

Biological Process	Gene #	Expected	Over/Under	Fold Enrichment	P-Value
response to stimulus (GO:0050896)	474	280.85	+	1.69	5.58E-38
response to light stimulus (GO:0009416)	160	60.46	+	2.65	1.03E-24
response to radiation (GO:0009314)	161	61.73	+	2.61	3.37E-24
response to abiotic stimulus (GO:0009628)	244	124.18	+	1.96	8.25E-22
response to organic substance (GO:0010033)	214	105.83	+	2.02	8.63E-20
response to chemical (GO:0042221)	261	152.53	+	1.71	1.68E-15
response to endogenous stimulus (GO:0009719)	160	76.73	+	2.09	1.15E-14
response to hormone (GO:0009725)	158	75.71	+	2.09	2.11E-14
response to external stimulus (GO:0009605)	160	89.56	+	1.79	5.46E-09
response to auxin (GO:0009733)	43	11.62	+	3.7	7.79E-09
biological process involved in interspecies interaction between organisms (GO:0044419)	138	75.07	+	1.84	4.07E-08
response to external biotic stimulus (GO:0043207)	137	74.59	+	1.84	5.47E-08
response to other organism (GO:0051707)	137	74.59	+	1.84	5.47E-08
response to biotic stimulus (GO:0009607)	137	74.65	+	1.84	5.55E-08
cellular nitrogen compound metabolic process (GO:0034641)	41	97.8	-	0.42	7.99E-08
response to oxygen-containing compound (GO:1901700)	159	93.18	+	1.71	1.98E-07
response to stress (GO:0006950)	238	159.56	+	1.49	3.60E-07
response to lipid (GO:0033993)	112	58.41	+	1.92	4.36E-07
nucleobase-containing compound metabolic process (GO:0006139)	23	68.64	-	0.34	4.67E-07
nucleic acid metabolic process (GO:0090304)	16	56.63	-	0.28	5.97E-07
defense response to other organism (GO:0098542)	115	63.87	+	1.8	8.27E-06
defense response (GO:0006952)	127	73.68	+	1.72	1.27E-05

response to red or far red light (GO:0009639)	35	11.32	+	3.09	6.12E-05
response to organic cyclic compound (GO:0014070)	56	24.66	+	2.27	1.73E-04
gene expression (GO:0010467)	19	51.74	-	0.37	6.31E-04
response to bacterium (GO:0009617)	73	37.49	+	1.95	6.76E-04
response to wounding (GO:0009611)	54	24.6	+	2.19	9.57E-04
cellular aromatic compound metabolic process (GO:0006725)	48	91.04	-	0.53	1.19E-03
response to light intensity (GO:0009642)	32	11.26	+	2.84	1.41E-03
heterocycle metabolic process (GO:0046483)	46	87.03	-	0.53	2.39E-03
RNA metabolic process (GO:0016070)	14	41.93	-	0.33	2.61E-03
secondary metabolic process (GO:0019748)	52	24.45	+	2.13	3.02E-03
cell wall organization or biogenesis (GO:0071554)	59	29.19	+	2.02	3.15E-03
response to fungus (GO:0009620)	60	30.03	+	2	4.42E-03
response to gibberellin (GO:0009739)	16	3.74	+	4.27	1.13E-02
signaling (GO:0023052)	116	74.68	+	1.55	1.24E-02
cellular response to organic substance (GO:0071310)	80	46.79	+	1.71	2.07E-02
response to alcohol (GO:0097305)	66	36.04	+	1.83	2.14E-02
defense response to fungus (GO:0050832)	45	21.19	+	2.12	2.22E-02
cell communication (GO:0007154)	121	81.14	+	1.49	4.74E-02
lipid metabolic process (GO:0006629)	68	38.85	+	1.75	4.74E-02
organic acid metabolic process (GO:0006082)	99	63.03	+	1.57	4.87E-02
Molecular Function	Gene #	Expected	Over/Under	Fold Enrichment	P-Value
RNA binding (GO:0003723)	10	48.9	-	0.2	3.66E-08
mRNA binding (GO:0003729)	5	31.94	-	0.16	1.42E-05

catalytic activity, acting on a nucleic acid (GO:0140640)	5	23.27	-	0.21	2.07E-02
amide transmembrane transporter activity (GO:0042887)	10	1.69	+	5.92	3.79E-02
Cellular Component	Gene #	Expected	Over/Under	Fold Enrichment	P-Value
protein-containing complex (GO:0032991)	28	93.4	-	0.3	3.52E-13
cell periphery (GO:0071944)	179	108.1	+	1.66	1.99E-08
intracellular non-membrane-bounded organelle (GO:0043232)	13	51.38	-	0.25	1.32E-07
non-membrane-bounded organelle (GO:0043228)	13	51.38	-	0.25	1.32E-07
plasma membrane (GO:0005886)	148	92.88	+	1.59	1.67E-05
extracellular region (GO:0005576)	149	94.84	+	1.57	4.04E-05
catalytic complex (GO:1902494)	12	40.87	-	0.29	1.11E-04
ribonucleoprotein complex (GO:1990904)	2	20.89	-	0.1	3.41E-04
nuclear lumen (GO:0031981)	7	29.46	-	0.24	1.14E-03
intracellular organelle lumen (GO:0070013)	11	34.83	-	0.32	3.22E-03
membrane-enclosed lumen (GO:0031974)	11	34.83	-	0.32	3.22E-03
organelle lumen (GO:0043233)	11	34.83	-	0.32	3.22E-03
envelope (GO:0031975)	14	38.73	-	0.36	4.66E-03
organelle envelope (GO:0031967)	14	38.73	-	0.36	4.66E-03
membrane (GO:0016020)	203	151.84	+	1.34	8.61E-03
intracellular protein-containing complex (GO:0140535)	5	22.46	-	0.22	1.54E-02
nucleus (GO:0005634)	263	319.94	-	0.82	3.83E-02
plastid stroma (GO:0009532)	6	22.67	-	0.26	4.72E-02

Supplemental Table 1: Significant, down-regulated GO Terms for artificially acidified Arabidopsis.

Biological Process	Gene #	Expected	Over/Under	Fold Enrichment	P-Value
response to stress (GO:0006950)	373	139.52	+	2.67	1.55E-77
response to chemical (GO:0042221)	341	133.37	+	2.56	2.09E-63
response to stimulus (GO:0050896)	477	245.57	+	1.94	3.29E-63
cellular response to hypoxia (GO:0071456)	85	6.31	+	13.47	3.07E-57
cellular response to decreased oxygen levels (GO:0036294)	85	6.36	+	13.36	5.37E-57
cellular response to oxygen levels (GO:0071453)	85	6.39	+	13.31	7.09E-57
cellular response to chemical stimulus (GO:0070887)	201	54.03	+	3.72	1.14E-54
response to hypoxia (GO:0001666)	89	8.53	+	10.44	2.88E-52
response to decreased oxygen levels (GO:0036293)	89	8.74	+	10.19	1.64E-51
response to oxygen-containing compound (GO:1901700)	243	81.48	+	2.98	1.87E-51
response to oxygen levels (GO:0070482)	89	8.79	+	10.13	2.52E-51
response to abiotic stimulus (GO:0009628)	277	108.59	+	2.55	1.76E-47
cellular response to stimulus (GO:0051716)	266	102.23	+	2.6	1.47E-46
cellular response to stress (GO:0033554)	142	32.07	+	4.43	1.93E-44
response to wounding (GO:0009611)	110	21.51	+	5.11	1.50E-38
response to chitin (GO:0010200)	71	8.13	+	8.73	1.26E-36
response to organic substance (GO:0010033)	232	92.54	+	2.51	1.91E-36
response to external biotic stimulus (GO:0043207)	189	65.22	+	2.9	4.12E-36
response to other organism (GO:0051707)	189	65.22	+	2.9	4.12E-36
response to biotic stimulus (GO:0009607)	189	65.27	+	2.9	4.58E-36
biological process involved in interspecies interaction between organisms (GO:0044419)	189	65.64	+	2.88	9.54E-36
response to external stimulus (GO:0009605)	207	78.31	+	2.64	1.23E-34

response to inorganic substance (GO:0010035)	170	55.72	+	3.05	2.21E-34
defense response (GO:0006952)	180	64.43	+	2.79	4.33E-32
response to organonitrogen compound (GO:0010243)	90	17.1	+	5.26	1.06E-31
cellular process (GO:0009987)	552	392.01	+	1.41	1.85E-30
response to nitrogen compound (GO:1901698)	95	20.85	+	4.56	3.93E-29
defense response to other organism (GO:0098542)	159	55.85	+	2.85	1.75E-28
response to fungus (GO:0009620)	103	26.26	+	3.92	6.38E-27
response to oxidative stress (GO:0006979)	81	16.18	+	5.01	7.34E-27
response to alcohol (GO:0097305)	111	31.51	+	3.52	1.42E-25
response to lipid (GO:0033993)	145	51.07	+	2.84	2.18E-25
response to bacterium (GO:0009617)	111	32.78	+	3.39	3.12E-24
response to endogenous stimulus (GO:0009719)	168	67.09	+	2.5	4.23E-24
response to hormone (GO:0009725)	166	66.2	+	2.51	5.57E-24
defense response to fungus (GO:0050832)	82	18.53	+	4.43	6.39E-24
response to abscisic acid (GO:0009737)	102	28.32	+	3.6	6.69E-24
response to osmotic stress (GO:0006970)	92	23.6	+	3.9	1.68E-23
defense response to bacterium (GO:0042742)	98	27.16	+	3.61	6.98E-23
response to temperature stimulus (GO:0009266)	89	22.86	+	3.89	1.37E-22
cellular response to organic substance (GO:0071310)	122	40.91	+	2.98	2.15E-22
response to organic cyclic compound (GO:0014070)	86	21.56	+	3.99	2.25E-22
regulation of response to stress (GO:0080134)	88	23.23	+	3.79	1.51E-21
regulation of defense response (GO:0031347)	79	19.64	+	4.02	1.59E-20
regulation of response to stimulus (GO:0048583)	108	35.26	+	3.06	3.12E-20

