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(54) Title: TREATMENT AND DIAGNOSIS OF EPIGENETIC DISORDERS AND CONDITIONS

(57) Abstract: The present disclosure relates generally to the field of epigenetics and in particular epigenetic profiles associated with a pathological condition. The present specification teaches screening of individuals and populations for epigenetic profiles associated with a pathological condition. The epigenetic profiles can be from an intron, an intron/exon boundary or a splicing region. Epigenetic profiles are disclosed from the following sites in the FMR locus: FREE3, intron 2 of FMR1, the genomic FREE2 region as a whole or specific FREE2 fragments including FREE2 (D) or FREE2 (E). Kits and diagnostic assays are also taught herein as are computer programs to monitor changes in epigenetic patterns and profiles. Further enabled herein is a method for screening for agents which can reduce or mask the adverse effects of epigenetic modification and the use of these agents in therapy and prophylaxis.

TREATMENT AND DIAGNOSIS OF EPIGENETIC DISORDERS AND CONDITIONS

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[0001] This application is associated with and claims priority from Australian Provisional Patent Application No. 2010903595, filed on 11 August 2010, entitled "Treatment and diagnosis of epigenetic disorders and conditions", the entire contents of which, are incorporated herein by reference.

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FIELD

[0002] The present disclosure relates generally to the field of epigenetics and in particular epigenetic profiles associated with a pathological condition. The present specification
15 teaches screening of individuals and populations for epigenetic profiles associated with a pathological condition. Kits and diagnostic assays are also taught herein as are computer programs to monitor changes in epigenetic patterns and profiles. Further enabled herein is a method for screening for agents which can reduce or mask the adverse effects of epigenetic modification and the use of these agents in therapy and prophylaxis.

20

BACKGROUND

[0003] Bibliographic details of the publications referred to in this specification are also collected at the end of the description.

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[0004] Reference to any prior art in this specification is not, and should not be taken as, an acknowledgment or any form of suggestion that this prior art forms part of the common general knowledge in any country.

30 [0005] It is apparent that DNA methylation and other epigenetic modifications play a role in the regulation of gene expression in higher organisms. The importance of epigenetic

modification has been highlighted by its involvement in several human diseases. Methylation, for example, of cytosine at the 5' position is the only known methylation modification of genomic DNA. In particular, methylation of CpG islands within regulatory regions of the genome appears to be highly tissue specific. Methylation of cytosines distal to the islands is also important. These regions are called "shores" or "island shores" (Irizarry *et al., Nature Genetics 41(2)*:178-186, 2009). Epigenetic modifications include histone modification, changes in acetylation, methylation, obiquitylation, phosphorylation, sumoylation, activation or deactivation, chromatin altered transcription factor levels and the like.

[0006] Another genetic condition which can affect gene expression arises from expansion or increase in the number of repeats in a specific tandem repeat array. Such nucleotide expansion can result in repeat expansion disease conditions. A critical threshold of repeat expansion determines the level of pathologenicity (Orr and Zoghbi, *Ann Rev Neurosci 30*:575-621, 2007). Many diseases arise from expansion of a repeat located in an open reading frame resulting in a protein with a long polyQ[2] tract that is toxic to neurons (Orr and Zoghbi, 2007 *supra*). Other expansion disease conditions such as Fragile X syndrome (FXS), Fragile XE mental retardation (FRAXE), Fragile X-associated primary ovarian insufficiency (FXPOI), Fragile type, folic acid type, rare 12 (FRA12A), mental retardation (MR), Friedrich's ataxia (FRDA) and myotonic dystrophy (DM), arise from altered transcription of the repeats which are not translated.

[0007] A particular type of expansion disorder is referred to as a trinucleotide repeat disorder (also known as trinucleotide repeat expansion disorder, triplet repeat expansion disorder and codon reiteration disorder) and results from trinucleotide repeats in certain genetic loci. An example occurs in the Fragile X Mental Retardation genetic locus ("FMR genetic locus").

[0008] The FMR genetic locus includes the FMR1 gene which is composed of 17 exons, spanning 38Kb, and encodes Fragile X Mental Retardation Protein (FMRP), essential for normal neurodevelopment (Verkerk *et al., Cell 65(5)*:905-914, 1991; Terracciano *et al., Am J Med Genet C Semin Med Genet 137C(1)*:32-37, 2005). A CGG repeat

segment is located within the 5' untranslated region (UTR) of the gene. Its normal range is < 40 repeats. When expanded, these repeats have been implicated in a number of pathologies, including the Fragile X syndrome (FXS), Fragile X-associated Tremor Ataxia Syndrome (FXTAS) and Fragile X-associated primary ovarian insufficiency (FXPOI; formerly referred to as Premature Ovarian Failure [POF]). FXS is neurodevelopmental in nature with a frequency of 1/1400 males and 1/8000 females, associated with a Fragile site at the Xq27.3 locus (Jin and Warren, *Hum. Mol. Genet 9(6)*:901-908, 2000).

[0009] This syndrome is caused by a CGG expansion to "full mutation" (FM) which comprises >200 repeats, leading to a gross deficit of FMRP and subsequent synaptic abnormalities (Pieretti *et al., Cell 66(4)*:817-822, 1991; Irwin *et al., Cereb Cortex 10(10)*:1038-1044, 2000). The FXS clinical phenotype ranges from learning disabilities to severe mental retardation and can be accompanied by a variety of physical and behavioral characteristics. FXTAS is prevalent in ~30% of premutation individuals (PM), comprising 55 to 199 repeats (Nolin *et al., Am J Hum Genet 72(2)*:454-464, 2003) and is a progressive neurodegenerative late-onset disorder with a frequency of 1/3000 males in the general population (Jacquemont *et al., Am J Ment Retard 109(2)*:154-164, 2004), manifesting as tremor, imbalance and distinct MRI and histological changes (Hagerman *et al., Neurology 57(1)*:127-130, 2001; Jacquemont *et al., J Med Genet 42(2)*:e14, 2005; L oesch *et al., C lin Genet 67(5)*:412-417, 2005). It is often associated with 'toxicity' of elevated FMR1 mRNA, which has been linked to the intranuclear inclusions and cell death observed during neurodegeneration (Jin *et al., Neuron 39(5)*:739-747, 2003).

[0010] FXTAS can occur in females carrying PM, but with much lower frequency as can be expected from X-linked inheritance. The intermediate or Gray Zone (GZ) alleles comprising 41 to 54 repeats (Bodega *et al., Hum Reprod 21(4)*:952-957, 2006) are the most common form of the expansion, 1 in 30 males and 1 in 15 females. As with PM alleles, increased levels of FMR1 mRNA have been reported in the GZ individuals, proportional to the size of CGG expansion (Kenneson *et al., Hum Mol Genet 10(14)*:14491454, 2001; Mitchell *et al., Clin Genet 67(1)*:38-46, 2005; Loesch *et al., J Med Genet 44(3)*:200-204, 2007). Female carriers of both PM and GZ allelic

types have an increased risk of developing POF (Allingham-Hawkins *et al.*, *Am J Med Genet 83(4)*:322-325, 1999; Sullivan *et al.*, *Hum Reprod 20(2)*:402-412, 2005) which has incidence of approximately 1% in the general population, and often unknown etiology (Coulam, *Fertil Steril 38(6)*:645-655, 1982).

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[0011] Expansion related abnormalities in FMR1 are involved in pathologies with a wide spectrum of patho-mechanisms all pointing to involvement of multiple factors at the Xq27.3 locus in addition to FMR1. A number of antisense transcripts have been described embedded within the FMR1 sequence, ASFMR1 (Ladd *et al.*, *Hum Mol Genet*
10 *16(24)*:3174-3187, 2007) and FMR4 (Khalil *et al.*, *PLoS ONE 3(1)*:e1486, 2008). The ASFMR1 and FMR4 transcripts have been suggested to share the bi-directional promoter with FMR1, which is heavily regulated by the state of the surrounding chromatin environment (Pietrobono *et al.*, *Nucleic Acids Res 30(14)*:3278-3285, 2002; Chiurazzi *et al.*, *Hum Mol Genet 7(1)*:109113, 1998).

15

[0012] Transcription of ASFMR1 is also regulated by another promoter located in the exon 2 of FMR1, with the resulting transcript spanning the CGG repeat in the antisense direction (Ladd *et al.*, 2007, *supra*), and an open reading frame (ORF) with the CGG encoding a polyproline peptide (Ladd *et al.*, 2007, *supra*). FMR4, however, is a long non-
20 coding RNA, involved in regulation of apoptosis (Khalil *et al.*, 2008, *supra*).

[0013] The length of the CGG repeat has been reported to effect transcription of all three genes FMR1, FMR4 and ASFMR1 (Ladd *et al.*, 2007, *supra*; Khalil *et al.*, 2008, *supra*). However, although it is well documented that FMR1 transcription is promoter methylation
25 dependent, linked to the CGG expansion size, the relationship between FMR4 and ASFMR1 transcription and methylation remains elusive.

[0014] One of the current problems is in the diagnosis of subjects with FM in the FMR genetic locus. Diagnostic assays targeting only the CGG expansion have hitherto been
30 inconclusive. Therefore, currently Southern DNA analysis, which is expensive and time consuming, is used as a gold standard assay for diagnosis in many laboratories.

[0015] Despite the availability of a range of methylation and nucleotide expansion assays (see, for example, Rein *et al., Nucleic Acids Res. 26*:2255, 1998 in relation to methylation assays), selection of regions to amplify and screen is an important aspect of determining an epigenetic profile characteristic of a disease condition. There is a need to identify crucial regions which are associated with epigenetic change linked to a pathological condition to assay and/or therapeutically target.

SUMMARY

[0016] Throughout this specification, unless the context requires otherwise, the word "comprise" or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element or integer or method step or group of elements or integers or method steps but not the exclusion of any element or integer or method step or group of elements or integers or method steps.

[0017] Nucleotide and amino acid sequences are referred to by a sequence identifier number (SEQ IN NO:). The SEQ ID NOs: correspond numerically to the sequence identifiers <400>1 (SEQ ID NO:1), <400>2 (SEQ ID NO:2), etc. A summary of sequence identifiers is given in Table 1.

[0018] Aspects enabled herein are predicated in part on the determination of an association between epigenetic modification of intronic regions including intron/exon boundaries and splicing regions within a genetic locus and a pathological condition including a trinucleotide expansion disorder. In an embodiment, the epigenetic modification occurs in:

(i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; and/or

(ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region;

within a genetic locus.

[0019] In an embodiment, the epigenetic modification occurs within a genetic locus which leads to a condition including a pathoneurological condition such as a pathoneurodevelopmental and pathoneurodegenerative condition as well as a non-neurological condition. Conditions and disorders including trinucleotide expansion disorders associated with a change in the epigenetic profile from that observed in healthy controls associated with a change in epigenetic profile in intronic regions including intron/exon boundary regions, include Fragile X syndrome (FXS), Fragile X-associated

tremor or ataxia (FXTAS), Fragile X-associated primary ovarian insufficiency (FXPOI), autism, mental retardation, cognitive impairment, a modified X-chromosome, Huntington's disease (HD), dentatorubropallid-oluysiantrophy (DRPLA), spinobulbar muscular atrophy or Kennedy disease (SBMA), spinocerebella ataxia Type 1 (SCA1), spinocerebella ataxia
5 Type 2 (SCA2), spinocerebella ataxia Type 3 or Machado-Joseph disease (SCA3), spinocerebella ataxia Type 6 (SCA6), spinocerebella ataxia Type 7 (SCA7), spinocerebella ataxia Type 17 (SCA17), Fragile XE mental retardation (FRAXE), Friedrich's ataxia (FRDA), Fragile type, folic acid type, rare 12 (FRA12A), myotonic dystrophy (DM), spinocerebella ataxia (SCA8) and spinocerebella ataxias Type 12 (SCA12), Klinefelter's
10 syndrome and Turner's syndrome. Reference to a "control" means relative to a healthy subject which means a subject with a normal size of expansion repeats and/or who is phenotypically normal meaning that the subject does not have symptoms of, for example, a trinucleotide expansion disorder and/or is the epigenetic (e.g. methylation) profile observed in healthy control subjects.

15

[0020] It is proposed herein that epigenetic changes in an intron, intron/exon boundary and/or splicing region within a particular genetic locus are associated with the development, progression and severity of a range of pathological conditions including trinucleotide expansions disorders such as but not limited to those listed above. In relation
20 to the FMR genetic locus, the epigenetic modification may occur in:

(i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; and/or

(ii) approximately one seventh or greater of an intron including an intron/exon
25 boundary and/or a splicing region;

within the genetic locus. These regions also include promoter regions. Epigenetic changes may occur on either strand of double stranded genomic DNA including either strand of a promoter or other regulatory region and either strand may be targeted for epigenetic
30 analysis. The ASFMR1 promoter is an example. The location of this promoter can be seen in Figures 6A and 6C and has a transcription start site in FREE3 of intron 2. Hence, another aspect of the present disclosure provides a method for identifying FXS or a related

condition in a human subject, the method comprising screening for a change relative to a control in the extent of epigenetic modification in the FMR genetic locus at a location selected from:

5 (i) Fragile X-related Epigenetic Element 3 in FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions; and

10 (ii) genomic FREE2 region as a whole or specific fragments of FREE2 including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under

15 medium stringency conditions;

wherein a change in extent of epigenetic modification relative to a control is indicative of the presence or severity of the pathological condition or a propensity to develop same.

20 **[0021]** In an embodiment, a method is provided for identifying a trinucleotide expansion disorder in a mammalian subject including a human, the method comprising screening for a change relative to a healthy control in the extent of epigenetic modification within (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; and/or (ii) approximately one seventh or greater of an intron including an intron/exon boundary

25 and/or a splicing region of the FMR genetic locus; wherein a change in extent of epigenetic modification relative to the control is indicative of the presence or severity of the trinucleotide expansion disorder or a propensity to develop same wherein the intron, intron/exon boundary and/or splicing region is selected from the list consisting of:

30 (i) Fragile X-related Epigenetic Element 3 in FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which

hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions;

(ii) intron 2 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or a portion or fragment thereof defined by having at least 80%
5 nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions; and

(iii) genomic FREE2 region as a whole or specific fragments of FREE2 including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof
10 defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditions.

[0022] By "epigenetic modification" is meant changes in extent, level and/or profile or
15 epigenetic modification including changes in methylation including hypermethylation and hypomethylation, histone modification, acetylation, obiquitylation, phosphorylation and/or sumoylation, as well as changes in chromatin altered transcription factor levels and the like leading to activation or deactivation of genetic locus expression. The epigenetic modification extends to an increase or decrease in epigenetic change relative to a normal
20 control. It also extends to either strand of these target regions which includes either strand of a promoter region. In an embodiment, epigenetic modification includes the methylation state of CpG and CpNpG sites within an intron of a genetic locus. In an embodiment, the genetic locus is the FMR genetic locus which includes FMR1, FMR4 and ASFMR1 genes. In an embodiment, the epigenetic modification occurs in the FMR genetic locus within a
25 region selected from:

(i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region;

(ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region;

30 (iii) the 3' boundar y of the FREE2 region and the FMR1 promoter located between CpG unit 1 of the FREE2 (E) amplicon and CpG unit 2/3 of the FREE2 (E) amplicon;

(iv) the FREE2 region alone or in combination with the FREE1 region;

(v) the FREE3 region; and

(vi) an intron including an intron/exon boundary and/or splicing region downstream of intron 1 within the FMR1 gene including the FREE2 region alone or in combination with the FREE1 region (D) region or FREE2 (D)/(E) boundary.

[0023] These regions include either strand of a double stranded genomic sequence and includes either strand of the promoter region such as the ASFMR1 promoter with a transcription initiation site in FREE3 of intron 2.

[0024] Furthermore, the epigenetic profile of the FMR genetic locus is also informative as to the spectrum of disease conditions associated with the genetic locus, such as whether the subject is normal or has a PM, GZ or FM pathology and/or whether the epigenetic change and/or CGG expansion is heterozygous or homozygous at the FMR allele. Reference to "FREE2" include FREE2 (A), FREE2 (B), FREE2 (C), FREE2 (D) and FREE2 (E) including any exon/intron boundaries therein such as the FREE2(D)/FREE2 (E) boundary. The boundary regions include a promoter region. A "promoter region" includes either or both nucleic acid strands within double stranded genomic DNA.

[0025] Accordingly, an aspect enabled herein is a method for identifying an epigenetic profile in the genome of a cell indicative of a pathological condition, the method comprising screening for a change relative to a control in the extent of epigenetic modification within (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; and/or (ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region of a genetic locus wherein the extent of epigenetic change relative to a control is indicative of the presence or severity of the pathological condition or a propensity to develop same.

[0026] In an embodiment, the epigenetic profile is determined within a genetic locus, the epigenetic profile of which, is associated with a pathological condition including a trinucleotide disorder associated with a change in epigenetic profile from that observed in healthy controls selected from Fragile X syndrome (FXS), Fragile X-associated tremor or

ataxia (FXTAS), Fragile X-associated primary ovarian insufficiency (FXPOI), autism, mental retardation, cognitive impairment, a modified X-chromosome, Huntington's disease (HD), dentatorubropallid-oluysiantrophy (DRPLA), spinobulbar muscular atrophy or Kennedy disease (SBMA), spinocerebella ataxia Type 1 (SCA1), spinocerebella ataxia Type 2 (SCA2), spinocerebella ataxia Type 3 or Machado-Joseph disease (SCA3), spinocerebella ataxia Type 6 (SCA6), spinocerebella ataxia Type 7 (SCA7), spinocerebella ataxia Type 17 (SCA17), Fragile XE mental retardation (FRAXE), Friedrich's ataxia (FRDA), Fragile type, folic acid type, rare 12 (FRA12A), myotonic dystrophy (DM), spinocerebella ataxia (SCA8) and spinocerebella ataxias Type 12 (SCA12), Klinefelter's syndrome and Turner's syndrome.

[0027] In an embodiment, the epigenetic change is within the FMR genetic locus and is associated with one or more of FXS, FXTAS, FXPOI, autism, mental retardation, a modified X-chromosome and/or cognitive impairment.

[0028] In relation to the latter aspect, the method comprises screening for a change relative to the control in the extent of epigenetic modification within the FMR genetic locus within a region selected from:

(i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region;

(ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region;

(iii) the 3' boundary of the FREE2 region and the FMR1 promoter located between CpG unit 1 of the FREE2 (E) amplicon and CpG unit 2/3 of the FREE2 (E) amplicon;

(iv) the FREE2 region alone or in combination with the FREE1 region;

(v) the FREE3 region; and

(vi) an intron including an intron/exon boundary and/or splicing region downstream of intron 1 within the FMR1 gene including FREE2 (D) or FREE2(D)/(E) boundary. These regions may be assessed on either strand of double stranded genomic DNA and include either strand of a promoter region. An example of a promoter region is

the ASFMR1 promoter with an initiation site in FREE3 of intron 2 (see Figure 6).

[0029] The extent of epigenetic change is indicative of the presence of severity of the pathological condition or a propensity to developing same. As indicated above, a "pathological condition" includes a trinucleotide expansion disorder.

[0030] A further aspect taught herein is a method for identifying an epigenetic profile in the genome of a cell indicative of a pathological condition associated with the FMR genetic locus, the method comprising extracting genomic DNA from the cell and subjecting the DNA to an amplification reaction using primers selective for (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; and/or (ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region, within the FMR genetic locus including the FMR1 gene, subjecting the amplified DNA to an epigenetic assay to determine the extent of epigenetic modification of the DNA wherein a change in the extent of epigenetic modification is indicative of the presence or severity of the pathological condition or propensity to develop same. The region within the FMR genetic locus is selected from:

(i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region;

(ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region;

(iii) the 3' boundary of the FREE2 region and the FMR1 promoter located between CpG unit 1 of the FREE2 (E) amplicon and CpG unit 2/3 of the FREE2 (E) amplicon;

(iv) the FREE2 region alone or in combination with the FREE1 region;

(v) the FREE3 region; and

(vi) an intron including an intron/exon boundary and/or splicing region downstream of intron 1 within the FMR1 gene including the FREE2 (D) region or FREE2 (D)/(E) boundary.

[0031] A similar method applies to epigenetic changes in other genetic loci. Reference to

the "FMR genetic locus" includes the FMR1, FMR4 and ASFMR1 genes and corresponds to Xq27.3 as well as promoter regions associated with these sites. The term "FMR locus" means the "FMR genetic locus". In an embodiment, an aspect taught herein determines that the intronic region downstream of intron 1 comprises Fragile X-related Epigenetic Element 3 as defined by SEQ ID NO:1 or a homolog thereof or a portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions; or is intron 2 as defined by SEQ ID NO:2 or a homolog thereof or a portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions. The nucleotide sequence of intron 1 of the FMR1 gene is set forth in SEQ ID NO:3. The genomic nucleotide sequence of FREE2 region alone or in combination with the FREE1 region (D), FREE2 (E) and FREE3 are set forth in SEQ ID NOs:48, 49 and 47, respectively, and the present disclosure extends to homologs thereof having at least 80% identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or a complement thereof under medium stringency conditions. The present disclosure further contemplates amplifying all or part of an expansion mutation and/or and detecting extent of epigenetic change therein in combination with an epigenetic change (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; and/or (ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region of the FMR genetic locus including the FMR1 gene. The extent of epigenetic change in two or more of an intron, an intron/exon boundary and/or a splicing region or in one seventh or greater of an intron within the FMR genetic locus may be determined alone or in combination with extent of $(CGG)_n$ expansion and/or any other epigenetic change therein. The determination of epigenetic change may also be conducted in combination with an assay as contemplated by International Patent Application No. PCT/AU2010/000169 filed on 17 February 2010, the contents of which are incorporated herein by reference in their entirety. In an embodiment, the epigenetic modification is a change in extent of methylation which includes hypermethylation and hypomethylation and profile of methylation.

[0032] Another aspect of the present disclosure contemplates a method for identifying a

pathological condition in a mammalian subject including a human, the method comprising screening for a change relative to a control in the extent of change in methylation or other epigenetic modification within a region selected from:

5 (i) Fragile X-related Epigenetic Element 3 in FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions;

10 (ii) intron 2 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or a portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions;

(iii) genomic FREE2 region as a whole or specific fragments of FREE2 15 including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditions;

20 . (iv) an intron, intron/exon boundary and/or splicing region downstream of intron 2 of FMR1 or a homolog thereof or a portion or fragment thereof;

(v) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing regions within the FMR genetic locus; and

(vi) approximately one seventh or greater of an intron including an intron/exon 25 boundary and/or a splicing region within the FMR genetic locus;

wherein a change in epigenetic modification relative to a control is indicative of the presence or severity of the pathological condition or a propensity to develop same. In an embodiment, the pathological condition is a trinucleotide expansion disorder.

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[0033] As indicated above, the region within the FMR genetic locus assayed for epigenetic change is selected from:

(i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region;

(ii) approximately one seventh or greater of an intron including an intron/exon
5 boundary and/or a splicing region;

(iii) the 3' boundary of the FREE2 region and the FMR1 promoter located between CpG unit 1 of the FREE2 (E) amplicon and CpG unit 2/3 of the FREE2 (E) amplicon;

(iv) the FREE2 region alone or in combination with the FREE1 region;

10 (v) the FREE3 region; and

(vi) an intron including an intron/exon boundary and/or splicing region downstream of intron 1 within the FMR1 gene including the FREE2 (D) region or FREE2 (D)/(E) boundary.

15 **[0034]** Hence, in relation to detecting epigenetic changes in (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; and/or (ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region or FREE3 within intron 2, the present disclosure enables the diagnosis monitoring or analyzing of a spectrum of neurodegenerative or neurodevelopmental pathologies such
20 as Fragile X-related conditions including FXS, FXTAS, FXPOI, autism, mental retardation, a modified X-chromosome and cognitive impairment. Certain tri-nucleotide disorders are also included.

[0035] A "modified" X-chromosome includes an inactivated X-chromosome or an X-
25 chromosome having a skewed X- inactivation, or inversion, insertion, deletion, duplication or is a hybrid.

[0036] The epigenetic profile is determined in the genome of a cell of a subject. Any cell may be tested such as a cell from a post-natal or pre-natal human or embryo. More
30 particularly, the cell is a cultured or uncultured chorionic villi sample (CVS) cell, a lymphoblast cell, a blood cell, a buccal cell, epithelial cells, fibroblast cells, an amniocyte or an EBV transformed lymphoblast cell line.

[0037] In a particular embodiment of the present disclosure, the epigenetic modification is methylation of CpG and/or CpNpG sites. Methylation is determined by a range of assays including bisulfite MALDI-TOF methylation assay. In an alternative embodiment, methylation is determined by use of methylation sensitive PCR, methylation specific melting curve analysis (MS-MCA) or *high resolution melting* (MS-HRM); *quantification* of methylation by MALDI-TOF MS; methylation specific MLPA; methylated-DNA precipitation and methylation-sensitive restriction enzymes (COMPARE-MS); single molecule (SMRT) sequencing; or methylation sensitive oligonucleotide microarray; or antibodies. Other methods include NEXT generation (GEN) and DEEP sequencing or pyrosequencing. However, any assay of methylation status may be employed. Regardless of the method, either strand of genomic double stranded DNA may be assessed for its epigenetic profile.

[0038] Further taught herein is a method for screening for an agent which modulates epigenetic change of (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; and/or (ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region within a genetic locus, the method comprising screening for a change relative to a control in the extent of epigenetic modification within the intron 1n the presence or absence of an agent to be tested, wherein an agent is selected if it induces a change in the epigenetic modification.

[0039] In an embodiment, the epigenetic modification is associated with a polyglutamine (polyQ) disease such as Fragile X syndrome (FXS), Fragile X-associated tremor or ataxia (FXTAS), Fragile X-associated primary ovarian insufficiency (FXPOI), autism, mental retardation, cognitive impairment, a modified X-chromosome, Huntington's disease (HD), dentatorubropallid-oluysiantrophy (DRPLA), spinobulbar muscular atrophy or Kennedy disease (SBMA), spinocerebella ataxia Type 1 (SCA1), spinocerebella ataxia Type 2 (SCA2), spinocerebella ataxia Type 3 or Machado-Joseph disease (SCA3), spinocerebella ataxia Type 6 (SCA6), spinocerebella ataxia Type 7 (SCA7), spinocerebella ataxia Type 17 (SCA17), Fragile XE mental retardation (FRAXE), Friedrich's ataxia (FRDA), Fragile type, folic acid type, rare 12 (FRA12A), myotonic dystrophy (DM), spinocerebella ataxia

(SCA8) and spinocerebella ataxias Type 12 (SCA12), Klinefelter's syndrome and Turner's syndrome. The "association" is based on a change in epigenetic profile from that of healthy controls.

5 **[0040]** In an embodiment, the agent modulates genetic change in the FMR genetic locus *within a region selected from:*

(i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region;

10 (ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region;

(iii) the 3' boundary of the FREE2 region and the FMR1 promoter located between CpG unit 1 of the FREE2 (E) amplicon and CpG unit 2/3 of the FREE2 (E) amplicon;

15 (iv) the FREE2 region alone or in combination with the FREE1 region;

(v) the FREE3 region; and

(vi) an intron including an intron/exon boundary and/or splicing region downstream of intron 1 within the FMR1 gene including the FREE2 (D) region or FREE2 (D)/(E) boundary.

20

[0041] In an embodiment, a method is also provided for screening for an agent which modulates epigenetic modification of an FMR genetic locus in a mammalian cell including a human cell, the method comprising screening for a change relative to a healthy control in the extent of epigenetic change in (i) two or more of (a) an intron; (b) an intron/exon 25 boundary; and/or (c) a splicing region; and/or (ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region of the FMR genetic locus; wherein the intron, intron/exon boundary and/or splicing region is selected from the list consisting of:

30 (i) Fragile X-related Epigenetic Element 3 in FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which

hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions;

(ii) intron 2 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or a portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions; and

(iii) genomic FREE2 region as a whole or specific fragments of FREE2 including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditions;

in the presence or absence of an agent to be tested wherein the agent is selected if it induces a change in extent of epigenetic modification. Such an agent is useful in treating a trinulceotide expansion disorder or other pathological conditions.

[0042] A method is also provided for screening for an agent which modulates epigenetic change of an FMR genetic locus in a mammalian cell including a human cell, the method comprising screening for a change relative to a control in the extent of epigenetic modification within a region selected from:

(i) Fragile X-related Epigenetic Element 3 in FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions;

(ii) intron 2 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or a portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions;

(iii) genomic FREE2 region as a whole or specific fragments of FREE2

including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under
5 medium stringency conditions;

(iv) an intron, intron/exon boundary and/or splicing region downstream of intron 2 of FMR1 or a homolog thereof or a portion or fragment thereof;

(v) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing regions within the FMR genetic locus; and

10 (vi) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region within the FMR genetic locus;

in the presence or absence of an agent to be tested wherein the agent is selected if (i) it induces a change in extent of epigenetic modification and /or (ii) causes an improvement in
15 disease phenotype based on the type and degree of epigenetic modification. A change in extent of methylation includes hypermethylation, hypomethylation and a change in the profile of methylation.

[0043] As indicated above, in an embodiment, the epigenetic modification is methylation.
20 De-methylation as well as pro-methylation agents are contemplated herein.

