Supplementary Note

Considering the propagation of rice cultivation areas, we expect that other genes were also involved in the adaptation of landraces within local areas in addition to the three major domestication-related genes involved in *japonica* rice domestication. Number of grains per panicle could have been a target trait for local adaptation in rice domestication. *Gn1a*, involved in grain number, has been cloned through natural variation between an *indica* cultivar, Habataki, and a temperate *japonica* cultivar, Koshihikari, and shown to encode a cytokinin oxidase[24]. In this case, the Habataki-type allele was defective. There is so far no evidence that *Gn1a* was a domestication-related gene. Therefore, we partly sequenced *Gn1a* in our rice collections and found that the major allele in the "heritage" landraces was distinct from both the defective *indica* allele and the reportedly functional Koshihikari allele (**Supplementary Fig. 7a, b** on line). The Koshihikari allele became a major allele in rice landraces produced after crossing of the *qsw5* and *wx* mutations, but only in the temperate *japonica* group (especially in Japanese landraces) (**Supplementary Fig. 6 and 7** online). It was likely that fixation of the Koshihikari allele occurred in this case of *Gn1a*, since the Koshihikari allele existed in the "heritage" landraces as a minor allele as well as in *qsw5* and *wx* landraces. It is possible that the current Koshihikari allele was favored during domestication, since it may be a weaker *Gn1a* allele than the original *Gn1a* allele that we found in the "heritage" landraces. This example in *Gn1a* may imply that more genes were involved in rice domestication from the point of view of local adaptation.

There have been several distinct models of the local origin of *japonica* domesticated rice. In such models, the China and Bengal areas have been proposed as points of origin[6, 7]. Our results, however, strongly suggest that the origin was a different area. Although ancestral rice with all functional alleles of the three domestication-related genes might be distributed throughout the tropical areas of Asia, landraces with naturally occurring mutations in the domestication-related genes were likely to have propagated to broader areas from the local areas of origin. Therefore, in these local areas of origin, "heritage" landraces and landraces with a single mutation among the FNPs are still being grown at the moment. Furthermore, landraces with single mutations, such as those of *qsw5* and *wx*, were likely to have been distributed over broader areas along with the propagation of rice cultivation. This distribution of landraces with the single defective FNPs, *qsw5* and *wx*, could be seen to occur in accordance with the gradual changes in the RFLP genome pattern (**Fig. 3b** and **Supplementary Figs. 4, 5** online). Considering the adaptation of landraces to local areas, very rapid migration of the landraces was unlikely. These results indicate that the process of domestication of *japonica* rice was complex but divided into the several key events (**Supplementary Fig. 6** online); it was a process of fixation of segregating loci in local groups from the original "heritage" alleles to Nipponbare-type alleles in accordance with expansion in the area of cultivation of rice to Far Eastern Asia. Nipponbare is a modern Japanese cultivar typical of the temperate *japonica* group, and the temperate *japonica* subgroup was imported into Japan about

3000 years ago through China and/or Korea [6, 7, 13].

In these processes, our analysis of the genome RFLP patterns of the *japonica* landraces failed to find any landraces derived from crossings between relatively distant ancient rice intermediates, with the exception of some landraces of Japanese upland rice and of Bangladesh, which had some additional Kasalath-type alleles in some loci around the genome (**Supplementary Fig. 5**). Note that crossings between genetically distant rice landraces must have made brand-new mixed genome structures. These observations in *japonica* landraces indicated that gradual changes in genome structures occurred in accordance with fixation to Nipponbare-type alleles in the segregating loci among local subgroups during *japonica* rice domestication. Therefore, it is still possible that some other, unidentified, loci may have been selected and favored to fix to the selected allele in terms of local adaptation processes, as was the case with *Gn1a* (**Supplementary Fig. 7** on line). Therefore, we concluded that *japonica* cultivated rice was largely domesticated with the combined selection of the three major FNPs in the domestication-related genes and with gradual fixation of alleles (sometimes favored ones) at various loci genome-wide in relative crossings and selfings, but not by crossings between distant ancient intermediates (**Supplementary Fig. 6** on line).

Another domestication-related gene for seed shattering, termed *sh4*, has also been reported[12]. All tested cultivars, including *japonica* and *indica* rice, contain the defective *sh4* allele. We therefore

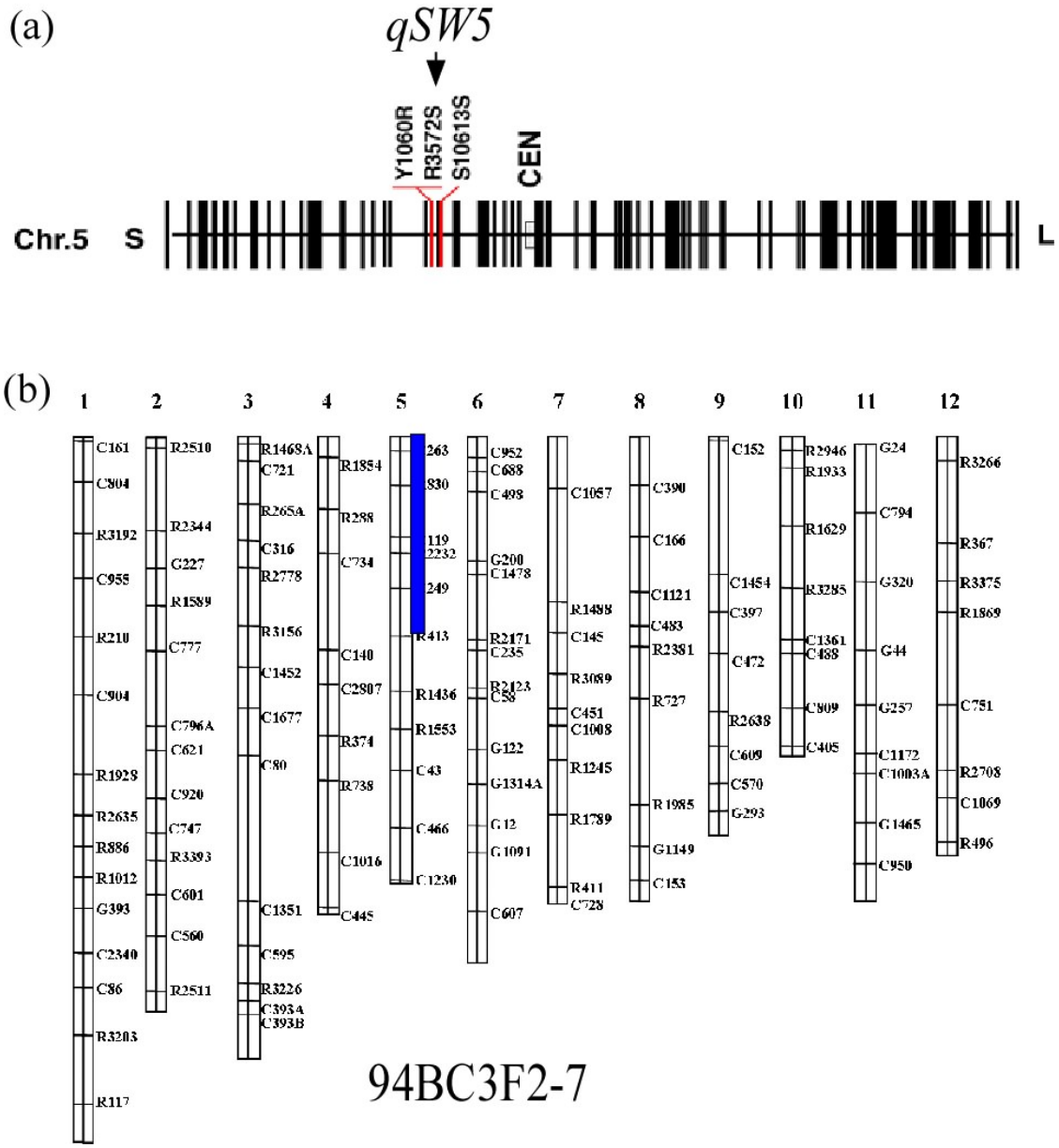
confirmed that several accessions (W1954, W1958, and W1976) of *O. rufipogon* that were very close to *japonica* rice[21] already had the defective allele (data not shown). This indicates that the *sh4* defective allele was a standing natural variation in wild species and was selected at the very beginning of *japonica* rice domestication for its reduction in seed shattering traits. Further analysis of wild rice remains to address this question in more detail.

