





IMAGp998E211117	GARS	glycyl-tRNA synthetase	NM_002047	2617	-1.79	-1.19	-
2.05	-1.42	-1.81	-2.17	-0.41	0	-0.71	-0.6
	0.31	-0.47	-0.1	-0.14	0.77		
	1.14	0.4	0.75				
IMAGp998E20194	GCLM	glutamate-cysteine ligase, modifier subunit	NM_002061	2730	-0.83	-1.01	-0.91
	-1.44	-1.17	-1.11	-0.03	-0.37	-0.26	-
0.09	0.09	0.18	0.01	-0.09	0.57	0.34	0.2
	0.35						
IMAGp998J051786	GNB4	guanine nucleotide binding protein (G protein), beta polypeptide 4	NM_021629	59345	0.21	0.27	0.01
	0.52	0.76	0.09	-0.23	-0.3	-0.54	
0.15	-0.18	0.45	0.17	-0.05	-0.2	-0.23	-0.49
	-0.23	-0.23	-0.3	-0.54			
IMAGp998F241862	GOSR1	golgi SNAP receptor complex member 1	NM_001007025				
	9527	0.47	0.86	0.4	0.82	0.13	0.11
	0.31	0.24	0.02	0.29	0.99		
0.47	-0.15	-0.01	0.07	0.01	0	-0.03	
IMAGp998F18976	GPC6	glypican 6		10082	0.4	0.56	0.31
	1.01	1.12					
0.77	-0.11	0.48	-0.05	0.37	0.23	0.14	-0.22
	0.09	-0.62	-0.44	-0.2	-		
0.28							
IMAGp998O04462	GTPBP4	GTP binding protein 4	NM_012341	23560	-0.8	-	
	0.66	-0.5	-0.94	-0.15	-1.22	-0.16	-0.77
	-0.58	-1.32	-0.24	-0.55	0.17	-0.05	
	1.41	0.87	0.3	0.59			
IMAGp998P012577	HIST1H2BA	histone 1, H2ba	NM_170610	255626		0.07	
	0.6	-0.04	0.73	0.59	0.68	-0.29	0.24
	0.78	0.28	0.34	0.18	-0.22	-	
0.2	-0.25	-0.11	0	-0.52			
IMAGp998B144117	HNRPLL	heterogeneous nuclear ribonucleoprotein L-like					
	92906	-0.05	0.57	0.38	0.8	-0.16	0.64
	0.02	-0.14	0.07	0.24	0.66		
	0.45	-0.16	-0.08	-0.67	-0.51	-0.2	-0.29
IMAGp998C131008	HSMPP8	M-phase phosphoprotein, mpp8		54737	0.03		
	0.59	0.11	0.62	0.63	0.23	-0.08	0.04
	0.1	0.28	-0.05	0.4	-0.1	-	
0.23	-0.29	-0.07	0	-0.34			
IMAGp998K17615	HSPA9B	heat shock 70kDa protein 9B (mortalin-2)					
	NM_004134	3313	-0.87	-0.8	-0.96	-0.97	-0.75
	0.06	-0.12	-0.41	-0.86	-		
0.58	-0.92	-0.47	0.1	-0.12	1.52	1.24	0.6
	0.99						
IMAGp998G04114	HSPC111	hypothetical protein HSPC111	NM_016391	51491	-		
	1.32	-0.45	-1.17	-0.31	-0.32	-0.05	-1.4
	-0.86	-1.86	-1.42	-2.02	-1.96	0.13	-
0.57	0.43	0.57	0.4	-0.22			
IMAGp998O16868	HSPD1	heat shock 60kDa protein 1 (chaperonin)	NM_199440				
	3329	-0.48	-1.2	-0.9	-1.36	-0.58	-0.31
	-0.02	-0.14	-0.6	-0.94	-1.13	-	
0.44	0.13	-0.15	1	0.88	0.3	0.24	
IMAGp998L222014	HSPH1	heat shock 105kDa/110kDa protein 1	NM_006644	10808	-		
	0.88	-1.24	-1.04	-1.28	-1.25	-1.73	-0.32
	-0.26	-0.7	-0.28	-0.09	0.12	-0.25	
	0.27	0.94	0.73	0.1	0.67		
IMAGp998P191938	HSU79274	protein predicted by clone 23733	NM_013300				
	29902	-0.94	-0.8	-0.99	-1.2	-1.04	-0.82
	-0.53	-0.61	-0.46	-0.3	-0.92		
	0.01	0.05	-0.15	0.77	0.51	0	1
