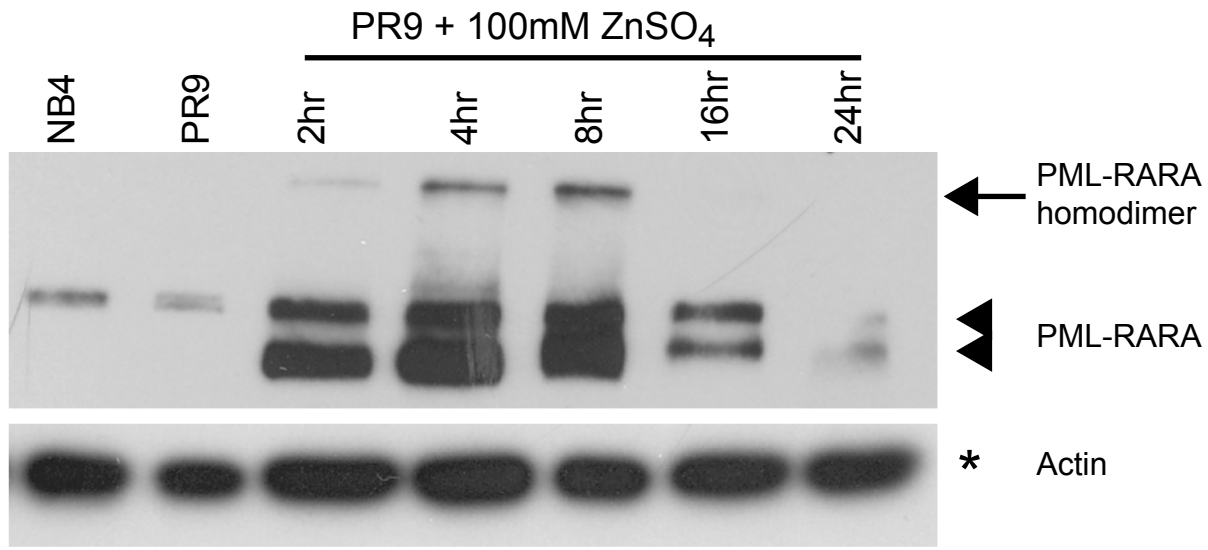
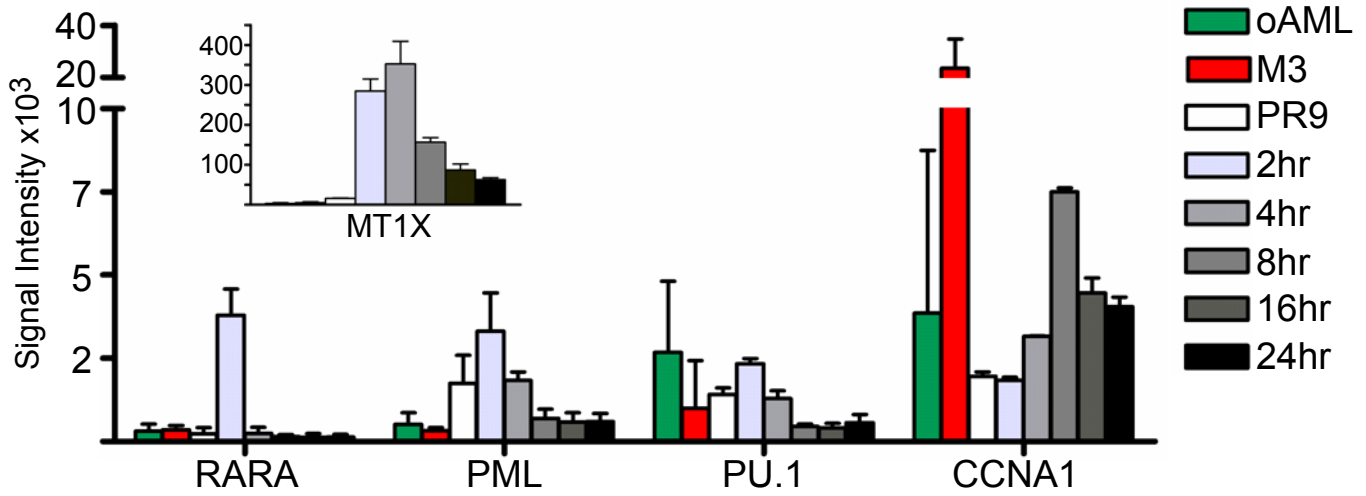


Supplemental Figure 1. Identification of genes with significantly different expression in M3 compared to normal myeloid cell fractions. A. Heatmap of microarray data shows genes that are normally expressed only in CD34+ cells, but are aberrantly expressed in M3 cells. B. Heatmap of microarray data shows genes that are normally expressed in promyelocytes, but not expressed in M3 AML cells. C. Heatmap of microarray data shows genes with very high expression levels in M3 cells, but little or no expression in any normal myeloid fraction.

A



B



Supplemental Figure 2. Zn²⁺ treatment induces PML-RARA expression and up-regulation of known downstream targets in PR-9 cells. A. Western blot showing PML-RARA and actin protein levels at 0, 2, 4, 8, 16 and 24 hours post Zn²⁺-induction. NB4 cells, which express PML-RARA, serve as a positive control in lane 1. B. Expression of PML, RARA, PU.1 and CCNA1 in other AML (oAML) subtypes, M3, and PR-9 cells 0-24 hours post Zn²⁺-induction. All are upregulated after PML-RARA induction, as expected. Inset: MTX1, a known Zn-responsive gene, is also upregulated after Zn²⁺ treatment.

Supplemental Table 1. M3-specific dysregulome (510 genes)

Figure 2B Probeset	Gene Symbol	Entrez Gene	Gene Title
215409_at	AGPAT7	254531	1-acylglycerol-3-phosphate O-acyltransferase 7 (lysophosphatidic acid acyltransferase, eta)
228264_at	ACCS	84680	1-aminocyclopropane-1-carboxylate synthase homolog (Arabidopsis)(non-functional)
200862_at	DHCR24	1718	24-dehydrocholesterol reductase
218043_s_at	AZ12	64343	5-azacytidine induced 2
218051_s_at	NT5DC2	64943	5'-nucleotidase domain containing 2
201790_s_at	DHCR7	1717	7-dehydrocholesterol reductase
215483_at	AKAP9	10142	A kinase (PRKA) anchor protein (yotiao) 9
225098_at	ABI2	10152	abl interactor 2
49452_at	ACACB	32	acetyl-Coenzyme A carboxylase beta
200974_at	ACTA2	59	actin, alpha 2, smooth muscle, aorta
208002_s_at	ACOT7	11332	acyl-CoA thioesterase 7
210278_s_at	AP4S1	11154	adaptor-related protein complex 4, sigma 1 subunit
204497_at	ADCY9	115	adenylate cyclase 9
225342_at	AK3L1	205	adenylate kinase 3-like 1
204348_s_at	AK3L1 /// AK3L2		adenylate kinase 3-like 1 /// adenylate kinase 3-like 2
226718_at	AMIGO1	57463	adhesion molecule with Ig-like domain 1
228094_at	AMICA1	120425	adhesion molecule, interacts with CXADR antigen 1
209122_at	ADFP	123	adipose differentiation-related protein
201792_at	AEBP1	165	AE binding protein 1
212285_s_at	AGRN	375790	agrin
202053_s_at	ALDH3A2	224	aldehyde dehydrogenase 3 family, member A2
223136_at	AIG1	51390	androgen-induced 1
223092_at	ANKH	56172	ankylosis, progressive homolog (mouse)
229307_at	ANKRD28	23243	ankyrin repeat domain 28
201590_x_at	ANXA2	302	annexin A2
201301_s_at	ANXA4	307	annexin A4
	ANXA8 /// ANXA8L1 /// ANXA8L2		annexin A8-like 2 /// annexin A8 /// annexin A8-like 1
219366_at	AVEN	57099	apoptosis, caspase activation inhibitor
39248_at	AQP3	360	aquaporin 3 (Gill blood group)
207076_s_at	ASS1	445	argininosuccinate synthetase 1
218694_at	ARMCX1	51309	armadillo repeat containing, X-linked 1
230244_at	UNQ830	389084	ASCL830
205047_s_at	ASNS	440	asparagine synthetase
210192_at	ATP8A1	10396	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1
219660_s_at	ATP8A2	51761	ATPase, aminophospholipid transporter-like, class I, type 8A, member 2
201242_s_at	ATP1B1	481	ATPase, Na ⁺ /K ⁺ transporting, beta 1 polypeptide
203505_at	ABCA1	19	ATP-binding cassette, sub-family A (ABC1), member 1
203196_at	ABCC4	10257	ATP-binding cassette, sub-family C (CFTR/MRP), member 4
212599_at	AUTS2	26053	autism susceptibility candidate 2
214575_s_at	AZU1	566	azurocidin 1 (cationic antimicrobial protein 37)
222746_s_at	BSPRY	54836	B-box and SPRY domain containing
1559078_at	BCL11A	53335	B-cell CLL/lymphoma 11A (zinc finger protein)
205681_at	BCL2A1	597	BCL2-related protein A1
205839_s_at	BZRAP1	9256	benzodiazapine receptor (peripheral) associated protein 1
217904_s_at	BACE1	23621	beta-site APP-cleaving enzyme 1
225285_at	BCAT1	586	branched chain aminotransferase 1, cytosolic

Supplemental Table 1. M3-specific dysregulome (510 genes)

Figure 2B Probeset	Gene Symbol	Entrez Gene	Gene Title
207693_at	CACNB4	785	calcium channel, voltage-dependent, beta 4 subunit
221042_s_at	CLMN	79789	calmin (calponin-like, transmembrane)
221879_at	CALML4	91860	calmodulin-like 4
212586_at	CAST	831	calpastatin
200935_at	CALR	811	calreticulin
211031_s_at	CLIP2	7461	CAP-GLY domain containing linker protein 2
201850_at	CAPG	822	capping protein (actin filament), gelsolin-like
227522_at	CMBL	134147	carboxymethylenebutenolidase homolog (Pseudomonas)
205624_at	CPA3	1359	carboxypeptidase A3 (mast cell)
209790_s_at	CASP6	839	caspace 6, apoptosis-related cysteine peptidase
225647_s_at	CTSC	1075	cathepsin C
205653_at	CTSG	1511	cathepsin G
214450_at	CTSW	1521	cathepsin W
203324_s_at	CAV2	858	caveolin 2
214523_at	CEBPE	1053	CCAAT/enhancer binding protein (C/EBP), epsilon
217078_s_at	CD300A	11314	CD300a molecule
218529_at	CD320	51293	CD320 molecule
206488_s_at	CD36	948	CD36 molecule (thrombospondin receptor)
213539_at	CD3D	915	CD3d molecule, delta (CD3-TCR complex)
204489_s_at	CD44	960	CD44 molecule (Indian blood group)
200663_at	CD63	967	CD63 molecule
201005_at	CD9	928	CD9 molecule
206761_at	CD96	10225	CD96 molecule
201028_s_at	CD99	4267	CD99 molecule
221556_at	CDC14B /// CDC14C		CDC14 cell division cycle 14 homolog B (S. cerevisiae) /// CDC14 cell division cycle 14 homolog C (S. cerevisiae)
217849_s_at	CDC42BPB	9578	CDC42 binding protein kinase beta (DMPK-like)
232355_at	---		CDNA FLJ10247 fis, clone HEMBB1000705
233422_at	---		CDNA FLJ10277 fis, clone HEMBB1001199
236787_at	---		CDNA FLJ35091 fis, clone PLACE6005786
243937_x_at	BMS1P5 /// CTGLF1 /// CTGLF6 /// CTGLF7		centaurin, gamma-like family, member 1 /// BMS1 pseudogene 5 /// centaurin, gamma-like family, member 6 /// centaurin, gamma-like family, member 7
221850_x_at	CTGLF1 /// CTGLF3 /// CTGLF4 /// CTGLF5 /// KIAA1975		centaurin, gamma-like family, member 1 /// KIAA1975 protein similar to MRIP2 /// centaurin, gamma-like family, member 3 /// centaurin, gamma-like family, member 4 /// centaurin, gamma-like family, member 5
239151_at	CTGLF6	642517	centaurin, gamma-like family, member 6
223513_at	CENPJ	55835	centromere protein J
242041_at	CSPP1	79848	centrosome and spindle pole associated protein 1
224794_s_at	CERCAM	51148	cerebral endothelial cell adhesion molecule
229958_at	CLN8	2055	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)
213385_at	CHN2	1124	chimerin (chimaerin) 2
226473_at	CBX2	84733	chromobox homolog 2 (Pc class homolog, Drosophila)
226123_at	CHD7	55636	chromodomain helicase DNA binding protein 7
205944_s_at	CLTCL1	8218	clathrin, heavy chain-like 1
208792_s_at	CLU	1191	clusterin
205229_s_at	COCH	1690	coagulation factor C homolog, cochlin (Limulus polyphemus)

Supplemental Table 1. M3-specific dysregulome (510 genes)

Figure 2B Probeset	Gene Symbol	Entrez Gene	Gene Title
204363_at	F3	2152	coagulation factor III (thromboplastin, tissue factor)
201161_s_at	CSDA	8531	cold shock domain protein A
229168_at	COL23A1	91522	collagen, type XXIII, alpha 1
205382_s_at	CFD	1675	complement factor D (adipsin)
215388_s_at	CFH /// CFHR1		complement factor H /// complement factor H-related 1
225129_at	CPNE2	221184	copine II
202118_s_at	CPNE3	8895	copine III
205538_at	CORO2A	7464	coronin, actin binding protein, 2A
211709_s_at	CLEC11A	6320	C-type lectin domain family 11, member A
232466_at	CUL4A	8451	Cullin 4A
1560018_at	ARPP-21	10777	cyclic AMP-regulated phosphoprotein, 21 kD
205899_at	CCNA1	8900	cyclin A1
200953_s_at	CCND2	894	cyclin D2
224851_at	CDK6	1021	cyclin-dependent kinase 6
213348_at	CDKN1C	1028	cyclin-dependent kinase inhibitor 1C (p57, Kip2)
209644_x_at	CDKN2A	1029	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)
205518_s_at	CMAH	8418	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminate monooxygenase) pseudogene
217889_s_at	CYBRD1	79901	cytochrome b reductase 1
209975_at	CYP2E1	1571	cytochrome P450, family 2, subfamily E, polypeptide 1
223377_x_at	CISH	1154	cytokine inducible SH2-containing protein
219837_s_at	CYTL1	54360	cytokine-like 1
222101_s_at	DCHS1	8642	dachsous 1 (Drosophila)
239648_at	DCUN1D3	123879	DCN1, defective in cullin neddylation 1, domain containing 3 (S. cerevisiae)
224215_s_at	DLL1	28514	delta-like 1 (Drosophila)
228293_at	DEPDC7	91614	DEP domain containing 7
218854_at	DSE	29940	dermatan sulfate epimerase
226817_at	DSC2	1824	desmocollin 2
201681_s_at	DLG5	9231	discs, large homolog 5 (Drosophila)
215761_at	DMXL2	23312	Dmx-like 2
215433_at	DPY19L1	23333	Dpy-19-like 1 (C. elegans)
215102_at	DPY19L1P 1	89231	dpy-19-like 1 pseudogene 1 (C. elegans)
238784_at	DPY19L2	283417	dpy-19-like 2 (C. elegans)
215116_s_at	DNM1	1759	dynamamin 1
212838_at	DNMBP	23268	dynamamin binding protein
233850_s_at	EBF4	57593	early B-cell factor 4
227404_s_at	EGR1	1958	Early growth response 1
204160_s_at	ENPP4	22875	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)
211200_s_at	EFCAB2	84288	EF-hand calcium binding domain 2
206580_s_at	EFEMP2	30008	EGF-containing fibulin-like extracellular matrix protein 2
206871_at	ELA2	1991	elastase 2, neutrophil
204163_at	EMILIN1	11117	elastin microfibril interfacier 1
213779_at	EMID1	129080	EMI domain containing 1
204503_at	EVPL	2125	envoplakin
223253_at	EPDR1	54749	ependymin related protein 1 (zebrafish)
231944_at	ERO1LB	56605	ERO1-like beta (S. cerevisiae)
226432_at	ETNK1	55500	ethanolamine kinase 1
236700_at	EIF3C	8663	eukaryotic translation initiation factor 3, subunit C
209365_s_at	ECM1	1893	extracellular matrix protein 1

Supplemental Table 1. M3-specific dysregulome (510 genes)

