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 7.0 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 7.0 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 1516571 to 4215826 of chromosome 2;
(2) QTL region 2, extending from nucleotide 4858549 to 5594262 of chromosome 2;
(3) QTL region 3, extending from nucleotide 33949264 to 34110104 of chromosome 2;
(4) QTL region 4, extending from nucleotide 43405853 to 43834266 of chromosome 3;
(5) QTL region 5, extending from nucleotide 44126148 to 44193097 of chromosome 3;
(6) QTL region 6, extending from nucleotide 30702027 to 31148630 of chromosome 4;
(7) QTL region 7, extending from nucleotide 33166529 to 33451554 of chromosome 4;
(8) QTL region 8, extending from nucleotide 35906266 to 36257708 of chromosome 7;
(9) QTL region 9, extending from nucleotide 29233675 to 29612202 of chromosome 10;
(10) QTL region 10, extending from nucleotide 13470988 to 13734716 of chromosome 11;
(11) QTL region 11, extending from nucleotide 24620951 to 24989005 of chromosome 13; or
(12) QTL region 12, extending from nucleotide 6941783 to 7160542 of chromosome 15.

2. The method of claim 1, wherein the high-oil-production trait comprises decreased shell-to-fruit, increased mesocarp-to-fruit, or a combination thereof, in *tenera* oil palm plants.

3. The method of claim 1, wherein:

the first QTL corresponds to one of QTL regions 1, 2, 3, 4, 5, 6, 7, or 10;

the high-oil-production trait comprises decreased shell-to-fruit; and

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

4. The method of claim 1, wherein:

the first QTL corresponds to one of QTL regions 1, 8, 9, 11, or 12;

the high-oil-production trait comprises increased mesocarp-to-fruit; 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 first QTL corresponds to QTL region 1;

the high-oil-production trait comprises decreased shell-to-fruit and increased mesocarp-to-fruit; and

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

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

7. 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 7.0 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 7.0 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 12, with the proviso that the first QTL and the second QTL correspond to different QTL regions.

8. The method of claim 7, 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.

9. 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 -log10(p-value) of at least 7.0 in the population or having a linkage disequilibrium r2 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 -log10(p-value) of at least 7.0 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 1516571 to 4215826 of chromosome 2;

(2) QTL region 2, extending from nucleotide 4858549 to 5594262 of chromosome 2;

(3) QTL region 3, extending from nucleotide 33949264 to 34110104 of chromosome 2;

(4) QTL region 4, extending from nucleotide 43405853 to 43834266 of chromosome 3;

(5) QTL region 5, extending from nucleotide 44126148 to 44193097 of chromosome 3;

(6) QTL region 6, extending from nucleotide 30702027 to 31148630 of chromosome 4;

(7) QTL region 7, extending from nucleotide 33166529 to 33451554 of chromosome 4;

(8) QTL region 8, extending from nucleotide 35906266 to 36257708 of chromosome 7;

(9) QTL region 9, extending from nucleotide 29233675 to 29612202 of chromosome 10;

(10) QTL region 10, extending from nucleotide 13470988 to 13734716 of chromosome 11;

(11) QTL region 11, extending from nucleotide 24620951 to 24989005 of chromosome 13; or

(12) QTL region 12, extending from nucleotide 6941783 to 7160542 of chromosome 15; 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).

10. The method of claim 1, wherein positional information of the SNP markers in the QTL regions 1 to 12 comprises as follows:

SNP No.	SNP ID	QTL region	Chromosome	Position
1	SD_SNP_000009674	1	2	2839498
2	SD_SNP_000034184	1	2	2663542
3	SD_SNP_000034185	1	2	2665765
4	SD_SNP_000001499	1	2	2382629
5	SD_SNP_000035651	1	2	1759437
6	SD_SNP_000035648	1	2	1771297
7	SD_SNP_000022297	1	2	1846961
8	SD_SNP_000012522	1	2	1885428
9	SD_SNP_000031778	1	2	2126909
10	SD_SNP_000032978	1	2	2221505
11	SD_SNP_000032977	1	2	2222803
12	SD_SNP_000052843	1	2	2248781
13	SD_SNP_000022228	1	2	2252803
14	SD_SNP_000049001	1	2	2278583
15	SD_SNP_000012251	1	2	2334302
16	SD_SNP_000039744	1	2	2420710
17	SD_SNP_000051255	1	2	2441311
18	SD_SNP_000034181	1	2	2667048
19	SD_SNP_000042600	1	2	2695780
20	SD_SNP_000042602	1	2	2703264
21	SD_SNP_000018126	1	2	2716684
22	SD_SNP_000014865	1	2	2743533
23	SD_SNP_000013344	1	2	2823760
24	SD_SNP_000009676	1	2	2832871
25	SD_SNP_000052431	1	2	2916362
26	SD_SNP_000052409	1	2	2930303
27	SD_SNP_000045278	1	2	2950494
28	SD_SNP_000053629	1	2	2981286
29	SD_SNP_000053733	1	2	3012316
30	SD_SNP_000050894	1	2	3058428
31	SD_SNP_000044826	1	2	3088072
32	SD_SNP_000044827	1	2	3091668
33	SD_SNP_000054426	1	2	3097626
34	SD_SNP_000049523	1	2	3102809
35	SD_SNP_000049522	1	2	3106023
36	SD_SNP_000032638	1	2	3138520
37	SD_SNP_000032635	1	2	3164271
38	SD_SNP_000032634	1	2	3178475
39	SD_SNP_000035300	1	2	3208657
40	SD_SNP_000015816	1	2	3231524
41	SD_SNP_000015817	1	2	3234434
42	SD_SNP_000015818	1	2	3244642
43	SD_SNP_000020090	1	2	3261964

44	SD_SNP_000042701	1	2	3516726
45	SD_SNP_000042699	1	2	3525144
46	SD_SNP_000021289	1	2	3628967
47	SD_SNP_000021286	1	2	3642032
48	SD_SNP_000025837	1	2	3758742
49	SD_SNP_000025836	1	2	3768336
50	SD_SNP_000025835	1	2	3772793
51	SD_SNP_000044908	1	2	4074998
52	SD_SNP_000044907	1	2	4077752
53	SD_SNP_000020230	2	2	5097780
54	SD_SNP_000025305	2	2	5363657
55	SD_SNP_000042900	3	2	34075248
56	SD_SNP_000042901	3	2	34075791
57	SD_SNP_000042902	3	2	34078593
58	SD_SNP_000038061	4	3	43585962
59	SD_SNP_000038060	4	3	43590008
60	SD_SNP_000003552	5	3	44177007
61	SD_SNP_000045016	5	3	44193097
62	SD_SNP_000010805	11	13	24755265
63	SD_SNP_000033505	6	4	30941927
64	SD_SNP_000030856	7	4	33272835
65	SD_SNP_000032245	8	7	36083819
66	SD_SNP_000006564	9	10	29394849
67	SD_SNP_000032106	10	11	13717993
68	SD_SNP_000044156	12	15	6941783

11. The method of claim 1, wherein the first SNP marker comprises one or more SNP markers for the high-oil-production trait of decreased shell-to-fruit in *tenera* oil palm plants as follows:

SNP No.	Major allele	Minor allele	Minor allele freq.	Min. S/F geno.	Max. S/F geno.	[-$\log_{10}$(*p-value*)] for decreased shell-to-fruit (%)		
						Genotype	Dominant	Recessive
1	C	A	0.289	A/C	C/C	9.552	0.000	8.421
2	C	A	0.2303	A/C	A/A	10.505	0.000	9.411
3	A	C	0.4547	C/C	A/A	11.490	8.208	7.565
4	G	A	0.1151	G/G	A/A	17.581	0.000	12.028
5	G	A	0.1283	G/G	A/A	7.368	0.000	5.906
6	G	A	0.1212	G/G	A/G	7.646	0.000	5.103
7	G	A	0.1783	G/G	A/A	7.004	0.000	2.271
8	A	G	0.2036	A/A	G/G	7.268	0.000	5.646
9	A	C	0.4742	A/A	C/C	9.589	4.995	8.071
10	C	A	0.3228	A/A	C/C	8.543	3.768	6.628
11	A	G	0.291	A/A	G/G	14.269	4.103	9.206
12	A	G	0.2108	A/A	G/G	11.103	0.000	11.508
13	G	A	0.4926	G/G	A/A	11.532	11.800	4.821
14	A	G	0.3232	A/A	G/G	9.188	1.927	7.977
15	G	A	0.1473	G/G	A/A	9.266	0.000	8.756
16	A	G	0.1336	A/A	G/G	15.395	0.000	12.353
17	A	G	0.1394	A/A	G/G	16.511	0.000	12.619
18	A	G	0.3148	G/A	A/A	11.722	0.000	8.301

