Table S4 Theoretical frequencies of the nine identifiable genotypes in the double cross population for Scenario 13 and 14. A_1 and B_1 are the two alleles at locus 1; A_2 and B_2 are the two alleles at locus 2. The combined recombination frequency is denoted as *r*. The last column gives the symbol of observed sample size of each genotype.

Genotype	Locus 1	Locus 2	Expected frequency		Sample size
			Scenario 13	Scenario 14	
1	A_1A_1	A_2A_2	$\frac{1}{4}r(1-r)$	$\frac{1}{4}(1-r)^2$	n_1
2	A_1A_1	A_2B_2	$\frac{1}{4}(1-2r+2r^2)$	$\frac{1}{2}r(1-r)$	n_2
3	A_1A_1	B_2B_2	$\frac{1}{4}r(1-r)$	$\frac{1}{4}r^2$	n_3
4	A_1B_1	A_2A_2	$\frac{1}{4}(1-2r+2r^2)$	$\frac{1}{2}r(1-r)$	n_4
5	A_1B_1	A_2B_2	$r(1-r)$	$\frac{1}{2}(1-2r+2r^2)$	n_5
6	A_1B_1	B_2B_2	$\frac{1}{4}(1-2r+2r^2)$	$\frac{1}{2}r(1-r)$	n_6
7	B_1B_1	A_2A_2	$\frac{1}{4}r(1-r)$	$\frac{1}{4}r^2$	n_7
8	B_1B_1	A_2B_2	$\frac{1}{4}(1-2r+2r^2)$	$\frac{1}{2}r(1-r)$	n_8
9	B_1B_1	B_2B_2	$\frac{1}{4}r(1-r)$	$\frac{1}{4}(1-r)^2$	n_9