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Cortical Plate Gene Expression During Gyrification in Sheep

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Dedicated to Jessica Elise Markham.

May this humble piece of work act as a game-changer in our lives, my dear, so it translates into my enhanced ability to help us build our home, so I can provide shelter, education, health and guidance for our future children.

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Summary

The development of the cerebral cortex is comprised by a series of events that are common to all mammals, however, not all mammalian cortices show the same architecture. While some species such as the mouse and the rat have a smooth cortex, others like sheep and humans have folded cortices. Due to the presence of outer and inner folds (referred to as gyri and sulci, respectively), the process of folding of the cortex is referred to as gyrification, and species with folded cortices are thus referred to as gyrencephalic. In contrast, species with smooth cortices are referred to as lissencephalic.

Considering the appropriate folding of the cortex is tightly associated with the function of the cortex in humans (i.e. misfolding of the cortex has been associated with mental retardation, epilepsy, attention deficit hyperactivity disorder [ADHD], autism, etc.), this gyrification process has been intensely studied. However, the mechanisms driving the folding process remain elusive. This has encouraged scientists to develop interesting theories on what drives the cortex to fold, and how does it do it. For example, the axonal tension hypothesis posits that axons within different regions of the cortex "pull" connected regions together, thus creating the buckling or folding of the cerebral cortex. Another hypothesis, the differential tangential expansion hypothesis, states that the buckling is generated as a way to dissipate the tension created by the differential growth of the upper layers of the cortical wall (cerebral cortex) and the lower ones (cerebral white matter). However, most theories fail to account for the reproducibility of the gyrification pattern, which is species-specific and highly conserved among individuals of the same species. These theories of gyrification can aptly explain why the brain folds, but not how the reproducible pattern is acquired.

The most recent theories of gyrification have focused on the role of one of the uppermost layers of the cerebral wall - the cortical plate (CP). It is hypothesised that the tangential expansion of the CP (about a thousandfold increase) during gyrification plays a substantial role during gyrification. However, again, the tangential expansion of the CP alone cannot explain the reproducibility of the folding pattern; it can only explain randomised folding patterns. One possibility is that cortical folding is driven, not only by cellular processes, but genetic ones too. This thesis aimed to determine whether the CP has a genetic fingerprint that could explain the consistent formation of gyri and sulci during gyrification. Specifically, the aim of this thesis was to determine whether CP cells from gyri and sulci showed differentially expressed genes, as a first step to determine genetically-driven regional variation in the CP. This work was performed in fetal sheep, mainly due to the fact that,

similarly to human's, the cerebral cortex of the sheep folds *in utero*, and it also folds at similar developmental times (i.e. second and third trimesters).

Chapter 3 of this thesis focused on determining the *in silico* genetic differences between CP cells from gyri and sulci during gyrification in fetal sheep (GA 90, term GA ~147), determined through RNA Seq and subsequent bioinformatic analyses. Analysis of the data revealed a large number of potentially differentially-expressed genes between gyri and sulci. Some of these genes had been previously identified to be associated with cortical folding malformations, while others had been reported to be involved in processes that are known to occur concomitantly with gyrification (e.g. dendrogenesis and axonogenesis). Therefore, a subset of these genes (namely BDNF, CDK5, NeuroD6, HDAC5 and MeCP2) was selected to validate these differences using histological approaches.

Chapter 4 of this thesis aimed to determine the differences in expression of these genes between CP cells from gyri and sulci throughout the cerebral cortex at GA 90 using immunohistochemistry (BDNF, CDK5 and NeuroD6) and fluorescent *in situ* hybridisation (HDAC5 and MeCP2). Immunoreactivity for BDNF, CDK5 and NeuroD6 was consistently greater in gyri compared to sulci throughout the cerebral cortex during gyrification, whereas mRNA levels for HDAC5 and MeCP2 were lower in gyri compared to sulci at this developmental stage. It was then hypothesised that this pattern of immunoreactivity and gene expression is observed before gyrification (GA 70), but not after gyrification was complete (GA 110), thus providing a genetic signature distinguishing gyri from sulci. The findings of this chapter show that none of the patterns of immunoreactivity and gene expression were observed in the GA 70 CP cells. However, at GA 110 only BDNF retained its gyri-to-sulci immunoreactivity pattern; gyri-to-sulci immunoreactivity patterns for CDK5 and NeuroD6, as well as gene expression patterns for HDAC5 and MeCP2 were no longer evident.

Considering that the genes being studied have previously been reported to be associated with neurite outgrowth, and that neurite outgrowth has been described to occur concomitantly with gyrification at GA 90, **Chapter 5** of this thesis aimed to determine whether neurite outgrowth occurred differentially between gyri and sulci. An additional aim of Chapter 5 was to determine if gyri-to-sulci immunoreactivity patterns for BDNF, CDK5, and NeuroD6, and gene expression patterns for HDAC5 and MeCP2 (from Chapter 4) were associated with dendrogenesis using MAP2 (a marker for dendrite outgrowth but more specifically for dendrogenesis), and whether these genes were associated with neurons, microglia or astrocytes. Immunoreactivity for MAP2 was higher in gyri compared to sulci throughout the cortex at GA 90, therefore suggesting differential dendrogenesis between gyri and sulci. To determine whether this differential immunoreactivity for MAP2 between

gyri and sulci translated into changes in cellular architecture between these regions, diffusion tension imaging (DTI) and neurite orientation dispersion and density imaging (NODDI) were performed in gyri and sulci of GA 98 fetal sheep brains. DTI and NODDI results strongly suggested greater cell dispersion and increased neurite size in gyral CP cells compared to sulcal CP cells, which was in line with the differences in MAP2 immunoreactivity. Furthermore, there was a reduction in total cell density (assessed using DAPI staining) in GA 90 gyri compared to sulci, although neuron, microglia and astrocyte cell densities in gyri and sulci were not different. Immunoreactivity for BDNF, CDK5, and NeuroD6, and mRNA expression of HDAC5 and MeCP2, were found to be associated with MAP2-positive cells and with NeuN-positive neurons in both gyri and sulci. Immunoreactivity for BDNF and NeuroD6, and mRNA expression HDAC5 and MeCP2, were found associated with astrocytes. Finally, immunoreactivity for BDNF and mRNA expression of MeCP2 only, were found associated with microglia.

Overall, this thesis demonstrated differential patterns of immunoreactivity and gene expression in the CP of the fetal sheep brain during gyrification that are absent before cortical folding starts (GA70) and mostly absent after cortical folding is complete (GA 110). It has also demonstrated architectural differences between gyri and sulci that appear to be correlated with the differential immunoreactivity and gene expression observed. This study therefore strongly suggests that dendrogenesis is indeed occurring differentially between gyri and sulci (i.e. sooner and/or more extensively in gyri than sulci), and that this might explain the architectural differences between gyri and sulci observed through MRI analyses. Further experiments are needed to conclusively show that differential dendrogenesis plays a role in the regional patterning of the CP during gyrification.

Declaration

This thesis contains no material which has been accepted for the award of any other degree or diploma at any university or equivalent institution and that, to the best of my knowledge and belief, this thesis contains no material previously published or written by another person, except where due reference is made in the text of the thesis.

Publications during enrolment

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Introduction

The folding of the cerebral cortex on some species has for long been an unsolved mystery for scientists all around the world. This process is not unique to humans, having a wide number of mammal species with folded cortices, including lions, porpoises, cats, ferrets and most primates. However, not all mammals have their cortices folded, like mice, rats and some primates like the marmoset. Species who have a folded cortex are called gyrencephalic, while those who have a smooth, non-folded cortex are called lissencephalic. The terms derive from the presence in the former of outward and inward folding, called gyri and sulci respectively, and the process of folding of the cortex is referred to as gyrification. The patterns of the cerebral cortex folding are very specific for every species, and highly heritable.

Many theories have been drawn to explain the gyrification process, based on biological evidence and/or mathematical and computational approaches, and all these theories have evidence backing them up and militating against them as well. The most recent theories focus on the widely accepted evidence of the expansion of the cortical plate –one of the uppermost layer in the brain architecture– during the gyrification process, where it can grow up to a thousand-fold tangentially, while it only does it around two-fold in depth. However, these theories also harbour shortcomings, because the biological mechanisms proposed to explain them are not sufficient to account for the gyrification process, neither when it started nor throughout the whole process. Neither they explain the inheritability of the patterns. These theories have been complemented with genetic studies that have shed light on a massive number of genes reported to be associated with cortical malformations such as lissencephaly (loss of folding), microcephaly (reduction in brain volume and alteration of the gyrification pattern), pachygyria (wider and thicker gyri), polymicrogyria (too many folds) and many others; all of them having clinical implications that can range from schizophrenia and autism to behavioural impairment, cognitive deficits, cerebral palsy, epilepsy and many more.

Considering the inheritability of the gyrification pattern, the evidence of these gene mutations associated with cortical malformations, and the recent theories pointing at the cortical plate as being the main responsible for the cerebral cortex folding process, it is highly feasible that the patterns of expression of these genes –and/or some other not yet described– are associated with the gyrification process, and it might be possible that differential expression of such genes between gyri and sulci is indeed acting as a molecular beacon to drive the folding of the cortex.

Therefore, studying such gene expression differences in the cortical plate during development is the main drive of this study.

Chapter 1 – Background, aims and hypotheses

Background

Development of the Cerebral Cortex

The development of the cerebral cortex is a complex but organized process common to all mammals, although the timing of the stages of cortex development differs among them (1). In the human, formation of the brain starts with the closure of the neural tube around 30 days post conception (E30). The brain arises from the rostral end of the neural tube, and thereafter the cerebral cortex starts developing from a single layer or zone –namely the ventricular zone (VZ)– into a multi-layered complex structure, harbouring different cell types and features in each of its zones (reviewed in (2)).

The VZ is the first germinating layer, homogenously composed of cells that divide symmetrically, quickly thickening this layer (Fig 1a). At approximately 33 days post-conception these cells begin dividing asymmetrically, starting the neurogenic process, with one daughter cell remaining in a proliferative state while the other enters either the glial or neuronal cell lineage. At the start of neurogenesis these neuroepithelial stem cells start differentiating into many proliferative cell lines, including radial glial cells (RGC) (2-4). RGC have important functions in brain development: they not only produce new subsets of cortical neurons and intermediate progenitor (IP) cells through asymmetrical division, but they also act as a scaffold to guide the newly generated neurons away from the VZ. This outwards migration of newly generated neurons forms the first neuronal layer of the cortex known as the preplate (PP) (3, 5, 6), a transient zone harbouring cells that regulate the formation of the future cortical layers (Fig 1b). Eventually, new cells accumulate between the VZ and the PP, giving rise to a new proliferative zone: the subventricular zone (SVZ). At this point of brain development, the SVZ continues to proliferate and becomes the main source of progenitor cells (7), while the VZ slowly reduces its size to a single cell-thick layer (Fig 1c).

The SVZ is subdivided into two main layers: *the inner SVZ* (iSVZ), proximal to the VZ, with a primary role to inhibit cell division of the VZ (8), and *the outer SVZ* (oSVZ), comprising intermediate radial glial cells (iRGC), which serve as secondary scaffolds for the RGC, and aid in the process of generating the cortical plate (CP). As the SVZ keeps producing new cells, the PP starts sub-compartmentalizing. Cajal-Retzius cells present in the PP migrate to the surface of this structure to start outlining the future marginal zone (MZ), leaving the inner zone that extends down to the SVZ to become part of the future subplate (SP) (9). These progenitor cells, arising from the SVZ –aided in

their outward migration by the RGC and iRGC–, begin to accumulate progressively to form the CP. This migration starts around 50 days post-conception and continues into the third trimester of human pregnancy (Fig 1d).

As the CP begins to form, the intermediate zone (IZ), a layer between the post-migratory neurons and the SVZ, also arises (Fig 1d). This structure is defined by the complete absence of precursor or post-migratory cells, and is composed of radially and tangentially migrating cells and a thickening layer of axons, positioned directly under the SP, a transformed remnant of the PP and a distinctive neuronal compartment containing an heterogeneous population of cells (2). It should be noted that current nomenclature refers to the zone between the CP and the SVZ as intermediate/suplate zone (IZ/SP) because there are no clear boundaries between these zones at this developmental stage (2). Following myelination, the IZ/SP zone is largely transformed into the subcortical white matter layer (10). Additionally, at gestational week (GW) 11, cells originating from the SVZ migrate tangentially to the top of the MZ, giving rise to the sub-pial granular (SG) layer, a transient structure covering the entire cerebral cortex by GW14.

Following GW14, and continuing throughout gestation, the cerebral wall (Figure 1e) continues to develop, and the CP starts slowly transforming into the six-layered cerebral cortex (grey matter), while the IZ slowly transforms into the white matter (11), and the SG progressively disappears after GW28 (12).

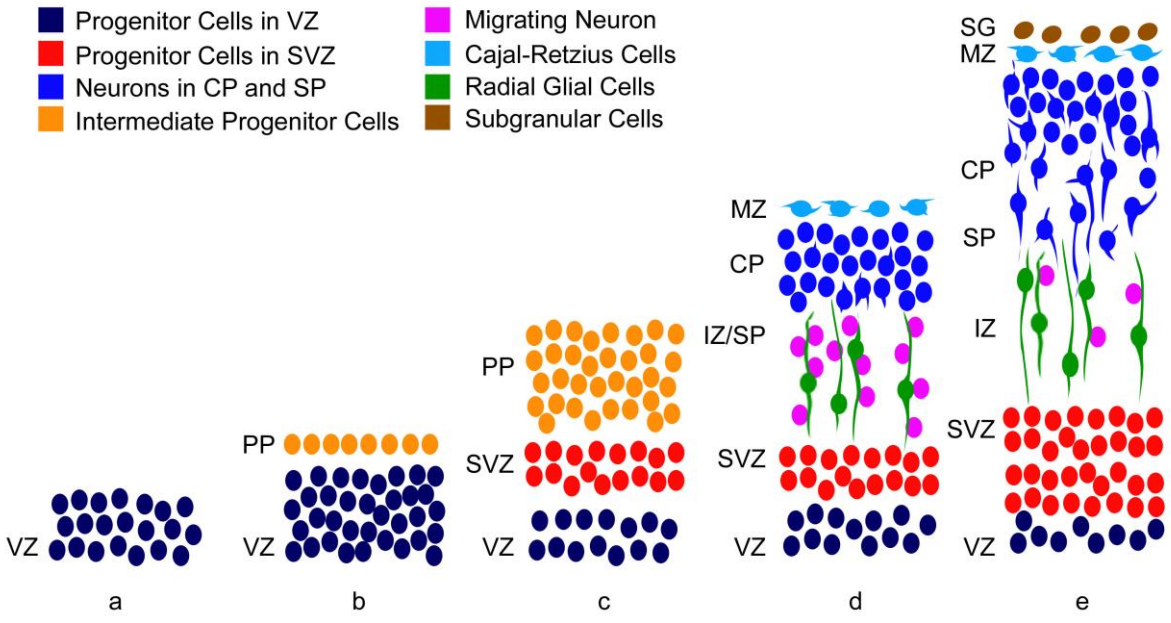


Figure 1. Corticogenesis. Schematic representation of the brain cortex development process during the first stages of development. a: embryonic day (E) 30; b: E31-E32; c: E45; d: E55; e: gestational week 14. CP, cortical plate; IZ, intermediate zone; MZ, marginal zone; PP, preplate; SVZ, subventricular zone; SG, subpial granular layer; SP, subplate; VZ, ventricular zone. Modified with permission from Bystron et al, 2008.

Folding Pattern of the Cerebral Cortex

Although the basic process of formation of the cerebral cortex described above holds true for all mammals, specific aspects of the neuronal architecture differ between species. While some have cortical hemispheres that show complex folding into 'hills' (gyri) and 'valleys' (sulci), and thus referred to as *gyrencephalic*, others have almost completely smooth cortical surfaces and are referred to as *lissencephalic* (13, 14). Furthermore, the degree and complexity of cortical folding differs even between gyrencephalic mammals. The gyrification index (GI) is used to describe the degree and complexity of the folds. The gyrification index (GI) was originally proposed and calculated by Zilles and colleagues (15), and it was obtained by manually calculating the ratio of the length of the cortical surface to the perimeter of the exposed outer surface of the brain, also known as the cortical hull. However, the method is highly dependent on the slicing direction of the histological sections and has difficulty in accounting for the rostro-caudal variation in gyrification. The advancement of MRI techniques has led to improvements in assessing the gyrification index, developing the global (16) and local GI (17), making the measurement of the GI more accurate, reproducible and less biased. Yet, the measurement remains the same, despite the method used to calculate it: GI reflects the degree of folding of the cerebral cortex compared to the perimeter of the exposed cortical surface. For example, the GI is lower in lissencephalic animals like the mouse (GI = 1.03) and in less complexly folded brains such as in the baboon (GI = 1.89), while the GI is higher in more complex brains such as the human (GI = 2.53). Importantly, amongst individuals, in humans the GI highly correlated with general cognitive ability (18).

It is generally accepted that gyrification exists to expand the cortical surface area within the confines of the cranium. However, there is evidence that the size of the cranium is determined by the brain, not the other way around (see "theories of gyrification" section). In humans, the gyrification process starts during fetal development, occurring primarily in the second trimester and being completed prior to term. Cortical folds can be classified as primary, secondary, and tertiary, and this classification is based on the timing of formation of folds and their consistency between individuals. Primary folds develop between GW16 to GW29 and are highly constant between individuals. Secondary folds start at approximately GW32 and have slight individual variation, and tertiary folds start by GW36, with high individual variation. Interestingly, gyri and sulci develop in a

region-dependent fashion among the different lobes of the brain, in a caudal-to-rostral and ventral-to-dorsal fashion (19-21). Moreover, the inheritability of the folding pattern (20, 22, 23) shows that gyrification is precisely controlled and not a random process.

Furthermore, many neurological diseases are attributed to cortical misfolding (3, 24-32). These folding malformations have been associated with aggressive traits in children (33), schizophrenia (34), autism (35-37), inclination to alcohol consumption (38), anorexia nervosa (39), cognitive deficits (40-42), and many others. These conditions can be caused by mutations in genes (reviewed in (3) and (43)) or by a suboptimal intrauterine environment (reviewed in (44)). Lissencephaly, one of these conditions, which results from abnormal neuronal migration, is associated with profound mental retardation and seizures. Pachygyria is also caused by abnormal neuronal migration, and is associated with seizures, feeding and swallowing difficulties, and poor muscle control. Therefore, understanding gyrification and the processes underlying it poses an endeavour of the utmost importance for the clinical welfare of the individual.

Gyrogenesis

Thoroughly reviewed by Welker in (14), gyrogenesis (or gyrification) is a complex process, where several interconnected steps are hypothesised to occur:

1. *Neuronal differentiation and dendrogenesis*: occurring earlier and more extensively in gyri than in sulci, this process involves neuronal growth and differentiation and development of a greater degree of elaboration of the dendrites,
2. *Neuronal orientation*: in which pyramidal cell bodies elongate vertically extending their apical dendrites perpendicular to the cortex and parallel to afferent axons in gyri, but more or less tangentially in the sulci,
3. *Afferent arrival, penetration, fasciculation and arborisation*: also occurring more extensively in gyri than in sulci, and during which thalamo-cortical and cortico-cortical axons penetrate the cortex between vertical columns of cell bodies, and intracortical axons increase in number, density, diameter and degree of myelination, and the terminal plexuses of these axons arborize more profusely,
4. *Synaptogenesis*: where, as axons arborize, the dendritic spines and synaptic bulbs differentiate and increase in size and number, a process thought to be more profuse in gyri than in sulci,

5. *Glial proliferation and myelin ensheathment*: where glial cells, –specifically, oligodendrocytes– aid in myelination, synaptogenesis and the formation of segregated specialised neuronal assemblies (glomeruli), more predominantly in gyri than in sulci,
6. *Laminar aggregation and segregation*: where differently arranged layers of cells bodies, axons and synaptic neuropil differentiate, again earlier in gyri than in sulci,
7. *"Plasticity" changes*: which consist of further changes within the different cortical layers and involves selective apoptosis, axonal and dendrite sprouting, and establishment and rearrangement of local synaptic circuits,
8. *Rearrangement of cell adhesion molecules and related membrane structures*: where alteration of the proteins regulating cell-cell adhesions is hypothesized to have a profound effect over the shape of cell columns and laminae, therefore modifying the shape of the cortex itself.

Welker also proposes that processes (2) and (3) result in the *height of cortical columns* being greater in gyri than in sulci. The cerebral cortex also expands tangentially as a consequence of the increasing volume of the neuropil, generating several mechanical forces throughout it, which further contribute to brain development and give the brain its folded appearance (14, 45). Interestingly, gyrification does not start until human fetuses reach around 500g body weight and 200 mm in crown-ramp length (46).

Gyrification is gradual process and continues after birth, subsequently declining with aging (47). Also, brain structure formation is not a symmetric process, with differences in cortical area, thickness and gyrification between hemispheres found when individuals are assessed early (48) and later (49) in life. In addition, sex and age impact on gyrification (47). Gyrification follows a ventral-to-dorsal and caudal-to-rostral timeline (50), and increases asymmetrically between hemispheres (51). Early in life, the GI increases 16.1% in the first year of life, and 6.6% in the second (52). During this period of development, growth is heterogeneous throughout the brain, with the association cortex more highly developed than the sensorimotor, auditory, and visual cortices. Furthermore, by the second year of life males have a larger GI than females (52). During early childhood, both cortical volume and trajectories of growth, but not cortical thickness, are different between males and females, with cortical volume peaking later in boys (47). However, at present we still do not know what drives cortical folding, and many theories have been proposed.

Theories of gyrification

If we consider Cope's rule – that is, the trend in evolution towards having larger body size (53) – the brain folding process might have appeared as a means to fit an enlarged brain into a skull that could not grow proportionally due to the stress over the spine that such skull growth might impose. A larger body requires a larger number of neurons, and the neuronal number and brain size problems cannot be solved by thickening the cerebral cortex, due to constraints in the pattern of connectivity. Therefore, this problem is solved by enlarging the cortex surface area, so cortical folding might be a consequence of a larger cortex surface fitting into a skull not big enough to keep it smooth and fully expanded.

One of the first hypotheses of brain folding suggested that the cranium posed a physical constraint that caused the brain to fold as it grew during fetal development. However, a classical experiment by Barron (54) led to the conclusion that the cranial compartment apparently plays no role in the ongoing cortical folding process. In this experiment, large parts of the fetal sheep brain were removed, and the remaining regions of brain were then allowed to continue to develop within an artificially increased internal cranial space. Interestingly, the remaining regions of the cerebral cortex folded despite the removal of a large portion of the brain, suggesting that the folding process is an intrinsic characteristic of the brain, and not just a result of its lack of space for further growth.

Evidence from humans tells a similar story. Human brain growth occurs until around 4 years of age, showing very small variations thereafter (20, 55-57). In contrast, ossification of the cranial sutures –which defines the final size and shape of the skull– occurs rapidly during early stages of postnatal life and early childhood, and then decreases as the brain stops growing until is complete by the third decade of adult life (58). Premature closure of the sutures (craniostenosis) leads to restriction in growth of the brain (59), elevated intracranial pressure in children and severe mental retardation, epilepsy, and other symptoms (59, 60). Craniostenosis can be reversed by surgery, allowing the brain to grow fully (61). In addition, mice genetically modified to grow larger brains develop an enlarged skull (62), similar to what is seen in conditions such as hydrocephaly. Individuals suffering microcephaly and microhydranencephaly develop distorted skull in line with the distorted architecture of their brains. These observations strongly support the contention that brain volume determines skull volume, and not *vice versa*.

From another perspective, if cortical folding was indeed only a consequence of cranial restraint, one would expect the folding patterns to be quite variable. This is because the brain would have no reason to fold in the definite, conserved pattern that is highly conserved between members

of the same species. However, the actual mechanisms which underlie gyrification remain elusive. Currently there are only a few widely cited theories explaining why and how the brain folds (reviewed in (4) and (63)). These theoretical mechanism may not be mutually exclusive. Thus, gyrification may not be based on a single mechanism, but rather the interplay of multiple factors in a well-orchestrated process.

Axonal Tension Hypothesis

Proposed by Van Essen in 1997, this theory postulates that axonal tracts exert mechanical tension over the laminar cortical surface layers, and that adjacent groups of neurons pass axons between them creating a regional tension that pulls the regions together (Figure 2) (64). This mechanical tension has been demonstrated in many studies (65-69), and is based on the observation that after homogenisation, the brain 'soup' is composed of many 'synaptosomes' in which the presynaptic and postsynaptic membranes remain adhered together – hence the view that, once formed, synaptic contacts are able to withstand considerable retractile force. However, contrary to this hypothesis, Xu and collaborators (69) microdissected the axonal fibres between adjacent folding regions in the developing ferret brain, and demonstrated that even though axonal tension was indeed present, it was not responsible for driving gyrification. Furthermore, the tension was located in deep white matter tracts and not within the core of the individual gyrus, and was therefore not likely to play a role in the folding of the cortical mantle and creation of a gyrus (69). In addition, mathematical modelling has shown that folding of the cerebral cortex may occur in complete absence of these cortico-cortical axonal fibres, and could be a consequence of just surface instability driven by differential growth of the cortical surface compared to inner layers (70), rendering the idea of adjacent retractile tension unnecessary.

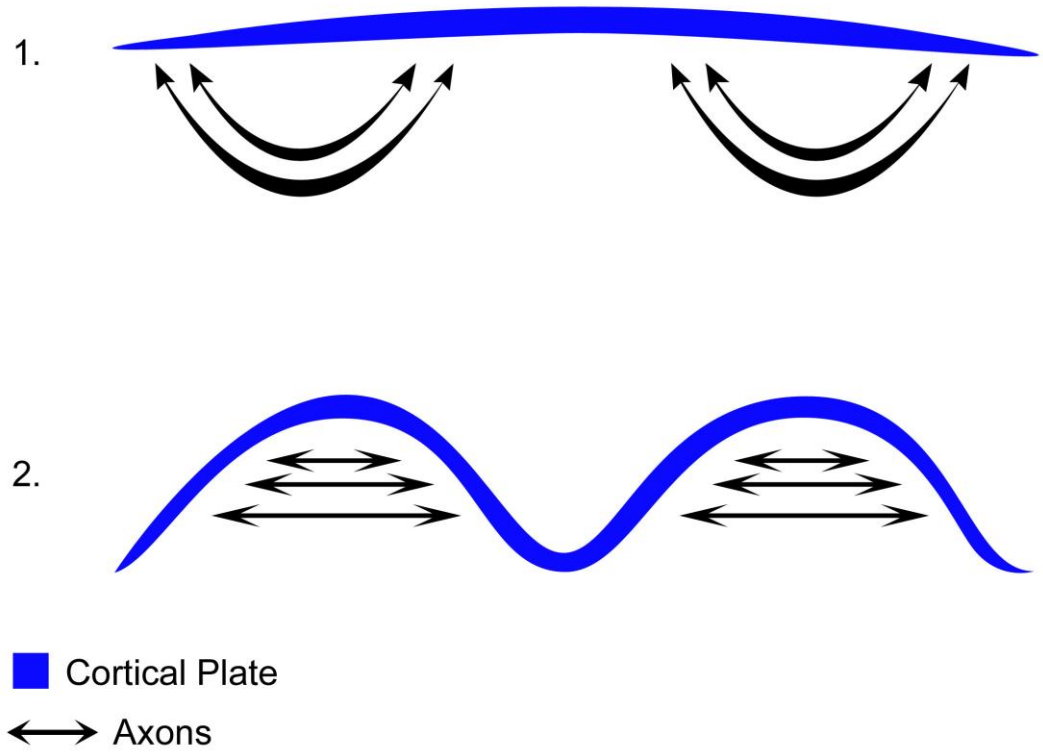


Figure 2. Axonal tension hypothesis. A schematic representation of the axonal tension hypothesis, stating that axons (black arrows) pull related and connected regions in the cortical plate (blue) closer, to transit from an initially smooth surface (1) into the creation of gyri and sulci (2) as a consequence.

Radial Expansion Hypothesis

First proposed by Richman et al (71), this theory suggests that the cortical folding is a consequence of differential growth between the upper and lower layers of the cerebral wall (Figure 3), although at the time the authors did not provide a developmental neurobiological mechanism for why the upper layers expanded tangentially more rapidly than the lower ones. The hypothesis gained new light several years later when the radial unit hypothesis proposed by Rakic (72) came into play. The latter explained cortical folding as a consequence of differential expansion of progenitor cells in the germinating layers and subsequent orchestrated migration of newly formed cortical neurons through radial glial "scaffolds" (further reviewed in (73)).

Recent evidence largely supports this idea. In ferret brains the manipulation on the outer SVZ proliferation rates can modify size and shape of cortical folds without modifying lamination or cortical area identity (74, 75). Furthermore, the presence of basal RGC and IPC in the outer SVZ

greatly impacts tangential expansion of the cortex in gyrencephalic models (74, 76), while the number of basal RGC also correlates with the degree of gyrification (74, 77). Additionally, the number of basal RGC is significantly larger in the cortex of gyrencephalic brains compared to lissencephalic ones (74, 78). In humans, mutations in a specific receptor (namely FGFR3) result in macrocephaly, presumably by expansion of the apical RGC population (79).

In ferrets, the brain shows regional differences in abundance of SVZ progenitors, leading to the proposal that these differences might pre-date the positions of the future gyri and sulci (80). Similarly, in both macaques and humans the SVZ is thicker directly under some of the developing gyri than in adjacent sulci (81), and gyri contain significantly more neurons than sulci (82). In addition, reduction in intermediate RGC proliferation achieved in enucleation experiments significantly reduced cortical surface area and fold size without reduction in the number of cortical neurons (74). It is noteworthy that modification of the proliferation rates in the germinal layers in mice without altering the type or relative number of neurons did not induce a gyrification pattern (75).

Studies in ferrets have also determined that before gyrification, neuronal migration is predominantly radial, while during gyrification neuronal migration becomes less frequent, and more "tortuous" and less radial (83), suggesting a way neurons might disseminate tangentially in a gyrencephalic brain.

The duration of mitosis in the VZ has been also linked to the degree of gyrification (72), and manipulation of neural precursors leading to overpopulation in the VZ in mutant mice has also led to the appearance of folds due to abnormal expansion in the proliferative zone (62). This latter observation came from transgenic mice overexpressing β-catenin –which led to an increase in cell cycle re-entry in the neural precursor pool, ultimately causing an enlarged brain which folded. However, the causes by which this normally lissencephalic brain actually folded after enlarging were not addressed.

Conversely, however, some studies have reported evidence not consistent with this hypothesis. For example, the presence and incidence of basal RGC in different species is similar between gyrencephalic and lissencephalic models (84, 85), and humans suffering from lissencephaly or polymicrogyria have roughly the normal numbers of neurons (6). Another limitation to this model is that differential proliferation by itself cannot explain gyrification as a whole, because it would only increase the thickness of the CP in certain zones, while in reality gyri and sulci are born from a CP that starts buckling while keeping its thickness relatively constant (63, 86). In fact, the cortical

surface expands a thousand-fold with only about a two-fold increase in cortical thickness (87), so it has been proposed that the increase in the upper layer cells are actually responsible for the formation of the gyri (81, 88, 89), although the mechanisms by which this occurs remain undefined. An early report shows that migration of neurons into the CP is largely complete by mid-gestation in humans (10), before the major changes that result in gyrification have taken place. However, more recent studies now show that neurogenesis can be observed until at least GW 30 (90), strongly suggesting that neuronal migration occurs until at least this stage of fetal development. Yet, the effect that late versus early neurogenesis and neuronal migration has on gyrification remains to be addressed. In ferrets, for example, neuronal migration is thought to be largely complete by two weeks after birth (91), while gyrification continues past the first month of postnatal life (92), suggesting that the effects of these late neurodevelopmental processes might be negligible. Still, a species-specific effect cannot be discarded, and therefore the net effects of these late processes on gyrification remains to be addressed in humans.

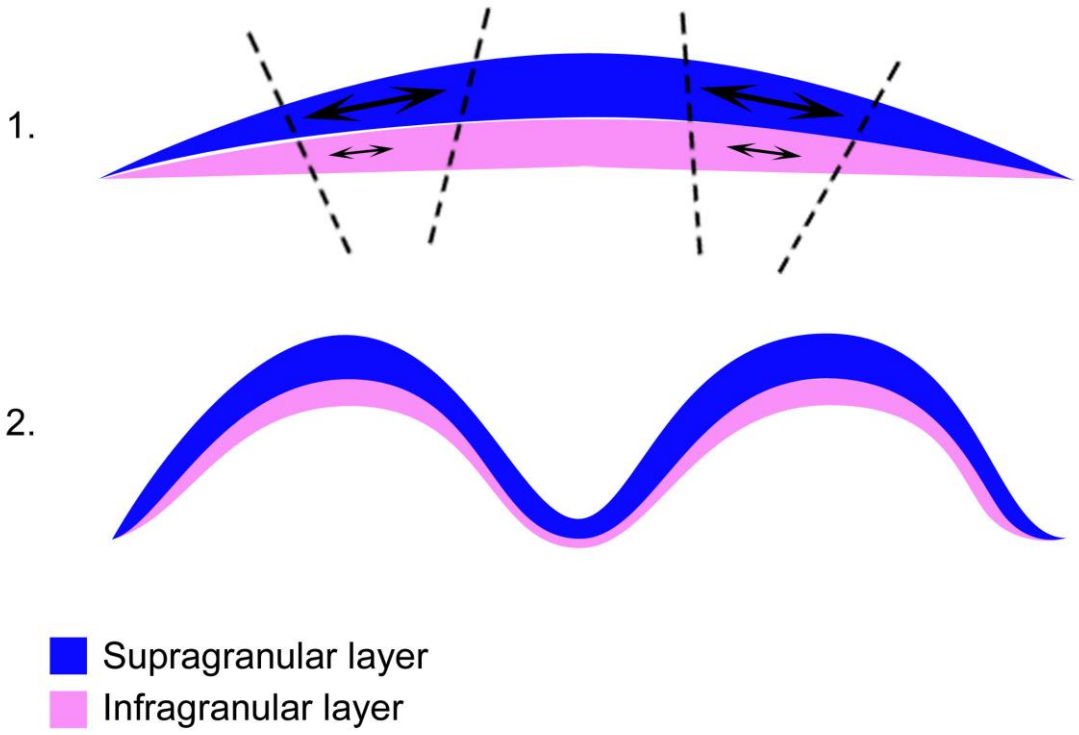


Figure 3. Radial expansion hypothesis. A schematic representation of the radial expansion hypothesis, in which the supragranular layer (blue) expands at a more accelerated pace than the infragranular layer (pink), that allows transit from a smooth surface (1) into a folded one (2), creating gyri and sulci as a consequence.

Differential Tangential Expansion Hypothesis

As the cerebral cortex folds, three major events occur at the same time in the upper cortical layers:

1. The surface area of the cortex expands significantly,
2. Axons from the subplate extend to the CP, and
3. Neurons differentiate and extend both axons and dendrites.

Little changes occur after these events (45). These observations led to the conjecture that gyrification is a process involving maturation and differentiation of the upper layers without further addition of migrating neurons.

Ronan and colleagues (93) speculate that folding of the cerebral cortex is driven by a tangential expansion of the CP that is different in gyri compared to sulci, causing the whole CP to fold because of its subsequent mechanical instability (Figure 4). Not surprisingly, many experimental observations and mechanical models agree with this theory, as during gyrification the brain is subject to many different mechanical forces (reviewed in (45), (94) and (95)).

Computational modelling showed that faster tangential expansion of the outer layer compared to the core resulted in buckling (70). Inclusion of both radial growth of the core and radial stress in modelling resulted in outward buckles resembling gyri (96).

A different approach was developed by Tallinen and colleagues (97). Using a gel composed of different layers that expanded at different rates after taking in a chemical compound, the gel mimicked the differential expansion of the inner and outer layer of the cerebral cortex. Indeed, the layered gel behaved according to predictions, and displayed convolutions that were consistent with a wide array of gyrencephalic and lissencephalic brains. Furthermore, this model fitted with the growing genetic evidence linking proliferation and migration of cells with increasing brain size, cortical thickness and gyrification degree (97).

A more recent approach by Mota and Herculano-Houzel (98) described cortical folding to be like a paper ball, where the number of folds correlates with the thickness of the paper and the area of the paper to be folded. This theory predicts that thicker cortices (e.g. a cardboard surface) will have less tendency to fold compared to thinner cortices (e.g. a paper surface). In addition, if the surface area increases, both cortices will start to fold, however the thinner one will do it more frequently. This is consistent with the fact that larger brains with greater surface areas are usually

more convoluted (e.g. cetaceans) compared to smaller brains, keeping in mind that cortical thickness varies little between species (99, 100). Consequently, gyrification can be viewed as the highly coordinated radial expansion and lateral dispersion of CP neurons, and not just a simple differential cell proliferation that results in a folded epithelium (62). However, the main problem with this 'paper sheet' analogy is that it is modelled after a surface that is not growing (like the paper or cardboard), and does not take into account a brain that folds as it grows, which is what we observe (101).

Another approach by Budday and colleagues (102) established a mechanical model that successfully mimicked cortical folding based on differential growth of two layers. In this model, based on the observations that gyral buckling in the ferret brain is a consequence of mechanical stress (96), the outer layer grew at a constant pace while the inner layer grew in response to overstretch (102). This approach integrated the axonal tension and the differential growth hypotheses, predicting that deviations in the growth of the CP and cortical thickness would induce morphological abnormalities such as lissencephaly and polymicrogyria (102).

However, each of the models described above failed to provide a developmental mechanism at the level of the constituent cells to explain the tangential expansion of the CP.

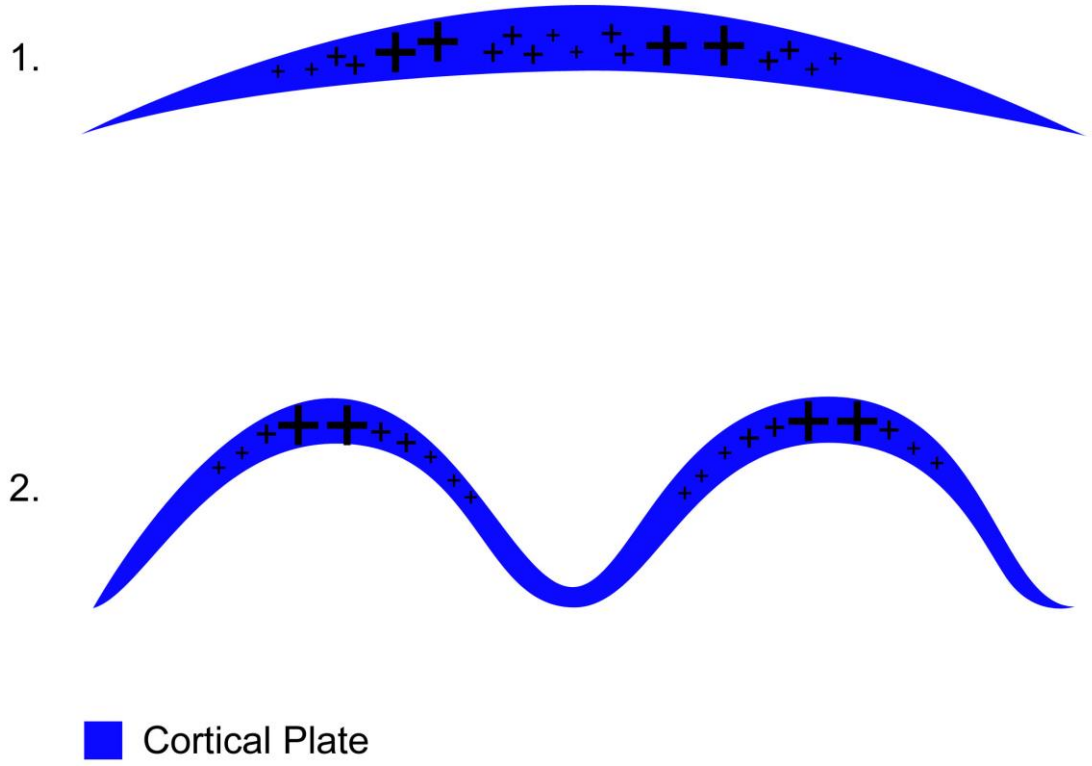


Figure 4. Differential tangential expansion hypothesis. A schematic representation of the differential tangential expansion hypothesis, in which the cortical plate (blue) expands tangentially at different paces in different regions of the initially smooth cortex (1), creating a folded cortex (2) as a consequence.

Differential Tangential Expansion by Radial Intercalation

A recent review by Striedter and colleagues (63) proposed that the differential tangential expansion hypothesis held by Ronan and colleagues harboured shortcomings, such as the fact that tangential dispersion of neurons does not result in tangential spread of force (63). Also, the view that hypertrophy of the neurons in the CP is a major driving force for gyrification (93, 103) is unlikely because this would thicken the CP as much as it would expand it tangentially, which does not occur. Thus, magnification of cellular size is unlikely to explain the tangential expansion of the cerebral cortex.

To overcome these limitations, Striedter and colleagues proposed a modification of the differential tangential expansion theory, in which radial intercalation of new neurons at the top of the CP result in significant tangential expansion. According to this theory, as neurons migrate and approach the CP, they shorten their leading processes and are subsequently pulled into the CP

(terminal translocation; (63)), and thus they push other neurons aside, creating regional, non-uniform tangential expansion (Figure 5). Furthermore, variations in the folding degree are inversely correlated with the corresponding cortical thickness, regardless of the age of the subject (104). However, in both the ferret (91) and human (16) brains, gyrification is a slow process that continues well beyond the time of the wave of neuronal migration into the CP (see previous sections).

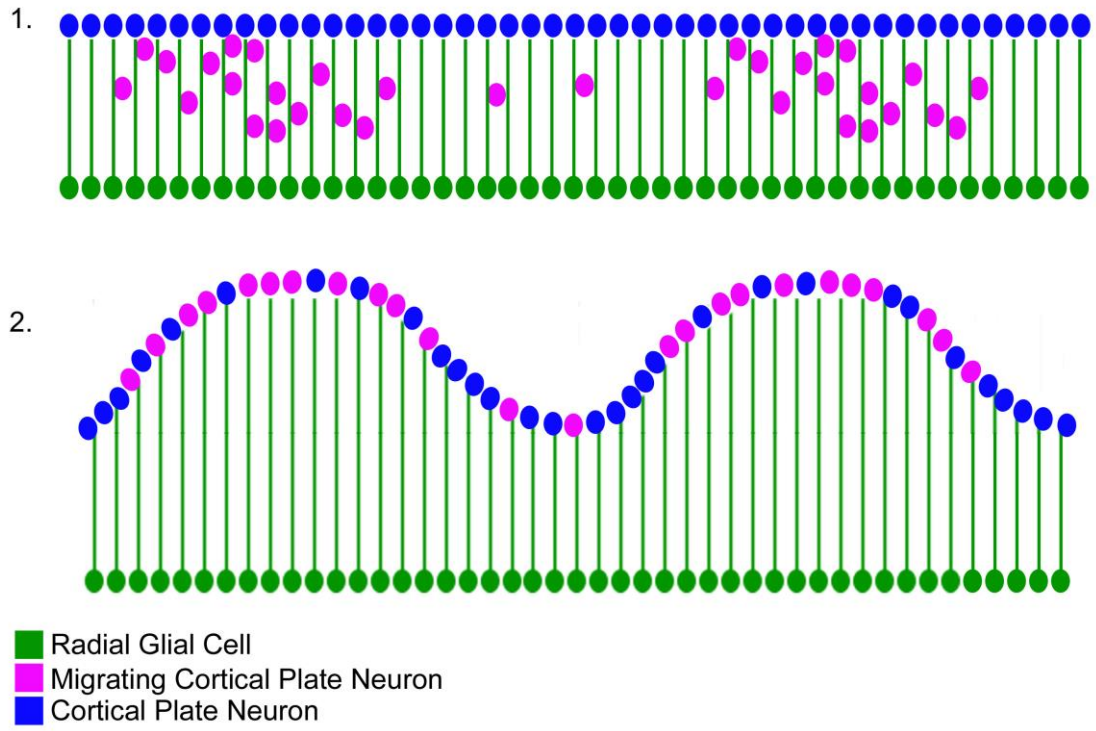


Figure 5. Differential tangential expansion by radial intercalation hypothesis. A schematic representation of the differential tangential expansion by radial intercalation hypothesis, in which newly created cortical plate neurons (pink) migrate using radial glial cells (green) as scaffolds, and create tangential tension among the pre-existing cortical plate neurons (blue), which is dissipated by buckling the cortex, allowing the smooth cortex (1) to fold into the convoluted mature shape of the brain (2).

Gyrification across species

Originally, it was thought that brains among species were scaled versions of the same structure, having somewhat similar organization, neuronal density and functionality (105, 106). Thus, previous observations in large brains such as cetaceans or elephants being gyrencephalic led to the belief that cortical folding should indeed be a direct function of neuron number in the cortex (107). However, recent studies suggest that only some features of the brain appear to be conserved widely between different animal clades and phyla in evolution. The development of the isotropic fractionator (108) –a technique similar but faster than stereology that allows quantification of neurons and non-neurons in defined brain regions– brought to light evidence about different scaling rules across mammalian orders and even across structures within the same brain, demonstrating that using volume or surface to conclude about cellular composition might be misleading (109, 110). Thus, several primate species do not have a constant number of neurons beneath the cortical surface as previously thought (111), despite having very similar gyrification indices (112).

Primates also have different relationship of cerebral cortex mass and neuron number in it compared to afrotherians (mammals living in or originally from Africa), lagomorphs (rabbits, hares and pikas) and rodents (109, 113). That is, cortical mass, as a function of neuron number, increases faster in rodents than in primates (109). However, primate cortices have larger densities compared to rodents of comparable size (reviewed in (114)). Afrotherians also share with eulipotyphlans (hedgehogs, gymnures, moles and others) and rodents the scaling rules applying to the cerebral cortex, but not with primates; the former share the scaling rules in cerebellum with rodents (113). Artiodactyls (even-toed ungulates) also share the non-neuronal scaling rules of cerebral cortex and cerebellum with afrotherians and rodents, but not with primates (115). White matter and cortical folding also scale differently between rodents and primates: rodents have greater connectivity and more white matter volume for a similar number of neurons when compared to primates, and have a faster increase in white matter volume as the cortex gains neurons compared to the latter (116).

Cetaceans share the same ancestor with artiodactyls (even-toed ungulates) and, given their big and convoluted brains, they also pose an interesting animal clade to study. A species of dolphin, the long-finned pilot whale (*Globicephala melas*), has been found to harbour more neocortical neurons than any mammal studied, including humans, almost doubling them (117). The brains of modern cetaceans are the largest of mammals in terms of mass and related to body size. The encephalization quotient (EQ) – the relative brain size defined as a ratio of the actual brain size and the predicted brain mass for an animal of a given size – for almost all odontocetes (toothed cetacean) is above average, ranging from 4.0 to 5.0 (reviewed in (118)). These EQs are even larger

than nonhuman anthropoid primates (highest EQ of 3.3) and seconds only to humans (EQ = 7.0) (119), in far contrast to mysticete (whalebone whales) brains which are all below 1.0, which is thought to be due to an uncoupling in brain size and body size in very large (and especially aquatic) animals (120). Recent comparative studies have hypothesized that, apparently, encephalization and brain organization followed different evolutionary pathways (121). In contrast, nonetheless, it appears that non-neuronal scaling rules are shared across mammalian orders and structures as reviewed in (122).

Taking all this evidence together, there is no reason to expect cortical folding to be a simple universal function of cortical neuronal numbers for all mammals, given that large cetaceans and artiodactyls have more folded cerebral cortices than primates with similarly sized brains (123), and artiodactyls have a much more folded brain than primate or rodents sharing similar neuronal number (115). Comparisons between GI, brain size and number of neurons in some of these species can be observed in Table 1.

Table 1. Differences in gyrification, neuron number and brain volume in different species. GI values taken from reference (112). *: estimate calculated from data from one hemisphere.

Order	Species	Common name	GI	Mean number of neurons in cortex (reference)	Mean cortical mass (reference)
Rodentia	*Rattus norvegicus*	Rat	1.02	31.02 million (114)	0.769 g (114)
Rodentia	*Mus musculus*	Mouse	1.03	13.69 million (114)	0.173 g (114)
Lagomorpha	*Oryctolagus cuniculus*	Rabbit	1.15	71.45 million (114)	4.448 g (114)
Cetacea	*Phocaena phocaena*	Harbor porpoise	3.00	14.9 billion (124)	302 g* (124)
Cetacea	*Globicephala melas*	Atlantic pilot whale	5.03	37.4 billion (117)	2893 g (125)
Artiodactyla	*Sus scrofa domestica*	Domestic pig	2.16	307 million (126)	42.404 g (126)
Primates	*Callithrix jacchus*	Marmoset	1.18	244.72 million (127)	5.561 g (127)
Primates	*Homo sapiens*	Human	2.56	16.34 billion (126)	1232.93 g (126)
Carnivora	*Mustela putorius*	Ferret	1.63	38.95 million (128)	3.123 g (128)
Carnivora	*Procyon lotor*	Raccoon	1.85	437.94 million (128)	24.491 g (128)

Again, comparative studies have shed light to important observations about the evolution of cortical folding. Previously, it has been reported that distribution of gyri and sulci is conserved between members belonging to the same order of mammals (14). Indeed, the developmental pattern of gyrification is homologous between primate species, with differential progression of cortical infolding in frontal and temporo-parieto-occipital regions (129), although humans represent an interesting outlying case of gyrification being 30% more convoluted than chimps (130). Interestingly though, cortices of Old World Monkeys are much more convoluted than those belonging to New World Monkeys (131), and small rodents usually have lissencephalic cortices, while large ones like the agouti and capybara are gyrencephalic (132).

In cynomolgus monkeys, chronology of the pattern of appearance of primary sulci (reviewed through MRI in (133)) is homologous to humans with very slight differences (129). Cynomolgus monkeys also show an increase in the gyrification index postnatally, just as humans (16, 134, 135), and also exhibit asymmetry patterns (136) and sexual dimorphism (137) in their gyrification maps.

Another interesting primate model for study gyrification is the nearly-lissencephalic marmoset (*Callithrix jacchus*) which, having a GI of only 1.2 (138), has been hypothesized to be an example of evolution where gyrification was simply a discarded trait towards selection of smaller body sizes (reviewed in (139)). It is also worthy of mention that findings about basal RGC in marmoset have a similar abundance in the SVZ as humans and ferrets, yet it is lissencephalic, raising the possibility that this high abundance of basal RGC is necessary but not sufficient for gyrencephaly (84).

Comparisons with the ferret, another gyrencephalic non-primate mammal, suggested that even when both primate and non-primate species cortices transform rapidly from lissencephalic to gyrencephalic with accelerated expansion of cortical surface area and growth in brain volume, these cortices grow in different fashion. For example, the rate of development of the length of the primary sulci in baboons is far faster than the evolution of its depth, in contrast to ferrets (140). The ferret develops characteristic gyrification patterns, similar to those found in dogs (141, 142) and cats (143), but highly different from primates (133). Also similar to humans and marmosets, the brain of ferrets presents sexual dimorphism in sulcal morphology (144) and shares striking similarities with primates in its development, with transcription factors expression indicating that germinal layers in the ferret may contain identical subpopulations of progenitor cells as in primates, although with different emergence timing, iRGC abundance and cell cycle kinetics (145).

However, the aforementioned homologies in cortex folding go missing when comparing more evolutionary distant species. The scaling of the gyrification index in correlation with neuronal number is not shared between either afrotherians, rodents, primates (113) or artiodactyla (115), having the latter more convoluted brains than primates, but with a similar number of neurons. An interesting recent study (146) addressing brain morphology in phocoenidae (odontocete cetacean such as the porpoise) revealed, even more, that degree of gyrification can vary interspecifically and intra-specifically between members of the same family, in which gyrification can no longer be used as a phylogenetically or ontogenetically informative feature. Here, gyrification appears to be a secondary feature derived from accommodation to different habitats (146), similar to the marmoset example presented above. On the other hands, species such as the echidna have shown throughout their evolution that despite differences in diet, habitats and body sizes, most of their neurological specializations have been conserved, where all the extant and extinct species studied show the same cortical gyrification pattern (147). This strongly suggests that different species have taken different evolutionary paths to achieve or discard their convoluted cortices. We should be wary of the implications of these assumptions, and these hypotheses and findings should be taken into account when studying gyrification in species distant to the human, as mechanisms discovered in said species might not readily translate into medical advances for humans due to these differences.

So far, the evidence hitherto presented suggests there is no reliable predictor of gyrification from an evolutionary perspective. Gyrification appears to be a mechanism by which species are able to fit an enlarged brain necessary for higher functions into a skull that cannot grow proportionally due to physiological constraints, but with, apparently, little regard of the number of neurons or progenitor cells in it, or its internal architecture. Thus, we are compelled to think that gyrification as a process of reorganisation of the cerebral cortex that does not alter the number of neurons present in it, as the differential tangential expansion hypothesis might suggest. This would allow our current understanding on the matter and data collected so far to fit nicely into a unified idea that gyrification is a process of transformation of the neurons inside the cerebral cortex. This would imply gyrification as a consequence of similar number of neurons transformed differently by dissimilar habitats throughout evolution.

Genetic regulation of the cerebral cortex folding

A general overview

All the theories of gyrification presented above could potentially explain the mechanism by which the cerebral cortex folds. However, they cannot explain why it folds in the distinctive pattern it does. Gyrification is not only folding, but rather pattern-specific folding of the cerebral cortex; a pattern that is highly conserved between members of the same species (20, 22, 23). Therefore, any comprehensive theory on gyrification must include an explanation for the rise and reproducibility of the folding pattern. Genetic studies on cortical malformations could therefore give us further insight on how gyrification is ultimately regulated.

Since the discovery around twenty years ago of the lissencephaly-related genes LIS1 (also known as PAFAH1B1) (148) and doublecortin (DCX) (149, 150), a wide number of genes from different experimental approaches have been related to cortical misfolding and to psychological diseases. These genes affect, but are not limited to, DNA repair efficiency, radial migration, cytoskeleton regulation, cortical lamination and neuronal migration, among others (reviewed in (43) and (3)). This has allowed us to expand our knowledge of genes such as Phosphatidylinositol 4-Kinase Alpha (PI4KA), implied in perisylvian polymicrogyria, cerebellar hypoplasia and arthrogryposis (151); G protein-coupled receptor 56 (GPR56), related to frontal cortex development (25), Tubulin Beta 2B Class IIb (TUBB2B), related to asymmetrical polymicrogyria (152); Tubulin alpha-1A (TUBA1A), involved in lissencephaly and pachygyria (153, 154) and Reelin (RELN), involved in lissencephaly with cerebral hypoplasia (154, 155), for example. Also, variations in Collagen alpha-1(IV) (COL4A1) and 2, Myristoylated Alanine-Rich Protein Kinase C Substrate (MARCKS), Occludin (OCLN), ALX Homeobox 4 (ALX4), Msh homeobox 2 (MSX2), Tubulin Alpha 8 (TUBA8) and Eomesodermin (EOMES), as well as the 22q11.2 cluster, underlie polymicrogyria (26). The latter has also been associated with cortical changes, as deletion of it can cause massive changes to surface morphology in the brain in humans (156-158). The list of genes associated directly or indirectly to cerebral cortex malformations spans several hundreds, further expanded by studies on microcephaly primary hereditary (reviewed in (31)), studies on patients with diverse brain structural malformations (159), and studies on inheritable brain traits (160). Gyrification of the normally lissencephalic brain of the mouse can be induced by injection of fibroblast growth factor 2 (FGF2) (161), and recently it has been shown that FGF signalling is necessary for gyrification in the mammalian brain (162). Also, TMF-regulated nuclear protein 1 (TRNP1) appears to play direct part in the expansion and folding regulation of the cortex, by controlling tangential and radial expansion of the cells (163).

But although the aforementioned evidence strongly suggests these genes are directly related to the gyrification process, direct evidence of their role on the onset of gyri and sulci formation is still lacking. These findings cannot speak for their direct involvement in gyrification *during* gyrification. For example, whether the expression of such genes –or the absence of it– by the time of gyrification onset is detrimental for a region of the brain cortex to be programmed and induced into a gyrus or a sulcus, or what drives different cortical regions to develop their characteristic architecture. This has led scientists to inquire about the presence of differential genetic programs throughout the cerebral cortex during development, which expression seal the fate of the specific regions they act upon, and act as a genetic blueprint to build the cortex. Indeed, genetic markers such as the ones determining segmentation in the body of the fruit fly or expression maps such as those found in the developmental mouse brain (164) could potentially be the master regulators of the specific folding patterns we observe throughout the cortex in gyrencephalic animals.

Modules of genetic expression: the protomap.

Following the first description on how cerebral cortical areas are specified through coordinated cell dynamics and interactions in 1988 by Pasko Rakic (87), an interest on the underlying genetic mechanisms driving these processes grew. Eleven years later, in 1999, Donoghue and Rakic identified differential ephrins and Eph receptors' expression throughout the developing primate cortex, proving for the first time that differential molecular expression could "correspond to particular presumptive cortical areas during their formation" (165); an idea that was reinforced with the identification of β-catenin and its control over neural precursors, and how its manipulation could induce cerebral cortex folding in the otherwise lissencephalic mouse (62). This molecular blueprint is referred to as the protomap (reviewed In (166), (167) and (168)).

The protomap is specified early in the cortical progenitor cells, which determine diffusible morphogens and transcription factor expression patterns throughout the cortex (169, 170). These patterns are later propagated to the CP through a cascade involving transcription factors PAX6, EOMES and TBR1, specifying regional identity rostro-caudally in mice (171). Also, there is recent evidence of involvement of small enhancer elements in driving gene expression in discrete domains throughout the cortex (172, 173). However, little is known about what genetic expression patterns in the cerebral cortex distinguish between lissencephalic and gyrencephalic animals.

An outstanding recent approach taken by de Juan Romero and colleagues (174) has uncovered the existence of several domains of gene expression present in the germinal layers cortex of human and ferret (namely the VZ, iSVZ and oSVZ), but absent in the lissencephalic mouse, that are also differential in the germinal layers underlying gyri and sulci. This approach has delineated several genetic expression maps that could be used as proxy for determining the positioning of gyri and sulci throughout the cortex, following the remarkable correlation between the oSVZ expression patterns and the eventual location of gyri and sulci. Yet, the role of the CP, if any, remains to be elucidated.

The cortical plate during brain folding

Although there is now a consensus that corticogenesis occurs as described at the beginning of this chapter, it appears there is little agreement on the timeline of the stages and changes undergone by the CP as it transforms into the mature cerebral cortex in humans. For example, Bentivoglio and collaborators published a diagram showing an undifferentiated CP between GW16-22, a partially differentiated CP – showing only layers V and VI being differentiated– between GW23-34, and from GW35 onwards, a fully differentiated cerebral cortex showing all distinctive layers from I to VI (175). On the other hand, Mrzljak and collaborators published a diagram in which is claimed that the six cortical layers can be observed and differentiated from GW26 onwards (176). Consistent with the latter, it has been reported that at GW29, the six cortical layers can be clearly distinguished by immunohistochemistry, but the CP at GW23 appears undifferentiated (177). Similarly, Budday and colleagues have published a diagram that suggests that layers II to VI are observable from as early as GW18 (11). In monkeys, some diagrams treat the same region as either “CP” as a whole at E94 (178) while others show a cortex in which different layers can be differentiated at similar embryonic ages (179). In fetal sheep, authors have referred to the grey matter as the “CP” at GA 63, 80, 85, and 150 (180), while others have referred to it as the “cerebral cortex” at GA 70, 94, 125 and 140 (181). This lack of consistency in the nomenclature previously used to describe the CP, cortical layers and cerebral cortex across neurodevelopment can therefore become a problem when studying and reporting results on the development of the CP/cerebral cortex in the context of gyrification, which spans from GW24 until late gestation, therefore encompassing developmental stages in which the limits between the CP, as an immature entity, and the cerebral cortex, as a differentiated one, are not easily distinguishable.

Nonetheless, the study of the CP/ cerebral cortex during gyrification posits an interesting avenue for finding new genetic and metabolic regulators that could have an active role in regulating

the region-dependent development of the cortex during gyrification, as the most recent theories of cerebral cortex folding strongly suggest that the CP is one of the main responsible layers in this process (63, 93). By the time the cortex starts folding the CP is composed largely by post-migration pyramidal neurons already in place and some newly-migrating ones, and the apical processes of radial glial cells along which the former have travelled. These pyramidal neurons present in the CP can be subdivided into two major classes: corticocortical projection neurons and subcortical projection neurons. The former are found in the upper layers, are responsible for connections between the hemispheres and express several gene markers including SATB2, while the latter are found in the deeper layers, are responsible for subcortical connections, and express different neuronal markers, including CTIP2 (182). The presence of interneurons, who are mainly born outside the cortex and must travel long distances to find their final positions in the CP (14, 183, 184) in the sheep CP at this point is uncertain, however human evidence suggest that by the time the brain starts to fold they might be slowly starting to migrate into the CP (185). Also, it is worth mentioning that at this stage the CP has not yet developed its six-layered conformation, which is observable later in fetal development and during postnatal life (182, 186, 187), with corticocortical and subcortical projection neurons taking different positions and having different roles in the CP (182). As stated in the previous sections, there are several events that are hypothesised to take place inside the CP while the brain cortex starts and keeps folding (14, 45) and some of them are believed to occur differentially between gyri and sulci (14). These events, like neuronal differentiation and dendrogenesis, neuronal orientation and synaptogenesis, could be key cellular changes behind the mechanical forces observed during the tangential expansion of the CP.

In humans, at 21 post-conception weeks (some weeks before gyrification begins), the CP shows enrichment of genetic processes indicating microtubule family cytoskeletal protein, protein modification, synaptic transmission and axonogenesis (185). Around GW28, the time when gyrification has started, cortical synapse increases exponentially, resulting in a six-fold increase of synaptic density (188).

Consistent with observations in the human neocortex (189), early studies on the sheep CP formation and progression throughout gyrification show a layer densely packed with neurons (180) that starts progressively “unpacking” –i.e. the cells start spreading as brain development proceeds– as gyrification advances (190, 191). In sheep, CP neurons start being generated at GA 32 (full term: GA ~150) (192), creating the first densely populated layer that can be visible from approximately GA 35 (190). These cells keep accumulating, and around GA 60 the fetal sheep appears to have a cortical development comparable to that of a 5 month-old human fetus (191). At this stage, the first major

lateral fissure starts forming (193). Shortly after, the fetal CP of the sheep starts to slowly change its cytoarchitecture and "unpack" (190, 191). Gyrification in sheep starts around GA 75-80, with the CP containing mature neurons in the inner layers (190), many of them pyramidal in morphology (180). Considering the sheep has a gestational period of approximately 150 days, gyrification in this species starts at the end of the second trimester, similar to humans. This process continues at least to GA 110 (194), when the CP is observed to be highly differentiated (190). Furthermore, some similarities and differences have been found between humans and sheep (for a table listing human gyral and sulcal development, see (19). Similar to humans, sheep also have been described to have an ansate (central) sulcus, callosal sulcus, sylvian fissure, sulcus diagonalis (frontalis inferior), and others (195). However, others such as sulcus coronalis and ectolateralis that are present in sheep, appear to be absent in humans (196). Regrettably, lack of in-depth study of the ontology of sulcation in sheep and differences in the patterning of cortical folding make thorough comparisons between human and sheep gyrification difficult. A comparative timeline of gyrification in humans and sheep is presented in Figure 6.

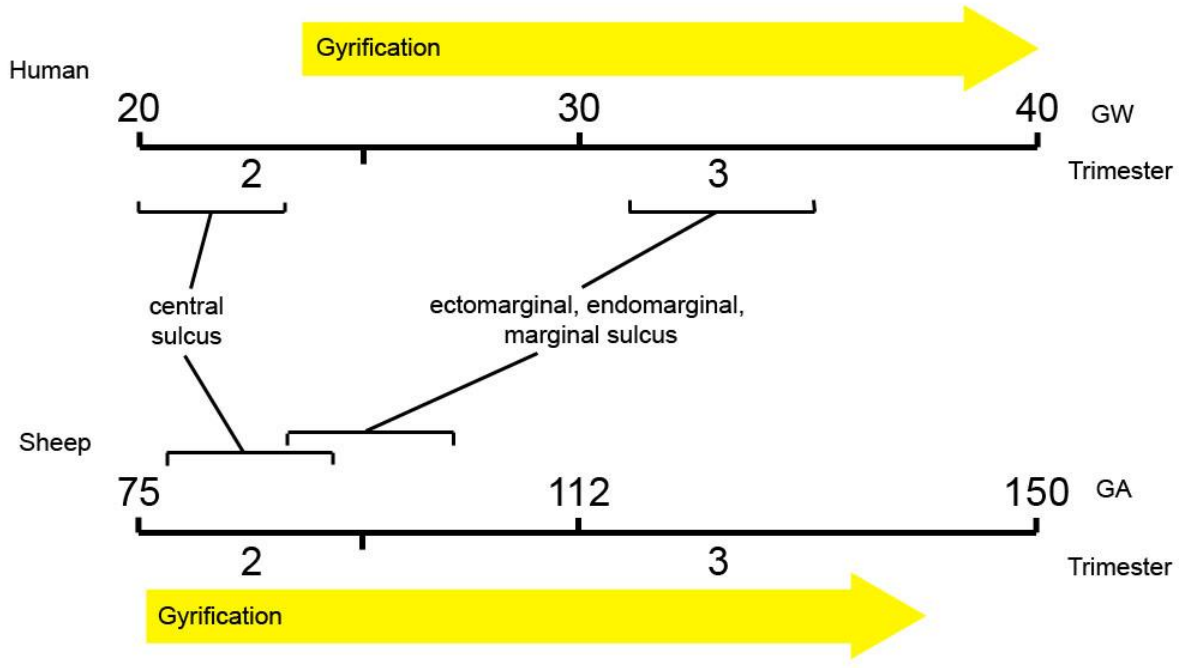


Figure 6. Comparative gyrification between human and sheep. A schematic comparison of gyrification in human and sheep, indicating the time of development of central, ectomarginal, endomarginal and marginal sulci. GA: gestational age; GW: gestational week.

Thus, these processes of CP unpacking, differentiation and maturation occur concomitantly with the cerebral cortex folding, making a strong case for neuronal differentiation and neurite outgrowth as the main driver for gyrification. Consistently in the ferret, neurite outgrowth in the CP occurs concomitantly with gyrification (197). Recently in the rhesus monkey, strong correlation

between maturation of dendrites and loss of diffusion anisotropy was found, while also finding that these changes in diffusion anisotropy were strongly associated with cortical folding (198). This provides a strong suggestion that dendritic changes might underlie gyrification in the CP. However regrettably, *no comparisons between gyri and sulci CP during gyrification have been performed so far*. Thus, the main objective of this present study is to address differences between gyri and sulci CP.

Among all the animal models that are commonly used to study brain development, the sheep presents some advantages that distinguish it from its counterparts and make it suitable for our study. In contrast to rodents such as the mice and rats which have been used to study brain folding, the sheep brain naturally folds whereas the former brains do not. Furthermore, and in contrast to ferrets –another commonly used animal model to study brain folding– the sheep brain folds *in utero*, whereas the ferret brain does it postnatally, making the sheep more resemblant of the natural process of human brain folding, which also occurs prenatally. This is of further importance considering that recent evidence suggests that gyrification in humans is also sensitive to the intrauterine environment (44).

Also, the process of folding of the brain in the sheep starts around GA 75 (i.e. second gestational trimester), and is described to be mostly complete by GA 110, in third trimester of pregnancy (194), similar to humans. These similarities make the sheep an excellent animal model to address our hypotheses about brain folding and make inferences regarding our own cerebral cortex folding process.

Considering the aforementioned lack of consensus in the appropriate terminology to describe the different developmental stages of the CP/cerebral cortex during gyrification, in this study the following terms have been used to describe the three developmental ages studied: early CP (eCP) describes the state of the CP before gyrification (GA 70); transitioning CP (tCP) describes the state of the CP/cerebral cortex during gyrification (GA 90) as it transitions from CP to a more mature cerebral cortex; and "cortex" is used to refer to the cerebral cortex after gyrification (GA 110). Labels indicating layers I to VI have been added for orientation purposes only, even at developmental stages where they cannot yet be told apart.

Further Perspectives

All the evidence laid out so far point to consider gyrification as both

- the last step of shaping a cerebral cortex insofar moulded by neuronal proliferation and migration mechanisms present in both lissencephalic and gyrencephalic animals, and
- a process in itself, that only occurs in gyrencephalic animals, despite all the previous steps of the cerebral cortex development being shared between gyrencephalic and lissencephalic animals.

This view of gyrification has two seemingly contradicting but not mutually-excluding implications. First, that we should not understand gyrification as a standalone process only, because it depends on all the preceding processes of the cerebral cortex development being deployed timely and effectively, without alterations. This means that alterations of early processes such as proliferation rates in the germinal zones or neuronal migration towards the CP could indeed alter the outcome of gyrification without directly impacting the processes that drive it. And second, that we should not understand gyrification as just a step of a more complex cortical process, because it is a process that only occurs in certain species despite the common cortical development pattern. Thus, gyrification in itself is a standalone process driven by mechanisms only present in gyrencephalic species. This encourages us to see gyrification as a process that modifies the cerebral cortex shape by taking the building blocks already placed by previous processes and creating a convoluted landscape throughout the cortex that is imperative to fit this growing brain into the much-smaller skull; again, a process only present in gyrencephalic animals.

Previous studies have addressed the importance for gyrification of basal progenitors (75, 80), neuronal migration (199) and even the subplate (14). However, this evidence points to processes that occur before gyrification, which might indirectly impact gyrification without altering the processes that drive it, as stated above. This way, LIS1 and DCX, for example, have been implied in radial and/or neuronal migration deficits (200, 201), which results in a lissencephalic phenotype. Mutation of ASPM, a gene involved in proper division of neural progenitor cells, also causes cortical malformations (3). Other genes whose correlation with gyrification is less evident, such as NHEJ1 (involved in DNA repair efficiency, (202)) and some members of the tubulin family like TUBB2B and TUBA1A (which are important for cytoskeleton regulation, (26)) also cause cortical malformations. Yet, evidence of the involvement of these genes *during* gyrification is missing.

Another problematic concerning the study of the genetic control over the folding pattern of the cortex refers to what has been recently referred to as "*pseudo* cortical folding", as opposed to true or "*bona fide* cortical folding" (203). True cortical folding involves folding of the upper layers of

the cortex (pial, layers II-IV) while the underlying white matter remains smooth. On the other hand, pseudo cortical folding is achieved through, for example, artificial overgrowth of the early neuroepithelium with little neurogenesis (204), or blockage of embryonic apoptosis (205), which are both events unnatural to proper gyrencephaly. This pseudo-gyrification has been the result of exploring the effects on cortical shape of manipulation of the normal cortical development in lissencephalic models such as mice. And while still highly informative and useful, they can produce results that might be misleading or difficult to interpolate and compare with naturally gyrencephalic models such as the ferret.

As no one can deny the invaluable information and contributions to the field that mutant models and gene silencing approaches have given us, these approaches lack the subtleties that imply studying gyrification as a standalone process. Because mutations such as the ones observed in knockout models could impact processes prior to gyrification, this could alter the gyrification pattern but not necessarily altering the processes that drive gyrification. Therefore, this implies that an approach for better understanding gyrification as a standalone process rather than a step on a bigger process –i.e. understanding how and what drives the cerebral cortex to fold despite the shared similarities between gyrencephalic and lissencephalic models– should be focused on sampling and studying a cerebral cortex while gyrification unfolds, in a context void of scientific manipulation.

Additionally, because cortical thickness and sulcal depth changes dynamically over a long time (many years in humans (206)), further investigation of the formation of secondary and tertiary gyri might be useful to distinguish between the process where the gross macroscopic changes develop during embryogenesis between GW26 and GW44 (19), and those that happen after birth. It is possible that mechanisms governing the formation of gyri and sulci *in utero* are distinct from those present later, therefore leading to the conclusion that gyrification (or loss of) as a dynamic ongoing process cannot be explained by a single equation, theory, or mathematical model, and might respond to more variables than we might address in a single experiment.

Aims and Hypotheses

General

The general hypothesis of this project that t*CP cells in gyri and sulci differentially express genes that are associated with gyrification in sheep, and these differential expression correlates with structural differences between gyri and sulci throughout the cortex*. The aim of this project is *to address whether there is a differential gene expression in the transitioning cortical plate (tCP) cells belonging to either a gyrus or a sulcus in the developing brain of the fetal sheep, and correlate such gene expression to the gyrification process*. Therefore, this project was designed to be divided in three studies, each one with its own aim and hypothesis.

Study 1

The hypothesis of this study is that t*CP cells coming from a gyrus and a sulcus at GA 90 in the sheep differentially express genes that are associated with gyrification.* Therefore, the aims of this study are 1) *to determine whether there is a differential gene expression in tCP cells belonging to either a gyrus or a sulcus in brain of the sheep at gestational age (GA) 90 that can be associated to gyrification.*

Study 2

The hypothesis of this study is that *one or more of the selected genes is expressed differently between gyri and sulci in the GA 70, 90 and 110 fetal sheep brain*. Therefore, the aim of this study is *to study a subset of differentially expressed genes in CP cells coming from gyri and sulci on fetal sheep brains before (GA 70), during (GA 90) and after gyrification (GA 110)*.

Study 3

The hypotheses of this study are:

- *Neurite outgrowth occurs concomitantly with gyrification in sheep,*
- *Neurite outgrowth is differentially regulated between gyri and sulci,*
- *Gyri and sulci become micro-structurally different during gyrification,*

- *BDNF, CDK5, HDAC5, MeCP2 and NeuroD6 expression/transcription is associated with neurite outgrowth,*
- *BDNF, CDK5, HDAC5, MeCP2 and NeuroD6 expression/transcription is mainly associated. with neurons (as opposed to glia and astrocytes) in the tCP during gyrification,* and
- *Gyri and sulci tCP is mainly composed by neurons during gyrification.*

The aims of this study are:

- *To determine the development of neurite outgrowth during gyrification in sheep,*
- *To determine the level of expression of MAP2, a neurite outgrowth marker, between gyri and sulci during gyrification in sheep,*
- *To determine the differences in microstructure between gyri and sulci during gyrification in sheep,*
- *To determine whether BDNF, CDK5, HDAC5, MeCP2 and NeuroD6 expressions are associated with neurite outgrowth, and/or specific cellular types (namely neurons, astrocytes and/or microglia),* and
- *To determine the cellular composition of gyri and sulci tCP during gyrification*.

Chapter 2 – General Methods

Based on the aims and studies stated above, the following project was divided in three stages. In the first stage of the project, the differential gene expression between the tCP cells was addressed using a fixed developmental stage of the sheep, namely GA 90. This stage represents an ideal point for analysis of the tCP cells during gyrification, as gyri and sulci can be easily distinguished, and the gyrification process is still continuing. The cells of the tCP were sampled accordingly, the genetic material extracted, sequenced and analysed *in silico*, to select candidate genes to be further analysed and studied. In the second stage of the project, the results for the genes selected in the first stage were further validated using tissue-labelling techniques, such as fluorescence in situ hybridisation and immunohistochemistry, and these results were evaluated at different developmental stages of the brain in sheep, namely before (GA 70), during (GA 90) and after (GA 110) gyrification. Finally, in the third stage of the project, the expression/transcription of these genes were co-localised with specific markers for neurite outgrowth, neurons, astrocytes, and microglia, and the level of neurite outgrowth was assessed between gyri and sulci, and structural differences between gyri and sulci were assessed. The methodologies for the these studies is presented below.

2.1 Animals and tissue collection

The following experiments were approved by Monash University bioethics MMCA 2013-20.

For all experiments, time-mated pregnant Border Leicester ewes carrying twins were obtained from a local supplier (Kernalow P/L, Victoria, Australia). Pregnant ewes were euthanised at GA 70 (n = 5), 90 (n = 9), 98 (n = 3), or 110 (n = 5), using a lethal dose of pentobarbitone (100 mg/kg; IV), and the fetuses were rapidly delivered by caesarean section. Fetal brains were prepared for laser capture microdissection (LCM), immunohistochemistry (IHC), fluorescent *in situ* hybridisation (FISH) and neurite orientation dispersion and density imaging (NODDI) analysis in the appropriate matter for downstream experimentation, as follows.

2.1.1 For LCM, fetuses at GA 90 (n = 4) were used. The cerebral hemispheres were removed from the brain, hemisected, orientated in a uniform manner and cut transversely into 5 mm-thick coronal blocks from the rostral to the caudal extent of the brain (Figure 7). The ansate sulcus (at the level of region R2 in Figure 7B) was used as reference point to ensure consistency across animals. Blocks were immediately placed in cryo-moulds, immersed in optimum cutting temperature formulation (OCT, Sakura Finetek, USA), and snap-frozen in isopentane cooled in liquid nitrogen. Blocks were stored at -80^{o} C until sectioning.

2.1.2 For IHC and FISH, fetuses at GA 70 (n = 5), GA 90 (n = 5) and GA 110 (n = 5) were used. At post-mortem, brains were transcardially perfused with 0.9% saline followed by 4% paraformaldehyde (PFA) in 0.1M phosphate buffer saline (PBS; pH 7.4); the brain was then removed from the skull, hemisected along the midline, and blocked using the same procedure described for LCM (Figure 7). Blocks from the right cerebral hemisphere were cryoprotected by immersion in 20% sucrose in 0.1M PBS (pH 7.4) for 48 hours at 4° C, then immersed in OCT and snap frozen in isopentane over liquid nitrogen. Blocks from the left cerebral hemisphere were embedded in paraffin.

2.1.3 For NODDI analyses, fetuses at GA 98 (n = 3) were used. At post-mortem, brains were removed from the skull, hemisected along the midline, and the left cerebral hemisphere was immersed in 4% PFA for 2 weeks. Subsequently, the tissue was transferred into 0.1M PBS for 8 weeks prior to NODDI acquisitions and analysis at the Laboratoire du Service du Developpement de la Criossance, in Geneva, Switzerland.

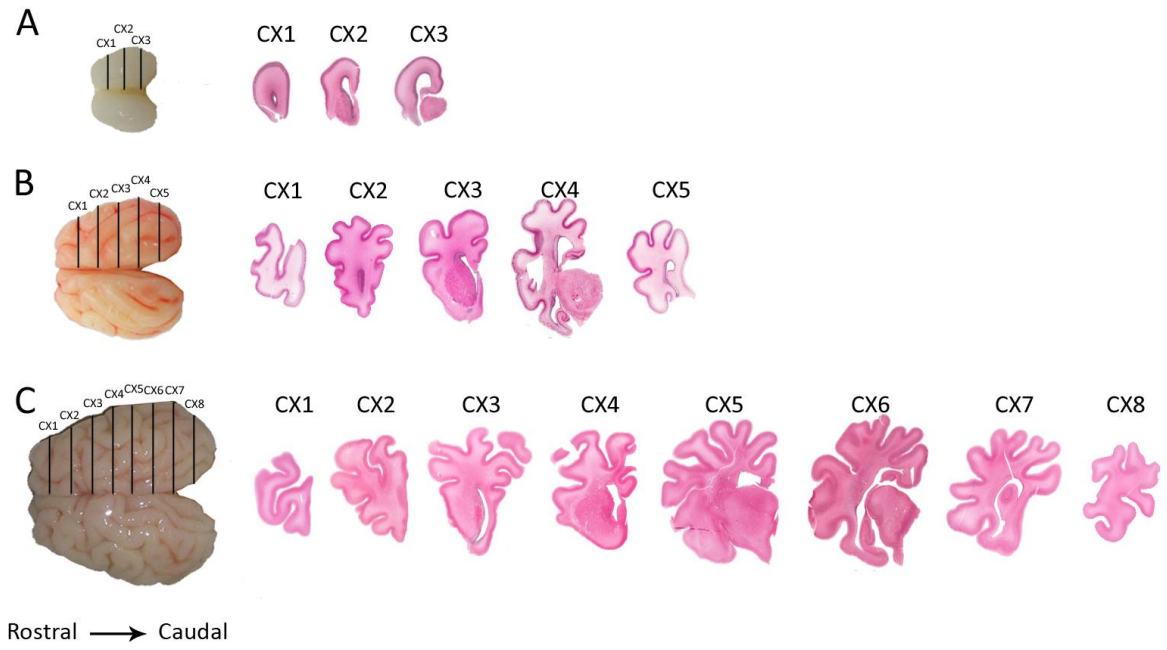


Figure 7. Blocking of fetal sheep brains. A representation of fetal brains at GA 70 (A), GA 90 (B), and GA 110 (C), and a HE staining of a representative slide at every cerebral region (R).

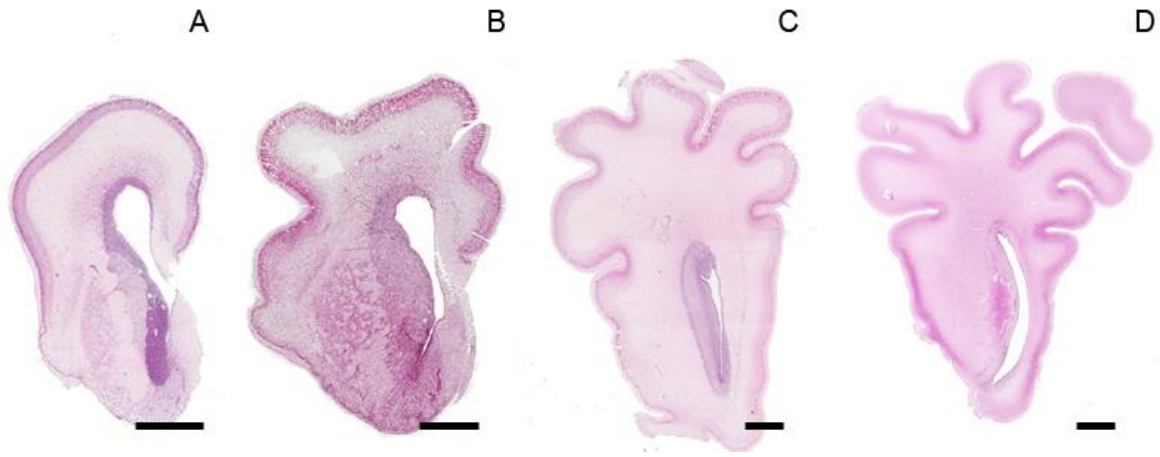


Figure 8: Cortical folding in sheep. Sequence of different stages of the cerebral cortex folding process in the sheep brain. Gestational ages A, 70 days; B, 80 days; C, 90 days; D, 110 days. Bars are 5 mm each. Haematoxylin-eosin staining.

2.2 Laser capture microdissection

For RNA Seq experiments, LCM was performed to isolate the tCP cells from a gyrus and sulcus. For each GA 90 brain (n = 4), fifty coronal 20 µm-thick sections were taken from region R2 (i.e. level of ansate sulcus; Figure 7B,). Sections were cut at -13° C to -15° C using a Leica CM1850 cryostat (Leica Biosystems, Germany), mounted on nuclease-free PEN membrane-covered slides (ZEISS Australia), air-dried for 2 minutes, fixed in ice-cold nuclease-free 95% ethanol (Sigma-Aldrich, Australia) and stored at -80° C with desiccant beads (Sigma-Aldrich, Australia) in a tightly sealed container until staining.

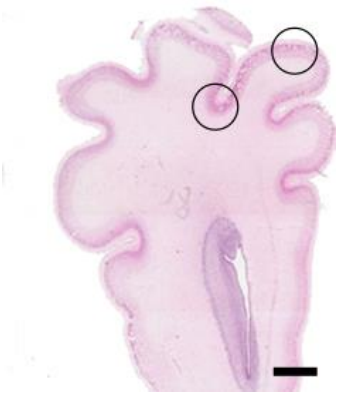


Figure 9: Sectioning of the fetal sheep brain. Histological diagram from section 2 of the fetal sheep brain (Cx2) at 90 days-gestation, showing the selected gyrus and sulcus for further sampling. Haematoxylin-Eosin staining. Bar: 5 mm.

Staining of the slides was performed as previously described (207) to ensure proper visibility of the tCP. Sections were brought to room temperature (RT) for 5 minutes and progressively rehydrated in solutions of 95%, 75% and 70% ethanol (30 seconds in each), stained with 1% Cresyl

Violet and dehydrated progressively in solutions of 70%, 75%, 95%, 100% and 100% ethanol (30 seconds in each), as described before (207). Sections were then stored at -80° C with desiccant beads in a tightly sealed container until further sampling.

LCM was performed using a Zeiss PALM laser capture microdissection microscope (ZEISS, Australia) with PALMRobo software (v3.2). Regions of the tCP from layers II to VI of approximately 500,000 µm^2 per slide were extracted (Figure 10). Tissue was captured in RNA lysis buffer (QIAGEN, Australia) in a nuclease-free Eppendorf tube and stored on dry ice until RNA was extracted.

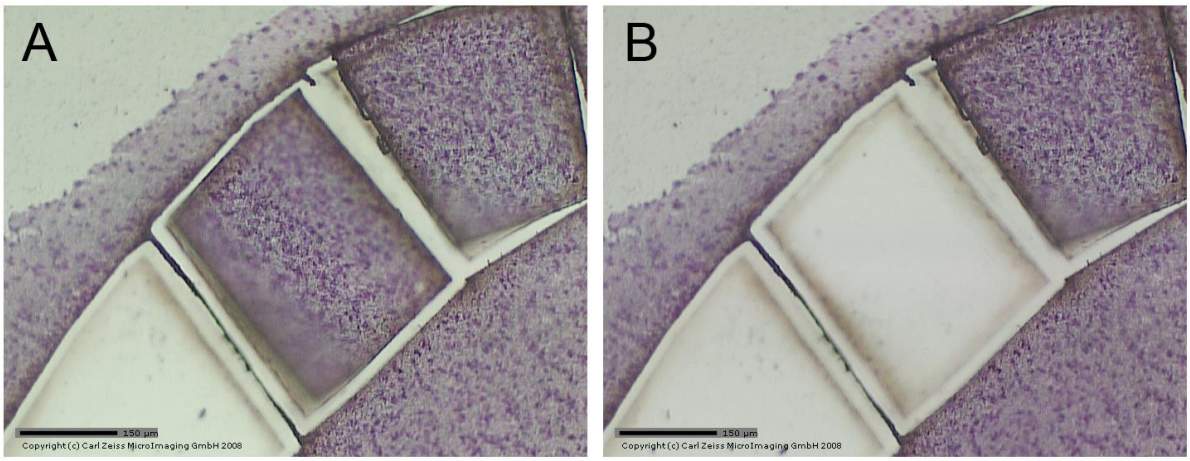


Figure 10: Laser Capture Microdissection (LCM). Histological record from selected gyrus at 90 days-gestation being sampled through LCM. A, section before LCM; B, section after LCM. Nissl staining. Bar: 150 µm.

2.3 RNA extraction and sequencing

RNA was extracted using a RNA Micro Kit (QIAGEN, Australia) following manufacturer instructions with a DNase in-column treatment. Quality of RNA extracted was assessed using an Agilent Bioanalyzer 2100 (Agilent Technologies, Australia). 20 ng of total RNA were used for sequencing using single reads SPIA sequencing (208), using 7 cycles of amplification to minimise amplification effects (Nugen Ovation RNA-Seq system) in an Illumina HiSeq 3000 sequencer (Illumina Inc, Australia).

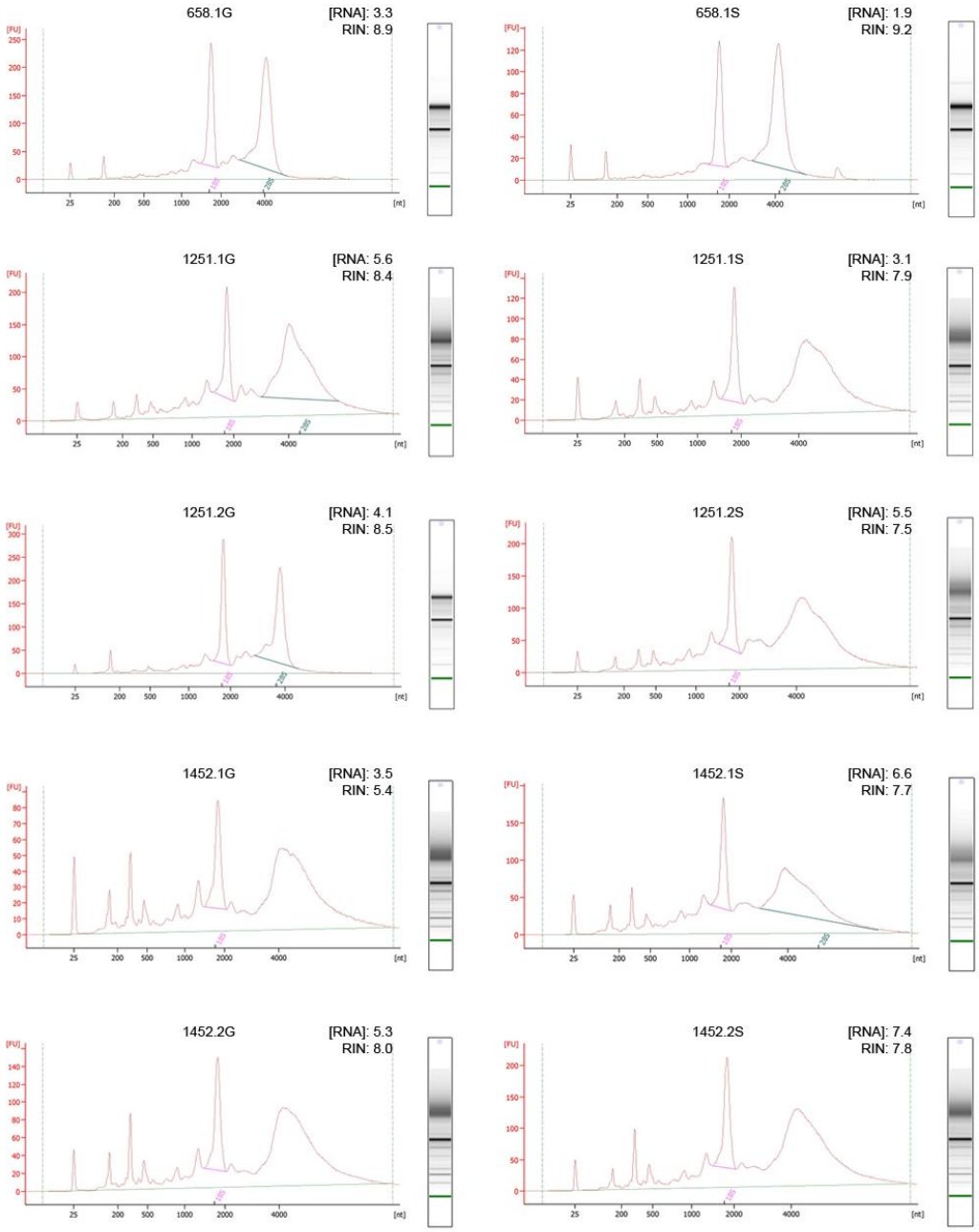


Figure 11: Bioanalyzer report for RNA extracts. Histograms, concentration and RIN for RNA extracted from sheep cortical plate cells at 90 days-gestation. Sample names are sheep number + sample type, G: gyrus; S: sulcus. RNA concentration is given in ng/µL.

Table 2. RNA Quality check summary for samples extracted from either gyrus (G) or sulcus (S). Concentration, RNA Integrity Numbers, mean size and reads passed the analyser filter are given for each sample.

	Conc. (ng/ul)	RIN	Mean size (bp)	Reads Passed Filter (million)
658.1 G	0.3	7.8	296	112.3
658.1 S	0.5	8.6	300	108.7
1251.1 G	10.5	8.4	310	95

1251.1 S	6.4	7.9	306	92.8
1251.2 G	6.2	8.5	312	100.6
1251.2 S	8.7	7.5	308	88.3
1452.1 G	6.6	7.7	295	77.4
1452.1 S	3.5	5.4	304	94.5
1452.2 G	7.4	7.8	303	83.6
1542.2 S	5.7	8	307	89.1

Table 3. Sequencing QC. Quality check for sequencing the gyri and sulci samples. Sample names are animal number with sample type (G, gyrus; S, sulcus).

	658.1 G	**658.1 S**	**1251.1 G**	**1251.1 S**	**1251.2 G**
Total Sequences	112298516	108746314	95042870	92816161	100619309
Sequences flagged as poor quality	0	0	0	0	0
Sequence length	35-51	35-51	35-51	35-51	35-51
%GC	46	42	41	41	43
Basic Statistics summary	Pass	pass	pass	pass	pass
Per base sequence quality	Pass	pass	pass	pass	pass

	1251.2 S	**1452.1 G**	**1452.1 S**	**1452.2 G**	**1542.2 S**
Total Sequences	88269301	94483647	77373939	89060055	83647014
Sequences flagged as poor quality	0	0	0	0	0
Sequence length	35-51	35-51	35-51	35-51	35-51
%GC	42	39	35	41	41
Basic Statistics summary	Pass	pass	pass	Pass	pass
Per base sequence quality	Pass	pass	pass	Pass	pass

2.4 Mapping and differential expression analysis

Fully annotated sheep genome (v 3.1) and annotations files were obtained from the International Sheep Genome Consortium online, through the ENSEMBL database available in June 2016. Raw data obtained from the sequencer was mapped using STAR (v 2.4.2a) (209), and summarization was read inside R environment using RStudio (v 0.98.1103) using featureCounts from package RSubread (v 1.12.6) (210). Total gene list was filtered down removing all genes with counts of less than 10 counts per million (cpm) in any sheep sample. Differential expression analysis was performed using edgeR (v 3.4.2) (211, 212) and edgeRun (v 1.0.9) (213). All bioinformatics analyses were performed on the Monash Bioinformatics Platform server.

2.5 Gene ontology analysis and selection of candidate genes

Genes retrieved from edgeRun output with unadjusted p value < 0.05 were used for selecting candidate genes. Gene ontology analysis was performed using DAVID Bioinformatics Resources online (v 6.8) (214, 215) as at January 2017, using Ensembl IDs extracted from the annotation files. Pathway database information was also retrieved during January 2017 from BIOCARTA, EBI, KEGG and WIKIPATH, and analysis was performed comparing gene symbols in both edgeRun output and the databases obtained.

Selection of genes of interest was performed by selecting genes using the following criteria:

a) selection based on arbitrary score, calculated as

$$score = |logFC| + logCPM + (1 - Unadj\ p\ value)$$

b) cross-matching a list of potential genes of interest with EBI and KEGG pathway databases (Supplementary Table 4).

c) Evidence in literature of direct or potential involvement of the gene in brain folding malformation.

Genes that were annotated as “NA” in the sheep genome annotation file were ignored when applying these criteria.

The three criteria are applied and combined as follows:

Score criterion: score was calculated for the 1963 genes that showed unadjusted p < 0.05 using the formula provided. A literature search was performed for the top 100 genes with highest score, and the genes that did not have direct evidence of involvement in central nervous system development (e.g evidence for neuronal and/or dendrite activity, neurogenesis, migration, cell survival or death, neural differentiation) or had not been implicated in brain malformations, were excluded from further analysis. The top 20 genes remaining from this selection procedure were pre-selected. This list was called “gene list 1”.

Pathway criterion: the 1963 genes mentioned before were cross-matched with pathway databases available in BIOCARTA, EBI, KEGG and WIKIPATH for a number of neuronal processes of interest, producing a list with several genes included in the edgeRun output and their associated pathway of interest. Genes involved in two or more pathways were pre-selected. This list was called “gene list 2”.

Literature criterion: the 1063 genes were cross-matched with a list containing all the genes of interest based on their direct or potential involvement in brain folding malformation as provided by a literature search using the terms “gyrification”, “brain folding” and/or “brain development”. This list was called “gene list 3”.

Gene lists 1, 2 and 3 were compared side by side, and those genes who appeared in two or all lists were selected.

2.6 Probe design for FISH procedures

Probe set design was performed by selecting available reported sequences from the NCBI nucleotide database (NIH), and then performing a multiple sequence alignment with Clustal Omega online interface (EMBL-EBI). Subsequently, the most highly-conserved regions were selected to design the corresponding probe sets using the Stellaris probe designer algorithm online (LGC Biosearch Technologies, USA). Probes generated were analysed through BLAST (NIH) to validate their specificity. See supplementary information for sequence ID, multiple sequence alignment and probes generated.

2.7 Fluorescence *In Situ* Hybridization (FISH)

FISH was performed on 5-µm-thick frozen sections using Stellaris RNA FISH probes and reagents (LGC Biosearch Technologies, USA), according to manufacturer recommendations. For each fetal brain at each GA, one coronal section per brain region was used (GA 70, 3 sections; GA 90, 5 sections; GA 110, 8 sections, Figure 7). Sections were cut using a cryostat (-15 to -12^{o}C) and collected on to RNase-free Superfrost slides, air-dried for 2 minutes at RT and kept in the cryostat before freezing for long-term storage at -80° C. To perform FISH, sections were defrosted at RT for 30 minutes, fixed for 10 minutes in 4% formaldehyde in nuclease-free 0.1M PBS (Ambion, Invitrogen Australia), washed twice in nuclease-free 0.1M PBS and permeabilised in nuclease-free 70% ethanol overnight at 4^{o} C. The following day sections were incubated in Stellaris wash buffer A, and hybridised with the corresponding probe in Stellaris hybridisation buffer overnight at 37^{o} C in a humid chamber. On day 3, sections were washed in Stellaris wash buffer A, incubated with 1 µg/ml DAPI solution in 0.1M PBS for 5 minutes, washed in Stellaris wash buffer B, mounted in fluorescent medium (Dako North America, USA), coverslipped and visualised immediately using a Nikon Confocal C1 microscope with NIS-elements software v4.30.02 (build 1053, Nikon Instruments Inc.) Negative controls with no probe were also included.

2.8 Immunohistochemistry (IHC)

IHC was performed on 8 µm-thick paraffin sections using selected commercial antibodies (Table 4). As above for each fetal brain at each GA, one coronal section per brain region was used (GA 70, 3 sections; GA 90, 5 sections; GA 110, 8 sections, Figure 7). Sections were dewaxed in xylene, rehydrated in progressively diluted concentrations of ethanol, and washed with 20mM Tris buffered saline (TBS; pH 7.6) three times for 5 minutes each. Heat-mediated antigen retrieval was performed in a microwave by simmering in 11.4 mM sodium citrate buffer (pH 6.0) for 7 minutes. Sections were washed three times for 5 minutes in TBS, blocked using Dako protein block serum-free (Dako North America, USA) for 30 minutes, and incubated with the primary antibody diluted in Dako antibody diluent (Dako North America, USA) overnight at 4^{o} C; antibody dilutions are listed in Table 4. The following day sections were washed using TBS, and incubated with the secondary antibody diluted in TBS (see Table 4 for secondary antibody details and dilutions) at RT for 60 minutes, the Vectastain ABC kit (Vector Laboratories, USA) for 60 minutes, and DAB (3,3'-diaminobenzidine, MP Biomedicals, Australia) for 5 minutes. When the primary antibody was replaced with PBS (pH 7.4) as a negative control, immunoreactivity failed to occur. For each antibody, sections from each age group were stained simultaneously to ensure uniform conditions for subsequent analysis. For CDK5 only, prior to antigen retrieval, sections were permeabilized in 70% ethanol, overnight at 4^{o} C. Immunoreactive sections were digitalised using an Aperio ScanScope AT turbo (Leica Biosystems, Germany) slide scanner, and visualised using Aperio ImageScope (v12.3.0.5056, Leica Biosystems, Germany).

2.9 Immunofluorescence for co-localization

Co-localization of BDNF, CDK5 and NeuroD6 with MAP2, NeuN, GFAP, and Iba1 was performed on 8 µm-thick paraffin sections using commercial antibodies (Table 4). Paraffin sections were dewaxed and cleared in xylene, rehydrated in progressively diluted concentrations of ethanol, washed with 0.1M PBS (pH 7.4) for 15 minutes, and heat-mediated antigen retrieval in citrate buffer was performed as described above. Sections were then incubated in 0.1% Sudan Black in 70% ethanol for 10 minutes (to block autofluorescence), washed in 0.1M PBS, and incubated in 2.0 mM glycine for one hour at RT. Sections were further blocked with Dako protein block serum-free (Dako North America, USA) for 30 minutes, and incubated with the first primary antibody in Dako antibody diluent (Dako North America, USA) overnight at 4^{o} C. The following day sections were washed in 0.1M PBS and incubated with the appropriate secondary antibody in 0.1 M PBS for 60 minutes at RT. Sections were then washed in 0.1M PBS and blocked with 10% normal goat serum for 30 minutes at RT. The second primary antibody diluted in Dako antibody diluent, was then applied to the sections, and incubated overnight at 4^{o} C. Sections were then washed in 0.1 M PBS and incubated for 60 minutes with the appropriate secondary antibody in 0.1 M PBS at RT. Sections were washed in 0.1M

PBS and 1 μg/ml DAPI solution in 0.1M PBS was applied for 5 minutes. Finally, sections were washed in 0.1M PBS, mounted with Dako fluorescent mounting media (Dako North America, USA), coverslipped and kept at 4^{o} C until visualisation.

FISH probes for HDAC5 and MeCP2 were colocalised with MAP2, NeuN, GFAP, or Iba1 antibodies on 5 μm-thick frozen cryostat sections using the general FISH procedure described above. Sections were co-incubated with the primary antibody and the FISH probe, and the appropriate secondary was added to the second wash buffer A, as per manufacturer recommendations. Fluorescent co-localisation slides were visualised using a Nikon Confocal C1 microscope with NIS-elements software v4.30.02 (build 1053, Nikon Instruments Inc.).

Table 4. Antibodies. Antibodies and concentrations used in this study for either immunohistochemistry with DAB precipitation (IHC) or immunofluorescence (IF), and brief mention whether the general protocol was modified to include an overnight permeabilization before antigen retrieval (for IHC) to increase signal. For IF with FISH probes, the permeabilization is recommended by the manufacturer.

Method	**Primary antibody (dilution)**	**Manufacturer (Cat. No/Lot)**	**Secondary antibody (dilution)**	**Conjugation**	**Manufacturer (Cat. No/Lot)**
IHC	Rabbit α-CDK5 (1:200)	Abcam (ab40773/GR103646-18)	Goat α-Rabbit IgG (1:200)	Biotin	Vector Labs (BA-1000/ZB0318)
IF	Rabbit α-CDK5 (1:200)	Abcam (ab40773/GR103646-18)	Goat α-Rabbit IgG (1:500)	Alexa Fluor 546	Invitrogen (A11035/442417)
IHC	Chicken α-BDNF (1:100)	Promega (G1641/ 0000265206)	Goat α-Chicken IgY (1:200)	Biotin	Vector Labs (BA-9010/ZB1005)
IF	Chicken α-BDNF (1:500)	Promega (G1641/ 0000265206)	Goat α-Chicken IgG (1:500)	Alexa Fluor 546	Invitrogen (A11040/1927941)
IHC	Rabbit α-NEUROD6 (1:1000)	Sigma-Aldrich (AV32416/QC1884)	Goat α-Rabbit IgG (1:200)	Biotin	Vector Labs (BA-1000/ZB0318)
IF	Rabbit α-NEUROD6 (1:1000)	Sigma-Aldrich (AV32416/QC1884)	Goat α-Rabbit IgG (1:500)	Alexa Fluor 546	Invitrogen (A11035/442417)
IHC	Mouse α-MAP2a,b (1:200)	ThermoFisher (MS-249-S1/249S1802B)	Goat α-Mouse (1:200)	Biotin	Vector Labs (BA-9200/Y0907)
IF	Mouse α-MAP2a,b (1:100)	ThermoFisher (MS-249-S1/249S1802B)	Goat α-Mouse IgG (1:500)	Alexa Fluor 488	Invitrogen (A11029/47683)
IF	Mouse α-NeuN (1:500)	Merck (MAB377/2607740)	Goat α-Mouse IgG (1:500)	Alexa Fluor 488	Invitrogen (A11029/47683)

IF	Mouse α-Iba1 (1:500)	Sigma-Aldrich (SAB2702364/42128)	Goat α-Mouse IgG (1:500)	Alexa Fluor 488	Invitrogen (A11029/47683)
IF	Mouse α-GFAP (1:500)	Sigma-Aldrich (SAB1405864)	Goat α-Mouse IgG (1:500)	Alexa Fluor 488	Invitrogen (A11029/47683)

2.10 NODDI analysis

Whole fixed left cerebral hemispheres were subjected to diffusion tensor magnetic resonance (MR) imaging as well as (Neurite Orientation Dispersion and Density Imaging) NODDI analysis. MR experiments were performed on an actively-shielded 9.4T/31 cm magnet (Agilent) equipped with 12 cm gradient coils (400 mT/m, 120 μs) with a 3.5 mm diameter birdcage coil. A multi-b-value shell protocol was acquired using a spin-echo sequence with the following parameters: FOV = 30×25 mm2, matrix size = 212×148, 20 slices of 1 mm thickness in the axial plane with a gap of 0.5 mm between each, 3 averages with TE/TR = 45/3000 ms. A total of 96 diffusion weighted images were acquired, 15 of them as b0 reference images. The remaining 81 were separated in 3 shells with the following distribution (# of directions/b-value in s/mm2): 21/1750, 30/3400 and 30/5100. All 81 directions were non-collinear and were uniformly distributed in each shell. The total acquisition time was 15 hours per brain. During acquisition, brains were bathed into Fomblin. Axial (AD), radial (RD) and mean diffusivity (MD) values, as well as fractional anisotropy (FA) were derived from the tensor using DTI toolkit. Acquired data were then fitted using the NODDI toolbox (216) to extract NODDI estimates, adapted for ex-vivo data: intra-neurite volume fraction (fin) isotropic volume fraction (irfrac) and orientation dispersion index (ODI). Regions of interest corresponding to two gyri and two sulci at each coronal section were manually drawn and analysed at a resolution of 150x195 μm^2 and 1 mm slice thickness on all regions of interest. Data for each parameter (DTI-derived parameters and NODDI estimates) was averaged between gyri and sulci separately at each coronal section and used for statistical analysis. For quality control, acquisition at single b value of 1750 was performed in all three brains.

2.11 Imaging analysis

For rostro-caudal analysis of BDNF, CDK5, NeuroD6, MAP2, HDAC5 and MeCP2, non-overlapping CP/cortex regions were selected for each coronal region of the brain (Figure 7), depending on fetal GA, as follows. For GA 70 brains, six regions were randomly selected across the medial-lateral section of the eCP. For GA 90 and 110 brains, two gyri and two sulci tCP/cortex

regions were randomly selected. In each region of interest (ROI), analysis was performed as follows. For BDNF, CDk5, NeuroD6 and MAP2 expression, two non-overlapping 200-µm wide areas of the eCP/tCP/cortex spanning from layers II to VI were analysed. For HDAC5 and MeCP2 transcription, two non-overlapping 200 x 200 µm areas of the eCP/tCP/cortex spanning from layers II to III were analysed. Analysis for each ROI was performed using FIJI software (v 1.51, NIH) (217) as previously described (218-220).

Cell density for BDNF, CDK5, NeuroD6 was analysed as follows. Images were converted to 16-bits, background subtracted, area of interest delimited, detection threshold applied, binary functions “fill holes” and “watershed” applied, and the “analyse particles” plugin run. Number of particles per area in each ROI was recorded as cells per tissue area and used for statistical analysis. These will be referred to as “positive cell density” in the text.

Area coverage of MAP2 was analysed as follows. Images were converted to 16-bits, background subtracted, area of interest delimited, detection threshold applied, and “analyse particles” plugin was run. Area covered by the stain in each ROI was recorded as area of staining per tissue area and used for statistical analysis. This will be referred to as “immunoreactivity” in the text.

For HDAC5 and MeCP2 transcription density was analysed as follows. Images were converted to 16-bits, background subtracted, area of interest delimited, detection threshold applied, binary functions “fill holes” and “watershed” applied, and the “analyse particles” plugin run. Number of particles per area in the ROI was recorded as mRNA molecules per tissue area and used for statistical analysis. These will be referred to as “mRNA expression density” in the text.

The threshold values applied for immunohistochemistry and FISH were calculated as follows:

One randomly selected gyrus and one randomly selected sulcus were combined into a single image, and this image was analysed using the same procedure that was used for analysing all the individual gyri and sulci. The analysis of the image containing both one gyrus and one sulcus ensured that the effects of the background reduction before the selection of the threshold were minimised. The appropriate signal intensity threshold for each analysis was chosen by analysing the combined image and selecting a signal intensity threshold level that could reliably distinguish positive signal from background. This procedure was repeated in ten such combined images independently, and the threshold for the full analysis was calculated by averaging the thresholds selected for each of the ten combined images. After the signal intensity threshold was calculated, the appropriate size threshold for each analysis was calculated by analysing five gyri and five sulci images separately and

determining a size restriction that excluded background noise and potential artefacts. The size threshold for the full analysis was calculated by averaging the thresholds selected for each analysed image. The selection of these thresholds were also contrasted against, and validated with, the criteria of an experienced analyst. No restriction to the shape of the signal was applied. See Supplementary Figure 1 for representative images of this procedure.

Additionally to the counts provided for the genes of interest, $\log_2$ ratios of expression between gyri and sulci were also calculated. These were calculated by applying $\log_2$ to the quotient between gyri and sulci counts, with gyri always as dividend, and sulci always as divisor.

For analysis of NeuN, GFAP and Iba1 expression in the gyri and sulci at GA 90, fields from the tCP from two gyri and two sulci at R2 were analysed. Two non-overlapping transverse areas with 200-µm width from layers II to VI were analysed in each gyrus and sulcus. NeuN-, GFAP- and Iba1-positive cells were manually counted and only included if they had a DAPI-stained nucleus. To determine total number of cells DAPI-stained nuclei were counted within the analysed area. The proportions of NeuN, GFAP and Iba-1 cells were then calculated using the total number of cells and used for statistical analysis.

2.12 Statistical analyses

For RNA Seq analyses, Fisher's exact test and unconditional exact test were applied using edgeR (v 3.4.2) and edgeRun (v 1.0.9), respectively, in R-environment using RStudio (v 0.98.1103).

For BDNF, CDK5, NeuroD6, MAP2, HDAC5, MeCP2 and NODDI parameters analyses, two-way ANOVA with Sidak post hoc was performed to compare differences between averages from gyri and sulci and averages between rostro-caudal regions. For NeuN, GFAP, Iba1, and total cell analyses, unpaired t-tests were performed in all pair-wise comparisons to determine differences in averages from gyri and sulci. Statistical tests for these analyses were performed using GraphPad Prism (v6.01, GraphPad Software, USA). Results shown are mean ± SEM.

Chapter 3 – *in silico* differential expression analysis on the cortical plate between a gyrus and a sulcus in the developing brain of the sheep, and selection of genes for further study

Rationale

Consistent with our view of gyrification as a standalone process which should be studied in a context completely void of previous human intervention –i.e. without previously induced mutations or alterations–, we decided that the best way to address the differences between gyri and sulci tCP is using normally developing fetal sheep, collecting their brains and studying the tissues without further manipulation.

Given that most recent theories on gyrification point to the CP as the main factor driving this process (see background section), we hypothesise that tCP cells have gene expression profiles that differ between gyri and sulci. Such differences in tCP genetic expression between gyri and sulci, to the best of our knowledge, have not been previously addressed. These genetic expression profiles were studied by sampling the tCP cells of both gyri and sulci in normally-developing fetal sheep brain cortices using Laser Capture Microdissection, and then comparing the RNA contents of both regions through RNA Seq approaches, to investigate what genes are differentially expressed between gyri and sulci. These genes might play a key role into the folding of the cerebral cortex.

Methods

Please refer to sections 2.1, 2.2, 2.3, 2.4, 2.5 and 2.12 for the detailed methodology corresponding to this study.

Results

Laser capture microdissection (LCM), RNA extraction and quality check

After checking the RNA purification and integrity (RNA Integrity numbers (RIN) 7.85 ± 1.04, concentration 4.31 ± 1.73 ng/µL, Table 2, Figure 11), the RNA was sequenced and quality check reports were obtained. An average of 9.37 ± 1.07 x 10^7 sequences of 35-51 bp length were analysed, containing an average 41.01 ± 2.81 % GC content (Table 3, Supplementary Figure 2).

Using STAR, the raw data delivered by the sequencer was aligned to the sheep genome, which yielded an average of 56.14 ± 7.24 % uniquely mapped reads, with an average 34.62 ± 9.25 % multi-mappers and an average 6.15 ± 9.25 % unmapped reads. Summarization using featureCounts deemed an average of 9.88 ± 1.64 uniquely assigned reads (Table 5).

Table 5: Alignment output. Summary statistics of the alignment and read summarization processes through STAR and featureCounts, respectively, using isolated fetal sheep cortical plate cells RNA from either gyrus or sulcus. Numbers are total reads per category and percentage of total input reads in brackets. Sample names are sheep number + sample type, G: gyrus; S: sulcus.

	STAR alignment			featureCounts summarization
Sample	Uniquely mapped (% total reads)	Multi-mapping reads (% total reads)	Unmapped reads (% total reads)	Successfully assigned reads (% total reads)
658.1G	46828481 (41.7)	28265536 (25.17)	37204498 (33.13)	12240538 (10.9)
658.1S	67194347 (61.79)	37017245 (34.04)	4534721 (4.17)	13375797 (12.3)
1251.1G	55419497 (58.31)	33426577 (35.17)	6196795 (6.52)	9694373 (10.2)
1251.S	53313603 (57.44)	35706377 (38.47)	3796181 (4.09)	8075006 (8.7)
1251.2G	60120037 (59.75)	35780226 (35.56)	4719046 (4.69)	10766266 (10.7)
1251.2S	50048694 (56.7)	33180430 (37.59)	5040177 (5.71)	8826930 (10)
1452.1G	47903209 (50.7)	43131785 (45.65)	3448653 (3.65)	6519372 (6.9)
1452.1S	39174425 (50.63)	27158253 (35.1)	11041261 (14.27)	6499411 (8.4)
1452.2G	59946323 (67.31)	25729450 (28.89)	3384282 (3.8)	10687207 (12)
1452.2S	51493102 (61.56)	28816396 (34.45)	3337516 (3.99)	8364701 (10)

Differential Expression (DE) analysis

Analysis using edgeR multi-dimensional scaling (MDS, Figure 12) showed an expected sample clustering, where samples were more similar between those obtained from the same animal (sharing same animal number), compared to samples of the same region (i.e., gyrus or sulcus), which accounted for approximately 55% of sample variability. However, MDS also showed irregular behaviour of samples coming from one animal (658.1, Figure 12) which did not show this clustering, suggesting a methodological error, and so these samples were not analysed further. After removing these samples (Figure 13), the new MDS analysis showed expected clustering of RNA samples, albeit with again more variability in the sequences obtained from different animals compared to samples from gyri and sulci. Finally, this new MDS showed that the two main components can together explain about 80% of the variation in the data set. The first dimension –genetic differences between twin sets–, accounted for about 50% of the variation, while the second dimension –genetic differences between twins– accounted for about 30% of the variation. Lastly, the third dimension –genetic differences between gyri and sulci– accounted for only ~10% of the variation in the dataset. This is further appreciated when plotting dimension 3 (Supplementary Figure 3).

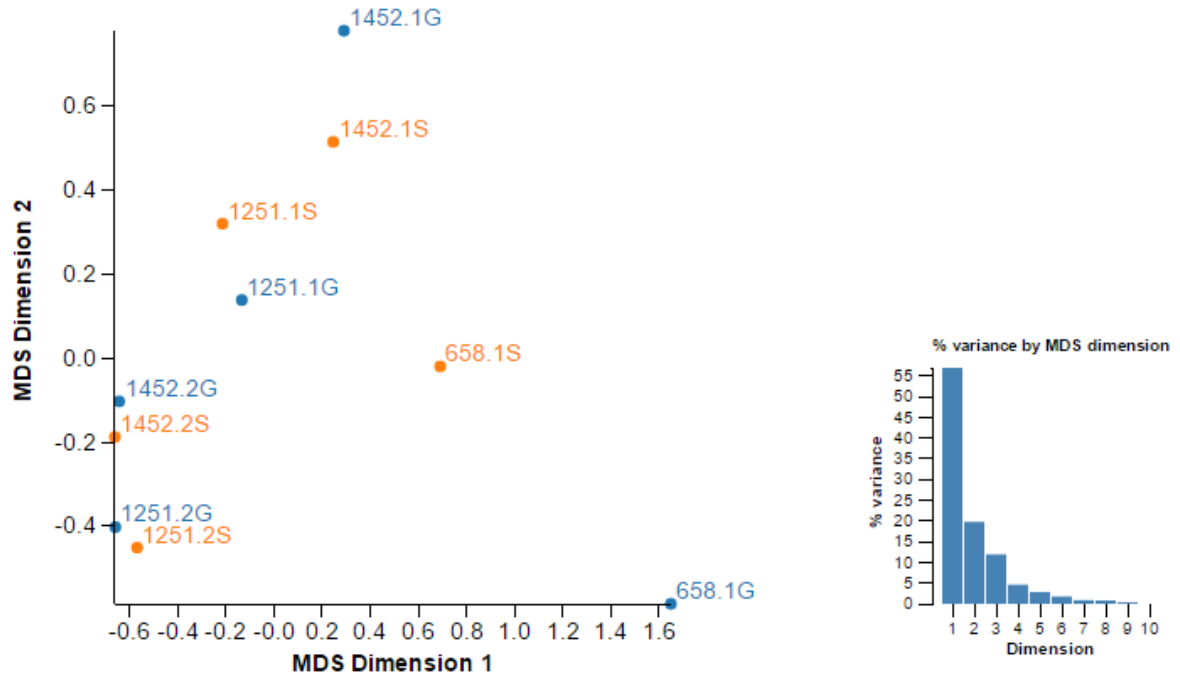


Figure 12: Preliminary multi-dimensional scaling (MDS) for RNA samples. MDS showing correspondence of the RNA samples obtained from fetal sheep cortical plate cells. Sample names are sheep number + sample type, G: gyrus; S: sulcus.

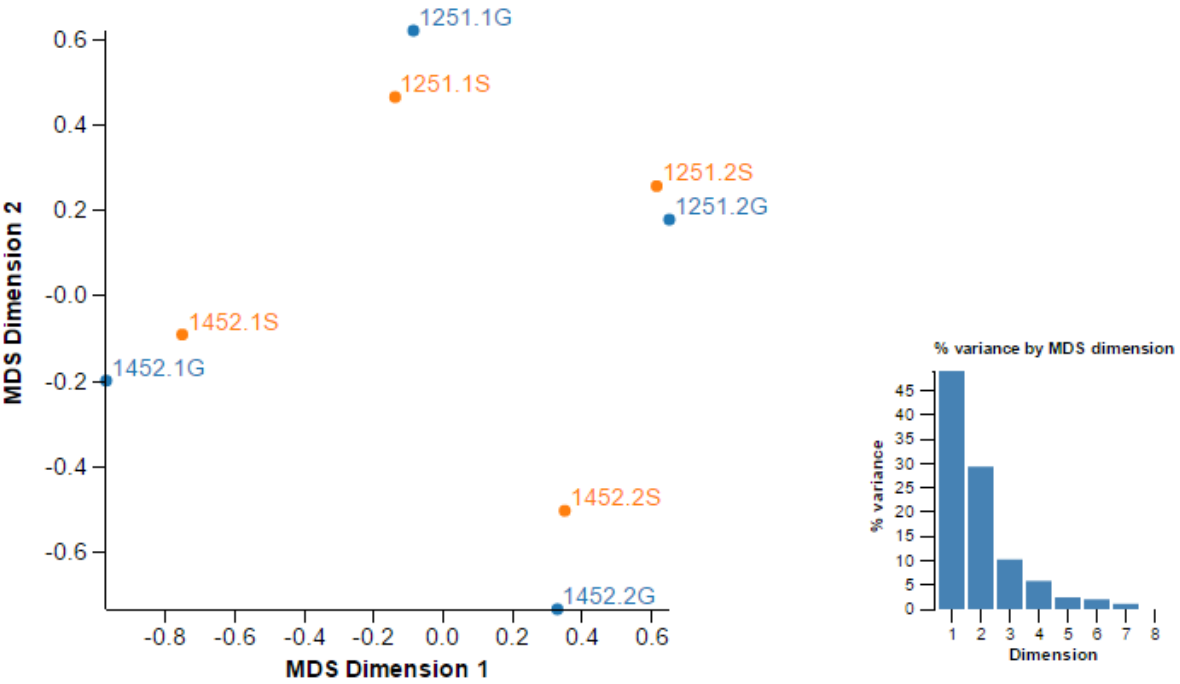


Figure 13: Multi-dimensional scaling of RNA samples. Multi-dimensional scaling showing correspondence of the RNA samples obtained from fetal sheep cortical plate cells after outliers were removed. Sample names are sheep number + sample type, G: gyrus; S: sulcus.

In performing the DE analysis, the first step was filtering out all the genes with a count number lower than 10 in every sample, as recommended to reduce the impact of multiple-testing adjustments of poorly expressed transcripts or uninformative background (221, 222). This filtering step reduced the number of identified "genes" from 27,054 to 11,167. Subsequent DE analysis performed with edgeRun with 50,000 iterations over the filtered samples showed no differentially expressed genes when samples from sulci and gyri were compared (Figure 14). The analysis also calculated dispersion in 0.09356 and the biological coefficient of variability (BCV) in 0.3059, while the calculated false discovery ratio (FDR) for the genes was 0.1849. Visualisation of the samples using a mean average (MA) plot (Figure 14) and a volcano plot (Figure 15) showed a typical trend in distribution of genes, but with again no statistically significant differences in expression between gyrus and sulcus.

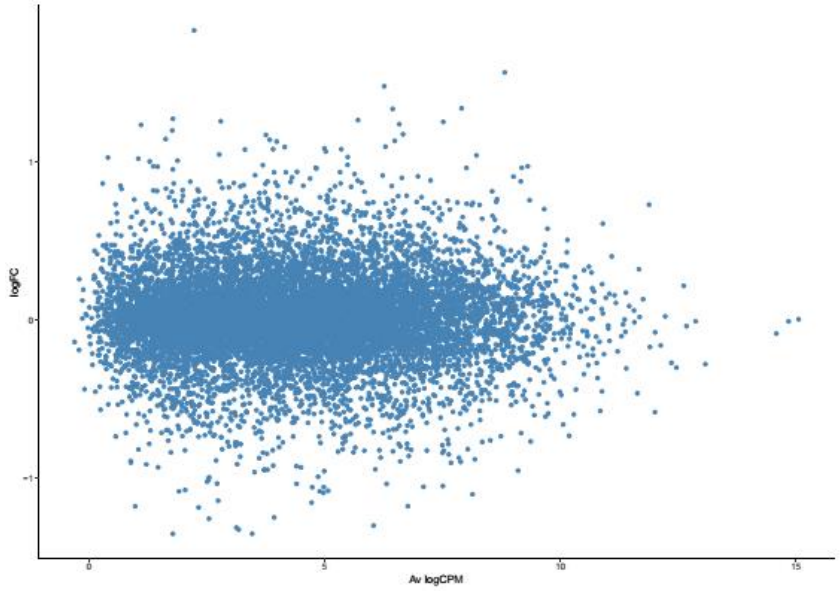


Figure 14: MA plot of analysed RNA samples. MA plot showing the average log of fold change in expression for all the evaluated genes between gyrus and sulcus tCP cells (logFC) and the average logarithm of that gene expression (Avg log expr). Each dot represents a gene in the dataset. Blue dots represent non-significant differential gene expression between the two studied conditions (gyrus and sulcus).

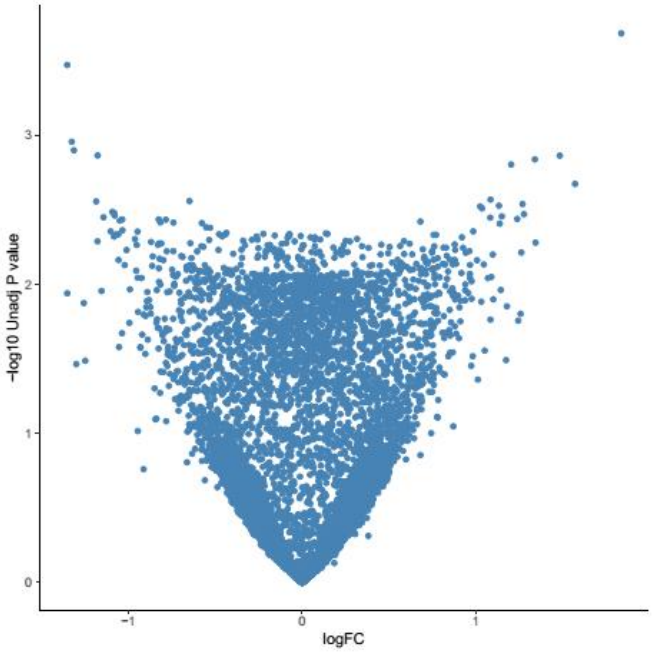


Figure 15. Volcano plot of analysed RNA samples. Volcano plot showing the average log of fold change in expression for all the evaluated genes between gyrus and sulcus tCP cells (logFC) and the average negative logarithm of the unadjusted p value obtained from the edgeRun analysis. Each dot represents a gene in the dataset. Blue dots represent non-significant differential gene expression between the two studied conditions (gyrus and sulcus).

Gene Ontology (GO) analysis and selection of genes for further study

From the genes passed on to DAVID database (n = 1963, Supplementary Table 1), 1424 were recognised as belonging to sheep (*Ovis aries*), and 539 were deemed as "unknown", presumably due to lack of proper annotation in the DAVID database. Gene Functional Classification analysis was performed at medium stringency.

Thirty-seven functional clusters were obtained, with enrichment scores ranging from 2.22 to 0.01 (Supplementary Table 2). Thirty-seven annotation groups had an association with biological processes (GOTERM_BP_DIRECT), 14 annotation groups were associated with cellular components (GOTERM_CC_DIRECT), 10 annotation groups were related to molecular function (GOTERM_MF_DIRECT), and 19 annotation groups were associated with pathways (KEGG_PATHWAY) such as "Ribosome", "Acute myeloid leukemia", "Non-alcoholic fatty liver disease", among others. However, only one term had a corrected $p < 0.05$ (GOTERM_CC_DIRECT = Mitochondrion; Supplementary Table 3).

Selection of the genes of further study was performed in a sequential three-step analysis (see methods). First, an arbitrary score was calculated for all genes based on their fold change between gyri and sulci, the number of counts for each gene, and their individual unadjusted p value.

Then, a literature search was performed for the top 100 genes, and those genes with no direct evidence for involvement in central nervous system development (e.g evidence for neuronal and/or dendrite activity, neurogenesis, migration, cell survival or death, neural differentiation) or had not been implicated in brain malformations, were excluded from further analysis. The top 20 genes remaining from this selection procedure were retained for further analysis (Table 6)

Table 6. Top 20 genes based on score, identity, and literature. ID, symbol, logarithm of fold change (logFC), logarithm of counts per million (logCPM), unadjusted p value (Unadj p value) and score (see methods) are presented.

Ensembl Gene ID	Gene symbol	logFC	logCPM	Unadj p value	Score
ENSOARG00000008435	NEUROD6	0.53977	7.940096	0.027698	9.452169
ENSOARG00000006902	HDAC5	0.529798	6.280473	0.048911	7.76136
ENSOARG00000003312	DIRAS2	0.508674	6.044235	0.030424	7.522486
ENSOARG00000004165	ISLR2	0.299774	6.090372	0.007343	7.382803
ENSOARG00000000847	PRRT1	0.350907	5.856211	0.017835	7.189283
ENSOARG00000015727	LUM	-0.04594	6.071919	0.025685	7.092179
ENSOARG00000005284	FKBP2	0.547028	5.292303	0.043607	6.795724
ENSOARG00000004402	DYNLT1	0.596243	5.151107	0.035557	6.711793
ENSOARG00000017717	SPG21	0.867319	4.83069	0.011911	6.686097
ENSOARG00000002633	CDK5	0.592752	4.834952	0.033558	6.394147
ENSOARG00000010129	BACE2	-0.6142	4.579773	0.012373	6.1816
ENSOARG00000002748	NRXN3	0.016192	5.118738	0.007699	6.12723
ENSOARG00000001772	FOXP2	-1.30088	3.858729	0.034249	6.125356
ENSOARG00000012674	SLC39A12	-0.22008	4.883856	0.01108	6.092859
ENSOARG00000013997	STARD7	-0.56315	4.515657	0.048961	6.029843
ENSOARG00000009812	FREM2	-0.63401	4.32726	0.035621	5.925645
ENSOARG00000017383	HTR2C	-0.43699	4.423833	0.004506	5.856317
ENSOARG00000014075	KCNIP3	0.273411	4.541936	0.015748	5.799598
ENSOARG00000015737	DCN	-0.83616	3.938382	0.017175	5.757365

Second, the list of 1963 genes obtained from the edgeRun output was cross-matched with pathway databases available in BIOCARTA, EBI, KEGG and WIKIPATH for a number of neuronal processes of interest, producing a list with several genes included in the edgeRun output and their associated pathway of interest (Supplementary Table 4). Genes involved in two or more pathways were pre-selected; specifically, BDNF, CDK5, CXCR4, DRD1, DVL1, HDAC5 and MeCP2.

Lastly, the edgeRun output was cross-matched with a list containing all the genes of interest based on their direct or potential involvement in brain folding malformation as provided by a literature search using the terms “gyrification”, “brain folding” and/or “brain development”, and using the references on the literature to find more literature. This approach matched 9 genes from the bioinformatic output to the literature database (Supplementary Table 5).

Combining the lists generated from these three criteria we identified 9 genes of interest for further testing: BDNF, CDK5, DIRAS2, DYNLT1, HDAC5, MeCP2, NEUROD6, NRXN3 and PAX6. See Table 7 for information on these genes. We then proceeded to investigate the expression differences between gyri and sulci of a subset of these genes, namely BDNF, CDK5, HDAC5, MeCP2 and NeuroD6 using immunohistochemistry and/or fluorescent *in situ* hybridisation. This validation was performed in the next study.

Table 7. Genes of interest for further testing.

Gene	logFC	logCPM	Unadj p value	Evidence
BDNF	0.975	0.943	0.01	Modulates axonal and dendritic branching (223), synaptic efficacy (224), plasticity (225), and more. Mutant BDNF is associated with altered gyrification (226) (227).
CDK5	0.593	4.835	0.034	Involved in neuronal survival (228), migration (229-232), synaptic transmission (233), and cell death (234), among others. Mutation causes impaired gyrification (235).
DIRAS2	0.509	6.044	0.03	Little is known about the involvement of this protein during neurodevelopment. It is thought to regulate neurogenesis (236). Polymorphism in promoter region linked to ADHD (236, 237), while ADHD has been associated with reduced cortical folding (238).
DYNLT1	0.596	5.151	0.036	Important for axonal growth (239). Association to gyrification unknown.
HDAC5	0.53	6.28	0.049	Associated with axonal regeneration (240), regulates neurogenesis and differentiation in neurons (241), and

				neurite development (242). Association to gyrification unknown.
MeCP2	0.183	2.506	0.014	MECP2 controls neuronal differentiation (243), dendritic growth and maturation (244). Associated with polymicrogyria (245).
NEUROD6	0.54	7.94	0.028	Implicated in neuronal differentiation (246), neurite regrowth (247) and neuron survival (248, 249). Association with gyrification unknown.
NRXN3	0.016	5.119	0.008	Essential for synaptic function (250). Mutations linked to ASD patients (251), which usually display alterations in gyrification (252, 253). Mutations found in schizophrenia patients (254), who have also been shown to have impaired gyrification (34, 255-258).
PAX6	0.29	3.343	0.014	Influences proper cerebral cortex morphology (259), orientation and cell division mode in the progenitor cells (260), and regulates cortical cell fate function and position of upper layer neurons (261, 262). Linked to polymicrogyria (263).

Discussion and Conclusion

Based on previous work performed in our laboratory at different developmental ages, we decided that GA 90 was a proper sampling stage to address our hypothesis. Using LCM we extracted tCP cells from gyri and sulci, extracted their RNA and sequenced it. Using RNA Seq pipelines, we were unable to detect differences between gyri and sulci. However, when applying alternative complementary bioinformatic approaches, we were able to obtain a list of nine candidates genes to validate as differentially expressed between gyri and sulci, despite the differences between gyri and sulci samples not being large enough to be detected by conventional RNA Seq pipelines. The degree to which the methodology applied might have contributed to our inability to detect differences between our samples of interest is discussed.

Staining of the slides for LCM was performed following the protocol described by Wang and colleagues (207), which is a modification of a Nissl staining. The LCM was performed over fifty 20-µm slices cut consecutively from the selected brain section, accounting for approximately 1 mm in-depth sampled tissue. LCM procedure was performed successfully and RNA was further extracted. The RNA quality obtained with this protocol (RIN = 7.85 ± 1.04) was in accordance with the expected quality described by the literature protocol (207), and was therefore suitable for downstream sequencing.

RNA sequencing for whole transcriptome usually requires large amounts of genetic material to perform either poly-A selection or ribodepletion (depletion of rRNA) to take away ribosomal RNA, which can constitute 60-80% of total RNA in a cell, leaving only mRNA as the target. However, acquiring such amounts of RNA is not always possible, especially when analysing individual or small numbers of cells or performing acquisition procedures such as LCM. Single Primer Isothermal Amplification (SPIA) sequencing was developed to overcome those limitations by using a linear amplification reaction based on random DNA-RNA chimeric hexamers, while maintaining the relative amounts of all the RNA species proportional within the total RNA pool (208).

Due to its nature, whole transcriptome sequencing through SPIA has the constraint of not select mRNA over other types of RNA, which can make the subsequent bioinformatic analysis problematic. 'Ovation RNA-Seq' system was therefore introduced as a modification for SPIA to overcome this problem, using the hexamers described above but also adding poly-T primers. This system has been shown to produce excellent quality sequencing data without the rRNA depletion steps –which are known to be responsible for loss of rare transcripts in cDNA preparation protocols– when compared with other systems (264).

We compared the sequencing data coming from two different zones (namely a gyrus and a sulcus) of the tCP in the sheep brain at GA 90 obtained using LCM and later sequenced by Ovation SPIA sequencing, analysed by both edgeR and edgeRun pipelines. Our results are consistent with other reports for this pipeline (264), having an average of 56.7 ±7.24% uniquely mapped reads, 34.69 ± 5.35% multi-mappers, 6.15 ± 9.25% unmapped reads, and 9.88 ± 1.65% of the uniquely mapped reads referred unambiguously to the sheep genome features using featureCounts, even when using a genome presumably less sequenced and annotated than those of reference animal models, and using different mapping and read-summarisation programs.

Initial analysis of the samples after reading summarisation through a multi-dimensional scale (MDS) plot suggested the samples obtained from fetus 658.1 were technical errors (Figure 12), and

the gyrus sample coming from this specimen also showed an unusual level of unmapped reads in STAR (Table 5) and an unusual GC content distribution (Supplementary Figure 2). Based on these interpretations, the dataset of fetus 658.1 was removed, and the new filtered MDS plot showed a much more expected distribution of the samples.

Analysis of the filtered MDS plot showed that the main driver of variation in the samples is the genetic background of the animals, because they were genetically independent. Although the twin fetuses 1251.1 and 1251.2 came from the same ewe (number 1251), and 1452.1 and 1452.2 were twins from another ewe (number 1452), they still showed significantly greater between-animal variation compared to the differences found between gyrus and sulcus in the same fetus. It was not possible for us to determine if the fetal sheep coming from multiple pregnancies are monochorionic or dichorionic twins, and thus further infer about their genetic similarity (or dissimilarity), but monochorionic twinning in sheep is rare (265-267), so we can assume they were both dichorionic. The between-animal variability was consistent with the biological coefficient of variation (BCV, 0.3059) and the calculated common dispersion (0.09356), which was expected for an experiment with genetically unrelated subjects as stated in the edgeR user guide, and also by Hart and colleagues (268). BCV values, as the name suggests, represent a measure of the biological variability of the samples analysed, and it is expected to be smaller for highly similar samples (e.g. samples coming from tightly regulated cell culture conditions) and larger for highly variable ones (e.g. samples from genetically unrelated individuals), while the common dispersion is the BCV squared. For example, samples coming from zebrafish values have been reported to have BCV values ranging from 0.19 to 0.26, while samples from humans ranging from 0.32 to 0.74, with a median of 0.43 (268). Our samples therefore present a value that falls within predicted parameters expected for genetically unrelated individuals.

The first step in performing differential expression analysis is to filter out those genes in the featureCounts output count table with low or no counts to reduce the background 'noise' level which can directly impact the statistical power of the tests performed over the selected gene set, and which also reduces the ability of the test to effectively detect differentially expressed genes (221, 222). The number of minimum reads defined as threshold for inclusion is arbitrary, and is defined by the user at the moment of analysis. Too many genes filtered out will increase the power of the statistical test by reduction of impact of multiple test correction (221), but will filter out genes that might possibly be lowly expressed in the sample and still be of interest, such as transcription factors (269). On the other hand, including these genes might effectively be a good way to keep lowly expressed genes in the analysis, but will impact the statistical power of the test. In the filtering

used here, the featureCounts output list was reduced from 27,054 to 11,167 genes. One gene known to be a key determinant of neuronal survival, differentiation, and synaptic plasticity –the transcription factor MEF2– was thereby left out of the list, but other genes known to be differentially regulated by it in human progenitor cells (e.g. WDR37, SMOC1, STARD7 and others (270)), were kept in the analysis (Supplementary Table 1).

Several tools have been developed in order to address differences in gene expression between samples and experimental conditions coming from high-throughput RNA sequencing methodologies. The digital gene expression data produced by these technologies, after the mapping and read summarisation steps, is observed as "counts" reflecting the overall number of "tags" or "exons" that have been successfully assigned to an annotated gene in the genome they have been mapped to. To address the differences in genetic expression between two different conditions (in our case, gyrus versus sulcus), tools such as edgeR (211) and DESeq2 (271) treat the problem as a pairwise comparison of mean values for each gene, which results in a fold-change measure of change between the two conditions studied, adding a p-value to address the statistical significance of the comparison. Particularly, edgeR models count data using an over-dispersed Poisson model fitting a negative binomial distribution, and uses a quantile adjustment to adjust the counts of a library depending on the library size, called quantile adjusted conditional maximum likelihood, therefore reducing the dispersions of the counts towards a common value, normalising the libraries and the counts.

The edgeR package also contains the statistical tools necessary to determine differences in expression between samples associated with the two conditions under study. After normalising the samples to account for the RNA composition effect (i.e. variability that comes from differences in gene expression in RNA libraries of different sizes), negative binomial models are fitted and dispersions are estimated, edgeR calculates the differences between the two conditions using an exact test, which calculates the difference in mean expression between the two conditions for every gene that has not been filtered out, and assigns a p-value to this comparison to address the statistical significance of the comparison. However, given the big number of genes that usually compose a gene expression library –and considering the exact test is performed for each gene individually–, the possibility for type I errors (i.e. false positive genes) becomes substantive. To correct for this, the edgeR also performs the Benjamini-Hochberg method to control for False Discovery Rate (FDR), and adjusts the p values.

However, the differences in gene expression between the samples coming from each experimental condition need to be large enough to reach significance using edgeR. This poses an

important constraint to experimental designs where the differential expression between the samples, although plausible, might be too small to pass the FDR threshold, which appears to be the case for our samples coming from gyri and sulci. This becomes especially important if the samples present high biological variability, and in cases where only few biological replicates are available. To tackle these problems an extension of the edgeR package, called edgeRun, has recently been developed (213). In contrast to edgeR, which performs a conditional test that suffers from a loss of power the fewer replicates a condition has, edgeRun performs a test based on the unconditional probability of the observed data, using a user-determined number of iterations for the calculation of the appropriate p values for the comparison of the conditions analysed. Although computationally demanding, this test becomes more powerful than the conditional test when analysing datasets with high variability and/or low biological replicates, as the number of iterations can be adjusted to increase the accuracy of the p-values calculated for the dataset. However, for the 1963 candidate genes had a significant but unadjusted p-value between gyrus and sulcus ($p < 0.05$), the calculated FDR was greater than 0.05, and therefore the output classified them as non-significant.

One way to surpass this constraint is increasing the number of subjects in the experiment, as this usually brings down variability. However, it has also been reported that little gain is obtained by increasing biological replicates after the optimal sequence depth is reached (268, 272), and in general terms, 30 to 40 million reads are sufficient for technical precision for most genes when measuring gene expression (268, 273). Also, and regardless of whether the pipeline used identifies differentially expressed genes or not, chances are that some of these genes will still be false positives, as shown previously (274, 275). In order to complement such results and select genes that may be truly useful for further validation by complementary approaches such as *in situ* hybridisation or real time qPCR, we applied a combination of three criteria: *score*, relevant *pathways*, and *literature*-based reports.

The *score* criterion focused on three main parameters derived from the bioinformatic analysis: absolute value of the difference in expression between gyrus and sulcus, the amount of reads for each gene in the sequencer output, and the unadjusted p value obtained from the edgeRun analysis. The *score* will be higher for a given gene when the difference in expression between gyrus and sulcus is higher, the overall expression of the gene is high, and when the edgeRun analysis provides a low unadjusted p value for the gyrus/sulcus difference for the given gene. However, a major disadvantage of this approach is that it is naturally biased to highly expressed genes, leaving out others that might play an important role but have low expression, such as transcription factors, regulatory ncRNA and many others. For example, MeCP2 and PAX6, which

have been associated with polymicrogyria (26), had relatively low scores (3.67 and 4.62, respectively) in comparison to the ribosomal protein RPS11 (score = 10.07), despite evidence of the involvement of MeCP2 (276, 277) and PAX6 (3, 245) in the morphological abnormalities of brain development. On the other hand, genes like NEUROD6 –which is important in neural induction (248, 278)– and HDAC5 –which has been implicated in axon regeneration (240)– were successfully selected by the *score* method.

The second criterion – *pathway* – was based on the interrogation of biological pathway databases of biological processes that are, or might be, important for the onset and/or progress of the gyrification process in early cortical development. However, this criterion has the disadvantage that it is based on mammalian databases that might not reflect the species *Ovis aries*, which in practice is much less studied than other mammalian species. Also, these databases do not necessarily contain the pathways in which genes thought to be associated with normal and abnormal cortical folding malformations are involved. For example, POMT1 (associated with lissencephaly; (43)), and TNNI3 (associated with focal cortical dysplasia; (159)), were not picked up by this method. On the other hand, this method identified both HDAC5 and MeCP2, although the *score* method had failed to identify the latter. Nevertheless, an important feature of the *pathway* method is its ability to detect groups of genes related to a pathway, whereas gene ontology analysis using DAVID failed to give such association. For example, this method of analysis showed up several genes associated with the KEGG Axon Guidance pathway and EBI Neuron Projection pathways (Supplementary Table 4), whereas some of these genes were not recognised by the DAVID database as belonging to sheep, even though all the Ensembl gene IDs were extracted from the sheep genome annotation file. Whether these pathways are truly differentially regulated in gyrus and sulcus in the fetal sheep brain remains to be addressed.

