

SEQ_ID	Fold change	Log Fold of Absolute F-Regulation	Fold change Log Fold of Absolute F-Regulation	Fold change Log Fold of Absolute F-Regulation	Fold change Log Fold of Absolute F-Regulation	FC[log2] (Stable)	FC[log2] (AE-1)	FC[log2] (AE-3)	FC[log2] (AE-10)	GENE	SYNONYM	DESCRIPTION	NCBI	GENCHROMO	STRAND	START	STOP	GO	biological GO	cellular GO	molecular GO	UniGene	Dbid	TIGRID									
NM_03180	5.053987	2.337422	5.053987	8.482920	3.084558	8.482920	8.392629	5.069128	8.392629	6.035794	2.953453	6.035794	189.31242	956.7825	16059.9188	1588.8289	1425.6508	DKCZP541	MGC10500	hypochlorite	283846	chr18	-	11609741	11623796	GO:0008159	GO:0005778	GO:0006016	Ha.552700	gBd	A314	TICR1D	
NM_010935	5.020261	2.416533	5.020261	7.194262	2.826848	7.194262	7.542684	2.913467	7.542684	308.1064	2.913467	308.1064	209.12278	3.546571	2097.0261	2525.0251	4102.118	FNPA1	FB161ECL	ephrin-A1	1942	chr11	-	15336972	15374010	GO:0007226	GO:0005858	GO:0004687	Ha.516664	reFNM_004	THC24678		
NM_009295	5.130059	2.358974	5.130059	11.605559	3.536744	11.605559	9.255011	3.120346	9.255011	22.13182	4.668465	22.13182	27.47131	1409.2943	3188.199	2524.917	6081.684	LKOC53722	-	-	-	-	chr19	-	5683824	5684423	-	-	-	-	-	-	
NM_01925	5.179447	2.327298	5.179447	83.86752	3.900044	83.86752	72.62577	3.182047	72.62577	51.64661	1634.821	2472.457	21.41082	DEF4A	DEF4H	defensin, alpha 1	1669	chr2	-	-	-	-	-	-	6780574	6783196	GO:0006800	GO:0005575	GO:0004254	Ha.591391	reFNM_002	THC24718	
BC018523	5.1999545	2.378499	5.1999545	19.592552	4.292233	19.592552	25.329245	4.627232	25.329245	7.013664	2.8101683	7.013664	1883.807	9795.938	36909.445	47216.516	13212.605	LTF	GLG12H1F	lactoferrin	4057	chr2	-	40652162	40648140	GO:0006081	GO:0005575	GO:0004254	Ha.529517	reFNM_002	THC24851		
NM_133505	5.2028546	2.379035	5.2028546	34.860336	5.1235147	34.860336	39.959152	5.320454	39.959152	47.89806	5.5819954	47.89806	105.72747	550.08466	3685.0953	4224.7803	5064.1006	DCN	DSPG2	PG4	ecoron	1634	chr2	-	94002655	94009640	GO:0009888	GO:0005575	GO:0005511	Ha.156316	reFNM_001	THC25247	
NM_001005	5.2263603	2.388806	5.2263603	22.848629	4.5140357	22.848629	16.197774	4.027698	16.197774	9.757754	3.286549	9.757754	158.76872	8293.2653	3627.6477	2587.926	1549.2261	ATP1B1	ATP1B1	ATPase, Na/K	481	chr1	-	167342570	167368884	GO:0006081	GO:0005890	GO:0005575	Ha.291196	reFNM_001	THC25382		
NM_010935	5.2026261	2.416533	5.2026261	8.780781	3.1224575	8.780781	10.48613	3.2904104	10.48613	10.172728	3.546571	10.172728	240.79668	1374.368	2097.0261	2525.0251	4102.118	FNPA1	FB161ECL	ephrin-A1	1942	chr11	-	65390394	65397899	GO:0007226	GO:0005858	GO:0004687	Ha.516664	reFNM_016	THC15559		
NM_010018	5.3622456	2.422873	5.3622456	23.78455	4.571953	23.78455	16.29977	4.18087	16.29977	20.31058	4.343483	20.31058	30.98657	120.8205	7230.1836	5133.4277	6112.499	SCN11A	ATP2B4	ATPase, Na/K	6337	chr12	-	6326273	6354796	GO:0006081	GO:0005575	GO:0005523	Ha.591047	reFNM_001	THC25918		
NM_93461	5.49468	2.458055	5.49468	5.7801957	2.531184	5.7801957	6.847401	2.755566	6.847401	5.1561046	2.6622815	5.1561046	434.13446	2385.43	2509.3823	2972.6299	2238.4246	RLG1	GLG12585M	laminin	57139	chr19	-	11365744	11309957	GO:0007116	GO:0005662	GO:0005088	Ha.375142	enSTO	THC251173		
NM_050448	5.5001073	2.4589458	5.5001073	30.251492	4.9194833	30.251492	49.993004	6.364563	49.993004	27.046692	7.0757267	27.046692	128.30162	705.67267	3881.3152	6474.1836	3404.1634	HLC3	MJC1114	haplotaglin	3245	chr19	-	76044008	76052458	GO:0006500	GO:0005575	GO:0004254	Ha.513711	reFNM_005	THC26053		
AY327595	5.547538	2.4718475	5.547538	5.924253	2.566632	5.924253	8.356234	2.6062829	8.356234	1269.9286	7044.9766	7509.496	7523.378	10611.82	10611.82	10611.82	10611.82	CG127	FB127EM	myosin	418	chr2	-	153425222	153429282	GO:0005575	GO:0004254	Ha.579973	reFNM_002	THC24671			
BC104987	5.5692067	2.4774718	5.5692067	12.916048	3.647515	12.916048	5.706553	3.2512619	5.706553	10.16728	5.266728	12.72807	580.2012	521.1857	B4GAL1	B4GAL1	UDP-Galactase	933	chr20	-	-	-	-	-	47689599	47763667	GO:0005970	GO:01602	GO:0008377	Ha.370487	reFNM_004	THC24671	
BC098342	5.5747455	2.5217521	5.5747455	6.702051	2.578098	6.702051	8.127568	3.0228238	8.127568	11.03481	683.4987	1156.3528	1292.4212	1102.8944	1102.8944	1102.8944	1102.8944	CSDMG1	CSDMG1	cytosine synthase	4280	chr12	-	15345222	153429282	GO:00019752	GO:0005575	GO:0003377	Ha.89063	reFNM_005	THC24759		
BC021584	5.841166	2.56997	5.841166	8.583511	3.0623114	8.583511	9.64278	3.269492	9.64278	11.540425	3.2528425	11.540425	202.74951	1190.4237	7340.4067	8474.135	30301.451	MFAP4	-	-	-	-	chr1	-	19227569	19259284	GO:0007115	GO:0001512	GO:0003377	Ha.296049	reFNM_002	THC211437	
BC062415	5.874101	2.537047	5.874101	41.61852	5.3710896	41.61852	5.706553	3.2512619	5.706553	3.5355713	2.4156427	3.5355713	11.54866	681.0051	612.2913	662.5035	616.18695	N/A	N/A	Myosin sapie	N/A	chr14	-	23993419	239952779	-	-	-	-	-	-		
NM_100245	5.896833	2.559943	5.896833	5.1390064	2.4065113	5.1390064	5.282973	2.520226	5.282973	12.726988	777.4048	2306.738	2969.048	3082.6072	LITBP2	LITBP2	laminin	4053	chr2	-	-	-	-	-	-	4470638	4471887	GO:0000070	GO:0005575	GO:0005509	Ha.512776	reFNM_000	THC24811
NM_001296	5.910528	2.611510	5.910528	42.204933	5.3993397	42.204933	24.68008	4.622278	24.68008	6.537094	2.6683074	6.537094	46.80358	2835.5742	19449.547	11347.4407	2929.577	CEACAM6	CD66G	carcinoembryonic	1084	chr19	-	46992243	47007148	-	-	-	-	-	-		
BC098342	5.5747455	2.5217521	5.5747455	11.605559	3.536744	11.605559	9.255011	3.120346	9.255011	11.03481	683.4987	1156.3528	1292.4212	1102.8944	1102.8944	1102.8944	1102.8944	CSDMG1	CSDMG1	cytosine synthase	4280	chr12	-	15345222	153429282	GO:00019752	GO:0005575	GO:0003377	Ha.89063	reFNM_005	THC24759		
NM_007278	6.272283	2.650403	6.272283	15.415518	3.946315	15.415518	17.160553	4.110224	17.160553	212.4045	1334.8047	3277.9636	3640.0286	4473.594	FKBP9	ATP2C2	FK506	bind	11238	chr7	-	-	-	-	-	32962576	33013067	GO:0006458	GO:0003775	Ha.103934	reFNM_001	THC251319	
NM_02525	6.333117	2.6629157	6.333117	13.862817	3.7931485	13.862817	9.980825	4.176806	9.980825	6.981393	2.80515	6.981393	16.92781	1063.5121	2327.9648	3036.2727	1127.3763	CLA0A	Cor2E92C	actin	cor2	80776	chr16	-	3193974	31954736	-	-	-	-	-	-	
AK02438	6.3402376	2.6624537	6.3402376	7.5230184	2.9113116	7.5230184	8.980759	3.159423	8.980759	6.2480796	2.6517015	6.2480796	13.5252	833.9011	989.4665	1309.8064	826.5149	FLJ14327	-	-	-	-	chr1	-	80158915	80164449	-	-	-	-	-	-	
NM_00018	6.4326296	2.684806	6.4326296	17.679386	4.1439962	17.679386	18.85934	4.267554	18.85934	10.989832	3.579792	10.989832	40.43463	2595.157	7132.5808	7036.1166	4433.354	COL3A1	MGC9568	collagen, type	1295	chr3	-	100840413	100997848	GO:0006081	GO:0005575	GO:0005519	Ha.654548	reFNM_001	THC24720		
NM_001296	5.910528	2.611510	5.910528	56.182167	5.8120403	56.182167	36.949802	5.2760497	36.949802	36.949802	3.144237	36.949802	17.47623	839.0219	7611.895	5306.8516	4710.224	FN1	CG1CZP	fibronectin	1235	chr3	-	21593421	21600936	GO:0006095	GO:0005575	GO:0005020	Ha.654548	reFNM_005	THC24720		
NM_004435	6.601213	2.727361	6.601213	22.598763	5.0267455	22.598763	38.844537	5.279633	38.844537	37.7369	4.3028235	37.7369	18.7269	4.3028235	6637.207	7908.8286	4014.493	ELF3	EPF-1	ERT	7-E4-like	1999	chr1	-	200243695	200251756	GO:0006353	GO:0005653	GO:0000176	Ha.67928	reFNM_004	THC25523	
BC048333	6.6380895	2.729681	6.6380895	16.100217	4.0143747	16.100217	8.494577	3.086542	8.494577	11.1159	3.4801336	11.1159	8.494577	3.086542	8.494577	8.494577	8.494577	KIAA070A	ATP2C2	FK506	bind	11238	chr7	-	83959633	8305202	GO:0006081	GO:01602	GO:0000176	Ha.67928	reFNM_004	THC26496	
NM_123498	6.710685	2.746611	6.710685	10.401051	3.3786753	10.401051	12.157213	3.6037407	12.157213	27.100206	2.760232	27.100206	132.8199	314.123	1813.4666	1614.72	3599.447	N/A	N/A	Myosin sapie	N/A	chr21	-	41758354	41760885	-	-	-	-	-	-		
NM_00577	6.73734	2.7521791	6.73734	12.58744	3.852009	12.58744	10.137152	3.341804	10.137152	815.9848	5496.961	11782.093	10270.63	820.849	PRSS8	CAP1	PROS	protease	5652	chr16	-	-	-	-	-	31050256	31054662	GO:0006500	GO:0005575	GO:0004254	Ha.75799	reFNM_002	THC61592
NM_004435	6.601213	2.727361	6.601213	13.744004	3.782703	13.744004	10.73359	3.4240068	10.73359	15.420822	1043.4504	2122.8458	6004.684	1655.2079	810.275	810.275	810.275	HIT1	75635	immunoglobulin	3671	chr15	-	72253139	72256265	GO							

AL173101	-6.119443	-2.613401	6.119443	down	-9.489696	-3.246362	9.489696	down	-9.541381	-3.254198	9.541381	down	-10.00003	-3.321932	10.000026	down	4347.295	710.40686	458.1069	455.62534	434.72836	C21orf7	TAKIL	chromosom:6911	chr21	+	2942486	29470064	GO:000551:hs.222802	ref:NM_020THC61828	
XM_93159	-6.186644	-2.629157	6.186644	down	-11.41454	-3.512801	11.414543	down	-9.541708	-2.522083	9.541707	down	-7.402883	-2.888087	7.402883	down	1313.487	212.30391	115.06802	228.66019	177.42395	LOC643514	hypothetical:643514	chr8	+	10002766	10002747				
NM_13836	-6.276377	-2.649932	6.276377	down	-11.5046	-3.524139	11.504601	down	-7.347457	-2.877245	7.347456	down	-10.00002	-3.322623	10.000021	down	2227.4153	354.88887	193.61082	303.15457	221.62793	NRP2	hypothetical:47553	chr12	+	43188331	43564605	GO:000715:GO:000557:GO:000519:hs.505326	ref:NM_006THC251221		
NM_002346	-6.692009	-2.742439	6.692008	down	-8.152088	-3.027171	8.152088	down	-7.358062	-2.879926	7.358062	down	-6.52728	-2.706482	6.52728	down	1991.0325	297.52339	244.23857	270.9195	305.03247	LY9	CD229:SLA	lymphocyte:4063	chr2	+	15903251	15906469	GO:000715:GO:001602:GO:000367:hs.403857	ref:NM_002THC260375	
XM_93485	-6.890036	-2.784512	6.890036	down	-14.58177	-3.862766	14.58177	down	-11.224681	-3.679233	11.224675	down	-9.41295	-3.234647	9.41295	down	2026.3582	294.0998	139.28612	157.23189	215.27347	LY9	CD229:SLA	lymphocyte:4063	chr2	+	84911269	84961721			
BC062589	-6.941211	-2.795188	6.941211	down	-7.265337	-2.86103	7.265336	down	-7.124588	-2.832807	7.124588	down	-5.465092	-2.450246	5.465092	down	11661.9404	239.8631	229.16219	233.68936	304.65002	LY9	CD229:SLA	lymphocyte:4063	chr1	+	159059026	159064667	GO:000715:GO:001602:GO:000367:hs.403857	ref:NM_002THC260375	
XM_93414	-7.021789	-2.811839	7.021789	down	-7.540285	-2.914619	7.540284	down	-11.021269	-3.488859	11.022674	down	-6.198253	-2.631862	6.198253	down	1631.8488	161.19093	105.1609	100.81781	182.6077	KIAA0748	HSPC257	KIAA0748	9840	chr12	+	53629494	5363930		
BC085067	-7.292628	-2.866441	7.292628	down	-6.276096	-2.650005	6.276096	down	-7.512347	-2.909264	7.512346	down	-7.71396	-2.947272	7.713959	down	4777.2285	655.07575	671.1056	635.61993	619.29625	C7orf7	TAKIL	chromosom:6911	chr21	+	29424676	29497499			
NM_13836	-7.786442	-2.869964	7.786442	down	-6.35867	-2.668725	6.358669	down	-5.867333	-2.527705	5.867332	down	-5.233062	-2.387655	5.233062	down	3097.3176	397.78345	487.1015	57.80197	591.8749	CD2345	colicoid:490799	chr7	+	59933619	59964526	GO:000551:hs.569713	ref:NM_001THC402281		
BC072140	-7.842644	-2.971734	7.842644	down	-11.48244	-4.564306	11.48244	down	-18.04891	-4.17672	18.04974	down	-32.289579	-5.017925	32.285053	down	7126.6793	908.711	161.42409	394.0673	220.74294	UNQ470	CAA1470	375704	chr7	+	3451104	34513027			
BC027920	-7.863331	-2.975141	7.863331	down	-6.237559	-2.640982	6.2375593	down	-5.838262	-2.455539	5.838261	down	-5.345279	-2.418265	5.345279	down	2220.777	282.4194	356.8302	380.3827	415.46515	LY9	CD229:SLA	lymphocyte:4063	chr1	+	15903261	159064667	GO:000715:GO:001602:GO:000367:hs.403857	ref:NM_002THC260375	
BC038996	-8.122065	-3.037745	8.122065	down	-8.16998	-3.029804	8.169988	down	-10.57849	-3.403062	10.578494	down	-9.816098	-3.310748	9.816098	down	1317.6743	160.4559	161.3415	124.56162	133.62349	AK5	AK6:MGK3	adenylate:ki:26289	chr1	+	77520874	77797007	GO:000613:GO:000573:GO:000178:hs.559718	ref:NM_1474THC248432	
NM_085151	-10.74784	-3.425974	10.747836	down	-8.720418	-3.124397	8.720418	down	-5.104356	-2.351729	5.104356	down	-7.382225	-2.884056	7.382224	down	1156.867	107.6372	132.66188	226.64308	156.70981	YPLM1	C14orf170:YLP	motif:c6252	chr14	+	74299827	74372853	GO:0008159:GO:000557:GO:000367:hs.531111	gb:BC0235THC275442	
NM_01455	-16.80003	-4.07198	16.800032	down	-21.7658	-4.443991	21.7658	down	-32.03665	-5.001681	32.036648	down	-14.88979	-3.890252	14.889792	down	4558.0938	283.46298	209.41559	142.27748	386.12207	TF1PCL1	CRTR1:LB	transcription:29842	chr4	-	121695003	121759245	GO:000012:GO:000563:GO:000370:hs.156471	ref:NM_014THC215106	
NM_01016	-21.03073	-3.944427	21.030733	down	-27.92748	-4.803614	27.927485	down	-18.68745	-4.222998	18.687447	down	-18.59982	-3.810522	18.599817	down	4255.381	201.39006	151.66537	226.64308	227.71089	SCP2	DKFZ:26868	steroid:camer6342	chr1	+	53165555	53232492	GO:000669:GO:000573:GO:000549:hs.476365	ref:NM_002THC269388	

