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Treatment protocols

Patients were treated on one of the following intensive cytarabine/daunorubicin-based Cancer and Leukemia Group B (CALGB) frontline treatment protocols: 8525 (n=17),[1] 8923 (n=11),[2] 9420 (n=5),[3] 9720 (n=65),[4,5] or 10201 (n=60).[6] Among these protocols, CALGB 9420, 9720, and 10201 included investigational agents other than chemotherapy. CALGB 9720[4,5] was initiated as a phase III trial in untreated acute myeloid leukemia (AML) patients 60 years and older evaluating multidrug resistance (MDR) modulation by valspodar (PSC-833) during induction and consolidation therapy with cytarabine, daunorubicin, and etoposide. The valspodar (PSC-833) arm was closed after only random assignment of 120 patients because of excessive early deaths. Enrollment on this protocol continued on the chemotherapy-only control arm. CALGB 10201[6] evaluated the *BCL2* antisense, oblimersen sodium (Genasense; G3139) administered with induction and consolidation chemotherapy; preliminary results showed no impact of the antisense on outcome. CALGB 9420[3] and CALGB 9720[4,5] evaluated a subcutaneous IL-2 regimen in older AML patients as maintenance therapy, which was demonstrated to induce no clear benefit. Per the protocols, patients enrolled on these studies did not receive stem cell transplantation in first complete remission (CR).

Sample Preparation

Patients enrolled on the aforementioned treatment protocols were also enrolled on the companion protocols CALGB 9665 (Leukemia Tissue Bank) and CALGB 20202 [molecular studies in AML], and gave informed consent for pretreatment marrow and blood collection and their research use in accordance with the Declaration of Helsinki. Mononuclear cells from pretreatment blood were enriched by Ficoll-Hypaque gradient and cryopreserved in liquid nitrogen until they were thawed at 37°C for the analysis. DNA and total RNA sample extraction and quality control was performed as reported previously.[7–10] Two micrograms of total RNA were used to derive complementary DNA.

Definition of clinical end points

CR was defined as recovery of morphologically normal bone marrow and blood counts (ie, neutrophils ≥1,500/μl and platelets >100,000/μl), and no circulating leukemic blasts or evidence of extramedullary leukemia. Disease-free survival (DFS) was measured from the date of CR until date of relapse or death, regardless of cause. Overall survival (OS) was measured from the date on study until date of death. Patients alive at last follow-up were censored for both DFS and OS.

Multivariable models

Multivariable logistic regression models were constructed to analyze factors related to the probability of achieving CR using a limited backwards selection procedure. Variables in addition to *BAALC* and *ERG* expression that were considered for univariable analyses were age, sex, race, hemoglobin, platelet count, white blood count (WBC), *NPM1* (mutated vs wild-type), *FLT3*-ITD (present vs absent), *FLT3*-TKD (present vs absent), and *CEBPA* (mutated vs wild-type). Variables considered for inclusion in the logistic models were those significant at $\alpha=.20$ from the univariable models. Variables remaining in the final models were significant at $\alpha=.05$.

Multivariable proportional hazards models were constructed for DFS and OS to evaluate the impact of *BAALC* and *ERG* expression by adjusting for other variables using a limited backwards selection procedure. Variables in addition to *BAALC* and *ERG* expression that were considered for univariable analyses were age, sex, race, hemoglobin, platelet count, WBC, *NPM1* (mutated v wild-type), *FLT3*-ITD (present v absent), *FLT3*-TKD (present v absent), *CEBPA* (mutated v wild-type) and *WT1* (mutated v wild-type). Variables significant at α=.20 from the univariable analyses were considered for multivariable analyses. The proportional hazards assumption was checked for each variable individually. If the proportional hazards assumption was not met for a particular variable, then an artificial time dependent covariate was included in all models that contained that variable.[11]

Best model selection

Because we recently reported a strong prognostic impact of *NPM1* mutations on CR rates, DFS and OS in older cytogenetically normal AML patients,[12] it was of particular interest to us to investigate the relationship of *NPM1* mutation status with *BAALC* and *ERG* expresser status. Consequently we compared different multivariable models for CR, DFS and OS.

The Akaike information criterion (AIC) is a model selection tool that aids in choosing between competing statistical models by taking into consideration the goodness-of-fit and complexity of the model. The AIC score was calculated for competing models estimating CR attainment, DFS, and OS. Among the AIC scores calculated for each model, the lowest score is indicative of the best model, irrespective of the amount of difference in the numerical values.

For the achievement of CR, the best Akaike score had the model reported in the main text of this article, consisting of *BAALC* expression, WBC and *NPM1* mutation status, whereas a model that included only *NPM1* mutation status and WBC had a higher (ie, worse) score (Supplemental Table S1a). For DFS, the model including *BAALC* expression, *FLT3*-ITD and age was best, while both the model including *NPM1* mutation status in addition to the aforementioned variables and the model including *NPM1* mutation status, *FLT3*-ITD and WBC, but not *BAALC* expression, were worse (Supplemental Table S1b). For OS, the model including only *BAALC* and *ERG* expression status was better than models including *BAALC* and *ERG* expression and *NPM1* mutation status, or *NPM1* mutation status, *FLT3*-ITD and WBC (Supplemental Table S1c).

Outcome and WBC

336 *de novo* CN-AML patients, 60 years or older, enrolled on CALGB protocols 8525, 8923, 9420, 9720, 10201. A subset of 158 cases had adequate material available to be included in our study. The subset of studied patients had higher CR rates, when compared to the remaining 178 cases without adequate material (70% vs. 58%, *P*=.02). There was no significant difference observed for DFS (*P*=.57) and OS (*P*=.20). Furthermore the WBC was significantly higher in the studied cases compared to the cases not included in our study (*P*<.001). This is a result of availability of adequate material for reliable molecular studies in patients with higher WBCs. To rule out any potential confounding effect due to this fact, we evaluated WBC in all final multivariable models that did not include WBC. WBC was not significant in either the DFS (*P*=.47) or in the OS (*P*=.42) models. The estimates and significance of our main variables, *BAALC* and *ERG* expression, did not change.

Gene- and microRNA-expression profiling

For gene-expression microarrays, summary measures of gene expression were computed for each probe set using the robust multichip average (RMA) method, which incorporates quantile normalization of arrays. Expression values were logged (base 2) before analysis. A filtering step was performed to remove probe sets that did not display significant variation in expression across arrays. In this procedure, a chi-square test was used to test whether the observed variance in expression of a probe set was significantly larger than the median observed variance in expression for all probe sets using α=.01 as the significance level. A total of 24,437 probe sets passed the filtering criterion and were examined in the derivation of signatures. A comparison of gene expression was made between low and high *BAALC* expression and low and high *ERG* expression respectively, using a univariable significance level of .001.

For microRNA microarrays, signal intensities were calculated for each spot making an adjustment for local background. Intensities were log-transformed and log-intensities from replicate spots were averaged. Quantile normalization was performed on arrays using all human and mouse microRNA probes represented on the array. For each microRNA probe, an adjustment was made for batch effects (ie, differences in expression related to the batch in which arrays were hybridized). Further analysis was limited to 895 unique human probes. A comparison of microRNA-expression was made between low and high *BAALC* expression and low and high *ERG* expression respectively, using a univariable significance level of .005.

Analyses were performed using BRB-ArrayTools Version 3.8.0 Beta_1 Release developed by Dr. Richard Simon and Amy Peng Lam. For *in silico* target prediction of microRNAs, the online applications miRBase Targets Version 5 and Targetscan Release 5.0 were used.

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Table S1a. Akaike information criterion (AIC) of CR achievement models

Model	Log likelihood (LL)	No. of Covariates (c)	No. of Ancillary Parameters (a)	AIC*
BAALC, *NPM1*, WBC	−82.14	3	1	172.3
NPM1, WBC	−88.27	2	1	182.5

*AIC=−2LL+2(c+a)

Table S1b. Akaike information criterion (AIC) of DFS models

Model	Log likelihood (LL)	No. of Covariates (c)	No. of Ancillary Parameters (a)	AIC*
BAALC, *FLT3*-ITD, Age	−374.06	3	1	756.1
BAALC, *FLT3*-ITD, Age, *NPM1*	−373.65	4	1	757.3
NPM1, *FLT3*-ITD, WBC	−377.06	3	1	762.1

*AIC=−2LL+2(c+a)

Table S1c. Akaike information criterion (AIC) of OS models

Model	Log likelihood (LL)	No. of Covariates (c)	No. of Ancillary Parameters (a)	AIC*
BAALC, *ERG*	−577.52	2	1	1161.0
BAALC, *ERG*, *NPM1*	−577.06	3	1	1162.1
NPM1, *FLT3*-ITD, WBC	−585.99	3	1	1178.0

*AIC=−2LL+2(c+a)

Note: Among the AIC scores calculated for each model, the lowest score is indicative of the best model, irrespective of the amount of difference in the numerical values.

Table S2. 482 probe sets associated with low *BAALC* expression in older CN-AML patients

Probe set	gene symbol	Fold-change: Low/High	P-value
204304_s_at	PROM1	0.1640	4.54E-05
218899_s_at	BAALC	0.1672	1.00E-07
222780_s_at	BAALC	0.1717	1.00E-07
219789_at	NPR3	0.1843	3.00E-07
1566363_at	DNTT	0.1958	0.000617
210487_at	DNTT	0.1998	0.000598
205330_at	MN1	0.2030	2.00E-07
209543_s_at	CD34	0.2037	< 1e-07
219054_at	C5orf23	0.2189	1.00E-07
1562433_at	FLJ10489	0.2673	7.95E-05
218589_at	LPAR6	0.2679	0.000361
211597_s_at	HOPX	0.2842	0.000635
241133_at	TRBV27	0.2843	0.000653
210755_at	HGF	0.2868	0.000218
204439_at	IFI44L	0.2883	0.000582
229390_at	FAM26F	0.3073	6.20E-06
214953_s_at	APP	0.3108	0.000144
207655_s_at	BLNK	0.3141	0.000556
226517_at	BCAT1	0.3169	0.000441
209583_s_at	CD200	0.3169	1.06E-05
202283_at	SERPINF1	0.3243	0.000144
200665_s_at	SPARC	0.3266	1.05E-05
209576_at	GNAI1	0.3271	0.000122
227692_at	GNAI1	0.3351	4.79E-05
227198_at	AFF3	0.3362	4.39E-05
211991_s_at	HLA-DPA1	0.3386	0.000342
230896_at	BEND4	0.3467	0.00038
213506_at	F2RL1	0.3474	7.20E-05
211990_at	HLA-DPA1	0.3506	0.000115
225285_at	BCAT1	0.3610	0.000633
224428_s_at	CDCA7	0.3754	0.00063
210997_at	HGF	0.3768	0.000148
219790_s_at	NPR3	0.3813	5.90E-06
209723_at	SERPINB9	0.3854	0.000863
227923_at	SHANK3	0.3905	0.00013
209993_at	ABCB1	0.3918	0.000319
203987_at	FZD6	0.4008	0.000408
224579_at	SLC38A1	0.4010	4.88E-05
214452_at	BCAT1	0.4037	0.000579
242064_at	SDK2	0.4040	0.000752
205984_at	CRHBP	0.4044	0.000306
219648_at	MREG	0.4050	0.000558
221491_x_at		0.4053	8.37E-05
217979_at	TSPAN13	0.4068	8.77E-05
211474_s_at	SERPINB6	0.4076	0.000778

Probe set	gene symbol	Fold-change: Low/High	P-value
201137_s_at	HLA-DPB1	0.4082	0.000327
202242_at	TSPAN7	0.4102	0.000293
208116_s_at	MAN1A1	0.4106	1.30E-06
229391_s_at	FAM26F	0.4113	5.90E-06
226878_at	HLA-DOA	0.4157	6.18E-05
218237_s_at	SLC38A1	0.4213	1.62E-05
211675_s_at	MDFIC	0.4225	0.000134
206233_at	B4GALT6	0.4296	4.10E-06
214022_s_at	IFITM1	0.4299	0.000504
201601_x_at	IFITM1	0.4312	0.000212
235333_at	B4GALT6	0.4334	0.000184
209199_s_at	MEF2C	0.4386	0.00033
228831_s_at	GNG7	0.4391	5.00E-07
213241_at	PLXNC1	0.4393	0.000193
223125_s_at	C1orf21	0.4396	0.000481
209200_at	MEF2C	0.4518	0.000599
221760_at	MAN1A1	0.4554	1.38E-05
209795_at	CD69	0.4558	0.000485
227108_at	STARD9	0.4610	0.000171
206232_s_at	B4GALT6	0.4637	3.30E-06
209994_s_at		0.4652	0.000294
229543_at	FAM26F	0.4752	4.09E-05
212607_at	AKT3	0.4757	0.000113
204972_at	OAS2	0.4775	0.000338
205101_at	CIITA	0.4781	3.20E-06
217478_s_at	HLA-DMA	0.4798	0.000565
216766_at		0.4808	2.30E-06
210192_at	ATP8A1	0.4828	7.10E-05
221004_s_at	ITM2C	0.4838	3.76E-05
213618_at	ARAP2	0.4883	0.00054
225105_at	C12orf75	0.4885	0.00054
204896_s_at		0.4887	0.000104
208965_s_at	IFI16	0.4923	3.71E-05
209582_s_at	CD200	0.4927	0.000518
230481_at	ACY3	0.4943	0.000354
213106_at	ATP8A1	0.4953	8.69E-05
1553183_at	UMODL1	0.5015	0.000282
227875_at	KLHL13	0.5028	0.00073
208966_x_at	IFI16	0.5032	6.51E-05
209574_s_at	C18orf1	0.5042	8.10E-05
206332_s_at	IFI16	0.5110	0.000121
214255_at	ATP10A	0.5127	0.000136
226018_at	C7orf41	0.5156	0.000492
212573_at	ENDOD1	0.5203	0.000105
209933_s_at	CD300A	0.5223	0.000839
214390_s_at	BCAT1	0.5232	0.000345
201015_s_at	JUP	0.5267	0.000401
228557_at	L3MBTL4	0.5279	0.000277

