

Fig. S1. Consensus map of maize with projected QTLs controlling resistance against *Aspergillus flavus*

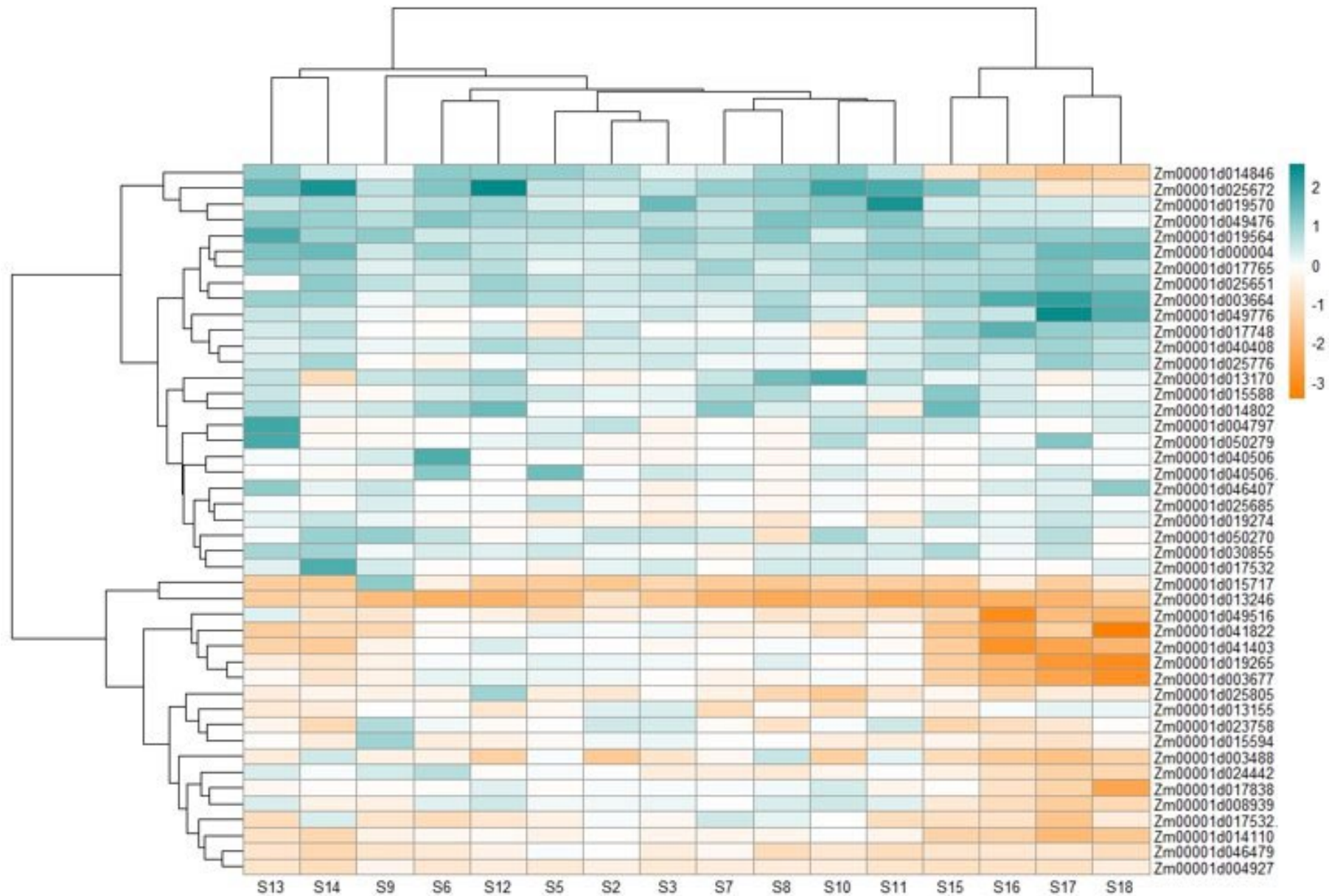


Fig. S2. Heatmap showing differential expression of 43 putative *Aspergillus flavus* specific genes in MQTL intervals at various stages of *Aspergillus flavus* infection (Musungu et al. 2020). These genes did not have any match with published genes expressed under other stresses