19	A	G	0.3497	G/A	G/G	7.352	0.000	8.615
20	G	A	0.3487	A/G	A/A	8.390	0.000	10.433
21	A	G	0.2639	G/A	A/A	12.417	0.000	13.202
22	A	C	0.2534	C/A	A/A	12.202	0.000	11.570
23	A	G	0.409	A/A	G/G	8.394	8.159	3.005
24	A	G	0.3011	G/A	A/A	7.305	1.200	10.625
25	C	A	0.2237	A/C	C/C	9.596	0.000	8.138
26	G	A	0.2601	A/G	G/G	11.635	0.000	10.126
27	C	A	0.2649	C/C	A/A	9.605	0.000	10.837
28	G	A	0.3846	A/G	A/A	25.486	0.000	22.077
29	G	A	0.2129	A/G	A/A	11.613	0.000	11.878
30	C	A	0.4227	A/C	C/C	6.054	2.713	17.188
31	G	A	0.2129	A/G	A/A	17.961	0.000	12.531
32	G	A	0.4929	G/G	A/A	19.665	5.049	13.979
33	A	G	0.4796	A/A	G/G	23.007	5.167	18.883
34	A	G	0.2678	A/A	G/G	14.486	0.000	14.055
35	A	C	0.2648	A/A	C/C	10.686	0.000	10.250
36	A	G	0.1138	A/A	G/G	22.568	0.000	16.519
37	C	A	0.1627	C/C	A/C	22.541	0.000	22.336
38	A	G	0.05755	G/A	G/G	7.034	0.000	7.381
39	A	G	0.2953	A/A	G/G	31.785	5.232	22.543
40	A	C	0.2532	C/A	C/C	23.397	0.000	24.469
41	A	G	0.2234	G/A	G/G	8.239	0.000	8.508
42	A	G	0.2442	G/G	A/A	8.924	0.000	4.156
43	A	C	0.4702	C/C	A/A	18.199	13.996	8.498
44	G	A	0.2543	A/G	G/G	11.044	0.000	10.142
45	C	A	0.3308	C/C	A/A	16.351	5.002	8.967
46	A	G	0.3413	G/A	A/A	7.310	5.868	2.711
47	G	A	0.3505	A/G	G/G	8.461	4.970	2.748
48	G	A	0.1785	A/G	G/G	10.440	0.000	7.475
49	A	C	0.1966	C/A	A/A	10.668	0.000	8.079
50	G	A	0.2799	G/G	A/A	25.085	1.979	20.074
51	A	G	0.3255	A/A	G/G	20.122	8.825	8.797
52	C	A	0.381	C/C	A/A	14.791	4.912	6.827
53	A	G	0.2368	A/A	G/G	7.647	0.000	6.088
54	G	A	0.1073	G/G	A/A	7.639	0.000	3.049
55	A	C	0.3162	A/A	C/C	7.419	3.187	3.383
56	A	G	0.3166	A/A	G/G	7.321	3.251	3.612
57	G	A	0.3151	G/G	A/A	7.766	2.859	3.308
58	A	G	0.1425	G/G	G/A	8.146	0.000	3.435
59	A	G	0.1326	G/G	G/A	8.414	0.000	6.963
60	G	A	0.3228	A/G	A/A	7.146	4.094	1.324
61	A	G	0.4	G/A	G/G	7.510	5.273	1.005
62	G	A	0.2863	A/G	G/G	4.189	0.272	0.823
63	G	A	0.1906	A/G	G/G	7.787	0.000	0.032
64	A	G	0.1502	A/A	G/G	7.070	0.000	0.847
65	G	A	0.2913	A/A	G/G	6.510	0.500	1.428
66	G	A	0.08552	A/A	A/G	2.459	0.000	0.473
67	C	A	0.2453	C/C	A/C	7.507	0.000	0.600
68	A	G	0.2879	G/A	G/G	5.448	0.220	0.617

