Figure S1: Sequence length distribution of non-redundant (NR) unique unitranscript sequences after sequencing and de novo assembly of *R. stylosa* leaf transcriptome. The X-axis represents the length range bins in bp. The Y-axis represents the frequency of transcripts in each bin.
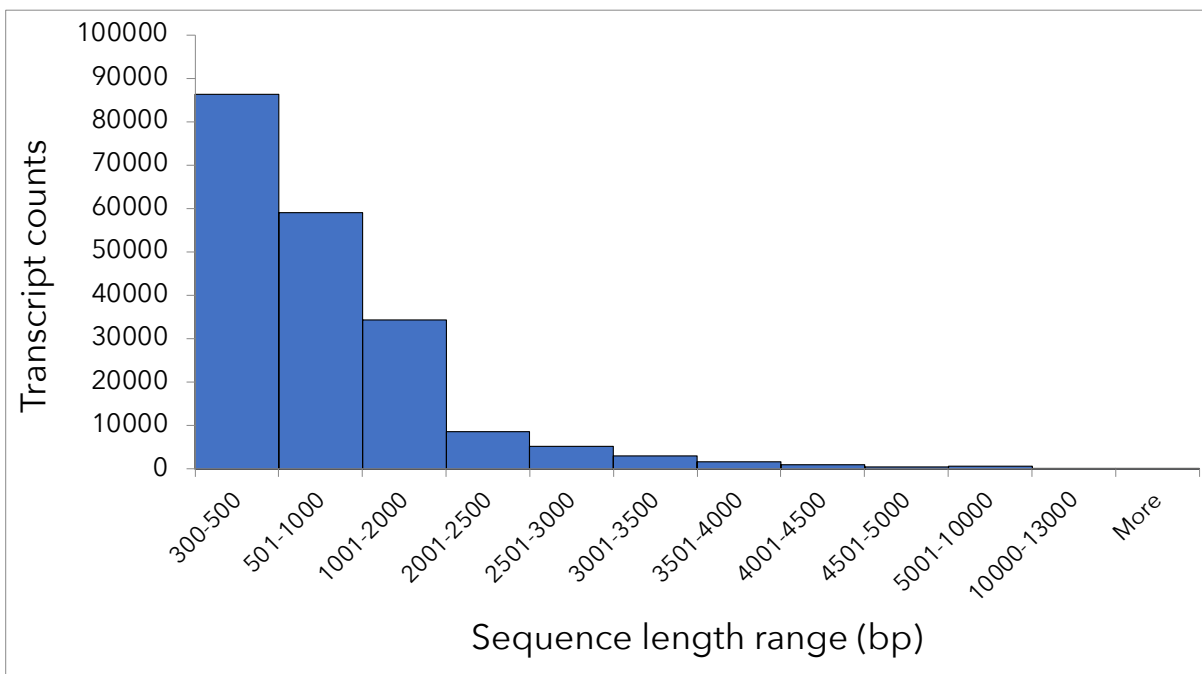
Figure S2. BLAST Top-Hits species distribution for *R. stylosa* leaf transcriptome when compared with nr database (BLASTx).