IMAGp998H23652	KIAA0355	KIAA0355	NM_014686	9710	0.5	0.23	0.47
	0.45	0.53	1.11	0.32	0.57	0.15	0.18
	0.34	0.55	-0.39	-0.15	-0.29	-	
0.09	-0.1	-0.31					
IMAGp998F072040	KIF11	kinesin family member 11	NM_004523	3832	-0.02	-	
	0.62	-1.17	-1.27	-1.01	-1.34	-0.44	-0.66
	-0.2	-0.67	-0.74	0.57	-0.11	0.2	
	0.87	0.5	0.4	0.8			
IMAGp998B192011	KLF9	Kruppel-like factor 9	NM_001206	687	-0.24	-0.49	-
	0.42	-0.54	-0.17	-0.29	0.09	-0.15	-0.14
	-0.56	0.24	0.16	0.06	0.22	0.66	
	0.4	0.4	0.59				
IMAGp998M1818	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)					
	NM_002266	3838	-0.35	-0.53	-1.14	-1.25	-1.03
	-1.1	-0.19	-0.42	-1.18	-		
0.2	-0.97	-0.31	0.64	-0.37	2.24	1.97	0.8
	2.11						
IMAGp998E191786	LDHC	lactate dehydrogenase C		3948	-0.15	0.75	-0.05
	0.61	0.56	0.49	-0.31	0.28	-0.42	0.09
	0.68	0.05	-0.41	-0.25	-0.44	-	
0.2	-0.6	-0.46					

IMAGp998A19123	LNK	lymphocyte adaptor protein	NM_005475	10019	-0.39	-
0.69	-0.43	-0.73	-0.36	-0.1	-0.13	-0.36
	1.6	1.15	0.7	1.04		
IMAGp998I171779	LOC115294	similar to hypothetical protein FLJ10883				
	NM_052937	115294	-0.06	0.54	-0.03	0.71
	1.08	0.91	1.62	1.15	-0.25	-0.05
IMAGp998O06929	LOC285556	hypothetical protein LOC285556				
	285556		-0.8	-2.04	-1.19	-1.84
0.49	-0.85	0.04	0.11	1.44	1.27	0.2
IMAGp998F17116	LOC388214	hypothetical LOC388214				
			0.63	0.36	0.05	-0.13
0.17	-0.41	-0.15	-0.4	-0.44	0.06	-0.16
IMAGp998N211962	LOC389730	similar to chromosome 9 open reading frame 36				
	XM_372094	389730	0.33	0.34	-0.27	0.48
	0.99	0.03	-0.1	0.4	-0.22	-0.37
IMAGp998I191963	MELK	maternal embryonic leucine zipper kinase	NM_014791			
	9833		-0.02	-0.75	-0.79	-0.74
	0.25	0.32	0.22	1.08	0.49	0.4
IMAGp998L09196	MGC10744	hypothetical protein MGC10744	NM_183065	84314		
			0.04	0.24	-0.09	0.32
0.11	-0.23	-0.24	-0.15	-0.6	-0.34	
IMAGp998C07136	MGC15912	hypothetical protein MGC15912	NM_032886	84972		
			0.09	0.3	0.07	0.56
0.15	0	-0.46	-0.18	-0.2	-0.33	
IMAGp998B06642	MGC40214	hypothetical protein MGC40214		137682		
			0.12	0.07	0.09	0.59
0.21	-0.32	-0.63	-0.39	-1.8	-0.44	
IMAGp998A216113	MGC42367	similar to 2010300C02Rik protein	NM_207362			
	343990		-1.63	-0.29	-1.83	-0.35
	0.03	-0.35	-0.01	0.11	0.35	0.4
IMAGp998O03131	MKI67IP	MKI67 (FHA domain) interacting nucleolar				
phosphoprotein	NM_032390	84365	-1.13	-0.95	-0.96	-0.82
0.6	-1.12	-0.52	-0.84	-0.44	0.06	-0.23
IMAGp998A09421	MRPL36	mitochondrial ribosomal protein L36	NM_032479			
	64979		-0.38	-0.36	-0.05	-0.6
0.92	0.12	0.15	0.5	0.13	0.2	0.33
IMAGp998E111206	MRPS9	mitochondrial ribosomal protein S9		64965	-1.13	-