The third criterion was based on published *literature* findings of the genes found to be directly or potentially involved in cortical folding malformations, and then cross-matched with the output list obtained from edgeRun. This approach has the advantage of confirming if the relatively unbiassed 'hits' identified in the bioinformatic approaches have a credible biological role in cortical development, but has the disadvantage that the list of genes generated from a literature review is by definition incomplete, and relies heavily on hypothesized involvement of specific genes in malformations of brain folding. For example, a gyrification malformation could be secondary to another more fundamental defect, and therefore not directly related to the process of gyrification, as discussed previously. Yet, the literature method allowed us to again select MeCP2, and others like CDK5 and BDNF who have been correlated with gyrification malformations. Nonetheless, the

combination of these three selection methods of analysing the gene expression data consistently identified a number of genes that are strongly hypothesised to be differentially expressed between gyri and sulci (e.g., CDK5, HDAC5), validating the selection of these genes for further study.

Finally, it is important to note that the use of these criteria in combination might prove to be advantageous for selecting important differentially expressed genes in the absence of statistically significant data derived from the bioinformatic analysis. However, it is not useful for detecting genes that might still be differentially expressed and potentially important, but are relatively novel and therefore lack evidence linking them to the brain and the cortex development, in which case the bioinformatic analysis is by far a superior and more reliable approach that should be used whenever possible.

Chapter 4 – Differential expression analysis on the cortical plate between gyri and sulci in the developing cortex of the sheep

Rationale

Based on our findings described in Chapter 3, BDNF, CDK5, HDAC5, MeCP2 and NeuroD6 were selected as a subset of the nine genes in the list of genes we obtained from Study 1 due to their relevance during gyrification –based on further literature research–, which is presented below.

BDNF

Brain-Derived Neurotrophic Factor (BDNF), part of the nerve growth factor family, is an important growth factor that is implied in memory development and maintenance (279), modulates axonal and dendritic branching (223), synaptic efficacy (224), plasticity (225) and potentiation (280), and it is expressed widely both across the brain and throughout the body in mice and rats (281), sheep (279, 282, 283), ferret (284), and humans (285).

During brain development, BDNF has been shown to directly impact over survival and growth of neurons in both the hippocampus and the cortex, and has a direct effect over developing and maintaining cortical circuitry (286). In developing mice, disruption of BDNF affects brain neuron development, with homozygous mutant mice having significantly reduced number of sensory neurons, which die soon after birth (287). Furthermore, a mutant variation of BDNF that only exists in humans has been correlated with reduced in dorsolateral prefrontal cortex (288), smaller temporal and occipital grey matter volume (289), reduced hippocampal volume, and abnormal hippocampal-related tasks (reviewed in (290)). Noteworthy, transgenic mice harbouring this BDNF variant also showed reduced hippocampal volume, reduced dendritic complexity, and similar hippocampal-dependent learning impairment (291).

BDNF expression stimulates directed migration of embryonic cortical neurons (292), although interestingly, it differentially stimulates neurons in from different cerebral cortex layers at least in the developing visual cortex (293). However, BDNF overexpression induces aberrant cortical lamination in mice developing cerebral cortex (294, 295), by inducing premature RGC differentiation, thus impairing neuronal migration (296).

Yet, our understanding of the role of BDNF in gyrification is limited and conflicting. Bipolar disorder patients carrying a mutant allele for BDNF show greater losses in GI compared to individuals without it (226), and individuals with autism spectrum disorder (ASD) showed altered local surface area (which alters gyrification) associated with this allele (227). Interestingly, brain areas where this

mutant allele influences cortical volume match those that are altered in ASD patients (227). However, other studies have found no structural changes associated with the mutant allele (297, 298).

The role of BDNF during in utero gyrification has not yet been addressed. Nonetheless, evidence from gyrencephalic animals suggest BDNF could be influencing cerebral cortex folding. During gyrification in ferrets, BDNF heavily influences dendritic arborisation in the CP (293) –a process known to occur concomitantly with gyrification. Also, in cats, BDNF expression increases in the CP as gyrification unfolds (284). These observations support the notion that BDNF might be playing a role during gyrification not only on these animals, but also on both the sheep and the human.

CDK5

Cyclin-dependent protein kinase 5 (CDK5) is a serine/threonine kinase that, unlike other members of the CDK family, has no known role in cell cycle regulation (299, 300). CDK5 is active mainly in post-mitotic neurons and it is essential for maintaining this state (301), however it shows no activity as a monomer, as it requires association and activation by regulatory proteins p35 and p39 (302). After activation, it interacts with many downstream targets, thus being important in very diverse cellular functions, such as neuronal survival (228), migration (229-232), synaptic transmission (233), and cell death (234), among others (reviewed in (299)). CDK5 is ubiquitously expressed in the central nervous system of humans (303), mice (304), rats (305), ferrets (235), and sheep (306), and its kinase activity has been demonstrated only in mammal brains (307).

During development in mice, alterations in the expression pattern of either CDK5 or its activators impacts the normal positioning of post-mitotic neurons in the brain, with neurons failing to reach their final positions in the CP during migration, being arrested in the SVZ and IZ, and showing abnormal orientation (229-231). CDK5-null mice showed impaired layering of the cerebral cortex, and die perinatally (230, 231). Also, they show abnormal dendritic morphology, altered neuron polarity (231) and abnormal positioning of neurons from layer II to V (308). Mice deficient in p35 and p39 regulators of CDK5 display similar cortical aberrant phenotype, with abnormal layering phenotype (230).

CDK5 is essential for neuronal migration and positioning, and neuronal migration and/or positioning defects are linked to cortical malformations such as lissencephaly, polymicrogyria,

cortical dysplasia, and microcephaly (309-311). Also, CDK5 is mutated in some patients with lissencephaly (312, 313). Hence, evidence points to CDK5 being a strong candidate molecule implicated in the normal gyrification process in mammals. Indeed, during the development of this second year of this research project (2017), Shinmyo and colleagues (235) reported CDK5 to be necessary for normal folding of the ferret brain, suggesting its involvement in the correct positioning of upper-layer neurons is essential for proper folding of gyrencephalic mammals. Further study of the expression of CDK5 during gyrification is essential for understanding the molecular bases of cerebral cortex folding.

HDAC5

Histone deacetylases (HDACs) play an important role in controlling gene expression through the removal of acetyl groups from the histone complex, and even though little is known about their role in brain growth, they are known to be important for normal neural development (314).

HDAC5 has been mainly associated with axonal regeneration, albeit in peripheral neurons, deacetylating tubulin to change the dynamics of the microtubules (240), and has been associated with addiction to drugs (315), depression, and stress (316). Also, the activity of HDAC5 is dependent on its cellular localisation in hippocampal neurons (317).

HDAC5, alongside many other members of the HDAC family, regulates neurogenesis and differentiation in neurons (241), and also regulates neurite development through another important family of transcription factors: MEF2 (242).

HDAC5 has been described to be up-regulated by MEF2 in human neural progenitor cells (270), while MEF2 transcription factors are important in neuron survival (318, 319) and synapse regulation (318). Interestingly, HDAC5 also interacts with MEF2 to repress its transcriptional activity (320), although this repression has not been reported in the context of neural development. Nonetheless, and considering the evidence that neuronal differentiation, dendrogenesis, and axonal growth and orientation are important features of gyrification (14), in addition with its association with MEF2, HDAC5 makes an interesting candidate for study in gyrification.

MeCP2

Methyl-CpG binding protein 2 (MeCP2) binds methylated DNA and has been implied in long-term gene silencing (321, 322), although recent studies have proposed this protein as a transcriptional modulator, both down- and up-regulating gene expression (323, 324). MeCP2 has at least three transcription variants (325), and their transcription levels are tissue-dependent (326). MeCP2 is involved in a wide array of neurological syndromes, which depend on the severity of the loss of function of the gene (323), and is the main gene associated with Rett Syndrome, a rare disease affecting mainly women, and characterised for loss of language and motor skills, among other symptoms (276, 322, 325). However, given that this syndrome is evident during childhood development, most of what we know about MeCP2 is concentrated during postnatal development.

MeCP2 controls neuronal differentiation (243), dendritic growth and maturation (244), and its expression is enriched in post-mitotic neurons in the central nervous system (243). MeCP2 expression also correlates with CNS maturity (325), while its deletion leads to impaired learning and memory (327). Interestingly, loss of MeCP2 at juvenile and adult stages also leads to shrinkage of the brain, as MeCP2 is critical for maintaining mature neuronal connections and overall neuron and brain structure (328).

Interestingly, MeCP2 has been associated with polymicrogyria (245), and pathways controlling MeCP2 are altered in ASD individuals (329), which usually display alterations in gyrification (252, 253). These observations make MeCP2 a very promising candidate for an active role during gyrification development.

NeuroD6

Neuronal Differentiation 6 (NeuroD6, also called Math2 or Nex1) is an important transcription factor implied in neuronal differentiation (246), neurite regrowth (247) and neuron survival (248, 249), and during apical-to-basal progression in neuronal progenitor cells (330).

During embryonic development, NeuroD6 is selectively expressed in post-mitotic pyramidal neurons of the dorsal telencephalon (331, 332), and neocortical projections are disrupted in absence of it (333). Therefore, NeuroD6 is an important regulator of axonal genesis in the neocortex (333). Also, cell lines constitutively expressing NeuroD6 upregulate genes related to neuronal differentiation and cell cycle arrest (248).

NeuroD6 expression is upregulated in differentiating neurons in early stages of brain neurogenesis, and this expression is maintained during later stages of neuron maturation (330).

Interestingly, NeuroD6 binds the *trkB* gene promoter, which is involved in the Nerve Growth Factor (NGF) and BDNF signalling pathway, therefore suggesting that NeuroD6 and BDNF might share similar downstream effects (249). In addition, NeuroD6 has been shown critical in the NGF signalling pathway promoting neurite outgrowth (247), and cell lines overexpressing NeuroD6 imitate NGF effects on differentiation and survival (247, 334).

Considering that in human, NeuroD6 expression starts increasing towards the second semester of gestation, some weeks before gyrification starts (335), and, again, some of the processes controlled by NeuroD6 like neuronal differentiation, dendrogenesis, and axonal growth are all important features of gyrification hypothesised to be occurring differentially between gyri and sulci (14), NeuroD6 rises as an interesting candidate for studying during gyrification.

The literature hereby presented makes the aforementioned genes interesting candidates for validation between gyri and sulci, as they may be underlying a metabolic process that could be differential between these regions during gyrification. Considering the results we got from Study 1 were obtained comparing only one gyrus and one sulcus in only one region of the brain (CX2), we decided to explore whether these differences in gene expression were not only valid between gyri and sulci in this region, but also present consistently between gyri and sulci throughout the cerebral cortex during gyrification (GA 90). Additionally, we also decided to explore whether these differences in expression between different zones of the CP could be seen before gyrification (GA 70) and after the main changes in gyrification occurred (post-gyrification, GA 110).

Methods

Please refer to sections 2.1, 2.6, 2.7, 2.8, 2.11 and 2.12 for the detailed methodology corresponding to this study.

Results

Genetic expression between gyri and sulci tCP during gyrification

We addressed the average density of BDNF- (Figure 16), CDK5- (Figure 18), and NeuroD6-positive (Figure 20) cells between multiple gyri and sulci throughout the sheep brain at GA 90 using immunohistochemical approaches. We also addressed the level of HDAC5 (Figure 22), MeCP2 (Figure 24) mRNA expression density based on the average number of mRNA molecules detected per area unit between gyri and sulci at this developmental stage, using a fluorescent *in situ* hybridisation approach.

During gyrification, both gyri and sulci throughout the cortex showed marked ~~expression~~ differences. Gyri displayed higher BDNF (1294 ± 67.06 positive cells/mm^2), CDK5 (398.6 ± 15.18 positive cells/mm^2), and NeuroD6 (1607 ± 142.8 positive cells/mm^2) average positive cell density, but with lower HDAC5 (486.2 ± 106.1 mRNA molecules/mm^2), and MeCP2 (1145 ± 83.04 mRNA molecules/mm^2) average mRNA expression density. Sulci, on the contrary, showed the opposing pattern: lower BDNF (207.8 ± 73.38 positive cells/mm^2), CDK5 (105.5 ± 8.793 positive cells/mm^2), and NeuroD6 (663.4 ± 102.3 positive cells/mm^2) average positive cell density, but higher HDAC5 (1387 ± 323.6 mRNA molecules/mm^2), and MeCP2 (1751 ± 177.7 mRNA molecules/mm^2) average mRNA expression density.

We then performed a two-way ANOVA ~~analyses~~ to determine whether these differences in positive cell or mRNA expression density levels both between gyri and sulci and rostro-caudally throughout the cerebral cortex was statistically significant. Confirming our previous results, there were major differences between gyri and sulci. We consistently found higher BDNF- ($F(1, 40) = 42.95$, $p < 0.0001$, Figure 16, panel 4B), CDK5- ($F(1, 40) = 44.26$, $p < 0.0001$, Figure 18, panel 4B), and NeuroD6-positive cell density in gyri compared to sulci ($F(1, 40) = 15.31$, $p < 0.001$, Figure 20, panel 4B). In contrast, we found lower mRNA expression density in gyri compared to sulci for both HDAC5 ($F(1, 40) = 11.06$, $p < 0.01$, Figure 22, panel 4B), and MeCP2 ($F(1, 40) = 14.38$, $p < 0.001$, Figure 24, panel 4B). Post-hoc analyses, however, showed statistically significant differences between gyri and sulci only for BDNF (CX2 (adjusted p = 0.0499), CX3 (adjusted p = 0.0146), CX4 (adjusted p = 0.0076) and CX5 (adjusted p = 0.0146)), CDK5 (CX2 (adjusted p = 0.0450), CX3 (adjusted p = 0.0131), CX4 (adjusted p = 0.0152) and CX5 (adjusted p = 0.0134)), and HDAC5 (CX5 (adjusted p = 0.0178)). These results show a consistent genetic difference between gyri and sulci tCP, adding to our previous results obtained through *in silico* approaches. This consistency can be further appreciated in the

evaluation of the log_2 gyri/sulci ratios for either BDNF (Figure 17, panel 1A), CDK5 (Figure 19, panel 1A), and NeuroD6 (Figure 21, panel 1A) average positive cell densities, and HDAC5 (Figure 23, panel 1A), and MeCP2 (Figure 25, panel 1A) average mRNA expression densities, with only a few exceptions. Log_2 ratios represent a different visual interpretation of the data for exploring how the biological variability in the differences between gyri and sulci levels of either mRNA expression or positive cell density per individuals could impact the data and the conclusions. Therefore, these results strongly suggest that, despite the inherent biological variation in the levels of either mRNA expression or positive cell density between individuals, the gyri-to-sulci effect is indeed substantial and statistically significant.

Nonetheless, rostro-caudally, the analyses showed no differences between the different sections of the brain for neither BDNF ($F(4, 40) = 0.4931$, $p = 0.7408$), CDK5 ($F(4, 40) = 0.2291$, $p = 0.9205$), NeuroD6 ($F(4, 40) = 0.9595$, $p = 0.4402$), HDAC5 ($F(4, 40) = 1.870$, $p = 0.1347$), nor MeCP2 ($F(4, 40) = 2.485$, $p = 0.0588$), showing the levels of positive cell density and mRNA expression for the analysed genes were consistent throughout the tCP during gyrification.

Our investigations regarding the differential expression of BDNF, CDK5, NeuroD6, HDAC5 and MeCP2 during gyrification led us to enquire whether these differences between different zones of the tCP could be observed before (GA 70) and after (GA 110) gyrification. We hypothesised that the differences we found during gyrification were not seen before this process started, but were sustained between gyri and sulci after cortical folding was mainly completed.

Genetic expression throughout the eCP before gyrification

Considering no gyri or sulci can be observed before gyrification (GA 70), we took six different regions of the eCP and compared them. Again, we addressed the average BDNF- (Figure 16), CDK5- (Figure 18), and NeuroD6-positive cell density (Figure 20), and the level of HDAC5 (Figure 22), MeCP2 (Figure 24) mRNA expression density.

At this developmental stage, all regions analysed showed similar BDNF (659.40 ± 39.40 positive cells/mm^2), CDK5 (33.15 ± 5.99 positive cells/mm^2), and NeuroD6 (369.02 ± 65.24 positive cells/mm^2) positive cell density levels, with also similar HDAC5 (683.47 ± 43.34 mRNA molecules/mm^2), and MeCP2 (505.43 ± 35.78 mRNA molecules/mm^2) mRNA expression density levels.

As hypothesised, there were no differences between the six regions of eCP analysed for neither BDNF ($F(5, 72) = 0.09687$, $p = 0.9924$, Figure 16, panel 4A), CDK5 ($F(5, 72) = 0.1315$, $p = 0.9847$, Figure 18, panel 4A), NeuroD6 ($F(5, 72) = 0.2493$, $p = 0.9388$, Figure 20, panel 4A), HDAC5 ($F(5, 72) = 0.2877$, $p= 0.9184$, Figure 22, panel 4A) nor MeCP2 ($F(5, 72) = 0.2204$, $p = 0.9527$, Figure 24, panel 4A), showing consistent homogeneity throughout the eCP at this developmental stage.

Again, there were also no differences rostro-caudally for neither BDNF ($F(2, 72) = 0.4481$, $p = 0.6406$), CDK5 ($F(2, 72) = 0.6878$, $p = 0.5060$), NeuroD6 ($F(2, 72) = 1.843$, $p = 0.1658$), HDAC5 ($F(2, 72) = 0.7433$, $p = 0.4792$) nor MeCP2 ($F(2, 72) = 0.7306$, $p = 0.4851$), showing again the consistency of the eCP throughout the eCP before gyrification.

Genetic expression between gyri and sulci cortex after gyrification

Finally, we addressed the average BDNF- (Figure 16), CDK5- (Figure 18), and NeuroD6- (Figure 20) positive cell density, and the level of HDAC5 (Figure 22), MeCP2 (Figure 24) mRNA expression density between gyri and sulci cortex after gyrification was mainly complete, at GA 110.

We hypothesised that the differences seen at GA 90 between gyri and sulci tCP would be sustained at GA 110 as a permanent feature of gyri and sulci. However, only BDNF sustained a gyri-to-sulci difference in positive cell density (gyri: 497.3 ± 72.98 positive cells/mm^2, sulci: 283.4 ± 24.49 positive cells/mm^2, $F(1, 64) = 22.84$, $p < 0.0001$, Figure 16, panel 4C), while this difference was lost for CDK5 (gyri: 195.4 ± 22.23 positive cells/mm^2, sulci: 140.9 ± 17.59 positive cells/mm^2, $F(1, 64) = 3.392$, $p = 0.0701$, Figure 18, panel 4C), NeuroD6 (gyri: 460.71 ± 120.73 positive cells/mm^2, sulci: 433.16 ± 116.86 positive cells/mm^2, $F(1, 64) = 0.1870$, $p = 0.6669$, Figure 20, panel 4C), HDAC5 (gyri: 312.3 ± 38.63 mRNA molecules/mm^2, sulci: 291.2 ± 26.92 mRNA molecules/mm^2, $F(1, 64) = 0.3003$, $p = 0.5856$, Figure 22, panel 4C) and MeCP2 (gyri: 243.5 ± 12.6 mRNA molecules/mm^2, sulci: 240.8 ± 27.53 mRNA molecules/mm^2, $F(1, 64) = 0.01013$, $p = 0.9202$, Figure 24, panel 4C). Post-hoc analyses showed statistically significant differences between gyri and sulci, again, only for BDNF in the rostral portion of the brain (CX1, adjusted $p = 0.0021$; CX2, adjusted $p = 0.0326$). The differences in consistency can be further appreciated in the distribution of the $\log_2$ gyri/sulci ratios for BDNF (Figure 17, panel 2A), CDK5 (Figure 19, panel 2A), and NeuroD6 (Figure 21, panel 2A) average positive cell densities, or HDAC5 (Figure 23, panel 2A), and MeCP2 (Figure 25, panel 2A) average mRNA expression densities, showing that the consistent gyri-to-sulci effect observed at GA 90 is lost at this later developmental stage.

However, at this developmental stage two genes showed rostro-caudal differences in positive cell density in the cortex. Both BDNF ($F(7, 64) = 4.390$, $p = 0.0005$) and NeuroD6 ($F(7, 64) = 4.261$, $p = 0.0006$) showed differential expression throughout the rostro-caudal axis, although BDNF showed higher positive cell density towards the rostral side of the cortex (CX1 = 667.15 ± 54.51 positive cells/mm^2, CX2 = 444.10 ± 35.53 positive cells/mm^2, Figure 16, panel 4C), while NeuroD6 showed increased positive cell density towards the caudal side (CX8 = 859.15 ± 197.63 positive cells/mm^2, Figure 20, panel 4C). In contrast, CDK5 ($F(7, 64) = 1.598$, $p = 0.1522$, Figure 18, panel 4C), HDAC5 ($F(7, 64) = 1.762$, $p = 0.1107$, Figure 22, panel 4C) and MeCP2 ($F(7, 64) = 1.311$, $p = 0.2597$, Figure 24, panel 4C) did not show rostro-caudal differences in positive cell density or mRNA expression density.

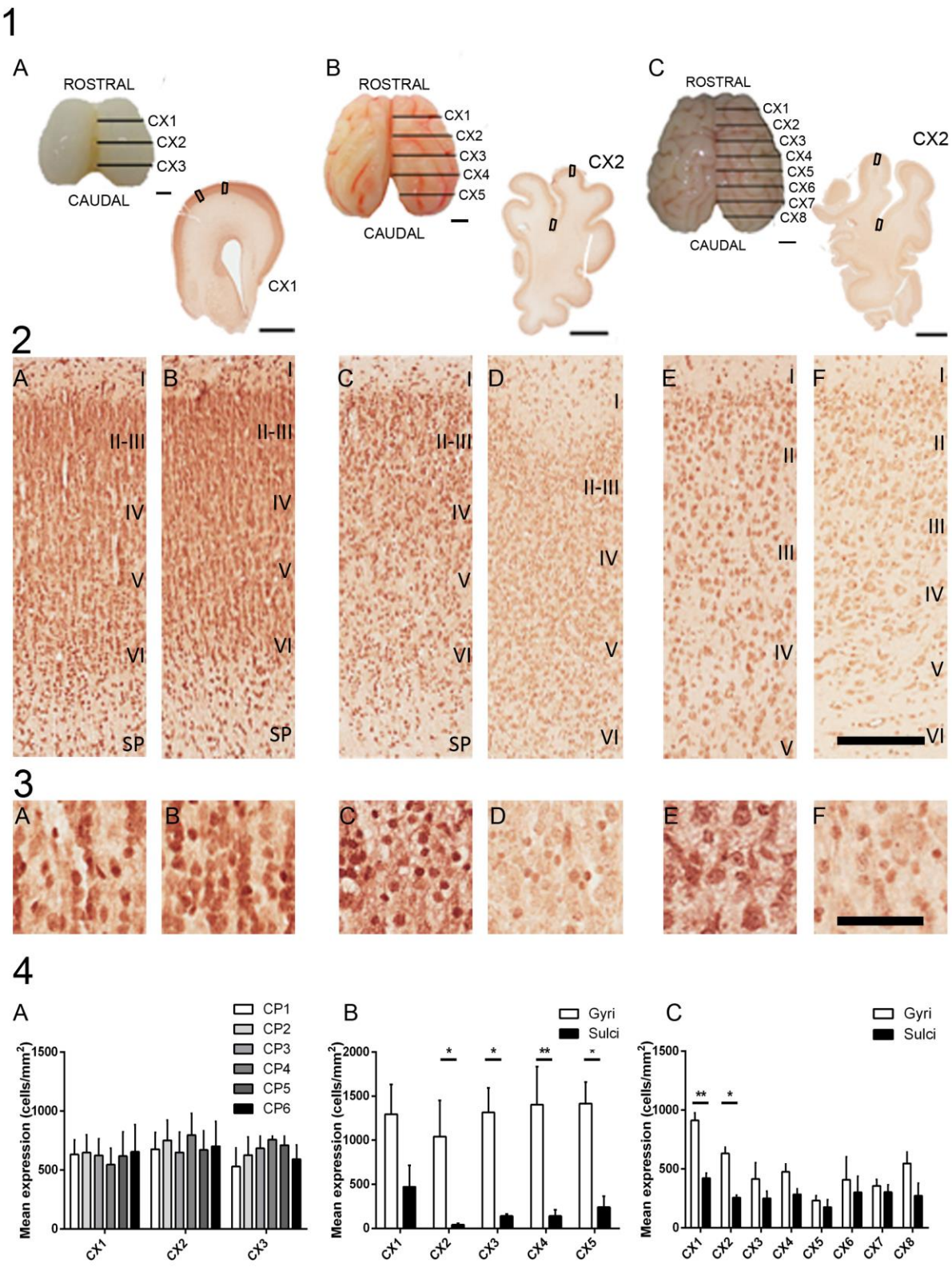


Figure 16. BDNF expression in the eCP/tCP/cortex during gyrification. Immunohistochemistry analysis for BDNF expression in the fetal sheep brain eCP/tCP/cortex at GA 70, 90 and 110. 1: Diagrams showing brain sections analysed at GA 70 (A), 90 (B) and 110 (C), and a representative brain section. 2, 3:. Immunohistochemistry analysis of BDNF expression in the eCP at GA 70 (A-B), and between gyri (C,E) and sulci tCP/cortex (D,F) at GA 90 (C-D) and 110 (E-F). 4: Mean BDNF positive cell density in the eCP throughout the brain at GA 70 (A), and between gyri and sulci tCP/cortex at GA 90 (B) and 110 (C). Bars are means ± SEM. *: $p < 0.05$; **: $p < 0.01$. n = 5. Bars in 1A: 3 mm, 1B: 4 mm; 1C: 5 mm; 2(A-F): 200 µm; 3(A-F): 50 µm.

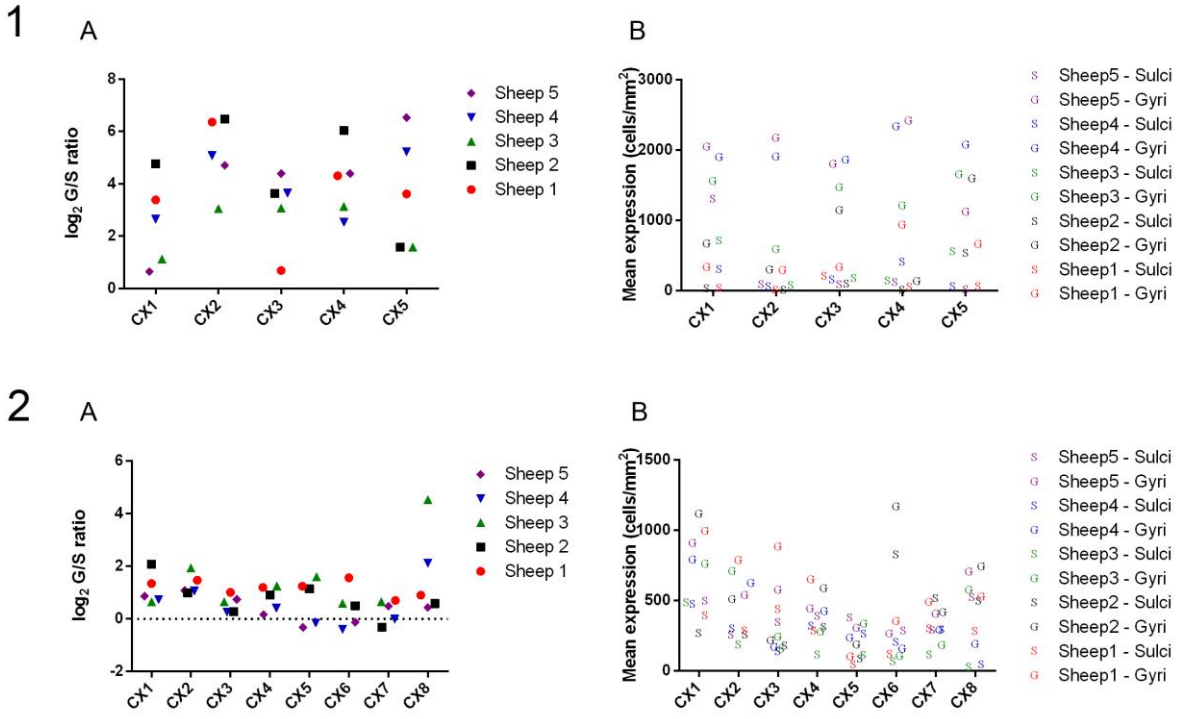


Figure 17. BDNF expression. BDNF expression at 1) GA 90 and 2) GA 110 between gyri and sulci. A. Log_2 values of BDNF expression ratios between gyri and sulci plotted for each individual sheep analysed, per brain section. B. Means obtained for BDNF expression for gyri (G) and sulci (S) for every individual sheep analysed, per brain section.

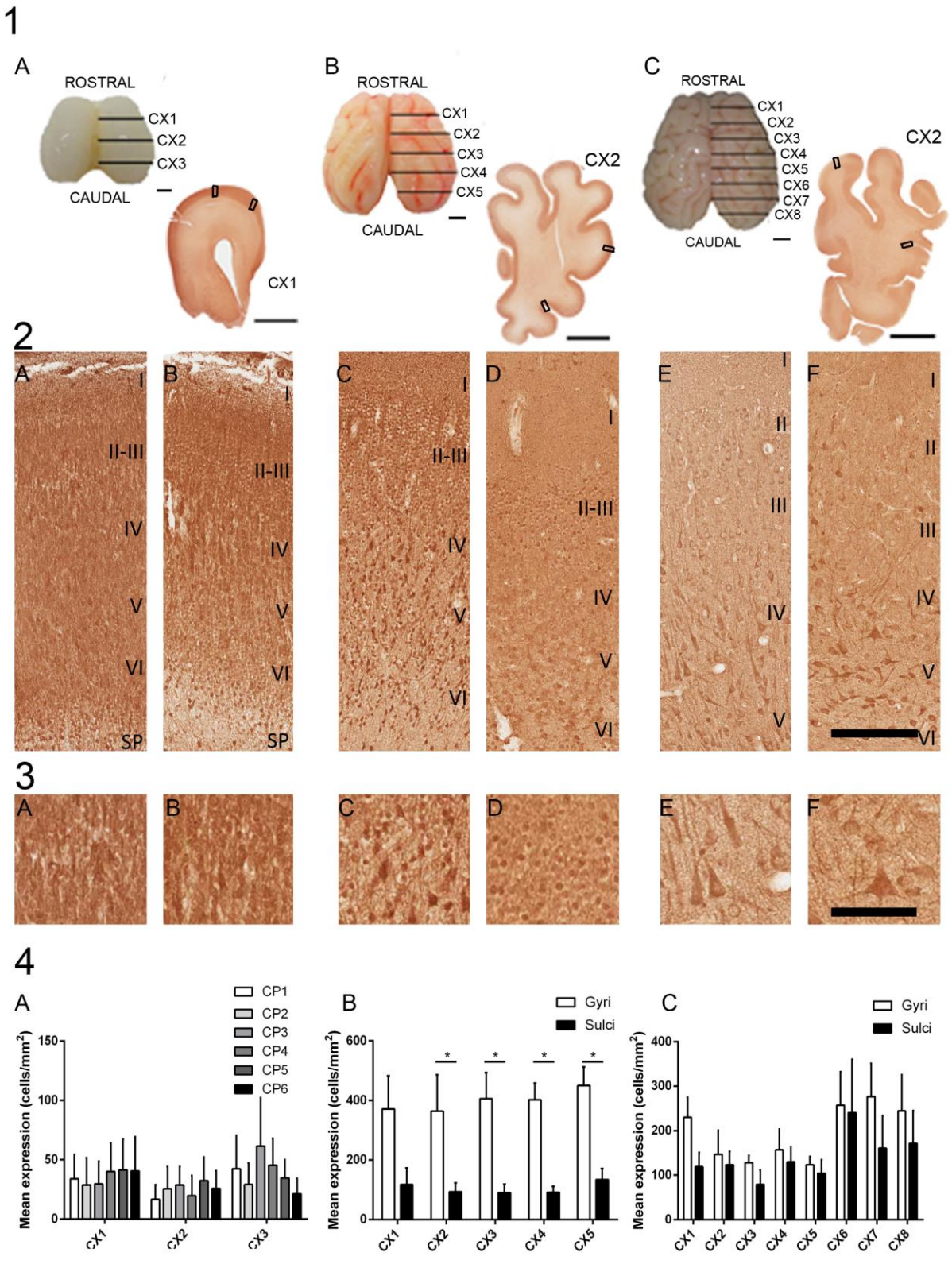


Figure 18. CDK5 expression in the eCP/tCP/cortex during gyrification. Immunohistochemistry analysis for CDK5 expression in the fetal sheep brain eCP/tCP/cortex at GA 70, 90 and 110. 1: Diagrams showing brain sections analysed at GA 70 (A), 90 (B) and 110 (C), and a representative brain section. 2, 3:. Immunohistochemistry analysis of CDK5 expression in the eCP at GA 70 (A-B), and between gyri (C,E) and sulci tCP/cortex (D,F) at GA 90 (C-D) and GA 110 (E-F). 4: Mean CDK5 positive cell density in the eCP throughout the brain at GA 70 (A), and between gyri and sulci tCP/cortex at GA 90 (B) and GA 110 (C). Bars are means ± SEM. *: $p < 0.05$. n = 5. Bars in 1A: 3 mm, 1B: 4 mm; 1C: 5 mm; 2(A-F): 200 µm; 3(A-F): 50 µm.

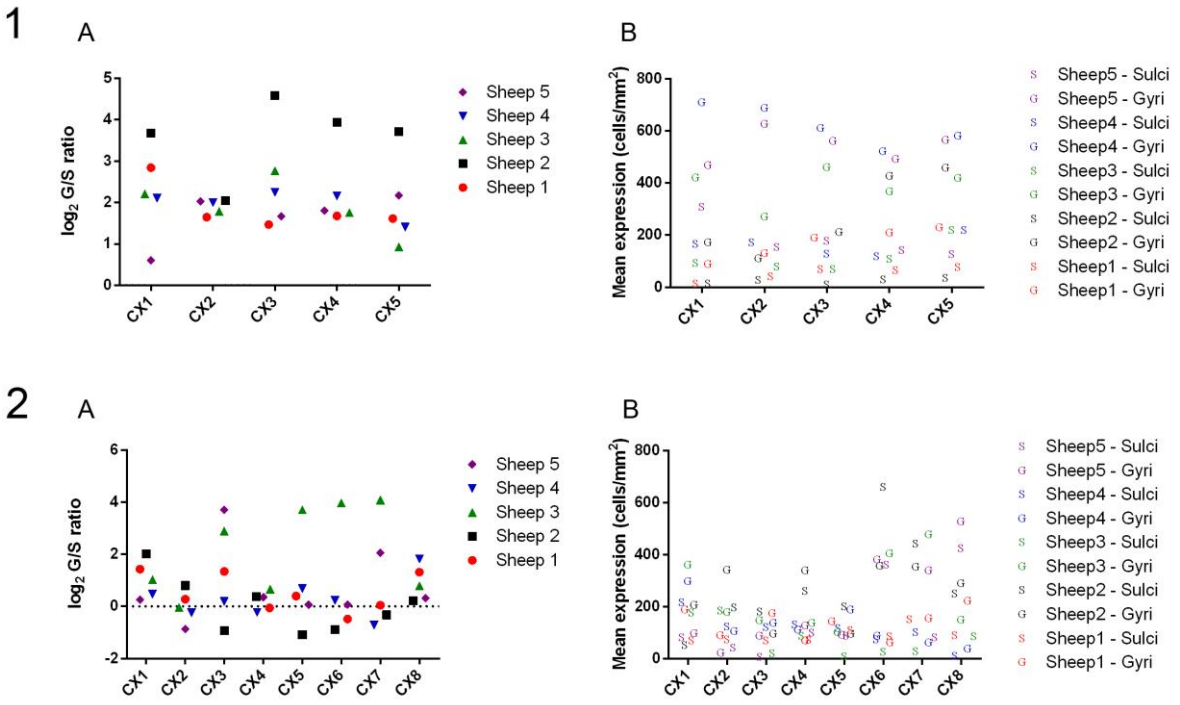


Figure 19. CDK5 expression. CDK5 expression at 1) GA 90 and 2) GA 110 between gyri and sulci. A. Log_2 values of CDk5 expression ratios between gyri and sulci plotted for each individual sheep analysed, per brain section. B. Means obtained for CDK5 expression for gyri (G) and sulci (S) for every individual sheep analysed, per brain section.

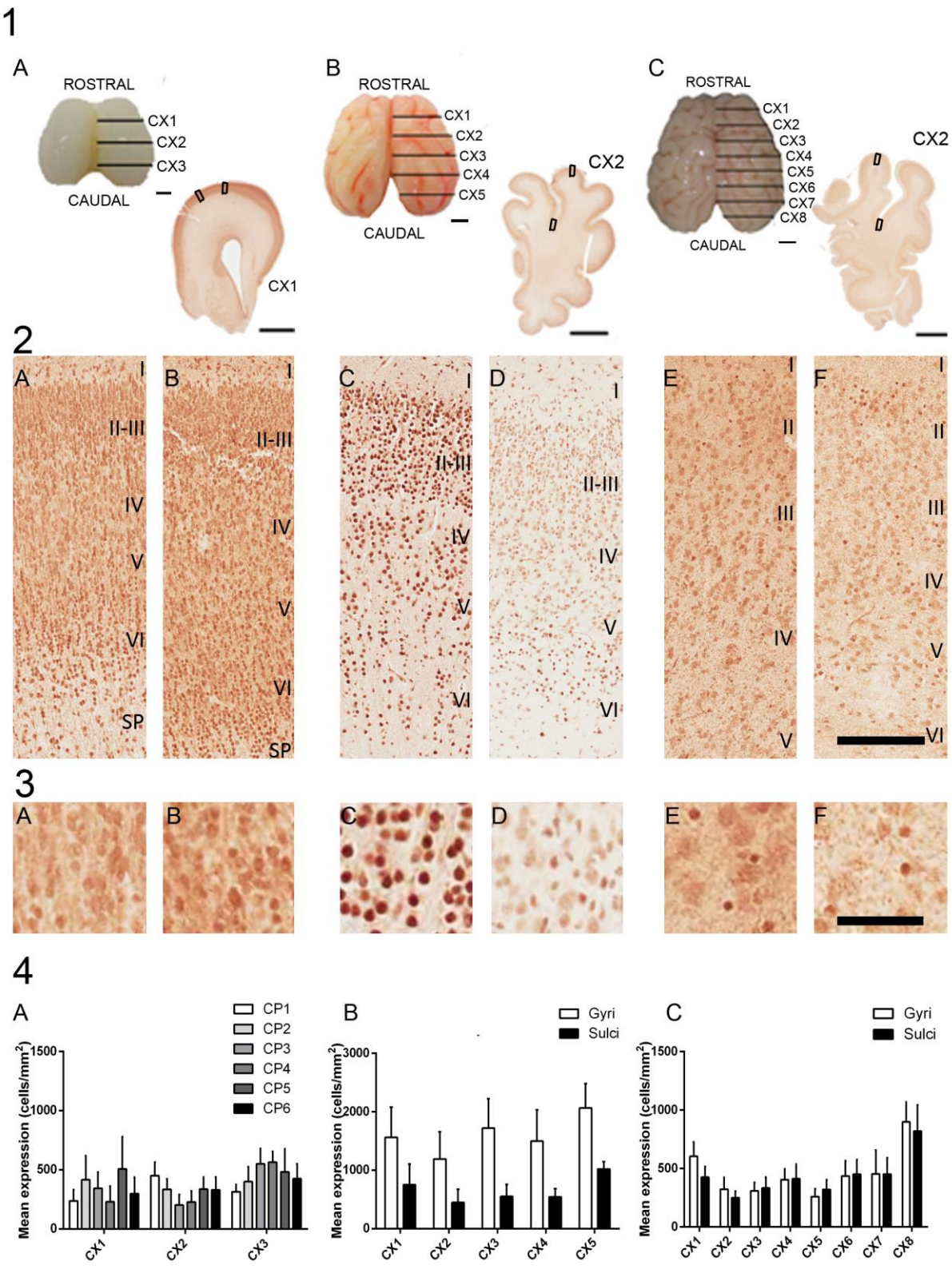


Figure 20. NeuroD6 expression in the eCP/tCP/cortex during gyrification. Immunohistochemistry analysis for NeuroD6 expression in the fetal sheep brain eCP/tCP/cortex at GA 70, 90 and 110. 1: Diagrams showing brain sections analysed at GA 70 (A), 90 (B) and 110 (C), and a representative brain section. 2, 3:. Immunohistochemistry analysis of NeuroD6 expression in the eCP at GA 70 (A-B), and between gyri (C,E) and sulci tCP/cortex (D,F) at GA 90 (C-D) and 110 (E-F). 4: Mean NeuroD6 positive cell density in the eCP throughout the brain at GA 70 (A), and between gyri and sulci tCP/cortex at GA 90 (B) and 110 (C). Bars are means ± SEM. *: $p < 0.05$. n = 5. Bars in 1A: 3 mm, 1B: 4 mm; 1C: 5 mm; 2(A-F): 200 µm; 3(A-F): 50 µm.

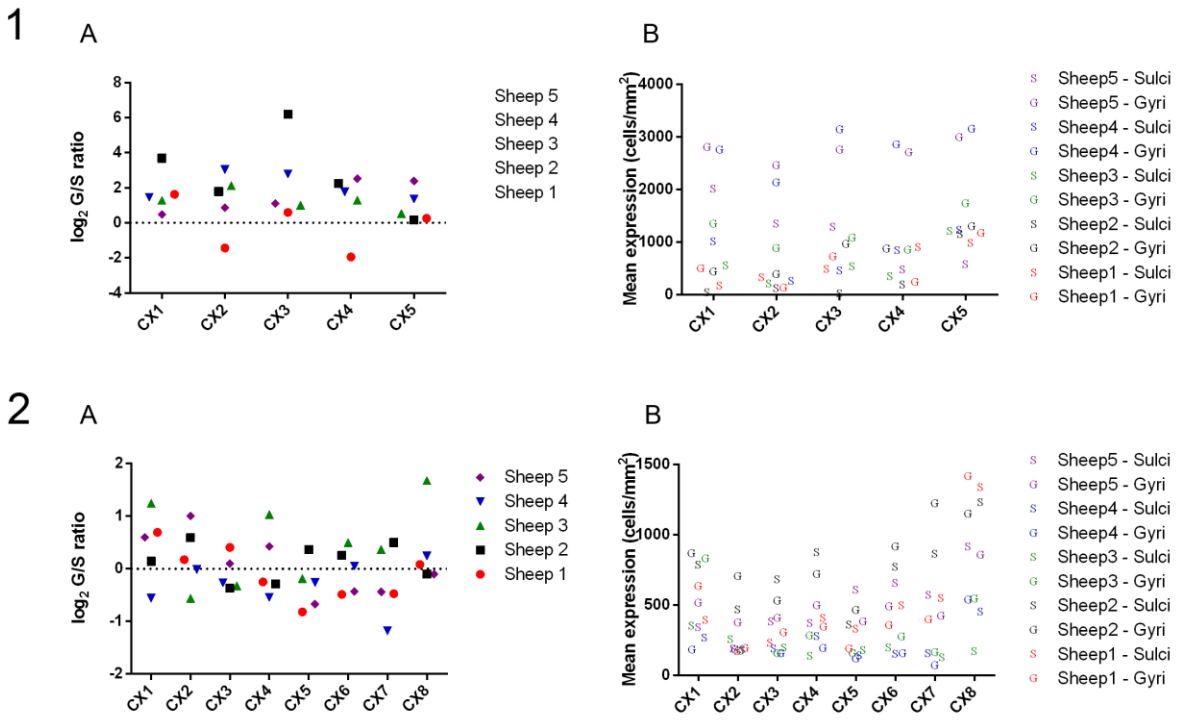


Figure 21. NeuroD6 expression. NeuroD6 expression levels at 1) GA 90 and 2) GA 110 between gyri and sulci. A. Log_2 values of NeuroD6 expression level ratios between gyri and sulci plotted for each individual sheep analysed, per brain section. B. Means obtained for NeuroD6 expression levels for gyri (G) and sulci (S) for every individual sheep analysed, per brain section.

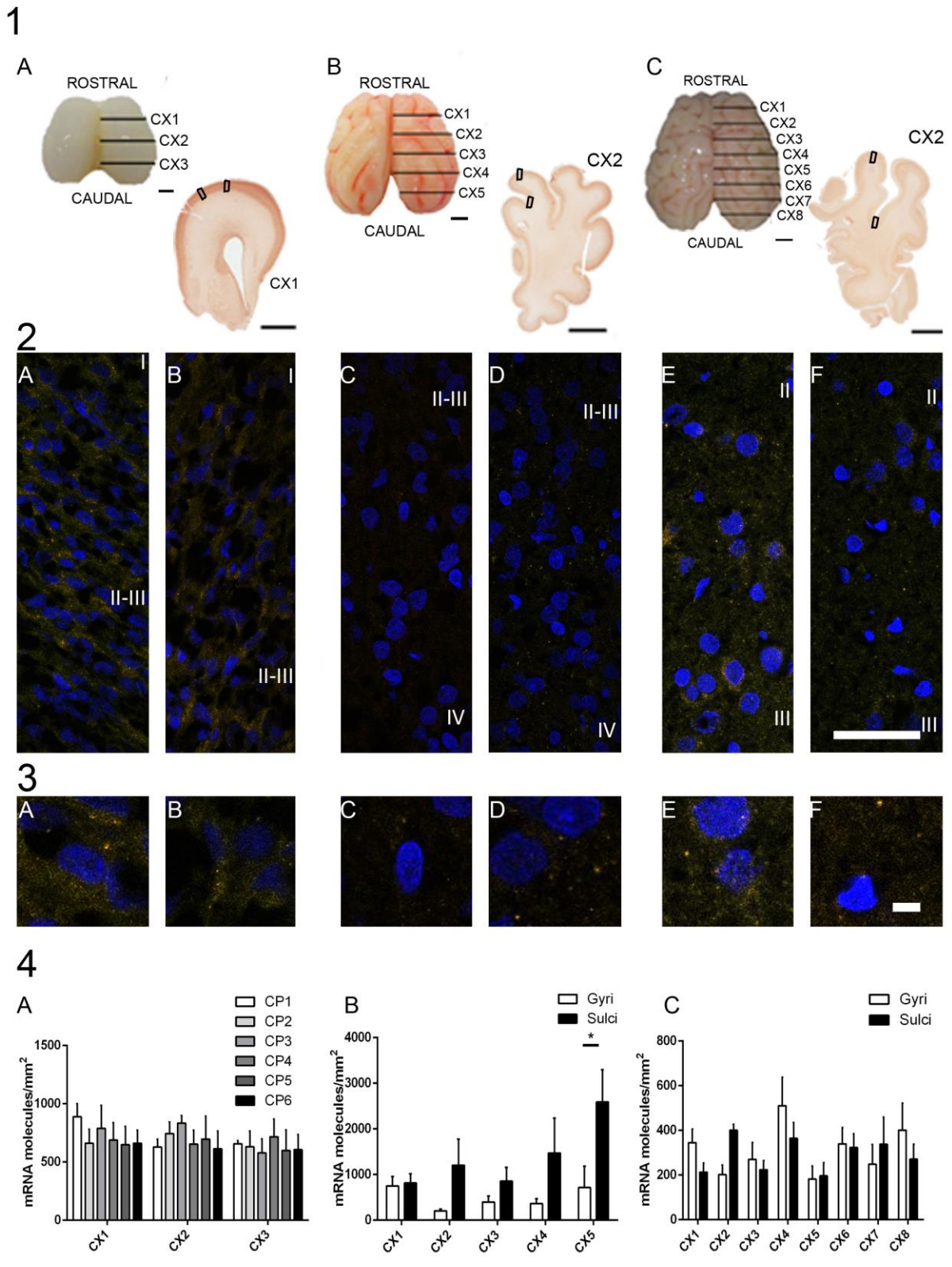


Figure 22. HDAC5 transcription in the eCP/tCP/cortex during gyrification. Fluorescent in situ hybridisation (FISH) analysis for HDAC5 transcription in the fetal sheep brain eCP/tCP/cortex at GA 70, 90 and 110. 1: Diagrams showing brain sections analysed at GA 70 (A), 90 (B) and 110 (C), and a representative brain section. 2, 3:. FISH analysis of HDAC5 transcription in the eCP at GA 70 (A-B), and between gyri (C,E) and sulci tCP/cortex (D,F) at GA 90 (C-D) and 110 (E-F). 4: Mean HDAC5 mRNA expression density in the eCP throughout the brain at GA 70 (A), and between gyri and sulci tCP/cortex at GA 90 (B) and 110 (C). Bars are means ± SEM. *: $p < 0.05$. n = 5. Bars in 1A: 3 mm, 1B: 4 mm; 1C: 5 mm; 2(A-F): 50 µm; 3(A-F): 5 µm. FISH images have been enhanced for visualisation purposes.

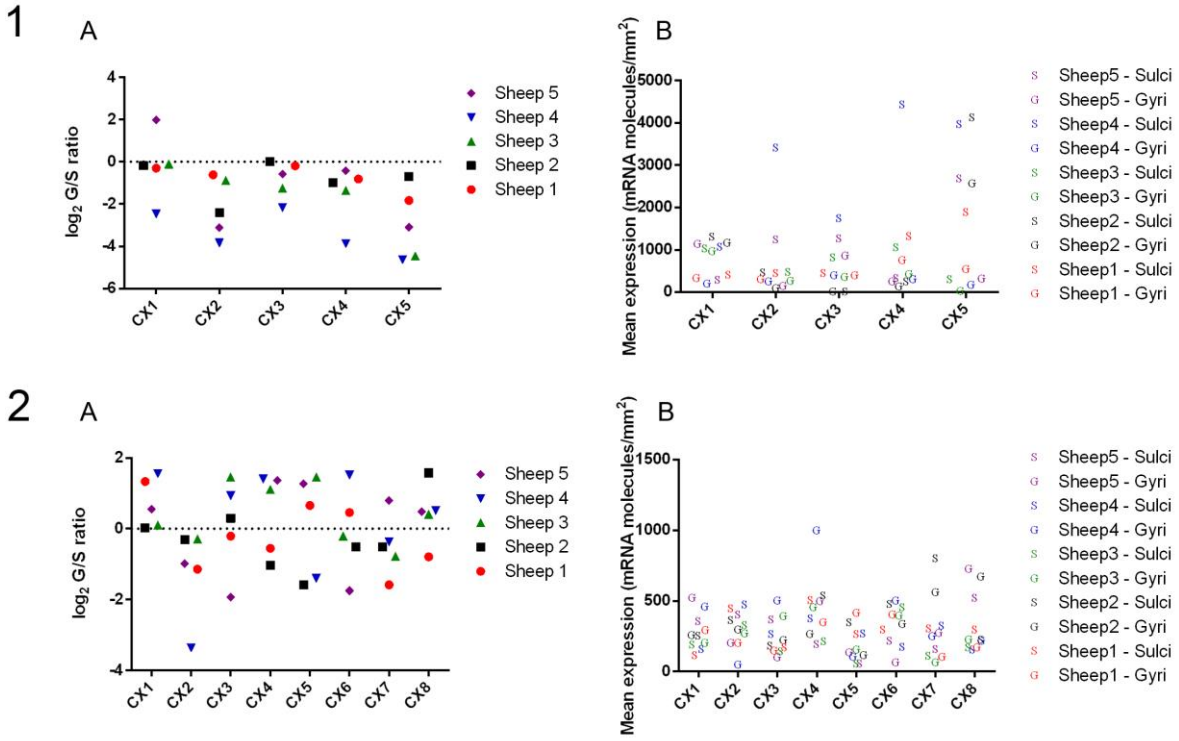


Figure 23. HDAC5 transcription. HDAC5 transcriptions levels at 1) GA 90 and 2) GA 110 between gyri and sulci. A. Log_2 values of HDAC5 transcription level ratios between gyri and sulci plotted for each individual sheep analysed, per brain section. B. Means obtained for HDAC5 transcription levels for gyri (G) and sulci (S) for every individual sheep analysed, per brain section.

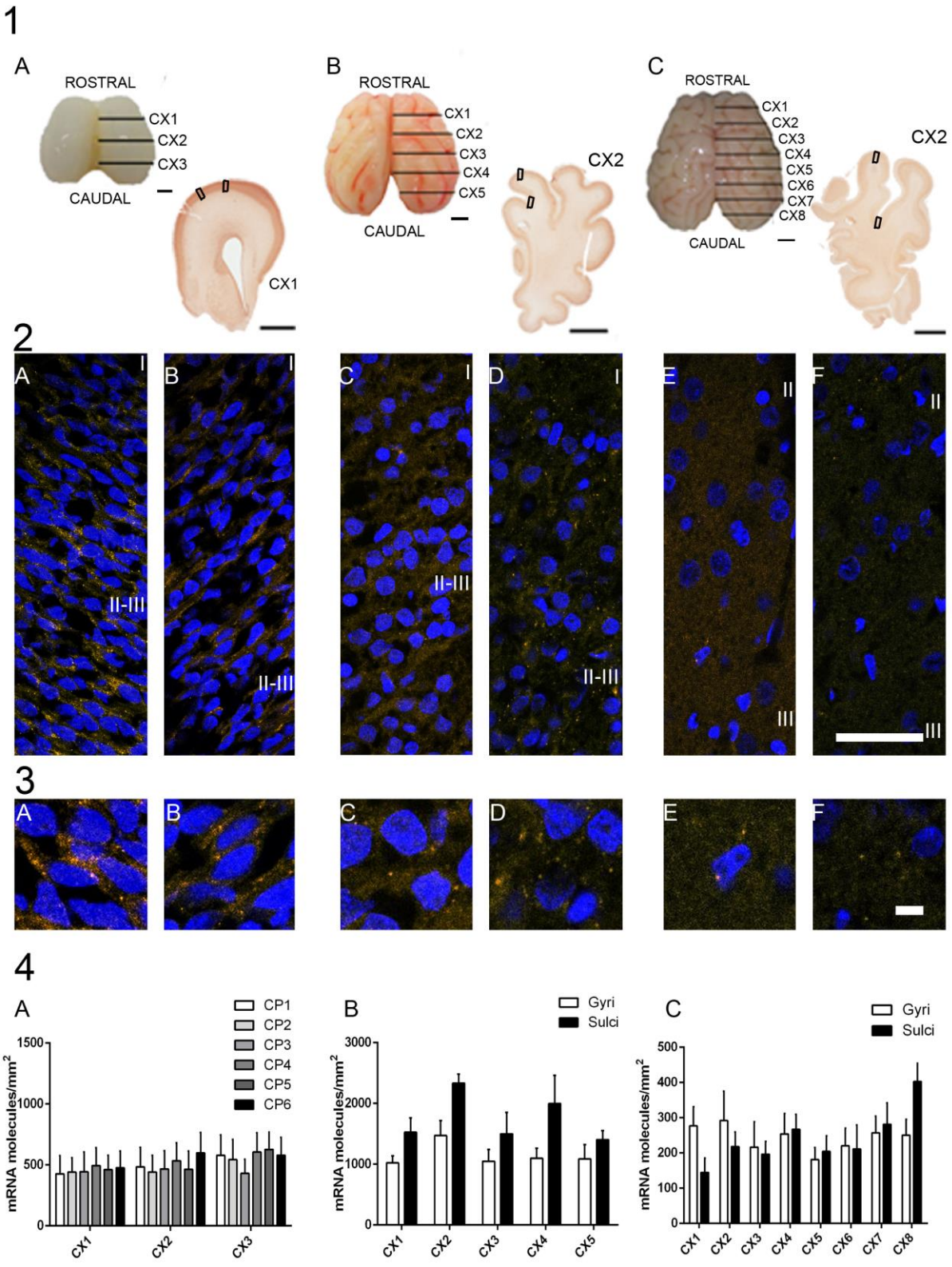


Figure 24. MeCP2 transcription in the eCP/tCP/cortex during gyrification. Fluorescent in situ hybridisation (FISH) analysis for MeCP2 transcription in the fetal sheep brain eCP/tCP/cortex at GA 70, 90 and 110. 1: Diagrams showing brain sections analysed at GA 70 (A), 90 (B) and 110 (C), and a representative brain section. 2, 3:. FISH analysis of MeCP2 transcription in the eCP at GA 70 (A-B), and between gyri (C,E) and sulci tCP/cortex (D,F) at GA 90 (C-D) and 110 (E-F). 4: Mean MeCP2 mRNA expression density in the eCP throughout the brain at GA 70 (A), and between gyri and sulci tCP/cortex at GA 90 (B) and 110 (C). Bars are means ± SEM. *: $p < 0.05$. n = 5. Bars in 1A: 3 mm, 1B: 4 mm; 1C: 5 mm; 2(A-F): 50 µm; 3(A-F): 5 µm. FISH images have been enhanced for visualisation purposes.

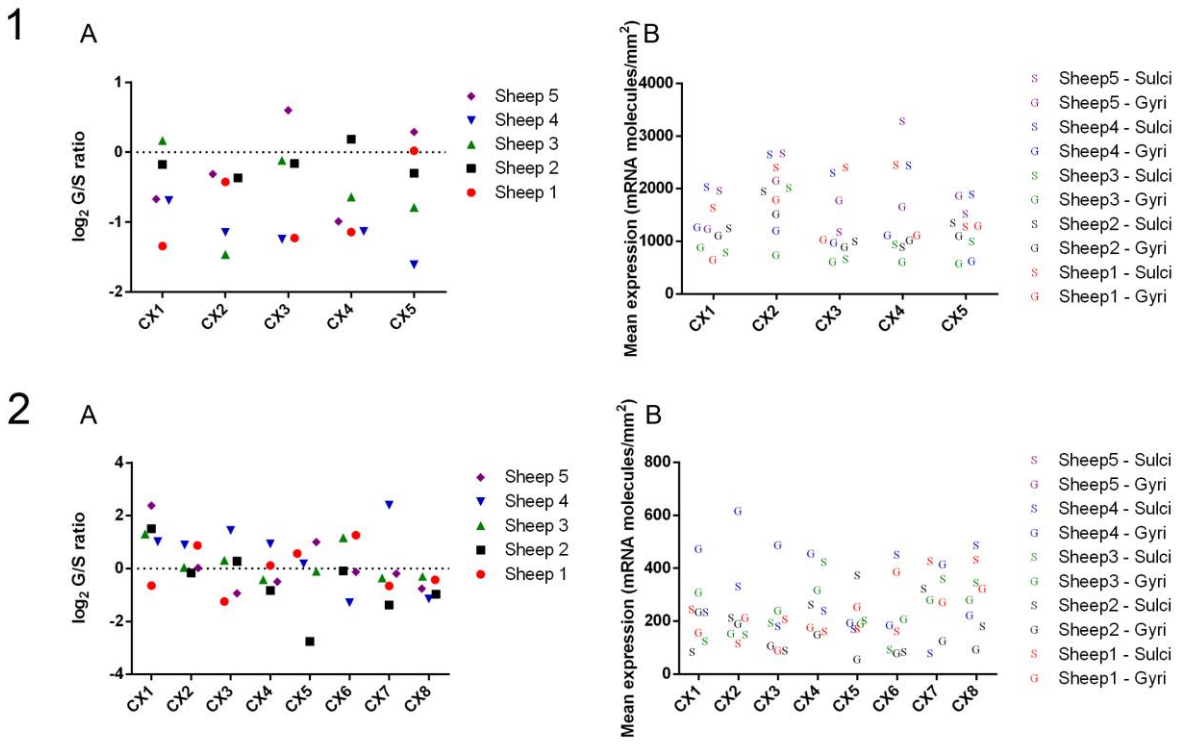


Figure 25. MeCP2 transcription. MeCP2 transcriptions levels at 1) GA 90 and 2) GA 110 between gyri and sulci. A. Log_2 values of MeCP2 transcription level ratios between gyri and sulci plotted for each individual sheep analysed, per brain section. B. Means obtained for MeCP2 transcription levels for gyri (G) and sulci (S) for every individual sheep analysed, per brain section.

Discussion and Conclusion

This study evaluated the positive cell density levels of BDNF, CDK5, and NeuroD6, and the mRNA expression density levels of HDAC5 and MeCP2 in the sheep tCP between gyri and sulci throughout the cerebral cortex during gyrification (GA 90), to validate our *in silico* results and hypotheses. It then expanded these results to the eCP before (GA 70) and the cortex after (GA 110) gyrification. However, given that no gyri or sulci can be observed before gyrification, the eCP was randomly sampled at different places to compare differences in expression and transcription.

The expression of these genes was ubiquitous throughout the cortex at every developmental stage. However, we found that the positive cell densities or mRNA expression densities of these genes, although changing throughout gyrification, follow a similar trend: they are lower before gyrification, peak during this process and lower again after the process is completed. Our evidence partly agrees with previous studies showing increasing expression of BDNF (336-338), CDK5 (305, 339, 340) and NeuroD6 (341), and increased transcription of MeCP2 (342) concomitantly with maturation of the brain at similar developmental stages. However, our results show that the positive

cell densities of BDNF, CDK5 and NeuroD6, and the mRNA expression densities of HDAC5 and MeCP2 diminish after gyrification. The pattern of positive cell density of NeuroD6 observed in sheep holds similarities with reports in mice, in which transcription increases as the brain matures, and then decreases, albeit this final decrease is seen post-natally (341). This difference in the timing of the NeuroD6 transcription and expression patterns might reflect a species-specific timing of cerebral cortex maturation. HDAC5 at fetal stages in the cortex has also been reported (343), but to our knowledge the patterns of expression throughout the fetal cortex have not been addressed. Nonetheless, this general pattern of positive cell density and mRNA expression density decrease after gyrification could be due to a combined effect partly due to the dispersion of the neurons in the cortex –which is a feature of the maturing cortex–, therefore decreasing the number of cells per area unit, and partly due to a decrease in the number of positive cells, which can be observed in some regions. This decrease in the number of positive signal per area in the developing cortex has been reported for at least BDNF (337) and CDK5 (339). It is also possible that these discrepancies could be due to differences in the analytical procedures used (e.g. positive cells per area versus gene mRNA per total RNA).

However, the most interesting feature of the tCP during gyrification was the difference in positive cell densities and mRNA expression densities between gyri and sulci. We consistently found higher BDNF, CDK5 and NeuroD6 positive cell density in gyri compared to sulci, and lower HDAC5 and MeCP2 mRNA expression density in gyri compared to sulci. This evidence agrees with several studies. CDK5 has been reported enhancing BDNF activity (344), while absence of CDK5 results in reduced BDNF expression (345). NeuroD6 and BDNF have been identified as a co-expressed genes in nervous system development, and NeuroD6 has been proposed to be regulated by similar subset of transcription factors than BDNF (346). This strongly suggests a connection in both BDNF and NeuroD6 expression that might explain the observed expression pattern. Previous studies have also shown lower expression of HDAC5 in line with increased BDNF expression (242, 343), and others have shown dynamic regulation of BDNF expression by CpG methylation (347), which has been shown to be driven at least by MeCP2 (348, 349). This is also consistent with previous reports showing lack of MeCP2 concomitantly with augmented BDNF expression during development (350). And although spatial differences in BDNF distribution had been observed during gyrification stages in previous studies (337), to our knowledge no gyri-to-sulci analyses have been performed previously.

Still, the differences we found during gyrification were not seen in the eCP before gyrification, as hypothesised. However, these genetic differences between gyri and sulci, contrary to our hypothesis, were lost for all genes except BDNF after gyrification. This loss of difference in

expression between gyri and sulci becomes evident when observing the biological variability observing the $\log_2$ gyri/sulci ratios at this stage for CDK5 (Figure 19), NeuroD6 (Figure 21), HDAC5 (Figure 23) and MeCP2 (Figure 25). BDNF was the only gene to show rather consistent gyri-to-sulci differences in expression after gyrification (Figure 17). This biological variation in either the level of positive cell density or mRNA expression density or in the gyri-to-sulci ratio could be responsible for the variation that prevented post-hoc analyses reaching significance, both during and after gyrification for most evaluated cortex regions. This biological variability between individuals has been reported for at least MeCP2 transcription (351).

Interestingly at this later stage (GA 110), we found two genes showing rostro-caudal differences in positive cell density. BDNF showed increased positive cell density towards the rostral side of the cortex, which resembles previous evidence showing differential BDNF expression between lobes in adult human (285). This higher positive cell density in the frontal cortex after gyrification might reflect the delayed maturation of the frontal cortex (352), in which some functions such as memory (279) and inhibitory control (353) have been correlated with BDNF.

NeuroD6 showed increased positive cell density towards the caudal pole. This might suggest a role for NeuroD6 in the development of the visual cortex, which undergoes important changes in late brain development (354). Interestingly, another member of the NeuroD6 family (basic helix-loop-helix), BHLHB5, has been reported more expressed in the occipital lobe compared to the rest of the cortex in the adult human (355), suggesting that NeuroD6 might be found in the same patterns.

Yet, no other genes showed rostro-caudal differences in positive cell density or mRNA expression density. This mimics evidence for HDAC5 in the adult rat brain showing nearly no differences in transcription levels between different parts of the cortex (356), and evidence showing apparently no differences in CDK5 expression rostro-caudally in the development of rat (305) and mouse (357) neocortices. Other studies have shown differential MeCP2 expression in different zones the cerebral cortex (358), and different layers of the cortex (358, 359), but to the best of our knowledge no rostro-caudal analyses have been performed.

Despite our results, this study harbours some shortcomings. The first and most important one is that we never sought to address whether these genetic expression differences are present mainly in neurons, astrocytes, glia or other cells present in the tCP during gyrification, or a combination of them. Our aim was to characterise the differences between gyri and sulci tCP, if any, as a whole, not on a cell type-specific basis. This indeed might mask individual expression differences among these cells that might also be differential between gyri and sulci that indeed are valuable to

uncover. This is worth considering, in the light of recent studies that have proposed that neuronal growth and axonal elongation might be key mechanisms by which the cerebral cortex folds (102); this implicates neurons, rather than glia, as the primary cell type involved in gyrification. By showing that neurons and not glia express BDNF, CDK5, NeuroD6, HDAC5 and MeCP2 in the tCP of the fetal sheep brain, this would enable us to more confidently conclude that it is the differential expression of these neuron-specific genes that contributes to cortical folding in our study. Nonetheless, our results help to understand a possible general trend that might explain a tissue region behaviour. Further studies are needed to uncover the full extent of the genetic differences not only between the different cell types present in the tCP during gyrification, but also between gyri and sulci as fundamental regions of the tCP that share the common task of driving gyrification correctly.

Another limitation of this study comes from the methodological procedures used. For example, we used an ani-BDNF antibody that recognises both proBDNF and BDNF in its mature form, regardless of the specific exons expressed, in which the number and regulatory units vary among species (281, 285). This raises the possibility that the sheep might have a completely different BDNF expression machinery. Thus, our results account for the complete BDNF expression differences between gyri and sulci eCP/tCP/cortex in the sheep, and dismiss any differences that might be present at a transcriptional, post-transcriptional and post-translational level. We also used FISH probes that recognised conserved regions of the genes regardless of the isoform expressed, therefore our results again dismiss variations in expression among isoforms, which is the case for MeCP2, which has been showed to have different expression levels in the cortex during development in at least two of its known isoforms (342). Again, this masks more subtle differences regarding MeCP2 expression that might be happening in the cortex during the developmental ages addressed. Future studies will be needed to fully dissect the nature of BDNF and MeCP2 expression and regulation between gyri and sulci in the cortex before, during and after gyrification.

Nonetheless, all the evidence collected so far strongly suggests that, at least during gyrification, gyri and sulci undergo differential processes that encompass BDNF, CDK5, NeuroD6, HDAC5 and MeCP2. A strong candidate for this process that might be occurring differentially between gyri and sulci during gyrification is neurite outgrowth. Not only this process has been reported occurring at the same time that gyrification unfolds (197, 360), but also BDNF (244, 344), CDK5 (344, 361), NeuroD6 (247), HDAC5 (242), and MeCP2 (244, 350, 362, 363) have been correlated with it. Furthermore, it falls in line with previous studies proposing gyrification as a function of differential growth between lower and upper layers of the cerebral wall (70, 96, 97, 102), and in line with the differential tangential expansion hypothesis proposed early by Ronan *et al*. (93).

This study, in which differential genetic expression between gyri and sulci tCP have been addressed and concluded, highlights the possibility that differential genetic expression maps through the tCP, as shown before (see Chapter 1), might be one of the missing pieces of the cortical folding theory jigsaw, in which a lot of progress has been obtained in explaining why and how the cerebral cortex folds, but little in explaining why the folding patterns are so consistent. We hypothesise that neurite outgrowth is one of the developmental processes that is differentially regulated between gyri and sulci during gyrification, and that it is one of the main actors driving gyrification in the tCP in a region-dependent fashion.

Chapter 5 – Neurite outgrowth in gyri and sulci during gyrification in fetal sheep

Rationale

As reported in Study 2, there were consistent differences in gene expression in the tCP of gyri and sulci of the sheep brain during the gyrification period (GA 90) that were absent before (GA 70) and after (GA 110) the main changes in the folding of the cerebral cortex, specifically with regards to BDNF, CDK5, HDAC5, MeCP2 and NeuroD6. Based on a more extensive and in-depth literature search on these genes, we determined that the genes we had selected and validated as being differentially expressed between gyri and sulci were all involved in the process of neurite outgrowth –i.e. neuronal differentiation for dendritic and axonal growth. In addition, several genes, such as MEF2 and some of its targets, that were deemed as differentially expressed in our *in silico* approach (Supplementary Table 1) are also known to play a role in the same process. Thus, we hypothesise that neurite outgrowth represents a strong candidate for a process that could at least partly explain gyrification, and that this process is differential between gyri and sulci, as explained below.

Recently, mechanical models that explain and predict folding as a function of differential growth between lower and upper layers of the cerebral wall have been proposed (70, 96, 97, 102), (see Differential Tangential Expansion Hypothesis in Chapter 1). Thus, growth in the upper layers –mainly the cortex– could be partly responsible for the gyrification process according to this theory. This growth could be attained by incorporating newly migrating cells –as suggested by Striedter *et al*. (63)– or through regional changes throughout the cortex –as suggested by Ronan *et al*. (93)–, or a mixture of both. However, the possibility that this growth is achieved mainly through migration is unlikely, as it has been observed that neuronal migration is mostly complete by the time gyrification starts (10), and the volume of neurons –and by extension the effect of later migration on gyrification– has not been assessed. Furthermore, in ferrets the neuronal migration towards the CP occurs mainly before gyrification starts, with some few late-migrating neurons changing migration direction as folding onsets (83). Additionally, a recent study in the physics of the folding of human brain organoids revealed that by the onset of folding, the nuclei of cells in the outer layers of the organoid have reached near maximum density (364). At the same time, the evidence presented in such study shows that the during the folding of the organoid, the nuclei of the cells in the outer layer undergo distinctive changes in nuclei morphology (364). This suggests that, at least in this organoid model, folding of the outer layers seems to be driven mainly by changes in cellular morphology rather than just an increase in the number of cells per area. Also, by the time the last wave of neurons leave the SVZ the cerebral cortex shows little regional architecture (14), meaning that if

folding should be attained by newly migrating neurons, this last wave needs to produce *all* the mechanical force needed to produce the observed buckling; a process that seems unlikely.

On the other hand, early studies on the sheep cortex formation and progression throughout gyrification –and other gyrencephalic species such as rhesus monkey (179) and ferrets (365)– show a layer densely packed with neurons (180) that starts unpacking progressively as gyrification advances (190, 191). Also, the eCP displays mature neurons in the inner layers (190), and many of them showing pyramidal morphology (180) as gyrification starts around GA 80. By GA 110 the cortex is already differentiated (190), when gyrification is mostly complete. Thus, these processes of cortical unpacking, differentiation and maturation occur concomitantly with the cerebral cortex folding, suggesting this differentiation and rearrangement of the tCP during gyrification might play a significant role in the process of the folding of the cerebral cortex, and not just be a consequence of it.

This differentiation and rearrangement of the tCP could be attained through neurite outgrowth. This hypothesis is consistent with previous reports showing neurite outgrowth concomitantly with gyrification in ferrets (197) and humans (360). Also, recently, a study showed both regional and temporal changes in fractal anisotropy throughout the cerebral cortex in association with gyrification in rhesus macaque (198), thus supporting the hypothesis that neuronal differentiation and neurite outgrowth might be responsible for cerebral cortex folding. This way little, if any, would be the impact of late migration on gyrification when compared to neurite outgrowth.

So, we hypothesize that this mechanism indeed plays a major role during gyrification in sheep that is differential between gyri and sulci. The data presented in Chapter 4 supports this hypothesis, as the genes we characterised as differentially expressed between gyri and sulci during gyrification are all involved in genetic pathways and processes that promote neurite outgrowth.

MeCP2 regulates expression of the BDNF gene (348, 349) by binding to one of its promoters, impeding transcription. This binding reverses by a calcium-dependent phosphorylation of MeCP2 that releases BDNF gene upon physiological stimuli. Thus, MeCP2 regulates BDNF-dependent dendritic growth (244). Furthermore, mouse models of Rett syndrome –which lack MeCP2– show higher levels of BDNF at birth (350), and MeCP2-deficient mice models show abnormal dendritic arborization (362, 363). This evidences an important role for MeCP2 in neurite outgrowth control via BDNF regulation.

HDAC5 is also shown to regulate BDNF, as inhibition of HDAC5 leads to increased BDNF expression and augmented neurite development (242) via regulation of BDNF promoter sites in cortical neurons (343). On the other hand, BDNF also stimulates phosphorylation and relocation of HDAC5 to the nucleus, and this correlates with an increase in MEF2 activity at least in hippocampal neurons (366). Also, BDNF is shown to activate MEF2-mediated transcription in cortical neurons (367, 368), which is consistent with our data showing various MEF2-regulated genes (e.g. APOD, SOX9, NEXN) to be differentially expressed between gyri and sulci (Supplementary Table 1).

CDK5, in association with p35, also modulates BDNF-induced neurite growth activity at least in hippocampal neurons by interaction with TrkB receptor (344). Also, BDNF expression is reduced in neurons lacking CDK5, and these neurons display reduced number of neurites (345). BDNF/TrkB also activates downstream ERK, which is necessary for dendritic growth (369), and induces strong expression of p35 (361), which activates CDK5. This activation of ERK and induction of p35 is also observed through the NGF pathway –which also induces neurite outgrowth (370, 371)– in which inhibition of CDK5 blocks NGF-induced neurite outgrowth in PC12 cells (361). Most interestingly, NGF also increases MEF2 activity in these cells (372).

This NGF-induced neurite outgrowth also requires expression of NeuroD6. NeuroD6 is induced by NGF treatment, and can regulate neurite outgrowth even in absence of NGF (247). Also, NeuroD6 is an essential component of the neuron differentiation mechanism (373), and its expression is dramatically changed in BDNF-deficient mice embryonic cortices (374). Most interestingly, NeuroD6 expression peaks when neurite outgrowth is highly active (341, 375).

Also, ablation of Pax6 also reduced expression of NeuroD6 in mouse cortex development, revealing NeuroD6 as a target of Pax6 regulation (376). This is reinforced by analyses on the Pax6 binding sites, which reveal a consensus binding site that is shared by proteins of the same family as NeuroD6, including it (377). This might suggest a role for Pax6 in regulating neurite outgrowth in cortical neurons at least through the NGF-Pax6-NeuroD6 pathway.

So, again, we hypothesize that neurite outgrowth is a central process by which gyrification unfolds, and that this process occurs differentially between gyri and sulci. This hypothesis would perfectly encompass our experimental data with histological observations of the sheep tCP and the structural analyses obtained through MRI in previous studies. It would also align the aforementioned evidence with the mechanical models proposed to explain gyrification, and would provide a feasible biological mechanism by which the cerebral cortex could obtain its convoluted shape following discrete domains of differential expression.

To investigate whether neurite outgrowth occurs concomitantly with gyrification in sheep, hereby we describe the neurite outgrowth process before (GA 70), during (GA 90), and after (GA 110) gyrification using fluorescent immunohistochemistry staining for microtubule-associated protein 2 (MAP2), a well-known marker for neurite outgrowth which is specific for neurons (378), in similar regions used for study 2. It is worth noting that even when both dendrites and axons are collectively known as neurites –and therefore neurite outgrowth encompasses both dendro and axonogenesis– and both axonal and dendritic sprouting occur concomitantly with gyrification (360), MAP2 shows specific subcellular localisation to dendrites while being mostly absent from axons (378-381). Therefore, even when generally known as a marker for neurite outgrowth, MAP2 is more specifically a marker for dendrogenesis rather than axonogenesis, and therefore we will be hereafter referring to MAP2 as a marker of dendrites.

To investigate whether BDNF, CDK5, NeuroD6, HDAC5 and MeCP2 were correlated with this process during gyrification, we co-localised the expression of this genes with MAP2 at GA 90 in sheep. MAP2, interestingly, has been found having: increased expression concomitantly with increased NeuroD6 expression in PC12 cells (334), altered expression in Rett syndrome (MeCP2-deficient) neocortex (382), decreased expression in CDK5-deficient mice (231), and increased expression following BDNF administration (383). Also, neurons transfected with DYNLT1 –another gene we found differentially expressed between gyri and sulci during gyrification on study 1– showed longer and more elaborate MAP2-positive dendrites (239). Furthermore, MAP2 is also affected my MEF2 expression (384).

To investigate whether dendrogenesis occurs differentially between gyri and sulci, we analysed the expression of MAP2 between gyri and sulci throughout the cortex at GA 90. To address differences in the microstructure of gyri and sulci, we performed NODDI analysis (216) over three GA 98 brains and compared gyri and sulci throughout the cortex. This age was chosen for the NODDI analysis because it represented the mid-point between the ages of “during-gyrification” (GA 90) and “after-gyrification” (GA 110), and would allow us to observe whether the differences in genetic expression observed at GA 90 translated in microarchitectural differences shortly after. NODDI has been described as a powerful technique for assessment of neurite microstructure in the brain, whose utilization will aid into the assessment of the structural differences between gyri and sulci during gyrification that other histological approaches cannot render.

We also aimed to further characterise the differential expression observed in the tCP during gyrification, to understand its correspondence with neurons, astrocytes and microglia. To investigate this, we co-localised BDNF, CDK5, NeuroD6, HDAC5 and MeCP2 with neuronal marker NeuN,

astrocyte marker GFAP, and microglia marker Iba-1. These experiments also allowed us to examine the cellular composition of the tCP between gyri and sulci during gyrification.

Methods

Please refer to sections 2.1, 2.8, 2.9, 2.10, 2.11 and 2.12 for the detailed methodology corresponding to this study.

Results

Neurite outgrowth progression in fetal sheep

We performed a fluorescent immunohistochemistry against MAP2 to observe mature neurons in the sheep tCP, as this marker is essential in the process of ~~neurite outgrowth~~ dendrogenesis and the staining allows us to observe neuronal morphology. Figure 26 shows the temporal distribution of MAP2 in the eCP/tCP/cortex before (GA 70, panels A-B), during (GA 90, panels C-D) and after gyrification (GA 110, panels E-F).

Before gyrification, the eCP shows little MAP2 immunoreactivity, and the neuronal morphology characteristic of mature pyramidal neurons cannot yet be observed (panels A-B). However, increased MAP2 immunoreactivity and distinct neuronal morphology can begin to be observed concomitant with gyrification in both gyri (panel C) and sulci (panel D) at GA 90, with neurites of pyramidal neurons becoming evident especially in layers IV-V. Also, cells appear more dispersed as compared to the highly compacted pre-gyrification eCP. After gyrification is mostly complete, the neurite architecture appears even more complex in structure in both gyri (panel E) and sulci (panel F), with pyramidal morphology now being observed from layers II to VI, and increased arborisation and neuronal complexity as well as greater number of visible neurites throughout the cortex. Furthermore, the cells appear even more dispersed than in mid-gyrification, especially in gyri. The bundling of the apical dendrites at this later gyrification stage resemble those already reported in species such as cats, mice and monkey (reviewed in (385)), and appear to be more spread in gyri compared to sulci. Proper characterisation of these cortical columns, their structure in sheep, and whether they are different in gyri compared to sulci, will require future experimental approaches. So far, to the best of our knowledge, this cortical organisation has not been observed before in sheep.

However, even when both gyri and sulci showed increased maturation in pyramidal neuron morphology and neurite outgrowth during gyrification, more subtle differences between gyri and

sulci regarding this process remain unclear. Therefore, we proceeded to elucidate whether there is differential MAP2 immunoreactivity between gyri and sulci during gyrification.

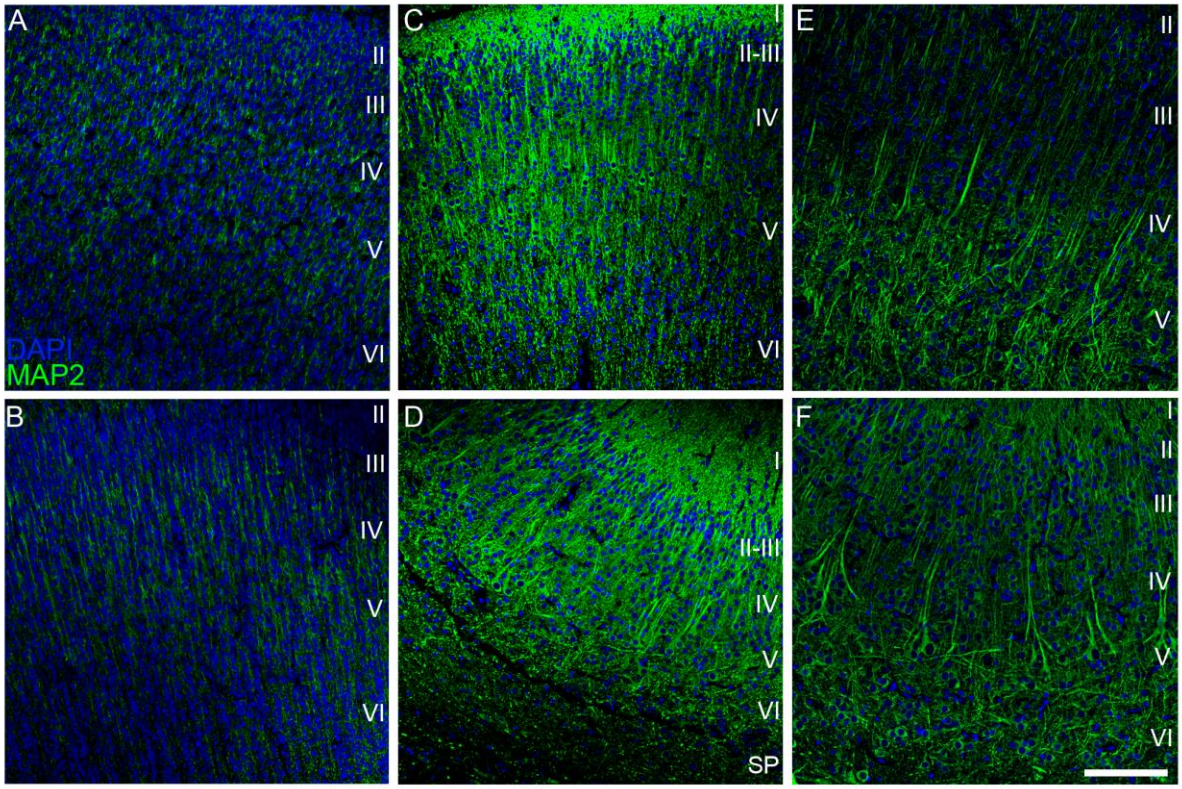


Figure 26. Dendrogenesis progression in the eCP/tCP/cortex. Progression of dendrogenesis in the sheep cortex as defined by MAP2 immunoreactivity (green) before (GA 70, A-B), during (GA 90, C-D) and after gyrification (GA 110, E-F). Two regions of the eCP (A-B), gyri (C, E) and sulci tCP/cortex (D, F) are depicted. I-VI: layers I to VI; SP: subplate. Bar size = 150 **µm**.

Differential MAP2 immunoreactivity and neurite outgrowth between gyri and sulci

In order to study whether dendrogenesis might be occurring differently between gyri and sulci during gyrification, we investigated the immunoreactivity levels of MAP2 between gyri and sulci throughout the sheep cortex tCP at GA 90 (Figure 27).

Gyri displayed higher MAP2 immunoreactivity (0.073 ± 0.004 mm^2 signal/mm^2 tissue) than sulci (0.019 ± 0.003 mm^2 signal/mm^2 tissue). There were also major differences between gyri and sulci, showing consistently higher MAP2 immunoreactivity in gyri than sulci ($F(1, 40) = 20.94$, $p < 0.0001$, Figure 27, panel 4). Nonetheless, post-hoc analysis failed to reach significance, again, probably due to biological variation (Figure 28). These differences were not observed rostro-caudally, though, with gyri and sulci displaying similar MAP2 immunoreactivity throughout the tCP.

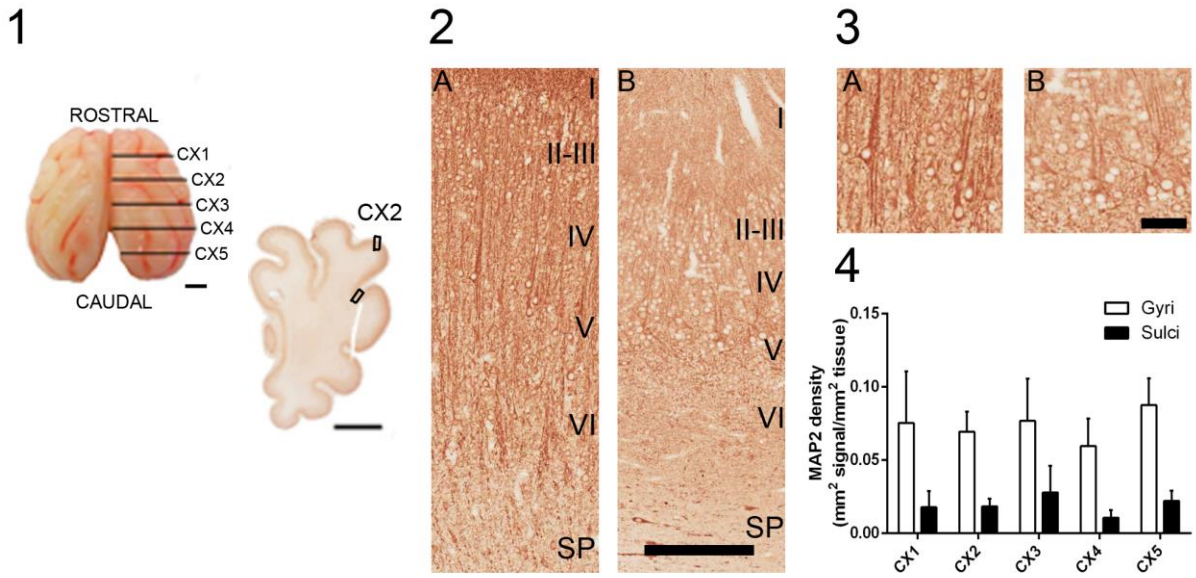


Figure 27. MAP2 immunoreactivity in gyri and sulci tCP during gyrification. MAP2 immunoreactivity in the sheep tCP between gyri (2A, 3A) and sulci (2B, 3B) during gyrification (GA 90) throughout the cerebral cortex. 1: Diagram showing brain sections analysed, and a representative brain section. 2, 3: Immunohistochemistry analysis of MAP2 expression in the tCP between gyri (2A, 3A) and sulci (2B, 3B). 4: Mean MAP2 immunoreactivity in the tCP of gyri and sulci throughout the cerebral cortex. Bars are means ± SEM. I-VI: layers I to VI; SP: subplate. Bar sizes in 1: 4mm, 2: 200 µm, 3: 50 µm.

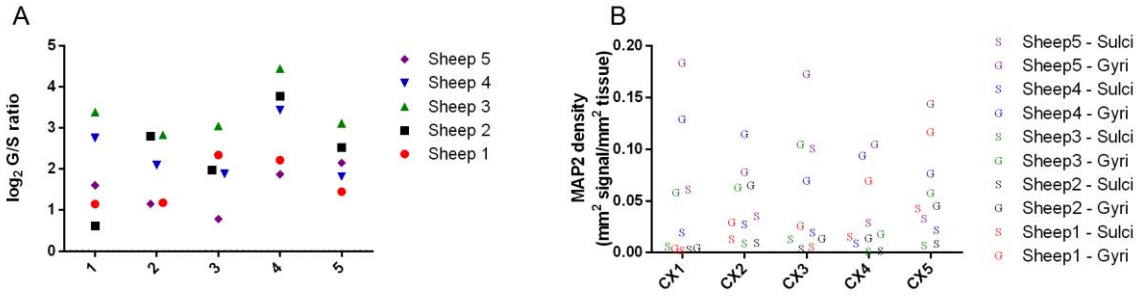


Figure 28. MAP2 immunoreactivity. MAP2 immunoreactivity levels at GA 90 between gyri and sulci. A. Log_2 values of MAP2 expression density level ratios between gyri and sulci plotted for each individual sheep analysed, per brain section. B. Means obtained for MAP2 expression density levels for gyri (G) and sulci (S) for every individual sheep analysed, per brain section.

We also performed NODDI analysis over two gyri and two sulci for each brain region, from CX2 to CX5 (Table 8, Figure 29). The NODDI toolbox rendered the following parameters: AD (axial diffusivity [also known as parallel diffusivity], i.e. diffusivity alongside the main axis of diffusion), RD (radial diffusivity [also known as perpendicular diffusivity], i.e. diffusivity perpendicular to the main axis of diffusion), MD (mean diffusivity, i.e. the mean diffusivity of all three eigenvectors), FA (fractional anisotropy), FECVF and FICVF (extracellular and intracellular volume fractions, i.e. volume of extracellular and intracellular spaces, respectively), IRFRAC (isotropic restricted fraction, i.e. water

that is not diffusing), FISO (isotropic free volume, i.e. free water around neurites), and ODI (orientation-dispersion index, that quantifies the spread of the neurites).

NODDI parameters in the GA 98 cortex showed that both gyri and sulci presented distinctive microarchitecture, which largely remained constant rostro-caudally. Gyri showed higher AD, higher RD, higher MD and lower FA values than sulci (Table 8). Gyri also appeared less radially-oriented than in sulci. Gyri also showed higher FECVF and lower FICVF values in compared to sulci, which matches with higher FISO in gyri than sulci, and lower IRFRAC compared to sulci. However, surprisingly and contrary to our expectations, ODI values were persistently lower in gyri than sulci (Table 8). Interestingly, however, ODI values for both gyri and sulci were significantly higher towards the rostral side of the cortex (CX2-3, gyri 0.077 ± 0.012, sulci 0.115 ± 0.015) when compared to the caudal side (CX4-5, gyri 0.031 ± 0.007, sulci 0.079 ± 0.010). Quality control values showed similar trends (Supplementary Table 6).

Table 8. Comparison between sulci and gyri of GA 98 fetal sheep brains using NODDI. AD, axial diffusivity; RD, radial diffusivity; MD, mean diffusivity; FA, fractional anisotropy; FECVF, extracellular volume fraction; FICVF, intracellular volume fraction; IRFRAC, isotropic restricted fraction; FISO, isotropic free volume; ODI, orientation-dispersion index. NS, non-significant; G, gyri; S, sulci; R, rostral; C, caudal. n = 3.

NODDI Parameter	Gyri (mean ± SEM)	Sulci (mean ± SEM)	Gyri to Sulci relationship	Effect size	p value	Rostro-caudal relationship
AD	0.471 ± 0.006	0.389 ± 0.013	G > S	F (1, 16) = 37.77	< 0.0001	NS
RD	0.315 ± 0.009	0.237 ± 0.005	G > S	F (1, 16) = 147.0	< 0.0001	NS
MD	0.367 ± 0.007	0.288 ± 0.007	G > S	F (1, 16) = 128.1	< 0.0001	NS
FA	0.247 ± 0.018	0.302 ± 0.009	G < S	F (1, 16) = 8.739	0.0093	NS
FECVF	0.826 ± 0.007	0.722 ± 0.007	G > S	F (1, 16) = 39.89	< 0.0001	NS
FICVF	0.181 ± 0.007	0.280 ± 0.007	G < S	F (1, 16) = 41.95	< 0.0001	NS
IRFRAC	0.070 ± 0.006	0.104 ± 0007	G < S	F (1, 16) = 15.06	0.0013	NS
FISO	0.107 ± 0.009	0.062 ± 0.003	G > S	F (1, 16) = 8.897	0.0088	NS
ODI	0.054 ± 0.014	0.097 ± 0.011	G < S	F (1, 16) = 13.33	0.0022	R > C F (3, 16) = 4.07, p = 0.0251

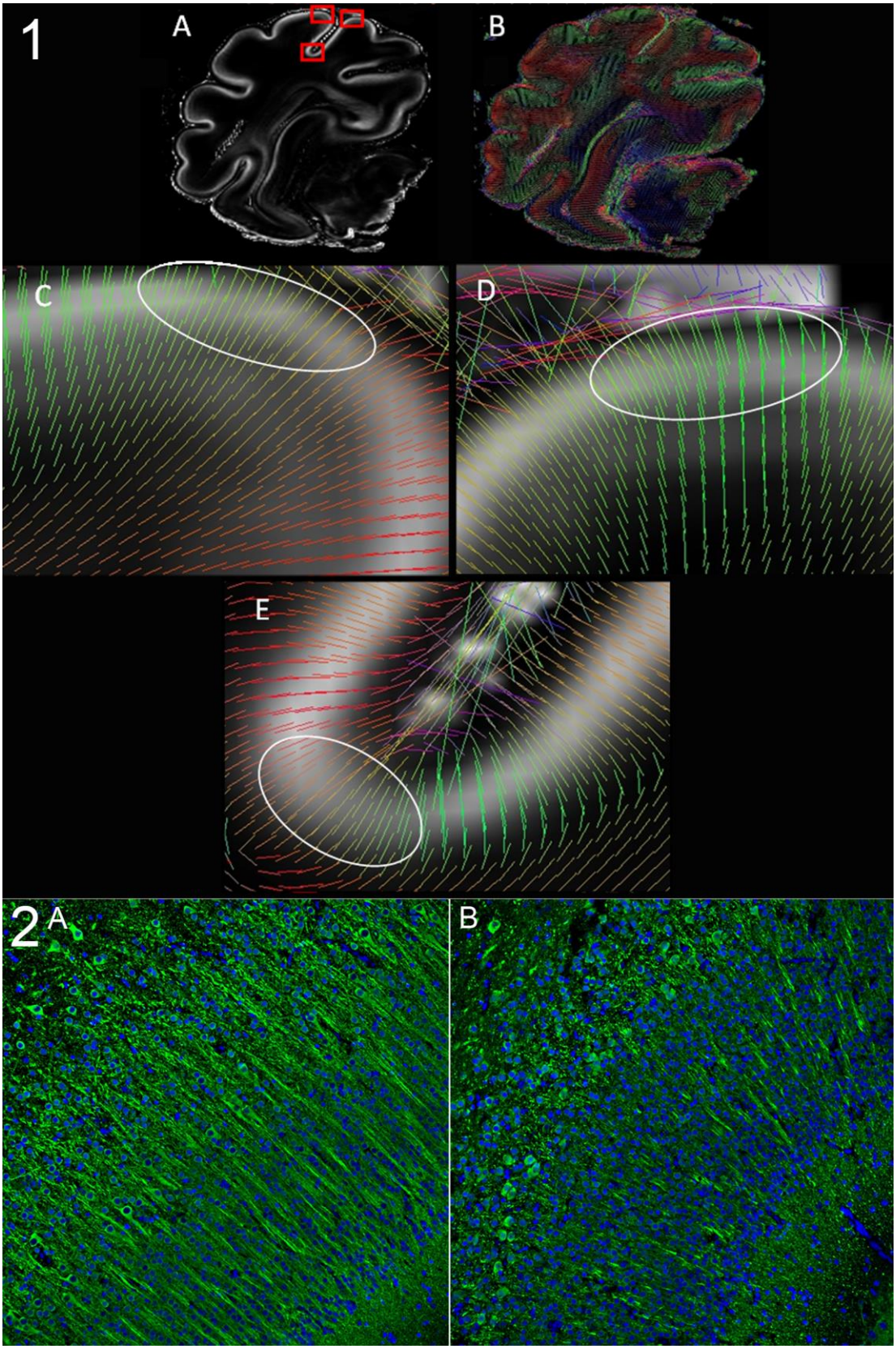


Figure 29. NODDI and MAP2 analysis during gyrification. Graphical representation of the DTI analysis performed over the cortex (1), and MAP2 immunoreactivity (2) at GA 98. FA map (1A) and principal eigenvector map (1B) of a sample region of the fetal sheep brain. 1C-1E: zooms with eigenvectors overlaid on FA map in gyri (1C, 1D) and sulci (1E) as shown with red rectangles in 1A. White ovals in 1C, 1D and 1E represent the tCP areas over which the NODDI analysis was performed. (2) MAP2 immunoreactivity in a representative gyrus (2A) and a representative sulcus (2B).

Co-localisation of BDNF, CDK5, NeuroD6, HDAC5 and MeCP2 with neurite outgrowth.

In order to correlate the differences in gene expression between gyri and sulci observed in Study 2 with neurite outgrowth, we performed double-labelling experiments through immunohistochemistry and FISH, exploring the pattern of immunoreactivity of BDNF, CDK5, and NeuroD6, and the mRNA expression of HDAC5 and MeCP2 concomitantly with MAP2. However, considering we found no rostro-caudal differences in the expression levels of these genes on the previous studies, we performed these analyses only on one region of the cortex, namely CX2. Figure 30 shows the immunoreactivity of BDNF, CDK5, and NeuroD6, and the mRNA expression of HDAC5, MeCP2 (red channel, black arrows) concomitantly with MAP2 immunoreactivity (green channel, white arrows) in the tCP. All these genes were found to be co-localised with MAP2 in both gyri and sulci.

BDNF was immunoreactive in every cell in the tCP, including MAP2-positive neurons, suggesting that BDNF immunoreactivity is observed not only in other neurons during gyrification, but also astrocytes and glia. CDK5 immunoreactivity, on the other hand, mimicked MAP2 ~~expression~~ immunoreactivity in the tCP accurately, suggesting that CDK5 is only expressed in MAP2-positive neurons. HDAC5 mRNA expression was found co-localised with MAP2-positive neurons as well, but some signal was also observed elsewhere, suggesting, similar to BDNF, that other tCP cells might be expressing HDAC5 during gyrification. However, only weak MeCP2 mRNA signal was co-localised MAP2 expression, and can be seen more intensely in cells with lower immunoreactivity of MAP2. Finally, NeuroD6 immunoreactivity, similar to BDNF, was found co-localised with many cells including MAP2 neurons, but unlike BDNF, there were some NeuroD6-negative cells in the tCP, showing that not all cells express this protein in the tCP during gyrification.

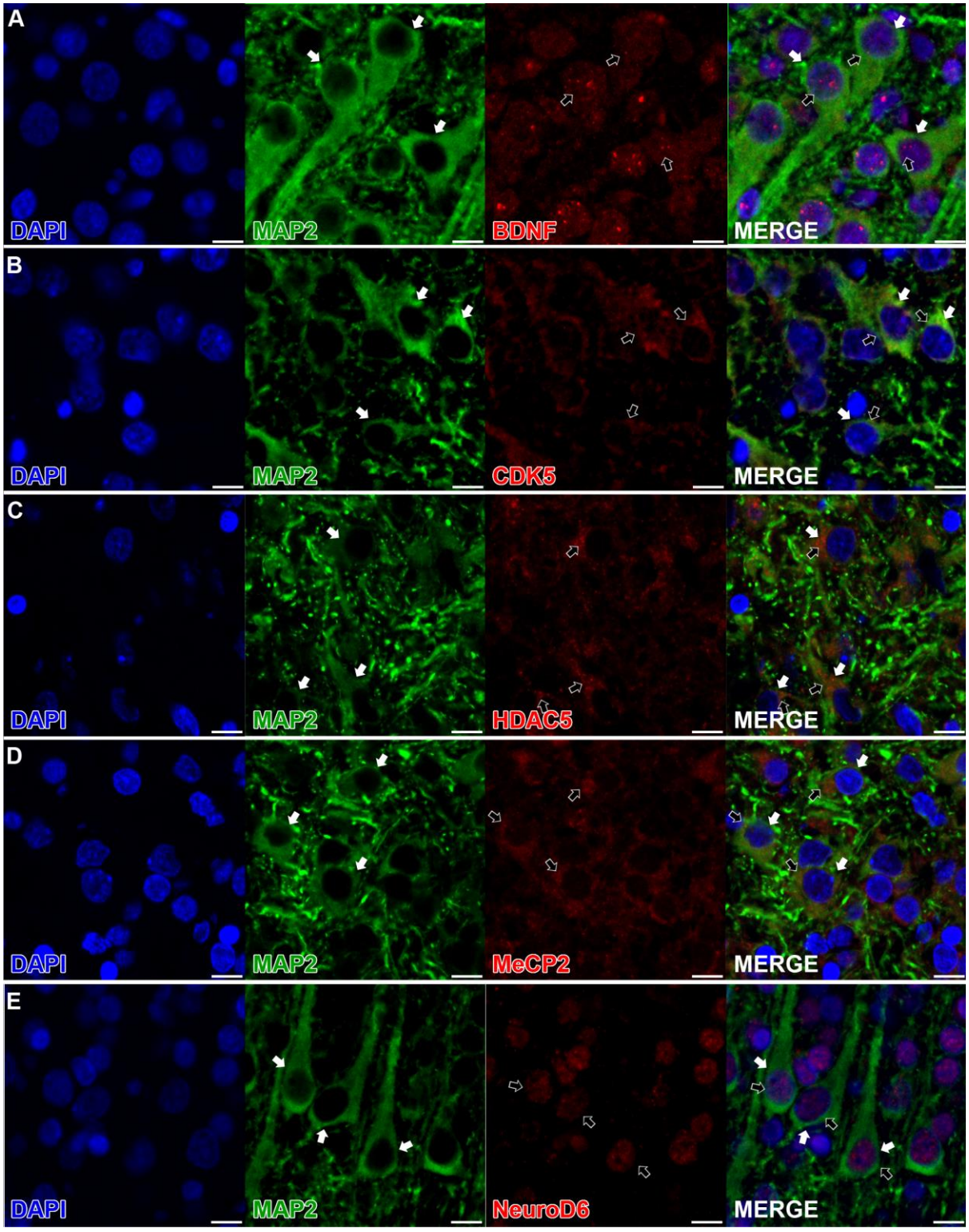


Figure 30. Gene expression association with dendrogenesis. Co-localisation of BDNF (A), CDK5 (B), HDAC5 (C), MeCP2 (D) and NeuroD6 (E) with dendrogenesis-specific marker MAP2. Blue, DAPI; green, MAP2; red, gene of interest. White arrows indicate MAP2-positive cell of interest. Black arrows indicate gene of interest-positive cell. Bars, 10 µm.

Characterisation of cell types in tCP expressing BDNF, CDK5, NeuroD6, HDAC5 and MeCP2 during gyrification

The results obtained through co-localisation of our proteins and mRNAs of interest with MAP2 suggested that the expression of these genes in the tCP during gyrification is associated with many more cell types, not only MAP2-positive neurons. Thus, we co-localised our genes of interest with cell type-specific markers for neurons, astrocytes and microglia. Figure 31, Figure 32 and Figure 33 show the co-localisation of our genes of interest with neuron-specific marker NeuN, astrocyte-specific marker GFAP, and microglia-specific maker Iba1, respectively. None of the genes studied here showed differences between gyri and sulci in co-localisation with the cell type-specific markers.

As stated before, BDNF immunoreactivity was ubiquitous in the tCP during gyrification. We found BDNF not only co-localised with NeuN-positive neurons (Figure 31, panel A), but also with GFAP-positive astrocytes (Figure 32, panel A) and Iba1-positive microglia (Figure 33, panel A). In contrast, CDK5 was present only in NeuN-positive neurons (Figure 31, panel B), but neither in GFAP-positive astrocytes (Figure 32, panel B) nor in Iba1-positive microglia (Figure 33, panel B), complementing our previous hypothesis of CDK5-expression being neuron-specific in the tCP at this developmental stage. Interestingly, HDAC5 was co-localised primarily in NeuN-positive neurons (Figure 31, panel C) but only faint signal was co-localised with GFAP-positive astrocytes (Figure 32, panel C). However, HDAC5 was not found co-localised with Iba1-positive microglia (Figure 33, panel C). MeCP2 was found strongly expressed in NeuN-positive neurons (Figure 31, panel D), while being only weakly expressed in GFAP-positive astrocytes (Figure 32, panel D) and Iba1-positive microglia (Figure 33, panel D). Finally, NeuroD6 showed a pattern similar to HDAC5: it was mainly found co-localised to NeuN-positive neurons (Figure 31, panel E), and only faint signal was co-localised with GFAP-positive astrocytes (Figure 32, panel E) and not observed in Iba1-positive microglia (Figure 33, panel E).

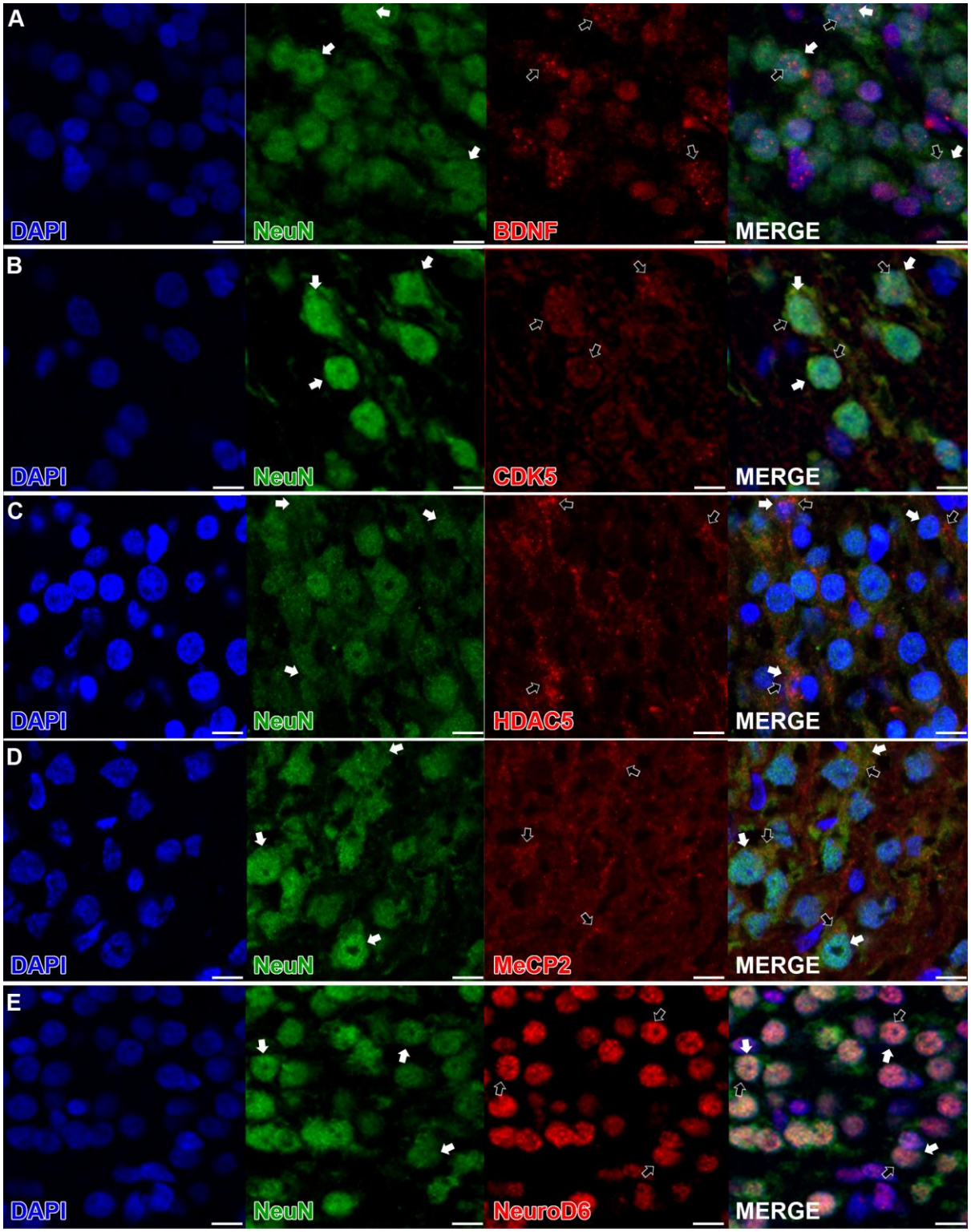


Figure 31. Gene expression association with neurons. Co-localisation of BDNF (A), CDK5 (B), HDAC5 (C), MeCP2 (D) and NeuroD6 (E) with neuron-specific marker NeuN. Blue, DAPI; green, NeuN; red, gene of interest. White arrows indicate NeuN-positive cell of interest. Black arrows indicate gene of interest-positive cell. Bars, 10 µm.

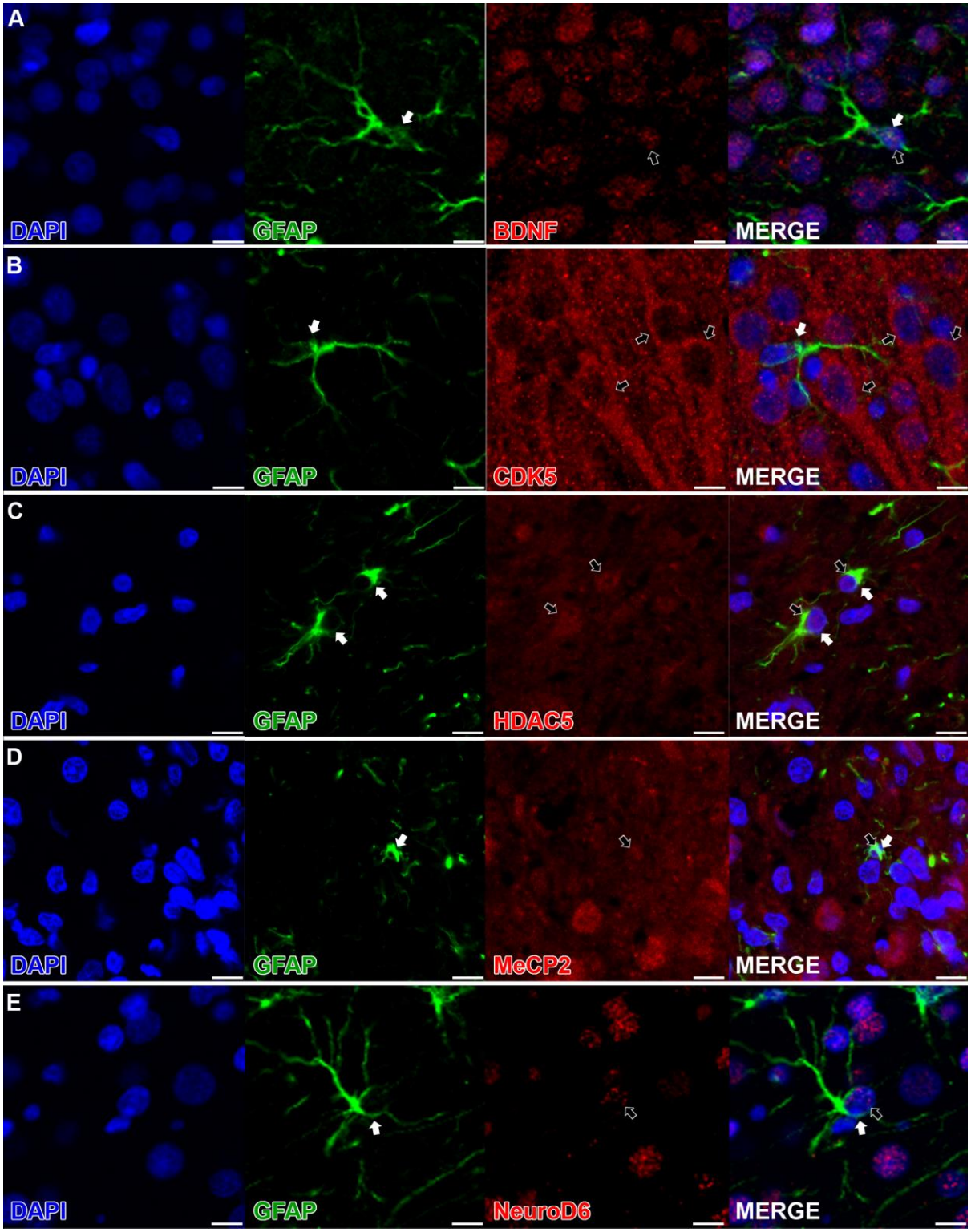


Figure 32. Gene expression association with astrocytes. Co-localisation of BDNF (A), CDK5 (B), HDAC5 (C), MeCP2 (D) and NeuroD6 (E) with astrocyte-specific marker GFAP. Blue, DAPI; green, GFAP; red, gene of interest. White arrows indicate GFAP-positive cell of interest. Black arrows indicate gene of interest-positive cell. Bars, 10 µm

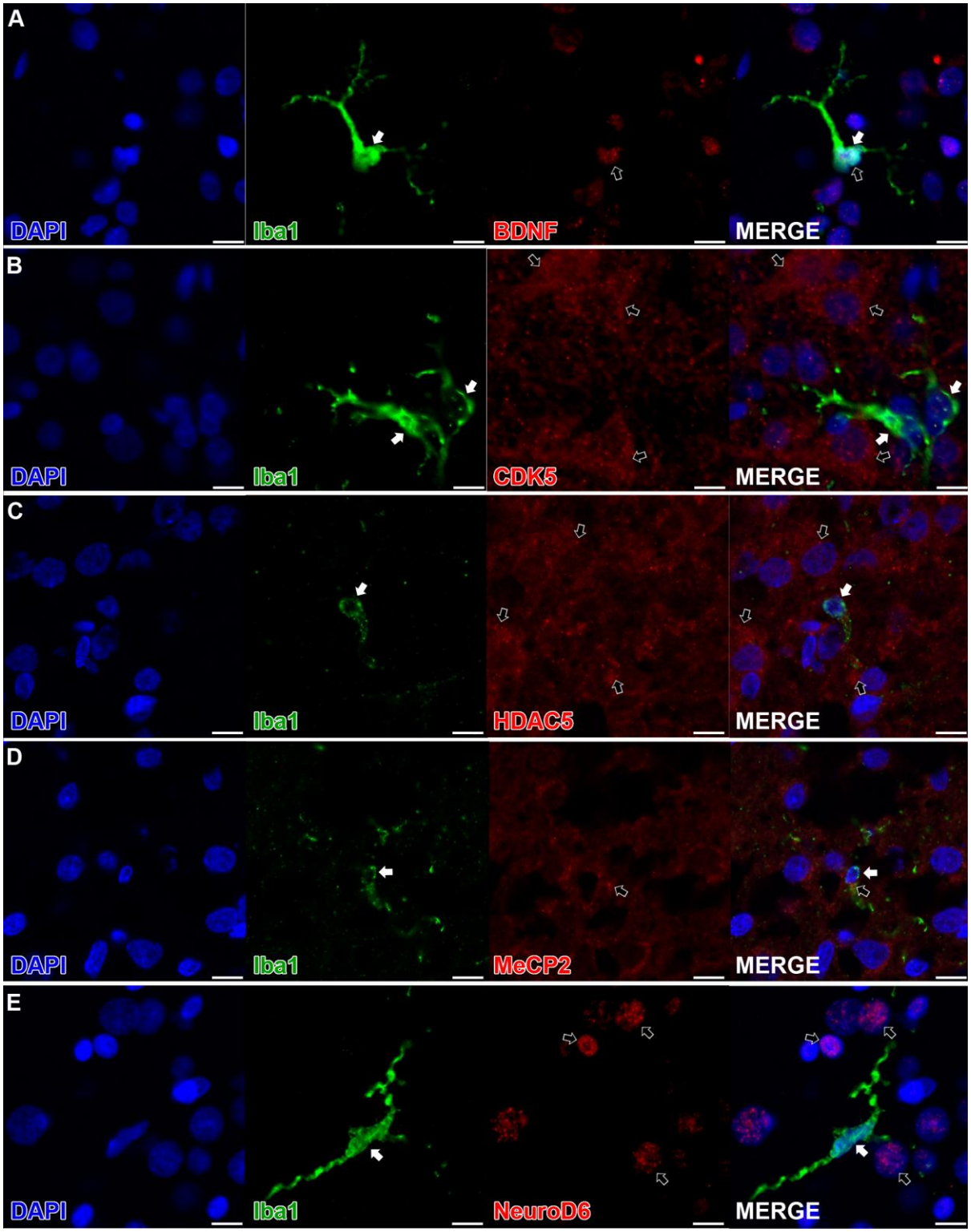


Figure 33. Gene expression association with microglia. Co-localisation of BDNF (A), CDK5 (B), HDAC5 (C), MeCP2 (D) and NeuroD6 (E) with microglia-specific marker Iba1. Blue, DAPI; green, Iba1; red, gene of interest. White arrows indicate Iba1-positive cell of interest. Black arrows indicate gene of interest-positive cell. Bars, 10 µm

Composition of the tCP between gyri and sulci during gyrification.

Our previous co-localisation experiments also allowed us to investigate and characterise the overall composition of the tCP between gyri and sulci during gyrification (GA 90). Using our previous results we quantified, in both gyri and sulci of a section of the brain (namely CX2), the number of NeuN-positive, GFAP-positive, and Iba1-positive cells per area, and also what proportion of the total cell number in the area these cells represent. We also compared the total number of cells per area in both gyri and sulci. Figure 34 shows the results of our composition analyses for NeuN-positive neurons (panels 1A-B), GFAP-positive astrocytes (panels 1C-D) and Iba1-positive microglia (panels 1E-F) for both gyri (panels 1A, C, E) and sulci (panels 1B, D, F).

Our results indicated that there were no differences neither in the number of NeuN-positive (gyri 3706 ± 91.65, sulci 3981 ± 190.3, $p = 0.2297$), GFAP-positive (gyri 298.9 ± 18.10, sulci 313.6 ± 27.02, $p = 0.6630$), and Iba1-positive (gyri 28.28 ± 2.6, sulci 33.44 ± 4.9, $p = 0.3842$) cells per area (panels 2A, B and C, respectively), nor in their proportion of NeuN-positive (gyri 88.17 ± 0.86, sulci 87.06 ± 1.18, $p = 0.4688$), GFAP-positive (gyri 7.642 ± 0.38, sulci 7.012 ± 0.50, $p = 0.3493$) or Iba1-positive (gyri 0.7160 ± 0.05, sulci 0.7980 ± 0.14, $p = 0.5954$) cells of the total number of cells in the regions analysed (panels 3A, B and C, respectively). Nonetheless, the number of total cells per area – which includes not only neurons, astrocytes and microglia, but *all* cells including, for example, oligodendrocytes– showed a small but significant difference. While gyri showed an average of 4290 ± 159 cells per area, sulci showed 4907 ± 199 cells per area ($p < 0.05$, panel 4). This result agrees with our previous observations during NODDI analysis suggesting less-compacted gyri than sulci during gyrification.

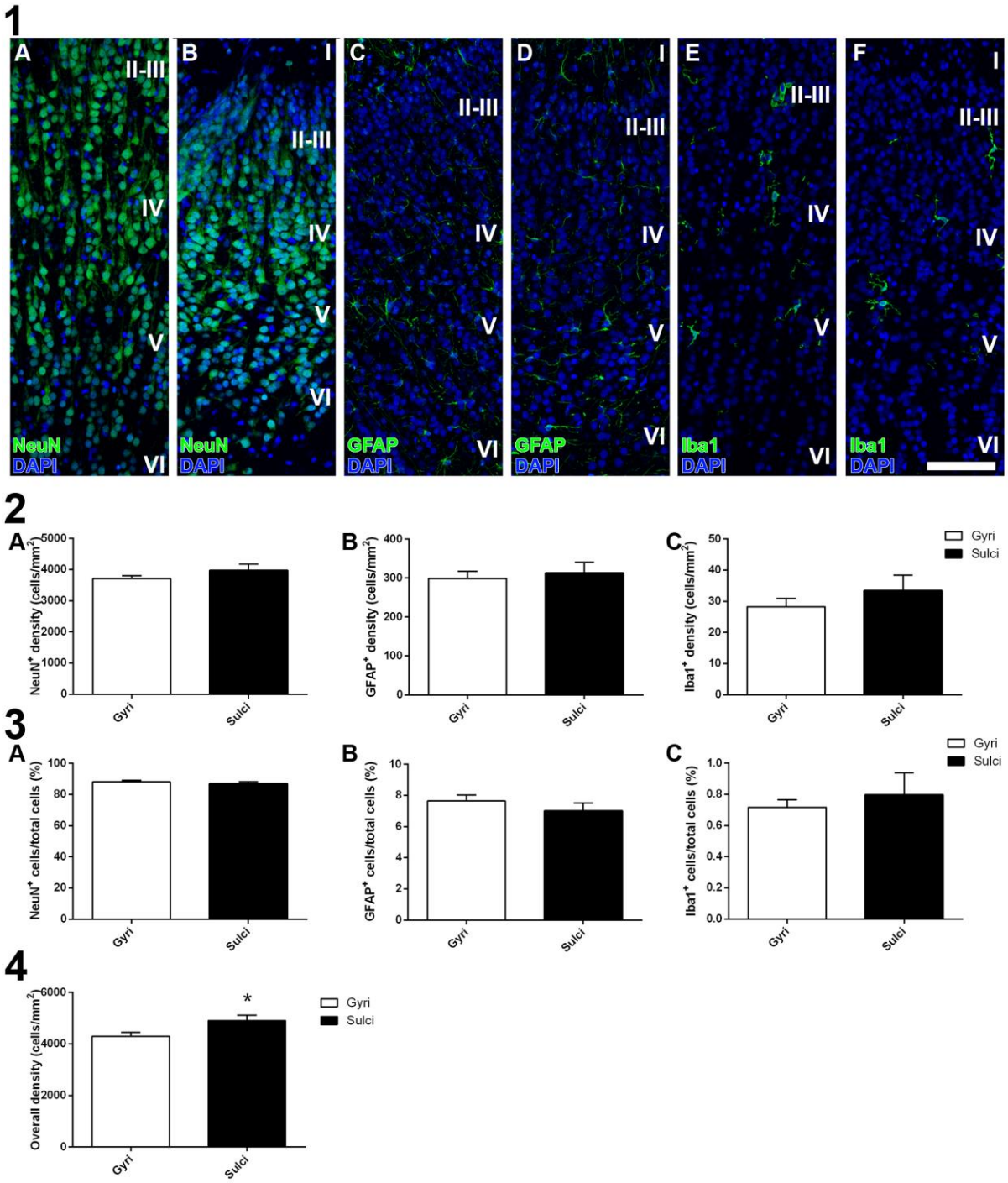


Figure 34. Composition analysis of the gyri and sulci tCP during gyrification. 1. Fluorescent immunohistochemistry for NeuN (A-B), GFAP (C-D) and GFAP (E-F) in both gyri (A, C, E) and sulci (B, D, F). 2. NeuN (A), GFAP (B) and Iba1 (C) density analyses between gyri and sulci. 3. NeuN (A), GFAP (B) and Iba1 (C) proportion analyses between gyri and sulci. 4. Density analysis for total cells between gyri and sulci. Results are mean ± SEM. *, $p < 0.05$. n = 5. Bar in 1, 100 µm

Discussion and Conclusion

This study was aimed at evaluating the presence of MAP2 immunoreactivity as an indicator of dendrogenesis between gyri and sulci tCP during gyrification in sheep. It was also set to deepen our understanding of both the previously addressed immunoreactivity of BDNF, CDK5, and NeuroD6, and also the mRNA expression of HDAC5 and MeCP2 in the tCP, and the neuron, astrocyte and microglia composition of the tCP during cortical folding.

We first addressed the normal progression of dendrogenesis between gyri and sulci tCP during gyrification in sheep. This has been assessed in the past by Astrom on early development until GA 90 (191). Our results partly agree with those described by Astrom at the same developmental stages in the CP, however we could not observe the more developed neurons at ~GA 70 in the inner layers of the eCP. The dendrogenesis developmental state of the tCP at GA 90 hereby described resembles much more the results described by Astrom for the same developmental stage, although the long neurites described in that work could not be observed by us through MAP2 staining until later in development (GA 110). Nonetheless, the changes in neuronal structure observed through MAP2 immunostaining we observed during gyrification largely agree with previous reports (197, 198). The differences observed with Astrom's work might obviously arise from the differences in sensitivity of Golgi staining versus MAP2 immunohistochemistry. A thorough Golgi staining analysis of the GA 90 tCP might prove useful to directly contrast our results with those obtained in the past. However, the Nissl staining presented in Astrom's work confirm that the developmental stages described by both his and our work are consistent, so the differences in neurite outgrowth results are most likely due to the differences in methodology, rather than developmental stage mismatch.

Still, the most interesting findings arose from the comparison between gyri and sulci during (GA 90) and after (GA 110) gyrification. Our results suggest the tCP in gyri had more disperse cells than in sulci –especially in the upper layers–, and neurons were on average shorter but more abundant. The deeper pyramidal layers (IV-V) were the ones that showed the most dramatic changes in morphology throughout gyrification, enlarging their processes both towards the MZ and laterally alongside the tCP. We therefore wondered if there might be differences in the expression levels of MAP2 that could account for these differences between gyri and sulci.

We observed a consistently higher MAP2 immunoreactivity in gyri compared to sulci, in both upper (II-III) and deeper (IV-V) layers of the tCP, confirming that in gyri the dendrogenesis process is upregulated when compared to sulci. To the best of our knowledge, MAP2 immunoreactivity

differences between gyri and sulci during gyrification have not been addressed before. However, more subtle differences between gyri and sulci cannot be rendered through simple immunohistochemistry, especially those concerning structural dissimilarities that might be a consequence of this differential MAP2 expression. This is essential to understand whether these MAP2 differences between gyri and sulci correlate and/or translate into structural differences between these two regions *in vivo*, and whether they could be a feasible mechanism to explain how the tCP matures in a region-dependent manner. We therefore performed NODDI analysis throughout the cerebral cortex in order to gain detailed insight of the structural differences between gyri and sulci rostro-caudally during gyrification.

Two MRI acquisitions were performed. The first one was performed on all brains at a resolution of 150x195 μm^2 and 1 mm slice thickness on all regions of interest, using the protocol described in the methods section with three b values. The second acquisition was performed at single b value of 1750 and was used to corroborate the trend of the data in the first acquisition. Both acquisitions resulted in similar data and showed similar trends between gyri and sulci (Supplementary Table 6), thus making us confident in the data we obtained. However, we cannot exclude partial volume effect in the region of interest, because of how thin the analysed regions are, but we can clearly delineate the cortical plate with this resolution. Furthermore, given the same resolution was used to analyse both gyri and sulci, the partial volume effect is expected to be the same between the two regions, therefore unlikely to impact gyri and sulci differentially.

The NODDI toolbox (216) was developed as an extension of Diffusion Tension Imaging techniques to investigate and evaluate the microarchitecture of different regions of the brain, including the tCP, and has been successfully used in many studies for this purpose (386-389). Higher AD, RD, MD and lower FA values in gyri compared to sulci strongly suggest neurites in gyri on average being less compacted and less radially-oriented than in sulci. Previous reports have shown a reduction of FA (198, 390-392) and increase in MD (390, 393) values as the brain matures and neurite outgrowth unfolds during gyrification, therefore suggesting that the lower FA and higher MD values in gyri correspond to a sooner neurite outgrowth development in these areas when compared to sulci throughout the cortex. This is further supported by the consistent difference in MAP2 immunoreactivity between gyri and sulci. Higher FECVF and lower FICVF values in gyri compared to sulci also suggest on average gyri have smaller neurites while sulci have larger ones, or neurites being more dispersed in gyri compared to sulci. The latter matches the observation that neurites in gyri are suggested to have more free water surrounding them than do neurites in sulci (higher FISO in gyri than sulci), and less fixated water (lower IRFRAC in gyri than sulci), again

suggesting more dispersion between cells in gyri than sulci. Overall, these observations suggest a difference in average neuronal polarity between gyri and sulci during this developmental age, with gyri containing more multipolar neurons, while sulci harbours more immature, bipolar ones. This again is consistent with the generalised increased MAP2 immunoreactivity observed in gyri compared to sulci at this stage.

However, surprisingly and contrary to our expectations, ODI values were persistently lower in gyri than sulci, suggesting less dispersed neurites in gyri than sulci; the opposite pattern suggested by AD, RD, MD, FA, FECVF, FICVF FISO and IRFRAC values. The ODI values obtained between gyri and sulci are largely puzzling for us. Our hypothesis of gyri having increased dendrite outgrowth and lower cellular density compared to sulci is supported by both histological data and the rest of the Diffusion Tensor Imaging data, as the evidence hitherto collected agrees with previous studies mentioned before for FA and MD. However, ODI values were expected to have the opposing pattern: being higher in gyri than sulci. Yet, they consistently showed lower values in gyri compared to sulci. This may reflect the effects of histological data that is yet to be acquired, such as changes in axon and radial glial cell morphology between gyri and sulci, currently unknown to us. ODI discrepancies could be also due to the curvature of the sulci more pronounced than in gyri. Eigenvector images match well with this explanation.

Interestingly, however, ODI values were significantly higher towards the rostral side of the cortex (CX2-3) when compared to the caudal side (CX4-5) during gyrification. This resembles not only previous observations in adult macaques where the motor cortex had significantly less densely packed neurons compared to the visual cortex (394), but also the rostro-caudal expression pattern of BDNF hereby observed later in gyrification (Figure 16). This suggests that BDNF might have an important role in the maturation and spreading of the neurons in the cortex in a rostro-caudal fashion later in development, and also suggests that ODI values could be more sensitive than FA in measuring changes in microstructure.

Thus, our NODDI results account for a structurally different tCP between gyri and sulci that is associated with, and is hereby hypothesised to be a consequence of at least, differential MAP2 immunoreactivity between these two regions throughout the cortex. More specifically, a consequence of at least differential dendrogenesis between gyri and sulci during gyrification. This hypothesis needs to be further pursued by future *de novo* knock out studies –with no disruption of previous processes of cortical maturation– such as the ones performed by Shinmyo and colleagues (235), so causality can be established.

Also, it is important to keep in mind that even when MAP2 shows specific subcellular localisation for dendrites and cell bodies, the NODDI approach addresses the general structure of neurites in the tCP, therefore accounting for both dendrites and axons, even when in the grey matter it has been described to quantify the pattern and structure of dendrites (216).

Taking together both our MAP2 and NODDI results, we hereby show that dendrogenesis is more active in gyri than sulci, and this difference appears to correlate with a structural difference between gyri and sulci. Gyri shows either more dispersion of the neurons, more and or thinner dendrites per neuron, less axonal density, or a mixture of these or other observations we may have not accounted for, when compared to sulci. This hypothesis is plausible in light that not only neurite outgrowth occurs concomitantly with gyrification, but also synaptogenesis and axonal growth (360). Considering no attention has been paid to axonal growth in this study, future analyses on the distribution and expression of axon-specific proteins (e.g. Tau (395)) between gyri and sulci will undoubtedly lead to better understanding of the precise structural differences between these two regions by considering the separate effects of both dendro and axonogenesis during gyrification. Again, performing a Golgi staining at this developmental stage and comparing gyri and sulci could also prove essential to bring our results to a better explanation, and to have better accounting for the differences in dendrogenesis between gyri and sulci during gyrification. The Golgi staining will allow us to account for primary and secondary branches structures, and for the length and number of neuronal projections, confirming differences in neuronal morphology between gyri and sulci.

For the purpose of further understanding the relationship between the observed genetic expression and the dendrogenesis process, we sought to perform co-localisation experiments between these genes and MAP2. We found all BDNF, CDK5, HDAC5, MeCP2 and NeuroD6 in MAP2-positive neurons, with varying degrees of intensity, showing that indeed these genes are associated with dendrogenesis during gyrification in sheep. These results largely agree with previous studies showing BDNF (383), CDK5 (345), HDAC5 (242), MeCP2 (359) and NeuroD6 (247) in association with MAP2-positive neurons. Nonetheless, further knock-out experiments are needed to establish causality between these genes and dendrogenesis during gyrification, and their impact over cortical folding during cortical folding. The previously described CDK5 knock-out causing impaired cortical folding during gyrification did not evaluate the impact of the absence of this protein over dendrogenesis, and only describes misfolding of the cortex as a function of impaired migration of neurons to the upper layers of the CP (235). Therefore, it is not conclusive about the impact of CDK5 over dendrogenesis on gyrification during gyrification. Still, our results suggest these genes might be

controlling neurite outgrowth during gyrification in fetal sheep, making them promising candidates for future targeting and evaluation.

To further deepen our understanding of the genetic expression patterns observed between different cell types other than MAP2-positive neurons, we hypothesised that this expression was mainly correlated to neurons, as opposed to astrocytes and microglia. We observed BDNF being expressed by all neurons, astrocytes and microglia. These results agree with previous reports showing BDNF being produced mainly by neurons (396, 397), but also by astrocytes (398) and microglia (399) during development. This highlights the importance of BDNF expression during gyrification, as both astrocytes (400) and microglia (401) have been observed promoting neurite outgrowth. CDK5, on the contrary, was found only associated with neurons, agreeing with previous studies showing this protein mainly expressed and active in neurons, specifically post-mitotic neurons (402). Nonetheless, CDK5 has also been reported expressed in neonatal cultured astrocytes from mice, although at much lower levels (403). These discrepancies might result from our antibody not being sensitive enough to detect the low-level production of CDK5 in astrocytes, combined with the high levels of background it produced in the grey matter, which can make more subtle associations harder. In microglia, to the best of our knowledge, CDK5 expression has yet to be reported. Results obtained for HDAC5 partially mimic previous reports showing cell-type specificity in HDAC5 transcription for neurons mainly, with no expression in astrocytes (356, 404) or microglia (404), whereas we observed only very faint signal coming from astrocytes. These differences might arise from different developmental stages –fetal versus adult stages–, species-specific differences –sheep versus mice and rat–, or due to methodological approaches, as cut-off criteria for positive-to-negative signal largely depends on personal criteria. Nonetheless, a recent study reports that HDAC5 may be present in these three cell types (315). We observed MeCP2 expression expressed mainly in neurons, and only weakly in astrocytes and microglia. These agrees with previous reports showing MeCP2 being mainly neuronal (405), while being expressed in much lower levels in astrocytes (405) and microglia (406). Interestingly, this expression in astrocytes and microglia has been shown to be critical for neurite outgrowth of at least hippocampal neurons in vitro (406, 407). Finally, our results showed NeuroD6 expression mainly in neurons, but we also observed some little expression associated with astrocytes. Yet, to the best of our knowledge, NeuroD6 has only been reported in neurons (248, 333, 334).

Finally, to further deepen our understanding of the tCP during gyrification, we determined both the densities and proportions of neurons, astrocytes and microglia in the tCP of gyri and sulci during gyrification, finding the tCP being composed of around 85% neurons, around 8% astrocytes

and around 0.8% microglia, with no differences between gyri and sulci. Our results contrast with previously reported data on the number of neuronal and non-neuronal cells in the grey matter showing much greater glial/neuron ratios (108, 394, 408). This might undoubtedly reflect a developmental stage difference, as the subjects addressed in previous studies were adult specimens (108, 394, 408), and the glia/neuron rate changes dramatically with later development of the brain (409). Nonetheless, this could also be a species-specific difference (410), or a mixture of both. Furthermore, it has been reported that both astrocytes and microglia increase their numbers in early post-natal development, at least in mice (411), and the proportion of astrocytes and glia in the adult brain is 3-4 to 1 (408), and that microglia maintain their numbers through a process of self-renewal (412). Again, we hypothesise that the difference in the numbers of neurons, astrocytes and microglia between ours and other reports reflect mainly a mixture of developmental age and species-specific effects. Yet, we only found a small but significant difference between gyri and sulci in terms of the density of the total number of cells, but not in the densities of neurons, astrocytes or glial cells when using markers specific for cell type. It might be that the combined effect of the small, non-significant reductions of densities in all cell types in gyri compared to sulci translates into a significant difference in the density of the total number of cells between gyri and sulci. This effect, nonetheless, agrees with the NODDI parameters showing gyri being less cellular dense compared to sulci.

Hereby we have shown that the dendrogenesis process, similar to other gyrencephalic species, occurs concomitantly with gyrification, beyond the stages previously described. This process is also upregulated in gyri compared to sulci throughout the cortex during gyrification, and correlates with microstructural changes that distinguish gyri from sulci mainly in, we hypothesise, general neuronal polarity. Furthermore, we have shown that BDNF, CDK5, HDAC5, MeCP2 and NeuroD6 expression co-localises with a marker for this process (MAP2), and this expression is mainly found in neurons, which account for the majority of the cells found in the tCP during gyrification in sheep.

However, our results overlook several plausible hypotheses and effects we have not accounted for (e.g. axonogenesis and synaptogenesis) which reside outside the scope of this study. This is especially important when putting our results in broader context, because BDNF (223), CDK5 (413), MeCP2 (414) and NeuroD6 (333) have been associated with axonogenesis, and BDNF (415), CDK5 (402) and MeCP2 (416) have been associated with synaptogenesis. Furthermore, our results only account for association of this genetic expression differences with differences in microstructure and cellular densities defining gyri from sulci during gyrification. It is imperative for proper understanding of cortical folding that causality is established through further experiments. Nonetheless, these results argue in favour of a hypothesis where these genes have central roles in

regulating dendrogenesis sooner and more extensively in gyri compared to sulci, shaping distinct microstructural fingerprints between these two regions. Thus, we hypothesise that both these genes and the aforementioned process are pivotal for gyrification during gyrification; a conjecture that needs to be further pursued by proper knock out studies.

Chapter 6 – Project Discussion and Conclusion

Discussion and Conclusion

The main aim of this project was to further elucidate the genetic drivers underlying the development of gyri and sulci during gyrification, and to determine whether differences in gene expression might be associated with the architectural differences between these two structures. It is well documented that gyrification is associated with a number of clinical implications for the individual (32, 153, 417), and although many theories have been proposed for this process (64, 93, 101), the exact mechanisms driving cortical folding remain elusive. To date, a number of studies have uncovered a myriad of genes with known implications for gyrification (for recent reviews, see (4), (3), and (43)). However, the fact that some genes have been associated with gyrification does not readily mean that those genes are involved in gyrification *during* gyrification, i.e. involved in the formation of gyri and sulci during the process of cortical folding. This, in combination with other challenges discussed before (see "Further perspectives" in Chapter 1) makes the study of gyrification a complex matter. We used the sheep model to account for these challenges and evaluate whether there are regional genetic differences between gyri and sulci tCP *during* gyrification that could account for the different morphologies exhibited by said regions. This has been evaluated in the past for deeper layers of the cortex in the ferret (174).

Given that gyrification in sheep is known to start around gestational age (GA) 70, after the first major lateral fissure starts forming (193) and continues at least until GA 110 (194), we decided to sample the tCP in detail at GA 90 to evaluate our hypothesis of DE genes involved in gyrification during gyrification.

We extracted RNA from cells coming from a fixed gyrus and sulcus tCP obtained through LCM, sequenced it and compared the results from both regions using edgeR and edgeRun analyses. While our results are consistent with other reports using similar bioinformatic approaches (264), we could not determine DE genes between gyri and sulci using this approach alone. We hypothesised that the biological variability and genetic differences between the analysed specimens were more robust than the genetic differences between gyri and sulci (Figure 13), which could explain the inability of the pipeline to discern statistically significant differences in gene expression between gyri and sulci. Nonetheless, when applying a complementary pipeline which selected DE genes based on (i) a combination of the unadjusted p values from the edgeRun output, (ii) the fold change in the counts analysed in the sequencer, (iii) the number of total reads, (iv) the presence of these genes in developmentally important pathways and (v) in previous reports, we found a number of genes worth

validating as potentially DE between gyri and sulci. These genes included, but were not limited to, BDNF, CDK5, HDAC5, MeCP2 and NeuroD6, which have been described involved in several cellular processes associated with gyrification in the cortex (see chapter 5).

We firstly validated these genes at the same developmental stage (GA 90) that we used for the *in silico* analysis, and found that not only the differences in these genes between gyri and sulci suggested by our previous *in silico* analysis were correct, but they were a feature of gyri and sulci throughout the rostro-caudal extent of the cortex during gyrification. Interestingly, as the samples we collected RNA from originated exclusively from the frontal (CX2) portion of the cortex, our findings suggested that we might have tapped onto a general feature of gyri and sulci. We then moved on to determine whether the observed differences in gene expression were still present later in gyrification (GA 110), or before the process had taken place (GA 70). We found that prior to gyrification, the eCP of fetal sheep showed no differences in genetic expression throughout the eCP or rostro-caudally throughout the cortex between sulci and gyri. Nevertheless, the differences between gyri and sulci for CDK5, HDAC5, MeCP2 and NeuroD6 found during gyrification (GA 90) were not sustained after gyrification had occurred (GA 110). Only BDNF-positive cell density sustained this gyri-to-sulci difference. Also, at this later stage of brain development we found BDNF having increased positive cell density towards the rostral side of the cortex, which might reflect the delayed maturation of the frontal cortex (352), in which some functions such as memory (279) and inhibitory control (353) have been correlated with BDNF. NeuroD6 showed increased positive cell density towards the caudal pole at this later stage, which might suggest a role for NeuroD6 in the development of the visual cortex, which undergoes important changes in late brain development (354). However, technical difficulties and financial constraints impeded the extraction of RNA of sufficient quantity to perform both sequencing and qRT-PCR on the samples to validate a larger number of DE genes between gyri and sulci; the RNA extracted using LCM was exhausted in the sequencing step. Nonetheless, detection and analysis of RNA using FISH validates our results for HDAC5 and MeCP2. Future approaches for validation of other genes at the RNA level consider the utilisation of qRT-PCR and other techniques.

