

**Additional file 1:** This PDF contains all of the additional material (Figures S1-S7)

**Figure S1.** The bamboo seedlings of different ages.

**Figure S2.** oxplot of the log fragments per kilobase of exon per million fragments mapped (FPKM) expression values.

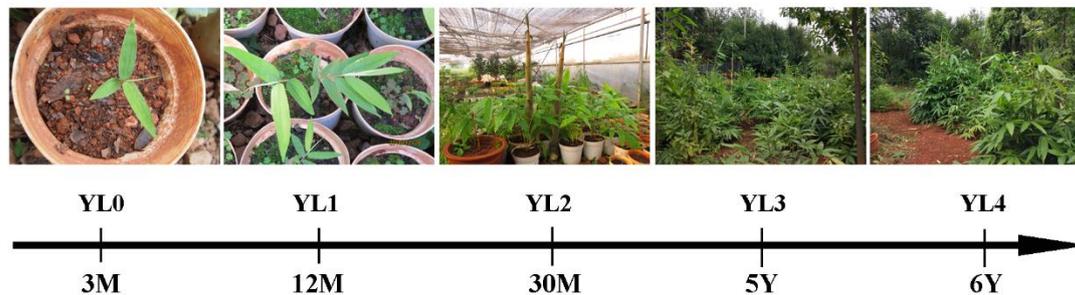
**Figure S3.** Boxplot distribution of coefficient of variation, in percentage, among biological replicates.

**Figure S4.** Quantitative RT-PCR validations.

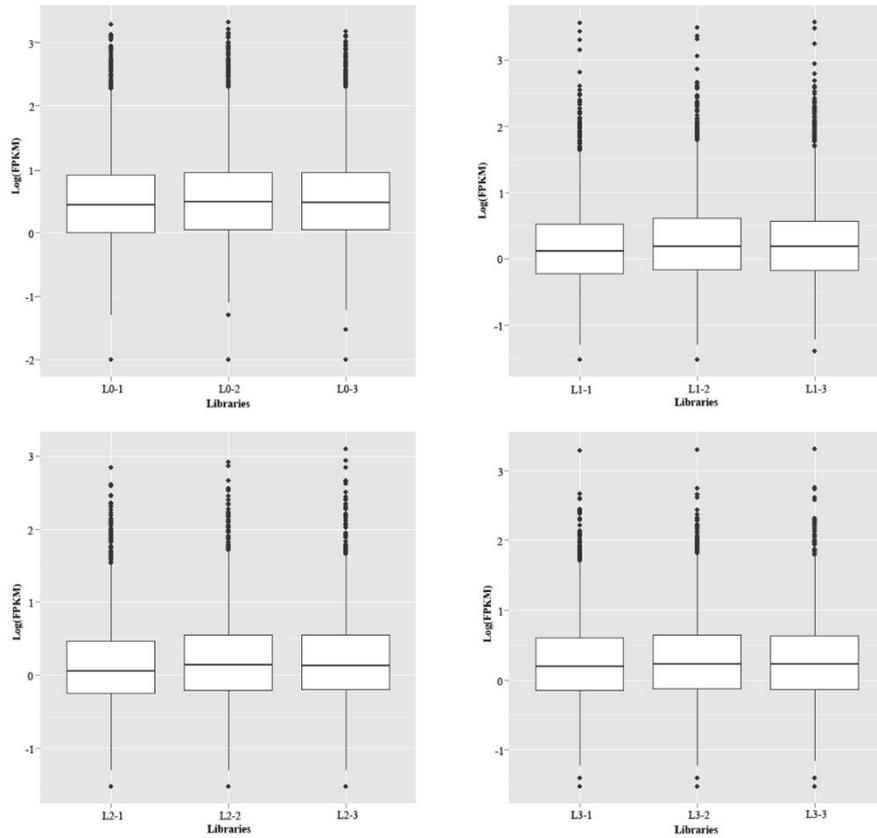
**Figure S5.** These unigenes were assigned into different pathways.

