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(12) **United States Patent**
Alisch et al.

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(45) **Date of Patent: Jan. 3, 2023**

(54) **BLOOD DNA METHYLATION BIOMARKER DIAGNOSTIC TEST FOR ANXIETY AND DEPRESSIVE DISORDERS**

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(73) Assignees: **Wisconsin Alumni Research Foundation;**, Madison, WI (US); **Emory University**, Atlanta, GA (US)

(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 208 days.

(21) Appl. No.: **16/898,897**

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(65) **Prior Publication Data**

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Related U.S. Application Data

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(51) **Int. Cl.**
C12Q 1/686 (2018.01)
C12Q 1/6883 (2018.01)

(52) **U.S. Cl.**
CPC ***C12Q 1/686*** (2013.01); ***C12Q 1/6883*** (2013.01); *C12Q 2600/154* (2013.01)

(58) **Field of Classification Search**
CPC C12Q 2600/154
See application file for complete search history.

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(57) **ABSTRACT**

A method for diagnosing or giving a prognosis for anxious temperament or trait-like anxiety in a human or non-human primate subject comprising the steps of (a) obtaining DNA from a blood or saliva sample from the subject and (b) quantifying methylation in a set of differentially methylated regions (DMRs) selected from SEQ ID NOs:1-75 or DMR-associated genes selected from DIP2C, GRB10, INPP5A, C17ORF97, PDXK, CACNA2D4, TRAPPC9, CRTC1, MEGF6, HIVEP3, OPCML, PITPNM2, ZFPM1, RAP1GAP2, NFATC1, RNF126, FSTL3, GNAS, SH3BP2, NEURL1B, MAD1L1, HSPA12B, IGF2, PEG10, PEG3, SLC16A3, SYTL1, and ZIM2, wherein a significant change methylation indicates the present of anxious temperament or trait-like anxiety, wherein the change is relative to DNA from a second human or non-human primate who does not have anxious temperament or trait-like anxiety. Also disclosed is a biomarker panel of DMR and DMR-associated genes for the diagnosis or prognosis of anxious temperament or trait-like anxiety.

11 Claims, 33 Drawing Sheets
(32 of 33 Drawing Sheet(s) Filed in Color)

Specification includes a Sequence Listing.

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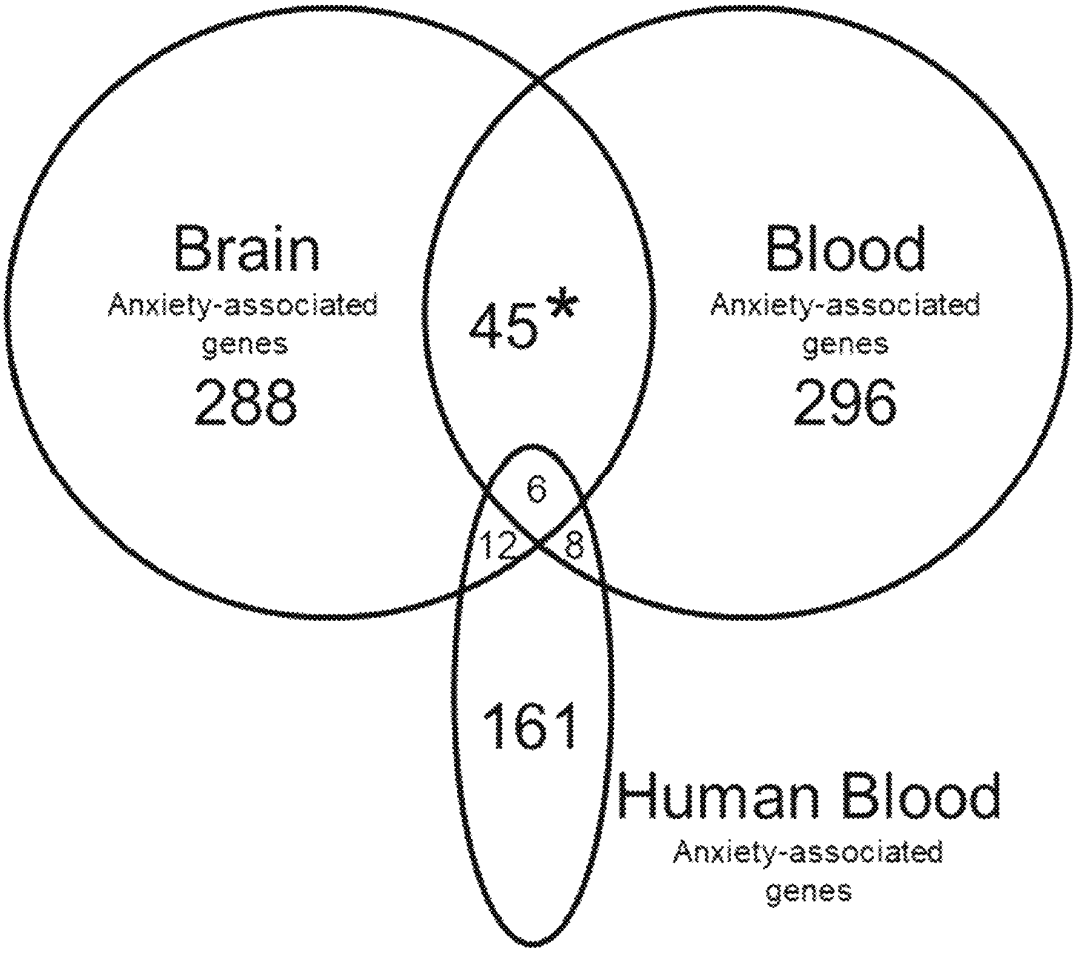

Brain
Anxiety-associated genes
288
45*
Blood
Anxiety-associated genes
296
6
12
8
161
Human Blood
Anxiety-associated genes
*P-value < 0.05

FIG. 1

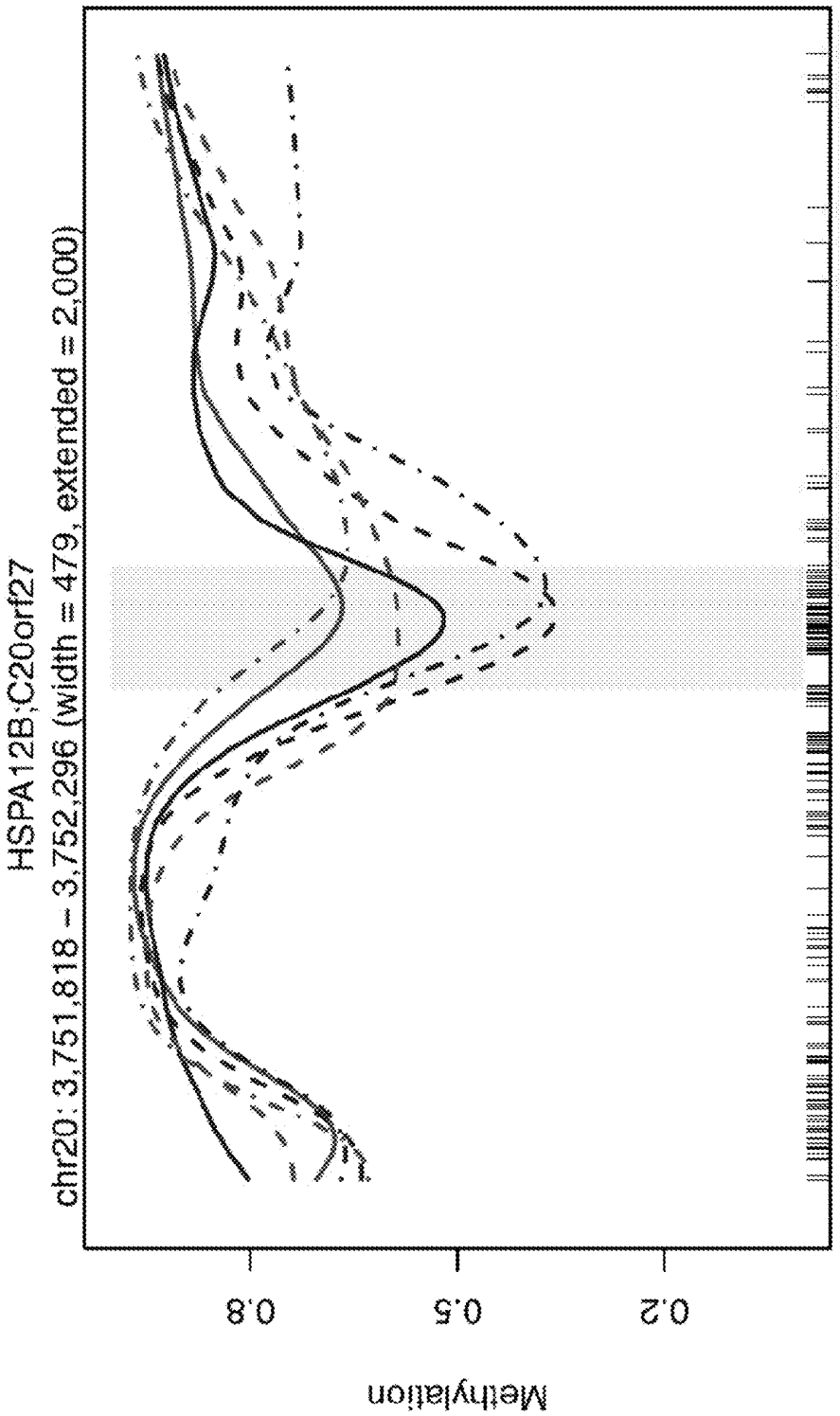
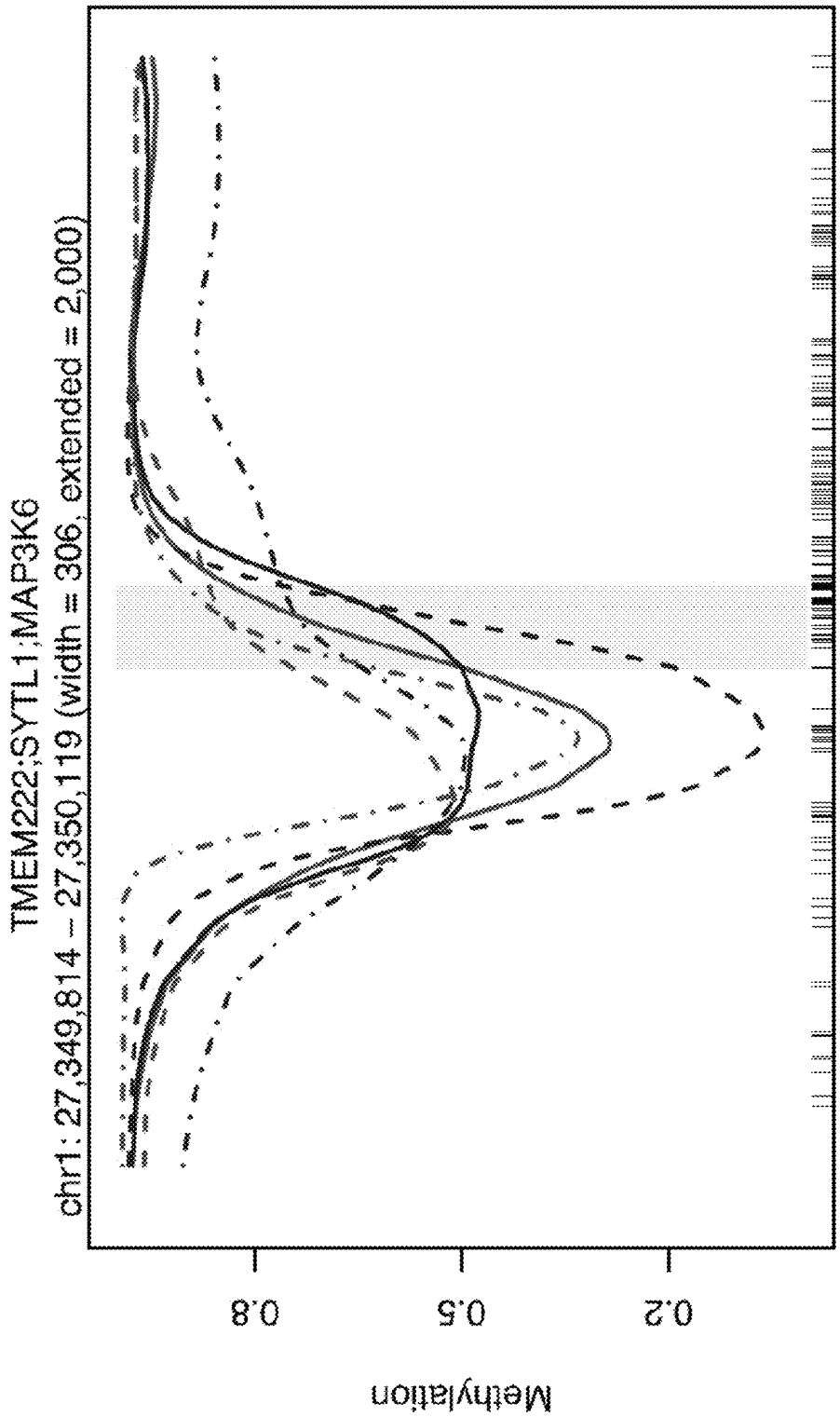

HSPA12B;C20orf27
chr20: 3,751,818 – 3,752,296 (width = 479, extended = 2,000)
Methylation
0.2
0.5
0.8

FIG. 2



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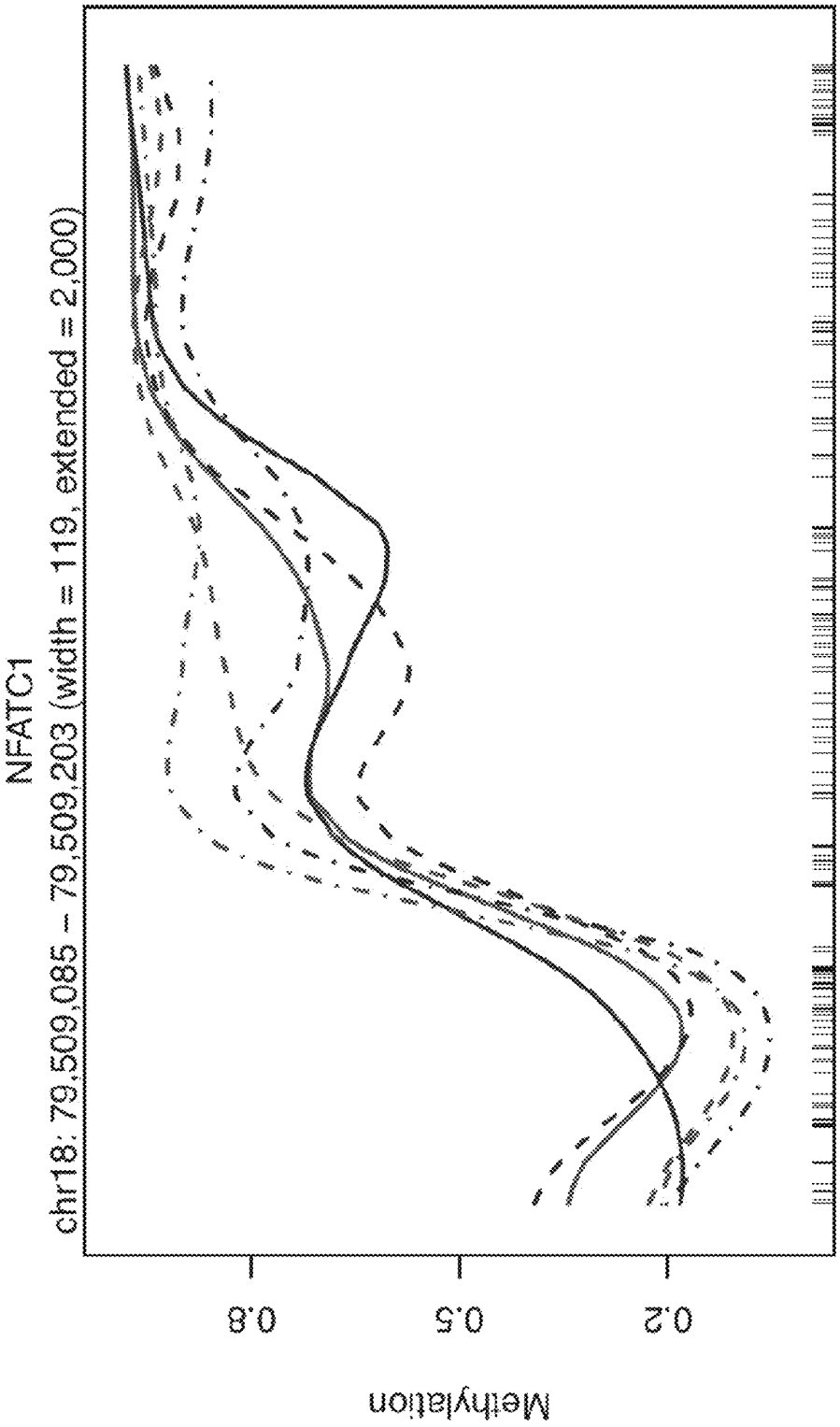

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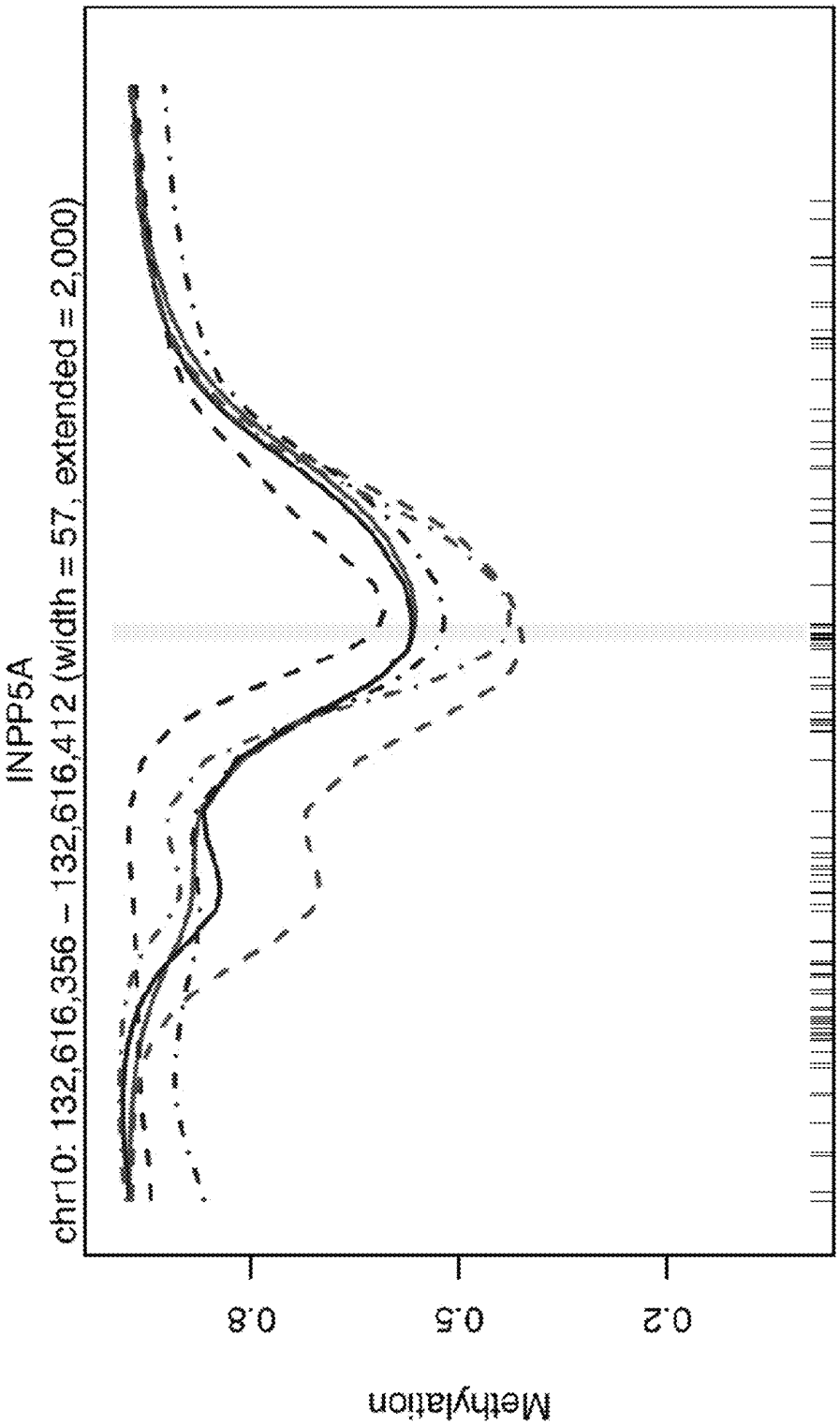

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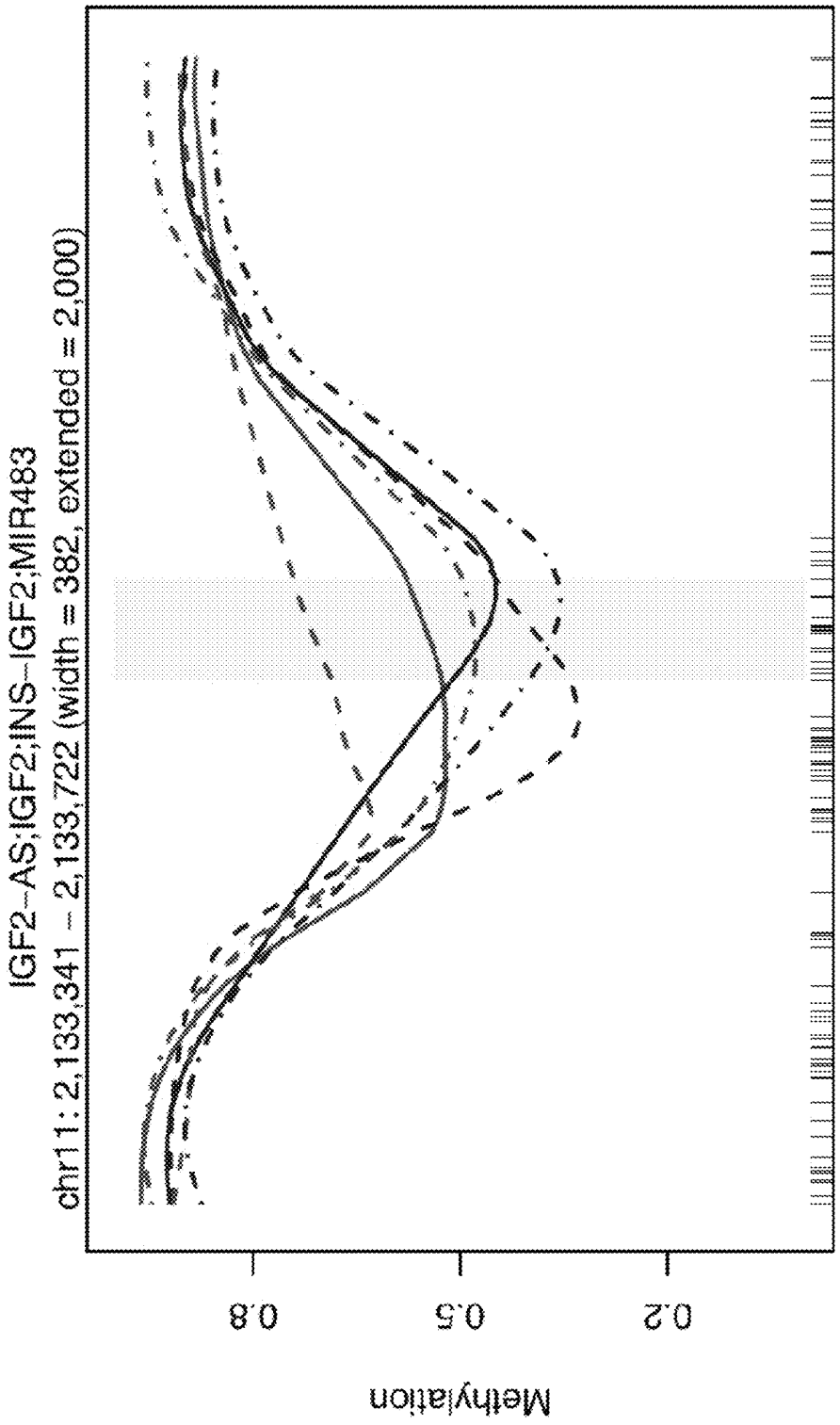

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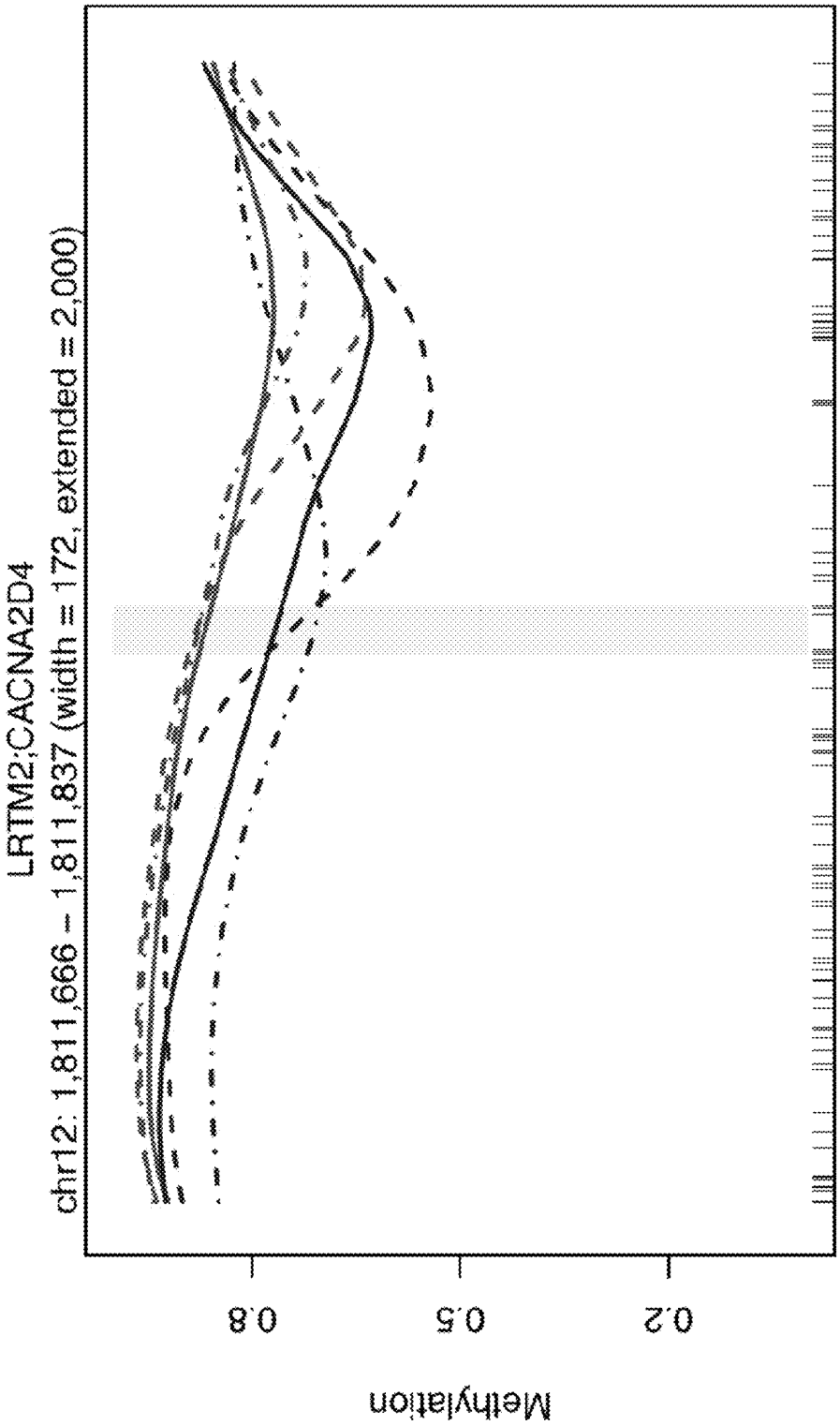

