

Complete list of differentially expressed genes (DEGs) in GSE45267

Probe ID	Gene Symbol	P Value	Adj. P	logFC
220496_at	CLEC1B	2.06E-40	1.13E-35	-4.18929
207804_s_at	FCN2	4.91E-38	1.34E-33	-4.41547
1559065_a_at	CLEC4G	1.40E-37	2.10E-33	-4.01568
230135_at	HHIP	1.53E-37	2.10E-33	-3.44002
230478_at	OIT3	1.01E-36	1.04E-32	-4.31539
205866_at	FCN3	1.14E-36	1.04E-32	-4.77552
210481_s_at	CLEC4M	1.76E-35	1.37E-31	-3.03856
220114_s_at	STAB2	7.30E-35	4.99E-31	-2.56257
209365_s_at	ECM1	1.17E-34	7.12E-31	-2.75002
222484_s_at	CXCL14	4.53E-33	2.47E-29	-4.73506
205984_at	CRHBP	2.75E-32	1.37E-28	-4.00468
1559573_at	LINC01093	5.54E-32	2.53E-28	-4.50884
228186_s_at	RSP03	7.19E-32	3.02E-28	-2.34851
218002_s_at	CXCL14	1.22E-31	4.76E-28	-4.36318
222077_s_at	RACGAP1	2.10E-31	7.65E-28	3.17621
219787_s_at	ECT2	4.48E-31	1.53E-27	3.092112
214710_s_at	CCNB1	8.97E-31	2.89E-27	3.428023
219918_s_at	ASPM	3.02E-30	9.17E-27	3.97677
223699_at	CNDP1	3.78E-30	1.09E-26	-4.21811
206380_s_at	CFP	7.61E-30	2.08E-26	-2.55426
206797_at	NAT2	1.78E-29	4.63E-26	-4.06924
218009_s_at	PRC1	2.24E-29	5.58E-26	3.211852
204822_at	TTK	2.60E-29	6.19E-26	3.268899

207995_s_at	CLEC4M	8.98E-29	2.05E-25	-3.14792
228273_at	PRR11	1.97E-28	4.10E-25	3.228725
218039_at	NUSAP1	2.14E-28	4.18E-25	2.969405
1559577_at	FCN2	3.23E-28	6.10E-25	-2.2601
209714_s_at	CDKN3	3.39E-28	6.19E-25	3.241534
231358_at	MRO	1.27E-27	2.25E-24	-2.04492
205819_at	MARCO	1.75E-27	2.99E-24	-3.04255
204641_at	NEK2	2.58E-27	4.15E-24	2.878395
226936_at	CENPW	4.75E-27	7.43E-24	2.492128
223967_at	ANGPTL6	6.49E-27	9.86E-24	-2.05867
209469_at	GPM6A	8.02E-27	1.19E-23	-2.52059
204428_s_at	LCAT	1.12E-26	1.61E-23	-3.1961
207165_at	HMMR	1.30E-26	1.79E-23	3.105503
202705_at	CCNB2	1.31E-26	1.79E-23	2.505347
206102_at	GINS1	1.36E-26	1.81E-23	3.235325
204162_at	NDC80	1.44E-26	1.88E-23	2.82618
209470_s_at	GPM6A	2.54E-26	3.23E-23	-2.26219
207828_s_at	CENPF	2.83E-26	3.51E-23	2.699834
201292_at	TOP2A	2.89E-26	3.51E-23	3.561832
206680_at	CD5L	4.69E-26	5.57E-23	-2.90117
1568638_a_at	IDO2	4.93E-26	5.73E-23	-3.26431
203213_at	CDK1	5.53E-26	6.29E-23	3.106181
220186_s_at	CDHR2	5.85E-26	6.53E-23	-2.39953
237350_at	TTC36	1.08E-25	1.18E-22	-3.90366

208079_s_at	AURKA	1.12E-25	1.20E-22	3.091297
203755_at	BUB1B	1.56E-25	1.64E-22	2.806799
204023_at	RFC4	2.47E-25	2.51E-22	2.241682
1555758_a_at	CDKN3	3.08E-25	3.01E-22	3.216614
222608_s_at	ANLN	4.50E-25	4.32E-22	3.173786
230165_at	SGO2	5.17E-25	4.87E-22	2.336186
219059_s_at	LYVE1	5.41E-25	5.01E-22	-2.63682
203554_x_at	PTTG1	7.70E-25	7.01E-22	2.446468
232449_at	BCO2	9.19E-25	8.23E-22	-3.40654
201890_at	RRM2	1.28E-24	1.09E-21	3.536905
202095_s_at	BIRC5	1.80E-24	1.51E-21	2.807619
218350_s_at	GMNN	2.01E-24	1.64E-21	2.336514
222843_at	FIGNL1	2.66E-24	2.08E-21	2.091988
207584_at	LPA	2.75E-24	2.11E-21	-3.36079
218585_s_at	DTL	2.93E-24	2.22E-21	3.234068
205019_s_at	VIPR1	5.69E-24	4.21E-21	-2.08594
223307_at	CDCA3	7.81E-24	5.69E-21	2.065612
219014_at	PLAC8	1.24E-23	8.94E-21	-3.23437
206210_s_at	CETP	1.92E-23	1.34E-20	-2.69695
203358_s_at	EZH2	2.36E-23	1.64E-20	2.401126
218662_s_at	NCAPG	7.19E-23	4.85E-20	2.6187
204825_at	MELK	7.90E-23	5.27E-20	2.413434
233604_at	FLJ22763	8.51E-23	5.61E-20	-3.27144
218355_at	KIF4A	8.99E-23	5.85E-20	2.662587

