Supplemental Table 1. List of SSR markers used to evaluate genetic divergence and diversity

Locus	Chromo-some	Genome position	Motif	Forward primer	Reverse primer	*Na*	*He*
RM6405	1	31266464	(GGA)7	GGAGGAGCTATAGGATCGGG	CGCTCGAATCTGCGGTAC	3	0.273
RM6840	1	43499589	(CCT)22	TACCAAGACTCCGCTATGGC	GAAGAAGGATCATGGATCG	11	0.811
RM6853	2	8985893	(TGC)8	CAACACGCACATCCTGTACC	CTCCAAAGACGAGACCAAGG	3	0.219
RM3688	2	23227884	(GA)15	GTTGAATCAAGCTGTGCAGC	AGCTAGGCAAAGCATGCATG	5	0.661
RM3730	2	27098371	(GA)13	TGCGAGTATCTTCAAGGCAG	ATTGAGGGGGCTAATCATCC	6	0.659
RM6301	3	2631471	(CTT)8	CGCTACCTTATGCTGCTGTC	TCGGCTACAACCTCTCCTTC	2	0.198
RM3180	3	18220879	(CT)12	GGGTCGGATAGCCACACAC	GAGGTAATCTCGCGGAGTTG	7	0.660
RM8208	3	22357040	(AG)8	GCCCAAACTACACTCTCTTG	GTAAATGCCTGAGTGCCTAC	13	0.769
SSR5	4	27568679	(AT)5	CTTGTCAACTACTGTGGCAAG	AGAAGATCAACGGTGGTATAG	2	0.094
AP005527	6	8324649	(TC)10	CAGTCCAAGAATCGTACTTC	GCTTTTGCTGTGATTTGGTG	12	0.860
RM3827	6	22297202	(GA)21	CACCAGCTTCACTTCATCTC	CCTTTCTTCAATCTGCATTC	10	0.506
SSR2	6	25602910	(CCG)5	CTCCACCGTGAATGTACGTAAG	GCGATCACCTCCTGCAAC	3	0.588
+29Cat	6	30917713	(CT)10	CACGATCTAGAAGACGAGAG	CCAAATTACGCCTTCCTACC	5	0.381
AP005454	7	3140437	(ATT)24	CAGATATAGGCTCCAGATAC	AGTACGAGGAAGCTGTTGGC	12	0.860
RM214	7	13444643	(TC)32	CTGATGATAGAAACCTCTTCTC	AAGAACAGCTGACTTCACAA	14	0.830
RM3691	7	19886294	(GA)15	GCTGATGGTCAAAGATCAGG	ATGTGTCTGCTGGCACAGAG	9	0.698
wags74	7	29197874	(CGC)6	GCCTGCCTACCCCATACTTA	ATCGGTACGGCGTCAGTAAG	2	0.178
RM1309	8	19178297	(AG)19	AGGAGACTGCAGATCACAAC	CCCTCAGCTTACCTTAATCC	8	0.472
RM8264	8	19833194	(GA)15	ACGCTCCTCGCTTTCTAC	GCACCTCACACCAGTAATTC	7	0.736
SSRat7	8	20379336	(AT)7	TGATGTGCCCTCTCCTTTC	CATAAATAATGGCATCTTCTATATA	4	0.510
RM1109	8	20483289	(AG)12	TCAAAATCACGTGTATGTAAGC	TTTACAAAGGACAGAGGGC	4	0.668
RM3459	8	20519942	(CT)20	ATGGACTTTCGAGAATGTTG	GAGTACGAAATGAAGGCAAG	8	0.775
AP003898	8	20665998	(AT)9	CTCCACCTCTCACTTTCTC	GCTTTCACCTTGCTCCTC	3	0.329
AP004617	8	20773444	(AT)5	GAAATGGCAAGGTCCTTGTG	GGAGATTGCCGGAAAGTTATG	2	0.071
RM6850	8	22150412	(TGA)13	CTAGCTCCAAGAGAGAATGC	GCCCTTGATTTACTAATCTCG	6	0.510
RM311	10	9487243	(TG)5	TGGTAGTATAGGTACTAAACAT	TCCTATACACATACAAACATAC	6	0.307
RM441	11	6067219	(GA)17	ACACCAGAGAGAGAGAGAGAGAG	TCTGCAACGGCTGATAGATG	5	0.555
RM5379	11	21796175	(TC)13	AGGGCATGCTTACATCCAAC	CATTTGCTTCTATGCCCCAG	6	0.437
RM4112	11	24646853	(TA)14	TGGCAAAGTCAGTAGTCCTTCCACAA	GCCATTCCCCCAACAGCTCC	19	0.876
RM17	12	269554668	(TC)15	TGCCCTGTTATTTTCTTCTCTC	GGTGATCCTTTCCCATTTCA	3	0.296

Supplemental Table 2. Additional SSR markers around *Badh2* in order to evaluate selective sweep

