Table S3.

Process	GO number	CNAG #	Function	FPKM, WT	FPKM, kcs1	Log2 (kcs1/ WT)	Q-value	Significant
Glycolysis and pyruvate decraboxylation (6 genes)								**4**
biological_process	GO:0006096	CNAG_03769	hexokinase	357.50	515.89	0.53	0.5841	
biological_process	GO:0006096	CNAG_05480	hexokinase	65.67	149.86	1.19	0.0005	yes
biological_process	GO:0006096	CNAG_04676	6-phosphofructokinase	22.91	103.29	2.17	0.0005	yes
biological_process	GO:0006096	CNAG_01820	pyruvate kinase	53.69	322.45	2.59	0.0005	yes
biological_process	GO:0008152	CNAG_01120	pyruvate dehydrogenase complex E2 component dihydrolipoamide acetyltransferase	101.37	219.77	1.12	0.0005	yes
biological_process	GO:0008152	CNAG_07660	pyruvate dehydrogenase (acetyl-transferring) E1 component, alpha subunit	105.44	220.38	1.06	0.2379	
Citric acid cycle (16 genes)								**5**
biological_process	GO:0006096	CNAG_03225	malate dehydrogenase, NAD-dependent	542.05	393.71	-0.46	0.1568	
biological_process	GO:0006096	CNAG_03266	malate dehydrogenase, NAD-dependent	418.84	212.30	-0.98	0.0005	
biological_process	GO:0044262	CNAG_00061	citrate synthase, mitochondrial	351.42	251.37	-0.48	0.2178	
biological_process	GO:0008152	CNAG_07363	isocitrate dehydrogenase, NAD-dependent	187.56	194.13	0.05	0.9135	
biological_process	GO:0008152	CNAG_07851	isocitrate dehydrogenase, NAD-dependent	232.39	221.89	-0.07	0.8845	
biological_process	GO:0006099	CNAG_01137	aconitate hydratase, mitochondrial	397.72	226.19	-0.81	0.0084	
biological_process	GO:0006099	CNAG_03226	succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	637.58	299.74	-1.09	0.0005	yes
biological_process	GO:0006099	CNAG_03427	aconitate hydratase, mitochondrial	20.65	8.79	-1.23	0.0005	yes
biological_process	GO:0006099	CNAG_03596	2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase)	571.47	425.04	-0.43	0.2248	
biological_process	GO:0006099	CNAG_04189	succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	741.37	283.18	-1.39	0.0005	yes
biological_process	GO:0006099	CNAG_06723	succinate dehydrogenase (ubiquinone) membrane anchor subunit	1287.65	571.45	-1.17	0.0005	yes
biological_process	GO:0006099	CNAG_07356	succinate dehydrogenase, cytochrome b556 subunit	875.97	421.19	-1.06	0.0005	yes
biological_process	GO:0006099	CNAG_07363	isocitrate dehydrogenase, NAD-dependent	187.56	194.13	0.05	0.9135	
biological_process	GO:0006099	CNAG_07851	isocitrate dehydrogenase, NAD-dependent	232.39	221.89	-0.07	0.8845	
biological_process	GO:0006099	CNAG_07908	aconitate hydratase, mitochondrial	14.38	13.96	-0.04	0.9328	
biological_process	GO:0006106	CNAG_01657	fumarate hydratase, mitochondrial	181.56	248.63	0.45	0.1296	
Fatty acid beta-oxidation and peroxisomal organisation (24 genes)								**18**
biological_process	GO:0006635	CNAG_07747	acyl-CoA oxidase	99.86	21.78	-2.20	0.0005	yes
biological_process	GO:0006810	CNAG_02764	ATP-binding cassette, subfamily D (ALD), peroxisomal long-chain fatty acid import protein	58.38	4.85	-3.59	0.0005	yes
biological_process	GO:0008152	CNAG_02562	acyl-CoA dehydrogenase	114.58	9.03	-3.66	0.0005	yes
biological_process	GO:0008152	CNAG_03666	acyl-CoA dehydrogenase	541.90	24.11	-4.49	0.0005	yes
biological_process	GO:0008152	CNAG_04688	acyl-CoA dehydrogenase	199.96	25.38	-2.98	0.0005	yes
biological_process	GO:0008152	CNAG_04308	3-hydroxyacyl-CoA dehydrogenase Had1	441.78	49.38	-3.16	0.0005	yes
biological_process	GO:0008152	CNAG_05378	3-hydroxyacyl-CoA dehydrogenase	9.95	12.47	0.32	0.5101	