202503_s_at	KIAA0101	1.05E-22	6.58E-20	2.750903
215712_s_at	IGFALS	1.10E-22	6.84E-20	-2.04793
228191_at	FLVCR1	1.14E-22	6.92E-20	2.273226
209960_at	HGF	1.25E-22	7.54E-20	-3.14256
227350_at	HELLS	1.36E-22	8.10E-20	2.337789
204026_s_at	ZWINT	2.22E-22	1.26E-19	2.762074
203362_s_at	MAD2L1	2.72E-22	1.52E-19	2.415291
223593_at	AADAT	3.01E-22	1.66E-19	-2.18358
211813_x_at	DCN	3.14E-22	1.72E-19	-3.36051
225834_at	FAM72A///FAM72D///FAM72B///FAM72C	3.24E-22	1.74E-19	2.835552
205773_at	CPEB3	3.46E-22	1.84E-19	-2.46492
225571_at	LIFR	3.79E-22	1.98E-19	-3.07928
220491_at	HAMP	8.51E-22	4.21E-19	-5.59396
204146_at	RAD51AP1	1.11E-21	5.27E-19	2.154155
219148_at	PBK	1.97E-21	9.11E-19	2.67069
202580_x_at	FOXM1	2.01E-21	9.17E-19	2.162251
206424_at	CYP26A1	2.05E-21	9.26E-19	-3.16845
231683_at	GLYAT	3.63E-21	1.60E-18	-2.78608
205942_s_at	ACSM3	4.11E-21	1.77E-18	-2.50137
213706_at	GPD1	5.08E-21	2.15E-18	-2.33242
201291_s_at	TOP2A	5.25E-21	2.20E-18	3.961336
202870_s_at	CDC20	5.30E-21	2.20E-18	2.831922
205554_s_at	DNASE1L3	5.58E-21	2.29E-18	-3.50273
207262_at	APOF	6.05E-21	2.47E-18	-3.98133

202954_at	UBE2C	6.50E-21	2.63E-18	2.197432
1553977_a_at	CYP39A1	7.02E-21	2.80E-18	-2.62612
223381_at	NUF2	7.31E-21	2.89E-18	2.739658
227654_at	FAM65C	7.52E-21	2.96E-18	-2.51459
205225_at	ESR1	7.99E-21	3.12E-18	-3.41591
206030_at	ASPA	8.27E-21	3.21E-18	-2.30803
219954_s_at	GBA3	9.05E-21	3.45E-18	-3.65126
211896_s_at	DCN	1.37E-20	5.13E-18	-3.95253
218883_s_at	CENPU	1.98E-20	7.13E-18	2.600744
204092_s_at	AURKA	2.97E-20	1.04E-17	2.463062
218755_at	KIF20A	2.97E-20	1.04E-17	2.379003
201893_x_at	DCN	3.89E-20	1.33E-17	-3.54551
218663_at	NCAPG	4.23E-20	1.44E-17	2.381345
222906_at	FLVCR1	4.70E-20	1.59E-17	2.171307
232224_at	MASP1	6.72E-20	2.21E-17	-2.10899
228729_at	CCNB1	7.17E-20	2.35E-17	2.132308
204318_s_at	GTSE1	8.55E-20	2.77E-17	2.280897
237765_at	SLC25A47	8.71E-20	2.80E-17	-3.1764
203666_at	CXCL12	9.13E-20	2.90E-17	-2.5578
207609_s_at	CYP1A2	1.08E-19	3.34E-17	-4.02507
225575_at	LIFR	1.10E-19	3.35E-17	-2.93866
1553296_at	ADGRG7	1.20E-19	3.64E-17	-2.16691
225655_at	UHRF1	1.26E-19	3.78E-17	2.371424
209773_s_at	RRM2	1.28E-19	3.81E-17	2.935162

