

Clone Id	Gene Name	Description	Refseq	GeneID	HDMVEC_6h
	HDMVEC_6h	HDMVEC_12h	HDMVEC_12h	HDMVEC_12h	Fibro_6h
	Fibro_6h	Fibro_12h	Fibro_12h	Fibro_12h	U87_6h
	U87_6h	U87_12h	U87_12h	U87_12h	U87_12h
IMAGp998I17793	AES	amino-terminal enhancer of split	NM_198970	166	-
0.21	0.34	-0.07	0.23	0.18	0.35
				0.19	0.22
				0.2	0.47
				0.47	0.58
				0.79	-0.21
				0	
				-0.32	-0.39
				-0.4	-0.34
IMAGp998J2273	ARL6IP	ADP-ribosylation factor-like 6 interacting protein	NM_015161	23204	-0.51
				0.16	-0.92
				0.6	1.25
				1.25	-1.02
				0.57	0.57
				-0.9	-0.35
0.52	-0.21	0.57	0.78	1.16	2.91
				2.16	2.6
				3.45	
IMAGp998A06732	ARPC5L	actin related protein 2/3 complex, subunit 5-like	NM_030978	81873	-1.04
				0.05	-0.73
				-0.86	-0.65
				-0.21	-0.25
				-0.57	-0.91
1.09	-1.34	-0.83	0.29	-0.15	0.91
				0.6	0.1
				0.07	
IMAGp998D082010	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	NM_000489	546	-0.68
				-0.31	-0.46
				0.17	-
0.35	0	0.29	-0.23	0.39	-0.9
				-0.47	-0.08
				0.45	0.59
				1.56	1.14
				1.8	
				1.62	
IMAGp998G09191	BNIP1	BCL2/adenovirus E1B 19kDa interacting protein 1	NM_662	0.38	0.29
				0.4	0.48
				1.17	0.99
				-0.27	-0.11
				0.23	-0.11
				0.51	-
0.01	-0.05	-0.23	-0.58	-0.27	-0.4
				-0.29	
IMAGp998G144334	BRRN1	barren homolog (Drosophila)	NM_-0.73	-1.03	-0.93
				0.02	-0.03
				-0.1	-1.21
				-1.27	0.11
				0.04	-0.07
				0.48	
0.38	0.6	0.52			
IMAGp998D041904	BXDC1	brix domain containing 1	NM_032194	84154	-1.58
				-0.85	-1.04
0.87	-1.36	-0.8	-0.66	-0.37	-0.95
				-0.63	-1.31
				-0.81	0.07
				-0.39	
0.81	1.03	0.2	0.01		
IMAGp998P16979	C10orf11	chromosome 10 open reading frame 11	NM_0.17	0.44	-0.1
				0.7	0.21
				0.48	-0.02
				0.09	0.08
				0.06	-0.02
				1.12	-
0.05	-0.13	-0.53	-0.39	-0.2	-0.37
IMAGp998H175002	C10orf117	chromosome 10 open reading frame 117	NM_022451	64318	-1.04
				-0.1	-0.8
				0.33	0.34
				-1.88	-0.43
				-0.69	-0.04
0.44	-0.02	0.22	0.24	0.19	0.9
				0.59	1
				1.18	
IMAGp998L051853	C12orf11	chromosome 12 open reading frame 11	NM_55726	-0.82	-0.88
				-0.9	-0.81
				-0.08	-0.28
				-0.16	-0.3
				-0.07	0
				-0.89	-
0.02	0.02	0.07	0.8	0.51	0.7
				0.61	
IMAGp998J03130	C1orf8	chromosome 1 open reading frame 8	NM_0.13	0.72	0.03
				0.76	0.43
				0.68	-0.2
				0.08	-0.06
				0.27	0.34
				-0.14	-
0.16	-0.06	-0.29	-0.32	-0.3	-0.71
IMAGp998F18651	C20orf129	chromosome 20 open reading frame 129	NM_030919	81610	-0.31
				-0.75	-1.2
				-1.18	-1.21
				-2.47	-0.37
				-1.16	-0.57
