

Table S1. Primer Sequences

	Primer sequence
h C/EBPα forward	5'-TGG ACA AGA ACA GCA ACG AG-3'
h C/EBPα reverse	5'-TTG TCA CTG GTC AGC TCC AG-3'
m C/EBPα forward	5'-GAC CAT TAG CCT TGT GTG TAC TGT ATG-3'
m C/EBPα reverse	5'-TGG ATC GAT TGT GCT TCA AGT T-3'
GCSF-R forward	5'-ACC TGG GCA CAG CTG GAG TGG-3'
GCSF-R reverse	5'-CAG GCT GCT GTG AGC TGG GTC TGG-3'
Notch1 forward	5'-CAA CAT CCA GGA CAA CAT GG-3'
Notch1 reverse	5'-GGA CTT GCC CAG GTC ATC TA-3'
GAPDH forward	5'-ACC ACA GTC CAT GCC ATC AC-3'
GAPDH reverse	5'-TCC ACC ACC CTG TTG CTG TA-3'
mature miR-30c forward	5'-TGC TGT GTA AAC ATC CTA CAC TCT CAG CGT TTT GGC CAC TGA CTG ACG CTG AGA GTA GGA TGT TTA CA-3'
mature miR-30c reverse	5'-CCT GTG TAA ACA TCC TAC TCT CAG CGT CAG TCA GTG GCC AAA ACG CTG AGA GTG TAG GAT GTT TAC AC-3'
Notch1 3'UTR mut forward	5'-CAT GAC CAG ATG CGT CCC AAG ATG TTG ATT TTT ACT GTG TTT TAT AAA ATA CTG TCA AGT AAT CAG AAA AAG ACT TTA AAA GTG ATC TAC AT-3'
Notch1 3'UTR mut reverse	5'-ATG TAG ATC ACT TTT AAA GTC TTT TTC TGA TTA CTT GAC AGT ATT TTA TAA AAC ACA GTA AAA ATC AAC ATC TTG GGA CGC ATC TGG TCA TG-3'
Primer #1 forward	5'-ACA TCT GTC TCT ACA ATC TCA ACA-3'
Primer #1 reverse	5'-CAG GCA CTC TAT TTG ATG AAT GAA T-3'
Primer #2 forward	5'-CGA CCT TCA TCC CCC AGT TC-3'
Primer #2 reverse	5'-CAC CCT GCC TAT CCT TGT GG-3'
Primer #3 forward	5'-CAA GCC CTG TAG TTG GGG AG-3'
Primer #3 reverse	5'-AGC TTT AGT GGG GCA GAA GTC-3'
Primer #4 forward	5'-ACT CCA TTC ATG TGT ATG CCT CT-3'
Primer #4 reverse	5'-ATG CAG CTT CTC ACT CTC TGG-3'

h – human; m – mouse; mut – mutant; 3'UTR – 3' untranslated region

Table S2. Genetic and morphological characteristics of AML patients used for miRNA-30c analysis.

Patient No.	Morphology by FAB	karyotype	FLT3 mutation status	% blast cells	age	gender
	healthy	-	-	-	-	unknown
	healthy	-	-	-	-	unknown
	healthy	-	-	-	-	unknown
1	M4/5	normal	unknown	unknown	75	m
2	M1	normal	unknown	unknown	72	m
3	unclassified	normal	negative	unknown	21	m
4	unclassified	normal	TKD	unknown	39	f
5	unclassified	normal	negative	unknown	43	f
6	unclassified	normal	TKD	unknown	58	m
7	unclassified	normal	ITD	unknown	70	f
8	M5	complex	negative	90	65	f
9	M5	complex	unknown	unknown	73	m
10	M5	complex	unknown	90	56	m
11	M1	complex	unknown	unknown	60	m
12	unclassified	complex	ITD/ TKD	unknown	29	m
13	unclassified	complex	ITD	unknown	30	f
14	M3	t(15;17)	unknown	unknown	32	f
15	M3	t(15;17)	TKD	unknown	23	f
16	M3	t(15;17)	negative	unknown	50	m
17	M3	t(15;17)	negative	unknown	70	m
18	unclassified	t(8;21)	ITD	unknown	42	m
19	unclassified	t(8;21)	ITD/ TKD	unknown	67	m
20	M2	t(8;21)	unknown	unknown	40	m
21	M2	t(8;21)	unknown	23	43	f
22	unclassified	t(8;21)	negative	unknown	53	f
23	unclassified	t(8;21)	negative	unknown	42	m
24	unclassified	Inv(16)	negative	unknown	60	m
25	unclassified	Inv(16)	TKD	unknown	40	m
26	unclassified	Inv(16)	TKD	unknown	39	m
27	unclassified	Inv(16)	TKD	unknown	42	m
28	unclassified	Inv(16)	TKD	unknown	29	m
29	unclassified	Inv(16)	negative	unknown	41	f
30	unclassified	Inv(16)	negative	unknown	45	f

FAB indicates French-American-British; TKD - Tyrosinkinasedomaine; ITD - Internal Tandem Duplication; m - male; f – female

Table S3. Genetic and morphological characteristics of normal karyotype AML patients with *CEBPA* mutations and *CEBPA* wildtyp used for miRNA-30c analysis.

Patient No.	Morphology by FAB	Karyotype	CEBPA mutation status	% blast cells	FLT3 mutation status	age	gender
1	s-AML	normal	WT	46	negative	78	f
2	M4	normal	WT	unknown	negative	74	m
3	M5a	normal	WT	99	negative	82	m
4	M0	normal	WT	90	negative	63	f
5	unclassified	normal	monoallelic	unknown	negative	65	m
6	unclassified	normal	monoallelic	unknown	negative	50	m
7	unclassified	normal	monoallelic	unknown	negative	73	f
8	unclassified	normal	monoallelic	unknown	ITD	60	f
9	M2	normal	biallelic	66	negative	68	f
10	M2	normal	biallelic	22	negative	66	f
11	unclassified	normal	biallelic	unknown	negative	66	f
12	M1	normal	biallelic	58,5	negative	82	m

FAB indicates French-American-British; s-AML – secondary AML; WT - wildtype; m - male; f – female; ITD – Internal Tandem Duplication