1313.487	212.30391	115.06802	228.66019	177.42395	LOC643514	hypothetical:643514	chr8	+	10002766	10002747				
2227.4153	354.88887	193.61082	303.15457	221.62793	NRP2	hypothetical:47553	chr12	+	43188331	43564605	GO:000715:GO:000557:GO:000519:hs.505326	ref:NM_006THC251221		
1991.0325	297.52339	244.23857	270.9195	305.03247	LY9	CD229:SLA	lymphocyte:4063	chr2	+	15903251	15906469	GO:000715:GO:001602:GO:000367:hs.403857	ref:NM_002THC260375	
2026.3582	294.0998	139.28612	157.23189	215.27347	LY9	CD229:SLA	lymphocyte:129293	chr2	+	84911269	84961721			
11661.9404	239.8631	229.16219	233.68936	304.65002	LY9	CD229:SLA	lymphocyte:4063	chr1	+	159059026	159064667	GO:000715:GO:001602:GO:000367:hs.403857	ref:NM_002THC260375	
1631.8488	161.19093	105.1609	100.81781	182.6077	KIAA0748	HSPC257	KIAA0748	9840	chr12	+	53629494	5363930		
4777.2285	655.07575	671.1056	635.61993	619.29625	C7orf7	TAKIL	chromosom:6911	chr21	+	29424676	29497499			
3097.3176	397.78345	487.1015	57.80197	591.8749	CD2345	colicoid:490799	chr7	+	59933619	59964526	GO:000551:hs.569713	ref:NM_001THC402281		
7126.6793	908.711	161.42409	394.0673	220.74294	UNQ470	CAA1470	375704	chr7	+	3451104	34513027			
2220.777	282.4194	356.8302	380.3827	415.46515	LY9	CD229:SLA	lymphocyte:4063	chr1	+	15903261	159064667	GO:000715:GO:001602:GO:000367:hs.403857	ref:NM_002THC260375	
1317.6743	160.4559	161.3415	124.56162	133.62349	AK5	AK6:MGK3	adenylate:ki:26289	chr1	+	77520874	77797007	GO:000613:GO:000573:GO:000178:hs.559718	ref:NM_1474THC248432	
1156.867	107.6372	132.66188	226.64308	156.70981	YPLM1	C14orf170:YLP	motif:c6252	chr14	+	74299827	74372853	GO:0008159:GO:000557:GO:000367:hs.531111	gb:BC0235THC275442	
4558.0938	283.46298	209.41559	142.27748	386.12207	TF1PCL1	CRTR1:LB	transcription:29842	chr4	-	121695003	121759245	GO:000012:GO:000563:GO:000370:hs.156471	ref:NM_014THC215106	
4255.381	201.39006	151.66537	226.64308	227.71089	SCP2	DKFZ:26868	steroid:camer6342	chr1	+	53165555	53232492	GO:000669:GO:000573:GO:000549:hs.476365	ref:NM_002THC269388	

(AE-1 vs Con) (AE-1 vs Stable) (AE-3 vs Con) (AE-3 vs Stable) (AE-10 vs Con) (AE-10 vs Stable) (AE-10 vs 8P) GENE\_N/SYNONY/DESCRIP NCBI\_GE CHROMSTART

SEQ_ID	Fold chnq	Log Fold	Absolute FRegulation	Fold chnq	Log Fold	Absolute FRegulation	Fold chnq	Log Fold	Absolute FRegulation	Fold chnq	Log Fold	Absolute FRegulation	Fold chnq	Log Fold	Absolute FRegulation	Fold chnq	Log Fold	Absolute FRegulation	Fold chnq	Log Fold	Absolute FRegulation	Con PBM	Stable PBM	AE-1 PBM	AE-3 PBM	AE-10 8P PBM	GENE_N/SYNONY/DESCRIP	NCBI_GE	CHROMSTART						
AB191261	12.0543	3.591476	12.0543	up	6.931292	2.793124	6.931292	up	11.74042	3.553412	11.74042	up	6.758088	2.75506	6.758088	up	10.1716	3.364475	10.1716	up	5.84873	2.548123	5.84873	up	253.8776	441.5218	3060.316	2980.629	2582.342	FN1	CIG/DKZF2	fibronectin:2335	chr2	2.16E+08	
AX7289814	12.64951	3.66101	12.64951	up	12.97689	3.697873	12.97689	up	20.04907	4.325643	20.04907	up	20.56796	3.462327	20.56796	up	9.831717	3.297443	9.831717	up	10.08617	3.334307	10.08617	up	550.0894	536.2117	6958.362	11028.78	5408.323	ALPL	AP-TNAP1	alkaline ph:249	chr7	21708465	
BC004940	19.274201	4.777788	19.274201	up	28.56771	4.836313	28.56771	up	33.53661	5.067665	33.53661	up	34.92505	3.12619	34.92505	up	13.19787	3.722233	13.19787	up	13.74427	3.780758	13.74427	up	709.8009	681.583	19471.26	23804.32	9367.857	CEAC	c-fos	v-fos	FBJ:1253	chr14	74815312
BC005008	19.12746	4.257573	19.12746	up	12.47856	3.874391	12.47856	up	12.47856	3.874391	12.47856	up	5.678633	3.258197	5.678633	up	8.446976	2.695252	8.446976	up	6.746761	2.695252	6.746761	up	40.1248	62.1863	9183.566	591.265	4055.603	CEACAM	CD66c	CEACAM:66c	carcinoem:4680	chr19	44951346
BC005322	8.366265	3.064584	8.366265	up	21.15465	4.402903	21.15465	up	9.203319	3.202154	9.203319	up	23.2712	4.540474	23.2712	up	10.46855	3.879899	10.46855	up	26.47041	4.726308	26.47041	up	495.6132	196.0128	4146.582	4561.452	5188.537	DCN	DSPG2PG	decorin:1634	chr12	90063644	
BC007628	29.69084	4.891946	29.69084	up	8.770476	3.132655	8.770476	up	34.44355	5.106162	34.44355	up	10.1744	3.346871	10.1744	up	6.13455	3.575306	6.13455	up	10.6739	3.416106	10.6739	up	116.26119	134.5263	3423.449	3971.412	4166.428	KRT19	CK19	K19	keratin:19	chr17	36933395
BC007695	7.101755	2.828176	7.101755	up	7.540242	2.821112	7.540242	up	9.336472	3.222878	9.336472	up	7.54653	2.915813	7.54653	up	6.785271	2.762406	6.785271	up	5.844432	2.455													

BC004490	27.43201	4.777788	27.43201	up	28.56771	4.836313	28.56771	up	33.53661	5.067665	33.53661	up	34.92505	5.12619	34.92505	up	13.19787	3.722233	13.19787	up	13.74427	3.780758	13.74427	up	709.8009	681.583	19471.26	23804.32	9367.857	FOS	c-fos	v-fos	FBI	r2353	chr14	74815312
AB042648	-2.27021	-1.18283	2.270213	down	-3.40858	-1.76917	3.408584	down	-2.13113	-1.09162	2.131131	down	-1.19976	-1.67796	3.199761	down	-2.08251	-1.05832	2.082505	down	-1.12675	-1.64466	3.126752	down	611.453	918.0587	269.3372	286.9147	293.6142	MYO1B	DKFZP434myosin	XV	84700	chr22	24495993	
AF072385	-4.30153	-2.10485	4.30153	down	-2.41748	-1.2735	2.417481	down	-3.67128	-1.87628	3.671276	down	-2.06328	-1.04494	2.063275	down	-3.64245	-1.86491	3.642451	down	-2.04708	-1.03356	2.047075	down	515.1675	289.5266	119.7638	140.3238	141.4343	KIR2DL8	HDMCPH	chromosome	283600	chr14	99859431	
AF002258	-2.12843	-1.17848	2.263388	down	-2.09308	-1.06563	2.09308	down	-2.60304	-1.3802	2.603044	down	-2.53811	-1.34375	2.53811	down	-2.90006	-1.56008	2.900099	down	-2.82772	-1.49366	2.827717	down	1617.851	1577.944	760.1166	621.523	557.8685	KIR4DL4	103A51	killer	cell	r3805	chr10	60090922
AF074087	-3.0983	-1.63147	3.098295	down	-2.48749	-1.31469	2.487485	down	-4.79671	-2.26205	4.796712	down	-3.85107	-1.94526	3.851069	down	-2.64845	-1.40515	2.648447	down	-2.12632	-1.08836	2.126322	down	1678.65	1347.715	541.7982	349.9586	633.8245	KIR2DS2	183ACT1	killer	cell	r3807	chr19	rand721465
AF929086	-2.26339	-1.17848	2.263388	down	-2.09308	-1.06563	2.09308	down	-5.05448	-2.33756	5.05448	down	-4.67416	-2.22471	4.674155	down	-3.32307	-1.73252	3.323071	down	-3.07303	-1.61966	3.073027	down	2701.184	1915.338	915.0813	409.772	623.2741	SLA2	C20orf156	Src-like	ad	84174	chr20	34675682
AF924278	-3.45213	-1.78429	3.452131	down	-6.52236	-2.70539	6.522363	down	-2.85623	-1.51411	2.856232	down	-5.39649	-2.43202	5.396487	down	-2.09048	-1.06384	2.090481	down	-3.9497	-1.98174	3.949699	down	560.9077	1059.764	162.4816	196.3803	268.3511	PRDM16	KIAA1675	Prc domain	63976	chr1	2975620	
AF320053	-2.28872	-1.19454	2.28872	down	-2.14865	-1.10343	2.148653	down	-2.64802	-1.40491	2.648016	down	-2.48596	-1.3138	2.485965	down	-3.18266	-1.67023	3.182663	down	-2.98788	-1.57912	2.987882	down	62.50703	402.3416	187.253	161.8458	134.6578	MYCN	MODED1	Nr-myc	myc	4613	chr2	15998136
AF367023	-3.72848	-1.89859	3.728477	down	-2.44498	-1.23982	2.444979	down	-3.13334	-1.63846	3.133336	down	-2.0416	-1.0297	2.041596	down	-3.06304	-1.61496	3.063039	down	-2.00861	-1.0062	2.008613	down	379.2629	248.484	101.6305	121.7019	123.7095	KCNIP3	CSEEN1	Kv channel	30818	chr2	95329136	
AF646521	-3.21799	-1.21287	2.317984	down	-3.33105	-1.73598	3.331046	down	-2.35737	-1.23497	2.357366	down	-3.38246	-1.75807	3.382464	down	-2.1042	-1.14432	2.104149	down	-2.11767	-1.06742	2.117667	down	1668.677	2397.961	719.8823	708.399	754.9144	FAM71B	MGC269R6	family	153745	chr5	1.57E+08	
AJ002102	-3.71957	-1.89513	3.719565	down	-3.82965	-1.93721	3.829654	down	-7.40683	-2.88886	7.406831	down	-7.62605	-2.93094	7.626052	down	-4.23646	-2.08286	4.236462	down	-4.36185	-2.12494	4.361849	down	1355.273	1395.385	364.3632	182.9761	319.9067	KIR2DS2	183ACT1	killer	cell	r3807	chr19	rand164628
AJ002104	-3.71957	-1.89513	3.719565	down	-3.82965	-1.93721	3.829654	down	-7.40683	-2.88886	7.406831	down	-7.62605	-2.93094	7.626052	down	-4.23646	-2.08286	4.236462	down	-4.36185	-2.12494	4.361849	down	831.2791	797.4266	358.8875	223.046	310.4958	KIR2DS2	183ACT1	killer	cell	r3807	chr19	rand164628
AJ421515	-25.3616	-4.66457	25.3616	up	-4.54459	-1.88443	4.544589	down	-12.4696	-3.64034	12.469578	down	-2.23445	-1.15992	2.234446	down	-11.9072	-3.57377	11.90723	down	-2.13368	-1.09304	2.133677	down	513.8294	956.7823	210.5322	428.1968	448.4195	TRTAC1	ASPIC1	Cartilage	a	55118	chr10	90629401
AK000262	-3.12871	-1.64557	3.12871	down	-3.00774	-1.58845	3.007741	down	-3.29717	-1.72123	3.297171	down	-3.16969	-1.66434	3.169688	down	-2.291	-1.19598	2.290998	down	-2.20242	-1.13939	2.202419	down	95.52938	915.0281	304.2244	288.6808	415.4652	MTM1	OM14FLJ00001	transmem	protein	113178	chr19	21954521
AK026367	-3.14972	-1.65522	3.149716	down	-2.61595	-1.40705	2.615945	down	-2.91653	-1.54426	2.916535	down	-2.45562	-1.29608	2.455615	down	-3.44457	-1.78432	3.444567	down	-2.9002	-1.5365	2.900199	down	541.7061	456.9662	171.9857	185.7362	157.2639	N/A	N/A	Homo sapi	N/A	chrY	Y	
AK074586	-2.73972	-1.45403	2.739719	down	-2.30367	-1.20393	2.303668	down	-2.75698	-1.46309	2.75698	down	-2.31818	-1.12129	2.318182	down	-2.6511	-1.40659	2.651104	down	-2.22916	-1.1565	2.229157	down	520.1008	774.4226	336.1694	334.0647	347.4061	SCAMP4	FLJ33847	secretory	protein	113178	chr19	11856570
AK091878	-6.26776	-2.64795	6.267757	down	-2.13082	-1.09141	2.130824	down	-7.1578	-2.83952	7.157802	down	-2.43341	-1.28298	2.433409	down	-10.5356	-3.39721	10.53564	down	-3.58176	-1.84067	3.581759	down	1612.649	548.246	257.2929	225.2995	153.0661	LOC123874	923A4	1,11	hypothetic	123876	chr16	20394189
AK097866	-2.4492	-1.29231	2.449197	down	-2.57334	-1.36364	2.573343	down	-3.10072	-1.63562	3.100722	down	-3.88757	-2.03413	3.887572	down	-4.30377	-2.10547	4.303774	down	-4.30377	-2.10547	4.303774	down	743.3167	584.3455	230.2041	239.2231	149.8188	N/A	N/A	Homo sapi	N/A	chr1	54381652	
AK122760	-3.22895	-1.69106	3.228946	down	-2.53838	-1.34391	2.53838	down	-3.10721	-1.63562	3.107212	down	-2.44268	-1.28847	2.44268	down	-4.96144	-2.31076	4.961437	down	-3.90035	-1.9636	3.900347	down	743.3167	584.3455	230.2041	239.2231	149.8188	N/A	N/A	Homo sapi	N/A	chr1	54381652	
AK124690	-2.04036	-1.02883	2.040363	down	-2.66624	-1.41481	2.666245	down	-3.10721	-1.63562	3.107212	down	-2.71898	-1.44307	2.718984	down	-2.31326	-1.20993	2.313263	down	-3.02285	-1.59591	3.022851	down	59.7703	490.0353	199.5328	143.4259	155.4441	N/A	N/A	Homo sapi	N/A	chr3	1.36E+08	
AK126846	-2.90564	-1.52886	2.905638	down	-2.45591	-1.29626	2.455913	down	-4.0423	-2.01518	4.042298	down	-3.41664	-1.77258	3.416645	down	-3.72977	-1.89909	3.729767	down	-3.15249	-1.65649	3.152486	down	45.81539	5394.662	2069.694	1944.429	1984.604	N/A	N/A	Homo sapi	N/A	chr7	77555509	
AK126997	-2.18319	-1.12644	2.183192	down	-2.0665	-1.38212	2.066503	down	-2.32384	-1.21651	2.323839	down	-2.77442	-1.47219	2.77442	down	-2.2768	-1.18701	2.276976	down	-2.71826	-1.44268	2.718256	down	62.86251	466.0561	198.7176	178.1543	209.6147	N/A	N/A	Homo sapi	N/A	chr9	87325324	
AK127390	-2.43517	-1.28402	2.43517	down	-2.34532	-1.22978	2.345319	down	-2.71625	-1.44162	2.716248	down	-2.61603	-1.38738	2.616026	down	-2.30857	-1.207	2.308574	down	-2.22339	-1.15276	2.223394	down	346.5911	496.7902	119.8809	160.8999	164.6979	N/A	N/A	Homo sapi	N/A	chr3	52071149	
AK127904	-3.02511	-1.59699	3.025108	down	-4.58614	-2.19728	4.586139	down	-2.2529	-1.17422	2.252902	down	-3.41697	-1.77272	3.416971	down	-2.20193	-1.13877	2.201926	down	-3.33817	-1.73906	3.338174	down	682.9326	957.2303	215.3326	237.4556	162.2483	N/A	N/A	Homo sapi	N/A	chr12	64353993	
AK128072	-2.20923	-1.14355	2.209235	down	-2.68065	-1.42258	2.680645	down	-2.00341	-1.00246	2.003407	down	-2.44309	-1.28149	2.443098	down	-2.93205	-1.55191	2.932051	down	-3.5577	-1.83094	3.557697	down	10.7492	57.2303	215.3326	237.4556	162.2483	N/A	N/A	Homo sapi	N/A	chr12	64353993	
AK130913	-2.97954	-1.57509	2.979536	down	-2.49586	-1.31953	2.495855	down	-2.98149	-1.54432	2.981468	down	-2.44149	-1.28776	2.441493	down	-3.38279	-1.72834	3.382789	down	-2.83365	-1.52066	2.833647	down	47.50081	879.0302	352.196	360.038	310.2117	N/A	N/A	Homo sapi	N/A	chr8	1.46E+08	
AK131481	-2.64532	-1.40344	2.645323	down	-3.95819	-1.98484	3.958193	down	-3.18947	-1.67332	3.189472	down	-4.7724	-2.25472	4.772401	down	-3.68313	-1.88093	3.68313	down	-5.51106	-2.46233	5.511063	down	564.1364	844.1165	213.2581	178.6746	153.1677	G3orf2	DKFZP43	chromosome	84077	chr3	14691651	
AK172756	-2.01668	-1.01198	2.016682	down	-2.04966	-1.03538	2.04966	down	-2.32616	-1.21795	2.326163	down	-2.3642	-1.24135	2.364202	down	-3.4448	-1.78442	3.444803	down	-3.50113	-1.80782	3.501132	down	442.1628	449.3925	219.2527	190.0825	128.3566	GLDN	COMO	CO	glomiosin	342035	chr5	49421168
AY758752	-2.39774	-1.26167	2.397736	down	-2.60005	-1.37854	2.600055	down	-2.23401	-1.15964	2.234014	down	-2.42822	-1.27651	2.428218	down	-2.11244	-1.09489	2.112435	down	-2.29608	-1														





