

Clone Id	Gene Name	Description	Refseq	GeneID	HDMVEC_6h	Fibro_6h	U87_6h						
	HDMVEC_6h	HDMVEC_12h	HDMVEC_12h	HDMVEC_12h	HDMVEC_12h	Fibro_6h	U87_6h						
	Fibro_6h	Fibro_12h	Fibro_12h	Fibro_12h	Fibro_12h	Fibro_12h	U87_6h						
	U87_6h	U87_12h	U87_12h	U87_12h	U87_12h	U87_12h	U87_12h						
IMAGp998L05332	ABCC8	ATP-binding cassette, sub-family C (CFTR/MRP), member 8											
	NM_000352	6833	-0.17	0.12	-0.48	0.15	0.1	0.18	-0.5	-0.39	-0.47	-	
0.3	-0.9	-0.37	0	-0.17	0	0.39	0.8	0.41					
IMAGp998I235646	ACTG1	actin, gamma 1		NM_001614	71	0.16	-0.26	-0.59	-				
1.77	-1.11	-0.79	-0.46	0.17	-0.54	-0.97	1.04	0.18	-0.02	0.36	1.46	0.99	
	0.4	0.7											
IMAGp998C21738	ACTG1	actin, gamma 1		71	0.34	-0.23	-0.38	-0.61	-				
0.1	-0.55	0.38	-0.53	0.3	-0.54	-0.37	0.13	-0.1	0.39	1.19	0.66	0.1	
	0.99												
IMAGp998C16233	ADAM12	a disintegrin and metalloproteinase domain 12 (meltrin alpha)		8038	-0.16	0.16	-0.1	-0.08	-0.66	0.37	-0.46	-0.47	-
1.01	-0.54	-1.65	-0.4	-0.25	0.35	0.61	0.21	-0.2	0.6				
IMAGp998P131933	ADAT1	adenosine deaminase, tRNA-specific 1											23536
	0.33	0.38	0.24	0.25	2.39	0.65	0.05	0.14	-0.66	-0.61	-0.24	-0.58	-
0.21	-0.08	1.02	1.07	1.8	0.5								
IMAGp998H23972	AFG3L1	AFG3 ATPase family gene 3-like 1 (yeast)											
	NM_001132	172	-0.65	0.15	-0.92	0.2	-0.07	-0.66	0.01	0.46	-0.27		
	0.33	0.56	0.52	-0.53	-0.22	-0.62	0.01	-0.7	-0.38				
IMAGp998N211942	AMACR	alpha-methylacyl-CoA racemase								23600	-0.53	0.19	-
0.16	-0.15	-0.43	-0.11	0.12	0.15	0.35	0.28	1.03	0.52	-0.02	-0.27	0.13	-
	0.29	-0.2	-0.02										
IMAGp998F181867	ANKRA2	ankyrin repeat, family A (RFXANK-like), 2											
	57763	-0.78	0.21	0.09	-0.06	-0.02	-0.54	0.35	0.77	0.48	0.12	0.85	
	0.3	-0.09	-0.4	0.09	0.16	-1	-0.23						
IMAGp998K03526	APH1A	anterior pharynx defective 1 homolog A (C. elegans)											
	NM_016022	51107	0.17	0.77	-0.06	0.7	1	1.32	-0.18	-0.13	-0.44	-	
0.12	-0.49	0.06	-0.11	-0.21	0.24	0.71	1.4	0.36					
IMAGp998J08460	APOBEC3B	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B		9582	-0.26	0.11	-0.28	-0.09	0.01	0.16	0.17		
	0.35	0.53	0.69	0.42	0.18	0.19	-0.45	0.34	0.33	0	-0.32		
IMAGp998I132615	AQP9	aquaporin 9		NM_020980	366	0.78	0.19	-0.22	-0.06	-			
0.09	-0.05	-0.18	-0.12	-0.58	-0.49	-1.24	-0.91	0.03	-0.5	0.58	0.06	0.3	
	0.48												
IMAGp998A18727	ARL4A	ADP-ribosylation factor-like 4A								NM_005738	10124	-	
0.32	0.06	-0.41	-0.01	-0.32	-0.09	-0.56	-0.57	-0.45	-0.63	-1.16	-0.33	-0.07	
	0.03	0.39	0.28	-0.4	0.09								
IMAGp998J011196	ARL6IP5	ADP-ribosylation-like factor 6 interacting protein 5											
	NM_006407	10550	-0.19	-0.37	0.01	-0.3	0.05	0	0.25	0.38	0.74		
	0.26	0.41	0.84	0.05	0	0.61	0.35	-0.8	-0.38				
IMAGp998M13236	ARMCX1	armadillo repeat containing, X-linked 1											
	51309	-0.26	-0.03	-0.06	-0.29	0.46	0.29	0.74	0.28	0.6	0.46	0.81	
	0.63	0.06	-0.32	0.51	0.59	0.2	0.43						
IMAGp998P151784	ATP5G2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2		NM_005176	517	0.46	0.13	0.48					
	0.38	0.66	0.9	0.15	-0.06	0.13	0.02	-0.13	0.22	0.22	-0.03	1.12	
	0.7	0	0.28										
IMAGp998E04653	BET1	BET1 homolog (S. cerevisiae)								NM_005868	10282	-0.23	
	0.32	0.2	0.17	-0.36	0.09	0.63	0.59	0.68	0.83	0.35	0.71	0.01	-
0.11	0.14	0.36	0.3	1.08									
IMAGp998B111865	C10orf33	chromosome 10 open reading frame 33								NM_032709			
	84795	-0.15	0.58	-0.76	-0.22	-0.49	0.12	0.59	0.57	0.41	0.43	1.34	
	0.57	-0.09	-0.16	-0.59	0.34	-0.2	-1.01						

