Supplementary Table 12. Comparison of the number of peptides in tryptic digested soluble and membrane proteomes (OD$_{600}$= 0.7 and 1.2) identified by MS/MS. Only the proteins with a *Protein/Peptide Prophet* probability ≥ 0.9 were tabulated. The numbers of transmembrane domains predicted by *TMHMM* program are shown in the last column.

Multiple or single unique peptide identification	**Protein information**				**Number of peptides indentified in membrane and soluble fractions at OD 0.7 and 1.2**								**Estimation of expression level changes**					**Membrane of soluble specificity**					
	Locus name	**Accession no.**	**Gene name**	**Protein description**	**OD 0.7 memb**		**OD 0.7 sol**		**OD 1.2 memb**		**OD 1.2 sol**		**No. peptides in OD 0.7**	**No. peptides in OD 1.2**	**Total no. peptides**	**OD 0.7/1.2**	**Remark 1**	**No. peptides (membrane)**	**No. peptides (soluble)**	**% membrane / total**	**Remark 2**	**Protein length**	***TMHMM***
					total	**unique**	**total**	**unique**	**total**	**unique**	**total**	**unique**											
≥ 2 unique peptides	pNG5138	Q5V7F4_HALMA	*csg1*	Cell surface glycoprotein	2282	85	33	14	1739	77	122	17	2315	1861	4176	1.2	**No dramatic change**	4021	155	96.3	Memb predominant	887	2
≥ 2 unique peptides	rrnAC1803	Q5V1B0_HALMA	*rrnAC1803*	Hypothetical protein	1294	62	15	7	1314	59	10	4	1309	1324	2633	1.0	**No dramatic change**	2608	25	99.1	Memb predominant	396	1
≥ 2 unique peptides	rrnAC3098	Q5UY43_HALMA	*rrnAC3098*	Hypothetical protein	1198	39	13	4	863	38	24	8	1211	887	2098	1.4	**No dramatic change**	2061	37	98.2	Memb predominant	357	1
≥ 2 unique peptides	rrnAC3099	Q5UY42_HALMA	*edp*	Proteinase IV-like	1061	48	1	1	791	39	1	1	1062	792	1854	1.3	**No dramatic change**	1852	2	99.9	Memb predominant	308	1
≥ 2 unique peptides	rrnAC3155	Q5UXZ2_HALMA	*atpC1*	H+ ATP synthase sununit C (EC 3.6.3.14)	940	10	0	0	871	14	0	0	940	871	1811	1.1	**No dramatic change**	1811	0	100.0	Memb only	86	2
≥ 2 unique peptides	rrnAC2228	Q5V092_HALMA	*dppD*	Dipeptide ABC transporter ATP-binding	551	26	0	0	392	21	0	0	551	392	943	1.4	**No dramatic change**	943	0	100.0	Memb only	575	0
≥ 2 unique peptides	rrnAC2149	Q5V0G0_HALMA	*yqgG*	Phosphate ABC transporter binding	79	14	0	0	723	23	3	2	79	726	805	0.1	1.2 (>3X)	802	3	99.6	Memb predominant	384	0
≥ 2 unique peptides	rrnAC3299	Q5UXL1_HALMA	*dppA*	Dipeptide ABC transporter dipeptide-binding	437	21	0	0	354	21	1	1	437	355	792	1.2	**No dramatic change**	791	1	99.9	Memb predominant	621	0
≥ 2 unique peptides	rrnAC0510	Q5V4M1_HALMA	*hcp9*	Halocyanin-like	260	14	0	0	492	17	2	2	260	494	754	0.5	**No dramatic change**	752	2	99.7	Memb predominant	297	0
≥ 2 unique peptides	rrnAC2706	MDH_HALMAReview	*mdh*	Malate dehydrogenase (EC 1.1.1.37)	0	0	267	30	3	2	216	27	267	219	486	1.2	**No dramatic change**	3	483	0.6	Soluble predominant	304	0
≥ 2 unique peptides	rrnAC2158	Q5V0F1_HALMA	*acnB*	Aconitate hydratase (EC 4.2.1.3)	42	15	205	29	46	16	182	29	247	228	475	1.1	**No dramatic change**	88	387	18.5	Soluble predominant	677	0
≥ 2 unique peptides	rrnAC2571	Q5UZD8_HALMA	*rrnAC2571*	Hypothetical protein	6	1	295	19	5	1	132	11	301	137	438	2.2	0.7 (2>3X)	11	427	2.5	Soluble predominant	55	0
≥ 2 unique peptides	rrnAC0831	SODM_HALMAReview	*sod*	Superoxide dismutase [Mn] (EC 1.15.1.1)	0	0	164	17	4	3	254	16	164	258	422	0.6	**No dramatic change**	4	418	0.9	Soluble predominant	203	0
≥ 2 unique peptides	pNG7111	Q5V6M9_HALMA	*pNG7111*	Hypothetical protein	26	13	108	20	20	11	226	18	134	246	380	0.5	**No dramatic change**	46	334	12.1	Soluble predominant	342	0
≥ 2 unique peptides	rrnAC3160	Q5UXY7_HALMA	*ntpB*	V-type sodium ATP synthase subunit B (EC 3.6.3.14)	49	13	131	26	69	16	114	23	180	183	363	1.0	**No dramatic change**	118	245	32.5	Memb + Sol	470	0
≥ 2 unique peptides	rrnAC2406	EF1A_HALMAReview	*tuf*	Elongation factor 1-alpha (EF-1-alpha) (Elongation factor Tu) (EF-Tu)	16	7	125	26	24	8	198	30	141	222	363	0.6	**No dramatic change**	40	323	11.0	Soluble predominant	421	0
≥ 2 unique peptides	rrnAC0170	Q5V5G6_HALMA	*rrnAC0170*	Hypothetical protein	198	18	0	0	154	17	0	0	198	154	352	1.3	**No dramatic change**	352	0	100.0	Memb only	323	0
≥ 2 unique peptides	rrnB0319	Q5UW70_HALMA	*phnD1*	ABC tranporter phosphate-binding protein	250	27	0	0	73	15	0	0	250	73	323	3.4	0.7 (>3X)	323	0	100.0	Memb only	389	0
≥ 2 unique peptides	rrnAC1171	CATA_HALMAReview	*perA*	Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase)	0	0	161	46	3	3	152	42	161	155	316	1.0	**No dramatic change**	3	313	0.9	Soluble predominant	731	0
≥ 2 unique peptides	rrnAC0472	Q5V4Q4_HALMA	*sucC*	Succinyl-CoA synthetase beta chain (EC 6.2.1.5)	7	2	130	27	11	4	166	25	137	177	314	0.8	**No dramatic change**	18	296	5.7	Soluble predominant	382	0
≥ 2 unique peptides	rrnAC2526	FER1_HALMAReview	*fer1*	Ferredoxin-1	0	0	174	2	0	0	132	5	174	132	306	1.3	**No dramatic change**	0	306	0.0	Soluble only	129	0
≥ 2 unique peptides	rrnAC1097	Q5V345_HALMA	*sdhA1*	Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)	113	28	8	5	179	31	1	1	121	180	301	0.7	**No dramatic change**	292	9	97.0	Memb predominant	608	0
≥ 2 unique peptides	rrnAC2413	EF2_HALMAReview	*fusA*	Elongation factor 2 (EF-2)	3	2	145	41	6	3	135	39	148	141	289	1.0	**No dramatic change**	9	280	3.1	Soluble predominant	728	0
≥ 2 unique peptides	rrnB0311	Q5UW77_HALMA	*ugpB*	Glycerol-3-phosphate-binding protein	22	7	0	0	258	18	3	3	22	261	283	0.1	1.2 (>3X)	280	3	98.9	Memb predominant	453	0
≥ 2 unique peptides	rrnAC1914	Q5V116_HALMA	*lon*	ATP-dependent protease LA (EC 3.4.21.53)	173	39	1	1	105	28	0	0	174	105	279	1.7	**No dramatic change**	278	1	99.6	Memb predominant	709	1
≥ 2 unique peptides	rrnAC0792	Q5V3X3_HALMA	*cdc48b*	Cell division control protein 48	1	1	121	45	7	5	144	44	122	151	273	0.8	**No dramatic change**	8	265	2.9	Soluble predominant	757	0
≥ 2 unique peptides	rrnAC1267	Q5V2P4_HALMA	*korA*	2-oxoglutarate ferredoxin oxidoreductase subunit alpha (EC 1.2.7.3)(EC 1.2.7.1)	6	4	120	23	13	8	124	26	126	137	263	0.9	**No dramatic change**	19	244	7.2	Soluble predominant	632	0
≥ 2 unique peptides	rrnAC1083	Q5V357_HALMA	*hbd1*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) (EC 4.2.1.17)	1	1	121	28	5	4	131	32	122	136	258	0.9	**No dramatic change**	6	252	2.3	Soluble predominant	669	0
≥ 2 unique peptides	rrnAC2656	Q5UZ68_HALMA	*yufN*	ABC transporter	125	10	0	0	127	9	0	0	125	127	252	1.0	**No dramatic change**	252	0	100.0	Memb only	393	0
≥ 2 unique peptides	rrnAC0080	Q5V5P3_HALMA	*rrnAC0080*	Predicted hydrolase	35	18	103	29	28	15	81	29	138	109	247	1.3	**No dramatic change**	63	184	25.5	Memb + Sol	460	0
≥ 2 unique peptides	rrnAC2605	Q5UZA8_HALMA	*hdrD*	Heterodisulfide reductase	130	20	0	0	111	21	0	0	130	111	241	1.2	**No dramatic change**	241	0	100.0	Memb only	693	4
≥ 2 unique peptides	rrnAC3026	Q5UYA2_HALMA	*yfmJ1*	Quinone oxidoreductase (EC 1.6.5.5)	30	9	97	19	15	9	95	21	127	110	237	1.2	**No dramatic change**	45	192	19.0	Soluble predominant	348	0
≥ 2 unique peptides	rrnAC2473	Q5UZM4_HALMA	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	2	2	81	17	15	5	125	19	83	140	223	0.6	**No dramatic change**	17	206	7.6	Soluble predominant	522	0
≥ 2 unique peptides	rrnAC2891	Q5UYL7_HALMA	*cctA2*	Thermosome alpha subunit	4	3	87	25	13	8	117	24	91	130	221	0.7	**No dramatic change**	17	204	7.7	Soluble predominant	590	0
≥ 2 unique peptides	rrnAC1525	Q5V207_HALMA	*rrnAC1525*	Hypothetical protein	20	12	98	29	19	12	71	21	118	90	208	1.3	**No dramatic change**	39	169	18.8	Soluble predominant	380	0
≥ 2 unique peptides	rrnAC1622	Q5V1R5_HALMA	*nrdA*	Ribonucleoside-diphosphate reductase alpha chain(EC 1.17.4.1)	2	2	106	34	3	2	88	28	108	91	199	1.2	**No dramatic change**	5	194	2.5	Soluble predominant	1032	0
≥ 2 unique peptides	rrnAC1782	THI4_HALMAReview	*rrnAC1782*	Putative thiazole biosynthetic enzyme	10	7	64	10	17	9	107	20	74	124	198	0.6	**No dramatic change**	27	171	13.6	Soluble predominant	310	0
≥ 2 unique peptides	rrnAC3228	Q5UXS3_HALMA	*acs5*	Putative acetyl-coenzyme A synthetase (EC 6.2.1.1)	0	0	64	18	5	3	129	30	64	134	198	0.5	1.2 (2~3X)	5	193	2.5	Soluble predominant	664	0
≥ 2 unique peptides	rrnAC1449	Q5V277_HALMA	*ndHG5*	NADH dehydrogenase/oxidoreductase	88	28	2	2	101	27	3	2	90	104	194	0.9	**No dramatic change**	189	5	97.4	Memb predominant	560	0
≥ 2 unique peptides	rrnB0265	Q5UWB7_HALMA	*acs4*	Acyl-coenzyme A synthetases (EC 6.2.1.1)	4	4	102	25	4	3	83	26	106	87	193	1.2	**No dramatic change**	8	185	4.1	Soluble predominant	616	0
≥ 2 unique peptides	rrnAC3419	Q5UXA4_HALMA	*icd*	Isocitrate dehydrogenase (EC 1.1.1.42)	3	3	93	23	8	6	82	23	96	90	186	1.1	**No dramatic change**	11	175	5.9	Soluble predominant	420	0
≥ 2 unique peptides	rrnAC0028	Q5V5U1_HALMA	*fumC*	Fumarate hydratase class-II (EC 4.2.1.2)	4	2	97	26	4	2	80	19	101	84	185	1.2	**No dramatic change**	8	177	4.3	Soluble predominant	468	0
≥ 2 unique peptides	rrnAC2780	Q5UYW5_HALMA	*glnA*	Glutamine synthetase (EC 6.3.1.2)	5	4	94	23	13	7	70	21	99	83	182	1.2	**No dramatic change**	18	164	9.9	Soluble predominant	480	0
≥ 2 unique peptides	rrnAC2939	Q5UYH9_HALMA	*cctB*	Thermosome beta subunit	4	2	93	23	7	5	77	21	97	84	181	1.2	**No dramatic change**	11	170	6.1	Soluble predominant	559	0
≥ 2 unique peptides	pNG4049	Q5V7X3_HALMA	*cas3*	CRISPR-associated protein	10	6	90	23	4	1	73	23	100	77	177	1.3	**No dramatic change**	14	163	7.9	Soluble predominant	357	0
≥ 2 unique peptides	rrnAC0345	Q5V510_HALMA	*fba*	Fructose-bisphosphate aldolase (EC 4.1.2.13)	38	13	50	16	33	12	56	12	88	89	177	1.0	**No dramatic change**	71	106	40.1	Memb + Sol	260	0
≥ 2 unique peptides	rrnAC1787	Q5V1C3_HALMA	*hutU*	Urocanate hydratase (EC 4.2.1.49)	3	3	54	16	10	8	105	28	57	115	172	0.5	1.2 (2~3X)	13	159	7.6	Soluble predominant	582	0
≥ 2 unique peptides	rrnAC2115	Q5V0I7_HALMA	*rrnAC2115*	Hypothetical protein	64	10	0	0	96	13	0	0	64	96	160	0.7	**No dramatic change**	160	0	100.0	Memb only	197	0
≥ 2 unique peptides	rrnAC1093	Q5V347_HALMA	*sdhB*	Succinate dehydrogenase iron-sulfur protein subunit(EC 1.3.99.1)	71	17	1	1	82	16	1	1	72	83	155	0.9	**No dramatic change**	153	2	98.7	Memb predominant	295	0
≥ 2 unique peptides	rrnAC0718	Q5V441_HALMA	*porA*	Pyruvate ferredoxin oxidoreductase subunit alpha (EC 1.2.7.3)(EC 1.2.7.1)	1	1	82	24	0	0	69	23	83	69	152	1.2	**No dramatic change**	1	151	0.7	Soluble predominant	586	0

≥ 2 unique peptides	rrnAC3019	Q5UYA9_HALMA	*cobN*	Cobalamin biosynthesis protein	0	0	111	39	0	0	40	21	111	40	151	2.8	0.7 (2>3X)	0	151	0.0	Soluble only	1312	0
≥ 2 unique peptides	pNG7157	Q5V6I7_HALMA	*gudB*	NAD(P)-specific glutamate dehydrogenase (EC 1.4.1.3)	11	4	65	18	8	3	67	16	76	75	151	1.0	**No dramatic change**	19	132	12.6	Soluble predominant	431	0
≥ 2 unique peptides	rrnAC1154	Q5V2Z7_HALMA	*coxA3*	Cytochrome c oxidase polypeptide I (EC 1.9.3.1)	74	8	0	0	76	10	0	0	74	76	150	1.0	**No dramatic change**	150	0	100.0	Memb only	562	13
≥ 2 unique peptides	rrnAC0770	Q5V3Z3_HALMA	*acdB*	Acyl-coA dehydrogenase (EC 1.3.99.-)	2	2	72	19	6	3	70	17	74	76	150	1.0	**No dramatic change**	8	142	5.3	Soluble predominant	382	0
≥ 2 unique peptides	rrnAC1611	RL3_HALMAReview	*rpl3p*	50S ribosomal protein L3P (Hmal3) (Hl1)	91	19	0	0	57	14	0	0	91	57	148	1.6	**No dramatic change**	148	0	100.0	Memb only	338	0
≥ 2 unique peptides	rrnAC3147	Q5UXZ9_HALMA	*etfA2*	Electron transfer flavoprotein alpha-subunit	4	2	56	10	3	2	83	11	60	86	146	0.7	**No dramatic change**	7	139	4.8	Soluble predominant	316	0
≥ 2 unique peptides	rrnAC0382	Q5V4X8_HALMA	*gabT*	4-aminobutyrate aminotransferase	3	2	63	19	5	4	74	20	66	79	145	0.8	**No dramatic change**	8	137	5.5	Soluble predominant	440	0
≥ 2 unique peptides	pNG7145	Q5V6J8_HALMA	*nosL*	NosL protein	55	7	0	0	86	8	0	0	55	86	141	0.6	**No dramatic change**	141	0	100.0	Memb only	200	0
≥ 2 unique peptides	rrnAC3159	Q5UXY8_HALMA	*ntpA*	V-type sodium ATP synthase subunit A (EC 3.6.3.14)	9	6	56	16	17	9	56	19	65	73	138	0.9	**No dramatic change**	26	112	18.8	Soluble predominant	586	0
≥ 2 unique peptides	rrnAC1268	Q5V2P3_HALMA	*korB*	Putative 2-ketoglutarate ferredoxin oxidoreductase (Beta) (EC 1.2.7.3)(EC 1.2.7.1)	2	1	61	15	5	2	70	17	63	75	138	0.8	**No dramatic change**	7	131	5.1	Soluble predominant	312	0
≥ 2 unique peptides	pNG7361	Q5V5Z8_HALMA	*gcvT5*	Probable aminomethyltransferase (EC 2.1.2.10)	0	0	32	13	5	3	99	24	32	104	136	0.3	1.2 (>3X)	5	131	3.7	Soluble predominant	458	0
≥ 2 unique peptides	rrnAC0923	Q5V3K5_HALMA	*rbsB-2*	Sugar ABC transporter substrate binding protein	76	14	0	0	60	14	0	0	76	60	136	1.3	**No dramatic change**	136	0	100.0	Memb only	509	1
≥ 2 unique peptides	rrnAC3012	Q5UYB5_HALMA	*rrnAC3012*	Hypothetical protein	2	2	67	6	6	3	58	6	69	64	133	1.1	**No dramatic change**	8	125	6.0	Soluble predominant	123	0
≥ 2 unique peptides	rrnAC1443	Q5V283_HALMA	*rrnAC1443*	Hypothetical protein	61	16	5	2	66	19	1	1	66	67	133	1.0	**No dramatic change**	127	6	95.5	Memb predominant	465	0
≥ 2 unique peptides	rrnAC2227	Q5V093_HALMA	*dppF*	Dipeptide ABC transporter ATP-binding	64	28	4	3	65	26	0	0	68	65	133	1.0	**No dramatic change**	129	4	97.0	Memb predominant	890	0
≥ 2 unique peptides	rrnAC0201	Q5V5E0_HALMA	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	4	1	35	11	8	4	86	20	39	94	133	0.4	1.2 (2~3X)	12	121	9.0	Soluble predominant	508	0
≥ 2 unique peptides	rrnAC0732	Q5V427_HALMA	*petB1*	Cytochrome b6	58	5	0	0	74	5	0	0	58	74	132	0.8	**No dramatic change**	132	0	100.0	Memb only	267	5
≥ 2 unique peptides	rrnAC0474	Q5V4Q3_HALMA	*sucD*	Succinyl-CoA synthetase alpha chain (EC 6.2.1.5)	3	1	59	12	10	4	59	12	62	69	131	0.9	**No dramatic change**	13	118	9.9	Soluble predominant	290	0
≥ 2 unique peptides	rrnAC0979	Q5V3F5_HALMA	*rrnAC0979*	Putative nuclease	0	0	63	22	1	1	65	25	63	66	129	1.0	**No dramatic change**	1	128	0.8	Soluble predominant	726	0
≥ 2 unique peptides	rrnAC0158	Q5V5H6_HALMA	*rrnAC0158*	Hypothetical protein	75	9	0	0	54	10	0	0	75	54	129	1.4	**No dramatic change**	129	0	100.0	Memb only	359	1
≥ 2 unique peptides	rrnAC3339	DNAK_HALMAReview	*dnaK*	Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDaprotein) (HSP70)	8	4	49	16	21	10	50	18	57	71	128	0.8	**No dramatic change**	29	99	22.7	Soluble predominant	635	0
≥ 2 unique peptides	rrnAC2956	Q5UYG3_HALMA	*pdhB1*	Pyruvate dehydrogenase (EC 1.2.4.1)	8	4	51	13	12	5	57	15	59	69	128	0.9	**No dramatic change**	20	108	15.6	Soluble predominant	332	0
≥ 2 unique peptides	rrnAC0384	Q5V4X6_HALMA	*gdhA1*	NADP-specific glutamate dehydrogenase (EC 1.4.1.3)	18	8	58	22	7	6	44	15	76	51	127	1.5	**No dramatic change**	25	102	19.7	Soluble predominant	427	0
≥ 2 unique peptides	rrnAC0759	Q5V402_HALMA	*cat*	Cationic amino acid transporter	68	22	0	0	59	20	0	0	68	59	127	1.2	**No dramatic change**	127	0	100.0	Memb only	754	12
≥ 2 unique peptides	rrnAC0852	Q5V3R9_HALMA	*rrnAC0852*	Hypothetical protein	63	18	0	0	63	15	0	0	63	63	126	1.0	**No dramatic change**	126	0	100.0	Memb only	321	1
≥ 2 unique peptides	rrnAC1570	Q5V1W4_HALMA	*trp-7*	ABC transporter ATP-binding protein	77	15	0	0	46	13	0	0	77	46	123	1.7	**No dramatic change**	123	0	100.0	Memb only	601	4
≥ 2 unique peptides	rrnAC0734	Q5V425_HALMA	*rrnAC0734*	Hypothetical protein	58	14	0	0	64	16	0	0	58	64	122	0.9	**No dramatic change**	122	0	100.0	Memb only	139	2
≥ 2 unique peptides	rrnAC0653	Q5V495_HALMA	*cysH*	Phospho-adenylyl-sulfate Reductase (EC 1.8.4.8)	7	2	56	14	10	6	49	13	63	59	122	1.1	**No dramatic change**	17	105	13.9	Soluble predominant	325	0
≥ 2 unique peptides	rrnAC0451	Q5V4S0_HALMA	*rrnAC0451*	Hypothetical protein	1	1	62	16	6	2	52	13	63	58	121	1.1	**No dramatic change**	7	114	5.8	Soluble predominant	177	0
≥ 2 unique peptides	rrnAC1464	Q5V263_HALMA	*rrnAC1464*	Hypothetical protein	1	1	60	16	0	0	59	16	61	59	120	1.0	**No dramatic change**	1	119	0.8	Soluble predominant	278	0
≥ 2 unique peptides	rrnAC1429	RS3A_HALMAReview	*rps3Ae*	30S ribosomal protein S3Ae	33	16	47	14	19	9	20	8	80	39	119	2.1	0.7 (2>3X)	52	67	43.7	Memb + Sol	213	0
≥ 2 unique peptides	pNG5070	Q5V7M2_HALMA	*pNG5070*	Hypothetical protein	59	17	0	0	57	17	0	0	59	57	116	1.0	**No dramatic change**	116	0	100.0	Memb only	549	1
≥ 2 unique peptides	rrnAC0775	Q5V3Y8_HALMA	*gdhA2*	NAD(P)-specific glutamate dehydrogenase (EC 1.4.1.3)	0	0	52	17	1	1	63	22	52	64	116	0.8	**No dramatic change**	1	115	0.9	Soluble predominant	418	0
≥ 2 unique peptides	rrnAC1153	Q5V2Z8_HALMA	*coxB2*	Cytochrome c oxidase subunit II (EC 1.9.3.1)	35	3	0	0	79	5	0	0	35	79	114	0.4	1.2 (2~3X)	114	0	100.0	Memb only	190	1
≥ 2 unique peptides	rrnAC2667	Q5UZ58_HALMA	*thrC3*	Threonine synthase	74	19	1	1	32	10	6	4	75	38	113	2.0	**No dramatic change**	106	7	93.8	Memb predominant	463	0
≥ 2 unique peptides	rrnAC1965	Q5V0X0_HALMA	*aceB*	Malate synthase	0	0	50	14	0	0	63	15	50	63	113	0.8	**No dramatic change**	0	113	0.0	Soluble only	435	0
≥ 2 unique peptides	rrnAC1589	SECY_HALMAReview	*secY*	Preprotein translocase subunit secY (Protein transport protein SEC61subunit alpha homolog)	62	11	0	0	51	8	0	0	62	51	113	1.2	**No dramatic change**	113	0	100.0	Memb only	487	9
≥ 2 unique peptides	rrnAC2428	Q5UZR4_HALMA	*rpoA*	DNA-directed RNA polymerase (EC 2.7.7.6)	28	12	42	19	7	4	34	18	70	41	111	1.7	**No dramatic change**	35	76	31.5	Memb + Sol	969	0
≥ 2 unique peptides	rrnAC3156	Q5UXZ1_HALMA	*atpE*	V-type ATP synthase subunit E (EC 3.6.3.14)	18	6	47	12	21	5	25	9	65	46	111	1.4	**No dramatic change**	39	72	35.1	Memb + Sol	194	0
≥ 2 unique peptides	rrnAC3325	Q5UXI8_HALMA	*rrnAC3325*	Sulfatase arylsulfatase A-like (EC 3.1.6.-)	6	3	44	15	14	8	47	18	50	61	111	0.8	**No dramatic change**	20	91	18.0	Soluble predominant	447	0
≥ 2 unique peptides	rrnAC1815	Q5V199_HALMA	*cctA3*	Thermosome alpha subunit	5	4	38	14	8	5	59	17	43	67	110	0.6	**No dramatic change**	13	97	11.8	Soluble predominant	526	0
≥ 2 unique peptides	rrnAC1754	Q5V1F0_HALMA	*maeB*	NAD-dependent malate dehydrogenase (EC 1.1.1.40)	0	0	53	20	3	2	53	22	53	56	109	0.9	**No dramatic change**	3	106	2.8	Soluble predominant	750	0
≥ 2 unique peptides	rrnB0246	Q5UWD2_HALMA	*aldY5*	Aldehyde dehydrogenase (EC 1.2.1.3)	0	0	47	15	1	1	61	17	47	62	109	0.8	**No dramatic change**	1	108	0.9	Soluble predominant	483	0
≥ 2 unique peptides	rrnAC1972	Q5V0W4_HALMA	*gcdH*	Glutaryl-CoA dehydrogenase (EC 1.3.99.7)	0	0	46	12	3	3	60	15	46	63	109	0.7	**No dramatic change**	3	106	2.8	Soluble predominant	387	0
≥ 2 unique peptides	rrnAC2815	Q5UYT2_HALMA	*aca2*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	0	0	57	17	2	2	49	14	57	51	108	1.1	**No dramatic change**	2	106	1.9	Soluble predominant	377	0
≥ 2 unique peptides	rrnAC0232	Q5V5B1_HALMA	*rrnAC0232*	Hypothetical protein	5	4	28	7	17	7	57	15	33	74	107	0.4	1.2 (2~3X)	22	85	20.6	Soluble predominant	347	0
≥ 2 unique peptides	rrnAC3157	Q5UXZ0_HALMA	*ntpC*	V-type ATP synthase subunit C (EC 3.6.3.14)	34	14	16	8	44	15	13	7	50	57	107	0.9	**No dramatic change**	78	29	72.9	Memb + Sol	357	0
≥ 2 unique peptides	rrnAC1455	Q5V271_HALMA	*nuoL2*	NADH dehydrogenase I L subunit	44	6	0	0	63	6	0	0	44	63	107	0.7	**No dramatic change**	107	0	100.0	Memb only	697	16
≥ 2 unique peptides	rrnAC3215	Q5UXT5_HALMA	*secD*	Protein-export membrane protein SecD	59	15	0	0	47	13	0	0	59	47	106	1.3	**No dramatic change**	106	0	100.0	Memb only	518	6
≥ 2 unique peptides	rrnAC2457	Q5UZN9_HALMA	*rrnAC2457*	Hypothetical protein	52	7	0	0	52	8	0	0	52	52	104	1.0	**No dramatic change**	104	0	100.0	Memb only	255	6
≥ 2 unique peptides	rrnAC1795	Q5V1B6_HALMA	*ppsA*	Phosphoenolpyruvate synthase (EC 2.7.9.2)	6	3	48	16	8	3	42	20	54	50	104	1.1	**No dramatic change**	14	90	13.5	Soluble predominant	786	0
≥ 2 unique peptides	rrnAC3306	Q5UXK6_HALMA	*trpD1*	Anthranilate phosphoribosyltransferase (EC 2.4.2.18)	0	0	51	14	1	1	52	14	51	53	104	1.0	**No dramatic change**	1	103	1.0	Soluble predominant	361	0
≥ 2 unique peptides	rrnAC3297	Q5UXL3_HALMA	*oppC*	Oligopeptide ABC transporter permease protein	65	11	0	0	39	8	0	0	65	39	104	1.7	**No dramatic change**	104	0	100.0	Memb only	486	8
≥ 2 unique peptides	rrnAC0002	Q5V5W4_HALMA	*accC2*	Carbamoyl phosphate synthase L chain (EC 6.3.4.16)	2	2	45	17	4	3	52	22	47	56	103	0.8	**No dramatic change**	6	97	5.8	Soluble predominant	616	0
≥ 2 unique peptides	rrnAC1527	Q5V205_HALMA	*cdc48d*	Cell division control protein 48	46	22	5	4	49	23	2	1	51	51	102	1.0	**No dramatic change**	95	7	93.1	Memb predominant	741	0
≥ 2 unique peptides	rrnAC0731	Q5V428_HALMA	*rrnAC0731*	Cytochrome b(C-terminal)/b6	55	15	0	0	46	12	0	0	55	46	101	1.2	**No dramatic change**	101	0	100.0	Memb only	254	4

≥ 2 unique peptides	rrnAC1830	Q5V185_HALMA	*yurF*	ABC transporter ATP-binding protein	0	0	50	18	2	1	49	18	50	51	101	1.0	**No dramatic change**	2	99	2.0	Soluble predominant	309	0
≥ 2 unique peptides	rrnAC1230	Q5V2S8_HALMA	*slyD*	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	1	1	42	12	1	1	56	13	43	57	100	0.8	**No dramatic change**	2	98	2.0	Soluble predominant	314	0
≥ 2 unique peptides	rrnAC0371	Q5V4Y8_HALMA	*htr*	MCP domain signal transducer	49	19	0	0	51	20	0	0	49	51	100	1.0	**No dramatic change**	100	0	100.0	Memb only	640	2
≥ 2 unique peptides	rrnAC2511	Q5UZI9_HALMA	*citZ*	Citrate synthase II (EC 2.3.3.1)	2	2	49	13	2	1	45	13	51	47	98	1.1	**No dramatic change**	4	94	4.1	Soluble predominant	381	0
≥ 2 unique peptides	rrnAC3154	Q5UXZ3_HALMA	*atpI*	V-type ATP synthase subunit I (EC 3.6.3.14)	48	14	0	0	50	14	0	0	48	50	98	1.0	**No dramatic change**	98	0	100.0	Memb only	623	7
≥ 2 unique peptides	rrnAC1283	PURA_HALMAReview	*purA*	Adenylosuccinate synthetase (EC 6.3.4.4) (IMP--aspartate ligase)(AdSS) (AMPSase)	1	1	47	18	0	0	50	14	48	50	98	1.0	**No dramatic change**	1	97	1.0	Soluble predominant	458	0
≥ 2 unique peptides	rrnAC1592	RS5_HALMAReview	*rps5p*	30S ribosomal protein S5P (HmaS5)	11	6	52	15	5	4	30	11	63	35	98	1.8	**No dramatic change**	16	82	16.3	Soluble predominant	212	0
≥ 2 unique peptides	rrnAC2429	Q5UZR3_HALMA	*rpoB*	DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)	2	2	54	26	1	1	39	22	56	40	96	1.4	**No dramatic change**	3	93	3.1	Soluble predominant	608	0
≥ 2 unique peptides	rrnAC0562	Q5V4H5_HALMA	*pepC*	Phosphoenolpyruvate carboxylase (EC 4.1.1.31)	2	2	50	17	1	1	43	24	52	44	96	1.2	**No dramatic change**	3	93	3.1	Soluble predominant	898	0
≥ 2 unique peptides	rrnAC1507	Q5V224_HALMA	*pstA2*	Phosphate ABC transporter permease protein	59	5	0	0	37	6	0	0	59	37	96	1.6	**No dramatic change**	96	0	100.0	Memb only	566	14
≥ 2 unique peptides	rrnAC1259	Q5V2Q1_HALMA	*alkK2*	Medium-chain-fatty-acid-CoA ligase	0	0	45	16	1	1	49	20	45	50	95	0.9	**No dramatic change**	1	94	1.1	Soluble predominant	550	0
≥ 2 unique peptides	rrnAC1657	SYD_HALMAReview	*aspS*	Aspartyl-tRNA synthetase (EC 6.1.1.12) (Aspartate--tRNA ligase)(AspRS)	1	1	39	14	1	1	51	21	40	52	92	0.8	**No dramatic change**	2	90	2.2	Soluble predominant	434	0
≥ 2 unique peptides	rrnAC2726	Q5UZ11_HALMA	*pepB3*	Aminopeptidase	0	0	31	12	1	1	60	13	31	61	92	0.5	**No dramatic change**	1	91	1.1	Soluble predominant	363	0
≥ 2 unique peptides	rrnAC0266	Q5V579_HALMA	*rrnAC0266*	Hypothetical protein	16	5	21	5	27	7	26	6	37	53	90	0.7	**No dramatic change**	43	47	47.8	Memb + Sol	237	0
≥ 2 unique peptides	rrnAC1732	PDXS_HALMAReview	*pdxS*	Pyridoxal biosynthesis lyase pdxS (EC 4.-.-.-)	2	2	44	14	2	2	42	15	46	44	90	1.0	**No dramatic change**	4	86	4.4	Soluble predominant	302	0
≥ 2 unique peptides	rrnAC0431	Q5V4T7_HALMA	*tot*	Transmembrane oligosaccharyl transferase	55	15	0	0	35	10	0	0	55	35	90	1.6	**No dramatic change**	90	0	100.0	Memb only	937	13
≥ 2 unique peptides	rrnAC0250	Q5V595_HALMA	*rrnAC0250*	Hypothetical protein	47	14	0	0	42	13	0	0	47	42	89	1.1	**No dramatic change**	89	0	100.0	Memb only	497	2
≥ 2 unique peptides	rrnAC0771	Q5V3Z2_HALMA	*paaH*	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.35)	0	0	31	9	0	0	58	9	31	58	89	0.5	**No dramatic change**	0	89	0.0	Soluble only	285	0
≥ 2 unique peptides	rrnAC2430	Q5UZR2_HALMA	*rpoB*	DNA-directed RNA polymerase subunit B	21	12	33	12	7	5	27	16	54	34	88	1.6	**No dramatic change**	28	60	31.8	Memb + Sol	521	0
≥ 2 unique peptides	rrnAC1812	Q5V1A2_HALMA	*pnm*	N-methyltransferase-like	52	13	0	0	36	9	0	0	52	36	88	1.4	**No dramatic change**	88	0	100.0	Memb only	174	0
≥ 2 unique peptides	rrnAC1174	PSMA1_HALMAReview	*psmA1*	Proteasome alpha subunit (EC 3.4.25.1) (Multicatalytic endopeptidasecomplex alpha subunit)	0	0	50	10	1	1	37	12	50	38	88	1.3	**No dramatic change**	1	87	1.1	Soluble predominant	260	0
≥ 2 unique peptides	rrnAC2600	Q5UZB4_HALMA	*rrnAC2600*	Hypothetical protein	49	13	0	0	38	12	0	0	49	38	87	1.3	**No dramatic change**	87	0	100.0	Memb only	475	2
≥ 2 unique peptides	rrnAC3161	Q5UXY6_HALMA	*bop*	Bacteriorhodopsin	32	5	0	0	55	5	0	0	32	55	87	0.6	**No dramatic change**	87	0	100.0	Memb only	250	7
≥ 2 unique peptides	rrnAC1698	Q5V1J8_HALMA	*moxR2*	Methanol dehydrogenase regulatory protein	11	5	40	13	12	6	23	11	51	35	86	1.5	**No dramatic change**	23	63	26.7	Memb + Sol	315	0
≥ 2 unique peptides	rrnAC3467	Q5UX61_HALMA	*pspA1*	Transcription regulator	45	13	0	0	40	11	0	0	45	40	85	1.1	**No dramatic change**	85	0	100.0	Memb only	280	0
≥ 2 unique peptides	rrnAC1067	Q5V373_HALMA	*prk1*	Protein kinase	1	1	44	20	2	2	38	20	45	40	85	1.1	**No dramatic change**	3	82	3.5	Soluble predominant	690	0
≥ 2 unique peptides	rrnAC2229	Q5V091_HALMA	*dppB1*	Dipeptide ABC transporter permease	47	10	0	0	38	7	0	0	47	38	85	1.2	**No dramatic change**	85	0	100.0	Memb only	360	6
≥ 2 unique peptides	rrnAC3295	Q5UXL5_HALMA	*ykfD*	Oligopeptide ABC transporter ATP-binding	43	13	0	0	42	15	0	0	43	42	85	1.0	**No dramatic change**	85	0	100.0	Memb only	469	0
≥ 2 unique peptides	rrnAC0847	Q5V3S4_HALMA	*alkK3*	Medium-chain acyl-CoA ligase	0	0	35	12	2	2	47	16	35	49	84	0.7	**No dramatic change**	2	82	2.4	Soluble predominant	539	0
≥ 2 unique peptides	rrnAC3148	Q5UXZ8_HALMA	*etfB1*	Electron transfer flavoprotein beta subunit	1	1	40	3	2	1	41	6	41	43	84	1.0	**No dramatic change**	3	81	3.6	Soluble predominant	263	0
≥ 2 unique peptides	rrnAC1001	Q5V3D5_HALMA	*rrnAC1001*	Hypothetical protein	0	0	47	11	2	1	35	10	47	37	84	1.3	**No dramatic change**	2	82	2.4	Soluble predominant	272	0
≥ 2 unique peptides	pNG5004	Q5V7G7_HALMA	*pNG5004*	Hypothetical protein	38	9	0	0	44	9	0	0	38	44	82	0.9	**No dramatic change**	82	0	100.0	Memb only	355	1
≥ 2 unique peptides	rrnAC2955	Q5UYG4_HALMA	*pdhC2*	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenasecomplex (EC 2.3.1.12)	4	4	32	15	8	5	38	19	36	46	82	0.8	**No dramatic change**	12	70	14.6	Soluble predominant	545	0
≥ 2 unique peptides	rrnAC2947	Q5UYH2_HALMA	*leuS2*	Leucyl-tRNA synthetase (EC 6.1.1.4)	0	0	35	13	0	0	46	19	35	46	81	0.8	**No dramatic change**	0	81	0.0	Soluble only	895	0
≥ 2 unique peptides	rrnAC2439	Q5UZQ5_HALMA	*tnaA*	Tryptophanase (EC 4.1.99.1)	3	2	9	4	11	4	57	21	12	68	80	0.2	1.2 (>3X)	14	66	17.5	Soluble predominant	447	0
≥ 2 unique peptides	rrnAC3346	KAD_HALMAReview	*adk*	Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase)	0	0	39	14	0	0	40	13	39	40	79	1.0	**No dramatic change**	0	79	0.0	Soluble only	216	0
≥ 2 unique peptides	rrnAC0358	Q5V4Z8_HALMA	*imp-1*	Immunogenic protein	35	13	0	0	44	15	0	0	35	44	79	0.8	**No dramatic change**	79	0	100.0	Memb only	382	0
≥ 2 unique peptides	rrnAC0890	Q5V3N4_HALMA	*frt*	Ferritin	0	0	34	11	2	2	42	15	34	44	78	0.8	**No dramatic change**	2	76	2.6	Soluble predominant	179	0
≥ 2 unique peptides	rrnB0207	Q5UWG3_HALMA	*rrnB0207*	Putative extracellular ligand binding protein	59	16	0	0	19	8	0	0	59	19	78	3.1	0.7 (>3X)	78	0	100.0	Memb only	414	0
≥ 2 unique peptides	rrnAC2129	Q5V0H6_HALMA	*sseA2*	Thiosulfate sulfurtransferase	0	0	45	9	4	2	29	8	45	33	78	1.4	**No dramatic change**	4	74	5.1	Soluble predominant	297	0
≥ 2 unique peptides	rrnAC1791	Q5V1C0_HALMA	*hutH*	Histidine ammonia-lyase (EC 4.3.1.3)	3	2	20	8	5	2	50	15	23	55	78	0.4	1.2 (2~3X)	8	70	10.3	Soluble predominant	549	0
≥ 2 unique peptides	rrnAC1820	Q5V195_HALMA	*rrnAC1820*	Hypothetical protein	0	0	44	17	0	0	33	12	44	33	77	1.3	**No dramatic change**	0	77	0.0	Soluble only	296	0
≥ 2 unique peptides	rrnAC1828	Q5V187_HALMA	*rrnAC1828*	Hypothetical protein	0	0	37	12	0	0	39	11	37	39	76	0.9	**No dramatic change**	0	76	0.0	Soluble only	403	0
≥ 2 unique peptides	rrnAC2414	Q5UZS6_HALMA	*metB*	Cystathionine gamma-synthase (EC 2.5.1.48)	0	0	30	5	1	1	45	10	30	46	76	0.7	**No dramatic change**	1	75	1.3	Soluble predominant	411	0
≥ 2 unique peptides	rrnAC3125	Q5UY19_HALMA	*usp33*	Universal stress protein	4	3	27	6	13	7	32	8	31	45	76	0.7	**No dramatic change**	17	59	22.4	Soluble predominant	132	0
≥ 2 unique peptides	rrnAC2423	RS7_HALMAReview	*rps7p*	30S ribosomal protein S7P (HmaS7)	13	7	22	12	22	10	18	8	35	40	75	0.9	**No dramatic change**	35	40	46.7	Memb + Sol	206	0
≥ 2 unique peptides	rrnAC0233	Q5V5B0_HALMA	*ykfB2*	Chloromuconate cycloisomerase	0	0	11	5	7	3	56	11	11	63	74	0.2	1.2 (>3X)	7	67	9.5	Soluble predominant	359	0
≥ 2 unique peptides	rrnAC1605	RS3_HALMAReview	*rps3p*	30S ribosomal protein S3P (HmaS3) (HS1)	1	1	52	14	0	0	21	9	53	21	74	2.5	0.7 (2>3X)	1	73	1.4	Soluble predominant	304	0
≥ 2 unique peptides	rrnAC0906	Q5V3M0_HALMA	*ibp*	Iron-binding protein	52	5	0	0	22	4	0	0	52	22	74	2.4	0.7 (2>3X)	74	0	100.0	Memb only	401	0
≥ 2 unique peptides	rrnAC3053	Q5UY81_HALMA	*rrnAC3053*	ABC transporter ATP-binding protein	43	11	0	0	31	9	0	0	43	31	74	1.4	**No dramatic change**	74	0	100.0	Memb only	312	0
≥ 2 unique peptides	rrnAC0381	Q5V4X9_HALMA	*glnH1*	Glutamine ABC transporter permease protein	43	6	0	0	31	7	0	0	43	31	74	1.4	**No dramatic change**	74	0	100.0	Memb only	262	0
≥ 2 unique peptides	rrnAC0159	Q5V5H5_HALMA	*rrnAC0159*	Hypothetical protein	32	11	8	4	30	10	3	3	40	33	73	1.2	**No dramatic change**	62	11	84.9	Memb predominant	195	0
≥ 2 unique peptides	rrnAC2716	Q5UZ20_HALMA	*cysD*	O-acetylhomoserine (Thiol)-lyase (EC 2.5.1.49)	2	1	29	9	3	2	39	12	31	42	73	0.7	**No dramatic change**	5	68	6.8	Soluble predominant	432	0
≥ 2 unique peptides	rrnAC0748	Q5V413_HALMA	*guaB3*	Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	0	0	35	9	1	1	35	13	35	36	71	1.0	**No dramatic change**	1	70	1.4	Soluble predominant	494	0
≥ 2 unique peptides	rrnAC3296	Q5UXL4_HALMA	*oppD2*	Oligopeptide ABC transporter ATPase component	31	10	0	0	40	12	0	0	31	40	71	0.8	**No dramatic change**	71	0	100.0	Memb only	406	0

≥ 2 unique peptides	rrnAC1252	Q5V2Q8_HALMA	*lrp*	Leucine responsive regulatory protein	0	0	41	13	1	1	28	11	41	29	70	1.4	**No dramatic change**	1	69	1.4	Soluble predominant	164	0
≥ 2 unique peptides	rrnAC2108	Q5V0J4_HALMA	*npdG-1*	F420-dependent NADP reductase (EC 1.6.8.-)	1	1	36	9	3	2	30	8	37	33	70	1.1	**No dramatic change**	4	66	5.7	Soluble predominant	222	0
≥ 2 unique peptides	pNG7110	Q5V6N0_HALMA	*pNG7110*	Putative permease	35	13	0	0	35	12	0	0	35	35	70	1.0	**No dramatic change**	70	0	100.0	Memb only	318	4
≥ 2 unique peptides	rrnAC2634	SYI_HALMAReview	*ileS*	Isoleucyl-tRNA synthetase (EC 6.1.1.5) (Isoleucine--tRNA ligase)(IleRS)	0	0	25	13	0	0	45	21	25	45	70	0.6	**No dramatic change**	0	70	0.0	Soluble only	1074	0
≥ 2 unique peptides	rrnAC3189	Q5UXV9_HALMA	*pepF*	Oligoendopeptidase F (EC 3.4.24.-)	1	1	37	9	1	1	30	10	38	31	69	1.2	**No dramatic change**	2	67	2.9	Soluble predominant	596	0
≥ 2 unique peptides	pNG7059	Q5V6S5_HALMA	*prrC*	Regulatory protein PrrC	38	9	1	1	29	8	0	0	39	29	68	1.3	**No dramatic change**	67	1	98.5	Memb predominant	225	0
≥ 2 unique peptides	rrnAC1542	Q5V1Z1_HALMA	*rrnAC1542*	Hypothetical protein	37	14	0	0	31	14	0	0	37	31	68	1.2	**No dramatic change**	68	0	100.0	Memb only	547	1
≥ 2 unique peptides	rrnB0264	Q5UWB8_HALMA	*acdH*	Acyl-CoA dehydrogenase (EC 1.3.99.3)	0	0	37	11	0	0	31	13	37	31	68	1.2	**No dramatic change**	0	68	0.0	Soluble only	388	0
≥ 2 unique peptides	rrnAC1010	Q5V3C7_HALMA	*rfbB1*	DTDP-glucose 4-6-dehydratase (EC 4.2.1.46)	7	6	22	6	6	5	33	11	29	39	68	0.7	**No dramatic change**	13	55	19.1	Soluble predominant	353	0
≥ 2 unique peptides	rrnAC1404	Q5V2B9_HALMA	*usp28*	Universal stress protein	2	1	35	12	4	2	27	10	37	31	68	1.2	**No dramatic change**	6	62	8.8	Soluble predominant	137	0
≥ 2 unique peptides	rrnAC2160	Q5V0E9_HALMA	*rrnAC2160*	Putative DNA binding protein	3	2	37	6	4	2	23	7	40	27	67	1.5	**No dramatic change**	7	60	10.4	Soluble predominant	219	0
≥ 2 unique peptides	rrnAC1829	Q5V186_HALMA	*rrnAC1829*	Hypothetical protein	0	0	31	14	0	0	36	11	31	36	67	0.9	**No dramatic change**	0	67	0.0	Soluble only	476	0
≥ 2 unique peptides	rrnAC1225	PYRB_HALMAReview	*pyrB*	Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartatetranscarbamylase) (ATCase)	4	4	29	15	2	2	32	11	33	34	67	1.0	**No dramatic change**	6	61	9.0	Soluble predominant	304	0
≥ 2 unique peptides	rrnAC2953	DLDH2_HALMAReview	*lpdA2*	Dihydrolipoyl dehydrogenase 2 (EC 1.8.1.4) (Dihydrolipoamidedehydrogenase 2)	0	0	30	11	0	0	37	13	30	37	67	0.8	**No dramatic change**	0	67	0.0	Soluble only	472	0
≥ 2 unique peptides	rrnAC1773	PSMA2_HALMAReview	*psmA2*	Proteasome alpha subunit (EC 3.4.25.1) (Multicatalytic endopeptidasecomplex alpha subunit)	0	0	47	13	0	0	20	8	47	20	67	2.4	0.7 (2>3X)	0	67	0.0	Soluble only	244	0
≥ 2 unique peptides	rrnAC0064	RL18E_HALMAReview	*rpl18e*	50S ribosomal protein L18e (Hl29) (L19)	37	10	4	3	26	10	0	0	41	26	67	1.6	**No dramatic change**	63	4	94.0	Memb predominant	116	0
≥ 2 unique peptides	rrnAC3116	PFDA_HALMAReview	*pfdA*	Prefoldin alpha subunit (GimC alpha subunit)	0	0	33	10	0	0	33	9	33	33	66	1.0	**No dramatic change**	0	66	0.0	Soluble only	154	0
≥ 2 unique peptides	rrnAC2590	Q5UZC2_HALMA	*cstA*	Carbon starvation protein CstA	26	5	0	0	40	6	0	0	26	40	66	0.7	**No dramatic change**	66	0	100.0	Memb only	631	13
≥ 2 unique peptides	pNG6189	Q5V7C3_HALMA	*pNG6189*	Hypothetical protein	0	0	28	13	0	0	37	19	28	37	65	0.8	**No dramatic change**	0	65	0.0	Soluble only	1097	0
≥ 2 unique peptides	rrnAC1152	Q5V2Z9_HALMA	*hcp5*	Halocyanin-like	38	5	0	0	27	5	0	0	38	27	65	1.4	**No dramatic change**	65	0	100.0	Memb only	409	2
≥ 2 unique peptides	rrnAC1109	Q5V336_HALMA	*purD2*	Phosphoribosylamine-glycine ligase (EC 6.3.4.13)	0	0	33	12	2	1	30	10	33	32	65	1.0	**No dramatic change**	2	63	3.1	Soluble predominant	450	0
≥ 2 unique peptides	rrnAC3285	Q5UXM4_HALMA	*nolA*	NADH dehydrogenase/oxidoreductase-like protein	9	4	18	8	23	5	15	7	27	38	65	0.7	**No dramatic change**	32	33	49.2	Memb + Sol	299	0
≥ 2 unique peptides	pNG6088	Q5V746_HALMA	*pNG6088*	Hypothetical protein	31	16	0	0	32	15	1	1	31	33	64	0.9	**No dramatic change**	63	1	98.4	Memb predominant	435	0
≥ 2 unique peptides	rrnAC3021	Q5UYA7_HALMA	*cbiJ*	Precorrin-3 methylase	0	0	38	15	1	1	25	11	38	26	64	1.5	**No dramatic change**	1	63	1.6	Soluble predominant	254	0
≥ 2 unique peptides	rrnAC2755	Q5UYY6_HALMA	*rrnAC2755*	Hypothetical protein	31	7	0	0	32	8	0	0	31	32	63	1.0	**No dramatic change**	63	0	100.0	Memb only	418	6
≥ 2 unique peptides	rrnAC0741	Q5V418_HALMA	*hat2*	Probable acetyltransferase	0	0	35	7	0	0	28	6	35	28	63	1.3	**No dramatic change**	0	63	0.0	Soluble only	179	0
≥ 2 unique peptides	rrnAC1973	Q5V0W3_HALMA	*aldY4*	Aldehyde dehydrogenase (EC 1.2.1.3)	0	0	21	5	1	1	41	9	21	42	63	0.5	1.2 (2~3X)	1	62	1.6	Soluble predominant	489	0
≥ 2 unique peptides	rrnAC1347	Q5V2H4_HALMA	*rrnAC1347*	Putative mechanosensitive ion channel	34	7	0	0	28	6	0	0	34	28	62	1.2	**No dramatic change**	62	0	100.0	Memb only	293	3
≥ 2 unique peptides	rrnAC1680	PFDB_HALMAReview	*pfdB*	Prefoldin beta subunit (GimC beta subunit)	0	0	30	12	1	1	30	11	30	31	61	1.0	**No dramatic change**	1	60	1.6	Soluble predominant	129	0
≥ 2 unique peptides	rrnAC0457	Q5V4R5_HALMA	*top6B*	Type II DNA topoisomerase VI subunit B (EC 5.99.1.3)	13	7	24	13	4	2	20	10	37	24	61	1.5	**No dramatic change**	17	44	27.9	Memb + Sol	796	0
≥ 2 unique peptides	rrnAC0220	Q5V5C3_HALMA	*rrnAC0220*	Hypothetical protein	30	6	1	1	29	5	1	1	31	30	61	1.0	**No dramatic change**	59	2	96.7	Memb predominant	95	0
≥ 2 unique peptides	rrnAC0189	Q5V5F0_HALMA	*purH*	Bifunctional purine biosynthesis protein PurH (EC 3.5.4.10)(EC 2.1.2.3) (EC 2.1.2.2)	0	0	28	9	0	0	33	10	28	33	61	0.8	**No dramatic change**	0	61	0.0	Soluble only	526	0
≥ 2 unique peptides	rrnAC2092	Q5V0K8_HALMA	*cxp*	Probable carboxypeptidase	0	0	22	10	5	1	34	13	22	39	61	0.6	**No dramatic change**	5	56	8.2	Soluble predominant	500	0
≥ 2 unique peptides	rrnAC2301	Q5V028_HALMA	*hpyA*	Archaeal histone A1	2	1	21	8	2	1	35	11	23	37	60	0.6	**No dramatic change**	4	56	6.7	Soluble predominant	145	0
≥ 2 unique peptides	rrnB0261	Q5UWC0_HALMA	*pccB*	Propionyl-CoA carboxylase beta subunit	0	0	40	17	0	0	20	13	40	20	60	2.0	0.7 (2>3X)	0	60	0.0	Soluble only	572	0
≥ 2 unique peptides	rrnAC3020	Q5UYA8_HALMA	*cbiC*	Precorrin-8X methylmutase (EC 5.4.1.2)	1	1	35	9	2	1	22	8	36	24	60	1.5	**No dramatic change**	3	57	5.0	Soluble predominant	241	0
≥ 2 unique peptides	rrnAC2568	Q5UZE1_HALMA	*pmm*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	0	0	22	10	3	3	34	14	22	37	59	0.6	**No dramatic change**	3	56	5.1	Soluble predominant	479	0
≥ 2 unique peptides	rrnAC1182	THIC_HALMAReview	*thiC*	Thiamine biosynthesis protein thiC	0	0	0	0	2	1	57	21	0	59	59	0.0	1.2 only	2	57	3.4	Soluble predominant	480	0
≥ 2 unique peptides	rrnAC1251	Q5V2Q9_HALMA	*aspB1*	Aspartate aminotransferase (EC 2.6.1.1)	2	1	34	10	0	0	22	10	36	22	58	1.6	**No dramatic change**	2	56	3.4	Soluble predominant	381	0
≥ 2 unique peptides	rrnAC0633	Q5V4B1_HALMA	*rffH2*	Glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	0	0	35	9	0	0	23	9	35	23	58	1.5	**No dramatic change**	0	58	0.0	Soluble only	335	0
≥ 2 unique peptides	rrnAC2957	Q5UYG2_HALMA	*pdhA3*	Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1)(EC 1.2.4.4)	0	0	31	13	0	0	27	11	31	27	58	1.1	**No dramatic change**	0	58	0.0	Soluble only	368	0
≥ 2 unique peptides	rrnAC0302	ILVD_HALMAReview	*ilvD*	Dihydroxy-acid dehydratase (EC 4.2.1.9) (DAD)	0	0	26	9	0	0	32	12	26	32	58	0.8	**No dramatic change**	0	58	0.0	Soluble only	575	0
≥ 2 unique peptides	rrnAC3267	Q5UXP0_HALMA	*rrnAC3267*	Molybdate transport protein	31	2	0	0	27	2	0	0	31	27	58	1.1	**No dramatic change**	58	0	100.0	Memb only	320	0
≥ 2 unique peptides	rrnAC2851	PCNA_HALMAReview	*pcn*	DNA polymerase sliding clamp (Proliferating cell nuclear antigenhomolog) (PCNA)	2	2	22	9	3	2	30	8	24	33	57	0.7	**No dramatic change**	5	52	8.8	Soluble predominant	247	0
≥ 2 unique peptides	rrnAC2307	Q5V022_HALMA	*rrnAC2307*	Hypothetical protein	34	7	0	0	23	5	0	0	34	23	57	1.5	**No dramatic change**	57	0	100.0	Memb only	368	7
≥ 2 unique peptides	rrnAC1372	Q5V2F1_HALMA	*ccpA*	Cytochrome c551 peroxidase	34	7	0	0	23	6	0	0	34	23	57	1.5	**No dramatic change**	57	0	100.0	Memb only	474	2
≥ 2 unique peptides	rrnAC0065	RL13_HALMAReview	*rpl13p*	50S ribosomal protein L13P (Hmal13)	30	7	0	0	26	8	1	1	30	27	57	1.1	**No dramatic change**	56	1	98.2	Memb predominant	145	0
≥ 2 unique peptides	pNG7149	Q5V6J5_HALMA	*drrA-2*	ABC transporter ATP-binding protein	29	8	0	0	28	6	0	0	29	28	57	1.0	**No dramatic change**	57	0	100.0	Memb only	241	0
≥ 2 unique peptides	rrnAC0502	Q5V4M8_HALMA	*ycdH*	Adhesion protein	26	11	0	0	31	9	0	0	26	31	57	0.8	**No dramatic change**	57	0	100.0	Memb only	361	0
≥ 2 unique peptides	pNG6087	Q5V747_HALMA	*pNG6087*	Hypothetical protein	26	7	0	0	30	9	0	0	26	30	56	0.9	**No dramatic change**	56	0	100.0	Memb only	353	0
≥ 2 unique peptides	rrnB0240	Q5UWD8_HALMA	*aca1*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	2	1	29	11	0	0	25	10	31	25	56	1.2	**No dramatic change**	2	54	3.6	Soluble predominant	381	0
≥ 2 unique peptides	rrnAC0229	Q5V5B4_HALMA	*nhaC1*	Na+/H+ antiporter	28	8	0	0	28	7	0	0	28	28	56	1.0	**No dramatic change**	56	0	100.0	Memb only	517	11
≥ 2 unique peptides	rrnAC1278	Q5V2N6_HALMA	*coxA1*	Cytochrome c oxidase polypeptide I (EC 1.9.3.1)	26	4	0	0	29	4	0	0	26	29	55	0.9	**No dramatic change**	55	0	100.0	Memb only	594	13
≥ 2 unique peptides	rrnAC1613	Q5V1S2_HALMA	*rrnAC1613*	Hypothetical protein	8	4	19	8	9	5	19	10	27	28	55	1.0	**No dramatic change**	17	38	30.9	Memb + Sol	215	0
≥ 2 unique peptides	rrnAC1301	Q5V2L5_HALMA	*yjlD2*	NADH dehydrogenase	14	6	15	5	16	5	10	5	29	26	55	1.1	**No dramatic change**	30	25	54.5	Memb + Sol	389	0

