

Figure S1A

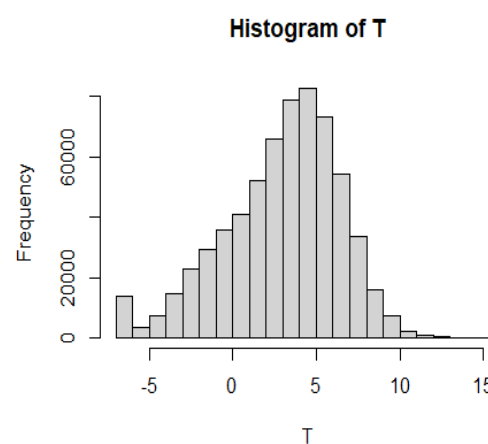


Figure S1B

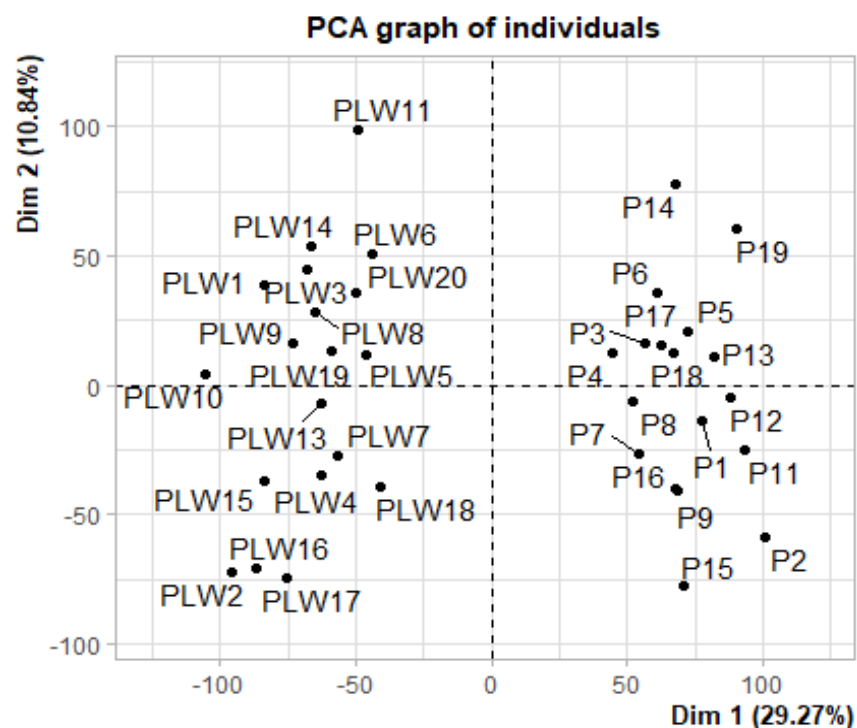
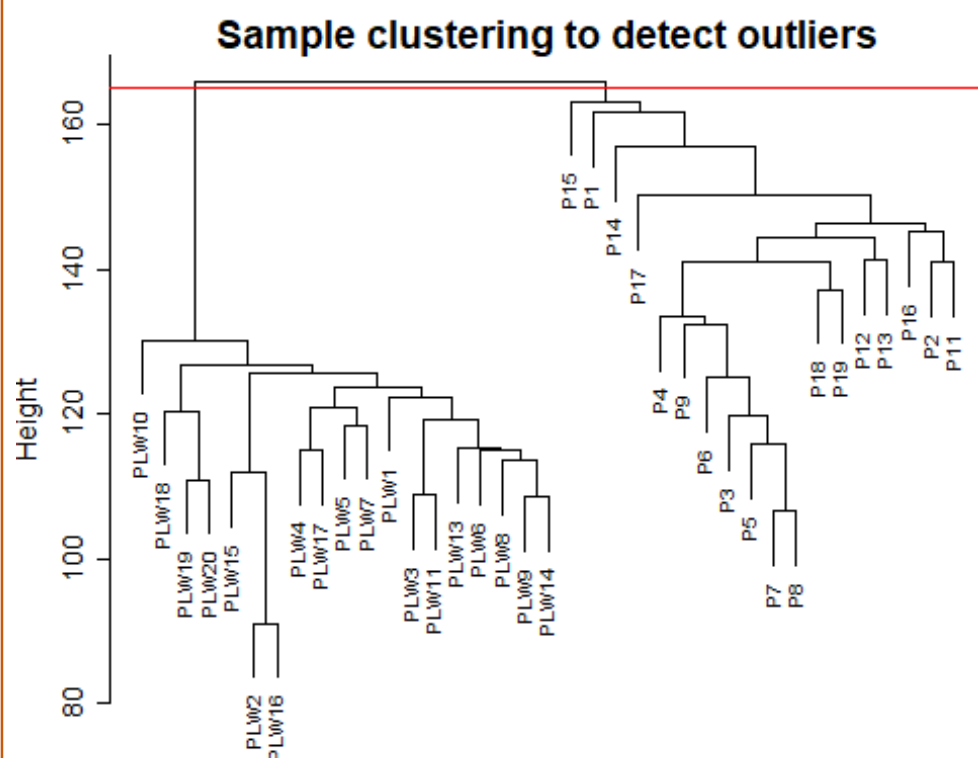
