CLAIMS

1. A panel of isolated polynucleotides comprising, consisting of, or consisting essentially of at least two isolated polynucleotides, each of said isolated polynucleotides having a polynucleotide sequence of any of Target 1 to Target 1849 listed in Table 1, or a complementary or substantially complementary sequence thereof.

2. The panel of claim 1, which comprises, consists of, or consists essentially of at least 10, 50, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1,000, 1,100, 1,200, 1,300, 1,400, 1,500, 1,600, 1,700, 1,800, more of the isolated polynucleotides, or the isolated polynucleotides corresponding to all of Target 1 to Target 1849 listed in Table 1.

3. The panel of claim 1 or 2, which comprises at least 10, 50, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1,000, 1,100, 1,200, 1,300, 1,400, 1,500, 1,600, 1,700, 1,800, more of the isolated polynucleotides, or the isolated polynucleotides corresponding to all of Target 1 to Target 1849 listed in Table 1.

4. The panel of claim 1 or 2, which consists of at least 10, 50, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1,000, 1,100, 1,200, 1,300, 1,400, 1,500, 1,600, 1,700, 1,800, more of the isolated polynucleotides, or the isolated polynucleotides corresponding to all Target 1 to Target 1849 listed in Table 1.

5. The panel of claim 1 or 2, which consists essentially of at least 10, 50, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1,000, 1,100, 1,200, 1,300, 1,400, 1,500, 1,600, 1,700, 1,800, or more of the isolated polynucleotides, or the isolated polynucleotides corresponding to all of Target 1 to Target 1849 listed in Table 1.

6. A kit or system, which comprises reagents for assessing methylation status of at least two of Target 1 to Target 1849 listed in Table 1.

7. The kit or system of claim 6, which comprises reagents for assessing methylation status of at least 10, 50, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1,000, 1,100, 1,200, 1,300, 1,400, 1,500, 1,600, 1,700, 1,800, or all of Target 1 to Target 1849 listed in Table 1.

8. The kit or system of claim 6 or 7, wherein the reagents comprise, consist essentially of, or consist of a probe or primer configured for hybridizing with each of the targets whose methylation status is to be assessed.

9. The kit or system of claim 8, wherein the reagents comprise, consist essentially of, or consist of a single probe or primer configured for hybridizing with each of the targets whose methylation status is to be assessed.

10. The kit or system of claim 8, wherein the reagents comprise, consist essentially of, or consist of multiple probes or primers configured for hybridizing with each of the targets whose methylation status is to be assessed.

11. A method for assessing cancer or neoplasia in a subject, which method comprises:

a) providing a sample from a subject containing at least two target polynucleotides of said subject, said at least two target polynucleotides having polynucleotide sequences of at least two of Target 1 to Target 1849 listed in Table 1, or a complementary or substantially complementary sequence thereof;

b) assessing methylation status of said at least two target polynucleotides; and

c) assessing cancer or neoplasia in said subject based on assessment of methylation status of said at least two target polynucleotides.

12. The method of claim 11, wherein the sample comprises circulating cell-free or tumor DNA (ctDNA).

13. The method of claim 11 or 12, wherein the sample is a blood, serum, plasma, or body fluid sample, or any combination thereof.