Supplementary Information

人工光源對黃緣螢幼蟲基因表現之影響

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附表一、黃緣螢光害實驗使用次世代定序技術定序後產出之 read 產量、有效 read 量、轉錄組組裝所使用的 read 量、與轉錄組和 RNA-seq read 比對率

sTable 1. Read numbers for the transcriptome assembly as well as the mapping rate in A. ficta light treatment and control

	FFC-1	FFC-2	FFC-3	FFL-1	FFL-2	FFL-3	Total paired-end read numbers	Total bases
total reads	36,053,903	43,158,444	37,706,602	60,995,302	54,259,270	34,432,345	266,605,866	39,990,879,900
after removed bad / rRNA read	36,022,675	43,140,885	37,676,575	60,967,364	54,237,080	34,413,092	266,457,671	39,968,650,650
Reads for transcriptome assembly	36,022,675	43,140,885	37,676,575	60,967,364	54,237,080	34,413,092	266,457,671	39,968,650,650
mapped reads	33,320,502	39,842,215	35,477,450	56,797,733	50,733,536	32,241,741	248,413,177	37,261,976,550
mapping rate	92.50%	92.35%	94.16%	93.16%	93.54%	93.69%	93.23%	

FFC：無光照對照組；FFL：光照處理組

FFC: control; FFL: light treatment

附表二、黃緣螢表現量上升 / 啟動的差異性表現基因在控制組與夜間光照組中轉錄子表現量與表現量改變倍數。

Table S2. Expression levels, annotation, and expression fold chnages of (A) up-regulated unigenes and (B) activated unigenes of A. ficta larvae underwent either regular light/dark cycle (control) or light treatment during night (experiment).

(A)

Unigene ID	Controls (FPKM)			Light treatment (FPKM)			Average expression level		Standard diviation		fold change	subject sequence ID	% match	NCBI accession number	annotation
	replicate 1	replicate 2	replicate 3	replicate 1	replicate 2	replicate 3	control	experiment	control	experiment					
TRINITY_DN52275_c0_g1_i1	66.94	162.53	5.40	4480.31	461.00	62.95	78.29	1668.09	79.18	2443.58	21.31				
TRINITY_DN50800_c1_g1_i1	26.35	4.32	18.76	406.47	17.04	89.79	16.48	171.10	11.19	207.06	10.38	PE1_ANOGA	45.83	gi|2224921|	insect intestinal mucin IIM22 [Trichoplusia ni]
TRINITY_DN68372_c0_g2_i1	102.66	74.62	9.98	1528.89	208.57	53.41	62.42	596.96	47.53	810.80	9.56				
TRINITY_DN56035_c0_g1_i1	49.23	0.00	0.00	187.53	185.03	52.01	16.41	141.53	28.42	77.53	8.63	UXUA_STRA5	31.11	gi|149143243|	putative orphan protein [Roseovarius sp. TM1035]
TRINITY_DN79295_c0_g1_i3	4.07	5.07	0.00	37.96	10.98	24.26	3.05	24.40	2.69	13.49	8.01	LCAP_HUMAN	34.2	gi|157111305|	aminopeptidase AAEL005806-PA, partial [Aedes aegypti]
TRINITY_DN10957_c0_g1_i1	11.46	17.36	10.33	98.04	20.86	166.46	13.05	95.12	3.78	72.84	7.29				
TRINITY_DN75296_c2_g5_i1	1614.10	2022.20	145.78	20710.91	5028.69	1543.96	1260.69	9094.52	986.87	10209.86	7.21				
TRINITY_DN64939_c1_g1_i1	164.09	291.60	50.51	2540.65	759.71	335.76	168.73	1212.04	120.61	1169.97	7.18	CUD1_SCHGR	51.96	gi|399154152|	cuticular protein 21 precursor [Apis mellifera]
TRINITY_DN74959_c0_g12_i4	9.16	32.79	22.89	249.56	153.36	22.36	21.62	141.76	11.87	114.04	6.56				
TRINITY_DN74626_c0_g3_i1	9.69	5.45	0.00	55.33	20.80	10.95	5.05	29.02	4.86	23.31	5.75	JHAMT_DROME	32.18	gi|89258596|	juvenile hormone acid methyl transferase [Aedes aegypti]
TRINITY_DN35140_c0_g1_i1	8.50	12.59	0.00	47.23	37.75	28.76	7.03	37.91	6.42	9.24	5.39	CP6B1_PAPPO	29.03	gi|270012827|	cytochrome P450 9Z6 [Tribolium castaneum]
TRINITY_DN96734_c0_g1_i1	23.98	4.37	4.51	43.51	71.08	51.21	10.95	55.27	11.28	14.23	5.05	JHAMT_BOMMO	27.75	gi|728678581|	juvenile hormone acid methyltransferase [Neocaridina denticulata]
TRINITY_DN5946_c0_g1_i1	84.41	48.95	99.07	365.21	397.77	288.10	77.47	350.36	25.77	56.32	4.52				
TRINITY_DN87624_c0_g1_i1	7.18	20.33	3.37	48.11	34.00	57.34	10.29	46.48	8.90	11.75	4.52	VNNL2_DROME	35.05	gi|295393189|	FI11051p [Drosophila melanogaster]
TRINITY_DN55953_c0_g1_i1	16.35	13.47	0.00	36.39	50.83	46.88	9.94	44.70	8.73	7.47	4.50	LA1D_UROYA	27.59	gi|642927671|	uncharacterized protein LOC103313566 [Tribolium castaneum]
TRINITY_DN90741_c0_g3_i1	54.42	16.07	22.65	130.32	105.47	180.38	31.05	138.72	20.51	38.16	4.47	GLBL3_HUMAN	37.72	gi|636630774|	beta-galactosidase [Periplaneta americana]
TRINITY_DN86310_c0_g1_i1	20.86	11.28	9.34	50.52	74.44	57.94	13.83	60.97	6.17	12.25	4.41	CBPA1_ANOGA	43.77	gi|86279351|	putative carboxypeptidase A-like [Tenebrio molitor]
TRINITY_DN87322_c1_g1_i1	12.80	12.56	4.53	61.00	22.95	40.08	9.96	41.34	4.71	19.06	4.15	CBPB_ASTAS	44.08	gi|429327023|	carboxypeptidase [Coptotermes formosanus]
TRINITY_DN89726_c0_g1_i1	7.65	3.99	4.11	18.20	17.34	13.79	5.25	16.44	2.08	2.34	3.13	YH24_CAEEL	42.13	gi|646718860|	putative aminopeptidase W07G4.4 [Zootermopsis nevadensis]
TRINITY_DN90456_c1_g1_i1	25.15	28.27	17.89	36.68	94.21	85.05	23.77	71.98	5.33	30.91	3.03	CP9E2_BLAGE	46.01	gi|741829289|	cytochrome P450 [Leptinotarsa decemlineata]
TRINITY_DN56580_c2_g1_i1	246.31	225.68	168.36	541.46	627.57	737.55	213.45	635.52	40.39	98.29	2.98	MMP20_HUMAN	43.37	gi|676778926|	interstitial collagenase, partial [Calypte anna]
TRINITY_DN78027_c0_g1_i1	159.72	123.86	68.22	314.92	380.10	280.38	117.26	325.14	46.10	50.64	2.77				
TRINITY_DN79572_c0_g1_i1	74.57	70.22	43.52	170.89	192.81	144.89	62.77	169.53	16.81	23.99	2.70	THIC_HUMAN	56.49	gi|24655093|	acetyl-CoA acetyltransferase CG9149 [Drosophila melanogaster]

(B)

Unigene ID	Controls (FPKM)			Light treatment (FPKM)			Average expression level		Standard diviation		fold change	subject sequence ID	% match	NCBI accession number	annotation
	replicate 1	replicate 2	replicate 3	replicate 1	replicate 2	replicate 3	control	experiment	control	experiment					
TRINITY_DN84496_c0_g1_i4	0.00	6.17	0.00	111.30	15.39	3.01	2.06	43.23	3.56	59.27					
TRINITY_DN50395_c0_g1_i1	3.94	0.00	0.00	10.34	79.00	7.00	1.31	32.11	2.28	40.64					
TRINITY_DN82778_c0_g2_i1	0.00	0.00	4.38	49.84	7.58	18.89	1.46	25.44	2.53	21.88		CTR2_ANOGA	35.14	gi|568255267|	chymotrypsin 1 [Anopheles darlingi]
TRINITY_DN86731_c0_g1_i1	6.72	8.39	4.78	13.55	18.63	21.37	6.63	17.85	1.81	3.97		OXDD_PIG	33.73	gi|170047888|	d-amino acid oxidase [Culex quinquefasciatus]
TRINITY_DN145178_c0_g1_i1	0.00	0.00	0.00	0.00	20.34	30.12	0.00	16.82	0.00	15.36		RL39_SPOFR	85.29	gi|225708742|	60S ribosomal protein L39 [Caligus rogercresseyi]
TRINITY_DN120152_c0_g1_i1	4.77	0.00	0.00	14.00	19.39	10.41	1.59	14.60	2.76	4.52		JHAMT_DROME	31.03	gi|607030597|	juvenile hormone acid methyltransferase [Aphis gossypii]
TRINITY_DN201218_c0_g1_i1	0.00	0.00	0.00	8.57	24.27	10.30	0.00	14.38	0.00	8.61		RL38A_SCHPO	59.09	gi|761966387|	60S ribosomal protein L38 [Monoraphidium neglectum]
TRINITY_DN127104_c0_g1_i1	0.00	0.00	0.00	6.67	28.25	4.82	0.00	13.25	0.00	13.03		RS21_ASPFU	57.32	gi|759278829|	40S ribosomal protein S21 [Exophiala xenobiotica]
TRINITY_DN172675_c0_g1_i1	0.00	0.00	0.00	0.00	29.50	4.05	0.00	11.18	0.00	15.99		RS27A_CAEBR	61.22	gi|545703418|	40S ribosomal protein S27Ae [Galdieria sulphuraria]
TRINITY_DN193140_c0_g1_i1	0.00	0.00	0.00	0.00	25.25	4.32	0.00	9.86	0.00	13.50		RL31_CYAPA	61.02	gi|700589126|	60S ribosomal protein [Phragmatopoma lapidosa]
TRINITY_DN213693_c0_g1_i1	0.00	0.00	0.00	3.10	25.87	0.00	0.00	9.66	0.00	14.13		RL291_ARATH	56.45	gi|7959366|	ribosomal protein L29 [Panax ginseng]
TRINITY_DN85029_c0_g2_i1	3.53	0.00	0.00	7.19	6.12	10.31	1.18	7.87	2.04	2.18		CP6K1_BLAGE	36.2	gi|47779232|	antennae-rich cytochrome P450 [Phyllopertha diversa]
TRINITY_DN54988_c0_g1_i1	0.00	0.00	0.00	8.59	10.46	3.30	0.00	7.45	0.00	3.71		ACT1_DICDI	97.18	gi|332672680|	beta-actin [Sepia officinalis]
TRINITY_DN171107_c0_g1_i1	0.00	0.00	0.00	17.19	4.10	0.00	0.00	7.10	0.00	8.98					
TRINITY_DN168506_c0_g1_i1	0.00	0.00	0.00	0.00	16.19	3.20	0.00	6.47	0.00	8.58		RL23A_RAT	68.1	gi|166952305|	ribosomal protein rpl23a [Lineus viridis]
TRINITY_DN191407_c0_g1_i1	0.00	0.00	0.00	0.00	15.68	3.28	0.00	6.32	0.00	8.27		RL27A_PONAB	65.77	gi|478621094|	60S ribosomal protein L27a [Gallus gallus]
TRINITY_DN116174_c0_g1_i1	0.00	0.00	0.00	3.36	15.21	0.00	0.00	6.19	0.00	7.99		RS23_CIOIN	70.63	gi|223646526|	40S ribosomal protein S23 [Salmo salar]
TRINITY_DN214737_c0_g1_i1	0.00	0.00	0.00	4.90	7.90	5.45	0.00	6.09	0.00	1.60		RL12_CAEEL	49.44	gi|313586509|	60S ribosomal protein L12A [Hevea brasiliensis]
TRINITY_DN104464_c0_g1_i1	0.00	0.00	0.00	12.02	6.12	0.00	0.00	6.05	0.00	6.01		CYTX_BOVIN	30	gi|586730450|	cystatin domain protein [Tetrahymena thermophila SB210]
TRINITY_DN59349_c0_g1_i1	0.00	0.00	0.00	11.89	4.48	0.00	0.00	5.45	0.00	6.00					
TRINITY_DN127242_c0_g1_i1	0.00	0.00	0.00	3.07	8.57	3.77	0.00	5.14	0.00	2.99					
TRINITY_DN56440_c0_g3_i1	0.00	0.00	0.00	9.57	5.77	0.00	0.00	5.11	0.00	4.82					
TRINITY_DN40369_c0_g1_i1	0.00	0.00	0.00	0.00	8.41	6.65	0.00	5.02	0.00	4.44		COX2_DROYA	62.04	gi|341605664|	cytochrome c oxidase subunit II (mitochondrion) [Alcithoe larochei]
TRINITY_DN180457_c0_g1_i1	0.00	0.00	0.00	0.00	7.02	7.50	0.00	4.84	0.00	4.20					
TRINITY_DN70978_c0_g2_i1	0.00	0.00	0.00	7.92	5.14	0.00	0.00	4.35	0.00	4.02					
TRINITY_DN49364_c0_g2_i1	0.00	0.00	0.00	0.00	5.28	7.27	0.00	4.18	0.00	3.76					
TRINITY_DN56652_c0_g1_i1	0.00	0.00	0.00	0.00	7.01	5.09	0.00	4.03	0.00	3.62		COX1_LUMTE	71.65	gi|567767395|	cytochrome c oxidase subunit I (mitochondrion) [Nerita versicolor]
TRINITY_DN44766_c0_g1_i1	0.00	0.00	0.00	0.00	8.48	3.62	0.00	4.03	0.00	4.26		CAH3_BOVIN	64.71	gi|99082886|	putative cytoplasmic carbonic anhydrase [Anopheles gambiae]
TRINITY_DN68879_c0_g2_i1	0.00	0.00	0.00	5.56	6.25	0.00	0.00	3.94	0.00	3.43		RS20_DROME	46.02	gi|195353879|	ribosomal protein GM23136 [Drosophila sechellia]
TRINITY_DN1720_c0_g1_i1	0.00	0.00	0.00	4.69	0.00	6.49	0.00	3.73	0.00	3.35					
TRINITY_DN57148_c0_g1_i1	0.00	0.00	0.00	5.73	0.00	4.95	0.00	3.56	0.00	3.11					
TRINITY_DN60115_c0_g1_i1	0.00	0.00	0.00	4.30	6.15	0.00	0.00	3.48	0.00	3.15					
TRINITY_DN65331_c0_g2_i1	0.00	0.00	0.00	5.09	4.87	0.00	0.00	3.32	0.00	2.88		RL36A_TETTS	65.14	gi|241669024|	ribosomal protein TA01007p [Drosophila melanogaster]
TRINITY_DN65931_c0_g1_i1	0.00	0.00	0.00	4.65	4.97	0.00	0.00	3.20	0.00	2.78		RL21_TETTS	53.5	gi|678329162|	ribosomal protein l21 [Stylonychia lemnae]
TRINITY_DN148112_c0_g1_i1	0.00	0.00	0.00	4.69	0.00	4.87	0.00	3.18	0.00	2.76					

附表三、黃緣螢表現量 (A) 下降 / (B) 關閉的差異性表現基因在控制組與夜間光照組中轉錄子表現量與表現量改變倍數。

Table S3. Expression levels, annotation, and expression fold chnages of (A) down-regulated unigenes and (B) inactivated unigenes of A. ficta larvae underwent either regular light/dark cycle (control) or light treatment during night (experiment).

(A)

Unigene ID	Controls (FPKM)			Light treatment (FPKM)			Average expression level		Standard diviation		fold change	subject sequence ID	% match	NCBI accession number	annotation
	replicate 1	replicate 2	replicate 3	replicate 1	replicate 2	replicate 3	control	experiment	control	experiment					
TRINITY_DN76602_c2_g7_i1	308.91	491.70	181.11	4.88	7.69	0.00	327.24	4.19	156.10	3.89	0.01	U88A1_ARATH	36.84	gi|734545061|	hypotheticalproteinTcan_00040
TRINITY_DN25891_c0_g1_i1	126.26	296.95	59.46	0.00	0.00	10.68	160.89	3.56	122.47	6.16	0.02	PBP6_DROME	26.6	gi|22022285|	pheromone-bindingprotein[Anomalacuprea]
TRINITY_DN82391_c3_g4_i1	182.41	206.62	210.64	3.30	23.43	5.42	199.89	10.72	15.27	11.06	0.05	ACT1_ACACA	98.02	gi|470402520|	Actin1[Acanthamoebacastellaniistr.Neff]>gi|470511936|ref|XP_004352077.1|actin-1
TRINITY_DN28599_c0_g1_i1	15.52	55.18	76.55	0.00	9.40	0.00	49.08	3.13	30.97	5.43	0.06	CHIT_BRUMA	38.89	gi|157361591|	peritrophin-likeprotein[Phlebotomuspapatasi]
TRINITY_DN25933_c0_g2_i1	34.24	119.85	10.00	0.00	4.53	6.17	54.70	3.57	57.71	3.20	0.07	OB99A_DROME	27.78	gi|194765282|	GF23357[Drosophilaananassae]>gi|190615028|gb|EDV30552.1|GF23357[Drosophilaananassae]
TRINITY_DN193886_c0_g2_i1	25.45	122.95	56.10	3.95	6.62	3.48	68.16	4.68	49.86	1.69	0.07				
TRINITY_DN84003_c0_g1_i1	112.89	30.90	186.64	10.12	6.87	9.59	110.14	8.86	77.91	1.74	0.08	SAB_ARATH	31.58	gi|759719309|	hypotheticalprotein[Cystobacterfuscus]
TRINITY_DN71202_c0_g1_i1	79.02	31.70	126.50	9.48	5.30	5.20	79.07	6.66	47.40	2.44	0.08	TBB_TETPY	99.21	gi|422900825|	beta-tubulin
TRINITY_DN46853_c2_g2_i1	1198.36	2797.08	617.96	60.02	191.52	222.77	1537.80	158.10	1128.52	86.37	0.10				
TRINITY_DN4344_c0_g1_i1	49.32	28.99	44.07	4.89	4.46	4.05	40.79	4.47	10.55	0.42	0.11				
TRINITY_DN140163_c2_g1_i1	717.57	1379.36	1018.69	27.56	177.68	161.15	1038.54	122.13	331.34	82.32	0.12	PE1_ANOGA	33.33	gi|752878828|	PREDICTED:peritrophin-1[Camponotusfloridanus]
TRINITY_DN51599_c4_g1_i1	389.96	1008.61	864.52	16.95	199.57	79.07	754.36	98.53	323.70	92.85	0.13				
TRINITY_DN64658_c0_g6_i1	24.65	10.11	32.75	3.87	5.24	0.00	22.50	3.03	11.47	2.72	0.13	ACT10_SOLTU	98.91	gi|724970643|	PREDICTED:actin
TRINITY_DN66574_c0_g2_i1	41.42	6.63	36.15	5.89	5.67	0.00	28.07	3.85	18.75	3.34	0.14	RS241_ARATH	47.17	gi|669029828|	unnamedproteinproduct[Triticumaestivum]
TRINITY_DN71279_c0_g2_i1	51.46	22.00	39.11	9.05	4.17	3.36	37.52	5.53	14.79	3.08	0.15	TBB_TETPY	99.29	gi|149212511|	beta-tubulin
TRINITY_DN166008_c0_g1_i1	115.66	55.56	137.17	12.45	23.96	9.95	102.80	15.45	42.30	7.47	0.15				
TRINITY_DN80134_c0_g1_i1	22.57	12.06	66.13	5.27	5.46	7.44	33.58	6.05	28.67	1.20	0.18				
TRINITY_DN6547_c1_g2_i1	41.68	14.67	67.50	8.67	6.08	8.32	41.28	7.69	26.42	1.41	0.19	Y4654_MYCGI	30.49	gi|678310018|	UNKNOWN[Stylonychialemnae]
TRINITY_DN76902_c0_g1_i1	19.63	6.89	35.67	3.77	3.25	4.89	20.73	3.97	14.42	0.84	0.19	CATB_MACFA	49.84	gi|678004657|	PREDICTED:cathepsinB[Acanthisittachloris]
TRINITY_DN143135_c0_g1_i1	34.08	17.62	20.24	7.22	0.00	6.61	23.98	4.61	8.84	4.00	0.19				
TRINITY_DN84655_c0_g1_i1	24.45	11.12	47.36	4.72	4.50	6.98	27.65	5.40	18.33	1.37	0.20	GSTM2_CHICK	34.13	gi|586738842|	glutathioneS-transferase
TRINITY_DN28120_c0_g1_i1	15.17	8.02	43.75	4.39	4.36	4.76	22.31	4.50	18.91	0.22	0.20				
TRINITY_DN86144_c1_g1_i2	8.90	12.04	30.42	3.37	3.80	3.30	17.12	3.49	11.62	0.27	0.20	Y132A_HAEIN	34.48	gi|795010534|	PREDICTED:uncharacterizedproteinLOC105561931[Vollenhoviaemeryi]
TRINITY_DN78906_c0_g1_i1	91.27	31.57	133.39	16.26	15.24	21.48	85.41	17.66	51.16	3.35	0.21	XCP1_ARATH	43.87	gi|260516678|	cysteineprotease1[Brachiariahybridcultivar]
TRINITY_DN87539_c3_g6_i8	54.99	27.30	119.18	12.57	14.36	15.37	67.15	14.10	47.13	1.42	0.21	TBA_CHLVU	94.99	gi|135433|	RecName:Full=Tubulinalphachain[Oxytrichagranulifera]>gi|578450|emb|CAA77810.1|alpha-Tubulin[Oxytrichagranulifera]
TRINITY_DN212772_c0_g1_i1	485.26	351.27	566.30	121.97	184.55	131.41	467.61	145.98	108.60	33.74	0.31				

(B)

Unigene ID	Expression level in control (FPKM)			Expression level in experiment (FPKM)			Average expression level		Standard diviation		fold change	subject sequence ID	% match	NCBI accession number	annotation
	replicate 1	replicate 2	replicate 3	replicate 1	replicate 2	replicate 3	control	experiment	control	experiment					
TRINITY_DN80177_c1_g1_i1	391.16	148.57	264.23	0.00	0.00	0.00	267.99	0.00	121.34	0.00	0.00	H2B2_TETTS	75.22	gi|544214317|	histoneH2B[Cyanidioschyzonmerolaestrain10D]>gi|544214335|ref|XP_005537314.1|histoneH2B[Cyanidioschyzonmerolaestrain10D]>gi|449017867|dbj|BAM81269.1|histoneH2B[Cyanidioschyzonmerolaestrain10D]>gi|449017876|dbj|BAM81278.1|histoneH2B[Cyanidioschyzonmerolaestrain10D]
TRINITY_DN38693_c0_g1_i1	215.72	280.86	254.76	0.00	0.00	0.00	250.44	0.00	32.78	0.00	0.00	ATPD_CHLAD	38.1	gi|326501204|	predictedprotein[Hordeumvulgaresubsp.vulgare]
TRINITY_DN15787_c0_g1_i1	242.76	241.77	177.68	0.00	0.00	0.00	220.74	0.00	37.29	0.00	0.00				
TRINITY_DN189287_c0_g1_i1	197.46	115.85	221.45	8.24	0.00	0.00	178.25	2.75	55.36	4.76	0.02				
TRINITY_DN45292_c0_g2_i1	173.71	80.67	277.65	5.26	0.00	0.00	177.35	1.75	98.54	3.04	0.01	TBA_TETPY	97.12	gi|94692110|	putativetubulinalpha1chain[Fagussylvatica]
TRINITY_DN213458_c0_g1_i1	151.05	181.62	177.17	0.00	0.00	0.00	169.95	0.00	16.52	0.00	0.00				
TRINITY_DN105920_c0_g1_i1	207.77	158.38	126.21	0.00	0.00	0.00	164.12	0.00	41.08	0.00	0.00	CATR_ATRNU	34.92	gi|296206094|	PREDICTED:calmodulin-likeprotein5[Callithrixjacchus]
TRINITY_DN140722_c0_g1_i1	243.71	87.40	138.87	0.00	0.00	0.00	156.66	0.00	79.66	0.00	0.00	RS28_ICTPU	63.64	gi|511000226|	30SribosomalproteinS28e[Mucorcircinelloidesf.circinelloides1006PhL]
TRINITY_DN186724_c0_g1_i1	147.70	131.91	186.98	0.00	0.00	0.00	155.53	0.00	28.36	0.00	0.00				
TRINITY_DN97982_c0_g1_i1	152.12	143.70	140.99	0.00	0.00	0.00	145.60	0.00	5.80	0.00	0.00				
TRINITY_DN165646_c0_g1_i1	181.93	68.04	159.83	0.00	0.00	0.00	136.60	0.00	60.39	0.00	0.00				
TRINITY_DN211883_c0_g1_i1	143.42	173.79	73.69	0.00	0.00	0.00	130.30	0.00	51.32	0.00	0.00				
TRINITY_DN74644_c0_g1_i2	134.76	112.39	104.08	0.00	0.00	0.00	117.08	0.00	15.87	0.00	0.00	APTX_RAT	35.85	gi|118385490|	hypotheticalproteinTTHERM_00713220[Tetrahymenathermophila]>gi|89307641|gb|EAS05629.1|hypotheticalproteinTTHERM_00713220[Tetrahymenathermophila SB210]
TRINITY_DN66354_c0_g1_i1	149.39	115.76	61.76	0.00	3.03	0.00	108.97	1.01	44.21	1.75	0.01	RS30_PLAF7	72.73	gi|749841441|	hypotheticalproteinPAXINDRAFT_10917[PaxillusinvolutusATCC200175]
TRINITY_DN189772_c0_g1_i1	38.89	12.21	264.56	0.00	0.00	0.00	105.22	0.00	138.63	0.00	0.00				
TRINITY_DN78288_c2_g4_i1	203.09	86.61	23.56	0.00	0.00	0.00	104.42	0.00	91.08	0.00	0.00	RL29_TETTH	58.73	gi|72011326|	ribosomalproteinL29[Sterkiellahistriomuscorum]>gi|72011329|gb|AAZ66133.1|ribosomalproteinL29[Sterkiellahistriomuscorum]>gi|403343981|gb|EJY71327.1|Ribosomalprotein L29[Oxytrichatrifallax]
TRINITY_DN85683_c0_g1_i3	91.65	110.11	109.84	0.00	3.54	0.00	103.87	1.18	10.58	2.04	0.01				
TRINITY_DN187439_c0_g1_i1	193.74	70.08	35.40	0.00	0.00	0.00	99.74	0.00	83.24	0.00	0.00				
TRINITY_DN52417_c0_g3_i1	133.40	102.72	55.66	0.00	0.00	0.00	97.26	0.00	39.16	0.00	0.00				
TRINITY_DN72206_c1_g1_i2	139.56	50.26	93.63	0.00	0.00	0.00	94.49	0.00	44.66	0.00	0.00	H2AX_TETPY	73.87	gi|224083032|	PREDICTED:histoneH2A.x-like[Taeniopygiaguttata]
TRINITY_DN49051_c0_g2_i1	209.80	15.69	47.53	3.38	0.00	0.00	91.01	1.13	104.11	1.95	0.01	H41_TETPY	90.59	gi|195618484|	histoneH4[Zeamays]
TRINITY_DN117045_c0_g1_i1	126.11	90.13	48.59	0.00	0.00	0.00	88.28	0.00	38.79	0.00	0.00	YCNE_BACSU	34.04	gi|663751327|	antibioticbiosynthesismonooxygenase[Phycicoccusjejuensis]
TRINITY_DN214364_c0_g1_i1	93.89	86.06	74.86	0.00	0.00	0.00	84.94	0.00	9.56	0.00	0.00				
TRINITY_DN45754_c0_g2_i1	98.29	48.99	93.30	3.74	0.00	0.00	80.19	1.25	27.13	2.16	0.02	TBA_TETTH	97.14	gi|54287295|	alpha-tubulin[Cucumissativus]
TRINITY_DN122268_c0_g1_i1	64.95	107.00	66.08	0.00	0.00	0.00	79.34	0.00	23.96	0.00	0.00	MEND_HISS2	38.1	gi|326501204|	predictedprotein[Hordeumvulgaresubsp.vulgare]
TRINITY_DN172794_c0_g1_i1	114.10	77.04	44.20	0.00	0.00	0.00	78.45	0.00	34.97	0.00	0.00				
TRINITY_DN212212_c0_g1_i1	95.24	44.36	87.51	0.00	0.00	0.00	75.70	0.00	27.42	0.00	0.00				
TRINITY_DN72206_c1_g1_i1	147.88	19.59	59.10	0.00	0.00	0.00	75.52	0.00	65.70	0.00	0.00	H2AX_TETPY	73.87	gi|224083032|	PREDICTED:histoneH2A.x-like[Taeniopygiaguttata]

TRINITY_DN167503_c0_g1_i1	93.96	30.09	94.39	0.00	0.00	0.00	72.81	0.00	37.00	0.00	0.00				
TRINITY_DN116345_c0_g1_i1	84.68	76.37	51.82	0.00	0.00	0.00	70.96	0.00	17.09	0.00	0.00	CMOA_PSYIN	31.15	gi|326501204|	predictedprotein[Hordeumvulgaresubsp.vulgare]
TRINITY_DN190728_c0_g1_i1	182.33	9.33	13.44	0.00	0.00	0.00	68.37	0.00	98.72	0.00	0.00				
TRINITY_DN59727_c0_g1_i1	118.56	41.89	42.07	0.00	0.00	0.00	67.51	0.00	44.21	0.00	0.00	RLA1_DAVTA	40	gi|528295470|	60sacidicribosomalproteinP1[Blumeriagraminisf.sp.hordeiDH14]
TRINITY_DN79424_c0_g3_i1	24.38	157.41	19.17	0.00	0.00	0.00	66.99	0.00	78.35	0.00	0.00				
TRINITY_DN12153_c0_g2_i1	104.92	19.52	75.10	0.00	0.00	0.00	66.51	0.00	43.34	0.00	0.00	H41_TETPY	88.89	gi|4376214|	histoneH4
TRINITY_DN190806_c0_g1_i1	83.95	54.68	60.60	0.00	0.00	0.00	66.41	0.00	15.47	0.00	0.00				
TRINITY_DN96379_c1_g1_i1	22.11	9.46	160.20	0.00	0.00	0.00	63.92	0.00	83.62	0.00	0.00	RS29_CANGA	58.82	gi|50286045|	40SribosomalproteinS29[CandidaglabrataCBS138]>gi|74637844|sp|Q6FWE3.1|RS29_CANGARecName:Full=40SribosomalproteinS29[CandidaglabrataCBS138]>gi|49524756|emb|CAG58362.1|unnamedproteinproduct[Candidaglabrata]
TRINITY_DN116364_c0_g1_i1	77.82	55.19	51.89	0.00	0.00	0.00	61.63	0.00	14.12	0.00	0.00				
TRINITY_DN193998_c0_g1_i1	77.47	31.86	72.71	0.00	0.00	0.00	60.68	0.00	25.07	0.00	0.00				
TRINITY_DN79978_c0_g2_i1	104.37	27.87	40.24	0.00	0.00	0.00	57.49	0.00	41.06	0.00	0.00	H2AZ_CHICK	80.17	gi|567755092|	ChainC
TRINITY_DN190808_c0_g1_i1	78.37	39.97	52.18	0.00	0.00	0.00	56.84	0.00	19.62	0.00	0.00				
TRINITY_DN79203_c0_g1_i2	116.44	6.11	46.54	0.00	0.00	0.00	56.36	0.00	55.81	0.00	0.00	CATL2_PARTE	44.4	gi|145510090|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124408217|emb|CAK73581.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN90964_c2_g2_i9	66.45	25.68	76.80	0.00	0.00	0.00	56.31	0.00	27.03	0.00	0.00	TBB_TETTH	99.61	gi|302026149|	beta-tubulin[Gymnophryssp.ATCC50923]
TRINITY_DN142037_c0_g1_i1	96.99	33.86	31.83	0.00	0.00	0.00	54.23	0.00	37.05	0.00	0.00	RL35_SCHPO	39.32	gi|125590092|	hypotheticalproteinOsJ_14490[OryzasativaJaponicaGroup]
TRINITY_DN73840_c1_g1_i1	123.38	6.16	31.86	0.00	0.00	0.00	53.80	0.00	61.61	0.00	0.00	RS28_ICTPU	57.69	gi|156083811|	40SribosomalproteinS28[BabesiabovisT2Bo]>gi|154796640|gb|EDO05821.1|40SribosomalproteinS28[Babesiabovis]>gi|527098979|dbj|BAN64549.1|40SribosomalproteinS28[Babesiabovis]>gi|656187643|emb|CDR97969.1|40SribosomalproteinS28
TRINITY_DN42398_c0_g1_i1	61.19	41.48	58.17	0.00	0.00	0.00	53.61	0.00	10.62	0.00	0.00	UBC5_YEAST	79.31	gi|698794030|	ubiquitin-conjugatingenzymeE2-17kDa[Aphanomycesastaci]>gi|574114633|gb|ETV80120.1|ubiquitin-conjugatingenzymeE2-17kDa[Aphanomycesastaci]
TRINITY_DN94621_c0_g1_i1	82.84	26.00	49.90	0.00	0.00	0.00	52.92	0.00	28.54	0.00	0.00	RL34_TETTS	57.01	gi|242078237|	hypotheticalproteinSORBIDRAFT_07g003770[Sorghumbicolor]>gi|514793400|ref|XP_004972805.1|PREDICTED:60SribosomalproteinL34-like[Setariaitalica]>gi|241940237|gb|EES13382.1|hypotheticalproteinSORBIDRAFT_07g003770[Sorghumbicolor]
TRINITY_DN41070_c0_g2_i1	64.44	51.35	41.42	0.00	0.00	0.00	52.41	0.00	11.55	0.00	0.00				
TRINITY_DN55239_c0_g1_i1	86.43	36.64	33.58	0.00	0.00	0.00	52.21	0.00	29.67	0.00	0.00	RL36A_TETTS	66.98	gi|820108972|	60SribosomalproteinL36a-like[Scleropagesformosus]
TRINITY_DN148830_c0_g1_i1	66.93	39.80	47.71	0.00	0.00	0.00	51.48	0.00	13.95	0.00	0.00				
TRINITY_DN118406_c0_g1_i1	69.03	28.05	55.55	0.00	0.00	0.00	50.88	0.00	20.88	0.00	0.00	RS28_DICDI	48.28	gi|156083811|	40SribosomalproteinS28[BabesiabovisT2Bo]>gi|154796640|gb|EDO05821.1|40SribosomalproteinS28[Babesiabovis]>gi|527098979|dbj|BAN64549.1|40SribosomalproteinS28[Babesiabovis]>gi|656187643|emb|CDR97969.1|40SribosomalproteinS28
TRINITY_DN75857_c0_g1_i1	76.59	56.27	17.89	0.00	0.00	0.00	50.25	0.00	29.81	0.00	0.00	RS29_GRIJA	74.55	gi|759100021|	PREDICTED:LOWQUALITYPROTEIN:40SribosomalproteinS29[Pteropusvampyrus]
TRINITY_DN69756_c0_g2_i1	54.52	61.94	33.21	0.00	0.00	0.00	49.89	0.00	14.91	0.00	0.00	RL392_ARATH	80.39	gi|645227824|	PREDICTED:60SribosomalproteinL39-1[Prunusmume]
TRINITY_DN2834_c0_g1_i1	60.57	27.41	57.15	0.00	0.00	0.00	48.38	0.00	18.24	0.00	0.00	H2AX_TETPY	68.66	gi|562975223|	histoneH2A[OgataeaparapolymorphaDL-1]
TRINITY_DN180861_c0_g1_i1	49.54	47.95	47.28	0.00	0.00	0.00	48.26	0.00	1.16	0.00	0.00				
TRINITY_DN187286_c0_g1_i1	48.97	51.51	43.84	0.00	0.00	0.00	48.11	0.00	3.91	0.00	0.00				
TRINITY_DN96875_c0_g1_i1	49.72	24.66	66.46	0.00	0.00	0.00	46.95	0.00	21.04	0.00	0.00	BAR3_CHITE	23.03	gi|118367704|	hypotheticalproteinTTHERM_01532560[Tetrahymenathermophila]
TRINITY_DN81323_c1_g3_i1	42.26	78.98	19.19	0.00	0.00	0.00	46.81	0.00	30.16	0.00	0.00	APE1_AERPE	88.24	gi|398395201|	hypotheticalproteinMYCGRDRAFT_45280[ZymoseptoriatriticiIPO323]>gi|339470938|gb|EGP86035.1|hypotheticalproteinMYCGRDRAFT_45280[ZymoseptoriatriticiIPO323]>gi|452836072|gb|EME38021.1|hypotheticalproteinDOTSEDRAFT_67407[DothistromaseptosporumNZE10]
TRINITY_DN216304_c0_g1_i1	49.30	18.04	70.24	0.00	0.00	0.00	45.86	0.00	26.27	0.00	0.00				
TRINITY_DN172276_c0_g1_i1	85.16	29.22	22.87	0.00	0.00	0.00	45.75	0.00	34.28	0.00	0.00				
TRINITY_DN13083_c0_g1_i1	44.63	24.71	66.48	0.00	0.00	0.00	45.27	0.00	20.89	0.00	0.00	CALM2_BRAFL	37.76	gi|758367768|	hypotheticalprotein[Parasitellaparasitica]
TRINITY_DN145827_c0_g1_i1	46.34	38.68	48.86	0.00	0.00	0.00	44.63	0.00	5.30	0.00	0.00				
TRINITY_DN47085_c0_g1_i1	103.80	5.81	20.50	0.00	0.00	0.00	43.37	0.00	52.85	0.00	0.00	Y572_OCEIH	33.33	gi|326501204|	predictedprotein[Hordeumvulgaresubsp.vulgare]
TRINITY_DN59173_c0_g1_i2	44.64	32.25	51.26	0.00	0.00	0.00	42.72	0.00	9.65	0.00	0.00	CATR6_PARTE	61.94	gi|224000107|	centrin-likeprotein[ThalassiosirapseudonanaCCMP1335]>gi|220974934|gb|EED93263.1|centrin-likeprotein[ThalassiosirapseudonanaCCMP1335]
TRINITY_DN118777_c0_g1_i1	41.18	39.00	47.28	0.00	0.00	0.00	42.49	0.00	4.29	0.00	0.00				
TRINITY_DN194448_c0_g1_i1	41.67	58.47	25.93	0.00	0.00	0.00	42.02	0.00	16.27	0.00	0.00				
TRINITY_DN77670_c0_g1_i2	50.21	49.90	18.27	0.00	0.00	0.00	39.46	0.00	18.35	0.00	0.00	RS28B_SCHPO	85.11	gi|472584676|	40Sribosomalproteins28[RhodosporidiumtoruloidesNP11]>gi|647399217|emb|CDR43777.1|RHTO0S08e05512g1_1[Rhodosporidiumtoruloides]
TRINITY_DN148003_c0_g1_i1	30.69	49.43	37.44	0.00	0.00	0.00	39.19	0.00	9.49	0.00	0.00				
TRINITY_DN73121_c0_g1_i1	42.26	57.09	17.20	0.00	0.00	0.00	38.85	0.00	20.16	0.00	0.00				
TRINITY_DN67444_c0_g1_i1	58.52	21.24	36.68	0.00	0.00	0.00	38.81	0.00	18.73	0.00	0.00	RL23_PONAB	67.39	gi|4583511|	ribosomalproteinL17[Dicentrarchuslabrax]
TRINITY_DN166239_c0_g2_i1	49.01	22.91	44.10	0.00	0.00	0.00	38.67	0.00	13.87	0.00	0.00				
TRINITY_DN115786_c0_g1_i1	58.61	28.16	29.12	0.00	0.00	0.00	38.63	0.00	17.31	0.00	0.00				
TRINITY_DN72262_c0_g2_i1	76.52	21.10	18.18	0.00	0.00	0.00	38.60	0.00	32.87	0.00	0.00	CMOB_KLEP3	30.65	gi|813214640|	hypotheticalproteinG7K_1412-t1[SaitoellacomplicataNRRLY-17804]
TRINITY_DN74657_c0_g4_i1	60.50	29.79	24.69	0.00	0.00	0.00	38.33	0.00	19.37	0.00	0.00	RL30_TETTS	65.35	gi|261195114|	60SribosomalproteinL30[BlastomycesdermatitidisSLH14081]>gi|239587833|gb|EEQ70476.1|cytosoliclargeribosomalsubunitproteinL30[BlastomycesdermatitidisSLH14081]>gi|239610679|gb|EEQ87666.1|cytosoliclargeribosomalsubunitproteinL30[BlastomycesdermatitidisER-3]>gi|327348885|gb|EGE77742.1|ribosomalproteinL30[BlastomycesdermatitidisATCC18188]>gi|531987432|gb|EQL38019.1|60SribosomalproteinL30[BlastomycesdermatitidisATCC26199]
TRINITY_DN212162_c0_g1_i1	48.64	21.78	43.80	0.00	0.00	0.00	38.08	0.00	14.32	0.00	0.00				
TRINITY_DN19217_c0_g1_i1	51.78	37.02	22.42	0.00	0.00	0.00	37.07	0.00	14.68	0.00	0.00	NLTP_CHICK	47.47	gi|460384923|	PREDICTED:non-specificlipid-transferprotein-like[Solanumlycopersicum]
TRINITY_DN65269_c0_g4_i1	32.65	58.01	19.09	0.00	0.00	0.00	36.58	0.00	19.76	0.00	0.00				
TRINITY_DN187717_c0_g1_i1	19.05	10.38	80.09	0.00	0.00	0.00	36.51	0.00	37.99	0.00	0.00				

TRINITY_DN214074_c0_g1_i1	56.60	28.92	23.27	0.00	0.00	0.00	36.26	0.00	17.84	0.00	0.00				
TRINITY_DN63245_c0_g1_i2	42.16	40.09	24.83	0.00	0.00	0.00	35.70	0.00	9.46	0.00	0.00	LITAF_XENTR	38.78	gi|662502957|	hypotheticalproteinM437DRAFT_10438
TRINITY_DN115209_c0_g1_i1	68.84	21.39	14.65	0.00	0.00	0.00	34.96	0.00	29.53	0.00	0.00	NEDD8_RABIT	44.59	gi|50540180|	neuralprecursorcellexpressed
TRINITY_DN57671_c0_g1_i1	78.68	0.00	25.54	0.00	0.00	0.00	34.74	0.00	40.14	0.00	0.00	BIOB1_PARDP	42.86	gi|678314685|	UNKNOWN[Stylonychialemnae]
TRINITY_DN63507_c0_g2_i1	34.85	21.52	46.29	0.00	0.00	0.00	34.22	0.00	12.40	0.00	0.00	DYL1_HELCR	89.77	gi|640800030|	PREDICTED:dyneinlightchain2
TRINITY_DN50656_c0_g1_i1	39.19	41.30	21.51	0.00	0.00	0.00	34.00	0.00	10.87	0.00	0.00	RL44_CAEEL	73.74	gi|312068963|	hypotheticalproteinLOAG_01874[Loaloa]>gi|3122756|sp|P90702.3|RL44_BRUMARecName:Full=60SribosomalproteinL44[Brugiamalayi]>gi|1813690|gb|AAC47627.1|ribosomalproteinL44[Brugiamalayi]>gi|307767384|gb|EFO26618.1|60SribosomalproteinL44[Loaloa]>gi|402588167|gb|EJW82101.1|60SribosomalproteinL44[Wuchereriabancrofti]>gi|671408793|emb|CDP98126.1|ProteinBM-RPL-41[Brugiamalayi]
TRINITY_DN127098_c0_g1_i1	41.54	12.07	48.13	0.00	0.00	0.00	33.91	0.00	19.20	0.00	0.00				
TRINITY_DN120740_c0_g1_i1	50.23	33.23	18.24	0.00	0.00	0.00	33.90	0.00	16.01	0.00	0.00				
TRINITY_DN55859_c0_g4_i2	45.87	26.94	27.56	0.00	0.00	0.00	33.46	0.00	10.75	0.00	0.00	UBIQP_XENLA	94.51	gi|343960965|	ubiquitin[Pantroglodytes]
TRINITY_DN67489_c0_g1_i1	37.49	29.64	33.17	0.00	0.00	0.00	33.43	0.00	3.93	0.00	0.00	RS26_NEUCR	68	gi|691793744|	hypotheticalproteinBN946_scf184845.g70[Trametescinnabarina]
TRINITY_DN188416_c0_g1_i1	35.45	25.86	38.54	0.00	0.00	0.00	33.28	0.00	6.61	0.00	0.00				
TRINITY_DN99880_c0_g1_i1	40.91	24.45	33.99	0.00	0.00	0.00	33.11	0.00	8.27	0.00	0.00				
TRINITY_DN233600_c0_g1_i1	12.80	46.63	39.25	0.00	0.00	3.54	32.90	1.18	17.79	2.04	0.04				
TRINITY_DN145860_c0_g1_i1	27.59	44.78	25.90	0.00	0.00	0.00	32.76	0.00	10.44	0.00	0.00	MATP_ECO8A	29.51	gi|145508171|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124407241|emb|CAK72638.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN34006_c0_g1_i1	36.91	35.03	24.39	0.00	0.00	0.00	32.11	0.00	6.75	0.00	0.00	RS21_DICDI	58.57	gi|749874142|	hypotheticalproteinM422DRAFT_75438[SphaerobolusstellatusSS14]
TRINITY_DN39162_c0_g1_i1	68.25	0.00	26.85	0.00	0.00	0.00	31.70	0.00	34.38	0.00	0.00	RL8_TETTS	72.73	gi|734673978|	60SribosomalproteinL2[ParacoccidioidesbrasiliensisPb18]>gi|699752250|gb|EEH46099.2|60SribosomalproteinL2[ParacoccidioidesbrasiliensisPb18]>gi|719930595|gb|EEH16618.2|60SribosomalproteinL2[ParacoccidioidesbrasiliensisPb03]
TRINITY_DN52789_c0_g2_i1	33.82	31.85	29.43	0.00	0.00	0.00	31.70	0.00	2.20	0.00	0.00	H4_STYLE	55.24	gi|669313955|	hypotheticalproteinM513_01512[Trichurissuis]>gi|669326302|gb|KFD66515.1|hypotheticalproteinM514_01512[Trichurissuis]
TRINITY_DN66983_c0_g1_i1	35.89	33.86	25.14	0.00	0.00	0.00	31.63	0.00	5.71	0.00	0.00	COAA_DICDI	47.89	gi|751065784|	hypotheticalproteinPAXRUDRAFT_821784[PaxillusrubicundulusVe08.2h10]
TRINITY_DN63209_c3_g1_i3	27.63	33.24	33.83	0.00	0.00	0.00	31.57	0.00	3.42	0.00	0.00	ACT1_ACACA	99.07	gi|387598137|	actin
TRINITY_DN19091_c0_g1_i1	30.37	48.04	16.07	0.00	0.00	0.00	31.49	0.00	16.01	0.00	0.00	HN1_MOUSE	33.9	gi|678314685|	UNKNOWN[Stylonychialemnae]
TRINITY_DN51285_c0_g1_i1	51.72	23.12	19.58	0.00	0.00	0.00	31.48	0.00	17.63	0.00	0.00	CYC_TETPY	58.33	gi|294882136|	cytochromec
TRINITY_DN70448_c0_g1_i1	31.68	32.82	29.39	0.00	0.00	0.00	31.30	0.00	1.75	0.00	0.00	RL26_CHICK	57.72	gi|319401865|	60SribosomalproteinL26[Ictaluruspunctatus]>gi|15293919|gb|AAK95152.1|AF401580_1ribosomalproteinL26[Ictaluruspunctatus]
TRINITY_DN30375_c0_g1_i1	73.03	4.44	16.07	0.00	0.00	0.00	31.18	0.00	36.71	0.00	0.00	ZNUC_MANSM	28.4	gi|326501204|	predictedprotein[Hordeumvulgaresubsp.vulgare]
TRINITY_DN186970_c0_g1_i1	45.60	25.09	22.75	0.00	0.00	0.00	31.14	0.00	12.57	0.00	0.00				
TRINITY_DN39488_c0_g1_i1	34.83	19.32	39.17	0.00	0.00	0.00	31.11	0.00	10.43	0.00	0.00				
TRINITY_DN74894_c0_g1_i1	37.17	35.53	19.81	0.00	0.00	0.00	30.84	0.00	9.58	0.00	0.00	RL38_IXOSC	62.12	gi|695075758|	PREDICTED:60SribosomalproteinL38[Musaacuminatasubsp.malaccensis]
TRINITY_DN68773_c0_g1_i1	46.19	29.37	16.53	0.00	0.00	0.00	30.70	0.00	14.88	0.00	0.00				
TRINITY_DN164491_c0_g1_i1	40.35	14.33	36.73	0.00	0.00	0.00	30.47	0.00	14.10	0.00	0.00				
TRINITY_DN211670_c0_g1_i1	24.14	25.13	40.60	0.00	0.00	0.00	29.96	0.00	9.23	0.00	0.00				
TRINITY_DN96356_c0_g1_i1	43.04	15.19	31.61	0.00	0.00	0.00	29.95	0.00	14.00	0.00	0.00	RS254_ARATH	44.78	gi|385304892|	40sribosomalproteins25-b[BrettanomycesbruxellensisAWRI1499]
TRINITY_DN67522_c0_g1_i1	37.69	30.46	20.92	0.00	0.00	0.00	29.69	0.00	8.41	0.00	0.00	ACTP_ACACA	59.85	gi|646304782|	hypotheticalproteinPLEOSDRAFT_1058112[PleurotusostreatusPC15]
TRINITY_DN147515_c0_g1_i1	35.00	25.85	27.75	0.00	0.00	0.00	29.53	0.00	4.83	0.00	0.00				
TRINITY_DN193811_c0_g1_i1	33.41	20.40	34.44	0.00	0.00	0.00	29.42	0.00	7.83	0.00	0.00				
TRINITY_DN38852_c0_g1_i1	49.48	0.00	38.21	0.00	0.00	0.00	29.23	0.00	25.93	0.00	0.00	TIL_ARATH	34.67	gi|518288178|	membraneprotein[Acinetobactersp.GG2]
TRINITY_DN166041_c0_g1_i1	52.40	20.86	13.83	0.00	0.00	0.00	29.03	0.00	20.54	0.00	0.00				
TRINITY_DN78251_c0_g1_i2	36.55	30.23	20.25	0.00	0.00	0.00	29.01	0.00	8.22	0.00	0.00	RS27_SCHPO	73.49	gi|669167945|	40Sribosomalprotein[SaprolegniadiclinaVS20]>gi|813184508|ref|XP_012206426.1|40Sribosomalprotein[SaprolegniaparasiticaCBS223.65]>gi|530728863|gb|EQC27105.1|40Sribosomalprotein[SaprolegniadiclinaVS20]>gi|641528656|gb|KDO22869.1|40Sribosomalprotein[SaprolegniaparasiticaCBS223.65]
TRINITY_DN5115_c0_g1_i1	24.94	19.10	42.44	8.04	0.00	0.00	28.82	2.68	12.14	4.64	0.09	RL10_BOMMA	73.81	gi|268306444|	ribosomalproteinL10[Manducasexta]
TRINITY_DN225180_c0_g1_i1	53.70	0.00	32.75	0.00	0.00	0.00	28.82	0.00	27.07	0.00	0.00				
TRINITY_DN62845_c1_g1_i2	36.69	26.06	23.49	0.00	0.00	0.00	28.75	0.00	7.00	0.00	0.00	1433D_SOYBN	56.79	gi|731339701|	PREDICTED:14-3-3protein2-likeisoformX1[Betavulgarissubsp.vulgaris]
TRINITY_DN66994_c0_g4_i1	43.14	16.41	25.82	0.00	0.00	0.00	28.46	0.00	13.56	0.00	0.00	RS272_ARATH	60.98	gi|698519309|	PREDICTED:40SribosomalproteinS27-3-like[Nicotianasylvestris]>gi|698519311|ref|XP_009804520.1|PREDICTED:40SribosomalproteinS27-3-like[Nicotianasylvestris]
TRINITY_DN146909_c0_g1_i1	22.48	56.96	5.84	0.00	0.00	0.00	28.43	0.00	26.07	0.00	0.00				
TRINITY_DN94169_c0_g1_i1	32.85	15.20	36.91	0.00	0.00	0.00	28.32	0.00	11.54	0.00	0.00	IF5A3_ARATH	40.38	gi|294895634|	eukaryotictranslationinitiationfactor5A-2
TRINITY_DN63206_c0_g1_i1	46.90	11.94	26.06	0.00	0.00	0.00	28.30	0.00	17.59	0.00	0.00	TBB_TETPY	98.86	gi|407316678|	beta-tubulin
TRINITY_DN70630_c0_g1_i1	43.17	14.01	27.33	0.00	0.00	0.00	28.17	0.00	14.60	0.00	0.00	RS20_RAT	44.54	gi|585651716|	PREDICTED:40SribosomalproteinS20-like[Elephantulusedwardii]
TRINITY_DN46521_c0_g2_i1	30.60	30.18	23.42	0.00	0.00	0.00	28.07	0.00	4.03	0.00	0.00	PRO1A_ACACA	67.46	gi|664512127|	hypotheticalprotein[Streptomycessp.NRRLWC-3725]
TRINITY_DN43964_c0_g2_i1	47.26	14.68	21.21	0.00	0.00	0.00	27.72	0.00	17.23	0.00	0.00	RS26B_SCHPO	53.19	gi|695036712|	PREDICTED:40SribosomalproteinS26-1-like[Musaacuminatasubsp.malaccensis]
TRINITY_DN100884_c0_g1_i1	14.76	5.48	61.90	0.00	0.00	0.00	27.38	0.00	30.25	0.00	0.00	SC61G_BRABE	52	gi|685828235|	ProteintransportproteinSec61subunitgamma[Strongyloidesratti]
TRINITY_DN67027_c0_g1_i1	29.25	24.92	27.41	0.00	0.00	0.00	27.19	0.00	2.17	0.00	0.00	RL30_SPOFR	73.87	gi|391325479|	PREDICTED:60SribosomalproteinL30-likeisoform1[Metaseiulusoccidentalis]>gi|391325481|ref|XP_003737262.1|PREDICTED:60SribosomalproteinL30-likeisoform2[Metaseiulusoccidentalis]
TRINITY_DN34963_c0_g1_i1	31.17	20.87	28.54	0.00	0.00	0.00	26.86	0.00	5.36	0.00	0.00				
TRINITY_DN64977_c0_g1_i1	33.34	32.23	14.61	0.00	0.00	0.00	26.73	0.00	10.51	0.00	0.00	RL37A_CRYST	66.25	gi|761923604|	60SribosomalproteinL43[FistulinahepaticaATCC64428]
TRINITY_DN19417_c0_g1_i1	48.09	13.21	18.27	0.00	0.00	0.00	26.52	0.00	18.85	0.00	0.00	RLA1_CHLRE	56.36	gi|557117270|	60SacidicribosomalproteinP1
TRINITY_DN228004_c0_g1_i1	22.54	23.74	33.15	0.00	0.00	0.00	26.48	0.00	5.81	0.00	0.00				
TRINITY_DN188746_c0_g1_i1	27.78	31.23	19.52	0.00	0.00	0.00	26.18	0.00	6.02	0.00	0.00				
TRINITY_DN23874_c0_g1_i1	62.56	4.78	10.40	0.00	0.00	0.00	25.91	0.00	31.86	0.00	0.00	RL31_TETTS	53.91	gi|221057283|	60SribosomalsubunitproteinL31[PlasmodiumknowlesistrainH]>gi|457872111|ref|XP_004222975.1|60SribosomalproteinL31[PlasmodiumcynomolgistrainB]>gi|193809851|emb|CAQ40555.1|60SribosomalsubunitproteinL31
TRINITY_DN43151_c0_g1_i1	42.93	13.32	21.48	0.00	0.00	0.00	25.91	0.00	15.30	0.00	0.00	RL14_TETTS	50.91	gi|597763415|	PREDICTED:60SribosomalproteinL14-like[Astyanaxmexicanus]

