

Table S3. Differentially expressed genes (DEGs) in both LMAFvar1IDN vs LXIDN and LMAFvar2IDN vs LXIDN-transduced CD34+ HPCs.

Probeset ID	Gene Symbol	Gene Title	RefSeq Transcript ID	FDR (LMAFVAR1IDN vs. LXIDN)	Fold-Change(LMAFVAR 1IDN vs. LXIDN)	FDR (LMAFVAR2IDN vs. LXIDN)	Fold-Change(LMAFVAR 2IDN vs. LXIDN)	FDR (LMAFVAR2IDN vs. LMAFVAR1IDN)	Fold-Change(LMAFVAR 2IDN vs. LMAFVAR 1IDN)
11725979_a_at	CALB1	calbindin 1, 28kDa	NM_004929	0,0281	78,0309	0,0367	44,7699	0,9906	-1,7429
11719684_a_at	NTS	neurotensin	NM_006183	0,0269	73,0019	0,0327	66,7170	0,9949	-1,0942
11754472_a_at	CALB1	calbindin 1, 28kDa	NM_004929	0,0282	47,3451	0,0381	25,9458	0,9906	-1,8248
11755730_x_at	SPP1	secreted phosphoprotein 1	NM_000582 /// ↑	0,0366	31,5761	0,0476	22,4343	0,9906	-1,4075
11723068_at	CRHBP	corticotropin releasing hormone binding protein	NM_001882	0,0266	30,9736	0,0333	22,2337	0,9906	-1,3931
11737943_a_at	SPP1	secreted phosphoprotein 1	NM_000582 /// ↑	0,0343	25,7248	0,0443	19,2564	0,9910	-1,3359
11716384_at	CCL2	chemokine (C-C motif) ligand 2	NM_002982	0,0302	18,3654	0,0360	16,1870	0,9910	-1,1346
11752076_s_at	SEPT10	septin 10	NM_144710 /// ↑	0,0212	15,9336	0,0231	18,2133	0,9906	1,1431
11719853_s_at	SEPT10	septin 10	NM_144710 /// ↑	0,0251	15,0360	0,0269	17,2773	0,9906	1,1491
11741434_s_at	SEPT10	septin 10	NM_144710 /// ↑	0,0338	14,4201	0,0359	17,0318	0,9906	1,1811
11724931_a_at	MERTK	c-mer proto-oncogene tyrosine kinase	NM_006343	0,0212	14,2657	0,0231	14,1249	0,9992	-1,0100
11729094_a_at	GAD1	glutamate decarboxylase 1 (brain, 67kDa)	NM_000817 /// ↑	0,0277	13,5590	0,0342	11,6039	0,9906	-1,1685
11739503_at	ABCA1	ATP-binding cassette, sub-family A (ABC1), mem1	NM_005502	0,0251	12,7932	0,0338	6,8480	0,9906	-1,8682
11722159_a_at	SLC7A8	solute carrier family 7 (amino acid transporter high affinity)	NM_001267036	0,0346	11,9403	0,0447	8,9381	0,9906	-1,3359
11763851_a_at	CRHBP	corticotropin releasing hormone binding protein	NM_001882	0,0272	11,6233	0,0394	6,7958	0,9906	-1,7104
11733355_x_at	C5AR1	complement component 5a receptor 1	NM_001736	0,0280	10,4510	0,0352	8,7379	0,9906	-1,1961
11748110_a_at	LGMN	legumain	NM_001008530	0,0341	10,0064	0,0480	6,5881	0,9906	-1,5189
11720994_x_at	CCL3	chemokine (C-C motif) ligand 3 /// c-C motif chemokine 3	NM_002983 /// >	0,0457	9,9040	0,0367	8,8956	0,9949	-1,1134
11746287_x_at	LGMN	legumain	NM_001008530	0,0311	9,3539	0,0459	5,6740	0,9906	-1,6486
11733729_s_at	LGMN	legumain	NM_001008530	0,0337	8,9239	0,0433	6,9732	0,9906	-1,2797
11752744_a_at	LGMN	legumain	NM_001008530	0,0288	8,9209	0,0411	5,8186	0,9906	-1,5332
11741079_x_at	CREM	cAMP responsive element modulator	NM_001267562	0,0258	8,7346	0,0302	7,8946	0,9906	-1,1064
11743732_a_at	RCAN1	regulator of calcineurin 1	NM_004414 /// ↑	0,0237	8,6324	0,0275	6,9419	0,9906	-1,2435
11743733_s_at	RCAN1	regulator of calcineurin 1	NM_004414 /// ↑	0,0252	8,3257	0,0282	7,8601	0,9916	-1,0592
11740030_s_at	CREM	cAMP responsive element modulator	NM_001267562	0,0429	7,8444	0,0447	9,1123	0,9906	1,1616
11746995_a_at	NPL	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate dependent)	NM_001200050	0,0303	7,7567	0,0345	8,1167	0,9949	1,0464
11718983_x_at	CCL4	chemokine (C-C motif) ligand 4 /// chemokine (C-C motif) ligand 4	NM_001001435	0,0457	7,7355	0,0405	7,1814	0,9951	-1,0772
11753445_a_at	HMOX1	heme oxygenase (decycling) 1	NM_002133	0,0337	7,5756	0,0451	5,5472	0,9906	-1,3657
11733796_s_at	RCAN1	regulator of calcineurin 1	NM_004414 /// ↑	0,0237	7,4649	0,0269	7,2951	0,9951	-1,0233
11731027_s_at	CREM	cAMP responsive element modulator	NM_001267562	0,0403	7,1910	0,0411	8,4529	0,9906	1,1755
11740028_a_at	CREM	cAMP responsive element modulator	NM_001267562	0,0305	7,1525	0,0366	6,5574	0,9910	-1,0908
11723884_at	SOWAHC	sonosdowah ankyrin repeat domain family member 1	NM_023016	0,0271	7,1194	0,0326	7,1782	0,9997	1,0083
11728228_at	HAVCR2	hepatitis A virus cellular receptor 2	NM_032782	0,0281	6,9476	0,0338	6,5197	0,9920	-1,0656
11718014_a_at	CELA2B	chymotrypsin-like elastase family, member 2B	NM_015849	0,0212	6,9259	0,0231	13,6610	0,9906	1,9725
11716939_a_at	HMOX1	heme oxygenase (decycling) 1	NM_002133	0,0414	6,8027	0,0494	6,1388	0,9915	-1,1082
11719657_a_at	MMP9	matrix metalloproteinase 9 (gelatinase B, 92kDa glycoprotein)	NM_004994	0,0427	6,7834	0,0375	5,5583	0,9910	-1,2204
11723803_a_at	TREM2	triggering receptor expressed on myeloid cells 2	NM_001271821	0,0382	6,6521	0,0377	8,1387	0,9906	1,2235
11718061_at	PVALB	parvalbumin	NM_002854	0,0212	6,6490	0,0269	3,0850	0,9906	-2,1553
11741874_x_at	SEPP1	selenoprotein P, plasma, 1	NM_001085486	0,0214	6,4161	0,0269	5,3087	0,9906	-1,2086
11723883_at	SOWAHC	sonosdowah ankyrin repeat domain family member 1	NM_023016	0,0311	6,3999	0,0344	6,8932	0,9916	1,0771
11741567_x_at	SLCO2B1	solute carrier organic anion transporter family, member 2B1	NM_001145211	0,0314	6,0770	0,0444	4,4452	0,9906	-1,3671
11722728_a_at	EGR2	early growth response 2	NM_000399 /// ↑	0,0267	5,9926	0,0312	5,6667	0,9916	-1,0575
11724463_a_at	GNPMB	glycoprotein (transmembrane) nmb	NM_001005340	0,0269	5,8620	0,0359	4,2312	0,9906	-1,3854
11755337_a_at	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	NM_001040092	0,0269	5,6443	0,0375	3,8737	0,9906	-1,4571
11731433_a_at	SEPP1	selenoprotein P, plasma, 1	NM_001085486	0,0319	5,3077	0,0422	4,2500	0,9906	-1,2489
11717672_s_at	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	NM_001040092	0,0312	5,2760	0,0425	4,0147	0,9906	-1,3142
11753130_at	TM4SF1	transmembrane 4 L six family member 1	NM_014220	0,0395	5,2317	0,0458	4,8688	0,9923	-1,0746
11715931_s_at	SGK1	serum/glucocorticoid regulated kinase 1	NM_001143676	0,0267	5,0998	0,0311	4,8467	0,9916	-1,0522
11740752_a_at	FOLR2	folate receptor 2 (fetal)	NM_000803 /// ↑	0,0419	5,0915	0,0377	7,2640	0,9906	1,4267
11728763_x_at	GAL3ST4	galactose-3-O-sulfotransferase 4	NM_024637	0,0266	5,0258	0,0243	9,6638	0,9906	1,9228
11717661_a_at	PPP1R16B	protein phosphatase 1, regulatory subunit 16B	NM_001172735	0,0255	4,9599	0,0269	5,8403	0,9906	1,1775
11759566_a_at	NPL	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate dependent)	NM_001200050	0,0212	4,8477	0,0231	5,2152	0,9906	1,0758
11720263_a_at	MITF	microphthalmia-associated transcription factor	NM_000248 /// ↑	0,0212	4,7928	0,0242	4,4380	0,9906	-1,0800
11719120_a_at	KYNU	kynureninase	NM_001032998	0,0217	4,7893	0,0269	3,8507	0,9906	-1,2438
11733698_s_at	SGK1	serum/glucocorticoid regulated kinase 1	NM_001143676	0,0214	4,7278	0,0243	4,4341	0,9906	-1,0662
11737312_at	CCL1	chemokine (C-C motif) ligand 1	NM_002981	0,0221	4,6211	0,0234	6,5592	0,9906	1,4194
11728156_s_at	LACC1	laccase (multicopper oxidoreductase) domain containing	NM_001128303	0,0312	4,6092	0,0359	4,5118	0,9962	-1,0216

11737750_s_at	SGK1	serum/glucocorticoid regulated kinase 1	NM_001143676	0,0232	4,5931	0,0269	4,2891	0,9906	-1,0709
11724275_s_at	TMEM158	transmembrane protein 158 (gene/pseudogene)	NM_015444	0,0346	4,5260	0,0422	4,0713	0,9906	-1,1117
11716161_s_at	LBH	limb bud and heart development	NM_030915	0,0267	4,4356	0,0338	3,5931	0,9906	-1,2345
11716162_at	LBH	limb bud and heart development	NM_030915	0,0295	4,3789	0,0359	4,1034	0,9910	-1,0672
11721467_s_at	CD276	CD276 molecule	NM_001024736	0,0214	4,3137	0,0251	4,1688	0,9915	-1,0348
11752395_a_at	NFATC1	nuclear factor of activated T-cells, cytoplasmic, calcium dependent	NM_006162 /// ↑	0,0443	4,2599	0,0447	4,9337	0,9906	1,1582
11744715_a_at	SLC38A6	solute carrier family 38, member 6	NM_001172702	0,0269	4,2386	0,0338	3,6861	0,9906	-1,1499
11726725_a_at	NABP1	nucleic acid binding protein 1	NM_001031716	0,0255	4,2293	0,0297	3,9664	0,9906	-1,0663
11756780_a_at	MS4A7	membrane-spanning 4-domains, subfamily A, member 7	NM_021201 /// ↑	0,0276	4,2127	0,0375	3,3188	0,9906	-1,2693
11743350_a_at	C15orf48	chromosome 15 open reading frame 48	NM_032413 /// ↑	0,0214	4,2012	0,0263	3,7123	0,9906	-1,1317
11745612_a_at	TREM2	triggering receptor expressed on myeloid cells 2	NM_001271821	0,0255	4,1968	0,0301	3,7957	0,9906	-1,1057
11719447_s_at	GBP2	guanylate binding protein 2, interferon-inducible	NM_004120	0,0249	4,1891	0,0269	4,3949	0,9906	1,0491
11729741_x_at	CD68	CD68 molecule	NM_001040059	0,0212	4,1849	0,0231	3,9693	0,9906	-1,0543
11763367_at	---	---	---	0,0269	4,1746	0,0334	3,8256	0,9906	-1,0912
11735045_at	ATP6V0D2	ATPase, H ⁺ transporting, lysosomal 38kDa, V0 subunit	NM_152565	0,0287	4,1718	0,0370	3,5942	0,9906	-1,1607
11726190_a_at	DOCK4	dedicator of cytokinesis 4	NM_014705	0,0413	4,1458	0,0497	3,7636	0,9906	-1,1016
11717994_a_at	NR4A1	nuclear receptor subfamily 4, group A, member 1	NM_001202233	0,0455	4,1408	0,0395	6,1249	0,9906	1,4792
11721305_a_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	NM_007350	0,0266	4,1392	0,0338	3,3462	0,9906	-1,2370
11720062_s_at	IER3	immediate early response 3	NM_003897 /// ↑	0,0302	4,1317	0,0359	4,0015	0,9949	-1,0325
11716580_s_at	CYSTM1	cysteine-rich transmembrane module containing 1	NM_032412	0,0299	4,0502	0,0388	3,3786	0,9906	-1,1988
11716479_s_at	F13A1	coagulation factor XIII, A1 polypeptide	NM_000129	0,0413	4,0475	0,0494	3,6994	0,9906	-1,0941
11734874_x_at	PPFIBP1	PTPRF interacting protein, binding protein 1 (liprin beta 1)	NM_001198915	0,0272	4,0394	0,0334	3,9047	0,9940	-1,0345
11725175_x_at	ADAP2	ArfGAP with dual PH domains 2	NM_018404	0,0212	4,0389	0,0231	3,8193	0,9906	-1,0575
11733240_at	IRAK2	interleukin-1 receptor-associated kinase 2	NM_001570	0,0214	4,0388	0,0252	3,6110	0,9906	-1,1185
11754206_a_at	HIVEP2	human immunodeficiency virus type I enhancer binding protein 2	NM_006734	0,0214	4,0183	0,0251	3,8302	0,9906	-1,0491
11740871_a_at	MS4A7	membrane-spanning 4-domains, subfamily A, member 7	NM_021201 /// ↑	0,0276	3,9007	0,0339	3,5879	0,9906	-1,0872
11745007_s_at	SDC2	syndecan 2	NM_002998	0,0269	3,8406	0,0354	3,1523	0,9906	-1,2184
11762406_s_at	GBP2	guanylate binding protein 2, interferon-inducible	NM_004120	0,0321	3,8393	0,0377	3,6606	0,9923	-1,0488
11721720_s_at	CELA2A	chymotrypsin-like elastase family, member 2A	NM_033440	0,0414	3,8179	0,0334	6,9784	0,9906	1,8278
11721630_at	MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene	NM_005461	0,0352	3,8015	0,0444	3,3572	0,9906	-1,1324