[0044] Further enabled herein is a method for monitoring the treatment of a disease condition including trinucleotide expansion disorders associated with a change in epigenetic profile from that observed in healthy controls such as Fragile X syndrome
25 (FXS), Fragile X-associated tremor or ataxia (FXTAS), Fragile X-associated primary ovarian insufficiency (FXPOI), autism, mental retardation, cognitive impairment, a modified X-chromosome, Huntington's disease (HD), dentatorubropallid-oluysiantrophy (DRPLA), spinobulbar muscular atrophy or Kennedy disease (SBMA), spinocerebella ataxia Type 1 (SCA1), spinocerebella ataxia Type 2 (SCA2), spinocerebella ataxia Type 3
30 or Machado-Joseph disease (SCA3), spinocerebella ataxia Type 6 (SCA6), spinocerebella ataxia Type 7 (SCA7), spinocerebella ataxia Type 17 (SCA17), Fragile XE mental retardation (FRAXE), Friedrich's ataxia (FRDA), Fragile type, folic acid type, rare 12

(FRA12A), myotonic dystrophy (DM), spinocerebella ataxia (SCA8) and spinocerebella ataxias Type 12 (SCA12), Klinefelter's syndrome and Turner's syndrome, the method comprising screening for a change relative to the control in the extent of epigenetic modification within a genetic locus wherein the epigenetic profile of the genetic locus is
5 associated with the disease or condition, wherein the extent of epigenetic change is indicative of the presence or severity of the pathological condition, wherein the treatment modulates the extent of epigenetic change of (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; and/or (ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region within
10 the genetic locus, the method comprising monitoring for a change relative to a control in a pre- and post-treatment sample in the extent of epigenetic modification within the intron, wherein a change in extent of epigenetic modification after or during treatment is indicative of effective treatment.

15 **[0045]** In an embodiment, the genetic locus is the FMR genetic locus and the disease or condition is FXS or a related condition such as FXTAS, FXPOI, autims, mental retardation, a modified X-chromosome or cognitive impairment.

[0046] By "monitoring" in this context includes diagnosis of disease, monitoring progress
20 of the disease before or after treatment, prognosis of the disease development or remission as well as the pharmacoresponsiveness or pharmacosensitivity of a subject or agent.

[0047] The present disclosure also teaches the use of an epigenetic profile within (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; and/or (ii)
25 approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region of a genetic locus in a cell in the manufacture of an assay to identify an epigenetic profile of gene associated with a pathological condition. In an embodiment, the genetic locus is the FMR genetic locus and epigenetic change is monitored within a region selected from:

30

(i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region;

(ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region;

(iii) the 3' boundary of the FREE2 region and the FMR1 promoter located between CpG unit 1 of the FREE2 (E) amplicon and CpG unit 2/3 of the FREE2 (E) amplicon;

(iv) *the FREE2 region alone or in combination with the FREE1 region;*

(v) the FREE3 region; and

(vi) an intron including an intron/exon boundary and/or splicing region downstream of intron 1 within the FMR1 gene including the FREE2 (D) region or FREE2 (D)/(E) boundary.

[0048] An embodiment herein is directed to the use of an epigenetic profile within the FMR genetic locus in a mammalian cell including a human cell, the epigenetic profile including methylation of CpG and/or CpNpG sites located in a region selected from:

(i) Fragile X-related Epigenetic Element 3 in FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions;

(ii) intron 2 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or a portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions;

(iii) genomic FREE2 region as a whole or specific fragments of FREE2 including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditions;

(iv) an intron, intron/exon boundary and/or splicing region downstream of intron 2 of FMR1 or a homolog thereof or a portion or fragment thereof;

(v) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing regions within the FMR genetic locus; and

(vi) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region within the FMR genetic locus;

5

in the manufacture of an assay to identify an epigenetic profile of an FMR locus-associated pathological condition.

[0049] The assay taught herein may also be used alone or in combination with assays to detect extent of a nucleotide expansion such as a $(CGG)_n$ expansion, such as using PCR and Southern blot assays. This is useful in determining homozygosity, heterozygosity and mosaicism of a disease or condition. The assay of the present disclosure is also useful in population studies such as epidemiological studies as well as studies based on ethnic populations. Accordingly, another aspect enabled herein provides a method of identifying epigenetic profile in populations of subjects indicative of a pathological condition associated with epigenetic modifications or changes in an intron, intron/exon boundary and/or splicing region, the method comprising screening for a change, relative to a control in a statistically significant number of subjects, in the extent of epigenetic change within (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; and/or (ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region of a genetic locus, the epigenetic change including extent of methylation of CpG and/or CpNpG sites located within the intron, intron/exon boundary and/or splicing region wherein a change in extent of epigenetic modification is indicative of the presence or severity of the pathological condition or a propensity to develop same.

[0050] In an embodiment, the epigenetic modification is determiend in the FMR genetic locus within a region selected from:

(i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region;

(ii) approximately one seventh or greater of an intron including an intron/exon

boundary and/or a splicing region;

(iii) the 3' boundary of the FREE2 region and the FMR1 promoter located between CpG unit 1 of the FREE2 (E) amplicon and CpG unit 2/3 of the FREE2 (E) amplicon;

5 (iv) the FREE2 region alone or in combination with the FREE1 region;

(v) the FREE3 region; and

(vi) an intron including an intron/exon boundary and/or splicing region downstream of intron 1 within the FMR1 gene including the FREE2 (D) region or FREE2 (D)/(E) boundary.

10

[0051] Contemplated herein is a method of identifying a methylation or other epigenetic profile in a population of subjects indicative of a pathological condition associated with the FMR locus, the method comprising screening for a change, relative to a control, in a statistically significant number of subjects in the extent of epigenetic modification 15 including extent of change in methylation of CpG and/or CpNpG sites within a region selected from:

(i) Fragile X-related Epigenetic Element 3 in FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or fragment thereof 20 defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions;

(ii) intron 2 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or a portion or fragment thereof defined by having at least 80% 25 nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions;

(iii) genomic FREE2 region as a whole or specific fragments of FREE2 including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof 30 defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditions;

(iv) an intron, intron/exon boundary and/or splicing region downstream of intron 2 of FMR1 or a homolog thereof or a portion or fragment thereof;

(v) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing regions within the FMR genetic locus; and

5 (vi) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region within the FMR genetic locus;

wherein a change in extent of epigenetic modification is indicative of the presence of the pathological condition or a propensity to develop same in the population.

10

[0052] In accordance with this method the assay may comprise the further step of determining the extent of a nucleotide expansion such as a (CGG)n expansion such as by PCR and/or Southern blot analysis. The regions investigated for epigenetic change within the FMR genetic locus include:

15

(i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region;

(ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region;

20 (iii) the 3' boundary of the FREE2 region and the FMR1 promoter located between CpG unit 1 of the FREE2 (E) amplicon and CpG unit 2/3 of the FREE2 (E) amplicon;

(iv) the FREE2 region alone or in combination with the FREE1 region;

(v) the FREE3 region; and

25 (vi) an intron including an intron/exon boundary and/or splicing region downstream of intron 1 within the FMR1 gene including the FREE2 (D) region or FREE2 (D)/(E) boundary.

[0053] Aspects herein extend to the use of the epigenetic profile of an intron within a 30 genetic locus to determine the status, prognosis or disease development or recovery and/or treatment options including responsiveness of the subject to pharmacological agents and/or behavioral intervention strategies.

[0054] Computer programs to monitor changes in epigenetic modification or profile over time that may assist in making decisions regarding treatment options including responsiveness of the subject to pharmacological agents and/or behavioral intervention strategies, are also enabled herein.

[0055] Accordingly, another aspect provides a method of allowing a user to determine the status, prognosis and/or treatment response of a subject with respect to an FMR locus-associated pathology, the method including:

(a) receiving data in the form of extent of methylation or other epigenetic modification at a site within (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; and/or (ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region of a genetic locus associated with the pathology, wherein the extent of methylation or other epigenetic modification provides a correlation to the presence, state, classification or progression of the pathology;

(b) transferring the data from the user *via* a communications network;

(c) processing the subject data *via* multivariate or univariate analysis to provide a disease value;

(d) determining the status of the subject in accordance with the results of the disease value in comparison with predetermined values; and

(e) transferring an indication of the status of the subject to the user *via* the communications network.

[0056] In an embodiment, the genetic locus is the FMR genetic locus. The epigenetic profile is determined within the FMR genetic locus from a region selected from:

(i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region;

(ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region;

(iii) the 3' boundary of the FREE2 region and the FMR1 promoter located

between CpG unit 1 of the FREE2 (E) amplicon and CpG unit 2/3 of the FREE2 (E) amplicon;

(iv) the FREE2 region alone or in combination with the FREE1 region;

(v) the FREE3 region; and

5 (vi) an intron including an intron/exon boundary and/or splicing region downstream *of intron 1 within the FMR1 gene including* the FREE2 (D) region or FREE2 (D)/(E) boundary.

[0057] In an embodiment, a method is provided of allowing a user to determine the status, 10 prognosis and/or treatment response of a subject with respect to an FMR locus-associated pathology, the method including:

(a) receiving data in the form of extent of methylation or other epigenetic modification at a site selected from:

15 (i) Fragile X-related Epigenetic Element 3 in FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions;

20 (ii) intron 2 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or a portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions;

(iii) genomic FREE2 region as a whole or specific fragments of FREE2 25 including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditions;

30 (iv) an intron, intron/exon boundary and/or splicing region downstream of intron 2 of FMR1 or a homolog thereof or a portion or fragment thereof;

(v) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a

splicing regions within the FMR genetic locus; and

(vi) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region within the FMR genetic locus;

5 wherein the extent of methylation or other epigenetic modification provides a correlation to the presence, state, classification or progression of the pathology;

(b) transferring the data from the user *via* a communications network;

(c) processing the subject data *via* multivariate or univariate analysis to provide
10 a disease index value;

(d) determining the status of the subject in accordance with the results of the disease index value in comparison with predetermined values; and

(e) transferring an indication of the status of the subject to the user *via* the communications network.

15

[0058] A further embodiment enabled herein is a kit comprising primers which amplify regions of the FMR genetic locus, comprising CpG and/or CpNpG sites located within a region selected from:

20 (i) Fragile X-related Epigenetic Element 3 in FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions;

25 (ii) intron 2 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or a portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions;

(iii) genomic FREE2 region as a whole or specific fragments of FREE2
30 including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47

or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditions;

(iv) an intron, intron/exon boundary and/or splicing region downstream of intron 2 of FMR1 or a homolog thereof or a portion or fragment thereof;

5 (v) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing regions within the FMR genetic locus; and

(vi) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region within the FMR genetic locus;

10 in the manufacture of a diagnostic kit or device to detect epigenetic modification of the FMR locus-associated with a pathological condition.

[0059] In an embodiment, the epigenetic modification relates to extent of, or change in, methylation at CpG and/or CpNpG sits within the selected regions of the FMR genetic 15 locus, defined as FREE3, intron 2 and an intron, intron/exon boundary and/or splicing region downstream of intron 2 of the FMR gene. In an embodiment, the epigenetic modification occurs in the FMR genetic locus within a region selected from:

(i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a 20 splicing region;

(ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region;

(iii) the 3' boundary of the FREE2 region and the FMR1 promoter located between CpG unit 1 of the FREE2 (E) amplicon and CpG unit 2/3 of the FREE2 (E) 25 amplicon;

(iv) the FREE2 region alone or in combination with the FREE1 region;

(v) the FREE3 region; and

(vi) an intron including an intron/exon boundary and/or splicing region downstream of intron 1 within the FMR1 gene including the FREE2 (D) region or FREE2 30 (D)/(E) boundary.

[0060] In an embodiment, the primers useful in practicing the subject assay are selected

from the list consisting of SEQ ID NOs:6 through 11. Those sequences include tag sequences. The present disclosure extends to the primer only portions of SEQ ID NOs:6 through 11.

TABLE 1

Summary of sequence identifiers

SEQUENCE ID NO:	DESCRIPTION
1	Nucleotide sequence of FREE3 within the FMR1 gene
2	Nucleotide sequence of intron 2 of the FMR1 gene
3	Nucleotide sequence of intron 1 of FMR1 gene
4	Nucleotide sequence of FREE2 (B)
5	Nucleotide sequence of FREE2 (C)
6	Forward primer and tag sequence for FREE2 (B)
7	Reverse primer and tag sequecne for FREE2 (B)
8	FREE 2 (C) forward primer and tag
9	FREE2 (C) reverse primer and tag
10	FREE3 forward primer and tag
11	FREE3 reverse primer and tag
12	Nucleotide sequecne of regulatory motif GATA-1
13	Nucleotide sequence of regulatory motif HSF2
14	Nucleotide sequence of regulatory motif C/EBP
15	Nucleotide sequence of regulatory motif CdxA
16	Nucleotide sequence of regulatory motif AML-1a
17	Nucleotide sequence of regulatory motif AML-1a
18	Nucleotide sequence of regulatory motif CdxA
19	Nucleotide sequence of regulatory motif CdxA
20	Nucleotide sequence of regulatory motif CdxA
21	Nucleotide sequence of regulatory motif HFH-1/HFH-2
22	Nucleotide sequence of regulatory motif Cdx2
23	Nucleotide sequence of regulatory motif SRY
24	Nucleotide sequence of regulatory motif SRY
25	Nucleotide sequence of regulatory motif SRY
26	Nucleotide sequence of regulatory motif S8
27	Nucleotide sequence of regulatory motif SRY
28	Nucleotide sequence of regulatory motif CdxA

SEQUENCE ID NO:	DESCRIPTION
29	Nucleotide sequence of regulatory motif Oct-1
30	Nucleotide sequence of intron1 downstream of FREE2 (C)
31	Nucleotide sequence of exon2 upstream of FREE3
32	Nucleotide sequence of CGG amplification primer (r)
33	Nucleotide sequence of CGG amplification primer (f)
34	ASFMR1 (-1) forward primer
35	ASFMR1 (-1) reverse primer
36	ASFMR1 (-1) probe
37	ASFMR1 (-2) forward primer
38	ASFMR1 (-2) reverse primer
39	ASFMR1 (-2) probe
40	ASFMR1 (-3) forward primer
41	ASFMR1 (-3) reverse primer
42	ASFMR1 (-3) probe
43	Forward primer FREE2 (D)
44	Reverse primer FREE2 (D)
45	Forward primer FREE2 (E)
46	Reverse primer FREE2 (E)
47	Genomic target sequence FREE3
48	Genomic target sequence FREE2 (D)
49	Genomic target sequence FREE2 (E)
50	Forward primer FREE3
51	Forward primer FREE3
52	Tag forward primer FREE2 (D)
53	Tag reverse primer FREE2 (D)
54	Tag forward primer FREE2 (E)
55	Tag reverse primer FREE2 (E)
56	Tag forward primer FREE3
57	Tag reverse primer FREE3

[0061] A list of abbreviations used herein is provided in Table 2.

TABLE 2

Abbreviations

ABBREVIATION	DESCRIPTION
Ab	Antibody
ASFMR1	Antisense Fragile X mental retardation 1 gene
$(CGG)_n$	CGG repeat element located within 5' untranslated region of the FMR1 gene
CpG	Cytosine and guanine separated by a phosphate (C-phosphate-G), which links the two nucleosides together in DNA
CpNpG	Cytosine and guanine separated by a nucleotide (N) where N is any nucleotide but guanine. The cytosine and N nucleotide are phosphorylated.
CVS	Cultured or uncultured Chorionic Villi Sample
DM	Mytotonic dystrophy
DNA	Deoxyribonuceic acid
DRPLA	dentatorubropallid oluysiantrophy
FIQ	Full scale IQ
FM	Full Mutation
FMR	Fragile X mental retardation genetic locus comprising of FMR1 and FMR4 genes
FMR1	Fragile X mental retardation 1 gene
FMRP	Fragile X mental retardation protein
FRA12A	Fragile type, folic acid type, rare 12
FRAXE	Fragile X E mental retardation
FRDA	Friedrich's ataxia
FREE	Fragile X related Epigenetic Element (e.g. FREE2 and FREE3)
FREE2 (D)/(E) boundary	Boundary of FREE2 (D) and FREE2 (E)
FXPOI	Fragile X-associated primary ovarian insufficiency

ABBREVIATION	DESCRIPTION
FXS	Fragile X Syndrome
FXTAS	Fragile X-associated Tremor Ataxia Syndrome
GZ	Gray Zone
HD	Hungtington's disease
HRM	Heat Resolution Melt
MR	Mental retardation
ORF	Open Reading Frame
PCR	Polymerase Chain Reaction
PM	Premutation
POF	Premature Ovarian Failure
PolyQ	Polyglutamine
SBMA	spinobullar muscular atrophy (Kennedy disease)
SCA1	spinocerebellar ataxia Type 1
SCA17	spinocerebellar ataxia Type 17
SCA2	spinocerebellar ataxia Type 2
SCA3	spinocerebellar ataxia Type 3
SCA6	spinocerebellar ataxia Type 6
SCA7	spinocerebellar ataxia Type 7
SCA8	spinocerebellar ataxia Type 8

BRIEF DESCRIPTION OF THE FIGURES

[0062] Some figures contain color representations or entities. Color photographs are available from the Patentee upon request or from an appropriate Patent Office. A fee may be imposed if obtained from a Patent Office.

[0063] **Figure 1A** is a representation of the intron and exon regions 5' of the FMR1 CGG expansion (sequence numbering from GenBank L29074 L38501). (A) is a diagrammatic representation of the organization of the FMR genetic locus in relation to FMR1 and ASFMR1 transcription start sites, FMR1 promoter, the Fragile X-related epigenetic elements (FREE), FMR1 gene has 17 exons, and encodes FMRP. A CGG repeat is located within the 5' (UTR) of the FMR1 gene. ASFMR1 spans the CGG expansion in the antisense direction and is also regulated by another promoter located in the exon 2 of FMR1. The FREE2 located downstream of the CGG expansion. The FREE3 region is located within intron 2 of FMR1 downstream of the second ASFMR1 promoter. (B) Primers utilized for MALDI-TOF methylation analysis targeted 4 regions at the Xq27.3 locus designated as FREE2(A) [described as amplicon 5 in Godler *et al.*, *Hum Mol Genet 10(8)*:1618-1632. [Epub 2010]; Godler *et al.*, *J. Mol Diagn.* 2011 [Epub ahead of print] PMID:21723415,; HMG); FREE2(B); FREE2(C) and FREE3 (color coded). Individual CPG sites within each region are numbered accordingly. Prominent transcription factor binding sites and methylation sensitive restriction enzyme recognition sites are indicated in capital font, and are listed/identified in Table 1. << Indicates ASFMR1 transcription start site.

[0064] **Figure 2** is a graphical representation of the methylation pattern variation between healthy controls and FXS individuals within the body of the FMR1 gene, 5' of the CGG expansion. DNA from lymphoblasts of (A) healthy controls (n=4) and (B) Fragile X syndrome affected patients (n=3). Methylation of individual CpGs, were analyzed within the 9.762 kb region 5' CGG expansion, inclusive of intron 1, exon 2 and intron 2 (sequence numbering from GenBank L29074 L38501) using 3 SEQUENOM mass spectrometry assays (see Table 2). * - represent missing values. OL – represent CpG unit/s with

overlaying fragment peak; DUP – represent CpG unit/s with peak/s of the same size.

[0065] Figures 3A through C are graphical representations of a spiking experiment indicating the quantification limits of the MALDI-TOF methylation analysis of the Fragile X Syndrome (FXS) DNA within the 9.762 kb region 5' CGG expansion, inclusive of intron 1, exon 2 and intron 2 (sequence numbering from *GenBank* L29074 L38501) using 3 SEQUENOM mass spectrometry assays (A: FREE2(B); B: FREE2(C); C: FREE3). Healthy control DNA was spiked with FXS DNA at 1:0; 2:1; 1:1; 1:2; 0:1 ratios corresponding to 0, 33.3, 50, 66.6, 100% FXS DNA in the sample. The spiked DNA samples were analyzed using MALDI-TOF methylation analysis at three sequential regions at the Xq27.3 locus (see Figure 1 for locations). The methylated vs unmethylated ratios at each analysable CpG unit were expressed as output methylation ratios on Y axis, with FXS DNA input % expressed on the X axis (each point represents mean of duplicate PCRs from a single bisulfite converted DNA mixture). Methylation output ratios for CpG sites within FREE2B and FREE2C amplicons (A and B) were positively correlated with increasing FXS DNA input %; while FREE3 Methylation output ratios were negatively correlated with increasing FXS DNA input %.

[0066] Figure 4A is a diagrammatic representation of the intron and exon regions at the Xq27.3 locus (sequence numbering from GenBank L29074 L38501), locations of FMR1 and ASFMR1 transcription start sites and alternative splicing events. The locations of target sequences for FMR1 and ASFMR1 real-time PCR assays used are also indicated: ASFMR1 (-1) real-time assay: detects unspliced and splice variant C (positioned -282 to -343 from FMR1 transcription start site), ASFMR1 (-2) real-time assay: detects unspliced only (positioned -588 to -663 from FMR1 transcription start site), ASFMR1 real-time assay: detects all (positioned -1299 to -1360 from FMR1 transcription start site).

[0067] Figure 4B is a graphical representation of standard curve and amplification real-time PCR plots showing that in the FXS cell lines with fully methylated FMR1 promoter and silenced FMR1 and FMRP, ASFMR1 is expressed. RNA was extracted from 3 FXS cell lines whose methylation profiles are presented in Figure 2; Sample 849 was taken from the male 490 CGG repeat line; Sample 862 was taken from the male 530 CGG repeat

line; Sample 865 was taken from the female 563 and 47 CGG repeat line. Each RNA sample was split in two, with one half subjected to RNase A treatment prior to ASFMR1 (-3) relative standard curve analysis. The ASFMR1 (-3) real-time PCR analysis was performed in quadruplicate reactions. The difference in Ct values between RNase A treated
5 and untreated samples represents the level of ASFMR1 expression.

[0068] Figures 4C and D are graphical representations of standard curve and amplification real-time PCR plots indicating that in the FXS cell lines, ASFMR1RNA forms RNA:DNA complexes. FXS RNA samples were treated with TURBO DNase (C)
10 and RQ1 DNase (D) respectively. These DNase treatments caused complete loss of real-time-PCR signal for the ASFMR1(-3) assay. Because DNase can only degrade RNA molecules if they form complexes with DNA, loss of ASFMR1 after DNase treatment suggests that ASFMR1RNA forms RNA:DNA complexes in FXS samples with fully methylated FMR1 promoter and silenced FMR1 expression.
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[0069] Figures 5A and B are graphical representations of different FMR1 and ASFMR1 transcripts in RNA samples from lymphoblast lines of 6 male controls, two FXS males (samples 849 and 862) and one FXS female (865). The control and FXS RNA samples were either treated with TURBO DNase (A), RQ1 DNase (B), RNase A (C), or were
20 untreated. Addition of TURBO DNase or RQ1 DNAse buffers to RNA samples without DNase were included as additional controls in A and B. The FMR1 and ASFMR1 transcripts were quantified using real-time RT-PCR relative standard curve method, normalized to mRNA levels of three internal control genes, GUS, GAPDH and B2M. FMR15' and 3' assays showed no signal for the FXS RNA samples, while similar levels
25 were detected in all control samples (upper two panels in A, B and C). TURBO and RQ1 DNAse treatment caused ~50% decrease in the FMR1 levels in most of the control samples; while RNase A treatment caused complete loss of FMR1 and ASFMR1 signals. While decrease of ASMFR1 (-1)(-2) and (-3) levels was also observed in all control samples caused by TURBO and RQ1 DNAse treatment, in FXS samples (with analogous
30 to control ASFMR1 levels in the untreated samples) TURBO and RQ1 DNAse treatment resulted in complete loss of signal for all three ASFMR1 assays. Because DNase can only degrade RNA molecules if they form complexes with DNA, this suggests that ASFMR1

RNA forms RNA:DNA complexes more readily in FXS samples than in controls. Increase in RNA:DNA interaction of ASFMR1 in FXS may lead to methylated FMR1 promoter and adjacent regions (Figure 1) and silencing FMR1 expression leading to loss of FMRP and the resulting FXS clinical phenotype.

5

[0070] Figure 6(A) is a representation of the intron and exon regions 5' of the FMR1 CGG expansion (sequence numbering from GenBank L29074 L38501) in relation to FMR1 and ASFMR1 transcription start sites, FMR1 promoter, the Fragile X-related epigenetic elements 2 and 3 (FREE). A CGG repeat is located within the 5' (UTR) of the FMR1 gene. 10 ASFMR1 spans the CGG expansion in the antisense direction and is also regulated by another promoter located in the exon 2 of FMR1. The FREE2 located downstream of the CGG expansion. The FREE3 region is located within intron 2 of FMR1 and spans the potential second ASFMR1 promoter of transcription in the antisense direction. **(B)** Primers utilized for MALDI-TOF methylation analysis targeted 5 regions at the Xq27.3 locus 15 designated as FREE2(A) (described as amplicon 5 in Godler *et al., Hum Mol Genet*, 2010; [Epub ahead of print] doi:10.1093/hmg/ddq 1037); FREE2(D); FREE2(E), and FREE3 (color coded). Individual CPG sites within each region are numbered accordingly. Prominent transcription factor binding sites and methylation sensitive restriction enzyme recognition sites are indicated in capital font, and are listed/identified in Tables 3 and 4. << 20 Indicates ASFMR1 transcription start site. The red arrow indicates the FREE2 3' Boundary located at CpG1 of FREE2(E) which is underlined in the sequence. **(C)** is a representation of the CG dinucleotide density in the regions proximal to the FREE2 3' Boundary. The CpG sites that have been analysed for methylation status are represented in Blue on the X axis, while sites not covered by our assays are represented in red. The coordinates of the 25 FREE2(D) and FREE2(E) assays on the GenBank L29074 L38501 are also indicated.

[0071] Figure 7 is a graphical representation of the methylation pattern variation in lymphoblasts and blood between **(A)** healthy controls, **(B)** unmethylated FM 'high functioning' males with full scale IQ (FIQ) greater than 70, **(C)** FXS affected individuals 30 full scale IQ (FIQ) less than 70. Methylation output ratio (Y axis) of individual CpG units (X axis), were analyzed within the 27 kb region 3' CGG expansion, inclusive of intron 1, exon 2 and intron 2 (sequence numbering from GenBank L29074 L38501). The

SEQUENOM mass spectrometry assays FREE2(D) and FREE2(E) (see Tables 3 and 4) were the most proximal to the FREE2 3' Boundary highlighted with the RED arrow as the CpG 1 of the FREE2(E) assay. It is evident from the representation that this CpG unit is the last one within the FREE2 region which is unmethylated in healthy controls and high functioning FM individuals while being hyper methylated in FXS affected individuals. It is evident from the representation that the FREE3 region methylation status is an important biomarker of the FXS phenotype as it is hypermethylated in high functioning FM individuals as well as in healthy controls, while being hypomethylated in FXS affected individuals. It is also evident from the representation that the methylation patterns are consistent between lymphoblasts and blood. LB- represents lymphoblasts.

DETAILED DESCRIPTION

[0072] Taught herein is to a method for identifying an epigenetic profile of an intron, intron/exon boundary and/or splicing region within a genetic locus associated with or indicative, instructive or informative of a pathological condition. The epigenetic modification occurs in:

(i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; and/or

(ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region;

within a genetic locus. In an embodiment, the pathological condition is a trinucleotide expansion disorder such as in association with a change in epigenetic profile from that of a healthy control subject.

[0073] By "epigenetic profile" includes epigenetic modifications such as methylation including hypermethylation and hypomethylation, RNA/DNA interactions, expression profiles of non-coding RNA, histone modification, changes in acetylation, obiquitylation, phosphorylation and sumoylation, as well as chromatin altered transcription factor levels and the like leading to activation or deactivation of genetic locus expression. Particularly, the extent of methylation, RNA/DNA interaction and non-coding RNA expression are determined as well as any changes therein. In an aspect, the epigenetic modification is an elevation in methylation, a decrease in methylation or an alteration in distribution of methylation sites. The epigenetic profile may be determined on either strand of genomic double stranded DNA or an amplified fragment thereof. Hence, primers may be generated to amplify either strand of a genomic DNA target.

[0074] The pathological condition may be a neurological or non-neurological condition. Insofar as the condition is neurological, it may be described as a neuropathological condition or a pathoneurological condition which encompasses neurodegenerative and

neurodevelopmental disorders. Non-neurological pathologies are also contemplated herein as well as any nucleotide expansion disease or condition. Reference to a pathological conditions includes a trinucleotide expansion disorder. Reference to a "control" means relative to a healthy subject which means a subject with a normal size of expansion repeats and/or who is phenotypically normal meaning that the subject does not have symptoms of, *for example, a trinucleotide expansion disorder and/or is the epigenetic profile* observed in healthy control subjects.

[0075] In an embodiment, the pathological diesease or condition including trinucleotides expansion disorders associated with a change in the epigenetic profile from that observed in healthy controls associated with the intronic epigenetic change is Fragile X syndrome (FXS), Fragile X-associated tremor or ataxia (FXTAS), Fragile X-associated primary ovarian insufficiency (FXPOI), autism, mental retardation, cognitive impairment, a modified X-chromosome, Huntington's disease (HD), dentatorubropallid-oluysiantrophy (DRPLA), spinobulbar muscular atrophy or Kennedy disease (SBMA), spinocerebella ataxia Type 1 (SCA1), spinocerebella ataxia Type 2 (SCA2), spinocerebella ataxia Type 3 or Machado-Joseph disease (SCA3), spinocerebella ataxia Type 6 (SCA6), spinocerebella ataxia Type 7 (SCA7), spinocerebella ataxia Type 17 (SCA17), Fragile XE mental retardation (FRAXE), Friedrich's ataxia (FRDA), Fragile type, folic acid type, rare 12 (FRA12A), myotonic dystrophy (DM), spinocerebella ataxia (SCA8) and spinocerebella ataxias Type 12 (SCA12), Klinefelter's syndrome and Turner's syndrome. The present disclsoure also identifies nucleotide expansion diseases and conditions. In an embodiment, the genetic locus is the FMR genetic locus and the pathology is FXS or related condition such as FXTAS, FXPOI, autism, mental retardation, a modified X-chromosome or cognitive impairment.

