

Cichlid_GeneID	GeneName (Human Ortholog)	Description	logFC	P.Value
aanat	AANAT	aralkylamine	-3.5289353	0.00438605
aars2	AARS2	alanyl-tRNA s	-5.0509256	3.26E-05
aasdh	AASDH	aminoadipate	-9.3172152	1.23E-13
abcf3	ABCF3	ATP-binding c	-4.5538683	0.00044009
LOC101469557	ABHD12	abhydrolase c	-4.6065848	2.16E-07
abhd16a	ABHD16A	abhydrolase c	-3.1498871	0.0078678
LOC101474210	ABI3BP	ABI family, m	-4.9831925	0.00010346
abl2	ABL2	v-abl Abelson	-5.5681401	0.00013176
abt1	ABT1	activator of b	-4.0386603	0.00061494
acat2	ACAT2	acetyl-CoA ac	-3.4866658	0.00020643
ace2	ACE2	angiotensin I	-7.0494774	5.26E-11
acer1	ACER1	alkaline cerar	-7.1628266	2.09E-08
LOC106676906	ACOT11	acyl-CoA thio	-4.5627744	0.00024523
LOC101484036	ACP5	acid phospho	-5.7927255	2.17E-06
LOC101476622	ACTB	actin, beta [S	-6.2493126	2.07E-08
actn3	ACTN2	actinin, alpha	-2.8066137	0.00773227
LOC101467323	ACVR1	activin A rece	-2.9139681	0.00021413
LOC101464677	ACY3	aspartoacylas	-3.3271638	0.00231881
LOC101479803	ACY3	aspartoacylas	-2.5036492	0.00660774
LOC101465362	ACYP2	acylphosphat	-6.7275296	3.75E-09
LOC101473447	ADAM9	ADAM metall	-4.1954336	0.00103951
LOC101464246	ADH4	alcohol dehyd	-3.2472517	0.00658593
adipor2	ADIPOR2	adiponectin r	-5.6681701	5.48E-05
LOC105941219	ADM	adrenomedul	-3.5795871	0.00181082
LOC101478205	ADSS	adenylosuccir	-6.0098743	3.35E-07
LOC101481961	ADTRP	androgen-dej	-1.8392015	0.00730245
LOC101487596	AEN	apoptosis enl	-5.7214987	1.98E-06
LOC101480149	AGXT	alanine-glyox	-3.3810457	0.00206802
LOC101482817	AGXT	alanine-glyox	-2.6022544	0.01102592
phykpl	AGXT2L2	alanine-glyox	-2.36839	0.000156
LOC106674550	AHNAK	AHNAK nucle	-5.6439179	1.50E-06
LOC101466712	AIM1L	absent in mel	-3.5704198	0.00530782
aimp1	AIMP1	aminoacyl tRI	-3.4589824	0.00509645
ak4	AK4	adenylate kin	-3.8679781	0.00301018
akip1	AKIP1	A kinase (PRK	-6.4827592	5.70E-07
LOC101487903	ALDOB	aldolase B, fru	-3.5712908	0.00365051
LOC101475106	ALG11	asparagine-lir	-4.5681529	1.17E-07
alg12	ALG12	asparagine-lir	-3.4492097	0.00232925
alkbh1	ALKBH1	alkB, alkylatic	-3.6964259	0.00134813
LOC101479875	AMICA1	adhesion mol	-2.937695	0.01136543

LOC101478708	AMOT	angiomotin [S	-3.3566769	0.00626071
LOC101473164	AMPD3	adenosine mo	-5.2306346	0.00012571
anapc2	ANAPC2	anaphase pro	-4.7705619	0.00015854
ankfy1	ANKFY1	ankyrin repea	-2.80099	0.00034854
ankrd22	ANKRD22	ankyrin repea	-3.0272516	0.00994805
ankrd61	ANKRD61	ankyrin repea	-2.1666121	0.00286499
anks1a	ANKS1A	ankyrin repea	-3.7452728	0.00085599
ano1	ANO1	anoctamin 1,	-3.8091656	0.00266089
LOC101483809	ANXA1	annexin A1 [S	-7.5898567	2.14E-08
anxa1	ANXA1	annexin A1 [S	-4.2780184	2.07E-05
LOC101468000	ANXA11	annexin A11	-3.8902902	0.00028888
LOC101486457	AP1G2	adaptor-relat	-3.3164052	0.00403545
LOC101476758	AP1M2	adaptor-relat	-4.3725153	0.0005461
LOC101487710	AP1S3	adaptor-relat	-4.1660901	0.0016154
LOC101484620	APBA1	amyloid beta	-3.1446659	0.00376277
apc2	APC2	adenomatosi:	-3.6164604	4.42E-05
apmap	APMAP	adipocyte pla	-5.560602	1.80E-05
LOC101472019	APOA1	apolipoprotei	-3.7840035	0.0004276
LOC101479002	APOLD1	apolipoprotei	-4.8817968	0.00010631
LOC101466403	AQP3	aquaporin 3 (-6.0348324	3.32E-06
ar	AR	androgen rec	-4.6185909	0.00014025
LOC101481239	AREG	amphiregulin	-3.205355	0.0107162
LOC101474876	ARHGAP4	Rho GTPase a	-3.4247387	0.0061049
arhgap42	ARHGAP42	Rho GTPase a	-3.605956	0.0081964
LOC101478428	ARHGEF15	Rho guanine	-4.3778932	0.00017045
arhgef16	ARHGEF16	Rho guanine	-3.8504701	0.00059199
LOC101480595	ARHGEF18	Rho/Rac guar	-2.6269367	0.00799061
LOC101485626	ARHGEF19	Rho guanine	-3.0250532	0.00250456
arhgef38	ARHGEF38	Rho guanine	-3.2186377	0.00144513
LOC101465638	ARID5A	AT rich intera	-3.55332	0.00194718
arl4a	ARL4A	ADP-ribosylat	-4.0783732	0.00065485
nrap	ARL5B	ADP-ribosylat	-3.7131002	0.00137612
arl9	ARL9	ADP-ribosylat	-4.0327991	0.00115676
LOC101487707	ARMC1	armadillo rep	-5.8625432	1.42E-05
armc3	ARMC3	armadillo rep	-4.3666456	0.00012621
LOC101471957	ARPC1A	actin related	-5.4718691	1.81E-05
LOC101487389	ARRDC1	arrestin doma	-2.9807923	0.00474286
LOC101478001	AS3MT	arsenic (+3 o)	-3.8852987	0.000606
asb12	ASB12	ankyrin repea	-2.2146464	0.00028854
asb14	ASB14	ankyrin repea	-1.8881786	0.00613077
asb7	ASB7	ankyrin repea	-3.4446576	0.0070932

ass1	ASS1	argininosucci	-4.5787345	0.00085655
LOC101472547	ASTE1	asteroid hom	-5.0176944	1.01E-05
LOC101485633	ASTL	astacin-like r	-3.8374703	4.37E-06
atat1	ATAT1	alpha tubulin	-8.0276443	1.32E-11
atp10b	ATP10B	ATPase, class	-3.4275408	0.00144141
atp13a2	ATP13A2	ATPase type :	-3.1067007	0.00340096
atp8b1	ATP8B1	ATPase, amin	-3.1248851	0.00506389
atp8b4	ATP8B4	ATPase, class	-6.711058	3.44E-07
LOC101479299	AVIL	advillin [Sour	-3.3645602	0.00792656
avpr2	AVPR2	arginine vaso	-4.8543544	7.96E-05
LOC101485333	B3GALT5	UDP-Gal:beta	-6.1877809	1.67E-07
LOC101465145	B3GALT5	UDP-Gal:beta	-3.0177403	0.00419685
LOC101465460	B3GALT5	UDP-Gal:beta	-2.9684003	0.00657817
LOC101486761	B4GALT1	UDP-Gal:beta	-2.999639	0.00970185
bag4	BAG4	BCL2-associat	-4.8036233	3.53E-05
baiap2l1	BAIAP2L1	BAI1-associat	-3.8993398	0.00167884
LOC101468796	BANF1	barrier to aut	-4.5139227	0.00016733
LOC101480297	BANF2	barrier to aut	-4.0894139	0.0002308
barx2	BARX2	BARX homeol	-3.7156722	0.00697085
LOC101473120	BCOR	BCL6 corepre	-3.4507028	0.00211749
LOC101469974	BDKRB1	bradykinin re	-6.9510191	5.71E-08
bfsp2	BFSP2	beaded filam	-7.0699864	9.66E-08
LOC101487058	BICD2	bicaudal D hc	-3.5661311	0.00095156
LOC101465152	BICD2	bicaudal D hc	-2.7074812	0.01143143
blcap	BLCAP	bladder canc	-3.7119839	0.0030606
blzf1	BLZF1	basic leucine	-2.9959707	0.00801464
LOC101467782	BMPR1A	bone morphc	-3.1407411	0.00550417
LOC101474392	BNIP2	BCL2/adenov	-5.4831057	3.60E-06
LOC101480739	BOK	BCL2-related	-3.552707	0.00532377
brat1	BRAT1	BRCA1-associ	-1.8835692	0.00719716
LOC101483850	BRD4	bromodomai	-5.6175759	3.59E-06
LOC101472078	BRSK2	BR serine/thr	-3.6483507	1.20E-05
LOC101466116	BTBD11	BTB (POZ) do	-4.9236899	9.41E-05
btbd3	BTBD3	BTB (POZ) do	-2.7517403	0.00701694
LOC101481147	BTBD6	BTB (POZ) do	-3.3622354	0.00035222
bzrap1	BZRAP1	benzodiazapi	-3.3134085	0.00477883
LOC101483108	BZRAP1	benzodiazapi	-2.2441168	0.00545826
ddias	C11orf82	chromosome	-4.3733562	0.00045486
LOC105941258	C11orf89	chromosome	-5.4164638	2.72E-08
faap100	C17orf70	chromosome	-3.1456378	0.00380504
LOC101473408	C18orf8	chromosome	-3.5437122	0.00215289

LOC101481331	C1orf106	chromosome	-3.4367403	0.0071006
LOC101473750	C1orf172	chromosome	-3.615942	0.00061598
LOC101484289	C21orf2	chromosome	-3.2614295	0.00036535
LOC101482640	C22orf23	chromosome	-3.5094001	0.00938698
LOC101473019	C2orf42	chromosome	-8.4416053	6.47E-09
LOC101466831	C3orf52	chromosome	-3.5630892	0.00191009
c6	C6	complement	-4.0490554	0.00322963
tbc1d32	C6orf170	chromosome	-2.9789431	0.0054282
LOC101478077	C6orf174	C6orf174 pro	-2.5207361	0.0117835
LOC101481886	C7orf62	chromosome	-5.3991589	6.18E-06
ca5a	CA5A	carbonic anhy	-4.3063804	0.00070005
LOC101465884	CABP2	calcium bindi	-5.7716753	3.56E-05
LOC101475539	CABP4	calcium bindi	-2.2951414	0.00315768
cacna1i	CACNA1I	calcium chan	-4.4316343	0.00065635
LOC101466725	CACNB4	calcium chan	-5.7753632	8.29E-05
cad	CAD	carbamoysl-ph	-7.8667793	4.00E-09
LOC101468863	CAPN1	calpain 1, (m	-3.9403287	0.0002174
LOC101486012	CAPN14	calpain 14 [Sc	-13.645225	1.69E-15
LOC101473607	CAPN14	calpain 14 [Sc	-3.6614021	0.00049174
LOC101468385	CAPN2	calpain 2, (m	-3.1068496	0.00138666
capn9	CAPN9	calpain 9 [Sou	-9.7218743	1.49E-10
capn12	CAPN9	calpain 9 [Sou	-5.7720494	8.26E-07
LOC101473853	CAPNS2	calpain, small	-3.7666696	0.00357144
card14	CARD10	caspase recru	-5.5082633	7.91E-06
LOC101478214	CARD6	caspase recru	-8.5505972	1.05E-09
LOC101487093	CASKIN2	CASK interact	-3.6787856	0.00343129
LOC106676547	CASP6	caspase 6, ap	-3.8879386	0.00032014
LOC101478827	CASP8	caspase 8, ap	-2.9671906	0.00547159
LOC101486104	CASQ1	calsequestrin	-2.8112861	0.00677663
LOC101467330	CASQ1	calsequestrin	-2.7517403	0.00701694
cast	CAST	calpastatin [S	-3.5349227	4.40E-05
LOC101465189	CBR1	carbonyl redu	-3.519469	0.00487593
LOC101487143	CBS	cystathionine	-8.7540045	8.19E-13
LOC101479719	CBS	cystathionine	-2.6022544	0.01102592
ccdc12	CCDC12	coiled-coil do	-4.7079878	0.00027914
ccdc146	CCDC146	coiled-coil do	-3.1454651	0.00555552
ccdc167	CCDC167	coiled-coil do	-3.0123576	0.00713519
ccdc50	CCDC50	coiled-coil do	-3.806149	0.00044202
LOC101475644	CCDC64B	coiled-coil do	-5.6891878	8.44E-06
LOC101484920	CCDC64B	coiled-coil do	-4.2665663	0.00080191
ccdc86	CCDC86	coiled-coil do	-3.1851833	0.00870037