11716716_x_at	CTSB	cathepsin B	NM_001908 /// ↑	0,0308	3,7569	0,0375	3,4714	0,9906	-1,0822
11719959_at	SGPL1	sphingosine-1-phosphate lyase 1	NM_003901	0,0316	3,7439	0,0366	3,7052	0,9992	-1,0105
11726963_s_at	SGTB	small glutamine-rich tetratricopeptide repeat (TPR)	NM_019072	0,0237	3,7161	0,0269	3,5897	0,9915	-1,0352
11759525_at	GADD45B	growth arrest and DNA-damage-inducible, beta	NM_015675	0,0286	3,6445	0,0338	3,7523	0,9949	1,0296
11739379_a_at	FAM198B	family with sequence similarity 198, member B	NM_001031700	0,0255	3,6411	0,0338	2,8573	0,9906	-1,2743
11729051_a_at	PPFIBP1	PTPRF interacting protein, binding protein 1 (liprin beta 1)	NM_001198915	0,0270	3,6273	0,0327	3,5811	0,9978	-1,0129
11718810_at	PRKCH	protein kinase C, eta	NM_006255	0,0393	3,6127	0,0411	3,8243	0,9920	1,0586
11742911_at	IGSF6	immunoglobulin superfamily, member 6	NM_005849	0,0269	3,6081	0,0320	3,6215	0,9997	1,0037
11740896_s_at	MIR22 ///	microRNA 22 /// MIR22 host gene (non-protein coding)	NM_001001870	0,0413	3,5908	0,0491	3,3794	0,9919	-1,0625
11746798_x_at	SDC2	syndecan 2	NM_002998	0,0335	3,5104	0,0484	2,7020	0,9906	-1,2992
11743071_a_at	LPAR6	lysophosphatidic acid receptor 6	NM_001162497	0,0426	3,4945	0,0494	3,3371	0,9940	-1,0472
11729424_s_at	CCRL2	chemokine (C-C motif) receptor-like 2	NM_001130910	0,0283	3,4829	0,0351	3,2630	0,9906	-1,0674
11726727_a_at	NABP1	nucleic acid binding protein 1	NM_001031716	0,0312	3,4829	0,0387	3,1081	0,9906	-1,1206
11717886_a_at	PLAU	plasminogen activator, urokinase	NM_001145031	0,0399	3,4780	0,0444	3,5332	0,9985	1,0159
11725174_a_at	ADAP2	ArfGAP with dual PH domains 2	NM_018404	0,0285	3,4707	0,0384	2,8891	0,9906	-1,2013
11755248_x_at	PPFIBP1	PTPRF interacting protein, binding protein 1 (liprin beta 1)	NM_001198915	0,0363	3,4639	0,0395	3,5345	0,9962	1,0204
11737428_a_at	MSR1	macrophage scavenger receptor 1	NM_002445 /// ↑	0,0281	3,4493	0,0340	3,3063	0,9916	-1,0432
11718841_s_at	IL8	interleukin 8	NM_000584	0,0214	3,4373	0,0251	3,3354	0,9910	-1,0305
11754777_a_at	SH2D2A	SH2 domain containing 2A	NM_001161441	0,0458	3,4330	0,0426	4,4741	0,9906	1,3033
11757798_s_at	MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene	NM_005461	0,0346	3,4231	0,0444	3,0336	0,9906	-1,1284
11733799_a_at	SLC31A2	solute carrier family 31 (copper transporters), member 2	NM_001860	0,0268	3,4181	0,0334	3,0590	0,9906	-1,1174
11744435_a_at	DUSP6	dual specificity phosphatase 6	NM_001946 /// ↑	0,0369	3,4104	0,0377	3,7363	0,9906	1,0956
11726726_s_at	NABP1	nucleic acid binding protein 1	NM_001031716	0,0255	3,4073	0,0275	3,4341	0,9992	1,0079
11740872_a_at	MS4A7	membrane-spanning 4-domains, subfamily A, member 7	NM_021201 /// ↑	0,0255	3,3805	0,0289	3,2970	0,9941	-1,0253
11740113_x_at	NIPSNAP3	nipsnap homolog 3B (C. elegans)	NM_018376	0,0212	3,3642	0,0231	3,0778	0,9906	-1,0930
11716974_a_at	PDK4	pyruvate dehydrogenase kinase, isozyme 4	NM_002612	0,0288	3,3440	0,0359	3,1177	0,9906	-1,0726
11754810_a_at	ITGB5	integrin, beta 5	NM_002213	0,0237	3,3426	0,0284	2,8299	0,9906	-1,1812
11746878_s_at	ID2	inhibitor of DNA binding 2, dominant negative helix-loop-helix	NM_002166	0,0338	3,3317	0,0377	3,3521	0,9997	1,0061
11741980_a_at	DUSP6	dual specificity phosphatase 6	NM_001946 /// ↑	0,0269	3,3139	0,0298	3,5589	0,9906	1,0739
11720836_a_at	RIN2	Ras and Rab interactor 2	NM_001242581	0,0214	3,2961	0,0252	3,1250	0,9906	-1,0548
11725937_a_at	LGALS3	lectin, galactoside-binding, soluble, 3	NM_001177388	0,0212	3,2887	0,0242	2,8915	0,9906	-1,1374
11743288_at	PEAK1	NKF3 kinase family member	NM_024776	0,0212	3,2839	0,0231	3,5661	0,9906	1,0859
11731281_a_at	NFATC1	nuclear factor of activated T-cells, cytoplasmic, calcium dependent	NM_006162 /// ↑	0,0427	3,2833	0,0401	3,9877	0,9906	1,2145
11744618_a_at	DUSP6	dual specificity phosphatase 6	NM_001946 /// ↑	0,0478	3,2509	0,0488	3,7464	0,9906	1,1524
11755796_a_at	ADAM9	ADAM metallopeptidase domain 9	NM_001005845	0,0212	3,2339	0,0242	2,8758	0,9906	-1,1245
11725987_a_at	MMP14	matrix metallopeptidase 14 (membrane-inserted)	NM_004995	0,0341	3,2287	0,0375	3,3411	0,9942	1,0348

11755695_a_at	FUCA1	fucosidase, alpha-L- 1, tissue	NM_000147	0,0296	3,1838	0,0384	2,7481	0,9906	-1,1586
11723641_a_at	FUCA1	fucosidase, alpha-L- 1, tissue	NM_000147	0,0341	3,1704	0,0444	2,7542	0,9906	-1,1511
11758147_s_at	MAPK13	mitogen-activated protein kinase 13	NM_002754 /// ↑	0,0306	3,1572	0,0351	3,2074	0,9962	1,0159
11758263_s_at	CYBB	cytochrome b-245, beta polypeptide	NM_000397	0,0277	3,1383	0,0342	2,9268	0,9906	-1,0723
11728265_a_at	LILRB2	leukocyte immunoglobulin-like receptor, subfamily	NM_001080978	0,0214	3,1205	0,0243	3,0891	0,9953	-1,0102
11715994_x_at	ID2	inhibitor of DNA binding 2, dominant negative heli	NM_002166	0,0248	3,1068	0,0269	3,0925	0,9997	-1,0046
11717118_a_at	P4HA2	prolyl 4-hydroxylase, alpha polypeptide II	NM_001017973	0,0447	3,1027	0,0483	3,2678	0,9923	1,0532
11719344_a_at	ATF3	activating transcription factor 3	NM_001030287	0,0426	3,0891	0,0470	3,1324	0,9989	1,0140
11757534_s_at	FAM198B	family with sequence similarity 198, member B	NM_001031700	0,0237	3,0850	0,0269	2,8919	0,9906	-1,0668
11743289_s_at	PEAK1	NKF3 kinase family member	NM_024776	0,0412	3,0823	0,0400	3,5454	0,9906	1,1502
11759343_x_at	FMN1	formin 1	NM_001103184	0,0475	3,0738	0,0500	3,3630	0,9906	1,0941
11729053_x_at	PPFIBP1	PTPRF interacting protein, binding protein 1 (lipri	NM_001198915	0,0269	3,0425	0,0338	2,7929	0,9906	-1,0894
11755797_x_at	ADAM9	ADAM metallopeptidase domain 9	NM_001005845	0,0237	3,0370	0,0286	2,6015	0,9906	-1,1674
11720440_at	OLFML2B	olfactomedin-like 2B	NM_015441	0,0279	3,0094	0,0470	2,1306	0,9906	-1,4125
11728423_a_at	PILRA	paired immunoglobulin-like type 2 receptor alpha	NM_013439 /// ↑	0,0271	2,9931	0,0353	2,6396	0,9906	-1,1339
11754989_a_at	DMXL2	Dmx-like 2	NM_001174116	0,0428	2,9796	0,0447	3,2123	0,9906	1,0781
11721099_at	C3AR1	complement component 3a receptor 1	NM_004054	0,0399	2,9287	0,0488	2,6852	0,9906	-1,0907
11726611_x_at	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogen	NM_001161572	0,0445	2,9223	0,0401	3,6794	0,9906	1,2591
11743000_at	CD83	CD83 molecule	NM_001040280	0,0248	2,9131	0,0269	3,0390	0,9906	1,0432
11757868_a_at	PIK3IP1	phosphoinositide-3-kinase interacting protein 1	NM_001135911	0,0407	2,9045	0,0434	3,0604	0,9916	1,0537
11716019_at	RAB31	RAB31, member RAS oncogene family	NM_006868	0,0337	2,8894	0,0422	2,6092	0,9906	-1,1074
11724509_a_at	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	NM_021127	0,0212	2,8830	0,0231	2,5628	0,9906	-1,1249
11755223_a_at	JHDM1D	jumonji C domain containing histone demethylase	NM_030647	0,0316	2,8702	0,0359	2,8917	0,9993	1,0075
11722049_a_at	DUSP6	dual specificity phosphatase 6	NM_001946 /// ↑	0,0302	2,8693	0,0334	3,1454	0,9906	1,0962
11736065_x_at	P2RX7	purinergic receptor P2X, ligand-gated ion channel	NM_002562 /// ↑	0,0297	2,8667	0,0344	2,8867	0,9993	1,0070
11741990_s_at	CCRL2	chemokine (C-C motif) receptor-like 2	NM_001130910	0,0390	2,8660	0,0494	2,5333	0,9906	-1,1313
11741223_s_at	FAM198B	family with sequence similarity 198, member B	NM_001031700	0,0237	2,8570	0,0269	2,6573	0,9906	-1,0752
11730096_a_at	BCL2A1	BCL2-related protein A1	NM_001114735	0,0391	2,8475	0,0411	2,9660	0,9923	1,0416
11744128_x_at	CXCL2	chemokine (C-X-C motif) ligand 2	NM_002089	0,0269	2,8398	0,0289	3,0480	0,9906	1,0733
11734614_a_at	GABRE ///	gamma-aminobutyric acid (GABA) A receptor, eps	NM_004961 /// ↑	0,0302	2,8377	0,0384	2,5398	0,9906	-1,1173
11717836_a_at	AIF1	allograft inflammatory factor 1	NM_001623 /// ↑	0,0237	2,8147	0,0251	3,1689	0,9906	1,1258
11757860_s_at	QKI	QKI, KH domain containing, RNA binding	NM_006775 /// ↑	0,0212	2,7775	0,0231	2,7248	0,9906	-1,0193
11734938_x_at	CSF2RA	colony stimulating factor 2 receptor, alpha, low-aff	NM_001161529	0,0302	2,7707	0,0359	2,6577	0,9910	-1,0425
11732585_a_at	IL1RAP	interleukin 1 receptor accessory protein	NM_001167928	0,0377	2,7703	0,0384	3,0152	0,9906	1,0884
11743062_a_at	PLAUR	plasminogen activator, urokinase receptor	NM_001005376	0,0368	2,7660	0,0461	2,4860	0,9906	-1,1127
11755766_x_at	SNX30	sorting nexin family member 30	NM_001012994	0,0357	2,7634	0,0377	2,9311	0,9906	1,0607
11731679_x_at	FAM20C	family with sequence similarity 20, member C	NM_020223	0,0214	2,7466	0,0245	2,6513	0,9906	-1,0359
11755606_x_at	IFI30 /// PI	interferon, gamma-inducible protein 30 /// phosph	NM_005027 /// ↑	0,0255	2,7443	0,0312	2,4962	0,9906	-1,0994
11744067_s_at	SYNGR2	synaptogyrin 2	NM_004710	0,0277	2,7405	0,0359	2,4171	0,9906	-1,1338
11721347_a_at	MPEG1	macrophage expressed 1	NM_001039396	0,0266	2,7398	0,0327	2,5007	0,9906	-1,0956
11716743_s_at	TJP2	tight junction protein 2	NM_001170414	0,0447	2,7356	0,0462	2,9584	0,9906	1,0815
11726962_at	SGTB	small glutamine-rich tetratricopeptide repeat (TPR	NM_019072	0,0212	2,7276	0,0231	2,8868	0,9906	1,0584
11746363_x_at	SYNGR2	synaptogyrin 2	NM_004710	0,0269	2,7081	0,0340	2,4658	0,9906	-1,0983
11732349_at	LILRA6	leukocyte immunoglobulin-like receptor, subfamily	NM_024318 /// >	0,0413	2,7000	0,0465	2,6851	0,9997	-1,0056
11758208_s_at	KLF2	Kruppel-like factor 2 (lung)	NM_016270	0,0311	2,6918	0,0395	2,3937	0,9906	-1,1245
11716715_a_at	CTSB	cathepsin B	NM_001908 /// ↑	0,0380	2,6676	0,0480	2,4028	0,9906	-1,1102
11723186_at	FGD6	FYVE, RhoGEF and PH domain containing 6	NM_018351	0,0466	2,6592	0,0494	2,8713	0,9906	1,0797
11717703_a_at	KIFC3	kinesin family member C3	NM_001130099	0,0363	2,6590	0,0387	2,7470	0,9937	1,0331
11734529_x_at	PILRA	paired immunoglobulin-like type 2 receptor alpha	NM_013439 /// ↑	0,0237	2,6584	0,0286	2,3409	0,9906	-1,1356
11722111_at	HLX	H2.0-like homeobox	NM_021958	0,0341	2,6522	0,0338	3,0850	0,9906	1,1632
11732432_a_at	GK	glycerol kinase	NM_000167 /// ↑	0,0271	2,6461	0,0334	2,5679	0,9923	-1,0305
11743063_x_at	PLAUR	plasminogen activator, urokinase receptor	NM_001005376	0,0285	2,6454	0,0382	2,2987	0,9906	-1,1508
11723769_at	SNX24	sorting nexin 24	NM_014035	0,0448	2,6412	0,0395	3,3672	0,9906	1,2749
11728477_at	CXCL3	chemokine (C-X-C motif) ligand 3	NM_002090	0,0357	2,6342	0,0360	2,9193	0,9906	1,1082
11736141_a_at	ITSN1	intersectin 1 (SH3 domain protein)	NM_001001132	0,0248	2,6297	0,0360	1,9034	0,9906	-1,3816