[0076] A method is enabled for identifying an epigenetic profile in a genome of a cell indicative of a pathological condition selected from Fragile X syndrome (FXS), Fragile X-associated tremor or ataxia (FXTAS), Fragile X-associated primary ovarian insufficiency (FXPOI), autism, mental retardation, cognitive impairment, a modified X-chromosome, Huntington's disease (HD), dentatorubropallid-oluysiantrophy (DRPLA), spinobulbar muscular atrophy or Kennedy disease (SBMA), spinocerebella ataxia Type 1 (SCA1),

spinocerebella ataxia Type 2 (SCA2), spinocerebella ataxia Type 3 or Machado-Joseph disease (SCA3), spinocerebella ataxia Type 6 (SCA6), spinocerebella ataxia Type 7 (SCA7), spinocerebella ataxia Type 17 (SCA17), Fragile XE mental retardation (FRAXE), Friedrich's ataxia (FRDA), Fragile type, folic acid type, rare 12 (FRA12A), myotonic dystrophy (DM), spinocerebella ataxia (SCA8) and spinocerebella ataxias Type 12 (SCA12), Klinefelter's syndrome and Turner's syndrome, the method comprising screening for a change relative to the control in the extent of epigenetic modification in a genetic locus within (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; and/or (ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region of a genetic locus associated with the pathological condition wherein the extent of epigenetic change is indicative of the presence or severity of the pathological condition or a propensity to develop same. In an embodiment, the genetic locus is the FMR locus and the region assayed for epigenetic change is selected from:

(i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region;

(ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region;

(iii) the 3' boundary of the FREE2 region and the FMR1 promoter located between CpG unit 1 of the FREE2 (E) amplicon and CpG unit 2/3 of the FREE2 (E) amplicon;

(iv) the FREE2 region alone or in combination with the FREE1 region;

(v) the FREE3 region; and

(vi) an intron including an intron/exon boundary and/or splicing region downstream of intron 1 within the FMR1 gene including the FREE2 (D) region or FREE2 (D)/(E) boundary.

[0077] In an embodiment, a method is provided for identifying an epigenetic profile in a genome of a cell indicative of FXS or related condition the method comprising screening for a change relative to the control in the extent of epigenetic modification in the FMR genetic locus within (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or

(c) a splicing region; and/or (ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region of a genetic locus associated with the pathological condition wherein the extent of epigenetic change is indicative of the presence or severity of the pathological condition or a propensity to develop same. A related condition includes FXTAS, FXPOI, autism, mental retardation, a modified X-chromosome and cognitive impairment.

[0078] In relation to this aspect, an "intron", "intron/exon boundary" and "splicing region", are regarded as an intron, intron/exon boundary and splicing region within a genetic locus or a gene within a genome. The intron, intron/exon boundary and splicing region may also encode a regulatory RNA species. Either strand of a double stranded genomic DNA or an amplified fragment or region thereof may be assayed for its epigenetic profile.

[0079] In an embodiment, the pathological condition is associated with an epigenetic profile of the FMR genetic locus. For the purposes of the present disclosure, the "FMR genetic locus" includes the FMR1, FMR4 and ASFMR1 genes as well as promoter and regulatory regions and introns and exons and intron/exon boundaries. In particular, the FMR genetic locus comprises a promoter region, a $(CGG)_n$ region proximal to the promoter and exonic and intronic regions of the FMR1, FMR4 and ASFMR1 genes as depicted in Figures 1A and 4A and 6A. The promoter is generally referred to as the "FMR1 promoter" or "ASFMR1 promoter" for the promoter with an initiation site in FREE3 of intron 2 (see Figure 6). The FMR locus includes introns, intron/exon boundaries and splicing regions wherein it is proposed herein that epigenetic changes occur within (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing regions; and/or (ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region of the FMR genetic locus including the FMR1 gene or a part thereof such as FREE3 or FREE2 region alone or in combination with the FREE1 region (D) or FREE2 (E) which are indicative or diagnostic of a pathological condition or its severity involving the FMR1, FMR4 and/or ASFMR1 genes. FREE3, FREE2 (D) and FREE2 (E) are is further defined below. As indicated above, when determining an epigenetic profile either or both strands of the double stranded genomic DNA or an amplified product therefrom may be assayed. This also applies to a

promoter region or other regulatory region.

[0080] In an embodiment, the epigenetic profile is determined within a genetic locus which enables the determination of an epigenetic profile in a genome of a cell indicative of a pathological condition and in particular a trinucleotide expansion disorder selected from Fragile X syndrome (FXS), Fragile X-associated tremor or ataxia (FXTAS), Fragile X-associated primary ovarian insufficiency (FXPOI), autism, mental retardation, cognitive impairment, a modified X-chromosome, Huntington's disease (HD), dentatorubropallid-oluysiantrophy (DRPLA), spinobulbar muscular atrophy or Kennedy disease (SBMA), spinocerebella ataxia Type 1 (SCA1), spinocerebella ataxia Type 2 (SCA2), spinocerebella ataxia Type 3 or Machado-Joseph disease (SCA3), spinocerebella ataxia Type 6 (SCA6), spinocerebella ataxia Type 7 (SCA7), spinocerebella ataxia Type 17 (SCA17), Fragile XE mental retardation (FRAXE), Friedrich's ataxia (FRDA), Fragile type, folic acid type, rare 12 (FRA12A), myotonic dystrophy (DM), spinocerebella ataxia (SCA8) and spinocerebella ataxias Type 12 (SCA12), Klinefelter's syndrome and Turner's syndrome. Epigenetic changes in intronic, intronic/exonic boundaries and promoter or other regulatory regions in certain geentic loci are instructive to the development of these conditions.

[0081] In an embodiment, the genetic locus is the FMR genetic locus and the method comprises screening for a change relative to the control in the extent of epigenetic modification within the FMR genetic locus within a region selected from:

(i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region;

(ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region;

(iii) the 3' boundary of the FREE2 region and the FMR1 promoter located between CpG unit 1 of the FREE2 (E) amplicon and CpG unit 2/3 of the FREE2 (E) amplicon;

(iv) the FREE2 region alone or in combination with the FREE1 region;

(v) the FREE3 region; and

(vi) an intron including an intron/exon boundary and/or splicing region downstream of intron 1 within the FMR1 gene including the FREE2 (D) region or FREE2 (D)/(E) boundary.

5 **[0082]** The extent of epigenetic change is indicative of the presence of severity of the pathological condition or a propensity to developing same. Disease conditions contemplated herein associated with the FMR genetic locus include the trinucleotide expansion disorder FXS and related conditions such as FXTAS, FXPOI, autism, mental retardation, a modified X-chromosome and cognitive impairment. In an embodiment, the 10 present disclosure teaches a method for identifying FXS or a related condition in a human subject, the method comprising screening for a change relative to a control in the extent of epigenetic modification in the FMR genetic locus at a location selected from:

(i) Fragile X-related Epigenetic Element 3 in FMR1 comprising the nucleotide 15 sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions; and

(ii) genomic FREE2 region as a whole or specific fragments of FREE2 20 including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditions;

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wherein a change in extent of epigenetic modification relative to a control is indicative of the presence or severity of the pathological condition or a propensity to develop same.

[0083] In an embodiment a method is provided for identifying a trinucleotide expansion 30 disorder in a mammalian subject including a human, the method comprising screening for a change relative to a healthy control in the extent of epigenetic modification within (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; and/or

(ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region of the FMR genetic locus; wherein a change in extent of epigenetic modification relative to the control is indicative of the presence or severity of the trinucleotide expansion disorder or a propensity to develop same wherein the intron, intron/exon boundary and/or splicing region is selected from the list consisting of:

(i) Fragile X-related Epigenetic Element 3 in FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions;

(ii) intron 2 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or a portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions; and

(iii) genomic FREE2 region as a whole or specific fragments of FREE2 including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditions.

[0084] The present disclosure teaches the manufacture of an assay to identify an epigenetic profile of an FMR genetic locus-associated pathological condition. Reference to an FMR genetic locus-associated pathological condition includes a trinucleotide expansion disorder associated with a change in epigenetic profile from that observed in a healthy subject.

[0085] The FMR genetic locus is depicted in part in Figures 1A, 4A and 6A. Reference to the "FMR genetic locus" includes the FMR1, FMR4 and ASFMR1 genes and corresponds to Xq27.3. The term "FMR locus" means the "FMR genetic locus". In an embodiment, an aspect taught herein determines that the intronic region downstream of intron 1 comprises Fragile X-related Epigenetic Element 3 as defined by SEQ ID NO:1 or a homolog thereof

or a portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions; or is intron 2 as defined by SEQ ID NO:2 or a homolog thereof or a portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions. The nucleotide sequence of intron 1 of the FMR1 gene is set forth in SEQ ID NO:3. The nucleotide sequence of genomic FREE2 (D), FREE2 (E) and FREE3 are set forth in SEQ ID NOs:48, 49 and 47, respectively and the present disclosure extends to homology thereof having at least 80% identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or a complement thereof under medium stringency conditions. The present disclosure extends to both strands and hence, for example, reference to a particular SEQ ID NO: includes the corresponding complementary sequence.

[0086] The present disclosure further contemplates amplifying all or part of an expansion mutation and/or and detecting extent of epigenetic change therein in combination with an epigenetic change (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; and/or (ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region of the FMR genetic locus including the FMR1 gene. The extent of epigenetic change in two or more of an intron, an intron/exon boundary and/or a splicing region or in one seventh or greater of an intron within the FMR genetic locus may be determined alone or in combination with extent of $(CGG)_n$ expansion and/or any other epigenetic change therein. The determination of epigenetic change may also be conducted in combination with an assay as contemplated by International Patent Application No. PCT/AU2010/000169 filed on 17 February 2010, the contents of which are incorporated herein by reference in their entirety. In an embodiment, the epigenetic modification is a change in extent of methylation which includes hypermethylation and hypomethylation and profile of methylation. Without limiting the present disclosure to any one theory or mode of action, epigenetic changes in these introns may affect the ability of the introns, intron/exon boundaries and/or splicing regions to transcribe regulatory RNAs which in turn have an effect on bidirectional transcription capability.

[0087] Hence, an aspect taught herein is a method for identifying a pathological condition in a mammalian subject including a human, the method comprising screening for a change relative to a control in the extent of epigenetic modification within a region selected from:

5 (i) Fragile X-related Epigenetic Element 3 in FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions;

10 (ii) intron 2 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or a portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions;

(iii) genomic FREE2 region as a whole or specific fragments of FREE2 15 including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditions;

20 (iv) an intron, intron/exon boundary and/or splicing region downstream of intron 2 of FMR1 or a homolog thereof or a portion or fragment thereof;

(v) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing regions within the FMR genetic locus; and

(vi) approximately one seventh or greater of an intron including an intron/exon 25 boundary and/or a splicing region within the FMR genetic locus;

wherein a change in extent of genetic modification relative to a control is indicative of the presence or severity of the pathological condition or a propensity to develop same.

30 [0088] The present disclosure teaches a method for identifying in a genome of a mammalian cell including a human cell, a pathological condition associated with methylation and other epigenetic change within the FMR locus, the method comprising

extracting genomic DNA from the cell and subjecting the DNA to an amplication reaction using primers selective of a region of the FMR genetic locus comprising CpG and/or CpNpG sites, the CpG and CpNpG sites located in a region selected from:

5 (i) Fragile X-related Epigenetic Element 3 in FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions;

10 (ii) intron 2 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or a portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions;

(iii) genomic FREE2 region as a whole or specific fragments of FREE2 15 including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditions;

20 (iv) an intron, intron/exon boundary and/or splicing region downstream of intron 2 of FMR1 or a homolog thereof or a portion or fragment thereof;

(v) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing regions within the FMR genetic locus; and

(vi) approximately one seventh or greater of an intron including an intron/exon 25 boundary and/or a splicing region within the FMR genetic locus;

and subjecting the amplified DNA to a methylation or other epigenetic assay to determine the extent of epigenetic modification of the DNA wherein a change in extent of epigenetic modification relative to a control is indicative of the presence or severity of the 30 pathological condition or propensity to develop same. In an embodiment, the above assay is useful in detecting FXS or a related condition. Examples of related conditions include FXTAS, FXPOI, autism, mental retardation, a modified X-chromosome and cognitive

impairment.

[0089] In an embodiment, the epigenetic modification is methylation of CpG and/or CpNpG sites and the assay identifies the extent of methylation change in either strand of
5 double stranded genomic DNA or an amplified fragment thereof including either strand of a promoter region. This change may be an *elevation or increase in methylation* or a decrease in methylation relative to a control. Alternatively, the epigenetic modification is extent of change in RNA/DNA interaction and/or change in profile of expression of expression of non-coding RNA. Yet in another embodiment, the epigenetic profile is a
10 change in histone modification, changes in acetylation, obiquitylation, phosphorylation, sumoylation, activation or deactivation, chromatin altered transcription factor levels and the like.

[0090] In accordance with the present disclosure, a method is provided wherein the extent
15 of methylation *or other epigenetic modification* provides a quantitative or semi-quantitative or qualitative indication of extent of change in epigenetic profile in (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; and/or (ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region within the FMR genetic locus including the FMR1 gene, ASFMR1
20 gene and promoter gene (including an FMR1 promoter and an ASFMR1 promoter) and as such the level of epigenetic modification defines the severity of the pathological condition alone or in combination with the extent of $(CGG)_n$ expansion. The number of repeats indicate whether a subject is a healthy control or has a Gray Zone (GZ) pathology, premutation (PM) pathology or full mutation (FM) pathology. The method disclosed
25 herein may also be used in conjunction with other assays such as Southern blot or PCR to measure $(CGG)_n$ expansion. Examples of pathology conditions associated with inronic epigenetic changes include the polyQ and non-polyQ conditions listed above.

[0091] The present disclosure, however, is not limited to the FMR genetic locus and
30 pathological conditions only associated therewith. Rather, the present disclosure extends to any epigenetic modification in any genetic locus selected from (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; and/or (ii) approximately

one seventh greater of an intron including an intron/exon boundary and/or splicing region and which epigenetic change is associated with a pathological condition.

[0092] By "approximately one seventh or greater" means from about 14% or greater or nucleotides capable of epigenetic change or modification have undergone a change. This includes 14.5, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 67, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 and 100% of the nucleotides.

[0093] The regions within the FMR genetic locus identified above include a region selected from:

(i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region;

(ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region;

(iii) the 3' boundary of the FREE2 region and the FMR1 promoter located between CpG unit 1 of the FREE2 (E) amplicon and CpG unit 2/3 of the FREE2 (E) amplicon;

(iv) the FREE2 region alone or in combination with the FREE1 region;

(v) the FREE3 region; and

(vi) an intron including an intron/exon boundary and/or splicing region downstream of intron 1 within the FMR1 gene including the FREE2 (D) region or FREE2 (D)/(E) boundary.

[0094] As taught herein a "pathological condition" or "disease condition" includes an abnormal condition including a neurodevelopmental condition or a neurodegenerative condition or a non-neurological condition as defined by objective or subjective manifestations of disease. In an embodiment, it is a trinucleotide expansion disorder. A particular condition is FXS or a related condition such as FXTAS, FXPOI, autism, mental

retardation, a modified X-chromosome and cognitive impairment. The assay herein described is useful for diagnosing nucleotide expansion diseases or conditions. The assay enabled herein includes a genetic determination to be made to complement other symptom-based diagnoses such as based on behavioral studies or may be made in its own right. The assay may be part of a suit of diagnostic or prognostic genetic assays of embryos, pre- and post-natal subjects. The terms "method", "assay", "system", "test", "determination", "prognostic", "diagnostic", "report" and the like may all be used to describe the methylation assay of selected regions of the FMR genetic locus or other genetic locus. The epigenetic assay such as a methylation assay determines the epigenetic profile or extent of epigenetic change compared to a control which suggests or indicates or is instructive of a disease or condition associated with epigenetic modification of an intron within a genetic locus. The present assay is also useful in population studies such as epidemiological studies including studies of ethnic populations.

[0095] Accordingly, the present disclosure further provides a method of identifying a methylation or other epigenetic profile in populations of subjects indicative of a pathological condition, the method comprising screening for a change relative to a control in a statistically significant number of subjects the extent of epigenetic modification in (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; and/or (ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region within a genetic locus wherein a change in extent of epigenetic modification is indicative of the presence or severity of the pathological condition or a propensity to develop same.

[0096] In an embodiment, the genetic locus is the FMR genetic locus and the region screened for epigenetic change is selected from:

(i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region;

(ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region;

(iii) the 3' boundary of the FREE2 region and the FMR1 promoter located

between CpG unit 1 of the FREE2 (E) amplicon and CpG unit 2/3 of the FREE2 (E) amplicon;

(iv) the FREE2 region alone or in combination with the FREE1 region;

(v) the FREE3 region; and

5 (vi) an intron including an intron/exon boundary and/or splicing region downstream of intron 1 *within the FMR1 gene including the* FREE2 (D) region or FREE2 (D)/(E) boundary.

[0097] The present disclosure teaches a method of identifying a methylation or other 10 epigenetic profile in a population of subjects indicative of a pathological condition associated with the FMR locus, the method comprising screening for a change, relative to a control, in a statistically significant number of subjects in the extent of epigenetic modification including extent of change in methylation of CpG and/or CpNpG sites within a region selected from:

15

(i) Fragile X-related Epigenetic Element 3 in FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency 20 conditions;

(ii) intron 2 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or a portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions;

25 (iii) genomic FREE2 region as a whole or specific fragments of FREE2 including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under 30 medium stringency conditions;

(iv) an intron, intron/exon boundary and/or splicing region downstream of intron 2 of FMR1 or a homolog thereof or a portion or fragment thereof;

(v) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing regions within the FMR genetic locus; and

(vi) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region within the FMR genetic locus;

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wherein a change in extent of epigenetic modification is indicative of the presence of the pathological condition or a propensity to develop same in the population. In an embodiment, the pathological condition is FXS or a related condition such as FXTAS, FXPOI, autism, mental retardation, a modified X-chromosome and cognitive impairment.

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[0098] In accordance with this method, a further step may be conducted of determining the extent of $(CGG)_n$ expansion such as by PCR and/or Southern blot analysis of bisulfite converted and/or non converted DNA. Furthermore, this assay may be conducted with one or more assays contemplated and described in International Patent Application NO.
15 PCT/AU2010/000169 filed on 17 February 2010, the contents of which are incorporated by reference in their entirety.

[0099] In an embodiment, the extent of methylation or change in extent of methylation is detected and associated with the pathology condition such as but not limited to an
20 expansion disease or condition.

[0100] An epigenetic map and in particular a methylation map of introns, intron/exon boundaries and/or splicing regions within the FMR locus has thus been constructed in accordance with the present disclosure using standard techniques such as high throughput
25 mass spectrometry in the genome of various cells. Any cell type cell may be assayed. These cells include cultured or uncultured Chorionic Villi Sample (CVS) cells, lymphoblasts, blood cells, buccal cells, epithelial cells, fibroblast cells, an amniocyte and EBV transformed lymphoblast cell lines from male and female subjects with either no symptoms or from a spectrum of a pathological condition such as Fragile X mental
30 retardation symptoms. In an embodiment a Fragile X-related Epigenetic Element 3 (FREE3) has been identified within intron 2 of the FMR1 gene. It is proposed that this region [FREE3] or other regions of intron 2 or other introns or parts thereof including

intron/exon boundaries and splicing regions downstream of intron 2 of FMR1 or elsewhere in the FMR genetic locus are responsible for the regulation of transcription of FMR4 and ASFMR1 and FMR1 and expression of FMRP. Another region is an ASFMR1 promoter having an initiation site in FREE3 of intron 2 (see Figure 6A).

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[0101] *In an embodiment, the present disclosure teaches that the extent of methylation in* CpG and/or CpNpG sites located within the region downstream of intron 1 or part thereof such as FREE3 closely corresponds to a healthy condition or a level or severity of disease within the spectrum of PM to FM including GZ subjects such a correspondence may be in
10 a further association with other epigenetic modifications within the FMR genetic locus and/or CGG expansion. Furthermore, using the methylation assay, methylation levels of the FREE3 region provide fully quantitative results, which also reflect the degree of X-chromosome modification in females. This can be more informative than methylation patterns of FMR1 CpG islands only which may be biased due to its proximity to a
15 nucleotide expansion, and hence can only provide a qualitative assessment of methylation. Other regions of interest include FREE2 (A), (B), (C) and (D) and the FREE2 (D)/FREE2 (E) boundary defined herein.

[0102] Hence, in an embodiment, the present disclosure contemplates a change in extent of
20 methylation which includes an increase or decrease in extent of methylation. There may also be no change in the extent of methylation within an intron of a genetic locus. However, the present disclosure extends to the detection of the change in extent of any epigenetic modification. Such a change or level of methylation in an intron ls proposed to be associated with a pathological condition or its severity. In this context, an "intron"
25 includes an intron/exon boundary and/or a splicing region.

[0103] A "normal" or "control" in the assay of the present disclosure may be a control genome from a healthy individual performed at the same time or the epigenetic pattern may be compared to a statistically validated standard. In relation to a nucleotide expansion
30 disease condition, a healthy individual includes a subject with a nucleotide repeat within the normal range with no clinically apparent pathological phenotype. For example, in relation to $(CGG)_n$ expansion conditions within the FMR genetic locus, this includes when

n is <40.

[0104] The present disclosure also explores the relationship between transcription and epigenetic profile of introns or parts thereof and pathological conditions. A "part" includes an intron/exon boundary and splicing region. In an embodiment, methylated CpG sites are identified within *FREE3* or *intron 2 of the FMR1 gene in subjects with* Fragile X mental retardation conditions. In another embodiment, the methylated CpG sites are identified in (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; and/or (ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region of the FMR genetic locus. Fragile X mental retardation conditions include FXS as well as FXTAS, FXPOI, autism, mental retardation, a modified X-chromosome and cognitive impairment.

[0105] As used herein, the terms "subject", "patient", "individual", "target" and the like refer to any organism or cell of the organism on which an assay of the present disclosure is performed whether for experimental, diagnostic, prophylactic, and/or therapeutic purposes. Typical subjects include both male and female humans but the present disclosure extends to experimental animals such as non-human primates, (e.g., mammals, mice, rats, rabbits, pigs and guinea pigs/hamsters). The "subject" may also be referred to as a population since the present disclosure teaches an assay useful in populations studies including epidemiological studies or assays of ethnic population. In a particular embodiment, the subject is a human. The test may be tailored to human females or human males or pre-natal humans. A control subject has epigenetic (e.g. methylation) profile of a healthy subject.

[0106] The terms "Fragile X mental retardation-like condition" and FMR condition" refer to a neurological disease, disorder and/or condition characterized by one or more of the following symptoms: (1) behavioral symptoms, including but not limited to hyperactivity, stereotypy, anxiety, seizure, impaired social behavior, and/or cognitive delay; (2) defective synaptic morphology, such as an abnormal number, length, and/or width of dendritic spines; and/or (3) defective synaptic function, such as enhanced long-term depression (LTD); and/or reduced long-term potentiation (LTP); and/or impaired cognitive ability. The pathological condition is a disease, disorder, and/or condition caused by and/or

associated with epigenetic changes within an intron or part thereof within the FMR genetic locus such as downstream of intron 1 of the FMR1 gene. Such epigenetic changes may be alone or in combination with one or more of the following: (1) a mutation in FMRl or FMR4 or ASFMR1; (2) defective FMRl/FMR4/ASFMR1 expression; (3) increased and/or
5 decreased levels of FMRP; (4) defective FMRP function; (5) increased and/or decreased expression of genes or genetic functions regulated by FMR1, FMRP, FMR4 transcript or ASFMR1 transcript; (6) the increased methylation of FMR locus at CpG or CpNpG sites in the region upstream of FMR1 promoter and/or the region downstream of the $(CGG)_n$ portion of the FMR1 promoter but not including the $(CGG)_n$ portion; (7) an increased
10 and/or decreased function of the FMR locus *via* miRNAs and/or members of the miRNA pathway; (8) an increased and/or decreased ability of FMRP to interact with its known target RNAs, such as RNAs encoding Racl, microtubule-associated protein IB, activity-regulated cytoskeleton-associated protein, and/or alpha-calcium/calmodulin-dependent protein kinase II; (9) symptoms of FXS, FXTAS, FXPOI, mental retardation, a modified
15 X-chromosome, autism and/or autism spectrum disorders; and/or (10) cognitive impairment. Generally, the FMR condition is a trinucleotide expansion disorder, particularly associated with a changed epigenetic profile from that of a healthy subject.

[0107] Those of ordinary skill in the art will appreciate that the teachings of the present
20 disclosure are applicable to any neurodevelopmental or neurodegenerative disorders linked, associated or otherwise influenced by the function of the FMR genetic locus or genes therein such as FMR1, FMR4 and ASFMR1 as well as their promoters or other regulatory regions. Non-neurological disorders are also contemplated herein including FXPOI and other tri-nucleotide expansion disorders.

25

[0108] Furthermore, the present disclosure teaches a range of nucleotide expansion disorders. Conditions and disorders contemplated herein include diseases such as Fragile X syndrome (FXS), Fragile X-associated tremor or ataxia (FXTAS), Fragile X-associated primary ovarian insufficiency (FXPOI), autism, mental retardation, cognitive impairment,
30 a modified X-chromosome, Huntington's disease (HD), dentatorubropallid-oluysiantrophy (DRPLA), spinobulbar muscular atrophy or Kennedy disease (SBMA), spinocerebella ataxia Type 1 (SCA1), spinocerebella ataxia Type 2 (SCA2), spinocerebella ataxia Type 3

or Machado-Joseph disease (SCA3), spinocerebella ataxia Type 6 (SCA6), spinocerebella ataxia Type 7 (SCA7), spinocerebella ataxia Type 17 (SCA17), Fragile XE mental retardation (FRAXE), Friedrich's ataxia (FRDA), Fragile type, folic acid type, rare 12 (FRA12A), myotonic dystrophy (DM), spinocerebella ataxia (SCA8) and spinocerebella
5 ataxias Type 12 (SCA12), Klinefelter's syndrome and Turner's syndrome.

[0109] The term "genomic DNA" includes all DNA in a cell, group of cells, or in an organelle of a cell and includes exogenous DNA such a transgenes introduced into a cell. Either strand or both strands of double stranded DNA may be assayed.

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[0110] In a particular aspect, the present disclosure enables the determination of the presence of an FMR genetic locus-associated pathology based on extent of methylation of CpG/CpNpG sites located within (i) an intron downstream of intron 1 of the FMR1 gene or part of an intron; (ii) two or more or (a) an intron; (b) an intron/exon boundary; (c) a
15 splicing region; and/or (iii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region within the FMR genetic locus. The downstream FMR1 introns may extend beyond the FMR1 gene. In an embodiment, the extent of methylation in part of intron 2 [FREE3] is identified in the FMR1 gene which includes all or part of an ASFMR1 promoter with a transcription start site in FREE3 of
20 intron 2 (see Figure 6A).

[0111] Hence, the present disclosure teaches a method for identifying a methylation or other epigenetic profile in the genome of a cell indicative of a pathological condition associated with the FMR genetic locus, the method comprising screening for a change
25 relative to the control in the extent of epigenetic modification of CpG and/or CpNpG sites located within:

(i) (a) FREE3; (b) intron 2; and (c) an intron downstream of intron 2 or a homolog thereof or a portion or fragment thereof within the FMR1 gene;

30 (ii) two or more of (a) an intron; (b) an intron/exon boundary; (c) a splicing region within the FMR genetic locus; and/or

(iii) approximately one seventh or greater of an intron including an intron/exon

boundary and/or a splicing region within the FMR genetic locus;

wherein a change in the extent of epigenetic modification is indicative of the presence of the pathological condition or a propensity to develop same. The nucleotide sequences of FREE3 and intron 2 are set forth in SEQ ID NOs: 1 and 2, respectively and the present disclosure extends to their homologs and portions and parts thereof having at least 80% identity thereto or a nucleotide sequence capable of hybridizing to these sequences or their complementary forms under medium stringency conditions. Reference to FREE3 and an intron such as intron 2 includes portions, fragments, parts, regions and domains thereof. The nucleotide genomic sequences of genome FREE2 (D), FREE2 (E) and FREE3 are set forth in SEQ ID NOs:48, 49 and 47, respectively and the present disclosure extends to their homologs and portions and parts thereof having at least 80% identity thereto or a nucleotide sequence capable of hybridizing to these sequences or their complementary forms under medium stringency conditions. Reference to FREE3 and an intron such as intron 2 includes portions, fragments, parts, regions and domains thereof as well as one or both strands of double stranded genomic DNA.

[0112] In a particular embodiment, the epigenetic modification is methylation and RNA/DNA interactions.

