



Table S1

Table S1: Accessions used in the study, with the exiting haplotypes for HRY in hotspot regions of chromosome 8 and 11.

 Favourable haplotype identified for high HRY
 Missing/heterozygous

Accession IDs	chr8 (block1)	chr11	Average % HRY
IRIS_313-10000	TTATTATTATATTA	TTGG	57.50
IRIS_313-10001	CCGCCGGCGCCCCG	TTGG	35.43
IRIS_313-10007	TTATTATTATATTA	TTGG	46.87
IRIS_313-10016	CCGCCGGCGCCCCG	TTGG	35.10
IRIS_313-10026	CCGCCGGCGCCCCG	TTGG	24.23
IRIS_313-10030	CCGCCGGCGCCCCG	TTGG	14.17
IRIS_313-10034	CCGCCGGCGCCCCG	TTGG	36.40
IRIS_313-10040	CCGCCGGCGCCCCG	TTGG	63.33
IRIS_313-10045	CCGCCGGCGCCCCG	TTGG	28.13
IRIS_313-10046	CCGCCGGCGCCCCG	TTGG	53.37
IRIS_313-10047	CCGCCGGCGCCCCG	TTGG	39.43
IRIS_313-10048	CCGCCGGCGCCCCG	TTGG	32.73
IRIS_313-10050	CCGCCGGCGCCCCG	TTGG	35.73
IRIS_313-10054	CCGCCGGCGCCCCG	TTGG	45.03
IRIS_313-10102	-	TTGG	41.77
IRIS_313-10103	CCGCCGGCGCCCCG	TTGG	32.97
IRIS_313-10109	CCGCCGGCGCCCCG	TTGG	35.23
IRIS_313-10113	-	TTGG	53.47
IRIS_313-10114	CCGCCGGCGCCCCG	TTGG	13.07
IRIS_313-10129	CCGCCGGCGCCCCG	TTGG	41.60
IRIS_313-10147	CCGCCGGCGCCCCG	TTGG	43.17
IRIS_313-10148	CCGCCGGCGCCCCG	TTGG	55.00
IRIS_313-10151	-	-	51.07
IRIS_313-10154	CCGCCGGCGCCCCG	TTGG	43.13
IRIS_313-10167	CCGCCGGCGCCCCG	TTGG	38.93
IRIS_313-10168	CCGCCGGCGCCCCG	GCAA	26.10
IRIS_313-10170	CCGCCGGCGCCCCG	TTGG	36.33
IRIS_313-10171	CCGCCGGCGCCCCG	TTGG	40.93
IRIS_313-10177	CCGCCGGCGCCCCG	TTGA	57.40
IRIS_313-10178	CCGCCGGCGCCCCG	TTGG	50.43
IRIS_313-10179	CCGCCGGCGCCCCG	TTGG	52.43
IRIS_313-10191	TTATTATTATATTA	TTGG	59.73
IRIS_313-10220	-	TTGG	48.90
IRIS_313-10221	TTATTATTATATTA	TTGG	59.13
IRIS_313-10224	CCGCCGGCGCCCCG	TTGG	40.43
IRIS_313-10226	CCGCCGGCGCCCCG	TTGG	45.57
IRIS_313-10234	TTATTATTATATTA	TTGG	42.80
IRIS_313-10235	CCGCCGGCGCCCCG	TTGG	47.90
IRIS_313-10237	TTATTATTATATTA	TTGG	48.67
IRIS_313-10238	TTATTATTATATTA	TTGG	60.97
IRIS_313-10247	CCGCCGGCGCCCCG	TTGG	45.50
IRIS_313-10257	CCGCCGGCGCCCCG	TTGG	30.73
IRIS_313-10260	CCGCCGGCGCCCCG	TTGG	55.20
IRIS_313-10263	CCGCCGGCGCCCCG	TTGG	39.73
IRIS_313-10268	TTATTATTATATTA	TTGG	50.13
IRIS_313-10271	CCGCCGGCGCCCCG	TTGG	48.67
IRIS_313-10274	-	TTGG	59.43

Table S1

Accession IDs	chr8 (block1)	chr11	Average % HRY
IRIS_313-10275	-	TTGG	40.20
IRIS_313-10279	CCGCCGGCGCCCCG	TTGG	30.60
IRIS_313-10285	-	TTGG	46.90
IRIS_313-10287	TTATTATTATATTA	TTGG	54.07
IRIS_313-10289	CCGCCGGCGCCCCG	TTGG	57.03
IRIS_313-10293	CCGCCGGCGCCCCG	TTGG	46.00
IRIS_313-10294	CCGCCGGCGCCCCG	TTGG	46.40
IRIS_313-10298	CCGCCGGCGCCCCG	TTGG	31.60
IRIS_313-10300	CCGCCGGCGCCCCG	TTGG	53.27
IRIS_313-10301	CCGCCGGCGCCCCG	TTGG	43.73
IRIS_313-10307	-	TTGG	52.37
IRIS_313-10314	CCGCCGGCGCCCCG	TTGG	48.70
IRIS_313-10318	CCGCCGGCGCCCCG	TTGG	44.70
IRIS_313-10325	CCGCCGGCGCCCCG	TTGG	40.57
IRIS_313-10332	CCGCCGGCGCCCCG	TTGG	58.20
IRIS_313-10333	CCGCCGGCGCCCCG	TTGG	49.47
IRIS_313-10334	CCGCCGGCGCCCCG	TTGG	49.53
IRIS_313-10337	CCGCCGGCGCCCCG	GCAA	33.43
IRIS_313-10340	TTATTATTATATTA	TTGG	50.70
IRIS_313-10349	CCGCCGGCGCCCCG	GCAA	35.50
IRIS_313-10352	CCGCCGGCGCCCCG	TTGG	47.73
IRIS_313-10353	TTATTATTATATTA	TTGG	31.27
IRIS_313-10355	CCGCCGGCGCCCCG	TTGG	37.33
IRIS_313-10357	CCGCCGGCGCCCCG	TTGG	46.37
IRIS_313-10360	CCGCCGGCGCCCCG	TTGG	52.67
IRIS_313-10361	TTATTATTATATTA	TTGG	59.43
IRIS_313-10366	CCGCCGGCGCCCCG	TTGG	48.53
IRIS_313-10371	CCGCCGGCGCCCCG	TTGG	31.70
IRIS_313-10374	TTATTATTATATTA	TTGG	54.50
IRIS_313-10375	CCGCCGGCGCCCCG	TTGG	32.70
IRIS_313-10385	CCGCCGGCGCCCCG	TTGG	38.97
IRIS_313-10392	TTATTATTATATTA	TTGG	46.37
IRIS_313-10394	CCGCCGGCGCCCCG	TTGG	56.80
IRIS_313-10396	TTATTATTATATTA	TTGG	55.67
IRIS_313-10397	CCGCCGGCGCCCCG	TTGG	57.50
IRIS_313-10398	CCGCCGGCGCCCCG	TTGG	59.50
IRIS_313-10399	CCGCCGGCGCCCCG	TTGG	51.80
IRIS_313-10400	CCGCCGGCGCCCCG	TTGG	46.37
IRIS_313-10401	-	TTGG	50.13
IRIS_313-10402	CCGCCGGCGCCCCG	TTGG	54.43
IRIS_313-10403	TTATTATTATATTA	TTGG	60.50
IRIS_313-10404	CCGCCGGCGCCCCG	TTGG	50.20
IRIS_313-10412	CCGCCGGCGCCCCG	TTGG	49.70
IRIS_313-10417	CCGCCGGCGCCCCG	TTGG	31.30
IRIS_313-10421	-	TTGG	54.67
IRIS_313-10422	-	TTGG	35.17
IRIS_313-10423	CCGCCGGCGCCCCG	GCAA	34.67
IRIS_313-8288	CCGCCGGCGCCCCG	TTGG	27.97
IRIS_313-8303	TTATTATTATATTA	TTGG	59.37
IRIS_313-8305	CCGCCGGCGCCCCG	TTGG	49.73
IRIS_313-8315	CCGCCGGCGCCCCG	TTGG	53.60
IRIS_313-8332	CCGCCGGCGCCCCG	TTGG	44.27
IRIS_313-8368	CCGCCGGCGCCCCG	TTGG	32.97
IRIS_313-8380	CCGCCGGCGCCCCG	TTGG	43.10

