Genome-wide pedigree analysis of elite rice ShuHui527 reveals key regions for breeding

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Appendix A-K

Appendix A Characteristics of upstream progenitors

Cultivar	**Morphological character**
GU154	*Indica* type, medium late maturity, semi-dwarf, strong in division, strong in rice quality, strong in resilience and resistant to rice blast.
G630	*Indica* type, medium late maturity, semi-dwarf, large 1000-grain weight, strong recovery system, high combining ability.
IR1544	*Indica* type, medium late maturity, semi-dwarf, strong division, strong rice, strong resilience, resistance to rice blast.
R1318	*Indica* type, medium late maturity, semi-dwarf, resistant to fertilizer, plant type loose, medium millet, late leaf color yellow, 1000-grain major, high resistance to rice blast, strong resilience.
F36-2	*Indica* type, medium mature, good plant type, resistant to fertilizer, and the number of spikes is moderate and strong, and the recovery is strong.
IR24	*Indica* type, medium late maturity, disease resistance, good plant type, resistant to fertilizer, moderate to high number of spikes, excellent rice quality, strong resilience and wide adaptability.
SH527	*Indica* type, medium late maturity, disease resistance, good plant type, resistant to fertilizer, over the middle of the number of spikes, thousands of grains, excellent rice quality, strong resilience and high combining ability.

Information of upstream progenitors was obtained from the China Rice Data Center (http://www.ricedata.cn/variety/).

Appendix B Basic information of downstream derivatives restorer

Cultivar	Morphological character	Breeding pedigree
SH781	Strong restoring ability	IRBB60/SH527(♀) SH527(♂)
LH11	Compact plant type, good leaf shape, excellent rice quality, and strong restoring ability.	SH527(♀) FH828(♂)
3301	High number of grains per panicle	MH436(♀) SH527(♂)
SH238	R238, compact plant type, straight leaves, strong growth, and strong restoring ability.	SH527(♀) 677(♂)(MH77/C64/G3)
SH158	Loose and moderate plant type, good leaf shape, hard stalk to resist, strong tillering force , strong restoring ability, and high combining ability	SH527(♀) MH725(♂)
CH727	Good resistance, stable and high yield, strong restoring ability	CH177(♀) SH527(♂)
SH205	Moderate plant type, large grain size, strong resistance, strong restoring ability and high combining ability	Molecular marker-assisted selection was used to introduce disease resistance genes Xa21 and Xa4 into SH527.
NH511	Wide recovery spectrum, strong restoring ability, high combining ability, good rice quality and excellent comprehensive traits	SH881(♀) SH527(♂)
LH5240	High quality, stress resistance, strong combining ability, high seed production	R0211(♀) SH527(♂)
SH707	High yield, high yield, stable yield, wide adaptability, superior rice quality, high seed production	SH527(♀) E32(♂)
SHH287	Moderate plant type, long panicle, relatively rare grain, high 1000-grain weight, strong restoring ability and high combining ability	SH527(♀) LH130(♂)
SHH8281	High yield, moderate growth period, wide adaptability, superior rice quality and strong restoring ability	SH527/R130(♀) SH527(♂)

JH275	High yield, high yield and stable yield, moderate growth period, wide adaptability, strong disease resistance and superior rice quality	SH527/R130(♀) R130(♂)
SH288	Large number of grains per spike, high seed setting rate and strong restoring ability	R130(♀) SH527(♂)
R674	High yield, high quality, strong resistance, wide adaptability, moderate growth period, strong restoring ability and high combining ability	SH527(♀) 9311(♂)
B4114	Compact plant type, thick stems, high seed setting rate and strong resilience	YD6(♀) SH527(♂)
M2008	Strong hybridization, high yield, good quality, strong disease resistance, great potential for increased yield	H7954/SH527 (♀) SH527(♂)

Information of downstream derivatives restorer was obtained from the China Rice Data Center (http://www.ricedata.cn/variety/).