≥ 2 unique peptides	rrnAC0428	Q5V4U0_HALMA	*yidJ*	Putative sulfatase	18	9	9	5	23	12	5	4	27	28	55	1.0	**No dramatic change**	41	14	74.5	Memb + Sol	451	0
≥ 2 unique peptides	rrnAC0719	Q5V440_HALMA	*porB*	Pyruvate ferredoxin oxidoreductase subunit beta (EC 1.2.7.3)(EC 1.2.7.1)	1	1	26	8	0	0	28	10	27	28	55	1.0	**No dramatic change**	1	54	1.8	Soluble predominant	287	0
≥ 2 unique peptides	rrnAC1458	Q5V269_HALMA	*ndhG3*	NADH dehydrogenase/oxidoreductase	24	5	0	0	31	5	0	0	24	31	55	0.8	**No dramatic change**	55	0	100.0	Memb only	516	13
≥ 2 unique peptides	rrnAC3071	Q5UY65_HALMA	*ilvE1*	Branched-chain amino acid aminotransferase	0	0	20	5	0	0	35	12	20	35	55	0.6	**No dramatic change**	0	55	0.0	Soluble only	382	0
≥ 2 unique peptides	rrnAC3353	Q5UXG1_HALMA	*noxA2*	NADH oxidase	0	0	19	6	1	1	35	11	19	36	55	0.5	**No dramatic change**	1	54	1.8	Soluble predominant	416	0
≥ 2 unique peptides	rrnB0272	Q5UWB0_HALMA	*rrnB0272*	Hypothetical protein	45	19	0	0	9	7	0	0	45	9	54	5.0	0.7 (>3X)	54	0	100.0	Memb only	521	2
≥ 2 unique peptides	rrnAC0830	Q5V3U0_HALMA	*rrnAC0830*	Hypothetical protein	32	6	0	0	22	4	0	0	32	22	54	1.5	**No dramatic change**	54	0	100.0	Memb only	458	0
≥ 2 unique peptides	rrnAC2993	Q5UYD0_HALMA	*rrnAC2993*	Hypothetical protein	1	1	25	8	3	2	25	8	26	28	54	0.9	**No dramatic change**	4	50	7.4	Soluble predominant	203	0
≥ 2 unique peptides	rrnAC0160	Q5V5H4_HALMA	*rrnAC0160*	Hypothetical protein	24	7	0	0	30	8	0	0	24	30	54	0.8	**No dramatic change**	54	0	100.0	Memb only	227	0
≥ 2 unique peptides	rrnAC2110	Q5V0J2_HALMA	*trxA3*	Thioredoxin	0	0	26	6	0	0	27	7	26	27	53	1.0	**No dramatic change**	0	53	0.0	Soluble only	88	0
≥ 2 unique peptides	rrnAC0840	Q5V3T0_HALMA	*rrnAC0840*	Hypothetical protein	30	6	0	0	23	5	0	0	30	23	53	1.3	**No dramatic change**	53	0	100.0	Memb only	103	2
≥ 2 unique peptides	rrnAC1173	Q5V2X9_HALMA	*rrnAC1173*	Hypothetical protein	0	0	26	13	0	0	27	11	26	27	53	1.0	**No dramatic change**	0	53	0.0	Soluble only	242	0
≥ 2 unique peptides	rrnB0263	Q5UWB9_HALMA	*accC1*	Carbamoyl phosphate synthase L chain	0	0	32	12	0	0	21	8	32	21	53	1.5	**No dramatic change**	0	53	0.0	Soluble only	594	0
≥ 2 unique peptides	rrnAC0799	Q5V3W6_HALMA	*cdlM*	Endoglucanase	0	0	25	8	0	0	28	9	25	28	53	0.9	**No dramatic change**	0	53	0.0	Soluble only	355	0
≥ 2 unique peptides	rrnAC2147	Q5V0G2_HALMA	*pstA1*	Phosphate ABC transporter permease protein	14	4	0	0	39	6	0	0	14	39	53	0.4	1.2 (2~3X)	53	0	100.0	Memb only	884	24
≥ 2 unique peptides	rrnAC2910	Q5UYK2_HALMA	*radA*	DNA repair and recombination protein RadA	1	1	24	8	0	0	27	10	25	27	52	0.9	**No dramatic change**	1	51	1.9	Soluble predominant	351	0
≥ 2 unique peptides	pNG3012	Q5V7Y3_HALMA	*pNG3012*	Hypothetical protein	34	7	0	0	18	5	0	0	34	18	52	1.9	**No dramatic change**	52	0	100.0	Memb only	373	0
≥ 2 unique peptides	rrnAC1432	Q5V293_HALMA	*dpm5*	Dolichyl-phosphate-mannose-protein mannosyltransferase (EC 2.4.1.-)(EC 2.4.1.109)	32	10	0	0	20	6	0	0	32	20	52	1.6	**No dramatic change**	52	0	100.0	Memb only	665	10
≥ 2 unique peptides	rrnAC0630	Q5V4B4_HALMA	*sppA*	Putative signal peptide peptidase SppA (EC 3.4.21.-)	25	9	0	0	27	12	0	0	25	27	52	0.9	**No dramatic change**	52	0	100.0	Memb only	331	1
≥ 2 unique peptides	rrnB0306	Q5UW82_HALMA	*rrnB0306*	Hypothetical protein	0	0	40	13	0	0	11	5	40	11	51	3.6	0.7 (>3X)	0	51	0.0	Soluble only	95	0
≥ 2 unique peptides	rrnAC1448	Q5V278_HALMA	*nuoB*	NADH dehydrogenase I B subunit	27	9	0	0	24	9	0	0	27	24	51	1.1	**No dramatic change**	51	0	100.0	Memb only	230	0
≥ 2 unique peptides	pNG7150	Q5V6J4_HALMA	*nosD1*	Copper-binding protein	21	8	0	0	30	9	0	0	21	30	51	0.7	**No dramatic change**	51	0	100.0	Memb only	637	1
≥ 2 unique peptides	rrnAC1600	RS4E_HALMAReview	*rps4e*	30S ribosomal protein S4E (HS3)	4	2	30	10	5	2	12	5	34	17	51	2.0	0.7 (2>3X)	9	42	17.6	Soluble predominant	234	0
≥ 2 unique peptides	rrnAC1160	Q5V2Z1_HALMA	*rrnAC1160*	Von Willebrand factor type A like metal binding protein	0	0	22	11	0	0	29	13	22	29	51	0.8	**No dramatic change**	0	51	0.0	Soluble only	394	0
≥ 2 unique peptides	pNG5011	Q5V7G9_HALMA	*pNG5011*	Hypothetical protein	33	13	0	0	17	9	0	0	33	17	50	1.9	**No dramatic change**	50	0	100.0	Memb only	835	10
≥ 2 unique peptides	rrnAC1572	Q5V1W2_HALMA	*rfbB2*	DTDP-glucose-46-dehydratase (EC 4.2.1.46)	1	1	26	8	1	1	22	8	27	23	50	1.2	**No dramatic change**	2	48	4.0	Soluble predominant	353	0
≥ 2 unique peptides	rrnAC3303	Q5UXK8_HALMA	*ppiB1*	Peptidyl-prolyl cis-trans isomerase slr1251 (EC 5.2.1.8)	2	1	23	6	5	2	20	6	25	25	50	1.0	**No dramatic change**	7	43	14.0	Soluble predominant	209	0
≥ 2 unique peptides	rrnAC2502	Q5UZJ6_HALMA	*phzC*	Phenazine biosynthesis-like protein	0	0	25	8	1	1	24	9	25	25	50	1.0	**No dramatic change**	1	49	2.0	Soluble predominant	292	0
≥ 2 unique peptides	rrnAC2364	PGK_HALMAReview	*pgk*	Phosphoglycerate kinase (EC 2.7.2.3)	0	0	18	5	3	1	29	13	18	32	50	0.6	**No dramatic change**	3	47	6.0	Soluble predominant	400	0
≥ 2 unique peptides	rrnAC1790	Q5V1C1_HALMA	*hutI*	Imidazolonepropionase (EC 3.5.2.7)	0	0	15	7	0	0	35	11	15	35	50	0.4	1.2 (2~3X)	0	50	0.0	Soluble only	420	0
≥ 2 unique peptides	rrnAC1602	RL14_HALMAReview	*rpl14p*	50S ribosomal protein L14P (Hmal14) (Hl27)	19	7	2	1	29	9	0	0	21	29	50	0.7	**No dramatic change**	48	2	96.0	Memb predominant	132	0
≥ 2 unique peptides	rrnAC0043	Q5V5S7_HALMA	*coxB1*	Cytochrome c oxidase polypeptide II (EC 1.9.3.1)	24	7	0	0	25	7	0	0	24	25	49	1.0	**No dramatic change**	49	0	100.0	Memb only	253	3
≥ 2 unique peptides	rrnAC3510	Q5UX24_HALMA	*rrnAC3510*	Hypothetical protein	0	0	25	7	1	1	23	7	25	24	49	1.0	**No dramatic change**	1	48	2.0	Soluble predominant	252	0
≥ 2 unique peptides	rrnAC3169	SYR_HALMAReview	*argS*	Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS)	0	0	25	16	0	0	24	11	25	24	49	1.0	**No dramatic change**	0	49	0.0	Soluble only	579	0
≥ 2 unique peptides	rrnAC3008	Q5UYB9_HALMA	*cbiH*	Precorrin-3B C17-methyltransferase (EC 2.1.1.131)	6	2	18	3	0	0	25	5	24	25	49	1.0	**No dramatic change**	6	43	12.2	Soluble predominant	240	0
≥ 2 unique peptides	rrnAC3323	Q5UXJ0_HALMA	*ipp*	Inorganic pyrophosphatase (EC 3.6.1.1)	0	0	18	9	0	0	31	13	18	31	49	0.6	**No dramatic change**	0	49	0.0	Soluble only	177	0
≥ 2 unique peptides	pNG7293	Q5V663_HALMA	*yafB*	Aldehyde reductase	0	0	18	6	0	0	31	10	18	31	49	0.6	**No dramatic change**	0	49	0.0	Soluble only	279	0
≥ 2 unique peptides	pNG7366	Q5V5Z4_HALMA	*gcvT3*	Sacrosine dehydrogenase/glycine cleavage T-protein (EC 1.5.3.1)(EC 2.1.2.10)	0	0	9	5	0	0	40	19	9	40	49	0.2	1.2 (>3X)	0	49	0.0	Soluble only	857	0
≥ 2 unique peptides	rrnAC2498	Q5UZK1_HALMA	*trkA6*	TRK potassium uptake system protein	0	0	20	6	0	0	29	7	20	29	49	0.7	**No dramatic change**	0	49	0.0	Soluble only	221	0
≥ 2 unique peptides	rrnAC0915	Q5V3L2_HALMA	*rrnAC0915*	Hypothetical protein	29	8	0	0	19	5	0	0	29	19	48	1.5	**No dramatic change**	48	0	100.0	Memb only	458	0
≥ 2 unique peptides	rrnAC3162	Q5UXY5_HALMA	*atpD*	V-type ATP synthase subunit D (EC 3.6.3.14)	0	0	32	14	5	1	11	7	32	16	48	2.0	0.7 (2>3X)	5	43	10.4	Soluble predominant	230	0
≥ 2 unique peptides	rrnAC2577	UPP_HALMAReview	*upp*	Probable uracil phosphoribosyltransferase (EC 2.4.2.9) (UMPpyrophosphorylase) (UPRTase)	3	2	26	11	0	0	19	8	29	19	48	1.5	**No dramatic change**	3	45	6.3	Soluble predominant	225	0
≥ 2 unique peptides	rrnAC0204	Q5V5D7_HALMA	*dapD*	23,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase(EC 2.3.1.117)	0	0	27	8	0	0	21	9	27	21	48	1.3	**No dramatic change**	0	48	0.0	Soluble only	276	0
≥ 2 unique peptides	pNG7017	Q5V6W1_HALMA	*pNG7017*	4Fe-S protein	18	9	0	0	30	12	0	0	18	30	48	0.6	**No dramatic change**	48	0	100.0	Memb only	726	0
≥ 2 unique peptides	rrnAC3402	Q5UXC0_HALMA	*rrnAC3402*	Hypothetical protein	1	1	30	7	2	1	14	5	31	16	47	1.9	**No dramatic change**	3	44	6.4	Soluble predominant	166	0
≥ 2 unique peptides	rrnAC0899	Q5V3M6_HALMA	*rrnAC0899*	Hypothetical protein	27	10	0	0	20	9	0	0	27	20	47	1.4	**No dramatic change**	47	0	100.0	Memb only	388	0
≥ 2 unique peptides	rrnAC2969	PYRD_HALMAReview	*pyrD*	Dihydroorotate dehydrogenase (EC 1.3.3.1) (Dihydroorotate oxidase)(DHOdehase) (DHODase) (DHOD)	32	9	0	0	15	7	0	0	32	15	47	2.1	0.7 (2>3X)	47	0	100.0	Memb only	350	0
≥ 2 unique peptides	rrnAC3472	GUAAB_HALMAReview	*guaAB*	GMP synthase [glutamine-hydrolyzing] subunit B (EC 6.3.5.2) (GMPsynthetase)	0	0	27	10	0	0	20	10	27	20	47	1.4	**No dramatic change**	0	47	0.0	Soluble only	305	0
≥ 2 unique peptides	rrnAC1450	Q5V276_HALMA	*ndhG4*	NADH dehydrogenase/oxidoreductase	25	4	0	0	22	5	0	0	25	22	47	1.1	**No dramatic change**	47	0	100.0	Memb only	347	9
≥ 2 unique peptides	rrnAC0069	ENO_HALMAReview	*eno*	Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)	0	0	24	8	0	0	23	9	24	23	47	1.0	**No dramatic change**	0	47	0.0	Soluble only	401	0
≥ 2 unique peptides	rrnAC3546	Q5UWZ1_HALMA	*pan2*	Proteasome-activating nucleotidase 2	0	0	21	11	1	1	25	10	21	26	47	0.8	**No dramatic change**	1	46	2.1	Soluble predominant	404	0
≥ 2 unique peptides	rrnAC3289	Q5UXM0_HALMA	*trkA3*	TRK potassium uptake system protein	0	0	24	10	2	1	21	9	24	23	47	1.0	**No dramatic change**	2	45	4.3	Soluble predominant	228	0
≥ 2 unique peptides	rrnAC1393	Q5V2D0_HALMA	*rrnAC1393*	Hypothetical protein	22	3	0	0	24	3	0	0	22	24	46	0.9	**No dramatic change**	46	0	100.0	Memb only	80	1
≥ 2 unique peptides	rrnAC0325	Q5V527_HALMA	*rrnAC0325*	Hypothetical protein	18	5	2	1	22	7	4	2	20	26	46	0.8	**No dramatic change**	40	6	87.0	Memb predominant	226	0

≥ 2 unique peptides	rrnAC0896	Q5V3M8_HALMA	*acaB3*	3-ketoacyl-CoA thiolase (EC 2.3.1.9)	0	0	30	8	0	0	16	10	30	16	46	1.9	**No dramatic change**	0	46	0.0	Soluble only	430	0
≥ 2 unique peptides	rrnAC3495	Q5UX36_HALMA	*aspB2*	Aspartate aminotransferase (EC 2.6.1.1)	0	0	26	5	1	1	19	5	26	20	46	1.3	**No dramatic change**	1	45	2.2	Soluble predominant	373	0
≥ 2 unique peptides	rrnAC0227	Q5V5B6_HALMA	*ocd3*	Ornithine cyclodeaminase (EC 4.3.1.12)	0	0	21	9	0	0	24	9	21	24	45	0.9	**No dramatic change**	0	45	0.0	Soluble only	337	0
≥ 2 unique peptides	rrnAC1441	Q5V285_HALMA	*recJ3*	Putative exonuclease recJ-like	0	0	19	9	1	1	24	14	19	25	44	0.8	**No dramatic change**	1	43	2.3	Soluble predominant	637	0
≥ 2 unique peptides	rrnAC1800	SYM_HALMAReview	*metG*	Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)(MetRS)	0	0	24	9	0	0	20	10	24	20	44	1.2	**No dramatic change**	0	44	0.0	Soluble only	717	0
≥ 2 unique peptides	rrnAC2837	Q5UYR3_HALMA	*trzA3*	N-ethylammeline chlorohydrolase	0	0	23	6	0	0	21	8	23	21	44	1.1	**No dramatic change**	0	44	0.0	Soluble only	432	0
≥ 2 unique peptides	rrnAC3424	Q5UX99_HALMA	*rrnAC3424*	Rieske [2Fe-2S] domain protein	17	5	0	0	27	6	0	0	17	27	44	0.6	**No dramatic change**	44	0	100.0	Memb only	295	0
≥ 2 unique peptides	rrnAC0070	RS2_HALMAReview	*rps2p*	30S ribosomal protein S2P (HS2) (ORFMSG)	0	0	26	10	0	0	18	9	26	18	44	1.4	**No dramatic change**	0	44	0.0	Soluble only	267	0
≥ 2 unique peptides	rrnAC0004	Q5V5W2_HALMA	*accA*	Acetyl-CoA carboxylase alpha subunit	0	0	23	8	1	1	19	8	23	20	43	1.2	**No dramatic change**	1	42	2.3	Soluble predominant	451	0
≥ 2 unique peptides	rrnAC0444	Q5V4S4_HALMA	*manB2*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	0	0	18	9	0	0	25	13	18	25	43	0.7	**No dramatic change**	0	43	0.0	Soluble only	455	0
≥ 2 unique peptides	rrnAC2696	Q5UZ36_HALMA	*serA1*	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	0	0	17	8	0	0	26	12	17	26	43	0.7	**No dramatic change**	0	43	0.0	Soluble only	528	0
≥ 2 unique peptides	rrnB0320	PHNC2_HALMAReview	*phnC2*	Phosphonates import ATP-binding protein phnC 2 (EC 3.6.3.28)	33	12	1	1	9	6	0	0	34	9	43	3.8	0.7 (>3X)	42	1	97.7	Memb predominant	271	0
≥ 2 unique peptides	rrnAC0703	Q5V453_HALMA	*ftsZ1*	Cell division protein FtsZ	4	2	15	5	5	3	18	5	19	23	42	0.8	**No dramatic change**	9	33	21.4	Soluble predominant	386	0
≥ 2 unique peptides	rrnAC0535	Q5V4J9_HALMA	*rrnAC0535*	HTH DNA-binding protein	0	0	16	5	0	0	26	10	16	26	42	0.6	**No dramatic change**	0	42	0.0	Soluble only	175	0
≥ 2 unique peptides	rrnAC2885	Q5UYM1_HALMA	*rrnAC2885*	Hypothetical protein	25	6	0	0	17	5	0	0	25	17	42	1.5	**No dramatic change**	42	0	100.0	Memb only	181	0
≥ 2 unique peptides	rrnAC2308	Q5V021_HALMA	*rrnAC2308*	Hypothetical protein	0	0	24	7	0	0	18	6	24	18	42	1.3	**No dramatic change**	0	42	0.0	Soluble only	148	0
≥ 2 unique peptides	pNG7158	Q5V6I6_HALMA	*pNG7158*	Hypothetical protein	0	0	19	8	0	0	23	7	19	23	42	0.8	**No dramatic change**	0	42	0.0	Soluble only	47	0
≥ 2 unique peptides	rrnAC2683	ASSY_HALMAReview	*argG*	Argininosuccinate synthase (EC 6.3.4.5) (Citrulline--aspartateligase)	0	0	20	9	0	0	22	12	20	22	42	0.9	**No dramatic change**	0	42	0.0	Soluble only	420	0
≥ 2 unique peptides	rrnAC2811	Q5UYT6_HALMA	*mthK*	Potassium channel related protein	21	11	0	0	21	10	0	0	21	21	42	1.0	**No dramatic change**	42	0	100.0	Memb only	375	4
≥ 2 unique peptides	rrnAC1528	Q5V204_HALMA	*rrnAC1528*	Hypothetical protein	0	0	18	6	0	0	23	8	18	23	41	0.8	**No dramatic change**	0	41	0.0	Soluble only	138	0
≥ 2 unique peptides	rrnAC3471	PYRG_HALMAReview	*pyrG*	CTP synthase (EC 6.3.4.2) (UTP--ammonia ligase) (CTP synthetase)	0	0	24	9	0	0	17	8	24	17	41	1.4	**No dramatic change**	0	41	0.0	Soluble only	553	0
≥ 2 unique peptides	rrnAC0874	Q5V3P9_HALMA	*acdA*	Acyl-CoA dehydrogenase (EC 1.3.99.-)	0	0	20	9	0	0	21	9	20	21	41	1.0	**No dramatic change**	0	41	0.0	Soluble only	375	0
≥ 2 unique peptides	rrnAC2638	Q5UZ82_HALMA	*hit2*	Histidine triad protein	0	0	19	5	2	2	20	5	19	22	41	0.9	**No dramatic change**	2	39	4.9	Soluble predominant	142	0
≥ 2 unique peptides	rrnAC1434	Q5V291_HALMA	*aspC3*	Aspartate aminotransferase (EC 2.6.1.1)	0	0	10	6	0	0	31	9	10	31	41	0.3	1.2 (>3X)	0	41	0.0	Soluble only	386	0
≥ 2 unique peptides	rrnAC1608	RL2_HALMAReview	*rpl2p*	50S ribosomal protein L2P (Hmal2) (Hl4)	22	6	2	1	16	6	1	1	24	17	41	1.4	**No dramatic change**	38	3	92.7	Memb predominant	240	0
≥ 2 unique peptides	rrnAC3052	Q5UY82_HALMA	*nosY2*	ABC-type transport system involved in multi-copper enzyme maturationpermease component	24	8	0	0	17	7	0	0	24	17	41	1.4	**No dramatic change**	41	0	100.0	Memb only	334	6
≥ 2 unique peptides	rrnAC2528	Q5UZH2_HALMA	*rrnAC2528*	Hypothetical protein	14	6	0	0	26	9	0	0	14	26	40	0.5	**No dramatic change**	40	0	100.0	Memb only	306	2
≥ 2 unique peptides	rrnAC0677	Q5V473_HALMA	*yusZ4*	Short-chain dehydrogenase/oxidoreductase	24	6	0	0	16	5	0	0	24	16	40	1.5	**No dramatic change**	40	0	100.0	Memb only	274	0
≥ 2 unique peptides	rrnAC0904	Q5V3M2_HALMA	*fabG1*	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)	0	0	22	7	0	0	18	10	22	18	40	1.2	**No dramatic change**	0	40	0.0	Soluble only	247	0
≥ 2 unique peptides	rrnAC3159	Q5UZ65_HALMA	*rrnAC2659*	Hypothetical protein	0	0	18	8	0	0	22	9	18	22	40	0.8	**No dramatic change**	0	40	0.0	Soluble only	202	0
≥ 2 unique peptides	rrnAC1962	Q5V0X3_HALMA	*malA*	Putative alpha-D-14-glucosidase	0	0	8	5	0	0	32	15	8	32	40	0.3	1.2 (>3X)	0	40	0.0	Soluble only	663	0
≥ 2 unique peptides	rrnAC0550	GLPK_HALMAReview	*glpK*	Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase)(Glycerokinase) (GK)	0	0	8	2	0	0	32	10	8	32	40	0.3	1.2 (>3X)	0	40	0.0	Soluble only	510	0
≥ 2 unique peptides	rrnAC3395	Q5UXC7_HALMA	*usp24*	Universal stress protein family	10	2	0	0	24	3	6	3	10	30	40	0.3	1.2 (>3X)	34	6	85.0	Memb predominant	146	0
≥ 2 unique peptides	rrnAC3344	Q5UXG9_HALMA	*htlB*	HTR-like protein	22	6	0	0	17	4	0	0	22	17	39	1.3	**No dramatic change**	39	0	100.0	Memb only	296	4
≥ 2 unique peptides	rrnAC1308	Q5V2K9_HALMA	*rrnAC1308*	Glutaredoxin	0	0	20	7	0	0	19	5	20	19	39	1.1	**No dramatic change**	0	39	0.0	Soluble only	132	0
≥ 2 unique peptides	rrnAC2520	Q5UZI0_HALMA	*gstN*	Glutathione S-transferase N-terminal domain	1	1	18	4	3	1	17	4	19	20	39	1.0	**No dramatic change**	4	35	10.3	Soluble predominant	82	0
≥ 2 unique peptides	rrnAC0931	Q5V3J7_HALMA	*rrnAC0931*	Hypothetical protein	28	8	0	0	10	6	1	1	28	11	39	2.5	0.7 (2>3X)	38	1	97.4	Memb predominant	313	0
≥ 2 unique peptides	rrnAC3016	Q5UYB1_HALMA	*rrnAC3016*	Hypothetical protein	26	3	0	0	13	2	0	0	26	13	39	2.0	0.7 (2>3X)	39	0	100.0	Memb only	68	1
≥ 2 unique peptides	rrnAC1898	Q5V129_HALMA	*rrnAC1898*	Hypothetical protein	19	9	0	0	20	8	0	0	19	20	39	1.0	**No dramatic change**	39	0	100.0	Memb only	459	4
≥ 2 unique peptides	rrnAC1456	Q5V270_HALMA	*ndhD*	NADH dehydrogenase subunit 4	22	3	0	0	17	4	0	0	22	17	39	1.3	**No dramatic change**	39	0	100.0	Memb only	511	14
≥ 2 unique peptides	rrnAC1982	Q5V0V6_HALMA	*hbd2*	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.35) (EC 4.2.1.17)	0	0	17	4	0	0	22	6	17	22	39	0.8	**No dramatic change**	0	39	0.0	Soluble only	654	0
≥ 2 unique peptides	rrnAC0106	NDK_HALMAReview	*ndk*	Nucleoside diphosphate kinase (EC 2.7.4.6) (NDK) (NDP kinase)(Nucleoside-2-P kinase)	0	0	17	5	0	0	22	4	17	22	39	0.8	**No dramatic change**	0	39	0.0	Soluble only	154	0
≥ 2 unique peptides	rrnAC3460	Q5UX67_HALMA	*usp26*	Universal stress protein	0	0	16	6	0	0	23	8	16	23	39	0.7	**No dramatic change**	0	39	0.0	Soluble only	143	0
≥ 2 unique peptides	rrnAC0252	Q5V593_HALMA	*abcS-2*	ABC transporter permease protein	22	9	0	0	17	7	0	0	22	17	39	1.3	**No dramatic change**	39	0	100.0	Memb only	377	4
≥ 2 unique peptides	rrnAC0743	Q5V416_HALMA	*rrnAC0743*	Putative PRC-barrel domain	0	0	16	5	1	1	22	7	16	23	39	0.7	**No dramatic change**	1	38	2.6	Soluble predominant	101	0
≥ 2 unique peptides	rrnAC2427	Q5UZR5_HALMA	*rpoC*	RNA polymerase Rpb1 domain 5 (EC 2.7.7.6)	10	6	12	6	3	2	13	7	22	16	38	1.4	**No dramatic change**	13	25	34.2	Memb + Sol	395	0
≥ 2 unique peptides	rrnAC1118	Q5V327_HALMA	*hlx1*	HoxA-like transcriptional regulator	0	0	17	8	0	0	21	10	17	21	38	0.8	**No dramatic change**	0	38	0.0	Soluble only	194	0
≥ 2 unique peptides	rrnB0013	Q5UWX6_HALMA	*rrnB0013*	Hypothetical protein	34	15	0	0	4	3	0	0	34	4	38	8.5	0.7 (>3X)	38	0	100.0	Memb only	420	0
≥ 2 unique peptides	rrnAC0258	Q5V587_HALMA	*rrnAC0258*	Hypothetical protein	0	0	25	10	2	2	11	6	25	13	38	1.9	**No dramatic change**	2	36	5.3	Soluble predominant	190	0
≥ 2 unique peptides	rrnAC2469	Q5UZM8_HALMA	*rrnAC2469*	Hypothetical protein	21	2	0	0	17	2	0	0	21	17	38	1.2	**No dramatic change**	38	0	100.0	Memb only	473	0
≥ 2 unique peptides	rrnAC2971	Q5UYE9_HALMA	*rrnAC2971*	Hypothetical protein	0	0	9	5	1	1	28	7	9	29	38	0.3	1.2 (>3X)	1	37	2.6	Soluble predominant	116	0
≥ 2 unique peptides	rrnAC2262	G3P_HALMAReview	*gap*	Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.59) (GAPDH)(NAD(P)-dependent glyceraldehyde-3-phosphate dehydrogenase)	12	6	7	4	5	4	14	6	19	19	38	1.0	**No dramatic change**	17	21	44.7	Memb + Sol	354	0
≥ 2 unique peptides	rrnAC0134	Q5V5J6_HALMA	*ilvB1*	Acetolactate synthase large subunit (EC 2.2.1.6)	1	1	15	6	0	0	22	10	16	22	38	0.7	**No dramatic change**	1	37	2.6	Soluble predominant	549	0
≥ 2 unique peptides	rrnAC0575	Q5V4G3_HALMA	*dgoA4*	Mandelate racemase/muconate lactonizing enzyme family	0	0	9	6	0	0	29	8	9	29	38	0.3	1.2 (>3X)	0	38	0.0	Soluble only	416	0
≥ 2 unique peptides	rrnAC1867	Q5V154_HALMA	*rrnAC1867*	Putative Hsp20	6	1	10	5	14	5	8	4	16	22	38	0.7	**No dramatic change**	20	18	52.6	Memb + Sol	251	0

≥ 2 unique peptides	rrnAC2474	IF1A_HALMAReview	*eif1a*	Translation initiation factor 1A (aIF-1A)	1	1	18	3	2	2	17	3	19	19	38	1.0	**No dramatic change**	3	35	7.9	Soluble predominant	95	0
≥ 2 unique peptides	rrnAC1590	RL15_HALMAReview	*rpl15p*	50S ribosomal protein L15P (Hmal15) (Hl9)	5	4	5	3	28	11	0	0	10	28	38	0.4	1.2 (2~3X)	33	5	86.8	Memb predominant	165	0
≥ 2 unique peptides	rrnAC3298	Q5UXL2_HALMA	*dppB*	Dipeptide ABC transporter permease	20	5	0	0	18	4	0	0	20	18	38	1.1	**No dramatic change**	38	0	100.0	Memb only	346	6
≥ 2 unique peptides	rrnAC0259	Q5V586_HALMA	*rpb4*	RNA polymerase Rpb4	0	0	20	6	1	1	16	6	20	17	37	1.2	**No dramatic change**	1	36	2.7	Soluble predominant	118	0
≥ 2 unique peptides	pNG6093	Q5V751_HALMA	*pNG6093*	Hypothetical protein	0	0	21	5	0	0	16	5	21	16	37	1.3	**No dramatic change**	0	37	0.0	Soluble only	55	0
≥ 2 unique peptides	rrnAC0166	SYP_HALMAReview	*proS*	Prolyl-tRNA synthetase (EC 6.1.1.15) (Proline--tRNA ligase) (ProRS)	0	0	19	7	0	0	18	9	19	18	37	1.1	**No dramatic change**	0	37	0.0	Soluble only	484	0
≥ 2 unique peptides	rrnAC0887	Q5V3N7_HALMA	*cbiA1*	Cobyrinic acid ac-diamide synthase	0	0	19	9	0	0	18	5	19	18	37	1.1	**No dramatic change**	0	37	0.0	Soluble only	358	0
≥ 2 unique peptides	rrnAC3210	G6PI_HALMAReview	*pgi*	Probable glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI)(Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI)	0	0	18	8	0	0	19	8	18	19	37	0.9	**No dramatic change**	0	37	0.0	Soluble only	436	0
≥ 2 unique peptides	rrnAC0772	Q5V3Z1_HALMA	*fbp2*	Fructose-16-bisphosphatase (EC 3.1.3.11)	0	0	18	8	0	0	19	8	18	19	37	0.9	**No dramatic change**	0	37	0.0	Soluble only	291	0
≥ 2 unique peptides	rrnAC3179	RS19E_HALMAReview	*rps19e*	30S ribosomal protein S19e (HS12) (E1.3)	2	1	20	7	3	2	12	5	22	15	37	1.5	**No dramatic change**	5	32	13.5	Soluble predominant	153	0
≥ 2 unique peptides	rrnAC2146	PSTB2_HALMAReview	*pstB2*	Phosphate import ATP-binding protein pstB 2 (EC 3.6.3.27) (Phosphate-transporting ATPase 2) (ABC phosphate transporter 2)	0	0	0	0	37	13	0	0	0	37	37	0.0	1.2 only	37	0	100.0	Memb only	313	0
≥ 2 unique peptides	rrnAC2267	Q5V057_HALMA	*uvrD*	Repair helicase	2	1	25	12	0	0	9	5	27	9	36	3.0	0.7 (>3X)	2	34	5.6	Soluble predominant	613	0
≥ 2 unique peptides	rrnAC0991	Q5V3E3_HALMA	*htlD*	Sensor protein (EC 2.7.13.3)	19	9	0	0	17	7	0	0	19	17	36	1.1	**No dramatic change**	36	0	100.0	Memb only	644	5
≥ 2 unique peptides	pNG4051	Q5V7X1_HALMA	*pNG4051*	Putative helicase	1	1	14	8	1	1	20	13	15	21	36	0.7	**No dramatic change**	2	34	5.6	Soluble predominant	893	0
≥ 2 unique peptides	rrnAC3530	Q5UX06_HALMA	*nuoL1*	NADH dehydrogenase I L subunit	22	7	0	0	14	4	0	0	22	14	36	1.6	**No dramatic change**	36	0	100.0	Memb only	565	12
≥ 2 unique peptides	rrnAC1881	Q5V141_HALMA	*deoC2*	Deoxyribose-phosphate aldolase	0	0	21	7	0	0	15	7	21	15	36	1.4	**No dramatic change**	0	36	0.0	Soluble only	267	0
≥ 2 unique peptides	rrnAC0999	GLYA_HALMAReview	*glyA*	Serine hydroxymethyltransferase (EC 2.1.2.1) (Serine methylase)(SHMT)	0	0	20	9	0	0	16	8	20	16	36	1.3	**No dramatic change**	0	36	0.0	Soluble only	415	0
≥ 2 unique peptides	rrnAC2808	SYS_HALMAReview	*serS*	Seryl-tRNA synthetase (EC 6.1.1.11) (Seryl-tRNA(Ser/Sec) synthetase)(Serine--tRNA ligase) (SerRS)	0	0	19	10	0	0	17	9	19	17	36	1.1	**No dramatic change**	0	36	0.0	Soluble only	460	0
≥ 2 unique peptides	rrnAC0833	Q5V3T7_HALMA	*ech2*	Enoyl-CoA hydratase (EC 4.2.1.17)	1	1	12	3	2	1	21	8	13	23	36	0.6	**No dramatic change**	3	33	8.3	Soluble predominant	285	0
≥ 2 unique peptides	rrnAC0322	Q5V530_HALMA	*pepQ*	Xaa-Pro aminopeptidase (EC 3.4.11.9)	0	0	15	6	0	0	21	9	15	21	36	0.7	**No dramatic change**	0	36	0.0	Soluble only	400	0
≥ 2 unique peptides	rrnAC1730	Q5V1G9_HALMA	*rrnAC1730*	Hypothetical protein	0	0	16	6	0	0	19	7	16	19	35	0.8	**No dramatic change**	0	35	0.0	Soluble only	58	0
≥ 2 unique peptides	rrnAC2967	SYFB_HALMAReview	*pheT*	Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20) (Phenylalanine--tRNA ligase beta chain) (PheRS)	0	0	20	12	1	1	14	9	20	15	35	1.3	**No dramatic change**	1	34	2.9	Soluble predominant	584	0
≥ 2 unique peptides	rrnAC0537	TPIS_HALMAReview	*tpiA*	Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphateisomerase)	0	0	20	5	0	0	15	5	20	15	35	1.3	**No dramatic change**	0	35	0.0	Soluble only	215	0
≥ 2 unique peptides	rrnAC0081	Q5V5P2_HALMA	*idsA*	Geranylgeranyl diphosphate synthase (EC 2.5.1.1) (EC 2.5.1.10)	0	0	19	9	0	0	16	7	19	16	35	1.2	**No dramatic change**	0	35	0.0	Soluble only	346	0
≥ 2 unique peptides	rrnAC2699	Q5UZ34_HALMA	*rrnAC2699*	Putative inosine monophosphate dehydrogenase (EC 1.1.1.205)	0	0	19	8	0	0	16	5	19	16	35	1.2	**No dramatic change**	0	35	0.0	Soluble only	289	0
≥ 2 unique peptides	rrnAC0012	Q5V5V5_HALMA	*adh11*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	0	0	18	7	1	1	16	8	18	17	35	1.1	**No dramatic change**	1	34	2.9	Soluble predominant	360	0
≥ 2 unique peptides	pNG6056	Q5V6Y2_HALMA	*copA2*	Copper-transporting ATPase CopA	15	9	0	0	20	12	0	0	15	20	35	0.8	**No dramatic change**	35	0	100.0	Memb only	760	8
≥ 2 unique peptides	rrnAC0289	Q5V557_HALMA	*eif2BD1*	Translation initiation factor eIF-2B subunit delta	0	0	16	6	0	0	19	8	16	19	35	0.8	**No dramatic change**	0	35	0.0	Soluble only	283	0
≥ 2 unique peptides	rrnAC3089	Q5UY49_HALMA	*pspA2*	Transcription regulator	21	9	1	1	12	6	0	0	22	12	34	1.8	**No dramatic change**	33	1	97.1	Memb predominant	241	0
≥ 2 unique peptides	rrnAC0681	Q5V470_HALMA	*tbpE*	TATA-box binding protein E	5	2	17	5	2	1	10	2	22	12	34	1.8	**No dramatic change**	7	27	20.6	Soluble predominant	186	0
≥ 2 unique peptides	pNG5069	Q5V7M3_HALMA	*pNG5069*	Hypothetical protein	24	8	0	0	10	4	0	0	24	10	34	2.4	0.7 (2>3X)	34	0	100.0	Memb only	760	10
≥ 2 unique peptides	pNG4046	Q5V7W8_HALMA	*pNG4046*	Hypothetical protein	0	0	21	5	0	0	13	8	21	13	34	1.6	**No dramatic change**	0	34	0.0	Soluble only	270	0
≥ 2 unique peptides	rrnAC3149	Q5UXZ7_HALMA	*rrnAC3149*	Hypothetical protein	19	9	0	0	15	9	0	0	19	15	34	1.3	**No dramatic change**	34	0	100.0	Memb only	364	2
≥ 2 unique peptides	pNG4047	Q5V7W7_HALMA	*pNG4047*	Hypothetical protein	0	0	18	11	0	0	16	11	18	16	34	1.1	**No dramatic change**	0	34	0.0	Soluble only	710	0
≥ 2 unique peptides	rrnB0206	Q5UWG4_HALMA	*aspC1*	Aspartate aminotransferase (EC 2.6.1.1)	4	2	24	8	0	0	6	1	28	6	34	4.7	0.7 (>3X)	4	30	11.8	Soluble predominant	372	0
≥ 2 unique peptides	rrnAC3531	Q5UX05_HALMA	*ndhG2*	NADH dehydrogenase/oxidoreductase	22	2	0	0	12	3	0	0	22	12	34	1.8	**No dramatic change**	34	0	100.0	Memb only	497	13
≥ 2 unique peptides	rrnAC1642	GATB_HALMAReview	*gatB*	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B(EC 6.3.5.-) (Asp/Glu-ADT subunit B)	0	0	15	5	0	0	19	7	15	19	34	0.8	**No dramatic change**	0	34	0.0	Soluble only	505	0
≥ 2 unique peptides	rrnAC0650	Q5V498_HALMA	*acs1*	Acyl-coenzyme A synthetases (EC 6.2.1.1)	0	0	13	8	1	1	20	9	13	21	34	0.6	**No dramatic change**	1	33	2.9	Soluble predominant	673	0
≥ 2 unique peptides	rrnAC1409	Q5V2B4_HALMA	*gloA1*	Lactoylglutathione lyase (EC 4.4.1.5)	0	0	5	2	0	0	29	11	5	29	34	0.2	1.2 (>3X)	0	34	0.0	Soluble only	250	0
≥ 2 unique peptides	rrnAC0059	RS4_HALMAReview	*rps4p*	30S ribosomal protein S4P (HmaS4)	0	0	27	8	0	0	7	4	27	7	34	3.9	0.7 (>3X)	0	34	0.0	Soluble only	171	0
≥ 2 unique peptides	rrnAC1509	Q5V222_HALMA	*phoX*	Phosphate ABC transporter phosphate-binding protein	20	7	0	0	14	4	0	0	20	14	34	1.4	**No dramatic change**	34	0	100.0	Memb only	337	0
≥ 2 unique peptides	rrnAC1282	Q5V2N2_HALMA	*rrnAC1282*	Hypothetical protein	0	0	20	5	0	0	13	6	20	13	33	1.5	**No dramatic change**	0	33	0.0	Soluble only	101	0
≥ 2 unique peptides	rrnAC2612	Q5UZA2_HALMA	*rrnAC2612*	Hypothetical protein	16	5	0	0	17	7	0	0	16	17	33	0.9	**No dramatic change**	33	0	100.0	Memb only	468	1
≥ 2 unique peptides	rrnB0210	Q5UWG0_HALMA	*galE10*	UDP-glucose 4-epimerase	3	3	21	7	0	0	9	6	24	9	33	2.7	0.7 (2>3X)	3	30	9.1	Soluble predominant	319	0
≥ 2 unique peptides	rrnB0255	Q5UWC4_HALMA	*rrnB0255*	Amidohydrolase	0	0	24	8	0	0	9	4	24	9	33	2.7	0.7 (2>3X)	0	33	0.0	Soluble only	259	0
≥ 2 unique peptides	rrnB0249	Q5UWC9_HALMA	*paaC*	Phenylacetic acid degradation protein PaaC	0	0	20	8	0	0	13	7	20	13	33	1.5	**No dramatic change**	0	33	0.0	Soluble only	277	0
≥ 2 unique peptides	rrnAC1707	PHS_HALMAReview	*rrnAC1707*	Putative pterin-4-alpha-carbinolamine dehydratase (EC 4.2.1.96) (PHS)(4-alpha-hydroxy-tetrahydropterin dehydratase) (Pterin carbinolaminedehydratase) (PCD)	0	0	17	6	0	0	16	7	17	16	33	1.1	**No dramatic change**	0	33	0.0	Soluble only	92	0
≥ 2 unique peptides	rrnAC2150	Q5V0F9_HALMA	*prp1*	Phosphate regulatory protein-like	0	0	7	3	4	2	22	7	7	26	33	0.3	1.2 (>3X)	4	29	12.1	Soluble predominant	334	0
≥ 2 unique peptides	rrnAC2230	Q5V090_HALMA	*oppC1*	Oligopeptide transport system permease protein OppC	21	6	0	0	12	4	0	0	21	12	33	1.8	**No dramatic change**	33	0	100.0	Memb only	309	6
≥ 2 unique peptides	rrnAC1750	Q5V1F3_HALMA	*argT*	Amino acid ABC transporter amino acid-binding protein	19	4	0	0	14	3	0	0	19	14	33	1.4	**No dramatic change**	33	0	100.0	Memb only	266	0
≥ 2 unique peptides	rrnAC1281	Q5V2N3_HALMA	*rrnAC1281*	Hypothetical protein	3	2	12	8	1	1	16	12	15	17	32	0.9	**No dramatic change**	4	28	12.5	Soluble predominant	863	0
≥ 2 unique peptides	rrnAC0892	Q5V3N2_HALMA	*rrnAC0892*	Hypothetical protein	14	3	0	0	18	4	0	0	14	18	32	0.8	**No dramatic change**	32	0	100.0	Memb only	194	0

