

Supplementary Figure 1. Diagram displaying CpG-methylation status around the BCL7A TSS. Genomic DNA from the NB4 cell line was subjected to bisulfite 2 conversion and used for subsequent TA-cloning. Then, nine independent amplicons were analysed by Sanger sequencing. 61 CpG sites included in the 579 bp

amplicon (chr12:122,459,192 - 122,459,770 GRCh37; hg19 genome assembly) were assessed. 4

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Long isoform extended sequence

Lentiviral plasmid expressing BCL7A versions

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- 6 Supplementary Figure 2. Schematic representation of the different lentiviral plasmids used in the experimental procedures. The specific region of the long
- 7 isoform of BCL7A is colored in blue. The specific region that is deleted in the BCL7A mutant (Δ27-BCL7A) is colored in green. The Empty Vector (EV) has the
- 8 pLVX-IRES-ZsGreen1 structure without any insert.



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Supplementary Figure 3. Western blot including the Decitabine (DAC) treatment over the NB4 cell line shown in Fig. 2c. Here we also show the rest of the lanes including a negative control of BCL7A expression (KM-H2 cell line, which has no BCL7A expression), and a positive control (Daudi cell line) which expresses average BCL7A levels. The band which appears in KM-H2 sample is an inespecific band due to an inespecific binding of the anti-BCL7A (Cat#HPA019762) that we used.

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30 Fraction (1kb upstream TSS) vs BCL7A expression level. NB4 and M07e are marked.





Supplementary Figure 6. Competition cell growth effect of BCL7A expression restoration *on in vitro* proliferation. Competition cell growth assay of non-transduced M-07e cells vs M-07e cells
transduced with either pLVX-IRES-ZsGreen1 plasmid expressing wild-type BCL7A, mutant BCL7A
(Δ27-BCL7A), or empty vector. All constructs were evaluated in a time course of ZsGreen1+ %
measurements on days 0, 3, 9, 12, 18, 23 and 26. This assay involves the co-culture of an M-07e
model transduced with one of the plasmids together with non-transduced M-07e cells.

39 Supplementary Table 1

Cell line	Subtype	BCL7A mRNA, log2(TPM+1)
OCI-AML3	AML	0,028569152
AML-193	AML	0,604071324
NB4	AML	1,007195501
BDCM	AML	1,827819025
HEL	AML	2,039138394
OCI-M2	AML	2,056583528
HEL 92.1.7	AML	2,341985747
NA	AML	2,40053793
HL-60	AML	2,580145484
MUTZ-8	AML	2,587364991
NOMO-1	AML	2,587364991
TF-1	AML	2,733354341
F-36P	AML	2,752748591
OCI-M1	AML	2,794935663
MOLM-14	AML	2,944858446
SHI-1	AML	3,016139703
OCI-AML4	AML	3,025028794
SKM-1	AML	3,026800059
СМК	AML	3,08236197
NA	AML	3,116031993
CMK-11-5	AML	3,122672719
SKNO-1	AML	3,148934105
MV4;11	AML	3,277984747
U-937	AML	3,353323291
PL-21	AML	3,49057013
KO52	AML	3,614709844
KASUMI-1	AML	3,626439137
ME-1	AML	3,635754391
SIG-M5	AML	3,708187236
EOL-1	AML	3,786596362
M-07e	AML	3,881664619
OCI-AML5	AML	3,944858446
MONO-MAC-1	AML	3,956056652
P31/FUJ	AML	3,957914599
NA	AML	3,9800253
Set-2	AML	4,06436554
KG-1	AML	4,196134881
Kasumi-6	AML	4,239550797
MOLM-16	AML	4,268284667
THP-1	AML	4,283180979
MONO-MAC-6	AML	4,436961338
GDM-1	AML	4,467931546
MOLM-13	AML	4,627023106
OCI-AML2	AML	4,757023247

Cell line	Subtype	BCL7A mRNA, log2(TPM+1)
A4/Fuk	DLBCL	1,250961574
A3/KAW	DLBCL	2,386810946
OCILY-13	DLBCL	3,399171094
KML-1	DLBCL	3,777156666
SU-DHL-8	DLBCL	4,341274184
RC-K8	DLBCL	4,622930351
HT	DLBCL	4,657068301
NU-DHL-1	DLBCL	4,894817763
OCI-LY3	DLBCL	4,905447179
WSU-NHL	DLBCL	5,058316496
RL	DLBCL	5,086189313
SU-DHL-5	DLBCL	5,298291731
OCI-LY-19	DLBCL	5,362469889
OCI-LY7	DLBCL	5,479618608
Farage	DLBCL	5,482202926
OCI-LY18	DLBCL	5,560714954
NU-DUL-1	DLBCL	5,646738698
SU-DHL-4	DLBCL	5,935223994
Pfeiffer	DLBCL	6,013238915
SU-DHL-10	DLBCL	6,31596467
DB	DLBCL	6,464831606
WSU-DLCL2	DLBCL	6,594399256
Toledo	DLBCL	6,599020177
VAL	DLBCL	6,627606838
SU-DHL-6	DLBCL	6,657354182
DOHH-2	DLBCL	6,827692021
U-2904	DLBCL	6,874059203
KARPAS-422	DLBCL	6,912649865
RI-1	DLBCL	7,126601235

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41 **Supplementary Table 1.** *BCL7A* mRNA expression level in log2(TPM+1) and subtype of the cell

42 lines included in Fig. 2a. Data from DepMap Portal database (22Q2).