**Figure S6.** Plant hormone signal transduction for unigenes by KEGG annotation.

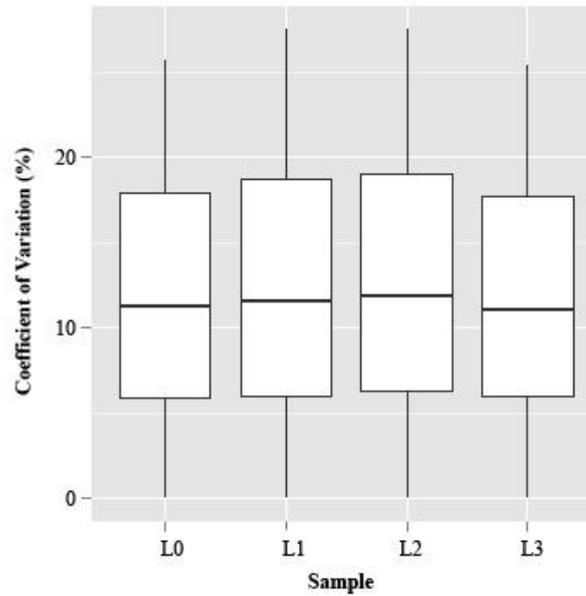
**Figure S7.** Phylogenetic analysis of the CONSTANS or CONSTANS-like proteins.



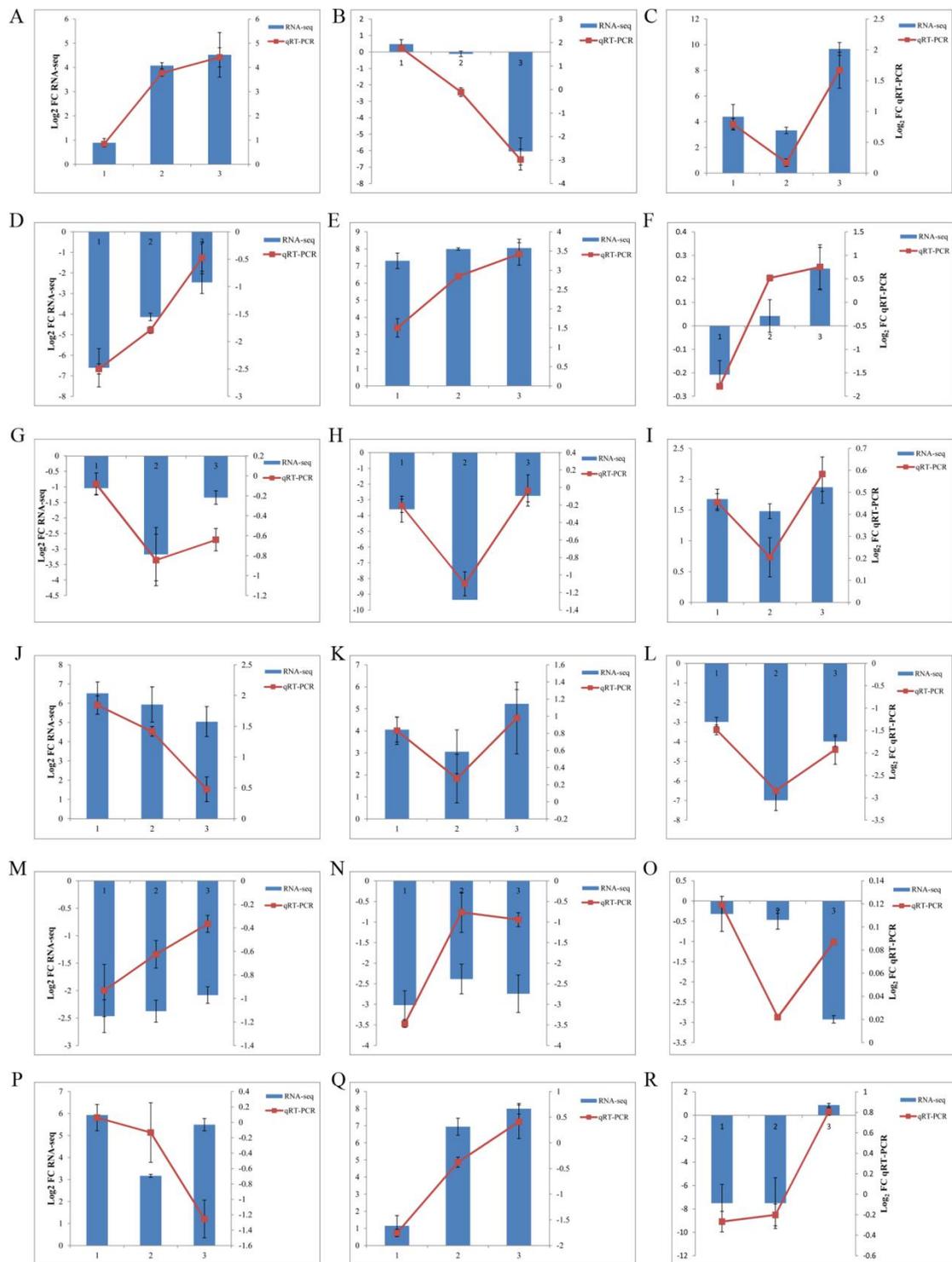
**Figure S1. The bamboo seedlings of different ages.** YL0: the seedlings of 3 months; YL1: the seedlings of 12 months; YL2: the seedlings of 30 months; YL3: the seedlings of 5 years; YL4: the seedlings of 6 years. YL0, YL1 and YL2 were planted in the greenhouse. YL3 and YL4 were planted out of the greenhouse.