ccdc97	CCDC97	coiled-coil do	-3.8285322	3.78E-05
LOC106675061	CCKAR	cholecystokin	-3.3371008	0.00288387
cckar	CCKAR	cholecystokin	-3.3234734	0.00313464
LOC101467602	CCL19	chemokine (C	-4.4280797	0.00019729
LOC101472946	CCL20	chemokine (C	-6.7204899	1.07E-07
LOC101475896	CCL20	chemokine (C	-3.5245688	0.00059731
LOC106676255	CCL25	chemokine (C	-4.4958334	1.30E-05
ccndbp1	CCNDBP1	cyclin D-type	-4.4105507	0.00014356
LOC101486478	CCNE2	cyclin E2 [Sou	-2.235771	0.00779636
LOC101478668	CCR9	chemokine (C	-4.6318568	7.37E-05
ccs	CCS	copper chape	-6.7415713	1.08E-06
LOC101470447	CCSAP	centriole, cilia	-3.4818383	0.00774099
LOC101479353	CD101	CD101 molec	-3.693486	0.00604319
cd109	CD109	CD109 molec	-6.9757619	2.49E-07
LOC106674898	CD22	CD22 molecu	-3.5153964	0.00271779
LOC101486696	CD22	CD22 molecu	-3.5084766	0.00072676
LOC106675279	CD276	CD276 molec	-4.6424962	2.51E-05
LOC101486239	CD300LG	CD300 molec	-7.6572874	1.30E-08
LOC105941287	CD300LG	CD300 molec	-4.1121189	0.00064275
LOC101476613	CD4	CD4 molecule	-11.988141	1.06E-13
LOC101467428	CD53	CD53 molecu	-2.8796378	0.0062699
LOC101467196	CD86	CD86 molecu	-5.9080775	9.27E-07
LOC106676430	CD86	CD86 molecu	-3.7478329	0.00087441
LOC101486014	CD86	CD86 molecu	-3.7467182	0.00033687
LOC101486694	CD86	CD86 molecu	-3.5924346	0.00261079
LOC101485270	CD86	CD86 molecu	-3.5040393	0.00181857
LOC106674899	CD86	CD86 molecu	-3.3471802	0.00205361
LOC106676048	CD86	CD86 molecu	-3.1870453	0.0018869
LOC101470971	CD8A	CD8a molecu	-5.1230142	5.01E-06
cdadc1	CDADC1	cytidine and c	-2.9619134	0.00437532
cdc123	CDC123	cell division c	-3.747179	0.00189734
LOC101479607	CDC42	cell division c	-3.10783	0.00988542
LOC101477078	CDH12	cadherin 12, t	-5.1176785	9.31E-05
cdh20	CDH20	cadherin 20, t	-4.2685573	0.00039088
LOC101469563	CDIP1	cell death-inc	-11.741215	9.61E-15
cdipt	CDIPT	CDP-diacylgly	-3.0943142	0.00941257
LOC101474553	CDKN1A	cyclin-depend	-5.0508934	9.91E-05
LOC101477495	CDR2L	cerebellar de	-3.5245575	0.00467435
LOC101467689	CEACAM21	carcinoembry	-5.3225732	9.32E-06
LOC101485975	CEBPB	CCAAT/enhar	-3.3236485	0.00126847
cebpd	CEBPD	CCAAT/enhar	-5.4495497	2.65E-07

cecr6	CECR6	cat eye syndr	-3.390943	0.00504226
cep152	CEP152	centrosomal	-3.8280926	0.0013882
LOC101474144	CERK	ceramide kin	-5.264449	3.18E-05
cetp	CETP	cholesteryl es	-3.0387785	0.00610321
LOC101476252	CFP	complement	-8.5226839	6.53E-12
LOC101478526	CGNL1	cingulin-like 1	-6.3583342	2.01E-07
LOC101481696	CHAC1	ChaC, cation f	-4.8543799	0.00016837
chac1	CHAC1	ChaC, cation f	-4.1487771	0.00340632
chchd2	chchd2	coiled-coil-he	-3.8129294	0.00231057
LOC101485554	CHL1	cell adhesion	-2.8658632	0.00763968
LOC101480991	CHMP6	charged mult	-3.1126219	0.0026774
chpf2	CHPF2	chondroitin p	-9.4928447	5.16E-13
LOC101470861	CHRNA2	cholinergic re	-4.3622305	0.00092511
LOC101467859	CHST1	carbohydrate	-3.5749273	0.00114109
LOC101477544	CHST8	carbohydrate	-5.5719504	1.75E-06
cinp	CINP	cyclin-depend	-2.881329	0.00258544
cish	CISH	cytokine indu	-2.3274866	0.00159455
LOC101479976	CLDN18	claudin 18 [Sc	-3.2118506	0.00513398
LOC101472769	CLDN23	claudin 23 [Sc	-5.3719318	1.06E-05
LOC101476456	CLDN7	claudin 7 [Sou	-6.5793135	1.91E-06
LOC101476694	CLDN8	claudin 8 [Sou	-7.800482	1.18E-09
LOC101466430	CLDN8	claudin 8 [Sou	-7.3076768	8.29E-09
LOC101480961	CLDN8	claudin 8 [Sou	-3.8401255	0.00099455
LOC101475374	CLDN8	claudin 8 [Sou	-3.71101	0.00134039
LOC101464975	CLDN8	claudin 8 [Sou	-3.2021314	0.00389906
LOC101475811	CLDN8	claudin 8 [Sou	-2.8580946	0.00414315
LOC101481769	CLEC3B	C-type lectin	-3.5251898	4.56E-07
LOC101481774	CLIC3	chloride intra	-8.0135964	1.69E-09
clip3	CLIP3	CAP-GLY dom	-4.0647122	0.00063604
LOC106675732	CLMP	CXADR-like m	-4.0511512	9.46E-05
clta	CLTA	clathrin, light	-3.3055709	0.00512672
LOC101469899	CLUH	clustered mit	-2.9939616	0.00695201
LOC101479291	CLUL1	clusterin-like	-3.5255358	5.99E-06
fsd2	CMYA5	cardiomyopa	-1.9926177	0.00550919
LOC101469064	CNDP2	CNDP dipepti	-4.0906891	0.0025254
LOC101468473	CNDP2	CNDP dipepti	-2.8796378	0.0062699
LOC105940421	CNGA3	cyclic nucleot	-3.5706884	0.00065715
cnot10	CNOT10	CCR4-NOT tra	-4.3968171	9.74E-05
cnst	CNST	consortin, coi	-6.4410592	2.41E-05
col19a1	COL19A1	collagen, type	-3.4629599	0.00150951
LOC101477258	COL28A1	collagen, type	-4.7713106	0.00014247

commd1	COMMD1	copper metal	-2.9697672	0.0056482
commd5	COMMD5	COMM doma	-2.9052351	0.00702872
commd6	commd6	COMM doma	-3.2764442	0.00164211
LOC101484041	CORO6	coronin 6 [So	-5.973905	2.57E-05
LOC101487158	COX17	cytochrome c	-3.4361197	0.0082244
cpox	CPOX	coproporphyr	-2.3745666	0.00191241
cps1	CPS1	carbamoyl-ph	-4.6049008	0.0003075
LOC101477396	CR1L	complement	-2.4070868	0.00086544
LOC101486360	CRADD	CASP2 and RI	-2.8854426	0.00591975
crip1	CRIP2	cysteine-rich	-5.4800138	5.46E-05
LOC101471604	CRIP2	cysteine-rich	-3.3020604	0.00878971
crtc3	CRTC3	CREB regulat	-3.3987614	0.0046072
LOC101480452	CRY1	cryptochrome	-4.3466674	0.00077118
ctc1	ctc1	CTS telomere	-2.2964543	0.00718364
ctif	CTIF	CBP80/20-de	-3.0627065	0.00902254
ctsh	CTSH	cathepsin H [-3.2181679	0.00433495
LOC101485929	CTSS	cathepsin S [S	-2.8596395	0.00996434
LOC101485887	CXXC11	CXXC finger p	-4.250939	0.00042799
LOC101468594	CYCS	cytochrome c	-3.5249121	0.00315183
LOC101481861	CYGB	cytoglobin [Sc	-3.7972865	0.00153814
LOC101463871	CYP11B2	cytochrome F	-3.6919124	0.00034566
LOC101472203	CYP1A1	cytochrome F	-3.1747873	0.00551154
LOC101478374	CYP27A1	cytochrome F	-4.7835622	9.28E-05
LOC101473743	CYP27A1	cytochrome F	-4.0377855	0.00034226
LOC101481994	CYP2D6	cytochrome F	-2.8796378	0.0062699
LOC101472746	CYP2J2	cytochrome F	-3.6908013	0.00106571
LOC101471528	CYP3A43	cytochrome F	-5.6841522	1.86E-05
LOC101477063	CYP3A43	cytochrome F	-3.1927746	0.011206
cyth3	CYTH3	cytohesin 3 [S	-2.2328178	0.00216519
LOC101464010	DAB2IP	DAB2 interact	-7.2045413	5.91E-07
dazap1	DAZAP1	DAZ associat	-4.2041979	0.00061878
LOC101468996	DBNL	drebrin-like [S	-3.8403962	0.00147083
LOC101484131	DCAF7	DDB1 and CU	-2.4180582	0.00205158
LOC101465766	DCK	deoxycytidine	-3.0133401	0.00529606
ddc	DDC	dopa decarbc	-8.2474031	8.56E-09
ddx43	DDX43	DEAD (Asp-Gl	-4.2985593	0.00020964
kiaa0907	DDX46	DEAD (Asp-Gl	-3.4240183	0.00050944
LOC101480720	DENND1A	DENN/MADD	-5.4964791	4.83E-06
dffa	DFFA	DNA fragmen	-3.0165173	0.00924487
LOC101474081	DGUOK	deoxyguanos	-3.4718851	0.00137076
dhrs11	DHRS11	dehydrogena	-4.3401326	0.00017325

dhrsx	DHRSX	dehydrogena	-5.6568287	4.62E-06
dlg1	DLG1	discs, large ho	-3.981688	0.00176951
LOC101464331	DMBX1	diencephalon	-3.4521734	0.00622985
dnaaf2	DNAAF2	dynein, axone	-6.4723293	1.18E-07
dnai2	DNAI2	dynein, axone	-3.6604809	0.00294876
LOC101476475	DNAJC3	DnaJ (Hsp40)	-3.5537105	0.00307518
dnajc6	DNAJC6	DnaJ (Hsp40)	-5.1848399	3.73E-05
LOC101485654	DNASE1L1	deoxyribonuc	-6.7177023	4.03E-06
LOC101485000	DNASE1L1	deoxyribonuc	-5.4078231	5.52E-05
LOC101477732	DNASE1L1	deoxyribonuc	-5.0995066	4.27E-05
dnase1l3	DNASE1L1	deoxyribonuc	-4.6967824	0.00010628
LOC101473965	DNMT3L	DNA (cytosine	-2.7555949	0.00980269
dohh	DOHH	deoxyhypusir	-3.5510036	0.00365556
LOC101468029	DOK1	docking prote	-6.6989199	1.70E-07
dqx1	DQX1	DEAQ box RN	-3.9378033	0.00052147
LOC101475702	DSC1	desmocollin 1	-8.1339888	4.69E-09
LOC101482365	DSC1	desmocollin 1	-5.6341599	5.31E-07
LOC105940471	DSC1	desmocollin 1	-5.2142395	5.44E-06
LOC101473374	DSC1	desmocollin 1	-4.8142271	0.00019621
LOC101474133	DSC1	desmocollin 1	-4.3218758	0.00013752
dsel	DSEL	dermatan sul	-4.4204683	0.00052267
LOC101474660	DSP	desmoplakin	-6.6885252	2.79E-09
LOC101468104	DUSP10	dual specificit	-3.2991885	0.00675551
dusp12	DUSP12	dual specificit	-2.8608717	0.00708726
LOC101468287	DUSP14	dual specificit	-3.4982413	0.00085466
dusp7	DUSP7	dual specificit	-6.2004759	2.96E-09
LOC101486034	E2F5	E2F transcript	-7.849987	3.06E-09
LOC101482309	EEF1A2	eukaryotic tra	-2.1624451	0.01052799
eef1e1	EEF1E1	eukaryotic tra	-3.4803479	0.00519991
efcab14	EFCAB14	EF-hand calci	-1.9962493	0.01033052
eftud1	EFTUD1	elongation fa	-3.908096	0.00143667
LOC101477281	EGFR	epidermal gro	-3.301889	0.01067002
LOC101482048	EGR3	early growth	-3.4794101	0.00838626
eif1ad	EIF1AD	eukaryotic tra	-7.5316933	1.43E-07
eif2ak1	EIF2AK1	eukaryotic tra	-2.4123666	0.00057563
eif2b4	EIF2B4	eukaryotic tra	-3.7569963	0.00183117
LOC101480970	EIF4E1B	eukaryotic tra	-3.2063374	0.00493933
LOC101474559	ELF3	E74-like facto	-6.3036768	1.60E-06
LOC101472138	ELL	elongation fa	-3.7790512	0.00023485
elmsan1	ELMSAN1	ELM2 and My	-5.429201	6.76E-05
LOC101481208	ELOVL1	ELOVL fatty a	-3.9959527	0.00071481

elovl7	ELOVL7	ELOVL fatty a	-6.5850224	2.15E-06
emc9	EMC9	ER membran	-4.1770135	1.06E-07
LOC101482971	EMP1	epithelial me	-2.4163348	0.00650671
LOC101471457	EMP3	epithelial me	-3.3187131	0.00399931
LOC101471758	ENDOD1	endonucleas	-6.2933206	4.78E-08
LOC101477672	ENTPD2	ectonucleosic	-3.7139869	0.00069768
LOC101473382	ENTPD3	ectonucleosic	-7.3114196	3.52E-07
LOC101479109	EPB41L1	erythrocyte n	-7.2242223	9.61E-08
epb41l4b	EPB41L4B	erythrocyte n	-7.534323	3.53E-08
LOC101475160	EPB42	erythrocyte n	-8.4404576	4.75E-08
LOC101483349	EPB42	erythrocyte n	-7.4845409	5.34E-08
LOC101483944	EPB42	erythrocyte n	-7.1945491	9.00E-07
LOC101476154	EPCAM	epithelial cell	-5.4149425	2.87E-05
LOC106675788	EPM2AIP1	EPM2A (lafor	-3.9313874	0.00090703
LOC106674795	EPM2AIP1	EPM2A (lafor	-3.3279767	0.00233418
eps8l1	EPS8L1	EPS8-like 1 [S	-7.6452618	1.51E-09
eps8l2	EPS8L2	EPS8-like 2 [S	-6.0594756	2.56E-06
erbb2	ERBB2	v-erb-b2 eryt	-4.5055909	0.00042559
erbb3	ERBB3	v-erb-b2 eryt	-6.5904829	7.09E-06
ergic3	ERGIC3	ERGIC and go	-2.3911406	3.17E-05
LOC101468631	ERLIN2	ER lipid raft a	-4.8507547	0.00013246
LOC101475569	ERN1	endoplasmic	-2.7498986	0.00757498
LOC101469072	ESR2	estrogen rece	-4.6524552	5.98E-05
esrp1	ESRP1	epithelial spli	-7.0919951	1.98E-08
LOC101470769	EVA1C	eva-1 homolc	-3.3078187	0.00513895
LOC101470648	EVPL	envoplakin [S	-9.1034874	5.53E-10
evpl	EVPL	envoplakin [S	-8.4231011	3.10E-10
LOC101486492	EXTL1	exostoses (m	-3.3756764	0.00353466
ezr	EZR	ezrin [Source	-5.5337802	8.76E-06
fa2h	FA2H	fatty acid 2-h	-3.5891636	0.00836317
LOC101485489	FABP6	fatty acid bin	-5.5204504	2.25E-05
LOC101484077	FAM102A	family with se	-7.5611006	2.57E-08
fam103a1	FAM103A1	family with se	-7.9118428	1.15E-10
LOC101474680	FAM105B	family with se	-3.2883598	3.86E-05
LOC101481643	FAM109A	family with se	-2.7517403	0.00701694
fam117a	FAM117A	family with se	-3.2295865	0.00338887
LOC101484850	FAM129A	family with se	-3.9013101	0.0011208
fam160b1	FAM160B1	family with se	-3.5001063	1.86E-05
fam183a	FAM183A	family with se	-1.8539274	0.00121469
fam189a1	FAM189A1	family with se	-3.023633	0.0077034
fam195a	FAM195A	family with se	-3.3214956	0.00216118