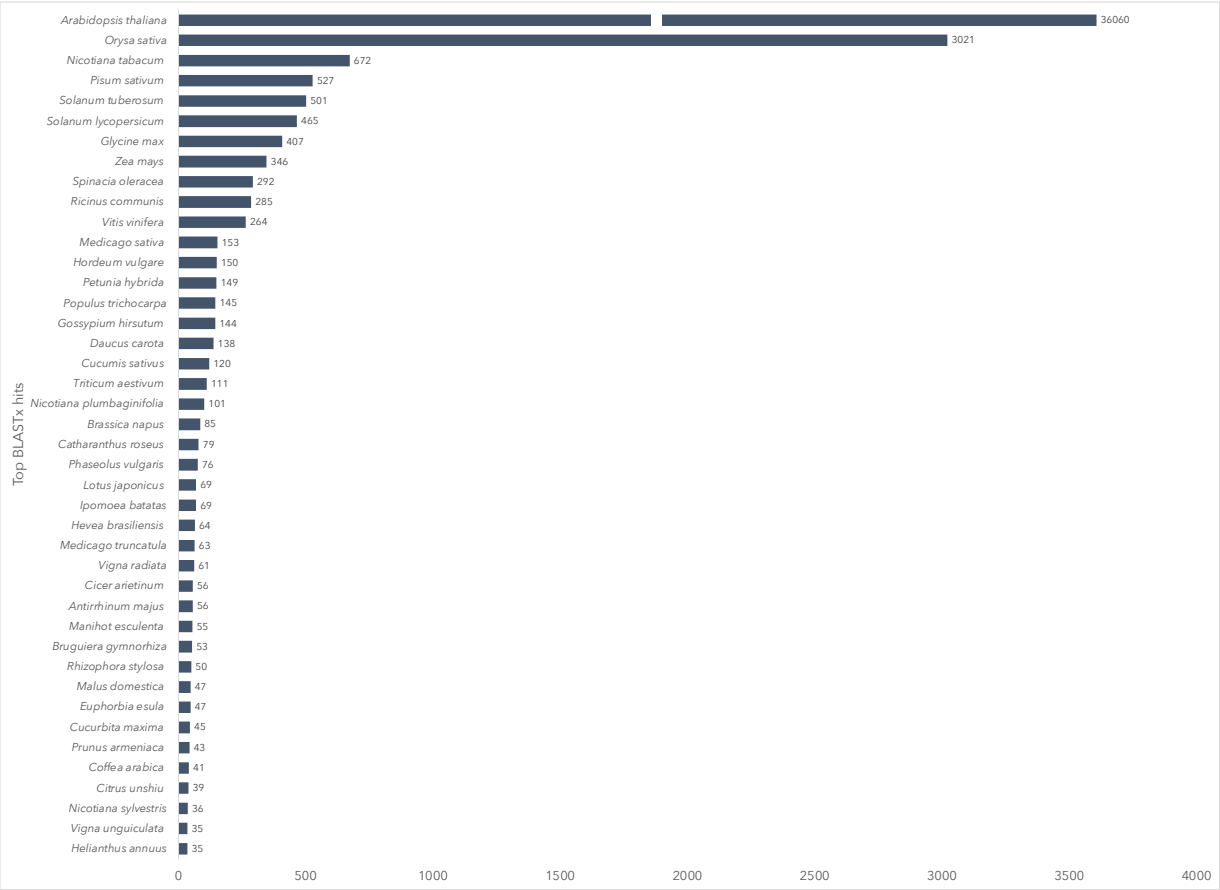
Figure S3. BLAST Top-Hits species distribution for *R. stylosa* leaf transcriptome when compared with Swiss-Prot database (BLASTp).

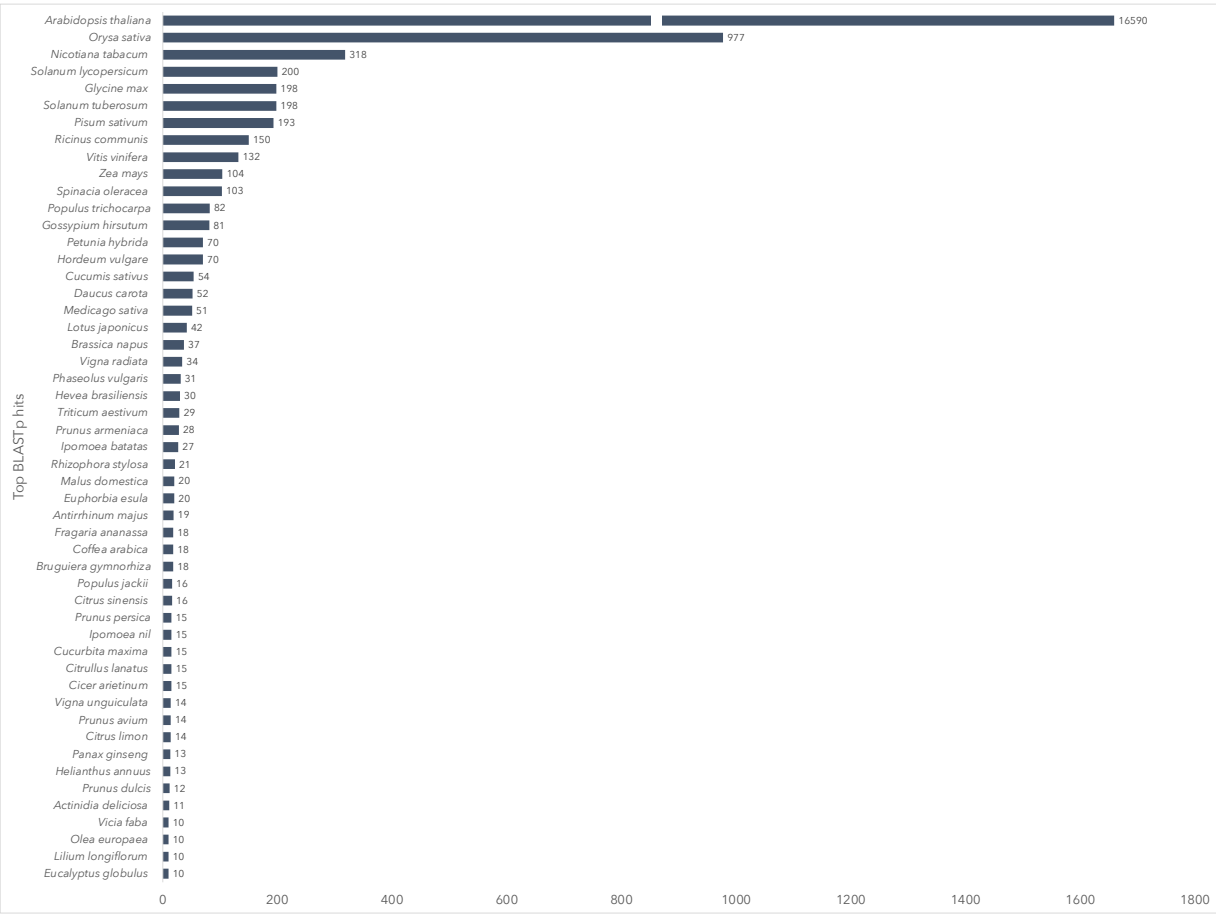| Species	Top BLASTp hits
Arabidopsis thaliana	16590
Orysa sativa	977
Nicotiana tabacum	318
Solanum lycopersicum	200
Glycine max	198
Solanum tuberosum	198
Pisum sativum	193
Ricinus communis	150
Vitis vinifera	132
Zea mays	104
Spinacia oleracea	103
Populus trichocarpa	82
Gossypium hirsutum	81
Petunia hybrida	70
Hordeum vulgare	70
Cucumis sativus	54
Daucus carota	52
Medicago sativa	51
Lotus japonicus	42
Brassica napus	37
Vigna radiata	34
Phaseolus vulgaris	31
Hevea brasiliensis	30
Triticum aestivum	29
Prunus armeniaca	28
Ipomoea batatas	27
Rhizophora stylosa	21
Malus domestica	20
Euphorbia esula	20
Antirrhinum majus	19
Fragaria ananassa	18
Coffea arabica	18
Bruguiera gymnorhiza	18
Populus jackii	16
Citrus sinensis	16
Prunus persica	15
Ipomoea nil	15
Cucurbita maxima	15
Citrullus lanatus	15
Cicer arietinum	15
Vigna unguiculata	14
Prunus avium	14
Citrus limon	14
Panax ginseng	13
Helianthus annuus	13
Prunus dulcis	12
Actinidia deliciosa	11
Vicia faba	10
Olea europaea	10
Lilium longiflorum	10
Eucalyptus globulus	10

Figure S4. Gene ontology (GO) functional classification of *R. stylosa* leaf transcriptome BLAST Top-Hits species distribution when compared with nr database. Histograms of the frequency of transcripts annotated to specific GO categories; biological process, cellular components, and molecular functions are represented by blue, green, and orange bars, respectively.