Figure 2B Probeset	Gene Symbol	Entrez Gene	Gene Title
231846_at	FOXRED2	80020	FAD-dependent oxidoreductase domain containing 2
229459_at	FAM19A5	25817	family with sequence similarity 19 (chemokine (C-C motif)-like), member A5
1568865_at	FNTB	2342	Farnesyltransferase, CAAX box, beta
210933_s_at	FSCN1	6624	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)
216080_s_at	FADS3	3995	fatty acid desaturase 3
227222_at	FBXO10	26267	F-box protein 10
224162_s_at	FBXO31	79791	F-box protein 31
1560031_at	FRMD4A	55691	FERM domain containing 4A
205110_s_at	FGF13	2258	fibroblast growth factor 13
211535_s_at	FGFR1	2260	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)
204379_s_at	FGFR3	2261	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)
223321_s_at	FGFRL1	53834	fibroblast growth factor receptor-like 1
218618_s_at	FNDC3B	64778	fibronectin type III domain containing 3B
202994_s_at	FBLN1	2192	fibulin 1
219118_at	FKBP11	51303	FK506 binding protein 11, 19 kDa
210220_at	FZD2	2535	frizzled homolog 2 (Drosophila)
202862_at	FAH	2184	fumarylacetoacetate hydrolase (fumarylacetoacetase)
229312_s_at	GKAP1	80318	G kinase anchoring protein 1
228770_at	GPR146	115330	G protein-coupled receptor 146
221902_at	GPR153	387509	G protein-coupled receptor 153
232912_at	GPR180	160897	G protein-coupled receptor 180
204537_s_at	GABRE	2564	gamma-aminobutyric acid (GABA) A receptor, epsilon
208438_s_at	FGR	2268	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog
215659_at	GSDML	55876	Gasdermin-like
210358_x_at	GATA2	2624	GATA binding protein 2
220773_s_at	GPHN	10243	gephyrin
224839_s_at	GPT2	84706	glutamic pyruvate transaminase (alanine aminotransferase) 2
205164_at	GCAT	23464	glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase)
208798_x_at	GOLGA8A	23015	golgi autoantigen, golgin subfamily a, 8A
210425_x_at	GOLGA8A /// GOLGA8B		golgi autoantigen, golgin subfamily a, 8A /// golgi autoantigen, golgin subfamily a, 8B
238002_at	GOLIM4	27333	golgi integral membrane protein 4
217771_at	GOLM1	51280	golgi membrane protein 1
31874_at	GAS2L1	10634	growth arrest-specific 2 like 1
216860_s_at	GDF11	10220	growth differentiation factor 11
209409_at	GRB10	2887	growth factor receptor-bound protein 10
229377_at	GRTP1	79774	growth hormone regulated TBC protein 1
219777_at	GIMAP6	474344	GTPase, IMAP family member 6
40562_at	GNA11	2767	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)
207124_s_at	GNB5	10681	guanine nucleotide binding protein (G protein), beta 5
226840_at	H2AFY	9555	H2A histone family, member Y
211936_at	HSPA5	3309	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
1570200_at	HELB	92797	helicase (DNA) B
209458_x_at	HBA1 /// HBA2		hemoglobin, alpha 1 /// hemoglobin, alpha 2
227361_at	HS3ST3B1	9953	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1
201655_s_at	HSPG2	3339	heparan sulfate proteoglycan 2

Supplemental Table 1. M3-specific dysregulome (510 genes)

Figure 2B Probeset	Gene Symbol	Entrez Gene	Gene Title
203821_at	HBEGF	1839	heparin-binding EGF-like growth factor
210755_at	HGF	3082	hepatocyte growth factor (hepapoietin A; scatter factor)
210997_at	HGF	3082	hepatocyte growth factor (hepapoietin A; scatter factor)
1555653_at	HNRNPA3	220988	heterogeneous nuclear ribonucleoprotein A3
235500_at	HNRNPC	3183	heterogeneous nuclear ribonucleoprotein C (C1/C2)
	HRNBP3 ///		hexaribonucleotide binding protein 3 ///
	LOC10013		hypothetical protein LOC100130312 ///
235468_at	0312 ///		hypothetical protein LOC100133332
	LOC10013		
	3332		
205936_s_at	HK3	3101	hexokinase 3 (white cell)
225601_at	HMGB3	3149	high-mobility group box 3
222126_at	HRBL	3268	HIV-1 Rev binding protein-like
226651_at	HOMER1	9456	homer homolog 1 (Drosophila)
231050_at	HRASLS5	117245	HRAS-like suppressor family, member 5
211728_s_at	HYAL3 ///		hyaluronoglucosaminidase 3 ///
	NAT6		N-acetyltransferase 6
200825_s_at	HYOU1	10525	hypoxia up-regulated 1
1554452_a_at	HIG2	29923	hypoxia-inducible protein 2
	ING5 ///		inhibitor of growth family, member 5 ///
229197_at	LOC72777		
	3		
202662_s_at	ITPR2	3709	inositol 1,4,5-triphosphate receptor, type 2
226216_at	INSR	3643	insulin receptor
202718_at	IGFBP2	3485	insulin-like growth factor binding protein 2, 36kDa
211959_at	IGFBP5	3488	insulin-like growth factor binding protein 5
201163_s_at	IGFBP7	3490	insulin-like growth factor binding protein 7
202747_s_at	ITM2A	9452	integral membrane protein 2A
1555349_a_at	ITGB2	3689	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)
226535_at	ITGB6	3694	integrin, beta 6
224514_x_at	IL17RC	84818	interleukin 17 receptor C
212195_at	IL6ST	3572	interleukin 6 signal transducer (gp130, oncostatin M receptor)
213392_at	IQCK	124152	IQ motif containing K
230472_at	IRX1	79192	iroquois homeobox 1
229638_at	IRX3	79191	iroquois homeobox 3
210239_at	IRX5	10265	iroquois homeobox 5
202069_s_at	IDH3A	3419	isocitrate dehydrogenase 3 (NAD+) alpha
216268_s_at	JAG1	182	jagged 1 (Alagille syndrome)
211202_s_at	JARID1B	10765	jumonji, AT rich interactive domain 1B
201466_s_at	JUN	3725	jun oncogene
	JAM3 ///		junctional adhesion molecule 3 ///
212813_at	LOC10013		hypothetical protein LOC100133502
	3502		
220010_at	KCNE1L	23630	KCNE1-like
243428_at	KCNQ1OT	10984	KCNQ1 overlapping transcript 1 (non-protein coding)
	1		
212236_x_at	KRT17	3872	keratin 17
201596_x_at	KRT18	3875	keratin 18
234307_s_at	KIF26A	26153	kinesin family member 26A
216264_s_at	LAMB2	3913	laminin, beta 2 (laminin S)
200771_at	LAMC1	3915	laminin, gamma 1 (formerly LAMB2)
244881_at	LMLN	89782	leishmanolysin-like (metallopeptidase M8 family)

Supplemental Table 1. M3-specific dysregulome (510 genes)

Figure 2B Probeset	Gene Symbol	Entrez Gene	Gene Title
205381_at	LRRC17	10234	leucine rich repeat containing 17
206076_at	LRRC23	10233	leucine rich repeat containing 23
1559502_s_at	LRRC25	126364	leucine rich repeat containing 25
227423_at	LRRC28	123355	leucine rich repeat containing 28
235359_at	LRRC33	375387	leucine rich repeat containing 33
215063_x_at	LRRC40	55631	leucine rich repeat containing 40
210784_x_at	LILRA6 /// LILRB3		leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 /// leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 6
207106_s_at	LTK	4058	leukocyte receptor tyrosine kinase
208771_s_at	LTA4H	4048	leukotriene A4 hydrolase
206480_at	LTC4S	4056	leukotriene C4 synthase
218656_s_at	LHFP	10186	lipoma HMGIC fusion partner
212658_at	LHFPL2	10184	lipoma HMGIC fusion partner-like 2
204381_at	LRP3	4037	low density lipoprotein receptor-related protein 3
209468_at	LRP5	4041	low density lipoprotein receptor-related protein 5
207734_at	LAX1	54900	lymphocyte transmembrane adaptor 1
206960_at	LPAR4	2846	lysophosphatidic acid receptor 4
227145_at	LOXL4	84171	lysyl oxidase-like 4
205614_x_at	MST1	4485	macrophage stimulating 1 (hepatocyte growth factor-like)
213380_x_at	MSTP9	11223	macrophage stimulating, pseudogene 9
211654_x_at	HLA-DQB1	3119	major histocompatibility complex, class II, DQ beta 1
			major histocompatibility complex, class II, DQ beta 1 /// major histocompatibility complex, class II, DQ beta 2 /// major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 2 (pseudogene) /// major histocompatibility complex, class II, DR beta 3 /// major histocompatibility complex, class II, DR beta 4 /// major histocompatibility complex, class II, DR beta 5 /// ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) /// zinc finger protein 749 /// hypothetical protein LOC730415 /// similar to Major histocompatibility complex, class II, DR beta 4 /// similar to major histocompatibility complex, class II, DQ beta 1 /// similar to HLA class II histocompatibility antigen, DR-W53 beta chain /// similar to hCG1992647
206111_at	hCG_1998 957 /// HLA- DQB1 /// HLA-DQB2 /// HLA- DRB1 /// HLA-DRB2 /// HLA- DRB3 /// HLA-DRB4 /// HLA- DRB5 ///		
	LOC10013 3484 ///		
	LOC10013 3583 ///		
	LOC10013 3661 ///		
	LOC10013 3811 ///		
	LOC73041 5 ///		
	RNASE2 ///		
	ZNF749		
239108_at	MLSTD1	55711	Male sterility domain containing 1
204059_s_at	ME1	4199	malic enzyme 1, NADP(+)-dependent, cytosolic
37408_at	MRC2	9902	mannose receptor, C type 2

Supplemental Table 1. M3-specific dysregulome (510 genes)

Figure 2B Probeset	Gene Symbol	Entrez Gene	Gene Title
221713_s_at	MAP6D1	79929	MAP6 domain containing 1
226210_s_at	MEG3	55384	maternally expressed 3
204575_s_at	MMP19	4327	matrix metalloproteinase 19
201069_at	MMP2	4313	matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)
212509_s_at	MXRA7	439921	matrix-remodelling associated 7
235409_at	MGA	23269	MAX gene associated
35147_at	MCF2L	23263	MCF.2 cell line derived transforming sequence-like
230461_s_at	MUM1	84939	Melanoma associated antigen (mutated) 1
210254_at	MS4A3	932	membrane-spanning 4-domains, subfamily A, member 3 (hematopoietic cell-specific)
224356_x_at	MS4A6A	64231	membrane-spanning 4-domains, subfamily A, member 6A
211456_x_at	MT1P2	645745	metallothionein 1 pseudogene 2
213629_x_at	MT1F	4494	metallothionein 1F
206461_x_at	MT1H	4496	metallothionein 1H
208581_x_at	MT1X	4501	metallothionein 1X
212185_x_at	MT2A	4502	metallothionein 2A
223311_s_at	MTA3	57504	metastasis associated 1 family, member 3
1554127_s_at	MSRB3	253827	methionine sulfoxide reductase B3
201761_at	MTHFD2	10797	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase
224918_x_at	MGST1	4257	microsomal glutathione S-transferase 1
203151_at	MAP1A	4130	microtubule-associated protein 1A
200836_s_at	MAP4	4134	microtubule-associated protein 4
203208_s_at	MTFR1	9650	mitochondrial fission regulator 1
35617_at	MAPK7	5598	mitogen-activated protein kinase 7
214786_at	MAP3K1	4214	mitogen-activated protein kinase kinase kinase 1
205447_s_at	MAP3K12	7786	mitogen-activated protein kinase kinase kinase 12
225997_at	MOBK1A	92597	MOB1, Mps One Binder kinase activator-like 1A (yeast)
226844_at	MOBK2B	79817	MOB1, Mps One Binder kinase activator-like 2B (yeast)
221636_s_at	MOSC2	54996	MOCO sulphurase C-terminal domain containing 2
243857_at	MORF4L2	9643	Mortality factor 4 like 2
234224_at	---		MRNA; cDNA DKFZp434O0919 (from clone DKFZp434O0919)
226869_at	MEGF6	1953	multiple EGF-like-domains 6
225185_at	MRAS	22808	muscle RAS oncogene homolog
1565436_s_at	MLL	4297	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)
239289_x_at	MTMR15	22909	myotubularin related protein 15
228424_at	NAALADL1	10004	N-acetylated alpha-linked acidic dipeptidase-like 1
215850_s_at	NDUFA5	4698	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa
228523_at	NANOS1	340719	nanos homolog 1 (Drosophila)
220429_at	NDST3	9348	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3
224802_at	NDFIP2	54602	Nedd4 family interacting protein 2
227870_at	NOPE	57722	neighbor of Punc E11
223638_at	NBPF3	84224	neuroblastoma breakpoint family, member 3
218888_s_at	NETO2	81831	neuropilin (NRP) and tolloid (TLL)-like 2
209949_at	NCF2	4688	neutrophil cytosolic factor 2 (65kDa, chronic granulomatous disease, autosomal 2)
212803_at	NAB2	4665	NGFI-A binding protein 2 (EGR1 binding protein 2)
202237_at	NNMT	4837	nicotinamide N-methyltransferase
1552553_a_at	NLRC4	58484	NLR family, CARD domain containing 4
231798_at	NOG	9241	noggin

Supplemental Table 1. M3-specific dysregulome (510 genes)

Figure 2B Probeset	Gene Symbol	Entrez Gene	Gene Title
227556_at	NME7	29922	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)
202599_s_at	NRIP1	8204	nuclear receptor interacting protein 1
219557_s_at	NRIP3	56675	nuclear receptor interacting protein 3
203920_at	NR1H3	10062	nuclear receptor subfamily 1, group H, member 3
207202_s_at	NR1I2	8856	nuclear receptor subfamily 1, group I, member 2
1559139_at	NOC2L	26155	nucleolar complex associated 2 homolog (S. cerevisiae)
212775_at	OBSL1	23363	obscurin-like 1
213125_at	OLFML2B	25903	olfactomedin-like 2B
213825_at	OLIG2	10215	oligodendrocyte lineage transcription factor 2
228170_at	OLIG1	116448	oligodendrocyte transcription factor 1
201364_s_at	OAZ2	4947	ornithine decarboxylase antizyme 2
225105_at	OCC-1	387882	overexpressed in colon carcinoma-1
223464_at	OSBPL5	114879	oxysterol binding protein-like 5
226435_at	PAPLN	89932	papilin, proteoglycan-like sulfated glycoprotein
227204_at	PARD6G	84552	par-6 partitioning defective 6 homolog gamma (C. elegans)
209815_at	PTCH1	5727	patched homolog 1 (Drosophila)
210139_s_at	PMP22	5376	peripheral myelin protein 22
212012_at	PXDN	7837	peroxidasin homolog (Drosophila)
208510_s_at	PPARG	5468	peroxisome proliferator-activated receptor gamma
204604_at	PFTK1	5218	PFTAIRE protein kinase 1
232279_at	PHF15	23338	PHD finger protein 15
226150_at	PPAPDC1 B	84513	phosphatidic acid phosphatase type 2 domain containing 1B
207621_s_at	PEMT	10400	phosphatidylethanolamine N-methyltransferase
230352_at	PRPS2	5634	Phosphoribosyl pyrophosphate synthetase 2
201481_s_at	PYGB	5834	phosphorylase, glycogen; brain
222688_at	PHCA	55331	phytoceramidase, alkaline
235411_at	PGBD1	84547	piggyBac transposable element derived 1
219225_at	LOC10013 4440 /// PGBD5		piggyBac transposable element derived 5 /// similar to PGBD5 protein
220798_x_at	PRG2	79948	plasticity-related gene 2
205463_s_at	PDGFA	5154	platelet-derived growth factor alpha polypeptide
220952_s_at	PLEKHA5	54477	pleckstrin homology domain containing, family A member 5
228171_s_at	PLEKHG4	25894	pleckstrin homology domain containing, family G (with RhoGef domain) member 4
203623_at	PLXNA3	55558	plexin A3
241742_at	PRAM1	84106	PML-RARA regulated adaptor molecule 1
212662_at	PVR	5817	poliovirus receptor
224701_at	PARP14	54625	poly (ADP-ribose) polymerase family, member 14
203688_at	PKD2	5311	polycystic kidney disease 2 (autosomal dominant)
226246_at	KCTD1	284252	potassium channel tetramerisation domain containing 1
212192_at	KCTD12	115207	potassium channel tetramerisation domain containing 12
222668_at	KCTD15	79047	potassium channel tetramerisation domain containing 15
239763_at	LOC10012 9965 /// PRDM11		PR domain containing 11 /// hypothetical protein LOC100129965
214177_s_at	PBXIP1	57326	pre-B-cell leukemia homeobox interacting protein 1
226065_at	PRICKLE1	144165	prickle homolog 1 (Drosophila)
200654_at	P4HB	5034	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide

Supplemental Table 1. M3-specific dysregulome (510 genes)

Figure 2B Probeset	Gene Symbol	Entrez Gene	Gene Title
226423_at	PAQR8	85315	progesterin and adiponQ receptor family member VIII
214203_s_at	PRODH	5625	proline dehydrogenase (oxidase) 1
205618_at	PRRG1	5638	proline rich Gla (G-carboxyglutamic acid) 1
212187_x_at	PTGDS	5730	prostaglandin D2 synthase 21kDa (brain)
207650_x_at	PTGER1	5731	prostaglandin E receptor 1 (subtype EP1), 42kDa
213933_at	PTGER3	5733	prostaglandin E receptor 3 (subtype EP3)
231323_at	PSMB2	5690	proteasome (prosome, macropain) subunit, beta type, 2
229453_at	PDIA3	2923	Protein disulfide isomerase family A, member 3
208658_at	PDIA4	9601	protein disulfide isomerase family A, member 4
226101_at	PRKCE	5581	protein kinase C, epsilon
237107_at	PRKRA /// PRKRAP1		protein kinase, interferon-inducible double stranded RNA dependent activator /// protein kinase, interferon-inducible double stranded RNA dependent activator pseudogene 1
225203_at	PPP1R16A	84988	protein phosphatase 1, regulatory (inhibitor) subunit 16A
1569323_at	PTPRG	5793	protein tyrosine phosphatase, receptor type, G
1555579_s_at	PTPRM	5797	protein tyrosine phosphatase, receptor type, M
219654_at	PTPLA	9200	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member A
232473_at	PRPF18	8559	PRP18 pre-mRNA processing factor 18 homolog (S. cerevisiae)
240846_at	PCBD2	84105	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 2
220005_at	P2RY13	53829	purinergic receptor P2Y, G-protein coupled, 13
206277_at	P2RY2	5029	purinergic receptor P2Y, G-protein coupled, 2
235634_at	PURG	29942	purine-rich element binding protein G
1558290_a_at	PVT1	5820	Pvt1 oncogene homolog (mouse)
218018_at	PD XK	8566	pyridoxal (pyridoxine, vitamin B6) kinase
201251_at	PKM2	5315	pyruvate kinase, muscle
201482_at	QSOX1	5768	quiescin Q6 sulfhydryl oxidase 1
202252_at	RAB13	5872	RAB13, member RAS oncogene family
219412_at	RAB38	23682	RAB38, member RAS oncogene family
230266_at	RAB7B	338382	RAB7B, member RAS oncogene family
214487_s_at	RAP2A /// RAP2B		RAP2A, member of RAS oncogene family /// RAP2B, member of RAS oncogene family
222810_s_at	RASAL2	9462	RAS protein activator like 2
215620_at	RREB1	6239	ras responsive element binding protein 1
219167_at	RASL12	51285	RAS-like, family 12
226597_at	REEP6	92840	receptor accessory protein 6
212589_at	RRAS2	22800	related RAS viral (r-ras) oncogene homolog 2
220570_at	RETN	56729	resistin
228550_at	RTN4R	65078	reticulon 4 receptor
226638_at	ARHGAP2 3	57636	Rho GTPase activating protein 23
202975_s_at	RHOBTB3	22836	Rho-related BTB domain containing 3
212912_at	RPS6KA2	6196	ribosomal protein S6 kinase, 90kDa, polypeptide 2
207735_at	RNF125	54941	ring finger protein 125
226106_at	RNF141	50862	ring finger protein 141
205228_at	RBMS2	5939	RNA binding motif, single stranded interacting protein 2
228802_at	RBPM S2	348093	RNA binding protein with multiple splicing 2
225743_at	RPUSD3	285367	RNA pseudouridylate synthase domain containing 3
218394_at	ROGDI	79641	rogdi homolog (Drosophila)
213939_s_at	RUFY3	22902	RUN and FYVE domain containing 3
202917_s_at	S100A8	6279	S100 calcium binding protein A8

Supplemental Table 1. M3-specific dysregulome (510 genes)

Figure 2B Probeset	Gene Symbol	Entrez Gene	Gene Title
203535_at	S100A9	6280	S100 calcium binding protein A9
209686_at	S100B	6285	S100 calcium binding protein B
201825_s_at	SCCPDH	51097	saccharopine dehydrogenase (putative)
206671_at	SAG	6295	S-antigen; retina and pineal gland (arrestin)
202375_at	SEC24D	9871	SEC24 related gene family, member D (<i>S. cerevisiae</i>)
209875_s_at	SPP1	6696	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)
203021_at	SLPI	6590	secretory leukocyte peptidase inhibitor
219689_at	SEMA3G	56920	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G
224407_s_at	RP6-213H19.1	51765	serine/threonine protein kinase MST4
220030_at	STYK1	55359	serine/threonine/tyrosine kinase 1
202628_s_at	SERPINE1	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1
200986_at	SERPING1	710	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1, (angioedema, hereditary)
207714_s_at	SERPINH1	871	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)
212921_at	SMYD2	56950	SET and MYND domain containing 2
224817_at	SH3PXD2A	9644	SH3 and PX domains 2A
220059_at	STAP1	26228	signal transducing adaptor family member 1
244889_at	LOC388210	388210	Similar to LD15094p
204900_x_at	SAP30	8819	Sin3A-associated protein, 30kDa
203787_at	SSBP2	23635	single-stranded DNA binding protein 2
221562_s_at	SIRT3	23410	sirtuin (silent mating type information regulation 2 homolog) 3 (<i>S. cerevisiae</i>)
206634_at	SIX3	6496	SIX homeobox 3
232636_at	SLITRK4	139065	SLIT and NTRK-like family, member 4
232020_at	SMURF2	64750	SMAD specific E3 ubiquitin protein ligase 2
219480_at	SNAI1	6615	snail homolog 1 (<i>Drosophila</i>)
237106_at	SLC11A2	4891	Solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2
219593_at	SLC15A3	51296	solute carrier family 15, member 3
207057_at	SLC16A7	9194	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)
204430_s_at	SLC2A5	6518	solute carrier family 2 (facilitated glucose/fructose transporter), member 5
219090_at	SLC24A3	57419	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3
225305_at	SLC25A29	123096	solute carrier family 25, member 29
205097_at	SLC26A2	1836	solute carrier family 26 (sulfate transporter), member 2
220475_at	SLC28A3	64078	solute carrier family 28 (sodium-coupled nucleoside transporter), member 3
238418_at	SLC35B4	84912	solute carrier family 35, member B4
234976_x_at	SLC4A5	57835	Solute carrier family 4, sodium bicarbonate cotransporter, member 5
201195_s_at	SLC7A5	8140	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5
220129_at	SOHLH2	54937	spermatogenesis and oogenesis specific basic helix-loop-helix 2
228654_at	SPIN4	139886	spindlin family, member 4
224995_at	SPIRE1	56907	spire homolog 1 (<i>Drosophila</i>)
243361_at	SFRS12	140890	splicing factor, arginine/serine-rich 12

Supplemental Table 1. M3-specific dysregulome (510 genes)

Figure 2B Probeset	Gene Symbol	Entrez Gene	Gene Title
218638_s_at	SPON2	10417	spondin 2, extracellular matrix protein
225639_at	SKAP2	8935	src kinase associated phosphoprotein 2
213355_at	ST3GAL6	10402	ST3 beta-galactoside alpha-2,3-sialyltransferase 6
204150_at	STAB1	23166	stabilin 1
38487_at	STAB1	23166	stabilin 1
231891_at	STAMBPL1	57559	STAM binding protein-like 1
225662_at	ZAK	51776	sterile alpha motif and leucine zipper containing kinase AZK
204548_at	STAR	6770	steroidogenic acute regulatory protein
201061_s_at	STOM	2040	stomatin
212926_at	SMC5	23137	structural maintenance of chromosomes 5
202260_s_at	STXBP1	6812	syntaxin binding protein 1
208608_s_at	SNTB1	6641	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)
216920_s_at	TARP /// TRGC2		T cell receptor gamma constant 2 /// TCR gamma alternate reading frame protein
233719_s_at	TASP1	55617	taspase, threonine aspartase, 1
222116_s_at	TBC1D16	125058	TBC1 domain family, member 16
227632_at	TBC1D24	57465	TBC1 domain family, member 24
206301_at	TEC	7006	tec protein tyrosine kinase
218872_at	TESC	54997	tescalcin
223838_at	TSGA10	80705	testis specific, 10
214606_at	TSPAN2	10100	tetraspanin 2
219587_at	TTC12	54970	tetratricopeptide repeat domain 12
219838_at	TTC23	64927	tetratricopeptide repeat domain 23
215146_s_at	TTC28	23331	tetratricopeptide repeat domain 28
225308_s_at	TANC1	85461	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1
203313_s_at	TGIF1	7050	TGFB-induced factor homeobox 1
229253_at	THEM4	117145	thioesterase superfamily member 4
220384_at	TXNDC3	51314	thioredoxin domain containing 3 (spermatzoa)
219477_s_at	THSD1 /// THSD1P		thrombospondin, type I, domain containing 1 /// thrombospondin, type I, domain containing 1 pseudogene
201666_at	TIMP1	7076	TIMP metalloproteinase inhibitor 1
204043_at	TCN2	6948	transcobalamin II; macrocytic anemia
222317_at	---		Transcribed locus
226192_at	---		Transcribed locus
230391_at	---		Transcribed locus
230408_at	---		Transcribed locus
230684_at	---		Transcribed locus
231550_at	---		Transcribed locus
237945_at	---		Transcribed locus
1555348_at	TFAP2E	339488	transcription factor AP-2 epsilon (activating enhancer binding protein 2 epsilon)
238520_at	TRERF1	55809	transcriptional regulating factor 1
203221_at	TLE1	7088	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)
244716_x_at	TMIGD2	126259	transmembrane and immunoglobulin domain containing 2
1554077_a_at	TMEM53	79639	transmembrane protein 53
215583_at	TMEM63A	9725	Transmembrane protein 63A
223771_at	TMEM87A	25963	Transmembrane protein 87A
235245_at	TMEM92	162461	transmembrane protein 92
223814_at	TRNT1	51095	tRNA nucleotidyl transferase, CCA-adding, 1
241402_at	TSEN54	283989	tRNA splicing endonuclease 54 homolog (S. cerevisiae)
203476_at	TPBG	7162	trophoblast glycoprotein

Supplemental Table 1. M3-specific dysregulome (510 genes)

Figure 2B Probeset	Gene Symbol	Entrez Gene	Gene Title
209344_at	TPM4	7171	tropomyosin 4
215111_s_at	TSC22D1	8848	TSC22 domain family, member 1
239742_at	TULP4	56995	Tubby like protein 4
209191_at	TUBB6	84617	tubulin, beta 6
228285_at	TDRD9	122402	tudor domain containing 9
207113_s_at	TNF	7124	tumor necrosis factor (TNF superfamily, member 2)
203508_at	TNFRSF1B	7133	tumor necrosis factor receptor superfamily, member 1B
214228_x_at	TNFRSF4	7293	tumor necrosis factor receptor superfamily, member 4
202286_s_at	TACSTD2	4070	tumor-associated calcium signal transducer 2
213943_at	TWIST1	7291	twist homolog 1 (acrocephalosyndactyly 3; Saethre-Chotzen syndrome) (Drosophila)
206828_at	TXK	7294	TXK tyrosine kinase
238057_at	USP45	85015	ubiquitin specific peptidase 45
232621_at	USP48	84196	ubiquitin specific peptidase 48
236597_at	UGT3A1	133688	UDP glycosyltransferase 3 family, polypeptide A1
203188_at	B3GNT1	11041	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1
219956_at	GALNT6	11226	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)
1562434_at	UNK	85451	unkempt homolog (Drosophila)
205844_at	VNN1	8876	vanin 1
235818_at	VSTM1	284415	V-set and transmembrane domain containing 1
219251_s_at	WDR60	55112	WD repeat domain 60
243526_at	WDR86	349136	WD repeat domain 86
206067_s_at	WT1	7490	Wilms tumor 1
218775_s_at	WWC2	80014	WW and C2 domain containing 2
213996_at	YPEL1	29799	yippee-like 1 (Drosophila)
223382_s_at	ZNRF1	84937	zinc and ring finger 1
226137_at	ZFH3	463	zinc finger homeobox 3
205739_x_at	ZNF107	51427	zinc finger protein 107
234394_at	ZNF124	7678	zinc finger protein 124
235728_at	ZFP3	124961	zinc finger protein 3 homolog (mouse)
222016_s_at	ZNF323	64288	zinc finger protein 323
205514_at	ZNF415	55786	zinc finger protein 415
205964_at	ZNF426	79088	zinc finger protein 426
235176_at	ZNF545	284406	zinc finger protein 545
223680_at	ZNF607	84775	zinc finger protein 607
212620_at	ZNF609	23060	zinc finger protein 609
228864_at	ZNF653	115950	zinc finger protein 653
227080_at	ZNF697	90874	zinc finger protein 697
228988_at	ZNF711	7552	zinc finger protein 711
206059_at	ZNF91	7644	zinc finger protein 91
1562303_at	ZKSCAN3	80317	zinc finger with KRAB and SCAN domains 3
219247_s_at	ZDHHC14	79683	zinc finger, DHHC-type containing 14
240859_at	ZFYVE16	9765	zinc finger, FYVE domain containing 16
219628_at	ZMAT3	64393	zinc finger, matrin type 3
210282_at	ZMYM2	7750	zinc finger, MYM-type 2
207130_at	ZMYND8	23613	zinc finger, MYND-type containing 8

Supplemental Table 2. Data from nCounter assays of AML samples and normal CD34+, promyelocytes, and neutrophils (PMNs).

Accession No.	Gene Name/Sample ID	M0	M0	M0	M0	M0	M0	M0	M0	M0	M0	M0	M0	M1	M1	M1	M1	M1
		4528	4528	4528	4532	4532	4532	6742	6742	6742	17366	17366	17366	4534	4534	4534	6747	6747
NM_002841.2	PTPRG	5	2	4	0	1	0	2	2	0	3	0	3	1	0	2	2	0
NM_145256.2	LRRC25	176	175	165	2	1	3	3	3	2	9	10	8	23	22	21	8	3
NM_001972.2	ELA2	5	2	2	0	4	0	2	2	1	24	23	22	174	188	150	38	33
NM_000597.2	IGFBP2	25	12	23	0	1	0	9	5	6	8	1	5	90	79	66	131	98
NM_005413.1	SIX3	5	17	0	7	1	1	2	1	1	8	4	3	3	0	2	2	0
NM_006272.1	S100B	7	3	8	1	0	6	6	4	6	14	20	11	3	4	3	2	0
NM_003327.2	TNFRSF4	5	3	0	0	1	1	0	3	1	3	0	4	1	2	3	2	5
NM_004049.2	BCL2A1	356	363	334	17	15	10	86	76	75	42	44	35	69	61	57	17	20
NM_001911.2	CTSG	7	5	4	1	0	3	0	1	1	45	30	42	456	481	469	29	45
NM_001557.2	IL8RB	36	47	36	6	1	1	3	1	4	9	10	11	15	9	14	0	3
NM_001066.2	TNFRSF1B	845	862	760	9	5	7	19	11	11	35	49	43	115	139	101	38	30
NM_002046.3	GAPDH	3533	3587	3208	1929	1762	1790	4100	3649	3447	2494	2367	2687	4885	5088	4813	5798	5066
NM_006169.2	NNMT	2	2	4	0	2	3	2	2	1	3	6	5	6	3	1	12	10
NM_015381.3	FAM19A5	2	0	0	4	0	1	1	1	1	1	0	1	2	0	0	0	0
NM_015136.2	STAB1	194	195	178	7	7	8	156	112	114	14	19	26	151	115	123	21	18
NM_002029.3	FPR1	282	255	283	4	1	3	5	8	5	10	19	15	38	29	19	27	8
NM_003930.3	SCAP2	52	45	32	21	19	25	12	15	15	14	10	14	19	32	21	33	25
NM_006486.2	FBLN1	2	2	0	0	0	1	0	0	0	1	1	0	0	0	1	0	0
NM_153206.1	AMICA1	2	5	2	0	0	0	1	1	0	3	0	1	1	1	0	0	0
NM_002965.2	S100A9	6135	6132	5334	11	6	3	290	231	214	873	809	849	895	792	794	602	684
NM_021209.3	CARD12/NLRC4	56	33	38	2	1	10	2	2	4	13	9	12	13	9	9	4	5
NM_000433.2	NCF2	933	1005	861	4	2	6	13	9	9	90	104	103	105	128	102	27	20
NM_003489.2	NRIP1	74	65	56	54	56	51	1	3	2	36	30	26	33	17	19	35	28
NM_001040084.1	LOC653107/ANXA8	2	2	4	0	1	0	2	1	1	3	0	1	2	0	0	4	0
NM_016582.1	SLC15A3	83	83	114	0	1	6	1	3	1	19	9	14	8	9	8	8	5
NM_000211.2	ITGB2	1710	1648	1340	109	85	117	147	134	129	196	151	174	418	427	382	346	298
NM_000601.4	HGF	56	35	53	31	29	32	31	41	30	9	13	15	2	2	4	62	78
NM_001042729.1	FGR	1649	1506	1370	9	1	8	90	86	67	101	87	124	339	306	270	44	35
NM_001614.2	ACTG1	4209	4072	3381	2051	1782	1754	2154	1778	1840	2854	2726	2720	4114	3423	3280	2949	3035
NM_138444.2	KCTD12	264	260	221	1	1	4	2	8	7	17	14	14	36	34	30	8	13
NM_002964.3	S100A8	9494	9373	8823	21	23	19	637	531	509	2010	2096	1911	1532	1347	1274	1121	1165
NM_001025109.1	CD34	18	17	11	131	123	128	159	151	116	22	20	20	2	2	1	17	13
NM_000474.3	TWIST1	2	3	6	1	0	0	2	0	1	0	3	3	3	4	2	2	5
NM_015869.3	PPARG	7	8	9	0	1	0	2	0	1	1	1	3	4	5	2	0	10
NM_004666.1	VNN1	9	12	11	4	2	4	3	1	3	1	3	0	17	12	21	2	8
NM_005874.1	LILRB2	509	516	490	39	44	39	37	34	27	32	49	37	98	77	86	12	15
NM_001005463.1	EBF3	2	5	4	6	2	1	5	3	2	0	3	3	3	5	2	8	0
NM_152852.1	MS4A6A	79	68	53	1	4	0	2	1	1	15	9	18	8	8	6	0	0

Supplemental Table 2. Data from nCounter assays of AML samples and normal CD34+, promyelocytes, and neutrophils (PMNs).