IMAGp998C02972	C14orf102	chromosome 14 open reading frame 102												
	NM_017970	55051	-0.71	0.22	-0.08	-0.14	0.11	-0.31	-0.41	-0.31	-0.94	-		
0.48	-0.93	-0.47	-0.19	-0.29	0.5	0.48	0.4	0.33						
IMAGp998H21470	C14orf118	Chromosome 14 open reading frame 118												
	55668	0.24	0.13	0.66	-0.01	0.56	0.38	0.15	-0.02	-0.16	-0.21	-0.29	0	
	-0.02	0.22	0.81	0.38	1	1.57								
IMAGp998I04734	C15orf12	chromosome 15 open reading frame 12												NM_018285
	55272	-1.05	0.59	-0.47	0	0	0.14	-0.59	-0.66	-0.89	-0.79	-1.42	-	
0.75	-0.26	-0.09	-0.04	-0.06	0.4	-0.47								
IMAGp998A182010	C20orf9	chromosome 20 open reading frame 9												NM_016004
	51098	0.08	-0.18	-0.18	-0.04	0.06	-0.45	0.54	-0.11	0.6	0.1	0.28		
	0.5	0.24	0.04	0.24	0.13	-0.6	-2.54							
IMAGp998D23820	C6orf80	chromosome 6 open reading frame 80												25901
	0.19	0.6	0.54	0.6	1.56	-0.3	0.87	0.85	0.99	0.69	0.95	0.75		
	0.2	0.2	0.3	0.18	-0.4	-0.05								
IMAGp998H11135	C7orf23	chromosome 7 open reading frame 23												79161
	0.19	-0.17	-0.09	-0.14	-0.46	0.1	0.3	0.51	0.21	0.25	0.86	0.19	-0.13	-
	0.14	0.32	0.13	0.4	-1.12									
IMAGp998N22623	Cab45	calcium binding protein Cab45 precursor												NM_016176
	51150	-0.33	-0.06	-0.26	-0.73	0.09	-0.61	0.16	-0.03	0.92	0.42	1.19		
	0.65	0.2	0.49	0.07	-0.63	-0.4	-0.45							
IMAGp998N04533	CASK	calcium/calmodulin-dependent serine protein kinase												
(MAGUK family)	8573	-0.12	1.63	0.65	0.11	-0.1	-0.34	-0.48	-0.23	-				
0.39	-0.49	-1.07	-0.36	-0.48	-0.01	0.44	0.3	1	-0.25					
IMAGp998L2280	CCL2	chemokine (C-C motif) ligand 2												6347
	0.23	0.33	0	0.26	0.68	0.53	0.15	1.72	1.25	2.17	1.32	-0.13	0.16	-
	0.07	-0.36	0.5	-0.21										
IMAGp998B16822	CCNE1	cyclin E1												
	0.25	-0.1	-0.03	-0.06	0.31	0.42	0.16	-0.42	0	-0.48	-0.39	-2.3	-	
	1.1													
IMAGp998C121895	CCNE2	cyclin E2												
	9134	-0.4	-0.76	0.05	-0.69	-								
0.44	-0.3	1.26	0.72	0.77	-0.23	0.5	0.1	-0.36	1.06	-0.79	-1.38	-0.8	-	
	1.68													
IMAGp998D18199	CDYL	chromodomain protein, Y-like												
	9425	-0.22	-											
0.3	-0.1	-0.29	-0.35	0.29	-0.03	-0.29	-0.4	-0.58	-0.81	-0.42	0	-0.29		
	0.35	0.01	0.2	1.24										
IMAGp998I22373	CERK	ceramide kinase												
	64781	0.3	0.04	0.22										
	0.13	0.57	0.14	-0.1	-0.51	-0.29	-0.55	-0.72	-0.35	-0.02	0.19	0.07	-	
0.07	-0.7	-0.29												
IMAGp998B021861	CHAF1B	chromatin assembly factor 1, subunit B (p60)												
	8208	-0.2	0.22	-0.59	-0.25	-0.18	-0.45	0.05	0.63	0.1	0.15	0.27		
	0.29	-0.65	0.23	-0.71	-0.53	-0.7	-0.82							
IMAGp998M07224	CHD9	chromodomain helicase DNA binding protein 9												
	80205	0.38	0.35	0.83	0.52	1.1	1.02	0.09	-0.22	-0.1	-			
0.11	-0.15	-0.29	0.29	0.02	1.44	1.13	1	1.44						
IMAGp998L071853	CHIC2	cysteine-rich hydrophobic domain 2												
	26511													
	0.17	0.28	0.89	0.35	1.1	0.22	0.09	-0.26	0.15	-0.49	0.13	-0.72		
	1.63	0.3	0.4	0.06	0.2	1.01								
IMAGp998G01671	CHST2	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase												
	2	9435	-0.34	0	-0.85	-0.08	-0.21	0.06	-0.84	-0.63	-1.67	-1.71	-	
2.08	-0.78	-0.18	-0.26	-0.33	0.01	0.2	-0.11							
IMAGp998J14406	CHST2	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase												
	2	9435	-0.52	0.13	-0.96	0.21	-0.16	-0.07	-0.74	-0.57	-1.56	-1.44	-	
0.94	-1.07	-0.11	-0.15	-0.21	-0.15	0.1	0.22							
IMAGp998O181782	CHST5	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase												