biological_process	GO:0006637	CNAG_03393	acyl-CoA thioesterase II	78.27	9.77	-3.00	0.0005	yes
biological_process	GO:0006637	CNAG_04274	acyl-CoA thioesterase II	29.91	16.42	-0.87	0.0016	
biological_process	GO:0008152	CNAG_00861	3-hydroxyacyl-CoA dehydrogenase	8.22	4.37	-0.91	0.0162	
biological_process	GO:0006118	CNAG_06431	acyl-CoA oxidase	768.18	22.10	-5.12	0.0005	yes
biological_process	GO:0008152	CNAG_03010	enoyl-CoA hydratase/isomerase family protein	516.44	22.25	-4.54	0.0005	yes
biological_process	GO:0008152	CNAG_04228	2,4-dienoyl-CoA reductase	95.26	16.77	-2.51	0.0005	yes
biological_process	GO:0008152	CNAG_04238	peroxisomal 2,4-dienoyl-CoA reductase	232.15	21.14	-3.46	0.0005	yes
biological_process	GO:0008152	CNAG_04531	enoyl-CoA hydratase	1969.33	199.73	-3.30	0.0005	yes
biological_process	GO:0008152	CNAG_01947	2,4-dienoyl-CoA reductase	8.08	339.78	5.39	0.0005	yes
biological_process	GO:0008152	CNAG_01135	delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase	21.95	12.83	-0.77	0.3261	
biological_process	GO:0007031	CNAG_00171	peroxin-2	51.47	13.12	-1.97	0.0005	yes
biological_process	GO:0007031	CNAG_02939	peroxin-3	41.37	22.60	-0.87	0.3996	
biological_process	GO:0007031	CNAG_04937	peroxin-12	17.85	4.26	-2.07	0.0005	yes
biological_process	GO:0007031	CNAG_05564	peroxin-10	59.16	25.67	-1.20	0.0005	yes
biological_process	GO:0007031	CNAG_07403	peroxin-1	46.07	9.93	-2.10	0.4260	
biological_process	GO:0008152	CNAG_05721	multifunctional beta-oxidation protein Mfe2	370.16	17.62	-4.39	0.0003	yes
biological_process	GO:0006631	CNAG_03134	3-hydroxyacyl-CoA dehydrogenase Had2	264.66	23.92	-3.47	0.0003	yes
Glyoxylate cycle and gluconeogenesis (5 genes)								**3**
biological_process	GO:0005975	CNAG_00057	fructose-1,6-bisphosphatase I	1105.45	815.94	-0.44	0.3014	
biological_process	GO:0006094	CNAG_04217	phosphoenolpyruvate carboxykinase (PCK1)	1103.07	54.26	-4.35	0.0005	yes

biological_process	GO:0006094	CNAG_05907	pyruvate carboxylase	93.24	140.45	0.59	0.0559	
biological_process	GO:0008152	CNAG_05303	isocitrate lyase	1035.28	3.88	-8.06	0.0005	yes
biological_process	GO:0006097	CNAG_05653	malate synthase A	916.08	44.54	-4.36	0.0005	yes
Translation/ribosomal biogenesis (160 genes)								**91**
biological_process	GO:0006412	CNAG_00007	methionine-tRNA ligase	46.05	41.27	-0.16	0.7637	
biological_process	GO:0006412	CNAG_00034	large subunit ribosomal protein L9e	409.66	1581.66	1.95	0.0005	yes
biological_process	GO:0006412	CNAG_00084	glutamine-tRNA ligase	13.99	25.79	0.88	0.0052	
biological_process	GO:0006412	CNAG_00109	large subunit ribosomal protein L34	38.15	46.81	0.30	0.5121	
biological_process	GO:0006412	CNAG_00116	small subunit ribosomal protein S3	141.03	452.63	1.68	0.0005	yes
biological_process	GO:0006412	CNAG_00143	phosphoribosylaminoimidazolesuccinocarboxamide synthase	20.84	50.78	1.28	0.0012	yes
biological_process	GO:0006412	CNAG_00232	large subunit ribosomal protein L30e	1158.08	3145.83	1.44	0.0005	yes
biological_process	GO:0006412	CNAG_00238	isoleucine-tRNA ligase	45.00	100.62	1.16	0.0005	yes
biological_process	GO:0006412	CNAG_00347	DEAH box polypeptide 36	6.35	6.79	0.10	0.8799	
biological_process	GO:0006412	CNAG_00370	polyubiquitin	788.64	2141.44	1.44	0.0005	yes
biological_process	GO:0006412	CNAG_00451	cytoplasmic protein	7.15	7.40	0.05	0.9318	
biological_process	GO:0006412	CNAG_00502	large subunit ribosomal protein L35	69.29	83.34	0.27	0.4703	
