

Supplementray Materials

Table S1. Differentially expressed proteins in *P. neglecta* after treatment with SPA.

Accession	Sequence Description	Score	Coverage [%]	Fold change	P-value
Gene.10060::TRINITY_DN16389_c0_g1::g.10060::m.10060	40S ribosomal protein S20	157.918	47	0.83094	0.01302
Gene.101::TRINITY_DN10172_c0_g1::g.101::m.101	40S ribosomal protein S16	295.819	7	0.79533	0.01735
Gene.10267::TRINITY_DN16452_c0_g2::g.10267::m.10267	Benzoate 4-monooxygenase	623.239	4	1.50983	0.02603
Gene.10322::TRINITY_DN16467_c0_g1::g.10322::m.10322	Sexual differentiation process protein isp4	584.719	5	1.73394	0.03287
Gene.10367::TRINITY_DN16488_c0_g3::g.10367::m.10367	Cyclic pyranopterin monophosphate synthase, mitochondrial	157.532	4	1.22095	0.03621
Gene.10394::TRINITY_DN16500_c0_g1::g.10394::m.10394	Bifunctional cytochrome P450 / NADPH-P450 reductase	1315.06	20	1.45399	0.02816
Gene.10420::TRINITY_DN16509_c0_g1::g.10420::m.10420	Neutrophil cytosol factor 2	147.132	6	1.4777	0.03805
Gene.10479::TRINITY_DN16533_c0_g2::g.10479::m.10479	Deoxyuridine 5'-triphosphate nucleotidohydrolase	228.024	37	0.69252	0.00487
Gene.10500::TRINITY_DN16540_c0_g2::g.10500::m.10500	Vacuolar morphogenesis protein 6	171.4	8	1.23048	0.00953
Gene.10529::TRINITY_DN16547_c0_g1::g.10529::m.10529	Actin-related protein 2/3 complex subunit 3	138.658	4	0.77755	0.00885
Gene.1064::TRINITY_DN11092_c1_g5::g.1064::m.1064	Flavohemoprotein A	259.225	64	0.62014	0.007
Gene.10646::TRINITY_DN16581_c0_g1::g.10646::m.10646	GPI-anchored CFEM domain protein ARB_01545	58.5362	6	1.99401	0.03057
Gene.10655::TRINITY_DN16584_c0_g1::g.10655::m.10655	Clustered mitochondria protein homolog	1596.64	50	0.77096	0.0245
Gene.10989::TRINITY_DN16697_c0_g1::g.10989::m.10989	Cyclic AMP-dependent transcription factor ATF-2	97.8265	8	0.76626	0.01514
Gene.11119::TRINITY_DN16746_c0_g2::g.11119::m.11119	ATP synthase subunit delta, mitochondrial	272.707	28	0.657	0.00967
Gene.11200::TRINITY_DN16770_c0_g3::g.11200::m.11200	Activator of stress genes 1	280.026	3	1.29308	0.01491
Gene.11294::TRINITY_DN16802_c0_g1::g.11294::m.11294	40S ribosomal protein S2	590.882	8	1.25432	0.02736
Gene.11570::TRINITY_DN16893_c0_g1::g.11570::m.11570	BolA-like protein 1	91.2781	20	0.74043	0.03728
Gene.1158::TRINITY_DN11156_c0_g1::g.1158::m.1158	Pre-rRNA-processing protein, PNO1	371.703	14	0.75879	0.03031
Gene.11689::TRINITY_DN16928_c0_g3::g.11689::m.11689	Glucan endo-1,3-alpha-glucosidase, agn1	206.068	17	1.25225	0.03723
Gene.11768::TRINITY_DN16953_c0_g2::g.11768::m.11768	SWI/SNF chromatin-remodeling complex subunit, sol1	176.022	7	0.77253	0.00105
Gene.11850::TRINITY_DN16978_c0_g1::g.11850::m.11850	Vegetative incompatibility protein, HET-E-1	60.8474	58	0.71674	0.01031
Gene.11946::TRINITY_DN16993_c0_g1::g.11946::m.11946	N-alpha-acetyltransferase 30	161.384	17	1.97471	0.04182
Gene.12075::TRINITY_DN17038_c0_g2::g.12075::m.12075	54S ribosomal protein L12, mitochondrial	128.257	38	0.56878	0.01654
Gene.12096::TRINITY_DN17043_c0_g1::g.12096::m.12096	Protein BCP1	353.214	38	0.8229	0.03779
Gene.12114::TRINITY_DN17046_c0_g4::g.12114::m.12114	Guanine deaminase	80.1073	9	1.6404	0.00122
Gene.12223::TRINITY_DN17085_c0_g1::g.12223::m.12223	Regulator of V-ATPase in vacuolar membrane protein 2	44.2838	8	1.2805	0.00042
Gene.12281::TRINITY_DN17100_c1_g2::g.12281::m.12281	Probable DNA primase large subunit	749.199	5	0.79319	0.03209
Gene.12414::TRINITY_DN17133_c0_g3::g.12414::m.12414	mRNA export factor rsm1	72.0182	2	0.71478	0.00086
Gene.12419::TRINITY_DN17137_c0_g2::g.12419::m.12419	Calcium-binding protein NCS-1	321.627	40	0.75431	0.00669
Gene.12493::TRINITY_DN1715_c0_g1::g.12493::m.12493	Probable proteasome subunit beta type-2	348.977	17	0.68161	0.01104
Gene.12606::TRINITY_DN17194_c1_g4::g.12606::m.12606	Mitochondrial fission 1 protein	252.292	27	0.638	0.0188
Gene.12607::TRINITY_DN17195_c0_g2::g.12607::m.12607	Probable D-xylulose reductase A	115.931	24	1.82134	0.02358
Gene.12867::TRINITY_DN17252_c0_g2::g.12867::m.12867	Bleomycin hydrolase	138.658	11	0.70891	0.00626
Gene.12872::TRINITY_DN17253_c0_g1::g.12872::m.12872	Sphingolipid long chain base-responsive protein PIL1	190.274	60	1.50585	0.03836
Gene.12894::TRINITY_DN17257_c0_g1::g.12894::m.12894	UBX domain-containing protein 1	107.071	35	0.79533	0.02442
Gene.12944::TRINITY_DN17272_c1_g1::g.12944::m.12944	Single-stranded TG1-3 DNA-binding protein	124.79	63	0.79211	0.03038

Gene.13076::TRINITY_DN17309_c0_g1::g.13076::m.13076	RING finger protein ETP1 homolog	313.538	2	1.23714	0.01577
Gene.13103::TRINITY_DN17314_c0_g1::g.13103::m.13103	Uncharacterized oxidoreductase	208.764	69	0.70746	0.00308
Gene.13204::TRINITY_DN17341_c0_g1::g.13204::m.13204	Probable eukaryotic translation initiation factor 2 subunit beta	227.254	50	0.8276	0.01538
Gene.13208::TRINITY_DN17342_c0_g2::g.13208::m.13208	Probable fumarate hydratase, mitochondrial	669.848	58	0.81464	0.02774
Gene.13435::TRINITY_DN17399_c0_g1::g.13435::m.13435	Myosin regulatory light chain cdc4	181.03	83	0.76991	0.02569
Gene.13462::TRINITY_DN17404_c0_g5::g.13462::m.13462	Putative glycine cleavage system H protein, mitochondrial	116.316	39	0.62839	0.00105
Gene.13489::TRINITY_DN17410_c0_g2::g.13489::m.13489	Hit family protein 1	72.4034	16	0.77148	0.04045
Gene.13507::TRINITY_DN17416_c0_g1::g.13507::m.13507	NAD(P)H-dependent D-xylose reductase, xyl1	255.758	4	1.2779	0.02825
Gene.13533::TRINITY_DN17418_c1_g8::g.13533::m.13533	Ammonium transporter 1	497.278	3	2.44687	0.00833
Gene.1380::TRINITY_DN11320_c1_g1::g.1380::m.1380	Methyltransferase, ustM	128.257	28	1.28311	0.00646
Gene.13831::TRINITY_DN17504_c0_g1::g.13831::m.13831	Xanthocillin biosynthesis cluster protein D	94.7449	12	1.22845	0.0067
Gene.13904::TRINITY_DN17526_c0_g1::g.13904::m.13904	NADH-dependent flavin oxidoreductase, nadA	405.601	29	1.25141	0.00979
Gene.14155::TRINITY_DN17584_c0_g3::g.14155::m.14155	NA polymerase-associated protein C651.09c	126.716	7	1.24757	0.00202
Gene.14393::TRINITY_DN17631_c0_g3::g.14393::m.14393	Protein IVY1	102.449	5	1.23547	0.04438
Gene.14578::TRINITY_DN17679_c0_g3::g.14578::m.14578	Secretory component protein SHR3	60.4622	29	1.32919	0.03613
Gene.14582::TRINITY_DN1767_c0_g2::g.14582::m.14582	Mitochondrial import receptor subunit tom22	149.058	28	0.63177	0.01677
Gene.14686::TRINITY_DN17702_c0_g8::g.14686::m.14686	Mitochondrial protein cyt-4	628.632	9	0.75182	0.01388
Gene.14752::TRINITY_DN17717_c0_g1::g.14752::m.14752	Phosphatidylinositol 4,5-bisphosphate-binding protein	300.056	16	1.24551	0.00186
Gene.14900::TRINITY_DN17742_c0_g4::g.14900::m.14900	Ferrochelatase, mitochondrial	426.017	41	0.82815	0.0232
Gene.15070::TRINITY_DN17778_c0_g1::g.15070::m.15070	Protein transport protein SEC61 subunit alpha	935.636	14	1.41895	0.00325
Gene.15106::TRINITY_DN17785_c1_g5::g.15106::m.15106	Ornithine aminotransferase	642.884	52	0.7613	0.02381
Gene.15162::TRINITY_DN17799_c0_g1::g.15162::m.15162	Phosphatidylglycerol/phosphatidylinositol transfer protein	189.504	42	1.3261	0.04914
Gene.15167::TRINITY_DN17800_c0_g1::g.15167::m.15167	40S ribosomal protein S21	154.451	45	1.31303	0.00863
Gene.15236::TRINITY_DN17818_c0_g1::g.15236::m.15236	Methionine aminopeptidase 1	428.328	38	0.78991	0.00232
Gene.15286::TRINITY_DN17832_c0_g2::g.15286::m.15286	3,4-dihydroxy-2-butanone 4-phosphate synthase	265.388	56	0.70455	0.01971
Gene.15351::TRINITY_DN17839_c0_g1::g.15351::m.15351	Rho GDP-dissociation inhibitor	177.563	64	0.79587	0.0314
Gene.15486::TRINITY_DN17870_c0_g1::g.15486::m.15486	Succinate--CoA ligase [ADP-forming] subunit alpha, mitochondrial	326.25	37	0.81683	0.00463
Gene.15571::TRINITY_DN17883_c0_g1::g.15571::m.15571	GTPase-activating protein, GYP7	631.713	4	1.25781	0.00185
Gene.15710::TRINITY_DN178_c0_g1::g.15710::m.15710	ATP synthase assembly factor FMC1, mitochondrial	51.9878	15	1.37208	0.00185
Gene.15800::TRINITY_DN17919_c0_g3::g.15800::m.15800	Microsomal glutathione S-transferase 3	77.411	15	1.95081	0.00526
Gene.15833::TRINITY_DN17927_c1_g4::g.15833::m.15833	Glyoxalase 3	78.5666	25	1.58398	0.04093
Gene.15852::TRINITY_DN17933_c0_g3::g.15852::m.15852	Cytochrome c oxidase subunit 6, mitochondrial	57.3806	10	0.45278	0.00422
Gene.1586::TRINITY_DN11491_c0_g1::g.1586::m.1586	DNA-directed RNA polymerase II subunit RPB9	91.2781	3	0.75446	0.02215
Gene.15860::TRINITY_DN17934_c2_g15::g.15860::m.15860	Putative 26S proteasome complex subunit sem-1	72.4034	32	0.5064	0.02429
Gene.15986::TRINITY_DN17950_c0_g2::g.15986::m.15986	Tyrosine--tRNA ligase, mitochondrial	629.402	25	0.72612	0.00879
Gene.16301::TRINITY_DN18014_c1_g3::g.16301::m.16301	Uncharacterized transcriptional regulatory protein C15D4.02	85.1149	2	1.31036	0.00757
Gene.16335::TRINITY_DN18020_c0_g2::g.16335::m.16335	40S ribosomal protein S15	232.646	23	0.7194	0.00595
Gene.16569::TRINITY_DN18053_c0_g5::g.16569::m.16569	2,3-dihydroxybenzoate decarboxylase	201.06	3	1.2531	0.01843
Gene.16616::TRINITY_DN18059_c0_g2::g.16616::m.16616	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3	62.003	18	0.82205	0.03211
Gene.16630::TRINITY_DN18061_c0_g1::g.16630::m.16630	40S ribosomal protein S28	129.028	30	0.81105	0.01723
Gene.16658::TRINITY_DN18066_c1_g12::g.16658::m.16658	Vacuolar protein sorting-associated protein 41 homolog	199.904	4	1.26112	0.01993
Gene.1696::TRINITY_DN11594_c0_g1::g.1696::m.1696	NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial	359.762	41	1.25602	0.00657