Accession No.	Gene Name/Sample ID	M0	M0	M0	M0	M0	M0	M0	M0	M0	M0	M0	M0	M1	M1	M1	M1	M1
		4528	4528	4528	4532	4532	4532	6742	6742	6742	17366	17366	17366	4534	4534	4534	6747	6747
NM_000954.5	PTGDS	0	0	0	2	0	0	0	0	1	0	3	0	1	0	0	2	8
NM_000222.1	KIT	5	12	2	66	67	60	24	24	22	4	6	9	38	52	57	60	83
NM_004961.3	GABRE	0	2	2	2	0	3	2	1	0	1	0	1	3	2	1	2	0
NM_007261.2	CD300A	11	17	9	6	10	6	9	3	8	56	53	57	9	8	11	4	8
NM_002115.1	HK3	99	75	64	1	1	0	2	1	1	8	4	9	10	9	12	2	3
NM_023914.2	P2RY13	340	316	291	17	11	10	6	16	8	18	11	11	55	52	44	40	35
NM_033642.1	FGF13	0	2	0	1	1	1	1	1	1	1	1	0	1	1	0	2	5

AF324996.2	Athal_Spike_S23	1829	1841	1822	1853	1765	1800	1846	1855	1837	1832	1873	1858	1806	1871	1823	1924	1796
AF325027.2	Athal_Spike_S14	692	759	762	726	775	755	730	728	715	746	759	738	731	729	716	667	739
AF325042.2	Athal_Spike_S19	527	479	505	518	546	533	532	518	519	497	493	502	548	504	569	506	510
AY058560.1	DrosSpike8	194	158	189	179	158	202	171	165	184	195	181	180	181	183	175	175	219
AF325027.2	Athal_Spike_S13	95	72	58	79	94	68	69	87	78	82	64	78	66	80	71	92	78
AF324998.2	Athal_Spike_S22	81	98	96	77	100	88	84	83	91	88	67	73	87	72	76	79	91
AY058658.1	DrosSpike7	32	37	23	33	27	14	31	27	36	21	24	30	42	23	28	29	33
AF325032.2	Athal_Spike_S17	34	40	28	25	23	24	26	23	27	24	27	28	26	26	31	21	25
DQ412624	SarsSpike3	7	15	13	5	7	11	7	6	6	8	3	7	10	8	6	4	5
AY058658.1	DrosSpike6	9	0	4	4	4	6	2	6	6	5	7	4	1	3	3	2	3
AY058560.1	DrosSpike10	2	2	2	0	2	0	2	0	1	4	0	1	2	0	1	4	3
AY058658.1	DrosSpike11	2	0	2	1	5	0	0	2	0	0	0	3	2	3	0	2	0
AF325014.2	Athal_Spike_S12	2	3	0	4	6	3	3	2	5	4	1	9	5	3	3	2	0
AF325016.2	Athal_Spike_S15	5	2	0	6	1	8	4	2	3	3	3	3	3	2	3	2	5
AF325016.2	Athal_Spike_S16	2	5	8	2	1	3	2	2	1	5	1	0	3	4	3	0	0
AF325032.2	Athal_Spike_S18	7	5	2	2	1	0	3	2	0	3	1	1	2	2	2	2	0
AF324998.2	Athal_Spike_S20	2	2	2	0	4	6	0	2	3	9	1	3	4	2	2	8	5
AF324998.2	Athal_Spike_S21	0	5	0	2	2	4	3	3	3	8	6	1	4	2	2	2	3
AF324998.2	Athal_Spike_S24	0	10	6	2	2	6	0	1	1	4	4	3	4	2	5	6	3
DQ412624	SarsSpike4	5	3	0	2	0	1	7	1	4	5	6	1	3	2	6	0	0
AY058560.1	DrosSpike9	5	2	0	2	2	1	2	1	1	0	0	0	3	1	0	2	3

Supplemental Table 2. Data from nCounter assays of AML samples and normal CD34+, promyelocytes, and neutrophils (PMNs).

Accession No.	Gene Name/Sample ID	M1	M1	M1	M1	M1	M1	M1	M1	M1	M1	M2	M2	M2	M2	M2	M2
		6747	15599	15599	15599	16066	16066	16066	20900	20900	20900	4530	4530	4530	4983	4983	4983
NM_002841.2	PTPRG	2	1	0	0	0	2	3	0	0	1	1	1	3	2	2	2
NM_145256.2	LRRC25	0	63	29	38	5	3	4	2	3	2	4	5	7	23	18	19
NM_001972.2	ELA2	40	25	15	7	3	2	2	3	1	3	49	58	64	124	75	96
NM_000597.2	IGFBP2	125	39	18	22	11	3	11	11	30	18	2	2	7	4	7	7
NM_005413.1	SIX3	0	0	0	4	1	0	2	0	5	2	2	1	2	2	4	3
NM_006272.1	S100B	0	7	3	4	7	2	1	0	2	5	5	6	4	2	2	3
NM_003327.2	TNFRSF4	0	0	2	0	2	0	1	1	2	1	2	0	2	0	3	1
NM_004049.2	BCL2A1	35	14	21	18	8	12	5	9	13	8	26	46	19	78	78	83
NM_001911.2	CTSG	38	524	549	469	408	414	363	54	22	37	10	14	16	223	182	248
NM_001557.2	IL8RB	5	10	11	5	1	2	0	1	0	1	7	6	3	21	15	23
NM_001066.2	TNFRSF1B	24	310	252	264	111	101	92	29	40	35	28	29	35	90	60	93
NM_002046.3	GAPDH	6083	5419	5985	4994	4404	4284	4310	3726	3595	3359	3401	3593	3512	2823	1890	2450
NM_006169.2	NNMT	12	1	2	2	1	2	2	7	3	2	1	1	2	1	1	2
NM_015381.3	FAM19A5	0	1	0	2	1	0	0	0	0	1	0	0	0	2	0	1
NM_015136.2	STAB1	24	34	30	25	9	3	4	3	1	1	35	39	22	73	52	65
NM_002029.3	FPR1	12	1	15	9	4	3	3	3	2	3	10	19	16	86	63	69
NM_003930.3	SCAP2	40	22	33	24	31	26	15	20	23	22	19	11	14	25	7	21
NM_006486.2	FBLN1	0	1	2	2	0	0	1	0	0	0	2	0	0	0	0	1
NM_153206.1	AMICA1	0	1	6	2	0	0	0	0	0	0	1	0	0	2	0	5
NM_002965.2	S100A9	654	654	665	529	140	120	108	2	2	3	319	365	375	1814	1322	1642
NM_021209.3	CARD12/NLRC4	2	35	41	36	10	9	11	5	5	2	9	5	7	9	8	12
NM_000433.2	NCF2	19	353	309	306	118	122	115	3	4	5	50	59	51	156	121	156
NM_003489.2	NRIP1	59	21	20	29	57	56	54	59	52	50	26	41	36	14	10	12
NM_001040084.1	LOC653107/ANXA8	5	1	8	2	4	5	6	2	3	2	3	10	6	2	0	2
NM_016582.1	SLC15A3	0	18	12	13	2	0	1	3	2	3	4	5	7	11	6	8
NM_000211.2	ITGB2	391	1030	1175	900	666	585	660	132	135	123	90	106	94	414	275	400
NM_000601.4	HGF	75	186	154	186	9	16	11	56	59	49	203	214	233	5	3	8
NM_001042729.1	FGR	38	601	616	561	47	40	63	11	6	5	63	78	83	331	267	310
NM_001614.2	ACTG1	3403	5348	4840	4460	5820	5376	5246	3142	3097	3123	2513	2689	2595	2029	1559	1813
NM_138444.2	KCTD12	9	34	23	9	4	7	2	3	9	7	22	17	22	16	19	25
NM_002964.3	S100A8	1426	1091	916	934	246	310	272	4	2	1	645	670	656	3456	2593	3002
NM_001025109.1	CD34	31	7	9	2	21	10	13	3	5	2	125	128	134	2	4	2
NM_000474.3	TWIST1	0	4	0	2	0	3	4	4	2	4	3	3	5	1	2	1
NM_015869.3	PPARG	0	1	14	13	2	0	1	1	1	1	1	2	0	4	8	5
NM_004666.1	VNN1	2	13	11	9	5	9	10	2	0	1	23	20	22	14	12	13
NM_005874.1	LILRB2	16	159	142	165	142	125	139	46	55	55	57	56	52	62	48	59
NM_001005463.1	EBF3	5	9	2	4	3	3	3	3	5	3	5	0	5	5	6	5
NM_152852.1	MS4A6A	2	73	78	63	5	9	2	1	6	3	12	17	20	10	5	5

Supplemental Table 2. Data from nCounter assays of AML samples and normal CD34+, promyelocytes, and neutrophils (PMNs).

Accession No.	Gene Name/Sample ID	M1	M1	M1	M1	M1	M1	M1	M1	M1	M1	M2	M2	M2	M2	M2	M2
		6747	15599	15599	15599	16066	16066	16066	20900	20900	20900	4530	4530	4530	4983	4983	4983
NM_000954.5	PTGDS	2	0	0	0	0	0	0	1	0	1	0	0	0	3	2	4
NM_000222.1	KIT	99	22	18	11	15	12	5	59	74	71	41	54	40	12	6	9
NM_004961.3	GABRE	7	3	2	0	2	0	1	2	3	3	0	1	0	2	3	5
NM_007261.2	CD300A	7	10	14	11	13	12	8	0	7	9	4	4	1	7	7	5
NM_002115.1	HK3	5	24	14	36	4	2	5	1	1	1	5	8	2	17	8	6
NM_023914.2	P2RY13	40	148	121	100	42	47	29	5	3	1	28	28	20	74	49	63
NM_033642.1	FGF13	2	1	0	2	0	0	4	0	1	0	0	0	1	1	1	1

AF324996.2	Athal_Spike_S23	1859	1856	1870	1841	1840	1893	1875	1850	1803	1804	1824	1862	1825	1897	1764	1772
AF325027.2	Athal_Spike_S14	772	727	738	746	678	675	727	752	752	775	740	693	746	729	749	785
AF325042.2	Athal_Spike_S19	482	500	523	527	566	501	512	496	519	505	528	506	525	493	579	513
AY058560.1	DrosSpike8	174	185	155	183	198	188	180	173	204	188	180	185	163	161	172	190
AF325027.2	Athal_Spike_S13	85	66	63	67	72	77	67	70	60	71	79	73	73	77	82	80
AF324998.2	Athal_Spike_S22	71	97	72	80	88	108	64	91	94	82	83	97	102	71	90	87
AY058658.1	DrosSpike7	24	29	36	22	28	23	32	32	21	29	35	38	30	37	27	32
AF325032.2	Athal_Spike_S17	21	29	29	25	20	26	31	25	27	28	20	27	27	19	22	25
DQ412624	SarsSpike3	7	9	9	7	7	5	9	5	13	10	7	14	6	8	12	8
AY058658.1	DrosSpike6	5	1	3	2	3	3	2	3	6	5	2	5	4	7	3	8
AY058560.1	DrosSpike10	2	1	3	0	1	0	3	2	1	1	2	3	1	1	0	2
AY058658.1	DrosSpike11	2	0	0	0	3	2	0	0	3	1	0	1	1	2	2	1
AF325014.2	Athal_Spike_S12	0	1	5	2	6	5	4	2	6	6	5	3	1	2	3	3
AF325016.2	Athal_Spike_S15	2	7	5	2	3	2	10	5	5	4	4	5	7	3	4	3
AF325016.2	Athal_Spike_S16	0	1	2	5	4	2	1	0	1	3	4	2	2	3	0	2
AF325032.2	Athal_Spike_S18	0	0	2	0	1	2	4	1	3	2	2	3	3	6	6	1
AF324998.2	Athal_Spike_S20	2	3	5	2	2	2	3	3	3	3	2	3	6	4	4	4
AF324998.2	Athal_Spike_S21	0	5	5	4	5	2	1	2	2	4	0	2	2	5	5	5
AF324998.2	Athal_Spike_S24	2	1	3	0	5	2	4	0	2	5	0	3	2	2	3	3
DQ412624	SarsSpike4	2	3	0	2	5	2	1	6	4	5	2	6	3	5	6	5
AY058560.1	DrosSpike9	0	3	2	7	1	0	1	0	0	0	0	4	1	5	2	1

Supplemental Table 2. Data from nCounter assays of AML samples and normal CD34+, promyelocytes, and neutrophils (PMNs).