≥ 2 unique peptides	rrnAC1028	Q5V3A9_HALMA	*lolC*	Putative permease	15	8	0	0	17	9	0	0	15	17	32	0.9	**No dramatic change**	32	0	100.0	Memb only	1021	8
≥ 2 unique peptides	rrnAC2245	Q5V077_HALMA	*rrnAC2245*	M50 family metallopeptidase	15	2	0	0	17	3	0	0	15	17	32	0.9	**No dramatic change**	32	0	100.0	Memb only	289	3
≥ 2 unique peptides	rrnAC0103	RL7A_HALMAReview	*rpl7ae*	50S ribosomal protein L7Ae (Hs6)	0	0	16	2	3	1	13	2	16	16	32	1.0	**No dramatic change**	3	29	9.4	Soluble predominant	120	0
≥ 2 unique peptides	rrnAC2103	Q5V0J9_HALMA	*rli*	RNase L inhibitor	0	0	16	8	0	0	16	7	16	16	32	1.0	**No dramatic change**	0	32	0.0	Soluble only	609	0
≥ 2 unique peptides	rrnAC3516	Q5UX18_HALMA	*rrnAC3516*	Hypothetical protein	18	5	0	0	13	5	0	0	18	13	31	1.4	**No dramatic change**	31	0	100.0	Memb only	90	0
≥ 2 unique peptides	rrnAC3552	Q5UWY7_HALMA	*rrnAC3552*	Hypothetical protein	16	5	0	0	15	6	0	0	16	15	31	1.1	**No dramatic change**	31	0	100.0	Memb only	150	2
≥ 2 unique peptides	rrnAC1112	Q5V333_HALMA	*rrnAC1112*	Hypothetical protein	0	0	16	4	0	0	15	4	16	15	31	1.1	**No dramatic change**	0	31	0.0	Soluble only	129	0
≥ 2 unique peptides	pNG1025	Q5V882_HALMA	*pNG1025*	Hypothetical protein	0	0	12	8	0	0	19	8	12	19	31	0.6	**No dramatic change**	0	31	0.0	Soluble only	248	0
≥ 2 unique peptides	rrnAC0836	Q5V3T4_HALMA	*csg2*	Surface glycoprotein	0	0	11	6	0	0	20	7	11	20	31	0.6	**No dramatic change**	0	31	0.0	Soluble only	71	0
≥ 2 unique peptides	rrnAC2675	Q5UZ52_HALMA	*argD*	Acetylornithine aminotransferase (EC 2.6.1.11)	0	0	19	7	0	0	12	6	19	12	31	1.6	**No dramatic change**	0	31	0.0	Soluble only	375	0
≥ 2 unique peptides	rrnAC0546	Q5V4I8_HALMA	*pykA*	Pyruvate kinase (EC 2.7.1.40)	0	0	19	4	0	0	12	4	19	12	31	1.6	**No dramatic change**	0	31	0.0	Soluble only	610	0
≥ 2 unique peptides	rrnAC1656	Q5V1N3_HALMA	*rrnAC1656*	Nitrite/nitrate reduction protein	16	4	0	0	15	4	0	0	16	15	31	1.1	**No dramatic change**	31	0	100.0	Memb only	299	6
≥ 2 unique peptides	rrnAC0841	Q5V3S9_HALMA	*ech1*	Enoyl-CoA hydratase (EC 4.2.1.17)	0	0	15	5	0	0	16	8	15	16	31	0.9	**No dramatic change**	0	31	0.0	Soluble only	353	0
≥ 2 unique peptides	rrnAC3121	Q5UY23_HALMA	*eda*	2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutaratealdolase (EC 4.1.2.14)	0	0	14	4	0	0	17	4	14	17	31	0.8	**No dramatic change**	0	31	0.0	Soluble only	397	0
≥ 2 unique peptides	rrnAC3197	Q5UXV2_HALMA	*malE2*	Trehalose/maltose binding protein	14	7	0	0	17	8	0	0	14	17	31	0.8	**No dramatic change**	31	0	100.0	Memb only	446	0
≥ 2 unique peptides	rrnAC3326	Q5UXI7_HALMA	*ftsZ4*	Cell division protein	10	8	4	4	3	3	13	8	14	16	30	0.9	**No dramatic change**	13	17	43.3	Memb + Sol	357	0
≥ 2 unique peptides	rrnAC0079	Q5V5P4_HALMA	*rrnAC0079*	Hypothetical protein	19	10	0	0	11	6	0	0	19	11	30	1.7	**No dramatic change**	30	0	100.0	Memb only	496	2
≥ 2 unique peptides	rrnAC0776	Q5V3Y7_HALMA	*rrnAC0776*	Hypothetical protein	19	7	0	0	11	4	0	0	19	11	30	1.7	**No dramatic change**	30	0	100.0	Memb only	161	0
≥ 2 unique peptides	rrnAC2810	Q5UYT7_HALMA	*rrnAC2810*	Hypothetical protein	0	0	15	3	0	0	15	4	15	15	30	1.0	**No dramatic change**	0	30	0.0	Soluble only	329	0
≥ 2 unique peptides	rrnAC0726	Q5V433_HALMA	*rrnAC0726*	Hypothetical protein	6	5	8	5	10	5	6	3	14	16	30	0.9	**No dramatic change**	16	14	53.3	Memb + Sol	411	0
≥ 2 unique peptides	rrnAC3356	Q5UXF8_HALMA	*rrnAC3356*	Hypothetical protein	13	3	0	0	17	3	0	0	13	17	30	0.8	**No dramatic change**	30	0	100.0	Memb only	257	5
≥ 2 unique peptides	rrnAC1121	THYX_HALMAReview	*thyX*	Thymidylate synthase thyX (EC 2.1.1.148) (TS) (TSase)	0	0	19	8	0	0	11	9	19	11	30	1.7	**No dramatic change**	0	30	0.0	Soluble only	247	0
≥ 2 unique peptides	rrnAC2650	Q5UZ73_HALMA	*leuS1*	Leucyl-tRNA synthetase (EC 6.1.1.4)	0	0	16	6	0	0	14	8	16	14	30	1.1	**No dramatic change**	0	30	0.0	Soluble only	892	0
≥ 2 unique peptides	rrnAC0448	Q5V4S2_HALMA	*udp2*	Uridine phosphorylase (EC 2.4.2.3)	0	0	15	5	0	0	15	5	15	15	30	1.0	**No dramatic change**	0	30	0.0	Soluble only	274	0
≥ 2 unique peptides	rrnAC1426	RS15_HALMAReview	*rps15p*	30S ribosomal protein S15P/S13e (HmaS15) (HS11)	4	1	14	6	4	1	8	6	18	12	30	1.5	**No dramatic change**	8	22	26.7	Memb + Sol	156	0
≥ 2 unique peptides	rrnAC2424	RS12_HALMAReview	*rps12p*	30S ribosomal protein S12P	8	2	7	2	10	2	5	1	15	15	30	1.0	**No dramatic change**	18	12	60.0	Memb + Sol	142	0
≥ 2 unique peptides	rrnAC2829	Q5UYS0_HALMA	*rpoE'*	DNA-directed RNA polymerase subunit E'	0	0	22	4	0	0	7	3	22	7	29	3.1	0.7 (>3X)	0	29	0.0	Soluble only	192	0
≥ 2 unique peptides	rrnAC1133	Q5V314_HALMA	*rpaA*	Replication protein A	0	0	12	5	0	0	17	6	12	17	29	0.7	**No dramatic change**	0	29	0.0	Soluble only	426	0
≥ 2 unique peptides	rrnAC1135	Q5V313_HALMA	*rrnAC1135*	Hypothetical protein	0	0	18	8	0	0	11	6	18	11	29	1.6	**No dramatic change**	0	29	0.0	Soluble only	573	0
≥ 2 unique peptides	pNG2007	Q5V851_HALMA	*pNG2007*	Hypothetical protein	0	0	18	8	0	0	11	5	18	11	29	1.6	**No dramatic change**	0	29	0.0	Soluble only	372	0
≥ 2 unique peptides	pNG7179	Q5V6G7_HALMA	*pNG7179*	Hypothetical protein	1	1	14	5	1	1	13	2	15	14	29	1.1	**No dramatic change**	2	27	6.9	Soluble predominant	218	0
≥ 2 unique peptides	rrnAC0996	FOLD1_HALMAReview	*folD1*	Bifunctional protein folD 1 [Includes: Methylenetetrahydrofolatedehydrogenase (EC 1.5.1.5); Methenyltetrahydrofolate cyclohydrolase(EC 3.5.4.9)]	0	0	14	6	0	0	15	9	14	15	29	0.9	**No dramatic change**	0	29	0.0	Soluble only	297	0
≥ 2 unique peptides	pNG7380	FTHS_HALMAReview	*fhs*	Formate--tetrahydrofolate ligase (EC 6.3.4.3) (Formyltetrahydrofolatesynthetase) (FHS) (FTHFS)	0	0	2	1	1	1	26	11	2	27	29	0.1	1.2 (>3X)	1	28	3.4	Soluble predominant	553	0
≥ 2 unique peptides	rrnAC0061	RS11_HALMAReview	*rps11p*	30S ribosomal protein S11P (HmaS11) (HS19)	4	3	19	6	0	0	6	3	23	6	29	3.8	0.7 (>3X)	4	25	13.8	Soluble predominant	129	0
≥ 2 unique peptides	rrnAC0058	RS13_HALMAReview	*rps13p*	30S ribosomal protein S13P (HmaS13)	4	4	17	5	2	2	6	3	21	8	29	2.6	0.7 (2>3X)	6	23	20.7	Soluble predominant	177	0
≥ 2 unique peptides	pNG5003	Q5V7G2_HALMA	*yvrO-1*	ABC transporter ATP-binding protein	12	5	0	0	17	8	0	0	12	17	29	0.7	**No dramatic change**	29	0	100.0	Memb only	227	0
≥ 2 unique peptides	pNG7016	Q5V6W2_HALMA	*pNG7016*	Hypothetical protein	0	0	17	6	0	0	11	6	17	11	28	1.5	**No dramatic change**	0	28	0.0	Soluble only	452	0
≥ 2 unique peptides	rrnAC2250	Q5V072_HALMA	*rrnAC2250*	Hypothetical protein	0	0	16	7	0	0	12	9	16	12	28	1.3	**No dramatic change**	0	28	0.0	Soluble only	653	0
≥ 2 unique peptides	rrnAC1735	Q5V1G4_HALMA	*rrnAC1735*	Hypothetical protein	0	0	15	4	0	0	13	4	15	13	28	1.2	**No dramatic change**	0	28	0.0	Soluble only	193	0
≥ 2 unique peptides	pNG6187	Q5V7B7_HALMA	*pNG6187*	Hypothetical protein	0	0	14	10	0	0	14	11	14	14	28	1.0	**No dramatic change**	0	28	0.0	Soluble only	965	0
≥ 2 unique peptides	rrnAC3438	Q5UX86_HALMA	*rrnAC3438*	Hypothetical protein	13	5	0	0	15	6	0	0	13	15	28	0.9	**No dramatic change**	28	0	100.0	Memb only	606	3
≥ 2 unique peptides	rrnAC2581	Q5UZC9_HALMA	*rrnAC2581*	Hypothetical protein	0	0	9	3	0	0	19	7	9	19	28	0.5	1.2 (2~3X)	0	28	0.0	Soluble only	230	0
≥ 2 unique peptides	rrnAC3227	Q5UXS4_HALMA	*rrnAC3227*	Hypothetical protein	8	4	0	0	20	7	0	0	8	20	28	0.4	1.2 (2~3X)	28	0	100.0	Memb only	142	2
≥ 2 unique peptides	rrnAC0549	Q5V4I5_HALMA	*rrnAC0549*	Hypothetical protein	7	4	0	0	21	8	0	0	7	21	28	0.3	1.2 (>3X)	28	0	100.0	Memb only	362	8
≥ 2 unique peptides	rrnAC0903	Q5V3M3_HALMA	*accA*	Acetyl-CoA carboxylase alpha subunit	0	0	16	7	0	0	12	7	16	12	28	1.3	**No dramatic change**	0	28	0.0	Soluble only	527	0
≥ 2 unique peptides	rrnAC3152	Q5UXZ4_HALMA	*atpG*	Vacuolar (H+)-ATPase G subunit (EC 3.6.3.14)	5	2	10	3	7	2	6	2	15	13	28	1.2	**No dramatic change**	12	16	42.9	Memb + Sol	110	0
≥ 2 unique peptides	rrnAC2522	Q5UZH8_HALMA	*manB3*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	0	0	15	6	0	0	13	7	15	13	28	1.2	**No dramatic change**	0	28	0.0	Soluble only	459	0
≥ 2 unique peptides	rrnAC3238	Q5UXR6_HALMA	*rffH3*	Glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	1	1	9	3	2	1	16	3	10	18	28	0.6	**No dramatic change**	3	25	10.7	Soluble predominant	251	0
≥ 2 unique peptides	rrnAC2580	Q5UZD0_HALMA	*imp*	Immunogenic protein	17	2	0	0	11	1	0	0	17	11	28	1.5	**No dramatic change**	28	0	100.0	Memb only	345	0
≥ 2 unique peptides	rrnAC2782	Q5UYW3_HALMA	*rbn*	Ribonuclease BN	14	3	0	0	14	3	0	0	14	14	28	1.0	**No dramatic change**	28	0	100.0	Memb only	379	8
≥ 2 unique peptides	rrnAC0147	Q5V5I5_HALMA	*tppA*	Thiamine-binding periplasmic protein-like	21	8	0	0	7	4	0	0	21	7	28	3.0	0.7 (>3X)	28	0	100.0	Memb only	374	0
≥ 2 unique peptides	rrnAC3309	Y3309_HALMAReview	*rrnAC3309*	UPF0343 protein rrnAC3309	0	0	13	5	0	0	14	5	13	14	27	0.9	**No dramatic change**	0	27	0.0	Soluble only	309	0
≥ 2 unique peptides	rrnAC1702	Q5V1J4_HALMA	*rrnAC1702*	Hypothetical protein	18	10	0	0	9	5	0	0	18	9	27	2.0	0.7 (2>3X)	27	0	100.0	Memb only	405	2
≥ 2 unique peptides	rrnAC1130	Q5V317_HALMA	*rrnAC1130*	Hypothetical protein	1	1	15	4	0	0	11	4	16	11	27	1.5	**No dramatic change**	1	26	3.7	Soluble predominant	95	0

≥ 2 unique peptides	rrnAC3011	Q5UYB6_HALMA	*cbiK*	Colbalt chelase thioredoxin (EC 4.99.1.-)	6	3	12	3	1	1	8	2	18	9	27	2.0	0.7 (2>3X)	7	20	25.9	Memb + Sol	407	0
≥ 2 unique peptides	rrnAC0927	Q5V3K1_HALMA	*pyrE2*	Orotate phosphoribosyltransferase (EC 2.4.2.10)	0	0	15	6	2	2	10	6	15	12	27	1.3	**No dramatic change**	2	25	7.4	Soluble predominant	212	0
≥ 2 unique peptides	rrnAC3462	SYT_HALMAReview	*thrS*	Threonyl-tRNA synthetase (EC 6.1.1.3) (Threonine--tRNA ligase)(ThrRS)	0	0	15	7	0	0	12	6	15	12	27	1.3	**No dramatic change**	0	27	0.0	Soluble only	642	0
≥ 2 unique peptides	rrnAC1149	Q5V302_HALMA	*ctpB*	Cation transporting ATPase	13	8	0	0	14	7	0	0	13	14	27	0.9	**No dramatic change**	27	0	100.0	Memb only	793	7
≥ 2 unique peptides	rrnAC2561	SYA_HALMAReview	*alaS*	Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine--tRNA ligase) (AlaRS)	0	0	12	7	0	0	15	11	12	15	27	0.8	**No dramatic change**	0	27	0.0	Soluble only	927	0
≥ 2 unique peptides	rrnAC0438	Q5V4T0_HALMA	*purM*	Phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1)	0	0	12	6	0	0	15	7	12	15	27	0.8	**No dramatic change**	0	27	0.0	Soluble only	336	0
≥ 2 unique peptides	rrnAC1526	Q5V206_HALMA	*yfmJ2*	Quinone oxidoreductase (EC 1.6.5.5)	0	0	8	4	0	0	19	5	8	19	27	0.4	1.2 (2~3X)	0	27	0.0	Soluble only	337	0
≥ 2 unique peptides	rrnAC2065	RL15E_HALMAReview	*rpl15e*	50S ribosomal protein L15e (50S ribosomal protein LC12)	16	3	0	0	11	3	0	0	16	11	27	1.5	**No dramatic change**	27	0	100.0	Memb only	196	0
≥ 2 unique peptides	rrnAC1310	Q5V2K7_HALMA	*epf2a*	MRNA 3'-end processing factor-like	1	1	12	7	0	0	14	9	13	14	27	0.9	**No dramatic change**	1	26	3.7	Soluble predominant	640	0
≥ 2 unique peptides	rrnAC0524	Q5V4K8_HALMA	*rrnAC0524*	Putative sec-independent transolcation prot	16	1	0	0	11	2	0	0	16	11	27	1.5	**No dramatic change**	27	0	100.0	Memb only	90	1
≥ 2 unique peptides	rrnAC2030	Q5V0R5_HALMA	*xop1*	Bacteriorhodopsin	7	2	0	0	20	4	0	0	7	20	27	0.4	1.2 (2~3X)	27	0	100.0	Memb only	250	7
≥ 2 unique peptides	rrnAC1145	Q5V305_HALMA	*blp*	Bacterio-opsin linked product	13	4	0	0	14	4	0	0	13	14	27	0.9	**No dramatic change**	27	0	100.0	Memb only	154	0
≥ 2 unique peptides	rrnB0191	Q5UWH7_HALMA	*rrnB0191*	Hypothetical protein	1	1	18	5	0	0	7	4	19	7	26	2.7	0.7 (2>3X)	1	25	3.8	Soluble predominant	96	0
≥ 2 unique peptides	rrnAC0708	Q5V449_HALMA	*rrnAC0708*	Hypothetical protein	5	3	7	2	8	4	6	2	12	14	26	0.9	**No dramatic change**	13	13	50.0	Memb + Sol	195	0
≥ 2 unique peptides	pNG7148	Q5V6J6_HALMA	*pNG7148*	Hypothetical protein	11	4	0	0	15	5	0	0	11	15	26	0.7	**No dramatic change**	26	0	100.0	Memb only	270	7
≥ 2 unique peptides	pNG7088	Q5V6P9_HALMA	*qad*	Quinohemoprotein alcohol dehydrogenase (EC 1.1.99.-)	17	8	0	0	9	6	0	0	17	9	26	1.9	**No dramatic change**	26	0	100.0	Memb only	407	0
≥ 2 unique peptides	rrnAC3360	Q5UXF4_HALMA	*carB*	Carbamoylphosphate synthetase large subunit (EC 6.3.5.5)	0	0	17	7	0	0	9	6	17	9	26	1.9	**No dramatic change**	0	26	0.0	Soluble only	1083	0
≥ 2 unique peptides	rrnAC0419	Q5V4U8_HALMA	*gtl*	Glycosyl transferase-like	15	6	0	0	11	3	0	0	15	11	26	1.4	**No dramatic change**	26	0	100.0	Memb only	348	2
≥ 2 unique peptides	rrnAC2840	Q5UYR1_HALMA	*ahcY*	Adenosylhomocysteinase (EC 3.3.1.1) (AdoHcyase) (S-adenosyl-L-homocysteine hydrolase)	0	0	15	7	0	0	11	9	15	11	26	1.4	**No dramatic change**	0	26	0.0	Soluble only	425	0
≥ 2 unique peptides	rrnAC3005	Q5UYC1_HALMA	*cobH*	Precorrin-3B C17-methyltransferase (EC 2.1.1.131)	0	0	14	5	0	0	12	4	14	12	26	1.2	**No dramatic change**	0	26	0.0	Soluble only	332	0
≥ 2 unique peptides	rrnAC2663	Q5UZ62_HALMA	*lysC*	Aspartokinase (EC 2.7.2.4)	0	0	14	3	0	0	12	6	14	12	26	1.2	**No dramatic change**	0	26	0.0	Soluble only	391	0
≥ 2 unique peptides	rrnAC0246	Q5V599_HALMA	*folP3*	Dihydropteroate synthase (EC 2.5.1.15)	0	0	11	5	1	1	14	10	11	15	26	0.7	**No dramatic change**	1	25	3.8	Soluble predominant	385	0
≥ 2 unique peptides	rrnAC0239	Q5V5A5_HALMA	*mer2*	N5N10-methylenetetrahydromethanopterin reductase	0	0	11	7	0	0	15	10	11	15	26	0.7	**No dramatic change**	0	26	0.0	Soluble only	369	0
≥ 2 unique peptides	rrnAC3036	Q5UY93_HALMA	*aldY3*	Aldehyde dehydrogenase	0	0	10	5	0	0	16	8	10	16	26	0.6	**No dramatic change**	0	26	0.0	Soluble only	481	0
≥ 2 unique peptides	rrnAC1729	SYV_HALMAReview	*valS*	Valyl-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase) (ValRS)	0	0	8	5	0	0	18	10	8	18	26	0.4	1.2 (2~3X)	0	26	0.0	Soluble only	901	0
≥ 2 unique peptides	rrnAC1929	IF5A_HALMAReview	*eif5a*	Translation initiation factor 5A (eIF-5A) (Hypusine-containingprotein)	0	0	13	5	0	0	13	4	13	13	26	1.0	**No dramatic change**	0	26	0.0	Soluble only	126	0
≥ 2 unique peptides	rrnAC3537	Q5UWZ9_HALMA	*mnhE*	Na/H antiporter subunit	16	8	0	0	10	5	0	0	16	10	26	1.6	**No dramatic change**	26	0	100.0	Memb only	226	2
≥ 2 unique peptides	rrnAC2721	Q5UZ15_HALMA	*cat*	Cation efflux protein	16	4	0	0	10	5	0	0	16	10	26	1.6	**No dramatic change**	26	0	100.0	Memb only	323	5
≥ 2 unique peptides	rrnAC3517	Q5UX17_HALMA	*rrnAC3517*	Hypothetical protein	13	5	0	0	12	4	0	0	13	12	25	1.1	**No dramatic change**	25	0	100.0	Memb only	772	15
≥ 2 unique peptides	rrnAC1802	Q5V1B1_HALMA	*rrnAC1802*	Hypothetical protein	12	5	0	0	13	4	0	0	12	13	25	0.9	**No dramatic change**	25	0	100.0	Memb only	198	3
≥ 2 unique peptides	rrnB0228	Q5UWE7_HALMA	*rrnB0228*	Hypothetical protein	11	2	0	0	14	2	0	0	11	14	25	0.8	**No dramatic change**	25	0	100.0	Memb only	415	0
≥ 2 unique peptides	rrnB0199	Q5UWH0_HALMA	*pdhB2*	Pyruvate dehydrogenase (EC 1.2.4.1)	5	4	17	5	0	0	3	2	22	3	25	7.3	0.7 (>3X)	5	20	20.0	Soluble predominant	338	0
≥ 2 unique peptides	rrnAC1017	Q5V3C0_HALMA	*lpg2*	LPS glycosyltransferase	17	8	0	0	8	7	0	0	17	8	25	2.1	0.7 (2>3X)	25	0	100.0	Memb only	353	0
≥ 2 unique peptides	rrnAC2408	Q5UZT1_HALMA	*hom*	Homoserine dehydrogenase (EC 1.1.1.3)	0	0	15	6	0	0	10	5	15	10	25	1.5	**No dramatic change**	0	25	0.0	Soluble only	314	0
≥ 2 unique peptides	rrnAC1497	Q5V233_HALMA	*nifS*	Selenocysteine lyase (EC 4.4.1.16)	0	0	14	7	0	0	11	5	14	11	25	1.3	**No dramatic change**	0	25	0.0	Soluble only	568	0
≥ 2 unique peptides	rrnAC0340	Q5V514_HALMA	*ipmD*	3-isopropylmalate dehydrogenase (EC 1.1.1.85)	0	0	10	4	0	0	15	6	10	15	25	0.7	**No dramatic change**	0	25	0.0	Soluble only	327	0
≥ 2 unique peptides	rrnAC2181	Q5V0D0_HALMA	*pepB2*	Aminopeptidase	0	0	8	5	0	0	17	6	8	17	25	0.5	1.2 (2~3X)	0	25	0.0	Soluble only	408	0
≥ 2 unique peptides	rrnAC1417	RLA0_HALMAReview	*rplP0*	50S ribosomal protein L10E (Ribosomal protein L10) (Acidic ribosomalprotein P0 homolog) (L10E) (HMal10)	0	0	17	7	3	1	5	3	17	8	25	2.1	0.7 (2>3X)	3	22	12.0	Soluble predominant	348	0
≥ 2 unique peptides	pNG5052	Q5V7K5_HALMA	*usp8*	Universal stress protein	4	3	8	4	6	4	7	4	12	13	25	0.9	**No dramatic change**	10	15	40.0	Memb + Sol	138	0
≥ 2 unique peptides	rrnB0321	Q5UW68_HALMA	*phnE*	Phosphonates ABC tranporter permease protein	22	4	0	0	3	2	0	0	22	3	25	7.3	0.7 (>3X)	25	0	100.0	Memb only	271	5
≥ 2 unique peptides	rrnAC1765	Q5V1E0_HALMA	*tenA*	Transcriptional activator tenA	0	0	3	1	1	1	20	6	3	21	24	0.1	1.2 (>3X)	1	23	4.2	Soluble predominant	219	0
≥ 2 unique peptides	rrnAC3311	Q5UXK1_HALMA	*rrnAC3311*	Hypothetical protein	0	0	13	5	0	0	11	6	13	11	24	1.2	**No dramatic change**	0	24	0.0	Soluble only	537	0
≥ 2 unique peptides	rrnAC0733	Q5V426_HALMA	*rrnAC0733*	Rieske [2Fe-2S] domain protein	12	6	0	0	12	6	0	0	12	12	24	1.0	**No dramatic change**	24	0	100.0	Memb only	288	0
≥ 2 unique peptides	rrnAC1430	Q5V295_HALMA	*fbr2*	Cytochrome-like protein	12	2	0	0	12	2	0	0	12	12	24	1.0	**No dramatic change**	24	0	100.0	Memb only	147	0
≥ 2 unique peptides	rrnAC0023	Q5V5U5_HALMA	*gatE*	Glutamyl-tRNA(Gln) amidotransferase subunit E (EC 6.3.5.-)	0	0	12	6	0	0	12	6	12	12	24	1.0	**No dramatic change**	0	24	0.0	Soluble only	623	0
≥ 2 unique peptides	rrnAC0128	Q5V5K2_HALMA	*sdr*	Short chain dehydrogenase	0	0	10	5	0	0	14	7	10	14	24	0.7	**No dramatic change**	0	24	0.0	Soluble only	234	0
≥ 2 unique peptides	rrnAC2906	Q5UYK5_HALMA	*htpX1*	Probable protease htpX-like (EC 3.4.24.-)	13	5	0	0	11	5	0	0	13	11	24	1.2	**No dramatic change**	24	0	100.0	Memb only	292	4
≥ 2 unique peptides	rrnAC2047	Q5V0P9_HALMA	*sppA*	Protease IV-like (EC 3.4.21.-)	11	4	0	0	13	5	0	0	11	13	24	0.8	**No dramatic change**	24	0	100.0	Memb only	319	1
≥ 2 unique peptides	rrnAC2261	Q5V062_HALMA	*pepB1*	Aminopeptidase	0	0	8	4	0	0	16	5	8	16	24	0.5	1.2 (2~3X)	0	24	0.0	Soluble only	341	0
≥ 2 unique peptides	rrnAC1856	Q5V162_HALMA	*rrnAC1856*	Putative RNA binding protein	13	6	0	0	11	5	0	0	13	11	24	1.2	**No dramatic change**	24	0	100.0	Memb only	394	1
≥ 2 unique peptides	rrnB0315	Q5UW74_HALMA	*msmX-3*	Sugar ABC transporter ATP-binding protein	0	0	0	0	24	10	0	0	0	24	24	0.0	1.2 only	24	0	100.0	Memb only	379	0
≥ 2 unique peptides	rrnAC0436	Q5V4T2_HALMA	*traB*	Putative plasmid transfer protein	11	5	0	0	13	6	0	0	11	13	24	0.8	**No dramatic change**	24	0	100.0	Memb only	534	6
≥ 2 unique peptides	rrnAC0807	Q5V3V9_HALMA	*cdc48c*	Cell division control protein 48	0	0	11	7	0	0	12	8	11	12	23	0.9	**No dramatic change**	0	23	0.0	Soluble only	705	0
≥ 2 unique peptides	rrnB0156	Q5UWK8_HALMA	*rrnB0156*	Sensor protein (EC 2.7.13.3)	19	7	0	0	4	4	0	0	19	4	23	4.8	0.7 (>3X)	23	0	100.0	Memb only	964	2
≥ 2 unique peptides	rrnAC3456	Q5UX70_HALMA	*bcp1*	Bacterioferritin comigrating protein	0	0	7	1	0	0	16	2	7	16	23	0.4	1.2 (2~3X)	0	23	0.0	Soluble only	157	0

≥ 2 unique peptides	rrnAC0961	Q5V3H0_HALMA	*rrnAC0961*	Hypothetical protein	15	6	0	0	8	5	0	0	15	8	23	1.9	**No dramatic change**	23	0	100.0	Memb only	274	2
≥ 2 unique peptides	rrnAC0955	Q5V3H6_HALMA	*rrnAC0955*	Hypothetical protein	11	7	0	0	12	7	0	0	11	12	23	0.9	**No dramatic change**	23	0	100.0	Memb only	560	6
≥ 2 unique peptides	pNG7140	Q5V6K2_HALMA	*pNG7140*	Hypothetical protein	0	0	11	5	0	0	12	6	11	12	23	0.9	**No dramatic change**	0	23	0.0	Soluble only	149	0
≥ 2 unique peptides	pNG4050	Q5V7X2_HALMA	*pNG4050*	Hypothetical protein	4	1	6	4	3	1	10	5	10	13	23	0.8	**No dramatic change**	7	16	30.4	Memb + Sol	265	0
≥ 2 unique peptides	rrnAC2085	Q5V0L5_HALMA	*rrnAC2085*	Hypothetical protein	2	1	6	1	4	1	11	5	8	15	23	0.5	**No dramatic change**	6	17	26.1	Memb + Sol	173	0
≥ 2 unique peptides	rrnAC0365	Q5V4Z3_HALMA	*asd*	Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)	0	0	14	5	0	0	9	4	14	9	23	1.6	**No dramatic change**	0	23	0.0	Soluble only	345	0
≥ 2 unique peptides	rrnAC1451	Q5V275_HALMA	*nolD*	NADH dehydrogenase/oxidoreductase-like protein	10	3	0	0	13	3	0	0	10	13	23	0.8	**No dramatic change**	23	0	100.0	Memb only	153	0
≥ 2 unique peptides	rrnAC0272	HISX_HALMAReview	*hisD*	Histidinol dehydrogenase (EC 1.1.1.23) (HDH)	0	0	10	6	0	0	13	7	10	13	23	0.8	**No dramatic change**	0	23	0.0	Soluble only	422	0
≥ 2 unique peptides	rrnAC0423	Q5V4U5_HALMA	*rrnAC0423*	Arylsulfatase	6	5	3	3	10	7	4	3	9	14	23	0.6	**No dramatic change**	16	7	69.6	Memb + Sol	444	0
≥ 2 unique peptides	rrnB0238	Q5UWD9_HALMA	*hbd3*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	3	3	6	3	1	1	13	4	9	14	23	0.6	**No dramatic change**	4	19	17.4	Soluble predominant	295	0
≥ 2 unique peptides	rrnAC2776	Q5UYW8_HALMA	*matE2*	Multi antimicrobial extrusion drug/sodium antiporters	17	5	0	0	6	2	0	0	17	6	23	2.8	0.7 (2>3X)	23	0	100.0	Memb only	419	10
≥ 2 unique peptides	rrnAC2464	Q5UZN2_HALMA	*livF-6*	Branched-chain amino acid ABC transporter ATP-binding protein	11	3	0	0	11	3	1	1	11	12	23	0.9	**No dramatic change**	22	1	95.7	Memb predominant	240	0
≥ 2 unique peptides	rrnAC3132	Q5UY13_HALMA	*livK-2*	Branched-chain amino acid ABC transporter amino acid-bindingprotein	10	3	0	0	13	3	0	0	10	13	23	0.8	**No dramatic change**	23	0	100.0	Memb only	472	0
≥ 2 unique peptides	rrnB0314	Q5UW75_HALMA	*ugpE*	Sn-glycerol-3-phosphate transport system permease	0	0	0	0	23	6	0	0	0	23	23	0.0	1.2 only	23	0	100.0	Memb only	307	6
≥ 2 unique peptides	rrnAC2116	Q5V0I6_HALMA	*uvrA*	Excinuclease ABC subunit A	0	0	14	12	0	0	8	7	14	8	22	1.8	**No dramatic change**	0	22	0.0	Soluble only	992	0
≥ 2 unique peptides	rrnAC3185	Q5UXW3_HALMA	*rrnAC3185*	Hypothetical protein	14	5	0	0	8	5	0	0	14	8	22	1.8	**No dramatic change**	22	0	100.0	Memb only	115	1
≥ 2 unique peptides	rrnB0304	Q5UW84_HALMA	*rrnB0304*	Hypothetical protein	14	6	0	0	8	3	0	0	14	8	22	1.8	**No dramatic change**	22	0	100.0	Memb only	359	4
≥ 2 unique peptides	rrnAC2729	Q5UZ09_HALMA	*rrnAC2729*	Hypothetical protein	13	3	0	0	9	3	0	0	13	9	22	1.4	**No dramatic change**	22	0	100.0	Memb only	124	2
≥ 2 unique peptides	rrnAC2492	Q5UZK7_HALMA	*rrnAC2492*	Hypothetical protein	12	3	0	0	10	3	0	0	12	10	22	1.2	**No dramatic change**	22	0	100.0	Memb only	91	0
≥ 2 unique peptides	rrnAC1151	Q5V300_HALMA	*rrnAC1151*	Hypothetical protein	12	2	0	0	10	2	0	0	12	10	22	1.2	**No dramatic change**	22	0	100.0	Memb only	58	2
≥ 2 unique peptides	rrnAC3454	Q5UX72_HALMA	*rrnAC3454*	Hypothetical protein	0	0	11	4	0	0	11	6	11	11	22	1.0	**No dramatic change**	0	22	0.0	Soluble only	336	0
≥ 2 unique peptides	rrnAC2050	Q5V0P6_HALMA	*rrnAC2050*	Hypothetical protein	0	0	8	4	0	0	14	4	8	14	22	0.6	**No dramatic change**	0	22	0.0	Soluble only	108	0
≥ 2 unique peptides	rrnAC2334	Q5UZZ6_HALMA	*glcD2*	Putative oxidoreductase	16	9	0	0	6	2	0	0	16	6	22	2.7	0.7 (2>3X)	22	0	100.0	Memb only	1021	0
≥ 2 unique peptides	rrnAC1231	Q5V2S7_HALMA	*ilvA1*	Threonine dehydratase (EC 4.3.1.19)	2	1	10	6	3	1	7	4	12	10	22	1.2	**No dramatic change**	5	17	22.7	Soluble predominant	342	0
≥ 2 unique peptides	rrnAC0192	Q5V5E7_HALMA	*purB*	Adenylosuccinate lyase (EC 4.3.2.2)	0	0	11	6	0	0	11	6	11	11	22	1.0	**No dramatic change**	0	22	0.0	Soluble only	460	0
≥ 2 unique peptides	rrnAC0489	Q5V4N8_HALMA	*pip*	Putative intracellular protease (EC 3.2.-.-)	0	0	11	4	0	0	11	3	11	11	22	1.0	**No dramatic change**	0	22	0.0	Soluble only	196	0
≥ 2 unique peptides	rrnAC3151	Q5UXZ5_HALMA	*ubiE1*	Ubiquinone/menaquinone biosynthesis methyltransferase	9	2	1	1	8	2	4	1	10	12	22	0.8	**No dramatic change**	17	5	77.3	Memb predominant	206	0
≥ 2 unique peptides	rrnAC2369	PDXT_HALMAReview	*pdxT*	Glutamine amidotransferase subunit pdxT (EC 2.6.-.-) (Glutamineamidotransferase glutaminase subunit pdxT)	0	0	10	4	0	0	12	5	10	12	22	0.8	**No dramatic change**	0	22	0.0	Soluble only	197	0
≥ 2 unique peptides	rrnAC2610	Q5UZA4_HALMA	*hemB*	Delta-aminolevulinic acid dehydratase (EC 4.2.1.24)	0	0	10	3	0	0	12	5	10	12	22	0.8	**No dramatic change**	0	22	0.0	Soluble only	326	0
≥ 2 unique peptides	rrnAC3183	SYH_HALMAReview	*hisS*	Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)(HisRS)	0	0	9	4	0	0	13	7	9	13	22	0.7	**No dramatic change**	0	22	0.0	Soluble only	435	0
≥ 2 unique peptides	pNG7289	Q5V666_HALMA	*adh6*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	0	0	9	4	0	0	13	6	9	13	22	0.7	**No dramatic change**	0	22	0.0	Soluble only	338	0
≥ 2 unique peptides	rrnAC1490	Q5V239_HALMA	*cadT*	Cobalamin adenosyltransferase	0	0	9	4	0	0	13	4	9	13	22	0.7	**No dramatic change**	0	22	0.0	Soluble only	178	0
≥ 2 unique peptides	rrnAC1289	Q5V2M6_HALMA	*rrnAC1289*	Chelatase	0	0	8	2	1	1	13	4	8	14	22	0.6	**No dramatic change**	1	21	4.5	Soluble predominant	293	0
≥ 2 unique peptides	rrnAC0543	SYY_HALMAReview	*tyrS*	Tyrosyl-tRNA synthetase (EC 6.1.1.1) (Tyrosine--tRNA ligase) (TyrRS)	0	0	8	6	0	0	14	7	8	14	22	0.6	**No dramatic change**	0	22	0.0	Soluble only	346	0
≥ 2 unique peptides	rrnAC0855	Q5V3R6_HALMA	*galE4*	UDP-glucose 4-epimerase (EC 5.1.3.2)	0	0	7	4	0	0	15	7	7	15	22	0.5	1.2 (2~3X)	0	22	0.0	Soluble only	308	0
≥ 2 unique peptides	rrnAC1925	Q5V106_HALMA	*mhpC*	2-hydroxy-6-ketonona-24-dienedioic acid hydrolase (EC 3.7.1.-)	5	4	0	0	17	9	0	0	5	17	22	0.3	1.2 (>3X)	22	0	100.0	Memb only	349	0
≥ 2 unique peptides	rrnAC3170	Q5UXX7_HALMA	*rrnAC3170*	M50 metallopeptidase	11	4	0	0	11	5	0	0	11	11	22	1.0	**No dramatic change**	22	0	100.0	Memb only	588	7
≥ 2 unique peptides	rrnAC2488	RS24_HALMAReview	*rps24e*	30S ribosomal protein S24e (HS15) (E1.2)	1	1	15	6	2	1	4	4	16	6	22	2.7	0.7 (2>3X)	3	19	13.6	Soluble predominant	102	0
≥ 2 unique peptides	rrnAC1606	RL22_HALMAReview	*rpl22p*	50S ribosomal protein L22P (Hmal22) (Hl23)	5	2	7	3	10	5	0	0	12	10	22	1.2	**No dramatic change**	15	7	68.2	Memb + Sol	155	0
≥ 2 unique peptides	rrnAC2827	IF2G_HALMAReview	*eif2g*	Translation initiation factor 2 gamma subunit (eIF-2-gamma) (aIF2-gamma)	0	0	11	5	0	0	11	7	11	11	22	1.0	**No dramatic change**	0	22	0.0	Soluble only	409	0
≥ 2 unique peptides	rrnAC2072	Q5V0M7_HALMA	*vacB*	Ribonuclease R (EC 3.1.-.-)	0	0	10	6	0	0	12	8	10	12	22	0.8	**No dramatic change**	0	22	0.0	Soluble only	457	0
≥ 2 unique peptides	rrnAC2710	Q5UZ25_HALMA	*gbp3*	GTP-binding proteinlike	16	9	0	0	6	3	0	0	16	6	22	2.7	0.7 (2>3X)	22	0	100.0	Memb only	213	0
≥ 2 unique peptides	rrnAC1505	PSTB1_HALMAReview	*pstB1*	Phosphate import ATP-binding protein pstB 1 (EC 3.6.3.27) (Phosphate-transporting ATPase 1) (ABC phosphate transporter 1)	18	4	0	0	4	3	0	0	18	4	22	4.5	0.7 (>3X)	22	0	100.0	Memb only	299	0
≥ 2 unique peptides	rrnAC2349	Q5UZY4_HALMA	*malE1*	Maltose ABC transporter maltose-binding protein	11	4	0	0	11	4	0	0	11	11	22	1.0	**No dramatic change**	22	0	100.0	Memb only	426	0
≥ 2 unique peptides	rrnAC2965	Q5UYF5_HALMA	*trpS*	Tryptophanyl-tRNA synthetase (EC 6.1.1.2)	0	0	11	4	0	0	11	6	11	11	22	1.0	**No dramatic change**	0	22	0.0	Soluble only	549	0
≥ 2 unique peptides	rrnAC2154	Q5V0F5_HALMA	*rrnAC2154*	Hypothetical protein	11	3	0	0	10	5	0	0	11	10	21	1.1	**No dramatic change**	21	0	100.0	Memb only	137	1
≥ 2 unique peptides	rrnAC3269	Q5UXN8_HALMA	*rrnAC3269*	Hypothetical protein	0	0	11	4	0	0	10	4	11	10	21	1.1	**No dramatic change**	0	21	0.0	Soluble only	84	0
≥ 2 unique peptides	rrnAC0856	Q5V3R5_HALMA	*rrnAC0856*	Hypothetical protein	10	6	0	0	11	5	0	0	10	11	21	0.9	**No dramatic change**	21	0	100.0	Memb only	222	0
≥ 2 unique peptides	rrnAC1348	Q5V2H3_HALMA	*rrnAC1348*	Hypothetical protein	0	0	10	2	1	1	10	2	10	11	21	0.9	**No dramatic change**	1	20	4.8	Soluble predominant	82	0
≥ 2 unique peptides	rrnAC1032	Q5V3A5_HALMA	*rrnAC1032*	Hypothetical protein	9	4	0	0	12	5	0	0	9	12	21	0.8	**No dramatic change**	21	0	100.0	Memb only	337	5
≥ 2 unique peptides	rrnAC0117	Q5V5L0_HALMA	*rrnAC0117*	Hypothetical protein	9	4	0	0	12	5	0	0	9	12	21	0.8	**No dramatic change**	21	0	100.0	Memb only	99	0
≥ 2 unique peptides	rrnAC1350	Q5V2H1_HALMA	*gtr-4*	Putative sugar transferase	15	6	0	0	6	3	0	0	15	6	21	2.5	0.7 (2>3X)	21	0	100.0	Memb only	396	0
≥ 2 unique peptides	rrnAC1186	Q5V2W7_HALMA	*moaE*	Molybdenum cofactor biosynthesis protein	0	0	12	8	0	0	9	7	12	9	21	1.3	**No dramatic change**	0	21	0.0	Soluble only	275	0
≥ 2 unique peptides	rrnAC3062	Q5UY73_HALMA	*moxR5*	Methanol dehydrogenase regulatory protein	4	3	6	4	5	4	6	3	10	11	21	0.9	**No dramatic change**	9	12	42.9	Memb + Sol	343	0

≥ 2 unique peptides	rrnAC0085	SYE_HALMAReview	*gltX*	Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)(GluRS)	0	0	10	6	0	0	11	5	10	11	21	0.9	**No dramatic change**	0	21	0.0	Soluble only	579	0
≥ 2 unique peptides	rrnAC2949	Q5UYH0_HALMA	*hsp20a*	Small heat shock protein	1	1	10	3	3	2	7	3	11	10	21	1.1	**No dramatic change**	4	17	19.0	Soluble predominant	135	0
≥ 2 unique peptides	rrnAC2357	RL10_HALMAReview	*rpl10e*	50S ribosomal protein L10e	14	7	0	0	7	3	0	0	14	7	21	2.0	0.7 (2>3X)	21	0	100.0	Memb only	177	0
≥ 2 unique peptides	rrnAC2212	RS6E_HALMAReview	*rps6e*	30S ribosomal protein S6e (HS13)	0	0	14	5	0	0	7	4	14	7	21	2.0	0.7 (2>3X)	0	21	0.0	Soluble only	129	0
≥ 2 unique peptides	rrnAC1511	RS8E_HALMAReview	*rps8e*	30S ribosomal protein S8e (HS23)	3	1	9	5	9	5	0	0	12	9	21	1.3	**No dramatic change**	12	9	57.1	Memb + Sol	123	0
≥ 2 unique peptides	rrnAC3512	IF2A_HALMAReview	*eif2a*	Translation initiation factor 2 alpha subunit (eIF-2-alpha) (aIF2-alpha)	0	0	8	2	0	0	13	4	8	13	21	0.6	**No dramatic change**	0	21	0.0	Soluble only	266	0
≥ 2 unique peptides	rrnAC0700	SECE_HALMAReview	*secE*	Preprotein translocase subunit secE (Protein transport protein SEC61gamma subunit homolog)	12	2	0	0	9	2	0	0	12	9	21	1.3	**No dramatic change**	21	0	100.0	Memb only	59	1
≥ 2 unique peptides	pNG6079	Q5V738_HALMA	*czcD*	Cation efflux system protein	10	3	0	0	11	3	0	0	10	11	21	0.9	**No dramatic change**	21	0	100.0	Memb only	311	6
≥ 2 unique peptides	rrnAC0933	Q5V3J6_HALMA	*argK*	ArgK protein	0	0	9	4	0	0	12	7	9	12	21	0.8	**No dramatic change**	0	21	0.0	Soluble only	352	0
≥ 2 unique peptides	rrnAC2818	Q5UYS9_HALMA	*ftsH*	Cell division protein FtsH (EC 3.4.24.-)	2	2	11	7	0	0	7	6	13	7	20	1.9	**No dramatic change**	2	18	10.0	Soluble predominant	492	0
≥ 2 unique peptides	rrnAC2179	Q5V0D2_HALMA	*fer2*	2Fe-2S iron-sulfur cluster binding domain	9	3	0	0	11	3	0	0	9	11	20	0.8	**No dramatic change**	20	0	100.0	Memb only	194	0
≥ 2 unique peptides	rrnAC1696	Q5V1J9_HALMA	*rrnAC1696*	Hypothetical protein	14	7	0	0	6	3	0	0	14	6	20	2.3	0.7 (2>3X)	20	0	100.0	Memb only	618	7
≥ 2 unique peptides	rrnAC1219	Q5V2T9_HALMA	*rrnAC1219*	Hypothetical protein	14	7	0	0	6	3	0	0	14	6	20	2.3	0.7 (2>3X)	20	0	100.0	Memb only	788	2
≥ 2 unique peptides	rrnAC1481	Q5V246_HALMA	*rrnAC1481*	Hypothetical protein	0	0	10	6	0	0	10	6	10	10	20	1.0	**No dramatic change**	0	20	0.0	Soluble only	364	0
≥ 2 unique peptides	pNG7051	Q5V6T2_HALMA	*pNG7051*	Hypothetical protein	8	3	0	0	12	4	0	0	8	12	20	0.7	**No dramatic change**	20	0	100.0	Memb only	441	8
≥ 2 unique peptides	rrnAC0383	Q5V4X7_HALMA	*arg2*	Arginase (EC 3.5.3.1)	0	0	16	8	0	0	4	3	16	4	20	4.0	0.7 (>3X)	0	20	0.0	Soluble only	315	0
≥ 2 unique peptides	rrnAC1356	Q5V2G5_HALMA	*gatC*	Glutamyl-tRNA(Gln) amidotransferase subunit C (EC 6.3.5.-)	0	0	9	4	0	0	11	5	9	11	20	0.8	**No dramatic change**	0	20	0.0	Soluble only	92	0
≥ 2 unique peptides	rrnAC1789	Q5V1C2_HALMA	*hutG*	Probable formimidoylglutamase (EC 3.5.3.8)	0	0	9	3	0	0	11	3	9	11	20	0.8	**No dramatic change**	0	20	0.0	Soluble only	307	0
≥ 2 unique peptides	rrnAC1960	Q5V0X5_HALMA	*graD4b*	Glucose-1-phosphate thymidylyltransferase	0	0	7	4	0	0	13	5	7	13	20	0.5	**No dramatic change**	0	20	0.0	Soluble only	314	0
≥ 2 unique peptides	rrnAC2701	Q5UZ33_HALMA	*glyS*	Glycyl-tRNA synthetase (EC 6.1.1.14)	0	0	6	4	0	0	14	9	6	14	20	0.4	1.2 (2~3X)	0	20	0.0	Soluble only	614	0
≥ 2 unique peptides	rrnAC0517	Q5V4L5_HALMA	*alaS2*	Alanyl-tRNA synthetase (EC 6.1.1.7)	0	0	6	4	0	0	14	8	6	14	20	0.4	1.2 (2~3X)	0	20	0.0	Soluble only	419	0
≥ 2 unique peptides	rrnB0243	Q5UWD5_HALMA	*paaK1*	Phenylacetyl-coenzyme A ligase	0	0	5	4	0	0	15	10	5	15	20	0.3	1.2 (>3X)	0	20	0.0	Soluble only	429	0
≥ 2 unique peptides	rrnAC3190	Q5UXV8_HALMA	*pan1*	Proteasome-activating nucleotidase 1	0	0	12	5	1	1	7	5	12	8	20	1.5	**No dramatic change**	1	19	5.0	Soluble predominant	406	0
≥ 2 unique peptides	pNG7253	Q5V698_HALMA	*rbsC-1*	Sugar ABC transporter permease protein	12	3	0	0	8	3	0	0	12	8	20	1.5	**No dramatic change**	20	0	100.0	Memb only	366	8
≥ 2 unique peptides	rrnAC2565	RFCS_HALMAReview	*rfcS*	Replication factor C small subunit (RFC small subunit) (Clamp loadersmall subunit)	0	0	12	7	0	0	7	4	12	7	19	1.7	**No dramatic change**	0	19	0.0	Soluble only	325	0
≥ 2 unique peptides	rrnAC2779	Q5UYW6_HALMA	*asnC1*	Transcription regulator AsnC family	0	0	10	6	0	0	9	6	10	9	19	1.1	**No dramatic change**	0	19	0.0	Soluble only	152	0
≥ 2 unique peptides	rrnAC3290	Q5UXL9_HALMA	*trh5*	Transcription regulator	0	0	9	6	0	0	10	6	9	10	19	0.9	**No dramatic change**	0	19	0.0	Soluble only	76	0
≥ 2 unique peptides	rrnAC0801	Q5V3W4_HALMA	*rrnAC0801*	Hypothetical protein	11	3	4	2	4	2	0	0	15	4	19	3.8	0.7 (>3X)	15	4	78.9	Memb predominant	356	0
≥ 2 unique peptides	rrnAC2884	Q5UYM2_HALMA	*rrnAC2884*	Hypothetical protein	11	4	0	0	8	4	0	0	11	8	19	1.4	**No dramatic change**	19	0	100.0	Memb only	185	0
≥ 2 unique peptides	rrnAC1035	Q5V3A2_HALMA	*rrnAC1035*	Hypothetical protein	9	2	0	0	9	2	1	1	9	10	19	0.9	**No dramatic change**	18	1	94.7	Memb predominant	565	1
≥ 2 unique peptides	pNG7131	Q5V6L0_HALMA	*pNG7131*	Hypothetical protein	0	0	9	2	0	0	10	3	9	10	19	0.9	**No dramatic change**	0	19	0.0	Soluble only	146	0
≥ 2 unique peptides	rrnAC0399	Q5V4W6_HALMA	*rrnAC0399*	Hypothetical protein	0	0	8	5	0	0	11	5	8	11	19	0.7	**No dramatic change**	0	19	0.0	Soluble only	365	0
≥ 2 unique peptides	rrnB0175	Q5UWJ2_HALMA	*imd2*	Inosine monophosphate dehydrogenase (EC 1.1.1.205)	13	5	0	0	6	4	0	0	13	6	19	2.2	0.7 (2>3X)	19	0	100.0	Memb only	356	3
≥ 2 unique peptides	rrnAC2912	Q5UYK1_HALMA	*gsp*	General stress protein 69	0	0	12	5	0	0	7	6	12	7	19	1.7	**No dramatic change**	0	19	0.0	Soluble only	350	0
≥ 2 unique peptides	rrnAC3003	Q5UYC3_HALMA	*cbiG*	Cobalamin biosynthesis protein G	0	0	12	6	0	0	7	4	12	7	19	1.7	**No dramatic change**	0	19	0.0	Soluble only	323	0
≥ 2 unique peptides	rrnAC0124	Q5V5K5_HALMA	*aroC*	Chorismate synthase (EC 4.2.3.5) (5-enolpyruvylshikimate-3-phosphatephospholyase)	0	0	12	4	0	0	7	4	12	7	19	1.7	**No dramatic change**	0	19	0.0	Soluble only	399	0
≥ 2 unique peptides	rrnAC2628	GSA_HALMAReview	*hemL*	Glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) (GSA)(Glutamate-1-semialdehyde aminotransferase) (GSA-AT)	0	0	10	6	0	0	9	4	10	9	19	1.1	**No dramatic change**	0	19	0.0	Soluble only	445	0
≥ 2 unique peptides	rrnAC2471	Q5UZM6_HALMA	*yusM*	Proline dehydrogenase	2	2	7	6	5	4	5	3	9	10	19	0.9	**No dramatic change**	7	12	36.8	Memb + Sol	278	0
≥ 2 unique peptides	rrnAC2950	Q5UYG9_HALMA	*pheA*	Prephenate dehydratase (EC 4.2.1.51)	0	0	9	5	0	0	10	6	9	10	19	0.9	**No dramatic change**	0	19	0.0	Soluble only	271	0
≥ 2 unique peptides	rrnAC0207	DAPA_HALMAReview	*dapA*	Dihydrodipicolinate synthase (EC 4.2.1.52) (DHDPS)	0	0	9	5	0	0	10	5	9	10	19	0.9	**No dramatic change**	0	19	0.0	Soluble only	306	0
≥ 2 unique peptides	rrnAC1446	Q5V280_HALMA	*purE*	Phosphoribosylaminoimidazole carboxylase catalytic subunit(EC 4.1.1.21)	0	0	8	6	0	0	11	6	8	11	19	0.7	**No dramatic change**	0	19	0.0	Soluble only	216	0
≥ 2 unique peptides	rrnAC1879	Q5V143_HALMA	*aroB*	3-dehydroquinate synthase (EC 4.2.3.4)	0	0	7	6	0	0	12	6	7	12	19	0.6	**No dramatic change**	0	19	0.0	Soluble only	388	0
≥ 2 unique peptides	rrnAC0261	EF1B_HALMAReview	*ef1b*	Elongation factor 1-beta (EF-1-beta) (aEF-1beta)	0	0	13	4	0	0	6	2	13	6	19	2.2	0.7 (2>3X)	0	19	0.0	Soluble only	88	0
≥ 2 unique peptides	rrnAC0758	Q5V403_HALMA	*usp17*	Universal stress protein	3	2	4	3	5	2	7	3	7	12	19	0.6	**No dramatic change**	8	11	42.1	Memb + Sol	151	0
≥ 2 unique peptides	rrnAC0754	Q5V407_HALMA	*trkA1*	Trk potassium uptake system protein	6	3	4	2	5	2	4	2	10	9	19	1.1	**No dramatic change**	11	8	57.9	Memb + Sol	227	0
≥ 2 unique peptides	rrnAC0251	Q5V594_HALMA	*yvrO-2*	ABC transporter ATP-binding protein	9	3	0	0	10	3	0	0	9	10	19	0.9	**No dramatic change**	19	0	100.0	Memb only	227	0
≥ 2 unique peptides	rrnAC0566	Q5V4H2_HALMA	*livK-1*	Branched chain amino acid ABC transporter branched chain amino acid-binding protein	6	4	0	0	13	5	0	0	6	13	19	0.5	1.2 (2~3X)	19	0	100.0	Memb only	470	0
≥ 2 unique peptides	rrnAC3284	Q5UXM5_HALMA	*ftsZ5*	Cell division protein	3	3	5	4	3	3	7	5	8	10	18	0.8	**No dramatic change**	6	12	33.3	Memb + Sol	393	0
≥ 2 unique peptides	rrnAC0185	Q5V5F3_HALMA	*rrnAC0185*	Hypothetical protein	12	4	0	0	6	3	0	0	12	6	18	2.0	0.7 (2>3X)	18	0	100.0	Memb only	238	1
≥ 2 unique peptides	rrnAC1168	Q5V2Y3_HALMA	*rrnAC1168*	Hypothetical protein	0	0	8	5	0	0	10	4	8	10	18	0.8	**No dramatic change**	0	18	0.0	Soluble only	480	0
≥ 2 unique peptides	rrnAC2373	Q5UZW4_HALMA	*rrnAC2373*	Hypothetical protein	0	0	6	3	0	0	12	3	6	12	18	0.5	1.2 (2~3X)	0	18	0.0	Soluble only	105	0
≥ 2 unique peptides	rrnB0006	Q5UWY2_HALMA	*rrnB0006*	Acetamidase/formamidase family protein	0	0	15	5	0	0	3	2	15	3	18	5.0	0.7 (>3X)	0	18	0.0	Soluble only	302	0
≥ 2 unique peptides	rrnB0257	Q5UWC3_HALMA	*citE2*	Citrate lyase beta chain (EC 4.1.3.6) (EC 4.1.2.20)	0	0	12	5	0	0	6	3	12	6	18	2.0	0.7 (2>3X)	0	18	0.0	Soluble only	295	0
≥ 2 unique peptides	rrnAC2741	Q5UYZ8_HALMA	*ywfD2*	Glucose dehydrogenase (EC 1.1.1.47)	0	0	12	4	0	0	6	4	12	6	18	2.0	0.7 (2>3X)	0	18	0.0	Soluble only	260	0