Gene.17002::TRINITY_DN18107_c1_g1::g.17002::m.17002	Nuclear distribution protein, PAC1	627.476	17	1.29973	0.00398
Gene.17208::TRINITY_DN18131_c1_g9::g.17208::m.17208	Arginine metabolism regulation protein II	57.7658	2	1.66002	0.00039
Gene.17295::TRINITY_DN18137_c0_g17::g.17295::m.17295	Uncharacterized oxidoreductase C26F1.07	224.172	11	1.21239	0.01273
Gene.17340::TRINITY_DN18141_c1_g13::g.17340::m.17340	Phosphatidylserine decarboxylase proenzyme 1, mitochondrial	384.8	16	0.78336	0.02447
Gene.17343::TRINITY_DN18141_c1_g16::g.17343::m.17343	Molybdopterin synthase catalytic subunit	263.077	6	0.76115	0.00371
Gene.17355::TRINITY_DN18141_c1_g7::g.17355::m.17355	60 kDa lysophospholipase	317.775	25	0.78253	0.04835
Gene.17472::TRINITY_DN18150_c0_g7::g.17472::m.17472	Reticulocyte-binding protein 2 homolog a	59.6918	2	0.79647	0.03988
Gene.17654::TRINITY_DN18184_c1_g12::g.17654::m.17654	Transcriptional regulator RPN4	93.9745	6	0.689	0.04913
Gene.17713::TRINITY_DN18185_c0_g1::g.17713::m.17713	UBP9-binding protein, bun107	191.045	6	1.21157	0.01472
Gene.17795::TRINITY_DN18190_c1_g1::g.17795::m.17795	Uncharacterized protein YJL213W	45.4394	16	1.34283	0.04048
Gene.17797::TRINITY_DN18190_c1_g10::g.17797::m.17797	Uncharacterized protein PYUK71.03c	668.692	25	1.24757	0.01714
Gene.17835::TRINITY_DN18191_c1_g1::g.17835::m.17835	Nucleoporin POM33	350.903	27	1.25094	0.03085
Gene.17838::TRINITY_DN18191_c1_g4::g.17838::m.17838	Temperature-induced lipocalin-1	59.3066	24	9.10101	0.00538
Gene.17875::TRINITY_DN18199_c0_g10::g.17875::m.17875	Copper amine oxidase 1	861.677	29	1.39004	0.00066
Gene.17879::TRINITY_DN18199_c0_g2::g.17879::m.17879	Splicing factor 3B subunit 4	267.314	5	0.77357	0.01656
Gene.17904::TRINITY_DN18200_c1_g1::g.17904::m.17904	60S ribosomal protein L23-B	241.506	17	1.68261	0.00808
Gene.17937::TRINITY_DN18205_c3_g16::g.17937::m.17937	Pyridoxal phosphate homeostasis protein	201.06	27	0.74469	0.00248
Gene.18::TRINITY_DN10041_c0_g1::g.18::m.18	Ribosome-releasing factor 2, mitochondrial	597.045	5	1.23003	0.04671
Gene.18091::TRINITY_DN18224_c2_g4::g.18091::m.18091	Catalase	613.609	21	1.67261	0.0215
Gene.18227::TRINITY_DN18240_c1_g1::g.18227::m.18227	NEDD8-specific protease 2	105.916	5	1.21774	0.01676
Gene.18345::TRINITY_DN18257_c0_g2::g.18345::m.18345	40S ribosomal protein S9	163.31	65	1.3015	0.01379
Gene.18346::TRINITY_DN18257_c0_g3::g.18346::m.18346	40S ribosomal protein S9-A	312.768	24	1.75023	0.00137
Gene.18356::TRINITY_DN18258_c0_g2::g.18356::m.18356	Pinoresinol reductase 2	55.0694	15	1.92826	3.8E-05
Gene.18439::TRINITY_DN18267_c2_g7::g.18439::m.18439	Uncharacterized protein YJL213W	132.109	10	1.22103	0.03057
Gene.18454::TRINITY_DN18269_c1_g1::g.18454::m.18454	Uncharacterized membrane protein YJR124C	263.462	14	1.32378	0.04306
Gene.18573::TRINITY_DN18277_c0_g4::g.18573::m.18573	Uncharacterized protein C354.08c	427.557	2	1.51467	0.0031
Gene.1873::TRINITY_DN11773_c0_g1::g.1873::m.1873	C-1-tetrahydrofolate synthase, cytoplasmic	1187.17	48	0.78761	0.02697
Gene.18766::TRINITY_DN18291_c0_g2::g.18766::m.18766	Putative fungistatic metabolite	58.151	14	1.70758	0.01876
Gene.18956::TRINITY_DN18310_c3_g5::g.18956::m.18956	Probable dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	481.1	47	0.79533	0.02147
Gene.19092::TRINITY_DN18321_c2_g6::g.19092::m.19092	Histidine biosynthesis trifunctional protein	1296.18	44	0.75901	0.00774
Gene.19190::TRINITY_DN18327_c3_g6::g.19190::m.19190	Mannose-1-phosphate guanylttransferase	641.728	50	0.82871	0.00242
Gene.19251::TRINITY_DN1832_c0_g1::g.19251::m.19251	Dicarboxylic amino acid permease	382.489	5	1.79367	0.02976
Gene.19281::TRINITY_DN18331_c0_g8::g.19281::m.19281	Probable secreted lipase ARB_02369	179.104	9	1.77778	0.01863
Gene.194::TRINITY_DN10320_c0_g1::g.194::m.194	Peroxisomal multifunctional enzyme type 2	100.138	7	2.52113	0.04521
Gene.19591::TRINITY_DN18354_c0_g19::g.19591::m.19591	Putative glutathione-dependent formaldehyde-activating enzyme	43.5134	7	1.47893	0.00523
Gene.19635::TRINITY_DN18357_c0_g1::g.19635::m.19635	Pyruvate decarboxylase	1047.73	6	1.56849	0.02976
Gene.19663::TRINITY_DN18362_c0_g2::g.19663::m.19663	Heat shock protein SSC1, mitochondrial	106.301	28	2.125	0.00674
Gene.1972::TRINITY_DN11828_c0_g2::g.1972::m.1972	UPF0676 protein C1494.01	60.077	13	1.20832	0.03941
Gene.19755::TRINITY_DN18365_c0_g2::g.19755::m.19755	60S ribosomal protein L10a	361.303	28	0.81159	0.04803
Gene.19848::TRINITY_DN18370_c2_g3::g.19848::m.19848	Protein-lysine N-methyltransferase EFM4	157.532	8	1.537	0.0081
Gene.19894::TRINITY_DN18373_c0_g3::g.19894::m.19894	Heat shock protein 60	959.903	61	0.7369	0.03357

