Transcriptional upregulation of *p21/WAF/Cip1* in myeloid leukemic blasts expressing AML1-ETO

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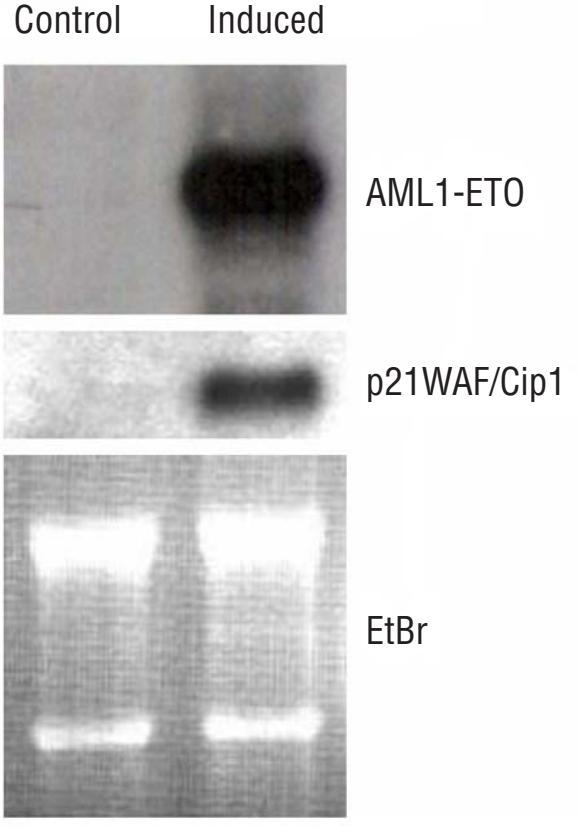
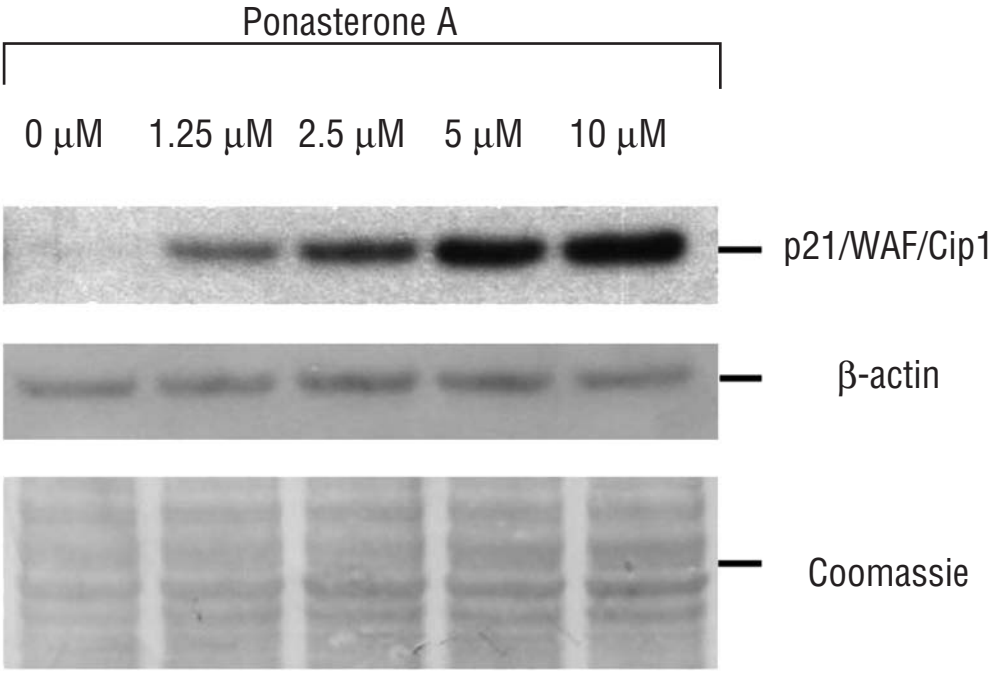
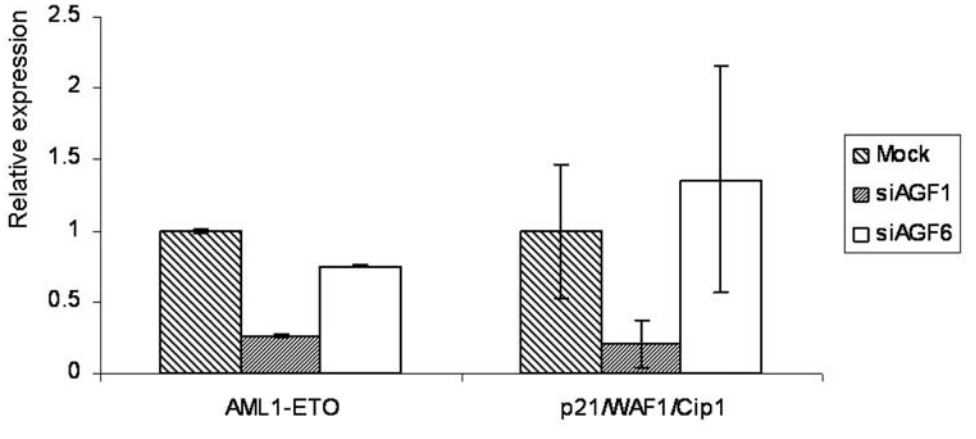


