Supplemental Figures

QTL Mapping in Outbred Tetraploid (and Diploid) Diallel Populations

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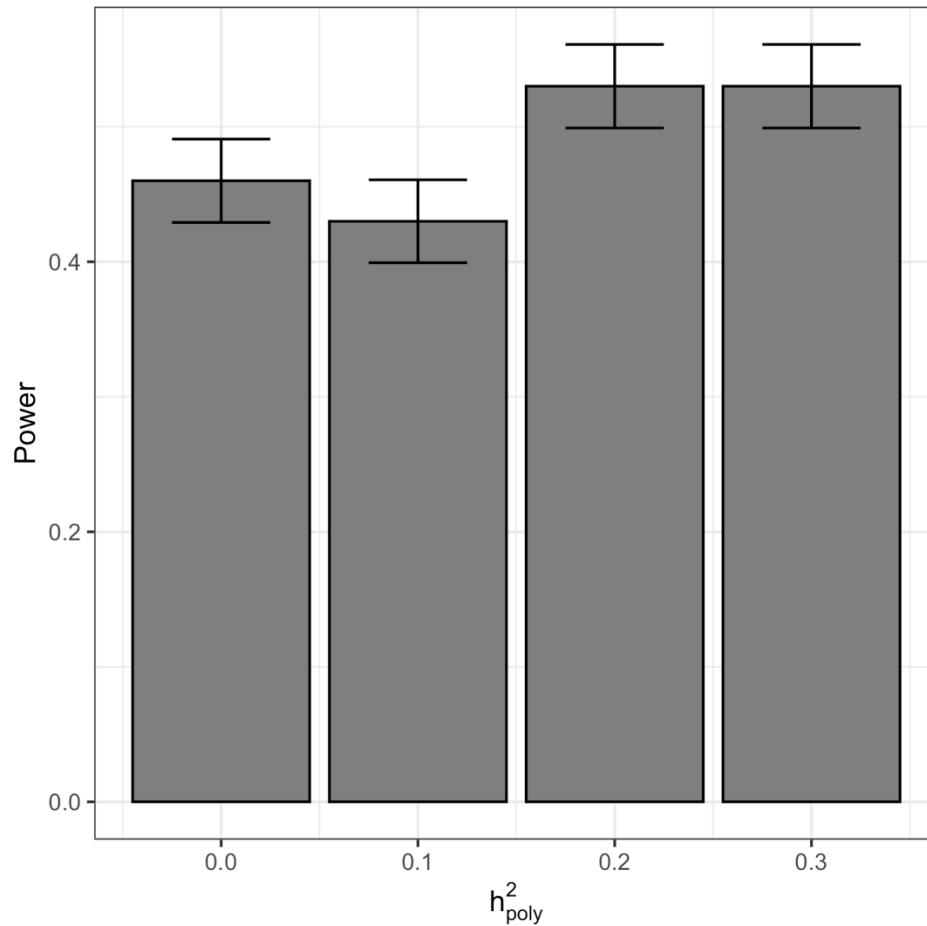[‡]Department of Horticulture, University of Wisconsin, Madison, WI, USA

Figure S1. The influence of simulating polygenic effects on statistical power for detecting an additive QTL with $h^2 = 0.2$ in a half-diallel with 4 parents and total population size N = 200. The height of each bar is the proportion of 1000 simulations in which the QTL was detected, and the error bars are $\pm 1.96\,\mathrm{SE}$ for the standard error (SE) of a binomial proportion.
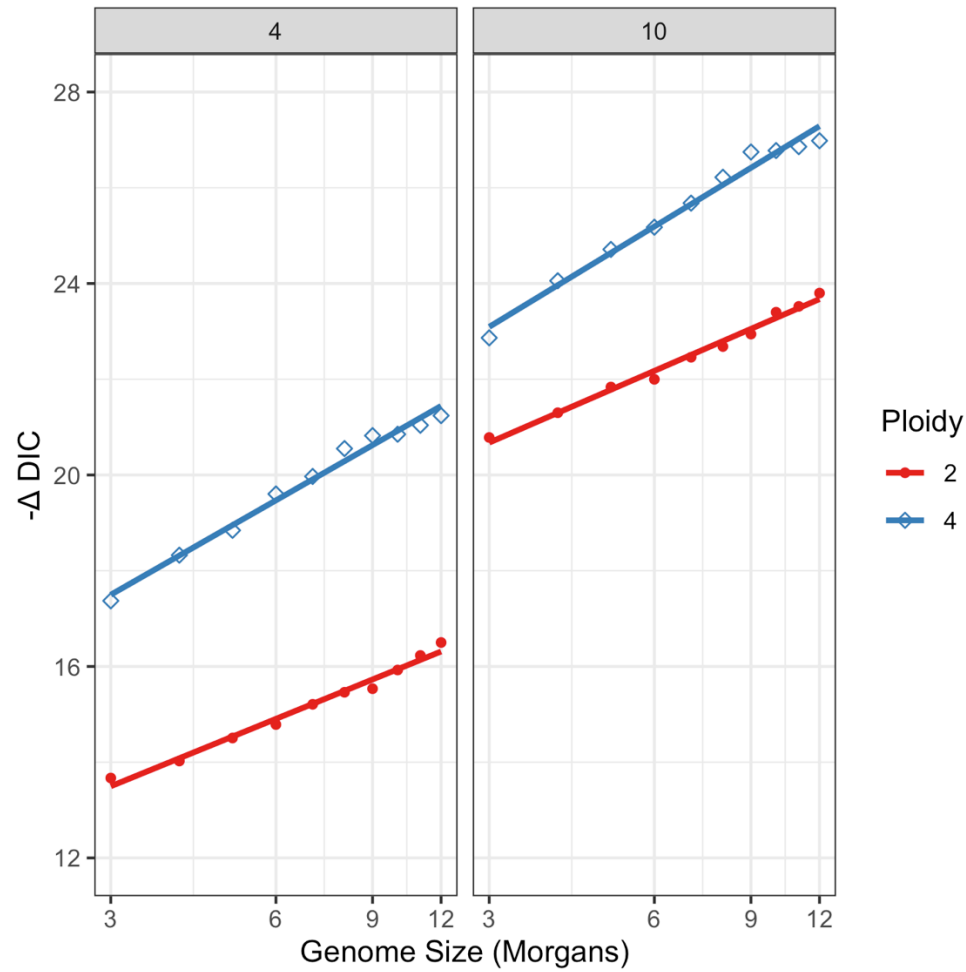
