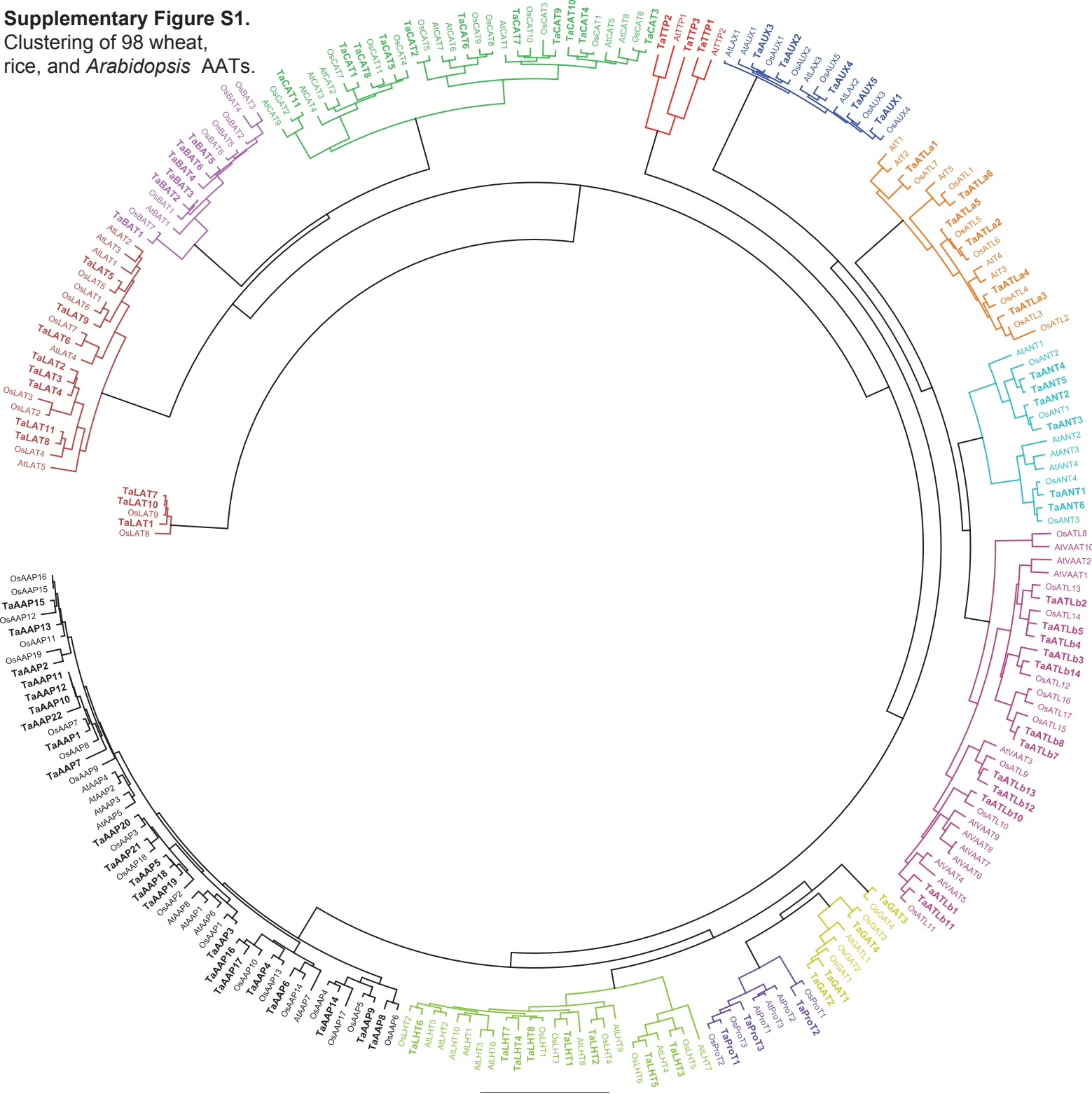


Spatiotemporal expression patterns of wheat amino acid transporters reveal their putative roles in nitrogen transport and responses to abiotic stress

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Supplementary Figure S1.
 Clustering of 98 wheat, rice, and *Arabidopsis* AATs.



Supplementary Figure S2a.