Supplementary Figure S1. p21/WAF-1/Cip 1 expression is induced by AML1-ETO demosnstrated by Northern Blot. AML1-ETO expression was induced by treatment of 9/14/18 cells with Ponasterone A for 48 hours.



Supplementary Figure S2. Dose-response for induction of p21/WAF-1/Cip 1. 9/14/18 cells were treated with the indicated doses of Ponasterone A for induction of AML1-ETO. Coomassie staining is shown as loading control. The following antibodies were used: polyclonal goat antbodies against ETO (sc-9737), and p21/waf/Cip1 (sc397g, both Santa Cruz Biotechnology, Heidelberg, Germany), b-actin (Sigma, Taufkirchen, Germany), donkey anti-goat IgG HRP (sc2033) and goat anti-mouse IgG HRP (sc2302, both Santa Cruz Biotechnology).



Supplementary Figure S3. Downregulation of p21/WAF1/Cip1 in Kasumi-1 by siRNA-mediated repression of AML1-ETO. *p21/WAF1/Cip1* and *AML1-ETO* mRNA and protein expression in Kasumi-1 after double-transfection with siRNAs (siAGF1 = active siRNA against AML1-ETO, siAGF6 = mismatch control siRNA, mock = mock siRNA). Results from a double transfection experiment are shown. Realtime PCR demonstrates that siAGF1 causes a reduced expression of AML1-ETO and p21/WAF1/Cip1 whereas MOCK and siAGF6 had no effects. Expression is normalized by GUSB expression. Relative expression is calculated in relation to the mock transfected samples. Error bars represent standard deviations of PCR replicates.

Supplementary Table I

Regulated genes by AML1-ETO in the inducible system

9/14/18 (1) and (2) represent two independent experiment in the inducible AML1-ETO expression system.

