Supplementary Table 6: Microarray statistical analyses for CIS genes differentially expressed from different AML patients in the 2 different Cohorts.

COHORT 1	Kruskal–Wallis statistic	Kruskal–Wallis *p*-value	-5/7(q) vs NK	8 vs NK	inv16 + t(8;21) vs NK	Other vs NK	t(15;17) vs NK	8 vs -5/7(q)	inv16 + t(8;21) vs -5/7(q)	Other vs -5/7(q)	t(15;17) vs -5/7(q)	inv16 + t(8;21) vs 8	t(15;17) vs 8	inv16 + t(8;21) vs Complex	t(15;17) vs Complex	Other vs inv16 + t(8;21)	t(15;17) vs inv16 + t(8;21)	t(15;17) vs Other
C2CD2212875sat	29,363270	0,000052	0,025631		0,000043													
CLCN3201735sat	19,747510	0,003071					0,023642											
HPGD203913sat	60,500389	< 0,000001	0,000233		< 0,000001						0,004124					0,006479	0,000052	
HPGD203914xat	61,939700	< 0,000001	0,000855		< 0,000001						0,006483					0,000471	0,000062	
HPGD211548sat	50,260534	< 0,000001			< 0,000001							0,006516				0,002091	0,000102	
HPGD211549sat	38,709304	0,000001	0,003468		0,000003						0,037275					0,010404	0,003665	
PCGF5226326at	29,078276	0,000059			0,000115											0,000999		
PCGF5229194at	40,478669	< 0,000001			0,000002				0,001998			0,032020				0,000044		
PCGF5235331xat	38,675400	0,000001			0,000007				0,000238					0,040353		0,000184		
TRPS1218502sat	45,113093	< 0,000001	0,014060	0,014179	0,001343		0,041619				0,000194		0,000098		0,017625		0,000021	0,018358
UBE3A213128sat	20,699939	0,002077			0,010378							0,037003				0,007301		

COHORT 2	Kruskal–Wallis statistic	Kruskal–Wallis *p*-value	-5/7(q) vs NK	8 vs NK	inv16 + t(8;21) vs NK	Other vs NK	t(15;17) vs NK	8 vs -5/7(q)	inv16 + t(8;21) vs -5/7(q)	Other vs -5/7(q)	t(15;17) vs -5/7(q)	inv16 + t(8;21) vs 8	t(15;17) vs 8	inv16 + t(8;21) vs Complex	t(15;17) vs Complex	Other vs inv16 + t(8;21)	t(15;17) vs inv16 + t(8;21)	t(15;17) vs Other
C2CD2212875sat	15,286023	0,018145			0,006122													
CLCN3201735sat	25,635072	0,000260					0,025069		0,009409									
HPGD203913sat	31,313617	0,000022	0,006103		0,000058													
HPGD203914xat	32,178426	0,000015			0,000028													
HPGD211548sat	31,885699	0,000017			0,000015													
HPGD211549sat	32,942632	0,000011			0,000518													
PCGF5226326at	34,889196	0,000005			0,000006									0,042645		0,004267		
PCGF5229194at	38,665092	0,000001			< 0,000001		0,037611							0,031657		0,017497		
PCGF5235331xat	27,196435	0,000133			0,000227													
TRPS1218502sat	25,221931	0,000311	0,033463															
UBE3A213128sat	21,947722	0,001238			0,000639													

Microarray statistical analyses for CIS genes differentially expressed from different AML patients in the 2 different Cohorts. As AML patients are characterized by different chromosomal aberrations or mutations, we divided the AML patients in different groups according to their mutation: 1) Normal karyotype (NK, N=101 Cohort1; 86 Cohort2); 2) CBF-associated AMLs (characterized by chromosomal abnormalities as inv(16) or t(8;21), N=18+21 Cohort1; 15+14 Cohort2); 3) PML/RARα translocations (t(15,17), N=17 Cohort1, 4 Cohort2); 4) complete or partial deletions of chromosomes 7 or 5 (N=17 Cohort1, 12 Cohort2); 5) trisomy of chromosome 8 (N=13 Cohort1, 7 Cohort2); 6) complex karyotype (N=7 Cohort1, 6 Cohort2); 7) patients with other translocations (N=30 Cohort1, 21 Cohort2). For microarray gene expression analyses of AML samples, nonparametric Kruskal–Wallis Analysis Of Variance (ANOVA) was performed to identify overall differences in gene expression between AML groups. Whenever significant, Wilcoxon rank sum test for pairwise comparisons adjusted with Bonferroni correction was applied. For each gene is reported: the value of the Kruskal-Wallis test statistic; the correspondent *p*-value and only significant pairwise contrasts after Bonferroni correction. For some genes different microarray probesets are provided. All the analyses were performed in R-statistical software (version 2.15.3; see http://www.R-project.org).