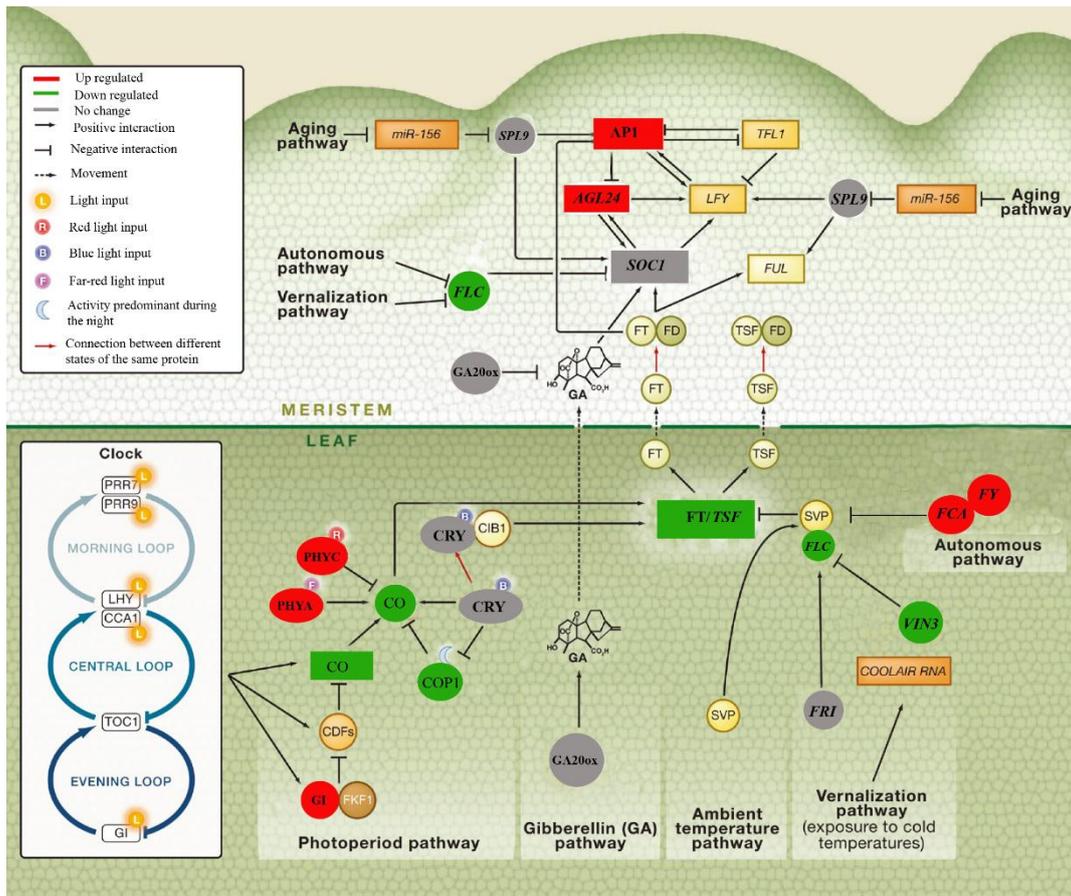
**Figure S2. Boxplot of the log fragments per kilobase of exon per million fragments mapped (FPKM) expression values.** The figure shows the boxplot of the log FPKM values in all the 12 libraries. The plot shows that the median of the FPKM values across the libraries being compared for differential expression are comparable. Further the different quartile values are almost identical among replicates.