TRINITY_DN166841_c0_g1_i1	57.46	0.00	20.24	0.00	0.00	0.00	25.90	0.00	29.15	0.00	0.00				
TRINITY_DN110334_c0_g1_i1	11.43	0.00	64.61	0.00	0.00	0.00	25.35	0.00	34.48	0.00	0.00				
TRINITY_DN95233_c0_g1_i1	68.45	0.00	7.19	0.00	0.00	0.00	25.21	0.00	37.62	0.00	0.00	RS21_ORYSJ	44	gi|218193460|	hypotheticalproteinOsI_12928[OryzasativaIndicaGroup]>gi|222625514|gb|EEE59646.1|hypotheticalproteinOsJ_12022[OryzasativaJaponicaGroup]
TRINITY_DN141181_c0_g1_i1	35.13	27.58	12.68	0.00	0.00	0.00	25.13	0.00	11.42	0.00	0.00	TNNC2_ANGAN	37.5	gi|145536037|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124421479|emb|CAK86349.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN226622_c0_g1_i1	45.24	16.59	12.99	0.00	0.00	0.00	24.94	0.00	17.67	0.00	0.00				
TRINITY_DN71280_c0_g1_i1	26.30	24.09	24.24	0.00	0.00	0.00	24.87	0.00	1.23	0.00	0.00	RL27_PYRST	46.32	gi|758366663|	hypotheticalprotein[Parasitellaparasitica]
TRINITY_DN79107_c0_g1_i1	27.37	19.34	27.27	0.00	0.00	0.00	24.66	0.00	4.61	0.00	0.00	ACTA_PHYPO	95.65	gi|208609318|	actin[Coptotermesformosanus]
TRINITY_DN134019_c0_g1_i1	37.32	19.30	16.89	0.00	0.00	0.00	24.50	0.00	11.17	0.00	0.00				
TRINITY_DN140904_c0_g1_i1	23.44	17.18	32.42	0.00	0.00	0.00	24.35	0.00	7.66	0.00	0.00	RS28_ICTPU	57.69	gi|511000226|	30SribosomalproteinS28e[Mucorcircinelloidesf.circinelloides1006PhL]
TRINITY_DN114582_c0_g1_i1	24.38	25.61	22.97	0.00	0.00	0.00	24.32	0.00	1.32	0.00	0.00	TIL_ARATH	35.48	gi|690974306|	membraneprotein[Acinetobacterbaumannii]>gi|572040516|gb|ETR94129.1|lipocalin-likedomainprotein[AcinetobacterbaumanniiCI78]
TRINITY_DN193866_c0_g1_i1	33.52	25.05	13.81	0.00	0.00	0.00	24.12	0.00	9.89	0.00	0.00				
TRINITY_DN77596_c0_g1_i1	53.16	3.37	15.66	0.00	0.00	0.00	24.06	0.00	25.94	0.00	0.00	RL37_TETTS	64.94	gi|682412838|	hypotheticalproteinV500_09067[PseudogymnoascuspannorumVKMF-4518(FW-2643)]>gi|682439031|gb|KFZ02863.1|hypotheticalproteinV502_11435[PseudogymnoascuspannorumVKMF-4520(FW-2644)]
TRINITY_DN61228_c1_g1_i1	26.75	15.71	29.35	0.00	0.00	0.00	23.94	0.00	7.24	0.00	0.00	RL21_CAEEL	47.56	gi|145521560|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124414113|emb|CAK79238.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN71303_c0_g1_i1	8.70	54.52	8.41	0.00	3.61	0.00	23.88	1.20	26.54	2.09	0.05	SDR1_AEDAE	41.57	gi|91084875|	PREDICTED:dehydrogenase/reductaseSDRfamilymember11[Triboliumcastaneum]>gi|270008975|gb|EFA05423.1|hypotheticalproteinTcasGA2_TC015599[Triboliumcastaneum]
TRINITY_DN116369_c0_g1_i1	36.33	31.09	3.68	0.00	0.00	0.00	23.70	0.00	17.53	0.00	0.00	TNNC1_MOUSE	33.33	gi|290986438|	predictedprotein[Naegleriagruberi]>gi|284089530|gb|EFC43187.1|predictedprotein[Naegleriagruberi]
TRINITY_DN66045_c0_g2_i1	49.00	0.00	21.83	0.00	0.00	0.00	23.61	0.00	24.55	0.00	0.00	CATL2_PARTE	42.4	gi|118366323|	Papainfamilycysteineproteasecontainingprotein[Tetrahymenathermophila]>gi|89298147|gb|EAR96135.1|papainfamilycysteineprotease[TetrahymenathermophilaSB210]
TRINITY_DN95258_c0_g1_i1	20.69	19.34	30.45	0.00	0.00	0.00	23.50	0.00	6.06	0.00	0.00				
TRINITY_DN41516_c0_g1_i1	14.75	35.92	18.95	0.00	0.00	0.00	23.21	0.00	11.21	0.00	0.00				
TRINITY_DN165290_c0_g1_i1	10.23	38.92	20.03	0.00	0.00	0.00	23.06	0.00	14.58	0.00	0.00				
TRINITY_DN62239_c0_g7_i2	34.91	3.92	29.27	0.00	3.55	0.00	22.70	1.18	16.51	2.05	0.05				
TRINITY_DN71903_c0_g2_i1	26.95	31.17	9.86	0.00	0.00	0.00	22.66	0.00	11.29	0.00	0.00	GBTR_ACIAD	36.36	gi|392876014|	hypotheticalprotein[Callorhinchusmilii]
TRINITY_DN54438_c0_g1_i1	51.37	0.00	16.56	0.00	0.00	0.00	22.64	0.00	26.22	0.00	0.00	CATD_CLUHA	38.71	gi|118366189|	Eukaryoticaspartylproteasefamilyprotein[Tetrahymenathermophila]>gi|89298080|gb|EAR96068.1|eukaryoticaspartylprotease[TetrahymenathermophilaSB210]
TRINITY_DN216719_c0_g1_i1	35.19	13.39	19.18	0.00	0.00	0.00	22.59	0.00	11.29	0.00	0.00				
TRINITY_DN71320_c0_g1_i1	4.97	0.00	62.74	0.00	0.00	0.00	22.57	0.00	34.88	0.00	0.00				
TRINITY_DN75669_c0_g1_i1	25.91	16.67	24.92	0.00	0.00	0.00	22.50	0.00	5.08	0.00	0.00				
TRINITY_DN117642_c0_g1_i1	24.61	23.13	19.58	0.00	0.00	0.00	22.44	0.00	2.59	0.00	0.00	PROA_LARHH	28.99	gi|326501204|	predictedprotein[Hordeumvulgaresubsp.vulgare]
TRINITY_DN219375_c0_g1_i1	27.35	22.40	17.24	0.00	0.00	0.00	22.33	0.00	5.05	0.00	0.00				
TRINITY_DN37665_c0_g2_i1	27.07	10.41	29.19	0.00	0.00	0.00	22.22	0.00	10.29	0.00	0.00	GBLP_DANRE	40.06	gi|158454999|	GNB2L1protein[Bostaurus]
TRINITY_DN56884_c1_g1_i1	20.68	8.71	37.18	0.00	4.33	4.47	22.19	2.94	14.30	2.54	0.13	CYSP_PEA	41.78	gi|525313731|	uncharacterizedproteinLOC101501911precursor[Cicerarietinum]>gi|3377952|emb|CAA08906.1|cysteineproteinase[Cicerarietinum]
TRINITY_DN180887_c0_g1_i1	29.10	23.34	13.26	0.00	0.00	0.00	21.90	0.00	8.02	0.00	0.00				
TRINITY_DN102722_c0_g1_i1	30.24	18.54	16.81	0.00	0.00	0.00	21.86	0.00	7.31	0.00	0.00	RS21_ORYSJ	37.33	gi|672171359|	PREDICTED:40SribosomalproteinS21[Phoenixdactylifera]>gi|672171361|ref|XP_008805750.1|PREDICTED:40SribosomalproteinS21[Phoenixdactylifera]
TRINITY_DN171473_c0_g1_i1	53.18	0.00	12.38	0.00	0.00	0.00	21.85	0.00	27.83	0.00	0.00				
TRINITY_DN39770_c0_g2_i1	38.75	16.43	9.96	0.00	0.00	0.00	21.71	0.00	15.10	0.00	0.00	RLA2_LEIDO	42.62	gi|385302239|	acidicribosomalproteinp2b[BrettanomycesbruxellensisAWRI1499]
TRINITY_DN181650_c0_g1_i1	33.76	8.24	23.04	0.00	0.00	0.00	21.68	0.00	12.81	0.00	0.00				
TRINITY_DN86347_c4_g8_i3	26.54	15.72	22.51	0.00	0.00	0.00	21.59	0.00	5.47	0.00	0.00	EF1A_TETPY	81.29	gi|554944813|	elongationfactor1-alpha(EF-1-alpha)[TrypanosomarangeliSC58]
TRINITY_DN53162_c0_g1_i1	23.76	17.66	23.12	0.00	0.00	0.00	21.52	0.00	3.35	0.00	0.00	CATR6_PARTE	30.77	gi|669156768|	centrin-2[SaprolegniadiclinaVS20]>gi|813121392|ref|XP_012196463.1|hypotheticalproteinSPRG_02500[SaprolegniaparasiticaCBS223.65]>gi|530734203|gb|EQC32445.1|centrin-2[SaprolegniadiclinaVS20]>gi|641538986|gb|KDO32807.1|hypotheticalproteinSPRG_02500[SaprolegniaparasiticaCBS223.65]
TRINITY_DN74363_c0_g1_i1	21.22	23.17	20.05	0.00	0.00	0.00	21.48	0.00	1.58	0.00	0.00	RS17_BOVIN	68.64	gi|632979108|	PREDICTED:40SribosomalproteinS17[Callorhinchusmilii]
TRINITY_DN120360_c0_g1_i1	15.94	16.41	31.75	0.00	0.00	0.00	21.36	0.00	8.99	0.00	0.00	CATR6_PARTE	58.33	gi|675190511|	hypotheticalproteinPPTG_10517[PhytophthoraparasiticaINRA-310]>gi|197320666|gb|ACH68461.1|calcium-dependentprotein4[Phytophthorasojae]>gi|566025545|gb|ETI48456.1|hypotheticalproteinF443_07513[PhytophthoraparasiticaP1569]>gi|566025555|gb|ETI48466.1|hypotheticalproteinF443_07508[PhytophthoraparasiticaP1569]>gi|567962891|gb|ETK88403.1|hypotheticalproteinL915_07339[Phytophthoraparasitica]>gi|567991600|gb|ETL41803.1|hypotheticalproteinL916_07285[Phytophthoraparasitica]>gi|568020841|gb|ETL94957.1|hypotheticalproteinL917_07173[Phytophthoraparasitica]>gi|568051290|gb|ETM48198.1|hypotheticalproteinL914_07232[Phytophthoraparasitica]>gi|568095617|gb|ETN10379.1|hypotheticalproteinPPTG_10517[PhytophthoraparasiticaINRA-310]>gi|570329301|gb|ETO77249.1|hypotheticalproteinF444_07528[PhytophthoraparasiticaP1976]>gi|570953000|gb|ETP18257.1|hypotheticalproteinF441_07495[PhytophthoraparasiticaCJ01A1]>gi|570987473|gb|ETP46195.1|hypotheticalproteinF442_07524[PhytophthoraparasiticaP10297]
TRINITY_DN99582_c0_g1_i1	28.05	17.34	18.39	0.00	0.00	0.00	21.26	0.00	5.90	0.00	0.00	RIDA_PYRFU	50.91	gi|544738387|	endoribonucleaseL-PSP[Sporomusaovata]>gi|530353184|gb|EQB29141.1|endoribonucleaseL-PSP[SporomusaovataDSM2662]>gi|808677805|emb|CQR72573.1|EndoribonucleaseL-PSP[Sporomusasp.An4]
TRINITY_DN120264_c0_g1_i1	12.09	6.56	45.08	0.00	0.00	0.00	21.24	0.00	20.83	0.00	0.00	SERP2_MOUSE	36.67	gi|557294350|	PREDICTED:stress-associatedendoplasmicreticulumprotein1-like[Alligatorsinensis]

TRINITY_DN42149_c0_g3_i1	45.84	3.29	14.53	0.00	0.00	0.00	21.22	0.00	22.05	0.00	0.00	HSBP1_HUMAN	52.31	gi|459378298|	heatshockfactorbindingprotein1
TRINITY_DN96306_c0_g1_i1	25.59	17.10	20.75	0.00	0.00	0.00	21.15	0.00	4.26	0.00	0.00	BGALA_PENSQ	37.78	gi|678306916|	UNKNOWN[Stylonychialemnae]
TRINITY_DN188613_c0_g1_i1	39.13	12.35	11.88	0.00	0.00	0.00	21.12	0.00	15.60	0.00	0.00				
TRINITY_DN74030_c0_g1_i1	30.94	19.94	12.45	0.00	0.00	0.00	21.11	0.00	9.30	0.00	0.00	RL37_DICDI	69.23	gi|238505483|	60SribosomalproteinL37[AspergillusflavusNRRL3357]>gi|317151433|ref|XP_003190519.1|60SribosomalproteinL37[AspergillusoryzaeRIB40]>gi|220690080|gb|EED46430.1|60SribosomalproteinL37[AspergillusflavusNRRL3357]
TRINITY_DN31199_c0_g1_i1	16.90	41.48	4.94	0.00	0.00	0.00	21.11	0.00	18.63	0.00	0.00				
TRINITY_DN56683_c0_g2_i1	29.73	9.61	23.92	0.00	0.00	0.00	21.09	0.00	10.36	0.00	0.00	RUXF_SCHPO	60.56	gi|576992714|	smallnuclearribonucleoproteinF[RhizoctoniasolaniAG-3Rhs1AP]
TRINITY_DN75345_c0_g2_i1	28.69	25.78	8.67	0.00	0.00	0.00	21.05	0.00	10.81	0.00	0.00	RL29_MACFA	64	gi|150982224|	largesubunitribosomalprotein29[Pristionchussp.15RS5229]
TRINITY_DN78562_c0_g1_i1	23.63	22.41	16.97	0.00	0.00	0.00	21.00	0.00	3.55	0.00	0.00	RL28_BOVIN	33.58	gi|115439475|	Os01g0706500[OryzasativaJaponicaGroup]>gi|113533548|dbj|BAF05931.1|Os01g0706500[OryzasativaJaponicaGroup]>gi|125571749|gb|EAZ13264.1|hypotheticalproteinOsJ_03190[OryzasativaJaponicaGroup]
TRINITY_DN48721_c0_g1_i1	25.94	19.33	17.70	0.00	0.00	0.00	20.99	0.00	4.37	0.00	0.00	RS20_RAT	63.21	gi|759041576|	PREDICTED:40SribosomalproteinS20[Cerapachysbiroi]
TRINITY_DN74557_c1_g1_i1	38.05	11.58	11.73	0.00	0.00	0.00	20.45	0.00	15.24	0.00	0.00	RS26B_SCHPO	53.19	gi|758365570|	hypotheticalprotein[Parasitellaparasitica]
TRINITY_DN97264_c0_g1_i1	32.02	20.56	8.17	0.00	0.00	0.00	20.25	0.00	11.93	0.00	0.00	FKBP1_DICDI	62.24	gi|391333973|	PREDICTED:12kDaFK506-bindingprotein-like[Metaseiulusoccidentalis]
TRINITY_DN79278_c0_g2_i1	15.16	22.60	22.95	0.00	0.00	0.00	20.24	0.00	4.40	0.00	0.00	RL10A_SPOFR	63.43	gi|815818871|	PREDICTED:60SribosomalproteinL10aisoformX1[Linepithemahumile]
TRINITY_DN68500_c0_g1_i1	25.95	17.32	17.43	0.00	0.00	0.00	20.23	0.00	4.95	0.00	0.00	RS15A_RAT	70	gi|449275996|	40SribosomalproteinS15a
TRINITY_DN74079_c1_g1_i1	22.05	21.09	17.16	0.00	0.00	0.00	20.10	0.00	2.59	0.00	0.00	ACT1_TETTH	77.99	gi|193890832|	actin[Amphidiniumcarterae]>gi|193890838|gb|ACF28582.1|actin[Amphidiniumcarterae]>gi|193890842|gb|ACF28584.1|actin[Amphidiniumcarterae]>gi|193890846|gb|ACF28586.1|actin[Amphidiniumcarterae]>gi|193890850|gb|ACF28588.1|actin[Amphidiniumcarterae]>gi|193890862|gb|ACF28594.1|actin[Amphidiniumcarterae]>gi|193890864|gb|ACF28595.1|actin[Amphidiniumcarterae]>gi|193890874|gb|ACF28600.1|actin[Amphidiniumcarterae]>gi|193890880|gb|ACF28603.1|actin[Amphidiniumcarterae]
TRINITY_DN26666_c0_g2_i1	31.67	11.90	16.70	0.00	0.00	0.00	20.09	0.00	10.31	0.00	0.00	RL34_TETTS	57.01	gi|514796360|	PREDICTED:60SribosomalproteinL34-like[Setariaitalica]
TRINITY_DN82347_c3_g3_i1	23.04	15.98	20.89	0.00	0.00	0.00	19.97	0.00	3.62	0.00	0.00	CYSP2_HOMAM	45.1	gi|501290391|	cathepsinL[Riptortuspedestris]
TRINITY_DN77677_c2_g1_i2	38.23	4.41	17.25	3.98	0.00	0.00	19.96	1.33	17.07	2.30	0.07	ACT1_ABSGL	92.79	gi|470237392|	actin[Dictyosteliumfasciculatum]>gi|470237524|ref|XP_004350719.1|actin[Dictyosteliumfasciculatum]>gi|470243688|ref|XP_004355576.1|actin[Dictyosteliumfasciculatum]>gi|328865559|gb|EGG13945.1|actin[Dictyosteliumfasciculatum]>gi|328865625|gb|EGG14011.1|actin[Dictyosteliumfasciculatum]>gi|328868714|gb|EGG17092.1|actin[Dictyosteliumfasciculatum]
TRINITY_DN45564_c0_g2_i2	13.88	22.22	23.57	0.00	4.03	0.00	19.89	1.34	5.25	2.33	0.07	ACT10_SOLTU	98	gi|59709763|	actin[Anophelesstephensi]
TRINITY_DN70312_c0_g2_i2	20.69	38.91	0.00	0.00	0.00	0.00	19.87	0.00	19.47	0.00	0.00				
TRINITY_DN195232_c0_g1_i1	28.36	13.01	18.19	0.00	0.00	0.00	19.85	0.00	7.81	0.00	0.00				
TRINITY_DN41296_c0_g1_i1	51.37	0.00	7.61	0.00	0.00	0.00	19.66	0.00	27.73	0.00	0.00	MAML1_MOUSE	42.11	gi|471231813|	hypotheticalproteinIMG5_062850
TRINITY_DN63167_c0_g1_i2	26.82	10.13	21.98	0.00	0.00	0.00	19.65	0.00	8.59	0.00	0.00	RS14_MOUSE	73.6	gi|602654012|	PREDICTED:40SribosomalproteinS14isoformX1[Pythonbivittatus]
TRINITY_DN83921_c0_g2_i1	22.96	12.13	23.57	0.00	0.00	0.00	19.55	0.00	6.44	0.00	0.00	RL18A_TETTH	58.82	gi|669137130|	50SribosomalproteinL18Ae[SaprolegniadiclinaVS20]>gi|530744468|gb|EQC42710.1|50SribosomalproteinL18Ae[SaprolegniadiclinaVS20]
TRINITY_DN2693_c0_g1_i1	14.81	0.00	43.62	0.00	0.00	0.00	19.48	0.00	22.18	0.00	0.00	RS29_CANGA	60.78	gi|636604195|	40SribosomalproteinS29A[TrametesversicolorFP-101664SS1]>gi|392571856|gb|EIW65028.1|40SribosomalproteinS29A[TrametesversicolorFP-101664SS1]
TRINITY_DN79787_c0_g2_i2	22.61	21.74	14.07	0.00	0.00	0.00	19.47	0.00	4.70	0.00	0.00	RS19B_SCHPO	50.75	gi|703073703|	40SribosomalproteinS19-1[Morusnotabilis]>gi|587847753|gb|EXB38086.1|40SribosomalproteinS19-1[Morusnotabilis]
TRINITY_DN160981_c0_g1_i1	11.52	38.31	8.57	0.00	3.64	0.00	19.47	1.21	16.38	2.10	0.06				
TRINITY_DN188223_c0_g1_i1	29.55	12.57	15.96	0.00	0.00	0.00	19.36	0.00	8.98	0.00	0.00				
TRINITY_DN66979_c0_g2_i1	21.34	13.37	23.16	0.00	0.00	0.00	19.29	0.00	5.21	0.00	0.00	RS10_DICDI	43.75	gi|672201698|	30SribosomalproteinS10e[PlasmodiuminuiSanAntonio1]>gi|577141791|gb|EUD65230.1|30SribosomalproteinS10e[PlasmodiuminuiSanAntonio1]
TRINITY_DN78902_c0_g1_i1	25.57	22.14	10.08	0.00	0.00	0.00	19.26	0.00	8.13	0.00	0.00	RS25_DICDI	53.73	gi|226493039|	40SribosomalproteinS25-1[Zeamays]>gi|195608352|gb|ACG26006.1|40SribosomalproteinS25-1[Zeamays]
TRINITY_DN106085_c0_g1_i1	43.84	4.30	9.41	0.00	0.00	0.00	19.18	0.00	21.51	0.00	0.00	RS272_ARATH	60.98	gi|678193760|	40SribosomalproteinS27-like
TRINITY_DN10903_c0_g1_i1	28.49	8.70	20.28	0.00	0.00	0.00	19.15	0.00	9.94	0.00	0.00	RL6_TETTS	46.91	gi|502140013|	PREDICTED:60SribosomalproteinL6-3-likeisoformX2[Cicerarietinum]
TRINITY_DN175450_c0_g1_i1	15.95	11.29	29.72	0.00	0.00	0.00	18.99	0.00	9.58	0.00	0.00				
TRINITY_DN70603_c0_g1_i1	18.24	19.36	19.34	0.00	0.00	0.00	18.98	0.00	0.64	0.00	0.00	RL193_ARATH	66.67	gi|357112310|	PREDICTED:60SribosomalproteinL19-3-likeisoformX2[Brachypodiumdistachyon]
TRINITY_DN70375_c0_g1_i1	39.81	3.56	13.13	0.00	0.00	0.00	18.83	0.00	18.79	0.00	0.00	HN1_RAT	62.07	gi|229596251|	hypotheticalproteinTTHERM_00106820[Tetrahymenathermophila]>gi|225565516|gb|EAR92081.3|hypotheticalproteinTTHERM_00106820[TetrahymenathermophilaSB210]
TRINITY_DN31653_c0_g2_i1	10.42	0.00	44.70	0.00	0.00	0.00	18.37	0.00	23.39	0.00	0.00	H2AX_MOUSE	84.62	gi|558205239|	PREDICTED:histoneH2AX-like[Myotislucifugus]>gi|641717578|ref|XP_008148302.1|PREDICTED:histoneH2AX[Eptesicusfuscus]
TRINITY_DN220724_c0_g1_i1	9.31	0.00	45.43	0.00	0.00	0.00	18.25	0.00	24.00	0.00	0.00				
TRINITY_DN74731_c1_g1_i1	19.39	9.90	25.13	0.00	0.00	0.00	18.14	0.00	7.69	0.00	0.00	RL9_TETTS	45.5	gi|597991149|	60SribosomalproteinL9[DichomitussqualensLYAD-421SS1]>gi|395328789|gb|EJF61179.1|60SribosomalproteinL9[DichomitussqualensLYAD-421SS1]
TRINITY_DN141344_c0_g1_i1	24.99	12.71	16.35	0.00	0.00	0.00	18.02	0.00	6.31	0.00	0.00	CYPH_SCHPO	73.46	gi|769863287|	PREDICTED:peptidyl-prolylcis-transisomerase-like[Pogonomyrmexbarbatus]
TRINITY_DN196261_c0_g1_i1	22.73	13.48	17.81	0.00	0.00	0.00	18.01	0.00	4.63	0.00	0.00				
TRINITY_DN217712_c0_g1_i1	15.12	20.11	18.47	0.00	0.00	0.00	17.90	0.00	2.54	0.00	0.00				
TRINITY_DN96757_c0_g1_i1	29.51	11.44	12.49	0.00	0.00	0.00	17.81	0.00	10.14	0.00	0.00				
TRINITY_DN193116_c0_g1_i1	15.76	17.56	19.98	0.00	0.00	0.00	17.77	0.00	2.12	0.00	0.00				
TRINITY_DN142560_c0_g1_i1	29.23	6.06	17.94	0.00	0.00	0.00	17.74	0.00	11.59	0.00	0.00	SC61B_MOUSE	41.46	gi|401400253|	agap011504-PA

TRINITY_DN37474_c0_g1_i1	17.11	18.85	17.26	0.00	0.00	0.00	17.74	0.00	0.96	0.00	0.00	ARF1_DAUCA	69.06	gi|636768425|	P-loopcontainingnucleosidetriphosphatehydrolase[GlarealozoyensisATCC20868]>gi|512198361|gb|EPE27196.1|P-loopcontainingnucleosidetriphosphatehydrolase[GlarealozoyensisATCC20868]>gi|751753822|gb|KIN02000.1|hypotheticalproteinOIDMADRAFT_18772[OidiodendronmaiusZn]
TRINITY_DN48308_c0_g1_i1	25.33	8.02	19.86	0.00	0.00	0.00	17.74	0.00	8.85	0.00	0.00	RS15_ORYSJ	53.15	gi|255551941|	40SribosomalproteinS15
TRINITY_DN63545_c0_g2_i1	48.04	0.00	5.14	0.00	0.00	0.00	17.73	0.00	26.38	0.00	0.00				
TRINITY_DN70173_c1_g1_i1	22.83	8.34	21.88	0.00	0.00	0.00	17.68	0.00	8.10	0.00	0.00	RS33_ARATH	50.75	gi|388494596|	unknown[Lotusjaponicus]>gi|388504726|gb|AFK40429.1|unknown[Lotusjaponicus]
TRINITY_DN68673_c0_g2_i1	49.68	0.00	3.32	0.00	0.00	0.00	17.67	0.00	27.77	0.00	0.00	LYG_STRCA	33.33	gi|326500768|	predictedprotein[Hordeumvulgaresubsp.vulgare]
TRINITY_DN56571_c0_g1_i1	19.27	15.90	17.73	0.00	0.00	0.00	17.64	0.00	1.68	0.00	0.00				
TRINITY_DN93587_c2_g27_i3	15.59	0.00	37.22	0.00	0.00	0.00	17.60	0.00	18.69	0.00	0.00	EF1A2_TRYB2	86.54	gi|71403916|	elongationfactor1-alpha(EF-1-alpha)[TrypanosomacruzistrainCLBrener]>gi|70867822|gb|EAN82859.1|elongationfactor1-alpha(EF-1-alpha)
TRINITY_DN141041_c0_g1_i1	29.37	7.32	16.05	0.00	0.00	0.00	17.58	0.00	11.10	0.00	0.00	RL23_PONAB	67.88	gi|544499563|	PREDICTED:60SribosomalproteinL23isoformX1[Macacafascicularis]
TRINITY_DN75245_c0_g1_i1	16.42	13.15	23.16	0.00	0.00	0.00	17.58	0.00	5.11	0.00	0.00	RL13_DICDI	59.52	gi|37700241|	60SribosomalproteinL13[Danionerio]>gi|528486331|ref|XP_005166723.1|PREDICTED:60SribosomalproteinL13isoformX1[Danionerio]>gi|21759388|sp|Q90Z10.3|RL13_DANRERecName:Full=60SribosomalproteinL13[Danionerio]>gi|14485765|gb|AAK63073.1|AF385081_160SribosomalproteinL13[Danionerio]>gi|45504889|gb|AAS66969.1|ribosomalproteinL13[Danionerio]>gi|50370041|gb|AAH75977.1|RibosomalproteinL13[Danionerio]
TRINITY_DN74842_c0_g1_i1	18.84	16.87	17.00	0.00	0.00	0.00	17.57	0.00	1.10	0.00	0.00	RL27A_BOVIN	67.2	gi|532009633|	PREDICTED:60SribosomalproteinL27a-like[Microtusochrogaster]
TRINITY_DN154644_c0_g1_i1	21.81	17.74	13.09	0.00	0.00	0.00	17.54	0.00	4.36	0.00	0.00				
TRINITY_DN44097_c0_g1_i1	10.70	13.06	28.80	0.00	0.00	0.00	17.52	0.00	9.84	0.00	0.00	RS11_SOYBN	54.12	gi|188572476|	putative40SribosomalproteinRPS11[Phoronismuelleri]
TRINITY_DN37339_c0_g1_i1	37.82	0.00	14.53	0.00	0.00	0.00	17.45	0.00	19.08	0.00	0.00	CATL1_PARTE	54.65	gi|118388482|	Papainfamilycysteineproteasecontainingprotein[Tetrahymenathermophila]>gi|89309108|gb|EAS07096.1|papainfamilycysteineprotease[Tetrahymenathermophila SB210]
TRINITY_DN3690_c0_g1_i1	21.00	14.82	16.52	0.00	0.00	0.00	17.45	0.00	3.19	0.00	0.00	RS12_PIG	51.69	gi|109088312|	PREDICTED:40SribosomalproteinS12-likeisoform3[Macacamulatta]>gi|297300560|ref|XP_002805617.1|PREDICTED:40SribosomalproteinS12-like[Macacamulatta]>gi|544456118|ref|XP_005564792.1|PREDICTED:40SribosomalproteinS12-like[Macacafascicularis]
TRINITY_DN54674_c0_g1_i1	22.26	0.00	29.64	0.00	0.00	0.00	17.30	0.00	15.43	0.00	0.00	CYSP_TRYCR	70.59	gi|237637246|	cysteineproteinase[Trypanosomacruzi]
TRINITY_DN116983_c0_g1_i1	20.51	14.20	17.08	0.00	0.00	0.00	17.26	0.00	3.16	0.00	0.00	GILT_BOVIN	37.95	gi|699210039|	gamma-interferon-inducible lysosomal thiol reductase[Stichopusmonotuberculatus]
TRINITY_DN114059_c0_g1_i1	21.63	9.53	20.62	0.00	0.00	0.00	17.26	0.00	6.71	0.00	0.00	FKBP2_DEBHA	50	gi|354545891|	hypotheticalproteinCPAR2_202630[Candidaparapsilosis]
TRINITY_DN57665_c1_g1_i1	21.48	7.71	22.50	0.00	0.00	0.00	17.23	0.00	8.26	0.00	0.00	RL31_TETTS	54.29	gi|145480865|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|145542522|ref|XP_001456948.1|hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124393530|emb|CAK59057.1|unnamedproteinproduct[Parameciumtetraurelia]>gi|124424762|emb|CAK89551.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN194033_c0_g1_i1	41.05	3.47	6.99	0.00	0.00	0.00	17.17	0.00	20.76	0.00	0.00				
TRINITY_DN134264_c0_g1_i1	8.17	12.48	30.83	0.00	0.00	0.00	17.16	0.00	12.04	0.00	0.00				
TRINITY_DN69774_c0_g1_i1	17.76	20.47	12.97	0.00	0.00	0.00	17.07	0.00	3.80	0.00	0.00	RL36_ICTPU	55.68	gi|743787162|	PREDICTED:60SribosomalproteinL36-3-like[Elaeisguineensis]>gi|743787166|ref|XP_010922349.1|PREDICTED:60SribosomalproteinL36-3-like[Elaeisguineensis]>gi|743787170|ref|XP_010922350.1|PREDICTED:60SribosomalproteinL36-3-like[Elaeisguineensis]
TRINITY_DN48961_c0_g1_i1	14.87	14.44	21.80	0.00	0.00	0.00	17.04	0.00	4.13	0.00	0.00	CATR5_PARTE	35.14	gi|510909189|	centrin
TRINITY_DN76178_c1_g1_i1	20.69	21.72	8.50	0.00	0.00	0.00	16.97	0.00	7.35	0.00	0.00	RL32_NEUCR	64.17	gi|576992669|	60SribosomalproteinL32[RhizoctoniasolaniAG-3Rhs1AP]>gi|660957922|gb|KEP46036.1|60SribosomalproteinL32[Rhizoctoniasolani123E]
TRINITY_DN106769_c0_g1_i1	16.57	20.06	14.08	0.00	0.00	0.00	16.90	0.00	3.00	0.00	0.00				
TRINITY_DN82709_c1_g1_i1	17.49	0.00	33.18	0.00	0.00	0.00	16.89	0.00	16.60	0.00	0.00	ACT_SPOLI	98.02	gi|525328807|	truncatedactin-4[Bombyxmori]
TRINITY_DN9657_c0_g1_i1	3.09	5.07	42.46	0.00	0.00	0.00	16.87	0.00	22.18	0.00	0.00				
TRINITY_DN46503_c0_g1_i1	20.42	9.02	20.49	0.00	0.00	0.00	16.64	0.00	6.60	0.00	0.00	RS2_DICDI	56.25	gi|755993672|	PREDICTED:40SribosomalproteinS2-like[Fopiusarisanus]
TRINITY_DN5390_c0_g1_i1	15.78	4.00	30.06	0.00	0.00	0.00	16.61	0.00	13.05	0.00	0.00	TBA_TRYCR	98.2	gi|604328526|	hypotheticalproteinMIMGU_mgv1a0196712mg
TRINITY_DN61307_c0_g1_i1	42.94	3.34	3.55	0.00	0.00	0.00	16.61	0.00	22.80	0.00	0.00	YCNE_BACSU	35.63	gi|753201633|	MULTISPECIES:monooxygenase[Bacillus]>gi|766988652|gb|KJF48969.1|monooxygenase[Bacillusinvictae]
TRINITY_DN63452_c0_g1_i1	12.00	22.11	15.61	0.00	0.00	0.00	16.57	0.00	5.12	0.00	0.00	TAR1_YEAST	61.7	gi|156356940|	predictedprotein[Nematostellavectensis]>gi|156210732|gb|EDO31884.1|predictedprotein
TRINITY_DN62883_c1_g1_i1	23.22	7.25	19.23	0.00	0.00	0.00	16.56	0.00	8.31	0.00	0.00				
TRINITY_DN57135_c0_g1_i1	21.46	16.72	11.44	0.00	0.00	0.00	16.54	0.00	5.02	0.00	0.00	RL31_RAT	60	gi|296221657|	PREDICTED:60SribosomalproteinL31[Callithrixjacchus]
TRINITY_DN169158_c0_g1_i1	39.74	0.00	9.71	0.00	0.00	0.00	16.49	0.00	20.72	0.00	0.00				
TRINITY_DN214039_c0_g1_i1	12.47	0.00	36.95	0.00	0.00	0.00	16.47	0.00	18.80	0.00	0.00				
TRINITY_DN115457_c0_g1_i1	27.62	8.69	12.78	0.00	0.00	0.00	16.36	0.00	9.96	0.00	0.00	RS10_DICDI	40.35	gi|528314652|	40SribosomalproteinS10[SchizosaccharomycescryophilusOY26]
TRINITY_DN147759_c0_g1_i1	36.79	0.00	12.19	0.00	0.00	0.00	16.33	0.00	18.74	0.00	0.00				
TRINITY_DN214582_c0_g1_i1	38.85	0.00	10.11	0.00	0.00	0.00	16.32	0.00	20.15	0.00	0.00				
TRINITY_DN43291_c0_g1_i1	10.61	0.00	38.27	0.00	0.00	0.00	16.29	0.00	19.76	0.00	0.00				
TRINITY_DN84058_c0_g1_i1	12.65	14.93	21.27	0.00	0.00	0.00	16.28	0.00	4.47	0.00	0.00	RL7A_TAKRU	57.39	gi|642093783|	unnamedproteinproduct[Oncorhynchusmykiss]
TRINITY_DN51830_c0_g2_i1	21.31	6.15	21.39	0.00	0.00	0.00	16.28	0.00	8.78	0.00	0.00	RL24_TETTS	47.83	gi|460408485|	PREDICTED:60SribosomalproteinL24[Solanumlycopersicum]
TRINITY_DN74579_c1_g1_i1	17.03	17.63	14.18	0.00	0.00	0.00	16.28	0.00	1.84	0.00	0.00	RL10_DICDI	74.77	gi|170587060|	60SribosomalproteinL10[Brugiamalayi]>gi|671409260|emb|CDP97543.1|ProteinBm13774
TRINITY_DN78676_c0_g1_i3	24.65	3.62	20.51	3.33	0.00	0.00	16.26	1.11	11.14	1.92	0.07	RS281_ARATH	54.72	gi|414865012|	TPA:40SribosomalproteinS28[Zeamays]
TRINITY_DN28238_c0_g1_i1	16.10	12.82	19.83	0.00	0.00	0.00	16.25	0.00	3.51	0.00	0.00	HSP70_ACHKL	71.08	gi|1051276|	Hsp70[Sterkiellanova]

TRINITY_DN166600_c0_g1_i1	25.08	15.60	7.83	0.00	0.00	0.00	16.17	0.00	8.64	0.00	0.00				
TRINITY_DN26064_c0_g1_i1	20.75	13.63	14.00	0.00	0.00	0.00	16.13	0.00	4.01	0.00	0.00	RL40_TETTS	90.24	gi|209879912|	60SribosomalproteinL40[CryptosporidiummurisRN66]>gi|209557002|gb|EEA07047.1|60SribosomalproteinL40
TRINITY_DN193344_c0_g1_i1	37.15	0.00	11.12	0.00	0.00	0.00	16.09	0.00	19.07	0.00	0.00				
TRINITY_DN80489_c0_g1_i1	18.20	7.93	22.11	0.00	0.00	0.00	16.08	0.00	7.33	0.00	0.00	RL26_TETTS	60.94	gi|17535693|	RPL-26
TRINITY_DN171737_c0_g1_i1	22.17	10.61	15.03	0.00	0.00	0.00	15.94	0.00	5.83	0.00	0.00				
TRINITY_DN114150_c0_g1_i1	28.89	8.01	10.32	0.00	0.00	0.00	15.74	0.00	11.44	0.00	0.00	VG34_EHV1B	25.97	gi|157093331|	unknown[Karlodiniumveneficum]
TRINITY_DN57325_c0_g1_i1	25.60	6.33	15.27	0.00	0.00	0.00	15.73	0.00	9.65	0.00	0.00	RS12_CAEEL	36.67	gi|735851075|	hypotheticalproteinSAMD00019534_099570[AcytosteliumsubglobosumLB1]
TRINITY_DN57782_c0_g1_i1	15.22	0.00	31.55	0.00	0.00	0.00	15.59	0.00	15.78	0.00	0.00	GBLP_TRYBR	29.1	gi|154431140|	activatedCkinaseprotein[Leishmaniachagasi]
TRINITY_DN82564_c0_g1_i1	15.47	16.21	14.94	0.00	0.00	0.00	15.54	0.00	0.63	0.00	0.00	RL74_ARATH	53.78	gi|674895505|	BnaC02g33760D[Brassicanapus]
TRINITY_DN67299_c0_g1_i1	13.95	16.26	16.32	0.00	0.00	0.00	15.51	0.00	1.35	0.00	0.00	RSSA_ORNPR	55.98	gi|698454805|	PREDICTED:40SribosomalproteinSAisoformX1[Cariamacristata]
TRINITY_DN211923_c0_g1_i1	17.20	6.63	22.67	0.00	0.00	0.00	15.50	0.00	8.15	0.00	0.00				
TRINITY_DN70297_c0_g1_i1	17.28	15.08	13.87	0.00	0.00	0.00	15.41	0.00	1.73	0.00	0.00	RL23A_RAT	66.67	gi|471407667|	PREDICTED:60SribosomalproteinL23a[Trichechusmanatuslatirostris]
TRINITY_DN75509_c0_g5_i1	22.89	10.08	13.23	0.00	0.00	0.00	15.40	0.00	6.68	0.00	0.00	RS8_MAIZE	56.94	gi|678333237|	ribosomalproteins8efamilyprotein[Stylonychialemnae]
TRINITY_DN79043_c0_g1_i1	16.67	12.13	17.38	0.00	0.00	0.00	15.39	0.00	2.85	0.00	0.00	RS7_XENLA	44.14	gi|598015149|	40SribosomalproteinS7[AuriculariadelicataTFB-10046SS5]>gi|393246418|gb|EJD53927.1|40SribosomalproteinS7[AuriculariadelicataTFB-10046SS5]
TRINITY_DN29802_c0_g1_i1	29.77	0.00	16.07	0.00	0.00	0.00	15.28	0.00	14.90	0.00	0.00	PYRH_STRSV	41.03	gi|403354757|	hypotheticalproteinOXYTRI_01541[Oxytrichatrifallax]
TRINITY_DN67445_c0_g1_i1	15.91	11.63	18.16	0.00	0.00	0.00	15.23	0.00	3.32	0.00	0.00	RL18A_DANRE	52.3	gi|188572433|	putative60SribosomalproteinRPL18A[Novocraniaanomala]
TRINITY_DN101191_c0_g1_i1	41.76	0.00	3.88	0.00	0.00	0.00	15.21	0.00	23.07	0.00	0.00				
TRINITY_DN122553_c0_g1_i1	13.67	6.06	25.67	0.00	0.00	0.00	15.14	0.00	9.89	0.00	0.00				
TRINITY_DN40117_c0_g1_i1	26.76	6.80	11.69	0.00	0.00	0.00	15.08	0.00	10.41	0.00	0.00	RS12_TETTH	73.94	gi|598072071|	hypotheticalproteinSPAPADRAFT_56791[SpathasporapassalidarumNRRLY-27907]>gi|344300510|gb|EGW30831.1|hypotheticalproteinSPAPADRAFT_56791[Spathasporapassalidarum NRRLY-27907]
TRINITY_DN33854_c0_g1_i1	9.57	16.01	19.34	0.00	0.00	0.00	14.97	0.00	4.96	0.00	0.00	HN1_BOVIN	65.22	gi|678314685|	UNKNOWN[Stylonychialemnae]
TRINITY_DN84210_c2_g2_i2	17.75	4.95	22.22	0.00	0.00	0.00	14.97	0.00	8.96	0.00	0.00	RS11_SOYBN	60.39	gi|340056660|	putativeribosomalproteinS17[TrypanosomavivaxY486]
TRINITY_DN195537_c0_g1_i1	12.56	15.91	16.35	0.00	0.00	0.00	14.94	0.00	2.07	0.00	0.00				
TRINITY_DN94230_c0_g1_i1	16.59	15.28	12.94	0.00	0.00	0.00	14.94	0.00	1.85	0.00	0.00				
TRINITY_DN66693_c0_g1_i1	19.23	8.86	16.64	0.00	0.00	0.00	14.91	0.00	5.40	0.00	0.00	RL10_TETTS	69.16	gi|170114921|	60SribosomalproteinL10[LaccariabicolorS238N-H82]>gi|164636351|gb|EDR00647.1|predictedprotein[LaccariabicolorS238N-H82]>gi|750946308|gb|KIK04208.1|hypotheticalproteinK443DRAFT_676174[Laccariamethystina LaAM-08-1]
TRINITY_DN164095_c0_g1_i1	13.03	7.32	24.35	0.00	0.00	0.00	14.90	0.00	8.67	0.00	0.00				
TRINITY_DN30732_c0_g1_i1	17.82	7.56	19.19	0.00	0.00	0.00	14.86	0.00	6.35	0.00	0.00				
TRINITY_DN203797_c0_g1_i1	22.00	13.30	9.24	0.00	0.00	0.00	14.85	0.00	6.52	0.00	0.00				
TRINITY_DN50985_c0_g1_i1	36.11	0.00	8.34	0.00	0.00	0.00	14.82	0.00	18.91	0.00	0.00				
TRINITY_DN70274_c0_g1_i1	19.07	16.36	8.98	0.00	0.00	0.00	14.80	0.00	5.22	0.00	0.00	RL33B_SCHPO	54.9	gi|631244633|	putative60sribosomalproteinl33protein[TogniniaminimaUCRPA7]>gi|500254374|gb|EON97982.1|putative60sribosomalproteinl33protein[TogniniaminimaUCRPA7]
TRINITY_DN62195_c0_g1_i1	24.23	3.85	16.24	0.00	0.00	0.00	14.77	0.00	10.27	0.00	0.00				
TRINITY_DN105794_c0_g1_i1	23.94	9.53	10.57	0.00	0.00	0.00	14.68	0.00	8.04	0.00	0.00	VA0E1_ARATH	32	gi|157093147|	hydrogen-transportingATPsynthase[Karlodiniumveneficum]
TRINITY_DN4510_c0_g1_i1	18.97	18.45	6.55	0.00	0.00	0.00	14.66	0.00	7.03	0.00	0.00	GCH1_FLAJ1	38.74	gi|647681997|	GTPcyclohydrolase[Prochlorococcussp.scB241_528K19]
TRINITY_DN116349_c0_g1_i1	31.32	0.00	12.41	0.00	0.00	0.00	14.58	0.00	15.77	0.00	0.00	ACT1_ABSGL	72.22	gi|257205968|	Actin5C[Schistosomajaponicum]
TRINITY_DN96728_c0_g1_i1	9.69	9.14	24.84	0.00	0.00	0.00	14.56	0.00	8.91	0.00	0.00	CTIF_MOUSE	57.89	gi|326489257|	predictedprotein[Hordeumvulgaresubsp.vulgare]
TRINITY_DN77818_c3_g1_i2	10.21	3.40	29.97	0.00	0.00	0.00	14.53	0.00	13.80	0.00	0.00	ACT1_ABSGL	93.48	gi|312073899|	hypotheticalproteinLOAG_04142[Loaloa]
TRINITY_DN17175_c0_g1_i1	18.97	10.92	13.39	0.00	0.00	0.00	14.43	0.00	4.12	0.00	0.00				
TRINITY_DN78305_c0_g1_i1	14.52	15.98	12.73	0.00	0.00	0.00	14.41	0.00	1.63	0.00	0.00	RL15A_PICMA	75.98	gi|747047646|	PREDICTED:60SribosomalproteinL15[Sesamumindicum]
TRINITY_DN57810_c0_g1_i2	19.89	0.00	23.25	0.00	0.00	0.00	14.38	0.00	12.56	0.00	0.00	RL32_DICDI	57.02	gi|554941689|	largesubunitribosomalproteinL32e[TrypanosomarangeliSC58]
TRINITY_DN49767_c0_g1_i1	22.79	4.14	16.02	0.00	0.00	0.00	14.32	0.00	9.44	0.00	0.00	RL44_CAEEL	69.32	gi|318054574|	60SribosomalproteinL36a[Ictaluruspunctatus]>gi|321267535|ref|NP_001189439.1|60SribosomalproteinL36a[Danio rerio]>gi|410914267|ref|XP_003970609.1|PREDICTED:60SribosomalproteinL36a[Takifugurubripes]>gi|551520152|ref|XP_005811568.1|PREDICTED:60SribosomalproteinL36a-like[Xiphophorusmaculatus]>gi|597788267|ref|XP_007257555.1|PREDICTED:60SribosomalproteinL36a-like[Astyanaxmexicanus]>gi|617460956|ref|XP_007571979.1|PREDICTED:60SribosomalproteinL36a[Poeciliaformosa]>gi|657795477|ref|XP_008324727.1|PREDICTED:60SribosomalproteinL36a[Cynoglossussemilaevis]>gi|658871714|ref|XP_008418798.1|PREDICTED:60SribosomalproteinL36a[Poeciliareticulata]>gi|736296674|ref|XP_010791647.1|PREDICTED:60SribosomalproteinL36a[Notothenia coriiceps]>gi|47605970|sp|P61485.2|RL36A_DANRERecName:Full=60SribosomalproteinL36a[Danio rerio]>gi|47605971|sp|P61486.2|RL36A_TAKRURecName:Full=60SribosomalproteinL36a;AltName:Full=60SribosomalproteinL44[Takifugurubripes]>gi|47605972|sp|P61487.2|RL36A_ICTPURecName:Full=60SribosomalproteinL36a[Ictaluruspunctatus]>gi|15293943|gb|AAK95164.1|AF401592_1ribosomalproteinL36a[Ictaluruspunctatus]>gi|15020805|emb|CAC44627.1|60sribosomalproteinL44(L36A)[Takifugurubripes]>gi|20502061|gb|AAM21715.1|60SribosomalproteinL36a[Danio rerio]>gi|32766551|gb|AAH55187.1|RibosomalproteinL36A[Danio rerio]>gi|164691011|dbj|BAF98688.1|ribosomalproteinL36a[Soleasenegalensis]>gi|225706216|gb|ACO08954.1|60SribosomalproteinL36a[Osmerusmordax]>gi|308322021|gb|ADO28148.1|60Sribosomalproteinl36a[Ictalurusfurcatus]>gi|808867832|gb|KKF18321.1|60SribosomalproteinL36a[Larimichthyscrocea]
TRINITY_DN65020_c0_g1_i1	15.52	13.67	13.54	0.00	0.00	0.00	14.25	0.00	1.11	0.00	0.00	RS3A_COPC7	58.88	gi|628834875|	ribosomalproteinS3Ae[ConiophoraputeanaRWD-64-598SS2]>gi|392593057|gb|EIW82383.1|ribosomalproteinS3Ae[ConiophoraputeanaRWD-64-598SS2]