response to salt stress (GO:0009651)	70	16.42	+	4.26	3.68E-19
response to acid chemical (GO:0001101)	94	29.19	+	3.22	1.45E-18
response to salicylic acid (GO:0009751)	58	11.61	+	4.99	2.08E-18
response to water (GO:0009415)	90	28.32	+	3.18	2.73E-17
response to water deprivation (GO:0009414)	86	26.39	+	3.26	5.02E-17
cellular response to endogenous stimulus (GO:0071495)	94	31.51	+	2.98	1.87E-16
cellular response to hormone stimulus (GO:0032870)	92	30.56	+	3.01	2.79E-16
hormone-mediated signaling pathway (GO:0009755)	81	24.55	+	3.3	3.57E-16
cell communication (GO:0007154)	150	70.95	+	2.11	2.06E-14
signaling (GO:0023052)	141	65.3	+	2.16	6.21E-14
immune system process (GO:0002376)	52	12.04	+	4.32	8.25E-14
signal transduction (GO:0007165)	138	63.64	+	2.17	8.61E-14
cellular response to oxygen-containing compound (GO:1901701)	85	30.09	+	2.82	2.81E-13
indole-containing compound metabolic process (GO:0042430)	33	4.8	+	6.87	5.08E-13
response to heat (GO:0009408)	40	7.89	+	5.07	3.60E-12
biological regulation (GO:0065007)	319	217.04	+	1.47	1.01E-11
response to cold (GO:0009409)	48	12.48	+	3.84	8.31E-11
response to reactive oxygen species (GO:0000302)	28	4.36	+	6.43	4.28E-10
response to fatty acid (GO:0070542)	53	16.1	+	3.29	1.12E-09
regulation of cellular process (GO:0050794)	250	163.78	+	1.53	2.22E-09
regulation of biological process (GO:0050789)	289	198.43	+	1.46	2.57E-09
response to jasmonic acid (GO:0009753)	52	16	+	3.25	2.94E-09
secondary metabolic process (GO:0019748)	61	21.38	+	2.85	5.62E-09

response to hydrogen peroxide (GO:0042542)	19	2.01	+	9.47	1.09E-08
toxin metabolic process (GO:0009404)	22	3.11	+	7.06	3.50E-08
metabolic process (GO:0008152)	376	285.75	+	1.32	7.12E-08
sulfur compound metabolic process (GO:0006790)	44	14.49	+	3.04	1.29E-06
camalexin metabolic process (GO:0052317)	10	0.42	+	23.68	1.33E-06
camalexin biosynthetic process (GO:0010120)	10	0.42	+	23.68	1.33E-06
toxin biosynthetic process (GO:0009403)	10	0.53	+	18.94	6.86E-06
phytoalexin biosynthetic process (GO:0052315)	10	0.53	+	18.94	6.86E-06
phytoalexin metabolic process (GO:0052314)	10	0.53	+	18.94	6.86E-06
indole phytoalexin biosynthetic process (GO:0009700)	10	0.53	+	18.94	6.86E-06
indole phytoalexin metabolic process (GO:0046217)	10	0.53	+	18.94	6.86E-06
cellular metabolic process (GO:0044237)	311	233.04	+	1.33	7.10E-06
photosynthesis (GO:0015979)	25	5.54	+	4.51	7.42E-06
small molecule metabolic process (GO:0044281)	126	75.41	+	1.67	6.18E-05
organic acid metabolic process (GO:0006082)	99	55.11	+	1.8	9.61E-05
response to molecule of bacterial origin (GO:0002237)	17	3.09	+	5.5	2.05E-04
protein folding (GO:0006457)	22	5.31	+	4.15	2.60E-04
oxoacid metabolic process (GO:0043436)	93	51.55	+	1.8	2.66E-04
cellular response to organic cyclic compound (GO:0071407)	25	6.84	+	3.66	3.28E-04
indole-containing compound biosynthetic process (GO:0042435)	13	1.87	+	6.94	6.90E-04
response to carbohydrate (GO:0009743)	20	4.72	+	4.23	7.40E-04
secondary metabolite biosynthetic process (GO:0044550)	20	4.75	+	4.21	8.03E-04
indole-containing compound catabolic process (GO:0042436)	7	0.34	+	20.4	1.28E-03

protein complex oligomerization (GO:0051259)	11	1.45	+	7.58	2.74E-03
regulation of immune system process (GO:0002682)	19	4.72	+	4.02	2.99E-03
cellular response to salicylic acid stimulus (GO:0071446)	15	2.96	+	5.07	3.06E-03
defense response by callose deposition (GO:0052542)	8	0.66	+	12.12	4.42E-03
aromatic compound biosynthetic process (GO:0019438)	48	22.22	+	2.16	4.65E-03
indole glucosinolate metabolic process (GO:0042343)	7	0.5	+	13.96	9.49E-03
sulfur compound biosynthetic process (GO:0044272)	17	4.22	+	4.03	1.09E-02
generation of precursor metabolites and energy (GO:0006091)	29	10.74	+	2.7	1.13E-02
immune response (GO:0006955)	19	5.25	+	3.62	1.26E-02
cellular response to lipid (GO:0071396)	34	13.91	+	2.44	1.43E-02
cellular response to ethylene stimulus (GO:0071369)	13	2.53	+	5.13	1.43E-02
callose localization (GO:0052545)	9	1.13	+	7.93	1.96E-02
aromatic compound catabolic process (GO:0019439)	20	5.97	+	3.35	2.03E-02
aromatic amino acid family catabolic process (GO:0009074)	7	0.58	+	12.05	2.11E-02
regulation of cellular ketone metabolic process (GO:0010565)	14	3.09	+	4.53	2.28E-02
organic substance metabolic process (GO:0071704)	318	258.85	+	1.23	2.72E-02
organonitrogen compound metabolic process (GO:1901564)	193	143.11	+	1.35	2.77E-02
cellular macromolecule biosynthetic process (GO:0034645)	6	25	-	0.24	2.98E-02
polysaccharide localization (GO:0033037)	9	1.21	+	7.41	3.16E-02
organic cyclic compound metabolic process (GO:1901360)	123	82.56	+	1.49	3.62E-02
innate immune response (GO:0045087)	17	4.7	+	3.62	3.97E-02
defense response by callose deposition in cell wall (GO:0052544)	6	0.42	+	14.21	4.55E-02
organic cyclic compound catabolic process (GO:1901361)	20	6.33	+	3.16	4.58E-02

organic cyclic compound biosynthetic process (GO:1901362)	49	25	+	1.96	4.67E-02
Molecular Function	Gene #	Expected	Over/Under	Fold Enrichment	P-Value
catalytic activity (GO:0003824)	317	220.34	+	1.44	1.90E-10
binding (GO:0005488)	372	272.44	+	1.37	2.25E-10
protein binding (GO:0005515)	224	151.11	+	1.48	6.85E-07
unfolded protein binding (GO:0051082)	18	3.01	+	5.98	1.57E-05
oxidoreductase activity (GO:0016491)	76	38.8	+	1.96	1.43E-04
tetrapyrrole binding (GO:0046906)	29	10.58	+	2.74	5.05E-03
ATP-dependent activity (GO:0140657)	42	19.22	+	2.19	1.31E-02
transferase activity (GO:0016740)	135	92.12	+	1.47	1.47E-02
chlorophyll binding (GO:0016168)	7	0.71	+	9.82	3.80E-02
Cellular Component					
cell periphery (GO:0071944)	152	94.52	+	1.61	4.12E-06
cytoplasm (GO:0005737)	470	391.56	+	1.2	4.46E-06
intracellular anatomical structure (GO:0005622)	630	569.43	+	1.11	8.28E-06
plant-type cell wall (GO:0009505)	37	13.59	+	2.72	9.80E-05
cell wall (GO:0005618)	37	14.12	+	2.62	2.36E-04
plasma membrane (GO:0005886)	127	81.22	+	1.56	5.05E-04
external encapsulating structure (GO:0030312)	37	14.75	+	2.51	7.38E-04
membrane (GO:0016020)	180	132.76	+	1.36	1.28E-02
plasmodesma (GO:0009506)	46	23.44	+	1.96	2.17E-02
cell-cell junction (GO:0005911)	46	23.44	+	1.96	2.17E-02
symplast (GO:0055044)	46	23.44	+	1.96	2.17E-02

anchoring junction (GO:0070161)	46	23.44	+	1.96	2.17E-02
cell junction (GO:0030054)	46	23.44	+	1.96	2.17E-02
Cellular Component	Gene #	Expected	Over/Under	Fold Enrichment	P-Value
cell periphery (GO:0071944)	152	94.52	+	1.61	4.12E-06
cytoplasm (GO:0005737)	470	391.56	+	1.2	4.46E-06
intracellular anatomical structure (GO:0005622)	630	569.43	+	1.11	8.28E-06
plant-type cell wall (GO:0009505)	37	13.59	+	2.72	9.80E-05
cell wall (GO:0005618)	37	14.12	+	2.62	2.36E-04
plasma membrane (GO:0005886)	127	81.22	+	1.56	5.05E-04
external encapsulating structure (GO:0030312)	37	14.75	+	2.51	7.38E-04
membrane (GO:0016020)	180	132.76	+	1.36	1.28E-02
plasmodesma (GO:0009506)	46	23.44	+	1.96	2.17E-02
cell-cell junction (GO:0005911)	46	23.44	+	1.96	2.17E-02
symplast (GO:0055044)	46	23.44	+	1.96	2.17E-02
anchoring junction (GO:0070161)	46	23.44	+	1.96	2.17E-02
cell junction (GO:0030054)	46	23.44	+	1.96	2.17E-02

Supplemental Table 2: Significant, up-regulated GO Terms for artificially acidified Arabidopsis.