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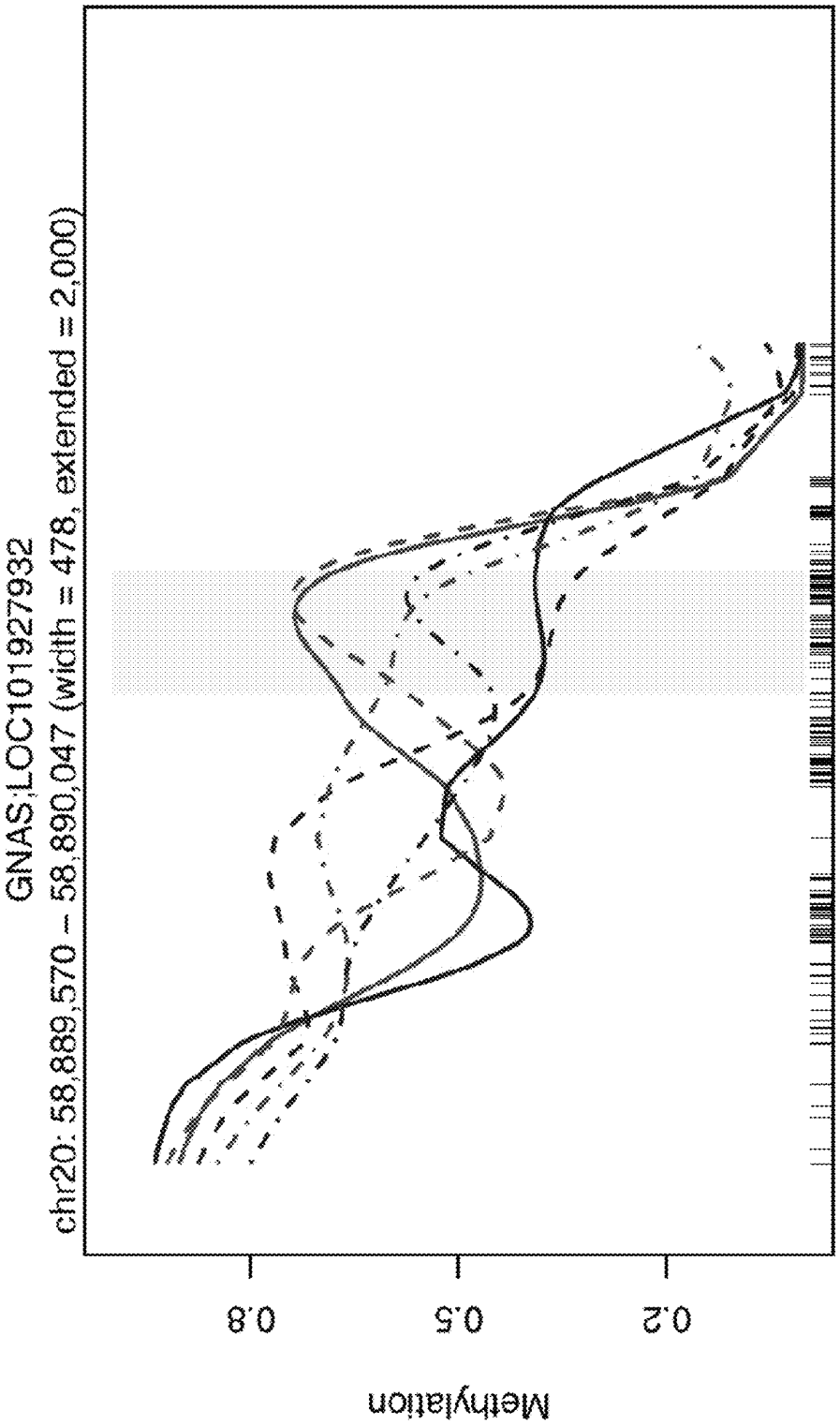

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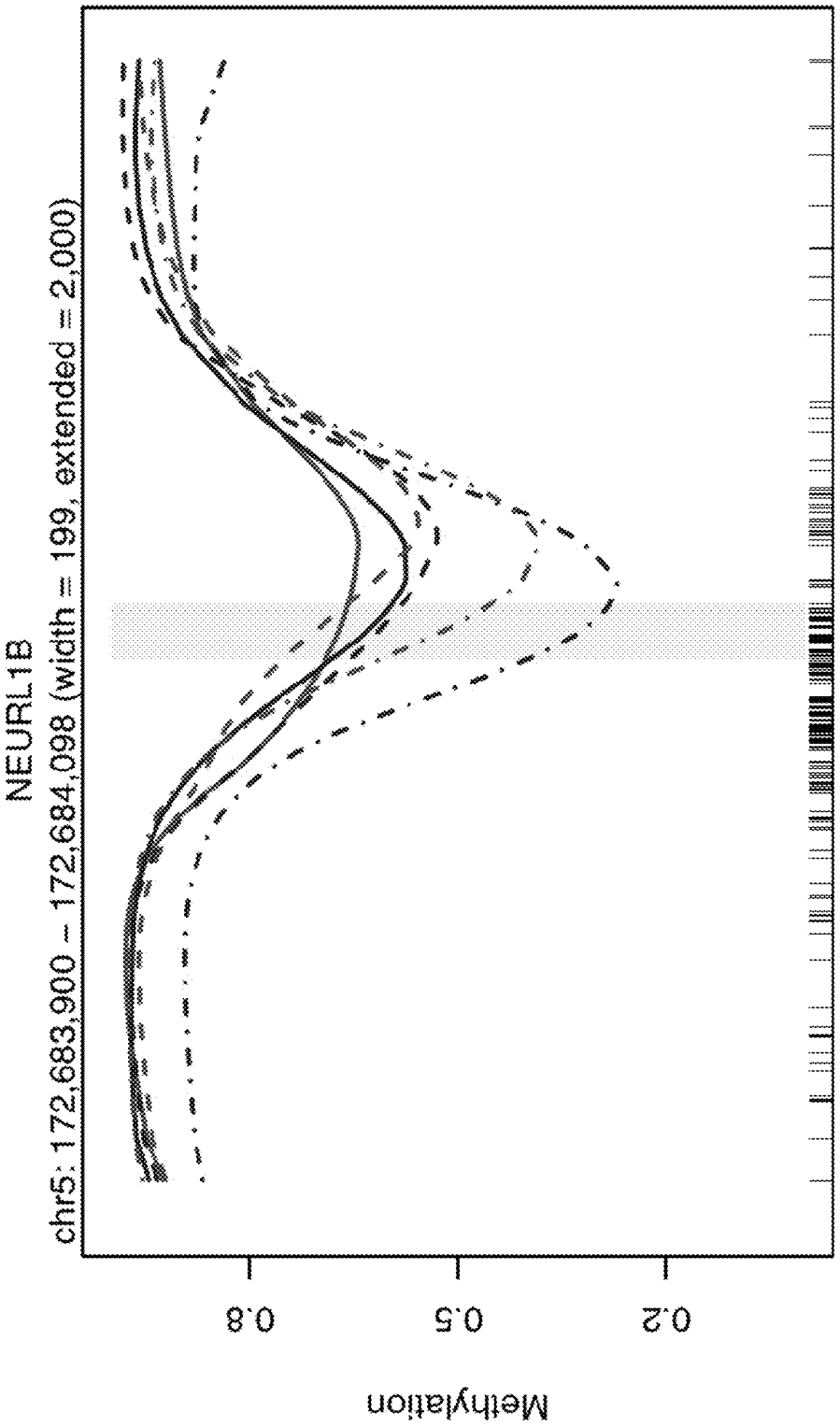

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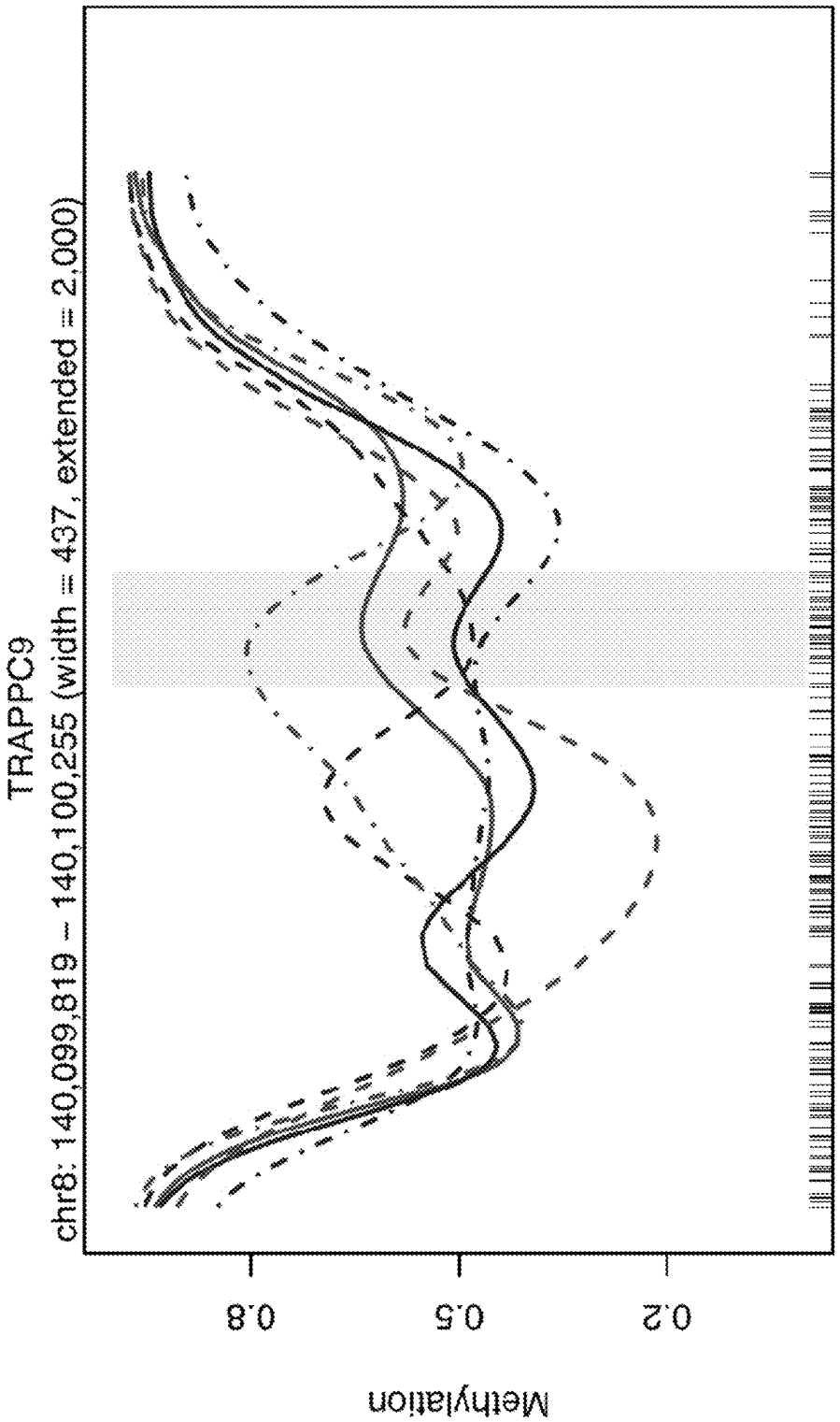

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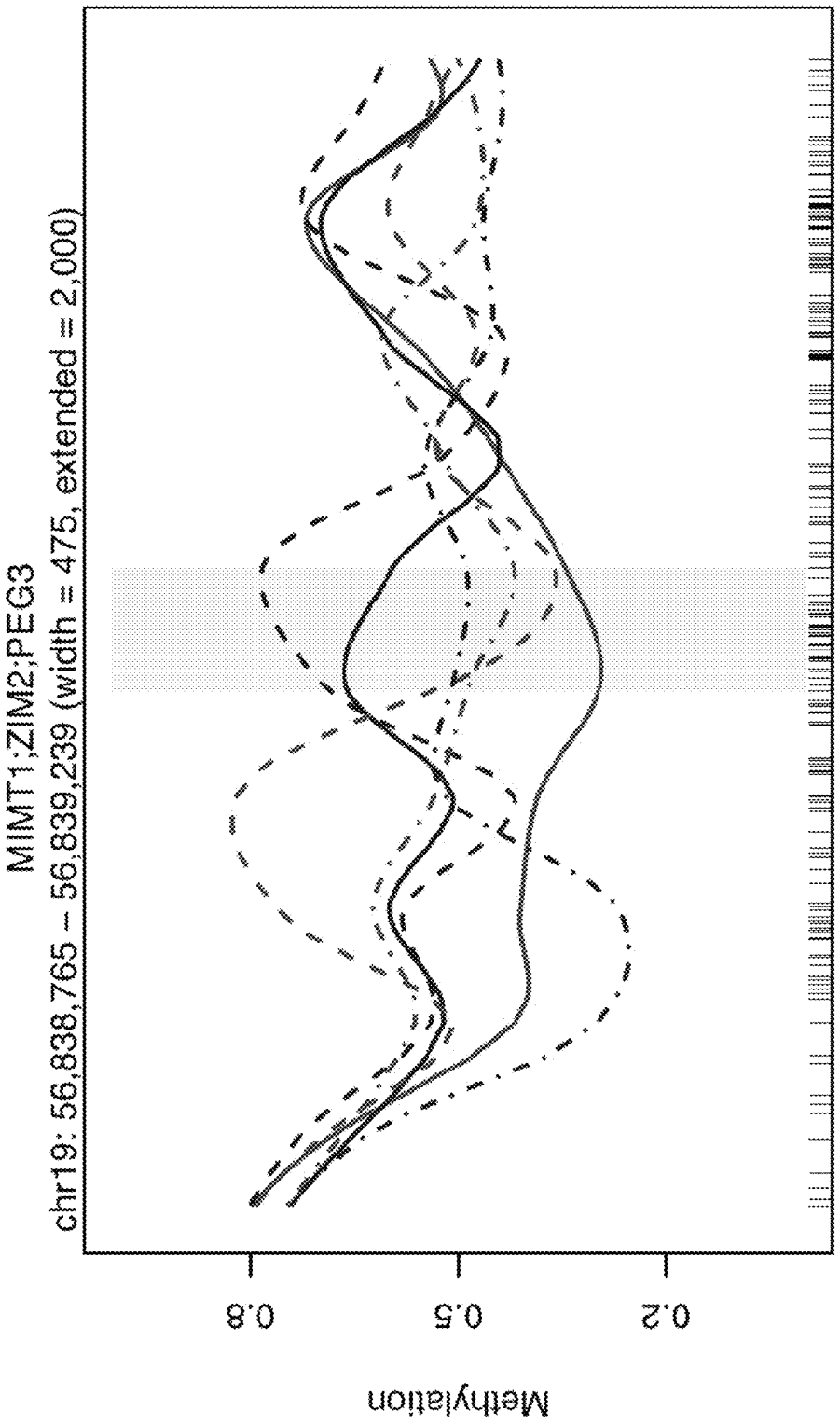

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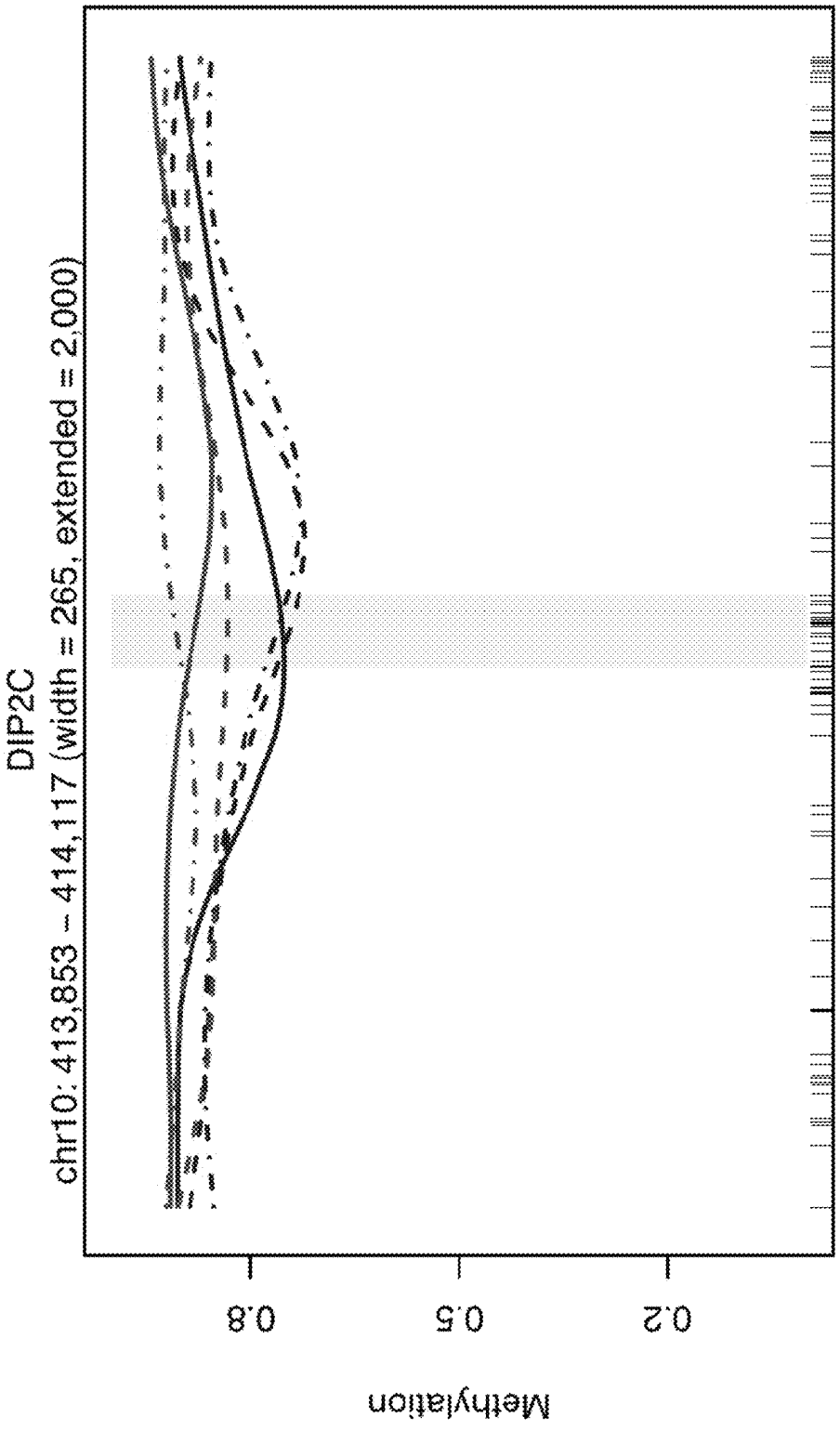

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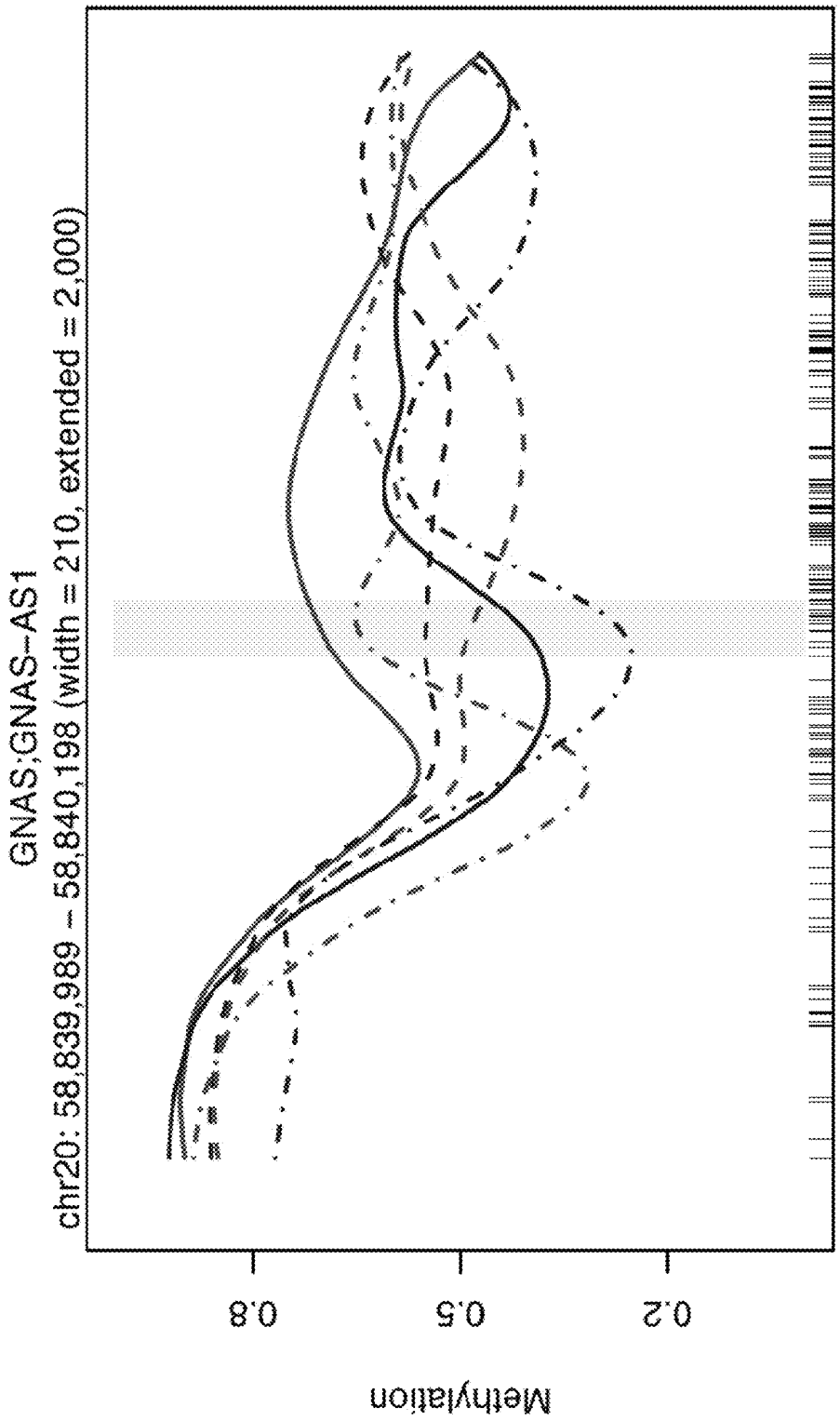

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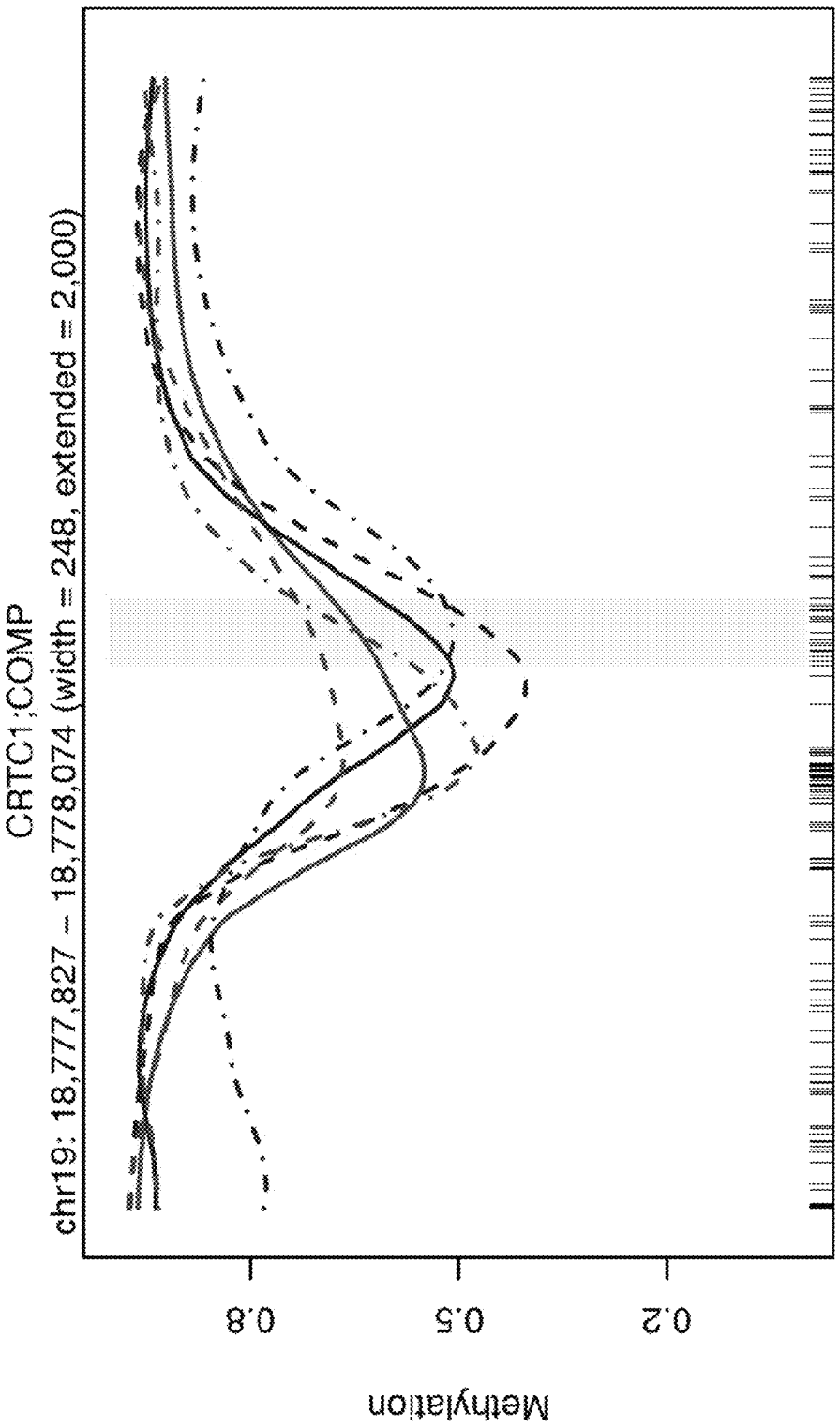