NM_0154-2.12958	-1.09057	2.129575	down	-2.147	-1.10233	2.147005	down	-2.26518	-1.19139	2.283719	down	-2.28372	-1.25619	2.381205	down	-2.40069	-1.26345	2.400694	down	502.684	506.7982	236.0489	221.9179	211.1049	CC2orf28	DKFZFP343:chromosom 25876	chr20	3760150	
NM_01554-2.34156	-1.42247	2.341562	down	-2.38093	-1.25153	2.380933	down	-3.07195	-1.61916	3.071951	down	-3.1236	-1.64321	3.123603	down	-2.84638	-1.50913	2.846379	down	639.736	650.5204	273.2208	208.2596	224.764	AC00711	BTBT/IFTT acyl-CoA 126027	chr1	54766488	
NM_01673-2.9655	-1.56828	2.965502	down	-2.01628	-1.10117	2.016284	down	-4.02826	-2.01016	4.028264	down	-2.73887	-1.45388	2.738869	down	-3.407	-1.7685	3.407	down	110.0273	642.7051	169.9687	125.1265	147.9432	PAC5	BSAP paired box 5079	chr9	36828350	
NM_01855-4.44697	-2.15282	4.446972	down	-2.53747	-1.34339	2.537471	down	-6.99485	-2.80629	6.994845	down	-3.9913	-1.74568	3.991304	down	-4.32221	-2.11147	4.322209	down	504.6475	365.9302	262.4421	166.8476	270.0177	SLC16A10	PROOR0813 solute carri 117427	chr6	1.12E+08	
NM_02190-2.42952	-1.28067	2.42952	down	-2.40832	-1.26802	2.408316	down	-2.98226	-1.57675	2.982965	down	-2.95693	-1.5641	2.956933	down	-2.2139	-1.14659	2.213903	down	1060.362	1051.2207	436.4987	355.5128	479.0102	SDMK2	FLJ10832 sidekick h. 54549	chr17	68845460	
NM_02192-2.27426	-1.1854	2.274264	down	-2.42557	-1.27832	2.425569	down	-2.15622	-1.1085	2.15622	down	-2.29967	-1.20143	2.299671	down	-2.1937	-1.11679	2.19371	down	226.126	241.1806	994.3258	1048.761	1028.185	HAMP	HEPC/HFE hepcidin ai 57817	chr19	408465249	
NM_02202-2.42164	-1.27598	2.421637	down	-2.32235	-1.21558	2.322347	down	-2.3355	-1.22373	2.335499	down	-2.23974	-1.16333	2.239741	down	-2.71867	-1.4429	2.718671	down	462.8627	827.4935	356.3177	369.4594	317.3875	PADP2A	PAP-2 pappalysin 60676	chr19	1.75E+08	
NM_03095-2.21941	-1.15018	2.219414	down	-2.63131	-1.39578	2.631311	down	-3.35448	-1.74609	3.354475	down	-3.97703	-1.99169	3.977025	down	-2.60773	-1.38279	2.607729	down	809.3671	532.6919	202.4436	133.9423	172.2979	ADAMTS	ADAM-TS ADAM h. 81794	chr19	8.55E+15	
NM_03391-4.83029	-2.07211	4.830294	down	-4.98916	-2.3188	4.989164	down	-9.83225	-3.29754	9.832348	down	-10.1557	-3.34422	10.15574	down	-3.02997	-1.5993	3.02997	down	5363.468	4559.874	1110.381	545.4921	1770.139	KSP37	Ksp37-pro 83888	chr4	15570963	
NM_03292-2.10301	-1.27245	2.103008	down	-2.4922	-1.31742	2.492202	down	-2.9012	-1.53665	2.901204	down	-3.43812	-1.78162	3.438116	down	-2.7835	-1.4769	2.783502	down	2996.053	3550.518	1424.651	1032.693	1076.361	SLA2	CC2orf156 Src-like-adt 84174	chr20	34674335	
NM_03312-2.25738	-1.17465	2.257376	down	-2.07746	-1.05482	2.077456	down	-2.68768	-1.42636	2.687683	down	-2.47347	-1.30653	2.473467	down	-3.17952	-1.66881	3.179518	down	737.7606	678.9591	326.8223	274.4969	232.0354	SCRT2	scrat h. 85508	chr20	590239	
NM_05328-2.30053	-1.7227	3.300533	down	-2.90813	-1.32661	2.908126	down	-2.96184	-1.56649	2.961838	down	-2.25075	-1.1704	2.250746	down	-2.99302	-1.5816	2.993017	down	22.7744	492.6343	196.4153	218.876	216.596	ODF3	CK6C CK6C keratin C. 140446	chr11	186760	
NM_05824-2.17617	-1.12179	2.176165	down	-2.82097	-1.49619	2.820969	down	-2.73761	-1.45292	2.737611	down	-2.61498	-1.3368	2.614978	down	-2.61498	-1.3368	2.614978	down	2573.205	3335.651	1182.448	939.945	984.0247	KRT6C	CK6C CK6C keratin C. 140446	chr11	51167243	
NM_13345-2.15468	-1.10747	2.15468	down	-2.19835	-1.13642	2.198352	down	-2.30775	-1.20262	2.307745	down	-2.35452	-1.23543	2.354519	down	-2.52268	-1.33496	2.522683	down	257.346	2405.126	1094.059	1021.493	934.4597	KRMI2	EM15 EM15 keratin 129800	chr22	27931952	
NM_13841-2.71525	-1.44109	2.715251	down	-3.00317	-1.58648	3.003167	down	-3.78884	-1.92175	3.788835	down	-4.19059	-2.06715	4.19059	down	-2.17034	-1.11792	2.17034	down	786.2566	869.6285	289.5705	207.5194	362.2735	CTUBH5	FLJ3472 chromosom 112817	chr10	99334107	
NM_13916-2.07113	-1.05042	2.07113	down	-2.34791	-1.23138	2.347909	down	-3.34032	-1.73999	3.340319	down	-2.43279	-1.92094	3.786709	down	-2.43279	-1.92094	3.786709	down	634.874	719.7167	306.5352	190.0639	260.9649	KRIB1	PUSA	Trub p5ub 142940	chr10	1.17E+08
NM_14715-2.61011	-1.38411	2.610116	down	-2.43978	-1.28075	2.439776	down	-3.58502	-1.84198	3.585018	down	-3.35107	-1.74462	3.351068	down	-2.62155	-1.39042	2.62155	down	785.127	733.8913	300.8027	219.0022	299.4896	TMIE	DNB6 transmem 259236	chr3	4671826	
NM_14896-2.62856	-2.64813	6.268561	down	-3.40161	-1.76622	3.401611	down	-3.95929	-1.98524	3.959291	down	-2.14849	-1.1033	1.48494	down	-3.99133	-1.99687	3.991329	down	2895.161	1571.048	461.8542	731.2322	725.3627	NLRF2A2	APP-3 DDB tumor necr 8718	chr1	6443797	
NM_15327-2.40262	-1.25461	2.402623	down	-3.09286	-1.62894	3.092862	down	-2.1432	-1.09977	2.143202	down	-2.75891	-1.4641	2.758913	down	-2.47129	-1.30526	2.47129	down	42.4713	543.8413	175.8376	172.1216	107.1717	KRHS2	FLJ38753 kelch dom 127707	chr1	18680452	
NM_15327-3.18917	-1.67318	3.189173	down	-2.79522	-1.48296	2.795216	down	-2.37894	-1.25032	2.378936	down	-2.08507	-1.06009	2.085067	down	-2.37364	-1.45293	2.373643	down	1504.348	1318.517	471.7048	332.3181	549.505	RP11-450F	MGC1256 thymosin 257240	chrX	21583529	
NM_15372-4.8727	-2.16584	4.87271	down	-3.04427	-1.6061	3.044268	down	-3.23554	-1.69401	3.235539	down	-2.19506	-1.13426	2.195064	down	-3.49436	-1.80503	3.494364	down	1596.226	1082.917	355.7232	493.3417	456.8003	VM142	MGC1266 vitellin form 26675	chr1	45021845	
NM_15366-2.08346	-1.05898	2.083458	down	-2.22303	-1.15253	2.223026	down	-2.03279	-1.18261	2.032785	down	-2.59575	-1.37615	2.595755	down	-2.23732	-1.16177	2.237322	down	791.2333	844.237	379.7693	325.2376	353.652	MYOC	MYOC myocardin 93649	chr17	12510230	
NM_15376-2.00747	-1.05308	2.007469	down	-3.40221	-1.76647	3.402209	down	-4.02574	-1.02555	2.057376	down	-3.45012	-1.07624	3.450115	down	-3.5735	-1.83734	3.573499	down	300.588	509.877	149.8696	147.7886	142.6858	RTYD	MGC354 receptor trk 13212	chr3	1.88E+08	
NM_17208-2.43712	-1.28517	2.437116	down	-2.31076	-1.20837	2.310762	down	-2.19132	-1.1318	2.191318	down	-2.07771	-1.05499	2.07708	down	-2.88747	-1.52981	2.88747	down	620.2306	588.0744	254.4937	283.04	214.8007	CAMK2B	CAM2C calcium mol 916	chr7	44225415	
NM_17211-12.7067	-3.66752	12.70671	down	-4.64383	-2.21532	4.643832	down	-23.4509	-4.55157	23.45086	down	-8.57042	-3.09937	8.570421	down	-7.07824	-3.28339	7.078241	down	3610.962	1319.673	284.1776	153.98	510.1497	CSDB	CDB2 CDB8 mol 926	chr2	86959970	
NM_17211-16.7673	-4.06758	16.76727	down	-6.36995	-2.67128	6.369953	down	-13.0408	-3.70496	13.04076	down	-4.95424	-2.30866	4.954239	down	-6.7835	-2.76203	6.783504	down	4202.895	1596.697	250.6607	322.2891	619.5758	CSDB	CDB18 CDB8 mol 926	chr2	86960022	
NM_17368-9.51829	-3.2507	9.518293	down	-2.53221	-1.34057	2.532508	down	-12.5777	-3.6528	12.5777	down	-3.34653	-1.74267	3.346531	down	-7.84843	-3.12902	8.478432	down	1376.339	366.2007	144.6001	109.427	157.3241	OTOP2	otopetropin 2 92736	chr7	1.5E+08	
NM_17375-3.13878	-1.6502	3.138778	down	-3.10573	-1.63493	3.105726	down	-2.05662	-1.04027	2.056618	down	-2.03496	-1.025	2.034962	down	-2.40295	-1.2648	2.402946	down	782.9844	774.6509	249.4267	380.6711	325.8063	VSIG9	DKFZFP57-V set and 2101633	chr3	1.15E+08	
NM_17816-2.36658	-1.42481	2.366584	down	-2.30336	-1.20374	2.303355	down	-2.11103	-1.07975	2.111033	down	-2.05463	-1.03888	2.054632	down	-2.68468	-1.42475	2.68468	down	2.417234	417.3167	181.1778	203.102	159.1708	OTOP2	otopetropin 2 92736	chr7	70431964	
NM_18251-2.78381	-1.47706	2.783808	down	-2.25768	-1.17484	2.257684	down	-2.66139	-1.44218	2.661394	down	-2.15841	-1.10997	2.158405	down	-4.1911	-2.06733	4.1911	down	567.3245	640.1032	203.7944	213.1681	135.3641	FLJ32252	-	hypothetic 146336	chr16	1054093
NM_18262-2.56659	-1.35985	2.566598	down	-2.01712	-1.0123	2.01712	down	-3.56531	-1.8088	3.565309	down	-2.75346	-1.46125	2.75346	down	-2.76188	-1.46565	2.761878	down	125.4665	989.942	490.7702	359.5267	456.0683	MGC5249	PRO171	hypothetic 348378	chr1	52871653
NM_18262-4.27224	-1.30582	4.272243	down	-2.63948	-1.40025	2.639476	down	-2.26578	-1.18001	2.265778	down	-2.41905	-1.27444	2.419047	down	-2.56969	-1.3616	2.569691	down	534.835	571.0135	216.336	236.0489	208.132	SLC6A18	FLJ12032 solute carri 348932	chr5	1278469	
NM_1944-2.90679	-1.53943	2.906791	down	-4.14164	-2.0502	4.141639	down	-3.83712	-1.94002	3.837116	down	-5.46718	-2.4508	5.467181	down	-3.68949	-1.88342	3.689486	down	52.5684	682.0287	164.676	124.7496	129.7413	LOC28549	MGC1266 vitellin form 26675	chr4	10525286	
NM_19807-2.9212	-1.54656	2.921203	down	-2.28141	-1.18993	2.281415	down	-2.83104	-1.50133	2.831042																			