209687_at	CXCL12	1.68E-19	4.89E-17	-3.3695
210377_at	ACSM3	1.68E-19	4.89E-17	-2.78626
203764_at	DLGAP5	2.78E-19	7.72E-17	2.477785
205440_s_at	NPY1R	3.07E-19	8.39E-17	-2.2302
219666_at	MS4A6A	3.25E-19	8.83E-17	-2.01478
206755_at	CYP2B6	3.86E-19	1.02E-16	-3.64507
224356_x_at	MS4A6A	3.97E-19	1.05E-16	-2.24863
207608_x_at	CYP1A2	4.28E-19	1.13E-16	-4.73596
210052_s_at	TPX2	4.50E-19	1.17E-16	2.108022
228401_at	ATAD2	5.42E-19	1.38E-16	2.017705
220432_s_at	CYP39A1	6.70E-19	1.68E-16	-3.67286
207027_at	HGFAC	7.51E-19	1.86E-16	-3.25395
205034_at	CCNE2	7.79E-19	1.92E-16	2.449971
209220_at	GPC3	7.85E-19	1.92E-16	4.672629
209335_at	DCN	8.65E-19	2.10E-16	-3.35346
204159_at	CDKN2C	9.43E-19	2.26E-16	2.368787
224061_at	INMT	9.69E-19	2.29E-16	-2.05325
213629_x_at	MT1F	9.72E-19	2.29E-16	-3.64529
202972_s_at	FAM13A	9.94E-19	2.33E-16	-2.03442
232138_at	MBNL2	9.98E-19	2.33E-16	-2.33066
204170_s_at	CKS2	1.24E-18	2.81E-16	2.166984
227554_at	MAGI2-AS3	1.27E-18	2.87E-16	-2.30331
236641_at	KIF14	1.61E-18	3.57E-16	2.014598
232428_at	MOGAT2	1.72E-18	3.80E-16	-2.80274

202107_s_at	MCM2	1.73E-18	3.80E-16	2.079808
204955_at	SRPX	2.35E-18	5.05E-16	-2.88747
226350_at	CHML	2.51E-18	5.33E-16	2.303039
209408_at	KIF2C	2.58E-18	5.47E-16	2.05213
214734_at	EXPH5	2.71E-18	5.62E-16	-2.52563
227695_at	LOC100287413///GLYATL1	3.16E-18	6.47E-16	-2.36444
223280_x_at	MS4A6A	3.37E-18	6.76E-16	-2.19461
223229_at	UBE2T	4.16E-18	8.20E-16	2.098877
218424_s_at	STEAP3	4.45E-18	8.65E-16	-2.07486
238756_at	GAS2L3	5.24E-18	1.01E-15	2.021005
205392_s_at	CCL15-CCL14///CCL14	6.75E-18	1.26E-15	-2.06301
209531_at	GSTZ1	7.57E-18	1.39E-15	-2.20516
222083_at	GLYAT	7.66E-18	1.40E-15	-3.5949
205194_at	PSPH	9.21E-18	1.66E-15	2.230648
208370_s_at	RCAN1	9.43E-18	1.69E-15	-2.04955
219343_at	CDC37L1	1.06E-17	1.85E-15	-2.08744
204962_s_at	SLC35F6///CENPA	1.50E-17	2.55E-15	2.137308
231691_at	C3P1	1.61E-17	2.71E-15	-3.36849
206898_at	CDH19	1.89E-17	3.17E-15	-2.2115
223784_at	TMEM27	1.93E-17	3.23E-15	-3.1657
209541_at	IGF1	2.26E-17	3.73E-15	-3.80194
205307_s_at	KMO	2.59E-17	4.21E-15	-2.71053
225316_at	MFSD2A	2.72E-17	4.38E-15	-2.93074
217165_x_at	MT1F	2.83E-17	4.55E-15	-3.29534

207544_s_at	ADH6	3.12E-17	4.96E-15	-2.6632
212551_at	CAP2	3.19E-17	5.05E-15	2.127299
229477_at	THRSP	3.26E-17	5.12E-15	-3.78245
227297_at	ITGA9	3.51E-17	5.44E-15	-2.1811
209540_at	IGF1	3.66E-17	5.64E-15	-3.53882
204745_x_at	MT1G	3.69E-17	5.66E-15	-3.37045
218162_at	OLFML3	4.07E-17	6.21E-15	-2.28083
205998_x_at	CYP3A4	4.49E-17	6.80E-15	-2.69168
222943_at	GBA3	4.95E-17	7.41E-15	-3.7636
216058_s_at	CYP2C19	5.22E-17	7.76E-15	-2.86748
217047_s_at	FAM13A	6.08E-17	8.86E-15	-2.39063
207201_s_at	SLC22A1	7.03E-17	1.01E-14	-4.23162
231156_at	HAO2	7.16E-17	1.02E-14	-3.07333
210095_s_at	IGFBP3	7.28E-17	1.03E-14	-2.16217
235086_at	THBS1	7.57E-17	1.06E-14	-2.3422
209614_at	ADH1B	1.15E-16	1.54E-14	-4.26759
206727_at	C9	1.26E-16	1.67E-14	-5.32251
225687_at	FAM83D	1.28E-16	1.69E-14	2.416409
217546_at	MT1M	1.32E-16	1.73E-14	-4.59815
220037_s_at	LYVE1	2.86E-16	3.47E-14	-2.02583
212554_at	CAP2	2.93E-16	3.55E-14	2.228124
206938_at	SRD5A2	2.96E-16	3.58E-14	-2.78739
216661_x_at	CYP2C9	3.28E-16	3.88E-14	-3.1121
206461_x_at	MT1H	3.35E-16	3.96E-14	-3.04841

