Table S1. Founder parents used in the genomic prediction experiment along with exome capture resequencing summaries.

Table S2. The number of private SNPs per population across three classes of genic variants.

Table S3. Summary of putatively dSNPs in the founder lines. BA: Busch Agricultural Resources, Inc.; MN: University of Minnesota; ND: North Dakota State University. Values listed include the number of dSNPs and private dSNPs per inbred line.

Table S4. The ancestral state of all variants was inferred with *Hordeum murinum* ssp. *glaucum* used as an outgroup. The number of SNPs in each class and the proportion of SNPs for which ancestral state could be inferred is shown.

Table S5. Basic descriptive statistics from genotyping of the Veracode 384 SNP assay. Values reported are based on observed genotypes in Illumina genotyping or exome capture resequencing (for C0 founder lines).

Table S6. Average pairwise diversity among progeny for sites that were polymorphic in the C0 founder lines. The data is based on phased and imputed genotypes given observed genotypes from the Veracode 384 SNP assay.

Table S7. Differences in means of fold change of DAF between various functional classes of SNPs.