XM_93227-2.1246	-1.08719	2.124599	down	-2.28349	-1.19124	2.28349	down	-2.23315	-1.15908	2.233152	down	-2.40016	-1.26313	2.400161	down	-2.07863	-1.05563	2.078631	down	-2.23408	-1.15968	2.234084	down	34935.43	37548.12	16443.31	15644	16806.95	LOC64463-	hypothetical:644635	chr12	54687343	
XM_93254-3.15358	-1.65699	3.15358	down	-2.45269	-1.29437	2.452693	down	-2.84256	-1.50719	2.842555	down	-2.21079	-1.14456	2.210793	down	-2.80899	-1.49005	2.80899	down	-2.18469	-1.12743	2.184688	down	439.2017	341.5885	139.2708	154.5095	156.3558	LOC65224-	similar to t653247	chr12	11435747	
XM_93255-2.75097	-1.45994	2.750975	down	-2.2287	-1.1562	2.2287	down	-2.70413	-1.45493	2.704147	down	-2.22096	-1.15119	2.220965	down	-2.99251	-1.58136	2.992509	down	-2.42438	-1.27762	2.424379	down	507.9933	411.5503	184.6594	185.3025	169.755	LOC64497-	hypothetical:644978	chr16	65471762	
XM_93255-5.65355	-2.49916	5.65355	down	-3.10746	-1.63574	3.107463	down	-4.54509	-2.17021	4.545087	down	-2.47391	-1.30679	2.473905	down	-4.28369	-2.09886	4.283693	down	-2.35452	-1.23544	2.354524	down	1530.203	841.0731	270.6623	339.9779	357.2157	LOC64502-	hypothetical:645023	chr17	1205967	
XM_93282-2.13332	-1.0931	2.133324	down	-2.31412	-1.21046	2.314119	down	-2.534	-1.34141	2.533996	down	-2.74875	-1.45877	2.748748	down	-2.22661	-1.13485	2.226613	down	-2.41531	-1.27221	2.415314	down	316.864	343.7177	148.5307	125.0452	142.3076	FBFI	FBFI-IFL Fas (TNFR 85302)	chr17	71433523	
XM_93282-2.75469	-1.46189	2.754685	down	-3.24688	-1.69905	3.246882	down	-2.67509	-1.41499	2.675091	down	-3.15307	-1.65676	3.153066	down	-2.52221	-1.15479	2.522211	down	-2.97287	-1.57186	2.972868	down	1391.962	1640.673	505.3073	520.342	551.8821	LOC64534-	hypothetical:645346	chr16	69029991	
XM_93282-2.27668	-1.18693	2.27668	down	-2.42878	-1.28023	2.428778	down	-2.2188	-1.14978	2.218797	down	-2.36703	-1.24308	2.367027	down	-2.84234	-1.50708	2.842342	down	-3.03223	-1.60038	3.03223	down	334.8268	357.1954	147.068	150.9407	117.7996	LOC64536-	hypothetical:645361	chr20	56186973	
XM_93282-3.61272	-1.85308	3.612718	down	-2.48047	-1.31061	2.48047	down	-4.93013	-2.30163	4.931332	down	-3.385	-1.75916	3.384999	down	-3.35067	-1.74748	3.350668	down	-2.30055	-1.20198	2.300548	down	727.8488	499.7366	201.4685	147.6327	217.225	LOC64541-	hypothetical:645411	chr18	75651000	
XM_93293-3.24373	-1.69766	3.243734	down	-3.10246	-1.63341	3.102464	down	-2.87504	-1.52528	2.875037	down	-2.74982	-1.45934	2.749824	down	-2.50003	-1.32194	2.500026	down	-2.39115	-1.2577	2.391146	down	813.7828	778.341	250.8784	283.0512	325.5907	LOC64557-	hypothetical:645574	chr22	17923032	
XM_93293-2.02118	-1.0152	2.021184	down	-2.53469	-1.34181	2.534692	down	-2.10361	-1.07027	2.10361	down	-2.62806	-1.39948	2.638059	down	-2.05113	-1.03642	2.05113	down	-2.57225	-1.36303	2.572246	down	549.9589	689.673	272.0934	261.432	268.1209	LOC65657-	hypothetical:645654	chr22	21852407	
XM_93342-2.46985	-1.30443	2.469853	down	-2.88042	-1.52628	2.880424	down	-2.24538	-1.16696	2.24538	down	-2.61864	-1.38882	2.618637	down	-2.03797	-1.02713	2.037967	down	-2.37675	-1.24899	2.376745	down	1124.939	1311.941	455.4678	501.0014	551.9905	LOC64613-	hypothetical:646130	chr11	33806897	
XM_93342-2.26882	-1.18194	2.26882	down	-2.21247	-1.14566	2.212469	down	-2.21684	-1.1485	2.216835	down	-2.16178	-1.11222	2.161776	down	-2.83566	-1.50369	2.835663	down	-2.76523	-1.4674	2.765234	down	946.7885	923.2731	417.3043	427.0901	333.8861	LOC64619-	hypothetical:646191	chr1	22472748	
XM_93347-3.40279	-1.76672	3.40279	down	-2.19126	-1.13176	2.191264	down	-4.26643	-2.09303	4.266432	down	-2.74742	-1.45808	2.747416	down	-3.38177	-1.75778	3.381773	down	-2.17773	-1.12283	2.17773	down	774.8968	499.0034	227.724	181.6264	269.1392	LOC64622-	hypothetical:646220	chr18	13207064	
XM_93378-2.35757	-1.23753	2.357569	down	-2.12754	-1.08919	2.127543	down	-2.79193	-1.48126	2.791925	down	-2.51952	-1.33315	2.51952	down	-2.47984	-1.31025	2.479842	down	-2.23789	-1.16214	2.237887	down	900.9075	813.0069	382.1341	322.6832	363.2922	LOC64662-	hypothetical:646632	chr2	2.22E+08	
XM_93386-6.48942	-2.69809	6.48942	down	-2.45807	-1.29752	2.458066	down	-5.92747	-2.56742	5.927473	down	-2.24521	-1.16685	2.245211	down	-9.19894	-3.20147	9.198939	down	-3.48438	-1.8009	3.484379	down	5483.29	2076.963	844.9583	925.0637	596.0785	LOC64666-	hypothetical:646663	chr2	1.48E+08	
XM_93406-2.76522	-1.46729	2.765218	down	-3.58676	-1.84268	3.586769	down	-2.39233	-1.25842	2.392331	down	-3.10309	-1.63731	3.103089	down	-2.09806	-1.06905	2.098057	down	-2.72139	-1.44434	2.721386	down	1973.948	2560.404	713.8489	825.1147	940.8457	LOC64452-	similar to t644529	chr9	1.27E+08	
XM_93412-2.36012	-1.23886	2.36012	down	-2.01925	-1.01832	2.019253	down	-3.01494	-1.59213	3.014938	down	-2.57949	-1.36709	2.579492	down	-2.38903	-1.25642	2.38903	down	-2.04938	-1.03138	2.049384	down	707.6205	605.4193	299.8234	334.7040	296.1958	GLYCAMA7	glycosylat:644076	chr12	55288243	
Y13054	-2.22808	-1.1558	2.228081	down	-2.52031	-1.3336	2.520311	down	-3.0233	-1.59612	3.023295	down	-3.41982	-1.77392	3.419824	down	-3.12407	-1.64343	3.124068	down	-3.53381	-1.82123	3.533814	down	681.6298	771.0309	305.9269	225.4592	218.1866	KIR2DL4	103AS15:killer cell t:805	chr19	60006918

SEQ_ID	Fold chang	Log Fold c	Absolute F	Regulation	Fold chang	Log Fold c	Absolute F	Regulation	Fold chang	Log Fold c	Absolute F	Regulation	Fold chang	Log Fold c	Absolute F	Regulation	Fold chang	Log Fold c	Absolute F	Regulation	Fold chang	Log Fold c	Absolute F	Regulation	Con	PBM	SB	AE-1	PBM	AE-10	8P	GENE	N/SYNONY	DESCRIP	NCLB	GE	CHROM	START
AJ002102	-3.71957	-1.89513	3.719565	down	-3.82965	-1.93721	3.829654	down	-7.40683	-3.88886	7.406831	down	-7.62605	-3.93904	7.626052	down	-4.23646	-2.02826	4.236462	down	-4.36185	-2.12494	4.361849	down	1355.273	1395.385	364.3632	182.9761	319.9067	KIR2DS3	183ACT1	killer cell c:807	chr19	rand	164628			
BC022407	-3.00703	-1.58834	3.007033	down	-3.66055	-1.87206	3.660546	down	-4.83658	-2.37399	4.836576	down	-5.8877	-2.5577	5.887699	down	-3.11696	-1.64014	3.116962	down	-3.79437	-1.92386	3.794365	down	1477.991	1799.163	491.5013	305.58	474.1671	SH2D1B	EAT2	SH2 domain	117157	chr1	1.61E+08			
BC066595	-3.57574	-1.83824	3.575743	down	-3.21577	-1.68517	3.215773	down	-9.9349	-3.3125	9.934986	down	-8.93475	-3.15943	8.934752	down	-3.57512	-1.83799	3.575125	down	-3.21522	-1.68492	3.215218	down	1423.849	1640.242	510.0617	183.5801	510.1497	SH2D1B	EAT2	SH2 domain	117157	chr1	1.61E+08			
BC100911	-1.12134	-3.48716	1.121345	down	-4.39859	-2.13704	4.398593	down	-15.6994	-3.99724	15.96944	down	-6.26418	-2.64713	6.264182	down	-7.89679	-2.98127	7.896788	down	-3.0976	-1.63115	3.097599	down	4300.045	1686.738	383.4722	269.2671	544.5309	CD8B	CD8B IL4 CD8b mole:926	chr2	86896190					
NM_00100	-3.65066	-1.87029	3.650663	down	-3.13065	-1.64466	3.130652	down	-4.68644	-2.22664	4.680437	down	-4.0781	-2.00282	4.07814	down	-3.67105	-1.87619	3.671048	down	-3.14348	-1.65236	3.143485	down	4700.465	321.7626	294.4315	229.9133	293.2295	OR2WS1	olfactory r:41932	chr1	2.46E+08					
NM_00491	-10.3033	-3.36503	10.30326	down	-5.28368	-2.40154	5.283679	down	-11.4902	-3.52233	11.49018	down	-5.89235	-2.55884	5.892348	down	-6.55496	-2.71259	6.554957	down	-3.36149	-1.7499	3.361487	down	5385.584	2761.814	522.7066	468.7119	821.6047	CD8B	CD8B IL4 CD8b mole:926	chr2	86922219					
NM_03194	-4.83029	-2.27211	4.830294	down	-4.98916	-2.3188	4.989164	down	-9.83235	-3.29754	9.832348	down	-10.1557	-3.34422	10.15574	down	-2.38903	-1.59923	2.389027	down	-3.12963	-1.69459	3.129626	down	5365.548	6539.874	1110.381	545.4921	170.1339	KSP37	Ksp37	chr8	88888	chr4	15570963			
NM_20161	-15.5828	-3.96189	15.58283	down	-5.55081	-2.4727	5.550806	down	-30.3645	-4.92432	30.36454	down	-10.8162	-3.43513	10.81624	down	-8.92242	-3.15744	8.922422	down	-3.17828	-1.66825	3.178282	down	14506.31	5167.336	930.9164	477.7387	1625.827	TCF7	MGC4773:transcript:6932	chr5	1.33E+08					

SEQ_ID	Fold chang	Log Fold c	Absolute F	Regulation	Fold chang	Log Fold c	Absolute F	Regulation	[AE-1] (norm)	[AE-3] (norm)	[AE-10] (norm)	GENE	NA	SYNONYM	DESCRIP	NCLB	GENE	CHROM	STRAND	START	STOP	GO	biologi	GO	cellular	GO	molecul	UniGene	Dbid	TIGRID	EnsemblID
XM_940804	-2.09598	-1.06894	2.095982	down	-2.02463	-1.01894	2.02463	down	5092.4067	2832.6348	1397.8221	WDR112	+	WAS protein:40253	chr15	+	2678.2969	68283543													
XM_92857	-2.017128	-1.012302	2.0171278	down	-2.584037	-1.369627	2.5840372	down	10108.737	5011.451	1939.3881	LOC64555-	+	hypothetical:645550	chr4	+	7411.345	7416216													
BC069310	-2.047157	-1.033622	2.047157	down	-2.141696	-1.098754	2.1416964	down	2749.0254	1342.8503	627.0031	GYPB	+	GYPB CD235G/glycophorin 29A	chr8	+	145136760	145159940													
NM_00051	-2.053443	-1.03804																													

