CLAIMS:

1. A method of making a DNA methylation array comprising a plurality of polynucleotides coupled to a matrix, wherein the plurality of polynucleotides are selected by a method comprising:

(a) performing a polynucleotide sequence alignment comprising comparing a human genome with a plurality of non-human mammalian genomes to identify polynucleotide sequences in the human genome comprising CpG methylation sites that are homologous to polynucleotide sequences within genomes of non-human mammalian species comprising CpG methylation sites;

(b) ranking the polynucleotide sequences in the human genome identified in (a), wherein the ranking criteria comprises sequence homology to polynucleotide sequences in genomes of non-human mammalian species; and

(c) using the ranking in (b) to select a plurality of polynucleotides in the human genome that cross hybridize to a plurality of polynucleotide sequences in the genomes of non-human mammalian species; and

(d) coupling selected sequences from step (c) to a matrix so as to form a DNA methylation array.

2. The method of claim 1, wherein the plurality of polynucleotides in the human genome are selected to have not more than a 3 base pair mismatch with polynucleotide sequences in genomes of non-human mammalian species.

3. The method of claim 2, wherein the ranking comprises homology comparisons to genomic polynucleotide sequences in non-placental mammalian species, and placental mammalian species in the Laurasiatheria, Euarchontoglires, Xenarthra and Afrotheria superordinal groups.

4. The method of claim 3, wherein the sequence alignment compares human genomic sequences with genomic sequences of at least 10 non-human mammalian species.

5. The method of claim 1, wherein the DNA methylation array comprises at least 30,000 unique polynucleotides coupled to the matrix.

6. The method of claim 5, wherein the 30,000 unique polynucleotides are between 40-80 nucleotides in length.

7. The method of claim 1, wherein the matrix is a bead or a chip.

8. A method of making a DNA methylation array comprising a plurality of polynucleotides coupled to a matrix, wherein each of the plurality of polynucleotides:

(a) comprise:

a CpG motif;

at least 2,000 unique polynucleotide sequences that hybridize to a 60 nucleotide segment in genomic polynucleotide sequences of a marsupial mammalian species, a monotreme mammalian species, a Laurasiatheria mammalian species, a Euarchontoglires mammalian species, a Xenarthra mammalian species and an Afrotheria mammalian species with less than a 3 base pair mismatch; and

(b) are selected by:

(i) performing a polynucleotide sequence alignment comparing a human genome with a plurality of non-human mammalian genomes to identify polynucleotide sequences in the human genome comprising CpG methylation sites that are homologous to polynucleotide sequences comprising CpG methylation sites within genomes of non-human mammalian species;

(ii) ranking the polynucleotide sequences in the human genome identified in (b), wherein the ranking criteria comprises a degree of sequence homology to polynucleotide sequences in the genomes of non-human mammalian species; and

(iii) using the ranking in (ii) to select a plurality of polynucleotides having CpG methylation sites that cross hybridize to a plurality of polynucleotide sequences having CpG methylation sites in the genomes of non-human mammalian species with not more than a 3 base pair mismatch; and

(c) coupling selected sequences from step (b) to a matrix so as to form a DNA methylation array;

so that the DNA methylation array is made.

9. A DNA methylation array comprising a plurality of polynucleotide sequences coupled to a matrix, wherein:

the polynucleotides comprise at least 40 nucleotides and a CpG motif at their terminal ends;

the polynucleotides comprise polynucleotide sequences present in a human genome; and:

at least 2,000 polynucleotides within the plurality of polynucleotide sequences can hybridize to a 40 nucleotide segment in genomic polynucleotide sequences of a marsupial mammalian species with less than a 3 base pair mismatch;

at least 2,000 polynucleotides within the plurality of polynucleotide sequences can hybridize to a 40 nucleotide segment in genomic polynucleotide sequences of a monotreme mammalian species with less than a 3 base pair mismatch;