Primer	Genome position (nt)	Motif	forward	reverse	Remark
319kup	20057887	(AG)14	CCTCTCCACTCCACTCACCAACC	GAAGCTTGCAGCGTGGGAACC	Nearly monomorphic
186kup	20191701	(AAG)9	GTTCATTTCGCGTTCTGATTCC	TTGCCGTTTGTTAATGCAGAGG	Monomorphic
160kup	20217308	(ATC)7	GAGCATGATCTCCACTTTGTTGG	GCCATCACAACAGCCTAACG	Monomorphic
65kup	20312594	(AG)11	CATGGTGTTTGGAGGAATGAGC	CAATAAGAGAGCACGCACATGG	Monomorphic
55kup (RM8264)	19833194	(GA)15	ACGCTCCTCGCTTTCTAC	GCACCTCACACCAGTAATTC	Polymorphic
45kup	20333065	(TA)5	CTTCTCAGTTCTCCACATTTCTCC	CTTTTCAATAATGTACATAGTC	Polymorphic
23kup	20353404	(AAAT)6	ATTTGAGGAGTGAGAAGCATAC	TATATCATAAGTAGTTTGATG	Monomorphic
18kup	20359599	(CT)6	AGGGATAGAACAATCTTTTC	GGTGATGCCGACAAAGCTTTG	Monomorphic
12kup	20365223	(GA)6	CCTCCTCTGCCGTTTGTCAG	CAGTCTAGTTAGTCATTTTC	Polymorphic
SSRat7	20379336	(AT)7	TGATGTGCCCTCTCCTTTC	CATAAATAATGGCATCTTCTATATA	Polymorphic
10kdwn	20396905	(CT)5	CGACATGGCGTGTGAGTCAG	AGCTCGTTGTCTTTGATCTC	Monomorphic
28kdwn	20405392	(CG)5	GAACGGCGAAGATGAACTCT	CTGCCGTTCGAAATGGTGGT	Monomorphic
44kdwn	20421435	(TA)5	ATATAGTAATATTCCTATCCC	TTCTGTTTCAAACATTGCGAC	Monomorphic
55kdwn	20432145	(AT)6	GCGAGAGAAGTCAAACTCGAG	AGTACTTATAGCATAGCTGC	Nearly monomorphic
80kdwn	20457312	(CCG)7	GCGACGTCACCGACATGAGG	GCATGATCGGTAGATCACCTTCTCG	Monomorphic
105kdwn (RM1109)	20483289	(AG)12	TCAAAATCACGTGTATGTAAGC	TTTACAAAGGACAGAGGGC	Polymorphic
142kdwn (RM3459)	20519942	(CT)20	ATGGACTTTCGAGAATGTTG	GAGTACGAAATGAAGGCAAG	Polymorphic
146kdwn	20523745	(AAAC)6	GTCAACTCCGACACCATCAGAGC	ACGAACAGCACCAAACACAATCC	Monomorphic
179kdwn	20556187	(AG)11	GGGAGCAGTCACCTAACATGTGG	GTGGCGCGTTAGGTTTCAGG	Monomorphic
224kdwn	20601431	(AT)23	ATCTAGGAGCGAAACTTTAGGG	CCCATTGTACGTAGAAAGAAGC	Monomorphic

Supplmental Table 3. INDEL primers of Up1136, Up1098, 5′-UTR, and I-986 and CAPS-r primer to detect novel allele at exon-intron junction with *Kpn* I restriction enzyme

INDEL	Genome position	Forward primer	Reverse primer
Up1136	20375802	CCGACTTAAATACGAACGATGTA	CTTAATACTATGGCATGTCTTAATA
Up1098	20375945	TATTAAGACATGCCATAGTATTAAG	GTTATATCGCAGTCAAACTCCCG
5′UTR	20377062	CTCAACGCTCCACTCC	GTGAGAGATACGGAGATGGATCG
I-986	20378011	GAGGGTGCGCAACAACAAG	CAACGGAATACCACAAAGGC
INDEL ex7		GGTTGCATTTACTGGGAGTT	CAGTGAAACAGGCTGTCAAG
CAPS-r primer			CCCTACCTTGGCCGCGATTG