Figure S2. The threshold for QTL discovery, −ΔDIC, increased approximately linearly with the logarithm of genome size. Results are shown for significance level $\alpha = 0.05$, using simulated half-diallel populations, and the number of parents (4 and 10) is shown at the top of each panel. Each point is based on 1000 simulations.
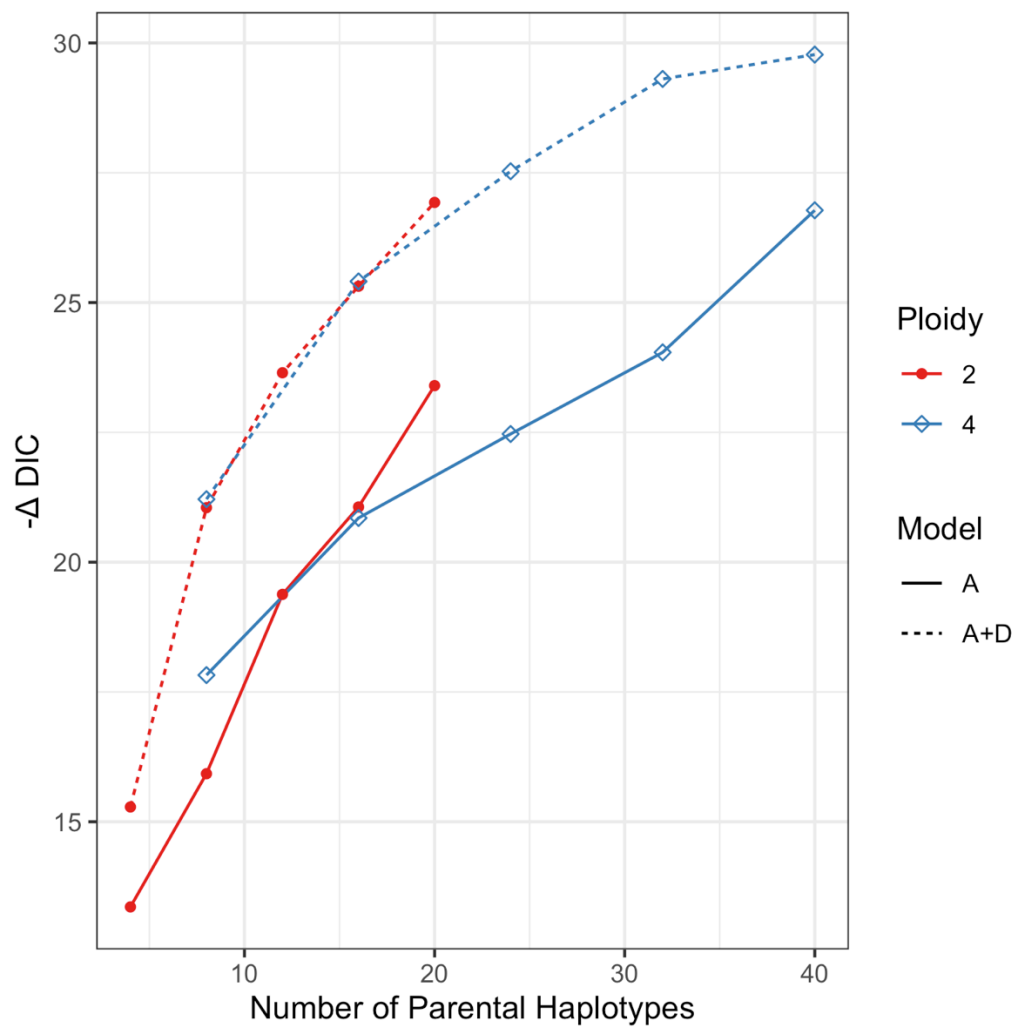
Figure S3. The threshold for QTL discovery, −ΔDIC, was higher for a QTL model with additive and dominance effects (A+D) compared to only additive (A) effects. Results are shown for significance level $\alpha = 0.05$, using 1000 simulated half-diallel populations. The number of parental haplotypes equals ploidy (2 or 4) times the number parents (2 to 10).
