Table SI. Sequences of primers used for qRT-PCR

Primer name	Primer sequence	PCR product size
717-4CL1-1-F02	5′-GCCAGGCATATAACTGAAG-3′	87 bp
717-4CL1-1-R01	5′-AACACTACAATGATTCGCAAG-3′	
717-4CL1-2-F02	5′-CTTGAGAGAGAGGTTGGCA-3′	117 bp
717-4CL1-2-R02	5′-AGGACTCAATGTAAGGTTTTCTC-3′	
aUbq-F03	5′-CTCTTTTGAAGTTGGTGTTTGC-3′	75 bp
aUbq-R03	5′-TCCAATGGAACGGCCATTAA-3′	

Figure S1. An expanded and labeled image from Figure 2Q. The blue-green fluorescence are phenolic extractives that are most prominent in the rays leading from the cambial zone inward. AB is air bubble (trapped under the water immersion lens used for imaging), CZ is cambial zone, CF is collapsed fibers, CV is collapsed vessels, TW is tension wood. TW cells dominate the lower left quadrant of this picture and can be identified by the presence of a thickened "G-layer" that often appears partially separated from the rest of the outer layers of the cell wall. TW G-layers also appear brown in color due to the apparently reduced autofluorescence in the red and blue spectra.

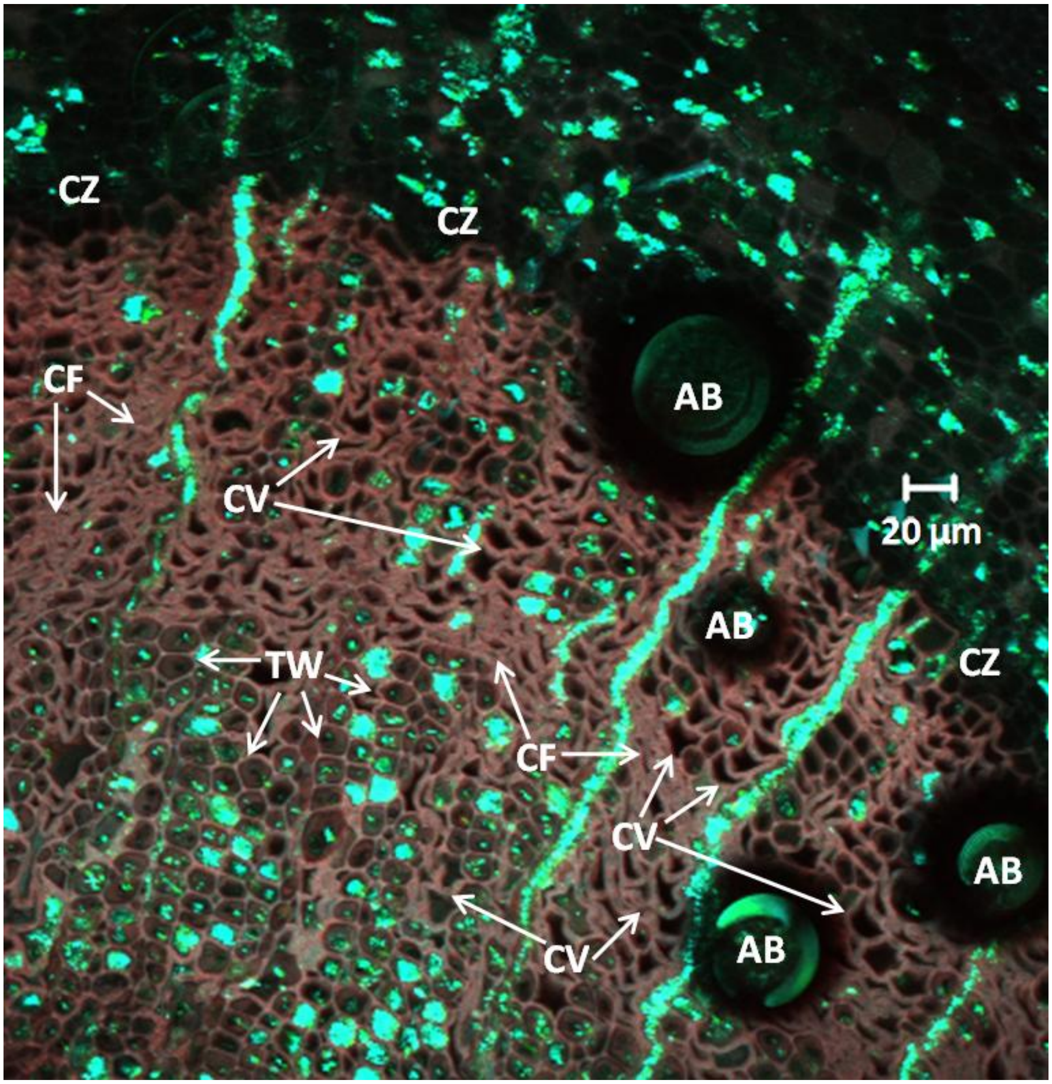

Figure S2. Examples of axial and cross-sectional patterns of brown wood distribution in fresh stem sections with bark removed. The stem sections were from the lower 20 cm of two year old trees harvested for biomass measurements. Sections from event 150 are left and sections from 713 are right. The cross-sections correspond to the nearest ends of stem samples located just below. Each stem section was about 1-1.5 cm in diameter.

Figure S3. Photographs of freshly harvested wood from transgenic event 210. The three cross-sections of the main stem were pictured at approximately 20 cm intervals from the base of the tree (left). Nine branch-to-stem junctions (i.e. knot cross-sections) are pictured on those same stem sections. Scale bars are 1 cm. On average, event 210 had 1% of the cross-sectional area in brown wood within stem bases (Table I), yet the branch junctions shown below had considerably more brown wood.