biological_process	GO:0006412	CNAG_00535	large subunit ribosomal protein L16	41.08	55.45	0.43	0.6481	
biological_process	GO:0006412	CNAG_00608	hypothetical protein	92.82	198.61	1.10	0.0368	yes
biological_process	GO:0006412	CNAG_00640	small subunit ribosomal protein S4-A	873.69	3002.20	1.78	0.0005	yes
biological_process	GO:0006412	CNAG_00656	large subunit ribosomal protein L7e	258.57	988.71	1.94	0.0005	yes
biological_process	GO:0006412	CNAG_00672	small subunit ribosomal protein S11	705.02	2654.13	1.91	0.0005	yes
biological_process	GO:0006412	CNAG_00703	large subunit ribosomal protein L31e	983.37	3293.43	1.74	0.0005	yes
biological_process	GO:0006412	CNAG_00722	large subunit ribosomal protein L27	106.98	143.41	0.42	0.4015	
biological_process	GO:0006412	CNAG_00771	large subunit ribosomal protein L29	523.89	1851.66	1.82	0.0005	yes
biological_process	GO:0006412	CNAG_00779	large subunit ribosomal protein L27e	475.08	1680.87	1.82	0.0005	yes
biological_process	GO:0006412	CNAG_00819	small subunit ribosomal protein S30	1160.19	2471.15	1.09	0.0019	yes
biological_process	GO:0006412	CNAG_00821	large subunit ribosomal protein L34e	351.16	1072.11	1.61	0.0005	yes
biological_process	GO:0006412	CNAG_01152	small subunit ribosomal protein S6e	248.71	1057.11	2.09	0.0005	yes
biological_process	GO:0006412	CNAG_01153	small subunit ribosomal protein S13e	249.70	773.51	1.63	0.0005	yes
biological_process	GO:0006412	CNAG_01170	small subunit ribosomal protein S17	713.01	2555.58	1.84	0.0005	yes
biological_process	GO:0006412	CNAG_01181	small subunit ribosomal protein S27Ae	627.68	1938.31	1.63	0.0005	yes
biological_process	GO:0006412	CNAG_01224	large subunit ribosomal protein L18-A	592.26	2232.13	1.91	0.0005	yes
biological_process	GO:0006412	CNAG_01300	small subunit ribosomal protein S21e	223.73	716.02	1.68	0.0005	yes
biological_process	GO:0006412	CNAG_01305	methionine-tRNA ligase	28.38	52.14	0.88	0.0012	
biological_process	GO:0006412	CNAG_01320	large subunit ribosomal protein L17	44.88	59.48	0.41	0.3855	
biological_process	GO:0006412	CNAG_01332	small subunit ribosomal protein S24e	387.57	1297.66	1.74	0.0005	yes
biological_process	GO:0006412	CNAG_01345	small subunit ribosomal protein S2	30.58	51.48	0.75	0.0082	
biological_process	GO:0006412	CNAG_01347	co-chaperone	142.94	96.93	-0.56	0.0887	
biological_process	GO:0006412	CNAG_01435	serine-tRNA ligase	62.00	142.00	1.20	0.0005	yes
biological_process	GO:0006412	CNAG_01455	large subunit ribosomal protein L39	378.41	1234.32	1.71	0.0005	yes
biological_process	GO:0006412	CNAG_01471	hypothetical protein	24.66	69.73	1.50	0.0005	yes
biological_process	GO:0006412	CNAG_01480	large subunit ribosomal protein L12	251.52	1740.10	2.79	0.0005	yes
biological_process	GO:0006412	CNAG_01486	large subunit ribosomal protein L15-A	340.05	1780.00	2.39	0.0005	yes
biological_process	GO:0006412	CNAG_01522	phenylalanine-tRNA ligase	21.06	75.09	1.83	0.0005	yes
biological_process	GO:0006412	CNAG_01544	histidyl-tRNA synthetase	67.53	175.88	1.38	0.0005	yes
biological_process	GO:0006412	CNAG_01590	large subunit ribosomal protein L32	57.82	207.59	1.84	0.0005	yes
biological_process	GO:0006412	CNAG_01599	hypothetical protein	14.03	41.69	1.57	0.1087	
biological_process	GO:0006412	CNAG_01628	small subunit ribosomal protein S20	348.23	2181.06	2.65	0.0005	yes
biological_process	GO:0006412	CNAG_01650	large subunit ribosomal protein L7	14.54	43.34	1.58	0.0005	yes