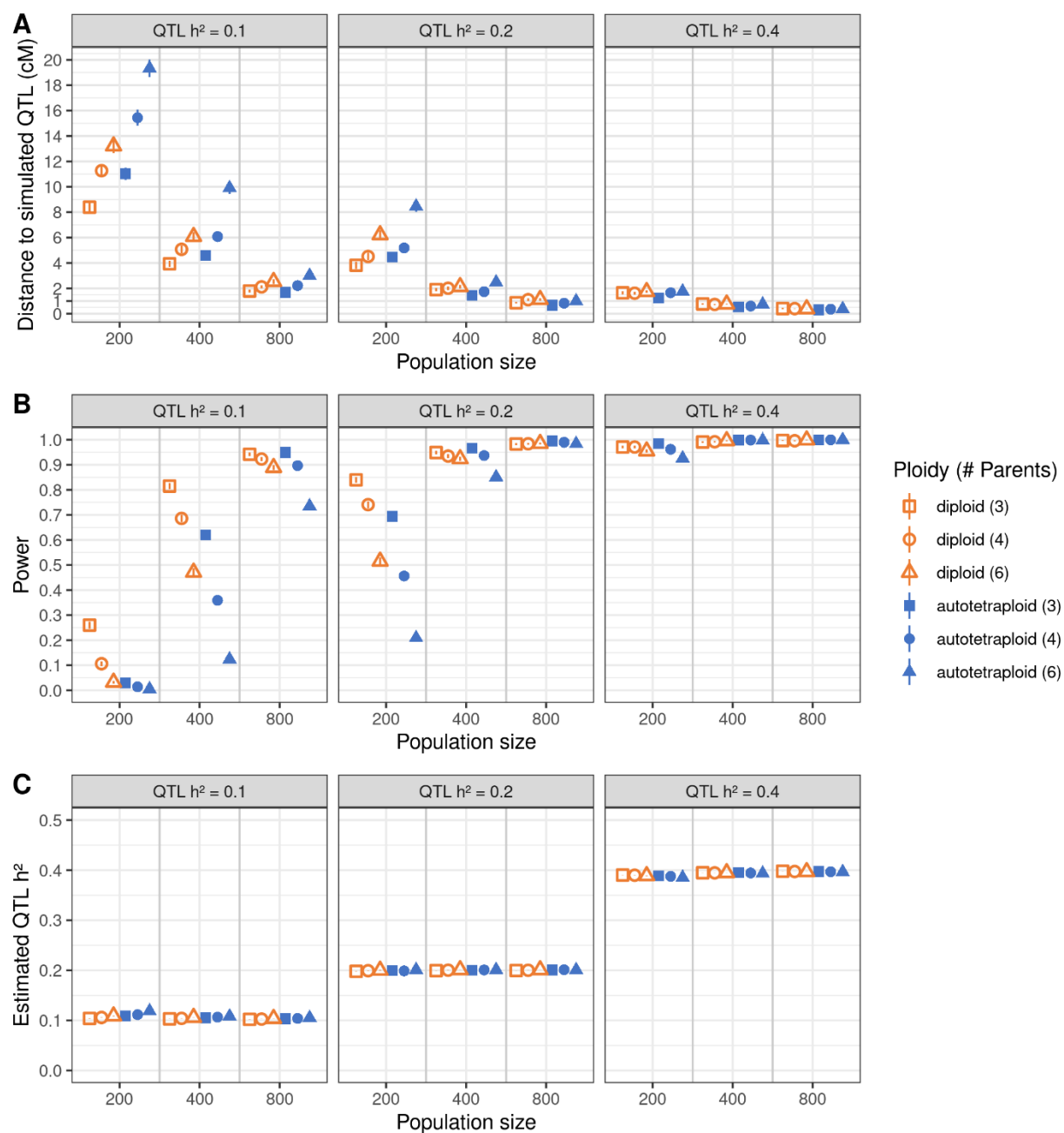
Figure S4. QTL mapping results from simulated half-diallel populations with varying population size, QTL heritability, number of parents, and ploidy. The genome-wide Type I error rate was controlled at $\alpha = 0.05$. A) Average distance in cM between the peak LOD score position and simulated QTL position. B) Average power to detect the QTL. C) Average estimated QTL heritability based on the diaQTL linear model. Error bars are standard errors based on 1,000 simulations.