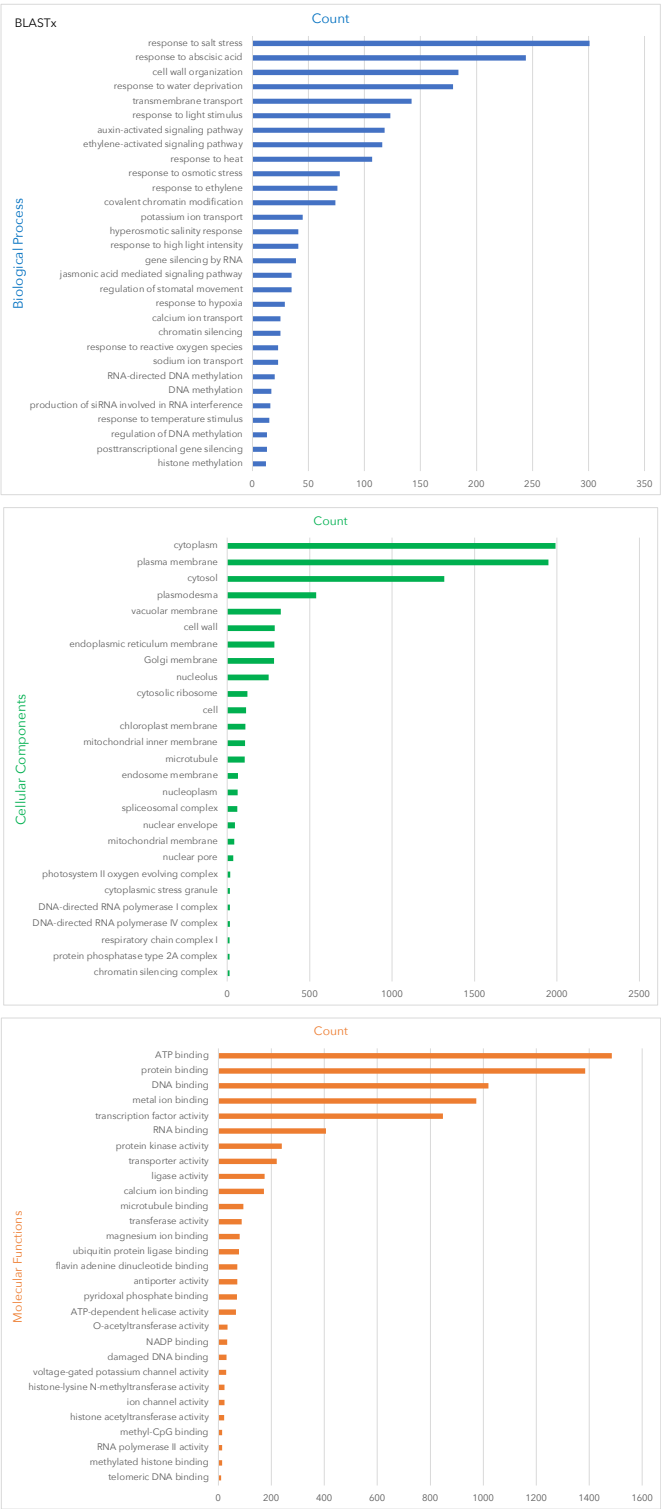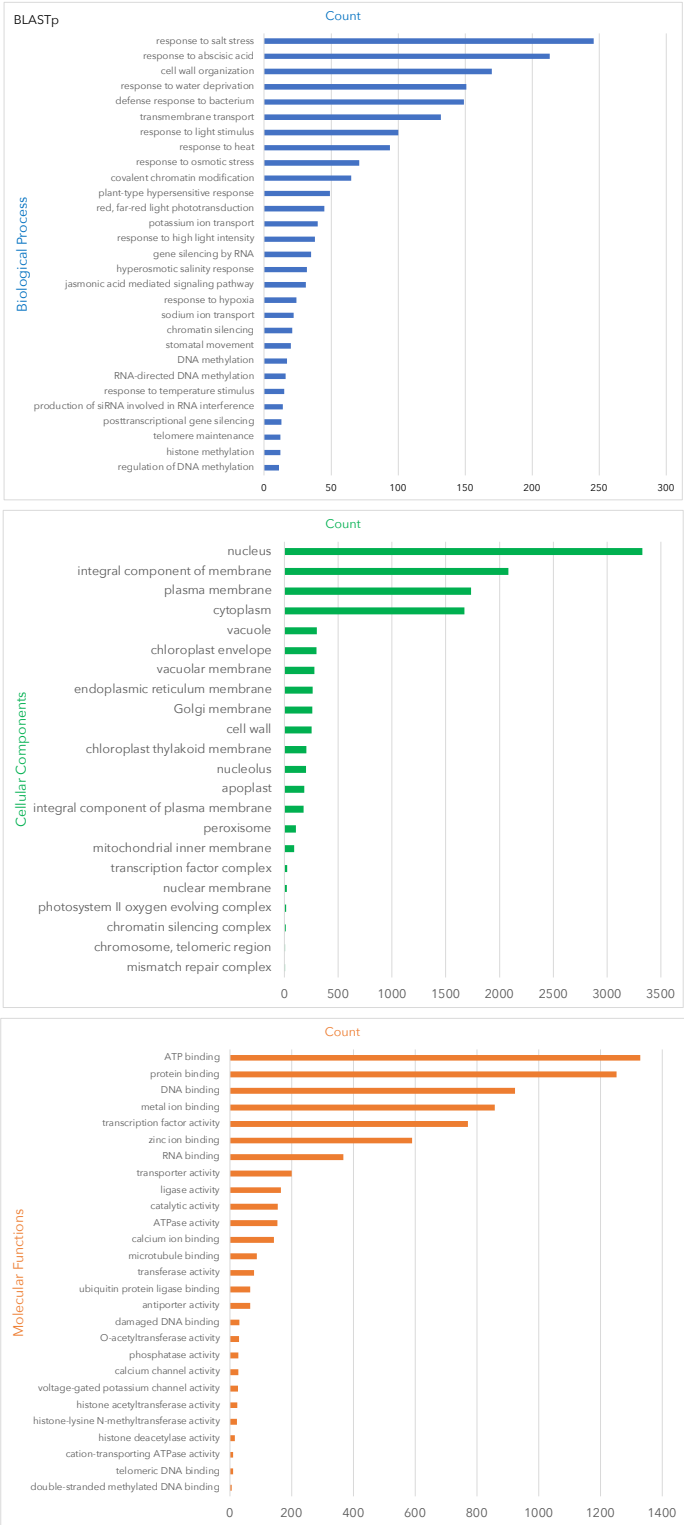
Figure S5. Gene ontology (GO) functional classification of *R. stylosa* leaf transcriptome BLAST Top-Hits species distribution when compared with Swiss-Prot database. Histograms of the frequency of transcripts annotated to specific GO categories; biological process, cellular components, and molecular