11744127_at	CXCL2	chemokine (C-X-C motif) ligand 2	NM_002089	0,0312	2,6244	0,0353	2,6926	0,9945	1,0260
11740895_a_at	MIR22 /// M	microRNA 22 /// MIR22 host gene (non-protein co	NM_001001870	0,0351	2,6139	0,0422	2,4760	0,9906	-1,0557
11755643_a_at	TNS3	tensin 3	NM_022748	0,0276	2,5963	0,0338	2,5162	0,9916	-1,0318
11732433_s_at	GK	glycerol kinase	NM_000167 /// ↑	0,0269	2,5873	0,0308	2,6914	0,9906	1,0402
11719483_a_at	P2RX4	purinergic receptor P2X, ligand-gated ion channel	NM_001256796	0,0490	2,5831	0,0483	3,0020	0,9906	1,1622
11738858_x_at	CSF2RA	colony stimulating factor 2 receptor, alpha, low-aff	NM_001161529	0,0413	2,5783	0,0494	2,4302	0,9906	-1,0610
11731197_a_at	PRR5L	proline rich 5 like	NM_001160167	0,0312	2,5773	0,0442	2,1757	0,9906	-1,1846
11742657_x_at	HIST2H2A,	histone cluster 2, H2aa3 /// histone cluster 2, H2a;	NM_001040874	0,0289	2,5756	0,0384	2,2616	0,9906	-1,1389
11719307_a_at	RASSF4	Ras association (RalGDS/AF-6) domain family me	NM_032023 /// ↑	0,0450	2,5680	0,0447	2,9075	0,9906	1,1322
11718861_a_at	HCK	hemopoietic cell kinase	NM_001172129	0,0346	2,5677	0,0447	2,2878	0,9906	-1,1224
11725989_x_at	MMP14	matrix metallopeptidase 14 (membrane-inserted)	NM_004995	0,0445	2,5673	0,0484	2,6566	0,9949	1,0348

11732188_at	PI4K2A	phosphatidylinositol 4-kinase type 2 alpha	NM_018425	0,0266	2,5599	0,0313	2,4254	0,9906	-1,0554
11750359_x_at	CD68 // S	CD68 molecule // small nucleolar RNA, H/ACA bc	NM_001040059	0,0325	2,5553	0,0422	2,2835	0,9906	-1,1190
11757306_s_at	CD59	CD59 molecule, complement regulatory protein	NM_000611 /// ↑	0,0314	2,5402	0,0405	2,2728	0,9906	-1,1177
11736375_a_at	CD86	CD86 molecule	NM_001206924	0,0271	2,5395	0,0395	2,0552	0,9906	-1,2357
11759037_s_at	IL6ST	interleukin 6 signal transducer (gp130, oncostatin	NM_001190981	0,0314	2,5366	0,0409	2,2483	0,9906	-1,1282
11758557_s_at	ZFP36L1	ZFP36 ring finger protein-like 1	NM_001244698	0,0212	2,5360	0,0231	2,7214	0,9906	1,0731
11719827_a_at	QPCT	glutaminy-peptide cyclotransferase	NM_012413	0,0266	2,5204	0,0277	2,7013	0,9906	1,0718
11754833_a_at	TLR2	toll-like receptor 2	NM_003264	0,0214	2,5184	0,0263	2,2022	0,9906	-1,1436
11719958_at	SGPL1	sphingosine-1-phosphate lyase 1	NM_003901	0,0212	2,5114	0,0231	2,4907	0,9949	-1,0083
11726823_at	ADORA3	adenosine A3 receptor	NM_000677 /// ↑	0,0451	2,5041	0,0494	2,5874	0,9949	1,0333
11723217_x_at	SFXN3	sideroflexin 3	NM_030971	0,0456	2,4982	0,0447	2,8920	0,9906	1,1577
11717758_x_at	RALA	v-ral simian leukemia viral oncogene homolog A (NM_005402	0,0212	2,4938	0,0231	2,4867	0,9995	-1,0029
11756897_x_at	TJP2	tight junction protein 2	NM_001170414	0,0447	2,4830	0,0488	2,5758	0,9937	1,0374
11727814_at	UBASH3B	ubiquitin associated and SH3 domain containing E	NM_032873	0,0373	2,4786	0,0394	2,5700	0,9923	1,0369
11721960_a_at	SNX30	sorting nexin family member 30	NM_001012994	0,0376	2,4775	0,0388	2,6203	0,9906	1,0576
11723477_x_at	SLC17A5	solute carrier family 17 (anion/sugar transporter),	NM_012434	0,0345	2,4755	0,0411	2,3362	0,9906	-1,0596
11741085_a_at	APLP2	amyloid beta (A4) precursor-like protein 2	NM_001142276	0,0212	2,4683	0,0231	2,5785	0,9906	1,0446
11717891_a_at	ECM1	extracellular matrix protein 1	NM_001202858	0,0279	2,4587	0,0358	2,2607	0,9906	-1,0876
11742819_at	PLAUR	plasminogen activator, urokinase receptor	NM_001005376	0,0365	2,4561	0,0422	2,3764	0,9923	-1,0335
11757816_s_at	MARCKS	myristoylated alanine-rich protein kinase C substr	NM_002356	0,0237	2,4504	0,0269	2,3095	0,9906	-1,0610
11716051_at	LAMC1	laminin, gamma 1 (formerly LAMB2)	NM_002293	0,0212	2,4471	0,0231	2,6252	0,9906	1,0728
11736273_a_at	TLR2	toll-like receptor 2	NM_003264	0,0324	2,4459	0,0410	2,2180	0,9906	-1,1028
11724997_a_at	CD86	CD86 molecule	NM_001206924	0,0305	2,4439	0,0359	2,4249	0,9992	-1,0078
11757383_a_at	CTSH	cathepsin H	NM_004390 /// ↑	0,0214	2,4341	0,0252	2,2942	0,9906	-1,0610
11751242_s_at	FCGR2A // Fc	fragment of IgG, low affinity IIa, receptor (CD32)	NM_001005410	0,0280	2,4300	0,0388	2,0554	0,9906	-1,1823
11727816_at	UBASH3B	ubiquitin associated and SH3 domain containing E	NM_032873	0,0269	2,4286	0,0286	2,6642	0,9906	1,0970
11716742_a_at	TJP2	tight junction protein 2	NM_001170414	0,0332	2,4244	0,0351	2,6245	0,9906	1,0825
11721957_at	YPEL2	yippee-like 2 (Drosophila)	NM_001005404	0,0442	2,4173	0,0377	3,1134	0,9906	1,2879
11718647_at	ACVR1	activin A receptor, type I	NM_0011105 /// ↑	0,0302	2,4159	0,0338	2,5487	0,9906	1,0550
11733115_a_at	CA2	carbonic anhydrase II	NM_000067	0,0346	2,4080	0,0494	2,0301	0,9906	-1,1861
11732469_at	IL3RA	interleukin 3 receptor, alpha (low affinity)	NM_001267713	0,0413	2,4042	0,0422	2,5810	0,9906	1,0735
11735511_x_at	PHTF2	putative homeodomain transcription factor 2	NM_001127357	0,0312	2,3854	0,0388	2,1901	0,9906	-1,0892
11718811_s_at	PRKCH	protein kinase C, eta	NM_006255	0,0269	2,3761	0,0286	2,6493	0,9906	1,1150
11723476_at	SLC17A5	solute carrier family 17 (anion/sugar transporter),	NM_012434	0,0269	2,3439	0,0286	2,5492	0,9906	1,0876
11724107_s_at	MRPS31P1	mitochondrial ribosomal protein S31 pseudogene	NM_018676 /// ↑	0,0445	2,3426	0,0403	2,8046	0,9906	1,1972
11717678_at	AVP1	arginine vasopressin-induced 1	NM_021732	0,0373	2,3415	0,0470	2,1367	0,9906	-1,0958
11721577_at	TNF	tumor necrosis factor	NM_000594	0,0214	2,3369	0,0234	2,6318	0,9906	1,1262
11739469_at	TMEM87B	transmembrane protein 87B	NM_032824	0,0399	2,3290	0,0388	2,5517	0,9906	1,0956
11743412_at	OTUD1	OTU domain containing 1	NM_001145373	0,0411	2,3239	0,0491	2,2139	0,9910	-1,0497
11737831_a_at	FNBP1L	formin binding protein 1-like	NM_001024948	0,0482	2,3158	0,0488	2,5839	0,9906	1,1158
11753292_x_at	CD44	CD44 molecule (Indian blood group)	NM_000610 /// ↑	0,0282	2,3111	0,0384	2,0121	0,9906	-1,1486
11718939_s_at	TNFAIP3	tumor necrosis factor, alpha-induced protein 3	NM_001270507	0,0276	2,3095	0,0274	2,7842	0,9906	1,2055
11752545_a_at	PDLIM5	PDZ and LIM domain 5	NM_001011513	0,0258	2,3087	0,0302	2,2020	0,9906	-1,0485
11721093_a_at	THBS1	thrombospondin 1	NM_003246	0,0395	2,3059	0,0377	2,6031	0,9906	1,1289
11742272_s_at	TM6SF1	transmembrane 6 superfamily member 1	NM_001144903	0,0269	2,3056	0,0320	2,3078	0,9997	1,0010
11717757_s_at	RALA	v-ral simian leukemia viral oncogene homolog A (NM_005402	0,0212	2,2982	0,0231	2,4328	0,9906	1,0586
11729099_a_at	IL1RAP	interleukin 1 receptor accessory protein	NM_001167928	0,0442	2,2940	0,0483	2,3571	0,9949	1,0275
11722094_s_at	PPIC	peptidylprolyl isomerase C (cyclophilin C)	NM_000943	0,0387	2,2906	0,0359	2,6726	0,9906	1,1668
11719528_at	PVRL2	poliovirus receptor-related 2 (herpesvirus entry me	NM_001042724	0,0250	2,2856	0,0252	2,6323	0,9906	1,1517
11758167_s_at	PHTF2	putative homeodomain transcription factor 2	NM_001127357	0,0251	2,2846	0,0300	2,1016	0,9906	-1,0870
11746940_a_at	CD9	CD9 molecule	NM_0011769	0,0271	2,2775	0,0359	2,0409	0,9906	-1,1159
11736047_a_at	ANTXR2	anthrax toxin receptor 2	NM_001145794	0,0220	2,2752	0,0252	2,3066	0,9941	1,0138
11719634_a_at	KLF4	Kruppel-like factor 4 (gut)	NM_004235	0,0281	2,2723	0,0359	2,1098	0,9906	-1,0770
11727817_at	UBASH3B	ubiquitin associated and SH3 domain containing E	NM_032873	0,0451	2,2722	0,0458	2,4973	0,9906	1,0991
11719367_a_at	PLEKH02	pleckstrin homology domain containing, family O	NM_001195059	0,0413	2,2710	0,0447	2,3179	0,9951	1,0206
11756011_a_at	PTPRJ	protein tyrosine phosphatase, receptor type, J	NM_001098503	0,0255	2,2708	0,0301	2,1466	0,9906	-1,0579
11758068_s_at	WDFY3	WD repeat and FYVE domain containing 3	NM_014991 /// ↑	0,0391	2,2685	0,0461	2,1621	0,9906	-1,0492
11740880_x_at	ANXA2	annexin A2	NM_001002857	0,0220	2,2649	0,0269	2,0654	0,9906	-1,0966
11746658_a_at	CD86	CD86 molecule	NM_001206924	0,0373	2,2642	0,0490	2,0233	0,9906	-1,1191
11728695_at	ARG2	arginase 2	NM_001172	0,0337	2,2622	0,0384	2,2219	0,9949	-1,0181
11724500_at	CRYBB1	crystallin, beta B1	NM_0011887	0,0411	2,2607	0,0269	4,7331	0,9906	2,0936
11757791_s_at	DUSP3	dual specificity phosphatase 3	NM_004090	0,0341	2,2600	0,0400	2,1631	0,9906	-1,0448
11755756_a_at	NHSL1	NHS-like 1	NM_001144060	0,0236	2,2591	0,0274	2,0533	0,9906	-1,1002
11758175_s_at	SLC36A1	solute carrier family 36 (proton/amino acid symport	NM_078483	0,0281	2,2589	0,0337	2,2676	0,9997	1,0039
11724768_s_at	FCGR2A // Fc	fragment of IgG, low affinity IIa, receptor (CD32)	NM_001005410	0,0269	2,2482	0,0306	2,2937	0,9935	1,0203
11737921_a_at	MILR1	mast cell immunoglobulin-like receptor 1	NM_001085423	0,0269	2,2347	0,0289	2,3391	0,9906	1,0467

11735242_s_at	ZC3H12C	zinc finger CCCH-type containing 12C	NM_033390	0,0267	2,2323	0,0300	2,2339	0,9997	1,0007
11715387_at	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	NM_000389 /// ↑	0,0212	2,2320	0,0231	2,3146	0,9906	1,0370
11715568_a_at	CD9	CD9 molecule	NM_001769	0,0282	2,2288	0,0327	2,3298	0,9906	1,0453
11743011_a_at	GPR137B	G protein-coupled receptor 137B	NM_003272	0,0255	2,2238	0,0327	1,9615	0,9906	-1,1337
11748126_a_at	TIMP2	TIMP metalloproteinase inhibitor 2	NM_003255	0,0427	2,2182	0,0466	2,2599	0,9952	1,0188
11720133_a_at	PROS1	protein S (alpha)	NM_000313	0,0248	2,2175	0,0269	2,2180	1,0000	1,0002
11757635_a_at	TYROBP	TYRO protein tyrosine kinase binding protein	NM_001173514	0,0308	2,2172	0,0367	2,1400	0,9910	-1,0360
11733841_a_at	EVI2A	ecotropic viral integration site 2A	NM_001003927	0,0349	2,2162	0,0388	2,2226	0,9997	1,0029
11750189_s_at	CD44	CD44 molecule (Indian blood group)	NM_000610 /// ↑	0,0248	2,2157	0,0289	2,0419	0,9906	-1,0851
11740879_s_at	ANXA2	annexin A2	NM_001002857	0,0269	2,2131	0,0334	2,1124	0,9906	-1,0477
11743389_s_at	PHTF2	putative homeodomain transcription factor 2	NM_001127357	0,0269	2,2126	0,0338	2,0903	0,9906	-1,0585
11720520_s_at	LOC10099	myomegalin-like /// myomegalin-like /// myomegali	NM_001002810	0,0450	2,2117	0,0474	2,3610	0,9906	1,0675
11723287_at	TYROBP	TYRO protein tyrosine kinase binding protein	NM_001173514	0,0357	2,2080	0,0434	2,0930	0,9906	-1,0549
11743916_a_at	NPC1	Niemann-Pick disease, type C1	NM_000271	0,0363	2,2078	0,0413	2,1633	0,9949	-1,0206
11754064_x_at	ANXA2	annexin A2	NM_001002857	0,0285	2,2043	0,0388	1,9284	0,9906	-1,1430
11716377_s_at	GRN	granulin	NM_001012479	0,0411	2,2007	0,0494	2,0903	0,9906	-1,0528