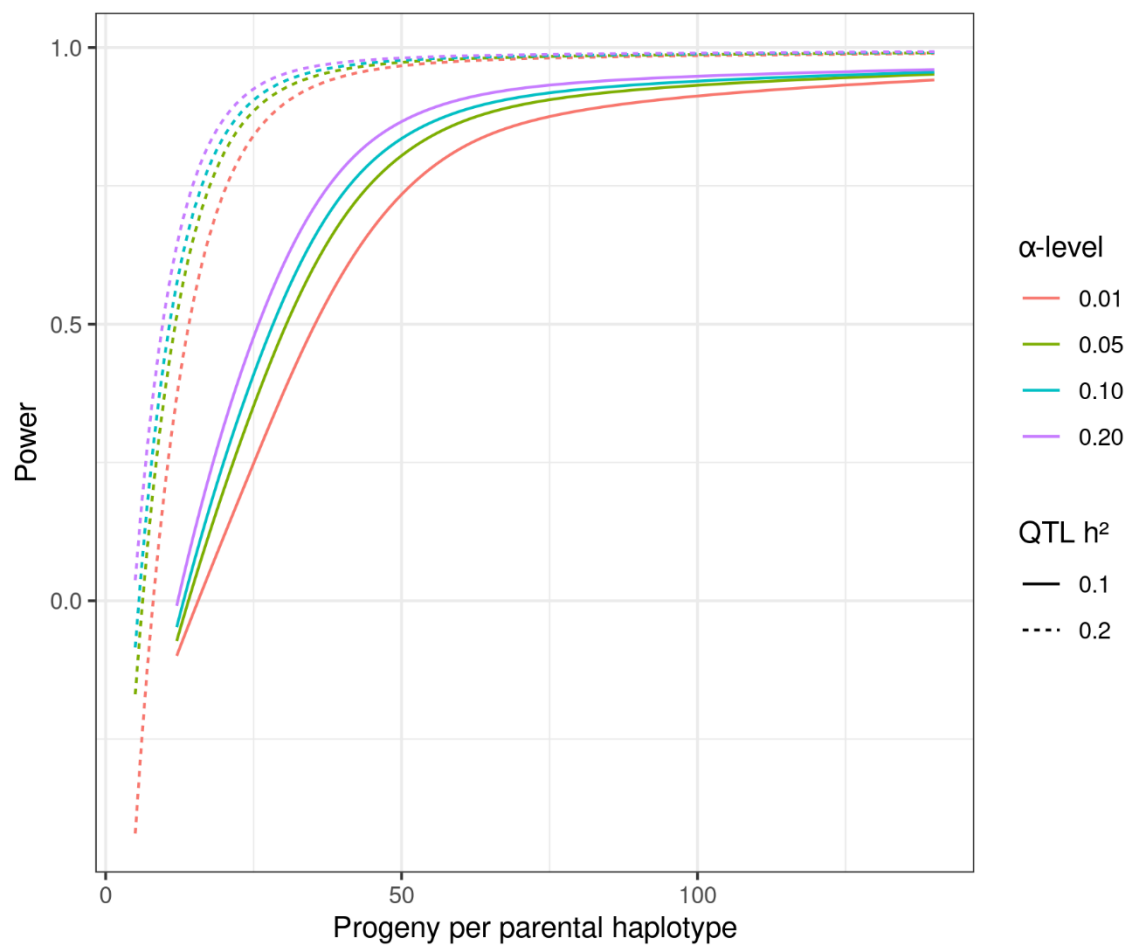
Figure S5. Statistical power to detect QTL for different significance levels α, as a function of the number of progeny per parental haplotype, number of parents, ploidy, and QTL heritability (h^2). Each point is the average of 1,000 simulations with an additive model. The dashed line is a monotone increasing, concave spline for $h^2 = 0.1$, and the solid line is the spline for $h^2 = 0.2$.
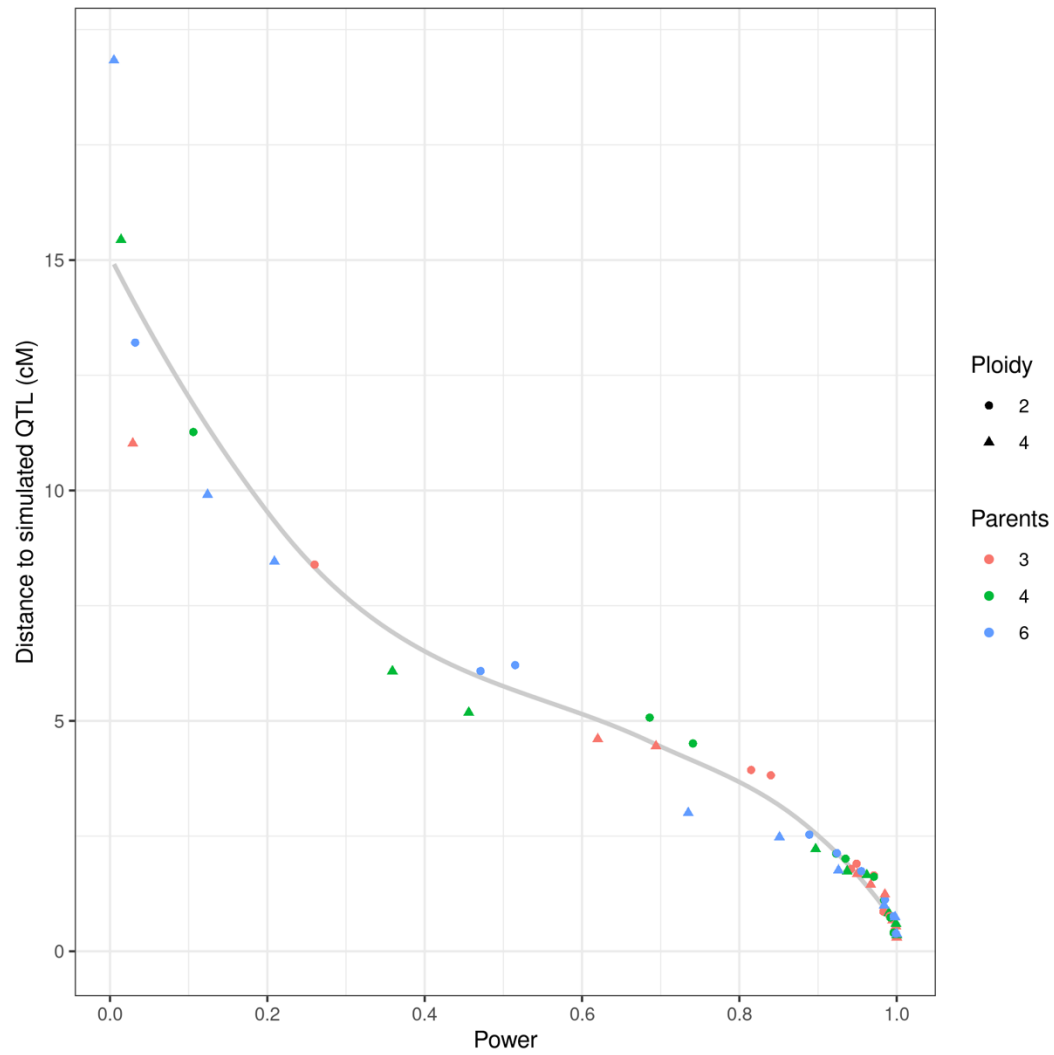