Biological Process	Gene #	Expected	Over/Under	Fold Enrichment	P-Value
response to external biotic stimulus (GO:0043207)	166	30	+	5.53	6.14E-77
response to other organism (GO:0051707)	166	30	+	5.53	6.14E-77
response to biotic stimulus (GO:0009607)	166	30.02	+	5.53	6.89E-77
biological process involved in interspecies interaction between organisms (GO:0044419)	166	30.19	+	5.5	1.56E-76
defense response (GO:0006952)	161	29.63	+	5.43	7.44E-73
response to external stimulus (GO:0009605)	170	36.02	+	4.72	3.39E-69
response to stress (GO:0006950)	216	64.17	+	3.37	6.01E-69
defense response to other organism (GO:0098542)	148	25.69	+	5.76	1.05E-68
response to bacterium (GO:0009617)	112	15.08	+	7.43	1.71E-59
response to stimulus (GO:0050896)	263	112.95	+	2.33	2.22E-59
response to fungus (GO:0009620)	93	12.08	+	7.7	3.23E-49
response to oxygen-containing compound (GO:1901700)	149	37.48	+	3.98	5.27E-49
cellular response to chemical stimulus (GO:0070887)	124	24.85	+	4.99	9.78E-49
defense response to bacterium (GO:0042742)	93	12.49	+	7.44	4.74E-48
response to chitin (GO:0010200)	61	3.74	+	16.31	1.21E-47
response to organic substance (GO:0010033)	156	42.56	+	3.67	1.51E-47
response to chemical (GO:0042221)	184	61.34	+	3	1.22E-46
cellular response to stimulus (GO:0051716)	162	47.02	+	3.45	1.66E-46
defense response to fungus (GO:0050832)	79	8.52	+	9.27	2.40E-46
response to organonitrogen compound (GO:0010243)	76	7.87	+	9.66	1.48E-45
response to organic cyclic compound (GO:0014070)	79	9.92	+	7.97	7.27E-42
response to nitrogen compound (GO:1901698)	77	9.59	+	8.03	6.77E-41

regulation of response to stress (GO:0080134)	79	10.68	+	7.39	1.10E-39
regulation of defense response (GO:0031347)	74	9.03	+	8.19	1.17E-39
response to salicylic acid (GO:0009751)	59	5.34	+	11.05	2.57E-37
cellular response to organic substance (GO:0071310)	96	18.82	+	5.1	1.53E-36
signal transduction (GO:0007165)	117	29.27	+	4	3.55E-36
signaling (GO:0023052)	118	30.03	+	3.93	7.45E-36
regulation of response to stimulus (GO:0048583)	89	16.22	+	5.49	9.88E-36
response to wounding (GO:0009611)	72	9.89	+	7.28	2.72E-35
cell communication (GO:0007154)	118	32.63	+	3.62	1.72E-32
response to endogenous stimulus (GO:0009719)	112	30.86	+	3.63	1.50E-30
response to hormone (GO:0009725)	110	30.45	+	3.61	1.08E-29
response to lipid (GO:0033993)	96	23.49	+	4.09	4.68E-29
cellular response to oxygen-containing compound (GO:1901701)	75	13.84	+	5.42	6.30E-29
cellular response to endogenous stimulus (GO:0071495)	74	14.5	+	5.11	6.56E-27
response to abiotic stimulus (GO:0009628)	137	49.94	+	2.74	9.38E-27
cellular response to hormone stimulus (GO:0032870)	72	14.06	+	5.12	3.84E-26
hormone-mediated signaling pathway (GO:0009755)	64	11.29	+	5.67	4.41E-25
regulation of cellular process (GO:0050794)	166	75.33	+	2.2	2.25E-23
response to jasmonic acid (GO:0009753)	51	7.36	+	6.93	5.67E-23
response to fatty acid (GO:0070542)	51	7.41	+	6.89	7.52E-23
cellular process (GO:0009987)	273	180.3	+	1.51	9.81E-23
regulation of biological process (GO:0050789)	182	91.27	+	1.99	1.02E-21
cellular response to hypoxia (GO:0071456)	34	2.9	+	11.72	5.67E-21

cellular response to decreased oxygen levels (GO:0036294)	34	2.93	+	11.62	7.23E-21
cellular response to oxygen levels (GO:0071453)	34	2.94	+	11.57	8.16E-21
biological regulation (GO:0065007)	188	99.83	+	1.88	8.73E-20
response to hypoxia (GO:0001666)	36	3.92	+	9.18	4.31E-19
response to decreased oxygen levels (GO:0036293)	36	4.02	+	8.96	9.12E-19
response to oxygen levels (GO:0070482)	36	4.04	+	8.91	1.10E-18
response to alcohol (GO:0097305)	62	14.5	+	4.28	4.32E-18
regulation of immune system process (GO:0002682)	27	2.17	+	12.42	9.63E-17
response to acid chemical (GO:0001101)	57	13.43	+	4.25	3.27E-16
response to molecule of bacterial origin (GO:0002237)	23	1.42	+	16.19	3.46E-16
response to water deprivation (GO:0009414)	54	12.14	+	4.45	4.82E-16
response to inorganic substance (GO:0010035)	79	25.63	+	3.08	1.15E-15
response to abscisic acid (GO:0009737)	55	13.03	+	4.22	1.98E-15
response to water (GO:0009415)	55	13.03	+	4.22	1.98E-15
cellular response to organic cyclic compound (GO:0071407)	28	3.14	+	8.91	5.46E-14
cellular response to salicylic acid stimulus (GO:0071446)	20	1.36	+	14.71	4.53E-13
immune system process (GO:0002376)	34	5.54	+	6.14	6.48E-13
systemic acquired resistance (GO:0009627)	20	1.41	+	14.2	8.27E-13
response to osmotic stress (GO:0006970)	46	10.85	+	4.24	1.77E-12
cellular response to stress (GO:0033554)	52	14.75	+	3.53	2.43E-11
response to temperature stimulus (GO:0009266)	41	10.51	+	3.9	1.06E-09
phosphorylation (GO:0016310)	48	14.19	+	3.38	1.28E-09
protein phosphorylation (GO:0006468)	45	12.83	+	3.51	2.30E-09

salicylic acid mediated signaling pathway (GO:0009863)	14	0.97	+	14.42	2.18E-08
response to oxidative stress (GO:0006979)	32	7.44	+	4.3	4.58E-08
regulation of cellular ketone metabolic process (GO:0010565)	15	1.42	+	10.56	2.08E-07
indole-containing compound metabolic process (GO:0042430)	17	2.21	+	7.69	1.05E-06
regulation of small molecule metabolic process (GO:0062012)	15	2.04	+	7.35	2.04E-05
phosphate-containing compound metabolic process (GO:0006796)	53	22.81	+	2.32	4.52E-05
phosphorus metabolic process (GO:0006793)	53	23.36	+	2.27	1.11E-04
response to cold (GO:0009409)	23	5.74	+	4.01	1.28E-04
jasmonic acid mediated signaling pathway (GO:0009867)	13	1.76	+	7.39	2.00E-04
cellular response to lipid (GO:0071396)	24	6.4	+	3.75	2.09E-04
response to salt stress (GO:0009651)	26	7.55	+	3.44	2.97E-04
cellular response to jasmonic acid stimulus (GO:0071395)	13	1.85	+	7.05	3.34E-04
cellular response to fatty acid (GO:0071398)	13	1.89	+	6.86	4.42E-04
gene expression (GO:0010467)	2	20.81	-	0.1	7.59E-04
immune response (GO:0006955)	14	2.42	+	5.8	1.02E-03
innate immune response (GO:0045087)	13	2.16	+	6.02	1.81E-03
oxoacid metabolic process (GO:0043436)	50	23.71	+	2.11	2.92E-03
regulation of response to biotic stimulus (GO:0002831)	13	2.37	+	5.49	4.74E-03
regulation of cell death (GO:0010941)	10	1.36	+	7.35	6.92E-03
regulation of response to external stimulus (GO:0032101)	13	2.55	+	5.1	1.02E-02
nucleobase-containing compound metabolic process (GO:0006139)	7	27.61	-	0.25	1.34E-02
positive regulation of defense response (GO:0031349)	9	1.18	+	7.64	1.67E-02
organic acid metabolic process (GO:0006082)	50	25.35	+	1.97	1.86E-02

