Supplementary Figure: 7 :Snapshot of PAGE SEACOMPARE. It is Cross comparison of PAGE of DETs at all 6 timepoints Top panel

GO Analysis Toolkit and Database for Agricultural Community

CAGRI

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GO Information				GO Information		СМ			🗌 Oh	ır	12		žhr 🗌			hr	48hr		hr		120	Jhr		240	40hr
No		Onto N	Numbe		12	34	56	Z-score	Mean	FDRnbsp;		Mean	• •		Mean	• •		Mean	•••		Mean	FDRnbsp;	Z-score		• •
1	GO:0019538	Р	84	protein metabolic process				4.5	1.8	0.00069	3.3	1.1	0.041	3.5	1.1	0.011	2.8	1.2	0.06	2.9	1.1	0.13	3.4	1.5	0.016
2	GO:0044267	Р	70	cellular protein metabolic process				4.5	1.9	0.00069	3.1	1.1	0.041	3.7	1.3	0.0093	2.7	1.3	0.07	2.8	1.1	0.13	3	1.5	0.032
3	GO:0043687	P	38	post-translational protein modification		-		4.2	2.5	0.0014	3.2	1.6	0.041	3.8	2	0.0093	2.7	1.6	0.07	2.6	1.4	0.13	3.5	2.2	0.016
4 5	GO:0006464 GO:0006468	P	39	protein modification process		-		4.2	2.4	0.0014	3.2 3.2	1.6	0.041	3.8	1.9	0.0093	2.6 2.3	1.6	0.07	2.6 2	1.4	0.13	3.4	2.1	0.016
6	GO:00043412	P	29 42	protein amino acid phosphorylation macromolecule modification		-		4.1 3.9	2.8	0.0019	3.2	1.9	0.041	3.7 3.8	2.3 1.9	0.0093	2.6	1.6 1.5	0.13	2.8	1.3 1.5	0.24	3.2 3.2	2.3	0.017
7		P	29	response to chitin		-		3.6	2.5	0.0074	3.4	2	0.041	3.1	1.8	0.039	2.5	1.7	0.092	1	0.71	0.67	1.2	0.93	0.57
8		P	16	immune response				3.5	3.2	0.01	2.5	2	0.08	2.4	2	0.14	1.9	1.7	0.27	2	1.7	0.24	2.1	2.1	0.15
9	GO:0002376		16	immune system process				3.5	3.2	0.01	2.5	2	0.08	2.4	2	0.14	1.9	1.7	0.27	2	1.7	0.24	2.1	2.1	0.15
10		Р	108	multicellular organismal process				3.3	1.1	0.02	2.6	0.69	0.08	3.6	0.96	0.011	2.2	0.91	0.14	2.6	0.88	0.13	2.2	0.91	0.14
11	GO:0009743	Р	34	response to carbohydrate stimulus				3.2	2	0.02	3.1	1.7	0.046	2.9	1.5	0.062	2.4	1.6	0.097	1	0.66	0.67	1.3	0.93	0.52
12	GO:0043170	Р	240	macromolecule metabolic process				3.2	0.73	0.02	2.7	0.41	0.08	2.5	0.27	0.13	2.9	0.82	0.048	2.5	0.6	0.13	3.4	0.93	0.016
13	GO:0016310	Р	35	phosphorylation				3.2	2	0.02	2.5	1.3	0.085	3	1.6	0.042	1.4	0.97	0.44	0.98	0.62	0.7	2.2	1.5	0.14
14	GO:0006796	Р	37	phosphate metabolic process				3.1	1.9	0.023	2.6	1.3	0.08	3.1	1.6	0.039	1.4	0.97	0.44	1	0.64	0.67	2.1	1.4	0.15
15	GO:0006793	Р	37	phosphorus metabolic process				3.1	1.9	0.023	2.6	1.3	0.08	3.1	1.6	0.039	1.4	0.97	0.44	1	0.64	0.67	2.1	1.4	0.15
16	GO:0051252	Р	74	regulation of RNA metabolic process				2.9	1.2	0.039	2.9	0.99	0.065	2.3	0.67	0.18	3	1.4	0.044	2.3	0.95	0.17	2.5	1.2	0.11