biological_process	GO:0006412	CNAG_01679	small subunit ribosomal protein S15	70.98	170.30	1.26	0.0231	yes
biological_process	GO:0006412	CNAG_01812	large subunit ribosomal protein L24e	45.35	121.98	1.43	0.0118	yes
biological_process	GO:0006412	CNAG_01819	large subunit ribosomal protein L1	9.35	63.05	2.75	0.0019	yes
biological_process	GO:0006412	CNAG_01884	large subunit ribosomal protein L3	252.31	1535.19	2.61	0.0005	yes
biological_process	GO:0006412	CNAG_01894	aspartate-tRNA ligase	9.71	38.45	1.98	0.3853	
biological_process	GO:0006412	CNAG_01951	small subunit ribosomal protein S22-A	451.56	2685.76	2.57	0.0005	yes
biological_process	GO:0006412	CNAG_01974	large subunit ribosomal protein L36	54.00	98.62	0.87	0.2034	
biological_process	GO:0006412	CNAG_01976	large subunit ribosomal protein L23	403.58	2473.50	2.62	0.0005	yes
biological_process	GO:0006412	CNAG_01990	small subunit ribosomal protein S5	730.34	5192.73	2.83	0.0005	yes
biological_process	GO:0006412	CNAG_02037	large subunit ribosomal protein L22	20.04	25.03	0.32	0.8750	
biological_process	GO:0006412	CNAG_02136	small subunit ribosomal protein S6	147.70	246.33	0.74	0.0097	
biological_process	GO:0006412	CNAG_02144	large subunit ribosomal protein L1-A	461.31	1525.44	1.73	0.0005	yes
biological_process	GO:0006412	CNAG_02234	large subunit ribosomal protein L6e	225.28	759.48	1.75	0.0005	yes
biological_process	GO:0006412	CNAG_02330	large subunit ribosomal protein L21e	107.87	452.41	2.07	0.0183	yes
biological_process	GO:0006412	CNAG_02331	small subunit ribosomal protein S9	815.88	3369.79	2.05	0.0009	yes
biological_process	GO:0006412	CNAG_02354	large subunit ribosomal protein L2	25.20	45.42	0.85	0.1226	

biological_process	GO:0006412	CNAG_02418	asparagine-tRNA ligase	22.81	79.49	1.80	0.0005	yes
biological_process	GO:0006412	CNAG_02709	small subunit ribosomal protein S19	66.30	91.74	0.47	0.2004	
biological_process	GO:0006412	CNAG_02754	small subunit ribosomal protein S12e	960.85	3408.42	1.83	0.0005	yes
biological_process	GO:0006412	CNAG_02763	phenylalanine-tRNA ligase, beta subunit	19.53	39.90	1.03	0.0869	
biological_process	GO:0006412	CNAG_02811	small subunit ribosomal protein S29	879.63	3252.14	1.89	0.0005	yes
biological_process	GO:0006412	CNAG_02813	large subunit ribosomal protein L30	185.64	190.28	0.04	0.9436	
biological_process	GO:0006412	CNAG_02838	small subunit ribosomal protein S17	42.45	62.37	0.56	0.0794	
biological_process	GO:0006412	CNAG_02914	hypothetical protein	15.90	23.45	0.56	0.0891	
biological_process	GO:0006412	CNAG_02923	large subunit ribosomal protein L14	79.00	101.16	0.36	0.2803	
biological_process	GO:0006412	CNAG_02928	large subunit ribosomal protein L5e	229.13	778.62	1.76	0.0005	yes
biological_process	GO:0006412	CNAG_03000	small subunit ribosomal protein S19e	704.36	2456.32	1.80	0.0005	yes
biological_process	GO:0006412	CNAG_03015	large subunit ribosomal protein L37-A	427.00	1315.86	1.62	0.0005	yes
biological_process	GO:0006412	CNAG_03053	large subunit ribosomal protein L23	264.37	1027.98	1.96	0.0005	yes
biological_process	GO:0006412	CNAG_03127	small subunit ribosomal protein S23	948.13	2100.79	1.15	0.0005	yes
biological_process	GO:0006412	CNAG_03221	large subunit ribosomal protein L29	824.08	2749.61	1.74	0.0005	yes
biological_process	GO:0006412	CNAG_03260	large subunit ribosomal protein L6	34.41	47.24	0.46	0.2481	
biological_process	GO:0006412	CNAG_03283	large subunit ribosomal protein L24e	353.83	1272.54	1.85	0.0005	yes