LOC101479720	FAM196A	family with se	-5.3717733	1.78E-05
fam210b	FAM210B	family with se	-6.9999113	4.94E-08
LOC101488081	FAM212A	family with se	-3.2763993	0.00221231
fam35a	FAM35A	family with se	-4.227314	9.58E-11
LOC101465551	FAM49B	family with se	-3.1874837	0.00222942
fam53b	FAM53B	family with se	-4.877608	2.50E-06
LOC101487817	FAM65C	family with se	-4.5191872	0.00010598
LOC101468946	FAM69A	family with se	-3.3644636	0.00367688
fam83b	FAM83B	family with se	-6.2604902	2.04E-06
LOC101475864	FAM83F	family with se	-5.6970247	2.94E-05
LOC101487448	FAM83F	family with se	-3.1250473	0.00677356
fam83g	FAM83G	family with se	-2.958995	0.00549788
fam83h	FAM83H	family with se	-4.2416972	3.78E-06
fanca	FANCA	Fanconi anem	-3.261683	0.00617854
fancl	FANCL	Fanconi anem	-1.891095	0.00158807
fancm	FANCM	Fanconi anem	-1.6107358	0.00793076
LOC101473631	FARP1	FERM, RhoGE	-2.4258258	0.01151289
farp2	FARP2	FERM, RhoGE	-4.0745511	1.80E-05
farsb	FARSB	phenylalanyl-	-3.9628338	0.00368196
fastk	FASTK	Fas-activated	-4.8843687	0.00026092
LOC101485697	FASTKD3	FAST kinase d	-3.1531803	0.00886611
fbf1	FBF1	Fas (TNFRSF6	-1.8140519	0.00519546
LOC101463775	FBXL3	F-box and leu	-3.4090518	0.00301842
fbxl6	FBXL6	F-box and leu	-8.0849837	2.73E-16
fbxo34	FBXO34	F-box protein	-2.7302834	0.00835471
LOC101486413	FCRLA	Fc receptor-li	-3.3552394	0.00396057
LOC101484479	FCRLA	Fc receptor-li	-2.9503317	0.00903929
fgd4	FGD4	FYVE, RhoGEF	-4.0342815	0.00135873
LOC101478795	FHDC1	FH2 domain c	-4.5170275	0.00046882
LOC101485431	FKBP5	FK506 binding	-3.2424882	0.00339338
LOC101472007	FNDC7	fibronectin ty	-2.8112861	0.00677663
fndc9	FNDC9	fibronectin ty	-1.984634	0.0002089
LOC101487312	FOS	FBJ murine os	-3.153837	0.01142601
LOC101467033	FOS	FBJ murine os	-2.7473855	0.00999749
LOC101486283	FOXB1	forkhead box	-3.5324797	0.00704142
foxc1	FOXC2	forkhead box	-4.041945	8.09E-05
frmd1	FRMD1	FERM domair	-3.7562852	0.00356324
LOC101475124	FRMD4B	FERM domair	-4.9580673	4.45E-05
fsd1	FSD1	fibronectin ty	-7.1518533	5.84E-08
fut11	FUT11	fucosyltransfe	-9.8474807	6.37E-13
LOC101487668	FYB	FYN binding p	-7.9915385	5.71E-09

fyn	FYN	FYN oncogen	-3.9148123	0.00016687
g3bp1	G3BP1	GTPase activa	-3.7374292	0.00147982
gabpa	GABPA	GA binding pr	-1.8649745	0.00435305
gabpb2	GABPB2	GA binding pr	-3.6914141	5.92E-06
LOC101473770	GAD1	glutamate de	-8.437895	7.13E-10
gadd45gip1	GADD45GIP1	growth arrest	-4.2280295	2.88E-05
galk2	GALK2	galactokinase	-6.2269595	4.00E-06
galnt14	GALNT14	UDP-N-acetyl	-3.4357011	0.00408781
LOC105941306	GALNT8	UDP-N-acetyl	-5.7656101	5.00E-06
LOC101472906	GARS	glycyl-tRNA s	-4.5098196	0.00027999
gart	GART	phosphoribos	-3.1871345	0.00012182
LOC101463747	GCK	glucokinase (l	-3.5519207	0.004048
gcsh	GCSH	glycine cleava	-7.0745159	1.63E-07
gda	GDA	guanine deam	-7.2984303	1.92E-08
LOC101473896	GGH	gamma-gluta	-3.2838223	0.00411762
LOC101464917	GHR	growth horm	-4.8687586	3.02E-05
gid4	GID4	GID complex	-7.687916	4.41E-09
LOC101470772	GIMAP4	GTPase, IMAF	-7.4365881	5.07E-09
LOC101483954	GIMAP4	GTPase, IMAF	-6.2601368	1.96E-06
LOC101472830	GIMAP4	GTPase, IMAF	-5.7575036	2.25E-05
LOC101473823	GIMAP4	GTPase, IMAF	-5.5324126	1.26E-06
LOC101482531	GIMAP4	GTPase, IMAF	-4.8654703	8.41E-06
LOC101480026	GIMAP4	GTPase, IMAF	-4.6076209	0.00014285
LOC101482533	GIMAP4	GTPase, IMAF	-4.116847	0.00024714
LOC101465760	GIMAP4	GTPase, IMAF	-4.0784497	0.00019207
LOC101468011	GIMAP4	GTPase, IMAF	-3.9583712	0.00072224
LOC105940615	GIMAP4	GTPase, IMAF	-3.9410316	0.00016152
LOC106674495	GIMAP4	GTPase, IMAF	-3.6614021	0.00049174
LOC101473531	GIMAP4	GTPase, IMAF	-3.6584855	0.00037187
LOC101473159	GIMAP4	GTPase, IMAF	-3.5495212	0.00140441
LOC101479274	GIMAP4	GTPase, IMAF	-3.4716269	0.0012606
LOC101470849	GIMAP4	GTPase, IMAF	-3.1446659	0.00376277
LOC106676236	GIMAP4	GTPase, IMAF	-3.0293915	0.00784797
LOC101488130	GIMAP4	GTPase, IMAF	-2.8704899	0.00423681
LOC101466893	GIMAP4	GTPase, IMAF	-2.4178457	0.01020335
LOC101486160	GJA3	gap junction	-3.0275479	0.0076366
LOC101469892	GJB3	gap junction	-4.5911373	0.00015591
LOC101471331	GJB5	gap junction	-4.4431741	0.00013001
gldc	GLDC	glycine dehy	-5.9136584	6.77E-06
glra2	GLRA2	glycine recep	-5.0133417	2.77E-05
glud1	GLUD1	glutamate de	-2.7369656	0.00254095

LOC101478711	GLUL	glutamate-an	-8.4682452	1.10E-10
gmds	GMDS	GDP-mannos	-8.7148657	3.38E-10
gmfb	GMFB	glia maturati	-3.153638	0.00055436
LOC106676909	GNA14	guanine nucle	-2.7161041	0.00283859
LOC101483250	GNAO1	guanine nucle	-2.8396565	0.01117833
gne	GNE	glucosamine	-8.1081853	3.31E-11
golp3	GOLPH3	golgi phospho	-3.6697178	2.29E-05
gorasp2	GORASP2	golgi reassem	-3.9517403	0.00109125
LOC101478913	GPA33	glycoprotein	-3.2965711	0.00344638
LOC101469872	GPC5	glypican 5 [Sc	-3.6163612	0.00259953
LOC101473153	GPD1	glycerol-3-ph	-7.6501924	1.57E-07
gpr101	GPR101	G protein-cou	-3.2897955	0.00802002
gpr157	GPR157	G protein-cou	-4.1408976	0.00312851
LOC101469645	GPR31	G protein-cou	-3.1953585	0.00302888
LOC101479735	GPR37	G protein-cou	-7.5773301	5.68E-08
LOC101475391	GPR64	G protein-cou	-3.1203786	0.0090886
LOC101472374	GPRC5D	G protein-cou	-7.9439221	4.02E-10
LOC101486521	GRAMD4	GRAM domai	-4.6111956	0.00021549
LOC101472205	GRB10	growth factor	-4.3158891	0.00013363
LOC101469335	GRB7	growth factor	-3.0202793	0.00533276
grhl1	GRHL1	grainyhead-lil	-6.8838713	1.92E-06
LOC101473111	GRHL2	grainyhead-lil	-4.03196	0.00060605
grhl3	GRHL3	grainyhead-lil	-6.4706772	1.14E-06
LOC101474374	GRIK2	glutamate rec	-4.4558553	0.0001975
LOC101468307	GRINA	glutamate rec	-3.6882075	0.00245163
LOC101472812	GRM2	glutamate rec	-5.0253581	6.35E-05
grwd1	GRWD1	glutamate-ric	-5.0266	8.24E-05
gsg1	GSG1	germ cell asso	-5.8946105	8.84E-05
LOC101487342	GSN	gelsolin [Sour	-5.039715	3.64E-07
LOC101469101	GSTA4	glutathione S	-2.4354319	0.01164577
gtpbp6	GTPBP6	GTP binding p	-8.0621125	4.99E-14
hace1	HACE1	HECT domain	-6.021049	1.65E-07
LOC101486868	HCFC1	host cell facto	-5.0427062	3.37E-07
heatr1	HEATR1	HEAT repeat	-2.8620517	0.00919449
hemk1	HEMK1	HemK methyl	-4.9819779	2.00E-10
LOC101478665	HEPACAM2	HEPACAM far	-2.9206915	0.0090908
LOC101464787	HHLA2	HERV-H LTR-α	-6.1117269	1.15E-06
LOC101465549	HHLA2	HERV-H LTR-α	-5.4658187	0.00013565
LOC101466245	HHLA2	HERV-H LTR-α	-4.7771412	1.35E-05
LOC101466873	HIBADH	3-hydroxyisol	-2.9326662	0.0054656
hid1	HID1	HID1 domain	-12.593126	1.05E-15

LOC101487316	HIP1R	huntingtin int	-5.871711	3.18E-06
LOC101486848	HIP1R	huntingtin int	-3.7915069	0.00192189
LOC101467042	HIST1H2BA	histone cluste	-2.8704899	0.00423681
LOC106674701	HIST2H2AC	histone cluste	-3.0852415	0.0023302
LOC101478967	HLA-DRA	major histocc	-3.6820496	0.00132586
hlf	HLF	hepatic leuke	-3.1650263	0.00540474
hmgcl	HMGCL	3-hydroxyme	-5.6937839	7.68E-11
hmgn1	hmgn1	high mobility	-3.7017766	1.85E-06
homer2	HOMER2	homer homo	-8.5425191	7.64E-09
homez	HOMEZ	homeobox ar	-3.4595135	0.0020248
hopx	hopx	HOP homeob	-4.8233327	0.00021064
hoxa13	HOXA13	homeobox A1	-5.3888718	1.44E-05
tmprss9	HPN	hepsin [Sourc	-5.4307972	3.18E-05
hsd17b12	HSD17B12	hydroxystero	-5.1359357	2.99E-05
LOC101482753	HTRA2	HtrA serine p	-2.1344334	0.00212781
iah1	IAH1	isoamyl aceta	-6.6162134	2.44E-06
LOC101487578	IDH3G	isocitrate def	-5.2603945	1.02E-05
LOC101464712	IFI27L2	interferon, al	-3.1125917	0.00213349
LOC101486260	IFI30	interferon, ga	-2.4734679	0.00035168
LOC101478727	IFIT5	interferon-inc	-5.8974517	5.24E-06
LOC101479007	IFIT5	interferon-inc	-4.9139084	0.00056725
ift172	IFT172	intraflagellar	-8.5133815	2.13E-09
ikzf2	IKZF2	IKAROS famil	-5.0303415	2.18E-05
ikzf5	IKZF5	IKAROS famil	-9.5816904	2.07E-11
LOC101479442	IL10RB	interleukin 10	-3.4799494	0.00362556
LOC101474421	IL12RB2	interleukin 12	-3.8218819	0.00293692
LOC101468842	IL13RA1	interleukin 13	-4.6457017	4.62E-05
LOC101482752	IL13RA2	interleukin 13	-4.8562336	4.32E-05
LOC101484732	IL16	interleukin 16	-3.0683751	0.01177198
il17d	IL17D	interleukin 17	-4.6273545	2.28E-10
LOC101463827	IL20RA	interleukin 20	-2.8802157	0.00620225
LOC105940966	IL21	interleukin 21	-3.3092862	0.00955325
LOC101478360	ILDR1	immunoglobu	-3.5513988	0.00524142
ino80e	INO80E	INO80 compl	-4.1996082	0.00106015
ipmk	ipmk	inositol polyp	-5.4274858	1.95E-05
ipp	IPP	intracisternal	-5.4278318	8.62E-05
LOC101475876	IRF2BP1	interferon reğ	-3.7141735	3.35E-06
LOC101481996	IRF2BP1	interferon reğ	-2.6086833	0.01115286
irf5	IRF5	interferon reğ	-4.1138675	0.0005932
LOC101482705	IRS2	insulin recept	-3.6769118	0.00184859
LOC101476715	IRS4	insulin recept	-3.8723812	0.0008655