17	GO:0006355	Р	74	regulation of transcription, DNA-dependent				2.9	1.2	0.039	2.9	0.99	0.065	2.3	0.67	0.18	3	1.4	0.044	2.3	0.95	0.17	2.5	1.2	0.11
18	GO:0032774	Р	76	RNA biosynthetic process				2.9	1.2	0.039	2.8	0.93	0.075	2.2	0.61	0.21	3	1.3	0.044	2.2	0.9	0.2	2.3	1.1	0.13
19	GO:0006351	Р	76	transcription, DNA-dependent				2.9	1.2	0.039	2.8	0.93	0.075	2.2	0.61	0.21	3	1.3	0.044	2.2	0.9	0.2	2.3	1.1	0.13
20	GO:0016070	Р	79	RNA metabolic process				2.8	1.1	0.042	2.8	0.9	0.077	2.1	0.56	0.23	3	1.3	0.044	2.2	0.89	0.2	2.3	1.1	0.13
21	GO:0042221	Р	129	response to chemical stimulus				2.8	0.88	0.042	2.1	0.44	0.2	2.2	0.38	0.21	2.5	0.92	0.092	2	0.66	0.24	1	0.46	0.59
22	GO:000003	Р	59	reproduction				2.8	1.3	0.045	2.4	0.89	0.12	2.8	1	0.071	1.5	0.82	0.44	1.9	0.89	0.29	2	1.1	0.19
23	GO:0044260	Ρ	223	cellular macromolecule metabolic process				2.8	0.65	0.045	2.4	0.35	0.12	2.3	0.23	0.19	2.7	0.78	0.07	2.1	0.55	0.23	2.8	0.82	0.051
24	GO:0003824	F	268	catalytic activity				4.5	0.97	0.00049	4.6	0.78	0.00033	4.4	0.68	0.00051	2.7	0.75	0.021	2.9	0.66	0.015	3	0.8	0.0094
25	GO:0017111	F	19	nucleoside-triphosphatase activity				4.1	3.5	0.00049	3.9	2.9	0.0012	4.1	3.2	0.00051	3.5	2.9	0.0078	4.2	3.2	0.00048	3.7	3.2	0.0012
26	GO:0016818	F	19	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides				4.1	3.5	0.00049	3.9	2.9	0.0012	4.1	3.2	0.00051	3.5	2.9	0.0078	4.2	3.2	0.00048	3.7	3.2	0.0012
27	GO:0016817	F	19	hydrolase activity, acting on acid anhydrides				4.1	3.5	0.00049	3.9	2.9	0.0012	4.1	3.2	0.00051	3.5	2.9	0.0078	4.2	3.2	0.00048	3.7	3.2	0.0012
28	GO:0016462	F	19	pyrophosphatase activity				4.1	3.5	0.00049	3.9	2.9	0.0012	4.1	3.2	0.00051	3.5	2.9	0.0078	4.2	3.2	0.00048	3.7	3.2	0.0012
29	GO:0032555	F	34	purine ribonucleotide binding				3.9	2.4	0.0011	3.6	2	0.0018	4	2.3	0.00051	3.1	1.9	0.013	3.6	2	0.0024	3.8	2.5	0.0012
30		F	34	ribonucleotide binding				3.9	2.4	0.0011	3.6	2	0.0018	4	2.3	0.00051	3.1	1.9	0.013	3.6	2	0.0024	3.8	2.5	0.0012
31	GO:0042623	F	10	ATPase activity, coupled				3.8	4.4	0.0011	3.9	4.1	0.0012	3.7	4	0.0014	3.2	3.6	0.013	3.5	3.6	0.0024	3.1	3.7	0.0079
32	GO:0016887	F	13	ATPase activity				3.7	3.8	0.0014	3.8	3.5	0.0012	3.7	3.5	0.0014	3.4	3.3	0.01	4.1	3.7	0.00057	3.6	3.8	0.0014
33	GO:0017076	F	35	purine nucleotide binding				3.6	2.2	0.002	3.4	1.8	0.0033	3.8	2.1	0.001	2.8	1.8	0.019	3.3	1.9	0.0038	3.6	2.3	0.0015
34	GO:0032559	F	31	adenyl ribonucleotide binding				3.6	2.3	0.002	3.6	2.1	0.0018	3.8	2.2	0.001	3.1	2	0.013	3.7	2.2	0.0017	4	2.7	0.0012
35		F	30	ATP binding				3.5	2.4	0.0021	3.7	2.2	0.0018	3.8	2.3	0.00099	3.2	2.1	0.013	3.8	2.3	0.0015	4.1	2.8	0.0012
