**Claims**

1. A method for predicting palm oil yield of a test oil palm plant, the method comprising the steps of:

(i) determining, from a sample of a test oil palm plant of a population of oil palm plants, at least a first single nucleotide polymorphism (SNP) genotype of the test oil palm plant, the first SNP genotype corresponding to a first SNP marker, the first SNP marker (a) being located in a first quantitative trait locus (QTL) for a high-oil-production trait and (b) being associated, after stratification and kinship correction, with the high-oil-production trait with a genome-wide $-\log_{10}(p\text{-}value)$ of at least 3.0 in the population or having a linkage disequilibrium $r^2$ value of at least 0.2 with respect to a first other SNP marker that is linked thereto and associated, after stratification and kinship correction, with the high-oil-production trait with a genome-wide $-\log_{10}(p\text{-}value)$ of at least 3.0 in the population;

(ii) comparing the first SNP genotype of the test oil palm plant to a corresponding first reference SNP genotype indicative of the high-oil-production trait in the same genetic background as the population; and

(iii) predicting palm oil yield of the test oil palm plant based on the extent to which the first SNP genotype of the test oil palm plant matches the corresponding first reference SNP genotype,

wherein the first QTL is a region of the oil palm genome corresponding to one of:
(1) QTL region 1, extending from nucleotide 18204491 to 18358401 of chromosome 1;
(2) QTL region 2, extending from nucleotide 18922390 to 19167923 of chromosome 1;
(3) QTL region 3, extending from nucleotide 19188077 to 19685080 of chromosome 1;
(4) QTL region 4, extending from nucleotide 23276098 to 23456770 of chromosome 1;
(5) QTL region 5, extending from nucleotide 26021716 to 26066534 of chromosome 1;
(6) QTL region 6, extending from nucleotide 28110016 to 28234799 of chromosome 1;
(7) QTL region 7, extending from nucleotide 29798161 to 30164329 of chromosome 1;
(8) QTL region 8, extending from nucleotide 30684639 to 31160129 of chromosome 1;
(9) QTL region 9, extending from nucleotide 37811723 to 38637229 of chromosome 1;
(10) QTL region 10, extending from nucleotide 38659012 to 39206652 of chromosome 1;
(11) QTL region 11, extending from nucleotide 39243858 to 39842157 of chromosome 1;
(12) QTL region 12, extending from nucleotide 61305818 to 61572106 of chromosome 1;
(13) QTL region 13, extending from nucleotide 1068379 to 1516571 of chromosome 2;
(14) QTL region 14, extending from nucleotide 1616491 to 2016169 of chromosome 2;
(15) QTL region 15, extending from nucleotide 17637996 to 17959911 of chromosome 2;
(16) QTL region 16, extending from nucleotide 20732085 to 20977490 of chromosome 2;
(17) QTL region 17, extending from nucleotide 31844836 to 31980071 of chromosome 2;
(18) QTL region 18, extending from nucleotide 50449700 to 50857310 of chromosome 2;

(19) QTL region 19, extending from nucleotide 50879601 to 51539414 of chromosome 2;
(20) QTL region 20, extending from nucleotide 52821582 to 52960520 of chromosome 2;
(21) QTL region 21, extending from nucleotide 42585292 to 42728875 of chromosome 3;
(22) QTL region 22, extending from nucleotide 9561644 to 9701199 of chromosome 4;
(23) QTL region 23, extending from nucleotide 12469969 to 13409114 of chromosome 4;
(24) QTL region 24, extending from nucleotide 14672228 to 14789226 of chromosome 4;
(25) QTL region 25, extending from nucleotide 395189 to 842107 of chromosome 5;
(26) QTL region 26, extending from nucleotide 47205529 to 47293291 of chromosome 5;
(27) QTL region 27, extending from nucleotide 48857594 to 48932286 of chromosome 5;
(28) QTL region 28, extending from nucleotide 5943980 to 6002717 of chromosome 6;
(29) QTL region 29, extending from nucleotide 6337822 to 6563232 of chromosome 6;
(30) QTL region 30, extending from nucleotide 6818733 to 7281658 of chromosome 6;
(31) QTL region 31, extending from nucleotide 17578027 to 18209857 of chromosome 6;
(32) QTL region 32, extending from nucleotide 26204516 to 26755007 of chromosome 6;
(33) QTL region 33, extending from nucleotide 36492757 to 36494757 of chromosome 6;
(34) QTL region 34, extending from nucleotide 219790 to 1533149 of chromosome 7;
(35) QTL region 35, extending from nucleotide 8700733 to 9242332 of chromosome 8;
(36) QTL region 36, extending from nucleotide 23767318 to 23957652 of chromosome 8;
(37) QTL region 37, extending from nucleotide 26648547 to 26848102 of chromosome 8;
(38) QTL region 38, extending from nucleotide 606020 to 1309231 of chromosome 9;
(39) QTL region 39, extending from nucleotide 3499347 to 3638435 of chromosome 9;
(40) QTL region 40, extending from nucleotide 28437588 to 28513671 of chromosome 9;
(41) QTL region 41, extending from nucleotide 28581068 to 28912034 of chromosome 9;
(42) QTL region 42, extending from nucleotide 32327318 to 32434321 of chromosome 9;
(43) QTL region 43, extending from nucleotide 32538074 to 32540074 of chromosome 9;
(44) QTL region 44, extending from nucleotide 32775289 to 33054696 of chromosome 9;
(45) QTL region 45, extending from nucleotide 33133902 to 33254107 of chromosome 9;
(46) QTL region 46, extending from nucleotide 15342814 to 15405953 of chromosome 10;
(47) QTL region 47, extending from nucleotide 15933273 to 15943963 of chromosome 11;
(48) QTL region 48, extending from nucleotide 12178551 to 12249693 of chromosome 12;
(49) QTL region 49, extending from nucleotide 2052746 to 2447722 of chromosome 13;
(50) QTL region 50, extending from nucleotide 14345084 to 14709650 of chromosome 13;
(51) QTL region 51, extending from nucleotide 22031000 to 22147560 of chromosome 13;
(52) QTL region 52, extending from nucleotide 23588504 to 24307350 of chromosome 15;
(53) QTL region 53, extending from nucleotide 1511530 to 1596020 of chromosome 16;
(54) QTL region 54, extending from nucleotide 2684531 to 2803682 of chromosome 16;
(55) QTL region 55, extending from nucleotide 5535711 to 5995857 of chromosome 16;

