Supporting information Figure S1 OrthoMCL cluster analysis of annotated Populus and Eucalyptus genes. (a) OrthoMCL identified 15,925 clusters of orthologs and paralogs representing 59,892 protein sequences in Populus trichocarpa and Eucalyptus grandis, of which 2,111 (7,087 proteins) were unique to poplar and 1,195 (5,116 proteins) were unique to eucalypt trees. (b) The fraction of predicted proteins in each species placed in the four cluster classes. A total of 12,619 clusters (47,689 proteins) contained in cluster classes 1×2 and N×2 shared orthology between species. Cluster analysis detected 2,111 clusters (7,087 proteins) unique to poplar and 1,195 clusters (5,116 proteins) unique to eucalypts (cluster class N×1). Class 1×1, about 25% of proteins in both species, contains proteins that did not cluster, i.e. are encoded by single copy genes with no detected orthologs in the other species.