To further put these differences in genetic expression between gyri and sulci during gyrification in context, we suggested several hypotheses regarding neurite outgrowth in the tCP between gyri and sulci and changes in their microstructure during gyrification. We also hypothesised about the previously validated genes and their association with both neurite outgrowth and the main components of the tCP: neurons, astrocytes and microglia. Importantly, neurite outgrowth was a pathway that was constantly repeated in our pathway analysis conducted for shortlisting our genes

for validation (Supplementary Table 4). Nonetheless, and even when many of the genes we hypothesised associated with neurite outgrowth during this developmental stage have been associated with other processes also known to occur concomitantly with gyrification (e.g. axonogenesis and synaptogenesis), we focused on neurite outgrowth because it represented a strong candidate process that could account for the mechanical forces necessary to explain the tangential expansion of the cortex during gyrification (see "Rationale" in Chapter 5).

Dendrogenesis in sheep had only been partially described in the past (until GA 90 (191)), whereas here we described it throughout gyrification (from GA 90 to GA 110). Furthermore, and most importantly, we described that this process is upregulated in gyri compared to sulci throughout the cortex, even when the gene we investigated as proxy for this cellular process (MAP2) was not found differentially expressed in our *in silico* analysis. However MAP1S, another microtubule-associated protein, was observed as potentially differentially expressed between gyri and sulci in study 1 (Supplementary Table 1). MAP1S, similarly to MAP2, shows subcellular distribution for both the soma and dendrites of, at least, cerebellar Purkinje cells (418), suggesting that MAP1S might also be indeed differentially expressed between gyri and sulci during gyrification in sheep, and also involved in dendrogenesis, as both MAP1S and MAP2 harbour similar functions in stabilising microtubules (418). Nonetheless, the prevalence of this difference in MAP2 immunoreactivity between gyri and sulci throughout the cortex showed us that this appears to be a general feature of gyri and sulci during gyrification.

We also showed that this upregulation in dendrogenesis in the tCP of gyri compared to sulci is associated with differential microstructure between these two regions, and these differences were also consistent throughout the cortex. The NODDI analysis performed in Chapter 5 strongly suggested us that the differences observed in genetic expression between gyri and sulci do actually translate into microstructural differences between gyri and sulci, which, similar to the genetic differences between gyri and sulci addressed here, are consistent throughout the cortex rostro-caudally during gyrification. We also showed that the genes we previously validated are associated with neurite outgrowth at GA 90, and are associated mainly with neurons, which comprise the majority of the cells in the tCP during gyrification. These results allow us to hypothesise that, during gyrification, neurite outgrowth is an essential process defining the regional architecture of the tCP. We further hypothesise that these regional differences in neurite outgrowth are controlled by regional differences in expression of the hereby validated genes, and possibly many more that we are yet to uncover or validate.

The genes hereby described in association with MAP2 and dendrogenesis might indeed only be a fraction of the genetic differences between gyri and sulci during gyrification. Another gene we shortlisted in study 1 but did not select for further studies (DYNLT1) also strengthens our hypothesis of dendrogenesis being central for the differences between in gyri and sulci during gyrification, as DYNLT1-transfected neurons develop longer and more elaborate MAP2-positive dendrites (239). Also, the list of potentially DE genes obtained from edgeRun showed a number of genes being controlled by the transcription factor MEF2, however MEF2 itself was not in the list. This is relevant because MAP2 expression is affected by MEF2 (384). Thus, the list of genes might indeed contain a number of DE genes between gyri and sulci that could point towards cellular processes other than dendrogenesis that might still be relevant in defining the microarchitecture of gyri and sulci.

We have just began to understand the genetic mechanisms controlling gyrification. We should keep moving towards developing appropriate models for studying cortical folding abnormalities and moving towards gyrencephalic models given that, for example, previous models of lissencephaly through mutation of PAFAH1B1 in mice fail to mimic the human phenotype (312). And while highly valuable and informative, the results arising from these models pose significant challenges in their translation to gyrencephalic animals, and ultimately into treatments for human conditions where abnormal folding occurs during development. Furthermore, we should also keep in mind that gyrification might only be partially controlled genetically, but is also sensitive to environmental (22) and intrauterine factors (44). This will in the future allow us to properly arrive at a complete picture of gyrification and how it is controlled and determined, and develop proper treatment, diagnostic and therapeutic approaches to prevent, mitigate or at least ameliorate the effects of a misfolded cerebral cortex.

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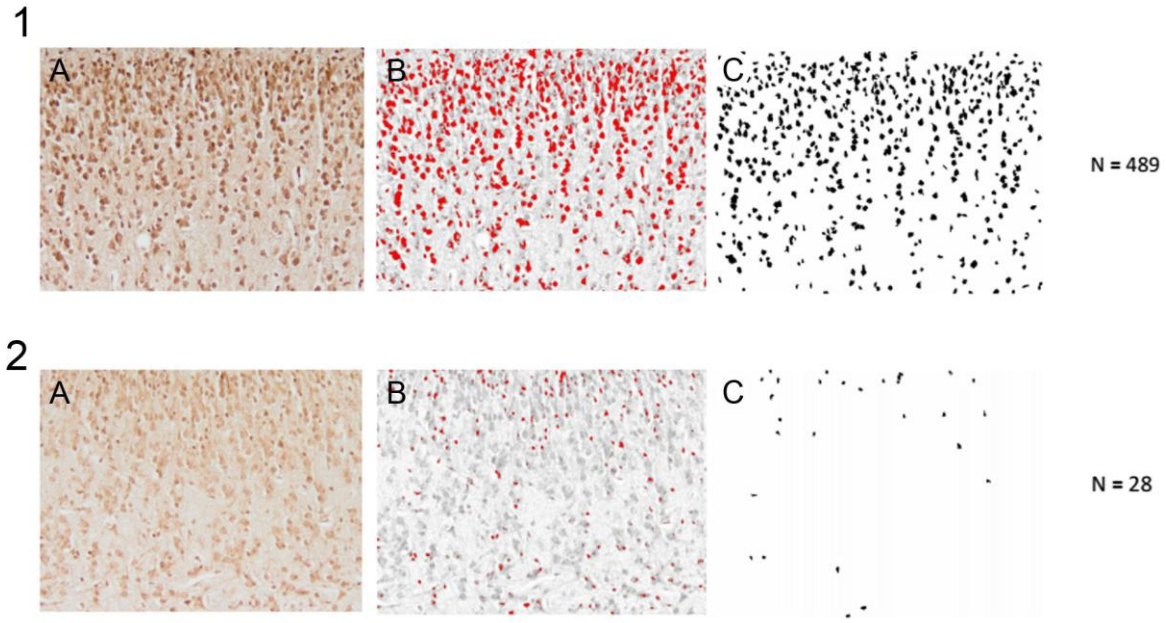
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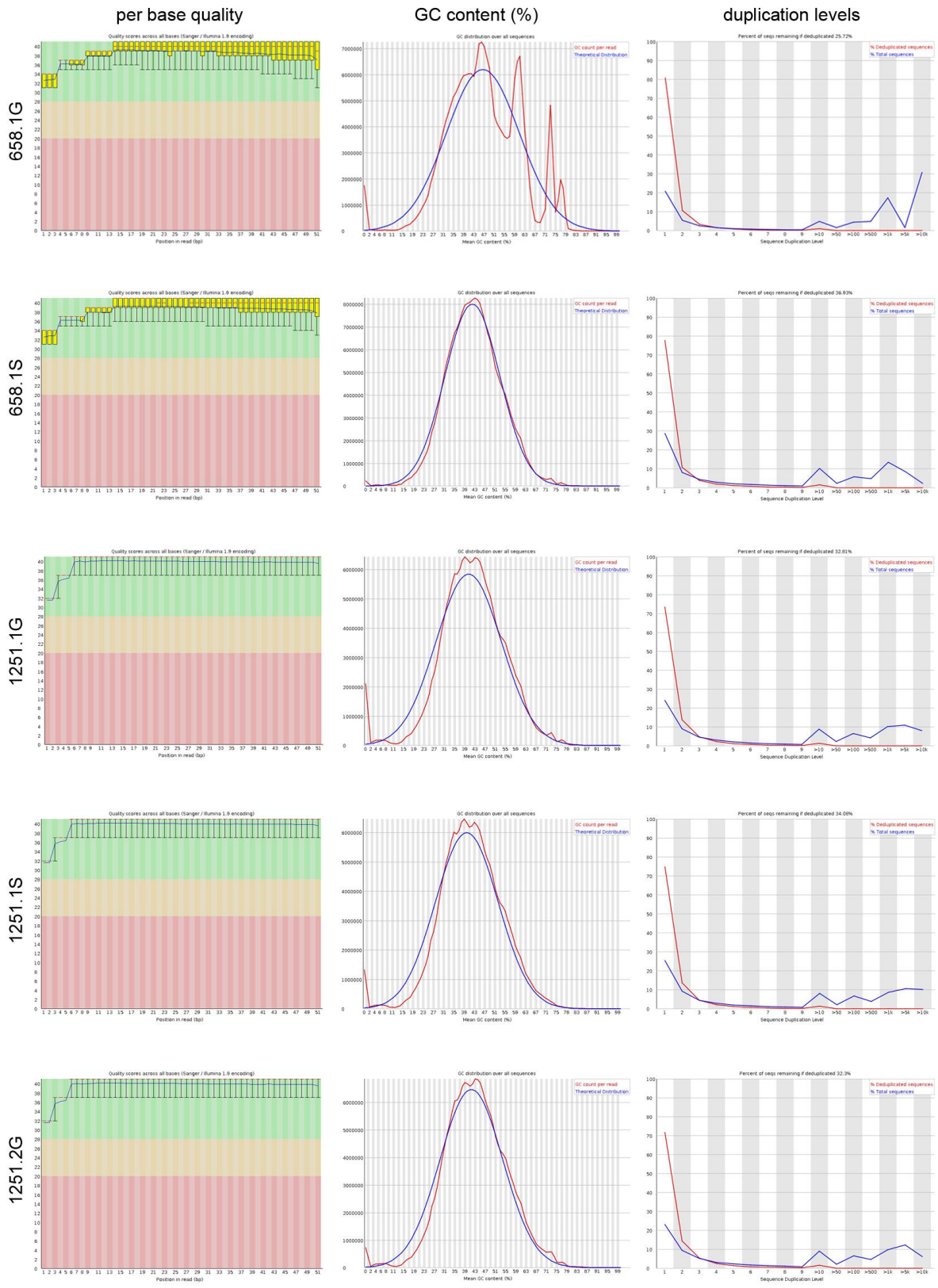
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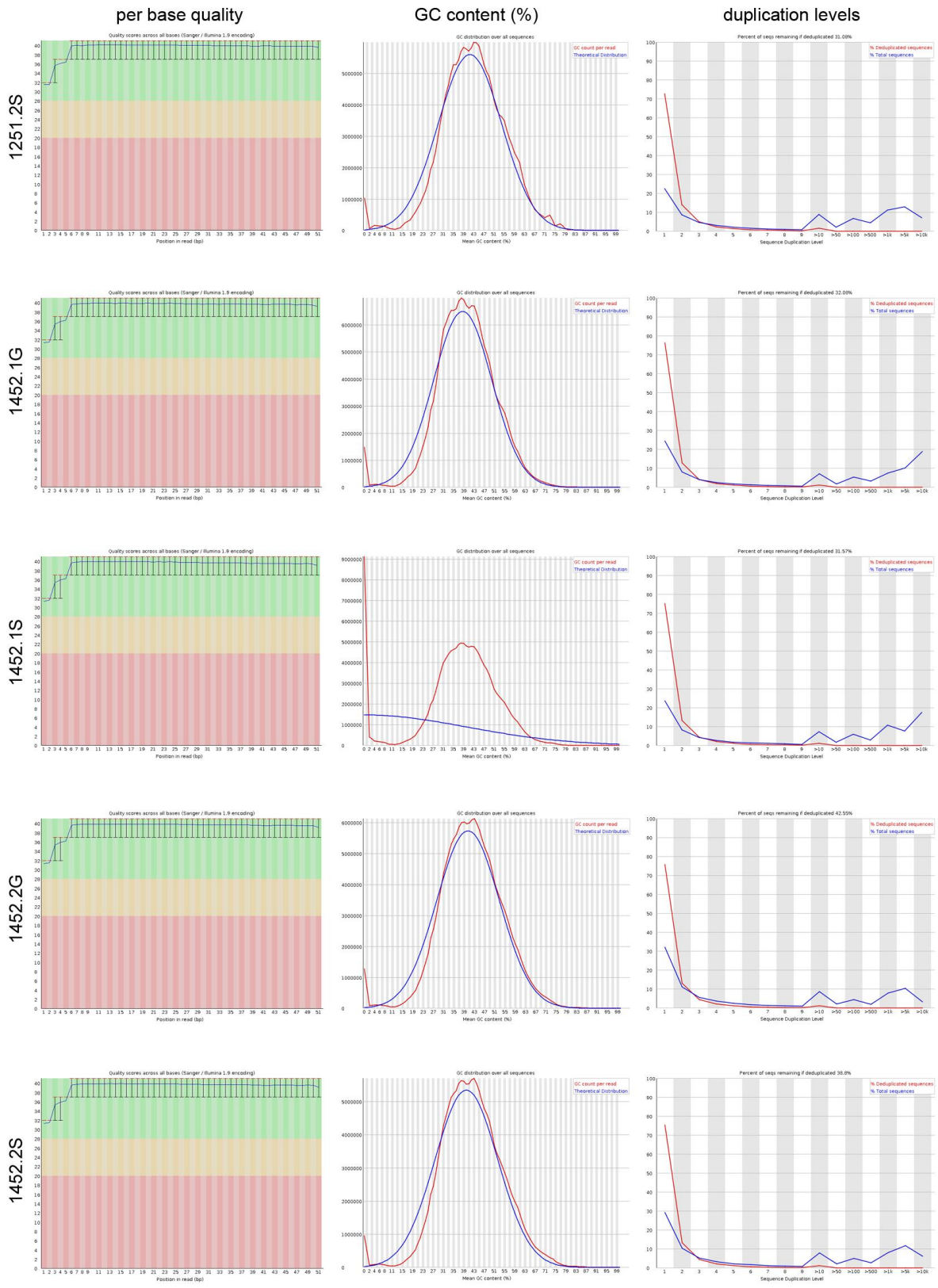
Appendix 1 – Supplementary Information

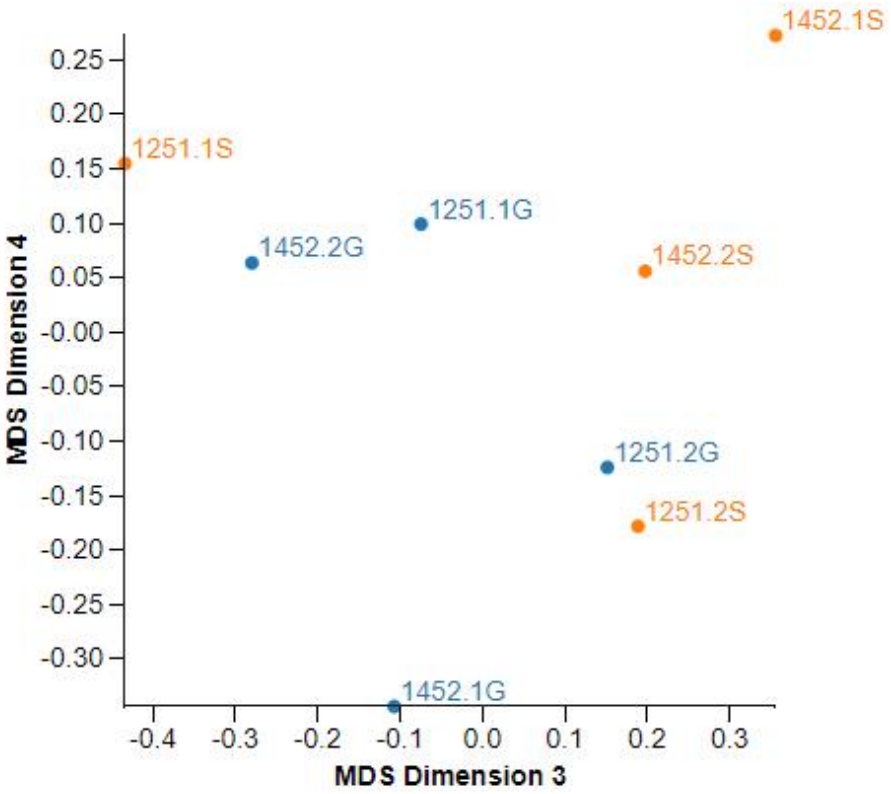


Supplementary Figure 1. Threshold analysis of expression. Example of a threshold analysis of expression for protein immunoreactivity in a gyrus (1) and a sulcus (2). A: photograph showing the upper layers of the cerebral cortex of a DAB immunohistochemistry reaction; B: in red, the signal that is above the previously determined threshold for detection; C: as in B, but the signal that is below the detection threshold has been removed. The counts (N) for each region analysed are presented.



Supplementary Figure 2. Sequencing QC. Overall look of the most important aspects of the quality control for sequencing the gyri and sulci samples RNA. Numbers are animal number with sample type (G, gyrus; S, sulcus). Per base quality, GC content histogram and duplication level plots are shown.


per base quality
GC content (%)
duplication levels
1251.2S
1452.1G
1452.1S
1452.2G
1452.2S



Supplementary Figure 3. MDS plot for dimensions 3 and 4. MDS plot showing the principal component analysis dimensions 3 and 4 of the RNA samples used in this study. Sample labels are sheep number + sample type; G: gyrus; S: sulcus.

Supplementary Table 1. edgeRun genes with unadjusted p < 0.05. Genes with an unadjusted p < 0.05 after the edgeRun analysis. ID, symbol, logarithm of fold change (logFC), logarithm of counts per million (logCPM), unadjusted p value (Unadj p value) and score (see methods) are presented.

Ensembl Gene ID	Gene Symbol	logFC	logCPM	Unadj p value	Score	Ensembl Gene ID	Gene Symbol	logFC	logCPM	Unadj p value	Score
ENSOARG00000005161	DNAH1	-0.128	2.861	0.016	3.973	ENSOARG00000016954	TTC32	-0.071	2.271	0.010	3.332
ENSOARG00000004785	PIK3CG	-1.156	1.439	0.011	3.584	ENSOARG00000015068	SLC10A5	-0.026	2.325	0.020	3.331
ENSOARG00000003199	SHC1	-0.376	2.350	0.016	3.710	ENSOARG00000006429	CYP2R1	0.291	2.069	0.029	3.330
ENSOARG00000004051	DVL1	0.761	1.943	0.009	3.695	ENSOARG00000004506	NA	-0.612	1.728	0.012	3.328
ENSOARG00000009438	APOE	-0.345	-0.004	0.016	1.325	ENSOARG00000001661	NA	0.898	1.441	0.012	3.326
ENSOARG00000010462	CXCR4	0.743	2.568	0.012	4.299	ENSOARG00000007757	RBM15B	-0.093	2.239	0.005	3.326
ENSOARG00000001337	CAV1	-0.234	2.975	0.017	4.192	ENSOARG00000004583	SNRNP35	0.263	2.070	0.011	3.323
ENSOARG00000020866	IL1B	-0.649	0.677	0.007	2.319	ENSOARG00000012232	WBSCR22	0.440	1.891	0.009	3.322
ENSOARG00000013457	PIN1	1.083	0.296	0.017	2.362	ENSOARG00000013827	NA	0.382	1.969	0.032	3.319
ENSOARG00000015899	EFNB3	0.170	3.332	0.046	4.457	ENSOARG00000003467	HMOX2	0.136	2.184	0.005	3.316
ENSOARG00000020173	SEMA5B	0.656	2.407	0.007	4.056	ENSOARG00000010551	PLEKHM1	0.038	2.283	0.011	3.311
ENSOARG00000006382	UNC5B	-1.011	1.673	0.006	3.679	ENSOARG00000019665	RPGRIP1	0.352	1.979	0.020	3.311
ENSOARG00000012066	SEMA4B	0.225	1.785	0.008	3.002	ENSOARG00000006698	RRP9	1.261	1.056	0.006	3.311
ENSOARG00000006187	MAPKAPK2	-0.222	3.312	0.016	4.518	ENSOARG00000009397	TRMT1	0.369	1.983	0.042	3.310
ENSOARG00000000156	PRKCD	0.232	2.034	0.028	3.238	ENSOARG00000001455	EXOG	-0.392	1.931	0.013	3.310
ENSOARG00000013329	MAP3K3	-0.701	0.846	0.016	2.530	ENSOARG00000017460	RAC3	0.001	2.337	0.029	3.309
ENSOARG00000011674	MATK	0.412	0.606	0.022	1.997	ENSOARG00000015392	SHCBP1	0.462	1.860	0.013	3.309
ENSOARG00000003246	IKBKB	0.047	0.804	0.025	1.825	ENSOARG00000002711	ADCK1	-1.103	1.208	0.004	3.307
ENSOARG00000015817	CACNG4	-0.400	2.264	0.034	3.629	ENSOARG00000002801	SLC4A2	0.568	1.778	0.042	3.304
ENSOARG00000008974	ADAM11	0.272	2.259	0.021	3.510	ENSOARG00000008168	NA	0.210	2.116	0.024	3.302
ENSOARG00000005434	ZIC1	-0.626	2.503	0.034	4.095	ENSOARG00000006169	SNRPE	0.544	1.763	0.008	3.300
ENSOARG00000017704	NOTCH4	-0.314	2.351	0.013	3.652	ENSOARG00000003661	TOX2	-0.932	1.395	0.026	3.300
ENSOARG00000016485	PMP22	-0.737	1.645	0.010	3.372	ENSOARG00000000077	NA	0.277	2.037	0.014	3.299
ENSOARG00000012718	NFKB1	-0.481	1.865	0.010	3.336	ENSOARG00000002488	NA	0.638	1.699	0.037	3.299
ENSOARG00000003820	NOTCH1	-0.655	1.340	0.011	2.983	ENSOARG00000018156	HAUS8	-0.737	1.572	0.010	3.299
ENSOARG00000011631	AXIN1	-0.035	0.594	0.010	1.619	ENSOARG00000015491	NA	-0.902	1.412	0.016	3.298
ENSOARG00000019441	RHOB	0.049	0.559	0.018	1.589	ENSOARG00000001936	RNF175	-0.211	2.100	0.014	3.296
ENSOARG00000003148	ZBTB2	0.099	3.957	0.018	5.038	ENSOARG00000007585	TANC1	-0.523	1.799	0.028	3.295
ENSOARG00000015505	KLF5	0.397	4.794	0.009	6.183	ENSOARG00000015028	DNAH9	-0.222	2.083	0.011	3.295
ENSOARG00000002924	CCND3	-0.187	2.137	0.028	3.296	ENSOARG00000018400	NA	-0.223	2.078	0.009	3.292
ENSOARG00000004119	MYCBPAP	0.755	0.830	0.007	2.578	ENSOARG00000006358	CSF1R	-0.191	2.112	0.011	3.291
ENSOARG00000020147	MYCL	-0.604	0.980	0.028	2.556	ENSOARG00000012960	DCP1B	-0.124	2.189	0.023	3.290
ENSOARG00000001680	SFRP2	-0.200	1.075	0.015	2.259	ENSOARG00000019145	TST	0.683	1.612	0.009	3.286
ENSOARG00000001851	FGF1	-0.430	0.799	0.020	2.209	ENSOARG00000000361	NA	1.082	1.207	0.004	3.286
ENSOARG00000008899	SFRP4	0.073	1.875	0.044	2.904	ENSOARG00000004941	PBLD	0.916	1.377	0.008	3.285
ENSOARG00000012212	PRR11	0.018	2.364	0.022	3.360	ENSOARG00000003372	FLNC	-0.415	1.912	0.047	3.281
ENSOARG00000012336	TLE4	-0.662	5.544	0.037	7.169	ENSOARG00000024537	NA	0.258	2.034	0.012	3.279
ENSOARG00000000855	SH3RF3	-0.363	2.108	0.049	3.422	ENSOARG00000009875	UBE2U	-0.703	1.606	0.031	3.278

ENSOARG00000010129	BACE2	-0.614	4.580	0.012	6.182	ENSOARG00000010523	JAG1	0.057	2.232	0.011	3.277
ENSOARG00000006744	POMT1	0.124	2.578	0.022	3.679	ENSOARG00000007400	ESYT3	-0.072	2.222	0.019	3.275
ENSOARG00000001811	TNNI3	0.502	1.567	0.033	3.035	ENSOARG00000016587	ESPL1	-0.710	1.579	0.015	3.274
ENSOARG00000009603	PNPLA4	0.236	0.812	0.030	2.018	ENSOARG00000008626	PRRG3	-0.114	2.167	0.009	3.272
ENSOARG00000002748	NRXN3	0.016	5.119	0.008	6.127	ENSOARG00000006664	LITAF	-0.318	1.985	0.033	3.270
ENSOARG00000002633	CDK5	0.593	4.835	0.034	6.394	ENSOARG00000014469	KLK14	-0.608	1.699	0.037	3.270
ENSOARG00000006843	NUMBL	-0.123	2.194	0.023	3.294	ENSOARG00000008265	CCDC130	0.061	2.225	0.017	3.270
ENSOARG00000016087	TSEN2	0.079	2.370	0.013	3.436	ENSOARG00000002065	IFT43	-0.450	1.845	0.028	3.267
ENSOARG00000015118	BDNF	0.975	0.943	0.010	2.909	ENSOARG00000012807	ADIPOR2	0.405	1.870	0.011	3.264
ENSOARG00000004402	DYNLT1	0.596	5.151	0.036	6.712	ENSOARG00000010864	SPTLC3	-0.817	1.450	0.004	3.263
ENSOARG00000011728	BCL9L	0.072	5.278	0.012	6.338	ENSOARG00000017675	RNASEH2C	0.770	1.497	0.005	3.263
ENSOARG00000000883	CACNG7	0.132	6.175	0.012	7.295	ENSOARG00000023941	Metazoa_SRP	-0.160	2.106	0.006	3.261
ENSOARG00000014590	CRYM	0.030	6.933	0.025	7.938	ENSOARG00000019148	NA	-0.333	1.960	0.035	3.257
ENSOARG00000013670	COX5B	0.681	5.648	0.041	7.288	ENSOARG00000018841	NA	0.103	2.156	0.005	3.254
ENSOARG00000000847	PRRT1	0.351	5.856	0.018	7.189	ENSOARG00000013667	TBC1D17	0.910	1.361	0.018	3.254
ENSOARG00000011032	PRAF2	0.071	5.183	0.005	6.249	ENSOARG00000014070	DGAT1	0.640	1.631	0.018	3.253
ENSOARG00000006902	HDAC5	0.530	6.280	0.049	7.761	ENSOARG00000016181	ITGA5	-1.327	0.926	0.001	3.252
ENSOARG00000011175	HYPK	0.646	6.234	0.013	7.867	ENSOARG00000017643	ASPSCR1	0.207	2.087	0.044	3.250
ENSOARG00000012674	SLC39A12	-0.220	4.884	0.011	6.093	ENSOARG00000005827	GLMP	0.195	2.060	0.006	3.249
ENSOARG00000017717	SPG21	0.867	4.831	0.012	6.686	ENSOARG00000016195	ZNF385A	-0.591	1.665	0.008	3.249
ENSOARG00000009812	FREM2	-0.634	4.327	0.036	5.926	ENSOARG00000007446	NA	-0.812	1.441	0.005	3.247
ENSOARG00000008435	NEUROD6	0.540	7.940	0.028	9.452	ENSOARG00000007657	CDK20	0.144	2.132	0.030	3.246
ENSOARG00000006607	PLD3	-0.187	6.718	0.045	7.860	ENSOARG00000011724	TOR2A	-0.123	2.138	0.016	3.245
ENSOARG00000000135	PBX2	0.566	6.209	0.021	7.754	ENSOARG00000013343	PIEZO1	-0.153	2.108	0.015	3.245
ENSOARG00000014075	KCNIP3	0.273	4.542	0.016	5.800	ENSOARG00000018885	METTL21A	0.372	1.885	0.012	3.245
ENSOARG00000020222	ITGB5	-1.353	1.591	0.000	3.944	ENSOARG00000009661	FAM229B	0.793	1.488	0.038	3.243
ENSOARG00000002463	LXN	-0.330	0.955	0.011	2.274	ENSOARG00000018257	TRIM3	-0.275	1.979	0.015	3.239
ENSOARG00000015727	LUM	-0.046	6.072	0.026	7.092	ENSOARG00000016344	METTL12	0.747	1.498	0.006	3.239
ENSOARG00000013997	STARD7	-0.563	4.516	0.049	6.030	ENSOARG00000008656	NA	-0.359	1.893	0.013	3.239
ENSOARG00000017383	HTR2C	-0.437	4.424	0.005	5.856	ENSOARG00000017557	SPECC1	0.469	1.791	0.022	3.238
ENSOARG00000015737	DCN	-0.836	3.938	0.017	5.757	ENSOARG00000019689	MANSC4	-0.636	1.610	0.008	3.238
ENSOARG00000020386	APOD	-0.099	4.649	0.011	5.736	ENSOARG00000015295	GLRA3	0.098	2.149	0.010	3.237
ENSOARG00000011271	TMOD1	0.391	4.284	0.010	5.664	ENSOARG00000001588	NA	1.243	1.011	0.018	3.236
ENSOARG00000020689	HTR2B	0.482	3.880	0.040	5.322	ENSOARG00000019141	PREB	-0.358	1.922	0.045	3.235
ENSOARG00000021190	SMOC1	-0.715	3.510	0.031	5.193	ENSOARG00000008090	PELP1	-0.527	1.727	0.020	3.234
ENSOARG00000011464	SYT17	-0.218	3.978	0.016	5.180	ENSOARG00000013335	IRF3	-0.662	1.591	0.020	3.233
ENSOARG00000019354	SLC7A8	0.743	3.371	0.022	5.092	ENSOARG00000018469	MTHFR	-0.504	1.733	0.010	3.227
ENSOARG00000013187	NEXN	0.105	3.988	0.011	5.082	ENSOARG00000000573	NA	-0.147	2.087	0.007	3.226
ENSOARG00000003329	SULF1	0.296	3.589	0.019	4.866	ENSOARG00000010421	SLC27A4	0.258	2.005	0.037	3.226
ENSOARG00000016952	ENDOD1	-0.738	3.064	0.028	4.773	ENSOARG00000003678	ZNF549	0.708	1.536	0.018	3.226
ENSOARG00000006068	ZFP36	0.716	2.959	0.013	4.662	ENSOARG00000003219	PLAGL2	0.417	1.832	0.025	3.225
ENSOARG00000011189	NUF2	0.285	3.330	0.030	4.585	ENSOARG00000025175	TOB2	-0.182	2.051	0.010	3.224
ENSOARG00000009349	KNTC1	-0.826	2.744	0.004	4.567	ENSOARG00000005908	ERCC6L	0.558	1.688	0.023	3.223
ENSOARG00000008440	CDC14B	-0.349	3.248	0.033	4.564	ENSOARG00000005473	GSN	-0.419	1.811	0.011	3.219

ENSOARG00000005787	WFS1	0.478	3.086	0.029	4.535	ENSOARG00000001319	ZNF205	0.440	1.823	0.045	3.218
ENSOARG00000020908	RAB27A	0.683	2.799	0.026	4.455	ENSOARG00000004578	PABPC1L	-0.416	1.832	0.031	3.217
ENSOARG00000012748	GPNMB	1.837	1.540	0.000	4.376	ENSOARG00000011529	ZFR2	0.495	1.734	0.011	3.217
ENSOARG00000015960	KCTD12	0.035	3.342	0.030	4.347	ENSOARG00000003475	NRDE2	-0.183	2.055	0.024	3.214
ENSOARG00000000106	VRK1	0.073	3.279	0.011	4.341	ENSOARG00000015755	NA	1.173	1.073	0.032	3.214
ENSOARG00000018923	PAMR1	0.616	2.734	0.013	4.336	ENSOARG00000017328	F3	-0.440	1.786	0.014	3.213
ENSOARG00000016482	FAM189A1	0.015	3.337	0.019	4.332	ENSOARG00000017714	CCDC184	0.335	1.891	0.015	3.210
ENSOARG00000016700	PHLDA1	0.070	3.294	0.041	4.323	ENSOARG00000007302	UBE3D	-0.675	1.555	0.021	3.209
ENSOARG00000003080	STK3	-0.675	2.690	0.042	4.323	ENSOARG00000017214	NR4A1	0.488	1.760	0.039	3.209
ENSOARG00000020887	CKAP2L	-0.229	3.045	0.012	4.262	ENSOARG00000008279	MRPS18A	0.758	1.495	0.047	3.206
ENSOARG00000020658	TXNIP	0.068	3.197	0.013	4.252	ENSOARG00000014325	DSCR3	-0.631	1.580	0.007	3.204
ENSOARG00000008358	CD79A	1.178	2.054	0.014	4.218	ENSOARG00000020862	AZIN2	1.099	1.116	0.013	3.203
ENSOARG00000014795	GLIPR1	1.024	2.185	0.003	4.206	ENSOARG00000004352	SIAH2	0.270	1.957	0.026	3.201
ENSOARG00000014133	ADAMTSL1	-0.331	2.890	0.030	4.191	ENSOARG00000016072	TWNK	0.403	1.805	0.008	3.200
ENSOARG00000014918	TSHZ2	-0.391	2.831	0.034	4.188	ENSOARG00000012840	RPP21	-0.027	2.184	0.012	3.199
ENSOARG00000004495	HELLS	-0.566	2.518	0.037	4.048	ENSOARG00000020669	HIST2H2BF	-0.607	1.598	0.009	3.196
ENSOARG00000015665	MAD2L1	0.060	2.981	0.033	4.007	ENSOARG00000000311	NA	0.171	2.036	0.014	3.192
ENSOARG00000000933	CYP46A1	0.034	3.017	0.044	4.006	ENSOARG00000020219	IVD	-0.459	1.760	0.027	3.192
ENSOARG00000004195	SLC16A9	-0.536	2.469	0.005	4.000	ENSOARG00000012624	C2orf81	1.132	1.062	0.003	3.191
ENSOARG00000014947	CCDC150	-1.080	1.886	0.003	3.963	ENSOARG00000021048	SHF	0.074	2.126	0.009	3.191
ENSOARG00000004813	SDC2	-0.217	2.788	0.043	3.962	ENSOARG00000000185	DPF3	-0.561	1.636	0.007	3.190
ENSOARG00000004800	EEPD1	0.094	2.851	0.025	3.920	ENSOARG00000015153	NA	0.160	2.042	0.012	3.190
ENSOARG00000005552	SPINT2	0.369	2.555	0.029	3.895	ENSOARG00000016086	GFRA3	1.045	1.152	0.007	3.189
ENSOARG00000019636	LBH	1.256	1.651	0.016	3.892	ENSOARG00000008070	TMEM241	0.042	2.160	0.014	3.187
ENSOARG00000015864	SOCS2	0.281	2.599	0.042	3.838	ENSOARG00000008203	CD99	0.982	1.235	0.030	3.186
ENSOARG00000017996	NIT2	0.176	2.651	0.016	3.811	ENSOARG00000015858	NA	1.006	1.186	0.007	3.186
ENSOARG00000000578	CDCA7	0.187	2.629	0.017	3.799	ENSOARG00000008441	NA	-0.140	2.077	0.039	3.178
ENSOARG00000015100	ANGPT1	-0.628	2.182	0.015	3.795	ENSOARG00000009405	TOMM40	0.426	1.773	0.022	3.177
ENSOARG00000004441	SLC41A1	0.729	2.072	0.031	3.770	ENSOARG00000025785	NA	-0.353	1.872	0.048	3.176
ENSOARG00000018865	KIAA1671	0.065	2.692	0.009	3.748	ENSOARG00000005282	ORC1	0.764	1.419	0.010	3.173
ENSOARG00000015964	TACC3	1.238	1.507	0.004	3.741	ENSOARG00000001777	RAB13	-0.290	1.894	0.011	3.173
ENSOARG00000017490	THBS4	-0.800	1.945	0.007	3.738	ENSOARG00000019051	SDR39U1	-0.119	2.059	0.010	3.168
ENSOARG00000011260	MFGE8	-0.555	2.190	0.021	3.724	ENSOARG00000008041	TXNRD3	-0.560	1.633	0.025	3.167
ENSOARG00000006371	ADAMTS6	-0.797	1.934	0.024	3.707	ENSOARG00000003986	ITPA	0.236	1.938	0.012	3.163
ENSOARG00000005231	WDR62	0.712	1.970	0.012	3.669	ENSOARG00000014631	JAK3	0.256	1.949	0.046	3.159
ENSOARG00000003163	PTPN21	-0.807	1.809	0.021	3.595	ENSOARG00000010220	ZDHHC16	0.034	2.146	0.022	3.158
ENSOARG00000017443	PDLIM5	-0.733	1.865	0.032	3.566	ENSOARG00000006678	JMJD6	-0.273	1.894	0.009	3.158
ENSOARG00000010682	PACSIN1	-0.017	2.554	0.017	3.554	ENSOARG00000008707	TICAM1	0.097	2.083	0.022	3.157
ENSOARG00000008988	PLCG2	-0.378	2.147	0.024	3.501	ENSOARG00000017219	TMED1	-0.749	1.416	0.008	3.157
ENSOARG00000002050	TGFB3	0.244	2.270	0.024	3.490	ENSOARG00000002706	ENTPD3	-0.568	1.603	0.015	3.155
ENSOARG00000020313	SGPP2	-0.610	1.874	0.015	3.469	ENSOARG00000020987	RFX5	-0.024	2.138	0.007	3.155
ENSOARG00000010283	MX1	-0.744	1.712	0.017	3.439	ENSOARG00000009978	FBXO32	0.406	1.786	0.037	3.155
ENSOARG00000008418	SOSTDC1	0.218	2.190	0.016	3.393	ENSOARG00000013282	NCAPD3	-0.078	2.080	0.005	3.154
ENSOARG00000014364	PIM1	-0.031	2.350	0.009	3.371	ENSOARG00000008999	ZNF234	-0.118	2.084	0.048	3.153

ENSOARG00000002158	VASH1	-0.517	1.883	0.038	3.361	ENSOARG00000019693	NA	-0.824	1.329	0.005	3.148
ENSOARG00000001113	COL16A1	0.866	1.494	0.029	3.332	ENSOARG00000005097	ERMARD	0.341	1.836	0.035	3.142
ENSOARG00000021097	PELI2	0.041	2.303	0.014	3.330	ENSOARG00000013180	SHROOM1	0.264	1.896	0.018	3.142
ENSOARG00000007469	ANKRD55	0.408	1.947	0.050	3.305	ENSOARG00000015055	KIF13B	-0.006	2.181	0.045	3.142
ENSOARG00000008473	PLAU	0.108	2.213	0.032	3.289	ENSOARG00000018385	PMM1	0.115	2.044	0.017	3.142
ENSOARG00000003370	MME	-0.850	1.476	0.050	3.276	ENSOARG00000026926	NA	0.006	2.166	0.031	3.141
ENSOARG00000016024	LIMS2	0.738	1.537	0.022	3.254	ENSOARG00000004773	AGPAT4	-0.401	1.752	0.013	3.140
ENSOARG00000007935	PLA2G4A	0.171	2.086	0.046	3.211	ENSOARG00000020493	ELMOD3	-0.436	1.727	0.023	3.140
ENSOARG00000018916	MYH15	-0.781	1.401	0.006	3.176	ENSOARG00000003249	CSK	-0.197	1.979	0.036	3.140
ENSOARG00000019985	DENND2C	-0.323	1.886	0.041	3.168	ENSOARG00000009894	SH3GL1	0.070	2.090	0.021	3.139
ENSOARG00000020018	SHANK3	-0.156	2.015	0.009	3.161	ENSOARG00000000535	CIB2	0.033	2.133	0.027	3.139
ENSOARG00000017007	GGA2	-0.076	2.077	0.011	3.142	ENSOARG00000004960	NA	-0.221	1.926	0.009	3.138
ENSOARG00000016152	MTMR10	-0.306	1.822	0.011	3.117	ENSOARG00000003894	THBS3	-0.715	1.462	0.038	3.138
ENSOARG00000003647	EFNA1	0.397	1.731	0.016	3.111	ENSOARG00000018733	NA	0.063	2.084	0.010	3.137
ENSOARG00000016515	CNIH3	-0.277	1.821	0.018	3.080	ENSOARG00000005087	PTCD2	-0.161	1.996	0.020	3.137
ENSOARG00000003451	SLC20A2	0.474	1.601	0.028	3.047	ENSOARG00000009890	NA	0.209	1.960	0.033	3.136
ENSOARG00000013649	VOPP1	0.779	1.238	0.007	3.010	ENSOARG00000006542	FAM159B	0.334	1.814	0.014	3.135
ENSOARG00000015211	KIF18A	0.179	1.824	0.010	2.993	ENSOARG00000019951	SSPN	0.159	1.993	0.018	3.135
ENSOARG00000001037	TWSG1	-0.263	1.733	0.023	2.974	ENSOARG00000010446	NA	-0.147	2.022	0.035	3.134
ENSOARG00000006008	KLHL14	-0.212	1.731	0.011	2.933	ENSOARG00000014267	LRWD1	-0.370	1.776	0.012	3.133
ENSOARG00000006142	IFIH1	-0.026	1.916	0.015	2.927	ENSOARG00000018794	CYB5D2	0.984	1.153	0.004	3.133
ENSOARG00000014141	ANKRD13A	-0.227	1.694	0.046	2.875	ENSOARG00000018498	PEX10	0.274	1.883	0.024	3.133
ENSOARG00000005603	KHDRBS2	0.465	1.424	0.035	2.853	ENSOARG00000004047	RBFA	0.268	1.876	0.012	3.132
ENSOARG00000008821	SLC25A34	-0.666	1.209	0.022	2.853	ENSOARG00000011578	TICRR	0.133	2.028	0.028	3.132
ENSOARG00000001470	LY6E	0.017	1.838	0.012	2.844	ENSOARG00000010966	NA	-1.144	0.988	0.004	3.129
ENSOARG00000005573	MAGEH1	0.457	1.269	0.021	2.706	ENSOARG00000004292	ADAMTS10	0.159	2.006	0.037	3.128
ENSOARG00000014754	CAPS2	0.183	1.536	0.017	2.702	ENSOARG00000011406	ARFGAP1	0.482	1.669	0.027	3.125
ENSOARG00000013281	HIST2H2AC	-0.158	1.554	0.016	2.697	ENSOARG00000022353	SNORA8	0.316	1.821	0.012	3.125
ENSOARG00000019414	MMP14	-0.335	1.259	0.047	2.548	ENSOARG00000010821	ARHGAP6	0.745	1.388	0.008	3.125
ENSOARG00000016663	INPP5A	-0.007	1.557	0.021	2.544	ENSOARG00000016716	MGAT1	-0.357	1.787	0.021	3.123
ENSOARG00000015876	IL17RB	-0.032	1.511	0.022	2.521	ENSOARG00000004516	UBOX5	-0.239	1.892	0.009	3.122
ENSOARG00000007690	S1PR3	0.209	1.301	0.016	2.494	ENSOARG00000007841	THUMPD2	-0.059	2.099	0.037	3.122
ENSOARG00000018135	MYO19	0.106	1.388	0.008	2.486	ENSOARG00000000953	NA	-0.183	1.958	0.022	3.120
ENSOARG00000006520	UBE2C	-0.226	1.267	0.009	2.483	ENSOARG00000011042	NA	0.560	1.583	0.024	3.120
ENSOARG00000001522	TAF7L	0.073	1.406	0.005	2.474	ENSOARG00000009542	DCAKD	-1.084	1.039	0.003	3.119
ENSOARG00000005591	KIF22	-0.461	1.006	0.005	2.463	ENSOARG00000004247	NA	0.905	1.229	0.014	3.119
ENSOARG00000004339	RHPN2	0.508	0.878	0.019	2.367	ENSOARG00000003375	NA	0.019	2.135	0.036	3.118
ENSOARG00000011997	UBA7	0.791	0.558	0.009	2.340	ENSOARG00000000582	SLC25A53	-0.619	1.537	0.039	3.117
ENSOARG00000013108	CHCHD10	0.003	1.323	0.024	2.302	ENSOARG00000009348	NA	-0.721	1.434	0.038	3.117
ENSOARG00000011508	ENAM	0.528	0.659	0.040	2.147	ENSOARG00000013022	TMEM182	0.200	1.929	0.013	3.116
ENSOARG00000014521	WDR37	-0.022	1.144	0.020	2.146	ENSOARG00000015940	TMCC3	0.094	2.049	0.028	3.115
ENSOARG00000003292	CKS1B	-0.035	1.099	0.016	2.118	ENSOARG00000007356	LRRC73	-0.033	2.103	0.022	3.114
ENSOARG00000014898	ADAMTS1	-0.014	1.105	0.010	2.108	ENSOARG00000001300	XYLB	0.486	1.659	0.036	3.109
ENSOARG00000014885	ANGPTL6	0.266	0.832	0.013	2.086	ENSOARG00000012419	NA	0.271	1.874	0.037	3.108

ENSOARG00000001274	CDC25B	-0.020	1.038	0.022	2.036	ENSOARG00000008496	ZNF646	-0.217	1.930	0.040	3.108
ENSOARG00000003341	IFI6	0.134	0.897	0.017	2.015	ENSOARG00000018515	NA	0.116	2.002	0.013	3.105
ENSOARG00000016322	ANGPTL1	-0.209	0.796	0.023	1.981	ENSOARG00000008067	SNX18	-0.161	1.966	0.023	3.104
ENSOARG00000010786	SLC35F2	0.270	0.713	0.015	1.968	ENSOARG00000000763	ASPHD2	-0.681	1.447	0.025	3.103
ENSOARG00000003114	DENND3	-0.595	0.402	0.029	1.967	ENSOARG00000014174	CCM2	0.021	2.091	0.010	3.102
ENSOARG00000012262	GPC4	0.247	0.471	0.017	1.701	ENSOARG00000020564	TMEM41A	-0.037	2.103	0.039	3.101
ENSOARG00000000918	TFPI2	0.290	0.390	0.015	1.665	ENSOARG00000016385	NA	0.391	1.728	0.018	3.101
ENSOARG00000018018	CHST12	0.127	0.381	0.032	1.475	ENSOARG00000011053	NA	-0.799	1.338	0.039	3.098
ENSOARG00000013734	DDIT4L	-0.094	0.282	0.036	1.340	ENSOARG00000014271	MOXD1	0.120	1.986	0.010	3.097
ENSOARG00000010442	ALDH4A1	0.062	0.285	0.029	1.318	ENSOARG00000007923	ACBD7	0.169	1.942	0.014	3.096
ENSOARG00000023742	SNORA79	-0.045	0.169	0.018	1.196	ENSOARG00000002346	PPP1R16A	-0.582	1.549	0.041	3.091
ENSOARG00000012444	BAX	0.295	0.928	0.010	2.212	ENSOARG00000009980	PCP4L1	0.108	2.005	0.022	3.091
ENSOARG00000018795	NTNG1	0.109	3.715	0.042	4.782	ENSOARG00000007092	NA	-0.774	1.343	0.027	3.090
ENSOARG00000020935	SEMA6C	-0.224	1.986	0.018	3.192	ENSOARG00000015456	POLN	0.483	1.644	0.040	3.087
ENSOARG00000014901	MYB	-0.263	2.435	0.015	3.683	ENSOARG00000009725	NA	-0.015	2.086	0.015	3.087
ENSOARG00000013779	SOX9	0.348	1.418	0.010	2.756	ENSOARG00000015698	MNT	-0.120	1.986	0.019	3.086
ENSOARG00000013030	SNAI2	0.582	0.520	0.019	2.083	ENSOARG00000010679	SLC25A19	-0.249	1.873	0.037	3.085
ENSOARG00000016191	PAX6	0.290	3.343	0.014	4.619	ENSOARG00000018035	MMP2	-0.447	1.649	0.012	3.084
ENSOARG00000005806	MECP2	0.183	2.506	0.014	3.675	ENSOARG00000006713	NA	-0.340	1.747	0.005	3.082
ENSOARG00000001772	FOXP2	-1.301	3.859	0.034	6.125	ENSOARG00000014933	HAS1	0.348	1.761	0.027	3.081
ENSOARG00000004165	ISLR2	0.300	6.090	0.007	7.383	ENSOARG00000007030	EVC2	-0.066	2.025	0.011	3.080
ENSOARG00000013191	RPS11	0.410	8.697	0.039	10.068	ENSOARG00000013157	TIMP1	0.316	1.767	0.005	3.078
ENSOARG00000009101	RPS18	0.532	6.785	0.050	8.267	ENSOARG00000013598	RGS12	0.003	2.090	0.015	3.077
ENSOARG00000014457	RPL18A	0.488	6.542	0.030	8.000	ENSOARG00000013644	PTOV1	0.110	1.969	0.009	3.070
ENSOARG00000012645	RPL8	0.471	6.237	0.037	7.671	ENSOARG00000000307	SMOX	-0.154	1.950	0.034	3.070
ENSOARG00000009322	ARAP2	-0.579	7.300	0.004	8.875	ENSOARG00000002208	PRELID2	-0.435	1.657	0.022	3.070
ENSOARG00000014799	RASGRF1	-0.153	6.231	0.035	7.348	ENSOARG00000011389	KCTD2	-0.138	1.953	0.026	3.065
ENSOARG00000003022	ATPIF1	0.745	5.701	0.014	7.433	ENSOARG00000020944	TSSK3	-0.214	1.860	0.009	3.065
ENSOARG00000011218	SARNP	0.500	6.688	0.032	8.156	ENSOARG00000009268	FAM219A	-0.328	1.767	0.031	3.064
ENSOARG00000017985	ARHGDIA	0.544	5.851	0.036	7.359	ENSOARG00000017040	STBD1	-0.397	1.701	0.035	3.063
ENSOARG00000003312	DIRAS2	0.509	6.044	0.030	7.522	ENSOARG00000015423	HIF1AN	-0.064	2.013	0.014	3.063
ENSOARG00000005284	FKBP2	0.547	5.292	0.044	6.796	ENSOARG00000012090	TMEM104	-0.667	1.402	0.008	3.061
ENSOARG00000014655	ZMIZ2	-0.084	6.331	0.007	7.408	ENSOARG00000014942	MMAB	-0.374	1.734	0.050	3.059
ENSOARG00000025253	NA	0.053	13.073	0.021	14.106	ENSOARG00000012647	MRPS18B	-0.174	1.904	0.021	3.058
ENSOARG00000018972	NA	0.105	7.888	0.009	8.983	ENSOARG00000017435	RRP8	-0.742	1.319	0.004	3.057
ENSOARG00000026777	NA	0.753	7.209	0.029	8.932	ENSOARG00000015752	TMEM109	0.527	1.554	0.024	3.057
ENSOARG00000021831	NA	0.194	6.811	0.014	7.991	ENSOARG00000019701	NA	0.367	1.713	0.024	3.056
ENSOARG00000007328	NA	0.683	6.156	0.013	7.826	ENSOARG00000016351	PGLS	0.077	2.020	0.043	3.054
ENSOARG00000018032	NA	0.595	6.240	0.014	7.821	ENSOARG00000019637	NA	-0.250	1.819	0.017	3.053
ENSOARG00000006531	NA	-0.510	6.267	0.015	7.762	ENSOARG00000010843	DTL	-0.087	1.986	0.022	3.050
ENSOARG00000006118	NA	0.636	6.105	0.022	7.719	ENSOARG00000017311	DFNB59	0.479	1.578	0.012	3.045
ENSOARG00000005384	NA	-0.115	6.592	0.015	7.692	ENSOARG00000000341	RNPEP	-0.541	1.537	0.035	3.044
ENSOARG00000008518	HOOK1	-0.474	6.043	0.043	7.473	ENSOARG00000006295	RIDA	-0.355	1.701	0.012	3.044
ENSOARG00000009588	NA	0.493	5.898	0.038	7.352	ENSOARG00000009232	PFDN6	0.257	1.800	0.015	3.043

ENSOARG00000006981	PRDX5	0.653	5.638	0.011	7.281	ENSOARG00000004712	FXYD7	-0.250	1.812	0.020	3.041
ENSOARG00000013126	RPS21	0.557	5.768	0.045	7.280	ENSOARG00000010860	GSS	-0.478	1.598	0.035	3.041
ENSOARG00000003689	RPS28	0.832	5.439	0.006	7.264	ENSOARG00000005358	TRAPPC12	-0.562	1.489	0.010	3.041
ENSOARG00000013861	MPDZ	-0.495	5.781	0.035	7.241	ENSOARG00000019976	GLB1L	0.106	1.966	0.035	3.037
ENSOARG00000000078	KIT	-1.037	5.184	0.004	7.217	ENSOARG00000014926	ADGRD1	-0.872	1.180	0.016	3.036
ENSOARG00000018666	NA	0.472	5.760	0.024	7.207	ENSOARG00000005388	MRPL2	0.975	1.073	0.013	3.036
ENSOARG00000002624	NA	0.635	5.517	0.025	7.127	ENSOARG00000017045	NA	0.489	1.552	0.008	3.032
ENSOARG00000015724	EDIL3	-0.584	5.554	0.026	7.112	ENSOARG00000001722	NA	-0.421	1.626	0.016	3.031
ENSOARG00000013155	NA	0.872	5.247	0.007	7.112	ENSOARG00000008206	CENPN	-0.306	1.739	0.015	3.030
ENSOARG00000008365	RPS19	0.655	5.503	0.048	7.110	ENSOARG00000026186	NA	0.451	1.612	0.033	3.029
ENSOARG00000006262	NA	0.605	5.495	0.008	7.092	ENSOARG00000008164	GRN	0.022	2.016	0.012	3.026
ENSOARG00000015199	P2RY1	-0.649	5.429	0.003	7.075	ENSOARG00000010111	NA	-0.684	1.385	0.044	3.024
ENSOARG00000010824	SPCS2	0.475	5.609	0.046	7.037	ENSOARG00000008612	IQCD	0.235	1.805	0.019	3.021
ENSOARG00000004010	SNRK	-0.534	5.491	0.024	7.002	ENSOARG00000012282	NA	0.260	1.799	0.038	3.020
ENSOARG00000010861	TACR3	0.941	4.975	0.006	6.909	ENSOARG00000016225	SFXN3	-0.387	1.645	0.014	3.018
ENSOARG00000005021	C11orf49	0.406	5.527	0.045	6.888	ENSOARG00000000876	PPFIA4	-0.426	1.611	0.020	3.017
ENSOARG00000016968	C11orf87	0.191	5.700	0.023	6.867	ENSOARG00000025585	NA	0.683	1.352	0.018	3.016
ENSOARG00000002297	CHST1	0.552	5.174	0.033	6.693	ENSOARG00000014253	SLC7A11	-0.291	1.766	0.042	3.015
ENSOARG00000004871	COL1A1	0.113	5.539	0.034	6.618	ENSOARG00000014770	TMEM170B	-0.251	1.785	0.022	3.014
ENSOARG00000021125	DHRS7	0.545	5.097	0.027	6.615	ENSOARG00000007437	VPS37B	0.384	1.640	0.011	3.013
ENSOARG00000010540	SV2B	-1.038	4.591	0.021	6.607	ENSOARG00000009347	DSE	-0.589	1.429	0.011	3.006
ENSOARG00000012837	NA	-0.407	5.112	0.043	6.475	ENSOARG00000010755	CYP39A1	-0.651	1.381	0.025	3.006
ENSOARG00000016652	PCNX3	-0.375	5.077	0.048	6.404	ENSOARG00000008433	TMCO3	0.004	2.007	0.006	3.005
ENSOARG00000004590	DAP3	0.594	4.794	0.021	6.367	ENSOARG00000011723	AADACL3	-0.151	1.863	0.011	3.003
ENSOARG00000018276	SMAD3	0.766	4.585	0.012	6.340	ENSOARG00000010405	BMP1	-0.266	1.751	0.014	3.003
ENSOARG00000011605	NA	0.547	4.819	0.042	6.324	ENSOARG00000001636	SI	0.283	1.752	0.033	3.001
ENSOARG00000004715	NA	-0.213	5.077	0.031	6.259	ENSOARG00000010427	IRF2BP1	0.360	1.660	0.019	3.000
ENSOARG00000006213	C1orf123	0.688	4.582	0.018	6.251	ENSOARG00000000637	EHMT1	-0.449	1.565	0.014	3.000
ENSOARG00000005542	NA	0.661	4.613	0.044	6.230	ENSOARG00000007261	NOM1	0.617	1.387	0.011	2.993
ENSOARG00000019965	FMN1	-0.070	5.117	0.018	6.169	ENSOARG00000014239	NFATC2	0.638	1.402	0.049	2.991
ENSOARG00000009775	SH3BGR	0.438	4.779	0.049	6.169	ENSOARG00000005257	GZF1	0.590	1.411	0.011	2.989
ENSOARG00000009954	NA	0.071	5.099	0.008	6.162	ENSOARG00000009883	ZSCAN29	0.249	1.749	0.008	2.989
ENSOARG00000012133	NA	0.736	4.388	0.012	6.112	ENSOARG00000006577	LRRC71	0.279	1.727	0.018	2.988
ENSOARG00000002429	SDF2	0.607	4.536	0.049	6.094	ENSOARG00000004651	MRPL27	0.055	1.941	0.009	2.988
ENSOARG00000025366	NA	-0.003	5.100	0.009	6.094	ENSOARG00000017270	NA	0.181	1.816	0.011	2.986
ENSOARG00000003264	TIMP2	-0.252	4.867	0.033	6.086	ENSOARG00000011146	PADI2	-0.194	1.804	0.013	2.986
ENSOARG00000015124	PTPRQ	-0.427	4.632	0.018	6.042	ENSOARG00000007562	C19orf70	1.083	0.903	0.003	2.984
ENSOARG00000010069	MYL6	0.615	4.446	0.042	6.019	ENSOARG00000020857	DUSP16	-0.002	1.991	0.010	2.984
ENSOARG00000017553	NA	0.643	4.373	0.033	5.983	ENSOARG00000011347	FBRSL1	-0.004	1.991	0.014	2.980
ENSOARG00000004091	NA	0.539	4.469	0.038	5.970	ENSOARG00000003715	NA	-0.113	1.887	0.021	2.980
ENSOARG00000000484	ALDOC	-0.511	4.495	0.049	5.957	ENSOARG00000005926	PCOLCE2	0.112	1.891	0.023	2.979
ENSOARG00000009260	QPCT	0.093	4.865	0.028	5.930	ENSOARG00000020268	ZNF684	0.638	1.348	0.008	2.978
ENSOARG00000020686	PYGL	-0.777	4.150	0.011	5.916	ENSOARG00000019279	ZNF641	-0.130	1.870	0.021	2.978
ENSOARG00000019904	NDUFB4	0.704	4.227	0.023	5.907	ENSOARG00000009296	NUDT2	0.312	1.681	0.016	2.977

ENSOARG00000010485	NA	0.062	4.834	0.011	5.885	ENSOARG00000020545	ELOVL1	0.268	1.755	0.046	2.977
ENSOARG00000012745	RNF123	-0.364	4.530	0.014	5.879	ENSOARG00000018821	NA	0.194	1.829	0.047	2.976
ENSOARG00000019216	EMC9	0.578	4.312	0.030	5.860	ENSOARG00000007284	ARHGAP10	-0.768	1.255	0.048	2.976
ENSOARG00000004464	KCTD15	-0.269	4.585	0.012	5.842	ENSOARG00000015279	NA	-0.258	1.724	0.007	2.976
ENSOARG00000015122	C11orf1	-0.536	4.318	0.013	5.841	ENSOARG00000007312	SCPEP1	0.228	1.764	0.016	2.975
ENSOARG00000002248	TBC1D9B	0.160	4.690	0.013	5.837	ENSOARG00000015230	BTD	-0.539	1.476	0.041	2.974
ENSOARG00000000751	NA	-0.053	4.806	0.033	5.825	ENSOARG00000016938	CXorf58	-1.023	0.959	0.007	2.974
ENSOARG00000004432	NA	0.878	3.944	0.007	5.815	ENSOARG00000002033	NADK	-0.013	1.967	0.009	2.970
ENSOARG00000017563	ZCCHC17	-0.482	4.330	0.006	5.806	ENSOARG00000004476	NA	0.326	1.648	0.010	2.964
ENSOARG00000015846	PLEC	-0.218	4.598	0.011	5.805	ENSOARG00000018763	UNC119	-0.374	1.608	0.018	2.964
ENSOARG00000010753	NA	-0.996	3.817	0.018	5.794	ENSOARG00000013735	ANKRD39	0.026	1.946	0.009	2.963
ENSOARG00000015804	TMEM132A	0.465	4.329	0.018	5.776	ENSOARG00000026770	NA	0.345	1.653	0.035	2.963
ENSOARG00000025327	NA	0.640	4.129	0.016	5.753	ENSOARG00000008733	ASB6	-0.581	1.392	0.012	2.961
ENSOARG00000011886	ZNF804B	-0.698	4.054	0.013	5.740	ENSOARG00000017642	THAP4	-0.193	1.779	0.012	2.960
ENSOARG00000014242	NA	0.289	4.479	0.033	5.735	ENSOARG00000013926	NA	0.256	1.716	0.012	2.960
ENSOARG00000000665	ATP6V0B	0.682	4.052	0.008	5.726	ENSOARG00000020087	HIST1H3I	0.120	1.846	0.010	2.956
ENSOARG00000004307	NA	0.757	3.973	0.019	5.711	ENSOARG00000009874	KCTD9	0.148	1.832	0.025	2.955
ENSOARG00000013051	SDHAF2	0.730	4.015	0.036	5.709	ENSOARG00000009407	AMER3	0.010	1.967	0.025	2.952
ENSOARG00000008916	TATDN1	0.623	4.113	0.042	5.694	ENSOARG00000019387	NA	-0.550	1.427	0.027	2.950
ENSOARG00000010704	ADRA2A	0.760	3.933	0.016	5.678	ENSOARG00000000381	RFT1	0.218	1.775	0.045	2.948
ENSOARG00000018901	PPIC	-0.101	4.582	0.018	5.665	ENSOARG00000009028	MKRN3	-0.227	1.730	0.009	2.948
ENSOARG00000004753	NA	-0.034	4.637	0.009	5.662	ENSOARG00000025504	NA	0.878	1.083	0.019	2.942
ENSOARG00000006456	RPL29	0.636	4.064	0.048	5.652	ENSOARG00000007357	PIGM	0.390	1.561	0.010	2.941
ENSOARG00000007985	NA	-0.010	4.645	0.028	5.628	ENSOARG00000010163	GCDH	0.247	1.705	0.015	2.937
ENSOARG00000008094	NA	-0.690	3.958	0.030	5.618	ENSOARG00000025168	CORT	-0.992	0.955	0.011	2.936
ENSOARG00000007064	NA	-0.121	4.493	0.011	5.604	ENSOARG00000016969	NA	-0.073	1.886	0.023	2.935
ENSOARG00000007080	CNTNAP4	-0.209	4.407	0.012	5.603	ENSOARG00000012489	AIP	0.144	1.836	0.045	2.934
ENSOARG00000000340	TCEB2	0.786	3.826	0.011	5.601	ENSOARG00000013943	ARG1	1.137	0.800	0.004	2.933
ENSOARG00000011718	INTS6L	-0.093	4.504	0.009	5.587	ENSOARG00000002607	LENG8	0.008	1.935	0.011	2.932
ENSOARG00000000037	NA	0.718	3.867	0.025	5.560	ENSOARG00000018079	MTERF4	-0.181	1.766	0.019	2.928
ENSOARG00000001771	CAMSAP3	0.151	4.404	0.020	5.535	ENSOARG00000008288	NECAB3	0.023	1.914	0.009	2.927
ENSOARG00000009504	NA	0.573	3.993	0.048	5.518	ENSOARG00000003311	POFUT1	-0.362	1.581	0.016	2.927
ENSOARG00000013658	TBC1D7	0.770	3.751	0.016	5.505	ENSOARG00000013141	MS4A13	-0.041	1.901	0.017	2.926
ENSOARG00000015186	ACSS3	0.403	4.115	0.018	5.499	ENSOARG00000000613	NA	-0.953	0.978	0.005	2.926
ENSOARG00000025737	NA	0.216	4.283	0.009	5.490	ENSOARG00000019389	CCDC121	0.220	1.730	0.024	2.925
ENSOARG00000004733	RXFP1	-0.410	4.100	0.043	5.468	ENSOARG00000000369	ECHS1	0.202	1.732	0.009	2.925
ENSOARG00000013027	NR1D1	-0.191	4.260	0.017	5.434	ENSOARG00000000695	ALKBH5	-0.209	1.726	0.010	2.925
ENSOARG00000020816	RORA	-0.720	3.731	0.024	5.427	ENSOARG00000006667	UCK1	0.372	1.580	0.028	2.925
ENSOARG00000020540	HAUS2	0.011	4.406	0.009	5.407	ENSOARG00000003724	NA	0.260	1.671	0.010	2.921
ENSOARG00000013448	POR	0.084	4.324	0.011	5.396	ENSOARG00000005654	PRIM2	0.074	1.854	0.008	2.920
ENSOARG00000008233	ECM2	-0.290	4.106	0.009	5.387	ENSOARG00000001296	ZNF696	-0.228	1.710	0.020	2.919
ENSOARG00000019935	NA	0.695	3.733	0.046	5.382	ENSOARG00000008963	PTER	-0.401	1.561	0.043	2.919
ENSOARG00000018267	NA	0.879	3.509	0.013	5.376	ENSOARG00000011232	KIAA0513	0.029	1.920	0.035	2.914
ENSOARG00000004647	ZNF385D	-0.089	4.305	0.018	5.376	ENSOARG00000019987	NA	-0.385	1.557	0.028	2.914

ENSOARG00000005149	KCNIP4	0.301	4.120	0.048	5.374	ENSOARG00000020986	USP50	0.739	1.191	0.017	2.913
ENSOARG00000015582	TBC1D4	-0.577	3.824	0.043	5.357	ENSOARG00000012990	TMEM256-PLSCR3	0.574	1.358	0.019	2.913
ENSOARG00000017596	NA	0.469	3.901	0.015	5.356	ENSOARG00000001162	NA	-0.260	1.677	0.023	2.913
ENSOARG00000006462	MAP3K10	0.223	4.124	0.006	5.342	ENSOARG00000012704	PCBP3	0.004	1.919	0.017	2.906
ENSOARG00000004284	PLPP4	0.423	3.945	0.029	5.339	ENSOARG00000017191	SIPA1	1.031	0.887	0.013	2.905
ENSOARG00000006390	GPR137	-0.044	4.298	0.005	5.337	ENSOARG00000022193	JPX_1	-0.217	1.706	0.019	2.904
ENSOARG00000003767	EPHX3	0.599	3.781	0.048	5.332	ENSOARG00000006125	NA	-0.474	1.438	0.010	2.902
ENSOARG00000001485	METAP1D	-0.591	3.749	0.035	5.305	ENSOARG00000013818	NA	-0.448	1.464	0.012	2.899
ENSOARG00000015805	WDR6	-0.167	4.138	0.010	5.295	ENSOARG00000005858	NR1H3	0.955	0.955	0.011	2.899
ENSOARG00000002391	MSRB2	0.212	4.091	0.018	5.284	ENSOARG00000020882	TEX9	-0.510	1.400	0.011	2.899
ENSOARG00000011891	PLEKHG5	-0.056	4.215	0.012	5.258	ENSOARG00000012879	SEMA4F	0.165	1.748	0.016	2.898
ENSOARG00000010384	PHYHIP	-0.312	3.958	0.025	5.245	ENSOARG00000003896	LAMTOR1	0.880	1.023	0.006	2.897
ENSOARG00000011479	CRTAC1	0.266	4.008	0.044	5.231	ENSOARG00000010269	FAM114A1	-0.186	1.716	0.005	2.897
ENSOARG00000011951	NA	0.450	3.785	0.006	5.229	ENSOARG00000000304	ACKR3	-0.018	1.910	0.032	2.895
ENSOARG00000006033	FAM198B	0.076	4.189	0.039	5.226	ENSOARG00000014583	PEX2	0.051	1.858	0.015	2.894
ENSOARG00000011298	EXOSC7	0.753	3.504	0.033	5.225	ENSOARG00000010962	ADAMTS9	-0.399	1.507	0.013	2.893
ENSOARG00000003506	ATP6V1F	0.851	3.365	0.011	5.204	ENSOARG00000000916	TNFAIP8L3	-0.864	1.035	0.008	2.892
ENSOARG00000011142	CRTC1	-0.124	4.056	0.011	5.169	ENSOARG00000020209	CHPF	0.142	1.762	0.017	2.887
ENSOARG00000008033	B4GALNT4	0.099	4.081	0.012	5.167	ENSOARG00000019578	ANO6	0.149	1.776	0.039	2.886
ENSOARG00000005894	CDH20	-0.021	4.151	0.007	5.166	ENSOARG00000003628	YIF1A	0.505	1.388	0.012	2.881
ENSOARG00000015743	SELENOK	0.666	3.533	0.040	5.159	ENSOARG00000008897	SMG9	-0.249	1.647	0.015	2.881
ENSOARG00000026257	NA	-0.578	3.591	0.011	5.158	ENSOARG00000019768	ADPRH	-0.117	1.787	0.026	2.878
ENSOARG00000000561	NA	0.711	3.458	0.021	5.148	ENSOARG00000004498	DHDDS	-0.083	1.802	0.009	2.876
ENSOARG00000006046	ICA1	-0.602	3.579	0.044	5.138	ENSOARG00000025513	NA	0.269	1.636	0.031	2.875
ENSOARG00000004212	NA	-0.508	3.654	0.029	5.132	ENSOARG00000000601	FLYWCH2	-0.159	1.720	0.005	2.874
ENSOARG00000009551	FYB	-0.222	3.917	0.011	5.128	ENSOARG00000010452	NA	1.149	0.727	0.003	2.872
ENSOARG00000006348	NA	0.612	3.541	0.035	5.118	ENSOARG00000020210	TMEM198	0.424	1.495	0.047	2.872
ENSOARG00000006396	USP35	-1.353	2.762	0.011	5.103	ENSOARG00000019605	BRD1	-0.149	1.732	0.009	2.872
ENSOARG00000018052	PTRHD1	0.143	3.986	0.026	5.103	ENSOARG00000008429	MRPL14	0.478	1.441	0.047	2.871
ENSOARG00000002042	CYBRD1	-0.194	3.922	0.028	5.087	ENSOARG00000009485	LRRK1	-0.477	1.408	0.015	2.870
ENSOARG00000025592	NA	0.402	3.715	0.031	5.086	ENSOARG00000013853	NARFL	0.846	1.043	0.020	2.869
ENSOARG00000011103	NA	0.556	3.544	0.041	5.059	ENSOARG00000009616	CLASRP	0.382	1.492	0.006	2.868
ENSOARG00000020582	MGST1	-0.892	3.178	0.011	5.058	ENSOARG00000017263	TMEM237	0.182	1.723	0.037	2.867
ENSOARG00000008751	GEMIN6	-0.139	3.930	0.014	5.055	ENSOARG00000018174	RPLP2	0.559	1.314	0.008	2.864
ENSOARG00000004887	TTYH3	-0.112	3.956	0.018	5.050	ENSOARG00000009697	GADD45GIP1	-0.361	1.527	0.026	2.862
ENSOARG00000003288	MAOB	-0.215	3.844	0.013	5.045	ENSOARG00000013008	FAM189A2	-0.086	1.786	0.010	2.862
ENSOARG00000008140	AHNAK2	-0.450	3.604	0.011	5.043	ENSOARG00000008898	POLRMT	0.873	0.998	0.011	2.859
ENSOARG00000012001	MLXIP	0.343	3.689	0.009	5.022	ENSOARG00000008498	NA	-0.252	1.618	0.012	2.858
ENSOARG00000018166	ADIPOR1	0.379	3.664	0.037	5.007	ENSOARG00000000255	NA	-0.046	1.821	0.009	2.858
ENSOARG00000012640	WDR54	-0.009	3.995	0.005	4.999	ENSOARG00000007324	SETD9	0.527	1.346	0.015	2.858
ENSOARG00000008561	UCP2	-0.266	3.749	0.016	4.999	ENSOARG00000007010	ARL6IP4	-0.134	1.734	0.011	2.857
ENSOARG00000008809	CADM4	-0.441	3.541	0.018	4.964	ENSOARG00000003982	NA	-0.538	1.330	0.012	2.856
ENSOARG00000015372	RGS9	0.222	3.745	0.014	4.953	ENSOARG00000013681	NA	0.316	1.545	0.008	2.853
ENSOARG00000017198	DDA1	0.610	3.375	0.035	4.950	ENSOARG00000005393	NA	0.107	1.759	0.013	2.853

ENSOARG00000004794	NA	0.690	3.299	0.041	4.948	ENSOARG00000020232	MYRFL	-0.330	1.528	0.006	2.852
ENSOARG00000007509	ZNF496	0.701	3.256	0.010	4.948	ENSOARG00000014248	LAYN	-0.537	1.334	0.022	2.849
ENSOARG00000002796	NA	0.054	3.914	0.028	4.939	ENSOARG00000016997	CCDC57	-0.476	1.385	0.014	2.848
ENSOARG00000019164	NEDD8	0.678	3.260	0.008	4.930	ENSOARG00000014255	BOP1	-0.136	1.720	0.009	2.847
ENSOARG00000009164	GALT	0.345	3.621	0.043	4.923	ENSOARG00000014647	TRIM66	-1.187	0.663	0.003	2.846
ENSOARG00000006443	PDZD4	0.273	3.665	0.021	4.916	ENSOARG00000011772	MRPL54	0.369	1.489	0.013	2.844
ENSOARG00000001551	BCHE	-0.487	3.464	0.036	4.915	ENSOARG00000018238	TEF	-0.018	1.835	0.010	2.842
ENSOARG00000009888	ZCCHC24	0.563	3.349	0.007	4.906	ENSOARG00000016973	NA	-0.090	1.762	0.013	2.840
ENSOARG00000020144	VANGL1	-0.783	3.140	0.020	4.902	ENSOARG00000012399	PIGQ	-0.045	1.803	0.009	2.839
ENSOARG00000013782	ALB	0.375	3.517	0.013	4.880	ENSOARG00000010079	SPATS1	0.503	1.341	0.006	2.838
ENSOARG00000003188	CREB3L1	0.074	3.809	0.024	4.859	ENSOARG00000005912	NA	0.043	1.810	0.017	2.836
ENSOARG00000001184	CHRNB4	0.068	3.793	0.018	4.843	ENSOARG00000011245	NAPA	0.076	1.781	0.020	2.836
ENSOARG00000013951	NRIP3	-0.374	3.486	0.021	4.839	ENSOARG00000010711	TSPAN9	0.588	1.268	0.021	2.835
ENSOARG00000004138	NA	0.682	3.178	0.036	4.824	ENSOARG00000025855	NA	1.069	0.773	0.009	2.833
ENSOARG00000002874	NA	0.342	3.487	0.013	4.816	ENSOARG00000010671	LZTS1	0.025	1.817	0.009	2.832
ENSOARG00000018063	DGCR8	0.703	3.121	0.014	4.811	ENSOARG00000001078	NA	0.075	1.772	0.015	2.832
ENSOARG00000003124	APOBR	0.129	3.683	0.007	4.805	ENSOARG00000015609	TMPPE	-0.831	1.000	0.005	2.826
ENSOARG00000019296	ZFHX2	-0.133	3.681	0.016	4.798	ENSOARG00000012374	TULP2	-0.385	1.459	0.019	2.825
ENSOARG00000015178	RNF4	-0.529	3.304	0.040	4.794	ENSOARG00000007541	CSF2RA	-0.488	1.351	0.014	2.825
ENSOARG00000015452	NA	-0.569	3.230	0.006	4.793	ENSOARG00000006831	DSC3	-0.826	1.006	0.008	2.824
ENSOARG00000000221	NA	0.060	3.745	0.013	4.792	ENSOARG00000006813	VEGFC	0.003	1.840	0.019	2.824
ENSOARG00000010995	NA	0.086	3.725	0.048	4.763	ENSOARG00000007524	PLEKHN1	0.423	1.411	0.011	2.823
ENSOARG00000012912	MAML3	0.284	3.494	0.025	4.753	ENSOARG00000013015	NA	0.376	1.460	0.014	2.823
ENSOARG00000014927	USP19	-0.696	3.062	0.006	4.752	ENSOARG00000004354	LMAN2	-0.160	1.689	0.028	2.822
ENSOARG00000012503	DTNBP1	0.610	3.183	0.042	4.751	ENSOARG00000000718	TGDS	-0.473	1.379	0.031	2.821
ENSOARG00000011661	SORCS2	-0.147	3.610	0.006	4.751	ENSOARG00000025407	NA	-0.170	1.668	0.018	2.820
ENSOARG00000003769	TRIM46	0.010	3.739	0.014	4.735	ENSOARG00000009312	RGL2	-0.065	1.758	0.008	2.815
ENSOARG00000006151	ANKFN1	0.006	3.713	0.012	4.708	ENSOARG00000018580	AASS	0.237	1.610	0.031	2.815
ENSOARG00000006760	LPAR1	-0.023	3.697	0.014	4.706	ENSOARG00000002192	ANGEL1	0.121	1.727	0.033	2.815
ENSOARG00000009832	KIAA1456	-0.678	3.069	0.047	4.699	ENSOARG00000011206	SPIDR	0.248	1.588	0.024	2.812
ENSOARG00000014122	C11orf88	1.343	2.359	0.005	4.696	ENSOARG00000005210	THAP8	0.178	1.679	0.044	2.812
ENSOARG00000017715	NHSL2	-0.516	3.181	0.010	4.688	ENSOARG00000016498	SLC27A1	0.347	1.466	0.007	2.806
ENSOARG00000007382	SDS	-0.063	3.634	0.011	4.685	ENSOARG00000008535	PRSS53	-0.249	1.583	0.027	2.805
ENSOARG00000000862	NA	-0.234	3.461	0.013	4.682	ENSOARG00000018379	EFEMP2	-0.708	1.109	0.011	2.805
ENSOARG00000003891	PTRH2	0.548	3.137	0.007	4.678	ENSOARG00000005176	LRFN3	0.029	1.808	0.033	2.804
ENSOARG00000019958	NA	-0.467	3.232	0.023	4.676	ENSOARG00000015870	PAH	0.000	1.818	0.017	2.802
ENSOARG00000015812	HFM1	-0.367	3.315	0.009	4.674	ENSOARG00000018845	NAGA	0.091	1.721	0.010	2.802
ENSOARG00000020586	CLCN2	-0.042	3.634	0.014	4.662	ENSOARG00000020234	CD58	-0.198	1.618	0.018	2.798
ENSOARG00000013025	SLC43A2	-0.161	3.507	0.006	4.662	ENSOARG00000010530	NA	-0.418	1.399	0.021	2.796
ENSOARG00000013810	MRPS14	0.725	2.947	0.010	4.662	ENSOARG00000004581	NA	0.553	1.251	0.009	2.795
ENSOARG00000015219	ZCCHC9	0.092	3.589	0.020	4.661	ENSOARG00000013528	RAI2	-0.112	1.713	0.033	2.792
ENSOARG00000003076	NDUFA3	0.764	2.905	0.018	4.651	ENSOARG00000018948	NA	0.760	1.037	0.006	2.791
ENSOARG00000012700	MRPL53	0.750	2.936	0.039	4.646	ENSOARG00000003086	KCNK10	-0.271	1.555	0.037	2.790
ENSOARG00000012989	CABLES2	-0.735	2.942	0.031	4.646	ENSOARG00000015442	MPP7	-0.044	1.756	0.013	2.788

ENSOARG00000009077	NKAPL	0.185	3.467	0.007	4.646	ENSOARG00000006572	NA	0.351	1.482	0.048	2.786
ENSOARG00000012162	ABLIM2	0.186	3.469	0.015	4.639	ENSOARG00000017313	GPC2	0.595	1.221	0.034	2.782
ENSOARG00000011683	NA	0.174	3.474	0.011	4.636	ENSOARG00000002802	DIO2	0.312	1.477	0.009	2.780
ENSOARG00000005323	HTR1A	-0.189	3.462	0.016	4.635	ENSOARG00000018076	CYB5R1	-0.419	1.391	0.031	2.779
ENSOARG00000006414	DIAPH3	-0.474	3.167	0.018	4.622	ENSOARG00000002018	WBP1L	-0.003	1.810	0.037	2.776
ENSOARG00000006369	MRPL55	0.481	3.156	0.015	4.622	ENSOARG00000021153	PLEKHG3	0.390	1.393	0.007	2.776
ENSOARG00000006538	PDGFRB	0.030	3.598	0.007	4.621	ENSOARG00000015551	MAP1S	-0.069	1.717	0.011	2.774
ENSOARG00000008978	ZNF283	0.124	3.493	0.011	4.606	ENSOARG00000019869	LMF2	0.333	1.453	0.013	2.773
ENSOARG00000008388	KDM4B	-0.262	3.368	0.026	4.604	ENSOARG00000001349	ISOC2	0.719	1.065	0.010	2.773
ENSOARG00000003838	AURKAIP1	0.506	3.098	0.009	4.596	ENSOARG00000012227	NA	0.237	1.570	0.041	2.766
ENSOARG00000014717	KIAA1462	0.209	3.393	0.011	4.591	ENSOARG00000005098	ST3GAL2	-0.204	1.570	0.009	2.765
ENSOARG00000002768	EVI5L	0.672	2.917	0.009	4.580	ENSOARG00000005511	NA	0.251	1.524	0.014	2.762
ENSOARG00000019702	NA	-0.565	3.021	0.008	4.577	ENSOARG00000016026	NA	-0.165	1.607	0.011	2.761
ENSOARG00000020657	LAMP3	-0.729	2.856	0.023	4.561	ENSOARG00000000770	ZNF202	-0.348	1.439	0.028	2.759
ENSOARG00000018183	NA	-0.074	3.490	0.005	4.560	ENSOARG00000011274	HSF2BP	0.495	1.293	0.029	2.758
ENSOARG00000016984	POLR2G	0.487	3.083	0.011	4.559	ENSOARG00000005300	NA	0.082	1.684	0.009	2.757
ENSOARG00000017982	FAM213B	0.813	2.731	0.006	4.539	ENSOARG00000004996	CCDC102B	-0.220	1.555	0.018	2.756
ENSOARG00000009774	NABP2	-0.029	3.501	0.011	4.518	ENSOARG00000024483	NA	0.438	1.345	0.027	2.756
ENSOARG00000015176	NUDT5	-0.716	2.804	0.009	4.511	ENSOARG00000015749	SLC12A9	0.443	1.325	0.012	2.756
ENSOARG00000000317	LOX	-0.398	3.114	0.006	4.505	ENSOARG00000026920	NA	0.054	1.734	0.032	2.756
ENSOARG00000014661	RNF144A	0.658	2.884	0.044	4.498	ENSOARG00000016312	LBHD1	-0.080	1.706	0.035	2.751
ENSOARG00000006032	NA	0.455	3.047	0.005	4.497	ENSOARG00000007293	ABCB9	0.345	1.428	0.026	2.747
ENSOARG00000014119	RARA	0.670	2.874	0.048	4.496	ENSOARG00000019557	CTDSP1	-0.441	1.317	0.011	2.747
ENSOARG00000008689	GAN	-0.291	3.214	0.013	4.493	ENSOARG00000012244	VTI1A	0.192	1.564	0.010	2.746
ENSOARG00000007018	NA	0.448	3.079	0.034	4.493	ENSOARG00000026625	NA	-0.160	1.598	0.013	2.746
ENSOARG00000013559	TMEM120A	0.925	2.569	0.006	4.488	ENSOARG00000006610	BCAR1	0.173	1.584	0.011	2.746
ENSOARG00000004781	NA	0.274	3.219	0.005	4.488	ENSOARG00000010687	MPG	0.118	1.651	0.024	2.745
ENSOARG00000010224	POLD3	-0.250	3.248	0.010	4.488	ENSOARG00000000818	TRIM68	0.278	1.474	0.009	2.743
ENSOARG00000007168	PYGB	-0.129	3.376	0.020	4.485	ENSOARG00000015148	NA	0.451	1.338	0.047	2.742
ENSOARG00000002228	NA	0.047	3.448	0.010	4.485	ENSOARG00000024996	uc_338	0.437	1.348	0.043	2.742
ENSOARG00000014183	SDPR	1.482	1.999	0.001	4.480	ENSOARG00000000400	IQCC	0.137	1.651	0.048	2.740
ENSOARG00000013402	PTGFR	0.691	2.822	0.034	4.479	ENSOARG00000012020	STMND1	0.677	1.107	0.047	2.737
ENSOARG00000005262	NA	0.516	2.966	0.009	4.473	ENSOARG00000005198	CENPS	0.109	1.666	0.046	2.729
ENSOARG00000014372	EFHC1	-0.017	3.461	0.007	4.471	ENSOARG00000019692	MLC1	-0.438	1.309	0.020	2.726
ENSOARG00000008813	NA	-0.416	3.077	0.023	4.470	ENSOARG00000026632	NA	0.512	1.243	0.032	2.723
ENSOARG00000007443	IRF2	0.530	2.932	0.009	4.452	ENSOARG00000004353	SALL3	-0.690	1.076	0.043	2.723
ENSOARG00000014813	IFT22	-0.735	2.743	0.027	4.452	ENSOARG00000019749	PPM1J	0.697	1.045	0.019	2.723
ENSOARG00000015209	NA	-0.824	2.644	0.020	4.448	ENSOARG00000008739	DCBLD1	-0.589	1.158	0.024	2.722
ENSOARG00000017663	MYBL1	-1.035	2.417	0.004	4.448	ENSOARG00000002966	NA	0.073	1.659	0.012	2.720
ENSOARG00000017917	GRIK4	-0.185	3.297	0.040	4.442	ENSOARG00000018994	IFT27	0.154	1.575	0.011	2.719
ENSOARG00000019446	TNS1	0.149	3.303	0.009	4.442	ENSOARG00000017334	NKD1	0.613	1.116	0.012	2.716
ENSOARG00000004121	NA	0.701	2.751	0.012	4.440	ENSOARG00000002074	NA	0.052	1.673	0.009	2.716
ENSOARG00000010535	NA	0.088	3.360	0.009	4.439	ENSOARG00000016877	NA	0.351	1.376	0.013	2.714
ENSOARG00000017360	NA	0.275	3.178	0.015	4.438	ENSOARG00000016348	SCRIB	-0.429	1.292	0.008	2.713

ENSOARG00000007640	PLEKHA6	0.118	3.328	0.011	4.435	ENSOARG00000000611	LDB3	0.418	1.312	0.018	2.712
ENSOARG00000007104	DLK2	0.092	3.352	0.011	4.433	ENSOARG00000010280	SORBS3	-0.541	1.179	0.008	2.712
ENSOARG00000015860	KSR1	-0.443	3.003	0.014	4.433	ENSOARG00000014866	FAS	-0.530	1.189	0.008	2.711
ENSOARG00000016001	CA8	-0.216	3.230	0.016	4.431	ENSOARG00000018313	B9D1	0.307	1.412	0.008	2.711
ENSOARG00000013135	YBEY	1.202	2.226	0.002	4.427	ENSOARG00000007305	NA	0.484	1.271	0.045	2.710
ENSOARG00000009115	GPR173	-0.452	2.976	0.004	4.423	ENSOARG00000003210	CCL25	-0.082	1.641	0.013	2.710
ENSOARG00000018288	NCKAP5L	0.314	3.149	0.040	4.423	ENSOARG00000010902	RCC2	-0.031	1.693	0.015	2.710
ENSOARG00000011188	MYH7B	-0.438	3.008	0.023	4.422	ENSOARG00000005354	SCAND1	0.161	1.561	0.015	2.707
ENSOARG00000003773	NA	-0.301	3.147	0.027	4.421	ENSOARG00000003556	EFCAB10	0.113	1.609	0.019	2.703
ENSOARG00000015251	TMEM184B	0.027	3.428	0.038	4.417	ENSOARG00000010774	ZIC3	-0.216	1.503	0.018	2.701
ENSOARG00000006799	ACOT8	0.249	3.187	0.020	4.415	ENSOARG00000007277	TRIM41	-0.510	1.199	0.009	2.700
ENSOARG00000002356	RARRES1	-0.294	3.144	0.024	4.414	ENSOARG00000003367	SMIM17	-0.037	1.673	0.013	2.697
ENSOARG00000018500	NA	-0.172	3.257	0.015	4.414	ENSOARG00000008605	CD9	-0.280	1.426	0.009	2.697
ENSOARG00000020462	IL1RAP	-0.522	2.917	0.028	4.411	ENSOARG00000000413	CHMP6	0.822	0.882	0.007	2.696
ENSOARG00000015127	SLC22A5	0.615	2.840	0.044	4.411	ENSOARG00000002814	NA	-0.250	1.466	0.020	2.696
ENSOARG00000011754	PGAP3	0.552	2.872	0.014	4.410	ENSOARG00000004562	ZADH2	0.128	1.577	0.009	2.695
ENSOARG00000015592	KITLG	0.145	3.273	0.009	4.409	ENSOARG00000002972	ZDHHC1	0.120	1.603	0.031	2.693
ENSOARG00000008526	PIK3AP1	-0.507	2.947	0.047	4.408	ENSOARG00000001785	TM2D2	-0.403	1.298	0.008	2.693
ENSOARG00000016529	LIPT1	0.310	3.094	0.009	4.395	ENSOARG00000011544	ARHGDIG	-0.193	1.539	0.040	2.692
ENSOARG00000020609	VWA5B2	0.329	3.090	0.039	4.380	ENSOARG00000017188	SPATA24	0.700	0.999	0.007	2.692
ENSOARG00000017345	SLC10A4	-0.417	2.975	0.013	4.379	ENSOARG00000016638	DPCD	0.716	1.012	0.037	2.692
ENSOARG00000004892	TSPAN4	0.688	2.732	0.042	4.379	ENSOARG00000007369	NA	0.164	1.537	0.010	2.692
ENSOARG00000003498	RMI1	0.275	3.130	0.028	4.377	ENSOARG00000009941	PARS2	0.480	1.248	0.036	2.691
ENSOARG00000016030	C6orf52	0.828	2.549	0.006	4.371	ENSOARG00000016852	CFLAR	-0.104	1.594	0.011	2.687
ENSOARG00000006703	SPTBN4	-0.419	2.996	0.048	4.367	ENSOARG00000006506	SLC29A3	0.074	1.652	0.043	2.683
ENSOARG00000004895	RPS6KA2	-0.283	3.103	0.021	4.365	ENSOARG00000015041	DEF8	-0.589	1.102	0.011	2.680
ENSOARG00000003394	AHDC1	-0.261	3.149	0.047	4.364	ENSOARG00000004315	ACSF2	-0.427	1.266	0.012	2.680
ENSOARG00000003101	COG2	-0.757	2.632	0.030	4.359	ENSOARG00000005157	NA	-0.026	1.668	0.016	2.678
ENSOARG00000016247	CETN3	0.186	3.186	0.015	4.357	ENSOARG00000010770	STARD13	-0.592	1.099	0.016	2.674
ENSOARG00000022919	U6	0.012	3.359	0.016	4.355	ENSOARG00000007760	EDEM1	-0.029	1.655	0.009	2.674
ENSOARG00000014483	MINOS1	0.681	2.698	0.036	4.342	ENSOARG00000019563	CERK	0.007	1.712	0.045	2.674
ENSOARG00000015666	MESDC1	0.417	2.947	0.022	4.342	ENSOARG00000015224	KRT27	-0.103	1.596	0.027	2.672
ENSOARG00000007948	HDDC2	0.680	2.653	0.004	4.330	ENSOARG00000009445	SLC35B2	-0.085	1.592	0.005	2.672
ENSOARG00000009024	IDNK	0.126	3.202	0.009	4.319	ENSOARG00000015360	SCRG1	-0.294	1.387	0.009	2.671
ENSOARG00000005138	GALNT3	-0.452	2.880	0.013	4.318	ENSOARG00000002091	ARMC3	-0.314	1.365	0.010	2.669
ENSOARG00000009559	NA	0.172	3.158	0.015	4.316	ENSOARG00000025376	NA	-0.003	1.674	0.010	2.667
ENSOARG00000006855	KCNA4	-0.224	3.095	0.005	4.314	ENSOARG00000014924	NA	0.937	0.741	0.013	2.666
ENSOARG00000003452	RAMP2	0.810	2.490	0.007	4.292	ENSOARG00000006300	WDR31	-0.228	1.448	0.011	2.665
ENSOARG00000004777	FAM217B	0.252	3.044	0.010	4.287	ENSOARG00000017042	RAD9B	0.568	1.113	0.017	2.664
ENSOARG00000014614	NA	0.119	3.187	0.029	4.277	ENSOARG00000001215	PRKAR1B	0.383	1.292	0.012	2.663
ENSOARG00000009301	COLEC12	-0.382	2.906	0.013	4.276	ENSOARG00000008108	ZACN	0.194	1.481	0.015	2.660
ENSOARG00000010837	TPMT	0.111	3.209	0.045	4.275	ENSOARG00000018676	NA	0.227	1.473	0.040	2.660
ENSOARG00000019342	HOMEZ	-0.727	2.555	0.009	4.273	ENSOARG00000011672	NA	-0.371	1.309	0.021	2.658
ENSOARG00000003460	SMIM19	-0.220	3.065	0.013	4.272	ENSOARG00000026502	NA	0.289	1.379	0.011	2.657

ENSOARG00000013028	KIRREL3	0.054	3.225	0.010	4.269	ENSOARG00000016081	NA	0.217	1.483	0.043	2.657
ENSOARG00000005881	KHSRP	-0.422	2.854	0.008	4.268	ENSOARG00000014481	PRKRIP1	-0.028	1.638	0.011	2.655
ENSOARG00000005266	POLR2I	0.722	2.552	0.007	4.267	ENSOARG00000011045	GALNT12	-0.763	0.902	0.011	2.654
ENSOARG00000026581	NA	-0.464	2.851	0.049	4.266	ENSOARG00000021168	PLEKHH1	0.621	1.039	0.008	2.652
ENSOARG00000009315	NACC1	0.115	3.159	0.009	4.264	ENSOARG00000002529	NA	-0.010	1.658	0.018	2.651
ENSOARG00000014165	RIPPLY3	1.339	1.927	0.001	4.264	ENSOARG00000010662	ACADVL	-0.003	1.678	0.033	2.649
ENSOARG00000010885	PHLDB1	-0.309	2.962	0.009	4.261	ENSOARG00000011585	NA	-0.288	1.394	0.034	2.648
ENSOARG00000014004	PCDHB15	-0.180	3.085	0.009	4.256	ENSOARG00000000808	ZC3H3	0.310	1.352	0.014	2.648
ENSOARG00000014515	MEX3B	0.149	3.112	0.012	4.248	ENSOARG00000002415	CCDC40	0.363	1.313	0.030	2.646
ENSOARG00000005780	EMP2	0.085	3.205	0.044	4.245	ENSOARG00000006947	ITPKC	0.041	1.621	0.018	2.644
ENSOARG00000011481	PIM2	-0.963	2.284	0.005	4.242	ENSOARG00000018011	ISCU	-0.066	1.608	0.030	2.644
ENSOARG00000004063	ZDHHC18	-0.216	3.035	0.010	4.241	ENSOARG00000005045	NA	0.055	1.614	0.027	2.642
ENSOARG00000004877	NA	0.912	2.341	0.013	4.240	ENSOARG00000011967	DBP	0.548	1.101	0.008	2.641
ENSOARG00000015861	ENOX2	0.300	2.958	0.021	4.237	ENSOARG00000021072	THEM4	0.375	1.287	0.021	2.641
ENSOARG00000026408	NA	0.384	2.866	0.015	4.235	ENSOARG00000005385	SMIM15	0.107	1.568	0.035	2.640
ENSOARG00000005110	SERPINB8	0.965	2.275	0.009	4.232	ENSOARG00000012692	MOGS	-0.168	1.481	0.009	2.640
ENSOARG00000006455	CPNE9	-0.361	2.885	0.014	4.231	ENSOARG00000005273	VEGFB	0.111	1.543	0.015	2.639
ENSOARG00000000004	NA	0.030	3.208	0.008	4.230	ENSOARG00000013614	FAM173A	0.072	1.590	0.023	2.639
ENSOARG00000019973	RASSF8	-0.904	2.352	0.029	4.226	ENSOARG00000019032	NA	-0.322	1.325	0.009	2.638
ENSOARG00000001515	TMEM150B	0.751	2.499	0.025	4.225	ENSOARG00000011972	SLC9B1	-0.142	1.514	0.019	2.636
ENSOARG00000001243	RAB31	0.307	2.926	0.008	4.224	ENSOARG00000006580	MFSD11	0.222	1.454	0.042	2.634
ENSOARG00000001146	ABRACL	0.246	2.990	0.013	4.223	ENSOARG00000009323	BCAM	-0.889	0.767	0.023	2.633
ENSOARG00000012749	PCGF1	0.678	2.553	0.030	4.201	ENSOARG00000001283	NA	-0.459	1.190	0.017	2.632
ENSOARG00000020901	CHCHD5	0.622	2.595	0.018	4.199	ENSOARG00000016922	CASP8	-0.203	1.446	0.018	2.631
ENSOARG00000000935	ABCC4	-0.118	3.084	0.007	4.196	ENSOARG00000009011	PSTK	0.507	1.156	0.034	2.630
ENSOARG00000020412	PHGDH	-0.102	3.108	0.017	4.193	ENSOARG00000015577	TMEM167A	0.131	1.524	0.025	2.630
ENSOARG00000008298	PARVA	-0.732	2.500	0.041	4.192	ENSOARG00000019274	AP1G2	0.453	1.185	0.009	2.630
ENSOARG00000007097	ATP13A1	-0.220	2.985	0.015	4.189	ENSOARG00000000758	SNAPIN	0.537	1.126	0.035	2.628
ENSOARG00000006314	SPRY3	-0.344	2.854	0.013	4.185	ENSOARG00000022315	SNORA63	0.255	1.389	0.017	2.627
ENSOARG00000006201	NA	0.221	3.010	0.047	4.184	ENSOARG00000012746	IGSF1	-0.792	0.850	0.017	2.625
ENSOARG00000025579	NA	-1.179	2.006	0.005	4.180	ENSOARG00000025113	DLX6-AS1_1	0.358	1.291	0.025	2.624
ENSOARG00000004923	NA	0.806	2.394	0.021	4.180	ENSOARG00000007360	DUSP9	0.761	0.871	0.009	2.623
ENSOARG00000003387	NA	0.338	2.855	0.014	4.179	ENSOARG00000002674	SHE	-0.386	1.270	0.035	2.621
ENSOARG00000014792	FAM151B	0.104	3.108	0.034	4.178	ENSOARG00000020259	NA	0.707	0.953	0.040	2.620
ENSOARG00000011484	POLG	-0.825	2.362	0.010	4.177	ENSOARG00000010123	EML2	0.271	1.368	0.020	2.620
ENSOARG00000005726	SLC25A11	0.756	2.417	0.005	4.168	ENSOARG00000024043	RMST_4	-0.581	1.044	0.006	2.619
ENSOARG00000007620	NA	0.028	3.132	0.011	4.149	ENSOARG00000002728	PEX16	0.313	1.315	0.009	2.619
ENSOARG00000013023	LSS	-0.242	2.922	0.021	4.144	ENSOARG00000020171	SLC22A15	0.342	1.294	0.018	2.618
ENSOARG00000002087	PET100	0.600	2.552	0.010	4.142	ENSOARG00000012488	NA	-0.444	1.179	0.005	2.618
ENSOARG00000019364	GTPBP8	0.302	2.855	0.016	4.142	ENSOARG00000026015	NA	0.230	1.414	0.027	2.617
ENSOARG00000017237	PRDM16	0.865	2.287	0.011	4.141	ENSOARG00000002553	NA	0.218	1.417	0.019	2.616
ENSOARG00000007146	LYPLA2	0.789	2.362	0.012	4.139	ENSOARG00000020414	SCO2	0.834	0.786	0.009	2.611
ENSOARG00000005133	C12orf57	0.466	2.691	0.019	4.137	ENSOARG00000005984	TMEM268	0.625	0.995	0.010	2.609
ENSOARG00000015272	RCHY1	0.253	2.895	0.012	4.135	ENSOARG00000021138	GNL3L	0.153	1.484	0.029	2.608

ENSOARG00000015284	P2RY12	-0.005	3.134	0.006	4.134	ENSOARG00000017421	SOWAHB	-0.572	1.035	0.009	2.598
ENSOARG00000019779	ARNTL2	-0.251	2.916	0.034	4.133	ENSOARG00000003756	ANKS3	0.114	1.511	0.028	2.597
ENSOARG00000014696	IGLON5	1.143	1.999	0.011	4.131	ENSOARG00000007794	WDR64	0.547	1.080	0.035	2.592
ENSOARG00000012153	CCDC160	0.279	2.881	0.029	4.131	ENSOARG00000019854	GPR156	-0.921	0.691	0.022	2.591
ENSOARG00000018130	NA	0.006	3.156	0.031	4.130	ENSOARG00000012868	NCLN	-0.220	1.380	0.011	2.589
ENSOARG00000017960	PLOD1	-0.692	2.447	0.018	4.121	ENSOARG00000007966	MYT1	0.411	1.219	0.041	2.589
ENSOARG00000016592	PRDX4	-0.121	3.002	0.006	4.117	ENSOARG00000025941	NA	0.495	1.111	0.020	2.586
ENSOARG00000008113	CHCHD1	0.627	2.527	0.037	4.117	ENSOARG00000013290	WDR38	0.420	1.192	0.027	2.585
ENSOARG00000001316	PUS10	0.163	2.958	0.009	4.112	ENSOARG00000001909	NA	0.335	1.265	0.015	2.585
ENSOARG00000020909	KIAA1522	0.193	2.968	0.050	4.111	ENSOARG00000006958	C19orf54	0.438	1.173	0.028	2.584
ENSOARG00000011927	EFCAB3	-0.761	2.386	0.040	4.108	ENSOARG00000003231	NA	-0.272	1.325	0.015	2.581
ENSOARG00000012943	CRTC3	-0.265	2.864	0.026	4.103	ENSOARG00000008795	NA	-0.368	1.224	0.011	2.581
ENSOARG00000019513	GRAMD1C	0.450	2.663	0.011	4.102	ENSOARG00000025465	NA	0.710	0.882	0.012	2.580
ENSOARG00000020159	NA	0.849	2.266	0.015	4.100	ENSOARG00000015782	PLEKHG7	-1.051	0.532	0.004	2.580
ENSOARG00000011552	DRD1	-0.263	2.827	0.005	4.085	ENSOARG00000002299	SH2B1	0.473	1.126	0.020	2.579
ENSOARG00000004661	FAM19A2	-0.284	2.841	0.040	4.084	ENSOARG00000011923	NECAP2	-0.025	1.589	0.037	2.577
ENSOARG00000018746	PCDHA11	-0.180	2.931	0.034	4.076	ENSOARG00000000081	NA	0.131	1.457	0.012	2.577
ENSOARG00000012229	WDR83	-0.403	2.702	0.029	4.076	ENSOARG00000015227	LTBP3	0.130	1.470	0.027	2.574
ENSOARG00000016346	NA	-0.027	3.066	0.019	4.074	ENSOARG00000005174	DMP1	-0.539	1.044	0.009	2.574
ENSOARG00000015451	NA	1.011	2.107	0.044	4.074	ENSOARG00000002934	TAF8	0.351	1.242	0.019	2.573
ENSOARG00000010487	UBXN8	-0.427	2.683	0.041	4.069	ENSOARG00000005920	NUBP1	0.355	1.264	0.046	2.573
ENSOARG00000006739	G6PC3	0.180	2.913	0.025	4.069	ENSOARG00000019539	GRAMD4	-0.253	1.353	0.036	2.571
ENSOARG00000013507	ZCCHC10	0.962	2.111	0.006	4.067	ENSOARG00000006183	NA	0.066	1.534	0.030	2.570
ENSOARG00000010514	GGT7	-0.349	2.755	0.039	4.065	ENSOARG00000014308	FAM173B	1.097	0.479	0.006	2.570
ENSOARG00000015829	PTPN18	0.677	2.431	0.043	4.065	ENSOARG00000001462	NA	0.297	1.301	0.030	2.568
ENSOARG00000005493	TKTL1	-0.948	2.125	0.009	4.064	ENSOARG00000018790	KCNH4	-0.774	0.821	0.030	2.565
ENSOARG00000008078	TAGLN2	-0.256	2.820	0.020	4.055	ENSOARG00000008940	LPO	0.331	1.260	0.025	2.565
ENSOARG00000016727	HGF	0.246	2.819	0.012	4.053	ENSOARG00000002332	DXO	-0.029	1.569	0.034	2.564
ENSOARG00000001815	NA	0.703	2.355	0.007	4.051	ENSOARG00000000376	NA	-0.225	1.378	0.042	2.562
ENSOARG00000007674	RNF40	-0.194	2.882	0.025	4.051	ENSOARG00000004788	PARK2	-0.861	0.706	0.007	2.560
ENSOARG00000001529	TRIM8	-0.260	2.796	0.010	4.046	ENSOARG00000015822	WRAP53	0.485	1.101	0.026	2.560
ENSOARG00000006968	PTPN3	-0.086	2.976	0.017	4.044	ENSOARG00000013928	MMP17	-0.365	1.213	0.019	2.558
ENSOARG00000012174	EIF6	0.433	2.617	0.013	4.038	ENSOARG00000001474	HIST3H2BB	-0.533	1.034	0.009	2.558
ENSOARG00000012456	NA	0.653	2.428	0.044	4.037	ENSOARG00000020053	HIST1H4L	0.122	1.457	0.023	2.555
ENSOARG00000012454	MYO1C	-0.050	2.991	0.012	4.029	ENSOARG00000001560	ARHGAP22	-0.475	1.100	0.020	2.555
ENSOARG00000003970	NA	-0.176	2.885	0.033	4.029	ENSOARG00000016926	FAM216A	0.072	1.502	0.019	2.555
ENSOARG00000016661	ZNF740	-0.117	2.920	0.009	4.028	ENSOARG00000011959	ZNF710	-0.293	1.293	0.032	2.555
ENSOARG00000005865	CD2BP2	0.471	2.566	0.010	4.027	ENSOARG00000011806	NA	-0.152	1.422	0.021	2.554
ENSOARG00000017791	FGD5	-0.605	2.425	0.006	4.024	ENSOARG00000017277	DUS1L	-0.364	1.206	0.017	2.553
ENSOARG00000005230	STOX1	0.566	2.476	0.019	4.023	ENSOARG00000007670	UBALD2	0.106	1.487	0.040	2.553
ENSOARG00000011066	KCNQ5	0.239	2.791	0.011	4.019	ENSOARG00000007716	BPGM	0.108	1.454	0.010	2.552
ENSOARG00000007965	GPX8	-0.421	2.627	0.029	4.019	ENSOARG00000016980	ZCWPW1	-0.323	1.242	0.014	2.551
ENSOARG00000013984	SNRPD3	0.489	2.548	0.019	4.018	ENSOARG00000020836	CCNB2	0.103	1.458	0.011	2.550
ENSOARG00000004631	ZNF599	-0.785	2.266	0.034	4.017	ENSOARG00000015571	TP53	-0.616	0.943	0.011	2.549

ENSOARG00000010919	STX17	0.221	2.802	0.010	4.012	ENSOARG00000020598	NA	-0.077	1.489	0.021	2.546
ENSOARG00000007890	ZNF629	-0.087	2.938	0.017	4.008	ENSOARG00000016812	AGFG2	0.425	1.129	0.009	2.545
ENSOARG00000011065	SLCO2B1	-0.134	2.886	0.014	4.006	ENSOARG00000026858	NA	0.839	0.711	0.008	2.542
ENSOARG00000019980	NA	0.200	2.826	0.024	4.002	ENSOARG00000012657	LYRM2	-0.380	1.164	0.008	2.537
ENSOARG00000020821	NA	-0.071	2.944	0.013	4.002	ENSOARG00000000155	CPM	-0.218	1.330	0.011	2.536
ENSOARG00000006611	STPG1	0.731	2.284	0.014	4.000	ENSOARG00000004470	B4GAT1	0.116	1.445	0.025	2.535
ENSOARG00000001641	C20orf27	0.328	2.681	0.010	3.999	ENSOARG00000016457	C12orf73	0.275	1.287	0.029	2.533
ENSOARG00000020786	APH1B	-0.642	2.379	0.028	3.993	ENSOARG00000005693	ZSCAN30	0.346	1.218	0.031	2.533
ENSOARG00000026420	NA	-0.433	2.566	0.008	3.991	ENSOARG00000014346	HACD4	0.085	1.457	0.011	2.530
ENSOARG00000013134	37316	0.065	2.941	0.016	3.990	ENSOARG00000010963	NA	0.208	1.368	0.046	2.530
ENSOARG00000004938	COG4	0.112	2.890	0.016	3.986	ENSOARG00000016244	NCKIPSD	-0.364	1.187	0.023	2.529
ENSOARG00000020086	NA	-0.458	2.540	0.012	3.986	ENSOARG00000006328	MPP2	-0.017	1.519	0.010	2.526
ENSOARG00000012813	NA	-0.766	2.239	0.020	3.985	ENSOARG00000012410	UNC45A	-0.110	1.428	0.014	2.523
ENSOARG00000002704	HSCB	0.398	2.595	0.011	3.983	ENSOARG00000004015	CD248	0.449	1.079	0.014	2.515
ENSOARG00000018625	FAM186B	0.116	2.908	0.043	3.981	ENSOARG00000008587	PXMP4	0.518	1.022	0.026	2.514
ENSOARG00000008293	RABAC1	0.493	2.508	0.022	3.979	ENSOARG00000006775	MEI4	0.153	1.383	0.022	2.514
ENSOARG00000016998	CBLN1	0.939	2.050	0.010	3.979	ENSOARG00000016610	HLA-DRA	-0.478	1.064	0.033	2.509
ENSOARG00000020302	VPS18	-0.553	2.429	0.004	3.978	ENSOARG00000016785	RPS19BP1	0.850	0.664	0.007	2.507
ENSOARG00000018927	XK	-0.124	2.888	0.035	3.977	ENSOARG00000026322	NA	0.247	1.268	0.011	2.504
ENSOARG00000007664	PIK3CD	0.777	2.214	0.015	3.976	ENSOARG00000007387	KCNJ10	-0.132	1.386	0.014	2.503
ENSOARG00000003325	DUS2	0.183	2.808	0.016	3.975	ENSOARG00000007174	KIRREL	-0.136	1.408	0.041	2.503
ENSOARG00000010316	LHPP	-0.094	2.919	0.039	3.974	ENSOARG00000005798	NA	0.064	1.462	0.027	2.500
ENSOARG00000017529	NA	-1.083	1.894	0.005	3.973	ENSOARG00000009632	SLC5A2	-0.103	1.416	0.024	2.495
ENSOARG00000011135	ATXN1L	0.003	2.977	0.012	3.968	ENSOARG00000017896	NA	0.007	1.520	0.032	2.494
ENSOARG00000011785	PPARD	0.748	2.220	0.006	3.961	ENSOARG00000011441	ATP13A2	0.231	1.269	0.010	2.490
ENSOARG00000014225	NA	0.264	2.714	0.017	3.961	ENSOARG00000012948	FHL2	0.486	1.015	0.011	2.489
ENSOARG00000012475	ABHD6	-0.009	2.965	0.014	3.959	ENSOARG00000004360	SNAPC4	0.602	0.895	0.019	2.478
ENSOARG00000006826	LTBP4	-0.016	2.969	0.026	3.959	ENSOARG00000007229	CD74	0.205	1.314	0.041	2.478
ENSOARG00000005172	NA	0.551	2.417	0.011	3.957	ENSOARG00000014354	ZNF276	-0.406	1.091	0.023	2.475
ENSOARG00000007864	LCP1	-0.564	2.409	0.017	3.956	ENSOARG00000018340	C15orf61	0.320	1.170	0.017	2.473
ENSOARG00000018891	TBC1D8B	-0.956	2.007	0.008	3.955	ENSOARG00000020284	ZFYVE19	0.255	1.227	0.009	2.473
ENSOARG00000002543	MRNIP	0.059	2.903	0.007	3.955	ENSOARG00000026769	NA	0.343	1.135	0.006	2.473
ENSOARG00000014572	CATSPER3	0.080	2.887	0.015	3.952	ENSOARG00000017340	NA	0.354	1.149	0.031	2.472
ENSOARG00000004480	TTC39A	-0.666	2.291	0.008	3.948	ENSOARG00000000724	NA	-0.029	1.469	0.030	2.469
ENSOARG00000019893	PROKR1	-0.304	2.650	0.013	3.941	ENSOARG00000020820	ECM1	0.049	1.432	0.015	2.466
ENSOARG00000015717	NA	-0.046	2.900	0.011	3.936	ENSOARG00000002989	MED18	0.083	1.392	0.011	2.464
ENSOARG00000018123	SARM1	-0.064	2.880	0.009	3.935	ENSOARG00000017630	NR2F6	0.375	1.103	0.013	2.464
ENSOARG00000001911	CCDC17	0.343	2.611	0.018	3.935	ENSOARG00000017392	TTC19	-0.260	1.253	0.050	2.462
ENSOARG00000016815	NA	-0.040	2.935	0.041	3.934	ENSOARG00000015786	NA	-0.486	0.985	0.009	2.462
ENSOARG00000003623	NA	-0.700	2.256	0.024	3.932	ENSOARG00000000846	CCDC28A	-0.283	1.194	0.016	2.462
ENSOARG00000015937	TMEM204	0.136	2.820	0.026	3.931	ENSOARG00000018243	SWSAP1	0.183	1.299	0.024	2.458
ENSOARG00000010939	NR4A3	-0.501	2.451	0.021	3.931	ENSOARG00000009563	STS	-0.569	0.921	0.033	2.456
ENSOARG00000001683	KCNC1	-0.313	2.626	0.011	3.929	ENSOARG00000005299	NA	0.738	0.734	0.019	2.454
ENSOARG00000017352	NA	-0.569	2.389	0.030	3.928	ENSOARG00000004233	PML	-0.188	1.273	0.012	2.449

ENSOARG00000003968	FBXO5	-1.093	1.836	0.003	3.926	ENSOARG00000018764	NA	-0.060	1.422	0.034	2.448
ENSOARG00000016509	CTHRC1	-0.207	2.726	0.008	3.925	ENSOARG00000012998	RHOF	0.150	1.311	0.014	2.447
ENSOARG00000006022	LRFN1	-0.128	2.822	0.029	3.921	ENSOARG00000026422	NA	0.347	1.108	0.008	2.446
ENSOARG00000014958	NA	-0.882	2.052	0.013	3.920	ENSOARG00000010256	DYDC1	0.062	1.396	0.013	2.445
ENSOARG00000009766	ADAMTS17	-0.614	2.351	0.046	3.919	ENSOARG00000025816	NA	0.001	1.446	0.007	2.440
ENSOARG00000009408	UEVLD	0.266	2.666	0.014	3.918	ENSOARG00000003004	MND1	0.543	0.910	0.016	2.437
ENSOARG00000000133	GJC1	0.000	2.952	0.039	3.913	ENSOARG00000009044	ZNF235	0.394	1.064	0.021	2.437
ENSOARG00000017093	SPRY1	0.107	2.845	0.040	3.912	ENSOARG00000025565	NA	-0.540	0.915	0.020	2.436
ENSOARG00000020454	P3H1	0.825	2.094	0.010	3.908	ENSOARG00000016564	HEXDC	-0.081	1.384	0.031	2.433
ENSOARG00000020716	NA	0.275	2.656	0.023	3.908	ENSOARG00000008186	SH3BP5L	-0.344	1.096	0.008	2.432
ENSOARG00000013659	SETD4	-0.243	2.682	0.018	3.907	ENSOARG00000004304	SYNJ2	-0.225	1.221	0.023	2.423
ENSOARG00000009726	TRIM35	0.375	2.547	0.014	3.907	ENSOARG00000003319	F8	-0.197	1.252	0.027	2.422
ENSOARG00000015794	NME5	0.966	1.948	0.007	3.906	ENSOARG00000019436	ABHD4	0.238	1.189	0.005	2.421
ENSOARG00000007549	LPAR2	0.215	2.702	0.014	3.904	ENSOARG00000014906	CCDC167	0.902	0.541	0.023	2.420
ENSOARG00000016278	GCNT2	-0.423	2.503	0.025	3.901	ENSOARG00000007340	SYCE1L	0.283	1.148	0.014	2.417
ENSOARG00000016534	TFPI	-0.323	2.596	0.022	3.897	ENSOARG00000010779	ZNF768	0.052	1.377	0.012	2.417
ENSOARG00000003420	NA	0.885	2.018	0.007	3.897	ENSOARG00000019673	UPK1B	-1.055	0.386	0.026	2.415
ENSOARG00000000928	ECT2L	-0.165	2.739	0.012	3.892	ENSOARG00000002396	NA	0.847	0.588	0.022	2.414
ENSOARG00000010061	PATZ1	0.023	2.887	0.019	3.890	ENSOARG00000016033	SOWAHC	-0.151	1.277	0.014	2.414
ENSOARG00000007617	NA	-0.142	2.764	0.016	3.890	ENSOARG00000017433	ZSWIM7	0.072	1.346	0.006	2.412
ENSOARG00000005483	NA	0.187	2.709	0.010	3.886	ENSOARG00000004438	NA	-0.462	0.967	0.019	2.410
ENSOARG00000019110	CTC1	-0.225	2.669	0.009	3.885	ENSOARG00000011201	B3GAT2	-0.431	0.989	0.013	2.407
ENSOARG00000007475	ADAMTS18	-0.012	2.882	0.011	3.883	ENSOARG00000010021	SUPT4H1	0.565	0.849	0.008	2.406
ENSOARG00000019413	FAM84A	0.382	2.541	0.041	3.881	ENSOARG00000019121	ABHD1	0.126	1.295	0.015	2.406
ENSOARG00000003725	UBL7	0.524	2.378	0.021	3.881	ENSOARG00000014343	SMYD4	0.282	1.155	0.031	2.406
ENSOARG00000003419	STK32A	-0.279	2.631	0.030	3.881	ENSOARG00000019106	RBCK1	-0.209	1.199	0.006	2.403
ENSOARG00000012289	MANBA	-1.178	1.702	0.001	3.879	ENSOARG00000013629	SLC39A3	0.363	1.050	0.010	2.402
ENSOARG00000001862	PITPNM3	-0.582	2.306	0.012	3.877	ENSOARG00000010722	CREB3L3	-0.600	0.847	0.046	2.401
ENSOARG00000014436	NA	-0.672	2.243	0.040	3.875	ENSOARG00000001918	TK2	-0.112	1.302	0.014	2.400
ENSOARG00000013246	NA	0.695	2.214	0.038	3.872	ENSOARG00000008998	PATJ	0.053	1.362	0.014	2.400
ENSOARG00000012383	KDELC2	-0.621	2.269	0.020	3.870	ENSOARG00000013050	SLC9A2	-0.201	1.239	0.041	2.398
ENSOARG00000013704	TMEM258	0.672	2.222	0.026	3.868	ENSOARG00000026219	NA	0.432	1.015	0.049	2.398
ENSOARG00000018526	NA	-0.500	2.376	0.019	3.858	ENSOARG00000015301	ACOT12	0.010	1.418	0.034	2.395
ENSOARG00000004095	ZNF414	-0.142	2.729	0.013	3.858	ENSOARG00000013947	PDXP	-0.318	1.121	0.045	2.394
ENSOARG00000018388	BBS2	-0.110	2.758	0.009	3.858	ENSOARG00000014182	CCDC124	0.708	0.690	0.008	2.390
ENSOARG00000004310	CXXC1	-0.119	2.742	0.006	3.855	ENSOARG00000008649	FKBP14	-0.016	1.389	0.016	2.390
ENSOARG00000007553	PLBD2	0.162	2.700	0.010	3.852	ENSOARG00000004318	NA	-0.777	0.648	0.035	2.390
ENSOARG00000005204	ACP1	0.755	2.139	0.043	3.851	ENSOARG00000000874	FBXO6	0.089	1.310	0.010	2.389
ENSOARG00000014097	CPNE7	0.973	1.913	0.035	3.850	ENSOARG00000010119	NA	-0.388	1.012	0.012	2.388
ENSOARG00000015886	RAVER1	0.241	2.623	0.016	3.849	ENSOARG00000017842	RGAG1	-0.077	1.319	0.010	2.386
ENSOARG00000000480	NA	-0.252	2.603	0.011	3.844	ENSOARG00000013229	GDF9	-0.049	1.357	0.021	2.385
ENSOARG00000001950	NA	-0.443	2.414	0.013	3.844	ENSOARG00000020208	NA	0.516	0.875	0.007	2.384
ENSOARG00000001030	ABCD4	0.227	2.623	0.006	3.843	ENSOARG00000005333	NA	0.460	0.934	0.010	2.384
ENSOARG00000007974	NA	-0.237	2.648	0.043	3.842	ENSOARG00000006920	JMJD4	0.612	0.785	0.018	2.379

ENSOARG00000008471	RAP1GAP	-0.874	1.981	0.014	3.841	ENSOARG00000014018	NA	0.724	0.676	0.022	2.377
ENSOARG00000011662	IQSEC3	0.057	2.798	0.014	3.840	ENSOARG00000006700	NA	0.004	1.382	0.011	2.375
ENSOARG00000009440	MAP4K2	-0.152	2.696	0.009	3.839	ENSOARG00000019775	CFAP65	-0.236	1.168	0.030	2.375
ENSOARG00000001691	TMEM176B	0.557	2.317	0.039	3.836	ENSOARG00000014824	MVK	0.727	0.688	0.042	2.373
ENSOARG00000001953	NA	-0.714	2.165	0.046	3.833	ENSOARG00000002275	NA	0.589	0.791	0.008	2.372
ENSOARG00000015790	BTG3	0.559	2.291	0.020	3.831	ENSOARG00000003339	RASSF3	-0.116	1.290	0.034	2.371
ENSOARG00000003476	EDC3	0.487	2.347	0.008	3.826	ENSOARG00000003644	RILPL2	-0.027	1.358	0.014	2.370
ENSOARG00000001988	RDH13	-0.744	2.090	0.009	3.825	ENSOARG00000002538	TBC1D16	0.065	1.324	0.018	2.370
ENSOARG00000013896	HOMER2	0.293	2.545	0.014	3.824	ENSOARG00000012669	NA	-0.180	1.213	0.025	2.369
ENSOARG00000004999	CEP85	0.149	2.694	0.019	3.824	ENSOARG00000008010	MAD2L1BP	-0.414	0.970	0.017	2.367
ENSOARG00000011162	NA	0.296	2.542	0.016	3.822	ENSOARG00000012761	FMO4	0.239	1.153	0.029	2.363
ENSOARG00000015603	MFSD8	0.342	2.518	0.039	3.821	ENSOARG00000003256	LCAT	0.493	0.885	0.014	2.363
ENSOARG00000018720	SNPH	-0.081	2.776	0.038	3.819	ENSOARG00000015072	NA	-0.380	1.026	0.044	2.362
ENSOARG00000016545	TEKT3	-0.251	2.577	0.011	3.817	ENSOARG00000002262	NA	-0.208	1.200	0.046	2.361
ENSOARG00000010468	PRDM15	0.660	2.180	0.025	3.816	ENSOARG00000001887	GAL3ST3	0.145	1.220	0.005	2.360
ENSOARG00000016740	EPHB6	0.171	2.654	0.011	3.814	ENSOARG00000016859	AXDND1	-0.644	0.761	0.045	2.360
ENSOARG00000005906	MAN1C1	-0.285	2.543	0.015	3.813	ENSOARG00000017812	CASKIN1	-0.050	1.348	0.040	2.357
ENSOARG00000011246	PRPS2	-0.189	2.639	0.020	3.807	ENSOARG00000018240	LCTL	-0.184	1.182	0.010	2.356
ENSOARG00000003391	PCGF6	-0.030	2.792	0.015	3.807	ENSOARG00000010307	C7orf31	0.824	0.548	0.021	2.351
ENSOARG00000013987	ROPN1L	-0.434	2.415	0.043	3.807	ENSOARG00000008951	LYPD5	0.721	0.636	0.012	2.345
ENSOARG00000015422	AIFM1	-0.074	2.743	0.011	3.805	ENSOARG00000015708	CHODL	-0.126	1.243	0.024	2.345
ENSOARG00000018006	TRIM4	-1.059	1.751	0.005	3.805	ENSOARG00000013793	LMAN2L	-0.371	0.984	0.010	2.345
ENSOARG00000011195	CHRNA4	0.083	2.748	0.027	3.805	ENSOARG00000015161	RAP2B	-0.095	1.267	0.019	2.344
ENSOARG00000004670	PHF7	-1.315	1.491	0.001	3.804	ENSOARG00000013729	LATS2	-0.143	1.230	0.030	2.343
ENSOARG00000010136	EXOSC1	0.639	2.171	0.009	3.801	ENSOARG00000015191	SHBG	0.293	1.060	0.011	2.343
ENSOARG00000022103	NA	0.720	2.086	0.007	3.799	ENSOARG00000019102	ADCY4	0.427	0.933	0.019	2.342
ENSOARG00000003686	WDTC1	-0.225	2.597	0.024	3.798	ENSOARG00000016265	NA	-0.817	0.559	0.038	2.337
ENSOARG00000018651	BAHCC1	0.137	2.674	0.013	3.798	ENSOARG00000000541	NA	0.139	1.202	0.011	2.330
ENSOARG00000010088	VIT	0.649	2.163	0.016	3.796	ENSOARG00000005426	BLCAP	0.554	0.791	0.016	2.330
ENSOARG00000009882	TOMM40L	0.243	2.559	0.010	3.793	ENSOARG00000003205	NA	0.556	0.783	0.012	2.328
ENSOARG00000001983	WDR5B	-0.141	2.690	0.039	3.791	ENSOARG00000008536	RCE1	0.097	1.235	0.009	2.323
ENSOARG00000012366	MFSD12	-0.159	2.668	0.037	3.791	ENSOARG00000010713	XRRA1	0.378	0.988	0.045	2.321
ENSOARG00000012778	FURIN	-0.272	2.529	0.010	3.790	ENSOARG00000000332	NA	0.919	0.401	0.005	2.315
ENSOARG00000000827	FAM35A	0.070	2.737	0.020	3.787	ENSOARG00000006970	NA	-0.048	1.284	0.017	2.314
ENSOARG00000010312	TSPAN14	0.358	2.443	0.015	3.786	ENSOARG00000004142	NA	0.710	0.636	0.032	2.314
ENSOARG00000008468	EMB	-0.443	2.358	0.016	3.784	ENSOARG00000015948	MCEE	-0.042	1.288	0.018	2.312
ENSOARG00000005275	PXDN	-0.786	2.013	0.021	3.778	ENSOARG00000010370	SLX4IP	-0.254	1.066	0.011	2.309
ENSOARG00000010291	DMWD	-0.771	2.035	0.029	3.778	ENSOARG00000014608	NA	-0.667	0.677	0.038	2.306
ENSOARG00000014994	TMED3	0.052	2.765	0.039	3.778	ENSOARG00000002496	NA	-0.378	0.942	0.013	2.306
ENSOARG00000013099	FBXL7	0.653	2.174	0.050	3.777	ENSOARG00000003070	ULK3	0.852	0.483	0.029	2.306
ENSOARG00000019873	YRDC	0.501	2.281	0.011	3.771	ENSOARG00000000817	CALY	0.250	1.066	0.012	2.304
ENSOARG00000005576	INTS1	0.008	2.768	0.006	3.770	ENSOARG00000025710	NA	-0.159	1.155	0.012	2.302
ENSOARG00000014630	MKNK2	-0.266	2.507	0.009	3.764	ENSOARG00000004207	MYO1F	0.015	1.296	0.010	2.302
ENSOARG00000009621	NA	0.025	2.750	0.012	3.762	ENSOARG00000012247	UBE2G2	0.475	0.875	0.048	2.301

ENSOARG00000010023	CFAP126	0.008	2.768	0.015	3.761	ENSOARG00000010812	NA	0.044	1.304	0.048	2.301
ENSOARG00000020633	L2HGDH	-0.282	2.523	0.045	3.760	ENSOARG00000017902	NA	0.591	0.719	0.009	2.301
ENSOARG00000013602	VWA3B	-0.925	1.834	0.009	3.750	ENSOARG00000000801	DMAP1	0.090	1.221	0.010	2.301
ENSOARG00000017618	STX5	-0.689	2.064	0.007	3.746	ENSOARG00000006479	ABHD14A	0.300	1.036	0.039	2.296
ENSOARG00000019192	PLCXD2	-0.232	2.526	0.013	3.745	ENSOARG00000004243	SDCCAG3	-0.216	1.085	0.007	2.294
ENSOARG00000015038	SDR16C5	0.760	2.024	0.040	3.744	ENSOARG00000020678	CCDC39	-0.628	0.695	0.029	2.294
ENSOARG00000026095	NA	-0.025	2.724	0.009	3.740	ENSOARG00000006000	B4GALT7	0.394	0.924	0.024	2.293
ENSOARG00000018850	SMDT1	1.570	1.167	0.002	3.735	ENSOARG00000004313	SLC10A6	0.817	0.511	0.041	2.287
ENSOARG00000000963	TMEM53	0.211	2.532	0.013	3.731	ENSOARG00000015369	SAP30	0.318	1.007	0.040	2.285
ENSOARG00000020444	PPIH	0.379	2.360	0.008	3.731	ENSOARG00000013594	NA	-0.058	1.247	0.020	2.285
ENSOARG00000013610	MYO7A	-0.063	2.680	0.016	3.727	ENSOARG00000016300	FN3KRP	0.086	1.230	0.033	2.283
ENSOARG00000015393	RASSF9	-0.465	2.296	0.037	3.724	ENSOARG00000000356	ZNF746	-0.269	1.022	0.011	2.280
ENSOARG00000025761	NA	-0.407	2.324	0.009	3.722	ENSOARG00000013213	DUSP10	-0.251	1.061	0.033	2.279
ENSOARG00000007445	RAD18	-0.804	1.938	0.022	3.721	ENSOARG00000001032	TMEM229B	-0.593	0.694	0.010	2.277
ENSOARG00000008509	NA	0.817	1.926	0.023	3.720	ENSOARG00000017827	AP5B1	0.400	0.887	0.015	2.272
ENSOARG00000024089	7SK	0.024	2.724	0.030	3.718	ENSOARG00000007893	NA	-0.111	1.199	0.038	2.272
ENSOARG00000013254	ARAF	-0.590	2.134	0.008	3.716	ENSOARG00000011492	SLC35A2	-0.638	0.640	0.007	2.271
ENSOARG00000011701	NA	0.099	2.621	0.006	3.714	ENSOARG00000016282	DGKQ	-0.205	1.108	0.043	2.270
ENSOARG00000012139	STOML2	0.756	1.965	0.008	3.713	ENSOARG00000003742	NA	-0.012	1.273	0.018	2.267
ENSOARG00000006484	APMAP	0.282	2.447	0.017	3.712	ENSOARG00000018198	SNAPC5	-0.932	0.362	0.027	2.267
ENSOARG00000013875	HUNK	-0.269	2.475	0.034	3.711	ENSOARG00000010550	NENF	0.407	0.884	0.024	2.267
ENSOARG00000013484	KIAA1211L	-0.251	2.469	0.009	3.711	ENSOARG00000006045	SERTM1	0.065	1.209	0.010	2.264
ENSOARG00000003393	USP36	-0.234	2.486	0.011	3.709	ENSOARG00000003856	NA	-0.146	1.128	0.011	2.263
ENSOARG00000020547	CHD1L	-0.094	2.661	0.047	3.708	ENSOARG00000001129	NA	0.403	0.887	0.029	2.261
ENSOARG00000008093	RSPH9	-0.003	2.720	0.019	3.705	ENSOARG00000001346	CST6	0.171	1.096	0.009	2.258
ENSOARG00000004780	KIF15	-0.082	2.629	0.007	3.704	ENSOARG00000020190	NA	-0.117	1.152	0.012	2.257
ENSOARG00000000399	TBC1D2B	-0.030	2.698	0.025	3.703	ENSOARG00000018069	NDST4	0.407	0.873	0.023	2.257
ENSOARG00000011694	B3GLCT	-0.912	1.806	0.016	3.702	ENSOARG00000001818	NA	0.385	0.918	0.049	2.254
ENSOARG00000019073	PRKG2	0.779	1.929	0.008	3.701	ENSOARG00000005280	ATP8B1	0.159	1.105	0.011	2.253
ENSOARG00000018085	L3MBTL2	-0.786	1.919	0.004	3.700	ENSOARG00000007744	CENPW	0.295	0.964	0.010	2.249
ENSOARG00000020854	TRIM62	-0.073	2.627	0.005	3.695	ENSOARG00000020459	GMNC	0.200	1.097	0.049	2.249
ENSOARG00000014444	PRSS23	-0.817	1.887	0.010	3.694	ENSOARG00000002512	COMMD4	0.216	1.044	0.011	2.249
ENSOARG00000009835	MFSD4B	-0.426	2.277	0.008	3.694	ENSOARG00000018957	NA	-0.275	0.990	0.021	2.244
ENSOARG00000005710	DDIAS	0.364	2.349	0.019	3.693	ENSOARG00000015527	NUDCD3	0.290	0.973	0.021	2.242
ENSOARG00000011062	ANKS6	-0.507	2.205	0.019	3.693	ENSOARG00000011941	TJP3	0.084	1.176	0.020	2.240
ENSOARG00000014986	CYYR1	-0.838	1.866	0.011	3.693	ENSOARG00000013513	SCML1	0.733	0.530	0.022	2.240
ENSOARG00000006704	ETV3	0.170	2.538	0.019	3.689	ENSOARG00000019617	NA	0.299	0.970	0.030	2.239
ENSOARG00000014787	MPDU1	0.853	1.858	0.022	3.689	ENSOARG00000003861	SPATA20	0.211	1.062	0.036	2.237
ENSOARG00000014026	CROT	-0.527	2.177	0.016	3.688	ENSOARG00000007742	ZFP92	-0.059	1.203	0.025	2.236
ENSOARG00000013389	HIST2H2AB	-0.214	2.488	0.014	3.687	ENSOARG00000011792	ACSL5	0.060	1.183	0.008	2.235
ENSOARG00000004656	NA	0.497	2.207	0.018	3.687	ENSOARG00000019824	DENND6B	0.174	1.096	0.034	2.235
ENSOARG00000006686	NA	-0.734	1.960	0.009	3.686	ENSOARG00000004192	NA	0.172	1.072	0.011	2.233
ENSOARG00000011417	FRMPD1	-1.076	1.610	0.005	3.682	ENSOARG00000020783	C1orf54	0.299	0.950	0.019	2.229
ENSOARG00000017989	NA	-0.389	2.307	0.016	3.680	ENSOARG00000020602	NUDT17	-0.544	0.713	0.029	2.228

ENSOARG00000010553	PRMT8	-0.669	2.019	0.009	3.679	ENSOARG00000015586	NA	0.413	0.831	0.017	2.227
ENSOARG00000004200	HCN3	-0.061	2.656	0.039	3.678	ENSOARG00000014215	C3orf62	0.528	0.697	0.009	2.217
ENSOARG00000012858	NSUN7	0.633	2.051	0.006	3.678	ENSOARG00000019797	NA	0.886	0.352	0.021	2.217
ENSOARG00000003096	FBXL18	-0.444	2.242	0.008	3.677	ENSOARG00000020446	NA	0.167	1.056	0.010	2.213
ENSOARG00000015003	ZNHIT1	0.815	1.878	0.016	3.676	ENSOARG00000011973	MOSPD1	-0.201	1.027	0.016	2.212
ENSOARG00000009575	MIS18BP1	-0.145	2.539	0.009	3.675	ENSOARG00000001654	PPP6R1	-0.035	1.192	0.016	2.211
ENSOARG00000010876	MRPL46	-0.350	2.330	0.006	3.674	ENSOARG00000003126	PBXIP1	0.118	1.122	0.030	2.210
ENSOARG00000001414	SUFU	-0.620	2.060	0.008	3.672	ENSOARG00000012006	LRRC3	0.376	0.846	0.013	2.210
ENSOARG00000013427	PTPN1	-0.871	1.805	0.005	3.671	ENSOARG00000016755	NA	0.054	1.162	0.008	2.209
ENSOARG00000014558	LGR5	-0.606	2.074	0.010	3.670	ENSOARG00000010854	JUNB	0.617	0.616	0.025	2.208
ENSOARG00000001561	TOE1	-0.531	2.143	0.004	3.670	ENSOARG00000001941	NA	0.789	0.452	0.035	2.205
ENSOARG00000008125	NA	0.938	1.739	0.011	3.666	ENSOARG00000001870	VSTM4	-0.087	1.135	0.018	2.203
ENSOARG00000004702	LRP4	-1.058	1.614	0.007	3.665	ENSOARG00000003313	DDX28	0.243	0.967	0.013	2.197
ENSOARG00000020555	ACP6	-0.090	2.588	0.014	3.665	ENSOARG00000006777	NA	0.156	1.061	0.020	2.197
ENSOARG00000001669	NA	0.305	2.373	0.013	3.665	ENSOARG00000019899	FBXO48	-0.170	1.049	0.025	2.194
ENSOARG00000007187	BCKDHB	0.053	2.630	0.019	3.664	ENSOARG00000004724	NA	-0.176	1.046	0.029	2.193
ENSOARG00000005979	TBC1D10B	0.240	2.433	0.008	3.664	ENSOARG00000012565	YPEL2	-0.330	0.900	0.045	2.186
ENSOARG00000015926	TEX11	0.170	2.504	0.011	3.663	ENSOARG00000005000	TESC	0.632	0.567	0.013	2.186
ENSOARG00000017479	LAMTOR4	0.743	1.964	0.044	3.663	ENSOARG00000008109	NA	0.198	1.018	0.030	2.186
ENSOARG00000015354	LRP5	-0.001	2.677	0.016	3.662	ENSOARG00000023242	NA	-0.126	1.069	0.011	2.185
ENSOARG00000008169	EDNRA	-0.840	1.838	0.018	3.660	ENSOARG00000004587	TOMM34	0.129	1.099	0.045	2.183
ENSOARG00000011830	OSBP	-0.269	2.401	0.010	3.660	ENSOARG00000005746	MAP4K1	0.477	0.716	0.010	2.183
ENSOARG00000011614	NA	-1.250	1.441	0.032	3.658	ENSOARG00000007403	BCKDHA	0.439	0.786	0.044	2.181
ENSOARG00000017511	NA	-0.178	2.497	0.018	3.657	ENSOARG00000015828	NA	-0.026	1.179	0.026	2.179
ENSOARG00000012405	MBNL3	0.128	2.541	0.012	3.656	ENSOARG00000013638	GNG7	-0.126	1.065	0.018	2.173
ENSOARG00000002842	TMEM208	-0.241	2.444	0.031	3.654	ENSOARG00000014139	TUBD1	-0.039	1.139	0.012	2.167
ENSOARG00000009901	NA	0.101	2.576	0.025	3.651	ENSOARG00000008614	PHLDB3	-0.060	1.131	0.025	2.166
ENSOARG00000017262	ARSK	-0.046	2.638	0.035	3.648	ENSOARG00000009600	GALK1	0.379	0.833	0.048	2.165
ENSOARG00000008598	MKS1	0.155	2.513	0.020	3.648	ENSOARG00000010993	ISM1	-0.479	0.688	0.005	2.163
ENSOARG00000003436	REXO4	-0.367	2.313	0.037	3.643	ENSOARG00000007354	PDYN	0.496	0.690	0.025	2.161
ENSOARG00000017502	NA	-0.669	2.017	0.043	3.643	ENSOARG00000012135	MROH9	0.564	0.622	0.026	2.160
ENSOARG00000011026	PDSS2	-0.385	2.268	0.012	3.641	ENSOARG00000011925	FAM129B	-0.196	1.011	0.049	2.158
ENSOARG00000022840	RNase_MRP	-0.598	2.055	0.019	3.634	ENSOARG00000013701	MRPS33	-0.200	0.963	0.005	2.157
ENSOARG00000014997	CHCHD7	0.191	2.490	0.047	3.633	ENSOARG00000008530	UHRF1	0.145	1.050	0.038	2.157
ENSOARG00000003240	RPA2	0.280	2.385	0.033	3.632	ENSOARG00000004906	HAUS5	0.080	1.100	0.023	2.157
ENSOARG00000008948	KIF17	0.771	1.875	0.014	3.631	ENSOARG00000003501	PDK4	-0.347	0.814	0.007	2.154
ENSOARG00000016549	LONRF3	-0.533	2.108	0.011	3.630	ENSOARG00000014723	CXCL14	-0.648	0.521	0.015	2.154
ENSOARG00000014617	PPP4R4	-0.406	2.236	0.013	3.630	ENSOARG00000005330	PGS1	0.282	0.882	0.011	2.153
ENSOARG00000002205	DNAH10	-0.214	2.431	0.014	3.630	ENSOARG00000000865	HCFC1R1	0.187	0.973	0.009	2.152
ENSOARG00000003516	THAP1	-0.113	2.528	0.012	3.629	ENSOARG00000017586	CNPY4	-0.210	0.947	0.006	2.151
ENSOARG00000007999	CCDC96	-0.771	1.880	0.026	3.625	ENSOARG00000020869	CTSK	0.104	1.075	0.027	2.151
ENSOARG00000014166	ZNF2	0.251	2.381	0.012	3.620	ENSOARG00000000909	THOC6	0.708	0.463	0.022	2.150
ENSOARG00000001685	MMACHC	0.204	2.435	0.021	3.619	ENSOARG00000012083	CORO1B	0.108	1.065	0.025	2.149
ENSOARG00000001965	CARS	0.097	2.537	0.015	3.618	ENSOARG00000010977	NA	0.531	0.632	0.015	2.147