LOC101482358	ITGB1BP2	integrin beta	-5.9004519	5.44E-06
itgb4	ITGB4	integrin, beta	-4.0285154	0.00058802
LOC101487045	ITIH3	inter-alpha-tr	-3.5901146	0.00015943
LOC101476763	ITSN2	intersectin 2	-3.9300634	0.0003894
ivns1abp	IVNS1ABP	influenza viru	-3.2846544	0.00197027
iws1	IWS1	IWS1 homolo	-4.325014	0.0001609
jagn1	JAGN1	jagunal homc	-9.2996936	4.53E-15
jmjd8	JMJD8	jumonji doma	-6.2374876	2.33E-07
jph2	JPH2	junction philin 2	-7.6704432	8.44E-09
LOC101482945	JUN	jun proto-onc	-3.3542557	0.00010936
LOC101478427	JUP	junction plak	-4.0341829	0.00016243
anos1	KAL1	Kallmann syn	-3.4545988	0.00394927
LOC101478713	KCNIP2	Kv channel in	-3.8250361	0.00106574
spidr	KIAA0146	KIAA0146 [So	-3.9189121	0.00063673
kiaa0922	KIAA0922	KIAA0922 [So	-3.40534	0.00156972
kiaa1211	KIAA1211	KIAA1211 [So	-6.4296467	1.57E-07
cep126	KIAA1377	KIAA1377 [So	-3.0218157	0.00875813
kiaa2026	kiaa2026	kiaa2026	-3.5559224	0.00244254
LOC101482075	KIF13B	kinesin family	-7.588249	2.16E-08
LOC101472005	KIF20B	kinesin family	-7.0360665	1.31E-07
LOC101473285	KIFC2	kinesin family	-3.7139869	0.00069768
LOC101463985	KISS1R	KISS1 receptc	-7.1686544	8.07E-08
klb	KLB	klotho beta [S	-4.0730282	0.00073083
klf11	KLF11	Kruppel-like f	-3.5051955	0.00162625
klf2	klf2	Kruppel like f	-4.3995681	3.17E-06
klf3	klf3	Kruppel like f	-4.0024731	0.00024131
klf4	klf4	Kruppel like f	-5.9466199	3.87E-06
klf5	klf5	Kruppel like f	-6.6986908	1.68E-06
klf9	KLF9	Kruppel-like f	-3.0917108	0.0074698
klhl26	klhl26	kelch like fam	-3.177801	0.00525302
LOC101476845	KLHL33	kelch-like 33	-3.3362749	0.00343305
LOC101467686	KNSTRN	kinetochore-l	-10.666691	4.73E-11
LOC101476354	KRT20	keratin 20 [Sc	-7.9659737	1.21E-07
LOC101476651	KRT23	keratin 23 (hi	-11.088085	4.87E-14
LOC101470433	KRT23	keratin 23 (hi	-11.016337	7.15E-11
LOC101469858	KRT23	keratin 23 (hi	-5.2585201	5.36E-05
LOC101476066	KRT23	keratin 23 (hi	-3.8527312	2.86E-06
LOC101482554	KRT23	keratin 23 (hi	-3.0799061	0.00799076
LOC101485955	KRT84	keratin 84 [Sc	-9.3743092	1.89E-15
LOC101486263	KRT84	keratin 84 [Sc	-3.4854467	3.76E-06
LOC101484446	KRTCAP3	keratinocyte	-4.0729995	0.00012223

lactb	LACTB	lactamase, be	-8.9101404	1.77E-10
LOC101470808	LALBA	lactalbumin, c	-4.2477735	0.00131693
LOC106675455	LBH	limb bud and	-3.5064184	0.00560383
lck	LCK	lymphocyte-s	-4.4772772	0.00109551
leng9	LENG9	leukocyte rec	-3.7700561	0.0034326
LOC101468553	LGALS1	lectin, galact	-6.7518434	2.65E-08
LOC101483893	LGALS1	lectin, galact	-3.0941786	0.00576166
LOC101473814	LGI1	leucine-rich, g	-4.1115564	0.0005526
LOC101487540	LGI2	leucine-rich r	-6.2429262	3.90E-06
lhfp15	LHFPL5	lipoma HMGI	-2.4287553	0.00249365
lmo7	LIMCH1	LIM and calpo	-4.6347697	7.06E-05
LOC101465963	LMLN	leishmanolysi	-11.299376	5.89E-14
lmod3	LMOD3	leiomodoin 3 (-7.4400353	1.24E-06
LOC101482740	LMX1A	LIM homeobc	-2.9674833	0.00636337
lnx1	LNX1	ligand of nurr	-3.713701	0.00444307
LOC101482875	LPAR2	lysophosphat	-10.443933	3.90E-11
lpcat4	LPCAT4	lysophosphat	-3.8752786	0.00065333
adgrl2	LPHN2	latrophilin 2 [-3.8798063	0.00025536
LOC101476956	LPO	lactoperoxida	-5.2749502	3.43E-06
LOC101483596	LPO	lactoperoxida	-3.9077703	0.00473246
lrp2	LRP2	low density li	-8.6152833	1.09E-10
lrr1	LRR1	leucine rich r	-3.6287775	0.001658
lrrc1	LRRC1	leucine rich r	-4.5300733	0.00012398
gp1bb	LRRC70	leucine rich r	-6.6277762	9.01E-08
LOC101466630	LRRFIP1	leucine rich r	-3.704723	0.00115207
lrrfip2	LRRFIP2	leucine rich r	-2.3661826	0.01112824
LOC101477090	LSM14B	LSM14B, SCD	-11.167697	7.20E-16
lsm5	LSM5	LSM5 homolc	-4.071884	0.00124827
LOC101476279	LTB4R	leukotriene B	-5.5196899	5.96E-06
LOC101476568	LTB4R	leukotriene B	-5.1415494	3.11E-05
ltk	LTK	leukocyte rec	-4.3361061	0.00064502
luc7l	LUC7L	LUC7-like (S. c	-3.1026399	0.00078012
luc7l3	LUC7L3	LUC7-like 3 (S	-2.2650983	0.00938011
lxn	LXN	latexin [Sourc	-3.9180316	5.80E-06
LOC101464585	LYRM5	LYR motif cor	-4.7350796	1.69E-05
lzic	LZIC	leucine zippe	-9.508351	7.38E-11
mad2l2	MAD2L2	MAD2 mitotic	-3.4630134	4.13E-05
LOC105941358	MAG	myelin associ	-5.2931891	8.00E-06
LOC106674858	MAG	myelin associ	-2.4559759	0.01170833
LOC101472626	MAGI3	membrane as	-4.6887473	0.00012644
LOC101485761	MAL	mal, T-cell dif	-7.6523223	6.60E-08

maneal	MANEAL	mannosidase	-6.7218903	1.07E-07
map3k12	MAP3K12	mitogen-activ	-3.9828293	0.00024023
map3k15	MAP3K15	mitogen-activ	-6.8274319	8.14E-08
map3k19	MAP3K19	mitogen-activ	-3.0474177	0.01035321
LOC101472584	MAP7	microtubule-i	-4.4354976	0.00056453
map7	MAP7	microtubule-i	-3.8694265	0.00314293
LOC101485680	MAPK12	mitogen-activ	-3.6470457	0.00127191
March1	March1	membrane as	-2.3946302	0.00877006
mau2	MAU2	MAU2 chrom	-6.2495623	1.32E-08
mcmdc2	MCMDC2	minichromos	-2.0307341	0.00234669
LOC101476817	MCTP2	multiple C2 d	-3.7829429	0.00035227
med19	MED19	mediator con	-4.096925	0.00106089
LOC101487076	MEP1B	mepirin A, bel	-3.5228488	0.00062382
mettl23	METTL23	methyltransfe	-5.0096232	0.00017559
mex3a	MEX3A	mex-3 homol	-6.432818	3.32E-07
mfap3	MFAP3	microfibrillar	-5.5578621	1.51E-06
mgarp	mgarp	mitochondria	-2.6720958	0.01109797
mgat4d	mgat4d	Glycosyltrans	-3.3599147	0.00096896
LOC101474131	MGST2	microsomal g	-4.897837	2.26E-05
LOC101468163	MICAL2	microtubule a	-4.7967434	4.55E-05
mid1ip1	MID1IP1	MID1 interacti	-7.4284553	9.32E-08
mlh1	mlh1	mutL homolo	-3.7035848	3.84E-07
LOC101477882	MLLT4	myeloid/lymph	-5.8088306	3.41E-10
LOC101468688	MMP25	matrix metall	-6.041322	1.66E-05
mn1	MN1	meningioma	-7.3901531	3.74E-07
LOC101484727	MOGAT3	monoacylglyc	-3.4007695	0.00242749
LOC101476831	MOV10	Mov10, Molo	-2.9450077	0.00494656
mrpl18	MRPL18	mitochondria	-3.2245785	0.01055384
mrpl34	MRPL34	mitochondria	-3.6325547	0.00200517
mrpl48	MRPL48	mitochondria	-7.8734826	3.79E-08
mrps26	MRPS26	mitochondria	-4.8011055	0.00011256
LOC101485729	MSLNL	mesothelin-li	-10.339063	5.47E-12
msra	MSRA	methionine s	-2.8249457	0.00235719
mtfr2	MTFR2	mitochondria	-8.9102871	1.29E-09
mthfd1l	MTHFD1L	methylenetet	-4.017799	0.00036696
mtif2	mtif2	mitochondria	-1.7049036	0.00712045
mtus2	MTUS2	microtubule a	-4.6256818	0.00115416
muc15	muc15	mucin 15, cel	-4.1796847	0.00129281
mus81	MUS81	MUS81 endo	-2.6855038	0.00233007
mvp	MVP	major vault p	-5.745741	3.03E-07
mxd3	MXD3	MAX dimeriza	-2.914579	0.00700778

myb	MYB	v-myb myelol	-5.8317072	2.06E-05
LOC101482181	MYCL1	v-myc myeloc	-6.2639855	2.95E-06
LOC101483420	MYH14	myosin, heav	-6.6794662	7.82E-08
LOC101463895	MYH6	myosin, heav	-5.0810475	5.37E-05
mylip	MYLIP	myosin regul	-3.3316233	0.00406084
LOC101467201	MYO1F	myosin IF [So	-6.8088836	1.14E-07
LOC101483740	MYO7B	myosin VIIB [:	-3.8055048	0.00198009
LOC101468518	MYOF	myoferlin [So	-3.0489779	0.00458538
n6amt2	N6AMT2	N-6 adenine-:	-5.0482348	0.00070341
LOC105941146	NA	NA	-14.91037	1.60E-23
LOC101465166	NA	NA	-11.285102	3.44E-14
LOC106676866	NA	NA	-11.089572	8.98E-12
LOC106676634	NA	NA	-10.928253	4.37E-11
LOC106676726	NA	NA	-10.607421	1.32E-12
LOC105940995	NA	NA	-10.56777	4.24E-19
LOC105941327	NA	NA	-10.262655	1.62E-11
LOC101483274	NA	NA	-9.4491836	4.59E-12
LOC101471434	NA	NA	-9.3934878	5.97E-11
LOC101476142	NA	NA	-9.1658966	9.78E-12
LOC101481752	NA	NA	-8.8429471	1.85E-10
LOC105940928	NA	NA	-8.7606967	1.37E-09
LOC106676502	NA	NA	-8.3705279	8.05E-14
LOC106676560	NA	NA	-8.0667379	2.19E-08
LOC101480360	NA	NA	-8.0380905	2.82E-11
LOC101471234	NA	NA	-7.8418426	1.53E-09
LOC101486921	NA	NA	-7.356798	3.77E-12
LOC105941180	NA	NA	-7.1894267	4.44E-07
LOC105940828	NA	NA	-6.7026732	5.91E-06
LOC105941329	NA	NA	-6.6991258	4.33E-07
LOC101469948	NA	NA	-6.4278291	8.04E-07
LOC101467316	NA	NA	-6.384163	1.51E-06
LOC105941187	NA	NA	-6.3642488	2.76E-07
LOC105940852	NA	NA	-6.3533697	5.82E-10
LOC105940775	NA	NA	-6.3344129	4.81E-06
LOC106676691	NA	NA	-6.0942592	2.76E-09
LOC101472574	NA	NA	-6.0260992	8.44E-06
LOC101463914	NA	NA	-5.9679485	4.89E-06
LOC101471754	NA	NA	-4.725091	0.00014836
LOC101463818	NA	NA	-4.6704533	0.00024922
LOC101481827	NA	NA	-4.666776	0.00012147
LOC101476414	NA	NA	-4.6365112	8.00E-05