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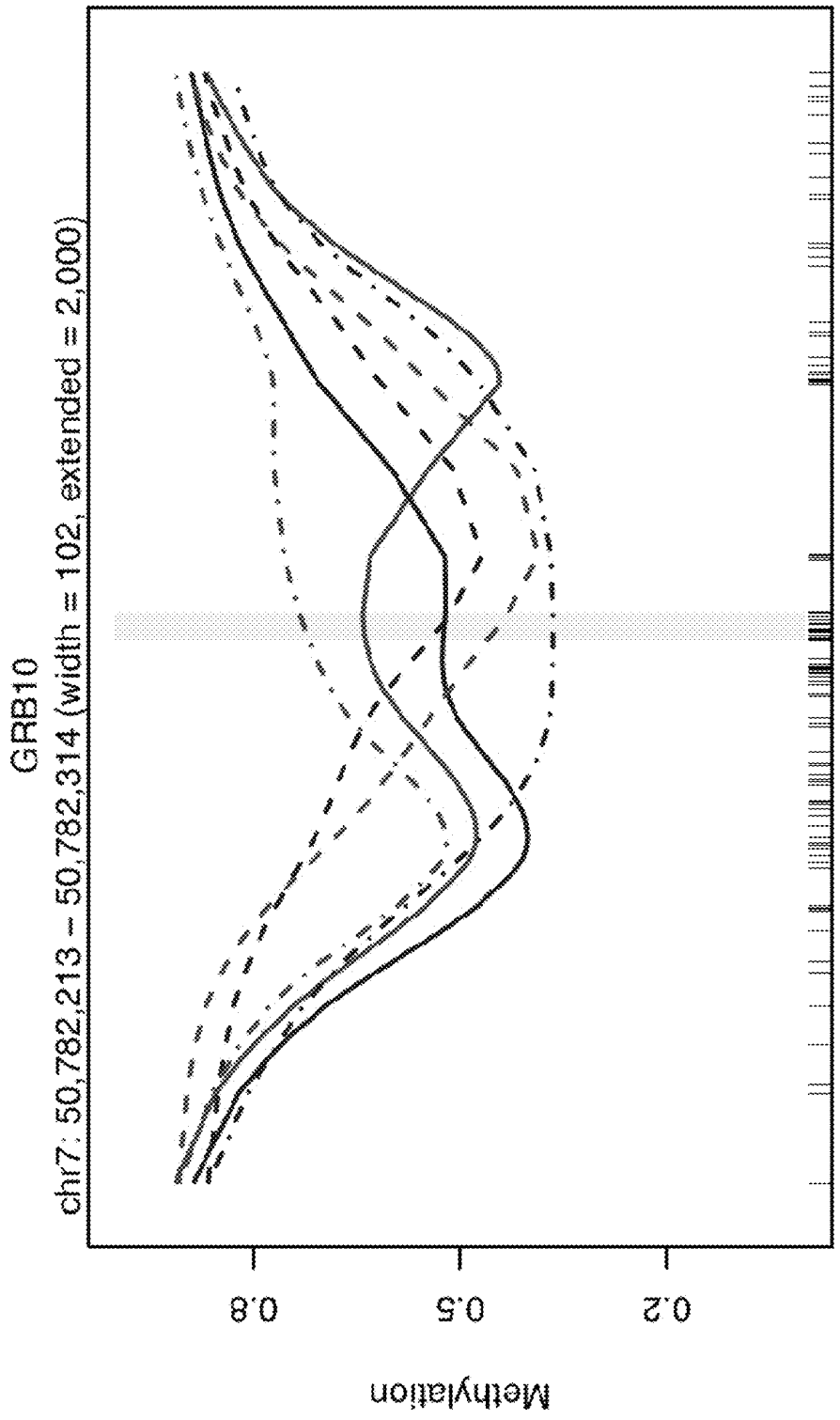

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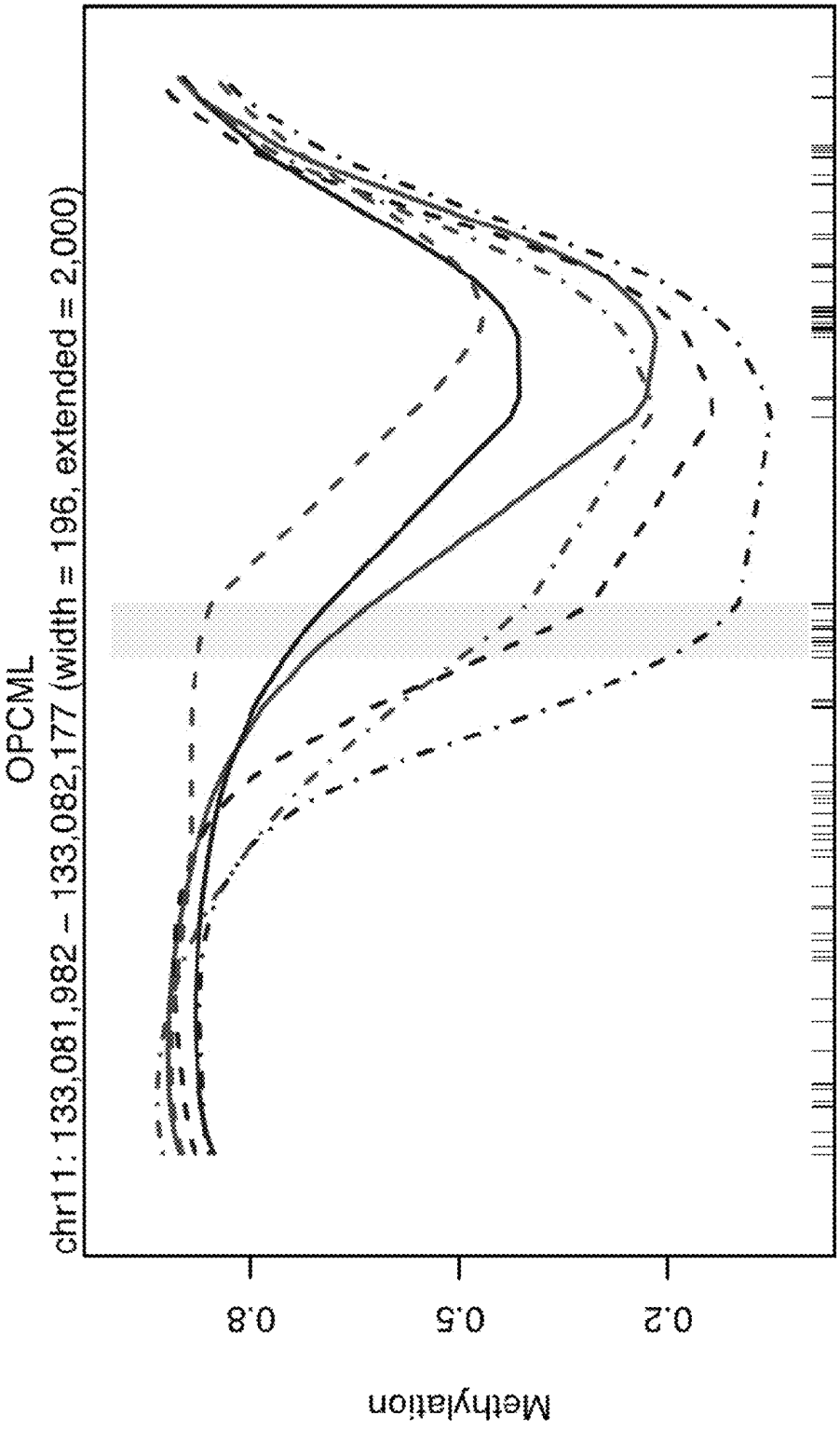

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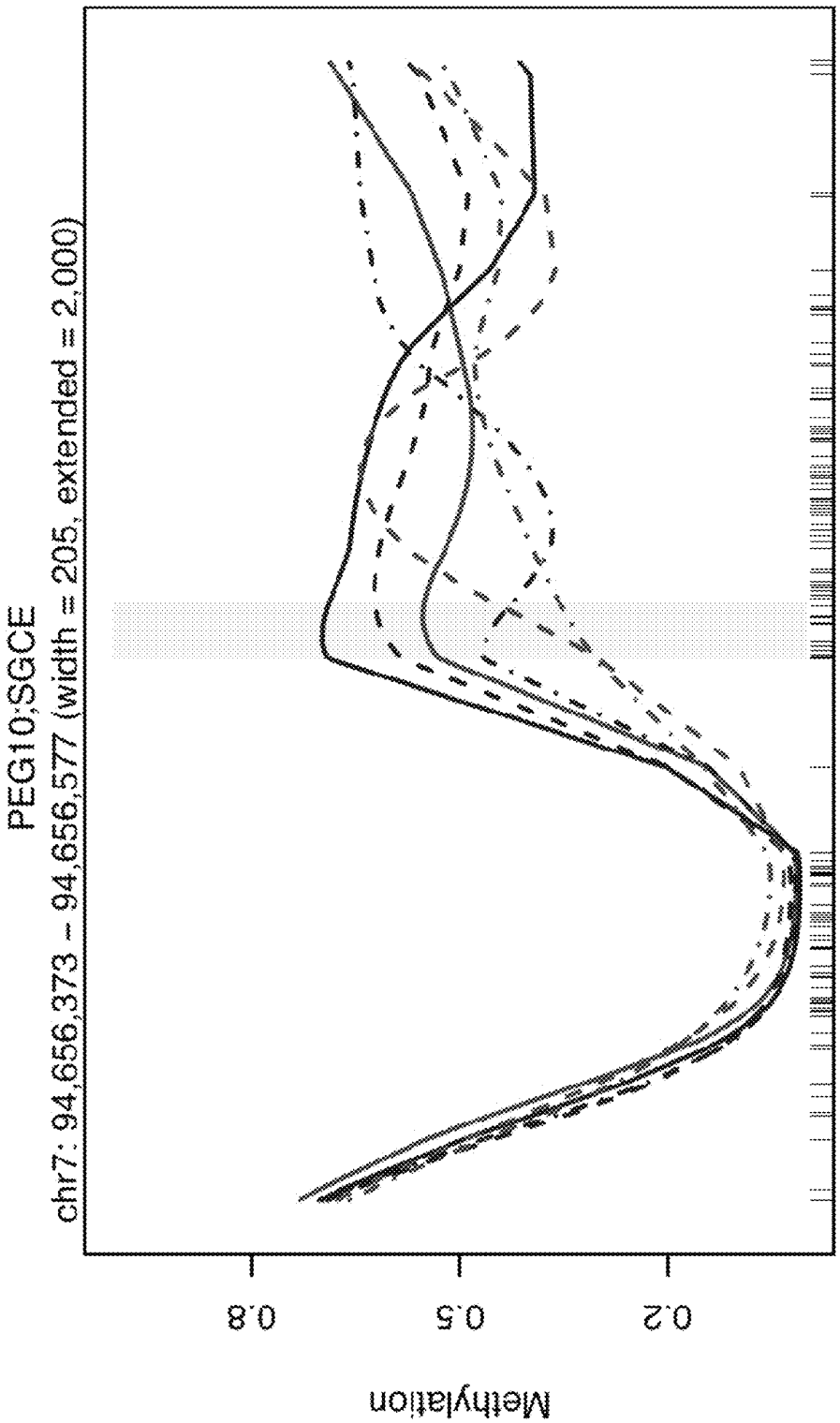

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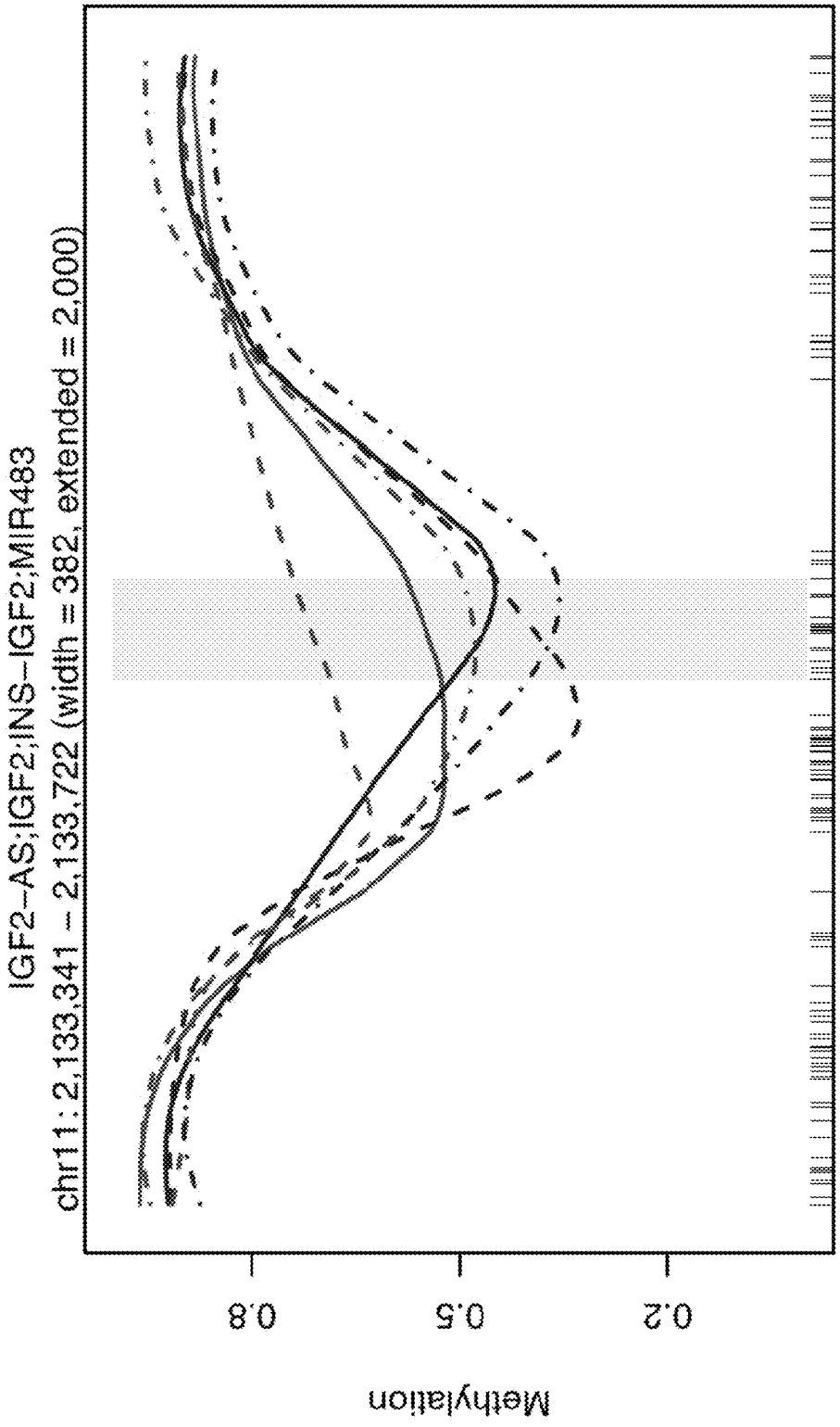

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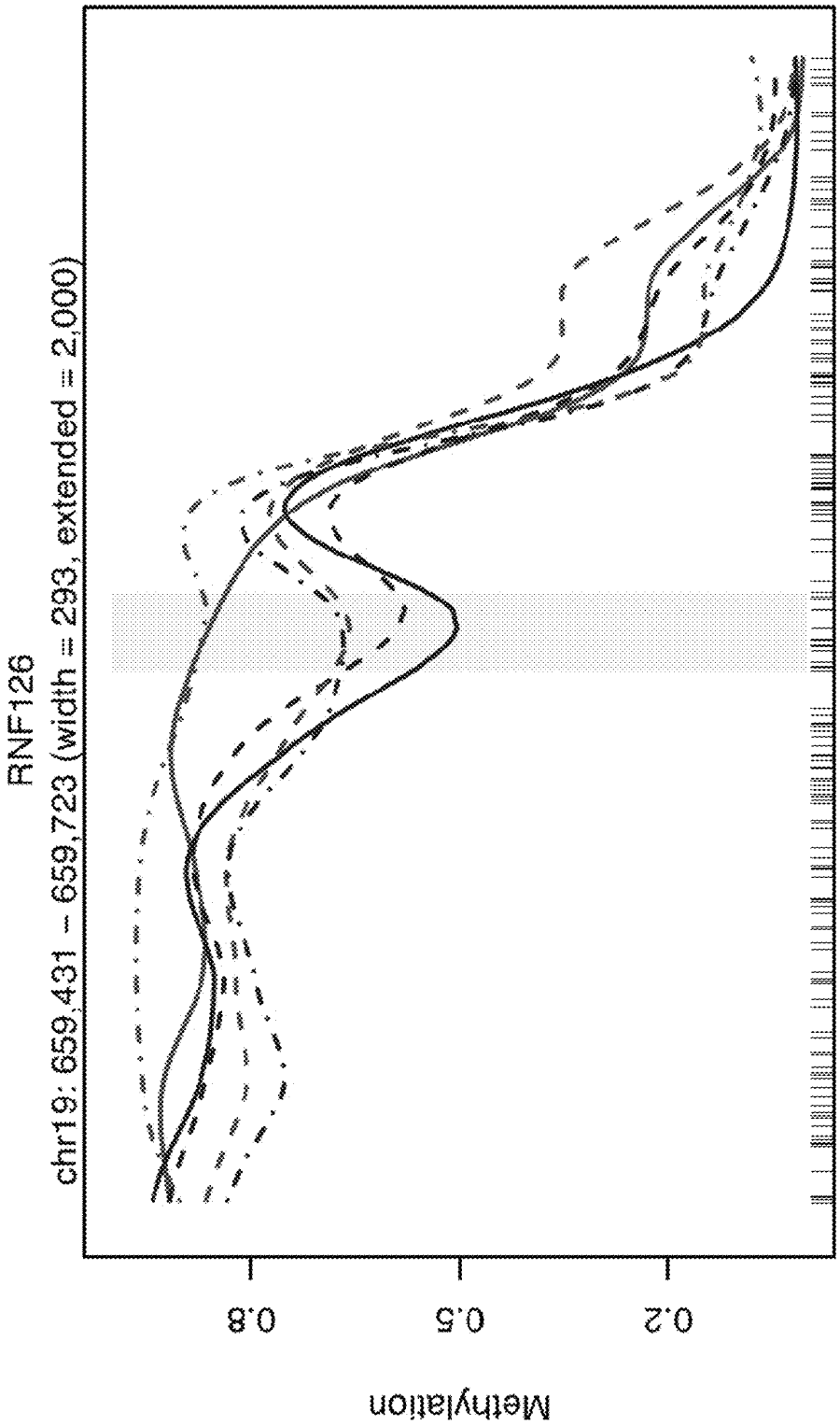

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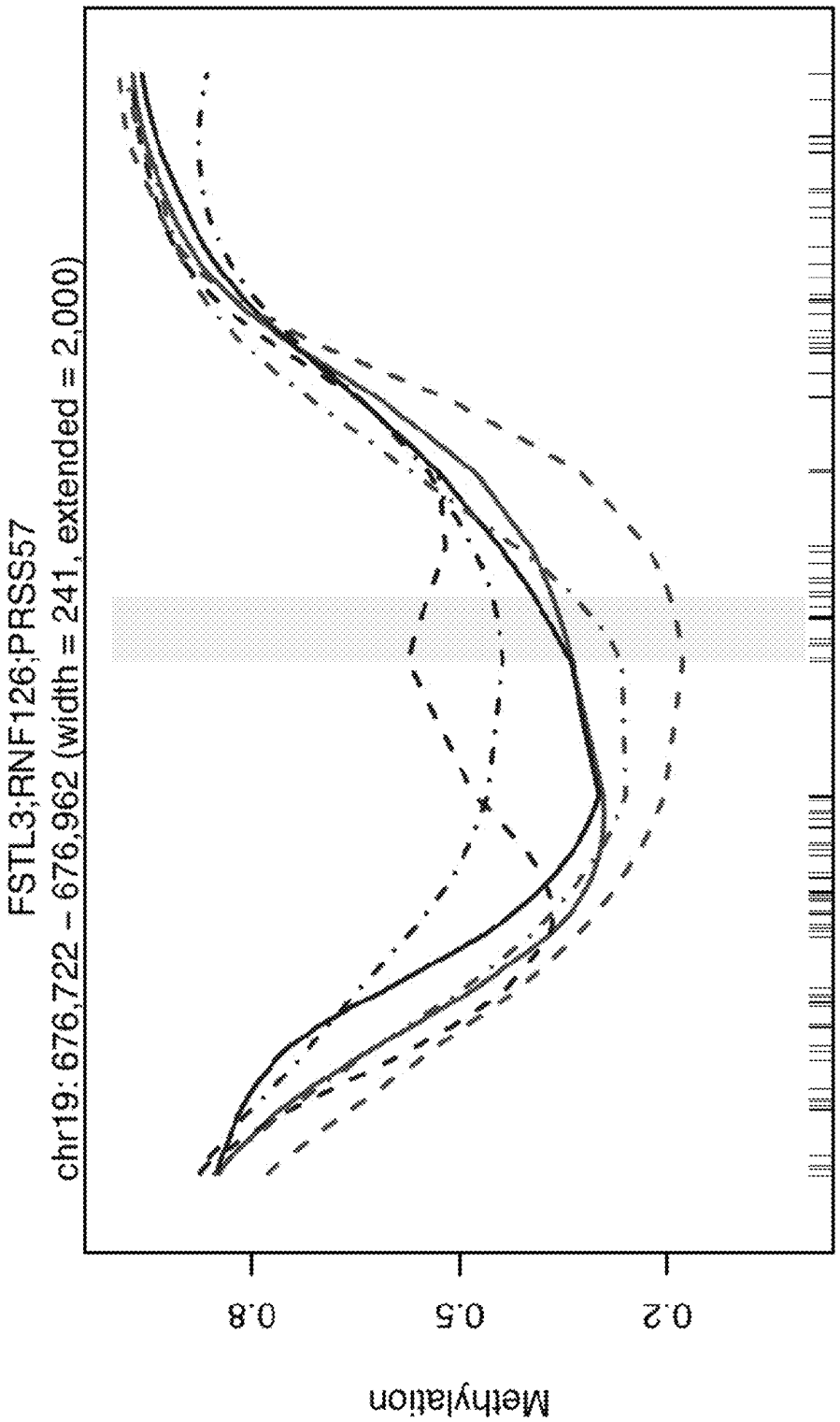

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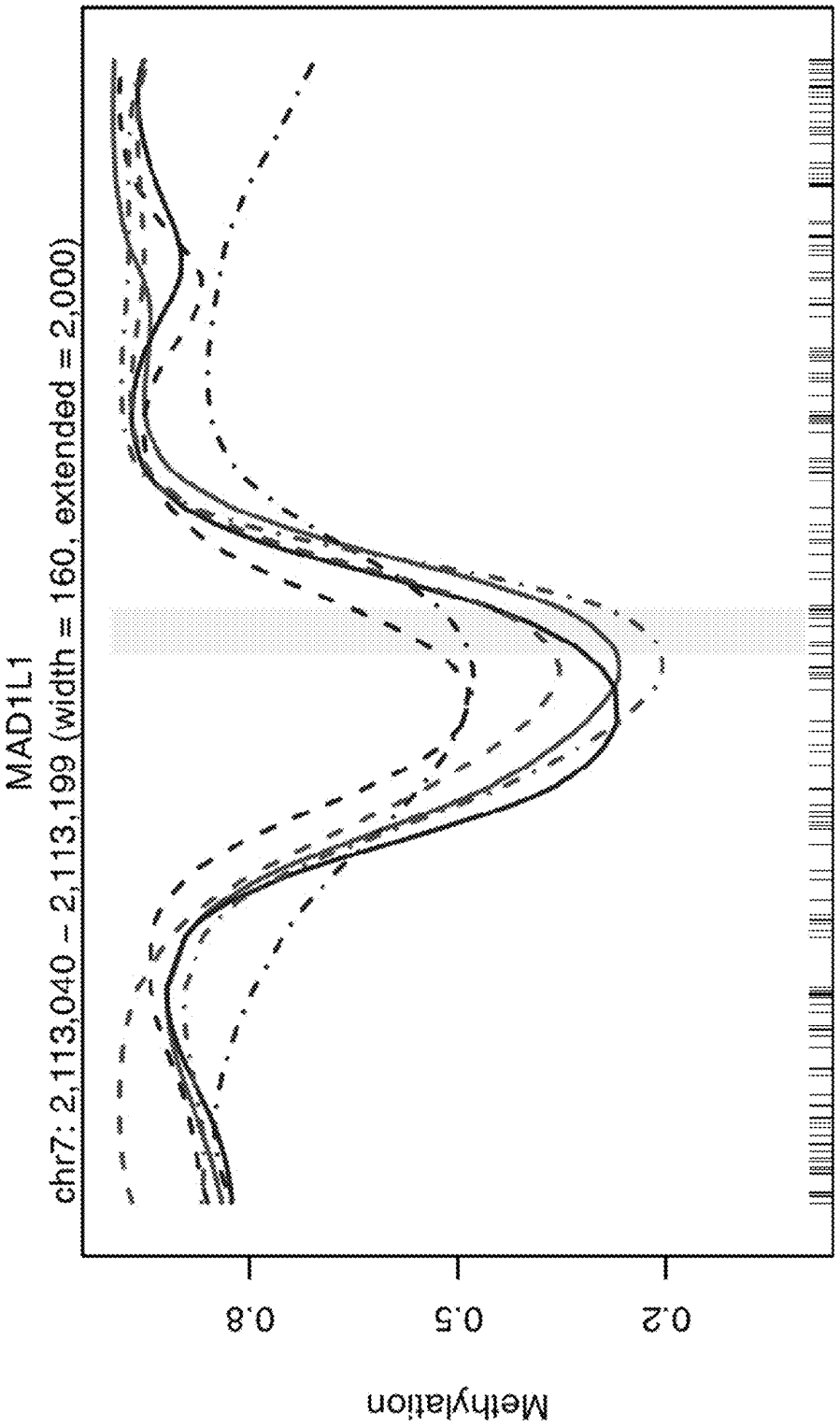

