SUPPLEMENTARY DATA

Supp. Figure 1. Large gene families have proportionally fewer strongly expressed genes. Each of the 76 CAZyme-encoding gene families in *Populus* was scored for the number of genes with observed ESTs in any of the 17 libraries (Table II) and expressed as a fraction of total gene family size. The histogram shows average number of genes with ESTs and a standard error. Families with 46 or more genes had a significantly smaller fraction of genes with ESTs. Note that some of the genes without ESTs might still be expressed at low levels or in tissues / conditions other than those sampled.

Supplementary Table I. List of all *P. trichocarpa* gene models identified as potentially encoding CAZymes and expansins and their corresponding ESTs.

Supplementary Table II. Arabidopsis gene expression data from AtGene Express project (http://www.uni-frankfurt.de/fb15/botanik/mcb/AFGN/atgenex.htm presented as the relative oligo array signal intensity tabulated for CAZyme encoding genes related to starch and cell wall polysaccharide metabolism.