	5	23563	-0.28	-0.14	-0.36	0.01	-0.6	0.07	0.13	0.1	0.41	0.1		
	0.5	0.33	-0.29	-0.47	-0.21	0.22	0.6	-0.38						

IMAGp998C161862	CLDN11	claudin 11 (oligodendrocyte transmembrane protein)											
NM_005602	5010		-0.16	-0.12	-0.67	-0.53	-0.99	-0.61	0.38	0.42	0.19		
	0.37	0.81	0.68	-0.23	-0.22	-0.38	0.02	-0.1	-1.4				
IMAGp998K211869	CLDN12	claudin 12	NM_012129	9069									
0.05	0.2	0.33	-0.09	0.05	-0.25	-0.24	-0.26	0.08	0.04	-0.22	1.15	1.08	
	1.1	1.62											
IMAGp998L031159	COL5A2	collagen, type V, alpha 2	NM_000393	1290									
0.42	0.25	-0.17	0.04	0.17	-0.25	0.35	0.34	0.44	0.38	0.65	0.76	-0.39	
	0.06	0.37	0.44	0.1	0.03								
IMAGp998O06236	COLM	collomin	NM_181789	342035									
	0.14	-0.12	-0.29	0.27	0.34	0.32	-0.07	0.12	0.07	0.01	-0.31	0.04	
0.39	-0.4	-0.38											
IMAGp998B05209	COQ6	coenzyme Q6 homolog (yeast)	NM_182480	51004									
0.07	-0.35	0.14	0.05	0.42	0.19	0.11	0.41	0.25	0.58	0.33	-0.16	0.07	
	0.04	0.06	-1.6	-1.14									
IMAGp998I03669	CRI2	CREBBP/EP300 inhibitor 2		163126									
0.61	-0.57	-0.72	-0.54	-0.24	-0.1	-0.11	0.3	0.16	0.23	0.47	0.12	-0.24	
	0.11	-0.01	0	-0.24									
IMAGp998A22374	CRLF3	cytokine receptor-like factor 3		51379									
	0.19	0.24	0.56	0.64	0.48	-0.13	0.02	-0.01	-0.05	-0.47	-0.29	0.02	
0.03	1.5	-0.21	0.1	0.35									
IMAGp998C04733	CSRP2	cysteine and glycine-rich protein 2		1466									
	0.08	-0.69	-0.13	-0.51	-0.29	0	-0.05	0.19	0.19	-0.03	0.34	-0.18	
0.18	-0.7	-0.52	-0.1	-0.33									
IMAGp998F23839	CYB5	cytochrome b-5		1528									
	0.45	-0.14	0.67	-0.02	0.64	0.28	0.7	0.42	0.11	-0.04	0.2	-0.42	0
	0.02												
IMAGp998D06191	DAAM1	dishevelled associated activator of morphogenesis 1											
	23002	-0.28	0.85	0.1	0.49	0.54	0.31	-0.22	-0.3	-0.07	0.09	-0.1	
0.14	0.89	0.31	0.04	-0.1	0.1	0.74							
IMAGp998K22829	DDIT4	DNA-damage-inducible transcript 4	NM_019058	54541									
1.43	-0.26	-1.53	-0.74	-1.93	-2.09	-0.24	0.26	0.38	0.71	1.41	1.05	1.86	
	0.41	-0.26	0.28	-1.4	0.11								
IMAGp998P161747	DDX21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	NM_004728										
	9188	-0.12	-0.87	0.23	-0.89	0.79	0.15	-0.53	-1.2	-1.88	-0.99	-1.93	
1.6	0.39	-0.1	0.92	0.37	0.1	0.29							
IMAGp998D106103	DDX21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	NM_004728										
	9188	-0.9	-0.17	-0.74	-0.37	2.33	-0.63	-0.67	-1.26	-1.89	-0.06	-1.83	
1.63	0.46	0.02	0.77	0.21	0.2	-0.11							
IMAGp998C15391	DDX5	Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 (DDX5), mRNA	NM_004396	1655									
	0.34	-0.67	-0.87	-0.82	-0.52	0.18	-0.13	1.03	0.88	0	0.47		
IMAGp998C11192	DKFZp434C0328	hypothetical protein DKFZp434C0328											
	NM_017577	54762	0.1	-0.09	0.26	0.36	0.9	0.88	-0.07	-0.27	-0.29		
0.35	0.24	-0.47	-0.14	-0.13	0.17	0.04	1.4	0.39					
IMAGp998I17617	DKFZP434F0318	hypothetical protein DKFZP434F0318											
	NM_030817	81575	-0.31	0.17	-1.2	-0.39	-1.07	-0.91	0.63	0.56	0.17		
	0.55	0.6	0.34	-0.09	-0.62	0.14	0.29	0.6	-0.48				
IMAGp998B20616	DKFZP564G2022	DKFZP564G2022 protein	NM_015497	25963									
	0.38	-0.58	0.1	0	0.27	-0.35	-0.11	-0.33	-0.79	-0.59	0.04	-0.42	
	0.2	-0.06	0.9	0.69	0.7	0.8							
IMAGp998J01134	DLG5	discs, large homolog 5 (Drosophila)	NM_004747	9231									
	0.3	0.78	-0.14	0.11	0.01	0.25	-0.12	-0.22	-0.24	-0.28	-0.75	-0.25	-0.09
0.15	0.62	0.37	0.6	0									
IMAGp998D061924	DNCL2B	dynein, cytoplasmic, light polypeptide 2B											
