

Suppl. Table 2: Summed allele combinations observed at *AtREV3* or *AtPOLH* loci among all progeny of a selfed F2 *AtPOLH*^{+/1} *AtREV3*^{+/2} double heterozygote.

	<i>AtREV3</i>			Total (2), (+)	<i>AtPOLH</i>			Total (1),
	2/2 ^a	+/2	+/+		1/1 ^a	+/1	+/+	
(+)								
Observed	202	362	195	766, 752	205	368	186	778, 740
Expected ^b	189	377	189	745, 745	189	377	189	745, 745

^a*AtREV3-2* and *AtPOLH-1* alleles contain a T-DNA insertion. + indicates the wild-type allele.

^bExpected progeny distribution for Mendelian segregation of a single locus. Chi-square test shows differences between observed vs. expected distributions to not be significant: for *AtREV3*, $\chi^2 = 1.7$, $P > 0.1$; for *AtPOLH*, $\chi^2 = 1.6$, $P > 0.1$