

Table 2 Genetic analysis of *badh2* in F₂ generation between Taiguoxiaoxiangzhan crossed with different restorer lines

Hybrid combinations	Non-fragrance homozygotes (<i>Badh2/Badh2</i>)	Non-fragrance heterozygotes (<i>Badh2/badh2</i>)	Fragrance homozygotes (<i>badh2/badh2</i>)	<i>p</i> value	Functional marker
Taiguoxiaoxiangzhan/R1	26	55	28	0.8756	InDel-E7
Taiguoxiaoxiangzhan/R2	32	70	38	0.8879	InDel-E7
Taiguoxiaoxiangzhan/R3	51	90	43	0.8407	FMbadh2-E7
Taiguoxiaoxiangzhan/R4	49	113	58	0.7880	FMbadh2-E7
Taiguoxiaoxiangzhan/R5	38	85	42	0.7888	FMbadh2-E7A
Taiguoxiaoxiangzhan/R6	62	112	53	0.7467	FMbadh2-E7A
Taiguoxiaoxiangzhan/R7	41	87	49	0.9178	FMbadh2-E7B
Taiguoxiaoxiangzhan/R8	55	101	42	0.8253	FMbadh2-E7B

Note: R1: Minghui2155; R2: Minghui86; R3: Minghui3009; R4: Fuhui673; R5: Minhui3301; R6: Jianghui151; R7: R527; R8: R498; *p* value > 0.05, No significant difference, which indicated that the segregation ratios were coincidence with the law of independent assortment