ENSOARG00000002037	CLDN10	-0.948	1.672	0.004	3.616	ENSOARG00000015848	FDX2	-0.190	0.993	0.037	2.146
ENSOARG00000020808	EMP1	0.659	1.983	0.026	3.616	ENSOARG00000020375	NA	-0.300	0.856	0.011	2.145
ENSOARG00000015971	IGSF6	-0.190	2.454	0.029	3.615	ENSOARG00000009747	HYAL3	0.043	1.126	0.024	2.145
ENSOARG00000003791	C12orf66	1.034	1.582	0.003	3.613	ENSOARG00000020707	KCNMB3	0.179	0.971	0.006	2.144
ENSOARG00000011856	ALOX5AP	0.139	2.498	0.025	3.612	ENSOARG00000010892	NEU3	-0.022	1.143	0.022	2.144
ENSOARG00000005192	ARFGAP2	0.152	2.470	0.009	3.612	ENSOARG00000005002	NA	0.001	1.165	0.024	2.143
ENSOARG00000012147	NPR3	-1.258	1.367	0.013	3.611	ENSOARG00000011896	NA	-0.009	1.179	0.046	2.142
ENSOARG00000019302	ZNF513	0.236	2.415	0.040	3.611	ENSOARG00000009157	NEK5	-0.087	1.082	0.030	2.139
ENSOARG00000011242	STK11	0.223	2.436	0.049	3.610	ENSOARG00000004428	NA	-0.253	0.889	0.007	2.136
ENSOARG00000017866	NA	0.571	2.044	0.007	3.608	ENSOARG00000013152	RNF114	-0.040	1.110	0.016	2.134
ENSOARG00000020877	IL1A	-0.644	1.972	0.009	3.608	ENSOARG00000015663	CCDC87	-0.114	1.044	0.028	2.131
ENSOARG00000013925	GNG5	0.239	2.385	0.017	3.607	ENSOARG00000001854	ARF5	-0.696	0.447	0.013	2.130
ENSOARG00000012962	NA	-0.285	2.338	0.016	3.607	ENSOARG00000012968	NA	0.154	0.979	0.009	2.124
ENSOARG00000020763	GUCY2C	0.165	2.451	0.010	3.606	ENSOARG00000015150	PDZD9	-0.002	1.160	0.042	2.121
ENSOARG00000018398	MMRN1	-0.389	2.246	0.035	3.601	ENSOARG00000003813	C16orf71	-0.011	1.117	0.013	2.115
ENSOARG00000020861	CTSS	-0.374	2.248	0.022	3.600	ENSOARG00000001960	EPM2A	-0.425	0.710	0.024	2.110
ENSOARG00000012548	NA	-0.037	2.572	0.009	3.599	ENSOARG00000011543	COQ7	0.055	1.074	0.019	2.110
ENSOARG00000005614	ACP2	0.457	2.142	0.008	3.590	ENSOARG00000009460	TMEM161A	-0.105	1.046	0.042	2.109
ENSOARG00000001153	NA	-0.179	2.431	0.020	3.590	ENSOARG00000006862	ST6GALNAC2	0.014	1.111	0.020	2.105
ENSOARG00000016194	FN3K	0.621	2.012	0.043	3.590	ENSOARG00000024080	NA	-0.100	1.031	0.032	2.098
ENSOARG00000019271	VWC2L	-0.068	2.539	0.019	3.588	ENSOARG00000003657	SURF2	-0.147	0.962	0.014	2.095
ENSOARG00000011040	NA	0.025	2.587	0.025	3.587	ENSOARG00000017505	SUGCT	0.158	0.961	0.027	2.092
ENSOARG00000012653	SLC19A1	0.273	2.327	0.014	3.586	ENSOARG00000024846	NA	0.160	0.948	0.018	2.090
ENSOARG00000014603	FBLL1	-0.480	2.120	0.014	3.585	ENSOARG00000014728	NA	-0.128	0.968	0.009	2.087
ENSOARG00000026365	NA	0.694	1.896	0.006	3.585	ENSOARG00000016953	GTPBP3	0.512	0.579	0.010	2.081
ENSOARG00000007095	NDUFA4L2	0.712	1.877	0.007	3.581	ENSOARG00000010058	NA	-0.521	0.568	0.009	2.079
ENSOARG00000019598	DBX2	0.068	2.539	0.026	3.580	ENSOARG00000014863	NA	1.089	-0.002	0.009	2.077
ENSOARG00000018791	C11orf63	0.186	2.430	0.037	3.579	ENSOARG00000003676	CD320	0.061	1.039	0.025	2.075
ENSOARG00000005207	PRPS1	0.184	2.405	0.011	3.578	ENSOARG00000013817	RGN	0.052	1.033	0.013	2.072
ENSOARG00000014188	ENPP1	-0.827	1.776	0.027	3.576	ENSOARG00000006532	KCNK4	-0.027	1.058	0.016	2.069
ENSOARG00000009040	ATOX1	0.637	1.968	0.031	3.574	ENSOARG00000011243	NT5C	-0.450	0.631	0.012	2.068
ENSOARG00000013848	C14orf132	0.018	2.571	0.016	3.573	ENSOARG00000004154	PEX5	-0.217	0.858	0.009	2.066
ENSOARG00000008527	PURB	0.668	1.929	0.023	3.573	ENSOARG00000006467	NA	0.195	0.895	0.029	2.062
ENSOARG00000009684	NA	0.576	2.016	0.020	3.572	ENSOARG00000016333	NA	0.740	0.356	0.035	2.061
ENSOARG00000001483	LETM2	-0.558	2.022	0.009	3.571	ENSOARG00000001093	NME6	0.586	0.479	0.005	2.060
ENSOARG00000011157	TFE3	0.819	1.787	0.040	3.566	ENSOARG00000001599	SFXN4	0.276	0.797	0.013	2.060
ENSOARG00000004044	UBAC2	-0.737	1.859	0.032	3.564	ENSOARG00000018187	COL4A5	-0.339	0.728	0.019	2.048
ENSOARG00000012184	GPC3	0.122	2.448	0.007	3.563	ENSOARG00000000147	NA	0.148	0.927	0.031	2.044
ENSOARG00000002124	ADGRB1	-0.303	2.271	0.014	3.560	ENSOARG00000025249	NA	0.036	1.023	0.016	2.043
ENSOARG00000003466	NA	0.340	2.227	0.009	3.558	ENSOARG00000007810	ANKRD16	-0.377	0.677	0.013	2.042
ENSOARG00000018556	NA	0.163	2.424	0.030	3.557	ENSOARG00000004991	TMEM219	0.100	0.964	0.023	2.040
ENSOARG00000014079	MOCS3	-0.557	2.008	0.008	3.557	ENSOARG00000001178	NA	0.114	0.935	0.010	2.038
ENSOARG00000004698	TECPR2	-0.105	2.459	0.010	3.554	ENSOARG00000015174	NA	0.123	0.927	0.012	2.037
ENSOARG00000004096	BNIP1	-0.479	2.098	0.025	3.552	ENSOARG00000011337	IGFBPL1	0.444	0.615	0.022	2.037

ENSOARG00000000664	ACSBG1	-0.548	2.025	0.021	3.552	ENSOARG00000010804	NA	-0.352	0.707	0.026	2.033
ENSOARG00000019885	ZFAND2B	0.417	2.144	0.012	3.550	ENSOARG00000018343	NA	0.394	0.662	0.022	2.033
ENSOARG00000011348	KCND1	0.310	2.255	0.017	3.548	ENSOARG00000011711	NA	0.047	0.986	0.005	2.028
ENSOARG00000009547	SHQ1	-0.894	1.663	0.013	3.545	ENSOARG00000010499	NA	-0.205	0.871	0.050	2.026
ENSOARG00000008006	RNF217	-0.167	2.407	0.029	3.544	ENSOARG00000021010	SHC4	0.089	0.974	0.039	2.024
ENSOARG00000015921	NA	0.487	2.073	0.018	3.541	ENSOARG00000003121	WIF1	-0.040	1.009	0.028	2.021
ENSOARG00000008539	GREB1L	-0.210	2.340	0.009	3.541	ENSOARG00000014008	SCRT1	0.192	0.837	0.023	2.006
ENSOARG00000013884	NA	-0.607	1.943	0.010	3.540	ENSOARG00000005645	CERS5	0.081	0.934	0.010	2.005
ENSOARG00000010949	CCDC190	0.270	2.287	0.018	3.539	ENSOARG00000011304	NA	0.126	0.924	0.045	2.005
ENSOARG00000009877	SLC16A10	-0.743	1.801	0.006	3.537	ENSOARG00000012084	NA	-0.014	1.001	0.010	2.005
ENSOARG00000015634	MARS2	-0.156	2.411	0.032	3.535	ENSOARG00000007862	CCDC110	-0.645	0.365	0.005	2.005
ENSOARG00000001823	TNNT1	0.447	2.095	0.007	3.535	ENSOARG00000006258	ZNF771	0.392	0.633	0.024	2.001
ENSOARG00000003409	PRMT7	0.007	2.555	0.031	3.531	ENSOARG00000018650	NRN1	0.618	0.386	0.005	1.999
ENSOARG00000011520	NA	-0.415	2.157	0.041	3.531	ENSOARG00000016465	LIPI	0.083	0.946	0.031	1.998
ENSOARG00000008310	TTC29	-0.081	2.485	0.037	3.529	ENSOARG00000014378	MTG2	-0.104	0.911	0.019	1.996
ENSOARG00000008163	POU2F2	0.694	1.876	0.041	3.528	ENSOARG00000012514	MRGBP	0.122	0.879	0.009	1.992
ENSOARG00000015966	KRCC1	0.171	2.385	0.029	3.527	ENSOARG00000013577	CA13	-0.821	0.174	0.007	1.989
ENSOARG00000003447	SEC22C	-0.094	2.443	0.012	3.526	ENSOARG00000001704	PLEKHA2	0.053	0.941	0.006	1.988
ENSOARG00000002175	DNASE1	0.331	2.218	0.026	3.524	ENSOARG00000009965	NR1I3	0.125	0.883	0.021	1.987
ENSOARG00000018964	STAT5B	-0.246	2.288	0.010	3.524	ENSOARG00000001548	CRYBB1	-0.160	0.840	0.014	1.986
ENSOARG00000027048	NA	-0.189	2.376	0.048	3.518	ENSOARG00000011088	NA	0.052	0.942	0.016	1.979
ENSOARG00000018629	SMPD1	-0.418	2.128	0.027	3.518	ENSOARG00000010190	TCF19	-0.163	0.824	0.008	1.979
ENSOARG00000000271	CLMP	-0.370	2.170	0.024	3.517	ENSOARG00000010508	DECR1	0.077	0.909	0.017	1.969
ENSOARG00000017527	ADHFE1	-0.741	1.819	0.043	3.517	ENSOARG00000003547	MYBL2	-0.326	0.649	0.012	1.963
ENSOARG00000006606	SNF8	0.081	2.476	0.044	3.513	ENSOARG00000026820	NA	-0.326	0.647	0.022	1.950
ENSOARG00000012898	CABIN1	-0.134	2.385	0.006	3.513	ENSOARG00000011264	TCP11	-0.105	0.870	0.029	1.946
ENSOARG00000008837	GHR	0.366	2.182	0.039	3.509	ENSOARG00000011712	SMYD5	0.049	0.914	0.019	1.944
ENSOARG00000018399	TTI1	-0.290	2.231	0.013	3.509	ENSOARG00000017216	STAG3	-0.175	0.783	0.014	1.944
ENSOARG00000007321	ATP5SL	1.276	1.235	0.003	3.508	ENSOARG00000002386	CRY2	-0.081	0.880	0.019	1.942
ENSOARG00000006415	NA	0.403	2.114	0.010	3.507	ENSOARG00000013807	MSANTD1	0.734	0.219	0.012	1.941
ENSOARG00000011557	NA	-0.408	2.109	0.012	3.506	ENSOARG00000010590	NA	-0.372	0.581	0.012	1.940
ENSOARG00000016897	TRPV2	0.260	2.251	0.006	3.505	ENSOARG00000026518	NA	0.229	0.722	0.014	1.937
ENSOARG00000017478	NAA38	0.615	1.907	0.017	3.505	ENSOARG00000012812	CYB561A3	-0.226	0.730	0.019	1.937
ENSOARG00000018014	RRM2B	-0.381	2.164	0.041	3.504	ENSOARG00000019921	NA	-0.150	0.824	0.037	1.937
ENSOARG00000010382	THSD7B	-0.547	1.988	0.032	3.503	ENSOARG00000010890	NA	-0.109	0.872	0.045	1.936
ENSOARG00000017608	D2HGDH	0.284	2.228	0.011	3.500	ENSOARG00000010598	SIRT6	-0.026	0.953	0.049	1.930
ENSOARG00000026623	NA	-0.784	1.735	0.020	3.498	ENSOARG00000021370	NA	0.027	0.920	0.019	1.928
ENSOARG00000006047	PLS1	-0.391	2.127	0.020	3.498	ENSOARG00000017901	TMEM199	0.129	0.813	0.013	1.928
ENSOARG00000016214	HN1L	0.866	1.638	0.007	3.497	ENSOARG00000005191	ALKBH6	0.484	0.455	0.011	1.928
ENSOARG00000001535	NA	-0.618	1.886	0.010	3.494	ENSOARG00000018436	ZNF133	0.027	0.919	0.023	1.924
ENSOARG00000013679	URB1	0.219	2.294	0.019	3.494	ENSOARG00000020994	SLC27A2	-0.252	0.691	0.022	1.921
ENSOARG00000010734	NA	-0.258	2.254	0.025	3.487	ENSOARG00000006652	METTL23	-0.534	0.392	0.013	1.913
ENSOARG00000014218	NA	-0.626	1.886	0.026	3.486	ENSOARG00000001193	NA	-0.176	0.752	0.021	1.907
ENSOARG00000003095	NA	1.268	1.219	0.003	3.484	ENSOARG00000016619	OGFOD3	0.139	0.779	0.013	1.904

ENSOARG00000011960	SPHK2	-0.544	1.967	0.027	3.484	ENSOARG00000001355	NA	0.050	0.864	0.010	1.904
ENSOARG00000015017	INTS9	-0.345	2.159	0.022	3.482	ENSOARG00000002344	MECR	0.036	0.910	0.045	1.901
ENSOARG00000008604	OSBP2	-0.166	2.333	0.018	3.481	ENSOARG00000008083	DYNLRB2	0.317	0.594	0.011	1.900
ENSOARG00000002615	CBX4	0.175	2.317	0.012	3.480	ENSOARG00000025138	NA	-0.237	0.701	0.038	1.899
ENSOARG00000011565	LIG1	-0.159	2.338	0.018	3.479	ENSOARG00000016856	SIL1	0.033	0.874	0.012	1.896
ENSOARG00000011378	SEC61G	0.425	2.065	0.012	3.478	ENSOARG00000015918	NA	0.133	0.793	0.033	1.893
ENSOARG00000020946	TMOD4	-0.277	2.212	0.012	3.477	ENSOARG00000011943	SLC9C2	0.443	0.463	0.015	1.892
ENSOARG00000001499	COQ8A	-0.086	2.413	0.025	3.474	ENSOARG00000007062	NA	-0.465	0.473	0.047	1.891
ENSOARG00000012100	SLC46A3	0.528	1.956	0.010	3.474	ENSOARG00000015398	NA	0.677	0.231	0.018	1.889
ENSOARG00000005073	GRK6	-0.492	2.004	0.022	3.474	ENSOARG00000000459	NA	-0.289	0.621	0.024	1.885
ENSOARG00000007438	EXOSC2	-0.095	2.402	0.025	3.472	ENSOARG00000017712	NA	0.286	0.621	0.022	1.885
ENSOARG00000021767	MIAT_exon5_3	0.002	2.493	0.023	3.472	ENSOARG00000005471	MEX3A	0.057	0.863	0.039	1.881
ENSOARG00000009516	NA	-0.047	2.444	0.022	3.470	ENSOARG00000020043	LRMP	-0.236	0.693	0.047	1.881
ENSOARG00000009262	CARD6	-0.358	2.139	0.029	3.468	ENSOARG00000007362	CCDC129	-0.290	0.596	0.005	1.881
ENSOARG00000009246	IL23A	-0.168	2.319	0.019	3.467	ENSOARG00000014065	C11orf16	0.169	0.721	0.010	1.880
ENSOARG00000019415	DLGAP3	0.443	2.069	0.046	3.466	ENSOARG00000002424	MAN2C1	0.027	0.869	0.019	1.876
ENSOARG00000022787	5_8S_rRNA	0.265	2.227	0.029	3.464	ENSOARG00000002269	IRF2BPL	-0.107	0.781	0.019	1.870
ENSOARG00000017754	PYCR1	0.696	1.780	0.013	3.462	ENSOARG00000015896	NA	-0.322	0.551	0.009	1.864
ENSOARG00000005178	MRPL11	0.744	1.737	0.020	3.461	ENSOARG00000024962	FTX_4	0.323	0.571	0.036	1.859
ENSOARG00000017343	PLK1	0.379	2.089	0.009	3.458	ENSOARG00000003807	LRRC51	0.237	0.633	0.013	1.857
ENSOARG00000015649	ORC6	0.202	2.285	0.030	3.457	ENSOARG00000011866	TMEM8A	-0.499	0.365	0.009	1.854
ENSOARG00000003493	CHTF8	0.966	1.499	0.009	3.456	ENSOARG00000014203	CCRL2	0.078	0.780	0.006	1.852
ENSOARG00000009596	LSM10	0.445	2.036	0.026	3.455	ENSOARG00000002394	NA	0.210	0.661	0.020	1.851
ENSOARG00000010548	TMEM116	-0.675	1.790	0.012	3.453	ENSOARG00000019316	MYH7	0.237	0.635	0.023	1.849
ENSOARG00000005613	TRAF1	0.166	2.295	0.011	3.450	ENSOARG00000003186	CENPT	0.338	0.546	0.041	1.844
ENSOARG00000003058	GALC	-0.142	2.314	0.007	3.449	ENSOARG00000013688	NA	0.006	0.846	0.009	1.843
ENSOARG00000004709	FXYD1	1.050	1.426	0.028	3.448	ENSOARG00000011312	TMEM218	0.418	0.432	0.010	1.840
ENSOARG00000010974	NAIF1	0.750	1.730	0.033	3.447	ENSOARG00000017470	NA	-0.057	0.796	0.014	1.839
ENSOARG00000019500	AAMP	0.192	2.264	0.013	3.443	ENSOARG00000015473	PRDM5	0.326	0.522	0.013	1.834
ENSOARG00000003392	ZIM2	0.856	1.605	0.018	3.443	ENSOARG00000004596	NA	0.025	0.832	0.026	1.831
ENSOARG00000011726	DAZAP1	-0.370	2.088	0.017	3.441	ENSOARG00000020599	LRR1	0.023	0.823	0.016	1.829
ENSOARG00000007719	NA	-0.124	2.342	0.025	3.441	ENSOARG00000015106	NA	-0.051	0.780	0.015	1.817
ENSOARG00000012189	DGAT2	0.712	1.737	0.009	3.440	ENSOARG00000002350	PLAC8L1	0.106	0.720	0.014	1.812
ENSOARG00000014398	ERN1	0.468	2.010	0.040	3.438	ENSOARG00000012820	LOXL3	-0.284	0.563	0.037	1.811
ENSOARG00000005689	CCDC125	0.474	2.012	0.049	3.438	ENSOARG00000017369	NA	0.200	0.607	0.011	1.797
ENSOARG00000009482	NA	-0.117	2.342	0.022	3.437	ENSOARG00000008044	RPRM	0.215	0.589	0.017	1.787
ENSOARG00000010201	ZDHHC5	-0.113	2.342	0.018	3.437	ENSOARG00000022743	SNORA25	0.409	0.382	0.011	1.780
ENSOARG00000005058	NA	0.486	1.962	0.013	3.435	ENSOARG00000026481	NA	-0.155	0.641	0.020	1.776
ENSOARG00000015458	SYCP2	0.434	2.011	0.010	3.435	ENSOARG00000003886	NA	-0.177	0.608	0.019	1.766
ENSOARG00000013316	PUS1	-0.253	2.187	0.006	3.434	ENSOARG00000002789	NA	0.078	0.727	0.042	1.764
ENSOARG00000000226	STARD4	0.172	2.299	0.037	3.434	ENSOARG00000002955	NA	-0.208	0.560	0.010	1.758
ENSOARG00000006441	SERPINB12	-0.041	2.424	0.031	3.434	ENSOARG00000008637	TPGS1	0.085	0.680	0.008	1.757
ENSOARG00000002340	NA	0.146	2.308	0.022	3.432	ENSOARG00000001076	NPC2	0.189	0.576	0.010	1.755
ENSOARG00000008923	OXCT1	-0.164	2.273	0.009	3.428	ENSOARG00000018851	MORC4	-0.258	0.499	0.005	1.752

ENSOARG00000013237	NA	0.250	2.183	0.005	3.428	ENSOARG00000009196	NA	-0.545	0.225	0.024	1.746
ENSOARG00000006096	WFDC2	0.033	2.420	0.025	3.428	ENSOARG00000003727	NA	-0.041	0.718	0.014	1.746
ENSOARG00000003358	TRERF1	-0.011	2.433	0.018	3.427	ENSOARG00000025267	NA	0.405	0.350	0.019	1.737
ENSOARG00000015939	NA	-0.024	2.413	0.010	3.426	ENSOARG00000009959	NA	0.227	0.543	0.036	1.734
ENSOARG00000007020	NA	0.269	2.171	0.015	3.425	ENSOARG00000016983	NA	-0.354	0.366	0.008	1.712
ENSOARG00000011346	SHB	0.180	2.269	0.024	3.424	ENSOARG00000016735	NA	0.002	0.722	0.020	1.703
ENSOARG00000013647	ACAD8	0.841	1.612	0.030	3.423	ENSOARG00000003614	NA	-0.102	0.625	0.025	1.702
ENSOARG00000006388	NA	0.494	1.934	0.006	3.422	ENSOARG00000007511	ALDOB	-0.001	0.724	0.029	1.696
ENSOARG00000017518	RWDD3	0.464	1.971	0.014	3.421	ENSOARG00000025896	NA	-0.094	0.606	0.007	1.693
ENSOARG00000020998	DTWD1	-0.050	2.385	0.016	3.418	ENSOARG00000008101	OSBPL7	-0.006	0.692	0.010	1.687
ENSOARG00000012461	FBLN5	-0.130	2.318	0.031	3.417	ENSOARG00000020565	CDAN1	-0.572	0.128	0.023	1.676
ENSOARG00000002649	ACAD9	-0.182	2.252	0.020	3.415	ENSOARG00000026720	NA	0.233	0.447	0.006	1.674
ENSOARG00000013231	NA	0.130	2.295	0.011	3.414	ENSOARG00000027057	NA	0.465	0.220	0.011	1.674
ENSOARG00000013370	FDX1	0.215	2.203	0.006	3.411	ENSOARG00000004376	FLRT1	-0.234	0.451	0.012	1.672
ENSOARG00000019928	AP4B1	0.448	1.979	0.016	3.411	ENSOARG00000011192	NA	0.564	0.113	0.006	1.671
ENSOARG00000002803	E2F4	0.141	2.301	0.031	3.411	ENSOARG00000002598	FAM205C	-0.009	0.668	0.007	1.670
ENSOARG00000018744	KCNH3	0.110	2.307	0.007	3.410	ENSOARG00000009048	GIMD1	-0.140	0.541	0.023	1.658
ENSOARG00000008016	TNIP1	-0.266	2.191	0.048	3.409	ENSOARG00000000978	ACAA1	-0.147	0.506	0.007	1.647
ENSOARG00000002781	MAS1	-0.320	2.125	0.037	3.408	ENSOARG00000008661	CFAP100	-0.328	0.341	0.026	1.643
ENSOARG00000015420	NA	-0.107	2.322	0.021	3.408	ENSOARG00000000540	NA	-0.424	0.223	0.010	1.636
ENSOARG00000020830	HEBP1	0.493	1.947	0.032	3.407	ENSOARG00000010961	NA	0.216	0.462	0.044	1.634
ENSOARG00000019989	GJD2	0.738	1.713	0.044	3.407	ENSOARG00000025878	NA	-0.305	0.329	0.011	1.624
ENSOARG00000012469	NA	-0.131	2.292	0.016	3.407	ENSOARG00000025819	NA	-0.425	0.200	0.008	1.617
ENSOARG00000020655	B3GNT5	-0.116	2.297	0.006	3.406	ENSOARG00000020886	NA	0.166	0.463	0.015	1.613
ENSOARG00000004190	CHAC2	0.130	2.297	0.022	3.405	ENSOARG00000005893	NA	0.136	0.477	0.014	1.599
ENSOARG00000011841	ANPEP	-0.321	2.128	0.045	3.404	ENSOARG00000005394	NA	0.461	0.178	0.046	1.593
ENSOARG00000012651	NA	0.227	2.224	0.048	3.403	ENSOARG00000010145	CLP1	0.084	0.515	0.010	1.590
ENSOARG00000002965	TPPP3	0.782	1.639	0.018	3.403	ENSOARG00000008020	ERF	-0.249	0.363	0.022	1.590
ENSOARG00000006434	C1orf35	0.186	2.244	0.028	3.402	ENSOARG00000026129	NA	0.253	0.378	0.044	1.586
ENSOARG00000003540	PRTFDC1	0.877	1.527	0.005	3.399	ENSOARG00000020188	NA	-0.124	0.495	0.034	1.585
ENSOARG00000000266	BCL11B	-0.188	2.235	0.027	3.397	ENSOARG00000020200	NA	-0.480	0.117	0.015	1.582
ENSOARG00000005688	RAB30	0.029	2.398	0.031	3.396	ENSOARG00000008735	NA	-0.328	0.281	0.032	1.577
ENSOARG00000010965	NA	-0.410	1.993	0.008	3.395	ENSOARG00000024094	U6	-0.158	0.427	0.009	1.576
ENSOARG00000019742	MXD1	0.097	2.307	0.011	3.394	ENSOARG00000020455	NA	-0.456	0.121	0.009	1.567
ENSOARG00000026957	NA	0.357	2.057	0.021	3.393	ENSOARG00000014801	CHMP4C	0.364	0.190	0.010	1.543
ENSOARG00000001121	NA	0.207	2.208	0.021	3.393	ENSOARG00000009645	SULT6B1	-0.201	0.358	0.018	1.540
ENSOARG00000000991	AKAP5	-0.454	1.972	0.039	3.387	ENSOARG00000014755	TMEM220	0.275	0.291	0.034	1.532
ENSOARG00000004251	NA	0.689	1.743	0.047	3.385	ENSOARG00000011558	NA	-0.095	0.455	0.024	1.525
ENSOARG00000003599	NA	0.368	2.036	0.022	3.382	ENSOARG00000014120	NA	-0.084	0.449	0.011	1.523
ENSOARG00000006858	ELF1	-0.462	1.932	0.013	3.382	ENSOARG00000005220	CARTPT	0.022	0.542	0.041	1.523
ENSOARG00000010072	ERRFI1	-0.349	2.034	0.011	3.372	ENSOARG00000004666	NA	0.238	0.291	0.016	1.513
ENSOARG00000011270	ZFYVE27	0.193	2.207	0.029	3.372	ENSOARG00000008757	NA	0.094	0.411	0.015	1.490
ENSOARG00000010691	S1PR1	0.063	2.325	0.016	3.371	ENSOARG00000019837	NA	-0.124	0.363	0.011	1.476
ENSOARG00000009905	MBOAT1	0.105	2.289	0.024	3.371	ENSOARG00000019527	TMBIM1	0.060	0.459	0.047	1.472

ENSOARG00000011597	SEC13	0.195	2.184	0.010	3.369	ENSOARG00000016959	IGHMBP2	-0.302	0.185	0.015	1.472
ENSOARG00000017804	ARX	0.041	2.338	0.011	3.367	ENSOARG00000010229	EXOSC8	0.023	0.441	0.009	1.455
ENSOARG00000003340	NA	0.346	2.047	0.026	3.367	ENSOARG00000007164	PPP1R17	-0.210	0.249	0.011	1.448
ENSOARG00000008880	SH2D5	0.179	2.203	0.019	3.364	ENSOARG00000000274	TEKT1	0.290	0.165	0.009	1.446
ENSOARG00000002358	NA	0.238	2.172	0.047	3.363	ENSOARG00000025054	SNORA9	-0.088	0.384	0.035	1.437
ENSOARG00000000805	ACTRT3	-0.644	1.730	0.012	3.363	ENSOARG00000003395	NA	-0.123	0.339	0.029	1.432
ENSOARG00000020522	TIE1	-0.096	2.279	0.014	3.360	ENSOARG00000002987	NA	0.175	0.282	0.030	1.427
ENSOARG00000006059	BEND7	-0.833	1.544	0.020	3.357	ENSOARG00000010252	AK9	0.231	0.195	0.014	1.412
ENSOARG00000015108	KRT25	-0.695	1.674	0.015	3.354	ENSOARG00000000215	NA	0.247	0.187	0.025	1.409
ENSOARG00000007858	RASAL1	-0.158	2.208	0.014	3.352	ENSOARG00000009594	PLA2G3	-0.184	0.226	0.006	1.404
ENSOARG00000004555	TSHZ1	-0.898	1.468	0.014	3.352	ENSOARG00000013148	ZSCAN2	0.024	0.402	0.023	1.403
ENSOARG00000003263	FAM129A	0.587	1.771	0.006	3.352	ENSOARG00000020093	UBE2N	-0.101	0.317	0.022	1.396
ENSOARG00000017323	HIRA	0.243	2.114	0.010	3.347	ENSOARG00000011400	SRRM5	-0.113	0.274	0.008	1.378
ENSOARG00000004014	NAA40	-0.333	2.025	0.013	3.345	ENSOARG00000001798	PRELID3A	0.033	0.356	0.025	1.364
ENSOARG00000016356	PPP1R11	0.133	2.220	0.010	3.343	ENSOARG00000021311	7SK	0.184	0.183	0.009	1.359
ENSOARG00000001457	REL	0.245	2.127	0.031	3.341	ENSOARG00000009368	NA	0.152	0.190	0.036	1.306
ENSOARG00000004907	ZC3HC1	0.334	2.011	0.009	3.336	ENSOARG00000022186	U1	-0.068	0.071	0.010	1.128
ENSOARG00000008843	GALM	-0.945	1.405	0.015	3.334	ENSOARG00000025385	NA	0.074	-0.109	0.038	0.927
ENSOARG00000019119	IQCA1	-0.569	1.777	0.012	3.334	ENSOARG00000020197	NA	-0.098	-0.224	0.020	0.855
ENSOARG00000025340	NA	0.058	-0.217	0.037	0.804						

Supplementary Table 2. DAVID Gene Functional Classification output. Functional classification output of DAVID database for the query including genes with an unadjusted p < 0.05 after the edgeRun analysis. Group enrichment score, Ensembl gene ID, gene name and gene symbol are presented.

Gene Group 1	**Enrichment Score: 2.2196860163284238**
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000013191	ribosomal protein S11(RPS11)
ENSOARG00000014242	ribosomal protein S6(RPS6)
ENSOARG00000020159	60S ribosomal protein L13a(LOC101109545)
ENSOARG00000019935	ribosomal protein S29(RPS29)
ENSOARG00000006456	ribosomal protein L29(RPL29)
ENSOARG00000005542	ribosomal protein lateral stalk subunit P2(RPLP2)
ENSOARG00000004651	mitochondrial ribosomal protein L27(MRPL27)
ENSOARG00000013810	mitochondrial ribosomal protein S14(MRPS14)
ENSOARG00000009101	ribosomal protein S18(RPS18)
ENSOARG00000012645	ribosomal protein L8(RPL8)
ENSOARG00000002624	ribosomal protein S27a(RPS27A)
ENSOARG00000008365	ribosomal protein S19(RPS19)
ENSOARG00000016333	60S ribosomal protein L36(LOC101103232)
ENSOARG00000018666	ribosomal protein lateral stalk subunit P1(RPLP1)
ENSOARG00000007328	ribosomal protein S14(RPS14)
ENSOARG00000005178	mitochondrial ribosomal protein L11(MRPL11)
ENSOARG00000013126	ribosomal protein S21(RPS21)
ENSOARG00000000332	60S ribosomal protein L23-like(LOC105612165)
ENSOARG00000000077	mitochondrial ribosomal protein S2(MRPS2)
ENSOARG00000004877	60S ribosomal protein L37(LOC101115154)
ENSOARG00000005388	mitochondrial ribosomal protein L2(MRPL2)
ENSOARG00000014457	ribosomal protein L18a(RPL18A)
ENSOARG00000012647	mitochondrial ribosomal protein S18B(MRPS18B)
ENSOARG00000019921	60S ribosomal protein L10a-like(LOC101108801)
ENSOARG00000011605	ribosomal protein L9(RPL9)
ENSOARG00000008429	mitochondrial ribosomal protein L14(MRPL14)
ENSOARG00000010977	40S ribosomal protein S27-like(LOC101119090)

Gene Group 2	**Enrichment Score: 1.7005999933414828**
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000020219	isovaleryl-CoA dehydrogenase(IVD)
ENSOARG00000013647	acyl-CoA dehydrogenase family member 8(ACAD8)
ENSOARG00000010163	glutaryl-CoA dehydrogenase(GCDH)
ENSOARG00000010662	acyl-CoA dehydrogenase, very long chain(ACADVL)
ENSOARG00000002649	acyl-CoA dehydrogenase family member 9(ACAD9)

Gene Group 3	**Enrichment Score: 1.475099533211555**
ENSEMBL_GENE_ID	Gene Name
ENSOARG00000014647	tripartite motif containing 66(TRIM66)
ENSOARG00000007277	tripartite motif containing 41(TRIM41)
ENSOARG00000014515	mex-3 RNA binding family member B(MEX3B)
ENSOARG00000004516	U-box domain containing 5(UBOX5)
ENSOARG00000007674	ring finger protein 40(RNF40)
ENSOARG00000013152	ring finger protein 114(RNF114)
ENSOARG00000009028	makorin ring finger protein 3(MKRN3)
ENSOARG00000008530	ubiquitin like with PHD and ring finger domains 1(UHRF1)
ENSOARG00000003769	tripartite motif containing 46(TRIM46)
ENSOARG00000012745	ring finger protein 123(RNF123)
ENSOARG00000012749	polycomb group ring finger 1(PCGF1)
ENSOARG00000014661	ring finger protein 144A(RNF144A)
ENSOARG00000014583	peroxisomal biogenesis factor 2(PEX2)
ENSOARG00000018257	tripartite motif containing 3(TRIM3)
ENSOARG00000009726	tripartite motif containing 35(TRIM35)
ENSOARG00000000185	double PHD fingers 3(DPF3)
ENSOARG00000015178	ring finger protein 4(RNF4)
ENSOARG00000018006	tripartite motif containing 4(TRIM4)
ENSOARG00000003391	polycomb group ring finger 6(PCGF6)
ENSOARG00000016983	tripartite motif-containing protein 59(LOC101108249)
ENSOARG00000019106	RANBP2-type and C3HC4-type zinc finger containing 1(RBCK1)
ENSOARG00000001529	tripartite motif containing 8(TRIM8)
ENSOARG00000000818	tripartite motif containing 68(TRIM68)

Gene Group 4	**Enrichment Score: 1.4162771758340147**
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000009766	ADAM metallopeptidase with thrombospondin type 1 motif 17(ADAMTS17)
ENSOARG00000010962	ADAM metallopeptidase with thrombospondin type 1 motif 9(ADAMTS9)
ENSOARG00000014898	ADAM metallopeptidase with thrombospondin type 1 motif 1(ADAMTS1)
ENSOARG00000004292	ADAM metallopeptidase with thrombospondin type 1 motif 10(ADAMTS10)
ENSOARG00000007475	ADAM metallopeptidase with thrombospondin type 1 motif 18(ADAMTS18)
ENSOARG00000006371	ADAM metallopeptidase with thrombospondin type 1 motif 6(ADAMTS6)
ENSOARG00000014133	ADAMTS like 1(ADAMTSL1)

Gene Group 5	**Enrichment Score: 1.3092604578928795**
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000015186	acyl-CoA synthetase short-chain family member 3(ACSS3)
ENSOARG00000004315	acyl-CoA synthetase family member 2(ACSF2)

ENSOARG00000011792	acyl-CoA synthetase long-chain family member 5(ACSL5)
ENSOARG00000000664	acyl-CoA synthetase bubblegum family member 1(ACSBG1)

Gene Group 6	**Enrichment Score: 1.079837086677482**
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000018845	alpha-N-acetylgalactosaminidase(NAGA)
ENSOARG00000018240	lactase like(LCTL)
ENSOARG00000019976	galactosidase beta 1 like(GLB1L)
ENSOARG00000012289	mannosidase beta(MANBA)

Gene Group 7	**Enrichment Score: 0.9950796819850072**
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000005257	GDNF inducible zinc finger protein 1(GZF1)
ENSOARG00000008496	zinc finger protein 646(ZNF646)
ENSOARG00000000185	double PHD fingers 3(DPF3)
ENSOARG00000010468	PR/SET domain 15(PRDM15)
ENSOARG00000010061	POZ/BTB and AT hook containing zinc finger 1(PATZ1)
ENSOARG00000003219	PLAG1 like zinc finger 2(PLAGL2)
ENSOARG00000004095	zinc finger protein 414(ZNF414)
ENSOARG00000003623	zinc finger protein OZF-like(LOC101113523)
ENSOARG00000001296	zinc finger protein 696(ZNF696)
ENSOARG00000014918	teashirt zinc finger homeobox 2(TSHZ2)
ENSOARG00000003392	zinc finger imprinted 2(ZIM2)
ENSOARG00000011959	zinc finger protein 710(ZNF710)
ENSOARG00000011270	zinc finger FYVE-type containing 27(ZFYVE27)
ENSOARG00000010774	Zic family member 3(ZIC3)
ENSOARG00000003358	transcriptional regulating factor 1(TRERF1)
ENSOARG00000007890	zinc finger protein 629(ZNF629)
ENSOARG00000002874	uncharacterized LOC105605861(LOC105605861)
ENSOARG00000015473	PR/SET domain 5(PRDM5)
ENSOARG00000013148	zinc finger and SCAN domain containing 2(ZSCAN2)
ENSOARG00000003724	zinc finger protein 211-like(LOC101110168)
ENSOARG00000002789	zinc finger protein 621-like(LOC105603383)
ENSOARG00000018972	PR/SET domain 8(PRDM8)
ENSOARG00000020284	zinc finger FYVE-type containing 19(ZFYVE19)
ENSOARG00000008978	zinc finger protein 283(ZNF283)
ENSOARG00000000147	zinc finger protein 282(LOC101107593)
ENSOARG00000007509	zinc finger protein 496(ZNF496)
ENSOARG00000005354	SCAN domain containing 1(SCAND1)
ENSOARG00000005434	Zic family member 1(ZIC1)
ENSOARG00000019279	zinc finger protein 641(ZNF641)

ENSOARG00000004631	zinc finger protein 599(ZNF599)
ENSOARG00000015505	Kruppel like factor 5(KLF5)
ENSOARG00000018515	SCAN domain-containing protein 1-like(LOC101103215)
ENSOARG00000020268	zinc finger protein 684(ZNF684)
ENSOARG00000010779	zinc finger protein 768(ZNF768)
ENSOARG00000019302	zinc finger protein 513(ZNF513)
ENSOARG00000004353	spalt like transcription factor 3(SALL3)
ENSOARG00000014166	zinc finger protein 2(ZNF2)
ENSOARG00000010190	transcription factor 19(TCF19)
ENSOARG00000009044	zinc finger protein 235(LOC105608474)
ENSOARG00000019296	zinc finger homeobox 2(ZFHX2)
ENSOARG00000000770	zinc finger protein 202(ZNF202)
ENSOARG00000014354	zinc finger protein 276(ZNF276)
ENSOARG00000011585	zinc finger protein 501-like(LOC101104423)
ENSOARG00000019885	zinc finger AN1-type containing 2B(ZFAND2B)
ENSOARG00000004647	zinc finger protein 385D(ZNF385D)
ENSOARG00000003678	zinc finger protein OZF-like(LOC101115059)
ENSOARG00000011886	zinc finger protein 804B(ZNF804B)

Gene Group 8	**Enrichment Score: 0.8790762537274741**
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000001960	epilepsy, progressive myoclonus type 2A, Lafora disease (laforin)(EPM2A)
ENSOARG00000013213	dual specificity phosphatase 10(DUSP10)
ENSOARG00000007360	dual specificity phosphatase 9(DUSP9)
ENSOARG00000008440	cell division cycle 14B(CDC14B)
ENSOARG00000008498	dual specificity phosphatase 18(DUSP18)
ENSOARG00000020857	dual specificity phosphatase 16(DUSP16)

Gene Group 9	**Enrichment Score: 0.8752390311126941**
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000010770	StAR related lipid transfer domain containing 13(STARD13)
ENSOARG00000015301	acyl-CoA thioesterase 12(ACOT12)
ENSOARG00000013997	StAR related lipid transfer domain containing 7(STARD7)
ENSOARG00000000226	StAR related lipid transfer domain containing 4(STARD4)

Gene Group 10	**Enrichment Score: 0.7643412153479223**
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000004207	myosin IF(MYO1F)
ENSOARG00000018916	myosin heavy chain 15(MYH15)
ENSOARG00000012454	myosin IC(MYO1C)
ENSOARG00000018135	myosin XIX(MYO19)

ENSOARG00000013610	myosin VIIA(MYO7A)
ENSOARG00000019316	myosin heavy chain 7(MYH7)
ENSOARG00000011188	myosin heavy chain 7B(MYH7B)

Gene Group 11	**Enrichment Score: 0.7378684547548892**
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000003894	thrombospondin 3(THBS3)
ENSOARG00000018398	multimerin 1(MMRN1)
ENSOARG00000018923	peptidase domain containing associated with muscle regeneration 1(PAMR1)
ENSOARG00000017704	notch 4(NOTCH4)
ENSOARG00000011479	cartilage acidic protein 1(CRTAC1)
ENSOARG00000017490	thrombospondin 4(THBS4)
ENSOARG00000004702	LDL receptor related protein 4(LRP4)
ENSOARG00000006826	latent transforming growth factor beta binding protein 4(LTBP4)
ENSOARG00000010405	bone morphogenetic protein 1(BMP1)
ENSOARG00000012461	fibulin 5(FBLN5)
ENSOARG00000018379	EGF containing fibulin like extracellular matrix protein 2(EFEMP2)
ENSOARG00000015724	EGF like repeats and discoidin domains 3(EDIL3)
ENSOARG00000011304	EGF like domain multiple 6(EGFL6)

Gene Group 12	**Enrichment Score: 0.6982413324231707**
ENSEMBL_GENE_ID	Gene Name
ENSOARG00000005858	nuclear receptor subfamily 1 group H member 3(NR1H3)
ENSOARG00000020816	RAR related orphan receptor A(RORA)
ENSOARG00000013027	nuclear receptor subfamily 1 group D member 1(NR1D1)
ENSOARG00000011785	peroxisome proliferator activated receptor delta(PPARD)
ENSOARG00000009965	nuclear receptor subfamily 1 group I member 3(NR1I3)
ENSOARG00000010939	nuclear receptor subfamily 4 group A member 3(NR4A3)

Gene Group 13	**Enrichment Score: 0.6905533035429205**
ENSEMBL_GENE_ID	Gene Name
ENSOARG00000019605	bromodomain containing 1(BRD1)
ENSOARG00000014647	tripartite motif containing 66(TRIM66)
ENSOARG00000004310	CXXC finger protein 1(CXXC1)
ENSOARG00000010190	transcription factor 19(TCF19)
ENSOARG00000007020	inhibitor of growth family member 1(ING1)
ENSOARG00000008388	lysine demethylase 4B(KDM4B)
ENSOARG00000000185	double PHD fingers 3(DPF3)
ENSOARG00000008530	ubiquitin like with PHD and ring finger domains 1(UHRF1)

Gene Group 14	**Enrichment Score: 0.6748428841728834**

ENSEMBL_GENE_ID	Gene Name
ENSOARG00000008656	filamin binding LIM protein 1(FBLIM1)
ENSOARG00000012948	four and a half LIM domains 2(FHL2)
ENSOARG00000017443	PDZ and LIM domain 5(PDLIM5)
ENSOARG00000016024	LIM zinc finger domain containing 2(LIMS2)

Gene Group 15	**Enrichment Score: 0.5639797924547291**
ENSEMBL_GENE_ID	Gene Name
ENSOARG00000007585	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1(TANC1)
ENSOARG00000016549	LON peptidase N-terminal domain and ring finger 3(LONRF3)
ENSOARG00000015926	testis expressed 11(TEX11)
ENSOARG00000012410	unc-45 myosin chaperone A(UNC45A)
ENSOARG00000005358	trafficking protein particle complex 12(TRAPPC12)
ENSOARG00000016954	tetratricopeptide repeat domain 32(TTC32)
ENSOARG00000008310	tetratricopeptide repeat domain 29(TTC29)
ENSOARG00000004587	translocase of outer mitochondrial membrane 34(TOMM34)

Gene Group 16	**Enrichment Score: 0.5278330324698647**
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000014901	MYB proto-oncogene, transcription factor(MYB)
ENSOARG00000017663	MYB proto-oncogene like 1(MYBL1)
ENSOARG00000003547	MYB proto-oncogene like 2(MYBL2)
ENSOARG00000009575	MIS18 binding protein 1(MIS18BP1)

Gene Group 17	**Enrichment Score: 0.49901187806585884**
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000015211	kinesin family member 18A(KIF18A)
ENSOARG00000016755	dynein axonemal heavy chain 14(DNAH14)
ENSOARG00000008948	kinesin family member 17(KIF17)
ENSOARG00000004780	kinesin family member 15(KIF15)
ENSOARG00000005591	kinesin family member 22(KIF22)
ENSOARG00000015055	kinesin family member 13B(KIF13B)
ENSOARG00000015491	kinesin family member 4A(KIF4A)
ENSOARG00000002205	dynein axonemal heavy chain 10(DNAH10)

Gene Group 18	**Enrichment Score: 0.3701325301507387**
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000009874	potassium channel tetramerization domain containing 9(KCTD9)
ENSOARG00000011389	potassium channel tetramerization domain containing 2(KCTD2)
ENSOARG00000004464	potassium channel tetramerization domain containing 15(KCTD15)
ENSOARG00000009315	nucleus accumbens associated 1(NACC1)

Gene Group 19	Enrichment Score: 0.333844238127253
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000011672	PWP2 periodic tryptophan protein homolog (yeast)(PWP2)
ENSOARG00000000909	THO complex 6(THOC6)
ENSOARG00000013290	WD repeat domain 38(WDR38)
ENSOARG00000006698	ribosomal RNA processing 9, small subunit (SSU) processome component, homolog (yeast)(RRP9)
ENSOARG00000010843	denticleless E3 ubiquitin protein ligase homolog(DTL)
ENSOARG00000019141	prolactin regulatory element binding(PREB)
ENSOARG00000012229	WD repeat domain 83(WDR83)
ENSOARG00000003114	DENN domain containing 3(DENND3)
ENSOARG00000010123	echinoderm microtubule associated protein like 2(EML2)
ENSOARG00000012336	transducin like enhancer of split 4(TLE4)
ENSOARG00000019500	angio associated migratory cell protein(AAMP)
ENSOARG00000012640	WD repeat domain 54(WDR54)
ENSOARG00000015822	WD repeat containing antisense to TP53(WRAP53)
ENSOARG00000014521	WD repeat domain 37(WDR37)
ENSOARG00000014267	leucine rich repeats and WD repeat domain containing 1(LRWD1)
ENSOARG00000006300	WD repeat domain 31(WDR31)
ENSOARG00000003686	WD and tetratricopeptide repeats 1(WDTC1)
ENSOARG00000001983	WD repeat domain 5B(WDR5B)
ENSOARG00000015805	WD repeat domain 6(WDR6)
ENSOARG00000007794	WD repeat domain 64(WDR64)
ENSOARG00000005231	WD repeat domain 62(WDR62)
ENSOARG00000011597	SEC13 homolog, nuclear pore and COPII coat complex component(SEC13)

Gene Group 20	Enrichment Score: 0.3310651104899716
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000000078	KIT proto-oncogene receptor tyrosine kinase(KIT)
ENSOARG00000020522	tyrosine kinase with immunoglobulin like and EGF like domains 1(TIE1)
ENSOARG00000006358	colony stimulating factor 1 receptor(CSF1R)
ENSOARG00000006538	platelet derived growth factor receptor beta(PDGFRB)

Gene Group 21	Enrichment Score: 0.2777133548116479
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000006520	ubiquitin conjugating enzyme E2 C(UBE2C)
ENSOARG00000018948	ubiquitin conjugating enzyme E2 F (putative)(UBE2F)
ENSOARG00000012247	ubiquitin conjugating enzyme E2 G2(UBE2G2)
ENSOARG00000020093	ubiquitin-conjugating enzyme E2 N(LOC105601864)
ENSOARG00000009875	ubiquitin conjugating enzyme E2 U (putative)(UBE2U)

Gene Group 22	Enrichment Score: 0.2647019467542983
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000001474	histone H2B type 3-B(LOC101102231)
ENSOARG00000013281	histone H2A type 2-C(LOC101122645)
ENSOARG00000009196	histone H2A type 1(LOC101120200)
ENSOARG00000013389	histone H2A type 2-B(LOC101122904)

Gene Group 23	Enrichment Score: 0.2334532775019263
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000010119	DEAD-box helicase 49(DDX49)
ENSOARG00000015812	HFM1, ATP dependent DNA helicase homolog(HFM1)
ENSOARG00000004495	helicase, lymphoid-specific(HELLS)
ENSOARG00000005908	ERCC excision repair 6 like, spindle assembly checkpoint helicase(ERCC6L)
ENSOARG00000020547	chromodomain helicase DNA binding protein 1 like(CHD1L)
ENSOARG00000017866	DEAH-box helicase 37(DHX37)

Gene Group 24	Enrichment Score: 0.232741031892927
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000001560	Rho GTPase activating protein 22(ARHGAP22)
ENSOARG00000009482	Rho GTPase activating protein 19(ARHGAP19)
ENSOARG00000007284	Rho GTPase activating protein 10(ARHGAP10)
ENSOARG00000009322	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2(ARAP2)

Gene Group 25	Enrichment Score: 0.22545693276483578
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000001683	potassium voltage-gated channel subfamily C member 1(KCNC1)
ENSOARG00000011348	potassium voltage-gated channel subfamily D member 1(KCND1)
ENSOARG00000007387	potassium voltage-gated channel subfamily J member 10(KCNJ10)
ENSOARG00000004200	hyperpolarization activated cyclic nucleotide gated potassium channel 3(HCN3)
ENSOARG00000006855	potassium voltage-gated channel subfamily A member 4(KCNA4)
ENSOARG00000011066	potassium voltage-gated channel subfamily Q member 5(KCNQ5)
ENSOARG00000018744	potassium voltage-gated channel subfamily H member 3(KCNH3)

Gene Group 26	Enrichment Score: 0.221271848797715O5
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000012998	ras homolog family member F, filopodia associated(RHOF)
ENSOARG00000015153	guanylate-binding protein 4-like(LOC101119773)
ENSOARG00000018994	intraflagellar transport 27(IFT27)
ENSOARG00000003312	DIRAS family GTPase 2(DIRAS2)
ENSOARG00000001854	ADP ribosylation factor 5(ARF5)

ENSOARG00000015072	guanylate-binding protein 1-like(LOC101119517)
ENSOARG00000005688	RAB30, member RAS oncogene family(RAB30)
ENSOARG00000001243	RAB31, member RAS oncogene family(RAB31)
ENSOARG00000015161	RAP2B, member of RAS oncogene family(RAP2B)
ENSOARG00000011103	ADP-ribosylation factor 2(LOC101120590)

Gene Group 27	**Enrichment Score: 0.21385453827007722**
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000005098	ST3 beta-galactoside alpha-2,3-sialyltransferase 2(ST3GAL2)
ENSOARG00000005138	polypeptide N-acetylgalactosaminyltransferase 3(GALNT3)
ENSOARG00000006862	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 2(ST6GALNAC2)
ENSOARG00000011045	polypeptide N-acetylgalactosaminyltransferase 12(GALNT12)

Gene Group 28	**Enrichment Score: 0.1778029936459451**
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000017917	glutamate ionotropic receptor kainate type subunit 4(GRIK4)
ENSOARG00000001184	cholinergic receptor nicotinic beta 4 subunit(CHRNB4)
ENSOARG00000011195	cholinergic receptor nicotinic alpha 4 subunit(CHRNA4)
ENSOARG00000015295	glycine receptor alpha 3(GLRA3)

Gene Group 29	**Enrichment Score: 0.16669710170493782**
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000013688	cleavage stimulation factor subunit 2 tau variant(CSTF2T)
ENSOARG00000004578	poly(A) binding protein cytoplasmic 1 like(PABPC1L)
ENSOARG00000007757	RNA binding motif protein 15B(RBM15B)
ENSOARG00000011726	DAZ associated protein 1(DAZAP1)
ENSOARG00000015886	ribonucleoprotein, PTB binding 1(RAVER1)
ENSOARG00000019797	zinc finger CCHC-type and RNA binding motif containing 1(ZCRB1)
ENSOARG00000015861	ecto-NOX disulfide-thiol exchanger 2(ENOX2)
ENSOARG00000004583	small nuclear ribonucleoprotein U11/U12 subunit 35(SNRNP35)

Gene Group 30	**Enrichment Score: 0.14855293068305875**
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000011481	Pim-2 proto-oncogene, serine/threonine kinase(PIM2)
ENSOARG00000007657	cyclin dependent kinase 20(CDK20)
ENSOARG00000013254	A-Raf proto-oncogene, serine/threonine kinase(ARAF)
ENSOARG00000002711	aarF domain containing kinase 1(ADCK1)
ENSOARG00000003249	c-src tyrosine kinase(CSK)
ENSOARG00000017343	polo like kinase 1(PLK1)
ENSOARG00000014631	Janus kinase 3(JAK3)
ENSOARG00000020522	tyrosine kinase with immunoglobulin like and EGF like domains 1(TIE1)

ENSOARG00000019073	protein kinase, cGMP-dependent, type II(PRKG2)
ENSOARG00000005073	G protein-coupled receptor kinase 6(GRK6)
ENSOARG00000005746	mitogen-activated protein kinase kinase kinase kinase 1(MAP4K1)
ENSOARG00000011674	megakaryocyte-associated tyrosine kinase(MATK)
ENSOARG00000003419	serine/threonine kinase 32A(STK32A)
ENSOARG00000014364	Pim-1 proto-oncogene, serine/threonine kinase(PIM1)
ENSOARG00000014630	MAP kinase interacting serine/threonine kinase 2(MKNK2)
ENSOARG00000020944	testis specific serine kinase 3(TSSK3)
ENSOARG00000000106	vaccinia related kinase 1(VRK1)

Gene Group 31	Enrichment Score: 0.09088929565972834
ENSEMBL_GENE_ID	Gene Name
ENSOARG00000001560	Rho GTPase activating protein 22(ARHGAP22)
ENSOARG00000000399	TBC1 domain family member 2B(TBC1D2B)
ENSOARG00000010885	pleckstrin homology like domain family B member 1(PHLDB1)
ENSOARG00000021168	pleckstrin homology, MyTH4 and FERM domain containing H1(PLEKHH1)

Gene Group 32	**Enrichment Score: 0.09031614382073533**
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000008288	N-terminal EF-hand calcium binding protein 3(NECAB3)
ENSOARG00000006047	plastin 1(PLS1)
ENSOARG00000017596	centrin-4(LOC101104012)
ENSOARG00000008649	FK506 binding protein 14(FKBP14)
ENSOARG00000005149	potassium voltage-gated channel interacting protein 4(KCNIP4)
ENSOARG00000014754	calcyphosine 2(CAPS2)
ENSOARG00000014075	potassium voltage-gated channel interacting protein 3(KCNIP3)
ENSOARG00000016247	centrin 3(CETN3)

Gene Group 33	**Enrichment Score: 0.08474668829938133**
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000011337	insulin like growth factor binding protein like 1(IGFBPL1)
ENSOARG00000001870	V-set and transmembrane domain containing 4(VSTM4)
ENSOARG00000019958	trophoblast glycoprotein(TPBG)
ENSOARG00000000271	CXADR like membrane protein(CLMP)
ENSOARG00000008358	CD79a molecule(CD79A)
ENSOARG00000014133	ADAMTS like 1(ADAMTSL1)
ENSOARG00000004376	fibronectin leucine rich transmembrane protein 1(FLRT1)
ENSOARG00000013187	nexilin F-actin binding protein(NEXN)
ENSOARG00000020462	interleukin 1 receptor accessory protein(IL1RAP)
ENSOARG00000015971	immunoglobulin superfamily member 6(IGSF6)
ENSOARG00000005275	peroxidasin(PXDN)

ENSOARG00000012746	immunoglobulin superfamily member 1(IGSF1)
ENSOARG00000008809	cell adhesion molecule 4(CADM4)
ENSOARG00000005176	leucine rich repeat and fibronectin type III domain containing 3(LRFN3)
ENSOARG00000013028	kin of IRRE like 3 (Drosophila)(KIRREL3)
ENSOARG00000006382	unc-5 netrin receptor B(UNC5B)
ENSOARG00000007174	kin of IRRE like (Drosophila)(KIRREL)
ENSOARG00000016969	coiled-coil domain containing 141(CCDC141)

Gene Group 34	**Enrichment Score: 0.07427573795841302**
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000016033	sosondowah ankyrin repeat domain family member C(SOWAHC)
ENSOARG00000017812	CASK interacting protein 1(CASKIN1)
ENSOARG00000011062	ankyrin repeat and sterile alpha motif domain containing 6(ANKS6)
ENSOARG00000013735	ankyrin repeat domain 39(ANKRD39)
ENSOARG00000008733	ankyrin repeat and SOCS box containing 6(ASB6)
ENSOARG00000007469	ankyrin repeat domain 55(ANKRD55)
ENSOARG00000006151	ankyrin repeat and fibronectin type III domain containing 1(ANKFN1)
ENSOARG00000014141	ankyrin repeat domain 13A(ANKRD13A)
ENSOARG00000003756	ankyrin repeat and sterile alpha motif domain containing 3(ANKS3)

Gene Group 35	**Enrichment Score: 0.05149411657284901**
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000019893	prokineticin receptor 1(PROKR1)
ENSOARG00000006760	lysophosphatidic acid receptor 1(LPAR1)
ENSOARG00000010462	C-X-C motif chemokine receptor 4(CXCR4)
ENSOARG00000010691	sphingosine-1-phosphate receptor 1(S1PR1)
ENSOARG00000014203	C-C motif chemokine receptor like 2(CCRL2)
ENSOARG00000015284	purinergic receptor P2Y12(P2RY12)
ENSOARG00000008837	growth hormone receptor(GHR)
ENSOARG00000007690	sphingosine-1-phosphate receptor 3(S1PR3)
ENSOARG00000009115	G protein-coupled receptor 173(GPR173)
ENSOARG00000010861	tachykinin receptor 3(TACR3)
ENSOARG00000000304	atypical chemokine receptor 3(ACKR3)
ENSOARG00000015876	interleukin 17 receptor B(IL17RB)
ENSOARG00000008169	endothelin receptor type A(EDNRA)
ENSOARG00000015199	purinergic receptor P2Y1(P2RY1)
ENSOARG00000010704	adrenoceptor alpha 2A(ADRA2A)
ENSOARG00000005323	5-hydroxytryptamine receptor 1A(HTR1A)
ENSOARG00000013402	prostaglandin F receptor(PTGFR)
ENSOARG00000002781	MAS1 proto-oncogene, G protein-coupled receptor(MAS1)
ENSOARG00000007549	lysophosphatidic acid receptor 2(LPAR2)

Gene Group 36	Enrichment Score: 0.04587562104987315
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000003676	CD320 molecule(CD320)
ENSOARG00000004284	phospholipid phosphatase 4(PLPP4)
ENSOARG00000002018	WW domain binding protein 1-like(WBP1L)
ENSOARG00000013141	membrane spanning 4-domains A13(MS4A13)
ENSOARG00000004247	translation initiation factor IF-2(LOC105616457)
ENSOARG00000010786	solute carrier family 35 member F2(SLC35F2)
ENSOARG00000016515	cornichon family AMPA receptor auxiliary protein 3(CNIH3)
ENSOARG00000002842	transmembrane protein 208(TMEM208)
ENSOARG00000011065	solute carrier organic anion transporter family member 2B1(SLCO2B1)
ENSOARG00000015876	interleukin 17 receptor B(IL17RB)
ENSOARG00000008070	transmembrane protein 241(TMEM241)
ENSOARG00000005573	MAGE family member H1(MAGEH1)
ENSOARG00000019893	prokineticin receptor 1(PROKR1)
ENSOARG00000010129	beta-site APP-cleaving enzyme 2(BACE2)
ENSOARG00000016968	chromosome 15 open reading frame, human C11orf87(C15H11orf87)
ENSOARG00000019673	uroplakin 1B(UPK1B)
ENSOARG00000011192	cytochrome c oxidase subunit 7A2, mitochondrial(LOC101110066)
ENSOARG00000010824	signal peptidase complex subunit 2(SPCS2)
ENSOARG00000010111	protein ARMCX6(LOC101106998)
ENSOARG00000007293	ATP binding cassette subfamily B member 9(ABCB9)
ENSOARG00000014572	cation channel sperm associated 3(CATSPER3)
ENSOARG00000020935	semaphorin 6C(SEMA6C)
ENSOARG00000012366	major facilitator superfamily domain containing 12(MFSD12)
ENSOARG00000001636	sucrase-isomaltase(SI)
ENSOARG00000007095	NDUFA4, mitochondrial complex associated like 2(NDUFA4L2)
ENSOARG00000000271	CXADR like membrane protein(CLMP)
ENSOARG00000001691	transmembrane protein 176B(TMEM176B)
ENSOARG00000003447	SEC22 homolog C, vesicle trafficking protein(SEC22C)
ENSOARG00000005906	mannosidase alpha class 1C member 1(MAN1C1)
ENSOARG00000017270	sodium- and chloride-dependent glycine transporter 1(LOC101119236)
ENSOARG00000018166	adiponectin receptor 1(ADIPOR1)
ENSOARG00000018018	carbohydrate sulfotransferase 12(CHST12)
ENSOARG00000020173	semaphorin 5B(SEMA5B)
ENSOARG00000005385	small integral membrane protein 15(SMIM15)
ENSOARG00000004063	zinc finger DHHC-type containing 18(ZDHHC18)
ENSOARG00000013793	lectin, mannose binding 2 like(LMAN2L)
ENSOARG00000013559	transmembrane protein 120A(TMEM120A)
ENSOARG00000005894	cadherin 20(CDH20)

ENSOARG00000020786	aph-1 homolog B, gamma-secretase subunit(APH1B)
ENSOARG00000020144	VANGL planar cell polarity protein 1(VANGL1)
ENSOARG00000007018	NADH:ubiquinone oxidoreductase subunit A11(NDUFA11)
ENSOARG00000009445	solute carrier family 35 member B2(SLC35B2)
ENSOARG00000011973	motile sperm domain containing 1(MOSPD1)
ENSOARG00000006506	solute carrier family 29 member 3(SLC29A3)
ENSOARG00000018744	potassium voltage-gated channel subfamily H member 3(KCNH3)
ENSOARG00000000665	ATPase H+ transporting V0 subunit b(ATP6V0B)
ENSOARG00000017345	solute carrier family 10 member 4(SLC10A4)
ENSOARG00000002553	stabilin-1-like(LOC101122261)
ENSOARG00000000963	transmembrane protein 53(TMEM53)
ENSOARG00000020232	myelin regulatory factor-like(MYRFL)
ENSOARG00000013008	family with sequence similarity 189 member A2(FAM189A2)
ENSOARG00000003628	Yip1 interacting factor homolog A, membrane trafficking protein(YIF1A)
ENSOARG00000013614	family with sequence similarity 173 member A(FAM173A)
ENSOARG00000007080	contactin associated protein like 4(CNTNAP4)
ENSOARG00000006390	G protein-coupled receptor 137(GPR137)
ENSOARG00000019958	trophoblast glycoprotein(TPBG)
ENSOARG00000001870	V-set and transmembrane domain containing 4(VSTM4)
ENSOARG00000016652	pecanex homolog 3 (Drosophila)(PCNX3)
ENSOARG00000001936	ring finger protein 175(RNF175)
ENSOARG00000020197	NADH:ubiquinone oxidoreductase subunit B1(NDUFB1)
ENSOARG00000014308	family with sequence similarity 173 member B(FAM173B)
ENSOARG00000011792	acyl-CoA synthetase long-chain family member 5(ACSL5)
ENSOARG00000004313	solute carrier family 10 member 6(SLC10A6)
ENSOARG00000001455	exo/endonuclease G(EXOG)
ENSOARG00000000935	multidrug resistance-associated protein 4(LOC101106534)
ENSOARG00000004441	solute carrier family 41 member 1(SLC41A1)
ENSOARG00000011032	PRA1 domain family member 2(PRAF2)
ENSOARG00000019692	megalencephalic leukoencephalopathy with subcortical cysts 1(MLC1)
ENSOARG00000020582	microsomal glutathione S-transferase 1(MGST1)
ENSOARG00000007357	phosphatidylinositol glycan anchor biosynthesis class M(PIGM)
ENSOARG00000014770	transmembrane protein 170B(TMEM170B)
ENSOARG00000015251	transmembrane protein 184B(TMEM184B)
ENSOARG00000012147	natriuretic peptide receptor 3(NPR3)
ENSOARG00000013022	transmembrane protein 182(TMEM182)
ENSOARG00000000541	store-operated calcium entry regulator STIMATE(LOC101108428)
ENSOARG00000012748	glycoprotein nmb(GPNMB)
ENSOARG00000006484	adipocyte plasma membrane associated protein(APMAP)
ENSOARG00000020657	lysosomal associated membrane protein 3(LAMP3)
ENSOARG00000019854	G protein-coupled receptor 156(GPR156)

ENSOARG00000009812	FRAS1 related extracellular matrix protein 2(FREM2)
ENSOARG00000010890	podoplanin(PDPN)
ENSOARG00000011045	polypeptide N-acetylgalactosaminyltransferase 12(GALNT12)
ENSOARG00000010548	transmembrane protein 116(TMEM116)
ENSOARG00000015752	transmembrane protein 109(TMEM109)
ENSOARG00000003467	heme oxygenase 2(HMOX2)
ENSOARG00000004991	transmembrane protein 219(TMEM219)
ENSOARG00000002396	ATP-binding cassette, sub-family B (MDR/TAP), member 1(ABCB1)
ENSOARG00000016969	coiled-coil domain containing 141(CCDC141)
ENSOARG00000000215	uncharacterized protein C1orf43 homolog pseudogene(LOC105607505)
ENSOARG00000020586	chloride voltage-gated channel 2(CLCN2)
ENSOARG00000006045	serine rich and transmembrane domain containing 1(SERTM1)
ENSOARG00000007549	lysophosphatidic acid receptor 2(LPAR2)
ENSOARG00000005097	ER membrane associated RNA degradation(ERMARD)
ENSOARG00000006831	desmocollin 3(DSC3)
ENSOARG00000004813	syndecan 2(SDC2)
ENSOARG00000001599	sideroflexin 4(SFXN4)
ENSOARG00000014203	C-C motif chemokine receptor like 2(CCRL2)
ENSOARG00000014253	solute carrier family 7 member 11(SLC7A11)
ENSOARG00000009835	major facilitator superfamily domain containing 4B(MFSD4B)
ENSOARG00000012807	adiponectin receptor 2(ADIPOR2)
ENSOARG00000014926	adhesion G protein-coupled receptor D1(ADGRD1)
ENSOARG00000011042	transmembrane protein 198-like(LOC101113745)
ENSOARG00000004470	beta-1,4-glucuronyltransferase 1(B4GAT1)
ENSOARG00000006777	transmembrane protein 170A(TMEM170A)
ENSOARG00000008561	uncoupling protein 2(UCP2)
ENSOARG00000014787	mannose-P-dolichol utilization defect 1(MPDU1)
ENSOARG00000015940	transmembrane and coiled-coil domain family 3(TMCC3)
ENSOARG00000020716	potassium calcium-activated channel subfamily M regulatory beta subunit 2(KCNMB2)
ENSOARG00000019121	abhydrolase domain containing 1(ABHD1)
ENSOARG00000000847	proline rich transmembrane protein 1(PRRT1)
ENSOARG00000008605	CD9 molecule(CD9)
ENSOARG00000004733	relaxin/insulin like family peptide receptor 1(RXFP1)
ENSOARG00000016482	family with sequence similarity 189 member A1(FAM189A1)
ENSOARG00000008974	ADAM metallopeptidase domain 11(ADAM11)
ENSOARG00000014661	ring finger protein 144A(RNF144A)
ENSOARG00000012262	glypican 4(GPC4)
ENSOARG00000001032	transmembrane protein 229B(TMEM229B)
ENSOARG00000013670	cytochrome c oxidase subunit 5B, mitochondrial(LOC101110664)
ENSOARG00000008821	solute carrier family 25 member 34(SLC25A34)

ENSOARG00000012100	solute carrier family 46 member 3(SLC46A3)
ENSOARG00000008626	proline rich and Gla domain 3(PRRG3)
ENSOARG00000015577	transmembrane protein 167A(TMEM167A)
ENSOARG00000003341	interferon alpha inducible protein 6(IFI6)
ENSOARG00000011866	transmembrane protein 8A(TMEM8A)
ENSOARG00000011066	potassium voltage-gated channel subfamily Q member 5(KCNQ5)
ENSOARG00000002394	adhesion G protein-coupled receptor E2-like(LOC105605924)
ENSOARG00000013050	solute carrier family 9 member A2(SLC9A2)
ENSOARG00000010487	UBX domain protein 8(UBXN8)
ENSOARG00000019904	NADH:ubiquinone oxidoreductase subunit B4(NDUFB4)
ENSOARG00000014795	GLI pathogenesis related 1(GLIPR1)
ENSOARG00000007690	sphingosine-1-phosphate receptor 3(S1PR3)
ENSOARG00000013704	transmembrane protein 258(TMEM258)
ENSOARG00000009632	solute carrier family 5 member 2(SLC5A2)
ENSOARG00000017470	natural resistance-associated macrophage protein 2-like(LOC101116391)
ENSOARG00000020086	solute carrier family 15 member 2(SLC15A2)
ENSOARG00000005726	solute carrier family 25 member 11(SLC25A11)
ENSOARG00000019141	prolactin regulatory element binding(PREB)
ENSOARG00000013629	solute carrier family 39 member 3(SLC39A3)
ENSOARG00000020209	chondroitin polymerizing factor(CHPF)
ENSOARG00000002706	ectonucleoside triphosphate diphosphohydrolase 3(ENTPD3)
ENSOARG00000014346	3-hydroxyacyl-CoA dehydratase 4(HACD4)
ENSOARG00000012746	immunoglobulin superfamily member 1(IGSF1)
ENSOARG00000000582	solute carrier family 25 member 53(SLC25A53)
ENSOARG00000010919	syntaxin 17(STX17)
ENSOARG00000009542	dephospho-CoA kinase domain containing(DCAKD)
ENSOARG00000010220	zinc finger DHHC-type containing 16(ZDHHC16)
ENSOARG00000010530	transmembrane protein 200C(TMEM200C)
ENSOARG00000015284	purinergic receptor P2Y12(P2RY12)
ENSOARG00000006580	major facilitator superfamily domain containing 11(MFSD11)
ENSOARG00000005426	bladder cancer associated protein(BLCAP)
ENSOARG00000006532	potassium two pore domain channel subfamily K member 4(KCNK4)
ENSOARG00000014004	protocadherin beta-15(LOC101103720)
ENSOARG00000008809	cell adhesion molecule 4(CADM4)
ENSOARG00000018240	lactase like(LCTL)
ENSOARG00000012868	nicalin(NCLN)
ENSOARG00000017618	syntaxin 5(STX5)
ENSOARG00000015603	major facilitator superfamily domain containing 8(MFSD8)
ENSOARG00000006542	family with sequence similarity 159 member B(FAM159B)
ENSOARG00000019869	lipase maturation factor 2(LMF2)
ENSOARG00000019989	gap junction protein delta 2(GJD2)

ENSOARG00000001483	leucine zipper and EF-hand containing transmembrane protein 2(LETM2)
ENSOARG00000009115	G protein-coupled receptor 173(GPR173)
ENSOARG00000000862	myeloid associated differentiation marker(MYADM)
ENSOARG00000011943	solute carrier family 9 member C2 (putative)(SLC9C2)
ENSOARG00000004195	solute carrier family 16 member 9(SLC16A9)
ENSOARG00000019354	solute carrier family 7 member 8(SLC7A8)
ENSOARG00000000381	RFT1 homolog(RFT1)
ENSOARG00000015609	transmembrane protein with metallophosphoesterase domain(TMPPE)
ENSOARG00000008293	Rab acceptor 1(RABAC1)
ENSOARG00000010382	thrombospondin type 1 domain containing 7B(THSD7B)
ENSOARG00000008739	discoidin, CUB and LCCL domain containing 1(DCBLD1)
ENSOARG00000020808	epithelial membrane protein 1(EMP1)
ENSOARG00000013231	ring finger protein 149(RNF149)
ENSOARG00000011723	arylacetamide deacetylase like 3(AADACL3)
ENSOARG00000015971	immunoglobulin superfamily member 6(IGSF6)
ENSOARG00000004887	tweety family member 3(TTYH3)
ENSOARG00000015199	purinergic receptor P2Y1(P2RY1)
ENSOARG00000004044	UBA domain containing 2(UBAC2)
ENSOARG00000012006	leucine rich repeat containing 3(LRRC3)
ENSOARG00000012879	ssemaphorin 4F(SEMA4F)
ENSOARG00000006744	protein O-mannosyltransferase 1(POMT1)
ENSOARG00000007030	EvC ciliary complex subunit 2(EVC2)
ENSOARG00000004354	lectin, mannose binding 2(LMAN2)
ENSOARG00000015708	chondrolectin(CHODL)
ENSOARG00000010679	solute carrier family 25 member 19(SLC25A19)
ENSOARG00000002037	claudin 10(CLDN10)
ENSOARG00000020171	solute carrier family 22 member 15(SLC22A15)
ENSOARG00000005827	glycosylated lysosomal membrane protein(GLMP)
ENSOARG00000009877	solute carrier family 16 member 10(SLC16A10)
ENSOARG00000005552	serine peptidase inhibitor, Kunitz type 2(SPINT2)
ENSOARG00000016983	tripartite motif-containing protein 59(LOC101108249)
ENSOARG00000009563	steroid sulfatase (microsomal), isozyme S(STS)
ENSOARG00000013246	interleukin 10 receptor subunit beta(IL10RB)
ENSOARG00000001030	ATP binding cassette subfamily D member 4(ABCD4)
ENSOARG00000002972	zinc finger DHHC-type containing 1(ZDHHC1)
ENSOARG00000019527	transmembrane BAX inhibitor motif containing 1(TMBIM1)
ENSOARG00000011520	family with sequence similarity 57 member A(FAM57A)
ENSOARG00000015749	solute carrier family 12 member 9(SLC12A9)
ENSOARG00000017901	transmembrane protein 199(TMEM199)
ENSOARG00000001785	TM2 domain containing 2(TM2D2)
ENSOARG00000003076	NADH:ubiquinone oxidoreductase subunit A3(NDUFA3)

ENSOARG00000003891	peptidyl-tRNA hydrolase 2(PTRH2)
ENSOARG00000015804	transmembrane protein 132A(TMEM132A)
ENSOARG00000007541	granulocyte-macrophage colony-stimulating factor receptor subunit alpha(LOC101115509)
ENSOARG00000015127	solute carrier family 22 member 5(SLC22A5)
ENSOARG00000013025	solute carrier family 43 member 2(SLC43A2)
ENSOARG00000010540	synaptic vesicle glycoprotein 2B(SV2B)
ENSOARG00000011270	zinc finger FYVE-type containing 27(ZFYVE27)
ENSOARG00000015068	solute carrier family 10 member 5(SLC10A5)
ENSOARG00000011997	cadherin related family member 4(CDHR4)
ENSOARG00000009347	dermatan sulfate epimerase(DSE)
ENSOARG00000011972	solute carrier family 9 member B1(SLC9B1)
ENSOARG00000011312	transmembrane protein 218(TMEM218)
ENSOARG00000020043	lymphoid restricted membrane protein(LRMP)
ENSOARG00000016619	2-oxoglutarate and iron dependent oxygenase domain containing 3(OGFOD3)
ENSOARG00000006201	protocadherin 20(PCDH20)
ENSOARG00000006607	phospholipase D family member 3(PLD3)
ENSOARG00000019689	MANSC domain containing 4(MANSC4)
ENSOARG00000005614	acid phosphatase 2, lysosomal(ACP2)
ENSOARG00000015899	ephrin B3(EFNB3)
ENSOARG00000003767	epoxide hydrolase 3(EPHX3)
ENSOARG00000012674	solute carrier family 39 member 12(SLC39A12)
ENSOARG00000012244	vesicle transport through interaction with t-SNAREs 1A(VTI1A)
ENSOARG00000004709	phospholemman(LOC101115476)
ENSOARG00000016952	endonuclease domain containing 1(ENDOD1)
ENSOARG00000010861	tachykinin receptor 3(TACR3)
ENSOARG00000013827	solute carrier family 52 member 2(SLC52A2)
ENSOARG00000012653	solute carrier family 19 member 1(SLC19A1)
ENSOARG00000007620	solute carrier family 25 member 30(SLC25A30)
ENSOARG00000016225	sideroflexin 3(SFXN3)
ENSOARG00000012066	semaphorin 4B(SEMA4B)
ENSOARG00000007400	extended synaptotagmin 3(ESYT3)
ENSOARG00000016716	mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase(MGAT1)
ENSOARG00000000817	calcyon neuron specific vesicular protein(CALY)
ENSOARG00000008108	zinc activated ion channel(ZACN)
ENSOARG00000014558	leucine rich repeat containing G protein-coupled receptor 5(LGR5)
ENSOARG00000015038	short chain dehydrogenase/reductase family 16C, member 5(SDR16C5)
ENSOARG00000004096	BCL2 interacting protein 1(BNIP1)
ENSOARG00000011492	solute carrier family 35 member A2(SLC35A2)
ENSOARG00000010201	zinc finger DHHC-type containing 5(ZDHHC5)

ENSOARG00000016485	peripheral myelin protein 22(PMP22)
ENSOARG00000010312	tetraspanin 14(TSPAN14)
ENSOARG00000004200	hyperpolarization activated cyclic nucleotide gated potassium channel 3(HCN3)
ENSOARG00000007965	glutathione peroxidase 8 (putative)(GPX8)
ENSOARG00000003256	lecithin-cholesterol acyltransferase(LCAT)
ENSOARG00000014994	transmembrane p24 trafficking protein 3(TMED3)
ENSOARG00000005912	transmembrane emp24 domain-containing protein 9(LOC101102809)
ENSOARG00000009905	membrane bound O-acyltransferase domain containing 1(MBOAT1)
ENSOARG00000003460	small integral membrane protein 19(SMIM19)
ENSOARG00000001515	transmembrane protein 150B(TMEM150B)
ENSOARG00000015921	uncharacterized protein C20orf24 homolog(LOC101121958)

Gene Group 37	**Enrichment Score: 0.01490801389194373**
ENSEMBL_GENE_ID	**Gene Name**
ENSOARG00000000135	PBX homeobox 2(PBX2)
ENSOARG00000019296	zinc finger homeobox 2(ZFHX2)
ENSOARG00000019342	homeobox and leucine zipper encoding(HOMEZ)
ENSOARG00000019598	developing brain homeobox 2(DBX2)

Supplementary Table 3. DAVID Functional annotation output. Functional annotation output of DAVID database for the query including genes with an unadjusted p < 0.05 after the edgeRun analysis. Gene Ontology category (Category), Term, number of genes per category (Count), percentage of total genes in category (%), calculated Fisher exact p value for category (PValue), list of gene IDs in category (Genes), total genes included in analysis (List total), number of genes annotated to given category on background list (Pop Hits), number of genes on the background list mapped to any gene set in this ontology (Pop Total), ratio of proportions between genes in list on category and genes in background on the same category (Fold Enrichment), Bonferroni statistic (Bonferroni), Benjamini-Hochberg statistic (Benjamini) and False Discovery Rate (FDR) are presented.

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_DIRECT	GO:0001666~response to hypoxia	14	0.983	8.9E-04	ENSOARG00000008473, ENSOARG00000011040, ENSOARG00000017960, ENSOARG00000018035, ENSOARG00000013853, ENSOARG00000004233, ENSOARG00000001337, ENSOARG00000008169, ENSOARG00000011195, ENSOARG00000008561, ENSOARG00000005806, ENSOARG00000018276, ENSOARG00000010462, ENSOARG00000002050	901	58	10659	2.856	0.891	0.891	1.562
GOTERM_BP_DIRECT	GO:0032060~bleb assembly	5	0.351	4.5E-03	ENSOARG00000020808, ENSOARG00000016485, ENSOARG00000005780, ENSOARG00000006760, ENSOARG00000019578	901	9	10659	6.572	1.000	0.996	7.649
GOTERM_BP_DIRECT	GO:0035469~determination of pancreatic left/right asymmetry	4	0.281	5.3E-03	ENSOARG00000002415, ENSOARG00000010774, ENSOARG00000008813, ENSOARG00000020678	901	5	10659	9.464	1.000	0.987	8.893
GOTERM_BP_DIRECT	GO:0071910~determination of liver left/right asymmetry	4	0.281	9.9E-03	ENSOARG00000002415, ENSOARG00000010774, ENSOARG00000008813, ENSOARG00000020678	901	6	10659	7.887	1.000	0.998	16.057
GOTERM_BP_DIRECT	GO:0006412~translation	27	1.896	1.0E-02	ENSOARG00000019935, ENSOARG00000020159, ENSOARG00000014457, ENSOARG00000000077, ENSOARG00000016333, ENSOARG00000008365, ENSOARG00000019921, ENSOARG00000016959, ENSOARG00000014242, ENSOARG00000005178, ENSOARG00000004651, ENSOARG00000011605, ENSOARG00000005388, ENSOARG00000013810, ENSOARG00000004877, ENSOARG00000008429,	901	191	10659	1.672	1.000	0.994	16.442

					ENSOARG00000012647, ENSOARG00000002624, ENSOARG00000012645, ENSOARG00000009101, ENSOARG00000013191, ENSOARG00000008279, ENSOARG00000000332, ENSOARG00000010977, ENSOARG00000013126, ENSOARG00000006456, ENSOARG00000007328							
GOTERM_BP_DIRECT	GO:0006635~fatty acid beta-oxidation	7	0.492	1.0E-02	ENSOARG00000020994, ENSOARG00000014026, ENSOARG00000004154, ENSOARG00000014583, ENSOARG00000010508, ENSOARG00000000978, ENSOARG00000011785	901	23	10659	3.600	1.000	0.986	16.691
GOTERM_BP_DIRECT	GO:0031589~cell-substrate adhesion	5	0.351	1.4E-02	ENSOARG00000008094, ENSOARG00000016181, ENSOARG00000010280, ENSOARG00000015100, ENSOARG00000011785	901	12	10659	4.929	1.000	0.994	22.581
GOTERM_BP_DIRECT	GO:0035234~ectopic germ cell programmed cell death	4	0.281	1.6E-02	ENSOARG00000000078, ENSOARG00000020877, ENSOARG00000015592, ENSOARG00000012444	901	7	10659	6.760	1.000	0.994	25.034
GOTERM_BP_DIRECT	GO:0045600~positive regulation of fat cell differentiation	8	0.562	2.1E-02	ENSOARG00000016195, ENSOARG00000003080, ENSOARG00000015505, ENSOARG00000006068, ENSOARG00000013030, ENSOARG00000001680, ENSOARG00000015354, ENSOARG00000003121	901	34	10659	2.784	1.000	0.997	31.673
GOTERM_BP_DIRECT	GO:0000038~very long-chain fatty acid metabolic process	4	0.281	2.4E-02	ENSOARG00000004154, ENSOARG00000014583, ENSOARG00000000978, ENSOARG00000000664	901	8	10659	5.915	1.000	0.998	35.224
GOTERM_BP_DIRECT	GO:0050731~positive regulation of peptidyl-tyrosine phosphorylation	10	0.702	2.5E-02	ENSOARG00000017490, ENSOARG00000009485, ENSOARG00000015592, ENSOARG00000016181, ENSOARG00000006813, ENSOARG00000016727, ENSOARG00000011242, ENSOARG00000007229, ENSOARG00000004702, ENSOARG00000015100	901	51	10659	2.320	1.000	0.997	36.496
GOTERM_BP_DIRECT	GO:0001822~kidney development	9	0.632	2.6E-02	ENSOARG00000005787, ENSOARG00000006678, ENSOARG00000014898, ENSOARG00000018014, ENSOARG00000012444, ENSOARG00000003370, ENSOARG00000005087, ENSOARG00000013928, ENSOARG00000004702	901	43	10659	2.476	1.000	0.995	36.666
GOTERM_BP_DIRECT	GO:0005975~carbohydrate metabolic process	15	1.053	2.6E-02	ENSOARG00000012289, ENSOARG00000007168, ENSOARG00000018845, ENSOARG00000018240, ENSOARG00000016564, ENSOARG00000016351,	901	94	10659	1.888	1.000	0.993	36.804

					ENSOARG00000009408, ENSOARG00000009747, ENSOARG00000019976, ENSOARG00000020686, ENSOARG00000001193, ENSOARG00000001636, ENSOARG00000001722, ENSOARG00000003058, ENSOARG00000006000							
GOTERM_BP_DIRECT	GO:0042593~glucose homeostasis	12	0.843	3.8E-02	ENSOARG00000018166, ENSOARG00000010598, ENSOARG00000005787, ENSOARG00000016191, ENSOARG00000002386, ENSOARG00000010704, ENSOARG00000012807, ENSOARG00000020686, ENSOARG00000017643, ENSOARG00000003498, ENSOARG00000003501, ENSOARG00000011242	901	72	10659	1.972	1.000	0.999	49.599
GOTERM_BP_DIRECT	GO:0031572~G2 DNA damage checkpoint	5	0.351	4.0E-02	ENSOARG00000017343, ENSOARG00000003387, ENSOARG00000006187, ENSOARG00000010843, ENSOARG00000008440	901	16	10659	3.697	1.000	0.999	51.712
GOTERM_BP_DIRECT	GO:0007596~blood coagulation	7	0.492	4.2E-02	ENSOARG00000018398, ENSOARG00000016534, ENSOARG00000012503, ENSOARG00000013246, ENSOARG00000017328, ENSOARG00000020908, ENSOARG00000019578	901	31	10659	2.671	1.000	0.999	53.337
GOTERM_BP_DIRECT	GO:0090090~negative regulation of canonical Wnt signaling pathway	12	0.843	4.5E-02	ENSOARG00000011631, ENSOARG00000003080, ENSOARG00000016509, ENSOARG00000008418, ENSOARG00000012184, ENSOARG00000008813, ENSOARG00000001337, ENSOARG00000013051, ENSOARG00000008899, ENSOARG00000004702, ENSOARG00000013030, ENSOARG00000001680	901	74	10659	1.918	1.000	0.999	55.839
GOTERM_BP_DIRECT	GO:0030574~collagen catabolic process	4	0.281	4.6E-02	ENSOARG00000020869, ENSOARG00000018035, ENSOARG00000020861, ENSOARG00000019414	901	10	10659	4.732	1.000	0.998	56.336
GOTERM_BP_DIRECT	GO:0030324~lung development	9	0.632	4.6E-02	ENSOARG00000001851, ENSOARG00000006678, ENSOARG00000002415, ENSOARG00000010774, ENSOARG00000012184, ENSOARG00000008813, ENSOARG00000000317, ENSOARG00000020678, ENSOARG00000019414	901	48	10659	2.218	1.000	0.998	56.420
GOTERM_BP_DIRECT	GO:0030317~sperm motility	8	0.562	5.4E-02	ENSOARG00000016545, ENSOARG00000002415, ENSOARG00000016638, ENSOARG00000005161, ENSOARG00000014572, ENSOARG00000020208,	901	41	10659	2.308	1.000	0.999	62.199

					ENSOARG00000015279, ENSOARG00000020678							
GOTERM_BP_DIRECT	GO:2000811~negative regulation of anoikis	4	0.281	5.9E-02	ENSOARG00000016181, ENSOARG00000001337, ENSOARG00000003501, ENSOARG00000013030	901	11	10659	4.302	1.000	0.999	65.948
GOTERM_BP_DIRECT	GO:0071907~determination of digestive tract left/right asymmetry	3	0.211	6.0E-02	ENSOARG00000002415, ENSOARG00000010774, ENSOARG00000020678	901	5	10659	7.098	1.000	0.999	66.381
GOTERM_BP_DIRECT	GO:0006012~galactose metabolic process	3	0.211	6.0E-02	ENSOARG00000009164, ENSOARG00000002297, ENSOARG00000008843	901	5	10659	7.098	1.000	0.999	66.381
GOTERM_BP_DIRECT	GO:0000712~resolution of meiotic recombination intermediates	3	0.211	6.0E-02	ENSOARG00000015926, ENSOARG00000005198, ENSOARG00000015812	901	5	10659	7.098	1.000	0.999	66.381
GOTERM_BP_DIRECT	GO:0006810~transport	11	0.772	7.4E-02	ENSOARG00000001862, ENSOARG00000005912, ENSOARG00000013782, ENSOARG00000008821, ENSOARG00000010786, ENSOARG00000014994, ENSOARG00000005726, ENSOARG00000016515, ENSOARG00000018276, ENSOARG00000000582, ENSOARG00000003447	901	71	10659	1.833	1.000	1.000	74.124
GOTERM_BP_DIRECT	GO:0030154~cell differentiation	8	0.562	8.1E-02	ENSOARG00000001851, ENSOARG00000001037, ENSOARG00000008435, ENSOARG00000013027, ENSOARG00000017704, ENSOARG00000004733, ENSOARG00000008527, ENSOARG00000011785	901	45	10659	2.103	1.000	1.000	77.563
GOTERM_BP_DIRECT	GO:0007018~microtubule-based movement	9	0.632	8.2E-02	ENSOARG00000015211, ENSOARG00000008083, ENSOARG00000016755, ENSOARG00000015055, ENSOARG00000008948, ENSOARG00000004780, ENSOARG00000005591, ENSOARG00000015491, ENSOARG00000002205	901	54	10659	1.972	1.000	1.000	77.805
GOTERM_BP_DIRECT	GO:0090263~positive regulation of canonical Wnt signaling pathway	9	0.632	8.2E-02	ENSOARG00000004051, ENSOARG00000009485, ENSOARG00000004871, ENSOARG00000014558, ENSOARG00000001337, ENSOARG00000012718, ENSOARG00000008899, ENSOARG00000001680, ENSOARG00000013457	901	54	10659	1.972	1.000	1.000	77.805
GOTERM_BP_DIRECT	GO:0008152~metabolic process	14	0.983	8.2E-02	ENSOARG00000015828, ENSOARG00000012968, ENSOARG00000011792, ENSOARG00000011723, ENSOARG00000004315, ENSOARG00000005906,	901	101	10659	1.640	1.000	1.000	77.992

					ENSOARG00000005493, ENSOARG00000000369, ENSOARG00000001349, ENSOARG00000007446, ENSOARG00000009563, ENSOARG00000000664, ENSOARG00000015186, ENSOARG00000017262							
GOTERM_BP_DIRECT	GO:0097192~extrinsic apoptotic signaling pathway in absence of ligand	5	0.351	8.3E-02	ENSOARG00000014866, ENSOARG00000020877, ENSOARG00000015592, ENSOARG00000012444, ENSOARG00000014630	901	20	10659	2.958	1.000	1.000	78.099
GOTERM_BP_DIRECT	GO:0043303~mast cell degranulation	3	0.211	8.5E-02	ENSOARG00000010939, ENSOARG00000000078, ENSOARG00000009594	901	6	10659	5.915	1.000	1.000	79.113
GOTERM_BP_DIRECT	GO:0007288~sperm axoneme assembly	3	0.211	8.5E-02	ENSOARG00000008637, ENSOARG00000009594, ENSOARG00000018388	901	6	10659	5.915	1.000	1.000	79.113
GOTERM_BP_DIRECT	GO:0051382~kinetochore assembly	3	0.211	8.5E-02	ENSOARG00000007744, ENSOARG00000003186, ENSOARG00000005198	901	6	10659	5.915	1.000	1.000	79.113
GOTERM_BP_DIRECT	GO:0001570~vasculogenesis	7	0.492	8.7E-02	ENSOARG00000003452, ENSOARG00000000304, ENSOARG00000010854, ENSOARG00000001337, ENSOARG00000000133, ENSOARG00000014174, ENSOARG00000001811	901	37	10659	2.238	1.000	1.000	80.076
GOTERM_BP_DIRECT	GO:0043393~regulation of protein binding	4	0.281	9.1E-02	ENSOARG00000017343, ENSOARG00000000758, ENSOARG00000006902, ENSOARG00000015100	901	13	10659	3.640	1.000	1.000	81.280
GOTERM_BP_DIRECT	GO:0042310~vasoconstriction	4	0.281	9.1E-02	ENSOARG00000005323, ENSOARG00000020689, ENSOARG00000001337, ENSOARG00000008169	901	13	10659	3.640	1.000	1.000	81.280
GOTERM_BP_DIRECT	GO:0045216~cell-cell junction organization	4	0.281	9.1E-02	ENSOARG00000018276, ENSOARG00000016024, ENSOARG00000014174, ENSOARG00000002050	901	13	10659	3.640	1.000	1.000	81.280
GOTERM_CC_DIRECT	GO:0005739~mitochondrion	97	6.812	1.3E-05	ENSOARG00000010163, ENSOARG00000012968, ENSOARG00000014787, ENSOARG00000001485, ENSOARG00000002386, ENSOARG00000017505, ENSOARG00000015948, ENSOARG00000010876, ENSOARG00000003341, ENSOARG00000013135, ENSOARG00000010679, ENSOARG00000019364, ENSOARG00000001093, ENSOARG00000009542, ENSOARG00000004154, ENSOARG00000014590, ENSOARG00000006295, ENSOARG00000008821, ENSOARG00000013254, ENSOARG00000020219, ENSOARG00000011242, ENSOARG00000010485,	1073	768	13162	1.549	0.006	0.006	0.018

					ENSOARG00000007382, ENSOARG00000006369, ENSOARG00000005388, ENSOARG00000007948, ENSOARG00000012475, ENSOARG00000003420, ENSOARG00000000770, ENSOARG00000013810, ENSOARG00000011243, ENSOARG00000018035, ENSOARG00000017754, ENSOARG00000012189, ENSOARG00000000369, ENSOARG00000010919, ENSOARG00000008429, ENSOARG00000006799, ENSOARG00000020862, ENSOARG00000014398, ENSOARG00000014655, ENSOARG00000015186, ENSOARG00000015848, ENSOARG00000020555, ENSOARG00000017996, ENSOARG00000016922, ENSOARG00000010974, ENSOARG00000003058, ENSOARG00000017527, ENSOARG00000012700, ENSOARG00000001685, ENSOARG00000015921, ENSOARG00000007321, ENSOARG00000011711, ENSOARG00000014942, ENSOARG00000006981, ENSOARG00000012657, ENSOARG00000010224, ENSOARG00000000077, ENSOARG00000001599, ENSOARG00000020994, ENSOARG00000016529, ENSOARG00000015571, ENSOARG00000005806, ENSOARG00000013370, ENSOARG00000018720, ENSOARG00000002649, ENSOARG00000014997, ENSOARG00000005087, ENSOARG00000005178, ENSOARG00000013701, ENSOARG00000004651, ENSOARG00000002711, ENSOARG00000016953, ENSOARG00000003838, ENSOARG00000014026, ENSOARG00000002344, ENSOARG00000004315, ENSOARG00000004562, ENSOARG00000003325, ENSOARG00000003891, ENSOARG00000012718, ENSOARG00000012647, ENSOARG00000015354, ENSOARG00000013316, ENSOARG00000001988, ENSOARG00000011026, ENSOARG00000002704, ENSOARG00000008923, ENSOARG00000009485, ENSOARG00000018014, ENSOARG00000020633,						

					ENSOARG00000018580, ENSOARG00000009296, ENSOARG00000010508, ENSOARG00000002087, ENSOARG00000002208							
GOTERM_CC_DIRECT	GO:0005578~proteinaceous extracellular matrix	18	1.264	1.6E-02	ENSOARG00000001851, ENSOARG00000007475, ENSOARG00000017313, ENSOARG00000012262, ENSOARG00000009766, ENSOARG00000004292, ENSOARG00000014898, ENSOARG00000006371, ENSOARG00000021190, ENSOARG00000015737, ENSOARG00000001113, ENSOARG00000010966, ENSOARG00000014133, ENSOARG00000012184, ENSOARG00000006826, ENSOARG00000011508, ENSOARG00000000317, ENSOARG00000010962	1073	119	13162	1.855	0.999	0.974	20.464
GOTERM_CC_DIRECT	GO:0005840~ribosome	17	1.194	2.6E-02	ENSOARG00000019935, ENSOARG00000011605, ENSOARG00000013810, ENSOARG00000004877, ENSOARG00000008429, ENSOARG00000002624, ENSOARG00000012647, ENSOARG00000018666, ENSOARG00000009101, ENSOARG00000000332, ENSOARG00000010977, ENSOARG00000016333, ENSOARG00000014242, ENSOARG00000005542, ENSOARG00000005178, ENSOARG00000004651, ENSOARG00000007328	1073	116	13162	1.798	1.000	0.980	30.918
GOTERM_CC_DIRECT	GO:0031410~cytoplasmic vesicle	12	0.843	2.8E-02	ENSOARG00000009747, ENSOARG00000013658, ENSOARG00000016181, ENSOARG00000014898, ENSOARG00000020866, ENSOARG00000004376, ENSOARG00000013861, ENSOARG00000005780, ENSOARG00000006981, ENSOARG00000000817, ENSOARG00000019692, ENSOARG00000019414	1073	71	13162	2.073	1.000	0.958	32.954
GOTERM_CC_DIRECT	GO:0005789~endoplasmic reticulum membrane	22	1.545	3.2E-02	ENSOARG00000006739, ENSOARG00000006744, ENSOARG00000019869, ENSOARG00000014927, ENSOARG00000010755, ENSOARG00000012444, ENSOARG00000001030, ENSOARG00000012503, ENSOARG00000010919, ENSOARG00000010283, ENSOARG00000008288, ENSOARG00000013793, ENSOARG00000010421, ENSOARG00000012761,	1073	168	13162	1.606	1.000	0.947	37.063

					ENSOARG00000015038, ENSOARG00000011856, ENSOARG00000014271, ENSOARG00000005912, ENSOARG00000014994, ENSOARG00000020545, ENSOARG00000002728, ENSOARG00000012868							
GOTERM_CC_DIRECT	GO:0070062~extracellular exosome	184	12.921	3.7E-02	ENSOARG00000008963, ENSOARG00000012968, ENSOARG00000014885, ENSOARG00000001854, ENSOARG00000015749, ENSOARG00000015804, ENSOARG00000020908, ENSOARG00000003288, ENSOARG00000004887, ENSOARG00000006059, ENSOARG00000008605, ENSOARG00000015752, ENSOARG00000001300, ENSOARG00000007437, ENSOARG00000020686, ENSOARG00000020093, ENSOARG00000006703, ENSOARG00000006606, ENSOARG00000004941, ENSOARG00000006607, ENSOARG00000011242, ENSOARG00000006441, ENSOARG00000006484, ENSOARG00000001037, ENSOARG00000007948, ENSOARG00000008809, ENSOARG00000011246, ENSOARG00000011245, ENSOARG00000007312, ENSOARG00000020866, ENSOARG00000019164, ENSOARG00000011243, ENSOARG00000018379, ENSOARG00000002624, ENSOARG00000010860, ENSOARG00000016619, ENSOARG00000020412, ENSOARG00000005138, ENSOARG00000000340, ENSOARG00000000341, ENSOARG00000008094, ENSOARG00000012778, ENSOARG00000014801, ENSOARG00000006479, ENSOARG00000019578, ENSOARG00000002175, ENSOARG00000016322, ENSOARG00000013947, ENSOARG00000019935, ENSOARG00000002965, ENSOARG00000012100, ENSOARG00000014866, ENSOARG00000017960, ENSOARG00000003644, ENSOARG00000013157, ENSOARG00000012692, ENSOARG00000003264, ENSOARG00000007229, ENSOARG00000015727, ENSOARG00000013943, ENSOARG00000012704, ENSOARG00000006981,	1073	1991	13162	1.134	1.000	0.943	41.767

					ENSOARG00000015724, ENSOARG00000013231, ENSOARG00000008365, ENSOARG00000009408, ENSOARG00000012184, ENSOARG00000001777, ENSOARG00000006826, ENSOARG00000001636, ENSOARG00000002074, ENSOARG00000001076, ENSOARG00000011260, ENSOARG00000015100, ENSOARG00000016952, ENSOARG00000005275, ENSOARG00000006187, ENSOARG00000015393, ENSOARG00000002972, ENSOARG00000015108, ENSOARG00000009301, ENSOARG00000005906, ENSOARG00000012998, ENSOARG00000009405, ENSOARG00000009196, ENSOARG00000008078, ENSOARG00000006455, ENSOARG00000012262, ENSOARG00000014787, ENSOARG00000017460, ENSOARG00000015224, ENSOARG00000010837, ENSOARG00000002091, ENSOARG00000006213, ENSOARG00000016545, ENSOARG00000016351, ENSOARG00000009600, ENSOARG00000005926, ENSOARG00000014590, ENSOARG00000005920, ENSOARG00000006295, ENSOARG00000015191, ENSOARG00000020386, ENSOARG00000013389, ENSOARG00000004470, ENSOARG00000011866, ENSOARG00000008164, ENSOARG00000007146, ENSOARG00000005614, ENSOARG00000012475, ENSOARG00000009260, ENSOARG00000008473, ENSOARG00000003256, ENSOARG00000020454, ENSOARG00000013281, ENSOARG00000019527, ENSOARG00000000369, ENSOARG00000011484, ENSOARG00000014444, ENSOARG00000001346, ENSOARG00000015127, ENSOARG00000013191, ENSOARG00000018629, ENSOARG00000007553, ENSOARG00000012147, ENSOARG00000000155, ENSOARG00000004578, ENSOARG00000011479, ENSOARG00000020197, ENSOARG00000007716, ENSOARG00000017996, ENSOARG00000003249,						

					ENSOARG00000019673, ENSOARG00000000271, ENSOARG00000019441, ENSOARG00000014097, ENSOARG00000013984, ENSOARG00000002356, ENSOARG00000012444, ENSOARG00000008988, ENSOARG00000016716, ENSOARG00000007174, ENSOARG00000018901, ENSOARG00000008940, ENSOARG00000011417, ENSOARG00000020821, ENSOARG00000020994, ENSOARG00000007511, ENSOARG00000015176, ENSOARG00000013782, ENSOARG00000004354, ENSOARG00000009812, ENSOARG00000006032, ENSOARG00000008998, ENSOARG00000002463, ENSOARG00000011841, ENSOARG00000017328, ENSOARG00000008843, ENSOARG00000007864, ENSOARG00000010462, ENSOARG00000005542, ENSOARG00000020820, ENSOARG00000003506, ENSOARG00000017490, ENSOARG00000007168, ENSOARG00000019145, ENSOARG00000012454, ENSOARG00000003370, ENSOARG00000018845, ENSOARG00000015870, ENSOARG00000019354, ENSOARG00000003676, ENSOARG00000006047, ENSOARG00000019557, ENSOARG00000009632, ENSOARG00000018014, ENSOARG00000005204, ENSOARG00000012461, ENSOARG00000010508, ENSOARG00000015161, ENSOARG00000006538, ENSOARG00000020830, ENSOARG00000011597, ENSOARG00000019904							
GOTERM_CC_DIRECT	GO:0005764~lysosome	14	0.983	3.8E-02	ENSOARG00000005614, ENSOARG00000018343, ENSOARG00000020866, ENSOARG00000020861, ENSOARG00000020908, ENSOARG00000007229, ENSOARG00000017479, ENSOARG00000007553, ENSOARG00000018629, ENSOARG00000009747, ENSOARG00000012184, ENSOARG00000001076, ENSOARG00000010462, ENSOARG00000005827	1073	93	13162	1.847	1.000	0.917	42.202
GOTERM_CC_DIRECT	GO:0009986~cell surface	32	2.247	4.2E-02	ENSOARG00000000271, ENSOARG00000003452,	1073	276	13162	1.422	1.000	0.910	45.490

					ENSOARG00000006358, ENSOARG00000004702, ENSOARG00000019958, ENSOARG00000016897, ENSOARG00000000304, ENSOARG00000015199, ENSOARG00000020821, ENSOARG00000004354, ENSOARG00000006032, ENSOARG00000014188, ENSOARG00000017328, ENSOARG00000008899, ENSOARG00000005176, ENSOARG00000010462, ENSOARG00000015876, ENSOARG00000006484, ENSOARG00000010962, ENSOARG00000016740, ENSOARG00000008473, ENSOARG00000007549, ENSOARG00000017704, ENSOARG00000005780, ENSOARG00000000155, ENSOARG00000012778, ENSOARG00000016534, ENSOARG00000006760, ENSOARG00000014253, ENSOARG00000015284, ENSOARG00000010312, ENSOARG00000019578							
GOTERM_CC_DIRECT	GO:0030425~dendrite	13	0.913	5.3E-02	ENSOARG00000016195, ENSOARG00000013027, ENSOARG00000010201, ENSOARG00000011270, ENSOARG00000003370, ENSOARG00000007585, ENSOARG00000002649, ENSOARG00000020908, ENSOARG00000015551, ENSOARG00000020862, ENSOARG00000014119, ENSOARG00000019102, ENSOARG00000007080	1073	88	13162	1.812	1.000	0.933	53.622
GOTERM_CC_DIRECT	GO:0031226~intrinsic component of plasma membrane	4	0.281	6.8E-02	ENSOARG00000018166, ENSOARG00000012807, ENSOARG00000006538, ENSOARG00000010691	1073	12	13162	4.089	1.000	0.958	63.194
GOTERM_CC_DIRECT	GO:0097342~ripoptosome	3	0.211	8.0E-02	ENSOARG00000016852, ENSOARG00000008707, ENSOARG00000016922	1073	6	13162	6.133	1.000	0.967	69.243
GOTERM_CC_DIRECT	GO:0005761~mitochondrial ribosome	4	0.281	8.3E-02	ENSOARG00000009697, ENSOARG00000008113, ENSOARG00000004590, ENSOARG00000014378	1073	13	13162	3.774	1.000	0.962	70.870
GOTERM_CC_DIRECT	GO:0016604~nuclear body	5	0.351	8.6E-02	ENSOARG00000008751, ENSOARG00000009315, ENSOARG00000002615, ENSOARG00000004516, ENSOARG00000007509	1073	21	13162	2.921	1.000	0.956	72.133
GOTERM_CC_DIRECT	GO:0016459~myosin complex	6	0.421	9.2E-02	ENSOARG00000011188, ENSOARG00000019316, ENSOARG00000013610, ENSOARG00000018916,	1073	30	13162	2.453	1.000	0.956	74.753

					ENSOARG00000018135, ENSOARG00000004207							
GOTERM_MF_DIRECT	GO:0008270~zinc ion binding	100	7.022	3.3E-04	ENSOARG00000008963, ENSOARG00000019797, ENSOARG00000007445, ENSOARG00000003769, ENSOARG00000009164, ENSOARG00000019605, ENSOARG00000008388, ENSOARG00000009028, ENSOARG00000010962, ENSOARG00000004292, ENSOARG00000002424, ENSOARG00000014354, ENSOARG00000014898, ENSOARG00000018035, ENSOARG00000013817, ENSOARG00000004233, ENSOARG00000015272, ENSOARG00000003391, ENSOARG00000019885, ENSOARG00000000341, ENSOARG00000020200, ENSOARG00000013152, ENSOARG00000005858, ENSOARG00000020816, ENSOARG00000017443, ENSOARG00000011785, ENSOARG00000019935, ENSOARG00000004647, ENSOARG00000006371, ENSOARG00000010220, ENSOARG00000008656, ENSOARG00000019296, ENSOARG00000013231, ENSOARG00000016195, ENSOARG00000013427, ENSOARG00000016959, ENSOARG00000004310, ENSOARG00000017433, ENSOARG00000015423, ENSOARG00000018257, ENSOARG00000007966, ENSOARG00000013027, ENSOARG00000002972, ENSOARG00000004516, ENSOARG00000014583, ENSOARG00000019414, ENSOARG00000010939, ENSOARG00000009726, ENSOARG00000007020, ENSOARG00000019106, ENSOARG00000005266, ENSOARG00000010021, ENSOARG00000018343, ENSOARG00000010405, ENSOARG00000004670, ENSOARG00000010201, ENSOARG00000016980, ENSOARG00000009888, ENSOARG00000014119, ENSOARG00000016983, ENSOARG00000014647, ENSOARG00000016549, ENSOARG00000018006, ENSOARG00000013928, ENSOARG00000015219, ENSOARG00000005613,	849	878	10488	1.407	0.177	0.177	0.481

					ENSOARG00000009260, ENSOARG00000014661, ENSOARG00000013507, ENSOARG00000004907, ENSOARG00000018629, ENSOARG00000000155, ENSOARG00000014655, ENSOARG00000008530, ENSOARG00000003516, ENSOARG00000018276, ENSOARG00000004063, ENSOARG00000014515, ENSOARG00000009766, ENSOARG00000007277, ENSOARG00000001529, ENSOARG00000000818, ENSOARG00000015178, ENSOARG00000012749, ENSOARG00000016001, ENSOARG00000011841, ENSOARG00000012745, ENSOARG00000001936, ENSOARG00000012948, ENSOARG00000007475, ENSOARG00000002344, ENSOARG00000000185, ENSOARG00000004562, ENSOARG00000003370, ENSOARG00000014133, ENSOARG00000018851, ENSOARG00000007674, ENSOARG00000009965, ENSOARG00000006142, ENSOARG00000016024							
GOTERM_MF_DIRECT	GO:0003735~structural constituent of ribosome	28	1.966	2.6E-03	ENSOARG00000019935, ENSOARG00000020159, ENSOARG00000014457, ENSOARG00000018666, ENSOARG00000000077, ENSOARG00000016333, ENSOARG00000008365, ENSOARG00000019921, ENSOARG00000014242, ENSOARG00000005542, ENSOARG00000005178, ENSOARG00000004651, ENSOARG00000011605, ENSOARG00000005388, ENSOARG00000013810, ENSOARG00000004877, ENSOARG00000008429, ENSOARG00000002624, ENSOARG00000012647, ENSOARG00000012645, ENSOARG00000009101, ENSOARG00000013191, ENSOARG00000008279, ENSOARG00000000332, ENSOARG00000010977, ENSOARG00000013126, ENSOARG00000006456, ENSOARG00000007328	849	189	10488	1.830	0.786	0.537	3.738
GOTERM_MF_DIRECT	GO:0050660~flavin adenine dinucleotide binding	10	0.702	2.2E-02	ENSOARG00000010163, ENSOARG00000012761, ENSOARG00000017277, ENSOARG00000010662, ENSOARG00000020219, ENSOARG00000003325,	849	52	10488	2.376	1.000	0.989	28.247

					ENSOARG00000002649, ENSOARG00000018469, ENSOARG00000008041, ENSOARG00000013647							
GOTERM_MF_DIRECT	GO:0005507~copper ion binding	8	0.562	2.7E-02	ENSOARG00000015571, ENSOARG00000014271, ENSOARG00000020414, ENSOARG00000018343, ENSOARG00000020877, ENSOARG00000012820, ENSOARG00000000317, ENSOARG00000003319	849	37	10488	2.671	1.000	0.982	32.922
GOTERM_MF_DIRECT	GO:0001227~transcriptional repressor activity, RNA polymerase II transcription regulatory region sequence-specific binding	8	0.562	3.5E-02	ENSOARG00000016191, ENSOARG00000015698, ENSOARG00000012718, ENSOARG00000003391, ENSOARG00000008527, ENSOARG00000012704, ENSOARG00000006704, ENSOARG00000011785	849	39	10488	2.534	1.000	0.985	40.616
GOTERM_MF_DIRECT	GO:0003995~acyl-CoA dehydrogenase activity	4	0.281	4.1E-02	ENSOARG00000010662, ENSOARG00000020219, ENSOARG00000002649, ENSOARG00000013647	849	10	10488	4.941	1.000	0.985	46.176
GOTERM_MF_DIRECT	GO:0003824~catalytic activity	12	0.843	4.8E-02	ENSOARG00000011792, ENSOARG00000015186, ENSOARG00000004315, ENSOARG00000005493, ENSOARG00000003767, ENSOARG00000000369, ENSOARG00000004941, ENSOARG00000006607, ENSOARG00000020862, ENSOARG00000001349, ENSOARG00000003861, ENSOARG00000000664	849	78	10488	1.901	1.000	0.985	51.838
GOTERM_MF_DIRECT	GO:0017017~MAP kinase tyrosine/serine/threonine phosphatase activity	4	0.281	5.3E-02	ENSOARG00000007360, ENSOARG00000020857, ENSOARG00000008498, ENSOARG00000013213	849	11	10488	4.492	1.000	0.983	55.377
GOTERM_MF_DIRECT	GO:0004879~RNA polymerase II transcription factor activity, ligand-activated sequence-specific DNA binding	5	0.351	7.3E-02	ENSOARG00000010939, ENSOARG00000005858, ENSOARG00000020816, ENSOARG00000005827, ENSOARG00000011785	849	20	10488	3.088	1.000	0.993	67.166
GOTERM_MF_DIRECT	GO:0038036~sphingosine-1-phosphate receptor activity	3	0.211	7.9E-02	ENSOARG00000007690, ENSOARG00000011960, ENSOARG00000010691	849	6	10488	6.177	1.000	0.993	70.179
INTERPRO	IPR001763:Rhodanese-like domain	7	0.492	4.2E-03	ENSOARG00000001274, ENSOARG00000007360, ENSOARG00000014079, ENSOARG00000020857, ENSOARG00000019145, ENSOARG00000011806, ENSOARG00000013213	1273	20	15550	4.275	1.000	1.000	6.965
INTERPRO	IPR017907:Zinc finger, RING-type, conserved site	19	1.334	9.4E-03	ENSOARG00000018257, ENSOARG00000010201, ENSOARG00000007445, ENSOARG00000014661,	1273	121	15550	1.918	1.000	1.000	14.964

					ENSOARG00000004516, ENSOARG00000004233, ENSOARG00000014583, ENSOARG00000003769, ENSOARG00000001529, ENSOARG00000016983, ENSOARG00000000818, ENSOARG00000015178, ENSOARG00000009726, ENSOARG00000013152, ENSOARG00000018006, ENSOARG00000012749, ENSOARG00000008530, ENSOARG00000007674, ENSOARG00000009028							
INTERPRO	IPR013273:Peptidase M12B, ADAM-TS	7	0.492	1.1E-02	ENSOARG00000007475, ENSOARG00000009766, ENSOARG00000004292, ENSOARG00000014133, ENSOARG00000014898, ENSOARG00000006371, ENSOARG00000010962	1273	24	15550	3.563	1.000	0.999	17.289
INTERPRO	IPR013786:Acyl-CoA dehydrogenase/oxidase, N-terminal	5	0.351	1.3E-02	ENSOARG00000010163, ENSOARG00000010662, ENSOARG00000020219, ENSOARG00000002649, ENSOARG00000013647	1273	12	15550	5.090	1.000	0.998	19.947
INTERPRO	IPR006089:Acyl-CoA dehydrogenase, conserved site	4	0.281	1.5E-02	ENSOARG00000010163, ENSOARG00000010662, ENSOARG00000020219, ENSOARG00000002649	1273	7	15550	6.980	1.000	0.997	22.589
INTERPRO	IPR009075:Acyl-CoA dehydrogenase/oxidase C-terminal	5	0.351	1.7E-02	ENSOARG00000010163, ENSOARG00000010662, ENSOARG00000020219, ENSOARG00000002649, ENSOARG00000013647	1273	13	15550	4.698	1.000	0.996	26.036
INTERPRO	IPR009100:Acyl-CoA dehydrogenase/oxidase	5	0.351	1.7E-02	ENSOARG00000010163, ENSOARG00000010662, ENSOARG00000020219, ENSOARG00000002649, ENSOARG00000013647	1273	13	15550	4.698	1.000	0.996	26.036
INTERPRO	IPR015395:C-myb, C-terminal	3	0.211	1.9E-02	ENSOARG00000003547, ENSOARG00000017663, ENSOARG00000014901	1273	3	15550	12.215	1.000	0.994	27.907
INTERPRO	IPR000195:Rab-GTPase-TBC domain	8	0.562	2.5E-02	ENSOARG00000000399, ENSOARG00000002248, ENSOARG00000013667, ENSOARG00000013658, ENSOARG00000018891, ENSOARG00000002768, ENSOARG00000002538, ENSOARG00000005979	1273	36	15550	2.714	1.000	0.997	34.708
INTERPRO	IPR001841:Zinc finger, RING-type	28	1.966	2.8E-02	ENSOARG00000004670, ENSOARG00000007445, ENSOARG00000007277, ENSOARG00000003769, ENSOARG00000001529, ENSOARG00000016983, ENSOARG00000000818, ENSOARG00000013231, ENSOARG00000016549, ENSOARG00000015178,	1273	225	15550	1.520	1.000	0.998	38.956

					ENSOARG00000018006, ENSOARG00000012749, ENSOARG00000012745, ENSOARG00000001936, ENSOARG00000009028, ENSOARG00000018257, ENSOARG00000015272, ENSOARG00000004233, ENSOARG00000014661, ENSOARG00000004516, ENSOARG00000014583, ENSOARG00000003391, ENSOARG00000009726, ENSOARG00000013152, ENSOARG00000008530, ENSOARG00000007674, ENSOARG00000019106, ENSOARG00000014515						
INTERPRO	IPR010909:PLAC	5	0.351	2.9E-02	ENSOARG00000007475, ENSOARG00000009766, ENSOARG00000004292, ENSOARG00000014133, ENSOARG00000006371	1273	15	15550	4.072	1.000	0.996	39.840
INTERPRO	IPR010294:ADAM-TS Spacer 1	6	0.421	3.0E-02	ENSOARG00000007475, ENSOARG00000009766, ENSOARG00000004292, ENSOARG00000014898, ENSOARG00000006371, ENSOARG00000010962	1273	22	15550	3.331	1.000	0.994	40.152
INTERPRO	IPR001609:Myosin head, motor domain	7	0.492	3.2E-02	ENSOARG00000011188, ENSOARG00000019316, ENSOARG00000012454, ENSOARG00000013610, ENSOARG00000018916, ENSOARG00000018135, ENSOARG00000004207	1273	30	15550	2.850	1.000	0.994	42.717
INTERPRO	IPR017853:Glycoside hydrolase, superfamily	9	0.632	3.9E-02	ENSOARG00000009747, ENSOARG00000019976, ENSOARG00000012289, ENSOARG00000001193, ENSOARG00000001636, ENSOARG00000018845, ENSOARG00000018240, ENSOARG00000016564, ENSOARG00000003058	1273	48	15550	2.290	1.000	0.997	49.666
INTERPRO	IPR000073:Alpha/beta hydrolase fold-1	6	0.421	4.2E-02	ENSOARG00000012475, ENSOARG00000006479, ENSOARG00000003767, ENSOARG00000019436, ENSOARG00000017717, ENSOARG00000019121	1273	24	15550	3.054	1.000	0.997	51.743
INTERPRO	IPR020845:AMP-binding, conserved site	6	0.421	4.2E-02	ENSOARG00000020994, ENSOARG00000010421, ENSOARG00000011792, ENSOARG00000015186, ENSOARG00000004315, ENSOARG00000000664	1273	24	15550	3.054	1.000	0.997	51.743
INTERPRO	IPR006091:Acyl-CoA oxidase/dehydrogenase, central domain	4	0.281	4.2E-02	ENSOARG00000010163, ENSOARG00000010662, ENSOARG00000020219, ENSOARG00000002649	1273	10	15550	4.886	1.000	0.996	52.279
INTERPRO	IPR008916:Retrovirus capsid, C-	6	0.421	4.9E-02	ENSOARG00000003392, ENSOARG00000000770,	1273	25	15550	2.932	1.000	0.997	57.462

	terminal				ENSOARG00000005354, ENSOARG00000007509, ENSOARG00000013148, ENSOARG00000018515							
INTERPRO	IPR000884:Thrombospondin, type 1 repeat	10	0.702	4.9E-02	ENSOARG00000007475, ENSOARG00000009766, ENSOARG00000004292, ENSOARG00000014133, ENSOARG00000020173, ENSOARG00000006382, ENSOARG00000014898, ENSOARG00000006371, ENSOARG00000010382, ENSOARG00000010962	1273	59	15550	2.070	1.000	0.996	57.757
INTERPRO	IPR000421:Coagulation factor 5/8 C-terminal type domain	5	0.351	5.4E-02	ENSOARG00000011260, ENSOARG00000008739, ENSOARG00000003319, ENSOARG00000015724, ENSOARG00000007080	1273	18	15550	3.393	1.000	0.997	61.318
INTERPRO	IPR001134:Netrin domain	5	0.351	5.4E-02	ENSOARG00000005926, ENSOARG00000013157, ENSOARG00000003264, ENSOARG00000008899, ENSOARG00000001680	1273	18	15550	3.393	1.000	0.997	61.318
INTERPRO	IPR003309:Transcription regulator SCAN	6	0.421	5.6E-02	ENSOARG00000003392, ENSOARG00000000770, ENSOARG00000005354, ENSOARG00000007509, ENSOARG00000013148, ENSOARG00000018515	1273	26	15550	2.819	1.000	0.997	62.982
INTERPRO	IPR002657:Bile acid:sodium symporter	3	0.211	5.7E-02	ENSOARG00000004313, ENSOARG00000017345, ENSOARG00000015068	1273	5	15550	7.329	1.000	0.996	63.046
INTERPRO	IPR009069:Cysteine alpha-hairpin motif superfamily	3	0.211	5.7E-02	ENSOARG00000005172, ENSOARG00000008113, ENSOARG00000014997	1273	5	15550	7.329	1.000	0.996	63.046
INTERPRO	IPR004032:PMP-22/EMP/MP20	3	0.211	5.7E-02	ENSOARG00000020808, ENSOARG00000016485, ENSOARG00000005780	1273	5	15550	7.329	1.000	0.996	63.046
INTERPRO	IPR016243:Tyrosine-protein kinase, CSF-1/PDGF receptor	3	0.211	5.7E-02	ENSOARG00000000078, ENSOARG00000006358, ENSOARG00000006538	1273	5	15550	7.329	1.000	0.996	63.046
INTERPRO	IPR019803:Glypican, conserved site	3	0.211	5.7E-02	ENSOARG00000017313, ENSOARG00000012262, ENSOARG00000012184	1273	5	15550	7.329	1.000	0.996	63.046
INTERPRO	IPR001863:Glypican	3	0.211	5.7E-02	ENSOARG00000017313, ENSOARG00000012262, ENSOARG00000012184	1273	5	15550	7.329	1.000	0.996	63.046
INTERPRO	IPR024079:Metallopeptidase, catalytic domain	12	0.843	6.0E-02	ENSOARG00000007475, ENSOARG00000009766, ENSOARG00000004292, ENSOARG00000010405, ENSOARG00000014898, ENSOARG00000006371, ENSOARG00000008974, ENSOARG00000018035, ENSOARG00000003370, ENSOARG00000013928, ENSOARG00000019414, ENSOARG00000010962	1273	80	15550	1.832	1.000	0.996	65.569

INTERPRO	IPR008993:Tissue inhibitor of metalloproteinases-like, OB-fold	5	0.351	6.4E-02	ENSOARG00000005926, ENSOARG00000013157, ENSOARG00000003264, ENSOARG00000008899, ENSOARG00000001680	1273	19	15550	3.215	1.000	0.997	67.828
INTERPRO	IPR015880:Zinc finger, C2H2-like	41	2.879	6.5E-02	ENSOARG00000003623, ENSOARG00000019302, ENSOARG00000010774, ENSOARG00000004647, ENSOARG00000010779, ENSOARG00000002789, ENSOARG00000007509, ENSOARG00000018972, ENSOARG00000019279, ENSOARG00000019296, ENSOARG00000016195, ENSOARG00000003358, ENSOARG00000004353, ENSOARG00000008978, ENSOARG00000003219, ENSOARG00000002874, ENSOARG00000004095, ENSOARG00000015505, ENSOARG00000004631, ENSOARG00000014166, ENSOARG00000010468, ENSOARG00000015473, ENSOARG00000005257, ENSOARG00000020268, ENSOARG00000014918, ENSOARG00000003392, ENSOARG00000014354, ENSOARG00000011585, ENSOARG00000000770, ENSOARG00000000185, ENSOARG00000009044, ENSOARG00000013148, ENSOARG00000003678, ENSOARG00000008496, ENSOARG00000001296, ENSOARG00000007890, ENSOARG00000005434, ENSOARG00000003724, ENSOARG00000010061, ENSOARG00000011959, ENSOARG00000013030	1273	383	15550	1.308	1.000	0.996	68.438
INTERPRO	IPR004172:L27	4	0.281	6.9E-02	ENSOARG00000008998, ENSOARG00000013861, ENSOARG00000006328, ENSOARG00000015442	1273	12	15550	4.072	1.000	0.996	70.398
INTERPRO	IPR000873:AMP-dependent synthetase/ligase	6	0.421	7.4E-02	ENSOARG00000020994, ENSOARG00000010421, ENSOARG00000011792, ENSOARG00000015186, ENSOARG00000004315, ENSOARG00000000664	1273	28	15550	2.618	1.000	0.997	73.057
INTERPRO	IPR001881:EGF-like calcium-binding	14	0.983	7.7E-02	ENSOARG00000017490, ENSOARG00000010405, ENSOARG00000018379, ENSOARG00000018923, ENSOARG00000017704, ENSOARG00000003894, ENSOARG00000004702, ENSOARG00000015724, ENSOARG00000018398, ENSOARG00000011479,	1273	103	15550	1.660	1.000	0.997	74.520

					ENSOARG00000010523, ENSOARG00000006826, ENSOARG00000012461, ENSOARG00000011304							
INTERPRO	IPR008979:Galactose-binding domain-like	11	0.772	7.8E-02	ENSOARG00000000874, ENSOARG00000019976, ENSOARG00000012289, ENSOARG00000008094, ENSOARG00000012778, ENSOARG00000011260, ENSOARG00000008739, ENSOARG00000003319, ENSOARG00000015724, ENSOARG00000007080, ENSOARG00000016740	1273	74	15550	1.816	1.000	0.997	75.155
INTERPRO	IPR020821:Extracellular Endonuclease, subunit A	3	0.211	8.0E-02	ENSOARG00000001455, ENSOARG00000014188, ENSOARG00000016952	1273	6	15550	6.108	1.000	0.997	76.108
INTERPRO	IPR011047:Quinonprotein alcohol dehydrogenase-like superfamily	6	0.421	9.4E-02	ENSOARG00000003114, ENSOARG00000010123, ENSOARG00000005231, ENSOARG00000019141, ENSOARG00000011672, ENSOARG00000014398	1273	30	15550	2.443	1.000	0.998	81.430
INTERPRO	IPR013785:Aldolase-type TIM barrel	7	0.492	9.5E-02	ENSOARG00000009747, ENSOARG00000007511, ENSOARG00000017277, ENSOARG00000001193, ENSOARG00000000480, ENSOARG00000018845, ENSOARG00000003325	1273	39	15550	2.192	1.000	0.998	81.886
KEGG_PATHWAY	oas03010:Ribosome	28	1.966	2.0E-03	ENSOARG00000019935, ENSOARG00000020159, ENSOARG00000014457, ENSOARG00000018666, ENSOARG00000020259, ENSOARG00000000077, ENSOARG00000016333, ENSOARG00000008365, ENSOARG00000019921, ENSOARG00000014242, ENSOARG00000005542, ENSOARG00000005178, ENSOARG00000004651, ENSOARG00000011605, ENSOARG00000005388, ENSOARG00000013810, ENSOARG00000004877, ENSOARG00000008429, ENSOARG00000002624, ENSOARG00000012645, ENSOARG00000009101, ENSOARG00000013191, ENSOARG00000008279, ENSOARG00000000332, ENSOARG00000010977, ENSOARG00000013126, ENSOARG00000006456, ENSOARG00000007328	520	224	7762	1.866	0.422	0.422	2.567
KEGG_PATHWAY	oas05221:Acute myeloid leukemia	11	0.772	3.6E-03	ENSOARG00000000078, ENSOARG00000014364, ENSOARG00000013254, ENSOARG00000018964, ENSOARG00000011481, ENSOARG00000004785,	520	56	7762	2.932	0.631	0.393	4.616

					ENSOARG00000004233, ENSOARG00000012718, ENSOARG00000014119, ENSOARG00000007664, ENSOARG00000011785								
KEGG_PATHWAY	oas04932:Non-alcoholic fatty liver disease (NAFLD)	21	1.475	3.6E-03	ENSOARG00000007018, ENSOARG00000018166, ENSOARG00000014866, ENSOARG00000012807, ENSOARG00000020877, ENSOARG00000012444, ENSOARG00000020866, ENSOARG00000003076, ENSOARG00000012718, ENSOARG00000011192, ENSOARG00000014398, ENSOARG00000020197, ENSOARG00000005858, ENSOARG00000001078, ENSOARG00000007095, ENSOARG00000004785, ENSOARG00000013670, ENSOARG00000016922, ENSOARG00000007664, ENSOARG00000019904, ENSOARG00000012001	520	156	7762	2.009	0.634	0.285	4.653
KEGG_PATHWAY	oas04142:Lysosome	18	1.264	4.2E-03	ENSOARG00000019274, ENSOARG00000007293, ENSOARG00000005614, ENSOARG00000019928, ENSOARG00000012289, ENSOARG00000017470, ENSOARG00000015603, ENSOARG00000018845, ENSOARG00000020861, ENSOARG00000006664, ENSOARG00000000665, ENSOARG00000003375, ENSOARG00000018629, ENSOARG00000011951, ENSOARG00000020657, ENSOARG00000017007, ENSOARG00000001076, ENSOARG00000003058	520	126	7762	2.132	0.687	0.252	5.356
KEGG_PATHWAY	oas01100:Metabolic pathways	107	7.514	1.1E-02	ENSOARG00000007935, ENSOARG00000003076, ENSOARG00000015948, ENSOARG00000003288, ENSOARG00000009164, ENSOARG00000010252, ENSOARG00000001300, ENSOARG00000020686, ENSOARG00000001193, ENSOARG00000020219, ENSOARG00000006607, ENSOARG00000007382, ENSOARG00000011792, ENSOARG00000012837, ENSOARG00000011246, ENSOARG00000006429, ENSOARG00000011243, ENSOARG00000010662, ENSOARG00000010864, ENSOARG00000017754, ENSOARG00000012189, ENSOARG00000013817,	520	1292	7762	1.236	0.956	0.464	13.738

					ENSOARG00000016278, ENSOARG00000006799, ENSOARG00000020862, ENSOARG00000010860, ENSOARG00000020412, ENSOARG00000005138, ENSOARG00000009747, ENSOARG00000018469, ENSOARG00000020209, ENSOARG00000011045, ENSOARG00000016081, ENSOARG00000013947, ENSOARG00000005654, ENSOARG00000004304, ENSOARG00000014942, ENSOARG00000012692, ENSOARG00000009905, ENSOARG00000000718, ENSOARG00000013943, ENSOARG00000018069, ENSOARG00000010224, ENSOARG00000001636, ENSOARG00000014188, ENSOARG00000013023, ENSOARG00000013647, ENSOARG00000005645, ENSOARG00000005906, ENSOARG00000018580, ENSOARG00000005266, ENSOARG00000006000, ENSOARG00000007018, ENSOARG00000010163, ENSOARG00000005493, ENSOARG00000000665, ENSOARG00000000664, ENSOARG00000016984, ENSOARG00000014018, ENSOARG00000016351, ENSOARG00000001093, ENSOARG00000009600, ENSOARG00000011960, ENSOARG00000000480, ENSOARG00000007095, ENSOARG00000015794, ENSOARG00000000978, ENSOARG00000004470, ENSOARG00000010485, ENSOARG00000009594, ENSOARG00000000369, ENSOARG00000005483, ENSOARG00000011484, ENSOARG00000011543, ENSOARG00000007357, ENSOARG00000006947, ENSOARG00000018629, ENSOARG00000020197, ENSOARG00000015186, ENSOARG00000007716, ENSOARG00000001722, ENSOARG00000013670, ENSOARG00000018733, ENSOARG00000003058, ENSOARG00000016716, ENSOARG00000008988, ENSOARG00000008735, ENSOARG00000005002, ENSOARG00000007511, ENSOARG00000016529, ENSOARG00000005172, ENSOARG00000002033,						

					ENSOARG00000011841, ENSOARG00000008843, ENSOARG00000003506, ENSOARG00000006739, ENSOARG00000007168, ENSOARG00000019145, ENSOARG00000002344, ENSOARG00000015870, ENSOARG00000006686, ENSOARG00000018014, ENSOARG00000005098, ENSOARG00000009347, ENSOARG00000003986, ENSOARG00000007403, ENSOARG00000019904							
KEGG_PATHWAY	oas05030:Cocaine addiction	9	0.632	1.3E-02	ENSOARG00000011552, ENSOARG00000003188, ENSOARG00000015372, ENSOARG00000002633, ENSOARG00000007354, ENSOARG00000012718, ENSOARG00000010722, ENSOARG00000003288, ENSOARG00000015118	520	48	7762	2.799	0.976	0.464	16.223
KEGG_PATHWAY	oas05200:Pathways in cancer	39	2.739	1.4E-02	ENSOARG00000001851, ENSOARG00000006358, ENSOARG00000014866, ENSOARG00000017460, ENSOARG00000018187, ENSOARG00000012444, ENSOARG00000008988, ENSOARG00000014119, ENSOARG00000011631, ENSOARG00000015571, ENSOARG00000007541, ENSOARG00000004051, ENSOARG00000015592, ENSOARG00000013254, ENSOARG00000001078, ENSOARG00000010462, ENSOARG00000005273, ENSOARG00000007664, ENSOARG00000002050, ENSOARG00000005613, ENSOARG00000003292, ENSOARG00000016727, ENSOARG00000007549, ENSOARG00000018035, ENSOARG00000018964, ENSOARG00000012718, ENSOARG00000004233, ENSOARG00000001414, ENSOARG00000008169, ENSOARG00000000340, ENSOARG00000000078, ENSOARG00000006813, ENSOARG00000006760, ENSOARG00000004785, ENSOARG00000018276, ENSOARG00000016922, ENSOARG00000006538, ENSOARG00000019102, ENSOARG00000011785	520	396	7762	1.470	0.982	0.437	17.366
KEGG_PATHWAY	oas04210:Apoptosis	10	0.702	1.9E-02	ENSOARG00000015571, ENSOARG00000015422,	520	61	7762	2.447	0.995	0.491	22.564

					ENSOARG00000014866, ENSOARG00000012444, ENSOARG00000016852, ENSOARG00000001078, ENSOARG00000004785, ENSOARG00000012718, ENSOARG00000016922, ENSOARG00000007664							
KEGG_PATHWAY	oas00240:Pyrimidine metabolism	13	0.913	3.4E-02	ENSOARG00000010252, ENSOARG00000005654, ENSOARG00000002706, ENSOARG00000001093, ENSOARG00000018014, ENSOARG00000011243, ENSOARG00000015794, ENSOARG00000009296, ENSOARG00000008041, ENSOARG00000005266, ENSOARG00000016984, ENSOARG00000016081, ENSOARG00000010224	520	100	7762	1.941	1.000	0.658	36.712
KEGG_PATHWAY	oas04931:Insulin resistance	14	0.983	3.6E-02	ENSOARG00000006739, ENSOARG00000000156, ENSOARG00000020994, ENSOARG00000010421, ENSOARG00000013427, ENSOARG00000003188, ENSOARG00000007168, ENSOARG00000020686, ENSOARG00000005858, ENSOARG00000004785, ENSOARG00000012718, ENSOARG00000010722, ENSOARG00000007664, ENSOARG00000012001	520	112	7762	1.866	1.000	0.636	38.076
KEGG_PATHWAY	oas05203:Viral carcinogenesis	23	1.615	4.0E-02	ENSOARG00000005613, ENSOARG00000006187, ENSOARG00000004318, ENSOARG00000013335, ENSOARG00000012444, ENSOARG00000006902, ENSOARG00000018964, ENSOARG00000012718, ENSOARG00000001474, ENSOARG00000012647, ENSOARG00000010722, ENSOARG00000020053, ENSOARG00000015571, ENSOARG00000014631, ENSOARG00000001457, ENSOARG00000003188, ENSOARG00000001078, ENSOARG00000005473, ENSOARG00000004785, ENSOARG00000016922, ENSOARG00000007664, ENSOARG00000020669, ENSOARG00000000751	520	222	7762	1.546	1.000	0.649	42.037
KEGG_PATHWAY	oas00030:Pentose phosphate pathway	6	0.421	4.1E-02	ENSOARG00000020598, ENSOARG00000016351, ENSOARG00000007511, ENSOARG00000011246, ENSOARG00000005493, ENSOARG00000013817	520	29	7762	3.088	1.000	0.622	42.489
KEGG_PATHWAY	oas00500:Starch and sucrose	6	0.421	5.3E-02	ENSOARG00000006739, ENSOARG00000007168,	520	31	7762	2.889	1.000	0.687	51.055

	metabolism				ENSOARG00000020686, ENSOARG00000001636, ENSOARG00000014188, ENSOARG00000018733							
KEGG_PATHWAY	oas05210:Colorectal cancer	9	0.632	5.7E-02	ENSOARG00000011631, ENSOARG00000015571, ENSOARG00000017460, ENSOARG00000012444, ENSOARG00000013254, ENSOARG00000004785, ENSOARG00000018276, ENSOARG00000007664, ENSOARG00000002050	520	63	7762	2.132	1.000	0.692	54.216
KEGG_PATHWAY	oas01130:Biosynthesis of antibiotics	22	1.545	6.2E-02	ENSOARG00000010163, ENSOARG00000011246, ENSOARG00000000369, ENSOARG00000005493, ENSOARG00000017754, ENSOARG00000013817, ENSOARG00000000718, ENSOARG00000013943, ENSOARG00000020412, ENSOARG00000014018, ENSOARG00000007511, ENSOARG00000010252, ENSOARG00000016351, ENSOARG00000001093, ENSOARG00000007716, ENSOARG00000018580, ENSOARG00000008843, ENSOARG00000015794, ENSOARG00000000978, ENSOARG00000013023, ENSOARG00000007403, ENSOARG00000007382	520	220	7762	1.493	1.000	0.695	56.977
KEGG_PATHWAY	oas04668:TNF signaling pathway	13	0.913	6.3E-02	ENSOARG00000005613, ENSOARG00000014866, ENSOARG00000003188, ENSOARG00000010854, ENSOARG00000016852, ENSOARG00000020866, ENSOARG00000001078, ENSOARG00000004785, ENSOARG00000012718, ENSOARG00000016922, ENSOARG00000010722, ENSOARG00000007664, ENSOARG00000019414	520	110	7762	1.764	1.000	0.678	57.584
KEGG_PATHWAY	oas04722:Neurotrophin signaling pathway	14	0.983	6.7E-02	ENSOARG00000006187, ENSOARG00000012444, ENSOARG00000008988, ENSOARG00000012718, ENSOARG00000013329, ENSOARG00000015118, ENSOARG00000000156, ENSOARG00000015571, ENSOARG00000002299, ENSOARG00000011674, ENSOARG00000004785, ENSOARG00000017985, ENSOARG00000021010, ENSOARG00000007664	520	123	7762	1.699	1.000	0.678	59.824
KEGG_PATHWAY	oas04750:Inflammatory mediator regulation of TRP	12	0.843	7.4E-02	ENSOARG00000016897, ENSOARG00000000156, ENSOARG00000017383, ENSOARG00000007935,	520	101	7762	1.773	1.000	0.694	63.538

	channels				ENSOARG00000020866, ENSOARG00000008988, ENSOARG00000020689, ENSOARG00000008735, ENSOARG00000004785, ENSOARG00000019102, ENSOARG00000007664, ENSOARG00000020462							
KEGG_PATHWAY	oas00230:Purine metabolism	18	1.264	9.3E-02	ENSOARG00000005654, ENSOARG00000011246, ENSOARG00000011243, ENSOARG00000020763, ENSOARG00000016984, ENSOARG00000014018, ENSOARG00000010224, ENSOARG00000010252, ENSOARG00000015176, ENSOARG00000001093, ENSOARG00000002706, ENSOARG00000018014, ENSOARG00000014188, ENSOARG00000009296, ENSOARG00000015794, ENSOARG00000005266, ENSOARG00000003986, ENSOARG00000019102	520	180	7762	1.493	1.000	0.762	72.538
PIR_SUPERFAMILY	PIRSF000615:tyrosine-protein kinase, CSF-1/PDGF receptor type	3	0.211	7.0E-02	ENSOARG00000000078, ENSOARG00000006358, ENSOARG00000006538	123	5	1324	6.459	1.000	1.000	56.465
SMART	SM00450:RHOD	6	0.421	8.4E-03	ENSOARG00000001274, ENSOARG00000014079, ENSOARG00000020857, ENSOARG00000019145, ENSOARG00000011806, ENSOARG00000013213	645	17	8147	4.458	0.955	0.955	11.016
SMART	SM00184:RING	24	1.685	1.7E-02	ENSOARG00000018257, ENSOARG00000007445, ENSOARG00000014661, ENSOARG00000015272, ENSOARG00000007277, ENSOARG00000014583, ENSOARG00000003769, ENSOARG00000003391, ENSOARG00000001529, ENSOARG00000016983, ENSOARG00000000818, ENSOARG00000013231, ENSOARG00000013152, ENSOARG00000016549, ENSOARG00000015178, ENSOARG00000009726, ENSOARG00000018006, ENSOARG00000008530, ENSOARG00000012749, ENSOARG00000007674, ENSOARG00000012745, ENSOARG00000019106, ENSOARG00000009028, ENSOARG00000014515	645	183	8147	1.657	0.998	0.960	21.508
SMART	SM00242:MYSc	7	0.492	2.8E-02	ENSOARG00000011188, ENSOARG00000019316, ENSOARG00000012454, ENSOARG00000013610, ENSOARG00000018916, ENSOARG00000018135,	645	30	8147	2.947	1.000	0.967	31.947

					ENSOARG00000004207							
SMART	SM00209:TSP1	10	0.702	3.7E-02	ENSOARG00000007475, ENSOARG00000009766, ENSOARG00000004292, ENSOARG00000014133, ENSOARG00000020173, ENSOARG00000006382, ENSOARG00000014898, ENSOARG00000006371, ENSOARG00000010382, ENSOARG00000010962	645	58	8147	2.178	1.000	0.968	40.471
SMART	SM00355:ZnF_C2H2	41	2.879	4.0E-02	ENSOARG00000003623, ENSOARG00000019302, ENSOARG00000010774, ENSOARG00000004647, ENSOARG00000010779, ENSOARG00000002789, ENSOARG00000007509, ENSOARG00000018972, ENSOARG00000019279, ENSOARG00000019296, ENSOARG00000016195, ENSOARG00000003358, ENSOARG00000004353, ENSOARG00000008978, ENSOARG00000003219, ENSOARG00000002874, ENSOARG00000004095, ENSOARG00000015505, ENSOARG00000004631, ENSOARG00000014166, ENSOARG00000010468, ENSOARG00000015473, ENSOARG00000005257, ENSOARG00000020268, ENSOARG00000014918, ENSOARG00000003392, ENSOARG00000014354, ENSOARG00000011585, ENSOARG00000000770, ENSOARG00000000185, ENSOARG00000009044, ENSOARG00000013148, ENSOARG00000003678, ENSOARG00000008496, ENSOARG00000001296, ENSOARG00000007890, ENSOARG00000005434, ENSOARG00000003724, ENSOARG00000010061, ENSOARG00000011959, ENSOARG00000013030	645	383	8147	1.352	1.000	0.949	42.836
SMART	SM00164:TBC	7	0.492	4.2E-02	ENSOARG00000000399, ENSOARG00000002248, ENSOARG00000013667, ENSOARG00000018891, ENSOARG00000002768, ENSOARG00000002538, ENSOARG00000005979	645	33	8147	2.679	1.000	0.928	44.701
SMART	SM00431:SCAN	6	0.421	4.3E-02	ENSOARG00000003392, ENSOARG00000000770, ENSOARG00000005354, ENSOARG00000007509, ENSOARG00000013148, ENSOARG00000018515	645	25	8147	3.031	1.000	0.900	45.378

SMART	SM00179:EGF_CA	14	0.983	6.2E-02	ENSOARG00000017490, ENSOARG00000010405, ENSOARG00000018379, ENSOARG00000018923, ENSOARG00000017704, ENSOARG00000003894, ENSOARG00000004702, ENSOARG00000015724, ENSOARG00000018398, ENSOARG00000011479, ENSOARG00000010523, ENSOARG00000006826, ENSOARG00000012461, ENSOARG00000011304	645	103	8147	1.717	1.000	0.946	58.308
SMART	SM00234:START	4	0.281	6.3E-02	ENSOARG00000010770, ENSOARG00000013997, ENSOARG00000015301, ENSOARG00000000226	645	12	8147	4.210	1.000	0.930	59.294
SMART	SM00181:EGF	18	1.264	7.9E-02	ENSOARG00000017490, ENSOARG00000010405, ENSOARG00000017704, ENSOARG00000018379, ENSOARG00000018923, ENSOARG00000003894, ENSOARG00000004702, ENSOARG00000015354, ENSOARG00000015724, ENSOARG00000018398, ENSOARG00000010523, ENSOARG00000006826, ENSOARG00000020522, ENSOARG00000012461, ENSOARG00000011260, ENSOARG00000011304, ENSOARG00000003121, ENSOARG00000007080	645	149	8147	1.526	1.000	0.951	67.845
SMART	SM00195:DSPc	6	0.421	9.3E-02	ENSOARG00000007360, ENSOARG00000020857, ENSOARG00000008440, ENSOARG00000008498, ENSOARG00000001960, ENSOARG00000013213	645	31	8147	2.445	1.000	0.962	74.126
UP_KEYWORDS	Proteoglycan	6	0.421	1.1E-03	ENSOARG00000017313, ENSOARG00000012262, ENSOARG00000012184, ENSOARG00000015737, ENSOARG00000010462, ENSOARG00000004813	1358	11	16570	6.656	0.231	0.231	1.421
UP_KEYWORDS	Glycosidase	9	0.632	1.4E-02	ENSOARG00000018629, ENSOARG00000009747, ENSOARG00000019976, ENSOARG00000007760, ENSOARG00000002424, ENSOARG00000001193, ENSOARG00000005906, ENSOARG00000018845, ENSOARG00000018240	1358	40	16570	2.745	0.968	0.820	16.996
UP_KEYWORDS	Acetylation	14	0.983	1.5E-02	ENSOARG00000001851, ENSOARG00000018343, ENSOARG00000013027, ENSOARG00000007168, ENSOARG00000001337, ENSOARG00000010283, ENSOARG00000003288, ENSOARG00000009040, ENSOARG00000020821, ENSOARG00000007511,	1358	82	16570	2.083	0.975	0.708	18.202

					ENSOARG00000015571, ENSOARG00000020686, ENSOARG00000013370, ENSOARG00000003986							
UP_KEYWORDS	Heparan sulfate	4	0.281	2.2E-02	ENSOARG00000017313, ENSOARG00000012262, ENSOARG00000012184, ENSOARG00000004813	1358	8	16570	6.101	0.995	0.739	25.347
UP_KEYWORDS	Phosphoprotein	22	1.545	6.3E-02	ENSOARG00000001851, ENSOARG00000013027, ENSOARG00000018343, ENSOARG00000007168, ENSOARG00000020877, ENSOARG00000008837, ENSOARG00000015108, ENSOARG00000013157, ENSOARG00000018964, ENSOARG00000013229, ENSOARG00000001337, ENSOARG00000006068, ENSOARG00000009040, ENSOARG00000012174, ENSOARG00000020821, ENSOARG00000007511, ENSOARG00000015571, ENSOARG00000013782, ENSOARG00000020686, ENSOARG00000013370, ENSOARG00000006760, ENSOARG00000001551	1358	180	16570	1.491	1.000	0.954	56.805
UP_KEYWORDS	Carbohydrate metabolism	5	0.351	6.4E-02	ENSOARG00000009164, ENSOARG00000007168, ENSOARG00000020686, ENSOARG00000001722, ENSOARG00000008843	1358	19	16570	3.211	1.000	0.928	57.604
UP_KEYWORDS	Myosin	6	0.421	6.5E-02	ENSOARG00000011188, ENSOARG00000019316, ENSOARG00000012454, ENSOARG00000013610, ENSOARG00000018916, ENSOARG00000004207	1358	27	16570	2.712	1.000	0.898	58.005
UP_KEYWORDS	EGF-like domain	15	1.053	6.9E-02	ENSOARG00000010405, ENSOARG00000008473, ENSOARG00000018379, ENSOARG00000018923, ENSOARG00000017704, ENSOARG00000003894, ENSOARG00000004702, ENSOARG00000015354, ENSOARG00000015724, ENSOARG00000018398, ENSOARG00000011479, ENSOARG00000010523, ENSOARG00000006826, ENSOARG00000012461, ENSOARG00000011304	1358	111	16570	1.649	1.000	0.880	60.265
UP_KEYWORDS	Actin-binding	9	0.632	8.5E-02	ENSOARG00000011188, ENSOARG00000019316, ENSOARG00000006047, ENSOARG00000006703, ENSOARG00000013610, ENSOARG00000003372, ENSOARG00000007864, ENSOARG00000002175, ENSOARG00000004207	1358	56	16570	1.961	1.000	0.902	67.952

UP_KEYWORDS	Motor protein	8	0.562	9.4E-02	ENSOARG00000011188, ENSOARG00000019316, ENSOARG00000015211, ENSOARG00000012454, ENSOARG00000013610, ENSOARG00000018916, ENSOARG00000005591, ENSOARG00000004207	1358	48	16570	2.034	1.000	0.904	72.086
UP_KEYWORDS	Ubl conjugation	7	0.492	9.6E-02	ENSOARG00000020821, ENSOARG00000015571, ENSOARG00000013027, ENSOARG00000008837, ENSOARG00000010283, ENSOARG00000006068, ENSOARG00000010462	1358	39	16570	2.190	1.000	0.885	72.583

Supplementary Table 4. Pathway database analysis. Matched genes involved in different pathways analysed. Database name, code (when available) and name of the pathway analysed, and genes matched are provided.