(56) QTL region 56, extending from nucleotide 8379248 to 8554851 of chromosome 16; or
(57) QTL region 57, extending from nucleotide 8883687 to 9269845 of chromosome 16.

2. The method of claim 1, wherein the high-oil-production trait comprises increased oil per palm plant.

3. The method of claim 1, wherein:

the population of oil palm plants comprises an *Ulu Remis dura* x AVROS *pisifera* population;

the first QTL corresponds to one of QTL regions 7, 8, 13, 14, 16, 18, 19, 25, 33, 52, or 54;

step (iii) further comprises applying a genotype model, thereby predicting the palm oil yield of the test oil palm plant; and

the first SNP marker is associated, after stratification and kinship correction, with the high-oil-production trait with a genome-wide $-\log_{10}(p\text{-}value)$ of at least 4.0 in the population or has a linkage disequilibrium $r^2$ value of at least 0.2 with respect to a first other SNP marker that is linked thereto and associated, after stratification and kinship correction, with the high-oil-production trait with a genome-wide $-\log_{10}(p\text{-}value)$ of at least 4.0 in the population.

4. The method of claim 1, wherein:

the population of oil palm plants comprises a *Banting dura* x AVROS *pisifera* population;

the first QTL corresponds to one of QTL regions 1, 3, 4, 5, 6, 9, 10, 11, 12, 21, 26, 27, 28, 29, 30, 31, 32, 34, 35, 36, 37, 38, 40, 41, 42, 43, 44, 47, 49, 50, 51, 53, 55, or 56; and

step (iii) further comprises applying a genotype model, thereby predicting the palm oil yield of the test oil palm plant.

5. The method of claim 1, wherein the test oil palm plant is a *tenera* candidate agricultural production plant.

6. The method of claim 1 , wherein the population of oil palm plants comprises an *Ulu Remis dura* x *Ulu Remis dura* population, an *Ulu Remis dura* x *Banting dura* population, a *Banting dura* x *Banting dura* population, an AVROS *pisifera* x AVROS *tenera* population, an AVROS *tenera* x AVROS *tenera* population, or a combination thereof.

7. The method of claim 1, wherein the test oil palm plant is a plant for mother palm selection and propagation, a plant for introgressed mother palm selection and propagation, or a plant for pollen donor selection and propagation.

8. The method of claim 1, wherein:

step (i) further comprises determining, from the sample of the test oil palm plant, at least a second SNP genotype of the test oil palm plant, the second SNP genotype corresponding to a second SNP marker, the second SNP marker (a) being located in a second QTL for the high-oil-production trait and (b) being associated, after stratification and kinship correction, with the high-oil-production trait with a genome-wide $-\log_{10}(p\text{-}value)$ of at least 3.0 in the population or having a linkage disequilibrium $r^2$ value of at least 0.2 with respect to a second other SNP marker that is linked thereto and associated, after stratification and kinship correction, with the high-oil-production trait with a genome-wide $-\log_{10}(p\text{-}value)$ of at least 3.0 in the population; and

step (ii) further comprises comparing the second SNP genotype of the test oil palm plant to a corresponding second reference SNP genotype indicative of the high-oil-production trait in the same genetic background as the population,

wherein the second QTL corresponds to one of QTL regions 1 to 57, with the proviso that the first QTL and the second QTL correspond to different QTL regions.

