

Supplementary data

Differentially expressed genes and *in silico* analysis in response to ozone (O₃) stress of soybean leaves

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Supplementary Table 1. Functional annotation results of DEGs upon ozone treatment.

Regulation	Seq. Name	Seq. Description	Seq. Length	No. of Hits	min. e-value	Mean Similarity
Up regulated	Glyma01g32750	lipid transfer protein precursor	357	20	9.15E-81	79.05%
	Glyma02g37990	metalloendoproteinase 1-like	918	20	0	67.90%
	Glyma02g39830	hypothetical protein MTR_7g046110 [Medicago truncatula]	1374	20	8.55E-172	69.60%
	Glyma04g01020	probable fructose-bisphosphate aldolase chloroplastic-like	1188	20	0	94.35%
	Glyma06g16600	cyclase dehydrase family protein	2061	20	0	76.90%
	Glyma11g01520	seed specific protein bn15d1b	357	20	5.72E-84	65.45%
	Glyma10g33710	superoxide dismutase	735	20	0	89.35%
	Glyma06g01310	40s ribosomal protein	327	20	6.25E-42	97.40%
	Glyma06g01310	40s ribosomal protein s25-2	303	20	1.32E-15	96.25%
	Glyma18g01860	histone h3	411	20	7.35E-91	99.40%
	Glyma01g43720	hydroxymethylbilane synthase	1071	20	0	91.10%
	Glyma15g40190	glutathione s-transferase	651	20	5.45E-141	92.30%
	Glyma16g20780	N/A	531	0		
	Glyma11g03470	uncharacterized protein	186	20	7.14E-39	79.20%
	Glyma16g28070	chlorophyll a/b-binding protein	795	20	0	97.90%
	Glyma11g14250	protein	447	20	4.61E-93	60.30%
	Glyma01g28440	upf0481 protein at3g47200-like	1131	20	3.55E-130	51.05%
	Glyma09g09100	protein tify 3b	621	20	2.78E-137	67.30%
	Glyma19g37100	udp-glycosyltransferase 73c2-like	1527	20	0	80.25%
	Glyma14g40590	histone h3	411	20	7.35E-91	99.40%
	Glyma14g14360	udp-n-acetylglucosamine udp-glucose gdp-mannose transporter	1038	20	0	86.30%
	Glyma18g04080	rubisco activase	1296	20	0	91.40%
	Glyma13g32680	methionine sulfoxide reductase type	609	20	3.07E-131	89.55%
	Glyma17g03350	pathogenesis-related protein class 10	477	20	9.43E-100	89.30%
	Glyma03g39200	N/A	492	20	8.62E-103	86.15%
	Glyma06g11970	nac domain protein	900	20	0	82.95%
	Glyma08g22600	phospholipase d alpha	2430	20	0	93.65%
	Glyma06g40330	protein	360	20	5.66E-62	85.45%
	Glyma08g08770	light-harvesting complex ii protein lhcb1	936	20	0	97.05%
	Glyma19g34480	cytochrome p450 94a1-like	1539	20	0	82.50%
	Glyma13g44080	uncharacterized protein	348	20	7.06E-70	68.75%