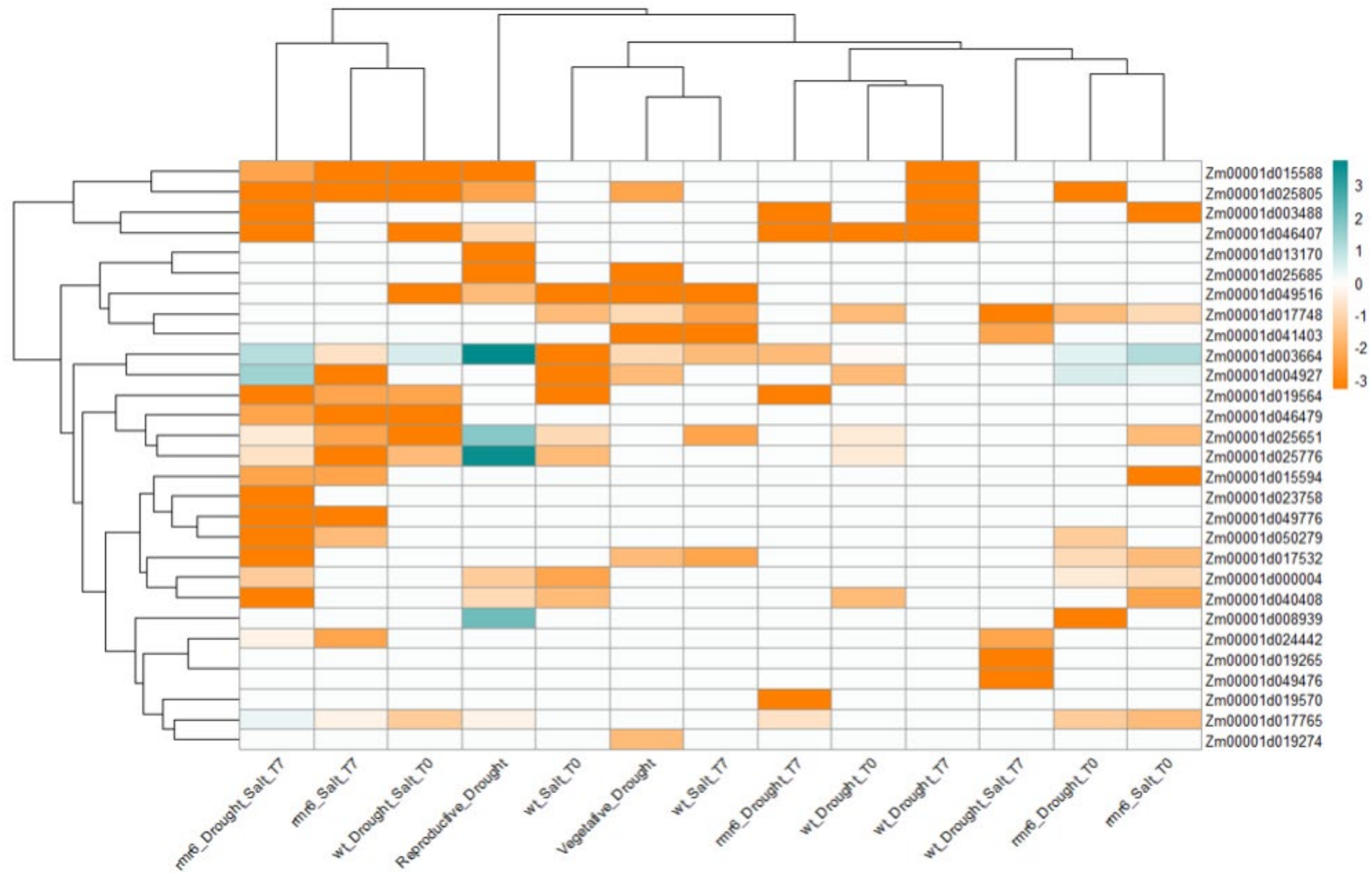


Fig. S3. Heatmap showing expression of 29 genes under drought and salt stresses in qTeller database. These genes belong to the set of 43 putative *Aspergillus flavus* specific genes in MQTL intervals that did not have any match with genes expressed under other stresses (Fig. S2)