1553583_a_at	THRSP	3.41E-16	4.01E-14	-2.26996
206840_at	AFM	3.49E-16	4.10E-14	-3.37951
211231_x_at	CYP4A11	3.52E-16	4.13E-14	-2.43922
209542_x_at	IGF1	3.55E-16	4.14E-14	-2.54881
225987_at	STEAP4	3.56E-16	4.14E-14	-2.55659
202238_s_at	LOC101928916///NNMT	3.87E-16	4.49E-14	-3.86786
208147_s_at	CYP2C8	4.52E-16	5.14E-14	-3.89272
214142_at	ZG16	4.58E-16	5.19E-14	-2.20107
209642_at	BUB1	4.65E-16	5.24E-14	2.085165
221188_s_at	CIDEB	5.19E-16	5.84E-14	-2.24847
203372_s_at	SOCS2	6.18E-16	6.82E-14	-2.96901
216336_x_at	MT1E	6.63E-16	7.24E-14	-2.88937
208581_x_at	MT1X	6.64E-16	7.24E-14	-3.08417
229476_s_at	THRSP	7.20E-16	7.73E-14	-4.60545
212724_at	RND3	7.90E-16	8.42E-14	-2.35161
204326_x_at	MT1X	8.21E-16	8.65E-14	-3.14207
206754_s_at	CYP2B7P///CYP2B6	9.98E-16	1.03E-13	-3.60299
203373_at	SOCS2	1.01E-15	1.04E-13	-2.6882
202992_at	C7	1.08E-15	1.10E-13	-3.39301
202973_x_at	FAM13A	1.28E-15	1.28E-13	-2.47927
211577_s_at	IGF1	1.31E-15	1.30E-13	-2.47331
211303_x_at	FOLH1B	1.34E-15	1.32E-13	-2.28035
223781_x_at	ADH4	1.49E-15	1.47E-13	-3.38915
206541_at	KLKB1	1.64E-15	1.60E-13	-2.09901

214261_s_at	ADH6	2.00E-15	1.90E-13	-2.18798
203854_at	CFI	2.21E-15	2.09E-13	-2.05196
214421_x_at	CYP2C9	2.28E-15	2.14E-13	-3.26429
210889_s_at	FCGR2B	2.54E-15	2.35E-13	-2.26843
228728_at	CPED1	2.75E-15	2.50E-13	-2.3839
216025_x_at	CYP2C9	3.09E-15	2.76E-13	-3.14906
220116_at	KCNN2	3.23E-15	2.85E-13	-3.10865
214420_s_at	CYP2C9	3.34E-15	2.94E-13	-2.0327
210559_s_at	CDK1	3.45E-15	3.03E-13	2.166538
211456_x_at	MT1HL1	3.46E-15	3.03E-13	-2.66337
220801_s_at	HAO2	3.61E-15	3.15E-13	-3.51486
209696_at	FBP1	3.87E-15	3.34E-13	-2.29448
218918_at	MAN1C1	4.16E-15	3.55E-13	-2.0738
230707_at	SORL1	4.23E-15	3.59E-13	-2.02806
212185_x_at	MT2A	4.31E-15	3.64E-13	-2.6048
230931_at	PLG	4.73E-15	3.96E-13	-2.89108
214621_at	GYS2	5.67E-15	4.62E-13	-3.97888
213226_at	CCNA2	6.32E-15	5.08E-13	2.053186
1554640_at	PALM2	7.62E-15	6.00E-13	-2.02619
202768_at	FOSB	7.84E-15	6.16E-13	-2.17056
207718_x_at	CYP2A7	8.47E-15	6.57E-13	-2.50166
207244_x_at	CYP2A6	9.84E-15	7.52E-13	-2.81527
209278_s_at	TFPI2	1.10E-14	8.33E-13	-2.14565
206753_at	RDH16	1.16E-14	8.67E-13	-2.85185

