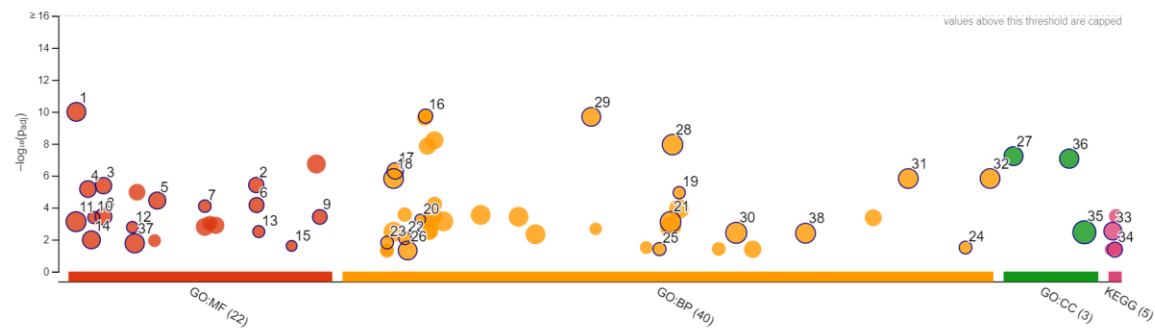


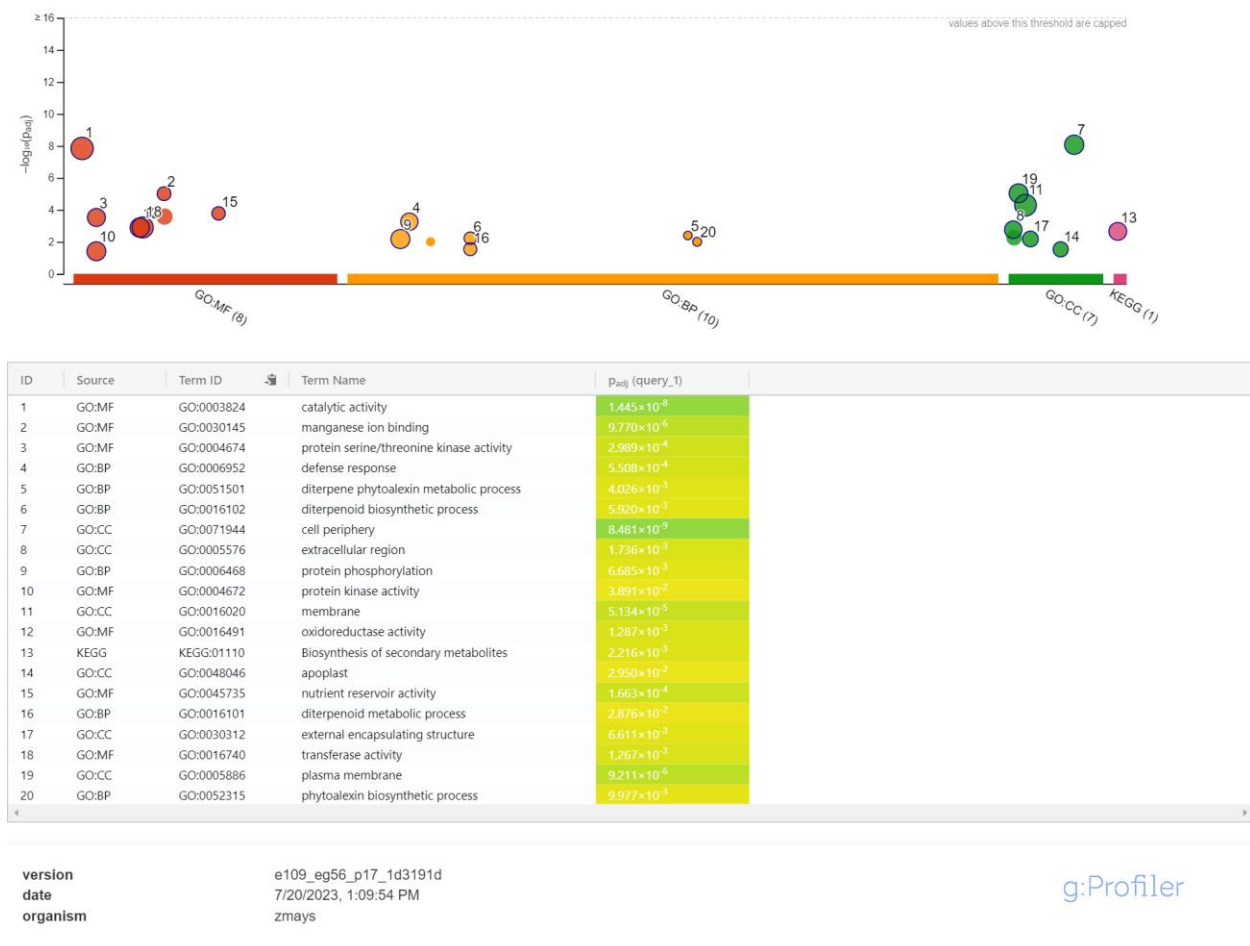


ID	Source	Term ID	Term Name	p _{adj} (query_1)
1	GO:MF	GO:0003700	DNA-binding transcription factor activity	1.014×10 ⁻¹⁰
2	GO:MF	GO:0051082	unfolded protein binding	3.842×10 ⁻⁶
3	GO:MF	GO:0005509	calcium ion binding	4.210×10 ⁻⁶
4	GO:MF	GO:0004497	monooxygenase activity	6.819×10 ⁻⁶
5	GO:MF	GO:0020037	heme binding	3.591×10 ⁻⁵
6	GO:MF	GO:0051213	dioxygenase activity	6.898×10 ⁻⁵
7	GO:MF	GO:0043621	protein self-association	8.052×10 ⁻⁵
8	GO:MF	GO:0005506	iron ion binding	3.634×10 ⁻⁴
9	GO:MF	GO:0140662	ATP-dependent protein folding chaperone	3.798×10 ⁻⁴
10	GO:MF	GO:0004805	trehalose-phosphatase activity	4.155×10 ⁻⁴
11	GO:MF	GO:0003677	DNA binding	7.555×10 ⁻⁴
12	GO:MF	GO:0016160	amylase activity	1.687×10 ⁻³
13	GO:MF	GO:0051787	misfolded protein binding	3.149×10 ⁻³
14	GO:MF	GO:0004674	protein serine/threonine kinase activity	1.035×10 ⁻²
15	GO:MF	GO:0102229	amylopectin maltohydrolase activity	2.481×10 ⁻²
16	GO:BP	GO:0009408	response to heat	1.861×10 ⁻¹⁰
17	GO:BP	GO:0006457	protein folding	4.990×10 ⁻⁷
18	GO:BP	GO:0006355	regulation of DNA-templated transcription	1.512×10 ⁻⁶
19	GO:BP	GO:0051259	protein complex oligomerization	1.154×10 ⁻⁵