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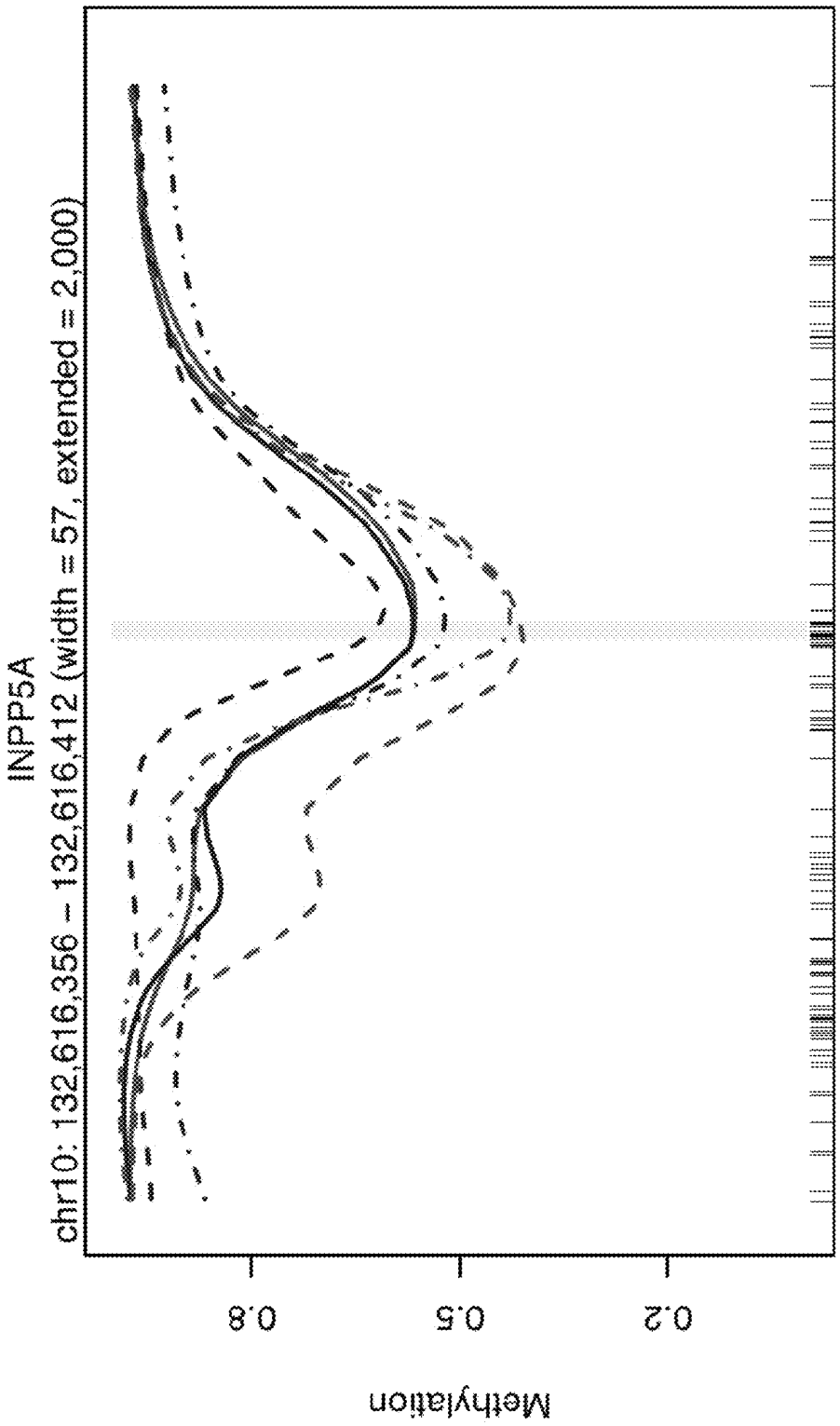

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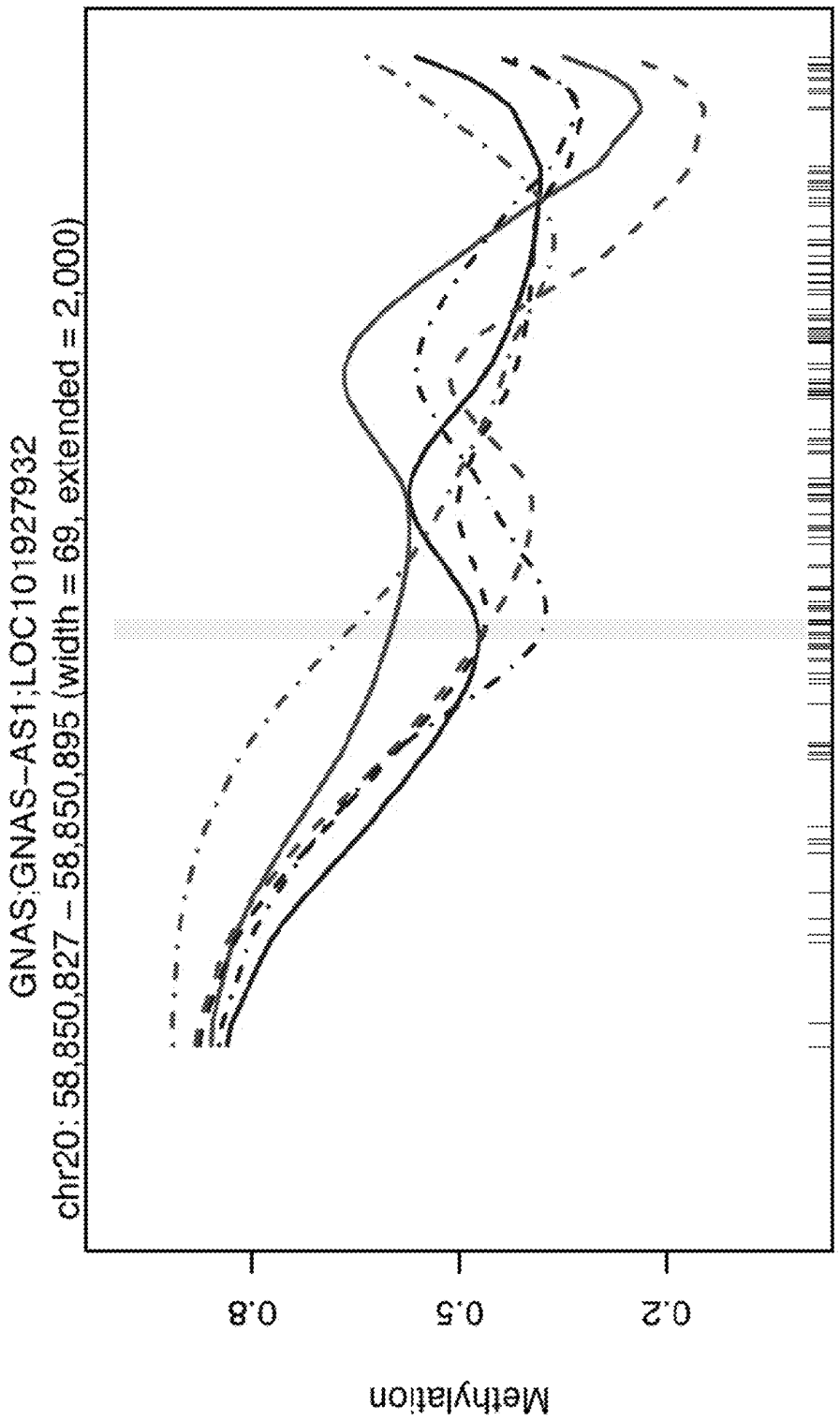

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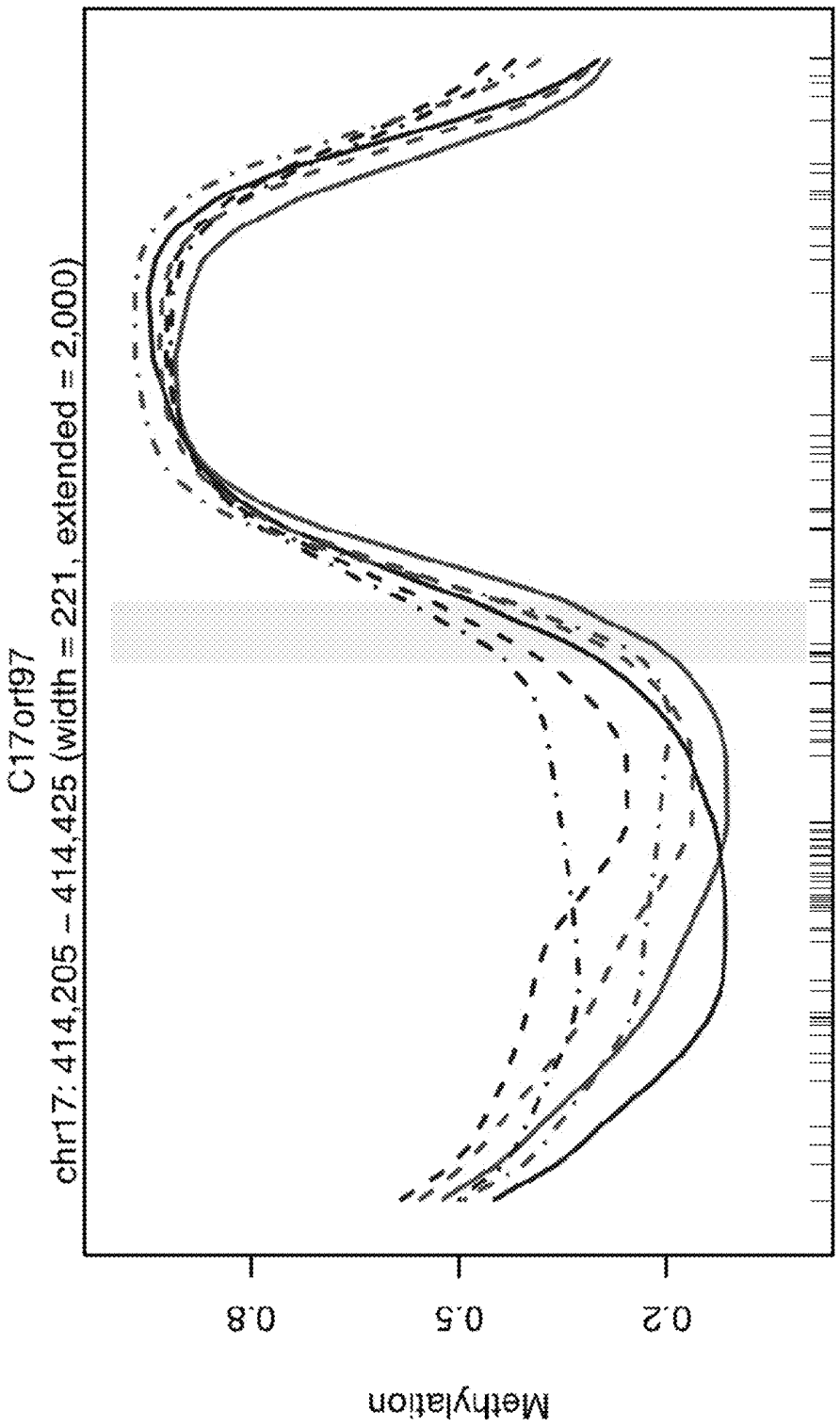

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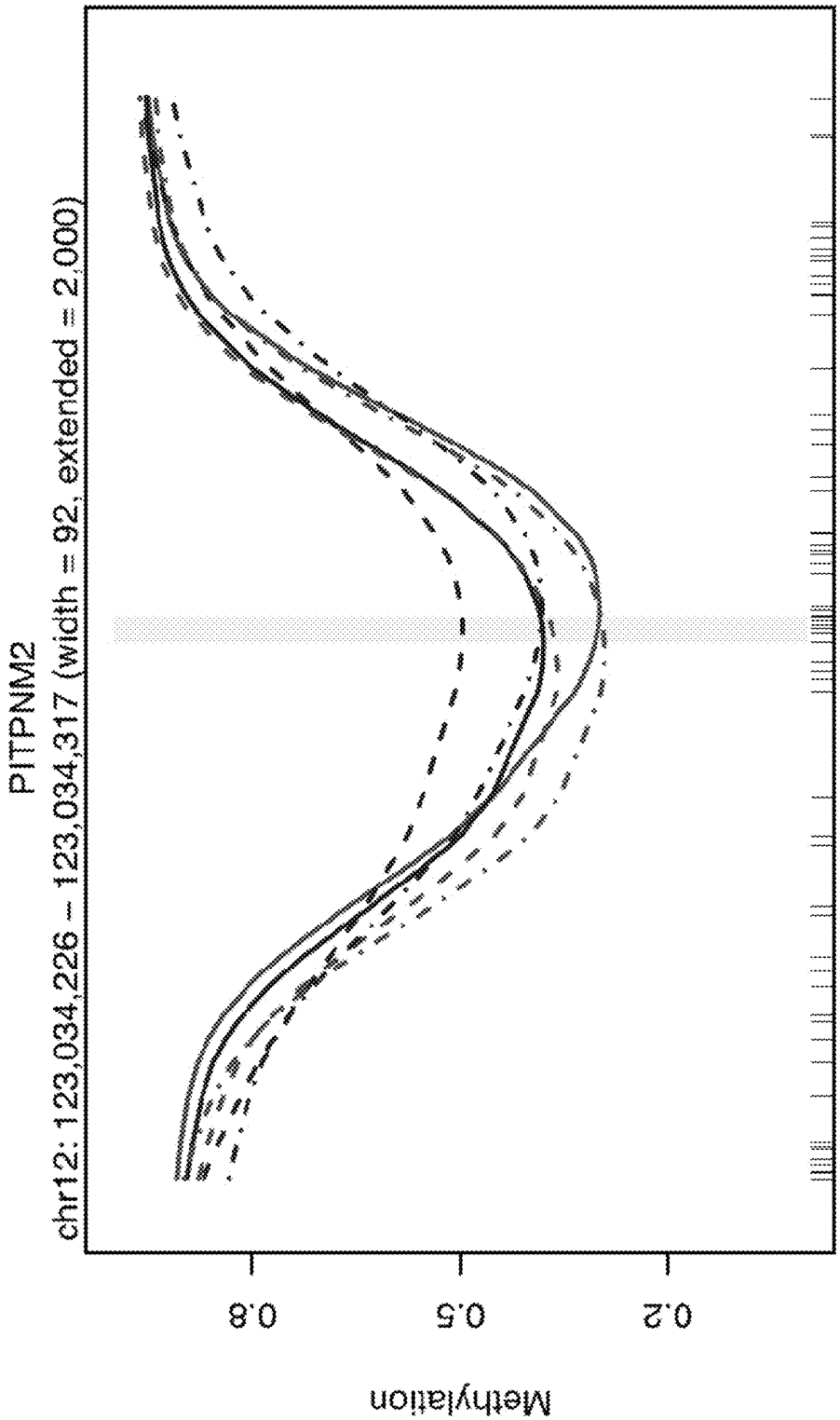

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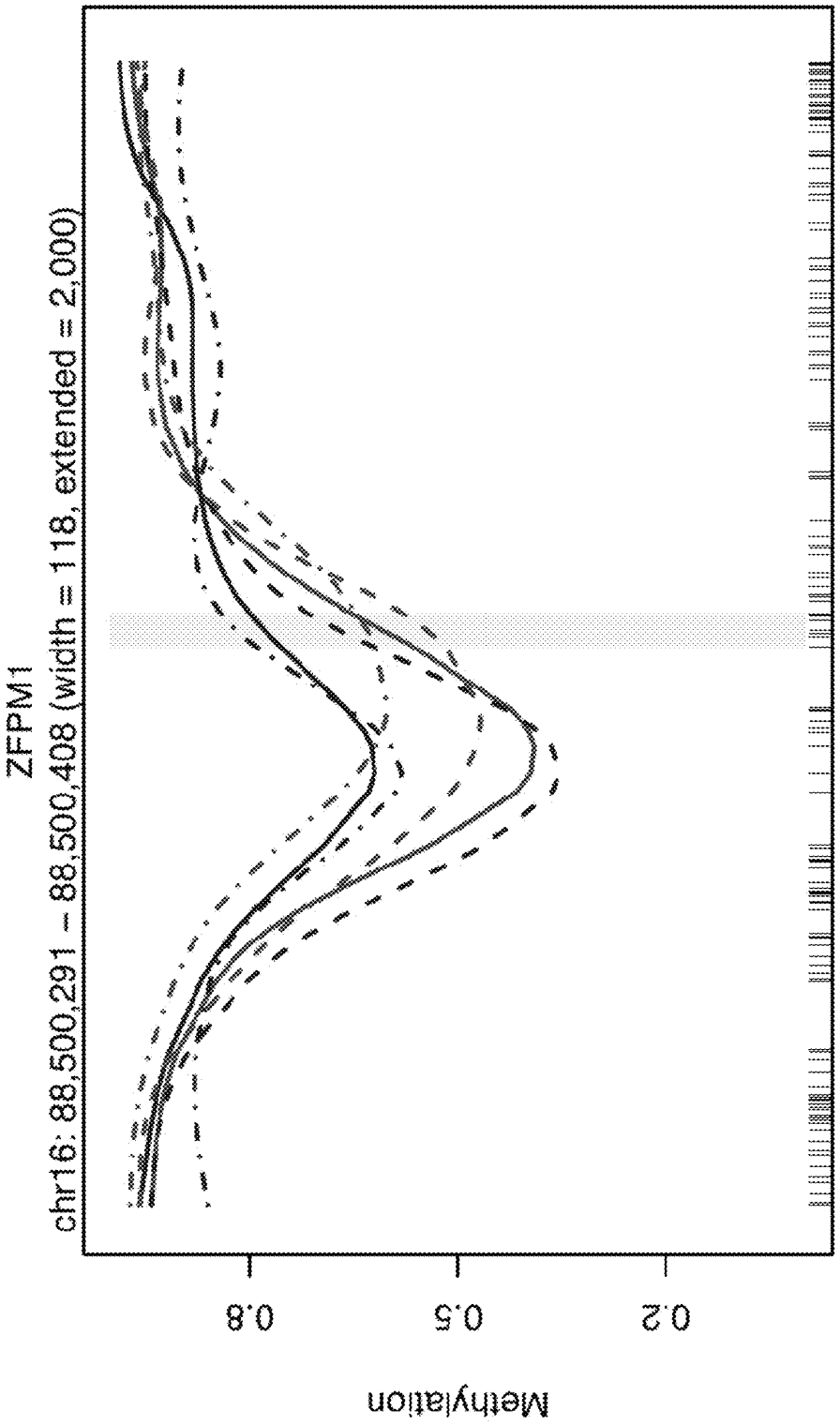

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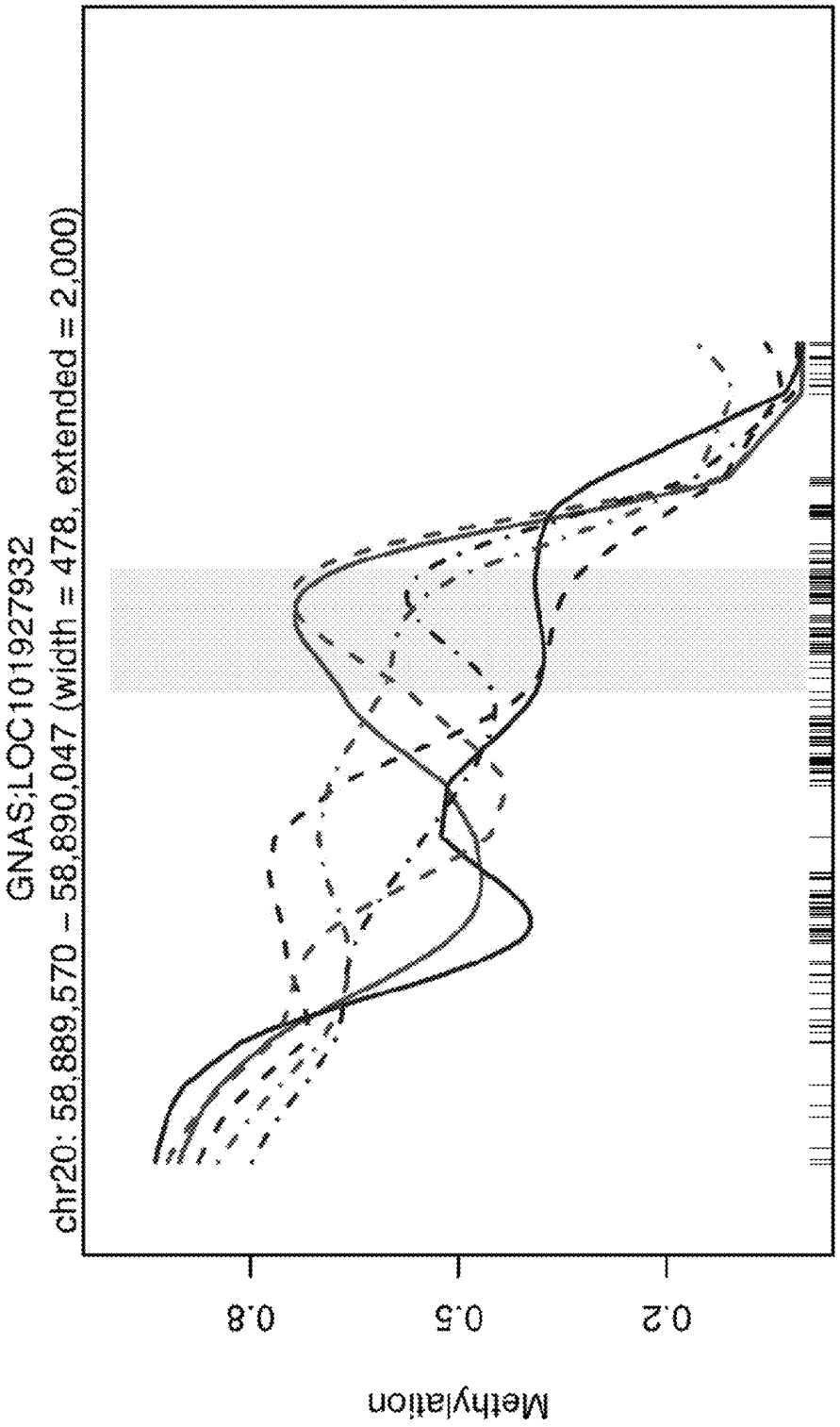

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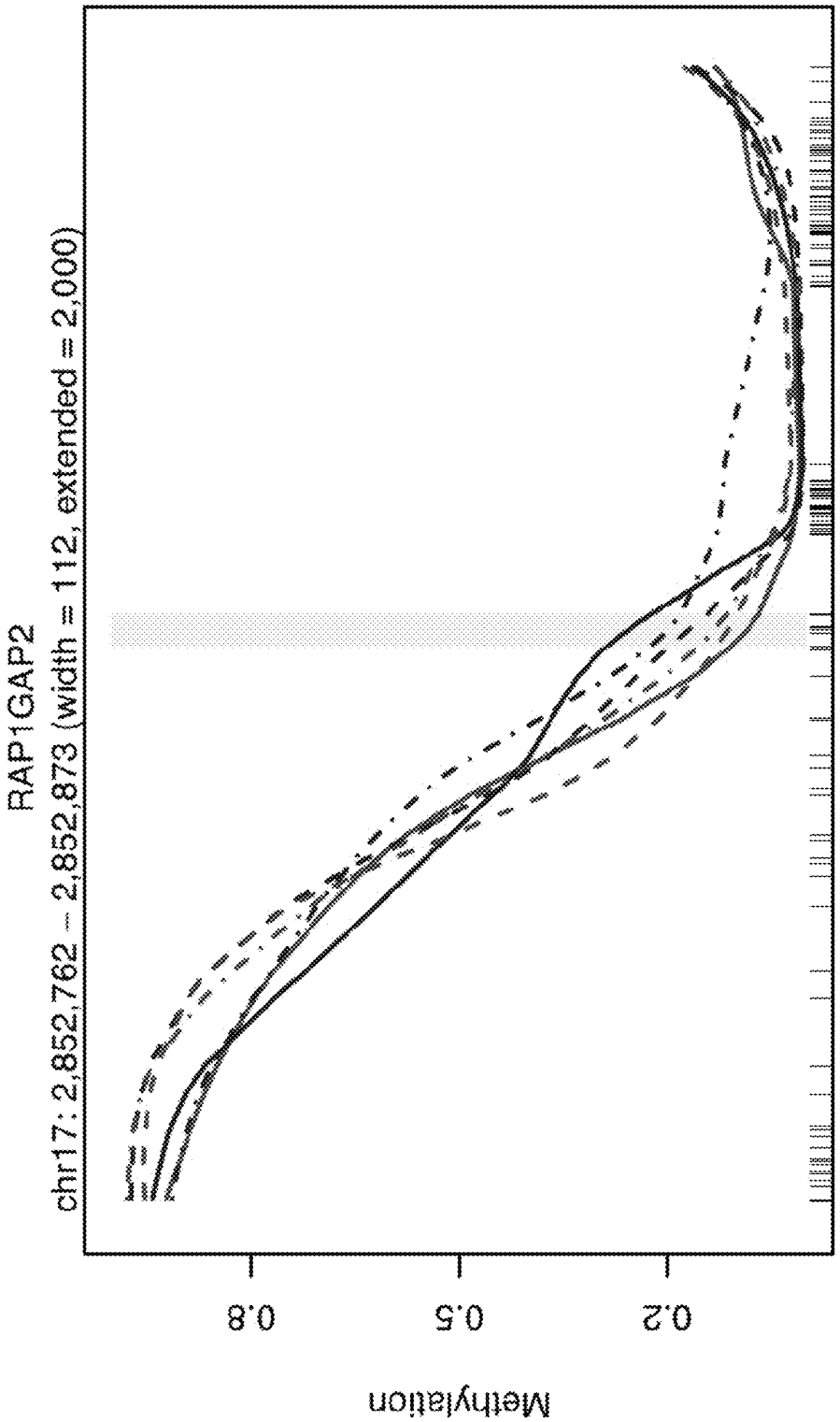