TRINITY_DN66110_c0_g1_i1	7.34	7.85	27.37	0.00	0.00	0.00	14.19	0.00	11.42	0.00	0.00	MARTX_VIBCH	33.96	gi|738956591|	hypotheticalprotein[Photorhabdustemperata]>gi|662547058|gb|KER01669.1|RtxArepeat/PeptidaseC80family[Photorhabdustemperatasubsp.temperataMeg1]
TRINITY_DN73799_c0_g1_i2	14.05	17.01	11.46	0.00	0.00	0.00	14.17	0.00	2.78	0.00	0.00	RS10B_DROME	62.37	gi|751477159|	PREDICTED:40SribosomalproteinS10b[Bactroceracucurbitae]
TRINITY_DN214438_c0_g1_i1	10.31	10.33	21.81	0.00	0.00	0.00	14.15	0.00	6.63	0.00	0.00				
TRINITY_DN67952_c0_g1_i1	13.16	5.00	24.23	0.00	0.00	0.00	14.13	0.00	9.65	0.00	0.00				
TRINITY_DN100415_c0_g1_i1	18.50	10.91	12.98	0.00	0.00	0.00	14.13	0.00	3.92	0.00	0.00	RLA22_ARATH	46.77	gi|671691312|	hypotheticalproteinLRAMOSA08577[Absidiaidahoensisvar.thermophila]
TRINITY_DN191105_c0_g1_i1	15.92	13.71	12.61	0.00	0.00	0.00	14.08	0.00	1.69	0.00	0.00				
TRINITY_DN114278_c0_g1_i1	20.56	9.84	11.77	0.00	0.00	0.00	14.06	0.00	5.72	0.00	0.00	RL35A_TETTS	55.66	gi|320586843|	60Sribosomalproteinl33[Grosmanniaclavigerakw1407]
TRINITY_DN76572_c0_g1_i1	13.11	12.10	16.91	0.00	0.00	0.00	14.04	0.00	2.54	0.00	0.00	RS15_PODAS	59.86	gi|604327047|	hypotheticalproteinMIMGU_mgv1a015638mg[Erythrantheguttata]
TRINITY_DN51661_c0_g1_i1	6.13	0.00	35.71	0.00	0.00	0.00	13.95	0.00	19.10	0.00	0.00	RL22_TETTS	59.09	gi|471219554|	ribosomalprotein
TRINITY_DN19397_c0_g1_i1	15.48	9.84	16.46	0.00	0.00	0.00	13.93	0.00	3.57	0.00	0.00	HISX_PSEAE	38.46	gi|74833933|	EPI21[Parameciumtetraurelia]
TRINITY_DN72975_c0_g1_i1	12.82	14.29	14.61	0.00	0.00	0.00	13.91	0.00	0.96	0.00	0.00	RS18_DICDI	64.34	gi|209880283|	40SribosomalproteinS18[CryptosporidiummurisRN66]>gi|209557187|gb|EEA07232.1|40SribosomalproteinS18
TRINITY_DN435_c0_g1_i1	24.25	12.23	5.06	0.00	0.00	0.00	13.85	0.00	9.70	0.00	0.00	POTA_UREPA	41.38	gi|678335294|	UNKNOWN[Stylonychialemnae]
TRINITY_DN60782_c0_g1_i1	11.89	4.52	25.09	0.00	3.35	0.00	13.83	1.12	10.42	1.93	0.08	MORA_RABIT	26.15	gi|145491710|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124398960|emb|CAK64456.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN69783_c1_g1_i1	22.96	9.37	9.13	0.00	0.00	0.00	13.82	0.00	7.92	0.00	0.00	H31_TETTH	87.22	gi|552812761|	hypotheticalproteinCHLNCDRAFT_59160[Chlorellavariabilis]>gi|307103418|gb|EFN51678.1|hypotheticalproteinCHLNCDRAFT_59160[Chlorellavariabilis]
TRINITY_DN33346_c0_g1_i1	10.97	0.00	30.48	0.00	0.00	0.00	13.81	0.00	15.44	0.00	0.00				
TRINITY_DN159114_c0_g1_i1	12.89	12.13	16.43	0.00	0.00	0.00	13.81	0.00	2.29	0.00	0.00				
TRINITY_DN139400_c0_g1_i1	19.30	5.42	16.46	0.00	0.00	0.00	13.73	0.00	7.33	0.00	0.00	RL7A_TETTH	55.56	gi|156089547|	ribosomalproteinL7Aefamilyprotein[Babesiabovis]>gi|154799434|gb|EDO08612.1|ribosomalproteinL7Aefamilyprotein[Babesiabovis]>gi|527101448|dbj|BAN64243.1|ribosomalproteinL7Aefamilyprotein[Babesiabovis]
TRINITY_DN125125_c0_g1_i1	15.87	6.21	19.05	0.00	0.00	0.00	13.71	0.00	6.69	0.00	0.00	RS30_SCHPO	51.67	gi|363750424|	hypotheticalproteinEcym_3104[EremotheciumcymbalariaeDBVPG#7215]>gi|356889063|gb|AET38612.1|HypotheticalproteinEcym_3104[EremotheciumcymbalariaeDBVPG#7215]
TRINITY_DN169567_c0_g1_i1	30.95	0.00	9.83	0.00	0.00	0.00	13.59	0.00	15.81	0.00	0.00				
TRINITY_DN94021_c0_g1_i1	15.99	9.12	15.59	0.00	0.00	0.00	13.57	0.00	3.85	0.00	0.00	RL7A_TETTH	56.41	gi|557116981|	60SribosomalproteinL7a
TRINITY_DN38711_c0_g2_i1	4.56	5.56	30.51	0.00	0.00	0.00	13.55	0.00	14.70	0.00	0.00	TBA1_CHICK	96.81	gi|21703250|	alpha-tubulin[Bolteniavillosa]
TRINITY_DN42917_c0_g1_i1	9.97	17.17	13.46	0.00	0.00	0.00	13.53	0.00	3.60	0.00	0.00	PPE1_HUMAN	34.57	gi|242014075|	Nicotinamidase
TRINITY_DN49558_c0_g2_i1	11.27	9.19	19.82	0.00	0.00	0.00	13.43	0.00	5.64	0.00	0.00	CATR5_PARTE	30.61	gi|401413544|	putativecaltractin[NeosporacaninumLiverpool]>gi|325120639|emb|CBZ56194.1|putativecaltractin[NeosporacaninumLiverpool]>gi|820695217|tpe|CEL70956.1|TPA:caltractin
TRINITY_DN115284_c0_g1_i1	17.90	11.33	11.02	0.00	0.00	0.00	13.42	0.00	3.88	0.00	0.00				
TRINITY_DN28158_c0_g1_i1	17.70	0.00	22.55	0.00	0.00	0.00	13.42	0.00	11.87	0.00	0.00	PABP_DROME	61.84	gi|751459418|	PREDICTED:polyadenylate-bindingprotein[Bactroceracucurbitae]>gi|751459420|ref|XP_011184425.1|PREDICTED:polyadenylate-bindingprotein[Bactroceracucurbitae]>gi|751459422|ref|XP_011184426.1|PREDICTED:polyadenylate-bindingprotein[Bactroceracucurbitae]>gi|751459424|ref|XP_011184427.1|PREDICTED:polyadenylate-bindingprotein[Bactroceracucurbitae]
TRINITY_DN88240_c0_g1_i4	16.34	3.47	20.34	0.00	0.00	0.00	13.38	0.00	8.82	0.00	0.00	RL34_TOBAC	52.83	gi|71420694|	60SribosomalproteinL34[TrypanosomacruzistrainCLBrener]>gi|71650763|ref|XP_814073.1|60SribosomalproteinL34[TrypanosomacruzistrainCLBrener]>gi|70876250|gb|EAN89722.1|60SribosomalproteinL34
TRINITY_DN74765_c0_g1_i1	15.43	7.29	17.32	0.00	0.00	0.00	13.35	0.00	5.33	0.00	0.00	RSSA_DICDI	51.26	gi|157877540|	putative40SribosomalproteinSA[LeishmaniamajorstrainFriedlin]>gi|157877562|ref|XP_001687098.1|putative40SribosomalproteinSA[LeishmaniamajorstrainFriedlin]>gi|75030566|sp|Q4Q0Q0.1|RSSA_LEIMAR ecName:Full=40SribosomalproteinSA[Leishmaniamajor]>gi|68130162|emb|CAJ09473.1|putative40SribosomalproteinSA[Leishmaniamajorstrain Friedlin]>gi|68130173|emb|CAJ09484.1|putative40SribosomalproteinSA[Leishmaniamajorstrain Friedlin]
TRINITY_DN172412_c0_g1_i1	17.10	11.50	11.37	0.00	0.00	0.00	13.32	0.00	3.27	0.00	0.00				
TRINITY_DN66408_c0_g1_i1	13.48	13.29	13.19	0.00	0.00	0.00	13.32	0.00	0.15	0.00	0.00	RL17_RAT	58.79	gi|700326628|	PREDICTED:60SribosomalproteinL17[Haliaeetusalbicilla]>gi|729768213|ref|XP_010581311.1|PREDICTED:60SribosomalproteinL17[Haliaeetusleucocephalus]>gi|729768215|ref|XP_010581312.1|PREDICTED:60SribosomalproteinL17[Haliaeetusleucocephalus]>gi|768382554|ref|XP_011588953.1|PREDICTED:60SribosomalproteinL17[Aquilachrysaetoscanadensis]>gi|768382556|ref|XP_011588954.1|PREDICTED:60SribosomalproteinL17[Aquilachrysaetoscanadensis]
TRINITY_DN84329_c0_g1_i1	16.54	8.08	15.28	0.00	0.00	0.00	13.30	0.00	4.56	0.00	0.00	RLA0_SOYBN	39.25	gi|145506509|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124406399|emb|CAK71818.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN14723_c0_g1_i1	8.73	31.12	0.00	0.00	0.00	0.00	13.28	0.00	16.05	0.00	0.00				
TRINITY_DN188352_c0_g1_i1	12.63	12.74	14.45	0.00	0.00	0.00	13.27	0.00	1.02	0.00	0.00				
TRINITY_DN73425_c0_g3_i1	13.24	12.72	13.85	0.00	0.00	0.00	13.27	0.00	0.57	0.00	0.00	PLAC8_BOVIN	33.33	gi|340055199|	conservedhypotheticalprotein[TrypanosomavivaxY486]
TRINITY_DN14108_c0_g1_i1	28.43	0.00	11.37	0.00	0.00	0.00	13.27	0.00	14.31	0.00	0.00	ALEU_HORVU	41.07	gi|685341094|	PREDICTED:ervatamin-B-like[Brassicarapa]
TRINITY_DN67635_c0_g3_i1	13.63	11.02	15.14	0.00	0.00	0.00	13.26	0.00	2.09	0.00	0.00	RAN_TETPY	71.96	gi|542173908|	PREDICTED:GTP-bindingnuclearproteinRan-likeisoformX2[Oreochromisniloticus]
TRINITY_DN158591_c0_g1_i1	3.52	0.00	36.21	0.00	0.00	0.00	13.24	0.00	19.97	0.00	0.00				
TRINITY_DN195903_c0_g1_i1	15.72	12.55	11.38	0.00	0.00	0.00	13.22	0.00	2.25	0.00	0.00				
TRINITY_DN67155_c0_g1_i1	12.51	13.54	13.59	0.00	0.00	0.00	13.21	0.00	0.61	0.00	0.00	RL24_BRABE	57.14	gi|118083604|	PREDICTED:60SribosomalproteinL24[Gallusgallus]>gi|527266977|ref|XP_005151635.1|PREDICTED:60SribosomalproteinL24[Melopsittacusundulatus]>gi|729738889|ref|XP_010565634.1|PREDICTED:60SribosomalproteinL24[Haliaeetusleucocephalus]>gi|733872175|ref|XP_010718751.1|PREDICTED:60SribosomalproteinL24[Meleagrisgallopavo]>gi|768340933|ref|XP_011582962.1|PREDICTED:60SribosomalproteinL24[Aquilachrysaetoscanadensis]
TRINITY_DN227444_c0_g1_i1	24.77	11.16	3.68	0.00	0.00	0.00	13.21	0.00	10.69	0.00	0.00				
TRINITY_DN117442_c0_g1_i1	13.73	12.19	13.66	0.00	0.00	0.00	13.19	0.00	0.87	0.00	0.00	GAT24_ARATH	30.3	gi|678339384|	UNKNOWN[Stylonychialemnae]

TRINITY_DN202151_c0_g1_i1	8.89	30.67	0.00	0.00	0.00	0.00	13.19	0.00	15.78	0.00	0.00			
TRINITY_DN64904_c1_g1_i1	35.75	0.00	3.76	0.00	0.00	0.00	13.17	0.00	19.65	0.00	0.00	RL37A_TETTS	68.18	gi|757348283| 60SribosomalproteinL37a[CryptococcusgattiiRu294]
TRINITY_DN74434_c0_g2_i1	17.43	5.96	16.07	0.00	0.00	3.16	13.16	1.05	6.27	1.83	0.08	CATL_SARPE	45.92	gi|118360450| Papainfamilycysteineproteasecontainingprotein[Tetrahymenathermophila]>gi|89295226|gb|EAR93214.1|papainfamilycysteineprotease[TetrahymenathermophilaSB210]
TRINITY_DN53323_c0_g1_i1	30.76	8.70	0.00	0.00	0.00	0.00	13.15	0.00	15.86	0.00	0.00			
TRINITY_DN53562_c0_g1_i1	16.64	8.86	13.81	0.00	0.00	3.81	13.10	1.27	3.93	2.20	0.10			
TRINITY_DN60019_c0_g1_i1	0.00	7.71	31.58	0.00	0.00	0.00	13.10	0.00	16.47	0.00	0.00			
TRINITY_DN26044_c0_g1_i1	16.55	9.16	13.26	0.00	0.00	0.00	12.99	0.00	3.70	0.00	0.00	RS131_ARATH	59.21	gi|213403730| 40SribosomalproteinS13[SchizosaccharomycesjaponicusyFS275]>gi|212000684|gb|EEB06344.1|40SribosomalproteinS13[SchizosaccharomycesjaponicusyFS275]
TRINITY_DN116136_c0_g1_i1	30.60	0.00	8.29	0.00	0.00	0.00	12.96	0.00	15.82	0.00	0.00	CEP2_ARATH	56.76	gi|570981538| hypotheticalproteinF442_11095[PhytophthoraparasiticaP10297]
TRINITY_DN32354_c0_g1_i1	30.22	0.00	8.63	0.00	0.00	0.00	12.95	0.00	15.57	0.00	0.00	GUAA_PROMH	30.67	gi|326502688| predictedprotein[Hordeumvulgaresubsp.vulgare]
TRINITY_DN140875_c0_g1_i1	20.68	6.74	11.40	0.00	0.00	0.00	12.94	0.00	7.10	0.00	0.00	VCAM1_CANLF	52	gi|145552232| hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124429628|emb|CAK94419.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN59524_c0_g1_i1	17.78	16.40	4.54	0.00	0.00	0.00	12.91	0.00	7.28	0.00	0.00			
TRINITY_DN57490_c0_g1_i1	31.79	0.00	6.91	0.00	0.00	0.00	12.90	0.00	16.72	0.00	0.00	RUXE_PIG	47.62	gi|318820229| smallnuclearribonucleoproteine[Ictaluruspunctatus]>gi|308324130|gb|ADO29200.1|smallnuclearribonucleoproteine[Ictaluruspunctatus]
TRINITY_DN116297_c0_g1_i1	15.26	8.12	15.22	0.00	0.00	0.00	12.87	0.00	4.11	0.00	0.00			
TRINITY_DN198439_c0_g1_i1	23.36	7.59	7.60	0.00	0.00	0.00	12.85	0.00	9.10	0.00	0.00			
TRINITY_DN141131_c0_g1_i1	20.79	11.45	6.24	0.00	0.00	0.00	12.82	0.00	7.37	0.00	0.00			
TRINITY_DN75540_c0_g1_i2	16.31	0.00	22.00	0.00	0.00	0.00	12.77	0.00	11.42	0.00	0.00	RL9_ORYSJ	51.67	gi|339898131| putative60SribosomalproteinL9[LeishmaniainfantumJPCM5]>gi|398014912|ref|XP_003860646.1|60SribosomalproteinL9
TRINITY_DN28928_c0_g1_i1	33.58	0.00	4.67	0.00	0.00	0.00	12.75	0.00	18.19	0.00	0.00	CAP6_ADE05	31.67	gi|678345141| UNKNOWN[Stylonychialemnae]
TRINITY_DN187014_c0_g1_i1	14.02	6.26	17.93	0.00	0.00	0.00	12.73	0.00	5.94	0.00	0.00			
TRINITY_DN79843_c0_g2_i1	13.42	13.65	11.14	0.00	0.00	0.00	12.73	0.00	1.38	0.00	0.00	RL212_ARATH	54.43	gi|698480070| PREDICTED:60SribosomalproteinL21-1-like[Nicotianasylvestris]
TRINITY_DN214269_c0_g1_i1	13.72	13.47	11.00	0.00	0.00	0.00	12.73	0.00	1.50	0.00	0.00			
TRINITY_DN42799_c0_g1_i1	8.99	8.20	20.97	0.00	0.00	0.00	12.72	0.00	7.15	0.00	0.00	FA8_CANLF	24.32	gi|145509561| hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124407947|emb|CAK73322.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN104434_c0_g1_i1	5.75	14.05	18.29	0.00	0.00	0.00	12.69	0.00	6.38	0.00	0.00			
TRINITY_DN66891_c0_g1_i1	18.56	9.15	10.37	0.00	0.00	0.00	12.69	0.00	5.12	0.00	0.00	RL8_TETTS	68.67	gi|751711734| hypotheticalproteinSCLCIDRAFT_1216482[SclerodermacitrinumFougA]
TRINITY_DN67684_c0_g1_i1	19.71	9.27	9.04	0.00	0.00	0.00	12.67	0.00	6.10	0.00	0.00			
TRINITY_DN215708_c0_g1_i1	12.46	16.07	9.09	0.00	0.00	0.00	12.54	0.00	3.49	0.00	0.00			
TRINITY_DN94118_c0_g1_i1	13.90	12.53	11.04	0.00	0.00	0.00	12.49	0.00	1.43	0.00	0.00			
TRINITY_DN189237_c0_g1_i1	13.20	8.19	15.99	0.00	0.00	0.00	12.46	0.00	3.96	0.00	0.00			
TRINITY_DN221379_c0_g1_i1	7.61	7.97	21.78	0.00	0.00	0.00	12.45	0.00	8.07	0.00	0.00			
TRINITY_DN141073_c0_g1_i1	14.88	10.58	11.87	0.00	0.00	0.00	12.44	0.00	2.21	0.00	0.00	HEXP_LEIMA	39.13	gi|121543757| zincfingerprotein-likeprotein[Maconellicoccushirsutus]
TRINITY_DN219909_c0_g1_i1	17.88	7.92	11.41	0.00	0.00	0.00	12.40	0.00	5.05	0.00	0.00			
TRINITY_DN187041_c0_g1_i1	11.83	16.50	8.80	0.00	0.00	0.00	12.38	0.00	3.88	0.00	0.00			
TRINITY_DN140876_c0_g1_i1	14.32	7.67	15.13	0.00	0.00	0.00	12.37	0.00	4.09	0.00	0.00	RS27A_CAEBR	44.3	gi|729392250| PREDICTED:ubiquitin-40SribosomalproteinS27a-1[Tarenayahassleriana]
TRINITY_DN57313_c0_g1_i1	18.90	4.36	13.86	0.00	0.00	0.00	12.37	0.00	7.38	0.00	0.00	NACA_CAEEL	38.56	gi|571443492| PREDICTED:uncharacterizedproteinLOC100527254isoformX1[Glycinemax]>gi|734417173|gb|KHN38800.1|Nascentpolypeptide-associatedcomplexsubunitalpha-likeprotein[Glycinesoja]
TRINITY_DN48407_c0_g1_i1	14.83	15.44	6.77	0.00	0.00	0.00	12.35	0.00	4.84	0.00	0.00			
TRINITY_DN141571_c0_g1_i1	10.28	14.54	12.22	0.00	0.00	0.00	12.35	0.00	2.14	0.00	0.00	FLVS_ELIME	21.62	gi|740035361| carbohydrate-bindingprotein[Streptomycessp.NRRLS-646]
TRINITY_DN74190_c0_g2_i1	28.09	0.00	8.86	0.00	0.00	0.00	12.32	0.00	14.36	0.00	0.00	RL21_TETTS	52.87	gi|597970755| hypotheticalproteinDICSQDRAFT_131707[DichomitussqualensLYAD-421SS1]>gi|395334995|gb|EJF67371.1|hypotheticalproteinDICSQDRAFT_131707[DichomitussqualensLYAD-421SS1]
TRINITY_DN77186_c0_g2_i1	8.47	11.89	16.46	0.00	0.00	0.00	12.27	0.00	4.01	0.00	0.00	RL81_ARATH	69.48	gi|675118838| largesubunitribosomalprotein2
TRINITY_DN95518_c0_g1_i1	20.10	7.67	8.94	0.00	0.00	0.00	12.24	0.00	6.84	0.00	0.00			
TRINITY_DN10233_c0_g2_i1	10.97	10.26	15.18	0.00	0.00	0.00	12.14	0.00	2.66	0.00	0.00			
TRINITY_DN6644_c0_g1_i1	32.46	0.00	3.95	0.00	0.00	0.00	12.14	0.00	17.71	0.00	0.00	GCSP_LEPIN	31.03	gi|145511902| hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124409134|emb|CAK74476.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN76141_c0_g2_i1	10.56	13.17	12.57	0.00	0.00	0.00	12.10	0.00	1.37	0.00	0.00	UBE2N_DICDI	70	gi|448081908| Piso0_005534[MillerozymafarinosaCBS7064]>gi|359376426|emb|CCE87008.1|Piso0_005534[MillerozymafarinosaCBS7064]
TRINITY_DN170254_c0_g1_i1	14.60	8.64	13.04	0.00	0.00	0.00	12.09	0.00	3.09	0.00	0.00			
TRINITY_DN167484_c0_g1_i1	16.10	5.73	14.27	0.00	0.00	0.00	12.03	0.00	5.53	0.00	0.00			
TRINITY_DN75292_c0_g1_i1	14.50	12.02	9.51	0.00	0.00	0.00	12.01	0.00	2.50	0.00	0.00	RS8_SPOFR	58.59	gi|675123520| ribosomalproteinRPS8[Hammondiahammondi]>gi|661337307|gb|KEP65436.1|ribosomalproteinRPS8[Hammondiahammondi]
TRINITY_DN194179_c0_g1_i1	20.42	6.79	8.70	0.00	0.00	0.00	11.97	0.00	7.38	0.00	0.00			
TRINITY_DN117678_c0_g1_i1	16.44	6.34	13.06	0.00	0.00	0.00	11.95	0.00	5.14	0.00	0.00	RS131_ARATH	59.21	gi|213403226| 40SribosomalproteinS13[SchizosaccharomycesjaponicusyFS275]>gi|212000432|gb|EEB06092.1|40SribosomalproteinS13[SchizosaccharomycesjaponicusyFS275]>gi|289449227|dbj|BAI77477.1|40SribosomalproteinS13[Schizosaccharomycesjaponicus]
TRINITY_DN28224_c0_g1_i1	19.60	8.31	7.74	0.00	0.00	0.00	11.88	0.00	6.69	0.00	0.00	RL31_TETTS	56.03	gi|14423905| RecName:Full=60SribosomalproteinL31[Cyanophoraparadoxa]>gi|5123727|emb|CAB45375.1|ribosomalproteinL31[Cyanophoraparadoxa]
TRINITY_DN72504_c0_g1_i1	18.24	3.61	13.79	0.00	0.00	0.00	11.88	0.00	7.50	0.00	0.00	RS20_SCHPO	56.9	gi|149286918| 40SribosomalproteinS20[Ornithodorosparkeri]
TRINITY_DN76648_c1_g2_i1	17.38	7.19	11.02	0.00	0.00	0.00	11.87	0.00	5.15	0.00	0.00	RS91_ARATH	58.86	gi|672189800| 40SribosomalprotEin[PlasmodiuminuiSanAntonio1]>gi|577145007|gb|EUD68321.1|40Sribosomalprotein[PlasmodiuminuiSanAntonio1]
TRINITY_DN19405_c0_g1_i1	17.86	7.72	10.01	0.00	0.00	0.00	11.86	0.00	5.32	0.00	0.00	RS19S_ASCSU	39.31	gi|225423503| PREDICTED:40SribosomalproteinS19-1[Vitisvinifera]>gi|147798403|emb|CAN70140.1|hypotheticalproteinVITISV_032083[Vitisvinifera]>gi|297738070|emb|CBI27271.3|unnamedproteinproduct[Vitisvinifera]
TRINITY_DN117217_c0_g1_i1	8.05	12.29	15.24	0.00	0.00	0.00	11.86	0.00	3.61	0.00	0.00			
TRINITY_DN143534_c0_g1_i1	17.10	11.00	7.42	0.00	0.00	0.00	11.84	0.00	4.89	0.00	0.00	BMBL_DANRE	31.34	gi|403355551| hypotheticalproteinOXYTRI_01013[Oxytrichatrifallax]

TRINITY_DN9387_c0_g1_i1	9.65	6.70	19.08	0.00	0.00	0.00	11.81	0.00	6.46	0.00	0.00	CATR2_PARTE	27.69	gi|145485548|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|75019017|sp|Q94726.1|CATR4_PARTERecName:Full=CaltractinICL1d;AltName:Full=Centrin-4[Parameciumtetraurelia]>gi|1667586|gb|AAC47490.1|ICL1dcentrin[Parameciumtetraurelia]>gi|74829685|emb|CAI38919.1|centrin1d-from-infraciliary-lattice[Parameciumtetraurelia]>gi|124395870|emb|CAK61384.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN115640_c0_g1_i1	4.96	18.88	11.48	0.00	0.00	0.00	11.77	0.00	6.96	0.00	0.00				
TRINITY_DN101243_c0_g1_i1	17.25	6.08	11.96	0.00	0.00	0.00	11.76	0.00	5.59	0.00	0.00	MKS3_HUMAN	27.05	gi|326498249|	predictedprotein[Hordeumvulgaresubsp.vulgare]
TRINITY_DN45374_c0_g1_i1	6.25	14.38	14.61	0.00	0.00	0.00	11.74	0.00	4.76	0.00	0.00				
TRINITY_DN70320_c0_g1_i1	16.32	0.00	18.85	0.00	0.00	0.00	11.72	0.00	10.23	0.00	0.00				
TRINITY_DN68358_c0_g1_i1	13.34	14.55	7.19	0.00	0.00	0.00	11.69	0.00	3.94	0.00	0.00				
TRINITY_DN198248_c0_g1_i1	22.87	5.24	6.93	0.00	0.00	0.00	11.68	0.00	9.73	0.00	0.00				
TRINITY_DN39911_c0_g2_i1	19.67	6.35	8.96	0.00	0.00	0.00	11.66	0.00	7.06	0.00	0.00	RL27A_RAT	62.16	gi|312086586|	60SribosomalproteinL27a[Loaloa]>gi|307759701|gb|EFO18935.1|60SribosomalproteinL27a[Loaloa]
TRINITY_DN166391_c0_g1_i1	17.42	5.81	11.72	0.00	0.00	0.00	11.65	0.00	5.80	0.00	0.00				
TRINITY_DN76573_c0_g2_i1	24.44	4.65	5.79	0.00	0.00	0.00	11.63	0.00	11.11	0.00	0.00	RL322_ARATH	56.49	gi|698562214|	PREDICTED:60SribosomalproteinL32-1-like[Nicotianasylvestris]>gi|698562218|ref|XP_009772348.1|PREDICTED:60SribosomalproteinL32-1-like[Nicotianasylvestris]
TRINITY_DN165021_c0_g1_i1	6.13	6.21	22.52	0.00	3.29	0.00	11.62	1.10	9.44	1.90	0.09				
TRINITY_DN99202_c0_g1_i1	14.34	11.46	9.04	0.00	0.00	0.00	11.61	0.00	2.65	0.00	0.00	PRDX3_PONAB	55.91	gi|657540054|	PREDICTED:peroxiredoxin-2[Stegastespartitus]
TRINITY_DN140586_c0_g1_i1	11.23	9.43	14.14	0.00	0.00	0.00	11.60	0.00	2.37	0.00	0.00	RL13A_TETTS	75.24	gi|158187860|	ribosomalproteinrpl13a[Eurythoecomplanata]
TRINITY_DN66667_c1_g1_i1	15.31	6.41	13.00	0.00	0.00	0.00	11.57	0.00	4.62	0.00	0.00	RS24_SPOFR	48.82	gi|752349202|	hypotheticalproteinM404DRAFT_14335[PisolithustinctoriusMarx270]
TRINITY_DN48992_c0_g1_i1	24.20	0.00	10.51	0.00	0.00	0.00	11.57	0.00	12.14	0.00	0.00	ADT1_MAIZE	31.33	gi|685346018|	PREDICTED:ADP
TRINITY_DN164106_c0_g1_i1	16.27	6.77	11.63	0.00	0.00	0.00	11.56	0.00	4.75	0.00	0.00				
TRINITY_DN214730_c0_g1_i1	27.25	7.42	0.00	0.00	0.00	0.00	11.55	0.00	14.09	0.00	0.00				
TRINITY_DN78712_c0_g1_i3	15.51	0.00	19.15	0.00	0.00	0.00	11.55	0.00	10.17	0.00	0.00	RL17_RAT	55.62	gi|528250753|	largesubunitribosomalproteinL17e[Strigomonasculicis]
TRINITY_DN188423_c0_g1_i1	18.72	0.00	15.88	0.00	0.00	0.00	11.53	0.00	10.09	0.00	0.00				
TRINITY_DN68842_c0_g2_i1	17.40	7.32	9.87	0.00	0.00	0.00	11.53	0.00	5.24	0.00	0.00	RS18_ARATH	50.75	gi|761929213|	40sribosomalprotein[FistulinahepaticaATCC64428]
TRINITY_DN57941_c0_g1_i1	12.35	10.44	11.74	0.00	0.00	0.00	11.51	0.00	0.98	0.00	0.00	RS24_DICDI	56.6	gi|514707845|	PREDICTED:40SribosomalproteinS24-1-like[Setariaitalica]
TRINITY_DN48908_c0_g1_i1	15.95	5.23	13.22	0.00	0.00	0.00	11.46	0.00	5.57	0.00	0.00	RL13A_TETTS	63.13	gi|360045055|	putative60sribosomalproteinL13a[Schistosomamansoni]
TRINITY_DN81858_c0_g1_i2	13.79	6.49	14.01	0.00	0.00	0.00	11.43	0.00	4.28	0.00	0.00	RS4_TETTH	56.13	gi|646305732|	hypotheticalproteinPLEOSDRAFT_1066177[PleurotusostreatusPC15]
TRINITY_DN79007_c0_g4_i2	14.43	3.19	16.64	0.00	0.00	0.00	11.42	0.00	7.21	0.00	0.00	IF5A_LEIMU	56.86	gi|565494166|	hypotheticalproteinCARUB_v10012030mg[Capsellarubella]>gi|482573433|gb|EOA37620.1|hypotheticalproteinCARUB_v10012030mg[Capsellarubella]
TRINITY_DN100744_c0_g1_i1	6.81	4.54	22.85	0.00	0.00	0.00	11.40	0.00	9.98	0.00	0.00				
TRINITY_DN74426_c0_g2_i2	15.44	11.73	7.03	0.00	0.00	0.00	11.40	0.00	4.21	0.00	0.00				
TRINITY_DN84375_c0_g1_i1	11.71	0.00	22.37	0.00	0.00	0.00	11.36	0.00	11.19	0.00	0.00	RS9_TRYBB	91.62	gi|342182386|	putative40SribosomalproteinS9[TrypanosomacongolenseIL3000]
TRINITY_DN74593_c0_g1_i1	11.37	8.94	13.74	0.00	0.00	0.00	11.35	0.00	2.40	0.00	0.00	RL13A_MACFA	69.08	gi|289472558|	putative60SribosomalproteinL13a[Amblyommamaculatum]
TRINITY_DN94772_c0_g1_i1	14.77	7.77	11.48	0.00	0.00	0.00	11.34	0.00	3.50	0.00	0.00	ATPD_MAGSA	31.55	gi|802778822|	atp-3
TRINITY_DN51813_c0_g1_i1	11.29	15.15	7.48	0.00	0.00	0.00	11.31	0.00	3.84	0.00	0.00	TCPZ_MOUSE	76.77	gi|257215846|	chaperonincontainingTCP1
TRINITY_DN81026_c0_g2_i1	13.40	12.29	8.18	0.00	0.00	0.00	11.29	0.00	2.74	0.00	0.00	RS13_SOYBN	72.85	gi|168004349|	predictedprotein[Physcomitrellapatens]>gi|168014677|ref|XP_001759878.1|predictedprotein[Physcomitrellapatens]>gi|168030653|ref|XP_001767837.1|predictedprotein[Physcomitrellapatens]>gi|162680919|gb|EDQ67351.1|predictedprotein[Physcomitrellapatens]>gi|162689008|gb|EDQ75382.1|predictedprotein[Physcomitrellapatens]>gi|162693978|gb|EDQ80328.1|predictedprotein[Physcomitrellapatens]
TRINITY_DN26294_c0_g2_i1	21.01	6.85	5.99	0.00	0.00	0.00	11.28	0.00	8.44	0.00	0.00	RL35A_TETTS	57.43	gi|440136300|	ribosomalproteinL35ae
TRINITY_DN83604_c0_g1_i1	10.17	11.16	12.50	0.00	0.00	0.00	11.28	0.00	1.17	0.00	0.00	RS6_CANGA	54.77	gi|50289221|	40SribosomalproteinS6[CandidaglabrataCBS138]>gi|50294420|ref|XP_449621.1|40SribosomalproteinS6[CandidaglabrataCBS138]>gi|54036325|sp|Q6FJH3.1|RS6_CANGARecName:Full=40SribosomalproteinS6[CandidaglabrataCBS138]>gi|49526350|emb|CAG59974.1|unnamedproteinproduct[Candidaglabrata]>gi|49528935|emb|CAG62597.1|unnamedproteinproduct[Candidaglabrata]
TRINITY_DN167135_c0_g1_i1	17.15	6.52	10.01	0.00	0.00	0.00	11.23	0.00	5.42	0.00	0.00				
TRINITY_DN78347_c0_g1_i3	22.21	0.00	11.46	0.00	0.00	0.00	11.22	0.00	11.10	0.00	0.00				
TRINITY_DN198718_c0_g1_i1	16.88	7.41	9.36	0.00	0.00	0.00	11.22	0.00	5.00	0.00	0.00				
TRINITY_DN1849_c0_g1_i1	13.64	4.67	15.26	0.00	0.00	0.00	11.19	0.00	5.70	0.00	0.00	BTF3_MOUSE	35.71	gi|673029620|	hypotheticalproteinH310_05735[Aphanomycesinvadans]>gi|574475166|gb|ETW02166.1|hypotheticalproteinH310_05735[Aphanomycesinvadans]
TRINITY_DN79769_c0_g1_i1	11.80	9.86	11.87	0.00	0.00	0.00	11.18	0.00	1.14	0.00	0.00	RL34_DICDI	56.25	gi|669196884|	50SribosomalproteinL34e[Plasmodiumvinckeivinckei]>gi|657010479|gb|KEG03529.1|50SribosomalproteinL34e[Plasmodiumvinckeivinckei]
TRINITY_DN165936_c0_g1_i1	24.15	0.00	9.35	0.00	0.00	0.00	11.17	0.00	12.17	0.00	0.00				
TRINITY_DN69917_c0_g1_i1	27.54	0.00	5.90	0.00	0.00	0.00	11.15	0.00	14.50	0.00	0.00	RL34_TETTS	58.82	gi|510907960|	60SribosomalproteinL34a
TRINITY_DN43415_c0_g1_i1	25.32	0.00	8.10	0.00	0.00	0.00	11.14	0.00	12.93	0.00	0.00	NEDD8_RABIT	44.59	gi|560132590|	Ubiquitindomaincontainingprotein[Haemonchuscontortus]
TRINITY_DN10768_c0_g1_i1	10.10	7.91	15.38	0.00	0.00	0.00	11.13	0.00	3.84	0.00	0.00	EF1A1_HORVU	74.29	gi|557159429|	elongationfactor1-alpha
TRINITY_DN73539_c0_g2_i1	17.43	6.41	9.48	0.00	0.00	0.00	11.11	0.00	5.68	0.00	0.00	RL11_MEDSA	73.65	gi|702245321|	PREDICTED:60SribosomalproteinL11-1-like[Eucalyptusgrandis]
TRINITY_DN77830_c0_g1_i1	17.47	0.00	15.78	0.00	0.00	0.00	11.08	0.00	9.64	0.00	0.00	RL35A_CAEEL	47.32	gi|528231908|	largesubunitribosomalproteinL35Ae[Strigomonasculicis]
TRINITY_DN100909_c0_g1_i1	17.12	12.35	3.78	0.00	0.00	0.00	11.08	0.00	6.76	0.00	0.00				
TRINITY_DN89449_c0_g1_i2	10.69	9.13	13.38	0.00	0.00	0.00	11.07	0.00	2.15	0.00	0.00				
TRINITY_DN26179_c0_g1_i1	14.71	5.92	12.51	0.00	0.00	0.00	11.05	0.00	4.57	0.00	0.00	RS71_ARATH	33.9	gi|568250054|	40SribosomalproteinS7[Anophelesdarlingi]
TRINITY_DN63140_c0_g1_i1	10.80	17.23	5.11	0.00	0.00	0.00	11.04	0.00	6.06	0.00	0.00	KBL_BOVIN	33.33	gi|656314262|	hypotheticalprotein[Schlesneriapaludicola]
TRINITY_DN64021_c0_g1_i1	22.11	3.00	7.96	0.00	0.00	0.00	11.03	0.00	9.91	0.00	0.00	TNNC2_ANGAN	34.72	gi|145537634|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124422294|emb|CAK87131.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN31001_c0_g1_i1	19.18	6.86	7.01	0.00	0.00	0.00	11.01	0.00	7.07	0.00	0.00	RL19_TETTS	68.31	gi|597897705|	hypotheticalproteinY032_0418g1120[Ancylostomaceylanicum]
TRINITY_DN19007_c0_g1_i1	13.64	6.19	12.98	0.00	0.00	0.00	10.94	0.00	4.12	0.00	0.00	MUC19_HUMAN	44	gi|393192137|	VspA-likeprotein
TRINITY_DN31969_c0_g1_i1	27.52	0.00	5.15	0.00	0.00	0.00	10.89	0.00	14.63	0.00	0.00	RL19_TETTS	59.7	gi|734547718|	60SribosomalproteinL19[Toxocaracanis]

TRINITY_DN62753_c0_g1_i1	5.67	9.09	17.88	0.00	0.00	0.00	10.88	0.00	6.30	0.00	0.00	SNU13_CANGA	60.83	gi|615440616|	ribonucleoprotein-associatedprotein[ColletotrichumfioriniaePJ7]>gi|588905028|gb|EXF84856.1|ribonucleoprotein-associatedprotein[ColletotrichumfioriniaePJ7]
TRINITY_DN73950_c0_g1_i2	12.64	0.00	19.94	0.00	0.00	0.00	10.86	0.00	10.09	0.00	0.00	RS17_BOVIN	58.26	gi|145345768|	RibosomalproteinS17
TRINITY_DN70408_c0_g2_i1	14.92	7.66	9.97	0.00	0.00	0.00	10.85	0.00	3.71	0.00	0.00	CATR2_PARTE	50.69	gi|325189489|	calciumdependentprotein4putative[AlbugolaibachiiNc14]
TRINITY_DN188526_c0_g1_i1	12.96	5.33	14.05	0.00	0.00	0.00	10.78	0.00	4.75	0.00	0.00				
TRINITY_DN167020_c0_g1_i1	13.07	7.33	11.83	0.00	0.00	0.00	10.74	0.00	3.02	0.00	0.00				
TRINITY_DN58667_c0_g2_i1	10.30	10.47	11.41	0.00	0.00	0.00	10.73	0.00	0.60	0.00	0.00	CATR5_PARTE	25.29	gi|145511448|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124408904|emb|CAK74252.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN54667_c0_g1_i1	27.82	0.00	4.32	0.00	0.00	0.00	10.71	0.00	14.97	0.00	0.00	RS13_MAIZE	71.79	gi|413921431|	hypotheticalproteinZEAMMB73_870097[Zeamays]>gi|413941712|gb|AFW74361.1|hypotheticalproteinZEAMMB73_979667[Zeamays]
TRINITY_DN395_c0_g1_i1	16.90	15.11	0.00	0.00	0.00	0.00	10.67	0.00	9.28	0.00	0.00				
TRINITY_DN50384_c0_g1_i1	18.00	10.52	3.40	0.00	0.00	0.00	10.64	0.00	7.30	0.00	0.00				
TRINITY_DN165855_c0_g1_i1	10.55	12.25	9.10	0.00	0.00	0.00	10.63	0.00	1.58	0.00	0.00				
TRINITY_DN222687_c0_g1_i1	12.74	4.31	14.82	0.00	0.00	0.00	10.62	0.00	5.57	0.00	0.00				
TRINITY_DN95546_c0_g1_i1	10.53	12.64	8.69	0.00	0.00	0.00	10.62	0.00	1.98	0.00	0.00	CATR6_PARTE	39.39	gi|673016758|	hypotheticalproteinH310_01097[Aphanomycesinvadans]>gi|574481543|gb|ETW08535.1|hypotheticalproteinH310_01097[Aphanomycesinvadans]
TRINITY_DN82133_c0_g1_i2	9.31	10.28	12.26	0.00	0.00	0.00	10.62	0.00	1.50	0.00	0.00	RL5_SUBDO	60.7	gi|302799842|	hypotheticalproteinSELMODRAFT_154687[Selaginellamoellendorffii]>gi|300150511|gb|EFJ17161.1|hypotheticalproteinSELMODRAFT_154687[Selaginellamoellendorffii]
TRINITY_DN56195_c0_g1_i1	26.54	0.00	5.28	0.00	0.00	0.00	10.61	0.00	14.05	0.00	0.00	RL35_TETTS	40.17	gi|366994067|	hypotheticalproteinNCAS_0E03710[NaumovozymacastelliiCBS4309]>gi|342302665|emb|CCC70441.1|hypotheticalproteinNCAS_0E03710[NaumovozymacastelliiCBS4309]
TRINITY_DN170699_c0_g1_i1	7.04	8.63	16.13	0.00	0.00	0.00	10.60	0.00	4.85	0.00	0.00				
TRINITY_DN116161_c0_g1_i1	26.63	0.00	5.01	0.00	0.00	0.00	10.54	0.00	14.15	0.00	0.00	PCR3_ARATH	35.71	gi|156409347|	predictedprotein[Nematostellavectensis]>gi|156229272|gb|EDO50068.1|predictedprotein[Nematostellavectensis]
TRINITY_DN56265_c0_g1_i1	24.61	0.00	7.00	0.00	0.00	0.00	10.54	0.00	12.68	0.00	0.00	ARF_CANAL	62.89	gi|459368883|	ADP-ribosylationfactor
TRINITY_DN159865_c0_g1_i1	6.90	10.52	14.18	0.00	0.00	0.00	10.54	0.00	3.64	0.00	0.00				
TRINITY_DN49263_c0_g1_i1	13.75	5.20	12.53	0.00	0.00	0.00	10.49	0.00	4.62	0.00	0.00	RL13_TETTS	50.25	gi|743854071|	PREDICTED:60SribosomalproteinL13-1[Elaeisguineensis]>gi|743854076|ref|XP_010940805.1|PREDICTED:60SribosomalproteinL13-1[Elaeisguineensis]
TRINITY_DN215061_c0_g1_i1	12.62	10.89	7.94	0.00	0.00	0.00	10.48	0.00	2.37	0.00	0.00				
TRINITY_DN88062_c0_g1_i1	14.74	6.78	9.92	0.00	0.00	0.00	10.48	0.00	4.01	0.00	0.00	RS3A_TETTS	44.49	gi|751006557|	hypotheticalproteinCY34DRAFT_797777[SuillusluteusUH-Slu-Lm8-n1]
TRINITY_DN14279_c0_g1_i1	8.76	10.18	12.44	0.00	0.00	0.00	10.46	0.00	1.85	0.00	0.00	DNAL1_XENLA	43.82	gi|698802396|	hypotheticalproteinH257_09639[Aphanomycesastaci]>gi|698802398|ref|XP_009834228.1|hypotheticalprotein
TRINITY_DN99035_c0_g1_i1	9.61	10.86	10.66	0.00	0.00	0.00	10.38	0.00	0.68	0.00	0.00	H31_TETTH	82.22	gi|221057978|	HistoneH3[PlasmodiumknowlesistrainH]>gi|194247502|emb|CAQ40902.1|HistoneH3
TRINITY_DN71567_c0_g1_i3	11.04	9.05	11.00	0.00	0.00	0.00	10.36	0.00	1.14	0.00	0.00	RL12_RAT	67.08	gi|803286756|	PREDICTED:60SribosomalproteinL12isoformX2[Ovisariesmusimon]
TRINITY_DN212129_c0_g1_i1	17.34	9.78	3.94	0.00	0.00	0.00	10.35	0.00	6.72	0.00	0.00				
TRINITY_DN86089_c0_g2_i1	10.01	0.00	20.97	0.00	0.00	0.00	10.33	0.00	10.49	0.00	0.00	KM11_TRYCR	93.48	gi|401429474|	kinetoplastidmembraneprotein-11[LeishmaniamexicanaMHOM/GT/2001/U1103]>gi|11225132|gb|AAG32958.1|AF193432_1kinetoplastmembraneprotein11[Leishmaniaamazonensis]>gi|322495469|emb|CBZ30774.1|kinetoplastidmembraneprotein-11[LeishmaniamexicanaMHOM/GT/2001/U1103]
TRINITY_DN76632_c0_g2_i1	22.36	0.00	8.56	0.00	0.00	0.00	10.31	0.00	11.28	0.00	0.00	PCKA2_SALRD	43.86	gi|685420345|	phosphoenolpyruvatecarboxykinase[Gaeumannomycesgraminisvar.triticiR3-111a-1]>gi|402073690|gb|EJT69242.1|phosphoenolpyruvatecarboxykinase[Gaeumannomycesgraminisvar.triticiR3-111a-1]
TRINITY_DN96142_c0_g1_i1	17.48	5.17	8.27	0.00	0.00	0.00	10.31	0.00	6.40	0.00	0.00	RL18_TETTH	55.26	gi|720043538|	PREDICTED:60SribosomalproteinL18-3[Nelumbonucifera]
TRINITY_DN140366_c0_g1_i1	11.92	9.10	9.87	0.00	0.00	0.00	10.30	0.00	1.46	0.00	0.00	ADT1_GOSHI	67.86	gi|470437283|	adeninenucleotidetranslocator
TRINITY_DN78957_c0_g2_i1	16.78	4.65	9.39	0.00	0.00	0.00	10.27	0.00	6.11	0.00	0.00	RL15_TETTS	72.55	gi|168009740|	predictedprotein[Physcomitrellapatens]>gi|162691257|gb|EDQ77620.1|predictedprotein[Physcomitrellapatens]
TRINITY_DN70124_c1_g2_i2	9.00	4.49	17.31	0.00	0.00	0.00	10.27	0.00	6.51	0.00	0.00				
TRINITY_DN65617_c0_g1_i1	7.89	14.89	7.92	0.00	0.00	0.00	10.24	0.00	4.03	0.00	0.00				
TRINITY_DN27993_c0_g1_i1	10.46	6.89	13.32	0.00	0.00	0.00	10.22	0.00	3.22	0.00	0.00				
TRINITY_DN59125_c0_g1_i1	14.00	8.31	8.35	0.00	0.00	0.00	10.22	0.00	3.27	0.00	0.00	CATD_DICDI	54.44	gi|195380081|	GJ21122[Drosophilavirilis]>gi|194143596|gb|EDW59992.1|GJ21122[Drosophilavirilis]
TRINITY_DN166205_c0_g1_i1	11.64	6.02	12.91	0.00	0.00	0.00	10.19	0.00	3.67	0.00	0.00				
TRINITY_DN33091_c0_g1_i1	8.13	6.18	16.20	0.00	0.00	0.00	10.17	0.00	5.31	0.00	0.00	EF1A_CRYPV	63.87	gi|255078526|	translationelongationfactorEF-1alpha/Tu[Micromonassp.RCC299]>gi|226518109|gb|ACO64101.1|translationelongationfactorEF-1alpha/Tu[Micromonassp.RCC299]
TRINITY_DN167519_c0_g1_i1	11.05	0.00	19.44	0.00	0.00	0.00	10.16	0.00	9.75	0.00	0.00				
TRINITY_DN47090_c0_g2_i1	21.32	0.00	9.10	0.00	0.00	0.00	10.14	0.00	10.70	0.00	0.00				
TRINITY_DN170236_c0_g1_i1	9.18	12.72	8.52	0.00	0.00	0.00	10.14	0.00	2.26	0.00	0.00				
TRINITY_DN15907_c0_g1_i1	10.73	7.13	12.51	0.00	0.00	0.00	10.13	0.00	2.74	0.00	0.00	KAD_CAUCR	30.37	gi|471220185|	hypotheticalproteinIMG5_190710[Ichthyophthiriusmultifiliis]>gi|340500877|gb|EGR27715.1|hypotheticalproteinIMG5_190710[Ichthyophthiriusmultifiliis]
TRINITY_DN81074_c0_g3_i1	11.71	8.93	9.74	0.00	0.00	0.00	10.13	0.00	1.43	0.00	0.00	VATL_CHRCT	65.19	gi|676395221|	hypotheticalproteinAURANDRAFT_32575[Aureococcusanophagefferens]>gi|323448604|gb|EGB04501.1|hypotheticalproteinAURANDRAFT_32575[Aureococcusanophagefferens]
TRINITY_DN84677_c0_g1_i2	8.03	11.96	10.36	0.00	0.00	0.00	10.12	0.00	1.98	0.00	0.00	GBLP_HYDVU	24.72	gi|30585331|	Homosapiensguaninenucleotidebindingprotein(Gprotein)
TRINITY_DN78497_c0_g1_i1	7.66	11.37	11.24	0.00	0.00	0.00	10.09	0.00	2.11	0.00	0.00	RS4_YARLI	66.15	gi|498970418|	PREDICTED:40SribosomalproteinS4[Ceratitiscapitata]>gi|751439300|ref|XP_011183473.1|PREDICTED:40SribosomalproteinS4[Bactroceracucurbitae]
TRINITY_DN21414_c0_g1_i1	13.75	10.66	5.81	0.00	0.00	0.00	10.08	0.00	4.00	0.00	0.00				
TRINITY_DN145811_c0_g1_i1	7.94	8.38	13.88	0.00	0.00	0.00	10.06	0.00	3.31	0.00	0.00	CB25_TETTH	26.39	gi|145513018|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124409773|emb|CAK75023.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN215331_c0_g1_i1	13.42	10.71	6.03	0.00	0.00	0.00	10.06	0.00	3.74	0.00	0.00				

