

Table S1. SNP/Indel number and function analysis of P1, P2, H and L bulks by BSA-seq sequencing.

Bulk		P1	P2	H	L
Number of SNPs		5,951,422	4,351,073	7,324,014	7,265,497
Number of indels		689,385	484,007	837,490	825,373
SNP location and function	downstream	162,648	110,808	195,226	195,695
	exonic	178,817	117,296	207,575	207,144
	exonic; splicing	163	106	195	190
	intergenic	4,797,977	3,573,314	5,952,845	5,894,409
	intronic	493,408	335,519	589,002	588,632
	splicing	730	534	872	864
	upstream	178,190	121,119	213,170	213,755
	upstream; downstream	18,790	13,116	22,691	22,851
	UTR3	71,364	46,936	84,278	84,027
	UTR5	47,947	31,374	56,480	56,253
	UTR5; UTR3	1,388	951	1,680	1,677
	nonsynonymous SNV	85,258	56,507	99,176	98,824
	stopgain	1,273	936	1,586	1,562
	synonymous SNV	92,449	59,959	107,008	106,948
	ts	4,210,793	3,095,013	5,185,449	5,150,740
	tv	1,740,629	1,256,060	2,138,565	2,114,757
	ts/tv	2.4191	2.4641	2.4247	2.4356
Indels location and function	downstream	36,482	24,916	43,773	43,416
	exonic	16,145	10,774	18,738	18,607
	exonic; splicing	29	20	33	33
	intergenic	432,224	312,221	533,644	523,404
	intronic	104,907	69,590	123,612	122,663
	splicing	538	365	619	621
	upstream	45,261	30,557	53,886	53,752
	upstream; downstream	5,563	3,798	6,644	6,644
	UTR3	25,617	16,966	30,157	30,012
	UTR5	21,841	14,246	25,424	25,255
	UTR5; UTR3	776	552	958	964
	frameshift deletion	2,845	2,062	3,367	3,338
	frameshift insertion	2,142	1,470	2,595	2,561
	nonframeshift deletion	6,027	4,007	6,879	6,865
	nonframeshift insertion	4,981	3,129	5,715	5,661
	stopgain	179	126	215	215

SNPs, single nucleotide polymorphisms; UTR3, 3' untranslated region; UTR5, 5' untranslated region; SNV, single nucleotide variant; ts, transition (the substitution between purines or between pyrimidines); tv, transversion (the substitution between purines and pyrimidines).

Table S2. QTLs conferring SGRL identified by four calculation models.

QTL names	Calculation models	CI	Chr	Start (bp)	End (bp)	Peak	Overlapping region (Mb)
<i>qSGRL1-1</i>	Δ (SNP-index)			970,001	12,300,000	0.484494	
	G' value			8,300,001	13,000,000	17.76683	
	Euclidean distance	0.95	1	10,400,001	12,300,000	0.524688	10.4–12.3
	Fisher's exact test			10,400,001	12,300,000	0.038513	
<i>qSGRL1-2</i>	Δ (SNP-index)			223,100,001	231,800,000	-0.67635	
	G' value	0.99	1	223,200,001	227,500,000	24.66762	224.1–225.1
	Euclidean distance			223,200,001	228,000,000	0.954488	