Appendix C Agronomic traits evaluated in the field from three years (2012-2014)

Cultivar	HD（day）	PH（cm）	TN	EPN	SpNPP	SeNPP	PSSR（%）	TKW（g）	WPPA（g）	WPPL（g）
SH527	103	116.6±1.0	13±2	55±2	125	116	92.17	35.67±0.3	4.12	45.36±3.01
Gu154	87	106.8±4.1	17±2	67±1	125	95	76.15	23.85±0.42	2.28	30.57±3.85
G630	105	116.3±2.9	11±5	48±5	165	152	92.36	31.03±0.48	4.74	45.54±6.13
IR1544	103	99.7±1.4	20±4	87±3	81	69	85.16	25.85±0.15	1.79	31.14±4.20
R1318	100	114.1±1.9	12±1	63±1	100	81	81.58	30.95±0.94	2.54	32.04±3.71
F36-2	86	91.4±3.2	20±5	71±3	113	85	75.17	21.53±0.5	1.83	26.04±6.05
IR24	103	96.1±1.9	12±4	54±3	96	86	89.08	29.32±0.27	2.61	28.17±5.47
SH781	99	123.0±0.7	10±2	44±2	122	112	91.71	33.52±0.62	3.77	33.16±6.89
LH11	99	127.8±2.2	15±2	63±2	175	155	88.44	31.86±0.63	4.96	62.45±9.24
3301	104	127.5±2.0	11±3	46±2	158	141	88.94	31.97±0.43	4.50	41.37±6.29
SH238	93	103.9±3.4	12±2	50±2	122	108	88.87	27.87±0.25	3.01	30.09±4.14
SH158	102	122.5±2.8	10±3	46±3	136	122	90.03	30.11±0.25	3.68	33.89±7.62
CH727	102	118.0±5.1	13±2	51±3	120	110	91.64	30.33±0.83	3.37	34.39±4.33
SH205	99	124.1±3.3	12±3	48±3	133	119	89.37	33.52±0.48	3.99	38.34±8.80
NH511	102	130.4±3.3	11±2	46±3	128	143	89.38	37.04±0.43	5.39	49.57±3.54
LH5240	102	120.9±1.0	11±3	49±3	131	120	91.97	34.59±0.76	4.20	41.12±5.47
SH707	104	121.1±5.2	10±3	44±3	125	115	91.39	34.17±1.06	4.18	36.80±3.03
SHH287	105	119.8±1.5	13±6	52±5	99	94	95.26	31.24±0.44	2.93	30.49±5.50
SHH8281	108	125.7±2.3	10±3	40±3	176	140	79.93	34.21±0.27	4.78	38.26±2.43
JH275	102	113.6±6.0	12±4	58±3	109	98	89.54	33.77±0.20	3.31	38.36±4.21
SH288	105	115.8±2.4	11±5	45±5	114	88	76.56	35.75±0.80	3.16	28.46±5.35
R674	106	119.1±5.1	12±2	52±2	111	103	92.90	32.84±0.61	4.40	44.00±5.90
B4114	106	114.8±2.1	13±5	58±4	141	135	96.24	26.25±0.21	3.56	41.26±8.65
M2008	103	113.2±2.3	14±2	43±5	147	132	89.80	28.17±0.23	3.72	31.98±2.24

Average data for the three years from 2012 to 2014. All the agronomic traits are measured as mean ± SD. Three replications. HD, heading date; PH, plant height; TN, tiller number; EPN, effective panicle number of 5 plants; SpNPP, spikelet number per panicle; SeNPP, seed number per panicle; PSSR, panicle seed-setting rate; TKW, thousand kernel weight; WPPA, seed weight per panicle; WPPL, seed weight per plant.

Appendix D Contribution of progenitors to the SH527 genome

Cultivar	Count	marker_number	Size	Ratio (%)
FU36_2	54	535	4394708	1.18
GUI630	149	6640	52875065	14.20
GU154	46	619	3652759	0.98
IR1544	7	37	251334	0.07
IR24	19	1757	13342968	3.58
F36_2_IR24	168	4199	32458924	8.72
G630_F36_2	49	461	2567945	0.69
G630_IR1544	98	1883	13542086	3.64
G630_IR24	33	813	5715721	1.54
GU154_F36_2	2	49	242856	0.07
GU154_G630	161	1864	12441818	3.34
GU154_IR1544	0	0	0	0
GU154_IR24	1	2	1093	0
IR1544_F36_2	1	27	243088	0.07
IR1544_IR24	2	14	80850	0.02
G630_F36_2_IR24	77	1265	8161283	2.19
G630_IR1544_F36_2	55	568	3769998	1.01
G630_IR1544_IR24	224	2774	20799959	5.59
GU154_F36_2_IR24	21	115	784276	0.21
GU154_G630_F36_2	95	811	5575498	1.50
GU154_G630_IR1544	59	542	3984557	1.07
GU154_G630_IR24	50	1171	8581697	2.31
GU154_IR1544_F36_2	1	3	363	0
GU154_IR1544_IR24	1	3	1047	0
IR1544_F36_2_IR24	36	652	5721245	1.54
G630_IR1544_F36_2_IR24	677	7434	52867704	14.20
GU154_G630_F36_2_IR24	302	2061	14652371	3.94
GU154_G630_IR1544_F36_2	58	245	1494422	0.40
GU154_G630_IR1544_IR24	229	2021	14749862	3.96
GU154_IR1544_F36_2_IR24	117	1108	8322082	2.24
GU154_G630_IR1544_F36_2_IR	3911	18011	118827110	31.91
527R_specific	60	174	716412	0.19