1554459_s_at	CFHR3	1.20E-14	8.93E-13	-3.21631
205860_x_at	FOLH1B///FOLH1	1.45E-14	1.06E-12	-2.18127
215363_x_at	FOLH1B///FOLH1	1.47E-14	1.07E-12	-2.18318
206305_s_at	C8A	1.49E-14	1.08E-12	-2.71072
213929_at	EXPH5	1.63E-14	1.17E-12	-2.11092
217319_x_at	CYP4A22///CYP4A11	1.65E-14	1.18E-12	-3.26772
210143_at	ANXA10	1.78E-14	1.25E-12	-2.6986
227794_at	LOC100287413///GLYATL1	1.79E-14	1.26E-12	-3.19239
210168_at	C6	1.89E-14	1.33E-12	-3.25912
220017_x_at	CYP2C9	1.96E-14	1.36E-12	-3.07006
211295_x_at	CYP2A6	2.51E-14	1.71E-12	-3.64564
207874_s_at	CFHR4	2.56E-14	1.74E-12	-3.51983
211138_s_at	KMO	2.66E-14	1.80E-12	-2.86141
229229_at	AGXT2	2.78E-14	1.87E-12	-2.17933
205306_x_at	KMO	2.78E-14	1.87E-12	-2.84159
212094_at	PEG10	2.82E-14	1.89E-12	4.146992
209189_at	FOS	2.91E-14	1.95E-12	-2.98266
207102_at	AKR1D1	3.34E-14	2.18E-12	-3.48314
210013_at	HPX	3.39E-14	2.21E-12	-2.32288
212859_x_at	MT1E	3.51E-14	2.28E-12	-3.03344
202237_at	LOC101928916///NNMT	3.57E-14	2.31E-12	-3.4083
206930_at	GLYAT	3.60E-14	2.32E-12	-2.78807
205999_x_at	CYP3A4	3.86E-14	2.46E-12	-3.61266
242817_at	PGLYRP2	4.01E-14	2.54E-12	-2.70715

1568765_at	SERPINE1	4.07E-14	2.58E-12	-2.8817
205141_at	ANG	4.29E-14	2.69E-12	-2.30261
207096_at	SAA2-SAA4///SAA4	4.36E-14	2.73E-12	-2.87579
219978_s_at	NUSAP1	4.72E-14	2.93E-12	2.401925
229777_at	CLRN3	5.17E-14	3.16E-12	-3.23155
203477_at	COL15A1	5.52E-14	3.33E-12	2.587065
225612_s_at	B3GNT5	5.73E-14	3.45E-12	2.428541
208367_x_at	CYP3A4	5.79E-14	3.47E-12	-3.28365
203790_s_at	RIDA	5.82E-14	3.48E-12	-2.0156
213293_s_at	TRIM22	6.04E-14	3.61E-12	-2.08759
209368_at	EPHX2	7.00E-14	4.07E-12	-2.0029
207407_x_at	CYP4A11	7.36E-14	4.26E-12	-3.23385
1494_f_at	CYP2A6	7.68E-14	4.44E-12	-3.71064
208937_s_at	ID1	8.42E-14	4.82E-12	-2.38449
218510_x_at	FAM134B	8.78E-14	4.98E-12	-2.4591
209035_at	MDK	9.71E-14	5.42E-12	2.34886
209774_x_at	CXCL2	1.03E-13	5.70E-12	-2.98331
214320_x_at	CYP2A6	1.19E-13	6.50E-12	-3.57757
231678_s_at	ADH4	1.30E-13	7.02E-12	-5.05029
206172_at	IL13RA2	1.38E-13	7.35E-12	-2.62342
213222_at	PLCB1	1.49E-13	7.90E-12	2.011448
237390_at	ADRA1A	1.59E-13	8.32E-12	-3.24301
206354_at	SLC01B3	1.79E-13	9.18E-12	-4.14032
210233_at	IL1RAP	1.82E-13	9.29E-12	-2.30467

214414_x_at	HBA2///HBA1	1.87E-13	9.48E-12	-2.24515
205498_at	GHR	1.89E-13	9.55E-12	-2.76932
238441_at	PRKAA2	1.94E-13	9.77E-12	2.174439
201743_at	CD14	1.99E-13	9.99E-12	-2.21574
207773_x_at	CYP3A43	2.24E-13	1.10E-11	-2.20227
224299_x_at	FTCD	2.29E-13	1.12E-11	-2.08588
205363_at	BBOX1	2.57E-13	1.25E-11	-2.74534
202145_at	LY6E	2.76E-13	1.32E-11	-2.07297
239093_at	HOGA1	2.87E-13	1.37E-11	-2.02682
228293_at	DEPDC7	3.23E-13	1.53E-11	-2.26551
230577_at	LINC00844	3.26E-13	1.54E-11	-3.66782
208126_s_at	CYP2C18	3.35E-13	1.58E-11	-2.21793
209374_s_at	IGHM	3.81E-13	1.77E-11	-2.53205
204018_x_at	HBA2///HBA1	4.30E-13	1.97E-11	-2.03379
243296_at	NAMPT	4.32E-13	1.98E-11	-2.02322
206068_s_at	ACADL	4.57E-13	2.08E-11	-2.11999
217014_s_at	AZGP1P1///AZGP1	4.90E-13	2.21E-11	-2.14478
1555564_a_at	CFI	5.11E-13	2.29E-11	-2.38622
1555175_a_at	PBLD	5.25E-13	2.35E-11	-2.40768
217414_x_at	HBA2///HBA1	5.25E-13	2.35E-11	-2.08403
209458_x_at	HBA2///HBA1	5.56E-13	2.46E-11	-2.14757
203967_at	CDC6	5.71E-13	2.52E-11	2.003505
211699_x_at	HBA2///HBA1	6.02E-13	2.64E-11	-2.12898
202345_s_at	FABP5	6.10E-13	2.67E-11	2.145349