Probe Set ID	Gene Symbol	9/14/18 - (2)	9/14/18 + (2)	9/14/18 - (1)	9/14/18 + (1)	U937 -	U937 +
201005_at	CD9	123.8	19.4	238.1	51.3	48.8	14.2
201367_s_at	ZFP36L2	448.7	184	748.7	348.8	494.9	529.2
202575_at	CRABP2	101.1	13.2	133	40.5	37.9	75
203015_s_at	SSX2IP	383.6	109.4	291.4	126	459	478.9
203238_s_at	NOTCH3	118.2	16.2	106.1	33.2	96.8	121.1
203289_s_at	C16orf35	114.9	46.7	121.4	31.8	28.3	139.7
203397_s_at	GALNT3	473	234.8	320.3	143.6	245	199
204008_at	DNAL4	103.1	22.6	132.8	65.3	26.2	99.7
204753_s_at	HLF	109.5	43	144.8	41.9	39.9	19
204921_at	GAS8	185.2	74.2	271.1	95.8	232.5	208.8
205543_at	HSPA4L	361.8	156.5	276.3	130.8	453.9	496.1
205843_x_at	CRAT	269.3	45.1	186.8	38.9	217.1	172.8
205864_at	SLC7A4	172.5	46.1	144.7	52.8	188.9	98.5
205980_s_at	ARHGAP8 /// LOC553158	207.9	22.1	217.4	53.8	143.8	283.7
206076_at	B7	123.7	9.6	140.4	50	70.7	68.5
206277_at	P2RY2	155.4	47.4	189.9	41	107.5	156.9
206470_at	PLXNC1	278.8	53.9	174.4	33.7	147.8	160.5
206471_s_at	PLXNC1	110.3	37.2	123.2	56.9	48.1	134.4
206500_s_at	C14orf106	257.7	51.6	205.8	99	194.6	134.9
206516_at	AMH	103.9	15	115.2	51.3	83.4	29
206643_at	HAL	171.6	79.4	192.9	48	260.7	177.4
206943_at	TGFBR1	591.8	98.5	1338.8	534.7	541.7	746.1
207193_at	AGRP	144.3	58.4	165.7	68.8	89	95
207511_s_at	C2orf24	169.4	51.5	335.3	117.2	180.3	70.9
207986_x_at	CYB561	204.5	91.7	145	66.1	228.2	96.6
208189_s_at	MYO7A	174.1	58.2	193.3	42.7	134.7	102
208191_x_at	PSG4	168.9	40.6	138.5	34.9	144	119.2
208217_at	GABRR2	105.9	52.5	163.4	78.5	92.7	125.7

208244_at	BMP3	161.1	15	112.7	20.9	82	104.9
209013_x_at	TRIO	148.4	68.8	375.4	174.4	53.4	107
209378_s_at	KIAA1128	160.4	54.9	133.2	53.4	56.3	105.5
209401_s_at	SLC12A4	145.7	12.6	142.2	49.6	168.2	65.3
210577_at	CASR	116.6	29.2	160.2	37.8	96	85.1
210796_x_at	SIGLEC6	771.8	346	1211.4	566.5	475.4	481.6
210972_x_at	TRA@ /// TRDV2 /// TRAV20 /// TRAJ17 /// TRAC	126.6	30.4	228.8	72.4	72.3	86.8
211077_s_at	TLK1	273.6	64.7	211	86.5	163	84.8
211172_x_at	AKAP7	176.1	54.3	167.5	55.4	133	46.9
211403_x_at	VCY /// VCX /// VCX2 /// VCX3A /// LOC401578 /// VCX-C	233	99.4	226.3	105.1	157.2	139.3
211613_s_at	GPD2	125.2	60.8	212.9	89	32.6	97.8
211852_s_at	ATRN	238.2	77.4	365.7	173.9	254.7	299
212827_at	IGHM	286.6	98.3	125.7	13.1	47.6	84.7
213739_at	---	146.3	31.5	100.7	26.8	48	105.8
213877_x_at	TCEB2	137.7	38.2	120.8	47.9	150.7	200.5
214616_at	HIST1H3E	152.2	34.1	131.5	28.6	120.6	39.7
215188_at	STK24	137.7	42.4	219.5	72	127.7	75.7
215920_s_at	LOC283970 /// LOC440350	147.6	41	324.8	106.4	184	133.8
216620_s_at	ARHGEF10	2649.6	962.6	2433.7	1082.3	1557	1648.5
216806_at	---	212.6	10.2	278.8	127.9	255.8	272.6
217441_at	USP33	110.9	4.2	115.2	52.5	99.4	63.4
217489_s_at	IL6R	131.9	51.3	241.4	116.7	268	263.2
218100_s_at	ESRRBL1	993.4	394.2	1096.8	538.1	392.5	448.7
218363_at	C14orf114	334.7	142.3	298.9	141.9	269.6	181

