



Heterosis and Genome-Scale Diversity Among High Yielding Hybrids of Strawberry



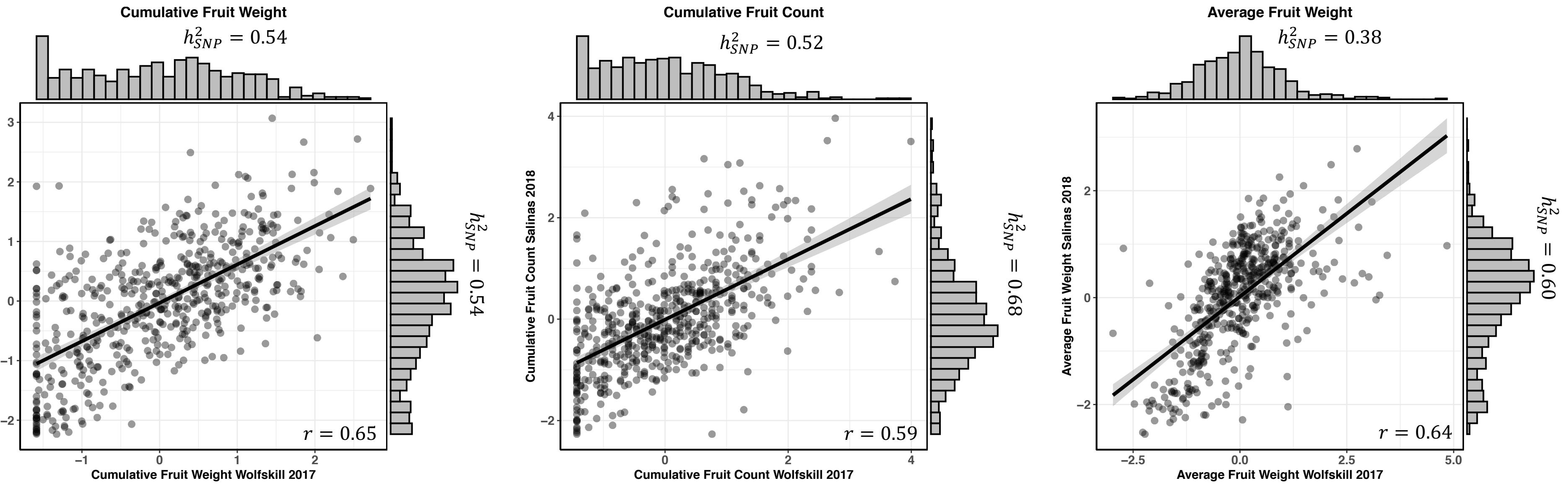
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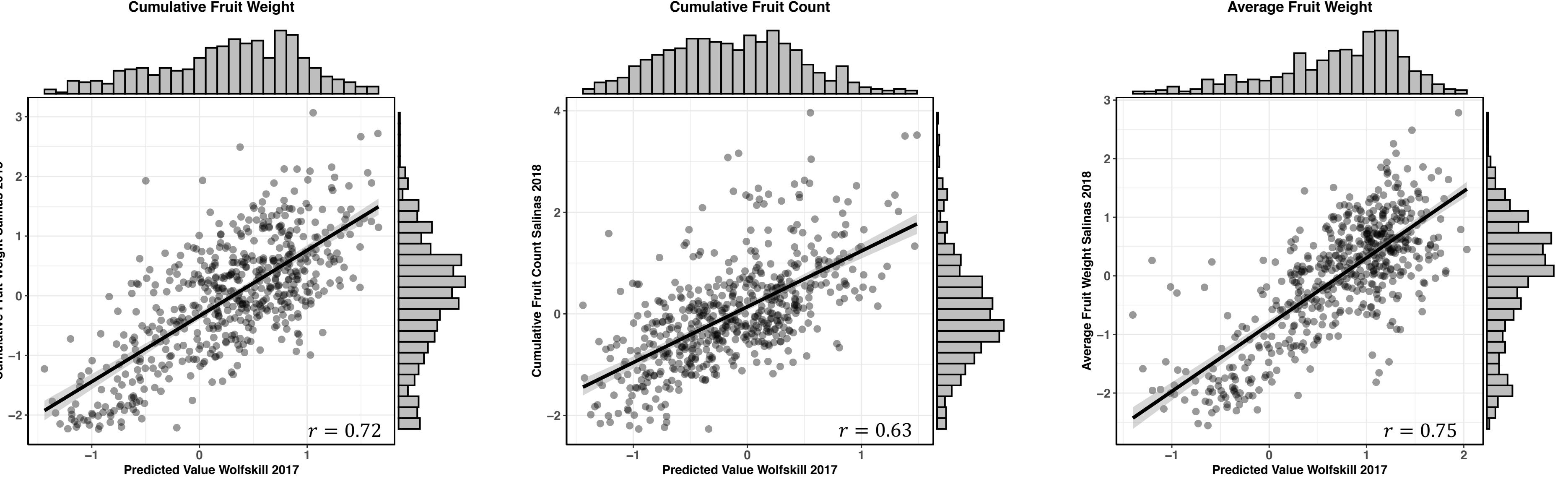
Introduction