TRINITY_DN67289_c0_g1_i1	9.53	7.10	13.40	0.00	0.00	0.00	10.01	0.00	3.18	0.00	0.00	SCG3_MOUSE	28.79	gi|678313288|	electrontransferflavoproteinubiquinoneoxidoreductase[Stylonychialemnae]
TRINITY_DN93833_c3_g8_i2	7.63	9.93	12.40	0.00	0.00	0.00	9.98	0.00	2.38	0.00	0.00	SDRD_STAAN	44.44	gi|737661294|	hypotheticalprotein
TRINITY_DN52943_c0_g2_i1	17.68	6.91	5.35	0.00	0.00	0.00	9.98	0.00	6.72	0.00	0.00	RS16_RAT	66.19	gi|384485990|	40SribosomalproteinS16[RhizopusdelemarRA99-880]>gi|384496508|gb|EIE86999.1|40SribosomalproteinS16[RhizopusdelemarRA99-880]
TRINITY_DN56967_c0_g2_i1	14.29	8.70	6.85	0.00	0.00	0.00	9.95	0.00	3.88	0.00	0.00	RBX1A_DROME	52.81	gi|588317221|	unnamedproteinproduct[Phytomonassp.isolateEM1]
TRINITY_DN20211_c0_g1_i1	10.35	8.78	10.67	0.00	0.00	0.00	9.93	0.00	1.01	0.00	0.00				
TRINITY_DN193509_c0_g1_i1	10.07	7.33	12.32	0.00	0.00	0.00	9.91	0.00	2.50	0.00	0.00				
TRINITY_DN212055_c0_g1_i1	11.43	3.83	14.29	0.00	0.00	0.00	9.85	0.00	5.40	0.00	0.00				
TRINITY_DN172040_c0_g1_i1	15.95	7.79	5.76	0.00	0.00	0.00	9.83	0.00	5.39	0.00	0.00				
TRINITY_DN44732_c0_g1_i1	3.47	0.00	25.74	0.00	0.00	0.00	9.74	0.00	13.97	0.00	0.00				
TRINITY_DN32467_c0_g1_i1	25.25	0.00	3.95	0.00	0.00	0.00	9.73	0.00	13.58	0.00	0.00				
TRINITY_DN212029_c0_g1_i1	9.84	5.57	13.76	0.00	0.00	0.00	9.72	0.00	4.10	0.00	0.00				
TRINITY_DN71569_c0_g1_i1	11.28	4.68	13.20	0.00	0.00	0.00	9.72	0.00	4.47	0.00	0.00	TBA_TETTH	98.91	gi|21632094|	alpha-tubulin
TRINITY_DN99760_c0_g1_i1	8.65	4.78	15.73	0.00	0.00	0.00	9.72	0.00	5.55	0.00	0.00	RIC1_ORYSJ	46.49	gi|212275502|	RasproteinRIC1[Zeamays]>gi|194690000|gb|ACF79084.1|unknown[Zeamays]>gi|195605598|gb|ACG24629.1|ras-relatedproteinRIC1[Zeamays]>gi|195606872|gb|ACG25266.1|ras-relatedproteinRIC1[Zeamays]>gi|223942789|gb|ACN25478.1|unknown[Zeamays]>gi|413950363|gb|AFW83012.1|RasproteinRIC1[Zeamays]
TRINITY_DN27885_c0_g1_i1	15.25	7.91	5.99	0.00	0.00	0.00	9.72	0.00	4.89	0.00	0.00	RL27A_RAT	63.51	gi|145510338|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|145549666|ref|XP_001460512.1|hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124408341|emb|CAK73705.1|unnamedproteinproduct[Parameciumtetraurelia]>gi|124428342|emb|CAK93115.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN188519_c0_g1_i1	7.44	0.00	21.64	0.00	0.00	0.00	9.70	0.00	11.00	0.00	0.00				
TRINITY_DN77101_c0_g1_i1	12.69	11.08	5.28	0.00	0.00	0.00	9.68	0.00	3.90	0.00	0.00	RS23_LUMRU	83.92	gi|524894332|	PREDICTED:40SribosomalproteinS23-like[Aplysiacalifornica]
TRINITY_DN116269_c0_g1_i1	12.83	7.39	8.78	0.00	0.00	0.00	9.67	0.00	2.82	0.00	0.00	PABP_YARLI	33.78	gi|321448546|	hypotheticalproteinDAPPUDRAFT_273146[Daphniapulex]
TRINITY_DN201124_c0_g1_i1	9.72	10.25	8.94	0.00	0.00	0.00	9.64	0.00	0.66	0.00	0.00				
TRINITY_DN68638_c0_g2_i1	0.00	13.02	15.82	0.00	0.00	0.00	9.61	0.00	8.44	0.00	0.00				
TRINITY_DN70043_c0_g1_i1	24.42	0.00	4.41	0.00	0.00	0.00	9.61	0.00	13.01	0.00	0.00	RL35A_TETTS	55.66	gi|557168142|	60sribosomalproteinL33-A
TRINITY_DN215240_c0_g1_i1	18.01	0.00	10.76	0.00	0.00	0.00	9.59	0.00	9.06	0.00	0.00				
TRINITY_DN187150_c0_g1_i1	6.54	3.97	18.23	0.00	0.00	0.00	9.58	0.00	7.60	0.00	0.00				
TRINITY_DN56164_c0_g1_i1	23.57	0.00	5.12	0.00	0.00	0.00	9.56	0.00	12.40	0.00	0.00	RS15A_DROYA	66.15	gi|766929433|	PREDICTED:40SribosomalproteinS15Aa[Ceratosolensolmsimarchali]
TRINITY_DN11547_c0_g1_i1	22.09	6.59	0.00	0.00	0.00	0.00	9.56	0.00	11.34	0.00	0.00	SYM_SHESW	46.88	gi|229596251|	hypotheticalproteinTTHERM_00106820[Tetrahymenathermophila]>gi|225565516|gb|EAR92081.3|hypotheticalproteinTTHERM_00106820[TetrahymenathermophilaSB210]
TRINITY_DN117181_c0_g1_i1	13.01	8.95	6.62	0.00	0.00	0.00	9.53	0.00	3.24	0.00	0.00				
TRINITY_DN43003_c0_g1_i1	8.48	13.85	6.20	0.00	0.00	0.00	9.51	0.00	3.93	0.00	0.00	DNAL4_MOUSE	34.41	gi|301757542|	PREDICTED:dyneinlightchain4
TRINITY_DN13359_c0_g1_i1	11.21	7.35	9.96	0.00	0.00	0.00	9.51	0.00	1.97	0.00	0.00	RL7_TETTH	59.56	gi|523421643|	BN860_16798g1_1[ZygosaccharomycesbailiiCLIB213]
TRINITY_DN76995_c0_g1_i1	10.43	9.66	8.35	0.00	0.00	0.00	9.48	0.00	1.05	0.00	0.00	RS16_CAEEL	70.21	gi|759308778|	40SribosomalproteinS16[FonsecaeapedrosoiCBS271.37]
TRINITY_DN79275_c0_g1_i1	6.91	8.31	13.20	0.00	0.00	0.00	9.48	0.00	3.30	0.00	0.00	RS31_ARATH	66.52	gi|586726574|	PREDICTED:40SribosomalproteinS3-3[Amborellatrichopoda]>gi|769805818|ref|XP_011625300.1|PREDICTED:40SribosomalproteinS3-3[Amborellatrichopoda]>gi|769805820|ref|XP_011625301.1|PREDICTED:40SribosomalproteinS3-3[Amborellatrichopoda]>gi|548853206|gb|ERN11212.1|hypotheticalproteinAMTR_s00024p00219330[Amborellatrichopoda]
TRINITY_DN120406_c0_g1_i1	8.36	5.81	14.13	0.00	0.00	0.00	9.44	0.00	4.26	0.00	0.00	CALM2_BRAFL	25	gi|590704747|	Centrin2isoform1[Theobromacacao]>gi|508699506|gb|EOX91402.1|Centrin2isoform1[Theobromacacao]
TRINITY_DN44000_c0_g2_i1	20.19	0.00	8.11	0.00	0.00	0.00	9.43	0.00	10.16	0.00	0.00	CATB_BOVIN	55.37	gi|555949073|	PREDICTED:cathepsinBisoformX2[Bosmutus]
TRINITY_DN83431_c0_g1_i1	10.34	10.55	7.38	0.00	0.00	0.00	9.42	0.00	1.77	0.00	0.00	NACA_DROME	41.96	gi|125552095|	hypotheticalproteinOsI_19723[OryzasativaIndicaGroup]
TRINITY_DN74820_c0_g3_i1	6.25	13.18	8.76	0.00	0.00	0.00	9.40	0.00	3.51	0.00	0.00				
TRINITY_DN140959_c0_g1_i1	22.89	0.00	5.26	0.00	0.00	0.00	9.38	0.00	11.99	0.00	0.00	PRVB_XENLA	32.2	gi|514698370|	hypotheticalprotein
TRINITY_DN221073_c0_g1_i1	12.86	0.00	15.10	0.00	0.00	0.00	9.32	0.00	8.15	0.00	0.00				
TRINITY_DN69138_c0_g1_i1	20.98	0.00	6.96	0.00	0.00	0.00	9.32	0.00	10.69	0.00	0.00	RL13_TETTS	50.75	gi|239835740|	60SribosomalproteinL13isoform1[Zeamays]>gi|238908779|gb|ACF86560.2|unknown[Zeamays]>gi|414878937|tpg|DAA56068.1|TPA:60SribosomalproteinL13isoform1[Zeamays]>gi|414878938|tpg|DAA56069.1|TPA:60SribosomalproteinL13isoform2[Zeamays]>gi|414878939|tpg|DAA56070.1|TPA:60SribosomalproteinL13isoform3[Zeamays]
TRINITY_DN179245_c0_g1_i1	13.33	6.23	8.19	0.00	0.00	0.00	9.25	0.00	3.67	0.00	0.00				
TRINITY_DN72131_c0_g1_i1	11.31	7.53	8.89	0.00	0.00	0.00	9.24	0.00	1.92	0.00	0.00	ATP5E_ARATH	41.38	gi|270004859|	stunted[Triboliumcastaneum]
TRINITY_DN224899_c0_g1_i1	20.97	0.00	6.70	0.00	0.00	0.00	9.23	0.00	10.71	0.00	0.00				
TRINITY_DN224896_c0_g1_i1	22.75	0.00	4.92	0.00	0.00	0.00	9.22	0.00	11.97	0.00	0.00				
TRINITY_DN70708_c0_g1_i1	9.05	3.47	15.14	0.00	0.00	0.00	9.22	0.00	5.84	0.00	0.00	PPGB_HUMAN	57.89	gi|367067078|	hypotheticalprotein2_8315_02
TRINITY_DN174993_c0_g1_i1	13.53	6.35	7.75	0.00	0.00	0.00	9.21	0.00	3.81	0.00	0.00				
TRINITY_DN147904_c0_g1_i1	10.59	10.57	6.45	0.00	0.00	0.00	9.20	0.00	2.38	0.00	0.00				
TRINITY_DN170348_c0_g1_i1	20.34	7.22	0.00	0.00	0.00	0.00	9.19	0.00	10.31	0.00	0.00				
TRINITY_DN37633_c0_g1_i1	9.89	8.52	8.98	0.00	0.00	0.00	9.13	0.00	0.69	0.00	0.00	TDRD5_AILME	39.68	gi|769203504|	hypotheticalprotein
TRINITY_DN48661_c0_g1_i1	16.65	0.00	10.72	0.00	0.00	0.00	9.12	0.00	8.44	0.00	0.00	RL4_TETTS	57.59	gi|674245589|	hypotheticalproteinAALP_AA3G103100[Arabisalpina]
TRINITY_DN52789_c0_g1_i1	20.00	0.00	7.36	0.00	0.00	0.00	9.12	0.00	10.12	0.00	0.00	H4_STYLE	52.88	gi|808863462|	HistoneH4[Larimichthyscrocea]
TRINITY_DN115892_c0_g1_i1	20.44	6.84	0.00	0.00	0.00	0.00	9.10	0.00	10.40	0.00	0.00				
TRINITY_DN80562_c0_g3_i1	11.89	7.61	7.78	0.00	0.00	0.00	9.09	0.00	2.43	0.00	0.00	RS15A_DROYA	65	gi|669143956|	40SribosomalproteinS15a[SaprolegniadiclinaVS20]>gi|813199586|ref|XP_012209364.1|40SribosomalproteinS15a[SaprolegniaparasiticaCBS223.65]>gi|530740474|gb|EQC38716.1|40SribosomalproteinS15a[SaprolegniadiclinaVS20]>gi|641525472|gb|KDO19925.1|40SribosomalproteinS15a[SaprolegniaparasiticaCBS223.65]

TRINITY_DN99975_c0_g1_i1	9.83	8.76	8.66	0.00	0.00	0.00	9.09	0.00	0.64	0.00	0.00	EPHB4_HUMAN	28	gi|326498249|	predictedprotein[Hordeumvulgaresubsp.vulgare]
TRINITY_DN10492_c0_g1_i1	7.97	3.56	15.69	0.00	0.00	0.00	9.07	0.00	6.14	0.00	0.00				
TRINITY_DN26778_c0_g1_i1	12.48	8.78	5.94	0.00	0.00	0.00	9.07	0.00	3.28	0.00	0.00	UBE2N_MACFA	41.41	gi|685308716|	PREDICTED:probableubiquitin-conjugatingenzymeE231[Brassicarapa]
TRINITY_DN73624_c1_g1_i1	7.89	6.01	13.30	0.00	0.00	0.00	9.07	0.00	3.79	0.00	0.00	EF1A_SOLLC	81.95	gi|159793379|	elongationfactor1-alpha
TRINITY_DN66271_c0_g2_i1	5.73	16.22	5.23	0.00	0.00	0.00	9.06	0.00	6.21	0.00	0.00				
TRINITY_DN22438_c0_g1_i1	14.29	6.96	5.88	0.00	0.00	0.00	9.04	0.00	4.58	0.00	0.00				
TRINITY_DN58793_c0_g1_i1	20.84	0.00	6.21	0.00	0.00	0.00	9.02	0.00	10.70	0.00	0.00	LDOX_PERFR	46.15	gi|471221620|	hypotheticalproteinIMG5_176490[Ichthyophthiriusmultifiliis]>gi|340501635|gb|EGR28393.1|hypotheticalproteinIMG5_176490[Ichthyophthiriusmultifiliis]
TRINITY_DN28075_c0_g1_i1	14.03	12.91	0.00	0.00	0.00	0.00	8.98	0.00	7.80	0.00	0.00	HPAB_ECOLX	34.04	gi|519093266|	hypotheticalprotein[BRC1bacteriumSCGCAAA252-M09]
TRINITY_DN68678_c0_g4_i1	11.55	6.91	8.42	0.00	0.00	0.00	8.96	0.00	2.37	0.00	0.00	CATR5_PARTE	72.3	gi|237836099|	caltractin
TRINITY_DN187105_c0_g1_i1	8.70	8.69	9.49	0.00	0.00	0.00	8.96	0.00	0.46	0.00	0.00				
TRINITY_DN6422_c0_g1_i1	12.82	14.03	0.00	0.00	0.00	0.00	8.95	0.00	7.77	0.00	0.00	MYCBP_DICDI	47.5	gi|294934535|	C-Myc-bindingprotein
TRINITY_DN90806_c0_g10_i1	9.06	10.62	7.14	0.00	0.00	0.00	8.94	0.00	1.74	0.00	0.00	H2A_TRYCR	65.52	gi|71649895|	histoneH2A[TrypanosomacruzistrainCLBrener]>gi|71649899|ref|XP_813660.1|histoneH2A[TrypanosomacruzistrainCLBrener]>gi|71649998|ref|XP_813706.1|histoneH2A[TrypanosomacruzistrainCLBrener]>gi|71650026|ref|XP_813720.1|histoneH2A[TrypanosomacruzistrainCLBrener]>gi|71664768|ref|XP_819361.1|histoneH2A[TrypanosomacruzistrainCLBrener]>gi|71664800|ref|XP_819377.1|histoneH2A[TrypanosomacruzistrainCLBrener]>gi|71664804|ref|XP_819379.1|histoneH2A[TrypanosomacruzistrainCLBrener]>gi|70878561|gb|EAN91807.1|histoneH2A
TRINITY_DN45198_c0_g1_i1	11.22	9.89	5.64	0.00	0.00	0.00	8.92	0.00	2.91	0.00	0.00				
TRINITY_DN63282_c0_g1_i1	20.52	0.00	6.20	0.00	0.00	0.00	8.91	0.00	10.53	0.00	0.00				
TRINITY_DN19340_c0_g1_i1	10.85	8.98	6.79	0.00	0.00	0.00	8.88	0.00	2.03	0.00	0.00	CATR4_PARTE	25.35	gi|697892044|	centrin[TheileriaorientalisstrainShintoku]>gi|403222830|dbj|BAM40961.1|centrin[TheileriaorientalisstrainShintoku]
TRINITY_DN9295_c0_g2_i1	9.17	8.64	8.80	0.00	0.00	0.00	8.87	0.00	0.27	0.00	0.00				
TRINITY_DN87698_c2_g1_i1	6.43	5.98	14.16	0.00	0.00	0.00	8.86	0.00	4.60	0.00	0.00				
TRINITY_DN100050_c0_g1_i1	3.19	13.46	9.88	0.00	0.00	0.00	8.84	0.00	5.21	0.00	0.00	LYS_BOMMO	32.98	gi|403347005|	hypotheticalproteinOXYTRI_05956[Oxytrichatrifallax]>gi|403367225|gb|EJY83427.1|hypotheticalproteinOXYTRI_18951[Oxytrichatrifallax]
TRINITY_DN169671_c0_g1_i1	12.37	7.25	6.80	0.00	0.00	0.00	8.81	0.00	3.09	0.00	0.00				
TRINITY_DN24684_c0_g2_i1	7.38	7.10	11.90	0.00	0.00	0.00	8.79	0.00	2.70	0.00	0.00	SMD2_DROME	71.11	gi|297604251|	Os05g0314100[OryzasativaJaponicaGroup]>gi|573915373|ref|XP_006645341.1|PREDICTED:smallnuclearribonucleoproteinSmD2-like[Oryzabrachyantha]>gi|54291778|gb|AAV32147.1|putativesmallnuclearribonucleoproteinD2[OryzasativaJaponicaGroup]>gi|215768148|dbj|BAH00377.1|unnamedproteinproduct[OryzasativaJaponicaGroup]>gi|215768714|dbj|BAH00943.1|unnamedproteinproduct[OryzasativaJaponicaGroup]>gi|218196532|gb|EEC78959.1|hypotheticalproteinOsI_19425[OryzasativaIndicaGroup]>gi|222631079|gb|EEE63211.1|hypotheticalproteinOsJ_18021[OryzasativaJaponicaGroup]>gi|255676234|dbj|BAF17082.2|Os05g0314100[OryzasativaJaponicaGroup]
TRINITY_DN70187_c0_g1_i1	16.74	6.52	3.11	0.00	0.00	0.00	8.79	0.00	7.10	0.00	0.00	EF2_CAEEL	57.06	gi|568249486|	eukaryotictranslationelongationfactor[Anophelesdarlingi]
TRINITY_DN86963_c0_g1_i1	7.38	7.73	11.26	0.00	0.00	0.00	8.79	0.00	2.14	0.00	0.00	PEPA1_RABIT	42.37	gi|1246039|	pepsinogen2[Scombridaegen.sp.]
TRINITY_DN228747_c0_g1_i1	8.51	8.62	9.24	0.00	0.00	0.00	8.79	0.00	0.39	0.00	0.00				
TRINITY_DN33911_c0_g1_i1	20.97	0.00	5.36	0.00	0.00	0.00	8.77	0.00	10.89	0.00	0.00				
TRINITY_DN139687_c0_g1_i1	3.36	19.28	3.68	0.00	0.00	0.00	8.77	0.00	9.10	0.00	0.00	S17P_SPIOL	46.8	gi|763807269|	hypotheticalproteinB456_011G279400[Gossypiumraimondii]>gi|763807271|gb|KJB74209.1|hypotheticalproteinB456_011G279400[Gossypiumraimondii]
TRINITY_DN89186_c0_g5_i1	9.21	8.01	9.05	0.00	0.00	0.00	8.76	0.00	0.65	0.00	0.00	H2B_TRYCR	61.4	gi|554930278|	histoneH2B[TrypanosomarangeliSC58]
TRINITY_DN165779_c0_g1_i1	11.70	8.71	5.84	0.00	0.00	0.00	8.75	0.00	2.93	0.00	0.00				
TRINITY_DN20260_c0_g1_i1	17.94	0.00	8.30	0.00	0.00	0.00	8.74	0.00	8.98	0.00	0.00	GBLP_BRANA	30.12	gi|729375758|	PREDICTED:guaninenucleotide-bindingproteinsubunitbeta-likeproteinB[Tarenayahassleriana]
TRINITY_DN18368_c0_g1_i1	15.86	4.33	6.03	0.00	0.00	0.00	8.74	0.00	6.23	0.00	0.00				
TRINITY_DN531_c0_g2_i1	19.54	6.63	0.00	0.00	0.00	0.00	8.72	0.00	9.93	0.00	0.00	RS27B_SCHPO	61.54	gi|471225568|	ubiquitinextensionprotein
TRINITY_DN12478_c0_g2_i1	7.62	10.37	8.16	0.00	0.00	0.00	8.72	0.00	1.46	0.00	0.00	RS14_PODCA	83.91	gi|751746696|	hypotheticalproteinOIDMADRAFT_21204[Oidiodendronmaius Zn]
TRINITY_DN26859_c0_g1_i1	22.89	0.00	3.24	0.00	0.00	0.00	8.71	0.00	12.39	0.00	0.00				
TRINITY_DN189743_c0_g1_i1	13.50	4.81	7.77	0.00	0.00	0.00	8.69	0.00	4.42	0.00	0.00				
TRINITY_DN64671_c0_g1_i1	20.23	5.65	0.00	0.00	0.00	0.00	8.62	0.00	10.44	0.00	0.00				
TRINITY_DN64466_c0_g1_i1	22.25	0.00	3.62	0.00	0.00	0.00	8.62	0.00	11.94	0.00	0.00				
TRINITY_DN10216_c0_g1_i1	16.99	0.00	8.87	0.00	0.00	0.00	8.62	0.00	8.50	0.00	0.00	RPON_METAR	57.35	gi|661184774|	dna-directedrnapolymerasesandiiisubunitrpabc5-like[LichtheimiacorymbiferaJMRC:FSU:9682]>gi|671686145|emb|CDS10711.1|PutativeDNA-directedRNApolymeraseI
TRINITY_DN171693_c0_g1_i1	3.12	3.07	19.63	0.00	0.00	0.00	8.60	0.00	9.55	0.00	0.00				
TRINITY_DN77510_c0_g1_i2	7.58	3.54	14.68	0.00	0.00	0.00	8.60	0.00	5.64	0.00	0.00	RS16_NEUCR	56.25	gi|545702826|	40SribosomalproteinS16e[Galdieriasulphuraria]>gi|452820175|gb|EME27221.1|40SribosomalproteinS16e[Galdieriasulphuraria]
TRINITY_DN68689_c0_g2_i1	7.51	4.89	13.38	0.00	0.00	0.00	8.59	0.00	4.34	0.00	0.00				
TRINITY_DN203786_c0_g1_i1	17.94	0.00	7.83	0.00	0.00	0.00	8.59	0.00	8.99	0.00	0.00				
TRINITY_DN84609_c1_g2_i1	11.93	6.74	7.09	0.00	0.00	0.00	8.59	0.00	2.90	0.00	0.00	RS6_KLUMA	54.07	gi|748510220|	hypotheticalproteinAOL_s00081g96[ArthrobotrysoligosporaATCC24927]>gi|345565147|gb|EGX48100.1|hypotheticalproteinAOL_s00081g96[ArthrobotrysoligosporaATCC24927]
TRINITY_DN119419_c0_g1_i1	4.12	16.36	5.26	0.00	0.00	0.00	8.58	0.00	6.76	0.00	0.00				
TRINITY_DN75523_c0_g1_i1	9.24	6.99	9.49	0.00	0.00	0.00	8.58	0.00	1.38	0.00	0.00	BDHA_CUPNH	53.91	gi|491912838|	D-beta-hydroxybutyratedehydrogenase[Massiliatimonae]>gi|425718932|gb|EKU81873.1|D-beta-hydroxybutyratedehydrogenase[MassiliatimonaeCCUG45783]
TRINITY_DN86505_c0_g3_i1	11.01	4.27	10.40	0.00	0.00	0.00	8.56	0.00	3.73	0.00	0.00	Y2R2_DROME	50	gi|733484|	reversetranscriptase[Drosophilatakahashii]
TRINITY_DN225024_c0_g1_i1	0.00	4.32	21.36	0.00	0.00	0.00	8.56	0.00	11.29	0.00	0.00				
TRINITY_DN118476_c0_g1_i1	15.86	5.19	4.52	0.00	0.00	0.00	8.52	0.00	6.36	0.00	0.00	MANA_DICDI	52.46	gi|19920972|	CG9466
TRINITY_DN147037_c0_g1_i1	9.46	8.23	7.78	0.00	0.00	0.00	8.49	0.00	0.87	0.00	0.00				

TRINITY_DN223167_c0_g1_i1	21.98	0.00	3.45	0.00	0.00	0.00	8.48	0.00	11.82	0.00	0.00				
TRINITY_DN167375_c0_g1_i1	9.98	5.37	10.08	0.00	0.00	0.00	8.47	0.00	2.69	0.00	0.00				
TRINITY_DN86854_c2_g1_i1	9.77	6.59	9.04	0.00	0.00	0.00	8.46	0.00	1.66	0.00	0.00	RS52_ARATH	70.68	gi|593690288|	hypotheticalproteinPHAVU_007G264200g[Phaseolusvulgaris]>gi|561018935|gb|ESW17739.1|hypotheticalproteinPHAVU_007G264200g[Phaseolusvulgaris]
TRINITY_DN142376_c0_g1_i1	7.07	10.34	7.96	0.00	0.00	0.00	8.46	0.00	1.69	0.00	0.00	TCTP1_DICDI	34.64	gi|301093462|	conservedhypotheticalprotein[PhytophthorainfestansT30-4]>gi|262110540|gb|EEY68592.1|conservedhypotheticalprotein[PhytophthorainfestansT30-4]
TRINITY_DN51914_c1_g1_i1	9.75	10.18	5.39	0.00	0.00	0.00	8.44	0.00	2.65	0.00	0.00	CSPL2_GINBI	48.28	gi|145478301|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124392242|emb|CAK57775.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN199464_c0_g1_i1	9.64	6.41	9.25	0.00	0.00	0.00	8.43	0.00	1.76	0.00	0.00				
TRINITY_DN66467_c0_g2_i1	13.15	4.88	7.17	0.00	0.00	0.00	8.40	0.00	4.27	0.00	0.00	RL123_ARATH	52.76	gi|475407355|	60SribosomalproteinL12[Aegilopstauschii]
TRINITY_DN71452_c0_g1_i1	10.73	8.97	5.43	0.00	0.00	0.00	8.38	0.00	2.70	0.00	0.00	RL35_DANRE	49.15	gi|679198243|	60SribosomalproteinL35
TRINITY_DN126901_c0_g1_i1	13.26	8.47	3.36	0.00	0.00	0.00	8.36	0.00	4.95	0.00	0.00				
TRINITY_DN79181_c0_g1_i1	7.91	9.54	7.61	0.00	0.00	0.00	8.35	0.00	1.04	0.00	0.00				
TRINITY_DN133701_c0_g1_i1	9.09	15.90	0.00	0.00	0.00	0.00	8.33	0.00	7.98	0.00	0.00				
TRINITY_DN45387_c0_g2_i1	16.05	0.00	8.88	0.00	0.00	0.00	8.31	0.00	8.04	0.00	0.00	RL40_TETTS	88.12	gi|671416448|	ProteinBM-UBQ-2[Brugiamalayi]
TRINITY_DN4034_c0_g1_i1	15.60	9.28	0.00	0.00	0.00	0.00	8.29	0.00	7.85	0.00	0.00				
TRINITY_DN65808_c1_g1_i1	9.82	7.18	7.85	0.00	0.00	0.00	8.28	0.00	1.38	0.00	0.00	NARG_BACSU	35.42	gi|678333512|	UNKNOWN[Stylonychialemnae]
TRINITY_DN82762_c0_g2_i2	7.53	0.00	17.19	0.00	0.00	0.00	8.24	0.00	8.61	0.00	0.00	RS3A2_TRYCC	60.73	gi|528226425|	smallsubunitribosomalproteinS3Ae[Angomonasdeanei]>gi|528232848|gb|EPY27109.1|smallsubunitribosomalproteinS3Ae[Angomonasdeanei]>gi|528260665|gb|EPY38278.1|smallsubunitribosomalproteinS3Ae[Angomonasdeanei]>gi|528262704|gb|EPY38958.1|smallsubunitribosomalproteinS3Ae[Angomonasdeanei]
TRINITY_DN37480_c0_g1_i1	8.36	5.33	11.02	0.00	0.00	0.00	8.24	0.00	2.85	0.00	0.00				
TRINITY_DN171003_c0_g1_i1	11.54	6.86	6.27	0.00	0.00	0.00	8.22	0.00	2.89	0.00	0.00				
TRINITY_DN97943_c0_g1_i1	12.55	5.62	6.48	0.00	0.00	0.00	8.22	0.00	3.78	0.00	0.00				
TRINITY_DN84984_c1_g2_i2	6.54	5.06	13.00	0.00	0.00	0.00	8.20	0.00	4.22	0.00	0.00	TBA1_VOLCA	90.51	gi|399146215|	alpha-tubulin
TRINITY_DN59575_c0_g1_i1	6.79	4.59	13.18	0.00	0.00	0.00	8.19	0.00	4.46	0.00	0.00	NEP1_CANGA	55.84	gi|597857569|	hypotheticalproteinY032_0072g642[Ancylostomaceylanicum]
TRINITY_DN20598_c0_g1_i1	16.79	0.00	7.78	0.00	0.00	0.00	8.19	0.00	8.40	0.00	0.00	ATPA_CAEEL	55	gi|677539274|	hypotheticalproteinY956_09339
TRINITY_DN100507_c0_g1_i1	7.48	11.82	5.26	0.00	0.00	0.00	8.19	0.00	3.33	0.00	0.00				
TRINITY_DN73099_c0_g1_i1	7.89	10.62	6.04	0.00	0.00	0.00	8.18	0.00	2.31	0.00	0.00	RS14_CHLRE	90.22	gi|224106672|	40SribosomalproteinS14-3[Populustrichocarpa]>gi|118483965|gb|ABK93870.1|unknown[Populustrichocarpa]>gi|222850653|gb|EEE88200.1|40SribosomalproteinS14-3[Populustrichocarpa]
TRINITY_DN126758_c0_g1_i1	9.40	5.61	9.54	0.00	0.00	0.00	8.18	0.00	2.23	0.00	0.00	CATR4_PARTE	33.85	gi|669156768|	centrin-2[SaprolegniadiclinaVS20]>gi|813121392|ref|XP_012196463.1|hypotheticalproteinSPRG_02500[SaprolegniaparasiticaCBS223.65]>gi|530734203|gb|EQC32445.1|centrin-2[SaprolegniadiclinaVS20]>gi|641538986|gb|KDO32807.1|hypotheticalproteinSPRG_02500[SaprolegniaparasiticaCBS223.65]
TRINITY_DN94690_c0_g1_i1	12.60	6.51	5.40	0.00	0.00	0.00	8.17	0.00	3.88	0.00	0.00	SODF_SHIFL	59.28	gi|672858045|	superoxidedismutase[Escherichiacoli]
TRINITY_DN115314_c0_g1_i1	9.27	7.89	7.34	0.00	0.00	0.00	8.17	0.00	0.99	0.00	0.00	ORC1_KLULA	41.67	gi|471222063|	hypotheticalproteinIMG5_206925[Ichthyophthiriusmultifiliis]>gi|340501868|gb|EGR28603.1|hypotheticalproteinIMG5_206925[Ichthyophthiriusmultifiliis]
TRINITY_DN71924_c0_g1_i1	7.51	7.24	9.59	0.00	0.00	0.00	8.11	0.00	1.28	0.00	0.00	CALM_AGABI	44	gi|750958942|	hypotheticalproteinPISMIDRAFT_686871[Pisolithusmicrocarpus441]
TRINITY_DN73122_c0_g1_i1	6.87	9.55	7.92	0.00	0.00	0.00	8.11	0.00	1.35	0.00	0.00	RL9_ORYSJ	54.5	gi|116782919|	unknown[Piceasitchensis]>gi|116784533|gb|ABK23381.1|unknown[Piceasitchensis]>gi|116791785|gb|ABK26107.1|unknown[Piceasitchensis]>gi|148909072|gb|ABR17638.1|unknown[Piceasitchensis]>gi|148909190|gb|ABR17695.1|unknown[Piceasitchensis]>gi|224285451|gb|ACN40448.1|unknown[Piceasitchensis]>gi|224286224|gb|ACN40821.1|unknown[Piceasitchensis]
TRINITY_DN72579_c0_g1_i2	8.28	3.29	12.75	0.00	0.00	0.00	8.11	0.00	4.73	0.00	0.00	RL31_CYAPA	46.49	gi|751006443|	hypotheticalproteinCY34DRAFT_798013[SuillusluteusUH-Slu-Lm8-n1]
TRINITY_DN68336_c0_g1_i1	9.96	0.00	14.30	0.00	0.00	0.00	8.09	0.00	7.33	0.00	0.00	RL13_DROME	56.49	gi|594149205|	unnamedproteinproduct[Phytomonassp.isolateHart1]
TRINITY_DN140953_c0_g1_i1	7.72	6.67	9.86	0.00	0.00	0.00	8.08	0.00	1.62	0.00	0.00	CISD3_HUMAN	39.51	gi|591374824|	PREDICTED:CDGSHiron-sulfurdomain-containingprotein3
TRINITY_DN142459_c0_g1_i1	12.24	7.47	4.50	0.00	0.00	0.00	8.07	0.00	3.90	0.00	0.00	RS173_ARATH	63.48	gi|604298004|	hypotheticalproteinMIMGU_mgv1a015102mg[Erythrantheguttata]
TRINITY_DN75195_c0_g2_i1	6.62	4.93	12.63	0.00	0.00	0.00	8.06	0.00	4.05	0.00	0.00	HMT2_SCHPO	29.19	gi|765283104|	sulfide:quinoneoxidoreductase[CryptococcusgattiiNT-10]
TRINITY_DN50217_c0_g1_i1	11.96	8.22	3.99	0.00	0.00	0.00	8.06	0.00	3.99	0.00	0.00	NDUA2_NEUCR	34.57	gi|118381896|	MitochondrialribosomalproteinL51/S25/CI-B8domaincontainingprotein[Tetrahymenathermophila]
TRINITY_DN71646_c0_g2_i1	9.80	3.95	10.39	0.00	0.00	0.00	8.05	0.00	3.56	0.00	0.00	YKWD_BACSU	39.47	gi|428233991|	SCP-likeextracellular[Calothrixsp.PCC6303]
TRINITY_DN35396_c0_g1_i1	5.74	5.61	12.78	0.00	0.00	0.00	8.04	0.00	4.11	0.00	0.00	FBRL_DROER	75	gi|698801100|	rRNA2'-O-methyltransferasefibrillarin[Aphanomycesastaci]>gi|574111171|gb|ETV76667.1|rRNA2'-O-methyltransferasefibrillarin[Aphanomycesastaci]
TRINITY_DN189789_c0_g1_i1	11.19	9.55	3.24	0.00	0.00	0.00	7.99	0.00	4.20	0.00	0.00				
TRINITY_DN70615_c0_g1_i2	10.58	0.00	13.31	0.00	0.00	0.00	7.96	0.00	7.03	0.00	0.00	RS18B_SCHPO	62.42	gi|700589108|	40Sribosomalprotein[Phragmatopomalapidosa]
TRINITY_DN42168_c0_g1_i1	17.98	0.00	5.91	0.00	0.00	0.00	7.96	0.00	9.17	0.00	0.00	YJD1_SCHPO	32.31	gi|145493503|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124399861|emb|CAK65350.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN221178_c0_g1_i1	14.06	9.78	0.00	0.00	0.00	0.00	7.95	0.00	7.21	0.00	0.00				
TRINITY_DN17211_c0_g2_i1	5.85	9.64	8.28	0.00	0.00	0.00	7.93	0.00	1.92	0.00	0.00	MYCBP_MOUSE	43.9	gi|551547077|	hypotheticalproteinEMIHUDRAFT_428176[EmilianiahuxleyiCCMP1516]>gi|551603183|ref|XP_005783112.1|hypotheticalproteinEMIHUDRAFT_232476[EmilianiahuxleyiCCMP1516]>gi|485610196|gb|EOD08966.1|hypotheticalproteinEMIHUDRAFT_428176[EmilianiahuxleyiCCMP1516]>gi|485636075|gb|EOD30683.1|hypotheticalproteinEMIHUDRAFT_232476[EmilianiahuxleyiCCMP1516]
TRINITY_DN117509_c0_g1_i1	7.09	11.99	4.66	0.00	0.00	0.00	7.91	0.00	3.74	0.00	0.00	GLMM_NEIMF	39.29	gi|662502957|	hypotheticalproteinM437DRAFT_10438
TRINITY_DN149624_c0_g1_i1	11.64	4.74	7.33	0.00	0.00	0.00	7.90	0.00	3.49	0.00	0.00				
TRINITY_DN117689_c0_g1_i1	12.72	4.88	5.93	0.00	0.00	0.00	7.84	0.00	4.25	0.00	0.00	RAB2B_MAIZE	76.25	gi|731439005|	PREDICTED:ras-relatedproteinRab-2-B[Vitisvinifera]
TRINITY_DN11698_c0_g1_i1	12.16	3.98	7.31	0.00	0.00	0.00	7.81	0.00	4.12	0.00	0.00	RL17_TETTS	56.79	gi|656187350|	ribosomalproteinL17
TRINITY_DN10028_c0_g1_i1	4.74	10.84	7.86	0.00	0.00	0.00	7.81	0.00	3.05	0.00	0.00				

TRINITY_DN101634_c0_g1_i1	15.62	0.00	7.79	0.00	0.00	0.00	7.80	0.00	7.81	0.00	0.00	IF5A_MAIZE	37.88	gi|156086812|	translationinitiationfactor5A[BabesiabovisT2Bo]>gi|154798066|gb|EDO07245.1|translationinitiationfactor5A
TRINITY_DN12968_c0_g1_i1	19.96	0.00	3.44	0.00	0.00	0.00	7.80	0.00	10.67	0.00	0.00	RL24_TETTS	53.12	gi|557209227|	60SribosomalproteinL24
TRINITY_DN191097_c0_g1_i1	9.44	6.62	7.24	0.00	0.00	0.00	7.77	0.00	1.48	0.00	0.00				
TRINITY_DN64198_c0_g1_i1	10.12	5.85	7.31	0.00	0.00	0.00	7.76	0.00	2.17	0.00	0.00	RS52_ARATH	63.59	gi|145498361|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124402298|emb|CAK67771.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN10802_c0_g1_i1	9.09	7.44	6.73	0.00	0.00	0.00	7.75	0.00	1.21	0.00	0.00				
TRINITY_DN82080_c0_g3_i1	8.78	3.49	10.93	0.00	0.00	0.00	7.74	0.00	3.83	0.00	0.00	R10A_ORYSJ	49.07	gi|457874870|	60SribosomalproteinL10a
TRINITY_DN211821_c0_g1_i1	8.09	6.28	8.78	0.00	0.00	0.00	7.72	0.00	1.29	0.00	0.00				
TRINITY_DN80096_c0_g1_i3	3.60	0.00	19.55	0.00	0.00	0.00	7.72	0.00	10.40	0.00	0.00	RP25L_MOUSE	33.61	gi|72387858|	hypotheticalprotein[TrypanosomabruceibruceiTREU927]>gi|788001749|ref|XP_011772780.1|hypotheticalprotein
TRINITY_DN89560_c0_g2_i1	7.80	7.94	7.38	0.00	0.00	0.00	7.71	0.00	0.29	0.00	0.00	RL3_ASPFU	63.5	gi|646293517|	hypotheticalproteinBOTBODRAFT_32448[Botryobasidiumbotryosum FD-172SS1]
TRINITY_DN139525_c0_g1_i1	8.11	8.60	6.38	0.00	0.00	0.00	7.70	0.00	1.16	0.00	0.00				
TRINITY_DN10294_c0_g1_i1	17.10	0.00	5.93	0.00	0.00	0.00	7.68	0.00	8.68	0.00	0.00	RLA1_CHLRE	63.46	gi|147905580|	uncharacterizedproteinLOC734491[Xenopuslaevis]>gi|66910680|gb|AAH97516.1|MGC114621protein[Xenopuslaevis]
TRINITY_DN66690_c0_g3_i1	18.24	0.00	4.66	0.00	0.00	0.00	7.63	0.00	9.48	0.00	0.00	RS24_SPOFR	47.17	gi|154091274|	ribosomalproteinS24[Heliconiusmelpomene]>gi|342356363|gb|AEL28840.1|ribosomalproteinS24[Heliconiusmelpomenecythera]
TRINITY_DN49826_c0_g1_i1	9.21	9.42	4.26	0.00	0.00	0.00	7.63	0.00	2.92	0.00	0.00	SYP_DESHY	32.39	gi|118381603|	hypotheticalproteinTTHERM_00474800[Tetrahymenathermophila]
TRINITY_DN76977_c0_g1_i1	6.15	7.40	9.33	0.00	0.00	0.00	7.62	0.00	1.60	0.00	0.00				
TRINITY_DN193080_c0_g1_i1	4.60	11.41	6.86	0.00	0.00	0.00	7.62	0.00	3.47	0.00	0.00				
TRINITY_DN39171_c0_g1_i1	7.84	5.98	9.01	0.00	0.00	0.00	7.61	0.00	1.53	0.00	0.00	FRAS1_HUMAN	24.78	gi|229596783|	hypotheticalproteinTTHERM_01237400[Tetrahymenathermophila]
TRINITY_DN45978_c0_g1_i1	12.64	6.11	4.02	0.00	0.00	0.00	7.59	0.00	4.50	0.00	0.00				
TRINITY_DN114728_c0_g1_i1	16.34	0.00	6.43	0.00	0.00	0.00	7.59	0.00	8.23	0.00	0.00				
TRINITY_DN57397_c1_g1_i1	8.42	0.00	14.32	0.00	0.00	0.00	7.58	0.00	7.20	0.00	0.00	RL7_CHICK	51.04	gi|343422616|	60SribosomalproteinL7
TRINITY_DN14745_c0_g1_i1	9.31	3.48	9.90	0.00	0.00	0.00	7.56	0.00	3.55	0.00	0.00	YPC4_CAEEL	28.17	gi|814460429|	DNA-directedRNAPolymeraseII%2Clargesubunit[Burkholderiapseudomallei]
TRINITY_DN69214_c0_g1_i1	3.24	3.69	15.75	0.00	0.00	0.00	7.56	0.00	7.10	0.00	0.00	RS25_LEIIN	66.67	gi|157875487|	ribosomalproteinS25[LeishmaniamajorstrainFriedlin]>gi|68129208|emb|CAJ07745.1|ribosomalproteinS25[LeishmaniamajorstrainFriedlin]
TRINITY_DN7042_c0_g2_i1	7.90	0.00	14.79	0.00	0.00	0.00	7.56	0.00	7.40	0.00	0.00	RL9_HAECO	46.25	gi|154337200|	putative60SribosomalproteinL9[LeishmaniabraziliensisMHOM/BR/75/M2904]>gi|154342021|ref|XP_001566962.1|putative60SribosomalproteinL9[LeishmaniabraziliensisMHOM/BR/75/M2904]>gi|134061871|emb|CAM38908.1|putative60SribosomalproteinL9[LeishmaniabraziliensisMHOM/BR/75/M2904]>gi|134064287|emb|CAM40487.1|putative60SribosomalproteinL9[LeishmaniabraziliensisMHOM/BR/75/M2904]
TRINITY_DN13227_c0_g1_i1	8.96	3.59	10.12	0.00	0.00	0.00	7.56	0.00	3.48	0.00	0.00	SR34_ARATH	33.77	gi|353229125|	putativefuse-bindingprotein-interactingrepressorsiahbp1[Schistosomamansoni]
TRINITY_DN74765_c0_g2_i1	15.82	0.00	6.76	0.00	0.00	0.00	7.53	0.00	7.94	0.00	0.00	RSSA_LEIBR	50	gi|648216098|	40SribosomalproteinSA[Acyrthosiphonpisum]>gi|239788258|dbj|BAH70817.1|ACYPI004271[Acyrthosiphonpisum]
TRINITY_DN43152_c0_g1_i1	9.40	7.14	6.03	0.00	0.00	0.00	7.52	0.00	1.72	0.00	0.00	TBA_TETTH	100	gi|399146173|	alpha-tubulin
TRINITY_DN61292_c0_g1_i1	18.39	0.00	4.18	0.00	0.00	0.00	7.52	0.00	9.64	0.00	0.00	RBX1A_DROME	40.45	gi|114052775|	ringboxprotein[Bombyxmori]>gi|87248591|gb|ABD36348.1|ringboxprotein[Bombyxmori]
TRINITY_DN47409_c0_g1_i1	19.00	0.00	3.56	0.00	0.00	0.00	7.52	0.00	10.10	0.00	0.00				
TRINITY_DN79103_c0_g1_i1	5.48	10.94	6.12	0.00	0.00	0.00	7.51	0.00	2.98	0.00	0.00				
TRINITY_DN167712_c0_g1_i1	9.42	5.47	7.65	0.00	0.00	0.00	7.51	0.00	1.98	0.00	0.00				
TRINITY_DN59345_c0_g1_i1	14.95	0.00	7.55	0.00	0.00	0.00	7.50	0.00	7.48	0.00	0.00	RL7A_TETTH	55.61	gi|678330300|	60sribosomalprotein[Stylonychialemnae]
TRINITY_DN161007_c0_g1_i1	5.70	0.00	16.80	0.00	0.00	0.00	7.50	0.00	8.54	0.00	0.00				
TRINITY_DN147896_c0_g1_i1	15.39	0.00	7.11	0.00	0.00	0.00	7.50	0.00	7.71	0.00	0.00				
TRINITY_DN18431_c0_g1_i1	4.93	0.00	17.56	0.00	0.00	0.00	7.50	0.00	9.06	0.00	0.00				
TRINITY_DN41526_c0_g2_i1	9.55	0.00	12.91	0.00	0.00	0.00	7.48	0.00	6.70	0.00	0.00	BTF3_MOUSE	34.71	gi|759059526|	PREDICTED:transcriptionfactorBTF3homolog4[Cerapachysbiroi]>gi|607359695|gb|EZA54048.1|TranscriptionfactorBTF3-likeprotein[Cerapachysbiroi]
TRINITY_DN99677_c0_g1_i1	17.62	4.81	0.00	0.00	0.00	0.00	7.48	0.00	9.11	0.00	0.00				
TRINITY_DN78841_c0_g1_i1	15.23	0.00	7.14	0.00	0.00	0.00	7.46	0.00	7.62	0.00	0.00	GILT_BOVIN	34.95	gi|698975134|	gamma-interferon-induciblelysosomalthiolreductase[Stichopusmonotuberculatus]
TRINITY_DN40553_c0_g1_i1	7.46	5.15	9.76	0.00	0.00	0.00	7.46	0.00	2.30	0.00	0.00	HSP90_EIMTE	69.91	gi|134037070|	heatshockprotein901[Alexandriumfundyense]
TRINITY_DN43434_c0_g1_i1	0.00	17.10	5.22	0.00	0.00	0.00	7.44	0.00	8.76	0.00	0.00				
TRINITY_DN83865_c0_g1_i1	4.08	5.89	12.33	0.00	0.00	0.00	7.43	0.00	4.34	0.00	0.00				
TRINITY_DN53320_c0_g1_i2	8.27	0.00	14.01	0.00	0.00	0.00	7.43	0.00	7.04	0.00	0.00				
TRINITY_DN63301_c1_g1_i1	10.22	0.00	12.05	0.00	0.00	0.00	7.42	0.00	6.49	0.00	0.00	RL22_TETTS	60.19	gi|734338066|	60SribosomalproteinL22-2[Glycinesoja]
TRINITY_DN87163_c1_g3_i2	11.96	0.00	10.29	0.00	0.00	0.00	7.42	0.00	6.48	0.00	0.00	RL40_TRYBB	95.73	gi|170595239|	ubiquitin-likeprotein[Brugiamalayi]>gi|402587591|gb|EJW81526.1|ubiquitin/ribosomalfusionprotein[Wuchereriabancrofti]
TRINITY_DN75026_c0_g1_i2	11.87	0.00	10.35	0.00	0.00	0.00	7.41	0.00	6.46	0.00	0.00	RS2_LEIAM	83.08	gi|157868060|	40SribosomalproteinS2[LeishmaniamajorstrainFriedlin]>gi|68126038|emb|CAJ07091.1|40SribosomalproteinS2[LeishmaniamajorstrainFriedlin]
TRINITY_DN102445_c0_g1_i1	7.15	6.80	8.27	0.00	0.00	0.00	7.41	0.00	0.77	0.00	0.00				
TRINITY_DN164522_c0_g1_i1	8.23	8.01	5.94	0.00	0.00	0.00	7.39	0.00	1.27	0.00	0.00				
TRINITY_DN62443_c0_g1_i2	8.29	0.00	13.84	0.00	0.00	0.00	7.38	0.00	6.97	0.00	0.00	RL4_TRYBB	82.86	gi|588320890|	unnamedproteinproduct[Phytomonassp.isolateEM1]
TRINITY_DN187510_c0_g1_i1	5.73	0.00	16.35	0.00	0.00	0.00	7.36	0.00	8.29	0.00	0.00				
TRINITY_DN67025_c0_g1_i1	4.20	6.92	10.89	0.00	0.00	0.00	7.33	0.00	3.36	0.00	0.00	ACTO_ACACA	61.64	gi|67467176|	actobindin[EntamoebahistolyticaHM-1:IMSS]>gi|672811386|ref|XP_008860731.1|actobindin
TRINITY_DN4100_c0_g1_i1	6.04	8.20	7.71	0.00	0.00	0.00	7.32	0.00	1.13	0.00	0.00				
TRINITY_DN167383_c0_g1_i1	10.02	6.43	5.41	0.00	0.00	0.00	7.29	0.00	2.42	0.00	0.00				
TRINITY_DN71873_c0_g1_i1	9.13	9.00	3.72	0.00	0.00	0.00	7.28	0.00	3.08	0.00	0.00	RS9_DICDI	63.59	gi|698587868|	PREDICTED:40SribosomalproteinS9-2-like[Nicotianasylvestris]
TRINITY_DN83552_c0_g1_i2	8.86	0.00	12.90	0.00	0.00	0.00	7.25	0.00	6.60	0.00	0.00	RL22L_MOUSE	42.24	gi|554947845|	60SribosomalproteinL22[TrypanosomarangeliSC58]
TRINITY_DN61121_c0_g1_i1	14.94	0.00	6.79	0.00	0.00	0.00	7.24	0.00	7.48	0.00	0.00				
TRINITY_DN28035_c0_g1_i1	18.15	3.56	0.00	0.00	0.00	0.00	7.24	0.00	9.62	0.00	0.00	TBA2_ELEIN	100	gi|224286005|	unknown[Piceasitchensis]
TRINITY_DN195822_c0_g1_i1	7.16	0.00	14.53	0.00	0.00	0.00	7.23	0.00	7.27	0.00	0.00				