functions are represented by blue, green, and orange bars, respectively.
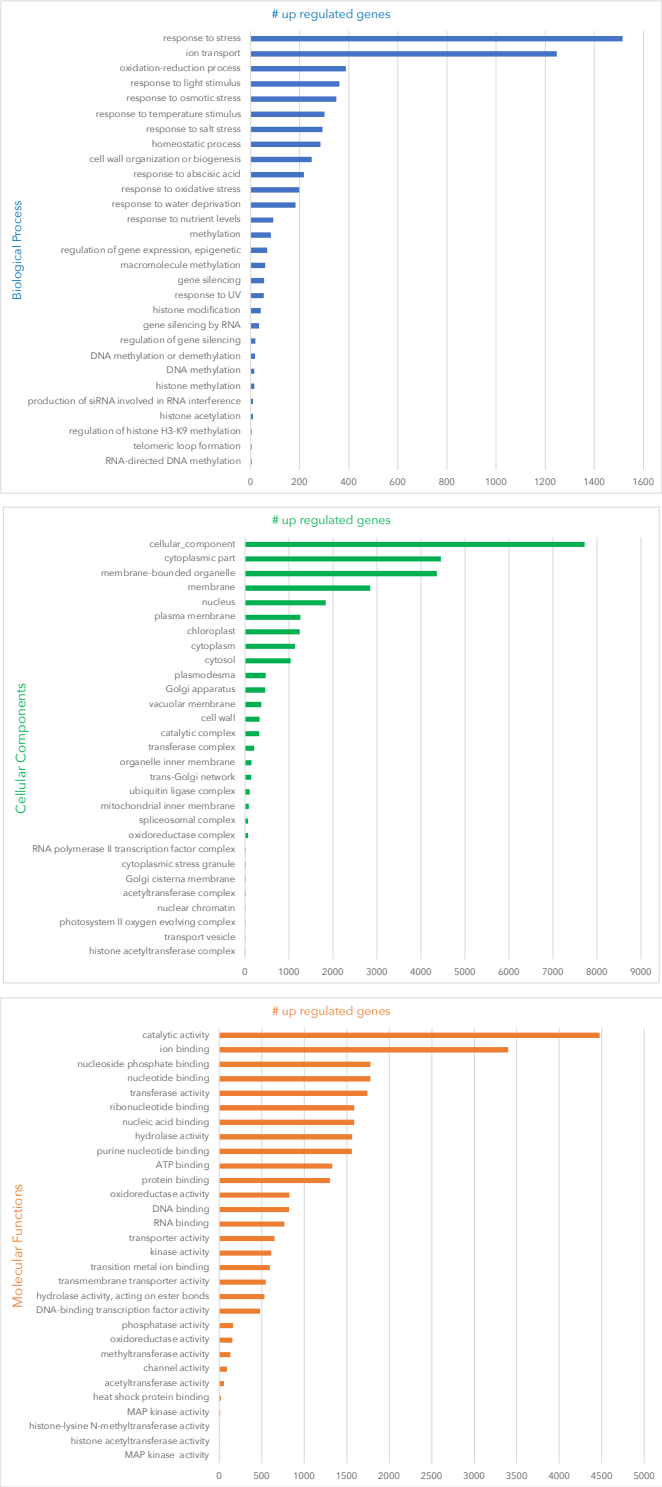
Figure S6. Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis of *R. stylosa* leaf transcriptome BLAST Top-Hits species distribution when compared with nr database (top) and Swiss-Prot database (bottom). Histograms of the frequency of transcripts annotated to KEGG pathways.

