Supplementary Figures

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

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Fig. S1

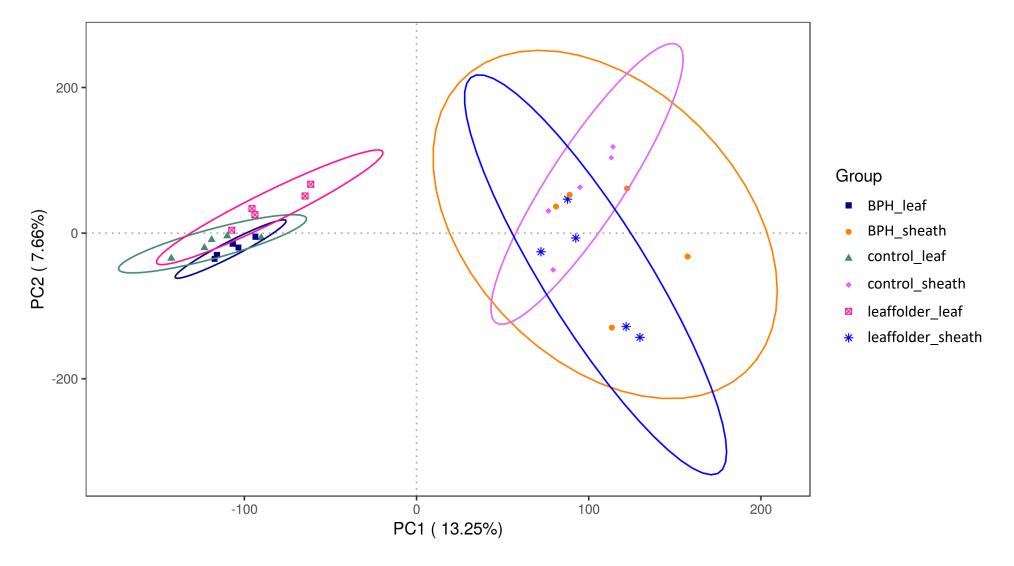
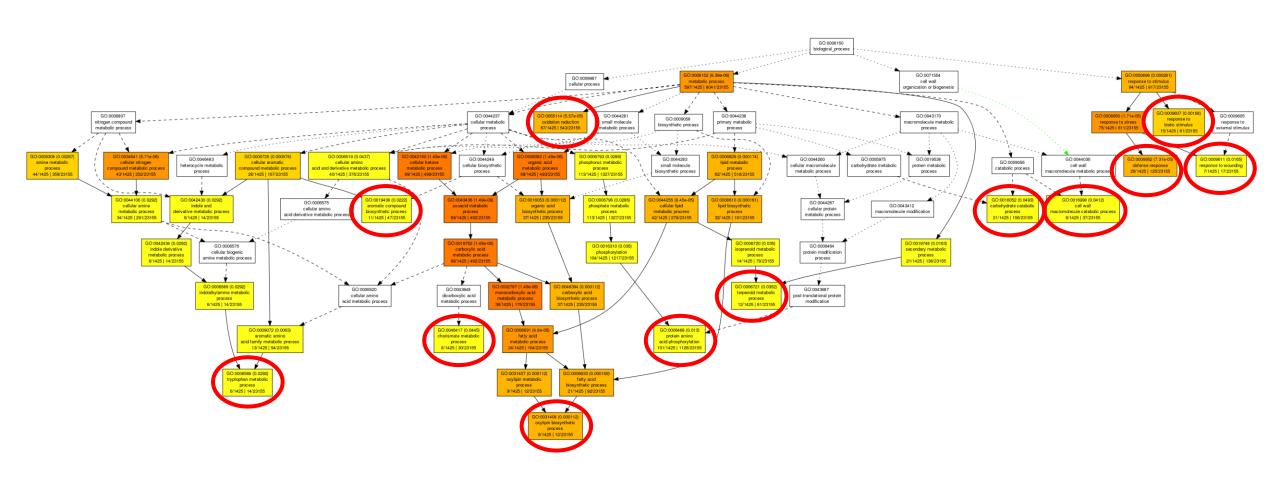