SEQ_ID	Fold change	Log Fold c	Absolute F	Regulation	Fold change	Log Fold c	Absolute F	Regulation	[AE-1]nor	[AE-3]nor	[AE-10]nor	GENE_NA	SYNONYM	DESCRIPTION	INCHI	GENE	CHROM	STRAND	START	STOP	GO biologi	GO cellular	GO molecu	UniGene	Dbid	TIGRID	Ensembl
NM_023126	-1.003792	-1.022345	1.003792	down	1.022345	1.003792	1.003792	down	1.022345	1.003792	1.003792	MM28		509180128	65018543	MM28	chr17	42377142	42377142	GO:0005737	GO:0005737	GO:0005737	U14633	ref:NM_023126	ref:G14633	ref:ENST00000338389	
BC020584	-2.007327	-1.003508	2.007327	down	2.007327	1.003508	2.007327	up	2.007327	1.003508	2.007327	CD9		2929.4002	1957.5294	5298.784	CD9	MIC2	MIC2	GO:0007154	GO:0005737	GO:0005118	G54534	ref:NM_002128	ref:G54534	ref:ENST00000338192	
AL113657	-2.012777	-1.009187	2.012778	down	2.012778	1.009187	2.012778	up	2.012778	1.009187	2.012778	P1P8		279.509	138.86736	291.6413	P1P8	ANN1	P1P8	GO:0007264	GO:0005058	GO:0005058	Hs.500197	ref:NM_006126	ref:G50058	ref:ENST00000225441	
AY093698	-2.022516	-1.016151	2.022516	down	2.022516	1.016151	2.022516	up	2.022516	1.016151	2.022516	CD28		805.2233	420.37894	1049.9675	CD28	MGC13829	CD28	GO:0006959	GO:0005588	GO:0001502	Hs.591629	ref:NM_006126	ref:G55829	ref:ENST00000331640	
BT775289	-2.022681	-1.016269	2.022681	down	2.022681	1.016269	2.022681	up	2.022681	1.016269	2.022681	PRMT1		8691.964	4297.249	11264.491	PRMT1	ANN1	PRMT1	GO:0001770	GO:0005653	GO:0005051	Hs.20521	ref:NM_198931	ref:G20521	ref:ENST00000326130	
AK131309	-2.030921	-1.022134	2.030926	down	2.030926	1.022134	2.030926	up	2.030926	1.022134	2.030926	ZSCAN2A		501.29095	246.82942	1070.169	ZSCAN2A	FLJ20595	zinc finger s45993	GO:0006351	GO:0005652	GO:0003708	Hs.594223	ref:NM_017324	ref:G59423	ref:ENST00000334141	
NM_000732	-2.031943	-1.022844	2.031943	down	2.031943	1.022844	2.031943	up	2.031943	1.022844	2.031943	CD247		38085.7183	2098.6528	95701.71	CD247	CD3-ZETA	CD247	GO:0008818	GO:0005573	GO:0004883	Hs.156445	ref:NM_198718	ref:G15645	ref:ENST00000336719	
NM_031954	-2.035589	-1.025425	2.035588	down	2.035588	1.025425	2.035588	up	2.035588	1.025425	2.035588	KSP37		1110.812	545.49207	578.1927	KSP37		Ksp37	GO:0003888				ref:NM_031954	ref:G38888	ref:ENST00000382324	
BC006063	-2.060292	-1.042849	2.060291	down	2.060291	1.042849	2.060291	up	2.060291	1.042849	2.060291	ZNF549		363.8042	176.56654	466.47098	ZNF549	FLJ34917	zinc finger p25601	GO:0006350	GO:0005652	GO:0003678	Hs.564295	ref:NM_153718	ref:G56429	ref:ENST00000240719	
NM_000544	-2.064993	-1.046093	2.064993	down	2.064993	1.046093	2.064993	up	2.064993	1.046093	2.064993	TNF53		812.82684	397.99255	1343.2498	TNF53	FLS1	JTRPS_tumor protein1751	GO:0006228	GO:0005652	GO:0007073	Hs.654481	ref:NM_000544	ref:G65448	ref:ENST00000269305	
NM_148414	-2.064933	-1.046093	2.064932	down	2.064932	1.046093	2.064932	up	2.064932	1.046093	2.064932	ATXN2L		2680.2505	1297.9843	3609.96	ATXN2L	A2D	ADZL	GO:0008151	GO:0005557	GO:0003667	Hs.460499	ref:NM_145N	ref:P080567	ref:ENST00000336783	
XM_933159	-2.065621	-1.046576	2.065621	down	2.065621	1.046576	2.065621	up	2.065621	1.046576	2.065621	FLJ14352		930.7989	450.61456	1029.4928	FLJ14352	FLJ14352	FLJ14352	GO:0001511	GO:0001511	GO:0001511	Hs.370937	ref:NM_172N	ref:P186276	ref:ENST00000374562	
BC080574	-2.071888	-1.059646	2.071881	down	2.071881	1.059646	2.071881	up	2.071881	1.059646	2.071881	TAPPB		4872.4946	2352.1957	8048.6025	TAPPB	NCG517TAT	bindin9692	GO:0006351	GO:0005653	GO:0003678	Hs.555947	ref:NM_016268	ref:G55947	ref:ENST00000265165	
NM_016268	-2.074857	-1.058312	2.074859	down	2.074859	1.058312	2.074859	up	2.074859	1.058312	2.074859	L66		708.8237	341.62534	804.5166	L66	DKFZ	S5860	lymphoblastoid cell line	GO:0006351	GO:0005653	GO:0003678	Hs.555947	ref:NM_016268	ref:G55947	ref:ENST00000265165
XI3890	-2.084304	-1.059566	2.084309	down	2.084309	1.059566	2.084309	up	2.084309	1.059566	2.084309	P0UP2		151.5631	7209.05066	3034.6174	P0UP2	GO:0008077	P0UP2	GO:0008077	GO:0005653	GO:0003678	Hs.525403	ref:NM_016268	ref:G55947	ref:ENST00000369477	
NM_017900	-2.088881	-1.06273	2.088881	down	2.088881	1.06273	2.088881	up	2.088881	1.06273	2.088881	TPCN1		407.14484	194.91049	405.8492	TPCN1	FLJ20612	two pore seq s5323	GO:0006351	GO:0001602	GO:0005244	Hs.524763	ref:NM_017900	ref:G52476	ref:ENST00000335509	
NM_016424	-2.089448	-1.063144	2.089497	down	2.089497	1.063144	2.089497	up	2.089497	1.063144	2.089497	ZNF219		216.10718	199.14392	865.337	ZNF219	ZFP219		GO:0006351	GO:0005653	GO:0003708	Hs.250493	ref:NM_016268	ref:G55947	ref:ENST00000369477	
NM_006754	-2.089497	-1.063156	2.089499	down	2.089499	1.063156	2.089499	up	2.089499	1.063156	2.089499	SURF5		460.51825	220.39671	592.3665	SURF5	MED22	ME surfeit 5	GO:0006351	GO:0005653	GO:0003678	Hs.6837	ref:NM_006754	ref:G6837	ref:ENST00000344469	
XM_931811	-2.091201	-1.064532	2.091209	down	2.091209	1.064532	2.091209	up	2.091209	1.064532	2.091209	LAC3795		247.21564	118.22468	282.5906	LAC3795		hypothetical:63795	GO:0008151	GO:0000011	GO:0003667	Hs.78354	ref:NM_016268	ref:G55947	ref:ENST00000344469	
BC031091	-2.092121	-1.064966	2.092129	down	2.092129	1.064966	2.092129	up	2.092129	1.064966	2.092129	GATAD1		226.1271	408.10661	256.81152	GATAD1	FLJ22489	GATA zinc finger 57998	GO:0006351	GO:0005653	GO:0003708	Hs.21145	ref:NM_016268	ref:G55947	ref:ENST00000287957	
NM_20784	-2.099672	-1.070164	2.099671	down	2.099671	1.070164	2.099671	up	2.099671	1.070164	2.099671	ENSA		886.20335	422.17096	852.61926	ENSA	MGC4319	endosomal protein	GO:0006351	GO:0005653	GO:0003678	Hs.632456	ref:NM_20784	ref:G63245	ref:ENST00000356527	
AJ22585	-2.119954	-1.084033	2.119954	down	2.119954	1.084033	2.119954	up	2.119954	1.084033	2.119954	EDG		384.7761	181.50209	209.2509	EDG	collagen-like	EDG2	GO:0001501	GO:0005605	GO:0001602	Hs.146735	ref:NM_089N	ref:P243138	ref:ENST00000338788	
NM_001002	-2.119991	-1.084058	2.119996	down	2.119996	1.084058	2.119996	up	2.119996	1.084058	2.119996	RP3-377H1		542.5135	255.90373	564.638	RP3-377H1	FLJ35429	hypothetical:28830	GO:0006351	GO:0001602	GO:0005653	Hs.655949	ref:NM_001002	ref:G65594	ref:ENST00000326012	
NM_929621	-2.122268	-1.085607	2.122268	down	2.122268	1.085607	2.122268	up	2.122268	1.085607	2.122268	EEF2		2495.8945	1176.0508	3031.3833	EEF2	EEF2	similar to ac646675	GO:0006351	GO:0005653	GO:0001602	Hs.515070	ref:NM_929621	ref:G51507	ref:ENST00000309311	
NM_001961	-2.125424	-1.08775	2.125427	down	2.125427	1.08775	2.125427	up	2.125427	1.08775	2.125427	EEF2		13524.476	6504.339	15292.803	EEF2	EEF2	eukaryotic t1938	GO:0006351	GO:0005653	GO:0005454	Hs.655333	ref:NM_001961	ref:G65533	ref:ENST00000228245	
NM_003324	-2.126116	-1.08822	2.126117	down	2.126117	1.08822	2.126117	up	2.126117	1.08822	2.126117	TPX2		491.68526	231.24718	822.34094	TPX2	ABC18A	kinetochore protein 26991	GO:0006351	GO:0005653	GO:0001602	Hs.50216	ref:NM_003324	ref:G50216	ref:ENST00000348977	
BC088854	-2.12946	-1.090488	2.129459	down	2.129459	1.090488	2.129459	up	2.129459	1.090488	2.129459	Clor2		497.60474	474.9977	1200.6333	Clor2	COTE1	cytochrome	GO:0006351	GO:0001602	GO:0003678	Hs.348308	ref:NM_003324	ref:G50216	ref:ENST00000361361	
NM_016661	-2.133663	-1.093332	2.133663	down	2.133663	1.093332	2.133663	up	2.133663	1.093332	2.133663	ARMXC3		304.52174	142.59596	296.36774	ARMXC3	ALEX3	ARMADILLO 3	GO:0006351	GO:0001602	GO:0005488	Hs.592225	ref:NM_016661	ref:G59225	ref:ENST00000341189	
AF119912	-2.138092	-1.096324	2.138092	down	2.138092	1.096324	2.138092	up	2.138092	1.096324	2.138092	N/A		2.3274452	1.218742	272.9358	N/A	N/A	Homo sapiens	GO:0006351	GO:0001602	GO:0005488	Hs.592225	ref:NM_016661	ref:G59225	ref:ENST00000341189	
AF466365	-2.141767	-1.098802	2.141767	down	2.141767	1.098802	2.141767	up	2.141767	1.098802	2.141767	MGC22014		834.11664	389.45255	903.93665	MGC22014	KIAA001	hypothetical:20024	GO:0006351	GO:0001602	GO:0005488	Hs.516107	ref:NM_016661	ref:G59225	ref:ENST00000341189	
NM_021972	-2.146671	-1.102665	2.146674	down	2.146674	1.102665	2.146674	up	2.146674	1.102665	2.146674	RELA		5.2530579	1701.7965	3.2530579	RELA	MGC13177	v-rel	GO:0006351	GO:0005653	GO:0003708	Hs.502875	ref:NM_021972	ref:G50287	ref:ENST00000308546	
BC002751	-2.1498	-1.104202	2.149798	down	2.149798	1.104202	2.149798	up	2.149798	1.104202	2.149798	TAP2		1294.1632	601.99243	1510.625	TAP2	ABC18A	kinetochore protein 26991	GO:0006351	GO:0005653	GO:0001602	Hs.50216	ref:NM_003324	ref:G50216	ref:ENST00000348977	
NM_002594	-2.158444	-1.109992	2.158443	down	2.158443	1.109992	2.158443	up	2.158443	1.109992	2.158443	PDE2A		216.41919	100.29999	207.9192	PDE2A	PDE2A	phosphodiesterase 2	GO:0006351	GO:0001602	GO:0003678	Hs.501163	ref:NM_002594	ref:G50116	ref:ENST00000334546	
NM_001011	-2.160076	-1.111082	2.160076	down	2.160076	1.111082	2.160076	up	2.160076	1.111082	2.160076	Gcom1		419.90652	194.39433	785.4945	Gcom1	FLJ30973	GRRINL1	GO:0006351	GO:0001602</						

BC013694	-2.826939	-1.499241	2.826939	down	3.2857369	1.7162169	3.2857369	up	4980.513	1761.8042	5788.825	P1BP1	HNRNPIH/poly(rimmin)5725	chr19	+	748478	762012	GO:000639	GO:000563	GO:00016	Hs.172550	ref:NM_002THC250052	ENST00000349038		
AK126599	-2.840814	-1.506304	2.8408137	down	4.5866613	2.1974444	4.5866613	up	445.05896	156.6632	718.56104	N/A	N/A	N/A	chr11	-	65147801	65149679							
AK123234	-2.86621	-1.571351	2.8662097	down	5.590797	2.4830514	5.590797	up	1591.444	3805.2485	21274.534	N/A	N/A	N/A	chr19	+	2996155	2996176							
NC110493	-2.881887	-1.527014	2.881887	down	2.765786	1.4676896	2.765786	up	3365.599	1167.7626	3229.718	MLXP	KIAA0867/MLX intera:2877	chr12	+	12117743	12119232	GO:004544	GO:000563	GO:003052	Hs.437153	ref:NM_014THC257876	ENST00000377037		
BC011971	-2.904925	-1.538501	2.9049247	down	2.4929599	1.3178597	2.4929599	up	596.9862	205.50832	512.324	AGPAT3	LPAAAT-GA1-acylglycerol:5684	chr21	+	44109569	44226862	GO:000815	GO:000557	GO:000384	Hs.248785	ref:NM_002THC246289	ENST00000358148		
UT7394	-2.912095	-1.542057	2.9120951	down	3.0655391	1.6161408	3.0655391	up	359.8534	123.57369	378.81998	KIR2DL4	103AS1:5.2.killer cell c1 3805	chr19	+	6006096	60017780	GO:000696	GO:000588	GO:000487	Hs.661219	ref:NM_002NP365687	ENST00000359085		
AY207007	-2.950101	-1.56072	2.9501013	down	4.126347	2.0448651	4.126347	up	584.6982	198.20209	817.85606	GCOM	FLJ30973/GRRIN.L1A c1 48571	chr15	+	55671522	55794235								
BC013009	-2.973775	-1.572296	2.9737755	down	3.1886917	1.679466	3.1886917	up	582.834	195.99126	624.55727	ZMYM3	DXS6073E/zinc finger_19203	chrX	-	70387579	70391148	GO:000727	GO:000563	GO:000367	Hs.522684	ref:NM_005THC248049	ENST00000314425		
NM_01612	-2.975538	-1.573151	2.9755381	down	4.111949	2.0395585	4.111949	up	1486.2148	499.47766	205.451	AKT2	PKBETA/1b-akt similar:208	chr19	+	4491455	4548336	GO:000646	GO:003002	GO:00016	Hs.631535	ref:NM_001THC252515	ENST00000311278		
AK054965	-2.991778	-1.585103	2.9917784	down	4.111949	2.0395585	4.111949	up	475.32324	158.87953	607.52774	N/A	N/A	chr19	+	56786847	56789442								
NM_00716	-2.995047	-1.582579	2.9950469	down	4.2882682	2.1003951	4.2882682	up	377.74107	1261.3965	5409.2605	SE3A2	PRP11/PRP11splicing fact:8175	chr19	+	2187815	2199678	GO:000388	GO:000562	GO:000367	Hs.115232	ref:NM_007THC246872	ENST00000221494		
XM_49695	-3.008958	-1.589264	3.0089578	down	2.9900639	1.5801763	2.9900639	up	1669.7161	554.9515	1659.2316	LOC44132	chromosom:441325	chr19	+	7083211	7083563								
AK026042	-3.05236	-1.609925	3.0523603	down	2.3764923	1.2488337	2.3764923	up	763.80055	200.23424	594.67975	NUP210	FLJ22389/Gnucleolar:25225	chr3	+	13368177	13392851	GO:000660	GO:000563	GO:000551	Hs.475525	ref:NM_024THC254813	ENST00000388753		
AK040603	-3.068948	-1.617744	3.0689485	down	5.0147589	2.3261803	5.0147589	up	825.0798	268.84772	1348.2055	AGPAT4	LPAAAT-GA1-acylglycerol:5684	chr21	+	44191238	44227206	GO:000815	GO:000557	GO:000384	Hs.248785	ref:NM_002THC246289	ENST00000358148		
BC021203	-3.082424	-1.624045	3.0824242	down	2.093137	1.0767373	2.093137	up	10446.399	3387.0508	7144.325	PZKX1P1	DD96MAP/PZKX1 inte:10538	chr16	+	4742185	47428271		GO:000576	extracellular:HS	Hs.431099	ref:NM_001THC246125	ENST00000294338		
BC014212	-3.131077	-1.646659	3.131077	down	3.9071353	1.9661112	3.9071353	up	3035.137	969.5858	3787.416	FBS1	FBS/FLJ116630:nt:1 64319	chr16	+	3058415	30588559								
BC031654	-3.131715	-1.646953	3.1317154	down	3.150161	1.6554256	3.150161	up	553.9955	176.89842	557.2585	FAM53B	KIAA1040/family with: 9679	chr10	+	126345752	126422828	GO:000815	GO:000557	GO:000367	Hs.129195	ref:NM_014THC247587	ENST00000337318		
BC031562	-3.173596	-1.666119	3.1735962	down	5.0967999	2.3478854	5.0967999	up	877.8108	276.59814	4840.0726	AKR7A3	AFAR2_alko-ecto:29277	chr1	+	1948166	1948789	GO:000608	GO:000582	GO:000403	Hs.6980	ref:NM_012THC247536	ENST00000361640		
BC028309	-3.20226	-1.679271	3.202604	down	2.2778954	1.1883917	2.2778954	up	8208.072	2562.8918	5840.793	MLXP	KIAA0867/MLX intera:2877	chr12	+	12178388	121184663	GO:004544	GO:000563	GO:003052	Hs.437153	ref:NM_014THC257876	ENST00000377037		
AY126869	-3.203304	-1.679561	3.2033039	down	3.7408102	1.9033508	3.7408102	up	473.8027	147.91063	555.2056	CENTG1	AGAP2/FLJcentaurin, g1 80769	chr12	+	56460661	56418296	GO:000716	GO:000562	GO:00016	Hs.302435	ens:ENST0THC267476	ENST00000257897		
NM_03296	-3.291968	-1.718195	3.291968	down	3.001638	1.5857143	3.001638	up	1913.7395	581.536	1744.9171	CLC14	CC-1CC-3/Chamactin: 6538	chr16	+	31334804	31337852								
AK126136	-3.311329	-1.72741	3.3113289	down	4.7013192	2.2330656	4.7013192	up	1673.5659	421.99661	1941.6265	AKNA	KIAA1968/AT-hook motif:1099	chr9	+	11617798	116200573								
NM_00073	-3.311783	-1.727608	3.3117833	down	2.9045762	1.5383277	2.9045762	up	334.23215	100.94599	293.21576	CHRM1	HIMJ1M1/cholesterin: 11328	chr11	+	62432726	62445588	GO:000646	GO:000562	GO:000158	Hs.632119	ref:NM_000THC270057	ENST00000306960		
BC027459	-3.33066	-1.735808	3.3306596	down	2.1970172	1.1355462	2.1970172	up	348.54956	104.64881	229.91524	PP5K2B	PIPSK1B/Phosphatidyl 8186	chr16	+	34185753	34209301	GO:000716	GO:000573	GO:000505	Hs.260603	ref:NM_003THC2586937			
NM_00363	-3.39068	-1.761575	3.39068	down	6.1342341	2.6168832	6.1342341	up	370.4958	907.33887	5569.328	KCNAB2	AKR6A5/Doestain c1 8154	chr1	+	6008966	6008310	GO:000681	GO:000573	GO:000521	Hs.444097	ref:NM_003THC246966	ENST00000341524		
NM_00687	-3.477512	-1.798056	3.4775125	down	5.5460015	2.471448	5.5460015	up	2827.494	813.07947	4509.324	DSTN	ACTDP/APdesmin (actin) 1134	chr20	+	17498958	17536652	GO:000815	GO:000562	GO:000377	Hs.304192	ref:NM_001THC247990	ENST00000246069		
BC104873	-3.625565	-1.858266	3.6255649	down	3.0362189	1.6022758	3.0362189	up	391.17813	107.89439	327.591	CREBL2	MGC11731_cAMP respo:189	chr12	+	12656149	12687308	GO:000635	GO:000563	GO:000378	Hs.591156	ref:NM_001THC250391	ENST00000228865		
NM_00476	-3.676933	-1.879443	3.6769330	down	3.2878839	1.1715951	3.2878839	up	18143.514	4931.2	16123.213	NRGN	RC7/rlng neurogranin:4900	chr11	+	124114951	124123209	GO:000716	GO:000562	GO:000551	Hs.524116	ref:NM_000THC246156	ENST00000284292		
BC036352	-3.698201	-1.898824	3.6982009	down	6.9462127	2.7962285	6.9462127	up	615.64136	166.4075	315.641	AGPAT3	LPAAAT-GA1-acylglycerol:5684	chr21	+	44169316	44227410	GO:000815	GO:000557	GO:000384	Hs.248785	ref:NM_002THC246289	ENST00000358148		
BC040943	-3.701461	-1.888095	3.7014616	down	2.2293232	1.1565476	2.2293232	up	3801.9624	1027.1517	2289.7067	WASF2	SCAR2/WAWAS protei:10163	chr1	+	27608887	27689247	GO:000718	GO:000585	GO:000377	Hs.590909	ref:NM_006THC254474	ENST00000374019		
XM_93295	-3.776419	-1.917019	3.7764192	down	3.1024985	1.6334305	3.1024985	up	2668.7747	706.6945	2192.5186	LOC653307	similar to hsp:653307	chr5	+	176985536	176914084								
BC028035	-3.816979	-1.932431	3.8169787	down	2.7978133	1.4842997	2.7978133	up	19404.535	5083.7417	14223.36	NRGN	RC3/rlng neurogranin:4900	chr11	+	124115150	124122312	GO:000716	GO:000562	GO:000551	Hs.524116	ref:NM_006THC246156	ENST00000284292		
AF225896	-3.920182	-1.970921	3.9201822	down	3.6298905	1.8599838	3.6298905	up	7033.781	1794.2485	6512.7803	N/A	N/A	N/A	chr2	+	218276876	218517006							
BC029098	-3.942846	-1.979238	3.9428465	down	3.931881	1.9752197	3.931881	up	1009.1406	255.94214	1006.3341	MTS1	FLJ44946/actin:9788	chr16	+	125634309	125682424	GO:000692	GO:000172	GO:000014	Hs.474751	ref:NM_002THC246530	ENST00000216181		
NM_93151	-3.989076	-1.99122	3.9890755	down	3.071743	1.6190575	3.071743	up	1308.808	328.7764	1009.9166	UBX3D7	KIAA0794_UBX domai:26043	chr14	+	19758062	197643672								
NM_00576	-4.329795	-2.114429	4.3297952	down	2.2114504	1.1449929	2.2114504	up	13880.122	3205.7224	7089.296	PZKX1P1	DD96MAP/PZKX1 inte:10538	chr16	+	47421847	47428358		GO:000576	extracellular:HS	Hs.431099	ref:NM_005THC261250	ENST00000294338		
BC026002	-4.590517	-2.198657	4.5905168	down	2.9709912	1.5709443	2.9709912	up	1009.8599	219.98828	653.58325	GRAP2	GAD5/GRAGR2B-retai:9402	chr22	+	38672801	38697330	GO:000724	GO:000573	GO:000507	Hs.517499	ref:NM_004THC262474	ENST00000344138		
AK127453	-4.679191	-2.226259	4.6791914	down	5.706807	2.5120597	5.706807	up	993.36005	212.2931	1211.3629	N/A	N/A	N/A	chr19	+	7441415	7444285							
NM_00394	-5.588296	-2.482409	5.5882964	down	4.1105312	2.0395248	4.1105312	up	13489.678	2415.916	9922.477	SELENBP1	FLJ138133_selenium bio:8991	chr1	+	149603403	149611788								
BC040920	-5.618144	-2.628801	5.6181435	down	4.1154795	2.0410605	4.1154795	up	3571.5598	577.4417	2376.495	MXR9	DFNA17/F17provia: hca:627	chr22	+	359510									