Gene.20005::TRINITY_DN18383_c0_g4::g.20005::m.20005	Poly [ADP-ribose] polymerase 2	326.25	12	0.74571	0.02553
Gene.20174::TRINITY_DN18390_c1_g15::g.20174::m.20174	Chitobiosyldiphosphodolichol beta-mannosyltransferase	327.405	16	1.26112	0.00172
Gene.20181::TRINITY_DN18390_c1_g4::g.20181::m.20181	Uncharacterized J domain-containing protein C3E7.11c	211.846	41	0.77515	0.00934
Gene.202::TRINITY_DN1032_c0_g1::g.202::m.202	tRNA-aminoacylation cofactor, ARC1	182.185	50	0.73661	0.03453
Gene.20269::TRINITY_DN18396_c0_g2::g.20269::m.20269	60S ribosomal protein L12	288.886	52	0.82039	0.00721
Gene.20316::TRINITY_DN18400_c0_g5::g.20316::m.20316	Membrane primary amine oxidase	297.36	36	1.80374	0.00119
Gene.20425::TRINITY_DN18403_c0_g6::g.20425::m.20425	Peptide-N4-(N-acetyl-beta-glucosaminy)l asparagine amidase A	198.364	2	2.00702	0.00811
Gene.20433::TRINITY_DN18404_c0_g2::g.20433::m.20433	Uncharacterized isomerase YHI9	74.7146	19	0.58746	0.00764
Gene.2044::TRINITY_DN11859_c0_g1::g.2044::m.2044	Probable helicase mot1	1607.42	12	1.22763	0.00842
Gene.20649::TRINITY_DN18413_c2_g1::g.20649::m.20649	Uncharacterized mitochondrial carrier C8C9.12c	308.531	12	0.79718	0.00371
Gene.20704::TRINITY_DN18416_c0_g2::g.20704::m.20704	Asparagine synthetase [glutamine-hydrolyzing] 1	286.189	17	0.82365	0.01301
Gene.20737::TRINITY_DN18421_c0_g8::g.20737::m.20737	Uncharacterized protein C13G1.09	315.079	11	0.83008	0.02942
Gene.20840::TRINITY_DN18428_c0_g2::g.20840::m.20840	Transcription factor himD	74.7146	4	1.22469	0.02631
Gene.20899::TRINITY_DN18431_c0_g3::g.20899::m.20899	Malate dehydrogenase, mitochondrial	312.768	69	0.66159	0.02604
Gene.20948::TRINITY_DN18435_c2_g1::g.20948::m.20948	Uncharacterized RING finger protein P32A8.03c	120.553	5	0.80693	0.03544
Gene.21021::TRINITY_DN18437_c0_g1::g.21021::m.21021	Ergothioneine biosynthesis protein 1	652.514	12	0.72414	0.00434
Gene.21089::TRINITY_DN18441_c1_g22::g.21089::m.21089	Aromatic amino acid aminotransferase C1773.13	182.185	2	1.27964	0.0013
Gene.21107::TRINITY_DN18441_c1_g7::g.21107::m.21107	Uncharacterized membrane protein YMR155W	174.866	2	1.45741	0.04476
Gene.21112::TRINITY_DN18441_c1_g9::g.21112::m.21112	Beta-1,3-glucan-binding protein	219.55	16	1.75482	0.01483
Gene.21117::TRINITY_DN18443_c0_g1::g.21117::m.21117	Protein sfk1	73.559	4	1.30985	0.00268
Gene.21160::TRINITY_DN18444_c0_g27::g.21160::m.21160	Secondary metabolism regulator LAE1	277.715	5	1.731	0.02191
Gene.21251::TRINITY_DN18452_c1_g14::g.21251::m.21251	Universal stress protein A family protein C25B2.10	154.451	11	1.28833	0.00435
Gene.21258::TRINITY_DN18452_c1_g19::g.21258::m.21258	Putative transferase CAF17, mitochondrial	285.419	14	0.71674	0.02726
Gene.21285::TRINITY_DN18452_c1_g6::g.21285::m.21285	T-complex protein 1 subunit gamma	838.18	66	0.79856	0.00228
Gene.21303::TRINITY_DN18454_c1_g12::g.21303::m.21303	Respiration factor 2	112.079	3	1.20066	0.00773
Gene.21613::TRINITY_DN18467_c1_g2::g.21613::m.21613	T-complex protein 1 subunit zeta	764.607	40	0.81239	0.02256
Gene.21665::TRINITY_DN18469_c0_g1::g.21665::m.21665	Inosine triphosphate pyrophosphatase	300.056	47	0.82396	0.01163
Gene.21700::TRINITY_DN18471_c0_g13::g.21700::m.21700	Probable phospholipase C20G8.02, mitochondrial	283.878	2	1.30376	0.01962
Gene.21723::TRINITY_DN18471_c0_g6::g.21723::m.21723	DNA-binding protein HEXBP	147.517	75	0.79964	0.02204
Gene.2177::TRINITY_DN11902_c0_g1::g.2177::m.2177	Cytochrome P450 monooxygenase, sdnE	188.734	4	1.53443	0.0398
Gene.21904::TRINITY_DN18478_c1_g6::g.21904::m.21904	UPF0588 membrane protein C20F10.02c	161.77	10	1.24841	0.00166
Gene.21921::TRINITY_DN1847_c0_g1::g.21921::m.21921	Alanyl-tRNA editing protein Aarsd1	51.2174	31	0.66833	0.04298
Gene.21940::TRINITY_DN18480_c1_g2::g.21940::m.21940	Aldehyde reductase 2	246.899	10	1.39577	0.03069
Gene.2206::TRINITY_DN11913_c0_g2::g.2206::m.2206	Translocator protein homolog	126.716	25	1.9975	0.00021
Gene.22089::TRINITY_DN18488_c2_g13::g.22089::m.22089	13 kDa ribonucleoprotein-associated protein	181.03	13	0.64249	0.01568
Gene.22151::TRINITY_DN18489_c2_g3::g.22151::m.22151	Spermidine synthase	458.759	47	0.76263	0.00178
Gene.22164::TRINITY_DN18489_c2_g8::g.22164::m.22164	Probable E3 ubiquitin-protein ligase WAVH2	56.9954	5	1.24169	0.04086
Gene.22218::TRINITY_DN18490_c1_g9::g.22218::m.22218	Uncharacterized protein YEL023C	49.2914	1	1.65722	0.02814
Gene.22411::TRINITY_DN18507_c0_g3::g.22411::m.22411	Heat shock protein hsp88	1060.44	66	0.80995	0.03876
Gene.22454::TRINITY_DN18511_c3_g14::g.22454::m.22454	60S acidic ribosomal protein P1	130.183	9	0.64564	0.01167
Gene.22461::TRINITY_DN18511_c3_g2::g.22461::m.22461	2-oxoglutarate-Fe(II) type oxidoreductase hxnY	146.747	59	1.3996	0.03335
Gene.22543::TRINITY_DN18513_c4_g16::g.22543::m.22543	GrpE protein homolog, mitochondrial	255.373	53	0.66556	0.042

Gene.22682::TRINITY_DN18517_c1_g9::g.22682::m.22682	Zinc-type alcohol dehydrogenase-like protein C16A3.02c	199.134	28	0.7994	0.02592
Gene.22745::TRINITY_DN18523_c0_g3::g.22745::m.22745	N14-3-3 family protein artA	291.197	73	0.83262	0.02938
Gene.22753::TRINITY_DN18523_c0_g7::g.22753::m.22753	Reticulocyte-binding protein 2 homolog a	50.447	1	2.23276	0.04862
Gene.22838::TRINITY_DN18529_c2_g2::g.22838::m.22838	Dothistromin biosynthesis peroxidase, dotB	228.794	3	1.43112	0.0294
Gene.22975::TRINITY_DN18534_c1_g5::g.22975::m.22975	Sphingolipid C9-methyltransferase	124.405	24	2.69354	0.00643
Gene.23010::TRINITY_DN18535_c0_g16::g.23010::m.23010	Dihydrofolate reductase	135.576	16	0.79021	0.0097
Gene.23060::TRINITY_DN18536_c3_g18::g.23060::m.23060	Mitochondrial import receptor subunit tom70	909.057	55	0.82896	0.01604
Gene.23077::TRINITY_DN18536_c3_g27::g.23077::m.23077	Mannose-6-phosphate isomerase	235.343	7	1.75229	0.00868
Gene.23123::TRINITY_DN18537_c1_g15::g.23123::m.23123	U3 small nucleolar RNA-associated protein 5	133.265	16	0.82346	0.01725
Gene.23196::TRINITY_DN18539_c0_g14::g.23196::m.23196	tRNA (guanine-N(7)-)-methyltransferase non-catalytic subunit trm82	301.982	15	0.80102	0.00059
Gene.2333::TRINITY_DN11983_c0_g1::g.2333::m.2333	Replication termination factor 2	122.865	3	0.83008	0.04722
Gene.23366::TRINITY_DN18553_c0_g1::g.23366::m.23366	ATP synthase subunit gamma, mitochondrial	310.071	67	0.8218	0.00478
Gene.23431::TRINITY_DN18560_c0_g3::g.23431::m.23431	Glutamine synthetase	663.685	2	0.66389	0.01378
Gene.2344::TRINITY_DN11985_c0_g1::g.2344::m.2344	Orotate phosphoribosyltransferase	283.493	47	0.81184	0.01483
Gene.23467::TRINITY_DN18562_c0_g14::g.23467::m.23467	Autophagy-related protein 11	1475.69	1	1.28311	0.03577
Gene.23498::TRINITY_DN18562_c0_g25::g.23498::m.23498	Trans-enoyl reductase fsr4	314.694	38	1.56739	0.01073
Gene.2358::TRINITY_DN12003_c0_g2::g.2358::m.2358	Homocysteine synthase	431.795	5	1.80767	0.03045
Gene.23683::TRINITY_DN18568_c2_g19::g.23683::m.23683	Probable nitrilase C965.09	84.7297	2	1.80421	0.02415
Gene.23766::TRINITY_DN18575_c0_g16::g.23766::m.23766	TATA element modulatory factor	81.6481	4	1.41061	0.00182
Gene.23785::TRINITY_DN18575_c0_g25::g.23785::m.23785	Bifunctional decalin synthase calF	352.058	5	1.22552	0.02478
Gene.24072::TRINITY_DN18582_c0_g23::g.24072::m.24072	Laccase-1	643.654	17	2.74703	0.00056
Gene.24075::TRINITY_DN18582_c0_g24::g.24075::m.24075	Laccase-2	601.282	2	1.8436	0.00762
Gene.24092::TRINITY_DN18582_c0_g3::g.24092::m.24092	WSC domain-containing protein ARB_07867	849.351	32	1.8342	0.01066
Gene.24116::TRINITY_DN18582_c0_g8::g.24116::m.24116	Laccase-1	646.351	10	1.6121	0.0213
Gene.24133::TRINITY_DN18583_c0_g8::g.24133::m.24133	Heat shock 70 kDa protein	731.48	56	0.6835	0.01143
Gene.24177::TRINITY_DN18586_c0_g11::g.24177::m.24177	Isoleucine--tRNA ligase, chloroplastic / mitochondrial	641.728	18	0.76493	0.02219
Gene.24250::TRINITY_DN18589_c1_g4::g.24250::m.24250	Ankyrin-1	197.978	5	0.77778	0.00204
Gene.24290::TRINITY_DN18590_c2_g3::g.24290::m.24290	Glutathione peroxidase-like peroxiredoxin 2	202.986	22	1.36913	0.00407
Gene.24391::TRINITY_DN18592_c2_g16::g.24391::m.24391	NAD(P) transhydrogenase, mitochondrial	1055.05	4	1.46812	0.02912
Gene.24446::TRINITY_DN18593_c0_g2::g.24446::m.24446	Mitochondrial protein import protein mas5	319.701	43	0.82039	0.02619
Gene.2445::TRINITY_DN12062_c0_g2::g.2445::m.2445	25-hydroxycholesterol 7-alpha-hydroxylase (Fragment)	93.2041	6	1.30808	0.0331
Gene.2466::TRINITY_DN1206_c0_g1::g.2466::m.2466	Tripeptidyl-peptidase sed1	586.645	4	1.35756	0.02477
Gene.24668::TRINITY_DN18601_c1_g16::g.24668::m.24668	C2H2 finger domain transcription factor crzA	400.979	3	0.6802	0.0198
Gene.24704::TRINITY_DN18602_c0_g14::g.24704::m.24704	Serine/threonine-protein kinase RIM15	412.535	1	1.83019	0.02033
Gene.24777::TRINITY_DN18603_c0_g14::g.24777::m.24777	Pyruvate dehydrogenase complex protein X component, mitochondrial	154.451	51	0.74723	0.00432
Gene.24803::TRINITY_DN18603_c0_g23::g.24803::m.24803	Galactose/lactose metabolism regulatory protein GAL80	126.716	29	1.36967	0.01193
Gene.24841::TRINITY_DN18604_c0_g9::g.24841::m.24841	5-methylcytosine rRNA methyltransferase NSUN4	83.9593	5	0.78625	0.0333
Gene.2487::TRINITY_DN12084_c0_g3::g.2487::m.2487	Elongator complex protein 4	146.747	3	1.55754	0.00378
Gene.24879::TRINITY_DN18607_c1_g19::g.24879::m.24879	Probable beta-glucosidase I	939.488	8	1.38663	0.00154
Gene.24887::TRINITY_DN18607_c1_g21::g.24887::m.24887	U3 small nucleolar RNA-associated protein 20	440.269	3	1.29797	0.00929
Gene.24918::TRINITY_DN18607_c1_g6::g.24918::m.24918	GBH/ACA ribonucleoprotein complex subunit GAR1	194.897	20	0.66945	0.01667
Gene.24941::TRINITY_DN18608_c1_g7::g.24941::m.24941	Serine/threonine-protein kinase ppk16	329.331	3	1.33827	0.01081

