SUPPLEMENTAL MATERIAL

Figure S1: Comparison between biological and technical replicates.

Pearson's correlation coefficients are given.

Table S1: List of unigenes from the cork subtractive library classified into functional categories and their expression pattern in the cork to wood microarray comparison.

For each gene, EST GenBank accession numbers, best BlastX in GenBank and in TAIR and gene description are given. The putative functions were assigned based on the highest BlastX score match (e-value $<10^{-20}$). The cork/wood expression ratio is given as FC (Fold Change) for genes with B>3. N is the number of ESTs present in the library.

Table S2: Experimental data for all ESTs represented on the microarray together with the detailed results of the hybridization experiments.

Each EST was spotted twice on the microarray. Annotation and GenBank data concerning to *Quercus suber* SSH library are given. Spots are considered absent if signal intensity <150; marginal if 150<signal intensity<250; present if 250<signal intensity<65000; and saturated if signal intensity>65000. The cork to wood hybridization was performed using three biological replicates with dye swap. Statistical B, $\log_2$-ratio (wood as a reference), cork and wood signal intensities and median of intensities (A) are given. The cork to embryo hybridization was performed using same RNA samples from SSH. Cork and embryo signal intensities, $\log_2$-ratio coefficient of variation (CV) among duplicated spots and median of intensities (A) are given. FC values and $\log_2$-ratio (taking embryo as a reference) are only given for ESTs showing CV < 0.3.

Table S3: Primers used for semiquantitative PCR.

Primer sequences are shown for each gene used in this analysis.