Appendix E Specific contribution of progenitors to the SH527 genome

Cultivar	Count	Size	Ratio (%)
F36_2	66	1018537	0.27
G630	366	5348693	1.44
GU154	51	506724	0.14
IR1544	6	89495	0.02
IR24	25	334755	0.09

Appendix F Summary of yield-related cloned gene information

Type	Gene	MSU_ID	Phenotypic characteristics
Grain Number	Gn1a; OsCKX2	LOC_Os01g10110	Number of grains per panicle (TO:0000447)
	Ghd7	LOC_Os07g15770	Number of grains per panicle (TO:0002759), High stalk (TO:0200207), Growth period related traits (TO:0000469), Late heading (TO:0010137)
	DEP1;DN1; qPE9-1	LOC_Os09g26999	Panicle type (TO:0000262), Number of grains per panicle(TO:0000447)
	DEP3	LOC_Os06g46350	Number of grains per panicle (TO:0000447), Panicle type (TO:0000089)
	SP1	LOC_Os11g12740	Short panicle (TO:0100040)
	OsAPO1; SCM2	LOC_Os06g45460	Stem strength (TO:0000051), Number of large vascular bundles (TO:0000539), Lodging rate (TO:0000068), Epidermal anatomical trait (TO:0000373), Number of grains per panicle (TO:0002759), Stem thickness (TO:0000976)
	OsSPL14; IPA1;WFP	LOC_Os08g39890	Number of grains per panicle (TO:0002759), Number of tillers (TO:0000346)
	PROG1	LOC_Os07g05900	tillerring force (TO:0000329), tillerring angle (TO:0000567), Number of effective panicles per plant (TO:0000152)
	OsJMT1	LOC_Os06g20920	Number of grains per panicle (TO:0002759)
	SQS	LOC_Os07g10130	Yield trait (TO:0000371), Drought resistance (TO:0000276)
	OsSDR	LOC_Os07g48640	Number of grains per panicle (TO:0002759)
	OsSIZ1	LOC_Os05g03430	Abiotic stress trait (TO:0000168), Plant height (TO:0000207), Seed setting rate (TO:0000448), Spikelet infertility (TO:0000436), Number of tillers (TO:0000346)
	WAF1	LOC_Os07g06970	Number of small flower organs (TO:0006038), Leaf shape (TO:0000492), Spike length (TO:0000040), Lethality (TO:0005285)
	OsOsAPC6APC6	LOC_Os03g13370	Grain size (TO:0000397), Female infertility (TO:0000358), Spike length (TO:0000040), Dwarf or semi-dwarf (TO:0100207)
	TAW1	(RAP-DB)Os10g0478000	Number of grains per panicle(TO:0002759), Secondary branch (TO:0000142)
	EP3	*LOC_Os02g15950*	Erect panicle (TO:0002621)
	OsFAD8	LOC_Os07g49310	Dwarf or semi-dwarf (TO:0100207), cold resistance (TO:0000303), Short panicle (TO:0100040)
	brd2;	(EMBL)AAM01136	Grain size (TO:0000397), Upright blade (PO:00200391), Infertility or low education (TO:0000485), Branch (PO:0009081), Small dwarf (TO:0120207), D6-type dwarf (TO:0230207), Sensitive to external BR (TO:0102677), Short panicle (TO:0100040)
Grain Weight; Grain Shape	GW2	LOC_Os02g14720	Grain width (TO:0000402), Thousand weight (TO:0000396), Number of effective panicles per plant (TO:0000152), Number of grains per panicle (TO:0002759), Late heading (TO:0010137)
	GS3	(RAP-DB)Os03g0407400	Grain length (TO:0000734), Grain width (TO:0000402), Grain thickness (TO:0000399), Thousand weight (TO:0000396)
	GS5	LOC_Os05g06660	Grain size (TO:0000397), Seed setting rate (TO:0000448), Thousand weight (TO:0000396)