9. The method of claim 8, wherein step (iii) further comprises predicting palm oil yield of the test oil palm plant based on the extent to which the second SNP genotype of the test oil palm plant matches the corresponding second reference SNP genotype.

10. A method of selecting a high-palm-oil-yielding oil palm plant for agricultural production of palm oil, the method comprising the steps of:

(a) predicting palm oil yield of a test oil palm plant comprising:

(i) determining, from a sample of a test oil palm plant of a population of oil palm plants, at least a first single nucleotide polymorphism (SNP) genotype of the test oil palm plant, the first SNP genotype corresponding to a first SNP marker, the first SNP marker (a) being located in a first quantitative trait locus (QTL) for a high-oil-production trait and (b) being associated, after stratification and kinship correction, with the high-oil-production trait with a genome-wide $-\log_{10}(p\text{-}value)$ of at least 3.0 in the population or having a linkage disequilibrium $r^2$ value of at least 0.2 with respect to a first other SNP marker that is linked thereto and associated, after stratification and kinship correction, with the high-oil-production trait with a genome-wide $-\log_{10}(p\text{-}value)$ of at least 3.0 in the population;

(ii) comparing the first SNP genotype of the test oil palm plant to a corresponding first reference SNP genotype indicative of the high-oil-production trait in the same genetic background as the population; and

(iii) predicting palm oil yield of the test oil palm plant based on the extent to which the first SNP genotype of the test oil palm plant matches the corresponding first reference SNP genotype,

wherein the first QTL is a region of the oil palm genome corresponding to one of:

(1) QTL region 1, extending from nucleotide 18204491 to 18358401 of chromosome 1;

(2) QTL region 2, extending from nucleotide 18922390 to 19167923 of chromosome 1;

(3) QTL region 3, extending from nucleotide 19188077 to 19685080 of chromosome 1;

(4) QTL region 4, extending from nucleotide 23276098 to 23456770 of chromosome 1;

(5) QTL region 5, extending from nucleotide 26021716 to 26066534 of chromosome 1;

(6) QTL region 6, extending from nucleotide 28110016 to 28234799 of chromosome 1;

(7) QTL region 7, extending from nucleotide 29798161 to 30164329 of chromosome 1;

(8) QTL region 8, extending from nucleotide 30684639 to 31160129 of chromosome 1;

(9) QTL region 9, extending from nucleotide 37811723 to 38637229 of chromosome 1;

(10) QTL region 10, extending from nucleotide 38659012 to 39206652 of chromosome 1;

(11) QTL region 11, extending from nucleotide 39243858 to 39842157 of chromosome 1;

(12) QTL region 12, extending from nucleotide 61305818 to 61572106 of chromosome 1;

(13) QTL region 13, extending from nucleotide 1068379 to 1516571 of chromosome 2;

(14) QTL region 14, extending from nucleotide 1616491 to 2016169 of chromosome 2;

(15) QTL region 15, extending from nucleotide 17637996 to 17959911 of chromosome 2;

(16) QTL region 16, extending from nucleotide 20732085 to 20977490 of chromosome 2;

(17) QTL region 17, extending from nucleotide 31844836 to 31980071 of chromosome 2;

(18) QTL region 18, extending from nucleotide 50449700 to 50857310 of chromosome 2;

(19) QTL region 19, extending from nucleotide 50879601 to 51539414 of chromosome 2;

(20) QTL region 20, extending from nucleotide 52821582 to 52960520 of chromosome 2;

(21) QTL region 21, extending from nucleotide 42585292 to 42728875 of chromosome 3;

(22) QTL region 22, extending from nucleotide 9561644 to 9701199 of chromosome 4;

(23) QTL region 23, extending from nucleotide 12469969 to 13409114 of chromosome 4;

(24) QTL region 24, extending from nucleotide 14672228 to 14789226 of chromosome 4;

(25) QTL region 25, extending from nucleotide 395189 to 842107 of chromosome 5;

(26) QTL region 26, extending from nucleotide 47205529 to 47293291 of chromosome 5;

(27) QTL region 27, extending from nucleotide 48857594 to 48932286 of chromosome 5;

(28) QTL region 28, extending from nucleotide 5943980 to 6002717 of chromosome 6;

(29) QTL region 29, extending from nucleotide 6337822 to 6563232 of chromosome 6;

(30) QTL region 30, extending from nucleotide 6818733 to 7281658 of chromosome 6;