LOC106676724	NA	NA	-4.6355485	0.00084508
LOC105940569	NA	NA	-4.6161143	7.35E-05
LOC106675221	NA	NA	-4.5009968	1.83E-06
LOC105941438	NA	NA	-4.4679115	7.93E-05
LOC106676072	NA	NA	-4.4657723	0.00019939
LOC101465749	NA	NA	-4.3386247	0.00013152
LOC106675389	NA	NA	-4.3036435	3.92E-05
LOC101484336	NA	NA	-4.2833386	0.00062719
LOC101484615	NA	NA	-4.2663832	0.00033105
LOC106676418	NA	NA	-4.244444	0.00019259
LOC105940766	NA	NA	-4.2133134	0.000229
LOC105941183	NA	NA	-4.1699794	0.00185835
LOC106676455	NA	NA	-4.0128885	0.00307483
LOC105940670	NA	NA	-4.001723	0.00086222
LOC101471044	NA	NA	-3.8598635	0.00185728
LOC105940988	NA	NA	-3.8349571	0.00524739
LOC106674675	NA	NA	-3.8318379	0.00207632
LOC106675740	NA	NA	-3.8277201	0.00158162
LOC106675500	NA	NA	-3.7443183	0.01158749
LOC105941043	NA	NA	-3.6657059	2.03E-05
LOC106675982	NA	NA	-3.6470457	0.00127191
LOC106675760	NA	NA	-3.6014889	0.00230971
LOC101465353	NA	NA	-3.4774562	0.00924417
LOC105940736	NA	NA	-3.3981061	3.67E-05
LOC106676504	NA	NA	-3.3490248	0.00852026
LOC101466287	NA	NA	-3.2765919	0.00467679
LOC106675074	NA	NA	-3.2592273	0.00178023
LOC106675439	NA	NA	-3.1932654	0.00402191
LOC101467309	NA	NA	-3.1694126	0.00782878
LOC101465469	NA	NA	-3.1076689	0.00243309
LOC105941398	NA	NA	-3.0805691	0.00678316
trnaq-cug	NA	NA	-3.0571773	0.00763076
LOC105940487	NA	NA	-3.0340999	0.00956643
LOC101471363	NA	NA	-3.0104346	0.00391114
LOC101475840	NA	NA	-2.9455279	0.00653347
LOC106676212	NA	NA	-2.9279605	0.00806884
LOC105940909	NA	NA	-2.8859001	0.00334499
LOC106674545	NA	NA	-2.8704899	0.00423681
LOC101486953	NA	NA	-2.8701668	0.0046371
LOC106676853	NA	NA	-2.8659325	0.00452743
LOC105940516	NA	NA	-2.8621532	0.00398792

LOC106675570	NA	NA	-2.8476975	0.01049433
LOC105941364	NA	NA	-2.6219823	2.95E-05
LOC105940488	NA	NA	-2.5826593	0.00518665
LOC105941032	NA	NA	-2.5523924	0.01105173
LOC106675615	NA	NA	-2.5207361	0.0117835
LOC101486729	NA	NA	-2.4559759	0.01170833
LOC106675110	NA	NA	-2.2843628	0.0001572
LOC105941293	NA	NA	-2.0660492	0.0064575
naif1	NAIF1	nuclear apop	-5.3102397	2.47E-05
LOC101475375	NAPSA	napsin A asp	-4.1496533	0.00063597
nars	NARS	asparaginytl	-3.6893315	0.00454474
LOC101483112	NCALD	neurocalcin d	-5.7069264	8.86E-06
LOC101468786	NCAM1	neural cell ad	-3.4466089	0.00051164
ncaph2	NCAPH2	non-SMC con	-2.4880291	0.00081192
LOC101483930	NCL	nucleolin [So	-2.695576	0.00283814
ndufa6	NDUFA6	NADH dehydr	-3.020835	0.00045224
ndufaf2	NDUFAF2	NADH dehydr	-3.9753054	0.00110095
LOC101485676	NDUFV1	NADH dehydr	-2.4662977	0.00305875
ndufv2	NDUFV2	NADH dehydr	-2.2692951	0.00218693
LOC101472925	NEFM	neurofilamen	-2.6507257	0.00268603
nek3	NEK3	NIMA-related	-4.704909	0.00013281
neu4	NEU4	sialidase 4 [Sc	-3.4774905	0.00836791
neurl4	NEURL2	neuralized hc	-2.5265336	0.00827647
nfatc2ip	NFATC2IP	nuclear facto	-3.7401818	0.00078432
LOC101471350	NFE2L1	nuclear facto	-4.9408267	0.00010148
nfkbil1	NFKBIL1	nuclear facto	-2.5224947	0.01132294
LOC101467620	NFKBIZ	nuclear facto	-4.0401763	0.0001218
nfrkb	NFRKB	nuclear facto	-9.9912892	2.21E-11
LOC101479895	NFX1	nuclear trans	-3.5134508	0.0031334
nip7	NIP7	nuclear impo	-2.5187254	0.00073386
nipa1	NIPA1	non imprinte	-5.8850253	5.26E-06
nipal4	NIPA2	non imprinte	-3.988692	0.00064525
nit2	NIT2	nitrilase fami	-9.1425942	3.89E-11
LOC101478757	NKX2-3	NK2 homeob	-4.0230276	0.00062676
LOC101483765	NME4	NME/NM23 r	-15.291179	4.21E-19
nmnat1	NMNAT1	nicotinamide	-8.0194866	4.27E-09
LOC101472624	NMRK1	nicotinamide	-5.5115867	2.78E-05
LOC105941157	NoAnnotation	NoAnnotatio	-18.365275	1.24E-19
LOC105940576	NoAnnotation	NoAnnotatio	-16.609699	8.43E-19
LOC106674558	NoAnnotation	NoAnnotatio	-13.131336	5.96E-15
LOC101474267	NoAnnotation	NoAnnotatio	-13.004463	3.17E-16

LOC101466847	NoAnnotation	NoAnnotation	-12.502949	6.47E-13
LOC105940575	NoAnnotation	NoAnnotation	-12.084649	2.32E-13
LOC101475848	NoAnnotation	NoAnnotation	-12.00536	2.49E-14
LOC101473175	NoAnnotation	NoAnnotation	-11.482494	1.23E-14
LOC106676574	NoAnnotation	NoAnnotation	-11.32839	1.14E-14
LOC101472879	NoAnnotation	NoAnnotation	-10.845746	6.58E-14
LOC106675996	NoAnnotation	NoAnnotation	-10.43531	1.04E-12
LOC106676246	NoAnnotation	NoAnnotation	-10.093978	4.92E-13
LOC106676062	NoAnnotation	NoAnnotation	-10.013895	1.52E-10
LOC101478955	NoAnnotation	NoAnnotation	-9.51117	1.34E-11
LOC105941246	NoAnnotation	NoAnnotation	-9.4525578	6.53E-12
LOC101468230	NoAnnotation	NoAnnotation	-9.3143199	2.75E-08
LOC101479207	NoAnnotation	NoAnnotation	-8.8873697	1.20E-10
LOC106674716	NoAnnotation	NoAnnotation	-8.0621258	2.83E-08
LOC101465183	NoAnnotation	NoAnnotation	-7.8708406	1.42E-07
LOC101463608	NoAnnotation	NoAnnotation	-7.5464664	4.47E-09
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LOC101465498	NoAnnotation	NoAnnotation	-6.6681575	2.76E-06
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LOC101473038	NoAnnotation	NoAnnotation	-6.0157763	1.81E-06
LOC106676108	NoAnnotation	NoAnnotation	-5.8083135	4.54E-10
LOC106676110	NoAnnotation	NoAnnotation	-5.7719529	8.01E-06
LOC106675205	NoAnnotation	NoAnnotation	-5.5970654	7.03E-09
LOC101469477	NoAnnotation	NoAnnotation	-5.5962268	3.54E-05
LOC106675957	NoAnnotation	NoAnnotation	-5.5458004	0.0001299
LOC101467402	NoAnnotation	NoAnnotation	-5.5117306	8.62E-06
LOC101478774	NoAnnotation	NoAnnotation	-5.4771876	8.59E-06
LOC101483183	NoAnnotation	NoAnnotation	-5.3983712	1.20E-05
LOC101471358	NoAnnotation	NoAnnotation	-5.3677137	0.00011752
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LOC101484134	NoAnnotation	NoAnnotation	-5.1983963	1.29E-05
LOC101475002	NoAnnotation	NoAnnotation	-5.1971196	0.00015398
LOC101465126	NoAnnotation	NoAnnotation	-5.1254038	7.13E-05
LOC101475037	NoAnnotation	NoAnnotation	-5.043006	3.72E-05
LOC101467796	NoAnnotation	NoAnnotation	-5.0294463	9.02E-06

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LOC106675304	NoAnnotation	NoAnnotation	-4.910182	1.97E-05
LOC106675134	NoAnnotation	NoAnnotation	-4.8864423	2.98E-05
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LOC106676687	NoAnnotation	NoAnnotation	-4.5818747	0.0072775
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LOC101471829	NoAnnotation	NoAnnotation	-4.4882488	0.00074237
LOC101476136	NoAnnotation	NoAnnotation	-4.4810199	0.00011444
LOC101464600	NoAnnotation	NoAnnotation	-4.4517011	0.00022121
LOC106674633	NoAnnotation	NoAnnotation	-4.3558069	6.34E-05
LOC101470155	NoAnnotation	NoAnnotation	-4.3424446	0.000242
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LOC101469353	NoAnnotation	NoAnnotation	-4.2897853	0.00075913
LOC101487210	NoAnnotation	NoAnnotation	-4.2866035	0.00023332
LOC101468467	NoAnnotation	NoAnnotation	-4.2494304	0.00014582
LOC101473401	NoAnnotation	NoAnnotation	-4.2318037	0.00078739
LOC101475026	NoAnnotation	NoAnnotation	-4.197133	0.00015666
LOC101483272	NoAnnotation	NoAnnotation	-4.1555972	0.00013887
LOC106676338	NoAnnotation	NoAnnotation	-4.1529826	0.00049239
LOC106675923	NoAnnotation	NoAnnotation	-4.1248786	0.00854519
LOC105940619	NoAnnotation	NoAnnotation	-4.0965154	0.00027522
LOC101470258	NoAnnotation	NoAnnotation	-4.0752627	0.00096408
LOC101463946	NoAnnotation	NoAnnotation	-4.0675594	0.00027583
LOC106675147	NoAnnotation	NoAnnotation	-4.0647623	0.00145601
LOC101487722	NoAnnotation	NoAnnotation	-4.0500871	0.00145205
LOC106674563	NoAnnotation	NoAnnotation	-3.9516294	0.00065172
LOC106676234	NoAnnotation	NoAnnotation	-3.8914549	0.00107411
LOC101468776	NoAnnotation	NoAnnotation	-3.8861151	0.00017839
LOC101483716	NoAnnotation	NoAnnotation	-3.860085	0.00112933
LOC101479484	NoAnnotation	NoAnnotation	-3.710309	0.00215439
LOC101470013	NoAnnotation	NoAnnotation	-3.6793614	0.00428826
LOC101474461	NoAnnotation	NoAnnotation	-3.664385	0.00204018
LOC101464544	NoAnnotation	NoAnnotation	-3.6517681	0.00181794
LOC106676852	NoAnnotation	NoAnnotation	-3.6418295	0.00084455
LOC101484466	NoAnnotation	NoAnnotation	-3.6315277	0.00414809
LOC101473487	NoAnnotation	NoAnnotation	-3.629869	0.00088225
LOC101467896	NoAnnotation	NoAnnotation	-3.6090428	0.00263368
LOC101485541	NoAnnotation	NoAnnotation	-3.5899565	0.00141992

LOC101471451	NoAnnotation	NoAnnotation	-3.5886318	0.0006929
LOC101474750	NoAnnotation	NoAnnotation	-3.5524037	0.00961291
LOC101471391	NoAnnotation	NoAnnotation	-3.5345718	0.00230756
LOC105941453	NoAnnotation	NoAnnotation	-3.5293417	0.00165275
LOC106675999	NoAnnotation	NoAnnotation	-3.5103124	0.00095569
LOC101478481	NoAnnotation	NoAnnotation	-3.4981024	0.00052346
LOC101468425	NoAnnotation	NoAnnotation	-3.4926966	0.00256364
LOC106675467	NoAnnotation	NoAnnotation	-3.4629599	0.00150951
LOC101481277	NoAnnotation	NoAnnotation	-3.4387177	0.001881
LOC101483238	NoAnnotation	NoAnnotation	-3.4256975	0.00326209
LOC101465215	NoAnnotation	NoAnnotation	-3.380034	0.00675834
LOC101465273	NoAnnotation	NoAnnotation	-3.354205	0.0020544
LOC101485971	NoAnnotation	NoAnnotation	-3.3468227	0.00897072
LOC106674947	NoAnnotation	NoAnnotation	-3.3452896	0.01025027
LOC101470285	NoAnnotation	NoAnnotation	-3.3303615	0.00344638
LOC101471383	NoAnnotation	NoAnnotation	-3.2830778	0.00452435
LOC101464915	NoAnnotation	NoAnnotation	-3.2820856	0.00529053
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LOC106676656	NoAnnotation	NoAnnotation	-3.2413271	0.00617732
LOC101485997	NoAnnotation	NoAnnotation	-3.225878	0.00507766
LOC106676128	NoAnnotation	NoAnnotation	-3.2192447	0.00477595
LOC106675956	NoAnnotation	NoAnnotation	-3.2054767	0.00569523
LOC101480915	NoAnnotation	NoAnnotation	-3.186431	0.00571356
LOC101474584	NoAnnotation	NoAnnotation	-3.1448238	0.00709059
LOC101478376	NoAnnotation	NoAnnotation	-3.0841738	0.00044235
LOC106675552	NoAnnotation	NoAnnotation	-3.0509477	0.00423606
LOC101482736	NoAnnotation	NoAnnotation	-3.0177403	0.00419685
LOC101476986	NoAnnotation	NoAnnotation	-3.0049362	0.01057674
LOC101471756	NoAnnotation	NoAnnotation	-2.9740785	0.00639848
LOC105940511	NoAnnotation	NoAnnotation	-2.972004	0.00538921
LOC101487050	NoAnnotation	NoAnnotation	-2.968832	0.00549063
LOC106674678	NoAnnotation	NoAnnotation	-2.8869991	0.00976295
LOC101476945	NoAnnotation	NoAnnotation	-2.8796378	0.0062699
LOC101480981	NoAnnotation	NoAnnotation	-2.8795035	0.00573816
LOC101482772	NoAnnotation	NoAnnotation	-2.8493562	0.0087942
LOC101463817	NoAnnotation	NoAnnotation	-2.7855606	0.00865175
LOC106676096	NoAnnotation	NoAnnotation	-2.4002444	0.00375711
LOC101474666	NoAnnotation	NoAnnotation	-2.3715806	2.53E-05
LOC101472336	NoAnnotation	NoAnnotation	-2.2271749	0.0029353
LOC101487883	NoAnnotation	NoAnnotation	-1.9963299	0.00368808
LOC101467927	NoAnnotation	NoAnnotation	-1.885811	0.00698391

