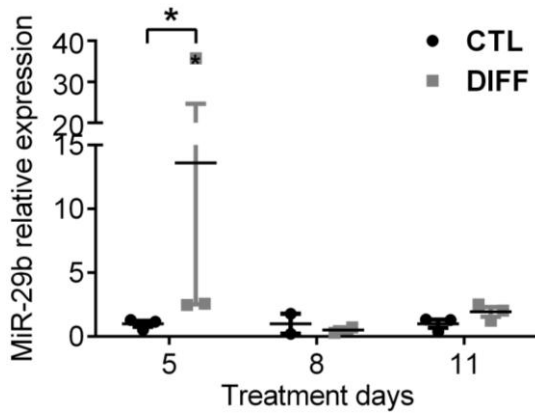


**Supplemental Figure 1. Differentiation of Sca1+ cardiac progenitor cells (CPC) by 5-azacytidine (AZA)/TGFbeta.** CPC were treated with AZA (5  $\mu$ M) and TGFbeta (1 ng/ml) for 12-26 days in culture. Relative gene expression indicative of cardiac myocyte lineage differentiation was measured by qRT-PCR and normalized to untreated controls. (A) Relative expression of mRNA for cardiac transcription factors (Nkx2.5 and Mef2C), and structural proteins (cardiac Troponin T, cTnT; alpha-Myosin Heavy Chain, alpha-MHC); n=3 different preparations; bounds of boxes are minimal and maximal values; internal line at mean value; \*: p<0.016 vs non-treated cells by Mann-Whitney test after correction for multiple comparisons. (B) Representative picture of CPC differentiating into cardiac myocytes upon treatment with AZA/TGFbeta (lower). Immunocytochemistry was performed using antibody against cTnT (green). DAPI staining is in blue. No differentiation is observed in control CPC in absence of treatment (upper).



Supplemental Figure 2 . Time-dependent expression of miR-29b in CPCs during differentiation. Relative gene expression was measured using qRT-PCR and normalized to 5S. \*  $p < 0.05$  vs. CTL,  $n=3$  experiments; Mann-Whitney test.

Gene symbol	Gene description	Sequences (5' to 3')
axin2	Axin2	F:CGGATTCAGGTCCTTCAAGA
		R:TGGATAACTCGCTGTCGTTG
Wnt4	wingless-type MMTV integration sit family, member 4	F:AGG AAG GCC ATC TTG ACA CA
		R:GCA CCG TCA AAC TTC TCC TT
Snai2	snail family zinc finger 2	F:CTA CAG CGA ACT GGA CAC ACA
		R:GGG TAA AGG AGA GTG GAG TGG
Lef1	lymphoid enhancer binding factor 1	F: GTC CCT TTC TCC ACC CAT C
		R: AAG TGC TCG TCG CTG TAG G
Wif-1	Wnt inhibitory factor 1	F: CCC ACG GAA CCT GCC ACG AA
		R: CTC GGG GCA TGC ATG AGG CTG
HBP1	high mobility group box transcription factor 1	F: ACT CAC AAG GGC TAT GGG TCT
		R: GCT TGG ATA AAA TGA CGA CCA
Nkx2.5	NK2 homeobox 5	F: ACC CGG GAG CCT ACG GTG AC
		R: GCG CCA TCC GTC TCG GCT TT
Myh6 (alpha-MHC)	myosin, heavy polypeptide 6, cardiac muscle, alpha	F: GAT GGC ACA GAA GAT GCT GA
		R: CTG CCC CTT GGT GAC ATA CT
Tnnt2 (cTnT)	troponin T2, cardiac	F: GTT GGT CCT GAT GAA GAA G
		R: GAG TCT GTA GCT CAT TCA G
Mef2C	myocyte enhancer factor 2C	F: CCG ATG CAG ACG ATT CAG TAG
		R: GTG TCA CAC CAG GAG ACA TAC
GAPDH	glyceraldehyde-3-phosphate dehydrogenase	F:ACCCCAGCAAGGACACTGAGCAAG
		R:TGGGGGTCTGGGATGGAAATTGTG

Table S1. Sense and anti-sense primers to amplify cDNA sequences of interest by RT-qPCR in *Mus musculus* samples.

DIANA-microT	TargetScanMouse	MicroCosm Targets	PicTar	miRanda
mmu-miR-5101	miR-29abcd	mmu-miR-29c	hsa-miR-328	mmu-miR-708
mmu-miR-29c-3p	miR-138	mmu-miR-719	hsa-miR-30e-5p	mmu-miR-28
mmu-miR-29a-3p	miR-138ab		hsa-miR-30d	mmu-miR-374
mmu-miR-1192	miR-101		hsa-miR-194	mmu-miR-361
mmu-miR-495-3p	miR-101ab		hsa-miR-101	mmu-miR-26b
mmu-miR-29b-3p	miR-30abcdef		hsa-miR-29a	mmu-miR-26a
mmu-miR-1231-5p	miR-330abe-5p		hsa-miR-30b	mmu-miR-1192
mmu-miR-667-5p	miR-384-5p		hsa-miR-30c	mmu-miR-495
mmu-miR-129-5p	miR-218		hsa-miR-30a-5p	mmu-miR-384-5p
mmu-miR-384-5p	miR-218a		hsa-miR-29c	mmu-miR-30b
mmu-miR-26a-5p	miR-26ab		hsa-miR-29b	mmu-miR-30c
mmu-miR-26b-5p	miR-1297		hsa-let-7d	mmu-miR-30a
mmu-miR-669b-5p	miR-4467			mmu-miR-30d
mmu-miR-3074-2-3p	miR-137			mmu-miR-30e
mmu-miR-5102	miR-137ab			mmu-miR-29a
mmu-miR-30e-5p				mmu-miR-29b
mmu-miR-543-3p				mmu-miR-29c
mmu-miR-30b-5p				mmu-miR-543
mmu-miR-450b-5p				mmu-miR-194
mmu-miR-30d-5p				mmu-miR-132
mmu-miR-30c-5p				mmu-miR-181a
mmu-miR-30a-5p				mmu-miR-181b
mmu-miR-194-5p				mmu-miR-181d
mmu-miR-671-5p				mmu-miR-181c
mmu-miR-3070b-3p				mmu-miR-212
mmu-miR-452-5p				
mmu-miR-325-3p				
mmu-miR-3099-3p				
mmu-miR-708-5p				
mmu-miR-3070a-3p				
mmu-miR-3070a-3p				
mmu-miR-3070a-3p				
mmu-miR-3070a-3p				
mmu-miR-3070a-3p				
mmu-miR-3070a-3p				

Table S2. Predicted miRNAs targeting Dnmt3a in *Mus musculus*. Displayed miRNAs from DIANA-microT-CDS analysis are ordered by miTG score, superior to 0.9. TargetScanMouse 6.2 search was performed on conserved sites for miRNA families broadly conserved among vertebrates. Targeted sites were sorted by aggregate  $P_{CT}$  superior to 0.9. PicTar search was performed on target predictions for all human microRNAs based on conservation in mammals (human, chimp, mouse, rat and dog). Displayed miRNAs are characterized by a *Mus musculus* probability superior to 0.9. Displayed miRNAs from MiRanda analysis were ordered by sum of mirSVR scores.