

34 up-regulated					76 down-regulated					9 discordant				
Gene name	Transcript type	Linear FC PIF (19) vs PIR (175)	Linear FC NUP98+ (21) vs Other AML (137)		Gene name	Transcript type	Linear FC PIF (19) vs PIR (175)	Linear FC NUP98+ (21) vs Other AML (137)		Gene name	Transcript type	Linear FC PIF (19) vs PIR (175)	Linear FC NUP98+ (21) vs Other AML (137)	
1	RNU7-115P	snRNA	22.1	2.5	1	GPR88	Coding	-54.0	-9.1	1	CLDN10	Coding	6.2	-13.0
2	AC092171.1	antisense	9.7	2.5	2	CLIP3	Coding	-51.8	-42.4	2	CHRN84	Coding	2.7	-9.1
3	TRGV2	TR_V_gene	9.3	4.1	3	XPNPEP2	Coding	-20.5	-6.8	3	NA	Coding	2.7	-2.2
4	SPINK2	Coding	8.3	4.7	4	NA	Coding	-20.5	-16.9	4	AC244035.1	antisense	2.5	-5.5
5	CCDC144CP	pseudogene	5.5	1.9	5	FLT4	Coding	-20.1	-55.3	5	LINC01006	processed transcript	2.2	-2.5
6	AP002812.2	antisense	4.6	2.1	6	ALPK3	Coding	-19.6	-5.2	6	GCH1	Coding	-2.3	1.8
7	TMA7	Coding	4.6	1.6	7	HSPG2	Coding	-18.2	-2.9	7	GASK1B	Coding	-3.4	3.0
8	DEFA4	Coding	4.3	5.8	8	VIT	Coding	-17.7	-41.4	8	STAB1	Coding	-3.5	3.8
9	SPCS2	Coding	4.2	1.5	9	RCOR2	Coding	-17.6	-10.4	9	DEFA1	Coding	-73.9	6.7
10	CDCP1	Coding	4.0	2.4	10	SEPN1	Coding	-14.4	-1.7					
11	ANP32E	Coding	4.0	2.2	11	PODXL2	Coding	-14.1	-2.6					
12	LINC01881	pseudogene	4.0	1.5	12	PACS1	Coding	-11.5	-1.5					
13	AC026124.1	sense intronic	3.6	2.5	13	GLIS3	Coding	-11.1	-20.5					
14	CAPZA1	Coding	3.2	1.5	14	GPR12	Coding	-10.2	-66.5					
15	NT5C3AP1	pseudogene	3.0	1.6	15	CELSR3	Coding	-10.1	-2.2					
16	PAFAH1B2	Coding	2.8	1.6	16	AADAT	Coding	-9.5	-6.5					
17	TRDMT1	Coding	2.7	1.6	17	AC104809.2	processed transcript	-9.2	-15.2					
18	LGALS12	Coding	2.6	2.1	18	LPAR5	Coding	-8.8	-5.8					
19	CCR6	Coding	2.6	3.0	19	EVC2	Coding	-7.9	-17.9					
20	NRG4	Coding	2.4	3.6	20	ABCD1	Coding	-7.5	-2.1					
21	GNB5	Coding	2.2	2.1	21	GRAMD1A	Coding	-7.3	-1.9					
22	FGFR10P2	Coding	2.2	1.5	22	SLC24A3	Coding	-7.0	-4.1					
23	TMEM241	Coding	2.2	1.6	23	LRP5	Coding	-6.7	-2.0					
24	PCNT	Coding	2.2	1.5	24	PAQR5	Coding	-6.4	-6.5					
25	NDUFA5	Coding	2.1	1.4	25	RD3	Coding	-6.2	-47.7					
