Claims:

1. A method of identifying a modified cytosine residue in a sample nucleotide sequence, the method comprising;

(i) providing a population of polynucleotides which comprise the sample nucleotide sequence,

(ii) reducing and deaminating a 5-methylcytosine (5mC) residue within the population,

(iii) sequencing the polynucleotides in the population or derivatives thereof following step (ii) to produce a treated nucleotide sequence, and;

(iv) identifying the residue in the treated nucleotide sequence which corresponds to a modified cytosine residue in the sample nucleotide sequence.

2. The method of claim 1, wherein the reduction is the reduction of the C5-C6 bond in a modified cytosine residue, and the deamination is the loss of the amino group at the C4 position in a modified cytosine residue, which is replaced with hydroxyl.

3. The method of claim 1 or claim 2, wherein the presence of a thymine residue in the treated nucleotide sequence is indicative that the modified cytosine residue in the sample nucleotide sequence is 5-methylcytosine (5mC).

4. A method of identifying 5-methylcytosine (5mC) or 5-carboxylcytosine (5caC) in a sample nucleotide sequence, the method comprising:

(i) providing a population of polynucleotides which comprise the sample nucleotide sequence,

(ii) treating the population with a radical initiator,

(iii) sequencing the polynucleotides in the population or derivatives thereof following step (ii) to produce a treated nucleotide sequence, and;

(iv) identifying the residue in the treated nucleotide sequence which corresponds to a modified cytosine residue in the sample nucleotide sequence,

wherein the presence of a thymine residue in the treated nucleotide sequence is indicative that the modified cytosine residue in the sample nucleotide sequence is 5-methylcytosine (5mC) or 5-carboxylcytosine (5caC).

5. A method of identifying a modified cytosine residue in a sample nucleotide sequence, the method comprising:

(i) providing a population of polynucleotides which comprise the sample nucleotide sequence,

(ii) oxidising a first portion of said population,

(iii) treating the oxidised first portion of said population with a radical initiator,

(iv) sequencing the polynucleotides in the first portions of the population or derivatives thereof following steps ii) and iii) to produce a first nucleotide sequence, and;

(v) identifying the residue in the first nucleotide sequences which corresponds to a modified cytosine residue in the sample nucleotide sequence.

6. The method of claim 5, wherein in step (ii), the oxidation is the oxidation of a C5 methyl group in a modified cytosine residue, and optionally wherein the oxidation is an oxidation by a ten-eleven-translocation (TET) oxygenase, such as an oxygenase selected from TET1, TET2 and TET3.

7. A method for modifying a polynucleotide, the method comprising converting a 5-methylcytosine (5mC) residue in a polynucleotide to a dihydrothymine (DHT) residue.

8. Use of a radical initiator to convert a 5-methylcytosine (5mC) residue in a polynucleotide to a dihydrothymine (DHT) residue, or to convert a 5-carboxylcytosine (5caC) residue in a polynucleotide to a dihydrouracil (DHU) residue.

9. The method or use according to any one of claims 4 to 8, wherein the radical initiator is a transition metal photocatalyst.

10. The method or use according to claim 9, wherein the transition metal photocatalyst is an iridium photocatalyst, wherein the iridium photocatalyst comprises $[Ir(dF(CF_3)ppy)_2(dtbpy)]^+$, such as the radical initiator $[Ir(dF(CF_3)ppy)_2(dtbpy)]Cl$.

11. The method or use according to any one of claims 4 to 10, wherein the radical initiator is provided together with a thiol compound, and/or the disulfide form thereof.

12. The method or use according to claim 11, wherein the thiol compound has one, two or three thiol groups, such as one, and the thiol compound optionally has one, two or three hydroxyl groups, such as one.

13. The method or use according to claim 12, wherein the thiol is an alkyl thiol.

14. The method or use according to claim 11, wherein the thiol is mercaptoethanol.

15. The method according to claim 5, wherein, in step (ii), the first portion of the polynucleotide is treated with a ten-eleven translocation (TET) dioxygenase.

16. The method or use according to any one of claims 1 to 15, wherein:

(i) the polynucleotides are genomic DNA, such as mammalian genomic DNA; or

(ii) the polynucleotides are RNA, such as wherein the RNA is genomic RNA, mRNA, tRNA, rRNA or non-coding RNA, such as mammalian, plant or viral genomic RNA.

17. The method or use according to any one of claims 1 to 16, wherein the population of polynucleotides or a portion of the population are immobilised.

18. The method or use according to any one of claims 1 to 17, wherein a portion of the population is amplified before sequencing.

19. The method or use according to claim 18, wherein a portion of the population is amplified following treatment with the radical initiator.

20. A kit for use in a method of identifying a modified cytosine residue according to any one of claims 1 to 19 comprising:

(a) a radical initiator, such as a transition metal photocatalyst, such as $[Ir(dF(CF_3)ppy)_2(dtbpy)]Cl$; and

(b) a nucleophile, such as a thiol compound, such as mercaptoethanol.