

Supplementary Figures

Transcriptomics identifies key defense mechanisms in rice resistant to both leaf-feeding and phloem feeding herbivores

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Fig. S1

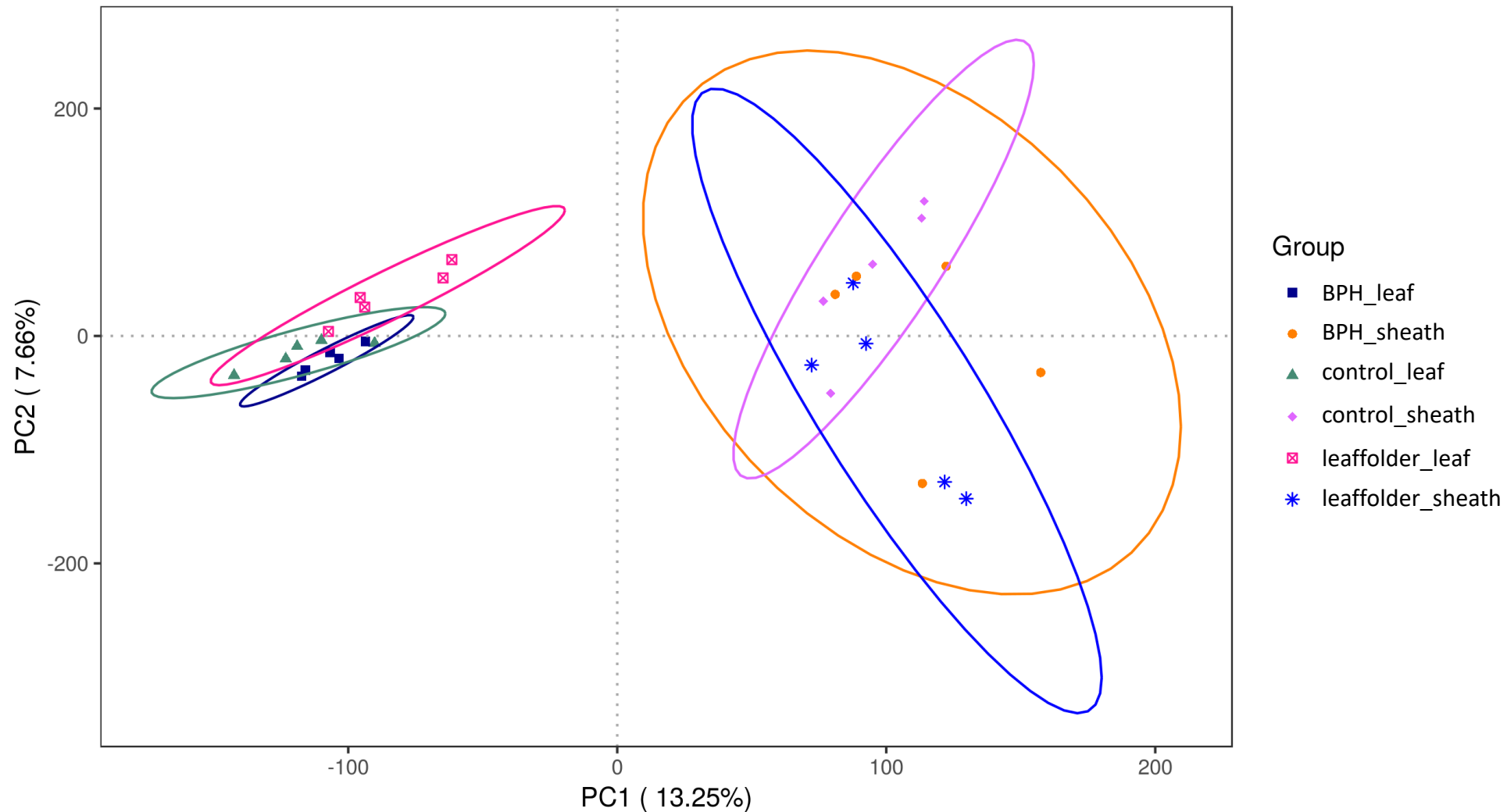
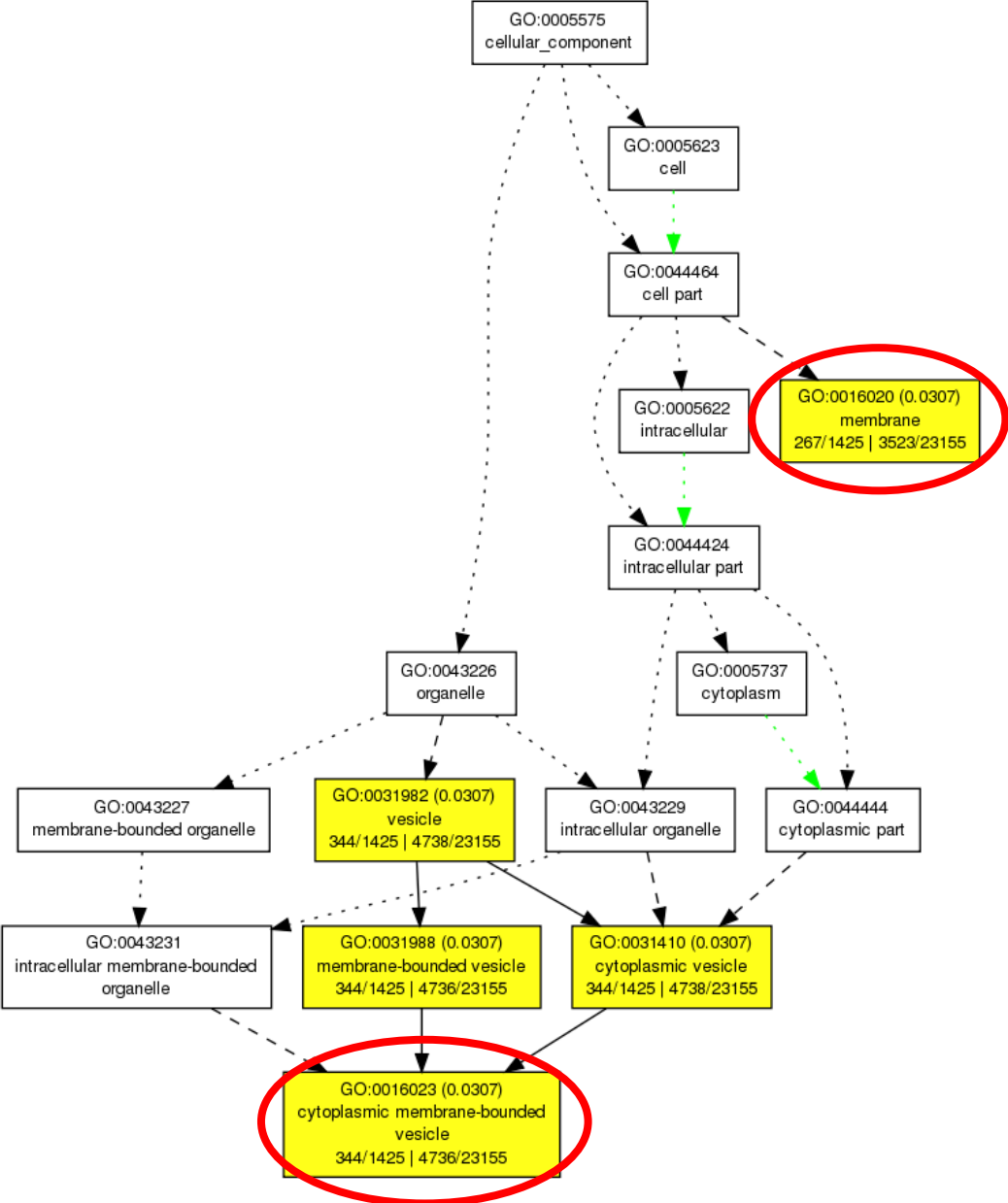
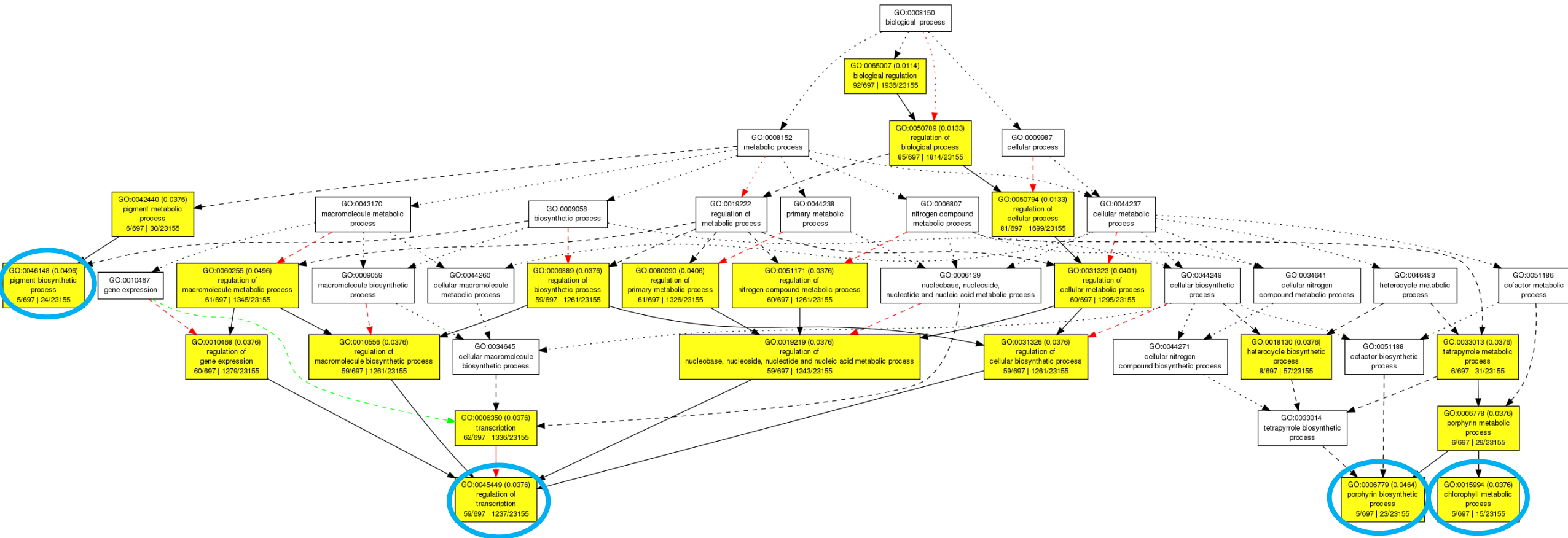