220604_x_at	FTCD	6.47E-13	2.81E-11	-2.01039
205531_s_at	GLS2	6.54E-13	2.84E-11	-3.13292
226225_at	MCC	7.60E-13	3.25E-11	-2.28084
217022_s_at	IGHA2///IGHA1///IGH	7.99E-13	3.39E-11	-3.49195
218541_s_at	C8orf4	8.00E-13	3.39E-11	-2.22887
202422_s_at	ACSL4	8.24E-13	3.48E-11	2.76926
227404_s_at	EGR1	8.77E-13	3.68E-11	-2.33703
218532_s_at	FAM134B	8.84E-13	3.70E-11	-2.63596
208650_s_at	CD24	8.86E-13	3.71E-11	3.350665
201109_s_at	THBS1	9.52E-13	3.96E-11	-2.39225
211745_x_at	HBA2///HBA1	1.00E-12	4.15E-11	-2.10695
39763_at	HPX	1.28E-12	5.20E-11	-2.00494
212143_s_at	IGFBP3	1.39E-12	5.56E-11	-2.44882
219543_at	PBLD	1.44E-12	5.73E-11	-2.20373
219733_s_at	SLC27A5	1.53E-12	6.04E-11	-2.5955
201693_s_at	EGR1	1.61E-12	6.29E-11	-2.23028
207820_at	ADH1A	1.73E-12	6.72E-11	-3.03251
206287_s_at	ITIH4	1.90E-12	7.27E-11	-2.19401
207218_at	F9	2.13E-12	8.01E-11	-3.76785
209976_s_at	CYP2E1	2.24E-12	8.36E-11	-4.82911
230120_s_at	PLGLB1///PLGLB2	2.32E-12	8.63E-11	-2.1408
209978_s_at	PLG///LPA	2.52E-12	9.25E-11	-2.47746
1431_at	CYP2E1	3.18E-12	1.15E-10	-4.93519
211470_s_at	SULT1C2	3.31E-12	1.19E-10	2.971229

212067_s_at	C1R	3.92E-12	1.38E-10	-2.00898
212592_at	JCHAIN	4.77E-12	1.66E-10	-2.88341
205442_at	MFAP3L	4.85E-12	1.68E-10	-2.71104
215049_x_at	CD163	5.19E-12	1.78E-10	-2.04317
205728_at	TENM1	5.33E-12	1.83E-10	-2.36942
207097_s_at	SLC17A2	5.49E-12	1.87E-10	-2.27034
211696_x_at	HBB	5.90E-12	2.00E-10	-2.22895
209116_x_at	HBB	6.43E-12	2.15E-10	-2.35664
207275_s_at	ACSL1	6.60E-12	2.20E-10	-2.3422
217232_x_at	HBB	6.92E-12	2.30E-10	-2.13594
206024_at	HPD	6.95E-12	2.31E-10	-3.962
206262_at	ADH1C	9.60E-12	3.04E-10	-3.27903
203645_s_at	CD163	9.96E-12	3.13E-10	-2.12393
210328_at	GNMT	1.31E-11	3.98E-10	-2.77161
207041_at	MASP2	1.44E-11	4.34E-10	-2.29098
217558_at	CYP2C9	1.46E-11	4.39E-10	-2.93788
209612_s_at	ADH1B	1.58E-11	4.69E-10	-3.37153
207409_at	LECT2	1.59E-11	4.72E-10	-3.35581
220061_at	ACSM5	1.75E-11	5.10E-10	-2.42178
205342_s_at	SULT1C2	1.89E-11	5.49E-10	2.626796
206085_s_at	CTH	2.04E-11	5.86E-10	-2.29154
209660_at	TTR	2.07E-11	5.94E-10	-2.09511
203131_at	PDGFRA	2.39E-11	6.79E-10	-2.7407
205830_at	CLGN	2.40E-11	6.82E-10	2.417351