gw5	(NCBI)DQ991205	Grain width (TO:0000402), Thousand weight (TO:0000396), Grain aspect ratio (TO:0002731)
qGW8; OsSPL16	LOC_Os08g41940	Grain size (TO:0000397), Steamed stuffed product (TO:0000667)
DEP2; EP2; SRS1	LOC_Os07g42410	Grain size (TO:0000397), Erect panicle (TO:0002621)
srs-3	LOC_Os05g06280	Grain size (TO:0000397)
TGW6	LOC_Os06g41850	Grain length (TO:0000734), Thousand weight (TO:0000396)
GIF1; OsCIN2	LOC_Os04g33740	Invertase activity (TO:0000311), Grain size (TO:0000397), Amylopectin content (TO:0000097), Viscous endosperm (TO:0000098), Grain filling degree (TO:0100928), Amylose content (TO:0000196)
flo-2	LOC_Os04g55230	Starch content (TO:0000696), Grain size (TO:0000397), Viscous endosperm (TO:0000098), High temperature resistance (TO:0000259)
OsGS1; GS1;OsGS1;1 ; OsGLN1;1 ; λGS28	LOC_Os02g50240	Grain filling degree (TO:0100928), Dwarf or semi-dwarf (TO:0100207), Late heading (TO:0010137)
OsPPKL3	LOC_Os12g42310	Grain length (TO:0000734), Thousand weight (TO:0000396)
OsPPKL2	LOC_Os05g05240	Grain length (TO:0000734), Thousand weight (TO:0000396)
PGL2	LOC_Os02g51320	Grain length (TO:0000734), Thousand weight (TO:0000396)
SG1	LOC_Os09g28520	Plant height (TO:0000207), Grain length (TO:0000734), Leaf width (TO:0000370), Spike length (TO:0000040), Leaf color (TO:0000326)
APG	LOC_Os05g04740	Grain length (TO:0000734), Thousand weight (TO:0000396)
PGL1	LOC_Os03g07510	Grain length (TO:0000734), Thousand weight (TO:0000396)
TH1; BSG1; BLS1	LOC_Os02g56610	Grain length (TO:0000734), Grain thickness (TO:0000399), Thousand weight (TO:0000396)
DEP3	LOC_Os06g46350	Number of grains per panicle (TO:0000447), Panicle type (TO:0000089)
CycT1;3	LOC_Os11g05850	Grain length (TO:0000734), Thousand weight (TO:0000396)
OsCD1	LOC_Os12g36890	Number of grains per panicle (TO:0000447), Dwarf or semi-dwarf (TO:0100207), Narrow leaf (TO:0200370), Short panicle (TO:0100040)
SGL1	LOC_Os08g36950	Plant height (TO:0000207), Grain length (TO:0000734), Leaf width (TO:0000370), Spike length (TO:0000040), Leaf color (TO:0000326)
LP	LOC_Os02g1590	Spike shape (TO:0000262), Spike length (TO:0000040)
OsPIP1;1	LOC_Os02g44630	Germination rate (TO:0000430), Salt sensitivity (TO:0000429), Thousand weight (TO:0000396)
HGW	LOC_Os06g06530	Thousand weight (TO:0000396), Heading period (TO:0000137)
OsNRAMP5	LOC_Os07g15370	Yield trait (TO:0000371)
OsFIE2	LOC_Os08g04270	Seed dormancy (TO:0000253), Grain size (TO:0000397), Grain filling degree (TO:0100928)
OsNADH-GOGAT2	LOC_Os05g48200	Leaf nitrogen content (TO:0000543), Number of grains per panicle (TO:0002759)