	NM_130897	83657	-0.41	0.36	-0.12	0.23	-0.3	0.87	-0.52	-0.24	-0.31		
0.26	-0.63	-0.46	0.16	-0.13	0.01	0.5	0	-0.47					

IMAGp998C03128	DTL	denticleless homolog (Drosophila)	NM_016448	51514	-									
0.89	0.3	-0.95	-0.36	-0.68	-0.54	0.53	0.55	0.18	0.27	0.39	0.7	-0.35	0	
		-0.22	-0.77	-0.6	-0.39									
IMAGp998N0278	EBF2	early B-cell factor 2	64641	-0.17	0.12	-0.18	-							
0.03	0.16	0.19	-0.21	-0.22	-0.45	-0.23	-0.24	-0.7	-0.05	-0.34	0.39	0.07	1	
		-0.18												
IMAGp998G04178	ECEL1	endothelin converting enzyme-like 1	9427	0.07	-									
0.47	-0.18	0.09	-0.93	-1.1	0.26	0.15	0.17	0.35	0.37	0.27	-0.29	-0.01	-	
		0.12	0.09	-1.3	0.58									
IMAGp998B215843	ERN1	endoplasmic reticulum to nucleus signalling 1												
		2081	-0.23	0.38	-0.16	0.57	0.38	0.12	-0.26	-0.9	-0.4	-0.65	-1.35	-
		0.55	-0.03	0.24	-0.23	-0.59	-0.5	0.47						
IMAGp998B22525	EZH2	enhancer of zeste homolog 2 (Drosophila)	NM_152998											
		2146	-0.91	0.11	-0.98	-0.36	-0.71	-1.04	-0.02	0.15	0.22	0.21	0.1	-
		0.2	-0.18	-0.01	-0.02	0.07	-1.1	-0.31						
IMAGp998C141794	FBXO4	F-box protein 4	NM_012176	26272	-0.26	0.31	-0.17	-						
		0.14	0.19	-0.3	0.3	0.01	0.13	0.29	0.58	0.33	-0.23	-0.53	-0.33	-
		0.1	-0.1	0.06										
IMAGp998G16882	FEM1A	fem-1 homolog a (C.elegans)	55527	-0.15	0.23	-								
0.24	0.17	0.07	0.23	-0.43	-0.3	-0.28	-0.33	-0.97	-0.42	-0.15	-0.05	0.13		
		0.23	0.9	0.44										
IMAGp998C09565	FES	feline sarcoma oncogene	NM_002005	2242	0.05	-0.38	-							
		0.15	-0.43	0.23	0.01	-0.07	-0.21	-0.63	-0.49	-0.24	-0.62	-0.24	0.23	
		0.34	0.2	0	0.21									
IMAGp998C091203	FLJ13639	hypothetical protein FLJ13639	79758	0.3	-									
0.71	0.73	0.04	0.99	1.27	-0.18	-0.41	-0.76	-0.5	-1.08	-0.42	-0.19	0.28		
		0.26	-0.19	0.2	-0.03									
IMAGp998G05794	FLJ20323	hypothetical protein FLJ20323	NM_019005	54468	-									
0.75	-0.14	-0.53	-0.19	-0.06	-0.12	-0.62	-0.33	-0.66	-0.45	-0.69	-0.54	-0.02	-	
		0.34	0.7	0.62	1.2	0.17								
IMAGp998B083711	FLJ25715	hypothetical protein FLJ25715	284241		-									
0.01	-0.09	-0.15	-0.11	-0.24	-1.16	0.49	-0.06	0.34	0.22	1.12	0.88	-0.09	-	
		0.3	-0.16	0.24	-0.4	-1.01								
IMAGp998E191785	FLJ32658	hypothetical protein FLJ32658	NM_144688	147872										
		-0.42	0.16	-0.6	-0.31	-0.72	-0.38	0.06	0.2	0.33	0.33	0.47	0.25	
		0.27	-0.5	-0.08	0.24	0.3	0.09							
IMAGp998K06189	FLJ33167	hypothetical protein FLJ33167	201973		-									
0.28	0.14	-0.46	-0.57	-0.26	-0.24	0.6	0.67	0.7	0.29	1.09	0.61	-0.15		
		0.26	-0.29	-0.35	-0.9	-0.49								
IMAGp998G034013	GBAS	glioblastoma amplified sequence	NM_001483	2631	-									
0.32	-0.38	-0.17	-0.3	-0.27	-0.13	0.33	0.4	0.36	0.41	0.94	0.99	0.03	-	
		0.03	0.18	0.28	0	0.7								
IMAGp998P201724	GCN1L1	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	NM_006836	10985	-0.06	0.04	-0.22	0.08	0.16	0.34	-0.36	-		
		0.04	-0.53	-0.18	-0.99	-0.21	-0.17	-0.04	0.15	0.17	-0.2	0.14		
IMAGp998C21593	HDAC9	Histone deacetylase 9	9734	0.08	0.84	0.32								
		0.99	0.59	0.85	-0.24	0.08	-0.36	-0.1	0.11	-0.25	-0.27	-0.02	-0.03	
		0.15	1	0.42										
IMAGp998F082039	HOP	homeodomain-only protein	84525	-0.64	0	-								
0.55	0.1	0.02	-1.14	0.43	0.39	0.45	0.29	0.21	0.12	-0.27	-0.2	-0.05	-	
		0.05	0.5	-0.38										
IMAGp998N181196	HOXA9	homeo box A9	NM_002142	3205	-0.3	0.09	-0.47	-						
0.44	0.01	-0.41	0.3	0.07	0.21	0.4	-0.01	0.8	-0.21	-0.41	-0.04	-0.11	0	
		-1.57												
IMAGp998F06112	HTATIP2	HIV-1 Tat interactive protein 2, 30kDa												