≥ 2 unique peptides	rrnAC3529	Q5UX07_HALMA	*rrnAC3529*	NADH-ubiquinone/plastoquinone	11	6	0	0	7	5	0	0	11	7	18	1.6	**No dramatic change**	18	0	100.0	Memb only	593	16
≥ 2 unique peptides	rrnAC3434	Q5UX90_HALMA	*udp1*	Uridine phosphorylase (EC 2.4.2.3)	0	0	11	5	0	0	7	2	11	7	18	1.6	**No dramatic change**	0	18	0.0	Soluble only	241	0
≥ 2 unique peptides	rrnAC0370	Q5V4Y9_HALMA	*lbp*	Leucine-binding protein	10	2	0	0	8	3	0	0	10	8	18	1.3	**No dramatic change**	18	0	100.0	Memb only	456	0
≥ 2 unique peptides	rrnAC1233	METK_HALMAReview	*mat*	S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionineadenosyltransferase) (AdoMet synthetase)	0	0	10	4	0	0	8	4	10	8	18	1.3	**No dramatic change**	0	18	0.0	Soluble only	400	0
≥ 2 unique peptides	rrnAC0267	Q5V578_HALMA	*imd1*	Inosine monophosphate dehydrogenase (EC 1.1.1.205)	0	0	10	3	0	0	8	2	10	8	18	1.3	**No dramatic change**	0	18	0.0	Soluble only	126	0
≥ 2 unique peptides	rrnAC3246	Q5UXQ9_HALMA	*sqdB*	UDP-sulfoquinovose synthase	0	0	8	5	0	0	10	5	8	10	18	0.8	**No dramatic change**	0	18	0.0	Soluble only	390	0
≥ 2 unique peptides	rrnAC1984	Q5V0V4_HALMA	*fabG4*	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)	0	0	8	3	0	0	10	5	8	10	18	0.8	**No dramatic change**	0	18	0.0	Soluble only	269	0
≥ 2 unique peptides	rrnAC0109	Q5V5L8_HALMA	*msrB*	Peptide methionine sulfoxide reductase msrB (EC 1.8.4.6)	0	0	7	4	0	0	11	4	7	11	18	0.6	**No dramatic change**	0	18	0.0	Soluble only	134	0
≥ 2 unique peptides	rrnAC1603	RS17_HALMAReview	*rps17p*	30S ribosomal protein S17P (HmaS17) (HS14)	0	0	10	5	1	1	7	4	10	8	18	1.3	**No dramatic change**	1	17	5.6	Soluble predominant	112	0
≥ 2 unique peptides	rrnAC2445	SUI1_HALMAReview	*sui1*	Protein translation factor SUI1 homolog	0	0	9	3	0	0	9	4	9	9	18	1.0	**No dramatic change**	0	18	0.0	Soluble only	97	0
≥ 2 unique peptides	pNG7169	Q5V6H7_HALMA	*nhaC4*	Na+/H+ antiporter	12	2	0	0	6	2	0	0	12	6	18	2.0	0.7 (2>3X)	18	0	100.0	Memb only	488	9
≥ 2 unique peptides	rrnAC0380	Q5V4Y0_HALMA	*glnP*	Glutamine-binding periplasmic protein of glutamine ABCtransporter	9	4	0	0	9	4	0	0	9	9	18	1.0	**No dramatic change**	18	0	100.0	Memb only	226	4
≥ 2 unique peptides	rrnAC3214	Q5UXT6_HALMA	*secF*	Protein-export membrane protein SecF	8	4	0	0	10	6	0	0	8	10	18	0.8	**No dramatic change**	18	0	100.0	Memb only	311	6
≥ 2 unique peptides	rrnAC2073	Q5V0M6_HALMA	*trp2*	ABC transporter ATP-binding protein	8	3	0	0	10	6	0	0	8	10	18	0.8	**No dramatic change**	18	0	100.0	Memb only	246	0
≥ 2 unique peptides	rrnAC1655	Q5V1N4_HALMA	*nosF-2*	ABC transporter ATP-binding protein	7	3	0	0	11	4	0	0	7	11	18	0.6	**No dramatic change**	18	0	100.0	Memb only	224	0
≥ 2 unique peptides	rrnAC3129	Q5UY15_HALMA	*livM-6*	Branched-chain amino acid ABC transporter permease protein	7	2	0	0	11	2	0	0	7	11	18	0.6	**No dramatic change**	18	0	100.0	Memb only	363	9
≥ 2 unique peptides	rrnAC0455	Q5V4R7_HALMA	*gyrA*	DNA gyrase subunit A (EC 5.99.1.3)	0	0	13	7	0	0	4	3	13	4	17	3.3	0.7 (>3X)	0	17	0.0	Soluble only	814	0
≥ 2 unique peptides	rrnAC0669	Q5V479_HALMA	*polX*	DNA polymerase IV	0	0	9	5	0	0	8	5	9	8	17	1.1	**No dramatic change**	0	17	0.0	Soluble only	578	0
≥ 2 unique peptides	rrnAC3443	Q5UX81_HALMA	*rrnAC3443*	Hypothetical protein	0	0	7	3	0	0	10	5	7	10	17	0.7	**No dramatic change**	0	17	0.0	Soluble only	199	0
≥ 2 unique peptides	rrnAC0430	Q5V4T8_HALMA	*exoM*	Succinoglycan biosynthesis protein	14	7	0	0	3	2	0	0	14	3	17	4.7	0.7 (>3X)	17	0	100.0	Memb only	324	1
≥ 2 unique peptides	rrnB0083	Q5UWR4_HALMA	*ski-1*	Putative 2-component system sensor kinase	13	3	0	0	4	1	0	0	13	4	17	3.3	0.7 (>3X)	17	0	100.0	Memb only	247	4
≥ 2 unique peptides	rrnAC1025	Q5V3B2_HALMA	*moxR6*	Methanol dehydrogenase regulatory protein	5	3	8	5	1	1	3	2	13	4	17	3.3	0.7 (>3X)	6	11	35.3	Memb + Sol	336	0
≥ 2 unique peptides	rrnAC1370	Q5V2F3_HALMA	*ccmF*	Cytochrome c-type biogenesis protein CcmF	9	5	0	0	8	5	0	0	9	8	17	1.1	**No dramatic change**	17	0	100.0	Memb only	788	15
≥ 2 unique peptides	rrnAC3046	Q5UY86_HALMA	*aspC2*	Aspartate aminotransferase	0	0	8	3	0	0	9	5	8	9	17	0.9	**No dramatic change**	0	17	0.0	Soluble only	381	0
≥ 2 unique peptides	rrnAC2486	Q5UZL2_HALMA	*nadE1*	NH(3)-dependent NAD(+) synthetase (EC 6.3.1.5)	0	0	8	4	0	0	9	4	8	9	17	0.9	**No dramatic change**	0	17	0.0	Soluble only	277	0
≥ 2 unique peptides	rrnAC2835	HIS1_HALMAReview	*hisG*	ATP phosphoribosyltransferase (EC 2.4.2.17) (ATP-PRTase) (ATP-PRT)	0	0	7	5	0	0	10	5	7	10	17	0.7	**No dramatic change**	0	17	0.0	Soluble only	282	0
≥ 2 unique peptides	rrnAC0191	Q5V5E8_HALMA	*adh3*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	0	0	6	3	1	1	10	4	6	11	17	0.5	**No dramatic change**	1	16	5.9	Soluble predominant	355	0
≥ 2 unique peptides	rrnAC1081	Q5V359_HALMA	*rffH1*	Glucose-1-phosphate thymidylyltransferase	0	0	6	3	0	0	11	6	6	11	17	0.5	**No dramatic change**	0	17	0.0	Soluble only	393	0
≥ 2 unique peptides	rrnAC3100	Y3100_HALMAReview	*rrnAC3100*	UPF0447 protein rrnAC3100	0	0	3	3	0	0	14	9	3	14	17	0.2	1.2 (>3X)	0	17	0.0	Soluble only	669	0
≥ 2 unique peptides	rrnAC1598	RL5_HALMAReview	*rpl5p*	50S ribosomal protein L5P (Hmal5) (Hl13)	8	3	5	1	3	1	1	1	13	4	17	3.3	0.7 (>3X)	11	6	64.7	Memb + Sol	177	0
≥ 2 unique peptides	rrnAC3164	RF1_HALMAReview	*prf1*	Peptide chain release factor subunit 1 (Translation termination factoraRF1)	0	0	11	6	0	0	6	4	11	6	17	1.8	**No dramatic change**	0	17	0.0	Soluble only	418	0
≥ 2 unique peptides	rrnAC1956	Q5V0X9_HALMA	*eif2BD2*	Translation initiation factor eIF-2B subunit delta	0	0	10	4	0	0	7	5	10	7	17	1.4	**No dramatic change**	0	17	0.0	Soluble only	283	0
≥ 2 unique peptides	rrnAC0402	Q5V4W4_HALMA	*usp15*	Universal stress protein	0	0	8	4	3	2	6	3	8	9	17	0.9	**No dramatic change**	3	14	17.6	Soluble predominant	149	0
≥ 2 unique peptides	rrnAC2111	SECG_HALMAReview	*secG*	Preprotein translocase secG subunit (Protein transport protein SEC61subunit beta homolog)	11	2	0	0	6	1	0	0	11	6	17	1.8	**No dramatic change**	17	0	100.0	Memb only	53	1
≥ 2 unique peptides	rrnAC0722	Q5V437_HALMA	*mop*	Molybdenum-pterin binding protein	0	0	9	2	0	0	8	2	9	8	17	1.1	**No dramatic change**	0	17	0.0	Soluble only	69	0
≥ 2 unique peptides	pNG5001	Q5V7G3_HALMA	*abcP-1*	ABC transporter permease protein	8	4	0	0	9	3	0	0	8	9	17	0.9	**No dramatic change**	17	0	100.0	Memb only	367	4
≥ 2 unique peptides	rrnAC1760	Q5V1E4_HALMA	*rrnAC1760*	Transporter possibly hexose	6	1	0	0	11	3	0	0	6	11	17	0.5	**No dramatic change**	17	0	100.0	Memb only	449	11
≥ 2 unique peptides	rrnAC0867	Q5V3Q4_HALMA	*rrnAC0867*	Transcription regulator	1	1	6	1	4	2	5	1	7	9	16	0.8	**No dramatic change**	5	11	31.3	Memb + Sol	187	0
≥ 2 unique peptides	pNG7172	Q5V6H4_HALMA	*pNG7172*	Hypothetical protein	11	6	0	0	5	4	0	0	11	5	16	2.2	0.7 (2>3X)	16	0	100.0	Memb only	356	0
≥ 2 unique peptides	rrnAC2098	Q5V0K4_HALMA	*rrnAC2098*	Hypothetical protein	0	0	10	7	0	0	6	6	10	6	16	1.7	**No dramatic change**	0	16	0.0	Soluble only	634	0
≥ 2 unique peptides	rrnAC1150	Q5V301_HALMA	*rrnAC1150*	Hypothetical protein	8	2	0	0	8	2	0	0	8	8	16	1.0	**No dramatic change**	16	0	100.0	Memb only	257	6
≥ 2 unique peptides	rrnAC0120	Q5V5K8_HALMA	*rrnAC0120*	Hypothetical protein	0	0	8	6	0	0	8	6	8	8	16	1.0	**No dramatic change**	0	16	0.0	Soluble only	250	0
≥ 2 unique peptides	rrnAC2546	Q5UZF8_HALMA	*rrnAC2546*	Hypothetical protein	6	2	0	0	10	2	0	0	6	10	16	0.6	**No dramatic change**	16	0	100.0	Memb only	285	7
≥ 2 unique peptides	rrnAC0171	Q5V5G5_HALMA	*rrnAC0171*	Hypothetical protein	0	0	4	3	0	0	12	7	4	12	16	0.3	1.2 (>3X)	0	16	0.0	Soluble only	359	0
≥ 2 unique peptides	rrnB0241	Q5UWD7_HALMA	*acaA*	Acyl carrier protein synthase (EC 2.3.1.41)	0	0	12	7	0	0	4	2	12	4	16	3.0	0.7 (>3X)	0	16	0.0	Soluble only	478	0
≥ 2 unique peptides	rrnAC1892	Q5V133_HALMA	*rrnAC1892*	DSBA-like thioredoxin domain	9	5	0	0	7	5	0	0	9	7	16	1.3	**No dramatic change**	16	0	100.0	Memb only	218	0
≥ 2 unique peptides	rrnAC1222	Q5V2T6_HALMA	*moxR4*	Methanol dehydrogenase regulatory protein	7	2	2	2	7	4	0	0	9	7	16	1.3	**No dramatic change**	14	2	87.5	Memb predominant	313	0
≥ 2 unique peptides	rrnAC0359	Q5V4Z7_HALMA	*rrnAC0359*	4-hydroxybenzoate 3-monooxygenase (EC 1.14.13.2)	8	5	0	0	8	6	0	0	8	8	16	1.0	**No dramatic change**	16	0	100.0	Memb only	452	0
≥ 2 unique peptides	rrnAC1489	Q5V240_HALMA	*dmd*	Diphosphomevalonate decarboxylase (EC 4.1.1.33)	1	1	7	4	0	0	8	4	8	8	16	1.0	**No dramatic change**	1	15	6.3	Soluble predominant	324	0
≥ 2 unique peptides	rrnAC3484	IDI_HALMAReview	*idi*	Isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) (IPP isomerase)(Isopentenyl pyrophosphate isomerase) (IPP:DMAPP isomerase)	0	0	7	4	0	0	9	6	7	9	16	0.8	**No dramatic change**	0	16	0.0	Soluble only	187	0
≥ 2 unique peptides	rrnAC0268	Q5V577_HALMA	*yrbE*	Oxidoreductase	0	0	7	4	0	0	9	5	7	9	16	0.8	**No dramatic change**	0	16	0.0	Soluble only	381	0
≥ 2 unique peptides	pNG6012	Q5V7D9_HALMA	*parA2*	Partition protein	0	0	7	2	0	0	9	4	7	9	16	0.8	**No dramatic change**	0	16	0.0	Soluble only	272	0
≥ 2 unique peptides	rrnAC1406	Q5V2B7_HALMA	*dph5*	Diphthine synthase (EC 2.1.1.98)	0	0	6	2	0	0	10	4	6	10	16	0.6	**No dramatic change**	0	16	0.0	Soluble only	259	0
≥ 2 unique peptides	rrnAC1980	Q5V0V7_HALMA	*aph*	Aminoglycoside phosphotransferase	0	0	5	3	0	0	11	3	5	11	16	0.5	1.2 (2~3X)	0	16	0.0	Soluble only	356	0

≥ 2 unique peptides	pNG7301	Q5V655_HALMA	*pphA*	Serine/threonine protein phosphatase (EC 3.1.3.16)	2	2	2	2	4	2	8	2	4	12	16	0.3	1.2 (>3X)	6	10	37.5	Memb + Sol	236	0
≥ 2 unique peptides	rrnAC2712	Q5UZ23_HALMA	*sec11a*	Signal sequence peptidase	9	3	0	0	7	2	0	0	9	7	16	1.3	**No dramatic change**	16	0	100.0	Memb only	279	1
≥ 2 unique peptides	rrnAC1591	RL30_HALMAReview	*rpl30p*	50S ribosomal protein L30P (Hmal30) (Hl20) (Hl16)	0	0	9	4	0	0	7	3	9	7	16	1.3	**No dramatic change**	0	16	0.0	Soluble only	154	0
≥ 2 unique peptides	rrnAC1114	Q5V331_HALMA	*htlD*	Sensor protein (EC 2.7.13.3)	7	4	0	0	9	4	0	0	7	9	16	0.8	**No dramatic change**	16	0	100.0	Memb only	575	6
≥ 2 unique peptides	rrnAC1745	Q5V1F6_HALMA	*yckA-2*	Amino acid ABC transporter permease protein	11	5	0	0	5	3	0	0	11	5	16	2.2	0.7 (2>3X)	16	0	100.0	Memb only	326	5
≥ 2 unique peptides	rrnAC0180	Q5V5F8_HALMA	*nhaC5*	Na+/H+ antiporter	8	2	0	0	8	1	0	0	8	8	16	1.0	**No dramatic change**	16	0	100.0	Memb only	717	13
≥ 2 unique peptides	rrnAC0010	Q5V5V7_HALMA	*nac*	Sodium-and chloride-dependent transporter	7	3	0	0	9	3	0	0	7	9	16	0.8	**No dramatic change**	16	0	100.0	Memb only	445	11
≥ 2 unique peptides	rrnAC2740	Q5UYZ9_HALMA	*rrnAC2740*	TRAM domain protein	0	0	6	2	0	0	10	3	6	10	16	0.6	**No dramatic change**	0	16	0.0	Soluble only	150	0
≥ 2 unique peptides	rrnAC0435	Q5V4T3_HALMA	*rrnAC0435*	Transcription regulator	0	0	11	3	0	0	4	1	11	4	15	2.8	0.7 (2>3X)	0	15	0.0	Soluble only	91	0
≥ 2 unique peptides	rrnAC3315	Q5UXJ8_HALMA	*rrnAC3315*	Hypothetical protein	10	3	0	0	5	3	0	0	10	5	15	2.0	0.7 (2>3X)	15	0	100.0	Memb only	285	0
≥ 2 unique peptides	pNG7152	Q5V6J2_HALMA	*pNG7152*	Hypothetical protein	10	3	0	0	5	1	0	0	10	5	15	2.0	0.7 (2>3X)	15	0	100.0	Memb only	103	1
≥ 2 unique peptides	rrnAC1704	Q5V1J2_HALMA	*rrnAC1704*	Hypothetical protein	8	6	0	0	7	4	0	0	8	7	15	1.1	**No dramatic change**	15	0	100.0	Memb only	258	2
≥ 2 unique peptides	pNG2015	Q5V844_HALMA	*pNG2015*	Hypothetical protein	8	3	0	0	7	3	0	0	8	7	15	1.1	**No dramatic change**	15	0	100.0	Memb only	204	1
≥ 2 unique peptides	rrnAC0862	Q5V3Q9_HALMA	*rrnAC0862*	Hypothetical protein	0	0	8	3	0	0	7	2	8	7	15	1.1	**No dramatic change**	0	15	0.0	Soluble only	224	0
≥ 2 unique peptides	rrnAC2125	Q5V0I0_HALMA	*rrnAC2125*	Hypothetical protein	7	2	0	0	8	3	0	0	7	8	15	0.9	**No dramatic change**	15	0	100.0	Memb only	159	3
≥ 2 unique peptides	rrnAC0655	Q5V493_HALMA	*rrnAC0655*	Hypothetical protein	0	0	7	2	0	0	8	3	7	8	15	0.9	**No dramatic change**	0	15	0.0	Soluble only	218	0
≥ 2 unique peptides	rrnAC2757	Q5UYY3_HALMA	*rrnAC2757*	Hypothetical protein	2	1	4	3	3	2	6	5	6	9	15	0.7	**No dramatic change**	5	10	33.3	Memb + Sol	729	0
≥ 2 unique peptides	rrnAC1089	Q5V351_HALMA	*rrnAC1089*	Hypothetical protein	0	0	6	5	0	0	9	6	6	9	15	0.7	**No dramatic change**	0	15	0.0	Soluble only	450	0
≥ 2 unique peptides	pNG2008	Q5V850_HALMA	*pNG2008*	Hypothetical protein	0	0	6	3	0	0	9	3	6	9	15	0.7	**No dramatic change**	0	15	0.0	Soluble only	244	0
≥ 2 unique peptides	rrnAC0895	Q5V3M9_HALMA	*rrnAC0895*	Hypothetical protein	0	0	4	2	0	0	11	5	4	11	15	0.4	1.2 (2~3X)	0	15	0.0	Soluble only	126	0
≥ 2 unique peptides	rrnAC3363	Q5UXF1_HALMA	*carA*	Carbamoyl-phosphate synthase small chain (EC 6.3.5.5)	0	0	10	4	0	0	5	3	10	5	15	2.0	0.7 (2>3X)	0	15	0.0	Soluble only	348	0
≥ 2 unique peptides	rrnAC2927	Q5UYI9_HALMA	*yafB-4*	Oxidoreductase	0	0	8	3	0	0	7	5	8	7	15	1.1	**No dramatic change**	0	15	0.0	Soluble only	264	0
≥ 2 unique peptides	rrnAC1955	Q5V0Y0_HALMA	*glpA*	Glycerol-3-phosphate dehydrogenase subunit A (EC 1.1.99.5)	0	0	6	3	0	0	9	5	6	9	15	0.7	**No dramatic change**	0	15	0.0	Soluble only	406	0
≥ 2 unique peptides	rrnAC1390	PURL_HALMAReview	*purL*	Phosphoribosylformylglycinamidine synthase II (EC 6.3.5.3) (FGAMsynthase II)	0	0	5	3	0	0	10	8	5	10	15	0.5	1.2 (2~3X)	0	15	0.0	Soluble only	720	0
≥ 2 unique peptides	rrnAC1977	Q5V0W0_HALMA	*alkK4*	Medium-chain fatty acid-CoA ligase	0	0	5	5	0	0	10	5	5	10	15	0.5	1.2 (2~3X)	0	15	0.0	Soluble only	551	0
≥ 2 unique peptides	rrnAC3505	Q5UX29_HALMA	*thrC1*	Threonine synthase (EC 4.2.3.1)	0	0	5	4	0	0	10	5	5	10	15	0.5	1.2 (2~3X)	0	15	0.0	Soluble only	390	0
≥ 2 unique peptides	rrnAC1711	Q5V1I6_HALMA	*nirH*	Heme biosynthesis protein NirH	0	0	5	2	0	0	10	3	5	10	15	0.5	1.2 (2~3X)	0	15	0.0	Soluble only	351	0
≥ 2 unique peptides	rrnAC2800	Q5UYU7_HALMA	*fprA*	Flavoprotein	0	0	3	3	1	1	11	3	3	12	15	0.3	1.2 (>3X)	1	14	6.7	Soluble predominant	232	0
≥ 2 unique peptides	rrnAC2220	Q5V0A0_HALMA	*usp5*	Universal stress protein	0	0	9	4	0	0	6	2	9	6	15	1.5	**No dramatic change**	0	15	0.0	Soluble only	154	0
≥ 2 unique peptides	pNG7139	Q5V6K3_HALMA	*usp13*	Universal stress protein	0	0	8	5	1	1	6	3	8	7	15	1.1	**No dramatic change**	1	14	6.7	Soluble predominant	300	0
≥ 2 unique peptides	rrnAC3225	Q5UXS6_HALMA	*usp22*	Universal stress protein	3	3	0	0	10	5	2	1	3	12	15	0.3	1.2 (>3X)	13	2	86.7	Memb predominant	157	0
≥ 2 unique peptides	rrnAC0827	Q5V3U2_HALMA	*livG-4*	Branched-chain amino acid ABC transporter ATP-binding protein	11	4	0	0	4	3	0	0	11	4	15	2.8	0.7 (2>3X)	15	0	100.0	Memb only	276	0
≥ 2 unique peptides	rrnAC0825	Q5V3U3_HALMA	*livM*	High-affinity branched-chain amino acid transport protein	9	3	0	0	6	2	0	0	9	6	15	1.5	**No dramatic change**	15	0	100.0	Memb only	460	8
≥ 2 unique peptides	rrnAC2004	Q5V0T7_HALMA	*ftsZ3*	Cell division protein FtsZ	3	2	6	3	1	1	4	4	9	5	14	1.8	**No dramatic change**	4	10	28.6	Memb + Sol	412	0
≥ 2 unique peptides	rrnAC2723	Q5UZ13_HALMA	*rrnAC2723*	Putative bacterial regulatory protein arsR family	8	4	0	0	6	4	0	0	8	6	14	1.3	**No dramatic change**	14	0	100.0	Memb only	229	2
≥ 2 unique peptides	rrnAC1916	Q5V114_HALMA	*rrnAC1916*	6-O-methylguanine DNA methyltransferase DNA binding domain	0	0	6	3	0	0	8	3	6	8	14	0.8	**No dramatic change**	0	14	0.0	Soluble only	167	0
≥ 2 unique peptides	rrnAC2202	Q5V0B5_HALMA	*kaiC1*	Circadian regulator	0	0	6	1	0	0	8	3	6	8	14	0.8	**No dramatic change**	0	14	0.0	Soluble only	241	0
≥ 2 unique peptides	rrnAC2801	Q5UYU6_HALMA	*rrnAC2801*	Hypothetical protein	8	4	0	0	6	3	0	0	8	6	14	1.3	**No dramatic change**	14	0	100.0	Memb only	301	4
≥ 2 unique peptides	rrnAC1022	Q5V3B5_HALMA	*rrnAC1022*	Hypothetical protein	8	4	0	0	6	3	0	0	8	6	14	1.3	**No dramatic change**	14	0	100.0	Memb only	481	1
≥ 2 unique peptides	rrnAC0228	Q5V5B5_HALMA	*rrnAC0228*	Hypothetical protein	7	4	0	0	7	2	0	0	7	7	14	1.0	**No dramatic change**	14	0	100.0	Memb only	90	0
≥ 2 unique peptides	pNG5010	Q5V7H0_HALMA	*pNG5010*	Hypothetical protein	7	2	0	0	7	2	0	0	7	7	14	1.0	**No dramatic change**	14	0	100.0	Memb only	292	1
≥ 2 unique peptides	rrnAC1304	Q5V2L2_HALMA	*rrnAC1304*	Hypothetical protein	0	0	6	3	0	0	8	4	6	8	14	0.8	**No dramatic change**	0	14	0.0	Soluble only	136	0
≥ 2 unique peptides	rrnAC2221	Q5V099_HALMA	*rrnAC2221*	Hypothetical protein	0	0	3	2	0	0	11	5	3	11	14	0.3	1.2 (>3X)	0	14	0.0	Soluble only	192	0
≥ 2 unique peptides	rrnAC1019	Q5V3B8_HALMA	*dpm1*	Dolichyl-phosphate beta-D-mannosyltransferase	12	6	0	0	2	1	0	0	12	2	14	6.0	0.7 (>3X)	14	0	100.0	Memb only	324	2
≥ 2 unique peptides	rrnAC1261	Q5V2P9_HALMA	*acdD*	Acyl-coA dehydrogenase (EC 1.3.99.-)	0	0	11	4	0	0	3	2	11	3	14	3.7	0.7 (>3X)	0	14	0.0	Soluble only	393	0
≥ 2 unique peptides	rrnAC0429	Q5V4T9_HALMA	*lpg3*	LPS glycosyltransferase	10	4	0	0	4	1	0	0	10	4	14	2.5	0.7 (2>3X)	14	0	100.0	Memb only	397	0
≥ 2 unique peptides	rrnAC2678	ARGC_HALMAReview	*argC*	N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) (AGPR) (N-acetyl-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase)	0	0	10	4	0	0	4	3	10	4	14	2.5	0.7 (2>3X)	0	14	0.0	Soluble only	345	0
≥ 2 unique peptides	rrnAC1818	Q5V196_HALMA	*rrnAC1818*	Putative hydrolase	8	4	0	0	6	4	0	0	8	6	14	1.3	**No dramatic change**	14	0	100.0	Memb only	623	0
≥ 2 unique peptides	rrnAC3304	Q5UXK7_HALMA	*yfhM*	Epoxide hydrolase-related protein	8	3	0	0	6	2	0	0	8	6	14	1.3	**No dramatic change**	14	0	100.0	Memb only	313	0
≥ 2 unique peptides	pNG6023	Q5V6Z0_HALMA	*pNG6023*	Putative metal ion permease	8	2	0	0	6	2	0	0	8	6	14	1.3	**No dramatic change**	14	0	100.0	Memb only	464	8
≥ 2 unique peptides	rrnAC0332	ILVC_HALMAReview	*ilvC*	Ketol-acid reductoisomerase (EC 1.1.1.86) (Acetohydroxy-acidisomeroreductase) (Alpha-keto-beta-hydroxylacil reductoisomerase)	0	0	8	5	0	0	6	4	8	6	14	1.3	**No dramatic change**	0	14	0.0	Soluble only	343	0
≥ 2 unique peptides	rrnAC0868	Q5V3Q3_HALMA	*coaD2*	Phosphopantetheine adenylyltransferase (EC 2.7.7.3)	0	0	8	4	0	0	6	3	8	6	14	1.3	**No dramatic change**	0	14	0.0	Soluble only	162	0
≥ 2 unique peptides	rrnAC3086	Q5UY52_HALMA	*hemC*	Porphobilinogen deaminase (EC 2.5.1.61)	0	0	7	5	0	0	7	3	7	7	14	1.0	**No dramatic change**	0	14	0.0	Soluble only	389	0
≥ 2 unique peptides	pNG6081	Q5V741_HALMA	*zntA1*	Zinc-transporting ATPase	6	6	0	0	8	7	0	0	6	8	14	0.8	**No dramatic change**	14	0	100.0	Memb only	894	6

≥ 2 unique peptides	pNG7164	Q5V6I2_HALMA	*hyuA*	N-methylhydaintoinase A (EC 3.5.2.9)	0	0	6	4	0	0	8	6	6	8	14	0.8	**No dramatic change**	0	14	0.0	Soluble only	664	0
≥ 2 unique peptides	rrnAC0511	Q5V4M0_HALMA	*hpcEa*	2-hydroxyhepta-24-diene-1,7-dioate isomerase	0	0	5	2	0	0	9	2	5	9	14	0.6	**No dramatic change**	0	14	0.0	Soluble only	257	0
≥ 2 unique peptides	rrnAC0970	Q5V3G2_HALMA	*aor3*	Flavin-containing amine-oxidoreductase	0	0	3	3	1	1	10	9	3	11	14	0.3	1.2 (>3X)	1	13	7.1	Soluble predominant	344	0
≥ 2 unique peptides	rrnAC1957	Q5V0X8_HALMA	*malQ*	4-alpha-glucanotransferase (EC 2.4.1.25)	0	0	2	1	0	0	12	7	2	12	14	0.2	1.2 (>3X)	0	14	0.0	Soluble only	556	0
≥ 2 unique peptides	rrnAC1772	Q5V1D5_HALMA	*psmA1*	Proteasome subunit alpha	0	0	5	4	0	0	9	6	5	9	14	0.6	**No dramatic change**	0	14	0.0	Soluble only	230	0
≥ 2 unique peptides	rrnAC1607	RS19_HALMAReview	*rps19p*	30S ribosomal protein S19P (HmaS19) (HS18)	1	1	11	4	2	1	0	0	12	2	14	6.0	0.7 (>3X)	3	11	21.4	Soluble predominant	140	0
≥ 2 unique peptides	rrnAC1597	RS8_HALMAReview	*rps8p*	30S ribosomal protein S8P (HmaS8) (HS16)	1	1	6	3	2	2	5	3	7	7	14	1.0	**No dramatic change**	3	11	21.4	Soluble predominant	130	0
≥ 2 unique peptides	rrnAC2000	Q5V0U0_HALMA	*usp9*	Universal stress protein family	0	0	3	2	0	0	11	4	3	11	14	0.3	1.2 (>3X)	0	14	0.0	Soluble only	272	0
≥ 2 unique peptides	rrnB0322	Q5UW67_HALMA	*phnD2*	Phosphonates ABC transporter permease protein	12	6	0	0	2	1	0	0	12	2	14	6.0	0.7 (>3X)	14	0	100.0	Memb only	264	5
≥ 2 unique peptides	rrnAC0819	Q5V3U8_HALMA	*rrnAC0819*	2-domain regulatory protein	0	0	7	3	0	0	6	5	7	6	13	1.2	**No dramatic change**	0	13	0.0	Soluble only	344	0
≥ 2 unique peptides	rrnAC0936	Q5V3J3_HALMA	*rrnAC0936*	Hypothetical protein	10	4	0	0	3	2	0	0	10	3	13	3.3	0.7 (>3X)	13	0	100.0	Memb only	128	3
≥ 2 unique peptides	rrnAC0591	Q5V4F0_HALMA	*rrnAC0591*	Hypothetical protein	0	0	10	4	0	0	3	2	10	3	13	3.3	0.7 (>3X)	0	13	0.0	Soluble only	279	0
≥ 2 unique peptides	rrnAC0752	Q5V409_HALMA	*rrnAC0752*	Hypothetical protein	0	0	10	4	0	0	3	1	10	3	13	3.3	0.7 (>3X)	0	13	0.0	Soluble only	97	0
≥ 2 unique peptides	rrnAC0219	Q5V5C4_HALMA	*rrnAC0219*	Hypothetical protein	9	3	0	0	4	3	0	0	9	4	13	2.3	0.7 (2>3X)	13	0	100.0	Memb only	364	4
≥ 2 unique peptides	rrnAC0285	Q5V561_HALMA	*rrnAC0285*	Hypothetical protein	8	4	0	0	5	3	0	0	8	5	13	1.6	**No dramatic change**	13	0	100.0	Memb only	353	3
≥ 2 unique peptides	rrnB0186	Q5UWI2_HALMA	*rrnB0186*	Hypothetical protein	0	0	8	3	0	0	5	3	8	5	13	1.6	**No dramatic change**	0	13	0.0	Soluble only	291	0
≥ 2 unique peptides	rrnAC1822	Q5V193_HALMA	*rrnAC1822*	Hypothetical protein	0	0	8	2	0	0	5	2	8	5	13	1.6	**No dramatic change**	0	13	0.0	Soluble only	221	0
≥ 2 unique peptides	rrnAC2981	Q5UYE1_HALMA	*rrnAC2981*	Hypothetical protein	7	3	0	0	6	3	0	0	7	6	13	1.2	**No dramatic change**	13	0	100.0	Memb only	408	1
≥ 2 unique peptides	rrnAC2752	Q5UYY8_HALMA	*rrnAC2752*	Hypothetical protein	0	0	7	4	0	0	6	3	7	6	13	1.2	**No dramatic change**	0	13	0.0	Soluble only	92	0
≥ 2 unique peptides	rrnAC2444	Q5UZQ0_HALMA	*rrnAC2444*	Hypothetical protein	6	5	0	0	7	4	0	0	6	7	13	0.9	**No dramatic change**	13	0	100.0	Memb only	744	5
≥ 2 unique peptides	rrnAC2434	Q5UZQ9_HALMA	*rrnAC2434*	Hypothetical protein	0	0	6	1	1	1	6	2	6	7	13	0.9	**No dramatic change**	1	12	7.7	Soluble predominant	100	0
≥ 2 unique peptides	rrnAC0216	Q5V5C7_HALMA	*rrnAC0216*	Hypothetical protein	2	2	3	3	5	3	3	2	5	8	13	0.6	**No dramatic change**	7	6	53.8	Memb + Sol	73	0
≥ 2 unique peptides	rrnAC2817	Q5UYT0_HALMA	*rrnAC2817*	Hypothetical protein	4	1	0	0	2	2	7	2	4	9	13	0.4	1.2 (2~3X)	6	7	46.2	Memb + Sol	535	4
≥ 2 unique peptides	rrnAC2410	Q5UZT0_HALMA	*rrnAC2410*	Hypothetical protein	0	0	4	4	0	0	9	6	4	9	13	0.4	1.2 (2~3X)	0	13	0.0	Soluble only	177	0
≥ 2 unique peptides	rrnAC0494	Q5V4N5_HALMA	*rrnAC0494*	Hypothetical protein	0	0	4	2	0	0	9	2	4	9	13	0.4	1.2 (2~3X)	0	13	0.0	Soluble only	101	0
≥ 2 unique peptides	rrnB0217	Q5UWF6_HALMA	*acs2*	Acyl-coenzyme A synthetases (EC 6.2.1.1)	0	0	11	6	0	0	2	2	11	2	13	5.5	0.7 (>3X)	0	13	0.0	Soluble only	666	0
≥ 2 unique peptides	rrnAC2069	Q5V0N0_HALMA	*crtB*	Phytoene synthase (EC 2.5.1.32) (EC 2.5.1.21)	8	5	0	0	5	4	0	0	8	5	13	1.6	**No dramatic change**	13	0	100.0	Memb only	323	0
≥ 2 unique peptides	rrnAC0545	Q5V4I9_HALMA	*pfk1*	Phosphofructokinase (EC 2.7.1.11)	0	0	8	5	0	0	5	4	8	5	13	1.6	**No dramatic change**	0	13	0.0	Soluble only	319	0
≥ 2 unique peptides	rrnB0113	Q5UWN9_HALMA	*gatA2*	Glutamyl-tRNA (Gln) amidotransferase subunit A (EC 6.3.5.-)	0	0	8	3	0	0	5	2	8	5	13	1.6	**No dramatic change**	0	13	0.0	Soluble only	519	0
≥ 2 unique peptides	rrnAC2966	Q5UYF4_HALMA	*pheS*	Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20)	0	0	7	5	0	0	6	3	7	6	13	1.2	**No dramatic change**	0	13	0.0	Soluble only	503	0
≥ 2 unique peptides	rrnAC0098	Q5V5M8_HALMA	*alkK1*	Medium-chain acyl-CoA ligase	0	0	6	4	0	0	7	6	6	7	13	0.9	**No dramatic change**	0	13	0.0	Soluble only	533	0
≥ 2 unique peptides	rrnAC0529	HIS8_HALMAReview	*hisC*	Histidinol-phosphate aminotransferase (EC 2.6.1.9) (Imidazole acetol-phosphate transaminase)	0	0	6	3	0	0	7	5	6	7	13	0.9	**No dramatic change**	0	13	0.0	Soluble only	360	0
≥ 2 unique peptides	rrnAC0452	Q5V4R9_HALMA	*galE*	UDP-glucose 4-epimerase (EC 5.1.3.2)	0	0	6	2	0	0	7	4	6	7	13	0.9	**No dramatic change**	0	13	0.0	Soluble only	305	0
≥ 2 unique peptides	rrnAC0038	Q5V5T2_HALMA	*ocd1*	Ornithine cyclodeaminase (EC 4.3.1.12)	0	0	5	3	0	0	8	5	5	8	13	0.6	**No dramatic change**	0	13	0.0	Soluble only	335	0
≥ 2 unique peptides	rrnAC3429	DEOC_HALMAReview	*deoC*	Probable deoxyribose-phosphate aldolase (EC 4.1.2.4)(Phosphodeoxyriboaldolase) (Deoxyriboaldolase) (DERA)	0	0	5	4	0	0	8	4	5	8	13	0.6	**No dramatic change**	0	13	0.0	Soluble only	231	0
≥ 2 unique peptides	rrnAC0717	Q5V442_HALMA	*rrnAC0717*	FAD/NAD binding oxidoreductase (EC 1.18.1.3)	0	0	5	4	0	0	8	4	5	8	13	0.6	**No dramatic change**	0	13	0.0	Soluble only	232	0
≥ 2 unique peptides	rrnAC1402	Q5V2C1_HALMA	*adh4*	Alcohol dehydrogenase (EC 1.1.1.1)	0	0	5	2	0	0	8	4	5	8	13	0.6	**No dramatic change**	0	13	0.0	Soluble only	347	0
≥ 2 unique peptides	rrnAC0934	Q5V3J5_HALMA	*mcmA3*	Putative methylmalonyl-CoA mutase	0	0	5	3	0	0	8	3	5	8	13	0.6	**No dramatic change**	0	13	0.0	Soluble only	156	0
≥ 2 unique peptides	rrnAC1595	RL32_HALMAReview	*rpl32e*	50S ribosomal protein L32e (Hl5)	2	1	6	3	4	3	1	1	8	5	13	1.6	**No dramatic change**	6	7	46.2	Memb + Sol	241	0
≥ 2 unique peptides	rrnAC0155	Q5V5H8_HALMA	*epf2b*	MRNA 3'-end processing factor-like	0	0	5	2	0	0	8	4	5	8	13	0.6	**No dramatic change**	0	13	0.0	Soluble only	638	0
≥ 2 unique peptides	rrnAC0214	NAC_HALMAReview	*nac*	Nascent polypeptide-associated complex protein	0	0	4	2	0	0	9	3	4	9	13	0.4	1.2 (2~3X)	0	13	0.0	Soluble only	130	0
≥ 2 unique peptides	rrnAC3203	IF2P_HALMAReview	*infB*	Probable translation initiation factor IF-2	0	0	3	2	0	0	10	5	3	10	13	0.3	1.2 (>3X)	0	13	0.0	Soluble only	601	0
≥ 2 unique peptides	rrnAC0738	Q5V421_HALMA	*usp29*	Universal stress protein	0	0	5	2	4	2	4	3	5	8	13	0.6	**No dramatic change**	4	9	30.8	Memb + Sol	168	0
≥ 2 unique peptides	rrnAC3171	Q5UXX6_HALMA	*usp19*	Universal stress protein	0	0	2	2	2	1	9	5	2	11	13	0.2	1.2 (>3X)	2	11	15.4	Soluble predominant	298	0
≥ 2 unique peptides	pNG7161	Q5V6I3_HALMA	*mntH*	Putative Mn transporter	7	2	0	0	6	2	0	0	7	6	13	1.2	**No dramatic change**	13	0	100.0	Memb only	402	11
≥ 2 unique peptides	rrnAC0187	Q5V5F2_HALMA	*rrnAC0187*	Putative transporter	6	5	0	0	7	6	0	0	6	7	13	0.9	**No dramatic change**	13	0	100.0	Memb only	328	6
≥ 2 unique peptides	rrnAC0706	Q5V451_HALMA	*nce1*	Na+/Ca2+-exchanging protein	6	4	0	0	7	4	0	0	6	7	13	0.9	**No dramatic change**	13	0	100.0	Memb only	489	12
≥ 2 unique peptides	rrnAC1070	Q5V370_HALMA	*spoVR*	Stage V sporulation protein R-like	0	0	5	3	0	0	7	4	5	7	12	0.7	**No dramatic change**	0	12	0.0	Soluble only	679	0
≥ 2 unique peptides	rrnAC0861	Q5V3R0_HALMA	*tfeA*	Transcription initiation factor IIE alpha subunit	0	0	9	4	0	0	3	2	9	3	12	3.0	0.7 (>3X)	0	12	0.0	Soluble only	176	0
≥ 2 unique peptides	rrnAC2432	Q5UZR1_HALMA	*rpoH*	DNA-directed RNA polymerase subunit H (EC 2.7.7.6)	0	0	9	3	0	0	3	1	9	3	12	3.0	0.7 (>3X)	0	12	0.0	Soluble only	75	0
≥ 2 unique peptides	rrnAC0456	Q5V4R6_HALMA	*gyrB*	DNA gyrase subunit B (EC 5.99.1.3)	0	0	7	4	0	0	5	5	7	5	12	1.4	**No dramatic change**	0	12	0.0	Soluble only	642	0
≥ 2 unique peptides	rrnB0067	Q5UWS9_HALMA	*rrnB0067*	Hypothetical protein	12	6	0	0	0	0	0	0	12	0	12	∞	0.7 only	12	0	100.0	Memb only	768	3
≥ 2 unique peptides	rrnAC3079	Q5UY58_HALMA	*rrnAC3079*	Hypothetical protein	0	0	8	3	0	0	4	3	8	4	12	2.0	0.7 (2>3X)	0	12	0.0	Soluble only	207	0
≥ 2 unique peptides	rrnAC1365	Q5V2F8_HALMA	*rrnAC1365*	Hypothetical protein	7	5	0	0	5	4	0	0	7	5	12	1.4	**No dramatic change**	12	0	100.0	Memb only	386	1
≥ 2 unique peptides	pNG6086	Q5V748_HALMA	*pNG6086*	Hypothetical protein	7	5	0	0	5	4	0	0	7	5	12	1.4	**No dramatic change**	12	0	100.0	Memb only	356	0

