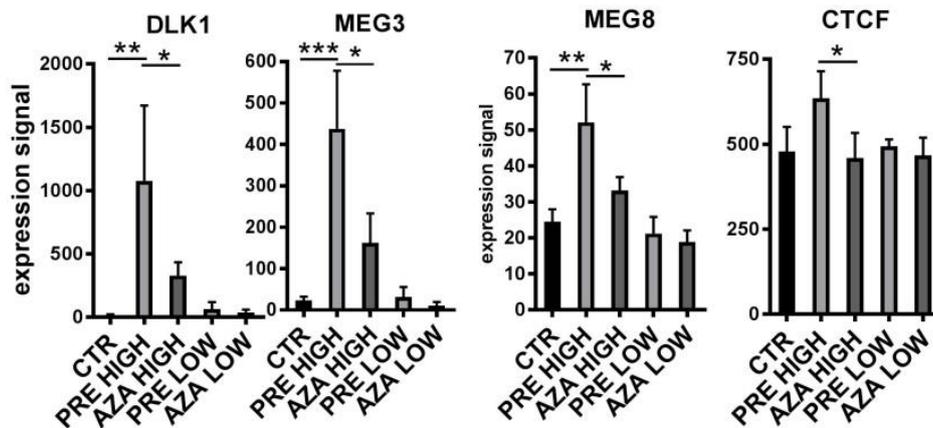
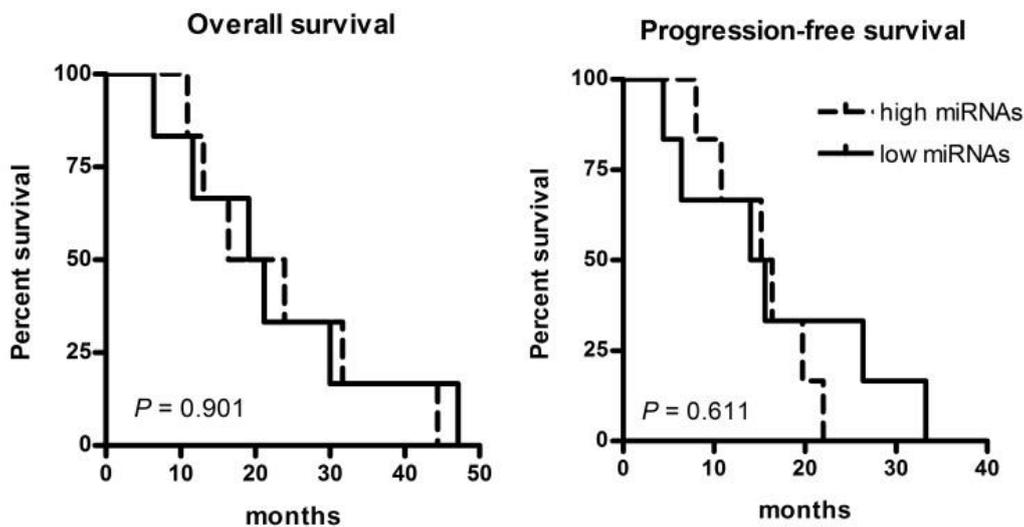


## SUPPLEMENTARY MATERIAL



**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.

| <b>Number of Patients</b>               | <b>12</b>       |
|---|-----------------|
| 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.

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