		10553	0.12	-0.33	-0.1	-0.14	0.02	0.01	0.24	0.12	0.32	0.24	0.64	
		0.21	-0.17	-0.06	-0.34	-0.08	-1.7	-0.3						

IMAGp998N08406	ID1	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	3397	0.1	0.09	0.38	0.12	0.58	1.02	-1.17	-										
			1.62	-1.25	-1.28	-2.03	-1.56	0.1	0.05	0.52	0.05	-0.1	0.65								
IMAGp998J061962	IDI1	isopentenyl-diphosphate delta isomerase	NM_004508	3422	-0.45	-0.1	-0.63	-0.44	-0.6	-0.35	0.18	0.32	0.04	0.23	0.78						
				0.33	0.21	-0.3	0.1	0.26	-0.1	-0.23											
IMAGp998L08626	IGF1R	insulin-like growth factor 1 receptor	3480	0.31	-0.1	-0.03	0.23	0.11	0.53	-0.35	-0.21	-1.63	-0.54	-1.34	-0.71	-0.38					
				0.23	0.16	0.22	0	0.44													
IMAGp998K153905	IRX2	iroquois homeobox protein 2	NM_033267	153572	0.29	-0.33	0.14	-0.02	0.5	-0.69	-0.43	-0.57	-0.56	-0.81	-1.58	-0.21					
				0.34	0.42	0.11	0.11	1	1.06												
IMAGp998C101962	ISL2	ISL2 transcription factor, LIM/homeodomain, (islet-2)	NM_145805	64843	-0.11	-0.07	-0.35	0.13	-0.32	0.12	0.14	0.35	0.15								
				0.49	0.11	0.11	0.11	-0.31	-0.13	0.01	-2.1	-0.55									
IMAGp998F06678	JDP2	jun dimerization protein 2	122953	0.19	-0.69	-0.28	-0.13	-1.36	0.07	-0.13	-0.06	0.27	0.45	0.63	-0.23	-0.34					
				0.59	0	-1.7	-0.3														
IMAGp998P0786	JMJD2C	jumonji domain containing 2C	23081	0.36	0.19	0.31	0.58	0.9	-1.19	-0.03	0.08	-0.18	-0.01	0.07	-0.03						
				0.07	0.33	0.37	0.7	0.31													
IMAGp998N202011	KBTBD6	kelch repeat and BTB (POZ) domain containing 6	NM_152903	89890	-0.3	-0.37	-0.18	-0.46	-0.15	-0.32	0.32	0.17	0.94								
				0.4	0.49	0.99	0.01	0.13	0.19	0.02	-0.4	0.99									
IMAGp998A041725	KCNMB3	potassium large conductance calcium-activated channel, subfamily M beta member 3	NM_171830	27094	-0.03	0	-0.14	-0.08													
				0.16	0.06	0.17	0.29	0.23	0.31	0.1	-0.05	-0.18	-0.11	0	-0.51	0					
				-0.3																	
IMAGp998B13204	KIAA1423	KIAA1423	XM_376550	57583	-0.5	0.06	-0.39	-	0.1	0.06	0.1	-0.3	-0.18	-0.74	-0.78	-0.77	-0.46	-0.16	-0.23	0.93	0.88
				0.9	-0.17																
IMAGp998E23314	KIAA1718	KIAA1718 protein	XM_376680	80853	-0.12	0.84			0.26	0.45	1.49	0.21	-0.3	-0.36	-0.26	-0.09	-1	-0.62	-0.33	-0.09	
				0.01	-0.16	-0.3	0.55														
IMAGp998I141163	KLF6	Kruppel-like factor 6	1316	0.39	1.1	0.84	-0.07	-0.65	-1.44	-1.78	-1.94	-1.16	0.07	0.06	1.02						
				0.9	0.4	0.79															
IMAGp998F173980	LOC150271	Hypothetical protein LOC150271	150271	-0.25	0.07	-0.1	-1.61	-0.86	-0.28	0.22	0.19	0.06	0.28	-0.11	-0.01	-					
				0.09	-0.18	-0.04	0.23	-0.1	-0.58												
IMAGp998M062035	LOC162073	Hypothetical protein LOC162073	162073	0.41	-0.24	0.43	-0.06	-0.21	0.66	0.27	-0.16	-1.18	-1.61	-1.04	-0.93						
				0.04	0.04	0.84	0.59	0	0.23												
IMAGp998C24181	LOC284018	hypothetical protein LOC284018	NM_181655	284018	-0.33	0.3	-0.25	-0.05	0.12	-1.28	0.14	0.32	0.2	0.05							
				0.81	0.34	-0.17	0.1	-0.3	-0.55	-0.7	0.21										
IMAGp998G134031	LOC284422	similar to HSPC323	XM_209196	284422	-0.1	0.28	-0.15	0.26	0.38	0.51	0.41	0.74	1	0.12	-						
				0.49	0.06	-0.5	-0.2	0.14													
IMAGp998O181199	LOC388796	hypothetical LOC388796	XM_373914	388796	-0.37	-0.87	-0.37	-0.11	-0.02	-0.73	-0.42	-0.71	-0.77	-1.05	-1.14	-0.23	-				
				0.24	0.02	0.26	0.7	-0.68													
IMAGp998E201119	LOC388969	hypothetical LOC388969	NM_001013649	388969	0.09	-0.28	-0.32	0.3	-0.02	-0.14	0.07	0.5	1.11	0.33	0.06	0.49					