Gene.25250::TRINITY_DN18617_c1_g22::g.25250::m.25250	Uncharacterized HTH La-type RNA-binding protein C1527.03	83.9593	26	0.70746	0.01231
Gene.25255::TRINITY_DN18617_c1_g27::g.25255::m.25255	Uncharacterized protein C736.07c	47.3654	3	1.20994	0.02903
Gene.25297::TRINITY_DN18619_c0_g1::g.25297::m.25297	Ubiquitin-conjugating enzyme E2-16 kDa	295.049	26	0.81928	0.0047
Gene.25429::TRINITY_DN18623_c2_g16::g.25429::m.25429	Nucleolar GTP-binding protein 2	776.163	9	0.83262	0.02578
Gene.25440::TRINITY_DN18623_c2_g18::g.25440::m.25440	40S ribosomal protein S13	242.276	30	1.57137	0.00257
Gene.25444::TRINITY_DN18623_c2_g2::g.25444::m.25444	Anucleate primary sterigmata protein A	427.172	7	1.20389	0.00173
Gene.25529::TRINITY_DN18625_c0_g14::g.25529::m.25529	CUE domain-containing protein C354.10	78.9518	18	0.74448	0.01152
Gene.25608::TRINITY_DN18626_c1_g4::g.25608::m.25608	NPC intracellular cholesterol transporter 1-related protein 1	867.455	9	1.22506	0.00701
Gene.25652::TRINITY_DN18627_c0_g19::g.25652::m.25652	Aldehyde dehydrogenase	393.66	2	1.29232	0.00682
Gene.25657::TRINITY_DN18627_c0_g20::g.25657::m.25657	Short-chain dehydrogenase/reductase ATR7	111.309	81	1.23343	0.0151
Gene.25721::TRINITY_DN18628_c3_g5::g.25721::m.25721	Probable Delta (7)-sterol 5(6)-desaturase	503.056	3	1.51403	0.02284
Gene.25910::TRINITY_DN18633_c3_g16::g.25910::m.25910	Deoxyribonuclease Tat-D	254.988	2	0.77567	0.01057
Gene.26051::TRINITY_DN18638_c0_g14::g.26051::m.26051	Putative serine/threonine-protein phosphatase C22H10.04	460.299	4	0.78678	0.00489
Gene.2617::TRINITY_DN12157_c0_g1::g.2617::m.2617	Aspartyl aminopeptidase	702.205	30	0.83293	0.00038
Gene.26220::TRINITY_DN18643_c1_g11::g.26220::m.26220	ATP synthase subunit H, mitochondrial	54.6842	36	0.76939	0.02042
Gene.26310::TRINITY_DN18646_c2_g8::g.26310::m.26310	Transcription factor SFP1	152.525	4	0.77989	0.00317
Gene.26317::TRINITY_DN18646_c2_g9::g.26317::m.26317	Probable inactive nicotinamidase At3g16190	46.2098	22	1.32648	0.00123
Gene.26454::TRINITY_DN18654_c0_g17::g.26454::m.26454	Small glutamine-rich tetratricopeptide repeat-containing protein 2	207.994	25	0.79051	0.00444
Gene.26667::TRINITY_DN18664_c0_g1::g.26667::m.26667	Ferric/cupric reductase transmembrane component 7	139.428	11	1.3175	0.01799
Gene.26690::TRINITY_DN18664_c0_g19::g.26690::m.26690	Non-specific lipid-transfer protein (Fragment)	448.358	9	1.32648	0.02921
Gene.26769::TRINITY_DN18665_c1_g6::g.26769::m.26769	Altered inheritance of mitochondria protein 6 homolog ARB_06966	331.643	19	1.51783	0.03495
Gene.27015::TRINITY_DN18671_c6_g7::g.27015::m.27015	Probable oxygen-dependent coproporphyrinogen-III oxidase	327.405	56	0.7336	0.03894
Gene.27281::TRINITY_DN18679_c2_g21::g.27281::m.27281	LETM1 domain-containing protein mdm28, mitochondrial	385.185	40	0.79563	0.02625
Gene.27399::TRINITY_DN18683_c5_g17::g.27399::m.27399	Cutinase transcription factor 1 alpha	76.2554	4	0.76678	0.02396
Gene.27431::TRINITY_DN18683_c5_g6::g.27431::m.27431	Morphogenesis-related protein MSB1	143.665	5	1.24346	0.01609
Gene.2753::TRINITY_DN12228_c0_g1::g.2753::m.2753	Signaling mucin HKR1	56.9954	1	1.96247	0.01314
Gene.27548::TRINITY_DN18693_c0_g1::g.27548::m.27548	Ketoisovalerate reductase BEA2	353.214	4	1.2193	0.01313
Gene.27586::TRINITY_DN18705_c0_g1::g.27586::m.27586	N-carbamoylputrescine amidase	82.8037	21	2.0633	0.02486
Gene.27759::TRINITY_DN18778_c0_g1::g.27759::m.27759	Mitochondrial import inner membrane translocase subunit tim16	216.083	70	0.66759	0.03458
Gene.27817::TRINITY_DN18800_c0_g1::g.27817::m.27817	Probable trafficking protein particle complex subunit 2	126.331	18	2.861	0.00945
Gene.27872::TRINITY_DN18827_c0_g1::g.27872::m.27872	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	283.108	34	0.7341	0.00594
Gene.27994::TRINITY_DN18897_c0_g1::g.27994::m.27994	Acid phosphatase PHO1	154.451	8	1.2363	0.01129
Gene.28064::TRINITY_DN1893_c0_g1::g.28064::m.28064	Mitochondrial respiratory chain complexes assembly protein	764.607	45	0.77725	0.02599
Gene.28174::TRINITY_DN19015_c0_g1::g.28174::m.28174	Short-chain dehydrogenase reductase 3a	71.633	31	0.75109	0.00331
Gene.28452::TRINITY_DN1928_c0_g1::g.28452::m.28452	Short chain dehydrogenase atnD	196.052	47	1.23881	0.03664
Gene.28634::TRINITY_DN19377_c0_g1::g.28634::m.28634	ATP-dependent RNA helicase MSS116, mitochondrial	352.058	27	0.81623	0.00082
Gene.28670::TRINITY_DN19389_c0_g1::g.28670::m.28670	ATP-dependent RNA helicase mrh4, mitochondrial	729.554	31	0.76783	0.02727
Gene.28724::TRINITY_DN19415_c0_g1::g.28724::m.28724	Protein priA	70.4774	5	2.88666	0.03666
Gene.28736::TRINITY_DN19425_c0_g1::g.28736::m.28736	Alpha N-terminal protein methyltransferase 1	163.31	3	1.35386	0.00255
Gene.28744::TRINITY_DN19432_c0_g1::g.28744::m.28744	Pre-mRNA-splicing factor SYF1	1459.51	10	1.27704	0.03184
Gene.28818::TRINITY_DN19467_c0_g1::g.28818::m.28818	Plasma alpha-L-fucosidase	198.749	3	1.43251	0.04929
Gene.28821::TRINITY_DN19469_c0_g1::g.28821::m.28821	Oxidase FUB9	305.834	17	1.26843	0.02801