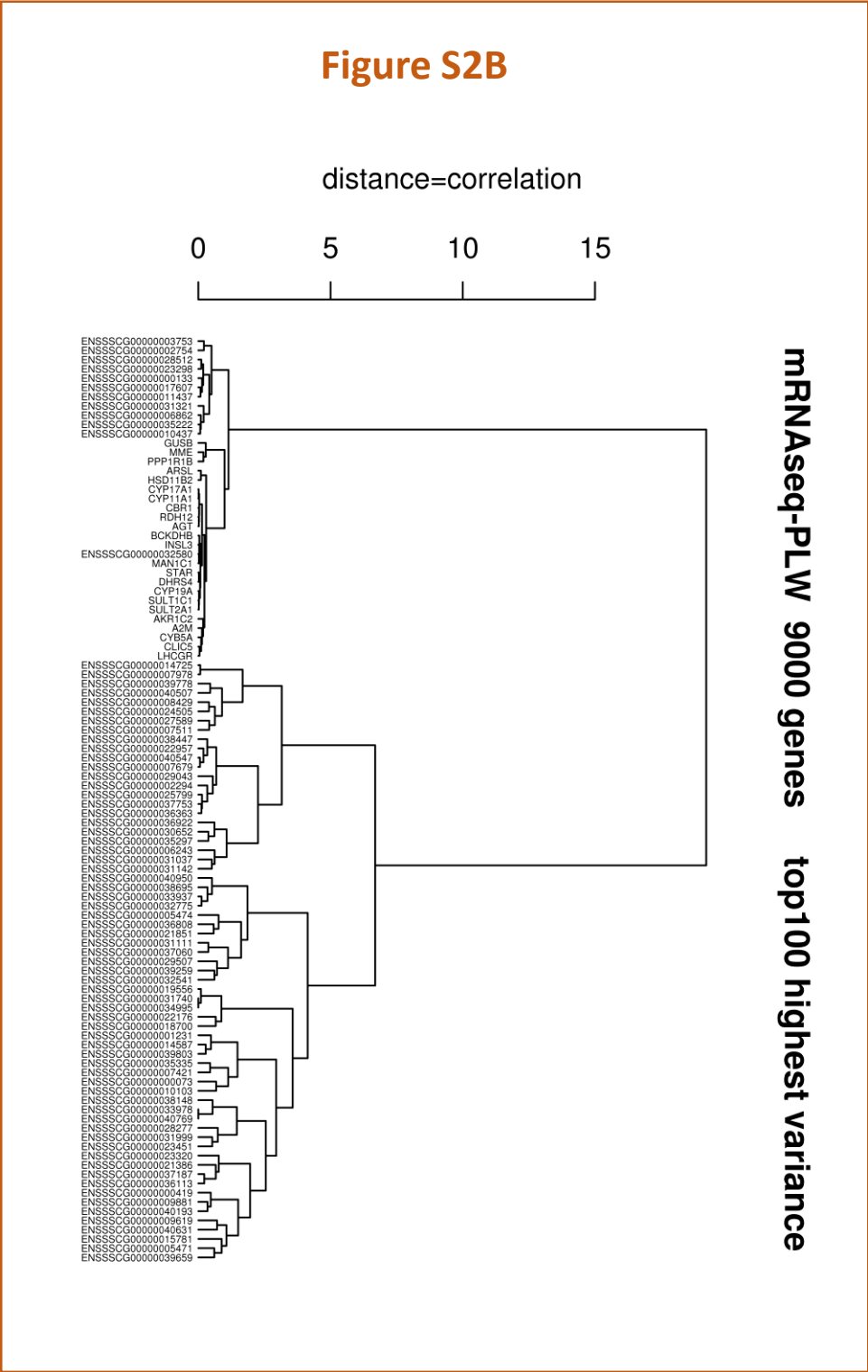
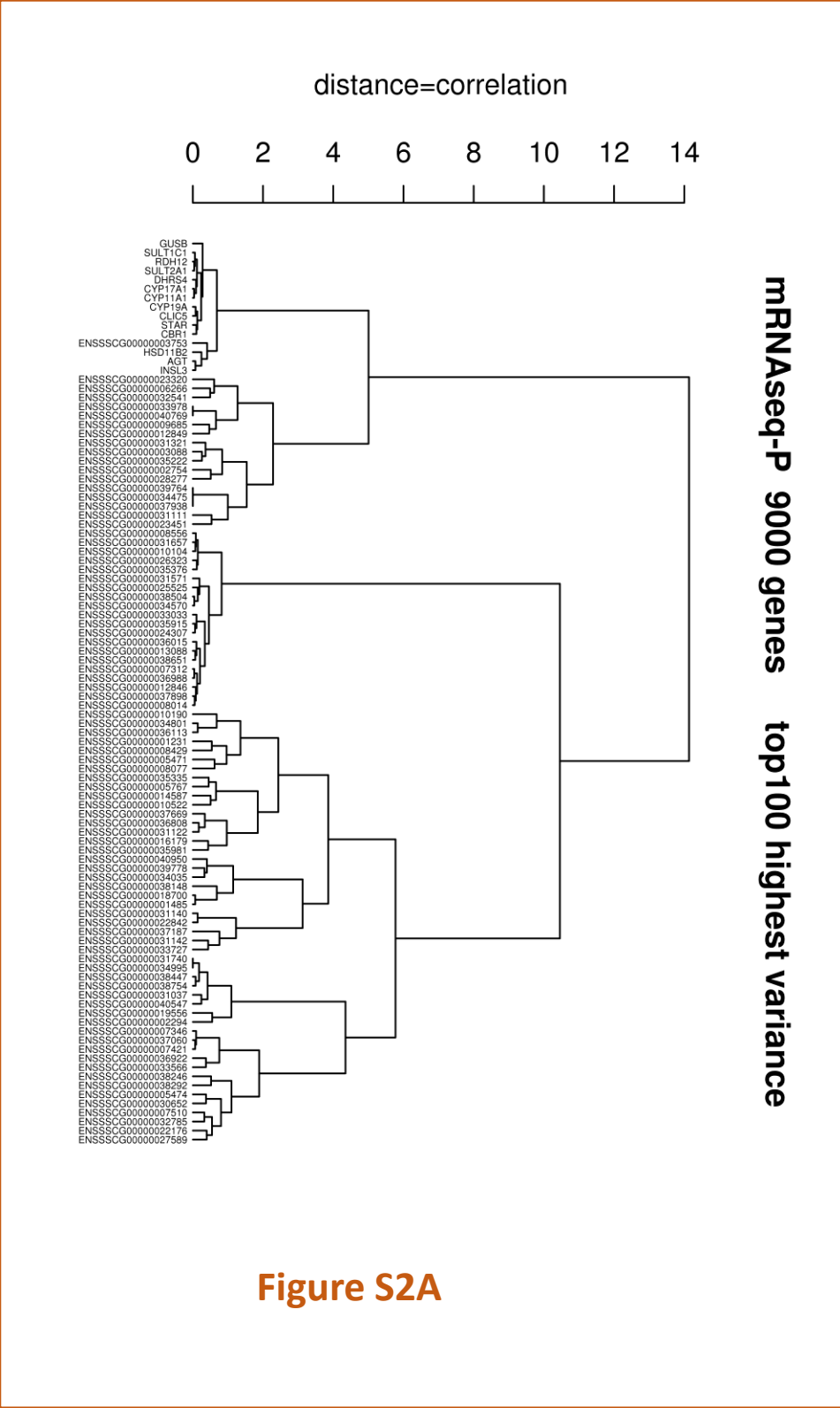