(31) QTL region 31, extending from nucleotide 17578027 to 18209857 of chromosome 6;
(32) QTL region 32, extending from nucleotide 26204516 to 26755007 of chromosome 6;
(33) QTL region 33, extending from nucleotide 36492757 to 36494757 of chromosome 6;
(34) QTL region 34, extending from nucleotide 219790 to 1533149 of chromosome 7;
(35) QTL region 35, extending from nucleotide 8700733 to 9242332 of chromosome 8;
(36) QTL region 36, extending from nucleotide 23767318 to 23957652 of chromosome 8;
(37) QTL region 37, extending from nucleotide 26648547 to 26848102 of chromosome 8;
(38) QTL region 38, extending from nucleotide 606020 to 1309231 of chromosome 9;
(39) QTL region 39, extending from nucleotide 3499347 to 3638435 of chromosome 9;
(40) QTL region 40, extending from nucleotide 28437588 to 28513671 of chromosome 9;
(41) QTL region 41, extending from nucleotide 28581068 to 28912034 of chromosome 9;
(42) QTL region 42, extending from nucleotide 32327318 to 32434321 of chromosome 9;
(43) QTL region 43, extending from nucleotide 32538074 to 32540074 of chromosome 9;
(44) QTL region 44, extending from nucleotide 32775289 to 33054696 of chromosome 9;
(45) QTL region 45, extending from nucleotide 33133902 to 33254107 of chromosome 9;
(46) QTL region 46, extending from nucleotide 15342814 to 15405953 of chromosome 10;
(47) QTL region 47, extending from nucleotide 15933273 to 15943963 of chromosome 11;
(48) QTL region 48, extending from nucleotide 12178551 to 12249693 of chromosome 12;
(49) QTL region 49, extending from nucleotide 2052746 to 2447722 of chromosome 13;
(50) QTL region 50, extending from nucleotide 14345084 to 14709650 of chromosome 13;
(51) QTL region 51, extending from nucleotide 22031000 to 22147560 of chromosome 13;
(52) QTL region 52, extending from nucleotide 23588504 to 24307350 of chromosome 15;
(53) QTL region 53, extending from nucleotide 1511530 to 1596020 of chromosome 16;
(54) QTL region 54, extending from nucleotide 2684531 to 2803682 of chromosome 16;
(55) QTL region 55, extending from nucleotide 5535711 to 5995857 of chromosome 16;
(56) QTL region 56, extending from nucleotide 8379248 to 8554851 of chromosome 16; or
(57) QTL region 57, extending from nucleotide 8883687 to 9269845 of chromosome 16; and

(b) field planting the test oil palm plant for agricultural production of palm oil if the palm oil yield of the test oil palm plant is predicted to be higher than average for the population based on step (a).

11. The method of claim 1, wherein the population of wherein the population of oil palm plants comprises a Ulu Remis *dura* x AVROS *pisifera* population, and the first SNP marker comprises one or more SNP markers as follows:

| | *Ulu Remis dura* x AVROS *pisifera* | | | | | |
|---|---|---|---|---|---|---|
| | Major | Minor | Minor allele | [-$\log_{10}$(*p-value*)] | | |
| SNP No. | allele | allele | frequency | Genotype | Dominant | Recessive |