biological_process	GO:0006412	CNAG_03303	small subunit ribosomal protein S27	368.07	962.36	1.39	0.0005	yes
biological_process	GO:0006412	CNAG_03320	mannose-1-phosphate guanylyltransferase	28.31	24.18	-0.23	0.8319	
biological_process	GO:0006412	CNAG_03353	hypothetical protein	37.46	80.45	1.10	0.0005	yes
biological_process	GO:0006412	CNAG_03441	small subunit ribosomal protein S21	33.68	44.73	0.41	0.2462	
biological_process	GO:0006412	CNAG_03457	arginine-tRNA ligase	32.05	96.83	1.59	0.0005	yes
biological_process	GO:0006412	CNAG_03510	large subunit ribosomal protein L36e	398.27	973.00	1.29	0.0116	yes
biological_process	GO:0006412	CNAG_03540	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase, B subunit	26.87	24.36	-0.14	0.7653	
biological_process	GO:0006412	CNAG_03554	coatomer protein complex, subunit alpha (xenin)	73.62	99.61	0.44	0.1884	
biological_process	GO:0006412	CNAG_03563	aspartate-tRNA(Asn) ligase	58.17	101.52	0.80	0.0116	
biological_process	GO:0006412	CNAG_03693	large subunit ribosomal protein L11	119.94	122.81	0.03	0.9607	
biological_process	GO:0006412	CNAG_03739	large subunit ribosomal protein L10-like	778.27	1867.45	1.26	0.0005	yes
biological_process	GO:0006412	CNAG_03747	large subunit ribosomal protein L27Ae	427.83	1536.99	1.85	0.0005	yes
biological_process	GO:0006412	CNAG_03779	large subunit ribosomal protein L4	16.80	18.97	0.18	0.8437	
biological_process	GO:0006412	CNAG_03780	small subunit ribosomal protein S16	364.78	1325.08	1.86	0.0005	yes
biological_process	GO:0006412	CNAG_03793	hypothetical protein	77.83	55.99	-0.48	0.6021	
biological_process	GO:0006412	CNAG_03810	large subunit ribosomal protein L13	173.98	162.92	-0.09	0.8589	
biological_process	GO:0006412	CNAG_03965	ribosome recycling factor	131.36	101.88	-0.37	0.2520	
biological_process	GO:0006412	CNAG_04004	small subunit ribosomal protein S1	908.90	3097.77	1.77	0.0005	yes
biological_process	GO:0006412	CNAG_04011	large subunit ribosomal protein L37a	733.09	2774.04	1.92	0.0005	yes
biological_process	GO:0006412	CNAG_04021	large subunit ribosomal protein L24	377.46	1361.80	1.85	0.0005	yes
biological_process	GO:0006412	CNAG_04068	large subunit ribosomal protein L28e	111.92	446.05	1.99	0.0005	yes
biological_process	GO:0006412	CNAG_04082	proline-tRNA ligase	29.30	68.56	1.23	0.0055	yes
biological_process	GO:0006412	CNAG_04114	small subunit ribosomal protein S0	51.66	283.79	2.46	0.0005	yes
biological_process	GO:0006412	CNAG_04179	lysine-tRNA ligase	46.15	88.73	0.94	0.0012	
biological_process	GO:0006412	CNAG_04180	large subunit ribosomal protein L15	74.92	121.53	0.70	0.0537	
biological_process	GO:0006412	CNAG_04292	hypothetical protein	25.93	44.75	0.79	0.0055	
biological_process	GO:0006412	CNAG_04400	small subunit ribosomal protein S10	26.41	36.43	0.46	0.7522	
biological_process	GO:0006412	CNAG_04445	small subunit ribosomal protein S7e	377.54	1451.02	1.94	0.0005	yes
biological_process	GO:0006412	CNAG_04448	large subunit ribosomal protein L19e	639.40	1988.41	1.64	0.0005	yes
biological_process	GO:0006412	CNAG_04452	small subunit ribosomal protein S18	59.02	84.64	0.52	0.2463	
biological_process	GO:0006412	CNAG_04604	tryptophan-tRNA ligase	39.36	66.66	0.76	0.0029	
biological_process	GO:0006412	CNAG_04641	general transcription factor 3C polypeptide 3 (transcription factor C subunit 4)	15.57	14.48	-0.11	0.8132	
biological_process	GO:0006412	CNAG_04726	large subunit ribosomal protein L18Ae	432.49	1639.13	1.92	0.0005	yes