12. The method of claim 1, wherein the first SNP marker comprises one or more SNP markers for the high-oil-production trait of increased mesocarp-to-fruit in *tenera* oil palm plants as follows:

SNP No.	Major allele	Minor allele	Minor allele freq.	Min. M/F geno.	Max. M/F geno.	[-$\log_{10}$(*p-value*)] for increased mesocarp-to-fruit (%)		
						Genotype	Dominant	Recessive
1	C	A	0.289	C/C	A/A	8.020	0.000	6.546
2	C	A	0.2303	C/C	A/C	5.764	0.000	4.622
3	A	C	0.4547	A/A	C/C	4.939	3.469	4.047
4	G	A	0.1151	A/A	G/G	11.099	0.000	7.057
5	G	A	0.1283	A/A	G/G	4.378	0.000	3.348
6	G	A	0.1212	A/G	A/A	5.334	0.000	3.949
7	G	A	0.1783	A/A	G/G	4.252	0.000	1.454
8	A	G	0.2036	G/G	A/A	2.713	0.000	2.126
9	A	C	0.4742	C/A	A/A	8.383	2.547	6.145
10	C	A	0.3228	C/C	A/A	4.074	2.269	2.927
11	A	G	0.291	G/G	A/A	5.877	1.190	4.629
12	A	G	0.2108	G/G	A/A	3.770	0.000	4.123
13	G	A	0.4926	A/A	G/G	4.272	5.548	1.588
14	A	G	0.3232	G/G	A/A	4.977	0.831	4.737
15	G	A	0.1473	A/A	G/G	4.980	0.000	5.279
16	A	G	0.1336	G/G	A/A	8.142	0.000	6.392
17	A	G	0.1394	G/G	A/A	8.921	0.000	6.741
18	A	G	0.3148	A/A	G/A	5.473	0.000	3.890
19	A	G	0.3497	G/G	G/A	5.787	0.000	6.195
20	G	A	0.3487	A/A	A/G	6.603	0.000	7.345
21	A	G	0.2639	A/A	G/A	6.822	0.000	7.515
22	A	C	0.2534	A/A	C/A	6.144	0.000	6.309
23	A	G	0.409	G/G	A/A	4.515	5.644	0.990
24	A	G	0.3011	A/A	G/G	6.725	1.779	7.273
25	C	A	0.2237	C/C	A/C	5.429	0.000	5.360
26	G	A	0.2601	G/G	A/G	7.053	0.000	6.606
27	C	A	0.2649	A/A	C/C	4.291	0.000	5.031
28	G	A	0.3846	G/G	A/G	16.331	0.000	13.937
29	G	A	0.2129	G/G	A/G	7.495	0.000	7.071
30	C	A	0.4227	C/C	A/C	8.847	0.198	11.846
31	G	A	0.2129	A/A	A/G	11.345	0.000	7.230
32	G	A	0.4929	A/G	G/G	5.638	0.118	6.461
33	A	G	0.4796	G/A	A/A	6.405	0.108	7.866
34	A	G	0.2678	G/G	A/A	7.230	0.000	6.516
35	A	C	0.2648	C/C	A/A	5.321	0.000	5.119
36	A	G	0.1138	G/G	A/A	13.365	0.000	9.047
37	C	A	0.1627	A/C	A/A	7.962	0.000	7.483
38	A	G	0.05755	G/G	G/A	4.787	0.000	5.364
39	A	G	0.2953	G/A	A/A	11.720	0.877	10.213
40	A	C	0.2532	C/C	C/A	15.178	0.000	15.856
41	A	G	0.2234	A/A	G/A	5.909	0.000	6.123
42	A	G	0.2442	A/A	G/G	4.021	0.000	1.643
43	A	C	0.4702	A/A	C/C	7.724	6.683	3.578
44	G	A	0.2543	G/G	A/G	3.554	0.000	5.222
45	C	A	0.3308	A/A	C/C	5.515	1.059	4.015