Table S1

Accession IDs	chr8 (block1)	chr11	Average % HRY
IRIS_313-8386	CCGTTATTATATTA	TTGG	51.80
IRIS_313-8392	CCGCCGGCGCCCCG	TTGG	30.50
IRIS_313-8401	-	TTGG	46.90
IRIS_313-8409	-	TTGG	57.40
IRIS_313-8412	-	TTGG	49.17
IRIS_313-8414	CCGCCGGCGCCCCG	TTGG	39.83
IRIS_313-8433	CCGCCGGCGCCCCG	TTGG	52.67
IRIS_313-8435	CCGCCGGCGCCCCG	TTGG	34.83
IRIS_313-8437	CCGCCGGCGCCCCG	TTGG	52.83
IRIS_313-8450	CCGTTATTATATTA	TTGG	53.93
IRIS_313-8453	CCGCCGGCGCCCCG	TTGG	49.83
IRIS_313-8454	CCGCCGGCGCCCCG	TTGG	52.70
IRIS_313-8458	CCGCCGGCGCCCCG	GCAA	46.37
IRIS_313-8509	CCGCCGGCGCCCCG	-	55.10
IRIS_313-8514	CCGCCGGCGCCCCG	TTGG	44.57
IRIS_313-8530	CCGCCGGCGCCCCG	TTGG	22.17
IRIS_313-8536	CCGCCGGCGCCCCG	TTGG	37.60
IRIS_313-8559	CCGCCGGCGCCCCG	TTGG	49.50
IRIS_313-8568	CCGCCGGCGCCCCG	TTGG	52.13
IRIS_313-8571	TTATTATTATATTA	TTGG	57.10
IRIS_313-8585	TTATTATTATATTA	TTGG	56.57
IRIS_313-8586	TTATTATTATATTA	GCAA	23.97
IRIS_313-8595	CCGCCGGCGCCCCG	TTGG	4.37
IRIS_313-8603	CCGCCGGCGCCCCG	TTGG	46.83
IRIS_313-8614	CCGTTATTATATTA	TTGG	63.13
IRIS_313-8616	CCGCCGGCGCCCCG	TTGG	47.37
IRIS_313-8621	-	TTGG	37.03
IRIS_313-8622	-	TTGG	25.37
IRIS_313-8631	CCGCCGGCGCCCCG	TTGG	32.17
IRIS_313-8632	CCGCCGGCGCCCCG	TTGG	51.67
IRIS_313-8638	TTATTATTATATTA	TTGG	44.13
IRIS_313-8643	CCGCCGGCGCCCCG	TTGG	47.60
IRIS_313-8645	CCGCCGGCGCCCCG	TTGG	39.23
IRIS_313-8647	CCGCCGGCGCCCCG	TTGG	58.10
IRIS_313-8659	CCGCCGGCGCCCCG	TTGG	40.83
IRIS_313-8660	-	TTGG	60.73
IRIS_313-8674	TTATTATTATATTA	TTGG	52.90
IRIS_313-8699	TTATTATTATATTA	TTGG	58.40
IRIS_313-8704	CCGCCGGCGCCCCG	TTGG	45.30
IRIS_313-8717	CCGCCGGCGCCCCG	TTGG	21.73
IRIS_313-8722	-	GCAA	36.77
IRIS_313-8725	CCGCCGGCGCCCCG	TTGG	51.47
IRIS_313-8727	CCGCCGGCGCCCCG	TTGG	46.23
IRIS_313-8731	CCGCCGGCGCCCCG	TTGG	56.70
IRIS_313-8732	CCGCCGGCGCCCCG	TTGG	42.73
IRIS_313-8733	CCGCCGGCGCCCCG	TTGG	24.77
IRIS_313-8737	CCGCCGGCGCCCCG	TTGG	29.67
IRIS_313-8743	CCGCCGGCGCCCCG	TTGG	46.60
IRIS_313-8744	CCGCCGGCGCCCCG	TTGG	29.47
IRIS_313-8751	TTATTATTATATTA	TTGG	55.63
IRIS_313-8754	CCGCCGGCGCCCCG	TTGG	39.13
IRIS_313-8757	CCGCCGGCGCCCCG	TTGG	45.00
IRIS_313-8781	CCGCCGGCGCCCCG	TTGG	47.23
IRIS_313-8785	TTATTATTATATTA	GCAA	36.50

Table S1

Accession IDs	chr8 (block1)	chr11	Average % HRY
IRIS_313-8796	CCGCCGGCGCCCCG	TTGG	55.20
IRIS_313-8812	CCGCCGGCGCCCCG	TTGG	54.53
IRIS_313-8831	CCGCCGGCGCCCCG	TTGG	37.73
IRIS_313-8844	CCGCCGGCGCCCCG	GCAA	37.23
IRIS_313-8846	CCGCCGGCGCCCCG	TTGG	45.60
IRIS_313-8850	CCGCCGGCGCCCCG	TTGG	28.70
IRIS_313-8854	CCGCCGGCGCCCCG	TTGG	50.93
IRIS_313-8889	TTATTATTATATTA	TTGG	60.73
IRIS_313-8900	CCGTTATTATATTA	TTGG	54.07
IRIS_313-8903	CCGCCGGCGCCCCG	TTGG	53.00
IRIS_313-8914	CCGCCGGCGCCCCG	TTGG	40.43
IRIS_313-8920	-	TTGG	38.50
IRIS_313-8924	CCGTTATTATATTA	TTGG	48.37
IRIS_313-8925	CCGCCGGCGCCCCG	TTGG	48.37
IRIS_313-8930	CCGCCGGCGCCCCG	TTGG	32.63
IRIS_313-8932	CCGCCGGCGCCCCG	TTGG	61.23
IRIS_313-8935	CCGCCGGCGCCCCG	TTGG	48.93
IRIS_313-8940	CCGCCGGCGCCCCG	TTGG	48.13
IRIS_313-8946	CCGCCGGCGCCCCG	TTGG	58.77
IRIS_313-8956	CCGCCGGCGCCCCG	TTGG	38.87
IRIS_313-8967	CCGCCGGCGCCCCG	TTGG	56.50
IRIS_313-8968	CCGCCGGCGCCCCG	TTGG	43.63
IRIS_313-8980	TTATTATTATATTA	GCAA	39.07
IRIS_313-8982	CCGCCGGCGCCCCG	TTGG	40.00
IRIS_313-8986	CCGCCGGCGCCCCG	TTGG	32.87
IRIS_313-8988	CCGCCGGCGCCCCG	TTGG	52.07
IRIS_313-8994	TTATTATTATATTA	TTGG	53.47
IRIS_313-9005	CCGCCGGCGCCCCG	TTGG	28.23
IRIS_313-9017	CCGCCGGCGCCCCG	TTGG	29.87
IRIS_313-9023	CCGCCGGCGCCCCG	TTGG	37.23
IRIS_313-9032	CCGCCGGCGCCCCG	TTGG	42.20
IRIS_313-9044	CCGCCGGCGCCCCG	TTGG	30.63
IRIS_313-9065	CCGCCGGCGCCCCG	TTGG	42.90
IRIS_313-9066	CCGCCGGCGCCCCG	TTGG	49.37
IRIS_313-9067	CCGCCGGCGCCCCG	TTGG	22.63
IRIS_313-9072	CCGTTATTATATTA	TTGG	47.40
IRIS_313-9111	-	TTGG	55.37
IRIS_313-9119	TTATTATTATATTA	TTGG	22.70
IRIS_313-9139	CCGCCGGCGCCCCG	TTGG	44.23
IRIS_313-9148	CCGCCGGCGCCCCG	TTGG	44.07
IRIS_313-9156	CCGTTATTATATTA	TTGG	53.77
IRIS_313-9174	CCGCCGGCGCCCCG	TTGG	46.53
IRIS_313-9184	CCGCCGGCGCCCCG	TTGG	49.50
IRIS_313-9190	CCGCCGGCGCCCCG	TTGG	54.20
IRIS_313-9198	-	TTGG	56.83
IRIS_313-9204	CCGCCGGCGCCCCG	TTGG	57.57
IRIS_313-9218	CCGCCGGCGCCCCG	TTGG	31.53
IRIS_313-9227	CCGCCGGCGCCCCG	TTGG	52.90
IRIS_313-9253	-	TTGG	38.03
IRIS_313-9256	CCGCCGGCGCCCCG	TTGG	28.47
IRIS_313-9259	CCGCCGGCGCCCCG	TTGG	53.10
IRIS_313-9262	CCGCCGGCGCCCCG	TTGG	50.93
IRIS_313-9271	CCGCCGGCGCCCCG	TTGG	43.00
IRIS_313-9281	CCGCCGGCGCCCCG	TTGG	46.90

Table S1



Accession IDs	chr8 (block1)	chr11	Average % HRY
IRIS_313-9286	CCGCCGGCGCCCCG	TTGG	26.30
IRIS_313-9287	CCGCCGGCGCCCCG	TTGG	37.97
IRIS_313-9313	CCGCCGGCGCCCCG	TTGG	42.13
IRIS_313-9314	CCGCCGGCGCCCCG	TTGG	35.00
IRIS_313-9317	TTATTATTATATTA	TTGG	55.70
IRIS_313-9320	CCGCCGGCGCCCCG	TTGG	41.40
IRIS_313-9324	CCGCCGGCGCCCCG	TTGG	23.50
IRIS_313-9325	CCGCCGGCGCCCCG	TTGG	47.03
IRIS_313-9348	CCGCCGGCGCCCCG	TTGG	44.17
IRIS_313-9351	CCGCCGGCGCCCCG	TTGG	55.00
IRIS_313-9360	CCGCCGGCGCCCCG	TTGG	50.70
IRIS_313-9372	CCGCCGGCGCCCCG	TTGG	40.70
IRIS_313-9384	CCGCCGGCGCCCCG	TTGG	51.37
IRIS_313-9388	CCGCCGGCGCCCCG	TTGG	39.20
IRIS_313-9400	-	TTGG	43.17
IRIS_313-9403	CCGCCGGCGCCCCG	TTGG	44.77
IRIS_313-9424	TTATTATTATATTA	TTGG	43.43
IRIS_313-9427	CCGCCGGCGCCCCG	TTGG	58.77
IRIS_313-9429	-	TTGG	58.30
IRIS_313-9433	CCGCCGGCGCCCCG	TTGG	40.33
IRIS_313-9451	-	TTGG	50.60
IRIS_313-9461	CCGCCGGCGCCCCG	GCAA	42.33
IRIS_313-9469	CCGCCGGCGCCCCG	TTGG	21.77
IRIS_313-9472	CCGCCGGCGCCCCG	TTGG	47.10
IRIS_313-9482	CCGCCGGCGCCCCG	TTGG	38.33
IRIS_313-9484	CCGCCGGCGCCCCG	TTGG	16.93
IRIS_313-9492	CCGCCGGCGCCCCG	TTGG	44.17
IRIS_313-9503	CCGCCGGCGCCCCG	TTGG	27.10
IRIS_313-9505	CCGCCGGCGCCCCG	TTGG	30.90
IRIS_313-9522	CCGCCGGCGCCCCG	TTGG	39.47
IRIS_313-9533	TTATTATTATATTA	TTGG	45.63
IRIS_313-9547	CCGCCGGCGCCCCG	TTGG	55.40
IRIS_313-9551	CCGCCGGCGCCCCG	TTGG	36.97
IRIS_313-9557	CCGCCGGCGCCCCG	TTGG	36.37
IRIS_313-9560	CCGCCGGCGCCCCG	TTGG	52.47
IRIS_313-9566	-	TTGG	54.97
IRIS_313-9570	CCGCCGGCGCCCCG	TTGG	44.57
IRIS_313-9572	CCGCCGGCGCCCCG	TTGG	33.60
IRIS_313-9574	CCGCCGGCGCCCCG	TTGG	27.93
IRIS_313-9590	CCGCCGGCGCCCCG	TTGG	49.73
IRIS_313-9593	CCGCCGGCGCCCCG	TTGG	59.90
IRIS_313-9594	CCGCCGGCGCCCCG	TTGG	50.90
IRIS_313-9602	CCGCCGGCGCCCCG	TTGG	48.93
IRIS_313-9604	CCGCCGGCGCCCCG	TTGG	52.33
IRIS_313-9605	CCGCCGGCGCCCCG	TTGG	51.77
IRIS_313-9609	-	TTGG	41.40
IRIS_313-9611	TTATTATTATATTA	TTGG	52.83
IRIS_313-9617	CCGCCGGCGCCCCG	TTGG	21.97
IRIS_313-9623	CCGCCGGCGCCCCG	TTGG	40.93
IRIS_313-9634	CCGCCGGCGCCCCG	TTGG	42.27
IRIS_313-9696	-	TTGG	57.33
IRIS_313-9705	CCGCCGGCGCCCCG	TTGG	43.13
IRIS_313-9706	-	TTGG	33.07
IRIS_313-9708	CCGCCGGCGCCCCG	TTGG	29.97