≥ 2 unique peptides	rrnAC2611	Q5UZA3_HALMA	*rrnAC2611*	Hypothetical protein	7	5	0	0	5	3	0	0	7	5	12	1.4	**No dramatic change**	12	0	100.0	Memb only	245	2
≥ 2 unique peptides	rrnAC0969	Q5V3G3_HALMA	*rrnAC0969*	Hypothetical protein	0	0	7	4	0	0	5	4	7	5	12	1.4	**No dramatic change**	0	12	0.0	Soluble only	717	0
≥ 2 unique peptides	pNG7058	Q5V6S6_HALMA	*pNG7058*	Hypothetical protein	6	2	0	0	6	2	0	0	6	6	12	1.0	**No dramatic change**	12	0	100.0	Memb only	166	0
≥ 2 unique peptides	rrnAC1492	Q5V237_HALMA	*rrnAC1492*	Hypothetical protein	0	0	5	2	0	0	7	2	5	7	12	0.7	**No dramatic change**	0	12	0.0	Soluble only	56	0
≥ 2 unique peptides	rrnAC2772	Q5UYX1_HALMA	*rrnAC2772*	Hypothetical protein	0	0	4	2	0	0	8	4	4	8	12	0.5	1.2 (2~3X)	0	12	0.0	Soluble only	538	0
≥ 2 unique peptides	rrnAC0403	Q5V4W3_HALMA	*rrnAC0403*	Hypothetical protein	0	0	4	2	0	0	8	2	4	8	12	0.5	1.2 (2~3X)	0	12	0.0	Soluble only	132	0
≥ 2 unique peptides	rrnAC2575	Q5UZD5_HALMA	*rrnAC2575*	Hypothetical protein	0	0	2	1	0	0	10	3	2	10	12	0.2	1.2 (>3X)	0	12	0.0	Soluble only	194	0
≥ 2 unique peptides	pNG6046	Q5V7E1_HALMA	*copA3*	Copper-transporting ATPase (EC 3.6.3.4)	7	5	0	0	5	4	0	0	7	5	12	1.4	**No dramatic change**	12	0	100.0	Memb only	868	8
≥ 2 unique peptides	rrnB0242	Q5UWD6_HALMA	*acaB2*	3-ketoacyl-CoA thiolase (EC 2.3.1.9) (EC 2.3.1.16)	0	0	7	4	0	0	5	3	7	5	12	1.4	**No dramatic change**	0	12	0.0	Soluble only	428	0
≥ 2 unique peptides	rrnAC1138	Q5V311_HALMA	*fbp1*	Fructose-16-bisphosphatase (EC 3.1.3.11)	0	0	7	4	0	0	5	3	7	5	12	1.4	**No dramatic change**	0	12	0.0	Soluble only	168	0
≥ 2 unique peptides	rrnAC2882	Q5UYM4_HALMA	*maoC1*	MaoC family protein	6	4	0	0	6	4	0	0	6	6	12	1.0	**No dramatic change**	12	0	100.0	Memb only	247	0
≥ 2 unique peptides	rrnAC0206	DAPB_HALMAReview	*dapB*	Dihydrodipicolinate reductase (EC 1.3.1.26) (DHPR)	0	0	6	4	0	0	6	4	6	6	12	1.0	**No dramatic change**	0	12	0.0	Soluble only	249	0
≥ 2 unique peptides	rrnAC2248	Q5V074_HALMA	*csd2*	Probable cysteine desulfurase (EC 4.4.1.-)	0	0	6	3	0	0	6	4	6	6	12	1.0	**No dramatic change**	0	12	0.0	Soluble only	367	0
≥ 2 unique peptides	rrnAC2232	Q5V088_HALMA	*pyrC*	Dihydroorotase (EC 3.5.2.3)	0	0	6	2	0	0	6	2	6	6	12	1.0	**No dramatic change**	0	12	0.0	Soluble only	443	0
≥ 2 unique peptides	rrnAC3458	Q5UX68_HALMA	*rrnAC3458*	Anhydrase family 3 protein	0	0	4	2	0	0	8	3	4	8	12	0.5	1.2 (2~3X)	0	12	0.0	Soluble only	170	0
≥ 2 unique peptides	rrnAC3272	Q5UXN5_HALMA	*purU*	Formyltetrahydrofolate deformylase (EC 3.5.1.10) (EC 2.1.2.2)	0	0	4	2	0	0	8	3	4	8	12	0.5	1.2 (2~3X)	0	12	0.0	Soluble only	277	0
≥ 2 unique peptides	rrnAC1906	Q5V122_HALMA	*tas*	Probable oxidoreductase	0	0	3	2	0	0	9	5	3	9	12	0.3	1.2 (>3X)	0	12	0.0	Soluble only	343	0
≥ 2 unique peptides	pNG7060	Q5V6S4_HALMA	*fmdA*	Formamidase	0	0	2	2	0	0	10	6	2	10	12	0.2	1.2 (>3X)	0	12	0.0	Soluble only	433	0
≥ 2 unique peptides	rrnAC0178	Q5V5G0_HALMA	*pop*	Prolyl oligopeptidase family protein	0	0	4	3	0	0	8	3	4	8	12	0.5	1.2 (2~3X)	0	12	0.0	Soluble only	574	0
≥ 2 unique peptides	rrnAC3112	RL39_HALMAReview	*rpl39e*	50S ribosomal protein L39e (Hl39e) (Hl46e)	7	2	0	0	5	1	0	0	7	5	12	1.4	**No dramatic change**	12	0	100.0	Memb only	50	0
≥ 2 unique peptides	rrnAC0056	Q5V5R4_HALMA	*mrp1*	Mrp protein-like	0	0	5	4	0	0	7	4	5	7	12	0.7	**No dramatic change**	0	12	0.0	Soluble only	353	0
≥ 2 unique peptides	rrnB0192	Q5UWH6_HALMA	*usp1*	Universal stress protein 1	6	3	4	2	0	0	2	2	10	2	12	5.0	0.7 (>3X)	6	6	50.0	Memb + Sol	294	0
≥ 2 unique peptides	rrnAC3127	Q5UY17_HALMA	*livF-7*	Branched-chain amino acid ABC transporter ATP-binding protein	3	2	0	0	9	4	0	0	3	9	12	0.3	1.2 (>3X)	12	0	100.0	Memb only	247	0
≥ 2 unique peptides	rrnAC2148	Q5V0G1_HALMA	*pstC2*	Phosphate ABC transporter permease protein	1	1	0	0	11	4	0	0	1	11	12	0.1	1.2 (>3X)	12	0	100.0	Memb only	373	8
≥ 2 unique peptides	rrnAC1165	Y1165_HALMAReview	*rrnAC1165*	UPF0212 protein rrnAC1165	0	0	5	2	0	0	6	2	5	6	11	0.8	**No dramatic change**	0	11	0.0	Soluble only	157	0
≥ 2 unique peptides	rrnAC0062	RPOD_HALMAReview	*rpoD*	DNA-directed RNA polymerase subunit D (EC 2.7.7.6)	0	0	4	3	0	0	7	5	4	7	11	0.6	**No dramatic change**	0	11	0.0	Soluble only	259	0
≥ 2 unique peptides	rrnAC0265	Q5V580_HALMA	*apl*	AP-endonuclease/AP-lyase (EC 3.1.21.2) (EC 4.2.99.18)	0	0	4	2	0	0	7	5	4	7	11	0.6	**No dramatic change**	0	11	0.0	Soluble only	322	0
≥ 2 unique peptides	rrnAC3015	Q5UYB2_HALMA	*rrnAC3015*	Hypothetical protein	11	2	0	0	0	0	0	0	11	0	11	∞	0.7 only	11	0	100.0	Memb only	236	6
≥ 2 unique peptides	pNG7384	Q5V5X8_HALMA	*pNG7384*	Hypothetical protein	8	4	0	0	3	2	0	0	8	3	11	2.7	0.7 (2>3X)	11	0	100.0	Memb only	241	0
≥ 2 unique peptides	rrnAC2913	Q5UYK0_HALMA	*rrnAC2913*	Hypothetical protein	7	5	0	0	4	2	0	0	7	4	11	1.8	**No dramatic change**	11	0	100.0	Memb only	337	8
≥ 2 unique peptides	rrnAC2421	Q5UZS0_HALMA	*rrnAC2421*	Hypothetical protein	7	4	0	0	4	1	0	0	7	4	11	1.8	**No dramatic change**	11	0	100.0	Memb only	460	0
≥ 2 unique peptides	rrnAC2226	Q5V094_HALMA	*rrnAC2226*	Hypothetical protein	0	0	7	4	0	0	4	3	7	4	11	1.8	**No dramatic change**	0	11	0.0	Soluble only	172	0
≥ 2 unique peptides	rrnAC2856	Q5UYP7_HALMA	*rrnAC2856*	Hypothetical protein	0	0	7	2	0	0	4	1	7	4	11	1.8	**No dramatic change**	0	11	0.0	Soluble only	58	0
≥ 2 unique peptides	rrnAC0863	Q5V3Q8_HALMA	*rrnAC0863*	Hypothetical protein	5	2	0	0	6	3	0	0	5	6	11	0.8	**No dramatic change**	11	0	100.0	Memb only	260	2
≥ 2 unique peptides	rrnAC1684	Q5V1K9_HALMA	*rrnAC1684*	Hypothetical protein	0	0	3	2	0	0	8	3	3	8	11	0.4	1.2 (2~3X)	0	11	0.0	Soluble only	153	0
≥ 2 unique peptides	rrnAC2241	Q5V081_HALMA	*rrnAC2241*	Quinolinate phosphoribosyl transferase (EC 2.4.2.19)	0	0	9	3	0	0	2	2	9	2	11	4.5	0.7 (>3X)	0	11	0.0	Soluble only	387	0
≥ 2 unique peptides	rrnAC0330	Q5V522_HALMA	*ilvB2*	Acetolactate synthase (EC 2.2.1.6)	3	2	5	2	1	1	2	1	8	3	11	2.7	0.7 (2>3X)	4	7	36.4	Memb + Sol	585	0
≥ 2 unique peptides	rrnAC1705	Q5V1J1_HALMA	*moeA1*	Molybdenum cofactor biosynthesis protein	0	0	8	6	0	0	3	3	8	3	11	2.7	0.7 (2>3X)	0	11	0.0	Soluble only	342	0
≥ 2 unique peptides	rrnAC0132	Q5V5J8_HALMA	*rrnAC0132*	Lysine-ketoglutarate reductase/saccharopine dehydrogenase (EC 1.5.1.7)(EC 1.5.1.10)	0	0	7	3	0	0	4	2	7	4	11	1.8	**No dramatic change**	0	11	0.0	Soluble only	429	0
≥ 2 unique peptides	rrnAC0357	Q5V4Z9_HALMA	*dcuC*	C4-dicarboxylate anaerobic carrier	6	2	0	0	5	2	0	0	6	5	11	1.2	**No dramatic change**	11	0	100.0	Memb only	689	15
≥ 2 unique peptides	rrnAC3173	SYK_HALMAReview	*lysS*	Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LysRS)	0	0	6	3	0	0	5	2	6	5	11	1.2	**No dramatic change**	0	11	0.0	Soluble only	545	0
≥ 2 unique peptides	rrnAC1438	Q5V287_HALMA	*taqD*	Glycerol-3-phosphate cytidyltransferase	0	0	6	2	0	0	5	1	6	5	11	1.2	**No dramatic change**	0	11	0.0	Soluble only	116	0
≥ 2 unique peptides	rrnAC2450	Q5UZP5_HALMA	*trxA9*	Thioredoxin	0	0	4	2	0	0	7	4	4	7	11	0.6	**No dramatic change**	0	11	0.0	Soluble only	211	0
≥ 2 unique peptides	rrnAC3039	Q5UY90_HALMA	*hpcEb*	2-hydroxyhepta-24-diene-1,7-dioate isomerase	0	0	4	2	0	0	7	3	4	7	11	0.6	**No dramatic change**	0	11	0.0	Soluble only	238	0
≥ 2 unique peptides	pNG7278	Q5V676_HALMA	*adh12*	Alcohol dehydrogenase (EC 1.1.1.1)	0	0	4	1	0	0	7	3	4	7	11	0.6	**No dramatic change**	0	11	0.0	Soluble only	384	0
≥ 2 unique peptides	rrnAC1616	Q5V1S0_HALMA	*mch*	N(5)N(10)-methenyltetrahydromethanopterin cyclohydrolase(EC 3.5.4.27)	0	0	2	2	0	0	9	6	2	9	11	0.2	1.2 (>3X)	0	11	0.0	Soluble only	310	0
≥ 2 unique peptides	rrnAC0334	LEU2_HALMAReview	*leuC*	3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)(Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI)	0	0	2	1	0	0	9	5	2	9	11	0.2	1.2 (>3X)	0	11	0.0	Soluble only	473	0
≥ 2 unique peptides	rrnAC2367	Q5UZW9_HALMA	*ribC*	Ribiflavin synthase alpha chain (EC 2.5.1.9)	0	0	2	2	0	0	9	4	2	9	11	0.2	1.2 (>3X)	0	11	0.0	Soluble only	192	0
≥ 2 unique peptides	rrnAC1740	Q5V1G0_HALMA	*mvaS*	Hydroxymethylglutaryl-CoA synthase (EC 2.3.3.10)	0	0	1	1	0	0	10	7	1	10	11	0.1	1.2 (>3X)	0	11	0.0	Soluble only	445	0
≥ 2 unique peptides	rrnAC0929	Q5V3J9_HALMA	*acaB4*	3-ketoacyl-CoA thiolase (EC 2.3.1.16)	0	0	1	1	0	0	10	7	1	10	11	0.1	1.2 (>3X)	0	11	0.0	Soluble only	388	0
≥ 2 unique peptides	pNG1026	Q5V881_HALMA	*flaA2*	Flagellin A protein	5	2	0	0	6	2	0	0	5	6	11	0.8	**No dramatic change**	11	0	100.0	Memb only	463	1
≥ 2 unique peptides	rrnAC0441	Y441_HALMAReview	*rrnAC0441*	UPF0212 protein rrnAC0441	0	0	6	2	0	0	5	3	6	5	11	1.2	**No dramatic change**	0	11	0.0	Soluble only	123	0
≥ 2 unique peptides	rrnAC3544	Q5UWZ3_HALMA	*htpX4*	Protease heat shock protein HtpX (EC 3.4.24.-)	4	2	0	0	6	1	1	1	4	7	11	0.6	**No dramatic change**	10	1	90.9	Memb predominant	353	4
≥ 2 unique peptides	rrnAC0055	RS17E_HALMAReview	*rps17e*	30S ribosomal protein S17e (Ribosomal protein HS26)	0	0	6	2	0	0	5	1	6	5	11	1.2	**No dramatic change**	0	11	0.0	Soluble only	63	0
≥ 2 unique peptides	rrnAC0138	Q5V5J2_HALMA	*eif2B1*	Probable translation initiation factor 2 beta subunit	0	0	4	4	0	0	7	3	4	7	11	0.6	**No dramatic change**	0	11	0.0	Soluble only	203	0

≥ 2 unique peptides	rrnAC0269	Q5V576_HALMA	*gbp1*	GTP-binding protein	0	0	6	4	0	0	5	3	6	5	11	1.2	**No dramatic change**	0	11	0.0	Soluble only	393	0
≥ 2 unique peptides	rrnAC2223	Q5V097_HALMA	*usp2*	Universal stress protein family	0	0	6	4	0	0	5	2	6	5	11	1.2	**No dramatic change**	0	11	0.0	Soluble only	128	0
≥ 2 unique peptides	rrnAC0716	Q5V443_HALMA	*usp6*	Universal stress protein	0	0	3	2	6	3	2	1	3	8	11	0.4	1.2 (2~3X)	6	5	54.5	Memb + Sol	288	0
≥ 2 unique peptides	rrnAC0379	Q5V4Y1_HALMA	*glnQ2*	Glutamine ABC transporter	5	3	1	1	3	2	2	1	6	5	11	1.2	**No dramatic change**	8	3	72.7	Memb + Sol	250	0
≥ 2 unique peptides	rrnAC3128	Q5UY16_HALMA	*livG-9*	Branched-chain amino acid ABC transporter ATP-binding protein	5	4	0	0	6	4	0	0	5	6	11	0.8	**No dramatic change**	11	0	100.0	Memb only	252	0
≥ 2 unique peptides	rrnAC2082	Q5V0L8_HALMA	*dhp*	Hypothetical protein dhp	0	0	4	2	0	0	7	4	4	7	11	0.6	**No dramatic change**	0	11	0.0	Soluble only	130	0
≥ 2 unique peptides	rrnAC2175	Q5V0D5_HALMA	*seb*	Selenium-binding protein	0	0	3	2	0	0	8	4	3	8	11	0.4	1.2 (2~3X)	0	11	0.0	Soluble only	464	0
≥ 2 unique peptides	rrnAC3013	Q5UYB4_HALMA	*tup1*	Tup1 like transcriptional repressor	0	0	8	3	0	0	2	1	8	2	10	4.0	0.7 (>3X)	0	10	0.0	Soluble only	421	0
≥ 2 unique peptides	rrnAC3381	Q5UXD9_HALMA	*lpdA1*	Dihydrolipoamide dehydrogenase (EC 1.8.1.4)	0	0	5	3	0	0	5	4	5	5	10	1.0	**No dramatic change**	0	10	0.0	Soluble only	466	0
≥ 2 unique peptides	rrnAC1218	Q5V2U0_HALMA	*rrnAC1218*	Hypothetical protein	7	6	0	0	3	3	0	0	7	3	10	2.3	0.7 (2>3X)	10	0	100.0	Memb only	606	2
≥ 2 unique peptides	rrnAC2074	Q5V0M5_HALMA	*rrnAC2074*	Hypothetical protein	7	4	0	0	3	2	0	0	7	3	10	2.3	0.7 (2>3X)	10	0	100.0	Memb only	536	12
≥ 2 unique peptides	pNG7166	Q5V6I0_HALMA	*pNG7166*	Hypothetical protein	7	2	0	0	3	1	0	0	7	3	10	2.3	0.7 (2>3X)	10	0	100.0	Memb only	330	4
≥ 2 unique peptides	rrnAC2598	Q5UZB5_HALMA	*rrnAC2598*	Hypothetical protein	0	0	6	3	0	0	4	3	6	4	10	1.5	**No dramatic change**	0	10	0.0	Soluble only	123	0
≥ 2 unique peptides	rrnAC2866	Q5UYN7_HALMA	*rrnAC2866*	Hypothetical protein	0	0	6	3	0	0	4	2	6	4	10	1.5	**No dramatic change**	0	10	0.0	Soluble only	128	0
≥ 2 unique peptides	rrnAC3202	Q5UXU7_HALMA	*rrnAC3202*	Hypothetical protein	5	3	0	0	5	4	0	0	5	5	10	1.0	**No dramatic change**	10	0	100.0	Memb only	602	0
≥ 2 unique peptides	rrnAC0675	Q5V475_HALMA	*rrnAC0675*	Hypothetical protein	5	3	0	0	5	3	0	0	5	5	10	1.0	**No dramatic change**	10	0	100.0	Memb only	314	6
≥ 2 unique peptides	rrnAC1031	Q5V3A6_HALMA	*rrnAC1031*	Hypothetical protein	4	1	0	0	6	4	0	0	4	6	10	0.7	**No dramatic change**	10	0	100.0	Memb only	674	1
≥ 2 unique peptides	rrnAC1808	Q5V1A6_HALMA	*rrnAC1808*	Hypothetical protein	0	0	4	2	0	0	6	5	4	6	10	0.7	**No dramatic change**	0	10	0.0	Soluble only	144	0
≥ 2 unique peptides	rrnAC0521	Q5V4L1_HALMA	*rrnAC0521*	Hypothetical protein	0	0	2	2	0	0	8	3	2	8	10	0.3	1.2 (>3X)	0	10	0.0	Soluble only	270	0
≥ 2 unique peptides	rrnB0219	Q5UWF4_HALMA	*gabD*	Succinate-semialdehyde dehydrogenase	0	0	9	4	0	0	1	1	9	1	10	9.0	0.7 (>3X)	0	10	0.0	Soluble only	453	0
≥ 2 unique peptides	rrnB0209	Q5UWG1_HALMA	*ilvB3*	Acetolactate synthase large subunit (EC 2.2.1.6)	0	0	7	3	0	0	3	3	7	3	10	2.3	0.7 (2>3X)	0	10	0.0	Soluble only	567	0
≥ 2 unique peptides	rrnAC0011	Q5V5V6_HALMA	*ywfD1*	Glucose 1-dehydrogenase (EC 1.1.1.47)	0	0	7	3	0	0	3	2	7	3	10	2.3	0.7 (2>3X)	0	10	0.0	Soluble only	236	0
≥ 2 unique peptides	rrnAC2521	Q5UZH9_HALMA	*pyrE1*	Orotate phosphoribosyltransferase (EC 2.4.2.10)	0	0	6	2	0	0	4	2	6	4	10	1.5	**No dramatic change**	0	10	0.0	Soluble only	183	0
≥ 2 unique peptides	rrnAC0320	Q5V532_HALMA	*ubiA*	Prenyltransferase	5	2	0	0	5	1	0	0	5	5	10	1.0	**No dramatic change**	10	0	100.0	Memb only	294	7
≥ 2 unique peptides	rrnAC0657	Q5V491_HALMA	*rrnAC0657*	P-hydroxybenzoate hydroxylase (EC 1.14.13.2)	3	3	1	1	6	6	0	0	4	6	10	0.7	**No dramatic change**	9	1	90.0	Memb predominant	472	0
≥ 2 unique peptides	rrnAC1983	Q5V0V5_HALMA	*acdI*	Acyl-CoA dehydrogenase (EC 1.3.99.3)	0	0	4	3	0	0	6	4	4	6	10	0.7	**No dramatic change**	0	10	0.0	Soluble only	584	0
≥ 2 unique peptides	rrnAC1485	Q5V242_HALMA	*yjlD4*	NADH dehydrogenase (EC 1.6.99.3)	0	0	4	2	0	0	6	3	4	6	10	0.7	**No dramatic change**	0	10	0.0	Soluble only	380	0
≥ 2 unique peptides	rrnAC3104	Q5UY37_HALMA	*csd1*	Probable cysteine desulfurase (EC 4.4.1.-)	0	0	3	1	1	1	6	3	3	7	10	0.4	1.2 (2~3X)	1	9	10.0	Soluble predominant	415	0
≥ 2 unique peptides	rrnAC0482	Q5V4P5_HALMA	*yajO*	Putative NAD(P)H-dependent xylose reductase	0	0	3	2	0	0	7	6	3	7	10	0.4	1.2 (2~3X)	0	10	0.0	Soluble only	325	0
≥ 2 unique peptides	rrnAC3232	Q5UXR9_HALMA	*graD4c*	Glucose-1-phosphate thymidylyltransferase	0	0	3	1	0	0	7	3	3	7	10	0.4	1.2 (2~3X)	0	10	0.0	Soluble only	396	0
≥ 2 unique peptides	pNG7279	Q5V675_HALMA	*pNG7279*	Putative pyridine nucleotide-disulphide oxidoreductase	0	0	2	2	0	0	8	6	2	8	10	0.3	1.2 (>3X)	0	10	0.0	Soluble only	199	0
≥ 2 unique peptides	rrnAC0296	Q5V551_HALMA	*htrA1*	Serine protease HtrA	7	4	0	0	3	3	0	0	7	3	10	2.3	0.7 (2>3X)	10	0	100.0	Memb only	361	0
≥ 2 unique peptides	rrnAC0442	Q5V4S6_HALMA	*psmA3*	Proteasome subunit alpha	0	0	6	2	0	0	4	3	6	4	10	1.5	**No dramatic change**	0	10	0.0	Soluble only	240	0
≥ 2 unique peptides	rrnAC2679	Q5UZ49_HALMA	*rimK*	Ribosomal protein S6 modification protein	0	0	9	5	0	0	1	1	9	1	10	9.0	0.7 (>3X)	0	10	0.0	Soluble only	326	0
≥ 2 unique peptides	rrnAC3340	Q5UXH3_HALMA	*grpE*	Heat shock protein GrpE protein	0	0	3	3	0	0	7	6	3	7	10	0.4	1.2 (2~3X)	0	10	0.0	Soluble only	226	0
≥ 2 unique peptides	rrnAC3113	RL31_HALMAReview	*rpl31e*	50S ribosomal protein L31e (L34) (Hl30)	2	1	2	2	5	2	1	1	4	6	10	0.7	**No dramatic change**	7	3	70.0	Memb + Sol	92	0
≥ 2 unique peptides	pNG7373	Q5V5Y9_HALMA	*usp25*	Universal stress protein	0	0	0	0	3	1	7	2	0	10	10	0.0	1.2 only	3	7	30.0	Memb + Sol	147	0
≥ 2 unique peptides	rrnAC3124	Q5UY20_HALMA	*srp54*	Signal recognition 54 kDa protein	2	2	6	3	0	0	2	2	8	2	10	4.0	0.7 (>3X)	2	8	20.0	Soluble predominant	469	0
≥ 2 unique peptides	rrnAC1029	Q5V3A8_HALMA	*rrnAC1029*	ABC transporter ATP-binding protein	6	2	0	0	4	2	0	0	6	4	10	1.5	**No dramatic change**	10	0	100.0	Memb only	254	0
≥ 2 unique peptides	rrnAC0665	Q5V483_HALMA	*abcP-2*	ABC transporter permease protein	5	4	0	0	5	4	0	0	5	5	10	1.0	**No dramatic change**	10	0	100.0	Memb only	411	4
≥ 2 unique peptides	rrnAC2465	Q5UZN1_HALMA	*livG-6*	Branched-chain amino acid ABC transporter ATP-binding protein	4	4	0	0	6	4	0	0	4	6	10	0.7	**No dramatic change**	10	0	100.0	Memb only	270	0
≥ 2 unique peptides	pNG7023	Q5V6V6_HALMA	*rbsB-1*	Putative ABC transporter substrate-binding protein	4	3	0	0	6	4	0	0	4	6	10	0.7	**No dramatic change**	10	0	100.0	Memb only	483	0
≥ 2 unique peptides	rrnAC1747	Q5V1F5_HALMA	*glnQ1*	Glutamine ABC transporter ATP-binding protein	4	3	0	0	6	3	0	0	4	6	10	0.7	**No dramatic change**	10	0	100.0	Memb only	250	0
≥ 2 unique peptides	rrnAC3369	Q5UXE7_HALMA	*htlA*	Hypothetical protein htlA	5	3	0	0	5	3	0	0	5	5	10	1.0	**No dramatic change**	10	0	100.0	Memb only	368	7
≥ 2 unique peptides	rrnAC2487	Q5UZL1_HALMA	*rfcC2*	Replication factor C small subunit	0	0	5	2	0	0	4	3	5	4	9	1.3	**No dramatic change**	0	9	0.0	Soluble only	335	0
≥ 2 unique peptides	rrnAC1767	Q5V1D9_HALMA	*tenA-2*	Transcriptional regulator putative	0	0	0	0	0	0	9	4	0	9	9	0.0	1.2 only	0	9	0.0	Soluble only	255	0
≥ 2 unique peptides	rrnAC3351	Q5UXG3_HALMA	*rrnAC3351*	Hypothetical protein	5	3	1	1	3	2	0	0	6	3	9	2.0	0.7 (2>3X)	8	1	88.9	Memb predominant	453	0
≥ 2 unique peptides	rrnAC1101	Q5V342_HALMA	*rrnAC1101*	Hypothetical protein	1	1	5	5	0	0	3	2	6	3	9	2.0	0.7 (2>3X)	1	8	11.1	Soluble predominant	346	0
≥ 2 unique peptides	pNG7225	Q5V6C4_HALMA	*pNG7225*	Hypothetical protein	0	0	6	3	0	0	3	2	6	3	9	2.0	0.7 (2>3X)	0	9	0.0	Soluble only	596	0
≥ 2 unique peptides	rrnB0271	Q5UWB1_HALMA	*rrnB0271*	Hypothetical protein	5	2	0	0	4	2	0	0	5	4	9	1.3	**No dramatic change**	9	0	100.0	Memb only	412	13
≥ 2 unique peptides	rrnAC2578	Q5UZD2_HALMA	*rrnAC2578*	Hypothetical protein	4	2	0	0	5	3	0	0	4	5	9	0.8	**No dramatic change**	9	0	100.0	Memb only	897	20
≥ 2 unique peptides	rrnAC0291	Q5V555_HALMA	*rrnAC0291*	Hypothetical protein	4	1	0	0	5	3	0	0	4	5	9	0.8	**No dramatic change**	9	0	100.0	Memb only	364	7
≥ 2 unique peptides	rrnAC2960	Q5UYG0_HALMA	*rrnAC2960*	Hypothetical protein	0	0	4	2	0	0	5	3	4	5	9	0.8	**No dramatic change**	0	9	0.0	Soluble only	125	0
≥ 2 unique peptides	rrnAC2242	Q5V080_HALMA	*rrnAC2242*	Hypothetical protein	0	0	4	1	0	0	5	2	4	5	9	0.8	**No dramatic change**	0	9	0.0	Soluble only	94	0
≥ 2 unique peptides	rrnAC3055	Q5UY79_HALMA	*rrnAC3055*	Hypothetical protein	0	0	0	0	0	0	9	4	0	9	9	0.0	1.2 only	0	9	0.0	Soluble only	442	0
≥ 2 unique peptides	rrnAC1378	Q5V2E5_HALMA	*pan1a*	Membrane protein Pan1	9	4	0	0	0	0	0	0	9	0	9	∞	0.7 only	9	0	100.0	Memb only	383	0

≥ 2 unique peptides	rrnAC2929	Q5UYI8_HALMA	*gfo1*	Glucose-fructose oxidoreductase	0	0	7	3	0	0	2	2	7	2	9	3.5	0.7 (>3X)	0	9	0.0	Soluble only	327	0
≥ 2 unique peptides	rrnAC2162	Q5V0E7_HALMA	*mgsA*	Methylglyoxal synthase (EC 4.2.3.3)	0	0	6	3	0	0	3	3	6	3	9	2.0	0.7 (2>3X)	0	9	0.0	Soluble only	127	0
≥ 2 unique peptides	rrnB0252	Q5UWC7_HALMA	*paaA*	Phenylacetic acid degradation protein PaaA	0	0	6	2	0	0	3	3	6	3	9	2.0	0.7 (2>3X)	0	9	0.0	Soluble only	354	0
≥ 2 unique peptides	rrnAC3239	Q5UXR5_HALMA	*ugd2*	UDP-glucose 6-dehydrogenase (EC 1.1.1.22)	0	0	6	3	0	0	3	1	6	3	9	2.0	0.7 (2>3X)	0	9	0.0	Soluble only	435	0
≥ 2 unique peptides	rrnB0254	Q5UWC5_HALMA	*ech6*	Enoyl-CoA hydratase (EC 4.2.1.17)	0	0	6	2	0	0	3	2	6	3	9	2.0	0.7 (2>3X)	0	9	0.0	Soluble only	253	0
≥ 2 unique peptides	rrnAC1936	Q5V0Z7_HALMA	*cobI*	Cobalamin adenosyltransferase (EC 2.5.1.17)	1	1	4	2	0	0	4	2	5	4	9	1.3	**No dramatic change**	1	8	11.1	Soluble predominant	216	0
≥ 2 unique peptides	rrnAC3243	Q5UXR1_HALMA	*galE7*	UDP-glucose 4-epimerase	0	0	4	3	0	0	5	4	4	5	9	0.8	**No dramatic change**	0	9	0.0	Soluble only	331	0
≥ 2 unique peptides	rrnAC2153	Q5V0F6_HALMA	*mutT2*	Mut/nudix family protein	0	0	4	2	0	0	5	2	4	5	9	0.8	**No dramatic change**	0	9	0.0	Soluble only	180	0
≥ 2 unique peptides	rrnAC1224	PYRI_HALMAReview	*pyrI*	Aspartate carbamoyltransferase regulatory chain	0	0	3	3	0	0	6	4	3	6	9	0.5	1.2 (2~3X)	0	9	0.0	Soluble only	155	0
≥ 2 unique peptides	rrnAC2897	Q5UYL1_HALMA	*galE2*	UDP-glucose 4-epimerase (EC 5.1.3.2)	0	0	3	3	0	0	6	4	3	6	9	0.5	1.2 (2~3X)	0	9	0.0	Soluble only	334	0
≥ 2 unique peptides	rrnAC0114	Q5V5L3_HALMA	*guaB5*	Inosine-5'-monophosphate dehydrogenase related protein V	0	0	2	1	0	0	7	5	2	7	9	0.3	1.2 (>3X)	0	9	0.0	Soluble only	194	0
≥ 2 unique peptides	rrnAC1515	Q5V216_HALMA	*pyrF*	Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23)	0	0	2	2	0	0	7	4	2	7	9	0.3	1.2 (>3X)	0	9	0.0	Soluble only	277	0
≥ 2 unique peptides	rrnAC1084	Q5V356_HALMA	*acdG*	Acyl-CoA dehydrogenase (EC 1.3.99.-)	0	0	2	2	0	0	7	4	2	7	9	0.3	1.2 (>3X)	0	9	0.0	Soluble only	385	0
≥ 2 unique peptides	pNG7370	Q5V5Z1_HALMA	*gcvT1*	Sacrosine dehydrogenase/glycine cleavage T-protein (EC 1.5.3.1)(EC 2.1.2.10)	0	0	0	0	1	1	8	4	0	9	9	0.0	1.2 only	1	8	11.1	Soluble predominant	850	0
≥ 2 unique peptides	rrnB0250	Q5UWC8_HALMA	*pacF*	PacF protein	0	0	5	3	0	0	4	2	5	4	9	1.3	**No dramatic change**	0	9	0.0	Soluble only	175	0
≥ 2 unique peptides	pNG7310	Q5V647_HALMA	*pNG7310*	Possible photosystem reaction center subunit H	0	0	5	3	0	0	4	3	5	4	9	1.3	**No dramatic change**	0	9	0.0	Soluble only	92	0
≥ 2 unique peptides	rrnB0212	Q5UWF9_HALMA	*pepB5*	Aminopeptidase	0	0	6	5	0	0	3	2	6	3	9	2.0	0.7 (2>3X)	0	9	0.0	Soluble only	422	0
≥ 2 unique peptides	rrnAC0260	RL21_HALMAReview	*rpl21e*	50S ribosomal protein L21e (Hl31)	2	2	3	2	4	2	0	0	5	4	9	1.3	**No dramatic change**	6	3	66.7	Memb + Sol	96	0
≥ 2 unique peptides	rrnAC2759	Q5UYY1_HALMA	*nso*	Transporter sodium/sulfate symporter family	7	4	0	0	2	2	0	0	7	2	9	3.5	0.7 (>3X)	9	0	100.0	Memb only	624	12
≥ 2 unique peptides	rrnAC0829	Q5V3U1_HALMA	*livF-4*	Branched-chain amino acid ABC transporter ATP-binding protein	4	1	1	1	4	2	0	0	5	4	9	1.3	**No dramatic change**	8	1	88.9	Memb predominant	251	0
≥ 2 unique peptides	rrnAC3265	Q5UXP2_HALMA	*pstB3*	Phosphate ABC transporter ATP-binding protein	4	3	0	0	5	2	0	0	4	5	9	0.8	**No dramatic change**	9	0	100.0	Memb only	254	0
≥ 2 unique peptides	rrnAC0647	Q5V4A0_HALMA	*abcS-1*	ABC transporter substrate-binding protein	2	2	0	0	7	3	0	0	2	7	9	0.3	1.2 (>3X)	9	0	100.0	Memb only	449	0
≥ 2 unique peptides	pNG7346	Q5V612_HALMA	*potD1*	Spermidine/putrescine transporter substrate binding protein	2	2	0	0	7	2	0	0	2	7	9	0.3	1.2 (>3X)	9	0	100.0	Memb only	397	0
≥ 2 unique peptides	rrnB0103	Q5UWP8_HALMA	*rbsB-3*	Putative ABC transporter substrate binding protein	0	0	0	0	9	6	0	0	0	9	9	0.0	1.2 only	9	0	100.0	Memb only	444	0
≥ 2 unique peptides	rrnB0312	Q5UW76_HALMA	*ugpA*	ABC transporter permease protein	0	0	0	0	9	3	0	0	0	9	9	0.0	1.2 only	9	0	100.0	Memb only	294	6
≥ 2 unique peptides	rrnAC3310	Q5UXK2_HALMA	*rrnAC3310*	Transcription regulator	0	0	6	2	0	0	2	1	6	2	8	3.0	0.7 (>3X)	0	8	0.0	Soluble only	270	0
≥ 2 unique peptides	rrnAC0842	Q5V3S8_HALMA	*cinR*	Transcription repressor CinR	0	0	5	4	0	0	3	2	5	3	8	1.7	**No dramatic change**	0	8	0.0	Soluble only	116	0
≥ 2 unique peptides	rrnAC1396	RPOL_HALMAReview	*rpoL*	DNA-directed RNA polymerase subunit L (EC 2.7.7.6)	0	0	4	3	0	0	4	1	4	4	8	1.0	**No dramatic change**	0	8	0.0	Soluble only	94	0
≥ 2 unique peptides	pNG7116	Q5V6M5_HALMA	*nthC*	Endonuclease III (EC 4.2.99.18)	0	0	4	1	0	0	4	2	4	4	8	1.0	**No dramatic change**	0	8	0.0	Soluble only	233	0
≥ 2 unique peptides	rrnAC3094	Q5UY46_HALMA	*recJ5*	RecJ-like exonuclease	0	0	3	3	0	0	5	3	3	5	8	0.6	**No dramatic change**	0	8	0.0	Soluble only	506	0
≥ 2 unique peptides	rrnAC0107	Q5V5M0_HALMA	*rrnAC0107*	Glutaredoxin-like	0	0	5	3	0	0	3	2	5	3	8	1.7	**No dramatic change**	0	8	0.0	Soluble only	85	0
≥ 2 unique peptides	rrnAC3254	Q5UXQ2_HALMA	*rrnAC3254*	Hypothetical protein	6	3	0	0	2	2	0	0	6	2	8	3.0	0.7 (>3X)	8	0	100.0	Memb only	727	0
≥ 2 unique peptides	rrnAC3406	Q5UXB6_HALMA	*rrnAC3406*	Hypothetical protein	0	0	6	3	0	0	2	2	6	2	8	3.0	0.7 (>3X)	0	8	0.0	Soluble only	163	0
≥ 2 unique peptides	rrnAC0802	Q5V3W3_HALMA	*rrnAC0802*	Hypothetical protein	0	0	6	2	0	0	2	2	6	2	8	3.0	0.7 (>3X)	0	8	0.0	Soluble only	176	0
≥ 2 unique peptides	rrnAC2807	Q5UYU0_HALMA	*rrnAC2807*	Hypothetical protein	1	1	4	2	1	1	2	2	5	3	8	1.7	**No dramatic change**	2	6	25.0	Soluble predominant	236	0
≥ 2 unique peptides	rrnAC0115	Q5V5L2_HALMA	*rrnAC0115*	Hypothetical protein	0	0	5	2	0	0	3	3	5	3	8	1.7	**No dramatic change**	0	8	0.0	Soluble only	302	0
≥ 2 unique peptides	rrnAC2744	Q5UYZ5_HALMA	*rrnAC2744*	Hypothetical protein	0	0	5	2	0	0	3	1	5	3	8	1.7	**No dramatic change**	0	8	0.0	Soluble only	314	0
≥ 2 unique peptides	rrnAC2443	Q5UZQ1_HALMA	*rrnAC2443*	Hypothetical protein	4	2	0	0	4	3	0	0	4	4	8	1.0	**No dramatic change**	8	0	100.0	Memb only	324	1
≥ 2 unique peptides	rrnAC1291	Q5V2M4_HALMA	*rrnAC1291*	Hypothetical protein	0	0	4	3	0	0	4	3	4	4	8	1.0	**No dramatic change**	0	8	0.0	Soluble only	161	0
≥ 2 unique peptides	pNG6121	Q5V7C8_HALMA	*pNG6121*	Hypothetical protein	0	0	4	3	0	0	4	2	4	4	8	1.0	**No dramatic change**	0	8	0.0	Soluble only	445	0
≥ 2 unique peptides	rrnAC0262	Q5V583_HALMA	*rrnAC0262*	Hypothetical protein	0	0	3	1	0	0	5	2	3	5	8	0.6	**No dramatic change**	0	8	0.0	Soluble only	59	0
≥ 2 unique peptides	rrnAC2305	Q5V024_HALMA	*rrnAC2305*	Hypothetical protein	0	0	3	2	0	0	5	1	3	5	8	0.6	**No dramatic change**	0	8	0.0	Soluble only	257	0
≥ 2 unique peptides	pNG4008	Q5V7S9_HALMA	*pNG4008*	Hypothetical protein	0	0	2	2	0	0	6	4	2	6	8	0.3	1.2 (>3X)	0	8	0.0	Soluble only	418	0
≥ 2 unique peptides	pNG7069	Q5V6R5_HALMA	*pNG7069*	Hypothetical protein	1	1	0	0	7	3	0	0	1	7	8	0.1	1.2 (>3X)	8	0	100.0	Memb only	135	0
≥ 2 unique peptides	rrnAC2886	Q5UYM0_HALMA	*phaC*	Poly(3-hydroxyalkanoate) synthase	7	3	0	0	1	1	0	0	7	1	8	7.0	0.7 (>3X)	8	0	100.0	Memb only	475	0
≥ 2 unique peptides	rrnB0270	Q5UWB2_HALMA	*zntA2*	Zinc-transporting ATPase	6	3	0	0	2	1	0	0	6	2	8	3.0	0.7 (>3X)	8	0	100.0	Memb only	806	5
≥ 2 unique peptides	rrnAC2674	Q5UZ53_HALMA	*gltCP*	Glutamate carboxypeptidase (EC 3.4.17.11)	0	0	6	3	0	0	2	2	6	2	8	3.0	0.7 (>3X)	0	8	0.0	Soluble only	353	0
≥ 2 unique peptides	rrnAC1102	COBB_HALMAReview	*cobB*	Probable cobyrinic acid A,C-diamide synthase	2	2	3	3	1	1	2	2	5	3	8	1.7	**No dramatic change**	3	5	37.5	Memb + Sol	439	0
≥ 2 unique peptides	rrnAC0329	Q5V523_HALMA	*leuA2*	2-isopropylmalate synthase 2 (EC 2.3.3.13)	0	0	5	3	0	0	3	2	5	3	8	1.7	**No dramatic change**	0	8	0.0	Soluble only	344	0
≥ 2 unique peptides	rrnAC2180	Q5V0D1_HALMA	*gnd*	6-phosphogluconate dehydrogenase (EC 1.1.1.44)	0	0	5	2	0	0	3	2	5	3	8	1.7	**No dramatic change**	0	8	0.0	Soluble only	299	0
≥ 2 unique peptides	pNG7175	Q5V6H1_HALMA	*sojA*	Putative plasmid partitioning protein Soj	0	0	4	3	1	1	3	2	4	4	8	1.0	**No dramatic change**	1	7	12.5	Soluble predominant	281	0
≥ 2 unique peptides	rrnAC2363	Q5UZX2_HALMA	*gapA*	Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.59)	0	0	4	2	0	0	4	4	4	4	8	1.0	**No dramatic change**	0	8	0.0	Soluble only	334	0
≥ 2 unique peptides	rrnAC1979	Q5V0V8_HALMA	*ech5*	Enoyl-CoA hydratase/isomerase (EC 4.2.1.17)	0	0	4	3	0	0	4	3	4	4	8	1.0	**No dramatic change**	0	8	0.0	Soluble only	196	0
≥ 2 unique peptides	pNG7165	Q5V6I1_HALMA	*hyuB*	N-methylhydantoinase B (EC 3.5.2.9)	0	0	4	1	0	0	4	4	4	4	8	1.0	**No dramatic change**	0	8	0.0	Soluble only	542	0
≥ 2 unique peptides	rrnAC0878	Q5V3P6_HALMA	*panB*	3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)	0	0	4	2	0	0	4	2	4	4	8	1.0	**No dramatic change**	0	8	0.0	Soluble only	260	0
≥ 2 unique peptides	rrnAC1459	Q5V268_HALMA	*rrnAC1459*	Metallo-beta-lactamase superfamily protein	0	0	3	2	0	0	5	3	3	5	8	0.6	**No dramatic change**	0	8	0.0	Soluble only	315	0

≥ 2 unique peptides	rrnAC1877	Q5V145_HALMA	*aroD*	3-dehydroquinate dehydratase (EC 4.2.1.10)	0	0	3	2	0	0	5	1	3	5	8	0.6	**No dramatic change**	0	8	0.0	Soluble only	229	0
≥ 2 unique peptides	rrnAC0982	Q5V3F2_HALMA	*ssuE1*	NADPH-dependent FMN reductase (EC 1.5.1.29)	0	0	2	2	0	0	6	3	2	6	8	0.3	1.2 (>3X)	0	8	0.0	Soluble only	192	0
≥ 2 unique peptides	rrnAC3523	APT_HALMAReview	*apt*	Adenine phosphoribosyltransferase (EC 2.4.2.7) (APRT)	0	0	2	1	0	0	6	3	2	6	8	0.3	1.2 (>3X)	0	8	0.0	Soluble only	189	0
≥ 2 unique peptides	rrnAC3034	Q5UY95_HALMA	*gfo6*	Xylose dehydrogenase	0	0	0	0	0	0	8	5	0	8	8	0.0	1.2 only	0	8	0.0	Soluble only	360	0
≥ 2 unique peptides	pNG7302	Q5V654_HALMA	*ppk*	Polyphosphate kinase (EC 2.7.4.1)	0	0	0	0	0	0	8	5	0	8	8	0.0	1.2 only	0	8	0.0	Soluble only	818	0
≥ 2 unique peptides	rrnAC3421	Q5UXA2_HALMA	*map*	Methionine aminopeptidase (EC 3.4.11.18)	0	0	4	2	0	0	4	3	4	4	8	1.0	**No dramatic change**	0	8	0.0	Soluble only	298	0
≥ 2 unique peptides	rrnAC2809	Q5UYT8_HALMA	*usp21*	Universal stress protein	0	0	3	1	0	0	5	2	3	5	8	0.6	**No dramatic change**	0	8	0.0	Soluble only	147	0
≥ 2 unique peptides	pNG7142	Q5V6K0_HALMA	*usp31*	Universal stress protein	0	0	0	0	0	0	8	5	0	8	8	0.0	1.2 only	0	8	0.0	Soluble only	140	0
≥ 2 unique peptides	rrnAC0377	Q5V4Y2_HALMA	*yckA-1*	Amino acid ABC transporter permease protein	6	4	0	0	2	2	0	0	6	2	8	3.0	0.7 (>3X)	8	0	100.0	Memb only	325	6
≥ 2 unique peptides	rrnAC0041	Q5V5S9_HALMA	*srp19*	Signal recognition particle 19 kDa protein	0	0	5	2	0	0	3	2	5	3	8	1.7	**No dramatic change**	0	8	0.0	Soluble only	112	0
≥ 2 unique peptides	rrnAC3266	Q5UXP1_HALMA	*modB*	Molybdenum ABC transporter permease protein	4	3	0	0	4	2	0	0	4	4	8	1.0	**No dramatic change**	8	0	100.0	Memb only	228	4
≥ 2 unique peptides	rrnAC0031	Q5V5T8_HALMA	*ugpC3*	Sugar ABC transporter ATP-binding protein (UGPC)	4	3	0	0	2	2	2	1	4	4	8	1.0	**No dramatic change**	6	2	75.0	Memb predominant	379	0
≥ 2 unique peptides	rrnAC0920	Q5V3K8_HALMA	*msmX-2*	Sugar ABC transporter ATP-binding protein	3	3	0	0	5	4	0	0	3	5	8	0.6	**No dramatic change**	8	0	100.0	Memb only	398	0
≥ 2 unique peptides	rrnAC1533	Q5V1Z9_HALMA	*phoU2*	Phosphate transport system regulatory protein PhoU	1	1	2	1	0	0	5	2	3	5	8	0.6	**No dramatic change**	1	7	12.5	Soluble predominant	235	0
≥ 2 unique peptides	rrnAC2034	Q5V0R2_HALMA	*htlA*	HTR-like protein	5	2	0	0	2	1	0	0	5	2	7	2.5	0.7 (2>3X)	7	0	100.0	Memb only	394	8
≥ 2 unique peptides	rrnAC1792	Q5V1B9_HALMA	*ruvB*	Holliday junction DNA helicase	4	3	1	1	0	0	2	2	5	2	7	2.5	0.7 (2>3X)	4	3	57.1	Memb + Sol	850	0
≥ 2 unique peptides	pNG6185	Q5V7B8_HALMA	*pNG6185*	Putative DEAD/H helicase	1	1	3	3	0	0	3	2	4	3	7	1.3	**No dramatic change**	1	6	14.3	Soluble predominant	1212	0
≥ 2 unique peptides	rrnAC0487	Q5V4P0_HALMA	*htlD*	Sensor protein (EC 2.7.13.3)	0	0	4	3	0	0	3	2	4	3	7	1.3	**No dramatic change**	0	7	0.0	Soluble only	461	0
≥ 2 unique peptides	rrnAC2861	Q5UYP2_HALMA	*mutS2*	Mismatch repair protein	0	0	2	2	0	0	5	5	2	5	7	0.4	1.2 (2~3X)	0	7	0.0	Soluble only	692	0
≥ 2 unique peptides	rrnAC0459	TOP6A_HALMAReview	*top6A*	Type II DNA topoisomerase VI subunit A (EC 5.99.1.3)	0	0	2	2	0	0	5	4	2	5	7	0.4	1.2 (2~3X)	0	7	0.0	Soluble only	368	0
≥ 2 unique peptides	pNG7223	Q5V6C6_HALMA	*boa*	Bacterio-opsin activator-like protein	0	0	1	1	0	0	6	2	1	6	7	0.2	1.2 (>3X)	0	7	0.0	Soluble only	1054	0
≥ 2 unique peptides	rrnAC1105	Q5V339_HALMA	*rrnAC1105*	Hypothetical protein	6	3	0	0	1	1	0	0	6	1	7	6.0	0.7 (>3X)	7	0	100.0	Memb only	264	5
≥ 2 unique peptides	rrnAC3543	Q5UWZ4_HALMA	*rrnAC3543*	Hypothetical protein	5	3	0	0	2	2	0	0	5	2	7	2.5	0.7 (2>3X)	7	0	100.0	Memb only	153	0
≥ 2 unique peptides	rrnAC2523	Q5UZH7_HALMA	*rrnAC2523*	Hypothetical protein	0	0	5	3	0	0	2	1	5	2	7	2.5	0.7 (2>3X)	0	7	0.0	Soluble only	383	0
≥ 2 unique peptides	rrnAC3437	Q5UX87_HALMA	*rrnAC3437*	Hypothetical protein	4	4	0	0	3	2	0	0	4	3	7	1.3	**No dramatic change**	7	0	100.0	Memb only	426	2
≥ 2 unique peptides	rrnAC2046	Q5V0Q0_HALMA	*rrnAC2046*	Hypothetical protein	4	3	0	0	3	2	0	0	4	3	7	1.3	**No dramatic change**	7	0	100.0	Memb only	347	1
≥ 2 unique peptides	rrnAC3463	Q5UX64_HALMA	*rrnAC3463*	Hypothetical protein	4	2	0	0	3	2	0	0	4	3	7	1.3	**No dramatic change**	7	0	100.0	Memb only	346	3
≥ 2 unique peptides	rrnAC1731	Q5V1G8_HALMA	*rrnAC1731*	Hypothetical protein	4	2	0	0	3	2	0	0	4	3	7	1.3	**No dramatic change**	7	0	100.0	Memb only	256	6
≥ 2 unique peptides	rrnAC0305	Q5V542_HALMA	*rrnAC0305*	Hypothetical protein	4	2	0	0	3	2	0	0	4	3	7	1.3	**No dramatic change**	7	0	100.0	Memb only	336	7
≥ 2 unique peptides	rrnAC3206	Q5UXU3_HALMA	*rrnAC3206*	Hypothetical protein	0	0	4	3	0	0	3	3	4	3	7	1.3	**No dramatic change**	0	7	0.0	Soluble only	152	0
≥ 2 unique peptides	rrnAC2249	Q5V073_HALMA	*rrnAC2249*	Hypothetical protein	0	0	4	3	0	0	3	3	4	3	7	1.3	**No dramatic change**	0	7	0.0	Soluble only	205	0
≥ 2 unique peptides	rrnAC2514	Q5UZI6_HALMA	*rrnAC2514*	Hypothetical protein	0	0	4	2	0	0	3	3	4	3	7	1.3	**No dramatic change**	0	7	0.0	Soluble only	318	0
≥ 2 unique peptides	rrnAC2112	Q5V0J0_HALMA	*rrnAC2112*	Hypothetical protein	0	0	4	2	0	0	3	1	4	3	7	1.3	**No dramatic change**	0	7	0.0	Soluble only	124	0
≥ 2 unique peptides	rrnAC3435	Q5UX89_HALMA	*rrnAC3435*	Hypothetical protein	3	2	0	0	4	3	0	0	3	4	7	0.8	**No dramatic change**	7	0	100.0	Memb only	504	4
≥ 2 unique peptides	rrnAC0629	Q5V4B5_HALMA	*rrnAC0629*	Hypothetical protein	0	0	3	2	0	0	4	3	3	4	7	0.8	**No dramatic change**	0	7	0.0	Soluble only	257	0
≥ 2 unique peptides	rrnAC1968	Q5V0W7_HALMA	*rrnAC1968*	Hypothetical protein	0	0	2	1	0	0	5	4	2	5	7	0.4	1.2 (2~3X)	0	7	0.0	Soluble only	432	0
≥ 2 unique peptides	pNG2029	Q5V830_HALMA	*pNG2029*	Hypothetical protein	0	0	2	1	0	0	5	3	2	5	7	0.4	1.2 (2~3X)	0	7	0.0	Soluble only	129	0
≥ 2 unique peptides	rrnAC1682	Q5V1L1_HALMA	*rrnAC1682*	Hypothetical protein	1	1	0	0	6	2	0	0	1	6	7	0.2	1.2 (>3X)	7	0	100.0	Memb only	110	2
≥ 2 unique peptides	rrnAC1254	Q5V2Q6_HALMA	*rrnAC1254*	Hypothetical protein	0	0	1	1	0	0	6	4	1	6	7	0.2	1.2 (>3X)	0	7	0.0	Soluble only	196	0
≥ 2 unique peptides	rrnAC3001	Q5UYC4_HALMA	*cbiF*	Cobalamin biosynthesis precorrin-3 methylase	0	0	7	3	0	0	0	0	7	0	7	∞	0.7 only	0	7	0.0	Soluble only	292	0
≥ 2 unique peptides	rrnB0214	Q5UWF8_HALMA	*rrnB0214*	Bacterial luciferase family monooxygenase	0	0	5	4	0	0	2	2	5	2	7	2.5	0.7 (2>3X)	0	7	0.0	Soluble only	334	0
≥ 2 unique peptides	pNG7284	Q5V671_HALMA	*glcD3*	Putative oxidoreductase	4	4	0	0	3	2	0	0	4	3	7	1.3	**No dramatic change**	7	0	100.0	Memb only	1014	0
≥ 2 unique peptides	rrnAC2178	Q5V0D3_HALMA	*rfbB3*	DTDP-glucose-46-dehydratase (EC 4.2.1.46)	4	2	0	0	3	2	0	0	4	3	7	1.3	**No dramatic change**	7	0	100.0	Memb only	294	0
≥ 2 unique peptides	rrnAC1368	Q5V2F5_HALMA	*trp-6*	ABC transporter ATP-binding protein	4	2	0	0	3	2	0	0	4	3	7	1.3	**No dramatic change**	7	0	100.0	Memb only	232	0
≥ 2 unique peptides	rrnAC1961	Q5V0X4_HALMA	*cga-1*	Glucoamylase	0	0	4	4	0	0	3	2	4	3	7	1.3	**No dramatic change**	0	7	0.0	Soluble only	1513	0
≥ 2 unique peptides	rrnAC0709	TRPE1_HALMAReview	*trpE1*	Anthranilate synthase component 1 1 (EC 4.1.3.27) (Anthranilatesynthase component I 1)	0	0	4	4	0	0	3	2	4	3	7	1.3	**No dramatic change**	0	7	0.0	Soluble only	489	0
≥ 2 unique peptides	rrnAC3174	Q5UXX3_HALMA	*pyrH*	Probable uridylate kinase (EC 2.7.4.-)	0	0	4	2	0	0	3	2	4	3	7	1.3	**No dramatic change**	0	7	0.0	Soluble only	228	0
≥ 2 unique peptides	pNG7288	Q5V667_HALMA	*pNG7288*	Putative phosphoesterase	3	3	0	0	4	2	0	0	3	4	7	0.8	**No dramatic change**	7	0	100.0	Memb only	448	2
≥ 2 unique peptides	rrnAC2280	Q5V048_HALMA	*cbiQ1*	Cobalt transport protein	3	2	0	0	4	2	0	0	3	4	7	0.8	**No dramatic change**	7	0	100.0	Memb only	263	5
≥ 2 unique peptides	rrnAC1011	Q5V3C6_HALMA	*rffG*	DTDP-glucose dehydratase (EC 4.2.1.46)	1	1	2	2	0	0	4	3	3	4	7	0.8	**No dramatic change**	1	6	14.3	Soluble predominant	333	0
≥ 2 unique peptides	rrnAC2056	Q5V0P1_HALMA	*serA3*	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	0	0	3	2	0	0	4	4	3	4	7	0.8	**No dramatic change**	0	7	0.0	Soluble only	320	0
≥ 2 unique peptides	rrnAC1355	GATA_HALMAReview	*gatA*	Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.-) (Glu-ADTsubunit A)	0	0	3	3	0	0	4	3	3	4	7	0.8	**No dramatic change**	0	7	0.0	Soluble only	425	0
≥ 2 unique peptides	rrnB0198	Q5UWH1_HALMA	*pdhC1*	Dihydrolipoamide S-acetyltransferase component of pyruvatedehydrogenase complex E2	0	0	3	3	0	0	4	3	3	4	7	0.8	**No dramatic change**	0	7	0.0	Soluble only	540	0
≥ 2 unique peptides	rrnAC0336	Q5V517_HALMA	*leuD*	3-isopropylmalate dehydratase small subunit (EC 4.2.1.33)	0	0	3	2	0	0	4	2	3	4	7	0.8	**No dramatic change**	0	7	0.0	Soluble only	214	0
≥ 2 unique peptides	rrnAC1498	Q5V232_HALMA	*gcvP1*	Glycine dehydrogenase subunit 1 (EC 1.4.4.2)	0	0	2	1	0	0	5	4	2	5	7	0.4	1.2 (2~3X)	0	7	0.0	Soluble only	447	0