at least 2,000 polynucleotides within the plurality of polynucleotide sequences can hybridize to a 40 nucleotide segment in genomic polynucleotide sequences of a Laurasiatheria mammalian species with less than a 3 base pair mismatch;

at least 2,000 polynucleotides within the plurality of polynucleotide sequences can hybridize to a 40 nucleotide segment in genomic polynucleotide sequences of a Euarchontoglires mammalian species with less than a 3 base pair mismatch;

at least 2,000 polynucleotides within the plurality of polynucleotide sequences can hybridize to a 40 nucleotide segment in genomic polynucleotide sequences of a Xenarthra mammalian species with less than a 3 base pair mismatch; and

at least 2,000 polynucleotides within the plurality of polynucleotide sequences can hybridize to a 40 nucleotide segment in genomic polynucleotide sequences of a Afrotheria mammalian species with less than a 3 base pair mismatch.

10. The DNA methylation array of claim 9, wherein:

the marsupial mammalian species is a Wallaby species; and/or

the monotreme mammalian species is a Platypus species; and/or

the Laurasiatheria mammalian species is a bat species; and/or

the Euarchontoglires mammalian species is a rodent species; and/or

the Xenarthra mammalian species is an armadillo species; and/or

the Afrotheria mammalian species is a tenrec species.

11. The DNA methylation array of any one of claims 9-10, wherein at least one polynucleotide within the plurality of polynucleotides is a polynucleotide having a sequence selected from SEQ ID NO: 1-SEQ ID NO: 50.

12. A method of observing a methylation profile in a non-human mammal comprising:

(a) obtaining genomic DNA from the non-human mammal;

(b) observing cytosine methylation of a plurality CG loci in the genomic DNA using a DNA methylation array of any one of claims 9-12; wherein at least one

observed polynucleotide within the plurality of polynucleotides is a polynucleotide having a sequence selected from SEQ ID NO: 1-SEQ ID NO: 50;

so that a methylation profile in the non-human mammal is observed.

13. The method of claim 12, further comprising:

(c) comparing the CG locus methylation observed in (b) to the CG locus methylation observed in genomic DNA derived from individuals in the non-human mammal species having known ages; and

(d) correlating the CG locus methylation observed in (b) with the known ages of the non-human mammal species;

so that information useful to determine the age of the non-human mammal is obtained.

14. The method of claim 12, wherein:

methylation is observed by a process comprising treatment of genomic DNA from the population of cells from the mammals with bisulfite to transform unmethylated cytosines of CpG dinucleotides in the genomic DNA to uracil;

the DNA methylation array is used to observe methylation profiles in a plurality of non-human mammalian species; and/or

genomic DNA is amplified by a polymerase chain reaction process.

15. A method of observing the effects of a test agent on genomic methylation associated epigenetic aging of mammalian cells, the method comprising:

(a) combining the test agent with mammalian cells;

(b) observing methylation status of methylation markers in genomic DNA from the mammalian cells using a DNA methylation array of any one of claims 9-12; wherein at least one observed polynucleotide within the plurality of polynucleotides is a polynucleotide having a sequence selected from SEQ ID NO: 1-SEQ ID NO: 50;

(c) comparing the observations from (b) with observations of the methylation status in genomic DNA from control mammalian cells not exposed to the test agent such that effects of the test agent on genomic methylation associated epigenetic aging in the mammalian cells is observed.

16. The method of claim 15, wherein a plurality of test agents are combined with the mammalian cells.

17. The method of claim 15, wherein the cells are human primary keratinocytes.

18. The method of claim 15, wherein the test agent is a compound having a molecular weight less than 3,000 g/mol, 2,000 g/mol, 1,000 g/mol or 500 g/mol.

19. The method of claim 15, wherein:

methylation is observed by a process comprising treatment of genomic DNA from the population of cells from the mammals with bisulfite to transform unmethylated cytosines of CpG dinucleotides in the genomic DNA to uracil; and/or

genomic DNA is amplified by a polymerase chain reaction process.