Gene.28834::TRINITY_DN19476_c0_g1::g.28834::m.28834	Protein FMP25, mitochondrial	120.553	41	0.80723	0.02333
Gene.28914::TRINITY_DN19516_c0_g1::g.28914::m.28914	6-phosphogluconate dehydrogenase, decarboxylating	396.356	9	1.26453	0.03721
Gene.28917::TRINITY_DN19521_c0_g1::g.28917::m.28917	Succinate-semialdehyde dehydrogenase, mitochondrial	412.92	2	0.79319	0.00544
Gene.28955::TRINITY_DN19545_c0_g1::g.28955::m.28955	Hydroxyacyl-thioester dehydratase type 2, mitochondrial	82.4185	13	1.31354	0.01068
Gene.2900::TRINITY_DN12282_c0_g3::g.2900::m.2900	Protein BNI4	83.5741	3	1.46324	0.00362
Gene.29072::TRINITY_DN19650_c0_g1::g.29072::m.29072	NADH-ubiquinone oxidoreductase 12 kDa subunit, mitochondrial	178.718	42	1.45139	0.00809
Gene.29175::TRINITY_DN1977_c0_g1::g.29175::m.29175	Probable nitrilase C965.09	74.3294	33	1.31392	0.03147
Gene.29243::TRINITY_DN1990_c0_g1::g.29243::m.29243	DnaJ homolog subfamily C member 7 homolog	325.865	31	0.73561	0.02797
Gene.29258::TRINITY_DN19938_c0_g1::g.29258::m.29258	Ubiquitin-conjugating enzyme E2 16	120.168	6	1.37758	0.01323
Gene.29373::TRINITY_DN20024_c0_g1::g.29373::m.29373	Nudix hydrolase 7	41.9726	42	0.7991	0.02455
Gene.29396::TRINITY_DN20036_c0_g1::g.29396::m.29396	Neutral ceramidase 2	501.516	4	1.2351	0.02762
Gene.29467::TRINITY_DN2006_c0_g1::g.29467::m.29467	UPF0768 protein YBL029C-A	39.6614	6	0.67673	0.03301
Gene.29625::TRINITY_DN20133_c0_g1::g.29625::m.29625	Ras-like protein	385.185	70	1.30238	0.03152
Gene.29694::TRINITY_DN20172_c0_g1::g.29694::m.29694	Elongator complex protein 2	560.066	3	1.28958	0.02862
Gene.2978::TRINITY_DN12352_c0_g1::g.2978::m.2978	Glycerophosphocholine permease, GIT4	259.996	11	1.75735	0.00396
Gene.29832::TRINITY_DN20250_c0_g1::g.29832::m.29832	54S ribosomal protein L28, mitochondrial	42.743	14	0.58228	0.01726
Gene.29848::TRINITY_DN20259_c0_g1::g.29848::m.29848	Tryprostatin B 6-hydroxylase	316.62	4	1.65913	0.02441
Gene.29876::TRINITY_DN20288_c0_g1::g.29876::m.29876	Putative agmatinase 1	533.487	19	1.58398	0.00681
Gene.29987::TRINITY_DN20384_c0_g1::g.29987::m.29987	Imidazoleglycerol-phosphate dehydratase	398.667	36	0.75622	0.0034
Gene.30027::TRINITY_DN20432_c0_g1::g.30027::m.30027	Probable proteasome subunit alpha type-6	315.849	56	0.8226	0.00154
Gene.30062::TRINITY_DN20461_c0_g1::g.30062::m.30062	54S ribosomal protein L19, mitochondrial	157.918	38	0.80451	0.04828
Gene.30115::TRINITY_DN20520_c0_g1::g.30115::m.30115	Monoxygenase CPUR_05431	202.601	30	1.61097	0.02665
Gene.30156::TRINITY_DN20574_c0_g1::g.30156::m.30156	Cytoplasmic tRNA 2-thiolation protein 2	120.939	14	1.28175	0.00296
Gene.30185::TRINITY_DN20617_c0_g1::g.30185::m.30185	Uncharacterized oxidoreductase C663.08c	114.005	6	1.53528	0.01423
Gene.30355::TRINITY_DN20867_c0_g1::g.30355::m.30355	Chromatin structure-remodeling complex subunit, sfh1	141.739	4	1.33463	0.03126
Gene.30439::TRINITY_DN20899_c0_g1::g.30439::m.30439	Phospholipid-transporting ATPase DNF1	1413.67	6	1.28311	0.01049
Gene.30587::TRINITY_DN20943_c0_g1::g.30587::m.30587	54S ribosomal protein L36, mitochondrial	55.0694	20	0.79802	0.01928
Gene.30618::TRINITY_DN20955_c0_g1::g.30618::m.30618	Mitochondrial zinc maintenance protein 1, mitochondrial	129.413	28	0.72534	0.00514
Gene.30640::TRINITY_DN20963_c0_g1::g.30640::m.30640	Uncharacterized protein C23C11.06c	270.396	9	1.47975	0.03452
Gene.30648::TRINITY_DN20966_c0_g1::g.30648::m.30648	Uncharacterized protein C32A11.02c	310.071	29	1.54453	0.01059
Gene.30686::TRINITY_DN20986_c0_g1::g.30686::m.30686	Uncharacterized protein C16G5.07c	372.474	59	0.75872	0.03873
Gene.30763::TRINITY_DN21028_c0_g1::g.30763::m.30763	FAD-linked oxidoreductase ZEB1	531.946	4	1.85987	0.04909
Gene.30836::TRINITY_DN21073_c0_g1::g.30836::m.30836	Calcium channel YVC1	450.284	6	1.25188	0.01931
Gene.30845::TRINITY_DN21077_c0_g1::g.30845::m.30845	Acetyl-coenzyme A transferase nodX	196.823	18	1.54669	0.00857
Gene.30971::TRINITY_DN21143_c0_g1::g.30971::m.30971	Pepsin B	43.8986	2	1.7688	0.01787
Gene.31032::TRINITY_DN21177_c0_g1::g.31032::m.31032	Vacuolar membrane protease	995.342	10	1.42188	0.00296
Gene.31097::TRINITY_DN21233_c0_g1::g.31097::m.31097	Mitochondrial import inner membrane translocase subunit tim44	327.02	53	0.7336	0.02742
Gene.31334::TRINITY_DN21478_c0_g1::g.31334::m.31334	40S ribosomal protein S11-A	221.861	16	4.28546	0.01486
Gene.31570::TRINITY_DN21748_c0_g1::g.31570::m.31570	Putative NADPH dehydrogenase C23G7.10c	309.301	2	1.38135	0.0324
Gene.31578::TRINITY_DN21751_c0_g1::g.31578::m.31578	Solute carrier family 25 member 40	233.417	3	0.79319	0.00465
Gene.31676::TRINITY_DN21789_c0_g1::g.31676::m.31676	Probable secreted lipase ARB_00047	212.616	3	1.75149	0.00321
Gene.31752::TRINITY_DN21824_c0_g1::g.31752::m.31752	Translation initiation factor IF-2, mitochondrial	489.96	12	0.82648	0.02754

Gene.31881::TRINITY_DN21893_c0_g1::g.31881::m.31881	Amino-acid permease 2	586.645	3	1.63968	0.03315
Gene.31888::TRINITY_DN21897_c0_g1::g.31888::m.31888	Phytoene desaturase	642.114	24	1.84091	0.00026
Gene.31951::TRINITY_DN21926_c0_g1::g.31951::m.31951	Mitochondrial carnitine carrier	273.863	23	1.34467	0.0301
Gene.32028::TRINITY_DN21962_c0_g1::g.32028::m.32028	3-dehydroshikimate dehydratase	150.599	9	2.96367	0.0111
Gene.32091::TRINITY_DN22004_c0_g1::g.32091::m.32091	Methyltransferase-like protein 7B	77.7962	17	1.26548	0.02139
Gene.32127::TRINITY_DN22021_c0_g1::g.32127::m.32127	Probable 54S ribosomal protein L32, mitochondrial	77.0258	7	1.71985	0.02186
Gene.32132::TRINITY_DN22024_c0_g1::g.32132::m.32132	Pre-mRNA-splicing factor sap61	416.387	14	1.29008	0.00052
Gene.32242::TRINITY_DN22121_c0_g1::g.32242::m.32242	Imidazole glycerol phosphate synthase hisHF	803.127	30	0.78253	0.01417
Gene.32261::TRINITY_DN22133_c0_g1::g.32261::m.32261	Uncharacterized protein tam6, mitochondrial	43.8986	6	0.82871	0.02084
Gene.32263::TRINITY_DN22137_c0_g1::g.32263::m.32263	Glycerol-3-phosphate dehydrogenase [NAD(+)]	639.032	18	0.82588	0.00354
Gene.32332::TRINITY_DN22203_c0_g1::g.32332::m.32332	Iron-sulfur assembly protein 2	80.8777	8	0.72662	0.0301
Gene.32520::TRINITY_DN22558_c0_g1::g.32520::m.32520	Uncharacterized protein C1840.09	183.341	41	0.7316	0.02021
Gene.32548::TRINITY_DN22567_c0_g1::g.32548::m.32548	Vacuolar morphogenesis protein 7 homolog	127.102	22	1.33775	0.03618
Gene.32551::TRINITY_DN22569_c0_g1::g.32551::m.32551	Protein BFR2	431.409	7	1.40152	0.00592
Gene.32564::TRINITY_DN22578_c0_g1::g.32564::m.32564	Cytochrome c oxidase polypeptide 5, mitochondrial	114.775	11	2.15126	0.0185
Gene.32600::TRINITY_DN22595_c0_g1::g.32600::m.32600	Probable lysosomal cobalamin transporter	808.135	5	1.23214	0.01591
Gene.32614::TRINITY_DN22599_c0_g1::g.32614::m.32614	Uncharacterized CDP-alcohol phosphatidyltransferase class-I family protein C22A12.08c	239.965	6	1.59516	0.02438
Gene.32678::TRINITY_DN22626_c0_g1::g.32678::m.32678	Lysine--tRNA ligase, mitochondrial	308.531	15	0.79319	0.00868
Gene.3268::TRINITY_DN12468_c0_g1::g.3268::m.3268	Retrograde regulation protein 2	231.106	5	1.2531	0.01833
Gene.32764::TRINITY_DN22658_c0_g1::g.32764::m.32764	Putative D-lactate dehydrogenase C713.03, mitochondrial	637.876	34	0.81214	0.03628
Gene.32848::TRINITY_DN22702_c0_g1::g.32848::m.32848	Mitochondrial amidoxime-reducing component 1	72.4034	3	1.3706	0.03866
Gene.32888::TRINITY_DN22717_c0_g1::g.32888::m.32888	Vacuolar transporter chaperone 3	455.292	28	1.3175	0.01562
Gene.32898::TRINITY_DN22719_c0_g1::g.32898::m.32898	AFG1-like ATPase	142.124	4	1.28002	0.02697
Gene.32918::TRINITY_DN22726_c0_g1::g.32918::m.32918	eEF1A lysine and N-terminal methyltransferase	58.5362	3	1.27407	0.00222
Gene.33030::TRINITY_DN22773_c0_g1::g.33030::m.33030	Cytochrome P450 monooxygenase paxP	145.591	4	1.73179	0.02279
Gene.33036::TRINITY_DN22777_c0_g1::g.33036::m.33036	Copper amine oxidase 1	444.121	3	0.73611	0.00166
Gene.33220::TRINITY_DN22865_c0_g1::g.33220::m.33220	Mitochondrial import inner membrane translocase subunit TIM50	603.208	34	0.73992	0.04134
Gene.33361::TRINITY_DN22949_c0_g1::g.33361::m.33361	54S ribosomal protein L17, mitochondrial	127.102	29	0.7508	0.01443
Gene.33380::TRINITY_DN22965_c0_g1::g.33380::m.33380	GTPase-activating protein GYP5	257.684	1	0.66113	0.01532
Gene.33429::TRINITY_DN229_c0_g1::g.33429::m.33429	Putative copper transporter crmD	43.8986	5	1.52419	0.04004
Gene.33434::TRINITY_DN23007_c0_g1::g.33434::m.33434	Microfibrillar-associated protein 1	112.849	2	1.57689	0.01842
Gene.33451::TRINITY_DN23016_c0_g1::g.33451::m.33451	54S ribosomal protein L11, mitochondrial	64.3142	34	0.76574	0.00504
Gene.33483::TRINITY_DN23034_c0_g1::g.33483::m.33483	HD domain-containing protein C4G3.17	141.739	22	1.26548	0.02747
Gene.33551::TRINITY_DN23102_c0_g1::g.33551::m.33551	Probable cytosolic iron-sulfur protein assembly protein 1	530.02	5	0.80505	0.00494
Gene.33576::TRINITY_DN2311_c0_g2::g.33576::m.33576	Agroclavine dehydrogenase	234.187	5	1.26672	0.04222
Gene.33630::TRINITY_DN23182_c0_g1::g.33630::m.33630	3-hydroxyacyl-CoA dehydrogenase type-2	56.9954	26	1.49273	0.02049
Gene.33667::TRINITY_DN2322_c0_g1::g.33667::m.33667	FAD-dependent monooxygenase sorC	180.644	8	1.76243	0.04917
Gene.33762::TRINITY_DN23337_c0_g1::g.33762::m.33762	Putative redox protein fmp46, mitochondrial	56.225	53	0.706	0.0366
Gene.33861::TRINITY_DN2367_c0_g1::g.33861::m.33861	Uncharacterized RNA-binding protein C1861.04c	298.13	14	1.41198	0.00796
Gene.33873::TRINITY_DN2371_c0_g1::g.33873::m.33873	U3 small nucleolar RNA-associated protein 15	345.51	6	0.72989	0.02025
Gene.33901::TRINITY_DN2396_c0_g1::g.33901::m.33901	Probable vacuolar protease A	90.8929	8	1.28746	0.03967