Probe set	gene symbol	Fold-change: Low/High	P-value
227210_at		0.5286	0.000139
209960_at	HGF	0.5329	0.000751
212203_x_at	IFITM3	0.5343	7.90E-06
229344_x_at	RIMKLB	0.5346	3.93E-05
205659_at	HDAC9	0.5362	0.000629
230405_at	C5orf56	0.5363	2.42E-05
225651_at	UBE2E2	0.5375	0.000807
213447_at		0.5474	0.000131
226164_x_at	RIMKLB	0.5476	0.000225
206429_at	F2RL1	0.5504	2.58E-05
225978_at	RIMKLB	0.5519	1.75E-05
217080_s_at	HOMER2	0.5542	0.000154
225999_at	RIMKLB	0.5550	2.05E-05
217078_s_at	CD300A	0.5557	0.000471
232286_at		0.5570	9.89E-05
212667_at	SPARC	0.5574	0.000317
204269_at	PIM2	0.5593	0.000432
207030_s_at	CSRP2	0.5647	0.000193
235574_at	GBP4	0.5675	0.000729
218825_at	EGFL7	0.5707	0.000853
207735_at	RNF125	0.5716	0.000141
216060_s_at	DAAM1	0.5727	0.000272
226550_at		0.5727	0.000602
209321_s_at	ADCY3	0.5758	0.000488
207124_s_at	GNB5	0.5761	2.83E-05
212875_s_at	C2CD2	0.5788	7.03E-05
228899_at	LOC100132884	0.5811	0.000929
226666_at	DAAM1	0.5825	0.000561
209679_s_at	SMAGP	0.5827	0.0004
220936_s_at	H2AFJ	0.5919	0.000445
212675_s_at	CEP68	0.5921	0.000144
212235_at	PLXND1	0.5970	0.000316
228167_at	KLHL6	0.5989	0.000875
235061_at	PPM1K	0.6012	0.000226
222731_at	ZDHHC2	0.6015	8.31E-05
206313_at	HLA-DOA	0.6026	7.36E-05
38671_at	PLXND1	0.6059	0.000251
204897_at	PTGER4	0.6069	0.00078
233138_at	C18orf1	0.6076	0.000149
224046_s_at	PDE7A	0.6094	0.000833
219282_s_at	TRPV2	0.6117	0.000917
221221_s_at	KLHL3	0.6155	0.000129
222857_s_at	KCNMB4	0.6165	0.000146
233379_at	PRR5L	0.6175	0.000268
204675_at	SRD5A1	0.6192	0.000284
226773_at		0.6192	0.000667
212677_s_at	CEP68	0.6199	0.000321
228049_x_at		0.6235	0.000202

Probe set	gene symbol	Fold-change: Low/High	P-value
1560156_at		0.6245	0.000194
228213_at	H2AFJ	0.6250	0.000667
203593_at	CD2AP	0.6287	0.000606
224580_at	SLC38A1	0.6302	0.000256
216286_at		0.6325	8.46E-05
235175_at	GBP4	0.6337	0.000646
219363_s_at	MTERFD1	0.6341	0.000121
222453_at	CYBRD1	0.6352	0.000793
242551_at		0.6361	0.000763
209163_at	CYB561	0.6389	0.000502
1555486_a_at	PRR5L	0.6391	4.17E-05
239317_at	CEACAM21	0.6401	2.00E-07
244721_at	TP53INP1	0.6419	0.000203
206896_s_at	GNG7	0.6440	2.70E-05
205961_s_at	PSIP1	0.6474	1.61E-05
219383_at	PRR5L	0.6480	0.000148
238376_at		0.6483	0.000203
218928_s_at	SLC37A1	0.6516	9.48E-05
201315_x_at	IFITM2	0.6572	0.000695
240454_at		0.6588	5.50E-05
243452_at	LOC646778	0.6602	0.000828
211056_s_at	SRD5A1	0.6635	0.000149
244561_at		0.6653	0.000985
227425_at	REPS2	0.6676	0.000425
209961_s_at	HGF	0.6681	0.000124
234089_at		0.6709	1.95E-05
204000_at	GNB5	0.6734	0.000414
220606_s_at	C17orf48	0.6737	0.000926
222855_s_at	TRPV2	0.6773	0.00044
242870_at	RIMKLB	0.6795	0.000697
226335_at	RPS6KA3	0.6800	5.90E-05
210757_x_at	DAB2	0.6806	0.000256
228362_s_at	FAM26F	0.6844	2.22E-05
336_at	TBXA2R	0.6932	0.000478
222730_s_at	ZDHHC2	0.6956	0.000804
216565_x_at		0.6960	0.000722
209337_at	PSIP1	0.6963	0.000173
201279_s_at	DAB2	0.6974	0.000917
1554360_at	FCHSD2	0.6986	0.000272
213628_at	CLCC1	0.7014	0.000637
212829_at	PIP4K2A	0.7048	0.000983
204109_s_at	NFYA	0.7050	0.000138
211871_x_at	GNB5	0.7089	0.000682
203843_at	RPS6KA3	0.7095	0.000162
218451_at	CDCP1	0.7156	0.000855
232948_at		0.7176	0.000518
205645_at	REPS2	0.7210	0.000704
1566880_at		0.7240	0.000756

Probe set	gene symbol	Fold-change: Low/High	P-value
41220_at	SEPT9	0.7315	0.000279
225879_at	TSEN54	0.7323	0.000842
229631_at	DNHD1	0.7357	0.00079
1556097_at		0.7406	0.000733
243951_at	ABCB1	0.7408	0.000981
215659_at	GSDMB	0.7589	0.000165
223334_at	TMEM126A	0.7708	7.00E-04
201222_s_at	RAD23B	0.7736	0.000309
212271_at	MAPK1	0.7881	0.000489
219313_at	GRAMD1C	0.8225	0.000458
221849_s_at	DCAF15	1.2408	0.000339
204177_s_at	KLHL20	1.2424	0.000943
239610_at		1.2448	0.000809
217784_at	YKT6	1.2472	0.000406
221953_s_at	EDEM2	1.2539	0.000909
241930_x_at	LOC442113	1.2542	0.000735
221799_at	CHPF2	1.2636	0.000696
223527_s_at	CDADC1	1.2665	0.000399
233101_at	MTMR9	1.2698	0.000453
211168_s_at	UPF1	1.2740	0.000304
44822_s_at	MIER2	1.2754	0.000763
221738_at	KIAA1219	1.2757	0.000482
201155_s_at	MFN2	1.2774	0.000215
233564_s_at	CDADC1	1.2785	0.000849
242337_at		1.2825	0.000612
232228_at	ZNF530	1.2828	0.000231
217888_s_at	ARFGAP1	1.2840	7.33E-05
231225_at		1.2859	0.000476
228138_at	ZNF498	1.2884	0.000613
242808_at		1.2896	0.000858
1554509_a_at	FAM188A	1.2897	0.000698
221927_s_at	ABHD11	1.2909	0.000123
210428_s_at	HGS	1.2920	0.000782
237064_x_at		1.2980	0.000504
213497_at	ABTB2	1.2996	0.00043
218749_s_at	SLC24A6	1.3000	0.00063
1570264_at		1.3003	0.000633
244664_at		1.3007	0.000242
220746_s_at	UIMC1	1.3025	0.000263
244218_at		1.3051	0.000111
218297_at	FAM188A	1.3059	0.000672
222767_s_at	C12orf49	1.3063	0.000262
203938_s_at	TAF1C	1.3077	6.91E-05
232135_at	SAP30L	1.3085	0.000719
234788_x_at		1.3102	0.000885
228139_at	RIPK3	1.3111	0.00058
211256_x_at	BTN2A1	1.3117	0.00028
1559759_at	KIFC3	1.3134	9.10E-05

Probe set	gene symbol	Fold-change: Low/High	P-value
228271_at		1.3170	0.00047
209222_s_at	OSBPL2	1.3208	0.00046
200977_s_at	TAX1BP1	1.3209	0.000537
218272_at	TTC38	1.3217	0.000425
215641_at	SEC24D	1.3217	0.000969
202851_at	AAGAB	1.3228	0.000241
226706_at		1.3234	0.000197
240175_at		1.3252	8.14E-05
213066_at	RUSC2	1.3267	0.000432
202361_at	SEC24C	1.3297	0.000104
225848_at	ZNF746	1.3313	0.000741
1564773_x_at		1.3318	8.84E-05
228683_s_at	KCTD15	1.3347	0.000124
226759_at	IKZF4	1.3356	0.000153
203943_at	KIF3B	1.3371	0.000903
204555_s_at	PPP1R3D	1.3430	0.000348
225205_at	KIF3B	1.3452	0.000219
213196_at	ZNF629	1.3454	7.65E-05
220140_s_at	SNX11	1.3457	3.50E-05
212297_at	ATP13A3	1.3474	0.000328
218821_at	NPEPL1	1.3485	0.000976
1555117_at		1.3492	0.00021
240151_at		1.3510	0.00079
204877_s_at	TAOK2	1.3543	2.97E-05
209211_at	KLF5	1.3545	2.13E-05
226229_s_at	SSU72	1.3559	6.60E-06
227547_at		1.3561	8.67E-05
238134_at		1.3572	0.000252
232148_at	NSMAF	1.3628	0.00023
226761_at	IKZF4	1.3628	0.000101
233936_s_at	GGNBP2	1.3717	0.000965
238295_at	C17orf42	1.3734	0.000848
237119_at		1.3748	0.000638
1556762_a_at		1.3754	0.000402
207023_x_at	KRT10	1.3763	0.000202
236346_at		1.3776	0.00036
214965_at	SPATA2L	1.3787	7.80E-06
229743_at	ZNF438	1.3802	0.000824
229059_at		1.3819	0.000279
222199_s_at	BIN3	1.3850	0.000106
242749_at		1.3853	7.39E-05
230528_s_at	MGC2752	1.3875	0.000519
232659_at		1.3884	0.000656
203590_at	DYNC1LI2	1.3886	6.83E-05
232906_at		1.3888	8.15E-05
1565894_at		1.3917	8.00E-06
205107_s_at	EFNA4	1.3934	0.000638
202197_at	MTMR3	1.3941	0.000113

Probe set	gene symbol	Fold-change: Low/High	P-value
215493_x_at	BTN2A1	1.3951	0.000121
203944_x_at	BTN2A1	1.3971	3.12E-05
242922_at		1.4012	3.76E-05
229776_at	SLCO3A1	1.4015	0.000425
1554860_at	PTPN7	1.4016	0.000108
241775_at		1.4061	0.00066
213287_s_at	KRT10	1.4079	0.000153
218941_at	FBXW2	1.4093	0.000774
227575_s_at	C14orf102	1.4096	0.000408
222894_x_at	C20orf7	1.4104	0.000487
210469_at	DLG5	1.4114	0.000975
1555303_at		1.4140	4.39E-05
205745_x_at	ADAM17	1.4147	0.000105
225381_at	LOC399959	1.4183	0.000696
239392_s_at	POGK	1.4191	0.000222
226566_at	TRIM11	1.4208	4.32E-05
239311_at		1.4239	3.80E-06
224616_at	DYNC1LI2	1.4281	0.000339
243280_at		1.4310	0.000942
226271_at	GDAP1	1.4313	6.55E-05
235595_at	ARHGEF2	1.4313	0.000398
1556416_s_at		1.4374	2.92E-05
1555872_a_at		1.4385	0.000886
46665_at	SEMA4C	1.4400	0.000952
233596_at		1.4559	0.000373
209438_at	PHKA2	1.4575	8.34E-05
227160_s_at	C20orf7	1.4598	0.000213
224614_at	DYNC1LI2	1.4607	2.88E-05
216548_x_at	HMGB3L1	1.4611	9.08E-05
219951_s_at	C20orf12	1.4618	0.000915
219028_at	HIPK2	1.4623	1.93E-05
241242_at		1.4633	0.000705
233122_at	KRTCAP2	1.4727	0.000209
205746_s_at	ADAM17	1.4730	0.000397
226298_at	RUNDC1	1.4749	0.000872
237096_at		1.4809	0.000259
227219_x_at	MAP1LC3A	1.4810	5.77E-05
205934_at	PLCL1	1.4815	0.000616
227949_at	PHACTR3	1.4889	0.00028
202807_s_at	TOM1	1.4926	0.000361
230974_at	DDX19B	1.4928	2.23E-05
222692_s_at	FNDC3B	1.4934	0.00094
213532_at	ADAM17	1.5047	2.58E-05
204998_s_at	ATF5	1.5078	2.51E-05
225097_at	HIPK2	1.5082	0.000406
228349_at		1.5100	1.85E-05
209439_s_at	PHKA2	1.5123	9.10E-06
228723_at		1.5138	0.000737

Probe set	gene symbol	Fold-change: Low/High	P-value
225116_at	HIPK2	1.5149	0.000771
223908_at	HDAC8	1.5154	0.000952
233229_at	SCFD1	1.5165	0.000339
223464_at	OSBPL5	1.5231	0.000278
1557810_at		1.5282	0.000501
228983_at		1.5316	0.000183
208499_s_at	DNAJC3	1.5365	0.000192
1556053_at	DNAJC7	1.5494	0.000368
244027_at		1.5518	0.000892
234978_at	SLC36A4	1.5562	0.000512
220795_s_at	BEGAIN	1.5570	0.00063
204999_s_at	ATF5	1.5591	3.24E-05
238000_at		1.5621	0.000809
242068_at		1.5641	0.000179
239022_at		1.5654	0.000174
214457_at	HOXA2	1.5693	2.57E-05
227334_at	USP54	1.5752	0.000886
232405_at		1.5761	0.000363
223393_s_at	TSHZ3	1.5804	0.000396
206862_at	ZNF254	1.5819	0.000276
224378_x_at	MAP1LC3A	1.5823	0.000154
233393_at		1.5842	0.000349
209333_at	ULK1	1.5892	1.02E-05
225522_at	AAK1	1.5899	0.000134
217620_s_at	PIK3CB	1.5973	0.000768
235009_at	BOD1L	1.5976	6.90E-05
206289_at	HOXA4	1.6082	0.000444
232011_s_at	MAP1LC3A	1.6116	0.000238
242343_x_at		1.6127	0.000424
239892_at		1.6138	3.79E-05
235662_at		1.6170	0.000316
226905_at	FAM101B	1.6184	1.20E-06
237798_at		1.6218	0.000101
205601_s_at	HOXB5	1.6229	0.000537
201482_at	QSOX1	1.6232	0.000433
215024_at	C7orf28B	1.6255	0.000328
229907_at		1.6260	1.20E-06
216417_x_at	HOXB9	1.6276	0.000368
210458_s_at	TANK	1.6379	0.000168
229897_at	ZNF641	1.6393	2.00E-07
219229_at	SLCO3A1	1.6407	0.000795
232113_at		1.6471	0.000857
236429_at	ZNF83	1.6572	3.03E-05
204363_at	F3	1.6626	5.44E-05
242827_x_at		1.6670	0.000403
214033_at	ABCC6	1.6688	0.000797
235749_at	UGGT2	1.6809	0.000466
205434_s_at	AAK1	1.6908	6.79E-05