Table S1

Accession IDs	chr8 (block1)	chr11	Average % HRY
IRIS_313-9723	CCGCCGGCGCCCCG	TTGG	47.27
IRIS_313-9727	CCGCCGGCGCCCCG	TTGG	39.80
IRIS_313-9730	CCGCCGGCGCCCCG	TTGG	54.97
IRIS_313-9732	CCGCCGGCGCCCCG	TTGG	34.67
IRIS_313-9740	CCGCCGGCGCCCCG	TTGG	32.97
IRIS_313-9758	CCGCCGGCGCCCCG	TTGG	52.50
IRIS_313-9767	CCGCCGGCGCCCCG	TTGG	54.73
IRIS_313-9791	CCGCCGGCGCCCCG	TTGG	31.73
IRIS_313-9795	-	TTGG	42.60
IRIS_313-9831	CCGCCGGCGCCCCG	GCAG	34.03
IRIS_313-9841	CCGCCGGCGCCCCG	TTGG	13.67
IRIS_313-9862	CCGCCGGCGCCCCG	TTGG	25.53
IRIS_313-9867	CCGCCGGCGCCCCG	TTGG	18.47
IRIS_313-9882	CCGCCGGCGCCCCG	TTGA	39.87
IRIS_313-9898	-	GCAA	20.20
IRIS_313-9917	CCGCCGGCGCCCCG	TTGG	50.20
IRIS_313-9922	CCGCCGGCGCCCCG	TTGG	50.50
IRIS_313-9924	-	TTGG	40.73
IRIS_313-9925	CCGCCGGCGCCCCG	TTGG	53.90
IRIS_313-9940	CCGCCGGCGCCCCG	TTGG	45.57
IRIS_313-9944	CCGCCGGCGCCCCG	TTGG	50.77
IRIS_313-9953	CCGCCGGCGCCCCG	TTGG	51.60
IRIS_313-9966	CCGCCGGCGCCCCG	TTGG	49.13

Table S2

Table S2: Accessions used in the study, with the exiting haplotypes for HRY stability within candidate region on chromosome 8.

 Favourable haplotype identified for high HRY stability
 Missing/heterozygous

Accession IDs	LOC_Os08g31340	HRY Stability
IRIS_313-10000	CTG	1.00
IRIS_313-10001	CTG	0.49
IRIS_313-10007	CTG	0.69
IRIS_313-10016	CTG	0.62
IRIS_313-10026	CTG	0.77
IRIS_313-10030	CTG	0.78
IRIS_313-10034	CTG	0.94
IRIS_313-10040	CTG	1.00
IRIS_313-10045	CTG	0.98
IRIS_313-10046	CTG	0.67
IRIS_313-10047	CTG	0.76
IRIS_313-10048	CTG	0.96
IRIS_313-10050	CTG	0.77
IRIS_313-10054	CTG	0.42
IRIS_313-10102	CTG	0.91
IRIS_313-10103	CTG	1.53
IRIS_313-10109	CTG	0.54
IRIS_313-10113	CTG	0.90
IRIS_313-10114	CTG	0.57
IRIS_313-10129	CTG	0.88
IRIS_313-10147	CTG	0.99
IRIS_313-10148	CTG	0.62
IRIS_313-10151	CTG	0.89
IRIS_313-10154	-	0.79
IRIS_313-10167	CTG	0.68
IRIS_313-10168	CTG	0.82
IRIS_313-10170	CTG	0.92
IRIS_313-10171	CTG	0.68
IRIS_313-10177	CTG	0.67
IRIS_313-10178	CTG	0.80
IRIS_313-10179	CTG	0.78
IRIS_313-10191	CTG	1.06
IRIS_313-10220	CTG	0.59
IRIS_313-10221	CTG	0.99
IRIS_313-10224	CTG	0.76
IRIS_313-10226	CTC	0.82
IRIS_313-10234	CTG	0.30
IRIS_313-10235	CTG	0.64
IRIS_313-10237	CTG	0.35
IRIS_313-10238	CTG	0.63
IRIS_313-10247	CTG	0.34
IRIS_313-10257	CTG	0.93
IRIS_313-10260	CTG	0.63
IRIS_313-10263	CTG	0.45
IRIS_313-10268	CTG	0.58
IRIS_313-10271	CTG	0.52
IRIS_313-10274	CTG	0.83

Table S2

Accession IDs	LOC_Os08g31340	HRY Stability
IRIS_313-10275	CTG	0.53
IRIS_313-10279	CTG	0.33
IRIS_313-10285	CTG	0.53
IRIS_313-10287	CTG	0.83
IRIS_313-10289	CTG	0.62
IRIS_313-10293	CTG	0.67
IRIS_313-10294	CTG	0.57
IRIS_313-10298	CTG	0.49
IRIS_313-10300	CTC	0.72
IRIS_313-10301	CTG	0.74
IRIS_313-10307	CTG	0.71
IRIS_313-10314	CTG	0.41
IRIS_313-10318	CTG	0.61
IRIS_313-10325	CTG	0.89
IRIS_313-10332	CTG	0.80
IRIS_313-10333	CTG	0.65
IRIS_313-10334	CTG	0.81
IRIS_313-10337	CTG	0.66
IRIS_313-10340	CTG	0.54
IRIS_313-10349	CTG	0.54
IRIS_313-10352	CTG	0.52
IRIS_313-10353	CTG	0.38
IRIS_313-10355	TCC	0.82
IRIS_313-10357	CTG	0.61
IRIS_313-10360	CTG	0.87
IRIS_313-10361	CTG	0.74
IRIS_313-10366	CTG	0.60
IRIS_313-10371	CTG	0.51
IRIS_313-10374	CTG	0.82
IRIS_313-10375	CTG	0.47
IRIS_313-10385	CTG	1.05
IRIS_313-10392	CTG	1.08
IRIS_313-10394	CTG	0.61
IRIS_313-10396	CTG	0.78
IRIS_313-10397	CTG	0.84
IRIS_313-10398	CTG	0.87
IRIS_313-10399	CTG	0.92
IRIS_313-10400	CTG	0.69
IRIS_313-10401	CTG	0.75
IRIS_313-10402	CTG	0.88
IRIS_313-10403	CTG	0.71
IRIS_313-10404	CTG	0.51
IRIS_313-10412	CTG	0.64
IRIS_313-10417	CTG	0.44
IRIS_313-10421	CTG	0.53
IRIS_313-10422	CTG	0.87
IRIS_313-10423	CTG	0.53
IRIS_313-8288	CTG	0.44
IRIS_313-8303	CTG	0.61
IRIS_313-8305	CTG	0.80
IRIS_313-8315	CTG	0.46
IRIS_313-8332	CTG	1.01
IRIS_313-8368	CTG	0.59

Table S2

Accession IDs	LOC_Os08g31340	HRY Stability
IRIS_313-8380	CTG	0.72
IRIS_313-8386	CTG	0.72
IRIS_313-8392	CTG	0.71
IRIS_313-8401	CTG	0.73
IRIS_313-8409	CTG	0.94
IRIS_313-8412	CTG	0.64
IRIS_313-8414	CTG	0.79
IRIS_313-8433	CTG	0.99
IRIS_313-8435	CTG	0.74
IRIS_313-8437	CTG	0.90
IRIS_313-8450	CTG	0.81
IRIS_313-8453	TCC	0.99
IRIS_313-8454	CTG	0.85
IRIS_313-8458	CTG	0.58
IRIS_313-8509	CTG	0.85
IRIS_313-8514	CTG	0.59
IRIS_313-8530	CTG	0.88
IRIS_313-8536	CTG	0.81
IRIS_313-8559	CTG	0.83
IRIS_313-8568	CTG	0.94
IRIS_313-8571	CTG	0.82
IRIS_313-8585	CTG	0.74
IRIS_313-8586	CTG	0.38
IRIS_313-8595	CTG	1.09
IRIS_313-8603	CTG	0.49
IRIS_313-8614	CTG	1.04
IRIS_313-8616	CTG	0.54
IRIS_313-8621	CTG	0.57
IRIS_313-8622	CTG	0.73
IRIS_313-8631	CTG	0.74
IRIS_313-8632	CTG	1.04
IRIS_313-8638	CTG	0.60
IRIS_313-8643	CTG	0.95
IRIS_313-8645	CTG	1.11
IRIS_313-8647	CTG	0.91
IRIS_313-8659	CTG	1.00
IRIS_313-8660	CTG	0.94
IRIS_313-8674	CTG	0.79
IRIS_313-8699	CTG	0.96
IRIS_313-8704	CTG	0.69
IRIS_313-8717	TCC	1.16
IRIS_313-8722	CTG	0.10
IRIS_313-8725	CTG	0.97
IRIS_313-8727	CTG	0.55
IRIS_313-8731	CTG	0.65
IRIS_313-8732	CTG	0.83
IRIS_313-8733	TCC	1.18
IRIS_313-8737	TCC	1.29
IRIS_313-8743	CTG	0.89
IRIS_313-8744	CTG	1.13
IRIS_313-8751	CTG	0.56
IRIS_313-8754	CTG	0.75
IRIS_313-8757	CTG	0.75

