**Supplementary figure legends**

Supplementary Figure S1.Length distribution of HQ unigenes

Supplementary Figure S2. GC content distribution of HQ unigenes

Supplementary Figure S3. EC numbers, to categorize unigenes into 6 EC Classes

Supplementary Figure S4. Validation of expression patterns of 7 randomly selected differentially expressed unigenes (based on FPKM values) using qRT-PCR to the show the similar patterns in both FPKM and qRT-PCR expression values, in blue and red color bar, respectively. The FPKM expression value of leaf tissue has been normalized with qRT-PCR. The respective unigenes id are shown at the top and Y-axis represents relative expression values

Supplementary Figure S5. Volcano and MA plots of DEGs for all 3 possible pair of tissue samples: Flower *vs* Leaf, Flower *vs* Shoot and Leaf *vs* Shoot, respectively, with red dots as significant expression and black ones representing ‘no significant expression’ [FDR=False Discovery Rate; FC=Fold Change]

Supplementary Figure S6. Aclustered heatmap showing the Pearson correlation matrix for pairwise comparison between three tissue samples by comparing the complete transcriptome

Supplementary Figure S7. Screenshot of ClustergeneDB, a database for retrieving information on the unigenes of cluster bean