36	GO:0016301	F	51	kinase activity				3.4	1.7	0.0033	2.9	1.2	0.014	3.6	1.6	0.0016	3.1	1.7	0.013	2.8	1.4	0.018	3.8	2.1	0.0012
37	GO:0030554		32	adenyl nucleotide binding				3.3	2.1	0.0033	3.4	1.9	0.0033	3.5	2	0.0017	2.8	1.8	0.019	3.5	2.1	0.0024	3.8	2.5	0.0012
38	GO:0001883		32	purine nucleoside binding				3.3	2.1	0.0033	3.4	1.9	0.0033	3.5	2	0.0017	2.8	1.8	0.019	3.5	2.1	0.0024	3.8	2.5	0.0012
39	GO:0001882		32	nucleoside binding				3.3	2.1	0.0033	3.4	1.9	0.0033	3.5	2	0.0017	2.8	1.8	0.019	3.5	2.1	0.0024	3.8	2.5	0.0012
40	GO:0016772		56	transferase activity, transferring phosphorus-containing groups				3.3	1.6	0.0033	2.9	1.2	0.013	3.5	1.4	0.0018	3	1.5	0.013	2.8	1.3	0.019	3.6	1.9	0.0015
41	GO:0016787		95	hydrolase activity				3.2	1.2	0.005	3.4	1	0.0033	3.4	0.97	0.0026	2.8	1.1	0.019	2.7	0.99	0.022	3.3	1.4	0.0043
42	GO:0016881		21	acid-amino acid ligase activity				3	2.4	0.0095	2.2	1.5	0.075	2.6	1.8	0.026	2.5	2	0.037	2.6	1.9	0.032	1.4	1.3	0.27
43	GO:0016879 GO:0004672		21	ligase activity, forming carbon-nitrogen bonds				3	2.4	0.0095	2.2	1.5	0.075	2.6	1.8	0.026	2.5	2	0.037	2.6	1.9	0.032	1.4	1.3	0.27
			26	protein kinase activity				3	2.1	0.0095	2.4 2.9	1.5	0.051	2.9	1.8	0.012	2	1.5	0.095	2.1	1.4	0.097	3.1	2.3	0.0079
45	GO:0000166		53 23	nucleotide binding ligase activity				2.9 2.8	1.4 2.2	0.011	2.9	1.2	0.014	3.3 2.7	1.4	0.0031	2.1	1.1	0.093	2.5 2.6	1.2	0.032	2.4 1.3	1.3	0.05
40	GO:0016773		31	phosphotransferase activity, alcohol group as acceptor				2.0	1.7	0.013	2.3	1.2	0.083	2.7	1.5	0.022	1.4	1	0.24	1.7	1.0	0.032	2.5	1.1	0.038
48	GO:0004842		18	ubiquitin-protein ligase activity				2.6	2.3	0.021	1.9	1.3	0.15	2.1	1.5	0.082	1.9	1.7	0.12	1.6	1.3	0.2	1.1	1.1	0.39
48	GO:0004842		85	transferase activity				2.6	2.3	0.021	2.8	0.87	0.15	2.1	0.82	0.082	1.9	0.79	0.12	1.6	0.68	0.2	2.3	1.1	0.39
50	GO:0010740		19	small conjugating protein ligase activity				2.4	2	0.024	1.6	1.1	0.22	1.9	1.3	0.13	1.6	1.4	0.18	1.3	1	0.34	0.82	0.82	0.51
51	GO:0048046		12	apoplast				-2.9	-3.1	0.035	-2.8	-3.1	0.045	-2.9	-3.5	0.014	-2.6	-2.3	0.017	-2.5	-2.2	0.029	-2.4	-2.4	0.032
52	GO:0034357		32	photosynthetic membrane				-2.9	-1.9	0.035	-2.9	-2	0.037	-4.1	-3.1	0.0014	-5.5	-3	5.1e-07	-6.2	-3.4		-5.8	-3.6	1.9e-07
53	GO:0030312		32	external encapsulating structure				-3	-2	0.034	-3.2	-2.2	0.019	-2.5	-2	0.04	-2.8	-1.4	0.012	-2.2	-1.2		-2.7	-1.6	0.018
54	GO:0005618		32	cell wall				-3	-2	0.034	-3.2	-2.2	0.019	-2.5	-2	0.04	-2.8	-1.4	0.012	-2.2	-1.2		-2.7	-1.6	0.018
