

**Suppl. Table 1:** Non-Mendelian segregation in F3 progeny of selfed *AtPOLH*<sup>+/-</sup> *AtREV3*<sup>+/-</sup> F2 heterozygotes.

F2 progeny genotype <sup>a</sup>		Obs. <sup>b</sup> (freq.)	Expect 1 <sup>*</sup> (freq.)	Expect 2 <sup>#</sup> (freq.)
<u><i>AtPOLH AtREV3</i></u>				
1/1	2/2	1 (.001)	47 (.062)	3 (.004)
+/-	2/2	55 (.07)	95 (.125)	40 (.053)
+/+	2/2	146 (.19)	47 (.062)	148 (.195)
1/1	+/-	43 (.06)	95 (.125)	40 (.053)
+/-	+/-	282 (.37)	190 (.25)	296 (.39)
+/+	+/-	37 (.05)	95 (.125)	40 (.053)
1/1	+/+	161 (.21)	47 (.062)	148 (.195)
+/-	+/+	31 (.04)	95 (.125)	40 (.053)
+/+	+/+	3 (.004)	47 (.062)	3 (.004)

<sup>a</sup>*AtREV3-2* and *AtPOLH-1* alleles contain a T-DNA insertion. + indicates wild-type alleles.

<sup>b</sup>Observed number of respective genotypes determined by PCR analysis of F3 progeny, as described under “Materials and methods”.

<sup>\*</sup>Expected progeny distribution for Mendelian segregation of two independent loci. Chi-square test of observed distribution:  $\chi^2 = 738.5$ ; for degrees freedom = 8,  $P < 0.005$ .

<sup>#</sup>Expected progeny distribution for segregation when *AtPOLH*<sup>+</sup> *AtREV3*<sup>+</sup> and *AtPOLH-1 AtREV3-2* gamete frequencies are reduced from 0.25 (normal) to 0.06 of total gametes. Chi-square test of observed distribution:  $\chi^2 = 11.2$ ; for degrees freedom = 8,  $P > 0.10$ .