Figure S6. Average distance between the position of the most significant marker and simulated QTL position, as function of power, ploidy and number of parents. Each point represents an average over the multiple population sizes and heritability values shown in Figure S4.
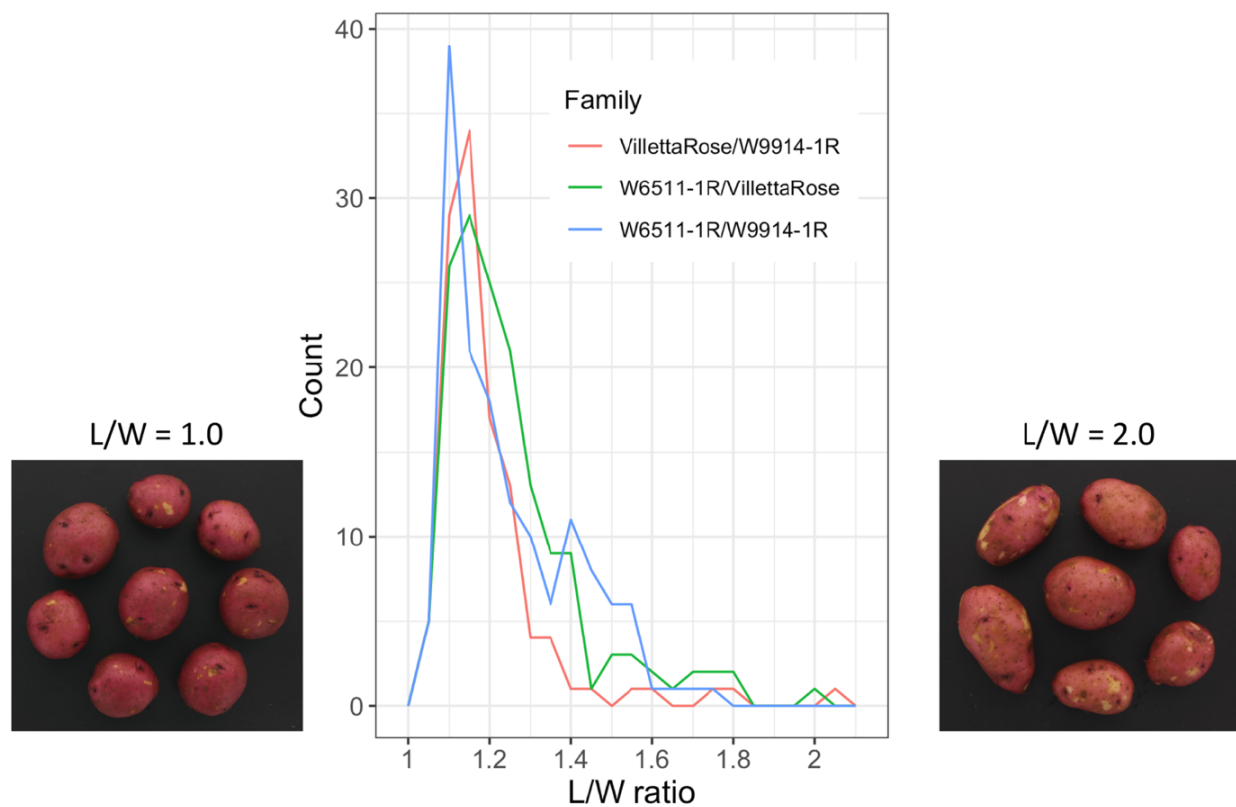
Figure S7. Distribution of the length to width (L/W) ratio for tubers of three full-sib families of autotetraploid potato. The images illustrate the extreme phenotypes of this population with L/W = 1.0 as a round tuber shape, L/W = 2.0 as an elongated tuber shape.