biological_process	GO:0006412	CNAG_04762	large subunit ribosomal protein L4e	165.05	540.16	1.71	0.0005	yes
biological_process	GO:0006412	CNAG_04799	large subunit ribosomal protein L14e	391.89	1499.48	1.94	0.0005	yes
biological_process	GO:0006412	CNAG_04800	phenylalanine-tRNA ligase, alpha subunit	109.18	125.86	0.21	0.5653	
biological_process	GO:0006412	CNAG_04830	large subunit ribosomal protein L33	234.78	219.34	-0.10	0.8555	
biological_process	GO:0006412	CNAG_04883	small subunit ribosomal protein S18	467.59	1451.03	1.63	0.0005	yes
biological_process	GO:0006412	CNAG_04884	large subunit ribosomal protein L44	861.38	2589.57	1.59	0.0005	yes
biological_process	GO:0006412	CNAG_04896	tyrosine-tRNA ligase	19.78	24.76	0.32	0.6314	
biological_process	GO:0006412	CNAG_05110	small subunit ribosomal protein S13	68.67	87.09	0.34	0.3321	
biological_process	GO:0006412	CNAG_05232	large subunit ribosomal protein L8	615.30	2054.82	1.74	0.0005	yes
biological_process	GO:0006412	CNAG_05507	small subunit ribosomal protein S8	252.54	258.01	0.03	0.9503	
biological_process	GO:0006412	CNAG_05525	small subunit ribosomal protein S26	864.06	2659.91	1.62	0.0005	yes
biological_process	GO:0006412	CNAG_05530	hypothetical protein	39.36	40.61	0.05	0.9405	
biological_process	GO:0006412	CNAG_05555	large subunit ribosomal protein L7Ae	411.68	1566.88	1.93	0.0005	yes

biological_process	GO:0006412	CNAG_05556	hypothetical protein	492.31	1882.61	1.94	0.0047	yes
biological_process	GO:0006412	CNAG_05580	hypothetical protein	4.22	2.64	-0.68	0.7885	
biological_process	GO:0006412	CNAG_05635	large subunit ribosomal protein L19	22.19	27.94	0.33	0.7345	
biological_process	GO:0006412	CNAG_05722	alanine-tRNA ligase	60.30	72.30	0.26	0.5626	
biological_process	GO:0006412	CNAG_05764	small subunit ribosomal protein S5	60.52	72.46	0.26	0.6730	
biological_process	GO:0006412	CNAG_05800	large subunit ribosomal protein L33-b	276.78	1066.97	1.95	0.0005	yes
biological_process	GO:0006412	CNAG_05825	minichromosome maintenance protein 7 (cell division control protein 47)	9.27	37.65	2.02	0.0005	yes
biological_process	GO:0006412	CNAG_05900	glycine-tRNA ligase	47.46	91.12	0.94	0.0005	
biological_process	GO:0006412	CNAG_05904	small subunit ribosomal protein S14	285.08	983.23	1.79	0.0005	yes
biological_process	GO:0006412	CNAG_05978	glutamate-tRNA ligase	60.67	92.26	0.60	0.0279	
biological_process	GO:0006412	CNAG_05980	large subunit ribosomal protein L7/L12	44.14	83.21	0.91	0.0019	
biological_process	GO:0006412	CNAG_06095	large subunit ribosomal protein L13e	510.02	1924.22	1.92	0.0005	yes
biological_process	GO:0006412	CNAG_06123	leucine-tRNA ligase	24.92	75.31	1.60	0.0005	yes
biological_process	GO:0006412	CNAG_06222	large subunit ribosomal protein L32e	1475.33	5286.23	1.84	0.0005	yes
biological_process	GO:0006412	CNAG_06231	large subunit ribosomal protein L13	139.83	569.85	2.03	0.0005	yes
biological_process	GO:0006412	CNAG_06441	isoleucine-tRNA ligase	19.18	25.00	0.38	0.2262	
biological_process	GO:0006412	CNAG_06447	large subunit ribosomal protein L22	274.94	1148.69	2.06	0.0005	yes
biological_process	GO:0006412	CNAG_06471	small subunit ribosomal protein S12	33.97	43.28	0.35	0.3608	
biological_process	GO:0006412	CNAG_06535	ribosome biogenesis protein UTP30	15.73	29.58	0.91	0.0023	
biological_process	GO:0006412	CNAG_06605	small subunit ribosomal protein S2	194.20	849.49	2.13	0.0005	yes
biological_process	GO:0006412	CNAG_06633	small subunit ribosomal protein S15	853.07	2933.37	1.78	0.0005	yes