20	GO:BP	GO:0009065	glutamine family amino acid catabolic process	5.459×10 ⁻⁴
21	GO:BP	GO:0050794	regulation of cellular process	7.781×10 ⁻⁴
22	GO:BP	GO:0006986	response to unfolded protein	8.067×10 ⁻³
23	GO:BP	GO:0005991	trehalose metabolic process	1.528×10 ⁻²
24	GO:BP	GO:1990961	xenobiotic detoxification by transmembrane expor...	3.146×10 ⁻²
25	GO:BP	GO:0048511	rhythmic process	3.933×10 ⁻²
26	GO:BP	GO:0007154	cell communication	4.835×10 ⁻²
27	GO:CC	GO:0005886	plasma membrane	5.965×10 ⁻⁸
28	GO:BP	GO:0050896	response to stimulus	1.138×10 ⁻⁸
29	GO:BP	GO:0042221	response to chemical	2.074×10 ⁻¹⁰
30	GO:BP	GO:0065007	biological regulation	3.754×10 ⁻³
31	GO:BP	GO:1903506	regulation of nucleic acid-templated transcription	1.512×10 ⁻⁶
32	GO:BP	GO:2001141	regulation of RNA biosynthetic process	1.512×10 ⁻⁶
33	KEGG	KEGG:01110	Biosynthesis of secondary metabolites	2.943×10 ⁻³
34	KEGG	KEGG:04141	Protein processing in endoplasmic reticulum	4.203×10 ⁻²
35	GO:CC	GO:0110165	cellular anatomical entity	3.482×10 ⁻³
36	GO:CC	GO:0071944	cell periphery	8.587×10 ⁻⁸
37	GO:MF	GO:0016491	oxidoreductase activity	1.693×10 ⁻²
38	GO:BP	GO:0097659	nucleic acid-templated transcription	3.977×10 ⁻³