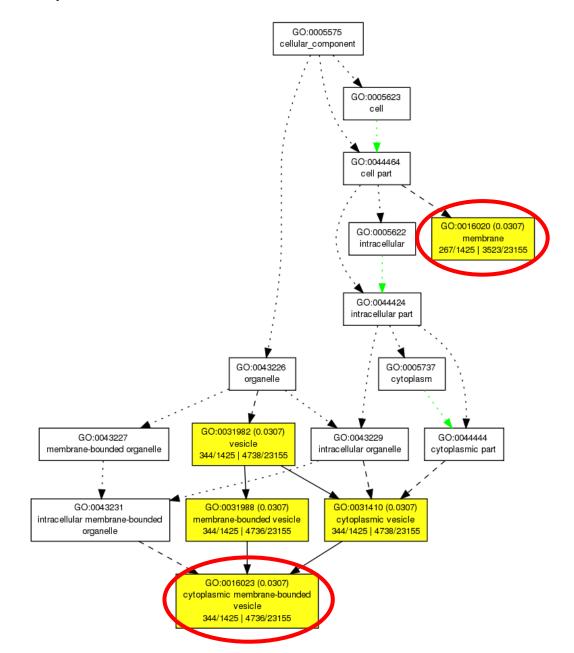
Fig. S1. Principal component analysis (PCA) plot of thirty RNA-Seq samples. The samples consisted of three experimental conditions (control, BPH or leaffolder infestation) and two tissues (leaves, sheaths) with five biological replicates for each combination.

Fig. S2

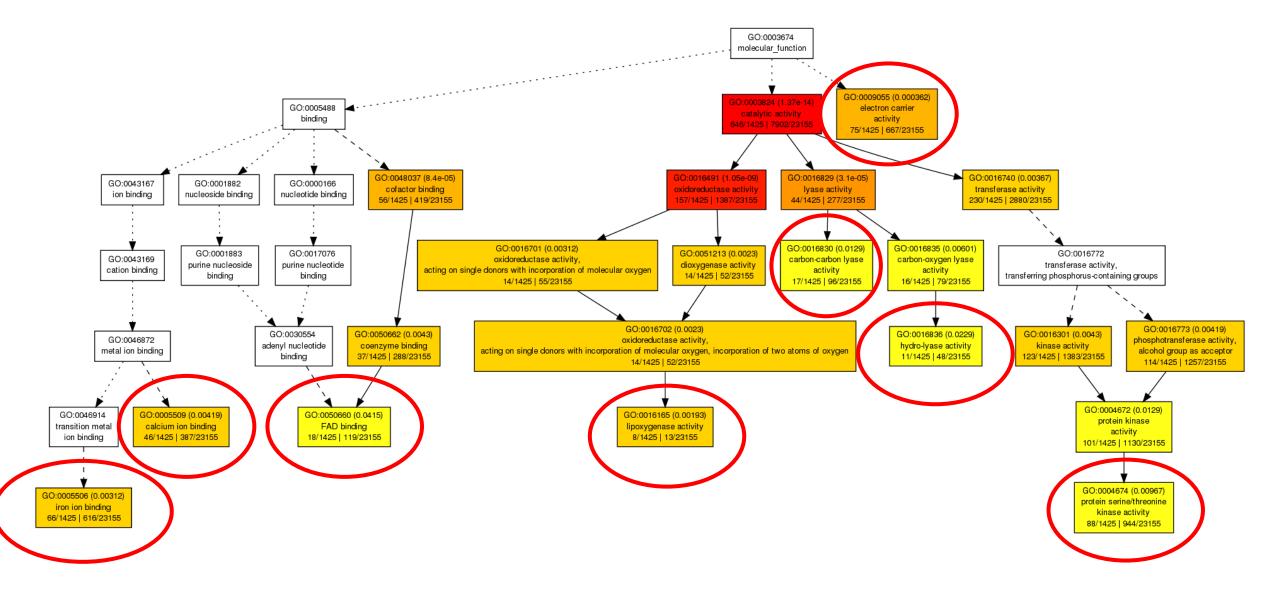
 a. GO enrichment of upregulated genes in the leaffolder vs control_leaf comparison (Biological process)