218525_s_at	HIF1AN	534.4	224.5	446.7	178.3	330.8	86.6
218971_s_at	HSPC049	179.8	73.4	277.8	107.5	335.4	329.3
219405_at	TRIM68	196.3	90.7	178.8	82	96.4	137.3
219592_at	MCPH1	108.1	51.4	153.2	71.3	33.1	58.6
220165_at	FLJ20309	137.5	54.5	101.9	21	137	76.1
220192_x_at	SPDEF	153.4	40.1	113.1	25.7	38.4	67.6
220257_x_at	NXF2	116.5	38.1	128.5	44.1	78.8	42.2
220264_s_at	GPR107	171.2	50.5	114.9	14.2	148.8	60.2
220292_at	ZNF434	162.5	32.5	126.7	53.7	122.7	153.2
220839_at	METTL5	136	50.6	108	44.6	97	156.8
220999_s_at	CYFIP2	189.2	79.5	166.3	69.5	125.1	112.5
221003_s_at	CAB39L	816.4	228.4	435	203	161.1	110.1
221042_s_at	CLMN	197.2	67.3	157.2	38.1	92.5	114.4
221602_s_at	FAIM3	170.7	15.3	144.1	14	25.8	19.8
221631_at	CACNA1I	197.2	43.1	143.9	27.7	71.8	84.8
221713_s_at	FLJ12748	117.7	51.6	123.9	52.6	121.4	58
221913_at	SIRT3	164.8	13.1	105	20.9	146.2	137.5
200797_s_at	MCL1	1568.7	5210.9	1699.2	3642	1793	1825.2
200798_x_at	MCL1	881.4	2412.3	1399.9	3955	1714.1	1509.6
200872_at	S100A10	1881.4	4454.8	1460.1	3613.3	1357.1	1248.4
201012_at	ANXA1	952.1	2814.5	929.6	2269.8	1794.9	1550.4
201059_at	CTTN	54.1	181.6	43.5	180.7	4.5	56.3
201340_s_at	ENC1	13.7	314.8	73.3	443.2	132.6	112.1
201341_at	ENC1	143.6	767.6	254.7	1199.1	150.1	268
201464_x_at	JUN	653	1477.8	675.9	1627.1	338.8	275.2
201466_s_at	JUN	137.2	459.4	107.4	258.8	5.3	45
201601_x_at	IFITM1	3466.2	10124.8	2465.6	5146.5	90.3	154.9
201798_s_at	FER1L3	196.4	416.8	183.4	620.2	217.3	152.1
202180_s_at	MVP	186	537.5	121.6	392	92.6	61
202241_at	TRIB1	49.2	492.4	82	404.7	16.6	2.7
202284_s_at	CDKN1A	413.4	1525.7	222.7	1210.9	28.8	87
202307_s_at	TAP1	592.5	2188.6	505.4	1019.9	269.1	303.8

202411_at	IFI27	164.4	2520.5	195.8	897.6	9.2	10.7
202499_s_at	SLC2A3	138.2	294.6	130.9	320.9	130.7	84.8
202638_s_at	ICAM1	334.1	865.9	335.5	794	201	164.5
202708_s_at	HIST2H2BE	95.8	213.9	90.2	189.6	167	95.6
202732_at	PKIG	111.2	261.4	105.4	224.3	175.5	101.6
202748_at	GBP2	98.8	214.2	18.1	123.8	87.8	55.8
202800_at	SLC1A3	313.4	1028.4	284.1	1023.6	267.8	299.2
202859_x_at	IL8	633.1	5190.8	720.9	4975	119.5	101.6
202869_at	OAS1	615.3	1291.4	418.9	885.6	102.9	110.8
203153_at	IFIT1	1112.5	3201.2	632.4	1840.5	311.8	279.9
203596_s_at	IFIT5	162.2	334.4	34.9	281.2	13	4.9
203623_at	PLXNA3	44.2	196.5	82	210.2	52.6	73.5
203671_at	TPMT	40.9	108.2	23	174.9	128.6	134.6
203787_at	SSBP2	109.6	348.1	62.3	259.6	91.8	95.9
203789_s_at	SEMA3C	18.2	129.3	6	131.5	38.4	18.8
203935_at	ACVR1	416.7	906.4	273.2	745.8	222.4	183
203936_s_at	MMP9	346.6	1127.7	280.1	1105.1	292.9	223.6
203946_s_at	ARG2	85.2	244	48	186	44	1.4
203980_at	FABP4	61.7	2080	9.5	704.6	12.8	27.1
204101_at	MTM1	73.2	148.3	36.8	158.8	51.4	113.1
204112_s_at	HNMT	407.5	1394.6	319.8	1220.5	221.8	239.5
204151_x_at	AKR1C1	235.9	599.6	143.5	291.8	119.9	146.2
204224_s_at	GCH1	370.7	1114.5	372.5	929.9	222.3	288.1
204248_at	GNA11	15.9	141.4	31.7	105.1	19.4	12.1
204439_at	IFI44L	129.3	469.1	11.1	240.9	2.8	3.8
204475_at	MMP1	248.5	5188.9	82.2	3927	16.3	30
204526_s_at	TBC1D8	545.4	1538.5	574	1524.4	615.3	823.9
204533_at	CXCL10	1703.8	16410.8	1473.7	14604.8	147.7	118.8