Fig. S1. Principal component analysis (PCA) plot of thirty RNA-Seq samples. The samples consisted of three experimental conditions (control, BPH or leaffolder infestation) and two tissues (leaves, sheaths) with five biological replicates for each combination.

(Cellular component)



b. GO enrichment of downregulated genes in the leaf folder vs control_leaf comparison (Biological process)



c. GO enrichment of upregulated genes in the leaffolder vs control_sheath comparison (Biological process)

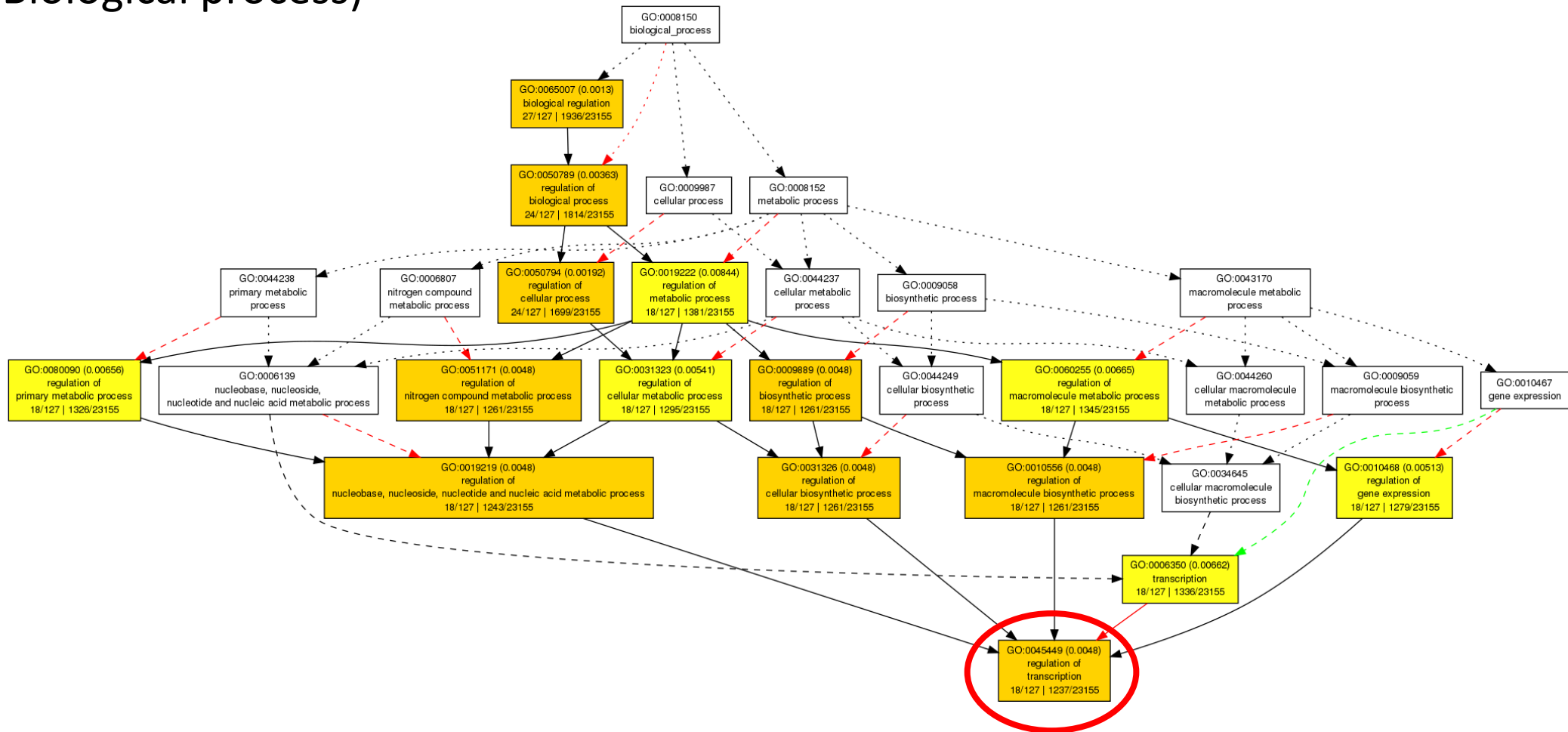
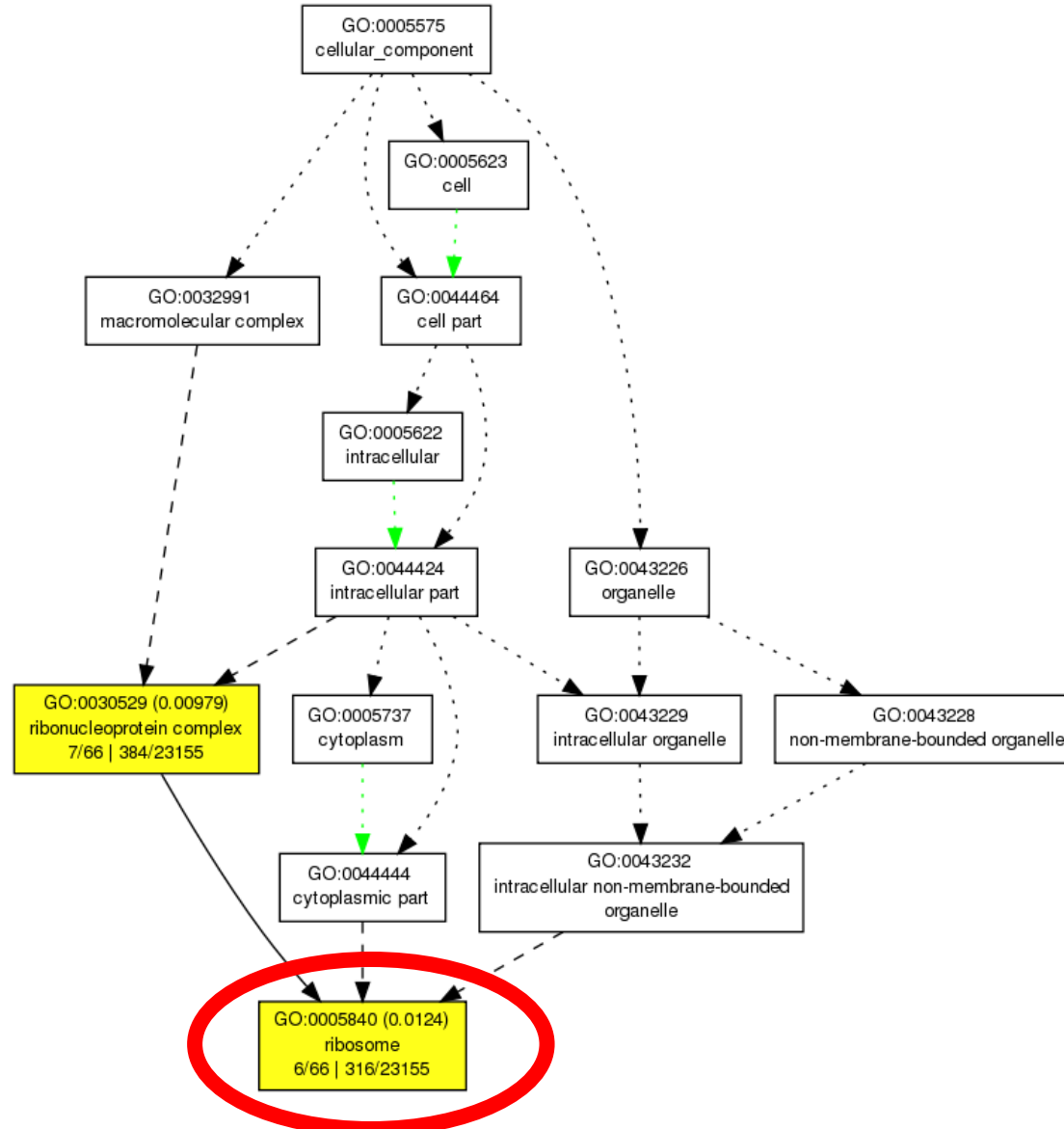