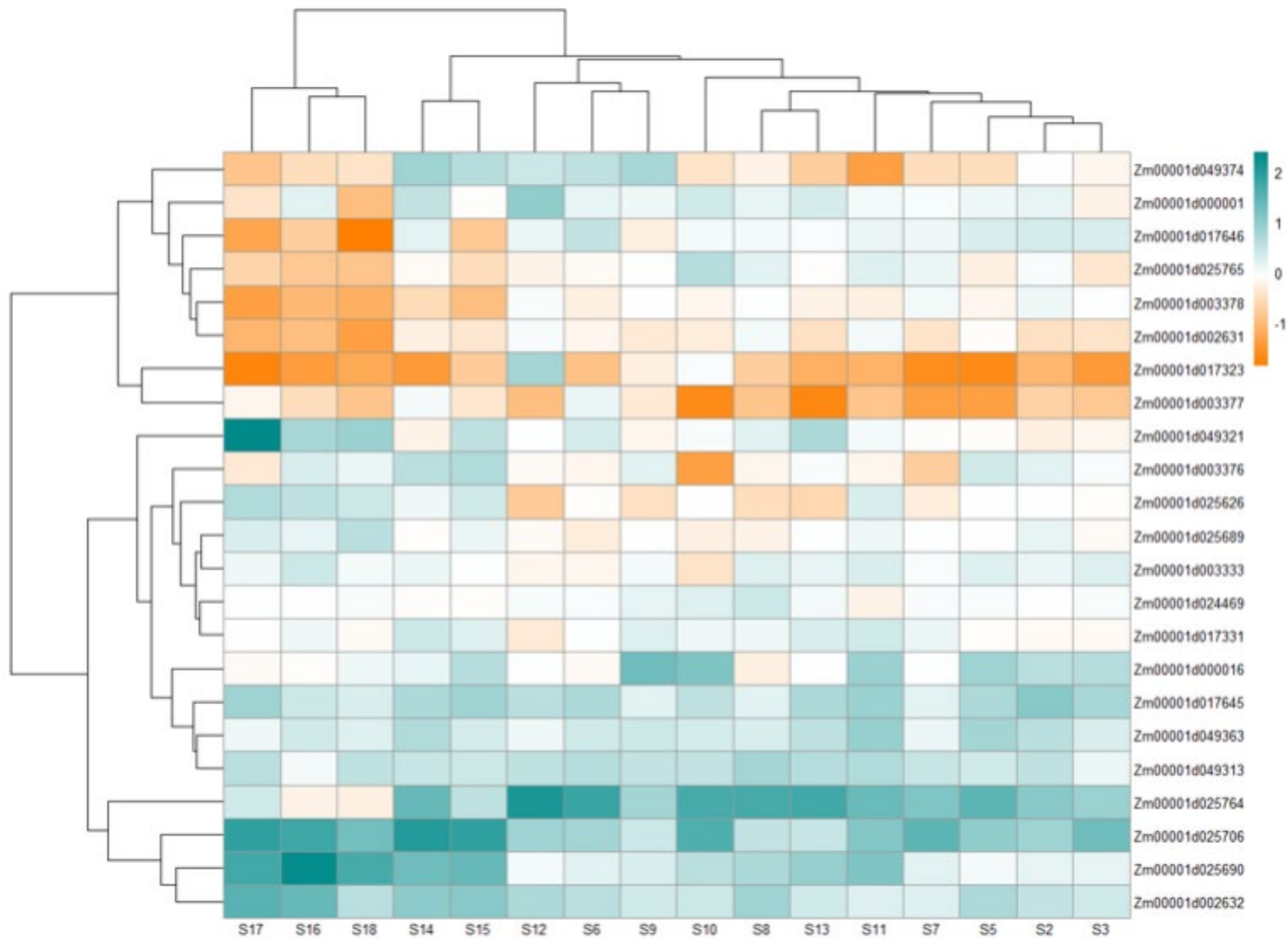


Fig. S4. Heatmap showing differential expression of 23 candidate genes flanking 10 Kb to GWAS SNPs at various stages of *Aspergillus flavus* infection