**Figure S3. Boxplot distribution of coefficient of variation, in percentage, among biological replicates.** The coefficient of variation was calculated by taking the ratio of the standard deviation and mean of the expression values, for every gene among the biological replicates. The 75<sup>th</sup> percentile in all the pairs has a variation of less than 20%, indication low variability among replicates.



**Figure S4. Quantitative RT-PCR validations.** 18 genes were selected for the quantitative RT-PCR analysis, including Unigene49490 (A), Unigene57034 (B), Unigene108692 (C), Unigene32545 (D), Unigene114564 (E), Unigene120387 (F), Unigene103892 (G), Unigene104205 (H), Unigene109097 (I), Unigene110315 (J), Unigene130058 (K), Unigene137345 (L), Unigene30387 (M), Unigene32039 (N), Unigene33763 (O), Unigene36923 (P), Unigene39652 (Q), Unigene28224 (R) in L0, L1, L2 and L3. 1, 2, 3 showed the relative expression level of L1, L2, L3 compared to L0. Vertical lines represent standard error for an average of three biological replicates.



**Figure S5.** These unigenes were assigned into different pathways. Red indicated up-regulated, green indicated down-regulated and gray indicated no change in gene expression level. The gene expression level displayed L3 compared to the expression level of L0(Fornara, de Montaigu, & Coupland, 2010).