	TAD1;TE; OsCCS52A	LOC_Os03g03150	Number of tillers (TO:0000346)
	OsPht1;8; OsPT8	LOC_Os10g30790	Arsenic content TO:0006054), Phosphorus content (TO:0001024), Seed setting rate (TO:0000448)
	OsEF3	LOC_Os01g38530	Thousand weight (TO:0000396), Early heading (TO:0020137)
	OsAP2-39	LOC_Os04g52090	Number of grains per panicle (TO:0002759), Dwarf or semi-dwarf (TO:0100207), Number of tillers (TO:0000346), Late heading (TO:0010137)
	OsCIN1	LOC_Os02g33110	Invertase activity (TO:0000311), Grain filling degree (TO:0100928)
	OsSUT2	LOC_Os12g44380	Plant height (TO:0000207), Thousand weight (TO:0000396), Number of tillers (TO:0000346)
	OsNAC10; ONAC122	LOC_Os11g03300	Yield trait (TO:0000371), Rice blast resistance TO:0000074), Drought resistance (TO:0000276)
Plant height	OsGS2;OsGLN2;λGS31	LOC_Os04g56400	Dwarf or semi-dwarf (TO:0100207), Number of tillers (TO:0000346)
	DST	LOC_Os03g57240	Plant height (TO:0000207), Cytokinin content (TO:0002660), Hydrogen peroxide content (TO:0000605), Drought resistance (TO:0000276), Salt sensitivity (TO:0000429), Number of grains per panicle (TO:0000447), Spike branch (TO:0000050)
	DTH8;Ghd8; OsHAP3H; LHD1	LOC_Os08g07740	Plant height (TO:0000207), Photoperiod sensitivity (TO:0000229), Heading period (TO:0000137), Number of grains per panicle (TO:0002759), Number of tillers (TO:0000346)
	EUI1; i-sd-1(t)	LOC_Os05g40384	High stalk (TO:0200207), Long spike (TO:0200040), Top internode elongation (TO:0101451)
	LGD1	LOC_Os09g32540	Plant height (TO:0000207), Spike shape (TO:0000262), Number of tillers (TO:0000346)
	OsDRM2	LOC_Os03g02010	Plant height (TO:0000207), Infertility or low education (TO:0000485), Number of tillers (TO:0000346)
Number of tillers	D3	LOC_Os06g06050	More tillers and dwarf (TO:0110207), Number of tillers (TO:0000346)
	D10; OsCCD8	LOC_Os01g54270	More tillers and dwarf (TO:0110207), Number of tillers (TO:0000346)
	OsMT2b	LOC_Os05g02070	Dwarf or semi-dwarf (TO:0100207), Number of tillers (TO:0000346)
	OGR1	LOC_Os12g17080	Infertility or low education (TO:0000485), Dwarf or semi-dwarf (TO:0100207), Number of tillers (TO:0000346)
	d-27	(RAP-DB)Os11g0587000	Dwarf or semi-dwarf (TO:0100207), Number of tillers (TO:0000346)
	HTD2; D88;D14	LOC_Os03g10620	More tillers and dwarf (TO:0110207), Number of tillers (TO:0000346)
	OsTB1; FC1	LOC_Os03g49880	Number of tillers (TO:0000346)
	OsTEF1	LOC_Os02g04160	Number of tillers (TO:0000346)
	OsTRXh1	LOC_Os07g08840	Plant height (TO:0000207), Salt sensitivity (TO:0000429), Number of tillers (TO:0000346)
	OsPIN2	LOC_Os06g44970	Plant height (TO:0000207), tillerring angle (TO:0000567), Number of tillers (TO:0000346)
	LAX2	LOC_Os04g32510	Number of tillers (TO:0000346), Spike branch (TO:0000050)
	OsEATB	LOC_Os09g28440	Internode length (TO:0000145), tillerring force (TO:0000329), Spike length (TO:0000040)

	OsJAG	LOC_Os01g03840	Flower organ developmental traits (TO:0006022), Male sterility (TO:0000437), Female infertility (TO:0000358), Number of tillers (TO:0000346)
	MIP1	LOC_Os04g46450	Dwarf or semi-dwarf (TO:0100207), Number of tillers (TO:0000346)
	OsPIN1; REH1	LOC_Os02g50960	Root to crown ratio (TO:0000278), Number of tillers (TO:0000346)
	MOC1	LOC_Os06g40780	tillerring force (TO:0000329)
Panicle seed setting rate	PTB1	LOC_Os05g05280	Seed setting rate (TO:0000448)
Yield	OsNAC5	LOC_Os11g08210	Yield trait (TO:0000371), Root thickness (TO:0000306), Drought resistance (TO:0000276), Salt sensitivity (TO:0000429)
	AID1	(EMBL)AY429017	Anther (PO:0006442), MYB transcription factor (GO:MYB3700), Pollen abortion (TO:0000053), Number of tillers (TO:0000346), Early heading (TO:0020137)

Datas on the known genes/QTLs was obtained from the National Rice Data Center (http://www.ricedata.cn/index.htm) and the Rice Genome Annotation Project (http://rice.plantbiology.msu.edu/).

