**Supporting Information**

**Supplemental Methods:** This section contains materials and methods details and code.

**Figure S1**: The frequencies of minor nucleotide calls (purple) and major nucleotide calls (green) among sites declared polymorphic between Red Fife and Chinese Spring. The major nucleotide is the nucleotide that occurs at the highest frequency at the polymorphic site. The minor nucleotide occurs at the lowest frequency.

**Figure S2:** The 1,503 genetic map positions to which 15,497 SNPs mapped.

**Figure S3**: The distributions of estimated genotypic trait values in the Red Fife (RF, Cross-hatched) x Stettler (S, Gray) doubled haploid population.

**Table S1:** Field data used in the correlation and QTL analyses

**Table S2:** Summary statistics from STAR read mapping of RNASeq reads.

**Table S3:** Attributes of SNPs including their genomic positions; predicted effects on gene functions; if they are in related/ unrelated genomic regions; the expression abundance of their resident gene; the triplication class of their resident gene; and the number of SNPs within their resident gene.

**Table S4:** SNP calls across 22,378 sites within the DH population.

**Table S5:** SNPs’ genetic map positions.

**Table S6:** Summary of genetic and physical maps.

**Table S7:** Summaries of expressed genes and SNP marker annotations within QTL regions.