| | | | | | | |
|---|---|---|---|---|---|---|
| 1 | G | A | 0.1942 | 0.786 | 0.000 | 0.582 |
| 2 | C | A | 0.2818 | 0.101 | 0.389 | 0.107 |
| 3 | G | A | 0.2444 | 0.691 | 0.000 | 0.551 |
| 4 | A | C | 0.1293 | 0.149 | 0.000 | 0.184 |
| 5 | A | G | 0.3062 | 0.164 | 0.144 | 0.314 |
| 6 | G | A | 0.2245 | 0.412 | 0.000 | 0.354 |
| 7 | G | A | 0.3777 | 4.176 | 0.000 | 3.549 |
| 8 | G | A | 0.2644 | 4.049 | 1.325 | 3.287 |
| 9 | A | G | 0.2642 | 4.084 | 1.325 | 3.432 |
| 10 | G | A | 0.2644 | 4.049 | 1.325 | 3.287 |
| 11 | A | G | 0.2648 | 4.577 | 2.375 | 2.907 |
| 12 | G | A | 0.3768 | 4.152 | 0.000 | 3.703 |
| 13 | A | C | 0.3771 | 4.195 | 0.000 | 3.703 |
| 14 | G | A | 0.1479 | 3.954 | 0.000 | 4.016 |
| 15 | A | G | 0.1434 | 4.437 | 0.000 | 4.760 |
| 16 | A | G | 0.3703 | 4.463 | 0.000 | 4.185 |
| 17 | A | G | 0.1671 | 2.798 | 0.000 | 4.050 |
| 18 | G | A | 0.3705 | 4.505 | 0.000 | 4.185 |
| 19 | A | G | 0.3703 | 4.463 | 0.000 | 4.185 |
| 20 | G | A | 0.3706 | 4.520 | 0.000 | 4.185 |
| 21 | A | G | 0.3702 | 4.449 | 0.000 | 4.185 |
| 22 | A | G | 0.2902 | 4.877 | 2.326 | 3.518 |
| 23 | A | G | 0.2221 | 3.674 | 1.963 | 4.739 |
| 24 | G | A | 0.4741 | 5.311 | 4.591 | 2.029 |
| 25 | A | G | 0.3729 | 4.646 | 0.000 | 4.185 |
| 26 | C | A | 0.372 | 4.807 | 0.000 | 4.185 |
| 27 | G | A | 0.3706 | 4.447 | 0.000 | 4.111 |
| 28 | A | G | 0.3387 | 0.961 | 0.000 | 0.907 |
| 29 | A | G | 0.3551 | 0.303 | 0.000 | 0.463 |
| 30 | G | A | 0.1881 | 0.790 | 0.000 | 0.580 |
| 31 | G | A | 0.1816 | 1.554 | 0.000 | 1.674 |
| 32 | G | A | 0.4762 | 0.528 | 0.926 | 0.160 |
| 33 | A | C | 0.3854 | 4.058 | 0.000 | 3.914 |
| 34 | A | G | 0.3851 | 4.127 | 0.000 | 4.097 |
| 35 | A | G | 0.2781 | 4.366 | 2.638 | 2.895 |
| 36 | G | A | 0.2798 | 4.270 | 2.638 | 2.833 |
| 37 | G | A | 0.107 | 0.089 | 0.000 | 0.046 |
| 38 | A | G | 0.3175 | 4.178 | 0.338 | 3.872 |
| 39 | G | A | 0.3888 | 0.341 | 0.097 | 0.284 |
| 40 | A | G | 0.2861 | 0.096 | 0.693 | 0.736 |
| 41 | A | G | 0.2344 | 4.226 | 0.000 | 4.234 |
| 42 | A | G | 0.2196 | 4.862 | 0.000 | 5.001 |
| 43 | A | G | 0.3599 | 4.036 | 0.567 | 4.505 |
| 44 | C | A | 0.3028 | 4.069 | 0.000 | 3.741 |
| 45 | G | A | 0.3028 | 4.112 | 0.000 | 3.741 |
| 46 | A | G | 0.298 | 4.016 | 0.000 | 3.893 |
| 47 | A | C | 0.3028 | 4.069 | 0.000 | 3.741 |
| 48 | G | A | 0.3144 | 0.678 | 0.000 | 0.621 |
| 49 | G | A | 0.4758 | 0.016 | 0.882 | 1.247 |
| 50 | G | A | 0.3392 | 2.800 | 0.000 | 4.692 |
| 51 | G | A | 0.3362 | 2.555 | 0.013 | 4.166 |
| 52 | A | G | 0.3251 | 2.523 | 0.020 | 4.078 |
| 53 | A | G | 0.2283 | 0.029 | 0.119 | 0.187 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 54 | G | A | 0.05629 | 4.061 | 0.000 | 3.915 |
| 55 | G | A | 0.05752 | 4.135 | 0.000 | 3.946 |
| 56 | A | G | 0.2999 | 0.381 | 0.000 | 0.241 |
| 57 | G | A | 0.4367 | 0.280 | 0.000 | 0.328 |
| 58 | C | A | 0.4232 | 0.193 | 0.168 | 0.801 |
| 59 | A | G | 0.4202 | 0.220 | 0.356 | 0.138 |