LOC101474399	NPHS1	nephrosis 1, c	-6.8742659	1.40E-09
LOC101465198	NPR2	natriuretic pe	-3.5587392	0.0007985
LOC101478879	NPR2	natriuretic pe	-3.0573711	0.00374773
LOC101463939	NPR2	natriuretic pe	-2.866977	0.0043701
LOC101479763	NRG1	neuregulin 1	-4.9675111	0.00011656
nsfl1c	NSFL1C	NSFL1 (p97) c	-3.8835859	0.00161362
LOC101468566	NT5C1B	5'-nucleotida	-3.6044374	0.00247419
nt5dc2	NT5DC2	5'-nucleotida	-2.8032193	0.00233936
ntmt1	NTMT1	N-terminal Xa	-4.433997	0.00025738
nudt13	NUDT13	nudix (nucleo	-4.359546	0.00070105
LOC101474324	NUGGC	nuclear GTPa	-3.0563976	0.00393579
LOC101473846	NUGGC	nuclear GTPa	-3.0139954	0.00507113
nus1	NUS1	nuclear unde	-3.4515842	0.00702104
nxph4	NXP4	neurexophilin	-3.7531189	0.00105891
obscn	OBSCN	obscurin, cyto	-3.2516046	0.00194338
LOC101466532	OCEL1	occludin/ELL	-3.1870004	0.00437677
omg	OMG	oligodendrocy	-2.9455279	0.00653347
LOC101466074	OSBP2	oxysterol bind	-4.1296933	0.00105171
LOC101485211	OSBPL7	oxysterol bind	-10.732715	2.31E-13
LOC101467260	OSMR	oncostatin M	-4.956783	0.00029819
LOC101469687	OSR1	odd-skipped 1	-5.2828199	2.58E-05
ovol1	OVOL1	ovo-like 1(Dro	-4.6286461	5.35E-05
LOC101471516	OXS1	oxidative-stre	-2.7904455	0.01055123
LOC101487202	PACS2	phosphofurin	-6.6332838	1.10E-06
LOC101469954	PACS2	phosphofurin	-2.438866	0.01166528
pacsin3	PACSIN3	protein kinase	-3.7784423	0.00183863
paics	PAICS	phosphoribos	-2.8207898	0.00081875
LOC101484450	PAK3	p21 protein (C	-3.3659011	0.00189193
LOC101464122	PAK6	p21 protein (C	-7.8710362	7.27E-09
LOC101482825	PAOX	polyamine ox	-6.4868255	7.34E-06
paqr6	PAQR6	progesterone	-3.7944595	0.00465872
LOC101478411	PARD6A	par-6 partitio	-3.9837197	0.0011586
LOC106674480	PARP12	poly (ADP-rib	-3.3965105	0.00140055
LOC101471084	PARP14	poly (ADP-rib	-4.6167873	0.00044806
LOC101473124	PARP14	poly (ADP-rib	-4.2582292	0.00047226
LOC101471969	PARP14	poly (ADP-rib	-3.8110772	0.00093145
LOC101465440	PARP15	poly (ADP-rib	-7.2445418	4.94E-07
LOC101464676	PARP15	poly (ADP-rib	-4.6122563	0.00145807
LOC106676250	PARP15	poly (ADP-rib	-4.1965842	0.00016415
LOC101465156	PARP15	poly (ADP-rib	-4.1444304	9.35E-05
LOC101464863	PARP15	poly (ADP-rib	-3.9504015	0.00131569

LOC101464392	PARP15	poly (ADP-rib	-3.8947244	0.00314952
patl1	PATL1	protein assoc	-3.7544487	0.00199722
LOC101487230	PBX2	pre-B-cell leu	-4.2410962	0.00080567
pbx4	PBX4	pre-B-cell leu	-4.8168546	9.96E-05
pck2	PCK2	phosphoenol	-4.582998	0.00045719
pcp4	PCP4	Purkinje cell p	-4.8162949	3.15E-05
pcsk7	PCSK7	proprotein cc	-4.7957569	6.82E-07
LOC101476669	PCSK7	proprotein cc	-2.890393	0.00901019
pdap1	PDAP1	PDGFA associ	-3.8030199	0.0008877
LOC106676169	PDCD1LG2	programmed	-6.2455318	6.71E-07
LOC106676168	PDCD1LG2	programmed	-4.6625001	0.00015649
LOC101486556	PDE4C	phosphodiect	-7.1907873	3.37E-07
LOC101464089	PDE4DIP	phosphodiect	-4.7998471	0.00012777
LOC101472679	PDE6H	phosphodiect	-4.3358446	0.00065068
pde7b	PDE7B	phosphodiect	-3.3246608	0.0027638
LOC101480551	PDIA2	protein disulf	-4.4270797	2.57E-05
LOC101481409	PDIK1L	PDLIM1 inter	-3.2641766	0.00364039
LOC101467182	PEAR1	platelet endo	-4.5541222	1.63E-07
pelo	PELO	pelota homol	-5.1103494	1.53E-05
perp	PERP	PERP, TP53 a	-3.4932832	0.00138678
pex11a	PEX11A	peroxisomal l	-3.0650255	0.00988373
LOC101465745	PFN3	profilin 3 [So	-5.3004726	0.00010653
pgap3	PGAP3	post-GPI atta	-3.4079674	0.00786032
LOC106675998	PGBD4	piggyBac tran	-2.4837638	0.00194217
LOC101473884	PGLYRP1	peptidoglycar	-4.7794801	0.00013274
LOC101475096	PHACTR4	phosphatase	-4.1553701	0.00014573
LOC101465856	PHB2	prohibitin 2 [-3.5996884	0.00871176
phgdh	PHGDH	phosphoglyce	-4.6922161	8.51E-05
LOC101480121	PHLDA3	pleckstrin hor	-3.8169657	0.00153706
phldb3	phldb3	pleckstrin hor	-4.7430532	7.95E-05
LOC101476416	PI4KB	phosphatidyli	-2.8572272	0.00724266
LOC101474114	PIK3CA	phosphatidyli	-4.7837511	0.00019717
LOC101481450	PIK3R1	phosphoinosi	-3.6271993	0.00057623
LOC101463967	PIK3R5	phosphoinosi	-3.1954985	0.00295687
pim1	PIM1	pim-1 oncoge	-7.1423789	2.27E-07
LOC106676929	PIM2	pim-2 oncoge	-4.06471	0.00097684
LOC101473319	PIM2	pim-2 oncoge	-3.2114451	0.00373561
LOC101482492	PIP5K1B	phosphatidyli	-3.1860058	0.00353273
LOC101468791	PITPNA	phosphatidyli	-4.5833819	0.00011663
LOC101487503	PKLR	pyruvate kina	-3.1898131	0.01062755
pkn2	PKN2	protein kinas	-2.9989345	0.00068182

LOC101478860	PKN3	protein kinase	-3.8987772	0.00494194
LOC101481283	PKP1	plakophilin 1	-3.1415083	0.00046898
pkp3	pkp3	plakophilin 3	-6.0788244	1.25E-07
oc90	PLA2G10	phospholipase	-2.8923818	0.00596381
LOC101469077	PLA2G16	phospholipase	-3.1074302	0.00435717
LOC101477336	PLA2G4C	phospholipase	-5.5682923	2.48E-06
LOC101472639	PLAC8L1	PLAC8-like 1	-5.9849897	7.03E-07
LOC101472126	PLAC8L1	PLAC8-like 1	-5.2578071	3.30E-06
LOC101484068	PLAC8L1	PLAC8-like 1	-3.0197143	0.00628915
LOC101470994	PLB1	phospholipase	-3.1923233	0.00528841
plcb3	PLCB3	phospholipase	-3.2863345	0.01042794
plce1	PLCE1	phospholipase	-4.1707303	0.00016808
LOC101485579	PLCXD1	phosphatidyli	-3.5535756	2.76E-05
LOC101480604	PLCXD1	phosphatidyli	-2.6250061	0.00770786
LOC101480937	PLCXD2	phosphatidyli	-3.8435747	0.00331466
LOC101487611	PLCZ1	phospholipase	-4.3675417	0.00044041
LOC101475558	PLEKHA6	pleckstrin hom	-3.9517015	0.00401183
LOC101473336	PLEKHF1	pleckstrin hom	-3.3730492	0.00303407
plekhg3	PLEKHG3	pleckstrin hom	-4.1913649	0.00294566
LOC101472683	PLEKHG4	pleckstrin hom	-3.5137735	0.00399439
plekhg6	PLEKHG6	pleckstrin hom	-7.3434425	1.01E-07
plekhg7	PLEKHG7	pleckstrin hom	-3.3250796	0.00369229
plekhs1	PLEKHS1	pleckstrin hom	-3.893597	0.00063345
LOC101477699	PLSCR4	phospholipid	-3.8871536	0.00335215
LOC101484021	PLXNC1	plexin C1 [So	-5.6858488	7.91E-06
pnkd	pnkd	paroxysmal n	-3.7815586	0.00015312
pnn	PNN	pinin, desmo	-2.3993167	0.00981214
LOC101477825	PNP	purine nuclec	-6.3505583	4.01E-07
poc1a	POC1A	POC1 centrio	-3.9877061	0.00043541
polq	POLQ	polymerase (l	-2.7223469	0.00022168
LOC101475101	PON1	paraoxonase	-1.9113205	0.00083255
pop4	POP4	processing of	-4.8754434	8.15E-05
pot1	POT1	protection of	-5.8657732	1.53E-06
pou1f1	POU1F1	POU class 1 h	-2.8112861	0.00677663
pou2af1	POU2AF1	POU class 2 a	-3.2766672	0.00138595
plpp6	PPAPDC2	phosphatidic	-6.0816246	5.26E-08
LOC101483779	PPFIA3	protein tyrosi	-4.3864689	0.00018774
ppil1	PPIL1	peptidylproly	-4.4879824	0.00017712
ppl	PPL	periplakin [Sc	-10.200566	2.48E-12
LOC101472635	PPP1CB	protein phosp	-1.9227667	0.00691008
ankrd66	PPP1R27	protein phosp	-5.4178007	0.00020938

LOC101466175	PPP1R3C	protein phosphatase 1	-9.3059105	2.54E-09
prkaa2	PRKAA2	protein kinase A2	-10.30273	1.89E-12
LOC101470867	PRKAB2	protein kinase A2	-2.9455279	0.00653347
prkx	PRKX	protein kinase X	-3.4760449	0.00447131
LOC101472831	PRLR	prolactin receptor	-3.5549151	0.00260499
prox1	PROX1	prospero homolog 1	-3.5499426	0.00274459
prpf38b	PRPF38B	PRP38 pre-mRNA splicing factor	-3.0169642	0.00014482
LOC101471970	PRR14	proline rich 14	-14.484647	5.80E-17
LOC101472909	PRR15	proline rich 15	-4.7652493	5.62E-05
LOC101477823	PRRG1	proline rich G1	-3.9927421	0.0001799
LOC101466526	PRRG4	proline rich G4	-5.074663	2.06E-05
LOC101476403	PRRT3	proline-rich transcript 3	-3.4775226	0.00391474
LOC105941023	PRSS42	protease, serine 42	-11.49934	2.26E-11
prss8	PRSS42	protease, serine 42	-6.1474055	2.15E-06
LOC101481279	PRSS42	protease, serine 42	-4.9547482	2.82E-05
LOC101486191	PRSS42	protease, serine 42	-4.8111193	7.50E-06
LOC101477959	PRUNE2	prune homolog 2	-6.457648	1.37E-06
psat1	PSAT1	phosphoserine aminotransferase 1	-3.9607854	0.0073649
LOC101472814	PSMB10	proteasome (20S) subunit 10	-3.464427	0.0057868
LOC101472537	PSMB9	proteasome (20S) subunit 9	-3.0846519	0.00223493
LOC101485841	PSME4	proteasome (26S) subunit 4	-4.7855985	0.00038459
LOC101469155	PSORS1C2	psoriasis susceptibility 1C2	-6.8861481	1.81E-07
LOC101468134	PTAFR	platelet-activating factor receptor	-7.9119271	1.55E-09
ptdss2	PTDSS2	phosphatidylserine decarboxylase 2	-4.0248722	0.00021248
LOC101466179	PTGDR2	prostaglandin synthase 2	-6.5394567	1.86E-05
aarsd1	PTGES3L-AARSD1	PTGES3L-AARSD1	-5.3244582	5.89E-07
ptgfrn	PTGFRN	prostaglandin synthase	-4.4706723	0.00028658
LOC101476415	PTGIS	prostaglandin synthase	-4.5767363	0.00013278
LOC101466406	PTPN18	protein tyrosine phosphatase 18	-3.8189337	0.00404985
LOC101482516	PTPN7	protein tyrosine phosphatase 7	-6.1360704	2.02E-06
LOC101474932	PTPRB	protein tyrosine phosphatase B	-5.5162853	9.74E-08
ptprz1	PTPRZ1	protein tyrosine phosphatase Z1	-5.419069	7.68E-06
pus10	PUS10	pseudouridylate synthase 10	-1.5222919	0.00430391
pusl1	PUSL1	pseudouridylate synthase 1	-3.3634367	0.00289273
pxmp4	PXMP4	peroxisomal membrane protein 4	-5.0852047	3.05E-05
qars	QARS	glutaminyl-tRNA synthetase	-3.0543978	0.00041244
LOC101474648	QRICH1	glutamine-rich protein 1	-6.2948685	4.73E-07
LOC101463597	RAB11FIP1	RAB11 family interacting protein 1	-5.3977454	1.54E-05
rab11fip2	RAB11FIP2	RAB11 family interacting protein 2	-3.0159971	0.00939048
LOC101475825	RAB25	RAB25, member 25	-6.6638916	7.04E-07
LOC101463638	RAB3B	RAB3B, member 3B	-3.4402437	0.00255878