BC104818	2.5415755	1.3457231	2.5415755	up	-7.763201	-2.965662	7.7632015	down	3628.0146	9220.873	1187.7668	ORM1	AGP-AJAgloromacoi5004	chr9	+	116125209	116128303	GO:000695	GO:000557	GO:000551	Hs.567311	ref:NM_0012HC255875	ENST0000259396	
NM_00395	2.5460857	1.348281	2.5460857	up	-2.085285	-1.060245	2.085285	down	2099.985	5346.7417	2564.534	SOCS3	CIS1(cch1)suppressor c9021	chr17	-	73864453	73867753	GO:001558	regulation	GO:000480	Hs.529773	ref:NM_0012HC246186	ENST0000330871	
NM_00063	2.6014512	1.3792654	2.6014512	up	-3.165678	-1.662837	3.165678	down	3004.8271	7817.5137	1765.1825	NT4	MG238109.neomycin-p1-4689	chr3	+	12884740	12885259	GO:000641	transactivation	GO:000552	Hs.107812	ref:NM_0012HC232591	ENST0000327744	
NM_016000	2.571005	1.3623324	2.571005	up	-3.497719	-1.80645	3.4977194	down	707.38763	1818.6911	519.96655	AHBD5	CDSC8GHis hydrolyase cs2599	chr3	+	43707378	43735296	GO:000650	GO:000581	GO:000417	Hs.19385	ref:NM_01612HC246405	ENST0000013894	
NM_012388	2.572496	1.3631688	2.572496	up	-6.511116	-2.706205	6.5111159	down	5337.828	13731.541	2109.9388	PAD1A	PADPCAD1peptidyl_4i_2169	chr1	+	15702778	15763082	GO:000635	GO:000563	GO:000466	Hs.522969	ref:NM_01212HC248926	ENST0000375448	
BC048107	2.5898415	1.3728638	2.5898415	up	-3.374525	-1.754864	3.3745249	down	570.7108	1478.0272	437.99564	ZNF333	KHIA1806_zinc_finger_h3442	chr19	+	14661880	14705557	GO:000635	GO:000562	GO:000367	Hs.15215	ens:ENST0000292530	ENST0000292530	
NM_021952	2.5900005	1.3729254	2.5900005	up	-2.87579	-1.523958	2.8757897	down	799.8725	2071.6702	720.38306	HLX1	HBA2_H2.0-like_hc8149	chr1	+	219119381	219125018	GO:000635	GO:000563	GO:000370	Hs.74870	ref:NM_02112HC275576	ENST0000366903	
NM_00773	2.597023	1.3785588	2.597023	up	-2.493384	-1.319262	2.4933836	down	2096.8174	7003.6973	2806.6166	TREM1	TRIM-1 triglycerin_e54210	chr6	-	41351717	41362416	GO:000695	GO:000588	GO:000408	Hs.283022	ref:NM_01812HC260703	ENST0000244709	
NM_00363	2.604889	1.3782274	2.604889	up	-4.428728	-2.146892	4.4287283	down	3004.8271	7817.5137	1765.1825	NT4	MG238109.neomycin-p1-4689	chr22	+	38540909	38540905	GO:000641	transactivation	GO:000552	Hs.107812	ref:NM_0012HC246402	ENST0000330951	
BC005051	2.607897	1.3828869	2.607897	up	-2.32974	-1.220169	2.3297402	down	1729.4148	4510.1357	1953.8964	CoIF6	HLJ103422.chromosom55122	chr6	-	88441693	88468382	GO:000007	GO:0005737	cytoplasm	Hs.104019	ref:NM_0012HC246405	ENST0000330951	
NM_00644	2.6113405	1.3847906	2.6113405	up	-2.014276	-1.010262	2.0142765	down	41.9567	105.7592	534.0673	MTHF6	FLJ19268.5.10-methen-15822	chr5	-	77924374	77976398	GO:000399	GO:000582	GO:000028	Hs.459049	ref:NM_00612HC270724	ENST0000258874	
NM_01473	2.6123878	1.3853691	2.6123878	up	-2.973147	-1.571991	2.973147	down	2182.723	5702.119	1917.8373	RASSF2	DKPZp781(Ras associated)5107	chr20	+	4708669	4752321	GO:000704	GO:000563	GO:000551	Hs.631504	ref:NM_01412HC246845	ENST0000379400	
NM_00100	2.6129408	1.3856744	2.6129408	up	-2.802053	-1.486484	2.8020528	down	132.96442	347.42816	123.99059	DSIP13	BEDPPIJ3.501 specifi51720	chr10	+	76524195	76538976	GO:000647	protein	GO:000472	Hs.178170	ref:NM_0112HC247508	ENST0000330673	
NM_00384	2.6234227	1.3912808	2.6234227	up	-3.493204	-2.168859	3.4932007	down	1012.8095	2657.0283	148.47624	CMT2E	CKLZP208.CKL-like_1130225	chr16	+	6555181	65579679	GO:000693	GO:000561	GO:000512	Hs.195685	ref:NM_0144NP140032	ENST0000268595	
BC093762	2.6259952	1.3928643	2.6259952	up	-3.618542	-1.855409	3.6184523	down	618.0896	1623.1003	448.55807	PPIA	CYPA/CYP_peptidyl_4i_5478	chr7	+	44802804	44807725	GO:000647	protein	foh	GO:000378	Hs.35631	ref:NM_0012HC256614	ENST0000359568
BC004564	2.6385442	1.3997422	2.6385442	up	-2.366543	-1.242781	2.3665425	down	7778.158	20523.014	8672.151	DOK3	FLJ22570F.docking_pp29925	chr5	-	176861520	176869992	GO:000547	GO:000573	GO:000515	Hs.153343	ref:NM_02412HC249773	ENST0000351798	
BC100942	2.641998	1.4016294	2.641998	up	-4.027571	-2.00991	4.0275712	down	245.59038	648.8493	161.10188	UNQ3033	MGC11916(LAIR long) 284415	chr19	+	59259252	59258996							
BC029125	2.66337	1.4132528	2.66337	up	-2.783581	-1.476929	2.783581	down	2550.738	6793.559	2404.5825	FRP1L	ALXR1P916(fornyl) pep2i_2584	chr19	+	56963709	56965589	GO:000692	GO:000588	GO:000158	Hs.99855	ref:NM_0012HC247886	ENST0000340023	
NM_00178	2.6717969	1.4178104	2.6717969	up	-4.579967	-2.193337	4.5799674	down	2583.0996	6901.5176	1506.8923	CDA	CDD_cytidine dea9778	chr1	+	20717112	20817983	GO:000574	GO:000557	GO:000188	Hs.466910	ref:NM_001NP1079190	ENST0000033701	
NM_00384	2.6988776	1.424263	2.6988776	up	-2.329141	-1.215331	2.3219408	down	2851.0842	7748.8037	3682.9985	SH2C	KIAA1725(dinghot_hc8564)	chr17	+	24977900	25281144	GO:000647	GO:000585	GO:000377	Hs.634754	gb:AB0272	THC254332	
NM_03338	2.7178446	1.442463	2.7178446	up	-2.33397	-1.222786	2.33397	down	1064.1598	2899.4778	1242.2944	CLIF	CS23CFL1.chemokine-151192	chr16	+	65143995	65157471	GO:000693	GO:000583	GO:000809	Hs.15159	ref:NM_01612HC250318	ENST0000264001	
BC004380	2.7246639	1.4460783	2.7246639	up	-4.300887	-2.104634	4.3008875	down	2124.9033	5885.7637	1361.292	GLT1F	FLJ31978.1 glycoyltran_14423	chr12	+	129404033	128035462	GO:000958	GO:000587	GO:001674	Hs.655668	ref:NM_14412HC247325	ENST0000281703	
NM_01534	2.7386129	1.4534453	2.7386129	up	-2.741129	-1.45477	2.7411287	down	1196.4146	3276.5164	1195.3165	DAAM2	KIAA0813(disevelhet) 23500	chr6	+	3988770	3998619	GO:0016043	cellular	GO:000377	Hs.652207	ref:NM_01512HC249547	ENST0000274867	
NM_00146	2.7393591	1.4538384	2.7393591	up	-2.459629	-1.298441	2.4596293	down	372.80374	1021.2433	415.20212	PYB	ADAPIR07.FYN bindin_2533	chr10	+	39141113	39255424	GO:000646	GO:000563	GO:000510	Hs.370503	ref:NM_0012HC2472026		
NM_00384	2.7554701	1.4622985	2.7554701	up	-3.926568	-1.973269	3.9265685	down	282.30994	777.8966	198.21105	HCCT2	FLJ40123(MHLA meta) 253018	chr6	+	31333592	31278775	GO:000693	GO:000563	GO:000370	Hs.654096	ref:NM_18112HC248079	ENST0000376240	
NM_00182	2.7557032	1.4624205	2.7557032	up	-2.321941	-1.215331	2.3219408	down	634.65715	1748.9174	753.2136	DLB	CCBL1(CBI_Ca-B_M) 0867	chr17	+	118581199	118664609	GO:000647	GO:000557	GO:000422	Hs.654979	ref:NM_0012HC247703	ENST0000262603	
NM_02448	2.7694968	1.4876251	2.7694968	up	-4.027571	-2.00991	4.0275712	down	6296.272	17408.857	2573.9617	MPM25	MPM2023(MHLA meta) 64386	chr6	+	3036682	3050728	GO:000027	GO:000557	GO:000422	Hs.654979	ref:NM_0012HC247511	ENST0000336577	
BC005044	2.7771483	1.4736042	2.7771483	up	-2.463346	-1.300619	2.4633457	down	5410.5044	15025.773	6099.742	NFE2	NFE2p245 nuclear fact4778	chr12	+	52972164	52981058	GO:000635	GO:000563	GO:000370	Hs.75643	ref:NM_00612HC260203	ENST0000312156	
AK007259	2.8087315	1.4899187	2.8087315	up	-4.303719	-2.105584	4.3037194	down	791.29706	2222.541	516.4233	N/A	N/A_Homo sapienNA	chr5	-	176868007	176869989							
NM_00569	2.8124222	1.4918132	2.8124222	up	-3.764341	-1.91297	3.7643414	down	220.78803	620.94073	164.95333	PYGM	GIL_phosphoryla5837	chr11	+	46427065	46428763	GO:000575	carbohydr	GO:000160	Hs.154804	ref:NM_0012HC246641	ENST00000164139	
NM_00384	2.8327772	1.5021272	2.8327772	up	-5.058708	-2.338769	5.0587078	down	1593.9141	4155.2036	895.4943	SIGLEC5	GO170CD3(Saaleic acid)8778	chr16	+	5680995	56831696	GO:000715	GO:001602	GO:000551	Hs.310333	ref:NM_0012HC2474272		
BC027951	2.8608493	1.5205225	2.8608493	up	-2.288792	-1.708758	2.2887924	down	2165.7941	621.3402	190.08249	C20a052	HEPL	CD3808222	chr20	+	54420770	54462337	GO:000688	GO:001562	GO:000377	Hs.473144	ref:NM_0012HC248833	ENST0000360314
AJ287588	2.8957028	1.5319135	2.8957028	up	-4.771567	-2.254463	4.7715669	down	1218.1829	3527.4956	739.27405	LRR4C	NAG14 leucine rich_61401	chr7	+	127455797	127482838	GO:001602	GO:000551	Hs.655003		ref:NM_02212HC247080	ENST0000249363	
NM_00103	2.9019863	1.5370407	2.9019863	up	-2.075563	-1.053053	2.0755634	down	457.4206	1327.4823	69.55084	PDE4B	FKZP686(phosphodiase) 5142	chr1	+	66570380	66612849	GO:000716	GO:000562	GO:000382	Hs.198072	ref:NM_0012HC263396	ENST0000371045	
NM_02508	2.9187834	1.5453672	2.9187834	up	-2.793561	-1.482105	2.7935606	down	507.06195	1480.004	529.79126	FEAR2	FFAZR2P6F(fire fatty acid)2697	chr1	+	40624356	40633449	GO:000716	GO:000588	GO:000158	Hs.248056	ref:NM_0012HC260286	ENST0000265459	
NM_00384	2.9229869	1.5474433	2.9229869	up	-3.60168	-1.84867	3.60168	down	1933.161	5650.604	1568.8802	C1orf24	FLJ32828(chromosom11)18646	chr1	+	183029674	183210267	GO:000815	GO:000557	GO:000367	Hs.518662	ref:NM_0012HC267749	ENST0000367511	
NM_00063	2.9261341	1.5489959	2.9261341	up	-5.766083	-2.527592	5.7660829	down	2359.4067	6903.9404	1197.3363	ILKRA	C.C.C.C - CKmerlekin_83577	chr2	+	218735812	218739961	GO:000693	GO:001602	GO:000158	Hs.194778	ref:NM_0012HC246694	ENST0000295843	
BC000213	2.9422234	1.5569068	2.9422234	up	-2.369891	-1.520996	2.3698914	down	639.61426	1878.582	654.5853	KHLH2	ABP_KHLH2-like_211275	chr1	+	3862125								