26	MAN1A2	Coding	2.1	1.6	26	NTNG2	Coding	-6.2	-2.6					
27	GCNT1	Coding	2.1	2.0	27	TRH	Coding	-5.9	-8.1					
28	NT5C3A	Coding	2.0	1.4	28	DCHS1	Coding	-5.8	-7.4					
29	C9orf78	Coding	2.0	1.4	29	KIF26B	Coding	-5.8	-3.7					
30	CPNE3	Coding	1.9	2.1	30	AC239798.1	lincRNA	-5.5	-4.6					
31	SRP54	Coding	1.8	1.4	31	FBLN2	Coding	-5.4	-2.9					
32	CCDC25	Coding	1.7	1.6	32	ARHGEF17	Coding	-5.3	-4.3					
33	CTR9	Coding	1.7	1.6	33	STK32B	Coding	-5.2	-4.4					
34	GOT1	Coding	1.4	1.7	34	CAPN15	Coding	-5.2	-1.5					
					35	TSC2	Coding	-5.2	-1.4					
					36	MAP4K2	Coding	-5.2	-1.6					
					37	HDAC7	Coding	-5.0	-1.5					
					38	CENPV	Coding	-4.9	-2.2					
					39	WHRN (DFNB31)	Coding	-4.8	-7.4					
					40	CACNA2D2	Coding	-4.8	-9.7					
					41	KCTD15	Coding	-4.7	-2.6					
					42	SHB	Coding	-4.5	-3.0					
					43	MMP25-AS1	antisense	-4.3	-3.0					
					44	PALM	Coding	-4.3	-9.7					
					45	TNFRSF21	Coding	-4.1	-2.4					
					46	DAGLA	Coding	-4.1	-3.2					
					47	ROBO4	Coding	-4.1	-10.3					
					48	RNF217	Coding	-4.0	-3.1					
					49	VSIG4	Coding	-4.0	-18.0					
					50	ENPP3	Coding	-4.0	-5.9					
					51	RNF217-AS1	antisense	-4.0	-6.3					
					52	SAP25	Coding	-3.9	-1.6					
					53	DCLK2	Coding	-3.8	-5.1					
					54	ZNF704	Coding	-3.8	-5.0					
					55	HPGD	Coding	-3.7	-7.1					
					56	DNM1	Coding	-3.7	-3.5					
					57	MMP28	Coding	-3.6	-8.1					
					58	ZNF467	Coding	-3.3	-3.1					
					59	ATP2A1	Coding	-3.3	-2.5					
					60	ARHGEF40	Coding	-3.2	-2.1					
					61	TANC1	Coding	-3.2	-10.9					
					62	PKN1	Coding	-3.1	-1.3					
					63	LOXHD1	Coding	-3.1	-11.8					
					64	TRIO	Coding	-3.1	-1.8					
					65	KDM4B	Coding	-3.0	-1.6					
					66	TRAK1	Coding	-3.0	-1.4					
					67	USP2	Coding	-3.0	-5.5					
					68	ZFYVE9	Coding	-2.9	-5.7					
					69	POU6F1	Coding	-2.4	-2.6					
					70	PRRT4	Coding	-2.3	-7.1					
					71	NAV1	Coding	-2.2	-8.1					
					72	SCMH1	Coding	-2.1	-1.8					
					73	SPTAN1	Coding	-2.1	-1.7					
					74	LPAR2	Coding	-1.9	-1.7					
					75	ZCCHC14	Coding	-1.8	-1.9					
					76	VGLL4	Coding	-1.4	-1.8					

