WHAT IS CLAIMED IS:

1. A method for detecting or predicting Mantle phenotype in an oil palm plant, the method comprising:

a) obtaining a biological sample from the plant;

b) detecting an increase or decrease in the methylation status of at least one cytosine within a differential methylation region (DMR) in the sample from the plant relative to a control locus, wherein the DMR is within a sequence of DNA at least 95% identical to SEQ ID NO:66; and

c) physically separating a plant predicted to have the Mantle phenotype from one or more plants predicted to lack the Mantle phenotype based on the detected methylation status.

2. The method of claim 1, wherein the physically separating comprises selecting plants predicted to have Mantle phenotype for destruction.

3. The method of claim 1, wherein the physically separating comprises selecting plants predicted to lack Mantle phenotype for cultivation.

4. The method of claim 3, wherein the plants selected for cultivation are planted or transplanted.

5. The method of claim 3, wherein the plants not selected for cultivation are discarded or destroyed.

6. The method of claim 3, wherein the plants not selected for cultivation are treated to reduce the likelihood of Mantle phenotype.

7. The method of claim 1, wherein the at least one cytosine is a first cytosine in a CHG sequence, wherein H is C, A, or T.

8. The method of claim 1, wherein the DMR is within a DNA region in the sample from the plant, and wherein the DNA region is at least 95% identical to SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, or SEQ ID NO: 46.

9. The method of claim 1, wherein the method comprises predicting the presence of Mantle phenotype when the methylation status of the at least one cytosine is reduced relative to a control locus.

10. The method of claim 9, wherein the control locus is an endogenous control locus.

11. The method of claim 9, wherein the control locus is an exogenous control locus.

12. The method of claim 1, wherein the detecting an increase or decrease in the methylation status comprises bisulfite conversion.

13. The method of claim 1, wherein the detecting an increase or decrease in the methylation status comprises digesting genomic DNA with a methylation-dependent endonuclease.

14. The method of claim 1, wherein the detecting an increase or decrease in the methylation status comprises digesting genomic DNA with a methylation-sensitive endonuclease.