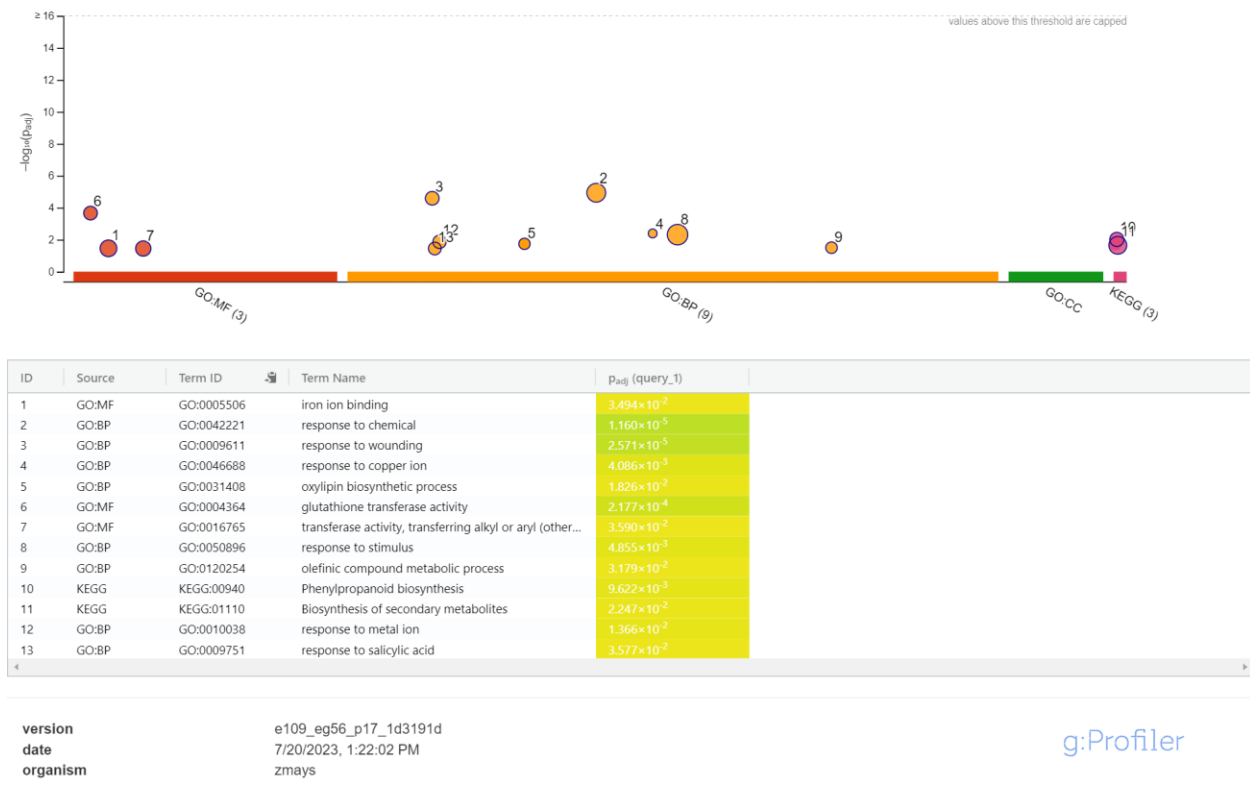
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date 7/20/2023, 12:54:05 PM
organism zmay

g:Profiler

Supplementary figure 1. GO enrichment analysis of the abiotic DEGs using g: Profiler



Supplementary figure 2. GO enrichment analysis of the biotic DEGs using g: Profiler



Supplementary figure 3. GO enrichment analysis of the co-DEGs using g: Profiler