[0113] The present disclosure further contemplates a method for identifying a pathological condition in a subject associated with methylation within the FMR locus, the method comprising extracting genomic DNA from a cell of the subject and subjecting the DNA to an amplication reaction using primers selective of a region of the FMR genetic locus comprising CpG and/or CpNpG sites, the CpG and CpNpG sites located in the FMR genetic locus within a region selected from:

(i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region;

(ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region;

(iii) the 3' boundary of the FREE2 region and the FMR1 promoter located

between CpG unit 1 of the FREE2 (E) amplicon and CpG unit 2/3 of the FREE2 (E) amplicon;

(iv) the FREE2 region alone or in combination with the FREE1 region;

(v) the FREE3 region; and

5 (vi) an intron including an intron/exon boundary and/or splicing region downstream of intron 1 within the FMR1 gene including the FREE2 (D) region or FREE2 (D)/(E) boundary.

and subjecting the DNA to a methylation assay to determine the extent of methylation of 10 the DNA wherein a change in extent of methylation relative to a control is indicative of the presence or severity of the pathological condition or propensity to develop same.

[0114] In an embodiment, the present disclsoure teaches a method for identifying FXS or a related condition assocaited with methylation of the FMR genetic locus, the method 15 comprising extracting genomic DNA from a cell of the subject and subjecting the DNA to an amplication reaction using primers selective of a region of the FMR genetic locus comprising CpG and/or CpNpG sites, the CpG and CpNpG sites located in the FMR genetic locus within a region selected from:

20 (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region;

(ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region;

(iii) the 3' boundary of the FREE2 region and the FMR1 promoter located 25 between CpG unit 1 of the FREE2 (E) amplicon and CpG unit 2/3 of the FREE2 (E) amplicon;

(iv) the FREE2 region alone or in combination with the FREE1 region;

(v) the FREE3 region; and

(vi) an intron including an intron/exon boundary and/or splicing region 30 downstream of intron 1 within the FMR1 gene including the FREE2 (D) region or FREE2 (D)/(E) boundary.

and subjecting the DNA to a methylation assay to determine the extent of methylation of the DNA wherein a change in extent of methylation relative to a control is indicative of the presence or severity of the pathological condition or propensity to develop same.

5 **[0115]** Any methylation assay may be employed such as methylation sensitive PCR, *methylation specific melting curve analysis (MS-MCA)* or *high resolution melting (MS-*HRM) [Dahl *et al., Clin Chem 53(4)*:790-793, 2007; Wojdacz *et al., Nucleic Acids Res. 35(6)*:e41, 2007]; quantification of CpG methylation by MALDI-TOF MS (Tost *et al., Nucleic Acids Res 31(9)*:e50, 2003); methylation specific MLPA (Nygren *et al., Nucleic* 10 *Acids Res. 33(14)*:e128, 2005); methylated-DNA precipitation and methylation-sensitive restriction enzymes (COMPARE-MS) [Yegnasubramanian *et al., Nucleic Acids Res. 34(3)*:e19, 2006] or methylation sensitive oligonucleotide microarray (Gitan *et al., Genome Res. 12(1)*:158-164, 2002), as well as *via* antibodies. Other assays include NEXT generation (GEN) and DEEP sequencing or pyrosequencing. Another assay is single 15 molecule (SMRT) sequencing.

[0116] Insofar as the methylation assay may involve an amplification, an amplification methodology may be employed. Amplification methodologies contemplated herein include the polymerase chain reaction (PCR) such as disclosed in U.S. Patent Nos. 4,683,202 and 20 4,683,195; the ligase chain reaction (LCR) such as disclosed in European Patent Application No. EP-A-320 308 and gap filling LCR (GLCR) or variations thereof such as disclosed in International Patent Publication No. WO 90/01069, European Patent Application EP-A-439 182, British Patent No. GB 2,225,112A and International Patent Publication No. WO 93/00447. Other amplification techniques include Qβ replicase such 25 as described in the literature; Stand Displacement Amplification (SDA) such as described in European Patent Application Nos. EP-A-497 272 and EP-A-500 224; Self-Sustained Sequence Replication (3SR) such as described in Fahy *et al., PCR Methods Appl. 1(1)*:25-33, 1991) and Nucleic Acid Sequence-Based Amplification (NASBA) such as described in the literature.

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[0117] A PCR amplification process is particularly useful in the practice of the present disclosure.

[0118] In an embodiment, prior to the PCR, either essentially all cytosines in the DNA sample are selectively delaminated, but 5-methylcytosines remain essentially unchanged or essentially all 5-methylcytosines in the DNA sample are selectively delaminated, but cytosines remain essentially unchanged. Cytosine-guanine (CpG) dinucleotides and CpNpG trinucleotides are detected, allowing conclusions about the methylation state of cytosines in the CpG dinucleotides and CpNpG trinucleotide in the DNA sample. This delamination is generally performed using a bisulfite reagent. After bisulfite treatment, the 5-methylcytosines residues are converted to thymine (T).

[0119] The sample DNA is only amplified by chosen PCR primers if a certain methylation state is present at a specific site in the sample DNA the sequence context of which is essentially complementary to one or more of the chosen PCR primers. This can be done using primers annealing selectively to bisulfite treated DNA which contains in a certain position either a TG or a CG or CNG, depending on the methylation status in the genomic DNA. Primers are designed based on particular regions around CpG and/or CpNpG sites or other FMR1 intronic regions. Introns or parts thereof including intron/exon boundaries and splicing regions downstream of intron 2 of FMR1 or downstream of the FMR1 gene itself are also contemplated herein as are (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; and/or (ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region, of the FMR genetic locus.

[0120] A technology which can alternatively be employed for methylation analysis utilizes base-specific cleavage followed by MALDI-TOF mass spectrometry on DNA after bisulfite treatment, where all the 5-methylcytosines residues are converted to thymine (T) or where all unmethylated cytosines residues are not converted to thymine (T). Primers are designed based on particular regions around CpG and/or CpNpG sites or other FMR1 intronic regions or downstream thereof. Primer sequences are designed to amplify without bias both converted and unconverted sequences using the PCR amplification process under the medium to high stringency conditions. The PCR products are *in vitro* transcribed and subjected to base specific cleavage and fragmentation analysis using MALDI-TOF MS.

The size ratio of the cleaved products provides quantitative methylation estimates for CpG sites within a target region. The shift in mass for non-methylated (NM) from methylated (M) fragments for a single CpG site is -16 daltons due to the presence of an adenosine residue in the place of a guanosine. A software is then used to calculate methylation for 5 each fragment based on this difference in mass, where the output methylation ratios are the *intensities of methylated signal/[methylated+unmethylated signal]*. If the fragment size overlaps for different CpGs, their methylation output ratio is calculated based on the sum of intensities for methylated/ [methylated+unmethylated signal]. To distinguish how well the methylation output ratio for multiple fragments of a similar size represented 10 methylation of separate CpG sites, for some amplicons both cytosine and thymidine cleave reactions can be performed (that produced fragments of different size) prior to fragment analysis. Silent peaks (S) – fragments of unknown origin, should not be taken into consideration if their size does not overlap with the fragments of interest. Methylation of CpG sites that have silent peaks (S) that overlap with the fragments of interest should be 15 included in the analysis.

[0121] Hence, a method is provided for determining the methylation profile of one or more CpG or CpNpG sites located within the genome of a eukaryotic cell or group of cells, the method comprising obtaining a sample of genomic DNA from the cell or group of cells 20 and subjecting the genomic DNA to primer-specific amplification within an intron of a genetic locus and assaying for extent of methylation relative to a control, including a change in the extent of methylation and associating this change with a pathological condition.

25 **[0122]** A "nucleic acid" as used herein, is a covalently linked sequence of nucleotides in which the 3' position of the phosphorylated pentose of one nucleotide is joined by a phosphodiester group to the 5' position of the pentose of the next nucleotide and in which the nucleotide residues are linked in specific sequence; i.e. a linear order of nucleotides. A "polynucleotide" as used herein, is a nucleic acid containing a sequence that is greater than 30 about 100 nucleotides in length. An "oligonucleotide" as used herein, is a short polynucleotide or a portion of a polynucleotide. An oligonucleotide typically contains a sequence of about two to about one hundred bases. The word "oligo" may be used in place

of the word "oligonucleotide". The term "oligo" also includes a particularly useful primer length in the practice of the present disclosure of up to about 10 nucleotides.

[0123] As used herein, the term "primer" refers to an oligonucleotide or polynucleotide that is capable of hybridizing to another nucleic acid of interest under particular stringency conditions. A primer may occur naturally as in a purified restriction digest or be produced synthetically, by recombinant means or by PCR amplification. The primer may be selected to amplify either or both stands of double stranded genomic DNA. This includes a promoter or other regulatory region. The terms "probe" and "primers" may be used interchangeably, although to the extent that an oligonucleotide is used in a PCR or other amplification reaction, the term is generally "primer". The ability to hybridize is dependent in part on the degree of complementarity between the nucleotide sequence of the primer and complementary sequence on the target DNA.

[0124] The terms "complementary" or "complementarity" are used in reference to nucleic acids (i.e. a sequence of nucleotides) related by the well-known base-pairing rules that A pairs with T or U and C pairs with G. For example, the sequence 5'-A-G-T-3' is complementary to the sequence 3'-T-C-A-5' in DNA and 3'-U-C-A-5' in RNA. Complementarity can be "partial" in which only some of the nucleotide bases are matched according to the base pairing rules. On the other hand, there may be "complete" or "total" complementarity between the nucleic acid strands when all of the bases are matched according to base-pairing rules. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of hybridization between nucleic acid strands as known well in the art. This is of particular importance in detection methods that depend upon binding between nucleic acids, such as those of the present disclosure. The term "substantially complementary" is used to describe any primer that can hybridize to either or both strands of the target nucleic acid sequence under conditions of low stringency as described below or, preferably, in polymerase reaction buffer heated to 95°C and then cooled to room temperature. As used herein, when the primer is referred to as partially or totally complementary to the target nucleic acid, that refers to the 3'-terminal region of the probe (i.e. within about 10 nucleotides of the 3'-terminal nucleotide position).

[0125] As discussed above, when reference is made to a genomic nucleotide sequence, the present disclosure extends to its complementary strand sequence. Either or both strands may be assayed from epigenetic change.

5 **[0126]** Reference herein to a stringency in relation to hybridization includes and encompasses from at least about 0 to at least about 15% v/v formamide and from at least about 1 M to at least about 2 M salt for hybridization, and at least about 1 M to at least about 2 M salt for washing conditions. Generally, low stringency is at from about 25-30°C to about 42°C. The temperature may be altered and higher temperatures used to replace
10 formamide and/or to give alternative stringency conditions. Alternative stringency conditions may be applied where necessary, such as medium stringency, which includes and encompasses from at least about 16% v/v to at least about 30% v/v formamide and from at least about 0.5 M to at least about 0.9 M salt for hybridization, and at least about 0.5 M to at least about 0.9 M salt for washing conditions, or high stringency, which
15 includes and encompasses from at least about 31% v/v to at least about 50% v/v formamide and from at least about 0.01 M to at least about 0.15 M salt for hybridization, and at least about 0.01 M to at least about 0.15 M salt for washing conditions. In general, washing is carried out $T_m = 69.3 + 0.41$ (G+C) % (Marmur and Doty, *J. Mol. Biol. 5:* 109, 1962). However, the T_m of a duplex DNA decreases by 1°C with every increase of 1% in
20 the number of mismatch base pairs (Bonner and Laskey, *Eur. J. Biochem. 46:* 83, 1974). Formamide is optional in these hybridization conditions. Accordingly, particularly preferred levels of stringency are defined as follows: low stringency is 6 x SSC buffer, 0.1% w/v SDS at 25-42°C; a moderate stringency is 2 x SSC buffer, 0.1% w/v SDS at a temperature in the range 20°C to 65°C; high stringency is 0.1 x SSC buffer, 0.1% w/v SDS
25 at a temperature of at least 65°C. Reference to at least "80% identity" includes 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 and 100%.

[0127] The present disclosure enables the determination of a methylation or other epigenetic profile of sites within an intron, intron/exon boundary and/or splicing region of
30 a genetic locus in a genome of a eukaryotic cell or group of cells, the method comprising obtaining a sample of genomic DNA from the cell or group of cells, subjecting the digested DNA to an amplification reaction using primers selected to amplify a region of

the genetic locus selected from:

(i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; and/or

5 (ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region of the genetic locus;

and then subjecting the amplified DNA to methylation or other epigenetic detection means to determine relative to control the extent of methylation or other epigenetic modification 10 wherein a change in epigenetic modification or other epigenetic modification relative to the control is indicative of a pathological condition associated with the genetic locus.

[0128] Examples of pathological conditions include Fragile X syndrome (FXS), Fragile X-associated tremor or ataxia (FXTAS), Fragile X-associated primary ovarian insufficiency 15 (FXPOI), autism, mental retardation, cognitive impairment, a modified X-chromosome, Huntington's disease (HD), dentatorubropallid-oluysiantrophy (DRPLA), spinobulbar muscular atrophy or Kennedy disease (SBMA), spinocerebella ataxia Type 1 (SCA1), spinocerebella ataxia Type 2 (SCA2), spinocerebella ataxia Type 3 or Machado-Joseph disease (SCA3), spinocerebella ataxia Type 6 (SCA6), spinocerebella ataxia Type 7 20 (SCA7), spinocerebella ataxia Type 17 (SCA17), Fragile XE mental retardation (FRAXE), Friedrich's ataxia (FRDA), Fragile type, folic acid type, rare 12 (FRA12A), myotonic dystrophy (DM), spinocerebella ataxia (SCA8) and spinocerebella ataxias Type 12 (SCA12), Klinefelter's syndrome and Turner's syndrome.

25 **[0129]** In an embodiment, the present disclosure enables determination of a methylation profile of the sites within the FMR locus in a genome of a eukaryotic cell or group of cells, the methylation profile comprising the extent or level of methylation within the FMR locus, the method comprising obtaining a sample of genomic DNA from the cell or group of cells, subjecting the digested DNA to an amplification reaction using primers selected to 30 amplify a region of the FMR genetic locus selected from:

(i) (a) FREE3; (b) intron 2; and (c) an intron, intron/exon boundary and/or

splicing region downstream of intron 2 or part thereof;

(ii) two or more of (a) an intron; (b) an intron/exon boundary; (c) a splicing region; and

(iii) approximately one seventh or greater of an intron including an intron/exon
5 boundary and/or a splicing region within the FMR genetic locus;

and then subjecting the amplified DNA to methylation detection means to determine relative to control the extent of methylation wherein a change in methylation relative to the control is indicative of a pathological condition associated with the FMR genetic locus.

10

[0130] In an embodiment, the region amplified within the FMR genetic locus is selected from:

(i) the 3' boundary of the FREE2 region and the FMR1 promoter located
15 between CpG unit 1 of the FREE2 (E) amplicon and CpG unit 2/3 of the FREE2 (E) amplicon;

(ii) the FREE2 region alone or in combination with the FREE1 region;

(iii) the FREE3 region; and

(iv) an intron including an intron/exon boundary and/or splicing region
20 downstream of intron 1 within the FMR1 gene including the FREE2 (D) region or FREE2 (D)/(E) boundary.

[0131] The present disclosure further provides a methylation profile of the sites within the FMR locus in a genome of a eukaryotic cell or group of cells, the methylation profile
25 comprising the extent or level of methylation within the FMR locus, the method comprising obtaining a sample of genomic DNA from the cell or group of cells, subjecting the digested DNA to an amplification reaction using primers selected to amplify FREE3 within the FMR1 gene and then subjecting the amplified DNA to methylation detection means to determine relative to control the extent of methylation wherein a change in
30 methylation relative to the control is indicative of a pathological condition associated with the FMR genetic locus.

[0132] In an embodiment, the present disclosure enables determination of a methylation profile of the sites within the FMR locus in a genome of a eukaryotic cell or group of cells, the methylation profile comprising the extent or level of methylation within the FMR locus, the method comprising obtaining a sample of genomic DNA from the cell or group of cells, subjecting the digested DNA to an amplification reaction using primers selected to amplify all or part of *FREE3* and then subjecting the amplified DNA to methylation detection means to determine relative to control the extent of methylation wherein a change in methylation relative to the control is indicative of a pathological condition associated with the FMR genetic locus. An adverse change in methylation or other epigenetic profile is associated with FXS or related condition such as FXTAS, FXPOI, autism, mental retardation and cognitive impairment.

[0133] As indicated above, the cells may be a lymphoblast, a CVS cell, a blood cell, a buccal cell, epthelial cell, fibroblast cell, an amniocyte or an EBV transformed lymphoblast cell line. In addition, the methylation profile may be determined or one or both alleles a genetic locus and in selected cells where mosaicism has occurred. In particular, the extent of methylation can determine homozygosity or heterozygosity or mosaicism. Reference to "mosaicism" includes the situation wherein two or more populations of cells have different genotypes or epigenetic profiles at the genetic locus.

[0134] The diagnostic assay herein can also detect heterozygosity or mosaicism where the methylation pattern is indicative of, for example, in relation to an FMR genetic locus-associated pathology, an FM. The latter may also be conducted in combination with an assay to detect $(CGG)_n$ expansion.

[0135] The present disclosure also teaches kits for determining the methylation or other epigenetic profile of one or more nucleotides at one or more sites within the genome of a eukaryotic cell or group of cells. The kits may comprise many different forms but in one embodiment, the kits comprise reagents for the bisulfite methylation assay.

[0136] A further embodiment of the present disclosure is a kit for the use in the above methods comprising primers to amplify an intron within a genetic locus.

[0137] In an embodiment, the present disclosure provides a use of primers which amplify regions of the FMR genetic locus, comprising CpG and/or CpNpG sites located within:

5 (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a *splicing region*;

(ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region;

(iii) the 3' boundary of the FREE2 region and the FMR1 promoter located 10 between CpG unit 1 of the FREE2 (E) amplicon and CpG unit 2/3 of the FREE2 (E) amplicon;

(iv) the FREE2 region alone or in combination with the FREE1 region;

(v) the FREE3 region; and

(vi) an intron including an intron/exon boundary and/or splicing region 15 downstream of intron 1 within the FMR1 gene.

in the manufacture of a diagnostic kit or device to detect methylation of the FMR locus-associated with a pathological condition.

20 [0138] In relation to one embodiment, a kit is provided for the use in the above methods comprising primers identified by SEQ ID NOs:6 through 11 to amplify an intronic site within the FMR1 genetic locus. The nucleotide sequences in SEQ ID NOs:6 through 11 comprise primer and tag sequences. The present disclosure extends to SEQ ID NO:6 through 11 as well as primer only portions therein. The primers may also include primers 25 disclosed in PCT/AU2010/000169.

[0139] The kit may also comprise instructions for use.

[0140] Conveniently, the kits are adapted to contain compartments for two or more of the 30 above-listed components. Furthermore, buffers, nucleotides and/or enzymes may be combined into a single compartment.

[0141] As stated above, instructions optionally present in such kits instruct the user on how to use the components of the kit to perform the various methods of the present disclosure. It is contemplated that these instructions include a description of the detection methods of the subject disclosure, including detection by gel electrophoresis.

5

[0142] The present disclosure further enables kits which contain a primer for a nucleic acid target of interest with the primer being complementary to a predetermined nucleic acid target. In another embodiment, the kit contains multiple primers or probes, each of which contains a different base at an interrogation position or which is designed to interrogate
10 different target DNA sequences. In a contemplated embodiment, multiple probes are provided for a set of nucleic acid target sequences that give rise to analytical results which are distinguishable for the various probes. The multiple probes may be in microarray format for ease of use.

15 [0143] The kit may comprise a vessel containing a purified and isolated enzyme whose activity is to release one or more nucleotides from the 3' terminus of a hybridized nucleic acid probe and a vessel containing pyrophosphate. In one embodiment, these items are combined in a single vessel. It is contemplated that the enzyme is either in solution or provided as a solid (e.g. as a lyophilized powder); the same is true for the pyrophosphate.
20 Preferably, the enzyme is provided in solution. Some contemplated kits contain labeled nucleic acid probes. Other contemplated kits further comprise vessels containing labels and vessels containing reagents for attaching the labels. Microtiter trays are particularly useful and these may comprise from two to 100,000 wells or from about six to about 10,000 wells or from about six to about 1,000 wells.

25

[0144] Another important application is in the high throughput screening of agents which are capable of demethylation genomes and in particular intronic regions within genomes. This may be important, for example, in de-differentiating cells and/or treating pathological conditions.

30

[0145] The present disclosure further enables a method for screening for an agent which modulates methylation or other epigenetic modification of a genetic locus, the method

comprising screening for a change relative to a control in the extent of methylation or other epigenetic modification in an intron, intron/exon boundary and/or splicing region within the genetic locus which is associated with a pathological condition in the presences or absence of an agent to be tested, wherein an agent is selected if it induces a change in the
5 extent of methylation or other epigenetic change. Agents include de-methylation agents and hyper-methylation agents, *global and site specific*.

[0146] In an embodiment, a method is also provided for screening for an agent which modulates epigenetic modification of an FMR genetic locus in a mammalian cell including
10 a human cell, the method comprising screening for a change relative to a healthy control in the extent of epigenetic change in (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; and/or (ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region of the FMR genetic locus; wherein the intron, intron/exon boundary and/or splicing region is selected from the
15 list consisting of:

(i) Fragile X-related Epigenetic Element 3 in FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which
20 hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions;

(ii) intron 2 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or a portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its
25 complementary form under medium stringency conditions;

(iii) genomic FREE2 region as a whole or specific fragments of FREE2 including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47
30 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditions;

[0147] in the presence or absence of an agent to be tested wherein the agent is selected if it induces a change in extent of epigenetic modification. Such an agent is useful in the treatment of a trinucleotide expansion disorder such as associated with a change in epigenetic profile from that of a healthy subject.

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[0148] In an embodiment, a method is provided for screening for an agent which modulates methylation of an FMR genetic locus in a mammalian cell including a human cell, the method comprising screening for a change relative to a control in the extent of methylation in a region selected from:

10

(i) Fragile X-related Epigenetic Element 3 in FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency
15 conditions;

(ii) intron 2 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or a portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions;

20 (iii) genomic FREE2 region as a whole or specific fragments of FREE2 including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under
25 medium stringency conditions;

(iv) an intron, intron/exon boundary and/or splicing region downstream of intron 2 of FMR1 or a homolog thereof or a portion or fragment thereof;

(v) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing regions within the FMR genetic locus; and

30 (vi) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region within the FMR genetic locus;

in the presence or absence of an agent to be tested wherein the agent is selected if it induces a change in extent of methylation.

[0149] The present disclosure further enables a method for monitoring the treatment of a genetic locus-associated disease including a nucleotide expansion disease in which the *treatment modulates the methylation of the genetic locus*, the method comprising monitoring for a change relative to a control or a pre and post-treatment sample in the extent of methylation within an intron, intron/exon boundary and/or splicing region of the genetic locus.

[0150] By "monitoring" includes diagnosis, prognosis, pharmacoresponsiveness, pharmacosensitivity, level of disease progression or remission, improving or declining health of a subject and the like.

[0151] As indicated above, conditions and disorders contemplated herein include a range of nucleotide expansion diseases such as but not limited to Fragile X syndrome (FXS), Fragile X-associated tremor or ataxia (FXTAS), Fragile X-associated primary ovarian insufficiency (FXPOI), autism, mental retardation, cognitive impairment, a modified X-chromosome, Huntington's disease (HD), dentatorubropallid-oluysiantrophy (DRPLA), spinobulbar muscular atrophy or Kennedy disease (SBMA), spinocerebella ataxia Type 1 (SCA1), spinocerebella ataxia Type 2 (SCA2), spinocerebella ataxia Type 3 or Machado-Joseph disease (SCA3), spinocerebella ataxia Type 6 (SCA6), spinocerebella ataxia Type 7 (SCA7), spinocerebella ataxia Type 17 (SCA17), Fragile XE mental retardation (FRAXE), Friedrich's ataxia (FRDA), Fragile type, folic acid type, rare 12 (FRA12A), myotonic dystrophy (DM), spinocerebella ataxia (SCA8) and spinocerebella ataxias Type 12 (SCA12), Klinefelter's syndrome and Turner's syndrome. Reference to a "modified" X-chromosome includes skewed X-inactivation, inversions, deletions, duplications, hybrids and any modification leading to X-chromosome inactivation. A particular condition assocaited with epigenetic changes to the FMR genetic locus include FXS and related disorders such as FXTAS, FXPOI, autism, mental retardation, a modified X-chromosome and cognitive impairment.

[0152] The present disclosure further teaches the identification of genes having introns with CpG or CpNpG sites or other methylation-sensitive restriction sites. The identification of these sites permits identification of potential regulatory regions which can be targeted by agonists or antagonists of abnormal gene expression.

5

[0153] In cases where the gene is methylated and silenced in affected individuals or tissues, compounds are screened in high throughput fashion in stable cell lines or individuals to identify drugs that result in demethylation and reactivation of the affected gene. Alternatively, a normal active copy of the affected gene is transfected as a transgene
10 into cells to correct the defect. Such transgenes are introduced with modulating sequences that protect the transgene from methylation and keep it unmethylated and transcriptionally active.

[0154] In cases where the gene is unmethylated and transcriptionally active or
15 transcriptionally over-active in affected individuals or tissues, compounds are screened in high throughput fashion in stable cell lines to identify drugs that result in methylation and silencing of the affected gene. Alternatively, a transgene encoding a double stranded RNA homologous to the affected sequences or homologs thereof, are transfected as a transgene into cells to methylate the gene, silence it and thereby correct the defect. Such double
20 stranded RNA-encoding transgenes are introduced with modulating sequences which protect it from methylation, keep it transcriptionally active and producing double stranded RNA.

[0155] The present disclosure further provides a computer program and hardware which
25 monitors the changing state, if any, of extent of methylation over time or in response to therapeutic and/or behavioral modification. Such a computer program has important utility in monitoring disease progression, response to intervention and may guide modification of therapy or treatment. The computer program is also useful in understanding the association between increasing methylation and disease progression.

30

[0156] The computer program monitors in a quantitative or semi-quantitative manner one or more features including extent of methylation or other epigenetic modification in an

intron of a genetic locus. In addition, the length of a nucleotide expansion may be determined or any epigenetic changes therein. In relation to a neuropathological condition, a behavioral assessment may be made using criteria associated with normal subjects or subjects considered to be suffering with a disease condition. For example, cognitive ability
5 can be measured as well as the general phenotype or clinical manifestations in subjects with a neurodevelopmental or neurodegenerative condition or other condition associated with nucleotide expansion.

[0157] Thus, in accordance with the present disclosure, values are assigned to the listed
10 features which are stored in a machine-readable storage medium, which is capable of processing the data to provide an extent of disease progression or change in methylation or other epigenetic modification for a subject.

[0158] In an aspect, the disclosure teaches a computer program product for assessing
15 progression of a pathological condition associated with the FMR locus in a subject, the product comprising:

(1) assigning a value to one or more of:

(a) change in of methylation or other epigenetic modification relative to
20 a control in FREE3 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or part thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions;

(b) change of methylation or other epigenetic modification relative to a
25 control in intron 2 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or portion or part thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions;

(c) change in methylation or other epigenetic modification relative to a
30 control in genomic FREE2 region as a whole or specific fragments of FREE2 including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by

having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditions;

(d) change of methylation in an intron, intron/exon boundary and/or
5 splicing region downstream of intron 2 of FMR1 or a homolog thereof or a portion or fragment thereof;

(e) two or more of (i) an intron; (ii) an intron/exon boundary; (iii) a splicing region within the FMR genetic locus;

(f) approximately one seventh or greater of an intron including an
10 intron/exon boundary and/or a splicing region within the FMR genetic locus;

(g) length of $(CGG)_n$ expansion within the FMR genetic locus when considered in combination with (a) and/or (b);

(h) general phenotype or clinical manifestations in subjects with a neurodevelopmental or neurodegenerative condition;

15 (i) behavioral assessment criteria associated with normal subjects, PM subjects, GZ subjects and FM subjects;

(j) cognitive ability;

(k) extent of transcription of genes within the FMR locus with the proviso that if any one of (d) through (k) is determined then one or more of (a) through (c)
20 is also determined;

(2) means to converting the value to a code; and

(3) means to store the code in a computer readable medium and compare code
25 to a knowledge database to determine whether the code corresponds to a pathological condition.

[0159] In a related aspect, the disclosure teaches a computer for assessing an association between extent of methylation or other epigenetic modification within the FMR locus, the
30 FMR locus and progression of a disease condition wherein the computer comprises:

(1) a machine-readable data storage medium comprising a data storage material

encoded with machine-readable data, wherein the machine-readable data comprise values associated with the features of one or more of:

(a) change in of methylation or other epigenetic modification relative to a control in FREE3 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or part thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions upstream;

(b) change of methylation or other epigenetic modification relative to a control in CpG and/or CpNpG islands and island shores in intron 2 of the FMR1 gene comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or portion or part thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions;

(c) change in methylation or other epigenetic modification relative to a control in genomic FREE2 region as a whole or specific fragments of FREE2 including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditions;

(d) change in methylation of an intron, intron/exon boundary and/or splicing region downstream of intron 2 of FMR1 or a homolog thereof or a portion or fragment thereof;

(e) two or more of (i) an intron; (ii) an intron/exon boundary; (iii) a splicing region within the FMR genetic locus;

(f) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region within the FMR genetic locus;

(g) length of $(CGG)_n$ expansion within the FMR genetic locus when considered in combination with (a) and/or (b);

(h) general phenotype or clinical manifestations in subjects with a neurodevelopmental or neurodegenerative condition;

(i) behavioral assessment criteria associated with normal subjects, PM

subjects, GZ subjects and FM subjects;

(j) cognitive ability;

(k) extent of transcription of genes within the FMR locus with the proviso that if one or more of (d) through (k) is determined, then one or more of (a)
5 through (c) or (k) is also determined;

(2) means to converting the value to a code; and

(3) means to store the code in a computer readable medium and compare code
10 to a knowledge database to determine whether the code corresponds to a pathological condition.