				0.19	-0.03	0.4	0.21	-2.6	-0.58												

IMAGp998L154547	PADI3	peptidyl arginine deiminase, type III	NM_016233											
	51702	-0.33	0.16	-0.27	0.72	-0.41	-1.06	0.47	0.2	0.44	0.37	0.2		
		0.64	-0.02	0.27	0.2	-0.66	-1.7	-0.06						
IMAGp998L19593	PAFAH1B2	platelet-activating factor acetylhydrolase, isoform Ib, beta subunit	30kDa	5049	0.22	0.22	0.34	0.26	0.69					
		0.79	0.25	0.16	-0.94	-0.53	-0.97	-0.84	0.18	3.32	1.05	0.82	0.7	
		0.53												
IMAGp998O0818	PDIR	protein disulfide isomerase-associated 5		10954	-									
	0.9	-0.16	-1.14	-0.17	0.15	-0.46	-0.2	0.34	-0.22	-0.02	0.25	-0.02	-0.41	-
	0.24	-0.33	0.06	-1	-1.76									
IMAGp998G011199	PDLIM5	PDZ and LIM domain 5	NM_006457	10611	0.57	-								
	0.28	0.9	0.05	0.7	1.09	-0.13	-0.55	-0.71	-0.48	-0.66	-0.36	-0.09	0.37	
		0.52	-0.01	-0.2	0.18									
IMAGp998P08679	PFDN2	prefoldin 2		5202	-0.23	-0.49	-0.28	-0.22	0.37					
	0.28	-0.19	-0.24	-0.82	-0.74	-0.88	-0.7	0.14	-0.03	1.12	0.87	0	-	
	0.21													
IMAGp998F21398	Pfs2	DNA replication complex GINS protein	PSF2	51659	-									
	0.83	0.41	-1.11	-0.25	-0.62	-1.34	0.14	0.51	0.34	0.44	0.99	-0.16	-0.3	0
		-0.43	-0.09	-0.7	-0.27									
IMAGp998J17653	PHYH	phytanoyl-CoA hydroxylase (Refsum disease)												
	5264	-0.3	0.01	-0.13	0.34	0.14	0.52	0.74	0.57	0.33	0.53	0.61		
		0.91	-0.17	0.13	0.17	0.48	0.2	0.29						
IMAGp998I064413	PKD1	polycystic kidney disease 1 (autosomal dominant)												
	5310	-0.46	0.29	0.02	0.44	0.7	1.32	0.56	0.9	0.42	0.76	0.66		
		0.53	-0.06	0	-0.3	-0.1	0	-0.89						
IMAGp998C144000	PKHD1	polycystic kidney and hepatic disease 1 (autosomal recessive)												
	5314	-0.04	-0.2	-0.25	-0.18	-2.04	0.01	0.39	-0.02	0.51				
	0.36	0.1	-0.2	-0.14	0.05	-0.06	-0.46	-0.2	-0.65					
IMAGp998E01326	PKM2	pyruvate kinase, muscle	NM_182471	5315	-0.78	-0.06	-							
	1.28	-0.09	-0.72	-0.35	-0.14	0.33	0.07	0.27	-0.13	0.37	-0.14	-0.08	-0.21	-
	0.11	0.1	-0.68											
IMAGp998C151780	PLEKHA2	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 2		59339	0.03	0.31	0.14							
	0.06	-0.24	0.07	-0.07	-0.56	-0.02	-0.23	-0.59	-0.34	-0.12	0.1	0.72		
	0.18	0.6	0.76											
IMAGp998L11214	PLEKHA5	pleckstrin homology domain containing, family A member 5	NM_019012	54477	-0.29	0.36	0.03	0.28	0.28	0.14	-0.01	-0.32	-	
	0.37	0.1	-0.54	-0.57	0.02	-0.47	0.27	0.45	1.4	0.82				
IMAGp998E15188	PLEKHM2	pleckstrin homology domain containing, family M (with RUN domain) member 2		23207	0.26	0.66	0.7	0.8	1.14	1.31	-			
	0.06	0.06	-0.15	-0.05	-0.6	-0.23	-0.09	-0.01	0.16	0.27	1.2	0.75		
IMAGp998C14217	PLSCR1	phospholipid scramblase 1		5359	-0.44	-								
	0.37	-0.18	-0.2	-0.32	-0.03	0.25	0.15	0.48	0.81	0.1	0.53	-0.16	-0.2	
		0.15	-0.02	0.1	0.38									
IMAGp998G17842	PMP22	peripheral myelin protein 22	NM_153321	5376	0.65	-								
	0.08	0.34	0	0.49	0.85	0.21	0.17	-0.27	-0.06	0.18	0.02	0.27	-	
	0.15	1.32	0.97	0.7	0.86									
IMAGp998O22388	PODXL	podocalyxin-like	NM_001018111	5420	0.26	-0.64	-							
	0.06	-0.33	0.22	0.5	-0.55	-0.4	-0.89	-0.15	-1.21	-0.35	-0.11	-0.12		
		0.32	0.23	0.7	0.25									
IMAGp998A07246	POLA	polymerase (DNA directed), alpha		5422	-0.56	-								
	0.01	-0.3	-0.35	-0.78	-0.85	-0.03	0.03	0.14	0.03	0.82	0.3	-0.19	0.08	-
	0.44	-0.15	-1	0.16										
IMAGp998F201861	POLR3GL	polymerase (RNA) III (DNA directed) polypeptide G (32kD) like	NM_032305	84265	-0.31	0.05	-0.2	-0.11	-0.56	0.21	0.36	0.36		
	0.46	0.46	0.38	0.58	0.09	-0.59	0.37	0.57	0.4	-2.74				