rabggt	RABGGTA	Rab geranylge	-6.7735357	8.51E-08
rad23b	RAD23A	RAD23 homo	-3.027313	0.00950353
rad9a	RAD9A	RAD9 homolc	-5.9526832	3.03E-05
rad9b	RAD9B	RAD9 homolc	-3.8568662	0.00240193
LOC101473598	RAP1GAP	RAP1 GTPase	-5.5359756	0.00060498
rapgef2	RAPGEF2	Rap guanine i	-3.2314346	0.00434945
LOC101468354	RARG	retinoic acid i	-3.4802078	0.00095229
LOC105940583	RARRES3	retinoic acid i	-3.8540782	0.00287194
LOC101481289	RASD2	RASD family,	-4.3222742	0.0004566
LOC101471002	RASEF	RAS and EF-h	-3.6760591	0.00449779
LOC101472166	RASGRP4	RAS guanyl re	-1.2115437	0.01001427
rbm41	RBM41	RNA binding i	-3.7271332	0.00132885
rbp7	RBP7	retinol bindin	-11.860667	7.29E-12
LOC101476276	RDH14	retinol dehyd	-8.0639035	2.49E-10
reep1	REEP1	receptor acce	-3.0343646	0.00023632
reep2	REEP2	receptor acce	-3.8011018	0.00486636
rfc2	RFC2	replication fa	-3.8240799	0.00071622
rfc5	RFC5	replication fa	-4.3108837	3.02E-06
LOC101472714	RFTN1	raftlin, lipid r	-1.8789673	0.00450776
LOC101483324	RGCC	regulator of c	-3.6539484	0.00167079
LOC101465819	RGS13	regulator of C	-4.3126841	0.00113937
LOC101472472	RGS18	regulator of C	-3.287928	0.00876409
LOC101466397	RGS2	regulator of C	-4.6890498	0.00014066
LOC101473767	RGS20	regulator of C	-3.3307049	0.00550939
rhbdl2	RHBDL2	rhomboid, ve	-3.3610035	0.00432193
LOC101469787	RHOV	ras homolog 1	-3.8025199	0.00350232
LOC101486182	RILPL1	Rab interactir	-3.2417232	0.0032425
ring1	RING1	ring finger pr	-3.2458383	0.00020167
riok3	RIOK3	RIO kinase 3 [-3.259403	0.00236006
ripk4	RIPK4	receptor-inte	-8.290768	6.25E-10
rnf113a	RNF113A	ring finger pr	-3.4961378	0.00131965
LOC101471368	RNF208	ring finger pr	-5.1145553	0.00024852
LOC101483179	RNF217	ring finger pr	-7.3180531	9.26E-07
rnf222	RNF222	ring finger pr	-2.9905123	0.00821413
LOC101471307	RNF38	ring finger pr	-4.6398165	0.0001095
LOC101478352	RNF41	ring finger pr	-3.2824774	0.00270582
rnls	RNLS	renalase, FAC	-4.4620075	2.58E-06
LOC101481672	ROBO3	roundabout,	-3.5796997	0.00378948
LOC101478009	RPGR	retinitis pigm	-3.9655815	0.00031294
LOC101472439	RPL19	ribosomal pro	-1.8901658	0.01113947
rpn1	RPN1	ribophorin I [-2.7755378	0.00420573

rpp30	RPP30	ribonuclease	-3.3395678	0.0047459
rpp40	RPP40	ribonuclease	-3.3599147	0.00096896
LOC101477757	RPS27L	ribosomal pro	-3.7111171	1.14E-07
LOC101475486	RPS6KA1	ribosomal pro	-5.3474235	7.69E-06
LOC101468435	RPS6KA5	ribosomal pro	-3.1501007	0.00668283
LOC101474829	RSPH6A	radial spoke f	-6.2113059	1.27E-05
rtnk	RTKN	rhotekin [Sou	-3.7964345	0.00185684
rufy1	RUFY1	RUN and FYV	-2.6333396	0.00730812
rundc1	RUNDC1	RUN domain	-3.7487735	0.00094043
LOC101465462	RUNDC3A	RUN domain	-2.132471	0.00296383
rundc3b	RUNDC3B	RUN domain	-2.8921268	0.00580242
LOC101485234	S100P	S100 calcium	-7.7260311	3.48E-09
LOC101467985	S100P	S100 calcium	-6.1309765	8.34E-07
LOC101471430	SAMD14	sterile alpha r	-6.8525873	2.00E-08
LOC101475261	SAMD9	sterile alpha r	-3.3998355	0.00122941
sap25	SAP25	Sin3A-associ	-7.1279976	4.89E-12
LOC101475165	SCAMP2	secretory cari	-3.9889399	0.00138402
scel	scel	sciellin	-10.70988	5.41E-14
LOC101470091	SCIN	scinderin [Sou	-3.4194047	0.00032535
scmh1	SCMH1	sex comb on	-3.3950221	0.01025718
scoc	SCOC	short coiled-c	-3.6793671	0.0043157
LOC101474415	SCOC	short coiled-c	-2.9831287	0.00272678
sdhd	SDHD	succinate def	-3.6759882	0.00277618
secisbp2	SECISBP2	SECIS binding	-6.8103005	1.16E-08
LOC101479196	SEMA4F	sema domain	-5.5408776	9.35E-06
LOC101475744	SEMA4F	sema domain	-4.1308909	0.00215749
LOC101478285	SERPINB2	serpin peptid	-6.1715291	1.88E-06
LOC106676165	SERPINB2	serpin peptid	-5.2124275	3.17E-05
serpind1	SERPIND1	serpin peptid	-4.1919073	0.00055778
LOC101485050	SESN2	sestrin 2 [Sou	-3.6372745	0.00322221
LOC101475491	Sgk3	Serine/threor	-3.3439876	0.00146226
sgpp2	SGPP2	sphingosine-1	-5.366254	7.62E-06
LOC101464567	SH2D3A	SH2 domain c	-5.0201534	9.09E-07
LOC101471217	SH2D4A	SH2 domain c	-3.5143678	0.00164933
sh3d19	SH3D19	SH3 domain c	-6.0354246	3.33E-07
LOC101472080	SH3KBP1	SH3-domain f	-2.9601438	0.00050316
LOC101469781	SH3RF2	SH3 domain c	-4.5432072	0.00046467
LOC101484394	SHISA5	shisa homolo	-3.8242398	0.00091189
LOC101470492	SHMT2	serine hydrox	-5.3498759	1.10E-05
LOC101478252	SHROOM3	shroom famil	-3.2834042	0.00021002
siah1	siah1	siah E3 ubiqu	-3.4171529	7.78E-06

LOC101471392	SIAH2	siah E3 ubiqu	-3.0552657	0.00419349
sigirr	SIGIRR	single immun	-3.0756752	0.00840792
sin3a	SIN3A	SIN3 transcrip	-4.1287038	6.06E-05
LOC101486976	SIPA1L2	signal-induce	-6.3322621	4.81E-07
six3	SIX3	SIX homeobo	-5.2007793	0.00015889
LOC101481621	SIX6	SIX homeobo	-4.4793004	0.00010629
ska2	SKA2	spindle and k	-3.9649967	0.00089148
LOC101475294	SLC12A3	solute carrier	-4.1557969	0.00015198
slc13a4	SLC13A4	solute carrier	-1.7624838	0.00559513
LOC101471059	SLC16A1	solute carrier	-3.8882764	0.0026185
slc16a12	SLC16A12	solute carrier	-4.4418159	0.0002368
slc16a6	SLC16A6	solute carrier	-3.7025337	0.00427357
slc17a6	SLC17A7	solute carrier	-4.2829069	0.00057338
LOC101484681	SLC17A7	solute carrier	-3.3599985	0.00327197
LOC101471102	SLC1A2	solute carrier	-4.0708476	1.19E-07
LOC101484092	SLC22A13	solute carrier	-8.1265326	7.71E-10
LOC101479579	SLC22A13	solute carrier	-2.9789431	0.0054282
slc22a16	SLC22A16	solute carrier	-2.9651008	0.01044562
LOC101464155	SLC22A5	solute carrier	-4.829644	0.00015481
LOC101463669	SLC22A5	solute carrier	-4.1524129	0.0008616
LOC101465478	SLC22A8	solute carrier	-3.2592273	0.00178023
LOC101488034	SLC24A3	solute carrier	-3.5858035	0.00162703
slc25a15	SLC25A15	solute carrier	-2.947433	0.00648431
LOC101474915	SLC25A30	solute carrier	-5.1605859	2.80E-05
slc25a37	SLC25A37	solute carrier	-3.334752	0.00349476
LOC101474466	SLC25A44	solute carrier	-3.438239	0.00011742
LOC101485866	SLC27A5	solute carrier	-10.396793	2.39E-13
slc2a13	SLC2A13	solute carrier	-4.2303568	0.0002134
slc30a3	SLC30A3	solute carrier	-2.7570548	0.0071785
slc31a2	SLC31A2	solute carrier	-4.5866616	2.22E-05
slc39a6	SLC39A6	solute carrier	-3.0884016	0.01131004
slc3a1	SLC3A1	solute carrier	-1.8613246	0.00928136
slc41a3	SLC41A3	solute carrier	-3.0250324	3.98E-06
LOC101470792	SLC4A7	solute carrier	-4.1857347	0.00073902
slc5a10	SLC5A10	solute carrier	-8.0648724	6.95E-11
LOC101475927	SLC6A12	solute carrier	-6.3299215	8.29E-07
LOC101464398	SLC6A12	solute carrier	-3.9106744	0.00083765
LOC101476219	SLC6A12	solute carrier	-3.5902035	0.00307234
LOC101471711	SLC6A13	solute carrier	-4.6238603	0.00015565
LOC101467277	SLC6A7	solute carrier	-5.373791	5.21E-05
slc7a11	SLC7A11	solute carrier	-3.6079526	0.00272135

LOC101468173	SLC7A11	solute carrier	-3.1446659	0.00376277
LOC101472120	SLC7A3	solute carrier	-3.6635354	0.0058829
slc7a5	SLC7A5	solute carrier	-7.6688578	3.91E-07
LOC101480678	SLC7A8	solute carrier	-3.1106923	0.00218254
LOC101474155	SLK	STE20-like kir	-4.0963577	5.05E-06
slx4	SLX4	SLX4 structur	-3.9548576	0.00049655
gypc	SMAGP	small cell adh	-4.4540857	8.14E-05
LOC101477562	SMCR8	Smith-Magen	-9.0312103	1.86E-10
smcr8	SMCR8	Smith-Magen	-5.2902213	2.06E-05
LOC101467774	SMTNL2	smoothelin-li	-8.3003513	3.37E-10
LOC101466871	SNAPC1	small nuclear	-4.8142017	5.98E-05
LOC101482807	SNRK	SNF related k	-5.6614758	7.78E-06
snrnp48	SNRNP48	small nuclear	-3.6261193	0.00586569
snrnp70	SNRNP70	small nuclear	-3.7175554	4.84E-07
snrpb	SNRPB	small nuclear	-2.7752725	0.01173731
snx29	snx29	sorting nexin	-4.9461109	4.16E-05
LOC101465854	SNX9	sorting nexin	-3.9125463	0.00262206
LOC101475426	SOAT2	sterol O-acylt	-6.1256938	3.59E-07
LOC101479828	SOLH	small optic lo	-4.5117883	4.71E-05
LOC101487636	SOWAHA	sosondowah	-3.2269997	0.00654729
LOC101479758	SOWAHC	sosondowah	-6.549878	1.47E-06
LOC101484987	SOX14	SRY (sex dete	-6.2891185	2.29E-06
sp8	SP8	Sp8 transcrip	-5.3727172	1.33E-05
LOC101483953	SPAG9	sperm associ	-5.5558598	8.57E-09
LOC101478750	SPATA13	spermatogen	-4.7348909	0.00011763
spen	SPEN	spen homolo	-3.2187006	0.00647591
LOC101464875	SPINT1	serine peptid	-7.2177273	2.71E-07
LOC101480474	SPIRE1	spire homolo	-4.3886384	0.00021781
LOC101476411	SRC	v-src sarcoma	-2.8704899	0.00423681
LOC101483482	SRRT	serrate RNA e	-3.2818596	0.00351123
ssbp3	SSBP3	single strand	-3.3191871	0.00353079
LOC101480440	SSC5D	scavenger rec	-10.253427	1.94E-14
ssfa2	SSFA2	sperm specifi	-3.4045764	0.00718209
LOC101468328	SST	somatostatin	-3.2088251	0.00235108
LOC101487446	SSUH2	ssu-2 homolo	-5.0203418	0.00021418
LOC101486466	SSX2IP	synovial sarcc	-5.6524522	3.23E-05
LOC101467249	ST14	suppression c	-5.8650982	9.23E-07
LOC101479765	ST14	suppression c	-5.5598124	2.55E-05
st14	ST14	suppression c	-4.9143486	7.33E-05
LOC101483776	ST3GAL1	ST3 beta-gala	-6.6451153	5.59E-08
LOC101484590	ST3GAL1	ST3 beta-gala	-3.2803336	0.00139602