	Glyma13g20200	polyubiquitin	465	20	1.48E-102	99.75%
	Glyma01g03070	N/A	480	0		
	Glyma14g39950	syringolide-induced protein 14-1-1	741	20	5.30E-140	56.30%
	Glyma05g00780	eukaryotic translation initiation factor 5a2	483	20	1.76E-114	97.60%
	Glyma17g11130	eukaryotic translation initiation factor 5a2	483	20	1.76E-114	97.60%
	Glyma18g13630	glutathione s-transferase	648	20	1.72E-157	88.70%
	Glyma13g35950	protein	351	20	9.22E-80	87.05%
	Glyma08g36390	cell wall-associated partial	180	6	8.03E-28	82.17%
	Glyma06g07400	gtp-binding nuclear protein ran-3-like	666	20	7.24E-153	98.15%
	Glyma14g38720	ubiquinol-cytochrome c reductase complex ubiquinone-binding protein qp-c	219	20	1.99E-47	89.25%
	Glyma07g25390	desacetoxyvindoline 4-	1197	20	0	71.35%
	Glyma02g38610	rna polymerase beta subunit	192	20	1.97E-26	87.25%
	Glyma10g05790	dna-binding protein s1fa2	249	20	3.02E-24	83.75%
	Glyma12g01080	42 kda peptidyl-prolyl isomerase	1113	20	0	88.75%
	Glyma15g01470	pleiotropic drug resistance protein 1-like	4281	20	0	90.10%
	Glyma13g12070	N/A	417			
	Glyma13g12070	cytochrome p450 liketbp	693	20	8.86E-57	80.00%
	Glyma19g39570	60s ribosomal protein	639	20	3.48E-126	96.40%
	Glyma18g02610	wound-induced protein 1-like	324	20	2.15E-71	73.90%
	Glyma08g11480	s-adenosyl-1-homocysteine hydrolase	1458	20	0	97.40%
	Glyma07g00520	mitogen-activated protein kinase kinase 5	1056	20	0	85.30%
	Glyma19g40690	adp-ribosylation factor	546	20	4.90E-129	99.80%
	Glyma05g36770	f-box protein skip8	657	20	1.01E-162	84.90%
Down regulated	Glyma07g00890	lipoxygenase	2580	20	0	86.10%
	Glyma08g18800	9-cis-epoxycarotenoid dioxygenase	1062	20	1.88E-131	74.30%
	Glyma13g26150	eri1 exoribonuclease	1245	20	0	78.25%
	Glyma09g04150	uncharacterized protein loc100526890	261	10	5.86E-39	71.60%
	Glyma18g08750	ribosomal protein s19	150	20	2.71E-29	97.00%
	Glyma05g31450	myo-inositol-1-phosphate synthase	1533	20	0	98.00%
	Glyma13g20830	rna-binding protein	840	20	4.74E-164	77.20%
	Glyma11g35500	protein	570	20	8.30E-125	85.85%
	Glyma18g03220	chlorophyll a/b binding protein	837	20	1.96E-167	83.50%
	Glyma19g36130	thioredoxin-like protein	771	20	9.76E-173	87.05%
	Glyma17g01800	rna-binding post-transcriptional regulator csx1-like	1209	20	0	84.10%
	Glyma06g12250	protein tolB	2100	20	0	73.10%
	Glyma07g38090	uncharacterized protein	567	20	1.38E-102	77.50%
	Glyma11g07160	uncharacterized protein	507	20	5.72E-99	80.95%
	Glyma19g06370	ribulose biphosphate carboxylase	537	20	3.47E-132	93.40%
	Glyma08g40850	ssdna-binding transcriptional regulator	810	20	2.54E-139	79.70%
	Glyma15g03050	lipoxygenase 1-5	2562	20	0	89.75%
	Glyma19g44200	aldose 1-	954	20	0	88.45%

Glyma09g07310	chlorophyll a b-binding protein	297	20	1.89E-67	99.50%
Glyma18g44510	cbl-interacting serine threonine-protein kinase 11-like	1332	20	0	75.80%
Glyma02g16000	photosystem ii reaction center w protein	402	20	9.02E-54	73.35%
Glyma15g12130	cytochrome b6 f complex subunit iv	378	20	1.20E-67	95.45%
Glyma12g06920	inner membrane protein albino3	1353	20	0	85.05%
Glyma05g25810	light-harvesting complex ii protein lhcb1	792	20	0	96.85%
Glyma15g41540	phosphoglycerate kinase	1452	20	0	96.60%
Glyma05g04210	elongation factor chloroplastic-like	2343	20	0	92.70%
Glyma09g24780	cell wall-associated hydrolase	207	10	8.35E-27	74.60%
Glyma03g31580	photosystem ii reaction center w protein	402	20	2.22E-54	71.30%
Glyma15g16060	dynein light chain cytoplasmic-like	357	20	3.88E-82	81.95%
Glyma12g16560	transcription factor ilr3	711	20	1.57E-106	85.60%
Glyma03g34310	tonoplast intrinsic protein	753	20	4.92E-156	92.55%
Glyma06g07200	ein3-binding f-box protein 1-like	1917	20	0	80.40%
Glyma10g06250	copper-binding protein	969	20	1.52E-139	69.25%
Glyma11g04900	lrr-like protein	810	20	5.45E-165	84.50%
Glyma06g06030	pentatricopeptide repeat-containing protein at4g33170-like	1740	20	0	74.90%
Glyma07g34440	40s ribosomal protein s17	405	20	2.28E-91	93.40%
Glyma17g05500	alpha-farnesene synthase	1707	20	0	70.50%
Glyma01g06260	uncharacterized protein loc100817240 isoform 1	561	20	3.98E-126	82.55%
Glyma01g06260	uncharacterized protein loc100817240 isoform 2	438	20	5.22E-93	70.10%
Glyma06g12720	transcriptional corepressor seuss-like	2862	20	0	77.60%
Glyma05g03340	atp synthase delta chain	747	20	5.80E-145	78.20%
Glyma06g16030	pentatricopeptide repeat-containing protein	1677	20	0	64.65%
Glyma08g14830	uncharacterized protein loc100779108 isoform 1	564	6	8.96E-22	85.50%
Glyma05g31610	uncharacterized protein loc100527462	573	8	5.31E-36	81.63%
Glyma14g31370	rna polymerase sigma factor rpod-like	1539	20	0	78.00%
Glyma04g39370	photosystem i reaction center subunit n	555	20	3.45E-74	81.50%
Glyma18g35300	uncharacterized protein	195	7	3.38E-20	94.00%
Glyma18g35300	unknown [Glycine max]	171	1	6.91E-20	97.00%
Glyma12g07160	60s ribosomal protein l23a	456	20	1.41E-93	93.30%
Glyma18g08900	30s ribosomal protein s10	618	20	1.60E-107	90.20%
Glyma06g38160	protochlorophyllide chloroplastic-like	1200	20	0	92.05%
Glyma13g37010	transcription activator glk1-like	1272	20	0	65.75%
Glyma19g28990	alpha-tubulin	1356	20	0	97.85%
Glyma14g36140	serine threonine-protein kinase ctr1-like	2712	20	0	73.25%
Glyma17g34690	glycine dehydrogenase	3171	20	0	93.75%
Glyma08g18750	glycolate oxidase	1116	20	0	96.40%
Glyma10g11570	trna-dihydrouridine synthase a	1461	20	0	86.85%
Glyma13g04640	ferredoxin-thioredoxin reductase	435	20	4.32E-105	87.60%
Glyma10g34970	phosphoenolpyruvate carboxylase	3084	20	0	91.20%