NM_177551.4.312451	2.1085081	4.312451	up	-7.542601	-2.915062	7.5426007	down	1228.3627	5297.254	702.31134	GPR109A	HM74aHMG protein-cc338442	chr12	-	121751792	121753857	GO:000716:GO:001602:GO:000158:Gs.524812	ref:NM_177THC246151ENST00000328880
NM_006014.4064444	2.139615	4.4064444	up	-5.103446	-2.351472	5.1034465	down	1524.9396	6719.5615	1316.6713	GPR109B	HM74bPUNG protein-cc8843	chr12	-	121765255	121767297	GO:000716:GO:000588:GO:000158:Gs.458425	ref:NM_006THC2461513
AF249277	4.5972298	2.207648	up	-5.255012	-2.393694	5.255012	down	493.6314	2269.337	431.8424	MTHFS	Hc119268 5,10-methen10588	chr15	-	77978301	78003099	GO:000939:GO:000582:GO:000028:Hs.459049	ref:NM_006THC270724ENST00000258874
AY234180	5.2228768	2.3848447	up	-4.00758	-2.002731	4.00758	down	307.69843	1607.071	401.00784	BCL2A1	BCL2L5BEBCL2-relate597	chr15	-	78040464	78050524	GO:000691:GO:000562:GO:000551:Gs.227817	ref:NM_004THC247733ENST00000267953
AB002384	5.3026741	2.4067201	up	-3.630673	-1.860237	3.630673	down	310.87164	1648.451	454.03455	C6orf32	D1PF40D1FChromosom9750	chr6	-	24912491	25019174	Hs.559459	gb:AB002384THC251509ENST00000378027
BC010952	6.0329695	2.5928683	up	-4.374521	-2.129125	4.3745211	down	170.35841	1027.7671	234.04391	PI3	ESI1MGC13peptidase in15266	chr20	+	43236956	43238595	GO:000762:GO:000557:GO:000486:Hs.112341	ref:NM_002THC246161ENST00000243924
NM_00224.7.0276518	2.8130427	7.0276518	up	-4.838379	-2.274524	4.8383791	down	597.60175	4199.737	868.00494	KCNJ15	KIR1.3KIR potassium ir.3772	chr21	+	38550533	38595618	GO:000681:GO:000562:GO:000524:Hs.411299	ref:NM_170THC247225ENST00000328656
AF035947	7.5599764	2.9183817	up	-2.435893	-1.284451	2.4358926	down	632.5817	4782.3027	1963.265	CISH	CIS/CIS-1(G)cytokine ind1154	chr3	-	50618924	50624196	GO:000155:GO:000557:GO:000367:Hs.655334	ref:NM_145THC246359ENST00000348721
NM_145071.0.417097	3.3808814	10.417097	up	-2.404833	-1.265937	2.4048333	down	592.09125	6167.872	2564.7815	CISH	CIS/CIS-1(G)cytokine ind1154	chr3	-	50618923	50624207	GO:000155:GO:000557:GO:000367:Hs.655334	ref:NM_145THC246359ENST00000348721
AF132297	10.723215	3.4226657	up	-2.769831	-1.469798	2.7698314	down	541.4777	5806.382	2096.2944	CISH	CIS/CIS-1(G)cytokine ind1154	chr3	-	50618950	50624207	GO:000155:GO:000557:GO:000367:Hs.655334	ref:NM_145THC246359ENST00000348721

SEQ_ID	Fold chang	Log Fold	Absolute Fc	Regulation	Fold chang	Log Fold	Absolute Fc	Regulation	[AE-1][nor]	[AE-3][nor]	[AE-10][no]	GENE_NAME	SYNONYM/DESCRIPTION	NCBI_GENCHROM	STRAND	START	STOP	GO biologi	GO cellular	GO molecu	UniGene	Dbid	TIGRID	EnsemblID	
Z15108	2.0241838	1.0173403	2.0241838	up	2.7610363	1.4652099	2.7610363	up	188.72653	382.01718	1054.7653	PRKCZ	protein kin 5590	chr1	+	1971947	2106686	GO:000646:GO:000562:GO:0000166:macuole	gb:AB0079:THC2527109						
BC037798	2.0484133	1.0345068	2.0484133	up	2.4251858	1.2780953	2.4251858	up	634.3157	1299.3407	3151.1426	CGI-38	brain specifi51673	chr16	-	65981214	65983350	Hs.534458	ref:NM_016NP211869	ENST00000290942					
NM_001033.2.103378	1.0727082	2.103378	up	2.7931822	1.4819097	2.7931822	up	334.29022	703.1387	1963.9945	PRKCZ	protein kin 5590	chr1	+	1998945	2106694	GO:000646:GO:000562:GO:0000166:macuole	gb:AB0079:THC2527109							
NM_007168.2.1274717	1.0891399	2.1274717	up	3.9825857	1.9937054	3.9825857	up	111.4468	237.09991	944.2707	ABCA8	KIAA0822 ATP-bindin10351	chr17	-	64375024	64463128	GO:000681:GO:001602:GO:000016:Hs.58351	ref:NM_007THC246363ENST00000269080							
AK022468	2.2809985	1.1896655	2.2809985	up	3.5298331	1.8196	3.5298331	up	151.83627	346.3383	1222.5164	SORBS1	CAPDKFZsorbin and S10580	chr10	-	97140403	97311120	GO:000681:GO:000172:GO:000377:Hs.38621	gb:AK0224:THC247915ENST00000371227						
NM_00640.2.2897658	1.1952	2.2897658	up	2.1812388	1.1251477	2.1812388	up	624.15515	1429.1691	3117.3591	NEDD9	CAS-L/CASneural precu4739	chr6	-	11291518	11340887	GO:000007:GO:000563:GO:000551:Hs.37982	ref:NM_006THC246839ENST00000379446							
NM_02303.2.2961893	1.1992416	2.2961893	up	2.0889467	1.0627757	2.0889467	up	156.49878	359.35083	750.66473	FRY	13CDNA73 furry homol 10129	chr13	+	31503436	31768771	GO:000635:GO:001602:GO:000552:Hs.591225	ref:NM_023THC256136ENST00000380250							
NM_01673.3.0155165	1.5924051	3.0155165	up	11.694855	3.5478021	11.694855	up	352.9474	1064.3187	12447.053	FOLR1	FBP/FOLR1hol recept2348	chr11	+	71578905	71584990	GO:000689:GO:000562:GO:000487:Hs.73769	ref:NM_016NP226704	ENST00000312293						

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Annotations

STOP	STRAND	GO biolog	GO cellula	GO molecu	UniGene	Dbid	TIGRID	EnsemblID
2.16E+08	-	GO:00069	GO:00055	GO:00052	Hs.203717	ref:NM_05	NP127642	ENST00000357867
21777491	+	GO:00015	GO:00160	GO:00002	Hs.75431	ref:NM_00	THC24671	ENST00000374832
31337907	-							
74818404	+	GO:00063	GO:00056	GO:00037	Hs.25647	ref:NM_00	THC25445	ENST00000303562
46967662	+	GO:00071	GO:00058	GO:00485	Hs.466814	gb:BC005008	gb:CB240801	
90096495	-	GO:00098	GO:00055	GO:00051	Hs.156316	ref:NM_00	THC25224	ENST00000052754
36938071	-	GO:00452	GO:00058	GO:00052	Hs.654568	ref:NM_00	THC25532	ENST00000361566
72548080	+	GO:00015	GO:00056	GO:00037	Hs.508234	ref:NM_00	NP284958	ENST00000377687
22847189	+	GO:00068	GO:00057	6(extracell)	Hs.467753	ref:NM_17	THC26777	ENST00000374637
93652783	+	GO:00069	GO:00057	GO:00036	Hs.532634	ref:NM_00	THC24736	ENST00000298902
22838686	+	GO:00068	GO:00056	GO:00020(comple)	Hs.632379	ref:NM_01	THC26912	ENST00000374642
54522973	-	GO:00002	GO:00055	GO:00042	Hs.591033	ref:NM_00	THC24883	ENST00000322569
42847743	-	GO:00018	GO:00055	GO:00084	Hs.275775	ref:NM_00	THC24989	ENST00000388827
19230746	-	GO:00071	GO:00015	GO:00036	Hs.296049	ref:NM_00	NP121143	ENST00000299610
20512677	+	GO:00015	GO:00056	GO:00001	Hs.502876	ref:NM_00	THC26414	ENST00000272233
70652454	+	GO:00065	GO:00055	GO:00042	Hs.513711	ref:NM_00	THC26053	ENST00000355906
2.16E+08	-	GO:00069	GO:00055	GO:00052	Hs.203717	ref:NM_05	NP127642	ENST00000357867
57138862	+	GO:00069	GO:00055	GO:00048	Hs.384598	ref:NM_00	THC25833	ENST00000278407
46967953	+	GO:00071	GO:00058	GO:00485	Hs.466814	gb:BC005008	gb:CB240801	
57138902	+	GO:00069	GO:00055	GO:00048	Hs.384598	ref:NM_00	THC25833	ENST00000278407
6671660	-	GO:00017	GO:00055	GO:00048	Hs.529053	ref:NM_00	THC24700	ENST00000389151
31589028	+	GO:00071	GO:00055	GO:00036	Hs.644633	ref:NM_00	THC25181	ENST00000266085
21777489	+	GO:00015	GO:00160	GO:00002	Hs.75431	ref:NM_00	THC24671	ENST00000374832
22860714	+	GO:00068	GO:00056	GO:00020(comple)	Hs.8986	ref:NM_00	THC24669	ENST00000314933
2.11E+08	+	GO:00063	GO:00056	GO:00036	Hs.4607	ref:NM_00	NP120535	ENST00000366987
85821978	+	GO:00015	GO:00055	GO:00055	Hs.8867	ref:NM_00	NP077848	ENST00000360431
1.89E+08	-	GO:00001	GO:00056	GO:00036	Hs.478588	ref:NM_13	THC24665	ENST00000232014
7136184	-	GO:00065	GO:00055	GO:00038	Hs.524224	ref:NM_00	THC2498629	
64996190	+	GO:00071	GO:00056	GO:00055	Hs.76206	ref:NM_00	NP146631	ENST00000341529
95165289	-	GO:00069	GO:00055	GO:00037	Hs.483454	ref:NM_00	THC25861	ENST00000370206
1.32E+08	-	GO:00015	GO:00055	GO:00051	Hs.591346	ref:NM_00	NP095144	ENST00000367976
90100937	-	GO:00098	GO:00055	GO:00055	Hs.156316	ref:NM_00	THC25224	ENST00000052754
1.86E+08	-	GO:00066	GO:00057	GO:00002	Hs.406678	ref:NM_00	THC25127	ENST00000281455
2.16E+08	-	GO:00069	GO:00055	GO:00052	Hs.203717	ref:NM_05	NP127642	ENST00000357867
36938160	-	GO:00452	GO:00058	GO:00052	Hs.654568	ref:NM_00	THC25532	ENST00000361566
58816033	-	GO:00071	GO:00058	GO:00048	Hs.23582	ref:NM_00	THC24688	ENST00000371225
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1.24E+08	+	GO:00015	GO:00055	GO:00042	Hs.501280	ref:NM_00	NP10487	ENST00000368984
12957867	+	GO:00071	GO:00058	GO:00048	Hs.631733	ref:NM_00	NP120629	ENST00000014914
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35764692	-	GO:00064	GO:00056	GO:00037	Hs.407190	ref:NM_00	THC27122	ENST00000357266
1.72E+08	-	GO:0006470	protein a	GO:00047	Hs.171695	ref:NM_00	THC25283	ENST00000239223
36227114	-	GO:00071	GO:00055	GO:00038	Hs.517033	ref:NM_19	THC2659478	
79752463	+	GO:00071	GO:00057	GO:00055	Hs.480042	ref:NM_00	THC27707	ENST00000264908
74818666	+	GO:00063	GO:00056	GO:00037	Hs.25647	ref:NM_00	THC25445	ENST00000303562
1.14E+08	+							
44375678	+	GO:00055	GO:00052	Hs.24601		ref:NM_00	THC25002	ENST00000262722
50670276	+	GO:00007	GO:00056	GO:00037	Hs.590958	ref:NM_00	THC25060	ENST00000353609
1.08E+08	-	GO:00064	GO:00057	GO:0004872	(receptor)	ens:ENST0000036900	ENST00000369002	
65176610	-							
90096460	-	GO:00098	GO:00055	GO:00055	Hs.156316	ref:NM_00	THC25224	ENST00000052754
90096460	-	GO:00098	GO:00055	GO:00055	Hs.156316	ref:NM_00	THC25224	ENST00000052754
90096460	-	GO:00098	GO:00055	GO:00055	Hs.156316	ref:NM_00	THC25224	ENST00000052754
22847190	+	GO:00068	GO:00057	6(extracell)	Hs.467753	ref:NM_17	THC26777	ENST00000374637
1.18E+08	+	GO:00071	GO:00058	GO:00048	Hs.496646	ref:NM_00	THC24886	ENST00000371666
72573179	-							
43922003	+							
36854135	-							

Hs.530443 ens:ENST0000033944 ENST00000339446

Annotations

STOP	STRAND	GO biolog	GO cellula	GO molecu	UniGene	Dbid	TIGRID	EnsemblID
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93652783 + GO:00069:GO:00057:GO:00036:Hs.532634 ref:NM\_001THC24736 ENST00000298902  
85821978 + GO:00015:GO:00055:GO:00055:Hs.8867 ref:NM\_001NP077848 ENST00000360431  
1.32E+08 - GO:00015:GO:00055:GO:00051:Hs.591346 ref:NM\_001NP095144 ENST00000367976  
12957867 + GO:00071:GO:00058:GO:00048:Hs.631733 ref:NM\_001NP120629 ENST0000014914  
50670276 + GO:00007 GO:00056:GO:00037:Hs.590958 ref:NM\_001THC25060 ENST00000353609  
90096460 + GO:000981 GO:00055:GO:00051:Hs.156316 ref:NM\_001THC25224 ENST00000052754  
43922003 + Hs.530443 ens:ENST0000033944 ENST00000339446

STOP	STRAND	GO biol	GO cellula	GO molec	UniGene	Dbid	TIGRID	EnsemblID	
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99866461	+	GO:00068	GO:00057	GO:00052	Hs.108268	ref:NM_20THC26246	ENST00000361529		
60017660	+	GO:00069	GO:00058	GO:00048	Hs.661219	ref:NM_001NP365687	ENST00000359085		
287963	+	GO:00069	GO:00058	GO:00048	Hs.512572	ref:NM_01NP084034	ENST00000291633		
34703152	-	GO:00001	GO:00057	GO:00050	Hs.693639	ref:NM_03THC24731	ENST00000262866		
3340717	+	GO:00063	GO:00056	GO:00036	Hs.99500	ref:NM_02THC26016	ENST00000270722		
15999716	+	GO:00063	GO:00078	GO:00037	Hs.25960	ref:NM_001THC24782	ENST00000281043		
95413524	+	GO:00063	GO:00056	GO:00036	Hs.437376	ref:NM_013434	ref:ENST00000295225		
1.57E+08	-				Hs.666099	ref:NM_13THC24723	ENST00000302938		
271823	+	GO:00069	GO:00058	GO:00048	Hs.512572	ref:NM_01NP084034	ENST00000291633		
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99761084	+				GO:00055	Hs.500736	ref:NM_01THC25030	ENST00000370597	
70347484	+				GO:001602	(membrar	Hs.370262	gb:AK0001THC24752	ENST00000335464
22023120	-								
1872817	+	GO:00150	GO:001602	(membrar	Hs.144980	gb:AK0741THC2482725			
20406034	+	GO:0008152	(metaboli	GO:00038	Hs.298252	ref:NM_001THC24745	ENST00000329697		
59728199	-								
54438334	-								
11252804	-								
1.36E+08	-								
77568569	+								
87328126	-								
52074168	-								
64562088	-								
1.46E+08	-								
14789544	+				GO:0005737	(cytoplasi	Hs.661452	ref:NM_03THC24911	ENST00000253697
49485509	+	GO:00068	GO:0005737	(cytoplasi	Hs.526441	ref:NM_18THC2605336			
19998424	-								
98211660	+	GO:00064	GO:00160	GO:00001	Hs.653244	gb:AL1336THC2612465			
60070260	+	GO:00069	GO:00058	GO:00048	Hs.645228	ref:NM_01THC24706	ENST00000326321		
35273967	-				GO:00056	GO:00036	Hs.444388	ref:NM_01NP124156	ENST00000293068
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27180439	-	GO:00063	GO:00056	GO:00037	Hs.592166	ref:NM_01NP140032	ENST00000283921		
31231446	-	GO:00068	GO:00055	GO:00048	Hs.514821	ref:NM_001THC24650	ENST00000293272		
18592843	+				GO:0005624	(membrar	Hs.329850	ref:NM_01THC24614	ENST00000262817
38654183	+	GO:0006396	(RNA pre	GO:00037	Hs.173311	ref:NM_15THC24633	ENST00000315616		
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54786072	+				GO:00055	GO:00051	Hs.35101	ref:NM_001THC24742	ENST00000246794
1.49E+08	-						Hs.652227	ref:NM_001THC26012	ENST00000378008
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54244175	+								
59956315	+								
6193546	+								
1.02E+08	-								
22090936	+								
39905106	+				Hs.693637	ref:NM_01THC2491244			
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1.77E+08	+				GO:0005737	(cytoplasi	Hs.101761	ref:NM_01THC24757	ENST00000274605
44175498	+	GO:00071	GO:00056	GO:00080	Hs.632404	ref:NM_05THC26629	ENST00000372354		
1.61E+08	-	GO:00072	GO:00055	GO:00036	Hs.350581	ref:NM_05THC24879	ENST00000367929		
21950353	+	GO:00063	GO:00078	GO:00036	Hs.131055	ref:NM_18NP800281			
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39094454	+	GO:00063	GO:00055	GO:00036	Hs.438	ref:NM_001THC24720	ENST00000318579		
22090933	+	GO:00069	GO:00058	GO:00048	Hs.74647	gb:BC0633NP1155360			
1.42E+08	+								
1.42E+08	+								
1.42E+08	+								
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42169399	+				GO:00055	Hs.501114	gb:BC0938NP1164839		
38502423	+	GO:00081	GO:00055	GO:00036	Hs.147695	ref:NM_14THC24843	ENST00000348862		
1.2E+08	-	GO:00071	GO:00058	GO:00015	Hs.248119	ref:NM_001THC24797	ENST00000239032		
226904	+	GO:00069	GO:00058	GO:00048	Hs.645228	ref:NM_01THC24706	ENST00000326321		