<i>qSGRL1-3</i>	Fisher's exact test	0.99	1	224,100,001	225,100,000	0.008814	225.9–226.9-
	$\Delta(\text{SNP-index})$			223,100,001	231,800,000	-0.67635	
	G' value			223,200,001	227,500,000	24.66762	
	Euclidean distance			223,200,001	228,000,000	0.954488	
	Fisher's exact test			225,900,001	226,900,000	0.00734	
<i>qSGRL1-4</i>	$\Delta(\text{SNP-index})$	0.99	1	223,100,001	231,800,000	-0.67635	228.2–230.0
	G' value			227,900,001	231,600,000	27.99551	
	Euclidean distance			228,100,001	231,600,000	0.907602	
	Fisher's exact test			228,200,001	230,000,000	0.008283	
	$\Delta(\text{SNP-index})$			221,500,001	251,200,000	-0.67635	
<i>qSGRL1-5</i>	G' value	0.95	1	236,400,001	251,100,000	17.71894	241.5–242.5
	Euclidean distance			236,500,001	251,100,000	0.722483	
	Fisher's exact test			241,500,001	242,500,000	0.049965	
	$\Delta(\text{SNP-index})$			221,500,001	251,200,000	-0.67635	
	G' value			236,400,001	251,100,000	17.71894	
<i>qSGRL1-6</i>	Euclidean distance	0.95	1	236,500,001	251,100,000	0.722483	243.1–244.3
	Fisher's exact test			243,100,001	244,300,000	0.043696	
	$\Delta(\text{SNP-index})$			221,500,001	251,200,000	-0.67635	
	G' value			236,400,001	251,100,000	17.71894	
	Euclidean distance			236,500,001	251,100,000	0.722483	
<i>qSGRL1-7</i>	Fisher's exact test	0.95	1	244,800,001	246,100,000	0.03049	244.8–246.1
	$\Delta(\text{SNP-index})$			67,700,001	70,500,000	0.533074	
	G' value			67,700,001	70,500,000	14.46116	
	Euclidean distance			67,400,001	70,500,000	0.626375	
	Fisher's exact test			68,300,001	69,300,000	0.041346	
<i>qSGRL2-1</i>	$\Delta(\text{SNP-index})$	0.95	2	67,700,001	70,500,000	0.533074	68.3–69.3
	G' value			67,700,001	70,500,000	14.46116	
	Euclidean distance			67,400,001	70,500,000	0.626375	
	Fisher's exact test			68,300,001	69,300,000	0.041346	
	$\Delta(\text{SNP-index})$			67,700,001	70,500,000	0.533074	
<i>qSGRL2-2</i>	G' value	0.95	2	67,700,001	70,500,000	14.46116	69.5–70.5
	Euclidean distance			67,400,001	70,500,000	0.626375	
	Fisher's exact test			69,500,001	70,500,000	0.046673	
	$\Delta(\text{SNP-index})$			157,300,001	170,000,000	0.669006	
	G' value			158,200,001	170,100,000	24.49339	
<i>qSGRL2-3</i>	Euclidean distance	0.95	2	158,200,001	170,000,000	0.944635	158.8–169.4

<i>qSGRL3</i>	Fisher's exact test			158,800,001	169,400,000	0.013121	231.1–232.1
	Δ (SNP-index)			230,900,001	232,100,000	0.581665	
	G' value	0.95	3	230,900,001	232,100,000	24.11769	
	Euclidean distance			231,000,001	232,100,000	0.713085	
	Fisher's exact test			231,100,001	232,100,000	0.011686	
<i>qSGRL7</i>	Δ (SNP-index)			172,400,001	181,600,000	-0.57091	173.0–176.2
	G' value	0.95	7	170,800,001	181,600,000	20.38417	
	Euclidean distance			172,700,001	181,600,000	0.701467	
	Fisher's exact test			173,000,001	176,200,000	0.029829	
	Δ (SNP-index)			155,100,001	160,200,000	-0.65785	
<i>qSGRL9</i>	G' value	0.95	9	155,100,001	159,800,000	22.56668	155.1–157.1
	Euclidean distance			155,100,001	159,800,000	0.905927	
	Fisher's exact test			155,100,001	157,100,000	0.010069	
	Δ (SNP-index)			2,900,001	4,900,000	0.657732	
	G' value			2,900,001	4,900,000	26.24168	
<i>qSGRL10</i>	Euclidean distance	0.99	10	2,900,001	4,400,000	0.973402	2.9–3.9
	Fisher's exact test			2,900,001	3,900,000	0.008801	

SNP, single nucleotide polymorphism; G, G-statistic; CI, Confidence Interval; Chr, chromosome.

Table S3. Summary of the RNA-seq data.

Sample	Raw Reads	Clean Reads	Clean Bases (Gb)	Q20 (%)	Q30 (%)	GC content (%)	Clean Reads Ratio (%)	Total Mapping (%)
P1-1	39,797,482	39,682,944	5.94	98.20	94.54	52.42	99.71	94.07
P1-2	39,439,870	39,306,088	5.88	98.29	94.67	51.56	99.66	94.84
P1-3	39,218,636	39,104,706	5.85	98.30	94.77	52.45	99.71	95.33
P2-1	40,798,352	40,662,196	6.08	98.31	94.82	52.19	99.67	92.79
P2-2	41,094,562	40,965,410	6.13	98.19	94.51	52.51	99.69	92.68
P2-3	41,915,340	41,782,288	6.24	98.32	94.85	52.45	99.68	91.21
H-1	41,041,526	40,921,162	6.12	97.85	93.65	51.64	99.71	91.90
H-2	41,008,880	40,898,494	6.12	98.28	94.69	52.10	99.73	92.91
H-3	44,273,096	44,152,490	6.61	98.36	94.91	52.13	99.73	92.53
L-1	44,880,798	44,745,210	6.70	98.09	94.32	53.17	99.70	91.67

L-2	42,853,28 6	42,690,690	6.38	97.73	93.51	53.72	99.62	90.79
L-3	43,166,15 2	43,040,310	6.44	98.17	94.47	53.17	99.71	90.71

Q20, the indicator of the proportion of bases with a quality value greater than or equal to 20;
Q30, the indicator of the proportion of bases with a quality value greater than or equal to 30.