Accession No.	Gene Name/Sample ID	M2	M2	M2	M2	M2	M2	M3	M3	M3	M3	M3	M3	M3	M3	M3	M3	M3	M3
		6744	6744	6744	6746	6746	6746	3038	3038	3038	4537	4537	4537	6947	6947	6947	9062	9062	9062
NM_002841.2	PTPRG	2	0	0	1	0	1	9	15	10	13	13	9	24	19	34	8	10	12
NM_145256.2	LRRC25	2	5	3	6	7	4	12	8	15	1	3	2	2	0	2	3	4	4
NM_001972.2	ELA2	3	4	2	95	107	87	239	263	283	109	91	101	325	245	353	438	351	372
NM_000597.2	IGFBP2	23	24	22	13	16	9	115	95	106	319	350	341	435	336	516	525	491	537
NM_005413.1	SIX3	3	7	7	7	8	4	16	16	12	24	27	27	4	4	9	21	22	18
NM_006272.1	S100B	3	19	14	8	19	7	23	32	25	134	126	135	43	26	43	196	165	213
NM_003327.2	TNFRSF4	0	1	3	1	0	1	0	5	0	20	17	18	16	12	16	16	11	8
NM_004049.2	BCL2A1	35	50	35	37	35	28	13	16	10	9	8	11	11	11	11	20	12	20
NM_001911.2	CTSG	107	103	108	6	5	7	671	707	634	156	144	163	534	434	617	2104	2089	2080
NM_001557.2	IL8RB	6	7	3	4	6	4	1	5	5	5	5	2	2	0	2	1	4	8
NM_001066.2	TNFRSF1B	11	18	11	20	12	13	14	11	7	5	4	6	6	8	4	5	6	6
NM_002046.3	GAPDH	2778	3455	3297	2787	2900	1919	4007	4085	3661	3195	2812	2996	4026	3047	4763	5197	5040	5239
NM_006169.2	NNMT	2	1	1	0	1	1	10	5	4	13	19	15	5	5	5	13	15	9
NM_015381.3	FAM19A5	0	1	0	1	0	1	2	3	2	12	7	11	2	5	5	17	17	17
NM_015136.2	STAB1	47	83	70	11	12	7	529	611	518	245	195	255	546	510	721	667	681	697
NM_002029.3	FPR1	2	3	4	11	4	5	3	9	4	2	4	2	6	4	7	14	8	3
NM_003930.3	SCAP2	16	25	24	12	16	7	1	3	1	3	3	7	1	0	2	3	3	5
NM_006486.2	FBLN1	1	3	0	0	0	0	0	0	2	10	6	6	0	2	1	4	6	10
NM_153206.1	AMICA1	0	0	1	0	0	1	0	0	0	2	0	0	2	0	0	1	1	0
NM_002965.2	S100A9	57	53	39	243	238	165	44	63	54	30	20	23	28	28	48	96	84	107
NM_021209.3	CARD12/NLRC4	2	3	3	4	3	4	1	3	2	5	3	2	0	1	2	2	1	3
NM_000433.2	NCF2	19	22	32	31	32	21	29	27	29	21	26	19	28	20	43	38	27	37
NM_003489.2	NRIP1	73	79	63	19	26	15	4	3	4	3	1	2	2	3	1	4	6	4
NM_001040084.1	LOC653107/ANXA8	1	3	0	1	4	0	60	55	72	33	39	62	243	201	301	45	37	41
NM_016582.1	SLC15A3	2	2	1	1	2	2	1	5	2	1	3	3	1	1	2	8	2	1
NM_000211.2	ITGB2	106	141	126	51	55	37	215	223	175	32	28	28	21	13	21	33	33	41
NM_000601.4	HGF	27	24	19	37	40	21	621	778	666	612	606	574	962	719	1118	940	931	887
NM_001042729.1	FGR	39	35	35	17	12	14	67	54	48	12	7	5	7	4	5	5	9	6
NM_001614.2	ACTG1	1849	2445	2162	2086	2190	1507	3295	3953	3430	1900	1984	1935	2937	2469	3799	4984	4897	4826
NM_138444.2	KCTD12	3	10	4	2	1	4	5	3	4	2	1	2	5	0	1	5	5	4
NM_002964.3	S100A8	100	111	99	662	662	416	119	203	128	31	47	44	89	84	101	149	138	147
NM_001025109.1	CD34	157	167	205	288	274	202	3	5	4	2	0	2	0	3	3	12	10	10
NM_000474.3	TWIST1	0	1	1	9	6	4	11	7	13	7	10	11	17	15	24	44	45	41
NM_015869.3	PPARG	2	0	2	1	2	2	17	16	12	24	30	30	33	20	32	28	27	23
NM_004666.1	VNN1	15	29	19	1	2	4	1	3	0	1	1	1	3	0	0	3	1	1
NM_005874.1	LILRB2	17	29	24	19	22	12	21	26	17	10	11	10	13	6	9	18	23	15
NM_001005463.1	EBF3	3	2	2	5	0	2	15	14	13	8	6	7	11	12	6	8	23	14
NM_152852.1	MS4A6A	6	3	3	2	3	2	1	1	2	0	5	3	4	2	1	2	2	0

Supplemental Table 2. Data from nCounter assays of AML samples and normal CD34+, promyelocytes, and neutrophils (PMNs).

Accession No.	Gene Name/Sample ID	M2	M2	M2	M2	M2	M2	M3	M3	M3	M3	M3	M3	M3	M3	M3	M3	M3	M3
		6744	6744	6744	6746	6746	6746	3038	3038	3038	4537	4537	4537	6947	6947	6947	9062	9062	9062
NM_000954.5	PTGDS	0	0	0	1	0	0	114	119	116	12	11	13	70	42	78	66	39	45
NM_000222.1	KIT	43	59	60	70	76	49	28	38	39	28	24	29	49	30	45	43	39	43
NM_004961.3	GABRE	1	1	1	0	3	1	21	31	17	2	7	3	24	28	26	11	8	8
NM_007261.2	CD300A	5	5	6	4	2	0	4	3	5	3	4	2	3	4	3	9	10	19
NM_002115.1	HK3	0	3	1	4	5	1	4	8	6	2	2	5	1	7	4	5	5	8
NM_023914.2	P2RY13	5	3	6	31	25	21	4	4	6	2	6	3	5	6	3	7	7	8
NM_033642.1	FGF13	0	2	2	1	3	5	22	15	11	9	16	9	29	20	25	25	24	20

AF324996.2	Athal_Spike_S23	1800	1810	1818	1792	1814	1808	1784	1759	1759	1820	1806	1800	1861	1772	1760	1810	1851	1792
AF325027.2	Athal_Spike_S14	760	783	776	794	754	757	782	812	803	729	753	782	741	803	801	757	744	748
AF325042.2	Athal_Spike_S19	530	516	504	512	507	524	512	484	490	533	517	512	502	547	507	525	481	486
AY058560.1	DrosSpike8	201	175	194	171	189	179	166	195	211	181	165	174	167	177	208	174	179	194
AF325027.2	Athal_Spike_S13	70	66	63	79	77	65	64	80	65	87	85	75	85	69	76	66	87	86
AF324998.2	Athal_Spike_S22	70	90	86	98	84	87	112	112	96	92	93	80	90	79	83	90	96	110
AY058658.1	DrosSpike7	28	26	23	22	31	39	34	30	32	25	32	27	21	24	29	37	26	36
AF325032.2	Athal_Spike_S17	29	26	23	21	32	32	38	24	29	22	35	33	23	16	27	29	28	33
DQ412624	SarsSpike3	7	4	7	9	9	4	3	1	10	6	9	11	5	9	7	8	3	10
AY058658.1	DrosSpike6	4	3	3	2	4	3	2	3	3	4	4	6	4	4	1	2	6	4
AY058560.1	DrosSpike10	1	0	2	1	1	1	0	1	6	1	0	2	2	2	1	1	1	1
AY058658.1	DrosSpike11	1	0	2	1	1	3	3	1	2	2	2	4	4	4	0	0	3	1
AF325014.2	Athal_Spike_S12	3	3	3	6	4	3	2	1	6	1	7	2	4	4	5	5	4	4
AF325016.2	Athal_Spike_S15	4	3	8	2	5	4	8	5	9	2	4	5	9	2	5	8	4	0
AF325016.2	Athal_Spike_S16	3	3	2	2	2	4	4	4	2	7	4	3	4	2	3	7	3	3
AF325032.2	Athal_Spike_S18	5	0	1	3	1	4	0	3	3	3	2	2	2	2	2	6	2	8
AF324998.2	Athal_Spike_S20	4	4	6	4	5	3	7	4	2	3	4	2	0	4	2	2	5	6
AF324998.2	Athal_Spike_S21	4	1	0	5	4	2	2	3	8	2	6	5	3	3	6	6	7	4
AF324998.2	Athal_Spike_S24	3	1	2	3	4	1	5	3	7	6	2	2	7	3	3	3	3	4
DQ412624	SarsSpike4	2	3	2	5	4	6	5	4	6	2	4	7	13	5	7	4	0	5
AY058560.1	DrosSpike9	2	2	1	1	1	1	1	0	3	2	0	0	2	2	0	2	2	1

Supplemental Table 2. Data from nCounter assays of AML samples and normal CD34+, promyelocytes, and neutrophils (PMNs).

Accession No.	Gene Name/Sample ID	M3	M3	M3	M3	M3	M3	M3	M3	M3	M3	M3	M3	M3	M3	M3
		15590	15590	15590	15591	15591	15591	15605	15605	15605	16060	16060	16060	17932	17932	17932
NM_002841.2	PTPRG	5	5	3	9	15	10	29	16	28	12	12	12	15	16	13
NM_145256.2	LRRC25	1	2	1	1	2	0	3	1	1	1	0	2	4	3	3
NM_001972.2	ELA2	388	408	352	183	192	186	213	215	319	219	164	124	175	131	174
NM_000597.2	IGFBP2	269	302	261	268	264	255	369	376	550	327	329	294	327	342	285
NM_005413.1	SIX3	34	22	18	15	14	13	78	71	133	46	37	32	30	29	18
NM_006272.1	S100B	108	113	122	44	36	39	86	86	116	92	101	93	66	87	78
NM_003327.2	TNFRSF4	16	18	23	11	6	3	73	50	87	29	32	49	7	4	6
NM_004049.2	BCL2A1	13	23	10	7	7	16	22	16	23	28	18	18	11	21	21
NM_001911.2	CTSG	829	976	939	610	646	613	1207	1252	1899	1650	1378	1236	448	447	370
NM_001557.2	IL8RB	5	3	4	2	1	2	6	4	7	2	4	6	1	1	3
NM_001066.2	TNFRSF1B	3	6	0	5	3	2	11	3	9	3	2	0	27	24	19
NM_002046.3	GAPDH	5816	6194	5803	2568	2787	2293	5517	5467	8500	6921	6006	5285	7955	8067	6548
NM_006169.2	NNMT	12	23	24	5	4	2	9	19	15	51	51	49	11	18	15
NM_015381.3	FAM19A5	17	23	21	21	20	15	29	42	65	7	8	10	48	54	43
NM_015136.2	STAB1	550	530	569	796	891	693	998	842	1295	886	879	832	977	933	766
NM_002029.3	FPR1	5	6	4	4	4	3	9	8	6	19	15	10	11	10	7
NM_003930.3	SCAP2	0	4	2	2	4	1	9	9	20	0	0	0	0	9	1
NM_006486.2	FBLN1	1	4	1	2	1	3	3	6	4	8	1	4	0	1	0
NM_153206.1	AMICA1	0	2	0	0	0	0	0	1	1	3	2	0	0	1	0
NM_002965.2	S100A9	16	25	20	9	4	10	5	5	4	46	55	35	194	219	179
NM_021209.3	CARD12/NLRC4	3	4	4	2	0	2	0	3	5	3	1	0	6	7	9
NM_000433.2	NCF2	26	22	23	18	26	14	31	17	20	31	18	12	82	84	65
NM_003489.2	NRIP1	16	6	8	3	3	2	6	7	14	8	9	2	10	3	9
NM_001040084.1	LOC653107/ANXA8	81	103	80	98	99	73	56	83	114	195	189	209	18	24	21
NM_016582.1	SLC15A3	1	5	4	2	2	1	1	2	6	2	1	6	7	6	9
NM_000211.2	ITGB2	16	21	23	11	7	22	29	27	54	13	15	6	84	90	72
NM_000601.4	HGF	828	884	785	527	522	470	1096	1000	1504	2554	2173	2297	896	873	723
NM_001042729.1	FGR	6	3	5	6	3	8	4	7	13	6	7	0	55	41	58
NM_001614.2	ACTG1	4636	4778	4599	2180	2432	2034	5431	4789	6845	3736	3420	3430	6033	5898	4910
NM_138444.2	KCTD12	5	2	6	2	0	1	5	3	4	1	5	8	11	4	15
NM_002964.3	S100A8	32	34	34	14	15	13	18	7	19	74	65	83	483	435	419
NM_001025109.1	CD34	3	5	4	2	2	2	5	7	9	0	2	4	4	1	3
NM_000474.3	TWIST1	48	47	37	15	13	14	11	24	27	18	18	20	46	31	38
NM_015869.3	PPARG	53	48	41	19	15	13	26	23	24	33	21	41	58	38	30
NM_004666.1	VNN1	3	2	4	2	1	1	4	3	6	3	4	2	1	6	3
NM_005874.1	LILRB2	5	12	14	5	6	2	5	9	16	10	16	10	39	25	25
NM_001005463.1	EBF3	61	65	55	20	29	16	11	21	29	70	69	49	92	103	69
NM_152852.1	MS4A6A	3	6	4	0	3	1	1	1	3	3	3	2	3	1	1

Supplemental Table 2. Data from nCounter assays of AML samples and normal CD34+, promyelocytes, and neutrophils (PMNs).

Accession No.	Gene Name/Sample ID	M3	M3	M3	M3	M3	M3	M3	M3	M3	M3	M3	M3	M3	M3	M3
		15590	15590	15590	15591	15591	15591	15605	15605	15605	16060	16060	16060	16060	17932	17932
NM_000954.5	PTGDS	32	29	21	49	50	59	36	36	66	17	16	10	7	13	7
NM_000222.1	KIT	68	81	72	37	46	35	57	66	69	46	21	32	86	84	59
NM_004961.3	GABRE	5	6	15	5	13	7	29	22	23	27	25	20	24	25	19
NM_007261.2	CD300A	1	6	8	4	6	5	9	4	9	3	7	10	15	10	3
NM_002115.1	HK3	3	10	9	2	3	3	4	6	4	6	4	4	4	0	7
NM_023914.2	P2RY13	12	9	10	2	5	0	6	6	9	6	4	6	13	10	12
NM_033642.1	FGF13	26	32	28	12	13	18	24	12	23	25	20	16	34	22	19

AF324996.2	Athal_Spike_S23	1816	1849	1821	1795	1877	1782	1808	1839	1795	1865	1797	1835	1801	1849	1889
AF325027.2	Athal_Spike_S14	754	755	802	799	758	757	796	789	787	754	760	806	750	709	741
AF325042.2	Athal_Spike_S19	542	501	491	519	475	542	505	464	518	478	532	447	504	499	491
AY058560.1	DrosSpike8	162	170	154	154	185	186	152	164	184	161	191	203	197	194	167
AF325027.2	Athal_Spike_S13	69	62	72	78	76	75	70	88	82	97	68	55	66	79	65
AF324998.2	Athal_Spike_S22	94	90	99	90	69	83	89	90	61	85	85	87	103	97	100
AY058658.1	DrosSpike7	27	30	23	28	28	37	28	30	27	28	24	37	34	25	16
AF325032.2	Athal_Spike_S17	27	31	25	25	25	25	29	26	27	21	30	12	34	31	24
DQ412624	SarsSpike3	4	6	11	9	4	8	15	3	10	9	12	12	4	12	4
AY058658.1	DrosSpike6	4	4	3	2	2	3	6	5	7	1	0	6	6	3	1
AY058560.1	DrosSpike10	1	4	0	2	0	3	4	0	2	2	3	2	0	1	1
AY058658.1	DrosSpike11	3	0	1	1	0	2	1	1	3	2	2	2	0	1	4
AF325014.2	Athal_Spike_S12	5	2	8	4	1	0	4	3	7	4	4	6	1	3	4
AF325016.2	Athal_Spike_S15	8	9	7	4	6	5	13	4	3	2	5	8	4	6	3
AF325016.2	Athal_Spike_S16	3	0	1	0	3	0	4	2	4	0	10	2	6	1	4
AF325032.2	Athal_Spike_S18	3	4	5	2	3	1	0	3	4	3	2	10	4	4	6
AF324998.2	Athal_Spike_S20	12	5	7	2	3	7	4	1	2	0	2	2	6	0	1
AF324998.2	Athal_Spike_S21	10	3	5	4	6	1	3	5	4	4	5	2	0	6	3
AF324998.2	Athal_Spike_S24	0	3	4	4	4	2	4	2	4	3	5	0	3	1	1
DQ412624	SarsSpike4	1	2	7	5	4	8	14	5	5	3	5	4	3	6	6
AY058560.1	DrosSpike9	1	0	1	0	1	1	0	1	2	1	1	0	0	1	0

Supplemental Table 2. Data from nCounter assays of AML samples and normal CD34+, promyelocytes, and neutrophils (PMNs).