209218_at	SQLE	2.74E-11	7.67E-10	2.057195
205871_at	PLGLB1///PLGLB2	3.05E-11	8.43E-10	-2.04017
232164_s_at	EPPK1	3.09E-11	8.53E-10	2.122744
232165_at	EPPK1	3.24E-11	8.87E-10	2.048573
209977_at	PLG	3.30E-11	9.01E-10	-2.30172
214478_at	SPP2	3.43E-11	9.33E-10	-2.95543
215103_at	CYP2C18	3.63E-11	9.80E-10	-2.08814
207185_at	SLC10A1	3.99E-11	1.07E-09	-3.16128
33323_r_at	SFN	4.02E-11	1.08E-09	2.425133
231790_at	DMGDH	4.05E-11	1.08E-09	-2.09128
241994_at	XDH	4.64E-11	1.22E-09	-2.30678
208471_at	HPR	4.67E-11	1.23E-09	-2.90586
238021_s_at	CRNDE	4.87E-11	1.27E-09	2.548568
236652_at	LOC149703	6.24E-11	1.59E-09	-2.32624
220554_at	SLC22A7	6.71E-11	1.69E-09	-2.10561
1564706_s_at	GLS2	6.77E-11	1.71E-09	-2.74808
210521_s_at	FETUB	6.96E-11	1.75E-09	-2.88666
201110_s_at	THBS1	8.57E-11	2.10E-09	-2.42605
209613_s_at	ADH1B	8.70E-11	2.13E-09	-3.39694
89977_at	ACSM5	9.57E-11	2.31E-09	-2.63842
204719_at	ABCA8	9.59E-11	2.32E-09	-2.77655
217127_at	CTH	1.05E-10	2.51E-09	-2.321
210387_at	HIST1H2BJ///HIST1H2BG	1.07E-10	2.56E-09	2.39547
214669_x_at	IGKC	1.31E-10	3.05E-09	-2.56142

204704_s_at	ALDOB	1.31E-10	3.05E-09	-3.12448
204438_at	MRC1	1.57E-10	3.59E-09	-2.05811
224795_x_at	IGK///IGKC	1.66E-10	3.78E-09	-3.00095
221671_x_at	IGK///IGKC	1.79E-10	4.04E-09	-2.91063
209975_at	CYP2E1	2.05E-10	4.56E-09	-4.22055
207202_s_at	NR1I2	2.32E-10	5.08E-09	-2.3135
221651_x_at	IGK///IGKC	2.32E-10	5.09E-09	-2.95395
1569203_at	CXCL2	2.97E-10	6.34E-09	-2.11904
232494_at	CYP8B1	3.28E-10	6.96E-09	-3.18753
218976_at	DNAJC12	3.34E-10	7.07E-09	-2.04769
205343_at	SULT1C2	3.48E-10	7.33E-09	2.042361
220148_at	ALDH8A1	4.15E-10	8.60E-09	-2.61462
206239_s_at	SPINK1	4.26E-10	8.81E-09	3.779106
238160_at	ACOT12	4.47E-10	9.16E-09	-2.24924
215176_x_at	IGK///IGKC	4.62E-10	9.46E-09	-2.34796
214456_x_at	SAA2///SAA1	5.19E-10	1.05E-08	-2.84494
209301_at	CA2	5.30E-10	1.07E-08	-2.03556
205433_at	BCHE	5.40E-10	1.08E-08	-2.83959
224244_s_at	APOA5	5.44E-10	1.09E-08	-2.16363
221590_s_at	ALDH6A1	5.67E-10	1.13E-08	-2.08265
210798_x_at	MASP2	6.96E-10	1.36E-08	-2.05867
207256_at	MBL2	7.10E-10	1.38E-08	-2.72849
202628_s_at	SERPINE1	7.17E-10	1.39E-08	-2.3368
205082_s_at	AOX1	7.76E-10	1.49E-08	-2.30683

208607_s_at	SAA2-SAA4///SAA2///SAA1	1.10E-09	2.04E-08	-3.08622
206345_s_at	PON1	1.13E-09	2.08E-08	-2.34022
223605_at	SLC25A18	1.31E-09	2.37E-08	-2.06471
214413_at	TAT	1.39E-09	2.51E-08	-2.19024
210272_at	CYP2B7P	1.61E-09	2.87E-08	-2.37268
211430_s_at	MIR8071-2///MIR8071-1///IGHV4-31///IGHM///IGHG2///IGHG1	1.72E-09	3.04E-08	-3.79812
205768_s_at	SLC27A2	1.78E-09	3.13E-08	-2.03252
205700_at	HSD17B6	2.17E-09	3.75E-08	-2.48777
266_s_at	CD24	2.23E-09	3.84E-08	2.318207
205229_s_at	COCH	2.24E-09	3.85E-08	2.250884
203820_s_at	IGF2BP3	2.30E-09	3.94E-08	2.421674
225681_at	CTHRC1	2.30E-09	3.94E-08	2.413351
215121_x_at	CYAT1///IGLV1-44///IGLC1	2.51E-09	4.26E-08	-2.54784
205943_at	TD02	3.06E-09	5.08E-08	-2.59529
224428_s_at	CDCA7	3.08E-09	5.10E-08	2.121424
208383_s_at	PCK1	3.26E-09	5.35E-08	-3.21299
209138_x_at	IGLC1	3.46E-09	5.63E-08	-2.7583
221008_s_at	ETNPPL	3.54E-09	5.75E-08	-2.43602
229819_at	A1BG	3.85E-09	6.21E-08	-2.24994
224367_at	BEX2	4.24E-09	6.76E-08	2.200713
215379_x_at	IGLV1-44	4.36E-09	6.94E-08	-2.6839
214677_x_at	IGLC1	4.42E-09	7.01E-08	-3.24769
226545_at	CD109	4.97E-09	7.82E-08	2.264992
241914_s_at	ACSM2B///ACSM2A	7.29E-09	1.10E-07	-2.3714