55	GO:0044425		54	membrane part				-3.4	-1.7	0.016	-3.2	-1.7	0.019	-3.2	-2	0.0065	-2.2	-0.79	0.053	-2.1	-0.82		-2.2	-0.94	0.05
56	GO:0031224	С	29	intrinsic to membrane				-4.3	-3	0.00048	-4.1	-2.9	0.001	-3.7	-3	0.0021	-1.6	-0.81	0.15	-1.4	-0.74	0.24	-1.7	-0.99	0.15
57	GO:0031225	с	23	anchored to membrane				-5.1	-4	2.2e-05	-4.9	-3.8	7.4e-05	-4.4	-3.8	0.00069	-2.2	-1.4	0.046	-2	-1.3	0.074	-2.3	-1.6	0.039
58	GO:0006631	Р	10	fatty acid metabolic process				-2	-2.4	0.18	-3.2	-3.8	0.041	-1.9	-2.6	0.31	-3.2	-3.2	0.044	-2.8	-2.8	0.13	-3.4	-3.7	0.016
59	GO:0007275	Р	99	multicellular organismal development				2.7	0.97	0.051	2.1	0.56	0.18	3.2	0.87	0.036	1.8	0.79	0.31	2.1	0.76	0.24	2.1	0.9	0.17
60	GO:0004091	F	16	carboxylesterase activity				2	1.8	0.11	1.9	1.4	0.15	2.4	1.9	0.045	2	1.8	0.11	1.1	0.98	0.41	1.3	1.3	0.32
61	GO:0005576	С	16	extracellular region				-2.3	-2.2	0.069	-2.4	-2.3	0.06	-2.5	-2.7	0.04	-1.8	-1.3	0.12	-1.4	-1.1	0.22	-1.8	-1.5	0.11
62	GO:0016020	С	172	membrane				-2.1	-0.65	0.1	-2	-0.75	0.12	-3	-1.2	0.012	-2.6	-0.46	0.019	-2.5	-0.52	0.029	-2.4	-0.53	0.034
63	GO:0044434	С	65	chloroplast part				-2.4	-1.2	0.052	-2.2	-1.2	0.08	-3.1	-1.8	0.0068	-5.2	-2	1.2e-06	-5.6	-2.1	1.4e-07	-4.8	-2	7.5e-06
64	GO:0044435	С	70	plastid part				-2.6	-1.2	0.052	-2.4	-1.2	0.06	-3.3	-1.8	0.005	-5.5	-2	5.1e-07	-5.8	-2.1	5.2e-08	-5	-2	3e-06
65	GO:0031090	С	36	organelle membrane				-2.3	-1.5	0.069	-2.2	-1.5	0.088	-3.3	-2.4	0.005	-4.5	-2.3	3.2e-05	-5	-2.6	2.1e-06	-4.8	-2.8	7.5e-06
66	GO:0009579	С	38	thylakoid				-2.5	-1.5	0.052	-2.4	-1.6	0.06	-3.4	-2.5	0.0031	-5.2	-2.6	1.2e-06	-5.8	-2.9	5.1e-08	-5.2	-2.9	1.4e-06
67	GO:0031984	С	28	organelle subcompartment				-2.5	-1.8	0.052	-2.4	-1.8	0.06	-3.6	-2.9	0.0021	-5.2	-3.1	1.2e-06	-5.8	-3.5	5.1e-08	-5.5	-3.7	2.6e-07
68	GO:0031976	С	28	plastid thylakoid				-2.5	-1.8	0.052	-2.4	-1.8	0.06	-3.6	-2.9	0.0021	-5.2	-3.1	1.2e-06	-5.8	-3.5	5.1e-08	-5.5	-3.7	2.6e-07
	GO:0009534	С	28	chloroplast thylakoid				-2.5	-1.8	0.052	-2.4	-1.8	0.06	-3.6	-2.9	0.0021	-5.2	-3.1	1.2e-06	-5.8	-3.5	5.1e-08	-5.5	-3.7	2.6e-07
69		C	31	thylakoid part				-2.5	-1.7	0.052	-2.4	-1.8	0.06	-3.6	-2.8	0.0021	-5.5	-3.1	5.1e-07	-6	-3.4	3.1e-08	-5.6	-3.5	2.6e-07
69 (70 (GO:0044436	C																							
	GO:0044436 GO:0055035		26	plastid thylakoid membrane				-2.5	-1.9	0.052	-2.4	-1.9	0.06	-3.6	-3	0.0021	-5.1	-3.1	1.5e-06	-5.8	-3.5	5.2e-08	-5.6	-3.9	2.6e-07
70		с	26 26					-2.5 -2.5	-1.9 -1.9	0.052	-2.4 -2.4	-1.9 -1.9	0.06	-3.6 -3.6	-3 -3	0.0021	-5.1 -5.1	-3.1 -3.1	1.5e-06 1.5e-06	-5.8 -5.8	-3.5 -3.5		-5.6 -5.6	-3.9 -3.9	