In addition, we demonstrated that during *indica* rice domestication, ancient humans did not utilize the same defective alleles of the three domestication genes at all to form the current *indica* rice landraces, although some modern *indica* cultivars may have the same alleles as a result of recent inbreeding. This fact strongly suggests that, in a future breeding program, the reuse of these alleles in an *indica* background may provide a chance to produce new rice cultivars improved through higher yield and quality (**Table 2, Fig. 2h**).

References

24. Ashikari, M. et al. Cytokinin oxidase regulates rice grain production. *Science* **309**, 741–745 (2005).

Supplementary Fig.1



Supplementary Fig. 1 Rough map of *qSW5* and materials used in this work. (**a**) Rough map position of *qSW5* flanking the primary DNA markers Y1060R and S10613S. R3572S was a cosegregating DNA marker. (**b**) Graphical genotype of the original material used for fine mapping of *qSW5*. Markers used for the genome-wide genotype data collection are indicated on the

chromosomes.

Supplementary Fig.2

Line1	Thin	Normal
Transgene +	16	-
Transgene -	-	3

Line2	Thin	Normal
Transgene +	11	-
Transgene -	-	1

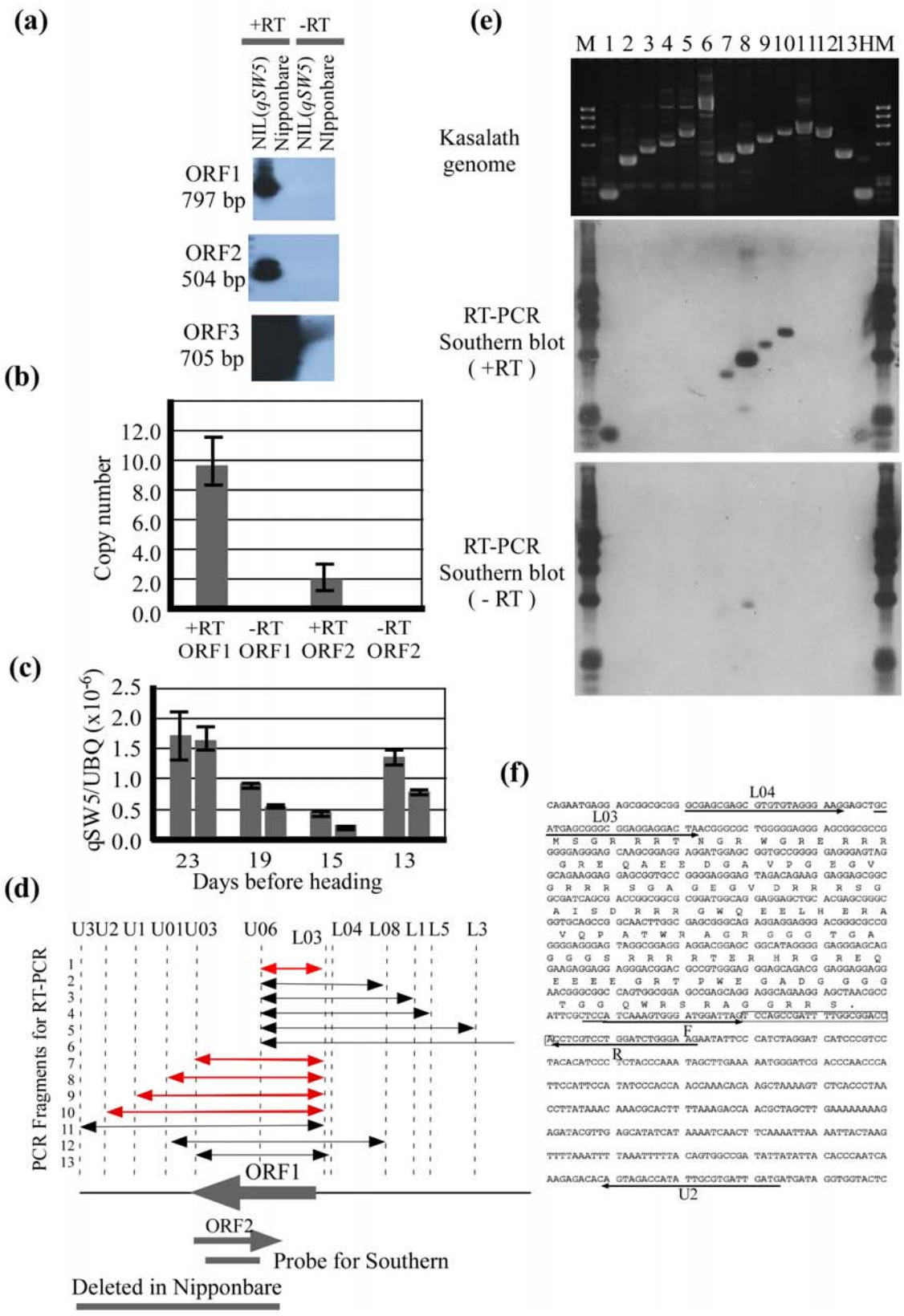
Line3	Thin	Normal
Transgene +	18	-
Transgene -	-	-