FIG. 2 CONTINUED

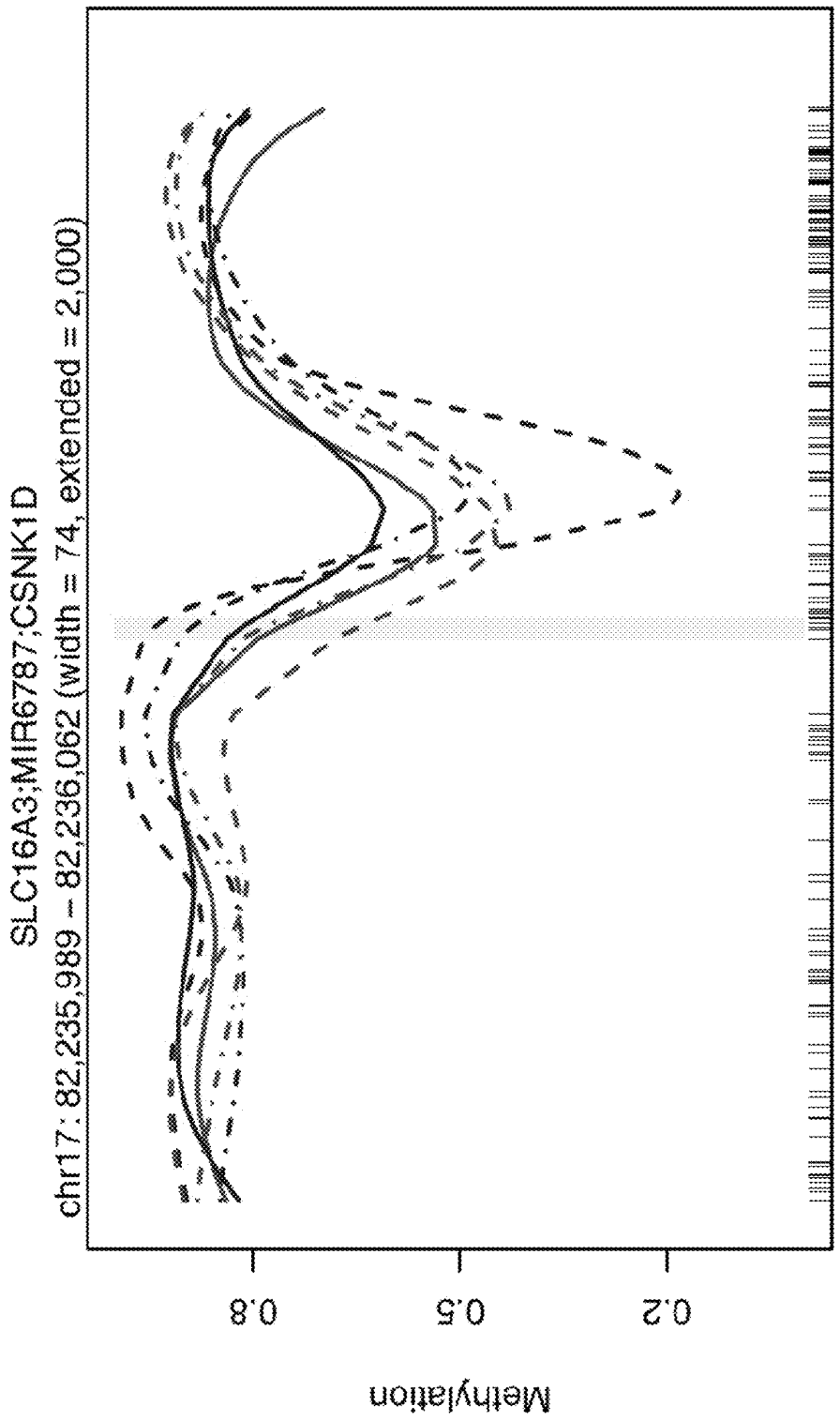

FIG. 2 CONTINUED

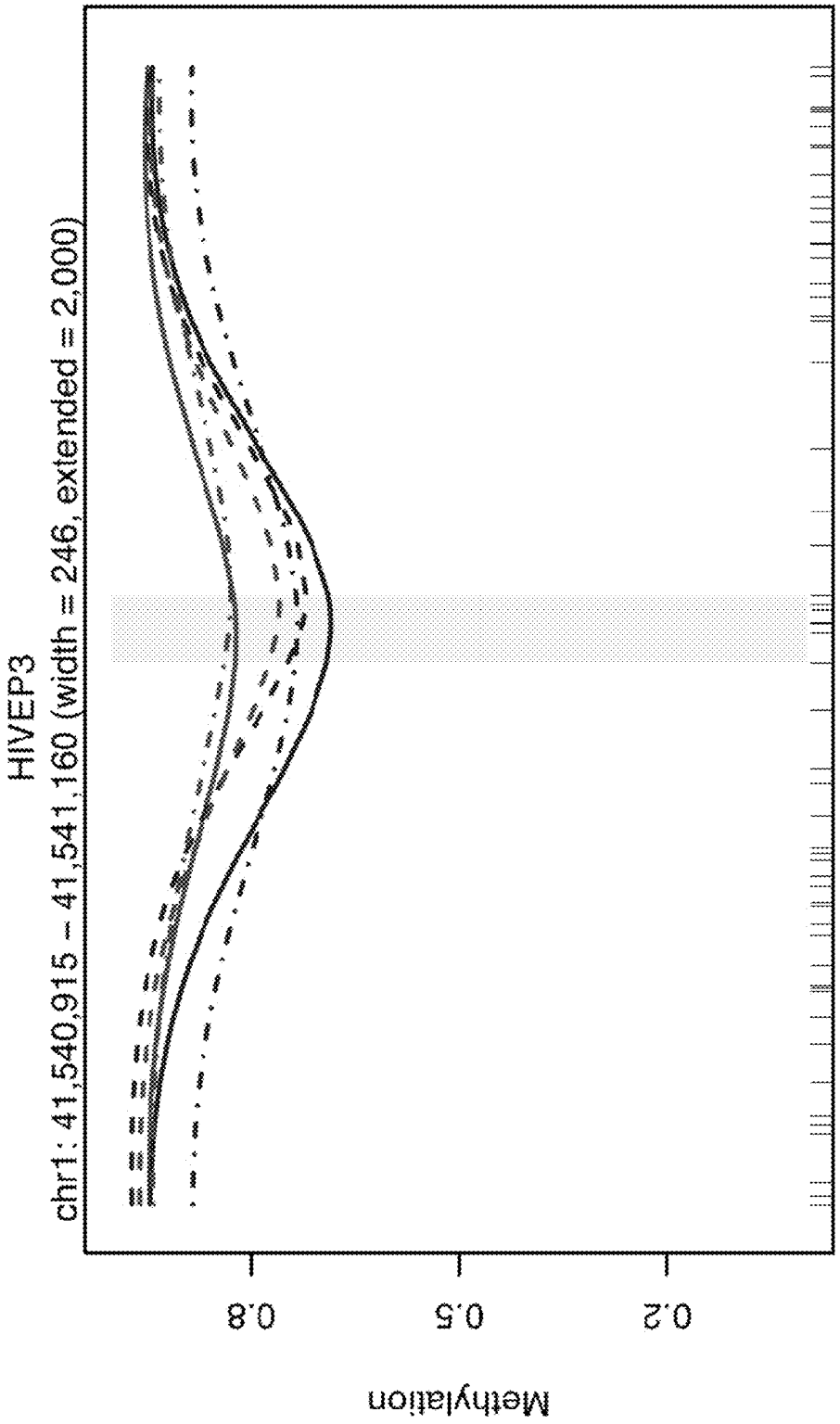

FIG. 2 CONTINUED

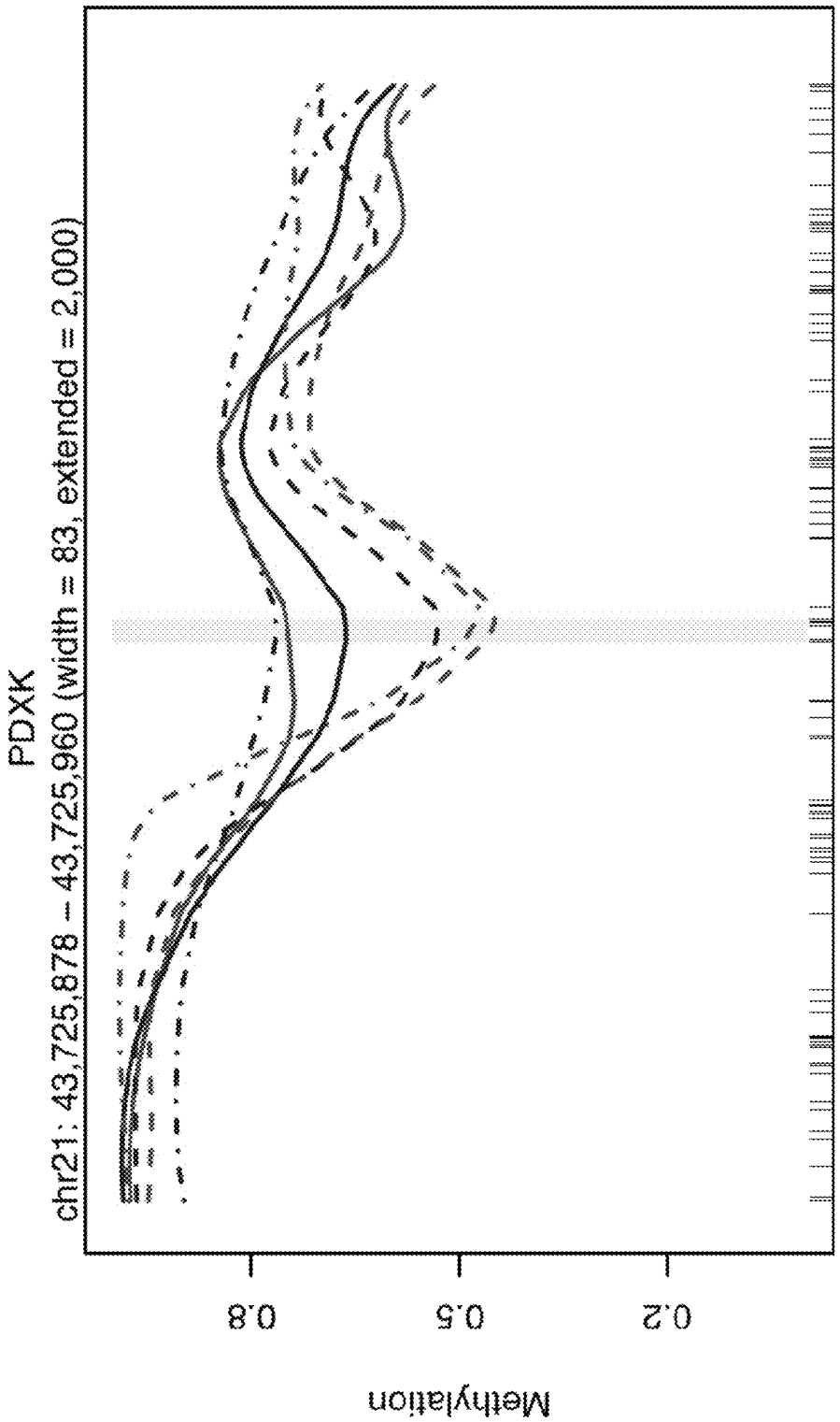

FIG. 2 CONTINUED

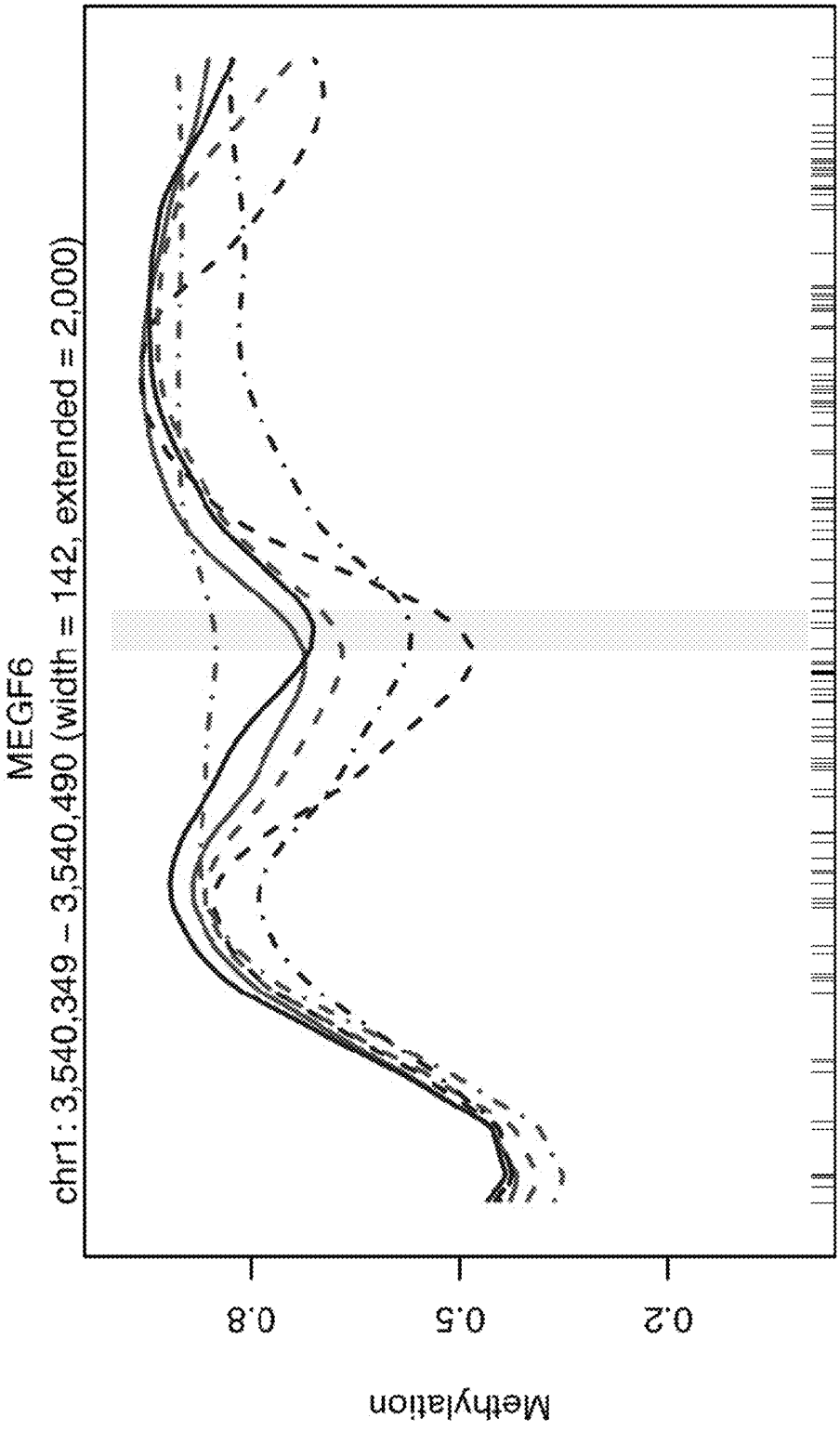

FIG. 2 CONTINUED

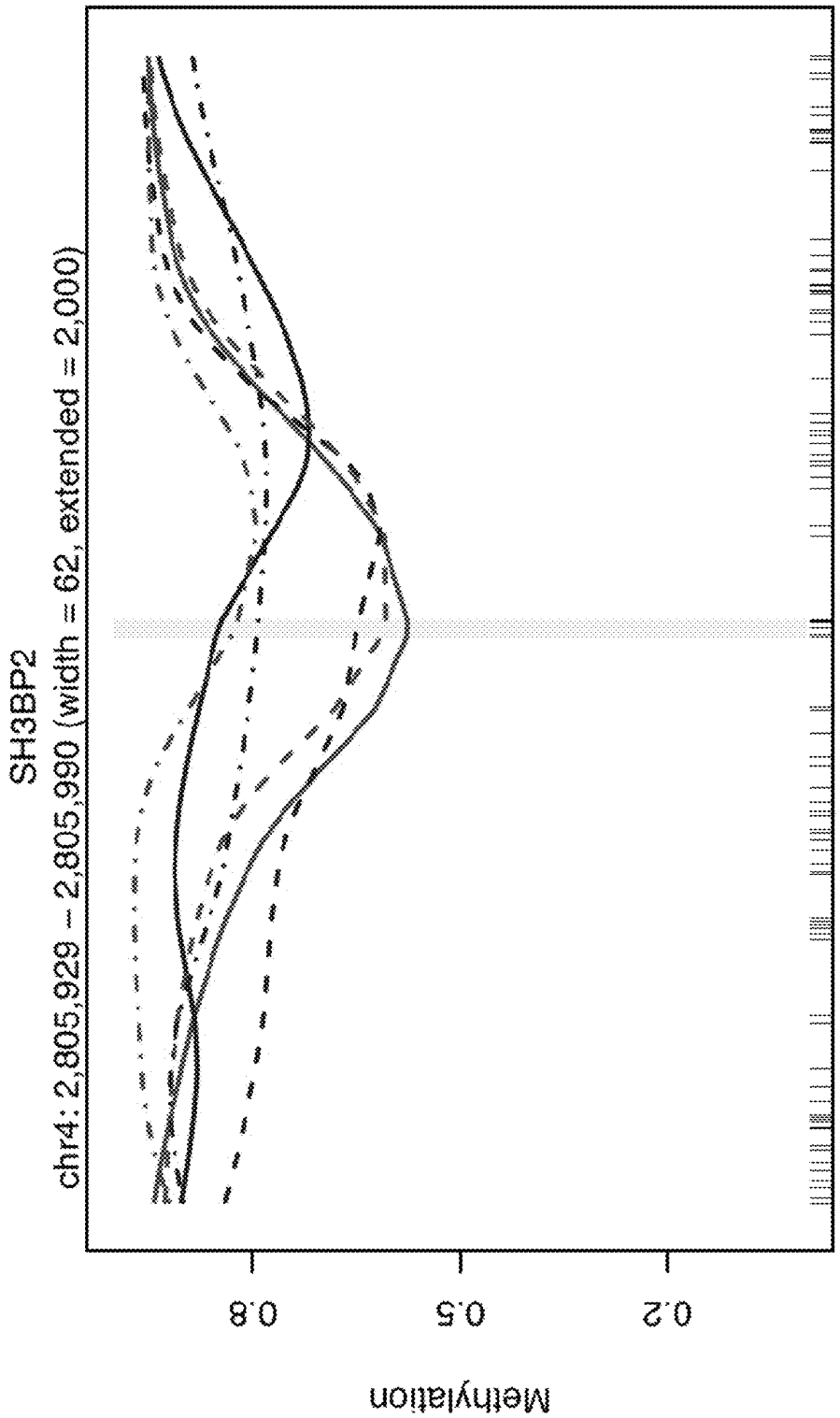

FIG. 2 CONTINUED

BLOOD DNA METHYLATION BIOMARKER DIAGNOSTIC TEST FOR ANXIETY AND DEPRESSIVE DISORDERS

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims priority to U.S. Provisional Application No. 62/860,022, filed Jun. 11, 2019, which is incorporated herein by reference in its entirety.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH

Not applicable

REFERENCE TO A SEQUENCE LISTING SUBMITTED VIA EFS-WEB

The content of the ASCII text file of the sequence listing named "960296 04029 ST25.txt" which is 44.6 kb in size was created on Jun. 4, 2020 and electronically submitted via EFS-Web herewith the application is incorporated herein by reference in its entirety.

BACKGROUND

Anxiety is frequently characterized by a negative affective response that is associated with the anticipation of encountering a potential threat. Trait-like anxiety in humans and non-human primates is associated with stable individual differences in hypothalamic-pituitary-adrenal (HPA) axis activation and amygdala function. HPA activation results in the release of cortisol, and increased cortisol concentrations in children and adolescents can be linked to inhibited behaviors and anxiety that often persist throughout life.

Additionally, a loss of the 'natural' circadian decline in afternoon/evening cortisol levels has been correlated with shyness and later alterations in behavior, including internalizing problems, suggesting that late-in-the day cortisol levels in children and adolescents may be an index of early life and current stress exposure as well as altered behaviors. High afternoon cortisol levels in childhood are also negatively correlated with amygdala-prefrontal cortex connectivity in adolescents and adults, indicating that a disruption in amygdala function is related to trait-like anxiety. In fact, anxiety prone individuals show greater amygdala activation during emotion processing tasks, further supporting a central role of the amygdala in processing of fearful stimuli.

Moreover, lesions in the central nucleus of the amygdala of non-human primates results in decreased adrenocorticotropic hormone (ACTH) concentrations before and after stressful conditions. Finally, higher and prolonged amygdala metabolism following a stressful challenge results in increased anxiety-like behaviors (e.g., freezing) in young rhesus monkeys, suggesting that the timing of amygdala activation and deactivation, in both humans and rhesus monkeys, is associated with trait-like anxiety.

Genetic data suggest that common anxiety disorders like generalized and social anxiety disorders are ~20%-40% heritable and that environmental factors—potentially including epigenetic modifications—likely account for much of the remaining variability. Studies using adult postmortem brain tissue support a role for DNA methylation (i.e., 5-methylcytosine [5mC]) in the development of anxiety, bipolar disorder, schizophrenia, and major depressive disorder.

SUMMARY OF THE INVENTION

In a first aspect, provided herein is a method of amplifying at least one of six differentially methylated region (DMR) associated genes comprising the steps of: (a) providing a reaction mixture comprising bisulfite modified target DNA from a subject and at least one pair of primers designed to amplify at least one DMR-associated gene selected from the group consisting of DIP2C, INPP5A, PDXK, GNAS, GRB10, and TRAPPC9 wherein the primer pair comprises a first and a second primer that are complementary to the DMR-associated gene; (b) heating the reaction mixture to a first predetermined temperature for a first predetermined time; (c) cooling the reaction mixture to a second predetermined temperature for a second predetermined time under conditions to allow the first and second primers to hybridize with their complementary sequences on the target DNA; and (d) repeating steps (b) and (c) wherein an amplified target DNA sample is formed. In some embodiments, the reaction mixture additionally comprises a polymerase and a plurality of free nucleotides comprising adenine, thymine, cytosine, and guanine. In some embodiments, the reaction mixture additionally comprises a reaction buffer and $MgCl_2$.

In some embodiments, in step (a), (i) a first reaction mixture comprising a first portion of bisulfite modified target DNA and a pair of primers designed to amplify DIP2C; (ii) a second reaction mixture comprising a second portion of bisulfite modified target DNA and a pair of primers designed to amplify INPP5A; (iii) a third reaction mixture comprising a third portion of bisulfite modified target DNA and a pair of primers designed to amplify PDXK; (iv) a forth reaction mixture comprising a forth portion of bisulfite modified target DNA and a pair of primers designed to amplify GNAS; (v) a fifth reaction mixture comprising a fifth portion of bisulfite modified target DNA and pair of primers designed to amplify GRB10; and (vi) a sixth reaction mixture comprising a sixth portion of bisulfite modified target DNA and a pair of primers designed to amplify TRAPPC9 are provided.

In some embodiments, the primers are specific for a DMR selected from the group consisting of SEQ ID NOs: 7-18, 50-59, 67-69, and 73-75. In some embodiments, at one of primers in the primer pair is biotinylated.

In some embodiments, the methods described herein include providing subsequent reaction mixtures comprising subsequent portions of bisulfite modified target DNA and a pair of primers designed to amplify one or more DMR-associated genes selected from the group consisting of C17ORF97, CACNA2D4, CRTC1, MEGF6, HIVEP3, OPCML, PITPNM2, ZFPM1, RAP1GAP2, NFATC1, RNF126, FSTL3, SH3BP2, NEURL1B, MAD1L1, HSPA12B, IGF2, PEG10, PEGS, SLC16A3, SYTL1, and ZIM2. In some embodiments, the primers are designed to amplify a DMR selected from the group consisting of SEQ ID NOs:1-6, 19-49, 60-66, and 70-72.

In some embodiments, the target DNA is isolated from a blood sample or a saliva sample form the subject. In some embodiments, the subject is a human or non-human primate.

In a second aspect, provided herein is a biomarker panel comprising probes specific to DIP2C, INPP5A, PDXK, GNAS, GRB10, and TRAPPC9. In some embodiments, the biomarker panel additionally comprises pairs of primers designed to amplify DIP2C, INPP5A, PDXK, GNAS, GRB10, and TRAPPC9.

In some embodiments, either the probes or the primers are arrayed on a substrate. In some embodiments, the substrate

is selected from the group consisting of a chip, a bead, a plate, a microfluidic device, or a multiwall plate.

In some embodiments, the primers are designed to amplify SEQ ID NOs: 7-18, 50-59, 67-69, and 73-75.

In some embodiments, the biomarker panel additionally comprises probes specific to HIVEP3, C17orf97, ZFPM1, RAP1GAP2, NFATC1, IGF2, SLC16A3, and SYTL1. In some embodiments, the probes are specific to SEQ ID NOs: 3-6, 19-20, 27-37.

In some embodiments, the biomarker panel additionally comprises probes specific to CACNA2D4, CRTC1, MEGF6, OPCML, PITPNM2, ZIM2, RNF126, FSTL3, SH3BP2, NEURL1B, MAD1L1, HSPA12B, PEG10, and PEGS. In some embodiments, the probes are specific to SEQ ID NOs: 1-2, 21-26, 38-49, 60-66, and 70-72.

In a third aspect, provided herein is a biomarker panel comprising the sequences of SEQ ID NOs: 7-18, 50-59, 67-69, and 73-75. In some embodiments, the sequences of SEQ ID NOs: 7-18, 50-59, 67-69, and 73-75 are arrayed on a substrate. In some embodiments, the substrate is selected from the group consisting of a chip, a bead, a plate, a microfluidic device, or a multiwall plate. In some embodiments, the biomarker panel additionally comprises the sequences of SEQ ID NOs: 1-2, 21-26, 38-49, 60-66, and 70-72. In some embodiments, the biomarker panel additionally comprise the sequences of SEQ ID NOs:3-6, 19-20, and 27-37.

In a forth aspect, provided herein is a method of diagnosing anxious temperament in a subject comprising the steps of: (a) obtaining a blood sample or saliva sample from the subject; (b) isolating target DNA from the sample obtained in (a); (c) contacting a biomarker panel as described herein with the isolated target DNA; (d) amplifying DMR-associated genes DIP2C, INPP5A, PDXK, GNAS, GRB10, and TRAPPC9; (e) quantifying methylation in the amplified DMR-associated genes, whereby a change in methylation of at least 10% compared to methylation in the same genes from a subject unaffected by anxious temperament indicates the presence of anxious temperament in the subject.

BRIEF DESCRIPTION OF DRAWINGS

The patent or patent application file contains at least one drawing in color. Copies of this patent or patent application publication with color drawings will be provided by the Office upon request and payment of the necessary fee.

FIG. **1** shows overlap of differentially methylated region associated genes identified from monkey brain, monkey blood, and human blood.

FIG. **2** shows differentially methylated region associated genes including multiple CpGs with greater than 10% differential methylation (shown as black tick marks at bottom). DNA methylation profiles for the anxious (red) and unaffected (control; blue) twin-pairs are shown and the genomic region of significance between twin-pairs is highlighted (peach). Each corresponding co-twin is indicated by a different line pattern (pair A=solid; B=dashed; C=dash+dot).

DETAILED DESCRIPTION OF THE DISCLOSURE

Recent study in young monkeys, as well as studies in humans, identified differentially methylated genes that are implicated as risk factors for anxiety and depressive disorders. Thus, these studies support the hypothesis that DNA methylation may have an important role in the risk to develop trait-like anxiety. However, these studies have relied heavily on the ability to access brain tissue. Focusing studies on anxiety-related DNA methylation profiles in blood has the potential to provide tools that could be clinically utilized to improve diagnostic and treatment strategies. Therefore, a need in the art exists for blood sample or saliva sample-based diagnostic tests for anxiety in primates.

The present disclosure describes blood sample or saliva sample based assays for the diagnosis, prognosis, and modified therapeutic response to anxiety in primates. The present disclosure describes differentially methylated regions (DMRs) associated with 22 different genes that are characteristic of anxious temperament and trait-like anxiety in primates. These characteristic biomarkers may be used to assay methylation in DNA isolated from a primate blood sample or a primate saliva sample. These characteristic biomarkers may be used in the development of a screening panel, a resequencing panel, or a diagnostic kit for the processing of DNA isolated from a primate blood sample or a primate saliva sample.

