



Supplementary Figure S6. The polygenetic tree of the characterized WRKY proteins in the RNA-seq database. A neighbor joining tree was generated by MEGA software using all of the ten WRKY proteins selected from our RNA-seq database (* star labeled) and their homologs from *Hordeum vulgare* (Hv), *Aegilops tauschii* (At), *Brachypodium distachyon* (Bd), *Triticum aestivum* (Ta), *Triticum urartu* (Tu), and *Sorghum bicolor* (Sb) obtained from GenBank nr database. All the WRKYs were temporally designated according to their closest homologs.