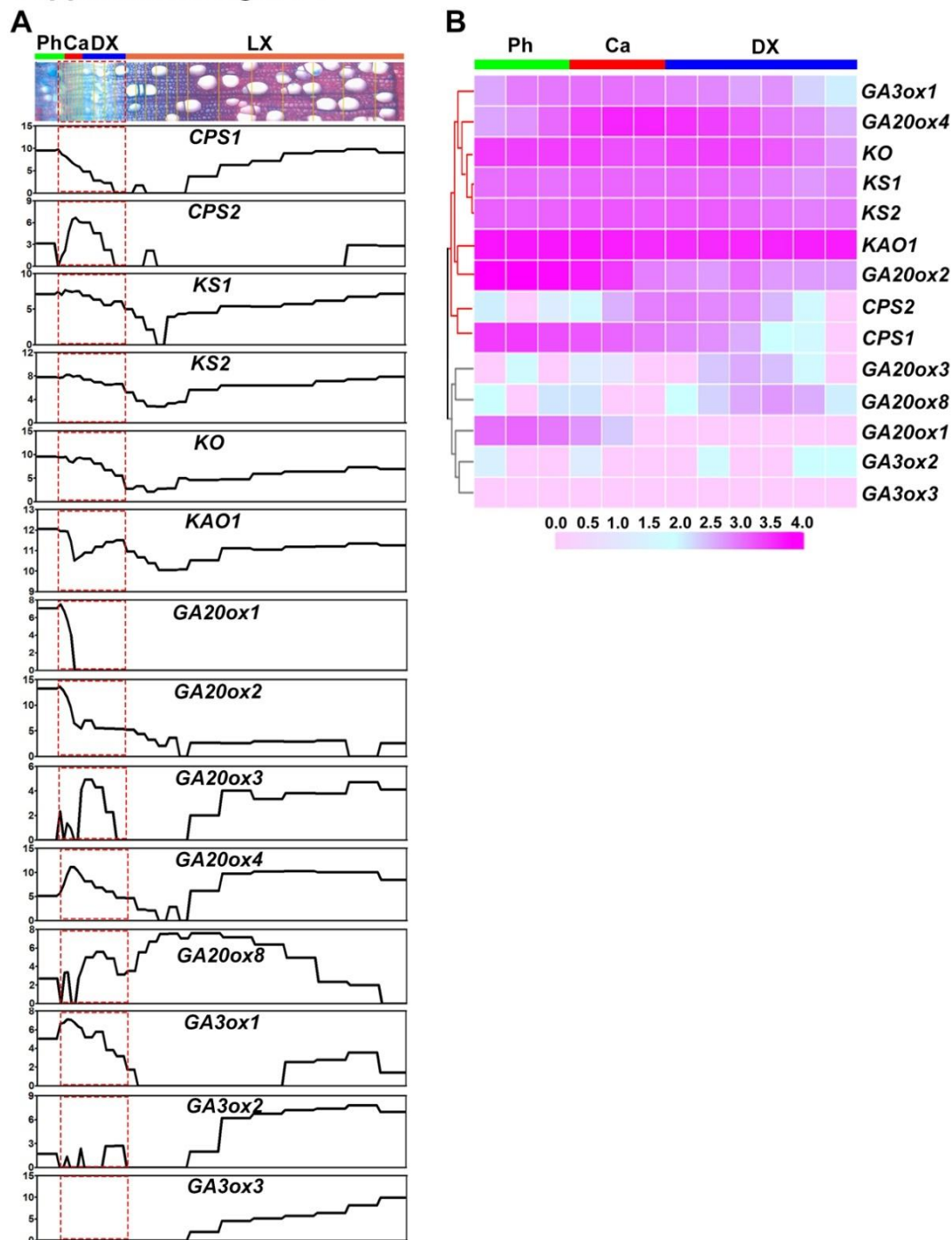## Supplemental figure 3

Figure S3. Expression patterns and co-expression correlations of genes encoding GA biosynthetic enzymes in wood-forming tissues of poplar stems.

(A) Expression patterns of genes encoding GA biosynthetic enzymes across the wood-forming tissues of poplar stems, based on the RNA-seq data from Tree 1 (Sundell et al., 2017). Curves were generated using expression values from cryo-sections of stem tissues. The red dotted lines represent early wood-forming tissues, including the phloem, cambium, and developing xylem. Abbreviations: Ph, phloem; Ca, cambium; DX, developing xylem; LX, lignified xylem. (B) Co-expression correlation of GA biosynthetic enzyme-encoding genes. Data is based on the RNA-seq databases corresponding to the red dotted lines in (A). The left-hand lines represent genes with co-expression correlations. Abbreviations: Ph, phloem; Ca, cambium; DX, developing xylem.