As used herein, "anxious temperament," or "AT" refers to the disposition of a human or non-human primate who is sensitive to new social experiences, shows increased freezing behavior, decreased communications, and increased pituitary-adrenal and autonomic activity. In non-human primates, AT can be computed and quantified as a composite measure among vocalizations, cortisol levels and freezing time assessed during the no eye contact condition of the human intruder paradigm. An individual can have an AT composite phenotype score between −1.48 to 1.43, with the higher scores correlated with increased freezing, decreased communication, increased cortisol levels, or a combination thereon. At risk children score at least 1.5 standard deviations above and below the mean on at least one of eight parent-reported symptom scales of the Health and Behavior Questionnaire (Essex M J, et al., Biological psychiatry, 2002). Because AT reflects a continuous trait-like variable, individuals will have a broad range of AT-related scores.

As used herein, "trait-like anxiety," refers to stable individual differences in hypothalamic-pituitary-adrenal (HPA) axis activation and amygdala function. (Kagan J, et al., Biological psychiatry. 1999; Kalin N H, Shelton S E. Ann N Y Acad Sci. 2003).

Biomarker Candidates

Described herein are differentially methylated regions associated with 22 different genes that are characteristic of anxious temperament and trait like anxiety.

As used herein, "differentially methylated region" or "DMR" refers to CpG dinucleotide regions with a significant increase (hypermethylation) or a significant decrease (hypomethylation) in methylation (e.g, 5-methylcytosine (5mC)) relative to control. The control is considered the level of methylation measured in a DNA sample from a primate unaffected by AT or trait-like anxiety. In some embodiments, the DMR corresponds to a region with a change in methylation of at least about 8%, at least about 10%, at least about 12%, at least about 15% or at least about 20% when compared to control. In some embodiments, the DMR corresponds to a region with at least 10% increase in methylation compared to control. In some embodiments, the DMR corresponds to a region with at least 10% decrease in methylation compared to control.

As used herein, "significant increase" refers to an increase with a statistical significance of $p<0.05$ when compared to control.

As used herein, "significant decrease" refers to a decrease with a statistical significance of $p<0.05$ when compared to control.

As used herein, "differentially methylated region-associated genes" or "DMR-associated genes" refers to the genes in which the DMRs are located or most closely associated with. In some embodiments, the DMR may be in the coding region of the DMR-associated gene. In some embodiments, the DMR may be in the promoter region of the DMR-associated gene.

DMR biomarker candidates associated with genes DIP2C, GRB10, INPP5A, C17ORF97, PDXK, CACNA2D4, TRAPPC9, CRTC1, MEGF6, HIVEP3, OPCML, PITPNM2, ZFPM1, RAP1GAP2, NFATC1, RNF126, FSTL3, GNAS, SH3BP2, NEURL1B, MADILL HSPA12B, IGF2, PEG10, PEGS, SLC16A3, SYTL1, and ZIM2 show significant ($p<0.05$) changes in methylation in target regions when DNA samples from anxious and unaffected (control) primates are compared.

Applicant notes that U.S. Provisional Application No. 62/860,022, the whole genome bisulfate sequence data was mapped to the rhesus macaque genome (rheMac8) and then annotated to "refseq" genes to get the gene symbols to orient the location of DNA methylation data to genes. This approach resulted in about ~6,000 gene symbol annotations to the data. However, this annotation was limited due to the low number of gene symbols found related to the data. Subsequence improved gene annotation methods and the use of Ensembl gene symbols provided more than 16,000 gene annotations to the rhesus macaque data. RNA sequencing data from the rhesus macaque brain tissue and the RSEM pipeline was also annotated to the Ensembl gene symbols. Using Ensembl gene symbols for both the DNA methylation and RNA sequence data allowed comprehensive comparisons between these data. Therefore, while particular gene symbols may be revised or updated from U.S. Provisional Application No. 62/860,022, this is an artifact of the gene annotation assembly used. The updated gene symbols are reflected herein and consistent with the DMRs recited in the provisional application.

TABLE 1

Anxiety-Associated Genes

Gene Symbol	Gene Name
DIP2C	disco interacting protein 2 homolog C
GRB10	growth factor receptor bound protein 10
INPP5A	inositol polyphosphate-5-phosphatase A
C17orf97	chromosome 16 open reading frame, human C17orf97
PDXK	pyridoxal kinase
CACNA2D4	calcium voltage-gated channel auxiliary subunit alpha2delta 4
TRAPPC9	trafficking protein particle complex 9
CRTC1	CREB regulated transcription coactivator 1
MEGF6	multiple epidermal growth factor-like domains protein 6
HIVEP3	human immunodeficiency virus type I enhancer-binding protein 3
OPCML	opioid-binding cell adhesion molecule
PITPNM2	phosphatidylinositol transfer protein membrane associated 2
ZFPM1	zinc finger protein multitype 1
RAP1GAP2	Ras-proximate-1 (RAP1) GTPase activating protein 2
NFATC1	nuclear factor of activated T-cells, cytoplasmic 1
RNF126	ring finger protein 126
FSTL3	follistatin Like 3
GNAS	guanine nucleotide-binding protein G(s) subunit alpha
SH3BP2	SH3 domain-binding protein 2
NEURL1B	neuralized E3 ubiquitin protein ligase 1B
MAD1L1	mitotic arrest deficient 1 like 1
HSPA12B	heat shock protein family A (Hsp70) member 12B
IGF2	insulin like growth factor 2
PEG10	paternally expressed 10
PEG3	paternally expressed 10
SLC16A3	solute carrier family 16 member 3
SYTL1	synaptotagmin like 1
ZIM2	zinc Finger Imprinted 2

DMR biomarkers are recited in Table 2. These biomarkers represent CpG regions with at least about 10% differential methylation in target regions when DNA samples from anxious and unaffected (control) primates are compared. Differential methylation includes both hypermethylation and hypomethylation.

TABLE 2

Overlapping AT-related DMRs

Chromosome	Start	End	Gene Symbol	ReSeq panel ID	Overlap	DMR Status	SEQ ID NO:
Chr 1	3503131	3503245	MEGF6	RhBrn_26	**	Hyper	1
Chr 1	3540349	3540490	MEGF6	HuBld_196	**	Hyper	2
Chr 1	27349740	27349796	SYTL1	RhBld_38	##	Hyper	3
Chr 1	27349814	27350119	SYTL1	HuBld_4	##	Hyper	4
Chr 1	41540915	41541160	HIVEP3	HuBld_171	##	Hyper	5
Chr 1	41618187	41618276	HIVEP3	RhBld_22	##	Hyper	6
Chr 10	309028	309164	DIP2C	RhBld_230	***	Hyper	7
Chr 10	329499	329561	DIP2C	RhBld_243	***	Hyper	8
Chr 10	355287	355459	DIP2C	RhBld_232	***	Hyper	9
Chr 10	355461	355490	DIP2C	RhBld_1000	***	Hyper	10
Chr 10	355492	355503	DIP2C	RhBld_1001	***	Hyper	11
Chr 10	355504	355516	DIP2C	RhBld_1002	***	Hyper	12
Chr 10	355517	355541	DIP2C	RhBld_1003	***	Hyper	13
Chr 10	413853	414117	DIP2C	HuBld_28	***	Hyper	14
Chr 10	484804	484931	DIP2C	RhBrn_215	***	Hyper	15
Chr 10	132607036	132607056	INPP5A	RhBrn_218	***	Hypo	16
Chr 10	132607057	132607061	INPP5A	RhBrn_1002	***	Hypo	17
Chr 10	132616356	132616412	INPP5A	HuBld_122	***	Hypo	18
Chr 11	2133265	2133335	IGF2;	RhBld_355	##	Hyper	19
Chr 11	2133341	2133722	IGF2; INS-IGF2	HuBld_67	##	Hyper	20

TABLE 2-continued

Overlapping AT-related DMRs

Chromosome	Start	End	Gene Symbol	ReSeq panel ID	Overlap	DMR Status	SEQ ID NO:
Chr 11	133081982	133082177	OPCML	HuBld_56	**	Hyper	21
Chr 12	1811666	1811837	CACNA2D4	HuBld_180	**	Hyper	22
Chr 12	1838231	1838295	CACNA2D4	RhBrn_300	**	Hyper	23
Chr 12	1842428	1842506	CACNA2D4	RhBrn_298	**	Hyper	24
Chr 12	123034226	123034317	PITPNM2	HuBld_153	**	Hypo	25
Chr 12	123077953	123078020	PITPNM2	RhBrn_295	**	Hypo	26
Chr 16	88500291	88500408	ZFPM1	HuBld_154	##	Hypo	27
Chr 16	88534642	88534701	ZFPM1	RhBld_495	##	Hypo	28
Chr 17	410141	410147	C17orf97	RhBld_1008	##	Hypo	29
Chr 17	414205	414425	C17orf97	HuBld_143	##	Hypo	30
Chr 17	2837445	2837518	RAP1GAP2	RhBld_403	##	Hypo	31
Chr 17	2852762	2852873	RAP1GAP2	HuBld_159	##	Hypo	32
Chr 17	82235989	82236062	SLC16A3	HuBld_170	##	Hypo	33
Chr 17	82238736	82238899	SLC16A3	RhBld_404	##	Hypo	34
Chr 18	79436203	79436269	NFATC1	RhBld_449	##	Hyper	35
Chr 18	79509085	79509203	NFATC1	HuBld_123	##	Hyper	36
Chr 18	79523293	79523358	NFATC1	RhBld_455	##	Hyper	37
Chr 19	659125	659132	RNF126	RhBrn_491	**	Hyper	38
Chr 19	659138	659172	RNF126	RhBrn_1011	**	Hyper	39
Chr 19	659175	659216	RNF126	RhBrn_1012	**	Hyper	40
Chr 19	659431	659723	RNF126	HuBld_79	**	Hyper	41
Chr 19	676722	676962	FSTL3	HuBld_108	**	Hypo	42
Chr 19	18762214	18762355	CRTC1	RhBrn_478	**	Hyper	43
Chr 19	18777827	18778074	CRTC1	HuBld_49	**	Hyper	44
Chr 19	56838765	56839239	ZIM2; PEG3	HuBld_13	**	Hypo	45
Chr 19	56840640	56840712	RF02151; PEG3	RhBrn_1009	**	Hypo	46
Chr 19	56840714	56840745	RF02151; PEG3	RhBrn_1010	**	Hypo	47
Chr 20	3751818	3752296	HSPA12B	HuBld_2	**	Hyper	48
Chr 20	3751944	3752172	HSPA12B	RhBrn_246	**	Hyper	49
Chr 20	58839989	58840198	GNAS; GNAS-AS1	HuBld_38	***	Hyper	50
Chr 20	58850827	58850895	GNAS; GNAS-AS1	HuBld_136	***	Hyper	51
Chr 20	58855291	58855453	GNAS	RhBrn_1000	***	Hyper	52
Chr 20	58889570	58890047	GNAS	HuBld_1	***	Hyper	53
Chr 20	58890242	58890319	GNAS	RhBld_1004	***	Hyper	54
Chr 21	43725878	43725960	PDXK	HuBld_195	***	Hypo	55
Chr 21	43727343	43727431	PDXK	RhBld_1007	***	Hypo	56
Chr 21	43758088	43758098	PDXK	RhBrn_1005	***	Hypo	57
Chr 21	43758106	43758177	PDXK	RhBrn_1006	***	Hypo	58
Chr 21	43758178	43758183	PDXK	RhBrn_1007	***	Hypo	59
Chr 4	2805929	2805990	SH3BP2	HuBld_199	**	Hypo	60
Chr 4	2825167	2825265	SH3BP2	RhBrn_141	**	Hypo	61
Chr 5	172669962	172670083	NEURL1B	RhBrn_145	**	Hyper	62
Chr 5	172683900	172684098	NEURL1B	HuBld_9	**	Hyper	63
Chr 7	1946572	1946581	MAD1L1	RhBrn_97	**	Hypo	64
Chr 7	1946583	1946636	MAD1L1	RhBrn_1003	**	Hypo	65
Chr 7	2113040	2113199	MAD1L1	HuBld_121	**	Hypo	66
Chr 7	50782213	50782314	GRB10	HuBld_52	***	Hyper	67
Chr 7	50782337	50782376	GRB10	RhBrn_1001	***	Hyper	68
Chr 7	50783121	50783181	GRB10	RhBld_1005	***	Hyper	69
Chr 7	94656373	94656577	PEG10	HuBld_60	**	Hypo	70
Chr 7	94658334	94658421	PEG10	RhBrn_68	**	Hypo	71
Chr 7	94658422	94658431	PEG10	RhBrn_1008	**	Hypo	72
Chr 8	140098781	140098880	TRAPPC9	RhBrn_192	***	Hyper	73
Chr 8	140098798	140098899	TRAPPC9	RhBld_208	***	Hyper	74
Chr 8	140099819	140100255	TRAPPC9	HuBld_12	***	Hyper	75

** monkey brain and human blood overlap

monkey blood and human blood overlap

*** monkey brain, monkey blood, and human blood overlap

TABLE 3

DMR Sequences:

SEQ ID NO:	Chr.	Start	End	hg38coord	cdna
1	Chr 1	3503131	3503245	chr1: 3503131-3503245	CGCTGAGGCCCTGAGGACACACCCTGGTGAACCCTTG TCACCAGGGCCCATCCCCAGGGGCACCCGCCCATAGG GACACAGGCACGTCCCTGGGACTACAGGCCTGGCACT CACC
2	Chr 1	3540349	3540490	chr1: 3540349-3540490	CGGGTTTCCCGCTGCACTGGGAAGACAGCCAGCTGAA GAATGTTGGCCTGGGGAGGCCCAGATTCAGCCACCCA CAGGAACGTGGCCCCAGCTTTGCAACCGGAAGGCCCA GGTTCAGGCCTGGGCTCCAGGGCCCATGGGC
3	Chr 1	27349740	27349796	chr1: 27349740-27349796	CGGTGTCCAGCCTTAACTCCTCCACGGTGAGGCGGGA GGGAGGGGACCCGGGCGGCC
4	Chr 1	27349814	27350119	chr1: 27349814-27350119	CGATGCGTAGCCCCTGCCTGCCCCTCCCTCGCCGCGG GACCCACCGCTGCAGCCCCCCAGCCTGCCACCTATGA CCCGGGTCTGAAGCCTCCGCGCTGCCCGCGGCCCCGA CGTGAGCCCTGCGAGCGGCCCTGACTCCCACCCACTC CCGTCCGCAGCTGAGCGGCAGCCAGATGAGCCTGTCA GGCGACGCGGAGGCGGTGCAGGTCCGCGGCTCCGTGC ACTTCGCGCTGCACTACGAGCCGGGCGCCGCCGAGCT GCGCGTGCACGTGATCCAGTGCCAGGGCCTGGCCGCC GCCCGGCGCC
5	Chr 1	41540915	41541160	chr1: 41540915-41541160	CGGGTTTAGCTGGACTCTAAATGGACACTGCAACCAC ACTGGTGCTCCAGACATAAACAGCCAGTAGGTGAGTG GGTGGGAAAACAGGAAGGAAGGGAGGGTGTGGTCACG GCTCAGAGGACTGAGGTGGCCTGTCTGATTAGGACGC TGCGAGTGCAGTGGTTAGGCATGGGGTGTTGATGCAT CAGACTGCCGAGTTCAAATCCTGCCTCCTCCGACCAG CTGTGTGATCCTGAGCAAGCACCC
6	Chr 1	41618187	41618276	chr1: 41618187-41618276	CGCTGCGGGATGGTGCCAGAGCCCGGAGCCACCAGGC TTGCCACTCTGGCTGCCACACAGAAGAGTCTCCTTGC GCTCAGCAGACTCTGC
7	Chr 4	2805929	2805990	chr4: 2805929-2805990	CGCGGGGAGACGCCTGTTCTGGAGGCCAGGCCCGCAG GCAGGAAGGAAAAGCACGGCCGGAC
8	Chr 4	2825167	2825265	chr4: 2825167-2825265	CGAAAAGAAAGACCTGCCCTTGGACACCAGGTGAGCC CGGGCCCAGGGCATACCGGGCAGTGAGGGTCCCTGGG GCGCCTGGGCCTGACCCGGGTGTCC
9	Chr 5	172669962	172670083	chr5: 172669962-172670083	CGTTCACGCAGCGGCCCATCCGGCTGTACGAGCAGGT GCGGCTGCGCCTGGTGGCCGTGCGCCCTGGCTGGAGC GGCGCGCTGCGCTTCGGCTTCACCGCGCACGATCCGT CGCTCATGAGC
10	Chr 5	172683900	172684098	chr5: 172683900-172684098	CGAGCTGCCCGCCGACCCAGACGCGCTGCTCGACCGC AAAGAGTACTGGGTGGTGGCGCGCGCCGGGCCCGTGC CGAGCGGCGGCGACGCGCTCAGCTTCACGCTGCGGCC CGGCGGCGACGTGCTCCTGGGCATCAACGGGCGTCCG CGCGGCCGCCTGCTGTGCGTCGACACCACGCAGGCGC TCTGGGCCTTCTTC
11	Chr 7	1946572	1946581	chr7: 1946572-1946581	TGACTCAACA
12	Chr 7	1946583	1946636	chr7: 1946583-1946636	AAATCTTTCACTTGCAGAGCGAGCAGGCGCTCTGGTG CTGCTACCCAGCGCGGT
13	Chr 7	2113040	2113199	chr7: 2113040-2113199	CGACGAGGGGCAGAGCCTCCCTCAGCAAAGCGTCCCA CTCAGGAAACGGGGACGAGGGGCAGAGCCTCCCTCAG CAAAGCGTCCCACTCAGGAAACGGGGACGAGGGGCAG AGCCTCCCTCAGCAAAGCGTCCCACTCAGGAAACACG GAAGAGACGGGC
14	Chr 7	50782213	50782314	chr7: 50782213-50782314	CGGCAACGAAGCTCGGGATCTCGGACTGCAGCGAGCC CGCGGCAGGCGGGCAGGGGGCCGCGCGGCAAGACCTC CCCGCCTCCCTCCCGGGCCCTGTCCGCC

TABLE 3-continued

DMR Sequences:

SEQ ID NO:	Chr.	Start	End	hg38coord	cdna
15	Chr 7	50782337	50782376	chr7: 50782337-50782376	GCGCAGGCCGATCCGCCCGCCGCCCCGGCTCGCGCCC ACC
16	Chr 7	50783121	50783181	chr7: 50783121-50783181	GCAGACAGGCGGGGGACATCGCGGCCGCGGCAAGCTA GAGATGCCGCCTGCTCGAGCAACC
17	Chr 7	94656373	94656577	chr7: 94656373-94656577	CGCGCTTCAACTTCGGTTGGTGTGTGTCGAAGAAACC TGACTGCGCCCTGAGGAGAACAGCGGAGAAGGTCCAC CGAGCCTGGCGAAAGGTCCGCTGAGCGGGCTGTCGTC CGGAGCCACTCCGGGCTGCGGAGCACCCAGTGGAGAC CGCGCCTGGCTCAGGTGTGGGACCCCATCCTTCCTGT CTTCGCAGAGGAGTCCTCGC
18	Chr 7	94658334	94658421	chr7: 94658334-94658421	CTGGGCCCGCCTCCTCTGAGGTGAACTGCCCAGGCCC CGCCTCTCCTGGGCCCGCCTCCTCTGATGTGAGCTCA CCCAGATCCCACCT
19	Chr 7	94658422	94658431	chr7: 94658422-94658431	CCCCAGGCCC
20	Chr 8	140098781	140098880	chr8: 140098781-140098880	CGCCCACCCAGGTCCTCCGCAGCTGTCCGCAGGGGAA GACACCAGCTAGATGTAAGTGCGCAGCTGCAGCAATC CCGCGATCCACAAAGTAATGACGCCC
21	Chr 8	140098798	140098899	chr8: 140098798-140098899	CGCAGCTGTCCGCAGGGGAAGACACCAGCTAGATGTA AGTGCGCAGCTGCAGCAATCCCGCGATCCACAAAGTA ATGACGCCCGCCCAGATCCTCCGCAGCC
22	Chr 8	140099819	140100255	chr8: 140099819-140100255	CGCTGGTCCTCCGCAGCCTTCTCCAGGGGAGGACACC CAGCTAGGTCTCTGCGCAGCTGCAGGAGTGCCACAAT CCTCAGGGTACTGACGCTCACCCAGGTCCTCCGCAGC CTTCCGCAGGGGAGATACCCAGCTAGGTCTCAGCGCG CAGCTTCAGCATCCCCGCGATCCGCAGAGTATTGACG CCCACCCGGGTCCTCCGCAGCCTAGAGCAAGGGACTG CGGAACGAGTGCCGCAATCTTCAGGGTATTGACGCCC ACCCGGGTCCTCCGCAGCCAAGAGCAAGGGACTGCGG AAGGAGTGCCGCAATCTTCAGGGTATTGACGCCCACC CGGGTCCTCCGCAGCCTAGAGCAGGGAACTGCGGAAA GAGTGCCACAATCCTCAGGGTATTGACGCCCACCCAA GTCCTCCGCAGCCTTCCGCAGGGGAGATAC
23	Chr 10	309028	309164	chr10: 309028-309164	CGGAGCGGCTGCTGACGGCGATAAGGGAAGGCACCAT GTCCCACGCACTTCACCTAAGCAACAATGAACGGGCA CCTCTACAGTCACCAAGTGGAAGATGATCTGTTTCAA CGGGGGAAGTCTGCAGTAAAAATGAC
24	Chr 10	329499	329561	chr10: 329499-329561	CGTGTCTCGGACTTTGTACTGACTCACGGCAAGAAGC CACAAGGCGGGGTTGGTTTCCAGCTC
25	Chr 10	355287	355459	chr10: 355287-355459	CGACACGCGCTTCTCTGGCAGAGGAGGAGGAGAGGTT GTTCCTATGAACTAAGCCACGTGCAGAGAATGGTCTG ATAACTGAAACTCAAACCAGAGAGTCGGGGAATAATT TCGTGATGCTGCTGGCATTTCCTTTTGTCTTCAATCT GCTGCTTCGCACACTAAGATTTTGA
26	Chr 10	355461	355490	chr10: 355461-355490	ACTCAGCAATTCTAAACAGCCATGACTTTT
27	Chr 10	355492	355503	chr10: 355492-355503	GAAGAGTTGCAA
28	Chr 10	355504	355516	chr10: 355504-355516	GTACCTATACTTG
29	Chr 10	355517	355541	chr10: 355517-355541	TCAAGAAGACTTACATTTTTCTTCC

TABLE 3-continued

DMR Sequences:

SEQ ID NO:	Chr.	Start	End	hg38coord	cdna
30	Chr 10	413853	414117	chr10: 413853-414117	CGTTCGGGAGTGGCTGTGCGAGGGGGTGGGCAAAGGG CAGAGAGTGAGCCTGGGGATTACCGTAAGTGAGGATG TAGAGGGGCTTCCCGTTGGTGTCCATGGTGGTCAGGC AGGGCGCCTTGGGCGAGATGGTGCCCCACCTCTGCAG TGCGGCCTCCAGCGACGGCGGCCAGTTCGTGACCACG CCCAGCTGCTCTCCGCGCATGGCCAGCATCTGGGCCC CCTCCGGCTTTGGTTGGTTCGGATCCGGTTGTTGAAC TAAATC
31	Chr 10	484804	484931	chr10: 484804-484931	CGGTTCCCTGCGGTGCTGGCCACCCGCTCCCGAGCCG CAGCTTCTCGGACGTCGCACACCCCGATGTGGGCAGA GCGGAATGTTCTCCTCGGCGCTCCTTCACTGTGCTGC AGTCTACACCGAACCAC
32	Chr 10	132607036	132607056	chr10: 132607036-132607056	CGGCTTGTGCTGAGTGCTCGC
33	Chr 10	132607057	132607061	chr10: 132607057-132607061	GCTCA
34	Chr 10	132616356	132616412	chr10: 132616356-132616412	CGTGGCGTGCGGGGACGCCGTGGGCGTGGTGTGAGGT ATGTGGCGTGCGGGGACGCC
35	Chr 11	2133265	2133335	chr11: 2133265-2133335	CGCTCTTCCGCCTGAGCCGCCCGCCTGACCTGACAGG CCACCCCTGTGACTGATCAGTGACTTGAGCTAAT
36	Chr 11	2133341	2133722	chr11: 2133341-2133722	CGGGCAGAGGGACAGAAGGAGCCAGCGTCTGAGCTGC TCCCGGGCCACACAGCAAGCAAGGAAGTCACGGGTCC TTGTCCCTGGCCAAGAGGTCCCAGAGGCCACAGGAAA CGCTGGGCGCCCGAAGCCCTATTTCTCTGTCTCTAGA GAGTGGGAAAGGGGCCCAGGACCCTCACCGGAAGCAC GGTCGGAGGGGTCGACACGTCCCTCTCGGACTTGGCG GGGGTAGCACAGTACGTCTCCAGGAGGGCCAGGTCAC AGCTGCGGAAACAGCACTCCTCAACGATGCCACGGCT GCGACGGCTCACACGGCTTGCGGGCCTGCCTGGAAGT CCCACAGCACAGAGAGAGCCGTGTTAGCACCGCACTG ACCCCAGCCCCC
37	Chr 11	133081982	133082177	chr11: 133081982-133082177	CGGGAAGTTCTGTCCCTGCTCCCGAGTGTGCCCAGAG TCCTGCCGTTTCCTTCTAGCGCGCGTTCTTTACTGGC GCCATTCCTGCTGCTAAGAGCCCTGAGACGGCCGGGG GTGACCCGGGCCCAGAGCAGCTCCCGGCTCAGGGACC CCTCCCCAGGCCAAGGGCAGGACAAGCCCGGGCCTGG GCCTCCGCCTC
38	Chr 12	1811666	1811837	chr12: 1811666-1811837	CGCGTTGCCGCCCAGAATTTGCGCTGGAGGAATTCCA GCTTCATTTGGACGCCCGCGGCTACAGGGCAGAAAGA GAGAGGGCAAGGCCAGGGAAGAGACGGGGAGAGAAAA AAATAGAGTCAAGTTAAAGAGAGGAGGTGCTTCCGCA GGAACTGAGGAGAGAGACCGCAGC
39	Chr 12	1838231	1838295	chr12: 1838231-1838295	CGGTGGTGTTATACACGGCAGTGACGCGCAGCCCGCC ACTGCCCCCGTGGCTGGGCTGAGTGCCC
40	Chr 12	1842428	1842506	chr12: 1842428-1842506	CGCGGTTGTTTTCCTTCTTTTGGGGTGGAAGGGAGTG TGCAGAGGTGGCCATGTGTCTAAGCGTGTGTGTGCGC TGAGC
41	Chr 12	123034226	123034317	chr12: 123034226-123034317	CGTCTGGGCCAGGGAGATAATGGTGCTGAACGCAAGG GCAAGTGTTCGCGTTGTAGGCGGCGGGACACAGTGCC GGAAAGCAATCTGATGCC
42	Chr 12	123077953	123078020	chr12: 123077953-123078020	CACGCAGCTCTCCCAGCAGCCCATGCCTGGAGACAGA GGACACTGAGGAGCACGCGTGTCCCCAGGAT