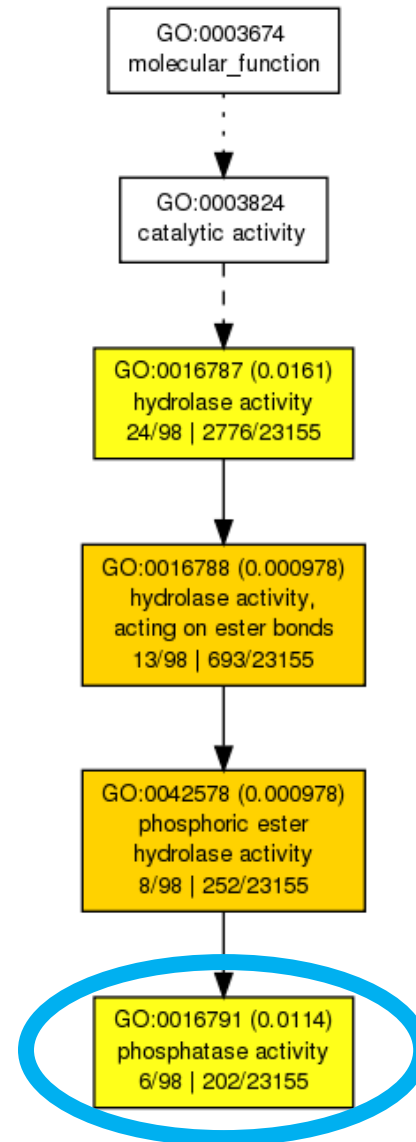
Fig. S2. Shortlisting nonredundant GO terms of leaffolder-responsive DEGs by manually curating the GO hierarchical tree graphs. GO enrichment of **a** upregulated genes in the leaffolder vs control_leaf comparison, **b** downregulated genes in the leaffolder vs control_leaf comparison and **c** upregulated genes in the leaffolder vs control_sheath comparison.