Probe set	gene symbol	Fold-change: Low/High	P-value
234186_at		1.6938	0.0004
1556761_at		1.6942	0.000155
239457_at	ATP8B3	1.7075	0.000394
230648_at	LOC283663	1.7177	0.000166
206589_at	GFI1	1.7407	0.000185
215209_at	SEC24D	1.7438	0.000229
226876_at	FAM101B	1.7631	7.00E-07
221766_s_at	FAM46A	1.7675	0.000386
214639_s_at	HOXA1	1.7715	0.000813
231858_x_at	DKFZp761E198	1.7802	5.59E-05
236899_at		1.7901	8.94E-05
229865_at	FNDC3B	1.7913	0.000904
232068_s_at	TLR4	1.8080	0.00061
238919_at		1.8091	0.000451
215623_x_at	SMC4	1.8203	8.90E-06
202766_s_at	FBN1	1.8216	0.0008
204778_x_at	HOXB7	1.8327	6.70E-06
1559049_a_at		1.8866	0.000992
232903_at		1.9030	6.20E-06
206847_s_at	HOXA7	1.9103	0.000185
235112_at		1.9432	0.00058
222363_at		1.9696	7.06E-05
235249_at	RDH13	1.9865	3.05E-05
232406_at		2.0013	0.000204
218865_at	MOSC1	2.0082	0.000201
204750_s_at	DSC2	2.0114	0.000726
230743_at	LOC404266	2.0186	0.000785
229715_at	DKFZp686O24166	2.0241	0.000349
213147_at	HOXA10	2.0295	0.000398
231183_s_at	JAG1	2.0319	8.49E-05
1556589_at		2.0408	0.00036
205600_x_at	HOXB5	2.0784	0.0005
241497_at		2.0818	3.43E-05
228790_at	FAM110B	2.0855	0.000399
210377_at	ACSM3	2.1104	0.000916
202728_s_at	LTBP1	2.1167	0.000577
209706_at	NKX3-1	2.1227	1.51E-05
221075_s_at	NCR2	2.1338	0.000834
208557_at	HOXA6	2.1449	0.000118
209098_s_at	JAG1	2.1677	2.49E-05
240772_at		2.1802	4.16E-05
204984_at	GPC4	2.1971	8.03E-05
220898_at		2.2378	0.000402
232979_at		2.2473	4.41E-05
204779_s_at	HOXB7	2.2677	0.000853
1559117_at		2.2779	0.000537
235753_at	HOXA7	2.2938	0.000392
226123_at	CHD7	2.2972	0.000257

Probe set	**gene symbol**	**Fold-change: Low/High**	**P-value**
209099_x_at	JAG1	2.2993	0.000521
218829_s_at	CHD7	2.3267	0.000787
215489_x_at		2.3448	0.000501
220798_x_at	PRG2	2.3496	5.40E-06
222222_s_at	HOMER3	2.3595	4.24E-05
216268_s_at	JAG1	2.4071	0.00037
224836_at	TP53INP2	2.4320	3.00E-07
204983_s_at	GPC4	2.4745	0.000127
230245_s_at	LOC283663	2.4768	4.86E-05
217521_at		2.4901	1.40E-06
219304_s_at	PDGFD	2.4930	0.000425
226461_at	HOXB9	2.4965	0.00025
236193_at	HIST1H2BC	2.5064	0.000231
206157_at	PTX3	2.5231	0.000903
1554453_at	HNRPLL	2.5448	3.75E-05
214455_at	HIST1H2BC	2.5620	0.000173
241692_at		2.5702	4.50E-05
225386_s_at	HNRPLL	2.5943	5.06E-05
239791_at		2.5988	0.000254
204751_x_at	DSC2	2.6018	0.000594
204647_at	HOMER3	2.6479	0.000113
205942_s_at	ACSM3	2.6539	0.000124
220110_s_at	NXF3	2.6857	0.000326
228497_at	SLC22A15	2.7598	0.000951
206111_at	RNASE2	2.7625	0.000747
205366_s_at	HOXB6	2.7632	8.79E-05
1556590_s_at		2.7866	0.000209
209905_at	HOXA9	2.8551	0.000771
215761_at	DMXL2	2.8563	3.61E-05
221959_at	FAM110B	2.8684	1.08E-05
205382_s_at	CFD	2.9108	0.000315
242172_at	MEIS1	3.1216	5.05E-05
232668_at		3.2436	0.000291
204069_at	MEIS1	3.2507	0.000149
212820_at	DMXL2	3.2875	1.70E-06
1558871_at		3.5201	0.000103
238022_at	CRNDE	3.5277	2.19E-05
206851_at	RNASE3	3.5559	1.09E-05
1559477_s_at	MEIS1	3.6059	8.52E-05
205801_s_at	RASGRP3	3.6196	1.80E-06
206643_at	HAL	3.6471	7.90E-06
238021_s_at	CRNDE	3.7246	2.87E-05
228904_at	HOXB3	3.8040	0.000432
213844_at	HOXA5	3.8611	0.000304
229638_at	IRX3	3.8844	9.50E-06
235521_at	HOXA3	3.9067	4.97E-05
214575_s_at	AZU1	3.9930	0.0001
218332_at	BEX1	4.2576	0.000157

Probe set	**gene symbol**	**Fold-change: Low/High**	**P-value**
210239_at	IRX5	4.2583	1.10E-06
236892_s_at		4.4202	4.75E-05
219737_s_at	PCDH9	4.5253	1.20E-06
1553613_s_at	FOXC1	4.9747	0.000653
205653_at	CTSG	6.0141	4.20E-06

Table S3. 1554 probe sets associated with low *ERG* expression in older CN-AML patients

Probe set	Gene Symbol	Fold-change: Low/High	P-value
1552908_at	C1orf150	0.2989	2.28E-05
203372_s_at	SOCS2	0.3480	0.000415
221942_s_at	GUCY1A3	0.3546	1.01E-05
227235_at	GUCY1A3	0.3631	7.20E-06
218858_at	DEPDC6	0.3788	1.80E-06
229530_at	GUCY1A3	0.3831	1.35E-05
227297_at	ITGA9	0.3842	0.000172
213541_s_at	ERG	0.3965	2.25E-05
225841_at	C1orf59	0.4136	4.25E-05
209537_at	EXTL2	0.4209	2.00E-07
223253_at	EPDR1	0.4330	5.47E-05
222603_at	ERMP1	0.4343	0.000128
202742_s_at	PRKACB	0.4374	2.00E-07
1554876_a_at	S100Z	0.4419	0.000186
235333_at	B4GALT6	0.4445	0.000235
203139_at	DAPK1	0.4501	0.000086
224285_at	GPR174	0.4546	0.000116
206233_at	B4GALT6	0.4576	1.84E-05
204521_at	C12orf24	0.4584	0.000022
222824_at		0.4626	1.66E-05
239963_at		0.4637	8.22E-05
227236_at	TSPAN2	0.4654	0.000756
224996_at	ASPH	0.4704	0.000696
220637_at	FAM124B	0.4715	1.30E-05
206232_s_at	B4GALT6	0.4743	4.80E-06
226126_at	TBCKL	0.4755	1.75E-05
1558956_s_at	IFT80	0.4771	0.000677
218491_s_at	THYN1	0.4775	1.35E-05
236918_s_at	LRRC34	0.4794	0.000159
239108_at	FAR2	0.4835	0.000148
225551_at	C1orf71	0.4841	1.40E-06
226794_at	STXBP5	0.4853	1.08E-05
223155_at	HDHD2	0.4856	0.000669
226478_at	TM7SF3	0.4861	8.53E-05
204839_at	POP5	0.4869	0.000125
219654_at	PTPLA	0.4870	0.00004
202890_at	MAP7	0.4875	0.000968
236917_at	LRRC34	0.4888	2.06E-05
218984_at	PUS7	0.4896	0.000106
215767_at	ZNF804A	0.4915	0.000402
202950_at	CRYZ	0.4941	1.06E-05
203284_s_at	HS2ST1	0.4946	6.10E-06
229391_s_at	FAM26F	0.4961	0.000432
213698_at	ZMYM6	0.4969	0.000249
201302_at	ANXA4	0.4981	0.000454
201307_at	SEPT11	0.5005	0.000017

Probe set	Gene Symbol	Fold-change: Low/High	P-value
239580_at	GUCY1A3	0.5017	1.28E-05
219032_x_at	OPN3	0.5051	0.000618
226098_at	IFT80	0.5053	0.000631
201301_s_at	ANXA4	0.5080	0.000519
206667_s_at	SCAMP1	0.5081	1E-07
231747_at	CYSLTR1	0.5084	0.000178
213427_at	RPP40	0.5101	7.57E-05
232383_at	TFEC	0.5101	0.000571
225485_at	TSGA14	0.5117	0.000133
220615_s_at	FAR2	0.5123	0.000054
225550_at	C1orf71	0.5138	4.00E-06
213246_at	C14orf109	0.5142	4.27E-05
225725_at		0.5150	9.89E-05
229971_at	GPR114	0.5161	2.41E-05
222477_s_at	TM7SF3	0.5161	0.000106
202741_at	PRKACB	0.5189	4.90E-06
213395_at	MLC1	0.5197	0.000266
1558105_a_at		0.5204	0.0004
230866_at	CYSLTR1	0.5219	0.00011
228697_at	HINT3	0.5226	0.000783
218557_at	NIT2	0.5229	2.23E-05
219553_at	NME7	0.5233	9.00E-07
225439_at	NUDCD1	0.5237	7.00E-07
224812_at	HIBADH	0.5253	1.00E-05
222746_s_at	BSPRY	0.5254	3.00E-07
226073_at	TMEM218	0.5268	0.000188
210653_s_at	BCKDHB	0.5270	0.000106
227522_at	CMBL	0.5272	0.000372
218788_s_at	SMYD3	0.5277	0.000258
225274_at	PCYOX1	0.5285	4.11E-05
227639_at	PIGK	0.5291	0.000171
235227_at		0.5293	1.22E-05
218342_s_at	ERMP1	0.5298	3.45E-05
219048_at	PIGN	0.5304	0.00005
220591_s_at	EFHC2	0.5313	0.000691
213346_at	C13orf27	0.5321	0.000471
1552386_at	GAPT	0.5325	0.000591
220307_at	CD244	0.5332	0.000131
226152_at	TTC7B	0.5336	1.17E-05
222428_s_at	LARS	0.5341	0.00057
201308_s_at	SEPT11	0.5345	1.29E-05
235287_at	CDK6	0.5362	0.000513
211031_s_at	CLIP2	0.5363	2.82E-05
212414_s_at		0.5366	0.000159
230298_at	MBLAC2	0.5368	4.00E-07
209409_at	GRB10	0.5370	0.000493
218795_at	ACP6	0.5374	0.00026
212175_s_at	AK2	0.5381	0.000317

Probe set	Gene Symbol	Fold-change: Low/High	P-value
222750_s_at	SRD5A3	0.5395	9.31E-05
212174_at	AK2	0.5396	0.000677
241991_at		0.5430	5.94E-05
212413_at	SEPT6	0.5434	2.27E-05
202502_at	ACADM	0.5436	2.85E-05
229905_at	RAP1GDS1	0.5436	3.06E-05
206272_at		0.5440	1.80E-06
220658_s_at	ARNTL2	0.5445	0.000255
209268_at	VPS45	0.5448	0.000538
213374_x_at	HIBCH	0.5454	0.000383
210154_at	ME2	0.5455	0.000336
212922_s_at	SMYD2	0.5462	4.30E-06
223451_s_at	CKLF	0.5465	0.000678
228661_s_at		0.5469	0.000252
209911_x_at	HIST1H2BD	0.5477	0.000345
205996_s_at	AK2	0.5484	0.000516
225647_s_at	CTSC	0.5487	0.000151
209707_at	PIGK	0.5489	0.000244
225835_at	SLC12A2	0.5491	0.000723
203545_at	ALG8	0.5493	9.17E-05
1557411_s_at	SLC25A43	0.5496	0.00021
211300_s_at	TP53	0.5500	0.00023
215022_x_at	ZNF33B	0.5514	5.00E-07
229693_at	TMEM220	0.5516	2.00E-07
222394_at	PDCD6IP	0.5520	0.000327
228841_at	LYRM7	0.5535	4.44E-05
228315_at		0.5537	0.000428
202330_s_at	UNG	0.5542	0.000411
235010_at	LOC729013	0.5545	5.08E-05
217892_s_at	LIMA1	0.5549	1.53E-05
228280_at	ZC3HAV1L	0.5553	1.14E-05
224847_at	CDK6	0.5564	4.87E-05
229402_at	SAMD13	0.5577	0.000139
213677_s_at	PMS1	0.5580	0.000262
207627_s_at	TFCP2	0.5590	1.51E-05
203148_s_at	TRIM14	0.5597	0.000781
201563_at	SORD	0.5602	0.000509
229210_at	RNASEH2B	0.5603	0.000535
243904_at		0.5606	0.000579
205078_at	PIGF	0.5611	9.63E-05
203282_at	GBE1	0.5613	9.10E-06
218477_at	TMEM14A	0.5615	0.000738
222427_s_at	LARS	0.5620	0.000511
203360_s_at	MYCBP	0.5628	7.69E-05
204283_at	FARS2	0.5633	0.000036
229983_at	TIGD2	0.5635	0.000169
223100_s_at	NUDT5	0.5637	2.34E-05
233642_s_at	HEATR5B	0.5638	6.00E-07

Probe set	Gene Symbol	Fold-change: Low/High	P-value
227556_at		0.5645	0.000875
217869_at	HSD17B12	0.5652	1.06E-05
226537_at	HINT3	0.5660	7.43E-05
200974_at	ACTA2	0.5666	0.000319
212415_at	SEPT6	0.5666	0.00011
227221_at		0.5674	0.000135
204513_s_at	ELMO1	0.5677	7.00E-07
209421_at	MSH2	0.5677	8.51E-05
205260_s_at	ACYP1	0.5679	0.000667
203711_s_at	HIBCH	0.5682	8.02E-05
235339_at	SETDB2	0.5684	1.93E-05
224848_at	CDK6	0.5684	0.000146
209175_at	SEC23IP	0.5688	1.69E-05
201614_s_at	RUVBL1	0.5693	0.000375
213129_s_at		0.5698	0.000338
212653_s_at	EHBP1	0.5703	0.000156
208097_s_at	TMX1	0.5705	8.50E-06
224410_s_at	LMBR1	0.5708	3.20E-06
223087_at	ECHDC1	0.5708	0.000732
224730_at	DCAF7	0.5710	2.84E-05
201847_at	LIPA	0.5712	0.000252
224959_at	SLC26A2	0.5713	0.000748
229491_at	NHEDC2	0.5721	0.000128
201487_at	CTSC	0.5722	0.000288
201503_at	G3BP1	0.5727	5.81E-05
219644_at	CCDC41	0.5730	0.000154
202472_at	MPI	0.5734	0.000144
219100_at	OBFC1	0.5736	9.46E-05
1558770_a_at	PIK3R6	0.5740	0.000423
231838_at	PABPC1L	0.5750	0.000884
222209_s_at	TMEM135	0.5752	2.68E-05
226760_at	MBTPS2	0.5752	0.000029
231955_s_at	HIBADH	0.5753	1.16E-05
205612_at	MMRN1	0.5757	0.000416
226291_at	ALS2	0.5758	0.00031
210338_s_at	HSPA8	0.5762	1.20E-06
213331_s_at	NEK1	0.5766	0.000051
227094_at	DHTKD1	0.5767	0.00023
209509_s_at	DPAGT1	0.5768	9.34E-05
225114_at	AGPS	0.5769	3.61E-05
225040_s_at	RPE	0.5772	0.000398
220741_s_at	PPA2	0.5774	0.000165
224722_at	MIB1	0.5776	0.000109
206295_at	IL18	0.5776	7.23E-05
233924_s_at	EXOC6	0.5777	8.00E-07
236769_at	LOC158402	0.5778	7.07E-05
226532_at		0.5788	6.22E-05
204045_at	TCEAL1	0.5790	3.90E-06