LOC101482673	STARD10	StAR-related	-5.4465842	1.77E-05
strbp	STRBP	spermatid pe	-3.8053522	0.00031563
LOC101480117	STUB1	STIP1 homolo	-3.7363908	0.00081751
LOC101481205	STX11	syntaxin 11 [S	-5.4994525	2.23E-05
LOC101481496	STX11	syntaxin 11 [S	-3.955844	0.0001579
LOC101469074	STYK1	serine/threor	-4.3702229	0.0003394
LOC101476872	SULT1E1	sulfotransfer	-5.1083201	3.80E-05
svop	SVOP	SV2 related p	-2.1599656	0.00510645
swt1	SWT1	SWT1 RNA er	-5.0307414	9.63E-05
syce1	syce1	synaptonema	-5.6779535	1.58E-08
syce2	SYCE2	synaptonema	-3.0133401	0.00529606
sycp1	SYCP1	synaptonema	-11.230222	6.63E-13
syne2	syne2	spectrin repe	-5.8657577	3.17E-06
syt13	SYTL3	synaptotagm	-3.7896443	0.00072906
LOC101478311	SZRD1	SUZ RNA binc	-4.1213785	0.00019428
tab3	TAB3	TGF-beta acti	-3.8805601	0.00077126
taf1a	TAF1A	TATA box bin	-3.5876507	0.00221986
taf8	TAF8	TAF8 RNA po	-2.7513034	0.01117979
LOC101479713	TAGAP	T-cell activati	-2.9854389	0.00919744
tagln	TAGLN	transgelin [Sc	-3.5999481	0.00401979
tars	TARS	threonyl-tRN	-5.0388808	6.74E-05
LOC101471744	TAS2R10	taste recepto	-3.5255609	0.00281487
tbcd23	TBC1D23	TBC1 domain	-6.3506862	1.71E-06
LOC101470948	TBC1D3	TBC1 domain	-3.3557287	0.00073193
tbl3	TBL3	transducin (b	-5.9949374	4.42E-06
LOC101466192	TBPL2	TATA box bin	-3.2485681	0.00415004
tcp1	TCP1	t-complex 1 [-1.7510778	0.00664341
LOC106676806	TDP2	tyrosyl-DNA p	-4.275401	0.00021035
LOC106676723	TDP2	tyrosyl-DNA p	-3.3875091	0.01014497
LOC105940876	TDP2	tyrosyl-DNA p	-3.092498	0.00487912
tecr	TECR	trans-2,3-enc	-4.8800945	3.58E-05
tep1	TEP1	telomerase-a	-3.3004487	0.00144122
LOC101487114	TERF2	telomeric rep	-3.4848523	0.00062358
LOC101463758	TESC	tescalcin [Sou	-3.0177403	0.00419685
tex11	TEX11	testis express	-5.9939768	2.15E-07
tfap2a	TFAP2A	transcription	-3.6366885	0.00246618
tfap2c	TFAP2C	transcription	-4.3825396	0.00041345
tgfbra1	TGFBRAP1	transforming	-4.9348729	0.00019674
tgm1	TGM1	transglutamir	-9.8339195	2.53E-12
LOC101467439	THADA	thyroid adenc	-8.0497049	2.14E-08
thap7	THAP7	THAP domain	-5.9590407	5.22E-07

thegl	THEGL	theg spermat	-3.0692556	0.00714929
thoc6	THOC6	THO complex	-5.258521	1.86E-05
LOC101477439	THRSP	thyroid horm	-2.9336713	0.00625705
thumpd1	THUMPD1	THUMP doma	-2.8704657	0.01015302
LOC101479171	TIGD1	tigger transp	-9.0674295	8.64E-08
LOC101470325	TJP3	tight junction	-6.4080208	1.53E-06
tlcd1	TLCD1	TLC domain c	-6.8075543	8.05E-08
LOC101463793	TLR2	toll-like recep	-3.3701941	0.00186421
tlr5	TLR5	toll-like recep	-3.2618242	0.00676103
LOC101484470	TMCC1	transmembra	-3.4372212	0.00213283
tmed1	TMED1	transmembra	-5.7535087	6.49E-06
tmem100	TMEM100	transmembra	-4.5250681	0.00078894
LOC101471304	TMEM120B	transmembra	-3.8318327	0.00150808
tmem130	TMEM130	transmembra	-6.1076114	5.87E-06
LOC101475208	TMEM132B	transmembra	-6.8979683	1.54E-07
LOC101473348	TMEM138	transmembra	-4.7174234	0.00024655
tmem163	TMEM163	transmembra	-5.3608606	6.77E-07
LOC101477618	TMEM198	transmembra	-6.8422271	2.68E-06
tmem242	TMEM242	transmembra	-3.4487965	0.0039729
tmem41a	TMEM41A	transmembra	-3.4683205	0.00526917
tmem47	TMEM47	transmembra	-3.0205353	0.00447137
tmem57	TMEM57	transmembra	-4.4723374	0.00018201
tmem98	TMEM98	transmembra	-5.3286061	8.35E-05
tmpo	TMPO	thymopoietin	-3.3629885	0.00072412
LOC101476381	TMPRSS13	transmembra	-4.1834899	0.00026883
tmub1	TMUB1	transmembra	-3.2095074	0.00326335
LOC101482032	TNFRSF14	tumor necros	-3.155598	0.00144144
LOC101483010	TNFRSF14	tumor necros	-2.8424879	0.0059156
tnfrsf9	TNFRSF21	tumor necros	-3.986705	0.00023694
LOC101483661	TNIK	TRAF2 and NC	-3.954071	0.00210516
tnik	TNIK	TRAF2 and NC	-3.4185618	0.00425487
tnk1	TNK1	tyrosine kinas	-4.1663945	0.00305838
LOC101473061	TNKS	tankyrase, TR	-4.3990789	0.00025969
LOC101483156	TNKS1BP1	tankyrase 1 b	-12.004749	2.09E-14
LOC101474343	TNNT2	troponin T tyj	-3.5601533	3.20E-05
LOC101466571	TOX4	TOX high mol	-2.2967509	0.00694143
tp53i13	TP53I13	tumor proteii	-2.1644435	0.0107295
tp63	TP63	tumor proteii	-5.3810026	4.68E-06
tpcn2	TPCN2	two pore segl	-3.0989325	0.01086419
LOC101474423	TPM2	tropomyosin	-2.1035649	0.00717414
tpo	TPO	thyroid perox	-3.5585052	0.00272653

tppp3	TPPP3	tubulin polyr	-5.8344706	1.82E-05
LOC101474409	TPRG1	tumor protei	-3.9021325	0.00128213
traf6	TRAF6	TNF receptor	-6.6169675	4.44E-07
LOC101486755	TRAK1	trafficking pro	-3.3354028	0.00189117
LOC101477892	TRIM16	tripartite mol	-3.1082758	0.00838968
LOC106675019	TRIM16L	tripartite mol	-4.600399	8.28E-05
LOC101481150	TRIM16L	tripartite mol	-2.9140812	0.00614875
LOC101470747	TRIM25	tripartite mol	-4.7496493	0.00022082
LOC101478395	TRIM25	tripartite mol	-4.212656	0.00063494
LOC101481878	TRIM25	tripartite mol	-3.8012817	0.00063229
LOC106675640	TRIM25	tripartite mol	-3.7615395	0.00260266
LOC101474025	TRIM25	tripartite mol	-3.5952236	0.00461843
LOC101475981	TRIM25	tripartite mol	-2.1145315	0.00720895
LOC101475734	TRIM35	tripartite mol	-5.1591253	3.81E-06
LOC101486807	TRIM35	tripartite mol	-3.9314058	0.00048492
LOC101481313	TRIM35	tripartite mol	-3.7418402	0.00099485
LOC106676453	TRIM35	tripartite mol	-3.5957378	0.00046379
LOC106676210	TRIM35	tripartite mol	-3.4790936	0.00207198
LOC106676760	TRIM35	tripartite mol	-3.0567474	0.00271913
LOC105940560	TRIM35	tripartite mol	-2.8764932	0.00542456
LOC101478914	TRIM47	tripartite mol	-4.7773256	0.00013691
LOC101479812	TRIM47	tripartite mol	-4.5610114	8.43E-05
LOC106676001	TRIM47	tripartite mol	-4.3268877	0.00033284
LOC101476686	TRIM47	tripartite mol	-4.0159667	0.00092897
LOC106676036	TRIM47	tripartite mol	-2.9450951	0.00300086
LOC101473709	TRIM47	tripartite mol	-2.7855784	0.00296476
trip10	TRIP10	thyroid horm	-2.8442633	0.01076578
trmt2a	TRMT2A	tRNA methylt	-2.4603542	1.25E-05
LOC101472910	TRPM4	transient rece	-3.6686065	0.00225742
trpm5	TRPM5	transient rece	-3.0858328	4.03E-06
trpv4	TRPV4	transient rece	-3.9704053	0.00054384
tsc2	TSC2	tuberous scle	-2.4085494	0.00244274
tsen54	TSEN54	tRNA splicing	-3.2708123	0.00335743
LOC101476679	TSPAN16	tetraspanin 1	-3.6297027	0.00549369
LOC101468263	TSPAN8	tetraspanin 8	-4.520664	0.00020344
tssc1	TSSC1	tumor suppre	-2.8580946	0.00414315
ttc22	TTC22	tetratricopep	-4.1278427	0.00019673
ttc37	TTC37	tetratricopep	-3.6478609	0.00096098
LOC101475575	TUBA8	tubulin, alph	-6.8323936	1.13E-07
LOC101486701	TUBA8	tubulin, alph	-4.6412573	0.00181409
LOC101473957	TUBB2B	tubulin, beta	-3.4410742	0.00311332

tube1	TUBE1	tubulin, epsil	-3.0140359	0.00921825
tubg1	TUBG1	tubulin, gamr	-7.5967277	2.79E-08
tubgcp2	TUBGCP2	tubulin, gamr	-3.674204	0.00126721
LOC101481929	TXN	thioredoxin [S	-6.4392919	1.04E-06
LOC101483363	TXN	thioredoxin [S	-3.7871402	0.00225363
tyro3	TYRO3	TYRO3 protei	-3.340648	0.00409447
tyrp1	TYRP1	tyrosinase-re	-3.4733979	0.00289922
ubb	UBC	ubiquitin C [S	-3.2842063	0.00159703
LOC101476756	UBE2G1	ubiquitin-con	-5.7418994	1.29E-05
ube2o	UBE2O	ubiquitin-con	-3.9584285	0.0001667
LOC101470020	UBXN1	UBX domain p	-4.5662244	9.60E-05
LOC101484608	UCP3	uncoupling p	-3.5796744	0.00209168
ufd1l	UFD1L	ubiquitin fusi	-3.5216708	0.00441495
ugcg	UGCG	UDP-glucose	-4.1234718	6.43E-09
uhrf1bp1	UHRF1BP1	UHRF1 bindin	-3.1552122	0.00862097
uimc1	UIMC1	ubiquitin inte	-4.9189041	6.54E-05
usp11	USP11	ubiquitin spe	-4.6508136	6.02E-05
usp45	USP45	ubiquitin spe	-4.4633221	2.19E-05
LOC101472044	VARS	valyl-tRNA sy	-4.15285	0.00094742
vgll1	VGLL1	vestigial like 1	-4.1654102	0.00011726
vill	VILL	villin-like [So	-6.0223233	7.00E-07
LOC101472268	VLDLR	very low dens	-7.4567608	7.13E-08
vps33b	VPS33B	vacuolar prot	-5.4153418	3.92E-08
LOC101486893	VRK2	vaccinia relat	-2.0104784	0.00583387
vsig10	VSIG10	V-set and imr	-8.6986223	2.92E-11
LOC101464556	VSIG8	V-set and imr	-5.891542	6.97E-07
vsx1	VSX1	visual system	-5.011465	4.38E-07
LOC101467109	VTCN1	V-set domain	-7.2352428	1.49E-07
LOC101466475	VWA7	von Willebrar	-3.7383983	0.00295842
vwc2	VWC2	von Willebrar	-7.6078303	1.27E-08
LOC101477445	WBSCR27	Williams Beu	-6.8372476	3.10E-08
LOC101470374	WDR37	WD repeat dc	-2.4958868	0.00363142
LOC101469834	WDR55	WD repeat dc	-2.8159901	0.0067217
wdr77	WDR77	WD repeat dc	-3.1482235	0.00726419
whamm	WHAMM	WAS protein	-5.6628915	7.40E-06
wisp3	WISP3	WNT1 inducil	-3.2188575	0.00017336
LOC101479331	WNT4	wingless-type	-5.9373662	5.23E-06
LOC101472383	XIAP	X-linked inhi	-3.5219928	0.00257492
LOC106675839	XKR8	XK, Kell blood	-6.2962175	3.41E-07
xylb	XYLB	xylulokinase t	-3.7171082	0.00158908
LOC101471951	YWHAZ	tyrosine 3-mc	-3.8886181	4.63E-05

zbtb11	ZBTB11	zinc finger an	-4.9075571	3.12E-05
LOC101486737	ZBTB7B	zinc finger an	-5.7614022	1.58E-06
zbtb7c	ZBTB7C	zinc finger an	-2.7529555	0.00963784
LOC101477172	ZC3H12A	zinc finger CC	-3.9336856	0.00351798
zc3h12d	ZC3H12D	zinc finger CC	-4.2962965	0.00044222
zdhhc16	ZDHHC16	zinc finger, DI	-8.3768309	4.28E-09
zdhhc9	ZDHHC9	zinc finger, DI	-3.0366721	0.00551885
LOC101473384	ZFAND3	zinc finger, AI	-6.8434887	1.96E-07
LOC101487224	ZFP36	ZFP36 ring fir	-3.7388657	0.00508544
LOC106675584	ZFP41	ZFP41 zinc fin	-2.8552009	0.00755762
LOC101483436	ZFYVE16	zinc finger, FY	-5.0069029	3.17E-05
LOC101485417	ZNF101	zinc finger pro	-5.9692037	1.97E-06
LOC101463705	ZNF101	zinc finger pro	-3.4680623	0.00194079
LOC101480628	ZNF296	zinc finger pro	-8.617733	4.15E-11
znf367	ZNF367	zinc finger pro	-5.5448013	9.30E-06
LOC101471277	ZNF502	zinc finger pro	-5.6555559	1.28E-05
LOC101478196	ZNF502	zinc finger pro	-2.9605714	0.00125729
LOC101481343	ZNF576	zinc finger pro	-3.6514477	0.00041389
LOC101466793	ZNF609	zinc finger pro	-3.1810286	0.00390325
LOC101463744	ZNF654	zinc finger pro	-3.6118227	0.00930072
znf703	ZNF703	zinc finger pro	-3.5603488	0.00346158
LOC101472631	ZNF706	zinc finger pro	-4.3713522	0.00070763
znf750	ZNF750	zinc finger pro	-7.1371333	6.49E-08
LOC101481586	ZP3	zona pellucid	-3.6480263	1.89E-05
LOC101466359	ZP3	zona pellucid	-3.2473931	0.00433398
LOC101487026	ZP3	zona pellucid	-2.8923818	0.00596381
zzef1	ZZEF1	zinc finger, Zz	-2.504284	0.01031543

adj.P.Val

0.02297115
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1.85E-11
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5.18E-06
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3.63E-05
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