Figure S1C





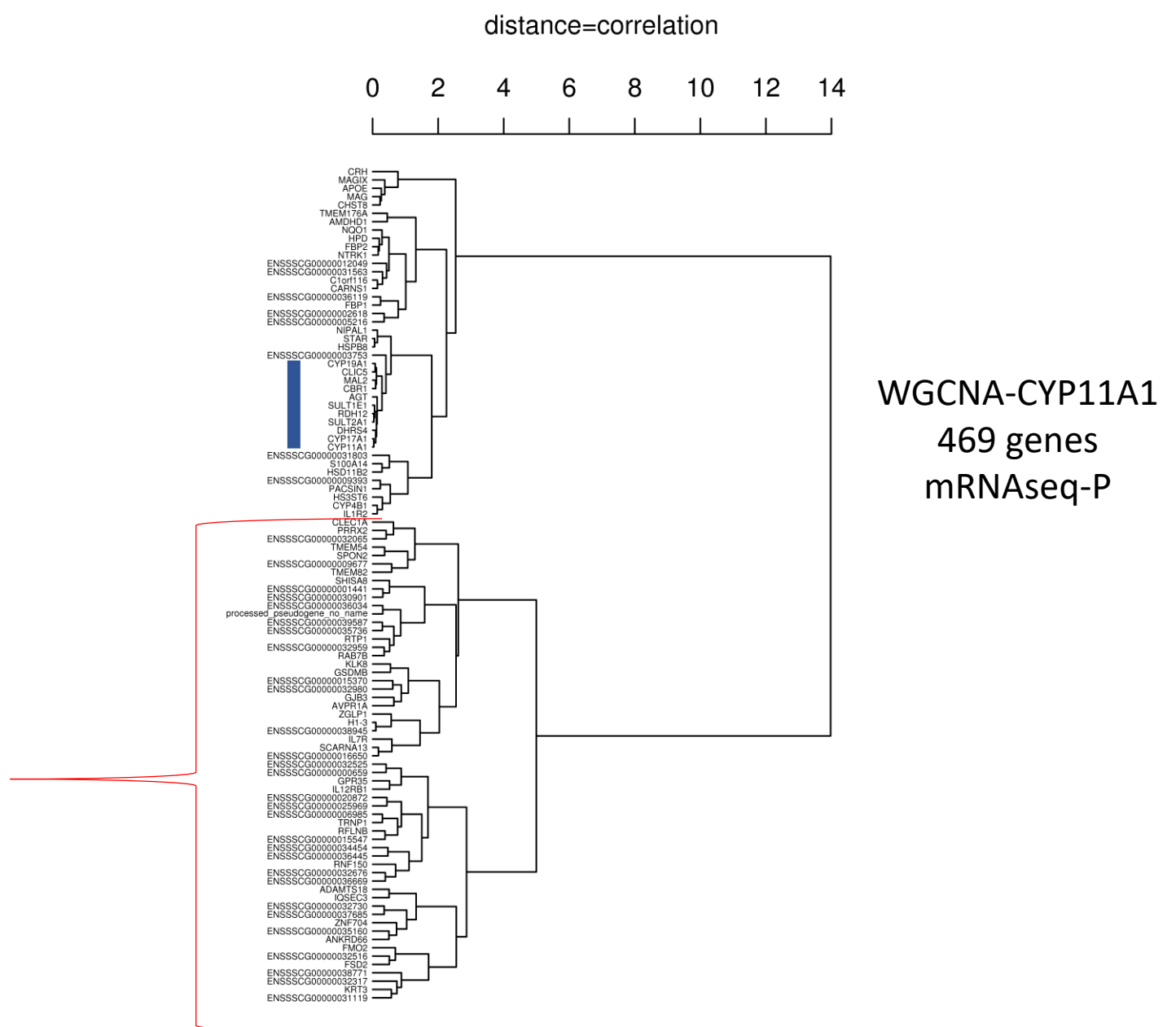


Figure S3

The top 100 genes with the biggest variance were retained to perform the hierarchical clustering using correlation as distance (agglomeration: ward).