Line4	Thin	Normal
Transgene +	18	1
Transgene -	-	1

Supplementary Fig. 2 Complementation test in T_1 generation. Progeny of four independent

transgenic plants that exhibited thinner seed grains in the T_0 generation were grown. Presence of the introduced transgene was checked by PCR, and the seed grain widths of T_1 plants were examined. Seed width was clearly segregated in the progeny. Note that it was easy to judge the phenotypes of T_2 seeds at first glance, since all T_2 seeds from a T_1 plant exhibited the same phenotype. A clear association of transgene presence with the phenotype was observed, except in one plant in Line 4, among the 69 T_1 plants tested. Numbers of T_1 plants are presented. Thin: T_1 plants with a thinner T_2 seed width than in Nipponbare. Normal: T_1 plants with the same T_2 seed width as in Nipponbare.

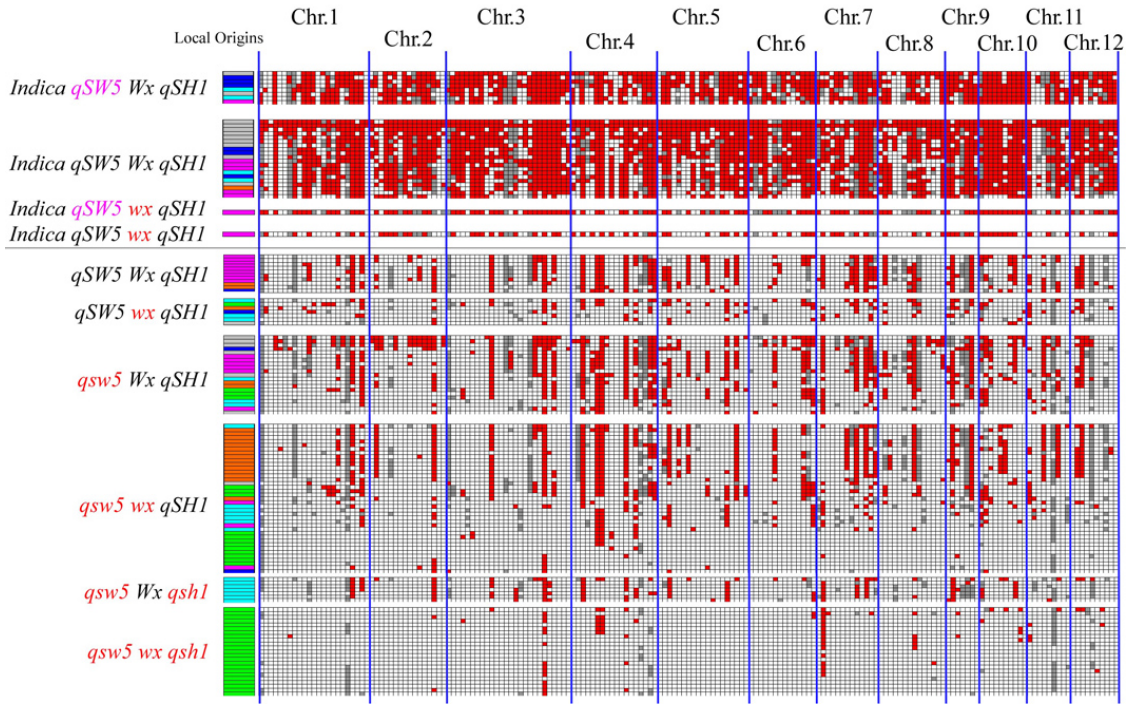
Supplementary Fig. 3



Supplementary Fig. 3 *qSW5* expression analysis and identification of *qSW5* transcripts. (**a**) Three ORFs (as shown in **Fig. 2d**) were examined by RT-PCR following Southern hybridization analysis to determine the real *qSW5* transcript. ORF1 and 2 were expressed only in NIL(*qSW5*) samples positive for reverse transcriptase. RT +, treated with reverse transcriptase; RT -, not treated with reverse transcriptases. RNA samples were prepared from developing young panicles at about 20 days before heading. (**b**) Confirmation of direction of *qSW5* transcription. ORF1 and ORF2 were predicted in opposite directions from the same genomic region (Fig. 2d).To confirm the direction of transcription, we performed a biased RT-PCR with the same RNA samples as in **a**. Only one primer "F" or "R" hybridized with ORF1 or ORF2 first-strand cDNA , respectively, was used in the first 20 cycles of the PCR reaction, followed by a typical Taq-Man PCR cycle with both primers and a probe (as shown in **f**). Predicted ORF1 mRNA made up the majority of the transcript. RT+, treated with reverse transcriptase; RT-, not treated with reverse transcriptases. (**c**) ORF1 mRNA expression by Taq-man quantitative RT-PCR. RNA samples were prepared from developing panicles at different stages judged by date relative to heading date. Relative *qSW5* mRNA expression was normalized against a ubiquitin gene. Two biological replicates were measured three times. (**d**) Schematic positions of primers for RT-PCR. Short gray line indicates position of the probe used for Southern analysis after RT-PCR. Red arrows correspond to the positive signals shown in the middle panel of **e. (e)** Results of RT-PCR for ORF1. Row numbers correspond to the PCR fragments in **d**. Top: Genome control to confirm amplification under the same PCR conditions.

Kasalath genomic DNA was used. Middle: RT-PCR followed by Southern blot analysis. mRNA samples were treated with reverse transcriptases (+RT). Bottom: RT-PCR followed by Southern blot analysis. mRNA samples were not treated with reverse transcriptases (-RT). H: RT-PCR control for histone cDNA. M: molecular DNA size markers. (**f**) cDNA sequence amplified by RT-PCR. cDNA was amplified by using primers L03 and U2, not primers L04 and U2. Predicted amino acid sequences of ORF1 (the qSW5 candidate protein) are shown with the DNA sequence. Primers (R and F) and probe for qRT-PCR (Taq-Man PCR) are indicated by arrows and the box, respectively.

