Differentially amplified repetitive sequences among *Aegilops tauschii* subspecies and genotypes



**Figure S1.** Composition of abundance of repetitive sequences in 29 *Ae. tauschii* genotypes belonging to *anathera*, *strangulata* and *tauschii* subspecies as revealed using RepeatExplorer2. The size of the rectangles is proportional to the number of reads in a cluster for each genotype. For a number of the clusters, the number of reads differs considerably among different subspecies and genotypes. Accession codes has been shown in red (for ssp. *anathera*), green (ssp. *meyeri*) and blue (ssp. *strangulata*).