Supplmental Table 4. *BADH2* sequence primers

Forward primer	Reverse primer	Forward start	Reverse start	Genome position
BADH2 up1400 f	BADH2 up 521r	CGTCCCAAGTTAGTATGCA	ATGTTGGAGGAGAGACGGT	20375719
BADH2 up 521f	BADH2 76r	ACCGTCTCTCCTCCAACAT	TGGTGTCAGGTGTGGAGTG	20376158
BADH2 up 19f	BADH2 533r	CTCAACGCTCCACTCC	GTCACCACCCTACCTTG	20377062
BADH2 RT f	BADH2-933r	ATCTCTCACCGACCCCAAATC	CTCTCCGCTTGAACCCATC	20377192
f2	r2	CCTCTGTTCTGGACTAGG	CTACACCGATAGGCTCTTTCCG	20377854
BADH2 1602f	BADH2 2107r	GGCTAGACTAGAGACGCTTG	GGAGAGAGTAGCTGCTAGG	20378682
BadhapG4 f	BadhapG4 r	ATCTTCGGAAAGAGCCTATCG	AGGAGCTACCTTCCATGTTGC	20378938
BADH2 1940-500f	BADH2 r4	ATATGTTGTCAGCATGATTCAC	CAGAGTCCATAACCAGAC	20379484
BADH2 1940-1000f	BADH2-4170r	CTGGTGTAGACAAGGTACAG	CAATCATAATCTATTGTTGTACTTG	20380015
BADH2 3766 f	BADH2-4506 r	GAAGGCAGTTAGGAAGGACTG	CCCATGCAACCATCCTT	20380846
BADH2-4220f	BADH2-5420r	ACTATTGCACAGAGCGAATA	AAAGCACAGCACCAG	20381300
BADH2 6301-1000f	BADH2 6131r	TTCTGACTGGTGGGGTTAGA	CAAGCCGATACGGAGAGAACC	20382126

Supplemental Table 5. Tropical and Temperate Japonica calssification performed with hull size ratio, methocothyl length, and endosperm degradation by KOH treatment among scented fragrant landraces

Clade	Landrace/Variety	Hull size (mm)			Mesocothyl length (mm)	KOH degradation (%)	Z2-score (Sato 1991)	Classification (Tr-Tm)
		Length	Width	Ratio				
Clade 2	Hokkaido-40-nichi-wase	7.30	3.60	2.03	50	85.43	0.91	Tr
	Jakou (Niigata)	7.80	3.50	2.23	1	25.84	–0.83	Tm
	Kaori-ine 4	7.20	3.30	2.18	3	4.64	0.25	Tr
	Kaori-wase 2	7.10	3.60	1.97	9	28.37	–0.79	Tm
	Kaori-wase 3	7.60	3.80	2.00	0	17.02	–0.42	Tm
	Nioi-wase 2	6.60	3.50	1.89	7	52.23	–1.77	Tm
Clade 3	Iwaka	6.60	3.20	2.06	2	16.20	–0.48	Tm
	Jakou-ine 2	7.30	3.50	2.09	3	52.44	–1.95	Tm
	Jakou (Ibaraki)	7.10	3.50	2.03	1	12.20	–0.43	Tm
	Jakou-wase	7.20	3.50	2.06	2	21.51	–0.71	Tm
	Kaori-ine 1	7.00	3.20	2.19	1	31.11	–1.10	Tm
	Kaori-ine 2	7.00	3.30	2.12	5	10.73	0.10	Tr
	Nioi-akako	7.10	3.40	2.09	1.5	29.65	–1.09	Tm
	Nioi-mai	7.50	3.50	2.14	10	84.18	–2.64	Tm
Clade 7	Hendoyori	7.20	3.60	2.00	5	27.55	–0.76	Tm
	Kabashiko A	6.90	3.50	1.97	2	44.98	–1.83	Tm
	Kabashiko B	7.20	3.80	1.89	7	47.15	–1.54	Tm
	Kabashiko C	7.30	3.70	1.97	1	58.45	–2.52	Tm
	Kaori-ine 3	7.70	3.50	2.20	6	55.98	–0.38	Tm
	Keitoku	7.50	3.80	1.97	2	74.64	–3.13	Tm
	Kumamoto	7.10	3.70	1.92	1	53.91	–2.37	Tm
	Mangoku	6.80	3.30	2.06	10	13.23	0.40	Tr
	Nioi-yoshi 1	7.00	3.70	1.89	16	46.30	0.80	Tr
	Nioi-yoshi 2	6.50	3.60	1.81	1	46.30	–2.15	Tm
	Seikoku-kawachi	7.00	3.70	1.89	0	27.57	–1.33	Tm
	Shiro-wase	6.90	3.90	1.77	6	3.10	0.18	Tm
Clade 8	Jakou-ine 1	7.00	3.60	1.94	9	27.39	–0.43	Tm
	Jakou-ine 4	6.80	3.80	1.79	9	27.39	–0.91	Tm
	Jakou-mochi	6.50	3.90	1.67	0	27.54	–1.56	Tm
	Nioi-mochi 1	6.60	3.80	1.74	10	54.41	–4.09	Tm
	Nioi-mochi 2	6.90	3.70	1.86	2	91.00	–1.61	Tm
	Kamari	6.80	3.50	1.94	1	24.98	–1.07	Tm
Clade 9	Hieri	6.80	3.70	1.84	3	30.00	–1.21	Tm
	Kaisen	6.40	3.60	1.78	0.1	70.92	–3.34	Tm
	Wase-hieri	6.50	3.60	1.81	1	45.87	–2.13	Tm