

Table S1 Statistic analysis of sequencing datum in each sample

Sample	Clean Base	Q30(%)	GC(%)	Ave depth	Cov- _ratio_10X(%)	Mapped(%)	Properly mapped(%)
KJ01	1672855240	94	45.72	38	88.4	97.52	90.06
Huaye 4	13466564590	93.8	45.54	31	90.19	97.77	91.14
L-pool	31934634710	93.8	46.04	70	95.23	95.51	88.31
S-pool	38091366320	93.9	46.03	83	95.89	95.75	88.57

Table S2 SNPs analysis for the four samples

Sample	SNP numbers	Transition	Transversion	Ti/Tv	Heterozygosity	Homozygosity	Het-ratio (%)
KJ01	1443316	1036169	407147	2.54	175341	1267975	12.14
Huaye 4	1245956	890859	355097	2.50	251407	994549	20.17
L-pool	2136482	1531309	605173	2.53	1545825	590657	72.35
S-pool	2216645	1590470	626175	2.53	1765226	451419	79.63

Table S3 The numbers of gene annotation in association region

Annotated databases	Annotated Gene Number
NR	37
NT	37
trEMBL	37
SwissProt	23
GO	33
KEGG	3
COG	9
Total	37

Table S4 TopGO analysis of 37 genes in associated regions

GO ID	Ontology	Term	Significant	Expected	KS
GO:0005886	CC	plasma membrane	3	2.79	1.40E-13
GO:0005634	CC	nucleus	4	4.01	2.00E-11
GO:0016021	CC	integral component of membrane	2	2.4	1.70E-09
GO:0005773	CC	vacuole	1	0.99	1.40E-05
GO:0005789	CC	endoplasmic reticulum membrane	2	0.16	0.00012
GO:0005524	MF	ATP binding	2	2.89	2.30E-06
GO:0006281	BP	DNA repair	2	0.3	0.00134
GO:0006882	BP	cellular zinc ion homeostasis	1	0.01	5.30E-05