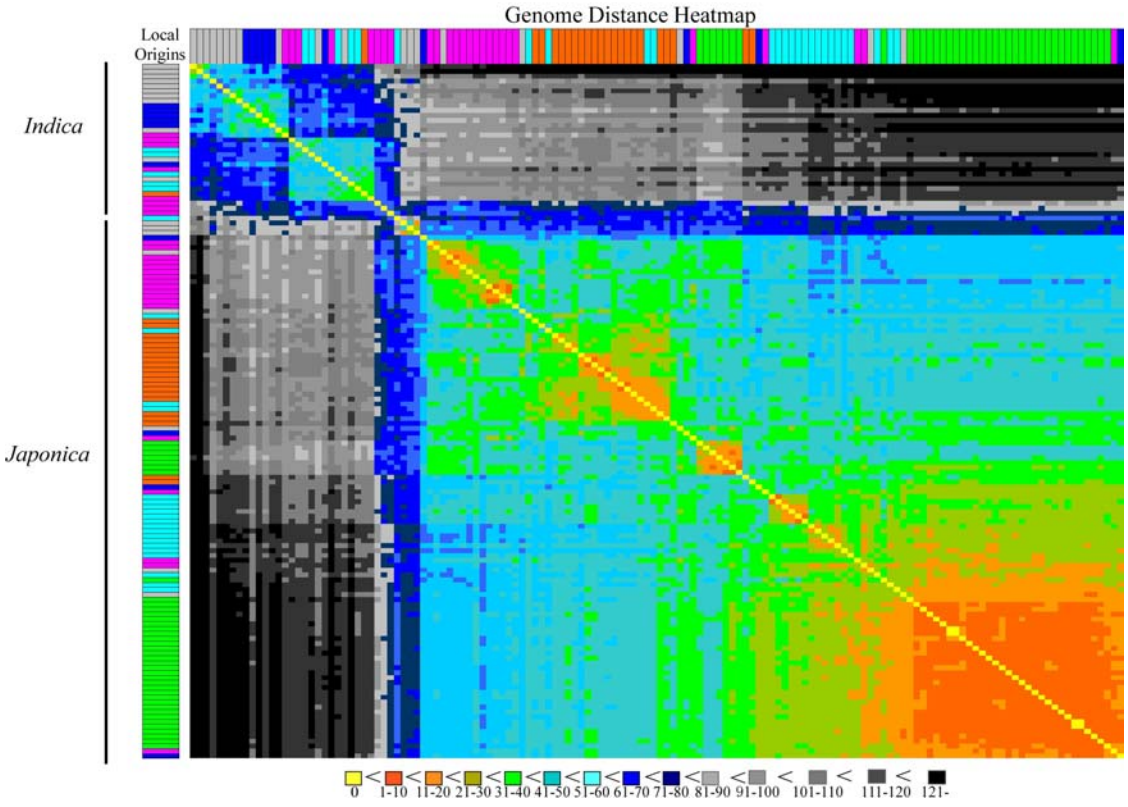
Supplementary Fig.4



Supplementary Fig. 4 RFLP data at 179 loci among all 12 chromosomes for three

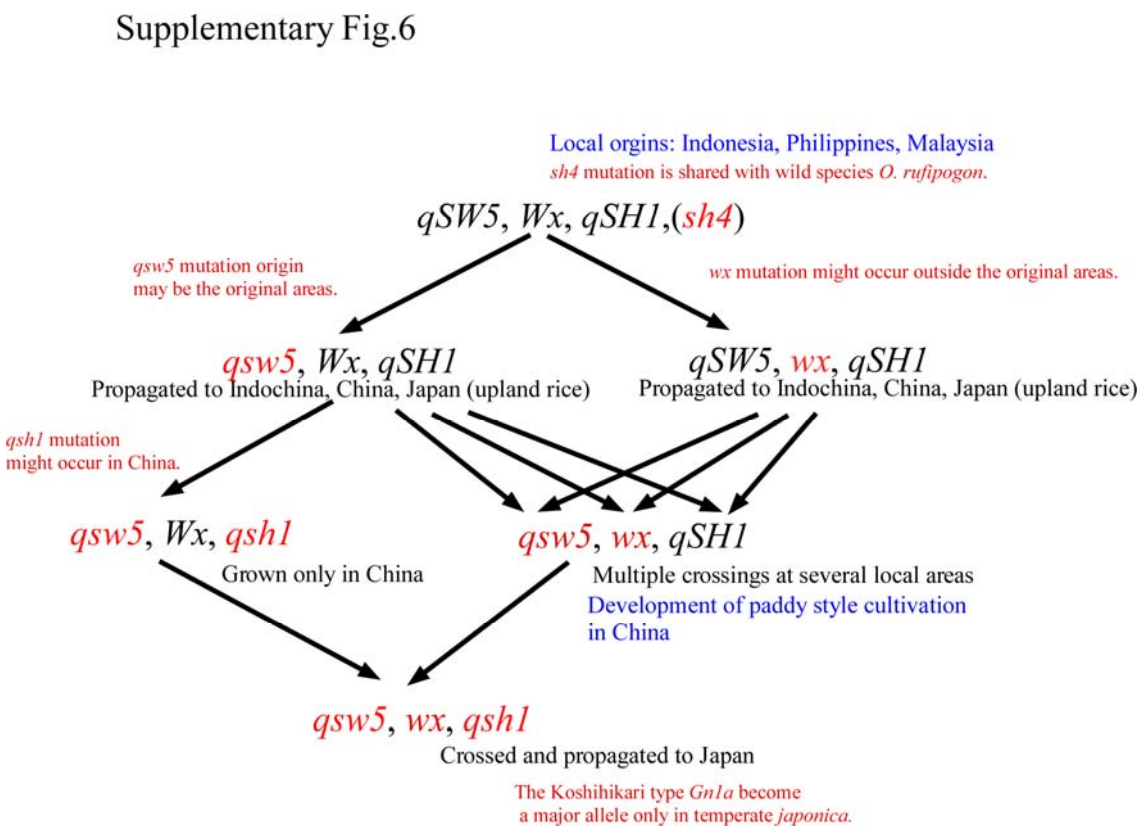
domestication genotypes. RFLP genotyping data for 141 landraces. Local origins are presented by bars of the same colors as in Fig. 3b. Each small square represents the genotype of an RFLP marker of a landrace. RFLP markers are aligned in the physical order of the chromosomes as shown at the top of the figure. Red squares indicate Kasalath alleles, white indicate Nipponbare, and grey indicate other types. Data for a landrace termed Danyu1 was removed owing to its complicated introgression between *indica* and *japonica.* The increase in the number of white squares was associated with gradual genomic changes to typical temperate *japonica*. These gradual genome changes clearly indicate that crossings between evolutionarily distant wild species (or intermediate landraces) did not occur during the rice domestication process, although crossings between relatives might have occurred (see also **Fig. 3c**). A *qSW5* allele found in *indica* (pink) corresponds to *indica* II-type in **Fig. 2g**. This allele did not affect the grain width clearly in the association analysis (**Fig. 2g**).