[0160] The computer system of the present disclosure may also be linked to detection systems such as MALDI-TOF mass spectrometry machines.

15

[0161] The present disclosure further provides a web-based system where data on extent of methylation within a genetic locus (optionally together with clinical phenotype) are provided by a client server to a central processor which analyzes and compares to a control and optionally considers other information such as patient age, sex, weight and other
20 medical conditions and then provides a report, such as, for example, a risk factor for disease severity or progression or status or response to treatment or an index of probability of a genetic locus-associated pathology in a subject.

[0162] Hence, knowledge-based computer software and hardware also form part of the
25 present disclosure.

[0163] In an embodiment, the assays herein may be used in existing or newly developed knowledge-based architecture or platforms associated with pathology services. For example, results from the assays are transmitted *via* a communications network (e.g. the
30 internet) to a processing system in which an algorithm is stored and used to generate a predicted posterior probability value which translates to the index of disease probability which is then forwarded to an end user in the form of a diagnostic or predictive report.

[0164] The assay may, therefore, be in the form of a kit or computer-based system which comprises the reagents necessary to detect the extent of methylation or other epigenetic modification within the genetic locus and includes computer hardware and/or software to facilitate determination and transmission of reports to a clinician.

[0165] The assay of the present disclosure permits integration into existing or newly developed pathology architecture or platform systems. For example, the present disclosure contemplates a method of allowing a user to determine the status of a subject with respect to an FMR locus-associated pathology, the method including:

(a) receiving data in the form of extent of methylation or other epigenetic modification at a site within:

(A) the FMR1 gene selected from:

(i) Fragile X-related Epigenetic Element 3 [FREE3] comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or part thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions;

(ii) intron 2 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or portion or part thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions; and

(iii) change in methylation or other epigenetic modification relative to a control in genomic FREE2 region as a whole or specific fragments of FREE2 including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditions;

(iv) an intron, intron/exon boundary and/or splicing region downstream of intron 2 or a homolog thereof or a fragment or portion thereof;

(B) the FMR genetic locus selected from:

(i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; or

(ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region;

wherein the extent of methylation or other epigenetic modification provides a correlation to the presence, state, classification or progression of the pathology; by transferring the data from the user *via* a communications network;

(c) processing the subject data *via* multivariate or univariate analysis to provide a disease value;

(d) determining the status of the subject in accordance with the results of the disease value in comparison with predetermined values; and

(e) transferring an indication of the status of the subject to the user *via* the communications network. Reference to the multivariate or univariate analysis includes an algorithm which performs the multivariate or univariate analysis function.

[0166] Conveniently, the method generally further includes:

(a) having the user determine the data using a remote end station; and

(b) transferring the data from the end station to the base station *via* the communications network.

[0167] The base station can include first and second processing systems, in which case the method can include:

(a) transferring the data to the first processing system;

(b) transferring the data to the second processing system; and

(c) causing the first processing system to perform the multivariate analysis function to generate the disease value.

[0168] The method may also include:

(a) transferring the results of the multivariate or univariate analysis function to the first processing system; and

5 (b) causing the first processing system to determine the status of the subject.

[0169] In this case, the method also includes at lest one of:

(a) transferring the data between the communications network and the first 10 processing system through a first firewall; and

(b) transferring the data between the first and the second processing systems through a second firewall.

[0170] The second processing system may be coupled to a database adapted to store 15 predetermined data and/or the multivariate analysis and/or univariate analysis function, the method including:

(a) querying the database to obtain at least selected predetermined data or access to the multivariate or univariate analysis function from the database; and

20 (b) comparing the selected predetermined data to the subject data or generating a predicted probability.

[0171] The second processing system can be coupled to a database, the method including storing the data in the database.

25

[0172] The method can also include having the user determine the data using a secure array, the secure array of elements capable of determining the extent of methylation in an intron with a genetic locus and having a number of features each located at respective position(s) on the respective code. In this case, the method typically includes causing the 30 base station to:

(a) determine the code from the data;

(b) determine a layout indicating the position of each feature on the array; and

(c) determine the parameter values in accordance with the determined layout, and the data.

5 [0173] The method can also include causing the base station to:

(a) determine payment information, the payment information representing the provision of payment by the user; and

(b) perform the comparison in response to the determination of the payment

10 information.

[0174] The present disclosure also teaches a base station for determining the status of a subject with respect to a pathology associated with a genetic locus such as the FMR locus. the base station including:

15

(a) a store method;

(b) a processing system, the processing system being adapted to;

(c) receive subject data from the user *via* a communications network, the data; including extent of methylation within the genetic locus wherein the level or methylation

20 or epigenetic modification relative to a control provides a correlation to the presence, state, classification or progression of the pathology;

(d) performing an algorithmic function including comparing the data to predetermined data;

(e) determining the status of the subject in accordance with the results of the

25 algorithmic function including the comparison; and

(f) output an indication of the status of the subject to the user *via* the communications network.

[0175] The processing system can be adapted to receive data from a remote end station

30 adapted to determine the data.

[0176] The processing system may include:

(a) a first processing system adapted to:

(i) receive the data; and

(ii) determine the status of the subject in accordance with the results of the multivariate or univariate analysis function including comparing the data; and

(b) a second processing system adapted to:

(i) receive the data from the processing system;

(ii) perform the multivariate or univariate analysis function including the comparison; and

(iii) transfer the results to the first processing system.

[0177] The determination of the extent of methylation or other epigenetic modification within the FMR locus at a site within the FMR1 gene selected from:

(i) Fragile X-related Epigenetic Element 3 [FREE3] comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or part thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions;

(ii) intron 2 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or portion or part thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions;

(iii) change in methylation or other epigenetic modification relative to a control in genomic FREE2 region as a whole or specific fragments of FREE2 including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditions;

(iv) an intron, intron/exon boundary and/or splicing region downstream of intron 2 or a homolog thereof or a portion or fragment thereof;

(v) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a

splicing region; or

(vi) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region within the FMR genetic locus;

5 enables establishment of a diagnostic or prognostic rule based on the extent of methylation relative to controls. Alternatively, the diagnostic or prognostic rule is based on the application of a statistical and machine learning algorithm. Such an algorithm uses relationships between methylation profiles and disease status observed in training data (with known disease status) to infer relationships which are then used to predict the status 10 of patients with unknown status. An algorithm is employed which provides an index of probability that a patient has an FMR locus-associated pathology. The algorithm performs a multivariate or univariate analysis function.

[0178] Hence, the present disclosure teaches a diagnostic rule based on the application of 15 statistical and machine learning algorithms. Such an algorithm uses the relationships between epigenetic profile and disease status observed in training data (with known disease status) to infer relationships which are then used to predict the status of patients with unknown status. Practitioners skilled in the art of data analysis recognize that many different forms of inferring relationships in the training data may be used without 20 materially changing the present disclosure.

[0179] The present disclosure teaches a knowledge base of training data comprising extent of methylation within a genetic locus such as the FMR genetic locus from a subject with locus-associated pathology to generate an algorithm which, upon input of a second 25 knowledge base of data comprising levels of the same biomarkers from a patient with an unknown pathology, provides a probability that predicts the nature of unknown pathology or response to treatment.

[0180] The term "training data" includes knowledge of the extent of methylation relative to 30 a control. A "control" includes a comparison to levels in a healthy subject devoid of a pathology or is cured of the condition or may be a statistically determined level based on trials.

[0181] The present disclosure contemplates, therefore, the use of the methylation, including epigenetic profile of intronic sites within the FMR genetic locus and in particular the FMR1 gene to assess or determine the status of a subject with respect to disease, to stratify a subject relative to normal controls or unhealthy subjects, to provide a prognosis of recovery or deterioration and/or to determine the pharmacoresponsiveness or pharmacosensitivity of a subject to treatment or an agent for use in treatment and/or determine applicability for other treatment options including behavioural intervention, and the like. By "intronic sites" includes intron/exon boundaries and splicing regions.

[0182] Hence, another aspect enabled herein is a method of allowing a user to determine the status, prognosis and/or treatment response of a subject with respect to an FMR locus-associated pathology, the method including:

(a) receiving data in the form of extent of methylation or other epigenetic modification at a site in:

(i) FMR1 gene selected from:

(ii) Fragile X-related Epigenetic Element 3 [FREE3] comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or part thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions;

(iii) intron 2 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or portion or part thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions;

(iv) change in methylation or other epigenetic modification relative to a control in genomic FREE2 region as a whole or specific fragments of FREE2 including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium

stringency conditions;

(v) an intron, intron/exon boundary and/or splicing region downstream of intron 2 or a homolog or a portion or fragment thereof;

(vi) two or more of (a) an intron; (b) an intron/exon boundary; (c) a splicing region within the FMR locus; or

(vii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region within the FMR genetic locus;

wherein the extent of methylation or epigenetic modification provides a correlation to the presence, state, classification or progression of the pathology;

(b) transferring the data from the user *via* a communications network;

(c) processing the subject data *via* multivariate or univariate analysis to provide a disease value;

(d) determining the status of the subject in accordance with the results of the disease value in comparison with predetermined values; and

(e) transferring an indication of the status of the subject to the user *via* the communications network.

[0183] Aspects disclosed herein are further described by the following non-limiting Example. In these Examples, materials and methods as outlined below were employed.

Patient Samples

[0184] FXS and premutation carrier EBV transformed lymphoblast cell lines were obtained from the tissue culture storage repository of the Murdoch Childrens Research Institute, Melbourne, Victoria, Australia or purchased from Coriell.

DNA extraction

[0185] DNA for CGG repeat size PCR and methylation analysis was obtained either from 200μl venous blood samples anti-coagulated with EDTA or from EBV transformed lymphoblasts 1 to $5x10^6$ cells per sample and extracted using a BIO ROBOT M48 DNA Extractor, as per manufacturer's instructions (Qiagen Inc., Hilden, Germany). DNA for Southern blot or methylation analysis was extracted from 3ml blood samples anti-

coagulated with EDTA or from EBV transformed lymphoblasts 5 to $10x10^6$ cells per sample.

CGG repeat size PCR amplification

5 **[0186]** CGG repeat size for all samples was initially assessed using a fully validated PCR assay with precision of +/- one triplet repeat across the normal and GZ ranges, performed using a fragment analyzer (MegaBace, GE Healthcare), with the higher detection limit of 170 repeats, as previously described (Khaniani *et al., Mol Cytogenet 1(1)*:5, 2008). Briefly, PCR amplifications were performed using primers:

10 (i) r (5'- *GCTCAGCTCCGTTTCGGTTTCACTTCCGGT*-3 [SEQ ID NO:32]); and
(ii) f (5'AGCCCCGCACTTCCACCACCAGCTCCTCCA-3' [SEQ ID NO:33]),

(Fu *et al., Cell 67(6)*:1047-1058, 1991) in a total volume of 25 μl containing 50ng of genomic DNA, 0.75 pmol of each primer, 8 μl of 5×Q-Solution (Qiagen Inc., Hilden,
15 Germany), 2.5 μl of 10×PCR Buffer and 1 unit of HotStarTaq Plus DNA polymerase (Qiagen Inc., Hilden, Germany) in a Gene Amp@ PCR System 9700. The PCR cycling profile was as follows: initial denaturation at 98°C for 5 minutes; 35 cycles at 98°C for 45 seconds, 70°C for 45 seconds, and 72°C for 2 minutes, and a final extension at 72°C for 10 minutes. Alleles were sized by capillary electrophoresis using an automatic
20 sequencer (MegaBACETM 1000 – GE HealthCare Amersham) with size standards (HealthCare) and controls of lengths 10, 23, 29, 30, 52 and 74 repeats determined by sequencing in-house or obtained from Coriel Cell Repositories web site (http://www.phppo.cdc.gov/dls/genetics/qcmaterials/).

25 **CGG repeat size by Southern Blot**

[0187] CGG sizes were assessed using a fully validated Southern Blot procedure with appropriate normal and abnormal controls for samples where the products could not be amplified using PCR (Fu *et al* 1991, *supra*; Francis *et al., Mol Diagn 5(3)*:221-225, 2000). Briefly, 5mg of DNA was digested with Pst1 (Boehringer Mannheim, Castle
30 Hill, Australia), separated on 1% w/v agarose gels, and analyzed by Southern blot hybridization. The FMR-1 gene was detected using Southern blot analysis with probe

Fxa3 and an X-chromosome control probe, pS8 (Yu *et al., Science 252(5010)*:1179-1181, 1991). Probes were labeled using random oligonucleotide priming (Boehringer, Mannheim) with [a32-P]CTP (NEN Dupont, Boston, MA). Autoradiography was performed at −80°C, with intensifying screens and Kodak XAR films (Sigma-Aldrich).

5

Methylation sensitive Southern Blot analysis

[0188] Methylation of the classical FMR1 CpG island was assessed using a fully validated methyl sensitive Southern Blot procedure with appropriate normal and abnormal controls, as previously described (Tassone *et al., J. Mol. Diagn 10*:43-49, 2008).
10 Briefly, *EcoRI* and *NruI* digestion was performed on 7 to 9μg of DNA, and separated on a 0.8% w/v agarose/Tris acetate EDTA (TAE) gel. The DNA was denatured with HCL and NAOH, transferred to a charged nylon membrane and analyzed by Southern blot hybridization. The FMR1 alleles were detected using Southern blot analysis with probe StB12.3, labeled with Dig-11-dUTP by PCR (PCR Dig Synthesis kit; Roche
15 Diagnostics). Autoradiography was performed with intensifying screens and Fuji Medical X-Ray film (Bedford, UK) and FMR1 methylation values for the expanded alleles were calculated as preciously described (Tassone *et al.*, 2008 *supra*). The FMR1 activation ratios for female samples were calculated based on the following formula: optically scanned density of the 2.8kb band / combined densities of the 2.8kb and 5.2kb
20 bands (where the 2.8kb band represents the proportion of normal active X and the 5.2kb band represents the proportion of normal inactive X), as previously described (de Vries *et al., Am J Hum Genet. 58*:1025-1032, 1996).

MALDI-TOF methylation analysis

25

Bisulfite Treatment

[0189] Bisulfite treatment of genomic DNA at 0.5μg per sample was performed using XCEED kit from MethylEasy (Human Genetic Signatures, Sydney, Australia) for sample sets of n<40. For sample sets n>40 96 well Methylamp kit from Epigentek
30 (Brookly, NY, USA) was used. Duplicate bisulfite reactions were made from each sample, and six of the same control DNA samples spiked with DNA from an FXS patient cell line at 0, 33.3, 50, 66.6 or 100% were included as standards within each run,

as an indicator of the inter-run variation in the degree of bisulfite related bias. Protocols were performed according to the manufacturer's instructions. Briefly, for the MethylEasy conversion, 20μl of genomic DNA (0.5μg total) was mixed with 2.2μl of 3μl NaOH, and incubated at 37°C for 15 minutes, then denatured by 45 minute
5 incubation at 80 °C. 240μl of the reagent #3 (XCEED kit, Human Genetic Signatures, Sydney, Australia) were then added to the mixture, which was transferred into the purification column and spun down at 10,000g for 1 minute. The captured DNA was then washed in Reagent #4 (XCEED kit, Human Genetic Signatures, Sydney, Australia), and DNA eluted twice by placing 50μl of the pre-warmed solution #5
10 (XCEED kit, Human Genetic Signatures, Sydney, Australia) onto column membrane, which was incubated for 1 minute at room temperature, and spun down at 10,000g for 1 minute. The eluted DNA was then incubated at 95°C for 20 minutes, with resulting final concentration at ~20ng/μl per sample.

15 **[0190]** For the Methylamp conversion, 7μl of genomic DNA (0.5μg total) was mixed with 5μl of the CF3 (Methylamp kit, Epigentek, Brookly, NY, USA) solution diluted 1:10 in distilled water, in each well of the 96 well plate. The DNA was denatured by placing the plate at 65°C for 90 minutes. It was then captured in the filter plate and washed in 150μl of the CF5 solution (Methylamp kit, Epigentek, Brookly, NY, USA),
20 then twice in 250μl of 80% v/v ethanol. The filter plate was then incubated in the CF3/90% ethanol solution, and washed twice in 90% v/v ethanol, as per manufacturer's instructions. The modified and cleaned DNA was then eluted with 40μl of the CF6 solution (Methylamp kit, Epigentek, Brookly, NY, USA), with resulting converted DNA final concentration at ~20ng/μl per sample. For the short term storage the
25 converted DNA was kept at -20°C, and for storage of more than 3 months it was kept at -80°C.

PCR and in vitro transcription

[0191] The primers used to amplify the target regions and the annealing temperatures
30 are listed in Tables 3 and 4. Each bisulfite converted sample was analyzed in duplicate PCR reactions, carried out in a total volume of 5μl using 1pmol of each primer, 40μM

dNTP, 0.2 U Hot Star Taq DNA polymerase (Qiagen Inc., Hilden, Germany), 1.5mM $MgCl_2$ and buffer supplied with the enzyme (final concentration 1X). The reaction mix was pre-activated for 15min at 95°C, followed by 45 cycles of amplification at 94°C for 20s, primer specific annealing for 30s and 72°C for 1 min followed by 72°C for 3 min.
5 The PCR products were run on 1.5% w/v agarose gel to confirm successful PCR amplification and efficiency. The DNA was then cleaned up and the T or C-cleavage reactions were carried out (T-cleave for Amplicons 1 to 5, C-cleave for Amplicon 5 only) as per manufacturer's instructions (SEQUENOM, San Diego, CA). Briefly, unincorporated dNTPs were dephosphorylated by adding 1.7μl H_2O and 0.3U Shrimp
10 Alkaline Phosphatase (SAP) [SEQUENOM, San Diego] to PCR products, which were incubated at 37°C for 20min, and 10min at 85°C to heat-inactivate the SAP. The transcription was performed on 2μl of template DNA in the 6.5ul reaction consisting of 20 U of the T7 R&DNA polymerase (Epicentre, Madison, WI) to incorporate either dCTP or dTTP; Ribonucleotides at 1nM and the dNTP substrate at 2.5mM, with other
15 components used as recommended (SEQUENOM, San Diego). RNase A (SEQUENOM, San Diego) was then added to the mix to cleave the *in vitro* transcript. The mix was diluted to 27μl in H_2O, and 6mg CLEAN Resin (SEQUENOM, San Diego, CA) was added for conditioning of the phosphate backbone prior to MALDI-TOF MS. The SEQUENOM Nanodispenser was then used to spot the samples onto a
20 SpectroCHIP for subsequent analysis. MassARRAY mass spectrometer (Bruker-SEQUENOM) was then used to collect mass spectra, which were analysed using the EpiTYPER software (Bruker-SEQUENOM). The calculation of the output methylation ratios for each CpG unit were based on the ratio of the signal intensities for the fragment from a methylated CpG unit/[methylated+unmethylated CpG units]. Further
25 details are described in (Godler *et al.*, 2010 supra).

RNA extractions and quality assessments

[0192] Total RNA was extracted and purified using the Rneasy extraction kit, as per manufacturer's instructions (Qiagen Inc., Hilden, Germany). RNA concentrations were
30 measured in triplicate using a NanoDrop ND-1000 Spectrophotometer, with purity being determined by the A260/A280 ratio using the expected values between 1.8 and 2. Total RNA quality and the degree of DNA contamination was also assessed using capillary

electrophoresis Standard Sens Kit (Bio-rad), which involved descriptive comparison of chromatographic features based on previous publications using this system (Fleige and Pfaffl, *Mol Aspects Med 27(2-3)*:126-139, 2006). Each RNA sample was then diluted to 30ng/ul, to be used in for reverse transcription real-time PCR analysis, where mRNA
5 quality at the Xq27.3 region was initially assessed by examining the relationship between 5' and 3' levels of FMR1 mRNA.

Standard reverse transcription real-time PCR

[0193] Reverse transcription was performed one reaction per sample using the Multiscribe Reverse Transcription System, 50 units/μl (Applied Biosystems). The 7900HT Fast Real Time PCR (Applied Biosystems) was used to quantify FMR1-5', FMR1-3', ASFMR1 (-1), (-2), (-3), GAPDH, B2M, and GUS, using the relative standard curve method. The target gene and the internal control gene dynamic linear ranges were performed on a series of doubling dilutions of an RNA standard (160-4 ng/μl). Since, both ASFMR1 assays do not target an exon/exon boundary, to minimize the impact of potential DNA contamination on the expression results, a no reverse transcription enzyme control was included for every sample. The difference between the plus and minus no reverse transcriptase control was considered as the ASFMR1 expression value for each sample. Previously published sequences were be used for primers and probe for: FMR1-5' and GUS (32); FMR1-3' (41). The following ASFMR1 primers and probes were designed using Primer Express 3.0 (Applied Biosystems):

ASFMR1 (-1) - Fw Primer (CCGCGGAATCCCAGAGA) [SEQ ID NO:34]; Rv Primer: (CAGTGGCGTGGGAAATCAA) [SEQ ID NO:35]; Probe: (FAM-TGGGATAACCGGATGCA-MGB) [SEQ ID NO:36].

ASFMR1 (-2) - Fw Primer: (ACACCCTGTGCCCTTTAAGG) [SEQ ID NO:37]; Rv Primer: (TCAAAGCTGGGTCTGAGGAAAG) [SEQ ID NO:38]; Probe: (VIC-TCGGGATCTCAAAATGT-TAMRA) [SEQ ID NO:39].

ASFMR1 (-3) - Fw Primer: (CCCCAGAATGAGAGGATGTTG) [SEQ ID NO:40]; Rv Primer: (GCCCTAGATCCACCGCTTTAA) [SEQ ID NO:41]; Probe: (FAM-TGCTGGTGGAACTC-MGB) [SEQ ID NO:42].

[0194] FMR1-5', FMR1-3', ASFMR1 primers and probes were be used at concentrations of 18μM and 2μM, respectively. GAPDH and B_2M primer/probe mixes will be obtained from PrimerDesign (PerfectProbe ge-PP-12-hu kit) and used at concentration of 2μM. All of the above assays were single-plexed, with each sample assayed in duplicate 10 μl PCR reactions. The reactions consisted of 5.8 mM MgCl2, 1 μl Buffer A (Applied Biosystems), 3.35 μl Rnase-free water, 1.2 mM dNTPs, 0.01 units/μl of AmpliTaq Gold, 0.5μl of

TaqMan probe and 0.5μl forward and 0.5μl reverse primers, and 1μl of the reverse transcription (cDNA) reaction. The annealing temperature for thermal cycling protocol was 60°C for 40 cycles. The samples were quantified in arbitrary units (au) in relation to the standard curves performed on each plate, standardized to the mean of the 3 internal control
5 genes (GUS, GAPDH and B_2M).

Amplicons

[0195] Amplicons were amplified using the primers and conditions shown in Tables 3 and 4. Table 5 shows prominent regulatory motif locations inclusive and proximal to FREE2
10 in FREE3. Amplicon 5 is as described by Godler *et al.*, *Hum Mol Genet 10(8)*:1618-1632. [Epub 2010]; Godler *et al.*, *J. Mol Diagn.* 2011 [Epub ahead of print] doi: 10.1093/hmg/ddq1037, the contents of which are incorporated by reference.

TABLE 3

Amplicon details used for MALDI-TOF methylation analysis of the regions greater than 0.2kb 3' of the CGG expansion at the Xq27.3 locus

Amplicon No.	Annealing Temperature	Size (kb)	Distance 3' of CGG (kb):	Primer sequence (in capitals) and tag (in lower case)
FREE2(B)	(I) 94 °C 4 min; 25 cycles of: touchdown PCR -0.5 °C per cycle - 94 °C 20s; 64 °C 30s; 72 °C 1 min. (II) 20 cycles of: 94°C for 20s, 59°C for 30s, 72°C for 1 min. (III) 72°C for 3min; 4 °C forever	500	0.207	Fw: 5'-aggaagagagGGTTTTTTTGAAATTTTTGGATTTA-3' Rv: 5'-cagtaatacgactcactatagggagaaggctTAAAACCTATTAAAAACCCCTCTCC-3'
FREE2(C)	(I) 94 °C 4 min; 25 cycles of: touchdown PCR -0.5 °C per cycle - 94 °C 20s; 64 °C 30s; 72 °C 1 min. (II) 20 cycles of: 94°C for 20s, 59°C for 30s, 72°C for 1 min. (III) 72°C for 3min; 4 °C forever	302	0.504	Fw: 5'-aggaagagagTAAGAGGGTTTTAGGTTTTTTTTGG -3' Rv: 5'-cagtaatacgactcactatagggagaaggctAAAACATATACATTCCTAAATTTACCCC-3'
FREE3 (ASFMR1)	(I) 94 °C 4 min; 25 cycles of: touchdown PCR -0.5 °C per cycle - 94 °C 20s; 64 °C 30s; 72 °C 1 min. (II) 20 cycles of: 94°C for 20s, 59°C for 30s, 72°C for 1 min. (III) 72°C for 3min; 4 °C forever	327	9.739	Fw: 5'-aggaagagagTTTTTTTTATATAGGTATTTGTAAAGGATG -3' Rv: 5'-cagtaatacgactcactatagggagaaggctTCTCTAATTTCTTTCTTCACATTCAAAA -3'

5

TABLE 4

Amplicon details used to define FREE2 3' Border region using MALDI-TOF methylation analysis within the FMR1 intron 1 sequence at the Xq27.3 locus

Amplicon No.	Annealing Temperature	Size (kb)	Distance 3' of CGG 3' end (kb):	Primer sequence (in capitals) and tag (in lower case)
FREE2(D) (pp4)	(I) 95 °C 15 min (II) 10 cycles of: 94 °C 20s; 56 °C 30s; 72 °C 1 min. 35 cycles of: 94°C for 20s, 62°C for 30s, 72°C for 1 min. (III) 72°C for 3min; 4 °C forever	374	0.790	Fw: 5'-aggaagagagAAAAGTTTTAGGAAGATTTTAATATGG-3' Rv: 5'-cagtaatacgactcactatagggagaaggctAAAAAACACAATAAACCCATAAATACC-3'
FREE2(E) (pp6)	(I) 95 °C 15 min (II) 10 cycles of: 94 °C 20s; 56 °C 30s; 72 °C 1 min. 35 cycles of: 94°C for 20s, 62°C for 30s, 72°C for 1 min. (III) 72°C for 3min; 4 °C forever	360	1.424	Fw: 5'-aggaagagagGAATGGTTTGAATGTTTTAGATAGGAT -3' Rv: 5'-cagtaatacgactcactatagggagaaggctACCAAAAATCTAATAACCAAAACCAC-3'
FREE3 (ASFMR1)	(I) 95 °C 15 min (II) 10 cycles of: 94 °C 20s; 56 °C 30s; 72 °C 1 min. 35 cycles of: 94°C for 20s, 62°C for 30s, 72°C for 1 min. (III) 72°C for 3min; 4 °C forever	327	9.908	Fw: 5'-aggaagagagTTTTTTTTATATAGGTATTTGTAAAGGATG -3' Rv: 5'-cagtaatacgactcactatagggagaaggctTCTCTAATTTCTTTCTTCACATTCAAAA -3'

5

TABLE 5

Prominent regulatory motif locations inclusive and proximal to FREE2 and FREE3 regions

TRANSCRIPTION FACTOR SITES/POTENTIAL REGULATORY MOTIFS:	SEQUENCE ON THE SENSE STRAND:	STRAND	SEQUENCE HOMOLOGY (%)	AMPLICON	CPG UNIT LOCATION:
GATA-1	GGCGATGGCT	LEADING	95	FREE2(A)	CpG15 and CpG16
HSF2	TGAATATTCG	LEADING	96	FREE2(B)	CpG7 and CpG8/9
C/EBP	AAGTTTCCAAAGA	LAGGING	95	FREE2(D)	CpG6 and CpG7
CdxA	TATTATTATT	LAGGING	99	FREE2(D)	CpG6 and CpG7
AML-1a	ACCACA	LAGGING	100	FREE2(D)	3' of CpG7
AML-1a	TGTGGTG	LEADING	100	FREE2(D)	3' of CpG7
CdxA	TATAAAT	LAGGING	100	N/A	Between FREE2(D) and FREE2(E)
CdxA	TATAAAT	LAGGING	100	N/A	Between FREE2(D) and FREE2(E)
CdxA	AATAATAT	LEADING	99	N/A	Between FREE2(D) and FREE2(E)
HFH-1/HFH-2	AAATAAACAAT	LAGGING	97	FREE2(E)	CpG1 and CpG2/3
CdxA	CATAAAT	LAGGING	100	FREE2(E)	CpG1 and CpG2/3
SRY	TTTGTTT	LAGGING	100	N/A	3' of FREE2(E) CpG6
SRY	TTTGTTT	LAGGING	100	N/A	3' of FREE2(E) CpG6
SRY	TTGTTTA	LAGGING	99	N/A	3' of FREE2(E) CpG6
S8	TTTATTTAATTAAGTT	LEADING	96	N/A	3' of FREE2(E) CpG6
SRY	AAACAAA	LEADING	100	5' of FREE3	5' of FREE3 CpG1
CdxA	TATAATT	LEADING	99	FREE3	CpG1
Oct-1	TTTATGCTAATT	LEADING	99	FREE3	Between CpG1 and CpG2

5

EXMAPLE 1

Mapping methylation of the FMR genetic locus using high throughput mass spectrometry

5 **[0196]** The structure of the FMR genetic locus is shown in Figure 1A and Figure 6A and comprises the FMR1 promoter, and FMR1 and ASFMR1 genes. A CGG repeat is located within the 5' (UTR) of the FMR1 gene. ASFMR1 spans the CGG expansion in the antisense direction and is also regulated by another promoter located in the exon 2 of FMR1. The FREE2 located downstream of the CGG expansion. The FREE3 region is 10 located within intron 2 of FMR1 downstream of the second ASFMR1 promoter.