Table S1. NUP98/PIF-associated DEGs: 34 upregulated (on the left); 76 downregulated (in the middle); 9 discordant (on the right, excluded for next analysis).

TARGET						
Gene symbol	Sensitivity (%)	Specificity (%)	PPV (%)	NPV (%)	AUC	<i>p</i> -value AUC
RNU7-115P	94.7	99.4	94.7	99.4	1.00	<0.0001
AC092171.1	94.7	93.1	60.0	99.4	0.97	<0.0001
TRGV2	84.2	85.7	39.0	98.0	0.87	<0.0001
SPINK2	78.9	86.3	38.5	97.4	0.89	<0.0001
CCDC144CP	89.5	82.9	44.7	98.6	0.93	<0.0001
AP002812.2	84.2	84.0	36.4	98.0	0.90	<0.0001
TMA7	100.0	100.0	100.0	100.0	1.00	<0.0001
DEFA4	78.9	70.9	22.7	96.9	0.79	<0.0001
SPCS2	94.7	100.0	100.0	99.4	0.99	<0.0001
CDCP1	52.6	89.7	35.7	94.6	0.76	0.0002
ANP32E	100.0	92.6	59.4	100.0	0.99	<0.0001
LINC01881	94.7	95.4	69.2	99.4	0.97	<0.0001
AC026124.1	73.7	78.9	27.5	96.5	0.76	0.0002
CAPZA1	89.5	94.9	65.4	98.8	0.95	<0.0001
NT5C3AP1	94.7	84.6	40.0	99.3	0.95	<0.0001
PAFAH1B2	84.2	86.9	41.0	98.1	0.91	<0.0001
TRDMT1	100.0	78.3	33.3	100.0	0.94	<0.0001
LGALS12	84.2	68.6	22.5	97.6	0.76	<0.0001
CCR6	47.4	89.7	33.3	94.0	0.64	0.0452
NRG4	89.5	68.6	23.6	98.7	0.78	<0.0001
GNB5	84.2	85.7	39.0	98.0	0.89	<0.0001
FGFR1OP2	84.2	90.3	48.5	98.1	0.92	<0.0001
TMEM241	94.7	78.3	32.1	99.3	0.92	<0.0001
PCNT	89.5	82.9	36.2	98.6	0.90	<0.0001
NDUFA5	78.9	95.4	65.2	97.7	0.93	<0.0001
MAN1A2	73.7	90.3	45.2	96.9	0.89	<0.0001
GCNT1	63.2	84.0	30.0	95.5	0.83	<0.0001
NT5C3A	89.5	88.6	45.9	98.7	0.93	<0.0001
C9orf78	100.0	86.3	44.2	100.0	0.97	<0.0001
CPNE3	94.7	68.6	24.7	99.2	0.84	<0.0001
SRP54	84.2	90.9	50.0	98.1	0.91	<0.0001
CCDC25	73.7	88.0	40.0	96.9	0.84	<0.0001
CTR9	94.7	61.1	20.9	99.1	0.82	<0.0001
GOT1	84.2	68.6	22.5	97.6	0.82	<0.0001

Table S2. A) Sensitivity, Specificity, Positive Predictive Value (PPV) and Negative Predictive Values (NPV) for all 34 upregulated highly confident NUP98/PIF-associated DEGs. All indices were calculated using best cut-off in Roc Curve for distinguishing PIF and PIR patients.

Gene symbol	Sensitivity (%)	Specificity (%)	PPV (%)	NPV (%)	AUC	p-value AUC
CACNA2D2	68.4	51.4	13.3	93.8	0.64	0.0505
CELSR3	84.2	73.1	25.4	97.7	0.86	<0.0001
SCMH1	89.5	34.3	12.9	96.8	0.68	0.0102
USP2	89.5	28.0	11.9	96.1	0.52	0.7291
FLT4	68.4	80.6	27.7	95.9	0.81	<0.0001
TRIO	89.5	47.4	15.6	97.6	0.71	0.0022
HDAC7	94.7	80.6	34.6	99.3	0.91	<0.0001
LPAR2	68.4	55.4	14.3	94.2	0.58	0.2325
GRAMD1A	100.0	88.6	48.7	100.0	0.96	<0.0001
DFNB31	78.9	64.6	19.5	96.6	0.74	0.0007
PALM	94.7	25.1	12.1	97.8	0.56	0.4286
LRP5L	5.3	62.9	1.5	85.9	0.62	0.0897
ABCD1	31.6	89.7	25.0	92.4	0.90	<0.0001
TSC2	94.7	88.0	46.2	99.4	0.94	<0.0001
CAPN15	100.0	74.9	30.2	100.0	0.92	<0.0001
CLIP3	94.7	42.9	15.3	98.7	0.68	0.0095
DNM1	89.5	44.0	14.8	97.5	0.72	0.0021
GLIS3	47.4	88.0	30.0	93.9	0.68	0.0097
SHB	73.7	70.3	21.2	96.1	0.75	0.0003
AADAT	68.4	86.3	35.1	96.2	0.81	<0.0001
ARHGEF17	57.9	88.0	34.4	95.1	0.79	<0.0001
PODXL2	94.7	66.3	23.4	99.1	0.87	<0.0001
TANC1	47.4	42.9	8.3	88.2	0.51	0.8922
XPNPEP2	68.4	89.7	41.9	96.3	0.81	<0.0001
PKN1	73.7	80.6	29.2	96.6	0.81	<0.0001
KDM4B	89.5	57.1	18.5	98.0	0.72	0.0016
MMP28	10.5	69.1	3.6	87.7	0.51	0.8549
GPR12	68.4	71.4	20.6	95.4	0.70	0.0034
NAV1	89.5	29.1	12.1	96.2	0.53	0.6499
DAGLA	94.7	36.6	14.0	98.5	0.68	0.0114
ALPK3	73.7	94.3	58.3	97.1	0.89	<0.0001
PAQR5	52.6	87.4	31.3	94.4	0.71	0.0028
ZCCHC14	84.2	36.0	12.5	95.5	0.55	0.4633
HSPG2	94.7	80.0	34.0	99.3	0.92	<0.0001
VGLL4	10.5	69.1	3.6	87.7	0.55	0.4425
TNFRSF21	94.7	43.4	15.4	98.7	0.67	0.0133
RNF217	73.7	64.0	18.2	95.7	0.69	0.0069
STK32B	78.9	57.7	16.9	96.2	0.67	0.0146