Accession No.	Gene Name/Sample ID	M3	M3	M3	M3	M3	M3	M4	M4	M4	M4	M4	M4	M4	M4	M4
		20898	20898	20898	20899	20899	20899	6039	6039	6039	15601	15601	15601	15602	15602	15602
NM_002841.2	PTPRG	12	12	7	27	19	19	1	2	2	0	1	4	2	2	2
NM_145256.2	LRRC25	4	1	2	2	2	5	34	19	22	28	24	20	94	118	104
NM_001972.2	ELA2	816	760	761	380	423	365	39	32	33	78	78	68	7	9	15
NM_000597.2	IGFBP2	280	236	223	1167	1011	1171	12	13	9	57	55	48	33	28	30
NM_005413.1	SIX3	76	70	73	70	67	65	0	4	9	6	5	1	3	5	3
NM_006272.1	S100B	179	189	149	362	356	406	2	0	1	8	16	11	6	9	8
NM_003327.2	TNFRSF4	39	26	28	79	79	87	0	4	0	4	0	1	7	2	4
NM_004049.2	BCL2A1	17	19	20	23	8	23	28	25	19	47	46	35	180	199	180
NM_001911.2	CTSG	3320	3186	2917	714	790	754	6	10	8	9	14	12	155	183	164
NM_001557.2	IL8RB	8	3	3	2	2	4	2	4	4	6	5	4	8	12	17
NM_001066.2	TNFRSF1B	7	16	5	14	14	23	153	142	143	126	106	92	440	460	432
NM_002046.3	GAPDH	7659	6995	6260	7903	7728	8005	3409	3494	3539	4175	4256	3942	4328	4325	4464
NM_006169.2	NNMT	138	95	102	42	59	53	4	4	3	10	8	8	1	3	2
NM_015381.3	FAM19A5	9	6	6	14	14	15	1	3	1	0	3	4	1	4	2
NM_015136.2	STAB1	571	531	453	710	591	690	57	58	53	23	34	24	214	223	218
NM_002029.3	FPR1	6	6	2	10	5	7	28	40	32	27	35	20	64	81	57
NM_003930.3	SCAP2	2	2	1	0	3	5	19	25	13	24	21	12	30	34	42
NM_006486.2	FBLN1	19	13	7	2	2	4	0	4	1	0	0	0	2	1	1
NM_153206.1	AMICA1	0	0	0	1	0	1	1	1	3	1	1	0	2	0	3
NM_002965.2	S100A9	21	23	16	53	46	44	1589	1610	1490	2243	2078	1948	1550	1667	1472
NM_021209.3	CARD12/NLRC4	5	0	5	8	2	8	24	19	28	14	13	23	39	46	33
NM_000433.2	NCF2	37	37	40	88	79	101	179	185	173	114	115	110	317	324	344
NM_003489.2	NRIP1	1	0	5	2	3	1	18	31	23	34	21	18	34	41	38
NM_001040084.1	LOC653107/ANXA8	19	19	10	203	212	218	7	4	6	6	5	3	3	1	2
NM_016582.1	SLC15A3	1	6	2	6	5	4	11	24	25	13	17	14	31	36	36
NM_000211.2	ITGB2	28	13	19	45	63	35	362	360	329	259	233	269	754	706	775
NM_000601.4	HGF	2321	2146	1725	3477	3564	3492	68	62	71	139	104	108	28	30	28
NM_001042729.1	FGR	15	8	3	21	29	35	275	267	252	176	164	200	591	602	611
NM_001614.2	ACTG1	5367	4817	4064	7911	7974	7995	2761	2655	2513	3267	2964	2951	3764	3904	3747
NM_138444.2	KCTD12	4	5	7	4	6	12	58	64	67	84	72	60	74	73	70
NM_002964.3	S100A8	50	38	30	107	87	87	2883	2798	2649	4377	3984	3749	3220	3314	3276
NM_001025109.1	CD34	5	8	7	14	14	11	6	12	18	55	68	76	8	8	5
NM_000474.3	TWIST1	31	19	24	18	11	18	4	3	2	3	2	2	8	2	4
NM_015869.3	PPARG	14	15	8	17	5	15	2	2	3	6	5	6	4	6	7
NM_004666.1	VNN1	4	2	1	1	3	3	23	19	23	3	3	3	54	56	47
NM_005874.1	LILRB2	9	5	3	16	25	27	100	112	118	75	69	74	487	473	440
NM_001005463.1	EBF3	11	18	12	45	59	49	1	2	2	10	5	4	3	3	2
NM_152852.1	MS4A6A	2	7	2	5	0	5	33	33	23	26	23	21	28	28	41

Supplemental Table 2. Data from nCounter assays of AML samples and normal CD34+, promyelocytes, and neutrophils (PMNs).

Accession No.	Gene Name/Sample ID	M3	M3	M3	M3	M3	M3	M4	M4	M4	M4	M4	M4	M4	M4	
		20898	20898	20898	20899	20899	20899	6039	6039	6039	15601	15601	15601	15602	15602	15602
NM_000954.5	PTGDS	4	6	12	21	25	31	1	2	3	1	2	0	0	0	0
NM_000222.1	KIT	88	84	86	17	17	19	12	10	17	59	65	56	23	30	24
NM_004961.3	GABRE	0	1	2	12	10	11	2	2	4	2	7	3	4	4	2
NM_007261.2	CD300A	13	7	5	7	11	3	0	4	2	12	4	8	17	14	9
NM_002115.1	HK3	7	2	6	1	6	4	24	12	14	6	12	12	25	29	36
NM_023914.2	P2RY13	11	4	7	7	2	4	39	51	46	52	56	60	94	105	91
NM_033642.1	FGF13	37	40	27	28	32	18	2	2	1	2	0	3	2	1	1

AF324996.2	Athal_Spike_S23	1863	1832	1850	1875	1833	1819	1801	1816	1872	1825	1866	1883	1858	1859	1909
AF325027.2	Athal_Spike_S14	754	699	745	737	768	768	811	734	689	761	766	676	730	744	713
AF325042.2	Athal_Spike_S19	489	514	515	472	464	516	483	540	527	521	506	516	501	501	497
AY058560.1	DrosSpike8	155	201	168	174	208	195	190	183	183	166	165	196	190	187	173
AF325027.2	Athal_Spike_S13	67	92	71	60	62	60	66	69	66	76	69	77	84	74	61
AF324998.2	Athal_Spike_S22	79	91	89	97	79	76	84	88	93	90	65	81	84	81	89
AY058658.1	DrosSpike7	32	29	31	25	25	29	32	22	26	23	28	31	21	23	21
AF325032.2	Athal_Spike_S17	38	24	17	37	51	30	26	36	36	23	29	29	23	25	27
DQ412624	SarsSpike3	18	11	9	18	5	4	6	6	5	10	4	6	5	4	5
AY058658.1	DrosSpike6	5	6	5	4	5	3	2	5	2	5	3	4	4	0	4
AY058560.1	DrosSpike10	2	3	1	2	2	0	5	1	3	3	1	2	2	1	0
AY058658.1	DrosSpike11	2	0	6	2	0	1	1	3	0	2	0	3	2	0	2
AF325014.2	Athal_Spike_S12	5	6	6	5	8	7	2	6	5	2	5	3	5	3	3
AF325016.2	Athal_Spike_S15	5	6	5	4	2	5	1	1	1	6	5	10	2	0	5
AF325016.2	Athal_Spike_S16	2	3	8	4	0	5	2	3	4	1	5	3	3	2	5
AF325032.2	Athal_Spike_S18	5	3	3	5	10	3	7	3	2	2	5	8	2	5	4
AF324998.2	Athal_Spike_S20	6	4	3	4	3	5	2	1	4	4	3	6	1	5	5
AF324998.2	Athal_Spike_S21	1	3	7	0	5	5	2	4	3	5	4	3	3	5	4
AF324998.2	Athal_Spike_S24	6	2	1	2	5	1	5	3	3	3	2	4	3	6	2
DQ412624	SarsSpike4	1	7	0	7	2	10	4	7	3	3	4	6	6	7	3
AY058560.1	DrosSpike9	0	1	0	4	2	3	0	2	0	4	1	1	0	1	2

Supplemental Table 2. Data from nCounter assays of AML samples and normal CD34+, promyelocytes, and neutrophils (PMNs).

Accession No.	Gene Name/Sample ID	M4	M4	M4	CD34	CD34	CD34	CD34	CD34	CD34	Pros	Pros	Pros	Pros	Pros
		20896	20896	20896	6	6	6	7	7	7	109055	109055	109055	109058	109058
NM_002841.2	PTPRG	1	1	0	1	1	1	0	0	7	8	13	9	10	9
NM_145256.2	LRRC25	14	8	18	1	1	2	3	3	0	17	15	10	28	25
NM_001972.2	ELA2	28	15	12	12	39	28	13	18	18	1199	1075	1244	868	789
NM_000597.2	IGFBP2	7	13	12	14	21	12	15	18	22	26	21	18	74	73
NM_005413.1	SIX3	1	0	2	1	0	3	4	1	0	57	44	55	55	63
NM_006272.1	S100B	25	19	15	3	5	3	0	0	4	10	10	11	4	0
NM_003327.2	TNFRSF4	1	0	1	2	0	0	0	1	0	3	5	2	2	2
NM_004049.2	BCL2A1	39	34	24	23	34	41	35	49	49	88	74	78	124	147
NM_001911.2	CTSG	222	220	205	100	90	97	48	43	60	2067	1769	1995	1946	1977
NM_001557.2	IL8RB	6	13	11	2	2	6	6	5	0	16	18	10	21	27
NM_001066.2	TNFRSF1B	90	58	78	17	16	12	9	11	9	44	44	37	63	86
NM_002046.3	GAPDH	5168	5296	5129	3824	4716	4995	3221	3288	3670	7616	6498	7234	6988	7429
NM_006169.2	NNMT	3	2	4	3	0	1	4	5	7	13	12	12	6	11
NM_015381.3	FAM19A5	1	1	0	15	12	19	3	4	0	9	7	6	7	14
NM_015136.2	STAB1	54	72	58	4	5	3	5	4	7	9	7	10	14	11
NM_002029.3	FPR1	21	28	21	8	9	7	6	4	4	22	27	9	27	25
NM_003930.3	SCAP2	20	26	18	17	12	13	14	5	4	32	18	15	41	16
NM_006486.2	FBLN1	0	1	0	2	0	1	1	0	0	1	2	2	2	2
NM_153206.1	AMICA1	0	0	3	1	1	1	1	0	0	12	1	5	10	2
NM_002965.2	S100A9	619	642	542	60	90	98	107	123	116	12420	11305	11278	13705	14343
NM_021209.3	CARD12/NLRC4	6	3	8	4	2	4	3	0	2	67	74	72	70	102
NM_000433.2	NCF2	120	151	154	14	12	33	18	34	24	271	260	227	334	358
NM_003489.2	NRIP1	22	28	19	130	146	149	70	86	109	40	27	32	35	48
NM_001040084.1	LOC653107/ANXA8	4	4	1	0	4	1	1	4	0	14	4	9	22	41
NM_016582.1	SLC15A3	7	8	4	4	6	0	5	4	2	28	18	21	33	23
NM_000211.2	ITGB2	283	247	216	67	72	83	39	32	44	554	450	499	658	655
NM_000601.4	HGF	78	68	87	23	44	39	18	23	18	21	10	15	31	20
NM_001042729.1	FGR	259	233	216	11	13	15	8	12	9	948	829	888	1172	1043
NM_001614.2	ACTG1	3575	3698	3542	3295	3986	4302	2823	3171	3121	4404	3904	3926	5081	5345
NM_138444.2	KCTD12	24	9	12	9	16	10	9	9	18	30	21	23	37	23
NM_002964.3	S100A8	1046	1055	967	169	195	228	301	339	371	39038	34512	34841	42709	46190
NM_001025109.1	CD34	39	23	29	112	118	149	54	61	62	4	4	7	1	2
NM_000474.3	TWIST1	4	1	3	4	5	10	1	4	4	22	14	16	22	9
NM_015869.3	PPARG	0	1	3	2	5	3	3	4	11	41	30	28	51	50
NM_004666.1	VNN1	17	18	15	3	2	3	3	5	0	14	17	16	12	9
NM_005874.1	LILRB2	39	54	48	35	34	33	42	31	42	177	162	155	189	177
NM_001005463.1	EBF3	6	4	4	2	8	3	3	3	7	12	7	10	11	11
NM_152852.1	MS4A6A	36	40	35	5	11	5	8	5	9	6	5	4	7	11

Supplemental Table 2. Data from nCounter assays of AML samples and normal CD34+, promyelocytes, and neutrophils (PMNs).

Accession No.	Gene Name/Sample ID	M4	M4	M4	CD34	CD34	CD34	CD34	CD34	CD34	Pros	Pros	Pros	Pros	Pros
		20896	20896	20896	6	6	6	7	7	7	109055	109055	109055	109058	109058
NM_000954.5	PTGDS	0	0	1	0	0	1	0	3	0	2	1	0	2	0
NM_000222.1	KIT	15	18	12	37	51	52	33	23	22	7	4	5	4	14
NM_004961.3	GABRE	0	2	4	1	4	3	0	0	2	12	23	17	25	18
NM_007261.2	CD300A	3	3	2	7	12	14	4	5	2	12	4	7	6	5
NM_002115.1	HK3	8	3	2	0	0	1	1	4	2	40	42	37	51	70
NM_023914.2	P2RY13	37	37	35	9	21	12	10	8	13	157	125	161	190	224
NM_033642.1	FGF13	1	1	0	4	0	3	3	0	2	15	25	27	4	7

AF324996.2	Athal_Spike_S23	1778	1871	1905	1838	1881	1839	1782	1827	1731	1797	1875	1830	1825	1907
AF325027.2	Athal_Spike_S14	757	722	717	741	704	736	732	759	755	669	659	703	753	621
AF325042.2	Athal_Spike_S19	595	503	496	491	550	521	517	483	544	580	538	525	530	510
AY058560.1	DrosSpike8	155	170	165	190	145	178	187	167	202	195	166	197	150	163
AF325027.2	Athal_Spike_S13	69	69	79	72	64	85	89	77	73	75	83	71	75	86
AF324998.2	Athal_Spike_S22	85	100	87	82	90	81	117	101	98	98	88	94	89	98
AY058658.1	DrosSpike7	20	26	25	46	29	20	33	36	42	41	35	38	32	34
AF325032.2	Athal_Spike_S17	30	22	13	25	26	25	36	34	47	26	38	28	25	68
DQ412624	SarsSpike3	9	11	9	8	7	10	5	9	4	12	8	6	12	7
AY058658.1	DrosSpike6	1	4	3	6	4	3	0	4	2	6	8	7	7	5
AY058560.1	DrosSpike10	4	1	1	0	0	0	3	1	2	3	4	4	4	2
AY058658.1	DrosSpike11	8	1	4	1	1	0	0	0	0	8	4	4	1	7
AF325014.2	Athal_Spike_S12	2	2	4	5	2	5	0	5	0	4	7	7	10	5
AF325016.2	Athal_Spike_S15	2	6	1	3	6	3	0	4	0	6	10	9	9	14
AF325016.2	Athal_Spike_S16	4	3	2	1	2	3	1	3	0	3	4	1	7	14
AF325032.2	Athal_Spike_S18	0	2	3	2	4	4	3	0	0	34	30	29	27	32
AF324998.2	Athal_Spike_S20	4	3	0	1	1	4	1	1	0	2	4	6	4	5
AF324998.2	Athal_Spike_S21	4	1	2	1	2	5	3	4	4	7	8	4	0	5
AF324998.2	Athal_Spike_S24	6	2	5	3	2	5	0	3	0	15	14	17	11	20
DQ412624	SarsSpike4	4	2	3	5	2	4	3	4	4	6	7	7	7	5
AY058560.1	DrosSpike9	1	1	1	2	0	0	0	0	2	5	1	4	5	0

Supplemental Table 2. Data from nCounter assays of AML samples and normal CD34+, promyelocytes, and neutrophils (PMNs).