Probe set	Gene Symbol	Fold-change: Low/High	P-value
222416_at	ALDH18A1	0.5795	0.000562
221589_s_at	ALDH6A1	0.5796	0.000578
220668_s_at	DNMT3B	0.5801	0.000203
204341_at	TRIM16	0.5802	0.000227
1555526_a_at	SEPT6	0.5803	4.57E-05
208875_s_at	PAK2	0.5805	3.45E-05
228167_at	KLHL6	0.5805	0.0003
202749_at	WRB	0.5806	3.32E-05
210317_s_at	YWHAE	0.5809	9.92E-05
216202_s_at	SPTLC2	0.5810	0.000796
203551_s_at	COX11	0.5823	0.000326
206544_x_at	SMARCA2	0.5823	1.28E-05
227722_at	RPS23	0.5829	0.000298
202371_at	TCEAL4	0.5835	0.000305
210347_s_at	BCL11A	0.5841	0.00012
222632_s_at	LZTFL1	0.5846	2.90E-06
226432_at	ETNK1	0.5857	3.42E-05
201892_s_at	IMPDH2	0.5861	0.00018
232101_s_at	PIGN	0.5863	0.000123
1557910_at	HSP90AB1	0.5869	4.79E-05
1554480_a_at	ARMC10	0.5872	0.000754
218147_s_at	GLT8D1	0.5875	0.000253
219083_at	SHQ1	0.5876	2.49E-05
218842_at	RPAP3	0.5878	2.42E-05
223330_s_at	SUGT1	0.5885	1.00E-07
227785_at	SDCCAG8	0.5888	0.000308
210519_s_at	NQO1	0.5898	4.15E-05
243000_at	CDK6	0.5899	0.000451
209143_s_at	CLNS1A	0.5900	0.000179
208393_s_at	RAD50	0.5901	5.81E-05
219055_at	SRBD1	0.5903	3.38E-05
219628_at	ZMAT3	0.5918	0.000983
217294_s_at	ENO1	0.5928	0.000415
226482_s_at		0.5931	0.000352
218983_at	C1RL	0.5935	0.000293
1554667_s_at	METTL8	0.5937	8.60E-06
219834_at	ALS2CR8	0.5938	5.40E-06
213189_at		0.5939	0.000205
203817_at	GUCY1B3	0.5939	0.000943
203367_at	DUSP14	0.5943	0.000055
227158_at	C14orf126	0.5946	4.42E-05
212110_at	SLC39A14	0.5951	0.000795
202438_x_at	IDS	0.5951	0.000047
214697_s_at	ROD1	0.5952	1.15E-05
215143_at	DPY19L2P2	0.5965	0.000341
228249_at	C11orf74	0.5969	2.61E-05
209444_at	RAP1GDS1	0.5973	7.04E-05
201564_s_at	FSCN1	0.5976	0.00066

Probe set	Gene Symbol	Fold-change: Low/High	P-value
203359_s_at	MYCBP	0.5984	2.72E-05
222388_s_at	VPS35	0.5984	0.000101
209349_at	RAD50	0.5986	0.000428
218792_s_at	BSPRY	0.5994	3.10E-06
233543_s_at	FAM175A	0.5997	0.000135
227157_at	CCDC111	0.5998	0.000495
211569_s_at	HADH	0.6000	0.00041
204333_s_at	AGA	0.6003	0.000527
217791_s_at	ALDH18A1	0.6005	0.000148
209123_at	QDPR	0.6005	0.000443
220985_s_at	RNF170	0.6008	2.65E-05
223328_at	ARMC10	0.6010	1.26E-05
235780_at	PRKACB	0.6011	0.000575
238488_at	LRRC70	0.6016	0.000287
200604_s_at	PRKAR1A	0.6016	9.09E-05
213391_at	DPY19L4	0.6020	0.000347
212121_at	TCTN3	0.6023	2.90E-06
222559_s_at	RPRD1A	0.6024	0.000831
242157_at	CHD9	0.6025	0.000169
219008_at	C2orf43	0.6027	0.000954
225366_at	PGM2	0.6028	1.94E-05
203069_at	SV2A	0.6028	0.000281
209806_at	HIST1H2BK	0.6039	0.000548
200841_s_at	EPRS	0.6039	2.00E-07
219924_s_at	ZMYM6	0.6040	0.000506
219204_s_at	SRR	0.6045	6.80E-06
1555830_s_at	ESYT2	0.6052	8.11E-05
223403_s_at	POLR1B	0.6053	1.20E-06
228006_at		0.6055	0.000623
218123_at	C21orf59	0.6059	0.000119
208817_at	COMT	0.6062	0.000516
218170_at	ISOC1	0.6064	0.000494
225769_at	COG6	0.6065	0.000146
225367_at	PGM2	0.6068	3.34E-05
218504_at	FAHD2A	0.6070	0.000223
218643_s_at	CRIPT	0.6071	1.17E-05
221104_s_at	NIPSNAP3B	0.6074	6.83E-05
208687_x_at	HSPA8	0.6077	5.01E-05
223306_at	EBPL	0.6079	0.000147
224392_s_at	OPN3	0.6082	0.000905
228045_at		0.6088	7.62E-05
225225_at	LOC729082	0.6099	9.48E-05
201746_at	TP53	0.6102	0.000518
206506_s_at	SUPT3H	0.6102	1.70E-06
219757_s_at	C14orf101	0.6104	0.000255
201448_at	TIA1	0.6107	0.000817
212946_at	KIAA0564	0.6110	0.000094
204226_at	STAU2	0.6112	0.000555

Probe set	Gene Symbol	Fold-change: Low/High	P-value
210667_s_at	C21orf33	0.6112	0.000525
206542_s_at	SMARCA2	0.6113	0.000122
220954_s_at	PILRB	0.6116	2.04E-05
218561_s_at	LYRM4	0.6121	9.02E-05
36830_at	MIPEP	0.6125	4.31E-05
237291_at	NCRNA00117	0.6128	0.000029
1559052_s_at	PAK2	0.6129	0.000027
220606_s_at	C17orf48	0.6130	1.75E-05
213461_at	NUDT21	0.6130	8.40E-06
222893_s_at	RPAP2	0.6131	5.40E-06
1554660_a_at	C1orf71	0.6133	1.28E-05
221745_at	DCAF7	0.6136	0.000174
218503_at	KIAA1797	0.6138	0.000424
224204_x_at	ARNTL2	0.6144	0.000107
201054_at	HNRNPA0	0.6145	0.000201
227808_at	DNAJC15	0.6147	0.000131
217900_at	IARS2	0.6147	1.78E-05
224523_s_at	C3orf26	0.6152	0.00044
210786_s_at	FLI1	0.6152	0.000225
231808_at	LOC729082	0.6152	9.30E-06
232423_at	ARSD	0.6153	0.000884
220172_at	DCAF17	0.6156	3.20E-06
218713_at	NARG2	0.6156	6.54E-05
219017_at	ETNK1	0.6157	0.000814
201675_at	AKAP1	0.6158	0.000438
228781_at	OBFC1	0.6159	2.40E-06
223892_s_at	TMBIM4	0.6159	0.000809
208818_s_at	COMT	0.6160	0.000999
222845_x_at	TMBIM4	0.6161	0.000785
212257_s_at	SMARCA2	0.6163	1.24E-05
224187_x_at	HSPA8	0.6164	3.91E-05
244050_at	PTPLAD2	0.6166	0.000598
221934_s_at	DALRD3	0.6167	1.10E-06
209623_at	MCCC2	0.6168	5.46E-05
223114_at	COQ5	0.6169	0.000145
209539_at	ARHGEF6	0.6170	0.000148
214298_x_at	SEPT6	0.6170	8.35E-05
1557302_at		0.6176	1.06E-05
218069_at	DCTPP1	0.6180	0.000195
218163_at	MCTS1	0.6182	0.000212
228062_at	NAP1L5	0.6189	0.000346
209849_s_at	RAD51C	0.6189	0.000741
202713_s_at	KIAA0391	0.6193	9.00E-07
221618_s_at	TAF9B	0.6193	0.000239
221864_at	ORAI3	0.6193	0.000128
211761_s_at	CACYBP	0.6198	2.01E-05
218322_s_at	ACSL5	0.6208	0.000875
203581_at	RAB4A	0.6210	2.56E-05

Probe set	Gene Symbol	Fold-change: Low/High	P-value
224916_at	TMEM173	0.6211	0.000021
217990_at	GMPR2	0.6213	0.000154
204091_at	PDE6D	0.6217	0.000348
224060_s_at	DPH5	0.6222	0.000178
212211_at	ANKRD17	0.6222	5.76E-05
200046_at	DAD1	0.6223	0.00025
228719_at	ZSWIM7	0.6224	0.00024
210541_s_at	TRIM27	0.6227	4.75E-05
228077_at	MRI1	0.6227	1.07E-05
208758_at	ATIC	0.6229	0.000337
232790_at		0.6229	1.52E-05
223272_s_at	C1orf57	0.6232	0.000668
212145_at	MRPS27	0.6233	3.80E-06
206976_s_at	HSPH1	0.6234	0.00094
223245_at	STRBP	0.6238	0.000505
224185_at		0.6238	0.000066
201036_s_at	HADH	0.6240	0.000889
218870_at	ARHGAP15	0.6240	8.57E-05
224748_at	DCAF7	0.6244	0.000042
1566472_s_at	RETSAT	0.6249	8.90E-06
1552310_at	C15orf40	0.6249	1.94E-05
227534_at	C9orf21	0.6252	0.000284
204807_at	TMEM5	0.6253	7.01E-05
221564_at	PRMT2	0.6254	0.000205
209916_at	DHTKD1	0.6258	0.000167
226455_at	CREB3L4	0.6260	0.000157
222369_at	NAT11	0.6261	9.76E-05
234111_at		0.6263	0.000744
211727_s_at	COX11	0.6264	0.000247
209624_s_at	MCCC2	0.6266	4.00E-07
205297_s_at	CD79B	0.6266	0.000426
222532_at	SRPRB	0.6269	0.000115
228620_at		0.6270	0.000238
221689_s_at	PIGP	0.6274	8.51E-05
226531_at	ORAI1	0.6275	0.000308
1555193_a_at	ZNF277	0.6277	0.000133
234975_at	GSPT1	0.6284	0.000236
226479_at	KBTBD6	0.6285	0.000102
217627_at	ZNF573	0.6285	0.000656
208608_s_at	SNTB1	0.6287	0.0006
222785_x_at	C11orf1	0.6287	0.000143
226361_at		0.6287	0.000763
202429_s_at	PPP3CA	0.6288	0.000227
204808_s_at	TMEM5	0.6288	8.23E-05
212568_s_at	DLAT	0.6290	4.10E-06
224881_at	VKORC1L1	0.6293	1.24E-05
224173_s_at	MRPL30	0.6293	1.22E-05
209150_s_at	TM9SF1	0.6295	0.000107

Probe set	Gene Symbol	Fold-change: Low/High	P-value
204305_at	MIPEP	0.6295	7.80E-06
225520_at	MTHFD1L	0.6297	0.000649
217809_at	BZW2	0.6299	0.000283
230370_x_at	STYXL1	0.6299	0.000548
214995_s_at		0.6304	2.48E-05
202444_s_at	ERLIN1	0.6306	0.000622
223057_s_at	XPO5	0.6306	1.30E-06
205133_s_at	HSPE1	0.6307	4.26E-05
218338_at	PHC1	0.6307	0.000388
218209_s_at	RPRD1A	0.6310	0.000289
208910_s_at	C1QBP	0.6311	3.82E-05
242794_at	MAML3	0.6311	0.00036
211563_s_at	C19orf2	0.6314	6.46E-05
213685_at		0.6315	9.00E-06
228113_at	RAB37	0.6315	0.00083
209512_at	HSDL2	0.6317	1.11E-05
219002_at	FASTKD1	0.6317	0.00025
212731_at	ANKRD46	0.6320	0.000842
1552978_a_at	SCAMP1	0.6320	9.00E-07
202529_at	PRPSAP1	0.6321	9.70E-06
201037_at	PFKP	0.6322	0.000642
227925_at	FLJ39051	0.6323	0.000236
219217_at	NARS2	0.6327	7.90E-06
213737_x_at	GOLGA9P	0.6328	0.000256
231576_at		0.6333	0.000295
200806_s_at	HSPD1	0.6333	0.00054
220500_s_at		0.6335	0.000138
218321_x_at	STYXL1	0.6336	0.000238
223335_at	TMEM69	0.6339	2.28E-05
202013_s_at	EXT2	0.6339	4.42E-05
233982_x_at	STYXL1	0.6341	0.000389
216392_s_at	SEC23IP	0.6344	2.00E-06
223212_at	ZDHHC16	0.6345	0.000482
209476_at	TMX1	0.6346	0.000144
217786_at	PRMT5	0.6347	0.000292
226688_at	C3orf23	0.6349	0.000472
225501_at	PHF6	0.6352	8.89E-05
226458_at		0.6352	0.000706
224623_at		0.6353	0.00003
1554661_s_at	C1orf71	0.6353	7.70E-06
219641_at	DET1	0.6353	0.000253
201825_s_at	SCCPDH	0.6354	9.93E-05
208848_at	ADH5	0.6355	0.000024
206833_s_at	ACYP2	0.6355	5.33E-05
209397_at	ME2	0.6355	0.000271
208644_at	PARP1	0.6357	6.47E-05
227451_s_at	CCDC90A	0.6359	1.02E-05
235840_at		0.6360	4.14E-05