1.26	0.08	-0.25	0.72	-0.16	2.1
				1.33	1.4
				2.19	
IMAGp998C17644	C3orf17	chromosome 3 open reading frame 17	NM_0.44	0.19	0.2
				0.48	0
				0.38	-0.1
				0.07	-0.09
				0.49	0.15
				0.15	-
0.08	-0.05	-0.15	-0.07	-0.1	-0.04
IMAGp998K151159	C6orf93	chromosome 6 open reading frame 93	NM_84946	-1.22	-0.91
				-0.96	-0.75
				0.62	-1.7
				-0.74	-0.99
				-0.87	-1.39
				-0.11	-
0.71	0.05	-0.02	0.88	0.63	0.1
				-0.1	-0.1
IMAGp998L154941	CCNB1	cyclin B1	NM_1.26	-2.63	0.52
				-0.83	0.1
				-0.55	-1.35
				-0.26	1.32
				1.29	2.32
				0.43	3
				1.33	
IMAGp998E011780	CCNB1	cyclin B1	NM_031966	891	-0.67
				-0.24	-1.8
1.19	-1.39	-0.27	-0.42	-1.05	-1.12
				-1.27	-0.69
				0.7	-0.73
				1.55	1.66
				0.7	0.96
IMAGp998D22135	CDC20	CDC20 cell division cycle 20 homolog (S. cerevisiae)	NM_001255	991	-0.65
				-0.29	-1.85
				-0.88	-1.12
				-0.95	-0.67
				-0.08	-1.07
1.06	-1.13	-1.48	0.22	-0.67	1.43
				1.66	1
				1.13	

IMAGp998E142011	CDCA8	cell division cycle associated 8	NM_018101	55143	0
-0.55	-1.14	-0.84	-1.25	-1.77	-0.02
0.17	1.69	0.79	0.9	1.16	
IMAGp998K211160	CEBPD	CCAAT/enhancer binding protein (C/EBP), delta			
NM_005195	1052	0.23	-0.09	-0.11	0.24
1.1	1.29	1.42	-0.43	-0.02	-1.09
0.89	-0.9	-0.4	-1.65	-0.15	-0.37
0.93	0.9	0.94			
IMAGp998I071779	CKS2	CDC28 protein kinase regulatory subunit 2	NM_001827		
1164	-0.22	-0.27	-0.12	-1.49	-0.77
1.19	0.54	-0.05	2.03	1.03	1.1
0.7	-0.76	-0.56	-0.15	0.04	0.22
IMAGp998D10578	CPSF6	cleavage and polyadenylation specific factor 6, 68kDa			
NM_007007	11052	-1.08	-1.11	-0.92	-0.93
0.44	-0.27	-0.2	-0.26	-0.51	-0.11
IMAGp998H09170	CYCS	cytochrome c, somatic	NM_018947	54205	-1.49
1.67	0.3	0.52	-0.87	0.06	-0.28
0.73	0.9	0.82	-0.77	-1.49	-0.73
IMAGp998B02519	CYP19A1	cytochrome P450, family 19, subfamily A, polypeptide 1			
0.67	0.13	1.2	0.73	-0.45	-0.12
IMAGp998G19624	DDA3	differential display and activated by p53		84722	-
0.17	-0.09	-0.62	-0.53	-1.27	-1.37
0.27	0.45	0.79	0.6	0.82	
IMAGp998D20115	DHX33	DEAH (Asp-Glu-Ala-His) box polypeptide 33	NM_020162		
56919	0.09	-0.48	-0.06	-0.45	-0.57
0.91	0.17	0.1	0.93	0.56	0.6
IMAGp998O011197	DKC1	dyskeratosis congenita 1, dyskerin	NM_001363	1736	-
0.9	-1.09	-0.69	-1.38	-0.59	-0.55
0.1	1.36	0.9	0.4	1.25	-0.05
IMAGp998I14645	EIF1AX	eukaryotic translation initiation factor 1A, X-linked			
NM_001412	1964	-0.35	-0.45	-0.37	-0.71
0.25	-0.63	-0.9	-0.41	-0.05	0.39
IMAGp998L081962	ELMO2	engulfment and cell motility 2 (ced-12 homolog, C. elegans)			