46	A	G	0.3413	A/A	G/A	3.150	2.503	1.306
47	G	A	0.3505	G/G	A/G	3.349	2.132	1.301
48	G	A	0.1785	G/G	A/A	5.135	0.000	3.866
49	A	C	0.1966	A/A	C/A	6.420	0.000	4.031
50	G	A	0.2799	A/G	G/G	9.796	0.379	8.126
51	A	G	0.3255	G/G	A/A	7.623	3.327	3.145
52	C	A	0.381	A/A	C/C	6.292	1.953	2.873
53	A	G	0.2368	G/G	A/A	3.428	0.000	2.867
54	G	A	0.1073	A/A	G/G	4.205	0.000	2.032
55	A	C	0.3162	C/C	A/A	5.096	2.622	1.767
56	A	G	0.3166	G/G	A/A	5.077	2.770	1.916
57	G	A	0.3151	A/A	G/G	5.388	2.406	1.747
58	A	G	0.1425	G/A	G/G	5.353	0.000	2.579
59	A	G	0.1326	G/A	G/G	6.624	0.000	5.847
60	G	A	0.3228	A/A	A/G	5.610	2.081	1.985
61	A	G	0.4	G/G	G/A	5.503	2.943	1.414
62	G	A	0.2863	G/G	A/A	7.229	0.942	1.251
63	G	A	0.1906	G/G	A/G	6.233	0.000	0.382
64	A	G	0.1502	G/G	G/A	2.763	0.000	0.439
65	G	A	0.2913	G/G	A/A	7.008	0.494	1.650
66	G	A	0.08552	G/G	A/A	7.781	0.000	0.894
67	C	A	0.2453	A/C	A/A	2.232	0.000	0.046
68	A	G	0.2879	G/G	A/A	8.052	0.326	1.070

13. The method of claim 1, wherein differences in mean shell-to-fruit and mean mesocarp-to-fruit of the SNP markers for a genotype model comprises as follows:

SNP No.	SNP effects (Genotype Model): Mean shell-to-fruit (%)			SNP effects (Genotype Model): Mean mesocarp-to-fruit (%)		
	Min	Max	δ	Min	Max	δ
1	10.350	11.620	1.270	78.840	80.780	1.940
2	10.190	12.280	2.090	79.010	80.750	1.740
3	10.030	11.960	1.930	78.560	80.860	2.300
4	10.570	14.870	4.300	74.970	80.470	5.500
5	10.640	14.210	3.570	76.240	80.380	4.140
6	10.620	12.090	1.470	77.890	82.700	4.810
7	10.640	13.780	3.140	75.510	80.390	4.880
8	10.380	13.220	2.840	78.540	80.480	1.940
9	10.470	11.310	0.840	79.590	80.350	0.760
10	10.410	11.600	1.190	78.900	81.310	2.410
11	10.050	12.750	2.700	78.190	80.830	2.640
12	10.500	13.870	3.370	77.310	80.540	3.230
13	9.880	12.130	2.250	78.130	81.320	3.190
14	9.930	12.960	3.030	77.100	81.200	4.100
15	10.590	13.260	2.670	76.390	80.490	4.100
16	10.570	14.600	4.030	75.900	80.470	4.570
17	10.520	14.600	4.080	75.900	80.520	4.620
18	10.500	11.550	1.050	79.190	80.320	1.130
19	10.590	13.270	2.680	77.930	80.520	2.590
20	10.590	13.210	2.620	78.030	80.520	2.490
21	10.280	11.650	1.370	78.990	80.640	1.650
22	10.250	11.650	1.400	78.910	80.740	1.830

