Table S2 Different barley TILLING plants and the corresponding positions of different amino acid substitution.

Mutant ID	population	SNP position	SNP	SNP allele	aa substitiution	Domain position	Conservation
10782-1	Barke	151	C→T	Heterozygote	R → C	-	-
10607-1	Barke	155	G→A	Heterozygote	G → D	-	-
12171-1	Barke	176	C→T	Heterozygote	P → L	-	conserved region
2723-1	Barke	308	G→A	Homozygote	R → H	within AP2/ERF domain	conserved region
3919-1	Barke	320	C→T	Heterozygote	S → F	within AP2/ERF domain	conserved region
6816-1	Barke	529	G→A	Homozygote	G → S	-	-
11023-1	Barke	541	G→A	Homozygote	G → S	-	-
11359-1	Barke	572	C→T	Homozygote	A → V	-	-
4913-1	Barke	587	G→A	Homozygote	S → N	-	-
13679-2	Barke	605	G→A	Homozygote	S → N	-	-
6872-1	Barke	631	A→T	Homozygote	S → C	-	-
9662-1	Barke	662	G→A	Homozygote	S → N	-	conserved region
6893-1	Barke	695	G→A	Homozygote	G → D	-	-
9624-1	Barke	748	G→T	Heterozygote	G → W	-	-
48	Morex	329	G→A	Heterozygote	G → D (110)	within AP2/ERF domain	conserved region
5865	Morex	286	G→A	Homozygote	E → K (96)	within AP2/ERF domain	conserved region
AP2/ERF domain				184 - 357 bp			
phylogenetically highly conserved domain				638 - 691 bp			