Fig. S3

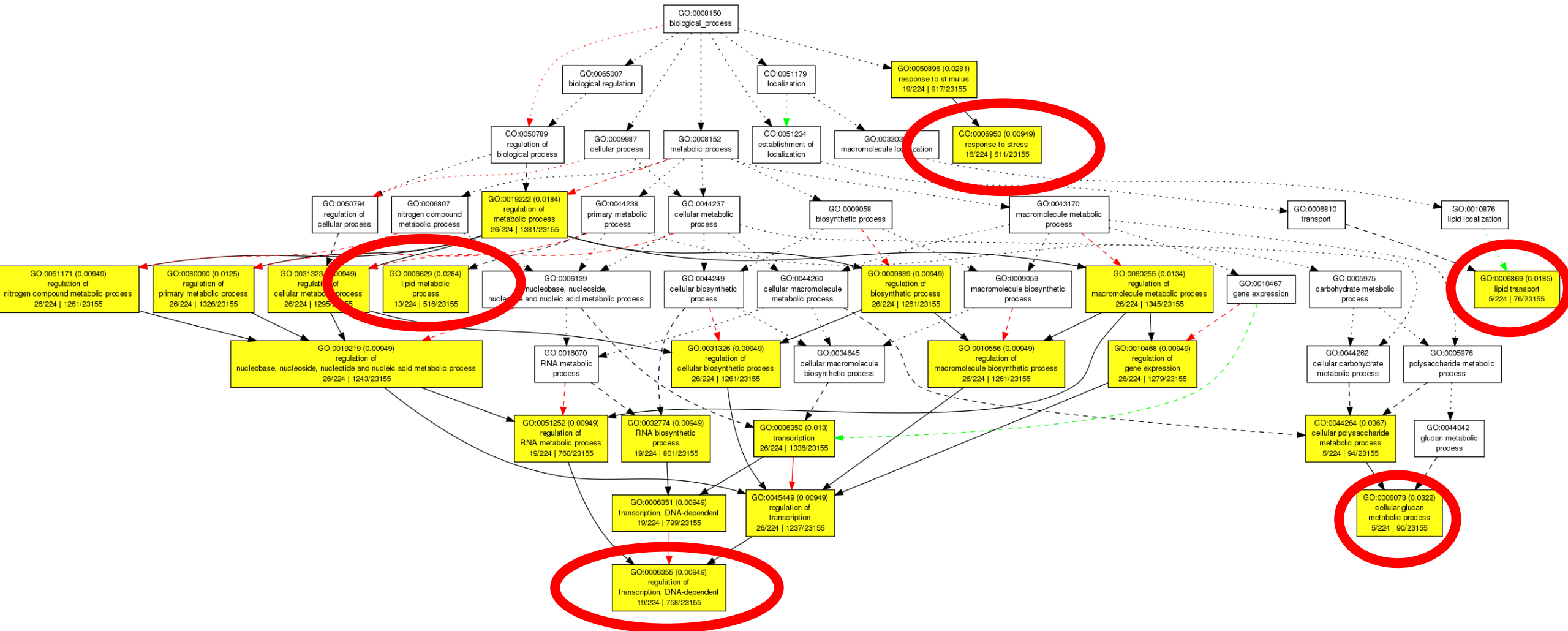
a. GO enrichment of upregulated genes in the BPH vs control_leaf comparison
(Cellular component)