Probe set	Gene Symbol	Fold-change: Low/High	P-value
235088_at	C4orf46	0.6360	0.00041
205395_s_at	MRE11A	0.6361	0.000131
225039_at	RPE	0.6361	6.75E-05
213761_at	MDM1	0.6361	0.000535
224879_at	C9orf123	0.6364	0.000453
203049_s_at	TTC37	0.6365	0.000115
228937_at	C13orf31	0.6366	0.000318
222744_s_at	TMLHE	0.6367	0.000468
205129_at	NPM3	0.6367	7.55E-05
204565_at	ACOT13	0.6380	0.000262
211704_s_at		0.6384	4.27E-05
219307_at	PDSS2	0.6384	0.000785
210482_x_at	MAP2K5	0.6384	2.37E-05
218471_s_at	BBS1	0.6389	1.60E-06
204683_at	ICAM2	0.6392	0.000489
215380_s_at	GGCT	0.6393	5.01E-05
223586_at	ARNTL2	0.6393	2.48E-05
217957_at	C16orf80	0.6394	0.00022
226116_at		0.6399	3.86E-05
204040_at	RNF144A	0.6403	0.000693
201619_at	PRDX3	0.6410	0.000203
217457_s_at	RAP1GDS1	0.6411	1.17E-05
212893_at	ZZZ3	0.6413	3.50E-06
217788_s_at	GALNT2	0.6415	0.000106
229189_s_at		0.6417	0.000115
230598_at		0.6420	0.000168
227796_at	ZFP62	0.6420	6.19E-05
203829_at	ELP4	0.6421	0.000647
217707_x_at	SMARCA2	0.6423	0.000285
212510_at	GPD1L	0.6423	0.000305
229810_at		0.6423	0.000152
228714_at		0.6425	0.000703
210567_s_at	SKP2	0.6430	0.000703
226521_s_at	FAM175A	0.6430	0.00009
201872_s_at	ABCE1	0.6431	4.99E-05
203972_s_at	PEX3	0.6432	0.000046
234304_s_at	IPO11	0.6434	1.10E-06
213188_s_at	MINA	0.6436	0.000815
222418_s_at	TMEM43	0.6437	1.30E-06
226779_at		0.6438	0.000288
235036_at	LIX1L	0.6439	6.95E-05
223273_at	C14orf142	0.6441	6.55E-05
224819_at	TCEAL8	0.6441	0.000132
219575_s_at		0.6444	1.80E-06
202930_s_at	SUCLA2	0.6445	0.000286
223764_x_at	NIPSNAP3B	0.6447	0.000871
201831_s_at	USO1	0.6448	3.16E-05
216591_s_at		0.6450	2.78E-05

Probe set	Gene Symbol	Fold-change: Low/High	P-value
208653_s_at	CD164	0.6450	4.23E-05
204960_at	PTPRCAP	0.6451	0.000904
207618_s_at	BCS1L	0.6454	0.00019
225029_at	LOC550643	0.6455	5.60E-06
222731_at	ZDHHC2	0.6457	0.000707
205401_at	AGPS	0.6459	1.13E-05
225321_s_at	PILRB	0.6465	0.000173
210978_s_at	TAGLN2	0.6466	5.73E-05
204354_at	POT1	0.6470	7.91E-05
221213_s_at	ZNF280D	0.6470	0.000203
203465_at	MRPL19	0.6472	0.000131
238590_x_at	TMEM107	0.6472	0.000744
202579_x_at	HMGN4	0.6473	0.000074
226259_at	EXOC6	0.6474	0.000454
206445_s_at	PRMT1	0.6475	0.000718
225675_at	C14orf101	0.6475	0.000785
211370_s_at	MAP2K5	0.6480	9.50E-06
206958_s_at	UPF3A	0.6482	2.87E-05
209338_at	TFCP2	0.6484	0.000198
205283_at	FKTN	0.6487	0.000291
210114_at	INVS	0.6488	3.82E-05
200848_at	AHCYL1	0.6490	5.40E-06
209786_at	HMGN4	0.6490	0.000202
219342_at	CASD1	0.6491	0.000342
230152_at	WDR52	0.6493	0.000451
223281_s_at	COX15	0.6493	9.19E-05
207223_s_at	ROD1	0.6500	0.0002
209434_s_at	PPAT	0.6501	0.000017
235134_at		0.6502	0.000648
203621_at	NDUFB5	0.6503	9.65E-05
1569503_at	HEATR5B	0.6503	0.00057
205652_s_at	TTLL1	0.6506	0.000613
214966_at	GRIK5	0.6509	6.33E-05
202889_x_at	MAP7	0.6510	0.000411
201514_s_at	G3BP1	0.6512	3.50E-06
222579_at	UBA5	0.6514	5.87E-05
202562_s_at	C14orf1	0.6518	1.99E-05
218930_s_at	TMEM106B	0.6520	0.000983
200890_s_at	SSR1	0.6520	0.000335
231319_x_at	KIF9	0.6521	0.000706
218568_at	AGK	0.6525	4.90E-06
209958_s_at	BBS9	0.6528	0.00022
214359_s_at	HSP90AB1	0.6530	0.000118
201259_s_at	SYPL1	0.6534	7.00E-06
226816_s_at	KIAA1143	0.6534	0.000393
222387_s_at	VPS35	0.6535	4.75E-05
218973_at	EFTUD1	0.6536	9.10E-06
223493_at	FBXO4	0.6538	0.000163

Probe set	Gene Symbol	Fold-change: Low/High	P-value
226912_at	ZDHHC23	0.6540	0.000699
228730_s_at	SCRN2	0.6541	8.94E-05
200605_s_at	PRKAR1A	0.6542	0.000264
221532_s_at	WDR61	0.6543	2.15E-05
235260_s_at	PACRGL	0.6543	1.49E-05
200760_s_at	ARL6IP5	0.6545	0.00041
217949_s_at	VKORC1	0.6546	0.000784
224576_at	ERGIC1	0.6547	0.000168
201708_s_at	NIPSNAP1	0.6548	6.21E-05
229058_at	ANKRD16	0.6548	8.05E-05
223361_at	C6orf115	0.6550	0.000231
213012_at	NEDD4	0.6551	0.000532
231819_at		0.6553	0.000112
203517_at	MTX2	0.6553	0.000298
201135_at	ECHS1	0.6553	0.000856
225804_at	CYB5D2	0.6555	5.10E-06
208478_s_at	BAX	0.6555	0.000349
229126_at	TMEM19	0.6556	0.000363
235273_at	DYX1C1	0.6559	0.00057
225793_at	LIX1L	0.6562	4.82E-05
225050_at	ZNF512	0.6564	0.000671
231530_s_at	C11orf1	0.6565	7.06E-05
218957_s_at	PAAF1	0.6565	0.000316
224699_s_at	ESYT2	0.6566	4.80E-06
228063_s_at	NAP1L5	0.6567	0.000658
222713_s_at	FANCF	0.6568	0.00049
201339_s_at	SCP2	0.6570	4.47E-05
224436_s_at	NIPSNAP3A	0.6575	0.000541
221744_at	DCAF7	0.6576	0.000169
211733_x_at	SCP2	0.6576	0.000453
212217_at	PREPL	0.6579	0.000577
223888_s_at	LARS	0.6579	0.000254
218970_s_at	CUTC	0.6579	2.28E-05
226781_at		0.6584	0.000115
200973_s_at	TSPAN3	0.6586	0.00013
202645_s_at	MEN1	0.6589	6.58E-05
37793_r_at	RAD51L3	0.6590	3.34E-05
224798_s_at	C15orf17	0.6590	7.26E-05
218351_at	COMMD8	0.6591	0.000222
219819_s_at	MRPS28	0.6594	6.89E-05
204119_s_at	ADK	0.6596	0.000196
219166_at	C14orf104	0.6602	0.000212
233999_s_at	TTC26	0.6602	8.00E-07
238440_at	CLYBL	0.6604	0.000867
241946_at	ZDHHC21	0.6605	3.67E-05
202069_s_at	IDH3A	0.6609	0.000457
225959_s_at	ZNRF1	0.6610	0.0009
209796_s_at	CNPY2	0.6613	0.000796

Probe set	Gene Symbol	Fold-change: Low/High	P-value
204178_s_at	RBM14	0.6613	0.000166
201836_s_at	SUPT7L	0.6614	0.000173
222640_at	DNMT3A	0.6615	0.000978
225335_at	ZNF496	0.6615	0.00016
210125_s_at	BANF1	0.6616	0.000896
213133_s_at	GCSH	0.6616	0.000271
221531_at	WDR61	0.6617	7.23E-05
1552733_at	KLHDC1	0.6620	0.000314
218545_at	CCDC91	0.6622	0.000445
204559_s_at	LSM7	0.6623	0.000807
223154_at	MRPL1	0.6627	0.000426
206831_s_at	ARSD	0.6628	0.000862
207761_s_at	METTL7A	0.6630	0.000536
218575_at	ANAPC1	0.6631	2.74E-05
223386_at	FAM118B	0.6633	0.00079
218512_at	WDR12	0.6634	0.000544
230434_at		0.6635	0.000671
209363_s_at	MED21	0.6637	8.20E-06
218146_at	GLT8D1	0.6643	5.83E-05
227134_at	SYTL1	0.6646	0.000962
1554029_a_at	TTC37	0.6648	0.00021
221622_s_at	TMEM126B	0.6649	2.41E-05
201938_at	CDK2AP1	0.6649	7.98E-05
228075_x_at	TFB1M	0.6652	4.29E-05
229850_at	KDSR	0.6653	0.000173
221891_x_at	HSPA8	0.6655	9.88E-05
243452_at	LOC646778	0.6659	0.000885
226628_at	THOC2	0.6660	0.000367
205512_s_at	AIFM1	0.6661	3.89E-05
224664_at	C10orf104	0.6661	0.000963
212216_at	PREPL	0.6663	0.000135
208722_s_at	ANAPC5	0.6663	0.000558
218307_at	RSAD1	0.6664	0.000985
206301_at	TEC	0.6671	0.000334
226995_at	LOC642852	0.6673	0.000751
201030_x_at	LDHB	0.6676	0.000254
224129_s_at	DPY30	0.6678	5.91E-05
205480_s_at	UGP2	0.6680	0.000266
201624_at	DARS	0.6680	0.00031
200845_s_at	PRDX6	0.6680	8.49E-05
228189_at	BAG4	0.6680	0.000149
219169_s_at	TFB1M	0.6690	0.000103
219258_at	TIPIN	0.6691	0.000655
215471_s_at	MAP7	0.6691	0.000279
209233_at	EMG1	0.6697	0.000273
220329_s_at	RMND1	0.6697	0.000109
203177_x_at	TFAM	0.6698	0.000131
226833_at	CYB5D1	0.6699	1.89E-05

Probe set	Gene Symbol	Fold-change: Low/High	P-value
208832_at	ATXN10	0.6700	0.00065
212221_x_at	IDS	0.6700	0.000619
217188_s_at	C14orf1	0.6700	2.32E-05
211684_s_at	DYNC1I2	0.6705	0.000104
210153_s_at	ME2	0.6708	0.000464
202641_at	ARL3	0.6709	3.15E-05
200008_s_at	GDI2	0.6710	1.46E-05
200889_s_at	SSR1	0.6718	0.000939
210802_s_at	DIMT1L	0.6718	2.84E-05
220477_s_at	C20orf30	0.6720	0.000418
218440_at	MCCC1	0.6726	0.000154
202213_s_at	CUL4B	0.6727	9.00E-07
1564238_a_at	WDR49	0.6728	0.000735
203686_at	MPG	0.6728	2.88E-05
219581_at	TSEN2	0.6729	0.000178
218375_at	NUDT9	0.6730	5.36E-05
221090_s_at	OGFOD1	0.6732	2.05E-05
204350_s_at	MED7	0.6735	0.000171
222805_at	MANEA	0.6738	0.000226
219130_at	CCDC76	0.6740	0.000328
229090_at	LOC220930	0.6740	0.00085
212815_at	ASCC3	0.6741	0.000141
202811_at	STAMBP	0.6742	0.000569
211812_s_at	B3GALNT1	0.6743	0.000967
225881_at	SLC35B4	0.6744	0.000663
222056_s_at	FAHD2A	0.6745	0.000695
65585_at	FAM86B1	0.6746	0.000282
228091_at	STX17	0.6749	0.000995
217777_s_at	PTPLAD1	0.6750	0.000718
221514_at	UTP14A	0.6751	0.000366
1553218_a_at	ZNF512	0.6754	0.000206
200708_at	GOT2	0.6754	3.82E-05
1557984_s_at	RPAP3	0.6755	1.62E-05
218005_at	ZNF22	0.6756	0.000437
204386_s_at	MRP63	0.6756	0.000137
200978_at	MDH1	0.6758	4.45E-05
226634_at	METTL10	0.6758	0.000367
1554883_a_at	ERCC8	0.6760	1.30E-06
1563111_a_at	PIGX	0.6762	6.19E-05
230032_at	OSGEPL1	0.6765	0.000309
212299_at	NEK9	0.6766	0.000546
223286_at	C17orf81	0.6768	0.000319
214214_s_at	C1QBP	0.6769	0.000195
218992_at	C9orf46	0.6771	0.00015
223677_at	ATG10	0.6772	0.000667
221449_s_at	ITFG1	0.6772	4.60E-06
218461_at	GPN3	0.6772	1.76E-05
1558511_s_at	ESYT2	0.6777	8.33E-05

Probe set	Gene Symbol	Fold-change: Low/High	P-value
221770_at	RPE	0.6780	0.000127
224815_at	COMMD7	0.6783	3.96E-05
202691_at	SNRPD1	0.6783	0.000644
224665_at	C10orf104	0.6785	0.000229
222683_at	RNF20	0.6785	0.000153
225577_at		0.6785	0.000418
204173_at	MYL6B	0.6786	0.00083
210849_s_at	VPS41	0.6787	0.00038
223221_at	SCO1	0.6788	1.80E-06
225106_s_at	OGFOD1	0.6790	4.58E-05
212640_at	PTPLB	0.6790	0.000274
207088_s_at	SLC25A11	0.6795	0.000943
1554774_at	MINA	0.6799	0.000124
222654_at	IMPAD1	0.6799	0.000919
203048_s_at	TTC37	0.6802	9.50E-06
219972_s_at	C14orf135	0.6802	0.000285
209463_s_at	TAF12	0.6802	0.000122
202319_at	SENP6	0.6803	0.000579
218734_at	NAT11	0.6805	2.07E-05
222140_s_at		0.6809	0.000133
212416_at	SCAMP1	0.6809	5.34E-05
203007_x_at	LYPLA1	0.6810	0.00021
218156_s_at	TSR1	0.6812	1.20E-06
202214_s_at	CUL4B	0.6812	4.64E-05
225101_s_at	SNX14	0.6812	0.000941
242423_x_at		0.6812	0.000976
225537_at	TRAPPC6B	0.6813	0.000217
34764_at	LARS2	0.6814	0.000175
235532_at	PIGM	0.6815	0.000501
238039_at	LOC728769	0.6818	0.000118
208721_s_at	ANAPC5	0.6819	4.44E-05
236834_at	SCFD2	0.6820	0.000503
218879_s_at	MTHFSD	0.6822	0.000117
214173_x_at	C19orf2	0.6823	0.000134
203415_at	PDCD6	0.6824	0.000087
225359_at	DNAJC19	0.6827	4.40E-06
223738_s_at	PGM2	0.6827	2.34E-05
217919_s_at	MRPL42	0.6828	4.84E-05
213564_x_at	LDHB	0.6833	0.000124
223711_s_at	THYN1	0.6834	0.000282
217968_at	TSSC1	0.6835	0.00094
219366_at	AVEN	0.6835	0.000518
226721_at	DPY19L4	0.6838	0.000152
227741_at	PTPLB	0.6839	3.69E-05
203077_s_at	SMAD2	0.6839	0.000157
208852_s_at	CANX	0.6840	0.000693
213463_s_at	FAM149B1	0.6840	3.08E-05
201613_s_at	AP1G2	0.6845	0.000644

