

1 **S2 Supporting Information: Maximum likelihood assignment method.**

2 The likelihood that seed genotype G_i belongs to a plant of cultivar v was calculated as:

3
$$L(G_i, v) = \sum_{g_v} f_{g_v} \cdot [sT(G_i/M_{g_v}, M_{g_v}) + (1 - s) \cdot \sum_{g_{v'}} f_{g_{v'}} T(G_i/M_{g_v}, F_{g_{v'}}),$$

4 where g_v represents all of the possible genotypes for the mother and $g_{v'}$ for the father, both of
5 cultivar v ; f_{g_v} and $f_{g_{v'}}$ are the genotype frequencies of g_v and $g_{v'}$; and s is the selfing rate [s
6 = 0.63, 17]. $T(G_i/M_{g_v}, F_{g_{v'}})$ is the Mendelian segregation probability that a mother of
7 genotype g_v and a father of genotype $g_{v'}$ produce offspring of genotype G_i .