220224_at	HA01	8.86E-09	1.30E-07	-2.23115
214069_at	ACSM2B///ACSM2A	1.34E-08	1.88E-07	-2.12825
205749_at	CYP1A1	1.35E-08	1.89E-07	-2.25937
37512_at	HSD17B6	1.38E-08	1.93E-07	-2.37198
205404_at	HSD11B1	1.52E-08	2.11E-07	-3.0705
208470_s_at	HPR///HP	1.89E-08	2.56E-07	-2.36698
210558_at	AKR1C4	2.04E-08	2.73E-07	-2.10426
206496_at	FMO3	2.42E-08	3.18E-07	-2.38419
205083_at	AOX1	2.76E-08	3.58E-07	-2.3124
205384_at	FXVD1	2.91E-08	3.74E-07	-2.01288
205568_at	AQP9	2.94E-08	3.78E-07	-2.3815
206119_at	BHMT	3.27E-08	4.15E-07	-2.07168
203819_s_at	IGF2BP3	3.82E-08	4.78E-07	2.143635
206697_s_at	HP	4.10E-08	5.09E-07	-2.01791
216238_s_at	FGB	4.23E-08	5.23E-07	-2.23982
209771_x_at	CD24	4.59E-08	5.64E-07	2.052465
207200_at	OTC	5.40E-08	6.52E-07	-2.21199
1555229_a_at	C1S	7.02E-08	8.26E-07	-2.43132
216379_x_at	CD24	1.08E-07	1.22E-06	2.08295
239380_at	LINC01554	1.20E-07	1.35E-06	-2.08537
228844_at	SLC13A5	1.29E-07	1.43E-06	-2.11211
229230_at	SLC51A	1.29E-07	1.43E-06	-2.21567
242881_x_at	DUXAP10	2.14E-07	2.24E-06	2.324599
206350_at	APCS	2.42E-07	2.51E-06	-2.09985

40665_at	FMO3	2.49E-07	2.56E-06	-2.38948
205892_s_at	FABP1	2.66E-07	2.72E-06	-2.05272
211548_s_at	HPGD	2.98E-07	3.02E-06	-2.16174
205753_at	CRP	3.53E-07	3.50E-06	-2.91196
203914_x_at	HPGD	3.84E-07	3.78E-06	-2.16394
231398_at	SLC22A7	3.85E-07	3.78E-06	-2.31598
201744_s_at	LUM	4.53E-07	4.36E-06	-2.46872
217238_s_at	ALDOB	5.43E-07	5.12E-06	-2.48483
1554491_a_at	SERPINC1	5.74E-07	5.37E-06	-2.1466
230554_at	ACSM2A	5.94E-07	5.53E-06	-2.06132
205695_at	SDS	6.84E-07	6.26E-06	-2.32749
205844_at	VNN1	7.79E-07	7.03E-06	-2.07609
235904_at	UGT3A1	9.10E-07	8.06E-06	-2.17605
206292_s_at	SULT2A1	1.18E-06	1.02E-05	-2.1674
243483_at	TRPM8	1.26E-06	1.08E-05	-2.035
217564_s_at	CPS1	2.22E-06	1.77E-05	-2.73918
37020_at	CRP	2.37E-06	1.88E-05	-2.82741
225491_at	SLC1A2	3.86E-06	2.89E-05	-2.18152
204920_at	CPS1	4.21E-06	3.13E-05	-2.56842
1556388_a_at	LOC100507389	6.25E-06	4.42E-05	-2.07568
206561_s_at	AKR1B10	1.13E-05	7.43E-05	2.756335
204351_at	S100P	1.76E-05	1.09E-04	2.165008
204602_at	DKK1	6.76E-05	3.56E-04	2.044545
203649_s_at	PLA2G2A	7.25E-05	3.77E-04	-2.06531

202409_at	INS-IGF2///IGF2	2.26E-04	1.02E-03	-2.19797
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