TRINITY_DN77016_c0_g1_i1	9.09	0.00	12.59	0.00	0.00	0.00	7.23	0.00	6.50	0.00	0.00	CC2H3_TRYBB	84.75	gi|157876562|	celldivisionrelatedproteinkinase2[LeishmaniamajorstrainFriedlin]>gi|4185262|gb|AAD08994.1|cdc2-relatedkinase[Leishmaniamajor]>gi|68129702|emb|CAJ09008.1|celldivisionrelatedproteinkinase2[LeishmaniamajorstrainFriedlin]
TRINITY_DN118229_c0_g1_i1	12.89	8.78	0.00	0.00	0.00	0.00	7.22	0.00	6.59	0.00	0.00				
TRINITY_DN83849_c0_g1_i1	7.78	6.78	7.10	0.00	0.00	0.00	7.22	0.00	0.51	0.00	0.00	RS2_DROME	68.18	gi|646721266|	40SribosomalproteinS2[Zootermopsisnevadensis]
TRINITY_DN70201_c0_g1_i1	11.53	0.00	10.09	0.00	0.00	0.00	7.21	0.00	6.28	0.00	0.00	CYSP2_MAIZE	56.6	gi|162460343|	cysteineprotease2precursor[Zeamays]>gi|1491774|emb|CAA68192.1|cysteineprotease[Zeamays]
TRINITY_DN71515_c0_g1_i1	7.59	0.00	14.03	0.00	0.00	0.00	7.21	0.00	7.02	0.00	0.00	RS10A_DROME	48.98	gi|780608837|	PREDICTED:40SribosomalproteinS10-like[Wasmanniaauropunctata]
TRINITY_DN77204_c0_g1_i1	4.42	4.03	13.09	0.00	0.00	0.00	7.18	0.00	5.12	0.00	0.00	HSP7M_EMENI	66.02	gi|31790767|	heatshockprotein70precursor[Neocallimastixpatriciarum]
TRINITY_DN42860_c0_g1_i1	17.72	0.00	3.78	0.00	0.00	0.00	7.17	0.00	9.33	0.00	0.00	YBEY_ECO81	37.21	gi|403355551|	hypotheticalproteinOXYTRI_01013[Oxytrichatrifallax]
TRINITY_DN60285_c0_g1_i1	0.00	8.78	12.71	0.00	0.00	0.00	7.16	0.00	6.51	0.00	0.00				
TRINITY_DN177746_c0_g1_i1	13.24	8.19	0.00	0.00	0.00	0.00	7.14	0.00	6.68	0.00	0.00				
TRINITY_DN90563_c0_g4_i1	11.08	3.61	6.73	0.00	0.00	0.00	7.14	0.00	3.75	0.00	0.00	H4_CANGA	56.25	gi|290994346|	histoneH4[Naegleriagruberi]>gi|284093411|gb|EFC47049.1|histoneH4[Naegleriagruberi]
TRINITY_DN2446_c0_g2_i1	10.53	0.00	10.86	0.00	0.00	0.00	7.13	0.00	6.18	0.00	0.00	RL31_TETTS	54.74	gi|301101838|	60SribosomalproteinL31
TRINITY_DN40389_c0_g1_i1	6.94	3.87	10.53	0.00	0.00	0.00	7.11	0.00	3.34	0.00	0.00				
TRINITY_DN81665_c0_g1_i1	8.24	0.00	13.07	0.00	0.00	0.00	7.10	0.00	6.61	0.00	0.00	CALM_TRYCR	100	gi|599385440|	hypotheticalproteinPHACADRAFT_259505[PhanerochaetecarnosaHHB-10118-sp]>gi|630361895|ref|XP_007870222.1|EF-hand[GloeophyllumtrabeumATCC11539]>gi|392050718|dbj|BAM24398.1|calmodulin[Phanerochaetechrysosporium]>gi|409043790|gb|EKM53272.1|hypotheticalproteinPHACADRAFT_259505[PhanerochaetecarnosaHHB-10118-sp]>gi|521720791|gb|EPQ51217.1|EF-hand[GloeophyllumtrabeumATCC11539]
TRINITY_DN39267_c0_g1_i1	9.44	11.87	0.00	0.00	0.00	0.00	7.10	0.00	6.27	0.00	0.00				
TRINITY_DN54495_c0_g1_i1	15.56	0.00	5.75	0.00	0.00	0.00	7.10	0.00	7.87	0.00	0.00	RS24B_SCHPO	58.82	gi|157690772|	TPA:putative40SribosomalproteinS24[Spadellacephaloptera]
TRINITY_DN74839_c0_g2_i1	13.74	0.00	7.52	0.00	0.00	0.00	7.09	0.00	6.88	0.00	0.00	CB25_TETTH	33.73	gi|471229598|	hypotheticalproteinIMG5_094250[Ichthyophthiriusmultifiliis]>gi|340505884|gb|EGR32162.1|hypotheticalproteinIMG5_094250[Ichthyophthiriusmultifiliis]
TRINITY_DN40768_c0_g1_i1	8.00	0.00	13.25	0.00	0.00	0.00	7.08	0.00	6.67	0.00	0.00	ATPA_CAEEL	81.94	gi|162719|	ATPsynthasealphasubunitprecursor
TRINITY_DN86102_c0_g1_i3	7.94	0.00	13.27	0.00	0.00	0.00	7.07	0.00	6.68	0.00	0.00	RS6_LEIMA	74.54	gi|528239961|	smallsubunitribosomalproteinS6e[Strigomonasculicis]
TRINITY_DN37048_c0_g1_i1	16.92	0.00	4.26	0.00	0.00	0.00	7.06	0.00	8.80	0.00	0.00	CATR4_PARTE	50.69	gi|1276639|	centrinICL1b
TRINITY_DN33046_c0_g1_i1	4.46	3.25	13.43	0.00	0.00	0.00	7.05	0.00	5.56	0.00	0.00	CAN13_HUMAN	35	gi|118397513|	hypotheticalproteinTTHERM_00939150[Tetrahymenathermophila]>gi|586729751|gb|EWS72332.1|hypotheticalproteinTTHERM_000939159[TetrahymenathermophilaSB210]
TRINITY_DN27324_c0_g1_i1	9.92	4.74	6.47	0.00	0.00	0.00	7.04	0.00	2.64	0.00	0.00	P4R2A_DANRE	37.88	gi|146182118|	hypotheticalproteinTTHERM_00475329[Tetrahymenathermophila]>gi|146143969|gb|EDK31410.1|serine/threonineproteinphosphatase4regulatorysubunit
TRINITY_DN213931_c0_g1_i1	6.47	7.13	7.45	0.00	0.00	0.00	7.02	0.00	0.50	0.00	0.00				
TRINITY_DN67780_c0_g1_i1	5.69	0.00	15.35	0.00	0.00	0.00	7.01	0.00	7.76	0.00	0.00	RL21_CYAPA	61.54	gi|594144037|	unnamedproteinproduct[Phytomonassp.isolateHart1]>gi|594150037|emb|CCW66440.1|unnamedproteinproduct[Phytomonassp.isolateHart1]
TRINITY_DN32649_c0_g1_i1	8.03	3.89	9.11	0.00	0.00	0.00	7.01	0.00	2.76	0.00	0.00				
TRINITY_DN77809_c0_g3_i1	6.29	6.14	8.59	0.00	0.00	0.00	7.01	0.00	1.37	0.00	0.00	HSS_RHILO	51.68	gi|653548826|	homospermidinesynthase[Bradyrhizobiumsp.Ai1a-2]
TRINITY_DN129430_c0_g1_i1	4.34	4.97	11.65	0.00	0.00	0.00	6.99	0.00	4.05	0.00	0.00	LYSG2_DICDI	46.25	gi|167520334|	hypotheticalprotein[MonosigabrevicollisMX1]>gi|163776837|gb|EDQ90455.1|predictedprotein[MonosigabrevicollisMX1]
TRINITY_DN80573_c0_g1_i1	5.96	8.44	6.53	0.00	0.00	0.00	6.97	0.00	1.30	0.00	0.00	TCTP_SCHPO	51.79	gi|6322794|	Tma19p[SaccharomycescerevisiaeS288c]>gi|549064|sp|P35691.1|TCTP_YEASTRecName:Full=Translationally-controlledtumorproteinhomolog;Short=TCTP;AltName:Full=Microtubuleandmitochondria-interactingprotein1;AltName:Full=Translationmachinery-associatedprotein19[SaccharomycescerevisiaeS288c]>gi|433641|emb|CAA53416.1|E167[Saccharomycescerevisiae]>gi|486151|emb|CAA81893.1|unnamedproteinproduct[Saccharomycescerevisiae]>gi|190409773|gb|EDV13038.1|hypotheticalproteinSCRG_03964[SaccharomycescerevisiaeRM11-1a]>gi|256272456|gb|EEU07437.1|Tma19p[SaccharomycescerevisiaeJAY291]>gi|259147782|emb|CAY81032.1|Tma19p[SaccharomycescerevisiaeEC1118]>gi|285813204|tpg|DAA09101.1|TPA:Tma19p[SaccharomycescerevisiaeS288c]>gi|323304090|gb|EGA57868.1|Tma19p[SaccharomycescerevisiaeFostersB]>gi|323308284|gb|EGA61532.1|Tma19p[SaccharomycescerevisiaeFostersO]>gi|323332782|gb|EGA74187.1|Tma19p[SaccharomycescerevisiaeAWRI796]>gi|323354092|gb|EGA85938.1|Tma19p[SaccharomycescerevisiaeVL3]>gi|365764608|gb|EHN06130.1|Tma19p[SaccharomycescerevisiaexSaccharomyceskudriavzeviiVIN7]>gi|392298082|gb|EIW09180.1|Tma19p[SaccharomycescerevisiaeCEN.PK113-7D]>gi|584370144|gb|EWG90095.1|Tma19p[SaccharomycescerevisiaeP301]>gi|584375052|gb|EWG94943.1|Tma19p[SaccharomycescerevisiaeR103]>gi|584475569|gb|EWH17324.1|Tma19p[SaccharomycescerevisiaeP283]>gi|628182327|gb|AHY76187.1|Tma19p[SaccharomycescerevisiaeYJM993]>gi|761508789|gb|AJP39981.1|Tma19p[SaccharomycescerevisiaeYJM1078]>gi|767008508|gb|AJS30179.1|Tma19p[SaccharomycescerevisiaeYJM189]>gi|767009279|gb|AJS30481.1|Tma19p[SaccharomycescerevisiaeYJM193]>gi|767009879|gb|AJS31079.1|Tma19p[SaccharomycescerevisiaeYJM244]>gi|767010175|gb|AJS31374.1|Tma19p[SaccharomycescerevisiaeYJM248]>gi|767010478|gb|AJS31676.1|Tma19p[SaccharomycescerevisiaeYJM270]>gi|767010796|gb|AJS31976.1|Tma19p[SaccharomycescerevisiaeYJM271]>gi|767027312|gb|AJS33720.1|Tma19p[SaccharomycescerevisiaeYJM453]>gi|767033254|gb|AJS34624.1|Tma19p[SaccharomycescerevisiaeYJM541]>gi|767039866|gb|AJS35224.1|Tma19p[SaccharomycescerevisiaeYJM555]>gi|767046533|gb|AJS36720.1|Tma19p[SaccharomycescerevisiaeYJM689]>gi|767049795|gb|AJS37019.1|Tma19p[SaccharomycescerevisiaeYJM693]>gi|767050096|gb|AJS37319.1|Tma19p[Saccharomycescer
TRINITY_DN31820_c0_g1_i1	7.82	5.07	8.00	0.00	0.00	0.00	6.96	0.00	1.64	0.00	0.00				

TRINITY_DN190912_c0_g1_i1	9.05	3.93	7.90	0.00	0.00	0.00	6.96	0.00	2.69	0.00	0.00				
TRINITY_DN86420_c0_g3_i1	7.91	0.00	12.93	0.00	0.00	0.00	6.95	0.00	6.52	0.00	0.00	RS13_SOYBN	71.23	gi|694420403|	PREDICTED:40SribosomalproteinS13-like[Pyrusxbretschneideri]>gi|694439924|ref|XP_009346809.1|PREDICTED:40SribosomalproteinS13-like[Pyrusxbretschneideri]
TRINITY_DN41793_c0_g1_i1	3.22	9.31	8.28	0.00	0.00	0.00	6.94	0.00	3.26	0.00	0.00				
TRINITY_DN54139_c0_g2_i1	7.40	9.85	3.52	0.00	0.00	0.00	6.92	0.00	3.19	0.00	0.00				
TRINITY_DN79463_c0_g1_i1	11.67	5.76	3.31	0.00	0.00	0.00	6.92	0.00	4.30	0.00	0.00				
TRINITY_DN147486_c0_g1_i1	14.11	6.63	0.00	0.00	0.00	0.00	6.91	0.00	7.06	0.00	0.00				
TRINITY_DN187091_c0_g1_i1	15.96	0.00	4.69	0.00	0.00	0.00	6.88	0.00	8.20	0.00	0.00				
TRINITY_DN133372_c0_g1_i1	12.30	4.01	4.32	0.00	0.00	0.00	6.88	0.00	4.70	0.00	0.00				
TRINITY_DN73841_c0_g1_i2	7.56	0.00	13.00	0.00	0.00	0.00	6.85	0.00	6.53	0.00	0.00	NTF2_ARATH	35.04	gi|573914311|	PREDICTED:nucleartransportfactor2-like[Oryzabrachyantha]
TRINITY_DN167910_c0_g1_i1	5.45	7.25	7.85	0.00	0.00	0.00	6.85	0.00	1.25	0.00	0.00				
TRINITY_DN92082_c4_g8_i2	7.26	0.00	13.24	0.00	0.00	0.00	6.83	0.00	6.63	0.00	0.00	CYSP_TRYCR	49.06	gi|72389853|	cysteinepeptidaseprecursor[Trypanosomabruceibruceiprecursor[Trypanosomabrucei]>gi|62359929|gb|AAX80354.1|cysteinepeptidaseprecursor[Trypanosomabrucei]>gi|70801756|gb|AAZ11662.1|cysteinepeptidaseprecursor[Trypanosomabruceibruceiprecursor[Trypanosomabrucei]
TRINITY_DN68976_c0_g1_i1	5.15	15.35	0.00	0.00	0.00	0.00	6.83	0.00	7.81	0.00	0.00				
TRINITY_DN77775_c0_g1_i1	7.21	5.94	7.34	0.00	0.00	0.00	6.83	0.00	0.77	0.00	0.00	RL14_HUMAN	47.15	gi|58260222|	ribosomalprotein[Cryptococcusneoformansvar.neoformansJEC21]>gi|134116346|ref|XP_773127.1|60SribosomalproteinL14[Cryptococcusneoformansvar.neoformansB-3501A]>gi|50255748|gb|EAL18480.1|hypotheticalproteinCNBJ1220[Cryptococcusneoformansvar.neoformansB-3501A]>gi|57229571|gb|AAW46004.1|ribosomalprotein
TRINITY_DN69982_c0_g1_i1	8.14	9.07	3.27	0.00	0.00	0.00	6.83	0.00	3.11	0.00	0.00	RL23_DANRE	75.38	gi|10121725|	ribosomalproteinL23[Gillichthysmirabilis]
TRINITY_DN60364_c0_g2_i1	9.86	4.32	6.27	0.00	0.00	0.00	6.82	0.00	2.81	0.00	0.00				
TRINITY_DN120260_c0_g1_i1	10.04	3.54	6.86	0.00	0.00	0.00	6.81	0.00	3.25	0.00	0.00	RS15_ORYSJ	53.66	gi|255551941|	40SribosomalproteinS15
TRINITY_DN17216_c0_g1_i1	13.60	0.00	6.78	0.00	0.00	0.00	6.79	0.00	6.80	0.00	0.00	RS29_ASHGO	66.67	gi|367014161|	40SribosomalproteinS29[Torulasporadelbrueckii]>gi|359749241|emb|CCE92369.1|hypotheticalproteinTDEL_0E01260[Torulasporadelbrueckii]
TRINITY_DN68127_c0_g1_i1	5.94	9.04	5.40	0.00	0.00	0.00	6.79	0.00	1.97	0.00	0.00	FRAS1_HUMAN	26.97	gi|154331996|	surfaceantigen-likeprotein[LeishmaniabraziliensisMHOM/BR/75/M2904]>gi|134059135|emb|CAM41611.1|surfaceantigen-likeprotein[LeishmaniabraziliensisMHOM/BR/75/M2904]
TRINITY_DN89629_c3_g26_i1	7.88	8.47	4.00	0.00	0.00	0.00	6.78	0.00	2.43	0.00	0.00	UBIQP_HORVU	94.68	gi|584233472|	polyubiquitin
TRINITY_DN61325_c0_g1_i1	3.66	0.00	16.66	0.00	0.00	0.00	6.77	0.00	8.76	0.00	0.00	ACT10_SOLTU	100	gi|301641376|	actin[Panonychuscitri]
TRINITY_DN77932_c0_g1_i1	6.13	8.37	5.79	0.00	0.00	0.00	6.76	0.00	1.40	0.00	0.00	NDK_GEOKA	65.31	gi|656013095|	nucleosidediphosphatekinase[Sporosarcinaureae]
TRINITY_DN63140_c0_g2_i1	8.64	7.79	3.83	0.00	0.00	0.00	6.75	0.00	2.57	0.00	0.00	BIKB_THET8	32.84	gi|403366781|	hypotheticalproteinOXYTRI_19183[Oxytrichatrifallax]
TRINITY_DN90568_c0_g5_i2	4.32	7.18	8.75	0.00	0.00	0.00	6.75	0.00	2.25	0.00	0.00	RL4A_ARATH	59.59	gi|567169707|	hypotheticalproteinEUTSA_v10013700mg[Eutremasalsugineum]>gi|557099833|gb|ESQ40196.1|hypotheticalproteinEUTSA_v10013700mg[Eutremasalsugineum]
TRINITY_DN193415_c0_g1_i1	7.53	4.54	8.17	0.00	0.00	0.00	6.75	0.00	1.94	0.00	0.00				
TRINITY_DN56465_c0_g1_i1	4.24	9.27	6.72	0.00	0.00	0.00	6.75	0.00	2.51	0.00	0.00	KEX1_CRYGW	27.27	gi|678314590|	UNKNOWN[Stylonychialemnae]
TRINITY_DN26318_c0_g1_i1	6.24	4.23	9.74	0.00	0.00	0.00	6.74	0.00	2.79	0.00	0.00	RL13A_TETTS	63.08	gi|634351824|	60SribosomalproteinL16[Microbotryumviolaceump1A1Lamole]
TRINITY_DN36590_c0_g1_i1	5.17	6.55	8.48	0.00	0.00	0.00	6.74	0.00	1.66	0.00	0.00				
TRINITY_DN65118_c0_g1_i1	16.58	0.00	3.57	0.00	0.00	0.00	6.72	0.00	8.73	0.00	0.00	RLA0_OXYRB	40.64	gi|302785041|	hypotheticalproteinSELMODRAFT_149765[Selaginellamoellendorffii]>gi|302807947|ref|XP_002985667.1|hypotheticalproteinSELMODRAFT_181962[Selaginellamoellendorffii]>gi|300146576|gb|EFJ13245.1|hypotheticalproteinSELMODRAFT_181962[Selaginellamoellendorffii]>gi|300157890|gb|EFJ24514.1|hypotheticalproteinSELMODRAFT_149765[Selaginellamoellendorffii]
TRINITY_DN189892_c0_g1_i1	12.52	3.80	3.81	0.00	0.00	0.00	6.71	0.00	5.03	0.00	0.00				
TRINITY_DN70861_c0_g1_i1	7.48	9.22	3.41	0.00	0.00	0.00	6.71	0.00	2.98	0.00	0.00	CYC_FRIAG	63.81	gi|670447187|	PREDICTED:cytochromec-like[Zeamays]>gi|413920117|gb|AFW60049.1|cytochromec[Zeamays]
TRINITY_DN87904_c0_g1_i1	6.29	5.29	8.51	0.00	0.00	0.00	6.70	0.00	1.65	0.00	0.00	PHYSA_PHYPO	45.57	gi|657734121|	PREDICTED:tripeptidyl-peptidase1isoformX1[Cynoglossussemilaevis]
TRINITY_DN39412_c0_g1_i1	16.86	0.00	3.19	0.00	0.00	0.00	6.69	0.00	8.96	0.00	0.00	ACBP_DROME	48.86	gi|564242440|	PREDICTED:acyl-CoA-bindingprotein[Alligatormississippiensis]
TRINITY_DN76810_c0_g1_i1	0.00	14.51	5.46	0.00	0.00	0.00	6.66	0.00	7.33	0.00	0.00	S12A3_HUMAN	50	gi|763086486|	osmoticallyinducibleproteinC[Anoxybacillusthermarum]>gi|756576233|gb|KIQ93774.1|peroxiredoxin
TRINITY_DN95942_c0_g1_i1	9.55	3.41	6.99	0.00	0.00	0.00	6.65	0.00	3.09	0.00	0.00	RL13_TETTS	50.25	gi|743872997|	PREDICTED:60SribosomalproteinL13-1-like[Elaeisguineensis]
TRINITY_DN83428_c0_g3_i1	4.26	3.45	12.15	0.00	0.00	0.00	6.62	0.00	4.81	0.00	0.00	EF1A2_TRYB2	83.56	gi|704459|	elongationfactor1alpha[Trypanosomacruzi]
TRINITY_DN27366_c0_g1_i1	10.61	0.00	9.24	0.00	0.00	0.00	6.62	0.00	5.77	0.00	0.00	DYL1_RAT	50	gi|350535837|	putativedyneincytoplasmiclightpeptidevariant3[Taeniopygiaguttata]>gi|327282608|ref|XP_003226034.1|PREDICTED:dyneinlightchain1
TRINITY_DN30452_c0_g1_i1	0.00	6.86	12.97	0.00	0.00	0.00	6.61	0.00	6.49	0.00	0.00				
TRINITY_DN65457_c0_g1_i1	15.50	4.32	0.00	0.00	0.00	0.00	6.60	0.00	8.00	0.00	0.00	SODM_PEA	66.67	gi|569406320|	superoxidedismutase[Reticulomyxafilosa]
TRINITY_DN47834_c0_g1_i1	13.11	6.70	0.00	0.00	0.00	0.00	6.60	0.00	6.56	0.00	0.00	RACB_DICDI	90.2	gi|754379811|	hypotheticalproteinPHLGIDRAFT_17570[Phlebiopsisgigantea11061_1CR5-6]
TRINITY_DN5479_c0_g1_i1	11.82	3.45	4.48	0.00	0.00	0.00	6.58	0.00	4.56	0.00	0.00	Y1608_CALS4	44.83	gi|403353014|	hypotheticalproteinOXYTRI_02457[Oxytrichatrifallax]
TRINITY_DN121835_c0_g1_i1	5.50	11.02	3.21	0.00	0.00	0.00	6.58	0.00	4.01	0.00	0.00	CATR5_PARTE	39.19	gi|145539173|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124423080|emb|CAK87884.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN172580_c0_g1_i1	0.00	8.70	11.03	0.00	0.00	0.00	6.58	0.00	5.81	0.00	0.00				
TRINITY_DN78575_c0_g1_i1	7.22	5.50	7.00	0.00	0.00	0.00	6.57	0.00	0.93	0.00	0.00				
TRINITY_DN9300_c0_g1_i1	12.01	0.00	7.70	0.00	0.00	0.00	6.57	0.00	6.09	0.00	0.00	YGU5_SCHPO	50	gi|818162564|	hypotheticalproteinTHAR02_05425[Trichodermaharzianum]
TRINITY_DN81856_c0_g1_i2	4.54	8.62	6.53	0.00	0.00	0.00	6.56	0.00	2.04	0.00	0.00	LEC_GALNI	44.44	gi|166353|	Ilectin
TRINITY_DN41852_c0_g1_i1	4.62	6.31	8.70	0.00	0.00	0.00	6.54	0.00	2.05	0.00	0.00				
TRINITY_DN186559_c0_g1_i1	7.44	5.41	6.68	0.00	0.00	0.00	6.51	0.00	1.03	0.00	0.00				
TRINITY_DN12648_c0_g1_i1	7.25	5.95	6.32	0.00	0.00	0.00	6.51	0.00	0.67	0.00	0.00	CATR6_PARTE	58.06	gi|635364260|	unnamedproteinproduct[Albugocandida]
TRINITY_DN48358_c0_g1_i1	9.41	5.32	4.75	0.00	0.00	0.00	6.50	0.00	2.54	0.00	0.00	RLA1_CHICK	62.5	gi|545368863|	ribosomalprotein60S[CoccomyxasubellipsoideaC-169]>gi|384251184|gb|EIE24662.1|ribosomalprotein60S[CoccomyxasubellipsoideaC-169]
TRINITY_DN117531_c0_g1_i1	5.92	7.37	6.19	0.00	0.00	0.00	6.49	0.00	0.77	0.00	0.00	MALE_SALTY	38.3	gi|667483467|	secretedprotein
TRINITY_DN114232_c0_g1_i1	4.95	4.01	10.50	0.00	0.00	0.00	6.49	0.00	3.50	0.00	0.00	CATZ_BOVIN	41.32	gi|325180819|	cathepsinlikecysteineproteaseputative[AlbugolaibachiiNc14]
TRINITY_DN7982_c0_g1_i1	6.15	4.01	9.26	0.00	0.00	0.00	6.48	0.00	2.64	0.00	0.00				

TRINITY_DN231682_c0_g1_i1	9.26	4.97	5.14	0.00	0.00	0.00	6.46	0.00	2.43	0.00	0.00			
TRINITY_DN14122_c0_g2_i1	8.85	3.36	7.14	0.00	0.00	0.00	6.45	0.00	2.81	0.00	0.00			
TRINITY_DN60436_c0_g1_i1	7.27	7.38	4.63	0.00	0.00	0.00	6.43	0.00	1.56	0.00	0.00	EF1A_ENTHI	83.15	gi|71406243| elongationfactor1-alpha(EF-1-alpha)[TrypanosomacruzistrainCLBrener]>gi|70869174|gb|EAN83825.1|elongationfactor1-alpha(EF-1-alpha)
TRINITY_DN109403_c0_g1_i1	0.00	3.41	15.87	0.00	0.00	0.00	6.43	0.00	8.35	0.00	0.00	UB2D4_HUMAN	83.78	gi|813212089| hypotheticalproteinG7K_2323-t1[SaitoellacomplicataNRRLY-17804]
TRINITY_DN12398_c0_g1_i1	9.42	6.22	3.62	0.00	0.00	0.00	6.42	0.00	2.91	0.00	0.00	GSTM3_HUMAN	31.56	gi|666420401| glutathioneS-transferase[Parameciumcaudatum]
TRINITY_DN189705_c0_g1_i1	8.01	7.69	3.53	0.00	0.00	0.00	6.41	0.00	2.50	0.00	0.00			
TRINITY_DN84524_c0_g1_i1	4.28	11.34	3.61	0.00	0.00	0.00	6.41	0.00	4.28	0.00	0.00	TRHN1_CHLMO	49.58	gi|652903285| globin[Methylobacterluteus]
TRINITY_DN143377_c0_g1_i1	8.45	5.39	5.38	0.00	0.00	0.00	6.41	0.00	1.77	0.00	0.00	YPTC1_CHLRE	66.67	gi|358248394| uncharacterizedproteinLOC100796206[Glycinemax]>gi|414832|gb|AAA34003.1|Rab7p[Glycinemax]>gi|734346277|gb|KHN11052.1|Ras-relatedproteinRABD1[Glycinesoja]
TRINITY_DN78541_c0_g1_i1	4.25	6.78	8.17	0.00	0.00	0.00	6.40	0.00	1.99	0.00	0.00	MD37E_ARATH	85.12	gi|595814637| hypotheticalproteinPRUPE_ppa002595mg[Prunuspersica]>gi|462399305|gb|EMJ04973.1|hypotheticalproteinPRUPE_ppa002595mg[Prunuspersica]
TRINITY_DN220223_c0_g1_i1	3.58	0.00	15.58	0.00	0.00	0.00	6.39	0.00	8.16	0.00	0.00			
TRINITY_DN38239_c0_g1_i1	12.53	6.62	0.00	0.00	0.00	0.00	6.38	0.00	6.27	0.00	0.00	CH10_BRANA	45.26	gi|695052315| PREDICTED:10kDachaperonin-like[Musaacuminatasubsp.malaccensis]
TRINITY_DN79496_c0_g2_i1	6.26	6.23	6.63	0.00	0.00	0.00	6.38	0.00	0.22	0.00	0.00	PRDX2_BOVIN	70.1	gi|27807469| peroxiredoxin-2[Bostaurus]>gi|528954915|ref|XP_005208710.1|PREDICTED:peroxiredoxin-2isoformX1[Bostaurus]>gi|555977262|ref|XP_005900588.1|PREDICTED:peroxiredoxin-2[Bosmutus]>gi|741931839|ref|XP_010805021.1|PREDICTED:peroxiredoxin-2isoformX1[Bostaurus]>gi|742184883|ref|XP_010853770.1|PREDICTED:peroxiredoxin-2[Bisonbisonbison]>gi|22095988|sp|Q9BGI3.1|PRDX2_BOVINRecName:Full=Peroxiredoxin-2[Bostaurus]>gi|12407847|gb|AAG53659.1|AF305562_1peroxiredoxin2[Bostaurus]>gi|74353992|gb|AAI02352.1|PRDX2protein[Bostaurus]>gi|296485908|tpg|DAA28023.1|TPA:peroxiredoxin-2[Bostaurus]>gi|440902071|gb|ELR52914.1|Peroxiredoxin-2[Bosmutus]
TRINITY_DN4181_c0_g2_i1	8.11	3.43	7.55	0.00	0.00	0.00	6.36	0.00	2.56	0.00	0.00			
TRINITY_DN13151_c0_g1_i1	3.21	0.00	15.84	0.00	0.00	0.00	6.35	0.00	8.37	0.00	0.00			
TRINITY_DN86325_c0_g1_i1	9.96	0.00	9.06	0.00	0.00	0.00	6.34	0.00	5.51	0.00	0.00	YOM2_SCHPO	29.41	gi|401421148| conservedhypotheticalprotein[LeishmaniamexicanaMHOM/GT/2001/U1103]>gi|322491299|emb|CBZ26567.1|conservedhypotheticalprotein[LeishmaniamexicanaMHOM/GT/2001/U1103]
TRINITY_DN85564_c0_g2_i1	3.68	3.95	11.37	0.00	0.00	0.00	6.33	0.00	4.36	0.00	0.00	RSSA_LEIIN	71.56	gi|528245450| smallsubunitribosomalproteinSAe[Angomonasdeanei]
TRINITY_DN202281_c0_g1_i1	15.72	3.26	0.00	0.00	0.00	0.00	6.33	0.00	8.30	0.00	0.00			
TRINITY_DN80494_c1_g1_i1	5.54	5.28	8.13	0.00	0.00	0.00	6.31	0.00	1.57	0.00	0.00	LPXD_CAMJR	25.74	gi|551559272| hypotheticalproteinEMIHUDRAFT_421996[EmilianiahuxleyiCCMP1516]>gi|485616891|gb|EOD14144.1|hypotheticalproteinEMIHUDRAFT_421996[EmilianiahuxleyiCCMP1516]
TRINITY_DN26320_c0_g1_i1	7.48	5.55	5.91	0.00	0.00	0.00	6.31	0.00	1.03	0.00	0.00			
TRINITY_DN69535_c0_g1_i1	4.11	7.83	6.97	0.00	0.00	0.00	6.30	0.00	1.95	0.00	0.00	RIDA_ARATH	60	gi|471865566| RutCfamilyproteinPH0854[RhizoctoniasolaniAG-1IB]>gi|751835258|emb|CEL56062.1|RutCfamilyproteinPH0854OS=Pyrococcushorikoshii(strainATCC700860/DSM12428/JCM9974/NBRC100139/OT-3)GN=PH0854PE=1SV=2[RhizoctoniasolaniAG-1IB]
TRINITY_DN71031_c0_g1_i1	7.83	3.20	7.86	0.00	0.00	0.00	6.30	0.00	2.68	0.00	0.00	CDPK4_PLAYO	50	gi|403360460| Proteinkinasedomaincontainingprotein[Oxytrichatrifallax]
TRINITY_DN103760_c0_g1_i1	3.68	6.39	8.77	0.00	0.00	0.00	6.28	0.00	2.54	0.00	0.00	CATR1_PARTE	33.33	gi|662536533| hypotheticalproteinAUEXF2481DRAFT_6419[AureobasidiumsubglacialeEXF-2481]
TRINITY_DN83818_c0_g1_i1	7.14	0.00	11.70	0.00	0.00	0.00	6.28	0.00	5.90	0.00	0.00	RL18_TRYB2	75.13	gi|154333852| putative60SribosomalproteinL18[LeishmaniabraziliensisMHOM/BR/75/M2904]>gi|134060193|emb|CAM45601.1|putative60SribosomalproteinL18[LeishmaniabraziliensisMHOM/BR/75/M2904]
TRINITY_DN52962_c0_g1_i1	15.22	0.00	3.61	0.00	0.00	0.00	6.28	0.00	7.95	0.00	0.00	RS14_MOUSE	74.4	gi|116488050| 40SribosomalproteinS14
TRINITY_DN89331_c0_g1_i2	7.66	0.00	11.16	0.00	0.00	0.00	6.27	0.00	5.71	0.00	0.00	RL10A_TRYBR	85.05	gi|528243988| largesubunitribosomalproteinL10Ae[Strigomonasculicis]
TRINITY_DN10543_c0_g1_i1	10.42	0.00	8.40	0.00	0.00	0.00	6.27	0.00	5.53	0.00	0.00	RL7_TETTH	60.09	gi|657386246| 60SribosomalproteinL7[Medicagotruncatula]
TRINITY_DN20173_c0_g1_i1	11.44	7.32	0.00	0.00	0.00	0.00	6.25	0.00	5.80	0.00	0.00			
TRINITY_DN18608_c0_g1_i1	6.28	5.36	7.11	0.00	0.00	0.00	6.25	0.00	0.87	0.00	0.00	CALM_TETPY	43.84	gi|545366875| EF-hand[CoccomyxasubellipsoideaC-169]>gi|384250284|gb|EIE23764.1|EF-hand[CoccomyxasubellipsoideaC-169]
TRINITY_DN128680_c0_g1_i1	3.50	4.46	10.79	0.00	0.00	0.00	6.25	0.00	3.96	0.00	0.00	ILVA_STAAR	41.67	gi|491688813| threoninedehydratase[Paenibacillusalvei]>gi|402508005|gb|EJW18526.1|threoninedehydratasebiosynthetic[PaenibacillusalveiDSM29]
TRINITY_DN56068_c0_g1_i1	5.70	3.61	9.43	0.00	0.00	0.00	6.25	0.00	2.95	0.00	0.00	EABF_STRCO	26.72	gi|739757258| galactosylceramidase[Streptacidiphilusrugosus]
TRINITY_DN77682_c0_g1_i1	5.37	5.80	7.56	0.00	0.00	0.00	6.24	0.00	1.16	0.00	0.00	NEP2_NEPGR	37.21	gi|636613253| acidprotease[TrametesversicolorFP-101664SS1]>gi|392566217|gb|EIW59393.1|acidprotease[TrametesversicolorFP-101664SS1]
TRINITY_DN115478_c0_g1_i1	7.09	4.00	7.60	0.00	0.00	0.00	6.23	0.00	1.95	0.00	0.00			
TRINITY_DN51185_c0_g1_i1	6.42	0.00	12.24	0.00	0.00	0.00	6.22	0.00	6.12	0.00	0.00	CB25_TETTH	33.78	gi|471229598| hypotheticalproteinIMG5_094250[Ichthyophthiriusmultifiliis]>gi|340505884|gb|EGR32162.1|hypotheticalproteinIMG5_094250[Ichthyophthiriusmultifiliis]
TRINITY_DN14025_c0_g1_i1	12.72	0.00	5.93	0.00	0.00	0.00	6.22	0.00	6.36	0.00	0.00	RS18_ARATH	68.75	gi|460391585| PREDICTED:40SribosomalproteinS18-like[Solanumlycopersicum]
TRINITY_DN28109_c0_g1_i1	10.25	5.27	3.13	0.00	0.00	0.00	6.21	0.00	3.65	0.00	0.00	MMS2_YEAST	56.2	gi|630352085| UBC-likeprotein[GloeophyllumtrabeumATCC11539]>gi|521726442|gb|EPQ56642.1|UBC-likeprotein[GloeophyllumtrabeumATCC11539]
TRINITY_DN82306_c0_g1_i1	6.09	5.63	6.91	0.00	0.00	0.00	6.21	0.00	0.65	0.00	0.00			
TRINITY_DN64301_c0_g1_i2	4.18	0.00	14.42	0.00	0.00	0.00	6.20	0.00	7.42	0.00	0.00			
TRINITY_DN27956_c0_g1_i1	7.48	5.35	5.68	0.00	0.00	0.00	6.17	0.00	1.15	0.00	0.00			
TRINITY_DN62644_c0_g2_i1	7.59	7.76	3.15	0.00	0.00	0.00	6.16	0.00	2.61	0.00	0.00	ZC3H3_HUMAN	36	gi|47228963| unnamedproteinproduct
TRINITY_DN82077_c2_g1_i1	5.72	3.31	9.45	0.00	0.00	0.00	6.16	0.00	3.10	0.00	0.00	RLA2_BRAFL	58.06	gi|748505041| hypotheticalproteinH072_5590[DactylellinahaptotylaCBS200.50]>gi|526199741|gb|EPS40551.1|hypotheticalproteinH072_5590[DactylellinahaptotylaCBS200.50]
TRINITY_DN121424_c0_g1_i1	9.97	0.00	8.50	0.00	0.00	0.00	6.16	0.00	5.38	0.00	0.00			

TRINITY_DN57957_c0_g2_i1	11.15	0.00	7.28	0.00	0.00	0.00	6.14	0.00	5.66	0.00	0.00				
TRINITY_DN76196_c0_g2_i1	11.91	6.51	0.00	0.00	0.00	0.00	6.14	0.00	5.96	0.00	0.00				
TRINITY_DN48481_c0_g1_i1	8.15	3.72	6.55	0.00	0.00	0.00	6.14	0.00	2.24	0.00	0.00				
TRINITY_DN19802_c0_g1_i1	11.86	0.00	6.53	0.00	0.00	0.00	6.13	0.00	5.94	0.00	0.00	RL30_TETTS	64.79	gi|682283886|	hypotheticalproteinO988_00832[PseudogymnoascuspannorumVKMF-3808]
TRINITY_DN15221_c0_g1_i1	10.57	7.78	0.00	0.00	0.00	0.00	6.12	0.00	5.48	0.00	0.00	VATG1_MOUSE	30.77	gi|453086419|	vacuolarATPsynthasesubunitG[SphaerulinamusivaSO2202]
TRINITY_DN146116_c0_g1_i1	4.95	8.34	4.94	0.00	0.00	0.00	6.08	0.00	1.96	0.00	0.00				
TRINITY_DN94225_c0_g1_i1	7.79	0.00	10.45	0.00	0.00	0.00	6.08	0.00	5.43	0.00	0.00				
TRINITY_DN167751_c0_g1_i1	5.57	6.15	6.49	0.00	0.00	0.00	6.07	0.00	0.47	0.00	0.00				
TRINITY_DN17092_c0_g1_i1	0.00	11.18	7.02	0.00	0.00	0.00	6.07	0.00	5.65	0.00	0.00				
TRINITY_DN120150_c0_g1_i1	5.68	12.51	0.00	0.00	0.00	0.00	6.06	0.00	6.26	0.00	0.00	SDR1_AEDAE	36.72	gi|91084883|	PREDICTED:dehydrogenase/reductaseSDRfamilymember11isoformX2[Triboliumcastaneum]>gi|270008569|gb|EFA05017.1|hypotheticalproteinTcasGA2_TC015100[Triboliumcastaneum]
TRINITY_DN139938_c0_g1_i1	6.36	6.22	5.61	0.00	0.00	0.00	6.06	0.00	0.40	0.00	0.00	SMD1_MOUSE	64.29	gi|359806624|	uncharacterizedproteinLOC100819089[Glycinemax]>gi|255647733|gb|ACU24327.1|unknown[Glycinemax]>gi|734354974|gb|KHN13859.1|SmallnuclearribonucleoproteinSmD1[Glycinesoja]
TRINITY_DN65952_c0_g1_i1	5.98	8.79	3.38	0.00	0.00	0.00	6.05	0.00	2.70	0.00	0.00				
TRINITY_DN43980_c0_g1_i1	6.58	3.02	8.50	0.00	0.00	0.00	6.03	0.00	2.78	0.00	0.00	MKS3_RAT	23.91	gi|751350949|	hypotheticalproteinFAVG1_07918[Fusariumavenaceum]
TRINITY_DN10694_c0_g1_i1	7.11	3.00	7.96	0.00	0.00	0.00	6.02	0.00	2.65	0.00	0.00	HNMT_BOVIN	45.16	gi|24474973|	p28protein[Tetrahymenathermophila]
TRINITY_DN69562_c0_g1_i1	8.90	5.42	3.74	0.00	0.00	0.00	6.02	0.00	2.63	0.00	0.00				
TRINITY_DN76809_c1_g2_i1	5.98	5.50	6.57	0.00	0.00	0.00	6.02	0.00	0.54	0.00	0.00	1433C_SOYBN	67.76	gi|356525282|	PREDICTED:14-3-3-likeproteinC-likeisoformX1[Glycinemax]>gi|571470968|ref|XP_006585166.1|PREDICTED:14-3-3-likeproteinC-likeisoformX2[Glycinemax]>gi|571470970|ref|XP_006585167.1|PREDICTED:14-3-3-likeproteinC-likeisoformX3[Glycinemax]>gi|734436286|gb|KHN47990.1|14-3-3-likeproteinC[Glycinesoja]
TRINITY_DN198243_c0_g1_i1	8.42	6.43	3.16	0.00	0.00	0.00	6.00	0.00	2.66	0.00	0.00				
TRINITY_DN64061_c0_g1_i1	7.02	3.85	7.08	0.00	0.00	0.00	5.98	0.00	1.85	0.00	0.00	RP25L_HUMAN	27.94	gi|694316599|	PREDICTED:ribonucleasePproteinsubunitp25-likeprotein[Pyrusxbretschneideri]
TRINITY_DN81714_c0_g1_i2	7.39	0.00	10.56	0.00	0.00	0.00	5.98	0.00	5.42	0.00	0.00	RL5_SUBDO	55	gi|195999960|	expressedhypotheticalprotein[Trichoplaxadhaerens]>gi|190587972|gb|EDV28014.1|expressedhypotheticalprotein[Trichoplaxadhaerens]
TRINITY_DN139277_c0_g1_i1	12.87	0.00	5.07	0.00	0.00	0.00	5.98	0.00	6.48	0.00	0.00	RL32_BOVIN	58.14	gi|470374500|	ribosomalproteinL32
TRINITY_DN87553_c0_g1_i1	5.79	5.05	7.08	0.00	0.00	0.00	5.97	0.00	1.03	0.00	0.00				
TRINITY_DN5992_c0_g1_i1	6.25	7.83	3.78	0.00	0.00	0.00	5.95	0.00	2.04	0.00	0.00	CATR4_PARTE	25.5	gi|145529061|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|74829821|emb|CAI38945.1|centrin6a-from-infraciliary-lattice[Parameciumtetraurelia]>gi|124417930|emb|CAK82922.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN169384_c0_g1_i1	5.86	8.72	3.22	0.00	0.00	0.00	5.93	0.00	2.75	0.00	0.00				
TRINITY_DN57134_c0_g1_i1	10.18	0.00	7.60	0.00	0.00	0.00	5.93	0.00	5.29	0.00	0.00				
TRINITY_DN78252_c0_g3_i1	6.04	7.84	3.89	0.00	0.00	0.00	5.93	0.00	1.98	0.00	0.00				
TRINITY_DN114302_c0_g1_i1	6.58	3.84	7.35	0.00	0.00	0.00	5.93	0.00	1.84	0.00	0.00	ATPG_DROME	39.72	gi|676388943|	hypotheticalproteinAURANDRAFT_53834[Aureococcusanophagefferens]>gi|323451892|gb|EGB07768.1|hypotheticalproteinAURANDRAFT_53834[Aureococcusanophagefferens]
TRINITY_DN64314_c0_g1_i2	7.56	3.32	6.89	0.00	0.00	0.00	5.92	0.00	2.28	0.00	0.00	DCD_PSYCK	30.67	gi|145489255|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124397729|emb|CAK63232.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN50031_c0_g1_i1	0.00	3.13	14.64	0.00	0.00	0.00	5.92	0.00	7.71	0.00	0.00				
TRINITY_DN218955_c0_g1_i1	3.12	11.12	3.52	0.00	0.00	0.00	5.92	0.00	4.50	0.00	0.00				
TRINITY_DN685_c0_g1_i1	7.41	5.68	4.67	0.00	0.00	0.00	5.92	0.00	1.39	0.00	0.00	CETN1_BOVIN	38.89	gi|209876844|	centrinprotein[CryptosporidiummurisRN66]>gi|209555470|gb|EEA05515.1|centrinprotein
TRINITY_DN193513_c0_g1_i1	5.35	7.32	5.08	0.00	0.00	0.00	5.92	0.00	1.22	0.00	0.00				
TRINITY_DN74565_c0_g1_i1	13.96	0.00	3.71	0.00	0.00	0.00	5.89	0.00	7.23	0.00	0.00	RSSA_MONBE	62.5	gi|74025154|	40SribosomalproteinSA[TrypanosomabruceibruceiTREU927]>gi|788025772|ref|XP_011780354.1|40SribosomalproteinSA
TRINITY_DN42093_c0_g1_i1	8.12	3.09	6.45	0.00	0.00	0.00	5.88	0.00	2.56	0.00	0.00	TC1D2_BOVIN	41.8	gi|676410740|	Tctex1domain-containingprotein2
TRINITY_DN80261_c1_g1_i1	5.63	6.21	5.80	0.00	0.00	0.00	5.88	0.00	0.29	0.00	0.00	H4_SOYBN	96.25	gi|195617798|	histoneH4[Zeamays]
TRINITY_DN72980_c0_g1_i1	4.23	5.43	7.97	0.00	0.00	0.00	5.88	0.00	1.91	0.00	0.00	CAPZA_DICDI	53.17	gi|432959402|	PREDICTED:F-actin-cappingproteinsubunitalpha-2[Oryziaslatipes]
TRINITY_DN118250_c0_g1_i1	5.63	11.87	0.00	0.00	0.00	0.00	5.83	0.00	5.94	0.00	0.00				
TRINITY_DN197754_c0_g1_i1	12.41	0.00	5.09	0.00	0.00	0.00	5.83	0.00	6.24	0.00	0.00				
TRINITY_DN57460_c1_g1_i1	5.27	0.00	12.22	0.00	0.00	0.00	5.83	0.00	6.13	0.00	0.00	ADT_PARKE	25	gi|157093149|	ATP/ADPtranslocator[Karlodiniumveneficum]
TRINITY_DN149729_c0_g1_i1	3.20	8.51	5.74	0.00	0.00	0.00	5.81	0.00	2.66	0.00	0.00				
TRINITY_DN56989_c0_g1_i1	14.38	3.04	0.00	0.00	0.00	0.00	5.81	0.00	7.58	0.00	0.00	RM36_DANRE	56.76	gi|727643791|	PREDICTED:uncharacterizedproteinLOC104770402[Camelinasativa]
TRINITY_DN86613_c0_g1_i2	5.51	6.29	5.60	0.00	0.00	0.00	5.80	0.00	0.43	0.00	0.00	ADT1_HUMAN	23.17	gi|795133081|	PREDICTED:ADP/ATPtranslocase4isoformX1[Colobusangolensispalliatus]
TRINITY_DN82922_c0_g1_i1	5.68	6.80	4.92	0.00	0.00	0.00	5.80	0.00	0.95	0.00	0.00	RL18_AEDAE	59.04	gi|475579567|	60SribosomalproteinL18-2[Aegilopstauschii]
TRINITY_DN11619_c0_g1_i1	4.04	0.00	13.31	0.00	0.00	0.00	5.79	0.00	6.83	0.00	0.00	CATR5_PARTE	75	gi|557148194|	caltractin
TRINITY_DN4072_c0_g1_i1	11.60	0.00	5.66	0.00	0.00	0.00	5.75	0.00	5.80	0.00	0.00	RS5_RAT	69.9	gi|728842581|	40SribosomalS5[Gossypiumarboreum]
TRINITY_DN89377_c0_g6_i1	6.15	0.00	11.09	0.00	0.00	0.00	5.75	0.00	5.56	0.00	0.00	SAHH_LEIDO	82.53	gi|686643453|	S-adenosylhomocysteinehydrolase[Trypanosomagrayi]>gi|657135386|gb|KEG07596.1|S-adenosylhomocysteinehydrolase[Trypanosomagrayi]
TRINITY_DN20067_c0_g1_i1	7.09	5.98	4.17	0.00	0.00	0.00	5.75	0.00	1.47	0.00	0.00	FAEA_ASPFN	26.24	gi|281209254|	hypotheticalproteinPPL_03573[PolysphondyliumpallidumPN500]
TRINITY_DN76359_c0_g1_i1	4.91	6.83	5.43	0.00	0.00	0.00	5.72	0.00	0.99	0.00	0.00	CHIA_FLAJ1	29.46	gi|750127063|	chitinase[Chitiniphilusshinanonensis]
TRINITY_DN81758_c1_g3_i1	12.15	0.00	4.99	0.00	0.00	0.00	5.71	0.00	6.10	0.00	0.00	RL8_TETTS	68.55	gi|384485790|	60SribosomalproteinL2[RhizopusdelemarRA99-880]>gi|384496254|gb|EIE86745.1|60SribosomalproteinL2[RhizopusdelemarRA99-880]>gi|384500526|gb|EIE91017.1|60SribosomalproteinL2[RhizopusdelemarRA99-880]>gi|384502039|gb|EIE92530.1|60SribosomalproteinL2[RhizopusdelemarRA99-880]
TRINITY_DN82575_c0_g2_i2	6.43	0.00	10.66	0.00	0.00	0.00	5.70	0.00	5.37	0.00	0.00	TBA1_NAEGR	93.52	gi|528228315|	tubulinalpha[Angomonasdeanei]