204661_at	CD52	162.8	432.4	20.5	261.5	10.8	20.2
204747_at	IFIT3	372.6	1531.5	457.7	957.5	272.1	205.5
204908_s_at	BCL3	130.4	298.2	56	274.6	43.9	39.8
205067_at	IL1B	240.3	647.1	274.4	688.6	707.5	654.6
205076_s_at	MTMR11	121.1	1013.4	152.9	669.5	104.7	87.5
205249_at	EGR2	59.5	148.4	44.1	220.7	54	6.2
205409_at	FOSL2	48	206.7	64.9	271.7	129.3	129.2
205552_s_at	OAS1	664.3	1528	514.9	1201.9	92.7	85.1
205568_at	AQP9	31.2	129.1	11.2	214.3	5.8	17.4
205660_at	OASL	414.8	1302.4	232.2	559.9	173.1	176.7
205749_at	CYP1A1	131.9	3467.3	92.3	3172.7	119.9	58.7
205789_at	CD1D	128.9	586	111.4	503.2	148.3	120
205797_s_at	TCP11L1	64.3	189.1	32.5	137.9	156.1	66.3
205798_at	IL7R	42.4	673.7	4.3	486.2	20.5	11.7
205847_at	PRSS22	50	136.1	49.5	151.6	187	148.4
205936_s_at	HK3	117.9	314	31.6	282.1	40.8	21.3
206026_s_at	TNFAIP6	64.1	291.2	77	205.3	19.5	53.5
206155_at	ABCC2	102.8	207.1	92	237.5	21.6	80.6
206181_at	SLAMF1	71.5	276.6	56.1	221.8	74.6	71.1
206187_at	PTGIR	22.1	301.9	16.5	148.4	41.6	13
206488_s_at	CD36	1075.9	3603.3	1354.4	3900.3	42.8	63.5
206548_at	FLJ23556	47.3	121.4	2.1	102.5	1.4	27.4
206584_at	LY96	140.7	330.6	67.6	246.5	42.8	108.5
206873_at	CA6	64.2	716.4	14.2	246.6	127.2	43
207147_at	DLX2	86	187.6	93.6	211.8	201.3	168.5
207191_s_at	ISLR	22.7	212	18.3	159.6	11.3	14.3
207674_at	FCAR	319.1	926.7	511.5	2538.4	153.4	142.4
208579_x_at	H2BFS	309.5	674.5	268.2	578.8	200.5	234.6
208937_s_at	ID1	224.3	464.9	181.1	464.2	303.4	288.9
208960_s_at	KLF6	210	464.2	257	743.7	95	82.8
208961_s_at	KLF6	327.8	779	360.5	758.9	118.9	97.7
209122_at	ADFP	1387.2	10299.8	840.6	6224.7	1161.8	1107.2
209189_at	FOS	95	747.2	45.4	1035.2	21.5	73.7
209199_s_at	MEF2C	94.5	206.7	99.7	275.7	135.1	98.7
209200_at	MEF2C	5.9	142.9	56.3	162.7	9.9	64.8