≥ 2 unique peptides	rrnAC3275	Q5UXN3_HALMA	*purC*	Phosphoribosylaminoimidazole-succinocarboxamide synthase(EC 6.3.2.6)	0	0	2	1	0	0	5	3	2	5	7	0.4	1.2 (2~3X)	0	7	0.0	Soluble only	344	0
≥ 2 unique peptides	rrnAC1999	Q5V0U1_HALMA	*spaT*	Aminotransferase class V	0	0	2	1	0	0	5	2	2	5	7	0.4	1.2 (2~3X)	0	7	0.0	Soluble only	402	0
≥ 2 unique peptides	rrnB0237	Q5UWE0_HALMA	*ech4*	Enoyl-CoA hydratase (EC 4.2.1.17)	0	0	1	1	0	0	6	3	1	6	7	0.2	1.2 (>3X)	0	7	0.0	Soluble only	270	0
≥ 2 unique peptides	rrnAC1129	Q5V318_HALMA	*trxB3*	Thioredoxin reductase (EC 1.8.1.9)	0	0	1	1	0	0	6	3	1	6	7	0.2	1.2 (>3X)	0	7	0.0	Soluble only	349	0
≥ 2 unique peptides	rrnAC1794	Q5V1B7_HALMA	*dapF*	Diaminopimelate epimerase (EC 5.1.1.7)	0	0	1	1	0	0	6	2	1	6	7	0.2	1.2 (>3X)	0	7	0.0	Soluble only	303	0
≥ 2 unique peptides	rrnAC3442	Q5UX82_HALMA	*asbA*	L-asparaginase (EC 3.5.1.1)	0	0	0	0	0	0	7	3	0	7	7	0.0	1.2 only	0	7	0.0	Soluble only	415	0
≥ 2 unique peptides	rrnAC2412	Q5UZS8_HALMA	*rrnAC2412*	Putative peptidase	4	2	0	0	3	2	0	0	4	3	7	1.3	**No dramatic change**	7	0	100.0	Memb only	238	4
≥ 2 unique peptides	rrnAC0514	SURE_HALMAReview	*surE*	5'-nucleotidase surE (EC 3.1.3.5) (Nucleoside 5'-monophosphatephosphohydrolase)	0	0	3	3	0	0	4	2	3	4	7	0.8	**No dramatic change**	0	7	0.0	Soluble only	269	0
≥ 2 unique peptides	rrnAC1594	RL19_HALMAReview	*rpl19e*	50S ribosomal protein L19e (Hmal19) (Hl24)	0	0	2	1	5	5	0	0	2	5	7	0.4	1.2 (2~3X)	5	2	71.4	Memb + Sol	149	0
≥ 2 unique peptides	pNG7084	Q5V6Q3_HALMA	*htr8*	MCP domain signal transducer	3	3	0	0	4	3	0	0	3	4	7	0.8	**No dramatic change**	7	0	100.0	Memb only	637	5
≥ 2 unique peptides	rrnAC1619	Q5V1R8_HALMA	*gbp2*	GTP-binding protein-like	0	0	2	2	0	0	5	2	2	5	7	0.4	1.2 (2~3X)	0	7	0.0	Soluble only	543	0
≥ 2 unique peptides	pNG7083	Q5V6Q4_HALMA	*usp23*	Putative universal stress protein family	0	0	4	2	0	0	3	2	4	3	7	1.3	**No dramatic change**	0	7	0.0	Soluble only	144	0
≥ 2 unique peptides	rrnB0204	Q5UWG6_HALMA	*livM-7*	High-affinity branched-chain amino acid transport protein	5	3	0	0	2	1	0	0	5	2	7	2.5	0.7 (2>3X)	7	0	100.0	Memb only	435	8
≥ 2 unique peptides	rrnAC0944	Q5V3I6_HALMA	*rrnAC0944*	Putative sugar transporter	5	2	0	0	2	1	0	0	5	2	7	2.5	0.7 (2>3X)	7	0	100.0	Memb only	449	10
≥ 2 unique peptides	rrnAC2468	Q5UZM9_HALMA	*livH-6*	Branched chain amino acid transporter permease protein	3	1	0	0	4	2	0	0	3	4	7	0.8	**No dramatic change**	7	0	100.0	Memb only	305	8
≥ 2 unique peptides	rrnAC0243	Q5V5A2_HALMA	*trkA7*	TRK potassium uptake system protein	0	0	2	2	0	0	5	3	2	5	7	0.4	1.2 (2~3X)	0	7	0.0	Soluble only	217	0
≥ 2 unique peptides	rrnAC2039	Q5V0Q7_HALMA	*oppA*	Oligopeptide ABC transporter solute-binding protein	1	1	0	0	6	3	0	0	1	6	7	0.2	1.2 (>3X)	7	0	100.0	Memb only	649	0
≥ 2 unique peptides	rrnAC0077	Q5V5P6_HALMA	*mvk*	Mevalonate kinase (EC 2.7.1.36)	0	0	3	2	0	0	4	3	3	4	7	0.8	**No dramatic change**	0	7	0.0	Soluble only	327	0
≥ 2 unique peptides	rrnB0325	Q5UW64_HALMA	*ftsZ2*	Cell division protein	5	4	1	1	0	0	0	0	6	0	6	∞	0.7 only	5	1	83.3	Memb predominant	425	0
≥ 2 unique peptides	rrnAC2205	Q5V0B2_HALMA	*cheA3*	Chemotaxis protein CheA (EC 2.7.3.-)	0	0	4	3	0	0	2	2	4	2	6	2.0	0.7 (2>3X)	0	6	0.0	Soluble only	662	0
≥ 2 unique peptides	rrnAC1397	Q5V2C6_HALMA	*rrnAC1397*	Putative DNA binding	5	2	0	0	1	1	0	0	5	1	6	5.0	0.7 (>3X)	6	0	100.0	Memb only	103	1
≥ 2 unique peptides	pNG6174	CDC6B_HALMAReview	*cdc6-11*	Cell division control protein 6 homolog 11 (CDC6 homolog 11)	0	0	5	2	0	0	1	1	5	1	6	5.0	0.7 (>3X)	0	6	0.0	Soluble only	422	0
≥ 2 unique peptides	rrnAC1144	Q5V306_HALMA	*mutS3*	DNA mismatch repair protein	0	0	5	2	0	0	1	1	5	1	6	5.0	0.7 (>3X)	0	6	0.0	Soluble only	585	0
≥ 2 unique peptides	rrnAC2217	Q5V0A2_HALMA	*recJ4*	RecJ-like exonuclease	0	0	4	3	0	0	2	2	4	2	6	2.0	0.7 (2>3X)	0	6	0.0	Soluble only	363	0
≥ 2 unique peptides	rrnAC1645	Q5V1P3_HALMA	*topA*	DNA topoisomerase I (EC 5.99.1.2)	0	0	4	3	0	0	2	2	4	2	6	2.0	0.7 (2>3X)	0	6	0.0	Soluble only	1364	0
≥ 2 unique peptides	rrnAC2847	Q5UYQ5_HALMA	*hjr*	Holliday junction resolvase	0	0	4	2	0	0	2	1	4	2	6	2.0	0.7 (2>3X)	0	6	0.0	Soluble only	172	0
≥ 2 unique peptides	pNG6143	Q5V782_HALMA	*mrr*	Mrr restriction system protein-like	3	2	0	0	3	2	0	0	3	3	6	1.0	**No dramatic change**	6	0	100.0	Memb only	454	1
≥ 2 unique peptides	rrnAC2044	Q5V0Q2_HALMA	*htlD*	Sensor protein (EC 2.7.13.3)	0	0	3	3	0	0	3	3	3	3	6	1.0	**No dramatic change**	0	6	0.0	Soluble only	782	0
≥ 2 unique peptides	rrnAC1311	Q5V2K6_HALMA	*recJ1*	RecJ exonuclease	0	0	3	3	0	0	3	2	3	3	6	1.0	**No dramatic change**	0	6	0.0	Soluble only	337	0
≥ 2 unique peptides	rrnAC3365	Q5UXF0_HALMA	*trh3*	Transcription regulator	0	0	3	2	0	0	3	2	3	3	6	1.0	**No dramatic change**	0	6	0.0	Soluble only	137	0
≥ 2 unique peptides	pNG1040	Q5V893_HALMA	*pNG1040*	Putative helicase	0	0	2	2	0	0	4	2	2	4	6	0.5	1.2 (2~3X)	0	6	0.0	Soluble only	862	0
≥ 2 unique peptides	rrnAC1996	Q5V0U4_HALMA	*rrnAC1996*	Putative DNA binding domain	0	0	0	0	0	0	6	3	0	6	6	0.0	1.2 only	0	6	0.0	Soluble only	216	0
≥ 2 unique peptides	rrnAC0656	Q5V492_HALMA	*ferA3*	Ferredoxin	0	0	0	0	5	2	1	1	0	6	6	0.0	1.2 only	5	1	83.3	Memb predominant	110	0
≥ 2 unique peptides	rrnAC2458	Q5UZN8_HALMA	*trxA1*	Thioredoxin	0	0	4	1	0	0	2	2	4	2	6	2.0	0.7 (2>3X)	0	6	0.0	Soluble only	115	0
≥ 2 unique peptides	rrnAC2816	Q5UYT1_HALMA	*rrnAC2816*	Hypothetical protein	0	0	6	3	0	0	0	0	6	0	6	∞	0.7 only	0	6	0.0	Soluble only	156	0
≥ 2 unique peptides	rrnAC2006	Q5V0T5_HALMA	*rrnAC2006*	Hypothetical protein	5	3	0	0	1	1	0	0	5	1	6	5.0	0.7 (>3X)	6	0	100.0	Memb only	232	0
≥ 2 unique peptides	rrnAC2121	Q5V0I3_HALMA	*rrnAC2121*	Hypothetical protein	4	3	0	0	2	1	0	0	4	2	6	2.0	0.7 (2>3X)	6	0	100.0	Memb only	760	3
≥ 2 unique peptides	rrnAC2021	Q5V0S3_HALMA	*rrnAC2021*	Hypothetical protein	0	0	4	2	0	0	2	2	4	2	6	2.0	0.7 (2>3X)	0	6	0.0	Soluble only	158	0
≥ 2 unique peptides	rrnAC1728	Q5V1H1_HALMA	*rrnAC1728*	Hypothetical protein	0	0	4	2	0	0	2	2	4	2	6	2.0	0.7 (2>3X)	0	6	0.0	Soluble only	305	0
≥ 2 unique peptides	rrnAC1439	Q5V286_HALMA	*rrnAC1439*	Hypothetical protein	0	0	4	2	0	0	2	2	4	2	6	2.0	0.7 (2>3X)	0	6	0.0	Soluble only	165	0
≥ 2 unique peptides	rrnAC1970	Q5V0W6_HALMA	*rrnAC1970*	Hypothetical protein	0	0	4	2	0	0	2	1	4	2	6	2.0	0.7 (2>3X)	0	6	0.0	Soluble only	376	0
≥ 2 unique peptides	rrnAC0803	Q5V3W2_HALMA	*rrnAC0803*	Hypothetical protein	3	2	0	0	3	2	0	0	3	3	6	1.0	**No dramatic change**	6	0	100.0	Memb only	514	0
≥ 2 unique peptides	rrnAC1643	Q5V1P5_HALMA	*rrnAC1643*	Hypothetical protein	0	0	3	1	0	0	3	3	3	3	6	1.0	**No dramatic change**	0	6	0.0	Soluble only	111	0
≥ 2 unique peptides	rrnAC0343	Q5V511_HALMA	*rrnAC0343*	Hypothetical protein	0	0	3	2	0	0	3	2	3	3	6	1.0	**No dramatic change**	0	6	0.0	Soluble only	375	0
≥ 2 unique peptides	rrnAC1658	Q5V1N1_HALMA	*rrnAC1658*	Hypothetical protein	2	2	0	0	4	2	0	0	2	4	6	0.5	1.2 (2~3X)	6	0	100.0	Memb only	60	2
≥ 2 unique peptides	rrnAC1026	Q5V3B1_HALMA	*rrnAC1026*	Hypothetical protein	2	1	0	0	4	2	0	0	2	4	6	0.5	1.2 (2~3X)	6	0	100.0	Memb only	364	1
≥ 2 unique peptides	rrnAC2259	Q5V064_HALMA	*rrnAC2259*	Hypothetical protein	0	0	2	2	0	0	4	2	2	4	6	0.5	1.2 (2~3X)	0	6	0.0	Soluble only	217	0
≥ 2 unique peptides	rrnAC2525	Q5UZH5_HALMA	*rrnAC2525*	Hypothetical protein	1	1	0	0	5	4	0	0	1	5	6	0.2	1.2 (>3X)	6	0	100.0	Memb only	244	3
≥ 2 unique peptides	rrnAC0253	Q5V592_HALMA	*rrnAC0253*	Hypothetical protein	0	0	1	1	0	0	5	5	1	5	6	0.2	1.2 (>3X)	0	6	0.0	Soluble only	170	0
≥ 2 unique peptides	rrnAC3455	Q5UX71_HALMA	*ykfB3*	Chloromuconate cycloisomerase	0	0	5	4	0	0	1	1	5	1	6	5.0	0.7 (>3X)	0	6	0.0	Soluble only	345	0
≥ 2 unique peptides	rrnAC2449	Q5UZP6_HALMA	*thiD*	Phosphomethylpyrimidine kinase (EC 2.7.4.7)	0	0	5	4	0	0	1	1	5	1	6	5.0	0.7 (>3X)	0	6	0.0	Soluble only	461	0
≥ 2 unique peptides	rrnAC1884	TRPA_HALMAReview	*trpA*	Tryptophan synthase alpha chain (EC 4.2.1.20)	0	0	5	2	0	0	1	1	5	1	6	5.0	0.7 (>3X)	0	6	0.0	Soluble only	293	0
≥ 2 unique peptides	rrnAC0637	Q5V4A8_HALMA	*mcmA1*	Methylmalonyl-CoA mutase subunit alpha	0	0	4	3	0	0	2	2	4	2	6	2.0	0.7 (2>3X)	0	6	0.0	Soluble only	560	0
≥ 2 unique peptides	rrnAC3343	KCY_HALMAReview	*cmk*	Cytidylate kinase (EC 2.7.4.14) (CK) (Cytidine monophosphate kinase)(CMP kinase)	0	0	4	2	0	0	2	2	4	2	6	2.0	0.7 (2>3X)	0	6	0.0	Soluble only	192	0
≥ 2 unique peptides	rrnAC3018	Q5UYB0_HALMA	*hmcA*	Protporphyrin IX magnesium chelatase	0	0	4	2	0	0	2	1	4	2	6	2.0	0.7 (2>3X)	0	6	0.0	Soluble only	719	0
≥ 2 unique peptides	rrnAC0639	Q5V4A6_HALMA	*rrnAC0639*	Acetyltransferase family	0	0	3	3	0	0	3	2	3	3	6	1.0	**No dramatic change**	0	6	0.0	Soluble only	194	0

≥ 2 unique peptides	rrnB0197	DLDH3_HALMAReview	*lpdA3*	Dihydrolipoyl dehydrogenase 3 (EC 1.8.1.4) (Dihydrolipoamidedehydrogenase 3)	0	0	3	1	0	0	3	2	3	3	6	1.0	**No dramatic change**	0	6	0.0	Soluble only	477	0
≥ 2 unique peptides	rrnAC2742	Q5UYZ7_HALMA	*manC*	Mannose-1-phosphate guanylyltransferase	0	0	3	2	0	0	3	1	3	3	6	1.0	**No dramatic change**	0	6	0.0	Soluble only	331	0
≥ 2 unique peptides	rrnAC0958	Q5V3H3_HALMA	*icfA2*	Carbonic anhydrase	0	0	3	1	0	0	3	2	3	3	6	1.0	**No dramatic change**	0	6	0.0	Soluble only	212	0
≥ 2 unique peptides	rrnAC0127	Q5V5K3_HALMA	*aroA*	3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)	0	0	3	1	0	0	3	2	3	3	6	1.0	**No dramatic change**	0	6	0.0	Soluble only	429	0
≥ 2 unique peptides	rrnAC1624	Q5V1R3_HALMA	*soxA3*	Probable sulfite oxidase	2	2	0	0	4	4	0	0	2	4	6	0.5	1.2 (2~3X)	6	0	100.0	Memb only	506	5
≥ 2 unique peptides	rrnAC2023	Q5V0S1_HALMA	*nuoC*	NADH dehydrogenase I chain C D	2	1	0	0	4	2	0	0	2	4	6	0.5	1.2 (2~3X)	6	0	100.0	Memb only	545	0
≥ 2 unique peptides	rrnAC0264	Q5V581_HALMA	*hbd-1*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	0	0	2	2	0	0	4	4	2	4	6	0.5	1.2 (2~3X)	0	6	0.0	Soluble only	290	0
≥ 2 unique peptides	rrnAC3139	Q5UY07_HALMA	*maoC2*	MaoC family protein	0	0	2	1	0	0	4	3	2	4	6	0.5	1.2 (2~3X)	0	6	0.0	Soluble only	297	0
≥ 2 unique peptides	rrnAC0888	Q5V3N6_HALMA	*scs*	Succinyl-Coa synthetase (EC 6.2.1.5)	0	0	2	1	0	0	4	3	2	4	6	0.5	1.2 (2~3X)	0	6	0.0	Soluble only	701	0
≥ 2 unique peptides	rrnAC3268	Q5UXN9_HALMA	*purQ*	Phosphoribosylformylglycinamidine synthase I (EC 6.3.5.3)	0	0	2	1	0	0	4	2	2	4	6	0.5	1.2 (2~3X)	0	6	0.0	Soluble only	165	0
≥ 2 unique peptides	rrnAC2484	Q5UZL4_HALMA	*ech3*	Enoyl-CoA hydratase (EC 4.2.1.17)	0	0	2	1	0	0	4	2	2	4	6	0.5	1.2 (2~3X)	0	6	0.0	Soluble only	224	0
≥ 2 unique peptides	rrnAC0555	Q5V4I1_HALMA	*gpdB*	Glycerol-3-phosphate dehydrogenase chain B	1	1	0	0	5	4	0	0	1	5	6	0.2	1.2 (>3X)	6	0	100.0	Memb only	424	0
≥ 2 unique peptides	rrnAC1068	Q5V372_HALMA	*prkA*	Kinase anchor protein	0	0	1	1	0	0	5	5	1	5	6	0.2	1.2 (>3X)	0	6	0.0	Soluble only	760	0
≥ 2 unique peptides	rrnAC1111	Q5V334_HALMA	*rrnAC1111*	Thioredoxin domain containing protein	0	0	1	1	0	0	5	4	1	5	6	0.2	1.2 (>3X)	0	6	0.0	Soluble only	733	0
≥ 2 unique peptides	rrnAC1917	Q5V113_HALMA	*glpQ2*	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)	0	0	0	0	0	0	6	3	0	6	6	0.0	1.2 only	0	6	0.0	Soluble only	333	0
≥ 2 unique peptides	pNG7291	Q5V665_HALMA	*htpX2*	Probable protease HtpX-like (EC 3.4.24.-)	5	4	0	0	1	1	0	0	5	1	6	5.0	0.7 (>3X)	6	0	100.0	Memb only	274	4
≥ 2 unique peptides	rrnAC1604	RL29_HALMAReview	*rpl29p*	50S ribosomal protein L29P (Hmal29) (Hl33)	0	0	5	2	0	0	1	1	5	1	6	5.0	0.7 (>3X)	0	6	0.0	Soluble only	71	0
≥ 2 unique peptides	rrnAC0965	Q5V3G6_HALMA	*pelA*	Cell division protein pelota	0	0	4	3	0	0	2	1	4	2	6	2.0	0.7 (2>3X)	0	6	0.0	Soluble only	355	0
≥ 2 unique peptides	rrnAC2084	Q5V0L6_HALMA	*nosF-3*	ABC transporter ATP-binding protein	4	3	0	0	2	2	0	0	4	2	6	2.0	0.7 (2>3X)	6	0	100.0	Memb only	314	0
≥ 2 unique peptides	rrnAC2858	Q5UYP5_HALMA	*tatC2*	Sec-independent protein translocase TatC	4	3	0	0	2	1	0	0	4	2	6	2.0	0.7 (2>3X)	6	0	100.0	Memb only	539	10
≥ 2 unique peptides	pNG7252	Q5V699_HALMA	*rbsA*	Ribose ABC transporter ATP-binding	3	3	0	0	3	3	0	0	3	3	6	1.0	**No dramatic change**	6	0	100.0	Memb only	595	0
≥ 2 unique peptides	pNG7375	Q5V5Y7_HALMA	*betL2*	Glycine betaine transporter	1	1	0	0	5	2	0	0	1	5	6	0.2	1.2 (>3X)	6	0	100.0	Memb only	586	12
≥ 2 unique peptides	rrnAC3490	Q5UX40_HALMA	*boa2*	Bacterio-opsin activator-like protein	1	1	0	0	2	1	3	2	1	5	6	0.2	1.2 (>3X)	3	3	50.0	Memb + Sol	215	0
≥ 2 unique peptides	rrnAC2354	Q5UZY0_HALMA	*rrnAC2354*	Transcription regulator	0	0	3	3	0	0	2	1	3	2	5	1.5	**No dramatic change**	0	5	0.0	Soluble only	350	0
≥ 2 unique peptides	rrnAC2015	END4_HALMAReview	*nfo*	Probable endonuclease 4 (EC 3.1.21.2) (Endonuclease IV)(Endodeoxyribonuclease IV)	0	0	3	2	0	0	2	1	3	2	5	1.5	**No dramatic change**	0	5	0.0	Soluble only	277	0
≥ 2 unique peptides	rrnAC2830	Q5UYR9_HALMA	*rpoE''*	DNA-directed RNA polymerase subunit E''	0	0	3	2	0	0	2	1	3	2	5	1.5	**No dramatic change**	0	5	0.0	Soluble only	65	0
≥ 2 unique peptides	rrnAC2070	Q5V0M9_HALMA	*boa*	Putative light-and oxygen-sensing transcription regulator	0	0	3	2	0	0	2	1	3	2	5	1.5	**No dramatic change**	0	5	0.0	Soluble only	526	0
≥ 2 unique peptides	rrnAC2550	Q5UZF5_HALMA	*mutL*	DNA mismatch repair protein mutL	0	0	2	2	0	0	3	3	2	3	5	0.7	**No dramatic change**	0	5	0.0	Soluble only	746	0
≥ 2 unique peptides	rrnAC2416	Q5UZS4_HALMA	*rrnAC2416*	Sensor protein (EC 2.7.13.3)	0	0	2	2	0	0	3	2	2	3	5	0.7	**No dramatic change**	0	5	0.0	Soluble only	1047	0
≥ 2 unique peptides	rrnAC0696	Q5V458_HALMA	*rrnAC0696*	Hypothetical protein	5	4	0	0	0	0	0	0	5	0	5	∞	0.7 only	5	0	100.0	Memb only	299	0
≥ 2 unique peptides	pNG6054	Q5V6Y4_HALMA	*pNG6054*	Hypothetical protein	4	2	0	0	1	1	0	0	4	1	5	4.0	0.7 (>3X)	5	0	100.0	Memb only	348	1
≥ 2 unique peptides	pNG4013	Q5V7T9_HALMA	*pNG4013*	Hypothetical protein	0	0	4	2	0	0	1	1	4	1	5	4.0	0.7 (>3X)	0	5	0.0	Soluble only	138	0
≥ 2 unique peptides	rrnAC1727	Q5V1H2_HALMA	*rrnAC1727*	Hypothetical protein	3	2	0	0	2	2	0	0	3	2	5	1.5	**No dramatic change**	5	0	100.0	Memb only	143	1
≥ 2 unique peptides	rrnAC2016	Q5V0S7_HALMA	*rrnAC2016*	Hypothetical protein	3	2	0	0	2	1	0	0	3	2	5	1.5	**No dramatic change**	5	0	100.0	Memb only	128	2
≥ 2 unique peptides	rrnAC3242	Q5UXR2_HALMA	*rrnAC3242*	Hypothetical protein	3	1	0	0	2	2	0	0	3	2	5	1.5	**No dramatic change**	5	0	100.0	Memb only	777	11
≥ 2 unique peptides	rrnB0220	Q5UWF3_HALMA	*rrnB0220*	Hypothetical protein	0	0	3	3	0	0	2	2	3	2	5	1.5	**No dramatic change**	0	5	0.0	Soluble only	239	0
≥ 2 unique peptides	rrnB0248	Q5UWD0_HALMA	*rrnB0248*	Hypothetical protein	0	0	3	3	0	0	2	1	3	2	5	1.5	**No dramatic change**	0	5	0.0	Soluble only	144	0
≥ 2 unique peptides	rrnAC1793	Q5V1B8_HALMA	*rrnAC1793*	Hypothetical protein	0	0	3	2	0	0	2	2	3	2	5	1.5	**No dramatic change**	0	5	0.0	Soluble only	249	0
≥ 2 unique peptides	rrnAC2745	Q5UYZ4_HALMA	*rrnAC2745*	Hypothetical protein	0	0	3	2	0	0	2	1	3	2	5	1.5	**No dramatic change**	0	5	0.0	Soluble only	204	0
≥ 2 unique peptides	pNG7138	Q5V6K4_HALMA	*pNG7138*	Hypothetical protein	0	0	3	2	0	0	2	1	3	2	5	1.5	**No dramatic change**	0	5	0.0	Soluble only	144	0
≥ 2 unique peptides	rrnAC1576	Q5V1V8_HALMA	*rrnAC1576*	Hypothetical protein	2	2	0	0	3	2	0	0	2	3	5	0.7	**No dramatic change**	5	0	100.0	Memb only	310	0
≥ 2 unique peptides	pNG7286	Q5V669_HALMA	*pNG7286*	Hypothetical protein	2	1	0	0	3	2	0	0	2	3	5	0.7	**No dramatic change**	5	0	100.0	Memb only	584	11
≥ 2 unique peptides	rrnB0234	Q5UWE2_HALMA	*rrnB0234*	Hypothetical protein	0	0	2	1	0	0	3	3	2	3	5	0.7	**No dramatic change**	0	5	0.0	Soluble only	108	0
≥ 2 unique peptides	rrnAC1721	Q5V1H6_HALMA	*rrnAC1721*	Hypothetical protein	0	0	2	2	0	0	3	2	2	3	5	0.7	**No dramatic change**	0	5	0.0	Soluble only	236	0
≥ 2 unique peptides	rrnAC1629	Q5V1Q9_HALMA	*rrnAC1629*	Hypothetical protein	0	0	2	2	0	0	3	2	2	3	5	0.7	**No dramatic change**	0	5	0.0	Soluble only	336	0
≥ 2 unique peptides	rrnAC0682	Q5V469_HALMA	*rrnAC0682*	Hypothetical protein	0	0	2	2	0	0	3	2	2	3	5	0.7	**No dramatic change**	0	5	0.0	Soluble only	146	0
≥ 2 unique peptides	rrnAC0592	Q5V4E9_HALMA	*rrnAC0592*	Hypothetical protein	0	0	2	2	0	0	3	2	2	3	5	0.7	**No dramatic change**	0	5	0.0	Soluble only	169	0
≥ 2 unique peptides	pNG4044	Q5V7W3_HALMA	*pNG4044*	Hypothetical protein	0	0	2	2	0	0	3	2	2	3	5	0.7	**No dramatic change**	0	5	0.0	Soluble only	79	0
≥ 2 unique peptides	rrnAC2864	Q5UYN9_HALMA	*rrnAC2864*	Hypothetical protein	0	0	2	2	0	0	3	1	2	3	5	0.7	**No dramatic change**	0	5	0.0	Soluble only	261	0
≥ 2 unique peptides	rrnAC3452	Q5UX73_HALMA	*rrnAC3452*	Hypothetical protein	1	1	0	0	4	3	0	0	1	4	5	0.3	1.2 (>3X)	5	0	100.0	Memb only	316	0
≥ 2 unique peptides	rrnAC1398	Q5V2C5_HALMA	*rrnAC1398*	Hypothetical protein	1	1	0	0	4	3	0	0	1	4	5	0.3	1.2 (>3X)	5	0	100.0	Memb only	518	11
≥ 2 unique peptides	rrnAC1654	Q5V1N5_HALMA	*rrnAC1654*	Hypothetical protein	1	1	0	0	4	2	0	0	1	4	5	0.3	1.2 (>3X)	5	0	100.0	Memb only	190	0
≥ 2 unique peptides	rrnAC2718	Q5UZ18_HALMA	*rrnAC2718*	Hypothetical protein	0	0	1	1	0	0	4	3	1	4	5	0.3	1.2 (>3X)	0	5	0.0	Soluble only	159	0
≥ 2 unique peptides	rrnAC3332	Q5UXI1_HALMA	*rrnAC3332*	Hypothetical protein	0	0	0	0	0	0	5	3	0	5	5	0.0	1.2 only	0	5	0.0	Soluble only	249	0
≥ 2 unique peptides	rrnAC3000	Q5UYC5_HALMA	*cbiL*	Precorrin-2 C20-methyltransferase	2	2	3	2	0	0	0	0	5	0	5	∞	0.7 only	2	3	40.0	Memb + Sol	265	0
≥ 2 unique peptides	rrnAC3258	ATGT_HALMAReview	*tgtA*	7-cyano-7-deazaguanine tRNA-ribosyltransferase (EC 2.4.2.-) (ArchaealtRNA-guanine transglycosylase)	0	0	5	2	0	0	0	0	5	0	5	∞	0.7 only	0	5	0.0	Soluble only	490	0

≥ 2 unique peptides	rrnB0259	Q5UWC2_HALMA	*fapS*	Cyclopropane-fatty-acyl-phospholipid synthase (EC 2.1.1.79)	0	0	5	2	0	0	0	0	5	0	5	∞	0.7 only	0	5	0.0	Soluble only	240	0
≥ 2 unique peptides	rrnAC1873	Q5V148_HALMA	*dpg*	Dolichol-P-glucose synthetase	4	4	0	0	1	1	0	0	4	1	5	4.0	0.7 (>3X)	5	0	100.0	Memb only	605	7
≥ 2 unique peptides	rrnAC1074	Q5V366_HALMA	*fadD3*	Long-chain fatty-acid-CoA ligase	3	3	1	1	1	1	0	0	4	1	5	4.0	0.7 (>3X)	4	1	80.0	Memb predominant	660	0
≥ 2 unique peptides	rrnAC2371	HIS2_HALMAReview	*hisE*	Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31) (PRA-PH)	0	0	4	3	0	0	1	1	4	1	5	4.0	0.7 (>3X)	0	5	0.0	Soluble only	98	0
≥ 2 unique peptides	rrnAC1910	Q5V119_HALMA	*fbr1*	Cytochrome-like protein Fbr	3	2	0	0	2	1	0	0	3	2	5	1.5	**No dramatic change**	5	0	100.0	Memb only	823	0
≥ 2 unique peptides	rrnAC1776	DCD_HALMAReview	*dcd*	Probable deoxycytidine triphosphate deaminase (EC 3.5.4.13) (dCTPdeaminase)	0	0	3	3	0	0	2	2	3	2	5	1.5	**No dramatic change**	0	5	0.0	Soluble only	195	0
≥ 2 unique peptides	rrnAC0866	CAAL_HALMAReview	*rrnAC0866*	Carboxylate-amine ligase rrnAC0866 (EC 6.3.-.-)	0	0	3	2	0	0	2	2	3	2	5	1.5	**No dramatic change**	0	5	0.0	Soluble only	359	0
≥ 2 unique peptides	rrnAC1004	Q5V3D2_HALMA	*suhB1*	Inositol-1-monophosphatase (EC 3.1.3.25)	0	0	3	1	0	0	2	2	3	2	5	1.5	**No dramatic change**	0	5	0.0	Soluble only	279	0
≥ 2 unique peptides	rrnAC1858	Q5V161_HALMA	*rrnAC1858*	Aldo/keto reductase	0	0	2	1	0	0	3	3	2	3	5	0.7	**No dramatic change**	0	5	0.0	Soluble only	361	0
≥ 2 unique peptides	rrnAC3480	Q5UX49_HALMA	*moaB2*	Molybdenum cofactor biosynthesis protein B	0	0	2	2	0	0	3	2	2	3	5	0.7	**No dramatic change**	0	5	0.0	Soluble only	321	0
≥ 2 unique peptides	rrnAC1893	Q5V132_HALMA	*ldc*	LD-carboxypeptidase	0	0	2	2	0	0	3	2	2	3	5	0.7	**No dramatic change**	0	5	0.0	Soluble only	353	0
≥ 2 unique peptides	rrnAC1236	Q5V2S2_HALMA	*cysK1*	Cysteine synthase (EC 2.5.1.47)	0	0	2	2	0	0	3	2	2	3	5	0.7	**No dramatic change**	0	5	0.0	Soluble only	303	0
≥ 2 unique peptides	rrnAC0102	Q5V5M4_HALMA	*npd*	2-nitropropane dioxygenase-related protein	0	0	2	1	0	0	3	2	2	3	5	0.7	**No dramatic change**	0	5	0.0	Soluble only	337	0
≥ 2 unique peptides	rrnAC2529	HIS4_HALMAReview	*hisA*	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase (EC 5.3.1.16)(Phosphoribosylformimino-5-aminoimidazole carboxamide ribotideisomerase)	0	0	1	1	0	0	4	4	1	4	5	0.3	1.2 (>3X)	0	5	0.0	Soluble only	246	0
≥ 2 unique peptides	rrnAC1650	PCRB_HALMAReview	*pcrB*	Protein pcrB homolog	0	0	1	1	0	0	4	2	1	4	5	0.3	1.2 (>3X)	0	5	0.0	Soluble only	253	0
≥ 2 unique peptides	rrnAC2671	Q5UZ55_HALMA	*inb*	Oxidoreductase-like	0	0	0	0	0	0	5	3	0	5	5	0.0	1.2 only	0	5	0.0	Soluble only	247	0
≥ 2 unique peptides	rrnAC1292	SYC_HALMAReview	*cysS*	Cysteinyl-tRNA synthetase (EC 6.1.1.16) (Cysteine--tRNA ligase)(CysRS)	0	0	0	0	0	0	5	3	0	5	5	0.0	1.2 only	0	5	0.0	Soluble only	492	0
≥ 2 unique peptides	pNG7328	FOLD2_HALMAReview	*folD2*	Bifunctional protein folD 2 [Includes: Methylenetetrahydrofolatedehydrogenase (EC 1.5.1.5); Methenyltetrahydrofolate cyclohydrolase(EC 3.5.4.9)]	0	0	0	0	0	0	5	2	0	5	5	0.0	1.2 only	0	5	0.0	Soluble only	297	0
≥ 2 unique peptides	rrnAC2435	Q5UZQ8_HALMA	*rrnAC2435*	Putative phosphoesterase	0	0	0	0	0	0	5	2	0	5	5	0.0	1.2 only	0	5	0.0	Soluble only	162	0
≥ 2 unique peptides	rrnAC0962	Q5V3G9_HALMA	*pcm3*	Protein-L-isoaspartate O-methyltransferase (EC 2.1.1.77)	0	0	0	0	0	0	5	2	0	5	5	0.0	1.2 only	0	5	0.0	Soluble only	204	0
≥ 2 unique peptides	rrnB0187	Q5UWI1_HALMA	*rrnB0187*	Putative cupin	0	0	4	3	0	0	1	1	4	1	5	4.0	0.7 (>3X)	0	5	0.0	Soluble only	142	0
≥ 2 unique peptides	rrnAC0659	Q5V489_HALMA	*ama*	N-acyl-L-amino acid amidohydrolase	0	0	1	1	1	1	3	2	1	4	5	0.3	1.2 (>3X)	1	4	20.0	Soluble predominant	423	0
≥ 2 unique peptides	rrnAC0939	Q5V3J0_HALMA	*dpm6*	Dolichyl-phosphate-mannose-protein mannosyltransferase	5	2	0	0	0	0	0	0	5	0	5	∞	0.7 only	5	0	100.0	Memb only	595	10
≥ 2 unique peptides	rrnAC1596	RL6_HALMAReview	*rpl6p*	50S ribosomal protein L6P (Hmal6) (Hl10)	0	0	5	2	0	0	0	0	5	0	5	∞	0.7 only	0	5	0.0	Soluble only	178	0
≥ 2 unique peptides	rrnAC2466	Q5UZN0_HALMA	*livM-5*	Branched-chain amino acid ABC transporter permease protein	4	4	0	0	1	1	0	0	4	1	5	4.0	0.7 (>3X)	5	0	100.0	Memb only	369	8
≥ 2 unique peptides	rrnAC1749	Q5V1F4_HALMA	*glnH2*	Glutamine ABC transporter permease protein	2	2	0	0	3	2	0	0	2	3	5	0.7	**No dramatic change**	5	0	100.0	Memb only	226	3
≥ 2 unique peptides	rrnAC2527	Q5UZH3_HALMA	*ylnA*	Anion permease	2	1	0	0	3	2	0	0	2	3	5	0.7	**No dramatic change**	5	0	100.0	Memb only	402	10
≥ 2 unique peptides	rrnAC1769	Q5V1D8_HALMA	*putP-2*	Sodium-solute symporter putative	0	0	0	0	5	4	0	0	0	5	5	0.0	1.2 only	5	0	100.0	Memb only	502	13
≥ 2 unique peptides	rrnAC0001	Q5V5W5_HALMA	*birA*	Biotin-(Acetyl-CoA carboxylase) ligase	0	0	0	0	0	0	5	4	0	5	5	0.0	1.2 only	0	5	0.0	Soluble only	315	0
≥ 2 unique peptides	rrnAC2691	DP2L_HALMAReview	*polC*	DNA polymerase II large subunit (EC 2.7.7.7) (Pol II) [Contains: HmapolC intein (Hma pol II intein)]	0	0	3	3	0	0	1	1	3	1	4	3.0	0.7 (>3X)	0	4	0.0	Soluble only	1395	0
≥ 2 unique peptides	rrnAC0475	Q5V4Q2_HALMA	*rrnAC0475*	Sensor protein (EC 2.7.13.3)	0	0	1	1	0	0	3	3	1	3	4	0.3	1.2 (>3X)	0	4	0.0	Soluble only	330	0
≥ 2 unique peptides	rrnAC0698	Q5V457_HALMA	*nusG*	Transcription antitermination protein NusG	0	0	1	1	0	0	3	2	1	3	4	0.3	1.2 (>3X)	0	4	0.0	Soluble only	145	0
≥ 2 unique peptides	pNG6070	Q5V731_HALMA	*trx*	DSBA-like thioredoxin	3	3	0	0	1	1	0	0	3	1	4	3.0	0.7 (>3X)	4	0	100.0	Memb only	328	0
≥ 2 unique peptides	rrnAC1046	Q5V392_HALMA	*rrnAC1046*	Hypothetical protein	4	3	0	0	0	0	0	0	4	0	4	∞	0.7 only	4	0	100.0	Memb only	255	0
≥ 2 unique peptides	rrnAC3540	Q5UWZ7_HALMA	*rrnAC3540*	Hypothetical protein	4	2	0	0	0	0	0	0	4	0	4	∞	0.7 only	4	0	100.0	Memb only	521	13
≥ 2 unique peptides	rrnAC1221	Q5V2T7_HALMA	*rrnAC1221*	Hypothetical protein	4	2	0	0	0	0	0	0	4	0	4	∞	0.7 only	4	0	100.0	Memb only	317	3
≥ 2 unique peptides	rrnAC0397	Q5V4W7_HALMA	*rrnAC0397*	Hypothetical protein	0	0	4	3	0	0	0	0	4	0	4	∞	0.7 only	0	4	0.0	Soluble only	298	0
≥ 2 unique peptides	pNG5051	Q5V7K6_HALMA	*pNG5051*	Hypothetical protein	0	0	4	3	0	0	0	0	4	0	4	∞	0.7 only	0	4	0.0	Soluble only	238	0
≥ 2 unique peptides	rrnAC2538	Q5UZG4_HALMA	*rrnAC2538*	Hypothetical protein	3	3	0	0	1	1	0	0	3	1	4	3.0	0.7 (>3X)	4	0	100.0	Memb only	394	1
≥ 2 unique peptides	rrnAC3097	Q5UY44_HALMA	*rrnAC3097*	Hypothetical protein	0	0	3	3	0	0	1	1	3	1	4	3.0	0.7 (>3X)	0	4	0.0	Soluble only	105	0
≥ 2 unique peptides	pNG7114	Q5V6M7_HALMA	*pNG7114*	Hypothetical protein	0	0	3	3	0	0	1	1	3	1	4	3.0	0.7 (>3X)	0	4	0.0	Soluble only	229	0
≥ 2 unique peptides	rrnAC2943	Q5UYH5_HALMA	*rrnAC2943*	Hypothetical protein	0	0	3	2	0	0	1	1	3	1	4	3.0	0.7 (>3X)	0	4	0.0	Soluble only	55	0
≥ 2 unique peptides	pNG6006	Q5V703_HALMA	*pNG6006*	Hypothetical protein	0	0	3	2	0	0	1	1	3	1	4	3.0	0.7 (>3X)	0	4	0.0	Soluble only	196	0
≥ 2 unique peptides	pNG6167	Q5V7A6_HALMA	*pNG6167*	Hypothetical protein	0	0	3	2	0	0	1	1	3	1	4	3.0	0.7 (>3X)	0	4	0.0	Soluble only	255	0
≥ 2 unique peptides	rrnAC3070	Q5UY66_HALMA	*rrnAC3070*	Hypothetical protein	2	2	0	0	2	2	0	0	2	2	4	1.0	**No dramatic change**	4	0	100.0	Memb only	219	2
≥ 2 unique peptides	rrnAC3056	Q5UY78_HALMA	*rrnAC3056*	Hypothetical protein	2	2	0	0	2	2	0	0	2	2	4	1.0	**No dramatic change**	4	0	100.0	Memb only	880	0
≥ 2 unique peptides	rrnAC0347	Q5V508_HALMA	*rrnAC0347*	Hypothetical protein	2	2	0	0	2	2	0	0	2	2	4	1.0	**No dramatic change**	4	0	100.0	Memb only	149	0
≥ 2 unique peptides	rrnAC2732	Q5UZ06_HALMA	*rrnAC2732*	Hypothetical protein	2	2	0	0	2	1	0	0	2	2	4	1.0	**No dramatic change**	4	0	100.0	Memb only	279	5
≥ 2 unique peptides	rrnAC1361	Q5V2G1_HALMA	*rrnAC1361*	Hypothetical protein	2	1	0	0	2	2	0	0	2	2	4	1.0	**No dramatic change**	4	0	100.0	Memb only	165	0
≥ 2 unique peptides	rrnAC0998	Q5V3D8_HALMA	*rrnAC0998*	Hypothetical protein	2	2	0	0	2	1	0	0	2	2	4	1.0	**No dramatic change**	4	0	100.0	Memb only	196	0
≥ 2 unique peptides	rrnAC1336	Q5V2I4_HALMA	*rrnAC1336*	Hypothetical protein	0	0	2	2	0	0	2	2	2	2	4	1.0	**No dramatic change**	0	4	0.0	Soluble only	141	0
≥ 2 unique peptides	rrnAC2754	Q5UYY5_HALMA	*rrnAC2754*	Hypothetical protein	0	0	2	2	0	0	2	1	2	2	4	1.0	**No dramatic change**	0	4	0.0	Soluble only	138	0
≥ 2 unique peptides	rrnAC2641	Q5UZ80_HALMA	*rrnAC2641*	Hypothetical protein	0	0	2	1	0	0	2	2	2	2	4	1.0	**No dramatic change**	0	4	0.0	Soluble only	305	0

≥ 2 unique peptides	rrnAC1513	Q5V218_HALMA	*rrnAC1513*	Hypothetical protein	0	0	2	2	0	0	2	1	2	2	4	1.0	**No dramatic change**	0	4	0.0	Soluble only	114	0
≥ 2 unique peptides	rrnAC1460	Q5V267_HALMA	*rrnAC1460*	Hypothetical protein	0	0	2	2	0	0	2	1	2	2	4	1.0	**No dramatic change**	0	4	0.0	Soluble only	89	0
≥ 2 unique peptides	rrnAC3178	Q5UXW9_HALMA	*rrnAC3178*	Hypothetical protein	1	1	0	0	3	2	0	0	1	3	4	0.3	1.2 (>3X)	4	0	100.0	Memb only	344	7
≥ 2 unique peptides	rrnAC0400	Q5V4W5_HALMA	*rrnAC0400*	Hypothetical protein	0	0	1	1	0	0	3	3	1	3	4	0.3	1.2 (>3X)	0	4	0.0	Soluble only	277	0
≥ 2 unique peptides	rrnAC2923	Q5UYJ2_HALMA	*rrnAC2923*	Hypothetical protein	0	0	1	1	0	0	3	2	1	3	4	0.3	1.2 (>3X)	0	4	0.0	Soluble only	158	0
≥ 2 unique peptides	rrnAC2567	Q5UZE2_HALMA	*rrnAC2567*	Hypothetical protein	0	0	1	1	0	0	3	2	1	3	4	0.3	1.2 (>3X)	0	4	0.0	Soluble only	150	0
≥ 2 unique peptides	rrnAC2554	Q5UZF1_HALMA	*rrnAC2554*	Hypothetical protein	0	0	1	1	0	0	3	2	1	3	4	0.3	1.2 (>3X)	0	4	0.0	Soluble only	167	0
≥ 2 unique peptides	rrnAC2323	Q5V006_HALMA	*rrnAC2323*	Hypothetical protein	0	0	1	1	0	0	3	2	1	3	4	0.3	1.2 (>3X)	0	4	0.0	Soluble only	202	0
≥ 2 unique peptides	rrnAC2200	Q5V0B6_HALMA	*rrnAC2200*	Hypothetical protein	0	0	1	1	0	0	3	2	1	3	4	0.3	1.2 (>3X)	0	4	0.0	Soluble only	111	0
≥ 2 unique peptides	rrnAC1859	Q5V160_HALMA	*rrnAC1859*	Hypothetical protein	0	0	1	1	0	0	3	2	1	3	4	0.3	1.2 (>3X)	0	4	0.0	Soluble only	56	0
≥ 2 unique peptides	rrnAC1181	Q5V2X1_HALMA	*rrnAC1181*	Hypothetical protein	0	0	1	1	0	0	3	2	1	3	4	0.3	1.2 (>3X)	0	4	0.0	Soluble only	274	0
≥ 2 unique peptides	rrnAC1069	Q5V371_HALMA	*rrnAC1069*	Hypothetical protein	0	0	1	1	0	0	3	2	1	3	4	0.3	1.2 (>3X)	0	4	0.0	Soluble only	437	0
≥ 2 unique peptides	rrnAC1733	Q5V1G6_HALMA	*rrnAC1733*	Hypothetical protein	0	0	0	0	4	3	0	0	0	4	4	0.0	1.2 only	4	0	100.0	Memb only	328	4
≥ 2 unique peptides	rrnAC3292	Q5UXL7_HALMA	*rrnAC3292*	Hypothetical protein	0	0	0	0	0	0	4	3	0	4	4	0.0	1.2 only	0	4	0.0	Soluble only	174	0
≥ 2 unique peptides	pNG5053	Q5V7K4_HALMA	*pNG5053*	Hypothetical protein	0	0	0	0	0	0	4	3	0	4	4	0.0	1.2 only	0	4	0.0	Soluble only	524	1
≥ 2 unique peptides	rrnAC1119	Q5V326_HALMA	*rrnAC1119*	Hypothetical protein	0	0	0	0	0	0	4	2	0	4	4	0.0	1.2 only	0	4	0.0	Soluble only	227	0
≥ 2 unique peptides	rrnAC2964	Q5UYF6_HALMA	*endA*	TRNA intron endonuclease (EC 3.1.27.9)	0	0	4	3	0	0	0	0	4	0	4	∞	0.7 only	0	4	0.0	Soluble only	335	0
≥ 2 unique peptides	rrnAC3549	Q5UWY9_HALMA	*rrnAC3549*	Putative HD family metal dependent phosphohydrolase	3	2	0	0	1	1	0	0	3	1	4	3.0	0.7 (>3X)	4	0	100.0	Memb only	407	0
≥ 2 unique peptides	rrnAC3427	Q5UX97_HALMA	*doxD2*	Terminal quinol oxidase subunit	3	2	0	0	1	1	0	0	3	1	4	3.0	0.7 (>3X)	4	0	100.0	Memb only	128	0
≥ 2 unique peptides	rrnAC3497	Q5UX35_HALMA	*yqeF*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	0	0	3	3	0	0	1	1	3	1	4	3.0	0.7 (>3X)	0	4	0.0	Soluble only	387	0
≥ 2 unique peptides	rrnAC2717	Q5UZ19_HALMA	*serB1*	Phosphoserine phosphatase (EC 3.1.3.3)	0	0	3	3	0	0	1	1	3	1	4	3.0	0.7 (>3X)	0	4	0.0	Soluble only	210	0
≥ 2 unique peptides	rrnAC0797	Q5V3W8_HALMA	*purF*	Amidophosphoribosyl transferase (EC 2.4.2.14)	0	0	3	2	0	0	1	1	3	1	4	3.0	0.7 (>3X)	0	4	0.0	Soluble only	480	0
≥ 2 unique peptides	rrnB0309	Q5UW79_HALMA	*acaB1*	3-ketoacyl-CoA thiolase (EC 2.3.1.9)	0	0	2	2	0	0	2	2	2	2	4	1.0	**No dramatic change**	0	4	0.0	Soluble only	389	0
≥ 2 unique peptides	rrnAC0875	Q5V3P8_HALMA	*rrnAC0875*	Putative haloacid dehalogenase-like hydrolase	0	0	2	2	0	0	2	2	2	2	4	1.0	**No dramatic change**	0	4	0.0	Soluble only	134	0
≥ 2 unique peptides	rrnAC3348	KHSE_HALMAReview	*thrB*	Homoserine kinase (EC 2.7.1.39) (HSK) (HK)	0	0	2	2	0	0	2	1	2	2	4	1.0	**No dramatic change**	0	4	0.0	Soluble only	291	0
≥ 2 unique peptides	rrnAC2914	Q5UYJ9_HALMA	*yvaI*	Acetyltransferase-like	0	0	2	1	0	0	2	2	2	2	4	1.0	**No dramatic change**	0	4	0.0	Soluble only	301	0
≥ 2 unique peptides	rrnAC0810	Q5V3V7_HALMA	*nitA*	Nitrilase	0	0	2	2	0	0	2	1	2	2	4	1.0	**No dramatic change**	0	4	0.0	Soluble only	272	0
≥ 2 unique peptides	rrnAC3312	Q5UXK0_HALMA	*cyp1*	Cytochrome P450 (EC 1.14.14.1) (EC 1.6.2.4)	1	1	0	0	3	3	0	0	1	3	4	0.3	1.2 (>3X)	4	0	100.0	Memb only	458	0
≥ 2 unique peptides	rrnAC0179	Q5V5F9_HALMA	*rfbU*	LPS biosynthesis protein	1	1	0	0	3	2	0	0	1	3	4	0.3	1.2 (>3X)	4	0	100.0	Memb only	352	0
≥ 2 unique peptides	rrnAC1500	GCST_HALMAReview	*gcvT*	Probable aminomethyltransferase (EC 2.1.2.10) (Glycine cleavage systemT protein)	0	0	1	1	0	0	3	3	1	3	4	0.3	1.2 (>3X)	0	4	0.0	Soluble only	363	0
≥ 2 unique peptides	rrnAC2508	Q5UZJ1_HALMA	*ilvA2*	Threonine dehydratase (EC 4.3.1.19)	0	0	1	1	0	0	3	3	1	3	4	0.3	1.2 (>3X)	0	4	0.0	Soluble only	403	0
≥ 2 unique peptides	rrnAC3483	Q5UX46_HALMA	*fabG2*	3-oxoacyl-[acyl-carrier protein] reductase	0	0	1	1	0	0	3	2	1	3	4	0.3	1.2 (>3X)	0	4	0.0	Soluble only	232	0
≥ 2 unique peptides	rrnAC3032	Q5UY97_HALMA	*dgoA2*	Mandelate racemase/muconate lactonizing enzyme family protein	0	0	1	1	0	0	3	2	1	3	4	0.3	1.2 (>3X)	0	4	0.0	Soluble only	391	0
≥ 2 unique peptides	rrnAC0241	Q5V5A3_HALMA	*hadL*	2-haloalkanoic acid dehalogenase (EC 3.8.1.2)	0	0	1	1	0	0	3	2	1	3	4	0.3	1.2 (>3X)	0	4	0.0	Soluble only	235	0
≥ 2 unique peptides	pNG7363	Q5V5Z7_HALMA	*metF*	5,10-methylenetetrahydrofolate reductase (EC 1.7.99.5)	0	0	0	0	4	2	0	0	0	4	4	0.0	1.2 only	4	0	100.0	Memb only	286	0
≥ 2 unique peptides	rrnAC1275	Q5V2N9_HALMA	*mcmA2*	Methylmalonyl-CoA mutase subunit alpha	0	0	0	0	0	0	4	3	0	4	4	0.0	1.2 only	0	4	0.0	Soluble only	567	0
≥ 2 unique peptides	rrnAC1113	Q5V332_HALMA	*bglX-2*	Beta-D-glucosidase	0	0	0	0	0	0	4	3	0	4	4	0.0	1.2 only	0	4	0.0	Soluble only	719	0
≥ 2 unique peptides	rrnAC2222	Q5V098_HALMA	*rrnAC2222*	Acetyltransferase (GNAT) family	0	0	0	0	0	0	4	2	0	4	4	0.0	1.2 only	0	4	0.0	Soluble only	173	0
≥ 2 unique peptides	rrnAC0016	Q5V5V1_HALMA	*tfbA*	Transcription initiation factor IIB	0	0	4	2	0	0	0	0	4	0	4	∞	0.7 only	0	4	0.0	Soluble only	319	0
≥ 2 unique peptides	rrnAC3513	Q5UX21_HALMA	*rps27E*	30S ribosomal protein S27e	0	0	1	1	0	0	3	2	1	3	4	0.3	1.2 (>3X)	0	4	0.0	Soluble only	57	0
≥ 2 unique peptides	rrnAC2405	RS10_HALMAReview	*rps10p*	30S ribosomal protein S10P (HmaS10)	0	0	1	1	0	0	3	2	1	3	4	0.3	1.2 (>3X)	0	4	0.0	Soluble only	103	0
≥ 2 unique peptides	rrnAC2374	Q5UZW3_HALMA	*gbp4*	GTP-binding protein	0	0	2	2	0	0	2	2	2	2	4	1.0	**No dramatic change**	0	4	0.0	Soluble only	331	0
≥ 2 unique peptides	rrnAC3508	Q5UX26_HALMA	*usp7*	Universal stress protein	1	1	0	0	0	0	3	3	1	3	4	0.3	1.2 (>3X)	1	3	25.0	Soluble predominant	296	0
≥ 2 unique peptides	rrnAC2836	Q5UYR4_HALMA	*dld*	Sugar and other transporter	3	2	0	0	1	1	0	0	3	1	4	3.0	0.7 (>3X)	4	0	100.0	Memb only	452	12
≥ 2 unique peptides	rrnAC0048	Q5V5S2_HALMA	*rrnAC0048*	ABC transporter ATP-binding protein	2	2	0	0	2	2	0	0	2	2	4	1.0	**No dramatic change**	4	0	100.0	Memb only	313	0
≥ 2 unique peptides	pNG7340	Q5V618_HALMA	*pNG7340*	Putative extracellular solute binding protein	2	2	0	0	2	1	0	0	2	2	4	1.0	**No dramatic change**	4	0	100.0	Memb only	452	0
≥ 2 unique peptides	rrnAC2512	Q5UZI8_HALMA	*pchB*	Potassium channel-related protein	0	0	2	2	0	0	2	2	2	2	4	1.0	**No dramatic change**	0	4	0.0	Soluble only	407	0
≥ 2 unique peptides	rrnAC2876	HELS_HALMAReview	*rrnAC2876*	Putative ski2-type helicase (EC 3.6.1.-)	0	0	0	0	0	0	4	3	0	4	4	0.0	1.2 only	0	4	0.0	Soluble only	799	0
≥ 2 unique peptides	rrnAC1840	Q5V177_HALMA	*smc1*	Structural maintenance of chromosomes	0	0	2	2	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	0	3	0.0	Soluble only	908	0
≥ 2 unique peptides	rrnB0041	Q5UWV1_HALMA	*xseA2*	Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)	3	3	0	0	0	0	0	0	3	0	3	∞	0.7 only	3	0	100.0	Memb only	403	1
≥ 2 unique peptides	rrnAC2532	MUTS1_HALMAReview	*mutS1*	DNA mismatch repair protein mutS 1	0	0	2	2	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	0	3	0.0	Soluble only	921	0
≥ 2 unique peptides	rrnAC1777	Q5V1D0_HALMA	*rrnAC1777*	DNA binding protein	0	0	2	2	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	0	3	0.0	Soluble only	298	0
≥ 2 unique peptides	rrnAC0832	Q5V3T8_HALMA	*phrB1*	Deoxyribodipyrimidine photolyase (EC 4.1.99.3)	0	0	2	2	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	0	3	0.0	Soluble only	465	0
≥ 2 unique peptides	rrnB0299	Q5UW88_HALMA	*oye*	Sensor protein (EC 2.7.13.3)	0	0	1	1	0	0	2	2	1	2	3	0.5	1.2 (2~3X)	0	3	0.0	Soluble only	1971	0
≥ 2 unique peptides	rrnAC1831	Q5V184_HALMA	*polB1*	DNA polymerase B elongation subunit (EC 2.7.7.7)	0	0	1	1	0	0	2	2	1	2	3	0.5	1.2 (2~3X)	0	3	0.0	Soluble only	1388	0
≥ 2 unique peptides	rrnAC0440	Q5V4S8_HALMA	*rrnAC0440*	Transcription regulator	0	0	1	1	0	0	2	2	1	2	3	0.5	1.2 (2~3X)	0	3	0.0	Soluble only	180	0