Homeolog gene scaled (row) FPKM values from salt stress RNA-seq data.

Genes without at least a single column above FPKM 3.0 before scaling were not included.

Root tissue used.

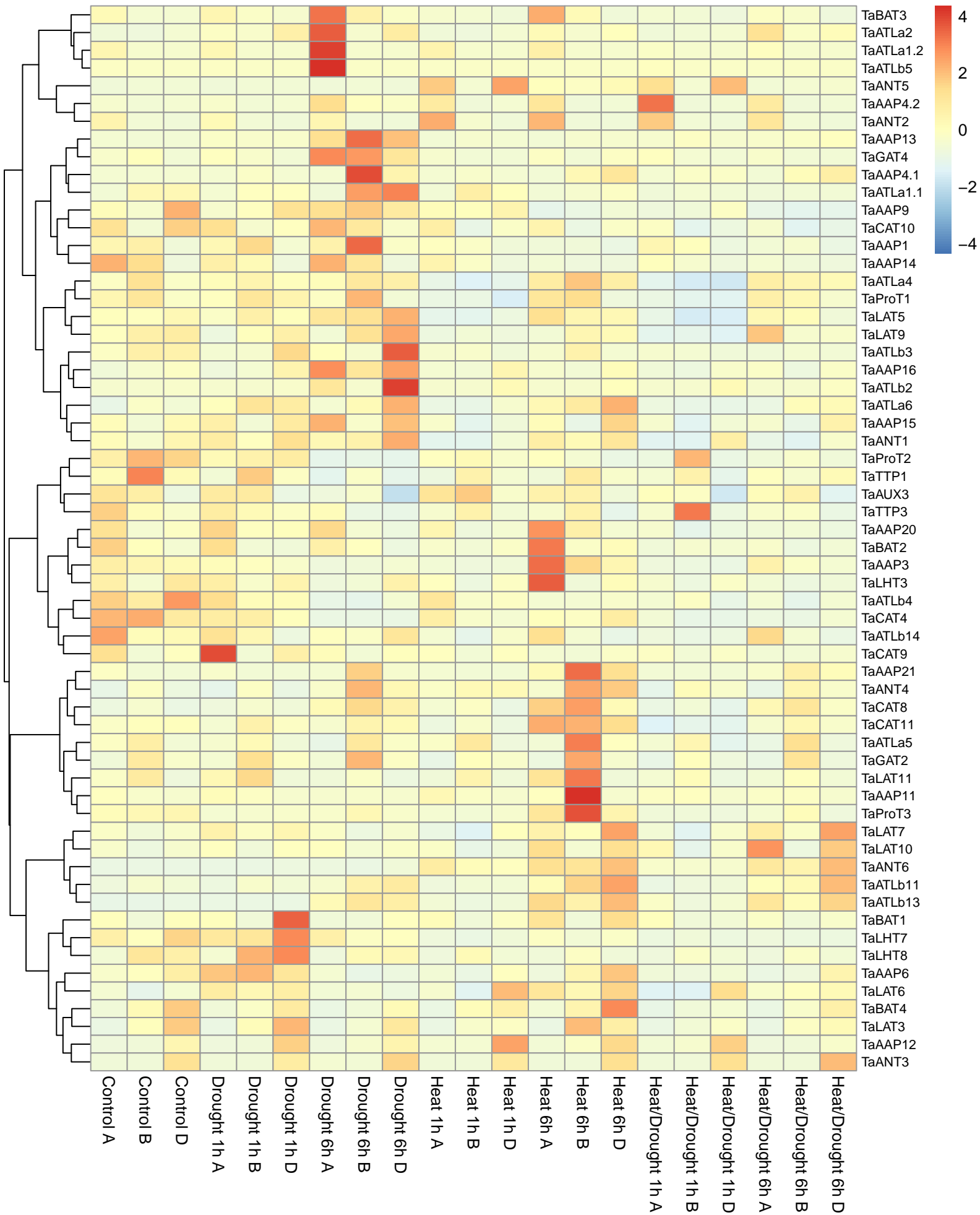


Supplementary Figure S2b.

Homeolog gene scaled (row) FPKM values from heat and drought RNA-seq data.

Genes without at least a single column above FPKM 3.0 before scaling were not included.

