

Fetal hemoglobin induction in azacytidine responders enlightens methylation patterns related to blast clearance in higher-risk MDS and CMML.

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Additional file 4: Supplementary tables and figures_2

Table S3. Genes with DMRs in patients treated with AZA and demonstration of response.

Patient ID	HMA given	Response	HbF regulating genes with changes in methylation patterns after AZA
A	AZA	CR	FOG-1, RCOR-1, ZBTB7A, MTA1, MTA2
B	AZA	mCR+HI	FOG-1, RCOR-1, ZBTB7A, BCL11A
C	AZA	mCR	FOG-1, ZBTB7A, MTA1, MTA2, MBD3, BCL11A
D	AZA	mCR+HI	No changes
E	AZA	NR	FOG-1, RCOR-1, ZBTB7A, MTA1, MDB3
F	AZA	NR	FOG-1, RCOR-1, ZBTB7A, MTA1, MTA2, MBD3
G	AZA	NR	No changes

NR: no response, mCR: marrow complete response, HI: hematological improvement, PR: partial response

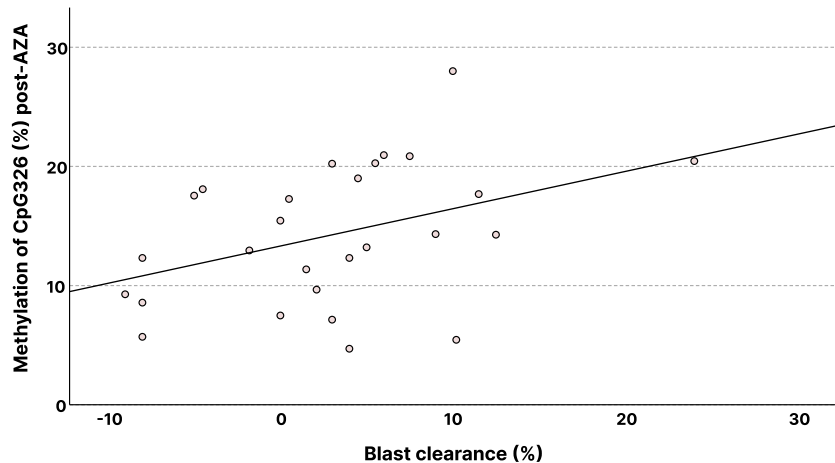


Figure S8. Methylation status of CpG326 island of *ZBTB7A* post-AZA treatment is related to blast cell clearance (p=0.026, $r_s=0.427$).

