

Table S1 List of symbols and their brief explanations.

| Category | Symbol | Explanation |
|--------------------|--------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Two-gene | (ab) | Two-gene IBD configurations include (11) and (12) |
| | $\alpha_t(ab)$ | Within-individual probability of configuration (ab) in generation t |
| | $\beta_t(ab)$ | Between-individual probability of configuration (ab) in generation t |
| | $\alpha_t(11)$ | Within-individual two-gene IBD probability in generation t |
| | $\alpha_t(12)$ | Within-individual two-gene non-IBD probability in generation t |
| | s_t | Two-gene coalescence probability that both come from a single individual of the previous generation $t - 1$ |
| Three-gene | (abc) | Three-gene IBD configurations include (111), (112), (121), (122), (123) |
| | $\alpha_t(abc)$ | Probability of configuration (abc) in generation t , given that genes a and c are in a single individual and gene b in another |
| | $\beta_t(abc)$ | Probability of configuration (abc) in generation t , given that the three genes are in three distinct individuals |
| | $\alpha_t(123)$ | Non-IBD probability of the three genes |
| | $\alpha_t(122)$ | Probability that the genes a and b are non-IBD and genes b and c are IBD |
| | $\alpha_t(1_2)$ | Marginal non-IBD probability between genes a and c |
| | q_t | Three-gene coalescence probability that one particular gene comes from one individual and other two genes come from another individual of the previous generation $t - 1$. |
| Four-gene | $(abcd)$ | Four-gene IBD configurations include the 15 configurations shown in Table 1 |
| | $D(abcd)$ | Two-locus probability of configuration $(abcd)$ |
| | $J_t(abcd)$ | Within-individual expected junction density of type $(abcd)$ in generation t . The seven junction types are shown in Table 1 |
| | $K_t(abcd)$ | Between-individual expected junction density of type $(abcd)$ in generation t |
| Breeding design | L | Number of distinct founder genome labels (FGL) |
| | U | Number of intercross generations |
| | V | Number of inbreeding generations |
| | N_t | Population size in generation t |
| | N_F | Constant size of founder population, and $N_F=L$ if founders are fully inbred |
| | N_I | Constant size of intercross populations |
| | N_{II} | Constant size of inbred populations. $N_{II} = 1$ if $\mathcal{M}_{II} = \text{Selfing}$, and $N_{II} = 2$ if $\mathcal{M}_{II} = \text{Sibling}$ |
| | \mathcal{M}_t | Mating scheme from the generation t to the next generation. |
| | \mathcal{M}_F | Constant mating scheme from the founder population to the F_1 population, $\mathcal{M}_F = \mathcal{M}_0$ |
| | \mathcal{M}_I | Constant mating scheme in the intercross stage, $\mathcal{M}_I = \mathcal{M}_1 = \dots = \mathcal{M}_U$ |
| \mathcal{M}_{II} | Constant mating scheme in the inbreeding stage, $\mathcal{M}_{II} = \mathcal{M}_{U+1} = \dots = \mathcal{M}_{U+V}$ | |
| Map resolution | R | Map expansion, the expected junction density (per Morgan) on one chromosome |
| | ρ | Overall expected junction density, the expected junction density (per Morgan) on two homologous chromosomes |