

Supplementary Figure: 3 :Snapshot of SEACOMPARE. It is Cross comparison of Singular Enrichment Analysis (SEA) of total DETs across all 6 time points. Top panel

AGRI90 *GO Analysis Toolkit and Database for Agricultural Community*

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[Suppress this table]

				CM						0hr		12hr		24hr		48hr		120hr		240hr	
GO Information				ID:535266206						ID:743244534		ID:803595330		ID:695983202		ID:340048613		ID:207254892			
No	GO Term	Onto	Description	1	2	3	4	5	6	FDR	Num	FDR	Num	FDR	Num	FDR	Num	FDR	Num	FDR	Num
1	GO:0010200	P	response to chitin							4.1e-09	24	4.2e-05	16	2.3e-07	21	1e-09	22	1.7e-05	17	4.1e-09	22
2	GO:0009743	P	response to carbohydrate stimulus							1.2e-07	27	0.00074	18	1.4e-06	24	2.6e-09	26	8.9e-05	19	5.4e-09	27
3	GO:0009889	P	regulation of biosynthetic process							1.8e-07	90	3e-07	85	1.8e-07	92	1e-09	86	8.9e-05	67	6.5e-12	100
4	GO:0031326	P	regulation of cellular biosynthetic process							1.8e-07	90	3e-07	85	1.8e-07	92	1e-09	86	8.9e-05	67	6.5e-12	100
5	GO:0031323	P	regulation of cellular metabolic process							1.8e-07	95	5.1e-07	87	4.3e-07	94	1e-09	90	0.00033	68	2.7e-11	102
6	GO:0010556	P	regulation of macromolecule biosynthetic process							2.2e-07	88	3e-07	83	1.8e-07	90	1.1e-09	84	8.9e-05	66	7.2e-12	98
7	GO:0019219	P	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process							2.2e-07	88	4.6e-07	82	2.7e-07	89	1.1e-09	84	8.9e-05	66	1.6e-11	97
8	GO:0080090	P	regulation of primary metabolic process							2.3e-07	91	3.2e-07	86	2.7e-07	92	1.1e-09	87	0.0002	67	1.7e-11	100
9	GO:0045449	P	regulation of transcription							2.3e-07	86	3e-07	82	1.8e-07	89	1e-09	84	8.9e-05	66	6.5e-12	97
10	GO:0051171	P	regulation of nitrogen compound metabolic process							2.3e-07	89	4.6e-07	83	2.7e-07	90	1e-09	86	0.00014	66	1.7e-11	98
11	GO:0010033	P	response to organic substance							2.5e-07	70	8.1e-05	58	7.4e-07	69	5e-07	61	0.0006	49	7e-07	66
12	GO:0050794	P	regulation of cellular process							2.5e-07	135	5.9e-06	121	5.7e-07	135	1.7e-08	122	0.00055	98	3.9e-10	140
13	GO:0019222	P	regulation of metabolic process							4.2e-07	98	2e-06	90	7.4e-07	98	2.6e-09	93	0.00079	70	2e-10	105
14	GO:0050896	P	response to stimulus							4.2e-07	154	4e-05	135	5e-07	156	7.8e-07	133	0.00044	114	1.4e-07	150
15	GO:0006350	P	transcription							6.5e-07	88	4.6e-07	84	4.7e-07	90	1.1e-09	86	0.00014	67	1.7e-11	99
16	GO:0060255	P	regulation of macromolecule metabolic process							8.3e-07	92	7.8e-07	87	5.3e-07	94	9.8e-09	87	0.00044	68	1.1e-10	101
17	GO:0010468	P	regulation of gene expression							8.3e-07	90	5.1e-07	86	2.7e-07	94	2.6e-09	87	0.00021	68	2.6e-11	101