biological_process	GO:0006412	CNAG_06713	cysteine-tRNA ligase	12.09	26.59	1.14	0.2149	
biological_process	GO:0006412	CNAG_06748	U3 small nucleolar RNA-associated protein 7	19.59	19.01	-0.04	0.9320	
biological_process	GO:0006412	CNAG_06755	threonine-tRNA ligase	36.71	78.70	1.10	0.0005	yes
biological_process	GO:0006412	CNAG_06763	serine-tRNA ligase	13.42	13.96	0.06	0.9114	
biological_process	GO:0006412	CNAG_06811	large subunit ribosomal protein L22e	277.11	1053.36	1.93	0.0005	yes
biological_process	GO:0006412	CNAG_06847	small subunit ribosomal protein S28	959.01	2965.93	1.63	0.0005	yes
biological_process	GO:0006412	CNAG_07309	mRNA surveillance protein pelota	68.24	136.39	1.00	0.0005	
biological_process	GO:0006412	CNAG_07400	aspartate-tRNA(Asn) ligase	83.32	111.59	0.42	0.1507	
biological_process	GO:0006412	CNAG_07429	asparagine-tRNA ligase	19.83	25.46	0.36	0.2854	
biological_process	GO:0006412	CNAG_07473	valine-tRNA ligase	39.11	53.14	0.44	0.1296	
biological_process	GO:0006412	CNAG_07535	small subunit ribosomal protein S16	21.11	31.01	0.55	0.1691	
biological_process	GO:0006412	CNAG_07563	glutamate-tRNA ligase	19.57	29.94	0.61	0.1560	
biological_process	GO:0006412	CNAG_07637	large subunit ribosomal protein L3	83.99	125.24	0.58	0.3869	
biological_process	GO:0006412	CNAG_07778	translation initiation factor 2 subunit 1	111.25	198.97	0.84	0.0016	
biological_process	GO:0006412	CNAG_07839	large subunit ribosomal protein L11	786.94	2681.61	1.77	0.0005	yes
Sugar transporters (51 genes)								**23**
molecular_function	GO:0005351	CNAG_00048	sugar transporter	11.79	1.82	-2.70	0.0005	yes
molecular_function	GO:0005351	CNAG_00097	MFS transporter, SP family, solute carrier family 2 (myo-inositol transporter), member 13	10.82	10.32	-0.07	0.9351	
molecular_function	GO:0005351	CNAG_00864	MFS transporter, SP family, solute carrier family 2 (myo-inositol transporter), member 13	15.32	1.03	-3.90	0.0125	yes
molecular_function	GO:0005351	CNAG_00867	MFS transporter, SP family, solute carrier family 2 (myo-inositol transporter), member 13	1.62	0.44	-1.87	0.5069	
molecular_function	GO:0005351	CNAG_01683	monosaccharide transporter	120.56	348.82	1.53	0.0005	
molecular_function	GO:0005351	CNAG_01835	hypothetical protein	81.67	53.74	-0.60	0.0279	
molecular_function	GO:0005351	CNAG_01862	hexose transporter	7.53	1.22	-2.63	0.0959	
molecular_function	GO:0005351	CNAG_01936	sugar transporter	130.18	6.90	-4.24	0.0005	yes
molecular_function	GO:0005351	CNAG_02254	quinate permease	25.95	5.16	-2.33	0.0005	yes
molecular_function	GO:0005351	CNAG_02479	monosaccharide transporter	3.87	4.82	0.32	0.4528	
molecular_function	GO:0005351	CNAG_02554	sugar transporter	9.73	6.68	-0.54	0.1240	
molecular_function	GO:0005351	CNAG_02733	monosaccharide transporter	18.69	1.27	-3.88	0.0077	yes
molecular_function	GO:0005351	CNAG_03087	maltose permease	1.26	0.38	-1.72	1.0000	
molecular_function	GO:0005351	CNAG_03320	mannose-1-phosphate guanylyltransferase	28.31	24.18	-0.23	0.8319	
molecular_function	GO:0005351	CNAG_03432	solute carrier family 2	36.41	15.49	-1.23	0.1396	
molecular_function	GO:0005351	CNAG_03438	hexose transporter	118.98	1025.80	3.11	0.0005	
molecular_function	GO:0005351	CNAG_03772	glucose transporter	687.02	13.25	-5.70	0.0005	yes
molecular_function	GO:0005351	CNAG_03910	D-xylose-proton symporter	239.02	20.04	-3.58	0.0005	yes
molecular_function	GO:0005351	CNAG_04024	sugar transporter	33.90	8.27	-2.03	0.0005	yes