Accession No.	Gene Name/Sample ID	Pros	Pros	Pros	Pros	Pros	Pros	Pros	Pros	Pros	Pros	PMNs	PMNs
		109058	114099	114099	114099	114100	114100	114100	114101	114101	114101	114101	109057
NM_002841.2	PTPRG	17	8	5	8	8	2	10	9	13	9	12	12
NM_145256.2	LRRC25	28	6	11	5	9	2	7	13	15	13	249	266
NM_001972.2	ELA2	867	216	247	272	354	259	317	310	324	323	47	35
NM_000597.2	IGFBP2	55	7	11	9	27	4	21	13	15	15	12	16
NM_005413.1	SIX3	64	48	52	60	77	4	67	104	86	80	61	43
NM_006272.1	S100B	6	1	2	5	4	0	2	6	6	2	5	8
NM_003327.2	TNFRSF4	5	3	2	4	4	0	2	5	5	4	5	9
NM_004049.2	BCL2A1	125	44	56	65	74	50	74	135	122	121	3264	2915
NM_001911.2	CTSG	1973	431	433	445	556	167	553	729	703	668	73	65
NM_001557.2	IL8RB	32	21	20	23	22	0	15	31	36	28	2153	1982
NM_001066.2	TNFRSF1B	65	75	69	69	75	59	59	115	111	104	1273	1202
NM_002046.3	GAPDH	7887	2952	3264	3296	3723	1530	3410	5675	5553	5591	3016	2697
NM_006169.2	NNMT	11	15	14	11	14	2	10	15	17	17	16	7
NM_015381.3	FAM19A5	10	4	6	7	5	1	4	14	11	10	12	3
NM_015136.2	STAB1	14	4	8	8	6	1	7	12	10	10	16	7
NM_002029.3	FPR1	45	19	22	19	29	16	30	96	96	85	2864	2610
NM_003930.3	SCAP2	30	11	11	12	18	8	9	22	22	25	56	60
NM_006486.2	FBLN1	3	2	3	1	1	0	0	1	1	1	2	0
NM_153206.1	AMICA1	4	11	14	12	11	6	15	20	20	20	17	14
NM_002965.2	S100A9	14743	3636	4143	4066	4738	520	4224	6612	6592	6666	18402	16585
NM_021209.3	CARD12/NLRC4	75	82	91	85	79	31	74	113	118	100	21	43
NM_000433.2	NCF2	374	167	153	171	198	93	199	288	319	267	2950	2698
NM_003489.2	NRIP1	42	13	19	24	25	2	31	37	33	33	19	27
NM_001040084.1	LOC653107/ANXA8	31	9	7	7	18	4	19	14	18	15	12	15
NM_016582.1	SLC15A3	34	18	12	18	19	3	18	32	24	17	185	190
NM_000211.2	ITGB2	763	294	322	344	386	143	339	513	504	500	1534	1479
NM_000601.4	HGF	30	10	11	8	13	4	11	20	11	15	16	18
NM_001042729.1	FGR	1256	968	990	1036	1004	1322	1018	1616	1601	1554	2959	2560
NM_001614.2	ACTG1	5497	1856	2023	2143	2709	1644	2497	3200	3382	3364	4005	3317
NM_138444.2	KCTD12	42	13	13	12	13	2	21	26	20	17	42	81
NM_002964.3	S100A8	47216	16732	18504	18732	20596	5219	18606	28528	28884	28963	38217	33320
NM_001025109.1	CD34	5	10	11	13	16	14	10	13	13	10	7	7
NM_000474.3	TWIST1	17	12	24	17	15	5	20	27	29	26	17	18
NM_015869.3	PPARG	49	27	34	33	41	2	26	40	43	51	33	31
NM_004666.1	VNN1	13	11	9	8	11	1	9	31	35	30	44	39
NM_005874.1	LILRB2	183	45	62	63	105	19	78	135	136	132	720	717
NM_001005463.1	EBF3	9	12	19	16	16	12	15	31	22	23	2	9
NM_152852.1	MS4A6A	11	4	2	1	3	1	2	5	6	4	0	4

Supplemental Table 2. Data from nCounter assays of AML samples and normal CD34+, promyelocytes, and neutrophils (PMNs).

Accession No.	Gene Name/Sample ID	Pros	Pros	Pros	Pros	Pros	Pros	Pros	Pros	Pros	Pros	PMNs	PMNs
		109058	114099	114099	114099	114100	114100	114100	114101	114101	114101	114101	109057
NM_000954.5	PTGDS	3	2	1	1	1	1	0	2	2	1	2	1
NM_000222.1	KIT	6	5	1	5	4	1	2	6	9	3	5	4
NM_004961.3	GABRE	18	17	17	22	16	2	17	22	26	24	23	16
NM_007261.2	CD300A	10	3	5	5	5	2	5	10	10	9	21	19
NM_002115.1	HK3	57	22	28	27	23	3	22	34	40	36	44	43
NM_023914.2	P2RY13	189	159	167	176	156	60	147	262	233	241	887	726
NM_033642.1	FGF13	9	5	4	5	9	1	7	13	11	11	2	7

AF324996.2	Athal_Spike_S23	1837	1794	1783	1850	1774	1961	1746	1837	1833	1798	1881	1817
AF325027.2	Athal_Spike_S14	674	377	411	407	424	327	388	381	400	396	657	688
AF325042.2	Athal_Spike_S19	555	620	658	644	637	547	671	634	648	639	528	535
AY058560.1	DrosSpike8	173	184	187	174	164	162	180	173	169	181	160	214
AF325027.2	Athal_Spike_S13	71	208	161	162	182	178	187	152	157	153	61	80
AF324998.2	Athal_Spike_S22	101	155	183	154	161	202	153	136	160	202	119	69
AY058658.1	DrosSpike7	35	22	34	23	33	21	27	35	35	33	31	35
AF325032.2	Athal_Spike_S17	35	116	55	55	91	82	119	98	62	61	47	46
DQ412624	SarsSpike3	11	11	13	15	20	12	14	20	16	15	9	14
AY058658.1	DrosSpike6	8	13	15	15	14	7	13	32	18	20	5	1
AY058560.1	DrosSpike10	5	8	8	9	12	2	9	8	10	14	2	4
AY058658.1	DrosSpike11	14	9	13	8	8	4	11	14	13	18	2	5
AF325014.2	Athal_Spike_S12	11	3	9	3	11	2	7	5	9	12	12	8
AF325016.2	Athal_Spike_S15	6	3	5	6	6	2	7	7	7	8	9	5
AF325016.2	Athal_Spike_S16	2	8	7	4	14	5	8	16	11	13	9	14
AF325032.2	Athal_Spike_S18	36	26	30	26	35	6	25	47	36	37	23	33
AF324998.2	Athal_Spike_S20	3	0	0	0	0	0	0	0	0	0	5	7
AF324998.2	Athal_Spike_S21	6	9	7	10	8	2	5	10	10	9	9	5
AF324998.2	Athal_Spike_S24	18	16	17	17	27	3	23	35	31	36	7	23
DQ412624	SarsSpike4	8	10	22	14	15	5	19	17	13	20	5	5
AY058560.1	DrosSpike9	8	5	11	9	10	1	6	15	6	12	2	3

Supplemental Table 2. Data from nCounter assays of AML samples and normal CD34+, promyelocytes, and neutrophils (PMNs).

Accession No.	Gene Name/Sample ID	PMNs	PMNs	PMNs	PMNs	Spike Only	Spike Only	Spike Only
		109057	109583	109583	109583			
NM_002841.2	PTPRG	9	4	6	2	0	0	0
NM_145256.2	LRRC25	208	198	159	180	1	0	0
NM_001972.2	ELA2	38	19	21	7	3	1	2
NM_000597.2	IGFBP2	12	3	4	10	1	4	0
NM_005413.1	SIX3	40	26	35	22	0	0	1
NM_006272.1	S100B	6	1	6	0	1	2	1
NM_003327.2	TNFRSF4	5	3	2	8	1	0	1
NM_004049.2	BCL2A1	2420	1615	1554	1612	2	1	1
NM_001911.2	CTSG	49	46	38	35	0	0	0
NM_001557.2	IL8RB	1803	1273	1220	1311	1	1	1
NM_001066.2	TNFRSF1B	1257	768	788	720	3	5	1
NM_002046.3	GAPDH	2588	1269	1124	1213	1	1	0
NM_006169.2	NNMT	11	10	8	7	0	1	1
NM_015381.3	FAM19A5	4	6	4	3	0	1	0
NM_015136.2	STAB1	4	6	6	3	1	1	0
NM_002029.3	FPR1	2391	1342	1274	1345	0	2	1
NM_003930.3	SCAP2	43	82	43	66	0	0	0
NM_006486.2	FBLN1	2	4	2	0	0	0	0
NM_153206.1	AMICA1	20	7	5	20	1	1	1
NM_002965.2	S100A9	14408	10883	9845	10712	0	0	1
NM_021209.3	CARD12/NLRC4	37	22	19	22	1	0	1
NM_000433.2	NCF2	2364	1581	1531	1616	0	1	2
NM_003489.2	NRIP1	21	11	2	15	0	0	0
NM_001040084.1	LOC653107/ANXA8	12	8	7	5	1	0	0
NM_016582.1	SLC15A3	139	100	74	94	0	0	0
NM_000211.2	ITGB2	1466	753	687	670	1	1	0
NM_000601.4	HGF	14	8	12	19	0	0	1
NM_001042729.1	FGR	2483	1530	1615	1518	3	4	1
NM_001614.2	ACTG1	2889	1479	1383	1486	0	0	0
NM_138444.2	KCTD12	44	17	18	19	0	1	0
NM_002964.3	S100A8	29862	18679	17602	18700	1	0	0
NM_001025109.1	CD34	2	3	4	0	5	8	7
NM_000474.3	TWIST1	20	8	11	12	1	2	1
NM_015869.3	PPARG	31	11	11	17	0	0	0
NM_004666.1	VNN1	30	59	57	56	0	0	0
NM_005874.1	LILRB2	663	369	335	367	0	1	0
NM_001005463.1	EBF3	10	4	4	2	3	4	1
NM_152852.1	MS4A6A	2	6	8	3	1	0	0

Supplemental Table 2. Data from nCounter assays of AML samples and normal CD34+, promyelocytes, and neutrophils (PMNs).

Accession No.	Gene Name/Sample ID	PMNs	PMNs	PMNs	PMNs	Spike Only	Spike Only	Spike Only
		109057	109583	109583	109583			
NM_000954.5	PTGDS	0	0	1	0	0	0	0
NM_000222.1	KIT	1	0	0	0	1	1	0
NM_004961.3	GABRE	14	11	12	12	2	2	1
NM_007261.2	CD300A	23	46	34	62	0	1	0
NM_002115.1	HK3	41	46	33	22	0	0	1
NM_023914.2	P2RY13	736	488	437	456	3	4	3
NM_033642.1	FGF13	4	1	6	7	0	0	0

AF324996.2	Athal_Spike_S23	1874	1840	1847	1875	1815	1882	1863
AF325027.2	Athal_Spike_S14	694	707	694	677	380	428	405
AF325042.2	Athal_Spike_S19	500	513	522	518	653	650	683
AY058560.1	DrosSpike8	191	183	157	197	180	179	180
AF325027.2	Athal_Spike_S13	69	79	72	81	192	141	135
AF324998.2	Athal_Spike_S22	85	102	109	84	154	133	152
AY058658.1	DrosSpike7	37	24	47	20	26	19	22
AF325032.2	Athal_Spike_S17	33	26	33	37	85	56	48
DQ412624	SarsSpike3	11	18	13	8	9	7	9
AY058658.1	DrosSpike6	4	7	6	2	5	4	3
AY058560.1	DrosSpike10	7	0	2	3	2	2	2
AY058658.1	DrosSpike11	2	1	1	3	3	4	3
AF325014.2	Athal_Spike_S12	9	3	4	3	3	4	5
AF325016.2	Athal_Spike_S15	10	3	1	3	3	2	1
AF325016.2	Athal_Spike_S16	2	3	2	0	8	7	5
AF325032.2	Athal_Spike_S18	19	12	15	8	2	2	1
AF324998.2	Athal_Spike_S20	2	0	6	3	0	0	0
AF324998.2	Athal_Spike_S21	4	1	5	8	4	2	2
AF324998.2	Athal_Spike_S24	8	3	9	15	1	1	0
DQ412624	SarsSpike4	6	8	7	2	10	8	3
AY058560.1	DrosSpike9	3	1	2	2	1	3	2

Supplemental Table 3. Detailed sequence information for nCounter CodeSet target regions, capture probes and reporter probes for 73 test (46) and control (28) genes.

Gene Symbol	Target-NSID	Reporter Probe Sequence
ACTG1	NM_001614.2:1615	CCACGGTGTCTGGCCAAAGACATCAGCTAAGAAAGGAAACTGGGTCTTA
AMICA1	NM_153206.1:125	CTTTGCCATCAGCTTTCCAGCCTCTAGGTGCTTCACACAGG
ANXA8	NM_001040084.1:775	GCAATTTTCTCATACTCTTCAAACACTCTCAGCAGGTGAGTGGCACTGCG
BCL2A1	NM_004049.2:80	CTGGTGGAGAGCAAAGTCTTGAGCTGGCTCACCTTGAAGCTGTTGA
CD300A	NM_007261.2:0	CTGCAGGTTCTTCGGCTATTTCTAGTGATGAGACCTCTCCC
CD34	NM_001025109.1:1580	AGTTCTCCAGACCTTGGCTTTCCCCCGTCACACGTTTACCCAAAGAAGA
CTSG	NM_001911.2:160	CAGGGTGACATTTATATTGCTTCCCAGCAATGAGCTGCTGTGACACACA
EBF3	NM_001005463.1:640	CCAGCACGTGGCCGTCCACGTTGACTGTTGTGCGATACAACAACCTGGA
ELA2	NM_001972.2:195	ACCACCCGCACCGCGCGGACGTTTACATTGCGCCACGCAGTG
FAM19A5	NM_015381.3:320	CTCCAGACACGGAAGCATGTCACACCACTGCTTGGTC
FBLN1	NM_006486.2:1260	GCTGGCACTCGTTGACATCGACACACATCCTGCTGATGCCGTCAAATAG
FGF13	NM_033642.1:620	TTCAACAGCACCTGGAGGTAAGGTTCTGTTACAGAGCCCTTCTTTTGGCC
FGR	NM_001042729.1:440	TATTGTTTCAAGATGTGGAACCTTCTCGCCCTTGGTGAAGGTGAGGTCATCC
FPR1	NM_002029.3:350	TGAGGGCGATCAGGAAGACACTTCCGAACAAGTTGATGTCCACTATGGTA
GABRE	NM_004961.3:65	GACAACATCACGGAAGAGGCTTCACTTTGATTCACTGAGGTCCT
GAPDH	NM_002046.3:245	ATCTCGCTCCTGGAAGATGGTGTGGGATTTCCATTGATGACAAGCTTCC
HGF	NM_000601.4:550	AAGCTGTGTTCTGTGGTATCATGGAAGTCCAGGGCTGACATTTGATGCC
HK3	NM_002115.1:495	GTCTGGTGACAAGGAAAGAGAAGCTGAAGCCAAGCTGCAGACCCTGTTT
IGFBP2	NM_000597.2:675	CAAGGTGATGCTTGCCACCCTTGCCCATCTGCCGG
IL8RB	NM_001557.2:2050	CTGAAGTTTTGAGGAAAGCTGCCATACTGTCTTCTGCAGTGGTCACACCA
ITGB2	NM_000211.2:520	CGGAGCAGGTCGCCACCTAGCTTCTTGACATTCCTGA
KCTD12	NM_138444.2:450	CTGCAAGTCCCGCAGGTAATCCAGGATGTAGCGGAAGAGGAA
KIT	NM_000222.1:5	AGATGGTTGAGAAGAGCCTGTCTGGACGCGAAGCAGTAGGAGCAGAACGC
LILRB2	NM_005874.1:595	GGCTGGGAGTTCAGGCATTGTGGGTGTTTCTCTCTTCTTACACAG
LRRC25	NM_145256.2:115	TCTGGTTTGCAGTCCCTGCACAGGTGCAAGTTCTAGAG
MS4A6A	NM_152852.1:65	TCTCAGTCCCATCAACGTTTCTACTTACCTTCTTCTGAAAGTCATC
NCF2	NM_000433.2:160	AGGGACATGATTAGGTAGAAACTAGGAGGCCAAGAGAGCTGCCAGGAGAC
NLRC4	NM_021209.3:840	TGCCAGGTATATCCAGGAGTTGATCACAGAGGGTTTCAAAAAGTCCACCC
NNMT	NM_006169.2:605	AAGCCAGGGAGTGACCCTGCAGAAGTTGTCTTCTCTGA
NRIP1	NM_003489.2:335	CCTGATCCCCCTGCTGCCTGATGCATTAGTAATCCTTCTAGGTAAGTTAA
P2RY13	NM_023914.2:2385	AGGTAAGGCCAGAAAGGTAGGCAAGTTCTAGGGCCTTTGAGGCCATGGAA
PPARG	NM_015869.3:1035	AAAACCAGGAATGCTTTTGGCATACTCTGTGATCTCCTGCACAGCCTCCA
PTGDS	NM_000954.5:180	TGGACAACGCCGCTTCTTCTCCCGGAGCCAGCTC
PTPRG	NM_002841.2:0	CCTGAAAGTTGTGGCTCCGGCGCAGGCTGGGAAGGAAC
S100A8	NM_002964.3:115	AGACGTCTGCACCCTTTTCTGATATACTGAGGACACTCGGTCTCTAGC
S100A9	NM_002965.2:75	CTTTGAATTTCCCTGGTTCAGGGTGTCTGGGTGC
S100B	NM_006272.1:40	CCCTCCCTTCCAGAATATTGGTGGAAAACGTCGATGAGGGCCACCATGGC
SCAP2	NM_003930.3:1270	AATATCATACATCTCCATTATGTAGGCTTTAGGCACCAAGCCAATGGCTC
SIX3	NM_005413.1:1305	GCGGCCTTGGCTATCATACATCACATTCCGAGTCGCTGG
SLC15A3	NM_016582.1:820	CAGCAGGAAGCTGATGTTCTGCTGAATAAACGCCACCACCAGCAGCGA