18	GO:0050789	P	regulation of biological process							1.3e-06	141	1.2e-05	128	7.4e-07	144	3.9e-08	129	0.00044	106	1.7e-10	151
19	GO:0065007	P	biological regulation							3.9e-06	153	1.2e-05	141	8.5e-07	158	8.5e-07	136	0.00057	116	1.1e-09	162
20	GO:0042221	P	response to chemical stimulus							1.6e-05	88	0.0019	74	3e-05	88	9.9e-06	78	0.0062	63	4.4e-05	83
21	GO:0010876	P	lipid localization							3.4e-05	8	2e-05	8	3.8e-05	8	0.0099	5	0.0073	5	0.0022	6
22	GO:0009791	P	post-embryonic development							0.00014	39	1e-05	40	5e-07	46	1.7e-05	37	0.0005	32	4.4e-05	39
23	GO:0032774	P	RNA biosynthetic process							0.002	47	0.0019	44	0.00016	51	2.5e-05	47	0.0023	39	1.2e-06	55
24	GO:0006351	P	transcription, DNA-dependent							0.002	47	0.0019	44	0.00016	51	2.5e-05	47	0.0023	39	1.2e-06	55
25	GO:0006950	P	response to stress							0.0021	86	0.046	73	0.019	82	0.00021	79	0.0028	70	0.00013	88
26	GO:0006355	P	regulation of transcription, DNA-dependent							0.0022	45	0.0015	43	9.8e-05	50	3.4e-05	45	0.0019	38	1.3e-06	53
27	GO:0051252	P	regulation of RNA metabolic process							0.0026	45	0.0017	43	0.00012	50	4.1e-05	45	0.0022	38	1.6e-06	53
28	GO:0002252	P	immune effector process							0.0096	6	0.035	5	---	---	0.025	5	0.02	5	0.0072	6
29	GO:0032501	P	multicellular organismal process							0.025	74	0.0059	72	0.0025	80	0.0099	66	0.0067	63	0.023	71
30	GO:0009620	P	response to fungus							0.029	12	0.014	12	0.031	12	0.021	11	0.044	10	0.045	11
31	GO:0009719	P	response to endogenous stimulus							0.034	43	0.022	41	0.0025	48	0.0078	40	---	---	0.014	43
32	GO:0051607	P	defense response to virus							0.035	5	---	---	---	---	---	---	---	---	0.025	5
33	GO:0009725	P	response to hormone stimulus							0.039	40	0.027	38	0.0053	44	0.011	37	---	---	0.017	40
34	GO:0003700	F	transcription factor activity							5.2e-15	121	7.9e-13	109	1.1e-15	124	6.1e-16	110	4.7e-09	88	2.7e-18	125
35	GO:0030528	F	transcription regulator activity							1.5e-13	125	4.7e-12	114	2.7e-15	131	1.4e-15	116	4e-08	91	4.3e-17	130
36	GO:0003677	F	DNA binding							5.2e-12	136	1.2e-10	124	1.7e-11	136	6.1e-12	120	7.3e-06	95	2.8e-14	138
37	GO:0005488	F	binding							1.4e-05	338	0.003	298	9e-06	344	5.3e-06	293	0.00066	262	2.4e-06	329
38	GO:0005515	F	protein binding							0.0019	105	---	---	0.0069	103	0.014	86	---	---	0.024	95
39	GO:0005199	F	structural constituent of cell wall							0.0056	7	0.0006	8	0.035	6	0.0019	7	0.0097	6	0.026	6
40	GO:0005516	F	calmodulin binding							0.038	15	---	---	---	---	---	---	---	---	---	---
41	GO:0003676	F	nucleic acid binding							0.048	147	---	---	0.042	149	0.011	131	---	---	0.0033	150
42	GO:0009507	C	chloroplast							5.3e-07	116	2.9e-06	105	3.4e-10	128	1.4e-17	131	1.1e-18	127	9.6e-18	143
43	GO:0044464	C	cell part							1.5e-06	441	6.1e-05	395	6.1e-07	449	6e-06	370	1e-06	350	2.7e-08	429