Gene symbol	Sensitivity (%)	Specificity (%)	PPV (%)	NPV (%)	AUC	p-value AUC
KCTD15	57.9	85.7	30.6	94.9	0.76	0.0002
ROBO4	57.9	87.4	33.3	95.0	0.67	0.0148
ENPP3	89.5	22.9	11.2	95.2	0.72	0.0013
VSIG4	63.2	56.0	13.5	93.3	0.52	0.7814
ZFYVE9	100.0	87.4	46.3	100.0	0.59	0.1761
SEPN1	78.9	58.9	17.2	96.3	0.97	<0.0001
KIF26B	73.7	37.1	11.3	92.9	0.71	0.0022
HPGDS	89.5	50.9	16.5	97.8	0.53	0.6546
FBLN2	47.4	81.7	22.0	93.5	0.73	0.0008
ZNF704	94.7	58.3	19.8	99.0	0.65	0.0381
ANXA8	68.4	74.3	22.4	95.6	0.76	0.0002
ARHGEF40	57.9	92.0	44.0	95.3	0.72	0.0015
DCHS1	94.7	70.3	25.7	99.2	0.77	0.0001
CENPV	42.1	90.3	32.0	93.5	0.88	<0.0001
LOXHD1	68.4	89.7	41.9	96.3	0.66	0.0266
RCOR2	100.0	74.3	29.7	100.0	0.83	<0.0001
MAP4K2	42.1	78.3	17.4	92.6	0.90	<0.0001
DCLK2	68.4	65.7	17.8	95.0	0.57	0.3277
TRH	47.4	69.1	14.3	92.4	0.68	0.0111
EVC2	100.0	95.4	70.4	100.0	0.57	0.3214
PACS1	78.9	60.6	17.9	96.4	0.99	<0.0001
ZNF467	68.4	82.9	30.2	96.0	0.71	0.0025
GPR88	89.5	68.0	23.3	98.3	0.79	<0.0001
TRAK1	89.5	38.9	13.7	97.1	0.80	<0.0001
POU6F1	26.3	82.9	14.3	91.2	0.64	0.0476
LPAR5	63.2	71.4	19.4	94.7	0.85	<0.0001
SLC24A3	89.5	62.3	20.5	98.2	0.71	0.0027
ATP2A1	84.2	68.0	22.2	97.5	0.73	0.0008
NTNG2	89.5	53.1	17.2	97.9	0.80	<0.0001
SPTAN1	89.5	37.1	13.4	97.0	0.62	0.0938
RD3	78.9	44.0	13.3	95.1	0.62	0.0753
VIT	31.6	90.9	27.3	92.4	0.61	0.1189
SAP25	78.9	27.4	10.6	92.3	0.89	<0.0001
AC104809.2	73.7	49.7	13.7	94.6	0.52	0.7259
PRRT4	84.2	50.9	15.7	96.7	0.62	0.0865
RP11-403I13.9	68.4	64.0	17.1	94.9	0.66	0.0206
RP11-510H23.1	84.2	62.3	19.5	97.3	0.61	0.1105
RP11-473M20.7	78.9	53.1	15.5	95.9	0.73	0.0008