Appendix G Genes found in various progenitor regions and the SH527 key regions

Region	Chr.	Gene	Function
F36-2.originated	chr06	AID1[1]	Fertility
G630.originated	chr08	GW8[2]	Grain size and weight
G630.originated	chr07	OsFAD8[3]	Stress and yield
G630.originated	chr11	OsNAC10[4]	Stress and yield
G630.originated	chr06	OsJMT1[5]	Stress and yield
G630.originated	chr12	OsCD1[6]	Plant architecture and yield
G630.originated	chr12	OsPPKL3[7]	Grain size and weight
G630.originated	chr05	GS5[8]	Grain size and weight
G630.originated	chr05	SRS3[9]	Grain size and weight
G630.originated	chr05	OsNADH-GOGAT2[10]	Spikelet number and yield
G630.originated	chr02	GW2[11]	Grain size and weight
G630.originated	chr02	EP3[12]	Panicle architecture and yield
G630.originated	chr02	LP[13]	Panicle architecture and yield
G630.originated	chr02	SGL1[14]	Panicle architecture,grain size and
IR24.originated	chr03	OsAPC6[15]	Fertility
IR24.originated	chr03	HTD2/D88/D14[16]	Tillering and plant architecture
IR24.originated	chr11	SP1[17]	Panicle architecture and yield
IR24.originated	chr11	d-27[18]	Tillering and plant architecture
SH527.key.region	chr04	OsAP2-39[19]	yield
SH527.key.region	chr03	TAD1[20]	Grain size and weight
SH527.key.region	chr03	qGL3.1[21]	Grain size and weight
SH527.key.region	chr03	OsTB1/FC1[22]	Tillering and plant architecture
SH527.key.region	chr03	DST[23]	Grain number and yield
SH527.key.region	chr07	SQS[24]	Stress and yield
SH527.key.region	chr07	Ghd7[25]	Grain number,plant height,grain
SH527.key.region	chr07	DEP2[26]	Panicle architecture and grain size
SH527.key.region	chr07	OsSDR[27]	Stress and yield
SH527.key.region	chr07	OsFAD8[3]	Stress and yield

SH527.key.region	chr11	d-27[18]	Tillering and plant architecture
SH527.key.region	chr06	OsJMT1[28]	Stress and yield
SH527.key.region	chr06	TGW6[29]	Grain size and weight
SH527.key.region	chr06	OsPIN2[30]	Tillering and plant architecture
SH527.key.region	chr06	APO1[31]	Grain number and yield
SH527.key.region	chr05	OsSIZ1[32]	Fertility
SH527.key.region	chr05	GS5[8]	Grain size and weight
SH527.key.region	chr05	EUI1[33]	Plant architecture
SH527.key.region	chr01	OsJAG[34]	Floral organ development and tillering
SH527.key.region	chr01	Gn1a[23]	Grain number and yield
SH527.key.region	chr01	OsEF3[35]	Flowering time
SH527.key.region	chr02	OsPIP1;1[36]	Stress and yield
SH527.key.region	chr02	REH1[37]	Tillering and plant architecture
SH527.key.region	chr02	SGL1[14]	Panicle architecture and grain size
SH527.key.region	chr02	TH1[38]	Grain size and weight

References

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Appendix H Key genomic regions of SH527 (> 200 kb)

Chr.	Beginning	Ending	Count	Beginning base	Ending base	size
chr06	2110	2120	11	18206974	18804121	597148
chr07	544	566	23	5202658	5553722	351065
chr02	1667	1675	9	13547380	13844186	296807
chr07	3215	3223	9	27105934	27377976	272043
chr11	131	151	21	1601944	1857800	255857
chr03	1391	1410	20	10575123	10814365	239243
chr07	435	449	15	4200115	4431697	231583
chr04	2818	2825	8	25720343	25948171	227829
chr12	242	259	18	2323291	2544788	221498

Appendix I GWAS result of important agronomic traits

Trait	HD	PH	TN	EPN	SpNPP	SeNPP	PSSR	TKW	WPPA	WPPL
Site	3	20	146	11	0	5	31	3	37	5

HD, heading date; PH, plant height; TN, tiller number; EPN, effective panicle number of 5 plants; SpNPP, spikelet number per panicle; SeNPP, seed number per panicle; PSSR, panicle seed-setting rate; TKW, thousand kernel weight; WPPA, seed weight per panicle; WPPL, seed weight per plant.

