



**S1 Fig. Schematic of conversion of array-based markers to PCR-based markers.** First, BlastN searches of reads/contig sequences of the markers were performed against the wheat survey genome sequence. The aligned sequences were searched for *Pst*I restriction sites for development of CAPS markers. If no *Pst*I sites were found, SSR motifs were searched and primers were designed to amplify these motifs. If no SSR motifs were present in the genomic sequence and if the read/contig sequence was derived from M808, SNPs and indels were searched because the genome sequence was derived from CS. In total, 12 markers were developed and used for further analyses.