TABLE 3-continued

DMR Sequences:

SEQ ID NO:	Chr.	Start	End	hg38coord	cdna
43	Chr 16	88500291	88500408	chr16: 88500291-88500408	CGGGGACACAGCCAGCTCCCCCCATGAGCTGGTGGCC TCGTCAGGAAGACGGCCACAGGGCGCTCTTGGGAGGA CCCTTGGGACAGTGGGCAGGCGCTGGGCAAGCCACAA GCGTGTC
44	Chr 16	88534642	88534701	chr16: 88534642-88534701	CGGCCGACCGCGGCCCCTCGCCCGCTCCCGCCCCCGC CGCCTCCCCGCAGCCCGGGTCCC
45	Chr 17	410141	410147	chr17: 410141-410147	CGCACCG
46	Chr 17	414205	414425	chr17: 414205-414425	CGTATCTGAAGGAAACAGATGTTCGGTACACGGACGA CGCCGACTCTCCCATCACCAAGCTGCCCTCGGTTGCC CAGGAGAGCCACAGTGCCTTGAGAACATAAGCAATTT AGTGAACAGAGTTCTTTTCAGAATTTCCTTTTTCTTA AGTAAGCATCTCTGTTACTTAATTTCTCACCACAGCT AGATGTCTATAATCTGCCCCAAAAAGAAAAGAAAGC
47	Chr 17	2837445	2837518	chr17: 2837445-2837518	CGGAGCAGGCAGAAAGGCATATTCCGCTTCGTCTGGT GATGGGCATCGGGAGTCTCTGGCCGAGTCAGCTCCTC
48	Chr 17	2852762	2852873	chr17: 2852762-2852873	CGGGAGGGGGCTGGGAGGCTGGGCAGCACCTGGAAGT GGATGAGGGCGATTGTGAGCGAGGCCCCGCGCCGATG GTAGGGACCAGGCCACAGCCCTTTCCCCAGGAGCCGG C
49	Chr 17	82235989	82236062	chr17: 82235989-82236062	CGGAACCAACCCTCCTGGCCATGGGAGGGGCCGTGGT GGACGAGGGCCCCACAGGCGTCAAGGCCCCTGACGGC
50	Chr 17	82238736	82238899	chr17: 82238736-82238899	CGTGTTCATCCTGGCGGGGGCCGAGGTGCTCACCTCC TCCCTGATTTTGCTGCTGGGCAACTTCTTCTGCATTA GGAAGAAGCCCAAAGAGCCACAGCCTGAGGTGGCGGC CGCGGAGGAGGAGAAGCTCCACAAGCCTCCTGCAGAC TCGGGGGTGGACTTGC
51	Chr 18	79436203	79436269	chr18: 79436203-79436269	CGCTTTTCAGAAACGAGGCTCATCGCACTGGCCTGGG GGCGCGAGGACGAGGCCGTGGGTAGTGGGC
52	Chr 18	79509085	79509203	chr18: 79509085-79509203	CGCATGGAAGGAAACGCCATTGCTGGGCAGTGTTGCA GCCTCCGCAGAGGTGTGTGGGCTCCGGGGAGAGGGAC GTGCTGGCCCCTGTGCAGTGGCGTGGCCCGTGTCCTT TCCCCGCC
53	Chr 18	79523293	79523358	chr18: 79523293-79523358	CGTTCAGGCCCTGGCAGCTCCGTTCTGGCCCTCATCA TTCCCAGCATAGAGAAACAAAACTCCTGC
54	Chr 19	659125	659132	chr19: 659125-659132	AGAGGCAG
55	Chr 19	659138	659172	chr19: 659138-659172	GGCTGTCACTGTCACGGTATCTGGCACAACCGCAG
56	Chr 19	659175	659216	chr19: 659175-659216	ACACAGAGCAAGCAGCGGCCAGAGACAGACCCAGGCC GTCTT
57	Chr 19	659431	659723	chr19: 659431-659723	CGGAGGTTGCAGGCGTTCGGGGGTGGGGGGTCGGCAG GCAGAGCTGGAACCACCCTAGGAACCACCCAGAGACG GGGAGGTCAGGGGCAAGGACGGCACGCAGGGCCACCT CCCTGCGCCCGCCTGGTTCCTGGGGGCTCAGTGCCCT CAGCAGCTCTCGCCCACACCCTACAGTCACAGCTCCA GTCAGTGCCTCCTCAGCAGGCTCGAGTCTGGGTCTGC GCAGCCGCCTGTGGCCTGAGCTCCAGCTGGCCTGTCT GGTTCCTGCCGCCACACGCCCCACTCTGGCTGAC

TABLE 3-continued

DMR Sequences:

SEQ ID NO:	Chr.	Start	End	hg38coord	cdna
58	Chr 19	676722	676962	chr19: 676722-676962	CGCTGACATTTATTGAGCGCTTAGTGTCTACCTCTCC CCTCCCTGAACCTGTGCCATCCCGATAGTGCCGGAGC TCTCTTCATCTCCGTCTTCCAGATGGGGAAACTGAGG CTCAGGGTCACACAGCCTGTAGCAGGCAAAGCCAGGG TTCTAGCCGCGACCGTCCGGGTCGGTCCTGGTGCCGA GAGGTAGTGCTGGGTGTCGGGAGCCAGGCCCTCCAGC TGGGGCTGAGAGCTTTCCC
59	Chr 19	18762214	18762355	chr19: 18762214-18762355	CGCCCGGGAGCTGCGCACCTCCAGCAGGCACCCAGTC TAAACAAGCACAAGGAAACACACAACATACGTGGAAG CTGGAGCCGGCGCTGGCCAGAGCGGCCCGGTAATGCC TGACATGTGTTGGGTTGTTTGTGAACCTGCC
60	Chr 19	18777827	18778074	chr19: 18777827-18778074	CGGTCCCCCAGCCCATCCGCCATCCCCAGCCCGTGGT CAGGTAGAGAGTGAGCCCCACGCCGCCCCCAGGGAGGA GGCGCCAGAGCGCGGGGCAGACGCAAAGTGAAATAAA CACTATTTTGACGGCTGTCTTTTATATTTCTGAGCAC ACACAGAGCCCTGGCGTCCACCGGGGCAGGCGCAAAG TGGACAGAGCATGCAGGGCGGCGGACCCCCCCACGAC CCTCCTCGCCCTGTCTCCATCCCCTC
61	Chr 19	56838765	56839239	chr19: 56838765-56839239	CGACCAGCACACACAGCCCAAGGAGCGCGGCACTCCA CAGCTTTCCATCACCGCAAGGCAGGCAAGCACAGCAA CCGTGGCCCCGCCCCTCCCTGTGGACAACCCCACACC TATGCGGCAAACCGCAGCCGCCCCGATCAAAGATGGC ACCCAGGTGGGCGGGGCTTGAACAGACCGTCCCGCCC ATGCCACCTGCAGCCACTTCAGCCTTGCCCCGCCGCA TCTGCCGCCAACCAATCCGGGCAACGCCTGCGCGGCA AACCTCAGCTGCCCCCATCAAAGATGGCGCCCAGGCG GGCGGGCCTTGTCTCGCCCAACCAACTAGGACAGCGC CTGCGCAGCAAATCTCAAGCACTTTCATTAAAGATGG CGCCCAGGTGGGTGGGGCTTGAACAAACCACTAGGTC CAATGCCACCCTGTCACTTCAGCCTTGCCCCGCCCCA TCTGCCACCAACCAACCAGGACAGCACCTGC
62	Chr 19	56840640	56840712	chr19: 56840640-56840712	GCCCGGCGCCCGGCGGCGCCACCAGCCCAGGGTGGAC ATCTCCCGCGCCTCCCAAACCTCTCCTCCCGCAGCT
63	Chr 19	56840714	56840745	chr19: 56840714-56840745	CCCAGACTTCTGCACCGAGGTGCAGCTCGACG
64	Chr 20	3751818	3752296	chr20: 3751818-3752296	CGACGTCTTCGAGCGCTTCGTGGCCGCCGAGCAGTCG GTGGCCCTGGGCGAGGAGGTGCGGCGCAGCTACTGCC CGGCGCGTCCCGGCCAGCGGCGCGTACTCATCAACCT GTACTGCTGCGCGGCAGAGGATGCGCGCTTCATCACC GACCCCGGCGTGCGCAAATGCGGCGCGCTCAGCCTCG AGCTTGAGCCCGCCGACTGCGGCCAGGACACCGCCGG CGCGCCTCCCGGCCGCCGCGAGATCCGCGCCGCCATG CAGTTTGGCGACACCGAAATTAAGGTCACCGCCGTCG ACGTCAGCACCAATCGCTCCGTGCGCGCGTCCATCGA CTTTCTTTCCAACTGAGGGCGCGCCGGCGCGGTGCCA GCGCCGTCTGCCCGGCCCCGCCCTCTTTCGGTTCAGG GGCCTGCGGAGCGGGTTGGGGCGGGGGAAACGATAGT TCTGCAGTCTGCGCCTTTCCACGCCCTCCAGCCCC
65	Chr 20	3751944	3752172	chr20: 3751944-3752172	AGAGGATGCGCGCTTCATCACCGACCCCGGCGTGCGC AAATGCGGCGCGCTCAGCCTCGAGCTTGAGCCCGCCG ACTGCGGCCAGGACACCGCCGGCGCGCCTCCCGGCCG CCGCGAGATCCGCGCCGCCATGCAGTTTGGCGACACC GAAATTAAGGTCACCGCCGTCGACGTCAGCACCAATC GCTCCGTGCGCGCGTCCATCGACTTTCTTTCCAACTG AGGGCGC
66	Chr 20	58839989	58840198	chr20: 58839989-58840198	CGGGCCAGCTTCTCACCTCATAGGGTGTACCTTTCCC GGCTCCAGCAGCCAATGTGCTTCGGAGCCACTCTCTG CAGAGCCAGAGGGCAGGCCGGCTTCTCGGTGTGTGCC TAAGAGGATGGATCGGAGGTCCCGGGCTCAGCAGTGG CGCCGAGCTCGCCATAATTACAACGACCTGTGCCCGC CCATAGGCCGCCGGGCAGCCACCGC

TABLE 3-continued

DMR Sequences:

SEQ ID NO:	Chr.	Start	End	hg38coord	cdna
67	Chr 20	58850827	58850895	chr20: 58850827-58850895	CGCCATACACCCGCCCCCCACCGGCTTCCAACCACCC CAGCAGCACCTCTTCGGGCGTTCCAACGCGGC
68	Chr 20	58855291	58855453	chr20: 58855291-58855453	GAAAAGATGGGCTACATGTGTACGCACCGCCTGCTGC TTCTAGGTAATGCGGCGGACTCTGCCTGCGGGCAGCA GGGCCGCCGGGGAACCGGGGAGGGGGTGGCAGGGCTG CCTGGTGGGGCTAGGGGCTCCGCAGTGGGAGGAGGGG GTCCAGCCAAAGGCG
69	Chr 20	58889570	58890047	chr20: 58889570-58890047	CGCGCCTTTGCACTTTTCTTTTTGAGTTGACATTTCT TGGTGCTTTTTGGTTTCTCGCTGTTGTTGGGTGCTTT TTGGTTTGTTCTTGTCCCTTTTTCGTTTGCTCATCCT TTTTGGCGCTAACTCTTAGGCAGCCAGCCCAGCAGCC CGAAGCCCGGGCAGCCGCGCTCCGCGGCCCCGGGGCA GCGCGGCGGGAACCGCAGCCAAGCCCCCCGACACGGG GCGCACGGGGGCCGGGCAGCCCGAGGCCGGGGGCAAG CAGGGAGCCCGGGCCAGGCGCGAGCCGAGCTCCCCGA GGTGGCCGGGCCACCATGCTGAAGATGGCCATGAAGC TCAAAGCCCGGGCGGCGGAGAGCGAGAAGAAGACGGC CGCGGCGGCTGCCGAGGTGGCTGCCGAAGCTGCGGCG GCGGCTGCGGCGTTGGCCGAGCCGAGAGAGCCGCTCG CGCCGCGGAAGAGCGGGGACCCCGAGAAGCTCGC
70	Chr 20	58890242	58890319	chr20: 58890242-58890319	GATGCCCCGAGGCCGCCGCCGCCGCGGCCGCCGCCGA CGACGACGAGGGCGCCGAGGAGGGCGCCGTCGGGGGC GCCG
71	Chr 21	43725878	43725960	chr21: 43725878-43725960	CGGTGGCCCGCACTAACTTCCTTAGAGGTGATGCTGA TGCTGTATGTTGGAGACGCTTCTGAGTGTCCTCGGAA CGTTCCCAC
72	Chr 21	43727343	43727431	chr21: 43727343-43727431	GCCGAGGAGGGGCCGGCAGCGCCTCCCTTCCTGCCCA CAGAGCAGCCGCCTTGTGCCCATCTATTCCCCGGCTC TGCATGGGGCCTCTG
73	Chr 21	43758088	43758098	chr21: 43758088-43758098	GCAGTGTCAGG
74	Chr 21	43758106	43758177	chr21: 43758106-43758177	CTCCTTCTGCCCCTGCAGTGGGTGTTACGGGCGGTGT GCCCTGGCGAGCAAGCTTTGATTCTTGGTTCTTTG
75	Chr 21	43758178	43758183	chr21: 43758178-43758183	AGCTCG

Any combination of DMRs outlined in Table 2 may be used to diagnose or give a prognosis of AT or trait-like anxiety in a human or non-human primate. Any combination of DMRs outlined in Table 2 may be used in an assay to quantify methylation. Any combination of DMRs outlined in Table 2 or DMR-associated genes outline in Table 1 may be used in an assay to amplify the DMRs or DMR-associated genes for sequencing to quantify methylation.

In some embodiments, the DMRs of interest are SEQ ID NOs:7-18, 50-59, 67-69, and 73-75. In some embodiments, the DMR-associated genes of interest are DIP2C, GRB10, INPP5A, GNAS, PDXK, and TRAPPC9. These DMRs and DMR-associated genes showed differential methylation across samples from non-human primate brain, non-human primate blood, and human blood. In some embodiments, at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 26, at least 27, or all 28 of the DMRs of SEQ ID NOs: 7-18, 50-59, 67-69, and 73-75 are assayed to diagnose or give a prognosis of AT or trait-like anxiety in a human or non-human primate. In some embodiments, at least 1, at least 2, at least 3, at least 4, at least 5, at least or all 6 of the DMR-associated genes are assayed to diagnose or give a prognosis of AT or trait-like anxiety in a human or non-human primate.

In some embodiments, the DMRs of interest are SEQ ID NOs:3-6, 19-20, and 27-37. In some embodiments, the DMR-associated genes of interest are HIVEP3, C17orf97, ZFPM1, RAP1GAP2, NFATC1, IGF2, SLC16A3, and SYTL1. These DMRs and DMR-associated genes showed differential methylation across samples from non-human primate blood and human blood. In some embodiments, at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, or all 17 of these DMRs are assayed to diagnose or given a prognosis of AT or trait-like anxiety in a human or non-human primate. In some embodiments, at least 1, at least 2, at least 3, at least

4, at least 5, at least 6, at least 7 or all 8 of the DMR-associated genes are assayed to diagnose or give a prognosis of AT or trait-like anxiety in a human or non-human primate.

In some embodiments, the DMRs of interest are SEQ ID NOs: 1-2, 21-26, 38-49, 60-66, and 70-72. In some embodiments, the DMR-associated genes of interest are CACNA2D4, CRTC1, MEGF6, OPCML, PITPNM2, ZIM2, RNF126, FSTL3, SH3BP2, NEURL1B, MAD1L1, HSPA12B, PEG10, and PEG3. These DMRs and DMR-associated genes showed differential methylation across samples from human blood and non-human primate brain. In some embodiments, at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 26, at least 27, at least 28, at least 29, or all 30 of these DMRs are assayed to diagnose or give a prognosis of AT or trait-like anxiety in a human or non-human primate. In some embodiments, at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, or all 14 of the DMR-associated genes are assayed to diagnose or give a prognosis of AT or trait-like anxiety in a human or non-human primate.

Biomarker Panels

In some embodiments, the biomarkers described herein are used in the production of a biomarker panel for use in assaying DNA methylation. The biomarker panel includes probes or primers specific to the sequences of the DMRs or DMR-associated genes disclosed herein. In some embodiments, the biomarker panel includes probes or primers specific to the sequences of the DMR-associated genes listed in Table 1. In some embodiments, the biomarker panel includes probes or primers specific to the DMRs listed in Table 2.

Primers specific to the DMRs or DMR-associated genes disclosed herein are between about 10 base pairs (bp) and about 40 bp and are complementary to sequences upstream and downstream of the DMR or DMR-associated gene of interest. Generally, a pair of forward and reverse primers that are designed to be complementary to the sequences flanking the DMR or DMR-associated gene are included. The size of the fragment to be amplified by the primer pair can range from less than 50 bp to greater than 10,000 bp. Primers can be designed that are complementary to a sequence less than 50 bp upstream of the DMR or more than 1,000 bp upstream depending on the sequence technology selected and the application of the biomarker panel. Therefore, it is possible to design many permutations of primer sets that are capable of amplifying a given DMR or DMR-associated gene of interest. For example, a given sample containing genomic DNA with a 500 bp DMR, a primer set can be designed to amplify i) the exact target region; or ii) a region encompassing the DMR including upstream and downstream regions.

Probes specific to the DMRs or DMR-associated genes disclosed herein are between about 10 bp and about 40 bp and are commentary to sequences including or adjacent to the DMR or DMR-associated gene of interest. In some embodiments, the probe is complementary to the DMR of interest.

The disclosure includes a number of preferred primers and probes for amplification, selection, and identification of specific DMRs or DMR-associated genes. However, a skilled artisan will appreciate that the DMRs and DMR-associated genes disclosed can be amplified, selected, and identified by primers and probes other than those specific disclosed, which have been presented for purposes of illustration. It is contemplated that the biomarker panel is compatible with a number of amplification and sequencing schemes and the scope of the claims should not be limited to the description of the embodiments contained herein.

Probes or primers for use in the biomarker panels described herein may be fused to a tag or label. Suitable tags and labels are known in the art, including but not limited to fluorescent labels (e.g., GFP, RFP, etc.), biotin, and combinations thereof. In some embodiments, the probe or primer is biotinylated and the biotinylated probe or primer bound sequence can be purified or captured with a streptavidin bound substrate.

In some embodiments, the primers or probes are covalently or non-covalently linked to a substrate. Suitable substrates for the biomarker panel include a bead, a plate, a microfluidic devise, a cuvette, a chip, a multiwell plate (e.g., 6-, 12-, 24-, 48-, 96-, 384-, or 1536-well plates).

In some embodiments, the biomarker panel is a microarray.

In some embodiments, the primers or probes are biotinylated and bind to streptavidin coated substrates for selection of the DMRs or DMR-associated genes targeted by the probe or primers. In some embodiments, the streptavidin-coated substrates are beads.

Methods

In some aspects, described herein are methods to assay the methylation status of DMRs or DMR-associated genes described herein to diagnose or give a prognosis for AT or trait-like anxiety in an individual. Methylation levels of at least one DMR or DMR-associated gene recited in Table 2, or any combination of DMRs or DMR-associated genes, is measured in target DNA from a blood sample or saliva sample from a human or non-human primate.

Methylation may be quantified by any suitable means known in the art. Suitable methods for assaying quantification are disclosed, for example, by Kurdyukov and Bullock ("DNA methylation analysis: Choosing the right method," Biology, 2016, 5(3)). Suitable methods for quantifying or assaying methylation may include, but are not limited to methylation specific polymerase chain reaction (PCR), high resolution melting, cold-PCR, pyrosequencing, PCR and sequencing, bead array, and digestion-based assay followed by PCR or quantitative PCR (qPCR).

In some embodiments, the target DNA is bisulfite modified. Bisulfite treatment mediates the deamination of cytosine to uracil, whereby the modified uracil residue will be read as a thymine as determined by PCR-amplification and sequencing. 5mC resides are protected from this conversion and will remain as cytosine.

To examine the methylation status of the DMR or DMR-associated gene, target genomic DNA may be isolated from a blood sample or a saliva sample from a subject. In some embodiments, the target DNA is isolated from a blood sample from a human or non-human primate. In some embodiments, the target DNA is isolated from a saliva sample from a human or non-human primate.

Following isolation of target DNA, the target DNA will be contacted with probes specific to the DMRs outlined in Table 2 to isolate and enrich these genomic regions from the target DNA sample. In some embodiments, sequences of the DMR is used as bait to isolate the genomic regions of interest for amplification and sequencing.

After isolation and enrichment of the genomic regions within the target DNA that include the DMR, methylated adapters are ligated to the enriched regions. The sample with

the ligated methylated adapters may then be subject to sodium bisulfite modification.

In general, target DNA or bisulfite modified target DNA is subject to amplification. The amplification may be polymerase chain reaction (PCR) amplification. PCR amplification will include single or multiple pair(s) of primers and probes at specific DMRs within the DIP2C, GRB10, INPP5A, C17ORF97, PDXK, CACNA2D4, TRAPPC9, CRTC1, MEGF6, HIVEP3, OPCML, PITPNM2, ZFPM1, RAP1GAP2, NFATC1, RNF126, FSTL3, GNAS, SH3BP2, NEURL1B, MAD1L1, HSPA12B, IGF2, PEG10, PEGS, SLC16A3, SYTL1, and ZIM2 genes as outlined in Table 2. The target DNA amplification and methylation quantification will be evaluated in one or multiple tubes.

In some embodiments, methylation is quantified by amplification and sequencing of target DNA. Bisulfite modified target DNA may be subject to PCR to amplify target regions outlined in Table 2. The PCR reaction mixture typically includes at least one pair of primers designed to target a DMR detailed in Table 2, PCR buffer, dNTPs (e.g., adenine, thymine, cytosine and guanine), $MgCl_2$, and polymerase. PCR amplification generally includes the steps of heating the reaction mixture to separate the strands of the target DNA, annealing the primers to the target DNA by cooling the reaction mixture, allowing the polymerase to extend the primers by addition of NTPs, and repeating the process at least 2, at least 5, at least 10, at least 15, at least 20, at least 25, or at least 30 times to produce a PCR amplification product. If the target DNA in the reaction mixture is single stranded, the initial heating step may be omitted, however this heating step will need to be included when the second and subsequent times the reaction is completed to separate the extended primer strands from the opposite strand and DNA (e.g., the target DNA or another previously extended primer strand). In some embodiments, the target DNA is bisulfite modified prior to amplification.

In some embodiments, the bisulfite modified target DNA is used in a methylation-specific-quantitative PCR (MS-QPCR) reaction such as MethylLight (WO 2000/070090A1) or HeavyMethyl (WO 2002/072880A2). For example, a reaction mixture for use in a MethylLight methylation specific PCR reaction would contain primers and probes specific to the DMRs recited in Table 2, PCR buffer, dNTPs (e.g., adenine, thymine, cytosine and guanine), $MgCl_2$, and polymerase. A typical kit for methylation specific PCR may include primers and probes specific to the DMRs recited in Table 2, wild type reference gene primers such as (3-actin, PCR buffer, dNTPs, $MgCl_2$, polymerase, positive and negative methylation controls, and a dilution reference. The MS-QPCR may be carried out in one or multiple reaction tubes.

In some embodiments, either the forward or reverse primer of the primer pair used in the PCR amplification reaction is biotinylated. When a biotinylated primer is used in a PCR amplification reaction, PCR products may be purified, captured, and/or sorted with a streptavidin coated substrate. In some embodiments, the substrate is a streptavidin coated bead. In some embodiments, the beads are streptavidin sepharose beads. In some embodiments, the beads are magnetic.

In some embodiments, the PCR amplification product is contacted with one or more probes specific for and complementary to a DMR detailed in Table 2. The probe may be biotinylated. The PCR amplification product and probe mixture can then be purified, captured and/or sorted with a streptavidin-coated substrate. In some embodiments, the substrate is a streptavidin-coated bead. In some embodiments, the beads are streptavidin sepharose beads. In some embodiments, the streptavidin beads are magnetic.

In some embodiments, methylation is quantified using pyrosequencing. Bisulfite modified target DNA may be subject to PCR to amplify target regions outlined in Table 2 as described above. PCR amplification products are purified, denatured to single-stranded DNA, and annealed to a sequencing primer for methylation quantification by pyrosequencing as the DMR or DMR-associated gene as detailed in Table 2. In some embodiments, methylation may be quantified with PyroMark™MD Pyrosequencing System (Qiagen) using PyroPyroMark® Gold Q96 Reagents (Qiagen, Cat #972804) (QIAGEN PyroMark Gold Q96 Reagents Handbook August 2009, 36-38).

In some embodiments, bisulfite treated DNA is subject to an Invader® assay to detect changes in methylation. The Invader® assay entails the use of Invader® chemistry (Hologic Inc.; invaderchemistry.com; Day, S., and Mast, A. Invader assay, 2004; Chapter in Encyclopedia of Diagnostic Genomics and Proteomics. Marcel Dekker, Inc., U.S. Pat. Nos. 7,011,944; 6,913,881; 6,875,572 and 6,872,816). In the Invader® assay, one would use a structure-specific flap endonuclease (FEN) to cleave a three-dimensional complex formed by hybridization of C/T specific overlapping oligonucleotides to target DNA containing a CG site. Initial PCR amplification of the bisulfite treated target DNA may be necessary if the quantity of the bisulfite treated target DNA is less than 20 ng.

The present invention has been described in terms of one or more preferred embodiments, and it should be appreciated that many equivalents, alternatives, variations, and modifications, aside from those expressly stated, are possible and within the scope of the invention.

Example 1

To investigate the role of DNA methylation in the development and expression of AT, we previously performed genome-wide DNA methylation and mRNA expression analyses in Ce tissue collected from young monkeys repeatedly phenotyped for AT and its associated brain metabolism. This approach identified twenty-two genes with a significant correlation between AT-associated methylation levels and gene expression (P-value <0.05), including two glutamate receptors, GRIN1 and GRM5, both of which have reported roles in fear and anxiety-like behaviors. These findings are also likely to provide insights into novel treatment targets for individuals that have already developed clinically significant anxiety and depressive disorders.