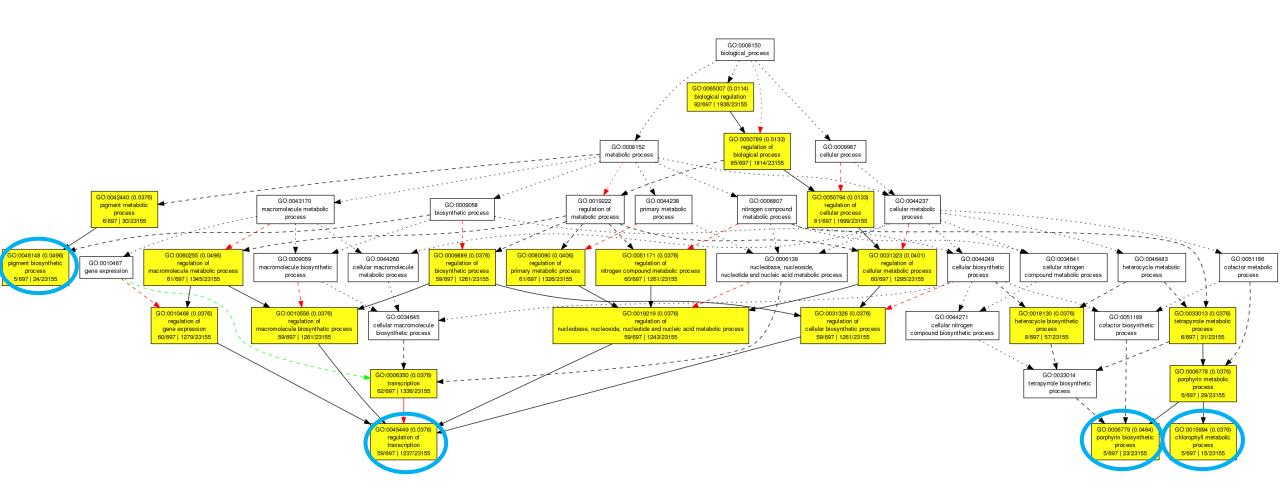
(Cellular component)



(Molecular function)



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



c. GO enrichment of upregulated genes in the leaffolder vs control_sheath comparison