Table S2

Accession IDs	LOC_Os08g31340	HRY Stability
IRIS_313-8781	CTG	0.92
IRIS_313-8785	TCC	0.98
IRIS_313-8796	CTG	0.74
IRIS_313-8812	CTG	0.89
IRIS_313-8831	CTG	1.10
IRIS_313-8844	TCC	0.98
IRIS_313-8846	CTG	0.86
IRIS_313-8850	CTG	1.10
IRIS_313-8854	CTG	0.78
IRIS_313-8889	CTG	0.88
IRIS_313-8900	CTG	0.92
IRIS_313-8903	CTG	0.74
IRIS_313-8914	CTG	0.84
IRIS_313-8920	TCC	1.18
IRIS_313-8924	CTG	0.74
IRIS_313-8925	TCC	1.04
IRIS_313-8930	CTG	0.63
IRIS_313-8932	CTG	0.84
IRIS_313-8935	CTG	0.82
IRIS_313-8940	CTG	0.96
IRIS_313-8946	CTG	0.76
IRIS_313-8956	CTG	1.24
IRIS_313-8967	CTG	0.68
IRIS_313-8968	CTG	0.99
IRIS_313-8980	CTG	0.43
IRIS_313-8982	CTG	0.84
IRIS_313-8986	CTG	0.78
IRIS_313-8988	CTG	0.58
IRIS_313-8994	CTG	0.80
IRIS_313-9005	CTG	0.62
IRIS_313-9017	CTG	0.55
IRIS_313-9023	CTG	0.52
IRIS_313-9032	-	0.83
IRIS_313-9044	CTG	0.71
IRIS_313-9065	-	1.09
IRIS_313-9066	CTG	0.99
IRIS_313-9067	TCC	0.96
IRIS_313-9072	CTG	0.88
IRIS_313-9111	CTG	0.97
IRIS_313-9119	CTG	0.91
IRIS_313-9139	CTG	0.91
IRIS_313-9148	CTG	0.73
IRIS_313-9156	CTG	0.78
IRIS_313-9174	CTG	0.93
IRIS_313-9184	CTG	0.90
IRIS_313-9190	TCC	0.73
IRIS_313-9198	TCC	0.87
IRIS_313-9204	CTG	0.91
IRIS_313-9218	TCC	0.95
IRIS_313-9227	CTG	0.49
IRIS_313-9253	CTG	0.76
IRIS_313-9256	CTG	0.67
IRIS_313-9259	CTC	0.70

Table S2

Accession IDs	LOC_Os08g31340	HRY Stability
IRIS_313-9262	CTG	0.56
IRIS_313-9271	CTG	0.71
IRIS_313-9281	CTG	0.70
IRIS_313-9286	CTG	0.75
IRIS_313-9287	CTG	0.55
IRIS_313-9313	CTG	0.71
IRIS_313-9314	CTG	0.90
IRIS_313-9317	CTG	0.94
IRIS_313-9320	CTG	0.70
IRIS_313-9324	CTG	0.77
IRIS_313-9325	CTG	0.61
IRIS_313-9348	CTG	0.66
IRIS_313-9351	CTG	0.68
IRIS_313-9360	TCC	0.78
IRIS_313-9372	CTG	0.73
IRIS_313-9384	CTG	1.11
IRIS_313-9388	CTG	0.90
IRIS_313-9400	CTG	0.56
IRIS_313-9403	TCC	0.99
IRIS_313-9424	CTG	0.88
IRIS_313-9427	CTG	0.69
IRIS_313-9429	CTG	0.90
IRIS_313-9433	CTG	0.86
IRIS_313-9451	CTG	0.84
IRIS_313-9461	CTG	0.92
IRIS_313-9469	CTG	0.85
IRIS_313-9472	CTG	0.58
IRIS_313-9482	CTG	0.62
IRIS_313-9484	CTG	0.39
IRIS_313-9492	CTG	0.75
IRIS_313-9503	-	0.45
IRIS_313-9505	CTG	0.77
IRIS_313-9522	CTG	0.85
IRIS_313-9533	CTG	0.73
IRIS_313-9547	CTG	0.92
IRIS_313-9551	CTG	0.90
IRIS_313-9557	CTG	1.15
IRIS_313-9560	CTG	0.68
IRIS_313-9566	CTG	0.76
IRIS_313-9570	CTG	0.83
IRIS_313-9572	CTG	0.91
IRIS_313-9574	TCC	1.40
IRIS_313-9590	CTG	0.98
IRIS_313-9593	CTG	0.70
IRIS_313-9594	CTG	0.88
IRIS_313-9602	CTG	0.85
IRIS_313-9604	CTG	0.79
IRIS_313-9605	CTG	0.89
IRIS_313-9609	TCC	0.99
IRIS_313-9611	CTG	0.75
IRIS_313-9617	TCC	1.30
IRIS_313-9623	CTG	0.72
IRIS_313-9634	CTC	0.39

Table S2

Accession IDs	LOC_Os08g31340	HRY Stability
IRIS_313-9696	CTG	0.95
IRIS_313-9705	CTG	0.87
IRIS_313-9706	CTG	0.90
IRIS_313-9708	CTG	0.48
IRIS_313-9723	CTG	1.03
IRIS_313-9727	CTG	0.91
IRIS_313-9730	CTG	0.70
IRIS_313-9732	CTG	0.65
IRIS_313-9740	CTG	0.60
IRIS_313-9758	CTG	0.93
IRIS_313-9767	CTG	0.89
IRIS_313-9791	CTG	0.55
IRIS_313-9795	CTG	0.61
IRIS_313-9831	CTG	1.12
IRIS_313-9841	CTG	0.72
IRIS_313-9862	CTG	1.13
IRIS_313-9867	CTG	0.83
IRIS_313-9882	CTG	0.81
IRIS_313-9898	-	0.46
IRIS_313-9917	CTG	0.86
IRIS_313-9922	CTG	0.85
IRIS_313-9924	CTG	0.70
IRIS_313-9925	CTG	0.81
IRIS_313-9940	CTG	0.49
IRIS_313-9944	CTG	0.85
IRIS_313-9953	CTG	0.50
IRIS_313-9966	CTG	0.30

Table S3

Table S3: Single locus GWAS for SNPs detected against Nipponbare reference genome with corresponding orthologous IDs in ZS97 and MH63.

Position	Chr	Ref	Alt	Beta	-log10 p-value	Region	Gene	Function of the Gene	Orthologous_ZS97	Orthologues_MH63
5117290	5	T	C	0.29	4.95	Upstream	LOC_Os05g09160	Unknown	Not Present	MH05g0088700
5237830	5	A	G	0.35	7.14	Upstream	LOC_Os05g09360	Unknown	ZS05g0108900	MH05g0091600
5299051	5	A	G	0.30	5.43	Upstream	LOC_Os05g09450	Unknown	Not present	Not present
5357676	5	C	A	-0.44	11.81	Upstream	LOC_Os05g09510	Unknown	ZS05g0109900	MH05g0092800
5358236	5	G	C	-0.42	9.89	Intergenic	LOC_Os05g09510, LOC_Os05g09520 (GW5)	Unknown, Signalling calcium	ZS05g0109900, ZS05g0110000	MH05g0092800, MH05g0093000
5359283	5	G	A	-0.39	10.26	Intergenic	LOC_Os05g09510, LOC_Os05g09520 (GW5)	Unknown, Signalling calcium	ZS05g0109900, ZS05g0110000	MH05g0092800, MH05g0093000
5359520	5	G	A	-0.48	14.45	Intergenic	LOC_Os05g09510, LOC_Os05g09520	Unknown, Signalling calcium	ZS05g0109900, ZS05g0110000	MH05g0092800, MH05g0093000
5361195	5	A	T	-0.37	9.83	Upstream	LOC_Os05g09520	Signalling calcium	ZS05g0110000	MH05g0093000
5361276	5	T	C	-0.49	15.04	Upstream	LOC_Os05g09520	Signalling calcium	ZS05g0110000	MH05g0093000
5363611	5	A	G	-0.42	12.26	Upstream	LOC_Os05g09520	Signalling calcium	ZS05g0110000	MH05g0093000
5368403	5	A	G	-0.34	8.61	Downstream	LOC_Os05g09520	Signalling calcium	ZS05g0110000	MH05g0093000
5369802	5	A	G	-0.42	11.82	Downstream	LOC_Os05g09520	Signalling calcium	ZS05g0110000	MH05g0093000
5373379	5	G	A	-0.38	10.21	Intergenic	LOC_Os05g09520, LOC_Os05g09530	Signalling calcium, Aspartate protease	ZS05g0110000- ZS05g0110100	MH05g0093000, MH05g0093100
5374961	5	C	T	-0.34	8.19	Intergenic	LOC_Os05g09520, LOC_Os05g09530	Signalling calcium, Aspartate protease	ZS05g0110000- ZS05g0110100	MH05g0093000, MH05g0093100
5377012	5	A	G	-0.28	5.73	Intergenic	LOC_Os05g09520, LOC_Os05g09530	Signalling calcium, Aspartate protease	ZS05g0110000- ZS05g0110100	MH05g0093000, MH05g0093100
5377744	5	T	A	-0.27	5.55	Intergenic	LOC_Os05g09520, LOC_Os05g09530	Signalling calcium, Aspartate protease	ZS05g0110000- ZS05g0110100	MH05g0093000, MH05g0093100
5378981	5	A	T	-0.37	9.01	Downstream	LOC_Os05g09520, LOC_Os05g09530	Signalling calcium, Aspartate protease	ZS05g0110000- ZS05g0110100	MH05g0093000, MH05g0093100
5433386	5	T	C	0.30	6.91	Downstream	LOC_Os05g09620	Unknown	ZS05g0110700	MH05g0094000

Table S4

Table S4 : Accessions used in the study, with the exiting haplotypes for lowering chalk in hotspot regions of chromosome 5.