209297_at	ITSN1	335.1	1110.5	207.7	807.9	243.1	460.8
209386_at	TM4SF1	12.9	329.3	24.4	194	15.7	93.2
209387_s_at	TM4SF1	51.6	139.7	6.6	153.1	16.5	2
209453_at	SLC9A1	27.1	385.6	55.9	365.6	162.4	96.6
209679_s_at	LOC57228	12.7	281.9	82.3	202.7	96.3	55.3
209691_s_at	DOK4	31.4	109.9	51.3	135.3	18.5	86.9
209774_x_at	CXCL2	8.1	234	86.5	894.6	45.1	33.3
209785_s_at	PLA2G4C	25.8	238.4	47.9	159.2	81.7	6.6
209806_at	HIST1H2BK	913.6	2165.9	524.7	1089.1	493.2	602.3
209875_s_at	SPP1	153.3	1050.3	8.7	699.9	20	5.4
209906_at	C3AR1	185.2	386.5	174.1	363.3	189	150.9
209911_x_at	HIST1H2BD	366.7	986.3	268.5	658.7	255	284.9
209949_at	NCF2	678.7	1894.5	516.4	1454.9	241.9	262.3
210147_at	ART3	543.4	2314.5	478.5	2000.6	170.6	173.4
210163_at	CXCL11	48.1	990.1	49.5	954.7	39.5	24.5
210394_x_at	SSX4	40.6	112.7	4.1	102.4	67.8	100.6
210483_at	MGC31957	40.1	169.6	28.9	176.2	82.4	41.3
210569_s_at	SIGLEC9	19.4	158	8.7	111.7	12.5	20.2
210829_s_at	SSBP2	93.8	199.3	94.5	222.4	150.3	187.3
210889_s_at	FCGR2B	210.4	862.1	122.4	763.7	158.2	282.2
211122_s_at	CXCL11	72.7	2119	41.5	2029.8	5	33.3
211181_x_at	RUNX1	232.7	2217.5	265.8	3756.8	109.8	165.2
211182_x_at	RUNX1	160.7	1002.7	227.3	1552.9	149.3	143.9
211307_s_at	FCAR	117.5	486.7	407.1	1518.2	4.6	37.9
211458_s_at	GABARAPL1 /// GABARAPL3	4.6	100.1	6	140.4	46.1	27.3
211506_s_at	IL8	137.7	737.5	92.4	1672.5	8.8	65.8
211535_s_at	FGFR1	19.9	117.4	68.9	143.2	109	138.8
211599_x_at	MET	12.3	147.9	56.3	187.3	79.9	153

211620_x_at	RUNX1	228.5	966.1	258.1	1509.4	166.7	61
211732_x_at	HNMT	376.9	1470.7	253.3	750.4	163.8	171.5
211864_s_at	FER1L3	46.6	180.2	128.2	293.8	101.2	144.3
211962_s_at	ZFP36L1	30	200.9	48.6	147.7	34.2	26.3
212614_at	ARID5B	127.4	660.8	136.3	451.8	83.7	140.8
212759_s_at	TCF7L2	40	220.5	54.1	173.7	18.7	8.6
212761_at	TCF7L2	385	1172	395.2	1184.8	342.1	401.2
212762_s_at	TCF7L2	147.8	426.5	177	440.3	213	121
212992_at	C14orf78	54.4	212.1	32.4	155.5	12.1	5
213038_at	IBRDC3	327.9	1576.8	434.4	1182	283.7	288.1
213059_at	CREB3L1	39.7	140.4	36.7	166.2	30.3	35.8
213146_at	---	111.1	237.8	53.7	218.7	67.3	74
213164_at	SLC5A3	921.1	2089.4	710.3	1451.7	879.5	881.2
213261_at	LBA1	117.5	267	60.5	240.3	212.6	172.5
213636_at	KIAA1045	58.3	139	35.2	148	18.5	91.8
214022_s_at	IFITM1	4306.1	10659.9	2562.4	5774.7	176.4	147.9
214056_at	MCL1	116.1	406	143.1	389.5	191.1	159
214290_s_at	HIST2H2AA	1456.6	3301	866.7	1968.6	597	541.2
214375_at	PPFIBP1 /// LOC440091	56.5	208.3	27.6	124.6	58	75.2
214401_at	PAX1	48.2	115.1	34.7	158.7	66.4	96.6
214453_s_at	IFI44	760.8	1978.3	769.6	2432.8	58.3	40.7
214696_at	MGC14376	7.4	204.4	74	381.9	91.8	68.7
214735_at	PIP3-E	131	666	292.2	664.5	35.6	102.3
214955_at	TMPRSS6	13.5	147.9	9.3	121.8	178.7	137.5
214995_s_at	APOBEC3G /// APOBEC3F	83.1	210.5	118.2	241.7	168.2	142.1
215034_s_at	TM4SF1	19	197.3	5	178.8	10.1	3.9
215049_x_at	CD163	61.7	166.5	17.1	140.1	68.1	91.6
215071_s_at	HIST1H2AC	87.5	435.8	69.1	227.5	24.5	14.7

