

Table S2. List of the significant results ($p < 0.01$) obtained from the enrichment gene ontology (GO) analysis of the DEGs. Only categories with more than five annotated genes are considered.

Total DEGs (Biological process)						
	GO.ID	Term	Annotated	Significant	Expected	classicFisher
1	GO:0010468	regulation of gene expression	1025	9	3.52	0.0071
2	GO:0060255	regulation of macromolecule metabolic process	1057	9	3.63	0.0086
3	GO:0019222	regulation of metabolic process	1076	9	3.69	0.0096
Up-regulated DEGs (Biological process)						
	GO.ID	Term	Annotated	Significant	Expected	classicFisher
1	GO:0019438	aromatic compound biosynthetic process	1389	9	3.66	0.008
2	GO:0018130	heterocycle biosynthetic process	1407	9	3.71	0.0087
Total DEGs (Molecular function)						
	GO.ID	Term	Annotated	Significant	Expected	classicFisher
1	GO:0001071	nucleic acid binding transcription factor	513	7	1.93	0.0031
2	GO:0003700	transcription factor activity, sequence-specific	513	7	1.93	0.0031
3	GO:0008378	galactosyltransferase activity	30	2	0.11	0.0057
Up-regulated DEGs (Molecular function)						
	GO.ID	Term	Annotated	Significant	Expected	classicFisher
2	GO:0001071	nucleic acid binding transcription factor	513	6	1.52	0.004
3	GO:0003700	transcription factor activity, sequence-specific	513	6	1.52	0.004
Down-regulated DEGs (Molecular function)						
	GO.ID	Term	Annotated	Significant	Expected	classicFisher
1	GO:0000287	magnesium ion binding	128	2	0.1	0.0045
2	GO:0005337	nucleoside transmembrane transporter activity	7	1	0.01	0.0055
3	GO:0015932	nucleobase-containing compound transmembrane	7	1	0.01	0.0055
4	GO:1901505	carbohydrate derivative transporter activity	12	1	0.01	0.0095