

SUPPLEMENTARY MATERIAL

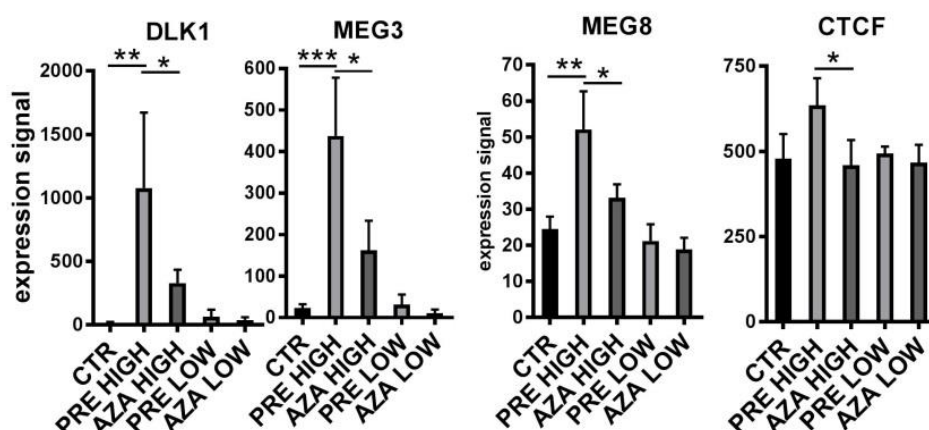


Figure S1. Expression of genes within the *DLK1–DIO3* region. The patient samples were divided according to miRNA expression and treatment status into four groups: PRE HIGH - untreated patients with high miRNA levels, AZA HIGH—AZA-treated patients with high miRNA levels, PRE LOW—untreated patients with low miRNA levels, AZA LOW—AZA-treated patients with low miRNA levels; CTR—controls. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

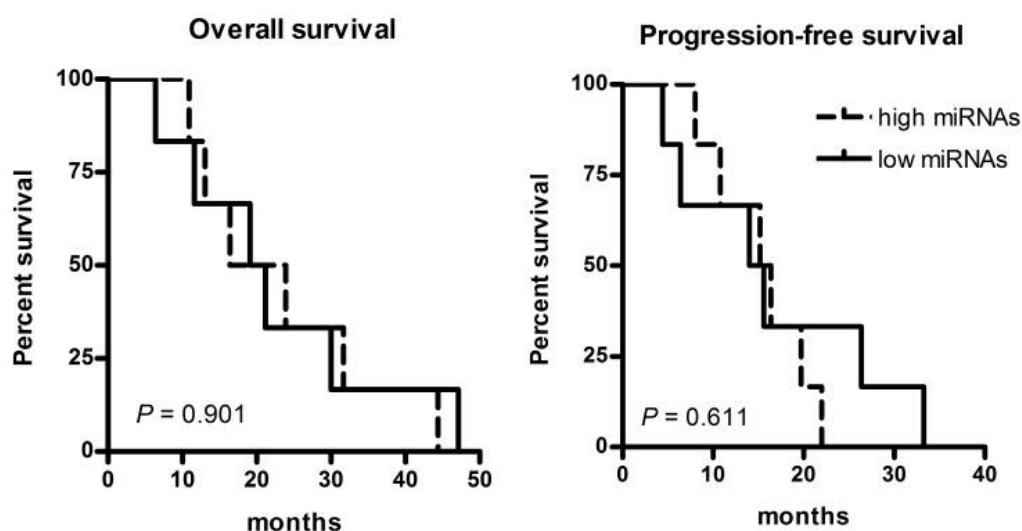


Figure S2. Overall survival (A) and progression-free survival (B) of MDS/AML-MRC patients after the initiation of AZA therapy according to pretreatment levels of 14q32 miRNAs.

Table S1. Patient characteristics.

Number of Patients	12
Age (years), mean (range)	69 (63–82)
Sex, female/male	6/6
Marrow blasts (%), mean (range)	18 (4–27)
Karyotype, normal/abnormal	3/9
Diagnosis, MLD/EB1/EB2/AML-MRC	1/1/5/5
IPSS, int-1/int-2/high	1/2/9
AZA cycles administered, median (range)	16 (4–34)
Response, responders/nonresponders	7/5
Follow-up (months), median (range)	25.4 (7.4–94.9)

Table S2. List of primers used for the generation of amplicons for bisulfite sequencing. Positions of amplicons on chr14 were defined according to the publication by Manodoro *et al.* [24] using genome assembly GRCh37/hg19.

Amplicon	Primer	Sequence	Position	Length	Regulatory Elements	CpG Density	Methylation Status in APL [24]
A1	Fwd	AAGTAGGATTGGAAGGTTTTTA GG	chr14:101,290,069- 101,290,515	447	- regulator binding sites: CTCF, OLF-1	0.30	hypermethylation (CpGs 127-421, incl. CTCF binding site)
	Rev	ACAACCCACAAAAACATAAATT AA					
A2	Fwd	GTATTTTATTTGAGGTTTGGGGTT T	chr14:101,290,455- 101,290,946	492	- CpG island - regulator binding sites: NFYA, RFX5, SP1	0.61	hypermethylation (whole region)
	Rev	CACCCCTTTACAACCTATAAAA CT					
A3	Fwd	TATTTTGGTTAAGGTGGAGGAA G	chr14:101,291,767- 101,292,194	428	- CpG island - regulator binding sites: CTCF, RBL2, POLR2A, CREB, PAX3	0.74	hypermethylation (CpGs 25-127 and 278-332, incl. CTCF binding site)
	Rev	CCAAACAAAATAAATTCAAACAC AATATAT					

Table S3. Matrix showing pairwise correlations between expression of mRNAs/miRNAs and methylation of CpG sites. Pearson correlation coefficients are provided for each pair of variables. Significant positive correlations are highlighted in a yellow-red scale, and significant negative correlations are shown in a blue scale as indicated at the top of the table. The table is accessible in a separate file at a higher resolution.

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