NM_182764	63916	-0.05	0.76	0.01	0.61
0.21	0.46	-0.38	0.05	-0.3	-0.1
IMAGp998D241165	FLJ10415	hypothetical protein FLJ10415	NM_018089	55139	-
0.11	0.39	0.05	0.84	0.73	0.85
0.36	-0.33	-0.33	0	-0.4	-0.28
IMAGp998D05669	FLJ11301	hypothetical protein FLJ11301	NM_018385	55341	-
0.08	-0.22	-0.19	-0.34	-0.85	-0.55
0.12	0.64	0.33	0	0.49	-0.17
IMAGp998M151817	ZC3H12A	zinc finger CCCH-type containing 12A			
NM_025079	80149	-0.55	0.26	-0.21	-0.31
0.14	-0.19	0	-0.51	-0.16	-0.65
IMAGp998A01519	FLJ35348	FLJ35348		266655	
0.66	1.17	0.46	0.3	0.27	0.43
0.09	-1.3	-0.54			
IMAGp998C05112	FLJ43663	hypothetical protein FLJ43663		378805	
0.32	1.03	0.45	0.94	0.88	1.31
0.03	0.16	-0.24	-0.01	-0.2	-0.27
IMAGp998M141931	GALK1	galactokinase 1	NM_000154	2584	-0.95
1.18	-0.73	-0.77	-0.48	-0.14	-0.95
0.4	0.4	0.55	-0.55	-0.6	-0.32
0.09	-1.3	-0.54	-0.16	-0.23	-0.48
0.09	-1.3	-0.54	-0.16	-0.23	-0.48

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
 0.15 -0.18 0.45 0.17 -0.05 -0.2 -0.23 -0.49 -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
 IMAGp998004462 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



IMAGp998C22891 NF1 neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) 4763 -0.39 -0.32 -0.44 -0.56 -0.41 -0.07  
 0.1 0 -0.1 -0.27 0.12 -0.17 0.01 0.14 1.39 1.21 0.9 1.14  
 IMAGp998P19615 NIPBL Nipped-B homolog (Drosophila) NM\_133433 25836 -0.86 -0.67 -1.03 -0.93 -0.88 -1.04 -0.25 -0.2 -0.89 -0.57 -0.29 -0.36 0.14 -0.07  
 1.52 1.4 0.9 0.77  
 IMAGp998B201942 NOL5A nucleolar protein 5A (56kDa with KKE/D repeat)  
 NM\_006392 10528 -1.48 -1.06 -1.74 -0.62 -0.74 -0.66 -0.91 -0.22 -1.59 -1.25 -0.73 -1.38 0.12 -0.36 0.17 0.45 -0.4 -0.17  
 IMAGp998D13688 NOLC1 nucleolar and coiled-body phosphoprotein 1  
 9221 -0.86 -1.01 -1 -1.13 -0.71 -0.78 -0.45 -0.23 -1.14 -0.98 -1.23 -1.03 -0.19 0.02 0.75 0.71 -0.1 -0.36  
 IMAGp998E093380 NP nucleoside phosphorylase NM\_000270 4860 -0.73  
 0.32 -0.55 -1.27 -0.35 0.6 -0.27 -0.5 -0.56 -0.5 -1.45 -0.92 0.34  
 0.17 0.95 0.44 0.8 0.43  
 IMAGp998D021119 NR2F1 nuclear receptor subfamily 2, group F, member 1  
 NM\_005654 7025 -0.43 -0.5 -0.87 -0.11 -0.97 -0.8 -0.45 -0.3 -0.35 -0.47 -1.14 -0.19 -0.22 -0.01 0.35 0.21 0 0.48  
 IMAGp998N081748 NUDT17 nudix (nucleoside diphosphate linked moiety X)-type motif 17 NM\_001012758 200035 -0.39 -0.05 -0.47 -0.13 -0.52 -0.31 -0.23 -0.36 -0.35 0.03 0.1 -0.24 0.17 -0.07 0.42 0.38 0.1 0.22  
 IMAGp998H05694 NUP35 nucleoporin 35kDa NM\_138285 129401 -0.88 -0.6 -0.82 -0.89 -0.9 -1.15 -0.43 -0.23 -0.6 -0.69 -0.78 -0.26 0.07 -0.31 0.91  