Figure S7. Biological process category of Gene ontology (GO) functional classification of upregulated transcripts BLAST Top-Hits species distribution when compared with Swiss-Prot database. Histograms of the frequency of transcripts annotated to specific GO categories; biological process, cellular components, and molecular functions are represented by blue, green and orange bars, respectively.
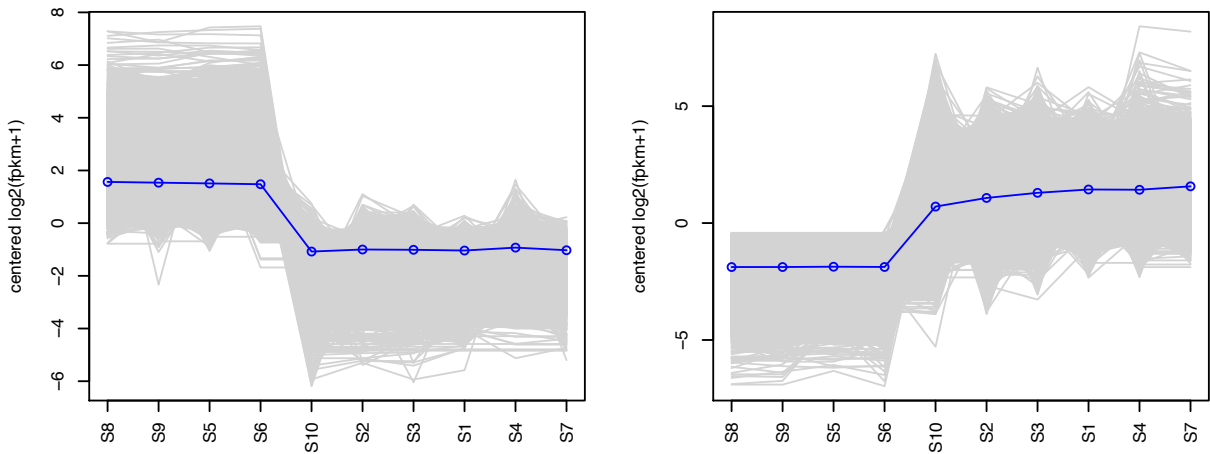
Figure S8. Transcript clusters extracted from the hierarchical clustering with R. X-axis: samples; y-axis: median-cantered log2(FPKM). Grey lines, individual transcripts; blue line, average expression values per cluster.

subcluster_1_log2_medianCentered_fpkm.matrix, 24512 tr

subcluster_2_log2_medianCentered_fpkm.matrix, 15676 tr

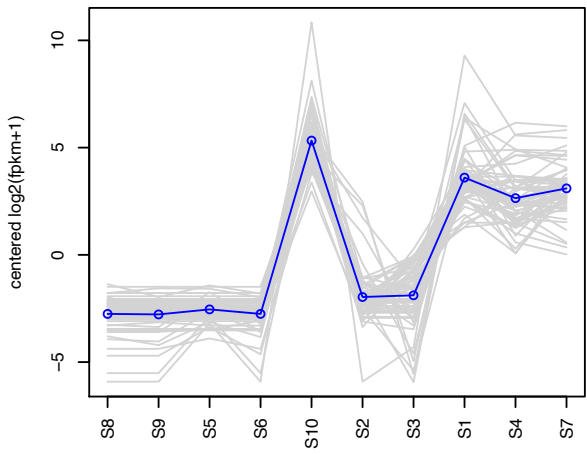**subcluster_3_log2_medianCentered_fpkm.matrix, 65 trar**

Figure S9. Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis of upregulated (Top) and downregulated (bottom) transcripts in oceanside samples of *R. stylosa*.