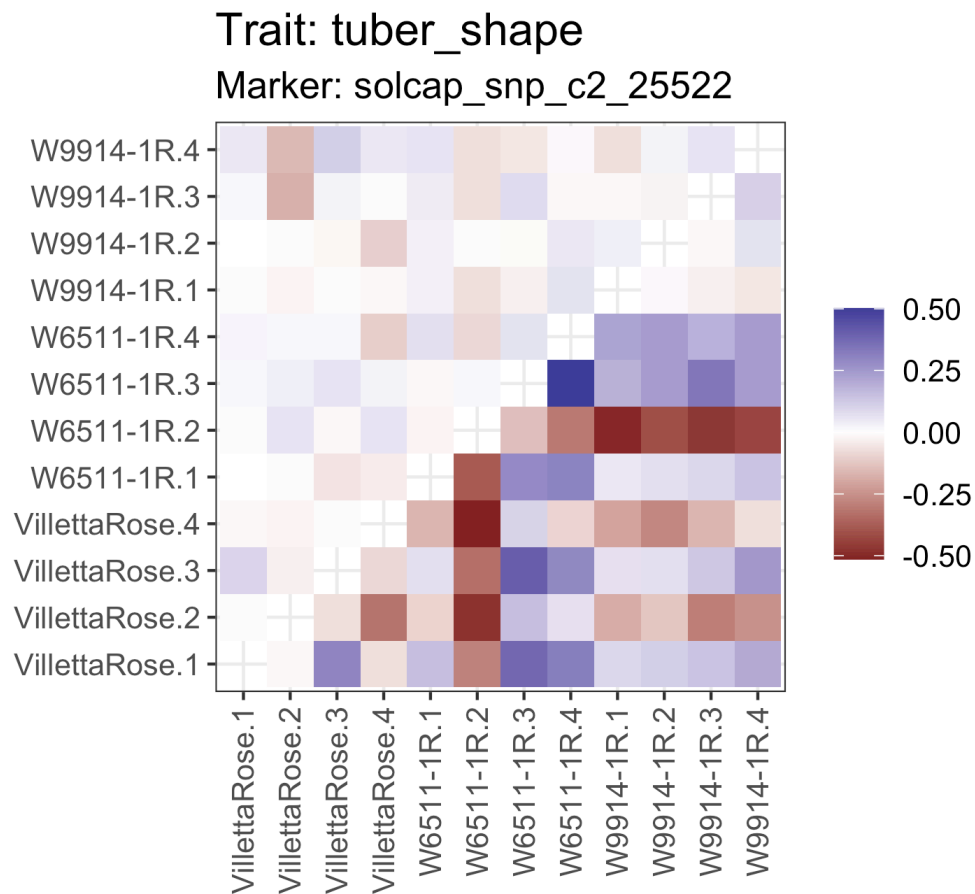
Figure S8. Estimated QTL effects for the 10@63 QTL with the digenic dominance model (#4 in Table 1). The digenic dominance effects are above the diagonal, and below the diagonal are the sum of the additive and digenic effects. The four haplotypes for each parent are labeled .1 to .4. The figure is part of the graphical output from diaQTL function *fitQTL.*
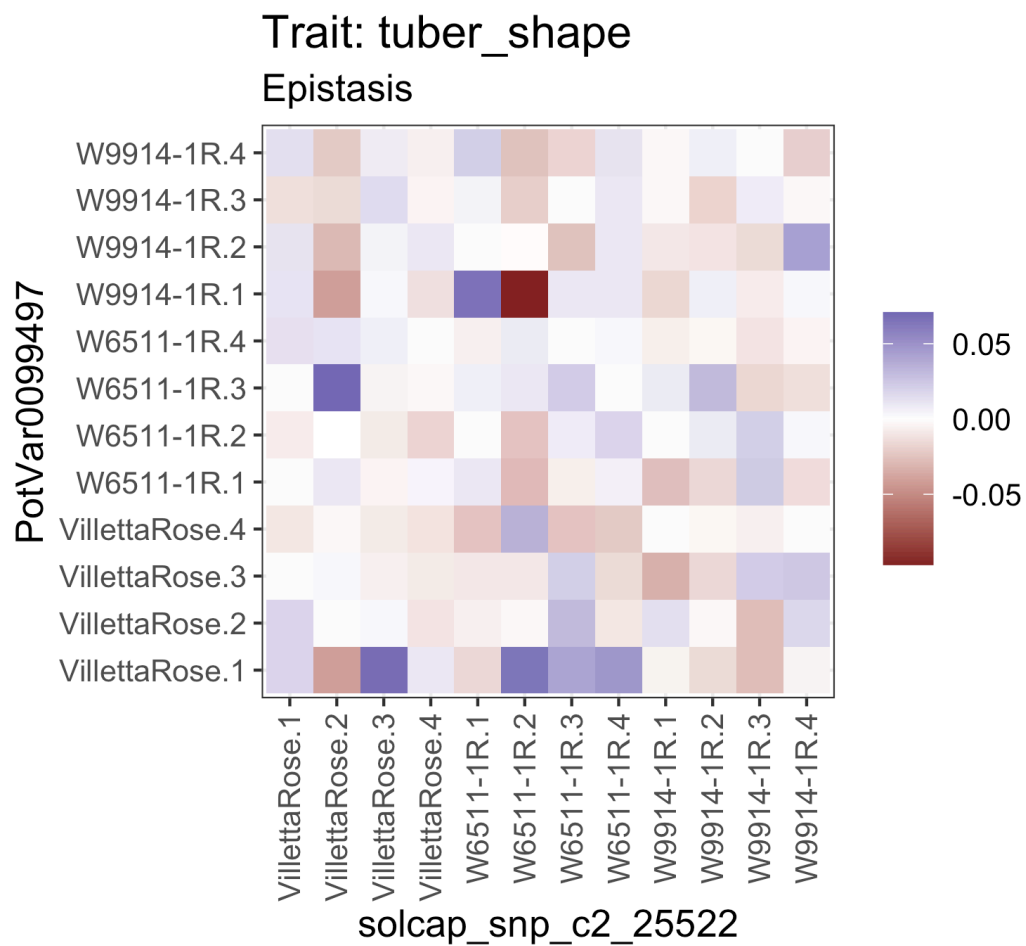
Figure S9. Estimated additive x additive epistatic effects between the 10@63 and 1@133 QTL (model #3 in Table 1). The four haplotypes for each parent