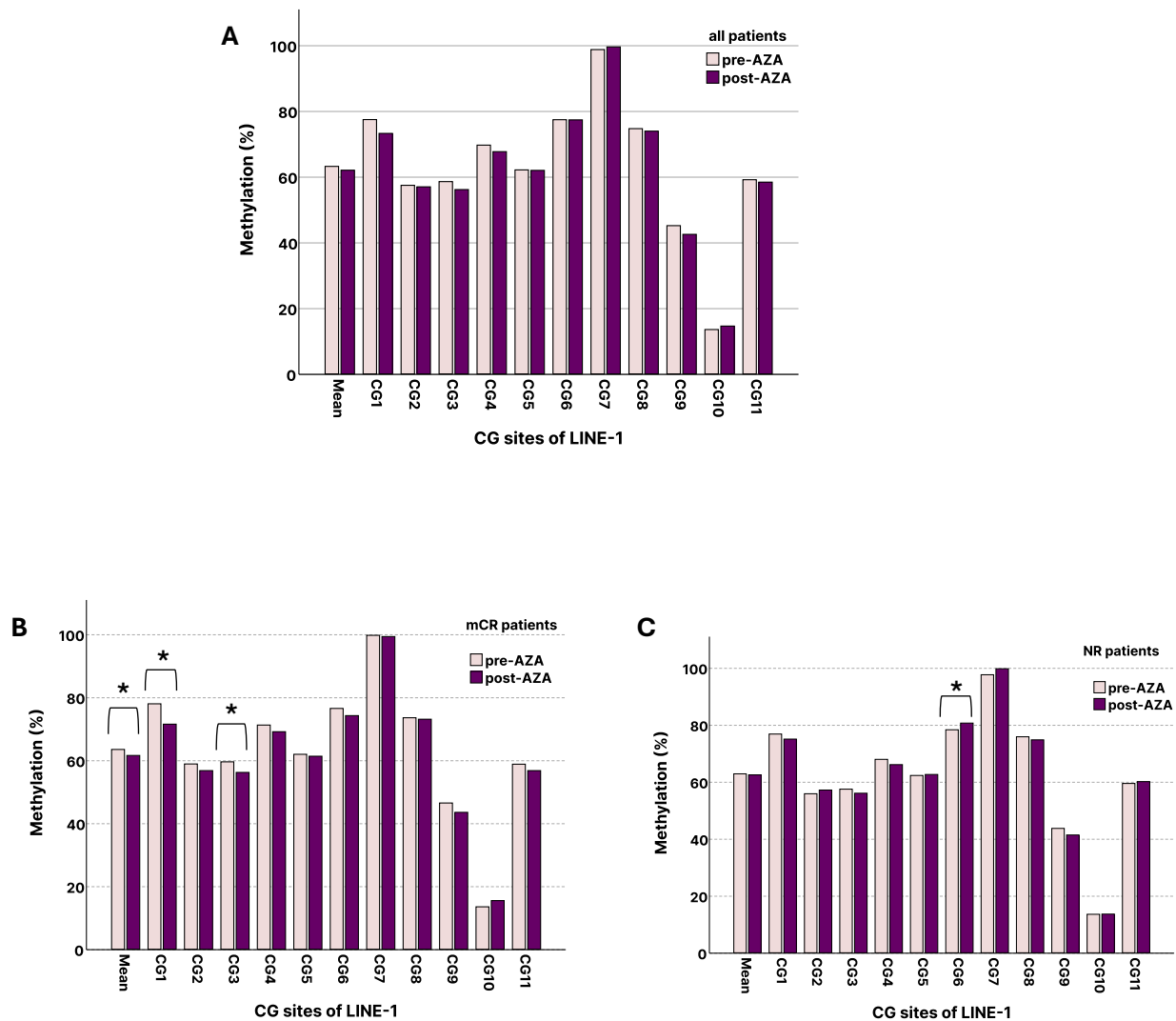


Figure S9. Methylation levels of LINE-1 CG sites tested pre- and post-AZA for A) all patients, B) marrow responders (mCR) and C) non-responding (NR) patients. Hypomethylation was observed only among responders ($p_{mCR}=0.012$) (B) and specifically at CG1 and CG3 sites ($p_1=0.001$, $p_3=0.028$). On the contrary, NR patients demonstrated hypermethylation of CG6 ($p=0.044$).

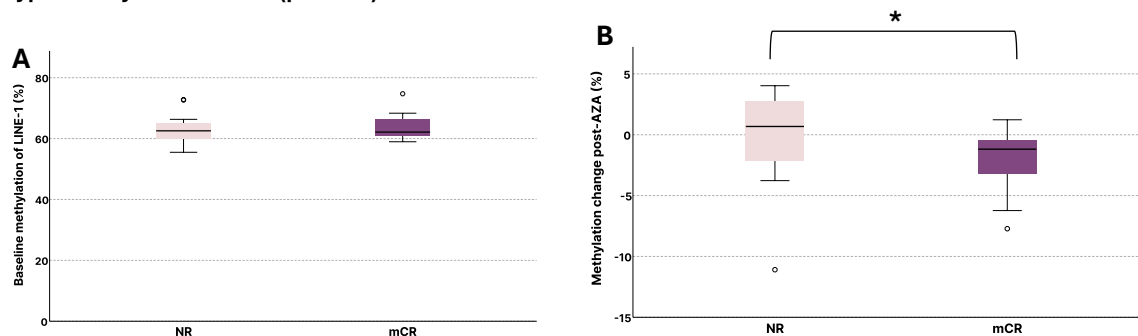


Figure S10. Methylation patterns of LINE-1 in AZA treated patients. A. No difference in pre-treatment LINE-1 methylation levels between mCR and NR patients ($p=0.348$). B. Methylation reduction post-AZA was greater in mCR responders ($p=0.047$).

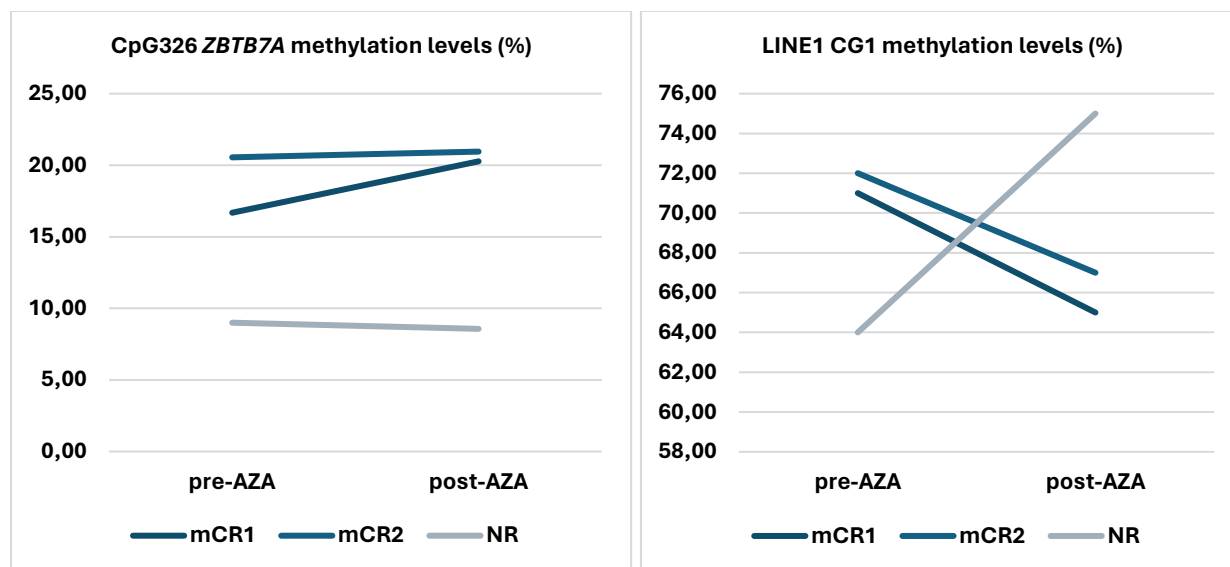


Figure S11. Methylation patterns of CpG326 of *ZBTB7A* and CG1 of LINE-1 in mCR and NR patients with stable cytogenetic/molecular status pre- and post-AZA.