Table S2. B) Sensitivity, Specificity, Positive Predictive Value (PPV) and Negative Predictive Values (NPV) for all 76 downregulated highly confident NUP98/PIF-associated DEGs. All indices were calculated using best cut-off in Roc Curve for distinguishing PIF and PIR patients.

Gene name	TARGET program	Adj. <i>p-value</i>	TARGET program	Adj. <i>p-value</i>	Noort Study Linear	Adj. <i>p-value</i>
	Linear		Linear		FoldChange	
	FoldChange NUP98+ vs NUP98-		FoldChange PIF vs PIR		NUP98-NSD1+ vs NUP98- NSD1-	
Upregulated						
NRG4	3.6	0.0006800	2.4	0.0073354	15.9	2.30E-16
DEFA4	5.8	0.0006774	4.3	0.0016807	3.7	0.0003144
SPINK2	4.7	0.0002229	8.3	2.16E-11	19.6	8.01E-14
CPNE3	2.1	0.0006891	1.9	0.0032273	2.1	0.0000009
LGALS12	2.1	0.0229131	2.6	0.0001047	3.1	1.38E-08
CDCP1	2.4	0.0268617	4.0	4.13E-07	8.1	1.82E-15
RP11-305O6.3	2.5	0.0042777	3.6	6.47E-07	2.9	0.0000095
GCNT1	2.0	0.0044462	2.1	0.0002831	2.7	1.74E-12
Downregulated						
XPNPEP2	-6.8	0.0025736	-20.5	7.21E-07	-3.5	1.18E-09
RCOR2	-10.4	7.79E-06	-17.6	3.62E-08	-5.9	6.36E-12
CELSR3	-2.2	0.0260854	-10.1	1.74E-11	-2.1	2.69E-07
FLT4	-55.3	9.77E-09	-20.1	1.40E-05	-4.4	0.0000051
DFNB31	-7.4	7.30E-11	-4.8	1.06E-06	-2.8	3.81E-09
FBLN2	-2.9	0.0345421	-5.4	0.0007283	-4.1	1.41E-07
VIT	-41.4	0.0027521	-17.7	0.0090988	-2.6	0.0001133
GPR12	-66.5	2.31E-06	-10.2	0.0044818	-6.1	1.39E-07
EVC2	-17.9	0.0010810	-7.9	0.0126903	-4.0	0.0000072
PRRT4	-7.1	1.75E-06	-2.3	0.0243112	-3.4	0.0000033
POU6F1	-2.6	1.98E-06	-2.4	3.83E-05	-2.6	1.72E-16
GLIS3	-20.5	0.0001184	-11.1	0.0005791	-4.0	0.0000048
LOXHD1	-11.8	4.05E-05	-3.1	0.0470452	-2.7	0.0057301
DCHS1	-7.4	3.05E-07	-5.8	1.70E-05	-4.3	6.37E-12
DCLK2	-5.1	0.0132501	-3.8	0.0219993	-3.6	0.0000083
ALPK3	-5.2	0.0016214	-19.6	1.52E-08	-3.4	1.64E-08
RP11-403I13.9	-4.6	0.0467955	-5.5	0.0117711	-3.0	0.0000176
CACNA2D2	-9.7	0.0001959	-4.8	0.0031621	-5.1	4.90E-10
RP11-510H23.1	-6.3	0.0053864	-4.0	0.0278720	-3.6	0.0000011
LPAR5	-5.8	1.23E-07	-8.8	2.59E-09	-2.3	5.94E-08
ZFYVE9	-5.7	0.0001245	-2.9	0.0154511	-4.7	4.19E-10
USP2	-5.5	0.0032263	-3.0	0.0401788	-7.1	1.02E-14
KCTD15	-2.6	0.0016137	-4.7	1.78E-07	-3.3	9.71E-10
TANC1	-10.9	4.79E-05	-3.2	0.0214368	-2.4	0.0011365
NAV1	-8.1	9.53E-08	-2.2	0.0496939	-2.6	0.0000136
AADAT	-6.5	0.0013006	-9.5	0.0003850	-10.9	4.53E-13
RNF217	-3.1	0.0399202	-4.0	0.0043638	-6.1	3.60E-08
ZNF704	-5.0	0.0054430	-3.8	0.0065976	-28.1	4.03E-29
SLC24A3	-4.1	0.0234298	-7.0	0.0014564	-3.1	0.0005889
TRH	-8.1	0.0066287	-5.9	0.0090749	-2.7	0.0402381
HPGD	-7.1	0.0011962	-3.7	0.0108997	-10.6	7.78E-18