Probe set	Gene Symbol	Fold-change: Low/High	P-value
224655_at	AK3	0.6847	3.35E-05
210255_at	RAD51L1	0.6848	1.77E-05
218395_at	ACTR6	0.6849	0.000655
221759_at	G6PC3	0.6849	0.000311
200992_at	IPO7	0.6850	0.00014
226529_at	TMEM106B	0.6850	0.000978
208860_s_at	ATRX	0.6852	0.000742
218549_s_at	FAM82B	0.6854	0.000509
207358_x_at	MACF1	0.6855	0.000211
238631_at	ZNF140	0.6858	0.000143
201512_s_at	TOMM70A	0.6859	0.000017
235189_at	NARG2	0.6860	3.67E-05
209497_s_at	RBM4B	0.6860	8.26E-05
222451_s_at	ZDHHC9	0.6860	0.000136
203405_at	PSMG1	0.6862	9.27E-05
209449_at	LSM2	0.6862	0.000181
223231_at	TATDN1	0.6863	0.000217
203714_s_at	TBCE	0.6867	1.73E-05
203226_s_at	TSPAN31	0.6868	9.30E-06
202783_at	NNT	0.6868	0.000118
211337_s_at	TUBGCP4	0.6870	2.96E-05
227674_at	ZNF585A	0.6875	4.70E-06
238565_at		0.6876	0.000166
239240_at		0.6876	9.32E-05
212352_s_at	TMED10	0.6876	0.000196
218654_s_at	MRPS33	0.6878	0.000066
225297_at	HAUS1	0.6882	0.000101
220642_x_at		0.6882	1.40E-06
203245_s_at	NCRNA00094	0.6882	0.000182
217301_x_at	RBBP4	0.6883	9.55E-05
213540_at	HSD17B8	0.6885	0.000127
202784_s_at	NNT	0.6889	0.000385
224151_s_at	AK3	0.6889	0.000457
222590_s_at	NLK	0.6889	0.000282
235387_at	GSTCD	0.6892	8.99E-05
225419_at	C7orf11	0.6892	6.17E-05
210621_s_at	RASA1	0.6893	0.000381
203633_at	CPT1A	0.6893	0.000046
212259_s_at	PBXIP1	0.6894	0.000217
221575_at	SCLY	0.6895	0.000561
221620_s_at	APOO	0.6896	0.0003
231921_at	DCAF17	0.6897	9.09E-05
225400_at	TSEN15	0.6897	2.17E-05
224834_at	UBTD2	0.6898	0.00047
224929_at	TMEM173	0.6902	0.000238
44654_at	G6PC3	0.6902	0.000552
235443_at	LOC100131067	0.6903	0.000808
212605_s_at		0.6906	0.000419

Probe set	Gene Symbol	Fold-change: Low/High	P-value
219023_at	C4orf16	0.6906	5.95E-05
228239_at	FAM165B	0.6907	0.000406
217942_at	MRPS35	0.6910	0.000177
211150_s_at	DLAT	0.6912	0.000017
225734_at	FBXO22	0.6914	8.28E-05
221513_s_at		0.6916	0.000119
208654_s_at	CD164	0.6919	6.24E-05
218628_at	CCDC53	0.6920	0.00099
203630_s_at	COG5	0.6922	0.000263
217725_x_at	SERBP1	0.6923	0.000348
213047_x_at	SET	0.6925	3.27E-05
1555846_a_at		0.6927	0.000706
211626_x_at	ERG	0.6927	8.95E-05
231896_s_at	DENR	0.6928	3.29E-05
200972_at	TSPAN3	0.6932	0.000564
218584_at	TCTN1	0.6936	0.000123
202457_s_at	PPP3CA	0.6936	0.00024
209362_at	MED21	0.6937	0.000438
237158_s_at	MPHOSPH9	0.6939	2.81E-05
213625_at	ZKSCAN4	0.6939	0.000838
226780_s_at		0.6940	0.000605
225670_at	FAM173B	0.6940	0.00097
211075_s_at	CD47	0.6941	0.000465
217795_s_at	TMEM43	0.6941	9.70E-06
213312_at	C6orf162	0.6943	0.000334
212957_s_at	LOC92249	0.6947	8.41E-05
225399_at	TSEN15	0.6947	1.06E-05
238615_at	ERLIN2	0.6949	0.000239
220007_at	METTL8	0.6949	1.49E-05
204925_at	CTNS	0.6949	0.00023
238662_at	ATPBD4	0.6951	0.000211
238418_at	SLC35B4	0.6952	0.000866
228671_at	TMEM201	0.6956	3.25E-05
208633_s_at	MACF1	0.6956	0.000245
223506_at	ZC3H8	0.6957	0.000078
225325_at	MFSD6	0.6959	0.000342
208669_s_at	EID1	0.6962	2.80E-06
223018_at	NOB1	0.6963	0.000109
201433_s_at	PTDSS1	0.6963	0.00025
225546_at	EEF2K	0.6963	0.000132
225113_at	AGPS	0.6964	0.000273
1561737_at		0.6965	0.000346
214323_s_at	UPF3A	0.6966	0.000349
235005_at	DIS3L	0.6968	4.52E-05
201562_s_at	SORD	0.6971	0.00038
221691_x_at	NPM1	0.6971	0.000187
225002_s_at	SUMF2	0.6973	0.000144
214894_x_at	MACF1	0.6974	0.000196

Probe set	Gene Symbol	Fold-change: Low/High	P-value
225600_at	C8orf83	0.6974	0.000306
205135_s_at	NUFIP1	0.6974	0.000624
228763_at	MDP1	0.6976	0.000967
210027_s_at	APEX1	0.6976	0.000595
226151_x_at	CRYZL1	0.6976	0.000368
221781_s_at	DNAJC10	0.6977	0.00027
1556285_s_at	PPA2	0.6978	0.000561
222849_s_at	SCRN3	0.6978	0.000906
223001_at	OSTC	0.6979	0.000121
205704_s_at	ATP6V0A2	0.6980	0.000339
212223_at	IDS	0.6981	0.000408
203075_at	SMAD2	0.6982	0.000988
224740_at	C5orf43	0.6983	0.000483
236042_at	LOC100130219	0.6983	4.46E-05
226314_at	CHST14	0.6984	0.000281
202845_s_at	RALBP1	0.6984	5.45E-05
219538_at	WDR5B	0.6984	0.000616
220206_at	ZMYM1	0.6988	0.000652
218757_s_at	UPF3B	0.6993	0.000505
233252_s_at	STRBP	0.6995	0.000465
202854_at	HPRT1	0.6995	4.17E-05
218046_s_at	MRPS16	0.6996	2.45E-05
221082_s_at	NDRG3	0.6996	0.000824
213896_x_at	FAM149B1	0.6996	0.000344
204353_s_at	POT1	0.6996	0.000101
238684_at		0.6997	0.000206
218288_s_at	CCDC90B	0.6998	0.000038
214045_at	LIAS	0.7000	0.000357
202012_s_at	EXT2	0.7001	0.000175
229741_at	MAVS	0.7003	0.000518
226127_at	ALKBH3	0.7004	0.000226
208847_s_at	ADH5	0.7004	3.70E-06
235338_s_at	SETDB2	0.7004	0.000369
215099_s_at	RXRB	0.7005	0.000141
225220_at	SNHG8	0.7005	0.000927
237105_at		0.7007	0.000864
216944_s_at	ITPR1	0.7007	0.00026
200064_at	HSP90AB1	0.7012	0.000149
204085_s_at	CLN5	0.7012	0.000708
218124_at	RETSAT	0.7014	8.36E-05
202754_at	R3HDM1	0.7014	1.08E-05
226583_at	C12orf76	0.7015	0.000288
201260_s_at	SYPL1	0.7015	0.000116
218689_at	FANCF	0.7016	0.000377
215222_x_at	MACF1	0.7017	0.000227
218439_s_at	COMMD10	0.7018	9.37E-05
203293_s_at	LMAN1	0.7018	0.00062
236032_at		0.7018	0.000293

Probe set	Gene Symbol	Fold-change: Low/High	P-value
203577_at	GTF2H4	0.7018	0.000473
202501_at	MAPRE2	0.7019	8.53E-05
201491_at	AHSA1	0.7024	0.000446
203032_s_at	FH	0.7025	7.95E-05
241926_s_at	ERG	0.7030	0.000679
36554_at	ASMTL	0.7031	0.000136
218349_s_at	ZWILCH	0.7033	0.000663
219242_at	CEP63	0.7038	0.000911
217921_at	MAN1A2	0.7039	0.000103
205588_s_at	FGFR1OP	0.7040	0.000561
224584_at	C20orf30	0.7040	0.000264
224946_s_at	CCDC115	0.7040	4.90E-06
229606_at		0.7041	0.000684
203257_s_at	C11orf49	0.7041	0.000222
213042_s_at	ATP2A3	0.7042	0.000599
234726_s_at	TMEM168	0.7043	0.000286
219974_x_at	ECHDC1	0.7043	0.000373
208802_at	SRP72	0.7044	0.000616
219003_s_at	MANEA	0.7045	4.15E-05
203294_s_at	LMAN1	0.7046	0.000774
229243_at		0.7048	0.00063
202049_s_at	ZMYM4	0.7049	0.000814
225412_at	TMEM87B	0.7054	0.000459
238056_at	SDHC	0.7057	1.78E-05
201332_s_at	STAT6	0.7057	0.000965
225014_at	LOC389203	0.7059	0.000619
218377_s_at	RWDD2B	0.7061	0.000147
221688_s_at	IMP3	0.7062	9.36E-05
223671_x_at	DPH5	0.7063	0.000221
219060_at	WDYHV1	0.7064	0.000523
224971_at	MRPL30	0.7067	0.000149
221550_at	COX15	0.7068	0.000641
204957_at	ORC5L	0.7073	0.000865
222609_s_at	EXOSC1	0.7074	4.56E-05
208787_at	MRPL3	0.7076	0.000366
205540_s_at	RRAGB	0.7077	0.000273
211934_x_at	GANAB	0.7082	0.000447
218946_at	NFU1	0.7086	7.39E-05
203960_s_at	HSPB11	0.7086	0.000152
225574_at	RWDD4A	0.7088	0.000198
219080_s_at	CTPS2	0.7089	0.000306
208861_s_at	ATRX	0.7094	0.000473
225358_at	DNAJC19	0.7099	0.000126
225676_s_at	DCAF13	0.7100	0.000213
206668_s_at	SCAMP1	0.7100	2.06E-05
227916_x_at	EXOSC3	0.7103	0.000738
234915_s_at	DENR	0.7103	4.63E-05
229018_at	C12orf26	0.7104	0.000381

Probe set	Gene Symbol	Fold-change: Low/High	P-value
204186_s_at	PPID	0.7105	0.000323
1554078_s_at	DNAJA3	0.7106	0.000842
220260_at	TBC1D19	0.7108	2.36E-05
222697_s_at	ABHD10	0.7110	0.000109
203941_at	INTS9	0.7115	7.50E-06
223847_s_at	ERGIC1	0.7115	0.000228
203340_s_at	SLC25A12	0.7116	9.86E-05
218715_at	UTP6	0.7118	0.000108
225599_s_at	C8orf83	0.7121	0.000507
222511_x_at	FAF1	0.7122	0.000742
211114_x_at	SIP1	0.7122	4.47E-05
212038_s_at	VDAC1	0.7122	0.000589
215535_s_at	AGPAT1	0.7123	0.0008
225712_at	GEMIN5	0.7124	0.000294
218989_x_at	SLC30A5	0.7124	0.00047
231727_s_at	MIF4GD	0.7126	0.000983
1559681_a_at	TRIM16L	0.7127	0.000381
1568678_s_at	FGFR1OP	0.7129	0.000618
216064_s_at	AGA	0.7129	0.00047
203947_at	CSTF3	0.7129	0.000661
229602_at		0.7133	0.00025
219658_at	PTCD2	0.7135	0.000213
222672_at	LYRM4	0.7136	0.000228
229360_at	ZNF280B	0.7138	0.000896
213149_at	DLAT	0.7139	0.000513
223401_at	C17orf48	0.7140	0.000363
226642_s_at	NUDCD2	0.7142	0.000192
201268_at		0.7144	0.000933
219858_s_at	MFSD6	0.7147	0.000753
205162_at		0.7148	6.20E-06
219539_at	GEMIN6	0.7149	0.000716
202261_at	VPS72	0.7149	0.000847
201653_at	CNIH	0.7150	6.35E-05
36566_at	CTNS	0.7151	0.000602
223156_at	MRPS23	0.7153	0.00048
222659_at	IPO11	0.7154	0.000202
243444_at		0.7155	0.000848
203678_at	MTMR15	0.7156	0.000837
1555803_a_at	C11orf57	0.7159	0.000363
210691_s_at	CACYBP	0.7161	0.000792
208858_s_at	ESYT1	0.7162	0.000569
208055_s_at	HERC4	0.7162	0.000236
224200_s_at	RAD18	0.7163	2.26E-05
235647_at	AP4S1	0.7164	0.000149
216960_s_at	ZNF133	0.7165	0.000804
209494_s_at	PATZ1	0.7168	1.43E-05
1554145_a_at	KLRAQ1	0.7168	1.96E-05
203611_at	TERF2	0.7170	0.00011

Probe set	Gene Symbol	Fold-change: Low/High	P-value
214507_s_at	EXOSC2	0.7173	0.000233
218882_s_at	WDR3	0.7173	0.000864
229803_s_at		0.7175	0.000709
223193_x_at	FAM162A	0.7176	0.000573
209751_s_at		0.7185	0.000248
210278_s_at	AP4S1	0.7189	8.23E-05
201873_s_at	ABCE1	0.7190	0.000445
221471_at	SERINC3	0.7191	0.000069
224196_x_at	DPH5	0.7191	0.000646
209426_s_at		0.7192	8.60E-06
242618_at		0.7193	1.12E-05
227650_at	HSPA14	0.7193	0.000369
231840_x_at	LYRM7	0.7193	0.000461
218363_at	EXD2	0.7194	0.000645
239715_at		0.7194	0.000534
229525_at	THOC7	0.7195	6.79E-05
238794_at	C10orf78	0.7196	0.00016
210892_s_at	GTF2I	0.7198	0.000381
1552562_at	ZNF570	0.7198	0.000184
219933_at	GLRX2	0.7201	3.54E-05
207838_x_at	PBXIP1	0.7204	0.000505
212424_at	PDCD11	0.7206	0.000229
224698_at	ESYT2	0.7207	0.000186
207621_s_at	PEMT	0.7208	0.000822
233341_s_at	POLR1B	0.7209	5.26E-05
230718_at	HSF5	0.7210	0.000706
207507_s_at	ATP5G3	0.7211	1.12E-05
202137_s_at	ZMYND11	0.7211	6.48E-05
208643_s_at	XRCC5	0.7213	4.80E-06
225545_at	EEF2K	0.7213	0.000203
228162_at	ESD	0.7214	0.00055
225463_x_at	GPR89A	0.7216	5.79E-05
219960_s_at	UCHL5	0.7217	0.000028
217099_s_at	GEMIN4	0.7219	7.20E-06
235177_at	FAM119A	0.7220	0.000902
222610_s_at	S100PBP	0.7222	0.000949
218229_s_at	POGK	0.7222	0.000476
211023_at	PDHB	0.7222	0.000188
235124_at	LOC645212	0.7223	2.66E-05
201076_at	NHP2L1	0.7224	0.000118
200916_at	TAGLN2	0.7225	9.72E-05
238448_at	MRPL19	0.7227	0.000207
214136_at	NUDT13	0.7228	6.60E-06
217185_s_at		0.7234	0.00028
218816_at	LRRC1	0.7235	0.000901
224700_at	STT3B	0.7236	5.16E-05
235830_at		0.7236	0.000901
217907_at	MRPL18	0.7237	0.000193