≥ 2 unique peptides	rrnB0280	Q5UWA4_HALMA	*rrnB0280*	Hypothetical protein	3	3	0	0	0	0	0	0	3	0	3	∞	0.7 only	3	0	100.0	Memb only	132	0
≥ 2 unique peptides	rrnAC0042	Q5V5S8_HALMA	*rrnAC0042*	Hypothetical protein	3	3	0	0	0	0	0	0	3	0	3	∞	0.7 only	3	0	100.0	Memb only	253	1
≥ 2 unique peptides	pNG2038	Q5V822_HALMA	*pNG2038*	Hypothetical protein	3	3	0	0	0	0	0	0	3	0	3	∞	0.7 only	3	0	100.0	Memb only	324	0
≥ 2 unique peptides	rrnB0307	Q5UW81_HALMA	*rrnB0307*	Hypothetical protein	3	2	0	0	0	0	0	0	3	0	3	∞	0.7 only	3	0	100.0	Memb only	318	7
≥ 2 unique peptides	rrnAC1586	Q5V1U8_HALMA	*rrnAC1586*	Hypothetical protein	3	2	0	0	0	0	0	0	3	0	3	∞	0.7 only	3	0	100.0	Memb only	470	5
≥ 2 unique peptides	rrnAC1092	Q5V348_HALMA	*rrnAC1092*	Hypothetical protein	3	2	0	0	0	0	0	0	3	0	3	∞	0.7 only	3	0	100.0	Memb only	121	3
≥ 2 unique peptides	pNG5104	Q5V7Q7_HALMA	*pNG5104*	Hypothetical protein	0	0	3	3	0	0	0	0	3	0	3	∞	0.7 only	0	3	0.0	Soluble only	371	0
≥ 2 unique peptides	rrnB0166	Q5UWK0_HALMA	*rrnB0166*	Hypothetical protein	0	0	3	2	0	0	0	0	3	0	3	∞	0.7 only	0	3	0.0	Soluble only	371	0
≥ 2 unique peptides	rrnAC0974	Q5V3F9_HALMA	*rrnAC0974*	Hypothetical protein	0	0	3	2	0	0	0	0	3	0	3	∞	0.7 only	0	3	0.0	Soluble only	551	0
≥ 2 unique peptides	rrnAC3528	Q5UX08_HALMA	*rrnAC3528*	Hypothetical protein	2	2	0	0	1	1	0	0	2	1	3	2.0	0.7 (2>3X)	3	0	100.0	Memb only	158	1
≥ 2 unique peptides	rrnAC0631	Q5V4B3_HALMA	*rrnAC0631*	Hypothetical protein	2	2	0	0	1	1	0	0	2	1	3	2.0	0.7 (2>3X)	3	0	100.0	Memb only	213	5
≥ 2 unique peptides	pNG7304	Q5V652_HALMA	*pNG7304*	Hypothetical protein	2	2	0	0	1	1	0	0	2	1	3	2.0	0.7 (2>3X)	3	0	100.0	Memb only	166	0
≥ 2 unique peptides	rrnAC2375	Q5UZW2_HALMA	*rrnAC2375*	Hypothetical protein	2	2	0	0	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	2	1	66.7	Memb + Sol	236	1
≥ 2 unique peptides	rrnAC2295	Q5V033_HALMA	*rrnAC2295*	Hypothetical protein	2	2	0	0	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	2	1	66.7	Memb + Sol	597	0
≥ 2 unique peptides	rrnB0286	Q5UW98_HALMA	*rrnB0286*	Hypothetical protein	0	0	2	2	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	0	3	0.0	Soluble only	413	0
≥ 2 unique peptides	rrnAC3083	Q5UY55_HALMA	*rrnAC3083*	Hypothetical protein	0	0	2	2	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	0	3	0.0	Soluble only	140	0
≥ 2 unique peptides	rrnAC1103	Q5V340_HALMA	*rrnAC1103*	Hypothetical protein	0	0	2	2	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	0	3	0.0	Soluble only	269	0
≥ 2 unique peptides	rrnAC3061	Q5UY74_HALMA	*rrnAC3061*	Hypothetical protein	1	1	0	0	2	2	0	0	1	2	3	0.5	1.2 (2~3X)	3	0	100.0	Memb only	136	2
≥ 2 unique peptides	rrnB0188	Q5UWI0_HALMA	*rrnB0188*	Hypothetical protein	0	0	1	1	0	0	2	2	1	2	3	0.5	1.2 (2~3X)	0	3	0.0	Soluble only	406	0
≥ 2 unique peptides	rrnAC2746	Q5UYZ3_HALMA	*rrnAC2746*	Hypothetical protein	0	0	1	1	0	0	2	2	1	2	3	0.5	1.2 (2~3X)	0	3	0.0	Soluble only	142	0
≥ 2 unique peptides	pNG1009	Q5V865_HALMA	*pNG1009*	Hypothetical protein	0	0	1	1	0	0	2	2	1	2	3	0.5	1.2 (2~3X)	0	3	0.0	Soluble only	287	0
≥ 2 unique peptides	pNG7317	Q5V640_HALMA	*pNG7317*	Hypothetical protein	0	0	0	0	0	0	3	3	0	3	3	0.0	1.2 only	0	3	0.0	Soluble only	243	0
≥ 2 unique peptides	rrnAC2803	Q5UYU4_HALMA	*rrnAC2803*	Hypothetical protein	0	0	0	0	0	0	3	2	0	3	3	0.0	1.2 only	0	3	0.0	Soluble only	365	0
≥ 2 unique peptides	rrnAC1780	Q5V1C8_HALMA	*rrnAC1780*	Hypothetical protein	0	0	0	0	0	0	3	2	0	3	3	0.0	1.2 only	0	3	0.0	Soluble only	253	0
≥ 2 unique peptides	rrnAC1015	Q5V3C2_HALMA	*gtr-7*	Glycosyltransferase (EC 2.4.1.-)	3	2	0	0	0	0	0	0	3	0	3	∞	0.7 only	3	0	100.0	Memb only	386	0
≥ 2 unique peptides	rrnAC1694	GUAAA_HALMAReview	*guaAA*	GMP synthase [glutamine-hydrolyzing] subunit A (EC 6.3.5.2) (Glutamineamidotransferase)	0	0	3	2	0	0	0	0	3	0	3	∞	0.7 only	0	3	0.0	Soluble only	189	0
≥ 2 unique peptides	rrnAC0257	KSGA_HALMAReview	*ksgA*	Probable dimethyladenosine transferase (EC 2.1.1.-) (S-adenosylmethionine-6-N',N'-adenosyl(rRNA) dimethyltransferase) (16SrRNA dimethylase)	0	0	2	2	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	0	3	0.0	Soluble only	285	0
≥ 2 unique peptides	rrnAC2159	Q5V0F0_HALMA	*dcd3*	Probable deoxyuridine 5'-triphosphate nucleotidohydrolase(EC 3.6.1.23)	0	0	2	2	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	0	3	0.0	Soluble only	202	0
≥ 2 unique peptides	rrnAC0223	Q5V5C0_HALMA	*camH3*	Creatinine amidohydrolase (EC 3.5.2.10)	0	0	2	2	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	0	3	0.0	Soluble only	256	0
≥ 2 unique peptides	rrnAC0554	Q5V4I2_HALMA	*gpdA*	Glycerol-3-phosphate dehydrogenase (EC 1.1.99.5)	1	1	0	0	2	2	0	0	1	2	3	0.5	1.2 (2~3X)	3	0	100.0	Memb only	576	0
≥ 2 unique peptides	rrnAC0321	Q5V531_HALMA	*crtI2*	Phytoene dehydrogenase (EC 1.3.99.-)	1	1	0	0	2	2	0	0	1	2	3	0.5	1.2 (2~3X)	3	0	100.0	Memb only	495	0
≥ 2 unique peptides	rrnAC1958	Q5V0X7_HALMA	*lpg1*	LPS glycosyltransferase	1	1	0	0	0	0	2	2	1	2	3	0.5	1.2 (2~3X)	1	2	33.3	Memb + Sol	359	0
≥ 2 unique peptides	rrnAC0073	Q5V5P9_HALMA	*cyc*	Cytochrome P450 (EC 1.14.14.1) (EC 1.6.2.4)	1	1	0	0	0	0	2	2	1	2	3	0.5	1.2 (2~3X)	1	2	33.3	Memb + Sol	445	0
≥ 2 unique peptides	rrnAC3391	PPNK_HALMAReview	*ppnK*	Probable inorganic polyphosphate/ATP-NAD kinase (EC 2.7.1.23)(Poly(P)/ATP NAD kinase)	0	0	1	1	0	0	2	2	1	2	3	0.5	1.2 (2~3X)	0	3	0.0	Soluble only	283	0
≥ 2 unique peptides	rrnAC3074	Q5UY62_HALMA	*rrnAC3074*	Hypothetical protein	0	0	1	1	0	0	2	2	1	2	3	0.5	1.2 (2~3X)	0	3	0.0	Soluble only	320	0
≥ 2 unique peptides	rrnAC2463	Q5UZN3_HALMA	*scp2*	Sterol carrier protein	0	0	1	1	0	0	2	2	1	2	3	0.5	1.2 (2~3X)	0	3	0.0	Soluble only	136	0
≥ 2 unique peptides	rrnAC1660	Q5V1M9_HALMA	*yafB-3*	Oxidoreductase aldo/keto reductase family	0	0	1	1	0	0	2	2	1	2	3	0.5	1.2 (2~3X)	0	3	0.0	Soluble only	253	0
≥ 2 unique peptides	rrnAC1573	Q5V1W1_HALMA	*galE8*	UDP-glucose 4-epimerase	0	0	1	1	0	0	2	2	1	2	3	0.5	1.2 (2~3X)	0	3	0.0	Soluble only	322	0
≥ 2 unique peptides	rrnAC1431	Q5V294_HALMA	*purK*	Phosphoribosylaminoimidazole carboxylase ATP binding subunit(EC 4.1.1.21)	0	0	1	1	0	0	2	2	1	2	3	0.5	1.2 (2~3X)	0	3	0.0	Soluble only	381	0
≥ 2 unique peptides	rrnAC1967	Q5V0W8_HALMA	*glcD1*	Glycolate oxidase subunit GlcD	0	0	0	0	3	2	0	0	0	3	3	0.0	1.2 only	3	0	100.0	Memb only	1012	0
≥ 2 unique peptides	pNG7318	Q5V639_HALMA	*fdhG*	Formate dehydrogenase alpha subunit	0	0	0	0	1	1	2	2	0	3	3	0.0	1.2 only	1	2	33.3	Memb + Sol	1103	0
≥ 2 unique peptides	rrnAC1986	Q5V0V2_HALMA	*acdC*	Acyl-CoA dehydrogenase (EC 1.3.99.-)	0	0	0	0	0	0	3	3	0	3	3	0.0	1.2 only	0	3	0.0	Soluble only	379	0
≥ 2 unique peptides	pNG7032	Q5V6U8_HALMA	*adh10*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	0	0	0	0	0	0	3	3	0	3	3	0.0	1.2 only	0	3	0.0	Soluble only	343	0
≥ 2 unique peptides	rrnAC2436	COFE_HALMAReview	*cofE*	F420-0:gamma-glutamyl ligase (EC 6.3.2.-)	0	0	0	0	0	0	3	2	0	3	3	0.0	1.2 only	0	3	0.0	Soluble only	257	0
≥ 2 unique peptides	rrnAC1394	HIS6_HALMAReview	*hisF*	Imidazole glycerol phosphate synthase subunit hisF (EC 4.1.3.-) (IGPsynthase cyclase subunit) (IGP synthase subunit hisF) (ImGP synthasesubunit hisF) (IGPS subunit hisF)	0	0	0	0	0	0	3	2	0	3	3	0.0	1.2 only	0	3	0.0	Soluble only	271	0
≥ 2 unique peptides	pNG4053	Q5V7X5_HALMA	*cas1*	CRISPR-associated protein Cas1	0	0	2	2	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	0	3	0.0	Soluble only	330	0
≥ 2 unique peptides	rrnAC1418	RL12_HALMAReview	*rpl12p*	50S ribosomal protein L12P (Hmal12)	0	0	3	2	0	0	0	0	3	0	3	∞	0.7 only	0	3	0.0	Soluble only	115	0
≥ 2 unique peptides	rrnAC1610	RL4_HALMAReview	*rpl4p*	50S ribosomal protein L4P (Hmal4) (Hl6)	0	0	2	2	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	0	3	0.0	Soluble only	246	0
≥ 2 unique peptides	rrnAC1415	RL1_HALMAReview	*rpl1p*	50S ribosomal protein L1P (Hmal1) (HL8)	0	0	1	1	2	2	0	0	1	2	3	0.5	1.2 (2~3X)	2	1	66.7	Memb + Sol	212	0
≥ 2 unique peptides	rrnAC0789	Q5V3X6_HALMA	*rrnAC0789*	Sensor protein (EC 2.7.13.3)	2	2	0	0	1	1	0	0	2	1	3	2.0	0.7 (2>3X)	3	0	100.0	Memb only	576	6
≥ 2 unique peptides	rrnAC1411	Q5V2B2_HALMA	*drg*	GTP-binding protein Drg	0	0	2	2	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	0	3	0.0	Soluble only	369	0
≥ 2 unique peptides	rrnAC2314	Q5V015_HALMA	*trp3*	ABC transport protein	2	2	0	0	1	1	0	0	2	1	3	2.0	0.7 (2>3X)	3	0	100.0	Memb only	640	5
≥ 2 unique peptides	rrnAC0755	Q5V406_HALMA	*trkH3*	TRK potassium uptake system protein	2	2	0	0	1	1	0	0	2	1	3	2.0	0.7 (2>3X)	3	0	100.0	Memb only	564	10

≥ 2 unique peptides	rrnB0225	Q5UWE9_HALMA	*livG-10*	Branched-chain amino acid ABC transporter ATP-binding protein	1	1	0	0	2	2	0	0	1	2	3	0.5	1.2 (2~3X)	3	0	100.0	Memb only	254	0
≥ 2 unique peptides	rrnAC1296	Q5V2M0_HALMA	*corA*	Magnesium Mg(2+)/cobalt Co(2+) transport protein	1	1	0	0	2	2	0	0	1	2	3	0.5	1.2 (2~3X)	3	0	100.0	Memb only	205	2
≥ 2 unique peptides	rrnAC3226	Q5UXS5_HALMA	*ssf*	Sodium/solute symporter	0	0	0	0	3	2	0	0	0	3	3	0.0	1.2 only	3	0	100.0	Memb only	532	12
≥ 2 unique peptides	rrnAC3316	Q5UXJ7_HALMA	*arsC*	Putative arsenate reductase	0	0	0	0	0	0	3	2	0	3	3	0.0	1.2 only	0	3	0.0	Soluble only	142	0
≥ 2 unique peptides	rrnAC3482	Q5UX47_HALMA	*ark-6*	Sensor protein (EC 2.7.13.3)	2	2	0	0	0	0	0	0	2	0	2	∞	0.7 only	2	0	100.0	Memb only	579	6
≥ 2 unique peptides	rrnB0062	Q5UWT3_HALMA	*parA3*	Chromosome partitioning protein ParA family ATPase	0	0	2	2	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	290	0
≥ 2 unique peptides	rrnAC2661	Q5UZ64_HALMA	*rad24*	DNA repair protein	0	0	2	2	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	232	0
≥ 2 unique peptides	rrnAC1338	Q5V2I2_HALMA	*arcR-6*	Transcription regulator	0	0	2	2	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	254	0
≥ 2 unique peptides	rrnAC0992	Q5V3E2_HALMA	*rrnAC0992*	DNA binding domain similar to hmvng1864	0	0	2	2	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	91	0
≥ 2 unique peptides	rrnAC0404	Q5V4W2_HALMA	*htr12*	MCP domain signal transducer	0	0	2	2	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	438	0
≥ 2 unique peptides	rrnAC0067	RPON_HALMAReview	*rpoN*	DNA-directed RNA polymerase subunit N (EC 2.7.7.6)	0	0	2	2	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	66	0
≥ 2 unique peptides	rrnAC2996	UVRB_HALMAReview	*uvrB*	UvrABC system protein B (Protein uvrB) (Excinuclease ABC subunit B)	0	0	2	2	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	686	0
≥ 2 unique peptides	pNG6094	Q5V755_HALMA	*xseA1*	Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)	0	0	0	0	2	2	0	0	0	2	2	0.0	1.2 only	2	0	100.0	Memb only	350	1
≥ 2 unique peptides	rrnAC2144	Q5V0G5_HALMA	*rrnAC2144*	Transcription regulator	0	0	0	0	0	0	2	2	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	353	0
≥ 2 unique peptides	rrnAC1303	Q5V2L3_HALMA	*rrnAC1303*	Transcription regulator	0	0	0	0	0	0	2	2	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	124	0
≥ 2 unique peptides	rrnAC1096	Q5V346_HALMA	*kinA4*	Sensor protein (EC 2.7.13.3)	0	0	0	0	0	0	2	2	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	449	0
≥ 2 unique peptides	rrnB0096	Q5UWQ4_HALMA	*rrnB0096*	Hypothetical protein	2	2	0	0	0	0	0	0	2	0	2	∞	0.7 only	2	0	100.0	Memb only	646	0
≥ 2 unique peptides	rrnAC3534	Q5UX02_HALMA	*rrnAC3534*	Hypothetical protein	2	2	0	0	0	0	0	0	2	0	2	∞	0.7 only	2	0	100.0	Memb only	181	5
≥ 2 unique peptides	rrnAC3317	Q5UXJ6_HALMA	*rrnAC3317*	Hypothetical protein	2	2	0	0	0	0	0	0	2	0	2	∞	0.7 only	2	0	100.0	Memb only	283	5
≥ 2 unique peptides	pNG6024	Q5V707_HALMA	*pNG6024*	Hypothetical protein	2	2	0	0	0	0	0	0	2	0	2	∞	0.7 only	2	0	100.0	Memb only	199	2
≥ 2 unique peptides	rrnAC1235	Q5V2S3_HALMA	*rrnAC1235*	Hypothetical protein	0	0	2	2	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	179	0
≥ 2 unique peptides	pNG5109	Q5V7R3_HALMA	*pNG5109*	Hypothetical protein	0	0	2	2	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	326	0
≥ 2 unique peptides	pNG3015	Q5V7Y7_HALMA	*pNG3015*	Hypothetical protein	0	0	2	2	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	155	0
≥ 2 unique peptides	rrnAC3368	Q5UXE8_HALMA	*rrnAC3368*	Hypothetical protein	0	0	0	0	2	2	0	0	0	2	2	0.0	1.2 only	2	0	100.0	Memb only	291	2
≥ 2 unique peptides	rrnAC3260	Q5UXP7_HALMA	*rrnAC3260*	Hypothetical protein	0	0	0	0	2	2	0	0	0	2	2	0.0	1.2 only	2	0	100.0	Memb only	381	0
≥ 2 unique peptides	rrnAC1644	Q5V1P4_HALMA	*rrnAC1644*	Hypothetical protein	0	0	0	0	2	2	0	0	0	2	2	0.0	1.2 only	2	0	100.0	Memb only	271	4
≥ 2 unique peptides	rrnAC0424	Q5V4U4_HALMA	*rrnAC0424*	Hypothetical protein	0	0	0	0	2	2	0	0	0	2	2	0.0	1.2 only	2	0	100.0	Memb only	322	0
≥ 2 unique peptides	pNG7055	Q5V6S9_HALMA	*pNG7055*	Hypothetical protein	0	0	0	0	2	2	0	0	0	2	2	0.0	1.2 only	2	0	100.0	Memb only	269	1
≥ 2 unique peptides	pNG6041	Q5V713_HALMA	*pNG6041*	Hypothetical protein	0	0	0	0	2	2	0	0	0	2	2	0.0	1.2 only	2	0	100.0	Memb only	177	4
≥ 2 unique peptides	rrnAC3217	Q5UXT3_HALMA	*rrnAC3217*	Hypothetical protein	0	0	0	0	0	0	2	2	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	425	0
≥ 2 unique peptides	rrnAC1189	Q5V2W4_HALMA	*rrnAC1189*	Hypothetical protein	0	0	0	0	0	0	2	2	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	170	0
≥ 2 unique peptides	rrnAC1090	Q5V350_HALMA	*rrnAC1090*	Hypothetical protein	0	0	0	0	0	0	2	2	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	340	0
≥ 2 unique peptides	rrnAC0994	Q5V3E1_HALMA	*rrnAC0994*	Hypothetical protein	0	0	0	0	0	0	2	2	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	239	0
≥ 2 unique peptides	rrnAC2850	Q5UYQ2_HALMA	*pcbD-1*	Hydrolase alpha/beta hydrolase fold family	2	2	0	0	0	0	0	0	2	0	2	∞	0.7 only	2	0	100.0	Memb only	298	0
≥ 2 unique peptides	rrnAC2139	Q5V0H0_HALMA	*imd3*	Inosine monophosphate dehydrogenase (EC 1.1.1.205)	2	2	0	0	0	0	0	0	2	0	2	∞	0.7 only	2	0	100.0	Memb only	358	3
≥ 2 unique peptides	rrnAC0532	Q5V4K1_HALMA	*pgsA*	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase(EC 2.7.8.5)	2	2	0	0	0	0	0	0	2	0	2	∞	0.7 only	2	0	100.0	Memb only	202	3
≥ 2 unique peptides	rrnAC0409	Q5V4V8_HALMA	*lemA*	LemA protein	2	2	0	0	0	0	0	0	2	0	2	∞	0.7 only	2	0	100.0	Memb only	193	1
≥ 2 unique peptides	pNG7073	Q5V6R2_HALMA	*qgd*	Quinoprotein glucose dehydrogenase (EC 1.1.5.2)	2	2	0	0	0	0	0	0	2	0	2	∞	0.7 only	2	0	100.0	Memb only	402	0
≥ 2 unique peptides	rrnB0310	Q5UW78_HALMA	*fmn*	Fmn oxidoreductase protein	0	0	2	2	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	407	0
≥ 2 unique peptides	rrnAC0857	Q5V3R4_HALMA	*rrnAC0857*	Hypothetical protein	0	0	2	2	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	180	0
≥ 2 unique peptides	rrnAC0331	Q5V521_HALMA	*ilvN*	Acetolactate synthase small subunit (EC 2.2.1.6)	0	0	2	2	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	199	0
≥ 2 unique peptides	rrnAC2788	TRM1_HALMAReview	*trm1*	N(2),N(2)-dimethylguanosine tRNA methyltransferase (EC 2.1.1.32)(tRNA(guanine-26,N(2)-N(2)) methyltransferase) (tRNA 2,2-dimethylguanosine-26 methyltransferase)(tRNA(m(2,2)G26)dimethyltransferase)	0	0	2	2	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	367	0
≥ 2 unique peptides	rrnAC3145	Q5UY01_HALMA	*adk*	Adenylate kinase	0	0	0	0	0	0	2	2	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	187	0
≥ 2 unique peptides	rrnAC2480	Q5UZL8_HALMA	*act*	Acyl-CoA thioester hydrolase	0	0	0	0	0	0	2	2	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	146	0
≥ 2 unique peptides	rrnAC0628	Q5V4B6_HALMA	*sun*	TRNA and rRNA cytosine-C5-methylases	0	0	0	0	0	0	2	2	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	318	0
≥ 2 unique peptides	rrnAC0453	Q5V4R8_HALMA	*arg1*	Arginase (EC 3.5.3.1)	0	0	0	0	0	0	2	2	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	304	0
≥ 2 unique peptides	rrnAC0078	Q5V5P5_HALMA	*argB1*	Acetylglutamate kinase (EC 2.7.2.8)	0	0	0	0	0	0	2	2	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	250	0
≥ 2 unique peptides	rrnAC2170	Q5V0E0_HALMA	*pepB4*	Aminopeptidase	0	0	0	0	0	0	2	2	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	442	0
≥ 2 unique peptides	rrnAC0864	Q5V3Q7_HALMA	*nop56/58*	Archaeal nucleolar protein-like	0	0	0	0	0	0	2	2	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	280	0
≥ 2 unique peptides	pNG7235	Q5V6B6_HALMA	*ern1*	Endoribonuclease L-PSP	0	0	0	0	0	0	2	2	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	126	0
≥ 2 unique peptides	rrnAC2359	Q5UZX5_HALMA	*usp16*	Universal stress protein	0	0	0	0	2	2	0	0	0	2	2	0.0	1.2 only	2	0	100.0	Memb only	59	0
≥ 2 unique peptides	rrnB0291	Q5UW94_HALMA	*usp27*	Universal stress protein	0	0	0	0	0	0	2	2	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	279	0
≥ 2 unique peptides	rrnAC2868	Q5UYN5_HALMA	*potD2*	Spermidine/putrescine ABC transporter spermidine/putrescine bindingprotein	2	2	0	0	0	0	0	0	2	0	2	∞	0.7 only	2	0	100.0	Memb only	357	1

≥ 2 unique peptides	rrnAC2244	Q5V078_HALMA	*rrnAC2244*	Putative ZIP domain zinc transporter	2	2	0	0	0	0	0	0	2	0	2	∞	0.7 only	2	0	100.0	Memb only	284	7
≥ 2 unique peptides	rrnAC1860	Q5V159_HALMA	*rrnAC1860*	Sugar transporter	2	2	0	0	0	0	0	0	2	0	2	∞	0.7 only	2	0	100.0	Memb only	378	10
≥ 2 unique peptides	rrnAC0029	Q5V5U0_HALMA	*rrnAC0029*	Sugar ABC transporter permease protein	2	2	0	0	0	0	0	0	2	0	2	∞	0.7 only	2	0	100.0	Memb only	354	6
≥ 2 unique peptides	rrnAC3118	Q5UY25_HALMA	*dpa*	Signal recognition particle receptor	0	0	2	2	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	429	0
single hit		Q5UZZ2_HALMA	*cspD3*	Cold shock protein	0	0	50	1	0	0	12	1	50	12	62	4.2	0.7 (>3X)	0	62	0.0	Soluble only	64	0
single hit		Q5V290_HALMA	*atpC2*	ATP synthase subunit C (EC 3.6.3.14)	8	1	0	0	45	1	0	0	8	45	53	0.2	1.2 (>3X)	53	0	100.0	Memb only	115	2
single hit		Q5UWJ3_HALMA	*rrnB0173*	Hypothetical protein	16	1	0	0	7	1	0	0	16	7	23	2.3	0.7 (2>3X)	23	0	100.0	Memb only	132	3
single hit		Q5V0Z0_HALMA	*rrnAC1944*	Hypothetical protein	10	1	0	0	7	1	0	0	10	7	17	1.4	No dramatic change	17	0	100.0	Memb only	170	0
single hit		Q5V2E6_HALMA	*hcp6*	Halocyanin-like	8	1	0	0	8	1	0	0	8	8	16	1.0	No dramatic change	16	0	100.0	Memb only	258	0
single hit		Q5V729_HALMA	*pNG6066*	Hypothetical protein	7	1	0	0	8	1	0	0	7	8	15	0.9	No dramatic change	15	0	100.0	Memb only	61	2
single hit		Q5UXM6_HALMA	*rrnAC3283*	Hypothetical protein	7	1	0	0	7	1	1	1	7	8	15	0.9	No dramatic change	14	1	93.3	Memb predominant	258	2
single hit		Q5V0H2_HALMA	*rrnAC2136*	Hypothetical protein	8	1	0	0	6	1	0	0	8	6	14	1.3	No dramatic change	14	0	100.0	Memb only	410	9
single hit		Q5UXI4_HALMA	*hcp3*	Halocyanin-like	6	1	0	0	4	1	0	0	6	4	10	1.5	No dramatic change	10	0	100.0	Memb only	219	1
single hit		UPPP_HALMAReview	*uppP*	Undecaprenyl-diphosphatase (EC 3.6.1.27) (Undecaprenyl pyrophosphatephosphatase)	6	1	0	0	4	1	0	0	6	4	10	1.5	No dramatic change	10	0	100.0	Memb only	270	6
single hit		Q5V859_HALMA	*pNG1001*	Hypothetical protein	5	1	0	0	5	1	0	0	5	5	10	1.0	No dramatic change	10	0	100.0	Memb only	216	4
single hit		Q5UZC1_HALMA	*arsA3*	Arsenical pump-driving ATPase (EC 3.6.3.16)	5	1	1	1	3	1	0	0	6	3	9	2.0	0.7 (2>3X)	8	1	88.9	Memb predominant	426	0
single hit		RS9_HALMAReview	*rps9p*	30S ribosomal protein S9P (HmaS9) (HS3) (F1)	1	1	5	1	1	1	2	1	6	3	9	2.0	0.7 (2>3X)	2	7	22.2	Soluble predominant	132	0
single hit		Q5UXJ9_HALMA	*rrnAC3314*	Hypothetical protein	5	1	0	0	4	1	0	0	5	4	9	1.3	No dramatic change	9	0	100.0	Memb only	185	3
single hit		Q5V1D2_HALMA	*rrnAC1775*	Hypothetical protein	5	1	0	0	4	1	0	0	5	4	9	1.3	No dramatic change	9	0	100.0	Memb only	240	5
single hit		Q5V4H6_HALMA	*usp14*	Universal stress protein	0	0	4	1	0	0	5	1	4	5	9	0.8	No dramatic change	0	9	0.0	Soluble only	150	0
single hit		Q5V3H5_HALMA	*rrnAC0956*	Hypothetical protein	3	1	0	0	6	1	0	0	3	6	9	0.5	1.2 (2~3X)	9	0	100.0	Memb only	178	2
single hit		Q5UZ60_HALMA	*rrnAC2665*	Hypothetical protein	5	1	0	0	3	1	0	0	5	3	8	1.7	No dramatic change	8	0	100.0	Memb only	324	10
single hit		Q5UYD1_HALMA	*nirA2*	Ferredoxin-nitrite reductase	0	0	5	1	0	0	3	1	5	3	8	1.7	No dramatic change	0	8	0.0	Soluble only	587	0
single hit		Q5UXD3_HALMA	*rrnAC3388*	Hypothetical protein	4	1	0	0	4	1	0	0	4	4	8	1.0	No dramatic change	8	0	100.0	Memb only	202	2
single hit		Q5UWX0_HALMA	*rrnB0019*	Hypothetical protein	5	1	0	0	2	1	0	0	5	2	7	2.5	0.7 (2>3X)	7	0	100.0	Memb only	148	2
single hit		Q5V2P2_HALMA	*asnC2*	Transcription regulator AsnC family	0	0	5	1	0	0	2	1	5	2	7	2.5	0.7 (2>3X)	0	7	0.0	Soluble only	142	0
single hit		Q5UX88_HALMA	*pch2*	Potassium channel-like	3	1	0	0	4	1	0	0	3	4	7	0.8	No dramatic change	7	0	100.0	Memb only	404	6
single hit		Q5UZ51_HALMA	*argB2*	Acetylglutamate kinase (EC 2.7.2.8)	0	0	3	1	0	0	4	1	3	4	7	0.8	No dramatic change	0	7	0.0	Soluble only	286	0
single hit		Q5V569_HALMA	*rrnAC0277*	Hypothetical protein	2	1	0	0	5	1	0	0	2	5	7	0.4	1.2 (2~3X)	7	0	100.0	Memb only	206	6
single hit		Q5V0U6_HALMA	*rrnAC1994*	Hypothetical protein	0	0	5	1	0	0	1	1	5	1	6	5.0	0.7 (>3X)	0	6	0.0	Soluble only	111	0
single hit		Q5UX48_HALMA	*rrnAC3481*	Hypothetical protein	4	1	0	0	2	1	0	0	4	2	6	2.0	0.7 (2>3X)	6	0	100.0	Memb only	106	2
single hit		Q5UYA5_HALMA	*cbiX*	Putative cobalamin biosynthesis protein	0	0	4	1	0	0	2	1	4	2	6	2.0	0.7 (2>3X)	0	6	0.0	Soluble only	257	0
single hit		Q5V516_HALMA	*rrnAC0338*	Hypothetical protein	0	0	4	1	0	0	2	1	4	2	6	2.0	0.7 (2>3X)	0	6	0.0	Soluble only	246	0
single hit		Q5V422_HALMA	*rrnAC0737*	Hypothetical protein	3	1	0	0	3	1	0	0	3	3	6	1.0	No dramatic change	6	0	100.0	Memb only	160	4
single hit		Q5V4S1_HALMA	*yjlD1*	NADH dehydrogenase	3	1	0	0	3	1	0	0	3	3	6	1.0	No dramatic change	6	0	100.0	Memb only	389	0
single hit		RL18_HALMAReview	*rpl18p*	50S ribosomal protein L18P (Hmal18) (Hl12)	3	1	0	0	3	1	0	0	3	3	6	1.0	No dramatic change	6	0	100.0	Memb only	187	0
single hit		Q5V4S3_HALMA	*cdd*	Cytidine deaminase (EC 3.5.4.5)	0	0	3	1	0	0	3	1	3	3	6	1.0	No dramatic change	0	6	0.0	Soluble only	128	0
single hit		Q5V6P4_HALMA	*pNG7095*	Hypothetical protein	0	0	3	1	0	0	3	1	3	3	6	1.0	No dramatic change	0	6	0.0	Soluble only	150	0
single hit		Q5UZ08_HALMA	*rrnAC2730*	Hypothetical protein	2	1	0	0	4	1	0	0	2	4	6	0.5	1.2 (2~3X)	6	0	100.0	Memb only	171	3
single hit		Q5V279_HALMA	*nolB*	NAD(P)H-quinone oxidoreductase chain 3 (EC 1.6.5.-)	2	1	0	0	4	1	0	0	2	4	6	0.5	1.2 (2~3X)	6	0	100.0	Memb only	177	3
single hit		Q5V6S1_HALMA	*cat1*	Cationic amino acid transporter	1	1	0	0	5	1	0	0	1	5	6	0.2	1.2 (>3X)	6	0	100.0	Memb only	476	12
single hit		Q5UX16_HALMA	*dgs*	Dolichol-P-glucose transferase	4	1	0	0	1	1	0	0	4	1	5	4.0	0.7 (>3X)	5	0	100.0	Memb only	255	0
single hit		Q5UX94_HALMA	*rrnAC3430*	Hypothetical protein	4	1	0	0	1	1	0	0	4	1	5	4.0	0.7 (>3X)	5	0	100.0	Memb only	278	7
single hit		Q5UWF5_HALMA	*npdG-2*	F420-dependent NADP reductase	0	0	4	1	0	0	1	1	4	1	5	4.0	0.7 (>3X)	0	5	0.0	Soluble only	223	0
single hit		Q5UY54_HALMA	*rrnAC3084*	Hypothetical protein	3	1	0	0	2	1	0	0	3	2	5	1.5	No dramatic change	5	0	100.0	Memb only	181	4
single hit		Q5V042_HALMA	*rrnAC2286*	Hypothetical protein	3	1	0	0	2	1	0	0	3	2	5	1.5	No dramatic change	5	0	100.0	Memb only	313	5
single hit		TRPD_HALMAReview	*trpD*	Anthranilate phosphoribosyltransferase (EC 2.4.2.18)	1	1	2	1	0	0	2	1	3	2	5	1.5	No dramatic change	1	4	20.0	Soluble predominant	331	0
single hit		Q5V7B2_HALMA	*pNG6172*	Hypothetical protein	0	0	3	1	0	0	2	1	3	2	5	1.5	No dramatic change	0	5	0.0	Soluble only	166	0
single hit		Q5UZS9_HALMA	*rrnAC2411*	Hypothetical protein	2	1	0	0	3	1	0	0	2	3	5	0.7	No dramatic change	5	0	100.0	Memb only	137	1
single hit		Q5UZW8_HALMA	*rrnAC2368*	Hypothetical protein	2	1	0	0	3	1	0	0	2	3	5	0.7	No dramatic change	5	0	100.0	Memb only	344	8
single hit		Q5V4K5_HALMA	*rrnAC0527*	Hypothetical protein	2	1	0	0	3	1	0	0	2	3	5	0.7	No dramatic change	5	0	100.0	Memb only	150	3
single hit		Q5UZZ1_HALMA	*rrnAC2340*	Hypothetical protein	0	0	2	1	0	0	3	1	2	3	5	0.7	No dramatic change	0	5	0.0	Soluble only	246	0
single hit		Q5V2L1_HALMA	*rrnAC1305*	Hypothetical protein	4	1	0	0	0	0	0	0	4	0	4	∞	0.7 only	4	0	100.0	Memb only	132	0
single hit		Q5UWF1_HALMA	*kdgR2*	Transcription regulator KdgR	0	0	4	1	0	0	0	0	4	0	4	∞	0.7 only	0	4	0.0	Soluble only	250	0
single hit		Q5V189_HALMA	*rrnAC1826*	Hypothetical protein	0	0	4	1	0	0	0	0	4	0	4	∞	0.7 only	0	4	0.0	Soluble only	78	0
single hit		Q5V679_HALMA	*fhuG1*	Ferrichrome ABC transporter permease protein	3	1	0	0	1	1	0	0	3	1	4	3.0	0.7 (>3X)	4	0	100.0	Memb only	371	8
single hit		Q5UWK2_HALMA	*rrnB0163*	Hypothetical protein	0	0	3	1	0	0	1	1	3	1	4	3.0	0.7 (>3X)	0	4	0.0	Soluble only	216	0
single hit		Q5V0L3_HALMA	*rrnAC2087*	Putative PUA domain RNA-binding protein	0	0	3	1	0	0	1	1	3	1	4	3.0	0.7 (>3X)	0	4	0.0	Soluble only	159	0
single hit		Q5V0P0_HALMA	*moaD*	Molybdopterin converting factor subunit 1	0	0	3	1	0	0	1	1	3	1	4	3.0	0.7 (>3X)	0	4	0.0	Soluble only	90	0
single hit		Q5V131_HALMA	*rrnAC1895*	Putative DNA binding	0	0	3	1	0	0	1	1	3	1	4	3.0	0.7 (>3X)	0	4	0.0	Soluble only	214	0
single hit		Q5V1I3_HALMA	*cspD5*	Cold shock protein	0	0	3	1	0	0	1	1	3	1	4	3.0	0.7 (>3X)	0	4	0.0	Soluble only	64	0
single hit		Q5UWJ5_HALMA	*rrnB0171*	Putative acyltransferase	2	1	0	0	2	1	0	0	2	2	4	1.0	No dramatic change	4	0	100.0	Memb only	278	8
single hit		Q5UWQ3_HALMA	*hcp7*	Halocyanin-like	2	1	0	0	2	1	0	0	2	2	4	1.0	No dramatic change	4	0	100.0	Memb only	173	0
single hit		Q5UX31_HALMA	*rrnAC3503*	Hypothetical protein	2	1	0	0	2	1	0	0	2	2	4	1.0	No dramatic change	4	0	100.0	Memb only	51	1
single hit		Q5UXE3_HALMA	*hemU*	Iron(III) dicitrate transport system permease protein FecD	2	1	0	0	2	1	0	0	2	2	4	1.0	No dramatic change	4	0	100.0	Memb only	356	8
single hit		Q5UY11_HALMA	*rrnAC3134*	Hypothetical protein	2	1	0	0	2	1	0	0	2	2	4	1.0	No dramatic change	4	0	100.0	Memb only	192	4
single hit		Q5UYW2_HALMA	*dip2*	DNA damage-inducible protein	2	1	0	0	2	1	0	0	2	2	4	1.0	No dramatic change	4	0	100.0	Memb only	431	10
single hit		Q5V0G7_HALMA	*rrnAC2142*	Hypothetical protein	2	1	0	0	2	1	0	0	2	2	4	1.0	No dramatic change	4	0	100.0	Memb only	99	3
single hit		Q5V0M1_HALMA	*rrnAC2079*	Hypothetical protein	2	1	0	0	2	1	0	0	2	2	4	1.0	No dramatic change	4	0	100.0	Memb only	221	1
single hit		Q5V1V1_HALMA	*icsA*	LPS glycosyltransferase	2	1	0	0	2	1	0	0	2	2	4	1.0	No dramatic change	4	0	100.0	Memb only	380	0
single hit		Q5V1Z0_HALMA	*rrnAC1543*	Hypothetical protein	2	1	0	0	2	1	0	0	2	2	4	1.0	No dramatic change	4	0	100.0	Memb only	149	0
single hit		Q5V2E9_HALMA	*rrnAC1374*	Hypothetical protein	2	1	0	0	2	1	0	0	2	2	4	1.0	No dramatic change	4	0	100.0	Memb only	40	1
single hit		Q5V3T1_HALMA	*dnaJ*	Chaperone protein DnaJ	2	1	0	0	2	1	0	0	2	2	4	1.0	No dramatic change	4	0	100.0	Memb only	317	4
single hit		Q5V5S1_HALMA	*rrnAC0049*	ABC transporter ATP-binding domain	2	1	0	0	2	1	0	0	2	2	4	1.0	No dramatic change	4	0	100.0	Memb only	246	6
single hit		Q5V687_HALMA	*fadD2*	Putative long-chain-fatty-acid-CoA ligase	2	1	0	0	2	1	0	0	2	2	4	1.0	No dramatic change	4	0	100.0	Memb only	617	0
single hit		Q5UWG9_HALMA	*pdhA2*	Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1)	0	0	2	1	0	0	2	1	2	2	4	1.0	No dramatic change	0	4	0.0	Soluble only	382	0
single hit		Q5UZ30_HALMA	*rrnAC2705*	Hypothetical protein	0	0	2	1	0	0	2	1	2	2	4	1.0	No dramatic change	0	4	0.0	Soluble only	242	0
single hit		Q5V316_HALMA	*ribG*	25-diamino-6-hydroxy-4-(5-phosphoribosylamino)pyrimidine 1-reductase(EC 1.1.1.-)	0	0	2	1	0	0	2	1	2	2	4	1.0	No dramatic change	0	4	0.0	Soluble only	219	0
single hit		Q5V3K0_HALMA	*rrnAC0928*	Hypothetical protein	0	0	2	1	0	0	2	1	2	2	4	1.0	No dramatic change	0	4	0.0	Soluble only	65	0
single hit		Q5V3M5_HALMA	*rrnAC0900*	Hypothetical protein	0	0	2	1	0	0	2	1	2	2	4	1.0	No dramatic change	0	4	0.0	Soluble only	61	0
single hit		Q5V3S2_HALMA	*rrnAC0849*	Hypothetical protein	0	0	2	1	0	0	2	1	2	2	4	1.0	No dramatic change	0	4	0.0	Soluble only	144	0
single hit		Q5V484_HALMA	*rrnAC0664*	Hypothetical protein	0	0	2	1	0	0	2	1	2	2	4	1.0	No dramatic change	0	4	0.0	Soluble only	159	0
single hit		Q5V4M7_HALMA	*rrnAC0503*	Transcription regulator	0	0	2	1	0	0	2	1	2	2	4	1.0	No dramatic change	0	4	0.0	Soluble only	196	0
single hit		Q5V7A8_HALMA	*pNG6177*	Hypothetical protein	0	0	2	1	0	0	2	1	2	2	4	1.0	No dramatic change	0	4	0.0	Soluble only	141	0