 0.62 1 0.44  
 IMAGp998B092976 PAPLN papilin, proteoglycan-like sulfated glycoprotein  
 89932 0.3 0.52 0.22 0.42 0.2 0.83 -0.07 0.04 -0.12 0.32 0.09  
 0.18 -0.08 -0.08 -0.1 -0.07 -0.2 -0.24  
 IMAGp998C23585 PCBD1 6-pyruvoyl-tetrahydropterin synthase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF) NM\_000281 5092 0.02  
 0.37 0.25 0.32 0.7 0.52 0.19 0.14 0.78 0.6 0.15 0.72 0.1 -0.4 -0.4 -0.31 -1.3 -0.37  
 IMAGp998J16870 PCBP1 poly(rC) binding protein 1 NM\_006196 5093 -0.16 -0.94 -0.1 -1.11 -0.35 -0.33 0.31 -0.5 -0.04 -0.6 -0.5 -0.37 -0.04 0.27  
 0.93 0.27 0.7 0.74  
 IMAGp998N16142 PCBP1 poly(rC) binding protein 1 NM\_006196 5093 -0.93 -0.41 -1.03 -0.05 0.44 0.12 0.25 -0.56 -0.14 -1.42 -1.07 -0.77 -0.01 0.38  
 1.05 0.49 0.4 0.76  
 IMAGp998N095451 PCMT1 protein-L-isoaspartate (D-aspartate) O-methyltransferase  
 NM\_005389 5110 -0.98 -0.26 -0.89 -0.14 -0.11 0.19 0.4 -0.26 -0.25 -1.36 -1.13 -0.63 0.49 0.14 1.1 0.68 0.2 1.23  
 IMAGp998F055360 PCMT1 protein-L-isoaspartate (D-aspartate) O-methyltransferase  
 5110 -1.07 0.37 -1.6 -0.37 -0.65 -0.55 0.08 0.05 -0.34 -1.49 -0.22 0.16 0.4 -0.15 0.84 0.6 0.6 0.77  
 IMAGp998K12677 PDCD4 programmed cell death 4 (neoplastic transformation inhibitor) NM\_145341 27250 0.33 0.57 0.63 0.52 1.52 0.91 0.6 1.2  
 0.76 0.3 1.4 1.08 -0.22 -0.07 -0.05 0.16 0 0.12  
 IMAGp998G201998 PLK1 polo-like kinase 1 (Drosophila) NM\_005030 5347 -0.32 0 -1.3 -0.66 -1.49 -0.84 -0.3 -0.49 -0.63 -0.85 -1.48 -0.35 0.37 -0.36 0.96 0.4 0.7 0.97  
 IMAGp998D13653 PPIL1 peptidylprolyl isomerase (cyclophilin)-like 1  
 NM\_016059 51645 -0.46 -0.73 -0.95 -0.76 -0.56 -0.25 -0.18 -0.09 -0.74 -0.09 -0.82 -0.15 0.29 -0.28 0.24 0.39 0.2 0.29  
 IMAGp998B02829 PRODH proline dehydrogenase (oxidase) 1 NM\_016335 5625 -0.03 0.12 0.02 0.26 0.59 0.62 0.06 0.1 0.26 0.24 0.42 0.4 0.02 -0.14 -0.25 -0.28 -0.1 -0.53

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 0.12 -0.03  
     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 -0.06 0.14  
     0.13 1.52 0.76 0.8 0.79  
 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 -0.35 -0.93 -  
 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 0.17 -0.27 -  
 0.53 -0.62 -0.14 -0.2 -0.46  
 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 -0.23 -0.43 -0.45 -  
 0.51 -0.06 0.24 0.4 -0.2 0 0.59  
 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 0.01 1.47  
     0.87 1.1 0.2  
