



Figure S2. RNA-Seq reveals meristem-specific expression pattern of cell wall genes, related to Figure 3.

(A) Reads from RNA-seq mapped to individual genes with enriched expression in SAM, flower or differentiated tissues.

(B) Gene ontology (GO) term enrichment of genes with increased or decreased transcript abundance in SAM or flower compared to their average expression in the whole plant. Red indicates level of enrichment. Cell wall-related categories are boxed. A selection of GO terms is shown.

(C) Relative expression of differentially expressed GT family genes in SAM and flower ($FC > 1.5$; $P < 0.05$). Red indicates higher, and blue indicates lower expression than average expression in the whole plant. Names of characterized genes are given in red.

(D) Network of GT genes after pairwise correlation coefficient analysis using CORNET

(https://bioinformatics.psb.ugent.be/cornet/versions/cornet_maize1.0/main/precalc). The highly correlated core part of the network, encompassing members of the *CESA* family, is circled. A floral subnetwork is highlighted (boxed).