215819_s_at	RHCE /// RHD	69.2	173	23.9	114.8	34.6	61.7
215887_at	ZNF277	93.8	245	65.6	135.8	107.9	69.2
216035_x_at	TCF7L2	197.4	426.3	176.1	503.4	167.5	245.4
216037_x_at	TCF7L2	189.3	472.1	246.4	613.4	178.1	179.2
216511_s_at	TCF7L2	145.1	314	128.2	435.1	148.9	166.5
216831_s_at	RUNX1T1	381.2	5123.1	442.1	3050.6	3.1	2.1
217192_s_at	PRDM1	35.9	119.8	23.8	118.6	19.1	45.3
217331_at	LOC283677	27.4	107.3	53.3	117.8	168.9	180.8
217374_x_at	TRGV5	58.8	130.9	144.8	323.2	39.6	189.5
217929_s_at	KIAA0319L	20	150.9	32	166.1	19.1	26.5
217996_at	PHLDA1	11.6	214.3	9.1	137.7	50.1	43.2
218113_at	TMEM2	71.3	169.6	18.2	147.6	167.6	128.9
218345_at	HCA112	79.6	227.7	15.2	138.3	173.6	205.2
218559_s_at	MAFB	166.2	561.4	172.6	617.2	74.1	9.4
218856_at	TNFRSF21	1161.3	3910.2	1173.4	3740	741.4	735.7
218880_at	FOSL2	140.1	884.6	227	579.4	256.6	144.7
218943_s_at	DDX58	313.1	1005	196.7	609	78.7	103.1
219036_at	Cep70	47.4	133.6	70.5	145.9	21.9	10.1
219222_at	RBKS	127	263.3	22.8	195.1	60.7	118
219235_s_at	PHACTR4	83.9	174.9	64.3	140.7	78.6	118.4
219424_at	EBI3	16.2	181.3	6.3	169.2	6.1	5.6
219434_at	TREM1	428.6	956.3	323.8	674	42.5	60.3
219442_at	MGC3020	35.4	132.8	30.6	109.2	34.3	65.3
219573_at	LRRC16	33.9	133.2	39.4	115.1	162.2	161.6
219607_s_at	MS4A4A	1066.3	2361.6	664.5	1526.4	116.8	106.7
219722_s_at	GDPD3	13.1	109.6	19.2	137.8	160.5	83.5
219763_at	DENND1A	422.1	1411.9	315.6	919.1	939.9	880.6
219799_s_at	DHRS9	243.5	872.3	83.4	466.7	227.8	230.3
220454_s_at	SEMA6A	27.9	144.1	79.3	201.8	119.4	76.7
220571_at	PRDM11	70.3	166.4	30.5	141.4	104.6	66.6
220778_x_at	SEMA6B	78.6	236.3	118.5	265.5	14.8	5.1
220973_s_at	SHARPIN	64.3	163.3	35.5	137.9	209.4	268.7

221246_x_at	TNS1	78.4	178	62.4	236.3	33.4	74.6
221560_at	MARK4	57.9	138.5	47.2	105.3	66.8	43.5
221710_x_at	C1orf78	15.1	146.1	16.9	111.4	12.9	12.2
221747_at	TNS1	128.3	273.7	8.1	268.8	26	34
221748_s_at	TNS1	84.2	605.7	104.3	482.1	107.3	77.1
221754_s_at	CORO1B	7.5	100.5	46.7	112.8	50.2	4.2
221870_at	EHD2	47.9	360.8	39.9	212.2	23.4	12.8
221928_at	ACACB	10.8	147.7	64.1	133.6	71.1	53.1
222067_x_at	HIST1H2BD	202.9	665.4	98.8	308.1	190.2	253.1
222160_at	AKAP8L	99.8	213.6	84.2	169.3	200.3	156.3
222195_s_at	C9orf156	70.5	150.7	54.9	128.5	215.2	292.5
33304_at	ISG20	135.7	972	97.9	412	91.7	93.2
34210_at	CD52	82.5	193.7	53.7	170.3	13.3	6.4
36564_at	IBRDC3	554.8	1465.5	401.4	1202.4	307.6	310.7