are labeled .1 to .4. The figure is part of the graphical output from diaQTL function *fitQTL*
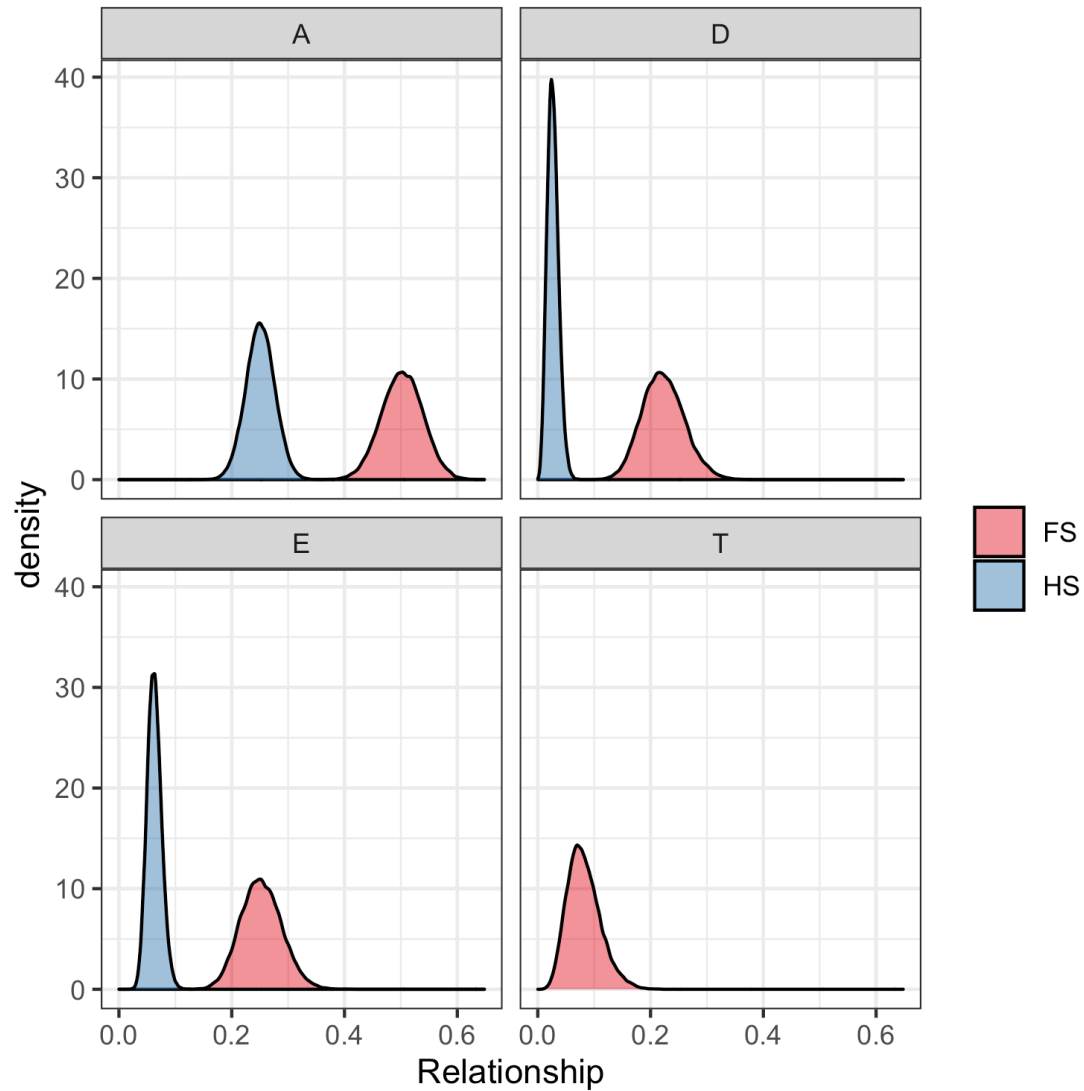
Figure S10. The distribution of realized relationships between full-sibs (FS) and half-sibs (HS) in the potato diallel population, computed with diaQTL function *IBDmat*. The four panels correspond to additive (A), digenic dominant (D), trigenic dominant (T), and additive x additive epistatic (E) effects. The expected values based on pedigree are A = 1/2, D = 2/9, T = 1/12, E = 1/4 for full-sibs and A = 1/4, D = 1/36, T = 0, E = 1/16 for half-sibs.