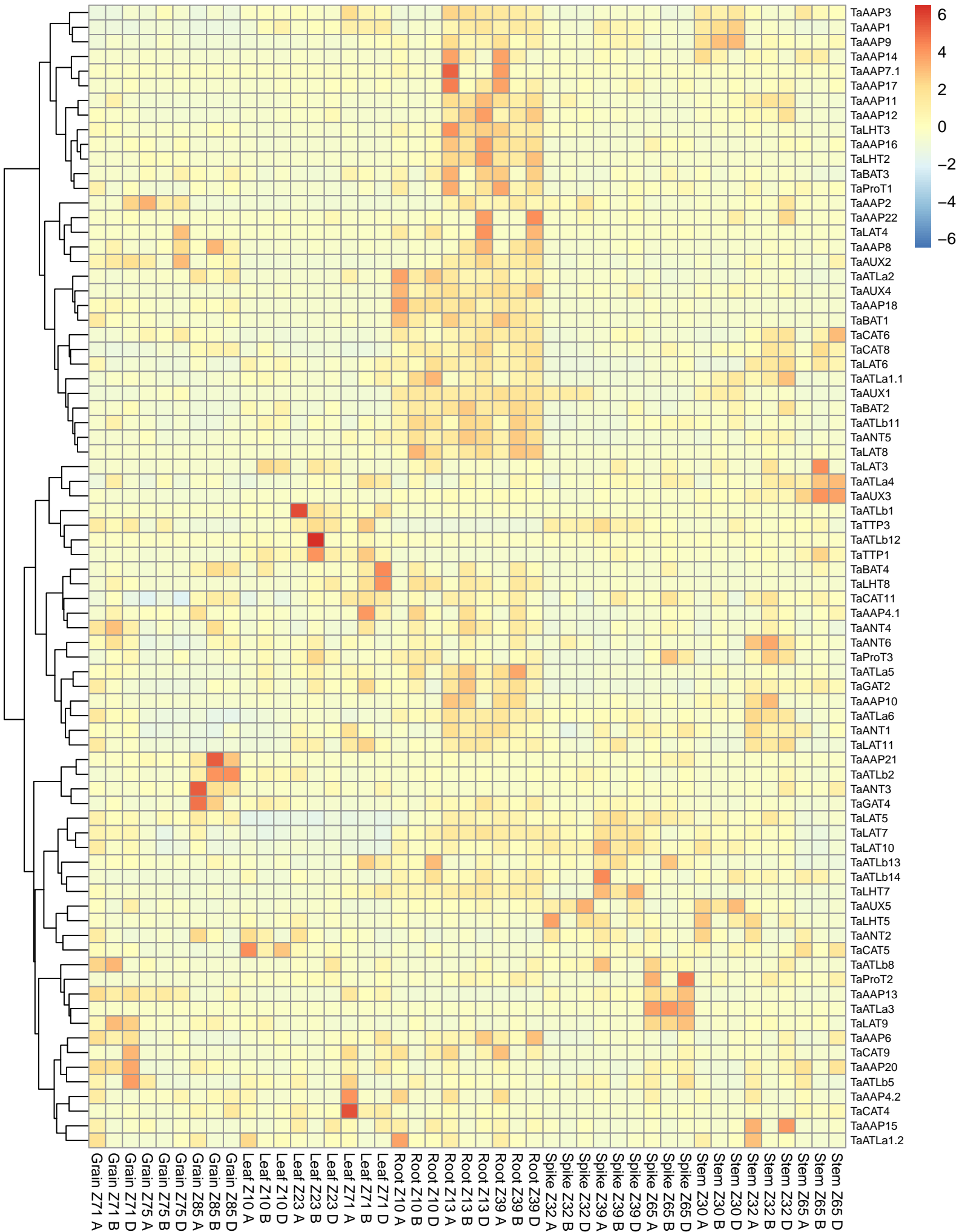
Leaf tissue used.



Supplementary Figure S2c.

Homeolog gene scaled (row) FPKM values from tissue specific RNA-seq data.

Genes without at least a single column above FPKM 3.0 before scaling were not included.



Supplementary Figure S3.

RNA-seq data expression (FPKM) from different organ tissues of four AATs that were used for qPCR in Figure 6.