indole glucosinolate metabolic process (GO:0042343)	5	0.23	+	21.68	2.60E-02
response to oomycetes (GO:0002239)	9	1.27	+	7.06	3.03E-02
RNA metabolic process (GO:0016070)	2	16.86	-	0.12	3.44E-02
nucleic acid metabolic process (GO:0090304)	5	22.77	-	0.22	4.05E-02
regulation of cell communication (GO:0010646)	18	5.39	+	3.34	4.30E-02
protein modification process (GO:0036211)	58	32.28	+	1.8	4.78E-02
Molecular Function	Gene #	Expected	Over/Under	Fold Enrichment	P-Value
ADP binding (GO:0043531)	22	2.08	+	10.6	3.77E-12
kinase activity (GO:0016301)	53	15.73	+	3.37	4.41E-11
protein kinase activity (GO:0004672)	44	12.64	+	3.48	3.15E-09
transferase activity, transferring phosphorus-containing groups (GO:0016772)	54	18.29	+	2.95	3.82E-09
protein serine/threonine kinase activity (GO:0004674)	36	9.26	+	3.89	2.09E-08
phosphotransferase activity, alcohol group as acceptor (GO:0016773)	45	14.56	+	3.09	7.83E-08
transferase activity (GO:0016740)	81	42.37	+	1.91	2.22E-05
adenyl ribonucleotide binding (GO:0032559)	28	8.12	+	3.45	5.37E-05
adenyl nucleotide binding (GO:0030554)	28	8.26	+	3.39	7.45E-05
catalytic activity, acting on a protein (GO:0140096)	63	31.61	+	1.99	2.98E-04
anion binding (GO:0043168)	39	15.53	+	2.51	5.36E-04
purine ribonucleotide binding (GO:0032555)	29	9.7	+	2.99	5.49E-04
purine nucleotide binding (GO:0017076)	29	9.86	+	2.94	7.55E-04
carbohydrate derivative binding (GO:0097367)	30	10.49	+	2.86	8.37E-04
ribonucleotide binding (GO:0032553)	29	10.05	+	2.89	1.11E-03
transmembrane signaling receptor activity (GO:0004888)	12	1.93	+	6.22	2.09E-03

ion binding (GO:0043167)	63	34.04	+	1.85	3.48E-03
signaling receptor activity (GO:0038023)	13	2.6	+	5	7.29E-03
transmembrane receptor protein kinase activity (GO:0019199)	10	1.52	+	6.59	1.01E-02
small molecule binding (GO:0036094)	37	16.45	+	2.25	1.10E-02
binding (GO:0005488)	164	125.31	+	1.31	3.36E-02
Cellular Component	Gene #	Expected	Over/Under	Fold Enrichment	P-Value
cell periphery (GO:0071944)	98	43.47	+	2.25	4.58E-12
plasma membrane (GO:0005886)	86	37.35	+	2.3	1.38E-10
membrane (GO:0016020)	109	61.06	+	1.79	2.69E-07

Supplemental Table 3: Significant, down-regulated GO Terms for severe-cold challenged Arabidopsis.

Biological Process	Gene #	Expected	Over/Under	Fold Enrichment	P-Value
response to stimulus (GO:0050896)	224	128.21	+	1.75	7.89E-20
response to chemical (GO:0042221)	137	69.63	+	1.97	1.85E-12
response to stress (GO:0006950)	138	72.84	+	1.89	3.23E-11
response to abiotic stimulus (GO:0009628)	113	56.69	+	1.99	9.74E-10
response to organic substance (GO:0010033)	97	48.31	+	2.01	6.95E-08
response to endogenous stimulus (GO:0009719)	78	35.03	+	2.23	9.49E-08
response to hormone (GO:0009725)	77	34.56	+	2.23	1.32E-07
cellular response to stimulus (GO:0051716)	98	53.37	+	1.84	6.05E-06
response to lipid (GO:0033993)	60	26.67	+	2.25	2.39E-05
biological regulation (GO:0065007)	167	113.32	+	1.47	2.82E-05
cellular response to chemical stimulus (GO:0070887)	61	28.21	+	2.16	6.37E-05
response to wounding (GO:0009611)	34	11.23	+	3.03	7.24E-05
response to oxygen-containing compound (GO:1901700)	79	42.54	+	1.86	2.44E-04
protein complex oligomerization (GO:0051259)	9	0.76	+	11.87	6.28E-04
cellular process (GO:0009987)	255	204.67	+	1.25	6.96E-04
cellular response to organic substance (GO:0071310)	48	21.36	+	2.25	8.60E-04
response to decreased oxygen levels (GO:0036293)	19	4.56	+	4.17	1.21E-03
cellular response to endogenous stimulus (GO:0071495)	40	16.45	+	2.43	1.28E-03
response to oxygen levels (GO:0070482)	19	4.59	+	4.14	1.32E-03
cellular response to hormone stimulus (GO:0032870)	39	15.96	+	2.44	1.63E-03
regulation of biological process (GO:0050789)	149	103.6	+	1.44	1.65E-03
response to radiation (GO:0009314)	56	28.18	+	1.99	3.54E-03

response to external stimulus (GO:0009605)	73	40.89	+	1.79	3.65E-03
response to hypoxia (GO:0001666)	18	4.45	+	4.04	3.66E-03
response to light stimulus (GO:0009416)	55	27.6	+	1.99	4.37E-03
response to alcohol (GO:0097305)	38	16.45	+	2.31	9.54E-03
response to abscisic acid (GO:0009737)	35	14.79	+	2.37	1.22E-02
negative regulation of response to stimulus (GO:0048585)	15	3.56	+	4.22	1.75E-02
response to osmotic stress (GO:0006970)	31	12.32	+	2.52	2.11E-02
regulation of phenylpropanoid metabolic process (GO:2000762)	6	0.4	+	15.01	2.16E-02
regulation of cellular process (GO:0050794)	124	85.51	+	1.45	2.36E-02
response to oxidative stress (GO:0006979)	24	8.45	+	2.84	2.49E-02
hormone-mediated signaling pathway (GO:0009755)	31	12.82	+	2.42	3.30E-02
response to external biotic stimulus (GO:0043207)	61	34.05	+	1.79	3.75E-02
response to other organism (GO:0051707)	61	34.05	+	1.79	3.75E-02
response to biotic stimulus (GO:0009607)	61	34.08	+	1.79	3.79E-02
biological process involved in interspecies interaction between organisms (GO:0044419)	61	34.27	+	1.78	4.09E-02
Molecular Function	Gene #	Expected	Over/Under	Fold Enrichment	P-Value
hormone binding (GO:0042562)	8	0.45	+	17.59	1.25E-04
RNA binding (GO:0003723)	4	22.32	-	0.18	6.95E-03
DNA-binding transcription factor activity (GO:0003700)	47	22.96	+	2.05	7.93E-03
Cellular Component	Gene #	Expected	Over/Under	Fold Enrichment	P-Value
plasma membrane (GO:0005886)	89	42.4	+	2.1	1.73E-08
cell periphery (GO:0071944)	98	49.35	+	1.99	2.38E-08
membrane (GO:0016020)	109	69.32	+	1.57	6.25E-04

Supplemental Table 4: Significant, up-regulated GO Terms for severe-cold challenged Arabidopsis.

Biological Process	Gene #	Expected	Over/Under	Fold enrichment	P-value
response to stimulus (GO:0050896)	402	279.15	+	1.44	1.33E-14
response to stress (GO:0006950)	260	158.6	+	1.64	4.08E-13
regulation of biological process (GO:0050789)	335	225.57	+	1.49	2.06E-12
response to chemical (GO:0042221)	248	151.61	+	1.64	3.90E-12
response to wounding (GO:0009611)	73	24.45	+	2.99	5.30E-12
response to oxygen-containing compound (GO:1901700)	171	92.62	+	1.85	3.15E-11
biological regulation (GO:0065007)	353	246.72	+	1.43	4.05E-11
regulation of cellular process (GO:0050794)	283	186.17	+	1.52	1.43E-10
cellular process (GO:0009987)	549	445.61	+	1.23	1.74E-09
cellular response to chemical stimulus (GO:0070887)	121	61.42	+	1.97	1.15E-08
response to external biotic stimulus (GO:0043207)	138	74.14	+	1.86	1.34E-08
response to other organism (GO:0051707)	138	74.14	+	1.86	1.34E-08
response to biotic stimulus (GO:0009607)	138	74.2	+	1.86	1.38E-08
biological process involved in interspecies interaction between organisms (GO:0044419)	138	74.62	+	1.85	2.31E-08
response to external stimulus (GO:0009605)	157	89.02	+	1.76	2.40E-08
response to organic substance (GO:0010033)	176	105.19	+	1.67	5.15E-08
response to endogenous stimulus (GO:0009719)	136	76.27	+	1.78	4.47E-07
cellular response to stimulus (GO:0051716)	186	116.2	+	1.6	4.69E-07
cellular response to organic substance (GO:0071310)	95	46.51	+	2.04	5.71E-07
response to salt stress (GO:0009651)	52	18.66	+	2.79	7.03E-07
regulation of response to stimulus (GO:0048583)	85	40.08	+	2.12	1.12E-06
response to hormone (GO:0009725)	133	75.25	+	1.77	1.16E-06