■ Favourable haplotype identified for lowering chalk
■ Missing/heterozygous

Accession IDs	New_gene	LOC_Os05g09520	LOC_Os05g09530	PGC
IRIS_313-10000	ATATGCTAAGAGCTA	GCTAGG	TGGTCTGTATTCGTTGGAA	60.30
IRIS_313-10001	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	3.95
IRIS_313-10007	ATATGCTAAGAGCTA	GCTAGG	TGGTCTGTATTCGTTGGAA	92.75
IRIS_313-10016	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	7.18
IRIS_313-10026	-	-	TGGGTCTGTGTTTCGTTGGAA	30.98
IRIS_313-10030	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCAGGACAACTAGG	84.87
IRIS_313-10034	ATATGCTAAGAGCTA	-	TGGGTCTGTATTCGTTGGAA	2.73
IRIS_313-10040	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCAGGACAACTAGG	2.78
IRIS_313-10045	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	7.28
IRIS_313-10046	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	4.47
IRIS_313-10047	-	GCTAGG	CAAGCTCAGGACAACTAGG	10.03
IRIS_313-10048	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	9.29
IRIS_313-10050	ATATGCTAAGAGCTA	GCTAGG	-	16.56
IRIS_313-10054	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	4.61
IRIS_313-10077	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	7.99
IRIS_313-10102	GCTCGCTGGGGGCCG	GCCGGT	TGGGTCTGTGTTTCGTTGGAA	7.40
IRIS_313-10103	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	68.30
IRIS_313-10109	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	8.38
IRIS_313-10113	-	ATCGTT	TGGGTCTGTATTCGTTGGAA	3.02
IRIS_313-10114	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	42.66
IRIS_313-10129	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCAGGACAACTAGG	30.79
IRIS_313-10147	-	GCTAGG	TGGTCTGTATTCGTTGGAA	1.38
IRIS_313-10148	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCAGGACAACTAGG	6.99
IRIS_313-10151	GCTCAAAGGAGATCG	GCTAGG	TGGTCTGTATTCGTTGGAA	0.89
IRIS_313-10154	ATATGCTAAGAGCTA	GCTAGG	TGGTCTGTATTCGTTGGAA	28.10
IRIS_313-10167	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	2.36
IRIS_313-10168	ATATGCTAAGAGCTA	GCTAGG	TGGTCTGTATTCGTTGGAA	58.20
IRIS_313-10170	-	-	TGGTCTGTATTCGTTGGAA	39.75
IRIS_313-10171	ATATGCTAAGAGCTA	GCTAGG	TGGTCTGTATTCGTTGGAA	35.57
IRIS_313-10177	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCAGGACAACTAGG	12.94
IRIS_313-10178	ATATGCTAAGAGCTA	GCTAGG	-	7.70
IRIS_313-10179	ATATGCTAAGAGCTA	GCTAGG	TGGGTCTGTATTCGTTGGAA	9.54
IRIS_313-10191	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	0.17
IRIS_313-10220	GCTCGCTGGGGGCCG	GCCGGT	TGGGTCTGTGTTTCGTTGGAA	4.36
IRIS_313-10221	ATATGCTAAGAGCTA	GCTAGG	TGGGTCTGTATTCGTTGGAA	9.33
IRIS_313-10224	-	-	TGGGTCTGTGTTTCGTTGGAA	21.80
IRIS_313-10226	ATATGCTAAGAGCTA	GCTAGG	-	42.54
IRIS_313-10234	ATATGCTAAGAGCTA	GCTAGG	TGGTCTGTATTCGTTGGAA	21.53
IRIS_313-10235	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	4.72
IRIS_313-10237	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	2.55
IRIS_313-10238	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	0.94
IRIS_313-10247	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	0.87
IRIS_313-10257	GCTCAAAGGAGATCG	ATCGTT	-	6.49
IRIS_313-10260	GCTCGCTGGGGGCCG	GCCGGT	TGGGTCTGTGTTTCGTTGGAA	6.47
IRIS_313-10263	-	GCCGGT	-	2.61
IRIS_313-10268	-	GCCGGT	TGGGTCTGTGTTTCGTTGGAA	5.86
IRIS_313-10271	GCTCGCTGGGGGCCG	GCCGGT	-	7.45
IRIS_313-10274	-	-	-	1.22

Table S4

Accession IDs	New_gene	LOC_Os05g09520	LOC_Os05g09530	PGC
IRIS_313-10275	GCTCGCTGGGGGCCG	GCCGGT	TGGGTCTGTGTTTCGTTGGAA	8.67
IRIS_313-10279	GCTCAAAGGAGAGCTA	GCTAGG	TGGTCTGTATTCGTTGGAA	6.67
IRIS_313-10285	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	4.59
IRIS_313-10287	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	4.75
IRIS_313-10289	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	3.95
IRIS_313-10293	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	0.91
IRIS_313-10294	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	1.15
IRIS_313-10298	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	12.73
IRIS_313-10300	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	2.69
IRIS_313-10301	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	11.13
IRIS_313-10307	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	6.77
IRIS_313-10314	-	GCCGGT	TGGGTCTGTGTTTCGTTGGAA	2.25
IRIS_313-10318	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	3.80
IRIS_313-10325	GCTCGCTGGGGGCCG	GCCGGT	TGGGTCTGTGTTTCGTTGGAA	3.40
IRIS_313-10332	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	1.83
IRIS_313-10333	ATATGCTAAGAGCTA	GCTAGG	TGGTCTGTATTCGTTGGAA	22.76
IRIS_313-10334	ATATGCTAAGAGCTA	GCTAGG	-	13.75
IRIS_313-10337	ATATGCTAAGAGCTA	GCTAGG	TGGGTCTGTATTCGTTGGAA	42.29
IRIS_313-10340	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	10.84
IRIS_313-10349	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	7.61
IRIS_313-10352	GCTCGCTGGGGGCCG	GCCGGT	TGGGTCTGTGTTTCGTTGGAA	4.86
IRIS_313-10353	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCACGACAACTAGG	92.38
IRIS_313-10355	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	9.22
IRIS_313-10357	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	3.54
IRIS_313-10359	-	-	TGGGTCTGTGTTTCGTTGGAA	16.02
IRIS_313-10360	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	1.54
IRIS_313-10361	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCACGACAACTAGG	30.73
IRIS_313-10366	-	-	TGGGTCTGTATTCGTTGGAA	1.23
IRIS_313-10371	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	5.48
IRIS_313-10374	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	4.75
IRIS_313-10375	ATATGCTAAGAGCTA	GCTAGG	CAAGCCCACGACAACTAGG	29.99
IRIS_313-10385	-	ATCGTT	TGGGTCTGTATTCGTTGGAA	1.33
IRIS_313-10392	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	3.83
IRIS_313-10394	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	9.40
IRIS_313-10396	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	2.38
IRIS_313-10397	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	0.43
IRIS_313-10398	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	0.83
IRIS_313-10399	-	GCTAGG	TGGTCTGTATTCGTTGGAA	3.88
IRIS_313-10400	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	0.61
IRIS_313-10401	-	ATCGTT	TGGGTCTGTATTCGTTGGAA	2.97
IRIS_313-10402	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	3.03
IRIS_313-10403	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	0.14
IRIS_313-10404	ATATGCTAAGAGCTA	-	TGGGTCTGTGTTTCGTTGGAA	9.65
IRIS_313-10412	-	-	TGGTCTGTATTCGTTGGAA	15.54
IRIS_313-10417	-	GCTAGG	CAAGCTCACGACAACTAGG	26.98
IRIS_313-10421	ATATGCTAAGAGCTA	GCTAGG	TGGGTCTGTATTCGTTGGAA	10.29
IRIS_313-10422	-	-	-	22.84
IRIS_313-10423	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCACGACAACTAGG	26.69
IRIS_313-11437	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	5.01
IRIS_313-11467	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	1.17
IRIS_313-11478	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	18.58
IRIS_313-11487	-	-	TGGGTCTGTATTCGTTGGAA	4.40
IRIS_313-11508	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	1.02
IRIS_313-11570	-	GCTAGG	TGGTCTGTATTCGTTGGAA	50.43

Table S4

Accession IDs	New_gene	LOC_Os05g09520	LOC_Os05g09530	PGC
IRIS_313-11573	-	ATCGTT	TGGGTCTGTATTCGTTGGAA	22.91
IRIS_313-11577	-	ATCGTT	TGGGTCTGTATTCGTTGGAA	19.46
IRIS_313-11580	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	0.08
IRIS_313-11585	ATTTGCTAAGAGCTA	GCTAGG	CAAGCTCAGGACAACTAGG	25.96
IRIS_313-11609	GCTCAAAGGAGATCG	-	TGGGTCTGTATTCGTTGGAA	9.21
IRIS_313-11650	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	5.33
IRIS_313-11671	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	4.68
IRIS_313-11724	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCAGGACAACTAGG	22.66
IRIS_313-11747	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	1.19
IRIS_313-11802	-	ATCGTT	TGGGTCTGTATTCGTTGGAA	29.04
IRIS_313-11828	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCAGGACAACTAGG	5.26
IRIS_313-7688	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	0.58
IRIS_313-7719	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	1.14
IRIS_313-7725	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	3.55
IRIS_313-8068	GCTCAAAGGAGATCG	ATCGTT	-	6.34
IRIS_313-8069	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	2.25
IRIS_313-8161	GCTCAAAGGAGATCG	ATCGTT	-	12.78
IRIS_313-8288	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	52.33
IRIS_313-8303	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	2.56
IRIS_313-8305	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	16.18
IRIS_313-8315	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	40.78
IRIS_313-8332	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	28.17
IRIS_313-8368	GCTCAAAGGAGATCG	ATCGTT	-	29.35
IRIS_313-8380	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCAGGACAACTAGG	84.21
IRIS_313-8383	-	-	-	43.08
IRIS_313-8386	ATATGCTAAGAGCTA	GCTAGG	TGGGTCTGTATTCGTTGGAA	6.39
IRIS_313-8392	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	12.67
IRIS_313-8401	-	-	-	63.93
IRIS_313-8405	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCAGGACAACTAGG	36.46
IRIS_313-8409	-	ATCGTT	TGGGTCTGTATTCGTTGGAA	7.58
IRIS_313-8412	GCTCAAAGGAGATCG	ATCGTT	-	8.00
IRIS_313-8414	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	17.89
IRIS_313-8433	ATATGCTAAGAGCTA	GCTAGG	-	17.77
IRIS_313-8435	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCAGGACAACTAGG	51.63
IRIS_313-8437	ATATGCTAAGAGCTA	GCTAGG	CAAGCCCAGGACAACTAGG	84.48
IRIS_313-8450	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	4.43
IRIS_313-8453	ATATGCTAAGAGCTA	GCTAGG	TGGGTCTGTATTCGTTGGAA	14.98
IRIS_313-8454	ATATGCTAAGAGCTA	GCTAGG	TGGTCTGTATTCGTTGGAA	8.48
IRIS_313-8458	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	6.71
IRIS_313-8509	-	ATCGTT	TGGGTCTGTATTCGTTGGAA	2.37
IRIS_313-8514	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCAGGACAACTAGG	20.98
IRIS_313-8530	ATATGCTAAGAGCTA	GCTAGG	CAAGCCCAGGACAACTAGG	46.36
IRIS_313-8536	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	9.37
IRIS_313-8559	-	GCTAGG	CAAGCTCAGGACAACTAGG	8.72
IRIS_313-8568	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	21.02
IRIS_313-8571	-	-	TGGGTCTGTATTCGTTGGAA	3.88
IRIS_313-8585	-	-	TGGGTCTGTATTCGTTGGAA	40.12
IRIS_313-8586	ATATGCTAAGAGCTA	GCTAGG	TGGGTCTGTATTCGTTGGAA	87.75
IRIS_313-8595	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	75.83
IRIS_313-8603	ATATGCTAAGAGCTA	GCTAGG	TGGTCTGTATTCGTTGGAA	93.84
IRIS_313-8614	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	0.58
IRIS_313-8616	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	1.05
IRIS_313-8621	-	ATCGTT	TGGGTCTGTATTCGTTGGAA	16.71
IRIS_313-8622	ATTTGCTAAGAGCTA	GCTAGG	TGGGTCTGTATTCGTTGGAA	40.04