molecular_function	GO:0005351	CNAG_04038	MFS quinate transporter QutD	12.92	10.07	-0.36	0.3294	
molecular_function	GO:0005351	CNAG_04092	sugar transporter	14.88	1.94	-2.94	0.0005	yes

molecular_function	GO:0005351	CNAG_04210	MFS transporter, SP family, general alpha glucoside:H symporter	43.30	57.36	0.41	0.1781	
molecular_function	GO:0005351	CNAG_04552	hypothetical protein	0.93	0.21	-2.17	1.0000	
molecular_function	GO:0005351	CNAG_04783	monosaccharide transporter	20.66	33.31	0.69	0.0166	
molecular_function	GO:0005351	CNAG_04784	monosaccharide transporter	1.78	0.52	-1.78	0.4783	
molecular_function	GO:0005351	CNAG_04920	galactose transporter	17.34	44.37	1.36	0.0055	
molecular_function	GO:0005351	CNAG_04938	hypothetical protein	117.25	163.60	0.48	0.2883	
molecular_function	GO:0005351	CNAG_05139	solute carrier family 35 (UDP-sugar transporter), member A1/2/3	18.88	21.26	0.17	0.7548	
molecular_function	GO:0005351	CNAG_05324	sugar transporter	3.08	0.42	-2.88	0.0005	yes
molecular_function	GO:0005351	CNAG_05330	MFS transporter, SP family, general alpha glucoside:H symporter	0.22	0.21	-0.07	1.0000	
molecular_function	GO:0005351	CNAG_05336	glucose transporter	35.21	5.18	-2.77	0.0026	yes
molecular_function	GO:0005351	CNAG_05340	monosaccharide transporter	26.39	2.97	-3.15	0.4952	
molecular_function	GO:0005351	CNAG_05377	MFS transporter, SP family, solute carrier family 2 (myo-inositol transporter), member 13	2.02	1.94	-0.06	0.9292	
molecular_function	GO:0005351	CNAG_05381	MFS transporter, SP family, solute carrier family 2 (myo-inositol transporter), member 13	15.77	0.75	-4.39	0.0005	yes
molecular_function	GO:0005351	CNAG_05387	galactose transporter	2301.50	240.34	-3.26	0.0005	yes
molecular_function	GO:0005351	CNAG_05471	alpha-glucosidase	14.37	5.88	-1.29	0.0005	yes
molecular_function	GO:0005351	CNAG_05662	sugar transporter	1074.95	9.75	-6.78	0.0005	yes
molecular_function	GO:0005351	CNAG_05667	MFS transporter, SP family, solute carrier family 2 (myo-inositol transporter), member 13	20.18	4.70	-2.10	0.0005	yes
molecular_function	GO:0005351	CNAG_05914	MFS transporter, SP family, general alpha glucoside:H symporter	26.40	7.79	-1.76	0.0636	
molecular_function	GO:0005351	CNAG_05929	MFS transporter, SP family, general alpha glucoside:H symporter	17.00	4.35	-1.97	0.0005	yes
molecular_function	GO:0005351	CNAG_05982	MFS transporter, SP family, general alpha glucoside:H symporter	21.57	3.71	-2.54	0.0005	yes
molecular_function	GO:0005351	CNAG_06259	MFS transporter, SP family, general alpha glucoside:H symporter	2.70	1.95	-0.47	0.3120	
molecular_function	GO:0005351	CNAG_06290	high-affinity glucose transporter SNF3	152.32	68.60	-1.15	0.4054	
molecular_function	GO:0005351	CNAG_06485	hexose transporter protein	7.86	5.94	-0.40	0.3021	
molecular_function	GO:0005351	CNAG_06521	hypothetical protein	8.43	6.36	-0.41	0.2984	
molecular_function	GO:0005351	CNAG_06527	MFS transporter, SP family, general alpha glucoside:H symporter	1.41	0.40	-1.81	0.0038	yes
molecular_function	GO:0005351	CNAG_06932	sugar transporter	32.10	0.69	-5.53	0.0077	yes
molecular_function	GO:0005351	CNAG_06934	hexose transporter protein	17.56	5.06	-1.79	0.0005	yes
molecular_function	GO:0005351	CNAG_06963	sugar transporter	11.06	65.50	2.57	0.0005	
molecular_function	GO:0005351	CNAG_07641	monosaccharide transporter	20.10	4.58	-2.13	0.0097	yes
molecular_function	GO:0005351	CNAG_07874	sugar transporter	122.59	1.76	-6.12	0.0005	yes