TRINITY_DN115814_c0_g1_i1	8.22	4.38	4.48	0.00	0.00	0.00	5.69	0.00	2.19	0.00	0.00	Y4844_ARATH	31.78	gi|56311577|	conservedhypotheticalprotein[AromatoleumaromaticumEbN1]
TRINITY_DN50129_c0_g1_i1	8.91	4.92	3.23	0.00	0.00	0.00	5.69	0.00	2.92	0.00	0.00				
TRINITY_DN71984_c1_g1_i1	7.16	9.88	0.00	0.00	0.00	0.00	5.68	0.00	5.10	0.00	0.00				
TRINITY_DN220201_c0_g1_i1	11.88	0.00	5.10	0.00	0.00	0.00	5.66	0.00	5.96	0.00	0.00				
TRINITY_DN49456_c0_g1_i1	5.74	4.98	6.22	0.00	0.00	0.00	5.65	0.00	0.62	0.00	0.00	RL121_ARATH	52.99	gi|118485188|	unknown[Populustrichocarpa]
TRINITY_DN77141_c0_g1_i1	9.43	7.49	0.00	0.00	0.00	0.00	5.64	0.00	4.98	0.00	0.00	RS27A_KLULA	52.38	gi|695073143|	PREDICTED:ubiquitin-40SribosomalproteinS27a-like[Musaacuminatasubsp.malaccensis]
TRINITY_DN74194_c0_g1_i1	3.40	4.48	9.03	0.00	0.00	0.00	5.64	0.00	2.99	0.00	0.00	DCD1B_DICDI	34.13	gi|514683371|	hypotheticalproteinPTSG_09912[Salpingoecarosetta]>gi|326433612|gb|EGD79182.1|hypotheticalproteinPTSG_09912[Salpingoecarosetta]
TRINITY_DN193317_c0_g1_i1	12.32	0.00	4.58	0.00	0.00	0.00	5.64	0.00	6.23	0.00	0.00				
TRINITY_DN52905_c0_g1_i1	6.84	0.00	10.06	0.00	0.00	0.00	5.63	0.00	5.14	0.00	0.00	ITH5_CUCMA	43.28	gi|514744052|	PREDICTED:subtilisin-chymotrypsininhibitor-2A-like[Setariaitalica]
TRINITY_DN51674_c0_g1_i1	10.16	3.52	3.21	0.00	0.00	0.00	5.63	0.00	3.93	0.00	0.00				
TRINITY_DN77693_c0_g1_i1	7.36	0.00	9.50	0.00	0.00	0.00	5.62	0.00	4.98	0.00	0.00	RL27_HIPCM	51.49	gi|401427265|	putativeribosomalproteinL27[LeishmaniamexicanaMHOM/GT/2001/U1103]>gi|322494363|emb|CBZ29664.1|putativeribosomalproteinL27[LeishmaniamexicanaMHOM/GT/2001/U1103]
TRINITY_DN146255_c0_g1_i1	6.76	4.11	5.94	0.00	0.00	0.00	5.61	0.00	1.36	0.00	0.00				
TRINITY_DN142577_c0_g1_i1	3.23	3.87	9.69	0.00	0.00	0.00	5.60	0.00	3.56	0.00	0.00	LYSC_DICDI	43.61	gi|330795839|	hypotheticalproteinDICPUDRAFT_53943[Dictyosteliumpurpureum]>gi|325084067|gb|EGC37504.1|hypotheticalproteinDICPUDRAFT_53943[Dictyosteliumpurpureum]
TRINITY_DN115979_c0_g1_i1	7.28	3.47	5.95	0.00	0.00	0.00	5.57	0.00	1.93	0.00	0.00	RK14_HELSJ	28.85	gi|471228965|	hypotheticalproteinIMG5_100110[Ichthyophthiriusmultifiliis]>gi|340505545|gb|EGR31862.1|hypotheticalproteinIMG5_100110[Ichthyophthiriusmultifiliis]
TRINITY_DN94699_c0_g1_i1	5.82	7.13	3.74	0.00	0.00	0.00	5.56	0.00	1.71	0.00	0.00	CLCA_VIBCB	34	gi|145495892|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124401059|emb|CAK66541.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN114692_c0_g1_i1	7.33	4.71	4.65	0.00	0.00	0.00	5.56	0.00	1.53	0.00	0.00	BGL38_ORYSJ	30	gi|145499745|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124402993|emb|CAK68460.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN43363_c0_g1_i1	8.68	0.00	7.95	0.00	0.00	0.00	5.54	0.00	4.82	0.00	0.00	DHE3_DICDI	36.11	gi|595498807|	glutamatedehydrogenase(NADP(+))GDH3[RhizophagusirregularisDAOM197198w]
TRINITY_DN68902_c0_g1_i1	11.88	4.75	0.00	0.00	0.00	0.00	5.54	0.00	5.98	0.00	0.00	RS27A_CAEBR	47.79	gi|50307755|	ubiquitin-40SribosomalproteinS31fusionprotein[KluyveromyceslactisNRRLY-1140]>gi|302393747|sp|P69061.2|RS27A_KLULARecName:Full=Ubiquitin-40SribosomalproteinS27a;Contains:RecName:Full=Ubiquitin;Contains:RecName:Full=40SribosomalproteinS27a;Flags:Precursor[KluyveromyceslactisNRRLY-1140]>gi|704360269|pdb|3J80|FFChainf
TRINITY_DN62929_c0_g1_i1	5.32	5.01	6.29	0.00	0.00	0.00	5.54	0.00	0.66	0.00	0.00				
TRINITY_DN92461_c3_g3_i9	5.03	0.00	11.59	0.00	0.00	0.00	5.54	0.00	5.81	0.00	0.00	TBB_TRYCR	95.51	gi|401421933|	betatubulin[LeishmaniamexicanaMHOM/GT/2001/U1103]>gi|13569565|gb|AAK31149.1|beta-tubulin[Leishmaniamexicana]>gi|322491692|emb|CBZ26965.1|betatubulin[LeishmaniamexicanaMHOM/GT/2001/U1103]
TRINITY_DN32045_c0_g1_i1	8.77	4.79	3.04	0.00	0.00	0.00	5.53	0.00	2.94	0.00	0.00				
TRINITY_DN65698_c0_g2_i1	12.29	0.00	4.30	0.00	0.00	0.00	5.53	0.00	6.24	0.00	0.00	RL13_DICDI	60.16	gi|541045010|	60sribosomalproteinl13[Ascarissuum]
TRINITY_DN88278_c0_g2_i2	7.21	0.00	9.37	0.00	0.00	0.00	5.52	0.00	4.90	0.00	0.00	XCP1_ARATH	44.29	gi|720087719|	PREDICTED:cysteineproteinaseRD21a-like[Nelumbonucifera]
TRINITY_DN41386_c0_g1_i1	3.60	6.86	6.03	0.00	0.00	0.00	5.50	0.00	1.69	0.00	0.00	AB8C_ARATH	21.62	gi|802577458|	PREDICTED:ABCtransporterCfamilymember8[Jatrophacurcas]>gi|643733954|gb|KDP40797.1|hypotheticalproteinJCGZ_24796[Jatrophacurcas]
TRINITY_DN11119_c0_g1_i1	6.10	5.60	4.79	0.00	0.00	0.00	5.50	0.00	0.66	0.00	0.00	CI116_DANRE	34.85	gi|557186313|	hypotheticalprotein
TRINITY_DN37280_c0_g1_i1	7.89	4.51	4.05	0.00	0.00	0.00	5.48	0.00	2.10	0.00	0.00				
TRINITY_DN83896_c0_g1_i2	5.29	0.00	11.15	0.00	0.00	0.00	5.48	0.00	5.58	0.00	0.00	GSTM4_HUMAN	29.86	gi|118350783|	GlutathioneS-transferase
TRINITY_DN47796_c0_g1_i1	6.23	6.57	3.64	0.00	0.00	0.00	5.48	0.00	1.61	0.00	0.00	YR614_MIMIV	30.3	gi|819034065|	SPFHdomain-containingprotein/band7familyprotein[Myxococcusfulvus]>gi|817713519|gb|AKF82720.1|hypotheticalproteinMFUL124B02_29930[Myxococcusfulvus124B02]
TRINITY_DN57526_c0_g1_i2	5.17	4.76	6.49	0.00	0.00	0.00	5.47	0.00	0.90	0.00	0.00	RPOD_PSEPH	24.59	gi|145492604|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124399410|emb|CAK64902.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN13174_c0_g1_i1	6.32	3.36	6.72	0.00	0.00	0.00	5.47	0.00	1.83	0.00	0.00	ARRD3_RAT	40.48	gi|669166040|	hypotheticalproteinSDRG_14245[SaprolegniadiclinaVS20]>gi|530729727|gb|EQC27969.1|hypotheticalproteinSDRG_14245[SaprolegniadiclinaVS20]
TRINITY_DN95472_c0_g1_i1	6.24	4.96	5.18	0.00	0.00	0.00	5.46	0.00	0.69	0.00	0.00	EF1B_YEAST	42.53	gi|570327874|	hypotheticalproteinF444_08640[PhytophthoraparasiticaP1976]
TRINITY_DN117425_c0_g1_i1	5.58	3.34	7.42	0.00	0.00	0.00	5.45	0.00	2.04	0.00	0.00	SODF_SALTY	59.28	gi|556426426|	MULTISPECIES:superoxidedismutase[Fe][Enterobacter]>gi|555087948|gb|ESM31096.1|superoxidedismutase[Fe][EnterobactercloacaeBWH31]>gi|555170330|gb|ESN12963.1|superoxidedismutase[Fe][Enterobactersp.MGH24]>gi|578179627|gb|EUL39958.1|superoxidedismutase[Fe][EnterobactercloacaeUCI49]>gi|584252637|gb|EWG72046.1|Superoxidedismutase(Fe)[Enterobactersp.DC1]>gi|667747824|gb|KFA86109.1|superoxidedismutase[Enterobactersp.EGD-HP1]>gi|721519697|gb|KGY63102.1|superoxidedismutase[Enterobactercloacae]>gi|736275349|gb|KHQ30298.1|superoxidedismutase[Enterobactercloacae]>gi|768650742|gb|KJI83132.1|superoxidedismutase[Enterobactercloacae]>gi|771216168|gb|KJN57445.1|superoxidedismutase[Enterobacterasburiae]>gi|771232912|gb|KJN70072.1|superoxidedismutase[Enterobacterasburiae]>gi|771391310|gb|KJP23417.1|superoxidedismutase[Enterobacterasburiae]>gi|772472319|gb|KJQ00917.1|superoxidedismutase[Enterobactercloacae]
TRINITY_DN114087_c0_g1_i1	12.97	0.00	3.35	0.00	0.00	0.00	5.44	0.00	6.73	0.00	0.00	RL26_TETTS	62.6	gi|388857113|	probable60SribosomalproteinL26[Ustilagohordei]
TRINITY_DN132743_c0_g1_i1	7.03	4.75	4.51	0.00	0.00	0.00	5.43	0.00	1.39	0.00	0.00	SUMO1_ORYSJ	63.64	gi|460397078|	PREDICTED:smallubiquitin-relatedmodifier1[Solanumlycopersicum]
TRINITY_DN381_c0_g1_i1	9.10	7.17	0.00	0.00	0.00	0.00	5.42	0.00	4.80	0.00	0.00				
TRINITY_DN23794_c0_g1_i1	10.39	0.00	5.88	0.00	0.00	0.00	5.42	0.00	5.21	0.00	0.00	ATM_CANAL	38.46	gi|118397356|	Leishmanolysinfamilyprotein[Tetrahymenathermophila]>gi|89285332|gb|EAR83348.1|leishmanolysinfamilyprotein[TetrahymenathermophilaSB210]
TRINITY_DN139934_c0_g1_i1	7.81	0.00	8.43	0.00	0.00	0.00	5.41	0.00	4.70	0.00	0.00	RNPH_BDEBA	32.43	gi|145552054|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124429539|emb|CAK94330.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN10114_c0_g1_i1	7.05	3.10	6.08	0.00	0.00	0.00	5.41	0.00	2.06	0.00	0.00	RLMN_LEGPC	26.77	gi|678332943|	UNKNOWN[Stylonychialemnae]
TRINITY_DN222898_c0_g1_i1	4.02	6.16	6.03	0.00	0.00	0.00	5.40	0.00	1.20	0.00	0.00				

TRINITY_DN30366_c0_g1_i1	11.82	0.00	4.37	0.00	0.00	0.00	5.40	0.00	5.98	0.00	0.00	RL18_TETTH	55.79	gi|159465349|	ribosomalproteinL18
TRINITY_DN144298_c0_g1_i1	4.50	11.66	0.00	0.00	0.00	0.00	5.39	0.00	5.88	0.00	0.00				
TRINITY_DN20149_c0_g1_i1	4.96	4.74	6.47	0.00	0.00	0.00	5.39	0.00	0.94	0.00	0.00	MPK7_ORYSJ	48.72	gi|570328714|	CMGC/MAPKproteinkinase
TRINITY_DN55302_c0_g1_i1	5.84	3.33	6.96	0.00	0.00	0.00	5.38	0.00	1.86	0.00	0.00	MNCP_OXYFA	28.57	gi|145546885|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124426948|emb|CAK91728.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN90410_c0_g1_i1	3.95	4.93	7.22	0.00	0.00	0.00	5.37	0.00	1.68	0.00	0.00				
TRINITY_DN189578_c0_g1_i1	6.20	9.89	0.00	0.00	0.00	0.00	5.36	0.00	5.00	0.00	0.00				
TRINITY_DN52776_c0_g1_i1	9.43	3.05	3.60	0.00	0.00	0.00	5.36	0.00	3.53	0.00	0.00	MMS2_YEAST	54.89	gi|27948830|	MMS2[Nakaseomycesdelphensis]
TRINITY_DN81808_c1_g2_i2	4.02	3.46	8.61	0.00	0.00	0.00	5.36	0.00	2.83	0.00	0.00				
TRINITY_DN215110_c0_g1_i1	13.02	0.00	3.04	0.00	0.00	0.00	5.36	0.00	6.81	0.00	0.00				
TRINITY_DN2419_c0_g1_i1	8.30	4.22	3.54	0.00	0.00	0.00	5.35	0.00	2.58	0.00	0.00	OPS3_DROPS	35.14	gi|403332136|	Protofilamentribbonprotein
TRINITY_DN98365_c0_g1_i1	7.43	3.51	5.12	0.00	0.00	0.00	5.35	0.00	1.97	0.00	0.00	RL123_ARATH	52.15	gi|168032176|	predictedprotein[Physcomitrellapatens]>gi|162680094|gb|EDQ66533.1|predictedprotein[Physcomitrellapatens]
TRINITY_DN4357_c0_g1_i1	0.00	8.72	7.33	0.00	0.00	0.00	5.35	0.00	4.69	0.00	0.00				
TRINITY_DN165814_c0_g1_i1	7.50	3.56	4.97	0.00	0.00	0.00	5.35	0.00	2.00	0.00	0.00				
TRINITY_DN781_c0_g1_i1	7.20	3.58	5.18	0.00	0.00	0.00	5.32	0.00	1.82	0.00	0.00	MPCP_CAEEL	49.83	gi|574995240|	hypotheticalproteinPFUGPA_01721[PlasmodiumfalciparumPaloAlto/Uganda]>gi|575000071|gb|ETW60549.1|hypotheticalproteinPFMC_03588[PlasmodiumfalciparumCAMP/Malaysia]
TRINITY_DN81226_c1_g1_i1	5.76	4.96	5.22	0.00	0.00	0.00	5.31	0.00	0.41	0.00	0.00	CYSP3_SOLLC	51.94	gi|527209146|	hypotheticalproteinM569_00815[Genliseaaurea]
TRINITY_DN88390_c2_g2_i3	5.76	4.28	5.89	0.00	0.00	0.00	5.31	0.00	0.90	0.00	0.00	EF2_CRYPV	58.77	gi|8918238|	elongationfactor2
TRINITY_DN167678_c0_g1_i1	10.47	0.00	5.45	0.00	0.00	0.00	5.31	0.00	5.24	0.00	0.00				
TRINITY_DN121890_c0_g1_i1	6.25	4.79	4.87	0.00	0.00	0.00	5.30	0.00	0.82	0.00	0.00				
TRINITY_DN213780_c0_g1_i1	3.95	0.00	11.94	0.00	0.00	0.00	5.30	0.00	6.08	0.00	0.00				
TRINITY_DN153813_c0_g1_i1	3.71	0.00	12.16	0.00	0.00	0.00	5.29	0.00	6.23	0.00	0.00				
TRINITY_DN217829_c0_g1_i1	9.30	6.57	0.00	0.00	0.00	0.00	5.29	0.00	4.78	0.00	0.00				
TRINITY_DN172461_c0_g1_i1	5.02	4.14	6.67	0.00	0.00	0.00	5.28	0.00	1.29	0.00	0.00				
TRINITY_DN115387_c0_g1_i1	8.10	7.72	0.00	0.00	0.00	0.00	5.28	0.00	4.57	0.00	0.00				
TRINITY_DN76479_c0_g1_i1	6.01	4.59	5.20	0.00	0.00	0.00	5.27	0.00	0.71	0.00	0.00	LIME_DICDI	61.36	gi|762084517|	PREDICTED:LIMandSH3domainproteinF42H10.3-likeisoformX12[Crassostreagigas]
TRINITY_DN22014_c0_g1_i1	9.85	0.00	5.95	0.00	0.00	0.00	5.27	0.00	4.96	0.00	0.00	CTL5_XENTR	31.18	gi|350643960|	unnamedproteinproduct[Schistosomamansoni]
TRINITY_DN228_c0_g1_i1	6.19	5.12	4.50	0.00	0.00	0.00	5.27	0.00	0.85	0.00	0.00	HN1_RAT	48.39	gi|403362832|	hypotheticalproteinOXYTRI_21453[Oxytrichatrifallax]
TRINITY_DN99539_c0_g1_i1	3.19	5.34	7.25	0.00	0.00	0.00	5.26	0.00	2.03	0.00	0.00				
TRINITY_DN53815_c0_g1_i1	0.00	7.48	8.29	0.00	0.00	0.00	5.26	0.00	4.57	0.00	0.00	STAM2_CHICK	44.83	gi|118388207|	hypotheticalproteinTTHERM_00977640[Tetrahymenathermophila]
TRINITY_DN114260_c0_g1_i1	5.91	5.03	4.82	0.00	0.00	0.00	5.25	0.00	0.58	0.00	0.00	TRMB_OCEIH	24.26	gi|326489009|	predictedprotein[Hordeumvulgaresubsp.vulgare]
TRINITY_DN11050_c0_g2_i1	6.24	3.18	6.34	0.00	0.00	0.00	5.25	0.00	1.80	0.00	0.00				
TRINITY_DN35977_c0_g1_i1	0.00	6.82	8.94	0.00	0.00	0.00	5.25	0.00	4.67	0.00	0.00				
TRINITY_DN12628_c0_g1_i1	4.15	4.04	7.56	0.00	0.00	0.00	5.25	0.00	2.00	0.00	0.00	IDLC_STRPU	55.83	gi|443696492|	hypotheticalproteinCAPTEDRAFT_153927[Capitellateleta]
TRINITY_DN52652_c0_g1_i1	7.22	0.00	8.50	0.00	0.00	0.00	5.24	0.00	4.58	0.00	0.00	EF1A_CRYPV	88.17	gi|758357232|	hypotheticalproteinMAM1_0002c00242[Mucorambiguus]
TRINITY_DN64686_c0_g1_i1	6.46	4.93	4.33	0.00	0.00	0.00	5.24	0.00	1.10	0.00	0.00	EF1G1_ARATH	31.13	gi|399217080|	unnamedproteinproduct[BabesiamicrotistrainRI]
TRINITY_DN63704_c0_g1_i1	5.58	6.76	3.31	0.00	0.00	0.00	5.22	0.00	1.75	0.00	0.00	CATLL_PHACE	28.78	gi|763799863|	hypotheticalproteinB456_010G159600[Gossypiumraimondii]>gi|763799864|gb|KJB66819.1|hypotheticalproteinB456_010G159600[Gossypiumraimondii]
TRINITY_DN32812_c0_g1_i1	9.64	0.00	6.01	0.00	0.00	0.00	5.22	0.00	4.87	0.00	0.00	DNAK_XANP2	79.52	gi|294907808|	heatshockprotein
TRINITY_DN143157_c0_g1_i1	4.85	0.00	10.80	0.00	0.00	0.00	5.22	0.00	5.41	0.00	0.00	SCONB_ASPFU	29.73	gi|145507440|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124406870|emb|CAK72278.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN141192_c0_g1_i1	4.51	5.64	5.48	0.00	0.00	0.00	5.21	0.00	0.61	0.00	0.00	SAHH_TOBAC	62.71	gi|301107277|	adenosylhomocysteinase[PhytophthorainfestansT30-4]>gi|262098595|gb|EEY56647.1|adenosylhomocysteinase[PhytophthorainfestansT30-4]
TRINITY_DN25718_c0_g1_i1	5.03	5.89	4.70	0.00	0.00	0.00	5.20	0.00	0.61	0.00	0.00	IMPG1_CHICK	27.83	gi|145491337|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124398773|emb|CAK64270.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN79701_c0_g1_i1	5.66	5.98	3.95	0.00	0.00	0.00	5.20	0.00	1.09	0.00	0.00	RL6_MESCR	57.72	gi|685367206|	PREDICTED:60SribosomalproteinL6-1[Brassicarapa]
TRINITY_DN68235_c0_g1_i1	5.63	4.99	4.97	0.00	0.00	0.00	5.20	0.00	0.37	0.00	0.00				
TRINITY_DN42813_c0_g1_i1	6.31	5.49	3.78	0.00	0.00	0.00	5.19	0.00	1.29	0.00	0.00				
TRINITY_DN13291_c0_g2_i1	7.07	3.76	4.70	0.00	0.00	0.00	5.18	0.00	1.70	0.00	0.00				
TRINITY_DN139056_c0_g1_i1	4.26	4.37	6.88	0.00	0.00	0.00	5.17	0.00	1.48	0.00	0.00	PUR9_CALBD	37.18	gi|752708579|	hypotheticalprotein[Nitrosococcushalophilus]
TRINITY_DN50636_c0_g1_i1	8.79	6.69	0.00	0.00	0.00	0.00	5.16	0.00	4.59	0.00	0.00	DYL1_SCHMA	45.12	gi|676454883|	hypotheticalproteinLOTGIDRAFT_203845[Lottiagigantea]>gi|556106658|gb|ESO95310.1|hypotheticalproteinLOTGIDRAFT_203845[Lottiagigantea]
TRINITY_DN147398_c0_g1_i1	9.22	0.00	6.25	0.00	0.00	0.00	5.16	0.00	4.71	0.00	0.00				
TRINITY_DN50646_c0_g2_i1	12.44	0.00	3.01	0.00	0.00	0.00	5.15	0.00	6.49	0.00	0.00	BTF3_MOUSE	34.57	gi|695032533|	PREDICTED:transcriptionfactorBTF3homolog4-like[Musaacuminatasubsp.malaccensis]
TRINITY_DN194177_c0_g1_i1	6.61	0.00	8.83	0.00	0.00	0.00	5.15	0.00	4.59	0.00	0.00				
TRINITY_DN134135_c0_g1_i1	3.71	0.00	11.72	0.00	0.00	0.00	5.14	0.00	5.99	0.00	0.00				
TRINITY_DN71822_c0_g1_i1	9.39	0.00	6.03	0.00	0.00	0.00	5.14	0.00	4.76	0.00	0.00	CY1_YEAST	31.29	gi|666428617|	cytochromec1/Cyt1[Aspergillusfumigatusvar.RP-2014]
TRINITY_DN80820_c0_g1_i1	5.51	4.83	5.07	0.00	0.00	0.00	5.14	0.00	0.34	0.00	0.00				
TRINITY_DN30579_c0_g1_i1	5.08	10.32	0.00	0.00	0.00	0.00	5.13	0.00	5.16	0.00	0.00	DHBB_BACSU	39.39	gi|145535963|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124421442|emb|CAK86312.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN67642_c0_g1_i2	5.40	0.00	9.98	0.00	0.00	0.00	5.13	0.00	5.00	0.00	0.00	FKBP4_RHIO9	30.48	gi|72392221|	nucleolarRNA-bindingprotein
TRINITY_DN213484_c0_g1_i1	7.67	0.00	7.68	0.00	0.00	0.00	5.12	0.00	4.43	0.00	0.00				
TRINITY_DN92248_c0_g1_i1	3.68	4.62	6.99	0.00	0.00	0.00	5.10	0.00	1.70	0.00	0.00				
TRINITY_DN83223_c1_g1_i3	10.58	0.00	4.71	0.00	0.00	0.00	5.09	0.00	5.30	0.00	0.00	RL3_TETTH	65.04	gi|313586457|	60SribosomalproteinL3A[Heveabrasiliensis]
TRINITY_DN54198_c0_g1_i1	5.79	0.00	9.43	0.00	0.00	0.00	5.07	0.00	4.76	0.00	0.00				

TRINITY_DN143391_c0_g1_i1	7.46	3.04	4.71	0.00	0.00	0.00	5.07	0.00	2.23	0.00	0.00	ETCG_EDWI9	34.38	gi|145540549|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|145543903|ref|XP_001457637.1|hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124423773|emb|CAK88567.1|unnamedproteinproduct[Parameciumtetraurelia]>gi|124425454|emb|CAK90240.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN67367_c0_g1_i1	9.24	0.00	5.95	0.00	0.00	0.00	5.06	0.00	4.68	0.00	0.00				
TRINITY_DN32670_c0_g1_i1	6.08	3.47	5.54	0.00	0.00	0.00	5.03	0.00	1.38	0.00	0.00				
TRINITY_DN171869_c0_g1_i1	6.62	5.39	3.08	0.00	0.00	0.00	5.03	0.00	1.80	0.00	0.00				
TRINITY_DN59186_c0_g1_i1	9.36	5.70	0.00	0.00	0.00	0.00	5.02	0.00	4.72	0.00	0.00	ALAT1_ARATH	53.97	gi|255584430|	alaninetransaminase
TRINITY_DN146110_c0_g1_i1	8.89	6.15	0.00	0.00	0.00	0.00	5.01	0.00	4.55	0.00	0.00				
TRINITY_DN104574_c0_g1_i1	5.83	0.00	9.21	0.00	0.00	0.00	5.01	0.00	4.66	0.00	0.00				
TRINITY_DN174586_c0_g1_i1	5.83	0.00	9.21	0.00	0.00	0.00	5.01	0.00	4.66	0.00	0.00				
TRINITY_DN214639_c0_g1_i1	8.67	0.00	6.31	0.00	0.00	0.00	4.99	0.00	4.48	0.00	0.00				
TRINITY_DN46007_c0_g1_i1	7.35	3.74	3.88	0.00	0.00	0.00	4.99	0.00	2.05	0.00	0.00	H3_CAEEL	56.08	gi|355561393|	HistoneH3/a[Macacamulatta]
TRINITY_DN49771_c0_g1_i1	3.99	4.61	6.35	0.00	0.00	0.00	4.98	0.00	1.22	0.00	0.00	LIP_THELA	22.75	gi|281209254|	hypotheticalproteinPPL_03573[PolysphondyliumpallidumPN500]
TRINITY_DN29771_c0_g1_i1	4.00	5.70	5.22	0.00	0.00	0.00	4.97	0.00	0.88	0.00	0.00	CB25_TETTH	37.66	gi|678310372|	transcriptioninitiationfactortfiidsubunit5-like[Stylonychialemnae]
TRINITY_DN212838_c0_g1_i1	4.51	4.46	5.94	0.00	0.00	0.00	4.97	0.00	0.84	0.00	0.00				
TRINITY_DN179608_c0_g1_i1	5.11	9.78	0.00	0.00	0.00	0.00	4.96	0.00	4.89	0.00	0.00				
TRINITY_DN147374_c0_g1_i1	6.93	0.00	7.96	0.00	0.00	0.00	4.96	0.00	4.33	0.00	0.00				
TRINITY_DN66112_c0_g1_i1	5.09	9.79	0.00	0.00	0.00	0.00	4.96	0.00	4.90	0.00	0.00				
TRINITY_DN81633_c0_g1_i1	11.00	0.00	3.83	0.00	0.00	0.00	4.94	0.00	5.58	0.00	0.00	RLA0_SOYBN	43.57	gi|209877763|	60SacidicribosomalproteinP0[CryptosporidiummurisRN66]>gi|209555929|gb|EEA05974.1|60SacidicribosomalproteinP0
TRINITY_DN21302_c0_g1_i1	5.85	4.52	4.41	0.00	0.00	0.00	4.93	0.00	0.80	0.00	0.00	CATL2_PARTE	40.85	gi|118348660|	Papainfamilycysteineproteasecontainingprotein[Tetrahymenathermophila]>gi|89289572|gb|EAR87560.1|papainfamilycysteineprotease[TetrahymenathermophilaSB210]
TRINITY_DN231154_c0_g1_i1	3.56	0.00	11.22	0.00	0.00	0.00	4.93	0.00	5.74	0.00	0.00				
TRINITY_DN154569_c0_g1_i1	4.16	5.30	5.30	0.00	0.00	0.00	4.92	0.00	0.66	0.00	0.00				
TRINITY_DN52748_c0_g1_i1	7.33	3.45	3.99	0.00	0.00	0.00	4.92	0.00	2.10	0.00	0.00	NDUV1_DICDI	69.17	gi|388507134|	unknown[Medicagotruncatula]
TRINITY_DN9117_c0_g1_i1	4.99	0.00	9.74	0.00	0.00	0.00	4.91	0.00	4.87	0.00	0.00				
TRINITY_DN149109_c0_g1_i1	4.19	6.37	4.16	0.00	0.00	0.00	4.91	0.00	1.27	0.00	0.00				
TRINITY_DN67519_c0_g1_i1	0.00	6.26	8.36	0.00	0.00	0.00	4.88	0.00	4.35	0.00	0.00				
TRINITY_DN65679_c0_g1_i1	11.44	0.00	3.17	0.00	0.00	0.00	4.87	0.00	5.91	0.00	0.00				
TRINITY_DN79831_c0_g4_i2	4.30	3.27	7.04	0.00	0.00	0.00	4.87	0.00	1.95	0.00	0.00	TBB_TRYCR	96.75	gi|91983184|	betatubulin
TRINITY_DN169876_c0_g1_i1	11.35	0.00	3.25	0.00	0.00	0.00	4.87	0.00	5.84	0.00	0.00				
TRINITY_DN116932_c0_g1_i1	8.89	5.68	0.00	0.00	0.00	0.00	4.86	0.00	4.50	0.00	0.00				
TRINITY_DN164906_c0_g1_i1	8.21	0.00	6.36	0.00	0.00	0.00	4.86	0.00	4.31	0.00	0.00				
TRINITY_DN9036_c0_g1_i1	4.06	3.39	7.11	0.00	0.00	0.00	4.85	0.00	1.98	0.00	0.00	RL17_TETTS	56.94	gi|528270932|	largesubunitribosomalproteinL17e[Angomonasdeanei]
TRINITY_DN165612_c0_g1_i1	5.28	0.00	9.26	0.00	0.00	0.00	4.85	0.00	4.64	0.00	0.00				
TRINITY_DN32558_c0_g1_i1	4.09	10.43	0.00	0.00	0.00	0.00	4.84	0.00	5.26	0.00	0.00				
TRINITY_DN57356_c0_g8_i1	0.00	5.34	9.18	0.00	0.00	0.00	4.84	0.00	4.61	0.00	0.00				
TRINITY_DN76351_c0_g1_i2	7.53	0.00	6.99	0.00	0.00	0.00	4.84	0.00	4.20	0.00	0.00	RS15_PODAS	59.87	gi|749886325|	hypotheticalproteinM422DRAFT_24237[SphaerobolusstellatusSS14]
TRINITY_DN60336_c0_g1_i1	10.03	0.00	4.47	0.00	0.00	0.00	4.84	0.00	5.03	0.00	0.00	CATR6_PARTE	30.77	gi|224000107|	centrin-likeprotein[ThalassiosirapseudonanaCCMP1335]>gi|220974934|gb|EED93263.1|centrin-likeprotein[ThalassiosirapseudonanaCCMP1335]
TRINITY_DN168449_c0_g1_i1	4.16	10.32	0.00	0.00	0.00	0.00	4.83	0.00	5.19	0.00	0.00				
TRINITY_DN38611_c0_g1_i1	4.49	4.89	5.10	0.00	0.00	0.00	4.83	0.00	0.31	0.00	0.00	VTSS1_HYOMU	34.62	gi|118362736|	hypotheticalproteinTTHERM_00046440[Tetrahymenathermophila]
TRINITY_DN10944_c0_g1_i1	4.04	0.00	10.35	0.00	0.00	0.00	4.79	0.00	5.22	0.00	0.00				
TRINITY_DN2776_c0_g2_i1	10.39	3.97	0.00	0.00	0.00	0.00	4.79	0.00	5.24	0.00	0.00				
TRINITY_DN54474_c0_g1_i1	0.00	5.96	8.39	0.00	0.00	0.00	4.79	0.00	4.32	0.00	0.00	BSL1_TRIVA	29.17	gi|475658736|	hypotheticalproteinI532_15491[BrevibacillusborstelensisAK1]
TRINITY_DN84931_c0_g1_i1	7.97	3.11	3.28	0.00	0.00	0.00	4.79	0.00	2.76	0.00	0.00				
TRINITY_DN166156_c0_g1_i1	9.62	0.00	4.74	0.00	0.00	0.00	4.78	0.00	4.81	0.00	0.00				
TRINITY_DN129033_c0_g1_i1	6.74	3.81	3.80	0.00	0.00	0.00	4.78	0.00	1.69	0.00	0.00	CDPKU_ARATH	38.1	gi|505789677|	PREDICTED:calmodulin-likeprotein5[Sorexaraneus]
TRINITY_DN187162_c0_g1_i1	6.90	4.39	3.05	0.00	0.00	0.00	4.78	0.00	1.95	0.00	0.00				
TRINITY_DN28440_c0_g1_i1	4.70	3.06	6.53	0.00	0.00	0.00	4.76	0.00	1.74	0.00	0.00	RL37A_TETTS	64.58	gi|666866363|	hypotheticalproteinSAPIO_CDS5295[Scedosporiumapiospermum]
TRINITY_DN74056_c0_g1_i1	3.09	0.00	11.18	0.00	0.00	0.00	4.76	0.00	5.77	0.00	0.00				
TRINITY_DN145472_c0_g1_i1	4.04	4.37	5.81	0.00	0.00	0.00	4.74	0.00	0.94	0.00	0.00	PSA7_DICDI	60.36	gi|813127846|	hypotheticalproteinSPRG_03500[SaprolegniaparasiticaCBS223.65]>gi|641537727|gb|KDO31571.1|hypotheticalproteinSPRG_03500[SaprolegniaparasiticaCBS223.65]
TRINITY_DN64662_c0_g1_i1	6.95	0.00	7.27	0.00	0.00	0.00	4.74	0.00	4.11	0.00	0.00	AP2M_DICDI	34.78	gi|325189003|	AP2complexsubunitmuputative[AlbugolaibachiiNc14]
TRINITY_DN141603_c0_g1_i1	3.76	4.88	5.56	0.00	0.00	0.00	4.73	0.00	0.91	0.00	0.00	SYE_OENOB	40.74	gi|118378435|	cystathioninebeta-synthasefamilyprotein[Tetrahymenathermophila]>gi|89304160|gb|EAS02148.1|cystathioninebeta-synthase[TetrahymenathermophilaSB210]
TRINITY_DN20410_c0_g1_i1	3.18	10.98	0.00	0.00	0.00	0.00	4.72	0.00	5.65	0.00	0.00				
TRINITY_DN167816_c0_g1_i1	6.25	3.84	4.05	0.00	0.00	0.00	4.71	0.00	1.34	0.00	0.00				
TRINITY_DN49409_c0_g1_i1	4.74	9.39	0.00	0.00	0.00	0.00	4.71	0.00	4.70	0.00	0.00	TRM7_HUMAN	65.52	gi|685380321|	PREDICTED:putativetRNA(cytidine(32)/guanosine(34)-2'-O)-methyltransferaseisoformX8[Brassicarapa]
TRINITY_DN71229_c0_g1_i1	8.94	5.10	0.00	0.00	0.00	0.00	4.68	0.00	4.49	0.00	0.00				
TRINITY_DN57106_c0_g2_i1	5.74	3.12	5.18	0.00	0.00	0.00	4.68	0.00	1.38	0.00	0.00	Y8928_DICDI	28.4	gi|146174104|	hypotheticalproteinTTHERM_00850630[Tetrahymenathermophila]>gi|146144813|gb|EAR99020.2|membranemagnesiumtransporter[TetrahymenathermophilaSB210]
TRINITY_DN42102_c0_g1_i1	3.55	5.05	5.42	0.00	0.00	0.00	4.68	0.00	0.99	0.00	0.00	GPTC4_MOUSE	29.85	gi|678326368|	gpatchdomaincontaining[Stylonychialemnae]
TRINITY_DN3006_c0_g1_i1	6.18	3.69	4.08	0.00	0.00	0.00	4.65	0.00	1.34	0.00	0.00	CAPZA_DEBHA	29.48	gi|675178037|	hypotheticalproteinPPTG_05916[PhytophthoraparasiticaINRA-310]>gi|566009675|gb|ETI32586.1|hypotheticalproteinF443_20623[PhytophthoraparasiticaP1569]>gi|568005319|gb|ETL79620.1|hypotheticalproteinL917_19776[Phytophthoraparasitica]>gi|568102121|gb|ETN16803.1|hypotheticalproteinPPTG_05916[PhytophthoraparasiticaINRA-310]

TRINITY_DN9892_c0_g1_i1	6.72	3.17	4.06	0.00	0.00	0.00	4.65	0.00	1.84	0.00	0.00	CATLL_FASHE	34.81	gi|118365752|	Papainfamilycysteineproteasecontainingprotein[Tetrahymenathermophila]>gi|89297863|gb|EAR95851.1|papainfamilycysteineprotease[TetrahymenathermophilaSB210]
TRINITY_DN237_c0_g1_i1	10.41	0.00	3.52	0.00	0.00	0.00	4.64	0.00	5.29	0.00	0.00	SYG_BOMMO	51.95	gi|662200536|	PREDICTED:glycine--tRNAligaseisoformX2[Diaphorinacitri]
TRINITY_DN97268_c0_g1_i1	8.76	0.00	5.16	0.00	0.00	0.00	4.64	0.00	4.40	0.00	0.00	NRTD_SYNY3	46.43	gi|471221527|	hypotheticalproteinIMG5_177530[Ichthyophthiriusmultifiliis]>gi|340501585|gb|EGR28350.1|hypotheticalproteinIMG5_177530[Ichthyophthiriusmultifiliis]
TRINITY_DN69952_c0_g1_i1	5.46	0.00	8.46	0.00	0.00	0.00	4.64	0.00	4.29	0.00	0.00				
TRINITY_DN87350_c0_g1_i3	4.24	4.88	4.80	0.00	0.00	0.00	4.64	0.00	0.35	0.00	0.00				
TRINITY_DN55129_c0_g2_i1	4.37	4.22	5.31	0.00	0.00	0.00	4.63	0.00	0.59	0.00	0.00	LYSG2_DICDI	40.7	gi|470500795|	glycosylhydrolase[Acanthamoebacastellaniistr.Neff]>gi|440800672|gb|ELR21707.1|glycosylhydrolase[Acanthamoebacastellaniistr.Neff]
TRINITY_DN42360_c0_g2_i1	6.81	3.71	3.34	0.00	0.00	0.00	4.62	0.00	1.91	0.00	0.00				
TRINITY_DN23697_c0_g1_i1	5.13	3.13	5.58	0.00	0.00	0.00	4.61	0.00	1.30	0.00	0.00	TBA1_ARATH	100	gi|238007614|	unknown[Zeamays]
TRINITY_DN20574_c0_g1_i2	4.84	0.00	8.99	0.00	0.00	0.00	4.61	0.00	4.50	0.00	0.00	SYE_PROMP	28.38	gi|678321290|	UNKNOWN[Stylonychialemnae]
TRINITY_DN36170_c0_g1_i1	4.04	3.08	6.68	0.00	0.00	0.00	4.60	0.00	1.86	0.00	0.00	IDHP_ASPNG	75.23	gi|586733391|	NADP-dependentisocitratedehydrogenase[TetrahymenathermophilaSB210]
TRINITY_DN231960_c0_g1_i1	8.30	0.00	5.49	0.00	0.00	0.00	4.60	0.00	4.22	0.00	0.00				
TRINITY_DN114212_c0_g1_i1	0.00	3.18	10.61	0.00	0.00	0.00	4.60	0.00	5.44	0.00	0.00				
TRINITY_DN86593_c0_g1_i1	4.92	0.00	8.87	0.00	0.00	0.00	4.60	0.00	4.44	0.00	0.00	TCTP_LUMRU	36	gi|594149587|	unnamedproteinproduct[Phytomonassp.isolateHart1]
TRINITY_DN54670_c0_g1_i1	9.37	0.00	4.41	0.00	0.00	0.00	4.59	0.00	4.69	0.00	0.00				
TRINITY_DN102670_c0_g1_i1	0.00	4.88	8.89	0.00	0.00	0.00	4.59	0.00	4.45	0.00	0.00				
TRINITY_DN47908_c0_g1_i1	5.95	4.25	3.57	0.00	0.00	0.00	4.59	0.00	1.22	0.00	0.00	PSB1_HUMAN	51.4	gi|54696302|	proteasome(prosome
TRINITY_DN88891_c0_g4_i2	6.99	0.00	6.75	0.00	0.00	0.00	4.58	0.00	3.97	0.00	0.00	RL8_SOLLC	67.66	gi|743854648|	PREDICTED:60SribosomalproteinL8-like[Elaeisguineensis]
TRINITY_DN26912_c0_g1_i1	9.10	0.00	4.63	0.00	0.00	0.00	4.58	0.00	4.55	0.00	0.00				
TRINITY_DN71000_c0_g1_i1	8.73	0.00	4.98	0.00	0.00	0.00	4.57	0.00	4.38	0.00	0.00	RS131_ARATH	58.94	gi|294944631|	40SribosomalproteinS13
TRINITY_DN91629_c1_g3_i1	6.92	0.00	6.75	0.00	0.00	0.00	4.56	0.00	3.95	0.00	0.00	HSP74_TRYBB	89.59	gi|133711697|	70kDaheatshockprotein[Trypanosomarangeli]
TRINITY_DN71571_c0_g1_i1	10.60	0.00	3.06	0.00	0.00	0.00	4.55	0.00	5.45	0.00	0.00	CYPH_SCHPO	72.84	gi|13377788|	cyclophilinA[Cryptococcusneoformansvar.neoformans]
TRINITY_DN32872_c0_g1_i1	9.66	0.00	3.96	0.00	0.00	0.00	4.54	0.00	4.86	0.00	0.00	CATR1_PARTE	34.18	gi|403331481|	Centrin
TRINITY_DN169349_c0_g1_i1	8.56	0.00	5.04	0.00	0.00	0.00	4.53	0.00	4.30	0.00	0.00				
TRINITY_DN36604_c0_g1_i1	4.53	0.00	9.04	0.00	0.00	0.00	4.52	0.00	4.52	0.00	0.00	EF1A2_TRYB2	88.76	gi|61207302|	elongationfactor1-alpha
TRINITY_DN54746_c0_g1_i1	8.20	0.00	5.37	0.00	0.00	0.00	4.52	0.00	4.16	0.00	0.00				
TRINITY_DN21636_c0_g1_i1	4.55	5.91	3.09	0.00	0.00	0.00	4.52	0.00	1.41	0.00	0.00				
TRINITY_DN31860_c0_g1_i1	4.45	9.09	0.00	0.00	0.00	0.00	4.51	0.00	4.54	0.00	0.00	RL7A_TAKRU	75	gi|52138653|	60SribosomalproteinL7a[Gallusgallus]>gi|417673|sp|P32429.2|RL7A_CHICKRecName:Full=60SribosomalproteinL7a[Gallusgallus]>gi|63778|emb|CAA44506.1|ribosomalproteinL7a[Gallusgallus]>gi|601884|dbj|BAA03395.1|ribosomalproteinL7a[Gallusgallus]>gi|28866784|dbj|BAC65169.1|ribosomalproteinL7a[Gallusgallus]
TRINITY_DN8966_c0_g1_i1	10.06	0.00	3.42	0.00	0.00	0.00	4.50	0.00	5.12	0.00	0.00	EF1A_TETPY	90.83	gi|630567684|	elongationfactor2
TRINITY_DN196184_c0_g1_i1	4.69	0.00	8.76	0.00	0.00	0.00	4.48	0.00	4.39	0.00	0.00				
TRINITY_DN2077_c0_g1_i1	9.02	4.41	0.00	0.00	0.00	0.00	4.48	0.00	4.51	0.00	0.00				
TRINITY_DN82968_c0_g1_i3	6.03	0.00	7.34	0.00	0.00	0.00	4.46	0.00	3.92	0.00	0.00	RS32_ARATH	62.33	gi|729329460|	PREDICTED:40SribosomalproteinS3-3[Tarenayahassleriana]
TRINITY_DN54002_c0_g1_i1	3.79	4.33	5.24	0.00	0.00	0.00	4.46	0.00	0.73	0.00	0.00				
TRINITY_DN95636_c0_g1_i1	6.01	7.35	0.00	0.00	0.00	0.00	4.45	0.00	3.91	0.00	0.00				
TRINITY_DN35556_c0_g2_i1	4.89	3.83	4.64	0.00	0.00	0.00	4.45	0.00	0.55	0.00	0.00	LAMC2_MOUSE	30.86	gi|145354416|	predictedprotein[OstreococcuslucimarinusCCE9901]>gi|144581718|gb|ABO99774.1|predictedprotein[OstreococcuslucimarinusCCE9901]
TRINITY_DN95447_c0_g1_i1	3.74	3.48	6.12	0.00	0.00	0.00	4.44	0.00	1.46	0.00	0.00	AB32G_ARATH	33.33	gi|145532070|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124419462|emb|CAK84399.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN172235_c0_g1_i1	7.99	5.33	0.00	0.00	0.00	0.00	4.44	0.00	4.07	0.00	0.00				
TRINITY_DN75632_c0_g1_i1	0.00	6.04	7.29	0.00	0.00	0.00	4.44	0.00	3.90	0.00	0.00				
TRINITY_DN54875_c0_g1_i1	4.17	6.08	3.04	0.00	0.00	0.00	4.43	0.00	1.53	0.00	0.00	RL22_RAT	54.44	gi|648171506|	hypotheticalproteinGALMADRAFT_233757[GalerinamarginataCBS339.88]
TRINITY_DN66582_c0_g1_i1	6.65	6.64	0.00	0.00	0.00	0.00	4.43	0.00	3.84	0.00	0.00	CYTA2_DICDI	45.65	gi|558127957|	PREDICTED:cystatin-B-like[Myotislucifugus]
TRINITY_DN70512_c0_g1_i1	9.54	0.00	3.74	0.00	0.00	0.00	4.43	0.00	4.81	0.00	0.00	SODM_CHLPN	59.09	gi|769938077|	superoxidedismutase[Chlamydophilaabortus]>gi|704849250|emb|CED80391.1|superoxidedismutase[Chlamydophilaabortus]
TRINITY_DN37906_c0_g1_i1	9.70	0.00	3.54	0.00	0.00	0.00	4.41	0.00	4.91	0.00	0.00				
TRINITY_DN81085_c0_g2_i1	4.31	4.16	4.74	0.00	0.00	0.00	4.40	0.00	0.30	0.00	0.00				
TRINITY_DN154110_c0_g1_i1	9.54	3.66	0.00	0.00	0.00	0.00	4.40	0.00	4.81	0.00	0.00				
TRINITY_DN33922_c0_g1_i1	5.89	3.06	4.23	0.00	0.00	0.00	4.39	0.00	1.42	0.00	0.00	PPGB_HUMAN	46.88	gi|507663926|	PREDICTED:lysosomalprotectiveprotein[Octodondegus]
TRINITY_DN64224_c0_g1_i1	3.05	5.93	4.18	0.00	0.00	0.00	4.39	0.00	1.45	0.00	0.00				
TRINITY_DN119879_c0_g1_i1	7.26	0.00	5.90	0.00	0.00	0.00	4.39	0.00	3.86	0.00	0.00	RL5A_XENLA	66.17	gi|638252880|	ribosomalproteinL5[Callorhinchusmilii]>gi|387914542|gb|AFK10880.1|60SribosomalproteinL5-A[Callorhinchusmilii]>gi|392874810|gb|AFM86237.1|60SribosomalproteinL5-A[Callorhinchusmilii]>gi|392875840|gb|AFM86752.1|60SribosomalproteinL5-A[Callorhinchusmilii]>gi|392876130|gb|AFM86897.1|60SribosomalproteinL5-A[Callorhinchusmilii]>gi|392879336|gb|AFM88500.1|60SribosomalproteinL5-A[Callorhinchusmilii]>gi|392882240|gb|AFM89952.1|60SribosomalproteinL5-A[Callorhinchusmilii]>gi|392883268|gb|AFM90466.1|60SribosomalproteinL5-A[Callorhinchusmilii]
TRINITY_DN87798_c0_g1_i1	4.29	5.16	3.68	0.00	0.00	0.00	4.38	0.00	0.75	0.00	0.00				
TRINITY_DN80980_c0_g1_i1	6.85	0.00	6.28	0.00	0.00	0.00	4.38	0.00	3.80	0.00	0.00	RL3_ORYSJ	58.82	gi|731694903|	ribosomalproteinL3
TRINITY_DN65235_c0_g1_i1	4.10	0.00	8.98	0.00	0.00	0.00	4.36	0.00	4.50	0.00	0.00	GSTMU_MESAU	52.44	gi|118373867|	GlutathioneS-transferase
TRINITY_DN88359_c0_g1_i1	4.03	0.00	9.05	0.00	0.00	0.00	4.36	0.00	4.53	0.00	0.00	YAHK_ECOLI	35.29	gi|736949173|	hydroxyaciddehydrogenase[Erwiniaoleae]
TRINITY_DN82010_c0_g1_i2	8.31	4.74	0.00	0.00	0.00	0.00	4.35	0.00	4.17	0.00	0.00				
TRINITY_DN32528_c0_g1_i1	0.00	3.76	9.27	0.00	0.00	0.00	4.35	0.00	4.66	0.00	0.00	CCD65_CHLRE	47.37	gi|302844556|	hypotheticalproteinVOLCADRAFT_106097[Volvoxcarterif.nagariensis]>gi|300260926|gb|EFJ45142.1|hypotheticalproteinVOLCADRAFT_106097
TRINITY_DN57028_c0_g1_i1	7.20	5.82	0.00	0.00	0.00	0.00	4.34	0.00	3.82	0.00	0.00				
TRINITY_DN86719_c0_g1_i3	3.29	5.09	4.64	0.00	0.00	0.00	4.34	0.00	0.94	0.00	0.00	LYSG2_DICDI	38.91	gi|735856890|	hypotheticalproteinSAMD00019534_042990
TRINITY_DN64431_c0_g2_i1	9.11	3.89	0.00	0.00	0.00	0.00	4.34	0.00	4.57	0.00	0.00				

