

Table 3 The strong association signals and functional annotation

Chromosome	Location	Adjacent gene	-log (p_value)	Minimum allele frequency	Distance	Base mutation
A05	16 943 383	BraA05g023100.3C	8.04	0.3 364	18 653	C→T
A05	16 943 901	BraA05g023110.3C	6.58	0.4 454	-7 228	G→A
A05	16 945 137	BraA05g023120.3C	6.71	0.2 629	-12 449	T→A
A10	5 004 502	BraA10g007660.3C	6.77	0.0 561	13 115	G→A
A10	5 004 502	BraA10g007670.3C	6.77	0.0 561	11 533	G→A
A10	5 004 502	BraA10g007680.3C	6.77	0.0 561	9 524	G→A
A10	5 004 502	BraA10g007690.3C	6.77	0.0 561	6 586	G→A
A10	5 004 502	BraA10g007700.3C	6.77	0.0 561	-2 773	G→A
A10	5 004 502	BraA10g007710.3C	6.77	0.0 561	-9 912	G→A