11718648_s_at	ACVR1	activin A receptor, type I	NM_001105 /// ↑	0,0285	2,1984	0,0334	2,2800	0,9906	1,0371
11740369_x_at	PDLIM5	PDZ and LIM domain 5	NM_001011513	0,0212	2,1981	0,0231	2,2169	0,9949	1,0086
11746025_a_at	MILR1	mast cell immunoglobulin-like receptor 1	NM_001085423	0,0457	2,1973	0,0492	2,3137	0,9910	1,0530
11739553_a_at	GAS7	growth arrest-specific 7	NM_001130831	0,0212	2,1959	0,0243	2,0406	0,9906	-1,0761
11729721_s_at	LILRA6 ///	leukocyte immunoglobulin-like receptor, subfamily	NM_001081450	0,0313	2,1944	0,0359	2,1846	0,9997	-1,0045
11722403_a_at	PLEKH01	pleckstrin homology domain containing, family O r	NM_016274	0,0285	2,1915	0,0377	1,9831	0,9906	-1,1051
11733060_a_at	PELI1	pellino E3 ubiquitin protein ligase 1	NM_020651	0,0251	2,1915	0,0286	2,0788	0,9906	-1,0542
11755327_s_at	LOC15476	family with sequence similarity 115, member C ps	NR_015421	0,0251	2,1898	0,0359	1,7523	0,9906	-1,2497
11722112_at	ADRA2A	adrenoceptor alpha 2A	NM_000681	0,0480	2,1872	0,0436	2,6634	0,9906	1,2177
11752119_x_at	SLC17A5	solute carrier family 17 (anion/sugar transporter),	NM_012434	0,0302	2,1790	0,0433	1,8801	0,9906	-1,1590
11715951_s_at	KCTD12	potassium channel tetramerisation domain contain	NM_138444	0,0399	2,1762	0,0436	2,2105	0,9953	1,0158
11743972_a_at	DDIT4	DNA-damage-inducible transcript 4	NM_019058	0,0305	2,1738	0,0334	2,3759	0,9906	1,0930
11718931_a_at	SLC35D2	solute carrier family 35, member D2	NM_007001	0,0449	2,1725	0,0417	2,5472	0,9906	1,1725
11744134_at	ZSWIM6	zinc finger, SWIM-type containing 6	NM_020928	0,0212	2,1608	0,0231	2,0369	0,9906	-1,0609
11745848_a_at	TJP2	tight junction protein 2	NM_001170414	0,0337	2,1605	0,0384	2,1227	0,9949	-1,0178
11757341_s_at	OPTN	optineurin	NM_001008211	0,0373	2,1561	0,0371	2,3579	0,9906	1,0936
11734162_a_at	TFEC	transcription factor EC	NM_001018058	0,0214	2,1545	0,0242	2,1752	0,9949	1,0096
11717464_at	LXN	latexin	NM_020169	0,0276	2,1475	0,0303	2,2987	0,9906	1,0704
11731634_at	HPGDS	hematopoietic prostaglandin D synthase	NM_014485	0,0373	2,1413	0,0353	2,4687	0,9906	1,1529
11730878_x_at	MYCT1	myc target 1	NM_025107	0,0285	2,1413	0,0269	2,7293	0,9906	1,2746
11757684_a_at	TPD52L2	tumor protein D52-like 2	NM_001243891	0,0461	2,1345	0,0482	2,3079	0,9906	1,0812
11750190_x_at	CD44	CD44 molecule (Indian blood group)	NM_000610 /// ↑	0,0349	2,1316	0,0399	2,1031	0,9953	-1,0136
11744619_a_at	SNX24	sorting nexin 24	NM_014035	0,0341	2,1294	0,0422	2,0012	0,9906	-1,0640
11746018_a_at	GRAMD3	GRAM domain containing 3	NM_001146319	0,0346	2,1267	0,0465	1,8947	0,9906	-1,1225
11753291_a_at	CD44	CD44 molecule (Indian blood group)	NM_000610 /// ↑	0,0269	2,1262	0,0360	1,8342	0,9906	-1,1592
11724769_x_at	FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32)	NM_001136219	0,0251	2,1242	0,0274	2,0842	0,9923	-1,0192
11721056_x_at	PRKX	protein kinase, X-linked	NM_005044	0,0467	2,1232	0,0484	2,2996	0,9906	1,0831
11763855_x_at	CD9	CD9 molecule	NM_001769	0,0281	2,1175	0,0363	1,9410	0,9906	-1,0909
11758377_s_at	TLR1	toll-like receptor 1	NM_003263	0,0261	2,1174	0,0311	2,0154	0,9906	-1,0506
11716093_a_at	KLF6	Kruppel-like factor 6	NM_001008490	0,0408	2,1143	0,0488	2,0244	0,9910	-1,0444
11733061_s_at	PELI1	pellino E3 ubiquitin protein ligase 1	NM_020651	0,0374	2,1099	0,0410	2,1271	0,9989	1,0081
11720746_s_at	BCL6	B-cell CLL/lymphoma 6	NM_001130845	0,0277	2,1092	0,0334	2,1031	0,9997	-1,0029
11715388_s_at	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	NM_000389 /// ↑	0,0255	2,1057	0,0275	2,1295	0,9951	1,0113
11742948_at	MARCKS	myristoylated alanine-rich protein kinase C substr	NM_002356	0,0332	2,1055	0,0494	1,7765	0,9906	-1,1852
11717465_s_at	LXN	latexin	NM_020169	0,0269	2,1037	0,0274	2,3179	0,9906	1,1018
11726961_at	SGTB	small glutamine-rich tetratricopeptide repeat (TPR)	NM_019072	0,0392	2,1036	0,0370	2,3780	0,9906	1,1304
11723707_a_at	AIFM2	apoptosis-inducing factor, mitochondrion-associat	NM_001198696	0,0417	2,0984	0,0384	2,4248	0,9906	1,1555
11718746_x_at	ARHGAP2	Rho GTPase activating protein 21	NM_020824	0,0393	2,0908	0,0384	2,2676	0,9906	1,0846
11716052_s_at	LAMC1	laminin, gamma 1 (formerly LAMB2)	NM_002293	0,0450	2,0907	0,0470	2,2301	0,9906	1,0667
11717552_s_at	FNBP1L	formin binding protein 1-like	NM_001024948	0,0294	2,0893	0,0313	2,3200	0,9906	1,1104
11733148_a_at	ANXA4	annexin A4	NM_001153	0,0399	2,0865	0,0494	1,9468	0,9906	-1,0717
11730864_s_at	CTTNBP2	CTTNBP2 N-terminal like	NM_018704	0,0401	2,0803	0,0408	2,2061	0,9906	1,0605
11737798_a_at	PROCR	protein C receptor, endothelial	NM_006404	0,0302	2,0729	0,0441	1,7909	0,9906	-1,1575
11735241_at	ZC3H12C	zinc finger CCCH-type containing 12C	NM_033390	0,0363	2,0688	0,0449	1,9284	0,9906	-1,0728
11744829_s_at	HLA-E	major histocompatibility complex, class I, E	NM_005516	0,0337	2,0661	0,0338	2,3096	0,9906	1,1179
11750041_s_at	ANXA5	annexin A5	NM_001154	0,0377	2,0617	0,0434	2,0273	0,9951	-1,0170
11723768_a_at	SNX24	sorting nexin 24	NM_014035	0,0458	2,0613	0,0491	2,1733	0,9906	1,0543
11716828_a_at	NPC2	Niemann-Pick disease, type C2	NM_006432	0,0370	2,0611	0,0367	2,2541	0,9906	1,0936
11718979_a_at	HTATIP2	HIV-1 Tat interactive protein 2, 30kDa	NM_001098520	0,0255	2,0602	0,0279	2,0719	0,9984	1,0057
11752817_s_at	TPP1	tripeptidyl peptidase I	NM_000391	0,0390	2,0572	0,0459	1,9731	0,9906	-1,0427

11744797_s_at	DAB2	Dab, mitogen-responsive phosphoprotein, homolo	NM_001244871	0,0269	2,0542	0,0334	1,9334	0,9906	-1,0624
11715915_a_at	CD44	CD44 molecule (Indian blood group)	NM_000610 /// ↑	0,0265	2,0532	0,0338	1,8510	0,9906	-1,1093
11747282_x_at	ANXA2 ///	annexin A2 /// annexin A2 pseudogene 2	NM_001002857	0,0270	2,0532	0,0353	1,8760	0,9906	-1,0944
11718724_at	ARRDC3	arrestin domain containing 3	NM_020801	0,0393	2,0492	0,0344	2,4999	0,9906	1,2200
11727992_at	STX11	syntaxin 11	NM_003764	0,0345	2,0457	0,0422	1,9364	0,9906	-1,0564
11745902_a_at	NPC2	Niemann-Pick disease, type C2	NM_006432	0,0220	2,0414	0,0245	2,1407	0,9906	1,0486
11716095_s_at	KLF6	Kruppel-like factor 6	NM_001008490	0,0314	2,0327	0,0370	1,9922	0,9940	-1,0203
11739617_x_at	CD44	CD44 molecule (Indian blood group)	NM_000610 /// ↑	0,0312	2,0320	0,0370	1,9676	0,9910	-1,0327
11729033_at	ITPRIPL2	inositol 1,4,5-trisphosphate receptor interacting pr	NM_001034841	0,0368	2,0256	0,0381	2,1195	0,9906	1,0464
11736655_a_at	PTGR1	prostaglandin reductase 1	NM_001146108	0,0404	2,0223	0,0447	2,0381	0,9992	1,0078
11758221_s_at	ARRDC3	arrestin domain containing 3	NM_020801	0,0341	2,0217	0,0405	1,9394	0,9906	-1,0424
11735293_x_at	TNFRSF11	tumor necrosis factor receptor superfamily, memb	NM_001270949	0,0249	2,0198	0,0324	1,7617	0,9906	-1,1465
11720134_s_at	PROS1	protein S (alpha)	NM_000313	0,0325	2,0192	0,0360	2,0568	0,9949	1,0186
11755110_a_at	LRIG1	leucine-rich repeats and immunoglobulin-like dom	NM_015541	0,0266	2,0153	0,0252	2,4925	0,9906	1,2368
11717568_s_at	NQO1	NAD(P)H dehydrogenase, quinone 1	NM_000903 /// ↑	0,0401	2,0116	0,0464	1,9574	0,9926	-1,0277
11748775_a_at	UPP1	uridine phosphorylase 1	NM_003364 /// ↑	0,0447	2,0083	0,0456	2,1401	0,9906	1,0656
11754763_a_at	GNPDA1	glucosamine-6-phosphate deaminase 1	NM_005471	0,0420	2,0075	0,0444	2,0987	0,9906	1,0454
11719728_s_at	SIRPA	signal-regulatory protein alpha	NM_001040022	0,0403	2,0047	0,0491	1,9033	0,9906	-1,0533
11717107_a_at	PDLIM5	PDZ and LIM domain 5	NM_001011513	0,0221	2,0047	0,0252	2,0068	0,9997	1,0011
11727905_a_at	IL13RA1	interleukin 13 receptor, alpha 1	NM_001560	0,0269	2,0035	0,0296	2,1371	0,9906	1,0667
11718319_at	CD93	CD93 molecule	NM_012072	0,0316	2,0012	0,0434	1,7981	0,9906	-1,1129
11743113_x_at	S100A10	S100 calcium binding protein A10	NM_002966	0,0258	2,0011	0,0353	1,7213	0,9906	-1,1625
11724409_a_at	MARCH2	membrane-associated ring finger (C3HC4) 2, E3	NM_001005415	0,0374	1,9992	0,0377	2,1361	0,9906	1,0685
11749587_x_at	FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32	NM_001136219	0,0369	1,9983	0,0447	1,8951	0,9906	-1,0544
11743112_at	S100A10	S100 calcium binding protein A10	NM_002966	0,0214	1,9975	0,0269	1,8280	0,9906	-1,0927
11728972_a_at	PTPRJ	protein tyrosine phosphatase, receptor type, J	NM_001098503	0,0255	1,9949	0,0308	1,8530	0,9906	-1,0766
11715949_s_at	KCTD12	potassium channel tetramerisation domain contain	NM_138444	0,0496	1,9947	0,0491	2,2068	0,9906	1,1063
11741959_x_at	IL6R	interleukin 6 receptor	NM_000565 /// ↑	0,0212	1,9881	0,0231	2,0383	0,9906	1,0253
11743033_x_at	ANXA5	annexin A5	NM_001154	0,0302	1,9875	0,0359	1,9508	0,9940	-1,0188
11754317_a_at	ANXA4	annexin A4	NM_001153	0,0341	1,9870	0,0366	2,0507	0,9910	1,0321
11758879_s_at	HLA-E	major histocompatibility complex, class I, E	NM_005516	0,0346	1,9834	0,0327	2,3791	0,9906	1,1995
11729406_a_at	IFNGR1	interferon gamma receptor 1	NM_000416	0,0255	1,9770	0,0289	1,9486	0,9937	-1,0146
11715570_x_at	CD9	CD9 molecule	NM_001769	0,0252	1,9746	0,0269	2,0051	0,9927	1,0155
11763704_a_at	SAT1	spermidine/spermine N1-acetyltransferase 1	NM_002970 /// ↑	0,0288	1,9708	0,0392	1,7709	0,9906	-1,1129
11717099_at	HIST1H2B	histone cluster 1, H2bk	NM_080593	0,0426	1,9646	0,0489	1,9376	0,9954	-1,0139
11744654_s_at	CD44	CD44 molecule (Indian blood group)	NM_000610 /// ↑	0,0419	1,9578	0,0471	1,9500	0,9997	-1,0040
11715569_at	CD9	CD9 molecule	NM_001769	0,0303	1,9545	0,0342	1,9959	0,9923	1,0212
11716453_s_at	MYO1C	myosin IC	NM_001080779	0,0302	1,9513	0,0348	1,9675	0,9964	1,0083
11748910_a_at	LOC10012	uncharacterized LOC100129518 /// superoxide dis	NM_000636 /// ↑	0,0237	1,9483	0,0269	1,9187	0,9923	-1,0154
11724836_at	NCEH1	neutral cholesterol ester hydrolase 1	NM_001146276	0,0413	1,9437	0,0491	1,8769	0,9915	-1,0356
11722970_a_at	CREB5 ///	cAMP responsive element binding protein 5 /// un	NM_001011666	0,0288	1,9414	0,0351	1,8993	0,9923	-1,0222
11731633_at	HPGDS	hematopoietic prostaglandin D synthase	NM_014485	0,0327	1,9345	0,0338	2,1275	0,9906	1,0998
11715926_s_at	PLEC	plectin	NM_000445 /// ↑	0,0316	1,9330	0,0384	1,8450	0,9906	-1,0477
11758318_s_at	CSTB	cystatin B (stefin B)	NM_000100	0,0271	1,9316	0,0338	1,8460	0,9906	-1,0464
11715917_a_at	CD44	CD44 molecule (Indian blood group)	NM_000610 /// ↑	0,0447	1,9272	0,0486	1,9738	0,9949	1,0242
11737066_x_at	GCSAML	germinal center-associated, signaling and motility	NM_145278	0,0387	1,9268	0,0384	2,0555	0,9906	1,0668