The monozygotic (MZ) twin difference design is an ideal way to probe non-shared environmentally or experientially based relationships between HPA activity and amygdala function. MZ co-twins are identical for DNA sequence variants with the exception of rare somatic mutations. MZ twins reared together also share many non-genetic factors (e.g., age, parenting, etc.); thus, reliable MZ twin differences are attributed to unique or non-shared environmental factors. In this context, "environmental" simply means "non-genetic" and "unique" means "not shared with the co-twin." Twin studies have shown that afternoon cortisol levels and amygdala volume are strongly influenced by environmental (i.e., non-genetic) factors. In addition, a substantial portion of the individual variability in anxiety level is due to variations in non-genetic factors. We recently used this design to examine the role of DNA methylation in the development and expression of human clinical anxiety using a multi-dimensional characterization method, to select

monozygotic twin pairs discordant for anxiety, and whole genome DNA methylation sequencing. Profiling the whole blood DNA methylation levels in discordant individuals revealed 230 anxiety-related differentially methylated loci that were annotated to 183 genes, including several known stress-related genes such as NAV1, IGF2, GNAS, and CRTCJ. As an initial validation of these findings, we tested the significance of an overlap of these data with anxiety-related differentially methylated loci in the Ce of young monkeys and found a significant overlap (P-value <0.05) of anxiety-related differentially methylated genes, including GNAS, SYN3, and JAG2. Together, these data demonstrate environmentally sensitive factors that may underlie the development of human anxiety and suggested that biomarkers of human anxiety can be detected in human blood.

Here we built upon these findings and used whole genome bisulfite sequencing to examine an average of 25.3 million CpG dinucleotides in genomic DNA from the hippocampal and blood tissue of 71 monkeys (including 23 females) and found significant overlaps of DMRs in these tissues, as well as with the previously reported anxiety-related DMRs in the monkey Ce and human blood. Together, these data suggest that blood can be used as a viable surrogate to brain tissue toward the development of a blood-based biomarker profile for clinical anxiety diagnosis, to improve estimates of clinical anxiety prognosis, and to guide personalized treatment of clinical anxiety.

Materials and Methods

Tissue Acquisition and DNA/RNA Extraction—

The whole brains from seventy-one young monkeys (including 23 females) with an average age of 1.3±0.2 years and a broad range of AT levels (−1.48 to 1.43) were sectioned into 4.5 mm slabs and functionally guided tissue biopsies of the hippocampus were conducted following animal housing and experimental procedures that are in accordance with institutional guidelines (UW IACUC protocol #G00181). Hippocampal regions were identified, thawed briefly on wet ice, and placed on an inverted glass Petri dish on top of wet ice. A circular 3-mm punch tool was used to biopsy the region best corresponding to the hippocampus. The tissue punches were collected into 1.5-mL microfuge tubes and placed on dry ice. Once acquired, approximately thirty milligrams of tissue were homogenized with glass beads (Sigma) and DNA and RNA extraction was performed using AllPrep DNA/RNA mini kit (Qiagen).

Whole blood was collected from the same seventy-one young monkeys in a BD vacutainer CPT cell preparation tube with sodium heparin (cat #362753). The peripheral blood mononuclear cells were isolated and genomic DNA was extracted using Promega wizard genomic DNA purification kit (cat #A1120), following the manufacturers protocol.

Library Preparation and high-throughput sequencing of genomic DNA—

To elucidate the utility of blood DNA methylation as a potential biomarker of anxiety and depressive disorders we will perform whole genome sequencing with bisulfite pretreatment. This unbiased approach uses bisulfite exposure and deamination chemistry to convert unmethylated cytosines to uracil, while leaving methylated cytosines unmodified. Subsequent sequencing of the treated DNAs provides single base-pair resolution of all methylated sites in the rhesus genome, and will expose novel genes and alleles of interest if present. To achieve this goal, extracted genomic DNA was resolved on a 1% agarose gel to verify that the DNA is of high molecular weight, and quantified using Qubit (Qiagen™, Hilden, Germany). Genome-wide methylation data was generated at WuXi NextCode (Cambridge, Mass.) using whole genome HiSeq technologies from Illumina™ (e.g., HiSeq X ten). High quality genomic DNAs were forwarded to WuXi NextCode™ for sodium bisulfite treatment, library preparation, and whole genome sequencing. To process the samples, genomic DNA (500 ng) was randomly fragmented, end-repaired, and ligated to NEBNext Methylated Adapters for Illumina sequencing following the manufacturer's protocol (Illumina™) Adapter-ligated DNA fragments, ranging from 200 to 400 base pairs (bp), are purified by Sample Purification Beads (Illumina™) and then treated with sodium bisulfite (ZymoResearch™ EZ DNA methylation gold kit), that converts unmethylated cytosines to uracil and leaves methylated cytosines unaltered. Libraries of converted DNA fragments are then amplified using KAPA HiFi Hot Start Uracil+Ready Mix (KAPA Biosystems™ KM2801), and Index Primer for Illumina and Universal PCR Primer for Illumina (NEB™ E7336A). Amplicons are purified by Sample Purification Beads (Illumina™) and sequenced on a Next-Generation sequencer (Illumina™ HiSeq X ten). This approach yields ~3 billion 150 bp-reads for each library, which provides the methylation status of ~25 million positions in the DNA where a cytosine nucleotide is followed by a guanine nucleotide in the linear sequence of bases along its 5' →3' direction (i.e., CpG sites) with a coverage >10 reads. Image processing and sequence extraction use the standard Illumina Pipeline. Raw fastq sequence files will be forwarded to our laboratory via FedEx on an encrypted external hard drive.

DNA Methylation Detection—

Quality control, mapping, and extraction of methylation information from the whole genome sequence data was done using bowtie2 and bismark (version 0.17.0). The average number of raw reads for each sample (N=142) was 404 million reads giving an average genomic coverage of 20.23× (median genomic coverage 19.53×). The sequence data will be filtered, and low quality and adapter sequences will be removed thereby arriving at an average genomic coverage of ~20×. Cleaned sequence data are then mapped to the human *Macaca mulatta* (Rhesus monkey) reference genome (rheMac8), and an average of 283.3 million uniquely mapped reads were obtained for each sample, giving an average coverage of 14.16× (median coverage 13.86×). Sequence reads from both DNA strands (forward and reverse) were combined to determine the DNA methylation level at all CpG dinucleotides (~27.4 million). Differentially methylated regions (DMRs) were identified using the DSS-single analysis method, which was selected because it incorporates the read depth into the DMR analysis and relies on smoothing so that neighborhood CpGs can be viewed as pseudo replicates and dispersion can be estimated across an entire genomic window. AT status was treated as a continuous independent variable, while methylation level was the dependent variable. All default settings were used in the DSS package (including a smoothing span of 500 bp) and the model was adjusted for gender and age. DMRs were identified using a generalized linear model in DSS, and limiting DMRs to those having a minimum of 5 consecutive CpG dinucleotides with a difference in mean methylation of 10% between the tested variables.

RNA Library Preparation and Sequencing—

One hundred nanograms of total RNA from hippcampal tissue was used for sequence library construction following instructions of the NuGen mRNA sample prep kit (cat #0348). In brief, total RNA was copied into first strand cDNA using reverse transcriptase and random primers. This process was followed by second strand cDNA synthesis

using DNA Polymerase I and RNaseH. The cDNA fragments were end repaired, a single "A" base was added, and then ligated to adapters. The products were gel purified and enriched by PCR to generate cDNA libraries. One hundred-cycle single-end sequencing was performed by Novogene Corporation (Sacramento, Calif. USA).

RNA-Seq Processing and Analysis—

After adapter trimming of reads, a median of 20.2 million paired-end reads were obtained per sample. Quality was assessed for each pair-mate using FastQC. After reads were assured for quality, paired-end reads were aligned to the Rhesus *Macaca mulatta* reference genome (Mmul_8.0.1) using RSEMv1.3.1, which utilized STAR v2.7.0. RNA transcription was quantified using RSEM which resulted in quantification for ~30,000 ensembl genes. Genes were filtered out if the total count for the gene was less than 500, or if it was present in less than 25 of the 31 samples. This resulted in a total of 12,768 ensembl genes, corresponding to a total of 11,471 gene symbols. The samples were classified as 'high' or 'low' anxiety depending on their AT_ToD score. If the score was below 0, the sample was classified as low, and if it was above 0, it was classified as high. Differential expression analysis was then performed using the DESeq function in the DESeq2 package. Any gene with a raw P-value <0.1 and a log 2 fold change >0.1 was deemed significant.

Results

The Hippocampal Methylome of Young Rhesus Monkeys—

To characterize the DNA methylation levels across the entire hippocampus genome (i.e., the hippocampal methylome) from young primates and reveal the epigenetic basis of anxious temperament, we extracted genomic DNA from the hippocampus of seventy-one rhesus macaques. All seventy-one monkeys were young (mean age=1.3±0.2 years) with a broad range of AT levels (−1.48 to 1.43). AT is computed as a composite measure among vocalizations, cortisol levels and time freezing (mean AT score) assessed during the no eye contact (NEC) condition of the human intruder paradigm. In this study, AT levels were assessed twice and the mean score for each monkey was used for analysis. The hippocampal genomic DNA from each monkey was treated with sodium bisulfite and sequenced on a Next-generation sequencer (Materials and Methods). This approach generated DNA methylation information at ~27.4 million CpG dinucleotides from the hippocampus of rhesus macaques. To investigate comparisons across the seventy-one individual monkey genomes, the high quality methylation data was filtered for CpG data that had a sequence read depth greater than 2 and less than 100 occurring in a minimum of thirty-six monkeys (N=26,497,371). This final dataset revealed a bimodal distribution of DNA methylation in monkey hippocampal tissue, with the majority (>60%) of CpGs being more than 60% methylated.

To examine whether the rhesus hippocampus harbors differential DNA methylation that is related to individual differences in AT levels, the methylation data were subjected to a differential methylation analysis that employed a statistical algorithm that incorporates sequence data read depth and does not need data from biological replicates (Materials and Methods). This analytical approach, which limited positive results to differentially methylated regions (DMRs) that have a minimum of 5 adjacent CpG dinucleotides with a minimum mean methylation difference of 10% across the seventy-one monkeys, revealed a total of 645 AT-related differentially methylated regions. AT-related increases in methylation were classified as hyper-DMRs and anxiety-related decreases in methylation were classified as hypo-DMRs. A total of 222 hyper- and 423 hypo-DMRs were identified and these loci were distributed across all the autosomes (Dataset 1), suggesting a genome-wide decrease in DNA methylation is associated with AT which is consistent with previous studies. Annotation of these DMRs to genomic structures revealed 515 genes that are enriched for neuronal ontological functions, such as synapse assembly and neuron development. Comparison of these genes to the genes previously found in the Ce revealed a significant overlap (P-value <0.05), indicating common AT-related epigenetic disruptions in these two brain structures. Importantly, a significant overlap (P-value <0.05) also was found between these differentially methylated genes from the monkey brain and anxiety-related differentially methylated genes reported in human blood, suggesting that blood may be an accessible tissue of value in the identification of differential methylation associated with the risk to develop trait-like anxiety.

The Whole Blood Methylome of Young Rhesus Monkeys—

The genomic DNA from whole blood of the same monkeys examined above was treated with sodium bisulfite and sequenced on a Next-generation sequencer (Materials and Methods). This approach generated DNA methylation information at ~27.6 million CpG dinucleotides from the blood tissue of rhesus macaques. To investigate comparisons across the seventy-one individual monkey genomes, the high quality methylation data was filtered for CpG data that had a read depth greater than 2 and less than 100 occurring in a minimum of thirty-six monkeys (N=26,973,327). This final dataset revealed a bimodal distribution of DNA methylation in monkey hippocampal tissue, with the majority (>60%) of CpGs being more than 60% methylated.

To examine whether the rhesus blood harbors differential DNA methylation that is related to individual differences in AT levels, the methylation data were subjected to the differential methylation analysis described for the hippocampal analysis (Materials and Methods). This analytical approach revealed a total of 719 AT-related differentially methylated regions (permutation P-value <0.01). AT-related increases in methylation were classified as hyper-DMRs and anxiety-related decreases in methylation were classified as hypo-DMRs. A total of 301 hyper- and 418 hypo-DMRs were identified and these loci were distributed across all the autosomes (Dataset 1), suggesting a genome-wide increase in DNA methylation is associated with AT which is consistent with previous studies. Comparison to monkey brain DMRs finds a significant overlap (N=51; P-value <0.0001), and the test statistics of these DMRs are significantly correlated, meaning these common DMRs are largely differentially methylated in the same direction (i.e., hyper-methylated or hypo-methylated; R-squared=0.701; P-value <0.0001).

For comparisons to the anxiety-related DMRs and DMR-associated genes previously found in human blood, the DMRs found in monkeys were mapped to the human reference genome (hg38). This approach revealed an overlap of six DMR-associated genes between monkey brain, monkey blood, and human blood anxiety-related blood DMRs, including DIP2C, GRB10, and CRTC1 (FIG. **1**). Furthermore, twelve DMR-associated genes were uniquely common to the monkey brain and human blood, and eight DMR-associated genes were uniquely common to monkey blood and human blood. These DMRs comprise multiple CpGs and a greater than 10% differential methylation related to anxiety (FIG. **2**), which serves to substantiate these

findings. Together, these data indicate that human blood contains anxiety-related changes in DNA methylation that provides the foundation for developing a blood-based biomarker profile for diagnosing the individual expression of clinical anxiety.

Using the overlapping genomic locations of the anxiety-related DMRs identified here and previously, we built a custom resequencing panel that will be used to detect deviations from healthy anxious trajectories and bolster diagnostic efforts with an epigenetic metric that integrates heritable and acquired variables that influence the expression of an anxious temperament and the development of clinical anxiety and depressive disorders. This resequencing panel will use Illumina Custom Enrichment Panel technology that enables custom panel design between 2,000-67,000 probes using DesignStudio. Nextera Flex methodologies will be used for enrichment. The initial enrichment panel (i.e., AT enrichment panel v3) will examine the DNA methylation levels at all the CpGs found in the 26 anxiety-related DMRs that are overlapping between monkey brain, monkey blood, and/or human blood (FIG. **1**; Table 2). This resequencing panel will be employed as a blood DNA methylation biomarker diagnostic test for clinical anxiety and depressive disorders, improving estimates of prognosis and to guide personalized treatment of clinical anxiety and depressive disorders.

RNA sequencing—The RNA sequencing was conducted using the same monkey brain tissue that was used to generate the DNA methylation data. Thus, these expression data provide a direct comparison with the monkey brain DNA methylation data to begin to identify a possible mechanism (DNA methylation) for the observed changes in expression that likely drive the AT phenotype. Approximately 60 genes have correlated changes in DNA methylation and gene expression levels in the monkey brain that are linked to the AT phenotype. Notably, 50% (3/6) of the genes that we find differentially methylated in all three tissues (human blood, monkey brain, and monkey blood) are among these 60 genes. These gene are GRB10, PDXK, and TRAPPC9. This additional connection to gene expression changes in the brain associated with the AT phenotype makes these three gene our top candidates. Ten more genes (13 in total) that have correlated changes in DNA methylation and gene expression levels in the monkey brain, also are differentially methylated in the monkey blood. These 10 genes (BRD3, DDX50, DUSP8, EHMT1, HCN2, IL17D, MICAL3, NACC2, PKD1, and VWA1) also are top candidates.

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SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 75

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tgcgagcggc cctgactccc acccactccc gtccgcagct gagcggcagc cagatgagcc 180

tgtcaggcga cgcggaggcg gtgcaggtcc gcggctccgt gcacttcgcg ctgcactacg 240

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ggcgcc 306

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actgaggtgg cctgtctgat taggacgctg cgagtgcagt ggttaggcat ggggtgttga 180

tgcatcagac tgccgagttc aaatcctgcc tcctccgacc agctgtgtga tcctgagcaa 240

gcaccc 246

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ac 62

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tgagggtccc tggggcgcct gggcctgacc cgggtgtcc 99

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c 61

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cggagaaggt ccaccgagcc tggcgaaagg tccgctgagc gggctgtcgt ccggagccac 120

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cctgtcttcg cagaggagtc ctcgc 205

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 19

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<212> TYPE: DNA
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cgatccacaa agtaatgacg cccgcccaga tcctccgcag cc 102

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gggagatacc cagctaggtc tcagcgcgca gcttcagcat ccccgcgatc cgcagagtat 180

tgacgcccac ccgggtcctc cgcagcctag agcaagggac tgcggaacga gtgccgcaat 240

cttcagggta ttgacgccca cccgggtcct ccgcagccaa gagcaaggga ctgcggaagg 300

agtgccgcaa tcttcagggt attgacgccc acccgggtcc tccgcagcct agagcaggga 360

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tctgcagtaa aaatgac 137

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<212> TYPE: DNA
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ctc 63

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cagagaatgg tctgataact gaaactcaaa ccagagagtc ggggaataat ttcgtgatgc 120

tgctggcatt tccttttgtc ttcaatctgc tgcttcgcac actaagattt tga 173

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<400> SEQUENCE: 26

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<400> SEQUENCE: 27

gaagagttgc aa 12

<210> SEQ ID NO 28
<211> LENGTH: 13
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 28

gtacctatac ttg 13

<210> SEQ ID NO 29
<211> LENGTH: 25
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 29

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<210> SEQ ID NO 30
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<400> SEQUENCE: 30

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cgtaagtgag gatgtagagg ggcttcccgt tggtgtccat ggtggtcagg cagggcgcct 120

tgggcgagat ggtgccccac ctctgcagtg cggcctccag cgacggcggc cagttcgtga 180

ccacgcccag ctgctctccg cgcatggcca gcatctgggc cccctccggc tttggttggt 240

tcggatccgg ttgttgaact aaatc 265

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<211> LENGTH: 128
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<400> SEQUENCE: 31

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 33

gctca 5

<210> SEQ ID NO 34
<211> LENGTH: 57
<212> TYPE: DNA
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<400> SEQUENCE: 34

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cttgagctaa t 71

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<400> SEQUENCE: 36

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cccgaagccc tatttctctg tctctagaga gtgggaaagg ggcccaggac cctcaccgga 180

agcacggtcg gaggggtcga cacgtccctc tcggacttgg cgggggtagc acagtacgtc 240

tccaggaggg ccaggtcaca gctgcggaaa cagcactcct caacgatgcc acggctgcga 300

cggctcacac ggcttgcggg cctgcctgga agtcccacag cacagagaga gccgtgttag 360

caccgcactg accccagccc cc 382

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cctgggcctc cgcctc 196

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<400> SEQUENCE: 38

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acagggcaga aagagagagg gcaaggccag ggaagagacg gggagagaaa aaaatagagt 120

caagttaaag agaggaggtg cttccgcagg aactgaggag agagaccgca gc 172

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<400> SEQUENCE: 39

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tgccc 65

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<211> LENGTH: 79
<212> TYPE: DNA
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<400> SEQUENCE: 40

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gcgtgtgtgt gcgctgagc 79

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<400> SEQUENCE: 41

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cgggacacag tgccggaaag caatctgatg cc 92

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 42

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cccaggat 68

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<400> SEQUENCE: 43

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cgctcttggg aggacccttg ggacagtggg caggcgctgg gcaagccaca agcgtgtc 118

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 45

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<211> LENGTH: 221
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tgccctcggt tgcccaggag agccacagtg ccttgagaac ataagcaatt tagtgaacag 120

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cagctagatg tctataatct gccccaaaaa gaaaagaaag c 221

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cgagtcagct cctc 74

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gccccgcgcc gatggtaggg accaggccac agccctttcc ccaggagccg gc 112

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<400> SEQUENCE: 49

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aggcccctga cggc 74

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cttcttctgc attaggaaga agcccaaaga gccacagcct gaggtggcgg ccgcggagga 120

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agtgggc 67

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 53

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tcctgc 66

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<400> SEQUENCE: 54

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<212> TYPE: DNA
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<400> SEQUENCE: 55

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<400> SEQUENCE: 56

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accacccaga gacggggagg tcaggggcaa ggacggcacg cagggccacc tccctgcgcc 120

cgcctggttc ctgggggctc agtgccctca gcagctctcg cccacaccct acagtcacag 180

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<400> SEQUENCE: 58

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gatagtgccg gagctctctt catctccgtc ttccagatgg ggaaactgag gctcagggtc 120

acacagcctg tagcaggcaa agccagggtt ctagccgcga ccgtccgggt cggtcctggt 180

gccgagaggt agtgctgggt gtcgggagcc aggccctcca gctggggctg agagctttcc 240

c 241

<210> SEQ ID NO 59
<211> LENGTH: 142
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 59

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aacatacgtg gaagctggag ccggcgctgg ccagagcggc ccggtaatgc ctgacatgtg 120

ttgggttgtt tgtgaacctg cc 142

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cgccccaggg aggaggcgcc agagcgcggg gcagacgcaa agtgaaataa acactatttt 120

gacggctgtc ttttatattt ctgagcacac acagagccct ggcgtccacc ggggcaggcg 180

caaagtggac agagcatgca gggcggcgga ccccccccacg accctcctcg ccctgtctcc 240

atcccctc 248

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ggcaagcaca gcaaccgtgg ccccgcccct ccctgtggac aaccccacac ctatgcggca 120

aaccgcagcc gccccgatca aagatggcac ccaggtgggc ggggcttgaa cagaccgtcc 180

cgcccatgcc acctgcagcc acttcagcct tgccccgccg catctgccgc caaccaatcc 240

gggcaacgcc tgcgcggcaa acctcagctg cccccatcaa agatggcgcc caggcgggcg 300

ggccttgtct cgcccaacca actaggacag cgcctgcgca gcaaatctca agcactttca 360

ttaaagatgg cgcccaggtg ggtggggctt gaacaaacca ctaggtccaa tgccaccctg 420

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<212> TYPE: DNA
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<400> SEQUENCE: 62

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tcctcccgca gct 73

<210> SEQ ID NO 63
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 63

cccagacttc tgcaccgagg tgcagctcga cg 32

<210> SEQ ID NO 64
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<213> ORGANISM: Homo sapiens

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cctcgagctt gagcccgccg actgcggcca ggacaccgcc ggcgcgcctc ccggccgccg 240

cgagatccgc gccgccatgc agtttggcga caccgaaatt aaggtcaccg ccgtcgacgt 300

cagcaccaat cgctccgtgc gcgcgtccat cgactttctt tccaactgag ggcgcgccgg 360

cgcggtgcca gcgccgtctg cccggccccg ccctctttcg gttcaggggc ctgcggagcg 420

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<210> SEQ ID NO 65
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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 65

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gcttgagccc gccgactgcg gccaggacac cgccggcgcg cctcccggcc gccgcgagat 120

ccgcgccgcc atgcagtttg gcgacaccga aattaaggtc accgccgtcg acgtcagcac 180

caatcgctcc gtgcgcgcgt ccatcgactt tctttccaac tgagggcgc 229

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<212> TYPE: DNA
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<400> SEQUENCE: 66

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<210> SEQ ID NO 67
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 67

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<211> LENGTH: 163
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 68

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gcctgcgggc agcagggccg ccggggaacc ggggaggggg tggcagggct gcctggtggg 120

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<210> SEQ ID NO 69
<211> LENGTH: 478
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<400> SEQUENCE: 69

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ttgttgggtg ctttttggtt tgttcttgtc ccttttttcgt ttgctcatcc tttttggcgc 120

taactcttag gcagccagcc cagcagcccg aagcccgggc agccgcgctc cgcggccccg 180

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<400> SEQUENCE: 71

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<400> SEQUENCE: 72

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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 73

gcagtgtcag g 11

<210> SEQ ID NO 74
<211> LENGTH: 72
<212> TYPE: DNA
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<400> SEQUENCE: 74

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<400> SEQUENCE: 75

agctcg 6

We claim:

1. A method of amplifying at least one of six differentially methylated region (DMR) associated genes comprising the steps of:

(a) providing a reaction mixture comprising bisulfite modified target DNA from a subject and at least one pair of primers designed to amplify at least one DMR-associated gene selected from the group consisting of DIP2C, GRB10, INPP5A, GNAS, PDXK, and TRAPPC9, wherein the primer pair comprises a first and a second primer that are complementary to the DMR-associated gene;

(b) heating the reaction mixture to a first predetermined temperature for a first predetermined time;

(c) cooling the reaction mixture to a second predetermined temperature for a second predetermined time under conditions to allow the first and second primers to hybridize with their complementary sequences on the target DNA; and

(d) repeating steps (b) and (c) wherein an amplified target DNA sample is formed.

2. The method of claim **1**, wherein the reaction mixture additionally comprises a polymerase and a plurality of free nucleotides comprising adenine, thymine, cytosine, and guanine.

3. The method of claim **1**, wherein the reaction mixture additionally comprises a reaction buffer and $MgCl_2$.

4. The method of claim **1**, wherein in step (a), (i) a first reaction mixture comprising a first portion of bisulfite modified target DNA and a pair of primers designed to amplify DIP2C; (ii) a second reaction mixture comprising a second portion of bisulfite modified target DNA and a pair of primers designed to amplify INPP5A; (iii) a third reaction mixture comprising a third portion of bisulfite modified target DNA and a pair of primers designed to amplify PDXK; (iv) a forth reaction mixture comprising a forth portion of bisulfite modified target DNA and a pair of primers designed to amplify GNAS; (v) a fifth reaction mixture comprising a fifth portion of bisulfite modified target DNA and pair of primers designed to amplify GRB10; (vi) and a sixth reaction mixture comprising a sixth portion of bisulfite modified target DNA and a pair of primers designed to amplify TRAPPC9 are provided.

5. The method of claim **1**, wherein the primers are specific for a DMR selected from the group consisting of SEQ ID NOs:7-18, 50-59, 67-69, and 73-75.

6. The method of claim **1**, wherein at least one of the primers in the primer pair is biotinylated.

7. The method of claim **4**, additionally comprising providing reaction mixtures comprising subsequent portions of bisulfite modified target DNA and a pair of primers designed to amplify one or more DMR-associated genes selected from the group consisting of C17ORF97, CACNA2D4, CRTC1, MEGF6, HIVEP3, OPCML, PITPNM2, ZFPM1, RAP1GAP2, NFATC1, RNF126, FSTL3, SH3BP2, NEURL1B, MAD1L1, HSPA12B, IGF2, PEG10, PEG3, SLC16A3, SYTL1, and ZIM2.

8. The method of claim **7**, wherein the primers are designed to amplify a DMR selected from the group consisting of SEQ ID NOs:1-6, 19-49, 60-66, and 70-72.

9. The method of claim **1**, wherein the target DNA is isolated from a blood sample or a saliva sample from the subject.

10. The method of claim **1**, wherein the subject is a human or non-human primate.

11. The method of claim **1**, wherein the providing the reaction mixture further comprises providing at least one pair of primers designed to amplify at least one DMR-associated gene selected from the group consisting of C17ORF97, CACNA2D4, CRTC1, MEGF6, HIVEP3,

OPCML, PITPNM2, ZFPM1, RAP1GAP2, NFATC1, RNF126, FSTL3, SH3BP2, NEURL1B, MAD1L1, HSPA12B, IGF2, PEG10, PEG3, SLC16A3, SYTL1, ZIM2, BRD3, DDX50, DUSP8, EHMT1, HCN2, IL17D, MICAL3, NACC2, PKD1, and VWA1.

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