**Supplemental Table S2. Pearson's correlation coefficients for canopy height and harsh flavor in collection of 433 carrot accessions and in core sets.** None of the correlations are significantly different from zero as determined by a t-test for differences in means.

|	correlation	N
Total collection	-0.076	433
Random Core	0.000	43
Geographic Core	-0.076	43
Genotypic Core	0.000	43
Core Hunter Core	-0.162	43
GBV Core	0.057	38
GTP core	0.000	43
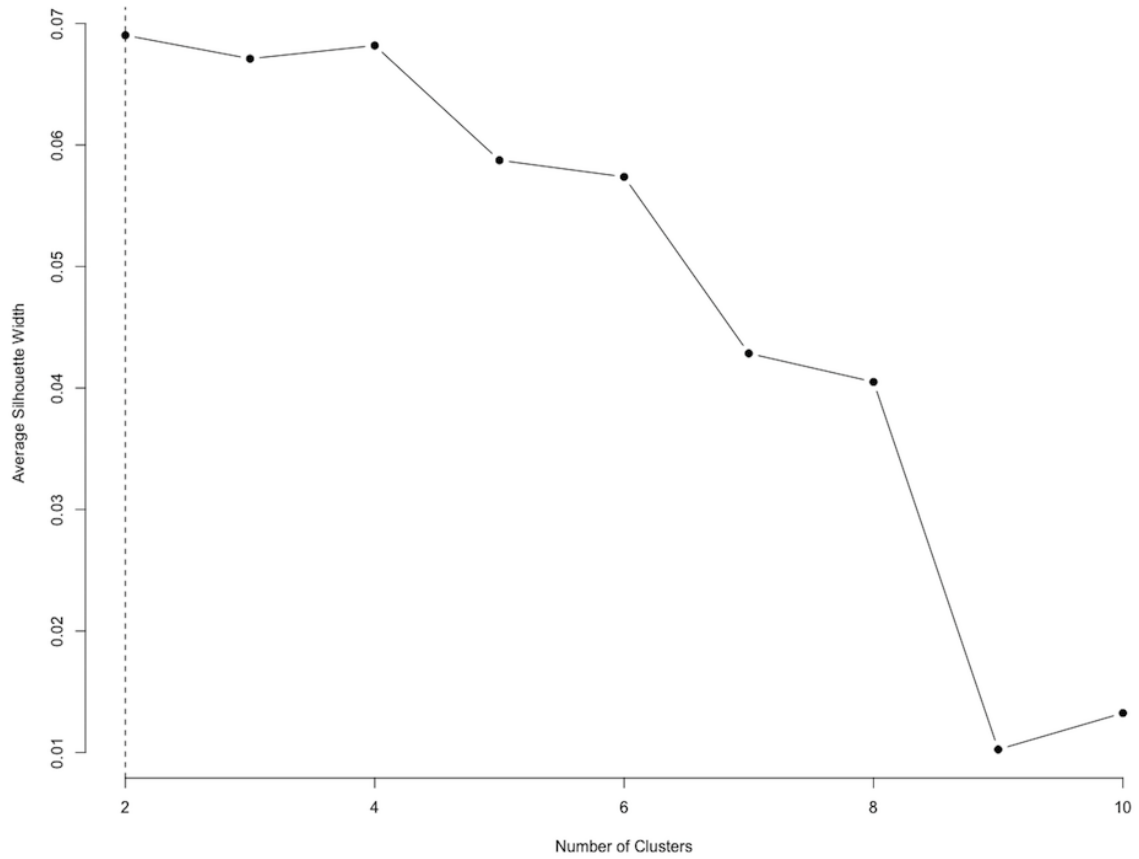
Supplemental Fig. S1: Average silhouette width of genotypic clusters. Silhouette width was calculated for K=2-10 clusters of accessions based on their genetic distances. The vertical dotted line indicates the most appropriate number of clusters.