Glyma15g07910	probable allantoinase 1-like	1542	20	0	85.35%
Glyma04g36250	elongation factor chloroplastic-like	1443	20	0	92.65%
Glyma02g46970	nuclear transcription factor y subunit b-3	498	20	1.57E-90	84.95%
Glyma07g36870	protein high chlorophyll fluorescent 107	1935	20	0	78.60%
Glyma17g23870	cell wall-associated hydrolase	267	9	1.13E-18	54.89%
Glyma11g34230	rubisco activase	1332	20	0	92.80%
Glyma11g34340	uncharacterized protein	1005	20	0	68.20%
Glyma09g38340	haloacid dehalogenase-like hydrolase domain-containing protein	1110	20	0	92.30%
Glyma09g38340	2-phosphoglycolate phosphatase 1	843	20	1.09E-149	90.85%
Glyma10g39780	polyubiquitin 10	918	20	0	99.85%
Glyma10g39780	ubiquitin	234	20	6.94E-48	99.90%
Glyma10g39780	polyubiquitin	690	20	1.51E-158	99.90%
Glyma08g17570	cation efflux family protein	1191	20	0	87.00%
Glyma01g06030	alpha-expansin 3	753	20	4.26E-164	92.75%
Glyma09g07590	lycopene epsilon cyclase	1599	20	0	86.55%
Glyma20g37940	acyl- binding protein 4	1980	20	0	84.30%
Glyma05g21350	atp synthase cf0 subunit iii	582	20	1.42E-13	82.35%
Glyma18g04510	dehydroascorbate reductase	786	20	1.28E-175	86.05%
Glyma01g35910	carotenoid cleavage dioxygenase 4	1530	20	0	87.45%
Glyma04g09550	aux iaa protein	1083	20	0	79.55%
Glyma09g00820	wrky transcription factor 6-like	1626	20	0	72.80%
Glyma10g41300	histidine-rich ca2+-binding protein	996	16	4.02E-67	85.63%
Glyma20g24430	lipoyl chloroplastic-like	1095	20	0	88.45%
Glyma18g48450	protein	813	20	0	63.55%
Glyma16g04460	arabinogalactan peptide 14	276	9	2.47E-19	72.67%
Glyma10g31080	ammonium transporter	1518	20	0	88.50%
Glyma20g01120	protein	384	20	4.15E-54	77.40%
Glyma14g06680	probable aquaporin pip-type 7a-like	870	20	0	94.30%
Glyma14g06680	aquaporin protein pip11	669	20	7.46E-153	92.20%
Glyma10g00520	50s ribosomal protein l28	411	20	1.13E-94	83.30%
Glyma13g28180	glutamine synthetase	1299	20	0	96.05%
Glyma19g35560	heat shock	1965	20	0	97.90%
Glyma19g35560	heat shock protein 70	1650	20	0	98.10%
Glyma10g39460	psi reaction center subunit ii	633	20	3.13E-128	84.65%
Glyma03g29710	transcription factor bhlh60	1203	20	0	71.40%
Glyma17g04210	dihydrolipoamide dehydrogenase precursor	1503	20	0	93.80%
Glyma18g00930	lipid transfer	582	20	1.75E-89	74.80%
Glyma05g35030	40s ribosomal protein s15-like protein	468	20	1.46E-97	97.85%
Glyma14g01470	plastidic fructose-bisphosphate aldolase	1074	20	0	92.45%
Glyma07g06590	60s ribosomal protein l5-like	951	20	0	94.95%
Glyma14g01130	chlorophyll a b binding protein	798	20	0	95.20%
Glyma12g08060	uncharacterized protein	513	20	1.94E-91	65.70%

Glyma15g11490	atp synthase gamma chain	1128	20	0	92.00%
Glyma06g08030	ring u-box domain-containing protein	1626	20	0	64.40%
Glyma19g00910	ferredoxin-thioredoxin variable chain-like	462	20	1.64E-93	71.50%
Glyma08g14280	protein chromosomal-like	972	20	0	89.90%
Glyma03g33990	cell division cycle protein 48 homolog	2427	20	0	96.95%
Glyma05g09390	ferredoxin-thioredoxin variable chain-like	438	20	1.38E-88	73.45%