Supplementary Fig.5



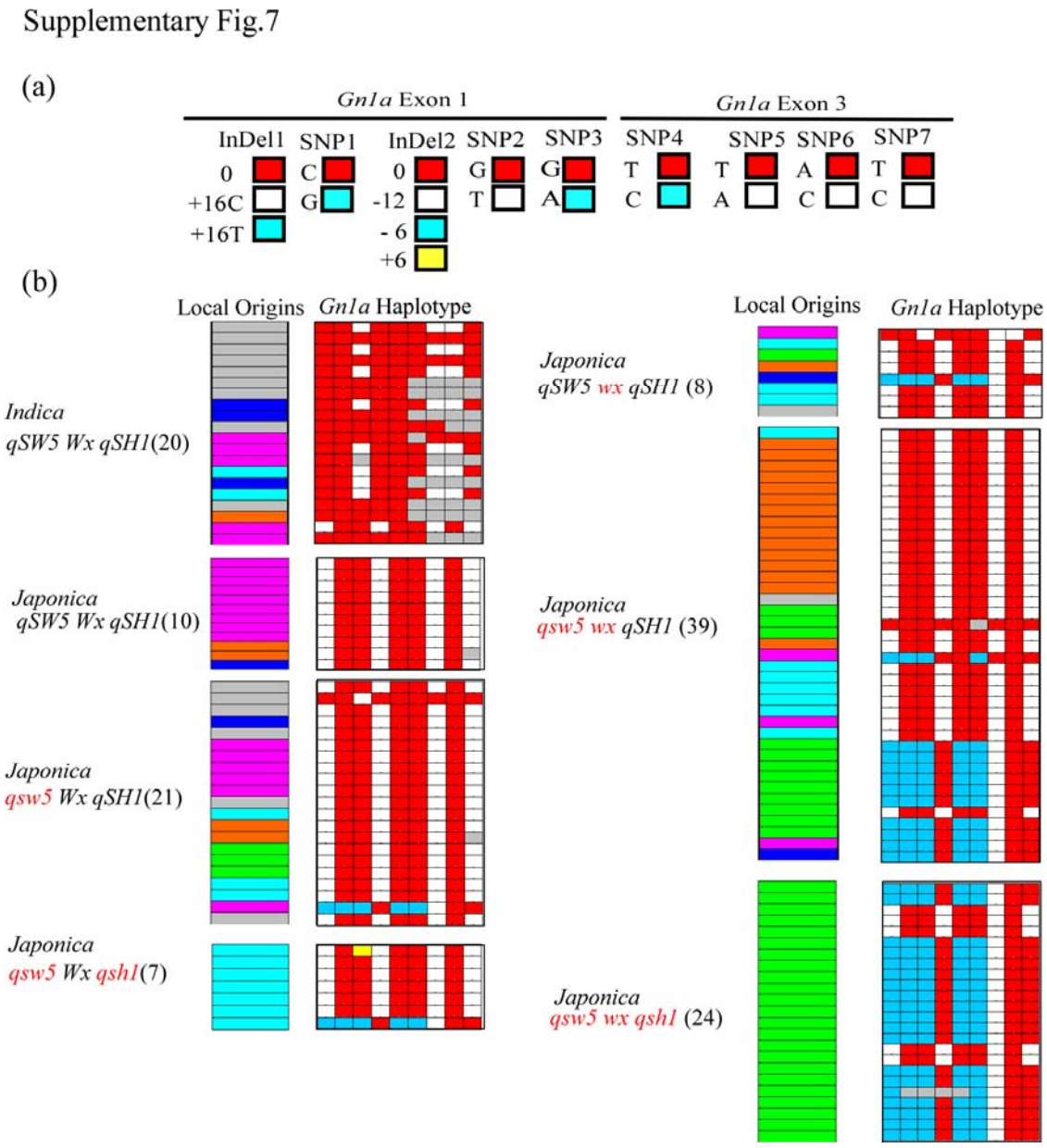
Supplementary Fig. 5 Genome distance heatmap with local origins represented by colors. Genome distances for all possible pairwise comparisons of 142 tested landraces (including a few modern cultivars) were calculated, and the genetic distance scores were used for clustering. Primarily, pvclust R software with an averaging method was used, and the results were fine-tuned manually. Colors in the heatmap indicate genome distances, as indicated at the bottom, from other landraces tested. A genome distance of 0 means that the RFLP patterns are identical at 179 loci. The order of landraces was determined by landrace alignment according to the relative genome similarities calculated by the RFLP patterns shown in Supplementary Fig. 4. Association of landrace order with local origin is apparent, indicating that clustering and alignment based on

genome similarity reflect the history of the propagation of rice cultivation. These landraces were largely classified into two groups, *indica* and *japonica*, with the exception of one termed Danyu1. The local origins of each landrace are indicated by color bars corresponding to the colors in **Fig. 3a**. See also **Supplementary Table 2** for details.



Supplementary Fig. 6 A model for *japonica* rice domestication. The local origin of ancient *japonica* rice was successfully assigned with domestication-related gene profiles. Propagation of each defective allele of *wx* and *qsw5* into the broader Asian area in accordance with local adaptation, and allele combination by natural crossing in several local areas, were key events in this

japonica domestication. Note that multiple independent crossings between *qsw5* single and *wx* single lines in several local areas are implicit in rice domestication.



Supplementary Fig. 7 How were *Gn1a* alleles facilitated in rice domestication? (**a**) Haplotype data used in this analysis. (**b**) Five polymorphisms on exon 1 and four on exon 3 were mapped with

the domestication genotypes of *qSW5*, *Wx*, and *qSH1* genes. A *Gn1a* allele with a haplotype with five blue bars became dominant only in temperate *japonica* after crossing between *qsw5* and *wx* in China (or Japan). Note that most *Gn1a* in *indica* contains the null allele, as represented by the red at InDel1 on exon 1[24].