Table S3. Thirty-nine differentially expressed genes in three different groups: NUP98+ vs NUP98- and PIF vs PIR from TARGET program, then NUP98-NSD1+ vs NUP98-NSD1- from Noort study. We show 8 upregulated and 31 downregulated transcripts, obtained by crossing our list of 110 NUP98/PIF-associated DEGs and 3026 NUP98-NSD1 differentially expressed genes reported by Noort et al.

	AIEOP LAM 2002/01	TARGET PROGRAM		LOCAL COHORT	
	Total AML patients	PIF	PIR	PIF	PIR
Patients, <i>n</i> (%)	482	19	175	4	8
Gender (male/female)	262 (52%)/ 220	12 (63%)/ 7	91(52%)/ 84	0/4	4/4
Age at diagnosis					
< 1 year	63 (13%)	0	8 (4%)	0	0
1-2 years	52 (10%)	3 (16%)	17 (10%)	0	0
2-10 years	181 (38%)	8 (42%)	63 (36%)	2 (50%)	3 (37,5%)
> 10 years	186 (39%)	8 (42%)	87 (50%)	2 (50%)	5 (62,5%)
WBC at diagnosis (×10⁹/l)					
<10	171 (35%)	2 (10%)	19 (11%)	2 (50%)	5 (62,5%)
10-99	236 (49%)	10 (53%)	116 (66%)	2 (50%)	3 (37,5%)
>100	75 (16%)	7 (37%)	40 (23%)	0	0
FAB Subtype					
M0	34 (7%)	3 (16%)	1 (0,6 %)	0	0
M1	88 (18%)	1 (5%)	25 (14%)	3 (75%)	2 (25%)
M2	91 (19%)	4 (21%)	42 (24%)	1 (25%)	2 (25%)
M4	83 (17%)	2 (11%)	44 (25%)	0	2 (25%)
M5	117 (24%)	3 (16%)	33 (19%)	0	1 (12,5%)
M6	5 (1%)	0	3 (2%)	0	0
M7	44 (9%)	1 (5%)	6 (3,4%)	0	1 (12,5%)
Unclassifiable/not known	20 (4%)	5 (26%)	21 (12%)	0	0
Patients with available cytogenetic data	418				
Normal	166 (39%)	7 (37%)	46 (26%)		
<i>t</i> (8;21), <i>t</i> (16;16) or <i>inv</i> (16)	99 (24%)	1 (5%)	55 (31%)	0	0
<i>t</i> (9;11) or MLL-t	65 (15%)	2 (11%)	31 (18%)	0	0
NUP98-rearrangements	25 (5%)	4 (21%)	12 (7%)	1 (25%)	4 (50%)
Other	61 (15%)	9 (47%)	34 (19%)	1 (25%)	6 (75%)
Complex karyotype*	27 (6%)	1 (5%)	23 (13%)	1 (25%)	2 (25%)
Unknown	0	0	9 (5%)	1 (25%)	0
Patients tested for molecular aberrations	384				
<i>FLT3</i> -ITD	42 (11%)	3 (16%)	21 (12%)	0	5 (62,5%)
<i>FLT3</i> activating loop mutations	10 (3%)	2 (11%)	14 (8%)	0	0
Other molecular aberration	244				
<i>NPM1</i> mutations	14 (6%)	0	11 (6%)	0	0
<i>CEBPA</i> mutations	18 (7%)	0	17 (10%)	0	0
<i>WT1</i>	NA	4 (21%)	9 (5%)	0	0
*Complex Karyotype, ≥ 3 abnormalities (numerical or structural)					