0.32	-0.95	-0.45	-0.97	0.39	-0.22	-0.4
	0.25	-0.02	0.3	0.16	0.29	-0.6
IMAGp998O07415	MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+				
dependent) 1-like	NM_015440	25902	-0.54	-0.61	-0.78	-1
0.4	-0.75	-0.6	-0.62	0.03	-0.09	0.02
IMAGp998J03598	MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+				
dependent) 2, methenyltetrahydrofolate cyclohydrolase	NM_006636	10797	-1.14	-		
1.17	-0.97	-1.67	-0.99	-0.98	0	-0.95
	0.9	0.4	-0.2	0.6	0	-0.25
IMAGp998P234167	NCBP2	nuclear cap binding protein subunit 2, 20kDa				
	NM_007362	22916	-1.24	0.11	-1.01	-0.25
1.14	-0.17	-0.19	0.13	0.15	0.89	0.66
IMAGp998F084789	NCL	nucleolin	NM_005381	4691	-0.5	-0.75
			0.26	-0.55	0.49	-0.94
	1.3	1.07	0.49	-0.94	0.28	-0.65
IMAGp998E08645	NEBL	nebullette	NM_006393	10529	-0.8	-0.5
0.89	-1.83	-0.04	-0.44	-0.13	-0.7	-0.06
	0.85					-0.07



IMAGp998B131156	PSME3	"proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)"	NM_005789	10197	-0.2	-0.45	-0.98	-0.67	-0.51	-0.54	-0.39	-
					0.6	-0.73	-0.8	-0.98	-0.16	0.07	-0.28	0.7
										0.48	0.3	0.57
IMAGp998P07460	PTDSR	phosphatidylserine receptor		23210	-0.13	-0.52	-					
					0.98	0.01	-0.05	-0.3	-1	-0.36	-0.86	-0.56
										-1.19	-0.22	-0.12
						0.23	0.4	0.67				
IMAGp998I04794	PYGM	"phosphorylase, glycogen; muscle (McArdle syndrome, glycogen storage disease type V)"		5837	0.39	-0.1	-0.06	0.01	-0.19	-		
					0.26	-0.13	-0.24	0.07	-0.17	0.21	0.2	0.3
										0.6	0.82	0.57
										0.2	0.62	
IMAGp998J17646	RAB18	RAB18, member RAS oncogene family	NM_021252	22931	-							
					0.38	-0.46	-0.53	-0.58	-0.47	-0.4	0.25	-0.21
										-0.22	-0.63	-0.38
						0.13	1.52	0.76	0.8	0.79		0.14
IMAGp998E16403	RBMS1	RNA binding motif, single stranded interacting protein 1		5937	-0.55	-0.67	-0.46	-0.96	-0.01	-1.22	0.08	-0.6
					1.01	-0.21	-0.13	0.28	1.15	0.69	0.8	0.84
IMAGp998A23474	RG9MTD1	RNA (guanine-9-) methyltransferase domain containing 1	NM_017819	54931	-0.98	-0.59	-0.67	0.54	0.07	-1.76	-1.35	-
					0.87	-0.06	-1.2	0.15	-0.34	0.22	0.01	0.77
										0.89	0.6	0.95
IMAGp998G05131	RHOU	ras homolog gene family, member U	NM_021205	58480	-							
					0.19	0.59	-0.25	0.79	0.24	-0.11	0.03	0.16
										-0.07	0.39	0.77
						0.53	-0.62	-0.14	-0.2	-0.46		-0.27
IMAGp998H17736	RNPS1	RNA binding protein S1, serine-rich domain		10921	-0.61	-0.47	-0.37	-0.96	-0.68	-0.82	-0.16	-0.6
					0.51	-0.06	0.24	0.4	-0.2	0	0.59	-0.23
												-0.43
												-0.45
IMAGp998A132000	RNU22	RNA, U22 small nucleolar		9304	-0.83	-1.28	-					