[0197] The primers utilized for MALDI-TOF methylation analysis targeted 4 regions at the Xq27.3 locus designated as FREE2(A) [described as amplicon 5 in Godler *et al.*, 2010 *supra*]; FREE2(B); FREE2(C) and FREE3 (color coded). Individual CPG sites within each 15 region are numbered accordingly. Prominent transcription factor binding sites and methylation sensitive restriction enzyme recognition sites are indicated in capital font, and are listed/identified in Tables 3 and 4. Numerous HpaII/MspI sites (CCGG) are located throughout the FREE2 A, B and C region.

20 **[0198]** Regions identified as biologically significant showed consistent differences in methylation between healthy controls and FXS samples (Figure 1B and Figures 2A and B). These include HpaII/MspI sites throughout FREE2 A, B and C regions including but not restricted to the FREE2B CCGG sites located at CpGs 6, 9, 13 and between CpGs 25 and 26; as well as FREE2 (C) CCGG site located at CpG1. These would be sensitive to HpaII 25 methylation specific digestion, which can be followed by PCR or other restriction enzyme based methods to assay differential methylation between healthy controls and FXS samples, and potentially carriers of smaller expansion alleles.

[0199] Other regions identified as biologically significant that showed consistent 30 differences in methylation between healthy controls and FXS samples (Figure 1B and Figure 2A and B and Table 5) included: (I) GATA-1 site (FREE2B between CpG 15 and 16); (II) HSF2 site (FREE2C between CpG 7, 8 and 9); (III) an SRY site located upstream

of FREE3; (IV) a CdxA/TATA box site located at CpG1 of FREE3; (V) an Oct-1 site located between CpG sites 1 and 2 within FREE3. Differential methylation of any of these sites in diseased individuals compared to controls may have an affect of relevant transcription factor binding and/or further epigenetic modification; which would inturn affect affect transcription of FMR1, ASFMR1 and/or FMR4. Or may result or reflect aberrant non coding RNA expression and/or RNA:DNA interactions or stability of RNA:DNA hybrids (Figures 4B and C and Figure 5).

EXAMPLE 2

Determining the impact of technical variation on quantitative analysis of methylation and evidence for disease specific methylation within intron 1 and intron 2 of FMR1.

[0200] DNA from lymphoblasts of healthy controls with 30 CGG repeats, normal levels of FMR1 mRNA and FMRP, and DNA from lymphoblasts of FXS patient with 530 CGG, silenced FMR1 transcription and absence of FMRP were mixed at ratios of 1:0; 2:1; 1:1; 1:2; 0:1 corresponding to 0, 33.3, 50, 66.6, 100% FXS DNA in the sample (Figure 3). The spiked DNA samples were bisulfite converted in duplicate reactions. Each reaction was amplified with primer sets (forward and reverse primers) as listed by SEQ ID NOs: which corresponded to 3 SEQUENOM mass spectrometry assays (A: FREE2(B); B: FREE2(C); C: FREE3). The spiked DNA samples were analysed using MALDI-TOF methylation analysis at three sequential regions at the Xq27.3 locus (see Figure 1 for locations). The methylated vs unmethylated ratios at each analysable CpG unit were expressed as output methylation ratios on Y axis, with FXS DNA input % expressed on the X axis (each point represents mean of duplicate PCRs from a single bisulfite converted DNA mixture). Methylation output ratios for CpG sites within FREE2B and FREE2C amplicons (A and B) were positively correlated with increasing FXS DNA input %; while FREE3 Methylation output ratios were negatively correlated with increasing FXS DNA input % with high Pierson's correlation. This clearly demonstrates that the FREE2 region comprising a large portion of FMR1 intron 1 is hypermethylated in FXS sample while FREE3 region within intron 2 of FMR1 is hypomethylated in the FXS sample. This methylation pattern is reversed in the healthy control sample, and supports the differential methylation patterns within FREE2 and FREE3 related to the disease state as shown in Figures 2A and B.

EXAMPLE 3

Evidence for expression of ASFMR1 in FXS and disease specific RNA:DNA interactions.

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[0201] Standard curve and amplification real-time PCR plots (of assays described in figure 4A) show that in the FXS cell lines, ASFMR1 RNA with fully methylated FMR1 promoter and silenced FMR1 and FMRP, ASFMR1 is expressed (Figure 4B). RNA was extracted from 3 FXS cell lines whose methylation profiles are presented in Figure 2; Sample 849 was taken from the male 490 CGG repeat line; Sample 862 was taken from the male 530 CGG repeat line; Sample 865 was taken from the female 563 and 47 CGG repeat line. Each RNA sample was split in two, with one half subjected to RNase A treatment prior to ASFMR1 (-3) relative standard curve analysis. The ASFMR1 (-3) real-time PCR analysis was performed in quadruplicate reactions. The difference in Ct values between RNase A treated and untreated samples represents the level of ASFMR1 expression.

[0202] Standard curve and amplification real-time PCR plots (Figures 4C and D) also indicate that in the FXS cell lines, ASFMR1RNA forms RNA:DNA complexes. FXS RNA samples were treated with TURBO DNase (C) and RQ1 DNase (D) respectively. These DNase treatments caused complete loss of real-time-PCR signal for the ASFMR1(-3) assay. Because DNase can only degrade RNA molecules if they form complexes with DNA, loss of ASFMR1 after DNase treatment suggests that ASFMR1RNA forms RNA:DNA complexes in FXS samples with fully methylated FMR1 promoter and silenced FMR1 expression.

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[0203] Expression of different FMR1 and ASFMR1 transcripts (detailed in Figure 4A) was detected in RNA samples from lymphoblast lines of 6 male controls, two FXS males (samples 849 and 862) and one FXS female (865) [Figures 5A and B]. The control and FXS RNA samples were either treated with TURBO DNase (A), RQ1 DNase (B), RNase A (C), or were untreated. Addition of TURBO DNase or RQ1 DNAse buffers to RNA samples without DNase were included as additional controls in (Figures 5A and B). The FMR1 and ASFMR1 transcripts were quantified using real-time RT-PCR relative standard

curve method, normalized to mRNA levels of three internal control genes, GUS, GAPDH and B2M. FMR1 5' and 3' assays showed no signal for the FXS RNA samples, while similar levels were detected in all control samples (upper two panels in Figures 5A, B and C). TURBO and RQ1 DNAse treatment caused ~50% decrease in the FMR1 levels in most
5 of the control samples; while RNase A treatment caused complete loss of FMR1 and ASFMR1 signals. While decrease of ASMFR1 (-1), (-2) and (-3) levels was also observed in all control samples caused by TURBO and RQ1 DNAse treatment, in FXS samples (with analogous to control ASFMR1 levels in the untreated samples) TURBO and RQ1 DNAse treatment resulted in complete loss of signal for all three ASFMR1 assays.
10 Because DNase can only degrade RNA molecules if they form complexes with DNA, this suggests that ASFMR1 RNA forms RNA:DNA complexes more readily in FXS samples than in controls. Increase in RNA:DNA interaction of ASFMR1 in FXS may lead to methylated FMR1 promoter and adjacent regions (Figure 1) and silencing FMR1 expression leading to loss of FMRP and the resulting FXS clinical phenotype.

EXAMPLE 4

Characterizing the 3' Boundary of the FMR1 promoter located within the FREE2 region – 1.3Kb from the 5' end of the FMR1 intron 1 - relative to transcription

[0204] There is significant inhibition of transcription of the FMR4, ASFMR1 and FMR1 genes in FXS patients which is likely caused by the methylation of the CpG units in Amplicon 1 (FREE 1 region), and/or Amplicon 5 (FREE 2 region) in association with the FMR1 promoter. It is demonstrated here that the FREE2 region and FMR1 promoter expands 1302 base pair into the FMR1 intron 1 from 5' end of the intron (Figures 6A through C). In subjects with FM affected with FXS with cognitive impairment (IQ<70) with no FMR1 mRNA or FMRP and significantly decreased from normal ASFMR1/FMR4 mRNA levels, FREE2 CpG units from FREE2(A) amplicon expanding to CpG unit 1 on the FREE2(E) amplicon have methylation status approaching 100% (Figure 7C) In these same cell lines the FREE1 and FREE2 regions and the FMR1 promoter were fully methylated. In healthy controls and the 'high functioning' FM males with IQ>70 the same region (FREE2 CpG units from FREE2(A) amplicon expanding to CpG unit 1 on the FREE2(E)) have methylation status approaching 0% (Figures 7A and B). The DNA regions 5' of the CpG unit 1 (eg CpG2/3 of FREE2E on the FREE2(E) do not show any difference in methylation between affected FM, healthy controls and 'high functioning full mutation males, as these regions have methylation status approaching 100% in all groups examined (Figure 7). Therefore, the assay enabled herein clearly identifies the 3' boundary of the FREE2 region and the FMR1 promoter, which is located between CpG unit 1 of the FREE2(E) amplicon and CpG unit 2/3 of the FREE2(E) amplicon.

[0205] These data also indicate that methylation of the FREE1 region is closely related to inhibition of bi-directional transcription and translation of the FMR locus required for normal neuronal development. As a consequence, this can lead to pathological conditions such as FXS, mental retardation and autism. Hence, the assay examining one or more biomarker sites herein can be used to diagnose, make a prognosis and detect the presence or predisposition to FXS, and potentially any other neuropathological condition/s associated with elevated methylation and/or altered distribution of methylated sites in the FMR locus described herein.

EXAMPLE 5

Methylation status of FREE3 in "high functioning" males and FM carrier females

[0206] To determine if FREE3 region is informative in biological settings, methylation of FREE3 was examined in blood and lymphoblast DNA samples of 'high functioning' FM males with IQ>70, FMR1 mRNA expression in blood which was 2.6 fold elevated above the normal levels and FMRP expression which was moderately reduced. The methylation results were compared to healthy control males and FXS affected FM males with no FMR1 expression and no FMRP expression and hypermethylated FMR1 promoter encompassing the FMR1 CpG island, FREE1 and FREE2 regions. It is evident from the representations in Figure 6 that the FREE3 region methylation status is an important biomarker of the FXS phenotype as it is hypermethylated in high functioning FM individuals as well as in healthy controls, while being hypomethylated in FXS affected individuals. It is also evident from the representation that the methylation patterns are consistent between lymphoblasts and blood.

[0207] These data indicate that decreased methylation of the FREE3 region is closely related to inhibition of bi-directional transcription and translation of the FMR locus required from normal neuronal development as ASFMR1 transcription start site is located between CpG units 1 and 2 of the FREE3 region. As a consequence, this can lead to pathological conditions such as FXS, mental retardation and autism. Hence, the assay examining one or more biomarker sites herein can be used to diagnose, make a prognosis and detect the presence or predisposition to FXS, and potentially any other neuropathological condition/s associated with elevated methylation and/or altered distribution of methylated sites in the FMR locus described herein.

[0208] Those skilled in the art will appreciate that aspects of the disclosure described herein are susceptible to variations and modifications other than those specifically described. It is to be understood that these aspects include all such variations and
5 modifications. These as pects also include all of the steps, features, compositions and compounds referred to or indicated in this specification, individually or collectively, and any and all combinations of any two or more of the steps or features.

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CLAIMS:

1. A method for identifying a trinucleotide expansion disorder in a mammalian subject including a human, said method comprising screening for a change relative to a healthy control in the extent of epigenetic modification within (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; and/or (ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region of the FMR genetic locus; wherein a change in extent of epigenetic modification relative to the control is indicative of the presence or severity of the trinucleotide expansion disorder or a propensity to develop same wherein the intron, intron/exon boundary and/or splicing region is selected from the list consisting of:

(i) Fragile X-related Epigenetic Element 3 in FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions;

(ii) intron 2 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or a portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions; and

(iii) genomic FREE2 region as a whole or specific fragments of FREE2 including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditions.

2. The method of Claim 1 wherein the trinucleotide expansion disorder is selected from Fragile X syndrome (FXS), Fragile X-associated tremor or ataxia (FXTAS), Fragile X-associated primary ovarian insufficiency (FXPOI), autism, mental retardation, cognitive

impairment, a modified X-chromosome.

3. The method of Claim 1 wherein the epigenetic modification is methylation.

4. The method of Claim 1 wherein a cell from the subject is a cultured or uncultured Chorionic Villi Sample (CVS) cell, a lymphoblast cell, a blood cell, buccal cell, epithelial cell, fibroblast cell, an amniocyte or an EBV transformed lymphoblast cell line.

5. The method according to any one of Claim 1 to 4 further comprising determining the length of $(CGG)_n$ expansion within the FMR genetic locus leading to a $(CGG)_n$ expansion pathology selected from a Gray Zone (GZ) pathology, a premutation (PM) pathology or a full mutation (FM) pathology.

6. A method for identifying FXS or a related condition in a human subject, said method comprising screening for a change relative to a healthy control in the extent of epigenetic modification in the FMR genetic locus at a location selected from:

(i) Fragile X-related Epigenetic Element 3 in FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions; and

(ii) genomic FREE2 region as a whole or specific fragments of FREE2 including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 . or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditions;

wherein a change in extent of epigenetic modification relative to a control is indicative of the presence or severity of the pathological condition or a propensity to develop same.

7. A method for screening for an agent which modulates epigenetic modification of an FMR genetic locus in a mammalian cell including a human cell, said method comprising screening for a change relative to a healthy control in the extent of epigenetic change in (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; and/or (ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region of the FMR genetic locus; wherein the intron, intron/exon boundary and/or splicing region is selected from the list consisting of:

(i) Fragile X-related Epigenetic Element 3 in FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions;

(ii) intron 2 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or a portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions; and

(iii) genomic FREE2 region as a whole or specific fragments of FREE2 including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditions;

in the presence or absence of an agent to be tested wherein the agent is selected if it induces a change in extent of epigenetic modification.

8. The method of Claim 7 wherein the epigenetic modification is methylation.

9. Use of epigenetic profile within a region of FMR genetic locus in a mammalian cell

including a human cell within (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; and/or (ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region of the FMR genetic locus; wherein the intron, intron/exon boundary and/or splicing region is selected from the list consisting of:

(i) Fragile X-related Epigenetic Element 3 in FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions;

(ii) intron 2 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or a portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions;

(iii) genomic FREE2 region as a whole or specific fragments of FREE2 including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditions;seventh

in the manufacture of an assay to identify an epigenetic profile of an FMR locus-associated trinucleotide expansion disorder.

10. Use of Claim 9 wherein the epigenetic modification is methylation.

11. Use of Claim 9 or 10 wherein the FMR locus-associated trinucleotide expansion disorder is FXS or a related condition selected from FXTAS, FXPOI, autism, mental retardation, a modified X-chromosome and cognitive impairment.

12. Use of an epigenetic assay specific for an intron, intron/exon boundary and/or splicing region within a genetic locus selected from (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; or (ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region conducted in conjunction with an assay which determines the length of a nucleotide expansion leading to an expansion pathology to diagnose a pathological condition.

13. Use of Claim 12 wherein the genetic locus is the FMR genetic locus.

14. Use of Claim 13 wherein the expansion pathology by GZ or FM pathology.

15. Use of Claim 13 or 14 wherein the region in the FMR genetic locus assayed is selected from:

(i) Fragile X-related Epigenetic Element 3 in FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions;

(ii) intron 2 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or a portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions;

(iii) genomic FREE2 region as a whole or specific fragments of FREE2 including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditionsseventh.

16. A method for identifying in a genome of a mammalian cell including a human cell,

a trinucleotide expansion disorder associated with methylation or other epigenetic modification within the FMR genetic locus said method comprising extracting genomic DNA from said cell and subjecting the DNA to an amplication reaction using primers selective of (i) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing region; and/or (ii) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region within the genetic locus and subjecting the amplified and/or enzyme digested DNA to a methylation or other epigenetic assay to determine the extent of methylation or other epigenetic modification of the DNA wherein a change in extent of methylation or other epigenetic modification relative to a healthy control is indicative of the presence of the trinucleotide expansion disorder or propensity to develop same wherein the intron, intron/exon boundary and/or splicing region is selected from the list consisting of:

(i) Fragile X-related Epigenetic Element 3 in FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions;

(ii) intron 2 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or a portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions; and

(iii) genomic FREE2 region as a whole or specific fragments of FREE2 including FREE2 FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditions.

17. The method of Claim 16 wherein the trinucleotide expansion disorder is FXS or a related condition selected from FXTAS, FXPOI, autism, mental retardation, a modified X-

chromosome and cognitive impairment.

18. Use of primers which amplify a region of the FMR genetic locus, said region within:

(i) Fragile X-related Epigenetic Element 3 in FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions;

(ii) intron 2 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or a portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions;

(iii) genomic FREE2 region as a whole or specific FREE2 fragemnts including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditions;

(iv) an intron, intron/exon boundary and/or splicing region downstream of intron 2 of FMR1 or a homolog thereof or a portion or fragment thereof;

(v) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing regions within the FMR genetic locus; and

(vi) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region within the FMR genetic locus;

in the manufacture of a diagnostic kit or device to detect methylation or other epigenetic modification of the FMR locus-associated with a pathological condition.

19. A kit for the use in a method of Claim 1 comprising primers which amplify a region with the FMR genetic locus, said region in:

(i) Fragile X-related Epigenetic Element 3 in FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions;

(ii) intron 2 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or a portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions;

(iii) genomic FREE2 region as a whole or specific FREE2 fragemnts including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditions;

(iv) an intron, intron/exon boundary and/or splicing region downstream of intron 2 of FMR1 or a homolog thereof or a portion or fragment thereof;

(v) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing regions within the FMR genetic locus; and

(vi) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region within the FMR genetic locus.

20. The kit of Claim 19 wherein the primers are selected from the list consisting of SEQ ID NOs:6 through 11.

21. A computer program product for assessing progression of a pathological condition associated with the FMR locus in a subject, the product comprising:

(1) assigning a value to one or more of:

(a) change in of methylation or other epigenetic modification relative to a control in FREE3 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or part thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions;

(b) change of methylation or other epigenetic modification relative to a control in intron 2 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or portion or part thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions;

(c) change in methylation or other epigenetic modification relative to a control in genomic FREE2 region as a whole or specific FREE2 fragemnts including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditions;

(d) change of methylation in an intron, intron/exon boundary and/or splicing region downstream of intron 2 of FMR1 or a homolog thereof or a portion or fragment thereof;

(e) two or more of (i) an intron; (ii) an intron/exon boundary; (iii) a splicing region within the FMR genetic locus;

(f) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region within the FMR genetic locus;

(g) length of $(CGG)_n$ expansion within the FMR genetic locus when considered in combination with (a) and/or (b);

(h) general phenotype or clinical manifestations in subjects with a

neurodevelopmental or neurodegenerative condition;

(i) behavioral assessment criteria associated with normal subjects, PM subjects, GZ subjects and FM subjects;

(j) cognitive ability;

(k) extent of transcription of genes within the FMR locus with the proviso that if any one of (d) through (k) is determined then one or more of (a) through (c) is also determined;

(2) means to converting the value to a code; and

(3) means to store the code in a computer readable medium and compare code to a knowledge database to determine whether the code corresponds to a pathological condition.

22. A computer for assessing an association between extent of methylation or other epigenetic modification within the FMR locus, the FMR locus and progression of a disease condition wherein the computer comprises:

(1) assigning a value to one or more of:

(a) change in of methylation or other epigenetic modification relative to a control in FREE3 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or part thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions;

(b) change of methylation or other epigenetic modification relative to a control in intron 2 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or portion or part thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions;

(c) change in methylation or other epigenetic modification relative to a control in genomic FREE2 region as a whole or specific FREE2 fragemnts including

FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditions;

(d) change of methylation in an intron, intron/exon boundary and/or splicing region downstream of intron 2 of FMR1 or a homolog thereof or a portion or fragment thereof;

(e) two or more of (i) an intron; (ii) an intron/exon boundary; (iii) a splicing region within the FMR genetic locus;

(f) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region within the FMR genetic locus;

(g) length of $(CGG)_n$ expansion within the FMR genetic locus when considered in combination with (a) and/or (b);

(h) general phenotype or clinical manifestations in subjects with a neurodevelopmental or neurodegenerative condition;

(i) behavioral assessment criteria associated with normal subjects, PM subjects, GZ subjects and FM subjects;

(j) cognitive ability;

(k) extent of transcription of genes within the FMR locus with the proviso that if any one of (d) through (k) is determined then one or more of (a) through (c) is also determined;

(2) means to converting the value to a code; and

(3) means to store the code in a computer readable medium and compare code to a knowledge database to determine whether the code corresponds to a pathological condition.

23. A method of identifying epigenetic profile in a population of human subjects indicative of a pathological condition associated with the FMR locus, said method comprising screening for a change relative to a control in a statistically significant number of subjects the extent of methylation or other epigenetic modification within:

(i) Fragile X-related Epigenetic Element 3 in FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions;

(ii) intron 2 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or a portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions;

(iii) genomic FREE2 region as a whole or specific fragments of FREE2 including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditions;

(iv) an intron, intron/exon boundary and/or splicing region downstream of intron 2 of FMR1 or a homolog thereof or a portion or fragment thereof;

(v) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing regions within the FMR genetic locus; and

(vi) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region within the FMR genetic locus;

wherein a change in extent of methylation or other epigenetic modification is indicative of the presence of the pathological condition or a propensity to develop same in the population.

24. A method of allowing a user to determine the status, prognosis and/or treatment response of a subject with respect to an FMR locus-associated pathology, the method including:

(1) receiving data in the form of extent of methylation or other epigenetic modification at a site in:

(i) Fragile X-related Epigenetic Element 3 in FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:1 or a homolog thereof or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:1 or which hybridizes to SEQ ID NO:1 or its complementary form under medium stringency conditions;

(ii) intron 2 of FMR1 comprising the nucleotide sequence set forth in SEQ ID NO:2 or a homolog thereof or a portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:2 or which hybridizes to SEQ ID NO:2 or its complementary form under medium stringency conditions;

(iii) genomic FREE2 region as a whole or specific FREE2 fragemnts including FREE2 (D), FREE2 (E) or FREE3 comprising the nucleotide sequence set forth in SEQ ID NO:48 or 49 or 47, respectively or a homolog or portion or fragment thereof defined by having at least 80% nucleotide sequence identity to SEQ ID NO:48 or 49 or 47 or which hybridizes to SEQ ID NO:48 or 49 or 47 or its complementary form under medium stringency conditions;

(iv) an intron, intron/exon boundary and/or splicing region downstream of intron 2 of FMR1 or a homolog thereof or a portion or fragment thereof;

(v) two or more of (a) an intron; (b) an intron/exon boundary; and/or (c) a splicing regions within the FMR genetic locus; and

(vi) approximately one seventh or greater of an intron including an intron/exon boundary and/or a splicing region within the FMR genetic locus;

wherein the extent of methylation or epigenetic modification provides a correlation to the presence, state, classification or progression of the pathology;

(2) transferring the data from the user *via* a communications network;

(3) processing the subject data *via* multivariate or univariate analysis to provide a disease index value;

(4) determining the status of the subject in accordance with thc results of the disease index value in comparison with predetermined values; and

(5) transferring an indication of the status of the subject to the user *via* the communications network.

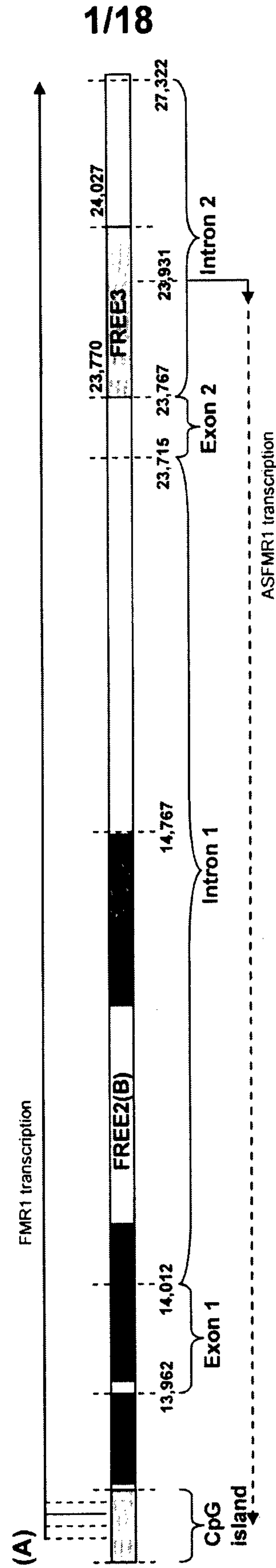

Figure 1A

(B)

FREE2(B)

(14,169)
tggggcctgtt ggaagcccct ctcc34gactcc33gagaggccct agc32gcctatc31g aaatgagag accagc30gagg agagggttct
ctttc29ggc28gcc27gagcccc26gc c25ggggtgagc tggggatggg c24gagggcc23gg c22ggcaggtac tagagcc21ggg c20gggaagggc
c19gaaatc18ggc17g ctaagtgac16G GC15GATGGCT tattcccct ttcctaaaca tcatctccca gc14gggatcc13gggcctgtc12gt gtgggtagtt
gtggaggagc11g gggggc10gct tcagcc9gggc c8gcctcctgc agc7gccaaga gggcttcagg tctcctttgg cttctctttt cc6ggtctagc attgggactt
c5ggagagctc cactgttctg ggc4gagggct gtgaagaaag agtagtaaga agc3ggtagtc2g gcaccaaat cacaatggca actgattttt agtggcttct
ctttgtggat ttc1ggaggag attttagatc caaaagtttc aggaagacc
(14,669)

5'end of FREE2(A) overlapping with section of amplicon 3

SEQ ID NO:4

FREE2(C)

5'end of FREE2(B) overlapping with section of FREE2(C)

SEQ ID NO:5

(14,668)
taacatggcc cagcagtgca ttgaagaagt tgatcatcgt gaatattcgc gtcccccttt ttgttaaacg gggtaaattc aggaatgcac atgcttcagc gtctaaaacc
attagcagcg ctgctactta aaaattgtgt gtgtgtgtttAAGTTTCCAA AGAcctaaat atatgccatg aaacttcagg taattaactg agagtaTATT ATTActaggg
catttttttt ttaactgagc gaaaatattt ttgtgcccct aagaacttg ACCACAtttcc tttgaatTTG TGGTGttgca gtggactgaa ttgttgaggc tttatatagg
cattcatggg tttactgtgc tttttaaagt tacaccattg cagatcaact aacacctttc agttttaaaa ggaagattta caaatttgat gtagcagtag tgcgtttgtt ggtatgtagg
tgctgTATAA ATtcatcTAT AAATtctcat ttcctttgga atgtctataa cctctttcAA TAATAtccca ccttactaca gtattttggc aatagaaggt gcgtgtggaa
ggaaggctgg aaaatagcta ttagcagtgt ccaacacaat tcttaaatgt attgtagaat ggcttgaatg tttcagacag gacacgtttg gctataggaA AATAAACAAT
tgactttatt ctgtgtttac caattttatg aagacatttg gagatcagta tatttCATAA ATgagtaaag tatgtaaact gttccatact ttgagcacaa agataaagcc
ttttgctgta aaaggaggca aaaggtaacc ccgcgtttat gttcttaaca gtctcatgaa tatgaaattg tttcagttga ctctgcagtc aaaattttaa tttcattgat tttattgatc
cataatttct tctggtgagt ttgcgtagaa tcgttcacgg tcctagatta gtggttttgg tcactagatt tctggcacta ataactataa tacatataca tatatatgtg tgagtaacgg
ctaatggtta ggcaagattt tgattgacct gtgatataaa cttagattgg atgccactaa agtttgctta tcacagaggg caagtagcac attatggcct tgaagtactt
attgttctct tccagcaact tatgatttgc tccagtgatt ttgcttgcac actgactgga atataagaaa tgccttctat ttttgctatt aattccctcc tttTTTGTTT TGTTTtgtaa
cgaagTTGTT TAacttgaag gtgaatgaag aataggttgg ttgcccctta gttccctgag gagaaatgtt aatacttgaa caagtgtgtg tcagacaaat tgctgttatg
TTTATTTAAT TAAGTTtgat ttctaagaaa atctcaaatg gtctgcactg atggaagaac agtttctgta acaaaaaagc ttgaaatttt tatatgactt ataatactgc
tgtgagtttt aaaagtaaag caaaagtaaa ctgagttgct tgtccagtgg gatggacagg
(16,200)

SEQ ID NO:30

(23461)
tcgagatgtt gaaatctgtg gagaattttt tctcatgttt agtgttttag ctatgtttat ctctagggta tagcacatac aaggtggcaa tatagatgtg cttaatgaat aaaatgatct
tcaaaaactg accttcattt gaagttctat tttattcata aacacataaa acgtttggta tcactgtaaa atttaactaa AAACAAAaac tatctttaag ctcacaagtt
aatttaacgt
(23700)