defense response to other organism (GO:0098542)	117	63.49	+	1.84	1.43E-06
positive regulation of biological process (GO:0048518)	92	45.82	+	2.01	3.06E-06
regulation of metabolic process (GO:0019222)	183	117.64	+	1.56	5.65E-06
cellular response to endogenous stimulus (GO:0071495)	77	35.82	+	2.15	5.82E-06
response to osmotic stress (GO:0006970)	63	26.82	+	2.35	5.93E-06
regulation of biosynthetic process (GO:0009889)	134	78.1	+	1.72	7.04E-06
cellular response to oxygen-containing compound (GO:1901701)	74	34.2	+	2.16	7.60E-06
response to lipid (GO:0033993)	107	58.06	+	1.84	8.92E-06
response to alcohol (GO:0097305)	76	35.82	+	2.12	1.02E-05
defense response (GO:0006952)	127	73.24	+	1.73	1.10E-05
cellular response to hormone stimulus (GO:0032870)	74	34.74	+	2.13	1.71E-05
hormone-mediated signaling pathway (GO:0009755)	63	27.9	+	2.26	3.62E-05
cell communication (GO:0007154)	134	80.65	+	1.66	3.64E-05
response to abscisic acid (GO:0009737)	69	32.19	+	2.14	4.13E-05
regulation of cellular biosynthetic process (GO:0031326)	128	76.42	+	1.67	6.38E-05
response to abiotic stimulus (GO:0009628)	185	123.43	+	1.5	6.85E-05
positive regulation of metabolic process (GO:0009893)	64	29.16	+	2.19	7.55E-05
signal transduction (GO:0007165)	122	72.34	+	1.69	8.72E-05
signaling (GO:0023052)	124	74.23	+	1.67	1.22E-04
regulation of DNA-templated transcription (GO:0006355)	112	65.53	+	1.71	1.88E-04
regulation of nucleic acid-templated transcription (GO:1903506)	112	65.56	+	1.71	1.91E-04
regulation of macromolecule biosynthetic process (GO:0010556)	119	70.99	+	1.68	1.92E-04
regulation of RNA biosynthetic process (GO:2001141)	112	65.62	+	1.71	1.95E-04

response to bacterium (GO:0009617)	73	37.26	+	1.96	4.19E-04
negative regulation of biological process (GO:0048519)	98	55.87	+	1.75	4.40E-04
developmental process (GO:0032502)	238	173.75	+	1.37	6.15E-04
response to organonitrogen compound (GO:0010243)	46	19.44	+	2.37	8.02E-04
positive regulation of cellular process (GO:0048522)	71	36.84	+	1.93	1.34E-03
response to acid chemical (GO:0001101)	66	33.18	+	1.99	1.39E-03
regulation of cellular metabolic process (GO:0031323)	145	95.14	+	1.52	1.53E-03
multicellular organism development (GO:0007275)	187	130.82	+	1.43	1.54E-03
regulation of nitrogen compound metabolic process (GO:0051171)	134	86.08	+	1.56	1.57E-03
response to water (GO:0009415)	64	32.19	+	1.99	1.63E-03
response to organic cyclic compound (GO:0014070)	53	24.51	+	2.16	1.64E-03
regulation of macromolecule metabolic process (GO:0060255)	147	97.36	+	1.51	2.01E-03
response to jasmonic acid (GO:0009753)	43	18.18	+	2.36	2.08E-03
regulation of RNA metabolic process (GO:0051252)	113	69.43	+	1.63	2.16E-03
defense response to bacterium (GO:0042742)	62	30.87	+	2.01	2.35E-03
response to fatty acid (GO:0070542)	43	18.3	+	2.35	2.38E-03
metabolic process (GO:0008152)	394	324.82	+	1.21	4.49E-03
regulation of gene expression (GO:0010468)	129	83.86	+	1.54	5.15E-03
protein ubiquitination (GO:0016567)	47	21.54	+	2.18	5.47E-03
response to nitrogen compound (GO:1901698)	50	23.7	+	2.11	6.08E-03
response to fungus (GO:0009620)	59	29.85	+	1.98	6.60E-03
response to chitin (GO:0010200)	27	9.24	+	2.92	6.77E-03
response to water deprivation (GO:0009414)	59	30	+	1.97	7.11E-03

multicellular organismal process (GO:0032501)	194	140.24	+	1.38	8.00E-03
anatomical structure development (GO:0048856)	215	159.32	+	1.35	1.01E-02
regulation of nucleobase-containing compound metabolic process (GO:0019219)	115	73.48	+	1.57	1.03E-02
regulation of primary metabolic process (GO:0080090)	132	87.49	+	1.51	1.05E-02
regulation of response to stress (GO:0080134)	53	26.4	+	2.01	1.23E-02
protein modification process (GO:0036211)	122	79.78	+	1.53	1.33E-02
organic substance metabolic process (GO:0071704)	359	294.25	+	1.22	1.44E-02
protein modification by small protein conjugation (GO:0032446)	47	22.59	+	2.08	1.75E-02
programmed cell death (GO:0012501)	13	2.67	+	4.87	2.60E-02
positive regulation of macromolecule metabolic process (GO:0010604)	50	25.08	+	1.99	2.94E-02
positive regulation of biosynthetic process (GO:0009891)	41	18.75	+	2.19	3.17E-02
secondary metabolic process (GO:0019748)	49	24.3	+	2.02	3.32E-02
programmed cell death induced by symbiont (GO:0034050)	10	1.56	+	6.41	3.48E-02
response to inorganic substance (GO:0010035)	100	63.34	+	1.58	3.73E-02
regulation of defense response (GO:0031347)	46	22.32	+	2.06	3.82E-02
biological process involved in interaction with symbiont (GO:0051702)	10	1.59	+	6.29	4.03E-02
negative regulation of cellular process (GO:0048523)	62	33.96	+	1.83	4.03E-02
Molecular Function	Gene #	Expected	Over/Under	Fold enrichment	P-value
protein binding (GO:0005515)	262	171.77	+	1.53	8.53E-10
binding (GO:0005488)	401	309.7	+	1.29	3.47E-07
transferase activity (GO:0016740)	160	104.71	+	1.53	1.54E-04
DNA binding (GO:0003677)	96	55.6	+	1.73	7.34E-04
DNA-binding transcription factor activity (GO:0003700)	82	49.99	+	1.64	4.46E-02

Cellular Component	Gene #	Expected	Over/Under	Fold enrichment	P-value
intracellular anatomical structure (GO:0005622)	709	647.3	+	1.1	4.75E-05
nucleus (GO:0005634)	380	318.01	+	1.19	1.05E-02
cellular anatomical entity (GO:0110165)	772	735.81	+	1.05	1.23E-02

Supplemental Table 5: Significant, down-regulated GO Terms for artificially acidified sorghum

Biological Process	Gene #	Expected	Over/Under	Fold enrichment	P-value
photosynthesis (GO:0015979)	74	8.46	+	8.75	1.28E-36
cellular metabolic process (GO:0044237)	570	355.67	+	1.6	2.50E-35
response to abiotic stimulus (GO:0009628)	336	165.73	+	2.03	3.86E-33
photosynthesis, light reaction (GO:0019684)	60	5.72	+	10.49	9.26E-33
response to light stimulus (GO:0009416)	208	80.69	+	2.58	1.48E-30
response to radiation (GO:0009314)	211	82.38	+	2.56	1.50E-30
metabolic process (GO:0008152)	639	436.12	+	1.47	6.16E-30
cellular process (GO:0009987)	794	598.3	+	1.33	8.43E-29
generation of precursor metabolites and energy (GO:0006091)	82	16.4	+	5	5.00E-26
cellular biosynthetic process (GO:0044249)	246	115.7	+	2.13	6.39E-25
biosynthetic process (GO:0009058)	270	134.03	+	2.01	1.63E-24
organic substance biosynthetic process (GO:1901576)	257	125.65	+	2.05	6.37E-24
tetrapyrrole metabolic process (GO:0033013)	63	10.68	+	5.9	9.42E-23
porphyrin-containing compound metabolic process (GO:0006778)	58	8.9	+	6.51	1.30E-22
response to stimulus (GO:0050896)	538	374.81	+	1.44	1.49E-19
organonitrogen compound biosynthetic process (GO:1901566)	143	57.65	+	2.48	3.27E-18
chlorophyll metabolic process (GO:0015994)	41	5.12	+	8.01	4.25E-18
cellular nitrogen compound biosynthetic process (GO:0044271)	131	52.73	+	2.48	2.44E-16
organic substance metabolic process (GO:0071704)	545	395.07	+	1.38	5.76E-16
plastid organization (GO:0009657)	60	13.78	+	4.36	8.31E-16
small molecule metabolic process (GO:0044281)	217	115.09	+	1.89	2.18E-15
tetrapyrrole biosynthetic process (GO:0033014)	31	3.63	+	8.55	8.01E-14

porphyrin-containing compound biosynthetic process (GO:0006779)	29	3.18	+	9.11	2.14E-13
photosynthetic electron transport chain (GO:0009767)	25	2.14	+	11.71	2.82E-13
response to temperature stimulus (GO:0009266)	94	34.89	+	2.69	5.13E-13
chlorophyll biosynthetic process (GO:0015995)	26	2.5	+	10.41	6.53E-13
protein-containing complex assembly (GO:0065003)	79	26.83	+	2.94	1.75E-12
pigment metabolic process (GO:0042440)	44	9.55	+	4.61	8.82E-12
protein-containing complex organization (GO:0043933)	81	29.81	+	2.72	5.80E-11
cellular component assembly (GO:0022607)	95	39.52	+	2.4	2.80E-10
photosynthesis, light harvesting (GO:0009765)	20	1.73	+	11.55	4.12E-10
organic cyclic compound biosynthetic process (GO:1901362)	91	38.15	+	2.39	1.37E-09
amide biosynthetic process (GO:0043604)	68	24.37	+	2.79	1.99E-09
cellular amide metabolic process (GO:0043603)	77	29.53	+	2.61	2.17E-09
organic cyclic compound metabolic process (GO:1901360)	210	126.01	+	1.67	2.27E-09
peptide metabolic process (GO:0006518)	69	25.06	+	2.75	2.34E-09
organonitrogen compound metabolic process (GO:1901564)	320	218.42	+	1.47	2.59E-09
pigment biosynthetic process (GO:0046148)	33	6.53	+	5.06	2.86E-09
electron transport chain (GO:0022900)	29	5.04	+	5.76	4.31E-09
translation (GO:0006412)	62	21.67	+	2.86	8.12E-09
peptide biosynthetic process (GO:0043043)	62	21.87	+	2.83	1.16E-08
chloroplast organization (GO:0009658)	41	10.59	+	3.87	1.20E-08
carboxylic acid metabolic process (GO:0019752)	122	61.92	+	1.97	2.35E-08
cellular aromatic compound metabolic process (GO:0006725)	200	121.5	+	1.65	2.40E-08
organic acid metabolic process (GO:0006082)	152	84.11	+	1.81	3.13E-08