					0.75	-1.17	-0.59	-0.72	-0.33	-0.83	-0.81	-1.24
										-0.57	-0.41	0.18
						0.87	1.1	0.2				0.01
												1.47
IMAGp998L20315	RPL11	ribosomal protein L11	NM_000975	6135	-0.34	-0.17	-					
					0.72	-0.56	-0.7	-0.22	0.09	-0.27	-0.52	-0.45
										-0.77	-0.3	0.17
						0.86	0.4	0.38				-0.11
												1.01
IMAGp998K1799	RPL24	ribosomal protein L24		6152	-0.56	-2.22	-0.82	-				
					2.04	-1.22	-0.19	0.58	-0.33	-0.29	-1.12	-0.83
										-0.83	0.22	0.43
						0.6	0.28					1.45
												0.65
IMAGp998P151197	SAP30	sin3-associated polypeptide, 30kDa	NM_003864	8819	-							
					0.13	-0.27	-0.66	-0.72	-0.49	-0.38	-0.38	-1.01
										-0.44	-0.07	-0.83
						0.09	0.54	-0.06	0.5	0.17		-0.11
												0.14
IMAGp998O0894	SASH1	SAM and SH3 domain containing 1		23328	0.21							
					0.27	0.36	0.31	1.37	0.93	-0.26	0.18	0.13
										0.36	0.29	0.62
						0.17	-0.58	-0.56	-0.9	-1.05		-0.32
IMAGp998L064578	SFRS2	splicing factor, arginine/serine-rich 2	NM_003016									
					6427	-0.88	0.04	-0.81	-0.49	-0.54	-0.04	0.1
										-0.4	-1.02	-0.16
						0.26	0.13	0.17	0.91	0.45	0.3	0.19
IMAGp998L20645	SFRS6	splicing factor, arginine/serine-rich 6	NM_006275									
					6431	-0.26	-0.66	-0.25	-0.85	-0.64	-0.84	-0.13
										-0.75	-0.91	-0.89
						0.78	0.16	0.28	0.83	0.28	0.1	0.29
IMAGp998L042012	SGOL2	shugoshin-like 2 (S. pombe)	NM_152524	151246	-							
					0.62	-0.62	-1.31	-1.18	-1.06	-1.06	-0.31	-0.57
										-0.64	-0.67	-0.88
						0.3	1.47	1.28	2.3	1.25		-0.05
												0.19
IMAGp998P192044	SLC1A1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 7	NM_004170	6505	0.29	1						
					0.32	0.94	0.26	0.39	0.22	0.25	-0.09	0.44
										0.47	0.66	-0.25
						0.05	0.02	0	0.05			0.09
												-
IMAGp998G01214	SLC30A7	solute carrier family 30 (zinc transporter), member 7		148867	-0.74	-0.55	-0.59	-0.69	-0.67	-1.13	0.1	-0.18
					0.34	-0.61	0.08	-0.25	-0.23	0.31	0.84	0.42
										0.3	0.52	

IMAGp998C152458	SLC39A14	solute carrier family 39 (zinc transporter), member 14	NM_015359	23516	-0.7	-0.34	-0.65	-0.81	-0.41	-0.12	-0.33	-0.61	-0.94	-0.57	-0.87	-1.1	-0.24	0.28	0.66	0.29	0	0.09
IMAGp998K06283	SLC39A14	solute carrier family 39 (zinc transporter), member 14	NM_015359	23516	-1.37	0.15	-1.33	0.48	-0.01	-1.99	-0.43	-0.6	-1.06	-0.31	-1.04	-0.6	-0.17	0.34	0.73	0.64	1.2	0.38
IMAGp998A10586	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	NM_003045	6541	-0.65	-0.58	-0.53	-1.04	-0.8	-0.32	-0.03	-0.63	-0.76	-0.65	-1.11	-0.46	-0.21	-0.09	0.8	0.23	0.4	0.25