SEQ ID NO:31

FREE3

(23,701)
ttttcttac acaggcattt gtaaaggatg ttcatgaaga ttcaataaca gttgcatttg aaaacaagta agtgtctc1gt taTATAATTt taatgatgag gttctttaat
atTTTATGCT AATTctattc ttcatttttt aaaaattcaa gtccagtttg agtgcttttc aggaatggat cttcatgtta ctgactgaga agtttctgaa caactcagta
ttaaactaat ggaatgactg tttctgctaa tgtcctggag gtcccttatt gtatggtatt gatccttac2g tcttaattcc cttgaatgtg aagaaagaaa ccagaga
(24,027)

SEQ ID NO:1

Figure 1B

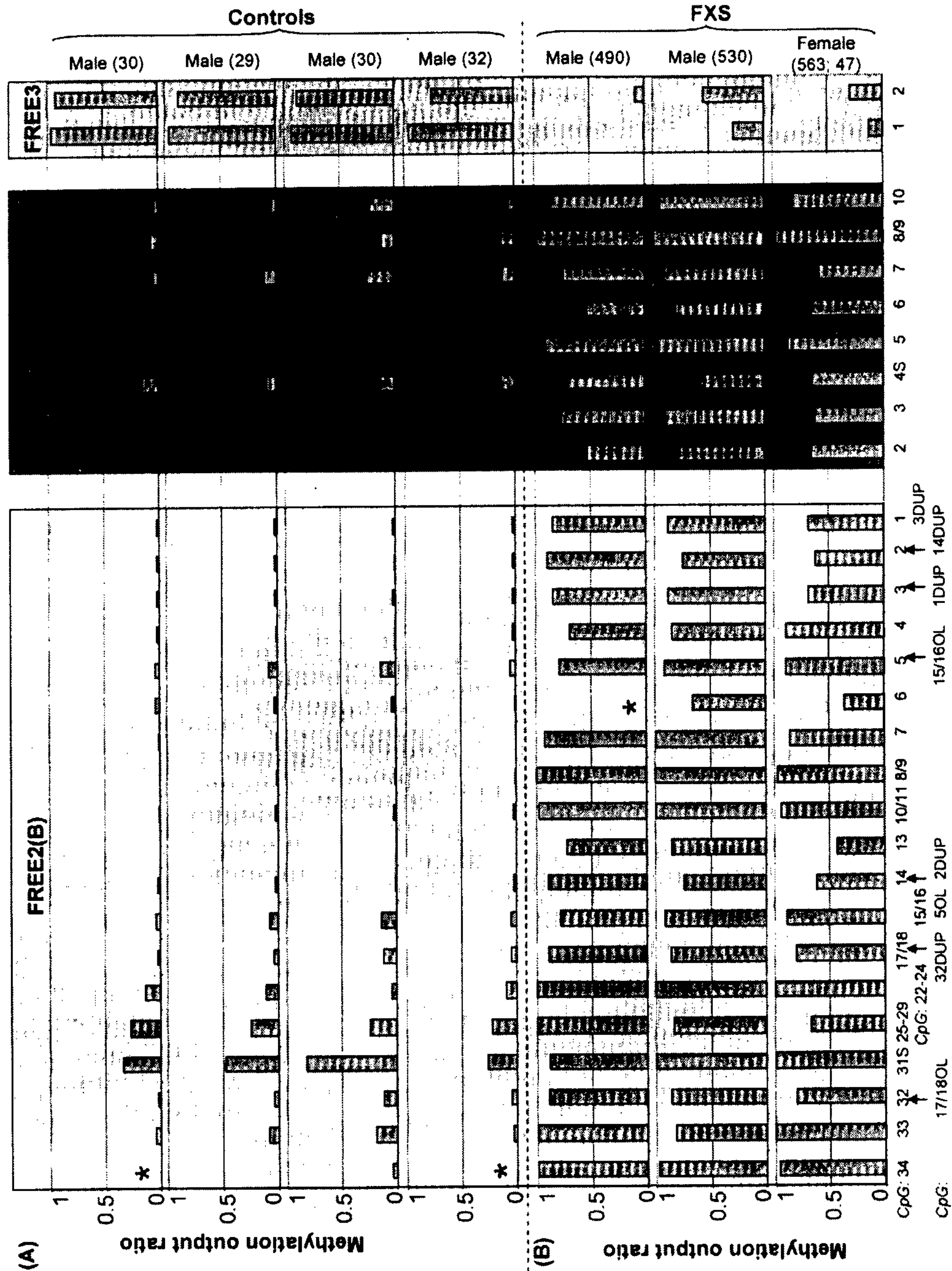

Figure 2

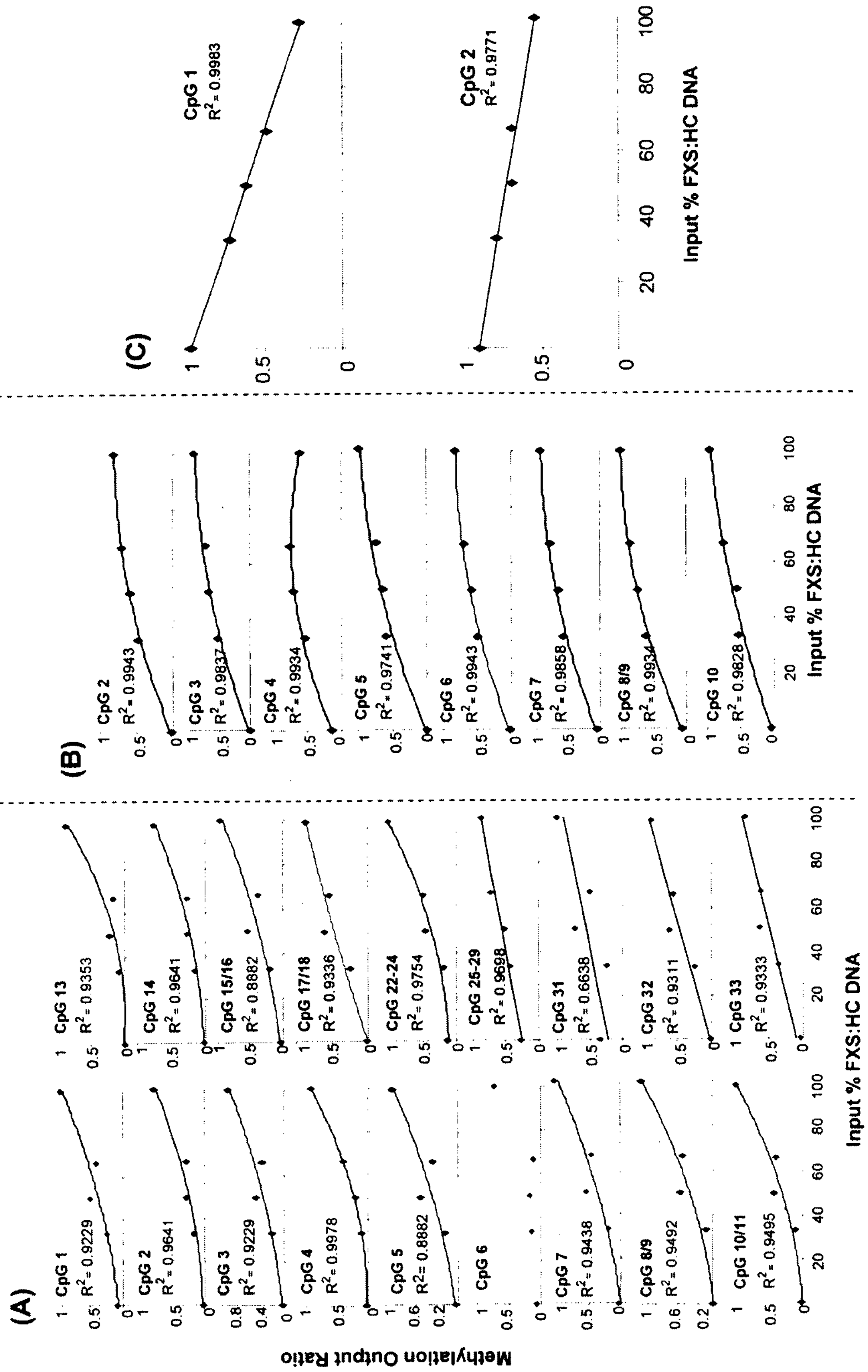

Figure 3

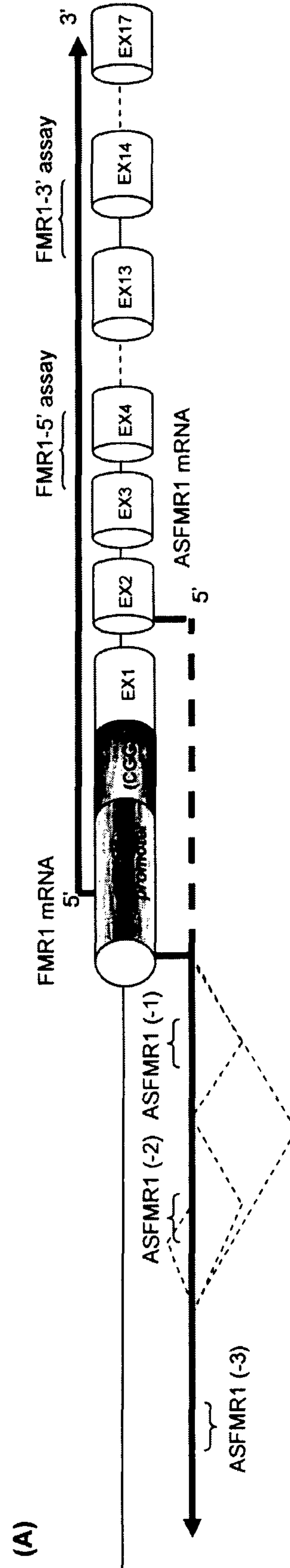

Figure 4A

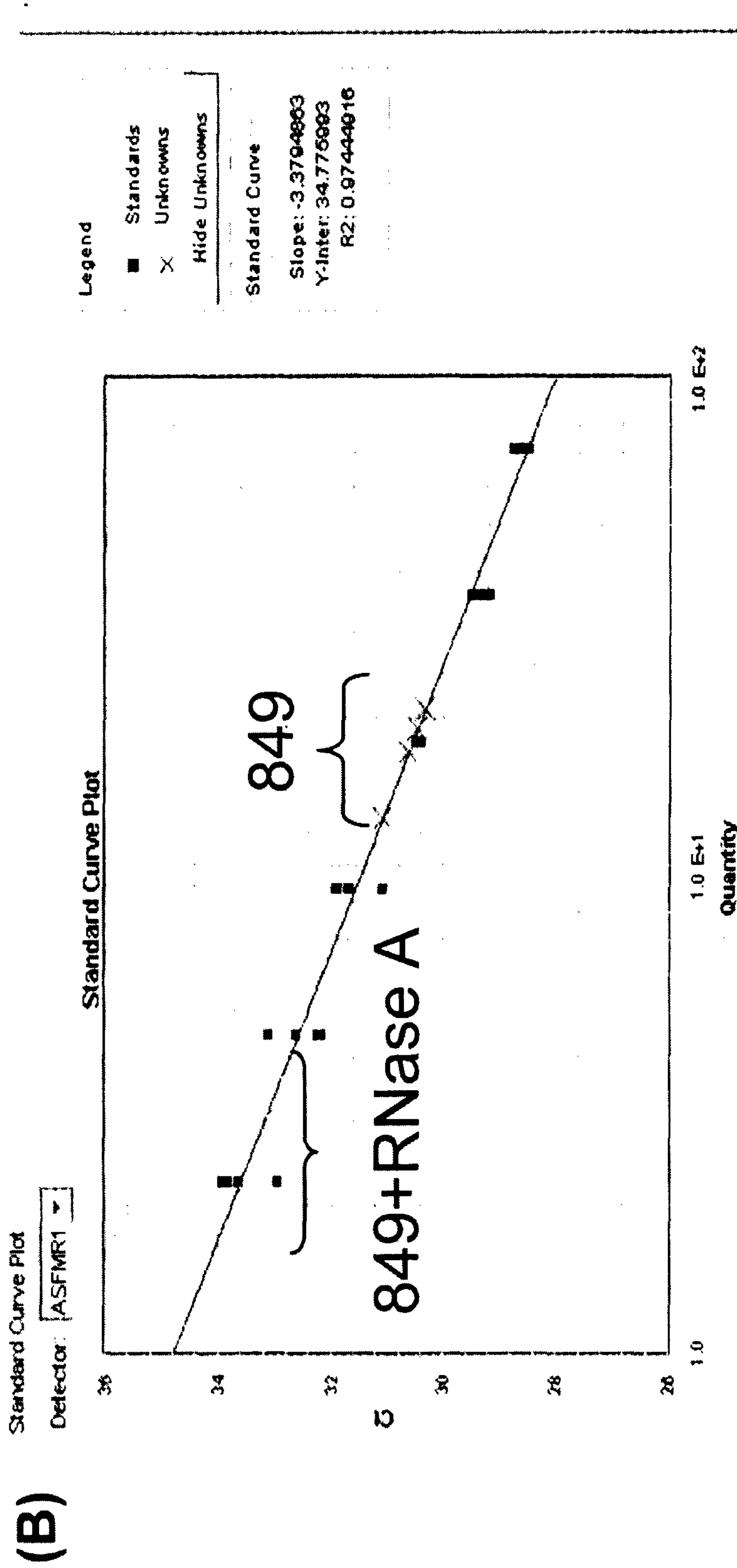

Figure 4B

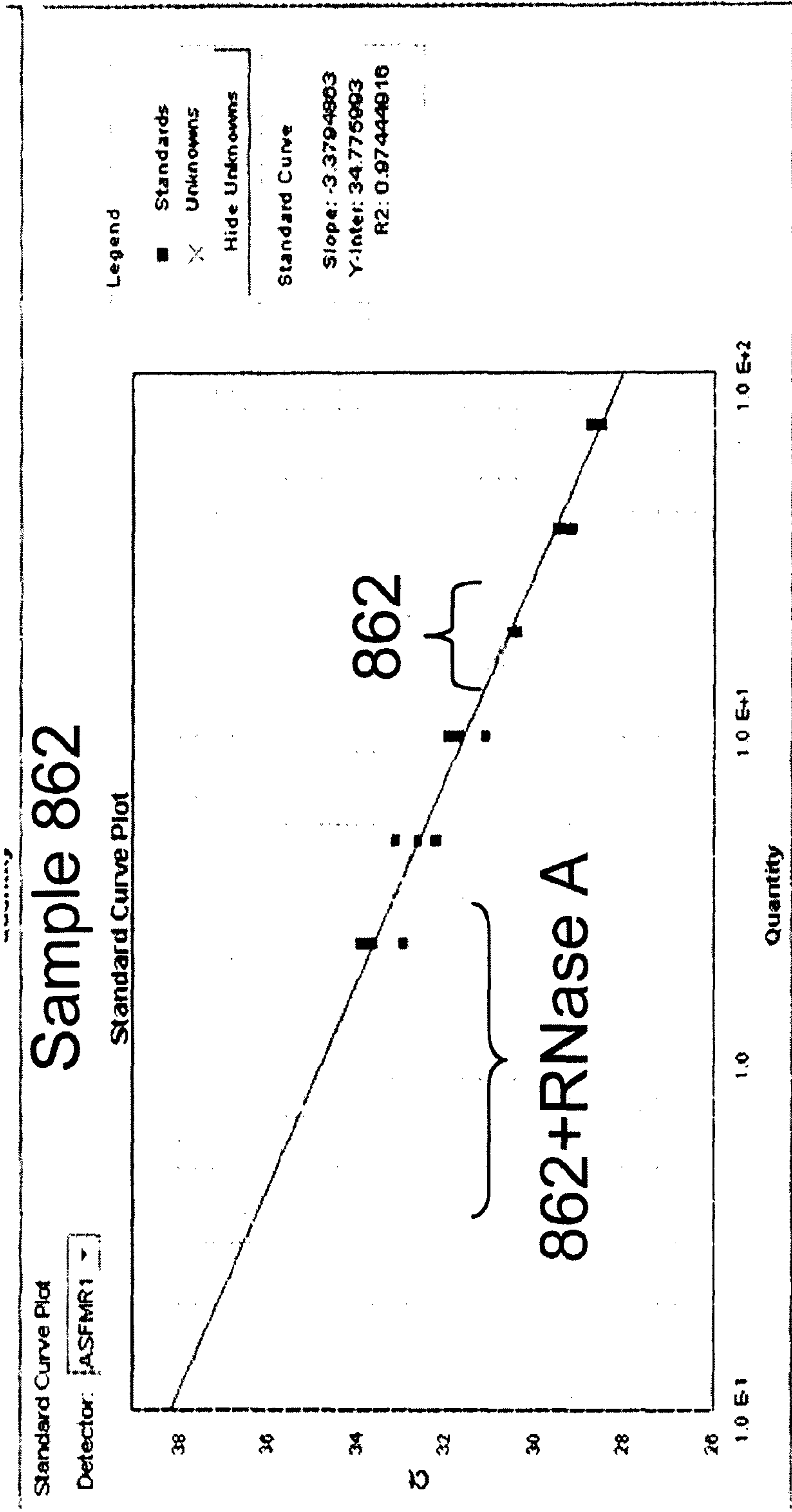

Figure 4B continued

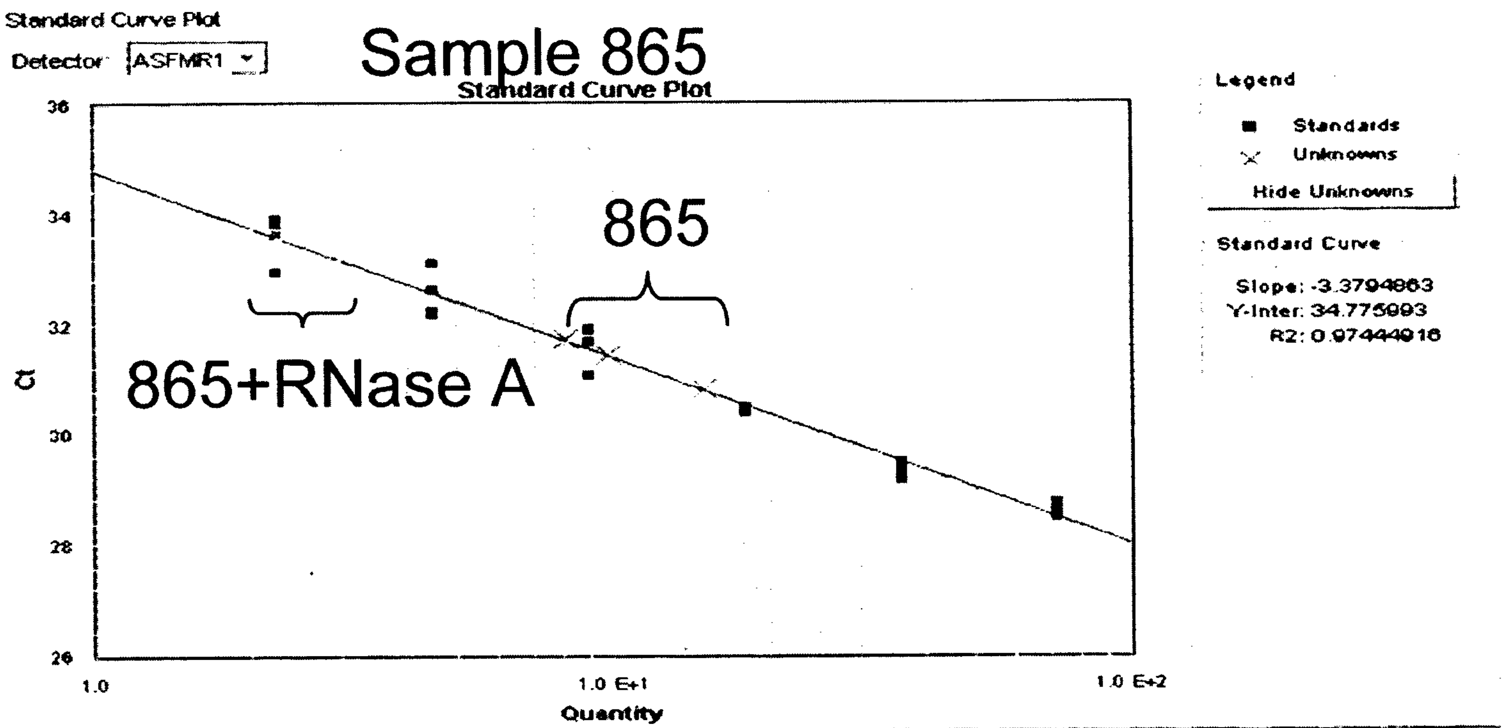

Figure 4B continued

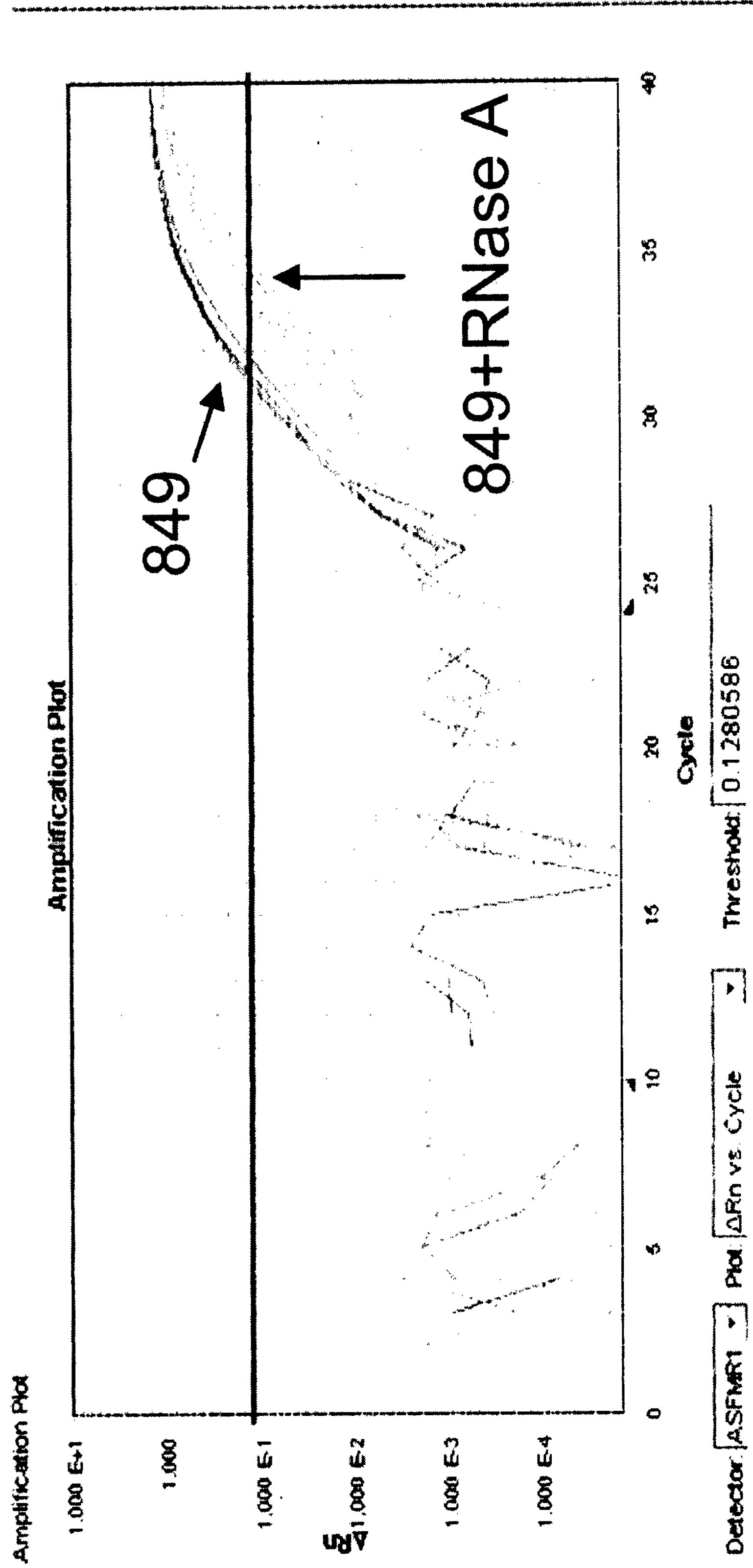

Figure 4B continued

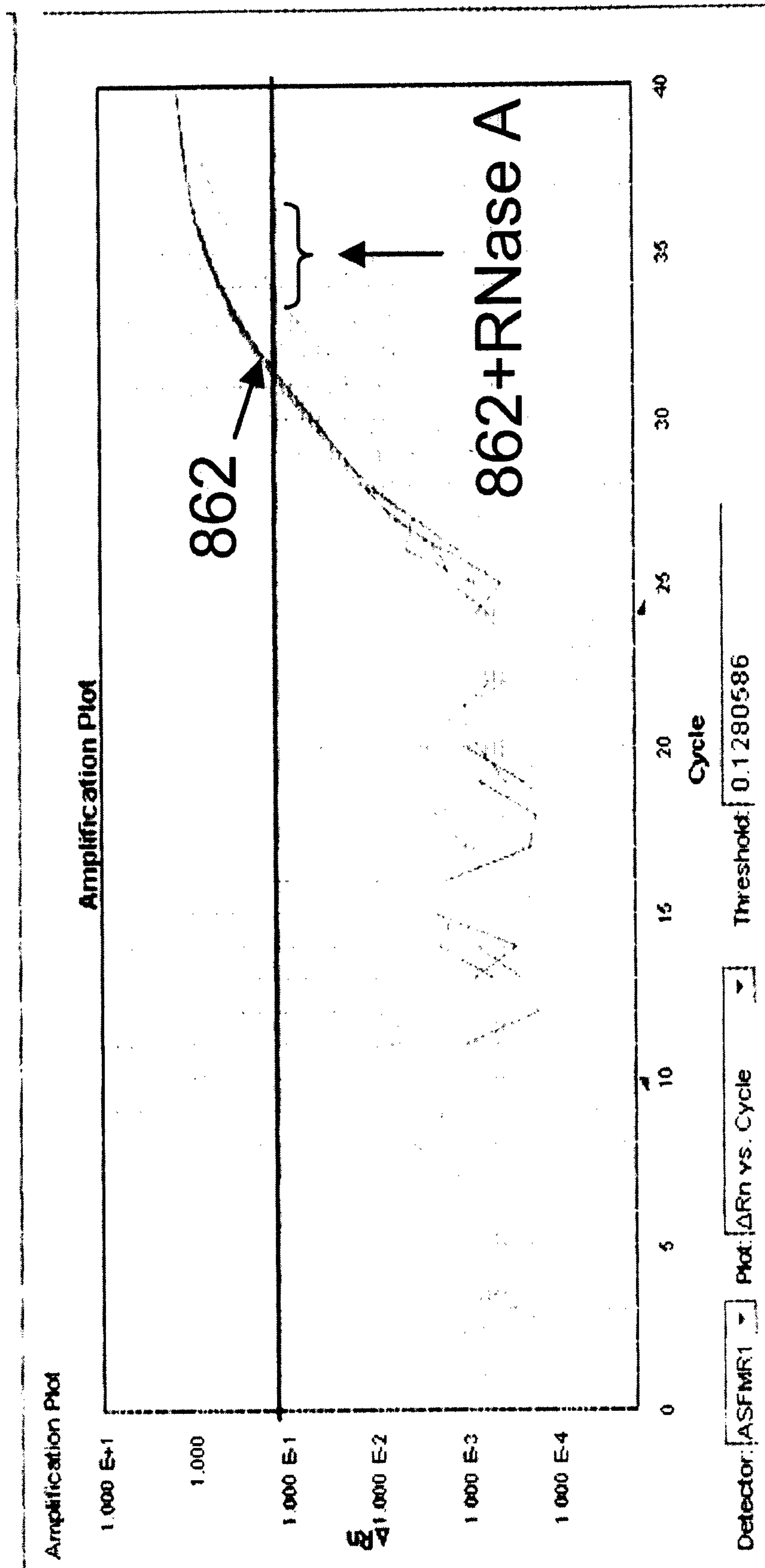

Figure 4B continued

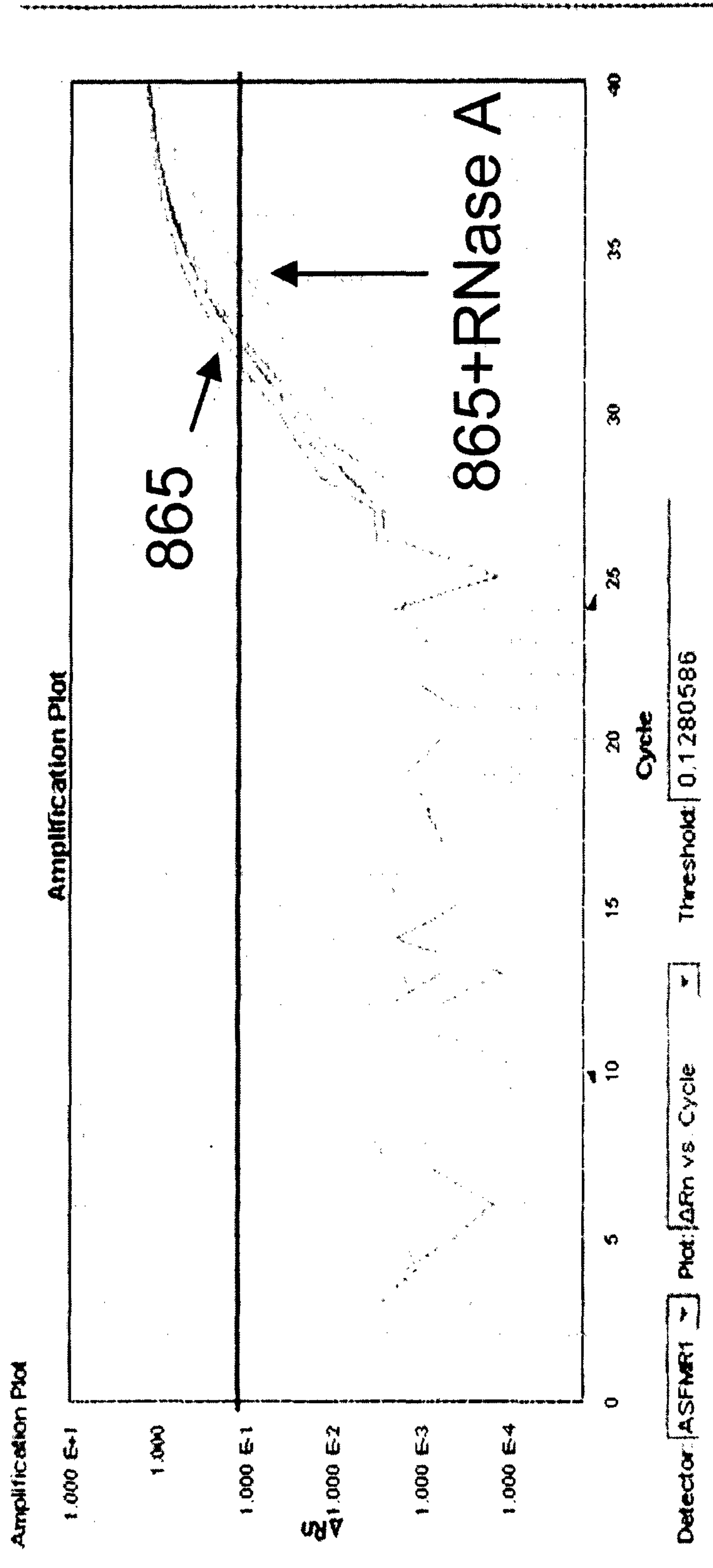

Figure 4B continued

(C)