Gene.33920::TRINITY_DN2411_c0_g1::g.33920::m.33920	Mitochondrial inner membrane protein OXA1L	108.612	16	0.77883	0.01179
Gene.33985::TRINITY_DN2457_c0_g1::g.33985::m.33985	Syntaxin-22	103.219	26	1.27311	0.00591
Gene.34003::TRINITY_DN2480_c0_g1::g.34003::m.34003	BSD domain-containing protein C22A12.14c	85.8853	39	0.77433	0.00108
Gene.34287::TRINITY_DN2699_c0_g1::g.34287::m.34287	Short chain dehydrogenase mpl6	143.28	46	2.38792	0.00029
Gene.3431::TRINITY_DN12520_c0_g1::g.3431::m.3431	Translation initiation factor eIF-2B subunit gamma	120.553	15	0.81159	0.03743
Gene.34314::TRINITY_DN2716_c0_g1::g.34314::m.34314	Citrinin biosynthesis transcriptional activator ctnR	165.236	1	1.2363	0.01511
Gene.3444::TRINITY_DN12530_c0_g3::g.3444::m.3444	Dihydropyrimidinase	399.053	22	1.48139	0.01219
Gene.34497::TRINITY_DN2901_c0_g1::g.34497::m.34497	Trafficking protein particle complex subunit 11	77.7962	2	0.77567	0.03019
Gene.34536::TRINITY_DN295_c0_g1::g.34536::m.34536	Protein Rf1, mitochondrial	70.8626	1	0.82704	0.00389
Gene.34606::TRINITY_DN3026_c0_g1::g.34606::m.34606	5-aminolevulinate synthase, erythroid-specific, mitochondrial	68.5514	7	1.44698	0.00095
Gene.34730::TRINITY_DN3158_c0_g1::g.34730::m.34730	Cytochrome P450 monooxygenase sdnH	465.692	9	2.05499	0.01929
Gene.34777::TRINITY_DN31_c0_g1::g.34777::m.34777	Dehydrogenase patE	555.058	31	1.74303	0.00458
Gene.34928::TRINITY_DN3372_c0_g1::g.34928::m.34928	Homoserine dehydrogenase	411.764	75	0.8105	0.01057
Gene.35013::TRINITY_DN3498_c0_g1::g.35013::m.35013	Zerumbone synthase	145.976	18	1.50522	0.01882
Gene.35141::TRINITY_DN3598_c0_g2::g.35141::m.35141	Elongation factor G, mitochondrial	1267.68	39	0.78808	0.00711
Gene.35235::TRINITY_DN3683_c0_g1::g.35235::m.35235	RNA-capping enzyme subunit alpha	255.758	4	1.20426	0.04758
Gene.35243::TRINITY_DN368_c0_g1::g.35243::m.35243	DNA-directed RNA polymerases I, II, and III subunit RPABC2	148.288	5	0.65062	0.01932
Gene.35256::TRINITY_DN3693_c0_g1::g.35256::m.35256	Outer spore wall protein RRT8	43.8986	3	1.55102	0.02058
Gene.35323::TRINITY_DN3764_c0_g1::g.35323::m.35323	Ubiquinone biosynthesis protein, coq9	134.42	12	0.75007	0.02403
Gene.35461::TRINITY_DN38_c0_g1::g.35461::m.35461	AB hydrolase superfamily protein C4A8.06c	57.3806	11	1.35849	0.01832
Gene.356::TRINITY_DN10547_c0_g1::g.356::m.356	Mitochondrial phosphate carrier protein 2	236.113	45	1.53915	0.03053
Gene.35605::TRINITY_DN4020_c0_g1::g.35605::m.35605	GPN-loop GTPase 1	409.068	14	0.73561	0.01049
Gene.35609::TRINITY_DN4020_c0_g2::g.35609::m.35609	DNA-directed RNA polymerases I, II, and III subunit RPABC4	77.411	21	0.69895	0.00207
Gene.35664::TRINITY_DN406_c0_g1::g.35664::m.35664	Glucose-6-phosphate isomerase	149.828	6	1.79367	0.03087
Gene.35806::TRINITY_DN4185_c0_g1::g.35806::m.35806	Aromatic amino acid aminotransferase C56E4.03	251.521	11	1.24551	0.00253
Gene.35818::TRINITY_DN4197_c0_g1::g.35818::m.35818	Probable exocyst complex component sec8	1415.59	9	1.23297	0.01422
Gene.35928::TRINITY_DN429_c0_g1::g.35928::m.35928	Uncharacterized leucine-rich repeat-containing protein C926.06c	243.432	1	1.40577	0.00903
Gene.35936::TRINITY_DN4303_c0_g1::g.35936::m.35936	Sexual differentiation process protein isp4	467.618	1	1.8851	0.02691
Gene.35941::TRINITY_DN4305_c0_g1::g.35941::m.35941	Iron-sulfur assembly protein 1	141.739	4	0.71478	5.7E-05
Gene.36053::TRINITY_DN4357_c0_g1::g.36053::m.36053	Serine/threonine-protein kinase KIN28	290.426	4	0.81573	0.02647
Gene.36240::TRINITY_DN4442_c0_g1::g.36240::m.36240	Uncharacterized protein C3B8.09	239.195	4	1.48798	0.03177
Gene.3639::TRINITY_DN12608_c0_g3::g.3639::m.3639	Exosome complex component CSL4	155.992	19	1.2805	0.0053
Gene.36401::TRINITY_DN450_c0_g2::g.36401::m.36401	Replication factor A protein 3	67.781	35	0.76753	0.01444
Gene.36449::TRINITY_DN4526_c0_g1::g.36449::m.36449	Dedicator of cytokinesis protein 1	338.576	3	1.35942	0.00126
Gene.36456::TRINITY_DN4529_c0_g1::g.36456::m.36456	DNA mismatch repair protein msh-2	1655.19	2	1.90508	0.046
Gene.36494::TRINITY_DN4550_c0_g1::g.36494::m.36494	Probable proteasome subunit alpha type-2	474.167	36	0.82785	0.00662
Gene.36611::TRINITY_DN4610_c0_g1::g.36611::m.36611	Septum-promoting GTP-binding protein 1	348.977	18	1.6455	0.00568
Gene.36616::TRINITY_DN4611_c0_g1::g.36616::m.36616	Trafficking protein particle complex subunit BET3	222.246	12	0.76419	0.00107
Gene.36618::TRINITY_DN4612_c0_g1::g.36618::m.36618	Uncharacterized boIA-like protein C4B3.11c	84.7297	6	0.79994	0.01144
Gene.36693::TRINITY_DN4636_c0_g2::g.36693::m.36693	Polyadenylation factor subunit 2	753.821	3	1.35756	0.0022
Gene.36763::TRINITY_DN4656_c0_g2::g.36763::m.36763	tRNA-specific adenosine deaminase subunit tad3	81.2629	5	1.41935	0.03064
Gene.36832::TRINITY_DN4684_c0_g1::g.36832::m.36832	Inner nuclear membrane protein SRC1	89.3521	18	1.22058	0.00592

Gene.36922::TRINITY_DN4728_c0_g2::g.36922::m.36922	Phosphatidylinositol 4-phosphate 5-kinase its3	559.681	3	0.7549	0.02121
Gene.36929::TRINITY_DN4729_c0_g1::g.36929::m.36929	Transforming growth factor-beta receptor-associated protein 1	100.523	1	1.28137	0.01534
Gene.36942::TRINITY_DN4733_c0_g1::g.36942::m.36942	Vacuolar transporter chaperone 1	175.252	15	1.21685	0.0421
Gene.36984::TRINITY_DN4756_c0_g1::g.36984::m.36984	SEH-associated protein 4	223.402	2	1.34703	0.00795
Gene.37026::TRINITY_DN4780_c0_g1::g.37026::m.37026	Lariat debranching enzyme	335.109	2	1.20588	0.02347
Gene.37064::TRINITY_DN4810_c0_g1::g.37064::m.37064	Uncharacterized methyltransferase C70.08c	70.4774	49	1.41643	0.03485
Gene.3726::TRINITY_DN12682_c0_g2::g.3726::m.3726	ADIPOR-like receptor IZH2	165.236	3	0.8018	0.00096
Gene.37269::TRINITY_DN5092_c0_g1::g.37269::m.37269	Ribose-phosphate pyrophosphokinase 5	389.808	20	1.21031	0.00194
Gene.3744::TRINITY_DN12690_c0_g1::g.3744::m.3744	WW domain-containing oxidoreductase	56.9954	18	1.45943	0.01585
Gene.37487::TRINITY_DN5320_c0_g1::g.37487::m.37487	WHI2-like protein P4H10.16c	162.925	26	1.44458	0.00266
Gene.37530::TRINITY_DN5351_c0_g1::g.37530::m.37530	Cytochrome P450 52A13	296.204	14	1.51889	0.02507
Gene.37726::TRINITY_DN5593_c0_g2::g.37726::m.37726	Dehydrololichyl diphosphate synthase complex subunit NUS1	176.022	8	1.21685	0.01111
Gene.37948::TRINITY_DN5805_c0_g2::g.37948::m.37948	Uncharacterized protein C9E9.15	115.931	9	0.71009	0.0249
Gene.37993::TRINITY_DN5827_c0_g1::g.37993::m.37993	Phosphatidylglycerol phospholipase C	113.235	16	0.67832	0.01385
Gene.3810::TRINITY_DN12739_c0_g2::g.3810::m.3810	Uncharacterized protein YLL056C	63.929	45	1.33372	0.02965
Gene.38197::TRINITY_DN596_c0_g1::g.38197::m.38197	Phenylalanine--tRNA ligase, mitochondrial	272.322	29	0.73611	0.00942
Gene.38273::TRINITY_DN6048_c0_g1::g.38273::m.38273	26S proteasome non-ATPase regulatory subunit 9	141.739	16	0.80807	0.03237
Gene.38307::TRINITY_DN6085_c0_g1::g.38307::m.38307	All-trans-retinol dehydrogenase [NAD(+)] ADH1B	151.754	34	1.24972	0.01105
Gene.38764::TRINITY_DN6515_c0_g2::g.38764::m.38764	Acetate permease A	279.256	9	1.7894	0.03858
Gene.3881::TRINITY_DN12771_c0_g1::g.3881::m.3881	V-type proton ATPase 16 kDa proteolipid subunit	260.766	12	1.46264	0.0005
Gene.38843::TRINITY_DN6555_c0_g1::g.38843::m.38843	Kynureninase 2	666.381	4	0.75879	0.00466
Gene.39008::TRINITY_DN6665_c0_g2::g.39008::m.39008	Solute carrier family 28 member 3	281.182	2	1.46163	0.04352
Gene.3904::TRINITY_DN12783_c0_g3::g.3904::m.3904	Putative arrestin-related trafficking adapter C2D10.04	265.774	4	1.32558	0.00275
Gene.39087::TRINITY_DN6726_c0_g1::g.39087::m.39087	Putative mitochondrial carnitine O-acetyltransferase	516.924	8	1.31622	0.01688
Gene.39179::TRINITY_DN67_c0_g1::g.39179::m.39179	Coactosin	106.686	42	0.82315	0.00414
Gene.3927::TRINITY_DN12792_c0_g1::g.3927::m.3927	Mitochondrial import inner membrane translocase subunit tim22	234.958	24	0.41878	0.01354
Gene.39288::TRINITY_DN6902_c0_g1::g.39288::m.39288	Putative nucleosome assembly protein C36B7.08c	85.1149	20	0.82562	0.0462
Gene.39374::TRINITY_DN7016_c0_g1::g.39374::m.39374	Acetyl-CoA--deacetylcephalosporin C acetyltransferase	61.6178	7	1.39561	0.00839
Gene.3939::TRINITY_DN1279_c0_g2::g.3939::m.3939	Acetamidase	165.622	17	1.25649	0.02072
Gene.39422::TRINITY_DN7076_c0_g1::g.39422::m.39422	ATP synthase subunit epsilon, mitochondrial	44.669	22	0.81984	0.02458
Gene.39539::TRINITY_DN717_c0_g1::g.39539::m.39539	Sphingosine N-acyltransferase-like protein FUM18	358.607	1	1.25602	0.03607
Gene.39616::TRINITY_DN7212_c0_g1::g.39616::m.39616	Choline monooxygenase, chloroplastic	130.568	2	1.8342	0.03263
Gene.39624::TRINITY_DN7218_c0_g3::g.39624::m.39624	Carboxyvinyl-carboxyphosphonate phosphorylmutase, chloroplastic	157.918	19	1.29747	0.00833
Gene.39704::TRINITY_DN7262_c0_g1::g.39704::m.39704	Protein SIP5	499.975	6	1.27752	0.01059
Gene.39760::TRINITY_DN7290_c0_g1::g.39760::m.39760	Mitochondrial ATPase complex subunit ATP10	97.4413	19	0.72068	0.02554
Gene.39769::TRINITY_DN7299_c0_g1::g.39769::m.39769	Trans-enoyl reductase fsdC	132.109	3	1.38434	0.01649
Gene.39801::TRINITY_DN7350_c0_g2::g.39801::m.39801	Acetyl-CoA acetyltransferase, mitochondrial	172.94	5	0.72911	0.03328
Gene.39819::TRINITY_DN7374_c0_g2::g.39819::m.39819	Alpha-L-arabinofuranosidase C	583.948	3	2.30943	0.04115
Gene.39901::TRINITY_DN7465_c0_g2::g.39901::m.39901	pH-response regulator protein palA/RIM20	1119.76	10	1.20913	0.00073
Gene.39907::TRINITY_DN747_c0_g1::g.39907::m.39907	Cytochrome P450 monooxygenase aclL	370.163	3	1.47219	0.01285
Gene.40007::TRINITY_DN75_c0_g1::g.40007::m.40007	Uncharacterized membrane protein C24H6.13	395.586	3	1.21848	0.02898
Gene.40045::TRINITY_DN7629_c0_g1::g.40045::m.40045	Uncharacterized membrane protein YJR124C	218.779	10	1.55168	0.01086