| 60 | A | G | 0.4638 | 0.957 | 0.499 | 0.833 |
| 61 | A | G | 0.2898 | 0.931 | 0.247 | 0.780 |
| 62 | A | G | 0.2914 | 0.097 | 0.532 | 0.979 |
| 63 | A | G | 0.009465 | 0.000 | 0.000 | 0.000 |
| 64 | G | A | 0.08703 | 0.185 | 0.000 | 0.153 |
| 65 | A | G | 0.08429 | 0.156 | 0.000 | 0.129 |
| 66 | C | A | 0.08463 | 0.142 | 0.000 | 0.080 |
| 67 | G | A | 0.08456 | 0.147 | 0.000 | 0.097 |
| 68 | A | G | 0.08792 | 0.005 | 0.000 | 0.068 |
| 69 | A | G | 0.08785 | 0.009 | 0.000 | 0.052 |
| 70 | C | A | 0.08622 | 0.011 | 0.000 | 0.001 |
| 71 | C | A | 0.08799 | 0.009 | 0.000 | 0.068 |
| 72 | C | A | 0.1127 | 0.294 | 0.000 | 0.345 |
| 73 | A | G | 0.4975 | 4.213 | 0.000 | 0.000 |
| 74 | A | C | 0.3324 | 1.078 | 0.776 | 0.869 |
| 75 | A | G | 0.3411 | 0.046 | 0.000 | 0.214 |
| 76 | C | A | 0.3396 | 0.027 | 0.000 | 0.197 |
| 77 | G | A | 0.3218 | 0.915 | 0.569 | 0.735 |
| 78 | A | G | 0.3303 | 0.608 | 0.448 | 0.523 |
| 79 | C | A | 0.2797 | 0.496 | 0.573 | 0.175 |
| 80 | G | A | 0.07677 | 0.333 | 0.000 | 0.324 |
| 81 | A | G | 0.4811 | 0.318 | 0.193 | 0.932 |
| 82 | G | A | 0.4117 | 0.108 | 0.000 | 0.318 |
| 83 | G | A | 0.4116 | 0.105 | 0.000 | 0.318 |
| 84 | A | G | 0.1602 | 0.038 | 0.000 | 0.070 |
| 85 | A | G | 0.226 | 0.534 | 0.000 | 0.694 |
| 86 | A | G | 0.3699 | 0.433 | 0.469 | 0.010 |
| 87 | G | A | 0.4975 | 1.157 | 0.565 | 0.522 |
| 88 | G | A | 0.07622 | 0.926 | 0.000 | 1.082 |
| 89 | A | G | 0.4035 | 0.107 | 0.038 | 0.258 |
| 90 | G | A | 0.2651 | 0.073 | 0.000 | 0.132 |
| 91 | G | A | 0.2486 | 0.023 | 0.000 | 0.032 |
| 92 | A | G | 0.424 | 0.566 | 0.806 | 0.121 |
| 93 | G | A | 0.2798 | 0.180 | 0.000 | 0.006 |
| 94 | G | A | 0.486 | 0.071 | 0.104 | 0.088 |
| 95 | G | A | 0.2463 | 0.018 | 0.000 | 0.037 |
| 96 | G | A | 0.08694 | 3.808 | 0.000 | 5.308 |
| 97 | G | A | 0.2516 | 0.691 | 0.041 | 0.955 |
| 98 | G | A | 0.01322 | 0.000 | 0.000 | 0.000 |
| 99 | A | G | 0.2227 | 0.479 | 0.000 | 0.367 |
| 100 | A | G | 0.2699 | 0.111 | 0.012 | 0.133 |
| 101 | G | A | 0.3258 | 0.089 | 0.000 | 0.225 |
| 102 | G | A | 0.3269 | 0.095 | 0.000 | 0.205 |
| 103 | G | A | 0.09252 | 0.044 | 0.000 | 0.013 |
| 104 | G | A | 0.09367 | 0.106 | 0.000 | 0.185 |
| 105 | A | G | 0.3265 | 4.527 | 2.439 | 3.206 |
| 106 | A | C | 0.3237 | 4.445 | 2.568 | 3.206 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 107 | C | A | 0.3235 | 4.520 | 2.805 | 3.137 |
| 108 | A | G | 0.3232 | 4.408 | 2.414 | 3.098 |
| 109 | C | A | 0.3248 | 4.509 | 2.805 | 2.990 |
| 110 | A | C | 0.325 | 4.327 | 2.568 | 3.057 |
| 111 | A | G | 0.3366 | 4.087 | 2.982 | 2.335 |
| 112 | G | A | 0.3377 | 4.255 | 3.230 | 2.393 |
| 113 | A | C | 0.02997 | 0.000 | 0.000 | 0.038 |
| 114 | G | A | 0.4376 | 4.244 | 2.827 | 2.149 |
| 115 | A | C | 0.3525 | 1.542 | 0.000 | 1.591 |
| 116 | G | A | 0.3528 | 1.514 | 0.000 | 1.478 |
| 117 | G | A | 0.3531 | 1.528 | 0.000 | 1.478 |
| 118 | A | G | 0.186 | 0.166 | 0.000 | 0.256 |
| 119 | G | A | 0.2685 | 0.218 | 0.470 | 0.020 |