TRINITY_DN89491_c0_g1_i1	3.93	3.04	6.02	0.00	0.00	0.00	4.33	0.00	1.53	0.00	0.00	COROA_DICDI	57.05	gi|384493922|	hypotheticalproteinRO3G_09123[RhizopusdelemarRA99-880]
TRINITY_DN77314_c0_g1_i1	5.02	0.00	7.97	0.00	0.00	0.00	4.33	0.00	4.03	0.00	0.00				
TRINITY_DN77249_c0_g1_i1	6.22	6.75	0.00	0.00	0.00	0.00	4.32	0.00	3.75	0.00	0.00	ACBP_CHAVI	46.75	gi|495451013|	MULTISPECIES:acyl-CoA-bindingprotein[Marinobacter]>gi|311696368|gb|ADP99241.1|acyl-coA-bindingprotein
TRINITY_DN20228_c0_g1_i1	9.21	0.00	3.75	0.00	0.00	0.00	4.32	0.00	4.63	0.00	0.00				
TRINITY_DN146837_c0_g1_i1	0.00	5.58	7.36	0.00	0.00	0.00	4.32	0.00	3.84	0.00	0.00				
TRINITY_DN90685_c0_g1_i6	3.87	3.37	5.70	0.00	0.00	0.00	4.31	0.00	1.23	0.00	0.00	RAC1_RAT	85.38	gi|675883478|	hypotheticalproteinHELRODRAFT_69003[Helobdellarobusta]>gi|260667435|gb|ACX47928.1|RacsmallGTPase[Helobdellasp.DHK-2009]>gi|555691179|gb|ESN94411.1|hypotheticalproteinHELRODRAFT_69003[Helobdellarobusta]
TRINITY_DN105017_c0_g1_i1	7.14	5.79	0.00	0.00	0.00	0.00	4.31	0.00	3.79	0.00	0.00				
TRINITY_DN221334_c0_g1_i1	0.00	7.52	5.40	0.00	0.00	0.00	4.31	0.00	3.88	0.00	0.00				
TRINITY_DN18464_c0_g1_i1	8.11	4.80	0.00	0.00	0.00	0.00	4.30	0.00	4.08	0.00	0.00	MYCB2_MOUSE	41.18	gi|780616715|	PREDICTED:E3ubiquitin-proteinligaseMYCBP2[Wasmanniaauropunctata]
TRINITY_DN79201_c0_g2_i1	5.54	0.00	7.34	0.00	0.00	0.00	4.29	0.00	3.83	0.00	0.00	BIP5_TOBAC	69.52	gi|763751521|	hypotheticalproteinB456_003G074600[Gossypiumraimondii]
TRINITY_DN79018_c0_g1_i1	0.00	6.60	6.28	0.00	0.00	0.00	4.29	0.00	3.72	0.00	0.00	PPIB_DICDI	78.95	gi|728829212|	Peptidyl-prolylcis-transisomeraseCYP20-1-likeprotein[Gossypiumarboreum]
TRINITY_DN85908_c0_g1_i2	5.03	0.00	7.84	0.00	0.00	0.00	4.29	0.00	3.97	0.00	0.00	EF2_CHICK	67.72	gi|554930505|	elongationfactor2[TrypanosomarangeliSC58]>gi|554931566|gb|ESL05986.1|elongationfactor2[TrypanosomarangeliSC58]>gi|554939383|gb|ESL09195.1|elongationfactor2[TrypanosomarangeliSC58]
TRINITY_DN48346_c0_g1_i1	8.95	3.91	0.00	0.00	0.00	0.00	4.29	0.00	4.49	0.00	0.00				
TRINITY_DN217778_c0_g1_i1	6.14	0.00	6.72	0.00	0.00	0.00	4.29	0.00	3.72	0.00	0.00				
TRINITY_DN40692_c0_g2_i1	6.61	0.00	6.22	0.00	0.00	0.00	4.28	0.00	3.71	0.00	0.00	GRP78_PIG	64.45	gi|224058097|	BiPisoformAfamilyprotein[Populustrichocarpa]>gi|222846706|gb|EEE84253.1|BiPisoformAfamilyprotein[Populustrichocarpa]
TRINITY_DN6839_c0_g2_i1	3.07	4.69	5.03	0.00	0.00	0.00	4.26	0.00	1.04	0.00	0.00	LUZP4_HUMAN	28.36	gi|749824634|	hypotheticalproteinPAXINDRAFT_46183
TRINITY_DN140806_c0_g1_i1	8.31	0.00	4.42	0.00	0.00	0.00	4.24	0.00	4.16	0.00	0.00				
TRINITY_DN95170_c0_g1_i1	7.21	5.51	0.00	0.00	0.00	0.00	4.24	0.00	3.77	0.00	0.00	VA0E_ASHGO	38.89	gi|403333085|	Hydrogen-transportingATPsynthase[Oxytrichatrifallax]
TRINITY_DN101169_c0_g1_i1	7.60	0.00	5.10	0.00	0.00	0.00	4.23	0.00	3.87	0.00	0.00	SC61B_MOUSE	43.9	gi|729435322|	PREDICTED:uncharacterizedproteinLOC104799494[Tarenayahassleriana]
TRINITY_DN137185_c0_g1_i1	4.74	0.00	7.86	0.00	0.00	0.00	4.20	0.00	3.96	0.00	0.00				
TRINITY_DN62405_c0_g1_i1	3.09	0.00	9.50	0.00	0.00	0.00	4.20	0.00	4.85	0.00	0.00				
TRINITY_DN193501_c0_g1_i1	9.53	0.00	3.01	0.00	0.00	0.00	4.18	0.00	4.87	0.00	0.00				
TRINITY_DN220098_c0_g1_i1	7.49	0.00	5.04	0.00	0.00	0.00	4.18	0.00	3.82	0.00	0.00				
TRINITY_DN146232_c0_g1_i1	5.97	0.00	6.54	0.00	0.00	0.00	4.17	0.00	3.62	0.00	0.00	CTL2A_MOUSE	45	gi|229594208|	Papainfamilycysteineproteasecontainingprotein[Tetrahymenathermophila]>gi|225567000|gb|EAR83984.3|papainfamilycysteineprotease[TetrahymenathermophilaSB210]
TRINITY_DN167228_c0_g1_i1	5.71	0.00	6.80	0.00	0.00	0.00	4.17	0.00	3.65	0.00	0.00				
TRINITY_DN206614_c0_g1_i1	8.99	0.00	3.50	0.00	0.00	0.00	4.17	0.00	4.53	0.00	0.00				
TRINITY_DN118112_c0_g1_i1	4.96	7.54	0.00	0.00	0.00	0.00	4.16	0.00	3.83	0.00	0.00	ACBD5_PONAB	45.78	gi|471271538|	acyl-CoA-bindingprotein3[Rhodniusprolixus]
TRINITY_DN27764_c0_g1_i1	8.58	3.92	0.00	0.00	0.00	0.00	4.16	0.00	4.29	0.00	0.00	CITA_KLEPN	33.33	gi|145507440|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124406870|emb|CAK72278.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN85670_c0_g1_i1	4.88	3.72	3.90	0.00	0.00	0.00	4.16	0.00	0.62	0.00	0.00	H2BE2_PSAMI	71.03	gi|544429568|	PREDICTED:histoneH2Btype1-F/J/L-likeisoformX1[Macacafascicularis]>gi|544429570|ref|XP_005553795.1|PREDICTED:histoneH2Btype1-F/J/L-likeisoformX2[Macacafascicularis]
TRINITY_DN79581_c0_g1_i1	3.76	4.19	4.54	0.00	0.00	0.00	4.16	0.00	0.39	0.00	0.00	NH2L1_XENTR	71.43	gi|543263164|	PREDICTED:NHP2-likeprotein1[Geospizafortis]
TRINITY_DN42983_c0_g1_i1	8.91	0.00	3.57	0.00	0.00	0.00	4.16	0.00	4.48	0.00	0.00				
TRINITY_DN20127_c0_g1_i1	9.15	0.00	3.33	0.00	0.00	0.00	4.16	0.00	4.63	0.00	0.00	GBLP_DROME	23.19	gi|524939691|	PREDICTED:guaninenucleotide-bindingproteinsubunitbeta-2-like1[Mesocricetusauratus]
TRINITY_DN12118_c0_g1_i1	0.00	7.46	5.01	0.00	0.00	0.00	4.16	0.00	3.80	0.00	0.00				
TRINITY_DN79686_c0_g2_i1	3.77	0.00	8.67	0.00	0.00	0.00	4.15	0.00	4.35	0.00	0.00	GPX4_SOLLC	40.72	gi|502782833|	glutathioneperoxidase[Stackebrandtianassauensis]>gi|290569273|gb|ADD42238.1|Peroxiredoxin[StackebrandtianassauensisDSM44728]
TRINITY_DN189994_c0_g1_i1	5.87	0.00	6.57	0.00	0.00	0.00	4.15	0.00	3.61	0.00	0.00				
TRINITY_DN9922_c0_g1_i1	0.00	6.00	6.43	0.00	0.00	0.00	4.14	0.00	3.59	0.00	0.00				
TRINITY_DN3010_c0_g1_i1	3.72	0.00	8.66	0.00	0.00	0.00	4.13	0.00	4.34	0.00	0.00				
TRINITY_DN34264_c0_g1_i1	8.42	0.00	3.95	0.00	0.00	0.00	4.12	0.00	4.21	0.00	0.00	HCDH_RAT	48.39	gi|471190487|	hypotheticalproteinEIN_408930[EntamoebainvadensIP1]>gi|440292409|gb|ELP85614.1|hypotheticalproteinEIN_408930[EntamoebainvadensIP1]
TRINITY_DN147028_c0_g1_i1	8.05	0.00	4.31	0.00	0.00	0.00	4.12	0.00	4.03	0.00	0.00				
TRINITY_DN220641_c0_g1_i1	4.52	3.43	4.40	0.00	0.00	0.00	4.12	0.00	0.60	0.00	0.00				
TRINITY_DN41782_c0_g1_i1	6.50	5.84	0.00	0.00	0.00	0.00	4.11	0.00	3.58	0.00	0.00	4CLL7_ORYSJ	40	gi|290984607|	predictedprotein[Naegleriagruberi]>gi|284088612|gb|EFC42274.1|predictedprotein[Naegleriagruberi]
TRINITY_DN53821_c0_g1_i1	0.00	7.21	5.12	0.00	0.00	0.00	4.11	0.00	3.71	0.00	0.00				
TRINITY_DN23087_c0_g1_i1	6.23	6.10	0.00	0.00	0.00	0.00	4.11	0.00	3.56	0.00	0.00	MYBAA_DICDI	44.57	gi|731335829|	PREDICTED:transcriptionfactorMYB98-like[Betavulgarissubsp.vulgaris]
TRINITY_DN4079_c0_g1_i1	3.73	3.39	5.20	0.00	0.00	0.00	4.11	0.00	0.96	0.00	0.00				
TRINITY_DN86834_c0_g2_i4	3.19	0.00	9.12	0.00	0.00	0.00	4.10	0.00	4.63	0.00	0.00	RL13_SCHMA	44.87	gi|407397276|	60SribosomalproteinL13
TRINITY_DN32116_c0_g1_i1	5.38	3.16	3.76	0.00	0.00	0.00	4.10	0.00	1.15	0.00	0.00	SLD3_YEAST	36.36	gi|471228073|	hypotheticalproteinIMG5_109590[Ichthyophthiriusmultifiliis]>gi|340505070|gb|EGR31441.1|hypotheticalproteinIMG5_109590[Ichthyophthiriusmultifiliis]
TRINITY_DN174048_c0_g1_i1	4.60	0.00	7.68	0.00	0.00	0.00	4.09	0.00	3.87	0.00	0.00				
TRINITY_DN92298_c0_g2_i1	5.26	0.00	7.02	0.00	0.00	0.00	4.09	0.00	3.65	0.00	0.00				
TRINITY_DN220486_c0_g1_i1	4.02	3.08	5.17	0.00	0.00	0.00	4.09	0.00	1.05	0.00	0.00				
TRINITY_DN52371_c0_g1_i1	3.29	4.26	4.70	0.00	0.00	0.00	4.08	0.00	0.72	0.00	0.00	TRXR1_EMIHU	53.73	gi|551535335|	thioredoxinreductase[EmilianiahuxleyiCCMP1516]>gi|485603363|gb|EOD04034.1|thioredoxinreductase[EmilianiahuxleyiCCMP1516]
TRINITY_DN147175_c0_g1_i1	8.60	0.00	3.63	0.00	0.00	0.00	4.08	0.00	4.31	0.00	0.00				
TRINITY_DN70454_c0_g1_i1	0.00	3.57	8.64	0.00	0.00	0.00	4.07	0.00	4.34	0.00	0.00	MGLL_RAT	28.96	gi|566214819|	hypotheticalproteinPOPTR_0018s08180g[Populustrichocarpa]>gi|550318313|gb|ERP49833.1|hypotheticalproteinPOPTR_0018s08180g[Populustrichocarpa]
TRINITY_DN96703_c0_g1_i1	9.05	3.12	0.00	0.00	0.00	0.00	4.06	0.00	4.60	0.00	0.00	GLRX5_HUMAN	47.47	gi|739627709|	glutaredoxin[Sphaerotilusnatans]>gi|633286246|gb|KDB51207.1|glutaredoxin-likeprotein[Sphaerotilusnatanssubsp.natansDSM6575]

TRINITY_DN55201_c0_g1_i1	7.45	0.00	4.72	0.00	0.00	0.00	4.05	0.00	3.77	0.00	0.00	QCR1_BOVIN	31.03	gi|146183516|	Insulinase(PeptidasefamilyM16)[Tetrahymenathermophila]>gi|146143565|gb|EAS06124.2|peptidaseM16inactivedomainprotein[TetrahymenathermophilaSB210]
TRINITY_DN171536_c0_g1_i1	8.56	0.00	3.60	0.00	0.00	0.00	4.05	0.00	4.30	0.00	0.00				
TRINITY_DN71412_c0_g1_i2	4.69	0.00	7.47	0.00	0.00	0.00	4.05	0.00	3.77	0.00	0.00	TBA_TETPY	99.1	gi|399146179|	alpha-tubulin
TRINITY_DN60086_c0_g1_i1	0.00	3.25	8.90	0.00	0.00	0.00	4.05	0.00	4.50	0.00	0.00	SPAG6_MOUSE	28.08	gi|298714886|	Putative[Ectocarpussiliculosus]
TRINITY_DN1321_c0_g1_i1	0.00	7.67	4.47	0.00	0.00	0.00	4.05	0.00	3.85	0.00	0.00	CLP1_DEBHA	43.9	gi|471225781|	lightintermediatepolypeptide2
TRINITY_DN64468_c0_g1_i1	3.86	3.38	4.89	0.00	0.00	0.00	4.04	0.00	0.77	0.00	0.00	DCOR_DATST	36.11	gi|28627544|	putativeornithinedecarboxylase1[Capsicumannuum]
TRINITY_DN48920_c0_g2_i1	6.95	0.00	5.16	0.00	0.00	0.00	4.04	0.00	3.61	0.00	0.00	CATR5_PARTE	26.09	gi|66359714|	centrin
TRINITY_DN113928_c0_g1_i1	6.39	0.00	5.72	0.00	0.00	0.00	4.04	0.00	3.51	0.00	0.00				
TRINITY_DN52314_c0_g1_i1	4.01	3.59	4.50	0.00	0.00	0.00	4.03	0.00	0.46	0.00	0.00				
TRINITY_DN177850_c0_g1_i1	6.11	5.99	0.00	0.00	0.00	0.00	4.03	0.00	3.49	0.00	0.00				
TRINITY_DN176873_c0_g1_i1	3.17	3.22	5.70	0.00	0.00	0.00	4.03	0.00	1.45	0.00	0.00				
TRINITY_DN219602_c0_g1_i1	3.47	8.59	0.00	0.00	0.00	0.00	4.02	0.00	4.32	0.00	0.00				
TRINITY_DN139952_c0_g1_i1	5.28	3.22	3.56	0.00	0.00	0.00	4.02	0.00	1.10	0.00	0.00				
TRINITY_DN52867_c0_g1_i1	4.96	3.27	3.81	0.00	0.00	0.00	4.02	0.00	0.86	0.00	0.00				
TRINITY_DN38827_c0_g1_i1	4.85	0.00	7.20	0.00	0.00	0.00	4.02	0.00	3.67	0.00	0.00	GGPPS_MOUSE	35.63	gi|557867574|	polyprenylsynthase[TrypanosomacruziDm28c]
TRINITY_DN50960_c0_g1_i1	4.84	3.68	3.53	0.00	0.00	0.00	4.02	0.00	0.72	0.00	0.00				
TRINITY_DN213118_c0_g1_i1	3.23	3.40	5.40	0.00	0.00	0.00	4.01	0.00	1.21	0.00	0.00				
TRINITY_DN80243_c0_g1_i1	3.65	4.66	3.71	0.00	0.00	0.00	4.01	0.00	0.57	0.00	0.00	PEF1_XENLA	25.27	gi|326491983|	predictedprotein[Hordeumvulgaresubsp.vulgare]
TRINITY_DN78853_c0_g2_i1	3.13	5.04	3.83	0.00	0.00	0.00	4.00	0.00	0.96	0.00	0.00	PCKA_DICDI	54.77	gi|589291436|	phosphoenolpyruvatecarboxykinase[Halorhodospirahalochlorisstr.A]
TRINITY_DN215245_c0_g1_i1	3.69	5.05	3.24	0.00	0.00	0.00	4.00	0.00	0.94	0.00	0.00				
TRINITY_DN55451_c0_g1_i1	8.22	3.75	0.00	0.00	0.00	0.00	3.99	0.00	4.12	0.00	0.00				
TRINITY_DN62466_c0_g1_i1	3.92	4.58	3.42	0.00	0.00	0.00	3.98	0.00	0.58	0.00	0.00	BGBP_PENMO	49.41	gi|57490775|	beta-1
TRINITY_DN182153_c0_g1_i1	5.66	0.00	6.27	0.00	0.00	0.00	3.98	0.00	3.46	0.00	0.00				
TRINITY_DN63834_c0_g2_i1	5.20	0.00	6.72	0.00	0.00	0.00	3.97	0.00	3.52	0.00	0.00				
TRINITY_DN115685_c0_g1_i1	5.63	0.00	6.27	0.00	0.00	0.00	3.97	0.00	3.45	0.00	0.00				
TRINITY_DN84665_c0_g2_i1	7.62	0.00	4.26	0.00	0.00	0.00	3.96	0.00	3.82	0.00	0.00	PPIB_DICDI	75.31	gi|636626609|	cyclophilin[TrametesversicolorFP-101664SS1]>gi|392559726|gb|EIW52910.1|cyclophilin[TrametesversicolorFP-101664SS1]
TRINITY_DN8468_c0_g1_i1	8.60	3.27	0.00	0.00	0.00	0.00	3.96	0.00	4.34	0.00	0.00				
TRINITY_DN100942_c0_g1_i1	0.00	5.96	5.91	0.00	0.00	0.00	3.96	0.00	3.43	0.00	0.00				
TRINITY_DN220073_c0_g1_i1	6.39	5.47	0.00	0.00	0.00	0.00	3.95	0.00	3.45	0.00	0.00				
TRINITY_DN133866_c0_g1_i1	8.06	0.00	3.78	0.00	0.00	0.00	3.95	0.00	4.03	0.00	0.00				
TRINITY_DN32446_c0_g1_i1	4.44	0.00	7.35	0.00	0.00	0.00	3.93	0.00	3.70	0.00	0.00	AP1M_DICDI	49.17	gi|470242484|	mu1[Dictyosteliumfasciculatum]>gi|328868111|gb|EGG16491.1|mu1[Dictyosteliumfasciculatum]
TRINITY_DN79455_c0_g2_i1	3.93	3.75	4.11	0.00	0.00	0.00	3.93	0.00	0.18	0.00	0.00	IDHC_PONAB	68.56	gi|617494329|	PREDICTED:isocitratedehydrogenase[NADP]cytoplasmic[Poeciliaformosa]
TRINITY_DN218147_c0_g1_i1	6.05	0.00	5.72	0.00	0.00	0.00	3.92	0.00	3.40	0.00	0.00				
TRINITY_DN43928_c0_g1_i1	4.12	3.13	4.51	0.00	0.00	0.00	3.92	0.00	0.71	0.00	0.00	TVP23_YARLI	27.62	gi|339243095|	proteinFAM18B[Trichinellaspiralis]>gi|316973723|gb|EFV57282.1|proteinFAM18B[Trichinellaspiralis]
TRINITY_DN167566_c0_g1_i1	4.09	4.17	3.49	0.00	0.00	0.00	3.92	0.00	0.37	0.00	0.00				
TRINITY_DN222234_c0_g1_i1	7.28	4.47	0.00	0.00	0.00	0.00	3.92	0.00	3.67	0.00	0.00				
TRINITY_DN40441_c0_g1_i1	4.91	6.84	0.00	0.00	0.00	0.00	3.92	0.00	3.53	0.00	0.00	YM9I_CAEEL	40	gi|736194079|	PREDICTED:putativeserineproteaseF56F10.1
TRINITY_DN70753_c0_g1_i1	5.86	0.00	5.89	0.00	0.00	0.00	3.92	0.00	3.39	0.00	0.00				
TRINITY_DN68238_c0_g1_i1	6.82	4.93	0.00	0.00	0.00	0.00	3.92	0.00	3.52	0.00	0.00	TTYH2_XENTR	30.36	gi|471227411|	hypotheticalproteinIMG5_117260[Ichthyophthiriusmultifiliis]>gi|340504712|gb|EGR31133.1|hypotheticalproteinIMG5_117260[Ichthyophthiriusmultifiliis]
TRINITY_DN65365_c0_g1_i1	0.00	6.87	4.87	0.00	0.00	0.00	3.91	0.00	3.53	0.00	0.00				
TRINITY_DN7261_c0_g1_i1	5.48	6.25	0.00	0.00	0.00	0.00	3.91	0.00	3.41	0.00	0.00				
TRINITY_DN2061_c0_g1_i1	3.05	5.41	3.25	0.00	0.00	0.00	3.90	0.00	1.31	0.00	0.00				
TRINITY_DN221133_c0_g1_i1	6.03	0.00	5.68	0.00	0.00	0.00	3.90	0.00	3.39	0.00	0.00				
TRINITY_DN118878_c0_g1_i1	8.48	3.23	0.00	0.00	0.00	0.00	3.90	0.00	4.28	0.00	0.00	RL19_TETTS	71.83	gi|582044903|	ChainR
TRINITY_DN218800_c0_g1_i1	8.45	3.24	0.00	0.00	0.00	0.00	3.90	0.00	4.26	0.00	0.00				
TRINITY_DN59202_c0_g1_i1	3.97	3.34	4.33	0.00	0.00	0.00	3.88	0.00	0.50	0.00	0.00				
TRINITY_DN39713_c0_g1_i1	3.10	3.71	4.83	0.00	0.00	0.00	3.88	0.00	0.88	0.00	0.00	PCSK5_MOUSE	27.53	gi|542190209|	PREDICTED:proproteinconvertasesubtilisin/kexintype5-likeisoformX1[Oreochromisniloticus]
TRINITY_DN149132_c0_g1_i1	0.00	4.79	6.82	0.00	0.00	0.00	3.87	0.00	3.50	0.00	0.00				
TRINITY_DN25758_c0_g1_i1	4.97	0.00	6.63	0.00	0.00	0.00	3.87	0.00	3.45	0.00	0.00				
TRINITY_DN64519_c0_g1_i1	7.39	0.00	4.20	0.00	0.00	0.00	3.86	0.00	3.71	0.00	0.00	RL13_TETTS	50.51	gi|630030314|	hypotheticalproteinPFICI_10372[PestalotiopsisficiW106-1]>gi|573058473|gb|ETS78310.1|hypotheticalproteinPFICI_10372[PestalotiopsisficiW106-1]
TRINITY_DN187981_c0_g1_i1	6.67	0.00	4.91	0.00	0.00	0.00	3.86	0.00	3.46	0.00	0.00				
TRINITY_DN94743_c0_g1_i1	7.04	0.00	4.48	0.00	0.00	0.00	3.84	0.00	3.56	0.00	0.00				
TRINITY_DN214289_c0_g1_i1	7.58	0.00	3.93	0.00	0.00	0.00	3.84	0.00	3.79	0.00	0.00				
TRINITY_DN65913_c0_g1_i2	7.67	0.00	3.84	0.00	0.00	0.00	3.84	0.00	3.84	0.00	0.00				
TRINITY_DN41130_c1_g1_i1	4.88	0.00	6.62	0.00	0.00	0.00	3.83	0.00	3.43	0.00	0.00	RL11_MEDSA	80	gi|658015503|	PREDICTED:60SribosomalproteinL11-likeisoformX1[Malusdomestica]
TRINITY_DN187606_c0_g1_i1	4.23	0.00	7.25	0.00	0.00	0.00	3.83	0.00	3.64	0.00	0.00				
TRINITY_DN149865_c0_g1_i1	4.52	6.94	0.00	0.00	0.00	0.00	3.82	0.00	3.52	0.00	0.00				
TRINITY_DN73058_c0_g1_i1	7.00	4.46	0.00	0.00	0.00	0.00	3.82	0.00	3.54	0.00	0.00				
TRINITY_DN64779_c0_g2_i1	8.03	3.42	0.00	0.00	0.00	0.00	3.82	0.00	4.03	0.00	0.00				
TRINITY_DN4057_c0_g1_i1	4.87	6.59	0.00	0.00	0.00	0.00	3.82	0.00	3.42	0.00	0.00				
TRINITY_DN56065_c0_g1_i1	3.08	0.00	8.36	0.00	0.00	0.00	3.81	0.00	4.23	0.00	0.00				
TRINITY_DN37282_c0_g1_i1	6.84	0.00	4.59	0.00	0.00	0.00	3.81	0.00	3.49	0.00	0.00				
TRINITY_DN188856_c0_g1_i1	0.00	7.61	3.81	0.00	0.00	0.00	3.81	0.00	3.81	0.00	0.00				
TRINITY_DN219301_c0_g1_i1	4.05	7.38	0.00	0.00	0.00	0.00	3.81	0.00	3.69	0.00	0.00				

TRINITY_DN11997_c0_g1_i1	7.81	3.59	0.00	0.00	0.00	0.00	3.80	0.00	3.91	0.00	0.00				
TRINITY_DN177817_c0_g1_i1	7.55	3.85	0.00	0.00	0.00	0.00	3.80	0.00	3.78	0.00	0.00				
TRINITY_DN190156_c0_g1_i1	7.49	0.00	3.89	0.00	0.00	0.00	3.79	0.00	3.74	0.00	0.00				
TRINITY_DN33682_c0_g1_i1	0.00	3.33	8.04	0.00	0.00	0.00	3.79	0.00	4.04	0.00	0.00				
TRINITY_DN206914_c0_g1_i1	6.39	0.00	4.97	0.00	0.00	0.00	3.79	0.00	3.36	0.00	0.00				
TRINITY_DN128758_c0_g1_i1	5.28	6.06	0.00	0.00	0.00	0.00	3.78	0.00	3.30	0.00	0.00	UBC4_YEAST	45.16	gi|268637909|	hypotheticalproteinDDB_G0282783[DictyosteliumdiscoideumAX4]>gi|256012934|gb|EAL66251.2|hypotheticalproteinDDB_G0282783[DictyosteliumdiscoideumAX4]
TRINITY_DN151389_c0_g1_i1	4.32	0.00	7.01	0.00	0.00	0.00	3.78	0.00	3.54	0.00	0.00				
TRINITY_DN66715_c0_g1_i2	3.85	3.01	4.46	0.00	0.00	0.00	3.77	0.00	0.73	0.00	0.00	CTNS_CAEEL	41.08	gi|24649193|	CG17119
TRINITY_DN75888_c0_g1_i1	6.08	0.00	5.21	0.00	0.00	0.00	3.76	0.00	3.29	0.00	0.00	MAP1_STAAW	26.19	gi|154337423|	conservedhypotheticalprotein[LeishmaniabraziliensisMHOM/BR/75/M2904]>gi|134061983|emb|CAM45069.1|conservedhypotheticalprotein[LeishmaniabraziliensisMHOM/BR/75/M2904]
TRINITY_DN149668_c0_g1_i1	4.05	3.08	4.12	0.00	0.00	0.00	3.75	0.00	0.58	0.00	0.00				
TRINITY_DN83048_c0_g2_i1	4.06	0.00	7.19	0.00	0.00	0.00	3.75	0.00	3.60	0.00	0.00	EF2_NAUCC	63.06	gi|528254324|	elongationfactor2[Strigomonasculicis]
TRINITY_DN30039_c0_g1_i1	7.49	3.75	0.00	0.00	0.00	0.00	3.75	0.00	3.74	0.00	0.00	NOTC4_HUMAN	41.03	gi|403347829|	hypotheticalproteinOXYTRI_05523[Oxytrichatrifallax]
TRINITY_DN174225_c0_g1_i1	0.00	5.19	6.03	0.00	0.00	0.00	3.74	0.00	3.26	0.00	0.00				
TRINITY_DN140833_c1_g2_i1	5.26	5.95	0.00	0.00	0.00	0.00	3.74	0.00	3.25	0.00	0.00				
TRINITY_DN88374_c0_g1_i1	3.10	3.49	4.61	0.00	0.00	0.00	3.73	0.00	0.78	0.00	0.00	CYSP5_DICDI	54.43	gi|330805277|	hypotheticalproteinDICPUDRAFT_81345[Dictyosteliumpurpureum]>gi|325079250|gb|EGC32859.1|hypotheticalproteinDICPUDRAFT_81345[Dictyosteliumpurpureum]
TRINITY_DN75433_c0_g1_i2	3.10	4.53	3.55	0.00	0.00	0.00	3.72	0.00	0.73	0.00	0.00	BTF3_MOUSE	40.83	gi|374533578|	basictranscriptionfactor3
TRINITY_DN146847_c0_g1_i1	6.93	4.24	0.00	0.00	0.00	0.00	3.72	0.00	3.49	0.00	0.00				
TRINITY_DN212378_c0_g1_i1	3.89	3.63	3.64	0.00	0.00	0.00	3.72	0.00	0.14	0.00	0.00				
TRINITY_DN20216_c0_g1_i1	7.21	0.00	3.95	0.00	0.00	0.00	3.72	0.00	3.61	0.00	0.00				
TRINITY_DN52914_c0_g1_i1	3.56	3.20	4.39	0.00	0.00	0.00	3.72	0.00	0.61	0.00	0.00	VCP_AEDAE	31.62	gi|242007128|	conservedhypotheticalprotein[Pediculushumanuscorporis]>gi|212507794|gb|EEB11656.1|conservedhypotheticalprotein[Pediculushumanuscorporis]
TRINITY_DN36868_c0_g1_i1	6.75	4.40	0.00	0.00	0.00	0.00	3.72	0.00	3.42	0.00	0.00				
TRINITY_DN219636_c0_g1_i1	7.41	0.00	3.73	0.00	0.00	0.00	3.71	0.00	3.71	0.00	0.00				
TRINITY_DN144016_c0_g1_i1	6.80	4.33	0.00	0.00	0.00	0.00	3.71	0.00	3.44	0.00	0.00	AP1M_DICDI	60.81	gi|527205993|	hypotheticalproteinM569_03066
TRINITY_DN191229_c0_g1_i1	6.80	4.33	0.00	0.00	0.00	0.00	3.71	0.00	3.44	0.00	0.00				
TRINITY_DN115850_c0_g1_i1	0.00	3.84	7.28	0.00	0.00	0.00	3.71	0.00	3.64	0.00	0.00	Y4141_ARATH	22.95	gi|551559272|	hypotheticalproteinEMIHUDRAFT_421996[EmilianiahuxleyiCCMP1516]>gi|485616891|gb|EOD14144.1|hypotheticalproteinEMIHUDRAFT_421996[EmilianiahuxleyiCCMP1516]
TRINITY_DN88413_c0_g1_i2	4.24	3.39	3.49	0.00	0.00	0.00	3.71	0.00	0.47	0.00	0.00	AMY6_HORVU	26.72	gi|652415341|	hemeoxygenase[Arenibacterlatericius]
TRINITY_DN2257_c0_g2_i1	5.35	0.00	5.76	0.00	0.00	0.00	3.70	0.00	3.21	0.00	0.00				
TRINITY_DN37819_c0_g1_i1	3.02	8.09	0.00	0.00	0.00	0.00	3.70	0.00	4.09	0.00	0.00				
TRINITY_DN57463_c0_g1_i1	7.18	3.90	0.00	0.00	0.00	0.00	3.69	0.00	3.59	0.00	0.00	KCAB_SCHPO	40.54	gi|403354182|	Oxidoreductase
TRINITY_DN214722_c0_g1_i1	3.58	3.06	4.43	0.00	0.00	0.00	3.69	0.00	0.69	0.00	0.00				
TRINITY_DN215841_c0_g1_i1	4.03	0.00	7.03	0.00	0.00	0.00	3.69	0.00	3.53	0.00	0.00				
TRINITY_DN26467_c0_g1_i1	5.39	0.00	5.66	0.00	0.00	0.00	3.68	0.00	3.19	0.00	0.00	CATR_CHLRE	30.89	gi|817744998|	hypotheticalproteinAK88_04420[Plasmodiumfragile]>gi|772397581|gb|KJP85945.1|hypotheticalproteinAK88_04420[Plasmodiumfragile]
TRINITY_DN10688_c0_g1_i1	4.01	3.95	3.09	0.00	0.00	0.00	3.68	0.00	0.51	0.00	0.00	AGRG7_HUMAN	47.06	gi|118397443|	hypotheticalproteinTTHERM_00938790[Tetrahymenathermophila]>gi|89285376|gb|EAR83391.1|transportsystemkinase[TetrahymenathermophilaSB210]
TRINITY_DN61559_c0_g1_i1	4.37	0.00	6.67	0.00	0.00	0.00	3.68	0.00	3.39	0.00	0.00	LITAF_HUMAN	34.33	gi|224496030|	lipopolysaccharide-inducedtumornecrosisfactor-alphafactor-like[Danio rerio]
TRINITY_DN44095_c0_g2_i1	3.61	3.66	3.74	0.00	0.00	0.00	3.67	0.00	0.06	0.00	0.00	RIAD1_HUMAN	38.1	gi|657789134|	PREDICTED:RIIadomain-containingprotein1[Cynoglossussemilaevis]
TRINITY_DN96141_c0_g1_i1	5.19	0.00	5.82	0.00	0.00	0.00	3.67	0.00	3.19	0.00	0.00	FCA1_TRYRA	36.21	gi|686641885|	flagellarcalcium-bindingprotein[Trypanosomagrayi]>gi|657136661|gb|KEG08379.1|flagellarcalcium-bindingprotein[Trypanosomagrayi]
TRINITY_DN60796_c0_g3_i1	6.87	0.00	4.10	0.00	0.00	0.00	3.66	0.00	3.46	0.00	0.00	PSD_CLOCE	38.57	gi|170086309|	predictedprotein[LaccariabicolorS238N-H82]>gi|164651930|gb|EDR16170.1|predictedprotein[LaccariabicolorS238N-H82]
TRINITY_DN65222_c0_g1_i1	5.08	0.00	5.89	0.00	0.00	0.00	3.66	0.00	3.19	0.00	0.00	SCP50_ARATH	33.17	gi|255570118|	Vitellogeniccarboxypeptidase
TRINITY_DN75552_c0_g5_i2	6.51	4.45	0.00	0.00	0.00	0.00	3.65	0.00	3.33	0.00	0.00	ACT_PINCO	83.17	gi|146149539|	actin
TRINITY_DN84312_c0_g1_i1	5.57	0.00	5.37	0.00	0.00	0.00	3.65	0.00	3.16	0.00	0.00	METK_LEIIN	84.95	gi|529496470|	methionineadenosyltransferase[Strigomonasoncopelti]
TRINITY_DN66877_c0_g1_i1	5.64	0.00	5.29	0.00	0.00	0.00	3.64	0.00	3.16	0.00	0.00	ARRD2_MOUSE	32.18	gi|672286671|	MmgE/PrpDfamilyprotein[ToxoplasmagondiiFOU]
TRINITY_DN165625_c0_g1_i1	3.73	0.00	7.17	0.00	0.00	0.00	3.63	0.00	3.59	0.00	0.00				
TRINITY_DN16946_c0_g2_i1	7.47	3.41	0.00	0.00	0.00	0.00	3.63	0.00	3.74	0.00	0.00	WECC_SHIFL	29.03	gi|678345424|	UNKNOWN[Stylonychialemnae]
TRINITY_DN41522_c0_g2_i1	6.51	0.00	4.37	0.00	0.00	0.00	3.63	0.00	3.32	0.00	0.00	STC2_CAVPO	30.77	gi|528252101|	cytochromecoxidaseVII[Strigomonasculicis]
TRINITY_DN13757_c0_g1_i1	7.00	0.00	3.85	0.00	0.00	0.00	3.62	0.00	3.51	0.00	0.00	COMT_HUMAN	40	gi|179955|	catechol-O-methyltransferase[Homosapiens]
TRINITY_DN214670_c0_g1_i1	5.84	5.00	0.00	0.00	0.00	0.00	3.61	0.00	3.16	0.00	0.00				
TRINITY_DN222069_c0_g1_i1	0.00	6.74	4.09	0.00	0.00	0.00	3.61	0.00	3.39	0.00	0.00				
TRINITY_DN219186_c0_g1_i1	7.55	0.00	3.27	0.00	0.00	0.00	3.61	0.00	3.79	0.00	0.00				
TRINITY_DN32989_c0_g1_i1	6.05	0.00	4.75	0.00	0.00	0.00	3.60	0.00	3.19	0.00	0.00	LPLA_SALAR	25	gi|471232080|	hypotheticalproteinIMG5_059920[Ichthyophthiriusmultifiliis]>gi|340507168|gb|EGR33178.1|hypotheticalproteinIMG5_059920[Ichthyophthiriusmultifiliis]
TRINITY_DN49633_c0_g1_i1	5.12	0.00	5.68	0.00	0.00	0.00	3.60	0.00	3.13	0.00	0.00	HPPA_LEPIN	35.71	gi|118374727|	inorganicpyrophosphatase[Tetrahymenathermophila]>gi|89302318|gb|EAS00306.1|vacuolarH+-translocatinginorganicpyrophosphatase[TetrahymenathermophilaSB210]
TRINITY_DN91960_c0_g1_i1	0.00	4.60	6.17	0.00	0.00	0.00	3.59	0.00	3.21	0.00	0.00				
TRINITY_DN128613_c0_g1_i1	3.45	3.51	3.81	0.00	0.00	0.00	3.59	0.00	0.19	0.00	0.00				
TRINITY_DN23368_c0_g1_i1	5.56	5.20	0.00	0.00	0.00	0.00	3.59	0.00	3.11	0.00	0.00	VPS29_PONAB	43.18	gi|403372538|	hypotheticalproteinOXYTRI_15841[Oxytrichatrifallax]
TRINITY_DN41219_c0_g1_i1	6.14	0.00	4.63	0.00	0.00	0.00	3.59	0.00	3.20	0.00	0.00	R10A_ORYSJ	50	gi|669193910|	50SribosomalproteinL10Ae[Plasmodiumvinckeivinckei]>gi|577148190|gb|EUD71286.1|50SribosomalproteinL10Ae[Plasmodiumvinckeipetteri]>gi|657011446|gb|KEG04481.1|50SribosomalproteinL10Ae[Plasmodiumvinckeivinckei]>gi|675222311|emb|CDR15251.1|60SribosomalproteinL10a
TRINITY_DN68237_c0_g1_i1	0.00	7.00	3.74	0.00	0.00	0.00	3.58	0.00	3.50	0.00	0.00	CTL5_HUMAN	34.02	gi|556971720|	PREDICTED:cholinetransporter-likeprotein2isoformX3[Latimeriachalumnae]
TRINITY_DN18109_c0_g1_i1	4.61	0.00	6.14	0.00	0.00	0.00	3.58	0.00	3.20	0.00	0.00	RL6_TETTS	47.67	gi|727480763|	PREDICTED:60SribosomalproteinL6-3-like[Camelinasativa]

TRINITY_DN10097_c0_g1_i1	0.00	5.53	5.21	0.00	0.00	0.00	3.58	0.00	3.11	0.00	0.00				
TRINITY_DN94842_c0_g1_i1	6.42	0.00	4.32	0.00	0.00	0.00	3.58	0.00	3.27	0.00	0.00				
TRINITY_DN50197_c0_g1_i1	0.00	3.23	7.49	0.00	0.00	0.00	3.58	0.00	3.76	0.00	0.00	Y6051_PSEF5	31.68	gi|471227285|	hypotheticalproteinIMG5_117970[Ichthyophthiriusmultifiliis]>gi|340504647|gb|EGR31072.1|hypotheticalproteinIMG5_117970[Ichthyophthiriusmultifiliis]
TRINITY_DN120674_c0_g1_i1	0.00	3.36	7.36	0.00	0.00	0.00	3.57	0.00	3.69	0.00	0.00	IF172_CHLRE	46.91	gi|566022603|	hypotheticalproteinF443_09938[PhytophthoraparasiticaP1569]>gi|568017839|gb|ETL92016.1|hypotheticalproteinL917_09562[Phytophthoraparasitica]>gi|568048254|gb|ETM45313.1|hypotheticalproteinL914_09605[Phytophthoraparasitica]>gi|570950037|gb|ETP15294.1|hypotheticalproteinF441_09888[PhytophthoraparasiticaCJ01A1]
TRINITY_DN28076_c0_g1_i1	3.82	3.56	3.33	0.00	0.00	0.00	3.57	0.00	0.24	0.00	0.00	APE3_YEAST	37.84	gi|326489009|	predictedprotein[Hordeumvulgaresubsp.vulgare]
TRINITY_DN9933_c0_g1_i1	7.62	0.00	3.09	0.00	0.00	0.00	3.57	0.00	3.83	0.00	0.00				
TRINITY_DN196531_c0_g1_i1	4.60	0.00	6.10	0.00	0.00	0.00	3.56	0.00	3.18	0.00	0.00				
TRINITY_DN8180_c0_g1_i1	3.38	0.00	7.31	0.00	0.00	0.00	3.56	0.00	3.66	0.00	0.00				
TRINITY_DN63067_c0_g2_i1	7.01	0.00	3.67	0.00	0.00	0.00	3.56	0.00	3.51	0.00	0.00	RSMH_LEPCP	24.07	gi|678321290|	UNKNOWN[Stylonychialemnae]
TRINITY_DN230989_c0_g1_i1	4.96	5.69	0.00	0.00	0.00	0.00	3.55	0.00	3.09	0.00	0.00				
TRINITY_DN9038_c0_g1_i1	4.29	3.26	3.10	0.00	0.00	0.00	3.55	0.00	0.65	0.00	0.00				
TRINITY_DN37409_c0_g1_i1	3.34	0.00	7.30	0.00	0.00	0.00	3.55	0.00	3.65	0.00	0.00				
TRINITY_DN154495_c0_g1_i1	7.28	3.35	0.00	0.00	0.00	0.00	3.54	0.00	3.65	0.00	0.00				
TRINITY_DN154902_c0_g1_i1	0.00	6.26	4.36	0.00	0.00	0.00	3.54	0.00	3.21	0.00	0.00				
TRINITY_DN15804_c0_g2_i1	4.19	0.00	6.42	0.00	0.00	0.00	3.54	0.00	3.26	0.00	0.00	RS18_ARATH	52.34	gi|590601175|	S18ribosomalprotein[Theobromacacao]>gi|590601179|ref|XP_007019599.1|S18ribosomalproteinisoform1[Theobromacacao]>gi|590601183|ref|XP_007019600.1|S18ribosomalproteinisoform1[Theobromacacao]>gi|508724926|gb|EOY16823.1|S18ribosomalprotein[Theobromacacao]>gi|508724927|gb|EOY16824.1|S18ribosomalproteinisoform1[Theobromacacao]>gi|508724928|gb|EOY16825.1|S18ribosomalproteinisoform1[Theobromacacao]>gi|728816484|gb|KHG02167.1|40SribosomalS18-likeprotein[Gossypiumarboreum]>gi|728820336|gb|KHG03705.1|40SribosomalS18-likeprotein[Gossypiumarboreum]>gi|728821395|gb|KHG04314.1|40SribosomalS18-likeprotein[Gossypiumarboreum]>gi|763761711|gb|KJB28965.1|hypotheticalproteinB456_005G077200[Gossypiumraimondii]>gi|763792492|gb|KJB59488.1|hypotheticalproteinB456_009G258700[Gossypiumraimondii]>gi|763793028|gb|KJB60024.1|hypotheticalproteinB456_009G286200[Gossypiumraimondii]>gi|763793029|gb|KJB60025.1|hypotheticalproteinB456_009G286200[Gossypiumraimondii]>gi|763798919|gb|KJB65874.1|hypotheticalproteinB456_010G132100[Gossypiumraimondii]
TRINITY_DN88903_c0_g1_i1	3.22	0.00	7.39	0.00	0.00	0.00	3.54	0.00	3.70	0.00	0.00	CDC48_SOYBN	67.83	gi|565458171|	hypotheticalproteinCARUB_v10000247mg[Capsellarubella]>gi|482555791|gb|EOA19983.1|hypotheticalproteinCARUB_v10000247mg[Capsellarubella]
TRINITY_DN191722_c0_g1_i1	6.01	4.59	0.00	0.00	0.00	0.00	3.53	0.00	3.14	0.00	0.00				
TRINITY_DN52360_c0_g1_i1	0.00	4.32	6.27	0.00	0.00	0.00	3.53	0.00	3.21	0.00	0.00	L_RABVS	48.15	gi|347515146|	rhabdoviral-likepolymerase
TRINITY_DN31238_c0_g1_i1	3.80	3.15	3.64	0.00	0.00	0.00	3.53	0.00	0.34	0.00	0.00	SUI1_ASHGO	37.27	gi|171676077|	hypotheticalprotein[PodosporaanserinaSmat+]>gi|170936104|emb|CAP60764.1|unnamedproteinproduct[PodosporaanserinaSmat+]>gi|586941423|emb|CDN29956.1|Putativecytosolictranslationinitiationfactoreif-1[Podosporaanserina]>gi|681094023|emb|CDP24428.1|Putativecytosolictranslationinitiationfactoreif-1[PodosporaanserinaSmat+]
TRINITY_DN150648_c0_g1_i1	4.02	3.08	3.44	0.00	0.00	0.00	3.52	0.00	0.48	0.00	0.00				
TRINITY_DN49178_c0_g1_i1	4.69	0.00	5.84	0.00	0.00	0.00	3.51	0.00	3.09	0.00	0.00				
TRINITY_DN2989_c0_g1_i1	3.77	6.76	0.00	0.00	0.00	0.00	3.51	0.00	3.39	0.00	0.00				
TRINITY_DN61951_c0_g3_i1	5.87	4.65	0.00	0.00	0.00	0.00	3.51	0.00	3.10	0.00	0.00				
TRINITY_DN56960_c0_g2_i1	3.78	6.74	0.00	0.00	0.00	0.00	3.50	0.00	3.38	0.00	0.00	RGL3_MOUSE	43.75	gi|118367511|	hypotheticalproteinTTHERM_00758860[Tetrahymenathermophila]>gi|89298736|gb|EAR96724.1|hypotheticalproteinTTHERM_00758860[TetrahymenathermophilaSB210]
TRINITY_DN122625_c0_g1_i1	7.40	0.00	3.10	0.00	0.00	0.00	3.50	0.00	3.72	0.00	0.00	PEX4_ARATH	46.36	gi|674913394|	BnaA09g04490D[Brassicanapus]
TRINITY_DN139477_c0_g1_i1	3.18	3.55	3.78	0.00	0.00	0.00	3.50	0.00	0.30	0.00	0.00	GPX7_ARATH	46.34	gi|255577761|	glutathioneperoxidase
TRINITY_DN36031_c0_g1_i1	4.54	5.96	0.00	0.00	0.00	0.00	3.50	0.00	3.11	0.00	0.00	PH1_ARATH	29	gi|567987352|	hypotheticalproteinL916_10679[Phytophthoraparasitica]>gi|570948777|gb|ETP14034.1|hypotheticalproteinF441_10979[PhytophthoraparasiticaCJ01A1]
TRINITY_DN193102_c0_g1_i1	5.87	4.63	0.00	0.00	0.00	0.00	3.50	0.00	3.09	0.00	0.00				
TRINITY_DN221419_c0_g1_i1	5.57	0.00	4.91	0.00	0.00	0.00	3.50	0.00	3.04	0.00	0.00				
TRINITY_DN32780_c0_g1_i1	0.00	6.53	3.95	0.00	0.00	0.00	3.49	0.00	3.29	0.00	0.00	PSB3_DICDI	62.96	gi|751203370|	PREDICTED:proteasomesubunitbetatype-3[Solenopsisinvicta]
TRINITY_DN141845_c0_g1_i1	5.74	4.72	0.00	0.00	0.00	0.00	3.49	0.00	3.06	0.00	0.00	SUCA1_SOLLC	71.33	gi|325186353|	unnamedproteinproduct[AlbugolaibachiiNc14]
TRINITY_DN56127_c0_g1_i1	3.14	3.59	3.72	0.00	0.00	0.00	3.48	0.00	0.30	0.00	0.00	CHI2_ARTBC	32.67	gi|488119041|	chitinase[Bacilluscereus]>gi|401298415|gb|EJS04015.1|hypotheticalproteinIKO_02985[BacilluscereusVDM034]>gi|401310134|gb|EJS15467.1|hypotheticalproteinIKS_02126[BacilluscereusVDM062]
TRINITY_DN212412_c0_g1_i1	6.47	3.97	0.00	0.00	0.00	0.00	3.48	0.00	3.26	0.00	0.00				
TRINITY_DN50449_c0_g1_i1	0.00	3.08	7.32	0.00	0.00	0.00	3.46	0.00	3.67	0.00	0.00				
TRINITY_DN57132_c0_g1_i1	0.00	5.60	4.79	0.00	0.00	0.00	3.46	0.00	3.03	0.00	0.00				
TRINITY_DN171808_c0_g1_i1	5.63	4.76	0.00	0.00	0.00	0.00	3.46	0.00	3.03	0.00	0.00				
TRINITY_DN173461_c0_g1_i1	6.72	3.66	0.00	0.00	0.00	0.00	3.46	0.00	3.37	0.00	0.00				