Supplementary Table 1 Data used for association analysis in Fig.2g

qSW5 haplotype (cultivar number)	Landrace name	average width (pixel)	average width (mm)	average length (pixel)	average length (mm)	ratio (length/width)
Indica II (10)	ARC 7291	453.9	2.75	1092.9	6.62	2.69
	Nepal 8	508.2	3.08	1175.0	7.12	2.31
	Jena 035	512.4	3.11	1340.2	8.12	2.62
	Puluik Arang	516.9	3.13	1519.8	9.21	2.94
	Co13	528.3	3.20	1205.6	7.31	2.28
	Ryou Suisan Koumai	529.3	3.21	1181.4	7.16	2.23
	Kalo Dhan	540.3	3.27	1228.1	7.44	2.27
	Davao 1	544.6	3.30	1189.8	7.21	2.19
	Jinguoin	552.3	3.35	1343.0	8.14	2.43
	HASSOKUHO	571.9	3.47	1234.1	7.48	2.16
Nipponbare (44)	Cultivar name	average width (pixel)	average width (mm)	average length (pixel)	average length (mm)	ratio (length/width)
	Tupa729	514.5	3.12	1176.9	7.13	2.29
	JOUSHUU	526.5	3.19	1114.0	6.75	2.12
	BOUZU MOCHI	535.6	3.25	1283.7	7.78	2.40
	AKAMAI	547.5	3.32	1096.1	6.64	2.00
	ISHIJIRO	550.3	3.34	1134.7	6.88	2.06

	HOSOGARA	556.0	3.37	1072.8	6.50	1.93
	DANGO	557.1	3.38	1059.6	6.42	1.90
	Nipponbare	559.8	3.39	1130.3	6.85	2.02
	MANSAKU	563.5	3.42	1141.0	6.92	2.03
	Jaguary	565.0	3.42	1548.9	9.39	2.74
	NAGOYA SHIRO	565.6	3.43	1057.4	6.41	1.87
	AKAGE	568.7	3.45	1161.5	7.04	2.05
	HIMENOMOCHI	573.7	3.48	1118.9	6.78	1.95
	SHINYAMADAHO 2	575.0	3.48	1049.5	6.36	1.83
	HINODE	575.9	3.49	1282.3	7.77	2.23
	RIKUTOU RIKUU 2	577.8	3.50	1126.7	6.83	1.95
	MORITA WASE	578.0	3.50	1165.1	7.06	2.02
	KAMEJI	578.0	3.50	1078.4	6.54	1.87
	AIKOKU	579.6	3.51	1043.6	6.32	1.80
	AKAMAI	582.3	3.53	1327.6	8.05	2.28
	Urasan 1	583.1	3.53	1319.4	8.00	2.27
	FUKOKU	584.3	3.54	1110.1	6.73	1.90
	OMACHI	584.9	3.54	1131.9	6.86	1.94
	SHICHIMENCHOU MOCHI	584.9	3.55	1163.3	7.05	1.99
	OKABO	585.2	3.55	1372.8	8.32	2.35
	MEGURO MOCHI	588.2	3.57	1256.5	7.62	2.14
	HIYADACHITOU	591.6	3.59	1111.5	6.74	1.88
	SHIROINE(KEMOMI)	592.1	3.59	1095.1	6.64	1.85
	GINBOUZU	592.2	3.59	1122.7	6.80	1.90
	KAHEI	594.4	3.60	1347.8	8.17	2.27
	KYOUTOASAHI	596.3	3.61	1115.7	6.76	1.87
	SHINRIKI	596.7	3.62	1157.2	7.01	1.94
	GAISEN MOCHI	598.6	3.63	1470.9	8.91	2.46
	KANEKO	599.0	3.63	1245.4	7.55	2.08
	SEKIYAMA	605.3	3.67	1069.7	6.48	1.77
	HAKAMURI(YOKOYAMA)	607.0	3.68	1291.0	7.82	2.13
	SENSHOU	609.0	3.69	1247.2	7.56	2.05
	KABASHIKO	611.7	3.71	1142.9	6.93	1.87

	YAMADA BAKE	619.2	3.75	1173.1	7.11	1.90
	SHINRIKI MOCHI	621.2	3.76	1082.6	6.56	1.74
	OIRAN	623.0	3.78	1289.9	7.82	2.07
	IRIMA NISHIKI	636.6	3.86	1262.0	7.65	1.98
	Khao Nok	667.6	4.05	1361.1	8.25	2.04
	HIRAYAMA	670.6	4.06	1176.4	7.13	1.87
Kasalath (30)	Cultivar name	average width (pixel)	average width (mm)	average length (pixel)	average length (mm)	ratio (length/width)
	Basilanon	415.7	2.52	1236.4	7.49	2.98
	Surjamukhi	422.2	2.56	1329.3	8.06	3.15
	Rexmont	428.1	2.59	1550.1	9.39	3.62
	Tadukan	428.4	2.60	1257.6	7.62	2.94
	IR 58	429.5	2.60	1325.6	8.03	3.09
	ARC 5955	436.5	2.65	1133.0	6.87	2.60
	Anjana Dhan	439.5	2.66	1364.8	8.27	3.11
	Tupa 121-3	446.4	2.71	1329.4	8.06	2.98
	Kasalath	446.8	2.71	1219.4	7.39	2.73
	Naba	447.4	2.71	1322.8	8.02	2.96
	Bei Khe	449.2	2.72	1381.9	8.38	3.08
	Jhona 2	455.6	2.76	1517.7	9.20	3.34
	Asu	460.4	2.79	1222.8	7.41	2.66
	Jarjan	468.4	2.84	1329.1	8.06	2.84
	Lebed	470.2	2.85	1227.6	7.44	2.61
	Pinulupot 1	474.2	2.87	1266.3	7.67	2.67
	Ma sho	475.7	2.88	1163.4	7.05	2.45
	Muha	476.5	2.89	1497.2	9.07	3.14
	AKAMAI	478.3	2.90	1337.4	8.11	2.80
	AKAMAI	480.1	2.91	1348.8	8.17	2.81
	Nepal 555	482.3	2.92	1208.5	7.32	2.51
	TOUBOSHI	484.3	2.94	1314.4	7.97	2.72
	Milyang 23	493.5	2.99	1301.8	7.89	2.64
	Kaluheenati	497.4	3.01	1229.1	7.45	2.47
	Deng Pao Zhai (Toufutsusai)	505.4	3.06	1247.9	7.56	2.47

	OKKA MODOSHI	507.1	3.07	1372.8	8.32	2.71
	Shuusoushu	518.3	3.14	1366.9	8.28	2.64
	WATARIBUNE	540.7	3.28	1210.6	7.34	2.24
	KARAHOUSHI	552.9	3.35	1364.5	8.27	2.47
	Shwe Nang Gyi	580.5	3.52	1485.0	9.00	3.20

Supplementary Table 2 Genotype of FNPs in three domestication genes for 142 landraces