11751951_a_at	TJP2	tight junction protein 2	NM_001170414	0,0212	1,9264	0,0231	2,0124	0,9906	1,0447
11757933_s_at	BTG2	BTG family, member 2	NM_006763	0,0399	1,9256	0,0400	2,0472	0,9906	1,0631
11754319_at	SSH1	slingshot protein phosphatase 1	NM_001161330	0,0401	1,9189	0,0404	2,0283	0,9906	1,0570
11751905_a_at	NID1	nidogen 1	NM_002508	0,0251	1,9174	0,0242	2,3567	0,9906	1,2291
11738036_s_at	APLP2	amyloid beta (A4) precursor-like protein 2	NM_001142276	0,0288	1,9171	0,0334	1,9856	0,9906	1,0357
11716826_a_at	FMOD	fibromodulin	NM_002023	0,0346	1,9134	0,0242	3,7094	0,9906	1,9386
11758924_x_at	LOC10012	uncharacterized LOC100129518 /// superoxide dis	NM_000636 /// ↑	0,0447	1,9103	0,0494	1,9288	0,9984	1,0097
11724410_x_at	MARCH2	membrane-associated ring finger (C3HC4) 2, E3	NM_001005415	0,0220	1,9079	0,0252	1,8869	0,9937	-1,0111
11724448_a_at	DNMBP	dynamamin binding protein	NM_015221	0,0353	1,9079	0,0375	1,9890	0,9906	1,0425
11718100_s_at	CD59	CD59 molecule, complement regulatory protein	NM_000611 /// ↑	0,0269	1,9017	0,0334	1,8409	0,9906	-1,0330
11719029_at	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1	NM_152309	0,0357	1,8995	0,0375	1,9773	0,9906	1,0410
11743469_a_at	WDFY3	WD repeat and FYVE domain containing 3	NM_014991 /// ↑	0,0258	1,8977	0,0286	1,9103	0,9964	1,0067
11717937_at	SMIM3	small integral membrane protein 3	NM_032947	0,0324	1,8954	0,0411	1,7650	0,9906	-1,0739
11736539_x_at	RAB7L1	RAB7, member RAS oncogene family-like 1	NM_001135662	0,0255	1,8951	0,0269	2,0940	0,9906	1,1050
11759022_s_at	ELK3	ELK3, ETS-domain protein (SRF accessory protein)	NM_005230	0,0269	1,8951	0,0269	2,1142	0,9906	1,1156
11726019_at	EEDP1	endonuclease/exonuclease/phosphatase family d	NM_030636	0,0212	1,8926	0,0231	2,0108	0,9906	1,0624
11715615_at	BTG2	BTG family, member 2	NM_006763	0,0214	1,8923	0,0242	2,0144	0,9906	1,0646
11726464_a_at	IGFLR1	IGF-like family receptor 1	NM_024660	0,0251	1,8907	0,0269	1,9583	0,9906	1,0357
11754496_x_at	FMO1	flavin containing monooxygenase 1	NM_002021	0,0497	1,8904	0,0391	2,4393	0,9906	1,2904
11746893_a_at	MPP1	membrane protein, palmitoylated 1, 55kDa	NM_001166460	0,0485	1,8894	0,0464	2,1186	0,9906	1,1213

11723868_a_at	SYNJ1	synaptojanin 1	NM_001160302	0,0314	1,8885	0,0324	2,1114	0,9906	1,1181
11729747_a_at	IL10RA	interleukin 10 receptor, alpha	NM_001558 /// †	0,0212	1,8857	0,0231	1,8908	0,9962	1,0027
11746894_x_at	MPP1	membrane protein, palmitoylated 1, 55kDa	NM_001166460	0,0266	1,8857	0,0269	2,1131	0,9906	1,1206
11740300_x_at	MARCH2	membrane-associated ring finger (C3HC4) 2, E3	NM_001005415	0,0346	1,8765	0,0368	1,9543	0,9906	1,0415
11730719_x_at	AP1S2	adaptor-related protein complex 1, sigma 2 subun	NM_001272071	0,0316	1,8754	0,0448	1,6605	0,9906	-1,1294
11751618_x_at	HLA-E	major histocompatibility complex, class I, E	NM_005516	0,0346	1,8730	0,0359	1,9986	0,9906	1,0671
11718905_x_at	FILIP1L	filamin A interacting protein 1-like	NM_001042459	0,0458	1,8706	0,0480	1,9900	0,9906	1,0638
11756395_s_at	AP1S2	adaptor-related protein complex 1, sigma 2 subun	NM_001272071	0,0248	1,8702	0,0269	1,8372	0,9915	-1,0180
11741550_a_at	OSBPL6	oxysterol binding protein-like 6	NM_001201480	0,0451	1,8691	0,0387	2,2492	0,9906	1,2033
11721588_at	TRAF1	TNF receptor-associated factor 1	NM_001190945	0,0388	1,8625	0,0359	2,0991	0,9906	1,1270
11715916_a_at	CD44	CD44 molecule (Indian blood group)	NM_000610 /// †	0,0269	1,8571	0,0327	1,8010	0,9906	-1,0312
11721993_at	SLC6A6	solute carrier family 6 (neurotransmitter transporte	NM_001134367	0,0388	1,8554	0,0494	1,7243	0,9906	-1,0761
11724771_x_at	FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32	NM_001136219	0,0427	1,8537	0,0485	1,8443	0,9996	-1,0051
11756245_s_at	ANXA5	annexin A5	NM_0011154	0,0251	1,8473	0,0269	1,8966	0,9906	1,0267
11727994_at	STX11	syntaxin 11	NM_003764	0,0297	1,8444	0,0369	1,7644	0,9906	-1,0454
11750740_a_at	ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	NM_001042437	0,0212	1,8409	0,0231	1,8931	0,9906	1,0284
11718255_at	ABHD4	abhydrolase domain containing 4	NM_022060	0,0220	1,8397	0,0269	1,7740	0,9906	-1,0370
11723562_a_at	VWA5A	von Willebrand factor A domain containing 5A	NM_001130142	0,0449	1,8331	0,0461	1,9465	0,9906	1,0619
11756712_a_at	ACP2	acid phosphatase 2, lysosomal	NM_001131064	0,0269	1,8329	0,0320	1,8320	0,9999	-1,0005
11722548_at	HIVEP1	human immunodeficiency virus type I enhancer b	NM_002114	0,0219	1,8326	0,0269	1,6816	0,9906	-1,0898
11737748_a_at	GMFB	glia maturation factor, beta	NM_004124	0,0269	1,8318	0,0334	1,7659	0,9906	-1,0373
11732415_s_at	TIAM1	T-cell lymphoma invasion and metastasis 1	NM_003253	0,0456	1,8266	0,0377	2,2482	0,9906	1,2309
11741449_s_at	CD99	CD99 molecule	NM_001122898	0,0342	1,8250	0,0359	1,9113	0,9906	1,0473
11741086_x_at	APLP2	amyloid beta (A4) precursor-like protein 2	NM_001142276	0,0292	1,8225	0,0308	2,0019	0,9906	1,0985
11727415_at	CLN8	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progr	NM_001034061	0,0314	1,8224	0,0359	1,8249	0,9997	1,0014
11716717_a_at	NINJ1	ninjurin 1	NM_004148	0,0357	1,8210	0,0447	1,7211	0,9906	-1,0580
11728287_at	RHOQ	ras homolog family member Q	NM_012249	0,0442	1,8161	0,0456	1,9023	0,9906	1,0475
11728391_s_at	LRP12	low density lipoprotein receptor-related protein 12	NM_001135703	0,0214	1,8133	0,0262	1,7271	0,9906	-1,0499
11748401_x_at	TPM4	tropomyosin 4	NM_001145160	0,0324	1,8127	0,0422	1,6802	0,9906	-1,0789
11757872_s_at	PLSCR1	phospholipid scramblase 1	NM_021105	0,0436	1,8122	0,0447	1,9068	0,9906	1,0522
11730788_a_at	APLP2	amyloid beta (A4) precursor-like protein 2	NM_001142276	0,0288	1,8117	0,0315	1,9384	0,9906	1,0700
11715858_s_at	NCKAP1	NCK-associated protein 1	NM_013436 /// †	0,0391	1,8034	0,0447	1,7806	0,9951	-1,0128
11717837_x_at	AIF1	allograft inflammatory factor 1	NM_0011623 /// †	0,0447	1,8033	0,0395	2,0784	0,9906	1,1525
11749517_x_at	EHD1	EH-domain containing 1	NM_006795	0,0255	1,7972	0,0274	1,8141	0,9949	1,0094
11716071_s_at	PIM3	pim-3 oncogene	NM_001001852	0,0456	1,7963	0,0400	2,1036	0,9906	1,1711
11720300_a_at	SLA	Src-like-adaptor	NM_001045556	0,0434	1,7868	0,0444	1,8986	0,9906	1,0626
11723195_x_at	HLA-E	major histocompatibility complex, class I, E	NM_005516	0,0285	1,7850	0,0313	1,8952	0,9906	1,0617
11720302_a_at	SLA	Src-like-adaptor	NM_001045556	0,0449	1,7830	0,0438	1,9566	0,9906	1,0974
11745504_a_at	MPP1	membrane protein, palmitoylated 1, 55kDa	NM_001166460	0,0439	1,7735	0,0380	2,0667	0,9906	1,1653
11746543_a_at	SNX9	sorting nexin 9	NM_016224	0,0447	1,7676	0,0489	1,8031	0,9949	1,0201
11723863_a_at	DOCK10	dedicator of cytokinesis 10	NM_014689 /// †	0,0391	1,7628	0,0447	1,7402	0,9951	-1,0130
11728532_at	FCER1A	Fc fragment of IgE, high affinity I, receptor for; alp	NM_002001	0,0255	1,7596	0,0274	1,7952	0,9910	1,0202
11726218_a_at	PRDM1	PR domain containing 1, with ZNF domain	NM_001198 /// †	0,0337	1,7593	0,0377	1,7543	0,9997	-1,0028
11728617_at	CARD6	caspase recruitment domain family, member 6	NM_032587	0,0346	1,7578	0,0340	1,9379	0,9906	1,1025
11732132_a_at	IDS	iduronate 2-sulfatase	NM_000202 /// †	0,0293	1,7529	0,0351	1,7324	0,9949	-1,0119
11757843_s_at	PEA15	phosphoprotein enriched in astrocytes 15	NM_003768	0,0212	1,7517	0,0231	1,7686	0,9910	1,0097
11716072_s_at	ATP6V1B2	ATPase, H+ transporting, lysosomal 56/58kDa, V1	NM_001693	0,0320	1,7481	0,0375	1,7205	0,9940	-1,0161
11754318_at	SSH1	slingshot protein phosphatase 1	NM_001161330	0,0302	1,7478	0,0334	1,8429	0,9906	1,0544
11720864_s_at	SLC25A24	solute carrier family 25 (mitochondrial carrier; pho	NM_013386 /// †	0,0424	1,7473	0,0463	1,7634	0,9965	1,0092
11740974_a_at	CYFIP1	cytoplasmic FMR1 interacting protein 1	NM_001033028	0,0285	1,7466	0,0436	1,5348	0,9906	-1,1380
11725327_a_at	CAMK2D	calcium/calmodulin-dependent protein kinase II de	NM_0011221 /// †	0,0258	1,7426	0,0269	1,9065	0,9906	1,0941
11732084_a_at	TFEC	transcription factor EC	NM_001018058	0,0365	1,7422	0,0364	1,8620	0,9906	1,0687
11727412_a_at	CLN8	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progr	NM_001034061	0,0419	1,7421	0,0471	1,7377	0,9997	-1,0025
11736550_x_at	RAB7L1	RAB7, member RAS oncogene family-like 1	NM_001135662	0,0451	1,7417	0,0491	1,7881	0,9923	1,0267
11748400_s_at	TPM4	tropomyosin 4	NM_001145160	0,0313	1,7411	0,0400	1,6321	0,9906	-1,0668
11722558_x_at	MPP1	membrane protein, palmitoylated 1, 55kDa	NM_001166460	0,0345	1,7370	0,0338	1,9299	0,9906	1,1111
11731183_a_at	TFPI	tissue factor pathway inhibitor (lipoprotein-associa	NM_001032281	0,0345	1,7352	0,0481	1,5753	0,9906	-1,1015
11755046_a_at	SPHK1	sphingosine kinase 1	NM_001142601	0,0362	1,7289	0,0461	1,6223	0,9906	-1,0657
11722152_s_at	EIF2AK3	eukaryotic translation initiation factor 2-alpha kina	NM_004836	0,0405	1,7249	0,0320	2,2462	0,9906	1,3022
11725364_x_at	GAS7	growth arrest-specific 7	NM_001130831	0,0345	1,7248	0,0447	1,6193	0,9906	-1,0652
11736315_s_at	WBP5	WW domain binding protein 5	NM_001006612	0,0442	1,7244	0,0447	1,8184	0,9906	1,0545
11743458_a_at	FAM49A	family with sequence similarity 49, member A	NM_030797	0,0267	1,7224	0,0338	1,6053	0,9906	-1,0730
11716135_a_at	MVP	major vault protein	NM_005115 /// †	0,0438	1,7221	0,0447	1,8031	0,9906	1,0470
11720367_a_at	TMEM2	transmembrane protein 2	NM_001135820	0,0451	1,7211	0,0387	2,0173	0,9906	1,1721
11743010_at	NFIL3	nuclear factor, interleukin 3 regulated	NM_005384	0,0363	1,7196	0,0444	1,6527	0,9906	-1,0405
11733187_a_at	IL7R	interleukin 7 receptor	NM_002185	0,0402	1,7193	0,0411	1,7887	0,9906	1,0404

11758676_s_at	RHOQ	ras homolog family member Q	NM_012249	0,0251	1,7131	0,0334	1,5389	0,9906	-1,1132
11715584_a_at	CAV1	caveolin 1, caveolae protein, 22kDa	NM_001172895	0,0337	1,7127	0,0269	2,2751	0,9906	1,3283
11749802_a_at	ARL8B	ADP-ribosylation factor-like 8B	NM_018184	0,0251	1,7125	0,0306	1,5850	0,9906	-1,0804
11747808_a_at	WIP1	WD repeat domain, phosphoinositide interacting 1	NM_017983	0,0399	1,7110	0,0463	1,6673	0,9916	-1,0262
11756436_x_at	C1orf85	chromosome 1 open reading frame 85	NM_001256604	0,0325	1,7094	0,0359	1,7403	0,9923	1,0181
11722542_a_at	HIVEP2	human immunodeficiency virus type I enhancer binding protein 2	NM_006734	0,0269	1,7094	0,0351	1,5742	0,9906	-1,0859