Genetic gains for cumulative fruit yield have been significant in strawberry (*Fragaria x ananassa*) over the last 50 years, especially among hybrids selected for production in coastal California environments. From commercial production statistics, we estimate that strawberry yields have increased 10-fold since 1970 despite a stable production acreage. However, common garden experiments have not been conducted to quantify realized genetic gains for yield or to study the effect of intense selection for increased yield on the underlying genetic diversity. Moreover, we hypothesized that heterosis might have played a significant role in driving strawberry yields upwards. To explore these questions, we developed and studied 545 hybrids among elite short-day and long-day parents developed using a factorial mating design—parents and hybrids were genotyped with high-density SNP arrays. Genetic diversity appears to be comparatively narrow among the hybrids studied. Heterozygosity ranged 0.18 to 0.45 among the 545 factorial-study hybrids and was not correlated with fruit yield in either study. High-parent heterosis for cumulative fruit yield was virtually non-existent and was only statistically significant for 34 of the 545 hybrids tested (6.2%). Consistent with these results, we found no evidence for heterotic groups in the population under study, which includes public germplasm that has played an important role in the expansion of strawberry industry worldwide. We speculate that interactions among genes in homoeologous genomes, so-called fixed heterosis, might underlie genetic gains for yield in strawberry.

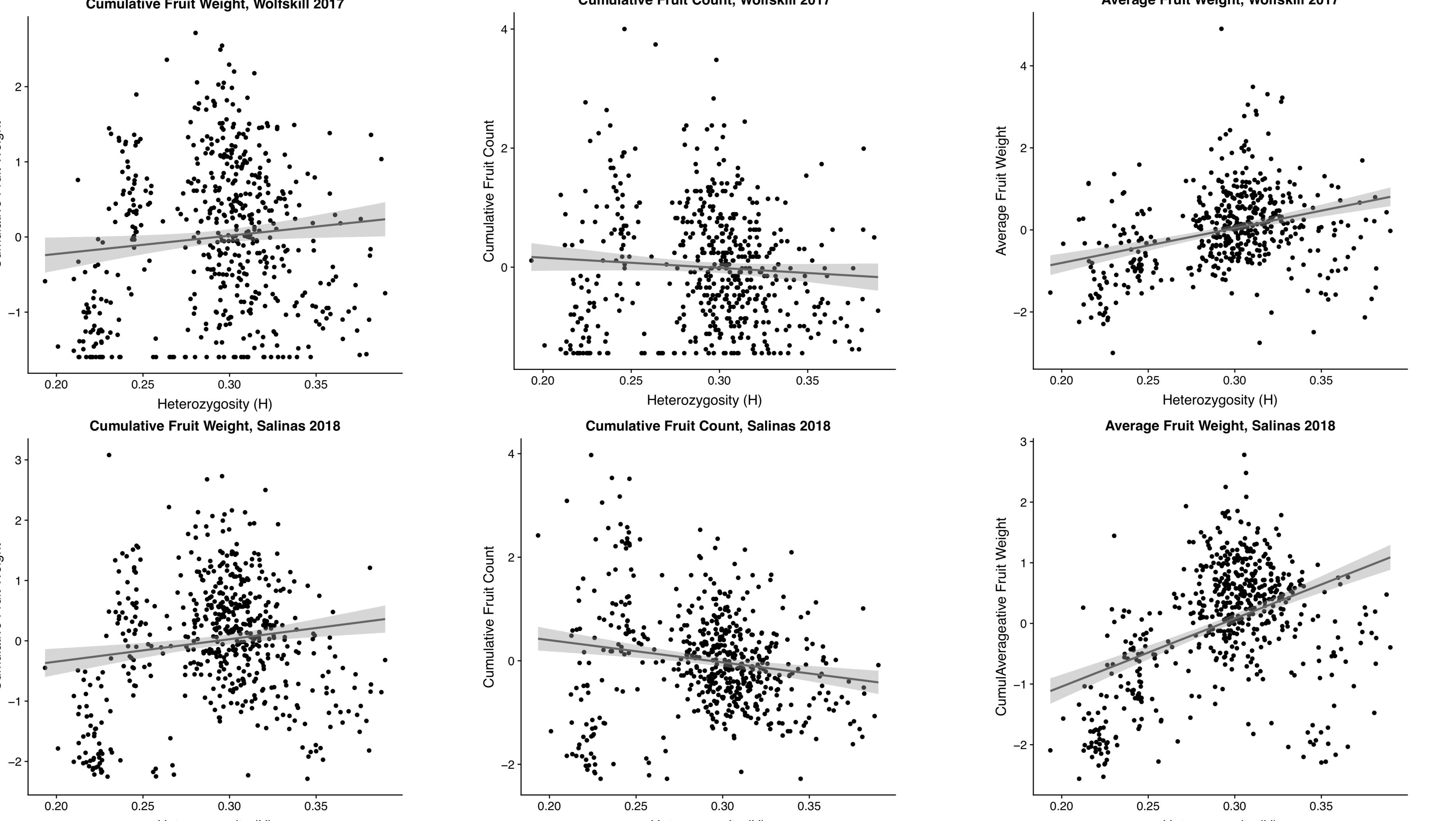
Phenotypic Predictions



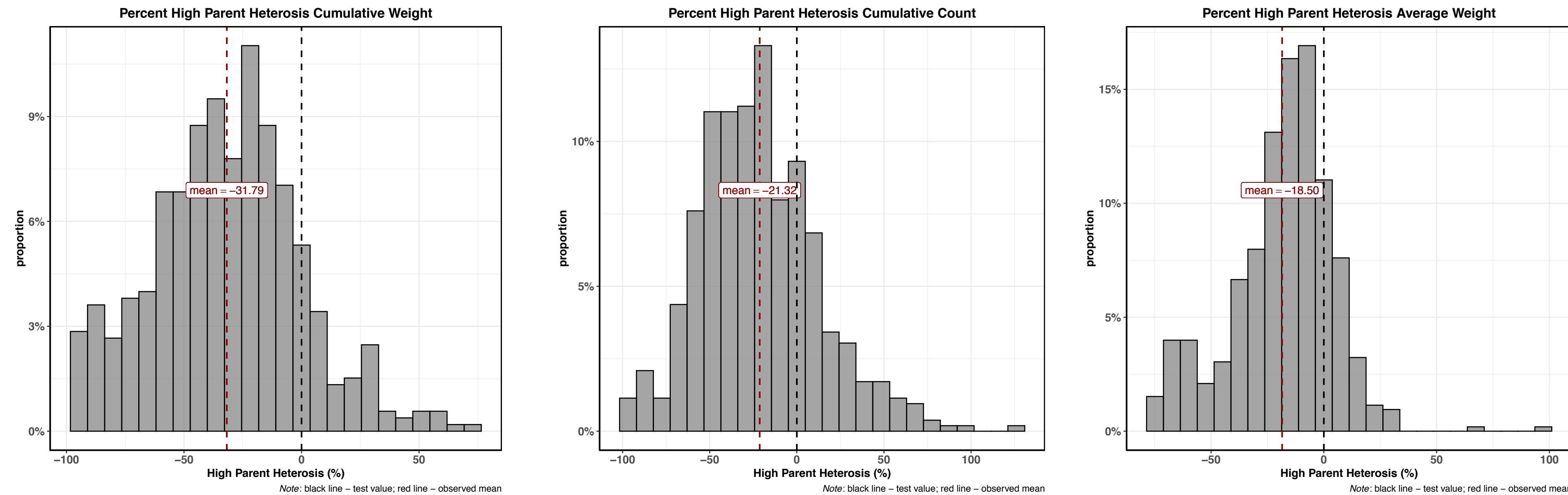
Genome-Wide Prediction



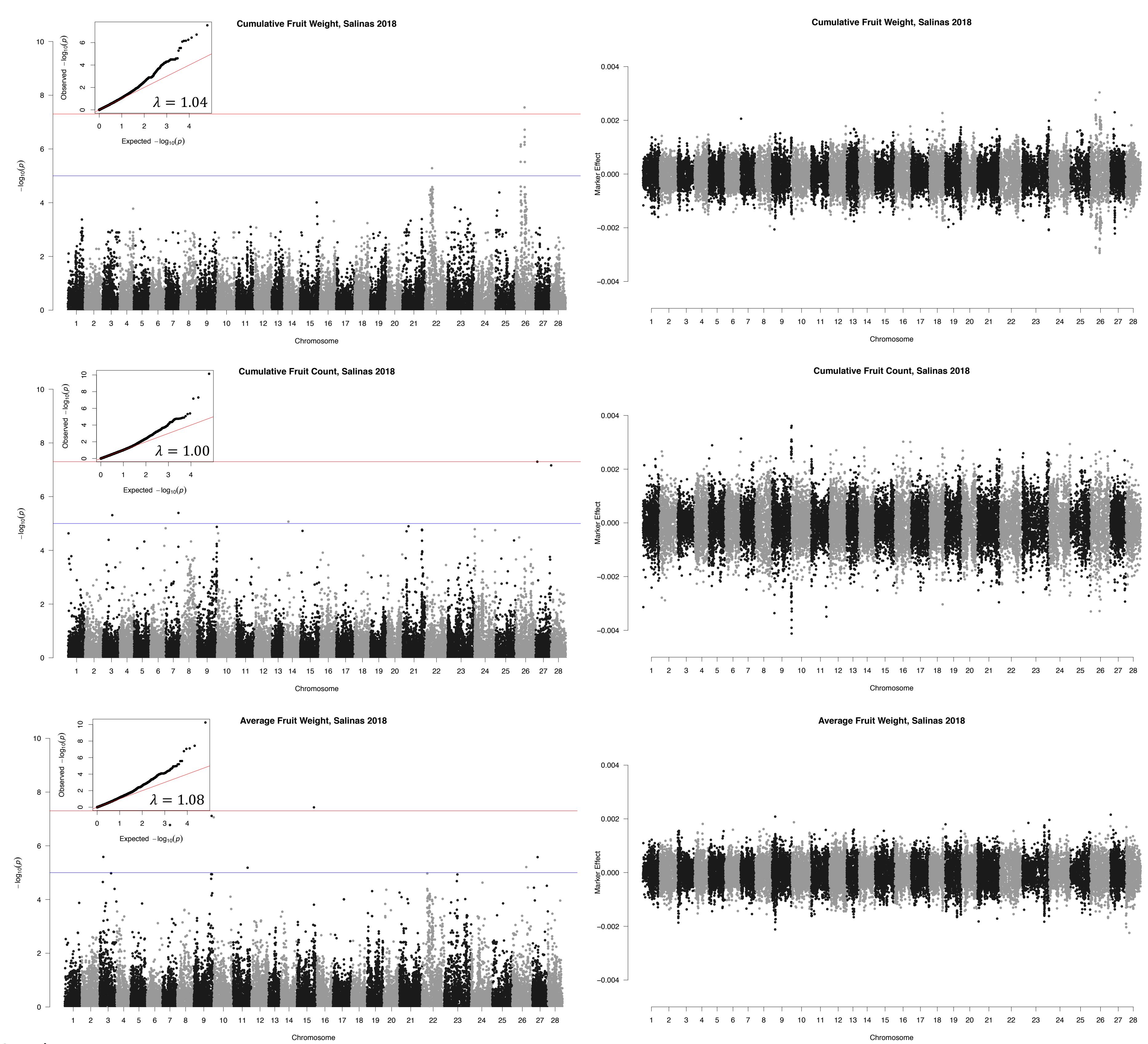
Residual Heterozygosity



High-Parent Hybrid Superiority



Genome-Wide Associations & Effects



Conclusions

- The relationship between genetic values estimated from unreplicated seedlings and the phenotypic value of replicated clones is stronger than the relationship between the phenotypic value of the seedling and that of the clone. This is true for cumulative fruit weight, cumulative fruit count, and average fruit weight. Hence, genomic prediction used selecting high yielding individuals has the potential to reduce the amount of space and time required to evaluate new individuals and to allow programs to focus on consumer centric traits.
- There is no significant, linear relationship between yield components and genome-wide heterozygosity. This could be a consequence of the octoploid genome of strawberry in which much of the observed heterozygosity could be distributed across sub-dominant genome. Hence, the specific quality of heterozygosity is likely more important than the overall quantity.
- There is little to no significant high-parent heterosis in strawberry. Only 34/545 (6.2%) individuals perform significantly better than their best performing parent regarding cumulative fruit weight. However, 153/545 (28.1%) of individuals perform significantly lesser than their worst performing parent.
- Genome-wise association analysis discovers genomic regions associated with yield components in strawberry. Fvb7-2 (26) and Fvb6-2 (22) associated with cumulative fruit weight and Fvb3-1 (9) associated with cumulative fruit count in Salinas 2018 are of primary interest.

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