

Supplementary Materials: Role of miR-34a-5p in Hematopoietic Progenitor Cells Proliferation and Fate Decision: Novel Insights into the Pathogenesis of Primary Myelofibrosis

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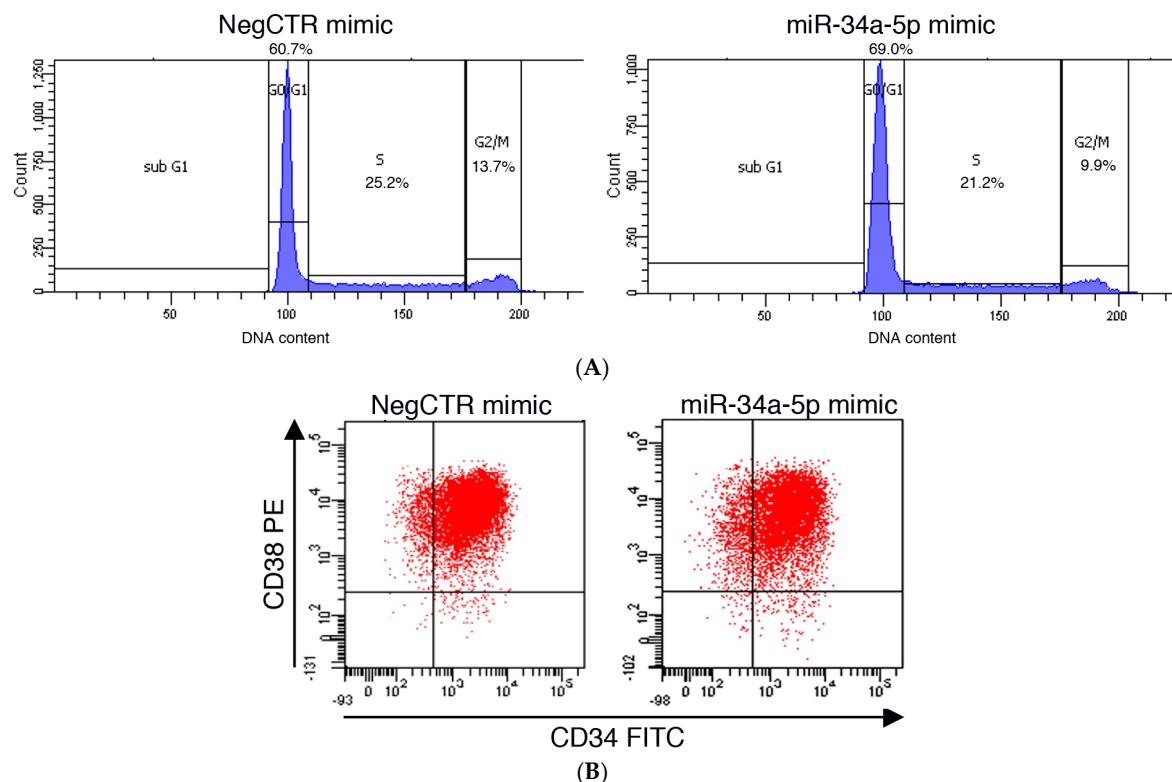


Figure S1. Effects of miR-34a-5p overexpression on CD34+ hematopoietic progenitor cells proliferation and commitment. (A) Representative histograms for the flow cytometric analysis of cell cycle distribution by propidium iodide staining in NegCTR mimic and miR-34a-5p mimic CD34+ cells; (B) Representative dot plots for the flow cytometric detection of CD34 and CD38 markers at 24 h post-nucleofection. No significant differences in the earliest CD34+CD38- stem cell population, the intermediate CD34+CD38+ hematopoietic progenitor cells fraction and the most committed CD34-CD38+ population were detected between NegCTR mimic and miR-34a-5p samples.