Gene.40282::TRINITY_DN7893_c1_g1::g.40282::m.40282	Probable U6 snRNA-associated Sm-like protein LSm3	110.538	14	0.80397	0.01806
Gene.40317::TRINITY_DN7917_c0_g2::g.40317::m.40317	Pre-rRNA-processing protein rix1	45.0542	10	0.8276	0.02956
Gene.40435::TRINITY_DN8040_c0_g1::g.40435::m.40435	Short-chain dehydrogenase/reductase tropE	274.633	34	1.9513	0.00662
Gene.40471::TRINITY_DN8072_c0_g1::g.40471::m.40471	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5-B	55.0694	44	1.57843	0.04246
Gene.40536::TRINITY_DN8105_c0_g1::g.40536::m.40536	tRNA-dihydrouridine(20) synthase [NAD(P)+]	244.973	4	1.21402	0.00079
Gene.40547::TRINITY_DN8111_c0_g1::g.40547::m.40547	NO-methyltransferase cnsE	99.3673	9	1.24972	0.03908
Gene.40636::TRINITY_DN8146_c0_g1::g.40636::m.40636	Dolichol kinase sec59	141.739	1	1.25442	0.01945
Gene.40734::TRINITY_DN8212_c0_g1::g.40734::m.40734	Microtubule integrity protein mal3	227.254	60	0.73489	0.00921
Gene.40760::TRINITY_DN8225_c0_g1::g.40760::m.40760	Subtilisin-like proteinase Spm1	589.726	30	1.20345	0.00331
Gene.40854::TRINITY_DN8256_c0_g1::g.40854::m.40854	Putative lipase YOR059C	51.6026	6	1.94551	0.00886
Gene.41031::TRINITY_DN8315_c0_g2::g.41031::m.41031	Carboxypeptidase S1 homolog A	593.964	7	1.4818	0.01807
Gene.4115::TRINITY_DN12879_c0_g5::g.4115::m.4115	Phytanoyl-CoA dioxygenase domain-containing protein 1 homolog	213.386	21	1.29446	0.00012
Gene.4122::TRINITY_DN12882_c0_g1::g.4122::m.4122	10 kDa heat shock protein, mitochondrial	128.257	11	0.62646	0.04336
Gene.41268::TRINITY_DN8412_c0_g2::g.41268::m.41268	Bax inhibitor 1	179.489	5	1.36274	0.01528
Gene.4136::TRINITY_DN12891_c0_g1::g.4136::m.4136	Aurofusarin biosynthesis cluster protein S	141.739	24	1.457	0.04935
Gene.41424::TRINITY_DN8547_c0_g1::g.41424::m.41424	Translation machinery-associated protein 46	267.314	22	0.83293	0.02048
Gene.41452::TRINITY_DN8568_c0_g1::g.41452::m.41452	Probable very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase	145.206	3	1.39672	0.03577
Gene.41478::TRINITY_DN8579_c0_g1::g.41478::m.41478	AP-3 complex subunit beta-2	418.698	7	1.36794	0.00072
Gene.41483::TRINITY_DN8580_c0_g1::g.41483::m.41483	Copper amine oxidase 1	823.543	21	1.27187	0.00281
Gene.41514::TRINITY_DN8604_c0_g2::g.41514::m.41514	Acyl-CoA synthetase FUM16	712.22	12	1.26159	0.00916
Gene.41602::TRINITY_DN8663_c0_g1::g.41602::m.41602	26S proteasome regulatory subunit rpn11	455.292	38	0.72414	0.00118
Gene.41644::TRINITY_DN8688_c0_g2::g.41644::m.41644	DNA-directed RNA polymerase III subunit rpc9	54.6842	19	0.80204	0.02398
Gene.41810::TRINITY_DN8831_c0_g1::g.41810::m.41810	Catalase-1	1064.29	26	1.45399	0.02659
Gene.4184::TRINITY_DN12913_c0_g2::g.4184::m.4184	Acyl-CoA dehydrogenase AFT10-1	356.681	12	1.34558	0.03338
Gene.41848::TRINITY_DN88_c0_g1::g.41848::m.41848	DnaJ homolog 1, mitochondrial	498.049	24	0.65472	0.01413
Gene.41898::TRINITY_DN8960_c0_g1::g.41898::m.41898	Methionine aminopeptidase 1	447.203	10	1.23501	0.01382
Gene.41997::TRINITY_DN905_c0_g1::g.41997::m.41997	2-aminomuconic semialdehyde dehydrogenase	425.246	7	1.42482	0.02231
Gene.42051::TRINITY_DN9119_c0_g1::g.42051::m.42051	Protein CASP	252.292	15	1.24551	0.00299
Gene.42102::TRINITY_DN9158_c0_g1::g.42102::m.42102	Probable transcriptional regulator ycf27	85.1149	66	2.67586	0.04451
Gene.42188::TRINITY_DN9248_c0_g1::g.42188::m.42188	Methylenetetrahydrofolate dehydrogenase [NAD(+)]	375.17	38	0.78731	0.04149
Gene.42189::TRINITY_DN9248_c0_g2::g.42189::m.42189	Signal peptidase complex subunit SPC2	69.707	17	1.21484	0.0085
Gene.42379::TRINITY_DN9404_c1_g2::g.42379::m.42379	Methyltransferase trt5	84.7297	20	1.25056	0.02366
Gene.42769::TRINITY_DN9682_c0_g2::g.42769::m.42769	Bifunctional lycopene cyclase/phytoene synthase	548.51	16	1.41198	0.01422
Gene.42789::TRINITY_DN9695_c0_g1::g.42789::m.42789	ABC multidrug transporter mdr1	1712.2	11	2.33148	9.1E-06
Gene.42884::TRINITY_DN9762_c0_g2::g.42884::m.42884	HD domain-containing protein C4G3.17	172.555	28	0.81354	0.01495
Gene.42922::TRINITY_DN9783_c0_g1::g.42922::m.42922	Iron-sulfur clusters transporter ATM1, mitochondrial	387.497	7	1.21529	0.02467
Gene.42927::TRINITY_DN9789_c0_g1::g.42927::m.42927	Adrenodoxin homolog, mitochondrial	168.318	6	0.68473	0.04773
Gene.42943::TRINITY_DN9792_c0_g1::g.42943::m.42943	Hydrolase tropI	192.971	32	1.25649	0.00151
Gene.4298::TRINITY_DN12969_c0_g1::g.4298::m.4298	ATP-dependent RNA helicase DBP8	776.548	7	1.38379	0.01127
Gene.43004::TRINITY_DN9842_c0_g1::g.43004::m.43004	Protein sum2	132.88	13	0.77335	0.0049
Gene.43085::TRINITY_DN9944_c0_g1::g.43085::m.43085	Tyrosine--tRNA ligase, cytoplasmic	160.229	7	0.81184	0.04814
Gene.4324::TRINITY_DN12984_c0_g1::g.4324::m.4324	Tubulin-specific chaperone D	70.8626	8	1.28871	0.01281