cellular nitrogen compound metabolic process (GO:0034641)	210	130.52	+	1.61	5.21E-08
aromatic compound biosynthetic process (GO:0019438)	80	33.92	+	2.36	7.42E-08
oxoacid metabolic process (GO:0043436)	143	78.68	+	1.82	8.54E-08
small molecule biosynthetic process (GO:0044283)	83	36.18	+	2.29	9.63E-08
cellular component biogenesis (GO:0044085)	137	75.29	+	1.82	2.61E-07
response to stress (GO:0006950)	304	212.94	+	1.43	2.74E-07
heterocycle biosynthetic process (GO:0018130)	73	30.98	+	2.36	4.56E-07
heterocycle metabolic process (GO:0046483)	188	116.14	+	1.62	5.37E-07
photosynthesis, light harvesting in photosystem I (GO:0009768)	13	0.97	+	13.45	1.88E-06
cellular macromolecule biosynthetic process (GO:0034645)	81	38.15	+	2.12	4.89E-06
protein folding (GO:0006457)	31	8.1	+	3.83	6.26E-06
cellular component organization (GO:0016043)	180	114.69	+	1.57	1.38E-05
response to light intensity (GO:0009642)	43	15.03	+	2.86	1.84E-05
photosynthetic electron transport in photosystem I (GO:0009773)	11	0.77	+	14.37	2.37E-05
monocarboxylic acid metabolic process (GO:0032787)	61	26.39	+	2.31	3.18E-05
response to cold (GO:0009409)	49	19.05	+	2.57	4.16E-05
nitrogen compound metabolic process (GO:0006807)	373	286.02	+	1.3	4.40E-05
cellular component organization or biogenesis (GO:0071840)	214	145.75	+	1.47	6.39E-05
cellular lipid metabolic process (GO:0044255)	79	39.28	+	2.01	6.54E-05
photosystem II assembly (GO:0010207)	12	1.17	+	10.27	9.15E-05
response to oxidative stress (GO:0006979)	57	24.69	+	2.31	1.14E-04
lipid metabolic process (GO:0006629)	95	51.85	+	1.83	1.87E-04
thylakoid membrane organization (GO:0010027)	14	2.09	+	6.68	5.67E-04

NAD(P)H dehydrogenase complex assembly (GO:0010275)	8	0.44	+	18.05	7.79E-04
chloroplast rRNA processing (GO:1901259)	10	0.93	+	10.79	9.14E-04
plastid membrane organization (GO:0009668)	14	2.42	+	5.79	2.50E-03
organic acid biosynthetic process (GO:0016053)	58	28.36	+	2.05	4.03E-03
energy quenching (GO:1990066)	8	0.6	+	13.24	4.40E-03
nonphotochemical quenching (GO:0010196)	8	0.6	+	13.24	4.40E-03
response to heat (GO:0009408)	32	12.05	+	2.66	6.80E-03
lipid biosynthetic process (GO:0008610)	61	30.98	+	1.97	7.09E-03
plastid translation (GO:0032544)	9	0.93	+	9.71	7.27E-03
chaperone-mediated protein folding (GO:0061077)	14	2.78	+	5.04	1.05E-02
response to reactive oxygen species (GO:0000302)	22	6.65	+	3.31	1.16E-02
carboxylic acid biosynthetic process (GO:0046394)	50	24.01	+	2.08	1.22E-02
gene expression (GO:0010467)	110	69.05	+	1.59	1.25E-02
serine family amino acid metabolic process (GO:0009069)	13	2.46	+	5.29	1.46E-02
cellular amino acid metabolic process (GO:0006520)	48	22.8	+	2.11	1.87E-02
fat-soluble vitamin metabolic process (GO:0006775)	8	0.81	+	9.93	2.35E-02
fat-soluble vitamin biosynthetic process (GO:0042362)	8	0.81	+	9.93	2.35E-02
macromolecule biosynthetic process (GO:0009059)	86	51.77	+	1.66	3.29E-02
cell cycle (GO:0007049)	7	27.03	-	0.26	3.46E-02
cellular response to environmental stimulus (GO:0104004)	27	10.19	+	2.65	4.31E-02
cellular response to abiotic stimulus (GO:0071214)	27	10.19	+	2.65	4.31E-02
regulation of photosynthesis (GO:0010109)	11	1.93	+	5.69	4.34E-02
Molecular Function	Gene #	Expected	Over/Under	Fold enrichment	P-value

oxidoreductase activity (GO:0016491)	138	59.22	+	2.33	2.37E-15
mRNA binding (GO:0003729)	110	42.62	+	2.58	1.04E-14
binding (GO:0005488)	552	415.82	+	1.33	6.26E-13
RNA binding (GO:0003723)	133	65.26	+	2.04	1.47E-10
catalytic activity (GO:0003824)	456	336.29	+	1.36	1.81E-10
structural constituent of ribosome (GO:0003735)	44	13.29	+	3.31	1.19E-07
structural molecule activity (GO:0005198)	50	19.42	+	2.58	1.66E-05
heterocyclic compound binding (GO:1901363)	281	205.85	+	1.37	8.38E-05
organic cyclic compound binding (GO:0097159)	282	207.46	+	1.36	1.14E-04
oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor (GO:0016616)	25	7.25	+	3.45	7.72E-04
unfolded protein binding (GO:0051082)	19	4.59	+	4.14	1.68E-03
chlorophyll binding (GO:0016168)	10	1.09	+	9.19	1.75E-03
oxidoreductase activity, acting on CH-OH group of donors (GO:0016614)	26	8.62	+	3.02	4.45E-03
protein folding chaperone (GO:0044183)	14	2.74	+	5.11	5.31E-03
tetrapyrrole binding (GO:0046906)	38	16.15	+	2.35	7.70E-03
isomerase activity (GO:0016853)	28	10.11	+	2.77	8.29E-03
Cellular Component	Gene #	Expected	Over/Under	Fold enrichment	P-value
chloroplast (GO:0009507)	572	204.16	+	2.8	4.09E-127
plastid (GO:0009536)	593	220.92	+	2.68	9.80E-126
plastid envelope (GO:0009526)	243	34.68	+	7.01	1.31E-113
thylakoid (GO:0009579)	194	22.04	+	8.8	1.29E-103
envelope (GO:0031975)	260	51.68	+	5.03	8.26E-94
organelle envelope (GO:0031967)	260	51.68	+	5.03	8.26E-94

plastid stroma (GO:0009532)	206	30.25	+	6.81	5.99E-93
plastid thylakoid (GO:0031976)	168	18.17	+	9.25	1.42E-91
chloroplast thylakoid (GO:0009534)	167	17.93	+	9.32	2.11E-91
chloroplast stroma (GO:0009570)	202	29.61	+	6.82	4.01E-91
photosynthetic membrane (GO:0034357)	146	15.55	+	9.39	1.21E-79
thylakoid membrane (GO:0042651)	145	15.35	+	9.45	2.33E-79
plastid membrane (GO:0042170)	157	19.5	+	8.05	4.59E-78
plastid thylakoid membrane (GO:0055035)	137	14.22	+	9.63	1.27E-75
chloroplast thylakoid membrane (GO:0009535)	134	13.9	+	9.64	6.55E-74
chloroplast envelope (GO:0009941)	161	24.49	+	6.57	2.06E-69
cytoplasm (GO:0005737)	881	597.62	+	1.47	1.61E-65
organelle subcompartment (GO:0031984)	196	44.88	+	4.37	9.46E-60
organelle membrane (GO:0031090)	201	62.52	+	3.21	1.47E-42
membrane (GO:0016020)	361	202.63	+	1.78	6.49E-26
cytosol (GO:0005829)	231	106.67	+	2.17	9.21E-25
intracellular anatomical structure (GO:0005622)	993	869.09	+	1.14	2.71E-19
nucleus (GO:0005634)	284	426.97	-	0.67	4.05E-16
intracellular membrane-bounded organelle (GO:0043231)	914	791.31	+	1.16	2.54E-14
membrane-bounded organelle (GO:0043227)	914	793.6	+	1.15	9.30E-14
thylakoid lumen (GO:0031977)	27	2.74	+	9.86	1.16E-13
intracellular organelle (GO:0043229)	918	800.29	+	1.15	2.52E-13
organelle (GO:0043226)	918	802.26	+	1.14	6.96E-13
chloroplast thylakoid lumen (GO:0009543)	23	1.97	+	11.65	1.17E-12

plastid thylakoid lumen (GO:0031978)	23	2.01	+	11.42	1.64E-12
photosystem (GO:0009521)	22	2.58	+	8.53	7.71E-10
cellular anatomical entity (GO:0110165)	1054	987.93	+	1.07	1.70E-09
plastoglobule (GO:0010287)	19	2.42	+	7.86	8.53E-08
chloroplast thylakoid membrane protein complex (GO:0098807)	13	1.05	+	12.41	8.96E-07
plastid inner membrane (GO:0009528)	18	2.7	+	6.67	2.38E-06
photosystem II (GO:0009523)	14	1.81	+	7.72	2.81E-05
chloroplast inner membrane (GO:0009706)	16	2.54	+	6.3	3.42E-05
NAD(P)H dehydrogenase complex (plastoquinone) (GO:0010598)	9	0.52	+	17.19	4.10E-05
apoplast (GO:0048046)	36	12.29	+	2.93	4.13E-05
chloroplast membrane (GO:0031969)	21	5.32	+	3.95	3.46E-04
nucleoid (GO:0009295)	14	2.54	+	5.52	9.29E-04
photosystem I (GO:0009522)	9	0.89	+	10.16	1.21E-03
ribosome (GO:0005840)	39	15.99	+	2.44	1.26E-03
plastid nucleoid (GO:0042646)	13	2.26	+	5.76	1.45E-03
organelle inner membrane (GO:0019866)	34	13.05	+	2.6	1.56E-03
nuclear protein-containing complex (GO:0140513)	12	36.86	-	0.33	2.49E-03
membrane protein complex (GO:0098796)	50	24.49	+	2.04	5.38E-03
chloroplast nucleoid (GO:0042644)	11	1.97	+	5.57	1.15E-02
organellar ribosome (GO:0000313)	13	3.18	+	4.08	3.68E-02