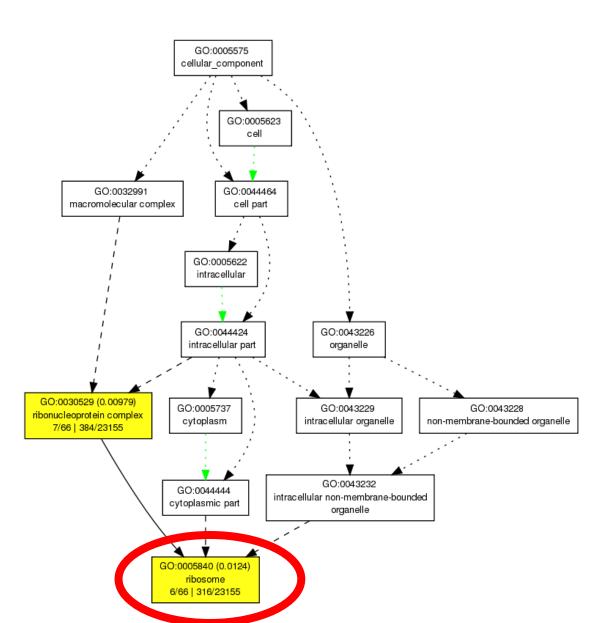
(Biological process) biological_process biological regulation 27/127 | 1936/23155 regulation of GO:0009987 biological process 24/127 | 1814/23155 GO:0019222 (0.00844) GO:0044237 GO:0044238 GO:0006807 regulation of regulation of primary metabolic nitrogen compound cellular metabolic cellular process metabolic process biosynthetic process process metabolic process process 24/127 | 1699/23155 18/127 | 1381/23155 GO:0051171 (0.0048) GO:0031323 (0.00541) O:0009889 (0.0048) GO:0006139 GO:0044249 GO:0044260 regulation of regulation of regulation of regulation of regulation of GO:0010467 nucleobase, nucleoside, cellular biosyntheti ellular macromolecule nacromolecule biosynthetic orimary metabolic process ogen compound metabolic process ellular metabolic process piosynthetic process acromolecule metabolic process gene expression nucleotide and nucleic acid metabolic process metabolic process process process 18/127 | 1326/23155 18/127 | 1261/23155 18/127 | 1295/23155 18/127 | 1261/23155 18/127 | 1345/23155 GO:0019219 (0.0048) GO:0031326 (0.0048) GO:0010556 (0.0048 :0010468 (0.00513) GO:0034645 regulation of cellular macromolecule ucleobase, nucleoside, nucleotide and nucleic acid metabolic process ellular biosynthetic process nacromolecule biosynthetic process gene expression biosynthetic process 18/127 | 1243/23155 18/127 | 1261/23155 18/127 | 1261/23155 18/127 | 1279/23155 18/127 | 1336/23155 regulation of 18/127 | 1237/23155

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.

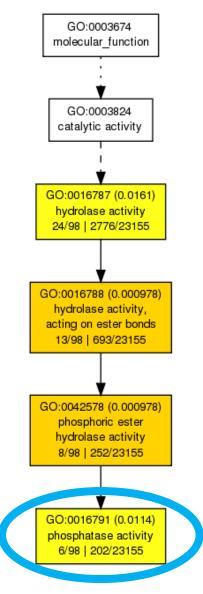
Fig. S3

a. GO enrichment of upregulated genes in the BPH vs control_leaf comparison

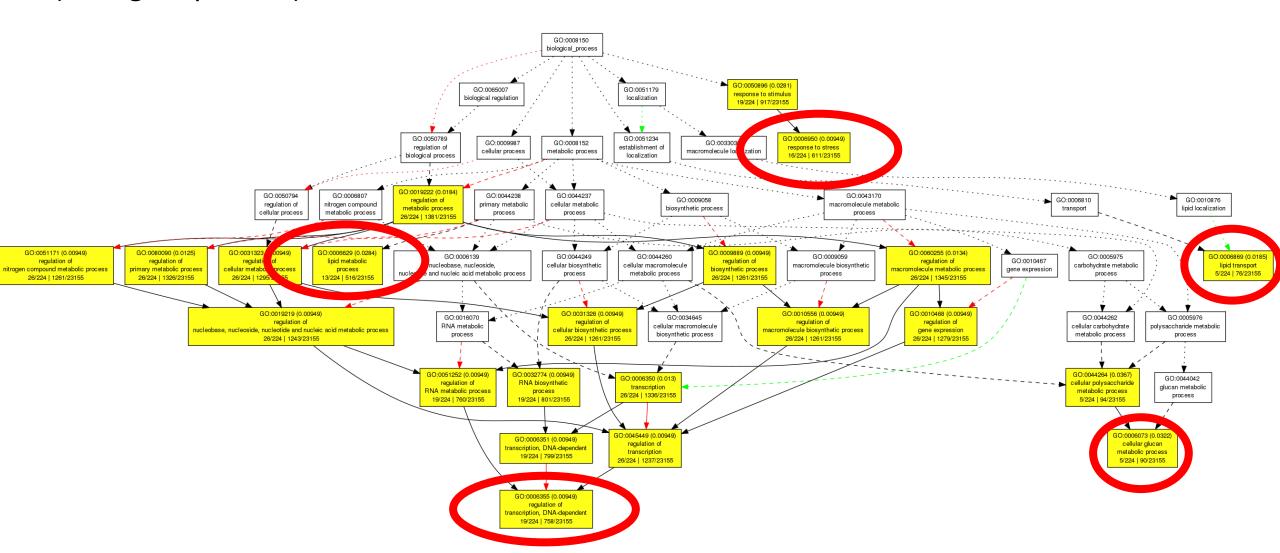
(Cellular component)