Table S4. **Characteristics of patients with AML included in our study.** PIF: Primary Induction Failure; PIR: Primary Induction Response; Number of cases (% of cases per category); N.A: not available; * Complex karyotype: ≥ than 3 chromosomal abnormalities numerical or structural).

	TARGET PROGRAM	
	NUP98r+	NUP98r-
Patients, n (%)	21	137
Gender (male/female)	15/ 6	70/ 67
Age at diagnosis		
< 1 year	0	11
1-2 years	3	13
2-10 years	9	46
> 10 years	9	67
WBC at diagnosis (×10⁹/l)		
<10	4	14
10-99	11	89
>100	6	34
FAB Subtype		
M0	0	3
M1	2	11
M2	7	35
M4	4	37
M5	4	34
M6	2	0
M7	1	4
Unclassifiable/not known	1	13
Overall Survival (days)	1214	Undefined
Patients with available cytogenetic data		
Normal	12	7
<i>t(8;21), t(16;16) or inv(16)</i>	0	68
<i>t(9;11) or MLL-t</i>	0	39
NUP98-rearrangements	21	0
Other	7	20
Complex karyotype*	3	11
Unknown	1	3
Patients tested for molecular aberrations		
<i>FLT3</i> -ITD	9	7
<i>FLT3</i> activating loop mutations	0	10
Other molecular aberration		
<i>NPM1</i> mutations	0	0
<i>CEBPA</i> mutations	1	1
<i>WT1</i>	6	6

Table S5. Clinical and pathological features and molecular alterations of selected TARGET samples, analyzed by transcriptome analysis and subdivided in NUP98r positive and NUP98r negative patients

Transcript (Accession number)	Forward Primer	Reverse Primer	Annealing Temperature	Fragment size
SPINK2 (NM_001271718.2)	2F- TCCCTCAATTGGTCTGTTTC	3R-CCTTCCCTGATTTTCATGCAC	60°C	151 bp
TMA7 (NM_183250.2)	2F- AGAAGCAGGCCAAGGAGATG	4R GCCAGATTTCCTTAATCCACCTG	59°C	140 bp
SPCS2 (NM_014752.3)	2F TGACAAGTGGGATGGATCAGC	3R TACAGATGGTGAGGCGACCA	58°C	122 bp
CDCP1 (NM_022842.5)	4F- TCAACCTCTCTCTGCAAGGC	5R-CGCTCATTACTCAAGTCAACC	58°C	133 bp
CAPZA1 (NM_006135.3)	7F ACCATCACACCACCTACAGC	9-10R TCACTAATTGCTGTCTGATACTCAT	60°C	197 bp
FGFR1OP2 (NM_015633.3)	3F- ACGGTCCACGTTAGTTATGG	4R-AAGTTCCAAGGCCGACTGAT	56°C	115 bp
MAN1A2 (NM_006699.5)	12F ATTGCCGAGTTAATGGTGGGT	13R TCGAACAGCAGGATTACCTGA	57°C	233 bp
NT5C3A (NM_001002010.5)	7F- AACATAGCATCCCCGTGTTC	7/8R-AATCCTTTGAGCACCCCAGTT	57°C	145 bp
SRP54 (NM_003136.4)	9F CATGCAAAAGGAGGTGGTGC	11R TCAGTCCTTCAATGTCGCCC	57°C	154 bp
MALAT1 (NR_002819.4)	3endF- AAAGCAAGGTCTCCCCACAAG	3endF- GGTCTGTGCTAGATCAAAAGGCA	61°C	73 bp

Table S6. Primers details used for qRT-PCR