Database	Code	Pathway Name	Genes matched
BIOCARTA	---	Lis1	CDK5, DNAH1
BIOCARTA	---	Neuroregulin	No Matches
BIOCARTA	---	Nerve Growth	PIK3CG, SHC1
EBI	GO:0048490	Anterograde synaptic vesicle transport	No Matches
EBI	GO:0048675	Axon extension pathway	BDNF, CDK5, DVL1
EBI	GO:0030517	Axon extension negative regulation	CDK5
EBI	GO:0045773	Axon extension positive regulation	No Matches
EBI	GO:0007409	Axonogenesis	CDK5, DVL1
EBI	GO:0050771	Axonogenesis negative regulation	No Matches
EBI	GO:0021954	Central Nervous system neuron development	CDK5
EBI	GO:0021895	Cortex neuron differentiation	No Matches
EBI	GO:0060079	Excitatory postsynaptic potential	BDNF, CDK5, MECP2
EBI	GO:0060080	Inhibitory postsynaptic potential	BDNF
EBI	GO:0060291	Long term synaptic potentiation	DRD1, MECP2
EBI	GO:0060292	Long term synaptic depression	DRD1
EBI	GO:0008045	Motor neuron axon guidance	CDK5
EBI	GO:0045665	Neuron negative differentiation	CAV1, IL1B
EBI	GO:0031914	Negative regulation of synaptic plasticity	CDK5
EBI	GO:1901214	Neuron death regulation	APOE
EBI	GO:0048666	Neuron development	No Matches
EBI	GO:0030182	Neuron differentiation	CDK5, HDAC5, MECP2, SHC1
EBI	GO:0045666	Neuron differentiation positive regulation	BDNF
EBI	GO:0021912	Neuron fate	PAX6
EBI	GO:0014041	Neuron maturation regulation	No Matches
EBI	GO:0001764	Neuron migration	BAX, CDK5, CXCR4
EBI	GO:2001223	Neuron migration negative regulation	No Matches

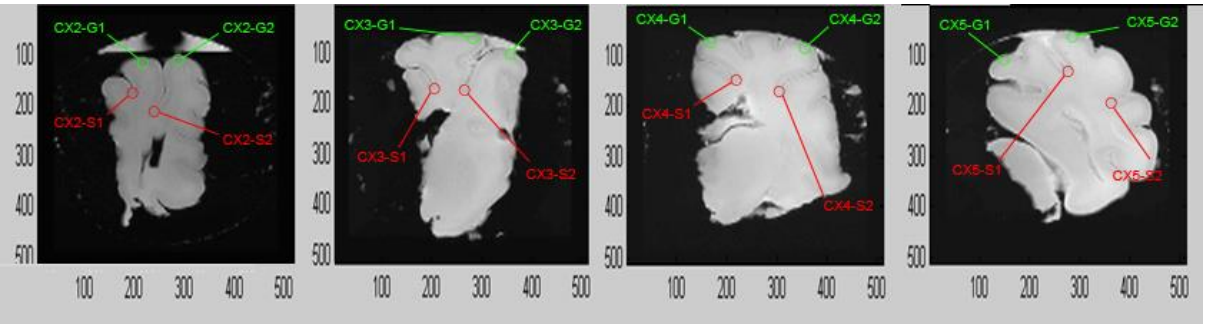
EBI	GO:0043005	Neuron projection	PIN1
EBI	GO:0010975	Neuron projection development regulation	No Matches
EBI	GO:0031175	Neuron projection development	CDK5, MECP2, SHC1
EBI	GO:1990138	Neuron projection extension	BDNF
EBI	GO:0048812	Neuron projection morphogenesis	BDNF, CDK5
EBI	GO:0097104	Postsynaptic membrane assembly	No Matches
EBI	GO:0097105	Presynaptic membrane assembly	No Matches
EBI	GO:0048168	Regulation of neuronal synaptic plasticity	APOE
EBI	GO:0032228	Regulation of synaptic transmission, GABAergic	No Matches
EBI	GO:0007271	Synaptic transmission, cholinergic	APOE
EBI	GO:0035249	Synaptic transmission, glutamaergic	CDK5
EBI	GO:0016188	Synaptic vesicle maturation	No Matches
Kegg	hsa04360	Axon guidance	CDK5, CXCR4, EFNB3, NTNG1, SEMA4B, SEMA5B, SEMA6C, UNC5B
Kegg	hsa04722	Neurotrophin pathway	BAX, BDNF, IKBKB, MAP3K3, MAPKAPK2, MATK, PRKCD
Wikipath	WP2276	Glial cell differentiation	No Matches
Wikipath	WP3392	LGI-ADAM interaction	ADAM11, CACNG4
Wikipath	WP2064	Neural crest differentiation	AXIN1, DVL1, HDAC5, MYB, NFKB1, NOTCH1, NOTCH4, PMP22, RHOB, SNAI2, SOX9, ZIC1

Supplementary Table 5. Genes in literature. Genes found in literature to be directly or potentially involved in gyrification. The genes that were matched from the bioinformatic output are depicted in bold font.

GENE	DOI	GENE	DOI
AKT3	10.1038/nrn3707	CHM	10.1002/humu.21585
ALX4	10.1186/s40478-014-0080-3	CLSTN1	10.1002/humu.21585
AMBP	10.1002/humu.21585	cluster miR-17-92	10.1038/nrn3707
APBA1	10.1002/humu.21585	CMPH1	10.15252/embj.201593701
aPKC	10.1038/nrn3707	COL4A1	10.1186/s40478-014-0080-3
APOER2	10.1186/1746-6148-9-156	COL4A2	10.1186/s40478-014-0080-3
ARFGEF2	10.15252/embj.201593701	CRKL	10.1002/humu.21585
ARL13B	10.1038/nrn3707	CTNNB1	10.1038/nrn3707
ASPM	10.1016/j.cortex.2015.10.010	Cyclin D1	10.1038/nrn3707
BACE2	10.1534/genetics.114.173443	DAB1	10.1186/1746-6148-9-156
BAZ1B	10.1534/genetics.114.173443	DACH2	10.1002/humu.21585
BDNF	10.1016/j.biopsych.2008.12.006	DCHS1	10.15252/embj.201593701
BRCA1	10.1038/nrn3707	DCX	10.1186/1746-6148-9-156
C6orf70	10.15252/embj.201593701	DNER	10.1534/genetics.114.173443
CASC5	10.1016/j.ejpn.2014.03.010	DOCK7	10.1038/nrn3707
CASP3	10.1038/nrn3707	DYNC1H1	10.1146/annurev-genom-090413-025600
CASP9	10.1038/nrn3707	**DYNLT1**	10.1038/nrn3707
CCND2	10.1038/nrn3707	DYRK1A	10.1534/genetics.114.173443
CDC42	10.1038/nrn3707	EFHD1	10.1534/genetics.114.173443
CDC42EP5	10.1002/humu.21585	ELAC2	10.1002/humu.21585
CDK4	10.1038/nrn3707	EML1	10.15252/embj.201593701
CDK5	10.1016/j.celrep.2017.08.024	EOMES	10.1186/s40478-014-0080-3
CDK5RAP2	10.1016/j.ejpn.2014.03.010	EPHA5	10.1038/nrn3707
CDK6	10.1016/j.ejpn.2014.03.010	EPHA7	10.1038/nrn3707
CDKN1C	10.1038/nrn3707	EPM2AIP	10.1002/humu.21585
CENPJ	10.1016/j.ejpn.2014.03.010	FANCA	10.1038/nrn3707
CEP120	10.1038/nrn3707	FANCG	10.1038/nrn3707
CEP135	10.1016/j.ejpn.2014.03.010	FAT4	10.15252/embj.201593701
CEP152	10.1016/j.ejpn.2014.03.010	FCMD	10.1002/humu.21585
CEP63	10.15252/embj.201593701	FGF10	10.1038/nrn3707

FGF2	10.1523/JNEUROSCI.3621-12.2013	LMO4	10.1038/nrn3707
FGF8	10.1038/srep15370	MALS3	10.1038/nrn3707
FGFR2	10.1038/nrn3707	MAP2K	10.1002/humu.21585
FGFR3	10.1038/nrn3707	MARCKS	10.1186/s40478-014-0080-3
FKRP	10.1146/annurev-genom-090413-025600	MCPH1	10.1016/j.ejpn.2014.03.010
FKTN	10.15252/embj.201593701	**MECP2**	10.1136/jmg.2004.023952
FLNA	10.1038/nrn3707	miR-124	10.1038/nrn3707
FZD9	10.1534/genetics.114.173443	miR-132	10.1038/nrn3707
GALR	10.1002/humu.21585	miR-134	10.1038/nrn3707
GIGYF2	10.1534/genetics.114.173443	miR-134	10.1038/nrn3707
GPSM2	10.1038/nrn3707	miR-17	10.1038/nrn3707
GRIK1	10.1534/genetics.114.173443	miR-9	10.1038/nrn3707
Gβgamma	10.1038/nrn3707	miR-9	10.1038/nrn3707
HNF1B	10.1002/humu.21585	miR-92	10.1038/nrn3707
HOOK3	10.1038/nrn3707	MLXIPL	10.1534/genetics.114.173443
IFT	10.1038/nrn3707	MOBKL2	10.1002/humu.21585
IFT88	10.1038/nrn3707	MSX2	10.1186/s40478-014-0080-3
IGF2	10.1038/nrn3707	MTOR	10.1038/nrn3707
INSC	10.1038/nrn3707	NDE1	10.1002/humu.21585
INSM1	10.1038/nrn3707	NGEF	10.1534/genetics.114.173443
ITPR1	10.1002/humu.21585	NHEJ1	10.15252/embj.201593701
KBP	10.15252/embj.201593701	NMUR1	10.1534/genetics.114.173443
KIF1A	10.1002/humu.21585	NOTCH1	10.1038/nrn3707
KIF2A	10.1146/annurev-genom-090413-025600	NUMB	10.1038/nrn3707
KIF5C	10.1146/annurev-genom-090413-025600	**NUMBL**	10.1038/nrn3707
LAMB1	10.15252/embj.201593701	OCLN	10.1186/s40478-014-0080-3
LARGE	10.15252/embj.201593701	OLIG2	10.1534/genetics.114.173443
LGN	10.1038/nrn3707	p57KIP2	10.1038/nrn3707
LIN7C	10.1038/nrn3707	PAFAH1B1	10.1002/humu.21585
LIS	10.1186/1746-6148-9-156	PAR complex	10.1038/nrn3707

PAR3	10.1038/nrn3707	STAU2	10.1038/nrn3707
PAR6	10.1038/nrn3707	STIL	10.1016/j.ejpn.2014.03.010
PAX6	10.1038/nrn3707	SUN1	10.1038/nrn3707
PEX7	10.1146/annurev-genom-090413-025600	SUN2	10.1038/nrn3707
PHC1	10.1016/j.ejpn.2014.03.010	TBR2	10.1038/srep29578
PIK3CA	10.1146/annurev-genom-090413-025600	TCOF1	10.1038/nrn3707
PIK3R2	10.1038/nrn3707	TCTEX	10.1038/nrn3707
PINS	10.1038/nrn3707	TEK	10.1002/humu.21585
PNCT	10.15252/embj.201593701	TFAP2A	10.1002/humu.21585
PNKP	10.15252/embj.201593701	TG737	10.1038/nrn3707
POMGNT1	10.15252/embj.201593701	TRNP1	10.1016/j.cell.2013.03.027
POMT1	10.15252/embj.201593701	TSC1	10.1097/01.jnen.0000171651.32460.19
POMT2	10.15252/embj.201593701	TSC2	10.1097/01.jnen.0000171651.32460.19
PP4C	10.1038/nrn3707	**TSEN2**	10.1016/j.ajhg.2014.03.003
PQBP1	10.1016/j.neuroimage.2014.07.057	TSEN34	10.1016/j.ajhg.2014.03.003
PTEN	10.1038/nrn3707	TSEN54	10.1016/j.ajhg.2014.03.003
QARS	10.1016/j.ajhg.2014.03.003	TUBA1A	10.1186/1746-6148-9-156
RAC1	10.1038/nrn3707	TUBA8	10.15252/embj.201593701
RARS2	10.1016/j.ajhg.2014.03.003	TUBA8	10.1186/s40478-014-0080-3
RCAN	10.1534/genetics.114.173443	TUBB2B	10.1002/humu.21585
RELN	10.1186/1746-6148-9-156	TUBB3	10.15252/embj.201593701
S100B	10.1534/genetics.114.173443	TUBB3	10.15252/embj.201593701
SEPSECS	10.1016/j.ajhg.2014.03.003	TUBB3	10.1146/annurev-genom-090413-025600
SIM2	10.1534/genetics.114.173443	TUBB5	10.1146/annurev-genom-090413-025600
SLC31A1	10.1002/humu.21585	TUBG1	10.1146/annurev-genom-090413-025600
SLC31A2	10.1002/humu.21585	VLDLR	10.1186/1746-6148-9-156
SMARCA2	10.1002/humu.21585	VPS13B	10.1146/annurev-genom-090413-025600
SNTG2	10.1002/humu.21585	WBSCR2	10.1534/genetics.114.173443
SNX13	10.1002/humu.21585	**WDR62**	10.1016/j.ejpn.2014.03.010
SPRX2	10.15252/embj.201593701	WNT	10.1038/nrn3707
		XLIS	10.1186/1746-6148-9-156
		YWHAE	10.1002/humu.21585
		ZNF238	10.1002/humu.21585
		ZNF335	10.1016/j.ejpn.2014.03.010



Supplementary Figure 4. NODDI regions. MRI images showing regions of interest used in NODDI analysis. Labels correspond to gyri (green) and sulci (red). Labels are cortex region + gyri/sulci number.

Supplementary Table 6. Quality control for DTI and NODDI acquisition. DTI and NODDI values acquired on GA 98 brains at b value of 1750. AD, axial diffusivity; RD, radial diffusivity; MD, mean diffusivity; FA, fractional anisotropy; FECVF, extracellular volume fraction; FICVF, intracellular volume fraction; NS, non-significant; G, gyri; S, sulci.

NODDI Parameter	Gyri (mean ± SEM)	Sulci (mean ± SEM)	Gyri to Sulci relationship	Effect size	p value	Rostro-caudal relationship
AD	0.6464 ± 0.0113	0.5356 ± 0.01111	G > S	F (1, 16) = 40.39	< 0.0001	NS
RD	0.3899 ± 0.01173	0.2937 ± 0.006504	G > S	F (1, 16) = 105.4	< 0.0001	NS
MD	0.4754 ± 0.009064	0.3743 ± 0.007135	G > S	F (1, 16) = 103.5	< 0.0001	NS
FA	0.3103 ± 0.02024	0.3624 ± 0.01070	G < S	F (1, 16) = 8.803	0.0091	NS
FECVF	0.6852 ± 0.004758	0.6056 ± 0.009768	G > S	F (1, 16) = 19.45	0.0004	NS
FICVF	0.1503 ± 0.006689	0.2351 ± 0.004285	G < S	F (1, 16) = 51.21	< 0.0001	NS

Appendix 2 – Sequence alignment and probe design

HDAC5

Sequence alignment

Sequences:

Ovis aries: XM_015098824.1, XM_012157406.2, XM_012157407.2, XM_012157408.2, XM_012157409.2, XM_012157411.2, XM_012157412.2, XM_012157413.2, XM_012157414.2, XM_012157415.2, XM_012157416.2

Bos taurus: XM_015458862.1, XM_005220824.3, XM_015458863.1, XM_010816322.2, XM_005220826.3

Homo sapiens: NM_005474.4, NM_001015053.1

Mus musculus: NM_001077696.1, NM_010412.3, NM_001284248.1, NM_001284249.1, NM_001284250.1

Sequence alignment (note in grey the selected sequence used for probe design):

```
Mm_HDAC5_v4          GGTCACGTGACGAGAGTGACGTCTCCGAATGTTGTTGTTGGTGGCGGCGGCGAGCGGAGC
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          GGTCACGTGACGAGAGTGACGTCTCCGAATGTTGTTGTTGGTGGCGGCGGCGAGCGGAGC
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          ------------------------------------------------------------
Hs_HDAC5_v3          ------------------------------------------------------------
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       ------------------------------------------------------------
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          CGGAGGAGCCGCCGCAAAGATGGAGGAGCCGTCGAGGAGGCGCTGCCGCTGCTGTTGCCG
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          CGGAGGAGCCGCCGCAAAGATGGAGGAGCCGTCGAGGAGGCGCTGCCGCTGCTGTTGCCG
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          ------------------------------------------------------------
```

```
Hs_HDAC5_v3          ------------------------------------------------------------
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       ------------------------------------------------------------
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          CCGCTGCTGCCGCCGCCGCCCGCGAAGCCGGAGCTCGAGCCGCAGCGGGGATGCCGTTCT
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          CCGCTGCTGCCGCCGCCGCCCGCGAAGCCGGAGCTCGAGCCGCAGCGGGGATGCCGTTCT
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          ------------------------------------------------------------
Hs_HDAC5_v3          ------------------------------------------------------------
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       ------------------------------------------------------------
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          GAGTGCCTGACTGCCTCGCCCCGCCCCGAAGGATGGCCTTGGATGGGCATTAGAGGCACT
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          GAGTGCCTGACTGCCTCGCCCCGCCCCGAAGGATGGCCTTGGATGGGCATTAGAGGCACT
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          ------------------------------------------------------------
Hs_HDAC5_v3          ------------------------------------------------------------
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       ------------------------------------------------------------
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          GCGGCCCTGGGCTCGGGCTCCTGTCCCGTCCGTCTGTCTGTTATCGTCTGTCTCTCTTGA
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          GCGGCCCTGGGCTCGGGCTCCTGTCCCGTCCGTCTGTCTGTTATCGTCTGTCTCTCTTGA
Mm_HDAC5_v5          ------------------------------------------------------------
```

```
Hs_HDAC5_v1          ------------------------------------------------------------
Hs_HDAC5_v3          ------------------------------------------------------------
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       ------------------------------------------------------------
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          CATCACAGCAGCTCCGCCCCCTCCCGTCCCAGCCCCCAACGTCAGCTTCCTGCAGGCCCA
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          CATCACAGCAGCTCCGCCCCCTCCCGTCCCAGCCCCCAACGTCAGCTTCCTGCAGGCCCA
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          ------------------------------------------------------------
Hs_HDAC5_v3          ------------------------------------------------------------
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       ------------------------------------------------------------
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          GAGCCGGCATGAACTCTCCCAACGAGTCGGATGGCATGTCAGGCCGGGAACCATCCTTGG
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          GAGCCGGCATGAACTCTCCCAACGAGTCGGCTTCCTTCCAGAGGGATTGGAGGCTCAGGA
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          ------------------CGAATGTTGTT----------------------------------
Hs_HDAC5_v3          ------------------CGAATGTTGTT----------------------------------
Bt_HDAC5_v1          --------------------------CTC----------------------------------
Bt_HDAC5_v5(P)       --------------TCTCCGAATGTTGTT----------------------------------
Bt_HDAC5_v4(P)       --------------TCTCCGAATGTTGTT----------------------------------
Bt_HDAC5_v2          --------------TCTCCGAATGTTGTT----------------------------------
Bt_HDAC5_v3(P)       --------------TCTCCGAATGTTGTT----------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ---CGGGAGTGACGTCTCCGAATGTTGTT----------------------------------
Oa_HDAC5_v6(P)       ---CGGGAGTGACGTCTCCGAATGTTGTT----------------------------------
Oa_HDAC5_v5(P)       ---CGGGAGTGACGTCTCCGAATGTTGTT----------------------------------
Oa_HDAC5_v2(P)       ---CGGGAGTGACGTCTCCGAATGTTGTT----------------------------------
Oa_HDAC5_v4(P)       ---CGGGAGTGACGTCTCCGAATGTTGTT----------------------------------

Mm_HDAC5_v4          AA------------------------ATCCTG------------------------------
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          CTGGCTGGTGAGGAGAGGCAGTATCAACCCAGAGAGGAAGTAGAAGATGACAAAAAAGGG
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Mm_HDAC5_v5          ------------------------------------------------------------GG
Hs_HDAC5_v1          ---GTTGGTGGC-------GGCGGCGAGCG-GAGCCGGAG---GAGCCGCCG--------
Hs_HDAC5_v3          ---GTTGGTGGC-------GGCGGCGAGCG-GAGCCGGAG---GAGCCGCCG--------
Bt_HDAC5_v1          ---ATTCGGGAA-------GGAGGAGCAGG-GAGCCGGGCCCAGAGCTGTCA--------
Bt_HDAC5_v5(P)       ---GTTGGTGGC-------GGCGGCGAGCG-GAGCCGGAG---GAGCCGCCG--------
Bt_HDAC5_v4(P)       ---GTTGGTGGC-------GGCGGCGAGCG-GAGCCGGAG---GAGCCGCCG--------
Bt_HDAC5_v2          ---GTTGGTGGC-------GGCGGCGAGCG-GAGCCGGAG---GAGCCGCCG--------
Bt_HDAC5_v3(P)       ---GTTGGTGGC-------GGCGGCGAGCG-GAGCCGGAG---GAGCCGCCG--------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ---GTTGGTGGC-------GGCGGCGAGCG-GAGCCGGAG---GAGCCGCCG--------
Oa_HDAC5_v6(P)       ---GTTGGTGGC-------GGCGGCGAGCG-GAGCCGGAG---GAGCCGCCG--------
Oa_HDAC5_v5(P)       ---GTTGGTGGC-------GGCGGCGAGCG-GAGCCGGAG---GAGCCGCCG--------
Oa_HDAC5_v2(P)       ---GTTGGTGGC-------GGCGGCGAGCG-GAGCCGGAG---GAGCCGCCG--------
Oa_HDAC5_v4(P)       ---GTTGGTGGC-------GGCGGCGAGCG-GAGCCGGAG---GAGCCGCCG--------


Mm_HDAC5_v4          -------------------------CCACGGACTC-------------------------
Mm_HDAC5_v1          ----GGTCACGTGACGAGAGTGACGTCTCCGAATGTTGTTGTTGGTGGCGGCGGCGAGCG
Mm_HDAC5_v3          GGAAGAGAGAAGATCCAGGCTGGCTGCTTGGTGTCCAGTCCGT--TGTTTGCCCCCAGCA
Mm_HDAC5_v5          TCACGTGACGAG------AGTGACGTCTCCGAATGTTGTTGTTGGTGGCGGCGGCGAGCG
Hs_HDAC5_v1          -------CAAAGATGGAGGAGCCGTCGAGGAGGTGCTGCCG-C-CGCTG---CCGCCGCC
Hs_HDAC5_v3          -------CAAAGATGGAGGAGCCGTCGAGGAGGTGCTGCCG-C-CGCTG---CCGCCGCC
Bt_HDAC5_v1          -------CCCAGGGCTGGGAGGGAACACAGAGAGCCCGCCTGC-CTGCC---CAGCTCCC
Bt_HDAC5_v5(P)       -------CAAAGATGGAGGAGCCGTCGAGGAGGTGCTGCCG-C-TGCTG---CCGCCGCC
Bt_HDAC5_v4(P)       -------CAAAGATGGAGGAGCCGTCGAGGAGGTGCTGCCG-C-TGCTG---CCGCCGCC
Bt_HDAC5_v2          -------CAAAGATGGAGGAGCCGTCGAGGAGGTGCTGCCG-C-TGCTG---CCGCCGCC
Bt_HDAC5_v3(P)       -------CAAAGATGGAGGAGCCGTCGAGGAGGTGCTGCCG-C-TGCTG---CCGCCGCC
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       -------CAAAGATGGAGGAGCCGTCGAGGAGGTGCTGCCG-C-TGCTG---CCGCCGCC
Oa_HDAC5_v6(P)       -------CAAAGATGGAGGAGCCGTCGAGGAGGTGCTGCCG-C-TGCTG---CCGCCGCC
Oa_HDAC5_v5(P)       -------CAAAGATGGAGGAGCCGTCGAGGAGGTGCTGCCG-C-TGCTG---CCGCCGCC
Oa_HDAC5_v2(P)       -------CAAAGATGGAGGAGCCGTCGAGGAGGTGCTGCCG-C-TGCTG---CCGCCGCC
Oa_HDAC5_v4(P)       -------CAAAGATGGAGGAGCCGTCGAGGAGGTGCTGCCG-C-TGCTG---CCGCCGCC


Mm_HDAC5_v4          ----------------------------------CTCT----------------GCAC--
Mm_HDAC5_v1          GAGCCGGAGGAGCCGCCGCAAAGATGGAGGAGCCGTCGAGGAGGCGCTGCCGCTGCTGTT
Mm_HDAC5_v3          GTGGC---CAAAGCTGACCCCAGATGCATGGGTCCTCTGCCTGCACCCTTC---TCTAGT
Mm_HDAC5_v5          GAGCCGGAGGAGCCGCCGCAAAGATGGAGGAGCCGTCGAGGAGGCGCTGCCGCTGCTGTT
Hs_HDAC5_v1          GCTGCTGCCGCCGCCGCCCGCGAAGCC---GGAGCTCGAGCCGCAGC-------------
Hs_HDAC5_v3          GCTGCTGCCGCCGCCGCCCGCGAAGCC---GGAGCTCGAGCCGCAGC-------------
Bt_HDAC5_v1          CTTCCTGTCCCC--TGAGTGCTCAGCC---AGACCCCGCTCCTG--GGACCTCTGGAGAG
Bt_HDAC5_v5(P)       GCTGCTGCCGCCGCCGCCCGCGAAGCC---GGAGCTCGAGCCGCAGG-------------
Bt_HDAC5_v4(P)       GCTGCTGCCGCCGCCGCCCGCGAAGCC---GGAGCTCGAGCCGCAGG-------------
Bt_HDAC5_v2          GCTGCTGCCGCCGCCGCCCGCGAAGCC---GGAGCTCGAGCCGCAGG-------------
Bt_HDAC5_v3(P)       GCTGCTGCCGCCGCCGCCCGCGAAGCC---GGAGCTCGAGCCGCAGGGGGCAGGGGCGCC
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       GCTGCTGCCGCCGCCGCCCGCGAAGCC---GGAGCTCGAGCCGCAGG-------------
Oa_HDAC5_v6(P)       GCTGCTGCCGCCGCCGCCCGCGAAGCC---GGAGCTCGAGCCGCAGG-------------
Oa_HDAC5_v5(P)       GCTGCTGCCGCCGCCGCCCGCGAAGCC---GGAGCTCGAGCCGCAGG-------------
Oa_HDAC5_v2(P)       GCTGCTGCCGCCGCCGCCCGCGAAGCC---GGAGCTCGAGCCGCAGG-------------
Oa_HDAC5_v4(P)       GCTGCTGCCGCCGCCGCCCGCGAAGCC---GGAGCTCGAGCCGCAGG-------------


Mm_HDAC5_v4          ------------------------AGCATCCCTGTGGCAG---------------GT----
Mm_HDAC5_v1          GCC-----GCCGCTGCTGCCGCCGCCGCCCGCGAAGCCG---------------GAGCTC
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Mm_HDAC5_v3          CCA-----GCCACTGGCCACCCAGAC-----TTTGGTCC---------------ACGCTC
Mm_HDAC5_v5          GCC-----GCCGCTGCTGCCGCCGCCGCCCGCGAAGCCG---------------GAGCTC
Hs_HDAC5_v1          --------GGGGATGCCGTTC--T----------------------GAGTGCCTGACTGC
Hs_HDAC5_v3          --------GGGGATGCCGTTC--T----------------------GAGTGCCTGACTGC
Bt_HDAC5_v1          GCCAGTGGTCGGATGCCCCTC--TAGAGGGGCACTGGGCCCGTAGCTCTGGGGCTCCTGG
Bt_HDAC5_v5(P)       --------GGGAATGCCGTTC--TGAATGCCTG----------------------ACTGC
Bt_HDAC5_v4(P)       --------GGGAATGCCGTTC--TGAATGCCTG----------------------ACTGC
Bt_HDAC5_v2          --------GGGAATGCCGTTC--TGAATGCCTG----------------------ACTGC
Bt_HDAC5_v3(P)       TTCCCTACAGGAATGCCGTTC--TGAATGCCTG----------------------ACTGC
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       --------GGGAATGCCGTTC--TGAATGCCTG----------------------ACTGC
Oa_HDAC5_v6(P)       --------GGGAATGCCGTTC--TGAATGCCTG----------------------ACTGC
Oa_HDAC5_v5(P)       --------GGGAATGCCGTTC--TGAATGCCTG----------------------ACTGC
Oa_HDAC5_v2(P)       --------GGGAATGCCGTTC--TGAATGCCTG----------------------ACTGC
Oa_HDAC5_v4(P)       --------GGGAATGCCGTTC--TGAATGCCTG----------------------ACTGC


Mm_HDAC5_v4          ----------------------GACC----TTGGACAAGCTCCCTCTG------------
Mm_HDAC5_v1          GAGCCGCAGCGGGGATGCCGTTCTGAGTGCCTGACTGCC----------------------
Mm_HDAC5_v3          CTGGAGCGGAGAGCAGGCCCTTCAGCCTCATTAGCCTCCCTGCGTCTGCTGCCTCCGGAG
Mm_HDAC5_v5          GAGCCGCAGCGGGGATGCCGTTCTGAGTG-----CCTGACTGCCT---------------
Hs_HDAC5_v1          CTCGCCCCGAAGGATGGCCTCGGATGGGCATTAGAGGCACGGC------GGCCCCGGGCT
Hs_HDAC5_v3          CTCGCCCCGAAGGATGGCCTCGGATGGGCATTAGAGGCACGGC------GGCCCCGGGCT
Bt_HDAC5_v1          CTCCTCCTGCCACCAGAAGTGCCCAGGCCGGATGAAGCACCTC------CCCATCGTGCT
Bt_HDAC5_v5(P)       CTCGCCCCGAAGGATGGCCTCGGATGGGCGTTAGAGGCACAGC------GGCCCCGGGCT
Bt_HDAC5_v4(P)       CTCGCCCCGAAGGATGGCCTCGGATGGGCGTTAGAGGCACAGC------GGCCCCGGGCT
Bt_HDAC5_v2          CTCGCCCCGAAGGATGGCCTCGGATGGGCGTTAGAGGCACAGC------GGCCCCGGGCT
Bt_HDAC5_v3(P)       CTCGCCCCGAAGGATGGCCTCGGATGGGCGTTAGAGGCACAGC------GGCCCCGGGCT
Oa_HDAC5_v11(P)      ------------GATGGCCTCGGATGGGCGTTAGAGGCACAGC------GGCCCCGGGCT
Oa_HDAC5_v10(P)      ------------GATGGCCTCGGATGGGCGTTAGAGGCACAGC------GGCCCCGGGCT
Oa_HDAC5_v8(P)       ------------GATGGCCTCGGATGGGCGTTAGAGGCACAGC------GGCCCCGGGCT
Oa_HDAC5_v9(P)       ------------GATGGCCTCGGATGGGCGTTAGAGGCACAGC------GGCCCCGGGCT
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       CTCGCCCCGAAGGATGGCCTCGGATGGGCGTTAGAGGCACAGC------GGCCCCGGGCT
Oa_HDAC5_v6(P)       CTCGCCCCGAAGGATGGCCTCGGATGGGCGTTAGAGGCACAGC------GGCCCCGGGCT
Oa_HDAC5_v5(P)       CTCGCCCCGAAGGATGGCCTCGGATGGGCGTTAGAGGCACAGC------GGCCCCGGGCT
Oa_HDAC5_v2(P)       CTCGCCCCGAAGGATGGCCTCGGATGGGCGTTAGAGGCACAGC------GGCCCCGGGCT
Oa_HDAC5_v4(P)       CTCGCCCCGAAGGATGGCCTCGGATGGGCGTTAGAGGCACAGC------GGCCCCGGGCT


Mm_HDAC5_v4          ----------------------------T------------------------GGCCTC
Mm_HDAC5_v1          -TCGCCCCGCCCCGAAGGATGGCCTTGGATGGGCATTAGAGGCACTGCGGCCCTGGGCTC
Mm_HDAC5_v3          CGCGCCCAGGCCGGATGAGGTGCCTCCT-TG-CCTCGTGGGTCCCAGCGGCAGTGGCCTG
Mm_HDAC5_v5          --CGCCCCGCCCCGAAGGATGGCCTTGGATGGGCATTAGAGGCACTGCGGCCCTGGGCTC
Hs_HDAC5_v1          CCCGTCCCGTCCGTCTGTC----------TGTTATCGTCTGTCTCTCTTGACATCACCGC
Hs_HDAC5_v3          CCCGTCCCGTCCGTCTGTC----------TGTTATCGTCTGTCTCTCTTGACATCACCGC
Bt_HDAC5_v1          GG-------TCCCAGTAGC----------CGTGGCCTGAGGGAGCCCCTGAGCAGCCGCG
Bt_HDAC5_v5(P)       CCTGTCCCGTCCGTCTGTC----------TGTTATCGTCTGTCTCTCTTGACATCACCGC
Bt_HDAC5_v4(P)       CCTGTCCCGTCCGTCTGTC----------TGTTATCGTCTGTCTCTCTTGACATCACCGC
Bt_HDAC5_v2          CCTGTCCCGTCCGTCTGTC----------TGTTATCGTCTGTCTCTCTTGACATCACCGC
Bt_HDAC5_v3(P)       CCTGTCCCGTCCGTCTGTC----------TGTTATCGTCTGTCTCTCTTGACATCACCGC
Oa_HDAC5_v11(P)      CCTGTCCCGTCCGTCTGTC----------TGTTATCGTCTGTCTCTCTTGACATCACCGC
Oa_HDAC5_v10(P)      CCTGTCCCGTCCGTCTGTC----------TGTTATCGTCTGTCTCTCTTGACATCACCGC
Oa_HDAC5_v8(P)       CCTGTCCCGTCCGTCTGTC----------TGTTATCGTCTGTCTCTCTTGACATCACCGC
Oa_HDAC5_v9(P)       CCTGTCCCGTCCGTCTGTC----------TGTTATCGTCTGTCTCTCTTGACATCACCGC
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       CCTGTCCCGTCCGTCTGTC----------TGTTATCGTCTGTCTCTCTTGACATCACCGC
Oa_HDAC5_v6(P)       CCTGTCCCGTCCGTCTGTC----------TGTTATCGTCTGTCTCTCTTGACATCACCGC
Oa_HDAC5_v5(P)       CCTGTCCCGTCCGTCTGTC----------TGTTATCGTCTGTCTCTCTTGACATCACCGC
Oa_HDAC5_v2(P)       CCTGTCCCGTCCGTCTGTC----------TGTTATCGTCTGTCTCTCTTGACATCACCGC
Oa_HDAC5_v4(P)       CCTGTCCCGTCCGTCTGTC----------TGTTATCGTCTGTCTCTCTTGACATCACCGC


Mm_HDAC5_v4          ACTTTCTCCTCCT----GCAGCTGGGG---------------------------------
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Mm_HDAC5_v1          GG---------------GCTCCTGTCCCGTCCGTCTGTCTGTTATCGTCTGTCTCTCTTG
Mm_HDAC5_v3          AGGGAGTCCTTGAGCAGCCAGCTGGCCCCGCTGACCACCTTTTCC---CTCACCGGCTTC
Mm_HDAC5_v5          GG---------------GCTCCTGTCCCGTCCGTCTGTCTGTTATCGTCTGTCTCTCTTG
Hs_HDAC5_v1          AGCTCCACCC----------------CC---TCCC-GTCCCAGCCCCCAACGCCAGCTTC
Hs_HDAC5_v3          AGCTCCACCC----------------CC---TCCC-GTCCCAGCCCCCAACGCCAGCTTC
Bt_HDAC5_v1          AGGGCCCCAC----------------CCGACCACC-TTCCCTGTGGCTGACTCCCCGCCT
Bt_HDAC5_v5(P)       AGCT--CCAC----------------CCC-CTCCC-GTCCCAGCCCCCAACGCCAGCTTC
Bt_HDAC5_v4(P)       AGCT--CCAC----------------CCC-CTCCC-GTCCCAGCCCCCAACGCCAGCTTC
Bt_HDAC5_v2          AGCT--CCAC----------------CCC-CTCCC-GTCCCAGCCCCCAACGCCAGCTTC
Bt_HDAC5_v3(P)       AGCT--CCAC----------------CCC-CTCCC-GTCCCAGCCCCCAACGCCAGCTTC
Oa_HDAC5_v11(P)      AGCT--CCAC----------------CCC-CTCCC-GTCCCAGCCCCCAACGCCAGCTTC
Oa_HDAC5_v10(P)      AGCT--CCAC----------------CCC-CTCCC-GTCCCAGCCCCCAACGCCAGCTTC
Oa_HDAC5_v8(P)       AGCT--CCAC----------------CCC-CTCCC-GTCCCAGCCCCCAACGCCAGCTTC
Oa_HDAC5_v9(P)       AGCT--CCAC----------------CCC-CTCCC-GTCCCAGCCCCCAACGCCAGCTTC
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       AGCT--CCAC----------------CCC-CTCCC-GTCCCAGCCCCCAACGCCAGCTTC
Oa_HDAC5_v6(P)       AGCT--CCAC----------------CCC-CTCCC-GTCCCAGCCCCCAACGCCAGCTTC
Oa_HDAC5_v5(P)       AGCT--CCAC----------------CCC-CTCCC-GTCCCAGCCCCCAACGCCAGCTTC
Oa_HDAC5_v2(P)       AGCT--CCAC----------------CCC-CTCCC-GTCCCAGCCCCCAACGCCAGCTTC
Oa_HDAC5_v4(P)       AGCT--CCAC----------------CCC-CTCCC-GTCCCAGCCCCCAACGCCAGCTTC


Mm_HDAC5_v4          ----------------------------------------------------CCGTTGAG
Mm_HDAC5_v1          ACATCACAGCAGCTCCGCCCCCTCCCGT-------------CCCAGCCCCCAACGTCAGC
Mm_HDAC5_v3          CGCCTCGGGCGGCCCCTCCCTGGCATGCTGCTGGTGCCCAAGGCACAGGGGCTTGTGGAG
Mm_HDAC5_v5          ACATCACAGCAGC---TCCGCCCCCTC------CCGTCC----CAGCCCCCAACGTCAGC
Hs_HDAC5_v1          CTGCAGGCCCAGAGC-----CGGCATGA--------------------------------
Hs_HDAC5_v3          CTGCAGGCCCAGAGC-----CGGCATGA--------------------------------
Bt_HDAC5_v1          CGGGCGGCCCCTCCT-----GGGCATGCTGCTAG---TGCCCAAGGCTCAGGGGCTGGTG
Bt_HDAC5_v5(P)       CTGCAGGCCCAGAGC-----CGGCATGAACTCTC---CCACCGAGTCG------------
Bt_HDAC5_v4(P)       CTGCAGGCCCAGAGC-----CGGCATGAACTCTC---CCACCGAGTCGGC----------
Bt_HDAC5_v2          CTGCAGGCCCAGAGC-----CGGCATGAACTCTC---CCACCGAGTCGGC----------
Bt_HDAC5_v3(P)       CTGCAGGCCCAGAGC-----CGGCATGAACTCTC---CCACCGAGTCGGC----------
Oa_HDAC5_v11(P)      CTGCAGGCCCAGAGC-----CGGCATGAACTCTC---CCACCGAGTCG------------
Oa_HDAC5_v10(P)      CTGCAGGCCCAGAGC-----CGGCATGAACTCTC---CCACCGAGTCGG-----------
Oa_HDAC5_v8(P)       CTGCAGGCCCAGAGC-----CGGCATGAACTCTC---CCACCGAGTCGG-----------
Oa_HDAC5_v9(P)       CTGCAGGCCCAGAGC-----CGGCATGAACTCTC---CCACCGAGTCG------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       CTGCAGGCCCAGAGC-----CGGCATGAACTCTC---CCACCGAGTCGGGAGCCTGCCTA
Oa_HDAC5_v6(P)       CTGCAGGCCCAGAGC-----CGGCATGAACTCTC---CCACCGAGTCGGGAGCCTGCCTA
Oa_HDAC5_v5(P)       CTGCAGGCCCAGAGC-----CGGCATGAACTCTC---CCACCGAGTCGGGAGCCTGCCTA
Oa_HDAC5_v2(P)       CTGCAGGCCCAGAGC-----CGGCATGAACTCTC---CCACCGAGTCGGGAGCCTGCCTA
Oa_HDAC5_v4(P)       CTGCAGGCCCAGAGC-----CGGCATGAACTCTC---CCACCGAGTCGGGAGCCTGCCTA


Mm_HDAC5_v4          TTGCTGAGC----------------------------------------------------
Mm_HDAC5_v1          TTCCTGCAGG------CCC-AGAGCCGGCATGAACTCTCCCAACGAGTCGGCAGATGGCA
Mm_HDAC5_v3          ATGCTGC-AG------ACC-ATCTATGAGACCGA---GTCCTGTTTCTCAGCAGATGGCA
Mm_HDAC5_v5          TTCCTGCAGG------CCC-AGAGCCGGCATGAA---CTCTCCCAACGAGTCGGATGGCA
Hs_HDAC5_v1          ---------------------------------ACTCTCCCAACGAGTCG---GATGGGA
Hs_HDAC5_v3          ---------------------------------ACTCTCCCAACGAGTCGGCAGATGGGA
Bt_HDAC5_v1          GAGA--------TGCTGCAGACCATCTATGAAACGGAATCCTGTTTTTCAGCAGATGGGA
Bt_HDAC5_v5(P)       ----------------------------------------------------GATGGGA
Bt_HDAC5_v4(P)       ---------------------------------------------------AGATGGGA
Bt_HDAC5_v2          ---------------------------------------------------AGATGGGA
Bt_HDAC5_v3(P)       ---------------------------------------------------AGATGGGA
Oa_HDAC5_v11(P)      ----------------------------------------------------GATGGGA
Oa_HDAC5_v10(P)      ---------------------------------------------------CAGATGGGA
Oa_HDAC5_v8(P)       ---------------------------------------------------CAGATGGGA
Oa_HDAC5_v9(P)       ----------------------------------------------------GATGGGA
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       GTGCTGCCAGAAATAGTCTGTGGGTGGGACTCCAGGCAGCTTTGTGCACGGCAGATGGGA
Oa_HDAC5_v6(P)       GTGCTGCCAGAAATAGTCTGTGGGTGGGACTCCAGGCAGCTTTGTGCACGG---ATGGGA
Oa_HDAC5_v5(P)       GTGCTGCCAGAAATAGTCTGTGGGTGGGACTCCAGGCAGCTTTGTGCACGGCAGATGGGA
Oa_HDAC5_v2(P)       GTGCTGCCAGAAATAGTCTGTGGGTGGGACTCCAGGCAGCTTTGTGCACGGCAGATGGGA
Oa_HDAC5_v4(P)       GTGCTGCCAGAAATAGTCTGTGGGTGGGACTCCAGGCAGCTTTGTGCACG---GATGGGA
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```
Mm_HDAC5_v4          -------------------------TCCTGGGCCTTTTCCTTACTGACATTCTGAGGGTC
Mm_HDAC5_v1          TGTCAGGCCGGGAACCATCCTTGGAAATCCTGCCACGGACTCCTCTGCACAGCATCCCTG
Mm_HDAC5_v3          TGTCAGGCCGGGAACCATCCTTGGAAATCCTGCCACGGACTCCTCTGCACAGCATCCCTG
Mm_HDAC5_v5          TGTCAGGCCGGGAACCATCCTTGGAAATCCTGCCACGGACTCCTCTGCACAGCATCCCTG
Hs_HDAC5_v1          TGTCAGGTCGGGAACCATCCTTGGAAATCCTGCCGCGGACTTCTCTGCACAGCATCCCTG
Hs_HDAC5_v3          TGTCAGGTCGGGAACCATCCTTGGAAATCCTGCCGCGGACTTCTCTGCACAGCATCCCTG
Bt_HDAC5_v1          TGCCAGGCCGGGAACCAGCCTTGGAAATCCTGCCCCGGACCCCTCTGCACGGCATCCCCG
Bt_HDAC5_v5(P)       TGCCAGGCCGGGAACCAGCCTTGGAAATCCTGCCCCGGACCCCTCTGCACGGCATCCCCG
Bt_HDAC5_v4(P)       TGCCAGGCCGGGAACCAGCCTTGGAAATCCTGCCCCGGACCCCTCTGCACGGCATCCCCG
Bt_HDAC5_v2          TGCCAGGCCGGGAACCAGCCTTGGAAATCCTGCCCCGGACCCCTCTGCACGGCATCCCCG
Bt_HDAC5_v3(P)       TGCCAGGCCGGGAACCAGCCTTGGAAATCCTGCCCCGGACCCCTCTGCACGGCATCCCCG
Oa_HDAC5_v11(P)      TGCCAGGCCGGGAACCAGCCTTGGAAATCCTGCCCCGGACCCCTCTGCACGGCATCCCCG
Oa_HDAC5_v10(P)      TGCCAGGCCGGGAACCAGCCTTGGAAATCCTGCCCCGGACCCCTCTGCACGGCATCCCCG
Oa_HDAC5_v8(P)       TGCCAGGCCGGGAACCAGCCTTGGAAATCCTGCCCCGGACCCCTCTGCACGGCATCCCCG
Oa_HDAC5_v9(P)       TGCCAGGCCGGGAACCAGCCTTGGAAATCCTGCCCCGGACCCCTCTGCACGGCATCCCCG
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       TGCCAGGCCGGGAACCAGCCTTGGAAATCCTGCCCCGGACCCCTCTGCACGGCATCCCCG
Oa_HDAC5_v6(P)       TGCCAGGCCGGGAACCAGCCTTGGAAATCCTGCCCCGGACCCCTCTGCACGGCATCCCCG
Oa_HDAC5_v5(P)       TGCCAGGCCGGGAACCAGCCTTGGAAATCCTGCCCCGGACCCCTCTGCACGGCATCCCCG
Oa_HDAC5_v2(P)       TGCCAGGCCGGGAACCAGCCTTGGAAATCCTGCCCCGGACCCCTCTGCACGGCATCCCCG
Oa_HDAC5_v4(P)       TGCCAGGCCGGGAACCAGCCTTGGAAATCCTGCCCCGGACCCCTCTGCACGGCATCCCCG

Mm_HDAC5_v4          TCTGAGTGGAGGTGAAGCCGGTGCTGCCAGGAGCCATGCCCAGCTCCATGGGGGGTGGAG
Mm_HDAC5_v1          TGGCAGTGGAGGTGAAGCCGGTGCTGCCAGGAGCCATGCCCAGCTCCATGGGGGGTGGAG
Mm_HDAC5_v3          TGGCAGTGGAGGTGAAGCCGGTGCTGCCAGGAGCCATGCCCAGCTCCATGGGGGGTGGAG
Mm_HDAC5_v5          TGGCAGTGGAGGTGAAGCCGGTGCTGCCAGGAGCCATGCCCAGCTCCATGGGGGGTGGAG
Hs_HDAC5_v1          TGACAGTGGAGGTGAAGCCGGTGCTGCCAAGAGCCATGCCCAGTTCCATGGGGGGTGGGG
Hs_HDAC5_v3          TGACAGTGGAGGTGAAGCCGGTGCTGCCAAGAGCCATGCCCAGTTCCATGGGGGGTGGGG
Bt_HDAC5_v1          TGACAGTAGAGGTGAAACCGGTGCTGCCAGGAGCCATGCCCAGCTCCATGGGGGGCGGGG
Bt_HDAC5_v5(P)       TGACAGTAGAGGTGAAACCGGTGCTGCCAGGAGCCATGCCCAGCTCCATGGGGGGCGGGG
Bt_HDAC5_v4(P)       TGACAG---AGGTGAAACCGGTGCTGCCAGGAGCCATGCCCAGCTCCATGGGGGGCGGGG
Bt_HDAC5_v2          TGACAGTAGAGGTGAAACCGGTGCTGCCAGGAGCCATGCCCAGCTCCATGGGGGGCGGGG
Bt_HDAC5_v3(P)       TGACAGTAGAGGTGAAACCGGTGCTGCCAGGAGCCATGCCCAGCTCCATGGGGGGCGGGG
Oa_HDAC5_v11(P)      TGACAG---AGGTGAAACCGGTGCTGCCAGGAGCCATGCCCAGCTCCATGGGGGGCGGGG
Oa_HDAC5_v10(P)      TGACAG---AGGTGAAACCGGTGCTGCCAGGAGCCATGCCCAGCTCCATGGGGGGCGGGG
Oa_HDAC5_v8(P)       TGACAGTAGAGGTGAAACCGGTGCTGCCAGGAGCCATGCCCAGCTCCATGGGGGGCGGGG
Oa_HDAC5_v9(P)       TGACAGTAGAGGTGAAACCGGTGCTGCCAGGAGCCATGCCCAGCTCCATGGGGGGCGGGG
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       TGACAGTAGAGGTGAAACCGGTGCTGCCAGGAGCCATGCCCAGCTCCATGGGGGGCGGGG
Oa_HDAC5_v6(P)       TGACAG---AGGTGAAACCGGTGCTGCCAGGAGCCATGCCCAGCTCCATGGGGGGCGGGG
Oa_HDAC5_v5(P)       TGACAG---AGGTGAAACCGGTGCTGCCAGGAGCCATGCCCAGCTCCATGGGGGGCGGGG
Oa_HDAC5_v2(P)       TGACAGTAGAGGTGAAACCGGTGCTGCCAGGAGCCATGCCCAGCTCCATGGGGGGCGGGG
Oa_HDAC5_v4(P)       TGACAGTAGAGGTGAAACCGGTGCTGCCAGGAGCCATGCCCAGCTCCATGGGGGGCGGGG

Mm_HDAC5_v4          GTGGAGGTAGCCCCAGCCCCGTGGAGCTTCGGGGGGCTCTGGCGGGCCCCATGGACCCTG
Mm_HDAC5_v1          GTGGAGGTAGCCCCAGCCCCGTGGAGCTTCGGGGGGCTCTGGCGGGCCCCATGGACCCTG
Mm_HDAC5_v3          GTGGAGGTAGCCCCAGCCCCGTGGAGCTTCGGGGGGCTCTGGCGGGCCCCATGGACCCTG
Mm_HDAC5_v5          GTGGAGGTAGCCCCAGCCCCGTGGAGCTTCGGGGGGCTCTGGCGGGCCCCATGGACCCTG
Hs_HDAC5_v1          GTGGAGGCAGCCCCAGCCCTGTGGAGCTACGGGGGGCTCTGGTGGGCTCTGTGGACCCCA
Hs_HDAC5_v3          GTGGAGGCAGCCCCAGCCCTGTGGAGCTACGGGGGGCTCTGGTGGGCTCTGTGGACCCCA
Bt_HDAC5_v1          GAGGAGGCAGCCCCAGCCCCGTGGAGCTGCGGGGGGCTCTGGCAGGCCCTGTGGACCCCA
Bt_HDAC5_v5(P)       GAGGAGGCAGCCCCAGCCCCGTGGAGCTGCGGGGGGCTCTGGCAGGCCCTGTGGACCCCA
Bt_HDAC5_v4(P)       GAGGAGGCAGCCCCAGCCCCGTGGAGCTGCGGGGGGCTCTGGCAGGCCCTGTGGACCCCA
Bt_HDAC5_v2          GAGGAGGCAGCCCCAGCCCCGTGGAGCTGCGGGGGGCTCTGGCAGGCCCTGTGGACCCCA
Bt_HDAC5_v3(P)       GAGGAGGCAGCCCCAGCCCCGTGGAGCTGCGGGGGGCTCTGGCAGGCCCTGTGGACCCCA
Oa_HDAC5_v11(P)      GAGGAGGCAGCCCCAGCCCCGTGGAGCTGCGGGGGGCTCTGGCAGGCCCTGTGGACCCCG
Oa_HDAC5_v10(P)      GAGGAGGCAGCCCCAGCCCCGTGGAGCTGCGGGGGGCTCTGGCAGGCCCTGTGGACCCCG
Oa_HDAC5_v8(P)       GAGGAGGCAGCCCCAGCCCCGTGGAGCTGCGGGGGGCTCTGGCAGGCCCTGTGGACCCCG
Oa_HDAC5_v9(P)       GAGGAGGCAGCCCCAGCCCCGTGGAGCTGCGGGGGGCTCTGGCAGGCCCTGTGGACCCCG
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       GAGGAGGCAGCCCCAGCCCCGTGGAGCTGCGGGGGGCTCTGGCAGGCCCTGTGGACCCCG
Oa_HDAC5_v6(P)       GAGGAGGCAGCCCCAGCCCCGTGGAGCTGCGGGGGGCTCTGGCAGGCCCTGTGGACCCCG
Oa_HDAC5_v5(P)       GAGGAGGCAGCCCCAGCCCCGTGGAGCTGCGGGGGGCTCTGGCAGGCCCTGTGGACCCCG
Oa_HDAC5_v2(P)       GAGGAGGCAGCCCCAGCCCCGTGGAGCTGCGGGGGGCTCTGGCAGGCCCTGTGGACCCCG
Oa_HDAC5_v4(P)       GAGGAGGCAGCCCCAGCCCCGTGGAGCTGCGGGGGGCTCTGGCAGGCCCTGTGGACCCCG
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Mm_HDAC5_v4          CGCTACGGGAGCAGCAACTGCAGCAGGAGCTCCTGGTCCTCAAGCAGCAGCAGCAGCTCC
Mm_HDAC5_v1          CGCTACGGGAGCAGCAACTGCAGCAGGAGCTCCTGGTCCTCAAGCAGCAGCAGCAGCTCC
Mm_HDAC5_v3          CGCTACGGGAGCAGCAACTGCAGCAGGAGCTCCTGGTCCTCAAGCAGCAGCAGCAGCTCC
Mm_HDAC5_v5          CGCTACGGGAGCAGCAACTGCAGCAGGAGCTCCTGGTCCTCAAGCAGCAGCAGCAGCTCC
Hs_HDAC5_v1          CACTGCGGGAGCAGCAACTGCAGCAGGAGCTCCTGGCGCTCAAGCAGCAGCAGCAGCTGC
Hs_HDAC5_v3          CACTGCGGGAGCAGCAACTGCAGCAGGAGCTCCTGGCGCTCAAGCAGCAGCAGCAGCTGC
Bt_HDAC5_v1          CGCTGCGGGAGCAGCAACTGCAGCAGGAGCTCCTGGCACTCAAGCAGCAGCAGCAACTGC
Bt_HDAC5_v5(P)       CGCTGCGGGAGCAGCAACTGCAGCAGGAGCTCCTGGCACTCAAGCAGCAGCAGCAACTGC
Bt_HDAC5_v4(P)       CGCTGCGGGAGCAGCAACTGCAGCAGGAGCTCCTGGCACTCAAGCAGCAGCAGCAACTGC
Bt_HDAC5_v2          CGCTGCGGGAGCAGCAACTGCAGCAGGAGCTCCTGGCACTCAAGCAGCAGCAGCAACTGC
Bt_HDAC5_v3(P)       CGCTGCGGGAGCAGCAACTGCAGCAGGAGCTCCTGGCACTCAAGCAGCAGCAGCAACTGC
Oa_HDAC5_v11(P)      CACTGCGGGAGCAGCAACTGCAGCAGGAGCTCCTGGCGCTCAAGCAGCAACAGCAATTGC
Oa_HDAC5_v10(P)      CACTGCGGGAGCAGCAACTGCAGCAGGAGCTCCTGGCGCTCAAGCAGCAACAGCAATTGC
Oa_HDAC5_v8(P)       CACTGCGGGAGCAGCAACTGCAGCAGGAGCTCCTGGCGCTCAAGCAGCAACAGCAATTGC
Oa_HDAC5_v9(P)       CACTGCGGGAGCAGCAACTGCAGCAGGAGCTCCTGGCGCTCAAGCAGCAACAGCAATTGC
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       CACTGCGGGAGCAGCAACTGCAGCAGGAGCTCCTGGCGCTCAAGCAGCAACAGCAATTGC
Oa_HDAC5_v6(P)       CACTGCGGGAGCAGCAACTGCAGCAGGAGCTCCTGGCGCTCAAGCAGCAACAGCAATTGC
Oa_HDAC5_v5(P)       CACTGCGGGAGCAGCAACTGCAGCAGGAGCTCCTGGCGCTCAAGCAGCAACAGCAATTGC
Oa_HDAC5_v2(P)       CACTGCGGGAGCAGCAACTGCAGCAGGAGCTCCTGGCGCTCAAGCAGCAACAGCAATTGC
Oa_HDAC5_v4(P)       CACTGCGGGAGCAGCAACTGCAGCAGGAGCTCCTGGCGCTCAAGCAGCAACAGCAATTGC

Mm_HDAC5_v4          AGAAGCAGCTCCTGTTCGCCGAGTTCCAGAAGCAGCACGACCACTTGACGCGGCAGCACG
Mm_HDAC5_v1          AGAAGCAGCTCCTGTTCGCCGAGTTCCAGAAGCAGCACGACCACTTGACGCGGCAGCACG
Mm_HDAC5_v3          AGAAGCAGCTCCTGTTCGCCGAGTTCCAGAAGCAGCACGACCACTTGACGCGGCAGCACG
Mm_HDAC5_v5          AGAAGCAGCTCCTGTTCGCCGAGTTCCAGAAGCAGCACGACCACTTGACGCGGCAGCACG
Hs_HDAC5_v1          AGAAGCAGCTCCTGTTCGCTGAGTTCCAGAAACAGCATGACCACCTGACAAGGCAGCATG
Hs_HDAC5_v3          AGAAGCAGCTCCTGTTCGCTGAGTTCCAGAAACAGCATGACCACCTGACAAGGCAGCATG
Bt_HDAC5_v1          AGAAGCAGCTTCTGTTCGCTGAGTTCCAGAAGCAGCATGACCACCTGACCCGGCAGCATG
Bt_HDAC5_v5(P)       AGAAGCAGCTTCTGTTCGCTGAGTTCCAGAAGCAGCATGACCACCTGACCCGGCAGCATG
Bt_HDAC5_v4(P)       AGAAGCAGCTTCTGTTCGCTGAGTTCCAGAAGCAGCATGACCACCTGACCCGGCAGCATG
Bt_HDAC5_v2          AGAAGCAGCTTCTGTTCGCTGAGTTCCAGAAGCAGCATGACCACCTGACCCGGCAGCATG
Bt_HDAC5_v3(P)       AGAAGCAGCTTCTGTTCGCTGAGTTCCAGAAGCAGCATGACCACCTGACCCGGCAGCATG
Oa_HDAC5_v11(P)      AGAAGCAGCTTCTGTTCGCTGAGTTTCAGAAACAGCATGACCACCTGACCCGGCAGCATG
Oa_HDAC5_v10(P)      AGAAGCAGCTTCTGTTCGCTGAGTTTCAGAAACAGCATGACCACCTGACCCGGCAGCATG
Oa_HDAC5_v8(P)       AGAAGCAGCTTCTGTTCGCTGAGTTTCAGAAACAGCATGACCACCTGACCCGGCAGCATG
Oa_HDAC5_v9(P)       AGAAGCAGCTTCTGTTCGCTGAGTTTCAGAAACAGCATGACCACCTGACCCGGCAGCATG
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       AGAAGCAGCTTCTGTTCGCTGAGTTTCAGAAACAGCATGACCACCTGACCCGGCAGCATG
Oa_HDAC5_v6(P)       AGAAGCAGCTTCTGTTCGCTGAGTTTCAGAAACAGCATGACCACCTGACCCGGCAGCATG
Oa_HDAC5_v5(P)       AGAAGCAGCTTCTGTTCGCTGAGTTTCAGAAACAGCATGACCACCTGACCCGGCAGCATG
Oa_HDAC5_v2(P)       AGAAGCAGCTTCTGTTCGCTGAGTTTCAGAAACAGCATGACCACCTGACCCGGCAGCATG
Oa_HDAC5_v4(P)       AGAAGCAGCTTCTGTTCGCTGAGTTTCAGAAACAGCATGACCACCTGACCCGGCAGCATG

Mm_HDAC5_v4          AGGTCCAGCTGCAGAAGCACCTCAAGCAGCAGCAGGAGATGCTGGCGGC-----------
Mm_HDAC5_v1          AGGTCCAGCTGCAGAAGCACCTCAAGCAGCAGCAGGAGATGCTGGCGGC-----------
Mm_HDAC5_v3          AGGTCCAGCTGCAGAAGCACCTCAAGCAGCAGCAGGAGATGCTGGCGGC-----------
Mm_HDAC5_v5          AGGTCCAGCTGCAGAAGCACCTCAAGCAGCAGCAGGAGATGCTGGCGGC-----------
Hs_HDAC5_v1          AGGTCCAGCTGCAGAAGCACCTCAAGCAGCAGCAGGAGATGCTGGCAGCCAAGCAGCAGC
Hs_HDAC5_v3          AGGTCCAGCTGCAGAAGCACCTCAAGCAGCAGCAGGAGATGCTGGCAGCCAAGCAGCAGC
Bt_HDAC5_v1          AAGTCCAGCTGCAGAAGCACCTCAAGCAGCAGCAGGAGATGCTGGCAGC-----------
Bt_HDAC5_v5(P)       AAGTCCAGCTGCAGAAGCACCTCAAGCAGCAGCAGGAGATGCTGGCAGC-----------
Bt_HDAC5_v4(P)       AAGTCCAGCTGCAGAAGCACCTCAAGCAGCAGCAGGAGATGCTGGCAGC-----------
Bt_HDAC5_v2          AAGTCCAGCTGCAGAAGCACCTCAAGCAGCAGCAGGAGATGCTGGCAGC-----------
Bt_HDAC5_v3(P)       AAGTCCAGCTGCAGAAGCACCTCAAGCAGCAGCAGGAGATGCTGGCAGC-----------
Oa_HDAC5_v11(P)      AAGTCCAGCTGCAGAAGCACCTCAAGCAGCAGCAGGAGATGCTGGCAGC-----------
Oa_HDAC5_v10(P)      AAGTCCAGCTGCAGAAGCACCTCAAGCAGCAGCAGGAGATGCTGGCAGC-----------
Oa_HDAC5_v8(P)       AAGTCCAGCTGCAGAAGCACCTCAAGCAGCAGCAGGAGATGCTGGCAGC-----------
Oa_HDAC5_v9(P)       AAGTCCAGCTGCAGAAGCACCTCAAGCAGCAGCAGGAGATGCTGGCAGC-----------
Oa_HDAC5_v1(P)       ---------------------------------------------GCA-----------
Oa_HDAC5_v7(P)       AAGTCCAGCTGCAGAAGCACCTCAAGCAGCAGCAGGAGATGCTGGCAGC-----------
Oa_HDAC5_v6(P)       AAGTCCAGCTGCAGAAGCACCTCAAGCAGCAGCAGGAGATGCTGGCAGC-----------
Oa_HDAC5_v5(P)       AAGTCCAGCTGCAGAAGCACCTCAAGCAGCAGCAGGAGATGCTGGCAGC-----------
Oa_HDAC5_v2(P)       AAGTCCAGCTGCAGAAGCACCTCAAGCAGCAGCAGGAGATGCTGGCAGC-----------
Oa_HDAC5_v4(P)       AAGTCCAGCTGCAGAAGCACCTCAAGCAGCAGCAGGAGATGCTGGCAGC-----------
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Mm_HDAC5_v4          ----------------TAAGAGGCAGCAGGAGCTGGAGCAGCAGCGGCAGCGGGAGCAGC
Mm_HDAC5_v1          ----------------TAAGAGGCAGCAGGAGCTGGAGCAGCAGCGGCAGCGGGAGCAGC
Mm_HDAC5_v3          ----------------TAAGAGGCAGCAGGAGCTGGAGCAGCAGCGGCAGCGGGAGCAGC
Mm_HDAC5_v5          ----------------TAAGAGGCAGCAGGAGCTGGAGCAGCAGCGGCAGCGGGAGCAGC
Hs_HDAC5_v1          AGGAGATGCTGGCAGCCAAGCGGCAGCAGGAGCTGGAGCAGCAGCGGCAGCGGGAGCAGC
Hs_HDAC5_v3          AGGAGATGCTGGCAGCCAAGCGGCAGCAGGAGCTGGAGCAGCAGCGGCAGCGGGAGCAGC
Bt_HDAC5_v1          ----------------CAAGAGGCAGCAGGAGCTGGAGCAGCAGCGGCAGCGGGAGCAGC
Bt_HDAC5_v5(P)       ----------------CAAGAGGCAGCAGGAGCTGGAGCAGCAGCGGCAGCGGGAGCAGC
Bt_HDAC5_v4(P)       ----------------CAAGAGGCAGCAGGAGCTGGAGCAGCAGCGGCAGCGGGAGCAGC
Bt_HDAC5_v2          ----------------CAAGAGGCAGCAGGAGCTGGAGCAGCAGCGGCAGCGGGAGCAGC
Bt_HDAC5_v3(P)       ----------------CAAGAGGCAGCAGGAGCTGGAGCAGCAGCGGCAGCGGGAGCAGC
Oa_HDAC5_v11(P)      ----------------CAAGAGGCAGCAGGAGCTGGAGCAGCAGCGGCAGCGGGAGCAGC
Oa_HDAC5_v10(P)      ----------------CAAGAGGCAGCAGGAGCTGGAGCAGCAGCGGCAGCGGGAGCAGC
Oa_HDAC5_v8(P)       ----------------CAAGAGGCAGCAGGAGCTGGAGCAGCAGCGGCAGCGGGAGCAGC
Oa_HDAC5_v9(P)       ----------------CAAGAGGCAGCAGGAGCTGGAGCAGCAGCGGCAGCGGGAGCAGC
Oa_HDAC5_v1(P)       ----------------GGAGATGCGGCAGGAGCTGGAGCAGCAGCGGCAGCGGGAGCAGC
Oa_HDAC5_v7(P)       ----------------CAAGAGGCAGCAGGAGCTGGAGCAGCAGCGGCAGCGGGAGCAGC
Oa_HDAC5_v6(P)       ----------------CAAGAGGCAGCAGGAGCTGGAGCAGCAGCGGCAGCGGGAGCAGC
Oa_HDAC5_v5(P)       ----------------CAAGAGGCAGCAGGAGCTGGAGCAGCAGCGGCAGCGGGAGCAGC
Oa_HDAC5_v2(P)       ----------------CAAGAGGCAGCAGGAGCTGGAGCAGCAGCGGCAGCGGGAGCAGC
Oa_HDAC5_v4(P)       ----------------CAAGAGGCAGCAGGAGCTGGAGCAGCAGCGGCAGCGGGAGCAGC
                                     **  ** **********************************

Mm_HDAC5_v4          AGCGGCAGGAGGAGCTGGAGAAACAGCGGCTGGAGCAGCAGCTGCTCATCCTGCGCAACA
Mm_HDAC5_v1          AGCGGCAGGAGGAGCTGGAGAAACAGCGGCTGGAGCAGCAGCTGCTCATCCTGCGCAACA
Mm_HDAC5_v3          AGCGGCAGGAGGAGCTGGAGAAACAGCGGCTGGAGCAGCAGCTGCTCATCCTGCGCAACA
Mm_HDAC5_v5          AGCGGCAGGAGGAGCTGGAGAAACAGCGGCTGGAGCAGCAGCTGCTCATCCTGCGCAACA
Hs_HDAC5_v1          AGCGGCAGGAAGAGCTGGAGAAGCAGCGGCTGGAGCAGCAGCTGCTCATCCTGCGGAACA
Hs_HDAC5_v3          AGCGGCAGGAAGAGCTGGAGAAGCAGCGGCTGGAGCAGCAGCTGCTCATCCTGCGGAACA
Bt_HDAC5_v1          AGCGGCAGGAGGAGCTGGAGAAGCAGCGGCTCGAGCAGCAGCTGCTCATCCTTCGAAACA
Bt_HDAC5_v5(P)       AGCGGCAGGAGGAGCTGGAGAAGCAGCGGCTCGAGCAGCAGCTGCTCATCCTTCGAAACA
Bt_HDAC5_v4(P)       AGCGGCAGGAGGAGCTGGAGAAGCAGCGGCTCGAGCAGCAGCTGCTCATCCTTCGAAACA
Bt_HDAC5_v2          AGCGGCAGGAGGAGCTGGAGAAGCAGCGGCTCGAGCAGCAGCTGCTCATCCTTCGAAACA
Bt_HDAC5_v3(P)       AGCGGCAGGAGGAGCTGGAGAAGCAGCGGCTCGAGCAGCAGCTGCTCATCCTTCGAAACA
Oa_HDAC5_v11(P)      AGCGGCAGGAGGAGCTGGAGAAGCAGCGGCTCGAGCAGCAGCTGCTCATCCTTCGAAACA
Oa_HDAC5_v10(P)      AGCGGCAGGAGGAGCTGGAGAAGCAGCGGCTCGAGCAGCAGCTGCTCATCCTTCGAAACA
Oa_HDAC5_v8(P)       AGCGGCAGGAGGAGCTGGAGAAGCAGCGGCTCGAGCAGCAGCTGCTCATCCTTCGAAACA
Oa_HDAC5_v9(P)       AGCGGCAGGAGGAGCTGGAGAAGCAGCGGCTCGAGCAGCAGCTGCTCATCCTTCGAAACA
Oa_HDAC5_v1(P)       AGCGGCAGGAGGAGCTGGAGAAGCAGCGGCTCGAGCAGCAGCTGCTCATCCTTCGAAACA
Oa_HDAC5_v7(P)       AGCGGCAGGAGGAGCTGGAGAAGCAGCGGCTCGAGCAGCAGCTGCTCATCCTTCGAAACA
Oa_HDAC5_v6(P)       AGCGGCAGGAGGAGCTGGAGAAGCAGCGGCTCGAGCAGCAGCTGCTCATCCTTCGAAACA
Oa_HDAC5_v5(P)       AGCGGCAGGAGGAGCTGGAGAAGCAGCGGCTCGAGCAGCAGCTGCTCATCCTTCGAAACA
Oa_HDAC5_v2(P)       AGCGGCAGGAGGAGCTGGAGAAGCAGCGGCTCGAGCAGCAGCTGCTCATCCTTCGAAACA
Oa_HDAC5_v4(P)       AGCGGCAGGAGGAGCTGGAGAAGCAGCGGCTCGAGCAGCAGCTGCTCATCCTTCGAAACA
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Mm_HDAC5_v4          AGGAGAAGAGCAAAGAGAGTGCCATCGCCAGCACCGAGGTAAAGCTGAGGCTCCAGGAAT
Mm_HDAC5_v1          AGGAGAAGAGCAAAGAGAGTGCCATCGCCAGCACCGAGGTAAAGCTGAGGCTCCAGGAAT
Mm_HDAC5_v3          AGGAGAAGAGCAAAGAGAGTGCCATCGCCAGCACCGAGGTAAAGCTGAGGCTCCAGGAAT
Mm_HDAC5_v5          AGGAGAAGAGCAAAGAGAGTGCCATCGCCAGCACCGAGGTAAAGCTGAGGCTCCAGGAAT
Hs_HDAC5_v1          AGGAGAAGAGCAAAGAGAGTGCCATTGCCAGCACTGAGGTAAAGCTGAGGCTCCAGGAAT
Hs_HDAC5_v3          AGGAGAAGAGCAAAGAGAGTGCCATTGCCAGCACTGAGGTAAAGCTGAGGCTCCAGGAAT
Bt_HDAC5_v1          AGGAGAAGAGCAAAGAGAGTGCCATCGCCAGCACTGAGGTGAAGCTACGGCTCCAGGAAT
Bt_HDAC5_v5(P)       AGGAGAAGAGCAAAGAGAGTGCCATCGCCAGCACTGAGGTGAAGCTACGGCTCCAGGAAT
Bt_HDAC5_v4(P)       AGGAGAAGAGCAAAGAGAGTGCCATCGCCAGCACTGAGGTGAAGCTACGGCTCCAGGAAT
Bt_HDAC5_v2          AGGAGAAGAGCAAAGAGAGTGCCATCGCCAGCACTGAGGTGAAGCTACGGCTCCAGGAAT
Bt_HDAC5_v3(P)       AGGAGAAGAGCAAAGAGAGTGCCATCGCCAGCACTGAGGTGAAGCTACGGCTCCAGGAAT
Oa_HDAC5_v11(P)      AGGAGAAGAGCAAAGAGAGTGCCATCGCCAGCACTGAGGTGAAGCTACGGCTCCAGGAAT
Oa_HDAC5_v10(P)      AGGAGAAGAGCAAAGAGAGTGCCATCGCCAGCACTGAGGTGAAGCTACGGCTCCAGGAAT
Oa_HDAC5_v8(P)       AGGAGAAGAGCAAAGAGAGTGCCATCGCCAGCACTGAGGTGAAGCTACGGCTCCAGGAAT
Oa_HDAC5_v9(P)       AGGAGAAGAGCAAAGAGAGTGCCATCGCCAGCACTGAGGTGAAGCTACGGCTCCAGGAAT
Oa_HDAC5_v1(P)       AGGAGAAGAGCAAAGAGAGTGCCATCGCCAGCACTGAGGTGAAGCTACGGCTCCAGGAAT
Oa_HDAC5_v7(P)       AGGAGAAGAGCAAAGAGAGTGCCATCGCCAGCACTGAGGTGAAGCTACGGCTCCAGGAAT
Oa_HDAC5_v6(P)       AGGAGAAGAGCAAAGAGAGTGCCATCGCCAGCACTGAGGTGAAGCTACGGCTCCAGGAAT
Oa_HDAC5_v5(P)       AGGAGAAGAGCAAAGAGAGTGCCATCGCCAGCACTGAGGTGAAGCTACGGCTCCAGGAAT
Oa_HDAC5_v2(P)       AGGAGAAGAGCAAAGAGAGTGCCATCGCCAGCACTGAGGTGAAGCTACGGCTCCAGGAAT
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Oa_HDAC5_v4(P)      AGGAGAAGAGCAAAGAGAGTGCCATCGCCAGCACTGAGGTGAAGCTACGGCTCCAGGAAT
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Mm_HDAC5_v4         TCCTGTTGTCCAAGTCAAAGGAGCCCACGCCAGGCGGCCTCAACCATTCCCTCCCACAGC
Mm_HDAC5_v1         TCCTGTTGTCCAAGTCAAAGGAGCCCACGCCAGGCGGCCTCAACCATTCCCTCCCACAGC
Mm_HDAC5_v3         TCCTGTTGTCCAAGTCAAAGGAGCCCACGCCAGGCGGCCTCAACCATTCCCTCCCACAGC
Mm_HDAC5_v5         TCCTGTTGTCCAAGTCAAAGGAGCCCACGCCAGGCGGCCTCAACCATTCCCTCCCACAGC
Hs_HDAC5_v1         TCCTCTTGTCGAAGTCAAAGGAGCCCACACCAGGCGGCCTCAACCATTCCCTCCCACAGC
Hs_HDAC5_v3         TCCTCTTGTCGAAGTCAAAGGAGCCCACACCAGGCGGCCTCAACCATTCCCTCCCACAGC
Bt_HDAC5_v1         TCCTCCTGTCGAAGTCAAAGGAGCCCACACCAGGCGGCCTCAACCATTCCCTCCCACAGC
Bt_HDAC5_v5(P)      TCCTCCTGTCGAAGTCAAAGGAGCCCACACCAGGCGGCCTCAACCATTCCCTCCCACAGC
Bt_HDAC5_v4(P)      TCCTCCTGTCGAAGTCAAAGGAGCCCACACCAGGCGGCCTCAACCATTCCCTCCCACAGC
Bt_HDAC5_v2         TCCTCCTGTCGAAGTCAAAGGAGCCCACACCAGGCGGCCTCAACCATTCCCTCCCACAGC
Bt_HDAC5_v3(P)      TCCTCCTGTCGAAGTCAAAGGAGCCCACACCAGGCGGCCTCAACCATTCCCTCCCACAGC
Oa_HDAC5_v11(P)     TCCTCCTGTCGAAGTCAAAGGAGCCCACACCAGGCGGCCTCAACCATTCCCTCCCACAGC
Oa_HDAC5_v10(P)     TCCTCCTGTCGAAGTCAAAGGAGCCCACACCAGGCGGCCTCAACCATTCCCTCCCACAGC
Oa_HDAC5_v8(P)      TCCTCCTGTCGAAGTCAAAGGAGCCCACACCAGGCGGCCTCAACCATTCCCTCCCACAGC
Oa_HDAC5_v9(P)      TCCTCCTGTCGAAGTCAAAGGAGCCCACACCAGGCGGCCTCAACCATTCCCTCCCACAGC
Oa_HDAC5_v1(P)      TCCTCCTGTCGAAGTCAAAGGAGCCCACACCAGGCGGCCTCAACCATTCCCTCCCACAGC
Oa_HDAC5_v7(P)      TCCTCCTGTCGAAGTCAAAGGAGCCCACACCAGGCGGCCTCAACCATTCCCTCCCACAGC
Oa_HDAC5_v6(P)      TCCTCCTGTCGAAGTCAAAGGAGCCCACACCAGGCGGCCTCAACCATTCCCTCCCACAGC
Oa_HDAC5_v5(P)      TCCTCCTGTCGAAGTCAAAGGAGCCCACACCAGGCGGCCTCAACCATTCCCTCCCACAGC
Oa_HDAC5_v2(P)      TCCTCCTGTCGAAGTCAAAGGAGCCCACACCAGGCGGCCTCAACCATTCCCTCCCACAGC
Oa_HDAC5_v4(P)      TCCTCCTGTCGAAGTCAAAGGAGCCCACACCAGGCGGCCTCAACCATTCCCTCCCACAGC
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Mm_HDAC5_v4         ACCCCAAATGCTGGGGAGCCCACCACGCTTCTTTGGACCAGAGTTCCCCTCCCCAGAGCG
Mm_HDAC5_v1         ACCCCAAATGCTGGGGAGCCCACCACGCTTCTTTGGACCAGAGTTCCCCTCCCCAGAGCG
Mm_HDAC5_v3         ACCCCAAATGCTGGGGAGCCCACCACGCTTCTTTGGACCAGAGTTCCCCTCCCCAGAGCG
Mm_HDAC5_v5         ACCCCAAATGCTGGGGAGCCCACCACGCTTCTTTGGACCAGAGTTCCCCTCCCCAGAGCG
Hs_HDAC5_v1         ACCCCAAATGCTGGGGAGCCCACCATGCTTCTTTGGACCAGAGTTCCCCTCCCCAGAGCG
Hs_HDAC5_v3         ACCCCAAATGCTGGGGAGCCCACCATGCTTCTTTGGACCAGAGTTCCCCTCCCCAGAGCG
Bt_HDAC5_v1         ATCCCAAATGCTGGGGAACCCACCATGCTTCTTTGGACCAGAGTTCCCCTCCCCAGAGCG
Bt_HDAC5_v5(P)      ATCCCAAATGCTGGGGAACCCACCATGCTTCTTTGGACCAGAGTTCCCCTCCCCAGAGCG
Bt_HDAC5_v4(P)      ATCCCAAATGCTGGGGAACCCACCATGCTTCTTTGGACCAGAGTTCCCCTCCCCAGAGCG
Bt_HDAC5_v2         ATCCCAAATGCTGGGGAACCCACCATGCTTCTTTGGACCAGAGTTCCCCTCCCCAGAGCG
Bt_HDAC5_v3(P)      ATCCCAAATGCTGGGGAACCCACCATGCTTCTTTGGACCAGAGTTCCCCTCCCCAGAGCG
Oa_HDAC5_v11(P)     ATCCTAAATGCTGGGGAACCCACCATGCTTCTTTGGACCAGAGTTCCCCTCCCCAGAGCG
Oa_HDAC5_v10(P)     ATCCTAAATGCTGGGGAACCCACCATGCTTCTTTGGACCAGAGTTCCCCTCCCCAGAGCG
Oa_HDAC5_v8(P)      ATCCTAAATGCTGGGGAACCCACCATGCTTCTTTGGACCAGAGTTCCCCTCCCCAGAGCG
Oa_HDAC5_v9(P)      ATCCTAAATGCTGGGGAACCCACCATGCTTCTTTGGACCAGAGTTCCCCTCCCCAGAGCG
Oa_HDAC5_v1(P)      ATCCTAAATGCTGGGGAACCCACCATGCTTCTTTGGACCAGAGTTCCCCTCCCCAGAGCG
Oa_HDAC5_v7(P)      ATCCTAAATGCTGGGGAACCCACCATGCTTCTTTGGACCAGAGTTCCCCTCCCCAGAGCG
Oa_HDAC5_v6(P)      ATCCTAAATGCTGGGGAACCCACCATGCTTCTTTGGACCAGAGTTCCCCTCCCCAGAGCG
Oa_HDAC5_v5(P)      ATCCTAAATGCTGGGGAACCCACCATGCTTCTTTGGACCAGAGTTCCCCTCCCCAGAGCG
Oa_HDAC5_v2(P)      ATCCTAAATGCTGGGGAACCCACCATGCTTCTTTGGACCAGAGTTCCCCTCCCCAGAGCG
Oa_HDAC5_v4(P)      ATCCTAAATGCTGGGGAACCCACCATGCTTCTTTGGACCAGAGTTCCCCTCCCCAGAGCG
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Mm_HDAC5_v4         GCCCTCCTGGGACGCCTCCCTCCTACAAATTGCCTTTGCTTGGGCCCTATGACAGCCGTG
Mm_HDAC5_v1         GCCCTCCTGGGACGCCTCCCTCCTACAAATTGCCTTTGCTTGGGCCCTATGACAGCCGTG
Mm_HDAC5_v3         GCCCTCCTGGGACGCCTCCCTCCTACAAATTGCCTTTGCTTGGGCCCTATGACAGCCGTG
Mm_HDAC5_v5         GCCCTCCTGGGACGCCTCCCTCCTACAAATTGCCTTTGCTTGGGCCCTATGACAGCCGTG
Hs_HDAC5_v1         GCCCCCCTGGGACGCCTCCCTCCTACAAACTGCCTTTGCCTGGGCCCTACGACAGTCGAG
Hs_HDAC5_v3         GCCCCCCTGGGACGCCTCCCTCCTACAAACTGCCTTTGCCTGGGCCCTACGACAGTCGAG
Bt_HDAC5_v1         GCCCCCCTGGGACGCCTTCCTCCTACAAACTGCCTTTGCTTGGGCCCTACGACAGCCGCG
Bt_HDAC5_v5(P)      GCCCCCCTGGGACGCCTTCCTCCTACAAACTGCCTTTGCTTGGGCCCTACGACAGCCGCG
Bt_HDAC5_v4(P)      GCCCCCCTGGGACGCCTTCCTCCTACAAACTGCCTTTGCTTGGGCCCTACGACAGCCGCG
Bt_HDAC5_v2         GCCCCCCTGGGACGCCTTCCTCCTACAAACTGCCTTTGCTTGGGCCCTACGACAGCCGCG
Bt_HDAC5_v3(P)      GCCCCCCTGGGACGCCTTCCTCCTACAAACTGCCTTTGCTTGGGCCCTACGACAGCCGCG
Oa_HDAC5_v11(P)     GCCCCCCTGGGACGCCTCCCTCCTACAAACTGCCTTTGCTTGGGCCCTATGACAGCCGCG
Oa_HDAC5_v10(P)     GCCCCCCTGGGACGCCTCCCTCCTACAAACTGCCTTTGCTTGGGCCCTATGACAGCCGCG
Oa_HDAC5_v8(P)      GCCCCCCTGGGACGCCTCCCTCCTACAAACTGCCTTTGCTTGGGCCCTATGACAGCCGCG
Oa_HDAC5_v9(P)      GCCCCCCTGGGACGCCTCCCTCCTACAAACTGCCTTTGCTTGGGCCCTATGACAGCCGCG
Oa_HDAC5_v1(P)      GCCCCCCTGGGACGCCTCCCTCCTACAAACTGCCTTTGCTTGGGCCCTATGACAGCCGCG
Oa_HDAC5_v7(P)      GCCCCCCTGGGACGCCTCCCTCCTACAAACTGCCTTTGCTTGGGCCCTATGACAGCCGCG
Oa_HDAC5_v6(P)      GCCCCCCTGGGACGCCTCCCTCCTACAAACTGCCTTTGCTTGGGCCCTATGACAGCCGCG
Oa_HDAC5_v5(P)      GCCCCCCTGGGACGCCTCCCTCCTACAAACTGCCTTTGCTTGGGCCCTATGACAGCCGCG
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Oa_HDAC5_v2(P)      GCCCCCCTGGGACGCCTCCCTCCTACAAACTGCCTTTGCTTGGGCCCTATGACAGCCGCG
Oa_HDAC5_v4(P)      GCCCCCCTGGGACGCCTCCCTCCTACAAACTGCCTTTGCTTGGGCCCTATGACAGCCGCG
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Mm_HDAC5_v4         ATGACTTTCCCCTCCGTAAAACGGCCTCGGAACCCAACTTAAAAGTACGTTCGAGGCTAA
Mm_HDAC5_v1         ATGACTTTCCCCTCCGTAAAACGGCCTCGGAACCCAACTTAAAAGTACGTTCGAGGCTAA
Mm_HDAC5_v3         ATGACTTTCCCCTCCGTAAAACGGCCTCGGAACCCAACTTAAAAGTACGTTCGAGGCTAA
Mm_HDAC5_v5         ATGACTTTCCCCTCCGTAAAACGGCCTCGGAACCCAACTTAAAAGTACGTTCGAGGCTAA
Hs_HDAC5_v1         ACGACTTCCCCCTCCGCAAAACAGCCTCTGAACCCAACTTGAAAGTGCGTTCAAGGCTAA
Hs_HDAC5_v3         ACGACTTCCCCCTCCGCAAAACAGCCTCTGAACCCAACTTGAAAGTGCGTTCAAGGCTAA
Bt_HDAC5_v1         ATGACTTCCCCCTCCGCAAAACAGCCTCCGAACCCAACTTAAAAGTACGTTCGAGGCTAA
Bt_HDAC5_v5(P)      ATGACTTCCCCCTCCGCAAAACAGCCTCCGAACCCAACTTAAAAGTACGTTCGAGGCTAA
Bt_HDAC5_v4(P)      ATGACTTCCCCCTCCGCAAAACAGCCTCCGAACCCAACTTAAAAGTACGTTCGAGGCTAA
Bt_HDAC5_v2         ATGACTTCCCCCTCCGCAAAACAGCCTCCGAACCCAACTTAAAAGTACGTTCGAGGCTAA
Bt_HDAC5_v3(P)      ATGACTTCCCCCTCCGCAAAACAGCCTCCGAACCCAACTTAAAAGTACGTTCGAGGCTAA
Oa_HDAC5_v11(P)     ATGACTTCCCCCTCCGCAAAACAGCCTCCGAACCCAACTTAAAAGTACGTTCGAGGCTAA
Oa_HDAC5_v10(P)     ATGACTTCCCCCTCCGCAAAACAGCCTCCGAACCCAACTTAAAAGTACGTTCGAGGCTAA
Oa_HDAC5_v8(P)      ATGACTTCCCCCTCCGCAAAACAGCCTCCGAACCCAACTTAAAAGTACGTTCGAGGCTAA
Oa_HDAC5_v9(P)      ATGACTTCCCCCTCCGCAAAACAGCCTCCGAACCCAACTTAAAAGTACGTTCGAGGCTAA
Oa_HDAC5_v1(P)      ATGACTTCCCCCTCCGCAAAACAGCCTCCGAACCCAACTTAAAAGTACGTTCGAGGCTAA
Oa_HDAC5_v7(P)      ATGACTTCCCCCTCCGCAAAACAGCCTCCGAACCCAACTTAAAAGTACGTTCGAGGCTAA
Oa_HDAC5_v6(P)      ATGACTTCCCCCTCCGCAAAACAGCCTCCGAACCCAACTTAAAAGTACGTTCGAGGCTAA
Oa_HDAC5_v5(P)      ATGACTTCCCCCTCCGCAAAACAGCCTCCGAACCCAACTTAAAAGTACGTTCGAGGCTAA
Oa_HDAC5_v2(P)      ATGACTTCCCCCTCCGCAAAACAGCCTCCGAACCCAACTTAAAAGTACGTTCGAGGCTAA
Oa_HDAC5_v4(P)      ATGACTTCCCCCTCCGCAAAACAGCCTCCGAACCCAACTTAAAAGTACGTTCGAGGCTAA
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Mm_HDAC5_v4         AACAGAAGGTAGCCGAGAGGAGAAGCAGTCCCCTCCTGCGTCGAAAGGATGGCACTGTTA
Mm_HDAC5_v1         AACAGAAGGTAGCCGAGAGGAGAAGCAGTCCCCTCCTGCGTCGAAAGGATGGCACTGTTA
Mm_HDAC5_v3         AACAGAAGGTAGCCGAGAGGAGAAGCAGTCCCCTCCTGCGTCGAAAGGATGGCACTGTTA
Mm_HDAC5_v5         AACAGAAGGTAGCCGAGAGGAGAAGCAGTCCCCTCCTGCGTCGAAAGGATGGCACTGTTA
Hs_HDAC5_v1         AACAGAAGGTGGCTGAGCGGAGAAGCAGTCCCCTCCTGCGTCGCAAGGATGGGACTGTTA
Hs_HDAC5_v3         AACAGAAGGTGGCTGAGCGGAGAAGCAGTCCCCTCCTGCGTCGCAAGGATGGGACTGTTA
Bt_HDAC5_v1         AGCAGAAGGTGGCCGAGCGGAGAAGCAGTCCCCTCTTGCGTCGCAAGGATGGGACTGTCA
Bt_HDAC5_v5(P)      AGCAGAAGGTGGCCGAGCGGAGAAGCAGTCCCCTCTTGCGTCGCAAGGATGGGACTGTCA
Bt_HDAC5_v4(P)      AGCAGAAGGTGGCCGAGCGGAGAAGCAGTCCCCTCTTGCGTCGCAAGGATGGGACTGTCA
Bt_HDAC5_v2         AGCAGAAGGTGGCCGAGCGGAGAAGCAGTCCCCTCTTGCGTCGCAAGGATGGGACTGTCA
Bt_HDAC5_v3(P)      AGCAGAAGGTGGCCGAGCGGAGAAGCAGTCCCCTCTTGCGTCGCAAGGATGGGACTGTCA
Oa_HDAC5_v11(P)     AGCAGAAGGTGGCCGAGCGGAGAAGCAGTCCTCTCTTGCGTCGCAAGGATGGGACTGTCA
Oa_HDAC5_v10(P)     AGCAGAAGGTGGCCGAGCGGAGAAGCAGTCCTCTCTTGCGTCGCAAGGATGGGACTGTCA
Oa_HDAC5_v8(P)      AGCAGAAGGTGGCCGAGCGGAGAAGCAGTCCTCTCTTGCGTCGCAAGGATGGGACTGTCA
Oa_HDAC5_v9(P)      AGCAGAAGGTGGCCGAGCGGAGAAGCAGTCCTCTCTTGCGTCGCAAGGATGGGACTGTCA
Oa_HDAC5_v1(P)      AGCAGAAGGTGGCCGAGCGGAGAAGCAGTCCTCTCTTGCGTCGCAAGGATGGGACTGTCA
Oa_HDAC5_v7(P)      AGCAGAAGGTGGCCGAGCGGAGAAGCAGTCCTCTCTTGCGTCGCAAGGATGGGACTGTCA
Oa_HDAC5_v6(P)      AGCAGAAGGTGGCCGAGCGGAGAAGCAGTCCTCTCTTGCGTCGCAAGGATGGGACTGTCA
Oa_HDAC5_v5(P)      AGCAGAAGGTGGCCGAGCGGAGAAGCAGTCCTCTCTTGCGTCGCAAGGATGGGACTGTCA
Oa_HDAC5_v2(P)      AGCAGAAGGTGGCCGAGCGGAGAAGCAGTCCTCTCTTGCGTCGCAAGGATGGGACTGTCA
Oa_HDAC5_v4(P)      AGCAGAAGGTGGCCGAGCGGAGAAGCAGTCCTCTCTTGCGTCGCAAGGATGGGACTGTCA
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Mm_HDAC5_v4         TTAGTACTTTTAAGAAGAGAGCAGTTGAGATCACCGGCACGGGGGCCTGGGGTGTCGTCCG
Mm_HDAC5_v1         TTAGTACTTTTAAGAAGAGAGCAGTTGAGATCACCGGCACGGGGGCCTGGGGTGTCGTCCG
Mm_HDAC5_v3         TTAGTACTTTTAAGAAGAGAGCAGTTGAGATCACCGGCACGGGGGCCTGGGGTGTCGTCCG
Mm_HDAC5_v5         TTAGTACTTTTAAGAAGAGAGCAGTTGAGATCACCGGCACGGGGGCCTGGGGTGTCGTCCG
Hs_HDAC5_v1         TTAGCACCTTTAAGAAGAGAGCTGTTGAGATCACAGGTGCCGGGGCCTGGGGCGTCGTCCG
Hs_HDAC5_v3         TTAGCACCTTTAAGAAGAGAGCTGTTGAGATCACAGGTGCCGGGGCCTGGGGCGTCGTCCG
Bt_HDAC5_v1         TTAGCACCTTTAAGAAGAGAGCTGTTGAGATCACAGGTGCCGGACCTGGGGTGTCCGCCG
Bt_HDAC5_v5(P)      TTAGCACCTTTAAGAAGAGAGCTGTTGAGATCACAGGTGCCGGACCTGGGGTGTCCGCCG
Bt_HDAC5_v4(P)      TTAGCACCTTTAAGAAGAGAGCTGTTGAGATCACAGGTGCCGGACCTGGGGTGTCCGCCG
Bt_HDAC5_v2         TTAGCACCTTTAAGAAGAGAGCTGTTGAGATCACAGGTGCCGGACCTGGGGTGTCCGCCG
Bt_HDAC5_v3(P)      TTAGCACCTTTAAGAAGAGAGCTGTTGAGATCACAGGTGCCGGACCTGGGGTGTCCGCCG
Oa_HDAC5_v11(P)     TTAGCACCTTTAAGAAGAGAGCTGTTGAGATCACAGGTGCCGGACCTGGGGTGTCCGCCG
Oa_HDAC5_v10(P)     TTAGCACCTTTAAGAAGAGAGCTGTTGAGATCACAGGTGCCGGACCTGGGGTGTCCGCCG
Oa_HDAC5_v8(P)      TTAGCACCTTTAAGAAGAGAGCTGTTGAGATCACAGGTGCCGGACCTGGGGTGTCCGCCG
Oa_HDAC5_v9(P)      TTAGCACCTTTAAGAAGAGAGCTGTTGAGATCACAGGTGCCGGACCTGGGGTGTCCGCCG
Oa_HDAC5_v1(P)      TTAGCACCTTTAAGAAGAGAGCTGTTGAGATCACAGGTGCCGGACCTGGGGTGTCCGCCG
Oa_HDAC5_v7(P)      TTAGCACCTTTAAGAAGAGAGCTGTTGAGATCACAG---------------TGTCCGCCG
Oa_HDAC5_v6(P)      TTAGCACCTTTAAGAAGAGAGCTGTTGAGATCACAGGTGCCGGACCTGGGGTGTCCGCCG
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Oa_HDAC5_v5(P)      TTAGCACCTTTAAGAAGAGAGCTGTTGAGATCACAGGTGCCGGACCTGGGGTGTCCGCCG
Oa_HDAC5_v2(P)      TTAGCACCTTTAAGAAGAGAGCTGTTGAGATCACAGGTGCCGGACCTGGGGTGTCCGCCG
Oa_HDAC5_v4(P)      TTAGCACCTTTAAGAAGAGAGCTGTTGAGATCACAGGTGCCGGACCTGGGGTGTCCGCCG
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Mm_HDAC5_v4         TGTGTAACAGTGCGCCCGGCTCTGGCCCCAGCTCTCCCAACAGTTCCCACAGCACCATCG
Mm_HDAC5_v1         TGTGTAACAGTGCGCCCGGCTCTGGCCCCAGCTCTCCCAACAGTTCCCACAGCACCATCG
Mm_HDAC5_v3         TGTGTAACAGTGCGCCCGGCTCTGGCCCCAGCTCTCCCAACAGTTCCCACAGCACCATCG
Mm_HDAC5_v5         TGTGTAACAGTGCGCCCGGCTCTGGCCCCAGCTCTCCCAACAGTTCCCACAGCACCATCG
Hs_HDAC5_v1         TGTGTAACAGCGCACCCGGCTCCGGCCCCAGCTCTCCCAACAGCTCCCACAGCACCATCG
Hs_HDAC5_v3         TGTGTAACAGCGCACCCGGCTCCGGCCCCAGCTCTCCCAACAGCTCCCACAGCACCATCG
Bt_HDAC5_v1         TGTGTAACAGCGCACCAGGCTCTGGCCCCAGCTCTCCCAACAGTTCCCACAGCACCATCG
Bt_HDAC5_v5(P)      TGTGTAACAGCGCACCAGGCTCTGGCCCCAGCTCTCCCAACAGTTCCCACAGCACCATCG
Bt_HDAC5_v4(P)      TGTGTAACAGCGCACCAGGCTCTGGCCCCAGCTCTCCCAACAGTTCCCACAGCACCATCG
Bt_HDAC5_v2         TGTGTAACAGCGCACCAGGCTCTGGCCCCAGCTCTCCCAACAGTTCCCACAGCACCATCG
Bt_HDAC5_v3(P)      TGTGTAACAGCGCACCAGGCTCTGGCCCCAGCTCTCCCAACAGTTCCCACAGCACCATCG
Oa_HDAC5_v11(P)     TGTGTAATAGCGCGCCAGGCTCTGGCCCCAGCTCTCCCAACAGCTCCCACAGCACCATCG
Oa_HDAC5_v10(P)     TGTGTAATAGCGCGCCAGGCTCTGGCCCCAGCTCTCCCAACAGCTCCCACAGCACCATCG
Oa_HDAC5_v8(P)      TGTGTAATAGCGCGCCAGGCTCTGGCCCCAGCTCTCCCAACAGCTCCCACAGCACCATCG
Oa_HDAC5_v9(P)      TGTGTAATAGCGCGCCAGGCTCTGGCCCCAGCTCTCCCAACAGCTCCCACAGCACCATCG
Oa_HDAC5_v1(P)      TGTGTAATAGCGCGCCAGGCTCTGGCCCCAGCTCTCCCAACAGCTCCCACAGCACCATCG
Oa_HDAC5_v7(P)      TGTGTAATAGCGCGCCAGGCTCTGGCCCCAGCTCTCCCAACAGCTCCCACAGCACCATCG
Oa_HDAC5_v6(P)      TGTGTAATAGCGCGCCAGGCTCTGGCCCCAGCTCTCCCAACAGCTCCCACAGCACCATCG
Oa_HDAC5_v5(P)      TGTGTAATAGCGCGCCAGGCTCTGGCCCCAGCTCTCCCAACAGCTCCCACAGCACCATCG
Oa_HDAC5_v2(P)      TGTGTAATAGCGCGCCAGGCTCTGGCCCCAGCTCTCCCAACAGCTCCCACAGCACCATCG
Oa_HDAC5_v4(P)      TGTGTAATAGCGCGCCAGGCTCTGGCCCCAGCTCTCCCAACAGCTCCCACAGCACCATCG
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Mm_HDAC5_v4         CTGAGAACGGCTTTACTGGCTCAGTCCCCAACATCCCCACTGAGATGATCCCCCAGCACC
Mm_HDAC5_v1         CTGAGAACGGCTTTACTGGCTCAGTCCCCAACATCCCCACTGAGATGATCCCCCAGCACC
Mm_HDAC5_v3         CTGAGAACGGCTTTACTGGCTCAGTCCCCAACATCCCCACTGAGATGATCCCCCAGCACC
Mm_HDAC5_v5         CTGAGAACGGCTTTACTGGCTCAGTCCCCAACATCCCCACTGAGATGATCCCCCAGCACC
Hs_HDAC5_v1         CTGAGAATGGCTTTACTGGCTCAGTCCCCAACATCCCCACTGAGATGCTCCCTCAGCACC
Hs_HDAC5_v3         CTGAGAATGGCTTTACTGGCTCAGTCCCCAACATCCCCACTGAGATGCTCCCTCAGCACC
Bt_HDAC5_v1         CGGAGAATGGCTTTACGGGCTCGGTTCCCAACATCCCCACCGAGATGCTCCCCCAGCACC
Bt_HDAC5_v5(P)      CGGAGAATGGCTTTACGGGCTCGGTTCCCAACATCCCCACCGAGATGCTCCCCCAGCACC
Bt_HDAC5_v4(P)      CGGAGAATGGCTTTACGGGCTCGGTTCCCAACATCCCCACCGAGATGCTCCCCCAGCACC
Bt_HDAC5_v2         CGGAGAATGGCTTTACGGGCTCGGTTCCCAACATCCCCACCGAGATGCTCCCCCAGCACC
Bt_HDAC5_v3(P)      CGGAGAATGGCTTTACGGGCTCGGTTCCCAACATCCCCACCGAGATGCTCCCCCAGCACC
Oa_HDAC5_v11(P)     CGGAGAATGGCTTTACAGGCTCGGTTCCCAACATCCCCACCGAGATGCTCCCCCAGCACC
Oa_HDAC5_v10(P)     CGGAGAATGGCTTTACAGGCTCGGTTCCCAACATCCCCACCGAGATGCTCCCCCAGCACC
Oa_HDAC5_v8(P)      CGGAGAATGGCTTTACAGGCTCGGTTCCCAACATCCCCACCGAGATGCTCCCCCAGCACC
Oa_HDAC5_v9(P)      CGGAGAATGGCTTTACAGGCTCGGTTCCCAACATCCCCACCGAGATGCTCCCCCAGCACC
Oa_HDAC5_v1(P)      CGGAGAATGGCTTTACAGGCTCGGTTCCCAACATCCCCACCGAGATGCTCCCCCAGCACC
Oa_HDAC5_v7(P)      CGGAGAATGGCTTTACAGGCTCGGTTCCCAACATCCCCACCGAGATGCTCCCCCAGCACC
Oa_HDAC5_v6(P)      CGGAGAATGGCTTTACAGGCTCGGTTCCCAACATCCCCACCGAGATGCTCCCCCAGCACC
Oa_HDAC5_v5(P)      CGGAGAATGGCTTTACAGGCTCGGTTCCCAACATCCCCACCGAGATGCTCCCCCAGCACC
Oa_HDAC5_v2(P)      CGGAGAATGGCTTTACAGGCTCGGTTCCCAACATCCCCACCGAGATGCTCCCCCAGCACC
Oa_HDAC5_v4(P)      CGGAGAATGGCTTTACAGGCTCGGTTCCCAACATCCCCACCGAGATGCTCCCCCAGCACC
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Mm_HDAC5_v4         GGGCCCTCCCTCTGGACAGTTCCCCAAACCAGTTCAGCCTCTATACGTCTCCTTCTCTGC
Mm_HDAC5_v1         GGGCCCTCCCTCTGGACAGTTCCCCAAACCAGTTCAGCCTCTATACGTCTCCTTCTCTGC
Mm_HDAC5_v3         GGGCCCTCCCTCTGGACAGTTCCCCAAACCAGTTCAGCCTCTATACGTCTCCTTCTCTGC
Mm_HDAC5_v5         GGGCCCTCCCTCTGGACAGTTCCCCAAACCAGTTCAGCCTCTATACGTCTCCTTCTCTGC
Hs_HDAC5_v1         GAGCCCTCCCTCTGGACAGCTCCCCCAACCAGTTCAGCCTCTACACGTCTCCTTCTCTGC
Hs_HDAC5_v3         GAGCCCTCCCTCTGGACAGCTCCCCCAACCAGTTCAGCCTCTACACGTCTCCTTCTCTGC
Bt_HDAC5_v1         GGGCCCTCCCTCCGGACACCTCCCCCAACCAGTTCAGCCTCTACACGTCTCCCTCTCTGC
Bt_HDAC5_v5(P)      GGGCCCTCCCTCCGGACACCTCCCCCAACCAGTTCAGCCTCTACACGTCTCCCTCTCTGC
Bt_HDAC5_v4(P)      GGGCCCTCCCTCCGGACACCTCCCCCAACCAGTTCAGCCTCTACACGTCTCCCTCTCTGC
Bt_HDAC5_v2         GGGCCCTCCCTCCGGACACCTCCCCCAACCAGTTCAGCCTCTACACGTCTCCCTCTCTGC
Bt_HDAC5_v3(P)      GGGCCCTCCCTCCGGACACCTCCCCCAACCAGTTCAGCCTCTACACGTCTCCCTCTCTGC
Oa_HDAC5_v11(P)     GGGCCCTCCCTCCGGACACCTCCCCCAACCAGTTCAGCCTCTACACGTCTCCCTCTCTGC
Oa_HDAC5_v10(P)     GGGCCCTCCCTCCGGACACCTCCCCCAACCAGTTCAGCCTCTACACGTCTCCCTCTCTGC
Oa_HDAC5_v8(P)      GGGCCCTCCCTCCGGACACCTCCCCCAACCAGTTCAGCCTCTACACGTCTCCCTCTCTGC
Oa_HDAC5_v9(P)      GGGCCCTCCCTCCGGACACCTCCCCCAACCAGTTCAGCCTCTACACGTCTCCCTCTCTGC
Oa_HDAC5_v1(P)      GGGCCCTCCCTCCGGACACCTCCCCCAACCAGTTCAGCCTCTACACGTCTCCCTCTCTGC
Oa_HDAC5_v7(P)      GGGCCCTCCCTCCGGACACCTCCCCCAACCAGTTCAGCCTCTACACGTCTCCCTCTCTGC
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Oa_HDAC5_v6(P)      GGGCCCTCCCTCCGGACACCTCCCCCAACCAGTTCAGCCTCTACACGTCTCCCTCTCTGC
Oa_HDAC5_v5(P)      GGGCCCTCCCTCCGGACACCTCCCCCAACCAGTTCAGCCTCTACACGTCTCCCTCTCTGC
Oa_HDAC5_v2(P)      GGGCCCTCCCTCCGGACACCTCCCCCAACCAGTTCAGCCTCTACACGTCTCCCTCTCTGC
Oa_HDAC5_v4(P)      GGGCCCTCCCTCCGGACACCTCCCCCAACCAGTTCAGCCTCTACACGTCTCCCTCTCTGC
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Mm_HDAC5_v4         CCAACATCTCCCTAGGGCTGCAGGCCACTGTCACTGTCACCAACTCGCACCTCACCGCCT
Mm_HDAC5_v1         CCAACATCTCCCTAGGGCTGCAGGCCACTGTCACTGTCACCAACTCGCACCTCACCGCCT
Mm_HDAC5_v3         CCAACATCTCCCTAGGGCTGCAGGCCACTGTCACTGTCACCAACTCGCACCTCACCGCCT
Mm_HDAC5_v5         CCAACATCTCCCTAGGGCTGCAGGCCACTGTCACTGTCACCAACTCGCACCTCACCGCCT
Hs_HDAC5_v1         CCAACATCTCCCTAGGGCTGCAGGCCACGGTCACTGTCACCAACTCACACCTCACTGCCT
Hs_HDAC5_v3         CCAACATCTCCCTAGGGCTGCAGGCCACGGTCACTGTCACCAACTCACACCTCACTGCCT
Bt_HDAC5_v1         CCAACATCTCCCTAGGGCTGCAGGCCACGGTCACTGTCACCAACTCGCACCTCACCGCCT
Bt_HDAC5_v5(P)      CCAACATCTCCCTAGGGCTGCAGGCCACGGTCACTGTCACCAACTCGCACCTCACCGCCT
Bt_HDAC5_v4(P)      CCAACATCTCCCTAGGGCTGCAGGCCACGGTCACTGTCACCAACTCGCACCTCACCGCCT
Bt_HDAC5_v2         CCAACATCTCCCTAGGGCTGCAGGCCACGGTCACTGTCACCAACTCGCACCTCACCGCCT
Bt_HDAC5_v3(P)      CCAACATCTCCCTAGGGCTGCAGGCCACGGTCACTGTCACCAACTCGCACCTCACCGCCT
Oa_HDAC5_v11(P)     CCAACATCTCCCTAGGGCTGCAGGCCACGGTCACAGTCACCAACTCGCACCTCACCGCCT
Oa_HDAC5_v10(P)     CCAACATCTCCCTAGGGCTGCAGGCCACGGTCACAGTCACCAACTCGCACCTCACCGCCT
Oa_HDAC5_v8(P)      CCAACATCTCCCTAGGGCTGCAGGCCACGGTCACAGTCACCAACTCGCACCTCACCGCCT
Oa_HDAC5_v9(P)      CCAACATCTCCCTAGGGCTGCAGGCCACGGTCACAGTCACCAACTCGCACCTCACCGCCT
Oa_HDAC5_v1(P)      CCAACATCTCCCTAGGGCTGCAGGCCACGGTCACAGTCACCAACTCGCACCTCACCGCCT
Oa_HDAC5_v7(P)      CCAACATCTCCCTAGGGCTGCAGGCCACGGTCACAGTCACCAACTCGCACCTCACCGCCT
Oa_HDAC5_v6(P)      CCAACATCTCCCTAGGGCTGCAGGCCACGGTCACAGTCACCAACTCGCACCTCACCGCCT
Oa_HDAC5_v5(P)      CCAACATCTCCCTAGGGCTGCAGGCCACGGTCACAGTCACCAACTCGCACCTCACCGCCT
Oa_HDAC5_v2(P)      CCAACATCTCCCTAGGGCTGCAGGCCACGGTCACAGTCACCAACTCGCACCTCACCGCCT
Oa_HDAC5_v4(P)      CCAACATCTCCCTAGGGCTGCAGGCCACGGTCACAGTCACCAACTCGCACCTCACCGCCT
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Mm_HDAC5_v4         CCCCGAAGCTGTCAACACAGCAGGAGGCTGAGAGGCAGGCCCTTCAGTCCCTGCGGCAGG
Mm_HDAC5_v1         CCCCGAAGCTGTCAACACAGCAGGAGGCTGAGAGGCAGGCCCTTCAGTCCCTGCGGCAGG
Mm_HDAC5_v3         CCCCGAAGCTGTCAACACAGCAGGAGGCTGAGAGGCAGGCCCTTCAGTCCCTGCGGCAGG
Mm_HDAC5_v5         CCCCGAAGCTGTCAACACAGCAGGAGGCTGAGAGGCAGGCCCTTCAGTCCCTGCGGCAGG
Hs_HDAC5_v1         CCCCGAAGCTGTCGACACAGCAGGAGGCCGAGAGGCAGGCCCTCCAGTCCCTGCGGCAGG
Hs_HDAC5_v3         CCCCGAAGCTGTCGACACAGCAGGAGGCCGAGAGGCAGGCCCTCCAGTCCCTGCGGCAGG
Bt_HDAC5_v1         CCCCGAAGCTGTCGACGCAGCAGGAGGCCGAGAGGCAGGCCCTCCAGTCCCTGCGGCAGG
Bt_HDAC5_v5(P)      CCCCGAAGCTGTCGACGCAGCAGGAGGCCGAGAGGCAGGCCCTCCAGTCCCTGCGGCAGG
Bt_HDAC5_v4(P)      CCCCGAAGCTGTCGACGCAGCAGGAGGCCGAGAGGCAGGCCCTCCAGTCCCTGCGGCAGG
Bt_HDAC5_v2         CCCCGAAGCTGTCGACGCAGCAGGAGGCCGAGAGGCAGGCCCTCCAGTCCCTGCGGCAGG
Bt_HDAC5_v3(P)      CCCCGAAGCTGTCGACGCAGCAGGAGGCCGAGAGGCAGGCCCTCCAGTCCCTGCGGCAGG
Oa_HDAC5_v11(P)     CCCCGAAGCTGTCGACGCAGCAGGAGGCCGAGAGGCAGGCCCTCCAGTCCCTGCGGCAGG
Oa_HDAC5_v10(P)     CCCCGAAGCTGTCGACGCAGCAGGAGGCCGAGAGGCAGGCCCTCCAGTCCCTGCGGCAGG
Oa_HDAC5_v8(P)      CCCCGAAGCTGTCGACGCAGCAGGAGGCCGAGAGGCAGGCCCTCCAGTCCCTGCGGCAGG
Oa_HDAC5_v9(P)      CCCCGAAGCTGTCGACGCAGCAGGAGGCCGAGAGGCAGGCCCTCCAGTCCCTGCGGCAGG
Oa_HDAC5_v1(P)      CCCCGAAGCTGTCGACGCAGCAGGAGGCCGAGAGGCAGGCCCTCCAGTCCCTGCGGCAGG
Oa_HDAC5_v7(P)      CCCCGAAGCTGTCGACGCAGCAGGAGGCCGAGAGGCAGGCCCTCCAGTCCCTGCGGCAGG
Oa_HDAC5_v6(P)      CCCCGAAGCTGTCGACGCAGCAGGAGGCCGAGAGGCAGGCCCTCCAGTCCCTGCGGCAGG
Oa_HDAC5_v5(P)      CCCCGAAGCTGTCGACGCAGCAGGAGGCCGAGAGGCAGGCCCTCCAGTCCCTGCGGCAGG
Oa_HDAC5_v2(P)      CCCCGAAGCTGTCGACGCAGCAGGAGGCCGAGAGGCAGGCCCTCCAGTCCCTGCGGCAGG
Oa_HDAC5_v4(P)      CCCCGAAGCTGTCGACGCAGCAGGAGGCCGAGAGGCAGGCCCTCCAGTCCCTGCGGCAGG
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Mm_HDAC5_v4         GCGGCACACTGACCGGCAAGTTCATGAGCACATCCTCCATCCCTGGCTGCCTGTTGGGAG
Mm_HDAC5_v1         GCGGCACACTGACCGGCAAGTTCATGAGCACATCCTCCATCCCTGGCTGCCTGTTGGGAG
Mm_HDAC5_v3         GCGGCACACTGACCGGCAAGTTCATGAGCACATCCTCCATCCCTGGCTGCCTGTTGGGAG
Mm_HDAC5_v5         GCGGCACACTGACCGGCAAGTTCATGAGCACATCCTCCATCCCTGGCTGCCTGTTGGGAG
Hs_HDAC5_v1         GTGGCACGCTGACCGGCAAGTTCATGAGCACATCCTCTATTCCTGGCTGCCTGCTGGGCG
Hs_HDAC5_v3         GTGGCACGCTGACCGGCAAGTTCATGAGCACATCCTCTATTCCTGGCTGCCTGCTGGGCG
Bt_HDAC5_v1         GCGGTGCACTGACGGGCAAGTTCATGAGCACATCCTCCATCCCTGGCTGCCTGCTGGGCG
Bt_HDAC5_v5(P)      GCGGTGCACTGACGGGCAAGTTCATGAGCACATCCTCCATCCCTGGCTGCCTGCTGGGCG
Bt_HDAC5_v4(P)      GCGGTGCACTGACGGGCAAGTTCATGAGCACATCCTCCATCCCTGGCTGCCTGCTGGGCG
Bt_HDAC5_v2         GCGGTGCACTGACGGGCAAGTTCATGAGCACATCCTCCATCCCTGGCTGCCTGCTGGGCG
Bt_HDAC5_v3(P)      GCGGTGCACTGACGGGCAAGTTCATGAGCACATCCTCCATCCCTGGCTGCCTGCTGGGCG
Oa_HDAC5_v11(P)     GCGGTGCACTGACCGGCAAGTTCATGAGCACATCCTCCATCCCTGGCTGCCTGCTGGGCG
Oa_HDAC5_v10(P)     GCGGTGCACTGACCGGCAAGTTCATGAGCACATCCTCCATCCCTGGCTGCCTGCTGGGCG
Oa_HDAC5_v8(P)      GCGGTGCACTGACCGGCAAGTTCATGAGCACATCCTCCATCCCTGGCTGCCTGCTGGGCG
Oa_HDAC5_v9(P)      GCGGTGCACTGACCGGCAAGTTCATGAGCACATCCTCCATCCCTGGCTGCCTGCTGGGCG
Oa_HDAC5_v1(P)      GCGGTGCACTGACCGGCAAGTTCATGAGCACATCCTCCATCCCTGGCTGCCTGCTGGGCG
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Oa_HDAC5_v7(P)      GCGGTGCACTGACCGGCAAGTTCATGAGCACATCCTCCATCCCTGGCTGCCTGCTGGGCG
Oa_HDAC5_v6(P)      GCGGTGCACTGACCGGCAAGTTCATGAGCACATCCTCCATCCCTGGCTGCCTGCTGGGCG
Oa_HDAC5_v5(P)      GCGGTGCACTGACCGGCAAGTTCATGAGCACATCCTCCATCCCTGGCTGCCTGCTGGGCG
Oa_HDAC5_v2(P)      GCGGTGCACTGACCGGCAAGTTCATGAGCACATCCTCCATCCCTGGCTGCCTGCTGGGCG
Oa_HDAC5_v4(P)      GCGGTGCACTGACCGGCAAGTTCATGAGCACATCCTCCATCCCTGGCTGCCTGCTGGGCG
                    * **  * ***** ********************** ** ************ **** *

Mm_HDAC5_v4         TGGCACTGGAGGGTGACACAAGCCCCCACGGGCACGCTTCCCTGCTGCAGCACGTTTTGC
Mm_HDAC5_v1         TGGCACTGGAGGGTGACACAAGCCCCCACGGGCACGCTTCCCTGCTGCAGCACGTTTTGC
Mm_HDAC5_v3         TGGCACTGGAGGGTGACACAAGCCCCCACGGGCACGCTTCCCTGCTGCAGCACGTTTTGC
Mm_HDAC5_v5         TGGCACTGGAGGGTGACACAAGCCCCCACGGGCACGCTTCCCTGCTGCAGCACGTTTTGC
Hs_HDAC5_v1         TGGCACTGGAGGGCGACGGGAGCCCCCACGGGCATGCCTCCCTGCTGCAGCATGTGCTGT
Hs_HDAC5_v3         TGGCACTGGAGGGCGACGGGAGCCCCCACGGGCATGCCTCCCTGCTGCAGCATGTGCTGT
Bt_HDAC5_v1         TGGCACTGGAGGGCGACTCGAGCCCCCACGGGCATGCCTCACTGCTGCAGCACGTGCTGC
Bt_HDAC5_v5(P)      TGGCACTGGAGGGCGACTCGAGCCCCCACGGGCATGCCTCACTGCTGCAGCACGTGCTGC
Bt_HDAC5_v4(P)      TGGCACTGGAGGGCGACTCGAGCCCCCACGGGCATGCCTCACTGCTGCAGCACGTGCTGC
Bt_HDAC5_v2         TGGCACTGGAGGGCGACTCGAGCCCCCACGGGCATGCCTCACTGCTGCAGCACGTGCTGC
Bt_HDAC5_v3(P)      TGGCACTGGAGGGCGACTCGAGCCCCCACGGGCATGCCTCACTGCTGCAGCACGTGCTGC
Oa_HDAC5_v11(P)     TGGCACTGGAGGGCGACTCGAGCCCCCACGGGCATGCCTCATTGCTGCAGCACGTGCTGC
Oa_HDAC5_v10(P)     TGGCACTGGAGGGCGACTCGAGCCCCCACGGGCATGCCTCATTGCTGCAGCACGTGCTGC
Oa_HDAC5_v8(P)      TGGCACTGGAGGGCGACTCGAGCCCCCACGGGCATGCCTCATTGCTGCAGCACGTGCTGC
Oa_HDAC5_v9(P)      TGGCACTGGAGGGCGACTCGAGCCCCCACGGGCATGCCTCATTGCTGCAGCACGTGCTGC
Oa_HDAC5_v1(P)      TGGCACTGGAGGGCGACTCGAGCCCCCACGGGCATGCCTCATTGCTGCAGCACGTGCTGC
Oa_HDAC5_v7(P)      TGGCACTGGAGGGCGACTCGAGCCCCCACGGGCATGCCTCATTGCTGCAGCACGTGCTGC
Oa_HDAC5_v6(P)      TGGCACTGGAGGGCGACTCGAGCCCCCACGGGCATGCCTCATTGCTGCAGCACGTGCTGC
Oa_HDAC5_v5(P)      TGGCACTGGAGGGCGACTCGAGCCCCCACGGGCATGCCTCATTGCTGCAGCACGTGCTGC
Oa_HDAC5_v2(P)      TGGCACTGGAGGGCGACTCGAGCCCCCACGGGCATGCCTCATTGCTGCAGCACGTGCTGC
Oa_HDAC5_v4(P)      TGGCACTGGAGGGCGACTCGAGCCCCCACGGGCATGCCTCATTGCTGCAGCACGTGCTGC
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Mm_HDAC5_v4         TCCTGGAGCAGGCCCGGCAACAGAGCACGCTCATAGCAGTGCCGCTCCATGGGCAGTCCC
Mm_HDAC5_v1         TCCTGGAGCAGGCCCGGCAACAGAGCACGCTCATAGCAGTGCCGCTCCATGGGCAGTCCC
Mm_HDAC5_v3         TCCTGGAGCAGGCCCGGCAACAGAGCACGCTCATAGCAGTGCCGCTCCATGGGCAGTCCC
Mm_HDAC5_v5         TCCTGGAGCAGGCCCGGCAACAGAGCACGCTCATAGCAGTGCCGCTCCATGGGCAGTCCC
Hs_HDAC5_v1         TGCTGGAGCAGGCCCGGCAGCAGAGCACCCTCATTGCTGTGCCACTCCACGGGCAGTCCC
Hs_HDAC5_v3         TGCTGGAGCAGGCCCGGCAGCAGAGCACCCTCATTGCTGTGCCACTCCACGGGCAGTCCC
Bt_HDAC5_v1         TGCTGGAACAAGCCCGGCAGCAGAGCACCCTCATTGCTGTGCCGCTCCACGGGCAGTCCC
Bt_HDAC5_v5(P)      TGCTGGAACAAGCCCGGCAGCAGAGCACCCTCATTGCTGTGCCGCTCCACGGGCAGTCCC
Bt_HDAC5_v4(P)      TGCTGGAACAAGCCCGGCAGCAGAGCACCCTCATTGCTGTGCCGCTCCACGGGCAGTCCC
Bt_HDAC5_v2         TGCTGGAACAAGCCCGGCAGCAGAGCACCCTCATTGCTGTGCCGCTCCACGGGCAGTCCC
Bt_HDAC5_v3(P)      TGCTGGAACAAGCCCGGCAGCAGAGCACCCTCATTGCTGTGCCGCTCCACGGGCAGTCCC
Oa_HDAC5_v11(P)     TGCTGGAACAAGCCCGGCAGCAGAGCACCCTCATTGCTGTGCCGCTCCACGGGCAGTCCC
Oa_HDAC5_v10(P)     TGCTGGAACAAGCCCGGCAGCAGAGCACCCTCATTGCTGTGCCGCTCCACGGGCAGTCCC
Oa_HDAC5_v8(P)      TGCTGGAACAAGCCCGGCAGCAGAGCACCCTCATTGCTGTGCCGCTCCACGGGCAGTCCC
Oa_HDAC5_v9(P)      TGCTGGAACAAGCCCGGCAGCAGAGCACCCTCATTGCTGTGCCGCTCCACGGGCAGTCCC
Oa_HDAC5_v1(P)      TGCTGGAACAAGCCCGGCAGCAGAGCACCCTCATTGCTGTGCCGCTCCACGGGCAGTCCC
Oa_HDAC5_v7(P)      TGCTGGAACAAGCCCGGCAGCAGAGCACCCTCATTGCTGTGCCGCTCCACGGGCAGTCCC
Oa_HDAC5_v6(P)      TGCTGGAACAAGCCCGGCAGCAGAGCACCCTCATTGCTGTGCCGCTCCACGGGCAGTCCC
Oa_HDAC5_v5(P)      TGCTGGAACAAGCCCGGCAGCAGAGCACCCTCATTGCTGTGCCGCTCCACGGGCAGTCCC
Oa_HDAC5_v2(P)      TGCTGGAACAAGCCCGGCAGCAGAGCACCCTCATTGCTGTGCCGCTCCACGGGCAGTCCC
Oa_HDAC5_v4(P)      TGCTGGAACAAGCCCGGCAGCAGAGCACCCTCATTGCTGTGCCGCTCCACGGGCAGTCCC
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Mm_HDAC5_v4         CACTGGTGACGGGTGAACGTGTGGCCACCAGCATGAGGACGGTGGGTAAGCTCCCGAGGC
Mm_HDAC5_v1         CACTGGTGACGGGTGAACGTGTGGCCACCAGCATGAGGACGGTGGGTAAGCTCCCGAGGC
Mm_HDAC5_v3         CACTGGTGACGGGTGAACGTGTGGCCACCAGCATGAGGACGGTGGGTAAGCTCCCGAGGC
Mm_HDAC5_v5         CACTGGTGACGGGTGAACGTGTGGCCACCAGCATGAGGACGGTGGGTAAGCTCCCGAGGC
Hs_HDAC5_v1         CACTAGTGACGGGTGAACGTGTGGCCACCAGCATGCGGACGGTAGGCAAGCTCCCGCGGC
Hs_HDAC5_v3         CACTAGTGACGGGTGAACGTGTGGCCACCAGCATGCGGACGGTAGGCAAGCTCCCGCGGC
Bt_HDAC5_v1         CGCTGGTGACGGGTGAGCGCGTGGCCACCAGCATGCGGACAGTGGGCAAGCTCCCGCGGC
Bt_HDAC5_v5(P)      CGCTGGTGACGGGTGAGCGCGTGGCCACCAGCATGCGGACAGTGGGCAAGCTCCCGCGGC
Bt_HDAC5_v4(P)      CGCTGGTGACGGGTGAGCGCGTGGCCACCAGCATGCGGACAGTGGGCAAGCTCCCGCGGC
Bt_HDAC5_v2         CGCTGGTGACGGGTGAGCGCGTGGCCACCAGCATGCGGACAGTGGGCAAGCTCCCGCGGC
Bt_HDAC5_v3(P)      CGCTGGTGACGGGTGAGCGCGTGGCCACCAGCATGCGGACAGTGGGCAAGCTCCCGCGGC
Oa_HDAC5_v11(P)     CGCTGGTGACGGGTGAGCGCGTGGCCACCAGCATGCGGACAGTGGGCAAGCTCCCGCGGC
Oa_HDAC5_v10(P)     CGCTGGTGACGGGTGAGCGCGTGGCCACCAGCATGCGGACAGTGGGCAAGCTCCCGCGGC
Oa_HDAC5_v8(P)      CGCTGGTGACGGGTGAGCGCGTGGCCACCAGCATGCGGACAGTGGGCAAGCTCCCGCGGC
Oa_HDAC5_v9(P)      CGCTGGTGACGGGTGAGCGCGTGGCCACCAGCATGCGGACAGTGGGCAAGCTCCCGCGGC
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Oa_HDAC5_v1(P)      CGCTGGTGACGGGTGAGCGCGTGGCCACCAGCATGCGGACAGTGGGCAAGCTCCCGCGGC
Oa_HDAC5_v7(P)      CGCTGGTGACGGGTGAGCGCGTGGCCACCAGCATGCGGACAGTGGGCAAGCTCCCGCGGC
Oa_HDAC5_v6(P)      CGCTGGTGACGGGTGAGCGCGTGGCCACCAGCATGCGGACAGTGGGCAAGCTCCCGCGGC
Oa_HDAC5_v5(P)      CGCTGGTGACGGGTGAGCGCGTGGCCACCAGCATGCGGACAGTGGGCAAGCTCCCGCGGC
Oa_HDAC5_v2(P)      CGCTGGTGACGGGTGAGCGCGTGGCCACCAGCATGCGGACAGTGGGCAAGCTCCCGCGGC
Oa_HDAC5_v4(P)      CGCTGGTGACGGGTGAGCGCGTGGCCACCAGCATGCGGACAGTGGGCAAGCTCCCGCGGC
                    * ** *********** ** *************** **** ** ** ********* ***

Mm_HDAC5_v4         ACCGACCTCTGAGCCGCACTCAGTCCTCCCCGCTGCCGCAGAGTCCCCAGGCCCTGCAGC
Mm_HDAC5_v1         ACCGACCTCTGAGCCGCACTCAGTCCTCCCCGCTGCCGCAGAGTCCCCAGGCCCTGCAGC
Mm_HDAC5_v3         ACCGACCTCTGAGCCGCACTCAGTCCTCCCCGCTGCCGCAGAGTCCCCAGGCCCTGCAGC
Mm_HDAC5_v5         ACCGACCTCTGAGCCGCACTCAGTCCTCCCCGCTGCCGCAGAGTCCCCAGGCCCTGCAGC
Hs_HDAC5_v1         ATCGGCCCCTGAGCCGCACTCAGTCCTCACCGCTGCCGCAGAGTCCCCAGGCCCTGCAGC
Hs_HDAC5_v3         ATCGGCCCCTGAGCCGCACTCAGTCCTCACCGCTGCCGCAGAGTCCCCAGGCCCTGCAGC
Bt_HDAC5_v1         ACCGGCCCCTGAGCCGCACCCAATCCTCGCCGCTGCCCCAGAGCCCCCAGGCCCTGCAGC
Bt_HDAC5_v5(P)      ACCGGCCCCTGAGCCGCACCCAATCCTCGCCGCTGCCCCAGAGCCCCCAGGCCCTGCAGC
Bt_HDAC5_v4(P)      ACCGGCCCCTGAGCCGCACCCAATCCTCGCCGCTGCCCCAGAGCCCCCAGGCCCTGCAGC
Bt_HDAC5_v2         ACCGGCCCCTGAGCCGCACCCAATCCTCGCCGCTGCCCCAGAGCCCCCAGGCCCTGCAGC
Bt_HDAC5_v3(P)      ACCGGCCCCTGAGCCGCACCCAATCCTCGCCGCTGCCCCAGAGCCCCCAGGCCCTGCAGC
Oa_HDAC5_v11(P)     ACCGGCCCCTGAGCCGCACCCAGTCCTCGCCGCTGCCCCAGAGCCCCCAGGCCCTGCAGC
Oa_HDAC5_v10(P)     ACCGGCCCCTGAGCCGCACCCAGTCCTCGCCGCTGCCCCAGAGCCCCCAGGCCCTGCAGC
Oa_HDAC5_v8(P)      ACCGGCCCCTGAGCCGCACCCAGTCCTCGCCGCTGCCCCAGAGCCCCCAGGCCCTGCAGC
Oa_HDAC5_v9(P)      ACCGGCCCCTGAGCCGCACCCAGTCCTCGCCGCTGCCCCAGAGCCCCCAGGCCCTGCAGC
Oa_HDAC5_v1(P)      ACCGGCCCCTGAGCCGCACCCAGTCCTCGCCGCTGCCCCAGAGCCCCCAGGCCCTGCAGC
Oa_HDAC5_v7(P)      ACCGGCCCCTGAGCCGCACCCAGTCCTCGCCGCTGCCCCAGAGCCCCCAGGCCCTGCAGC
Oa_HDAC5_v6(P)      ACCGGCCCCTGAGCCGCACCCAGTCCTCGCCGCTGCCCCAGAGCCCCCAGGCCCTGCAGC
Oa_HDAC5_v5(P)      ACCGGCCCCTGAGCCGCACCCAGTCCTCGCCGCTGCCCCAGAGCCCCCAGGCCCTGCAGC
Oa_HDAC5_v2(P)      ACCGGCCCCTGAGCCGCACCCAGTCCTCGCCGCTGCCCCAGAGCCCCCAGGCCCTGCAGC
Oa_HDAC5_v4(P)      ACCGGCCCCTGAGCCGCACCCAGTCCTCGCCGCTGCCCCAGAGCCCCCAGGCCCTGCAGC
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Mm_HDAC5_v4         AGCTGGTCATGCAGCAGCAGCACCAGCAGTTCCTGGAGAAGCAGAAGCAGCAGCAGATGC
Mm_HDAC5_v1         AGCTGGTCATGCAGCAGCAGCACCAGCAGTTCCTGGAGAAGCAGAAGCAGCAGCAGATGC
Mm_HDAC5_v3         AGCTGGTCATGCAGCAGCAGCACCAGCAGTTCCTGGAGAAGCAGAAGCAGCAGCAGATGC
Mm_HDAC5_v5         AGCTGGTCATGCAGCAGCAGCACCAGCAGTTCCTGGAGAAGCAGAAGCAGCAGCAGATGC
Hs_HDAC5_v1         AGCTGGTCATGCAACAACAGCACCAGCAGTTCCTGGAGAAGCAGAAGCAGCAGCAGCTAC
Hs_HDAC5_v3         AGCTGGTCATGCAACAACAGCACCAGCAGTTCCTGGAGAAGCAGAAGCAGCAGCAGCTAC
Bt_HDAC5_v1         AGCTGGTCATGCAGCAGCAGCACCAGCAGTTCCTGGAGAAGCAGAAGCAGCAGCAGCTGC
Bt_HDAC5_v5(P)      AGCTGGTCATGCAGCAGCAGCACCAGCAGTTCCTGGAGAAGCAGAAGCAGCAGCAGCTGC
Bt_HDAC5_v4(P)      AGCTGGTCATGCAGCAGCAGCACCAGCAGTTCCTGGAGAAGCAGAAGCAGCAGCAGCTGC
Bt_HDAC5_v2         AGCTGGTCATGCAGCAGCAGCACCAGCAGTTCCTGGAGAAGCAGAAGCAGCAGCAGCTGC
Bt_HDAC5_v3(P)      AGCTGGTCATGCAGCAGCAGCACCAGCAGTTCCTGGAGAAGCAGAAGCAGCAGCAGCTGC
Oa_HDAC5_v11(P)     AGCTGGTCATGCAGCAGCAGCACCAGCAATTCCTGGAGAAGCAGAAGCAGCAGCAGCTGC
Oa_HDAC5_v10(P)     AGCTGGTCATGCAGCAGCAGCACCAGCAATTCCTGGAGAAGCAGAAGCAGCAGCAGCTGC
Oa_HDAC5_v8(P)      AGCTGGTCATGCAGCAGCAGCACCAGCAATTCCTGGAGAAGCAGAAGCAGCAGCAGCTGC
Oa_HDAC5_v9(P)      AGCTGGTCATGCAGCAGCAGCACCAGCAATTCCTGGAGAAGCAGAAGCAGCAGCAGCTGC
Oa_HDAC5_v1(P)      AGCTGGTCATGCAGCAGCAGCACCAGCAATTCCTTGAGAAGCAGAAGCAGCAGCAGCTGC
Oa_HDAC5_v7(P)      AGCTGGTCATGCAGCAGCAGCACCAGCAATTCCTGGAGAAGCAGAAGCAGCAGCAGCTGC
Oa_HDAC5_v6(P)      AGCTGGTCATGCAGCAGCAGCACCAGCAATTCCTGGAGAAGCAGAAGCAGCAGCAGCTGC
Oa_HDAC5_v5(P)      AGCTGGTCATGCAGCAGCAGCACCAGCAATTCCTGGAGAAGCAGAAGCAGCAGCAGCTGC
Oa_HDAC5_v2(P)      AGCTGGTCATGCAGCAGCAGCACCAGCAATTCCTGGAGAAGCAGAAGCAGCAGCAGCTGC
Oa_HDAC5_v4(P)      AGCTGGTCATGCAGCAGCAGCACCAGCAATTCCTGGAGAAGCAGAAGCAGCAGCAGCTGC
                    ************* ** *********** ***** ********************* * *

Mm_HDAC5_v4         AGCTGGGCAAGATCCTTACCAAAACTGGGGAGCTGTCAAGGCAGCCCACCACTCACCCGG
Mm_HDAC5_v1         AGCTGGGCAAGATCCTTACCAAAACTGGGGAGCTGTCAAGGCAGCCCACCACTCACCCGG
Mm_HDAC5_v3         AGCTGGGCAAGATCCTTACCAAAACTGGGGAGCTGTCAAGGCAGCCCACCACTCACCCGG
Mm_HDAC5_v5         AGCTGGGCAAGATCCTTACCAAAACTGGGGAGCTGTCAAGGCAGCCCACCACTCACCCGG
Hs_HDAC5_v1         AGCTGGGCAAGATCCTCACCAAGACAGGGGAGCTGCCCAGGCAGCCCACCACCCACCCTG
Hs_HDAC5_v3         AGCTGGGCAAGATCCTCACCAAGACAGGGGAGCTGCCCAGGCAGCCCACCACCCACCCTG
Bt_HDAC5_v1         AGCTGGGCAAGATCCTTACCAAGACGGGGGAGCTGCCACGGCAGCCCACCACCCACCCCG
Bt_HDAC5_v5(P)      AGCTGGGCAAGATCCTTACCAAGACGGGGGAGCTGCCACGGCAGCCCACCACCCACCCCG
Bt_HDAC5_v4(P)      AGCTGGGCAAGATCCTTACCAAGACGGGGGAGCTGCCACGGCAGCCCACCACCCACCCCG
Bt_HDAC5_v2         AGCTGGGCAAGATCCTTACCAAGACGGGGGAGCTGCCACGGCAGCCCACCACCCACCCCG
Bt_HDAC5_v3(P)      AGCTGGGCAAGATCCTTACCAAGACGGGGGAGCTGCCACGGCAGCCCACCACCCACCCCG
Oa_HDAC5_v11(P)     AGCTGGGCAAGATCCTTACCAAGACGGGGGAGCTGCCACGGCAGCCCACCACCCACCCCG
Oa_HDAC5_v10(P)     AGCTGGGCAAGATCCTTACCAAGACGGGGGAGCTGCCACGGCAGCCCACCACCCACCCCG
Oa_HDAC5_v8(P)      AGCTGGGCAAGATCCTTACCAAGACGGGGGAGCTGCCACGGCAGCCCACCACCCACCCCG
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Oa_HDAC5_v9(P)      AGCTGGGCAAGATCCTTACCAAGACGGGGGAGCTGCCACGGCAGCCCACCACCCACCCCG
Oa_HDAC5_v1(P)      AGCTGGGCAAGATCCTTACCAAGACGGGGGAGCTGCCACGGCAGCCCACCACCCACCCCG
Oa_HDAC5_v7(P)      AGCTGGGCAAGATCCTTACCAAGACGGGGGAGCTGCCACGGCAGCCCACCACCCACCCCG
Oa_HDAC5_v6(P)      AGCTGGGCAAGATCCTTACCAAGACGGGGGAGCTGCCACGGCAGCCCACCACCCACCCCG
Oa_HDAC5_v5(P)      AGCTGGGCAAGATCCTTACCAAGACGGGGGAGCTGCCACGGCAGCCCACCACCCACCCCG
Oa_HDAC5_v2(P)      AGCTGGGCAAGATCCTTACCAAGACGGGGGAGCTGCCACGGCAGCCCACCACCCACCCCG
Oa_HDAC5_v4(P)      AGCTGGGCAAGATCCTTACCAAGACGGGGGAGCTGCCACGGCAGCCCACCACCCACCCCG
                    ********************* ***** ** ********* *  ************* ***** *

Mm_HDAC5_v4         AGGAGACAGAAGAGGAGCTGACGGAGCAGCAGGAGGCCTTGCTGGGAGAGGGGGCCCTGA
Mm_HDAC5_v1         AGGAGACAGAAGAGGAGCTGACGGAGCAGCAGGAGGCCTTGCTGGGAGAGGGGGCCCTGA
Mm_HDAC5_v3         AGGAGACAGAAGAGGAGCTGACGGAGCAGCAGGAGGCCTTGCTGGGAGAGGGGGCCCTGA
Mm_HDAC5_v5         AGGAGACAGAAGAGGAGCTGACGGAGCAGCAGGAGGCCTTGCTGGGAGAGGGGGCCCTGA
Hs_HDAC5_v1         AGGAGACAGAGGAGGAGCTGACGGAGCAGCAGGAGGTCTTGCTGGGGGAGGGAGCCCTGA
Hs_HDAC5_v3         AGGAGACAGAGGAGGAGCTGACGGAGCAGCAGGAGGTCTTGCTGGGGGAGGGAGCCCTGA
Bt_HDAC5_v1         AGGAGACAGAGGAGGAGCTGACGGAGCAGCAGGACGCCTTGCTGGGGGAGGGAGCCCTGA
Bt_HDAC5_v5(P)      AGGAGACAGAGGAGGAGCTGACGGAGCAGCAGGACGCCTTGCTGGGGGAGGGAGCCCTGA
Bt_HDAC5_v4(P)      AGGAGACAGAGGAGGAGCTGACGGAGCAGCAGGACGCCTTGCTGGGGGAGGGAGCCCTGA
Bt_HDAC5_v2         AGGAGACAGAGGAGGAGCTGACGGAGCAGCAGGACGCCTTGCTGGGGGAGGGAGCCCTGA
Bt_HDAC5_v3(P)      AGGAGACAGAGGAGGAGCTGACGGAGCAGCAGGACGCCTTGCTGGGGGAGGGAGCCCTGA
Oa_HDAC5_v11(P)     AGGAGACAGAGGAGGAGCTGACGGAGCAGCAGGACTCCTTGCTGGGGGAGGGAGCCCTCA
Oa_HDAC5_v10(P)     AGGAGACAGAGGAGGAGCTGACGGAGCAGCAGGACTCCTTGCTGGGGGAGGGAGCCCTCA
Oa_HDAC5_v8(P)      AGGAGACAGAGGAGGAGCTGACGGAGCAGCAGGACTCCTTGCTGGGGGAGGGAGCCCTCA
Oa_HDAC5_v9(P)      AGGAGACAGAGGAGGAGCTGACGGAGCAGCAGGACTCCTTGCTGGGGGAGGGAGCCCTCA
Oa_HDAC5_v1(P)      AGGAGACAGAGGAGGAGCTGACGGAGCAGCAGGACTCCTTGCTGGGGGAGGGAGCTCTCA
Oa_HDAC5_v7(P)      AGGAGACAGAGGAGGAGCTGACGGAGCAGCAGGACTCCTTGCTGGGGGAGGGAGCCCTCA
Oa_HDAC5_v6(P)      AGGAGACAGAGGAGGAGCTGACGGAGCAGCAGGACTCCTTGCTGGGGGAGGGAGCCCTCA
Oa_HDAC5_v5(P)      AGGAGACAGAGGAGGAGCTGACGGAGCAGCAGGACTCCTTGCTGGGGGAGGGAGCCCTCA
Oa_HDAC5_v2(P)      AGGAGACAGAGGAGGAGCTGACGGAGCAGCAGGACTCCTTGCTGGGGGAGGGAGCCCTCA
Oa_HDAC5_v4(P)      AGGAGACAGAGGAGGAGCTGACGGAGCAGCAGGACTCCTTGCTGGGGGAGGGAGCCCTCA
                    ********** ********************** ********* ***** ** ** * *

Mm_HDAC5_v4         CCATTCCCCGGGAAGGCTCTACAGAAAGTGAGAGCACCCAGGAAGACCTAGAAGAGGAGG
Mm_HDAC5_v1         CCATTCCCCGGGAAGGCTCTACAGAAAGTGAGAGCACCCAGGAAGACCTAGAAGAGGAGG
Mm_HDAC5_v3         CCATTCCCCGGGAAGGCTCTACAGAAAGTGAGAGCACCCAGGAAGACCTAGAAGAGGAGG
Mm_HDAC5_v5         CCATTCCCCGGGAAGGCTCTACAGAAAGTGAGAGCACCCAGGAAGACCTAGAAGAGGAGG
Hs_HDAC5_v1         CCATGCCCCGGGAGGGCTCCACAGAGAGTGAGAGCACACAGGAAGACCTGGAGGAGGAGG
Hs_HDAC5_v3         CCATGCCCCGGGAGGGCTCCACAGAGAGTGAGAGCACACAGGAAGACCTGGAGGAGGAGG
Bt_HDAC5_v1         CCATACCCCGAGAAGGCTCCACGGAGAGTGAGAGCACCCAGGAAGACCTGGAGGAGGAGG
Bt_HDAC5_v5(P)      CCATACCCCGAGAAGGCTCCACGGAGAGTGAGAGCACCCAGGAAGACCTGGAGGAGGAGG
Bt_HDAC5_v4(P)      CCATACCCCGAGAAGGCTCCACGGAGAGTGAGAGCACCCAGGAAGACCTGGAGGAGGAGG
Bt_HDAC5_v2         CCATACCCCGAGAAGGCTCCACGGAGAGTGAGAGCACCCAGGAAGACCTGGAGGAGGAGG
Bt_HDAC5_v3(P)      CCATACCCCGAGAAGGCTCCACGGAGAGTGAGAGCACCCAGGAAGACCTGGAGGAGGAGG
Oa_HDAC5_v11(P)     CCATACCCCGAGAAGGCTCCACGGAGAGTGAGAGCACCCAGGAAGACCTGGAGGAAGAGG
Oa_HDAC5_v10(P)     CCATACCCCGAGAAGGCTCCACGGAGAGTGAGAGCACCCAGGAAGACCTGGAGGAAGAGG
Oa_HDAC5_v8(P)      CCATACCCCGAGAAGGCTCCACGGAGAGTGAGAGCACCCAGGAAGACCTGGAGGAAGAGG
Oa_HDAC5_v9(P)      CCATACCCCGAGAAGGCTCCACGGAGAGTGAGAGCACCCAGGAAGACCTGGAGGAAGAGG
Oa_HDAC5_v1(P)      CCATACCCCGAGAAGGCTCCACGGAGAGTGAGAGCACCCAGGAAGACCTGGAGGAAGAGG
Oa_HDAC5_v7(P)      CCATACCCCGAGAAGGCTCCACGGAGAGTGAGAGCACCCAGGAAGACCTGGAGGAAGAGG
Oa_HDAC5_v6(P)      CCATACCCCGAGAAGGCTCCACGGAGAGTGAGAGCACCCAGGAAGACCTGGAGGAAGAGG
Oa_HDAC5_v5(P)      CCATACCCCGAGAAGGCTCCACGGAGAGTGAGAGCACCCAGGAAGACCTGGAGGAAGAGG
Oa_HDAC5_v2(P)      CCATACCCCGAGAAGGCTCCACGGAGAGTGAGAGCACCCAGGAAGACCTGGAGGAAGAGG
Oa_HDAC5_v4(P)      CCATACCCCGAGAAGGCTCCACGGAGAGTGAGAGCACCCAGGAAGACCTGGAGGAAGAGG
                    **** ***** ** ***** ** ** *********** *********** ** ** ****

Mm_HDAC5_v4         AGGAGGAG------------GAGGAGGAGGAAGAGGAGGACTGCATTCAGGTCAAGGATG
Mm_HDAC5_v1         AGGAGGAG------------GAGGAGGAGGAAGAGGAGGACTGCATTCAGGTCAAGGATG
Mm_HDAC5_v3         AGGAGGAG------------GAGGAGGAGGAAGAGGAGGACTGCATTCAGGTCAAGGATG
Mm_HDAC5_v5         AGGAGGAG------------GAGGAGGAGGAAGAGGAGGACTGCATTCAGGTCAAGGATG
Hs_HDAC5_v1         ACGAGGAAGA----------CGATGGGGAGGAGGAGGAGGATTGCATCCAGGTTAAGGACG
Hs_HDAC5_v3         ACGAGGAAGA----------CGATGGGGAGGAGGAGGAGGATTGCATCCAGGTTAAGGACG
Bt_HDAC5_v1         AAGAGGAGGAGGTGGTAGAGGAGGAGGAGGAGGAGGAGGACTGCATCCAGGTCAAGGACG
Bt_HDAC5_v5(P)      AAGAGGAGGAGGTGGTAGAGGAGGAGGAGGAGGAGGAGGACTGCATCCAGGTCAAGGACG
Bt_HDAC5_v4(P)      AAGAGGAGGAGGTGGTAGAGGAGGAGGAGGAGGAGGAGGACTGCATCCAGGTCAAGGACG
Bt_HDAC5_v2         AAGAGGAGGAGGTGGTAGAGGAGGAGGAGGAGGAGGAGGACTGCATCCAGGTCAAGGACG
Bt_HDAC5_v3(P)      AAGAGGAGGAGGTGGTAGAGGAGGAGGAGGAGGAGGAGGACTGCATCCAGGTCAAGGACG
Oa_HDAC5_v11(P)     AAGAGGAGGAGGAG------GAAGAGGAGGAGGAGGAGGACTGCATCCAGGTCAAGGATG
Oa_HDAC5_v10(P)     AAGAGGAGGAGGAG------GAAGAGGAGGAGGAGGAGGACTGCATCCAGGTCAAGGATG
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Oa_HDAC5_v8(P)      AAGAGGAGGAGGAG------GAAGAGGAGGAGGAGGAGGACTGCATCCAGGTCAAGGATG
Oa_HDAC5_v9(P)      AAGAGGAGGAGGAG------GAAGAGGAGGAGGAGGAGGACTGCATCCAGGTCAAGGATG
Oa_HDAC5_v1(P)      AAGAGGAGGAGGAG------GAAGAGGAGGAGGAGGAGGACTGCATCCAGGTCAAGGATG
Oa_HDAC5_v7(P)      AAGAGGAGGAGGAG------GAAGAGGAGGAGGAGGAGGACTGCATCCAGGTCAAGGATG
Oa_HDAC5_v6(P)      AAGAGGAGGAGGAG------GAAGAGGAGGAGGAGGAGGACTGCATCCAGGTCAAGGATG
Oa_HDAC5_v5(P)      AAGAGGAGGAGGAG------GAAGAGGAGGAGGAGGAGGACTGCATCCAGGTCAAGGATG
Oa_HDAC5_v2(P)      AAGAGGAGGAGGAG------GAAGAGGAGGAGGAGGAGGACTGCATCCAGGTCAAGGATG
Oa_HDAC5_v4(P)      AAGAGGAGGAGGAG------GAAGAGGAGGAGGAGGAGGACTGCATCCAGGTCAAGGATG
                    * *****             ** * ****** ******** ***** ***** ***** *

Mm_HDAC5_v4         AGGATGGCGAGAGTGGTCCTGATGAAGGCCCTGACTTAGAAGAGTCCAGTGCTGGTTACA
Mm_HDAC5_v1         AGGATGGCGAGAGTGGTCCTGATGAAGGCCCTGACTTAGAAGAGTCCAGTGCTGGTTACA
Mm_HDAC5_v3         AGGATGGCGAGAGTGGTCCTGATGAAGGCCCTGACTTAGAAGAGTCCAGTGCTGGTTACA
Mm_HDAC5_v5         AGGATGGCGAGAGTGGTCCTGATGAAGGCCCTGACTTAGAAGAGTCCAGTGCTGGTTACA
Hs_HDAC5_v1         AGGAGGGCGAGAGTGGTGCTGAGGAGGGGCCCGACTTGGAGGAGCCTGGTGCTGGATACA
Hs_HDAC5_v3         AGGAGGGCGAGAGTGGTGCTGAGGAGGGGCCCGACTTGGAGGAGCCTGGTGCTGGATACA
Bt_HDAC5_v1         AGGAGCGCGAGAGCGGTGCTGAAGAGGGGCCCGACTTGGAGGAGTCCAGTGCTGGTTACA
Bt_HDAC5_v5(P)      AGGAGCGCGAGAGCGGTGCTGAAGAGGGGCCCGACTTGGAGGAGTCCAGTGCTGGTTACA
Bt_HDAC5_v4(P)      AGGAGCGCGAGAGCGGTGCTGAAGAGGGGCCCGACTTGGAGGAGTCCAGTGCTGGTTACA
Bt_HDAC5_v2         AGGAGCGCGAGAGCGGTGCTGAAGAGGGGCCCGACTTGGAGGAGTCCAGTGCTGGTTACA
Bt_HDAC5_v3(P)      AGGAGCGCGAGAGCGGTGCTGAAGAGGGGCCCGACTTGGAGGAGTCCAGTGCTGGTTACA
Oa_HDAC5_v11(P)     AGGAGCGCGAGAGCGGTGCTGAAGAGGGGCCCGACTTGGAGGAGTCCAGTGCTGGTTACA
Oa_HDAC5_v10(P)     AGGAGCGCGAGAGCGGTGCTGAAGAGGGGCCCGACTTGGAGGAGTCCAGTGCTGGTTACA
Oa_HDAC5_v8(P)      AGGAGCGCGAGAGCGGTGCTGAAGAGGGGCCCGACTTGGAGGAGTCCAGTGCTGGTTACA
Oa_HDAC5_v9(P)      AGGAGCGCGAGAGCGGTGCTGAAGAGGGGCCCGACTTGGAGGAGTCCAGTGCTGGTTACA
Oa_HDAC5_v1(P)      AGGAGCGCGAGAGCGGTGCTGAAGAGGGGCCCGACTTGGAGGAGTCCAGTGCTGGTTACA
Oa_HDAC5_v7(P)      AGGAGCGCGAGAGCGGTGCTGAAGAGGGGCCCGACTTGGAGGAGTCCAGTGCTGGTTACA
Oa_HDAC5_v6(P)      AGGAGCGCGAGAGCGGTGCTGAAGAGGGGCCCGACTTGGAGGAGTCCAGTGCTGGTTACA
Oa_HDAC5_v5(P)      AGGAGCGCGAGAGCGGTGCTGAAGAGGGGCCCGACTTGGAGGAGTCCAGTGCTGGTTACA
Oa_HDAC5_v2(P)      AGGAGCGCGAGAGCGGTGCTGAAGAGGGGCCCGACTTGGAGGAGTCCAGTGCTGGTTACA
Oa_HDAC5_v4(P)      AGGAGCGCGAGAGCGGTGCTGAAGAGGGGCCCGACTTGGAGGAGTCCAGTGCTGGTTACA
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Mm_HDAC5_v4         AAAAGTTGTTCGCAGATGCCCAGCAGTTACAGCCCCTCCAGGTGTACCAGGCACCCCTCA
Mm_HDAC5_v1         AAAAGTTGTTCGCAGATGCCCAGCAGTTACAGCCCCTCCAGGTGTACCAGGCACCCCTCA
Mm_HDAC5_v3         AAAAGTTGTTCGCAGATGCCCAGCAGTTACAGCCCCTCCAGGTGTACCAGGCACCCCTCA
Mm_HDAC5_v5         AAAAGTTGTTCGCAGATGCCCAGCAGTTACAGCCCCTCCAGGTGTACCAGGCACCCCTCA
Hs_HDAC5_v1         AAAAACTGTTCTCAGATGCCCAGCCGCTGCAGCCTTTGCAGGTGTACCAGGCGCCCCTCA
Hs_HDAC5_v3         AAAAACTGTTCTCAGATGCCCAGCCGCTGCAGCCTTTGCAGGTGTACCAGGCGCCCCTCA
Bt_HDAC5_v1         AAAAGGCATTTGCAGACACCCAGCAGCTGCAGCCGCTGCAGGTGTACCAGGCACCCCTCA
Bt_HDAC5_v5(P)      AAAAGGCATTTGCAGACACCCAGCAGCTGCAGCCGCTGCAGGTGTACCAGGCACCCCTCA
Bt_HDAC5_v4(P)      AAAAGGCATTTGCAGACACCCAGCAGCTGCAGCCGCTGCAGGTGTACCAGGCACCCCTCA
Bt_HDAC5_v2         AAAAGGCATTTGCAGACACCCAGCAGCTGCAGCCGCTGCAGGTGTACCAGGCACCCCTCA
Bt_HDAC5_v3(P)      AAAAGGCATTTGCAGACACCCAGCAGCTGCAGCCGCTGCAGGTGTACCAGGCACCCCTCA
Oa_HDAC5_v11(P)     AAAAGGCATTTGCAGACACCCAGCAGCTGCAGCCGCTGCAGGTATACCAGGCACCCCTCA
Oa_HDAC5_v10(P)     AAAAGGCATTTGCAGACACCCAGCAGCTGCAGCCGCTGCAGGTATACCAGGCACCCCTCA
Oa_HDAC5_v8(P)      AAAAGGCATTTGCAGACACCCAGCAGCTGCAGCCGCTGCAGGTATACCAGGCACCCCTCA
Oa_HDAC5_v9(P)      AAAAGGCATTTGCAGACACCCAGCAGCTGCAGCCGCTGCAGGTATACCAGGCACCCCTCA
Oa_HDAC5_v1(P)      AAAAGGCATTTGCAGACACCCAGCAGCTGCAGCCGCTGCAGGTATACCAGGCACCCCTCA
Oa_HDAC5_v7(P)      AAAAGGCATTTGCAGACACCCAGCAGCTGCAGCCGCTGCAGGTATACCAGGCACCCCTCA
Oa_HDAC5_v6(P)      AAAAGGCATTTGCAGACACCCAGCAGCTGCAGCCGCTGCAGGTATACCAGGCACCCCTCA
Oa_HDAC5_v5(P)      AAAAGGCATTTGCAGACACCCAGCAGCTGCAGCCGCTGCAGGTATACCAGGCACCCCTCA
Oa_HDAC5_v2(P)      AAAAGGCATTTGCAGACACCCAGCAGCTGCAGCCGCTGCAGGTATACCAGGCACCCCTCA
Oa_HDAC5_v4(P)      AAAAGGCATTTGCAGACACCCAGCAGCTGCAGCCGCTGCAGGTATACCAGGCACCCCTCA
                    ****    **  ****  ****** * * *****  * ***** ******** *******

Mm_HDAC5_v4         GCCTGGCCACTGTGCCTCATCAGGCCCTGGGCCGCACCCAGTCCTCACCTGCTGCTCCTG
Mm_HDAC5_v1         GCCTGGCCACTGTGCCTCATCAGGCCCTGGGCCGCACCCAGTCCTCACCTGCTGCTCCTG
Mm_HDAC5_v3         GCCTGGCCACTGTGCCTCATCAGGCCCTGGGCCGCACCCAGTCCTCACCTGCTGCTCCTG
Mm_HDAC5_v5         GCCTGGCCACTGTGCCTCATCAGGCCCTGGGCCGCACCCAGTCCTCACCTGCTGCTCCTG
Hs_HDAC5_v1         GCCTGGCCACTGTGCCCCACCAGGCCCTGGGCCGTACCCAGTCCTCCCCTGCTGCCCCTG
Hs_HDAC5_v3         GCCTGGCCACTGTGCCCCACCAGGCCCTGGGCCGTACCCAGTCCTCCCCTGCTGCCCCTG
Bt_HDAC5_v1         GCCTGGCCACTGTGCCCCACCAGGCCCTGGGCCGCACCCAGTCCTCACCTGCTGCCCCTG
Bt_HDAC5_v5(P)      GCCTGGCCACTGTGCCCCACCAGGCCCTGGGCCGCACCCAGTCCTCACCTGCTGCCCCTG
Bt_HDAC5_v4(P)      GCCTGGCCACTGTGCCCCACCAGGCCCTGGGCCGCACCCAGTCCTCACCTGCTGCCCCTG
Bt_HDAC5_v2         GCCTGGCCACTGTGCCCCACCAGGCCCTGGGCCGCACCCAGTCCTCACCTGCTGCCCCTG
Bt_HDAC5_v3(P)      GCCTGGCCACTGTGCCCCACCAGGCCCTGGGCCGCACCCAGTCCTCACCTGCTGCCCCTG
Oa_HDAC5_v11(P)     GCCTGGCCACTGTGCCCCACCAGGCCCTGGGCCGCACCCAGTCCTCACCTGCTGCCCCTG
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Oa_HDAC5_v10(P)      GCCTGGCCACTGTGCCCCACCAGGCCCTGGGCCGCACCCAGTCCTCACCTGCTGCCCCTG
Oa_HDAC5_v8(P)       GCCTGGCCACTGTGCCCCACCAGGCCCTGGGCCGCACCCAGTCCTCACCTGCTGCCCCTG
Oa_HDAC5_v9(P)       GCCTGGCCACTGTGCCCCACCAGGCCCTGGGCCGCACCCAGTCCTCACCTGCTGCCCCTG
Oa_HDAC5_v1(P)       GCCTGGCCACTGTGCCCCACCAGGCCCTGGGCCGCACCCAGTCCTCACCTGCTGCCCCTG
Oa_HDAC5_v7(P)       GCCTGGCCACTGTGCCCCACCAGGCCCTGGGCCGCACCCAGTCCTCACCTGCTGCCCCTG
Oa_HDAC5_v6(P)       GCCTGGCCACTGTGCCCCACCAGGCCCTGGGCCGCACCCAGTCCTCACCTGCTGCCCCTG
Oa_HDAC5_v5(P)       GCCTGGCCACTGTGCCCCACCAGGCCCTGGGCCGCACCCAGTCCTCACCTGCTGCCCCTG
Oa_HDAC5_v2(P)       GCCTGGCCACTGTGCCCCACCAGGCCCTGGGCCGCACCCAGTCCTCACCTGCTGCCCCTG
Oa_HDAC5_v4(P)       GCCTGGCCACTGTGCCCCACCAGGCCCTGGGCCGCACCCAGTCCTCACCTGCTGCCCCTG
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Mm_HDAC5_v4          GGAGCATGAAGAGCCCCACAGACCAACCCACTGTGGTGAAGCACCTCTTCACCACAGGTG
Mm_HDAC5_v1          GGAGCATGAAGAGCCCCACAGACCAACCCACTGTGGTGAAGCACCTCTTCACCACAGGTG
Mm_HDAC5_v3          GGAGCATGAAGAGCCCCACAGACCAACCCACTGTGGTGAAGCACCTCTTCACCACAGGTG
Mm_HDAC5_v5          GGAGCATGAAGAGCCCCACAGACCAACCCACTGTGGTGAAGCACCTCTTCACCACAGGTG
Hs_HDAC5_v1          GGGGCATGAAGAGCCCCCCAGACCAGCCC------GTCAAGCACCTCTTCACCACAGGTG
Hs_HDAC5_v3          GGGGCATGAAGAGCCCCCCAGACCAGCCC------GTCAAGCACCTCTTCACCACAGGTG
Bt_HDAC5_v1          GGGGCATGAAGAGCCCCCCAGACCAGCCC------ACTAAGCACCTCTTCACCACAGGTG
Bt_HDAC5_v5(P)       GGGGCATGAAGAGCCCCCCAGACCAGCCC------ACTAAGCACCTCTTCACCACAGGTG
Bt_HDAC5_v4(P)       GGGGCATGAAGAGCCCCCCAGACCAGCCC------ACTAAGCACCTCTTCACCACAGGTG
Bt_HDAC5_v2          GGGGCATGAAGAGCCCCCCAGACCAGCCC------ACTAAGCACCTCTTCACCACAGGTG
Bt_HDAC5_v3(P)       GGGGCATGAAGAGCCCCCCAGACCAGCCC------ACTAAGCACCTCTTCACCACAGGTG
Oa_HDAC5_v11(P)      GGGGCATGAAGAGCCCCCCAGACCAGCCC------ACTAAGCACCTCTTCACCACAGGTG
Oa_HDAC5_v10(P)      GGGGCATGAAGAGCCCCCCAGACCAGCCC------ACTAAGCACCTCTTCACCACAGGTG
Oa_HDAC5_v8(P)       GGGGCATGAAGAGCCCCCCAGACCAGCCC------ACTAAGCACCTCTTCACCACAGGTG
Oa_HDAC5_v9(P)       GGGGCATGAAGAGCCCCCCAGACCAGCCC------ACTAAGCACCTCTTCACCACAGGTG
Oa_HDAC5_v1(P)       GGGGCATGAAGAGCCCCCCAGACCAGCCC------ACTAAGCACCTCTTCACCACAGGTG
Oa_HDAC5_v7(P)       GGGGCATGAAGAGCCCCCCAGACCAGCCC------ACTAAGCACCTCTTCACCACAGGTG
Oa_HDAC5_v6(P)       GGGGCATGAAGAGCCCCCCAGACCAGCCC------ACTAAGCACCTCTTCACCACAGGTG
Oa_HDAC5_v5(P)       GGGGCATGAAGAGCCCCCCAGACCAGCCC------ACTAAGCACCTCTTCACCACAGGTG
Oa_HDAC5_v2(P)       GGGGCATGAAGAGCCCCCCAGACCAGCCC------ACTAAGCACCTCTTCACCACAGGTG
Oa_HDAC5_v4(P)       GGGGCATGAAGAGCCCCCCAGACCAGCCC------ACTAAGCACCTCTTCACCACAGGTG
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Mm_HDAC5_v4          TGGTCTATGACACGTTCATGCTGAAGCACCAGTGTATGTGCGGAAACACACACGTGCACC
Mm_HDAC5_v1          TGGTCTATGACACGTTCATGCTGAAGCACCAGTGTATGTGCGGAAACACACACGTGCACC
Mm_HDAC5_v3          TGGTCTATGACACGTTCATGCTGAAGCACCAGTGTATGTGCGGAAACACACACGTGCACC
Mm_HDAC5_v5          TGGTCTATGACACGTTCATGCTGAAGCACCAGTGTATGTGCGGAAACACACACGTGCACC
Hs_HDAC5_v1          TGGTCTACGACACGTTCATGCTAAAGCACCAGTGCATGTGCGGGAACACACACGTGCACC
Hs_HDAC5_v3          TGGTCTACGACACGTTCATGCTAAAGCACCAGTGCATGTGCGGGAACACACACGTGCACC
Bt_HDAC5_v1          TGGTCTACGACACGTTCATGCTGAAGCACCAGTGCATGTGTGGGAACACACACGTGCACC
Bt_HDAC5_v5(P)       TGGTCTACGACACGTTCATGCTGAAGCACCAGTGCATGTGTGGGAACACACACGTGCACC
Bt_HDAC5_v4(P)       TGGTCTACGACACGTTCATGCTGAAGCACCAGTGCATGTGTGGGAACACACACGTGCACC
Bt_HDAC5_v2          TGGTCTACGACACGTTCATGCTGAAGCACCAGTGCATGTGTGGGAACACACACGTGCACC
Bt_HDAC5_v3(P)       TGGTCTACGACACGTTCATGCTGAAGCACCAGTGCATGTGTGGGAACACACACGTGCACC
Oa_HDAC5_v11(P)      TGGTCTACGACACGTTCATGCTGAAGCACCAGTGCATGTGCGGGAACACACATGTGCACC
Oa_HDAC5_v10(P)      TGGTCTACGACACGTTCATGCTGAAGCACCAGTGCATGTGCGGGAACACACATGTGCACC
Oa_HDAC5_v8(P)       TGGTCTACGACACGTTCATGCTGAAGCACCAGTGCATGTGCGGGAACACACATGTGCACC
Oa_HDAC5_v9(P)       TGGTCTACGACACGTTCATGCTGAAGCACCAGTGCATGTGCGGGAACACACATGTGCACC
Oa_HDAC5_v1(P)       TGGTCTACGACACGTTCATGCTGAAGCACCAGTGCATGTGCGGGAACACACATGTGCACC
Oa_HDAC5_v7(P)       TGGTCTACGACACGTTCATGCTGAAGCACCAGTGCATGTGCGGGAACACACATGTGCACC
Oa_HDAC5_v6(P)       TGGTCTACGACACGTTCATGCTGAAGCACCAGTGCATGTGCGGGAACACACATGTGCACC
Oa_HDAC5_v5(P)       TGGTCTACGACACGTTCATGCTGAAGCACCAGTGCATGTGCGGGAACACACATGTGCACC
Oa_HDAC5_v2(P)       TGGTCTACGACACGTTCATGCTGAAGCACCAGTGCATGTGCGGGAACACACATGTGCACC
Oa_HDAC5_v4(P)       TGGTCTACGACACGTTCATGCTGAAGCACCAGTGCATGTGCGGGAACACACATGTGCACC
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Mm_HDAC5_v4          CAGAGCACGCCGGCCGCATCCAGAGCATCTGGTCCCGGCTGCAGGAAACTGGTCTGCTCG
Mm_HDAC5_v1          CAGAGCACGCCGGCCGCATCCAGAGCATCTGGTCCCGGCTGCAGGAAACTGGTCTGCTCG
Mm_HDAC5_v3          CAGAGCACGCCGGCCGCATCCAGAGCATCTGGTCCCGGCTGCAGGAAACTGGTCTGCTCG
Mm_HDAC5_v5          CAGAGCACGCCGGCCGCATCCAGAGCATCTGGTCCCGGCTGCAGGAAACTGGTCTGCTCG
Hs_HDAC5_v1          CTGAGCATGCTGGCCGGATCCAGAGCATCTGGTCCCGGCTGCAGGAGACAGGCCTGCTTA
Hs_HDAC5_v3          CTGAGCATGCTGGCCGGATCCAGAGCATCTGGTCCCGGCTGCAGGAGACAGGCCTGCTTA
Bt_HDAC5_v1          CCGAGCACGCTGGCCGGATCCAGAGCATCTGGTCCCGGCTGCAGGAGACAGGCCTGCTCA
Bt_HDAC5_v5(P)       CCGAGCACGCTGGCCGGATCCAGAGCATCTGGTCCCGGCTGCAGGAGACAGGCCTGCTCA
Bt_HDAC5_v4(P)       CCGAGCACGCTGGCCGGATCCAGAGCATCTGGTCCCGGCTGCAGGAGACAGGCCTGCTCA
Bt_HDAC5_v2          CCGAGCACGCTGGCCGGATCCAGAGCATCTGGTCCCGGCTGCAGGAGACAGGCCTGCTCA
Bt_HDAC5_v3(P)       CCGAGCACGCTGGCCGGATCCAGAGCATCTGGTCCCGGCTGCAGGAGACAGGCCTGCTCA
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Oa_HDAC5_v11(P)      CCGAGCACGCTGGCCGGATCCAGAGCATCTGGTCCCGGCTGCAGGAGACAGGCCTGCTCA
Oa_HDAC5_v10(P)      CCGAGCACGCTGGCCGGATCCAGAGCATCTGGTCCCGGCTGCAGGAGACAGGCCTGCTCA
Oa_HDAC5_v8(P)       CCGAGCACGCTGGCCGGATCCAGAGCATCTGGTCCCGGCTGCAGGAGACAGGCCTGCTCA
Oa_HDAC5_v9(P)       CCGAGCACGCTGGCCGGATCCAGAGCATCTGGTCCCGGCTGCAGGAGACAGGCCTGCTCA
Oa_HDAC5_v1(P)       CCGAGCACGCTGGCCGGATCCAGAGCATCTGGTCCCGGCTGCAGGAGACAGGCCTGCTCA
Oa_HDAC5_v7(P)       CCGAGCACGCTGGCCGGATCCAGAGCATCTGGTCCCGGCTGCAGGAGACAGGCCTGCTCA
Oa_HDAC5_v6(P)       CCGAGCACGCTGGCCGGATCCAGAGCATCTGGTCCCGGCTGCAGGAGACAGGCCTGCTCA
Oa_HDAC5_v5(P)       CCGAGCACGCTGGCCGGATCCAGAGCATCTGGTCCCGGCTGCAGGAGACAGGCCTGCTCA
Oa_HDAC5_v2(P)       CCGAGCACGCTGGCCGGATCCAGAGCATCTGGTCCCGGCTGCAGGAGACAGGCCTGCTCA
Oa_HDAC5_v4(P)       CCGAGCACGCTGGCCGGATCCAGAGCATCTGGTCCCGGCTGCAGGAGACAGGCCTGCTCA
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Mm_HDAC5_v4          GCAAGTGTGAGCGGATCCGGGGTCGTAAAGCCACACTGGATGAAATCCAGACCGTGCACT
Mm_HDAC5_v1          GCAAGTGTGAGCGGATCCGGGGTCGTAAAGCCACACTGGATGAAATCCAGACCGTGCACT
Mm_HDAC5_v3          GCAAGTGTGAGCGGATCCGGGGTCGTAAAGCCACACTGGATGAAATCCAGACCGTGCACT
Mm_HDAC5_v5          GCAAGTGTGAGCGGATCCGGGGTCGTAAAGCCACACTGGATGAAATCCAGACCGTGCACT
Hs_HDAC5_v1          GCAAGTGCGAGCGGATCCGAGGTCGCAAAGCCACGCTAGATGAGATCCAGACAGTGCACT
Hs_HDAC5_v3          GCAAGTGCGAGCGGATCCGAGGTCGCAAAGCCACGCTAGATGAGATCCAGACAGTGCACT
Bt_HDAC5_v1          GCAAGTGTGAGCGAATCCGGGGTCGTAAAGCCACGCTGGATGAGATCCAGACGGTGCACT
Bt_HDAC5_v5(P)       GCAAGTGTGAGCGAATCCGGGGTCGTAAAGCCACGCTGGATGAGATCCAGACGGTGCACT
Bt_HDAC5_v4(P)       GCAAGTGTGAGCGAATCCGGGGTCGTAAAGCCACGCTGGATGAGATCCAGACGGTGCACT
Bt_HDAC5_v2          GCAAGTGTGAGCGAATCCGGGGTCGTAAAGCCACGCTGGATGAGATCCAGACGGTGCACT
Bt_HDAC5_v3(P)       GCAAGTGTGAGCGAATCCGGGGTCGTAAAGCCACGCTGGATGAGATCCAGACGGTGCACT
Oa_HDAC5_v11(P)      GCAAGTGTGAGCGAATCCGGGGTCGTAAAGCCACGCTGGATGAGATCCAGACGGTGCACT
Oa_HDAC5_v10(P)      GCAAGTGTGAGCGAATCCGGGGTCGTAAAGCCACGCTGGATGAGATCCAGACGGTGCACT
Oa_HDAC5_v8(P)       GCAAGTGTGAGCGAATCCGGGGTCGTAAAGCCACGCTGGATGAGATCCAGACGGTGCACT
Oa_HDAC5_v9(P)       GCAAGTGTGAGCGAATCCGGGGTCGTAAAGCCACGCTGGATGAGATCCAGACGGTGCACT
Oa_HDAC5_v1(P)       GCAAGTGTGAGCGAATCCGGGGTCGTAAAGCCACGCTGGATGAGATCCAGACGGTGCACT
Oa_HDAC5_v7(P)       GCAAGTGTGAGCGAATCCGGGGTCGTAAAGCCACGCTGGATGAGATCCAGACGGTGCACT
Oa_HDAC5_v6(P)       GCAAGTGTGAGCGAATCCGGGGTCGTAAAGCCACGCTGGATGAGATCCAGACGGTGCACT
Oa_HDAC5_v5(P)       GCAAGTGTGAGCGAATCCGGGGTCGTAAAGCCACGCTGGATGAGATCCAGACGGTGCACT
Oa_HDAC5_v2(P)       GCAAGTGTGAGCGAATCCGGGGTCGTAAAGCCACGCTGGATGAGATCCAGACGGTGCACT
Oa_HDAC5_v4(P)       GCAAGTGTGAGCGAATCCGGGGTCGTAAAGCCACGCTGGATGAGATCCAGACGGTGCACT
                     ******* ***** ***** ***** ******** ** ***** ******** *******

Mm_HDAC5_v4          CTGAGTACCACACCCTGCTCTATGGGACCAGCCCCCTTAACCGGCAGAAGCTGGACAGCA
Mm_HDAC5_v1          CTGAGTACCACACCCTGCTCTATGGGACCAGCCCCCTTAACCGGCAGAAGCTGGACAGCA
Mm_HDAC5_v3          CTGAGTACCACACCCTGCTCTATGGGACCAGCCCCCTTAACCGGCAGAAGCTGGACAGCA
Mm_HDAC5_v5          CTGAGTACCACACCCTGCTCTATGGGACCAGCCCCCTTAACCGGCAGAAGCTGGACAGCA
Hs_HDAC5_v1          CTGAATACCACACCCTGCTCTATGGGACCAGTCCCCTCAACCGGCAGAAGCTAGACAGCA
Hs_HDAC5_v3          CTGAATACCACACCCTGCTCTATGGGACCAGTCCCCTCAACCGGCAGAAGCTAGACAGCA
Bt_HDAC5_v1          CCGAGTACCACACCCTGCTGTACGGTACCAGCCCCCTCAACCGGCAGAAGCTGGACAGCA
Bt_HDAC5_v5(P)       CCGAGTACCACACCCTGCTGTACGGTACCAGCCCCCTCAACCGGCAGAAGCTGGACAGCA
Bt_HDAC5_v4(P)       CCGAGTACCACACCCTGCTGTACGGTACCAGCCCCCTCAACCGGCAGAAGCTGGACAGCA
Bt_HDAC5_v2          CCGAGTACCACACCCTGCTGTACGGTACCAGCCCCCTCAACCGGCAGAAGCTGGACAGCA
Bt_HDAC5_v3(P)       CCGAGTACCACACCCTGCTGTACGGTACCAGCCCCCTCAACCGGCAGAAGCTGGACAGCA
Oa_HDAC5_v11(P)      CCGAGTACCACACCCTGCTCTACGGTACCAGCCCCCTCAACCGGCAGAAGCTGGACAGCA
Oa_HDAC5_v10(P)      CCGAGTACCACACCCTGCTCTACGGTACCAGCCCCCTCAACCGGCAGAAGCTGGACAGCA
Oa_HDAC5_v8(P)       CCGAGTACCACACCCTGCTCTACGGTACCAGCCCCCTCAACCGGCAGAAGCTGGACAGCA
Oa_HDAC5_v9(P)       CCGAGTACCACACCCTGCTCTACGGTACCAGCCCCCTCAACCGGCAGAAGCTGGACAGCA
Oa_HDAC5_v1(P)       CCGAGTACCACACCCTGCTCTACGGTACCAGCCCCCTCAACCGGCAGAAGCTGGACAGCA
Oa_HDAC5_v7(P)       CCGAGTACCACACCCTGCTCTACGGTACCAGCCCCCTCAACCGGCAGAAGCTGGACAGCA
Oa_HDAC5_v6(P)       CCGAGTACCACACCCTGCTCTACGGTACCAGCCCCCTCAACCGGCAGAAGCTGGACAGCA
Oa_HDAC5_v5(P)       CCGAGTACCACACCCTGCTCTACGGTACCAGCCCCCTCAACCGGCAGAAGCTGGACAGCA
Oa_HDAC5_v2(P)       CCGAGTACCACACCCTGCTCTACGGTACCAGCCCCCTCAACCGGCAGAAGCTGGACAGCA
Oa_HDAC5_v4(P)       CCGAGTACCACACCCTGCTCTACGGTACCAGCCCCCTCAACCGGCAGAAGCTGGACAGCA
                     * ** ************** ** ** ***** ***** ************** *******

Mm_HDAC5_v4          AGAAGCTGCTTGGCCCCATCAGCCAGAAGATGTACGCCATGCTGCCCTGTGGGGGCATTG
Mm_HDAC5_v1          AGAAGCTGCTTGGCCCCATCAGCCAGAAGATGTACGCCATGCTGCCCTGTGGGGGCATTG
Mm_HDAC5_v3          AGAAGCTGCTTGGCCCCATCAGCCAGAAGATGTACGCCATGCTGCCCTGTGGGGGCATTG
Mm_HDAC5_v5          AGAAGCTGCTTGGCCCCATCAGCCAGAAGATGTACGCCATGCTGCCCTGTGGGGGCATTG
Hs_HDAC5_v1          AGAAGTTGCTCGGCCCCATCAGCCAGAAGATGTATGCTGTGCTGCCTTGTGGGGGCATCG
Hs_HDAC5_v3          AGAAGTTGCTCGGCCCCATCAGCCAGAAGATGTATGCTGTGCTGCCTTGTGGGGGCATCG
Bt_HDAC5_v1          AGAAGCTGCTCGGCCCCATCAGCCAGAAGATGTACGCCATGCTGCCTTGCGGGGGCATTG
Bt_HDAC5_v5(P)       AGAAGCTGCTCGGCCCCATCAGCCAGAAGATGTACGCCATGCTGCCTTGCGGGGGCATTG
Bt_HDAC5_v4(P)       AGAAGCTGCTCGGCCCCATCAGCCAGAAGATGTACGCCATGCTGCCTTGCGGGGGCATTG
Bt_HDAC5_v2          AGAAGCTGCTCGGCCCCATCAGCCAGAAGATGTACGCCATGCTGCCTTGCGGGGGCATTG
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Bt_HDAC5_v3(P)      AGAAGCTGCTCGGCCCCATCAGCCAGAAGATGTACGCCATGCTGCCTTGCGGGGGCATTG
Oa_HDAC5_v11(P)     AGAAGCTGCTCGGCCCCATCAGCCAGAAGATGTACGCCATGCTGCCTTGCGGGGGCATTG
Oa_HDAC5_v10(P)     AGAAGCTGCTCGGCCCCATCAGCCAGAAGATGTACGCCATGCTGCCTTGCGGGGGCATTG
Oa_HDAC5_v8(P)      AGAAGCTGCTCGGCCCCATCAGCCAGAAGATGTACGCCATGCTGCCTTGCGGGGGCATTG
Oa_HDAC5_v9(P)      AGAAGCTGCTCGGCCCCATCAGCCAGAAGATGTACGCCATGCTGCCTTGCGGGGGCATTG
Oa_HDAC5_v1(P)      AGAAGCTGCTCGGCCCCATCAGCCAGAAGATGTACGCCATGCTGCCTTGCGGGGGCATTG
Oa_HDAC5_v7(P)      AGAAGCTGCTCGGCCCCATCAGCCAGAAGATGTACGCCATGCTGCCTTGCGGGGGCATTG
Oa_HDAC5_v6(P)      AGAAGCTGCTCGGCCCCATCAGCCAGAAGATGTACGCCATGCTGCCTTGCGGGGGCATTG
Oa_HDAC5_v5(P)      AGAAGCTGCTCGGCCCCATCAGCCAGAAGATGTACGCCATGCTGCCTTGCGGGGGCATTG
Oa_HDAC5_v2(P)      AGAAGCTGCTCGGCCCCATCAGCCAGAAGATGTACGCCATGCTGCCTTGCGGGGGCATTG
Oa_HDAC5_v4(P)      AGAAGCTGCTCGGCCCCATCAGCCAGAAGATGTACGCCATGCTGCCTTGCGGGGGCATTG
                    ***** **** ********************** **  ******* ** ******** *

Mm_HDAC5_v4         GGGTGGACAGTGACACGGTGTGGAATGAGATGCACTCCTCAAGTGCCGTGCGAATGGCAG
Mm_HDAC5_v1         GGGTGGACAGTGACACGGTGTGGAATGAGATGCACTCCTCAAGTGCCGTGCGAATGGCAG
Mm_HDAC5_v3         GGGTGGACAGTGACACGGTGTGGAATGAGATGCACTCCTCAAGTGCCGTGCGAATGGCAG
Mm_HDAC5_v5         GGGTGGACAGTGACACGGTGTGGAATGAGATGCACTCCTCAAGTGCCGTGCGAATGGCAG
Hs_HDAC5_v1         GGGTGGACAGTGACACCGTGTGGAATGAGATGCACTCCTCCAGTGCTGTGCGCATGGCAG
Hs_HDAC5_v3         GGGTGGACAGTGACACCGTGTGGAATGAGATGCACTCCTCCAGTGCTGTGCGCATGGCAG
Bt_HDAC5_v1         GGGTGGACAGCGACACTGTGTGGAACGAGATGCACTCCTCCAGCGCCGTGCGCATGGCCG
Bt_HDAC5_v5(P)      GGGTGGACAGCGACACTGTGTGGAACGAGATGCACTCCTCCAGCGCCGTGCGCATGGCCG
Bt_HDAC5_v4(P)      GGGTGGACAGCGACACTGTGTGGAACGAGATGCACTCCTCCAGCGCCGTGCGCATGGCCG
Bt_HDAC5_v2         GGGTGGACAGCGACACTGTGTGGAACGAGATGCACTCCTCCAGCGCCGTGCGCATGGCCG
Bt_HDAC5_v3(P)      GGGTGGACAGCGACACTGTGTGGAACGAGATGCACTCCTCCAGCGCCGTGCGCATGGCCG
Oa_HDAC5_v11(P)     GGGTGGACAGCGACACTGTGTGGAACGAGATGCACTCCTCCAGCGCCGTGCGCATGGCGG
Oa_HDAC5_v10(P)     GGGTGGACAGCGACACTGTGTGGAACGAGATGCACTCCTCCAGCGCCGTGCGCATGGCGG
Oa_HDAC5_v8(P)      GGGTGGACAGCGACACTGTGTGGAACGAGATGCACTCCTCCAGCGCCGTGCGCATGGCGG
Oa_HDAC5_v9(P)      GGGTGGACAGCGACACTGTGTGGAACGAGATGCACTCCTCCAGCGCCGTGCGCATGGCGG
Oa_HDAC5_v1(P)      GGGTGGACAGCGACACTGTGTGGAACGAGATGCACTCCTCCAGCGCCGTGCGCATGGCGG
Oa_HDAC5_v7(P)      GGGTGGACAGCGACACTGTGTGGAACGAGATGCACTCCTCCAGCGCCGTGCGCATGGCGG
Oa_HDAC5_v6(P)      GGGTGGACAGCGACACTGTGTGGAACGAGATGCACTCCTCCAGCGCCGTGCGCATGGCGG
Oa_HDAC5_v5(P)      GGGTGGACAGCGACACTGTGTGGAACGAGATGCACTCCTCCAGCGCCGTGCGCATGGCGG
Oa_HDAC5_v2(P)      GGGTGGACAGCGACACTGTGTGGAACGAGATGCACTCCTCCAGCGCCGTGCGCATGGCGG
Oa_HDAC5_v4(P)      GGGTGGACAGCGACACTGTGTGGAACGAGATGCACTCCTCCAGCGCCGTGCGCATGGCGG
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Mm_HDAC5_v4         TGGGCTGCCTGGTGGAGCTGGCCTTCAAGGTGGCTGCAGGAGAGCTCAAGAATGGATTTG
Mm_HDAC5_v1         TGGGCTGCCTGGTGGAGCTGGCCTTCAAGGTGGCTGCAGGAGAGCTCAAGAATGGATTTG
Mm_HDAC5_v3         TGGGCTGCCTGGTGGAGCTGGCCTTCAAGGTGGCTGCAGGAGAGCTCAAGAATGGATTTG
Mm_HDAC5_v5         TGGGCTGCCTGGTGGAGCTGGCCTTCAAGGTGGCTGCAGGAGAGCTCAAGAATGGATTTG
Hs_HDAC5_v1         TGGGCTGCCTGCTGGAGCTGGCCTTCAAGGTGGCTGCAGGAGAGCTCAAGAATGGATTTG
Hs_HDAC5_v3         TGGGCTGCCTGCTGGAGCTGGCCTTCAAGGTGGCTGCAGGAGAGCTCAAGAATGGATTTG
Bt_HDAC5_v1         TGGGCTGCCTGGTGGAGCTGGCATTCAAGGTGGCTGCAGGGGAGCTCAAGAATGGATTTG
Bt_HDAC5_v5(P)      TGGGCTGCCTGGTGGAGCTGGCATTCAAGGTGGCTGCAGGGGAGCTCAAGAATGGATTTG
Bt_HDAC5_v4(P)      TGGGCTGCCTGGTGGAGCTGGCATTCAAGGTGGCTGCAGGGGAGCTCAAGAATGGATTTG
Bt_HDAC5_v2         TGGGCTGCCTGGTGGAGCTGGCATTCAAGGTGGCTGCAGGGGAGCTCAAGAATGGATTTG
Bt_HDAC5_v3(P)      TGGGCTGCCTGGTGGAGCTGGCATTCAAGGTGGCTGCAGGGGAGCTCAAGAATGGATTTG
Oa_HDAC5_v11(P)     TGGGCTGCCTGGTGGAGCTGGCATTCAAGGTGGCCGCAGGGGAGCTCAAGAATGGATTTG
Oa_HDAC5_v10(P)     TGGGCTGCCTGGTGGAGCTGGCATTCAAGGTGGCCGCAGGGGAGCTCAAGAATGGATTTG
Oa_HDAC5_v8(P)      TGGGCTGCCTGGTGGAGCTGGCATTCAAGGTGGCCGCAGGGGAGCTCAAGAATGGATTTG
Oa_HDAC5_v9(P)      TGGGCTGCCTGGTGGAGCTGGCATTCAAGGTGGCCGCAGGGGAGCTCAAGAATGGATTTG
Oa_HDAC5_v1(P)      TGGGCTGCCTGGTGGAGCTGGCATTCAAGGTGGCCGCAGGGGAGCTCAAGAATGGATTTG
Oa_HDAC5_v7(P)      TGGGCTGCCTGGTGGAGCTGGCATTCAAGGTGGCCGCAGGGGAGCTCAAGAATGGATTTG
Oa_HDAC5_v6(P)      TGGGCTGCCTGGTGGAGCTGGCATTCAAGGTGGCCGCAGGGGAGCTCAAGAATGGATTTG
Oa_HDAC5_v5(P)      TGGGCTGCCTGGTGGAGCTGGCATTCAAGGTGGCCGCAGGGGAGCTCAAGAATGGATTTG
Oa_HDAC5_v2(P)      TGGGCTGCCTGGTGGAGCTGGCATTCAAGGTGGCCGCAGGGGAGCTCAAGAATGGATTTG
Oa_HDAC5_v4(P)      TGGGCTGCCTGGTGGAGCTGGCATTCAAGGTGGCCGCAGGGGAGCTCAAGAATGGATTTG
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Mm_HDAC5_v4         CTATCATCCGGCCCCCAGGACACCATGCTGAGGAGTCCACAGCCATGGGATTCTGCTTCT
Mm_HDAC5_v1         CTATCATCCGGCCCCCAGGACACCATGCTGAGGAGTCCACAGCCATGGGATTCTGCTTCT
Mm_HDAC5_v3         CTATCATCCGGCCCCCAGGACACCATGCTGAGGAGTCCACAGCCATGGGATTCTGCTTCT
Mm_HDAC5_v5         CTATCATCCGGCCCCCAGGACACCATGCTGAGGAGTCCACAGCCATGGGATTCTGCTTCT
Hs_HDAC5_v1         CCATCATCCGGCCCCCAGGACACCACGCCGAGGAATCCACAGCCATGGGATTCTGCTTCT
Hs_HDAC5_v3         CCATCATCCGGCCCCCAGGACACCACGCCGAGGAATCCACAGCCATGGGATTCTGCTTCT
Bt_HDAC5_v1         CCATCATCCGGCCCCCAGGACACCACGCGGAGGAATCCACAGCCATGGGATTCTGCTTCT
Bt_HDAC5_v5(P)      CCATCATCCGGCCCCCAGGACACCACGCGGAGGAATCCACAGCCATGGGATTCTGCTTCT
Bt_HDAC5_v4(P)      CCATCATCCGGCCCCCAGGACACCACGCGGAGGAATCCACAGCCATGGGATTCTGCTTCT
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Bt_HDAC5_v2          CCATCATCCGGCCCCCAGGACACCACGCGGAGGAATCCACAGCCATGGGATTCTGCTTCT
Bt_HDAC5_v3(P)       CCATCATCCGGCCCCCAGGACACCACGCGGAGGAATCCACAGCCATGGGATTCTGCTTCT
Oa_HDAC5_v11(P)      CCATCATAAGGCCCCCAGGACACCACGCGGAAGAATCCACAGCCATGGGATTCTGCTTCT
Oa_HDAC5_v10(P)      CCATCATAAGGCCCCCAGGACACCACGCGGAAGAATCCACAGCCATGGGATTCTGCTTCT
Oa_HDAC5_v8(P)       CCATCATAAGGCCCCCAGGACACCACGCGGAAGAATCCACAGCCATGGGATTCTGCTTCT
Oa_HDAC5_v9(P)       CCATCATAAGGCCCCCAGGACACCACGCGGAAGAATCCACAGCCATGGGATTCTGCTTCT
Oa_HDAC5_v1(P)       CCATCATAAGGCCCCCAGGACACCACGCGGAAGAATCCACAGCCATGGGATTCTGCTTCT
Oa_HDAC5_v7(P)       CCATCATAAGGCCCCCAGGACACCACGCGGAAGAATCCACAGCCATGGGATTCTGCTTCT
Oa_HDAC5_v6(P)       CCATCATAAGGCCCCCAGGACACCACGCGGAAGAATCCACAGCCATGGGATTCTGCTTCT
Oa_HDAC5_v5(P)       CCATCATAAGGCCCCCAGGACACCACGCGGAAGAATCCACAGCCATGGGATTCTGCTTCT
Oa_HDAC5_v2(P)       CCATCATAAGGCCCCCAGGACACCACGCGGAAGAATCCACAGCCATGGGATTCTGCTTCT
Oa_HDAC5_v4(P)       CCATCATAAGGCCCCCAGGACACCACGCGGAAGAATCCACAGCCATGGGATTCTGCTTCT
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Mm_HDAC5_v4          TCAACTCCGTAGCCATCACAGCTAAACTCCTGCAGCAGAAGCTGAGCGTGGGCAAGGTCC
Mm_HDAC5_v1          TCAACTCCGTAGCCATCACAGCTAAACTCCTGCAGCAGAAGCTGAGCGTGGGCAAGGTCC
Mm_HDAC5_v3          TCAACTCCGTAGCCATCACAGCTAAACTCCTGCAGCAGAAGCTGAGCGTGGGCAAGGTCC
Mm_HDAC5_v5          TCAACTCCGTAGCCATCACAGCTAAACTCCTGCAGCAGAAGCTGAGCGTGGGCAAGGTCC
Hs_HDAC5_v1          TCAACTCTGTAGCCATCACCGCAAAACTCCTACAGCAGAAGTTGAACGTGGGCAAGGTCC
Hs_HDAC5_v3          TCAACTCTGTAGCCATCACCGCAAAACTCCTACAGCAGAAGTTGAACGTGGGCAAGGTCC
Bt_HDAC5_v1          TCAACTCAGTAGCTATCACAACCAAGCTCCTGCAGCAGAAGTTGAACGTGGGCAAGGTTC
Bt_HDAC5_v5(P)       TCAACTCAGTAGCTATCACAACCAAGCTCCTGCAGCAGAAGTTGAACGTGGGCAAGGTTC
Bt_HDAC5_v4(P)       TCAACTCAGTAGCTATCACAACCAAGCTCCTGCAGCAGAAGTTGAACGTGGGCAAGGTTC
Bt_HDAC5_v2          TCAACTCAGTAGCTATCACAACCAAGCTCCTGCAGCAGAAGTTGAACGTGGGCAAGGTTC
Bt_HDAC5_v3(P)       TCAACTCAGTAGCTATCACAACCAAGCTCCTGCAGCAGAAGTTGAACGTGGGCAAGGTTC
Oa_HDAC5_v11(P)      TCAACTCAGTAGCTATCACAACCAAGCTCCTGCAGCAGAAGTTGAACGTGGGCAAGGTTC
Oa_HDAC5_v10(P)      TCAACTCAGTAGCTATCACAACCAAGCTCCTGCAGCAGAAGTTGAACGTGGGCAAGGTTC
Oa_HDAC5_v8(P)       TCAACTCAGTAGCTATCACAACCAAGCTCCTGCAGCAGAAGTTGAACGTGGGCAAGGTTC
Oa_HDAC5_v9(P)       TCAACTCAGTAGCTATCACAACCAAGCTCCTGCAGCAGAAGTTGAACGTGGGCAAGGTTC
Oa_HDAC5_v1(P)       TCAACTCAGTAGCTATCACAACCAAGCTCCTGCAGCAGAAGTTGAACGTGGGCAAGGTTC
Oa_HDAC5_v7(P)       TCAACTCAGTAGCTATCACAACCAAGCTCCTGCAGCAGAAGTTGAACGTGGGCAAGGTTC
Oa_HDAC5_v6(P)       TCAACTCAGTAGCTATCACAACCAAGCTCCTGCAGCAGAAGTTGAACGTGGGCAAGGTTC
Oa_HDAC5_v5(P)       TCAACTCAGTAGCTATCACAACCAAGCTCCTGCAGCAGAAGTTGAACGTGGGCAAGGTTC
Oa_HDAC5_v2(P)       TCAACTCAGTAGCTATCACAACCAAGCTCCTGCAGCAGAAGTTGAACGTGGGCAAGGTTC
Oa_HDAC5_v4(P)       TCAACTCAGTAGCTATCACAACCAAGCTCCTGCAGCAGAAGTTGAACGTGGGCAAGGTTC
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Mm_HDAC5_v4          TCATCGTGGACTGGGATATTCACCATGGCAACGGCACCCAGCAAGCATTCTACAACGATC
Mm_HDAC5_v1          TCATCGTGGACTGGGATATTCACCATGGCAACGGCACCCAGCAAGCATTCTACAACGATC
Mm_HDAC5_v3          TCATCGTGGACTGGGATATTCACCATGGCAACGGCACCCAGCAAGCATTCTACAACGATC
Mm_HDAC5_v5          TCATCGTGGACTGGGATATTCACCATGGCAACGGCACCCAGCAAGCATTCTACAACGATC
Hs_HDAC5_v1          TCATCGTGGACTGGGACATTCACCATGGCAATGGCACCCAGCAGGCGTTCTACAATGACC
Hs_HDAC5_v3          TCATCGTGGACTGGGACATTCACCATGGCAATGGCACCCAGCAGGCGTTCTACAATGACC
Bt_HDAC5_v1          TCATCGTGGACTGGGACATTCACCATGGCAATGGCACCCAGCAAGCATTTTACAACGATC
Bt_HDAC5_v5(P)       TCATCGTGGACTGGGACATTCACCATGGCAATGGCACCCAGCAAGCATTTTACAACGATC
Bt_HDAC5_v4(P)       TCATCGTGGACTGGGACATTCACCATGGCAATGGCACCCAGCAAGCATTTTACAACGATC
Bt_HDAC5_v2          TCATCGTGGACTGGGACATTCACCATGGCAATGGCACCCAGCAAGCATTTTACAACGATC
Bt_HDAC5_v3(P)       TCATCGTGGACTGGGACATTCACCATGGCAATGGCACCCAGCAAGCATTTTACAACGATC
Oa_HDAC5_v11(P)      TCATCGTGGACTGGGATATTCACCATGGCAACGGCACCCAGCAAGCATTTTACAATGATC
Oa_HDAC5_v10(P)      TCATCGTGGACTGGGATATTCACCATGGCAACGGCACCCAGCAAGCATTTTACAATGATC
Oa_HDAC5_v8(P)       TCATCGTGGACTGGGATATTCACCATGGCAACGGCACCCAGCAAGCATTTTACAATGATC
Oa_HDAC5_v9(P)       TCATCGTGGACTGGGATATTCACCATGGCAACGGCACCCAGCAAGCATTTTACAATGATC
Oa_HDAC5_v1(P)       TCATCGTGGACTGGGACATTCACCATGGCAACGGCACCCAGCAAGCATTTTACAACGATC
Oa_HDAC5_v7(P)       TCATCGTGGACTGGGATATTCACCATGGCAACGGCACCCAGCAAGCATTTTACAATGATC
Oa_HDAC5_v6(P)       TCATCGTGGACTGGGATATTCACCATGGCAACGGCACCCAGCAAGCATTTTACAATGATC
Oa_HDAC5_v5(P)       TCATCGTGGACTGGGATATTCACCATGGCAACGGCACCCAGCAAGCATTTTACAATGATC
Oa_HDAC5_v2(P)       TCATCGTGGACTGGGATATTCACCATGGCAACGGCACCCAGCAAGCATTTTACAATGATC
Oa_HDAC5_v4(P)       TCATCGTGGACTGGGATATTCACCATGGCAACGGCACCCAGCAAGCATTTTACAATGATC
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Mm_HDAC5_v4          CCTCTGTGCTCTACATCTCCCTGCATCGCTACGACAACGGGAACTTCTTTCCAGGCTCTG
Mm_HDAC5_v1          CCTCTGTGCTCTACATCTCCCTGCATCGCTACGACAACGGGAACTTCTTTCCAGGCTCTG
Mm_HDAC5_v3          CCTCTGTGCTCTACATCTCCCTGCATCGCTACGACAACGGGAACTTCTTTCCAGGCTCTG
Mm_HDAC5_v5          CCTCTGTGCTCTACATCTCCCTGCATCGCTACGACAACGGGAACTTCTTTCCAGGCTCTG
Hs_HDAC5_v1          CCTCTGTGCTCTACATCTCTCTGCATCGCTATGACAACGGGAACTTCTTTCCAGGCTCTG
Hs_HDAC5_v3          CCTCTGTGCTCTACATCTCTCTGCATCGCTATGACAACGGGAACTTCTTTCCAGGCTCTG
Bt_HDAC5_v1          CCTCTGTGCTCTACATCTCCCTGCATCGCTATGACAACGGGAACTTCTTTCCGGGCTCTG
Bt_HDAC5_v5(P)       CCTCTGTGCTCTACATCTCCCTGCATCGCTATGACAACGGGAACTTCTTTCCGGGCTCTG
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Bt_HDAC5_v4(P)      CCTCTGTGCTCTACATCTCCCTGCATCGCTATGACAACGGGAACTTCTTTCCGGGCTCTG
Bt_HDAC5_v2         CCTCTGTGCTCTACATCTCCCTGCATCGCTATGACAACGGGAACTTCTTTCCGGGCTCTG
Bt_HDAC5_v3(P)      CCTCTGTGCTCTACATCTCCCTGCATCGCTATGACAACGGGAACTTCTTTCCGGGCTCTG
Oa_HDAC5_v11(P)     CCTCCGTGCTCTACATCTCCCTGCATCGCTATGACAATGGGAACTTCTTTCCGGGCTCCG
Oa_HDAC5_v10(P)     CCTCCGTGCTCTACATCTCCCTGCATCGCTATGACAATGGGAACTTCTTTCCGGGCTCCG
Oa_HDAC5_v8(P)      CCTCCGTGCTCTACATCTCCCTGCATCGCTATGACAATGGGAACTTCTTTCCGGGCTCCG
Oa_HDAC5_v9(P)      CCTCCGTGCTCTACATCTCCCTGCATCGCTATGACAATGGGAACTTCTTTCCGGGCTCCG
Oa_HDAC5_v1(P)      CCTCCGTGCTCTACATCTCCCTGCATCGCTATGACAATGGGAACTTCTTTCCGGGCTCCG
Oa_HDAC5_v7(P)      CCTCCGTGCTCTACATCTCCCTGCATCGCTATGACAATGGGAACTTCTTTCCGGGCTCCG
Oa_HDAC5_v6(P)      CCTCCGTGCTCTACATCTCCCTGCATCGCTATGACAATGGGAACTTCTTTCCGGGCTCCG
Oa_HDAC5_v5(P)      CCTCCGTGCTCTACATCTCCCTGCATCGCTATGACAATGGGAACTTCTTTCCGGGCTCCG
Oa_HDAC5_v2(P)      CCTCCGTGCTCTACATCTCCCTGCATCGCTATGACAATGGGAACTTCTTTCCGGGCTCCG
Oa_HDAC5_v4(P)      CCTCCGTGCTCTACATCTCCCTGCATCGCTATGACAATGGGAACTTCTTTCCGGGCTCCG
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Mm_HDAC5_v4         GGGCTCCTGAAGAGGTTGGTGGAGGGCCAGGTGTGGGGTACAACGTAAATGTGGCGTGGA
Mm_HDAC5_v1         GGGCTCCTGAAGAGGTTGGTGGAGGGCCAGGTGTGGGGTACAACGTAAATGTGGCGTGGA
Mm_HDAC5_v3         GGGCTCCTGAAGAGGTTGGTGGAGGGCCAGGTGTGGGGTACAACGTAAATGTGGCGTGGA
Mm_HDAC5_v5         GGGCTCCTGAAGAGGTTGGTGGAGGGCCAGGTGTGGGGTACAACGTAAATGTGGCGTGGA
Hs_HDAC5_v1         GGGCTCCTGAAGAGGTTGGTGGAGGACCAGGCGTGGGGTACAATGTGAACGTGGCATGGA
Hs_HDAC5_v3         GGGCTCCTGAAGAGGTTGGTGGAGGACCAGGCGTGGGGTACAATGTGAACGTGGCATGGA
Bt_HDAC5_v1         GGGCTCCTGAAGAGGTTGGCGGAGGGCCGGGCGTGGGGTACAATGTGAACGTGGCATGGA
Bt_HDAC5_v5(P)      GGGCTCCTGAAGAGGTTGGCGGAGGGCCGGGCGTGGGGTACAATGTGAACGTGGCATGGA
Bt_HDAC5_v4(P)      GGGCTCCTGAAGAGGTTGGCGGAGGGCCGGGCGTGGGGTACAATGTGAACGTGGCATGGA
Bt_HDAC5_v2         GGGCTCCTGAAGAGGTTGGCGGAGGGCCGGGCGTGGGGTACAATGTGAACGTGGCATGGA
Bt_HDAC5_v3(P)      GGGCTCCTGAAGAGGTTGGCGGAGGGCCGGGCGTGGGGTACAATGTGAACGTGGCATGGA
Oa_HDAC5_v11(P)     GGGCTCCTGAAGAGGTTGGCGGAGGGCCGGGCGTGGGGTACAATGTGAATGTGGCATGGA
Oa_HDAC5_v10(P)     GGGCTCCTGAAGAGGTTGGCGGAGGGCCGGGCGTGGGGTACAATGTGAATGTGGCATGGA
Oa_HDAC5_v8(P)      GGGCTCCTGAAGAGGTTGGCGGAGGGCCGGGCGTGGGGTACAATGTGAATGTGGCATGGA
Oa_HDAC5_v9(P)      GGGCTCCTGAAGAGGTTGGCGGAGGGCCGGGCGTGGGGTACAATGTGAATGTGGCATGGA
Oa_HDAC5_v1(P)      GGGCTCCTGAAGAGGTTGGCGGAGGGCCGGGCGTGGGGTACAATGTGAATGTGGCATGGA
Oa_HDAC5_v7(P)      GGGCTCCTGAAGAGGTTGGCGGAGGGCCGGGCGTGGGGTACAATGTGAATGTGGCATGGA
Oa_HDAC5_v6(P)      GGGCTCCTGAAGAGGTTGGCGGAGGGCCGGGCGTGGGGTACAATGTGAATGTGGCATGGA
Oa_HDAC5_v5(P)      GGGCTCCTGAAGAGGTTGGCGGAGGGCCGGGCGTGGGGTACAATGTGAATGTGGCATGGA
Oa_HDAC5_v2(P)      GGGCTCCTGAAGAGGTTGGCGGAGGGCCGGGCGTGGGGTACAATGTGAATGTGGCATGGA
Oa_HDAC5_v4(P)      GGGCTCCTGAAGAGGTTGGCGGAGGGCCGGGCGTGGGGTACAATGTGAATGTGGCATGGA
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Mm_HDAC5_v4         CAGGAGGTGTGGATCCCCCCATTGGAGATGTGGAATACCTGACAGCCTTCAGGACAGTGG
Mm_HDAC5_v1         CAGGAGGTGTGGATCCCCCCATTGGAGATGTGGAATACCTGACAGCCTTCAGGACAGTGG
Mm_HDAC5_v3         CAGGAGGTGTGGATCCCCCCATTGGAGATGTGGAATACCTGACAGCCTTCAGGACAGTGG
Mm_HDAC5_v5         CAGGAGGTGTGGATCCCCCCATTGGAGATGTGGAATACCTGACAGCCTTCAGGACAGTGG
Hs_HDAC5_v1         CAGGAGGTGTGGACCCCCCCCATTGGAGACGTGGAGTACCTTACAGCCTTCAGGACAGTGG
Hs_HDAC5_v3         CAGGAGGTGTGGACCCCCCCCATTGGAGACGTGGAGTACCTTACAGCCTTCAGGACAGTGG
Bt_HDAC5_v1         CGGGAGGTGTGGACCCCCCCCATCGGAGACGTGGAGTACCTAACGGCCTTCAGGACAGTGG
Bt_HDAC5_v5(P)      CGGGAGGTGTGGACCCCCCCCATCGGAGACGTGGAGTACCTAACGGCCTTCAGGACAGTGG
Bt_HDAC5_v4(P)      CGGGAGGTGTGGACCCCCCCCATCGGAGACGTGGAGTACCTAACGGCCTTCAGGACAGTGG
Bt_HDAC5_v2         CGGGAGGTGTGGACCCCCCCCATCGGAGACGTGGAGTACCTAACGGCCTTCAGGACAGTGG
Bt_HDAC5_v3(P)      CGGGAGGTGTGGACCCCCCCCATCGGAGACGTGGAGTACCTAACGGCCTTCAGGACAGTGG
Oa_HDAC5_v11(P)     CAGGAGGTGTGGACCCCCCCCATCGGAGACGTGGAGTACCTAACAGCCTTCAGGACAGTGG
Oa_HDAC5_v10(P)     CAGGAGGTGTGGACCCCCCCCATCGGAGACGTGGAGTACCTAACAGCCTTCAGGACAGTGG
Oa_HDAC5_v8(P)      CAGGAGGTGTGGACCCCCCCCATCGGAGACGTGGAGTACCTAACAGCCTTCAGGACAGTGG
Oa_HDAC5_v9(P)      CAGGAGGTGTGGACCCCCCCCATCGGAGACGTGGAGTACCTAACAGCCTTCAGGACAGTGG
Oa_HDAC5_v1(P)      CAGGAGGTGTGGACCCCCCCCATCGGAGACGTGGAGTACCTAACAGCCTTCAGGACAGTGG
Oa_HDAC5_v7(P)      CAGGAGGTGTGGACCCCCCCCATCGGAGACGTGGAGTACCTAACAGCCTTCAGGACAGTGG
Oa_HDAC5_v6(P)      CAGGAGGTGTGGACCCCCCCCATCGGAGACGTGGAGTACCTAACAGCCTTCAGGACAGTGG
Oa_HDAC5_v5(P)      CAGGAGGTGTGGACCCCCCCCATCGGAGACGTGGAGTACCTAACAGCCTTCAGGACAGTGG
Oa_HDAC5_v2(P)      CAGGAGGTGTGGACCCCCCCCATCGGAGACGTGGAGTACCTAACAGCCTTCAGGACAGTGG
Oa_HDAC5_v4(P)      CAGGAGGTGTGGACCCCCCCCATCGGAGACGTGGAGTACCTAACAGCCTTCAGGACAGTGG
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Mm_HDAC5_v4         TGATGCCCATTGCCCAGGAGTTCTCACCTGACGTCGTCCTAGTCTCCGCTGGGTTTGATG
Mm_HDAC5_v1         TGATGCCCATTGCCCAGGAGTTCTCACCTGACGTCGTCCTAGTCTCCGCTGGGTTTGATG
Mm_HDAC5_v3         TGATGCCCATTGCCCAGGAGTTCTCACCTGACGTCGTCCTAGTCTCCGCTGGGTTTGATG
Mm_HDAC5_v5         TGATGCCCATTGCCCAGGAGTTCTCACCTGACGTCGTCCTAGTCTCCGCTGGGTTTGATG
Hs_HDAC5_v1         TGATGCCCATTGCCCACGAGTTCTCACCTGATGTGGTCCTAGTCTCCGCCGGGTTTGATG
Hs_HDAC5_v3         TGATGCCCATTGCCCACGAGTTCTCACCTGATGTGGTCCTAGTCTCCGCCGGGTTTGATG
Bt_HDAC5_v1         TGATGCCCATTGCCCACGAGTTCTCACCTGATGTGGTCCTGGTCTCCGCTGGCTTTGATG
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Bt_HDAC5_v5(P)      TGATGCCCATTGCCCACGAGTTCTCACCTGATGTGGTCCTGGTCTCCGCTGGCTTTGATG
Bt_HDAC5_v4(P)      TGATGCCCATTGCCCACGAGTTCTCACCTGATGTGGTCCTGGTCTCCGCTGGCTTTGATG
Bt_HDAC5_v2         TGATGCCCATTGCCCACGAGTTCTCACCTGATGTGGTCCTGGTCTCCGCTGGCTTTGATG
Bt_HDAC5_v3(P)      TGATGCCCATTGCCCACGAGTTCTCACCTGATGTGGTCCTGGTCTCCGCTGGCTTTGATG
Oa_HDAC5_v11(P)     TGATGCCCATTGCCCACGAGTTCTCACCTGATGTGGTCCTGGTCTCCGCTGGCTTTGATG
Oa_HDAC5_v10(P)     TGATGCCCATTGCCCACGAGTTCTCACCTGATGTGGTCCTGGTCTCCGCTGGCTTTGATG
Oa_HDAC5_v8(P)      TGATGCCCATTGCCCACGAGTTCTCACCTGATGTGGTCCTGGTCTCCGCTGGCTTTGATG
Oa_HDAC5_v9(P)      TGATGCCCATTGCCCACGAGTTCTCACCTGATGTGGTCCTGGTCTCCGCTGGCTTTGATG
Oa_HDAC5_v1(P)      TGATGCCCATTGCCCACGAGTTCTCACCTGATGTGGTCCTGGTCTCCGCTGGCTTTGATG
Oa_HDAC5_v7(P)      TGATGCCCATTGCCCACGAGTTCTCACCTGATGTGGTCCTGGTCTCCGCTGGCTTTGATG
Oa_HDAC5_v6(P)      TGATGCCCATTGCCCACGAGTTCTCACCTGATGTGGTCCTGGTCTCCGCTGGCTTTGATG
Oa_HDAC5_v5(P)      TGATGCCCATTGCCCACGAGTTCTCACCTGATGTGGTCCTGGTCTCCGCTGGCTTTGATG
Oa_HDAC5_v2(P)      TGATGCCCATTGCCCACGAGTTCTCACCTGATGTGGTCCTGGTCTCCGCTGGCTTTGATG
Oa_HDAC5_v4(P)      TGATGCCCATTGCCCACGAGTTCTCACCTGATGTGGTCCTGGTCTCCGCTGGCTTTGATG
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Mm_HDAC5_v4         CTGTTGAAGGACATCTGTCTCCACTGGGTGGCTATTCTGTCACCGCCAGATGTTTTGGCC
Mm_HDAC5_v1         CTGTTGAAGGACATCTGTCTCCACTGGGTGGCTATTCTGTCACCGCCAGATGTTTTGGCC
Mm_HDAC5_v3         CTGTTGAAGGACATCTGTCTCCACTGGGTGGCTATTCTGTCACCGCCAGATGTTTTGGCC
Mm_HDAC5_v5         CTGTTGAAGGACATCTGTCTCCACTGGGTGGCTATTCTGTCACCGCCAGATGTTTTGGCC
Hs_HDAC5_v1         CTGTTGAAGGACATCTGTCTCCTCTGGGTGGCTACTCTGTCACCGCCAGATGTTTTGGCC
Hs_HDAC5_v3         CTGTTGAAGGACATCTGTCTCCTCTGGGTGGCTACTCTGTCACCGCCAGATGTTTTGGCC
Bt_HDAC5_v1         CTGTTGAGGGACACCTGTCTCCGCTGGGTGGCTACTCTGTCACCGCCAGATGTTTTGGCC
Bt_HDAC5_v5(P)      CTGTTGAGGGACACCTGTCTCCGCTGGGTGGCTACTCTGTCACCGCCAGATGTTTTGGCC
Bt_HDAC5_v4(P)      CTGTTGAGGGACACCTGTCTCCGCTGGGTGGCTACTCTGTCACCGCCAGATGTTTTGGCC
Bt_HDAC5_v2         CTGTTGAGGGACACCTGTCTCCGCTGGGTGGCTACTCTGTCACCGCCAGATGTTTTGGCC
Bt_HDAC5_v3(P)      CTGTTGAGGGACACCTGTCTCCGCTGGGTGGCTACTCTGTCACCGCCAGATGTTTTGGCC
Oa_HDAC5_v11(P)     CTGTTGAGGGACACCTGTCTCCGCTGGGTGGCTACTCTGTCACCGCCAGATGTTTTGGCC
Oa_HDAC5_v10(P)     CTGTTGAGGGACACCTGTCTCCGCTGGGTGGCTACTCTGTCACCGCCAGATGTTTTGGCC
Oa_HDAC5_v8(P)      CTGTTGAGGGACACCTGTCTCCGCTGGGTGGCTACTCTGTCACCGCCAGATGTTTTGGCC
Oa_HDAC5_v9(P)      CTGTTGAGGGACACCTGTCTCCGCTGGGTGGCTACTCTGTCACCGCCAGATGTTTTGGCC
Oa_HDAC5_v1(P)      CTGTTGAGGGACACCTGTCTCCGCTGGGTGGCTACTCTGTCACCGCCAGATGTTTTGGCC
Oa_HDAC5_v7(P)      CTGTTGAGGGACACCTGTCTCCGCTGGGTGGCTACTCTGTCACCGCCAGATGTTTTGGCC
Oa_HDAC5_v6(P)      CTGTTGAGGGACACCTGTCTCCGCTGGGTGGCTACTCTGTCACCGCCAGATGTTTTGGCC
Oa_HDAC5_v5(P)      CTGTTGAGGGACACCTGTCTCCGCTGGGTGGCTACTCTGTCACCGCCAGATGTTTTGGCC
Oa_HDAC5_v2(P)      CTGTTGAGGGACACCTGTCTCCGCTGGGTGGCTACTCTGTCACCGCCAGATGTTTTGGCC
Oa_HDAC5_v4(P)      CTGTTGAGGGACACCTGTCTCCGCTGGGTGGCTACTCTGTCACCGCCAGATGTTTTGGCC
                    ******* ***** ******** *********** ************************

Mm_HDAC5_v4         ACTTGACCAGGCAGCTCATGACACTGGCTGGGGGCCGGGTGGTGCTGGCCCTGGAGGGAG
Mm_HDAC5_v1         ACTTGACCAGGCAGCTCATGACACTGGCTGGGGGCCGGGTGGTGCTGGCCCTGGAGGGAG
Mm_HDAC5_v3         ACTTGACCAGGCAGCTCATGACACTGGCTGGGGGCCGGGTGGTGCTGGCCCTGGAGGGAG
Mm_HDAC5_v5         ACTTGACCAGGCAGCTCATGACACTGGCTGGGGGCCGGGTGGTGCTGGCCCTGGAGGGAG
Hs_HDAC5_v1         ACTTGACCAGGCAGCTGATGACCCTGGCAGGGGGCCGGGTGGTGCTGGCCCTGGAGGGAG
Hs_HDAC5_v3         ACTTGACCAGGCAGCTGATGACCCTGGCAGGGGGCCGGGTGGTGCTGGCCCTGGAGGGAG
Bt_HDAC5_v1         ACTTGACCAGGCAGCTGATGACGCTGGCAGGGGGCCGGGTGGTGCTGGCCCTGGAGGGAG
Bt_HDAC5_v5(P)      ACTTGACCAGGCAGCTGATGACGCTGGCAGGGGGCCGGGTGGTGCTGGCCCTGGAGGGAG
Bt_HDAC5_v4(P)      ACTTGACCAGGCAGCTGATGACGCTGGCAGGGGGCCGGGTGGTGCTGGCCCTGGAGGGAG
Bt_HDAC5_v2         ACTTGACCAGGCAGCTGATGACGCTGGCAGGGGGCCGGGTGGTGCTGGCCCTGGAGGGAG
Bt_HDAC5_v3(P)      ACTTGACCAGGCAGCTGATGACGCTGGCAGGGGGCCGGGTGGTGCTGGCCCTGGAGGGAG
Oa_HDAC5_v11(P)     ACTTGACCAGGCAGCTGATGACGCTGGCAGGGGGCCGGGTGGTGCTGGCCTTGGAGGGAG
Oa_HDAC5_v10(P)     ACTTGACCAGGCAGCTGATGACGCTGGCAGGGGGCCGGGTGGTGCTGGCCTTGGAGGGAG
Oa_HDAC5_v8(P)      ACTTGACCAGGCAGCTGATGACGCTGGCAGGGGGCCGGGTGGTGCTGGCCTTGGAGGGAG
Oa_HDAC5_v9(P)      ACTTGACCAGGCAGCTGATGACGCTGGCAGGGGGCCGGGTGGTGCTGGCCTTGGAGGGAG
Oa_HDAC5_v1(P)      ACTTGACCAGGCAGCTGATGACGCTGGCAGGGGGCCGGGTGGTGCTGGCCTTGGAGGGAG
Oa_HDAC5_v7(P)      ACTTGACCAGGCAGCTGATGACGCTGGCAGGGGGCCGGGTGGTGCTGGCCTTGGAGGGAG
Oa_HDAC5_v6(P)      ACTTGACCAGGCAGCTGATGACGCTGGCAGGGGGCCGGGTGGTGCTGGCCTTGGAGGGAG
Oa_HDAC5_v5(P)      ACTTGACCAGGCAGCTGATGACGCTGGCAGGGGGCCGGGTGGTGCTGGCCTTGGAGGGAG
Oa_HDAC5_v2(P)      ACTTGACCAGGCAGCTGATGACGCTGGCAGGGGGCCGGGTGGTGCTGGCCTTGGAGGGAG
Oa_HDAC5_v4(P)      ACTTGACCAGGCAGCTGATGACGCTGGCAGGGGGCCGGGTGGTGCTGGCCTTGGAGGGAG
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Mm_HDAC5_v4         GCCATGACTTGACCGCCATCTGTGATGCCTCTGAGGCCTGTGTCTCGGCTCTGCTCAGCG
Mm_HDAC5_v1         GCCATGACTTGACCGCCATCTGTGATGCCTCTGAGGCCTGTGTCTCGGCTCTGCTCAGCG
Mm_HDAC5_v3         GCCATGACTTGACCGCCATCTGTGATGCCTCTGAGGCCTGTGTCTCGGCTCTGCTCAGCG
Mm_HDAC5_v5         GCCATGACTTGACCGCCATCTGTGATGCCTCTGAGGCCTGTGTCTCGGCTCTGCTCAGCG
Hs_HDAC5_v1         GCCATGACTTGACCGCCATCTGTGATGCCTCTGAGGCTTGTGTCTCGGCTCTGCTCAGTG
Hs_HDAC5_v3         GCCATGACTTGACCGCCATCTGTGATGCCTCTGAGGCTTGTGTCTCGGCTCTGCTCAGTG
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Bt_HDAC5_v1          GCCACGACCTGACCGCCATCTGTGATGCCTCTGAGGCCTGTGTCTCGGCGCTGCTCAGCG
Bt_HDAC5_v5(P)       GCCACGACCTGACCGCCATCTGTGATGCCTCTGAGGCCTGTGTCTCGGCGCTGCTCAGCG
Bt_HDAC5_v4(P)       GCCACGACCTGACCGCCATCTGTGATGCCTCTGAGGCCTGTGTCTCGGCGCTGCTCAGCG
Bt_HDAC5_v2          GCCACGACCTGACCGCCATCTGTGATGCCTCTGAGGCCTGTGTCTCGGCGCTGCTCAGCG
Bt_HDAC5_v3(P)       GCCACGACCTGACCGCCATCTGTGATGCCTCTGAGGCCTGTGTCTCGGCGCTGCTCAGCG
Oa_HDAC5_v11(P)      GCCACGACCTGACCGCCATCTGTGATGCCTCTGAGGCCTGTGTCTCGGCGCTGCTCAGCG
Oa_HDAC5_v10(P)      GCCACGACCTGACCGCCATCTGTGATGCCTCTGAGGCCTGTGTCTCGGCGCTGCTCAGCG
Oa_HDAC5_v8(P)       GCCACGACCTGACCGCCATCTGTGATGCCTCTGAGGCCTGTGTCTCGGCGCTGCTCAGCG
Oa_HDAC5_v9(P)       GCCACGACCTGACCGCCATCTGTGATGCCTCTGAGGCCTGTGTCTCGGCGCTGCTCAGCG
Oa_HDAC5_v1(P)       GCCACGACCTGACCGCCATCTGTGATGCCTCTGAGGCCTGTGTCTCGGCGCTGCTCAGCG
Oa_HDAC5_v7(P)       GCCACGACCTGACCGCCATCTGTGATGCCTCTGAGGCCTGTGTCTCGGCGCTGCTCAGCG
Oa_HDAC5_v6(P)       GCCACGACCTGACCGCCATCTGTGATGCCTCTGAGGCCTGTGTCTCGGCGCTGCTCAGCG
Oa_HDAC5_v5(P)       GCCACGACCTGACCGCCATCTGTGATGCCTCTGAGGCCTGTGTCTCGGCGCTGCTCAGCG
Oa_HDAC5_v2(P)       GCCACGACCTGACCGCCATCTGTGATGCCTCTGAGGCCTGTGTCTCGGCGCTGCTCAGCG
Oa_HDAC5_v4(P)       GCCACGACCTGACCGCCATCTGTGATGCCTCTGAGGCCTGTGTCTCGGCGCTGCTCAGCG
                     **** *** *************************** *********** ******** *

Mm_HDAC5_v4          TGGAGCTGCAGCCCTTGGATGAAGCAGTCTTGCAGCAAAAGCCCAGCGTCAATGCGGTTG
Mm_HDAC5_v1          TGGAGCTGCAGCCCTTGGATGAAGCAGTCTTGCAGCAAAAGCCCAGCGTCAATGCGGTTG
Mm_HDAC5_v3          TGGAGCTGCAGCCCTTGGATGAAGCAGTCTTGCAGCAAAAGCCCAGCGTCAATGCGGTTG
Mm_HDAC5_v5          TGGAGCTGCAGCCCTTGGATGAAGCAGTCTTGCAGCAAAAGCCCAGCGTCAATGCGGTTG
Hs_HDAC5_v1          TAGAGCTGCAGCCCTTGGATGAGGCAGTCTTGCAGCAAAAGCCCAACATCAACGCAGTGG
Hs_HDAC5_v3          TAGAGCTGCAGCCCTTGGATGAGGCAGTCTTGCAGCAAAAGCCCAACATCAACGCAGTGG
Bt_HDAC5_v1          TGGAGCTGCAGCCCTTGGACGAGGCAGTCTTGCAGCAAAAGCCCAACATCAACGCAGTGG
Bt_HDAC5_v5(P)       TGGAGCTGCAGCCCTTGGACGAGGCAGTCTTGCAGCAAAAGCCCAACATCAACGCAGTGG
Bt_HDAC5_v4(P)       TGGAGCTGCAGCCCTTGGACGAGGCAGTCTTGCAGCAAAAGCCCAACATCAACGCAGTGG
Bt_HDAC5_v2          TGGAGCTGCAGCCCTTGGACGAGGCAGTCTTGCAGCAAAAGCCCAACATCAACGCAGTGG
Bt_HDAC5_v3(P)       TGGAGCTGCAGCCCTTGGACGAGGCAGTCTTGCAGCAAAAGCCCAACATCAACGCAGTGG
Oa_HDAC5_v11(P)      TGGAGCTACAGCCCTTGGACGAGGCAGTCTTGCAGCAGAAGCCCAACGCCAATGCAGTGG
Oa_HDAC5_v10(P)      TGGAGCTACAGCCCTTGGACGAGGCAGTCTTGCAGCAGAAGCCCAACGCCAATGCAGTGG
Oa_HDAC5_v8(P)       TGGAGCTACAGCCCTTGGACGAGGCAGTCTTGCAGCAGAAGCCCAACGCCAATGCAGTGG
Oa_HDAC5_v9(P)       TGGAGCTACAGCCCTTGGACGAGGCAGTCTTGCAGCAGAAGCCCAACGCCAATGCAGTGG
Oa_HDAC5_v1(P)       TGGAGCTACAGCCCTTGGACGAGGCAGTCTTGCAGCAGAAGCCCAACGCCAATGCAGTGG
Oa_HDAC5_v7(P)       TGGAGCTACAGCCCTTGGACGAGGCAGTCTTGCAGCAGAAGCCCAACGCCAATGCAGTGG
Oa_HDAC5_v6(P)       TGGAGCTACAGCCCTTGGACGAGGCAGTCTTGCAGCAGAAGCCCAACGCCAATGCAGTGG
Oa_HDAC5_v5(P)       TGGAGCTACAGCCCTTGGACGAGGCAGTCTTGCAGCAGAAGCCCAACGCCAATGCAGTGG
Oa_HDAC5_v2(P)       TGGAGCTACAGCCCTTGGACGAGGCAGTCTTGCAGCAGAAGCCCAACGCCAATGCAGTGG
Oa_HDAC5_v4(P)       TGGAGCTACAGCCCTTGGACGAGGCAGTCTTGCAGCAGAAGCCCAACGCCAATGCAGTGG
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Mm_HDAC5_v4          CCACACTAGAGAAAGTCATCGAGATCCAGAGCAAACACTGGAGCTGTGTACAGAGGTTTG
Mm_HDAC5_v1          CCACACTAGAGAAAGTCATCGAGATCCAGAGCAAACACTGGAGCTGTGTACAGAGGTTTG
Mm_HDAC5_v3          CCACACTAGAGAAAGTCATCGAGATCCAGAGCAAACACTGGAGCTGTGTACAGAGGTTTG
Mm_HDAC5_v5          CCACACTAGAGAAAGTCATCGAGATCCAGAGCAAACACTGGAGCTGTGTACAGAGGTTTG
Hs_HDAC5_v1          CCACGCTAGAGAAAGTCATCGAGATCCAGAGCAAACACTGGAGCTGTGTGCAGAAGTTCG
Hs_HDAC5_v3          CCACGCTAGAGAAAGTCATCGAGATCCAGAGCAAACACTGGAGCTGTGTGCAGAAGTTCG
Bt_HDAC5_v1          CCACGCTGGAGAAAGTCATCGAGATCCAGAGTAAACACTGGAGCTGTGTGCAGAGGTTCG
Bt_HDAC5_v5(P)       CCACGCTGGAGAAAGTCATCGAGATCCAGAGTAAACACTGGAGCTGTGTGCAGAGGTTCG
Bt_HDAC5_v4(P)       CCACGCTGGAGAAAGTCATCGAGATCCAGAGTAAACACTGGAGCTGTGTGCAGAGGTTCG
Bt_HDAC5_v2          CCACGCTGGAGAAAGTCATCGAGATCCAGAGTAAACACTGGAGCTGTGTGCAGAGGTTCG
Bt_HDAC5_v3(P)       CCACGCTGGAGAAAGTCATCGAGATCCAGAGTAAACACTGGAGCTGTGTGCAGAGGTTCG
Oa_HDAC5_v11(P)      CCACGCTGGAGAAAGTCATCGAGATCCAGAGCAAACACTGGAGCTGTGTGCAGAGGTTCG
Oa_HDAC5_v10(P)      CCACGCTGGAGAAAGTCATCGAGATCCAGAGCAAACACTGGAGCTGTGTGCAGAGGTTCG
Oa_HDAC5_v8(P)       CCACGCTGGAGAAAGTCATCGAGATCCAGAGCAAACACTGGAGCTGTGTGCAGAGGTTCG
Oa_HDAC5_v9(P)       CCACGCTGGAGAAAGTCATCGAGATCCAGAGCAAACACTGGAGCTGTGTGCAGAGGTTCG
Oa_HDAC5_v1(P)       CCACGCTGGAGAAAGTCATCGAGATCCAGAGCAAACACTGGAGCTGTGTGCAGAGGTTCG
Oa_HDAC5_v7(P)       CCACGCTGGAGAAAGTCATCGAGATCCAGAGCAAACACTGGAGCTGTGTGCAGAGGTTCG
Oa_HDAC5_v6(P)       CCACGCTGGAGAAAGTCATCGAGATCCAGAGCAAACACTGGAGCTGTGTGCAGAGGTTCG
Oa_HDAC5_v5(P)       CCACGCTGGAGAAAGTCATCGAGATCCAGAGCAAACACTGGAGCTGTGTGCAGAGGTTCG
Oa_HDAC5_v2(P)       CCACGCTGGAGAAAGTCATCGAGATCCAGAGCAAACACTGGAGCTGTGTGCAGAGGTTCG
Oa_HDAC5_v4(P)       CCACGCTGGAGAAAGTCATCGAGATCCAGAGCAAACACTGGAGCTGTGTGCAGAGGTTCG
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Mm_HDAC5_v4          CCGCTGGTCTGGGCTGCTCGCTGCGGGAGGCTCAGACAGGTGAGAAAGAGGAGGCCGAGA
Mm_HDAC5_v1          CCGCTGGTCTGGGCTGCTCGCTGCGGGAGGCTCAGACAGGTGAGAAAGAGGAGGCCGAGA
Mm_HDAC5_v3          CCGCTGGTCTGGGCTGCTCGCTGCGGGAGGCTCAGACAGGTGAGAAAGAGGAGGCCGAGA
Mm_HDAC5_v5          CCGCTGGTCTGGGCTGCTCGCTGCGGGAGGCTCAGACAGGTGAGAAAGAGGAGGCCGAGA
Hs_HDAC5_v1          CCGCTGGTCTGGGCCGGTCCCTGCGAGAGGCCCAAGCAGGTGAGACCGAGGAGGCCGAGA
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Hs_HDAC5_v3          CCGCTGGTCTGGGCCGGTCCCTGCGAGAGGCCCAAGCAGGTGAGACCGAGGAGGCCGAGA
Bt_HDAC5_v1          CTGCTGGCCTAGGCCGTTCCCTGCGGGAGGCCCAGGCAGGTGAGACAGAGGAGGCTGAGA
Bt_HDAC5_v5(P)       CTGCTGGCCTAGGCCGTTCCCTGCGGGAGGCCCAGGCAGGTGAGACAGAGGAGGCTGAGA
Bt_HDAC5_v4(P)       CTGCTGGCCTAGGCCGTTCCCTGCGGGAGGCCCAGGCAGGTGAGACAGAGGAGGCTGAGA
Bt_HDAC5_v2          CTGCTGGCCTAGGCCGTTCCCTGCGGGAGGCCCAGGCAGGTGAGACAGAGGAGGCTGAGA
Bt_HDAC5_v3(P)       CTGCTGGCCTAGGCCGTTCCCTGCGGGAGGCCCAGGCAGGTGAGACAGAGGAGGCTGAGA
Oa_HDAC5_v11(P)      CTGCTGGCCTAGGCCGTTCCCTGCGGGAGGCCCAGGCAGGTGAGACAGAGGAGGCTGAGA
Oa_HDAC5_v10(P)      CTGCTGGCCTAGGCCGTTCCCTGCGGGAGGCCCAGGCAGGTGAGACAGAGGAGGCTGAGA
Oa_HDAC5_v8(P)       CTGCTGGCCTAGGCCGTTCCCTGCGGGAGGCCCAGGCAGGTGAGACAGAGGAGGCTGAGA
Oa_HDAC5_v9(P)       CTGCTGGCCTAGGCCGTTCCCTGCGGGAGGCCCAGGCAGGTGAGACAGAGGAGGCTGAGA
Oa_HDAC5_v1(P)       CTGCTGGCCTAGGCCGTTCCCTGCGGGAGGCCCAGGCAGGTGAGACAGAGGAGGCTGAGA
Oa_HDAC5_v7(P)       CTGCTGGCCTAGGCCGTTCCCTGCGGGAGGCCCAGGCAGGTGAGACAGAGGAGGCTGAGA
Oa_HDAC5_v6(P)       CTGCTGGCCTAGGCCGTTCCCTGCGGGAGGCCCAGGCAGGTGAGACAGAGGAGGCTGAGA
Oa_HDAC5_v5(P)       CTGCTGGCCTAGGCCGTTCCCTGCGGGAGGCCCAGGCAGGTGAGACAGAGGAGGCTGAGA
Oa_HDAC5_v2(P)       CTGCTGGCCTAGGCCGTTCCCTGCGGGAGGCCCAGGCAGGTGAGACAGAGGAGGCTGAGA
Oa_HDAC5_v4(P)       CTGCTGGCCTAGGCCGTTCCCTGCGGGAGGCCCAGGCAGGTGAGACAGAGGAGGCTGAGA
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Mm_HDAC5_v4          CTGTGAGCGCCATGGCCCTGCTTTCCGTGGGGGCTGAGCAGGCCCAGGCTGTTGCCACTC
Mm_HDAC5_v1          CTGTGAGCGCCATGGCCCTGCTTTCCGTGGGGGCTGAGCAGGCCCAGGCTGTTGCCACTC
Mm_HDAC5_v3          CTGTGAGCGCCATGGCCCTGCTTTCCGTGGGGGCTGAGCAGGCCCAGGCTGTTGCCACTC
Mm_HDAC5_v5          CTGTGAGCGCCATGGCCCTGCTTTCCGTGGGGGCTGAGCAGGCCCAGGCTGTTGCCACTC
Hs_HDAC5_v1          CTGTGAGCGCCATGGCCTTGCTGTCGGTGGGGGCCGAGCAGGCCCAGGCTGCGGCAGCCC
Hs_HDAC5_v3          CTGTGAGCGCCATGGCCTTGCTGTCGGTGGGGGCCGAGCAGGCCCAGGCTGCGGCAGCCC
Bt_HDAC5_v1          CTGTGAGCGCCATGGCCTTGCTGTCGGTGGGGGCCGAGCAGGCCCAGGCGGCTGCAGCCC
Bt_HDAC5_v5(P)       CTGTGAGCGCCATGGCCTTGCTGTCGGTGGGGGCCGAGCAGGCCCAGGCGGCTGCAGCCC
Bt_HDAC5_v4(P)       CTGTGAGCGCCATGGCCTTGCTGTCGGTGGGGGCCGAGCAGGCCCAGGCGGCTGCAGCCC
Bt_HDAC5_v2          CTGTGAGCGCCATGGCCTTGCTGTCGGTGGGGGCCGAGCAGGCCCAGGCGGCTGCAGCCC
Bt_HDAC5_v3(P)       CTGTGAGCGCCATGGCCTTGCTGTCGGTGGGGGCCGAGCAGGCCCAGGCGGCTGCAGCCC
Oa_HDAC5_v11(P)      CTGTGAGTGCCATGGCCTTGCTGTCGGTGGGGGCCGAGCAGGCCCAGGCGGCTGCGGCCC
Oa_HDAC5_v10(P)      CTGTGAGTGCCATGGCCTTGCTGTCGGTGGGGGCCGAGCAGGCCCAGGCGGCTGCGGCCC
Oa_HDAC5_v8(P)       CTGTGAGTGCCATGGCCTTGCTGTCGGTGGGGGCCGAGCAGGCCCAGGCGGCTGCGGCCC
Oa_HDAC5_v9(P)       CTGTGAGTGCCATGGCCTTGCTGTCGGTGGGGGCCGAGCAGGCCCAGGCGGCTGCGGCCC
Oa_HDAC5_v1(P)       CTGTGAGTGCCATGGCCTTGCTGTCGGTGGGGGCCGAGCAGGCCCAGGCGGCTGCGGCCC
Oa_HDAC5_v7(P)       CTGTGAGTGCCATGGCCTTGCTGTCGGTGGGGGCCGAGCAGGCCCAGGCGGCTGCGGCCC
Oa_HDAC5_v6(P)       CTGTGAGTGCCATGGCCTTGCTGTCGGTGGGGGCCGAGCAGGCCCAGGCGGCTGCGGCCC
Oa_HDAC5_v5(P)       CTGTGAGTGCCATGGCCTTGCTGTCGGTGGGGGCCGAGCAGGCCCAGGCGGCTGCGGCCC
Oa_HDAC5_v2(P)       CTGTGAGTGCCATGGCCTTGCTGTCGGTGGGGGCCGAGCAGGCCCAGGCGGCTGCGGCCC
Oa_HDAC5_v4(P)       CTGTGAGTGCCATGGCCTTGCTGTCGGTGGGGGCCGAGCAGGCCCAGGCGGCTGCGGCCC
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Mm_HDAC5_v4          AAGAGCACAGCCCCAGG----CCAGCAGAGGAGCCCATGGAGCAGGAGCCTGCCCTGTGA
Mm_HDAC5_v1          AAGAGCACAGCCCCAGG----CCAGCAGAGGAGCCCATGGAGCAGGAGCCTGCCCTGTGA
Mm_HDAC5_v3          AAGAGCACAGCCCCAGGTAAGCCAGCAGAGGAGCCCATGGAGCAGGAGCCTGCCCTGTGA
Mm_HDAC5_v5          AAGAGCACAGCCCCAGGTAAGCCAGCAGAGGAGCCCATGGAGCAGGAGCCTGCCCTGTGA
Hs_HDAC5_v1          GGGAACACAGCCCCAGG----CCGGCAGAGGAGCCCATGGAGCAGGAGCCTGCCCTGTGA
Hs_HDAC5_v3          GGGAACACAGCCCCAGG----CCGGCAGAGGAGCCCATGGAGCAGGAGCCTGCCCTGTGA
Bt_HDAC5_v1          GGGAGCACAGCCCCAGG----TGA------------------------------------
Bt_HDAC5_v5(P)       GGGAGCACAGCCCCAGG----CCAGCAGAGGAGCCTATGGAACAGGAGCCTGCCCTGTGA
Bt_HDAC5_v4(P)       GGGAGCACAGCCCCAGG----CCAGCAGAGGAGCCTATGGAACAGGAGCCTGCCCTGTGA
Bt_HDAC5_v2          GGGAGCACAGCCCCAGG----CCAGCAGAGGAGCCTATGGAACAGGAGCCTGCCCTGTGA
Bt_HDAC5_v3(P)       GGGAGCACAGCCCCAGG----CCAGCAGAGGAGCCTATGGAACAGGAGCCTGCCCTGTGA
Oa_HDAC5_v11(P)      GGGAGCACAGCCCCAGG----CCGGCAGAGGAGCCTATGGAACAGGAGCCTGCCCTGTGA
Oa_HDAC5_v10(P)      GGGAGCACAGCCCCAGG----CCGGCAGAGGAGCCTATGGAACAGGAGCCTGCCCTGTGA
Oa_HDAC5_v8(P)       GGGAGCACAGCCCCAGG----CCGGCAGAGGAGCCTATGGAACAGGAGCCTGCCCTGTGA
Oa_HDAC5_v9(P)       GGGAGCACAGCCCCAGG----CCGGCAGAGGAGCCTATGGAACAGGAGCCTGCCCTGTGA
Oa_HDAC5_v1(P)       GGGAGCACAGCCCCAGG----CCGGCAGAGGAGCCTATGGAACAGGAGCCTGCCCTGTGA
Oa_HDAC5_v7(P)       GGGAGCACAGCCCCAGG----CCGGCAGAGGAGCCTATGGAACAGGAGCCTGCCCTGTGA
Oa_HDAC5_v6(P)       GGGAGCACAGCCCCAGG----CCGGCAGAGGAGCCTATGGAACAGGAGCCTGCCCTGTGA
Oa_HDAC5_v5(P)       GGGAGCACAGCCCCAGG----CCGGCAGAGGAGCCTATGGAACAGGAGCCTGCCCTGTGA
Oa_HDAC5_v2(P)       GGGAGCACAGCCCCAGG----CCGGCAGAGGAGCCTATGGAACAGGAGCCTGCCCTGTGA
Oa_HDAC5_v4(P)       GGGAGCACAGCCCCAGG----CCGGCAGAGGAGCCTATGGAACAGGAGCCTGCCCTGTGA
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Mm_HDAC5_v4          CACCCTGGCCCCCATCCCTCTGGGCTTCATCATTGTGATTTTGTTTATTTTTTCTATTAA
Mm_HDAC5_v1          CACCCTGGCCCCCATCCCTCTGGGCTTCATCATTGTGATTTTGTTTATTTTTTCTATTAA
Mm_HDAC5_v3          CACCCTGGCCCCCATCCCTCTGGGCTTCATCATTGTGATTTTGTTTATTTTTTCTATTAA
Mm_HDAC5_v5          CACCCTGGCCCCCATCCCTCTGGGCTTCATCATTGTGATTTTGTTTATTTTTTCTATTAA
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Hs_HDAC5_v1          CGCCCCGGCCCCCATCCCTCTGGGCTTCACCATTGTGATTTTGTTTATTTTTTCTATTAA
Hs_HDAC5_v3          CGCCCCGGCCCCCATCCCTCTGGGCTTCACCATTGTGATTTTGTTTATTTTTTCTATTAA
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       CGCCCTGGCCCCCATCTCTCTGGGCTTCATCATTGTGATTTTGTTTATTTTTTCTATTAA
Bt_HDAC5_v4(P)       CGCCCTGGCCCCCATCTCTCTGGGCTTCATCATTGTGATTTTGTTTATTTTTTCTATTAA
Bt_HDAC5_v2          CGCCCTGGCCCCCATCTCTCTGGGCTTCATCATTGTGATTTTGTTTATTTTTTCTATTAA
Bt_HDAC5_v3(P)       CGCCCTGGCCCCCATCTCTCTGGGCTTCATCATTGTGATTTTGTTTATTTTTTCTATTAA
Oa_HDAC5_v11(P)      CGCCCTGGCCCCCATCTCTCTGGGCTTCATCATTGTGATTTTGTTTATTTTTTCTATTAA
Oa_HDAC5_v10(P)      CGCCCTGGCCCCCATCTCTCTGGGCTTCATCATTGTGATTTTGTTTATTTTTTCTATTAA
Oa_HDAC5_v8(P)       CGCCCTGGCCCCCATCTCTCTGGGCTTCATCATTGTGATTTTGTTTATTTTTTCTATTAA
Oa_HDAC5_v9(P)       CGCCCTGGCCCCCATCTCTCTGGGCTTCATCATTGTGATTTTGTTTATTTTTTCTATTAA
Oa_HDAC5_v1(P)       CGCCCTGGCCCCCATCTCTCTGGGCTTCATCATTGTGATTTTGTTTATTTTTTCTATTAA
Oa_HDAC5_v7(P)       CGCCCTGGCCCCCATCTCTCTGGGCTTCATCATTGTGATTTTGTTTATTTTTTCTATTAA
Oa_HDAC5_v6(P)       CGCCCTGGCCCCCATCTCTCTGGGCTTCATCATTGTGATTTTGTTTATTTTTTCTATTAA
Oa_HDAC5_v5(P)       CGCCCTGGCCCCCATCTCTCTGGGCTTCATCATTGTGATTTTGTTTATTTTTTCTATTAA
Oa_HDAC5_v2(P)       CGCCCTGGCCCCCATCTCTCTGGGCTTCATCATTGTGATTTTGTTTATTTTTTCTATTAA
Oa_HDAC5_v4(P)       CGCCCTGGCCCCCATCTCTCTGGGCTTCATCATTGTGATTTTGTTTATTTTTTCTATTAA

Mm_HDAC5_v4          AAACAAAAAGTCACACATTCAAAAAAAAAAAAAAAAAAAA--------------------
Mm_HDAC5_v1          AAACAAAAAGTCACACATTCAAAAAAAAAAAAAAAAAAAA--------------------
Mm_HDAC5_v3          AAACAAAAAGTCACACATTCAAAAAAAAAAAAAAAAAAAA--------------------
Mm_HDAC5_v5          AAACAAAAAGTCACACATTCAAAAAAAAAAAAAAAAAAAA--------------------
Hs_HDAC5_v1          AAACAAAAAGTCACACATTCAACAAGGTGTGCCGTGTGGGTCTCTCAGCCTTGCCCCTCC
Hs_HDAC5_v3          AAACAAAAAGTCACACATTCAACAAGGTGTGCCGTGTGGGTCTCTCAGCCTTGCCCCTCC
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       AAACAAAAAGTCACACATTCAA----------------------------------------
Bt_HDAC5_v4(P)       AAACAAAAAGTCACACATTCAA----------------------------------------
Bt_HDAC5_v2          AAACAAAAAGTCACACATTCAA----------------------------------------
Bt_HDAC5_v3(P)       AAACAAAAAGTCACACATTCAA----------------------------------------
Oa_HDAC5_v11(P)      AAACAAAAAGTCACACATTCAA----------------------------------------
Oa_HDAC5_v10(P)      AAACAAAAAGTCACACATTCAA----------------------------------------
Oa_HDAC5_v8(P)       AAACAAAAAGTCACACATTCAA----------------------------------------
Oa_HDAC5_v9(P)       AAACAAAAAGTCACACATTCAA----------------------------------------
Oa_HDAC5_v1(P)       AAACAAAAAGTCACACATTCA-----------------------------------------
Oa_HDAC5_v7(P)       AAACAAAAAGTCACACATTCAA----------------------------------------
Oa_HDAC5_v6(P)       AAACAAAAAGTCACACATTCAA----------------------------------------
Oa_HDAC5_v5(P)       AAACAAAAAGTCACACATTCAA----------------------------------------
Oa_HDAC5_v2(P)       AAACAAAAAGTCACACATTCAAOaHDACvPTCTCCCCCAGGCTCCCCGGACGCGACACAG
Oa_HDAC5_v4(P)       AAACAAAAAGTCACACATTCAA----------------------------------------

Mm_HDAC5_v4          ------------------------------------------------------------
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          ------------------------------------------------------------
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          TGCTCCTCTACGCTGCCTCAGG---CCCCCAGCCCTGTGGCTTCCACCTCAGCTCTAGAA
Hs_HDAC5_v3          TGCTCCTCTACGCTGCCTCAGG---CCCCCAGCCCTGTGGCTTCCACCTCAGCTCTAGAA
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       TGCCCCCTCCTCCTGCCGTCGCTGCCCGCGGGCTCCCCGAGCGCGCGCCGAGCTCCGCGC
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          ------------------------------------------------------------
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          ------------------------------------------------------------
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Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         GCCTGCTCCCTCTGCAGGGGGTGGTGGTGTCTTCCCAGCCCTGTCCCATGTGTCCCT---
Hs_HDAC5_v3         GCCTGCTCCCTCTGCAGGGGGTGGTGGTGTCTTCCCAGCCCTGTCCCATGTGTCCCT---
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      CCCTCTTCCTTCCTCCCGGCGCCCGGGTGCCAGGCGGCGCCCCCCGGGAGCATCGCCAGC
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         -----------CCCCCCATTTTCCTGCATTCTGTCTGTCCTTTTCCTCCTTGGAGCCTGG
Hs_HDAC5_v3         -----------CCCCCCATTTTCCTGCATTCTGTCTGTCCTTTTCCTCCTTGGAGCCTGG
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      CCGGGAGCCGGGCCTCGGGGTTACTACCCGCGCCCCTCCCTGCCCTTCCCAGGCAGGGGC
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         GCCAGCTCAAGGTGGGCAC-----GGGGGCCCAGACAGTACTCTCCAG--TTCTGG----
Hs_HDAC5_v3         GCCAGCTCAAGGTGGGCAC-----GGGGGCCCAGACAGTACTCTCCAG--TTCTGG----
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      GCCTTCCCTACAGGAATGCCGTTCTGAATGCCTGACTGCCTCGCCCCGAAGGATGGCCTC
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
```