44	GO:0009536	C	plastid							1.5e-06	119	6.9e-06	108	3.5e-09	131	9.1e-17	135	1.5e-17	130	1.1e-16	147
45	GO:0005623	C	cell							1.5e-06	441	6.1e-05	395	6.1e-07	449	6e-06	370	1e-06	350	2.7e-08	429
46	GO:0009579	C	thylakoid							5.8e-06	29	2.9e-06	29	6.1e-07	31	1.5e-09	32	2.9e-12	35	9.8e-11	36
47	GO:0034357	C	photosynthetic membrane							6.9e-06	24	2.9e-06	24	6.1e-07	26	2e-09	27	3.1e-12	30	6.6e-11	31
48	GO:0044434	C	chloroplast part							2.6e-05	42	1.5e-05	40	1.8e-06	45	6.2e-11	50	3.8e-15	55	9.3e-12	55
49	GO:0043231	C	intracellular membrane-bounded organelle							3e-05	240	0.0004	214	1.4e-06	251	1.1e-10	233	2.1e-09	212	3.1e-13	269
50	GO:0043227	C	membrane-bounded organelle							3e-05	240	0.00041	214	1.1e-06	252	8.1e-11	234	1.4e-09	213	2.6e-13	270
51	GO:0042651	C	thylakoid membrane							3.4e-05	21	5.5e-06	22	3e-06	23	1.7e-08	24	4.1e-11	27	2.3e-09	27
52	GO:0044435	C	plastid part							4.4e-05	45	3.2e-05	43	6.1e-06	48	8.1e-11	54	2.3e-14	58	2.4e-11	59
53	GO:0009535	C	chloroplast thylakoid membrane							4.4e-05	20	6.4e-06	21	1.3e-05	21	1.2e-07	22	2.6e-10	25	1.3e-08	25
54	GO:0055035	C	plastid thylakoid membrane							4.4e-05	20	6.4e-06	21	1.3e-05	21	1.2e-07	22	2.6e-10	25	1.3e-08	25
55	GO:0044436	C	thylakoid part							6.4e-05	23	8.4e-06	24	9.2e-06	25	5.9e-08	26	1.7e-10	29	1.2e-08	29
56	GO:0005886	C	plasma membrane							6.4e-05	64	3.7e-05	61	4.4e-05	65	---	---	---	---	---	---
57	GO:0031225	C	anchored to membrane							0.0001	21	9.3e-05	20	0.00026	20	---	---	0.045	12	0.018	15
58	GO:0005622	C	intracellular							0.00023	285	0.0064	252	3e-05	295	1.2e-08	269	3.9e-07	244	2.2e-10	308
59	GO:0009534	C	chloroplast thylakoid							0.00023	21	3.2e-05	22	8.4e-05	22	2.8e-07	24	8.6e-10	27	1.7e-07	26
60	GO:0031976	C	plastid thylakoid							0.00025	21	3.3e-05	22	8.8e-05	22	3.2e-07	24	9.9e-10	27	1.9e-07	26
61	GO:0031984	C	organelle subcompartment							0.00026	21	3.4e-05	22	8.9e-05	22	3.5e-07	24	1.1e-09	27	2.1e-07	26
62	GO:0043229	C	intracellular organelle							0.00028	245	0.0037	219	1.9e-05	257	8.8e-09	236	8.9e-08	216	2.8e-11	274
63	GO:0043226	C	organelle							0.00028	245	0.0037	219	1.9e-05	257	8.8e-09	236	9e-08	216	2.8e-11	274
64	GO:0005618	C	cell wall							0.00034	25	0.00011	25	0.0058	22	0.0083	19	0.0072	18	0.0056	21
65	GO:0030312	C	external encapsulating structure							0.00038	25	0.00012	25	0.0063	22	0.009	19	0.0073	18	0.0061	21
66	GO:0044424	C	intracellular part							0.00067	271	0.02	239	8.4e-05	282	2.2e-07	254	2.4e-06	232	3.1e-09	293
67	GO:0009532	C	plastid stroma							0.0018	20	0.0007	20	0.0001	23	8.9e-10	30	1.1e-10	30	2.7e-08	29
68	GO:0009570	C	chloroplast stroma							0.0019	17	0.00082	17	8.8e-05	20						