Supplementary Table II

Regulated genes with an annotation to functions within the cell cycle or apoptosis

Probe Set ID	Gene Symbol	Gene Title	Entrez Gene ID	Chromosomal Location	Mean fold change
217996_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	22822	12q15	16,80
211506_s_at	IL8	interleukin 8	3576	4q13-q21	11,73
202859_x_at	IL8	interleukin 8	3576	4q13-q21	7,55
202284_s_at	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	1026	6p21.2	4,56
212759_s_at	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	6934	10q25.3	4,36
220454_s_at	SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	57556	5q23.1	3,85
203936_s_at	MMP9	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)	4318	20q11.2-q13.1	3,60
204908_s_at	BCL3	B-cell CLL/lymphoma 3	602	19q13.1-q13.2	3,60
218856_at	TNFRSF21	tumor necrosis factor receptor superfamily, member 21	27242	6p21.1-p12.2	3,28
214056_at	MCL1	Myeloid cell leukemia sequence 1 (BCL2-related)	4170	1q21	3,11
212761_at	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	6934	10q25.3	3,02
200798_x_at	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	4170	1q21	2,78
216511_s_at	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	6934	10q25.3	2,78
200797_s_at	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	4170	1q21	2,73
201012_at	ANXA1	annexin A1	301	9q12-q21.2|9q12-q21.2	2,70
212762_s_at	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	6934	10q25.3	2,69
205067_at	IL1B	interleukin 1, beta	3553	2q14	2,60
216035_x_at	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	6934	10q25.3	2,51
201601_x_at	IFITM1	interferon induced transmembrane protein 1 (9-27)	8519	11p15.5	2,50
216037_x_at	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	6934	10q25.3	2,49
203935_at	ACVR1	activin A receptor, type I	90	2q23-q24	2,45
214022_s_at	IFITM1	interferon induced transmembrane protein 1 (9-27)	8519	11p15.5	2,36
201464_x_at	JUN	jun oncogene	3725	1p32-p31	2,34
221560_at	MARK4	MAP/microtubule affinity-regulating kinase 4	57787	19q13.3	2,31
218100_s_at	IFT57	intraflagellar transport 57 homolog (Chlamydomonas)	55081	3q13.12	0,44
220999_s_at	CYFIP2	cytoplasmic FMR1 interacting protein 2	26999	5q33.3	0,42
211077_s_at	TLK1	tousled-like kinase 1	9874	2q31.1	0,32
221602_s_at	FAIM3	Fas apoptotic inhibitory molecule 3	9214	1q32.1	0,09

Supplementary Table III

Comparison of p21/WAF/Cip1 expression in AML1-ETO regulation from different data sets primary AML blasts (1, 2) and AML1-ETO *in vitro* models (3).

Reference	Microarray System	Material analyzed	Expression change P21/WAF1/CIP1
Bullinger et al., 2004	microarrays of complementary DNA (cDNA)	Samples from 116 adult AML patients including 11 A/E-positive leukemias	Upregulated
Ross et al., 2004	Affymetrix U133A	Samples from 130 pediatric patients with AML including 21 A/E-positive leukemias	Upregulated Signal log ratio 0.8
Berg et al, this dataset	Affymetrix U133A	Samples from 100 adult AML patients including 43 A/E-positive leukemias and 57 AE-negative AML M2 samples	Upregulated Signal log ratio 0.52
Mulloy et al., 2002	Affymetrix U95A	Retrovirally-mediated expression of AML1-ETO in hematopoetic precursor cell from cord blood and PB	Upregulated Signal log ratio 1.86
Berg et al, this dataset	Affymetrix U133A	Cell line model with inducible AML1-ETO expression	Upregulated Signal log ratio 2.18

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2. Ross ME, Mahfouz R, Onciu M, Liu HC, Zhou X, Song G, et al. Gene expression profiling of pediatric acute myelogenous leukemia. Blood. 2004 Dec 1;104(12):3679-87.
3. Mulloy JC, Cammenga J, MacKenzie KL, Berguido FJ, Moore MA, Nimer SD. The AML1-ETO fusion protein promotes the expansion of human hematopoietic stem cells. Blood. 2002 Jan 1;99(1):15-23.