Table S4

Accession IDs	New_gene	LOC_Os05g09520	LOC_Os05g09530	PGC
IRIS_313-8631	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCACGACAACTAGG	13.44
IRIS_313-8632	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	35.79
IRIS_313-8638	ATATGCTAAGAGCTA	GCTAGG	TGGTTCTGTATTCGTTGGAA	92.82
IRIS_313-8643	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCACGACAACTAGG	2.67
IRIS_313-8645	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCACGACAACTAGG	34.17
IRIS_313-8647	-	-	-	6.21
IRIS_313-8659	ATATGCTAAGAGCTA	GCTAGG	TGGGTCTGTATTCGTTGGAA	39.73
IRIS_313-8660	-	ATCGTT	TGGGTCTGTATTCGTTGGAA	10.65
IRIS_313-8674	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	0.82
IRIS_313-8697	-	ATCGTT	TGGGTCTGTATTCGTTGGAA	0.71
IRIS_313-8699	ATATGCTAAGAGCTA	GCTAGG	TGGGTCTGTTCGTTGGAA	12.43
IRIS_313-8704	-	-	-	5.31
IRIS_313-8717	ATATGCTAAGAGCTA	GCTAGG	TGGGTCTGTATTCGTTGGAA	47.75
IRIS_313-8722	ATATGCTAAGAGCTA	GCTAGG	TGGTTCTGTATTCGTTGGAA	87.13
IRIS_313-8725	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	52.53
IRIS_313-8727	ATATGCTAAGAGCTA	-	-	17.42
IRIS_313-8731	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCACGACAACTAGG	22.60
IRIS_313-8732	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	3.76
IRIS_313-8733	ATATGCTAAGAGCTA	GCTAGG	CAAGCCCACGACAACTAGG	24.39
IRIS_313-8737	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTTCGTTGGAA	24.38
IRIS_313-8743	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCACGACAACTAGG	33.54
IRIS_313-8744	ATATGCTAAGAGCTA	GCTAGG	TGGGTCTGTATTCGTTGGAA	54.46
IRIS_313-8751	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	2.32
IRIS_313-8754	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCACGACAACTAGG	35.63
IRIS_313-8757	ATATGCTAAGAGCTA	-	TGGGTCTGTATTCGTTGGAA	31.68
IRIS_313-8781	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	5.20
IRIS_313-8785	GCTCAAAGAGAGCTA	GCTAGG	TGGTTCTGTATTCGTTGGAA	3.67
IRIS_313-8796	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	4.13
IRIS_313-8812	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCACGACAACTAGG	41.84
IRIS_313-8831	-	GCTAGG	CAAGCTCACGACAACTAGG	17.93
IRIS_313-8844	-	ATCGTT	TGGGTCTGTATTCGTTGGAA	15.66
IRIS_313-8846	ATATGCTAAGAGCTA	GCTAGG	-	41.54
IRIS_313-8850	-	GCTAGG	TGGGTCTGTATTCGTTGGAA	37.35
IRIS_313-8854	-	ATCGTT	-	21.55
IRIS_313-8889	-	-	CAAGCTCACGACAACTAGG	9.61
IRIS_313-8900	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	9.42
IRIS_313-8903	GCTCAAAGGAGATCG	ATCGTT	-	8.00
IRIS_313-8914	ATATGCTAAGAGCTA	GCTAGG	TGGTTCTGTATTCGTTGGAA	7.98
IRIS_313-8920	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	3.85
IRIS_313-8924	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCACGACAACTAGG	10.06
IRIS_313-8925	ATATGCTAAGAGCTA	GCTAGG	CAAGCCCACGACAACTAGG	42.54
IRIS_313-8930	ATATGCTAAGAGCTA	GCTAGG	CAAGCCCACGACAACTAGG	53.00
IRIS_313-8932	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	2.30
IRIS_313-8935	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	2.68
IRIS_313-8940	ATATGCTAAGAGCTA	GCTAGG	TGGTTCTGTATTCGTTGGAA	28.46
IRIS_313-8946	ATATGCTAAGAGCTA	GCTAGG	TGGTTCTGTATTCGTTGGAA	78.73
IRIS_313-8948	ATATGCTAAGAGCTA	GCTAGG	TGGTTCTGTATTCGTTGGAA	4.91
IRIS_313-8956	GCTCGCTGGGGCCG	GCCGGT	-	7.02
IRIS_313-8967	-	ATCGTT	TGGGTCTGTATTCGTTGGAA	30.13
IRIS_313-8968	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCACGACAACTAGG	29.56
IRIS_313-8980	ATATGCTAAGAGCTA	GCTAGG	TGGTTCTGTATTCGTTGGAA	90.52
IRIS_313-8982	GCTCAAAGGAGATCG	ATCGTT	-	9.44
IRIS_313-8986	-	-	TGGGTCTGTTCGTTGGAA	12.38
IRIS_313-8987	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	2.58

Table S4

Accession IDs	New_gene	LOC_Os05g09520	LOC_Os05g09530	PGC
IRIS_313-8988	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	1.98
IRIS_313-8994	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	60.56
IRIS_313-9005	ATATGCTAAGAGCTA	GCTAGG	TGGGTCTGTATTCGTTGGAA	33.83
IRIS_313-9017	ATATGCTAAGAGCTA	GCTAGG	TGGTCTGTATTCGTTGGAA	48.05
IRIS_313-9023	ATATGCTAAGAGCTA	GCTAGG	TGGGTCTGTTCGTTGGAA	6.91
IRIS_313-9032	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	2.18
IRIS_313-9044	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	1.78
IRIS_313-9065	ATATGCTAAGAGCTA	GCTAGG	-	27.12
IRIS_313-9066	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	1.47
IRIS_313-9067	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	39.85
IRIS_313-9072	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	5.39
IRIS_313-9111	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	1.18
IRIS_313-9119	GCTCAAAGGAGATCG	ATCGTT	-	3.02
IRIS_313-9139	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	3.52
IRIS_313-9148	ATATGCTAAGAGCTA	GCTAGG	CAAGCCCACGACAAACTAGG	22.56
IRIS_313-9156	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	6.33
IRIS_313-9174	-	ATCGTT	TGGGTCTGTATTCGTTGGAA	43.79
IRIS_313-9184	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCACGACAAACTAGG	10.28
IRIS_313-9187	-	-	-	22.56
IRIS_313-9190	-	-	CAAGCTCACGACAAACTAGG	0.59
IRIS_313-9197	ATATGCTAAGAGCTA	GCTAGG	-	65.23
IRIS_313-9198	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	81.53
IRIS_313-9204	ATATGCTAAGAGCTA	-	TGGTCTGTATTCGTTGGAA	17.19
IRIS_313-9218	-	ATCGTT	-	22.12
IRIS_313-9227	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	4.51
IRIS_313-9253	ATTTGCTAAGAGCTA	GCTAGG	CAAGCTCACGACAAACTAGG	41.75
IRIS_313-9256	-	GCTAGG	CAAGCCCACGACAAACTAGG	35.09
IRIS_313-9259	GCTCAAAGGAGATCG	-	TGGGTCTGTATTCGTTGGAA	7.33
IRIS_313-9262	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	7.47
IRIS_313-9271	GCTCAAAGGAGATCG	ATCGTT	-	5.74
IRIS_313-9281	ATATGCTAAGAGCTA	GCTAGG	TGGTCTGTATTCGTTGGAA	18.29
IRIS_313-9285	ATATGCTAAGAGCTA	GCTAGG	-	21.72
IRIS_313-9286	GCTCAAAGGAGAGCTA	GCTAGG	TGGTCTGTATTCGTTGGAA	2.86
IRIS_313-9287	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	40.83
IRIS_313-9288	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	8.18
IRIS_313-9313	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	18.58
IRIS_313-9314	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	28.95
IRIS_313-9317	ATATGCTAAGAGCTA	-	TGGGTCTGTATTCGTTGGAA	8.11
IRIS_313-9320	ATATGCTAAGAGCTA	GCTAGG	-	100.00
IRIS_313-9324	ATATGCTAAGAGCTA	GCTAGG	TGGTCTGTATTCGTTGGAA	53.88
IRIS_313-9325	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	13.53
IRIS_313-9348	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	1.57
IRIS_313-9351	-	ATCGTT	TGGGTCTGTATTCGTTGGAA	23.12
IRIS_313-9360	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	2.71
IRIS_313-9372	ATATGCTAAGAGCTA	GCTAGG	TGGTCTGTATTCGTTGGAA	25.13
IRIS_313-9384	GCTCAAAGGAGATCG	ATCGTT	-	0.51
IRIS_313-9388	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCACGACAAACTAGG	40.26
IRIS_313-9400	GCTCAAAGGAGATCG	ATCGTT	-	17.30
IRIS_313-9403	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	2.50
IRIS_313-9424	ATATGCTAAGAGCTA	GCTAGG	TGGTCTGTATTCGTTGGAA	15.62
IRIS_313-9427	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	41.50
IRIS_313-9429	-	ATCGTT	TGGGTCTGTATTCGTTGGAA	7.20
IRIS_313-9433	-	ATCGTT	TGGGTCTGTATTCGTTGGAA	51.43
IRIS_313-9451	GCTCAAAGGAGAGCTA	GCTAGG	TGGTCTGTATTCGTTGGAA	14.68