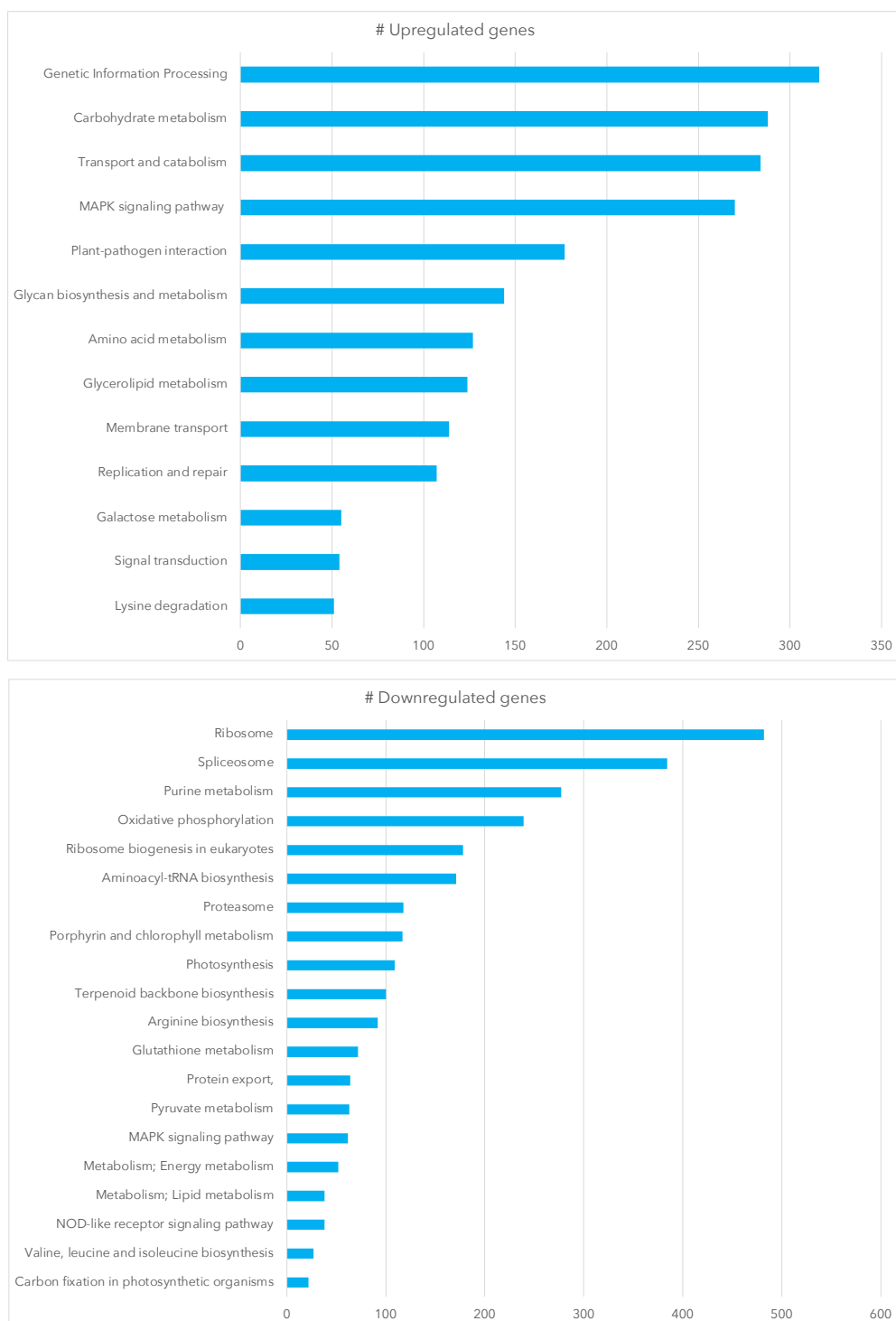
Figure S10. Comparison of BLAST Top-Hits species distribution for *R. stylosa* (green) and *B. gymnorhiza* (orange) leaf transcriptome when compared with nr database (BLASTx).