Probe set	Gene Symbol	Fold-change: Low/High	P-value
218593_at	RBM28	0.7237	0.000206
202470_s_at	CPSF6	0.7240	0.000537
204905_s_at	EEF1E1	0.7244	0.000199
223531_x_at		0.7244	0.000156
226262_at		0.7244	0.000879
219767_s_at	CRYZL1	0.7245	0.000614
212872_s_at	MED20	0.7246	0.000592
209825_s_at	UCK2	0.7248	0.000713
200987_x_at	PSME3	0.7249	0.000239
218932_at	ZNHIT6	0.7252	0.000409
205408_at	MLLT10	0.7254	0.000162
227865_at	C9orf103	0.7260	0.000371
219733_s_at	SLC27A5	0.7260	0.000204
202891_at	NIT1	0.7262	0.00056
215667_x_at	PMS2L1	0.7263	0.000259
223066_at	SNAPIN	0.7266	0.000907
218988_at	SLC35E3	0.7267	1.73E-05
216308_x_at	GRHPR	0.7267	0.000313
218526_s_at	RANGRF	0.7268	0.000116
201977_s_at	KIAA0141	0.7272	0.000232
206205_at	MPHOSPH9	0.7274	5.54E-05
218289_s_at	UBA5	0.7274	0.000109
208906_at	BSCL2	0.7275	0.000749
1556178_x_at	TAF8	0.7275	1.84E-05
209741_x_at	SCAPER	0.7277	0.000954
225398_at	RPUSD4	0.7278	0.000262
203179_at	GALT	0.7280	0.000476
200946_x_at	GLUD1	0.7282	0.000222
201381_x_at	CACYBP	0.7287	0.000445
230329_s_at	NUDT6	0.7288	0.000145
238511_at		0.7290	0.000055
202601_s_at	HTATSF1	0.7290	5.73E-05
212954_at	DYRK4	0.7291	0.000494
203264_s_at	ARHGEF9	0.7292	0.000447
205711_x_at	ATP5C1	0.7295	5.60E-06
213610_s_at	KLHL23	0.7296	0.000295
224602_at	C4orf3	0.7297	0.00016
223996_s_at	MRPL30	0.7301	2.77E-05
212996_s_at	URB1	0.7303	0.000306
241734_at	SRFBP1	0.7303	0.00017
224467_s_at	PDCD2L	0.7306	0.000783
214942_at	RBM34	0.7307	0.000574
203197_s_at	C1orf123	0.7309	0.000558
213893_x_at		0.7310	0.000143
225736_at	FBXO22	0.7312	0.000306
218838_s_at	TTC31	0.7312	0.000105
220397_at	MDM1	0.7313	0.000195
1566303_s_at	PPP1R11	0.7313	0.000433

Probe set	Gene Symbol	Fold-change: Low/High	P-value
224495_at	TMEM107	0.7316	0.000835
222741_s_at	C6orf64	0.7320	0.000974
212123_at	TCTN3	0.7322	0.00013
32836_at	AGPAT1	0.7324	0.000997
207011_s_at	PTK7	0.7327	0.000624
217106_x_at	DIMT1L	0.7328	0.000363
208405_s_at	CD164	0.7328	0.000333
202179_at	BLMH	0.7329	0.000264
210779_x_at	SIP1	0.7330	4.09E-05
227442_at	COX18	0.7331	5.81E-05
201468_s_at	NQO1	0.7334	8.74E-05
218398_at	MRPS30	0.7337	0.000029
214708_at	SNTB1	0.7339	0.000442
1555831_s_at	LRRC41	0.7340	0.000817
226835_s_at	C20orf199	0.7340	0.000781
227637_at	TFCP2	0.7341	0.000704
235736_at		0.7341	0.000176
203277_at	DFFA	0.7343	0.000218
224913_s_at	TIMM50	0.7346	0.000396
218285_s_at	BDH2	0.7346	0.000644
224863_at	GNAQ	0.7348	0.000364
240106_at	GNPTAB	0.7348	3.11E-05
220183_s_at	NUDT6	0.7349	0.000446
210131_x_at	SDHC	0.7350	0.000439
211115_x_at	SIP1	0.7352	0.000074
208870_x_at	ATP5C1	0.7354	7.50E-06
223056_s_at	XPO5	0.7355	0.000108
216652_s_at	DR1	0.7355	0.000249
203613_s_at	NDUFB6	0.7357	0.000576
208897_s_at	DDX18	0.7357	1.25E-05
200631_s_at	SET	0.7358	0.000199
241379_at	APLF	0.7359	0.000913
223157_at	C4orf14	0.7361	0.000135
225623_at		0.7362	0.000619
227374_at	EARS2	0.7362	0.000471
201051_at	ANP32A	0.7367	0.00084
203867_s_at	NLE1	0.7369	0.000796
227409_at	PPP1R3E	0.7370	0.000443
218748_s_at	EXOC5	0.7371	0.000346
231918_s_at	GFM2	0.7374	0.000186
215708_s_at	PRIM2	0.7374	4.96E-05
202050_s_at	ZMYM4	0.7375	0.000232
51146_at	PIGV	0.7376	0.000943
208675_s_at	DDOST	0.7380	0.000824
219004_s_at	C21orf45	0.7384	0.000831
232675_s_at	UCKL1	0.7385	0.000582
229425_at		0.7392	0.000063
243007_at		0.7392	0.00019

Probe set	Gene Symbol	Fold-change: Low/High	P-value
204405_x_at	DIMT1L	0.7392	0.000704
203905_at	PARN	0.7393	0.000359
216194_s_at	TBCB	0.7394	0.000627
200947_s_at	GLUD1	0.7395	0.000467
218527_at	APTX	0.7397	0.000636
211976_at		0.7398	0.000645
201657_at	ARL1	0.7398	0.000822
210337_s_at	ACLY	0.7401	0.000997
243790_at	ZNF585A	0.7401	6.37E-05
205702_at	PHTF1	0.7403	6.07E-05
214934_at	ATP9B	0.7408	0.000767
1563646_a_at	TMEM67	0.7410	0.000882
201515_s_at	TSN	0.7411	4.48E-05
235191_at	LOC148189	0.7412	0.000794
203076_s_at	SMAD2	0.7412	0.000137
219530_at	PALB2	0.7416	0.000172
221987_s_at	TSR1	0.7416	0.000107
200093_s_at	HINT1	0.7423	0.000795
201446_s_at	TIA1	0.7424	0.000267
201771_at	SCAMP3	0.7425	0.000087
204241_at	ACOX3	0.7426	0.000734
209009_at	ESD	0.7426	0.000392
234937_x_at	ZFP28	0.7427	4.79E-05
201175_at	TMX2	0.7428	2.97E-05
201607_at	PWP1	0.7429	6.97E-05
221699_s_at	DDX50	0.7429	0.000131
219418_at	NHEJ1	0.7430	1.36E-05
203582_s_at	RAB4A	0.7431	0.00053
225103_at		0.7434	0.000559
222665_at	FAM82B	0.7435	0.000378
233827_s_at	SUPT16H	0.7436	0.00053
222611_s_at	PSPC1	0.7437	0.000257
1564662_at	ZNF852	0.7437	0.000624
202004_x_at	SDHC	0.7438	0.000236
231824_at	LARP1B	0.7438	8.01E-05
219487_at	BBS10	0.7439	3.27E-05
242247_at	METT5D1	0.7443	0.000146
203176_s_at	TFAM	0.7444	0.000908
203283_s_at	HS2ST1	0.7445	0.000113
63009_at	SHQ1	0.7451	0.000308
222132_s_at	AGK	0.7453	7.40E-06
217981_s_at	FXC1	0.7454	0.000405
211323_s_at	ITPR1	0.7454	0.000274
210768_x_at	TMCO1	0.7459	0.000162
218250_s_at	CNOT7	0.7463	0.000242
240528_s_at	EXOC4	0.7466	0.000281
220083_x_at	UCHL5	0.7468	0.0006
201815_s_at	TBC1D5	0.7469	0.000288

Probe set	Gene Symbol	Fold-change: Low/High	P-value
203269_at	NSMAF	0.7469	0.000612
200009_at	GDI2	0.7470	0.000897
239792_at	LOC440288	0.7470	0.000722
214167_s_at		0.7470	0.000109
215691_x_at	HSPB11	0.7471	0.000505
218670_at	PUS1	0.7477	0.000982
213864_s_at	NAP1L1	0.7477	0.000694
204185_x_at	PPID	0.7478	0.000911
218991_at	HEATR6	0.7479	0.000791
225249_at	SPPL2B	0.7480	0.000707
244531_at	NNT	0.7483	0.000409
202306_at	POLR2G	0.7486	0.000149
210813_s_at	XRCC4	0.7498	0.000769
204666_s_at	SIKE1	0.7499	0.000121
208907_s_at	MRPS18B	0.7500	0.000719
223098_s_at	LONP2	0.7502	0.000229
211595_s_at	MRPS11	0.7502	0.000608
205634_x_at		0.7507	0.000522
211759_x_at	TBCB	0.7509	0.000345
213036_x_at	ATP2A3	0.7513	0.00065
201128_s_at	ACLY	0.7513	0.000254
203253_s_at	HISPPD1	0.7514	0.000616
217496_s_at	IDE	0.7514	0.000056
216411_s_at		0.7518	0.000837
226295_at	ITFG2	0.7519	0.000827
227873_at	TXNDC15	0.7520	0.000903
238677_at	WDR36	0.7521	0.00018
1556151_at	ITFG1	0.7524	0.000854
202757_at	COBRA1	0.7526	0.000931
203225_s_at	RFK	0.7526	0.000107
37549_g_at	BBS9	0.7528	0.000836
1555974_a_at		0.7528	0.000924
220647_s_at	CHCHD8	0.7530	0.000867
228743_at	TXNDC17	0.7531	0.000564
203165_s_at	SLC33A1	0.7531	0.000538
210250_x_at	ADSL	0.7532	0.000469
201727_s_at	ELAVL1	0.7533	0.00062
226024_at	COMMD1	0.7540	0.000327
213738_s_at	ATP5A1	0.7540	3.11E-05
209511_at	POLR2F	0.7541	0.00056
225317_at	ACBD6	0.7541	0.000516
224302_s_at	MRPS36	0.7542	9.82E-05
212035_s_at	EXOC7	0.7546	0.000357
203565_s_at	MNAT1	0.7546	0.000906
226696_at	RBBP9	0.7549	0.000177
208752_x_at	NAP1L1	0.7550	0.000555
213366_x_at	ATP5C1	0.7554	0.000429
225638_at	C1orf31	0.7554	0.000426

Probe set	Gene Symbol	Fold-change: Low/High	P-value
211973_at		0.7556	0.000797
204979_s_at	SH3BGR	0.7559	0.000642
216883_x_at	PDE6D	0.7561	0.000596
218203_at	ALG5	0.7564	7.66E-05
225088_at	C16orf63	0.7565	0.000536
205761_s_at	DUS4L	0.7567	0.000446
212896_at	SKIV2L2	0.7567	0.000394
232589_at		0.7568	0.000568
218316_at	TIMM9	0.7569	0.000619
1552306_at	ALG10	0.7571	0.000225
208826_x_at	HINT1	0.7578	0.000923
209853_s_at	PSME3	0.7582	0.000856
214756_x_at	PMS2L1	0.7582	0.000219
219576_at	MAP7D3	0.7582	0.000412
207438_s_at	SNUPN	0.7590	0.000818
226243_at	C2orf79	0.7595	0.000782
225244_at	SNAP47	0.7601	0.000617
207508_at	ATP5G3	0.7608	0.000706
225614_at	SAAL1	0.7609	0.000111
222555_s_at	MRPL44	0.7613	0.000252
241682_at	KLHL23	0.7615	0.000762
238578_at	TMEM182	0.7620	0.000204
225584_at		0.7622	0.000537
225908_at	IAH1	0.7625	8.83E-05
210573_s_at	POLR3C	0.7626	0.00083
224936_at	EIF2S3	0.7631	0.000882
226457_at		0.7634	0.000687
201007_at	HADHB	0.7635	0.000123
229984_at	DTWD1	0.7635	0.000576
200068_s_at	CANX	0.7638	0.000655
219988_s_at	RNF220	0.7645	0.000595
218213_s_at	C11orf10	0.7646	0.000753
230678_at	RGS5	0.7647	0.000344
212329_at	SCAP	0.7648	0.000595
238297_at		0.7652	0.000658
207243_s_at	CALM2	0.7654	0.000274
212720_at	PAPOLA	0.7656	0.000955
235628_x_at	FLJ33630	0.7658	0.00086
201804_x_at	TBCB	0.7662	0.000904
216958_s_at	IVD	0.7665	0.000236
228578_at	RBM45	0.7668	0.000246
214047_s_at	MBD4	0.7668	0.000504
201659_s_at	ARL1	0.7670	0.000433
203361_s_at	MYCBP	0.7670	0.000185
211392_s_at	PATZ1	0.7672	0.000617
222588_s_at	C11orf57	0.7674	0.000486
209394_at	ASMTL	0.7674	0.000587
1555679_a_at	RTN4IP1	0.7677	0.000362