12. The method of claim 1, wherein the population of wherein the population of oil palm plants comprises a Banting *dura* x AVROS *pisifera* population, and the first SNP marker comprises one or more SNP markers as follows:

| | *Banting dura* x AVROS *pisifera* | | | | | |
|---|---|---|---|---|---|---|
| | Major | Minor | Minor allele | [-$\log_{10}$(*p-value*)] | | |
| SNP No. | allele | allele | frequency | Genotype | Dominant | Recessive |
| 1 | G | A | 0.2623 | 3.265 | 0.000 | 2.855 |
| 2 | C | A | 0.3739 | 2.654 | 0.595 | 3.251 |
| 3 | G | A | 0.2298 | 3.023 | 0.000 | 2.532 |
| 4 | A | C | 0.2874 | 3.116 | 1.343 | 2.277 |
| 5 | A | G | 0.3619 | 3.791 | 0.812 | 3.431 |
| 6 | G | A | 0.2986 | 3.623 | 0.000 | 2.987 |
| 7 | G | A | 0.3492 | 0.994 | 0.144 | 1.306 |
| 8 | G | A | 0.3229 | 0.354 | 0.179 | 0.388 |
| 9 | A | G | 0.3548 | 0.237 | 0.411 | 0.099 |
| 10 | G | A | 0.3248 | 0.060 | 0.146 | 0.080 |
| 11 | A | G | 0.3282 | 0.457 | 0.377 | 0.374 |
| 12 | G | A | 0.2987 | 0.827 | 0.350 | 0.728 |
| 13 | A | C | 0.2697 | 0.363 | 0.030 | 0.489 |
| 14 | G | A | 0.2994 | 0.125 | 0.374 | 0.049 |
| 15 | A | G | 0.2372 | 0.695 | 0.000 | 0.928 |
| 16 | A | G | 0.3076 | 0.697 | 0.049 | 0.992 |
| 17 | A | G | 0.2963 | 0.203 | 0.114 | 0.490 |
| 18 | G | A | 0.3013 | 0.803 | 0.081 | 1.029 |
| 19 | A | G | 0.3459 | 1.079 | 0.509 | 0.955 |
| 20 | G | A | 0.3059 | 0.976 | 0.064 | 1.293 |
| 21 | A | G | 0.3365 | 0.714 | 0.375 | 0.643 |
| 22 | A | G | 0.2995 | 0.136 | 0.493 | 0.026 |
| 23 | A | G | 0.3365 | 0.689 | 0.614 | 0.879 |
| 24 | G | A | 0.486 | 0.996 | 0.374 | 1.275 |
| 25 | A | G | 0.3534 | 0.917 | 0.982 | 0.501 |
| 26 | C | A | 0.3243 | 0.654 | 0.271 | 0.633 |
| 27 | G | A | 0.3012 | 0.637 | 0.002 | 0.858 |
| 28 | A | G | 0.3374 | 3.162 | 0.000 | 3.143 |
| 29 | A | G | 0.3404 | 3.445 | 0.000 | 3.243 |
| 30 | G | A | 0.15 | 3.089 | 0.000 | 2.924 |
| 31 | G | A | 0.1774 | 3.104 | 0.000 | 2.984 |

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|---|---|---|---|---|---|---|
| 32 | A | G | 0.4897 | 3.456 | 2.348 | 2.018 |
| 33 | A | C | 0.2748 | 0.895 | 0.000 | 0.662 |
| 34 | A | G | 0.2787 | 1.036 | 0.000 | 0.797 |
| 35 | A | G | 0.3009 | 0.213 | 0.000 | 0.587 |
| 36 | G | A | 0.2641 | 0.193 | 0.000 | 0.432 |
| 37 | G | A | 0.2491 | 2.776 | 0.000 | 3.010 |
| 38 | A | G | 0.3444 | 0.325 | 0.435 | 0.384 |
| 39 | A | G | 0.4843 | 2.576 | 3.224 | 0.337 |
| 40 | A | G | 0.4543 | 2.096 | 0.056 | 3.390 |
| 41 | A | G | 0.3021 | 1.270 | 0.000 | 1.303 |
| 42 | A | G | 0.1542 | 1.258 | 0.000 | 1.264 |
| 43 | A | G | 0.3694 | 0.637 | 0.000 | 1.126 |
| 44 | C | A | 0.2658 | 0.010 | 0.000 | 0.103 |
| 45 | G | A | 0.2725 | 0.009 | 0.000 | 0.080 |
| 46 | A | G | 0.2429 | 0.114 | 0.000 | 0.208 |
| 47 | A | C | 0.2748 | 0.089 | 0.000 | 0.026 |
| 48 | G | A | 0.4652 | 2.710 | 3.105 | 0.942 |
| 49 | A | G | 0.465 | 3.064 | 2.714 | 0.812 |
| 50 | G | A | 0.135 | 0.045 | 0.000 | 0.094 |
| 51 | G | A | 0.4989 | 0.270 | 0.223 | 0.072 |
| 52 | A | G | 0.4494 | 0.048 | 0.207 | 0.090 |
| 53 | A | G | 0.1172 | 2.775 | 2.189 | 3.043 |
| 54 | G | A | 0.03162 | 0.000 | 0.000 | 0.096 |
| 55 | G | A | 0.03404 | 0.000 | 0.000 | 0.013 |
| 56 | A | G | 0.2519 | 3.246 | 0.000 | 3.351 |
| 57 | G | A | 0.3905 | 3.105 | 0.000 | 3.123 |
| 58 | A | C | 0.4693 | 3.112 | 0.595 | 3.973 |
| 59 | G | A | 0.4683 | 2.873 | 0.518 | 3.798 |
| 60 | A | G | 0.4401 | 3.393 | 0.525 | 3.706 |
| 61 | A | G | 0.2503 | 3.041 | 1.107 | 3.878 |
| 62 | A | G | 0.2056 | 3.408 | 0.000 | 2.918 |
| 63 | A | G | 0.06136 | 3.522 | 0.000 | 2.879 |
| 64 | G | A | 0.1656 | 3.298 | 0.000 | 4.769 |
| 65 | A | G | 0.1005 | 3.213 | 0.000 | 3.574 |
| 66 | C | A | 0.09914 | 2.982 | 0.000 | 3.299 |
| 67 | G | A | 0.1011 | 3.655 | 0.000 | 4.055 |
| 68 | A | G | 0.1368 | 3.082 | 0.000 | 4.459 |
| 69 | A | G | 0.1392 | 2.746 | 0.000 | 4.014 |
| 70 | C | A | 0.1278 | 2.612 | 0.000 | 3.679 |
| 71 | C | A | 0.1358 | 3.603 | 0.000 | 5.045 |
| 72 | C | A | 0.117 | 3.610 | 0.000 | 3.056 |
| 73 | A | G | 0.4297 | 1.141 | 0.000 | 1.170 |
| 74 | C | A | 0.4316 | 3.146 | 0.537 | 3.075 |
| 75 | A | G | 0.1294 | 3.023 | 0.000 | 3.303 |
| 76 | C | A | 0.1176 | 2.831 | 0.000 | 3.060 |
| 77 | A | G | 0.4745 | 3.033 | 0.859 | 2.665 |
| 78 | G | A | 0.4323 | 4.061 | 1.461 | 3.467 |
| 79 | C | A | 0.3158 | 3.109 | 0.708 | 2.867 |
| 80 | G | A | 0.1511 | 3.395 | 0.000 | 3.078 |
| 81 | A | G | 0.3742 | 3.446 | 1.352 | 2.500 |
| 82 | G | A | 0.3969 | 3.035 | 1.267 | 2.490 |
| 83 | G | A | 0.393 | 3.105 | 1.893 | 2.222 |
| 84 | A | G | 0.04615 | 2.824 | 0.000 | 3.011 |