Appendix J Distribution of the associated loci in each specific region

Region	Chr.	Snp_loci	Snp_name	Phenotype
G630.originated	chr06	7826314	F0607826314CT	TN
G630.originated	chr06	7827200	R0607827200GT	TN
G630.originated	chr02	1370860	F0201370860CT	HD
G630.originated	chr02	1047745	R0201047745TG	PSSR
G630.originated	chr02	1018930	F0201018930GT	PSSR
G630.originated	chr02	1012254	F0201012254CT	PSSR
G630.originated	chr10	910155	F1000910155TC	TN
G630.originated	chr10	1083370	R1001083370AG	TN
G630.originated	chr10	904922	R1000904922AC	TN
G630.originated	chr10	1086188	R1001086188GT	TN
G630.originated	chr10	908421	F1000908421AG	TN
IR24.originated	chr11	3802808	F1103802808AG	WPPA
IR24.originated	chr11	3757412	R1103757412AG	WPPA
IR24.originated	chr11	3825229	F1103825229TC	WPPA
IR24.originated	chr11	3805232	R1103805232TG	WPPA
IR24.originated	chr11	3751019	F1103751019AG	WPPA
IR24.originated	chr11	3800049	R1103800049TG	WPPA
IR24.originated	chr11	3790091	F1103790091CT	WPPA
IR24.originated	chr11	3799916	F1103799916TC	WPPA
IR24.originated	chr11	3805869	F1103805869AG	WPPA
IR24.originated	chr11	5562938	F1105562938TC	PH
IR24.originated	chr11	5584321	R1105584321AG	PH
IR24.originated	chr11	5588992	R1105588992GA	PH
IR24.originated	chr11	5629922	R1105629922CT	WPPA
IR24.originated	chr11	5584321	R1105584321AG	WPPA
IR24.originated	chr11	5630044	F1105630044CT	WPPA
IR24.originated	chr11	5588992	R1105588992GA	WPPA
IR24.originated	chr11	5741567	F1105741567CA	PH

IR24.originated	chr11	5754109	F1105754109AG	WPPA
IR24.originated	chr11	5753811	F1105753811TG	WPPA
IR24.originated	chr11	5887594	R1105887594AG	PH
IR24.originated	chr11	5899222	F1105899222CT	PH
IR24.originated	chr11	5886402	R1105886402CA	PH
IR24.originated	chr11	5886402	R1105886402CA	WPPA
IR24.originated	chr11	5887594	R1105887594AG	WPPA
IR24.originated	chr11	5899222	F1105899222CT	WPPA
IR24.originated	chr11	7401840	F1107401840GT	TN
IR24.originated	chr11	7410244	F1107410244GA	TN
IR24.originated	chr11	23240773	R1123240773GA	TKW
IR24.originated	chr11	23517419	F1123517419CT	TKW
IR24.originated	chr05	26995759	F0526995759CT	TN
IR24.originated	chr05	27024242	F0527024242GA	TN
IR24.originated	chr05	27015292	F0527015292GA	TN
IR24.originated	chr01	31318108	F0131318108CT	TN
SH527.key.region	chr05	26995759	F0526995759CT	TN
SH527.key.region	chr08	17688156	R0817688156AC	TN
SH527.key.region	chr08	17693208	R0817693208CT	TN
SH527.key.region	chr08	17708840	F0817708840GA	TN
SH527.key.region	chr08	17717860	R0817717860CT	TN
SH527.key.region	chr08	17727512	F0817727512TC	TN
SH527.key.region	chr08	17728978	F0817728978GA	TN
SH527.key.region	chr08	17820060	R0817820060TC	TN
SH527.key.region	chr08	17894172	F0817894172CT	TN
SH527.key.region	chr08	17921722	F0817921722CT	TN
SH527.key.region	chr08	17834484	R0817834484CA	TN
SH527.key.region	chr08	18008459	F0818008459CT	TN
SH527.key.region	chr08	18054909	F0818054909GA	TN
SH527.key.region	chr08	18099719	R0818099719TC	TN

SH527.key.region	chr08	18083452	R0818083452AG	TN
SH527.key.region	chr08	18130685	R0818130685CA	TN
SH527.key.region	chr08	18107067	R0818107067GA	TN
SH527.key.region	chr08	18118653	R0818118653CT	TN
SH527.key.region	chr08	18262805	R0818262805CA	TN
SH527.key.region	chr07	20006804	F0720006804TC	TN
SH527.key.region	chr07	20052503	R0720052503AT	TN
SH527.key.region	chr07	20079013	F0720079013TC	TN
SH527.key.region	chr07	20106452	F0720106452AC	TN
SH527.key.region	chr07	20874212	R0720874212AG	TN
SH527.key.region	chr07	21168311	R0721168311TG	TN
SH527.key.region	chr07	21212091	R0721212091CT	TN
SH527.key.region	chr07	21216049	R0721216049TC	TN
SH527.key.region	chr07	21295487	F0721295487TC	TN
SH527.key.region	chr07	21332936	F0721332936CT	TN
SH527.key.region	chr07	21365438	R0721365438CT	TN
SH527.key.region	chr07	21314534	R0721314534TC	TN
SH527.key.region	chr07	21344928	F0721344928GA	TN
SH527.key.region	chr07	21377088	R0721377088GA	TN
SH527.key.region	chr07	21437216	R0721437216AG	TN
SH527.key.region	chr07	22691148	R0722691148CA	TN
SH527.key.region	chr07	22641361	R0722641361GA	TN
SH527.key.region	chr07	22671293	F0722671293TC	TN
SH527.key.region	chr07	22784529	R0722784529TC	TN
SH527.key.region	chr07	22810816	F0722810816AG	TN
SH527.key.region	chr07	22873868	R0722873868AG	TN
SH527.key.region	chr07	23010115	R0723010115GT	TN
SH527.key.region	chr07	23094862	R0723094862TG	TN
SH527.key.region	chr07	23093142	F0723093142TC	TN
SH527.key.region	chr07	23104502	F0723104502TC	TN

