SI Table 4. Large-effect SNPs validation and false discovery rates

			Validation by dideoxy sequencing			
SNP Annotation	**# SNP sites[a]**	**# base calls[b]**	**# sequenced amplicons**	**True**	**False**	**FDR**
Premature stop	291	1290	90	72	18	0.20
Intron splice stop	101	632	80	65	16	0.20
Start/stop codon	74	562	39	39	0	0.00
Total	466	2484	209	176	34	0.163

[a] Number of SNP sites in the MBML-intersect data set with one or more cultivars different from the reference genome.

[b] Number of base calls in the MBML-intersect data set for all cultivars different from the reference at all SNP sites.