Canopy Height

Harsh Flavor
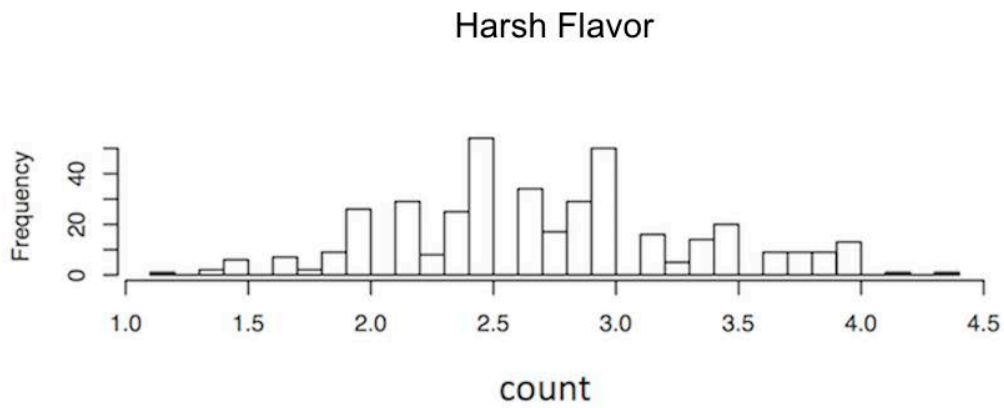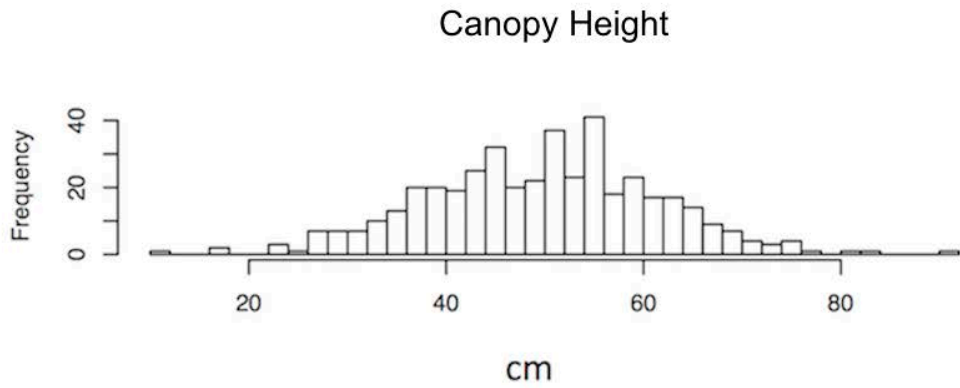
Supplemental Fig. S2. Distribution of phenotypes for collection of 433 carrot accessions. Four hundred thirty-three accessions were grown over two years in Hancock, Wisconsin in a randomized complete block design with 2 replications. Least-squares mean estimates of trait values, with within plot measurements averaged for height and harsh flavor, are plotted.
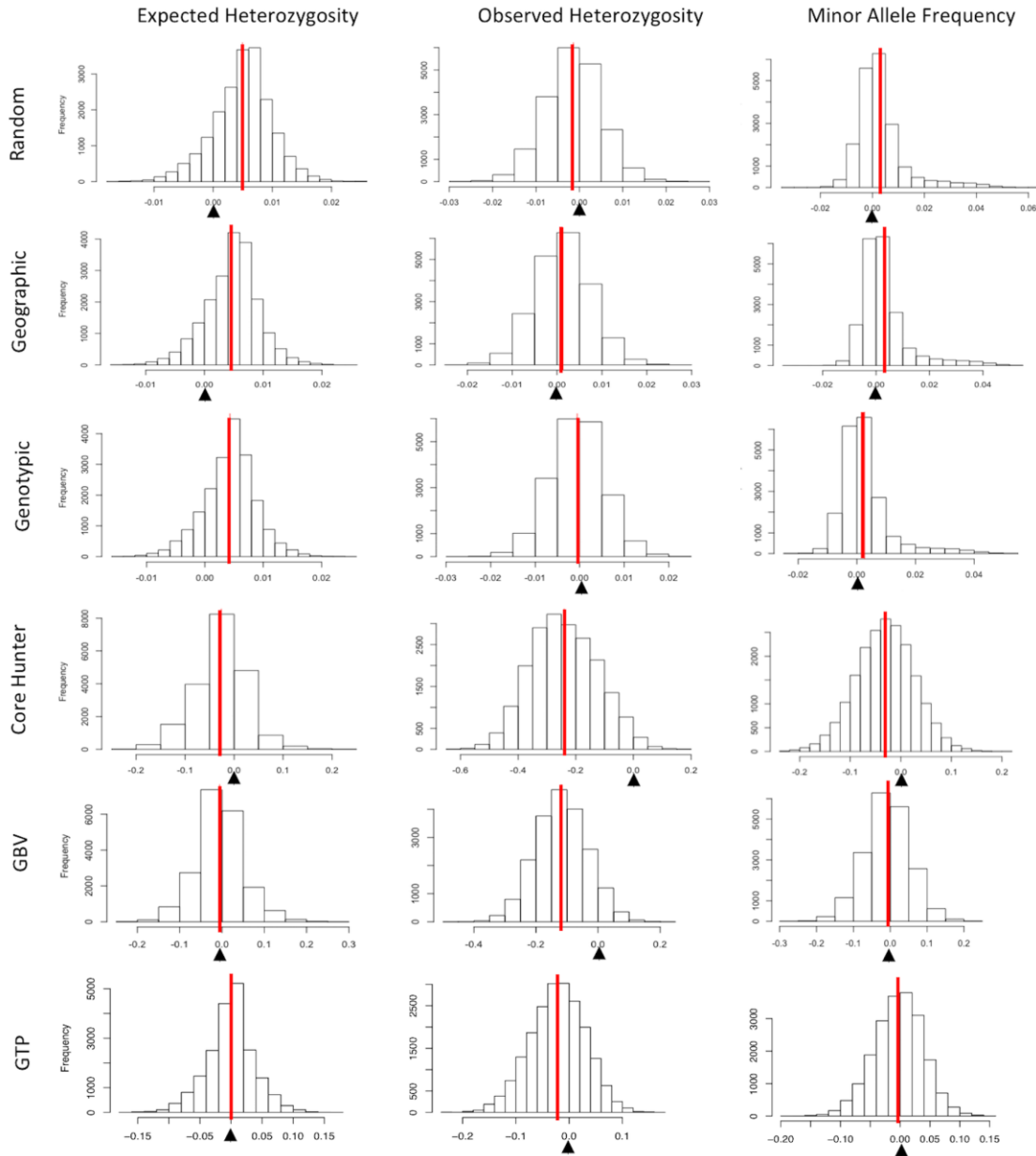
Supplemental Fig. S3. Per-locus distribution of differences in genetic diversity measurements between the collection of 433 carrot accessions and each core. Per-locus measurements of expected heterozygosity, observed heterozygosity, and minor allele frequency were calculated for the total collection and each core. Values calculated at each locus in a core collection were subtracted from the values at that locus in the total collection and the distribution of those differences is plotted. Vertical red lines indicate mean difference across loci and black triangles highlight zero.