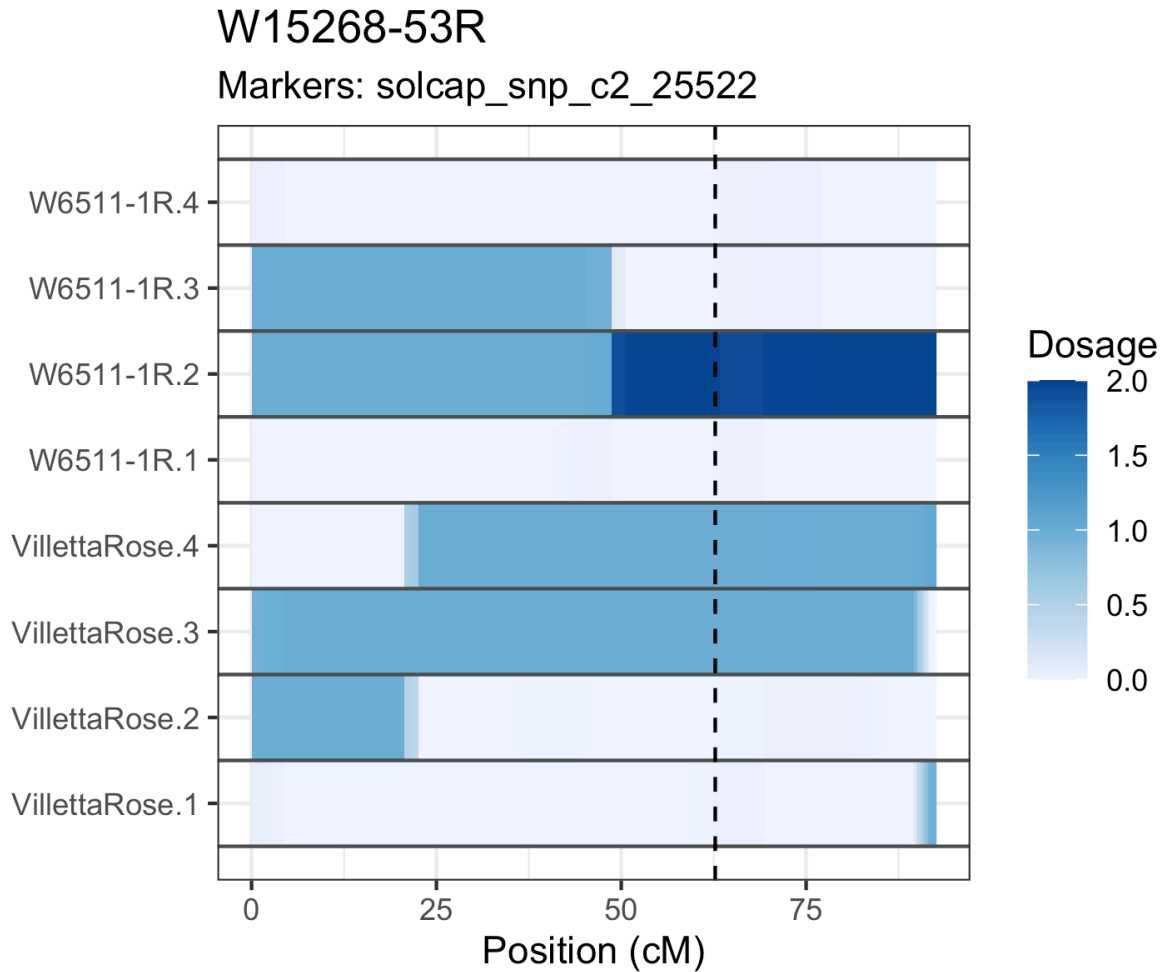
Figure S11. Visualizing the inheritance of parental haplotypes from VillettaRose and W6511-1R in one F1 offspring (W15268-53R), using diaQTL function *haplo_plot*. This clone was selected as one of three offspring containing two copies of the W6511-1R.2 haplotype, which was estimated to have the largest negative effect (Fig. 5) and is therefore desirable for breeding potato varieties with round tubers. The dashed line marks the position of the 10@63 QTL for tuber shape. The presence of two copies of a parental haplotype is possible in tetraploid offspring due to double reduction, a phenomenon in which the diploid gamete contains portions of both sister chromatids from one homologous chromosome.