11718137_a_at	PDXK	pyridoxal (pyridoxine, vitamin B6) kinase	NM_003681 /// ↑	0,0436	1,7087	0,0500	1,6862	0,9951	-1,0134
11717413_a_at	WIP1	WD repeat domain, phosphoinositide interacting 1	NM_017983	0,0281	1,7058	0,0342	1,6700	0,9910	-1,0215
11744054_a_at	ZNF1	zinc finger, NFX1-type containing 1	NM_021035	0,0251	1,7039	0,0269	1,7460	0,9906	1,0247
11719638_a_at	NEK3	NIMA-related kinase 3	NM_001146099	0,0456	1,6997	0,0338	2,2813	0,9906	1,3422
11723187_at	FGD6	FYVE, RhoGEF and PH domain containing 6	NM_018351	0,0269	1,6968	0,0286	1,7594	0,9906	1,0369
11727007_at	SORT1	sortilin 1	NM_001205228	0,0428	1,6963	0,0395	1,8725	0,9906	1,1039
11757793_s_at	TFPI	tissue factor pathway inhibitor (lipoprotein-association factor 1)	NM_001032281	0,0267	1,6953	0,0352	1,5411	0,9906	-1,1001
11725452_at	MCUR1	mitochondrial calcium uniporter regulator 1	NM_001031713	0,0427	1,6877	0,0306	2,3501	0,9906	1,3925
11758830_at	SLA	Src-like-adaptor	NM_001045556	0,0488	1,6819	0,0494	1,7839	0,9906	1,0606
11723563_at	VWA5A	von Willebrand factor A domain containing 5A	NM_001130142	0,0348	1,6782	0,0377	1,7104	0,9923	1,0192
11720208_a_at	IRF9	interferon regulatory factor 9	NM_006084	0,0493	1,6781	0,0491	1,8056	0,9906	1,0760
11718641_a_at	NDST2	N-deacetylase/N-sulfotransferase (heparan glucosaminase 2)	NM_003635	0,0449	1,6729	0,0422	1,8436	0,9906	1,1021
11748563_s_at	REEP5	receptor accessory protein 5	NM_005669	0,0341	1,6726	0,0404	1,6238	0,9906	-1,0300
11757515_s_at	ITGAV	integrin, alpha V	NM_001144999	0,0337	1,6725	0,0377	1,6700	0,9997	-1,0015
11729063_a_at	PDGFA	platelet-derived growth factor alpha polypeptide	NM_002607 /// ↑	0,0399	1,6670	0,0424	1,7013	0,9923	1,0206
11716041_a_at	PPP2CB	protein phosphatase 2, catalytic subunit, beta isoform	NM_001009552	0,0365	1,6664	0,0467	1,5677	0,9906	-1,0630
11716097_a_at	RAP1A	RAP1A, member of RAS oncogene family	NM_001010935	0,0443	1,6586	0,0442	1,7720	0,9906	1,0683
11749803_s_at	ARL8B	ADP-ribosylation factor-like 8B	NM_018184	0,0346	1,6548	0,0408	1,6210	0,9916	-1,0209
11756358_a_at	PLK3	polo-like kinase 3	NM_004073	0,0312	1,6528	0,0334	1,7525	0,9906	1,0604
11758506_s_at	RNF13	ring finger protein 13	NM_007282 /// ↑	0,0258	1,6510	0,0302	1,6068	0,9906	-1,0275
11722298_a_at	RAB7L1	RAB7, member RAS oncogene family-like 1	NM_001135662	0,0292	1,6499	0,0342	1,6511	0,9997	1,0007
11752620_s_at	YPEL5	yippee-like 5 (Drosophila)	NM_001127399	0,0212	1,6479	0,0231	1,6471	0,9997	-1,0005
11722379_at	GNG11	guanine nucleotide binding protein (G protein), gamma 11	NM_004126	0,0324	1,6465	0,0338	1,7511	0,9906	1,0635
11733644_s_at	NECAP2	NECAP endocytosis associated 2	NM_001145277	0,0449	1,6443	0,0448	1,7495	0,9906	1,0640
11757578_x_at	RHOC	ras homolog family member C	NM_001042678	0,0277	1,6369	0,0376	1,5122	0,9906	-1,0824
11743036_s_at	SAT1	spermidine/spermine N1-acetyltransferase 1	NM_002970 /// ↑	0,0265	1,6316	0,0297	1,6181	0,9949	-1,0084
11757839_s_at	NECAP2	NECAP endocytosis associated 2	NM_001145277	0,0212	1,6303	0,0231	1,6510	0,9906	1,0127
11749978_a_at	MVP	major vault protein	NM_005115 /// ↑	0,0450	1,6280	0,0456	1,7205	0,9906	1,0568
11735429_x_at	RNF135	ring finger protein 135	NM_001184992	0,0269	1,6243	0,0313	1,6064	0,9940	-1,0111
11748957_x_at	CORO1C	coronin, actin binding protein, 1C	NM_001105237	0,0214	1,6242	0,0242	1,6234	0,9997	-1,0005
11755603_a_at	ARL8B	ADP-ribosylation factor-like 8B	NM_018184	0,0281	1,6215	0,0351	1,5721	0,9906	-1,0314
11756303_a_at	SH3TC1	SH3 domain and tetratricopeptide repeats 1	NM_018986	0,0366	1,6205	0,0395	1,6362	0,9952	1,0097
11757894_x_at	NFKBIA	nuclear factor of kappa light polypeptide gene enhancer 1, alpha	NM_020529	0,0497	1,6201	0,0447	1,8360	0,9906	1,1333
11722031_s_at	RNF11	ring finger protein 11	NM_014372	0,0281	1,6174	0,0327	1,6577	0,9906	1,0249
11757513_at	NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer 1, zeta	NM_001005474	0,0365	1,6129	0,0334	1,8407	0,9906	1,1412
11723951_a_at	TFPI	tissue factor pathway inhibitor (lipoprotein-association factor 1)	NM_001032281	0,0332	1,6086	0,0394	1,5638	0,9906	-1,0286
11716042_x_at	PPP2CB	protein phosphatase 2, catalytic subunit, beta isoform	NM_001009552	0,0269	1,6073	0,0327	1,5778	0,9910	-1,0187
11744538_a_at	CALHM2	calcium homeostasis modulator 2	NM_015916 /// ↑	0,0251	1,6060	0,0297	1,5345	0,9906	-1,0466
11715432_a_at	TMBIM1	transmembrane BAX inhibitor motif containing 1	NM_022152	0,0308	1,6026	0,0384	1,5339	0,9906	-1,0448
11722141_at	RELB	v-rel reticuloendotheliosis viral oncogene homolog B	NM_006509	0,0214	1,5999	0,0231	1,6923	0,9906	1,0578
11731574_at	FRMD4B	FERM domain containing 4B	NM_015123	0,0388	1,5981	0,0388	1,6623	0,9906	1,0401
11754587_a_at	FYN	FYN oncogene related to SRC, FGR, YES	NM_001242779	0,0250	1,5979	0,0269	1,6202	0,9910	1,0140
11743962_at	CNST	consortin, connexin sorting protein	NM_001139459	0,0423	1,5951	0,0424	1,6730	0,9906	1,0489
11727920_a_at	OSTF1	osteoclast stimulating factor 1	NM_012383	0,0363	1,5945	0,0403	1,5909	0,9997	-1,0023
11739711_a_at	PHACTR2	phosphatase and actin regulator 2	NM_001100164	0,0493	1,5919	0,0475	1,7268	0,9906	1,0848
11732905_a_at	CABLES1	Cdk5 and Abl enzyme substrate 1	NM_001100619	0,0212	1,5914	0,0231	1,6342	0,9906	1,0269
11744000_a_at	NFKBIA	nuclear factor of kappa light polypeptide gene enhancer 1, alpha	NM_020529	0,0320	1,5887	0,0300	1,8169	0,9906	1,1437
11759092_at	USP12	ubiquitin specific peptidase 12	NM_182488	0,0212	1,5878	0,0231	1,6525	0,9906	1,0407
11716302_s_at	ACSL1	acyl-CoA synthetase long-chain family member 1	NM_0011995	0,0250	1,5858	0,0286	1,5273	0,9906	-1,0383
11744698_x_at	TPRG1L	tumor protein p63 regulated 1-like	NM_182752	0,0447	1,5831	0,0470	1,6341	0,9906	1,0322
11722602_at	PLEKHF1	pleckstrin homology domain containing, family F (1)	NM_024310	0,0324	1,5831	0,0395	1,5283	0,9906	-1,0358
11728733_at	ZBTB38	zinc finger and BTB domain containing 38	NM_001080412	0,0447	1,5803	0,0480	1,6218	0,9915	1,0263
11734317_a_at	STARD8	StAR-related lipid transfer (START) domain containing 8	NM_001142503	0,0281	1,5792	0,0348	1,5385	0,9906	-1,0265
11723329_a_at	GSN	gelsolin	NM_000177 /// ↑	0,0458	1,5707	0,0390	1,8025	0,9906	1,1476
11723910_a_at	CMKLR1	chemokine-like receptor 1	NM_001142343	0,0425	1,5656	0,0359	1,8111	0,9906	1,1569
11754845_a_at	FAM109A	family with sequence similarity 109, member A	NM_001177996	0,0413	1,5644	0,0395	1,6701	0,9906	1,0676
11718600_a_at	TM2D2	TM2 domain containing 2	NM_001024380	0,0258	1,5635	0,0289	1,5585	0,9989	-1,0032
11717409_at	SH2B3	SH2B adaptor protein 3	NM_005475	0,0456	1,5634	0,0492	1,6032	0,9916	1,0255
11716452_a_at	MYO1C	myosin IC	NM_001080779	0,0237	1,5628	0,0269	1,5746	0,9949	1,0076
11720252_s_at	C20orf194	chromosome 20 open reading frame 194	NM_001009984	0,0325	1,5597	0,0340	1,6310	0,9906	1,0457

11742923_a_at	LAPTM5	lysosomal protein transmembrane 5	NM_006762	0,0357	1,5590	0,0408	1,5464	0,9953	-1,0082
11721499_x_at	CTSA	cathepsin A	NM_000308 /// ↑	0,0369	1,5588	0,0375	1,6224	0,9906	1,0408
11720859_s_at	ABHD3	abhydrolase domain containing 3	NM_138340	0,0341	1,5538	0,0412	1,5020	0,9906	-1,0345
11724172_s_at	FCHO2	FCH domain only 2	NM_001146032	0,0403	1,5499	0,0375	1,6819	0,9906	1,0852
11716759_a_at	CASP4	caspase 4, apoptosis-related cysteine peptidase	NM_001225 /// ↑	0,0272	1,5475	0,0338	1,5204	0,9910	-1,0178
11756762_x_at	C1orf85	chromosome 1 open reading frame 85	NM_001256604	0,0314	1,5362	0,0338	1,6048	0,9906	1,0446
11754440_s_at	GAS6	growth arrest-specific 6	NM_000820 /// ↑	0,0473	1,5293	0,0467	1,6301	0,9906	1,0659
11719398_s_at	RRAGC	Ras-related GTP binding C	NM_001271851	0,0281	1,5180	0,0336	1,5190	0,9997	1,0007
11749662_a_at	KIFC3	kinesin family member C3	NM_001130099	0,0374	1,5174	0,0411	1,5189	0,9997	1,0010
11718896_x_at	SPAG9	sperm associated antigen 9	NM_001130527	0,0406	1,5140	0,0408	1,5757	0,9906	1,0408
11729998_a_at	B3GNT7	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosamin	NM_145236	0,0420	1,5127	0,0380	1,6479	0,9906	1,0894
11738552_x_at	ANXA2	annexin A2	NM_001002857	0,0269	1,5097	0,0306	1,5343	0,9910	1,0163
11742922_at	LAPTM5	lysosomal protein transmembrane 5	NM_006762	0,0427	1,5041	0,0447	1,5476	0,9906	1,0289
11724326_a_at	ARHGAP2	Rho GTPase activating protein 25	NM_001007231	0,0324	1,5010	0,0338	1,5709	0,9906	1,0465
11717589_a_at	EXOSC8	exosome component 8	NM_181503	0,0419	-1,5100	0,0457	-1,5229	0,9953	-1,0085
11718338_a_at	NHP2	NHP2 ribonucleoprotein	NM_001034833	0,0402	-1,5117	0,0447	-1,5187	0,9991	-1,0047
11744098_at	NOP58	NOP58 ribonucleoprotein	NM_015934	0,0212	-1,5131	0,0231	-1,5125	0,9997	1,0004
11733446_at	MMS22L	MMS22-like, DNA repair protein	NM_198468	0,0438	-1,5153	0,0388	-1,6696	0,9906	-1,1018
11715698_a_at	NOLC1	nucleolar and coiled-body phosphoprotein 1	NM_004741	0,0377	-1,5211	0,0372	-1,6033	0,9906	-1,0541
11725715_x_at	RPS14	ribosomal protein S14	NM_001025070	0,0346	-1,5223	0,0366	-1,5711	0,9906	-1,0320
11720970_at	TOP2A	topoisomerase (DNA) II alpha 170kDa	NM_001067	0,0376	-1,5241	0,0438	-1,5044	0,9949	1,0130
11732520_a_at	RAD51C	RAD51 homolog C (S. cerevisiae)	NM_002876 /// ↑	0,0337	-1,5258	0,0370	-1,5377	0,9952	-1,0078
11756156_s_at	TFRC	transferrin receptor (p90, CD71)	NM_001128148	0,0267	-1,5280	0,0277	-1,5819	0,9906	-1,0353
11739085_a_at	PCID2	PCI domain containing 2	NM_001127202	0,0421	-1,5289	0,0491	-1,5045	0,9937	1,0163
11729967_a_at	CLYBL	citrate lyase beta like	NM_138280 /// ↑	0,0332	-1,5337	0,0313	-1,7192	0,9906	-1,1209
11727353_a_at	CENPM	centromere protein M	NM_001002876	0,0387	-1,5363	0,0447	-1,5075	0,9919	1,0192
11727789_a_at	USP1	ubiquitin specific peptidase 1	NM_001017415	0,0346	-1,5370	0,0359	-1,5974	0,9906	-1,0393
11753942_a_at	UCA1	urothelial cancer associated 1 (non-protein coding	NR_015379	0,0411	-1,5371	0,0474	-1,5176	0,9949	1,0128
11754822_x_at	TDP1	tyrosyl-DNA phosphodiesterase 1	NM_001008744	0,0269	-1,5397	0,0289	-1,5901	0,9906	-1,0327
11743468_at	DKC1 /// M	dyskeratosis congenita 1, dyskerin /// microRNA 6	NM_001142463	0,0411	-1,5466	0,0483	-1,5192	0,9923	1,0180
11744082_at	MRPS31	mitochondrial ribosomal protein S31	NM_005830	0,0256	-1,5480	0,0300	-1,5136	0,9906	1,0227
11752128_a_at	IARS	isoleucyl-tRNA synthetase	NM_002161 /// ↑	0,0289	-1,5539	0,0340	-1,5539	1,0000	1,0000