Table S4

Accession IDs	New_gene	LOC_Os05g09520	LOC_Os05g09530	PGC
IRIS_313-9461	-	ATCGTT	TGGGTCTGTATTCGTTGGAA	0.45
IRIS_313-9469	ATTTGCTAAGAGCTA	GCTAGG	CAAGCTCAGGACAACTAGG	63.79
IRIS_313-9472	-	-	-	13.82
IRIS_313-9482	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	2.60
IRIS_313-9484	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	6.45
IRIS_313-9492	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	37.36
IRIS_313-9503	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	8.36
IRIS_313-9505	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	7.65
IRIS_313-9522	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCAGGACAACTAGG	36.93
IRIS_313-9533	-	ATCGTT	TGGGTCTGTATTCGTTGGAA	1.81
IRIS_313-9547	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	22.84
IRIS_313-9551	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	6.56
IRIS_313-9557	ATATGCTAAGAGCTA	GCTAGG	TGGGTCTGTATTCGTTGGAA	28.36
IRIS_313-9560	ATATGCTAAGAGCTA	GCTAGG	-	40.11
IRIS_313-9566	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	4.89
IRIS_313-9570	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	1.45
IRIS_313-9572	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	15.25
IRIS_313-9574	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	3.35
IRIS_313-9590	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	53.99
IRIS_313-9593	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	29.40
IRIS_313-9594	ATATGCTAAGAGCTA	GCTAGG	CAAGCCCAGGACAACTAGG	89.99
IRIS_313-9602	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	2.56
IRIS_313-9604	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	2.91
IRIS_313-9605	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCAGGACAACTAGG	8.44
IRIS_313-9609	ATATGCTAAGAGCTA	GCTAGG	TGGTCTGTATTCGTTGGAA	8.04
IRIS_313-9611	-	-	CAAGCTCAGGACAACTAGG	4.30
IRIS_313-9617	ATATGCTAAGAGCTA	GCTAGG	TGGGTCTGTATTCGTTGGAA	68.45
IRIS_313-9623	GCTCAAAGGAGATCG	ATCGTT	-	4.22
IRIS_313-9634	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	76.20
IRIS_313-9696	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	1.05
IRIS_313-9705	ATTTGCTAAGAGCTA	GCTAGG	-	18.71
IRIS_313-9706	ATTTGCTAAGAGCTA	GCTAGG	CAAGCTCAGGACAACTAGG	14.98
IRIS_313-9708	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCAGGACAACTAGG	4.31
IRIS_313-9723	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCAGGACAACTAGG	38.42
IRIS_313-9727	ATATGCTAAGAGCTA	GCTAGG	TGGTCTGTATTCGTTGGAA	37.02
IRIS_313-9730	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCAGGACAACTAGG	26.77
IRIS_313-9732	-	-	-	8.08
IRIS_313-9740	GCTCAAAGGAGATCG	ATCGTT	-	48.03
IRIS_313-9758	ATTTGCTAAGAGCTA	GCTAGG	CAAGCCCAGGACAACTAGG	19.15
IRIS_313-9767	-	GCCGGT	TGGGTCTGTGTTTCGTTGGAA	9.09
IRIS_313-9791	-	GCTAGG	-	34.96
IRIS_313-9795	GCTCAAAGGAGATCG	ATCGTT	CAAGCCCAGGACAACTAGG	9.49
IRIS_313-9831	ATATGCTAAGAGCTA	GCTAGG	-	34.49
IRIS_313-9841	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	2.32
IRIS_313-9862	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCAGGACAACTAGG	69.82
IRIS_313-9867	ATATGCTAAGAGCTA	GCTAGG	TGGTCTGTATTCGTTGGAA	67.46
IRIS_313-9882	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCAGGACAACTAGG	88.94
IRIS_313-9898	GCTCAAAGGAGATCG	-	TGGTCTGTATTCGTTGGAA	11.28
IRIS_313-9917	ATATGCTAAGAGCTA	GCTAGG	TGGTCTGTATTCGTTGGAA	9.71
IRIS_313-9922	GCTCAAAGGAGATCG	ATCGTT	CAAGCCCAGGACAACTAGG	5.62
IRIS_313-9924	ATATGCTAAGAGCTA	GCTAGG	TGGTCTGTATTCGTTGGAA	15.36
IRIS_313-9925	GCTCAAAGGAGATCG	ATCGTT	CAAGCCCAGGACAACTAGG	5.45
IRIS_313-9940	GCTCGCTGGGGGCCG	GCCGGT	TGGGTCTGTGTTTCGTTGGAA	8.65
IRIS_313-9944	GCTCAAAGGAGATCG	ATCGTT	-	3.67

Table S4

Accession IDs	New_gene	LOC_Os05g09520	LOC_Os05g09530	PGC
IRIS_313-9953	GCTCAAAGGAGATCG	ATCGTT	TGGGTCTGTATTCGTTGGAA	10.01
IRIS_313-9966	GCTCGCTGGGGGCCG	GCCGGT	TGGGTCTGTGTTTCGTTGGAA	6.97
IRIS_313-9968	ATATGCTAAGAGCTA	GCTAGG	-	30.61
IRIS_313-9969	ATATGCTAAGAGCTA	GCTAGG	TGGTTCTGTATTCGTTGGAA	90.56
IRIS_313-9970	ATATGCTAAGAGCTA	GCTAGG	CAAGCTCACGACAACTAGG	18.53
IRIS_313-9976	ATTTGCTAAGAGCTA	GCTAGG	CAAGCTCACGACAACTAGG	29.27

Table S5: Single locus GWAS for SNPs detected against ZS97 reference genome with corresponding orthologous ids in MH63 and Nipponbare.

Position	Chr	Ref	Alt	Beta	-log10 p-value	Region	Gene	Orthologues_MH63	Orthologues_Nipponbare
4104137	5	G	C	0.30	5.70	Upstream	ZS05g0093300	MH05g0082900	LOC_Os05g08670
4599654	5	T	A	-0.41	11.70	Upstream	ZS05g0110000 (GW5)	MH05g0093000 (GW5)	LOC_Os05g09520 (GW5)
4599671	5	A	G	-0.48	14.84	Upstream	ZS05g0110000	MH05g0093000	LOC_Os05g09520
4600629	5	A	G	-0.46	11.23	Upstream	ZS05g0110000	MH05g0093000	LOC_Os05g09520
4602339	5	G	T	-0.45	13.14	Upstream	ZS05g0110000	MH05g0093000	LOC_Os05g09520
4607243	5	A	T	-0.43	12.39	Downstream	ZS05g0110000	MH05g0093000	LOC_Os05g09520
4607689	5	A	T	-0.45	13.41	Downstream	ZS05g0110000	MH05g0093000	LOC_Os05g09520
4607936	5	A	G	-0.43	12.29	Downstream	ZS05g0110000	MH05g0093000	LOC_Os05g09520
4608886	5	T	C	-0.43	12.40	Downstream	ZS05g0110000	MH05g0093000	LOC_Os05g09520
4609180	5	T	C	-0.43	12.41	Downstream	ZS05g0110000	MH05g0093000	LOC_Os05g09520
4609667	5	C	A	-0.41	11.34	Downstream	ZS05g0110000	MH05g0093000	LOC_Os05g09520
4609747	5	A	G	-0.40	10.65	Downstream	ZS05g0110000	MH05g0093000	LOC_Os05g09520
4609824	5	C	T	-0.40	10.48	Downstream	ZS05g0110000	MH05g0093000	LOC_Os05g09520
4609854	5	G	A	-0.41	10.98	Downstream	ZS05g0110000	MH05g0093000	LOC_Os05g09520
4609910	5	G	A	-0.41	11.03	Downstream	ZS05g0110000	MH05g0093000	LOC_Os05g09520
4610087	5	C	G	-0.42	11.68	Downstream	ZS05g0110000	MH05g0093000	LOC_Os05g09520
4610188	5	C	T	-0.40	10.33	Downstream	ZS05g0110000	MH05g0093000	LOC_Os05g09520
4611979	5	C	T	-0.40	10.53	Intergenic	ZS05g0110000-ZS05g0110100	MH05g0093000-MH05g0093100	LOC_Os05g09520-LOC_Os05g09530
4612359	5	C	T	-0.40	10.33	Intergenic	ZS05g0110000-ZS05g0110100	MH05g0093000-MH05g0093100	LOC_Os05g09520-LOC_Os05g09530
4613099	5	C	T	-0.37	8.69	Intergenic	ZS05g0110000-ZS05g0110100	MH05g0093000-MH05g0093100	LOC_Os05g09520-LOC_Os05g09530
4613339	5	T	C	-0.36	8.10	Intergenic	ZS05g0110000-ZS05g0110100	MH05g0093000-MH05g0093100	LOC_Os05g09520-LOC_Os05g09530
4613365	5	T	C	-0.35	7.67	Intergenic	ZS05g0110000-ZS05g0110100	MH05g0093000-MH05g0093100	LOC_Os05g09520-LOC_Os05g09530
4613902	5	A	G	-0.35	7.72	Intergenic	ZS05g0110000-ZS05g0110100	MH05g0093000-MH05g0093100	LOC_Os05g09520-LOC_Os05g09530
4613924	5	G	A	-0.36	8.43	Intergenic	ZS05g0110000-ZS05g0110100	MH05g0093000-MH05g0093100	LOC_Os05g09520-LOC_Os05g09530
4613931	5	G	A	-0.34	7.44	Intergenic	ZS05g0110000-ZS05g0110100	MH05g0093000-MH05g0093100	LOC_Os05g09520-LOC_Os05g09530
4613987	5	C	A	-0.27	5.14	Intergenic	ZS05g0110000-ZS05g0110100	MH05g0093000-MH05g0093100	LOC_Os05g09520-LOC_Os05g09530
4614060	5	A	G	-0.35	8.01	Intergenic	ZS05g0110000-ZS05g0110100	MH05g0093000-MH05g0093100	LOC_Os05g09520-LOC_Os05g09530
4614276	5	G	A	-0.34	7.48	Intergenic	ZS05g0110000-ZS05g0110100	MH05g0093000-MH05g0093100	LOC_Os05g09520-LOC_Os05g09530
4614292	5	C	T	-0.30	6.15	Intergenic	ZS05g0110000-ZS05g0110100	MH05g0093000-MH05g0093100	LOC_Os05g09520-LOC_Os05g09530
4614299	5	A	G	-0.34	7.50	Intergenic	ZS05g0110000-ZS05g0110100	MH05g0093000-MH05g0093100	LOC_Os05g09520-LOC_Os05g09530
4614499	5	T	C	-0.29	5.99	Intergenic	ZS05g0110000-ZS05g0110100	MH05g0093000-MH05g0093100	LOC_Os05g09520-LOC_Os05g09530
4614515	5	A	G	-0.30	6.24	Intergenic	ZS05g0110000-ZS05g0110100	MH05g0093000-MH05g0093100	LOC_Os05g09520-LOC_Os05g09530
4615150	5	A	G	-0.31	6.39	Intergenic	ZS05g0110000-ZS05g0110100	MH05g0093000-MH05g0093100	LOC_Os05g09520-LOC_Os05g09530
4615250	5	T	A	-0.37	8.88	Intergenic	ZS05g0110000-ZS05g0110100	MH05g0093000-MH05g0093100	LOC_Os05g09520-LOC_Os05g09530
4615336	5	T	C	-0.37	8.94	Intergenic	ZS05g0110000-ZS05g0110100	MH05g0093000-MH05g0093100	LOC_Os05g09520-LOC_Os05g09530
4615445	5	A	G	-0.36	8.30	Intergenic	ZS05g0110000-ZS05g0110100	MH05g0093000-MH05g0093100	LOC_Os05g09520-LOC_Os05g09530
4615745	5	A	G	-0.37	8.74	Intergenic	ZS05g0110000-ZS05g0110100	MH05g0093000-MH05g0093100	LOC_Os05g09520-LOC_Os05g09530
4616584	5	T	A	-0.37	8.36	Intergenic	ZS05g0110000-ZS05g0110100	MH05g0093000-MH05g0093100	LOC_Os05g09520-LOC_Os05g09530