Figure S4 WGCNA-CYP11A1 (469 genes) mRNAseq-P

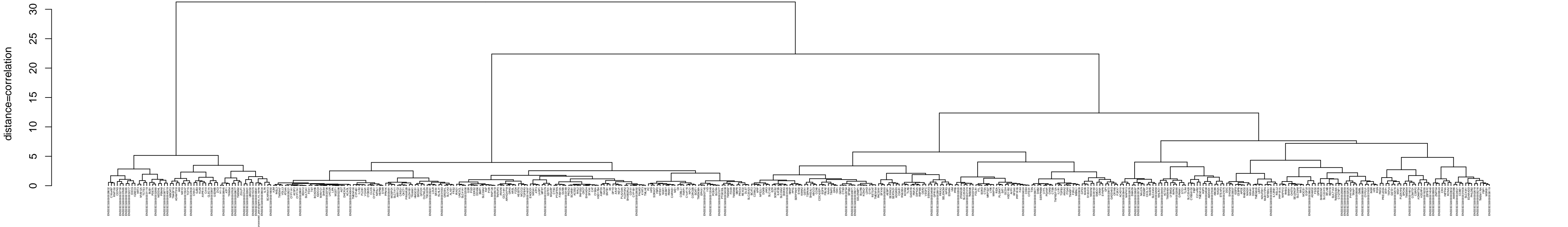


Figure S5 **WGCNA-CYP11A1 (469 genes) mRNAseq-PLW**

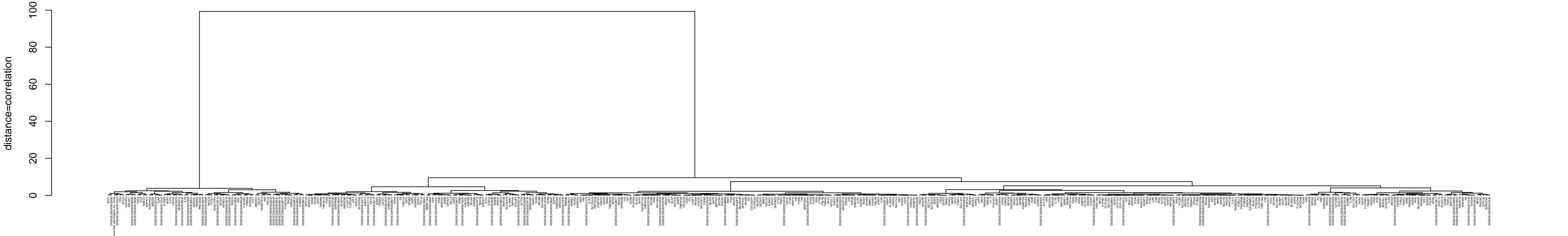


Figure S6 WGCNA-HSD17B3 (335 genes) mRNAseq-P