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|---|---|---|---|---|---|---|
| 85 | A | G | 0.1096 | 3.046 | 0.000 | 2.998 |
| 86 | G | A | 0.4871 | 3.230 | 2.054 | 1.424 |
| 87 | A | G | 0.3754 | 3.094 | 0.000 | 2.940 |
| 88 | G | A | 0.3428 | 2.449 | 1.303 | 3.167 |
| 89 | G | A | 0.4143 | 3.246 | 2.085 | 2.857 |
| 90 | G | A | 0.2958 | 3.082 | 0.000 | 1.986 |
| 91 | G | A | 0.3079 | 4.780 | 0.000 | 3.484 |
| 92 | G | A | 0.366 | 3.297 | 1.127 | 2.702 |
| 93 | G | A | 0.3243 | 3.514 | 0.000 | 2.799 |
| 94 | A | G | 0.4797 | 4.020 | 2.057 | 2.708 |
| 95 | G | A | 0.3013 | 3.288 | 0.000 | 3.326 |
| 96 | G | A | 0.2923 | 0.611 | 0.819 | 0.143 |
| 97 | G | A | 0.1317 | 2.188 | 0.000 | 3.691 |
| 98 | G | A | 0.07538 | 3.085 | 2.664 | 3.106 |
| 99 | A | G | 0.2421 | 2.213 | 0.000 | 3.363 |
| 100 | A | G | 0.4808 | 4.061 | 4.679 | 1.003 |
| 101 | G | A | 0.3077 | 3.114 | 0.000 | 3.197 |
| 102 | G | A | 0.2999 | 3.002 | 0.000 | 2.983 |
| 103 | G | A | 0.1898 | 3.015 | 0.000 | 3.094 |
| 104 | G | A | 0.1857 | 3.316 | 0.000 | 3.452 |
| 105 | A | G | 0.2288 | 0.416 | 0.000 | 0.005 |
| 106 | A | C | 0.2284 | 0.234 | 0.000 | 0.097 |
| 107 | C | A | 0.23 | 0.025 | 0.000 | 0.362 |
| 108 | A | G | 0.2286 | 0.140 | 0.000 | 0.203 |
| 109 | C | A | 0.2809 | 0.012 | 0.405 | 0.196 |
| 110 | A | C | 0.2781 | 0.007 | 0.459 | 0.201 |
| 111 | A | G | 0.2793 | 0.054 | 0.459 | 0.134 |
| 112 | G | A | 0.2753 | 0.175 | 0.497 | 0.505 |
| 113 | A | C | 0.07273 | 3.103 | 0.000 | 2.982 |
| 114 | A | G | 0.4569 | 0.372 | 0.055 | 0.512 |
| 115 | C | A | 0.3662 | 2.379 | 3.005 | 0.712 |
| 116 | A | G | 0.372 | 3.171 | 3.225 | 1.185 |
| 117 | A | G | 0.3766 | 3.711 | 3.404 | 1.562 |
| 118 | A | G | 0.3786 | 3.448 | 0.000 | 3.484 |
| 119 | G | A | 0.4838 | 2.233 | 0.125 | 3.937 |