1.13E+08 + GO:00069:GO:00055:GO:00051:Gs.211238 ref:NM\_01.NP861722 ENST00000259205  
5436786 - GO:00070:GO:00058:GO:00001:Gs.163079 ref:NM\_02.THC24788 ENST00000380419  
226904 + GO:00069:GO:00058:GO:00048:Gs.645228 ref:NM\_01.THC24706 ENST00000326321  
22090933 + GO:00069:GO:00058:GO:00048:Gs.74647 gb:BC0633NP1155360  
86942549 - GO:00069:GO:00058:GO:00051:Gs.405667 ref:NM\_17.THC24908 ENST00000337868  
69336254 - Gs.464079 ref:NM\_18.NP146566 ENST00000321800  
629117 - GO:00015:GO:00017:GO:00001:Gs.498570 ref:NM\_00.THC24717 ENST00000263125  
75113344 - GO:00069:GO:00056:GO:00048:Gs.24640 ref:NM\_00.THC24663 ENST00000261918  
1.14E+08 - GO:00069:GO:00055:GO:00051:Gs.278909 ref:NM\_17.THC24838 ENST00000327407  
60051298 + GO:00058:GO:00048:Gs.654608 ref:NM\_01.THC27529 ENST00000291633  
21173793 + GO:00000:GO:00056:GO:00080:Gs.111 ref:NM\_00.THC24806 ENST00000382353  
60070101 + GO:00069:GO:00058:GO:00048:Gs.645228 ref:NM\_00.THC24706 ENST00000326321  
288060 + GO:00069:GO:00058:GO:00048:Gs.512572 ref:NM\_01.NP084034 ENST00000291633  
85517555 + GO:0007242:(intracellular signal)Gs.209542 gb:BC110C.NP145707:ENST00000389938  
22090936 + GO:00069:GO:00058:GO:00048:Gs.74647 gb:BC0633NP1155360  
41219170 + GO:00076:GO:00055:GO:00036:Gs.302019 ref:NM\_02.THC24846 ENST00000378220  
3326560 + GO:00056:GO:00055:Gs.155995 ref:NM\_02.THC249436  
288306 + GO:00069:GO:00058:GO:00048:Gs.512572 ref:NM\_01.NP084034 ENST00000291633  
272126 + GO:00069:GO:00058:GO:00048:Gs.512572 ref:NM\_01.NP084034 ENST00000291633  
56648364 + GO:0006487:(protein a)GO:00048:Gs.654472 ref:NM\_00.THC24729 ENST00000299022  
17865897 + GO:00068 GO:00160:GO:00052:Gs.584804 ref:NM\_00.THC24826 ENST0000022248  
48638931 + GO:00068 GO:00056:GO:00052:Gs.130730 ref:NM\_00.THC24784 ENST00000199280  
25244956 + GO:00069:GO:00055:GO:00051:Gs.1897 ref:NM\_00.THC24810 ENST00000264708  
1.05E+08 - GO:0016020:(membran)Gs.680365 ref:NM\_00.THC24851 ENST00000329905  
8565237 +  
1.58E+08 +  
1.06E+08 +  
2.46E+08 +  
1.3E+08 + GO:00068:GO:00058:GO:00001:Gs.522413 ref:NM\_00.THC24938 ENST00000341179  
62186156 - Gs.570316 ref:NM\_00.THC24855 ENST00000308906  
38414444 - GO:00015:GO:00055:GO:00055:Gs.349705 ref:NM\_00.THC24798 ENST00000377694  
1.49E+08 - Gs.652227 ref:NM\_00.THC26012 ENST00000378008  
1.64E+08 - GO:00063:GO:00056:GO:00037:Gs.26550 ref:NM\_00.THC26061 ENST00000367892  
1766240 + Gs.7247 gb:AK074(THC2504155  
3059669 + GO:00069:GO:00056:GO:00051:Gs.943 ref:NM\_00.THC25889 ENST00000008180  
51109876 - Gs.646574 ref:NM\_00.THC24759 ENST00000321691  
53976682 - GO:00071:GO:00058:GO:00048:Gs.462529 ref:NM\_14.NP114549:ENST00000356876  
6448842 +  
37617144 +  
1.42E+08 +  
1.17E+08 + GO:00017:GO:00058:GO:00048:Gs.523500 ref:NM\_00.THC24719 ENST00000369478  
86871578 - GO:00069:GO:00058:GO:00055:Gs.85258 ref:NM\_00.THC24680 ENST00000283635  
27252717 + GO:00063:GO:00056:GO:00037:Gs.369879 ref:NM\_00.THC24849 ENST00000222761  
54365717 + GO:00065:GO:00057:GO:00042:Gs.277937 ref:NM\_00.THC24765 ENST00000231009  
60017783 + GO:00069:GO:00058:GO:00048:Gs.661219 ref:NM\_00.NP365687 ENST00000359085  
3752810 + GO:00000:GO:00056:GO:00001:Gs.631845 ref:NM\_13.THC27825 ENST00000310132  
1.34E+08 + GO:00063:GO:00056:GO:00036:Gs.573153 ref:NM\_00.THC24965 ENST00000342854  
1.14E+08 - GO:00063:GO:00056:GO:00037:Gs.469728 ref:NM\_01.NP207698 ENST00000348715  
1.44E+08 - GO:00071:GO:00056:GO:00055:Gs.415762 ref:NM\_00.THC24736 ENST00000301263  
1.74E+08 - GO:00071:GO:00058:GO:00015:Gs.248115 ref:NM\_00.THC26039 ENST00000241256  
19716846 - GO:00065:GO:00160:GO:00151:Gs.197116 ref:NM\_00.THC24751 ENST00000382932  
1.02E+08 - GO:00002:GO:00055:GO:00042:Gs.591946 ref:NM\_00.THC26655 ENST00000260228  
41426593 + GO:00069:GO:00058:GO:00048:Gs.194721 ref:NM\_00.THC24879 ENST00000373089  
29290876 + GO:00064:GO:00056:GO:00017:Gs.17958 ref:NM\_00.THC24717 ENST00000338911  
86942549 - GO:00069:GO:00058:GO:00055:Gs.405667 ref:NM\_17.THC24908 ENST00000337868  
1.01E+08 - GO:00063:GO:00056:GO:00037:Gs.520293 ref:NM\_00.THC24793 ENST00000262901  
5558225 + GO:00056:GO:00056:Gs.239600 ref:NM\_00.THC24726 ENST00000315238  
31347222 - GO:00061 GO:00057:GO:00041:Gs.250760 ref:NM\_005205:gb:BC029818  
27738789 - GO:00018:GO:00056:GO:00037:Gs.591663 ref:NM\_00.THC2631102  
9054610 + GO:00069:GO:00160:GO:00048:Gs.558446 ref:NM\_00.NP387863 ENST00000356986  
1E+08 + GO:00081:GO:00055:GO:00036:Gs.521083 ref:NM\_00.THC24727 ENST00000300176  
85779380 + GO:00068:GO:00056:Gs.105806 ref:NM\_00.THC26417 ENST00000263863  
10359227 + GO:00071:GO:00058:GO:00048:Gs.562457 ref:NM\_00.NP492171 ENST00000336164  
288431 + GO:00069:GO:00058:GO:00048:Gs.512572 ref:NM\_01.NP084034 ENST00000291633  
253356 +  
60051836 + GO:00058:GO:00048:Gs.654608 ref:NM\_01.THC27529 ENST00000291633  
1.09E+08 + Gs.436618 ref:NM\_01.THC27877 ENST00000389626  
49229100 + GO:00063:GO:00056:GO:00036:Gs.279840 ref:NM\_01.THC26374 ENST00000187879  
1.02E+08 -  
60651900 + GO:00080:GO:00058:GO:00050:Gs.58685 ref:NM\_01.THC2463150  
59987590 +  
37569963 - GO:00160:GO:00048:Gs.91622 ref:NM\_01.THC25010 ENST00000333039  
40899780 + GO:00001:GO:00056:GO:00036:Gs.99430 ref:NM\_01.THC27609 ENST00000262630  
59956316 +  
271801 + GO:00069:GO:00160:GO:00048:Gs.661101 ref:NM\_01.NP083697 ENST00000291633  
52735630 + GO:00063:GO:00056:GO:00037:Gs.549040 ref:NM\_01.THC24745 ENST00000303406  
150755 + GO:00056:GO:00050:Gs.536319 gb:BC0247NP437544 ENST00000326643

3710061 - GO:00081;GO:00055;GO:00036;Hs.72620 ref:NM\_01 THC24889 ENST00000356899  
54873005 + GO:00066;GO:00057;GO:00047;Hs.234786 ref:NM\_01 THC27076 ENST00000343744  
37024476 - GO:00063;GO:00056;GO:00036;Hs.654464 ref:NM\_01 THC24781 ENST00000377859  
1.12E+08 + GO:00068;GO:00160;GO:00052;Hs.591327 ref:NM\_01 THC24733 ENST00000368851  
68945808 - GO:00071;GO:00160;GO:00055;Hs.435719 gb:BC0663 THC2605019  
40467886 + GO:00068;GO:00055;GO:00051;Hs.8821 ref:NM\_02 THC24780 ENST00000222304  
1.75E+08 + GO:00015;GO:00056;GO:00082;Hs.187284 gb:AF3429 THC2490052  
8581588 - GO:00065;GO:00055;GO:00036;Hs.657508 ref:NM\_03 THC24643 ENST00000270328  
15573926 - GO:00198;Hs.98785 ref:NM\_03 THC24739 ENST00000382324  
34707972 - GO:00001;GO:00057;GO:00050;Hs.693639 ref:NM\_03 THC24731 ENST00000262866  
604823 - GO:00063;GO:00056;GO:00036;Hs.355284 ref:NM\_03 THC24776 ENST00000246104  
190258 + Hs.350949 ref:NM\_05 THC24833 ENST00000352113  
51173240 -  
27985586 + GO:00068;GO:00055;GO:00055;Hs.289106 ref:NM\_13 NP402577 ENST00000334018  
99362549 + GO:00081;GO:00057;GO:00168;Hs.180346 ref:NM\_13 THC24750 ENST00000370646  
1.17E+08 + GO:0008033(RNA pr GO:00047;Hs.21187 ref:NM\_13 NP116008 ENST00000298746  
46727205 + GO:00076;GO:001602(membran Hs.185777 ref:NM\_14 THC24802 ENST00000326431  
6448842 - GO:00071;GO:00058;GO:00048;Hs.462529 ref:NM\_14 NP114549 ENST00000356876  
18682886 + Hs.406913 ref:NM\_15 THC24850 ENST00000325337  
21886369 - GO:00055;Hs.448572 ref:NM\_15 THC24789 ENST00000379499  
45025964 - GO:00068;GO:00160;GO:00036;Hs.302513 ref:NM\_15 THC24886 ENST00000372207  
12607686 + GO:00063;GO:00056;GO:00036;Hs.567641 ref:NM\_15 NP540184 ENST00000343344  
1.88E+08 + GO:00512;GO:000986(cell surf Hs.518480 ref:NM\_15 NP541910 ENST00000382104  
44331749 - GO:0006468(protein a GO:00001;Hs.351887 ref:NM\_17 NP118865 ENST00000347193  
86942549 - GO:00069;GO:00058;GO:00055;Hs.405667 ref:NM\_17 THC24908 ENST00000337868  
86942549 - GO:00069;GO:00058;GO:00055;Hs.405667 ref:NM\_17 THC24908 ENST00000337868  
1.5E+08 - GO:000045(autophagic vacuole Hs.655505 ref:NM\_17 THC25198 ENST00000312968  
1.16E+08 + Hs.421750 ref:NM\_17 NP116530 ENST00000314309  
7041235 + Hs.352515 ref:NM\_17 NP115692 ENST00000314227  
1068674 - Hs.250557 gb:AK0568 THC2478752  
52907943 + Hs.424589 gb:AK128;THC2485408  
1299303 + GO:00068;GO:00058;GO:00052;Hs.213284 ref:NM\_18 NP398860 ENST00000324642  
1097350 - GO:00055;Hs.248290 ref:NM\_19 NP146562 ENST00000319237  
2.46E+08 - GO:00071;GO:00160;GO:00048;Hs.23491 ref:NM\_19 THC24845 ENST00000366487  
85517663 + GO:0007242(intracellular signalin Hs.209542 gb:BC110CNP145707;ENST00000389938  
7703008 - GO:00160;GO:00055;Hs.220649 ref:NM\_19 THC24791 ENST00000328853  
34513037 - Hs.522085 ref:NM\_19 THC26145 ENST00000303992  
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94983040 + GO:00071;GO:00160;GO:00015;Hs.143315 ref:NM\_19 THC26031 ENST00000316122  
1.34E+08 + GO:00063;GO:00056;GO:00036;Hs.573153 ref:NM\_00 THC24965 ENST00000342854  
5631911 - GO:00055;Hs.356626 ref:NM\_20 THC24966 ENST00000309324  
1.43E+08 - Hs.689547 ref:NM\_20 THC2480285  
48144348 -  
60034044 + GO:00069;GO:00058;GO:00048;Hs.645228 ref:NM\_01 THC24706 ENST00000262621  
60543369 + GO:00069;GO:00058;GO:00050;Hs.643167 ref:NM\_00 NP091718 ENST00000313421  
60017780 + GO:00069;GO:00058;GO:00048;Hs.661219 ref:NM\_00 NP365687 ENST00000359085  
84961721 -  
1.18E+08 +  
1.55E+08 +  
77498394 - GO:0016020(membran Hs.163451 ens:ENSTU THC26147 ENST00000330655  
38693156 - Hs.144075 gb:AK124;THC27852 ENST00000381390  
5620855 +  
1.45E+08 -  
1.79E+08 +  
47302669 +  
6483835 -  
88256899 -  
1876799 -  
1.76E+08 +  
39974822 +  
18761119 + Hs.632006 ref:NM\_02 THC2463453  
293088 +  
75242880 -  
5892515 +  
68038530 -  
1.52E+08 -  
35204356 +  
1.51E+08 -  
45398263 -  
1.05E+08 -  
1.12E+08 -  
48997409 -  
19948283 +  
71629939 -  
1.65E+08 -  
4790447 + Hs.558440 ens:ENSTU THC26344 ENST00000348624  
63293870 +

54689234 -  
 11439761 - GO:000711 GO:00055 GO:00015 Hs.654486 ref:NM\_006248;gb:K03208;gb:BC044827  
 65474181 -  
 18207722 +  
 71448618 - Hs.514494 ref:NM\_0017389  
 69030324 -  
 56189478 +  
 75659546 +  
 17924078 -  
 21853153 +  
 33807542 +  
 22485140 +  
 13210359 -  
 2.22E+08 -  
 1.48E+08 +  
 1.27E+08 +  
 53290507 - Hs.483519 ref:NR\_001988;Hs.98785 ref:NM\_03153  
 60017389 + GO:00069 GO:00058 GO:00048 Hs.661219 ref:NM\_0017389

Annotations								
STOP	STRAND	GO biolog	GO cellula	GO molec	UniGene	Dbid	TIGRID EnsemblID	
271823	+	GO:00069	GO:00058	GO:00048	Hs.512572	ref:NM_01	NP084034 ENST00000291633	
1.61E+08	-	GO:00072	GO:00055	GO:00036	Hs.350581	ref:NM_05	THC24879 ENST00000367929	
1.61E+08	-	GO:00072	GO:00055	GO:00036	Hs.350581	ref:NM_05	THC24879 ENST00000367929	
86942549	-	GO:00069	GO:00058	GO:00055	Hs.405667	ref:NM_17	THC24908 ENST00000337868	
2.46E+08	+							
86942549	-	GO:00069	GO:00058	GO:00055	Hs.405667	ref:NM_17	THC24908 ENST00000337868	
15573926	-				GO:00198	Hs.98785	ref:NM_03	THC24739 ENST00000382324
1.34E+08	+	GO:00063	GO:00056	GO:00036	Hs.573153	ref:NM_00	THC24965 ENST00000342854	