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Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         ----GGCCCCCCGAGTGAGGAGGGAACGGGAAGTCGGTGCCTTGGTTTCAGCTGATTTG-
Hs_HDAC5_v3         ----GGCCCCCCGAGTGAGGAGGGAACGGGAAGTCGGTGCCTTGGTTTCAGCTGATTTG-
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      GGATGGGCGTTAGAGGCACAGCGGCCCCGGGCTCCTGTCCCGTCCGTCTGTCTGTTATCG
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         --------GGGGGAAATGCCTTAATTTCACTCTCCTCCCTTCTCCAGCCTCA-GGGGAGG
Hs_HDAC5_v3         --------GGGGGAAATGCCTTAATTTCACTCTCCTCCCTTCTCCAGCCTCA-GGGGAGG
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      TCTGTCTCTCTTGACATCACCGCAGCTCCACCCCCTCCCGTCCCAGCCCCCAACGCCAGC
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         ATCTGGAGGATCCACTACTGTCTTTAAGATGCAGAGTGGAGGGGAGGTGGGCACCCACCC
Hs_HDAC5_v3         ATCTGGAGGATCCACTACTGTCTTTAAGATGCAGAGTGGAGGGGAGGTGGGCACCCACCC
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      TTC-------------------CTGCAGGCCCAGAGCCGGC-------ATGAACTCTCCC
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
```

```
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         TGCGATTCTCCACCCTTTCCCCTTCTTTCGTCCTCACCATCTCTGCAGACCCCTCTCCTC
Hs_HDAC5_v3         TGCGATTCTCCACCCTTTCCCCTTCTTTCGTCCTCACCATCTCTGCAGACCCCTCTCCTC
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      ACCGAGTCGGGAGCCTGCCTAGTGCTGCCAGAAATAG--TCTGTGGGTGGGACTCCAGGC
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         CTCCTTCCTCTTGGTCTCAGCACTGATGGGAGGCTGGTGCCCAAGCTGTGGCCTGCAGTC
Hs_HDAC5_v3         CTCCTTCCTCTTGGTCTCAGCACTGATGGGAGGCTGGTGCCCAAGCTGTGGCCTGCAGTC
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      AGCTTTGTGC---ACGGCAGATGGGATGCCAGGCCGGGAACCAGCCTTGGAAA-------
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         TGTGAGGAGGGGCTGTCTTGCCTCACACTCCTCACAGCCTACTTCCCCTTCCCCGGGGCTG
Hs_HDAC5_v3         TGTGAGGAGGGGCTGTCTTGCCTCACACTCCTCACAGCCTACTTCCCCTTCCCCGGGGCTG
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      --------------TCCTGCCCCGGACCCCTCTGC-------ACGGCATCCCCGTGACAG
Oa_HDAC5_v4(P)      ------------------------------------------------------------
```

```
Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         AGAGGGTGAAAGTGTGTGGGGAAGGAGAGGACTGGTTTCCTGGGTTCTCAGGGGCCAGGA
Hs_HDAC5_v3         AGAGGGTGAAAGTGTGTGGGGAAGGAGAGGACTGGTTTCCTGGGTTCTCAGGGGCCAGGA
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      TAGAGGTGAAACCGGTGCTGCCAGGAGC------CATGCCCAGCTCCATGGGGGGCGGGG
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         GGAGTAACAGAACCAG--------------------------------GTCTGCTCCCCA
Hs_HDAC5_v3         GGAGTAACAGAACCAG--------------------------------GTCTGCTCCCCA
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      GAGGAGGCAGCCCCAGCCCCGTGGAGCTGCGGGGGGCTCTGGCAGGCCCTGTGGACCCCG
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         CCTTACT--C------------GGATGGCCTCCCTGCCCCTCTGCTGGCACAGCCTGGGC
Hs_HDAC5_v3         CCTTACT--C------------GGATGGCCTCCCTGCCCCTCTGCTGGCACAGCCTGGGC
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      CACTGCGGGAGCAGCAACTGCAGCAGGAGCTCCTGGCGCTCAAGCAGCAACAGCAATTGC
Oa_HDAC5_v4(P)      ------------------------------------------------------------
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Mm_HDAC5_v4          ------------------------------------------------------------
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          ------------------------------------------------------------
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          AAGGGGAGAAGGTGGTCCCTGCAGAGGGGCTCCAGGCTGGTGAG----------------
Hs_HDAC5_v3          AAGGGGAGAAGGTGGTCCCTGCAGAGGGGCTCCAGGCTGGTGAG----------------
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       AGAAGCAGCTTCTGTTCGCTGAGTTTCAGAAACAGCATGACCACCTGACCCGGCAGCATG
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          ------------------------------------------------------------
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          ------------------------------------------------------------
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          ---------------AGCCCCCCTGCTGTCAGGACCAGATTTTCCCAGCCATCCAGCATG
Hs_HDAC5_v3          ---------------AGCCCCCCTGCTGTCAGGACCAGATTTTCCCAGCCATCCAGCATG
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       AAGTCCAGCTGCAGAAGCACCTCAAGCAGCAGCAGGAGATGCTGGCAGCCAAGAGGCAGC
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          ------------------------------------------------------------
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          ------------------------------------------------------------
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          CTGCGG----GGAGAAGGGGCAGAGGCTCACCTCCCTCCTGGGGCCTTTTG--TTTTGGA
Hs_HDAC5_v3          CTGCGG----GGAGAAGGGGCAGAGGCTCACCTCCCTCCTGGGGCCTTTTG--TTTTGGA
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       AGGAGCTGGAGCAGCAGCGGCAGCGGGAGCAGCAGCGGCAGGAGGAGCTGGAGAAGCAGC
Oa_HDAC5_v4(P)       ------------------------------------------------------------
```

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Mm_HDAC5_v4          ------------------------------------------------------------
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          ------------------------------------------------------------
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          TCCTGGGGATGGTGAGAATGGAGGTTCTAGAAGGGGTAAGGCCAGAACCCAGGGATCCAG
Hs_HDAC5_v3          TCCTGGGGATGGTGAGAATGGAGGTTCTAGAAGGGGTAAGGCCAGAACCCAGGGATCCAG
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       GGCTCGAGCAGCAGCTGCTCATCCTTCGAAACAAGGAGAAGAG--CAAAGA-GAGTGCCA
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          ------------------------------------------------------------
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          ------------------------------------------------------------
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          GAGTCGGCTCTCAGCTGGAGCTTCCATACCTTCTGGGCTCCCTTTGCTGACCACCAGCCC
Hs_HDAC5_v3          GAGTCGGCTCTCAGCTGGAGCTTCCATACCTTCTGGGCTCCCTTTGCTGACCACCAGCCC
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       TCGCCAGCACTGAGGTGAAGCTACGGCTCC---AGGAAT-----TCCTCCTGTCGAAGTC
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          ------------------------------------------------------------
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          ------------------------------------------------------------
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          AAGGGAGCTAAGACCAGGAGGGGGCTGGGCGCTGTCCCTTCTCTTTCCCAGGAGCCCTGC
Hs_HDAC5_v3          AAGGGAGCTAAGACCAGGAGGGGGCTGGGCGCTGTCCCTTCTCTTTCCCAGGAGCCCTGC
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       AAAGGAGCCCACACCAGGCGGCCTC--------AACCATTCCCTCCCACAGCATCCTA--
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Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         CAGGGGCTGTGGGCCTACAAGGCTTCCAGGGGATGCC-ATCCAGCCTGTAGGAAACCAAA
Hs_HDAC5_v3         CAGGGGCTGTGGGCCTACAAGGCTTCCAGGGGATGCC-ATCCAGCCTGTAGGAAACCAAA
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      -AATGCTGGGGAACCCACCATGCTTCTTTGGACCAGAGTTCCCCTCCCCAGAGCGGCCCC
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         GATGGGAAGTGGCTCCTAGGGGGCTGACTCTTCCTTCCTCC----TCCTCCCCAGTACCA
Hs_HDAC5_v3         GATGGGAAGTGGCTCCTAGGGGGCTGACTCTTCCTTCCTCC----TCCTCCCCAGTACCA
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      CCTGGG-------------ACGCCTCCCTCCTACAAACTGCCTTTGCTTGGGCCCTATGA
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         CATATACTTTCTCTCCTTCTATCTCCAGGGCCCCACCAATCTGTTTACATATTTATTATC
Hs_HDAC5_v3         CATATACTTTCTCTCCTTCTATCTCCAGGGCCCCACCAATCTGTTTACATATTTATTATC
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
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Oa_HDAC5_v2(P)       CAGCCGCGATGACTTCCCCCTCCGCAAAACAGC-----CTCCGAACCCAACTTAAAAGTA
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          ------------------------------------------------------------
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          ------------------------------------------------------------
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          CTATGGGGGCCTGAGCAGGATTGAGGGAGCCAGGGGAGGGGCAGGAGTCCC--AGCACCA
Hs_HDAC5_v3          CTATGGGGGCCTGAGCAGGATTGAGGGAGCCAGGGGAGGGGCAGGAGTCCC--AGCACCA
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       CGTTCGAGGCTAAAGCAGAAG-GTGG--CCGAGCGGAGAAGCAGTCCTCTCTTGCGTCGC
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          ------------------------------------------------------------
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          ------------------------------------------------------------
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          TCGGTTCATAGTGTGCTTGTGTGTTTGTTTTAGATCC----------TCCTGGGGGATGG
Hs_HDAC5_v3          TCGGTTCATAGTGTGCTTGTGTGTTTGTTTTAGATCC----------TCCTGGGGGATGG
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       AAGGATGGGACTGTCATTAGCACCTTTAAGAAGAGAGCTGTTGAGATCACAGGTGCCGGA
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          ------------------------------------------------------------
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          ------------------------------------------------------------
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          GGATGGGGCCAGGCTCAGTGTACTAGGCCTCTCTGTGCTGAGCCCCAGGCTCCCGGCCCC
Hs_HDAC5_v3          GGATGGGGCCAGGCTCAGTGTACTAGGCCTCTCTGTGCTGAGCCCCAGGCTCCCGGCCCC
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
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Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      CCTGGGGGTGTCCGCCGTGTGTAATAGCGCGCCAGGCTCTGGCCCCAGCTCTCCCAACAGC
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         TTACCCA-----CTCTCTCCCTGTGGCTGGTCTGGTTCTCATGTAAACCCACTCCTTGC-
Hs_HDAC5_v3         TTACCCA-----CTCTCTCCCTGTGGCTGGTCTGGTTCTCATGTAAACCCACTCCTTGC-
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      TCCCACAGCACCATCGCGGAGAATGGCTTTACAGGCTCGGTTCCCAACATCCCCACCGAG
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         TTTGTCTCCCTGGATATGGATTTCAGTTAAGTATTTT--GTAACCCGTTACACTGT----
Hs_HDAC5_v3         TTTGTCTCCCTGGATATGGATTTCAGTTAAGTATTTT--GTAACCCGTTACACTGT----
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      ATGCTCCCCCAGCACCGGGCCCTCCCTCCGGACACCTCCCCCAACCAGTTCAGCCTCTAC
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         --GTGTCCTTGTGTAAATAAACTTGTTTCTGGCAGTGCC--------------------
Hs_HDAC5_v3         --GTGTCCTTGTGTAAATAAACTTGTTTCTGGCAGTGCC--------------------
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
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Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      ACGTCTCCCTCTCTGCCCA-ACATCTCCCTAGGGCTGCAGGCCACGGTCACAGTCACCAA
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         ------------------------------------------------------------
Hs_HDAC5_v3         ------------------------------------------------------------
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      CTCGCACCTCACCGCCTCCCCGAAGCTGTCGACGCAGCAGGAGGCCGAGAGGCAGGCCCT
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         ------------------------------------------------------------
Hs_HDAC5_v3         ------------------------------------------------------------
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      CCAGTCCCTGCGGCAGGGCGGTGCACTGACCGGCAAGTTCATGAGCACATCCTCCATCCC
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         ------------------------------------------------------------
Hs_HDAC5_v3         ------------------------------------------------------------
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
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Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      TGGCTGCCTGCTGGGCGTGGCACTGGAGGGCGACTCGAGCCCCCACGGGCATGCCTCATT
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         ------------------------------------------------------------
Hs_HDAC5_v3         ------------------------------------------------------------
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      GCTGCAGCACGTGCTGCTGCTGGAACAAGCCCGGCAGCAGAGCACCCTCATTGCTGTGCC
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         ------------------------------------------------------------
Hs_HDAC5_v3         ------------------------------------------------------------
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      GCTCCACGGGCAGTCCCCGCTGGTGACGGGTGAGCGCGTGGCCACCAGCATGCGGACAGT
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         ------------------------------------------------------------
Hs_HDAC5_v3         ------------------------------------------------------------
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
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Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      GGGCAAGCTCCCGCGGCACCGGCCCCTGAGCCGCACCCAGTCCTCGCCGCTGCCCCAGAG
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         ------------------------------------------------------------
Hs_HDAC5_v3         ------------------------------------------------------------
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      CCCCCAGGCCCTGCAGCAGCTGGTCATGCAGCAGCAGCACCAGCAATTCCTGGAGAAGCA
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         ------------------------------------------------------------
Hs_HDAC5_v3         ------------------------------------------------------------
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      GAAGCAGCAGCAGCTGCAGCTGGGCAAGATCCTTACCAAGACGGGGGAGCTGCCACGGCA
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         ------------------------------------------------------------
Hs_HDAC5_v3         ------------------------------------------------------------
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
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Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      GCCCACCACCCACCCCGAGGAGACAGAGGAGGAGCTGACGGAGCAGCAGGACTCCTTGCT
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         ------------------------------------------------------------
Hs_HDAC5_v3         ------------------------------------------------------------
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      GGGGGAGGGAGCCCTCACCATACCCCGAGAAGGCTCCACGGAGAGTGAGAGCACCCAGGA
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         ------------------------------------------------------------
Hs_HDAC5_v3         ------------------------------------------------------------
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      AGACCTGGAGGAAGAGGAAGAGGAGGAGGAGGAAGAGGAGGAGGAGGAGGACTGCATCCA
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         ------------------------------------------------------------
Hs_HDAC5_v3         ------------------------------------------------------------
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
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Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      GGTCAAGGATGAGGAGCGCGAGAGCGGTGCTGAAGAGGGGCCCGACTTGGAGGAGTCCAG
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         ------------------------------------------------------------
Hs_HDAC5_v3         ------------------------------------------------------------
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      TGCTGGTTACAAAAAGGCATTTGCAGACACCCAGCAGCTGCAGCCGCTGCAGGTATACCA
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         ------------------------------------------------------------
Hs_HDAC5_v3         ------------------------------------------------------------
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      GGCACCCCTCAGCCTGGCCACTGTGCCCCACCAGGCCCTGGGCCGCACCCAGTCCTCACC
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         ------------------------------------------------------------
Hs_HDAC5_v3         ------------------------------------------------------------
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
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Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       TGCTGCCCCTGGGGGCATGAAGAGCCCCCCAGACCAGCCCACTAAGCACCTCTTCACCAC
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          ------------------------------------------------------------
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          ------------------------------------------------------------
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          ------------------------------------------------------------
Hs_HDAC5_v3          ------------------------------------------------------------
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       AGGTGTGGTCTACGACACGTTCATGCTGAAGCACCAGTGCATGTGCGGGAACACACATGT
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          ------------------------------------------------------------
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          ------------------------------------------------------------
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          ------------------------------------------------------------
Hs_HDAC5_v3          ------------------------------------------------------------
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       GCACCCCGAGCACGCTGGCCGGATCCAGAGCATCTGGTCCCGGCTGCAGGAGACAGGCCT
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          ------------------------------------------------------------
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          ------------------------------------------------------------
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          ------------------------------------------------------------
Hs_HDAC5_v3          ------------------------------------------------------------
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
```

```
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       GCTCAGCAAGTGTGAGCGAATCCGGGGTCGTAAAGCCACGCTGGATGAGATCCAGACGGT
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          ------------------------------------------------------------
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          ------------------------------------------------------------
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          ------------------------------------------------------------
Hs_HDAC5_v3          ------------------------------------------------------------
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       GCACTCCGAGTACCACACCCTGCTCTACGGTACCAGCCCCCTCAACCGGCAGAAGCTGGA
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          ------------------------------------------------------------
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          ------------------------------------------------------------
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          ------------------------------------------------------------
Hs_HDAC5_v3          ------------------------------------------------------------
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       CAGCAAGAAGCTGCTCGGCCCCATCAGCCAGAAGATGTACGCCATGCTGCCTTGCGGGGG
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          ------------------------------------------------------------
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          ------------------------------------------------------------
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          ------------------------------------------------------------
Hs_HDAC5_v3          ------------------------------------------------------------
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
```

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Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      CATTGGGGTGGACAGCGACACTGTGTGGAACGAGATGCACTCCTCCAGCGCCGTGCGCAT
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         ------------------------------------------------------------
Hs_HDAC5_v3         ------------------------------------------------------------
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      GGCGGTGGGCTGCCTGGTGGAGCTGGCATTCAAGGTGGCCGCAGGGGAGCTCAAGAATGG
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         ------------------------------------------------------------
Hs_HDAC5_v3         ------------------------------------------------------------
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      ATTTGCCATCATAAGGCCCCCAGGACACCACGCGGAAGAATCCACAGCCATGGGATTCTG
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         ------------------------------------------------------------
Hs_HDAC5_v3         ------------------------------------------------------------
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
```

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Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       CTTCTTCAACTCAGTAGCTATCACAACCAAGCTCCTGCAGCAGAAGTTGAACGTGGGCAA
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          ------------------------------------------------------------
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          ------------------------------------------------------------
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          ------------------------------------------------------------
Hs_HDAC5_v3          ------------------------------------------------------------
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       GGTTCTCATCGTGGACTGGGATATTCACCATGGCAACGGCACCCAGCAAGCATTTTACAA
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          ------------------------------------------------------------
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          ------------------------------------------------------------
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          ------------------------------------------------------------
Hs_HDAC5_v3          ------------------------------------------------------------
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       TGATCCCTCCGTGCTCTACATCTCCCTGCATCGCTATGACAATGGGAACTTCTTTCCGGG
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          ------------------------------------------------------------
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          ------------------------------------------------------------
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          ------------------------------------------------------------
Hs_HDAC5_v3          ------------------------------------------------------------
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
```

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Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      CTCCGGGGCTCCTGAAGAGGTTGGCGGAGGGCCGGGCGTGGGGTACAATGTGAATGTGGC
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         ------------------------------------------------------------
Hs_HDAC5_v3         ------------------------------------------------------------
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      ATGGACAGGAGGTGTGGACCCCCCCATCGGAGACGTGGAGTACCTAACAGCCTTCAGGAC
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         ------------------------------------------------------------
Hs_HDAC5_v3         ------------------------------------------------------------
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      AGTGGTGATGCCCATTGCCCACGAGTTCTCACCTGATGTGGTCCTGGTCTCCGCTGGCTT
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         ------------------------------------------------------------
Hs_HDAC5_v3         ------------------------------------------------------------
Bt_HDAC5_v1         ------------------------------------------------------------
```

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Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      TGATGCTGTTGAGGGACACCTGTCTCCGCTGGGTGGCTACTCTGTCACCGCCAGATGTTT
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         ------------------------------------------------------------
Hs_HDAC5_v3         ------------------------------------------------------------
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      TGGCCACTTGACCAGGCAGCTGATGACGCTGGCAGGGGGCCGGGTGGTGCTGGCCTTGGA
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         ------------------------------------------------------------
Hs_HDAC5_v3         ------------------------------------------------------------
Bt_HDAC5_v1         ------------------------------------------------------------
Bt_HDAC5_v5(P)      ------------------------------------------------------------
Bt_HDAC5_v4(P)      ------------------------------------------------------------
Bt_HDAC5_v2         ------------------------------------------------------------
Bt_HDAC5_v3(P)      ------------------------------------------------------------
Oa_HDAC5_v11(P)     ------------------------------------------------------------
Oa_HDAC5_v10(P)     ------------------------------------------------------------
Oa_HDAC5_v8(P)      ------------------------------------------------------------
Oa_HDAC5_v9(P)      ------------------------------------------------------------
Oa_HDAC5_v1(P)      ------------------------------------------------------------
Oa_HDAC5_v7(P)      ------------------------------------------------------------
Oa_HDAC5_v6(P)      ------------------------------------------------------------
Oa_HDAC5_v5(P)      ------------------------------------------------------------
Oa_HDAC5_v2(P)      GGGAGGCCACGACCTGACCGCCATCTGTGATGCCTCTGAGGCCTGTGTCTCGGCGCTGCT
Oa_HDAC5_v4(P)      ------------------------------------------------------------

Mm_HDAC5_v4         ------------------------------------------------------------
Mm_HDAC5_v1         ------------------------------------------------------------
Mm_HDAC5_v3         ------------------------------------------------------------
Mm_HDAC5_v5         ------------------------------------------------------------
Hs_HDAC5_v1         ------------------------------------------------------------
Hs_HDAC5_v3         ------------------------------------------------------------
```

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Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       CAGCGTGGAGCTACAGCCCTTGGACGAGGCAGTCTTGCAGCAGAAGCCCAACGCCAATGC
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          ------------------------------------------------------------
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          ------------------------------------------------------------
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          ------------------------------------------------------------
Hs_HDAC5_v3          ------------------------------------------------------------
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       AGTGGCCACGCTGGAGAAAGTCATCGAGATCCAGAGCAAACACTGGAGCTGTGTGCAGAG
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          ------------------------------------------------------------
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          ------------------------------------------------------------
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          ------------------------------------------------------------
Hs_HDAC5_v3          ------------------------------------------------------------
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       GTTCGCTGCTGGCCTAGGCCGTTCCCTGCGGGAGGCCCAGGCAGGTGAGACAGAGGAGGC
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          ------------------------------------------------------------
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          ------------------------------------------------------------
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          ------------------------------------------------------------
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Hs_HDAC5_v3          ------------------------------------------------------------
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       TGAGACTGTGAGTGCCATGGCCTTGCTGTCGGTGGGGGCCGAGCAGGCCCAGGCGGCTGC
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          ------------------------------------------------------------
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          ------------------------------------------------------------
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          ------------------------------------------------------------
Hs_HDAC5_v3          ------------------------------------------------------------
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       GGCCCGGGAGCACAGCCCCAGGCCGGCAGAGGAGCCTATGGAACAGGAGCCTGCCCTGTG
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          ------------------------------------------------------------
Mm_HDAC5_v1          ------------------------------------------------------------
Mm_HDAC5_v3          ------------------------------------------------------------
Mm_HDAC5_v5          ------------------------------------------------------------
Hs_HDAC5_v1          ------------------------------------------------------------
Hs_HDAC5_v3          ------------------------------------------------------------
Bt_HDAC5_v1          ------------------------------------------------------------
Bt_HDAC5_v5(P)       ------------------------------------------------------------
Bt_HDAC5_v4(P)       ------------------------------------------------------------
Bt_HDAC5_v2          ------------------------------------------------------------
Bt_HDAC5_v3(P)       ------------------------------------------------------------
Oa_HDAC5_v11(P)      ------------------------------------------------------------
Oa_HDAC5_v10(P)      ------------------------------------------------------------
Oa_HDAC5_v8(P)       ------------------------------------------------------------
Oa_HDAC5_v9(P)       ------------------------------------------------------------
Oa_HDAC5_v1(P)       ------------------------------------------------------------
Oa_HDAC5_v7(P)       ------------------------------------------------------------
Oa_HDAC5_v6(P)       ------------------------------------------------------------
Oa_HDAC5_v5(P)       ------------------------------------------------------------
Oa_HDAC5_v2(P)       ACGCCCTGGCCCCCATCTCTCTGGGCTTCATCATTGTGATTTTGTTTATTTTTTCTATTA
Oa_HDAC5_v4(P)       ------------------------------------------------------------

Mm_HDAC5_v4          ----------------------
Mm_HDAC5_v1          ----------------------
Mm_HDAC5_v3          ----------------------
Mm_HDAC5_v5          ----------------------
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Hs_HDAC5_v1          ----------------------
Hs_HDAC5_v3          ----------------------
Bt_HDAC5_v1          ----------------------
Bt_HDAC5_v5(P)       ----------------------
Bt_HDAC5_v4(P)       ----------------------
Bt_HDAC5_v2          ----------------------
Bt_HDAC5_v3(P)       ----------------------
Oa_HDAC5_v11(P)      ----------------------
Oa_HDAC5_v10(P)      ----------------------
Oa_HDAC5_v8(P)       ----------------------
Oa_HDAC5_v9(P)       ----------------------
Oa_HDAC5_v1(P)       ----------------------A
Oa_HDAC5_v7(P)       ----------------------
Oa_HDAC5_v6(P)       ----------------------
Oa_HDAC5_v5(P)       ----------------------
Oa_HDAC5_v2(P)       AAAACAAAAAGTCACACATTCAA
Oa_HDAC5_v4(P)       ----------------------
```

Probes designed

PROBE #	PROBE (5'-> 3')	PROBE POSITION	% GC
1	tctccttgtttcgaaggatg	91	45.00%
2	ttcgacaggaggaattcctg	158	50.00%
3	catttaggatgctgtgggag	215	50.00%
4	tctggtccaaagaagcatgg	247	50.00%
5	cagtttgtaggagggaggcg	297	60.00%
6	tgtcatagggcccaagcaaa	319	50.00%
7	ctgttttgcggagggggaag	349	60.00%
8	acttttaagttgggttcgga	371	40.00%
9	acgcaagagaggactgcttc	426	55.00%
10	ctattacacacggcggacac	515	55.00%
11	tgtgggagctgttgggagag	556	60.00%
12	tggggatgttgggaaccgag	604	60.00%
13	tgtagaggctgaactggttg	670	50.00%
14	tagggagatgttgggcagag	699	55.00%
15	tgcgagttggtgactgtgac	734	55.00%
16	tgctgcagcaatgaggcatg	917	55.00%
17	acagcaatgagggtgctctg	965	55.00%
18	cgtcttggtaaggatcttgc	1191	50.00%
19	ttctcggggtatggtgagag	1299	55.00%
20	ttttgtaaccagcactggac	1462	45.00%
21	tggtgaagaggtgcttagtg	1627	50.00%
22	tgaacgtgtcgtagaccaca	1651	50.00%
23	cacatgcactggtgcttcag	1673	55.00%
24	attcgctcacacttgctgag	1769	50.00%
25	tagagcagggtgtggtactc	1835	55.00%
26	cgtacatcttctggctgatg	1909	50.00%
27	atctcgttccacacagtgtc	1964	50.00%
28	ccttatgatggcaaatccat	2064	40.00%
29	aagaagcagaatcccatggc	2114	50.00%
30	ggttgtgatagctactgagt	2136	45.00%
31	ttcaacttctgctgcaggag	2159	50.00%
32	agtccacgatgagaaccttg	2185	50.00%

33	gtaaaatgcttgctgggtgc	2226	50.00%
34	atgtagagcacggagggatc	2249	55.00%
35	attgtcatagcgatgcaggg	2271	50.00%
36	cggagcccggaaagaagttc	2293	60.00%
37	catgccacattcacattgta	2351	40.00%
38	aaggctgttaggtactccac	2402	50.00%
39	caatgggcatcaccactgtc	2425	55.00%

40	cacatcaggtgagaactcgt	2448	50.00%
41	ctcaacagcatcaaagccag	2481	50.00%
42	aaacatctggcggtgacaga	2528	50.00%
43	ctcagaggcatcacagatgg	2628	55.00%
44	ttgggcttctgctgcaagac	2699	55.00%
45	ctggatctcgatgactttct	2742	45.00%
46	cagcgaacctctgcacacag	2776	60.00%

MECP2

Sequence alignment

Sequences:

Ovis aries: XM_012107079.1, XM_012164819.2, XM_015090226.1, XM_015090227.1

Bos taurus: NM_001206552.1

Homo sapiens: NM_004992.3, NM_001110792.1, NM_001316337.1

Mus musculus: NM_001081979.2, NM_010788.4

Sequence alignment (note in grey the selected sequence used for probe design):