11716822_a_at	BDH2 /// S	3-hydroxybutyrate dehydrogenase, type 2 /// solut	NM_020139 /// ↑	0,0258	-1,5550	0,0308	-1,5074	0,9906	1,0316
11742239_a_at	DEPDC1B	DEP domain containing 1B	NM_001145208	0,0314	-1,5563	0,0377	-1,5193	0,9906	1,0244
11757725_a_at	NHP2	NHP2 ribonucleoprotein	NM_001034833	0,0422	-1,5612	0,0458	-1,5795	0,9951	-1,0117
11720465_a_at	SKIV2L2	superkiller viralicidic activity 2-like 2 (S. cerevisiae)	NM_015360	0,0408	-1,5633	0,0494	-1,5094	0,9906	1,0357
11721512_a_at	TMM21	translocase of inner mitochondrial membrane 21 f	NM_014177	0,0299	-1,5649	0,0375	-1,5070	0,9906	1,0384
11743536_at	VRK1	vaccinia related kinase 1	NM_003384	0,0405	-1,5653	0,0479	-1,5334	0,9920	1,0208
11731578_s_at	ACSS1	acyl-CoA synthetase short-chain family member 1	NM_001252675	0,0276	-1,5669	0,0308	-1,6180	0,9906	-1,0326
11745463_x_at	PRDX2	peroxiredoxin 2	NM_005809 /// ↑	0,0425	-1,5669	0,0500	-1,5313	0,9916	1,0233
11715505_a_at	IARS	isoleucyl-tRNA synthetase	NM_002161 /// ↑	0,0269	-1,5723	0,0313	-1,5541	0,9926	1,0117
11750569_a_at	IARS	isoleucyl-tRNA synthetase	NM_002161 /// ↑	0,0277	-1,5748	0,0338	-1,5426	0,9906	1,0209
11734725_a_at	PNPT1	polyribonucleotide nucleotidyltransferase 1	NM_033109	0,0337	-1,5813	0,0388	-1,5548	0,9923	1,0170
11758640_s_at	FARSB	phenylalanyl-tRNA synthetase, beta subunit	NM_005687	0,0374	-1,5840	0,0447	-1,5393	0,9906	1,0291
11750373_a_at	BRCA1	breast cancer 1, early onset	NM_007294 /// ↑	0,0271	-1,5850	0,0338	-1,5327	0,9906	1,0341
11751966_a_at	IARS	isoleucyl-tRNA synthetase	NM_002161 /// ↑	0,0283	-1,5879	0,0359	-1,5318	0,9906	1,0366
11727808_s_at	FECH	ferrochelatase	NM_000140 /// ↑	0,0212	-1,5889	0,0242	-1,5274	0,9906	1,0403
11743519_at	DIDO1	death inducer-obliterator 1	NM_001193369	0,0295	-1,5907	0,0371	-1,5273	0,9906	1,0415
11743104_at	PTCD3	pentatricopeptide repeat domain 3	NM_017952	0,0384	-1,5963	0,0488	-1,5137	0,9906	1,0546
11726444_a_at	SAMD13	sterile alpha motif domain containing 13	NM_001010971	0,0376	-1,5971	0,0444	-1,5652	0,9919	1,0204
11719332_at	ARHGAP1	Rho GTPase activating protein 15	NM_018460	0,0383	-1,5972	0,0395	-1,6378	0,9910	-1,0255
11746829_x_at	DDX55	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55	NM_020936	0,0471	-1,5973	0,0465	-1,7151	0,9906	-1,0737
11745447_x_at	SAC3D1	SAC3 domain containing 1	NM_013299	0,0267	-1,5985	0,0297	-1,6046	0,9985	-1,0038
11722252_x_at	NEK2	NIMA-related kinase 2	NM_001204182	0,0448	-1,5989	0,0494	-1,6198	0,9951	-1,0131
11756405_s_at	GCSH /// L	glycine cleavage system protein H (aminomethyl C	NM_004483 /// ↑	0,0310	-1,6071	0,0351	-1,6229	0,9949	-1,0098
11733701_a_at	FKBP11	FK506 binding protein 11, 19 kDa	NM_001143781	0,0392	-1,6075	0,0377	-1,7112	0,9906	-1,0645
11746542_x_at	KIAA0146	KIAA0146 /// uncharacterized LOC100996383	NM_001080394	0,0245	-1,6077	0,0273	-1,5622	0,9906	1,0291
11725149_at	C9orf40	chromosome 9 open reading frame 40	NM_017998	0,0399	-1,6081	0,0494	-1,5364	0,9906	1,0467
11740366_a_at	SHMT1	serine hydroxymethyltransferase 1 (soluble)	NM_004169 /// ↑	0,0269	-1,6085	0,0334	-1,5785	0,9910	1,0190
11717511_a_at	CIRH1A	cirrrosis, autosomal recessive 1A (cirhin)	NM_032830	0,0248	-1,6098	0,0289	-1,5259	0,9906	1,0550
11755951_s_at	PRMT5	protein arginine methyltransferase 5	NM_001039619	0,0413	-1,6164	0,0447	-1,6407	0,9949	-1,0151
11743296_a_at	CENPF	centromere protein F, 350/400kDa	NM_016343	0,0456	-1,6180	0,0474	-1,6983	0,9906	-1,0496
11755600_a_at	GEMIN6	gem (nuclear organelle) associated protein 6	NM_024775	0,0283	-1,6180	0,0359	-1,5471	0,9906	1,0459
11724343_at	ITGA4	integrin, alpha 4 (antigen CD49D, alpha 4 subunit	NM_000885	0,0439	-1,6199	0,0462	-1,6677	0,9910	-1,0295
11715410_x_at	PRDX2	peroxiredoxin 2	NM_005809 /// ↑	0,0281	-1,6230	0,0338	-1,6044	0,9949	1,0116
11730421_x_at	FLVCR1	feline leukemia virus subgroup C cellular receptor	NM_014053	0,0302	-1,6241	0,0344	-1,6407	0,9949	-1,0102

11750272_a_at	LARS	leucyl-tRNA synthetase	NM_020117	0,0315	-1,6257	0,0384	-1,5707	0,9906	1,0351
11718142_a_at	TTC27	tetratricopeptide repeat domain 27	NM_001193509	0,0248	-1,6259	0,0269	-1,6259	1,0000	1,0000
11729688_s_at	LYRM7	LYR motif containing 7	NM_181705	0,0384	-1,6264	0,0428	-1,6236	0,9997	1,0017
11717773_a_at	THRA	thyroid hormone receptor, alpha	NM_001190918	0,0357	-1,6272	0,0447	-1,5526	0,9906	1,0480
11739515_at	CA8	carbonic anhydrase VIII	NM_004056	0,0387	-1,6282	0,0405	-1,6654	0,9916	-1,0228
11735992_a_at	LARS	leucyl-tRNA synthetase	NM_020117	0,0251	-1,6314	0,0297	-1,5527	0,9906	1,0507
11736596_s_at	GIN54	GIN5 complex subunit 4 (Sld5 homolog)	NM_032336	0,0399	-1,6322	0,0494	-1,5583	0,9906	1,0475
11756607_x_at	ZNF85	zinc finger protein 85	NM_001256171	0,0299	-1,6327	0,0302	-1,7975	0,9906	-1,1010
11727543_at	OIP5	Opa interacting protein 5	NM_007280	0,0372	-1,6334	0,0388	-1,6695	0,9916	-1,0221
11726630_a_at	HTRA2	HtrA serine peptidase 2	NM_013247 /// ↑	0,0373	-1,6356	0,0447	-1,5794	0,9906	1,0356
11736070_at	C8orf33	chromosome 8 open reading frame 33	NM_023080	0,0368	-1,6445	0,0447	-1,5853	0,9906	1,0373
11736050_s_at	FAM229B	family with sequence similarity 229, member B	NM_001033564	0,0285	-1,6453	0,0344	-1,6164	0,9916	1,0179
11718404_at	RFC3	replication factor C (activator 1) 3, 38kDa	NM_002915 /// ↑	0,0266	-1,6459	0,0338	-1,5257	0,9906	1,0788
11717677_a_at	CYFIP2	cytoplasmic FMR1 interacting protein 2	NM_001037332	0,0365	-1,6475	0,0470	-1,5484	0,9906	1,0640
11718303_a_at	PAFAH1B3	platelet-activating factor acetylhydrolase 1b, catalytic	NM_001145939	0,0332	-1,6478	0,0368	-1,6623	0,9952	-1,0088
11743603_a_at	RRM1	ribonucleotide reductase M1	NM_001033	0,0346	-1,6511	0,0408	-1,6116	0,9910	1,0245
11745391_x_at	MRPL3	mitochondrial ribosomal protein L3	NM_007208	0,0387	-1,6521	0,0422	-1,6634	0,9980	-1,0068
11724606_a_at	MAP2K6	mitogen-activated protein kinase kinase 6	NM_002758 /// ↑	0,0314	-1,6528	0,0376	-1,6129	0,9906	1,0248
11735234_a_at	SLC38A5	solute carrier family 38, member 5	NM_033518	0,0272	-1,6554	0,0269	-1,9488	0,9906	-1,1773
11747943_a_at	E2F8	E2F transcription factor 8	NM_001256371	0,0391	-1,6613	0,0377	-1,7750	0,9906	-1,0684
11757061_s_at	GCSH /// L	glycine cleavage system protein H (aminomethyltransferase)	NM_004483 /// ↑	0,0319	-1,6618	0,0384	-1,6119	0,9906	1,0310
11745979_a_at	LIG1	ligase I, DNA, ATP-dependent	NM_000234	0,0276	-1,6713	0,0338	-1,6241	0,9906	1,0290
11748475_a_at	TCERG1	transcription elongation regulator 1	NM_001040006	0,0391	-1,6714	0,0390	-1,7477	0,9906	-1,0457
11716388_a_at	BAZ1B	bromodomain adjacent to zinc finger domain, 1B	NM_023005 /// ↑	0,0269	-1,6719	0,0334	-1,6296	0,9906	1,0260
11760685_x_at	BRX1	BRX1, biogenesis of ribosomes, homolog (S. cerevisiae)	NM_018321	0,0401	-1,6726	0,0444	-1,6817	0,9992	-1,0054
11738457_a_at	C20orf197	chromosome 20 open reading frame 197	NM_173644	0,0413	-1,6742	0,0482	-1,6478	0,9949	1,0161
11734373_a_at	CSPP1	centrosome and spindle pole associated protein 1	NM_001077204	0,0327	-1,6765	0,0359	-1,7234	0,9906	-1,0280
11758737_s_at	PGRMC2	progesterone receptor membrane component 2	NM_006320	0,0212	-1,6794	0,0242	-1,6377	0,9906	1,0254
11751388_a_at	FEN1	flap structure-specific endonuclease 1	NM_004111	0,0411	-1,6808	0,0444	-1,7135	0,9937	-1,0195
11744699_a_at	TDP1	tyrosyl-DNA phosphodiesterase 1	NM_001008744	0,0269	-1,6811	0,0338	-1,5890	0,9906	1,0580
11757391_x_at	MRPL1	mitochondrial ribosomal protein L1	NM_020236	0,0269	-1,6859	0,0367	-1,5173	0,9906	1,1111
11720637_x_at	CXADR	coxsackie virus and adenovirus receptor	NM_001207063	0,0465	-1,6867	0,0497	-1,7459	0,9910	-1,0351
11716412_s_at	ALDH18A1	aldehyde dehydrogenase 18 family, member A1	NM_001017423	0,0352	-1,6886	0,0444	-1,6115	0,9906	1,0478
11715697_a_at	NOLC1	nucleolar and coiled-body phosphoprotein 1	NM_004741	0,0288	-1,6905	0,0390	-1,5574	0,9906	1,0855
11754598_s_at	DNAJA3	DnaJ (Hsp40) homolog, subfamily A, member 3	NM_001135110	0,0373	-1,6908	0,0412	-1,6891	0,9997	1,0010
11716381_x_at	MPC2	mitochondrial pyruvate carrier 2	NM_001143674	0,0448	-1,6910	0,0422	-1,8607	0,9906	-1,1004
11724492_a_at	LIG1	ligase I, DNA, ATP-dependent	NM_000234	0,0320	-1,6920	0,0366	-1,6913	0,9999	1,0005
11716380_a_at	MPC2	mitochondrial pyruvate carrier 2	NM_001143674	0,0447	-1,6972	0,0447	-1,7991	0,9906	-1,0601
11721109_a_at	NAP1L3	nucleosome assembly protein 1-like 3	NM_004538	0,0373	-1,7062	0,0462	-1,6208	0,9906	1,0527
11722213_at	NPM3	nucleophosmin/nucleoplamin 3	NM_006993	0,0314	-1,7067	0,0454	-1,5311	0,9906	1,1147
11756145_s_at	SLC25A15	solute carrier family 25 (mitochondrial carrier; ornithine carrier)	NM_014252	0,0297	-1,7070	0,0340	-1,7255	0,9949	-1,0108
11732584_a_at	WRN	Werner syndrome, RecQ helicase-like	NM_000553	0,0215	-1,7074	0,0252	-1,6932	0,9942	1,0084
11744398_a_at	LIG1	ligase I, DNA, ATP-dependent	NM_000234	0,0338	-1,7122	0,0447	-1,5912	0,9906	1,0760
11763518_x_at	PMS1	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	NM_000534 /// ↑	0,0319	-1,7157	0,0375	-1,6866	0,9928	1,0173
11715834_x_at	RUVBL1	RuvB-like 1 (E. coli)	NM_003707	0,0421	-1,7160	0,0461	-1,7307	0,9972	-1,0086
11751170_a_at	BZW2	basic leucine zipper and W2 domains 2	NM_001159767	0,0449	-1,7179	0,0500	-1,7343	0,9965	-1,0096
11746588_a_at	ALDH1B1	aldehyde dehydrogenase 1 family, member B1	NM_000692	0,0346	-1,7247	0,0454	-1,6061	0,9906	1,0738
11715734_a_at	NIPSNAP1	nipsnap homolog 1 (C. elegans)	NM_001202502	0,0402	-1,7289	0,0490	-1,6598	0,9906	1,0416
11725709_a_at	WDHD1	WD repeat and HMG-box DNA binding protein 1	NM_001008396	0,0280	-1,7298	0,0411	-1,5257	0,9906	1,1338
11734941_x_at	FAM212B	family with sequence similarity 212, member B	NM_019099 /// ↑	0,0269	-1,7312	0,0357	-1,5746	0,9906	1,0995
11719324_x_at	PTEN	phosphatase and tensin homolog	NM_000314	0,0255	-1,7413	0,0338	-1,5595	0,9906	1,1166
11743582_a_at	EEF1E1	eukaryotic translation elongation factor 1 epsilon 1	NM_001135650	0,0267	-1,7453	0,0306	-1,7287	0,9949	1,0096
11726837_a_at	SCAI	suppressor of cancer cell invasion	NM_001144877	0,0447	-1,7463	0,0482	-1,7963	0,9920	-1,0286
11744275_a_at	WDR12	WD repeat domain 12	NM_018256	0,0430	-1,7468	0,0497	-1,7155	0,9949	1,0182
11724919_a_at	HSD17B8	hydroxysteroid (17-beta) dehydrogenase 8	NM_014234	0,0384	-1,7487	0,0500	-1,6143	0,9906	1,0832