IMAGp998J154512	SMN1	survival of motor neuron 1, telomeric	NM_000344	6606	-0.77	0.02	-0.78	-0.28	-0.23	-0.29	0.03	-0.48	-0.38	-0.75	0.31	0.55	0.89	0.26	1.41	0.78	0.4	0.78
IMAGp998D034747	SNRPA1	small nuclear ribonucleoprotein polypeptide A'		6627	-1.58	-0.38	-1.95	0.42	-1.1	-2.53	-0.37	-0.11	-0.38	-0.7	-0.47	0.14	0.21	0.01	0.47	0.67	1.3	1.08
IMAGp998G08826	STK17A	serine/threonine kinase 17a (apoptosis-inducing)		9263	-0.75	-0.35	-0.51	-0.21	-0.35	-0.45	-0.3	-0.13	-0.52	-0.42	0.39	0.21	0.14	-0.2	0.88	0.98	0.7	0.88
IMAGp998A132001	TDP1	tyrosyl-DNA phosphodiesterase 1		55775	-0.61	-0.1	-0.87	-0.47	-0.57	-0.62	-0.25	-0.61	0.76	-0.71	-0.58	-0.51	0.18	-0.03	0.27	0.21	0.4	0.27
IMAGp998K18564	TOP2A	topoisomerase (DNA) II alpha 170kDa	NM_001067	7153	-0.52	-0.88	-1.29	-0.99	-0.77	-0.22	-0.65	-0.12	-0.49	-0.14	-0.06	0.45	0.31	1.58	0.9	1.3	1.13	
IMAGp998B06823	TRAM2	translocation associated membrane protein 2	NM_012288	9697	-0.67	-0.67	-0.6	-1.14	-0.97	-1.35	-0.07	-0.58	-0.61	0.89	-0.42	-0.33	0.05	-0.1	0.87	0.53	0.4	1.42
IMAGp998G10605	TRIP13	thyroid hormone receptor interactor 13	NM_004237	9319	-0.28	-0.33	-1.03	-1.13	-0.97	-0.9	0.25	-0.03	-0.45	0.3	-0.2	-0.21	0.11	0.06	0.73	0.34	0	0.6
IMAGp998C083938	TXNIP	thioredoxin interacting protein	NM_006472	10628	0.57	1.54	0.78	1.15	0.52	1.87	1.5	1.27	0.88	0.53	1.05	0.67	0.21	0.37	0.1	-0.23	-0.6	-1.27
IMAGp998F083938	TXNIP	thioredoxin interacting protein	NM_006472	10628	0.51	1.41	0.61	0.98	1.39	0.6	1.26	1.25	0.87	0.79	1.2	1.18	0.29	0.31	0.05	-0.11	-1.2	-0.71
IMAGp998E15659	UBE2C	ubiquitin-conjugating enzyme E2C	NM_007019	11065	0.25	-0.42	-0.38	-1.27	-0.92	-1	-0.25	-1.42	-0.51	-1.14	-0.03	-1.01	0.64	0.14	2.02	0.95	0.9	1.38
IMAGp998I054902	UBE2S	ubiquitin-conjugating enzyme E2S	NM_014501	27338	0.67	0.48	-1.88	0.69	-0.68	-1.55	-0.49	-0.53	-0.87	0.04	-0.81	-1.13	0.61	0.01	1	0.5	1	0.19
IMAGp998B22245	USP34	ubiquitin specific protease 34		9736	0.42	0.19	0.49	0.63	0.39	-0.04	0.02	0.03	0.15	0.51	-0.07	-0.05	0.1	-0.48	-0.1	-0.4	-0.25	
IMAGp998O10119	VCP	valosin-containing protein	NM_007126	7415	-0.89	-0.52	-0.6	-0.17	0.09	0.1	0.82	-0.56	-0.72	-0.28	0.58	0.27	0.29	0.86	0.55	1.1	0.39	
IMAGp998D08136	VDAC1	voltage-dependent anion channel 1	NM_003374	7416	-0.8	-0.43	-1.05	-0.53	-0.24	0.22	-0.1	-0.37	-0.3	-0.72	-0.57	0.01	0.46	0.06	1.46	1.05	0.9	0.81
IMAGp998A0394	WDR10	WD repeat domain 10		55764	-0.56	-0.16	0.14	-0.29	0.13	-0.81	-0.3	-0.41	0.28	0.42	1.34	0.52	0.66	1.3	0.92			