TRINITY_DN56796_c0_g1_i1	3.54	3.23	3.60	0.00	0.00	0.00	3.46	0.00	0.20	0.00	0.00	RS29_ICTPU	72.73	gi|4506717|
TRINITY_DN77388_c0_g1_i1	7.05	3.30	0.00	0.00	0.00	0.00	3.45	0.00	3.53	0.00	0.00	RP25L_HUMAN	27.41	gi|685287993|
TRINITY_DN150896_c0_g1_i1	5.37	4.99	0.00	0.00	0.00	0.00	3.45	0.00	3.00	0.00	0.00			
TRINITY_DN166283_c0_g1_i1	4.16	0.00	6.19	0.00	0.00	0.00	3.45	0.00	3.15	0.00	0.00			
TRINITY_DN12675_c0_g1_i1	6.02	4.31	0.00	0.00	0.00	0.00	3.44	0.00	3.10	0.00	0.00	NDUS6_ARATH	39.66	gi|630022058|
TRINITY_DN33989_c0_g1_i1	6.39	3.91	0.00	0.00	0.00	0.00	3.43	0.00	3.22	0.00	0.00	RS5_CICAR	65	gi|502078786|
TRINITY_DN166069_c0_g1_i1	3.73	3.09	3.47	0.00	0.00	0.00	3.43	0.00	0.32	0.00	0.00			
TRINITY_DN90350_c3_g1_i4	3.18	3.07	4.02	0.00	0.00	0.00	3.42	0.00	0.52	0.00	0.00	EF1A_CRYPV	44.73	gi|302832938|
TRINITY_DN116746_c0_g1_i1	3.78	3.23	3.22	0.00	0.00	0.00	3.41	0.00	0.32	0.00	0.00	CHI1_COCP7	28.51	gi|118364019|
TRINITY_DN152303_c0_g1_i1	4.09	0.00	6.11	0.00	0.00	0.00	3.40	0.00	3.11	0.00	0.00			
TRINITY_DN59351_c0_g1_i1	6.93	0.00	3.25	0.00	0.00	0.00	3.39	0.00	3.47	0.00	0.00			
TRINITY_DN77781_c1_g1_i1	7.14	0.00	3.03	0.00	0.00	0.00	3.39	0.00	3.59	0.00	0.00	RL5_TETTS	54.88	gi|525579191|
TRINITY_DN8379_c0_g2_i1	4.50	0.00	5.67	0.00	0.00	0.00	3.39	0.00	2.99	0.00	0.00	RL15_SINKN	64.79	gi|673047297|
TRINITY_DN26227_c0_g2_i1	0.00	5.00	5.13	0.00	0.00	0.00	3.38	0.00	2.93	0.00	0.00	LIP_THELA	29.47	gi|281209254|
TRINITY_DN35604_c0_g1_i1	4.99	5.15	0.00	0.00	0.00	0.00	3.38	0.00	2.93	0.00	0.00	PIN1_MOUSE	56.36	gi|584041781|
TRINITY_DN129509_c0_g1_i1	3.90	0.00	6.20	0.00	0.00	0.00	3.37	0.00	3.14	0.00	0.00			
TRINITY_DN18366_c0_g1_i1	4.82	5.29	0.00	0.00	0.00	0.00	3.37	0.00	2.93	0.00	0.00	Y8111_DICDI	50.67	gi|567146537|
TRINITY_DN27749_c0_g1_i1	5.17	4.91	0.00	0.00	0.00	0.00	3.36	0.00	2.92	0.00	0.00	Y4CA_RHISN	26.44	gi|229595761|
TRINITY_DN19912_c0_g1_i1	3.65	0.00	6.43	0.00	0.00	0.00	3.36	0.00	3.22	0.00	0.00			
TRINITY_DN19130_c0_g1_i1	4.83	0.00	5.24	0.00	0.00	0.00	3.36	0.00	2.91	0.00	0.00	HBSAG_HBVGO	30.19	gi|145480331|
TRINITY_DN81376_c0_g1_i2	3.08	3.79	3.16	0.00	0.00	0.00	3.34	0.00	0.39	0.00	0.00	RS20_RAT	56.88	gi|149286918|
TRINITY_DN46023_c0_g1_i1	3.54	0.00	6.49	0.00	0.00	0.00	3.34	0.00	3.25	0.00	0.00	EF2_PARKE	71.76	gi|71747296|
TRINITY_DN18442_c0_g1_i1	0.00	3.52	6.47	0.00	0.00	0.00	3.33	0.00	3.24	0.00	0.00			
TRINITY_DN189532_c0_g1_i1	3.71	0.00	6.28	0.00	0.00	0.00	3.33	0.00	3.16	0.00	0.00			
TRINITY_DN215356_c0_g1_i1	5.29	4.69	0.00	0.00	0.00	0.00	3.33	0.00	2.90	0.00	0.00			
TRINITY_DN50169_c0_g1_i1	3.02	6.94	0.00	0.00	0.00	0.00	3.32	0.00	3.48	0.00	0.00	TBA_TRYBR	91.46	gi|206598112|
TRINITY_DN41877_c0_g2_i1	4.11	0.00	5.81	0.00	0.00	0.00	3.31	0.00	2.99	0.00	0.00	SUCB2_DICDI	49.88	gi|391346848|
TRINITY_DN147832_c0_g1_i1	6.32	3.60	0.00	0.00	0.00	0.00	3.31	0.00	3.17	0.00	0.00			
TRINITY_DN100873_c0_g1_i1	6.31	3.60	0.00	0.00	0.00	0.00	3.31	0.00	3.17	0.00	0.00	RL24_TETTS	47.37	gi|557125314|
TRINITY_DN106069_c0_g1_i1	4.14	0.00	5.77	0.00	0.00	0.00	3.30	0.00	2.97	0.00	0.00			
TRINITY_DN19374_c0_g1_i1	4.93	0.00	4.97	0.00	0.00	0.00	3.30	0.00	2.86	0.00	0.00			

40SribosomalproteinS29isoform1[Homosapiens]>gi\|6677803\|ref\|NP_033119.1\|40SribosomalproteinS29[Musmusculus]>gi\|6981490\|ref\|NP_037008.1\|40SribosomalproteinS29[Rattusnorvegicus]>gi\|27807381\|ref\|NP_777229.1\|40SribosomalproteinS29[Bostaurus]>gi\|62857725\|ref\|NP_001016766.1\|ribosomalproteinS29[Xenopus(Silurana)tropicalis]>gi\|197098290\|ref\|NP_001127434.1\|40SribosomalproteinS29[Pongoabelii]>gi\|350535781\|ref\|NP_001232213.1\|putative40SribosomalproteinS29[Taeniopygiaguttata]>gi\|388596670\|ref\|NP_001254466.1\|40SribosomalproteinS29[Macacamulatta]>gi\|482677672\|ref\|NP_001264809.1\|40SribosomalproteinS29[Gallusgallus]>gi\|577019511\|ref\|NP_001276741.1\|40SribosomalproteinS29[Oryctolaguscuniculus]>gi\|73963693\|ref\|XP_853223.1\|PREDICTED:40SribosomalproteinS29isoform3[Canislupusfamiliaris]>gi\|291388310\|ref\|XP_002710749.1\|PREDICTED:40SribosomalproteinS29[Oryctolaguscuniculus]>gi\|301773224\|ref\|XP_002922032.1\|PREDICTED:40SribosomalproteinS29[Ailuropodamelanoleuca]>gi\|326921271\|ref\|XP_003206885.1\|PREDICTED:40SribosomalproteinS29[Meleagrisgallopavo]>gi\|332237004\|ref\|XP_003267690.1\|PREDICTED:40SribosomalproteinS29isoform1[Nomascusleucogenys]>gi\|332842161\|ref\|XP_003314358.1\|PREDICTED:40SribosomalproteinS29isoformX2[Pantroglodytes]>gi\|344273535\|ref\|XP_003408577.1\|PREDICTED:40SribosomalproteinS29[Loxodontaafricana]>gi\|390474494\|ref\|XP_003734787.1\|PREDICTED:40SribosomalproteinS29[Callithrixjacchus]>gi\|395504173\|ref\|XP_003756431.1\|PREDICTED:40SribosomalproteinS29-like[Sarcophilusharrisii]>gi\|395838634\|ref\|XP_003792217.1\|PREDICTED:40SribosomalproteinS29[Otolemurgarnettii]>gi\|397523558\|ref\|XP_003831796.1\|PREDICTED:40SribosomalproteinS29isoformX2[Panpaniscus]>gi\|402864580\|ref\|XP_003896536.1\|PREDICTED:40SribosomalproteinS29[Papioanubis]>gi\|410962194\|ref\|XP_003987659.1\|PREDICTED:40SribosomalproteinS29[Feliscatus]>gi\|426233080\|ref\|XP_004010545.1\|PREDICTED:40SribosomalproteinS29[Ovisaries]>gi\|426376821\|ref\|XP_004055181.1\|PREDICTED:40SribosomalproteinS29isoform1[Gorillagorillagorilla]>gi\|426376823\|ref\|XP_004055182.1\|PREDICTED:40SribosomalproteinS29isoform2[Gorillagorillagorilla]>gi\|441594602\|ref\|XP_004087178.1\|PREDICTED:40SribosomalproteinS29[Nomascusleucogenys]>gi\|470604151\|ref\|XP_004313287.1\|PREDICTED:40SribosomalproteinS29-likeTursiopstruncatus]>gi\|472377278\|ref\|XP_004408067.1\|PREDICTED:40Sribosomalp

PREDICTED:RNA-bindingproteincabezaisoformX2[Brassicarapa]

hypotheticalproteinPFICI_07547[PestalotiopsisficiW106-1]>gi\|573060256\|gb\|ETS80018.1\|hypotheticalproteinPFICI_07547[PestalotiopsisficiW106-1]

PREDICTED:40SribosomalproteinS5-like[Cicerarietinum]

eukaryotictranslationelongationfactor1alpha2[Volvoxcarterif.nagariensis]>gi\|300266835\|gb\|EFJ51021.1\|eukaryotictranslationelongationfactor1alpha2[Volvoxcarterif.nagariensis]

hypotheticalproteinTTHERM_00515220[Tetrahymenathermophila]>gi\|89296999\|gb\|EAR94987.1\|glycosidehydrolasefamily18protein[TetrahymenathermophilaSB210]

hypotheticalproteinPDE_00374[Penicilliumoxalicum114-2]

60Sribosomalprotein[Aphanomycesinvadans]>gi\|574466773\|gb\|ETV93800.1\|60Sribosomalprotein[Aphanomycesinvadans]

hypotheticalproteinPPL_03573[PolysphondyliumpallidumPN500]

PREDICTED:peptidyl-prolylcis-transisomeraseNIMA-interacting1[Myotisdavidii]>gi\|432099537\|gb\|ELK28678.1\|Peptidyl-prolylcis-transisomeraseNIMA-interacting1[Myotisdavidii]

hypotheticalproteinEUTSA_v10009098mg[Eutremasalsugineum]>gi\|557093312\|gb\|ESQ33894.1\|hypotheticalproteinEUTSA_v10009098mg[Eutremasalsugineum]

hypotheticalproteinTTHERM_00601860[Tetrahymenathermophila]

hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi\|124393261\|emb\|CAK58790.1\|unnamedproteinproduct[Parameciumtetraurelia]

40SribosomalproteinS20[Ornithodorosparkeri]

elongationfactor2[TrypanosomabruceibruceiTREU927]>gi\|71747298\|ref\|XP_822704.1\|elongationfactor2[TrypanosomabruceibruceiTREU927]>gi\|788017348\|ref\|XP_011777738.1\|elongationfactor2

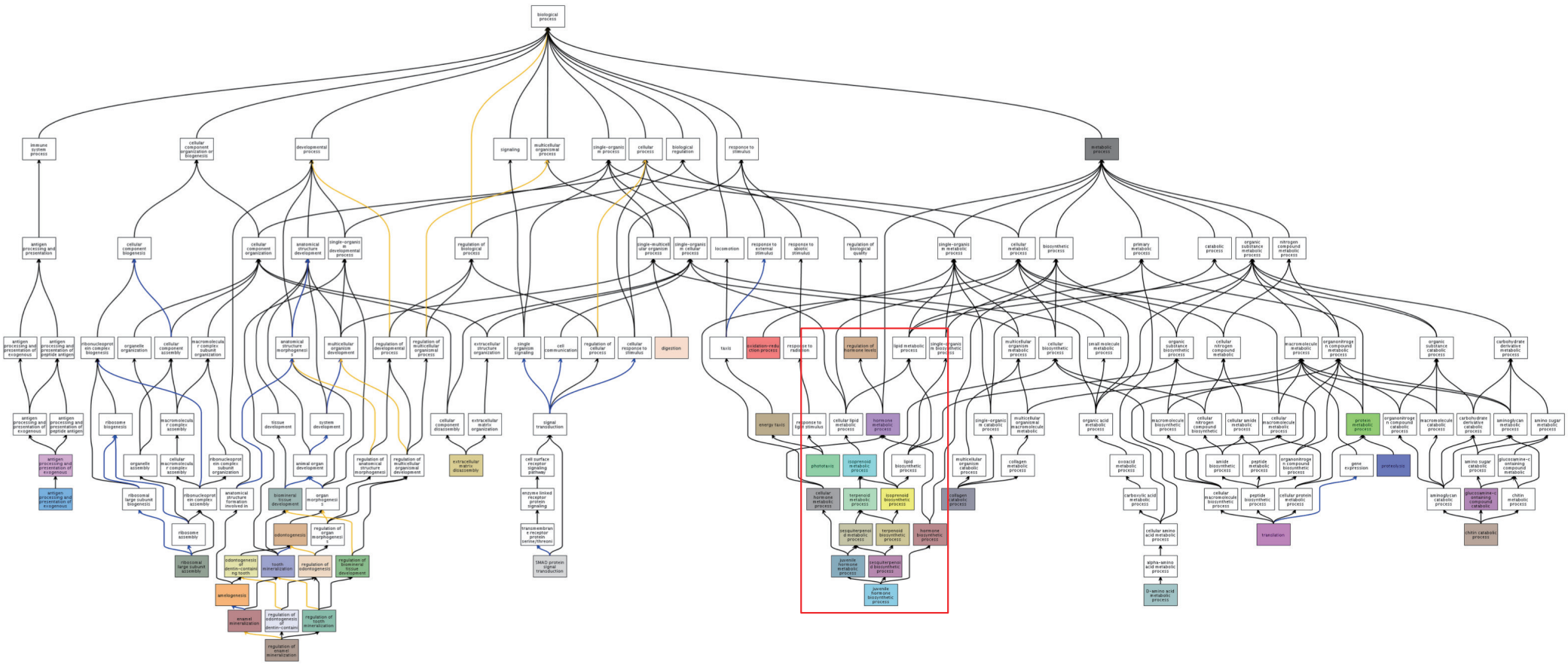
alpha-tubulin[Bodosaltans]

PREDICTED:succinyl-CoAligase[GDP-forming]subunitbeta

60SribosomalproteinL24

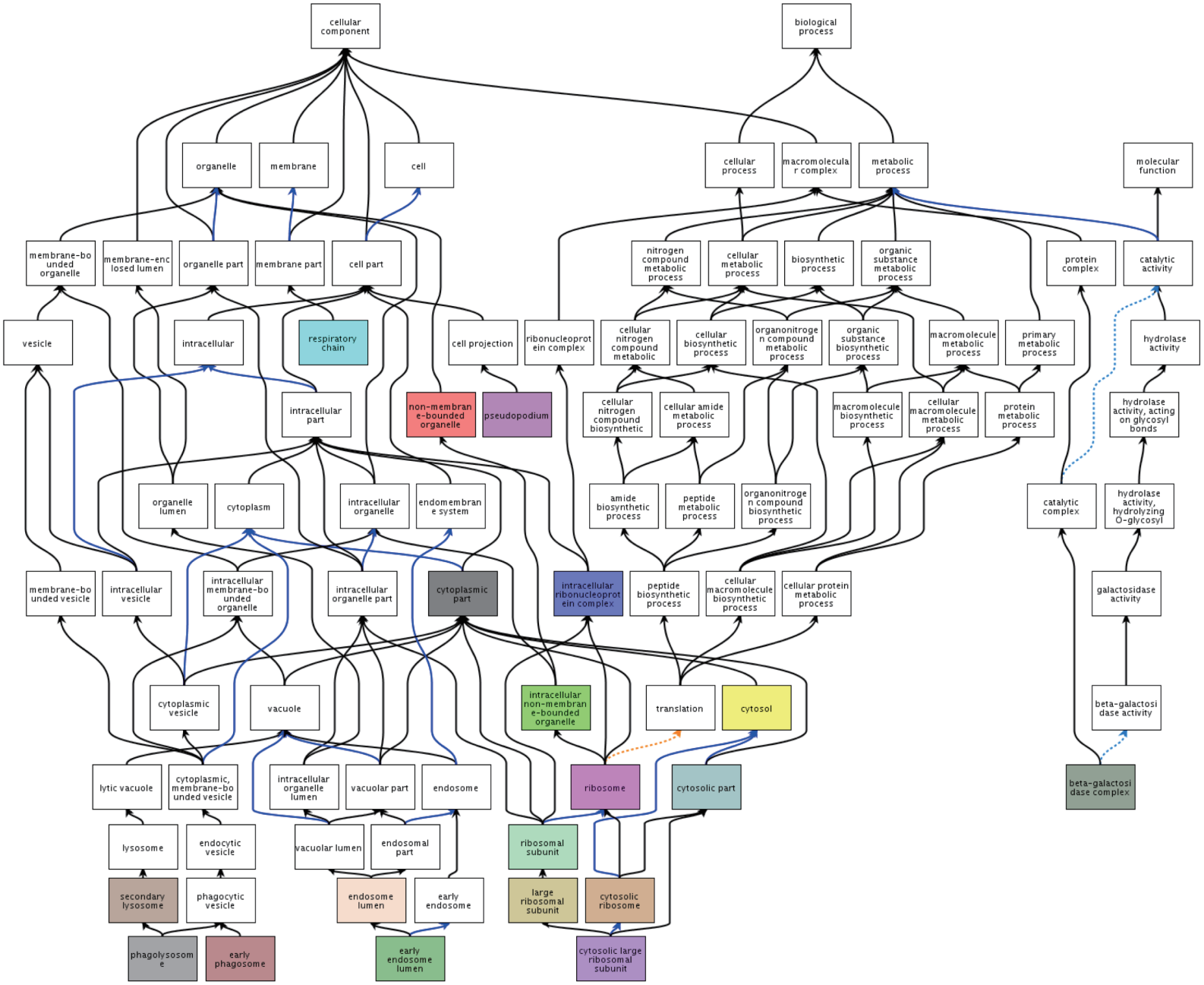
TRINITY_DN44066_c0_g2_i1	6.14	3.74	0.00	0.00	0.00	0.00	3.29	0.00	3.09	0.00	0.00	PUR4_VIBF1	30.19	gi|118353918|	hypotheticalproteinTTHERM_00561710[Tetrahymenathermophila]>gi|89291991|gb|EAR89979.1|hypotheticalproteinTTHERM_00561710[TetrahymenathermophilaSB210]
TRINITY_DN79476_c0_g2_i1	6.42	0.00	3.44	0.00	0.00	0.00	3.29	0.00	3.22	0.00	0.00				
TRINITY_DN71062_c0_g1_i1	3.33	0.00	6.52	0.00	0.00	0.00	3.28	0.00	3.26	0.00	0.00				
TRINITY_DN153859_c0_g1_i1	6.10	3.73	0.00	0.00	0.00	0.00	3.28	0.00	3.08	0.00	0.00				
TRINITY_DN49561_c0_g2_i1	3.55	6.29	0.00	0.00	0.00	0.00	3.28	0.00	3.15	0.00	0.00	OLA1_ARATH	72.97	gi|527189704|	hypotheticalproteinM569_13545
TRINITY_DN76356_c0_g1_i4	5.03	0.00	4.80	0.00	0.00	0.00	3.27	0.00	2.84	0.00	0.00				
TRINITY_DN74551_c0_g1_i1	4.74	5.06	0.00	0.00	0.00	0.00	3.27	0.00	2.83	0.00	0.00				
TRINITY_DN165548_c0_g1_i1	3.38	0.00	6.42	0.00	0.00	0.00	3.26	0.00	3.21	0.00	0.00				
TRINITY_DN196718_c0_g1_i1	5.43	0.00	4.37	0.00	0.00	0.00	3.26	0.00	2.88	0.00	0.00				
TRINITY_DN192345_c0_g1_i1	0.00	3.35	6.44	0.00	0.00	0.00	3.26	0.00	3.22	0.00	0.00				
TRINITY_DN231544_c0_g1_i1	0.00	4.12	5.67	0.00	0.00	0.00	3.26	0.00	2.93	0.00	0.00				
TRINITY_DN117655_c0_g1_i1	6.24	0.00	3.52	0.00	0.00	0.00	3.26	0.00	3.13	0.00	0.00	AGLU_BETVU	39.78	gi|731321888|	PREDICTED:alpha-glucosidase[Betavulgarissubsp.vulgaris]>gi|430726482|dbj|BAM72724.1|alpha-glucosidase[Betavulgaris]
TRINITY_DN233787_c0_g1_i1	5.00	0.00	4.74	0.00	0.00	0.00	3.25	0.00	2.82	0.00	0.00				
TRINITY_DN74745_c0_g1_i1	0.00	3.73	6.02	0.00	0.00	0.00	3.25	0.00	3.04	0.00	0.00	COMI_DICDI	57.14	gi|74231221|	agglutinin[Alliumtriquetrum]
TRINITY_DN201017_c0_g1_i1	5.03	4.68	0.00	0.00	0.00	0.00	3.24	0.00	2.81	0.00	0.00				
TRINITY_DN29320_c0_g1_i1	3.52	0.00	6.18	0.00	0.00	0.00	3.23	0.00	3.10	0.00	0.00				
TRINITY_DN82297_c0_g1_i1	6.21	0.00	3.45	0.00	0.00	0.00	3.22	0.00	3.11	0.00	0.00	CYC_STROO	82.46	gi|342182789|	putativecytochromec[TrypanosomacongolenseIL3000]
TRINITY_DN71077_c0_g1_i1	5.23	4.42	0.00	0.00	0.00	0.00	3.22	0.00	2.82	0.00	0.00				
TRINITY_DN86475_c2_g1_i1	4.20	0.00	5.46	0.00	0.00	0.00	3.22	0.00	2.86	0.00	0.00	IDHC_HUMAN	62.99	gi|557765933|	PREDICTED:isocitratedehydrogenase[NADP]cytoplasmicisoformX2[Muscadomestica]
TRINITY_DN17444_c0_g1_i1	4.77	4.88	0.00	0.00	0.00	0.00	3.22	0.00	2.79	0.00	0.00				
TRINITY_DN672_c0_g1_i1	4.77	4.88	0.00	0.00	0.00	0.00	3.22	0.00	2.79	0.00	0.00				
TRINITY_DN5413_c0_g1_i1	3.02	0.00	6.63	0.00	0.00	0.00	3.21	0.00	3.32	0.00	0.00				
TRINITY_DN52655_c0_g2_i1	0.00	5.60	3.99	0.00	0.00	0.00	3.20	0.00	2.88	0.00	0.00	MYSH_ACACA	42.31	gi|470490388|	myosin1
TRINITY_DN218963_c0_g1_i1	5.53	4.05	0.00	0.00	0.00	0.00	3.19	0.00	2.86	0.00	0.00				
TRINITY_DN82080_c0_g1_i1	4.82	0.00	4.74	0.00	0.00	0.00	3.19	0.00	2.76	0.00	0.00	R10A_ORYSJ	49.54	gi|457874870|	60SribosomalproteinL10a
TRINITY_DN14351_c0_g1_i1	0.00	3.24	6.27	0.00	0.00	0.00	3.17	0.00	3.14	0.00	0.00				
TRINITY_DN16153_c0_g1_i1	4.28	0.00	5.22	0.00	0.00	0.00	3.17	0.00	2.78	0.00	0.00	RS52_ARATH	64.1	gi|694410110|	PREDICTED:40SribosomalproteinS5-like[Pyrusxbretschneideri]>gi|694410112|ref|XP_009379665.1|PREDICTED:40SribosomalproteinS5-like[Pyrusxbretschneideri]>gi|694410115|ref|XP_009379666.1|PREDICTED:40SribosomalproteinS5-like[Pyrusxbretschneideri]
TRINITY_DN213825_c0_g1_i1	5.37	0.00	4.13	0.00	0.00	0.00	3.17	0.00	2.81	0.00	0.00				
TRINITY_DN761_c0_g2_i1	6.20	0.00	3.30	0.00	0.00	0.00	3.17	0.00	3.10	0.00	0.00				
TRINITY_DN83176_c0_g1_i1	0.00	4.58	4.92	0.00	0.00	0.00	3.17	0.00	2.75	0.00	0.00	CAP_DICDI	36.77	gi|602629477|	PREDICTED:adenylylcyclase-associatedprotein2isoformX1[Pythonbivittatus]>gi|602629479|ref|XP_007421666.1|PREDICTED:adenylylcyclase-associatedprotein2isoformX2[Pythonbivittatus]
TRINITY_DN213988_c0_g1_i1	3.56	0.00	5.90	0.00	0.00	0.00	3.15	0.00	2.97	0.00	0.00				
TRINITY_DN43746_c0_g1_i1	3.38	0.00	6.07	0.00	0.00	0.00	3.15	0.00	3.04	0.00	0.00	PSB6_MOUSE	46.23	gi|640833003|	PREDICTED:proteasomesubunitbetatype-6[Tarsiussyrichta]
TRINITY_DN149736_c0_g1_i1	5.20	0.00	4.23	0.00	0.00	0.00	3.14	0.00	2.77	0.00	0.00				
TRINITY_DN55568_c0_g1_i1	6.13	0.00	3.29	0.00	0.00	0.00	3.14	0.00	3.07	0.00	0.00	RS173_ARATH	67.92	gi|743868105|	PREDICTED:40SribosomalproteinS17-like[Populuseuphratica]>gi|743868109|ref|XP_011032912.1|PREDICTED:40SribosomalproteinS17-like[Populuseuphratica]>gi|743868113|ref|XP_011032913.1|PREDICTED:40SribosomalproteinS17-like[Populuseuphratica]>gi|743868117|ref|XP_011032914.1|PREDICTED:40SribosomalproteinS17-like[Populuseuphratica]>gi|743868119|ref|XP_011032915.1|PREDICTED:40SribosomalproteinS17-like[Populuseuphratica]>gi|743942241|ref|XP_011015616.1|PREDICTED:40SribosomalproteinS17-like[Populuseuphratica]>gi|743942243|ref|XP_011015617.1|PREDICTED:40SribosomalproteinS17-like[Populuseuphratica]>gi|743942245|ref|XP_011015619.1|PREDICTED:40SribosomalproteinS17-like[Populuseuphratica]>gi|743942247|ref|XP_011015620.1|PREDICTED:40SribosomalproteinS17-like[Populuseuphratica]>gi|743942249|ref|XP_011015621.1|PREDICTED:40SribosomalproteinS17-like[Populuseuphratica]
TRINITY_DN227009_c0_g1_i1	4.74	0.00	4.68	0.00	0.00	0.00	3.14	0.00	2.72	0.00	0.00				
TRINITY_DN86893_c0_g1_i1	3.36	0.00	6.05	0.00	0.00	0.00	3.14	0.00	3.03	0.00	0.00	EF1G_TRYCR	65.84	gi|731712800|	elongationfactor-1gamma[Leishmaniapanamensis]>gi|685201760|gb|AIN96012.1|elongationfactor-1gamma[Leishmaniapanamensis]
TRINITY_DN121248_c0_g1_i1	3.94	5.45	0.00	0.00	0.00	0.00	3.13	0.00	2.81	0.00	0.00	CISD3_HUMAN	50	gi|670471020|	glutamatesynthase[Vibrioparahaemolyticus]
TRINITY_DN43807_c0_g1_i1	0.00	4.97	4.37	0.00	0.00	0.00	3.11	0.00	2.71	0.00	0.00	DYHA_CHLRE	51.69	gi|401417747|	putativedyneinheavychain[LeishmaniamexicanaMHOM/GT/2001/U1103]>gi|322489595|emb|CBZ24853.1|putativedyneinheavychain[LeishmaniamexicanaMHOM/GT/2001/U1103]
TRINITY_DN131446_c0_g1_i1	0.00	5.96	3.36	0.00	0.00	0.00	3.11	0.00	2.99	0.00	0.00				
TRINITY_DN63273_c0_g1_i1	5.28	4.02	0.00	0.00	0.00	0.00	3.10	0.00	2.76	0.00	0.00	RSMB_DICDI	54.76	gi|674950502|	BnaC01g12160D[Brassicanapus]
TRINITY_DN199361_c0_g1_i1	3.29	0.00	6.01	0.00	0.00	0.00	3.10	0.00	3.01	0.00	0.00				
TRINITY_DN47786_c0_g1_i1	0.00	3.26	5.99	0.00	0.00	0.00	3.09	0.00	3.00	0.00	0.00				

TRINITY_DN45751_c0_g1_i1	3.87	5.39	0.00	0.00	0.00	0.00	3.09	0.00	2.78	0.00	0.00	PDI2_CAEEL	40.79	gi|597843602|	hypotheticalproteinY032_0185g1018[Ancylostomaceylanicum]
TRINITY_DN24099_c0_g2_i1	3.04	0.00	6.21	0.00	0.00	0.00	3.08	0.00	3.10	0.00	0.00	TCPD_RAT	71.43	gi|344291862|	PREDICTED:T-complexprotein1subunitdelta[Loxodontaafricana]
TRINITY_DN35525_c0_g1_i1	3.75	0.00	5.49	0.00	0.00	0.00	3.08	0.00	2.81	0.00	0.00				
TRINITY_DN61889_c0_g1_i1	3.73	0.00	5.45	0.00	0.00	0.00	3.06	0.00	2.79	0.00	0.00	PHOP_BACSU	25.86	gi|669319511|	hypotheticalproteinM514_11994[Trichurissuis]
TRINITY_DN154329_c0_g1_i1	3.56	0.00	5.61	0.00	0.00	0.00	3.06	0.00	2.84	0.00	0.00				
TRINITY_DN26884_c0_g1_i1	4.28	4.88	0.00	0.00	0.00	0.00	3.05	0.00	2.66	0.00	0.00				
TRINITY_DN13183_c0_g1_i1	4.41	0.00	4.75	0.00	0.00	0.00	3.05	0.00	2.65	0.00	0.00	SNRPA_BOVIN	50.54	gi|344298221|	PREDICTED:U1smallnuclearribonucleoproteinA[Loxodontaafricana]
TRINITY_DN69578_c0_g1_i2	4.80	0.00	4.34	0.00	0.00	0.00	3.05	0.00	2.65	0.00	0.00	DCD1A_DICDI	40.5	gi|585706203|	PREDICTED:proteindcd1A-like[Saccoglossuskowalevskii]
TRINITY_DN42621_c0_g1_i1	3.21	0.00	5.92	0.00	0.00	0.00	3.04	0.00	2.96	0.00	0.00	IF4G_DICDI	36	gi|145533070|	hypotheticalprotein[Parameciumtetraureliastraind4-2]>gi|124419973|emb|CAK84888.1|unnamedproteinproduct[Parameciumtetraurelia]
TRINITY_DN172683_c0_g1_i1	5.03	0.00	4.09	0.00	0.00	0.00	3.04	0.00	2.68	0.00	0.00				
TRINITY_DN57462_c0_g2_i1	3.94	5.18	0.00	0.00	0.00	0.00	3.04	0.00	2.70	0.00	0.00				
TRINITY_DN99350_c0_g1_i1	4.94	4.16	0.00	0.00	0.00	0.00	3.03	0.00	2.65	0.00	0.00	PCH2_MOUSE	29.21	gi|678306579|	UNKNOWN[Stylonychialemnae]
TRINITY_DN62214_c0_g1_i1	4.24	4.84	0.00	0.00	0.00	0.00	3.03	0.00	2.64	0.00	0.00	PSB3_DICDI	66.25	gi|511007417|	proteasomesubunitbetatype-3[Mucorcircinelloidesf.circinelloides1006PhL]
TRINITY_DN87205_c0_g1_i1	3.91	0.00	5.17	0.00	0.00	0.00	3.03	0.00	2.69	0.00	0.00	QCR1_BOVIN	26.53	gi|507620298|	PREDICTED:cytochromeb-c1complexsubunit1
TRINITY_DN227124_c0_g1_i1	3.31	0.00	5.75	0.00	0.00	0.00	3.02	0.00	2.89	0.00	0.00				
TRINITY_DN224097_c0_g1_i1	4.98	4.08	0.00	0.00	0.00	0.00	3.02	0.00	2.65	0.00	0.00				
TRINITY_DN64487_c0_g1_i1	6.00	3.05	0.00	0.00	0.00	0.00	3.01	0.00	3.00	0.00	0.00	RDH54_YEAS6	36.96	gi|586736585|	hypotheticalproteinTTHERM_00442010[TetrahymenathermophilaSB210]
TRINITY_DN213866_c0_g1_i1	5.98	0.00	3.04	0.00	0.00	0.00	3.01	0.00	2.99	0.00	0.00				
TRINITY_DN124811_c0_g1_i1	5.75	3.26	0.00	0.00	0.00	0.00	3.00	0.00	2.88	0.00	0.00				
TRINITY_DN171856_c0_g1_i1	3.96	5.05	0.00	0.00	0.00	0.00	3.00	0.00	2.66	0.00	0.00				
TRINITY_DN83830_c0_g2_i1	0.00	3.98	5.02	0.00	0.00	0.00	3.00	0.00	2.65	0.00	0.00	RL18_TRYCC	72.22	gi|401417529|	

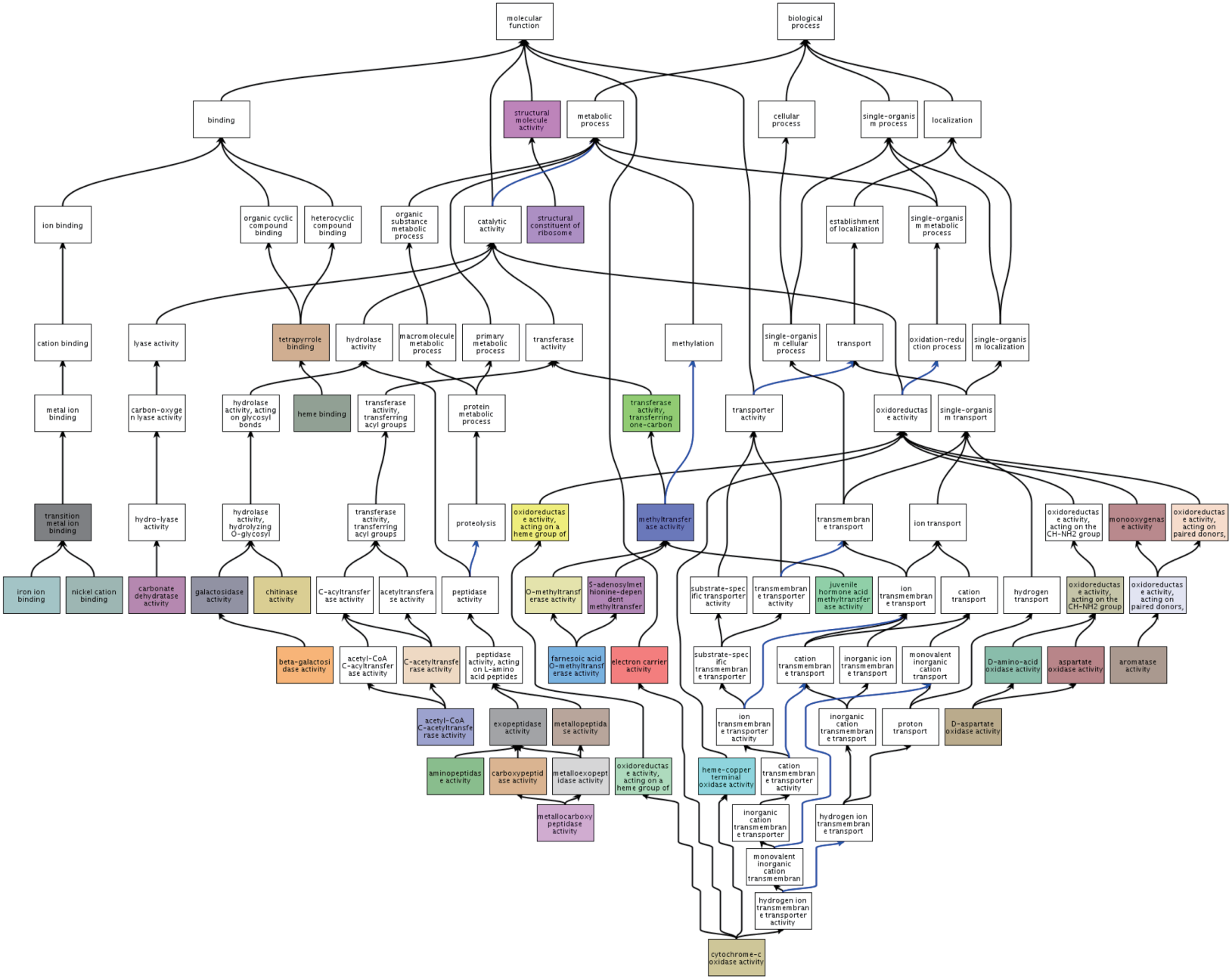


附圖一　表現量上升之差異性表現基因於 Biological process 層面功能群分佈圖。本研究中差異性表現基因座落之功能群以顏色標記。

sFig. 1　Distribution of GO terms related to the biological process of upregulated DEGs. Terms identified in this study are highlighted.

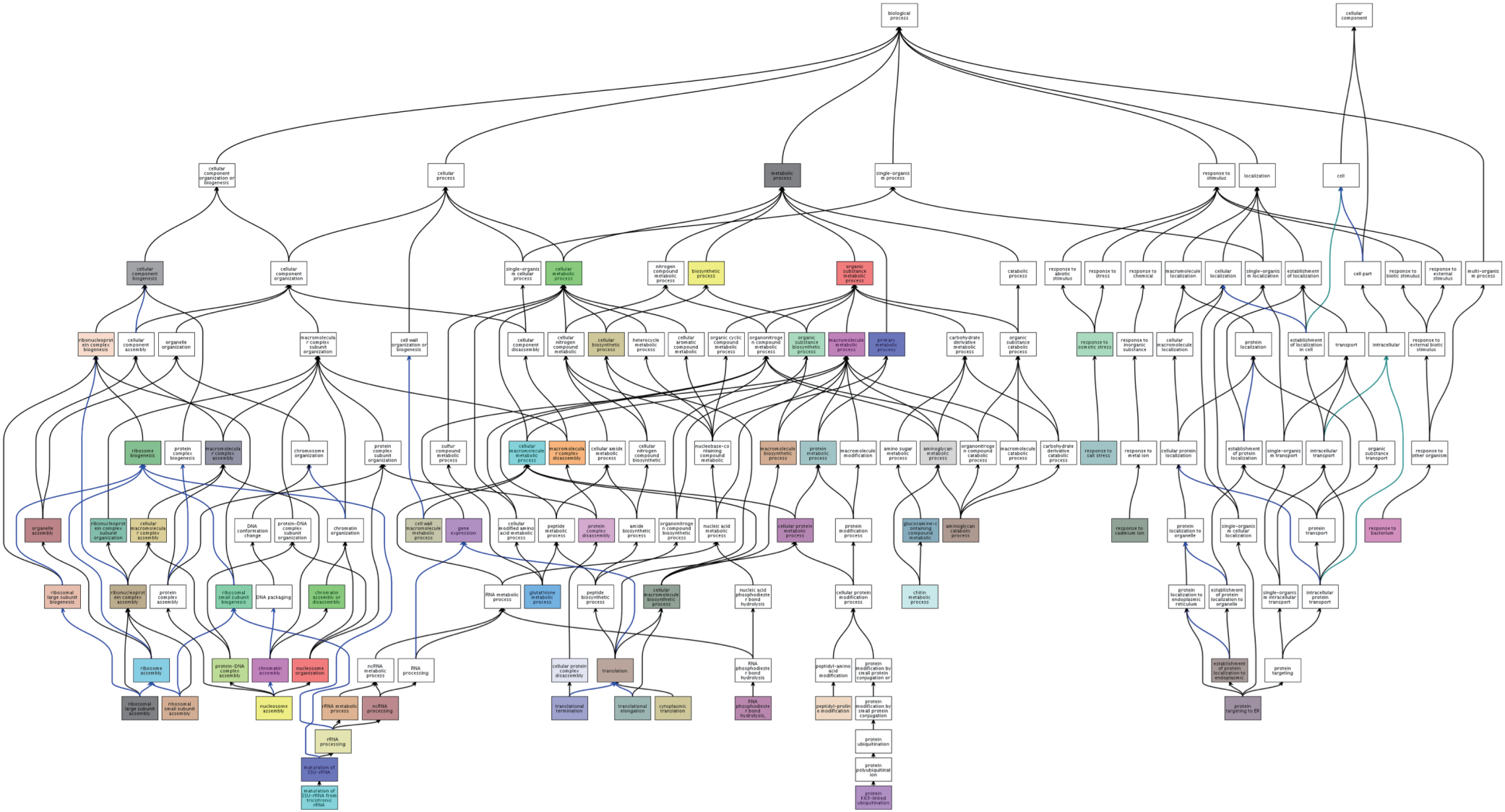


附圖二　表現量上升之差異性表現基因於 Cellular component 層面功能群分佈圖。本研究中差異性表現基因座落之功能群以顏色標記。
sFig. 2　Distribution of GO terms related to the cellular component of upregulated DEGs. Terms identified in this study are highlighted.



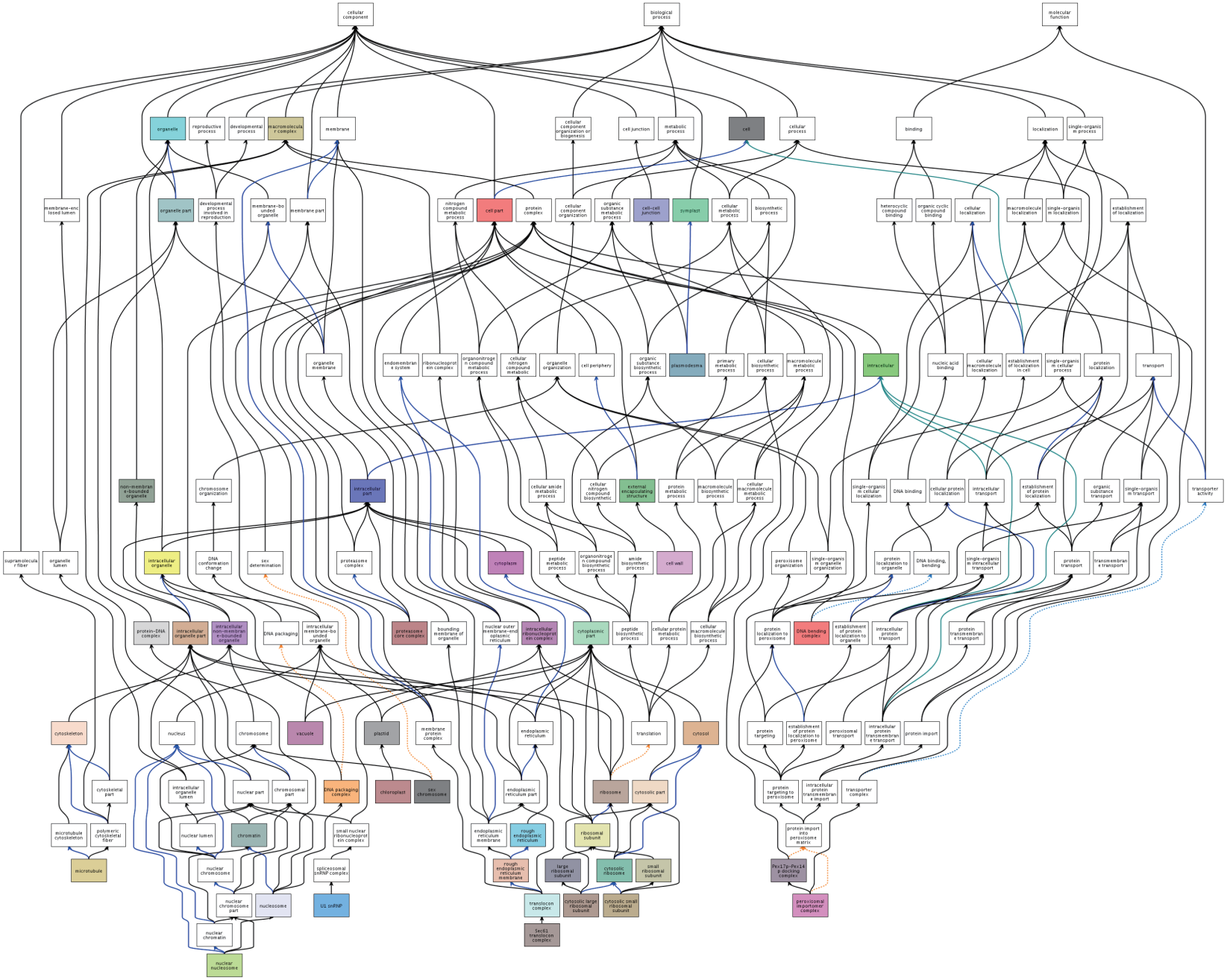
附圖三　表現量上升之差異性表現基因於 Molecular function 層面功能群分佈圖。本研究中差異性表現基因座落之功能群以顏色標記。

sFig. 3　Distribution of GO terms related to the molecular process of upregulated DEGs. Terms identified in this study are highlighted.



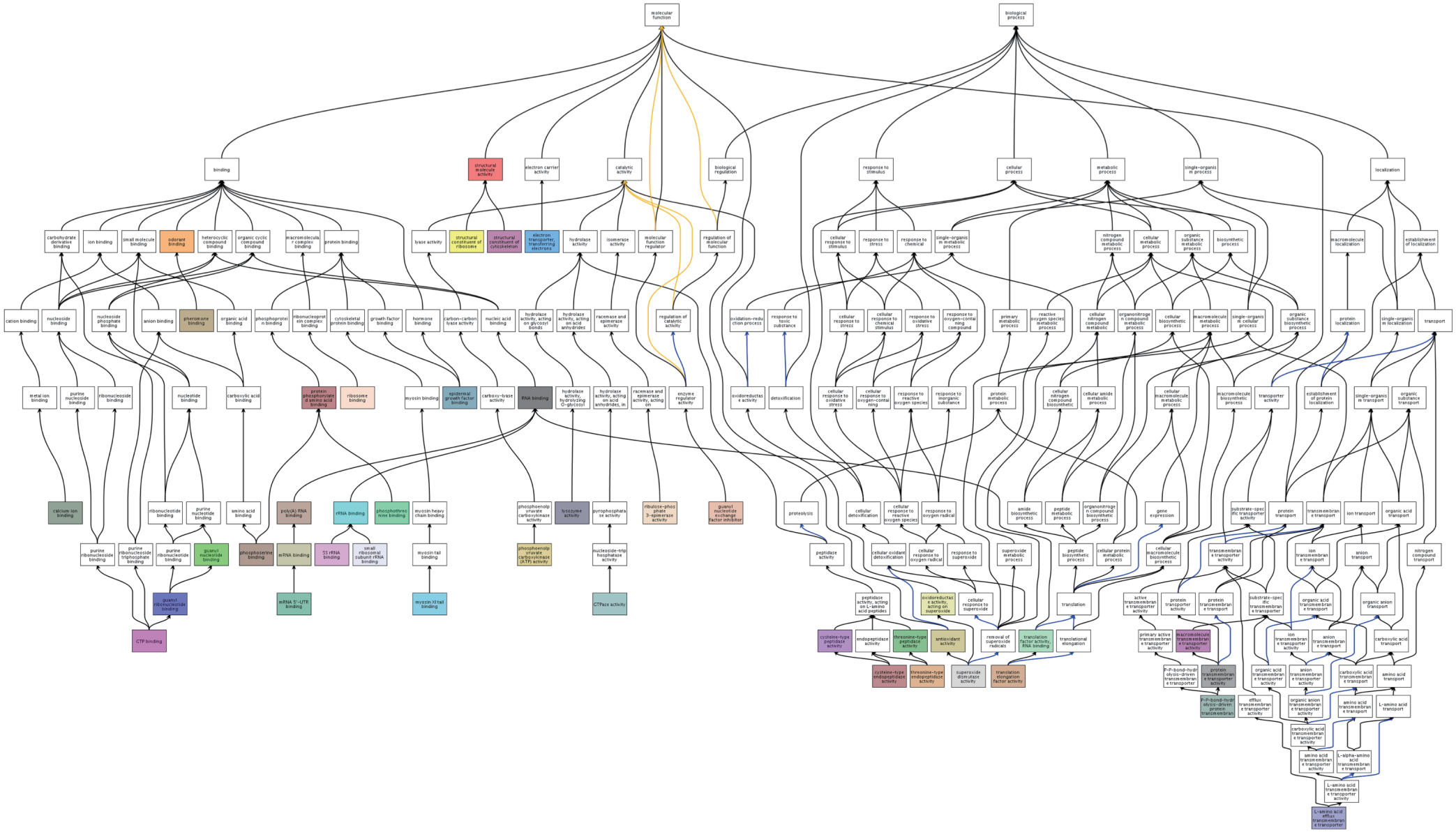
附圖四　表現量下降之差異性表現基因於 Biological process 層面功能群分佈圖。本研究中差異性表現基因座落之功能群以顏色標記。

sFig. 4　Distribution of GO terms related to the biological process of downregulated DEGs. Terms identified in this study are highlighted.



附圖五　表現量下降之差異性表現基因於 Cellular component 層面功能群分佈圖。本研究中差異性表現基因座落之功能群以顏色標記。

sFig. 5　Distribution of GO terms related to the cellular component of downregulated DEGs. Terms identified in this study are highlighted.



附圖六　表現量下降之差異性表現基因於 Molecular function 層面功能群分佈圖。本研究中差異性表現基因座落之功能群以顏色標記。

sFig. 6　Distribution of GO terms related to the molecular process of downregulated DEGs. Terms identified in this study are highlighted.