

**Table S3** Summary of LD analyses, excluding all sites with > 2 variants (and also excluding one female plant F13 plant in Table S1 whose sequences are incomplete). The phases of variants were inferred using HaploRec, using a minimum allele frequency for variants of 10%. The loci are ordered according to our estimated recombination distances from the PAR boundary.

Gene	Number of sequences analyzed	Sequence numbers excluded from analysis	Number of variants	Zns <sup>1</sup>	Number of significant Fisher's exact tests/Number of comparisons (after Bonferroni correction)	Rmin <sup>2</sup>
<i>E559</i>	40	F2, 12 (or also excluding M3, M18)	7	0.277	6/21 = 0.29	3
<i>E200</i>	38	M3, F2, 6	8	0.314	5/28 = 0.18	2
<i>E241</i>	38	M3, F1, F2	50	0.193	158/1225 = 0.13	9
<i>E284<sub>PAR</sub></i>	31	M3, 8, 23, F1, 4, 8a, 10	102	0.167	181/5151 = 0.04	19
<i>E592</i>	31	M11, 23, F2, 3b, 6, 9, 12	276	0.414	135/351 = 0.38	5
<i>E219</i>	38	F6, 8, 9	43	0.565	461/903 = 0.51	7
First 4 genes	25	M3, 8, 23, F1, 2, 4, 6, 8a, 10, 12	263	0.139	57/3240 = 0.018	19
All genes	20	As row above, plus M11, F3b, 9	224	0.139	— (too many variants to test)	38

<sup>1</sup> The linkage disequilibrium measure of JK Kelly (1997 A test of neutrality based on interlocus associations. *Genetics* 146, 1197-1206).

<sup>2</sup> The minimum number of recombination events (Hudson RR, Kaplan NL, 1985 Statistical properties of the number of recombination events in the history of a sample of DNA sequences. *Genetics* 111, 147-164).