Table S2 Theoretical frequencies of the twelve identifiable genotypes in the double cross population for Scenario 10. A_1 , B_1 , C_1 and D_1 are the four alleles at locus 1. A_2 and B_2 are the two alleles at locus 2. Recombination frequencies in the female and male parents are denoted as r_F and r_M , respectively. 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 | Frequency | Combined | Sample size |
|----------|----------|----------|---|--------------------------|------------------------|
| | | | | recombination | |
| | | | | frequency | |
| 1 | A_1C_1 | A_2A_2 | $\frac{1}{4}(1-r_F)r_M$ | $\frac{1}{4}r(1-r)$ | n_1 |
| 2 | A_1C_1 | A_2B_2 | $\frac{1}{4}(1-r_F)(1-r_M)+\frac{1}{4}r_Fr_M$ | $\frac{1}{4}(1-2r+2r^2)$ | n_2 |
| 3 | A_1C_1 | B_2B_2 | $\frac{1}{4}r_F(1-r_M)$ | $\frac{1}{4}r(1-r)$ | n_3 |
| 4 | A_1D_1 | A_2A_2 | $\frac{1}{4}(1-r_F)(1-r_M)$ | $\frac{1}{4}(1-r)^2$ | n_4 |
| 5 | A_1D_1 | A_2B_2 | $\frac{1}{4}(1-r_F)r_M + \frac{1}{4}r_F(1-r_M)$ | $\frac{1}{2}r(1-r)$ | n_5 |
| 6 | A_1D_1 | B_2B_2 | $\frac{1}{4} r_F r_M$ | $\frac{1}{4} r^2$ | n_6 |
| 7 | B_1C_1 | A_2A_2 | $\frac{1}{4} r_F r_M$ | $\frac{1}{4} r^2$ | n ₇ |
| 8 | B_1C_1 | A_2B_2 | $\frac{1}{4}(1-r_F)r_M + \frac{1}{4}r_F(1-r_M)$ | $\frac{1}{2}r(1-r)$ | n_8 |
| 9 | B_1C_1 | B_2B_2 | $\frac{1}{4}(1-r_F)(1-r_M)$ | $\frac{1}{4}(1-r)^2$ | n 9 |
| 10 | B_1D_1 | A_2A_2 | $\frac{1}{4}r_F(1-r_M)$ | $\frac{1}{4}r(1-r)$ | n_{10} |
| 11 | B_1D_1 | A_2B_2 | $\frac{1}{4}(1-r_F)(1-r_M)+\frac{1}{4}r_Fr_M$ | $\frac{1}{4}(1-2r+2r^2)$ | <i>n</i> ₁₁ |
| 12 | B_1D_1 | B_2B_2 | $\frac{1}{4}(1-r_F)r_M$ | $\frac{1}{4}r(1-r)$ | n_{12} |