Figure 4C

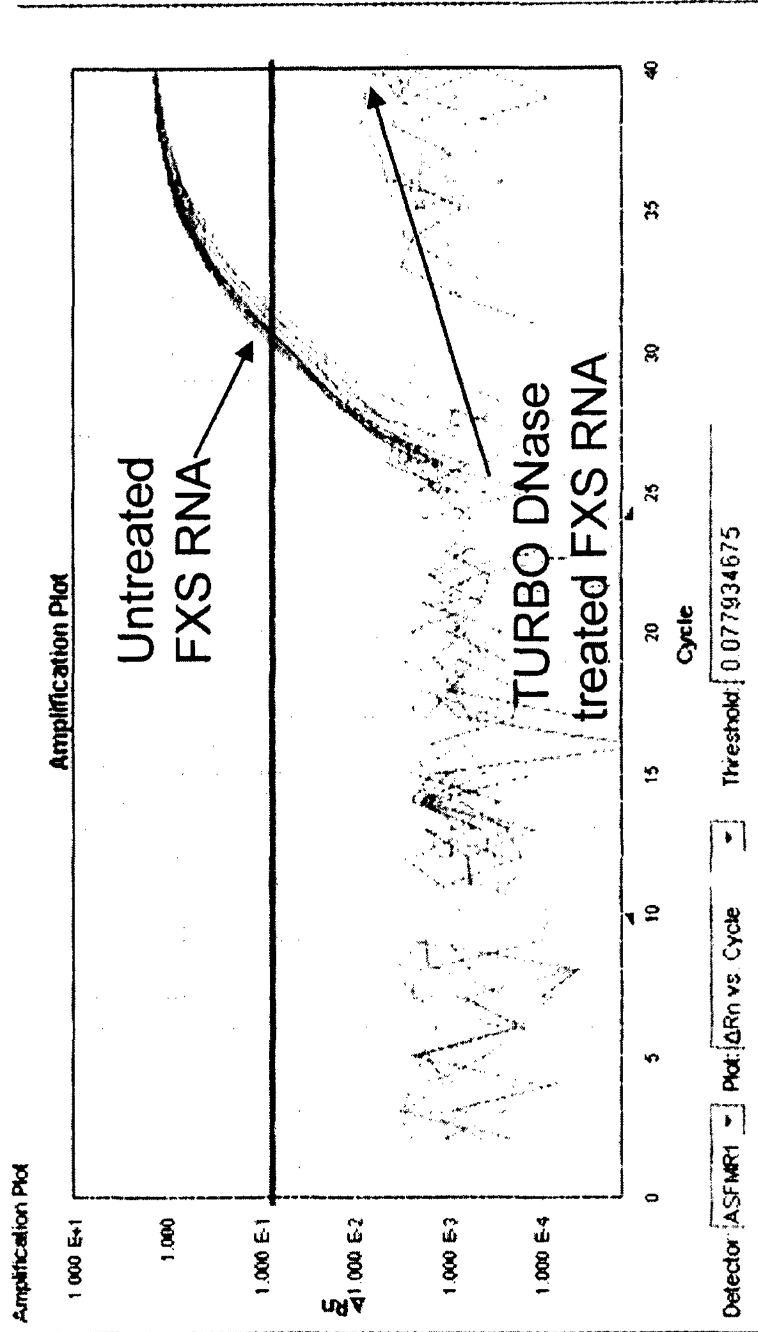

Figure 4C continued

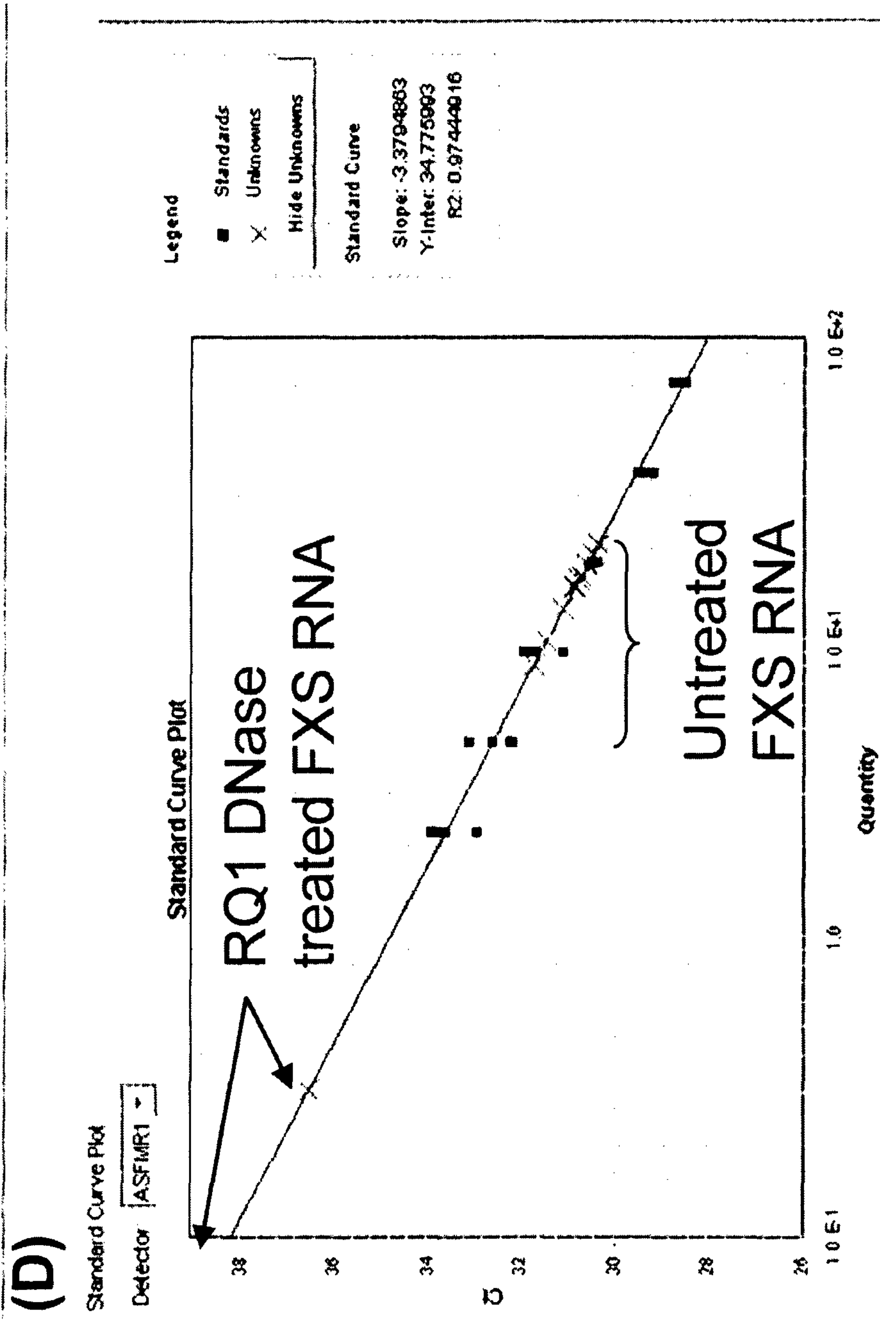

Figure 4D

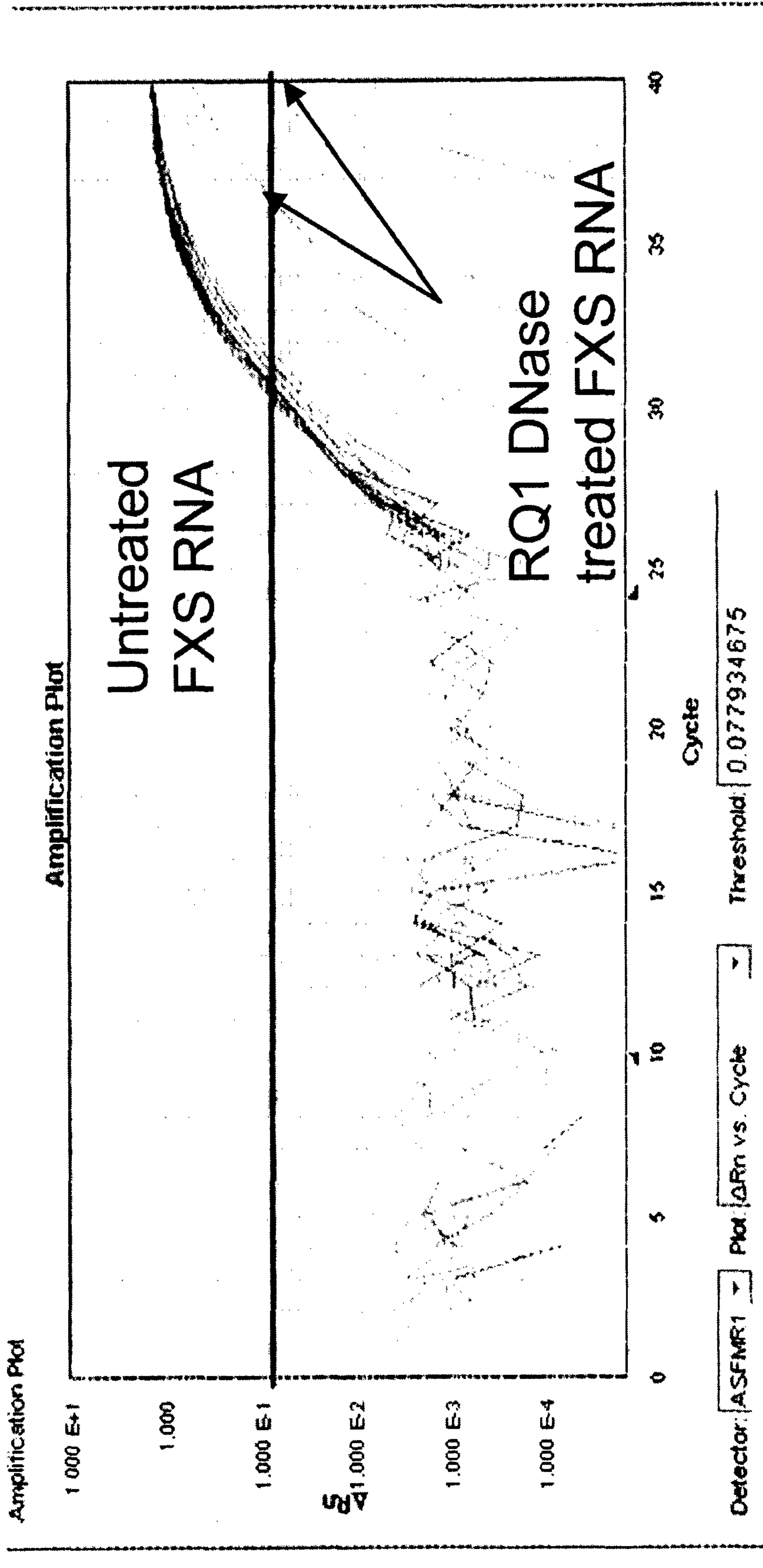

Figure 4D continued

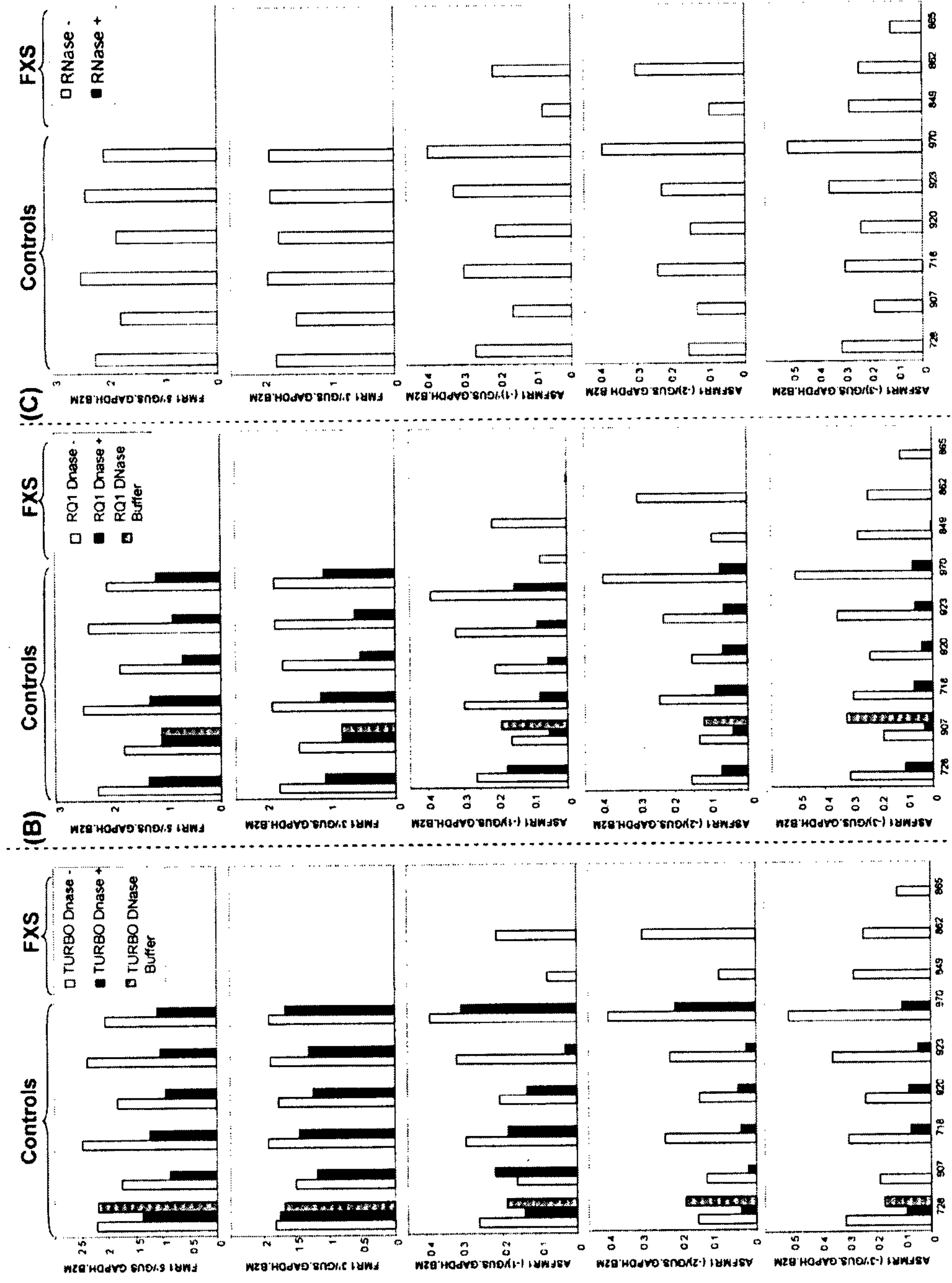

Figure 5

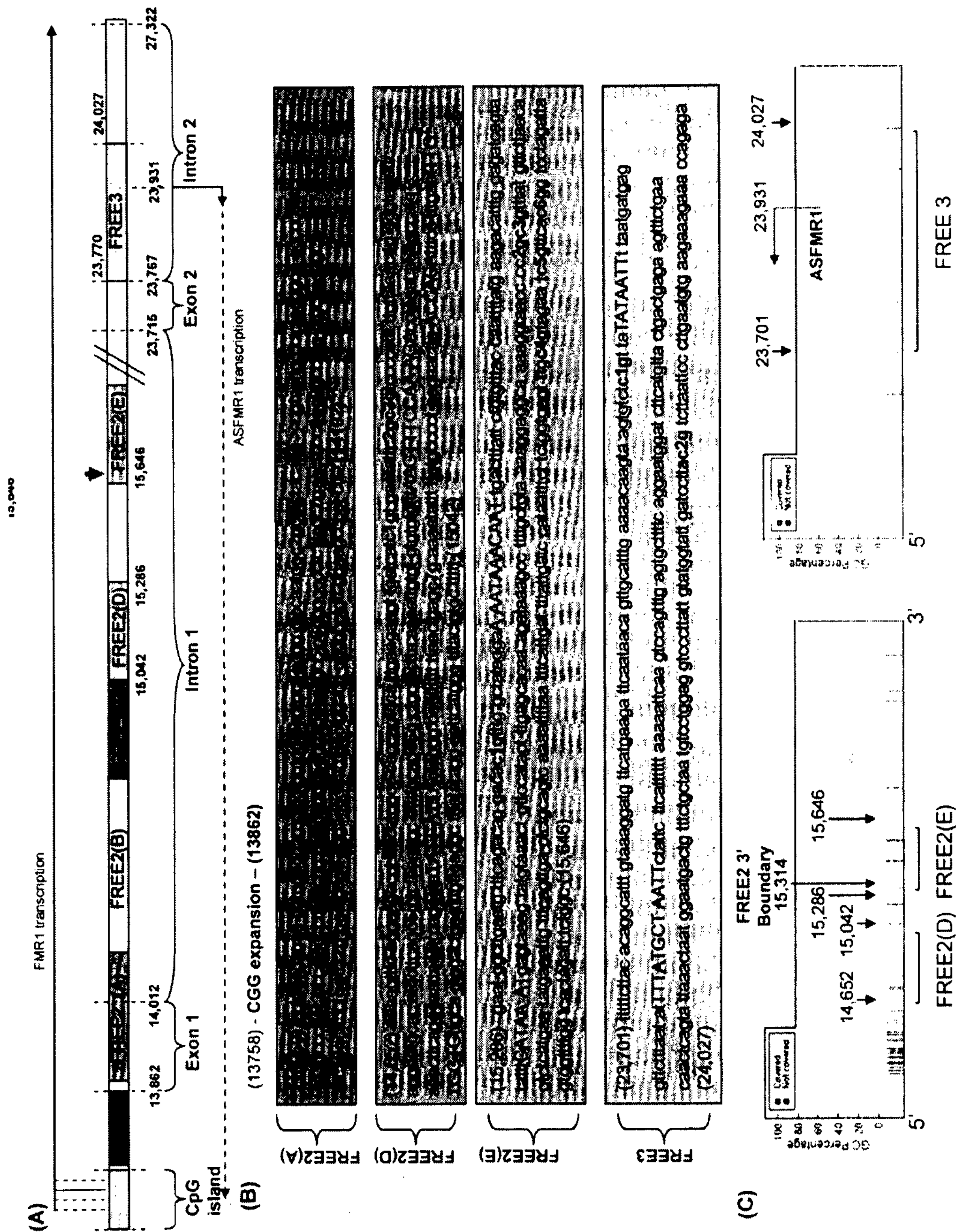

Figure 6

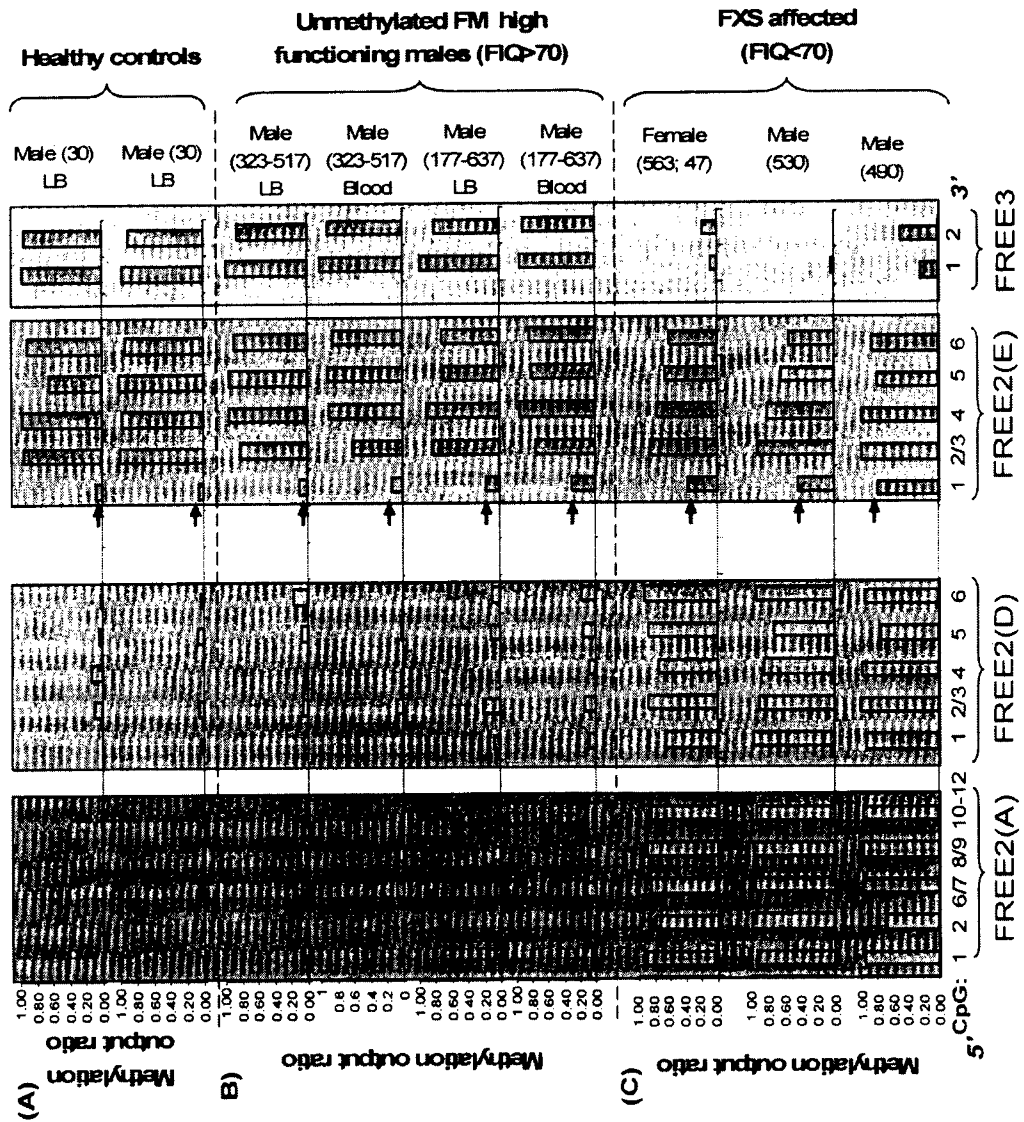

Figure 7

INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU2011/001024

A. CLASSIFICATION OF SUBJECT MATTER

Int. Cl.

C12Q 1/68 (2006.01)

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
GENOMEQUEST – subsequences of SEQ ID 1, 2, 45, 46, 47; EPODOC, WPI, CAPLUS, BIOSIS, MEDLINE – fragile X, fmr, epigenetic, methylation, intron, splice site, and like terms

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	WO 2010/094061 A1 (MURDOCH CHILDRENS RESEARCH INSTITUTE) 26 August 2010 See whole document, particularly claims and Figures 2 and 3	1-8, 15-17, 23
P,X	Godler, D.E. et al, "FMR1 Intron 1 Methylation Predicts FMRP Expression in Blood of Female Carriers of Expanded FMR1 Alleles" Journal of Molecular Diagnostics, 2011, Vol. 13, pps 528-536, published online 30 June 2011 See whole document, particularly abstract, conclusions	1-8, 15-17, 23
X	Godler, D.E. et al, "Methylation of novel markers of fragile X alleles is inversely correlated with FMRP expression and FMR1 activation ratio" Human Molecular Genetics, 2010, Vol. 19, pps 1618-1632, published online 29 January 2010 See whole document, particularly abstract, Fig 3, discussion	1-8, 15-17, 23
P, A	Kumari, D. et al, "The distribution of repressive histone modifications on silenced FMR1 alleles provides clues to the mechanism of gene silencing in fragile X syndrome" Human Molecular Genetics, 2010, Vol. 19, pps 4634-4642, published online 14 September 2010 See whole document, particularly Figures 1 and 2.	

☐ Further documents are listed in the continuation of Box C ☒ See patent family annex

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
04 October 2011	19/10/2011

Name and mailing address of the ISA/AU

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU2011/001024

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [X] Claims Nos.: **9-11, 21, 22, 24**
   because they relate to subject matter not required to be searched by this Authority, namely:
   (see supplemental sheet)

2. [ ] Claims Nos.:
   because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
   (see supplemental sheet)

3. [ ] Claims Nos.:
   because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
(see supplemental sheet)

1. [ ] As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. [X] As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.
3. [ ] As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. [ ] No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

[ ] The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

[ ] The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

[ ] No protest accompanied the payment of additional search fees.

Supplemental Box
(To be used when the space in any of Boxes I to IV is not sufficient)

Continuation of Box No: II – Observations where certain claims have been found unsearchable

Claims 9-11 are directed to the "use of an epigenetic profile" in the "manufacture of an assay". Since the epigenetic profile only consists of information, and no steps in the "manufacture of an assay" are actually defined, these claims are construed to be directed to the use of information in the design of an assay, which is a mental act and does not produce a defined useful, concrete or tangible result, and therefore excluded from international search and examination pursuant to PCT rule 39.1(iii).

Claims 21, 22 and 24 are directed to computers, computer programs and data processing methods. These programs merely carry out correlation of information, which do not produce a useful, concrete or tangible result, and are therefore excluded from international search and examination pursuant to PCT rule 39.1(vi).

Continuation of Box No: III – Lack of unity of invention
This International Application does not comply with the requirements of unity of invention because it does not relate to one invention or to a group of inventions so linked as to form a single general inventive concept.

This Authority has found that there are different inventions based on the following features that separate the claims into distinct groups:

- Invention 1: Claims 1-24 (each in part) characterised by determining epigenetic modification of FREE3 in FMR1
- Invention 2: As invention 1, but with respect to intron 2 in FMR1.
- Invention 3: As invention 1 but with respect to the genomic FREE2 region as a whole
- Invention 4: As invention 1 but with respect to FREE2 (D)
- Invention 5: As invention 1 but with respect to FREE2 (E)

PCT Rule 13.2, first sentence, states that unity of invention is only fulfilled when there is a technical relationship among the claimed inventions involving one or more of the same or corresponding special technical features. PCT Rule 13.2, second sentence, defines a special technical feature as a feature which makes a contribution over the prior art. When there is no special technical feature common to all the claimed inventions there is no unity of invention.

In the above groups of claims, the identified features may have the potential to make a contribution over the prior art but are not common to all the claimed inventions and therefore cannot provide the required technical relationship. The only feature common to all of the claimed inventions and which provides a technical relationship among them is determining the methylation status of an intron of FMR1 However this feature does not make a contribution over the prior art because it is disclosed in:

Godler et al (2010) Human Molecular Genetics vol. 19, pps 1618-1632

Therefore in the light of this document this common feature cannot be a special technical feature. Therefore there is no special technical feature common to all the claimed inventions and the requirements for unity of invention are consequently not satisfied *a posteriori*. Since it was possible to search all of these inventions with negligible additional effort, this search will cover the subject matter of all inventions.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No.
PCT/AU2011/001024

This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report		Patent Family Member
WO	2010094061	NONE

Due to data integration issues this family listing may not include 10 digit Australian applications filed since May 2001.

END OF ANNEX