Addition File 6: Snapshots of the analysis module

Figure S6-1. Snapshots of the analysis page: fetch structure information..................2
Figure S6-2. Snapshots of the analysis page: fetch function information. ..................3
Figure S6-3. Snapshots of the analysis page: fetch expression level information........5
Figure S6-4. Snapshots of the analysis page: enrichment analysis..........................7
Figure S6-5. Snapshots of the list compare page.....................................................9
Figure S6-6. Snapshots of the phylogenetic tree build page..................................10
Figure S6-1. Snapshots of the analysis page: fetch structure information. This snapshot displayed fetching transcript structure information in six genes in *G. hirsutum* (NAU assembly). Genes are: Gh_D11G0676, Gh_D02G0715, Gh_D06G1428, Gh_D10G2193, Gh_A12G2323 and Gh_A01G0120. The fetching results are in exactly the same order as the inputted IDs. (Note: this snapshot hid several columns in the result table in order to show the main ones.)
Figure S6-2. Snapshots of the analysis page: fetch function information. This snapshot displayed fetching associated GO terms in six genes in *G. hirsutum* (NAU assembly). Genes are: Gh_D11G0676, Gh_D02G0715, Gh_D06G1428, Gh_D10G2193, Gh_A12G2323 and Gh_A01G0120. Note that even for genes with no GO terms, they are still listed following the original order. Therefore, it is convenient to fetch different information type separately and then connect them together.
Select experiments (showing partial option only)

List expression level (FPKM) for each gene in selected experiments

Cluster input genes based on their expression atlas in selected experiments
Figure S6-3. Snapshots of the analysis page: fetch expression level information.

This snapshot displayed fetching expression levels (FPKM) in six genes of *G. hirsutum* (NAU assembly) in eight organs. Genes are: Gh_D11G0676, Gh_D02G0715, Gh_D06G1428, Gh_D10G2193, Gh_A12G2323 and Gh_A01G0120. In addition to the result table, CottonFGD will generate a heatmap clustered by the expression patterns for these query genes. The cluster is done by the pheatmap library (https://cran.r-project.org/web/packages/pheatmap/index.html).
Figure S6-4. Snapshots of the analysis page: enrichment analysis. This snapshot displayed doing KEGG pathway enrichment analysis in 96 genes of *G. hirsutum* (NAU assembly) using $P < 0.0001$ as thresholds.
Input two lists

Compare result:
Intersection
Union
Specific

Venn Graph showing count number
Figure S6-5. Snapshots of the list compare page. Note this page only conduct comparisons based on inputted IDs. Therefore, it could be applied to any ID lists instead of restricting on cotton gene IDs.
Figure S6-6. Snapshots of the phylogenetic tree build page. This snapshot
displayed a phylogenetic tree built by six *BZIP60* (Gh_A04G0770, Gh_A04G0769, Gh_D04G0051, Gh_A05G2508, Gh_D05G2786, Gh_D08G0879) and two *BZIP17* (Gh_A13G2071, Gh_D13G0009) genes in *G. hirsutum*.