23	9.980	12.080	2.100	77.570	81.220	3.650
24	10.190	11.730	1.540	78.660	80.740	2.080
25	10.270	11.510	1.240	79.070	80.760	1.690
26	10.250	11.680	1.430	78.890	80.730	1.840
27	10.080	11.950	1.870	77.980	80.790	2.810
28	10.580	12.680	2.100	77.700	80.450	2.750
29	10.040	11.890	1.850	78.940	80.990	2.050
30	10.470	12.280	1.810	77.510	80.440	2.930
31	10.000	12.030	2.030	78.570	81.050	2.480
32	9.530	12.330	2.800	79.620	81.040	1.420
33	9.570	12.320	2.750	79.590	80.950	1.360
34	9.950	14.400	4.450	75.920	81.090	5.170
35	10.020	12.880	2.860	78.220	80.970	2.750
36	10.570	22.400	11.830	68.200	80.460	12.260
37	10.480	12.060	1.580	78.400	80.690	2.290
38	10.700	11.620	0.920	78.620	79.920	1.300
39	9.900	12.650	2.750	78.670	80.940	2.270
40	10.030	12.370	2.340	78.220	80.980	2.760
41	10.030	12.050	2.020	78.820	81.040	2.220
42	9.520	11.570	2.050	79.060	81.310	2.250
43	9.530	12.240	2.710	78.210	81.630	3.420
44	10.190	11.830	1.640	78.740	80.790	2.050
45	9.910	12.720	2.810	78.780	80.930	2.150
46	10.620	11.480	0.860	79.350	80.210	0.860
47	10.630	11.440	0.810	79.360	80.190	0.830
48	10.030	11.500	1.470	79.100	82.700	3.600
49	10.110	11.440	1.330	79.150	80.930	1.780
50	9.940	12.630	2.690	78.650	80.860	2.210
51	9.920	13.010	3.090	78.090	80.920	2.830
52	9.740	12.890	3.150	77.820	81.270	3.450
53	10.300	14.080	3.780	77.390	80.430	3.040
54	10.680	14.300	3.620	76.950	80.240	3.290
55	10.780	11.520	0.740	78.550	80.100	1.550
56	10.780	11.520	0.740	78.540	80.110	1.570
57	10.780	11.510	0.730	78.560	80.110	1.550
58	10.020	11.640	1.620	78.840	81.050	2.210
59	10.020	11.770	1.750	78.570	81.050	2.480
60	10.660	11.980	1.320	78.850	80.350	1.500
61	10.440	11.940	1.500	78.670	80.630	1.960
62	10.970	11.110	0.140	79.340	80.620	1.280
63	10.870	10.890	0.020	79.830	80.040	0.210
64	10.900	13.900	3.000	76.620	80.000	3.380
65	10.460	11.380	0.920	79.400	81.150	1.750
66	10.490	11.270	0.780	79.560	82.310	2.750
67	10.700	11.130	0.430	79.800	82.700	2.900
68	10.470	11.830	1.360	77.890	80.440	2.550

14. The method of claim 1, wherein correlation accuracy for shell-to-mesocarp comprises as follows:

Number of QTLs represented in analysis (additive)	SNP No.	SNP ID	QTL region	Correlation accuracy for S/F (%)
1	39	SD_SNP_000035300	1	0.095
2	59	SD_SNP_000038060	4	0.097
3	63	SD_SNP_000033505	6	0.115
4	57	SD_SNP_000042902	3	0.309
5	53	SD_SNP_000020230	2	0.319
6	61	SD_SNP_000045016	5	0.324
7	67	SD_SNP_000032106	10	0.325
8	64	SD_SNP_000030856	7	0.324

15. The method of claim 1, wherein correlation accuracy for mesocarp-to-fruit comprises as follows:

Number of QTLs represented in analysis (additive)	SNP No.	SNP ID	QTL region	Correlation accuracy for M/F (%)
1	40	SD_SNP_000015816	1	0.079
2	68	SD_SNP_000044156	12	0.250
3	66	SD_SNP_000006564	9	0.257
4	62	SD_SNP_000010805	11	0.301
5	65	SD_SNP_000032245	8	0.303