Supplemental Table 6: Significant, up-regulated GO Terms for artificially acidified sorghum

Biological Process	Gene #	Expected	Over/Under	Fold Enrichment	P-Value
cellular process (GO:0009987)	387	261.52	+	1.48	1.09E-28
cellular metabolic process (GO:0044237)	273	155.47	+	1.76	5.07E-24
metabolic process (GO:0008152)	303	190.63	+	1.59	5.61E-21
organic substance metabolic process (GO:0071704)	280	172.69	+	1.62	2.92E-19
primary metabolic process (GO:0044238)	241	144.23	+	1.67	2.95E-16
cellular biosynthetic process (GO:0044249)	116	50.57	+	2.29	1.20E-13
biosynthetic process (GO:0009058)	125	58.58	+	2.13	1.18E-12
organic substance biosynthetic process (GO:1901576)	119	54.92	+	2.17	3.46E-12
nitrogen compound metabolic process (GO:0006807)	205	125.02	+	1.64	1.64E-11
organonitrogen compound metabolic process (GO:1901564)	165	95.47	+	1.73	7.41E-10
organic cyclic compound metabolic process (GO:1901360)	109	55.08	+	1.98	2.10E-08
cellular nitrogen compound metabolic process (GO:0034641)	111	57.05	+	1.95	2.96E-08
response to abiotic stimulus (GO:0009628)	131	72.44	+	1.81	3.27E-08
post-embryonic development (GO:0009791)	84	40.16	+	2.09	8.53E-07
small molecule biosynthetic process (GO:0044283)	46	15.81	+	2.91	1.03E-06
cellular aromatic compound metabolic process (GO:0006725)	101	53.11	+	1.9	1.56E-06
heterocycle metabolic process (GO:0046483)	97	50.77	+	1.91	2.97E-06
response to stimulus (GO:0050896)	229	163.83	+	1.4	4.72E-06
macromolecule metabolic process (GO:0043170)	164	105.44	+	1.56	5.01E-06
multicellular organism development (GO:0007275)	129	76.77	+	1.68	6.33E-06
reproductive structure development (GO:0048608)	74	35.16	+	2.1	7.29E-06
reproductive system development (GO:0061458)	74	35.2	+	2.1	7.54E-06

cellular amide metabolic process (GO:0043603)	39	12.91	+	3.02	9.09E-06
developmental process involved in reproduction (GO:0003006)	80	39.81	+	2.01	1.19E-05
fruit development (GO:0010154)	56	23.56	+	2.38	1.54E-05
response to stress (GO:0006950)	146	93.08	+	1.57	3.26E-05
cellular nitrogen compound biosynthetic process (GO:0044271)	54	23.05	+	2.34	7.05E-05
multicellular organismal process (GO:0032501)	132	82.3	+	1.6	7.42E-05
reproduction (GO:0000003)	86	46.61	+	1.85	1.37E-04
generation of precursor metabolites and energy (GO:0006091)	26	7.17	+	3.63	1.51E-04
small molecule metabolic process (GO:0044281)	91	50.31	+	1.81	1.60E-04
reproductive process (GO:0022414)	85	46.15	+	1.84	1.85E-04
seed development (GO:0048316)	52	22.66	+	2.29	1.98E-04
phosphorus metabolic process (GO:0006793)	68	33.88	+	2.01	2.66E-04
organonitrogen compound biosynthetic process (GO:1901566)	55	25.2	+	2.18	3.39E-04
plastid organization (GO:0009657)	23	6.02	+	3.82	3.81E-04
phosphate-containing compound metabolic process (GO:0006796)	66	33.09	+	1.99	5.31E-04
carboxylic acid metabolic process (GO:0019752)	57	27.06	+	2.11	8.04E-04
protein metabolic process (GO:0019538)	109	66.91	+	1.63	8.87E-04
embryo development (GO:0009790)	36	13.68	+	2.63	9.79E-04
tRNA aminoacylation for protein translation (GO:0006418)	10	1.06	+	9.47	1.05E-03
lipid metabolic process (GO:0006629)	50	22.66	+	2.21	1.26E-03
tRNA aminoacylation (GO:0043039)	10	1.09	+	9.16	1.38E-03
amino acid activation (GO:0043038)	10	1.09	+	9.16	1.38E-03
peptide metabolic process (GO:0006518)	31	10.95	+	2.83	1.53E-03

embryo development ending in seed dormancy (GO:0009793)	33	12.2	+	2.7	1.73E-03
response to chemical (GO:0042221)	134	88.98	+	1.51	1.94E-03
oxylipin biosynthetic process (GO:0031408)	7	0.4	+	17.28	1.96E-03
organic cyclic compound biosynthetic process (GO:1901362)	40	16.68	+	2.4	2.16E-03
amide biosynthetic process (GO:0043604)	30	10.65	+	2.82	2.59E-03
oxylipin metabolic process (GO:0031407)	7	0.44	+	15.9	3.15E-03
nucleobase-containing compound metabolic process (GO:0006139)	73	40.04	+	1.82	3.67E-03
oxoacid metabolic process (GO:0043436)	65	34.39	+	1.89	3.84E-03
jasmonic acid biosynthetic process (GO:0009695)	7	0.46	+	15.29	3.94E-03
anatomical structure development (GO:0048856)	138	93.5	+	1.48	4.14E-03
monocarboxylic acid metabolic process (GO:0032787)	31	11.53	+	2.69	4.32E-03
gene expression (GO:0010467)	59	30.18	+	1.95	5.36E-03
developmental process (GO:0032502)	147	101.97	+	1.44	6.67E-03
photosynthesis (GO:0015979)	16	3.7	+	4.33	7.14E-03
tRNA metabolic process (GO:0006399)	15	3.35	+	4.48	9.82E-03
response to heat (GO:0009408)	19	5.26	+	3.61	1.04E-02
response to osmotic stress (GO:0006970)	37	15.74	+	2.35	1.23E-02
carboxylic acid biosynthetic process (GO:0046394)	28	10.49	+	2.67	1.60E-02
monocarboxylic acid biosynthetic process (GO:0072330)	17	4.44	+	3.83	1.61E-02
response to temperature stimulus (GO:0009266)	36	15.25	+	2.36	1.67E-02
system development (GO:0048731)	101	64.45	+	1.57	1.77E-02
organic acid metabolic process (GO:0006082)	66	36.77	+	1.8	1.87E-02
jasmonic acid metabolic process (GO:0009694)	8	0.88	+	9.09	2.08E-02

translation (GO:0006412)	26	9.47	+	2.74	2.16E-02
organic acid biosynthetic process (GO:0016053)	31	12.4	+	2.5	2.45E-02
peptide biosynthetic process (GO:0043043)	26	9.56	+	2.72	2.52E-02
response to salt stress (GO:0009651)	28	10.95	+	2.56	3.40E-02
cellular component organization (GO:0016043)	82	50.13	+	1.64	3.70E-02
lipid biosynthetic process (GO:0008610)	32	13.54	+	2.36	3.92E-02
response to oxygen-containing compound (GO:1901700)	87	54.36	+	1.6	3.95E-02
RNA metabolic process (GO:0016070)	48	24.46	+	1.96	4.67E-02
Molecular Function	Gene #	Expected	Over/Under	Fold Enrichment	P-Value
catalytic activity (GO:0003824)	271	147	+	1.84	1.70E-27
binding (GO:0005488)	296	181.75	+	1.63	4.26E-22
mRNA binding (GO:0003729)	59	18.63	+	3.17	5.00E-11
protein binding (GO:0005515)	172	100.81	+	1.71	2.52E-10
RNA binding (GO:0003723)	74	28.53	+	2.59	4.34E-10
ATP-dependent activity (GO:0140657)	43	12.82	+	3.35	3.57E-08
organic cyclic compound binding (GO:0097159)	153	90.68	+	1.69	4.07E-08
heterocyclic compound binding (GO:1901363)	151	89.98	+	1.68	8.09E-08
ribonucleoside triphosphate phosphatase activity (GO:0017111)	33	8.36	+	3.95	1.80E-07
pyrophosphatase activity (GO:0016462)	35	9.47	+	3.69	2.58E-07
hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides (GO:0016818)	35	9.63	+	3.63	3.92E-07
hydrolase activity, acting on acid anhydrides (GO:0016817)	35	9.7	+	3.61	4.70E-07
hydrolase activity (GO:0016787)	90	47.44	+	1.9	1.02E-05
small molecule binding (GO:0036094)	56	23.86	+	2.35	1.97E-05