Landrace No.	WRC No.	Local Origin	Name	qSW5/FNP	Waxy/FNP	qSH1/FNP
1	WRC 35	IND	ARC 5955	Kasalath	G	G
2	WRC 02	IND	Kasalath	Kasalath	G	G
3	WRC 36	IND	Ratul	Kasalath	G	G
4	WRC 41	LKA	Kaluheenati	Kasalath	G	G
5	WRC 40	IND	Nepal 555	Kasalath	G	G
6	WRC 34	IND	ARC 7291	Indica type II	G	G
7	WRC 33	IND	Surjamukhi	Kasalath	G	G
8	WRC 32	BGD	Tupa 121-3	Kasalath	G	G
9	WRC 30	NPL	Anjana Dhan	Kasalath	G	G
10	WRC 29	NPL	Kalo Dhan	Indica type II	G	G
11	WRC 04	NPL	Jena 035	Indica type II	G	G
12	WRC 28	BTN	Jarjan	Kasalath	G	G
13	WRC 27	NPL	Nepal 8	Indica type II	G	G
14	WRC 26	IND	Jhona 2	Kasalath	G	G
15	WRC 25	IDN	Muha	Kasalath	G	G
16	WRC 14	PHL	IR 58	Kasalath	G	G
17	WRC 20	PHL	Tadukan	Kasalath	G	G
18	WRC 11	CHN	Jinguoin	Indica type II	G	G
19	WRC 19	CHN	Deng Pao Zhai (Toufutsusai)	Kasalath	G	G
20	WRC 15	IND	Co 13	Indica type II	G	G
21	WRC 13	BTN	Asu	Kasalath	G	G
22	WRC 06	IDN	Puluik Arang	Indica type II	T	G
23	WRC 10	CHN	Shuusoushu	Kasalath	G	G
24	WRC 05	IND	Naba	Kasalath	G	G
25	WRC 17	CHN	Keiboba	Indica type III	G	G

26	WRC 09	CHN	Ryou Suisan Koumai	Indica type II	G	G
27	WRC 03	CMB	Bei Khe	Kasalath	G	G
28	WRC 07	PHL	Davao 1	Indica type II	G	G
29	WRC 24	PHL	Pinulupot 1	Kasalath	G	G
30	WRC 23	PHL	Lebed	Kasalath	T	G
31	WRC 44	PHL	Basilanon	Kasalath	G	G
32	WRC 43	CHN	Dianyu 1	Nipponbare	T	T
33	WRC 55	BGD	Tupa729	Nipponbare	G	G
34		BGD	Kaloshahaita	Nipponbare	G	G
35		BGD	Tupa7-1	Nipponbare	G	G
36	WRC 53	BTN	Tima	Nipponbare	G	G
37		MYS	Turakin	Kasalath	G	G
38		MYS	Puteh/Rubon(H)	Kasalath	G	G
39		LKA	Godawee	Nipponbare	G	G
40		PHL	Kinan Kuda	Nipponbare	G	G
41		PHL	Binatangan 2	Nipponbare	G	G
42		PHL	Bincol (aromatic)	Nipponbare	G	G
43		PHL	Canabong bong	Nipponbare	G	G
44		PHL	Calutos	Kasalath	G	G
45		IDN	Masumikir	Kasalath	G	G
46		IDN	Siampang	Kasalath	G	G
47		IDN	Bodat Mayang	Kasalath	G	G
48		IDN	Padi Kenikir Puti	Kasalath	G	G
49		IDN	Simanoek	Indica type II	G	G
50		IDN	Ladang	Nipponbare	G	G
51	WRC 67	IND	Phulba	Nipponbare	G	G
52		CHN	Haohai	Nipponbare	G	G
53	WRC 45	MYN	Ma sho	Indica type III	G	G
54		MYN	Khauk Yoe	Kasalath	G	G
55		CHN	Bayuenuo	Nipponbare	T	G
56		VNM	Mu Bang Gu	Kasalath	G	G
57		VNM	Khau Van Lanh	Nipponbare	T	G
58		VNM	Bie Blau	Nipponbare	T	G
59		MYN	In Sitt	Nipponbare	G	G
60	WRC 48	VNM	Khau Mac Kho	Nipponbare	T	G

61		VNM	Cha Sen Lun	Nipponbare	T	G
62		VNM	Ngo Luu	Nipponbare	T	G
63		LAO	Khao Monh	Nipponbare	T	G
64		LAO	Khao Vay Deng	Nipponbare	T	G
65		THA	Daw Dam	Nipponbare	T	G
66		LAO	Mack Kheua	Nipponbare	T	G
67		LAO	Dam Ngo	Nipponbare	T	G
68		LAO	Deng Mak Tek	Nipponbare	T	G
69		LAO	Lep Xang	Nipponbare	T	G
70		CHN	Dabagu	Nipponbare	G	T
71		CHN	Haogang	Kasalath	T	G
72		MYN	Shwe War	Nipponbare	G	G
73		THA	KU 70-1	Nipponbare	T	G
74	WRC 46	LAO	Khao Nok	Nipponbare	T	G
75		BGD	Aus 38	Nipponbare	T	G
76		BTN	Kochum	Kasalath	G	G
77		IDN	Simedel	Indica type II	G	G
78		JPN(U)	Kahei	Nipponbare	T	G
79		JPN(U)	Aka Yakan	Kasalath	T	G
80	WRC 51	JPN(U)	Urasan 1	Nipponbare	T	G
81		JPN(U)	Mie	Nipponbare	G	G
82		JPN(U)	Bansei Tarou	Nipponbare	T	G
83		JPN(U)	Tamasari	Nipponbare	G	G
84		JPN(U)	Wase Sekitori F	Nipponbare	G	G
85	WRC 68	LAO	Khao Nam Jen	Nipponbare	T	G
86	WRC 52	VNM	Khau Tan Chiem	Kasalath	T	G
87		BTN	91-385	Kasalath	T	G
88		PHL	Dinalaga	Nipponbare	T	G
89		CHN	Ligihong	Nipponbare	G	T
90		CHN	Naxi	Nipponbare	G	T
91		CHN	Laolaihong	Nipponbare	G	T
92		CHN	Xiaobaigu	Nipponbare	G	T
93		CHN	Dabaigu	Nipponbare	T	G
94		CHN	Wahuigu	Nipponbare	G	T
95		CHN	Shoutan Zairai	Nipponbare	G	G
96		CHN	Moch Ine Sukensan	Nipponbare	T	G

