

Table S7. Sequence analysis of AML1-ETO target genes by the PSCAN algorithm against the JASPAR database. The full list of significantly enriched TFBS ($p < 0.01$) is reported.

TF_NAME	MATRIX_ID	Z_SCORE	P_VALUE
SP1	MA0079.2	19.1611	3.03E-84
Egr1	MA0162.1	19.0515	3.30E-84
TFAP2A	MA0003.1	18.4008	4.52E-77
PLAG1	MA0163.1	15.1082	1.98E-53
Klf4	MA0039.2	15.0755	7.09E-53
Zfx	MA0146.1	14.8979	6.66E-52
Pax5	MA0014.1	13.0516	1.18E-40
Mycn	MA0104.2	12.6139	2.92E-38
Arnt::Ahr	MA0006.1	12.4311	5.56E-37
NFKB1	MA0105.1	12.3661	1.09E-36
Myc	MA0147.1	10.711	3.41E-28
HIF1A::ARNT	MA0259.1	10.7559	4.86E-28
INSM1	MA0155.1	10.3506	2.74E-26
CTCF	MA0139.1	8.70288	3.24E-19
E2F1	MA0024.1	8.68949	3.27E-19
Zfp423	MA0116.1	8.26467	1.86E-17
MIZF	MA0131.1	7.7533	1.22E-15
Tcfcp2l1	MA0145.1	7.65411	2.95E-15
GABPA	MA0062.2	7.58255	5.77E-15
MZF1_1-4	MA0056.1	7.49379	1.87E-14
NHLH1	MA0048.1	6.73477	3.14E-12
EBF1	MA0154.1	6.68195	4.52E-12
ESR1	MA0112.2	6.40147	3.24E-11
RREB1	MA0073.1	5.92496	7.08E-10
NF-kappaB	MA0061.1	5.84013	1.23E-09
Arnt	MA0004.1	5.78783	1.66E-09
MZF1_5-13	MA0057.1	5.62863	4.64E-09
REST	MA0138.2	5.28561	3.52E-08
USF1	MA0093.1	4.74414	5.86E-07
ELK1	MA0028.1	4.2171	8.18E-06
ELK4	MA0076.1	4.19955	9.14E-06
EWSR1-FLI1	MA0149.1	3.80166	5.14E-05
znf143	MA0088.1	3.66744	9.03E-05
HNF4A	MA0114.1	2.93542	0.00131561
PPARG::RXRA	MA0065.2	2.81117	0.00202478
Myf	MA0055.1	2.63158	0.00362293
MYC::MAX	MA0059.1	2.28146	0.00985541