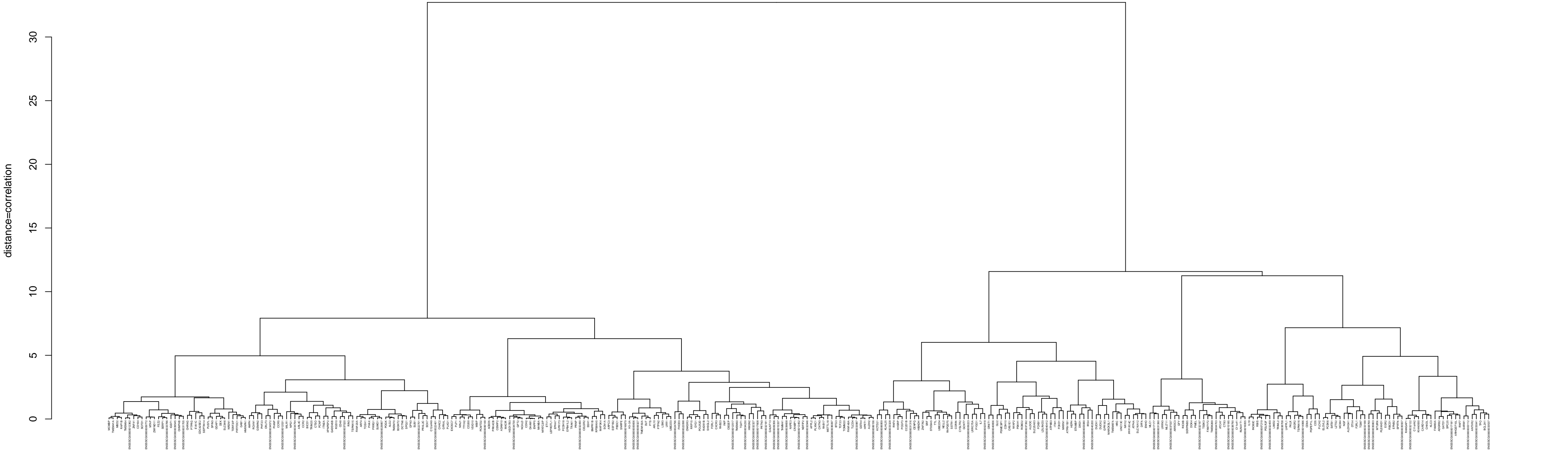


Figure S7A

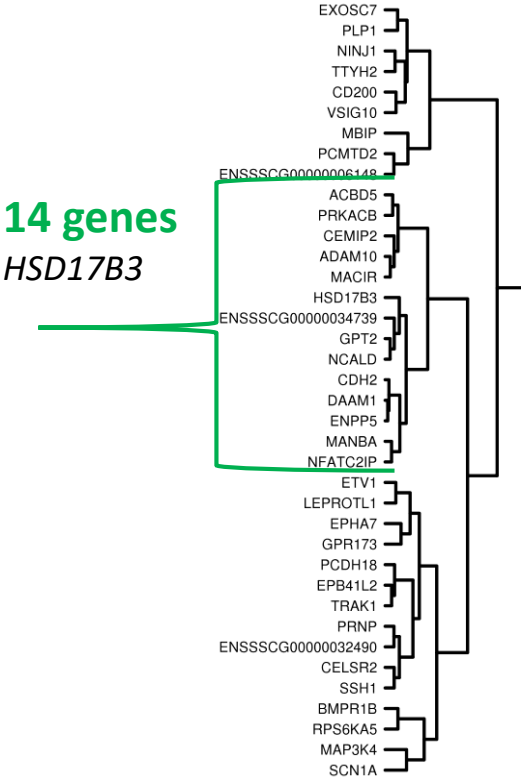


Figure S7B

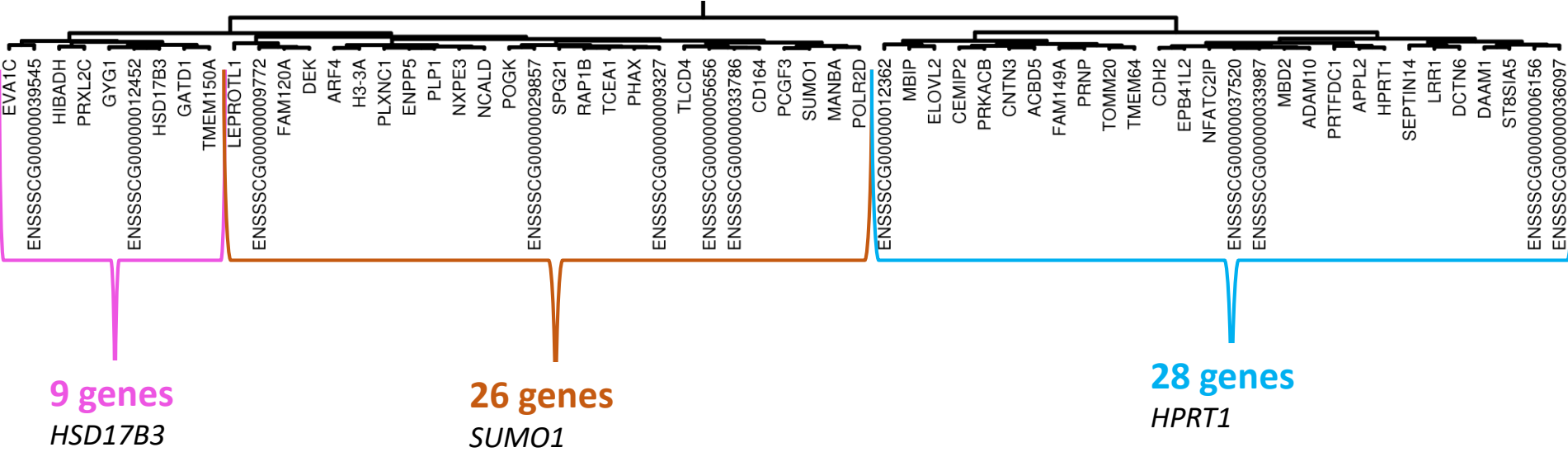


Figure S8 **WGCNA-HSD17B3 (335 genes) mRNAseq-PLW**