Position	Chr	Ref	Alt	Beta	-log10 p-value	Region	Gene	Orthologues_MH63	Orthologues_Nipponbare
4617119	5	A	T	-0.38	9.09	Intergenic	ZS05g0110000-ZS05g0110100	MH05g0093000-MH05g0093100	LOC_Os05g09520-LOC_Os05g09530
5054322	5	A	C	-0.31	5.27	Downstream	ZS05g0115200	MH05g0098900	LOC_Os05g10690
5069547	5	T	C	-0.27	5.16	Upstream	ZS05g0115300	MH05g0099000	LOC_Os05g10700

Table S6

Table S6: Single locus GWAS for SNPs detected against MH63 reference genome with corresponding Orthologous IDs in ZS97 and Nipponbare

Position	Chr	Ref	Alt	Beta	-log10 p-value	Effect	Gene	Orthologous_ZS97	Orthologous_Nipponbare
5012096	5	T	C	0.29	5.28	Synonymous	MH05g0089300	Not present	LOC_Os05g09200
5107094	5	A	G	0.35	8.16	Upstream	MH05g0091600	ZS05g0108900	LOC_Os05g09360
5192872	5	T	C	0.36	8.67	Upstream	MH05g0092200	Not present	LOC_Os05g09470
5269365	5	T	C	-0.32	7.30	Upstream	MH05g0093300	ZS05g0110300	LOC_Os05g09550
5298677	5	C	T	-0.30	6.63	Upstream	MH05g0094100	ZS05g0110700	LOC_Os05g09630
5302192	5	T	C	-0.30	6.60	Upstream	MH05g0094100	ZS05g0110700	LOC_Os05g09630

Table S7

Table S7: Genes/QTLs characterized in the mutants influencing the grain chalkiness.

Gene/QTL	Chr	Locus ID	Start-end positions (Mb)	Effect	Reference
<i>SUBSTANDARD STARCH GRAIN4 (SSG4)</i>	1	LOC_Os01g08420	4.13-4.14	Chalk endosperm	(Matsushima <i>et al.</i> , 2014)
<i>OsAPL2</i>	1	LOC_Os01g44220	25.35-25.36	Chalky endosperm	(Zhang <i>et al.</i> , 2012)
<i>SBEIIB</i>	2	LOC_Os02g32660	19.37-19.36	Amylose-Extender Mutation in Rice	(Butardo <i>et al.</i> , 2011; Nishi <i>et al.</i> , 2001)
<i>gif1 (grain incomplete Filling 1)/OsCIN2</i>	4	LOC_Os04g33740	20.42-20.43	Abnormally developed and loosely Packed starch granules	(Wang <i>et al.</i> , 2008)
<i>flo2 (FLOURY ENDOSPERM2)</i>	4	LOC_Os04g55230	32.84-32.85	Affects storage substance accumulation In the endosperm	(She <i>et al.</i> , 2010)
<i>Flo4 (OsPPDKB)</i>	5	LOC_Os05g33570	19.72-19.74	Affects metabolism and starch structure In the endosperm	(Kang <i>et al.</i> , 2005; Zhang <i>et al.</i> , 2018)
<i>Flo1</i>	5	NA*	17.70-20.70	floury endosperm	(Mo <i>et al.</i> , 2013a)
<i>flo7 (t)</i>	5	NA*	19.33-19.86	white-core floury endosperm	(Mo <i>et al.</i> , 2013b)
<i>OsSSIII/flo5</i>	8	LOC_Os08g09230	5.35-5.36	white-core floury endosperm	(Fujita <i>et al.</i> , 2007; Ryoo <i>et al.</i> , 2007)
<i>OsVPS22</i>	9	LOC_Os09g36020	20.75-20.75	chalky endosperm	(Zhang <i>et al.</i> , 2013)
<i>Flo7 (FLOURY ENDOSPERM7)</i>	10	LOC_Os10g32680	17.11-17.12	chalky or floury endosperm	(Zhang <i>et al.</i> , 2015)

*The gene ID was not detected.

References :

Butardo V, Jr., Fitzgerald MA, Bird AR, Gidley MJ, Flanagan BM, Larroque O, Resurreccion AP, Laidlaw HK, Jobling SA, Morell MK, Rahman S 2011. Impact of down-regulation of starch branching enzyme IIb in rice by artificial microRNA- and hairpin RNA-mediated RNA silencing. *Journal of Experimental Botany* **62**, 4927-4941.

Fujita N, Yoshida M, Kondo T, Saito K, Utsumi Y, Tokunaga T, Nishi A, Satoh H, Park J-H, Jane J-L 2007. Characterization of SSIIIa-deficient mutants of rice: the function of SSIIIa and pleiotropic effects by SSIIIa deficiency in the rice endosperm. *Plant Physiology* **144**, 2009-2023.

Table S7

- Kang HG, Park S, Matsuoka M, An G.** 2005. White-core endosperm floury endosperm-4 in rice is generated by knockout mutations in the C4-type pyruvate orthophosphate dikinase gene (OsPPDKB). *The Plant Journal* **42**, 901-911.
- Matsushima R, Maekawa M, Kusano M, Kondo H, Fujita N, Kawagoe Y, Sakamoto W.** 2014. Amyloplast-localized SUBSTANDARD STARCH GRAIN4 protein influences the size of starch grains in rice endosperm. *Plant Physiology* **164**, 623-636.
- Mo Y-J, Jeung J-U, Kang K-H, Lee J-S, Kim B-K.** 2013a. Genetic Analysis on Floury Endosperm Characteristics of Namil (SA)-flo1, a Japonica Rice Mutant Line. *Korean Journal of Crop Science* **58**, 283-291.
- Mo Y-J, Jeung J-U, Shin Y-S, Park CS, Kang K-H, Kim B-K.** 2013b. Agronomic and genetic analysis of Suweon 542, a rice floury mutant line suitable for dry milling. *Rice* **6**, 37.
- Nishi A, Nakamura Y, Tanaka N, Satoh H.** 2001. Biochemical and genetic analysis of the effects of amylose -extender mutation in rice endosperm. *Plant Physiology* **127**, 459-472.
- Ryoo N, Yu C, Park C-S, Baik M-Y, Park IM, Cho M-H, Bhoo SH, An G, Hahn T-R, Jeon J-S.** 2007. Knockout of a starch synthase gene OsSSIIIa/Flo5 causes white-core floury endosperm in rice (*Oryza sativa* L.). *Plant Cell Reports* **26**, 1083-1095.
- She K-C, Kusano H, Koizumi K, Yamakawa H, Hakata M, Imamura T, Fukuda M, Naito N, Tsurumaki Y, Yaeshima M.** 2010. A novel factor FLOURY ENDOSPERM2 is involved in regulation of rice grain size and starch quality. *The Plant Cell*, tpc. 109.070821.
- Wang E, Wang J, Zhu X, Hao W, Wang L, Li Q, Zhang L, He W, Lu B, Lin H.** 2008. Control of rice Grain-filling and yield by a gene with a potential signature of domestication. *Nature Genetics* **40**, 1370.