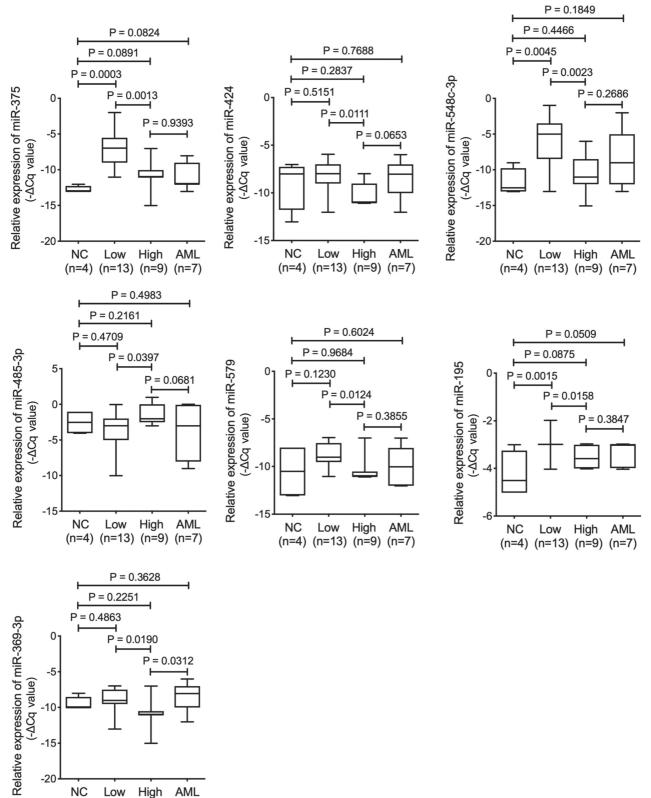
## Supplementary file 1: Quantitative RT-PCR of mature microRNAs

MicroRNAs were quantified using TaqMan<sup>®</sup> MicroRNA Assays (ThermoFisher Scientific, Inc.) with modifications. Briefly, 10 ng of total RNA was reverse transcribed (RT) by TaqMan<sup>®</sup> MicroRNA RT kit. 1.5  $\mu$ l of RT reactions contained 10xRT buffer, 0.15  $\mu$ l of 100 mM dNTPs with dTTP, 0.19  $\mu$ l of RNase-inhibitor (20 unit/ $\mu$ l), 1  $\mu$ l of MultiScribe<sup>TM</sup> Reverse Transcriptase (50 units/ $\mu$ l), 1  $\mu$ l of each of microRNA specific stem-loop primers (has-miR-101, cat. no. 000438; ath-miR-159, cat. no. 000338; ThermoFisher Scientific, Inc.) and 10  $\mu$ l of input RNA. The mixture was incubated at 16°C for 30 min, 42°C for 30 min and 85°C for 5 min subsequently, quantitative real time-PCR was performed using an ABI Prism 7900 sequence detection system (Applied Biosystems). For a 20  $\mu$ l of PCR reaction, 1  $\mu$ l of 20xTaqMan<sup>®</sup> MicroRNA Assays in which PCR primers and probes (5'-FAM and 3'-MGB) were contained, 1  $\mu$ l of RT product and 10  $\mu$ l of 2xTaqMan<sup>®</sup> Universal Master mix, No AmpErase<sup>®</sup> UNG (ThermoFisher Scientific, Inc.) were mixed. The reaction was first incubated at 95°C for 2 min, followed by 50 cycles of 95°C for 15 sec and 60°C for 1 min. Figure S1. Extracellular vesicle miR expression derived from BM-MSCs using TaqMan miRNA low-density array (Thermo Fisher Scientific, Inc.). In addition to miR-101 and miR-15b, a total of 7 EV-miRs (miR-375, miR-424, miR-548c-3p, miR-485-3p, miR-579, miR-195 and miR-369-3p) derived from BM-MSCs indicated a significant difference between low-risk MDS group (Low) and high-risk MDS group (High). However, these 7 miRs failed to exhibit any consistent pattern. miR, microRNA; BM-MSCs, bone marrow mesenchymal stromal cells; MDS, myelodysplastic syndrome.



(n=4) (n=13) (n=9) (n=7)

APP	EED	MYCN	SOX9
ARID1A	EYA1	NLK	SRF
ATG4D	EZH2	NOTCH1	STMN1
ATM	FBN2	PIK3CB	SUZ12
ATP5B	FMR1	PIM1	TET2
ATXN1	FOS	PRDM1	TGFBR1
CCDC88A	GRSF1	PRKDC	TLR2
CCND1	ITGA3	PTGER4	VEGFA
CDH5	JAK2	PTGS2	VEGFC
CDK8	KLF6	RAB1A	VHL
CFTR	MCL1	RAB5A	ZEB1
CPEB1	MEIS1	RAC1	ZEB2
CTNNB1	MET	RAP1B	
DNMT3A	MITF	RUNX1	
DUSP1	MTOR	SNHG1	

Table SI. List of the miR-101 target genes used for the gene ontology analysis.