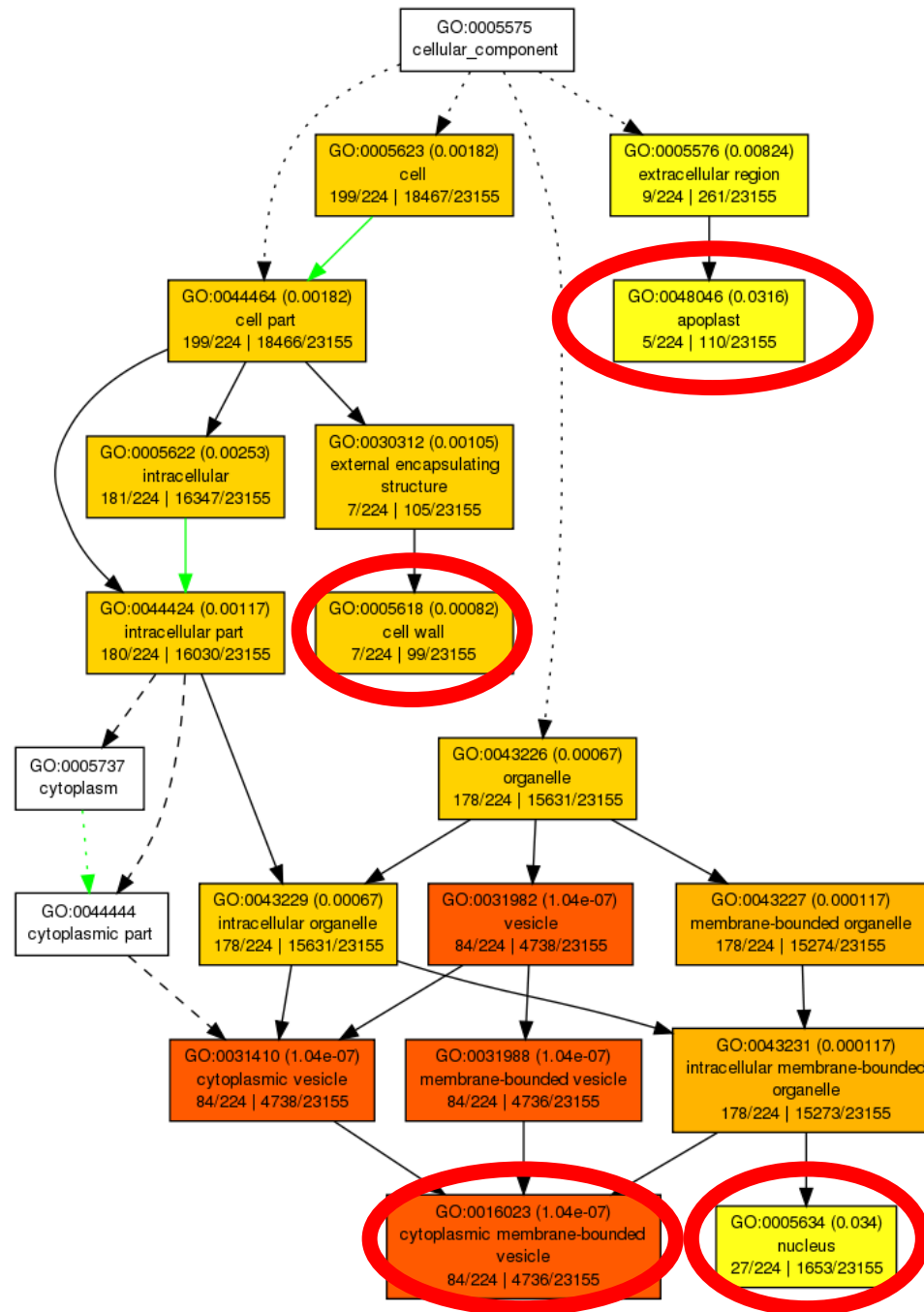
b. GO enrichment of downregulated genes in the BPH vs control_leaf comparison
(Molecular function)



c. GO enrichment of upregulated genes in the BPH vs control_sheath comparison (Biological process)