PLANT HORMONE SIGNAL TRANSDUCTION

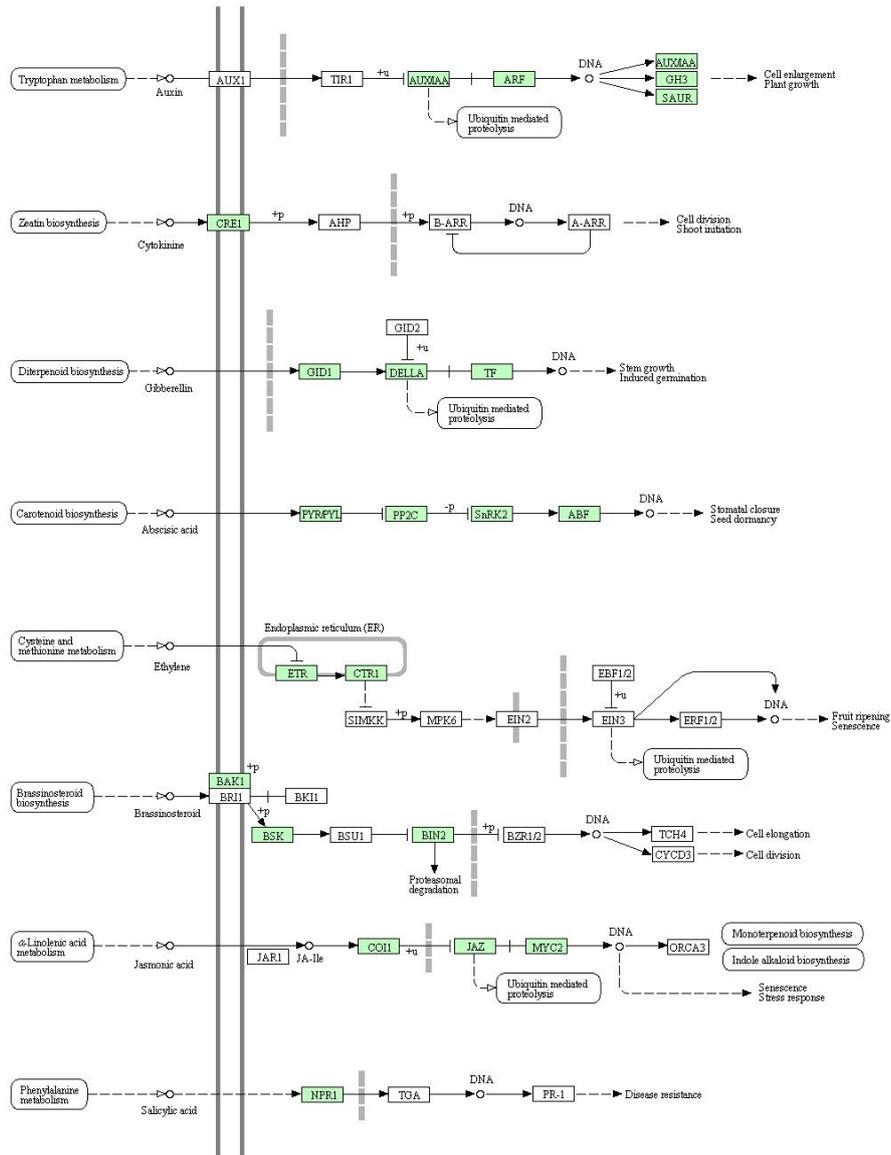
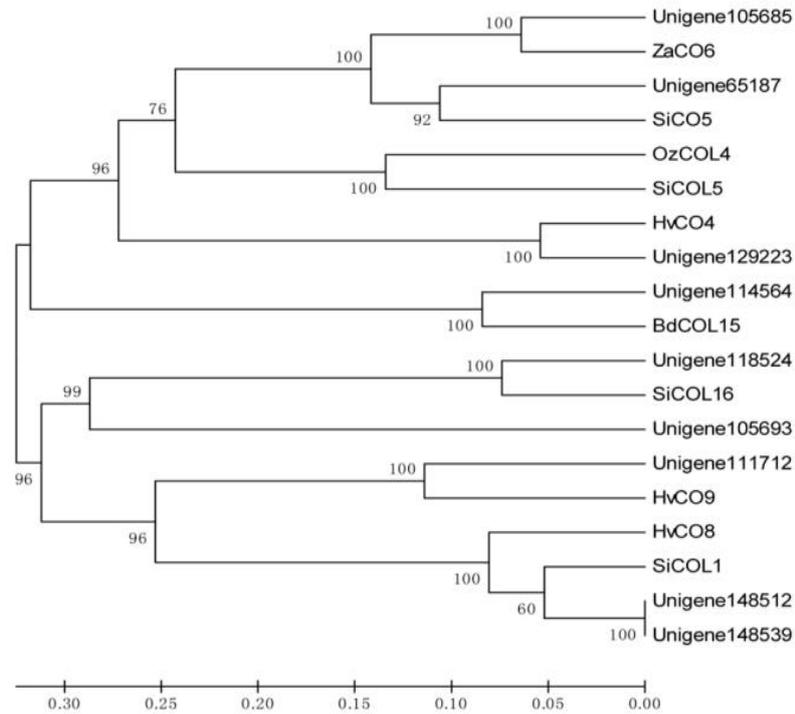


Figure S6. Plant hormone signal transduction for unigenes by KEGG annotation.



**Figure S7. Phylogenetic analysis of the CONSTANS or CONSTANS-like proteins.**

Different plant species (Za: *Zea mays*, Si: *Setaria italic*, Hv: *Hordeum vulgare*, Bd: *Brachypodium distachyon*). The proteins are as follows: ZaCO6 (accession no. NP\_001148229), SiCO5 (accession no. XP\_004976103), HvCO4 (accession no. AAM74069), BdCOL15 (accession no. XP\_003561634), SiCOL16 (accession no. XP\_004982006), HvCO9 (accession no. BAL02998), HvCO8 (accession no. AAL99270), SiCOL1 (accession no. XP\_004973094)