```
Bt_MECP2_v1          ------------------------------------------------------------
Oa_MECP2_v1(P)       ------------------------------------------------------------
Oa_MECP2_v4(P)       ------------------------------------------------------------
Oa_MECP2_v2(P)       ------------------------------------------------------------
Oa_MECP2_v3(P)       CCGGGTCTCCTGCATTGCAGGCAGATGCTTTACCATCTGAGCCACCATGGAAGCCCCCAT
Mm_MECP2_v1          ------------------------------------------------------------
Mm_MECP2_v2          ------------------------------------------------------------
Hs_MECP2_v3          ------------------------------------------------------------
Hs_MECP2_v1          ------------------------------------------------------------
Hs_MECP2_v2          ------------------------------------------------------------


Bt_MECP2_v1          ------------------------------------------------------------
Oa_MECP2_v1(P)       ------------------------------------------------------------
Oa_MECP2_v4(P)       ------------------------------------------------------------
Oa_MECP2_v2(P)       ------------------------------------------------------------
Oa_MECP2_v3(P)       TTAAGTGTACAATTCCATGGTATTAGGTATATTCATACTGTACAAACATTACCACCTTCC
Mm_MECP2_v1          ------------------------------------------------------------
Mm_MECP2_v2          ------------------------------------------------------------
Hs_MECP2_v3          ------------------------------------------------------------
Hs_MECP2_v1          ------------------------------------------------------------
```

```
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    ATCTTCCAGGAGCTGTTTAATCCAGTCCTGTTCTGCATGAATCAGCTAGACTTGGTCTGT
Mm_MECP2_v1       ------------------------------------------------------------
Mm_MECP2_v2       ------------------------------------------------------------
Hs_MECP2_v3       ------------------------------------------------------------
Hs_MECP2_v1       ------------------------------------------------------------
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    GTTGCTTACTACTAATAATCTGGAGAGATCCACCTGATTGTCTTTCTTCTCCTGCCTTGC
Mm_MECP2_v1       ------------------------------------------------------------
Mm_MECP2_v2       ------------------------------------------------------------
Hs_MECP2_v3       ------------------------------------------------------------
Hs_MECP2_v1       ------------------------------------------------------------
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    TCCTCTTTGTCTCCTCTGCTGACTCTCTCTCCTCATCATAGGGCCAGATAATGGGAGGGA
Mm_MECP2_v1       ------------------------------------------------------------
Mm_MECP2_v2       ------------------------------------------------------------
Hs_MECP2_v3       ------------------------------------------------------------
Hs_MECP2_v1       ------------------------------------------------------------
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    AATTGTCCATACTCATATCTAAGGGACCCTCACTTGCTCGCTGGCCTCTTCAGACATCCG
Mm_MECP2_v1       ------------------------------------------------------------
Mm_MECP2_v2       ------------------------------------------------------------
Hs_MECP2_v3       ------------------------------------------------------------
Hs_MECP2_v1       ------------------------------------------------------------
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    TGCTGAGAAGACTACCAGATCTCTGTCTCTAGCCTTGAACCCTCAAAGGCGAAATGCCTC
Mm_MECP2_v1       ------------------------------------------------------------
Mm_MECP2_v2       ------------------------------------------------------------
Hs_MECP2_v3       ------------------------------------------------------------
Hs_MECP2_v1       ------------------------------------------------------------
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    AACATGGAAAAAAATACAGAAGCCAGAATCCTGAATCTCCAGCGGTCCACCAGCACACAC
```

```
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      ATGCCCTCCCCTGATGGCACCTAGGCCAACCACAGTGTCCCCTGCTTAGACTCTGCACTA
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      CCCCCACAGCAGTCAAGGGGATGACCATGCAGATCCGCAGGAGTGCAGTCTGCAGGCCAC
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      CCCCAGCTGCCGGCCCCTTTGGGCTTGGCCTTGGCCCTGGTCTCAGCTGTGAGAGCTTCC
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      TCACCTGGTCAGGCTGATCCCAGGGCCGTGGGTGGGTGAAGGAGGGAGTGGGTACCAAAC
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      CCCTGCCCTACCATCACTGCCCATCATTCTTGCATGTCCTGGAACCTGCCAGATTGTTCC
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
```

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Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      TGGAGTTGGGGCCTTGGCTCTTCCTAGTCCTTAAGCCTGGACCCCTCTTTACATGATCCC
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      TTAAGGCACCTGAAGAATTCTTTACCCTTTATGTTCAGGACATTGACCACCATCCCTCTC
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      ACTGATGAGGTGTGTTTTTTTTAATCACTTTTTTTCGGAAGCATGGTGTGTTCTTTCAGC
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      CTGCAAATGCAGCTCACCTTTGTCTCAAATTAGTTCTCTTATATATCTTTGATGGCGTCT
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      ATGTGCCATTTGGGGTTCCCTACTGCAGGGACACGAATTATCCTTATGTTGGATTATCTT
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      TGTCTCTCTTCCAATGCTGTTAGTGTCACTCTAATTGCTTTTGCTTTTATCTCTTTCATC
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
```

```
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    TGCATACAGTGTTTGTCTGATTGGATTTTCAGCTATGCATATTCTGTTTCTGGCTGTCTT
Mm_MECP2_v1       ------------------------------------------------------------
Mm_MECP2_v2       ------------------------------------------------------------
Hs_MECP2_v3       ------------------------------------------------------------
Hs_MECP2_v1       ------------------------------------------------------------
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    TAAATGTACTTATTAGTTCCTTAATGGCACATCTTGGTCTGCAGTTTGTTTCCCTAGGTT
Mm_MECP2_v1       ------------------------------------------------------------
Mm_MECP2_v2       ------------------------------------------------------------
Hs_MECP2_v3       ------------------------------------------------------------
Hs_MECP2_v1       ------------------------------------------------------------
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    GGGAATTTGCCCTTTCATCTTACTGTGTTTTATCTTCTCATCTTTGAACTCTTATTGCGA
Mm_MECP2_v1       ------------------------------------------------------------
Mm_MECP2_v2       ------------------------------------------------------------
Hs_MECP2_v3       ------------------------------------------------------------
Hs_MECP2_v1       ------------------------------------------------------------
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    ACATGTTCTTATAAAATTGTAAGGAATTTCCTTCTCTTCCTTTTGTGTATTCGCTCCTTG
Mm_MECP2_v1       ------------------------------------------------------------
Mm_MECP2_v2       ------------------------------------------------------------
Hs_MECP2_v3       ------------------------------------------------------------
Hs_MECP2_v1       ------------------------------------------------------------
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    GTGAAAGTTTGACTTTCCTGAGCCATATCTCCCTCCCTGTCTCTCTTCTCCCCTTTTTTT
Mm_MECP2_v1       ------------------------------------------------------------
Mm_MECP2_v2       ------------------------------------------------------------
Hs_MECP2_v3       ------------------------------------------------------------
Hs_MECP2_v1       ------------------------------------------------------------
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    TTTTTTTTTTAGCTTTTGGCCATAAAATGTTTCTAGAAGTACCATGTGTTTTTTTGTCAA
```

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Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      CTTGGCTCAGGCTTCGACGGCTCCGTCCAGTTCTGTTTGTTGGCTTTGCTGCAGAGGGGA
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      GTTTTGGCTATCTCCTCCTGGTCCGCTGGCCTGTCTCGGTGCTTTCCCCTCTAGGCTGTC
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      GTGAGCTTGGCTCTTGTGGTCAGAACCAAGTTGCACAACCAGGGGAACTGCAGGCAGGGG
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      GACTCTTCGGCCACATCTGGAGTCACTAGCTTAGGAACAGTGTTCAGTGTTTTATGTCAC
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      GGCTCGCTCTAGCCCCTTGAAGGACATACATGCCATTCCTGGAAAGGGGCACCCCAGGCT
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
```

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Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      CCTGCTGGTTCCCTGAGCTGGGTGGCCCCAAGCACAGGCACCTCCTGCAGTGCTGGCCTC
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      TAGACCTGGGACATACGTGTGCTTGTGCCTGGTTCAAACTGTCACCCTGCAGAGACCAGC
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      ACGCCCCTATAAAGCAATTCTATTCCAATTCAAAAGGAGTTTTCAAGAGTGAGAGATGCC
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      TCCCCAGTTCCTCCGTTGCAGCTTATTGGAGAGATCTCGGGGCTCTCGTGAGCTTCCTGA
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      CATGGCTTCCAGGGGTGGAGCAGCCCTGCGGCTGCTTTGTTCTCTGGAGCCCTTTCCTCA
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      GCTGCCAGGTTGTGGCATGTGCTGCATGCAGTGTTACATCCCTTGCCTTCGCGGAATGAA
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
```

```
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    ATCTGCCCTTCCCACTCCTTGCTGTCTGTGTGTTTCCCCATCTTCTCTGGGATCAGGAGA
Mm_MECP2_v1       ------------------------------------------------------------
Mm_MECP2_v2       ------------------------------------------------------------
Hs_MECP2_v3       ------------------------------------------------------------
Hs_MECP2_v1       ------------------------------------------------------------
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    GAGCAGGTACGTGGGAGGTTGGAAGCTGCCGTTTGGACCAGATGCTCTCATCTGCGGTGA
Mm_MECP2_v1       ------------------------------------------------------------
Mm_MECP2_v2       ------------------------------------------------------------
Hs_MECP2_v3       ------------------------------------------------------------
Hs_MECP2_v1       ------------------------------------------------------------
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    CTTGATCGTGTCGTGTGGCTGCTGACGCAGGTCCCCGGAAGCACATCCCAGCCCCGCCAC
Mm_MECP2_v1       ------------------------------------------------------------
Mm_MECP2_v2       ------------------------------------------------------------
Hs_MECP2_v3       ------------------------------------------------------------
Hs_MECP2_v1       ------------------------------------------------------------
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    CCTCTGTTGTCTTCAGCTCTTCCCAGGTGCGGATTCCAGGCGACTTTCCACTGGCGGGCT
Mm_MECP2_v1       ------------------------------------------------------------
Mm_MECP2_v2       ------------------------------------------------------------
Hs_MECP2_v3       ------------------------------------------------------------
Hs_MECP2_v1       ------------------------------------------------------------
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    GGAAGTCAGTCTTCCATTGTATTTTCTACCCCATTAGTGCTTGTACACAGGGCCACCGCT
Mm_MECP2_v1       ------------------------------------------------------------
Mm_MECP2_v2       ------------------------------------------------------------
Hs_MECP2_v3       ------------------------------------------------------------
Hs_MECP2_v1       ------------------------------------------------------------
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    GACTTACTGATGTATGTCTTCTCACTTTTTCTCCGGTCCCCAGAGTTGTTTCAGGGAGCG
```