Gene.4349::TRINITY_DN12996_c0_g2::g.4349::m.4349	Uncharacterized oxidoreductase C162.03	157.147	5	1.37021	0.01715
Gene.4455::TRINITY_DN13039_c0_g2::g.4455::m.4455	Probable NADH dehydrogenase	304.294	14	0.69827	0.01245
Gene.4581::TRINITY_DN13079_c0_g3::g.4581::m.4581	Meiotically up-regulated gene 190 protein	806.979	3	1.27101	0.01762
Gene.4649::TRINITY_DN13109_c0_g2::g.4649::m.4649	Cytochrome c oxidase assembly protein COX20, mitochondrial	73.559	17	0.73461	0.00416
Gene.4665::TRINITY_DN13117_c0_g6::g.4665::m.4665	Monoxygenase CTB7	196.052	20	2.44037	0.01564
Gene.4868::TRINITY_DN13182_c0_g2::g.4868::m.4868	Mitochondrial presequence protease	1541.17	44	0.74672	0.0194
Gene.4965::TRINITY_DN13228_c0_g1::g.4965::m.4965	Probable T-complex protein 1 subunit eta	831.247	44	0.83094	0.03208
Gene.5140::TRINITY_DN13416_c0_g1::g.5140::m.5140	30S ribosomal protein S12, chloroplastic	204.912	28	2.12175	0.00542
Gene.5260::TRINITY_DN13571_c0_g2::g.5260::m.5260	Sphingolipid C4-hydroxylase SUR2	271.166	12	1.22222	0.00693
Gene.5288::TRINITY_DN13606_c0_g2::g.5288::m.5288	Monoxygenase	241.891	23	1.68456	0.01026
Gene.5452::TRINITY_DN13766_c0_g2::g.5452::m.5452	Mitochondrial-processing peptidase subunit alpha	694.501	37	0.78366	0.00091
Gene.55::TRINITY_DN10100_c0_g1::g.55::m.55	U3 small nucleolar ribonucleoprotein protein IMP3	141.739	10	0.77485	0.01533
Gene.5579::TRINITY_DN1390_c0_g1::g.5579::m.5579	Putative amidase ARB_02965	537.339	4	1.3482	0.03155
Gene.571::TRINITY_DN10722_c1_g1::g.571::m.571	Putative amidase C869.01	619.387	3	1.365	0.01406
Gene.5752::TRINITY_DN14117_c0_g1::g.5752::m.5752	Alpha-1,2-mannosyltransferase alg9	376.326	5	1.76927	0.02433
Gene.5807::TRINITY_DN14158_c0_g3::g.5807::m.5807	Altered inheritance of mitochondria protein 18, mitochondrial	119.398	35	0.78018	0.00356
Gene.5842::TRINITY_DN14178_c1_g2::g.5842::m.5842	Vacuolar protein-sorting-associated protein 11 homolog	444.121	3	1.23214	0.00232
Gene.5887::TRINITY_DN14221_c0_g1::g.5887::m.5887	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	548.51	61	0.79611	0.01204
Gene.5958::TRINITY_DN14264_c0_g4::g.5958::m.5958	UBX domain-containing protein 1	245.358	35	0.80156	0.0165
Gene.6376::TRINITY_DN14570_c0_g3::g.6376::m.6376	Lon protease homolog, mitochondrial	1607.81	39	0.7092	0.0051
Gene.6401::TRINITY_DN14592_c0_g2::g.6401::m.6401	Peroxisomal oxidoreductase	269.24	34	0.69539	0.0088
Gene.6534::TRINITY_DN14669_c0_g1::g.6534::m.6534	Mannan polymerase II complex ANP1 subunit	484.182	6	1.30858	0.02079
Gene.6555::TRINITY_DN14688_c0_g2::g.6555::m.6555	Exosome complex component rrp45	312.383	17	0.75	0.01021
Gene.6610::TRINITY_DN14705_c0_g6::g.6610::m.6610	Zinc-type alcohol dehydrogenase-like protein C16A3.02c	176.407	21	1.51298	0.01543
Gene.6752::TRINITY_DN14798_c0_g2::g.6752::m.6752	Nuclear polyadenylated RNA-binding protein NAB2	72.0182	7	0.80096	0.00476
Gene.6806::TRINITY_DN14838_c0_g2::g.6806::m.6806	Acyl-CoA dehydrogenase family member 9, mitochondrial	48.1358	17	1.28484	0.02829
Gene.6807::TRINITY_DN14840_c1_g1::g.6807::m.6807	Probable quinone oxidoreductase	229.565	2	0.81269	0.0371
Gene.683::TRINITY_DN10799_c0_g2::g.683::m.683	Short-chain dehydrogenase/reductase ATR7	80.4925	70	0.74672	0.01411
Gene.6863::TRINITY_DN14869_c0_g4::g.6863::m.6863	Tyrosinase ustQ	131.724	12	1.34611	0.0009
Gene.6949::TRINITY_DN14942_c0_g1::g.6949::m.6949	Histone acetyltransferase ESA1	770	3	1.23048	0.0074
Gene.6995::TRINITY_DN1496_c0_g1::g.6995::m.6995	Ribokinase	195.282	21	0.75901	0.00103
Gene.7044::TRINITY_DN15000_c0_g1::g.7044::m.7044	Uricase	373.244	40	1.57333	0.0009
Gene.7130::TRINITY_DN1505_c0_g1::g.7130::m.7130	Proline utilization trans-activator	55.0694	1	1.72773	0.04687
Gene.7292::TRINITY_DN15158_c0_g2::g.7292::m.7292	re-mRNA-splicing factor cwf19	400.593	2	1.32108	0.00065
Gene.7383::TRINITY_DN15207_c0_g1::g.7383::m.7383	DOA4-independent degradation protein 4	200.29	15	1.22717	0.00808
Gene.7421::TRINITY_DN15226_c0_g2::g.7421::m.7421	Transcriptional regulatory protein dep1	73.559	3	0.71625	0.03347
Gene.7453::TRINITY_DN1524_c0_g1::g.7453::m.7453	Oxidoreductase andH	149.443	16	1.33502	0.0311
Gene.7509::TRINITY_DN15280_c0_g2::g.7509::m.7509	O-acetyltransferase ptmV	110.923	2	1.69618	0.02163
Gene.7575::TRINITY_DN15315_c0_g2::g.7575::m.7575	Probable aminotransferase acII	449.514	2	1.23214	0.00928
Gene.7593::TRINITY_DN15322_c0_g1::g.7593::m.7593	SAGA-associated factor 29	102.834	3	1.24383	0.01895
Gene.7599::TRINITY_DN15326_c0_g1::g.7599::m.7599	Thioredoxin reductase gliT	279.641	33	1.45659	0.03178
Gene.763::TRINITY_DN10857_c0_g2::g.763::m.763	t-SNARE affecting a late Golgi compartment protein 1	56.9954	15	0.74927	0.01364

Gene.7630::TRINITY_DN15343_c0_g1::g.7630::m.7630	Uncharacterized transcriptional regulatory protein C3C7.04	129.798	2	1.32468	0.01331
Gene.7833::TRINITY_DN15451_c0_g4::g.7833::m.7833	Putative nitroreductase HBN1	42.743	34	0.77021	0.01314
Gene.7887::TRINITY_DN15476_c0_g2::g.7887::m.7887	Failed axon connections	75.0998	27	0.78412	0.00537
Gene.7910::TRINITY_DN15485_c0_g1::g.7910::m.7910	Bifunctional solanapyrone synthase	184.882	1	1.86533	0.00296
Gene.7920::TRINITY_DN15494_c0_g1::g.7920::m.7920	Probable RNA-binding protein 19	93.9745	53	0.75718	0.01876
Gene.797::TRINITY_DN10880_c0_g3::g.797::m.797	Acid phosphatase	152.525	10	1.67618	0.03717
Gene.8048::TRINITY_DN15572_c0_g1::g.8048::m.8048	Translation machinery-associated protein 7	53.5286	20	0.59872	0.00419
Gene.8237::TRINITY_DN15683_c0_g1::g.8237::m.8237	Uncharacterized transcriptional regulatory protein C1327.01c	60.8474	1	1.52674	0.04518
Gene.8367::TRINITY_DN15727_c0_g2::g.8367::m.8367	Trimethyllysine dioxygenase	494.197	11	1.29008	0.00744
Gene.8371::TRINITY_DN15728_c0_g1::g.8371::m.8371	Phosphatidylglycerol phospholipase C	134.806	8	1.59024	0.01076
Gene.838::TRINITY_DN10913_c0_g1::g.838::m.838	Ribosomal RNA-processing protein 14	90.8929	2	0.72237	0.00876
Gene.8380::TRINITY_DN15733_c1_g1::g.8380::m.8380	Probable D-xylulose reductase A	120.168	34	0.81628	0.00551
Gene.8557::TRINITY_DN15826_c0_g3::g.8557::m.8557	4-trimethylaminobutyraldehyde dehydrogenase	164.466	22	1.39848	0.03785
Gene.8690::TRINITY_DN1590_c0_g1::g.8690::m.8690	Proline iminopeptidase PfmaB	541.576	9	1.23131	0.00397
Gene.8743::TRINITY_DN15947_c0_g1::g.8743::m.8743	T-complex protein 1 subunit delta	742.265	49	0.80668	0.00732
Gene.8799::TRINITY_DN15972_c0_g1::g.8799::m.8799	Dihydrodipolyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	615.15	53	0.72761	0.00221
Gene.880::TRINITY_DN10955_c0_g1::g.880::m.880	Uncharacterized protein C56F8.02	1506.12	9	1.20147	0.00179
Gene.8809::TRINITY_DN15975_c0_g1::g.8809::m.8809	Probable U6 snRNA-associated Sm-like protein LSM4	143.665	41	0.79503	0.00594
Gene.8893::TRINITY_DN1601_c0_g1::g.8893::m.8893	Ribosome biogenesis protein nsa2	451.825	2	0.59251	0.00332
Gene.8981::TRINITY_DN16076_c0_g1::g.8981::m.8981	Probable T-complex protein 1 subunit beta	791.956	59	0.80699	0.00363
Gene.9102::TRINITY_DN16125_c0_g3::g.9102::m.9102	ABC multidrug transporter atrF	1181.39	3	1.36967	0.03644
Gene.9137::TRINITY_DN16132_c0_g2::g.9137::m.9137	Proteasome subunit alpha type-4	343.969	63	0.79235	0.00021
Gene.9235::TRINITY_DN16158_c0_g1::g.9235::m.9235	Nuclear cap-binding protein subunit 2	192.971	8	0.73511	0.00365
Gene.9273::TRINITY_DN16171_c0_g1::g.9273::m.9273	Phosphate-repressible acid phosphatase	292.352	5	1.45861	0.04885
Gene.9811::TRINITY_DN16322_c0_g1::g.9811::m.9811	15-cis-phytoene desaturase, chloroplastic/chromoplastic	52.7582	19	1.21113	0.0251
Gene.9826::TRINITY_DN16324_c0_g1::g.9826::m.9826	Uncharacterized protein YGR266W	397.127	2	1.21857	0.01486
Gene.9894::TRINITY_DN16342_c0_g1::g.9894::m.9894	Tat-binding homolog 7	671.389	5	1.2531	0.03254
Gene.9906::TRINITY_DN16346_c0_g1::g.9906::m.9906	Mitochondrial import inner membrane translocase subunit tim23	195.282	28	0.73461	0.01813
Gene.9944::TRINITY_DN16356_c0_g1::g.9944::m.9944	Nucleoprotein TPR	236.113	15	1.24346	0.02617
Gene.9988::TRINITY_DN16365_c0_g5::g.9988::m.9988	Itaconate transport protein	271.937	4	2.90371	0.02744