single hit		Q5UWE8_HALMA	*livH-9*	Branched-chain amino acid ABC transporter permease protein	1	1	0	0	3	1	0	0	1	3	4	0.3	1.2 (>3X)	4	0	100.0	Memb only	674	16
single hit		Q5V273_HALMA	*rrnAC1453*	Hypothetical protein	1	1	0	0	3	1	0	0	1	3	4	0.3	1.2 (>3X)	4	0	100.0	Memb only	132	2
single hit		Q5V2C4_HALMA	*cyoC*	Cytochrome c oxidase polypeptide III (EC 1.9.3.1)	1	1	0	0	3	1	0	0	1	3	4	0.3	1.2 (>3X)	4	0	100.0	Memb only	287	7
single hit		Q5UXY9_HALMA	*atpF*	V-type ATP synthase subunit F (EC 3.6.3.14)	1	1	0	0	2	1	1	1	1	3	4	0.3	1.2 (>3X)	3	1	75.0	Memb predominant	107	0
single hit		Q5UXL0_HALMA	*rrnAC3300*	Hypothetical protein	0	0	1	1	0	0	3	1	1	3	4	0.3	1.2 (>3X)	0	4	0.0	Soluble only	113	0
single hit		Q5V023_HALMA	*rrnAC2306*	Hypothetical protein	0	0	1	1	0	0	3	1	1	3	4	0.3	1.2 (>3X)	0	4	0.0	Soluble only	115	0
single hit		Q5V3F6_HALMA	*rrnAC0977*	Hypothetical protein	0	0	1	1	0	0	3	1	1	3	4	0.3	1.2 (>3X)	0	4	0.0	Soluble only	162	0
single hit		Q5V4L0_HALMA	*bcp-1*	Peroxiredoxin	0	0	1	1	0	0	3	1	1	3	4	0.3	1.2 (>3X)	0	4	0.0	Soluble only	155	0
single hit		Q5UZL5_HALMA	*rrnAC2483*	Hypothetical protein	0	0	0	0	0	0	4	1	0	4	4	0.0	1.2 only	0	4	0.0	Soluble only	218	0
single hit		Q5V1E1_HALMA	*rrnAC1764*	HTH DNA-binding protein	0	0	0	0	0	0	4	1	0	4	4	0.0	1.2 only	0	4	0.0	Soluble only	325	0
single hit		Q5UZ44_HALMA	*rrnAC2685*	Hypothetical protein	3	1	0	0	0	0	0	0	3	0	3	∞	0.7 only	3	0	100.0	Memb only	364	1
single hit		Q5V128_HALMA	*rrnAC1899*	Hypothetical protein	0	0	3	1	0	0	0	0	3	0	3	∞	0.7 only	0	3	0.0	Soluble only	396	0
single hit		Q5V5U2_HALMA	*hat7*	Putative acetyltransferase	0	0	3	1	0	0	0	0	3	0	3	∞	0.7 only	0	3	0.0	Soluble only	167	0
single hit		Q5V6R3_HALMA	*fabG7*	3-oxoacyl-[acyl-carrier protein] reductase 1 (EC 1.1.1.100)	0	0	3	1	0	0	0	0	3	0	3	∞	0.7 only	0	3	0.0	Soluble only	221	0
single hit		Q5UWZ6_HALMA	*rrnAC3541*	Hypothetical protein	2	1	0	0	1	1	0	0	2	1	3	2.0	0.7 (2>3X)	3	0	100.0	Memb only	409	0
single hit		Q5UYP6_HALMA	*tatC1*	Sec-independent protein translocase protein TatC	2	1	0	0	1	1	0	0	2	1	3	2.0	0.7 (2>3X)	3	0	100.0	Memb only	745	14
single hit		Q5UZ59_HALMA	*rrnAC2666*	Hypothetical protein	2	1	0	0	1	1	0	0	2	1	3	2.0	0.7 (2>3X)	3	0	100.0	Memb only	185	0
single hit		Q5V046_HALMA	*cbiM*	Cobalamin biosynthesis protein CbiM	2	1	0	0	1	1	0	0	2	1	3	2.0	0.7 (2>3X)	3	0	100.0	Memb only	212	6
single hit		Q5V0G9_HALMA	*sdr2*	Oxidoreductase short-chain dehydrogenase/reductase family	2	1	0	0	1	1	0	0	2	1	3	2.0	0.7 (2>3X)	3	0	100.0	Memb only	313	0
single hit		Q5V254_HALMA	*rrnAC1473*	Hypothetical protein	2	1	0	0	1	1	0	0	2	1	3	2.0	0.7 (2>3X)	3	0	100.0	Memb only	115	1
single hit		Q5V2H7_HALMA	*rrnAC1344*	Hypothetical protein	2	1	0	0	1	1	0	0	2	1	3	2.0	0.7 (2>3X)	3	0	100.0	Memb only	91	0
single hit		Q5V3S5_HALMA	*menA*	14-dihydroxy-2-naphthoate octaprenyltransferase	2	1	0	0	1	1	0	0	2	1	3	2.0	0.7 (2>3X)	3	0	100.0	Memb only	319	7
single hit		Q5V7M8_HALMA	*pNG5078*	Hypothetical protein	2	1	0	0	1	1	0	0	2	1	3	2.0	0.7 (2>3X)	3	0	100.0	Memb only	628	2
single hit		Q5UW56_HALMA	*parA5*	ParA/minD-like bacterial cell division regulator	1	1	1	1	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	1	2	33.3	Memb + Sol	334	0
single hit		Q5V3Y2_HALMA	*usp30*	Universal stress protein	1	1	1	1	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	1	2	33.3	Memb + Sol	138	0
single hit		CDC69_HALMAReview	*cdc6-9*	Cell division control protein 6 homolog 9 (CDC6 homolog 9)	0	0	2	1	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	0	3	0.0	Soluble only	408	0
single hit		GCP_HALMAReview	*gcp*	Putative O-sialoglycoprotein endopeptidase (EC 3.4.24.57)(Glycoprotease)	0	0	2	1	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	0	3	0.0	Soluble only	548	0
single hit		Q5UZ54_HALMA	*arcB*	Ornithine carbamoyltransferase (EC 2.1.3.3)	0	0	2	1	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	0	3	0.0	Soluble only	298	0
single hit		Q5UZD6_HALMA	*manB1*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	0	0	2	1	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	0	3	0.0	Soluble only	450	0
single hit		Q5V176_HALMA	*yhcR2*	Phosphoesterase	0	0	2	1	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	0	3	0.0	Soluble only	424	0
single hit		Q5V415_HALMA	*rrnAC0744*	Hypothetical protein	0	0	2	1	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	0	3	0.0	Soluble only	488	0
single hit		Q5V462_HALMA	*aspC4*	Aspartate aminotransferase (EC 2.6.1.1)	0	0	2	1	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	0	3	0.0	Soluble only	372	0
single hit		Q5V4A9_HALMA	*gloA2*	Lactoylglutathione lyase and related lyases	0	0	2	1	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	0	3	0.0	Soluble only	129	0
single hit		Q5V4P2_HALMA	*yqjF*	Hypothetical protein yqjF	0	0	2	1	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	0	3	0.0	Soluble only	234	0
single hit		Q5V4U2_HALMA	*rrnAC0426*	Putative sulfatase	0	0	2	1	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	0	3	0.0	Soluble only	487	0
single hit		Q5V6U4_HALMA	*trh2*	Transcription regulator	0	0	2	1	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	0	3	0.0	Soluble only	157	0
single hit		RL11_HALMAReview	*rpl11p*	50S ribosomal protein L11P (Hmal11)	0	0	2	1	0	0	1	1	2	1	3	2.0	0.7 (2>3X)	0	3	0.0	Soluble only	162	0
single hit		Q5UWM0_HALMA	*rrnB0138*	Hypothetical protein	1	1	0	0	2	1	0	0	1	2	3	0.5	1.2 (2~3X)	3	0	100.0	Memb only	98	3
single hit		Q5UX01_HALMA	*mnhG2*	Multisubunit Na+/H+ antiporter MnhG subunit	1	1	0	0	2	1	0	0	1	2	3	0.5	1.2 (2~3X)	3	0	100.0	Memb only	106	2
single hit		Q5UY99_HALMA	*rrnAC3030*	Hypothetical protein	1	1	0	0	2	1	0	0	1	2	3	0.5	1.2 (2~3X)	3	0	100.0	Memb only	1150	2
single hit		Q5V494_HALMA	*rrnAC0654*	Hypothetical protein	1	1	0	0	2	1	0	0	1	2	3	0.5	1.2 (2~3X)	3	0	100.0	Memb only	205	5
single hit		Q5V5I8_HALMA	*nhaC2*	Na+/H+ antiporter	1	1	0	0	2	1	0	0	1	2	3	0.5	1.2 (2~3X)	3	0	100.0	Memb only	491	10
single hit		Q5V0L9_HALMA	*rrnAC2081*	Hypothetical protein	1	1	0	0	1	1	1	1	1	2	3	0.5	1.2 (2~3X)	2	1	66.7	Memb + Sol	282	0
single hit		Q5UXP3_HALMA	*rrnAC3264*	Putative molybdenum-binding protein	0	0	1	1	0	0	2	1	1	2	3	0.5	1.2 (2~3X)	0	3	0.0	Soluble only	242	0
single hit		Q5UZ95_HALMA	*cheA2*	CHEA histidine kinase	0	0	1	1	0	0	2	1	1	2	3	0.5	1.2 (2~3X)	0	3	0.0	Soluble only	214	0
single hit		Q5V0L2_HALMA	*rrnAC2088*	Hypothetical protein	0	0	1	1	0	0	2	1	1	2	3	0.5	1.2 (2~3X)	0	3	0.0	Soluble only	303	0
single hit		Q5V0S0_HALMA	*msrA1*	Peptide methionine sulfoxide reductase MsrA (EC 1.8.4.6)	0	0	1	1	0	0	2	1	1	2	3	0.5	1.2 (2~3X)	0	3	0.0	Soluble only	177	0
single hit		Q5V235_HALMA	*htlD*	HTR-like protein	0	0	1	1	0	0	2	1	1	2	3	0.5	1.2 (2~3X)	0	3	0.0	Soluble only	122	0
single hit		Q5V2L8_HALMA	*moeA2*	Molybdopterin biosynthesis protein moeA	0	0	1	1	0	0	2	1	1	2	3	0.5	1.2 (2~3X)	0	3	0.0	Soluble only	407	0
single hit		Q5V3L3_HALMA	*trmB1*	Sugar-specific transcriptional regulator TrmB	0	0	1	1	0	0	2	1	1	2	3	0.5	1.2 (2~3X)	0	3	0.0	Soluble only	350	0
single hit		Q5V547_HALMA	*rrnAC0300*	Hypothetical protein	0	0	1	1	0	0	2	1	1	2	3	0.5	1.2 (2~3X)	0	3	0.0	Soluble only	239	0
single hit		Q5V860_HALMA	*pNG1006*	Hypothetical protein	0	0	1	1	0	0	2	1	1	2	3	0.5	1.2 (2~3X)	0	3	0.0	Soluble only	181	0
single hit		Q5V2I5_HALMA	*rrnAC1335*	Hypothetical protein	0	0	0	0	3	1	0	0	0	3	3	0.0	1.2 only	3	0	100.0	Memb only	346	6
single hit		Q5V059_HALMA	*rrnAC2265*	Hypothetical protein	0	0	0	0	0	0	3	1	0	3	3	0.0	1.2 only	0	3	0.0	Soluble only	224	0
single hit		Q5V1A8_HALMA	*htlD*	Sensor protein (EC 2.7.13.3)	0	0	0	0	0	0	3	1	0	3	3	0.0	1.2 only	0	3	0.0	Soluble only	626	0
single hit		Q5V3L4_HALMA	*rrnAC0913*	Hypothetical protein	0	0	0	0	0	0	3	1	0	3	3	0.0	1.2 only	0	3	0.0	Soluble only	258	0
single hit		Q5V5I9_HALMA	*sdhA2*	Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)	0	0	0	0	0	0	3	1	0	3	3	0.0	1.2 only	0	3	0.0	Soluble only	607	0
single hit		Q5V5Y3_HALMA	*folP2*	Dihydropteroate synthase (EC 2.5.1.15)	0	0	0	0	0	0	3	1	0	3	3	0.0	1.2 only	0	3	0.0	Soluble only	799	0
single hit		Q5UWR3_HALMA	*rrnB0084*	Hypothetical protein	2	1	0	0	0	0	0	0	2	0	2	∞	0.7 only	2	0	100.0	Memb only	116	0
single hit		Q5UWV5_HALMA	*nadC2*	Sodium dependent transporter	2	1	0	0	0	0	0	0	2	0	2	∞	0.7 only	2	0	100.0	Memb only	538	13
single hit		Q5UX79_HALMA	*rrnAC3446*	Hypothetical protein	2	1	0	0	0	0	0	0	2	0	2	∞	0.7 only	2	0	100.0	Memb only	521	12
single hit		Q5UZ75_HALMA	*rrnAC2647*	Hypothetical protein	2	1	0	0	0	0	0	0	2	0	2	∞	0.7 only	2	0	100.0	Memb only	234	5
single hit		Q5UZC6_HALMA	*rrnAC2586*	Phosphate transporter family protein	2	1	0	0	0	0	0	0	2	0	2	∞	0.7 only	2	0	100.0	Memb only	354	11
single hit		Q5V047_HALMA	*rrnAC2281*	Hypothetical protein	2	1	0	0	0	0	0	0	2	0	2	∞	0.7 only	2	0	100.0	Memb only	105	2
single hit		Q5V0L4_HALMA	*rrnAC2086*	Hypothetical protein	2	1	0	0	0	0	0	0	2	0	2	∞	0.7 only	2	0	100.0	Memb only	139	4
single hit		Q5V272_HALMA	*nolC*	NADH dehydrogenase/oxidoreductase-like protein	2	1	0	0	0	0	0	0	2	0	2	∞	0.7 only	2	0	100.0	Memb only	68	1
single hit		Q5V2Z6_HALMA	*rrnAC1155*	Hypothetical protein	2	1	0	0	0	0	0	0	2	0	2	∞	0.7 only	2	0	100.0	Memb only	182	1
single hit		Q5V4N6_HALMA	*rrnAC0492*	Hypothetical protein	2	1	0	0	0	0	0	0	2	0	2	∞	0.7 only	2	0	100.0	Memb only	56	1
single hit		Q5V4P6_HALMA	*rrnAC0481*	Hypothetical protein	2	1	0	0	0	0	0	0	2	0	2	∞	0.7 only	2	0	100.0	Memb only	297	5
single hit		Q5V4U9_HALMA	*rrnAC0418*	Hypothetical protein	2	1	0	0	0	0	0	0	2	0	2	∞	0.7 only	2	0	100.0	Memb only	108	0
single hit		Q5V626_HALMA	*pNG7332*	Hypothetical protein	2	1	0	0	0	0	0	0	2	0	2	∞	0.7 only	2	0	100.0	Memb only	310	10
single hit		Q5UZQ2_HALMA	*moxR3*	Methanol dehydrogenase regulatory protein	1	1	1	1	0	0	0	0	2	0	2	∞	0.7 only	1	1	50.0	Memb + Sol	319	0
single hit		Q5UWF7_HALMA	*rrnB0215*	Thioesterase	0	0	2	1	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	129	0
single hit		Q5UX66_HALMA	*rrnAC3461*	Hypothetical protein	0	0	2	1	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	188	0
single hit		Q5UZB3_HALMA	*gst2*	Glutathione S-transferase	0	0	2	1	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	92	0
single hit		Q5V004_HALMA	*repC*	Replication factor C	0	0	2	1	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	626	0
single hit		Q5V0P4_HALMA	*rrnAC2052*	Transcription regulator	0	0	2	1	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	263	0
single hit		Q5V124_HALMA	*rrnAC1904*	Hypothetical protein	0	0	2	1	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	100	0
single hit		Q5V164_HALMA	*rrnAC1854*	Hypothetical protein	0	0	2	1	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	144	0
single hit		Q5V1Y6_HALMA	*rrnAC1547*	Hypothetical protein	0	0	2	1	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	186	0
single hit		Q5V3H7_HALMA	*hel*	DNA helicase	0	0	2	1	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	911	0
single hit		Q5V4U7_HALMA	*trmB2*	Sugar-specific transcriptional regulator	0	0	2	1	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	280	0
single hit		Q5V565_HALMA	*rrnAC0281*	Hypothetical protein	0	0	2	1	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	79	0
single hit		Q5V591_HALMA	*metE*	5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase(EC 2.1.1.14)	0	0	2	1	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	357	0

single hit		Q5V5A0_HALMA	*trkA4*	Trk potassium uptake system protein	0	0	2	1	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	217	0
single hit		Q5V623_HALMA	*fabG5*	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)	0	0	2	1	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	280	0
single hit		Q5V7D8_HALMA	*pNG6003*	Hypothetical protein	0	0	2	1	0	0	0	0	2	0	2	∞	0.7 only	0	2	0.0	Soluble only	447	0
single hit		Q5UWW8_HALMA	*rrnB0021*	Hypothetical protein	1	1	0	0	1	1	0	0	1	1	2	1.0	**No dramatic change**	2	0	100.0	Memb only	156	2
single hit		Q5UY91_HALMA	*htpX3*	Heat shock protein X	1	1	0	0	1	1	0	0	1	1	2	1.0	**No dramatic change**	2	0	100.0	Memb only	318	4
single hit		Q5UYC6_HALMA	*cbiT*	Precorrin-8W decarboxylase (EC 1.-.-.-)	1	1	0	0	1	1	0	0	1	1	2	1.0	**No dramatic change**	2	0	100.0	Memb only	201	0
single hit		Q5UZ03_HALMA	*rrnAC2735*	Hypothetical protein	1	1	0	0	1	1	0	0	1	1	2	1.0	**No dramatic change**	2	0	100.0	Memb only	365	6
single hit		Q5V2G8_HALMA	*rrnAC1353*	Hypothetical protein	1	1	0	0	1	1	0	0	1	1	2	1.0	**No dramatic change**	2	0	100.0	Memb only	60	2
single hit		Q5V3C3_HALMA	*rrnAC1014*	Hypothetical protein	1	1	0	0	1	1	0	0	1	1	2	1.0	**No dramatic change**	2	0	100.0	Memb only	509	12
single hit		Q5V3D3_HALMA	*rrnAC1003*	Hypothetical protein	1	1	0	0	1	1	0	0	1	1	2	1.0	**No dramatic change**	2	0	100.0	Memb only	382	9
single hit		Q5V4U3_HALMA	*rrnAC0425*	Hypothetical protein	1	1	0	0	1	1	0	0	1	1	2	1.0	**No dramatic change**	2	0	100.0	Memb only	290	0
single hit		Q5V548_HALMA	*rrnAC0299*	Hypothetical protein	1	1	0	0	1	1	0	0	1	1	2	1.0	**No dramatic change**	2	0	100.0	Memb only	399	0
single hit		Q5V5T9_HALMA	*yurM*	ABC transporter permease protein	1	1	0	0	1	1	0	0	1	1	2	1.0	**No dramatic change**	2	0	100.0	Memb only	309	7
single hit		Q5V6A1_HALMA	*bmp-1*	Basic membrane protein	1	1	0	0	1	1	0	0	1	1	2	1.0	**No dramatic change**	2	0	100.0	Memb only	372	0
single hit		Q5V7W2_HALMA	*pNG4035*	Hypothetical protein	1	1	0	0	1	1	0	0	1	1	2	1.0	**No dramatic change**	2	0	100.0	Memb only	171	0
single hit		Q5V3R3_HALMA	*rrnAC0858*	Arylsulfatase (EC 3.1.6.8)	1	1	0	0	0	0	1	1	1	1	2	1.0	**No dramatic change**	1	1	50.0	Memb + Sol	450	0
single hit		CCA_HALMAReview	*cca*	CCA-adding enzyme (EC 2.7.7.25) (EC 2.7.7.21) (tRNAnucleotidyltransferase) (tRNA adenylyl-/cytidylyl- transferase) (tRNACCA-pyrophosphorylase) (tRNA-NT)	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	466	0
single hit		GPMI_HALMAReview	*gpmI*	2,3-bisphosphoglycerate-independent phosphoglycerate mutase(EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM) (iPGM)	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	519	0
single hit		KTHY_HALMAReview	*tmk*	Probable thymidylate kinase (EC 2.7.4.9) (dTMP kinase)	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	195	0
single hit		Q5UW66_HALMA	*rrnB0323*	Hypothetical protein	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	169	0
single hit		Q5UW87_HALMA	*hlx2*	HoxA-like transcriptional regulator	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	298	0
single hit		Q5UWV3_HALMA	*usp11*	Universal stress protein	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	147	0
single hit		Q5UX69_HALMA	*rrnAC3457*	Hypothetical protein	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	647	0
single hit		Q5UXT8_HALMA	*rrnAC3212*	Hypothetical protein	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	155	0
single hit		Q5UY34_HALMA	*tpr*	Tetratricopeptide repeat protein	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	242	0
single hit		Q5UYR8_HALMA	*rrnAC2831*	Hypothetical protein	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	136	0
single hit		Q5UYX8_HALMA	*mcm2*	Cell division control protein 21	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	1175	0
single hit		Q5UZF4_HALMA	*kdgK*	2-keto-3-deoxygluconate kinase (EC 2.7.1.45)	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	314	0
single hit		Q5UZX8_HALMA	*gst1*	Glutathione S-transferase	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	416	0
single hit		Q5V005_HALMA	*rrnAC2324*	Hypothetical protein	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	124	0
single hit		Q5V029_HALMA	*aup*	Acetoin utilization protein	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	335	0
single hit		Q5V0A5_HALMA	*dcd1*	Deoxycytidine triphosphate deaminase	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	140	0
single hit		Q5V0N4_HALMA	*aor1*	Aldehyde ferredoxin oxidoreductase	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	648	0
single hit		Q5V0V3_HALMA	*maoC1*	Monoamine oxidase regulatory protein	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	147	0
single hit		Q5V248_HALMA	*scrB*	Sucrose-6-phosphate hydrolase	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	703	0
single hit		Q5V2L0_HALMA	*rrnAC1307*	Putative transcriptional regulator	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	80	0
single hit		Q5V2L7_HALMA	*moeA3*	Molybdopterin biosynthesis protein moeA	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	567	0
single hit		Q5V2W6_HALMA	*moaC*	Molybdenum cofactor biosynthesis protein C	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	157	0
single hit		Q5V3W7_HALMA	*snp*	SnRNP-like protein	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	60	0
single hit		Q5V3W9_HALMA	*hat4*	Putative acetyltransferase	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	186	0
single hit		Q5V408_HALMA	*aroK*	Shikimate kinase (EC 2.7.1.71)	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	311	0
single hit		Q5V420_HALMA	*nthA*	Endonuclease III (EC 4.2.99.18)	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	227	0
single hit		Q5V450_HALMA	*aroE*	Shikimate 5-dehydrogenase (EC 1.1.1.25)	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	265	0
single hit		Q5V472_HALMA	*arsA2*	Arsenical pump-driving ATPase	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	362	0
single hit		Q5V487_HALMA	*apa*	Diadenosine tetraphosphate pyrophosphohydrolase	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	143	0
single hit		Q5V4B0_HALMA	*nudB*	NTP pyrophosphohydrolase	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	215	0
single hit		Q5V4B2_HALMA	*rrnAC0632*	Hypothetical protein	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	239	0
single hit		Q5V538_HALMA	*rrnAC0312*	Hypothetical protein	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	274	0
single hit		Q5V5B9_HALMA	*aglA1*	Alpha-glucosidase (EC 3.2.1.20)	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	565	0
single hit		Q5V5S4_HALMA	*rrnAC0046*	Hypothetical protein	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	79	0
single hit		Q5V643_HALMA	*adhC*	Formaldehyde dehydrogenase (EC 1.1.1.1)	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	387	0
single hit		Q5V7C2_HALMA	*pNG6190*	Hypothetical protein	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	46	0
single hit		Q5V866_HALMA	*pNG1008*	Hypothetical protein	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	117	0
single hit		RLX_HALMAReview	*rplX*	50S ribosomal protein LX (HL32)	0	0	1	1	0	0	1	1	1	1	2	1.0	**No dramatic change**	0	2	0.0	Soluble only	56	0
single hit		Q5UY36_HALMA	*rrnAC3105*	Hypothetical protein	0	0	0	0	2	1	0	0	0	2	2	0.0	1.2 only	2	0	100.0	Memb only	154	2
single hit		Q5UZW1_HALMA	*rrnAC2377*	Hypothetical protein	0	0	0	0	2	1	0	0	0	2	2	0.0	1.2 only	2	0	100.0	Memb only	307	6
single hit		Q5V0M2_HALMA	*rrnAC2078*	Hypothetical protein	0	0	0	0	2	1	0	0	0	2	2	0.0	1.2 only	2	0	100.0	Memb only	97	0
single hit		Q5V0N2_HALMA	*blh*	Brp-like protein-like	0	0	0	0	2	1	0	0	0	2	2	0.0	1.2 only	2	0	100.0	Memb only	343	8
single hit		Q5V567_HALMA	*rrnAC0279*	Hypothetical protein	0	0	0	0	2	1	0	0	0	2	2	0.0	1.2 only	2	0	100.0	Memb only	136	2
single hit		Q5V5K1_HALMA	*zip*	Zinc transporter	0	0	0	0	2	1	0	0	0	2	2	0.0	1.2 only	2	0	100.0	Memb only	288	9
single hit		Q5V633_HALMA	*betL1*	Glycine betaine transporter BetL	0	0	0	0	2	1	0	0	0	2	2	0.0	1.2 only	2	0	100.0	Memb only	645	15
single hit		Q5V6V4_HALMA	*malFG-1*	Sugar ABC transporter permease protein	0	0	0	0	2	1	0	0	0	2	2	0.0	1.2 only	2	0	100.0	Memb only	292	6
single hit		Q5UZX3_HALMA	*hsp20b*	Putative heat shock protein	0	0	0	0	1	1	1	1	0	2	2	0.0	1.2 only	1	1	50.0	Memb + Sol	128	0
single hit		Q5V6R4_HALMA	*fabG*	Oxidoreductase	0	0	0	0	1	1	1	1	0	2	2	0.0	1.2 only	1	1	50.0	Memb + Sol	309	0
single hit		Q5V7Q8_HALMA	*pNG5108*	Hypothetical protein	0	0	0	0	1	1	1	1	0	2	2	0.0	1.2 only	1	1	50.0	Memb + Sol	614	0
single hit		PTH_HALMAReview	*pth*	Peptidyl-tRNA hydrolase (EC 3.1.1.29) (PTH)	0	0	0	0	0	0	2	1	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	112	0
single hit		Q5UXK5_HALMA	*nirD*	Heme biosynthesis protein	0	0	0	0	0	0	2	1	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	345	0
single hit		Q5UXU4_HALMA	*rrnAC3205*	PRC-barrel domain posible photosystem reaction centre subunit H	0	0	0	0	0	0	2	1	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	79	0
single hit		Q5UY50_HALMA	*cysG1*	Uroporphyrin-III C-methyltransferase	0	0	0	0	0	0	2	1	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	260	0
single hit		Q5UYK6_HALMA	*galE6*	UDP-glucose 4-epimerase	0	0	0	0	0	0	2	1	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	297	0
single hit		Q5UZB9_HALMA	*rrnAC2594*	Hypothetical protein	0	0	0	0	0	0	2	1	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	68	0
single hit		Q5UZQ6_HALMA	*mer1*	F420-dependent N5N10-methylene-tetrahydromethanopterin reductase	0	0	0	0	0	0	2	1	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	325	0
single hit		Q5UZV2_HALMA	*rrnAC2386*	Hypothetical protein	0	0	0	0	0	0	2	1	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	244	0
single hit		Q5V1E2_HALMA	*serA2*	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	0	0	0	0	0	0	2	1	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	323	0
single hit		Q5V1K5_HALMA	*rrnAC1689*	Hypothetical protein	0	0	0	0	0	0	2	1	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	322	0
single hit		Q5V1X7_HALMA	*rrnAC1557*	Hypothetical protein	0	0	0	0	0	0	2	1	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	189	0
single hit		Q5V352_HALMA	*alkA*	DNA-3-methyladenine glycosylase	0	0	0	0	0	0	2	1	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	203	0
single hit		Q5V367_HALMA	*rrnAC1073*	Hypothetical protein	0	0	0	0	0	0	2	1	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	130	0
single hit		Q5V3D1_HALMA	*rrnAC1006*	Hypothetical protein	0	0	0	0	0	0	2	1	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	71	0
single hit		Q5V3U6_HALMA	*mogA*	Molybdenumm cofactor biosynthesis protein	0	0	0	0	0	0	2	1	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	231	0
single hit		Q5V499_HALMA	*bdhA*	D-beta-hydroxybutyrate dehydrogenase	0	0	0	0	0	0	2	1	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	289	0
single hit		Q5V507_HALMA	*rrnAC0348*	Hypothetical protein	0	0	0	0	0	0	2	1	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	427	0
single hit		Q5V509_HALMA	*rrnAC0346*	Hypothetical protein	0	0	0	0	0	0	2	1	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	47	0

single hit		Q5V5G2_HALMA	*gldA*	Glycerol-1-phosphate dehydrogenase [NAD(P)] (EC 1.1.1.6)(EC 1.1.1.261)	0	0	0	0	0	0	2	1	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	352	0
single hit		Q5V5L4_HALMA	*pai1*	Sporulation regulator-like	0	0	0	0	0	0	2	1	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	148	0
single hit		Q5V607_HALMA	*adh13*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	0	0	0	0	0	0	2	1	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	362	0
single hit		Q5V6Q7_HALMA	*trxB1*	Thioredoxin reductase (EC 1.8.1.9)	0	0	0	0	0	0	2	1	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	413	0
single hit		Q5V704_HALMA	*pNG6001*	Hypothetical protein	0	0	0	0	0	0	2	1	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	187	0
single hit		Q5V845_HALMA	*sojC*	Chromosome partitioning protein	0	0	0	0	0	0	2	1	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	255	0
single hit		Y1612_HALMAReview	*rrnAC1612*	Uncharacterized protein rrnAC1612	0	0	0	0	0	0	2	1	0	2	2	0.0	1.2 only	0	2	0.0	Soluble only	281	0
single hit		Q5UW97_HALMA	*rrnB0287*	Hypothetical protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	163	4
single hit		Q5UWA7_HALMA	*rrnB0275*	Putative-iron binding protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	354	0
single hit		Q5UWV9_HALMA	*rrnB0030*	Hypothetical protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	409	1
single hit		Q5UWZ5_HALMA	*rrnAC3542*	Hypothetical protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	247	2
single hit		Q5UX30_HALMA	*rrnAC3504*	Flavin-containing amine-oxidoreductase	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	417	0
single hit		Q5UX62_HALMA	*arsB*	Arsenite transport protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	653	11
single hit		Q5UX91_HALMA	*rrnAC3433*	Hypothetical protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	73	2
single hit		Q5UX98_HALMA	*cef*	Cation efflux system protein (Zinc/cadmium)	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	304	6
single hit		Q5UXU1_HALMA	*rrnAC3208*	Hypothetical protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	380	11
single hit		Q5UXX1_HALMA	*rrnAC3176*	Hypothetical protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	415	8
single hit		Q5UXZ6_HALMA	*rrnAC3150*	Hypothetical protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	410	1
single hit		Q5UY14_HALMA	*livH-7*	Branched-chain amino acid ABC transporter permease protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	214	4
single hit		Q5UYK4_HALMA	*rrnAC2907*	Hypothetical protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	205	0
single hit		Q5UYP0_HALMA	*rrnAC2863*	Hypothetical protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	285	0
single hit		Q5UZ72_HALMA	*rbsC*	Ribose ABC transporter permease	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	354	9
single hit		Q5UZ86_HALMA	*rrnAC2632*	Sodium symporter transmembrane region	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	469	14
single hit		Q5UZS1_HALMA	*bioY*	Dethiobiotin synthesis protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	193	5
single hit		Q5UZZ4_HALMA	*rrnAC2337*	Histidine kinase (EC 2.7.3.-)	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	409	4
single hit		Q5V041_HALMA	*rrnAC2287*	Hypothetical protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	177	3
single hit		Q5V0I8_HALMA	*rrnAC2114*	Hypothetical protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	468	1
single hit		Q5V0L7_HALMA	*yadH*	ABC transporter permease protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	255	6
single hit		Q5V1J6_HALMA	*rrnAC1700*	Sulfatase (EC 3.1.6.-)	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	472	0
single hit		Q5V1R6_HALMA	*rrnAC1621*	Hypothetical protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	152	0
single hit		Q5V282_HALMA	*xup*	Xanthine/uracil permease family protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	581	12
single hit		Q5V2B6_HALMA	*cyo*	Cytochrome oxidase subunit I-like	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	333	7
single hit		Q5V2E8_HALMA	*soxA2*	Putative sulfite oxidase	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	509	4
single hit		Q5V2T8_HALMA	*rrnAC1220*	Hypothetical protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	201	0
single hit		Q5V338_HALMA	*rrnAC1106*	Hypothetical protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	139	0
single hit		Q5V3C4_HALMA	*rrnAC1013*	Hypothetical protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	469	12
single hit		Q5V3K2_HALMA	*rrnAC0926*	Hypothetical protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	291	2
single hit		Q5V3U5_HALMA	*rrnAC0823*	Hypothetical protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	404	1
single hit		Q5V3X7_HALMA	*pssA*	CDP-diacylglycerol-serine O phosphatidyltransferase	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	228	5
single hit		Q5V412_HALMA	*rrnAC0749*	Hypothetical protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	295	8
single hit		Q5V4M3_HALMA	*hcp2*	Halocyanin-like protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	190	0
single hit		Q5V4M5_HALMA	*rrnAC0505*	Hypothetical protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	494	1
single hit		Q5V4N2_HALMA	*rrnAC0497*	Hypothetical protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	156	2
single hit		Q5V4U6_HALMA	*gtr-2*	Predicted glycosyltransferase	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	199	0
single hit		Q5V5D1_HALMA	*rrnAC0211*	Hypothetical protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	161	0
single hit		Q5V5S6_HALMA	*ctaB*	Heme synthase	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	463	13
single hit		Q5V646_HALMA	*pNG7311*	Hypothetical protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	395	1
single hit		Q5V688_HALMA	*pNG7264*	Hypothetical protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	157	4
single hit		Q5V697_HALMA	*rbsC-2*	Sugar ABC transporter permease protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	330	9
single hit		Q5V6P1_HALMA	*cpt*	CDP-alcohol phosphatidyltransferase (EC 2.7.8.-)	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	257	5
single hit		Q5V6S8_HALMA	*pNG7056*	Hypothetical protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	336	0
single hit		Q5V6U3_HALMA	*pNG7039*	Putative iron transport protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	414	0
single hit		Q5V6V5_HALMA	*sugA*	Sugar ABC transporter permease protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	310	7
single hit		Q5V6Z6_HALMA	*cadA*	Cadmium transporting P-type ATPase	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	639	5
single hit		Q5V723_HALMA	*copA1*	Copper-transporting ATPase CopA	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	790	7
single hit		Q5V744_HALMA	*pNG6084*	Hypothetical protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	88	1
single hit		Q5V803_HALMA	*pNG3042*	Hypothetical protein	1	1	0	0	0	0	0	0	1	0	1	∞	0.7 only	1	0	100.0	Memb only	137	0
single hit		ARLY_HALMAReview	*argH*	Argininosuccinate lyase (EC 4.3.2.1) (Arginosuccinase) (ASAL)	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	499	0
single hit		CDC61_HALMAReview	*cdc6-1*	Cell division control protein 6 homolog 1 (CDC6 homolog 1)	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	416	0
single hit		CDC65_HALMAReview	*cdc6-5*	Cell division control protein 6 homolog 5 (CDC6 homolog 5)	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	375	0
single hit		COFD_HALMAReview	*cofD*	LPPG:FO 2-phospho-L-lactate transferase (EC 2.7.8.-)	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	330	0
single hit		ENGB_HALMAReview	*engB*	Probable GTP-binding protein engB	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	205	0
single hit		Q5UW99_HALMA	*rrnB0285*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	81	0
single hit		Q5UWB3_HALMA	*rrnB0269*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	252	0
single hit		Q5UWD3_HALMA	*maoC2*	Monoamine oxidase regulatory protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	152	0
single hit		Q5UWR5_HALMA	*rrnB0082*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	81	0
single hit		Q5UWV7_HALMA	*rrnB0033*	Tautomerase	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	147	0
single hit		Q5UWX3_HALMA	*rrnB0016*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	132	0
single hit		Q5UXC6_HALMA	*rrnAC3396*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	616	0
single hit		Q5UXE1_HALMA	*rrnAC3378*	5-formyltetrahydrofolate cyclo-ligase (EC 6.3.3.2)	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	242	0
single hit		Q5UXJ1_HALMA	*rrnAC3322*	Transcription regulator	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	119	0
single hit		Q5UXP6_HALMA	*tgt*	Archaeosine tRNA-ribosyltransferase	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	595	0
single hit		Q5UY02_HALMA	*rrnAC3144*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	140	0
single hit		Q5UY27_HALMA	*rrnAC3115*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	45	0
single hit		Q5UYB7_HALMA	*rrnAC3010*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	219	0
single hit		Q5UYD4_HALMA	*rrnAC2988*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	225	0
single hit		Q5UYK7_HALMA	*nmd3*	Putative nonsense mediated mRNA decay protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	379	0
single hit		Q5UYL6_HALMA	*rrnAC2892*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	331	0
single hit		Q5UZ56_HALMA	*ort*	Orotate phosphoribosyltransferase (EC 2.4.2.10)	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	325	0
single hit		Q5UZ88_HALMA	*prsA*	Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	330	0
single hit		Q5UZC8_HALMA	*rrnAC2582*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	289	0
single hit		Q5UZG0_HALMA	*rrnAC2543*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	66	0
single hit		Q5UZJ7_HALMA	*araC*	Transcriptional regulator AraC family	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	203	0
single hit		Q5UZM1_HALMA	*prk2*	Protein kinase	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	193	0

single hit		Q5UZM7_HALMA	*prr*	Proline racemase (EC 5.1.1.4)	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	323	0
single hit		Q5V043_HALMA	*phrH2*	PhiH1 repressor-like	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	108	0
single hit		Q5V049_HALMA	*coaD1*	Phosphopantetheine adenylyltransferase (EC 2.7.7.3)	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	199	0
single hit		Q5V0A4_HALMA	*rrnAC2214*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	143	0
single hit		Q5V0K1_HALMA	*rrnAC2101*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	87	0
single hit		Q5V0K9_HALMA	*htr*	MCP domain signal transducer	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	328	0
single hit		Q5V0T3_HALMA	*rrnAC2009*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	216	0
single hit		Q5V0W2_HALMA	*aacC*	Aminoglycoside N3'-acetyltransferase (EC 2.3.1.81)	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	271	0
single hit		Q5V190_HALMA	*idr*	Iron-dependent repressor	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	144	0
single hit		Q5V1B5_HALMA	*htlC*	HTR-like protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	300	0
single hit		Q5V1I2_HALMA	*cspD1*	Cold shock protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	64	0
single hit		Q5V1I7_HALMA	*hemX*	Uroporphyrin-III C-methyltransferase	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	215	0
single hit		Q5V1K4_HALMA	*leuA1*	2-isopropylmalate synthase 2 (EC 2.3.3.13)	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	502	0
single hit		Q5V1P9_HALMA	*smc2*	Chromosome segregation protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	1195	0
single hit		Q5V1Q6_HALMA	*rrnAC1632*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	143	0
single hit		Q5V200_HALMA	*radB*	DNA repair and recombination protein RadB	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	192	0
single hit		Q5V203_HALMA	*rrnAC1529*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	438	0
single hit		Q5V231_HALMA	*gcvH*	Probable glycine cleavage system H protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	127	0
single hit		Q5V257_HALMA	*trxB2*	Thioredoxin reductase (EC 1.8.1.9)	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	199	0
single hit		Q5V2W3_HALMA	*rrnAC1190*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	105	0
single hit		Q5V319_HALMA	*rrnAC1128*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	94	0
single hit		Q5V329_HALMA	*rrnAC1116*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	274	0
single hit		Q5V3A0_HALMA	*rrnAC1037*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	160	0
single hit		Q5V3D4_HALMA	*rrnAC1002*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	569	0
single hit		Q5V3E9_HALMA	*rrnAC0985*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	179	0
single hit		Q5V3H9_HALMA	*moxR1*	Methanol dehydrogenase regulatory protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	401	0
single hit		Q5V3L1_HALMA	*sorD*	Sorbitol dehydrogenase (EC 1.1.1.140)	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	379	0
single hit		Q5V3N5_HALMA	*rrnAC0889*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	128	0
single hit		Q5V452_HALMA	*rrnAC0704*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	451	0
single hit		Q5V4N3_HALMA	*sirR*	Transcription repressor	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	230	0
single hit		Q5V560_HALMA	*rrnAC0286*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	244	0
single hit		Q5V5A6_HALMA	*rrnAC0238*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	230	0
single hit		Q5V5C6_HALMA	*rrnAC0217*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	118	0
single hit		Q5V5D3_HALMA	*rrnAC0208*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	165	0
single hit		Q5V5G7_HALMA	*gltB*	Glutamate synthase large subunit (EC 1.4.1.13)	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	1515	0
single hit		Q5V5K6_HALMA	*udg2*	Uracil DNA glycosylase superfamily protein (EC 3.2.2.-)	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	208	0
single hit		Q5V602_HALMA	*pNG7357*	Putative transcriptional regulator	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	217	0
single hit		Q5V628_HALMA	*cysE1*	Serine acetyltransferase (EC 2.3.1.30)	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	287	0
single hit		Q5V797_HALMA	*pNG6160*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	199	0
single hit		Q5V7C7_HALMA	*pNG6122*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	249	0
single hit		Q5V7Z7_HALMA	*pNG3032*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	390	0
single hit		Q5V856_HALMA	*pNG2002*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	138	0
single hit		Q5V878_HALMA	*pNG1021*	Hypothetical protein	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	309	0
single hit		RL23_HALMAReview	*rpl23p*	50S ribosomal protein L23P (Hmal23) (Hl25) (L21)	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	85	0
single hit		TRUD_HALMAReview	*truD*	Probable tRNA pseudouridine synthase D (EC 5.4.99.-) (tRNA-uridineisomerase D) (tRNA pseudouridylate synthase D)	0	0	1	1	0	0	0	0	1	0	1	∞	0.7 only	0	1	0.0	Soluble only	460	0
single hit		Q5UXL6_HALMA	*rrnAC3294*	Hypothetical protein	0	0	0	0	1	1	0	0	0	1	1	0.0	1.2 only	1	0	100.0	Memb only	135	3
single hit		Q5UXT2_HALMA	*mic*	Mechanosensitive ion channel	0	0	0	0	1	1	0	0	0	1	1	0.0	1.2 only	1	0	100.0	Memb only	371	5
single hit		Q5UXU5_HALMA	*hcp1*	Halocyanin-like	0	0	0	0	1	1	0	0	0	1	1	0.0	1.2 only	1	0	100.0	Memb only	184	0
single hit		Q5UYM5_HALMA	*rrnAC2881*	Hypothetical protein	0	0	0	0	1	1	0	0	0	1	1	0.0	1.2 only	1	0	100.0	Memb only	280	0
single hit		Q5UZ10_HALMA	*htr*	Putative HAMP and MCP domain signal transducer	0	0	0	0	1	1	0	0	0	1	1	0.0	1.2 only	1	0	100.0	Memb only	784	2
single hit		Q5UZP8_HALMA	*rrnAC2446*	Putative glycyl aminopeptidase	0	0	0	0	1	1	0	0	0	1	1	0.0	1.2 only	1	0	100.0	Memb only	770	1
single hit		Q5V0I5_HALMA	*rrnAC2117*	Hypothetical protein	0	0	0	0	1	1	0	0	0	1	1	0.0	1.2 only	1	0	100.0	Memb only	255	7
single hit		Q5V0P2_HALMA	*rrnAC2054*	Hypothetical protein	0	0	0	0	1	1	0	0	0	1	1	0.0	1.2 only	1	0	100.0	Memb only	259	1
single hit		Q5V0T2_HALMA	*rrnAC2010*	Hypothetical protein	0	0	0	0	1	1	0	0	0	1	1	0.0	1.2 only	1	0	100.0	Memb only	260	1
single hit		Q5V0V1_HALMA	*anf*	ABC transporter substrate-binding protein	0	0	0	0	1	1	0	0	0	1	1	0.0	1.2 only	1	0	100.0	Memb only	456	0
single hit		Q5V1N0_HALMA	*hop*	Halorhodopsin	0	0	0	0	1	1	0	0	0	1	1	0.0	1.2 only	1	0	100.0	Memb only	276	7
single hit		Q5V1R4_HALMA	*rrnAC1623*	Hypothetical protein	0	0	0	0	1	1	0	0	0	1	1	0.0	1.2 only	1	0	100.0	Memb only	96	0
single hit		Q5V2E2_HALMA	*rrnAC1381*	Hypothetical protein	0	0	0	0	1	1	0	0	0	1	1	0.0	1.2 only	1	0	100.0	Memb only	98	3
single hit		Q5V2F2_HALMA	*trxA7*	Thioredoxin	0	0	0	0	1	1	0	0	0	1	1	0.0	1.2 only	1	0	100.0	Memb only	154	1
single hit		Q5V3F7_HALMA	*htr8*	MCP domain signal transducer	0	0	0	0	1	1	0	0	0	1	1	0.0	1.2 only	1	0	100.0	Memb only	630	5
single hit		Q5V3K6_HALMA	*malFG-5*	Putative ABC transporter permease protein	0	0	0	0	1	1	0	0	0	1	1	0.0	1.2 only	1	0	100.0	Memb only	326	8
single hit		Q5V434_HALMA	*rrnAC0725*	Hypothetical protein	0	0	0	0	1	1	0	0	0	1	1	0.0	1.2 only	1	0	100.0	Memb only	389	0
single hit		Q5V4I0_HALMA	*gpdC*	Glycerol-3-phosphate dehydrogenase chain C	0	0	0	0	1	1	0	0	0	1	1	0.0	1.2 only	1	0	100.0	Memb only	458	0
single hit		Q5V4V2_HALMA	*rhoM*	Putative intramembrane serine protease	0	0	0	0	1	1	0	0	0	1	1	0.0	1.2 only	1	0	100.0	Memb only	552	10
single hit		Q5V504_HALMA	*ubiA*	Putative UbiA prenyltransferase	0	0	0	0	1	1	0	0	0	1	1	0.0	1.2 only	1	0	100.0	Memb only	284	7
single hit		Q5V5D9_HALMA	*rrnAC0202*	Hypothetical protein	0	0	0	0	1	1	0	0	0	1	1	0.0	1.2 only	1	0	100.0	Memb only	373	5
single hit		Q5V5E6_HALMA	*yfmO2*	Multidrug resistance protein-like	0	0	0	0	1	1	0	0	0	1	1	0.0	1.2 only	1	0	100.0	Memb only	435	11
single hit		Q5V5P1_HALMA	*rrnAC0082*	Hypothetical protein	0	0	0	0	1	1	0	0	0	1	1	0.0	1.2 only	1	0	100.0	Memb only	421	0
single hit		Q5V685_HALMA	*pNG7267*	Hypothetical protein	0	0	0	0	1	1	0	0	0	1	1	0.0	1.2 only	1	0	100.0	Memb only	92	1
single hit		Q5V6F7_HALMA	*pNG7190*	Ferrichrome-binding protein	0	0	0	0	1	1	0	0	0	1	1	0.0	1.2 only	1	0	100.0	Memb only	404	0
single hit		Q5V7K2_HALMA	*doxD3*	Terminal quinol oxidase subunit	0	0	0	0	1	1	0	0	0	1	1	0.0	1.2 only	1	0	100.0	Memb only	138	4
single hit		RL24_HALMAReview	*rpl24p*	50S ribosomal protein L24P (Hmal24) (Hl16) (Hl15)	0	0	0	0	1	1	0	0	0	1	1	0.0	1.2 only	1	0	100.0	Memb only	120	0
single hit		COBQ_HALMAReview	*cobQ*	Probable cobyric acid synthase	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	492	0
single hit		NADM_HALMAReview	*rrnAC1913*	Nicotinamide-nucleotide adenylyltransferase (EC 2.7.7.1) (NAD(+)pyrophosphorylase) (NAD(+) diphosphorylase) (NMN adenylyltransferase)	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	188	0
single hit		NPD_HALMAReview	*npdA*	NAD-dependent deacetylase (EC 3.5.1.-) (Regulatory protein SIR2homolog)	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	260	0
single hit		PRIS_HALMAReview	*priA*	Probable DNA primase small subunit (EC 2.7.7.-)	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	392	0
single hit		Q5UWF2_HALMA	*rrnB0221*	Putative metal dependent phosphohydrolase	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	194	0
single hit		Q5UWP9_HALMA	*suhB2*	Inositol-1-monophosphatase (EC 3.1.3.25)	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	265	0
single hit		Q5UWZ8_HALMA	*dfp*	Pantothenate metabolism flavoprotein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	388	0
single hit		Q5UX85_HALMA	*rrnAC3439*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	92	0
single hit		Q5UXC5_HALMA	*rrnAC3397*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	277	0
single hit		Q5UXC8_HALMA	*usp4*	Universal stress protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	174	0
single hit		Q5UXD0_HALMA	*kaiC2*	Circadian regulator	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	389	0

single hit		Q5UXG7_HALMA	*bcp2*	Bacterioferritin comigratory protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	176	0
single hit		Q5UXQ1_HALMA	*rrnAC3256*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	220	0
single hit		Q5UXS1_HALMA	*acs3*	Acyl-coenzyme A synthetase (EC 6.2.1.1)	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	652	0
single hit		Q5UYC2_HALMA	*fabG6*	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	254	0
single hit		Q5UYF8_HALMA	*rrnAC2962*	Putative haloacid dehalogenase-like hydrolase	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	218	0
single hit		Q5UYH4_HALMA	*rrnAC2944*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	94	0
single hit		Q5UYN1_HALMA	*phaJ1*	(R)-specific enoyl-CoA hydratase (EC 4.2.1.-)	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	148	0
single hit		Q5UYS3_HALMA	*rrnAC2826*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	295	0
single hit		Q5UYW7_HALMA	*rrnAC2777*	DNA binding protein putative transcriptional regulator	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	198	0
single hit		Q5UZ39_HALMA	*rrnAC2692*	Sensor protein (EC 2.7.13.3)	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	688	0
single hit		Q5UZ97_HALMA	*glnB*	Nitrogen regulatory protein P-II	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	121	0
single hit		Q5UZR0_HALMA	*rrnAC2433*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	217	0
single hit		Q5UZU7_HALMA	*rrnAC2392*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	544	0
single hit		Q5UZV1_HALMA	*rrnAC2387*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	119	0
single hit		Q5UZV6_HALMA	*tnp*	Phage integrase	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	340	0
single hit		Q5UZX4_HALMA	*rimK*	Ribosomal protein S6 modification protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	287	0
single hit		Q5V045_HALMA	*copG1*	Transcriptional regulator CopG family	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	136	0
single hit		Q5V0G4_HALMA	*phoU1*	Phosphate transport system regulatory protein PhoU	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	225	0
single hit		Q5V0I9_HALMA	*rrnAC2113*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	466	0
single hit		Q5V0J6_HALMA	*rrnAC2106*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	290	0
single hit		Q5V0N8_HALMA	*rrnAC2059*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	122	0
single hit		Q5V0R0_HALMA	*pkn*	Serine/threonine protein kinase	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	302	0
single hit		Q5V0S4_HALMA	*lpl*	Lipoate protein ligase (EC 6.3.4.-)	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	264	0
single hit		Q5V0W5_HALMA	*arcR5*	Transcription regulator	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	269	0
single hit		Q5V0X6_HALMA	*rrnAC1959*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	109	0
single hit		Q5V0Z8_HALMA	*rrnAC1935*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	241	0
single hit		Q5V163_HALMA	*rrnAC1855*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	109	0
single hit		Q5V1Q7_HALMA	*rrnAC1631*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	145	0
single hit		Q5V1Z7_HALMA	*trkA2*	Potassium uptake protein TrkA	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	464	1
single hit		Q5V229_HALMA	*rrnAC1501*	Sensor protein (EC 2.7.13.3)	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	598	0
single hit		Q5V252_HALMA	*rrnAC1475*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	413	0
single hit		Q5V2G3_HALMA	*mutT5*	Mut/nudix family protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	158	0
single hit		Q5V2K3_HALMA	*rrnAC1316*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	239	0
single hit		Q5V2P1_HALMA	*rrnAC1272*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	571	0
single hit		Q5V2P7_HALMA	*rrnAC1263*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	297	0
single hit		Q5V2Q2_HALMA	*cheC2*	Chemotaxis protein CheC	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	200	0
single hit		Q5V2W5_HALMA	*moaB1*	Molybdenum cofactor biosynthesis protein B	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	211	0
single hit		Q5V2Z3_HALMA	*rrnAC1158*	Protein phosphatase 2C like phosphatase	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	402	0
single hit		Q5V2Z4_HALMA	*rrnAC1157*	Putative DNA-binding protein with a phosphopeptide binding motif	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	377	0
single hit		Q5V343_HALMA	*rrnAC1100*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	83	0
single hit		Q5V394_HALMA	*rrnAC1044*	Putative acetamidase/formamidase (EC 3.5.1.-)	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	434	0
single hit		Q5V3R7_HALMA	*pebP*	Phosphatidylethanolamine-binding protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	229	0
single hit		Q5V3V6_HALMA	*rrnAC0811*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	143	0
single hit		Q5V3W0_HALMA	*rrnAC0806*	Putative C2H2 zinc finger DNA-binding protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	44	0
single hit		Q5V3Z6_HALMA	*rrnAC0767*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	95	0
single hit		Q5V444_HALMA	*rrnAC0715*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	101	0
single hit		Q5V4B8_HALMA	*msbA-1*	ABC transporter ATP-binding protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	602	5
single hit		Q5V4G4_HALMA	*htlD*	Sensor protein (EC 2.7.13.3)	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	631	0
single hit		Q5V4I7_HALMA	*glcK*	Glucokinase (EC 2.7.1.2)	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	323	0
single hit		Q5V4R0_HALMA	*ligA*	DNA ligase (EC 6.5.1.1)	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	554	0
single hit		Q5V4T5_HALMA	*rrnAC0433*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	151	0
single hit		Q5V575_HALMA	*rrnAC0271*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	308	0
single hit		Q5V5C5_HALMA	*rpoM*	DNA-directed RNA-polymerase subunit M	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	108	0
single hit		Q5V5E3_HALMA	*odc*	Diaminopimelate decarboxylase (EC 4.1.1.20)	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	434	0
single hit		Q5V5M9_HALMA	*mer3*	N5N10-methylenetetrahydromethanopterin reductase	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	324	0
single hit		Q5V5R7_HALMA	*citG*	CitG family protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	238	0
single hit		Q5V5V0_HALMA	*rrnAC0017*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	174	0
single hit		Q5V689_HALMA	*pNG7263*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	256	0
single hit		Q5V6A3_HALMA	*amaB*	N-carbamoyl-L-amino acid amidohydrolase (EC 3.5.1.-)	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	410	0
single hit		Q5V6G3_HALMA	*pNG7183*	Transcription regulator	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	199	0
single hit		Q5V6H2_HALMA	*pNG7174*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	126	0
single hit		Q5V6Q5_HALMA	*pNG7082*	Sulfatase (EC 3.1.6.-)	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	451	0
single hit		Q5V6V8_HALMA	*kdgR1*	Transcriptional regulator	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	255	0
single hit		Q5V773_HALMA	*pNG6134*	Transcription regulator	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	249	0
single hit		Q5V7E4_HALMA	*pNG5120*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	122	0
single hit		Q5V7I5_HALMA	*pNG5024*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	197	0
single hit		Q5V848_HALMA	*pNG2010*	Hypothetical protein	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	148	0
single hit		RS14_HALMAReview	*rps14p*	30S ribosomal protein S14P (HmaS14)	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	61	0
single hit		RS27A_HALMAReview	*rps27ae*	30S ribosomal protein S27ae (HSH)	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	44	0
single hit		TRPE3_HALMAReview	*trpE3*	Anthranilate synthase component 1 3 (EC 4.1.3.27) (Anthranilatesynthase component I 3)	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	503	0
single hit		Y1720_HALMAReview	*rrnAC1720*	UPF0095 protein rrnAC1720	0	0	0	0	0	0	1	1	0	1	1	0.0	1.2 only	0	1	0.0	Soluble only	445	0