11763093_x_at	GYPB	glycophorin B (MNS blood group)	NM_002100 /// ↑	0,0346	-1,7490	0,0434	-1,6685	0,9906	1,0482
11731984_at	CERKL	ceramide kinase-like	NM_001030311	0,0236	-1,7545	0,0269	-1,6983	0,9906	1,0331
11751479_a_at	CCDC152	coiled-coil domain containing 152	NM_001134848	0,0399	-1,7560	0,0489	-1,6754	0,9906	1,0481
11736985_a_at	NUBPL	nucleotide binding protein-like	NM_001201573	0,0374	-1,7577	0,0497	-1,6146	0,9906	1,0887
11719123_a_at	TIMELESS	timeless circadian clock	NM_003920	0,0214	-1,7661	0,0252	-1,6796	0,9906	1,0515
11727674_at	RFXAP	regulatory factor X-associated protein	NM_000538	0,0266	-1,7724	0,0335	-1,6544	0,9906	1,0713
11763965_s_at	MDN1	MDN1, midasin homolog (yeast)	NM_014611	0,0353	-1,7770	0,0422	-1,7199	0,9906	1,0332
11738840_a_at	NUDT10	nudix (nucleoside diphosphate linked moiety X)-type 10	NM_153183	0,0325	-1,7798	0,0384	-1,7299	0,9910	1,0289
11739820_at	ZNF714	zinc finger protein 714	NM_182515	0,0413	-1,7811	0,0476	-1,7578	0,9951	1,0132
11740098_a_at	ANK1	ankyrin 1, erythrocytic	NM_000037 /// ↑	0,0324	-1,7822	0,0342	-1,8757	0,9906	-1,0525
11741201_a_at	NAT10	N-acetyltransferase 10 (GCN5-related)	NM_001144030	0,0305	-1,7873	0,0395	-1,6595	0,9906	1,0770

11744515_a_at	SLC25A38	solute carrier family 25, member 38	NM_017875	0,0269	-1,7874	0,0384	-1,5642	0,9906	1,1427
11715755_a_at	ATIC	5-aminoimidazole-4-carboxamide ribonucleotide f	NM_004044	0,0252	-1,7894	0,0313	-1,6469	0,9906	1,0865
11758892_a_at	NDC1	NDC1 transmembrane nucleoporin	NM_001168551	0,0442	-1,7985	0,0497	-1,7925	0,9997	1,0034
11733454_a_at	CCDC41	coiled-coil domain containing 41	NM_001042399	0,0456	-1,8005	0,0460	-1,9348	0,9906	-1,0746
11748467_a_at	ALDH18A1	aldehyde dehydrogenase 18 family, member A1	NM_001017423	0,0302	-1,8068	0,0399	-1,6621	0,9906	1,0870
11730404_at	MEX3B	mex-3 homolog B (C. elegans)	NM_032246	0,0212	-1,8179	0,0231	-1,6647	0,9906	1,0920
11741856_s_at	LOC65350	zinc finger protein 658 pseudogene /// zinc finger	NM_001032297	0,0249	-1,8187	0,0359	-1,5090	0,9906	1,2053
11729458_a_at	FANCI	Fanconi anemia, complementation group I	NM_001113378	0,0285	-1,8193	0,0361	-1,7242	0,9906	1,0552
11757551_a_at	MRPL3	mitochondrial ribosomal protein L3	NM_007208	0,0251	-1,8251	0,0308	-1,6841	0,9906	1,0838
11739516_at	CA8	carbonic anhydrase VIII	NM_004056	0,0456	-1,8278	0,0447	-2,0089	0,9906	-1,0991
11722825_at	NCAPG	non-SMC condensin I complex, subunit G	NM_022346 /// ↑	0,0384	-1,8323	0,0425	-1,8291	0,9997	1,0017
11751171_x_at	BZW2	basic leucine zipper and W2 domains 2	NM_001159767	0,0269	-1,8399	0,0342	-1,7016	0,9906	1,0813
11740924_x_at	IMPDH2	IMP (inosine 5'-monophosphate) dehydrogenase 2	NM_000884	0,0320	-1,8405	0,0447	-1,6525	0,9906	1,1137
11721157_at	NTHL1	nth endonuclease III-like 1 (E. coli)	NM_002528	0,0269	-1,8426	0,0338	-1,7234	0,9906	1,0692
11755807_a_at	DNA2	DNA replication helicase/nuclease 2	NM_001080449	0,0271	-1,8451	0,0337	-1,7981	0,9906	1,0262
11757427_x_at	IMPDH2	IMP (inosine 5'-monophosphate) dehydrogenase 2	NM_000884	0,0341	-1,8501	0,0462	-1,6736	0,9906	1,1054
11715992_s_at	MCM2	minichromosome maintenance complex compone	NM_004526 /// ↑	0,0337	-1,8544	0,0447	-1,7021	0,9906	1,0895
11756160_x_at	CTNNA1	catenin (cadherin-associated protein), alpha-like 1	NM_003798	0,0302	-1,8596	0,0356	-1,8494	0,9990	1,0055
11752370_x_at	IMPDH2	IMP (inosine 5'-monophosphate) dehydrogenase 2	NM_000884	0,0288	-1,8689	0,0369	-1,7580	0,9906	1,0631
11715684_a_at	PPA1	pyrophosphatase (inorganic) 1	NM_021129	0,0266	-1,8689	0,0286	-1,9173	0,9906	-1,0259
11736528_a_at	SMC2	structural maintenance of chromosomes 2	NM_001042550	0,0297	-1,8700	0,0395	-1,7073	0,9906	1,0953
11757903_s_at	COL4A5	collagen, type IV, alpha 5	NM_000495 /// ↑	0,0271	-1,8711	0,0353	-1,7382	0,9906	1,0765
11724862_at	THNSL1	threonine synthase-like 1 (S. cerevisiae)	NM_024838	0,0269	-1,8815	0,0377	-1,6483	0,9906	1,1415
11715796_s_at	LUM	lumican	NM_002345	0,0345	-1,8950	0,0444	-1,7596	0,9906	1,0770
11723853_a_at	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	NM_018014 /// ↑	0,0325	-1,8969	0,0334	-2,1117	0,9906	-1,1133
11722908_a_at	KLHL13	kelch-like family member 13	NM_001168299	0,0272	-1,9151	0,0350	-1,8010	0,9906	1,0634
11742997_x_at	MCM3	minichromosome maintenance complex compone	NM_001270472	0,0271	-1,9194	0,0340	-1,8192	0,9906	1,0551
11758069_s_at	C1orf186	chromosome 1 open reading frame 186	NM_001007544	0,0332	-1,9224	0,0377	-1,9061	0,9966	1,0086
11736366_x_at	MCM10	minichromosome maintenance complex compone	NM_018518 /// ↑	0,0319	-1,9308	0,0363	-1,9319	0,9999	-1,0006
11736249_x_at	KIAA0101	KIAA0101	NM_001029989	0,0432	-1,9338	0,0485	-1,9358	0,9997	-1,0010
11721859_at	MIPEP	mitochondrial intermediate peptidase	NM_005932	0,0332	-1,9379	0,0366	-1,9734	0,9949	-1,0183
11721699_a_at	PMS1	PMS1 postmeiotic segregation increased 1 (S. ce)	NM_000534 /// ↑	0,0341	-1,9408	0,0436	-1,8064	0,9906	1,0744
11725052_a_at	TOP1MT	topoisomerase (DNA) I, mitochondrial	NM_001258446	0,0332	-1,9443	0,0410	-1,8306	0,9906	1,0621
11723903_at	PLEKHG1	pleckstrin homology domain containing, family G	(NM_001029884	0,0212	-1,9708	0,0252	-1,5984	0,9906	1,2329
11750140_x_at	TOP1MT	topoisomerase (DNA) I, mitochondrial	NM_001258446	0,0319	-1,9754	0,0461	-1,7205	0,9906	1,1481
11727839_x_at	ORC1	origin recognition complex, subunit 1	NM_001190818	0,0255	-1,9788	0,0301	-1,8955	0,9906	1,0440
11720884_a_at	HMBS	hydroxymethylbilane synthase	NM_000190 /// ↑	0,0413	-1,9856	0,0494	-1,9056	0,9910	1,0420
11755227_x_at	ANK1	ankyrin 1, erythrocytic	NM_000037 /// ↑	0,0255	-2,0010	0,0334	-1,8006	0,9906	1,1113
11718479_x_at	STAR	steroidogenic acute regulatory protein	NM_000349 /// ↑	0,0344	-2,0014	0,0422	-1,8892	0,9906	1,0594
11715814_a_at	TRAP1	TNF receptor-associated protein 1	NM_001272049	0,0281	-2,0027	0,0370	-1,8320	0,9906	1,0932
11716982_at	CMSS1	cms1 ribosomal small subunit homolog (yeast)	NM_001167924	0,0267	-2,0050	0,0334	-1,8662	0,9906	1,0743
11730300_a_at	FAM19A2	family with sequence similarity 19 (chemokine (C-	NM_178539	0,0248	-2,0056	0,0269	-1,9958	0,9985	1,0049
11728984_a_at	LOC10099	monofunctional C1-tetrahydrofolate synthase, mit	NM_001242767	0,0251	-2,0208	0,0362	-1,6397	0,9906	1,2324
11717775_s_at	GYPC	glycophorin C (Gerbich blood group)	NM_001256584	0,0297	-2,0223	0,0467	-1,6809	0,9906	1,2031
11753899_a_at	DLEU1	deleted in lymphocytic leukemia 1 (non-protein co	NM_005887 /// ↑	0,0494	-2,0263	0,0447	-2,4203	0,9906	-1,1944
11723995_a_at	GLCC1	glucocorticoid induced transcript 1	NM_138426	0,0377	-2,0396	0,0422	-2,0401	1,0000	-1,0003
11732058_a_at	CDC7	cell division cycle 7	NM_001134419	0,0391	-2,0430	0,0494	-1,8774	0,9906	1,0882
11726554_at	C1orf186	chromosome 1 open reading frame 186	NM_001007544	0,0455	-2,0593	0,0447	-2,2832	0,9906	-1,1087
11732057_a_at	CDC7	cell division cycle 7	NM_001134419	0,0447	-2,0699	0,0497	-2,0846	0,9993	-1,0071
11720867_x_at	PLAC8	placenta-specific 8	NM_001130715	0,0427	-2,0727	0,0448	-2,1580	0,9912	-1,0412
11759625_at	LOC10050	uncharacterized LOC100506965	XR_110300 /// X	0,0232	-2,0798	0,0269	-1,9926	0,9906	1,0438
11747185_x_at	ANK1	ankyrin 1, erythrocytic	NM_000037 /// ↑	0,0420	-2,0874	0,0497	-2,0058	0,9915	1,0407
11758478_s_at	CDCA7	cell division cycle associated 7	NM_031942 /// ↑	0,0295	-2,0876	0,0384	-1,9092	0,9906	1,0934
11744519_a_at	POLE2	polymerase (DNA directed), epsilon 2, accessory	NM_001197330	0,0283	-2,1104	0,0398	-1,8323	0,9906	1,1518
11721649_a_at	GPATCH4	G patch domain containing 4	NM_015590 /// ↑	0,0346	-2,1206	0,0444	-1,9519	0,9906	1,0864
11762504_a_at	ZRANB3	zinc finger, RAN-binding domain containing 3	NM_032143	0,0265	-2,1245	0,0338	-1,8945	0,9906	1,1214
11722964_a_at	AMMECR1	Alport syndrome, mental retardation, midface hyp	NM_001025580	0,0269	-2,1327	0,0338	-1,9531	0,9906	1,0919
11736367_a_at	MCM10	minichromosome maintenance complex compone	NM_018518 /// ↑	0,0311	-2,1433	0,0388	-1,9846	0,9906	1,0800
11758536_s_at	KCTD15	potassium channel tetramerisation domain contain	NM_001129994	0,0271	-2,1739	0,0338	-2,0656	0,9906	1,0525
11740178_x_at	ANKLE1	ankyrin repeat and LEM domain containing 1	NM_001278443	0,0292	-2,1940	0,0388	-1,9574	0,9906	1,1209
11758572_s_at	HELLS	helicase, lymphoid-specific	NM_018063	0,0219	-2,2234	0,0269	-2,0355	0,9906	1,0923
11718477_a_at	STAR	steroidogenic acute regulatory protein	NM_000349 /// ↑	0,0277	-2,2261	0,0342	-2,1271	0,9906	1,0466
11726386_at	PDZD8	PDZ domain containing 8	NM_173791	0,0442	-2,2461	0,0498	-2,2295	0,9993	1,0075
11725211_a_at	PLCXD1	phosphatidylinositol-specific phospholipase C, X	CN_018390 /// ↑	0,0258	-2,2811	0,0314	-2,1181	0,9906	1,0770
11739482_x_at	PLAC8	placenta-specific 8	NM_001130715	0,0277	-2,2976	0,0384	-1,9607	0,9906	1,1718
11753712_x_at	HBB	hemoglobin, beta	NM_000518	0,0449	-2,3117	0,0483	-2,4328	0,9910	-1,0524

11745300_a_at	DNAJC6	DnaJ (Hsp40) homolog, subfamily C, member 6	NM_001256864	0,0255	-2,3388	0,0289	-2,2327	0,9906	1,0476
11729291_a_at	SLC25A37	solute carrier family 25 (mitochondrial iron transp	NM_016612	0,0406	-2,3744	0,0491	-2,2363	0,9906	1,0618
11715167_at	ARHGAP2	Rho GTPase activating protein 22	NM_001256024	0,0395	-2,3933	0,0480	-2,2392	0,9906	1,0688
11736538_s_at	RHCE	/// R Rh blood group, CcEe antigens /// Rh blood group	NM_001127691	0,0403	-2,4524	0,0488	-2,3118	0,9906	1,0608
11755533_a_at	GPR125	G protein-coupled receptor 125	NM_145290	0,0346	-2,4653	0,0375	-2,5777	0,9910	-1,0456
11732805_at	EPX	eosinophil peroxidase	NM_000502	0,0363	-2,4975	0,0474	-2,2130	0,9906	1,1286
11742315_s_at	RHCE	/// R Rh blood group, CcEe antigens /// Rh blood group	NM_001127691	0,0303	-2,5684	0,0351	-2,5996	0,9964	-1,0121
11732341_at	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	NM_018014	0,0255	-2,6646	0,0282	-2,6721	0,9997	-1,0028
11732340_at	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	NM_018014	0,0337	-2,7322	0,0353	-2,9985	0,9906	-1,0975
11744559_a_at	SLC25A37	solute carrier family 25 (mitochondrial iron transp	NM_016612	0,0285	-2,7891	0,0327	-3,0027	0,9906	-1,0766
11745021_a_at	MYC	v-myc myelocytomatosis viral oncogene homolog	NM_002467	0,0390	-3,0782	0,0411	-3,2091	0,9928	-1,0425
11723070_a_at	CYTL1	cytokine-like 1	NM_018659	0,0252	-3,0966	0,0269	-3,3152	0,9906	-1,0706