97		CHN	North China 60	Nipponbare	T	G
98		CHN	Sousen	Nipponbare	T	G
99		CHN	Chuumoushi	Nipponbare	G	G
100		CHN	Aijiaonuo	Nipponbare	T	G
101		CHN	Nanjingxiangtao	Kasalath	T	G
102		PHL	Sinaba	Nipponbare	G	G
103		PHL	Curikit	Nipponbare	T	G
104		IND	K78	Nipponbare	G	G
105		CHN	China 830	Nipponbare	G	T
106		JPN	Ochikara	Nipponbare	T	T
107		CHN	Kamochi Kantonfukinsan	Kasalath	T	G
108		CHN	Chuutou	Nipponbare	T	G
109		IND	RM	Kasalath	T	G
110		JPN	Hokuto	Nipponbare	T	T
111		JPN	Wasekouriki	Nipponbare	T	G
112		JPN	Soushin 23	Nipponbare	T	G
113		JPN	Akage	Nipponbare	T	T
114		JPN	Komehikari	Nipponbare	T	T
115		JPN	Toyonishiki	Nipponbare	T	T
116		JPN	Shinsyukaneko	Nipponbare	T	T
117		JPN	Shinsyu	Nipponbare	T	T
118		JPN	Kinuhikari	Nipponbare	T	T
119		JPN	Koshihikari	Nipponbare	T	T
120		JPN	Ginbozu	Nipponbare	T	T
121		JPN	Akihikari	Nipponbare	T	T
122		JPN	Shinriki	Nipponbare	T	G
123		JPN	Asominori	Nipponbare	T	G
124		JPN	Chouhyouroku 1	Nipponbare	T	G
125	WRC 01	JPN	Nipponbare	Nipponbare	T	T
126		JPN	Norin 1	Nipponbare	T	T
127		JPN	Asahi	Nipponbare	T	G
128		JPN	Sasanishiki	Nipponbare	T	T
129		JPN	Shirakawa	Nipponbare	T	T
130		JPN	Fujisaka 5	Nipponbare	T	G
131		JPN	Sekiyama	Nipponbare	T	T
132		JPN	Oba	Nipponbare	T	T

133		JPN	Tamanishiki	Nipponbare	T	T
134		JPN	Jikkoku	Nipponbare	T	T
135		JPN	Norin 8	Nipponbare	T	T
136		JPN	Norin 29	Nipponbare	T	T
137		JPN	Kokuryoumiyako	Nipponbare	T	G
138		JPN	Banzai	Nipponbare	T	G
139		JPN	Kameji	Nipponbare	T	T
140		JPN	Kogyoku	Nipponbare	T	T
141		PHL	CS-S4	Nipponbare	T	G
142		BTN	91-382	Nipponbare	T	G

Supplementary Table 3 Primer information used in this work

mapping marker name	upper primer sequence	lower primer sequence	marker type
MS35029	5'-CCGGGCGTACCTGTACTACT-3'	5'-TACTATCATCCTTTCGTCCTTGG-3'	SSR
MS40671	5'-TTTGATTGCCATTATCGAGTTAG-3'	5'-GTGTGCGTGAAGAGAACAGT-3'	Indel
N1212del	5'-CGTCTTGCAACCAACGCCGATGTTATAC-3'	5'-GAGCGTGTGTAGGGAAGGAGCTGCATGA-3'	Indel
M15	-	-	SNP direct sequencing
M16	-	-	SNP direct sequencing
M17	-	-	SNP direct sequencing
M18	-	-	Indel direct sequencing
M23	5'-GATCGAATCCCGTGGTGATAAAC-3'	5'-GCATCAGCATCACGCATCTTTC-3'	Indel
GR42739	5'-CGAAACTTAATTTGACCATTGAA-3'	5'-CATCTTCCGTAAAGAAACTCAGG-3'	Indel
GR43920	5'-GGATCGGGAAGAGACAGATTACC-3'	5'-CGCATTTTTGGGAGGAAGTAGAA-3'	CAPS HhaI
GR48346	5'-GATATTTCAGGTCGGGAGTGG-3'	5'-AGGCAAGATAGGTGATGATTTGA-3'	CAPS AfaI

MS1898	5'-GTATTCAATTTTCAAGCCTCCTG-3'	5'-TTTTCTTTTCTTTCCTGGCATC-3'	SSR
ORF RT-PCR primer name			
predicted ORF1F	5'-TGGGATATGGAATGGAATGGGTTGG-3'		
predicted ORF1R	5'-GATAGGGGTGGGGATGGGATGAATG-3'		
predicted ORF2F	5'-TTCTTCCCAGATCCAGGACGAGGTG-3'		
predicted ORF2R	5'-GCGAGCGAGCGTGTGTAGGGAAG-3'		
predicted ORF3F	5'-ATGTTGACGTTGTGTGTTGGCGATG-3'		
predicted ORF3R	5'-TCTTGAAGTTGAACGCCTCCTGCAC-3'		
RT-PCR Southern primer name			
predicted ORF1SF	5'-GCTCGCCAAGTTGCCGGCTGCAC-3'		
predicted ORF1SR	5'-GCATGAGCGGGCGGAGGAGGACTA-3'		
predicted ORF2SF	5'-GCTCGCCAAGTTGCCGGCTGCAC-3'		
predicted ORF2SR	5'-GCATGAGCGGGCGGAGGAGGACTA-3'		

predicted ORF3SF	5'-ATGTTGACGTTGTGTGTTGGCGATG-3'		
predicted ORF3SR	5'-TCTTGAAGTTGAACGCCTCCTGCAC-3'		
U06	5'-GCTCGCCAAGTTGCCGGCTGCAC-3'		
U03	5'-TTCTTCCCAGATCCAGGACGAGGTG-3'		
U01	5'-TGGGATATGGAATGGAATGGGTTGG-3'		
U1	5'-GAAGTTGATTTTATGATATGCTCAACGT-3'		
U2	5'-CATCATCAATCACGCAATATGGTCTACT-3'		
U3	5'-CATGCTTTGTACCCCTTGTAGGATGCAT-3'		
L03	5'-CGGTGTCCAAGTGCCGTCCTCTT-3'		
L04	5'-GCGAGCGAGCGTGTGTAGGGAAG-3'		
L08	5'-GATAGGGGTGGGGATGGGATGAATG-3'		
L1	5'-GTGGGATAGGATGAAACCATACATG-3'		
L5	5'-GTTATAAACCATGTGCTCATAAGCTTTC-3'		

L3	5'-GAGTCTATGGAGTTAAGTCTAAGATCTG-3'		
L1	5'-CGATCGAGATGAGGCGGGGCAGCAA-3'		
qRT-PCR primer name			
F	5'-TCCATCAAAGTGGGATGGATTAG-3'		
R	5'-CTTCCCAGATCCAGGACGAG-3'		
Taq man probe for qSW5	5'FAM-TGGTCCGCCAAAATCGGCTGG-TAMRA3'		
PCR kit	TAKARA LA Taq weth GC buffer I		
94℃ 5min			
94℃ 45sec			
65℃ 45sec	30cycles		
72℃ 2min			
72℃ 10min			
4℃ ∞			