Probe set	Gene Symbol	Fold-change: Low/High	P-value
235031_at		0.7679	0.000838
217920_at	MAN1A2	0.7682	0.000442
219133_at	OXSM	0.7687	0.000617
223191_at	COX16	0.7691	0.000833
239790_s_at		0.7691	0.000351
1555902_at	ARMCX5	0.7691	0.000983
217874_at	SUCLG1	0.7692	0.00086
223197_s_at	SMARCAD1	0.7692	0.00099
228199_at	LOC729234	0.7693	0.000143
229075_at	SPATA5	0.7696	0.000554
241823_at		0.7700	0.000329
219030_at	TPRKB	0.7700	3.61E-05
219329_s_at	C2orf28	0.7704	0.000892
210290_at	ZNF174	0.7705	7.39E-05
209965_s_at	RAD51L3	0.7705	0.00043
238014_at	TMEM194B	0.7708	0.000368
200054_at	ZNF259	0.7709	0.000131
200705_s_at	EEF1B2	0.7712	0.000298
1569366_a_at	ZNF569	0.7714	6.01E-05
233268_s_at		0.7716	0.000593
222360_at	DPH5	0.7716	0.000658
213203_at	SNAPC5	0.7717	0.000682
230848_s_at	MGA	0.7718	0.000669
1554465_s_at		0.7721	8.91E-05
222014_x_at	MTO1	0.7721	0.000585
236994_at	FBXL4	0.7721	0.000404
217485_x_at	PMS2L1	0.7722	0.000201
243815_at	PGBD4	0.7726	0.000407
212544_at	ZNHIT3	0.7728	0.000379
218890_x_at	MRPL35	0.7732	0.000931
223219_s_at	CNOT10	0.7735	0.000121
218533_s_at	UCKL1	0.7736	0.000936
220128_s_at	NIPAL2	0.7740	0.000764
200955_at	IMMT	0.7740	0.000943
219770_at	GTDC1	0.7748	0.000452
224714_at	MKI67IP	0.7751	0.000491
202615_at	GNAQ	0.7752	0.000834
200063_s_at	NPM1	0.7754	0.000474
202358_s_at	SNX19	0.7755	0.000889
225737_s_at	FBXO22	0.7758	0.000176
218982_s_at		0.7762	0.000703
224723_x_at	LOC401397	0.7765	0.000744
219485_s_at	PSMD10	0.7768	0.00047
217956_s_at	ENOPH1	0.7771	0.000641
222510_s_at	MKRN2	0.7772	0.000515
209196_at	WDR46	0.7773	0.000592
212026_s_at	EXOC7	0.7777	0.000463
227903_x_at	C19orf20	0.7777	0.00077

Probe set	Gene Symbol	Fold-change: Low/High	P-value
215985_at		0.7785	0.000947
223355_at	ALG1	0.7787	0.000956
223334_at	TMEM126A	0.7787	0.000962
226815_at	C3orf31	0.7789	0.000154
203871_at	SENP3	0.7791	0.000627
243529_at	MARS2	0.7795	0.000744
211426_x_at	GNAQ	0.7797	0.000312
1554019_s_at	C6orf182	0.7804	0.000237
203715_at	TBCE	0.7815	0.000678
216843_x_at	PMS2L1	0.7815	0.000728
202417_at	KEAP1	0.7824	0.000262
1553940_a_at	LRRC28	0.7825	0.000255
209580_s_at	MBD4	0.7829	0.000989
210211_s_at	HSP90AA1	0.7829	0.000674
201239_s_at		0.7832	0.000538
224824_at	FAM36A	0.7832	8.05E-05
223277_at	C3orf75	0.7833	0.000673
219590_x_at	DPH5	0.7834	0.000721
1555702_a_at	ST3GAL3	0.7834	0.000932
227839_at	MBD5	0.7843	0.000385
206308_at	TRDMT1	0.7845	0.00055
202167_s_at	MMS19	0.7862	0.000413
1554885_a_at	PRIM2	0.7862	0.000472
48825_at	ING4	0.7865	0.000806
214738_s_at	NEK9	0.7868	0.000928
224805_s_at	C15orf17	0.7877	0.000803
203328_x_at	IDE	0.7881	0.000252
218049_s_at	MRPL13	0.7882	0.000446
223021_x_at	VTA1	0.7901	0.000922
203091_at	FUBP1	0.7910	0.000959
204699_s_at	C1orf107	0.7929	0.000771
217604_at		0.7936	0.000497
238490_at	KIAA2026	0.7939	0.000718
211212_s_at	ORC5L	0.7941	0.00056
212422_at	PDCD11	0.7949	0.000577
236240_at	C4orf29	0.7962	0.000177
1553726_s_at	C6orf170	0.7967	0.000788
220176_at	NUBPL	0.7970	0.00079
218869_at	MLYCD	0.7977	0.000921
1554577_a_at	PSMD10	0.7980	0.000301
200723_s_at	CAPRIN1	0.7982	0.000865
242515_x_at	C11orf17	0.7987	0.000859
208739_x_at	SUMO2	0.8018	0.000499
224474_x_at	SMEK2	0.8042	0.000257
207654_x_at	DR1	0.8044	0.000847
233013_x_at	LOC220906	0.8045	0.000469
1553158_at	C3orf34	0.8048	0.000744
223010_s_at	OCIAD1	0.8049	0.00042

Probe set	Gene Symbol	Fold-change: Low/High	P-value
222918_at	RAB9B	0.8051	0.000388
205763_s_at	DDX18	0.8054	0.000973
223436_s_at	TRPT1	0.8060	0.000533
1554321_a_at	NFS1	0.8118	0.00083
206001_at	NPY	1.1981	0.000972
225287_s_at	TMEM55B	1.2193	0.00049
217535_at	FAM49B	1.2267	0.000244
214294_at	KIAA0485	1.2337	0.000805
212822_at	HEG1	1.2432	0.000481
221417_x_at	S1PR5	1.2459	0.00065
40020_at	CELSR3	1.2489	0.000636
241930_x_at	LOC442113	1.2493	0.000751
232919_at	AFG3L2	1.2523	0.000796
226871_s_at	ATG4D	1.2525	0.000994
211410_x_at	KIR2DL5A	1.2548	0.000843
216537_s_at	SIGLEC7	1.2555	0.000506
208203_x_at	KIR2DS5	1.2571	0.000296
237460_x_at	C14orf182	1.2636	0.000427
235528_at	GUCA1B	1.2646	0.000821
215067_x_at	PRDX2	1.2672	0.000968
210059_s_at	MAPK13	1.2677	0.000277
217646_at	SURF1	1.2678	0.000406
33322_i_at	SFN	1.2692	0.000716
204952_at	LYPD3	1.2692	0.000828
201155_s_at	MFN2	1.2721	0.000219
216907_x_at		1.2748	0.000977
203916_at	NDST2	1.2781	0.000955
205494_at	ZNF821	1.2785	0.000602
1562853_x_at		1.2787	0.000159
212401_s_at		1.2798	0.000363
233101_at	MTMR9	1.2851	0.000164
211507_s_at	MTMR3	1.2856	0.000911
221619_s_at	MTCH1	1.2861	0.000594
225271_at	TMEM63B	1.2871	0.000594
207312_at	PHKG1	1.2879	0.000797
229247_at	FBLN7	1.2945	0.000152
201100_s_at	USP9X	1.2961	0.000836
214487_s_at		1.2977	0.000228
233168_s_at	RP3-402G11.5	1.2982	0.000713
215645_at	FLCN	1.3003	0.000815
204710_s_at	WIPI2	1.3009	0.000336
1556654_at		1.3037	0.000059
232579_at	LOC100134229	1.3065	0.000605
215588_x_at	RIOK3	1.3072	0.000465
204948_s_at	FST	1.3079	0.000287
218945_at	C16orf68	1.3086	0.000258
222160_at	AKAP8L	1.3113	0.000116
234362_s_at	CTLA4	1.3155	0.000342

Probe set	Gene Symbol	Fold-change: Low/High	P-value
33323_r_at	SFN	1.3161	0.000586
209222_s_at	OSBPL2	1.3204	0.000369
1568915_at		1.3216	0.000127
238888_at		1.3286	0.000261
221812_at	FBXO42	1.3340	0.00039
207840_at	CD160	1.3385	0.000938
47773_at	FBXO42	1.3416	0.000944
201006_at	PRDX2	1.3417	0.000819
241927_x_at	CDC34	1.3425	6.40E-06
232134_at		1.3439	0.00017
224783_at	FAM100B	1.3449	0.000966
224905_at	WDR26	1.3450	0.000648
242749_at		1.3462	0.000275
221490_at	UBAP1	1.3481	0.000293
241239_at	EPN2	1.3490	6.84E-05
1559436_x_at		1.3504	0.000429
229987_at		1.3512	0.000984
238042_at		1.3523	0.000221
208942_s_at	SEC62	1.3533	0.000695
241001_at		1.3561	0.000796
46270_at		1.3561	0.000265
219186_at	ZBTB7A	1.3567	0.00095
218208_at	PQLC1	1.3587	0.000203
231861_at	LRP10	1.3601	0.000483
238594_x_at	DUSP8	1.3602	0.000364
242742_at		1.3612	0.000252
202197_at	MTMR3	1.3617	0.000295
1561015_at		1.3624	0.000795
208707_at	EIF5	1.3662	0.00087
238430_x_at	SLFN5	1.3677	0.000092
223199_at	MKNK2	1.3693	0.000991
213579_s_at	EP300	1.3718	0.000713
204476_s_at	PC	1.3728	0.000185
202131_s_at	RIOK3	1.3752	0.000286
201749_at	ECE1	1.3755	0.000324
239585_at	KAT2B	1.3807	7.41E-05
208866_at	CSNK1A1	1.3820	0.00093
242725_at		1.3832	0.000115
209372_x_at		1.3842	0.000768
202130_at	RIOK3	1.3846	0.000185
244777_at	DCP2	1.3848	0.000473
219500_at	CLCF1	1.3859	8.16E-05
236533_at	ASAP1	1.3863	0.000842
231552_at		1.3871	0.0004
232307_at		1.3927	0.000976
1556820_a_at	DLEU2	1.3929	0.000253
230761_at		1.3942	0.000719
242837_at	SFRS4	1.3944	0.000255

Probe set	Gene Symbol	Fold-change: Low/High	P-value
223012_at	UBXN6	1.3945	0.000727
232342_at	MTMR14	1.4086	0.000109
232513_x_at	C20orf107	1.4094	0.000113
239633_at		1.4102	0.000648
244087_at		1.4125	0.000336
1557675_at	RAF1	1.4132	0.000937
225632_s_at	RAB43	1.4137	0.000464
236908_at		1.4143	0.000462
244408_at		1.4145	0.000383
229996_s_at	PCGF5	1.4160	0.000464
228866_at		1.4164	0.000961
213300_at	ATG2A	1.4168	0.000155
210598_at		1.4178	0.000652
44146_at	GMEB2	1.4180	4.42E-05
222251_s_at	GMEB2	1.4189	0.000119
218205_s_at	MKNK2	1.4229	1.62E-05
241865_at		1.4282	0.000591
235553_at	GAPVD1	1.4283	3.98E-05
237097_at		1.4304	0.000155
212356_at	KIAA0323	1.4392	0.000449
240451_at		1.4392	0.000181
231776_at	EOMES	1.4403	0.000385
205255_x_at	TCF7	1.4403	4.59E-05
212540_at	CDC34	1.4418	0.00074
227201_at	LOC643837	1.4424	0.000559
224897_at	WDR26	1.4429	0.000131
233728_at		1.4441	0.000401
239166_at		1.4564	0.000361
209270_at	LAMB3	1.4568	0.0004
227886_at	CTSD	1.4576	0.000749
232910_at	NCRNA00081	1.4614	1.56E-05
205377_s_at	ACHE	1.4614	0.000904
233308_at	COPB1	1.4629	0.000266
208868_s_at	GABARAPL1	1.4650	0.000975
228967_at	EIF1	1.4688	0.000202
203464_s_at	EPN2	1.4719	3.80E-06
218603_at	HECA	1.4755	0.000783
224889_at	FOXO3	1.4776	0.000555
230529_at	HECA	1.4816	3.91E-05
213343_s_at	GDPD5	1.4825	0.000454
242829_x_at	FBXL3	1.4857	0.000989
207460_at	GZMM	1.4967	0.000297
204131_s_at	FOXO3	1.4973	0.000497
233691_at		1.4985	0.000378
238360_s_at		1.5002	0.000473
233360_at	UBE2I	1.5066	0.000669
236379_at		1.5084	0.000716
1561130_at	C12orf51	1.5089	0.000702

Probe set	Gene Symbol	Fold-change: Low/High	P-value
238378_at		1.5100	0.000336
1563076_x_at		1.5111	0.000532
206571_s_at	MAP4K4	1.5187	0.000516
225005_at	PHF13	1.5188	0.000917
228674_s_at	EML4	1.5233	0.00042
230464_at	S1PR5	1.5241	0.000855
212441_at	KIAA0232	1.5267	1.99E-05
235983_at		1.5275	0.000516
35776_at	ITSN1	1.5318	0.000521
243286_at		1.5328	0.000573
208901_s_at	TOP1	1.5395	6.00E-07
230961_at		1.5408	0.000789
208900_s_at	TOP1	1.5537	1.27E-05
204180_s_at	ZBTB43	1.5588	0.000943
202492_at	ATG9A	1.5592	5.37E-05
233359_at		1.5639	1.39E-05
211458_s_at		1.5687	0.000487
1557543_at		1.5754	0.000586
213958_at	CD6	1.5841	0.000853
203936_s_at	MMP9	1.5859	0.000135
215592_at		1.5900	0.000144
204181_s_at	ZBTB43	1.5934	0.000252
1559101_at	FYN	1.5976	6.35E-05
217799_x_at	UBE2H	1.5990	0.00044
32502_at	GDPD5	1.5990	0.000156
217748_at	ADIPOR1	1.6092	0.000115
236755_at	TBC1D23	1.6125	0.000204
243675_at		1.6309	0.000275
218032_at	SNN	1.6391	0.000568
206374_at	DUSP8	1.6675	0.000292
202364_at	MXI1	1.6722	0.000174
202426_s_at	RXRA	1.6730	0.000486
1558299_at		1.6871	0.000724
238769_at		1.6891	0.000563
236248_x_at	TADA2B	1.7011	0.000342
240410_at		1.7056	0.000402
239845_at		1.7177	2.84E-05
231205_at		1.7210	1.25E-05
1560031_at	FRMD4A	1.7265	0.000825
240347_at		1.7275	0.000204
227867_at	LOC129293	1.7348	1.29E-05
222420_s_at	UBE2H	1.7447	0.000211
237082_at		1.7558	0.000365
225239_at		1.7737	0.000477
226561_at	AGFG1	1.7743	0.000423
204731_at	TGFBR3	1.7756	0.000658
203413_at	NELL2	1.7780	0.00077
222747_s_at	SCML1	1.7799	0.000498

Probe set	Gene Symbol	Fold-change: Low/High	P-value
232744_x_at		1.7949	0.000542
203827_at	WIPI1	1.8015	0.000236
243404_at		1.8149	2.11E-05
1564150_a_at	LOC256021	1.8232	0.000905
243509_at		1.8395	5.28E-05
209345_s_at	PI4K2A	1.8426	0.000399
224829_at	CPEB4	1.8548	0.000034
235652_at		1.8549	0.00094
1556385_at		1.8898	5.47E-05
218978_s_at	SLC25A37	1.8908	0.000832
243006_at		1.9030	0.000392
231911_at	ERMN	1.9752	0.000826
228361_at	E2F2	1.9968	0.000576
221778_at	JHDM1D	2.0076	0.000105
233289_at		2.0089	2.00E-07
226679_at	SLC26A11	2.0169	0.000807
243546_at		2.0454	0.000114
210031_at	CD247	2.0647	0.000108
223028_s_at	SNX9	2.1920	0.000508
223027_at	SNX9	2.2178	0.000372