SH527.key.region	chr07	23100443	F0723100443AG	TN
SH527.key.region	chr07	23155186	F0723155186AG	TN
SH527.key.region	chr07	23420882	F0723420882GA	TN
SH527.key.region	chr07	23415133	R0723415133TC	TN
SH527.key.region	chr07	26968406	R0726968406CT	TN
SH527.key.region	chr07	26972909	F0726972909AC	TN
SH527.key.region	chr07	27010519	F0727010519TC	TN
SH527.key.region	chr07	27010537	F0727010537TC	TN
SH527.key.region	chr07	27020591	R0727020591CT	TN
SH527.key.region	chr07	27022681	F0727022681CT	TN
SH527.key.region	chr07	27020954	F0727020954CT	TN
SH527.key.region	chr07	27736013	F0727736013AC	TN
SH527.key.region	chr07	27746264	F0727746264GA	TN
SH527.key.region	chr07	27800554	R0727800554GA	TN
SH527.key.region	chr07	27800219	R0727800219CA	TN
SH527.key.region	chr07	27776286	F0727776286CT	TN
SH527.key.region	chr07	27791602	R0727791602AT	TN
SH527.key.region	chr07	27778894	F0727778894CT	TN
SH527.key.region	chr07	27792775	R0727792775GA	TN
SH527.key.region	chr07	27781533	F0727781533GT	TN
SH527.key.region	chr07	27795366	F0727795366CT	TN
SH527.key.region	chr07	27796462	R0727796462CA	TN
SH527.key.region	chr07	27800162	F0727800162AC	TN
SH527.key.region	chr07	27763855	F0727763855AG	TN
SH527.key.region	chr07	28304354	R0728304354GA	TN
SH527.key.region	chr07	28302047	R0728302047CT	TN
SH527.key.region	chr07	28413937	R0728413937CT	TN
SH527.key.region	chr07	28411552	F0728411552TC	TN
SH527.key.region	chr07	28417878	F0728417878CT	TN
SH527.key.region	chr07	28415810	R0728415810TC	TN

SH527.key.region	chr07	28409173	F0728409173GA	TN
SH527.key.region	chr07	28525680	R0728525680CT	TN
SH527.key.region	chr11	5464969	F1105464969GA	TN
SH527.key.region	chr11	5452530	R1105452530GA	TN
SH527.key.region	chr11	5463158	R1105463158TC	TN
SH527.key.region	chr11	6100513	R1106100513TG	TN
SH527.key.region	chr11	6160757	R1106160757TC	TN
SH527.key.region	chr06	7826314	F0607826314CT	TN
SH527.key.region	chr06	7827200	R0607827200GT	TN
SH527.key.region	chr10	910155	F1000910155TC	TN
SH527.key.region	chr10	904922	R1000904922AC	TN
SH527.key.region	chr10	908421	F1000908421AG	TN
SH527.key.region	chr10	1083370	R1001083370AG	TN
SH527.key.region	chr10	1086188	R1001086188GT	TN

Appendix K Possible candidate genes at or adjacent to the associated sites

Gene	Chr	Snp_loci	Distance	Snp_name	Phenotype
D10	chr01	31318108	90841	F0131318108CT	TN
qGY2-1	chr02	2884335	94518	R0202884335CT	PSSR
qGY2-1	chr02	2749139	229714	F0202749139AG	PSSR
REH1	chr02	31078227	75776	F0231078227TC	TN
DEP3	chr06	28255300	145666	R0628255300GT	TN
TGW6	chr06	25112193	18896	R0625112193TC	WPPL
dwf1	chr10	13120470	168931	F1013120470GA	TN
SP1	chr11	7401840	209108	F1107401840GT	TN
SP1	chr11	7410244	217512	F1107410244GA	TN