Gene Symbol	Target-NSID	Reporter Probe Sequence
STAB1	NM_015136.2:95	GAGTGACAAACGTGGTTTTTCACATCACAGCCTTTGAACAGCACCTGCCCC
TNFRSF1B	NM_001066.2:835	GACACAGTTCACCACTCCTATTATTAGTAGACCCAAGGCTGTCACACCCA
TNFRSF4	NM_003327.2:200	CACTCCCACTTCTGAGGTTACACCACGTGCAGGGC
TWIST1	NM_000474.3:35	AAAAAGAAAGCGCCCAACGGCTGGACGCACACCCCGCCAGGCC
VNN1	NM_004666.1:195	GGGTAGAGAGAGTCCCTGTTGAAGTTCCAGCCATAAATAGCATCTTCTGG

Gene Symbol	Capture Probe Sequence
ACTG1	CGGCTTGGACTTTCCAACCCTGACAGACCCGCAAGACAAAACAACTGGTT
AMICA1	GACCCCTGCCATTATCTCTATGTTGCTCAAGCAATTTGAGCGGTCACT
ANXA8	CGTGCACAGGATGGTGTATGAATTCATCTCATCAGTCCCACGAATCTTCT
BCL2A1	GGCAATGTGCTGAGAATGCTCACTGAGCTTGACTGAGTTATGACACATGA
CD300A	TGTAGTGACTCCGTAGCTTGCAGGACTGATCCCCG
CD34	CCAGAGTCTGGCTCCAGGGAGCCGAATGTGTAAGGACAGGAGTTTAC
CTSG	AAGTCTTCTCGCACCAGGAACCCTCCACATCTGCT
EBF3	ATCTCCGCATATCTCGAGGGTTGCCTGCATTCTTCAAACAGTTCTGATTG
ELA2	CGCGGCCGACATGACGAAGTTGGGCGCAATCAGGGTGCG
FAM19A5	TTGATGATTCTTGCCTCCACACAGGCGGGCCGGGCT
FBLN1	TAACCCGTCTTGCATTTCGACGCGAAACTGCCGGGAGAGTTCACGCAGCG
FGF13	TCACTGGCTACGTTGATTCAATTGTGGCTCATGGATTTGCCTCCGTTCCAGC
FGR	TCAGTTCGAGCCTCATAGTCATACAGGGCAATGAACAGGGTCAC
FPR1	AAGACGAATTTGCACAGGAACCAGCCGAAAGGCCAATGTCCTCCCATGGC
GABRE	CGACCCTCGACTGGAGGATCAATAAGATGCCTAGGAGGACTGGAAGAACT
GAPDH	CGTTCTCAGCCTTGACGGTGCCATGGAATTTGCCATGGGTGGAATCATAT
HGF	ACTCTTAGTGATAGATACTGTTCCCTTGTAGCTGCGTCCTTTACCAATGA
HK3	GTTACACAGGCTGCGCATCCAGGAACCTCAGACAGGC
IGFBP2	TGCTGCTCAGTGACCTTCTCCCGAACACGGCCAG
IL8RB	TTTTACAATCCCCCCAGCAACGCTCGAGAGTTCCAGTTTCTCCTCTACA
ITGB2	GGTCATCAAGCATGGAGTAGGAGAGGTCCATCAGATAGTAC
KCTD12	GCCGTCCCGGTCCAGAAAGAAGCGGCCTTTGCTGT
KIT	AGAGAAAATCCCAGGCGCCGCGAGCGCCTCTCATCG
LILRB2	AATGAAGCCGCCAAATGCCACCTGTGACTCACACTGGAGGGTCACCCTTC
LRRC25	CCTCAGTCCTACCTTTTGGGTCCCCTGACCAGCTTTTG
MS4A6A	AGCCCTTCCTTATTCCAGTGTTTACAGCTATACAGGATGTGATACTCACA
NCF2	AGAGAGAAGACAGGTTGGAGCGTCTCCCCTAGCAG
NLRC4	TGGGCCCTGCTGAGACGGAGGAAGAAGACGAATTTGAACTTGGTCAGAGC
NNMT	GTCTCAGGCTAACAGCATTCTTCCATCAGTTCAGCCCTTCTTTTAGAAC
NRIP1	AACAATAGAATCCTGGTGCACATCAGAGCCAAGCTCTTCTCCATGAGTCA
P2RY13	GAAAACGTGGGCTTACCCTACGATGGTCGTGTTGGAGCTCGTGG
PPARG	CGGAGCGAAACTGGCAGCCCTGAAAGATGCGGATGGCCACCTCTTTG
PTGDS	GAGTTGGAGGCGAGGCCCGCGCTGAACCAGCGCCC
PTPRG	GAAGAGCGCGGCGCTGGAAACTGGCCATGCCTCCATACAGGAAGTAACAT
S100A8	AATTTCTTCAGGTCATCCCTGTAGACGGCATGGAAATCCCCTTTATCAG
S100A9	CCCAGTTCACAGAGTATTGGTGGAAGGTGTTGATGATGGTCTCTATGTT
S100B	CTTCTCCAGCTCAGACATCCTCTTCTTGTCTCAC
SCAP2	CCTTCATTTCTCCTACCCACCAGCCATATCTATTGTATTCTTGCTAAGA
SIX3	AGGTTACCGAGAGGATGGAGGTGCCGGTGTCCGCG
SLC15A3	CAGCACAGCACCCAGGTTGATGCTCCAGTAAAACCAGTTGAAGAAGCGGC

Gene Symbol	Capture Probe Sequence
STAB1	CTGACGAAGCTGAAGCCTGCCAGGCAGAAGGCCAG
TNFRSF1B	CAATCAGTCCAACCTGGAAGAGCGAAGTCGCCAGTGCTCCCTT
TNFRSF4	TTGCACGGCTTGGAGCTGACCACGTCGTTGTAGAAGCCCGG
TWIST1	TCCTGGAAACGGTGCCGGTGCTGCAGAGCCCGCGA
VNN1	AGTCACAATAATATGCGCACCCCTGATCTGCTGCTGATGTGATCGCT

Gene Symbol	Target Region Sequence
ACTG1	AACCAGTTGTTTTGTCTTGCGGGTCTGTCAGGGTTGAAAGTCCAAGCCGTAGGACCCAGTTTCCTTTCTTAGCTGATGTCTTTGGCCAGAACACCGTGG
AMICA1	AGTGACCCGCTCGAAATTGCTTGAGCAACATAGAGATAATGGGCAGGGTCCCTGTGTGAAGCACCTAGAGGCTGGAAAGCTGATGGCAAAGCTGGAGGGG
ANXA8	AGAAGATTCGTGGGACTGATGAGATGAAATTCATCACCATCCTGTGCACGCGCAGTGCCACTCACCTGCTGAGAGTGTGTAAGAGTATGAGAAAATTGC
BCL2A1	TCATGTGTCATAACTCAGTCAAGCTCAGTGAGCATTCTCAGCACATTGCCTCAACAGCTTCAAGGTGAGCCAGCTCAAGACTTTGCTCTCCACCAGGCAG
CD300A	CGGGGAAGTGAGAGTCTGGGGATCAGTCTGCAAGCTACGGAGTCACTACAGGGAGAGGTCTCATCACTAGAAATAGCCGAAGAACCTGCAGCCTCAACCA
CD34	AGGTAAACTCCTGTCTTTACACATTTCGGCTCCCTGGAGCCAGACTCTGGTCTTCTTTGGGTAAACGTGTGACGGGGGAAAGCCAAGGTCTGGAGAAGCT
CTSG	AGTCCAGCAGGTGAGAGCAGATGTGGAGGGTTCCTGGTGCAGAGACTTTGTGCTGACAGCAGCTCATTGCTGGGGAAGCAATATAAATGTCACCCTGG
EBF3	CAATCAGAACTGTTTGAAGAATGCAGGCAACCCTCGAGATATGCGGAGATTCCAGGTTGTTGTATCGACAACAGTCAACGTGGACGGCCACGTGCTGGCC
ELA2	ACTTCTGCGGCGCCACCCTGATTGCGCCCAACTTCGTCATGTCGGCCGCGCACTGCGTGGCGAATGTAACGTCCGCGCGGTGCGGGTGGTCTCTGGGAGC
FAM19A5	GCCGGCACCACGAGAGCCCGGCCCGCTGTGTGGACGCAAGAATCATCAAGACCAAGCAGTGGTGTGACATGCTTCCGTGTCTGGAGGGGAAAGGCTGCG
FBLN1	CGCTGCGTGAACCTCTCCCGCAGTTTCCGCTGCGAATGCAAGACGGGTACTATTTGACGGCATCAGCAGGATGTGTGTCGATGTCAACGAGTGCCAGC
FGF13	GCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAACGTAGCCAGTGAGGGCAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAA
FGR	ATTGGGGTGACCCTGTTCAATTGCCCTGTATGACTATGAGGCTCGAACTGAGGATGACCTCACCTTCACCAAGGGCGAGAAGTCCACATCCTGAACAATA
FPR1	GCCATGGGAGGACATTGGCCTTTCGGCTGGTTCCTGTGCAAATTCGTCCTTACCATAGTGGACATCAACTTGTTCGGAAGTGTCTTCTGATCGCCCTCA
GABRE	AGTTCCTCCAGTCTCCTAGGCATCTTATTGATCCTCCAGTCGAGGGTTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGTC
GAPDH	ATATGATTCCACCCATGGCAAATTCATGGCACCGTCAAGGCTGAGAACGGGAAGCTTGTATCAATGAAATCCCATCACCATCTTCCAGGAGCGAGAT
HGF	TCATTGGTAAAGGACGCAGCTACAAGGGAACAGTATCTATCACTAAGAGTGGCATCAAATGTCAGCCCTGGAGTTCATGATACCACACGAACACAGCTT
HK3	ACTTTGCTGCCCACTGCCTGTCTGAGTTCTTGATGCGCAGCCTGTGAACAAACAGGGTCTGCAGCTTGGCTTCAGCTTCTCTTCCCTTGTACCAGAC
IGFBP2	TCGGGTATGAAGGAGCTGGCCGTGTTCCGGGAGAAGGTCAGTGCAGCAGCACCGGCAGATGGGCAAGGGTGGCAAGCATCACCTTGGCCTGGAGGAGCCCA
IL8RB	TGTAGAGGAGAACTGAACTCTCGAGCGTTGCTGGGGGGATTGTAATAAGTGTGACCACTGCAGAAGACAGTATGGCAGCTTTCCTCAAAACTTCAG
ITGB2	CATCGACCTGTACTATCTGATGGACCTCTCCTACTCCATGCTTGTGACCTCAGGAATGTCAAGAAGCTAGGTGGCGACCTGCTCCGGGCCCTCAACGAG
KCTD12	AGGAGCTGGCCCGGACAGCAAAGGCCGCTTCTTCTGGACCGGGACGGCTTCTCTTCCGCTACATCCTGGATTACCTGCGGGACTTGCAGCTCGTGCT
KIT	CATCGCAGCTACCGCGATGAGAGGCGCTCGCGGCGCCTGGGATTTCTCTGCGTTCTGCTCCTACTGCTTCGCGTCCAGACAGGCTCTTCTCAACCATCT
LILRB2	GAAGGGTGACCCCTCCAGTGTGAGTCACAGGTGGCATTGGCGGCTCATTCTGTGTAAGGAAGGAGAAGATGAACACCCACAATGCCTGAACCTCCAGCC
LRRC25	CATCGCAGAGGCAAAGCGTGGCAGTGGGACCCAAAAGGTAGGACTGAGGCTCTAGAACTTGCACCTGTGCAGGGACTGCAAACCAGACCTGGGAGGACC
MS4A6A	TGTGAGTATCACATCCTGTATAGCTGTAACACTGGAATAAGGAAGGGCTGATGACTTTCAGAAGATGAAGGTAAGTAGAAACCGTTGATGGGACTGAGA
NCF2	GCCACTAAGGCAGCCCTGCTAGGGGAGACGCTCCAACCTGTCTTCTCTGTCTCCTGGCAGCTCTTGGCCTCCTAGTTTCTACCTAATCATGTCCCT
NLRC4	GCTCTGACCAAGTTCAAATTCGTCTTCTTCTCCGTCTCAGCAGGGCCAGGGTGGACTTTTTGAAACCCCTCTGTGATCAACTCCTGGATATACCTGGCA
NNMT	GTTCTAAAAGAAGGGCTGAACTGATGGAAGGAATGCTGTTAGCCTGAGACTCAGGAAGACAATTCTGCAGGGTCACTCCCTGGCTTCTGGAGGAAAGAG
NRIP1	TGACTCATGGAGAAGAGCTTGGCTCTGATGTGCACCAGGATTCTATTGTTTTAACTTACCTAGAAGGATTACTAATGCATCAGGCAGCAGGGGGATCAGG
P2RY13	ATGTGCCACGAGCTCCAACACGACCATCGTAGGGTGAAGCCACGTTTTCTTCCATGGCCTCAAAGGCCCTAGAACTTGCCTACCTTTCTGGCCTTACCT
PPARG	GAGCAAAGAGGTGGCCATCCGCATCTTTCAGGGCTGCCAGTTTCGCTCCGTGGAGGCTGTGCAGGAGATCACAGAGTATGCCAAAAGCATTCTGGTTTT
PTGDS	CAGGACAAGTTCCTGGGGCGCTGGTTCAGCGCGGGCCTCGCTCCAACCTCGAGCTGGCTCCGGGAGAAGAAGGCGGCGTTGTCCATGTGCAAGTCTGTGG
PTPRG	ATGTTACTTCTGTATGGAGGCATGGCCAGTTTCCAGCGCCGCGCTTCTCGTTCTTCCAGCCTGCGCCGAGCCACAACCTTTCAGGAGCATGGACTGA
S100A8	CTGATAAAGGGGAATTTCCATGCCGTCTACAGGGATGACCTGAAGAAATGCTAGAGACCGAGTGTCTCAGTATATCAGGAAAAAGGGTGCAGACGTCT
S100A9	AACATAGAGACCATCATCAACACCTTCCACCAATACTCTGTGAAGCTGGGGCACCCAGACACCCTGAACCAGGGGGAATTCAAAGAGCTGGTGCGAAAAG
S100B	GGAGACCAGGAAGGGGTGAGACAAGGAAGAGGATGTCTGAGCTGGAGAAGGCCATGGTGGCCCTCATCGACGTTTTCCACCAATATTCTGGAAGGGAGGG
SCAP2	TCTTAGCAAGGAATACAATAGATATGGCTGGTGGGTAGGAGAAATGAAGGGAGCCATTGGCTTGGTGCCTAAAGCCTACATAATGGAGATGTATGATATT
SIX3	CAGCCTGACGGAGCGCGGACACCGGCACCTCCATCCTCTCGGTAACCTCCAGCGACTCGGAATGTGATGTATGATAGCCAAGGCCGCCCTCCTCCCTC
SLC15A3	GCCGCTTCTCAACTGGTTTTACTGGAGCATCAACCTGGGTGCTGTGCTGTCGCTGCTGGTGGTGGCGTTTATTACGCAGAACATCAGCTTCTGCTGGG

Gene Symbol	Target Region Sequence
STAB1	CTCCCACTCTGCCTCCTGGCCTTCTGCCTGGCAGGCTTCAGCTTCGTCAGGGGGCAGGTGCTGTTCAAAGGCTGTGATGTGAAAACCACGTTTGTCACTC
TNFRSF1B	CCCAGCTGAAGGGAGCACTGGCGACTTCGCTCTTCCAGTTGGACTGATTGTGGGTGTGACAGCCTTGGGTCTACTAATAATAGGAGTGGTGAAGTGTGTC
TNFRSF4	CCGTGCGGGCCGGGCTTCTACAACGACGTGGTCAGCTCCAAGCCGTGCAAGCCCTGCACGTGGTGTAACTCAGAAGTGGGAGTGAGCGGAAGCAGCTGT
TWIST1	CAACTCCCAGACACCTCGCGGGCTCTGCAGCACCGGCACCGTTTCCAGGAGGCCTGGCGGGGTGTGCGTCCAGCCGTTGGGCGCTTTCTTTTTGGACCTC
VNN1	AAGGAGCGATCACATCAGCAGCAGATCAGGGTGCGCATATTATTGTGACTCCAGAAGATGCTATTTATGGCTGGAAGTTCAACAGGGACTCTCTTACCC