(Cellular component)



(Molecular function)

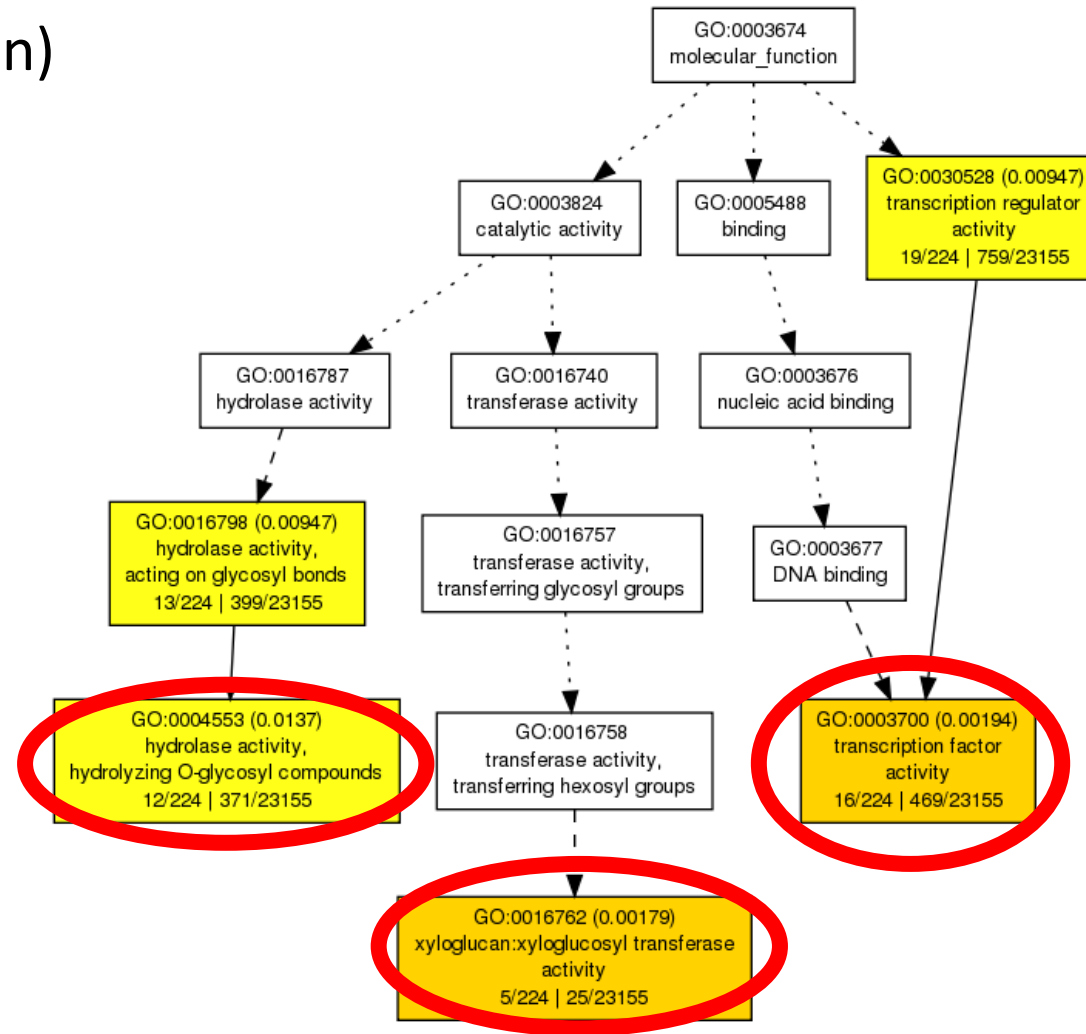


Fig. S3. Shortlisting nonredundant GO terms of BPH-responsive DEGs by manually curating the GO hierarchical tree graphs. GO enrichment of **a** upregulated genes in the BPH vs control_leaf comparison, **b** downregulated genes in the BPH vs control_leaf comparison and **c** upregulated genes in the BPH vs control_sheath comparison.