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Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      AGATTCAGTCCCTGCCAGTGACCCACAGAAACCCTGCAGCCTACTGGGGCCCTTGCCCTG
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      CAGGCTTCTCGGCCCTTCTGTCTGCCACGGGCAGACCGTGCTTTTCAGCCAGCCTGGCTC
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      CAGGTCCCCCTGTTGTGACCTTGAAGATTTCCTTGGGCTCTGCTAGTGGGGGTGGGGGTG
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      TCCTGTCCCAGACTGCCCCTCCAGCGGGTCACTCATGGTGCCTCAGCTTTGGATGTCACC
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      CCTTCTTTTTGTCTTTTGTTGCTCCTTTTCTTCAGCGGCTCCTGTGTTGTCATCAGGAAG
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
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Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      CAAGGCTGTCAGACCTGCAGCTGTGGGGTGACCTCCACTAGTGAGAGGAAAACAAACGGT
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      ATTAAGAGAAAAACTGCAGCAGGCAAGAGCTGTGGGAGCCTATTGCTGGGAACCAGAGAG
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      GCAGGCGCGACCAGAGTGTCTGTGCACACAGGCCATGGGGACCTGAAGCTGGATATATGG
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      CGAGGGGCCCCCAGAGGCCAGCTTTCCCCTGATGAGCATCCGTCTGTTTGTGCGAGGGCT
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      TGACATGAGTAGTCTGTAGCACAGATGTGCACAGGGGCCCAGAAACATGGTGGGAGAGAA
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      GTAGCTAGATATGGAGGCTGGGAAGAGACGAAGTGACGAAAATGTCAGTCATAAGACTTG
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
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Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    AGTTCTGGGTTTCCTCTCATTCTTAGCACATTTATCCAGCCCCCTTCAATGACCTACATG
Mm_MECP2_v1       ------------------------------------------------------------
Mm_MECP2_v2       ------------------------------------------------------------
Hs_MECP2_v3       ------------------------------------------------------------
Hs_MECP2_v1       ------------------------------------------------------------
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    GGACCCAATCCTTCCCACCCCAAGCAAGTCACACCACCTTCCAGAGCTCTCCCCTGGCTC
Mm_MECP2_v1       ------------------------------------------------------------
Mm_MECP2_v2       ------------------------------------------------------------
Hs_MECP2_v3       ------------------------------------------------------------
Hs_MECP2_v1       ------------------------------------------------------------
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    CTGGTATCTCCTCTCTGACAACACTCAGCAAAAGCGCTGTGATTTCGTTATTGACTCTTT
Mm_MECP2_v1       ------------------------------------------------------------
Mm_MECP2_v2       ------------------------------------------------------------
Hs_MECP2_v3       ------------------------------------------------------------
Hs_MECP2_v1       ------------------------------------------------------------
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    GCTTTATAAGATTGTTTGTACTGGAAGAAAGAGAAGAAACAGATGCAGGTAGAAAGCATA
Mm_MECP2_v1       ------------------------------------------------------------
Mm_MECP2_v2       ------------------------------------------------------------
Hs_MECP2_v3       ------------------------------------------------------------
Hs_MECP2_v1       ------------------------------------------------------------
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    CCTTGTTGCCAGAGCATCCACTATGGAGTGAATGAGGGGGTGACGTGAAACACTTCTCCC
Mm_MECP2_v1       ------------------------------------------------------------
Mm_MECP2_v2       ------------------------------------------------------------
Hs_MECP2_v3       ------------------------------------------------------------
Hs_MECP2_v1       ------------------------------------------------------------
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    CACTCCCAGCGTCTTGGTTGTGACAACTGTGTTCAAAGTTTGCCCCTCCCTGCTGGGCAT
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Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      TCCAGAGTAGAAGCCATTTCTGCCACCCCACTTTATTCCTATGGAGTTCTAGAACATTTT
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      CATCACCCCTAAAGGAAGCCATGTGGAAGACAGCCTGACGTTTCCTCAAAAGGTTACACG
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      TGGAATGCCCGTGTGACCCAGAAATTCCACTCTAGGTATAGACCCAAGAGAATCGAAAAT
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      ATACACCTGTGTAAAAACTTGTACACAAATATCCACAGCAGCTAAAAGGTAGAAGCAACC
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ----------------------------CTGAAGGAGGGCGTGGCAACCCACTCCAGTG
Oa_MECP2_v4(P)      ----------------------------CTGAAGGAGGGCGTGGCAACCCACTCCAGTG
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      CAGATGTCTATCAACAGATGAATGGATGAACACAGCATGGTGTGTCTATACAGTGGAATG
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
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Oa_MECP2_v1(P)      TTCTTTACTGGAGA----------------------------------------------------
Oa_MECP2_v4(P)      TTCTTTACTGGAGA----------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------------
Oa_MECP2_v3(P)      TTATTCAGCATAAAAAGGGAAGAAGTTCTAATACATGCTACAACATGGAAGAACCTTGAA
Mm_MECP2_v1         ------------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------------
Oa_MECP2_v3(P)      CACATGCTGAGTGAAAGAAGCCTGTCACAGAAAGCCATATATTGTATGATTCCATTTATA
Mm_MECP2_v1         ------------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------------
Oa_MECP2_v3(P)      TGAAAAGTCCAAGCAGATCCATAGAGACGTAAAGGAGATTAGTGTTTGCCAGGGGCTTGG
Mm_MECP2_v1         ------------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------------
Oa_MECP2_v3(P)      GAGTAAGGGGCTCTGGGGAAGTACCTGCTTAGTGGGTGTGAGGTTTCCTCCGGGGGGGTG
Mm_MECP2_v1         ------------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------------
Oa_MECP2_v3(P)      ACAAAATGTTCCGAAACTAAATAGTGGTGATGCTTGCACAACATTGTGAATGTACTAAGT
Mm_MECP2_v1         ------------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------------
Oa_MECP2_v3(P)      GCTGCTAATGGTAAATTTTGTATCATGGGTTTTACCACAATTTAAAAAAAAAGATTGATC
Mm_MECP2_v1         ------------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------------
```

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Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    AAACGCTTTCAGAATATTTAGCCAACAACCTTCAACTTGGCTACATGCCTAGTCATTAAA
Mm_MECP2_v1       ------------------------------------------------------------
Mm_MECP2_v2       ------------------------------------------------------------
Hs_MECP2_v3       ------------------------------------------------------------
Hs_MECP2_v1       ------------------------------------------------------------
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    CTTCTAGGACTAAATTCCTTTCTGACTGTCATGGTTACCATGTTCTGGGCTTTGGAGATT
Mm_MECP2_v1       ------------------------------------------------------------
Mm_MECP2_v2       ------------------------------------------------------------
Hs_MECP2_v3       ------------------------------------------------------------
Hs_MECP2_v1       ------------------------------------------------------------
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    TCATTTGGGTCAGCGTGGTCCAGTCCACCATGTGTCCCCATAGGTCCCCACGCTCACCTC
Mm_MECP2_v1       ------------------------------------------------------------
Mm_MECP2_v2       ------------------------------------------------------------
Hs_MECP2_v3       ------------------------------------------------------------
Hs_MECP2_v1       ------------------------------------------------------------
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    TTTCTCTTAAATGGGACAGCAGAGCTACTTGGCAGAGCATTGGAAAACCTGCCATAATGA
Mm_MECP2_v1       ------------------------------------------------------------
Mm_MECP2_v2       ------------------------------------------------------------
Hs_MECP2_v3       ------------------------------------------------------------
Hs_MECP2_v1       ------------------------------------------------------------
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    TTTAGGGTAATTGGTGAAGCTGGCTATCATTTTAGTGGGTTCTCACAAAATATAAGGTCG
Mm_MECP2_v1       ------------------------------------------------------------
Mm_MECP2_v2       ------------------------------------------------------------
Hs_MECP2_v3       ------------------------------------------------------------
Hs_MECP2_v1       ------------------------------------------------------------
Hs_MECP2_v2       ------------------------------------------------------------

Bt_MECP2_v1       ------------------------------------------------------------
Oa_MECP2_v1(P)    ------------------------------------------------------------
Oa_MECP2_v4(P)    ------------------------------------------------------------
Oa_MECP2_v2(P)    ------------------------------------------------------------
Oa_MECP2_v3(P)    AATTCACATATCATGACATTCACCCATTTAAAGGGTTCAGTGGCATTTAGTACATTTGCA
```

```
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      ATGTGCATTCTAATGGGAAAGATTGAAGGCAGAAGGAAAAGGGGGTAGCAGAGGATGAGA
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ----------------------------------------------------------ATCTTC
Oa_MECP2_v4(P)      ----------------------------------------------------------ATCTTC
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      TGGTTAGACAGCATCACCTACTCAATGAACATGAGTTTGAGCAAACTCCAGGAGATAGTG
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ATGGACAGAAGAGCCCAGGAGGCTACAGTCCATGGGGTTGCAAACAGTCGGACACGACAG
Oa_MECP2_v4(P)      ATGGACAGAAGAGCCCAGGAGGCTACAGTCCATGGGGTTGCAAACAGTCGGACACGACAG
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      GAGGACAGAGGAGCCTGGCGTGCTGTAGTCCATGGGGTCACAAAGAGTCAGGCACGACTT
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      AGCAACTAAGCCCAGCAAACCTGAGTAATACTGTGACTTTGACTTCTGAGATTTTAGAGC
Oa_MECP2_v4(P)      AGCAACTAAGCCCAGCAAACCTGAGTAATACTGTGACTTTGACTTCTGAGATTTTAGAGC
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      AGGGACTGAACAACAGTAACAAATGTACAACCATTGCTTCTATCT---AGTTCCAAAATA
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      GTTCTATGACTCGACTGTTTAAGGGAATTCTGAGGCCTCACTGCACCTCAATAGATAATT
Oa_MECP2_v4(P)      GTTCTATGACTCGACTGTTTAAGGGAATTCTGAGGCCTCACTGCACCTCAATAGATAATT
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      TTTGTATCACCCCCCCAAAAAAAAAAAAATCCCTGTGTCCATTAGGAGTCATTCTATATTA
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
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Oa_MECP2_v1(P)      CCAGATACC-----ATCCTGGTAGTTCCAGACCAGCAGTAAAAGACTTGGTTGGTGCTGC
Oa_MECP2_v4(P)      CCAGATACC-----ATCCTGGTAGTTCCAGACCAGCAGTAAAAGACTTGGTTGGTGCTGC
Oa_MECP2_v2(P)      ---------------------------------------------------------
Oa_MECP2_v3(P)      CTTACTACCTCTGGCCCCTGGCAGTGAATATCCTACTTGTAGTCTCTGGATTTTCCTATT
Mm_MECP2_v1         ---------------------------------------------------------
Mm_MECP2_v2         ---------------------------------------------------------
Hs_MECP2_v3         ---------------------------------------------------------
Hs_MECP2_v1         ---------------------------------------------------------
Hs_MECP2_v2         ---------------------------------------------------------

Bt_MECP2_v1         ---------------------------------------------------------
Oa_MECP2_v1(P)      ACTTCTGAGTTTGATTACATGAGTAATTGTGTGAATAGTCTCTTGTGTGAATAGTCTCTT
Oa_MECP2_v4(P)      ACTTCTGAGTTTGATTACATGAGTAATTGTGTGAATAGTCTCTTGTGTGAATAGTCTCTT
Oa_MECP2_v2(P)      ---------------------------------------------------------
Oa_MECP2_v3(P)      TCTGGATATTTCATATACATGAAATCTCATAATATTTGTCCTTTT---------------
Mm_MECP2_v1         ---------------------------------------------------------
Mm_MECP2_v2         ---------------------------------------------------------
Hs_MECP2_v3         ---------------------------------------------------------
Hs_MECP2_v1         ---------------------------------------------------------
Hs_MECP2_v2         ---------------------------------------------------------

Bt_MECP2_v1         ---------------------------------------------------------
Oa_MECP2_v1(P)      AAGTTGTACATGCTAGGCTTTTTTTAGTCTAAAGATAAAAGTGCAACTCTTGGGCCGGCA
Oa_MECP2_v4(P)      AAGTTGTACATGCTAGGCTTTTTTTAGTCTAAAGATAAAAGTGCAACTCTTGGGCCGGCA
Oa_MECP2_v2(P)      ---------------------------------------------------------
Oa_MECP2_v3(P)      ---------GTGTCTGGCTTACTTCACTTAGCATTAACATCTTCAGTTCATGGTCCATCC
Mm_MECP2_v1         ---------------------------------------------------------
Mm_MECP2_v2         ---------------------------------------------------------
Hs_MECP2_v3         ---------------------------------------------------------
Hs_MECP2_v1         ---------------------------------------------------------
Hs_MECP2_v2         ---------------------------------------------------------

Bt_MECP2_v1         ---------------------------------------------------------
Oa_MECP2_v1(P)      AGATATCAGCAATTAGCTAATATGAGGCGGTTGAGGTTTTAAGAAGGAAGTGATGGTTGT
Oa_MECP2_v4(P)      AGATATCAGCAATTAGCTAATATGAGGCGGTTGAGGTTTTAAGAAGGAAGTGATGGTTGT
Oa_MECP2_v2(P)      ---------------------------------------------------------
Oa_MECP2_v3(P)      ---------------------------------------------------------
Mm_MECP2_v1         ---------------------------------------------------------
Mm_MECP2_v2         ---------------------------------------------------------
Hs_MECP2_v3         ---------------------------------------------------------
Hs_MECP2_v1         ---------------------------------------------------------
Hs_MECP2_v2         ---------------------------------------------------------

Bt_MECP2_v1         ---------------------------------------------------------
Oa_MECP2_v1(P)      CTTGATGAAAAGTATAGTGGCGGAAGACCTTCTTTGAACATGTGTTCAAAGGCAAAAGAG
Oa_MECP2_v4(P)      CTTGATGAAAAGTATAGTGGCGGAAGACCTTCTTTGAACATGTGTTCAAAGGCAAAAGAG
Oa_MECP2_v2(P)      ---------------------------------------------------------
Oa_MECP2_v3(P)      ---------------------------------------------------------
Mm_MECP2_v1         ---------------------------------------------------------
Mm_MECP2_v2         ---------------------------------------------------------
Hs_MECP2_v3         ---------------------------------------------------------
Hs_MECP2_v1         ---------------------------------------------------------
Hs_MECP2_v2         ---------------------------------------------------------

Bt_MECP2_v1         ---------------------------------------------------------
Oa_MECP2_v1(P)      AAAGTATCACACTGTTAACTCAGTTTATTGAACATTTTACTGATCAGAGGCCTAAAAGTG
Oa_MECP2_v4(P)      AAAGTATCACACTGTTAACTCAGTTTATTGAACATTTTACTGATCAGAGGCCTAAAAGTG
Oa_MECP2_v2(P)      ---------------------------------------------------------
Oa_MECP2_v3(P)      ---------------------------------------------------------
Mm_MECP2_v1         ---------------------------------------------------------
Mm_MECP2_v2         ---------------------------------------------------------
Hs_MECP2_v3         ---------------------------------------------------------
Hs_MECP2_v1         ---------------------------------------------------------
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Hs_MECP2_v2        ------------------------------------------------------------

Bt_MECP2_v1        ------------------------------------------------------------
Oa_MECP2_v1(P)     AATGCTCAAAAACAGTCTTGTGTATGTCTGAGGATGGCTTAGGATCTCCCGGGGTACTTG
Oa_MECP2_v4(P)     AATGCTCAAAAACAGTCTTGTGTATGTCTGAGGATGGCTTAGGATCTCCCGGGGTACTTG
Oa_MECP2_v2(P)     ------------------------------------------------------------
Oa_MECP2_v3(P)     ----------------------------------------ATGCTGTACCAGGTGTCAGA
Mm_MECP2_v1        ------------------------------------------------------------
Mm_MECP2_v2        ------------------------------------------------------------
Hs_MECP2_v3        ------------------------------------------------------------
Hs_MECP2_v1        ------------------------------------------------------------
Hs_MECP2_v2        ------------------------------------------------------------

Bt_MECP2_v1        ------------------------------------------------------------
Oa_MECP2_v1(P)     GTTTCTGTTGGTTCCGTCTGTTTTTTTTCCTCT---CCTGGCTAAAGCCTTTTTATATGA
Oa_MECP2_v4(P)     GTTTCTGTTGGTTCCGTCTGTTTTTTTTCCTCT---CCTGGCTAAAGCCTTTTTATATGA
Oa_MECP2_v2(P)     ------------------------------------------------------------
Oa_MECP2_v3(P)     GTTTCCTTCTTTTTTTTTTTTTTTTTTTCCTTTTGGCCACCATGGGGCTTGTGGAATCTT
Mm_MECP2_v1        ------------------------------------------------------------
Mm_MECP2_v2        ------------------------------------------------------------
Hs_MECP2_v3        ------------------------------------------------------------
Hs_MECP2_v1        ------------------------------------------------------------
Hs_MECP2_v2        ------------------------------------------------------------

Bt_MECP2_v1        ------------------------------------------------------------
Oa_MECP2_v1(P)     TGTCACATCAGCTTGTTGCAACTTCAGCTGCTTGCAAATGACAGGATACTTTGCCTCT--
Oa_MECP2_v4(P)     TGTCACATCAGCTTGTTGCAACTTCAGCTGCTTGCAAATGACAGGATACTTTGCCTCT--
Oa_MECP2_v2(P)     ------------------------------------------------------------
Oa_MECP2_v3(P)     TGTTTCCTGACCAGGGATTGAACTCTGGCTCTTGGCAGTCAGAGCGCCAAGTCCTTCTTG
Mm_MECP2_v1        ------------------------------GTCGGGAGGGCGGGGCGCGACGTCTGCCGTG
Mm_MECP2_v2        ------------------------------GTCGGGAGGGCGGGGCGCGACGTCTGCCGTG
Hs_MECP2_v3        ------------------------------------------------------------
Hs_MECP2_v1        ------------------------------------------------------------
Hs_MECP2_v2        ------------------------------------------------------------

Bt_MECP2_v1        ------------------------------------------------------------
Oa_MECP2_v1(P)     --GCATTTCATGTGTTCTTGGGATGACATTTTGATGTTGCGTTTTCTCTGGAATATATCT
Oa_MECP2_v4(P)     --GCATTTCATGTGTTCTTGGGATGACATTTTGATGTTGCGTGTTCTCTGGAATATATCT
Oa_MECP2_v2(P)     ------------------------------------------------------------
Oa_MECP2_v3(P)     GGACCTTCTGGCTGCTGTGATGTGTGCTGTTAGGAACATCGTCATCCATGGGCTCTTGTT
Mm_MECP2_v1        CGGGGTCCCGGCATCGGTTGCGCGCGC---------------------------------
Mm_MECP2_v2        CGGGGTCCCGGCATCGGTTGCGCGCGC---------------------------------
Hs_MECP2_v3        -------CCGGCGTCGGCGGCGCGCGC---------------------------------
Hs_MECP2_v1        -------CCGGCGTCGGCGGCGCGCGC---------------------------------
Hs_MECP2_v2        -------CCGGCGTCGGCGGCGCGCGC---------------------------------

Bt_MECP2_v1        ------------------------------------------------------------
Oa_MECP2_v1(P)     TCTGTCTCTG--GATATTTCTGTATGAGATGTTGCCTGAAATACTTACTGGAGATCGCTT
Oa_MECP2_v4(P)     TCTGTCTCTG--GATATTTCTGTATGAGATGTTGCCTGAAATACTTACTGGAGATCGCTT
Oa_MECP2_v2(P)     ------------------------------------------------------------
Oa_MECP2_v3(P)     TGAGTCTCTGTTCTCAACTCTCCAGGGTTCATACCTTGGAGTGGAATCTCTGGGTCACAT
Mm_MECP2_v1        ------------------------------------------------------------
Mm_MECP2_v2        ------------------------------------------------------------
Hs_MECP2_v3        ------------------------------------------------------------
Hs_MECP2_v1        ------------------------------------------------------------
Hs_MECP2_v2        ------------------------------------------------------------

Bt_MECP2_v1        ------------------------------------------------------------
Oa_MECP2_v1(P)     CCTAACTGTATGTTT---------------------------------------------
Oa_MECP2_v4(P)     CCTAACTGTATGTTT---------------------------------------------
Oa_MECP2_v2(P)     ------------------------------------------------------------
Oa_MECP2_v3(P)     GGGAACTCTACATTTACCTTTTTGAGGAACTAACTGCCTGACTGTTCTCCACAGTGGCAG
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Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ---------------------------------TAGTGACAAAATGTCCCTCAGAGGTGA
Oa_MECP2_v4(P)      ---------------------------------TAGTGACAAAATGTCCCTCAGAGGTGA
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      TGTGTTTTCAAACTTGCTTATCTTTCCCACATGTAGTGGTTTCATGCTGTGACGAGGAGA
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      CAAGACCTGTGATAGTGTCAG--TTCTAACACTCATGAATCTTTCCTTTAGCACTGTGTG
Oa_MECP2_v4(P)      CAAGACCTGTGATAGTGTCAG--TTCTAACACTCATGAATCTTTCCTTTAGCACTGTGTG
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      CTTACCGTATGGCACTGACTGCCTTCATTTGGGGAGGGTTCTATCTTTGGGCGGCATGAA
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      TTATC--TGGCAGTAAATTTCAGTGTATCCTTTGTTTCTAGCTAGGTAAGCTGGGAAATA
Oa_MECP2_v4(P)      TTATC--TGGCAGTAAATTTCAGTGTATCCTTTGTTTCTAGCTAGGTAAGCTGGGAAATA
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      CTGTGTTTTGTACAGCTTTTCAAAGCATAGTTTCTTGCATCTTCTAAAAACTGGGCTATT
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ----------------------------CTGTGGTAAAAGCCGTCCGGAAAATGGCCGCCG
Oa_MECP2_v1(P)      GCATGGTACTTTGTCTGTATCTTCAAAATGTCCCAAATAGCCCTGGGAAAAAGGTCG---
Oa_MECP2_v4(P)      GCATGGTACTTTGTCTGTATCTTCAAAATGTCCCAAATAGCCCTGGGAAAAAGGTCG---
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      AAAGAATACACTGAGT--------------------------------------------
Mm_MECP2_v1         ----GCTCCCTCCTCTCGGAGAGAGGGCTGTGGTAAAACCCGTCCGGAAAATGGCCGCCG
Mm_MECP2_v2         ----GCTCCCTCCTCTCGGAGAGAGGGCTGTGGTAAAACCCGTCCGGAAAATGGCCGCCG
Hs_MECP2_v3         ----GCTCCCTCCTCTCGGAGAGAGGGCTGTGGTAAAAGCCGTCCGGAAAATGGCCGCCG
Hs_MECP2_v1         ----GCTCCCTCCTCTCGGAGAGAGGGCTGTGGTAAAAGCCGTCCGGAAAATGGCCGCCG
Hs_MECP2_v2         ----GCTCCCTCCTCTCGGAGAGAGGGCTGTGGTAAAAGCCGTCCGGAAAATGGCCGCCG

Bt_MECP2_v1         C---------------CGCCGCTGCCGCGCCGAGCGGAGGAGGAGGAGGAGGCGAGGAGG
Oa_MECP2_v1(P)      ----------------------TGCAGCACAATGGGGGCTTTCAACTTACGATTTTCTTT
Oa_MECP2_v4(P)      ----------------------TGCAGCACAATGGGGGCTTTCAACTTACGATTTTCTTT
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      -------------------------TCAGAACAGGGCCACTGAACTTTAGGTTCCACTG
Mm_MECP2_v1         CTGCCGCCACCGCCGCCGCCGCCGCCGCGCCGAGCGGAGGAGGAGGAGGAGGCGAGGAGG
Mm_MECP2_v2         CTGCCGCCACCGCCGCCGCCGCCGCCGCGCCGAGCGGAGGAGGAGGAGGAGGCGAGGAGG
Hs_MECP2_v3         C---------------CGCCGCCGCCGCGCCGAGCGGAGGAGGAGGAGGAGGCGAGGAGG
Hs_MECP2_v1         C---------------CGCCGCCGCCGCGCCGAGCGGAGGAGGAGGAGGAGGCGAGGAGG
Hs_MECP2_v2         C---------------CGCCGCCGCCGCGCCGAGCGGAG--------------------

Bt_MECP2_v1         AGAGACTGCTCCATAAAAATACAGACTCACCAGTTCCTGCTTTGATGTGACATGTGACTC
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Oa_MECP2_v1(P)      GTTTTAGGCTCCATAAAAATACAGACTCACCAGTTCCTGCTTTGATGTGACATGTGACTC
Oa_MECP2_v4(P)      GTTTTAGGCTCCATAAAAATACAGACTCACCAGTTCCTGCTTTGATGTGACATGTGACTC
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      TTGAAGCCTTCAAGCAGAACCCCGTCCCTCTTCCTCCT----------------------
Mm_MECP2_v1         AGAGA-------------------------------------------------------
Mm_MECP2_v2         AGAGACTGCTCCATAAAAATACAGACTCACCAGTTCCTGCTTTGATGTGACATGTGACTC
Hs_MECP2_v3         AGAGACTGCTCCATAAAAATACAGACTCACCAGTTCCTGCTTTGATGTGACATGTGACTC
Hs_MECP2_v1         AGAGACTGCTCCATAAAAATACAGACTCACCAGTTCCTGCTTTGATGTGACATGTGACTC
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CCCAGAATACATCTTGCTTCTGTAGACCAGCTCCAACAAGATTCCATGGTAGCTGGAATG
Oa_MECP2_v1(P)      CCCAGAATACATCTTGCTTCTGTAGACCAGCTCCAACAAGATTCCATGGTAGCTGGAATG
Oa_MECP2_v4(P)      CCCAGAATACATCTTGCTTCTGTAGACCAGCTCCAACAAGATTCCATGGTAGCTGGAATG
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      ------------------------------------------------------------
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         CCCAGAATACACCTTGCTTCTGTAGACCAGCTCCAACAGGATTCCATGGTAGCTGGGATG
Hs_MECP2_v3         CCCAGAATACACCTTGCTTCTGTAGACCAGCTCCAACAGGATTCCATGGTAGCTGGGATG
Hs_MECP2_v1         CCCAGAATACACCTTGCTTCTGTAGACCAGCTCCAACAGGATTCCATGGTAGCTGGGATG
Hs_MECP2_v2         -------------------------------------------GAGGAGGAGGAGGCGAG

Bt_MECP2_v1         TTAGGGCT----------------------------------------------------
Oa_MECP2_v1(P)      TTAGGGCT----------------------------------------------------
Oa_MECP2_v4(P)      TTAGGGCTCAGAGACCTCTGAGACCATCTTGCAGTGCCAGTTTGATTGCTCTCAGATCTT
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      -----CTGCAGAGACCTCTGAGACCATCTTGCAGTGCCAGTTTGATTGCTCTCAGATCTT
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         TTAGGGCT----------------------------------------------------
Hs_MECP2_v3         TTAGGGCT----------------------------------------------------
Hs_MECP2_v1         TTAGGGCT----------------------------------------------------
Hs_MECP2_v2         GAGGAGAG----------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      TAAAGGGACCAAAGCTGGAGACTCACAGTGCTGCTGCCTTGATGATTCGTGCAGAGAAAC
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      TAAAGGGACCAAAGCTGGAGACTCACAGTGCTGCTGCCTTGATGATTCGTGCAGAGAAAC
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      CTCCTGGATTCTGAGATGCTGTAGCTCGTACTTGACTCTTCGGGACAGAAGCAGCCTCTG
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      CTCCTGGATTCTGAGATGCTGTAGCTCGTACTTGACTCTTCGGGACAGAAGCAGCCTCTG
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      CCGGGAGGCCTGTTCTCGCCTCGGGTCCCAGACTATTGACGTGGAGAAGTAGCCACCCCC
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      CCGGGAGGCCTGTTCTCGCCTCGGGTCCCAGACTATTGACGTGGAGAAGTAGCCACCCCC
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
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Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      TCATCCTTCCAGTTCGTGGCTTCGTAGTGAGGCTTGGGCTCCTGACCAGACTCCACGAGG
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      TCATCCTTCCAGTTCGTGGCTTCGTAGTGAGGCTTGGGCTCCTGACCAGACTCCACGAGG
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      TGGCTGAAAGGTGGAAATGAAAGGTGCTGACACACGCATCTCCCAACATGGGCCTGATGC
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      TGGCTGAAAGGTGGAAATGAAAGGTGCTGACACACGCATCTCCCAACATGGGCCTGATGC
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      AAGCATGACTGAAATTAGGAAACGTCAGGATATCGCTGGGGCTCTGGAAATGTCCTAGAG
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      AAGCATGACTGAAATTAGGAAACGTCAGGATATCGCTGGGGCTCTGGAAATGTCCTAGAG
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      CTCACTCTGGGGCAGCCTGATTCCACTTCAAGGGAAGAATACCTTTTCAGCTACAGCCTT
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      CTCACTCTGGGGCAGCCTGATTCCACTTCAAGGGAAGAATACCTTTTCAGCTACAGCCTT
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      CACCTGGTTTTGTGGTCTGTCTGTCTTTAATATGAAATCCTTGGGGGTTGAGTAATCCCA
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      CACCTGGTTTTGTGGTCTGTCTGTCTTTAATATGAAATCCTTGGGGGTTGAGTAATCCCA
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      CCTGCGTGTCCATGGTCTGATCAGTGCAAGTGCCAAATGTCAGCGATCACACCCGTGGAA
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      CCTGCGTGTCCATGGTCTGATCAGTGCAAGTGCCAAATGTCAGCGATCACACCCGTGGAA
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Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      TTCACAGGAGCCTTGGATCCAAAGAGTGCCTGGTACGGCTTACCAAGGCTGCCTCCCGCT
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      TTCACAGGAGCCTTGGATCCAAAGAGTGCCTGGTACGGCTTACCAAGGCTGCCTCCCGCT
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      TGATTACTGGAGGTTCCTTTCATTAGGAAAATACAGTCAGTTCTTGCCATCAGACCCCTT
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      TGATTACTGGAGGTTCCTTTCATTAGGAAAATACAGTCAGTTCTTGCCATCAGACCCCTT
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      GGGATACAGTGATTTGGACTGAAGTCAAGATTCCTGCAACTCTTTTTCCTTTGCTAGGTC
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      GGGATACAGTGATTTGGACTGAAGTCAAGATTCCTGCAACTCTTTTTCCTTTGCTAGGTC
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      AAAGCAAGGATTTGATGTAATGTTTTTTGTTTCACGAGCATAATTAGCAAATGATTTTAT
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      AAAGCAAGGATTTGATGTAATGTTTTTTGTTTCACGAGCATAATTAGCAAATGATTTTAT
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      TTACATAAGAGCCTTCTCTCAGTCTTTATAGATGTTTAAGATTTGTGTAGCTCTTCTGCT
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      TTACATAAGAGCCTTCTCTCAGTCTTTATAGATGTTTAAGATTTGTGTAGCTCTTCTGCT
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
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Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      TCAATGTGATATGTCATTTCCTCCCCAAATCGTGTGTTTTGGTAATCACACATTGGAAAA
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      TCAATGTGATATGTCATTTCCTCCCCAAATCGTGTGTTTTGGTAATCACACATTGGAAAA
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      CAGAAGTTGTTATGGGAAAAACTGGATCAGAGTAGACCATGAGAAATGTGTGTGATTTGG
Oa_MECP2_v2(P)      ---------------------------GCGACGTCGGCCGTGC---------GGGGTCTCG
Oa_MECP2_v3(P)      CAGAAGTTGTTATGGGAAAAACTGGATCAGAGTAGACCATGAGAAATGTGTGTGATTTGG
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      TAATCAGAGCTCACAAAACCAGTAACCATTGTGGTTAAAGAAGCACCAGGGCTCACTGGA
Oa_MECP2_v2(P)      GCGTCGGCG---------------GC---------GCGCGCGCTCCCTCCTCTCAGAGAG
Oa_MECP2_v3(P)      TAATCAGAGCTCACAAAACCAGTAACCATTGTGGTTAAAGAAGCACCAGGGCTCACTGGA
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      GGCTCTATTGGTATTTGCAAGTGGCATCAATATCAGCTGACTGGTTTTTGCCATGACCCC
Oa_MECP2_v2(P)      AGGGCTG-TGGTAAAAGCC-GTCCGGAAAATGGCCGCCGCCGCCGCTGCCGCGCCGAGCG
Oa_MECP2_v3(P)      GGCTCTATTGGTATTTGCAAGTGGCATCAATATCAGCTGACTGGTTTTTGCCATGACCCC
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ----------------------------CAGGG-----------------------------
Oa_MECP2_v1(P)      ----------------------------CAGGG-----------------------------
Oa_MECP2_v4(P)      AGATTGGTGCTTCCTTCCCTGCATTGTACAGGG-----------------------------
Oa_MECP2_v2(P)      GAGGAGGAGGAGGAGGCGAGGAGGAGAGACTGG-----------------------------
Oa_MECP2_v3(P)      AGATTGGTGCTTCCTTCCCTGCATTGTACAGGG-----------------------------
Mm_MECP2_v1         ----------------------------CTGGAGGAAA-----------------------
Mm_MECP2_v2         ----------------------------CAGGGAGGAAA-----------------------
Hs_MECP2_v3         ----------------------------CAGCTGCAAGATGGGATTCAGATCTGTTCTCA
Hs_MECP2_v1         ----------------------------CAGGG-----------------------------
Hs_MECP2_v2         ----------------------------ACTGG-----------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      ------------------------------------------------------------
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         AGCCTGTCGTTCCAGGACCCAGGAGGGAGAAGCAGCTGCCAGGGGAAGTCTCTTCGTAGG
Hs_MECP2_v1         ------------------------------------------------------------
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Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      ------------------------------------------------------------
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         CGGAGGTCAGGAGTCCAAGAGGAGTGAGCAGAGTCACAGAAGCCTCTTAAAGCCTCTTCT
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ----------------------AAGAAAAGTCCGAAGAGCAGGATCTCCAGGGCCTGAAGG
Oa_MECP2_v1(P)      ----------------------AAGAAAAGTCCGAAGAGCAGGATCTCCAGGGCCTGAAGG
Oa_MECP2_v4(P)      ----------------------AAGAAAAGTCCGAAGAGCAGGATCTCCAGGGCCTGAAGG
Oa_MECP2_v2(P)      ----------------------AAGAAAAGTCCGAAGAGCAGGATCTCCAGGGCCTGAAGG
Oa_MECP2_v3(P)      ----------------------AAGAAAAGTCCGAAGAGCAGGATCTCCAGGGCCTGAAGG
Mm_MECP2_v1         ---------------------------AGTCAGAAGACCAGGATCTCCAGGGCCTCAGAG
Mm_MECP2_v2         ---------------------------AGTCAGAAGACCAGGATCTCCAGGGCCTCAGAG
Hs_MECP2_v3         TCCCCCATCCCATCAACACGGAAGAAAAGTCAGAAGACCAGGACCTCCAGGGCCTCAAGG
Hs_MECP2_v1         ----------------------AAGAAAAGTCAGAAGACCAGGACCTCCAGGGCCTCAAGG
Hs_MECP2_v2         ----------------------AAGAAAAGTCAGAAGACCAGGACCTCCAGGGCCTCAAGG
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Bt_MECP2_v1         ACAAACCTTTGAAGTTCAAAAAGGTGAAGAAGGATAAGAAAGAAGACAAAGAGGGCAAGC
Oa_MECP2_v1(P)      ACAAACCTTTGAAGTTCAAAAAGGTGAAGAAGGATAAGAAAGAAGACAAAGAGGGCAAGC
Oa_MECP2_v4(P)      ACAAACCTTTGAAGTTCAAAAAGGTGAAGAAGGATAAGAAAGAAGACAAAGAGGGCAAGC
Oa_MECP2_v2(P)      ACAAACCTTTGAAGTTCAAAAAGGTGAAGAAGGATAAGAAAGAAGACAAAGAGGGCAAGC
Oa_MECP2_v3(P)      ACAAACCTTTGAAGTTCAAAAAGGTGAAGAAGGATAAGAAAGAAGACAAAGAGGGCAAGC
Mm_MECP2_v1         ACAAGCCACTGAAGTTTAAGAAGGCGAAGAAAGACAAGAAGGAGGACAAAGAAGGCAAGC
Mm_MECP2_v2         ACAAGCCACTGAAGTTTAAGAAGGCGAAGAAAGACAAGAAGGAGGACAAAGAAGGCAAGC
Hs_MECP2_v3         ACAAACCCCTCAAGTTTAAAAAGGTGAAGAAAGATAAGAAAGAAGAGAAAGAGGGCAAGC
Hs_MECP2_v1         ACAAACCCCTCAAGTTTAAAAAGGTGAAGAAAGATAAGAAAGAAGAGAAAGAGGGCAAGC
Hs_MECP2_v2         ACAAACCCCTCAAGTTTAAAAAGGTGAAGAAAGATAAGAAAGAAGAGAAAGAGGGCAAGC
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Bt_MECP2_v1         ATGAGCCCCTGCAGCCAGCAGCCCACCACTCTGCCGAGCCAGCAGAGGCCGGCAAAGCAG
Oa_MECP2_v1(P)      ATGAGCCCCTGCAGCCAGCAGCCCACCACTCTGCCGAGCCAGCAGAGGCCGGCAAAGCAG
Oa_MECP2_v4(P)      ATGAGCCCCTGCAGCCAGCAGCCCACCACTCTGCCGAGCCAGCAGAGGCCGGCAAAGCAG
Oa_MECP2_v2(P)      ATGAGCCCCTGCAGCCAGCAGCCCACCACTCTGCCGAGCCAGCAGAGGCCGGCAAAGCAG
Oa_MECP2_v3(P)      ATGAGCCCCTGCAGCCAGCAGCCCACCACTCTGCCGAGCCAGCAGAGGCCGGCAAAGCAG
Mm_MECP2_v1         ATGAGCCACTACAACCTTCAGCCCACCATTCTGCAGAGCCAGCAGAGGCAGGCAAAGCAG
Mm_MECP2_v2         ATGAGCCACTACAACCTTCAGCCCACCATTCTGCAGAGCCAGCAGAGGCAGGCAAAGCAG
Hs_MECP2_v3         ATGAGCCCGTGCAGCCATCAGCCCACCACTCTGCTGAGCCCGCAGAGGCAGGCAAAGCAG
Hs_MECP2_v1         ATGAGCCCGTGCAGCCATCAGCCCACCACTCTGCTGAGCCCGCAGAGGCAGGCAAAGCAG
Hs_MECP2_v2         ATGAGCCCGTGCAGCCATCAGCCCACCACTCTGCTGAGCCCGCAGAGGCAGGCAAAGCAG
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Bt_MECP2_v1         AGACCTCAGAAGGGTCAGGCTCGGCCCCAGCCGTGCCAGAAGCTTCTGCATCCCCCAAGC
Oa_MECP2_v1(P)      AGACCTCAGAAGGGTCAGGCTCGGCCCCAGCCGTGCCAGAAGCTTCTGCGTCCCCCAAGC
Oa_MECP2_v4(P)      AGACCTCAGAAGGGTCAGGCTCGGCCCCAGCCGTGCCAGAAGCTTCTGCGTCCCCCAAGC
Oa_MECP2_v2(P)      AGACCTCAGAAGGGTCAGGCTCGGCCCCAGCCGTGCCAGAAGCTTCTGCGTCCCCCAAGC
Oa_MECP2_v3(P)      AGACCTCAGAAGGGTCAGGCTCGGCCCCAGCCGTGCCAGAAGCTTCTGCGTCCCCCAAGC
Mm_MECP2_v1         AAACATCAGAAAGCTCAGGCTCTGCCCCAGCAGTGCCAGAAGCCTCGGCTTCCCCCAAAC
Mm_MECP2_v2         AAACATCAGAAAGCTCAGGCTCTGCCCCAGCAGTGCCAGAAGCCTCGGCTTCCCCCAAAC
Hs_MECP2_v3         AGACATCAGAAGGGTCAGGCTCCGCCCCGGCTGTGCCGGAAGCTTCTGCCTCCCCCAAAC
Hs_MECP2_v1         AGACATCAGAAGGGTCAGGCTCCGCCCCGGCTGTGCCGGAAGCTTCTGCCTCCCCCAAAC
Hs_MECP2_v2         AGACATCAGAAGGGTCAGGCTCCGCCCCGGCTGTGCCGGAAGCTTCTGCCTCCCCCAAAC
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Bt_MECP2_v1         AGCGGCGCTCCATCATTCGTGATCGGGGCCCCATGTACGATGACCCCACTCTGCCGGAAG
Oa_MECP2_v1(P)      AGCGGCGCTCCATCATTCGTGATCGGGGCCCCATGTACGATGACCCCACTCTGCCGGAAG
Oa_MECP2_v4(P)      AGCGGCGCTCCATCATTCGTGATCGGGGCCCCATGTACGATGACCCCACTCTGCCGGAAG
Oa_MECP2_v2(P)      AGCGGCGCTCCATCATTCGTGATCGGGGCCCCATGTACGATGACCCCACTCTGCCGGAAG
Oa_MECP2_v3(P)      AGCGGCGCTCCATCATTCGTGATCGGGGCCCCATGTACGATGACCCCACTCTGCCGGAAG
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Mm_MECP2_v1         AGCGGCGCTCCATTATCCGTGACCGGGGACCTATGTATGATGACCCCACCTTGCCTGAAG
Mm_MECP2_v2         AGCGGCGCTCCATTATCCGTGACCGGGGACCTATGTATGATGACCCCACCTTGCCTGAAG
Hs_MECP2_v3         AGCGGCGCTCCATCATCCGTGACCGGGGACCCATGTATGATGACCCCACCCTGCCTGAAG
Hs_MECP2_v1         AGCGGCGCTCCATCATCCGTGACCGGGGACCCATGTATGATGACCCCACCCTGCCTGAAG
Hs_MECP2_v2         AGCGGCGCTCCATCATCCGTGACCGGGGACCCATGTATGATGACCCCACCCTGCCTGAAG
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Bt_MECP2_v1         GTTGGACCCGAAAGCTTAAGCAAAGGAAATCTGGCCGCTCCGCTGGGAAGTATGATGTGT
Oa_MECP2_v1(P)      GTTGGACCCGAAAGCTTAAGCAAAGGAAATCTGGCCGCTCCGCTGGGAAGTATGATGTGT
Oa_MECP2_v4(P)      GTTGGACCCGAAAGCTTAAGCAAAGGAAATCTGGCCGCTCCGCTGGGAAGTATGATGTGT
Oa_MECP2_v2(P)      GTTGGACCCGAAAGCTTAAGCAAAGGAAATCTGGCCGCTCCGCTGGGAAGTATGATGTGT
Oa_MECP2_v3(P)      GTTGGACCCGAAAGCTTAAGCAAAGGAAATCTGGCCGCTCCGCTGGGAAGTATGATGTGT
Mm_MECP2_v1         GTTGGACACGAAAGCTTAAACAAAGGAAGTCTGGCCGATCTGCTGGAAAGTATGATGTAT
Mm_MECP2_v2         GTTGGACACGAAAGCTTAAACAAAGGAAGTCTGGCCGATCTGCTGGAAAGTATGATGTAT
Hs_MECP2_v3         GCTGGACACGGAAGCTTAAGCAAAGGAAATCTGGCCGCTCTGCTGGGAAGTATGATGTGT
Hs_MECP2_v1         GCTGGACACGGAAGCTTAAGCAAAGGAAATCTGGCCGCTCTGCTGGGAAGTATGATGTGT
Hs_MECP2_v2         GCTGGACACGGAAGCTTAAGCAAAGGAAATCTGGCCGCTCTGCTGGGAAGTATGATGTGT
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Bt_MECP2_v1         ACTTGATCAATCCCCAGGGAAAAGCCTTTCGCTCTAAAGTGGAGTTGATTGCGTACTTCG
Oa_MECP2_v1(P)      ACTTGATCAATCCCCAGGGAAAAGCCTTTCGCTCTAAAGTGGAGTTGATTGCGTACTTCG
Oa_MECP2_v4(P)      ACTTGATCAATCCCCAGGGAAAAGCCTTTCGCTCTAAAGTGGAGTTGATTGCGTACTTCG
Oa_MECP2_v2(P)      ACTTGATCAATCCCCAGGGAAAAGCCTTTCGCTCTAAAGTGGAGTTGATTGCGTACTTCG
Oa_MECP2_v3(P)      ACTTGATCAATCCCCAGGGAAAAGCCTTTCGCTCTAAAGTGGAGTTGATTGCGTACTTCG
Mm_MECP2_v1         ATTTGATCAATCCCCAGGGAAAAGCTTTTCGCTCTAAAGTAGAATTGATTGCATACTTTG
Mm_MECP2_v2         ATTTGATCAATCCCCAGGGAAAAGCTTTTCGCTCTAAAGTAGAATTGATTGCATACTTTG
Hs_MECP2_v3         ATTTGATCAATCCCCAGGGAAAAGCCTTTCGCTCTAAAGTGGAGTTGATTGCGTACTTCG
Hs_MECP2_v1         ATTTGATCAATCCCCAGGGAAAAGCCTTTCGCTCTAAAGTGGAGTTGATTGCGTACTTCG
Hs_MECP2_v2         ATTTGATCAATCCCCAGGGAAAAGCCTTTCGCTCTAAAGTGGAGTTGATTGCGTACTTCG
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Bt_MECP2_v1         AAAAGGTAGGCGACACCTCCCTGGACCCTAATGATTTTGACTTCACGGTAACCGGGAGAG
Oa_MECP2_v1(P)      AAAAGGTAGGCGACACCTCCCTGGACCCTAATGATTTTGACTTCACGGTAACCGGGAGAG
Oa_MECP2_v4(P)      AAAAGGTAGGCGACACCTCCCTGGACCCTAATGATTTTGACTTCACGGTAACCGGGAGAG
Oa_MECP2_v2(P)      AAAAGGTAGGCGACACCTCCCTGGACCCTAATGATTTTGACTTCACGGTAACCGGGAGAG
Oa_MECP2_v3(P)      AAAAGGTAGGCGACACCTCCCTGGACCCTAATGATTTTGACTTCACGGTAACCGGGAGAG
Mm_MECP2_v1         AAAAGGTGGGAGACACCTCCTTGGACCCTAATGATTTTGACTTCACGGTAACTGGGAGAG
Mm_MECP2_v2         AAAAGGTGGGAGACACCTCCTTGGACCCTAATGATTTTGACTTCACGGTAACTGGGAGAG
Hs_MECP2_v3         AAAAGGTAGGCGACACATCCCTGGACCCTAATGATTTTGACTTCACGGTAACTGGGAGAG
Hs_MECP2_v1         AAAAGGTAGGCGACACATCCCTGGACCCTAATGATTTTGACTTCACGGTAACTGGGAGAG
Hs_MECP2_v2         AAAAGGTAGGCGACACATCCCTGGACCCTAATGATTTTGACTTCACGGTAACTGGGAGAG
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Bt_MECP2_v1         GGAGCCCCTCCCGGCGAGAACAGAAACCACCTAAGAAGCCCAAATCTCCCAAAGCTCCAG
Oa_MECP2_v1(P)      GGAGCCCCTCCCGGCGAGAACAGAAACCACCTAAGAAGCCCAAATCTCCCAAAGCTCCAG
Oa_MECP2_v4(P)      GGAGCCCCTCCCGGCGAGAACAGAAACCACCTAAGAAGCCCAAATCTCCCAAAGCTCCAG
Oa_MECP2_v2(P)      GGAGCCCCTCCCGGCGAGAACAGAAACCACCTAAGAAGCCCAAATCTCCCAAAGCTCCAG
Oa_MECP2_v3(P)      GGAGCCCCTCCCGGCGAGAACAGAAACCACCTAAGAAGCCCAAATCTCCCAAAGCTCCAG
Mm_MECP2_v1         GGAGCCCCTCCAGGAGAGAGCAGAAACCACCTAAGAAGCCCAAATCTCCCAAAGCTCCAG
Mm_MECP2_v2         GGAGCCCCTCCAGGAGAGAGCAGAAACCACCTAAGAAGCCCAAATCTCCCAAAGCTCCAG
Hs_MECP2_v3         GGAGCCCCTCCCGGCGAGAGCAGAAACCACCTAAGAAGCCCAAATCTCCCAAAGCTCCAG
Hs_MECP2_v1         GGAGCCCCTCCCGGCGAGAGCAGAAACCACCTAAGAAGCCCAAATCTCCCAAAGCTCCAG
Hs_MECP2_v2         GGAGCCCCTCCCGGCGAGAGCAGAAACCACCTAAGAAGCCCAAATCTCCCAAAGCTCCAG
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Bt_MECP2_v1         GAACTGGCAGAGGTCGGGGACGCCCCAAAGGGAGTGGCACCACGAGACCCAAGGCAGCTG
Oa_MECP2_v1(P)      GAACTGGCAGAGGTCGGGGACGCCCTAAAGGGAGTGGCACCACGAGACCCAAGGCAGCCG
Oa_MECP2_v4(P)      GAACTGGCAGAGGTCGGGGACGCCCTAAAGGGAGTGGCACCACGAGACCCAAGGCAGCCG
Oa_MECP2_v2(P)      GAACTGGCAGAGGTCGGGGACGCCCTAAAGGGAGTGGCACCACGAGACCCAAGGCAGCCG
Oa_MECP2_v3(P)      GAACTGGCAGAGGTCGGGGACGCCCTAAAGGGAGTGGCACCACGAGACCCAAGGCAGCCG
Mm_MECP2_v1         GAACTGGCAGGGGTCGGGGACGCCCCAAAGGGAGCGGCACTGGGAGACCAAAGGCAGCAG
Mm_MECP2_v2         GAACTGGCAGGGGTCGGGGACGCCCCAAAGGGAGCGGCACTGGGAGACCAAAGGCAGCAG
Hs_MECP2_v3         GAACTGGCAGAGGCCGGGGACGCCCCAAAGGGAGCGGCACCACGAGACCCAAGGCGGCCA
Hs_MECP2_v1         GAACTGGCAGAGGCCGGGGACGCCCCAAAGGGAGCGGCACCACGAGACCCAAGGCGGCCA
Hs_MECP2_v2         GAACTGGCAGAGGCCGGGGACGCCCCAAAGGGAGCGGCACCACGAGACCCAAGGCGGCCA
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Bt_MECP2_v1         CGTCAGAGGGTGTGCAAGTGAAAAGGGTTCTGGAGAAAAGTCCTGGAAAGCTACTCGTCA
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Oa_MECP2_v1(P)      CGTCAGAGGGTGTGCAGGTGAAAAGGGTTCTGGAGAAAAGTCCTGGAAAGCTGCTCGTCA
Oa_MECP2_v4(P)      CGTCAGAGGGTGTGCAGGTGAAAAGGGTTCTGGAGAAAAGTCCTGGAAAGCTGCTCGTCA
Oa_MECP2_v2(P)      CGTCAGAGGGTGTGCAGGTGAAAAGGGTTCTGGAGAAAAGTCCTGGAAAGCTGCTCGTCA
Oa_MECP2_v3(P)      CGTCAGAGGGTGTGCAGGTGAAAAGGGTTCTGGAGAAAAGTCCTGGAAAGCTGCTCGTCA
Mm_MECP2_v1         CATCAGAAGGTGTTCAGGTGAAAAGGGTCCTGGAGAAGAGCCCTGGGAAACTTGTTGTCA
Mm_MECP2_v2         CATCAGAAGGTGTTCAGGTGAAAAGGGTCCTGGAGAAGAGCCCTGGGAAACTTGTTGTCA
Hs_MECP2_v3         CGTCAGAGGGTGTGCAGGTGAAAAGGGTCCTGGAGAAAAGTCCTGGGAAGCTCCTTGTCA
Hs_MECP2_v1         CGTCAGAGGGTGTGCAGGTGAAAAGGGTCCTGGAGAAAAGTCCTGGGAAGCTCCTTGTCA
Hs_MECP2_v2         CGTCAGAGGGTGTGCAGGTGAAAAGGGTCCTGGAGAAAAGTCCTGGGAAGCTCCTTGTCA
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Bt_MECP2_v1         AGATGCCTTTCCAAGCTGCGCCGGGCAGCAAGGCAGAAGGGGGTGGGGCCACCACCTCAG
Oa_MECP2_v1(P)      AGATGCCTTTCCAAGCTGCGCCGGGCAGCAAGGCAGAAGGGGGTGGGGCCACCACCTCGG
Oa_MECP2_v4(P)      AGATGCCTTTCCAAGCTGCGCCGGGCAGCAAGGCAGAAGGGGGTGGGGCCACCACCTCGG
Oa_MECP2_v2(P)      AGATGCCTTTCCAAGCTGCGCCGGGCAGCAAGGCAGAAGGGGGTGGGGCCACCACCTCGG
Oa_MECP2_v3(P)      AGATGCCTTTCCAAGCTGCGCCGGGCAGCAAGGCAGAAGGGGGTGGGGCCACCACCTCGG
Mm_MECP2_v1         AGATGCCTTTCCAAGCATCGCCTGGGGGTAAGGGTGAGGGAGGTGGGGCTACCACATCTG
Mm_MECP2_v2         AGATGCCTTTCCAAGCATCGCCTGGGGGTAAGGGTGAGGGAGGTGGGGCTACCACATCTG
Hs_MECP2_v3         AGATGCCTTTTCAAACTTCGCCAGGGGGCAAGGCTGAGGGGGGTGGGGCCACCACATCCA
Hs_MECP2_v1         AGATGCCTTTTCAAACTTCGCCAGGGGGCAAGGCTGAGGGGGGTGGGGCCACCACATCCA
Hs_MECP2_v2         AGATGCCTTTTCAAACTTCGCCAGGGGGCAAGGCTGAGGGGGGTGGGGCCACCACATCCA
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Bt_MECP2_v1         CCCAGGTCATGGTCATCAAGCGCCCCGGCCGGAAGCGAAAAGCGGAGGCCGACCCCCAGG
Oa_MECP2_v1(P)      CCCAGGTTATGGTCATCAAGCGCCCCGGCCGGAAGCGAAAAGCGGAGGCCGACCCCCAGG
Oa_MECP2_v4(P)      CCCAGGTTATGGTCATCAAGCGCCCCGGCCGGAAGCGAAAAGCGGAGGCCGACCCCCAGG
Oa_MECP2_v2(P)      CCCAGGTTATGGTCATCAAGCGCCCCGGCCGGAAGCGAAAAGCGGAGGCCGACCCCCAGG
Oa_MECP2_v3(P)      CCCAGGTTATGGTCATCAAGCGCCCCGGCCGGAAGCGAAAAGCGGAGGCCGACCCCCAGG
Mm_MECP2_v1         CCCAGGTCATGGTGATCAAACGCCCTGGCAGAAAGCGAAAAGCTGAAGCTGACCCCCAGG
Mm_MECP2_v2         CCCAGGTCATGGTGATCAAACGCCCTGGCAGAAAGCGAAAAGCTGAAGCTGACCCCCAGG
Hs_MECP2_v3         CCCAGGTCATGGTGATCAAACGCCCCGGCAGGAAGCGAAAAGCTGAGGCCGACCCTCAGG
Hs_MECP2_v1         CCCAGGTCATGGTGATCAAACGCCCCGGCAGGAAGCGAAAAGCTGAGGCCGACCCTCAGG
Hs_MECP2_v2         CCCAGGTCATGGTGATCAAACGCCCCGGCAGGAAGCGAAAAGCTGAGGCCGACCCTCAGG
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Bt_MECP2_v1         CCATTCCCAAGAAACGAGGCCGAAAGCCGGGCAGTGTGGTTGCTGCCGCCACTGCCGAGG
Oa_MECP2_v1(P)      CCATTCCCAAGAAACGAGGCCGAAAGCCAGGCAGTGTGGTTGCTGCAGCTGCCGCCGAGG
Oa_MECP2_v4(P)      CCATTCCCAAGAAACGAGGCCGAAAGCCAGGCAGTGTGGTTGCTGCAGCTGCCGCCGAGG
Oa_MECP2_v2(P)      CCATTCCCAAGAAACGAGGCCGAAAGCCAGGCAGTGTGGTTGCTGCAGCTGCCGCCGAGG
Oa_MECP2_v3(P)      CCATTCCCAAGAAACGAGGCCGAAAGCCAGGCAGTGTGGTTGCTGCAGCTGCCGCCGAGG
Mm_MECP2_v1         CCATTCCTAAGAAACGGGGTAGAAAGCCTGGGAGTGTGGTGGCAGCTGCTGCAGCTGAGG
Mm_MECP2_v2         CCATTCCTAAGAAACGGGGTAGAAAGCCTGGGAGTGTGGTGGCAGCTGCTGCAGCTGAGG
Hs_MECP2_v3         CCATTCCCAAGAAACGGGGCCGAAAGCCGGGGAGTGTGGTGGCAGCCGCTGCCGCCGAGG
Hs_MECP2_v1         CCATTCCCAAGAAACGGGGCCGAAAGCCGGGGAGTGTGGTGGCAGCCGCTGCCGCCGAGG
Hs_MECP2_v2         CCATTCCCAAGAAACGGGGCCGAAAGCCGGGGAGTGTGGTGGCAGCCGCTGCCGCCGAGG
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Bt_MECP2_v1         CCAAAAAGAAAGCCGTGAAGGAGTCATCTATCCGGTCCGTTCAGGAGACCGTGCTCCCCA
Oa_MECP2_v1(P)      CCAAAAAGAAAGCCGTGAAGGAGTCGTCTATCCGGTCCGTGCAGGAGACCGTGCTCCCCA
Oa_MECP2_v4(P)      CCAAAAAGAAAGCCGTGAAGGAGTCGTCTATCCGGTCCGTGCAGGAGACCGTGCTCCCCA
Oa_MECP2_v2(P)      CCAAAAAGAAAGCCGTGAAGGAGTCGTCTATCCGGTCCGTGCAGGAGACCGTGCTCCCCA
Oa_MECP2_v3(P)      CCAAAAAGAAAGCCGTGAAGGAGTCGTCTATCCGGTCCGTGCAGGAGACCGTGCTCCCCA
Mm_MECP2_v1         CCAAAAAGAAAGCCGTGAAGGAGTCTTCCATACGGTCTGTGCATGAGACTGTGCTCCCCA
Mm_MECP2_v2         CCAAAAAGAAAGCCGTGAAGGAGTCTTCCATACGGTCTGTGCATGAGACTGTGCTCCCCA
Hs_MECP2_v3         CCAAAAAGAAAGCCGTGAAGGAGTCTTCTATCCGATCTGTGCAGGAGACCGTACTCCCCA
Hs_MECP2_v1         CCAAAAAGAAAGCCGTGAAGGAGTCTTCTATCCGATCTGTGCAGGAGACCGTACTCCCCA
Hs_MECP2_v2         CCAAAAAGAAAGCCGTGAAGGAGTCTTCTATCCGATCTGTGCAGGAGACCGTACTCCCCA
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Bt_MECP2_v1         TCAAGAAGCGCAAGACCCGGGAGACGGTGAGCATTGAGGTGAAGGAGGTAGTGAAGCCCC
Oa_MECP2_v1(P)      TCAAGAAGCGCAAGACCCGGGAGACGGTGAGCATTGAGGTGAAGGAGGTGGTGAAGCCCC
Oa_MECP2_v4(P)      TCAAGAAGCGCAAGACCCGGGAGACGGTGAGCATTGAGGTGAAGGAGGTGGTGAAGCCCC
Oa_MECP2_v2(P)      TCAAGAAGCGCAAGACCCGGGAGACGGTGAGCATTGAGGTGAAGGAGGTGGTGAAGCCCC
Oa_MECP2_v3(P)      TCAAGAAGCGCAAGACCCGGGAGACGGTGAGCATTGAGGTGAAGGAGGTGGTGAAGCCCC
Mm_MECP2_v1         TCAAGAAGCGCAAGACCCGGGAGACGGTCAGCATCGAGGTCAAGGAAGTGGTGAAGCCCC
Mm_MECP2_v2         TCAAGAAGCGCAAGACCCGGGAGACGGTCAGCATCGAGGTCAAGGAAGTGGTGAAGCCCC
Hs_MECP2_v3         TCAAGAAGCGCAAGACCCGGGAGACGGTCAGCATCGAGGTCAAGGAAGTGGTGAAGCCCC
Hs_MECP2_v1         TCAAGAAGCGCAAGACCCGGGAGACGGTCAGCATCGAGGTCAAGGAAGTGGTGAAGCCCC
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Hs_MECP2_v2         TCAAGAAGCGCAAGACCCGGGAGACGGTCAGCATCGAGGTCAAGGAAGTGGTGAAGCCCC
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Bt_MECP2_v1         TGCTGGTGTCCACGCTCGGCGAGAAGAGCGGGAAGGGACTGAAGACCTGCAAGAGCCCAG
Oa_MECP2_v1(P)      TGCTGGTGTCCACGCTTGGCGAGAAGAGCGGGAAGGGACTGAAGACCTGCAAGAGCCCAG
Oa_MECP2_v4(P)      TGCTGGTGTCCACGCTTGGCGAGAAGAGCGGGAAGGGACTGAAGACCTGCAAGAGCCCAG
Oa_MECP2_v2(P)      TGCTGGTGTCCACGCTTGGCGAGAAGAGCGGGAAGGGACTGAAGACCTGCAAGAGCCCAG
Oa_MECP2_v3(P)      TGCTGGTGTCCACGCTTGGCGAGAAGAGCGGGAAGGGACTGAAGACCTGCAAGAGCCCAG
Mm_MECP2_v1         TGCTGGTGTCCACCCTTGGTGAGAAAAGCGGGAAGGGACTGAAGACCTGCAAGAGCCCTG
Mm_MECP2_v2         TGCTGGTGTCCACCCTTGGTGAGAAAAGCGGGAAGGGACTGAAGACCTGCAAGAGCCCTG
Hs_MECP2_v3         TGCTGGTGTCCACCCTCGGTGAGAAGAGCGGGAAAGGACTGAAGACCTGTAAGAGCCCTG
Hs_MECP2_v1         TGCTGGTGTCCACCCTCGGTGAGAAGAGCGGGAAAGGACTGAAGACCTGTAAGAGCCCTG
Hs_MECP2_v2         TGCTGGTGTCCACCCTCGGTGAGAAGAGCGGGAAAGGACTGAAGACCTGTAAGAGCCCTG
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Bt_MECP2_v1         GGCGGAAAAGCAAGGAGAGCAGTCCCAAGGGGCGCAGCGGCAGCGCCTCCTCGCCCCCCA
Oa_MECP2_v1(P)      GGCGGAAAAGCAAGGAGAGCAGCCCCAAGGGGCGCAGCGGCAGCGCCTCCTCGCCACCCA
Oa_MECP2_v4(P)      GGCGGAAAAGCAAGGAGAGCAGCCCCAAGGGGCGCAGCGGCAGCGCCTCCTCGCCACCCA
Oa_MECP2_v2(P)      GGCGGAAAAGCAAGGAGAGCAGCCCCAAGGGGCGCAGCGGCAGCGCCTCCTCGCCACCCA
Oa_MECP2_v3(P)      GGCGGAAAAGCAAGGAGAGCAGCCCCAAGGGGCGCAGCGGCAGCGCCTCCTCGCCACCCA
Mm_MECP2_v1         GGCGTAAAAGCAAGGAGAGCAGCCCCAAGGGGCGCAGCAGCAGTGCCTCCTCCCCACCTA
Mm_MECP2_v2         GGCGTAAAAGCAAGGAGAGCAGCCCCAAGGGGCGCAGCAGCAGTGCCTCCTCCCCACCTA
Hs_MECP2_v3         GGCGGAAAAGCAAGGAGAGCAGCCCCAAGGGGCGCAGCAGCAGCGCCTCCTCACCCCCCA
Hs_MECP2_v1         GGCGGAAAAGCAAGGAGAGCAGCCCCAAGGGGCGCAGCAGCAGCGCCTCCTCACCCCCCA
Hs_MECP2_v2         GGCGGAAAAGCAAGGAGAGCAGCCCCAAGGGGCGCAGCAGCAGCGCCTCCTCACCCCCCA
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Bt_MECP2_v1         AGAAGGAGCACCACCACCACCACCACCACGTGGAGCCCCCGAAGGCCCCCGCGCCGCTGC
Oa_MECP2_v1(P)      AAAAGGAGCACCACCACCACCACCATCACGTGGAGCCCCCAAAGGCCCCCN---------
Oa_MECP2_v4(P)      AAAAGGAGCACCACCACCACCACCATCACGTGGAGCCCCCAAAGGCCCCCGCGCCTCTGC
Oa_MECP2_v2(P)      AAAAGGAGCACCACCACCACCACCATCACGTGGAGCCCCCAAAGGCCCCCGCGCCTCTGC
Oa_MECP2_v3(P)      AAAAGGAGCACCACCACCACCACCATCACGTGGAGCCCCCAAAGGCCCCCGCGCCTCTGC
Mm_MECP2_v1         AGAAGGAGCACCATCATCACCACCATCACTCAGAGTCCACAAAGGCCCCCATGCCACTGC
Mm_MECP2_v2         AGAAGGAGCACCATCATCACCACCATCACTCAGAGTCCACAAAGGCCCCCATGCCACTGC
Hs_MECP2_v3         AGAAGGAGCACCACCACCATCACCACCACTCAGAGTCCCCAAAGGCCCCCGTGCCACTGC
Hs_MECP2_v1         AGAAGGAGCACCACCACCATCACCACCACTCAGAGTCCCCAAAGGCCCCCGTGCCACTGC
Hs_MECP2_v2         AGAAGGAGCACCACCACCATCACCACCACTCAGAGTCCCCAAAGGCCCCCGTGCCACTGC
                    * *********** ** ** ***** ***   *** ** * *********

Bt_MECP2_v1         TCCTGCCCCCGCCCCCACCCCCGCCCGAGCCCCAGAGCTCCGAGGACCCTGCCAGCCCCC
Oa_MECP2_v1(P)      ---------NGCCCCCACCACCTCCTGAGCCCCAGAGCTCCCAGGACCCTGCCAGCCCCC
Oa_MECP2_v4(P)      TCCTGCCCCCGCCCCCACCCCCGCCTGAGCCCCAGAGCTCCGAGGACCCTGCCAGCCCCC
Oa_MECP2_v2(P)      TCCTGCCCCCGCCCCCACCCCCGCCTGAGCCCCAGAGCTCCGAGGACCCTGCCAGCCCCC
Oa_MECP2_v3(P)      TCCTGCCCCCGCCCCCACCCCCGCCTGAGCCCCAGAGCTCCGAGGACCCTGCCAGCCCCC
Mm_MECP2_v1         TCCCATCCCCAC------CCCCACCTGAGCCTGAGAGCTCTGAGGACCCCATCAGCCCCC
Mm_MECP2_v2         TCCCATCCCCAC------CCCCACCTGAGCCTGAGAGCTCTGAGGACCCCATCAGCCCCC
Hs_MECP2_v3         TCCCACCCCTGCCCCCACCTCCACCTGAGCCCGAGAGCTCCGAGGACCCCACCAGCCCCC
Hs_MECP2_v1         TCCCACCCCTGCCCCCACCTCCACCTGAGCCCGAGAGCTCCGAGGACCCCACCAGCCCCC
Hs_MECP2_v2         TCCCACCCCTGCCCCCACCTCCACCTGAGCCCGAGAGCTCCGAGGACCCCACCAGCCCCC
                              *      * ** ** *****  *******  *******   ********

Bt_MECP2_v1         CTGAGCCCCAGGACTTGAGCAGCAGCGTCTGCAAAGAGGAGAAGATGCCGAGAGCAGGCT
Oa_MECP2_v1(P)      CTGAGCCCCAGGACTTGAGCAGCAGCGTCTGCAAAGAGGAGAAGATGCCGAGAGCAGGCT
Oa_MECP2_v4(P)      CTGAGCCCCAGGACTTGAGCAGCAGCGTCTGCAAAGAGGAGAAGATGCCGAGAGCAGGCT
Oa_MECP2_v2(P)      CTGAGCCCCAGGACTTGAGCAGCAGCGTCTGCAAAGAGGAGAAGATGCCGAGAGCAGGCT
Oa_MECP2_v3(P)      CTGAGCCCCAGGACTTGAGCAGCAGCGTCTGCAAAGAGGAGAAGATGCCGAGAGCAGGCT
Mm_MECP2_v1         CTGAGCCTCAGGACTTGAGCAGCAGCATCTGCAAAGAAGAGAAGATGCCCCGAGGAGGCT
Mm_MECP2_v2         CTGAGCCTCAGGACTTGAGCAGCAGCATCTGCAAAGAAGAGAAGATGCCCCGAGGAGGCT
Hs_MECP2_v3         CTGAGCCCCAGGACTTGAGCAGCAGCGTCTGCAAAGAGGAGAAGATGCCCAGAGGAGGCT
Hs_MECP2_v1         CTGAGCCCCAGGACTTGAGCAGCAGCGTCTGCAAAGAGGAGAAGATGCCCAGAGGAGGCT
Hs_MECP2_v2         CTGAGCCCCAGGACTTGAGCAGCAGCGTCTGCAAAGAGGAGAAGATGCCCAGAGGAGGCT
                    ******* ****************** ********** ***********  *** *****

Bt_MECP2_v1         CGCTGGAGAGCGATGGCTGCCCCAAGGAGCCTGCTAAGACTCAGCCCGCGCTCGCCACCG
Oa_MECP2_v1(P)      CGCTGGAGAGCGATGGCTGCCCCAAGGAGCCTGCTAAGACTCAGCCCGCGCTCGCCACCG
Oa_MECP2_v4(P)      CGCTGGAGAGCGATGGCTGCCCCAAGGAGCCTGCTAAGACTCAGCCCGCGCTCGCCACCG
Oa_MECP2_v2(P)      CGCTGGAGAGCGATGGCTGCCCCAAGGAGCCTGCTAAGACTCAGCCCGCGCTCGCCACCG
Oa_MECP2_v3(P)      CGCTGGAGAGCGATGGCTGCCCCAAGGAGCCTGCTAAGACTCAGCCCGCGCTCGCCACCG
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Mm_MECP2_v1         CACTGGAAAGCGATGGCTGCCCCAAGGAGCCAGCTAAGACTCAGCCTATGGTCGCCACCA
Mm_MECP2_v2         CACTGGAAAGCGATGGCTGCCCCAAGGAGCCAGCTAAGACTCAGCCTATGGTCGCCACCA
Hs_MECP2_v3         CACTGGAGAGCGACGGCTGCCCCAAGGAGCCAGCTAAGACTCAGCCCGCGGTTGCCACCG
Hs_MECP2_v1         CACTGGAGAGCGACGGCTGCCCCAAGGAGCCAGCTAAGACTCAGCCCGCGGTTGCCACCG
Hs_MECP2_v2         CACTGGAGAGCGACGGCTGCCCCAAGGAGCCAGCTAAGACTCAGCCCGCGGTTGCCACCG
                    * ***** ***** ***************** **************   * * ******

Bt_MECP2_v1         CGGCCCCGGCCACAGAAAAGTACAAACACCGAGGGGAGGGAGAGCGCAAAGACATTGTCT
Oa_MECP2_v1(P)      CGGCCCCGGCCACAGAAAAGTACAAACACCGAGGGGAGGGAGAGCGCAAAGACATTGTCT
Oa_MECP2_v4(P)      CGGCCCCGGCCACAGAAAAGTACAAACACCGAGGGGAGGGAGAGCGCAAAGACATTGTCT
Oa_MECP2_v2(P)      CGGCCCCGGCCACAGAAAAGTACAAACACCGAGGGGAGGGAGAGCGCAAAGACATTGTCT
Oa_MECP2_v3(P)      CGGCCCCGGCCACAGAAAAGTACAAACACCGAGGGGAGGGAGAGCGCAAAGACATTGTCT
Mm_MECP2_v1         CTACCACAGTTGCAGAAAAGTACAAACACCGAGGGGAGGGAGAGCGCAAAGACATTGTTT
Mm_MECP2_v2         CTACCACAGTTGCAGAAAAGTACAAACACCGAGGGGAGGGAGAGCGCAAAGACATTGTTT
Hs_MECP2_v3         CCGCCACGGCCGCAGAAAAGTACAAACACCGAGGGGAGGGAGAGCGCAAAGACATTGTTT
Hs_MECP2_v1         CCGCCACGGCCGCAGAAAAGTACAAACACCGAGGGGAGGGAGAGCGCAAAGACATTGTTT
Hs_MECP2_v2         CCGCCACGGCCGCAGAAAAGTACAAACACCGAGGGGAGGGAGAGCGCAAAGACATTGTTT
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Bt_MECP2_v1         CATCCTCCATGCCAAGGCCAAACAGAGAGGAGCCTGTGGACAGCCGGACGCCCGTGACCG
Oa_MECP2_v1(P)      CATCCTCCATGCCAAGGCCAAACAGAGAGGAGCCTGTGGACAGCCGGACGCCCGTGACCG
Oa_MECP2_v4(P)      CATCCTCCATGCCAAGGCCAAACAGAGAGGAGCCTGTGGACAGCCGGACGCCCGTGACCG
Oa_MECP2_v2(P)      CATCCTCCATGCCAAGGCCAAACAGAGAGGAGCCTGTGGACAGCCGGACGCCCGTGACCG
Oa_MECP2_v3(P)      CATCCTCCATGCCAAGGCCAAACAGAGAGGAGCCTGTGGACAGCCGGACGCCCGTGACCG
Mm_MECP2_v1         CATCTTCCATGCCAAGGCCAAACAGAGAGGAGCCTGTGGACAGCCGGACGCCCGTGACCG
Mm_MECP2_v2         CATCTTCCATGCCAAGGCCAAACAGAGAGGAGCCTGTGGACAGCCGGACGCCCGTGACCG
Hs_MECP2_v3         CATCCTCCATGCCAAGGCCAAACAGAGAGGAGCCTGTGGACAGCCGGACGCCCGTGACCG
Hs_MECP2_v1         CATCCTCCATGCCAAGGCCAAACAGAGAGGAGCCTGTGGACAGCCGGACGCCCGTGACCG
Hs_MECP2_v2         CATCCTCCATGCCAAGGCCAAACAGAGAGGAGCCTGTGGACAGCCGGACGCCCGTGACCG
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Bt_MECP2_v1         AGAGAGTTAGCTGACTTTACGCAGAGCGGATTGCAAAGCAAACCAACAAGAATAAAGGCA
Oa_MECP2_v1(P)      AGAGAGTTAGCTGACTTTACGCAGAGCGGATTGCAAAGCAAACCAACAAGAATAAAGGCA
Oa_MECP2_v4(P)      AGAGAGTTAGCTGACTTTACGCAGAGCGGATTGCAAAGCAAACCAACAAGAATAAAGGCA
Oa_MECP2_v2(P)      AGAGAGTTAGCTGACTTTACGCAGAGCGGATTGCAAAGCAAACCAACAAGAATAAAGGCA
Oa_MECP2_v3(P)      AGAGAGTTAGCTGACTTTACGCAGAGCGGATTGCAAAGCAAACCAACAAGAATAAAGGCA
Mm_MECP2_v1         AGAGAGTTAGCTGACTTTACATAGAGCGGATTGCAAAGCAAACCAACAAGAATAAAGGCA
Mm_MECP2_v2         AGAGAGTTAGCTGACTTTACATAGAGCGGATTGCAAAGCAAACCAACAAGAATAAAGGCA
Hs_MECP2_v3         AGAGAGTTAGCTGACTTTACACGGAGCGGATTGCAAAGCAAACCAACAAGAATAAAGGCA
Hs_MECP2_v1         AGAGAGTTAGCTGACTTTACACGGAGCGGATTGCAAAGCAAACCAACAAGAATAAAGGCA
Hs_MECP2_v2         AGAGAGTTAGCTGACTTTACACGGAGCGGATTGCAAAGCAAACCAACAAGAATAAAGGCA
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Bt_MECP2_v1         GCTGTTGTCTCTTCTCCTTATGGGTAGGGCTCTGACAAAGCTTCCCGATTAACTGAAATA
Oa_MECP2_v1(P)      GCTGTTGTCTCTTCTCCTTATGGGTAGGGCTCTGACAAAGCTTCCCGATTAACTGAAATA
Oa_MECP2_v4(P)      GCTGTTGTCTCTTCTCCTTATGGGTAGGGCTCTGACAAAGCTTCCCGATTAACTGAAATA
Oa_MECP2_v2(P)      GCTGTTGTCTCTTCTCCTTATGGGTAGGGCTCTGACAAAGCTTCCCGATTAACTGAAATA
Oa_MECP2_v3(P)      GCTGTTGTCTCTTCTCCTTATGGGTAGGGCTCTGACAAAGCTTCCCGATTAACTGAAATA
Mm_MECP2_v1         GCTGTTGTCTCTTCTCCTTATGGGTAGGGCTCTGACAAAGCTTCCCGATTAACTGAAATA
Mm_MECP2_v2         GCTGTTGTCTCTTCTCCTTATGGGTAGGGCTCTGACAAAGCTTCCCGATTAACTGAAATA
Hs_MECP2_v3         GCTGTTGTCTCTTCTCCTTATGGGTAGGGCTCTGACAAAGCTTCCCGATTAACTGAAATA
Hs_MECP2_v1         GCTGTTGTCTCTTCTCCTTATGGGTAGGGCTCTGACAAAGCTTCCCGATTAACTGAAATA
Hs_MECP2_v2         GCTGTTGTCTCTTCTCCTTATGGGTAGGGCTCTGACAAAGCTTCCCGATTAACTGAAATA
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Bt_MECP2_v1         AAAAATATTTTTTTTTTCTTTCAGTAAACTTAGAGTTTCGTGGCTTCAGGGTGGGAGTAGT
Oa_MECP2_v1(P)      AAAAATATTTTTTTTTTCTTTCAGTAAACTTAGAGTTTCGTGGCTTCAGGGTGGGAGTAGT
Oa_MECP2_v4(P)      AAAAATATTTTTTTTTTCTTTCAGTAAACTTAGAGTTTCGTGGCTTCAGGGTGGGAGTAGT
Oa_MECP2_v2(P)      AAAAATATTTTTTTTTTCTTTCAGTAAACTTAGAGTTTCGTGGCTTCAGGGTGGGAGTAGT
Oa_MECP2_v3(P)      AAAAATATTTTTTTTTTCTTTCAGTAAACTTAGAGTTTCGTGGCTTCAGGGTGGGAGTAGT
Mm_MECP2_v1         AAAAATATTTTTTTTTTCTTTCAGTAAACTTAGAGTTTCGTGGCTTCGGGGTGGGAGTAGT
Mm_MECP2_v2         AAAAATATTTTTTTTTTCTTTCAGTAAACTTAGAGTTTCGTGGCTTCGGGGTGGGAGTAGT
Hs_MECP2_v3         AAAAATATTTTTTTTTTCTTTCAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
Hs_MECP2_v1         AAAAATATTTTTTTTTTCTTTCAGTAAACTTAGAGTTTCGTGGCTTCAGGGTGGGAGTAGT
Hs_MECP2_v2         AAAAATATTTTTTTTTTCTTTCAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
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Bt_MECP2_v1         TGGAGCATTGGGGATGTTTTTTTCTTATCGACAAGCACAGTCAGGTTGAAGACCTAACCA
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Oa_MECP2_v1(P)      TGGAGCATTGGGGGTGTTTTTTTCTTATCGACAAGCACAGTCAGGTTGAAGACCTAACCA
Oa_MECP2_v4(P)      TGGAGCATTGGGGGTGTTTTTTTCTTATCGACAAGCACAGTCAGGTTGAAGACCTAACCA
Oa_MECP2_v2(P)      TGGAGCATTGGGGGTGTTTTTTTCTTATCGACAAGCACAGTCAGGTTGAAGACCTAACCA
Oa_MECP2_v3(P)      TGGAGCATTGGGGGTGTTTTTTTCTTATCGACAAGCACAGTCAGGTTGAAGACCTAACCA
Mm_MECP2_v1         TGGAGCA-TTGGGATG--TTTTTCTTACCGACAAGCACAGTCAGGTTGAAGACCTAACCA
Mm_MECP2_v2         TGGAGCA-TTGGGATG--TTTTTCTTACCGACAAGCACAGTCAGGTTGAAGACCTAACCA
Hs_MECP2_v3         AAAAA-------------------------------------------------------
Hs_MECP2_v1         TGGAGCATTGGGGATG--TTTTTCTTACCGACAAGCACAGTCAGGTTGAAGACCTAACCA
Hs_MECP2_v2         AAAAA-------------------------------------------------------
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Bt_MECP2_v1         GGGCCAGAAGTAGCTTTGCACTTTTCTAAACTAGGCTCCTTCAACAAGGCTTGCTGCAGA
Oa_MECP2_v1(P)      GGGCCAGAAGTAGCTTTGCACTTTTCTAAACTAGGCTCCTTCAACAAGGCTTGCTGCAGA
Oa_MECP2_v4(P)      GGGCCAGAAGTAGCTTTGCACTTTTCTAAACTAGGCTCCTTCAACAAGGCTTGCTGCAGA
Oa_MECP2_v2(P)      GGGCCAGAAGTAGCTTTGCACTTTTCTAAACTAGGCTCCTTCAACAAGGCTTGCTGCAGA
Oa_MECP2_v3(P)      GGGCCAGAAGTAGCTTTGCACTTTTCTAAACTAGGCTCCTTCAACAAGGCTTGCTGCAGA
Mm_MECP2_v1         GGGCCAGAAGTAGCTTTGCACTTTTCTAAACTAGGCTCCTTCAACAAGGCTTGCTGCAGA
Mm_MECP2_v2         GGGCCAGAAGTAGCTTTGCACTTTTCTAAACTAGGCTCCTTCAACAAGGCTTGCTGCAGA
Hs_MECP2_v3         -------------------------------------------------------------
Hs_MECP2_v1         GGGCCAGAAGTAGCTTTGCACTTTTCTAAACTAGGCTCCTTCAACAAGGCTTGCTGCAGA
Hs_MECP2_v2         -------------------------------------------------------------


Bt_MECP2_v1         TACTACTGACCAGACAAGCTGTTGCCCAGGCTTCTTAGGGTGTGCCTGCACCTCCCTCCC
Oa_MECP2_v1(P)      TACTACTGACCAGACAAGCTGTTGCCCAGGCTTCTTAGGGTGTGCCTGCACCTCCCTCCC
Oa_MECP2_v4(P)      TACTACTGACCAGACAAGCTGTTGCCCAGGCTTCTTAGGGTGTGCCTGCACCTCCCTCCC
Oa_MECP2_v2(P)      TACTACTGACCAGACAAGCTGTTGCCCAGGCTTCTTAGGGTGTGCCTGCACCTCCCTCCC
Oa_MECP2_v3(P)      TACTACTGACCAGACAAGCTGTTGCCCAGGCTTCTTAGGGTGTGCCTGCACCTCCCTCCC
Mm_MECP2_v1         TACTACTGACCAGACAAGCTGTTGACCAGGCACTCCCCCCAACAATATCCTCCCTCTTCC
Mm_MECP2_v2         TACTACTGACCAGACAAGCTGTTGACCAGGCACTCCCCCCAACAATATCCTCCCTCTTCC
Hs_MECP2_v3         -------------------------------------------------------------
Hs_MECP2_v1         TACTACTGACCAGACAAGCTGTTGACCAGGCACCTCCCCTCCCGCCCAAACCTTTCCCC-
Hs_MECP2_v2         -------------------------------------------------------------


Bt_MECP2_v1         ACCCAGTCCCCCCCACGTGGTCACTAGGGACAGAGAGCACTTGAGAAGACACTCCTGGTT
Oa_MECP2_v1(P)      ACCCAGT-CCCCCTACGTGGTCACTAGGGACAGAGAGCACTTGAGAAGACACTCCTGGTT
Oa_MECP2_v4(P)      ACCCAGT-CCCCCTACGTGGTCACTAGGGACAGAGAGCACTTGAGAAGACACTCCTGGTT
Oa_MECP2_v2(P)      ACCCAGT-CCCCCTACGTGGTCACTAGGGACAGAGAGCACTTGAGAAGACACTCCTGGTT
Oa_MECP2_v3(P)      ACCCAGT-CCCCCTACGTGGTCACTAGGGACAGAGAGCACTTGAGAAGACACTCCTGGTT
Mm_MECP2_v1         CCCCCCCCACCCCCGCCCCGTG---TGCTCGTTAGGGCAATTGAGAGGACACTCCCATTT
Mm_MECP2_v2         CCCCCCCCACCCCCGCCCCGTG---TGCTCGTTAGGGCAATTGAGAGGACACTCCCATTT
Hs_MECP2_v3         -------------------------------------------------------------
Hs_MECP2_v1         ----CATGTGGTCGTTAGAGAC---AGAGCGACAGAGCAGTTGAGAGGACACTCCCGTTT
Hs_MECP2_v2         -------------------------------------------------------------


Bt_MECP2_v1         TGGGGGCCATCGGTACCCCAGTCTCAGCTCTCCTCTCCCCCCACACCCTGCCCAGCCTCG
Oa_MECP2_v1(P)      TGGGGGCCATCGCTACCCCAGTCTCAGCTCTCCTCTCCCCCCACACCCTGCCCAGCCTTG
Oa_MECP2_v4(P)      TGGGGGCCATCGCTACCCCAGTCTCAGCTCTCCTCTCCCCCCACACCCTGCCCAGCCTTG
Oa_MECP2_v2(P)      TGGGGGCCATCGCTACCCCAGTCTCAGCTCTCCTCTCCCCCCACACCCTGCCCAGCCTTG
Oa_MECP2_v3(P)      TGGGGGCCATCGCTACCCCAGTCTCAGCTCTCCTCTCCCCCCACACCCTGCCCAGCCTTG
Mm_MECP2_v1         TTGGTGCCATTGATGCCCTGTCCATAA---------------------------------
Mm_MECP2_v2         TTGGTGCCATTGATGCCCTGTCCATAA---------------------------------
Hs_MECP2_v3         -------------------------------------------------------------
Hs_MECP2_v1         TCGGTGCCATCAGTGCCCCGTCTACAG---------------------------------
Hs_MECP2_v2         -------------------------------------------------------------


Bt_MECP2_v1         AGCTCCACCACCCCACCCTCCAGTCCCCCTTATGCCCACCCACGTCGGGACCAGGAGGTC
Oa_MECP2_v1(P)      AGCTCCACCACCCCACCCTCCAGCCCCCCTTATGCCCACCCACGTCGGGACCAGGAGGTC
Oa_MECP2_v4(P)      AGCTCCACCACCCCACCCTCCAGCCCCCCTTATGCCCACCCACGTCGGGACCAGGAGGTC
Oa_MECP2_v2(P)      AGCTCCACCACCCCACCCTCCAGCCCCCCTTATGCCCACCCACGTCGGGACCAGGAGGTC
Oa_MECP2_v3(P)      AGCTCCACCACCCCACCCTCCAGCCCCCCTTATGCCCACCCACGTCGGGACCAGGAGGTC
Mm_MECP2_v1         -----TAGCTTCCCTGACTTTTACACCACCCCAACTCCCAATCTGAAGGACTGGGAGGTG
Mm_MECP2_v2         -----TAGCTTCCCTGACTTTTACACCACCCCAACTCCCAATCTGAAGGACTGGGAGGTG
Hs_MECP2_v3         -------------------------------------------------------------
Hs_MECP2_v1         -----CTCCCCCAGCTCCCCCCACCTCCCCCACTCCCAACCACGTTGGGACAGGGAGGTG
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Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CGAGGCAAGAGAGACAGTTGGATCCTTTAGAGATGGTG---GAGACGGCCAGTGGCTCCA
Oa_MECP2_v1(P)      CAGGGCAAAAGAGACAGTTGGATCCTTTCGAGACGGTG---GAGACGGCCAGTGGCTCCA
Oa_MECP2_v4(P)      CAGGGCAAAAGAGACAGTTGGATCCTTTCGAGACGGTG---GAGACGGCCAGTGGCTCCA
Oa_MECP2_v2(P)      CAGGGCAAAAGAGACAGTTGGATCCTTTCGAGACGGTG---GAGACGGCCAGTGGCTCCA
Oa_MECP2_v3(P)      CAGGGCAAAAGAGACAGTTGGATCCTTTCGAGACGGTG---GAGACGGCCAGTGGCTCCA
Mm_MECP2_v1         TGATGCAGGAGAAACTATGGGACTCTTGGGAGAAGACTATGGAGTTGGCCAGTGATTAAG
Mm_MECP2_v2         TGATGCAGGAGAAACTATGGGACTCTTGGGAGAAGACTATGGAGTTGGCCAGTGATTAAG
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TGAGGCAGGAGAGACAGTTGGATTCTTTAGAGAAGATG---GATATGACCAGTGGCTATG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GCCCGTGTGATCCCACACATGGGGGCACACAGACGGCTTCCCACCACCCCCAACCCCAGA
Oa_MECP2_v1(P)      GCCCGTGTGATCCCACCCATGGGGGTACACAGACGGCTCCCCACCAGCCCCAATCCCAAA
Oa_MECP2_v4(P)      GCCCGTGTGATCCCACCCATGGGGGTACACAGACGGCTCCCCACCAGCCCCAATCCCAAA
Oa_MECP2_v2(P)      GCCCGTGTGATCCCACCCATGGGGGTACACAGACGGCTCCCCACCAGCCCCAATCCCAAA
Oa_MECP2_v3(P)      GCCCGTGTGATCCCACCCATGGGGGTACACAGACGGCTCCCCACCAGCCCCAATCCCAAA
Mm_MECP2_v1         G-CCCAGTAATTCCAACTGTGGTAGCACAGATCTGGCTCCACAT-CAACCCAATCCAAAA
Mm_MECP2_v2         G-CCCAGTAATTCCAACTGTGGTAGCACAGATCTGGCTCCACAT-CAACCCAATCCAAAA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GCCTGTGCGATCCCACCCGTGGTGGCTCAAGTCTGGCCCCACACCAGCCCCAATCCAAAA
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TCGACCAGGACATTTCACAGGATGGGGACATAGCACCTGTTGGCCCCGGTTCTGGCCCAG
Oa_MECP2_v1(P)      TCGACCAGGACATTTCACAGGATGGGGACATAGCACCTGTCGGCCCCGGTTCTGGCCCAG
Oa_MECP2_v4(P)      TCGACCAGGACATTTCACAGGATGGGGACATAGCACCTGTCGGCCCCGGTTCTGGCCCAG
Oa_MECP2_v2(P)      TCGACCAGGACATTTCACAGGATGGGGACATAGCACCTGTCGGCCCCGGTTCTGGCCCAG
Oa_MECP2_v3(P)      TCGACCAGGACATTTCACAGGATGGGGACATAGCACCTGTCGGCCCCGGTTCTGGCCCAG
Mm_MECP2_v1         CTGACAAGGATATTTTGCAAAAAAAGAAAGTGGCACCTGTCTGATCCAGCTCTGACATGG
Mm_MECP2_v2         CTGACAAGGATATTTTGCAAAAAAAGAAAGTGGCACCTGTCTGATCCAGCTCTGACATGG
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CTGGCAAGGACGCTTCACAGGACAGGAAAGTGGCACCTGTCTGCTCCAGCTCTGGCATGG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CTAGGAGGGAGGCATCCTTTGAGCCCCCCTGGGTGTCGACTGGCCTGCGCCAGAGGCGAC
Oa_MECP2_v1(P)      CTAGGAGGGAGGCATCCTTTGAGCCCCCCTGGGTGTCGACTGGCCTGCGCCAGAGGCGAC
Oa_MECP2_v4(P)      CTAGGAGGGAGGCATCCTTTGAGCCCCCCTGGGTGTCGACTGGCCTGCGCCAGAGGCGAC
Oa_MECP2_v2(P)      CTAGGAGGGAGGCATCCTTTGAGCCCCCCTGGGTGTCGACTGGCCTGCGCCAGAGGCGAC
Oa_MECP2_v3(P)      CTAGGAGGGAGGCATCCTTTGAGCCCCCCTGGGTGTCGACTGGCCTGCGCCAGAGGCGAC
Mm_MECP2_v1         CTAGAGGTGAGTCCTAAA------CTGATGGCTTATAAACTAGCCTGAGCCACAGAAGAG
Mm_MECP2_v2         CTAGAGGTGAGTCCTAAA------CTGATGGCTTATAAACTAGCCTGAGCCACAGAAGAG
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CTAGGAGGGGGGAGTCCCTTGA--ACTACTGGGTGTAGACTGGCCTGAACCACAGGAGAG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ATTGGCCCAGGGCCGG----------------------------CCTCCAGCGGGTAGCA
Oa_MECP2_v1(P)      ATTGGCCCAGGGCTGG----------------------------CCTCCAGCGGGTAGCG
Oa_MECP2_v4(P)      ATTGGCCCAGGGCTGG----------------------------CCTCCAGCGGGTAGCG
Oa_MECP2_v2(P)      ATTGGCCCAGGGCTGG----------------------------CCTCCAGCGGGTAGCG
Oa_MECP2_v3(P)      ATTGGCCCAGGGCTGG----------------------------CCTCCAGCGGGTAGCG
Mm_MECP2_v1         TATGGCCCAGAGTGAAGTGTCATCATCTGTTCACAAGGCATGCTCCCCTAGAAGATAATG
Mm_MECP2_v2         TATGGCCCAGAGTGAAGTGTCATCATCTGTTCACAAGGCATGCTCCCCTAGAAGATAATG
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GATGGCCCAGGGTGAGGTGGCATGGTCCATTCTCAAGGGACGTCCTCCAACGGGTGGCGC
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CTAGACAGAGGCCACCAAGGCCATGGGCCGAGGCCCCAGCAGGCTGGCCCAGGCTGCAGC
Oa_MECP2_v1(P)      CTAGACAGAGGCCACCAAGGCCACGTGCCGAGGCCCCAGCAGGCTGGCCCAGGCTACAGC
Oa_MECP2_v4(P)      CTAGACAGAGGCCACCAAGGCCACGTGCCGAGGCCCCAGCAGGCTGGCCCAGGCTACAGC
Oa_MECP2_v2(P)      CTAGACAGAGGCCACCAAGGCCACGTGCCGAGGCCCCAGCAGGCTGGCCCAGGCTACAGC
Oa_MECP2_v3(P)      CTAGACAGAGGCCACCAAGGCCACGTGCCGAGGCCCCAGCAGGCTGGCCCAGGCTACAGC
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Mm_MECP2_v1         CTAAAGAGGTGCCATGGAGGCAGCAGGACAAAGTACAGGCAGGCTAGGTGGAGTCAAGC-
Mm_MECP2_v2         CTAAAGAGGTGCCATGGAGGCAGCAGGACAAAGTACAGGCAGGCTAGGTGGAGTCAAGC-
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         -----TAGAGGCCATGGAGGCAGTAGGACAAGGTGCAGGCAGGCTGGCCTGGGGTCAGGC
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CAGCGGAGTGCCGCAGGCCAGGCGGAAGGCATCCCTAGCTGCTCAGAGCAGTTGTGGCCA
Oa_MECP2_v1(P)      TGGCGGAGTGCCACAGGCCAGGTAGAAGGCATCCCTAGCTGCTCAGAGCAGTTGTGGCCG
Oa_MECP2_v4(P)      TGGCGGAGTGCCACAGGCCAGGTAGAAGGCATCCCTAGCTGCTCAGAGCAGTTGTGGCCG
Oa_MECP2_v2(P)      TGGCGGAGTGCCACAGGCCAGGTAGAAGGCATCCCTAGCTGCTCAGAGCAGTTGTGGCCG
Oa_MECP2_v3(P)      TGGCGGAGTGCCACAGGCCAGGTAGAAGGCATCCCTAGCTGCTCAGAGCAGTTGTGGCCG
Mm_MECP2_v1         ------------------------------CAGGCCTAGTGCCACAGAACA----------
Mm_MECP2_v2         ------------------------------CAGGCCTAGTGCCACAGAACA----------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ---CGGGCAGAGCACAGCGGGGTGAGAGGGATTCCTAATCACTCAGAGCA----------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CTAGTTCGAGCCTTAGTAGATGGGGCCAGGGGCCAGGGGGAAGGCAGAGGAAATGTTCTT
Oa_MECP2_v1(P)      CTAGTTCGAGCCTTAGTAGACAGGGCCAGGGGCCAGGGGGAAGGCAGGGGAAATGTTCTT
Oa_MECP2_v4(P)      CTAGTTCGAGCCTTAGTAGACAGGGCCAGGGGCCAGGGGGAAGGCAGGGGAAATGTTCTT
Oa_MECP2_v2(P)      CTAGTTCGAGCCTTAGTAGACAGGGCCAGGGGCCAGGGGGAAGGCAGGGGAAATGTTCTT
Oa_MECP2_v3(P)      CTAGTTCGAGCCTTAGTAGACAGGGCCAGGGGCCAGGGGGAAGGCAGGGGAAATGTTCTT
Mm_MECP2_v1         -----------AGAGAGCAGTCTGACTAGTAATTAAGAGGGAAGAAAGGAAAATATTCTT
Mm_MECP2_v2         -----------AGAGAGCAGTCTGACTAGTAATTAAGAGGGAAGAAAGGAAAATATTCTT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ---GTCTGTGACTTAGTGGACAGGGGAGGGGGCAAAGGGGGAGGAGAAGAAAATGTTCTT
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CCAAAACTTTTCCAATTCTCAACTCCTTTAGGGACAGCTTAGAACTATTTGCACTATTGA
Oa_MECP2_v1(P)      CCAAAACTTTTCCAATTCTCAACTCCTTTAGGGACAGCTTAGAACTATTTGCACTATTGA
Oa_MECP2_v4(P)      CCAAAACTTTTCCAATTCTCAACTCCTTTAGGGACAGCTTAGAACTATTTGCACTATTGA
Oa_MECP2_v2(P)      CCAAAACTTTTCCAATTCTCAACTCCTTTAGGGACAGCTTAGAACTATTTGCACTATTGA
Oa_MECP2_v3(P)      CCAAAACTTTTCCAATTCTCAACTCCTTTAGGGACAGCTTAGAACTATTTGCACTATTGA
Mm_MECP2_v1         CCAATTACTTTCCAGTT-----CTCCTTTAGGGACAGCTTAGAATTATTTGCACTATTGA
Mm_MECP2_v2         CCAATTACTTTCCAGTT-----CTCCTTTAGGGACAGCTTAGAATTATTTGCACTATTGA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CCAGTTACTTTCCAATT-----CTCCTTTAGGGACAGCTTAGAATTATTTGCACTATTGA
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GTCTTCATGTTCCCACTTCAAAACAAAC--CTGCTCTGCGAGCAACCTAGCGGGCTTGAC
Oa_MECP2_v1(P)      GTCTTCATGTTCCCACTTCAAAACAAAC--CTGCTTTGCGAGCAAGCTAGCGGGCTTGAC
Oa_MECP2_v4(P)      GTCTTCATGTTCCCACTTCAAAACAAAC--CTGCTTTGCGAGCAAGCTAGCGGGCTTGAC
Oa_MECP2_v2(P)      GTCTTCATGTTCCCACTTCAAAACAAAC--CTGCTTTGCGAGCAAGCTAGCGGGCTTGAC
Oa_MECP2_v3(P)      GTCTTCATGTTCCCACTTCAAAACAAAC--CTGCTTTGCGAGCAAGCTAGCGGGCTTGAC
Mm_MECP2_v1         GTCTTCATGTTCCCACTTCAAAACAAACAGATGCTCTGAAAGCAAACT----GGCTTGAA
Mm_MECP2_v2         GTCTTCATGTTCCCACTTCAAAACAAACAGATGCTCTGAAAGCAAACT----GGCTTGAA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GTCTTCATGTTCCCACTTCAAAACAAACAGATGCTCTGAGAGCAAACT----GGCTTGAA
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TTGGCGACCCTTTGTCCCTCAGGCCACTAGACGTGACGGTGTTGACAACTACCTGGAT--
Oa_MECP2_v1(P)      TTGGTGACCCTTTGTCCCTCAGGCCACTAGACGTGACAGTGTTGACAACTACCTGGAT--
Oa_MECP2_v4(P)      TTGGTGACCCTTTGTCCCTCAGGCCACTAGACGTGACAGTGTTGACAACTACCTGGAT--
Oa_MECP2_v2(P)      TTGGTGACCCTTTGTCCCTCAGGCCACTAGACGTGACAGTGTTGACAACTACCTGGAT--
Oa_MECP2_v3(P)      TTGGTGACCCTTTGTCCCTCAGGCCACTAGACGTGACAGTGTTGACAACTACCTGGAT--
Mm_MECP2_v1         ATGGTGACACTGTCC--CACAAGCCACCAGACATGGCAGTGTTCAGAACTACCTGTAT--
Mm_MECP2_v2         ATGGTGACACTGTCC--CACAAGCCACCAGACATGGCAGTGTTCAGAACTACCTGTAT--
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TTGGTGACATTTAGTCCCTCAAGCCACCAGATGTGACAGTGTTGAGAACTACCTGGATTT
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CTGTATATACCTGCGCTTGTTTTCAAGTGGGCTCAGCACATAGGGTTCCCACGAAGCTCC
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Oa_MECP2_v1(P)      CTGTATATACCTGCGCTTGTTTTCAAGTGGGCTCAGCACATAGGGTTCCCACGAAGCTCC
Oa_MECP2_v4(P)      CTGTATATACCTGCGCTTGTTTTCAAGTGGGCTCAGCACATAGGGTTCCCACGAAGCTCC
Oa_MECP2_v2(P)      CTGTATATACCTGCGCTTGTTTTCAAGTGGGCTCAGCACATAGGGTTCCCACGAAGCTCC
Oa_MECP2_v3(P)      CTGTATATACCTGCGCTTGTTTTCAAGTGGGCTCAGCACATAGGGTTCCCACGAAGCTCC
Mm_MECP2_v1         CTGTATATACCTGCGCTTGTTTTAAAGTGGGCTCAGCACATAGGATTCCCAAGAAGCTCC
Mm_MECP2_v2         CTGTATATACCTGCGCTTGTTTTAAAGTGGGCTCAGCACATAGGATTCCCAAGAAGCTCC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GTATATATACCTGCGCTTGTTTTAAAGTGGGCTCAGCACATAGGGTTCCCACGAAGCTCC
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GAAACTCTAAGTGTTTGCTGCAA-TTTATAAGGACTTCCTGATTGATTTCTCTCCTCTCC
Oa_MECP2_v1(P)      GAAACTCTAAGTGTTTGCTGCAA-TTTATAAGGACTTCCTGATTGGTTTCTCTCCTCTCC
Oa_MECP2_v4(P)      GAAACTCTAAGTGTTTGCTGCAA-TTTATAAGGACTTCCTGATTGGTTTCTCTCCTCTCC
Oa_MECP2_v2(P)      GAAACTCTAAGTGTTTGCTGCAA-TTTATAAGGACTTCCTGATTGGTTTCTCTCCTCTCC
Oa_MECP2_v3(P)      GAAACTCTAAGTGTTTGCTGCAA-TTTATAAGGACTTCCTGATTGGTTTCTCTCCTCTCC
Mm_MECP2_v1         GAAACTCTAAGTGTTTGCTGCAATTTTATAAGGACTTCCTGATTGCTTTCTCTCTCGTCC
Mm_MECP2_v2         GAAACTCTAAGTGTTTGCTGCAATTTTATAAGGACTTCCTGATTGCTTTCTCTCTCGTCC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GAAACTCTAAGTGTTTGCTGCAATTTTATAAGGACTTCCTGATTGGTTTCTCTTCTCCCC
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TTTGGTTTCTGTC-TCCTTTCATTTCAGCCTTTTCATTTCTCCCCTTCCTCCC-------
Oa_MECP2_v1(P)      TTTGGTTTCTGTC-TCCTTTCATTTCAGCCTTTTTATTTCTCCCCTTCCTCCC-------
Oa_MECP2_v4(P)      TTTGGTTTCTGTC-TCCTTTCATTTCAGCCTTTTTATTTCTCCCCTTCCTCCC-------
Oa_MECP2_v2(P)      TTTGGTTTCTGTC-TCCTTTCATTTCAGCCTTTTTATTTCTCCCCTTCCTCCC-------
Oa_MECP2_v3(P)      TTTGGTTTCTGTC-TCCTTTCATTTCAGCCTTTTTATTTCTCCCCTTCCTCCC-------
Mm_MECP2_v1         TTCCATTTCTTCCTTCCTTCCATTTCATGCTTTCATTTCTTCCCCTAGCTTCTAGTTGTT
Mm_MECP2_v2         TTCCATTTCTTCCTTCCTTCCATTTCATGCTTTCATTTCTTCCCCTAGCTTCTAGTTGTT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TTCCATTTCTGCCTTTTGTTCATTTCATCCTTTCACTTCTTTCCCTTCCTCCGTCCTCCT
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TCGTCCTCACTGCTCCCTTCTGTTCCAGGCAGCCGCAGTGCCCGACCGTACTTCGAGCCG
Oa_MECP2_v1(P)      TCGTCCTCACTGCTCCCTTCTGTTCCAGGCAGCCTCAGTGCCCAACCGTACTTTGAGCCG
Oa_MECP2_v4(P)      TCGTCCTCACTGCTCCCTTCTGTTCCAGGCAGCCTCAGTGCCCAACCGTACTTTGAGCCG
Oa_MECP2_v2(P)      TCGTCCTCACTGCTCCCTTCTGTTCCAGGCAGCCTCAGTGCCCAACCGTACTTTGAGCCG
Oa_MECP2_v3(P)      TCGTCCTCACTGCTCCCTTCTGTTCCAGGCAGCCTCAGTGCCCAACCGTACTTTGAGCCG
Mm_MECP2_v1         TCTTCT---------------GTTCCAGGCAGCTGCAGTGCTGAACCACATGGTTACCTA
Mm_MECP2_v2         TCTTCT---------------GTTCCAGGCAGCTGCAGTGCTGAACCACATGGTTACCTA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CCTTCCTAGTTCATCCCTTCTCTTCCAGGCAGCCGCGGTGCCCAACCACACTTGTCGGCT
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ACACTGGTCAGCTCAGGCCCCCAGAACT-CCCCCACCCTTGGCCTTCCCGCCGTCCAGCC
Oa_MECP2_v1(P)      ACGCTGGTCAGCTCAGGCCCCCAGAACTACCCCCACCCTTGGCCTTCCCGCCGTCCACCC
Oa_MECP2_v4(P)      ACGCTGGTCAGCTCAGGCCCCCAGAACTACCCCCACCCTTGGCCTTCCCGCCGTCCACCC
Oa_MECP2_v2(P)      ACGCTGGTCAGCTCAGGCCCCCAGAACTACCCCCACCCTTGGCCTTCCCGCCGTCCACCC
Oa_MECP2_v3(P)      ACGCTGGTCAGCTCAGGCCCCCAGAACTACCCCCACCCTTGGCCTTCCCGCCGTCCACCC
Mm_MECP2_v1         ACAGCAGTCAGCTGCAG-CCCTAGGATTCTTCCTGCCCTTTAACTTCCCATTGCCAGTGC
Mm_MECP2_v2         ACAGCAGTCAGCTGCAG-CCCTAGGATTCTTCCTGCCCTTTAACTTCCCATTGCCAGTGC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CCA------------GT-CCCCAGAACTCTGCCTGCCCTTTGTCCTCCTGCTGCCAGTAC
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CAGCTCCCCCTGCCACCCATTTCTGAGCCCTGAGGAAGCCCCAGACTCCGCTGAATCCAC
Oa_MECP2_v1(P)      CAGCCTCCCCTGCCACCCATTTCTGAGCCCTGAGGAAGCCCCAGACTCCGCTGAATCCAC
Oa_MECP2_v4(P)      CAGCCTCCCCTGCCACCCATTTCTGAGCCCTGAGGAAGCCCCAGACTCCGCTGAATCCAC
Oa_MECP2_v2(P)      CAGCCTCCCCTGCCACCCATTTCTGAGCCCTGAGGAAGCCCCAGACTCCGCTGAATCCAC
Oa_MECP2_v3(P)      CAGCCTCCCCTGCCACCCATTTCTGAGCCCTGAGGAAGCCCCAGACTCCGCTGAATCCAC
Mm_MECP2_v1         CAGGT-----------ATCATATTTAACCTTGAGCAAGAGCTGGGCTCTTTTGAGCCCTC
Mm_MECP2_v2         CAGGT-----------ATCATATTTAACCTTGAGCAAGAGCTGGGCTCTTTTGAGCCCTC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CAGCC-------CCACCCTGTTTTGAGCCCTGAGGAGGCCTTGGGCTCTGCTGAGTCCGA
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Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CCAGCTCTAGTACCCCAGCCTCTCTGAG-GGGCATGGGAGAGGCAAGATCTTGCTCTCCC
Oa_MECP2_v1(P)      CCAGCCCTAGTACCCCAGCCTCTCTGAG-GGGCATGGGAGAGGCAGGATCTTGCTCTCCC
Oa_MECP2_v4(P)      CCAGCCCTAGTACCCCAGCCTCTCTGAG-GGGCATGGGAGAGGCAGGATCTTGCTCTCCC
Oa_MECP2_v2(P)      CCAGCCCTAGTACCCCAGCCTCTCTGAG-GGGCATGGGAGAGGCAGGATCTTGCTCTCCC
Oa_MECP2_v3(P)      CCAGCCCTAGTACCCCAGCCTCTCTGAG-GGGCATGGGAGAGGCAGGATCTTGCTCTCCC
Mm_MECP2_v1         CCTAACCT-----------CTGTGAAGAAGAACAAGAAGGTAGGAAGCTCTTGC------
Mm_MECP2_v2         CCTAACCT-----------CTGTGAAGAAGAACAAGAAGGTAGGAAGCTCTTGC------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CCTGGCCT-----------GTCTGTGAA-GAGCAAGAGAGCAGCAAGGTCTTGCTCTCCT
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         AGGAGTCTCCTCCTT------------------------CGGTCAGACCCTGGATCCCA
Oa_MECP2_v1(P)      AGGAGTCCCCTCCTT------------------------CAGTCAGACCCTGGATCCCA
Oa_MECP2_v4(P)      AGGAGTCCCCTCCTT------------------------CAGTCAGACCCTGGATCCCA
Oa_MECP2_v2(P)      AGGAGTCCCCTCCTT------------------------CAGTCAGACCCTGGATCCCA
Oa_MECP2_v3(P)      AGGAGTCCCCTCCTT------------------------CAGTCAGACCCTGGATCCCA
Mm_MECP2_v1         ---------------TCTTGCTAAGAAAAATGTCAAAAGGCTTTCAGACCTTAAACA-AT
Mm_MECP2_v2         ---------------TCTTGCTAAGAAAAATGTCAAAAGGCTTTCAGACCTTAAACA-AT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         AGGTAGCCCCCTCTTCCCTGGTAAGAAAA-AGCAAAAGGCATTTCCCACCCTGAACAACG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GGTCTCCTCAGCCTTCCCACTCAACGGCAGTGGGTAGGAGAAGTGGACCAAGATTGGGAT
Oa_MECP2_v1(P)      GGTCTCCTCAGCCTTCCCACTCAACGGCAGTGGGTAGGAGAAGTGGACCCAGATTGGGAT
Oa_MECP2_v4(P)      GGTCTCCTCAGCCTTCCCACTCAACGGCAGTGGGTAGGAGAAGTGGACCCAGATTGGGAT
Oa_MECP2_v2(P)      GGTCTCCTCAGCCTTCCCACTCAACGGCAGTGGGTAGGAGAAGTGGACCCAGATTGGGAT
Oa_MECP2_v3(P)      GGTCTCCTCAGCCTTCCCACTCAACGGCAGTGGGTAGGAGAAGTGGACCCAGATTGGGAT
Mm_MECP2_v1         GAGCCTTTTCACCTT-TTACTCTAGAAAAGTGGACTAGAAAATCTGGGTCACATTGGGT-
Mm_MECP2_v2         GAGCCTTTTCACCTT-TTACTCTAGAAAAGTGGACTAGAAAATCTGGGTCACATTGGGT-
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         AGCCTTTTCACCCTT-CTACTCTAGAGAAGTGGACTGGAGGAGCTGGGCCCGATTTGGT-
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TGCAGAGCCAAGGGCAGCACAGAGACCCGCTGTGGCCTGCCAGTGTCACGGAGTGGCCAA
Oa_MECP2_v1(P)      TGCAGAGCCAAGGGCAGCACAGAGACCCACTGTGGCCTGCCAGCATCACGGAGTGGCCAA
Oa_MECP2_v4(P)      TGCAGAGCCAAGGGCAGCACAGAGACCCACTGTGGCCTGCCAGCATCACGGAGTGGCCAA
Oa_MECP2_v2(P)      TGCAGAGCCAAGGGCAGCACAGAGACCCACTGTGGCCTGCCAGCATCACGGAGTGGCCAA
Oa_MECP2_v3(P)      TGCAGAGCCAAGGGCAGCACAGAGACCCACTGTGGCCTGCCAGCATCACGGAGTGGCCAA
Mm_MECP2_v1         -----AGCTGAAGGAGATACAGAGGCCC-CTATGGCCTGCCAGAGTCGTTGCATGGCCCA
Mm_MECP2_v2         -----AGCTGAAGGAGATACAGAGGCCC-CTATGGCCTGCCAGAGTCGTTGCATGGCCCA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         -----AGTTGAGGAAAGCACAGAGGCCT-CCT-GTGGCCTGCCAGTCATCGAGTGGCCCA
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GCC---------------CTGACCTTGGCCTGTGCAGGACCCGGCTAGGGCGGGTTAGTT
Oa_MECP2_v1(P)      GCC---------------CTGACCTTGGCCTGTGCAGGACCCAGCTAGGGTGGGGTAGTC
Oa_MECP2_v4(P)      GCC---------------CTGACCTTGGCCTGTGCAGGACCCAGCTAGGGTGGGGTAGTC
Oa_MECP2_v2(P)      GCC---------------CTGACCTTGGCCTGTGCAGGACCCAGCTAGGGTGGGGTAGTC
Oa_MECP2_v3(P)      GCC---------------CTGACCTTGGCCTGTGCAGGACCCAGCTAGGGTGGGGTAGTC
Mm_MECP2_v1         ACAGGGGCTCCATGCCCACTACCCTTGACCCTACTCAGAAATCTAATGTCATACTTAGTG
Mm_MECP2_v2         ACAGGGGCTCCATGCCCACTACCCTTGACCCTACTCAGAAATCTAATGTCATACTTAGTG
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ACAGGGGCTCCATGCCAGCCGACCTTGACCTCACTCAGAAGTCCAGAGTCTAGCGTAGTG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GGGCCGGGCAGCAG-------------------------------------GCAAAATGA
Oa_MECP2_v1(P)      GGGCCAGGCAGCAG-------------------------------------GCAAAATGA
Oa_MECP2_v4(P)      GGGCCAGGCAGCAG-------------------------------------GCAAAATGA
Oa_MECP2_v2(P)      GGGCCAGGCAGCAG-------------------------------------GCAAAATGA
Oa_MECP2_v3(P)      GGGCCAGGCAGCAG-------------------------------------GCAAAATGA
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Mm_MECP2_v1         TGGGCAGGGGACCT--------GTCAGGACAGATGCAGACCTAAGCAGGGAGTGACACCA
Mm_MECP2_v2         TGGGCAGGGGACCT--------GTCAGGACAGATGCAGACCTAAGCAGGGAGTGACACCA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CAGCAGGGCAGTAGCGGTACCAATGCAGAACTCCCAAGACCCGAGCTGGGACCAGTACCT
Hs_MECP2_v2         ------------------------------------------------------------


Bt_MECP2_v1         GTGCAGATATCCC-----CTGCCACTCCTCTGAGCAGTAGTTCTCCTCTGCTGGGCCCTG
Oa_MECP2_v1(P)      GTGCAGATACCCC-----CTGCCACTCCTCTGAGCAGGAGTT---CTCTGCTGGGCCCCG
Oa_MECP2_v4(P)      GTGCAGATACCCC-----CTGCCACTCCTCTGAGCAGGAGTT---CTCTGCTGGGCCCCG
Oa_MECP2_v2(P)      GTGCAGATACCCC-----CTGCCACTCCTCTGAGCAGGAGTT---CTCTGCTGGGCCCCG
Oa_MECP2_v3(P)      GTGCAGATACCCC-----CTGCCACTCCTCTGAGCAGGAGTT---CTCTGCTGGGCCCCG
Mm_MECP2_v1         GGGCCCTTGGCCCTTCTTCTGACAAACATACACATCCCAAGTCTTTTTCTAGTGGAATTC
Mm_MECP2_v2         GGGCCCTTGGCCCTTCTTCTGACAAACATACACATCCCAAGTCTTTTTCTAGTGGAATTC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GGGTCCCCAGCCCTTCCTCTGCTCCCCCTTTTCCCTCGGAGTTCTTCTTGAATGGCAATG
Hs_MECP2_v2         ------------------------------------------------------------


Bt_MECP2_v1         TGCGGCCTTTGCTTGCTGGAGGCTGGTGGAAGGGGTTGGTACTTCACGCTTTTCCCCATC
Oa_MECP2_v1(P)      TGCGGCCTTTGCTTGCTGGAGGCTGGTAAGGGTGGCTGGTACTTCAGGCTTTTCCCCATC
Oa_MECP2_v4(P)      TGCGGCCTTTGCTTGCTGGAGGCTGGTAAGGGTGGCTGGTACTTCAGGCTTTTCCCCATC
Oa_MECP2_v2(P)      TGCGGCCTTTGCTTGCTGGAGGCTGGTAAGGGTGGCTGGTACTTCAGGCTTTTCCCCATC
Oa_MECP2_v3(P)      TGCGGCCTTTGCTTGCTGGAGGCTGGTAAGGGTGGCTGGTACTTCAGGCTTTTCCCCATC
Mm_MECP2_v1         TTAACCTCTTGCTCACTGGGGACTGG--GAAGCATCAGC-ACATCCCATATTTCAAACTC
Mm_MECP2_v2         TTAACCTCTTGCTCACTGGGGACTGG--GAAGCATCAGC-ACATCCCATATTTCAAACTC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TTTTGCTTTTGCTCGATGCAGACAGG--GGGCCAGAACACCACACATTTCACTGTCTGTC
Hs_MECP2_v2         ------------------------------------------------------------


Bt_MECP2_v1         AGCACCAGGGGCTGTGGTGTTGGGGCATCGAGGCTTGGGCTTGTTGCGGGGTGTTCATTT
Oa_MECP2_v1(P)      AGCACCA-GGGCTGTGGTGTTGGGGCGTCGAGGCTTGGGCTTGTTGCGGGGTGTTCATTT
Oa_MECP2_v4(P)      AGCACCA-GGGCTGTGGTGTTGGGGCGTCGAGGCTTGGGCTTGTTGCGGGGTGTTCATTT
Oa_MECP2_v2(P)      AGCACCA-GGGCTGTGGTGTTGGGGCGTCGAGGCTTGGGCTTGTTGCGGGGTGTTCATTT
Oa_MECP2_v3(P)      AGCACCA-GGGCTGTGGTGTTGGGGCGTCGAGGCTTGGGCTTGTTGCGGGGTGTTCATTT
Mm_MECP2_v1         TGCTCCA-TAAGTACAGTGGTGAATTTTATAGACTTGACTTTGCTGTGGGGTTTTAATTG
Mm_MECP2_v2         TGCTCCA-TAAGTACAGTGGTGAATTTTATAGACTTGACTTTGCTGTGGGGTTTTAATTG
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TGGTCCA-TAGCTGTGGTGTAGGGGCTTAGAGGCATGGGCTTGCTGTGGGTTTTTAATTG
Hs_MECP2_v2         ------------------------------------------------------------


Bt_MECP2_v1         GTCAGTTTCAATTCGAGACCCCGTGCTTTTACCCTCTGTTCAGGAAGTCCTTATCTAGCT
Oa_MECP2_v1(P)      GTCAGTTTCAATTTGAGACCCCGTGCTCTTACCCTCTGTTCAGGAAGTCCTTATCTAGCT
Oa_MECP2_v4(P)      GTCAGTTTCAATTTGAGACCCCGTGCTCTTACCCTCTGTTCAGGAAGTCCTTATCTAGCT
Oa_MECP2_v2(P)      GTCAGTTTCAATTTGAGACCCCGTGCTCTTACCCTCTGTTCAGGAAGTCCTTATCTAGCT
Oa_MECP2_v3(P)      GTCAGTTTCAATTTGAGACCCCGTGCTCTTACCCTCTGTTCAGGAAGTCCTTATCTAGCT
Mm_MECP2_v1         GTCAGTTTTAATTTGGGATCCCAAAGTTTTAACCTCCATTCAGGAAGTCCTTATCTAGCT
Mm_MECP2_v2         GTCAGTTTTAATTTGGGATCCCAAAGTTTTAACCTCCATTCAGGAAGTCCTTATCTAGCT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ATCAGTTTTCATGTGGGATCCCATCTTTTTAACCTCTGTTCAGGAAGTCCTTATCTAGCT
Hs_MECP2_v2         ------------------------------------------------------------


Bt_MECP2_v1         GCATATCTTCATCATATTGGTATATCCTTTTCTGTGTTTACAGAGATGTCTCTTATATCT
Oa_MECP2_v1(P)      GCATATCTTCATCATATTGGTATATCCTTTTCTGTGTTTACAGAGATGTCTCTTATATCT
Oa_MECP2_v4(P)      GCATATCTTCATCATATTGGTATATCCTTTTCTGTGTTTACAGAGATGTCTCTTATATCT
Oa_MECP2_v2(P)      GCATATCTTCATCATATTGGTATATCCTTTTCTGTGTTTACAGAGATGTCTCTTATATCT
Oa_MECP2_v3(P)      GCATATCTTCATCATATTGGTATATCCTTTTCTGTGTTTACAGAGATGTCTCTTATATCT
Mm_MECP2_v1         GCATATCTTCATCATATTGGTATATCCTTTTCTGTGTTTACAGAGATGTCTCATATCTA-
Mm_MECP2_v2         GCATATCTTCATCATATTGGTATATCCTTTTCTGTGTTTACAGAGATGTCTCATATCTA-
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GCATATCTTCATCATATTGGTATATCCTTTTCTGTGTTTACAGAGATGTCTCTTATATCT
Hs_MECP2_v2         ------------------------------------------------------------


Bt_MECP2_v1         AAATCTGTCCAACTGAGAAGTACCTTATCAAAGTAGCAAACGAGACAGCAGTCTTAGGCT
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Oa_MECP2_v1(P)      AAATCTGTCCAACTGAGAAGTACCTTATCAAAGTAGCAAACGAGACAGCAGTCTTATGCT
Oa_MECP2_v4(P)      AAATCTGTCCAACTGAGAAGTACCTTATCAAAGTAGCAAACGAGACAGCAGTCTTATGCT
Oa_MECP2_v2(P)      AAATCTGTCCAACTGAGAAGTACCTTATCAAAGTAGCAAACGAGACAGCAGTCTTATGCT
Oa_MECP2_v3(P)      AAATCTGTCCAACTGAGAAGTACCTTATCAAAGTAGCAAACGAGACAGCAGTCTTATGCT
Mm_MECP2_v1         -TCGAAATCTGTCTGAGAAGTACCTTATCAAAGTAGCAAATGAGACAGCAGTCTTATGCT
Mm_MECP2_v2         -TCGAAATCTGTCTGAGAAGTACCTTATCAAAGTAGCAAATGAGACAGCAGTCTTATGCT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         AAATCTGTCCAACTGAGAAGTACCTTATCAAAGTAGCAAATGAGACAGCAGTCTTATGCT
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TCCAGAAACACCCACAAGCACGTCCCATGTGAGCTGCTGCCATGAACTGTCAAGTGCGTG
Oa_MECP2_v1(P)      TCCAGAAACACCCACAAGCACGTCCCACGTGAGCTGCTGCCATGAACTGTCAAGTGCGTG
Oa_MECP2_v4(P)      TCCAGAAACACCCACAAGCACGTCCCACGTGAGCTGCTGCCATGAACTGTCAAGTGCGTG
Oa_MECP2_v2(P)      TCCAGAAACACCCACAAGCACGTCCCACGTGAGCTGCTGCCATGAACTGTCAAGTGCGTG
Oa_MECP2_v3(P)      TCCAGAAACACCCACAAGCACGTCCCACGTGAGCTGCTGCCATGAACTGTCAAGTGCGTG
Mm_MECP2_v1         TCCAGAAACACCCACAGGCACGTCCCATGTGAGCTGCTGCCATGAACTGTCGAGTGTGTA
Mm_MECP2_v2         TCCAGAAACACCCACAGGCACGTCCCATGTGAGCTGCTGCCATGAACTGTCGAGTGTGTA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TCCAGAAACACCCACAGGCATGTCCCATGTGAGCTGCTGCCATGAACTGTCAAGTGTGTG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TTGTCTCGTGTATTTCAGTTACTATCCCCCAGCTTTCCTCACTGCAGTGTAACCATGAAG
Oa_MECP2_v1(P)      TTGTCTCGTGTATTTCAGTTACTATCCCCCAGCTTTCCTCACTGCAGTGTAATCATGAAG
Oa_MECP2_v4(P)      TTGTCTCGTGTATTTCAGTTACTATCCCCCAGCTTTCCTCACTGCAGTGTAATCATGAAG
Oa_MECP2_v2(P)      TTGTCTCGTGTATTTCAGTTACTATCCCCCAGCTTTCCTCACTGCAGTGTAATCATGAAG
Oa_MECP2_v3(P)      TTGTCTCGTGTATTTCAGTTACTATCCCCCAGCTTTCCTCACTGCAGTGTAATCATGAAG
Mm_MECP2_v1         TTGTCTTGTGTATTTTCGTTAACGTTCCCCAGC-TTCCTTCCTGCGGTGTAATCATGGAA
Mm_MECP2_v2         TTGTCTTGTGTATTTTCGTTAACGTTCCCCAGC-TTCCTTCCTGCGGTGTAATCATGGAA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TTGTCTTGTGTATTTCAGTTATTG-TCCCTGGC-TTCCTTACTATGGTGTAATCATGAAG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GAGTGAAACATCTTAGAAACCATCTAGCACTTCCTTGCCAGTCCTTTAGTGATCAGGACC
Oa_MECP2_v1(P)      GAGTGAAACATCTTAGAAACCATCTAGCACTTCCTTGCCAGTCCTTTAGTGATCAGGACC
Oa_MECP2_v4(P)      GAGTGAAACATCTTAGAAACCATCTAGCACTTCCTTGCCAGTCCTTTAGTGATCAGGACC
Oa_MECP2_v2(P)      GAGTGAAACATCTTAGAAACCATCTAGCACTTCCTTGCCAGTCCTTTAGTGATCAGGACC
Oa_MECP2_v3(P)      GAGTGAAACATCTTAGAAACCATCTAGCACTTCCTTGCCAGTCCTTTAGTGATCAGGACC
Mm_MECP2_v1         GAGTGAAACATCATAGAAATCGTCTAGCACTTCCTGGCCAGTCC-TTAGTGATCAGGAAC
Mm_MECP2_v2         GAGTGAAACATCATAGAAATCGTCTAGCACTTCCTGGCCAGTCC-TTAGTGATCAGGAAC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GAGTGAAACATCATAGAAACTGTCTAGCACTTCCTTGCCAGTCT-TTAGTGATCAGGAAC
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CCTAGTTGACAGTTCCAATCAGTAGCTTCAGAAAAAAAAAT---GAAACTGTGTCTCTCT
Oa_MECP2_v1(P)      CCTAGTTGACAGTTCCAATCAGTAGCTTCAGAAAAAAAAAAAACGAAACTGTGTCTCTCT
Oa_MECP2_v4(P)      CCTAGTTGACAGTTCCAATCAGTAGCTTCAGAAAAAAAAAAAACGAAACTGTGTCTCTCT
Oa_MECP2_v2(P)      CCTAGTTGACAGTTCCAATCAGTAGCTTCAGAAAAAAAAAAAACGAAACTGTGTCTCTCT
Oa_MECP2_v3(P)      CCTAGTTGACAGTTCCAATCAGTAGCTTCAGAAAAAAAAAAAACGAAACTGTGTCTCTCT
Mm_MECP2_v1         CGTAGTTGACAGTTCCAATTGATAGCTTAAGAT-----------AAAACCATGTTTGTCT
Mm_MECP2_v2         CGTAGTTGACAGTTCCAATTGATAGCTTAAGAT-----------AAAACCATGTTTGTCT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CATAGTTGACAGTTCCAATCAGTAGCTTAAGAA-----------AAAACCGTGTTTGTCT
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CTCCCAGAACGGTTAAAAGCAAGGGAGTTTGCCC----TGTTCTGTTTGTGGA--GTTGT
Oa_MECP2_v1(P)      CTCCCAGAATGGTTAGAAGCAAGGGAATTTGCCC----TGTTCTGTTTGTGGA--GTTGT
Oa_MECP2_v4(P)      CTCCCAGAATGGTTAGAAGCAAGGGAATTTGCCC----TGTTCTGTTTGTGGA--GTTGT
Oa_MECP2_v2(P)      CTCCCAGAATGGTTAGAAGCAAGGGAATTTGCCC----TGTTCTGTTTGTGGA--GTTGT
Oa_MECP2_v3(P)      CTCCCAGAATGGTTAGAAGCAAGGGAATTTGCCC----TGTTCTGTTTGTGGA--GTTGT
Mm_MECP2_v1         CTTATGGAATGGTTAGAACTAAGTGAGAGATCTTGCCCCATTCTGTTTGCCGA--ATCAT
Mm_MECP2_v2         CTTATGGAATGGTTAGAACTAAGTGAGAGATCTTGCCCCATTCTGTTTGCCGA--ATCAT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CTTCTGGAATGGTTAGAAGTGAGGGAGTTTGCCC----CGTTCTGTTTGTAGAGTCTCAT
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Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         AGCTGCCCTTTCTAGCATTTTTGTATCCATTTCTTGATGCTGCAAAAGCAAGTCCCCCAA
Oa_MECP2_v1(P)      AGCTGCCCTTTCTAGCATTTTTGTATCCATTTCTTGATGCTGCAAAAGCAAGTCCCCCAA
Oa_MECP2_v4(P)      AGCTGCCCTTTCTAGCATTTTTGTATCCATTTCTTGATGCTGCAAAAGCAAGTCCCCCAA
Oa_MECP2_v2(P)      AGCTGCCCTTTCTAGCATTTTTGTATCCATTTCTTGATGCTGCAAAAGCAAGTCCCCCAA
Oa_MECP2_v3(P)      AGCTGCCCTTTCTAGCATTTTTGTATCCATTTCTTGATGCTGCAAAAGCAAGTCCCCCAA
Mm_MECP2_v1         AG-TTGGACTTTTAGTGTATTTGTATCCATTTCCTTGTGCTATAAAAGCAAACCCTGCAA
Mm_MECP2_v2         AG-TTGGACTTTTAGTGTATTTGTATCCATTTCCTTGTGCTATAAAAGCAAACCCTGCAA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         AGTTGGACTTTCTAGCATATATGTGTCCATTTCCTTATGCTGTAAAAGCAAGTCCTGCAA
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CCAA-----------------------------------ACCCACTCTGCTGTCCAC
Oa_MECP2_v1(P)      CCAA-----------------------------------ACCCACTCTGCTGTCCAC
Oa_MECP2_v4(P)      CCAA-----------------------------------ACCCACTCTGCTGTCCAC
Oa_MECP2_v2(P)      CCAA-----------------------------------ACCCACTCTGCTGTCCAC
Oa_MECP2_v3(P)      CCAA-----------------------------------ACCCACTCTGCTGTCCAC
Mm_MECP2_v1         CCAGCTTTCTGTCAGGCAGTCC----------------TTTTGCCTGCTCTGCTTTTGAT
Mm_MECP2_v2         CCAGCTTTCTGTCAGGCAGTCC----------------TTTTGCCTGCTCTGCTTTTGAT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CCAAACTCCCATCAGCCCAATCCCTGATCCCTGATCCCTTCCACCTGCTCTGCTGATGAC
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CTGCTGGGCTTCACTTCTGAGTCCTCCCCCAGGAAGGGATGGGAGTTGGAAGAGGGGGCA
Oa_MECP2_v1(P)      CTGCTGGGCTTCACTTCTGAGTCCTCCCCCAGGAAGGGATGGGAGTTGGAAGAGGGGGCG
Oa_MECP2_v4(P)      CTGCTGGGCTTCACTTCTGAGTCCTCCCCCAGGAAGGGATGGGAGTTGGAAGAGGGGGCG
Oa_MECP2_v2(P)      CTGCTGGGCTTCACTTCTGAGTCCTCCCCCAGGAAGGGATGGGAGTTGGAAGAGGGGGCG
Oa_MECP2_v3(P)      CTGCTGGGCTTCACTTCTGAGTCCTCCCCCAGGAAGGGATGGGAGTTGGAAGAGGGGGCG
Mm_MECP2_v1         CCTCTTAGTCTTGCTTCTGGTTCCTCCCTGGAGAGGGAGGAGGGGTCAGAAGAGGAATTC
Mm_MECP2_v2         CCTCTTAGTCTTGCTTCTGGTTCCTCCCTGGAGAGGGAGGAGGGGTCAGAAGAGGAATTC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CCCCCCAGCTTCACTTCTGACTCTTCCCCAGGAAGGGAAGGGGGGTCAGAAGAGAGGGTG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TGTTC-----------------GTTGGGGTCCCTCTTCCTCCAAGGACAAAAGGCTCCTG
Oa_MECP2_v1(P)      TGTTC-----------------ATTGGGGTCCCTCTTCCTCCAAGGACAAAAGGCTCCTG
Oa_MECP2_v4(P)      TGTTC-----------------ATTGGGGTCCCTCTTCCTCCAAGGACAAAAGGCTCCTG
Oa_MECP2_v2(P)      TGTTC-----------------ATTGGGGTCCCTCTTCCTCCAAGGACAAAAGGCTCCTG
Oa_MECP2_v3(P)      TGTTC-----------------ATTGGGGTCCCTCTTCCTCCAAGGACAAAAGGCTCCTG
Mm_MECP2_v1         TGGAGGATCCAGGATATGTCCTTCTGAACTCCTGCTTCTTCCAGTGACAAAAGGCCCCTA
Mm_MECP2_v2         TGGAGGATCCAGGATATGTCCTTCTGAACTCCTGCTTCTTCCAGTGACAAAAGGCCCCTA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         AGTCC----------------TCCAGAACTCTTC----CTCCAAGGACAGAAGGCTCCTG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         -------------------------GCACTCTCAGAGGACCCCTGTCCACA-TGAGCCCG
Oa_MECP2_v1(P)      -------------------------GCACTCTCAGAGGACTCCTGTCCACA-TGAGCCCG
Oa_MECP2_v4(P)      -------------------------GCACTCTCAGAGGACTCCTGTCCACA-TGAGCCCG
Oa_MECP2_v2(P)      -------------------------GCACTCTCAGAGGACTCCTGTCCACA-TGAGCCCG
Oa_MECP2_v3(P)      -------------------------GCACTCTCAGAGGACTCCTGTCCACA-TGAGCCCG
Mm_MECP2_v1         CTGCCCCACCCCAA-CCTGCCCCATGCACTCCTCTAGGACACCTTTCCATACTTTTCACA
Mm_MECP2_v2         CTGCCCCACCCCAA-CCTGCCCCATGCACTCCTCTAGGACACCTTTCCATACTTTTCACA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CCCCCATAGTGGCCTCGAACTCCTGGCACTACCAAAGGACACTTATCCACG-AGAGCGCA
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CTCTCCAGCCCATTTGTCATGGAGGTGCCATCTGGTTTCCTGGGTCAGG-TTTTGAGGCA
Oa_MECP2_v1(P)      CTCTCCAGCCCATTTGTCAGGGAGGTGCCATCTGGTTTGCTGGGTCAGG-TTTTGAGGCA
Oa_MECP2_v4(P)      CTCTCCAGCCCATTTGTCAGGGAGGTGCCATCTGGTTTGCTGGGTCAGG-TTTTGAGGCA
Oa_MECP2_v2(P)      CTCTCCAGCCCATTTGTCAGGGAGGTGCCATCTGGTTTGCTGGGTCAGG-TTTTGAGGCA
Oa_MECP2_v3(P)      CTCTCCAGCCCATTTGTCAGGGAGGTGCCATCTGGTTTGCTGGGTCAGG-TTTTGAGGCA
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Mm_MECP2_v1         ACACCTAGCCAGGTTGACACC---AAGTTGTTTATTGTGGTCTGCTTGGAATTTTACCTG
Mm_MECP2_v2         ACACCTAGCCAGGTTGACACC---AAGTTGTTTATTGTGGTCTGCTTGGAATTTTACCTG
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GCATCCGACCAGGTTGTCACTGAGAAGATGTTTATTTTGGTCAGTTGGG-TTTTTATGTA
Hs_MECP2_v2         ------------------------------------------------------------


Bt_MECP2_v1         TTAATTAAACCAAATCCATAAAACGTGGCTCCTGGAACCAGTCTCCAAAGCTGACCTCTC
Oa_MECP2_v1(P)      TTAATTACACCAAATCCATAAAATGTGGCTCCTGGGACCGGTCTCCAAAGCTGACCTCCC
Oa_MECP2_v4(P)      TTAATTACACCAAATCCATAAAATGTGGCTCCTGGGACCGGTCTCCAAAGCTGACCTCCC
Oa_MECP2_v2(P)      TTAATTACACCAAATCCATAAAATGTGGCTCCTGGGACCGGTCTCCAAAGCTGACCTCCC
Oa_MECP2_v3(P)      TTAATTACACCAAATCCATAAAATGTGGCTCCTGGGACCGGTCTCCAAAGCTGACCTCCC
Mm_MECP2_v1         TTAGGCTTACTTAG-------------TCCAATCAAAT-------------GGA-CTCCA
Mm_MECP2_v2         TTAGGCTTACTTAG-------------TCCAATCAAAT-------------GGA-CTCCA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TTATACTTAGTCAA---ATGTAATGTGGCTTCTGGAATCATTGTCCAGAGCTGC-TTCCC
Hs_MECP2_v2         ------------------------------------------------------------


Bt_MECP2_v1         CAGCAGCTTGGCACCATCTGGTCCTGGGCCAAGGAGAGCTGGGCCTGCCATGCCCCCCTT
Oa_MECP2_v1(P)      CAGCAGCTTGGCACCATCTGGTCCTGGGCCAAGGAGAGCTGGGCCTGTCATGCTCACCTC
Oa_MECP2_v4(P)      CAGCAGCTTGGCACCATCTGGTCCTGGGCCAAGGAGAGCTGGGCCTGTCATGCTCACCTC
Oa_MECP2_v2(P)      CAGCAGCTTGGCACCATCTGGTCCTGGGCCAAGGAGAGCTGGGCCTGTCATGCTCACCTC
Oa_MECP2_v3(P)      CAGCAGCTTGGCACCATCTGGTCCTGGGCCAAGGAGAGCTGGGCCTGTCATGCTCACCTC
Mm_MECP2_v1         AGTTGGGTATCCCTC-----ATCTTTGGAAGA---------------C------------
Mm_MECP2_v2         AGTTGGGTATCCCTC-----ATCTTTGGAAGA---------------C------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CGTCACCTGGGCGTCATCTGGTCCTGGTAAGAGGAGTGCGTGGCCCACCAGGCCCCCCTG
Hs_MECP2_v2         ------------------------------------------------------------


Bt_MECP2_v1         TGACCTGTAACAGTTGATTTTGGGGCTGACCGAT-GTGGTGGTCGAGAACACCGAATCTC
Oa_MECP2_v1(P)      TGACCTGTAACAGTTGATTTTGGAGCTGACCGATGGTGGTGGTCGAGAACACTGTATCTC
Oa_MECP2_v4(P)      TGACCTGTAACAGTTGATTTTGGAGCTGACCGATGGTGGTGGTCGAGAACAC--TATCTC
Oa_MECP2_v2(P)      TGACCTGTAACAGTTGATTTTGGAGCTGACCGATGGTGGTGGTCGAGAACAC--TATCTC
Oa_MECP2_v3(P)      TGACCTGTAACAGTTGATTTTGGAGCTGACCGATGGTGGTGGTCGAGAACAC--TATCTC
Mm_MECP2_v1         -----------------AACCTAGGCTGATTAGATATTTACTTTTGGGATTGCAGCACTTT
Mm_MECP2_v2         -----------------AACCTAGGCTGATTAGATATTTACTTTTGGGATTGCAGCACTTT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TCACCCATGACAGTTCATTCAGGGCCGATGGGGCAGTCGTGGTTGGGAACACAGCATTTC
Hs_MECP2_v2         ------------------------------------------------------------


Bt_MECP2_v1         AAGT-GGCGTTTCCTTTCTGCCCAGCCTGACCTGCAGGCCCCTTGCTCCGCAGCTCCCGC
Oa_MECP2_v1(P)      AAGT-GGTGTTTCCTTTCTGCCCAGCCTGACCTGCAGGCCCCTTGCTCCCCAGCTCCTGC
Oa_MECP2_v4(P)      AAGT-GGTGTTTCCTTTCTGCCCAGCCTGACCTGCAGGCCCCTTGCTCCCCAGCTCCTGC
Oa_MECP2_v2(P)      AAGT-GGTGTTTCCTTTCTGCCCAGCCTGACCTGCAGGCCCCTTGCTCCCCAGCTCCTGC
Oa_MECP2_v3(P)      AAGT-GGTGTTTCCTTTCTGCCCAGCCTGACCTGCAGGCCCCTTGCTCCCCAGCTCCTGC
Mm_MECP2_v1         GGGTGCCGTTTTTCTTTTACTTGGGTTTTATCTGCAGCTCCCTCACCACCACCACCACCC
Mm_MECP2_v2         GGGTGCCGTTTTTCTTTTACTTGGGTTTTATCTGCAGCTCCCTCACCACCACCACCACCC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         AAGC-GTCACTTTATTTCATTCGGGCCCCACCTGCAGCTCCCTCAAAGAGGCAGTTGC--
Hs_MECP2_v2         ------------------------------------------------------------


Bt_MECP2_v1         CCCTAGAGTTTCAAGGC-----------------------------TATAGGTGGCACCT
Oa_MECP2_v1(P)      CCCTAGAGTTTCAAGGC-----------------------------TGCAGGTGGCACCT
Oa_MECP2_v4(P)      CCCTAGAGTTTCAAGGC-----------------------------TGCAGGTGGCACCT
Oa_MECP2_v2(P)      CCCTAGAGTTTCAAGGC-----------------------------TGCAGGTGGCACCT
Oa_MECP2_v3(P)      CCCTAGAGTTTCAAGGC-----------------------------TGCAGGTGGCACCT
Mm_MECP2_v1         CCCACTTACCTGTATGTAGAACTGATTTCAAAACTGCAGGTGGTGGTAACTGCAGCTTCT
Mm_MECP2_v2         CCCACTTACCTGTATGTAGAACTGATTTCAAAACTGCAGGTGGTGGTAACTGCAGCTTCT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ----CCAGCCTCTTTCCCTTCCAGTTTATTCCAGAGCTGCCAGTGGGGCCTGAGGCTCCT
Hs_MECP2_v2         ------------------------------------------------------------


Bt_MECP2_v1         TAGGGTTTTCTCCC--------CCTTTGATCCACATTCCCTCTCCCCCAGATACAGGCAT
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Oa_MECP2_v1(P)      TAGGGTTTTCTCCC--------CCTTTCATCCACATCCCCTCTCCCCCAGATACAGGCAT
Oa_MECP2_v4(P)      TAGGGTTTTCTCCC--------CCTTTCATCCACATCCCCTCTCCCCCAGATACAGGCAT
Oa_MECP2_v2(P)      TAGGGTTTTCTCCC--------CCTTTCATCCACATCCCCTCTCCCCCAGATACAGGCAT
Oa_MECP2_v3(P)      TAGGGTTTTCTCCC--------CCTTTCATCCACATCCCCTCTCCCCCAGATACAGGCAT
Mm_MECP2_v1         TAGGGTTTTCTTCA--CTTCTTGCTTCTTTCCCCATTCCCTCATCCACAAATAAGGGCAT
Mm_MECP2_v2         TAGGGTTTTCTTCA--CTTCTTGCTTCTTTCCCCATTCCCTCATCCACAAATAAGGGCAT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TAGGGTTTTCTCTCTATTTCCCCCTTTCTTCCTCATTCCC-TCGTCTTTCCCAAAGGCAT
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TATGAGCGAGTCACCTTTGGGCAGGGG---------------------------------
Oa_MECP2_v1(P)      TACGAGCGAGTCACCTTTGGGCAGGGG---------------------------------
Oa_MECP2_v4(P)      TACGAGCGAGTCACCTTTGGGCAGGGG---------------------------------
Oa_MECP2_v2(P)      TACGAGCGAGTCACCTTTGGGCAGGGG---------------------------------
Oa_MECP2_v3(P)      TACGAGCGAGTCACCTTTGGGCAGGGG---------------------------------
Mm_MECP2_v1         CACAAGTCAGTCTCCTTTAAGCAGGCAGCTTTGGTGGGGTTTTTCCCCTGGAAGC-----
Mm_MECP2_v2         CACAAGTCAGTCTCCTTTAAGCAGGCAGCTTTGGTGGGGTTTTTCCCCTGGAAGC-----
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CACGAGTCAGTCGCCTTTCAGCAGGCAGCCTTGGCGGTTTATCGCCCTGGCAGGCAGGGG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CGCTGATGGTCCTGTACCACTT-TGTCCTGGAGACAGGTGGACAGAAGGTTGGAGGGCAG
Oa_MECP2_v1(P)      TGCTGAAGGTCCTGTACCACTTCTGTCCTGGAGACAGGTGGACAGAAGGTTGGAGGGCAG
Oa_MECP2_v4(P)      TGCTGAAGGTCCTGTACCACTTCTGTCCTGGAGACAGGTGGACAGAAGGTTGGAGGGCAG
Oa_MECP2_v2(P)      TGCTGAAGGTCCTGTACCACTTCTGTCCTGGAGACAGGTGGACAGAAGGTTGGAGGGCAG
Oa_MECP2_v3(P)      TGCTGAAGGTCCTGTACCACTTCTGTCCTGGAGACAGGTGGACAGAAGGTTGGAGGGCAG
Mm_MECP2_v1         CAGGGACCCTGTCAGGCTGCCTCTGCCTTGTGGTCAGGTTGACAGGAGGTTGGAGGGAAA
Mm_MECP2_v2         CAGGGACCCTGTCAGGCTGCCTCTGCCTTGTGGTCAGGTTGACAGGAGGTTGGAGGGAAA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CCCTGCAGCTCTCATGCTGCCCCTGCCTTGGGGTCAGGTTGACAGGAGGTTGGAGGGAAA
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         -GCCT--AGCCTTGGAATTCTCACCAGCTATGTCCGGCCCAGTTGGGGAGTATGATGTTG
Oa_MECP2_v1(P)      -GCCT--AGCCTTGGAATTCTCACCAGCTGTGTCCGGCCCAGTTGGGGAGTGTGACGTTG
Oa_MECP2_v4(P)      -GCCT--AGCCTTGGAATTCTCACCAGCTGTGTCCGGCCCAGTTGGGGAGTGTGACGTTG
Oa_MECP2_v2(P)      -GCCT--AGCCTTGGAATTCTCACCAGCTGTGTCCGGCCCAGTTGGGGAGTGTGACGTTG
Oa_MECP2_v3(P)      -GCCT--AGCCTTGGAATTCTCACCAGCTGTGTCCGGCCCAGTTGGGGAGTGTGACGTTG
Mm_MECP2_v1         AGCCTTAAGTCATGGGATTCTCACCAGCTGTGTCTGGCTCAGACCTGGAATGTGACCTTT
Mm_MECP2_v2         AGCCTTAAGTCATGGGATTCTCACCAGCTGTGTCTGGCTCAGACCTGGAATGTGACCTTT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         -GCCTTAAGCTGCAGGATTCTCACCAGCTGTGTCCGGCCCAGTTTTGGGGTGTGACCTCA
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ATTCTG------TGTGTACTTGAAGACCGCGAAGATTCAGGGGGCATCCCTTATAGACTG
Oa_MECP2_v1(P)      ATTCTG------TGTGTACTTGAACATTGCGAAGATTCAGGGGCCATCCCTTAGGGACTG
Oa_MECP2_v4(P)      ATTCTG------TGTGTACTTGAACATTGCGAAGATTCAGGGGCCATCCCTTAGGGACTG
Oa_MECP2_v2(P)      ATTCTG------TGTGTACTTGAACATTGCGAAGATTCAGGGGCCATCCCTTAGGGACTG
Oa_MECP2_v3(P)      ATTCTG------TGTGTACTTGAACATTGCGAAGATTCAGGGGCCATCCCTTAGGGACTG
Mm_MECP2_v1         ATTTTGTTGTATTTGAACATTGTAAAGTGT-----G---GGTGGTACCTTAAACTGAATA
Mm_MECP2_v2         ATTTTGTTGTATTTGAACATTGTAAAGTGT-----G---GGTGGTACCTTAAACTGAATA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ATTTCAATTTTGTCTGTACTTGAACATTATGAAGAT---GGGGGCCTCTTTCAGTGAATT
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TGTCCAGAAGGCAGGAATTGATAAGACAGCTTTCAGATACCCAAGGGACTAGGTCTGTCA
Oa_MECP2_v1(P)      TGTCCAGAAGGCAGGAATTGATAAGACAGCTTTCAGATACCCGAGGGGCTAGGTCCGTCA
Oa_MECP2_v4(P)      TGTCCAGAAGGCAGGAATTGATAAGACAGCTTTCAGATACCCGAGGGGCTAGGTCCGTCA
Oa_MECP2_v2(P)      TGTCCAGAAGGCAGGAATTGATAAGACAGCTTTCAGATACCCGAGGGGCTAGGTCCGTCA
Oa_MECP2_v3(P)      TGTCCAGAAGGCAGGAATTGATAAGACAGCTTTCAGATACCCGAGGGGCTAGGTCCGTCA
Mm_MECP2_v1         TGTGAAGAATCCAGAAACTGACCA-ACAGCTTTCA--GATACCTGGGGCTAGGTCACTAA
Mm_MECP2_v2         TGTGAAGAATCCAGAAACTGACCA-ACAGCTTTCA--GATACCTGGGGCTAGGTCACTAA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TGTGAAC---AGCAGAATTGACCG-ACAGCTTTCCAGTACCCATGGGGCTAGGTCATTAA
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Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CATTGGGTCTCCTTGCCC------------------------------------------
Oa_MECP2_v1(P)      CATTGGGTCTCCCCGCCC------------------------------------------
Oa_MECP2_v4(P)      CATTGGGTCTCCCCGCCC------------------------------------------
Oa_MECP2_v2(P)      CATTGGGTCTCCCCGCCC------------------------------------------
Oa_MECP2_v3(P)      CATTGGGTCTCCCCGCCC------------------------------------------
Mm_MECP2_v1         GGTCACATCCAGTCTTCC---CTACCCTGTTCTAGTTGTTAGCTACTACCTCTCCCAGAT
Mm_MECP2_v2         GGTCACATCCAGTCTTCC---CTACCCTGTTCTAGTTGTTAGCTACTACCTCTCCCAGAT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GGCCACATCCACAGTCTCCCCCACCCTTGTTCCAGTTGTTAGTTACTACCTCCTCTCCTG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------TGTGCCTGTCACT
Oa_MECP2_v1(P)      ------------------------------------------------CGTGCCTGTCACT
Oa_MECP2_v4(P)      ------------------------------------------------CGTGCCTGTCACT
Oa_MECP2_v2(P)      ------------------------------------------------CGTGCCTGTCACT
Oa_MECP2_v3(P)      ------------------------------------------------CGTGCCTGTCACT
Mm_MECP2_v1         AGATTGCTGTATATCCTCCAACTATGATCA-----TCCTGGCCCAAGCTTGCCTGTTCTT
Mm_MECP2_v2         AGATTGCTGTATATCCTCCAACTATGATCA-----TCCTGGCCCAAGCTTGCCTGTTCTT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ACAATACTGTATGTCGTCGAGCTCCCCCCAGGTCTACCCCTCCCGGCCCTGCCTGCTGGT
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TGGC-TGTCCTAACCCGTGTCGTTGCTGGCGTTGACACCACAGTGAGGCGTGGCCCCTGG
Oa_MECP2_v1(P)      TGGT-TGTCCTAACCTGTGTCGTTGCTGGCATTGACACCACAGTGAGGCGGGGCCCCTGG
Oa_MECP2_v4(P)      TGGT-TGTCCTAACCTGTGTCGTTGCTGGCATTGACACCACAGTGAGGCGGGGCCCCTGG
Oa_MECP2_v2(P)      TGGT-TGTCCTAACCTGTGTCGTTGCTGGCATTGACACCACAGTGAGGCGGGGCCCCTGG
Oa_MECP2_v3(P)      TGGT-TGTCCTAACCTGTGTCGTTGCTGGCATTGACACCACAGTGAGGCGGGGCCCCTGG
Mm_MECP2_v1         GAGTCTGTCTTAACCAGTGGAACTGCTGCCC-TTGGTGTGCAGTGAGTTGAGGACTCTTG
Mm_MECP2_v2         GAGTCTGTCTTAACCAGTGGAACTGCTGCCC-TTGGTGTGCAGTGAGTTGAGGACTCTTG
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GGGCTTGTCATAGCCAGTGGGATTGCCGGTCTTGACAGCTCAGTGAGCTGGAGATACTTG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GCCACAGCAAGGTCC----AGTACATGTCCCTTCTGC----ACCGTAGT-CCCTATCGAA
Oa_MECP2_v1(P)      GCCACAGCAAGGTCC----AGTACACGTCCCTTCTGC----ACCGTAGT-CCTTATCAAA
Oa_MECP2_v4(P)      GCCACAGCAAGGTCC----AGTACACGTCCCTTCTGC----ACCGTAGT-CCTTATCAAA
Oa_MECP2_v2(P)      GCCACAGCAAGGTCC----AGTACACGTCCCTTCTGC----ACCGTAGT-CCTTATCAAA
Oa_MECP2_v3(P)      GCCACAGCAAGGTCC----AGTACACGTCCCTTCTGC----ACCGTAGT-CCTTATCAAA
Mm_MECP2_v1         GTCACAGCCAGGCTCTAGTAGTACAGCTCCTTTCTGCTGGTGCTGTATTTCCATATCAAA
Mm_MECP2_v2         GTCACAGCCAGGCTCTAGTAGTACAGCTCCTTTCTGCTGGTGCTGTATTTCCATATCAAA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GTCACAGCCAGGC---GCTAGCACAGCTCCCTTCTGTTGATGCTGTATTCCCATATCAAA
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         AGGCACAGGAGACCCCCAGAAATGCCCTGCTCCC---CCCCACCACTCCCCTCAGCTCCC
Oa_MECP2_v1(P)      AGGCACAGGAGACCCCCAGAAATGCCCTG---CC---TCCCCCCACTCCCCTCAGCTCCC
Oa_MECP2_v4(P)      AGGCACAGGAGACCCCCAGAAATGCCCTG---CC---TCCCCCCACTCCCCTCAGCTCCC
Oa_MECP2_v2(P)      AGGCACAGGAGACCCCCAGAAATGCCCTG---CC---TCCCCCCACTCCCCTCAGCTCCC
Oa_MECP2_v3(P)      AGGCACAGGAGACCCCCAGAAATGCCCTG---CC---TCCCCCCACTCCCCTCAGCTCCC
Mm_MECP2_v1         AGGCACAGGGGAGATCTAGAAATGCCATCTCCCCCAGTCCATCAGTGCCAAACAAGCCCA
Mm_MECP2_v2         AGGCACAGGGGAGATCTAGAAATGCCATCTCCCCCAGTCCATCAGTGCCAAACAAGCCCA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         AGACACAGGGGACACCCAGAAACGCCACATCCCCCAATCCATCAGTGCCAAACTAGCCAA
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TGGACAGTGGAAGCCACAGTGGTGGCCTGGGCATGCCGGCCACAGCCAGCACCTGACTTC
Oa_MECP2_v1(P)      TGGACGGTGGAAGCCACAGCGGTGTCCTGGGCATGCTGG--TCAGTCAGCACCTGAC--C
Oa_MECP2_v4(P)      TGGACGGTGGAAGCCACAGCGGTGTCCTGGGCATGCTGG--TCAGTCAGCACCTGAC--C
Oa_MECP2_v2(P)      TGGACGGTGGAAGCCACAGCGGTGTCCTGGGCATGCTGG--TCAGTCAGCACCTGAC--C
Oa_MECP2_v3(P)      TGGACGGTGGAAGCCACAGCGGTGTCCTGGGCATGCTGG--TCAGTCAGCACCTGAC--C
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Mm_MECP2_v1         TGATCCCAGCATGGGTACAGACAACTCTGTTC----------------------------
Mm_MECP2_v2         TGATCCCAGCATGGGTACAGACAACTCTGTTC----------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CGGCCCCAGCTTCTCAGCTCGCTGGATGGCGGAAGCTGC--------------------T
Hs_MECP2_v2         ------------------------------------------------------------


Bt_MECP2_v1         TCTCCTGAGCCCCCATGCCATTGCTAGCAGCAGTCTGCTCAGTGGTGGTATGCCAGCCTA
Oa_MECP2_v1(P)      TCTCCTGAGCCCCCATGCCGGTGCTAGCAGCAGTCTGCTCAGTGGTGGCATGCCAGCCTA
Oa_MECP2_v4(P)      TCTCCTGAGCCCCCATGCCGGTGCTAGCAGCAGTCTGCTCAGTGGTGGCATGCCAGCCTA
Oa_MECP2_v2(P)      TCTCCTGAGCCCCCATGCCGGTGCTAGCAGCAGTCTGCTCAGTGGTGGCATGCCAGCCTA
Oa_MECP2_v3(P)      TCTCCTGAGCCCCCATGCCGGTGCTAGCAGCAGTCTGCTCAGTGGTGGCATGCCAGCCTA
Mm_MECP2_v1         ----------------------------------------AGTGCTATCACAACAGACTA
Mm_MECP2_v2         ----------------------------------------AGTGCTATCACAACAGACTA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ACTCGTGAGCGCCAGTGCGGGTGCAGACAATCTTCTGTTGGGTGGCATCATTCCAGGCCC
Hs_MECP2_v2         ------------------------------------------------------------


Bt_MECP2_v1         GAGGCCACGAGCAGTGGCGGTGGGACATGAAACAGCACCAGGTTGTCACCTGCCTCCCT-
Oa_MECP2_v1(P)      GAGGCCATGAGCAGTGGCAGTGGGACATGGAACAGCACCAGGTTGTCACCTGCCTCCCT-
Oa_MECP2_v4(P)      GAGGCCATGAGCAGTGGCAGTGGGACATGGAACAGCACCAGGTTGTCACCTGCCTCCCT-
Oa_MECP2_v2(P)      GAGGCCATGAGCAGTGGCAGTGGGACATGGAACAGCACCAGGTTGTCACCTGCCTCCCT-
Oa_MECP2_v3(P)      GAGGCCATGAGCAGTGGCAGTGGGACATGGAACAGCACCAGGTTGTCACCTGCCTCCCT-
Mm_MECP2_v1         GAGGCCATGAACATTGGACGTGGGAACCAGAGCAACCCG-----AATTGCTGCTGCTTTA
Mm_MECP2_v2         GAGGCCATGAACATTGGACGTGGGAACCAGAGCAACCCG-----AATTGCTGCTGCTTTA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         G-AAGCATGAACAGTGCACCTGGGACAGGGAGCAGCCCCAAATTGTCACCTGCTTCTCTG
Hs_MECP2_v2         ------------------------------------------------------------


Bt_MECP2_v1         ----GCCTGTCATTGCCGTGACGGCCATCATGAAGGAGGGTACTT-AATAGCCACAAGCA
Oa_MECP2_v1(P)      ----GCTTGTCATTGCCGTGACAGCCATCATGAAGGAGGATACTTAAATAGCCACAAGCA
Oa_MECP2_v4(P)      ----GCTTGTCATTGCCGTGACAGCCATCATGAAGGAGGATACTTAAATAGCCACAAGCA
Oa_MECP2_v2(P)      ----GCTTGTCATTGCCGTGACAGCCATCATGAAGGAGGATACTTAAATAGCCACAAGCA
Oa_MECP2_v3(P)      ----GCTTGTCATTGCCGTGACAGCCATCATGAAGGAGGATACTTAAATAGCCACAAGCA
Mm_MECP2_v1         TTCAGCTTTCCGTTGCTCTGACAATGAT---AAAACAAGGC-----AGTAACTTAAAACA
Mm_MECP2_v2         TTCAGCTTTCCGTTGCTCTGACAATGAT---AAAACAAGGC-----AGTAACTTAAAACA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CCCAGCTTTTCATTGCTGTGACAGTGATGGCGAAAGAGGGT-----AATAACCAGACACA
Hs_MECP2_v2         ------------------------------------------------------------


Bt_MECP2_v1         CGCTGCTATCTTTGGTGG-AAGAGCAGTTTCCTTAGCTGACAGGACCTCTGGATTTGAAG
Oa_MECP2_v1(P)      CGCTGCCATCTTTGGTGG-GAGAGCAGTTTCCTTAGCTGACAGGACCTCTGGATTTGAAG
Oa_MECP2_v4(P)      CGCTGCCATCTTTGGTGG-GAGAGCAGTTTCCTTAGCTGACAGGACCTCTGGATTTGAAG
Oa_MECP2_v2(P)      CGCTGCCATCTTTGGTGG-GAGAGCAGTTTCCTTAGCTGACAGGACCTCTGGATTTGAAG
Oa_MECP2_v3(P)      CGCTGCCATCTTTGGTGG-GAGAGCAGTTTCCTTAGCTGACAGGACCTCTGGATTTGAAG
Mm_MECP2_v1         GACTGCCAGGTTTGGCAGAGAAAGGAAATTCCTTAGCTGACAGCACCTCTGGATTTTAAA
Mm_MECP2_v2         GACTGCCAGGTTTGGCAGAGAAAGGAAATTCCTTAGCTGACAGCACCTCTGGATTTTAAA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         AACTGCCAAGTTGGGTGGAGAAAGGAGTTTCTTTAGCTGACAGAATCTCTGAATTTTAAA
Hs_MECP2_v2         ------------------------------------------------------------


Bt_MECP2_v1         TAACTTCTAACAAGCGGCGTGAGCCCAGGAGGGAACAGAGGGTGTAA-AGGGAAGCCACC
Oa_MECP2_v1(P)      TAACTTCTAACAAGCAGCGTGAGCCCAGGAGGGGACAGAGGGTGTAA-AGGGAAGCCACC
Oa_MECP2_v4(P)      TAACTTCTAACAAGCAGCGTGAGCCCAGGAGGGGACAGAGGGTGTAA-AGGGAAGCCACC
Oa_MECP2_v2(P)      TAACTTCTAACAAGCAGCGTGAGCCCAGGAGGGGACAGAGGGTGTAA-AGGGAAGCCACC
Oa_MECP2_v3(P)      TAACTTCTAACAAGCAGCGTGAGCCCAGGAGGGGACAGAGGGTGTAA-AGGGAAGCCACC
Mm_MECP2_v1         TAGGTTGTAATAAGTGGCTCAAACCCATCCAGGAAAAAGCAAAAGGG-TTAGAACTGACC
Mm_MECP2_v2         TAGGTTGTAATAAGTGGCTCAAACCCATCCAGGAAAAAGCAAAAGGG-TTAGAACTGACC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TCACTTAGTAAGCGGC--TCAAGCCCAGGAGGGAGCAGAGGGATACGAGCGGAGTCCCCT
Hs_MECP2_v2         ------------------------------------------------------------


Bt_MECP2_v1         AGGTATGGCAGCCTGGATCTC-----------GTGGAGCCTGGCAGT-TGAGCTCTGTGC
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Oa_MECP2_v1(P)      AGGTATGGTAGCCTGGATCTC-----------GTGGAGCCTGGCAGT-TGAGCTCTGTGC
Oa_MECP2_v4(P)      AGGTATGGTAGCCTGGATCTC-----------GTGGAGCCTGGCAGT-TGAGCTCTGTGC
Oa_MECP2_v2(P)      AGGTATGGTAGCCTGGATCTC-----------GTGGAGCCTGGCAGT-TGAGCTCTGTGC
Oa_MECP2_v3(P)      AGGTATGGTAGCCTGGATCTC-----------GTGGAGCCTGGCAGT-TGAGCTCTGTGC
Mm_MECP2_v1         AGATGAGACCAGCCTGATTTCATGCAGCCCAAATGGAGTCCAGCTGTCTGAACTCTGCAG
Mm_MECP2_v2         AGATGAGACCAGCCTGATTTCATGCAGCCCAAATGGAGTCCAGCTGTCTGAACTCTGCAG
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GCGCGGGACCATCTGGAATTGGTTTAGCCCAAGTGGAGCCTGACAGCCAGAACTCTGTGT
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CTC------------------CTCTCCAGAGTGTTCCTACCAGGCCCAACAAGG------
Oa_MECP2_v1(P)      CCC------------------CTCTCCAGAGTGTTCCTACCAGGCCTGACAAGG------
Oa_MECP2_v4(P)      CCC------------------CTCTCCAGAGTGTTCCTACCAGGCCTGACAAGG------
Oa_MECP2_v2(P)      CCC------------------CTCTCCAGAGTGTTCCTACCAGGCCTGACAAGG------
Oa_MECP2_v3(P)      CCC------------------CTCTCCAGAGTGTTCCTACCAGGCCTGACAAGG------
Mm_MECP2_v1         CACTTCTCTACTACAG-----TCTCCTAGAGCATTCCAGCCAGGCTCTTCAGGC------
Mm_MECP2_v2         CACTTCTCTACTACAG-----TCTCCTAGAGCATTCCAGCCAGGCTCTTCAGGC------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CCCCCGTCTAACCACAGCTCCTTTTCCAGAGCATTCCAGTCAGGCTCTCTGGGCTGACTG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         --CCAGGGGAGGTCACAGGCATCAGCCCTAGCTCAGCGCAGCCATTTCTAGCGGGTTCAT
Oa_MECP2_v1(P)      --CCAGGGGAGGTCACAGGCATCAGCCCTAGCTCAGCACAGCCATCTCTAGCAGGGTCAT
Oa_MECP2_v4(P)      --CCAGGGGAGGTCACAGGCATCAGCCCTAGCTCAGCACAGCCATCTCTAGCAGGGTCAT
Oa_MECP2_v2(P)      --CCAGGGGAGGTCACAGGCATCAGCCCTAGCTCAGCACAGCCATCTCTAGCAGGGTCAT
Oa_MECP2_v3(P)      --CCAGGGGAGGTCACAGGCATCAGCCCTAGCTCAGCACAGCCATCTCTAGCAGGGTCAT
Mm_MECP2_v1         --TGAGGAGACATCACAGGTGCC---------------------------------------
Mm_MECP2_v2         --TGAGGAGACATCACAGGTGCC---------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GGCCAGGGGAGGTTACAGGTACC---------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GGCCCCAAATTGTTTTTCTGATGTGAGTTGCCTATGTGGGTGGCCCAGACCATCCAGACC
Oa_MECP2_v1(P)      GGCCTCAAATTGTTTTTCTGATGTGAGTTGCCCGCGTGGGTGGCCCAGACCATCCAGACC
Oa_MECP2_v4(P)      GGCCTCAAATTGTTTTTCTGATGTGAGTTGCCCGCGTGGGTGGCCCAGACCATCCAGACC
Oa_MECP2_v2(P)      GGCCTCAAATTGTTTTTCTGATGTGAGTTGCCCGCGTGGGTGGCCCAGACCATCCAGACC
Oa_MECP2_v3(P)      GGCCTCAAATTGTTTTTCTGATGTGAGTTGCCCGCGTGGGTGGCCCAGACCATCCAGACC
Mm_MECP2_v1         ------------------------------------------------------------
Mm_MECP2_v2         ------------------------------------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TCGGGGAAGTGAGTTCTCTCTAGAGCCCTGTGGGCATCAGCCTACTGACCCCCTGAGTAC
Oa_MECP2_v1(P)      TTGGGGAAGTGAGTTCTCTCTAGAGCCCTGTGGGCATCAGCCTACTGACCCCCTGAGTAC
Oa_MECP2_v4(P)      TTGGGGAAGTGAGTTCTCTCTAGAGCCCTGTGGGCATCAGCCTACTGACCCCCTGAGTAC
Oa_MECP2_v2(P)      TTGGGGAAGTGAGTTCTCTCTAGAGCCCTGTGGGCATCAGCCTACTGACCCCCTGAGTAC
Oa_MECP2_v3(P)      TTGGGGAAGTGAGTTCTCTCTAGAGCCCTGTGGGCATCAGCCTACTGACCCCCTGAGTAC
Mm_MECP2_v1         -----------AGTTCTTCAAGAAGACTTTTGTGCATCAGT--TCATAGCCTATATCTTT
Mm_MECP2_v2         -----------AGTTCTTCAAGAAGACTTTTGTGCATCAGT--TCATAGCCTATATCTTT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         -----------AGTTCTTTAAGAAGATCTTTGGGCATATACATTTTTAGCCTGTGTCATT
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TGGCCAGTGCCTGGGGAGGGCT-AGGGGCACAGGCATGTTGCCAGGCTCGTAGTGGAATC
Oa_MECP2_v1(P)      TGGCCAGTGCCTGGGGAGGGCT-AGGGGCACAGGCGTGTTGCCAGGCTCGTAGTGGATTC
Oa_MECP2_v4(P)      TGGCCAGTGCCTGGGGAGGGCT-AGGGGCACAGGCGTGTTGCCAGGCTCGTAGTGGATTC
Oa_MECP2_v2(P)      TGGCCAGTGCCTGGGGAGGGCT-AGGGGCACAGGCGTGTTGCCAGGCTCGTAGTGGATTC
Oa_MECP2_v3(P)      TGGCCAGTGCCTGGGGAGGGCT-AGGGGCACAGGCGTGTTGCCAGGCTCGTAGTGGATTC
Mm_MECP2_v1         GCCCAAGATTGTAGA----TTC-AGGTTAACACTACAGATTCTAGGGCAGATGACTGAGA
Mm_MECP2_v2         GCCCAAGATTGTAGA----TTC-AGGTTAACACTACAGATTCTAGGGCAGATGACTGAGA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GCCCCAAATGGATTCCTGTTTCAAGTTCACACCTGCAGATTCTAGGACCTGTGTCCTAGA
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Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CCCGCT------------------------------------------------------
Oa_MECP2_v1(P)      CCCAAT------------------------------------------------------
Oa_MECP2_v4(P)      CCCAAT------------------------------------------------------
Oa_MECP2_v2(P)      CCCAAT------------------------------------------------------
Oa_MECP2_v3(P)      CCCAAT------------------------------------------------------
Mm_MECP2_v1         CTCAGAAAAAAAGCCCCTGTGGACTGTGGTATAGCGAAGTACAAAAACTGAAGGGGGCTA
Mm_MECP2_v2         CTCAGAAAAAAAGCCCCTGTGGACTGTGGTATAGCGAAGTACAAAAACTGAAGGGGGCTA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CTTCAG------------GGAGTCAGCTGTTTCTAGAGTTCCTACCATGGAGTGGGTCTG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ----------------------------CTCGAGCCCGACAGCCCCGCCACGTGTT----
Oa_MECP2_v1(P)      ----------------------------CTCGAG-CCGACAGCCCCGCCACGTTGTGTTC
Oa_MECP2_v4(P)      ----------------------------CTCGAG-CCGACAGCCCCGCCACGTTGTGTTC
Oa_MECP2_v2(P)      ----------------------------CTCGAG-CCGACAGCCCCGCCACGTTGTGTTC
Oa_MECP2_v3(P)      ----------------------------CTCGAG-CCGACAGCCCCGCCACGTTGTGTTC
Mm_MECP2_v1         GGGCAGATGCCGCATGCCTCATGCCAGAGCCAAGCCCTCTGCTCCATCCACATCCTTTTC
Mm_MECP2_v2         GGGCAGATGCCGCATGCCTCATGCCAGAGCCAAGCCCTCTGCTCCATCCACATCCTTTTC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GAGGACCTGCCCG-------GTGGGG--GGGCAGAGCCCTGCTCCCTC------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CCGGCTCTCAGT--TGCTCTCTGCAAGGGCCCTATCTCAGCGCTCTGCTCTACTGGAGGA
Oa_MECP2_v1(P)      CGGGCTCTCAGT--TGCTCCCTGCAAGGGCCCCATCTCAGCGCTCTGCTCTACTGGAGGG
Oa_MECP2_v4(P)      CGGGCTCTCAGT--TGCTCCCTGCAAGGGCCCCATCTCAGCGCTCTGCTCTACTGGAGGG
Oa_MECP2_v2(P)      CGGGCTCTCAGT--TGCTCCCTGCAAGGGCCCCATCTCAGCGCTCTGCTCTACTGGAGGG
Oa_MECP2_v3(P)      CGGGCTCTCAGT--TGCTCCCTGCAAGGGCCCCATCTCAGCGCTCTGCTCTACTGGAGGG
Mm_MECP2_v1         TGGCTCCTTCTTCCTGCTCTCTGCTTCAGTGAACCAGCCCCACTCTG----AAGAGATTT
Mm_MECP2_v2         TGGCTCCTTCTTCCTGCTCTCTGCTTCAGTGAACCAGCCCCACTCTG----AAGAGATTT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ----C--------------GGGTCTTCCTACTCTTCTCTCTGCTCTG----ACGGGATTT
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GTTTGTTGAG--TGTTTTTGCTTCTTTCTCTTTTTGAATCTGTATCAATCTTTAGAAAA-
Oa_MECP2_v1(P)      GTTTGTTGAGTCTGTTTTTGCTTCTTTCTCTTTTTGAAACTGTATCAATCTTTAGAAAA-
Oa_MECP2_v4(P)      GTTTGTTGAGTCTGTTTTTGCTTCTTTCTCTTTTTGAAACTGTATCAATCTTTAGAAAA-
Oa_MECP2_v2(P)      GTTTGTTGAGTCTGTTTTTGCTTCTTTCTCTTTTTGAAACTGTATCAATCTTTAGAAAA-
Oa_MECP2_v3(P)      GTTTGTTGAGTCTGTTTTTGCTTCTTTCTCTTTTTGAAACTGTATCAATCTTTAGAAAA-
Mm_MECP2_v1         GTTGATTCTCTCCATTTTTATGTCTTTCTCTTTTAGG--------TACTATATAGAAAAG
Mm_MECP2_v2         GTTGATTCTCTCCATTTTTATGTCTTTCTCTTTTAGG--------TACTATATAGAAAAG
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GTTGATTCTCTCCATTTTGGTGTCTTTCTCTTTTAGATATTGTATCAATCTTTAGAAAAG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         -CATAGCGGAATTATCAGAGCTCACTAGGATACTGCCTCACCCAGGGTCTAAAAGTTCCA
Oa_MECP2_v1(P)      -CATAGCTGAATTGTTAGAGCTCGCTAGGATACTGCCTCACCCAGGGTCT-AAAGTTCCA
Oa_MECP2_v4(P)      -CATAGCTGAATTGTTAGAGCTCGCTAGGATACTGCCTCACCCAGGGTCT-AAAGTTCCA
Oa_MECP2_v2(P)      -CATAGCTGAATTGTTAGAGCTCGCTAGGATACTGCCTCACCCAGGGTCT-AAAGTTCCA
Oa_MECP2_v3(P)      -CATAGCTGAATTGTTAGAGCTCGCTAGGATACTGCCTCACCCAGGGTCT-AAAGTTCCA
Mm_MECP2_v1         GCTTAGTCTAATTGTTATAAATTGCTAGAATACTGCCTCCCCCAGGGTCT-AAAAATATA
Mm_MECP2_v2         GCTTAGTCTAATTGTTATAAATTGCTAGAATACTGCCTCCCCCAGGGTCT-AAAAATATA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GCATAGTCTACTTGTTATAAATCGTTAGGATACTGCCTCCCCCAGGGTCT-AAAATTACA
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TGTTCAAGGGGAAAAAAAGGGAACACTGAAGCCCCTTGTCAACATTGCAGAAGGAAGACC
Oa_MECP2_v1(P)      TGTTCAAGGGG--AAAAAGGGAACACTGAAGCCCCTTGTCAACATTGCAGAAGAAAGACC
Oa_MECP2_v4(P)      TGTTCAAGGGG--AAAAAGGGAACACTGAAGCCCCTTGTCAACATTGCAGAAGAAAGACC
Oa_MECP2_v2(P)      TGTTCAAGGGG--AAAAAGGGAACACTGAAGCCCCTTGTCAACATTGCAGAAGAAAGACC
Oa_MECP2_v3(P)      TGTTCAAGGGG--AAAAAGGGAACACTGAAGCCCCTTGTCAACATTGCAGAAGAAAGACC
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Mm_MECP2_v1         TGCTAAAGGGG--AAAACTTGAACACTGAAACCAGTTCTGAACAATTTAGAAGGAAAACC
Mm_MECP2_v2         TGCTAAAGGGG--AAAACTTGAACACTGAAACCAGTTCTGAACAATTTAGAAGGAAAACC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TATTAGAGGGG--AAAAGCTGAACACTGAAGTCAGTTCTCAACAATTTAGAAGGAAAACC
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TAGGAAACCTTGAGCAAGAAACTACATCCTGAT-TTTCTGAGTGAATAAGAGCAAGCTTT
Oa_MECP2_v1(P)      TAGGAAACCTTGAGCAAGAAACTATATCCTGATGTTTCTGGGTGAATAAGAGCAAGCTTT
Oa_MECP2_v4(P)      TAGGAAACCTTGAGCAAGAAACTATATCCTGATGTTTCTGGGTGAATAAGAGCAAGCTTT
Oa_MECP2_v2(P)      TAGGAAACCTTGAGCAAGAAACTATATCCTGATGTTTCTGGGTGAATAAGAGCAAGCTTT
Oa_MECP2_v3(P)      TAGGAAACCTTGAGCAAGAAACTATATCCTGATGTTTCTGGGTGAATAAGAGCAAGCTTT
Mm_MECP2_v1         TTGAAAACATTTAACAAAAAATTATATTTTAATGTTTATGAATAAGAGG----AGGCTTT
Mm_MECP2_v2         TTGAAAACATTTAACAAAAAATTATATTTTAATGTTTATGAATAAGAGG----AGGCTTT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TAGAAAACATTTGGCAGAAAATTACATTTCGATGTTTTTGAATGAATACGAGCAAGCTTT
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TGCCCAAAAAAGGCTGATCTAAGAGGACTTGGAGCCTGGCCTGC--TGTGTGGCCAGTGC
Oa_MECP2_v1(P)      TG-CCAAAAAAGGCTGATCTAAGAGGACTTGCAACCTGGCCTGC--TGTGTGGCCAGCAT
Oa_MECP2_v4(P)      TG-CCAAAAAAGGCTGATCTAAGAGGACTTGCAACCTGGCCTGC--TGTGTGGCCAGCAT
Oa_MECP2_v2(P)      TG-CCAAAAAAGGCTGATCTAAGAGGACTTGCAACCTGGCCTGC--TGTGTGGCCAGCAT
Oa_MECP2_v3(P)      TG-CCAAAAAAGGCTGATCTAAGAGGACTTGCAACCTGGCCTGC--TGTGTGGCCAGCAT
Mm_MECP2_v1         TG---AAAAAATGTTGATCTATAAATACTTACTTTAGGC-CTGAGGTGTCTAATGAGTGA
Mm_MECP2_v2         TG---AAAAAATGTTGATCTATAAATACTTACTTTAGGC-CTGAGGTGTCTAATGAGTGA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TA---CAACAGTGCTGATCTAAAAATACTTAGCACTTGGCCTGAGATGCCTGGTGAGCAT
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TGCAGGTGAAGGGGAATCCAGCCTGAAA-CTGCTGGGTCTGCGCCTTGGAGCCCTTGGGT
Oa_MECP2_v1(P)      TGCAGGTGAAGGGGAATCCAGCCTGAAA-CTGCTGGGTCTGCGCCTTGGGGCCCTTGGGT
Oa_MECP2_v4(P)      TGCAGGTGAAGGGGAATCCAGCCTGAAA-CTGCTGGGTCTGCGCCTTGGGGCCCTTGGGT
Oa_MECP2_v2(P)      TGCAGGTGAAGGGGAATCCAGCCTGAAA-CTGCTGGGTCTGCGCCTTGGGGCCCTTGGGT
Oa_MECP2_v3(P)      TGCAGGTGAAGGGGAATCCAGCCTGAAA-CTGCTGGGTCTGCGCCTTGGGGCCCTTGGGT
Mm_MECP2_v1         ACTGAGCAATGGGAACTCAAGGCTGAAGCCTCCTGCATCAGAGGAGGTAGAACCAGGAGC
Mm_MECP2_v2         ACTGAGCAATGGGAACTCAAGGCTGAAGCCTCCTGCATCAGAGGAGGTAGAACCAGGAGC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TACAGGCAAGGGGAATCT------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CACTGGAGAGTCTATCTCTCTGTCTCTTTCTCTGGCTCTC---AGGTAGCGGTCCC----
Oa_MECP2_v1(P)      CACTGGAGAGTCTATCTCTCTGTCTCTTCCTCTGTCTCTC---CGGTAGCGGTCCC----
Oa_MECP2_v4(P)      CACTGGAGAGTCTATCTCTCTGTCTCTTCCTCTGTCTCTC---CGGTAGCGGTCCC----
Oa_MECP2_v2(P)      CACTGGAGAGTCTATCTCTCTGTCTCTTCCTCTGTCTCTC---CGGTAGCGGTCCC----
Oa_MECP2_v3(P)      CACTGGAGAGTCTATCTCTCTGTCTCTTCCTCTGTCTCTC---CGGTAGCGGTCCC----
Mm_MECP2_v1         CTCTTGAGATTTGAGGTGTTTTAGCATTGGAAAGCCACTCTTTGGGTAGCTGGCCC-CAG
Mm_MECP2_v2         CTCTTGAGATTTGAGGTGTTTTAGCATTGGAAAGCCACTCTTTGGGTAGCTGGCCC-CAG
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ----GGAG-------------------------------------GTAGCCGACCTGAGG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------TGCAGGGAGACCT---GCCTGTCTC
Oa_MECP2_v1(P)      ------------------------------------TGCAGGGAGACCT---GCCTGTTGC
Oa_MECP2_v4(P)      ------------------------------------TGCAGGGAGACCT---GCCTGTTGC
Oa_MECP2_v2(P)      ------------------------------------TGCAGGGAGACCT---GCCTGTTGC
Oa_MECP2_v3(P)      ------------------------------------TGCAGGGAGACCT---GCCTGTTGC
Mm_MECP2_v1         AAACTACTTCTGACCTTGTCATTTGGAAT------GGAGGTTAGTGGTCTGCCAGATGCC
Mm_MECP2_v2         AAACTACTTCTGACCTTGTCATTTGGAAT------GGAGGTTAGTGGTCTGCCAGATGCC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ACATGGCTTCTGAACCTGTCTTTTGGGAGTGGTATGGAAGGTGGAGCGTTCACCAGTGAC
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GAAGCTACAGGAGCCCAGCTC-CGGATGGGAAAGGGGGGCGCTCAGCAGAGAATTGTGAA
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Oa_MECP2_v1(P)      GAAGCTACAGGAGCCCAGCTC-CGGGTGGGAAAGGTGGGCGCTCAGCAGGAAATTGTAAA
Oa_MECP2_v4(P)      GAAGCTACAGGAGCCCAGCTC-CGGGTGGGAAAGGTGGGCGCTCAGCAGGAAATTGTAAA
Oa_MECP2_v2(P)      GAAGCTACAGGAGCCCAGCTC-CGGGTGGGAAAGGTGGGCGCTCAGCAGGAAATTGTAAA
Oa_MECP2_v3(P)      GAAGCTACAGGAGCCCAGCTC-CGGGTGGGAAAGGTGGGCGCTCAGCAGGAAATTGTAAA
Mm_MECP2_v1         AAAGCTGCATGAGACCAGCTCTTGGTTTATCAATTTGAACACTCAGTAACCTA----GAA
Mm_MECP2_v2         AAAGCTGCATGAGACCAGCTCTTGGTTTATCAATTTGAACACTCAGTAACCTA----GAA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CTGGAAGGCCCAGCACCACC------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GGCACGCAACCTCCTCACTACCTGACTTCACCTGTTCTTCCTCCTCTGTCATCTCCAGCG
Oa_MECP2_v1(P)      GGCACGCAACCTCCTCGCTACCTGACTTCACCTGTTCCTTCTCCTCTGTCATCTCCAGTG
Oa_MECP2_v4(P)      GGCACGCAACCTCCTCGCTACCTGACTTCACCTGTTCCTTCTCCTCTGTCATCTCCAGTG
Oa_MECP2_v2(P)      GGCACGCAACCTCCTCGCTACCTGACTTCACCTGTTCCTTCTCCTCTGTCATCTCCAGTG
Oa_MECP2_v3(P)      GGCACGCAACCTCCTCGCTACCTGACTTCACCTGTTCCTTCTCCTCTGTCATCTCCAGTG
Mm_MECP2_v1         GGCCCAGCACAAAGTGTCTG-------------------------CTCTCTTCTTAACTG
Mm_MECP2_v2         GGCCCAGCACAAAGTGTCTG-------------------------CTCTCTTCTTAACTG
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         -------CTCCTTCCCACTC-------------------------TTCTCATCTTGACAG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         AGCCTACCCCAAATGCCGAGGTGTCAGGAAGAATTGGTTCGAATTAGGGCC------CAG
Oa_MECP2_v1(P)      AGCCTGCCCCAATTGCCGAGGTGTCAGGAAGAATTAGTTCGAATTAGGGCC------CAG
Oa_MECP2_v4(P)      AGCCTGCCCCAATTGCCGAGGTGTCAGGAAGAATTAGTTCGAATTAGGGCC------CAG
Oa_MECP2_v2(P)      AGCCTGCCCCAATTGCCGAGGTGTCAGGAAGAATTAGTTCGAATTAGGGCC------CAG
Oa_MECP2_v3(P)      AGCCTGCCCCAATTGCCGAGGTGTCAGGAAGAATTAGTTCGAATTAGGGCC------CAG
Mm_MECP2_v1         AGCCTGCCCCAGC-ACTACTGCA----------------CAAATTAGGGAGGGTCTACTT
Mm_MECP2_v2         AGCCTGCCCCAGC-ACTACTGCA----------------CAAATTAGGGAGGGTCTACTT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         AGCCTGCCCCAGC-GCTGACGTGTCAGGAAAACACCCAGGGAACTAGGAAGGCACTTCTG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GCCACTAAGCAGGAGAAAGTGA-----------------------------------------
Oa_MECP2_v1(P)      GCCACTAAGCAGGAGAAGGTGA-----------------------------------------
Oa_MECP2_v4(P)      GCCACTAAGCAGGAGAAGGTGA-----------------------------------------
Oa_MECP2_v2(P)      GCCACTAAGCAGGAGAAGGTGA-----------------------------------------
Oa_MECP2_v3(P)      GCCACTAAGCAGGAGAAGGTGA-----------------------------------------
Mm_MECP2_v1         CCTACAGAGCATCCCTCCCTGGGCCCCCTCCCATCCTTTGTACTCTACCTACCTGACCTT
Mm_MECP2_v2         CCTACAGAGCATCCCTCCCTGGGCCCCCTCCCATCCTTTGTACTCTACCTACCTGACCTT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CCTGAGGGGCAGCCTGCCTTGC-CCACTCCTGCTCTGCTCGCCTCGGATCAGCTG-----
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------------------------------------------------------
Oa_MECP2_v1(P)      ------------------------------------------------------------
Oa_MECP2_v4(P)      ------------------------------------------------------------
Oa_MECP2_v2(P)      ------------------------------------------------------------
Oa_MECP2_v3(P)      ------------------------------------------------------------
Mm_MECP2_v1         CAGGATCTTGGCACATACGAAATGGCTGTGTAGCAAGCACTTTGGCATGCCCTCCTAAAC
Mm_MECP2_v2         CAGGATCTTGGCACATACGAAATGGCTGTGTAGCAAGCACTTTGGCATGCCCTCCTAAAC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------AGCC
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         -------------------TGTCTCCTCCACAGCGTCTACCTGTGGTGTGGCATGCCCCT
Oa_MECP2_v1(P)      -------------------TGTCTCCTCCACAGCGTCTGCCTGTGGTGTGGCCTGCCCCC
Oa_MECP2_v4(P)      -------------------TGTCTCCTCCACAGCGTCTGCCTGTGGTGTGGCCTGCCCCC
Oa_MECP2_v2(P)      -------------------TGTCTCCTCCACAGCGTCTGCCTGTGGTGTGGCCTGCCCCC
Oa_MECP2_v3(P)      -------------------TGTCTCCTCCACAGCGTCTGCCTGTGGTGTGGCCTGCCCCC
Mm_MECP2_v1         TTACCCCAGAGCCTCTCCCTGCCTCCTTAAGCCAGTCTGCCTGTCTTCTGGGGAGGTGTT
Mm_MECP2_v2         TTACCCCAGAGCCTCTCCCTGCCTCCTTAAGCCAGTCTGCCTGTCTTCTGGGGAGGTGTT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TTCTGAGCTGGCCTCTCACTGCCTCCCCAAGGCCCCCTGCCTGCCCTGTCAGGAGGCAGA
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Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GAGGACAGTCCCTGG-----------------------------------------------
Oa_MECP2_v1(P)      GAGGACAGTCCCTGG-----------------------------------------------
Oa_MECP2_v4(P)      GAGGACAGTCCCTGG-----------------------------------------------
Oa_MECP2_v2(P)      GAGGACAGTCCCTGG-----------------------------------------------
Oa_MECP2_v3(P)      GAGGACAGTCCCTGG-----------------------------------------------
Mm_MECP2_v1         AGAGCCCATAGAATGGAGAGGAGAAAGAAAAGAGGAAGAGGCAGGCAGGTAGTAAAAAGG
Mm_MECP2_v2         AGAGCCCATAGAATGGAGAGGAGAAAGAAAAGAGGAAGAGGCAGGCAGGTAGTAAAAAGG
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         AGGAAGCAGGTGTGAGGGCAGTGCAAGGAGGGAGCACAACC--------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         --CTCTGCGCTCATTTGGGGCCTGGGGCCAAGGGAGGGCAGGGGAGAGAACCCTCATGGA
Oa_MECP2_v1(P)      --CTCTGCGCTCC-TTGGGGCCTGGGGCTGAGGGAGGGCAGGGGAGAGGACCCTCATGGA
Oa_MECP2_v4(P)      --CTCTGCGCTCC-TTGGGGCCTGGGGCTGAGGGAGGGCAGGGGAGAGGACCCTCATGGA
Oa_MECP2_v2(P)      --CTCTGCGCTCC-TTGGGGCCTGGGGCTGAGGGAGGGCAGGGGAGAGGACCCTCATGGA
Oa_MECP2_v3(P)      --CTCTGCGCTCC-TTGGGGCCTGGGGCTGAGGGAGGGCAGGGGAGAGGACCCTCATGGA
Mm_MECP2_v1         CTCTGGGAGGAAAGACAGCCTCCTAGGCTTTGCACAAGCAGGACTCAGCCCCTTGTGGGA
Mm_MECP2_v2         CTCTGGGAGGAAAGACAGCCTCCTAGGCTTTGCACAAGCAGGACTCAGCCCCTTGTGGGA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         --CCCAGCTCCCGCTCCGGGCTCCGACTTGTGCACAGGCAGAGCCCAGA-----CCCTGG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         AGGGGCTTC-AGCTGGGGGTTTCCAAACATTGGGGAAACTTGC----CTTGGTTCTGCCG
Oa_MECP2_v1(P)      AGGGGCTTC-AGCTGGAGGTTTCCAAACATTGGGGAAACTTGC----CTTGGCTCTGCCG
Oa_MECP2_v4(P)      AGGGGCTTC-AGCTGGAGGTTTCCAAACATTGGGGAAACTTGC----CTTGGCTCTGCCG
Oa_MECP2_v2(P)      AGGGGCTTC-AGCTGGAGGTTTCCAAACATTGGGGAAACTTGC----CTTGGCTCTGCCG
Oa_MECP2_v3(P)      AGGGGCTTC-AGCTGGAGGTTTCCAAACATTGGGGAAACTTGC----CTTGGCTCTGCCG
Mm_MECP2_v1         ACTAAGTGCCATCTTGGAGTTTAAGAACATTTGGACAAGTTGCAAATGACCTTTG-----
Mm_MECP2_v2         ACTAAGTGCCATCTTGGAGTTTAAGAACATTTGGACAAGTTGCAAATGACCTTTG-----
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         AGGAAATCCTACCTTTGAATTCAAGAACATTTGGGGAATTTGGAAATCTCTTTGCCCCCA
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GCCACCCCCTCGGTCACCTGTCTCCTTGAGTCCTGCTCAGCGGTGAGGG----------G
Oa_MECP2_v1(P)      GCCTCCCCCTCGGTCACCTGTCTCCTCAAGTCCTGCTCAGCGGTGAGAG----------G
Oa_MECP2_v4(P)      GCCTCCCCCTCGGTCACCTGTCTCCTCAAGTCCTGCTCAGCGGTGAGAG----------G
Oa_MECP2_v2(P)      GCCTCCCCCTCGGTCACCTGTCTCCTCAAGTCCTGCTCAGCGGTGAGAG----------G
Oa_MECP2_v3(P)      GCCTCCCCCTCGGTCACCTGTCTCCTCAAGTCCTGCTCAGCGGTGAGAG----------G
Mm_MECP2_v1         --CTCCTTGCTCCTCTCACCTTTTATGGGGCCCTGCTTAGCACTGAAAGCAAATGCGCTG
Mm_MECP2_v2         --CTCCTTGCTCCTCTCACCTTTTATGGGGCCCTGCTTAGCACTGAAAGCAAATGCGCTG
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         AACCCCCATTCTGTCCTACCTTTAATCAGGTCCTGCTCAGCAGTGAGAGCAGATGAGGTG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         AAAAGGCCACGAGGTTTGGCTCCTGCCCACTGATAGTCCCTCTCCCCACAGTGTCTGTGT
Oa_MECP2_v1(P)      AAAAGGCCACGAGGTTTGGCTCCTGCCCACTGGTAGTCCCTCTCCCCACAGTGTCTCTGT
Oa_MECP2_v4(P)      AAAAGGCCACGAGGTTTGGCTCCTGCCCACTGGTAGTCCCTCTCCCCACAGTGTCTCTGT
Oa_MECP2_v2(P)      AAAAGGCCACGAGGTTTGGCTCCTGCCCACTGGTAGTCCCTCTCCCCACAGTGTCTCTGT
Oa_MECP2_v3(P)      AAAAGGCCACGAGGTTTGGCTCCTGCCCACTGGTAGTCCCTCTCCCCACAGTGTCTCTGT
Mm_MECP2_v1         AAAAGGCAAAGAGGTTTGGCTCCTGCCCACTGATAGTCC-TTTCCCTGCAGTGTTTGTGT
Mm_MECP2_v2         AAAAGGCAAAGAGGTTTGGCTCCTGCCCACTGATAGTCC-TTTCCCTGCAGTGTTTGTGT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         AAAAGGCCAAGAGGTTTGGCTCCTGCCCACTGATAGCCCCTCTCCCCGCAGTGTTTGTGT
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GTCAAGTGACAAAGCTGTTCTTCCTGGTGACCCGGATTATATCCAGTATCTTCTAGAC--
Oa_MECP2_v1(P)      GTCAAGTGACAAAGCTATTCTTCCTGGTGACCCTGATTATATCCGGTATCTTCTAGAC--
Oa_MECP2_v4(P)      GTCAAGTGACAAAGCTATTCTTCCTGGTGACCCTGATTATATCCGGTATCTTCTAGAC--
Oa_MECP2_v2(P)      GTCAAGTGACAAAGCTATTCTTCCTGGTGACCCTGATTATATCCGGTATCTTCTAGAC--
Oa_MECP2_v3(P)      GTCAAGTGACAAAGCTATTCTTCCTGGTGACCCTGATTATATCCGGTATCTTCTAGAC--
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Mm_MECP2_v1         GTCAAGTGGCAAAGCTGTTCTTCCTGGTGACTCTGATTAGATCCAGTAACTTAAGAGATT
Mm_MECP2_v2         GTCAAGTGGCAAAGCTGTTCTTCCTGGTGACTCTGATTAGATCCAGTAACTTAAGAGATT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GTCAAGTGGCAAAGCTGTTCTTCCTGGTGACCCTGATTATATCCAGTAACACATAGAC--
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TATACGCATAGACCTGCTTGGTCTTTTCTCTCCTGGGCTTTTGTTTTGCTCTTTAGTTTT
Oa_MECP2_v1(P)      TATACGAATAGACCTGCTTGGTCTTTTCTCTCCTGGGCTTTTGTTTTGCTCTTTAGTTTT
Oa_MECP2_v4(P)      TATACGAATAGACCTGCTTGGTCTTTTCTCTCCTGGGCTTTTGTTTTGCTCTTTAGTTTT
Oa_MECP2_v2(P)      TATACGAATAGACCTGCTTGGTCTTTTCTCTCCTGGGCTTTTGTTTTGCTCTTTAGTTTT
Oa_MECP2_v3(P)      TATACGAATAGACCTGCTTGGTCTTTTCTCTCCTGGGCTTTTGTTTTGCTCTTTAGTTTT
Mm_MECP2_v1         TGTATGCATAGGTCTGCTTTGACTCTTCTATTCTGGGCTTTTGATTTGTTTTTCAGTTTT
Mm_MECP2_v2         TGTATGCATAGGTCTGCTTTGACTCTTCTATTCTGGGCTTTTGATTTGTTTTTCAGTTTT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TGTGCGCATAGGCCTGCTTTGTCTCCTCTATCCTGGGCTTTTGTTTTGCTTTTTAGTTTT
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GCTTTTCCCTCTCCTGTCCCTTTTATTTAAATACACTGACTAGACACACAAAGCAGTTGA
Oa_MECP2_v1(P)      GCTTTTCCCTCTCCTGTCCCTTTTATTTAAATACACTGACTAGACACACAAAGCAGTTGA
Oa_MECP2_v4(P)      GCTTTTCCCTCTCCTGTCCCTTTTATTTAAATACACTGACTAGACACACAAAGCAGTTGA
Oa_MECP2_v2(P)      GCTTTTCCCTCTCCTGTCCCTTTTATTTAAATACACTGACTAGACACACAAAGCAGTTGA
Oa_MECP2_v3(P)      GCTTTTCCCTCTCCTGTCCCTTTTATTTAAATACACTGACTAGACACACAAAGCAGTTGA
Mm_MECP2_v1         GCTTTTAGTTTTCCTATTTTT---ATTT-TATGCACCAACTAGACACACAAAGCAGTTGA
Mm_MECP2_v2         GCTTTTAGTTTTCCTATTTTT---ATTT-TATGCACCAACTAGACACACAAAGCAGTTGA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GCTTTTAGTTTTTCTGTCCCTTTTATTT-AACGCACCGACTAGACACACAAAGCAGTTGA
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ATTTTTATATAT------ATATATA----TGTATATTGCACAGTTATAAACTCATTTTGC
Oa_MECP2_v1(P)      ATTTTTATATAT------ATATATATCTCTGTATATTGCACAGTTATAAACTCATTTTGC
Oa_MECP2_v4(P)      ATTTTTATATAT------ATATATATCTCTGTATATTGCACAGTTATAAACTCATTTTGC
Oa_MECP2_v2(P)      ATTTTTATATAT------ATATATATCTCTGTATATTGCACAGTTATAAACTCATTTTGC
Oa_MECP2_v3(P)      ATTTTTATATAT------ATATATATCTCTGTATATTGCACAGTTATAAACTCATTTTGC
Mm_MECP2_v1         ATTTATATATATATATATATATATATATCTGTATATTTCACAATTATAAACTCATTTTGC
Mm_MECP2_v2         ATTTATATATATATATATATATATATATCTGTATATTTCACAATTATAAACTCATTTTGC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ATTTTT------------ATATATATATCTGTATATTGCACAATTATAAACTCATTTTGC
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TTGTGGCTCCACACACACACACACACACACACACACACACACACAAAGACCTGTTAAAATTA
Oa_MECP2_v1(P)      TTGTGGCT----------------ACACACACACACACACACACAGACCTGTTAAAATTA
Oa_MECP2_v4(P)      TTGTGGCT--------------ACACACACACACACACACACAGACCTGTTAAAATTA
Oa_MECP2_v2(P)      TTGTGGCT--------------ACACACACACACACACACACAGACCTGTTAAAATTA
Oa_MECP2_v3(P)      TTGTGGCT--------------ACACACACACACACACACACAGACCTGTTAAAATTA
Mm_MECP2_v1         TTGTGACG----------------CCACACACACACAAAAAGAAAAACCTTTTAAAATTA
Mm_MECP2_v2         TTGTGACG----------------CCACACACACACAAAAAGAAAAACCTTTTAAAATTA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TTGTGGCT----------------CCACACACA----CAAAAAAAGACCTGTTAAAATTA
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TACCTGTTGCTTAATTACAATATTTCTGATAACCATAGCATAGGACAAGGGGAAATTTTA
Oa_MECP2_v1(P)      TACCTGTTGCTTAATTACAATATTTCTGATAACCATAGCATAGGACAAGGGAAAATTTTT
Oa_MECP2_v4(P)      TACCTGTTGCTTAATTACAATATTTCTGATAACCATAGCATAGGACAAGGGAAAATTTTT
Oa_MECP2_v2(P)      TACCTGTTGCTTAATTACAATATTTCTGATAACCATAGCATAGGACAAGGGAAAATTTTT
Oa_MECP2_v3(P)      TACCTGTTGCTTAATTACAATATTTCTGATAACCATAGCATAGGACAAGGGAAAATTTTT
Mm_MECP2_v1         TACCTGTTGCTTAATTACAATATTTCTGATAACCATAGAGTAGGACAAGGGAAAAAATTT
Mm_MECP2_v2         TACCTGTTGCTTAATTACAATATTTCTGATAACCATAGAGTAGGACAAGGGAAAAAATTT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TACCTGTTGCTTAATTACAATATTTCTGATAACCATAGCATAGGACAAGGGAAAATAAAA
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         AAAAACCAAAAAAAAAGAAAAAAAAAAAACACAAACGAAGAAAACAAACAACAA-AAAAA
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Oa_MECP2_v1(P)      AAAAACCAAAAAAAAAAAAAGAAAAAAAA--ACAAACGGAGAAAACAAAAAACAACAACAA
Oa_MECP2_v4(P)      AAAAACCAAAAAAAAAAAAAGAAAAAAAA--ACAAACGGAGAAAACAAAAAACAACAACAA
Oa_MECP2_v2(P)      AAAAACCAAAAAAAAAAAAAGAAAAAAAA--ACAAACGGAGAAAACAAAAAACAACAACAA
Oa_MECP2_v3(P)      AAAAACCAAAAAAAAAAAAAGAAAAAAAA--ACAAACGGAGAAAACAAAAAACAACAACAA
Mm_MECP2_v1         AAAAAGAAAAAAAAAAAAAGAAAAAACA----------------------------------
Mm_MECP2_v2         AAAAAGAAAAAAAAAAAAAGAAAAAACA----------------------------------
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         AAAGAAAA-AAAAGAAAAAAAAACGACA----------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         AAAACCTGACAAATCCGTCTGCTGGTCACTCGT---GTCCAAGCAGAACCGTGGTCT-TT
Oa_MECP2_v1(P)      CAAAAACGAAAAATCAGTCTGCTGGTCACTCGT---GTCCAAGCAGAGCCGTGGTCT-TT
Oa_MECP2_v4(P)      CAAAAACGAAAAATCAGTCTGCTGGTCACTCGT---GTCCAAGCAGAGCCGTGGTCT-TT
Oa_MECP2_v2(P)      CAAAAACGAAAAATCAGTCTGCTGGTCACTCGT---GTCCAAGCAGAGCCGTGGTCT-TT
Oa_MECP2_v3(P)      CAAAAACGAAAAATCAGTCTGCTGGTCACTCGT---GTCCAAGCAGAGCCGTGGTCT-TT
Mm_MECP2_v1         -----------CATCTGTCTGCTGGTCACTTCTTCAATCCAAGCAGATCTGTGATCT-TT
Mm_MECP2_v2         -----------CATCTGTCTGCTGGTCACTTCTTCAATCCAAGCAGATCTGTGATCT-TT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         -----------AATCTGTCTGCTGGTCACTTCTTCTGTCCAAGCAGATTCGTGGTCTTTT
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CCTCGCTTCTTTCAAGGGCTTCCCAGTGCCGAGCGAAGG-------AGGCAGCTCCTGGG
Oa_MECP2_v1(P)      CCTCGCTTCTTTCAAGGGCTTCCCAGTGCCGAGCGAAGG-------AGGCAGCTCCTGGA
Oa_MECP2_v4(P)      CCTCGCTTCTTTCAAGGGCTTCCCAGTGCCGAGCGAAGG-------AGGCAGCTCCTGGA
Oa_MECP2_v2(P)      CCTCGCTTCTTTCAAGGGCTTCCCAGTGCCGAGCGAAGG-------AGGCAGCTCCTGGA
Oa_MECP2_v3(P)      CCTCGCTTCTTTCAAGGGCTTCCCAGTGCCGAGCGAAGG-------AGGCAGCTCCTGGA
Mm_MECP2_v1         CCTCGCGTCTTTCAAAGACTTCCCTGTGCTAAGTGAAGGAAGCTCCAGGCTGCACCCAGG
Mm_MECP2_v2         CCTCGCGTCTTTCAAAGACTTCCCTGTGCTAAGTGAAGGAAGCTCCAGGCTGCACCCAGG
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CCTCGCTTCTTTCAAGGGCTTTCCTGTGCCAGGTGAAGGAGGCTCCAGGCAGCACCCAGG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TTTCGCACT---GTTTCTCCCAAGCTTGTGAGTGGGGCCCCAGGGCGCTGGTGTAGGCAG
Oa_MECP2_v1(P)      TTTCGCACT---GTTTTTCCCAAGCTTGTGAGTGCGGCCCCAGGGCACTGGTGTAGACAG
Oa_MECP2_v4(P)      TTTCGCACT---GTTTTTCCCAAGCTTGTGAGTGCGGCCCCAGGGCACTGGTGTAGACAG
Oa_MECP2_v2(P)      TTTCGCACT---GTTTTTCCCAAGCTTGTGAGTGCGGCCCCAGGGCACTGGTGTAGACAG
Oa_MECP2_v3(P)      TTTCGCACT---GTTTTTCCCAAGCTTGTGAGTGCGGCCCCAGGGCACTGGTGTAGACAG
Mm_MECP2_v1         TTTTGTGCTTTGTTTCTCCT--CTGTTGTGAAAGGGGCCCCAAGATTCTGG---GTACAG
Mm_MECP2_v2         TTTTGTGCTTTGTTTCTCCT--CTGTTGTGAAAGGGGCCCCAAGATTCTGG---GTACAG
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TTTTGCACTCTTGTTTCTCCCGTGCTTGTGAAAGAGGTCCCAAGGTTCTGG---GTGCAG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GACAGTTCGTTTCAGTGGG-----TGGATGCAAGCATGCTCCCTGGCTCTGGTGAAGCCC
Oa_MECP2_v1(P)      GACAGTTCGTTTCAGTGGG-----TGGATGCAAGCGTGTTCCCTGGCTCTGGCGAAGCCT
Oa_MECP2_v4(P)      GACAGTTCGTTTCAGTGGG-----TGGATGCAAGCGTGTTCCCTGGCTCTGGCGAAGCCT
Oa_MECP2_v2(P)      GACAGTTCGTTTCAGTGGG-----TGGATGCAAGCGTGTTCCCTGGCTCTGGCGAAGCCT
Oa_MECP2_v3(P)      GACAGTTCGTTTCAGTGGG-----TGGATGCAAGCGTGTTCCCTGGCTCTGGCGAAGCCT
Mm_MECP2_v1         GACAGTTCATTTCAGCATGGGGTCAGGAGACAAGAGCACTCCCTTTACATGCTGACGTAC
Mm_MECP2_v2         GACAGTTCATTTCAGCATGGGGTCAGGAGACAAGAGCACTCCCTTTACATGCTGACGTAC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GAGCGCTC----------------------------------CCTTGACCTGCTGAAGTCC
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         AGAATGTAGTTGGCACTGCCTGGGCCCCTTTGATCTCTGGGTGGGGCAGCTGGCGTTCAT
Oa_MECP2_v1(P)      AGAATGTAGTTGGCACTGCCTGGTCCCCTTTGATCTCTGGGTGGGGCAGCTGGCGTTCAT
Oa_MECP2_v4(P)      AGAATGTAGTTGGCACTGCCTGGTCCCCTTTGATCTCTGGGTGGGGCAGCTGGCGTTCAT
Oa_MECP2_v2(P)      AGAATGTAGTTGGCACTGCCTGGTCCCCTTTGATCTCTGGGTGGGGCAGCTGGCGTTCAT
Oa_MECP2_v3(P)      AGAATGTAGTTGGCACTGCCTGGTCCCCTTTGATCTCTGGGTGGGGCAGCTGGCGTTCAT
Mm_MECP2_v1         AGAACTTAGTGGGAATAGCCTAGTCCCCACCTCTA---GGGATGGGGAGCTAGCATGCAT
Mm_MECP2_v2         AGAACTTAGTGGGAATAGCCTAGTCCCCACCTCTA---GGGATGGGGAGCTAGCATGCAT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GGAACGTAGTCGGCACAGCCTGGTCGCCTTCCACC---TCT---GGGAGCTGGAGTCCAC
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Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GGGGGTGACCTGCCCCC--CCGACACCCTCCAGTGACC----CAGAGTGATA--GTGTGC
Oa_MECP2_v1(P)      GGGGGTGACCTGCCCCCCGCCGACACCCTCCAGTGACCCAGTCAGAGTGATG--GTGTGC
Oa_MECP2_v4(P)      GGGGGTGACCTGCCCCCCGCCGACACCCTCCAGTGACCCAGTCAGAGTGATG--GTGTGC
Oa_MECP2_v2(P)      GGGGGTGACCTGCCCCCCGCCGACACCCTCCAGTGACCCAGTCAGAGTGATG--GTGTGC
Oa_MECP2_v3(P)      GGGGGTGACCTGCCCCCCGCCGACACCCTCCAGTGACCCAGTCAGAGTGATG--GTGTGC
Mm_MECP2_v1         GGGGGTGACC--------CAACTCCCTCCACCTTTCCCTGGCCAGGAAGAGCCTGTGTAC
Mm_MECP2_v2         GGGGGTGACC--------CAACTCCCTCCACCTTTCCCTGGCCAGGAAGAGCCTGTGTAC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TGGGGTGGCCTGACTCCCCCAGTCCCCTTCCCGTGACCTGGTCAGGGTGAGCCCATGTGG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         AGACAGGCAGCAAGCCTCCCCACTGGTAGG-------------------------GCCTGT
Oa_MECP2_v1(P)      AGACAGGCAGCAAGCCTCTCTACTGGTAGG-------------------------GCTTGT
Oa_MECP2_v4(P)      AGACAGGCAGCAAGCCTCTCTACTGGTAGG-------------------------GCTTGT
Oa_MECP2_v2(P)      AGACAGGCAGCAAGCCTCTCTACTGGTAGG-------------------------GCTTGT
Oa_MECP2_v3(P)      AGACAGGCAGCAAGCCTCTCTACTGGTAGG-------------------------GCTTGT
Mm_MECP2_v1         AGTAAGTCTGACAAGCTTTCCCCAGTTAGCAGGGCTCAGAGCATTTAAAAACCCTCCAAA
Mm_MECP2_v2         AGTAAGTCTGACAAGCTTTCCCCAGTTAGCAGGGCTCAGAGCATTTAAAAACCCTCCAAA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         AGTCAGCCTCGCAGGCCTCCCTGCCAGTAG---GGTCCGAGT-GTGTTTCATCCTTCCCA
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CTCTGCCAAGTCTGGGGGCCGCAGGGGAGACGAAAGGCTGTGTCTCAATTCAGGAAGTGT
Oa_MECP2_v1(P)      CTCTGCCAAGTCCGGGGGGCTGAATGGGAGACAGAAGGCTGTGTCTCAGTTCAGAAAGCGT
Oa_MECP2_v4(P)      CTCTGCCAAGTCCGGGGGGCTGAATGGGAGACAGAAGGCTGTGTCTCAGTTCAGAAAGCGT
Oa_MECP2_v2(P)      CTCTGCCAAGTCCGGGGGGCTGAATGGGAGACAGAAGGCTGTGTCTCAGTTCAGAAAGCGT
Oa_MECP2_v3(P)      CTCTGCCAAGTCCGGGGGGCTGAATGGGAGACAGAAGGCTGTGTCTCAGTTCAGAAAGCGT
Mm_MECP2_v1         CTTTGCTGAGTCTAGGGACTAGAGAGAAGATAGAAGATTTGGTCTATCTCCAAGGTGTGT
Mm_MECP2_v2         CTTTGCTGAGTCTAGGGACTAGAGAGAAGATAGAAGATTTGGTCTATCTCCAAGGTGTGT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CTCTGTCGAGCCTGGGGGCTGGAGCGGAGACGGGAGGCCTGGCCTGTCT-CGGAACCTGT
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GAACCGTACCAGGTAGAACATCAGGGACCCCAGAACCACA-CATGCGGTCCAGCGGGTCC
Oa_MECP2_v1(P)      GAGCTGTACCAGGTAGAACATCAGGGACCCCAGAACCACA-CATGTGGTCCAGCGGGCCC
Oa_MECP2_v4(P)      GAGCTGTACCAGGTAGAACATCAGGGACCCCAGAACCACA-CATGTGGTCCAGCGGGCCC
Oa_MECP2_v2(P)      GAGCTGTACCAGGTAGAACATCAGGGACCCCAGAACCACA-CATGTGGTCCAGCGGGCCC
Oa_MECP2_v3(P)      GAGCTGTACCAGGTAGAACATCAGGGACCCCAGAACCACA-CATGTGGTCCAGCGGGCCC
Mm_MECP2_v1         AAGCTGTACCAGGTAGAATGCCAGGGACCCCAGAACCACATCCAACAGCCCAATGGGTCT
Mm_MECP2_v2         AAGCTGTACCAGGTAGAATGCCAGGGACCCCAGAACCACATCCAACAGCCCAATGGGTCT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GAGCTGCACCAGGTAGAACGCCAGGGACCCCAGAATCATGTGCGTCAGTCCAAGGGGTCC
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CCTCCAGGAGGTAGCGAAGACTCCAGAAACGTTCCTTCCTCTTCCCCCACTGCCCCAATC
Oa_MECP2_v1(P)      CCTCCAGGAGGTAGCGAAGACTCCAGAAACGTTCCTTCCTC-CCCACCCCCCCCCACCATC
Oa_MECP2_v4(P)      CCTCCAGGAGGTAGCGAAGACTCCAGAAACGTTCCTTCCTC-CCCACCCCCCCCCACCATC
Oa_MECP2_v2(P)      CCTCCAGGAGGTAGCGAAGACTCCAGAAACGTTCCTTCCTC-CCCACCCCCCCCCACCATC
Oa_MECP2_v3(P)      CCTCCAGGAGGTAGCGAAGACTCCAGAAACGTTCCTTCCTC-CCCACCCCCCCCCACCATC
Mm_MECP2_v1         CCTCCAGAAAGTAGTGAAGACTCCAGAAACATCCCTTTCTCTTC-------TCCCTGCTC
Mm_MECP2_v2         CCTCCAGAAAGTAGTGAAGACTCCAGAAACATCCCTTTCTCTTC-------TCCCTGCTC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CCTCCAGG-AGTAGTGAAGACTCCAGAAATGTCC--CTTTCTTC-------TCCCCCATC
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CTACGAGTAATTGCATTTGCTTTTGTAATTCTTACTGAGCAATATCTGCTAGAGAGTTT-
Oa_MECP2_v1(P)      CTATGAGTAATTGCATTTGCTTTTGTAATTCTTACCGAGCAATATCTGCT--AGAGTTT-
Oa_MECP2_v4(P)      CTATGAGTAATTGCATTTGCTTTTGTAATTCTTACCGAGCAATATCTGCT--AGAGTTT-
Oa_MECP2_v2(P)      CTATGAGTAATTGCATTTGCTTTTGTAATTCTTACCGAGCAATATCTGCT--AGAGTTT-
Oa_MECP2_v3(P)      CTATGAGTAATTGCATTTGCTTTTGTAATTCTTACCGAGCAATATCTGCT--AGAGTTT-
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Mm_MECP2_v1         CCATGAGTAACTGCATTTGCTTTTGTAATCCTTAATGAGCATTATCTGCTAAAAAAAAAA
Mm_MECP2_v2         CCATGAGTAACTGCATTTGCTTTTGTAATCCTTAATGAGCATTATCTGCTAAAAAAAAAA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CTACGAGTAATTGCATTTGCTTTTGTAATTCTTAATGAGCAATATCTGCTAGAGAGTTT-
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ----AGCCGTA--AGTTCTTTTTGATCA------TTTTTTAAGTAAGTAAAAACACCAAA
Oa_MECP2_v1(P)      ----AGCCGTA--AGTTCTTTTTGATCA------TTTTTTAAGTAAGTAAAAACACCAAA
Oa_MECP2_v4(P)      ----AGCCGTA--AGTTCTTTTTGATCA------TTTTTTAAGTAAGTAAAAACACCAAA
Oa_MECP2_v2(P)      ----AGCCGTA--AGTTCTTTTTGATCA------TTTTTTAAGTAAGTAAAAACACCAAA
Oa_MECP2_v3(P)      ----AGCCGTA--AGTTCTTTTTGATCA------TTTTTTAAGTAAGTAAAAACACCAAA
Mm_MECP2_v1         AATTAGCTGTAACAGTTCTTTTTGCAAAAGGATCATTCTTAAATAATTAAAAACACCCCC
Mm_MECP2_v2         AATTAGCTGTAACAGTTCTTTTTGCAAAAGGATCATTCTTAAATAATTAAAAACACCCCC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ----AGCTGTAACAGTTCTTTTTGATCATCTTTTTT----TAATAA---------TTAGA
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         AAAAAT-----AATAATATCCAGAAACTTGTTCTTCCAAAGCAGAGAGCATTATAATCAC
Oa_MECP2_v1(P)      AAAAAAATAAGAATAATATCCAGAAACTTGTTCTTCCAAAGCAGAGAGCATTATAATCAC
Oa_MECP2_v4(P)      AAAAAAATAAGAATAATATCCAGAAACTTGTTCTTCCAAAGCAGAGAGCATTATAATCAC
Oa_MECP2_v2(P)      AAAAAAATAAGAATAATATCCAGAAACTTGTTCTTCCAAAGCAGAGAGCATTATAATCAC
Oa_MECP2_v3(P)      AAAAAAATAAGAATAATATCCAGAAACTTGTTCTTCCAAAGCAGAGAGCATTATAATCAC
Mm_MECP2_v1         CCCCAA-----AAAAAAGTCCAGAACCTTGTTCTTCCAAAGCAGAGAGCATTATAATCAG
Mm_MECP2_v2         CCCCAA-----AAAAAAGTCCAGAACCTTGTTCTTCCAAAGCAGAGAGCATTATAATCAG
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         AACACC-----AAAAAAATCCAGAAACTTGTTCTTCCAAAGCAGAGAGCATTATAATCAC
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CAGGGCCAAAAGCTTCCCTCCCCGC---------------GTTATTACTTCTGAGGCCTA
Oa_MECP2_v1(P)      CAGGGCCAAAAGCTTCCCTCCCCGC---------------ATCATTACTTCTGAGGCCTA
Oa_MECP2_v4(P)      CAGGGCCAAAAGCTTCCCTCCCCGC---------------ATCATTACTTCTGAGGCCTA
Oa_MECP2_v2(P)      CAGGGCCAAAAGCTTCCCTCCCCGC---------------ATCATTACTTCTGAGGCCTA
Oa_MECP2_v3(P)      CAGGGCCAAAAGCTTCCCTCCCCGC---------------ATCATTACTTCTGAGGCCTA
Mm_MECP2_v1         GGCCAAAATCTGTCCCACACCTCTACCCCATCTCCTCATGATTGCTGCTTCTAAGGCCAG
Mm_MECP2_v2         GGCCAAAATCTGTCCCACACCTCTACCCCATCTCCTCATGATTGCTGCTTCTAAGGCCAG
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CAGGGCCAAAAGCTTCCCTCCCTGC-----------TGTCATTGCTTCTTCTGAGGCCTG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CGTCCA--AAAGAAACCCTTAGAGGCCCTTCAGGTGGCCAGGCACCACTCAGGCCCCTGG
Oa_MECP2_v1(P)      TGTCCA--AAAGAAACCCTTAGAGGCCCTTCAGGTGGCCAGGCACCCCTCAGGCCTTTGG
Oa_MECP2_v4(P)      TGTCCA--AAAGAAACCCTTAGAGGCCCTTCAGGTGGCCAGGCACCCCTCAGGCCTTTGG
Oa_MECP2_v2(P)      TGTCCA--AAAGAAACCCTTAGAGGCCCTTCAGGTGGCCAGGCACCCCTCAGGCCTTTGG
Oa_MECP2_v3(P)      TGTCCA--AAAGAAACCCTTAGAGGCCCTTCAGGTGGCCAGGCACCCCTCAGGCCTTTGG
Mm_MECP2_v1         AATACA--GCAAAGATATTTGTAGGCCCTTTGGGTGACTGGGCTACCCTTGGAGCTCTTG
Mm_MECP2_v2         AATACA--GCAAAGATATTTGTAGGCCCTTTGGGTGACTGGGCTACCCTTGGAGCTCTTG
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         AATCCAAAAGAAAAACAGCCATAGGCCCTTTCAGTGGCCGGGCTACCCGTGAGCCCTTCG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GAGGACCTG-----------------------GGCCTGGGGGCTGGGCCCCACCCTCAGT
Oa_MECP2_v1(P)      GAGGACCTG-----------------------GGCCTGGGGGCTGGGCCCCGCCTTCTGT
Oa_MECP2_v4(P)      GAGGACCTG-----------------------GGCCTGGGGGCTGGGCCCCGCCTTCTGT
Oa_MECP2_v2(P)      GAGGACCTG-----------------------GGCCTGGGGGCTGGGCCCCGCCTTCTGT
Oa_MECP2_v3(P)      GAGGACCTG-----------------------GGCCTGGGGGCTGGGCCCCGCCTTCTGT
Mm_MECP2_v1         GAAGATGGG--CTGGGGAAGCCTCTGAGACCCTATCCTAGGGCCTTGCTCTAGGGAGTAA
Mm_MECP2_v2         GAAGATGGG--CTGGGGAAGCCTCTGAGACCCTATCCTAGGGCCTTGCTCTAGGGAGTAA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GAGGACCAGGGCTGGGGCAGCCTCTGGG--CCCACATCCGGGGCCAGCTCCGGCGTGTGT
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TCAGTATTAGTGGTGGGTCCCTGCCTCTTCTCCTATCCAGCCTGGGCCAGGGCGGGCAGA
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Oa_MECP2_v1(P)      TCAGTATTAGTGGTGGGTCCCTGCCGCTT---CTACCCAGCCTGGGCCAGGG-TGGCAGA
Oa_MECP2_v4(P)      TCAGTATTAGTGGTGGGTCCCTGCCGCTT---CTACCCAGCCTGGGCCAGGG-TGGCAGA
Oa_MECP2_v2(P)      TCAGTATTAGTGGTGGGTCCCTGCCGCTT---CTACCCAGCCTGGGCCAGGG-TGGCAGA
Oa_MECP2_v3(P)      TCAGTATTAGTGGTGGGTCCCTGCCGCTT---CTACCCAGCCTGGGCCAGGG-TGGCAGA
Mm_MECP2_v1         TCAGTATTAGTAGAGTGTCACAACATTATTCCCCAGCCGGCATGAGATGGGGGCAGAAGA
Mm_MECP2_v2         TCAGTATTAGTAGAGTGTCACAACATTATTCCCCAGCCGGCATGAGATGGGGGCAGAAGA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TCAGTGTTAGCAGTGGGTCATGATGCTCTTTCCCACCCAGCCTGGGATAGGGGCAGAGGA
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GG--AAGCCGCTGCGACCACTGCT----GTCCAGCCTCTTGCAGATGGGTGTTGGCGCGT
Oa_MECP2_v1(P)      GG--AAGCTGCTGCGACCACTGCT----GTCCAGCTTCTTGCAGATGGGTGTTGGCGTGT
Oa_MECP2_v4(P)      GG--AAGCTGCTGCGACCACTGCT----GTCCAGCTTCTTGCAGATGGGTGTTGGCGTGT
Oa_MECP2_v2(P)      GG--AAGCTGCTGCGACCACTGCT----GTCCAGCTTCTTGCAGATGGGTGTTGGCGTGT
Oa_MECP2_v3(P)      GG--AAGCTGCTGCGACCACTGCT----GTCCAGCTTCTTGCAGATGGGTGTTGGCGTGT
Mm_MECP2_v1         AGCCAAAGGGTTGTCTCCACTGCTACTTACTTGGCCACTGACAGGTAGGTGACCATGTAT
Mm_MECP2_v2         AGCCAAAGGGTTGTCTCCACTGCTACTTACTTGGCCACTGACAGGTAGGTGACCATGTAT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GGCGAGGAGGCCGTTGCCGCTGAT----GTTTGGCCGTGAACAGGTGGGTGTCTGCGTGC
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GTCCA-------GTTCTGCCCGAGATCTGAAGGCGGCA-CCGAATTAGCCTCAGCCGGTG
Oa_MECP2_v1(P)      GTCCA-------GTTCTGCCTGAGATCTGAAGACAGCA-CCGAGTTAGCCTCAGCTGGTG
Oa_MECP2_v4(P)      GTCCA-------GTTCTGCCTGAGATCTGAAGACAGCA-CCGAGTTAGCCTCAGCTGGTG
Oa_MECP2_v2(P)      GTCCA-------GTTCTGCCTGAGATCTGAAGACAGCA-CCGAGTTAGCCTCAGCTGGTG
Oa_MECP2_v3(P)      GTCCA-------GTTCTGCCTGAGATCTGAAGACAGCA-CCGAGTTAGCCTCAGCTGGTG
Mm_MECP2_v1         GTCCATATGCATGTTTTATGGCTGATGTGAGATCAGCACCCAAGTTAGCTTCACCTGGTG
Mm_MECP2_v2         GTCCATATGCATGTTTTATGGCTGATGTGAGATCAGCACCCAAGTTAGCTTCACCTGGTG
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GTCCACGTGCGTGTTTTCTGACTGACATGAAATCGACGCCCGAGTTAGCCTCACCCGGTG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ACCTCTCACCCGGCCTGCCCCAGGCAGCAGGGCCCACCCAGTGCACTGTTCCTGGGTTGC
Oa_MECP2_v1(P)      ACCTCTCACCTGGCCTGCCCCAGGCAGCAGGGCCCACCCAGTGTACTGTTCCTGGGTTGC
Oa_MECP2_v4(P)      ACCTCTCACCTGGCCTGCCCCAGGCAGCAGGGCCCACCCAGTGTACTGTTCCTGGGTTGC
Oa_MECP2_v2(P)      ACCTCTCACCTGGCCTGCCCCAGGCAGCAGGGCCCACCCAGTGTACTGTTCCTGGGTTGC
Oa_MECP2_v3(P)      ACCTCTCACCTGGCCTGCCCCAGGCAGCAGGGCCCACCCAGTGTACTGTTCCTGGGTTGC
Mm_MECP2_v1         ACCTCTAACCCTGCCTG---GATGGAGCAG--GCCACCTGGTTCAATGTTTCTGGGCAGC
Mm_MECP2_v2         ACCTCTAACCCTGCCTG---GATGGAGCAG--GCCACCTGGTTCAATGTTTCTGGGCAGC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ACCTCTAGCCCTGCCCG---GATGGAGCGGGGCCCACCCGGTTCAGTGTTTCTGGGGAGC
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TGGACGGTGGCATGGCAAAGGCTTGCAGAACTCAAAACCTGCTCCTTCCCTTGCTCCCAA
Oa_MECP2_v1(P)      CGGACGGTAGCATGGCAAAGGCTTGCAGAACTCAAAACCTGCTCCTTCCCTTGCTCCCAA
Oa_MECP2_v4(P)      CGGACGGTAGCATGGCAAAGGCTTGCAGAACTCAAAACCTGCTCCTTCCCTTGCTCCCAA
Oa_MECP2_v2(P)      CGGACGGTAGCATGGCAAAGGCTTGCAGAACTCAAAACCTGCTCCTTCCCTTGCTCCCAA
Oa_MECP2_v3(P)      CGGACGGTAGCATGGCAAAGGCTTGCAGAACTCAAAACCTGCTCCTTCCCTTGCTCCCAA
Mm_MECP2_v1         TGGACAATGGAGTGCAAAAGGCTTACAGAACTTGAAGCCTTTTCCTTACTTTGCTAGCAC
Mm_MECP2_v2         TGGACAATGGAGTGCAAAAGGCTTACAGAACTTGAAGCCTTTTCCTTACTTTGCTAGCAC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TGGACAGTGGAGTGCAAAAGGCTTGCAGAACTTGAAGCCTGCTCCTTCCCTTGCTACCAC
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GGCCTCCTTTTCCATTTATATTGTCACTGCT----TCAATAACAGCCACTCCAGAGTCAG
Oa_MECP2_v1(P)      GCCCTCCTTTTCCCTTTGAGTTGTCACTGCTTCAATCAATAACAGCCGCTCCAGAGTCAG
Oa_MECP2_v4(P)      GCCCTCCTTTTCCCTTTGAGTTGTCACTGCTTCAATCAATAACAGCCGCTCCAGAGTCAG
Oa_MECP2_v2(P)      GCCCTCCTTTTCCCTTTGAGTTGTCACTGCTTCAATCAATAACAGCCGCTCCAGAGTCAG
Oa_MECP2_v3(P)      GCCCTCCTTTTCCCTTTGAGTTGTCACTGCTTCAATCAATAACAGCCGCTCCAGAGTCAG
Mm_MECP2_v1         GGCCTCCTTTTCCATTTGATTTGTCACTGCTTCAGTCAATAACAGCCGCTCCAGAGTCAG
Mm_MECP2_v2         GGCCTCCTTTTCCATTTGATTTGTCACTGCTTCAGTCAATAACAGCCGCTCCAGAGTCAG
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GGCCTCCT-TTCCGTTTGATTTGTCACTGCTTCAATCAATAACAGCCGCTCCAGAGTCAG
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Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TAGTTGATGAATATATGACCAAATATCATCAGGACTGTTACTCG--GTGTGCCGAGCCCT
Oa_MECP2_v1(P)      TAGTTGATGAATATATGACCAAATATCACCAGGACTGTTACTCG--GTGTGCCGAGCCCT
Oa_MECP2_v4(P)      TAGTTGATGAATATATGACCAAATATCACCAGGACTGTTACTCG--GTGTGCCGAGCCCT
Oa_MECP2_v2(P)      TAGTTGATGAATATATGACCAAATATCACCAGGACTGTTACTCG--GTGTGCCGAGCCCT
Oa_MECP2_v3(P)      TAGTTGATGAATATATGACCAAATATCACCAGGACTGTTACTCG--GTGTGCCGAGCCCT
Mm_MECP2_v1         TAGTTGATGAATATATGACCAAATATCACCAGGACTGTTACTCAACGTGTGCCGAGCCCT
Mm_MECP2_v2         TAGTTGATGAATATATGACCAAATATCACCAGGACTGTTACTCAACGTGTGCCGAGCCCT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TAGTCAATGAATATATGACCAAATATCACCAGGACTGTTACTCAATGTGTGCCGAGCCCT
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CTCCTCGCACGGGGCTCC---TGTACCCGGACACTGTACCGTGTGCTGTGTTTGCGCTCC
Oa_MECP2_v1(P)      CTCCTCGTGCAGGGCTCC---TGTACCCGGACACTGTACCGTGTGCTGTGTTTGCGCTCC
Oa_MECP2_v4(P)      CTCCTCGTGCAGGGCTCC---TGTACCCGGACACTGTACCGTGTGCTGTGTTTGCGCTCC
Oa_MECP2_v2(P)      CTCCTCGTGCAGGGCTCC---TGTACCCGGACACTGTACCGTGTGCTGTGTTTGCGCTCC
Oa_MECP2_v3(P)      CTCCTCGTGCAGGGCTCC---TGTACCCGGACACTGTACCGTGTGCTGTGTTTGCGCTCC
Mm_MECP2_v1         TTCCTTGTGCTGGGCTCCCTGTGTACCTGGACACTGTAATGTGTGCTGTGTTTGCTCTCC
Mm_MECP2_v2         TTCCTTGTGCTGGGCTCCCTGTGTACCTGGACACTGTAATGTGTGCTGTGTTTGCTCTCC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TGCCCATGCTGG--GCTCCCGTGTATCTGGACACTGTAACGTGTGCTGTGTTTGCTCCCC
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TCC-----CTTCCTCCACCCTCCCCTCGTCTCTCTGGGGTTGTTTCTGTTTGGGTTTGGT
Oa_MECP2_v1(P)      TCC-----CCTCCTCCGCCCTCCCCTCGTCTCTCTGGGGTTGTTTCTGTTTGGGTTTGGT
Oa_MECP2_v4(P)      TCC-----CCTCCTCCGCCCTCCCCTCGTCTCTCTGGGGTTGTTTCTGTTTGGGTTTGGT
Oa_MECP2_v2(P)      TCC-----CCTCCTCCGCCCTCCCCTCGTCTCTCTGGGGTTGTTTCTGTTTGGGTTTGGT
Oa_MECP2_v3(P)      TCC-----CCTCCTCCGCCCTCCCCTCGTCTCTCTGGGGTTGTTTCTGTTTGGGTTTGGT
Mm_MECP2_v1         TTCCTCTTCCTTCCTTGCCCTTTCCTTGTCTTTCTGGGGTT-TTTCTGTTGGGTTTGGTT
Mm_MECP2_v2         TTCCTCTTCCTTCCTTGCCCTTTCCTTGTCTTTCTGGGGTT-TTTCTGTTGGGTTTGGTT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TTCCCCTTCCTTCTTTGCCCTTTACTTGTCTTTCTGGGGTT-TTTCTGTTTGGGTTTGGT
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TTGGTTTTGAGTTCTCCTTTTGTGTTCCAAACATGAGCTTCTCTCTACTGGTCCTC-TTA
Oa_MECP2_v1(P)      TTGGTTTTGAGTTCTCCTTTTGTGTTCCAAACATGAGCTTCTCTCTACTGGTCCTC-TTA
Oa_MECP2_v4(P)      TTGGTTTTGAGTTCTCCTTTTGTGTTCCAAACATGAGCTTCTCTCTACTGGTCCTC-TTA
Oa_MECP2_v2(P)      TTGGTTTTGAGTTCTCCTTTTGTGTTCCAAACATGAGCTTCTCTCTACTGGTCCTC-TTA
Oa_MECP2_v3(P)      TTGGTTTTGAGTTCTCCTTTTGTGTTCCAAACATGAGCTTCTCTCTACTGGTCCTC-TTA
Mm_MECP2_v1         --TGGTTTTATTTTTCCTTTTGTGTTCCAAACATGAGGTTTTCTCTACTGGTCCTCTTTA
Mm_MECP2_v2         --TGGTTTTATTTTTCCTTTTGTGTTCCAAACATGAGGTTTTCTCTACTGGTCCTCTTTA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TTGGTTTTTATTTCTCCTTTTGTGTTCCAAACATGAGGTTCTCTCTACTGGTCCTC-TTA
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ACTGTGGTGTTGAGGCTTCTATTTGTGTAATTTTCGGTGGGTGAAGGGAATTTTGCGAAG
Oa_MECP2_v1(P)      ACTGTGGTGTTGAGGCTTCTATTTGTGTAATTTTCGGTGGGTGAAGGGAATTTTGCAAAG
Oa_MECP2_v4(P)      ACTGTGGTGTTGAGGCTTCTATTTGTGTAATTTTCGGTGGGTGAAGGGAATTTTGCAAAG
Oa_MECP2_v2(P)      ACTGTGGTGTTGAGGCTTCTATTTGTGTAATTTTCGGTGGGTGAAGGGAATTTTGCAAAG
Oa_MECP2_v3(P)      ACTGTGGTGTTGAGGCTTCTATTTGTGTAATTTTCGGTGGGTGAAGGGAATTTTGCAAAG
Mm_MECP2_v1         ACTGTGGTGTTGAGGCTTCTATTTGTGTAATTTTTGGTGGGTGAAAGGAACTTTGCTAAG
Mm_MECP2_v2         ACTGTGGTGTTGAGGCTTCTATTTGTGTAATTTTTGGTGGGTGAAAGGAACTTTGCTAAG
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ACTGTGGTGTTGAGGCTTATATTTGTGTAATTTTTGGTGGGTGAAAGGAATTTTGCTAAG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TAAATCTCTTCTGTGTTTGAACTGAAGTCTGTATTGTAACCATGTTTAAAGTAATTGTTC
Oa_MECP2_v1(P)      TAAATCTCTTCTGTGTTTGAACTGAAGTCTGTATTGTAACCATGTTTAAAGTAATTGTTC
Oa_MECP2_v4(P)      TAAATCTCTTCTGTGTTTGAACTGAAGTCTGTATTGTAACCATGTTTAAAGTAATTGTTC
Oa_MECP2_v2(P)      TAAATCTCTTCTGTGTTTGAACTGAAGTCTGTATTGTAACCATGTTTAAAGTAATTGTTC
Oa_MECP2_v3(P)      TAAATCTCTTCTGTGTTTGAACTGAAGTCTGTATTGTAACCATGTTTAAAGTAATTGTTC
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Mm_MECP2_v1         TAAATCTCTTCTGTGTTTGAAATGAAGTCTGTATTGTAACTATGTTTAAAGTAATTGTTC
Mm_MECP2_v2         TAAATCTCTTCTGTGTTTGAAATGAAGTCTGTATTGTAACTATGTTTAAAGTAATTGTTC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TAAATCTCTTCTGTGTTTGAACTGAAGTCTGTATTGTAACTATGTTTAAAGTAATTGTTC
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         CAGAGACAAATGCTTCTAGACACCTTTTCTTTACCAACAAAAGAATTTGGAGGGAGGGGA
Oa_MECP2_v1(P)      CAGAGACAAATGCTTCTAGACACCTTTTCTTTACCAACAAAAGAATTCAGAGGGAGGGGA
Oa_MECP2_v4(P)      CAGAGACAAATGCTTCTAGACACCTTTTCTTTACCAACAAAAGAATTCAGAGGGAGGGGA
Oa_MECP2_v2(P)      CAGAGACAAATGCTTCTAGACACCTTTTCTTTACCAACAAAAGAATTCAGAGGGAGGGGA
Oa_MECP2_v3(P)      CAGAGACAAATGCTTCTAGACACCTTTTCTTTACCAACAAAAGAATTCAGAGGGAGGGGA
Mm_MECP2_v1         CAGAGACAAATGCTTCTAGGTACATTTTCATTACAAACAAAGCATTTG-AAGGGAGGGAA
Mm_MECP2_v2         CAGAGACAAATGCTTCTAGGTACATTTTCATTACAAACAAAGCATTTG-AAGGGAGGGAA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CAGAGACAAATATTTCTAGACACTTTTTCTTTACAAACAAAAGCATTCGGAGGGAGGGGG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         -TGGTAACCAGAAGGAGAGGGGCTGTCCTCTTGCCCCAGGAGGGGGAGAGCCAAAGACAG
Oa_MECP2_v1(P)      -TGGTAACCAGAAGGAGAGGGGCTGTCCTCTTGCCCCAGGAGGGAGAGAGCCAAAAACAG
Oa_MECP2_v4(P)      -TGGTAACCAGAAGGAGAGGGGCTGTCCTCTTGCCCCAGGAGGGAGAGAGCCAAAAACAG
Oa_MECP2_v2(P)      -TGGTAACCAGAAGGAGAGGGGCTGTCCTCTTGCCCCAGGAGGGAGAGAGCCAAAAACAG
Oa_MECP2_v3(P)      -TGGTAACCAGAAGGAGAGGGGCTGTCCTCTTGCCCCAGGAGGGAGAGAGCCAAAAACAG
Mm_MECP2_v1         GTGGTGAATAAGACAAGAGGGGC------------------------AATCTGAA---TT
Mm_MECP2_v2         GTGGTGAATAAGACAAGAGGGGC------------------------AATCTGAA---TT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ATGGTGACTGAGATGAGAGGGGA------------------------GAGCTGAACAGAT
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GACCCCCTGCCCAGATCAGCCAGAAGCCACCCAAAGAAGTG-------------ACACCT
Oa_MECP2_v1(P)      GACCCCCTGCCCAGATCAGCCAGAAGCCACCCAAAGAAGTG-------------ACACCT
Oa_MECP2_v4(P)      GACCCCCTGCCCAGATCAGCCAGAAGCCACCCAAAGAAGTG-------------ACACCT
Oa_MECP2_v2(P)      GACCCCCTGCCCAGATCAGCCAGAAGCCACCCAAAGAAGTG-------------ACACCT
Oa_MECP2_v3(P)      GACCCCCTGCCCAGATCAGCCAGAAGCCACCCAAAGAAGTG-------------ACACCT
Mm_MECP2_v1         GA-TCCCTGCCCAGATCAGCCAGAAGCTACCAAAAGTTAAG---CACTGGTTTTCCATTC
Mm_MECP2_v2         GA-TCCCTGCCCAGATCAGCCAGAAGCTACCAAAAGTTAAG---CACTGGTTTTCCATTC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GA-CCCCTGCCCAGATCAGCCAGAAGCCACCCAAAGCAGTGGAGCCCAGGAGTCCCACTC
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         AGAGCTGACAAAGTAAATAGCTGACATGCTGCCATTTGTGAAGTCAGAGCAAAACCAGGT
Oa_MECP2_v1(P)      AGAGCTGACAAAGTGAATAGCTGACGTGCTGCCATTTGTGAAGTCAGAGCAAAACCAGGT
Oa_MECP2_v4(P)      AGAGCTGACAAAGTGAATAGCTGACGTGCTGCCATTTGTGAAGTCAGAGCAAAACCAGGT
Oa_MECP2_v2(P)      AGAGCTGACAAAGTGAATAGCTGACGTGCTGCCATTTGTGAAGTCAGAGCAAAACCAGGT
Oa_MECP2_v3(P)      AGAGCTGACAAAGTGAATAGCTGACGTGCTGCCATTTGTGAAGTCAGAGCAAAACCAGGT
Mm_MECP2_v1         CAAGTCA--AGAGACTGAAGCTGATGTTTTGCCATTTTCAAAGTCAAAGCAAAACCAGCT
Mm_MECP2_v2         CAAGTCA--AGAGACTGAAGCTGATGTTTTGCCATTTTCAAAGTCAAAGCAAAACCAGCT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CAAGCCAGCAAGCCGAATAGCTGATGTGTTGCCACTTTCCAAGTCACTGCAAAACCAGGT
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TTTGGTCCACTCCC--------------------------------AGATTAGTAGCATCAG
Oa_MECP2_v1(P)      TTTGGTCCACTCCC--------------------------------AGATTAATAGCATCAG
Oa_MECP2_v4(P)      TTTGGTCCACTCCC--------------------------------AGATTAATAGCATCAG
Oa_MECP2_v2(P)      TTTGGTCCACTCCC--------------------------------AGATTAATAGCATCAG
Oa_MECP2_v3(P)      TTTGGTCCACTCCC--------------------------------AGATTAATAGCATCAG
Mm_MECP2_v1         TTTCCACCCAATGG---ATTCT----TTGCTTCTCCTTCCCAGATTATTACTACTGCTGT
Mm_MECP2_v2         TTTCCACCCAATGG---ATTCT----TTGCTTCTCCTTCCCAGATTATTACTACTGCTGT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TTTGTTCCGCCCAGTGGATTCTTGTTTTGCTTCCCCTCCCCCCGAGATTATTACCACCAT
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GATTATTTTTTTAAGGACAGACAAGGTTGACGTTCCTGCAAGGGGAGCCAG---------
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Oa_MECP2_v1(P)      GATTATCTTTTTAAGGACAGACAAGGTTGACGTTCCTACAAGGGGAGCCAGGAGGGGTGT
Oa_MECP2_v4(P)      GATTATCTTTTTAAGGACAGACAAGGTTGACGTTCCTACAAGGGGAGCCAGGAGGGGTGT
Oa_MECP2_v2(P)      GATTATCTTTTTAAGGACAGACAAGGTTGACGTTCCTACAAGGGGAGCCAGGAGGGGTGT
Oa_MECP2_v3(P)      GATTATCTTTTTAAGGACAGACAAGGTTGACGTTCCTACAAGGGGAGCCAGGAGGGGTGT
Mm_MECP2_v1         AATAATCTAGGAGTGCCAGGAGGGAAAGGAGTATTAACACAGAGCTGTGCTCACTGA---
Mm_MECP2_v2         AATAATCTAGGAGTGCCAGGAGGGAAAGGAGTATTAACACAGAGCTGTGCTCACTGA---
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CCCGTGCTTTTAAGGAAAGGCAAGATTGATGTTTCC-TTGAGGGGAGCCAGGAGGGG---
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------------CCACATCTCGGCGGGAGAAGGTCGGGGTGGGCCTGCGGGGCAAGGCTC
Oa_MECP2_v1(P)      GAGCGGAACCAACCACACCTCGGTGGGAGAAGGTCAGGGTGGGCCTGTGGGGCAAGGCTC
Oa_MECP2_v4(P)      GAGCGGAACCAACCACACCTCGGTGGGAGAAGGTCAGGGTGGGCCTGTGGGGCAAGGCTC
Oa_MECP2_v2(P)      GAGCGGAACCAACCACACCTCGGTGGGAGAAGGTCAGGGTGGGCCTGTGGGGCAAGGCTC
Oa_MECP2_v3(P)      GAGCGGAACCAACCACACCTCGGTGGGAGAAGGTCAGGGTGGGCCTGTGGGGCAAGGCTC
Mm_MECP2_v1         --------------------GTATGGAAAGGCTTGGTCTGAGTTTTCAGGAGGATGACCC
Mm_MECP2_v2         --------------------GTATGGAAAGGCTTGGTCTGAGTTTTCAGGAGGATGACCC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         --------------------ATGTGTGTGTGCAGAGCTGAAGAGCTGGGGAGAATGGGGC
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GGCCAGAGGGTGGGCATCTCCTTGGAGACCTCCACTGTGGCCACAGGTCAGGCTTGTGTG
Oa_MECP2_v1(P)      GGCCTGAAGGTGGGCGTCTCCCAGGAGACCTCCACTGTGGCCACAGGTCAGGCGTGTGTG
Oa_MECP2_v4(P)      GGCCTGAAGGTGGGCGTCTCCCAGGAGACCTCCACTGTGGCCACAGGTCAGGCGTGTGTG
Oa_MECP2_v2(P)      GGCCTGAAGGTGGGCGTCTCCCAGGAGACCTCCACTGTGGCCACAGGTCAGGCGTGTGTG
Oa_MECP2_v3(P)      GGCCTGAAGGTGGGCGTCTCCCAGGAGACCTCCACTGTGGCCACAGGTCAGGCGTGTGTG
Mm_MECP2_v1         ACTGTGGACATGGGGAGAAGACAGAA---------------GATAAATTAGCCGCTCCCT
Mm_MECP2_v2         ACTGTGGACATGGGGAGAAGACAGAA---------------GATAAATTAGCCGCTCCCT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TGGGCCCACCCAAGCAGGAGGCTGGGACGCTCTGCTGTGGGCACAGGTCAGGCTAATGTT
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GACAGGG------CATTATGATTCGGGGGGGG----------------------------
Oa_MECP2_v1(P)      GACATGG------CATTATGATTC---GGGGG----------------------------
Oa_MECP2_v4(P)      GACATGG------CATTATGATTC---GGGGG----------------------------
Oa_MECP2_v2(P)      GACATGG------CATTATGATTC---GGGGG----------------------------
Oa_MECP2_v3(P)      GACATGG------CATTATGATTC---GGGGG----------------------------
Mm_MECP2_v1         GCCTAAGATACCTCTTAATAGATAAGTCAAGGCCATGGACATTATTGTCTACAAGGCATG
Mm_MECP2_v2         GCCTAAGATACCTCTTAATAGATAAGTCAAGGCCATGGACATTATTGTCTACAAGGCATG
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GGCAGATGCAGCTCTTCCTGGACAGGCCAGGT-GGTG-GGCATTCTCTCTCCAAGGTGTG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ------GGGCATTACCGTTCGGGATACCATCATCA-AATCCACCCCGCCCCACAGTGCAC
Oa_MECP2_v1(P)      ------GGACATTACTGTTCGGGGTACCATCATCA-AATCCACCCCGCCCCACAGTGCAG
Oa_MECP2_v4(P)      ------GGACATTACTGTTCGGGGTACCATCATCA-AATCCACCCCGCCCCACAGTGCAG
Oa_MECP2_v2(P)      ------GGACATTACTGTTCGGGGTACCATCATCA-AATCCACCCCGCCCCACAGTGCAG
Oa_MECP2_v3(P)      ------GGACATTACTGTTCGGGGTACCATCATCA-AATCCACCCCGCCCCACAGTGCAG
Mm_MECP2_v1         TTTCAAAGACATGACCAGTCAGGACACTTCTGTCATACTCCATGTTGCCCCCTAGTACAC
Mm_MECP2_v2         TTTCAAAGACATGACCAGTCAGGACACTTCTGTCATACTCCATGTTGCCCCCTAGTACAC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CCCCGTGGGCATTACTGTTTAAGACACTTCCGTCACATCCCACCCCATCCTCCAGGGCTC
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GACACTAACATAACCTCTGGATT-------CCCCACTTTCCTGGATGAGGAGATGATGGT
Oa_MECP2_v1(P)      GACACTAATGTTACCTCTGGATT-------CCCCACTTTCCTGGACAAAGAGATGATGAT
Oa_MECP2_v4(P)      GACACTAATGTTACCTCTGGATT-------CCCCACTTTCCTGGACAAAGAGATGATGAT
Oa_MECP2_v2(P)      GACACTAATGTTACCTCTGGATT-------CCCCACTTTCCTGGACAAAGAGATGATGAT
Oa_MECP2_v3(P)      GACACTAATGTTACCTCTGGATT-------CCCCACTTTCCTGGACAAAGAGATGATGAT
Mm_MECP2_v1         AGTACTAATCTGATATCTCTGTT-------CCCGCCATGCCTGGGGGATAAAATGATAGC
Mm_MECP2_v2         AGTACTAATCTGATATCTCTGTT-------CCCGCCATGCCTGGGGGATAAAATGATAGC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         AA---CACTGTGACATCTCTATTCCCCACCCTCCCCTTCCCAGGGCAATAAAATGACCAT
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Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GGGGTCGGGGGGTGGTGCATGCCCTTGGCTGTCATCTGATCCCCAGTAAAATTTGGATGT
Oa_MECP2_v1(P)      GGGGTGGGG----GGTGCACACCCTTGGCTGTCATCTGATCCCCAGCAAAATTTGGATAT
Oa_MECP2_v4(P)      GGGGTGGGG----GGTGCACACCCTTGGCTGTCATCTGATCCCCAGCAAAATTTGGATAT
Oa_MECP2_v2(P)      GGGGTGGGG----GGTGCACACCCTTGGCTGTCATCTGATCCCCAGCAAAATTTGGATAT
Oa_MECP2_v3(P)      GGGGTGGGG----GGTGCACACCCTTGGCTGTCATCTGATCCCCAGCAAAATTTGGATAT
Mm_MECP2_v1         AGAGACTC-----CTTTCC-----TTCAATGTGATCTAATTCCCAACAAAATCTGGGCCT
Mm_MECP2_v2         AGAGACTC-----CTTTCC-----TTCAATGTGATCTAATTCCCAACAAAATCTGGGCCT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GGAGGGGG-----CTTGCACTCTCTTGGCTGTCACCCGATCGCCAGCAAAACTTAGATGT
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GAGAAACCACCCCCCTTCTCGTTTCATGGCAAAACCCTATCCTCTTGAGTAGCCGTTACC
Oa_MECP2_v1(P)      GAGAA---ACCCCCCTTCTCGTTTCATGGCAAAACCCGATCCTCTTGAGTAGCCATTACC
Oa_MECP2_v4(P)      GAGAA---ACCCCCCTTCTCGTTTCATGGCAAAACCCGATCCTCTTGAGTAGCCATTACC
Oa_MECP2_v2(P)      GAGAA---ACCCCCCTTCTCGTTTCATGGCAAAACCCGATCCTCTTGAGTAGCCATTACC
Oa_MECP2_v3(P)      GAGAA---ACCCCCCTTCTCGTTTCATGGCAAAACCCGATCCTCTTGAGTAGCCATTACC
Mm_MECP2_v1         GAGATACCA----CCTGT---TTCTATGGCA--AACATC--CTCAG-TAAAGTGTTATTC
Mm_MECP2_v2         GAGATACCA----CCTGT---TTCTATGGCA--AACATC--CTCAG-TAAAGTGTTATTC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         GAGAAAACC----CCTTCCCATTCCATGGCGAAAACATCTCCTTAGAAAAGCCATTACCC
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TCC-CAGACACTATTGAGGACTGACAAAACAGGGGTGGCCATGTGCTCCCTTAGCACCCG
Oa_MECP2_v1(P)      TCC-CAGACACTATTGAGGACTGACGAAACA-GGGTGGCCACGTGCTCCCTTAGCGCCCG
Oa_MECP2_v4(P)      TCC-CAGACACTATTGAGGACTGACGAAACA-GGGTGGCCACGTGCTCCCTTAGCGCCCG
Oa_MECP2_v2(P)      TCC-CAGACACTATTGAGGACTGACGAAACA-GGGTGGCCACGTGCTCCCTTAGCGCCCG
Oa_MECP2_v3(P)      TCC-CAGACACTATTGAGGACTGACGAAACA-GGGTGGCCACGTGCTCCCTTAGCGCCCG
Mm_MECP2_v1         TCATTGCAGATTGTTCCAGCCTAATGTAAGAGGAACAGAGCAGTGTTCCCTTGGAGCCTC
Mm_MECP2_v2         TCATTGCAGATTGTTCCAGCCTAATGTAAGAGGAACAGAGCAGTGTTCCCTTGGAGCCTC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TCATTAGGCATGGTTTTGGGCTCCCAAAACACCTG----ACAGCCCCTCCCTCCTCTGAG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         GGGT--CGCCCCCTCTTCGAGGACAGTGCTGACCATTTGGGAATGGGGCTTAGGAGCGAG
Oa_MECP2_v1(P)      GGGTCCCCCCCCCCCTTCGAGGACAGTGCTGACCATTCGGGCATGGGGCTTAGGAATGAG
Oa_MECP2_v4(P)      GGGTCCCCCCCCCCCTTCGAGGACAGTGCTGACCATTCGGGCATGGGGCTTAGGAATGAG
Oa_MECP2_v2(P)      GGGTCCCCCCCCCCCTTCGAGGACAGTGCTGACCATTCGGGCATGGGGCTTAGGAATGAG
Oa_MECP2_v3(P)      GGGTCCCCCCCCCCCTTCGAGGACAGTGCTGACCATTCGGGCATGGGGCTTAGGAATGAG
Mm_MECP2_v1         ATGTGGACAGTTCT-------ACCTGTAGTGACCAGTTGGCTATAGTAGTTATTAGCTGG
Mm_MECP2_v2         ATGTGGACAGTTCT-------ACCTGTAGTGACCAGTTGGCTATAGTAGTTATTAGCTGG
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         AGGCGGAGAGTGCT-------GACTGTAGTGACCATTG-CATGCCGGGTGCAGCATCTGG
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         AAGAACCAAGCAGGGTCACCGCCCCCTCCTGAGTCGC-----------------------
Oa_MECP2_v1(P)      AAGAACCAAGCAGGATCACCGCCCCCTCCTGAGTCGC-----------------------
Oa_MECP2_v4(P)      AAGAACCAAGCAGGATCACCGCCCCCTCCTGAGTCGC-----------------------
Oa_MECP2_v2(P)      AAGAACCAAGCAGGATCACCGCCCCCTCCTGAGTCGC-----------------------
Oa_MECP2_v3(P)      AAGAACCAAGCAGGATCACCGCCCCCTCCTGAGTCGC-----------------------
Mm_MECP2_v1         AACAACCAGACAGGGTACATGCCCCCTCCAAAATCCATGTTGTACTCCCCTCTGCCAGCC
Mm_MECP2_v2         AACAACCAGACAGGGTACATGCCCCCTCCAAAATCCATGTTGTACTCCCCTCTGCCAGCC
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         AAGAGCTAGGCAGGGTGTCTGCCCCCTCCTGAGTTGAAGTCATGCTCCCCTGTGCCAGCC
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         -------------------------------AGGGACCCTGGTCACCCTGTGCAG-AGGG
Oa_MECP2_v1(P)      -------------------------------AGGGACCCTGGTCACCCTGTGCAG-AGGG
Oa_MECP2_v4(P)      -------------------------------AGGGACCCTGGTCACCCTGTGCAG-AGGG
Oa_MECP2_v2(P)      -------------------------------AGGGACCCTGGTCACCCTGTGCAG-AGGG
Oa_MECP2_v3(P)      -------------------------------AGGGACCCTGGTCACCCTGTGCAG-AGGG
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Mm_MECP2_v1         AGGGGGGGTGA-GATCTGTAGAATAGTGCAGCCAGTGACAAGCCACCTT---------GT
Mm_MECP2_v2         AGGGGGGGTGA-GATCTGTAGAATAGTGCAGCCAGTGACAAGCCACCTT---------GT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CAGAGGCCGAGAGCTATGGACAGCATTGCC-AGTAACACAGGCCACCCTGTGCAGAAGGG
Hs_MECP2_v2         ------------------------------------------------------------


Bt_MECP2_v1         AGCTGGCTCCAGCCCAGGAGGAAA---AGGGCTGGAAAAGTGTGTGTGGGGTGCGGGGAG
Oa_MECP2_v1(P)      AGCAGGCTCCAGCCCAGGAGGAAA---AGGGCTGGAAAAGTGTGTATGGGGTGAGGGGAG
Oa_MECP2_v4(P)      AGCAGGCTCCAGCCCAGGAGGAAA---AGGGCTGGAAAAGTGTGTATGGGGTGAGGGGAG
Oa_MECP2_v2(P)      AGCAGGCTCCAGCCCAGGAGGAAA---AGGGCTGGAAAAGTGTGTATGGGGTGAGGGGAG
Oa_MECP2_v3(P)      AGCAGGCTCCAGCCCAGGAGGAAA---AGGGCTGGAAAAGTGTGTATGGGGTGAGGGGAG
Mm_MECP2_v1         GTTTGTCACCAGCTCAAAAACTCATCTAAGGTTGGGAGCAGGCAGACAAGGCAGAGAGAA
Mm_MECP2_v2         GTTTGTCACCAGCTCAAAAACTCATCTAAGGTTGGGAGCAGGCAGACAAGGCAGAGAGAA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         AGCTGGCTCCAGCCTGGAAACCTGTCTGAGGTTGGGAGAGGTG-----CACTTGGGGCAC
Hs_MECP2_v2         ------------------------------------------------------------


Bt_MECP2_v1         TCACCCAGGACAGA-----CTTGGCTGGAGATGATCTCCAAAAGCCCTCTATCGCATTCA
Oa_MECP2_v1(P)      TCACCCAGGACAGA-----CTTGGCTGGAGATGATCTCCAAAAGCCCTCTATCGCATTCA
Oa_MECP2_v4(P)      TCACCCAGGACAGA-----CTTGGCTGGAGATGATCTCCAAAAGCCCTCTATCGCATTCA
Oa_MECP2_v2(P)      TCACCCAGGACAGA-----CTTGGCTGGAGATGATCTCCAAAAGCCCTCTATCGCATTCA
Oa_MECP2_v3(P)      TCACCCAGGACAGA-----CTTGGCTGGAGATGATCTCCAAAAGCCCTCTATCGCATTCA
Mm_MECP2_v1         AGATCCAGGACAGACCTAGCTGGGCTGGAGGGG-TCTTGAAAAGCCCTCTGTCGTATTCA
Mm_MECP2_v2         AGATCCAGGACAGACCTAGCTGGGCTGGAGGGG-TCTTGAAAAGCCCTCTGTCGTATTCA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         AGGGAGAGGCCGGGACACACTTAGCTGGAGATG-TCTCTAAAAGCCCTGTATCGTATTCA
Hs_MECP2_v2         ------------------------------------------------------------


Bt_MECP2_v1         CCTTCAGTTTTTGTGTTTTGGGACAATTACTTTAGAAAACTTAAGTAGGTCGTTTTAAAA
Oa_MECP2_v1(P)      CCTTCAGTTTTTGTGTTTTGGGACAATTACTTTAGAAAACTTAAGTAGATCGTTTTAAAA
Oa_MECP2_v4(P)      CCTTCAGTTTTTGTGTTTTGGGACAATTACTTTAGAAAACTTAAGTAGATCGTTTTAAAA
Oa_MECP2_v2(P)      CCTTCAGTTTTTGTGTTTTGGGACAATTACTTTAGAAAACTTAAGTAGATCGTTTTAAAA
Oa_MECP2_v3(P)      CCTTCAGTTTTTGTGTTTTGGGACAATTACTTTAGAAAACTTAAGTAGATCGTTTTAAAA
Mm_MECP2_v1         CCTTCAGTTTTTGTGCTTTGGGACAATTACTTTAGAAAA--TAAGTAGGTCGTTTTAAAA
Mm_MECP2_v2         CCTTCAGTTTTTGTGCTTTGGGACAATTACTTTAGAAAA--TAAGTAGGTCGTTTTAAAA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CCTTCAGTTTTTGTGTTTTGGGACAATTACTTTAGAAAA--TAAGTAGGTCGTTTTAAAA
Hs_MECP2_v2         ------------------------------------------------------------


Bt_MECP2_v1         AC--AAAAAATATTGATTGCTTTTTTGTAGTGTTCAAA--AAAAGGTTCTTTGTGTATAG
Oa_MECP2_v1(P)      ACAAAAAAAATATTGATTGCTTTTTTGTAGTGTTCAAA--AAAAGGTTCTTTGTGTATAG
Oa_MECP2_v4(P)      ACAAAAAAAATATTGATTGCTTTTTTGTAGTGTTCAAA--AAAAGGTTCTTTGTGTATAG
Oa_MECP2_v2(P)      ACAAAAAAAATATTGATTGCTTTTTTGTAGTGTTCAAA--AAAAGGTTCTTTGTGTATAG
Oa_MECP2_v3(P)      ACAAAAAAAATATTGATTGCTTTTTTGTAGTGTTCAAA--AAAAGGTTCTTTGTGTATAG
Mm_MECP2_v1         AC--AAAATA--TTGATTGCTTTTTTGTAGTGTTCAAAACAAAAGGTTCTTTGTGTATAG
Mm_MECP2_v2         AC--AAAATA--TTGATTGCTTTTTTGTAGTGTTCAAAACAAAAGGTTCTTTGTGTATAG
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         AC--AAAAATTATTGATTGCTTTTTTGTAGTGT-TCAGAAAAAAGGTTCTTTGTGTATAG
Hs_MECP2_v2         ------------------------------------------------------------


Bt_MECP2_v1         CCAAATGACTGAAAGCACTGATATATTTAAAAACAAAAGGCAATTTATTAAGGAAATTTG
Oa_MECP2_v1(P)      CCAAATGACTGAAAGCACTGATATATTTAAAAACAAAAGGCAATTTATTAAGGAAATTTG
Oa_MECP2_v4(P)      CCAAATGACTGAAAGCACTGATATATTTAAAAACAAAAGGCAATTTATTAAGGAAATTTG
Oa_MECP2_v2(P)      CCAAATGACTGAAAGCACTGATATATTTAAAAACAAAAGGCAATTTATTAAGGAAATTTG
Oa_MECP2_v3(P)      CCAAATGACTGAAAGCACTGATATATTTAAAAACAAAAGGCAATTTATTAAGGAAATTTG
Mm_MECP2_v1         CCAAATGACTGAAAGCACTGATATATTTAAAAACAAAAGGCAATTTATTAAGGAAATTTG
Mm_MECP2_v2         CCAAATGACTGAAAGCACTGATATATTTAAAAACAAAAGGCAATTTATTAAGGAAATTTG
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         CCAAATGACTGAAAGCACTGATATATTTAAAAACAAAAGGCAATTTATTAAGGAAATTTG
Hs_MECP2_v2         ------------------------------------------------------------


Bt_MECP2_v1         TACCATTTCAGTAAACCTGTCTGAATGTACCTGTATACGTTTCAAAAACACCCCC----C
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Oa_MECP2_v1(P)      TACCATTTCAGTAAACCTGTCTGAATGTACCTGTATACGTTTC-AAAACACCCCC----C
Oa_MECP2_v4(P)      TACCATTTCAGTAAACCTGTCTGAATGTACCTGTATACGTTTC-AAAACACCCCC----C
Oa_MECP2_v2(P)      TACCATTTCAGTAAACCTGTCTGAATGTACCTGTATACGTTTC-AAAACACCCCC----C
Oa_MECP2_v3(P)      TACCATTTCAGTAAACCTGTCTGAATGTACCTGTATACGTTTC-AAAACACCCCC----C
Mm_MECP2_v1         TACCATTTCAGTAAACCTGTCTGAATGTACCTGTATACGTTTCAAAAACACACCC----C
Mm_MECP2_v2         TACCATTTCAGTAAACCTGTCTGAATGTACCTGTATACGTTTCAAAAACACACCC----C
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         TACCATTTCAGTAAACCTGTCTGAATGTACCTGTATACGTTTCAAAAACACCCCCCCCCC
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ACTGAATCCCTGTAACCTATTTATTATATAAAGAGTTTGCCTTATAAATTTACATAAAAA
Oa_MECP2_v1(P)      ACTGAATCCCTGTAACCTATTTATTATATAAAGAGTTTGCCTTATAAATTTACATAAAAA
Oa_MECP2_v4(P)      ACTGAATCCCTGTAACCTATTTATTATATAAAGAGTTTGCCTTATAAATTTACATAAAAA
Oa_MECP2_v2(P)      ACTGAATCCCTGTAACCTATTTATTATATAAAGAGTTTGCCTTATAAATTTACATAAAAA
Oa_MECP2_v3(P)      ACTGAATCCCTGTAACCTATTTATTATATAAAGAGTTTGCCTTATAAATTTACATAAAAA
Mm_MECP2_v1         ACTGAACCCCTGTAACCTATTTATTATATAAAGAGTTTGCCTTATAAATTTACATAAAAA
Mm_MECP2_v2         ACTGAACCCCTGTAACCTATTTATTATATAAAGAGTTTGCCTTATAAATTTACATAAAAA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ACTGAATCCCTGTAACCTATTTATTATATAAAGAGTTTGCCTTATAAATTT---------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TGTCCGTTTGTGTCTTTTGTTGTAAAACCAAGTGATTTTTTCATAAGGTTCTTTTACTAT
Oa_MECP2_v1(P)      TGTCCGTTTGTGTCTTTTGTTGTAAAACCAAGTGATTTTTTCATAAGGTTCTTTTACTAT
Oa_MECP2_v4(P)      TGTCCGTTTGTGTCTTTTGTTGTAAAACCAAGTGATTTTTTCATAAGGTTCTTTTACTAT
Oa_MECP2_v2(P)      TGTCCGTTTGTGTCTTTTGTTGTAAAACCAAGTGATTTTTTCATAAGGTTCTTTTACTAT
Oa_MECP2_v3(P)      TGTCCGTTTGTGTCTTTTGTTGTAAAACCAAGTGATTTTTTCATAAGGTTCTTTTACTAT
Mm_MECP2_v1         TGTCCGTTTGTGTCTTTTGTTGTAAAATCAAGTGG-TTTTTCATAAGGTTCTTTTACTAT
Mm_MECP2_v2         TGTCCGTTTGTGTCTTTTGTTGTAAAATCAAGTGG-TTTTTCATAAGGTTCTTTTACTAT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         TTGAAAAGATGGGCAGCACGCAGTTTTATTTTATTTTTGTAAGTTTTTTAATACGTGTGA
Oa_MECP2_v1(P)      TTGAAAAGATGGGCAGCACGCAGTTTTATTTTATTTTTGTAAGTTTTTTAATACGTGTGA
Oa_MECP2_v4(P)      TTGAAAAGATGGGCAGCACGCAGTTTTATTTTATTTTTGTAAGTTTTTTAATACGTGTGA
Oa_MECP2_v2(P)      TTGAAAAGATGGGCAGCACGCAGTTTTATTTTATTTTTGTAAGTTTTTTAATACGTGTGA
Oa_MECP2_v3(P)      TTGAAAAGATGGGCAGCACGCAGTTTTATTTTATTTTTGTAAGTTTTTTAATACGTGTGA
Mm_MECP2_v1         TTGAAAAGATGGGCAGCACGCGGTTTCATTTTATTTTTGTAAGTTTTTTAATACATGTGA
Mm_MECP2_v2         TTGAAAAGATGGGCAGCACGCGGTTTCATTTTATTTTTGTAAGTTTTTTAATACATGTGA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         AAGCCAAGAATACTCAGCATGCCTTTCTAAGTGACGCGTTCGCACCTTTTGTTGGGAAGT
Oa_MECP2_v1(P)      AAGCCAAGAATACTCAGCATGCCTTTCTAAGTGACGCGTTCGCACCTTTTGTTGGGAAGT
Oa_MECP2_v4(P)      AAGCCAAGAATACTCAGCATGCCTTTCTAAGTGACGCGTTCGCACCTTTTGTTGGGAAGT
Oa_MECP2_v2(P)      AAGCCAAGAATACTCAGCATGCCTTTCTAAGTGACGCGTTCGCACCTTTTGTTGGGAAGT
Oa_MECP2_v3(P)      AAGCCAAGAATACTCAGCATGCCTTTCTAAGTGACGCGTTCGCACCTTTTGTTGGGAAGT
Mm_MECP2_v1         AAGCAAAGAATACTCAGCATGCCTTTCTAAGTGATGCGTTTGCACCTTTTGTTGGGAAGT
Mm_MECP2_v2         AAGCAAAGAATACTCAGCATGCCTTTCTAAGTGATGCGTTTGCACCTTTTGTTGGGAAGT
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
Hs_MECP2_v2         ------------------------------------------------------------

Bt_MECP2_v1         ACTGTATCCTGTGCTGTTAGCATTCTCGATAAATCTCTCTGTGAAAGTGA----------
Oa_MECP2_v1(P)      ACTGTATCCTGTGCTGTTAGCATTCTCGATAAATCTCTCTGTGAAAGTGA----------
Oa_MECP2_v4(P)      ACTGTATCCTGTGCTGTTAGCATTCTCGATAAATCTCTCTGTGAAAGTGA----------
Oa_MECP2_v2(P)      ACTGTATCCTGTGCTGTTAGCATTCTCGATAAATCTCTCTGTGAAAGTGA----------
Oa_MECP2_v3(P)      ACTGTATCCTGTGCTGTTAGCATTCTCGATAAATCTCTCTGTGAAAGTGA----------
Mm_MECP2_v1         ACTGTATCCTGTGCTGTTAGCATTCTCGATAAATCTCTCTGTGAAAGTGAAAAAAAAAAA
Mm_MECP2_v2         ACTGTATCCTGTGCTGTTAGCATTCTCGATAAATCTCTCTGTGAAAGTGAAAAAAAAAAA
Hs_MECP2_v3         ------------------------------------------------------------
Hs_MECP2_v1         ------------------------------------------------------------
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Hs_MECP2_v2          ------------------------------------------------------------

Bt_MECP2_v1          -------
Oa_MECP2_v1(P)       -------
Oa_MECP2_v4(P)       -------
Oa_MECP2_v2(P)       -------
Oa_MECP2_v3(P)       -------
Mm_MECP2_v1          AAAAAAA
Mm_MECP2_v2          AAAAAAA
Hs_MECP2_v3          -------
Hs_MECP2_v1          -------
Hs_MECP2_v2          -------
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Probes designed

PROBE #	PROBE (5'-> 3')	PROBE POSITION	PERCENT GC
1	tcaaaggtttgtccttcagg	26	45.00%
2	ccttcttcacctttttgaac	47	40.00%
3	cctctttgtcttctttctta	68	35.00%
4	cttctgaggtctctgctttg	146	50.00%
5	gacgcagaagcttctggcac	186	60.00%
6	gatcacgaatgatggagcgc	218	55.00%
7	agagtggggtcatcgtacat	246	50.00%
8	gatttcctttgcttaagctt	285	35.00%
9	tacacatcatacttcccagc	315	45.00%
10	tttccctggggattgatcaa	336	45.00%
11	ctccactttagagcgaaagg	358	50.00%
12	ctacctttttcgaagtacgca	383	45.00%
13	aaatcattagggtccaggga	411	45.00%
14	ttcttaggtggtttctgttc	471	40.00%
15	ctggagctttgggagatttg	494	50.00%
16	caggacttttctccagaacc	599	50.00%
17	gaaaggcatcttgacgagca	625	50.00%
18	cttgatgaccataacctggg	694	50.00%
19	cgtttcttgggaatggcctg	750	55.00%
20	cttcacggctttcttttgg	814	45.00%
21	cacggaccggatagacgact	835	60.00%
22	ttgcgcttcttgatggggag	867	55.00%
23	atcttctcctctttgcagac	1182	45.00%
24	tgtttgtacttttctgtggc	1284	40.00%
25	tggcatggaggatgagacaa	1330	50.00%
26	aagtcagctaactctctcgg	1393	50.00%
27	ttggtttgctttgcaatccg	1422	45.00%
28	caacagctgccttattctt	1443	40.00%
29	cctacccataaggagaagag	1464	50.00%
30	atcgggaagctttgtcagag	1485	50.00%
31	agccacgaaactctaagttt	1540	40.00%
32	aatgctccaactactcccac	1565	50.00%
33	ctgtgcttgtcgataagaaa	1596	40.00%
34	ctggttaggtcttcaacctg	1617	50.00%
35	agtgcaaagctacttctggc	1638	50.00%

36	tgaaggagcctagtttagaa	1659	40.00%
37	agtatctgcagcaagccttg	1680	50.00%
38	gcaacagcttgtctggtcag	1701	55.00%
39	tgcaggcacaccctaagaag	1726	55.00%
40	tagtgaccacgtaggggac	1761	60.00%
41	caggagtgtcttctcaagtg	1792	50.00%
42	gagaggagagctgagactgg	1832	60.00%