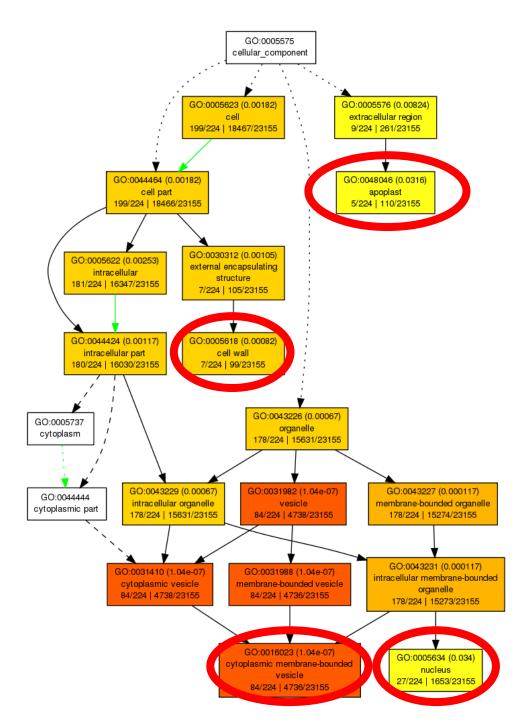
b. GO enrichment of downregulated genes in the BPH vs control_leaf comparison (Molecular function)



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



(Cellular component)



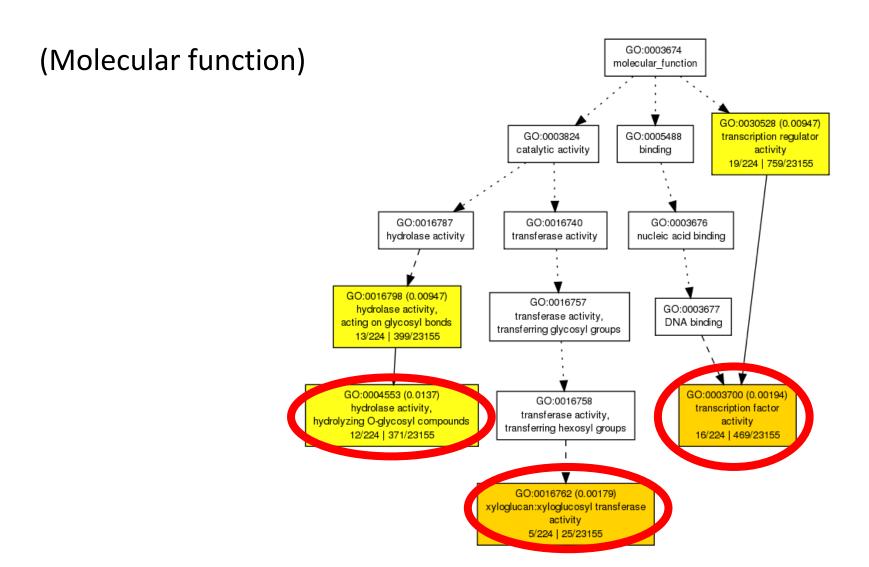


Fig. S3. Shortlisting nonredundant GO terms of BPH-responsive DEGs by manually curating the GO hierarchical tree graphs. GO enrichment of **a** upregulated genes in the BPH vs control_leaf comparison, **b** downregulated genes in the BPH vs control_leaf comparison and **c** upregulated genes in the BPH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