IMAGp998B10725	PPFIBP2	PTPRF interacting protein, binding protein 2 (liprin beta 2)	NM_003621	8495	-0.77	0.21	-0.3	0.34	-0.11	0.3	0.15									
					0.12	0.24	0.37	0.52	0.68	-0.34	-0.26	-0.06	0.12	-0.3	0.14					
IMAGp998N071907	PPIF	peptidylprolyl isomerase F (cyclophilin F)		10105	-0.74	-0.16	-0.77	-0.39	-0.26	0.02	-0.4	-0.46	-1.04	-0.97	-0.9	-				
					1.18	-0.03	-0.06	0.79	0.47	0.6	-0.61									
IMAGp998L24526	PRKCBP1	protein kinase C binding protein 1													23613	-				
					0.63	0.27	-0.4	0.19	-0.2	-0.2	0.48	0.28	0.01	0.29	0.27	0.01	-0.39			
						0.05	-0.13	-0.11	-0.2	-1.96										
IMAGp998O191854	PRKY	Protein kinase, Y-linked													5616	0.26	0.23			
						0.28	0.21	0.93	0.61	0.09	0.06	-0.04	-0.25	0.04	-0.2	-0.04	0.17			
						0.16	-0.09	0	0.29											
IMAGp998E14612	PSIP1	PC4 and SFRS1 interacting protein 1	NM_033222														11168	-		
					0.48	0.01	-0.45	-0.44	-0.29	-0.12	0.51	0.45	0.48	0.5	0.61	1.07	-0.19	-		
						0.22	0.17	0.44	1.3	-0.17										
IMAGp998A18791	PUM1	pumilio homolog 1 (Drosophila)															9698	0.25		
						0.16	0.28	0.35	1.07	0.43	0.11	-0.13	-0.35	-0.46	-0.46	-0.09	0.1			
						0.09	1.95	1.7	1.3	1.23										
IMAGp998K10518	PXN	paxillin	NM_002859	5829	-0.17	-0.05	0.01	-0.26												
						0.72	0.4	-0.11	-0.01	-0.42	-0.48	-0.87	-0.71	-0.21	0.39	0.32	0.18			
						0.1	0.15													
IMAGp998L0986	QKI	quaking homolog, KH domain RNA binding (mouse)																		
						NM_006775	9444	0.1	0.44	0.03	0.6	1.44	0.13	-0.25	0.14	-0.26				
								0.01	-0.49	-0.11	-0.18	-0.18	0.85	1.25	1.4	2.21				
IMAGp998A19163	RAB6IP2	RAB6 interacting protein 2															23085	1.21		
							0.82	0.18	-0.02	1.18	0.22	-0.27	-0.04	-0.69	-0.01	-1.26	-0.03	0.28		
							0.1	-0.04	0.57	1.3	1.02									
IMAGp998L052333	RABGEF1	RAB guanine nucleotide exchange factor (GEF) 1																		
						NM_014504	27342	-0.31	0.28	-0.06	-0.08	0.42	0.27	-0.11	-0.2	-0.25	-			
								0.13	-0.4	-0.12	-0.05	0.49	0.55	0.12	0.7	0.01				
IMAGp998G092332	RDX	radixin																		
							0.15	0	-0.44	-0.2	-0.29	-0.12	-0.31	0.17	-0.11	0.73	0.45	0.5		
							0.69													
IMAGp998C18473	REV3L	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)																		
							5980	0.23	0.59	0.45	0.48	0.78	0.51	-0.01	0.06	-0.05				
								0.17	-0.12	-0.1	0.09	-0.07	-0.11	-0.03	0.8	0.53				
IMAGp998P17514	RFP	ret finger protein																		
								0.06	0.08	-0.06	0.19	-0.27	-0.16	-0.58	-0.42	-0.83	-0.27	0.15	-0.24	0.36
									0.32	0.4	-0.23									
IMAGp998G05786	RHOB	ras homolog gene family, member B	NM_004040	388																
								0.06	1.68	1.21	0.64	0.86	1.32	-0.29	-0.51	-0.13	-0.19	-0.67	0.23	-
								0.27	0.32	0.24	-0.08	0.1	0.23							
IMAGp998J134543	RLN3R1	relaxin 3 receptor 1																		
								0.32	0.36	-0.52	0.11	0.49	0.29	0.37	0.28	0.83	0.53	0.14	0.13	0.08
									0.5	-0.4	-0.11									
IMAGp998E21692	RNF167	ring finger protein 167																		
								0.38	0.25	-0.42	-0.69	-0.1	0.26	0.35	0.56	1.24	0.98	-0.21	-0.13	-0.24
									0.1	-0.2	-0.35									
IMAGp998F05119	RNF4	ring finger protein 4	NM_002938	6047	-0.2	-0.3	-													
								0.11	-0.4	-0.06	0	-0.3	-0.63	-0.48	-0.51	-0.88	-0.23	-0.17	-0.06	0.09
									0.02	0	1.27									
IMAGp998J24820	RPA3	replication protein A3, 14kDa																		
								0.15	-0.14	0.42	-0.06	0.74	0.15	1.02	0.44	1.28	1.18	0.46	-0.25	
