Supplemental Table 1. Characteristics of the mutant families identified in the *Bradi5g03300* gene following screening of the Bd21-3 TILLING collection.

Family name	Nucleic acid transition[a]	Amino acid substitution[b]	Mutation type[c]	Location of the mutation
5617	G1477A	G269S	Missense	Exon 2
6570	C1542T	S290S	Silent	Exon 2
5648	C1585T	L305L	Silent	Exon 2
7273	G1589A	G306E	Missense	Exon 2
3698	G1660A	G330S	Missense	Exon 2
7079	G1686A	K337K	Silent	Exon 2
6829	G1707A	W345*	Nonsense	Exon 2 (PSPG box)
7850	C1726T	L352L	Silent	Exon 2 (PSPG box)
8156	C1778T	/	/	Intron 2
3658	G1792T	/	/	Intron 2
6491	G1878A	W366*	Nonsense	Exon 3 (PSPG box)
8637	C1883T	S368F	Missense	Exon 3 (PSPG box)
7945	G1922A	G381E	Missense	Exon 3 (PSPG box)
3714	A1923C	G381G	Silent	Exon 3 (PSPG box)
5775	G1966A	E396K	Missense	Exon 3

[a]Location of the point mutation in mutants are relative to the starting ATG on the genomic DNA sequence.
[b]Location of the amino acid substitution in mutants are relative to the starting methionine of the encoded protein.
[c]Missense, nucleic acid transition is a non-synonymous mutation and induce amino acid change in the translated protein; Nonsense, nucleic acid transition produces a stop codon and may induce a truncated protein; Silent, nucleic acid transition induces a synonymous mutation and therefore no change in the translated protein.