 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 -0.11 1.01  
     0.86 0.4 0.38  
 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 1.45 0.65  
     0.6 0.28  
 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 -0.11 0.14  
     0.09 0.54 -0.06 0.5 0.17  
 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 -0.32  
     0.17 -0.58 -0.56 -0.9 -1.05  
 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 -1.16  
     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 -0.18 -  
 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 -0.05 0.19 -  
 0.3 1.47 1.28 2.3 1.25  
 IMAGp998P192044 SLC1A1 solute carrier family 1 (neuronal/epithelial high  
 affinity glutamate transporter, system Xag), membe 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 0.09 -  
 0.05 0.02 0 0.05  
 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<sup>+</sup> 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 -0.15 -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 0.05 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 -0.45 -0.29 -0.89 -0.52 -0.6 -0.17 0.09 0.1 0.82 -0.56 -0.72 -0.28 0.58 0.27 0.86 0.55 1.1 0.39  
 IMAGp998D08136 VDAC1 voltage-dependent anion channel 1 NM\_003374 7416 -0.46 -0.8 -0.43 -1.05 -0.53 -0.24 0.22 -0.1 -0.37 -0.3 -0.72 -0.57 0.01 0.06 1.46 1.05 0.9 0.81  
 IMAGp998A0394 WDR10 WD repeat domain 10 55764 0.04 -0.33 -0.18 -0.66 -0.56 -0.16 0.14 -0.29 0.13 -0.81 -0.3 -0.41 0.28 0.42 1.34 0.52 1.3 0.92

IMAGp998L201787	ZC3HAV1	zinc finger	CCCH-type, antiviral 1	NM_020119
56829	-0.15	0.2	-0.08	-0.05 0.21 0.58 0.39 0.3 0.05 0.23 0.44
0.44	-0.41	-0.04	-0.44	-0.3 -0.1 -0.45
IMAGp998C07436	ZKSCAN1	zinc finger	with KRAB and SCAN domains 1	
7586	0.37	0.07	0.64	0.16 1.01 1.15 0.71 0.54 0.88 0.69 1.21
0.71	-0.31	0.3	0.01	-0.28 -0.2 0.02
IMAGp998N151821	ZNF305	zinc finger	protein 305	NM_014724 9753 0.24
0.44	0.07	0.48	0.55	0.7 -0.08 0.07 0.26 0.47 0.18 -0.03 -0.1 0
-0.15	0.03	-0.2	-0.2	
IMAGp998I133725	PDPK1	3-phosphoinositide dependent	protein kinase-1	
5170	0.31	0.38	0.32	0.62 0.6 0.54 -0.04 -0.05 -0.07 0.52 0.5
0.36	-0.1	-0.01	-0.17	-0.14 -0.4 0.05
IMAGp998B09629	HSDL2	Hydroxysteroid dehydrogenase like 2		84263 0.22
0.45	0.27	0.49	0.46	-0.02 -0.04 -0.08 0.1 0.34 0.78 0.56 -0.04 -
0.01	-0.03	-0.12	-0.2	-0.24
IMAGp998C233578	SLC28A2	Solute carrier family 28 (sodium-coupled nucleoside transporter), member 2	9153 0.11 0.55 0 0.62 0.66	
0.87	-0.2	0.07	-0.08	0.35 0.48 0.82 -0.17 -0.14 -0.09 -0.06 -0.3 -
0.55				