									0.79	0.16	-0.5	0.25								
IMAGp998I09694	RPL22L1	ribosomal protein L22 like 1	XM_114317	200916																
									-0.61	-0.42	-0.86	-0.67	-0.48	-1.44	0.2	0.12	0.31	0.22	1.17	1.26
									0.26	-0.28	0.69	0.56	-0.3	-0.65						

IMAGp998N2195	STAMBP	STAM binding protein	10617	-0.52	-0.27	-
0.68	-0.14	-0.11	-0.07	0.08	-0.01	0.15
0.34	-1	-0.32	-0.13	0.14	-0.14	0.16
						-0.33
IMAGp998H14626	STK38L	serine/threonine kinase 38 like	NM_015000			
23012	0.13	0.14	0.07	0.46	0.55	0.66
0.5	0.03	-0.21	0.58	0.49	-0.6	0.11
IMAGp998C221203	SUI1	putative translation initiation factor	NM_005801			
10209	1.22	0.17	1.24	0.46	1.01	0.84
1.5	-0.12	0.02	1.32	0.94	0.7	1.21
IMAGp998P151965	TBX15	T-box 15	NM_152380	6913	-0.91	-0.41
0.72	-1.12	0.4	0.47	0.23	0.15	0.97
	0.38				0.65	-0.18
					-0.03	0.2
					0.39	-0.8
IMAGp998A221154	TBX2	T-box 2	NM_005994	6909	0.32	-0.03
0.82	-0.76	-0.48	-0.36	-0.58	-0.3	-1.01
0.2	0.26				-0.31	-0.04
					-0.47	0.13
					0.41	-
IMAGp998G08415	TENC1	tensin like C1 domain containing phosphatase				
23371	-0.45	0.13	-0.69	0.42	-0.05	-0.02
0.51	-0.22	-0.09	-0.42	-0.88	0.1	-0.47
IMAGp998I01193	TMSB10	thymosin, beta 10	NM_021103	9168	0.08	0.61
0.36	0.63	0.16	0.96	-0.36	0.13	-0.35
	0.54	1.5	0.3		-0.15	-0.43
					-0.13	0.16
					-0.4	-0.09
IMAGp998I10392	TOP1	topoisomerase (DNA) I	7150	0.13	0.55	0
0.13	0.3	0.15	-0.43	0.15	-0.41	-0.3
0.07	0.7	1.65			-0.06	0.04
					-0.14	0.06
					0.16	
IMAGp998D231008	TRAPPC3	trafficking protein particle complex 3				
27095	0.13	-0.18	-0.13	0.24	-0.1	0.33
0.19	-0.01	-0.25	0.54	0.56	0.4	0.21
IMAGp998J10193	TTYH3	tweety homolog 3 (Drosophila)	NM_025250	80727	0.3	
0.09	0.29	-0.26	0.89	0.55	0.04	-0.24
0.05	0.43	0.26	0.4	0.09	-0.24	-0.39
					0	-0.56
					-0.42	-0.17
IMAGp998C14658	UGCG	UDP-glucose ceramide glucosyltransferase	7357			
0.37	-0.35	-0.56	-0.34	0.19	-0.49	0.6
	0.15	0.62	0.33	-0.6	-0.11	0.3
					0.77	0.43
					0.9	1.01
						-0.12
IMAGp998J24653	UNG	uracil-DNA glycosylase	7374	-0.32	-0.15	1.07
0.07	0.03	0.38	1.18	0.67	0.42	0.26
0.8	-0.56				0.54	0.89
					-0.4	0.2
					-0.02	-0.28
IMAGp998I22699	VPS39	vacuolar protein sorting 39 (yeast)	NM_015289	23339		
0.39	0.45	-0.42	0.12	-0.08	0.4	-0.13
0.29	-0.03	-0.25	-0.5	-0.53	0.39	0.35
					0.68	0.48
					0.68	0.68
						-0.58
IMAGp998M13839	YRDC	ischemia/reperfusion inducible protein	NM_024640			
79693	-0.04	0.07	-0.13	0.09	0.1	0.02
0.25	-0.1	0.05	0.35	0.16	0.1	-0.27
IMAGp998I07527	ZCCHC2	zinc finger, CCHC domain containing 2				
NM_017742	54877	-0.22	0.21	0.11	0.29	-0.27
0.06	-0.5	-0.16	-0.18	0.15	-0.17	0.2
					0.7	0.27
IMAGp998H08628	ZDHHC2	zinc finger, DHHC domain containing 2				
NM_016353	51201	-0.42	-0.08	-0.37	-0.92	0.05
0.23	0.6	0.23	0.22	-0.79	-0.18	-0.37
					0.8	-0.5
IMAGp998G18725	ZNF18	zinc finger protein 18 (KOX 11)	NM_144680	7566		
0.07	-0.27	-0.02	0.2	0.21	0.39	0.4
0.32	0.27	-0.37	0	-0.01	0.28	0.32
					0.23	0.35
					0.78	0.1
IMAGp998G10252	ZNF185	zinc finger protein 185 (LIM domain)				
NM_007150	7739	-0.52	-0.52	-0.69	-0.45	-0.52
0.63	0.53	0.48	0.17	-0.01	0.32	-0.01
					0.4	-1.14
IMAGp998F05835	ZNF262	zinc finger protein 262	9202	0.09	0.47	
0.67	0.39	0.47	1.15	0.17	-0.06	-0.21
0.4	0.08	1.2	0.81		-0.28	-0.65
					-0.26	-0.15
					0.11	

IMAGp998E201726	ZNFN1A1	zinc finger protein, subfamily 1A, 1 (Ikaros)									
NM_006060	10320	0.46	0.03	0.14	0.12	0.1	0.23	-0.32	-0.31	-0.14	-
2.11	-0.55	-0.37	0.01	-0.05	0.2	-0.09	-0.2	0.17			