ligase activity (GO:0016874)	19	4	+	4.75	1.23E-04
translation factor activity, RNA binding (GO:0008135)	13	1.83	+	7.1	2.30E-04
ATP hydrolysis activity (GO:0016887)	20	4.67	+	4.29	2.68E-04
translation regulator activity, nucleic acid binding (GO:0090079)	13	1.87	+	6.96	2.81E-04
ligase activity, forming carbon-oxygen bonds (GO:0016875)	10	1.06	+	9.47	6.17E-04
aminoacyl-tRNA ligase activity (GO:0004812)	10	1.06	+	9.47	6.17E-04
transferase activity (GO:0016740)	101	61.45	+	1.64	1.17E-03
catalytic activity, acting on a tRNA (GO:0140101)	14	2.52	+	5.56	1.18E-03
ion binding (GO:0043167)	85	49.37	+	1.72	2.00E-03
oxidoreductase activity (GO:0016491)	53	25.88	+	2.05	2.50E-03
catalytic activity, acting on RNA (GO:0140098)	27	9.26	+	2.92	2.91E-03
translation elongation factor activity (GO:0003746)	6	0.3	+	20.04	3.67E-03
translation regulator activity (GO:0045182)	13	2.39	+	5.43	3.76E-03
anion binding (GO:0043168)	48	22.52	+	2.13	3.94E-03
metallopeptidase activity (GO:0008237)	11	1.69	+	6.51	4.64E-03
protein folding chaperone (GO:0044183)	9	1.2	+	7.52	1.32E-02
nucleotide binding (GO:0000166)	42	19.86	+	2.11	1.65E-02
nucleoside phosphate binding (GO:1901265)	42	19.86	+	2.11	1.65E-02
ATP-dependent protein folding chaperone (GO:0140662)	8	0.95	+	8.41	2.03E-02
transferase activity, transferring phosphorus-containing groups (GO:0016772)	51	26.54	+	1.92	2.37E-02
catalytic activity, acting on a protein (GO:0140096)	76	45.85	+	1.66	2.90E-02
Cellular Component	Gene #	Expected	Over/Under	Fold Enrichment	P-Value
plastid (GO:0009536)	212	96.56	+	2.2	4.82E-29

chloroplast stroma (GO:0009570)	73	12.94	+	5.64	1.50E-28
plastid stroma (GO:0009532)	73	13.22	+	5.52	5.28E-28
chloroplast (GO:0009507)	198	89.24	+	2.22	5.05E-27
cytoplasm (GO:0005737)	370	261.22	+	1.42	2.77E-21
cytosol (GO:0005829)	114	46.63	+	2.44	5.60E-16
plastid envelope (GO:0009526)	57	15.16	+	3.76	5.09E-14
chloroplast envelope (GO:0009941)	45	10.71	+	4.2	2.78E-12
intracellular anatomical structure (GO:0005622)	442	379.88	+	1.16	3.90E-11
membrane (GO:0016020)	157	88.57	+	1.77	1.25E-10
envelope (GO:0031975)	64	22.59	+	2.83	1.74E-10
organelle envelope (GO:0031967)	64	22.59	+	2.83	1.74E-10
intracellular membrane-bounded organelle (GO:0043231)	414	345.88	+	1.2	3.58E-10
membrane-bounded organelle (GO:0043227)	414	346.89	+	1.19	6.86E-10
thylakoid (GO:0009579)	38	9.63	+	3.95	2.51E-09
intracellular organelle (GO:0043229)	414	349.81	+	1.18	4.70E-09
organelle (GO:0043226)	414	350.67	+	1.18	8.85E-09
cellular anatomical entity (GO:0110165)	470	431.83	+	1.09	6.43E-08
plasma membrane (GO:0005886)	101	54.18	+	1.86	8.35E-07
chloroplast thylakoid (GO:0009534)	30	7.84	+	3.83	9.68E-07
plastid thylakoid (GO:0031976)	30	7.94	+	3.78	1.30E-06
plasmodesma (GO:0009506)	43	15.64	+	2.75	4.43E-06
cell-cell junction (GO:0005911)	43	15.64	+	2.75	4.43E-06
symplast (GO:0055044)	43	15.64	+	2.75	4.43E-06

anchoring junction (GO:0070161)	43	15.64	+	2.75	4.43E-06
cell junction (GO:0030054)	43	15.64	+	2.75	4.43E-06
cell periphery (GO:0071944)	110	63.06	+	1.74	5.90E-06
apoplast (GO:0048046)	23	5.37	+	4.28	1.22E-05
organelle subcompartment (GO:0031984)	46	19.62	+	2.35	1.38E-04
vacuole (GO:0005773)	44	18.52	+	2.38	2.12E-04
plastid membrane (GO:0042170)	27	8.52	+	3.17	2.44E-04
thylakoid membrane (GO:0042651)	22	6.71	+	3.28	1.76E-03
photosynthetic membrane (GO:0034357)	22	6.8	+	3.24	2.14E-03
protein-containing complex (GO:0032991)	88	54.48	+	1.62	6.21E-03
plant-type vacuole (GO:0000325)	33	14.03	+	2.35	6.99E-03
cytoplasmic vesicle (GO:0031410)	31	12.94	+	2.4	9.77E-03
intracellular vesicle (GO:0097708)	31	12.98	+	2.39	1.02E-02
nucleolus (GO:0005730)	24	8.84	+	2.72	1.29E-02
chloroplast thylakoid membrane (GO:0009535)	19	6.07	+	3.13	1.57E-02
plastid thylakoid membrane (GO:0055035)	19	6.22	+	3.06	2.11E-02
Golgi apparatus (GO:0005794)	41	20.76	+	1.97	4.43E-02

Supplemental Table 7: Significant, down-regulated GO Terms for severe-cold-challenged sorghum

Biological Process	Gene #	Expected	Over/Under	Fold Enrichment	P-Value
response to light intensity (GO:0009642)	17	3.94	+	4.31	2.76E-03
electron transport chain (GO:0022900)	10	1.32	+	7.57	5.13E-03
regulation of shoot system development (GO:0048831)	11	2.03	+	5.42	3.23E-02
generation of precursor metabolites and energy (GO:0006091)	16	4.3	+	3.72	3.49E-02
Molecular Function	Gene #	Expected	Over/Under	Fold Enrichment	P-Value
protein binding (GO:0005515)	94	60.53	+	1.55	1.05E-02
electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity (GO:0045156)	4	0.12	+	34.39	2.62E-02
Cellular Component	Gene #	Expected	Over/Under	Fold Enrichment	P-Value
mitochondrial respirasome (GO:0005746)	13	1.22	+	10.69	6.83E-07
respiratory chain complex (GO:0098803)	13	1.26	+	10.33	1.00E-06
respirasome (GO:0070469)	13	1.32	+	9.84	1.73E-06
inner mitochondrial membrane protein complex (GO:0098800)	15	1.98	+	7.59	2.79E-06
oxidoreductase complex (GO:1990204)	14	1.72	+	8.12	4.12E-06
mitochondrial envelope (GO:0005740)	19	3.57	+	5.32	6.04E-06
envelope (GO:0031975)	38	13.56	+	2.8	1.20E-05
organelle envelope (GO:0031967)	38	13.56	+	2.8	1.20E-05
mitochondrial inner membrane (GO:0005743)	16	2.7	+	5.93	2.21E-05
transmembrane transporter complex (GO:1902495)	11	1.09	+	10.1	2.31E-05
transporter complex (GO:1990351)	11	1.13	+	9.72	3.31E-05
mitochondrial protein-containing complex (GO:0098798)	16	2.83	+	5.65	4.23E-05
membrane protein complex (GO:0098796)	24	6.43	+	3.73	4.57E-05
mitochondrial membrane (GO:0031966)	17	3.39	+	5.01	8.38E-05

integral component of membrane (GO:0016021)	22	5.7	+	3.86	9.48E-05
membrane (GO:0016020)	90	53.18	+	1.69	1.72E-04
cytosol (GO:0005829)	57	28	+	2.04	1.78E-04
cytochrome complex (GO:0070069)	7	0.4	+	17.42	2.83E-04
organelle inner membrane (GO:0019866)	16	3.43	+	4.67	4.80E-04
organelle membrane (GO:0031090)	39	16.41	+	2.38	5.05E-04
intrinsic component of membrane (GO:0031224)	27	9.12	+	2.96	5.94E-04
thylakoid membrane (GO:0042651)	16	4.03	+	3.97	3.54E-03
photosynthetic membrane (GO:0034357)	16	4.08	+	3.92	4.15E-03
chloroplast thylakoid membrane (GO:0009535)	15	3.65	+	4.11	4.71E-03
chloroplast thylakoid (GO:0009534)	17	4.7	+	3.61	5.96E-03
plastid thylakoid membrane (GO:0055035)	15	3.73	+	4.02	6.12E-03
thylakoid (GO:0009579)	19	5.78	+	3.29	6.51E-03
plastid thylakoid (GO:0031976)	17	4.77	+	3.57	7.05E-03
mitochondrial respiratory chain complex I (GO:0005747)	7	0.77	+	9.07	1.45E-02
respiratory chain complex I (GO:0045271)	7	0.8	+	8.71	1.84E-02
NADH dehydrogenase complex (GO:0030964)	7	0.85	+	8.28	2.50E-02

Supplemental Table 8: Significant, up-regulated GO Terms for severe-cold-challenged sorghum