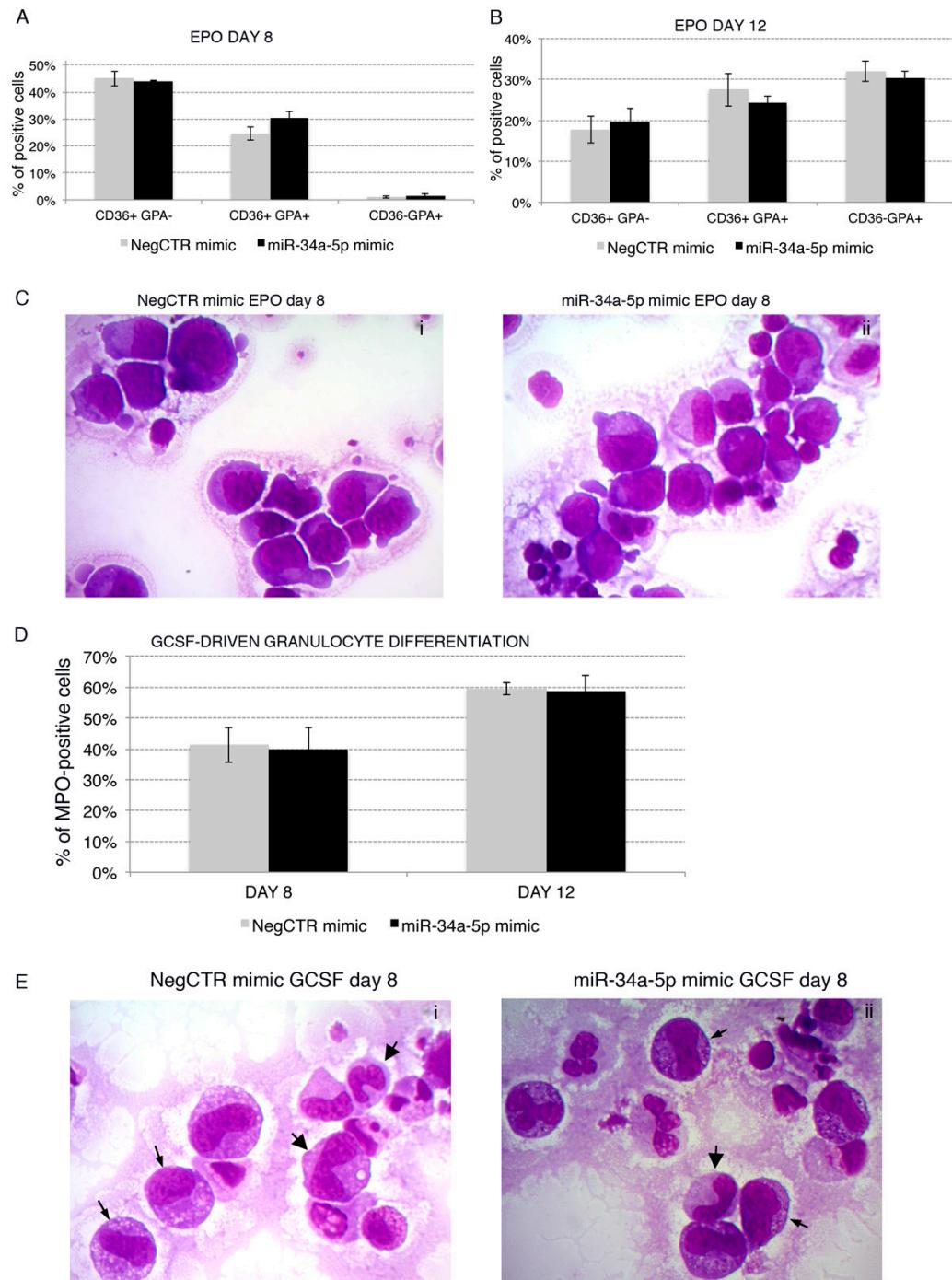


Figure S2. Effects of miR-34a-5p overexpression on erythroid and granulocyte differentiation. (A,B) Flow cytometric analysis (mean \pm SEM; $n = 3$) of CD36 and glycophorin A (GPA) expression at day 8 (A) and day 12 (B) of EPO-driven erythroid unilineage culture post-nucleofection; (C) Morphological analysis of NegCTR mimic (i) and miR-34a-5p mimic-transfected cells (ii) after May–Grünwald–Giemsa staining at day 8 of EPO-induced erythroid differentiation post-nucleofection in a representative experiment. Magnification, $\times 1000$; (D) Flow cytometric detection (mean \pm SEM; $n = 3$) of the myeloperoxidase (MPO) marker at day 8 and day 12 of GCSF-driven granulocyte unilineage culture post-nucleofection; (E) Morphological analysis of NegCTR mimic (i) and miR-34a-5p mimic-transfected cells (ii) after May–Grünwald–Giemsa staining at day 8 of GCSF-driven granulocyte differentiation post-nucleofection in a representative experiment. Thin arrows indicate myelocytes; thick arrows indicate band neutrophils. Magnification, $\times 1000$. Abbreviations: EPO, erythropoietin; GCSF, granulocyte colony stimulating factor.

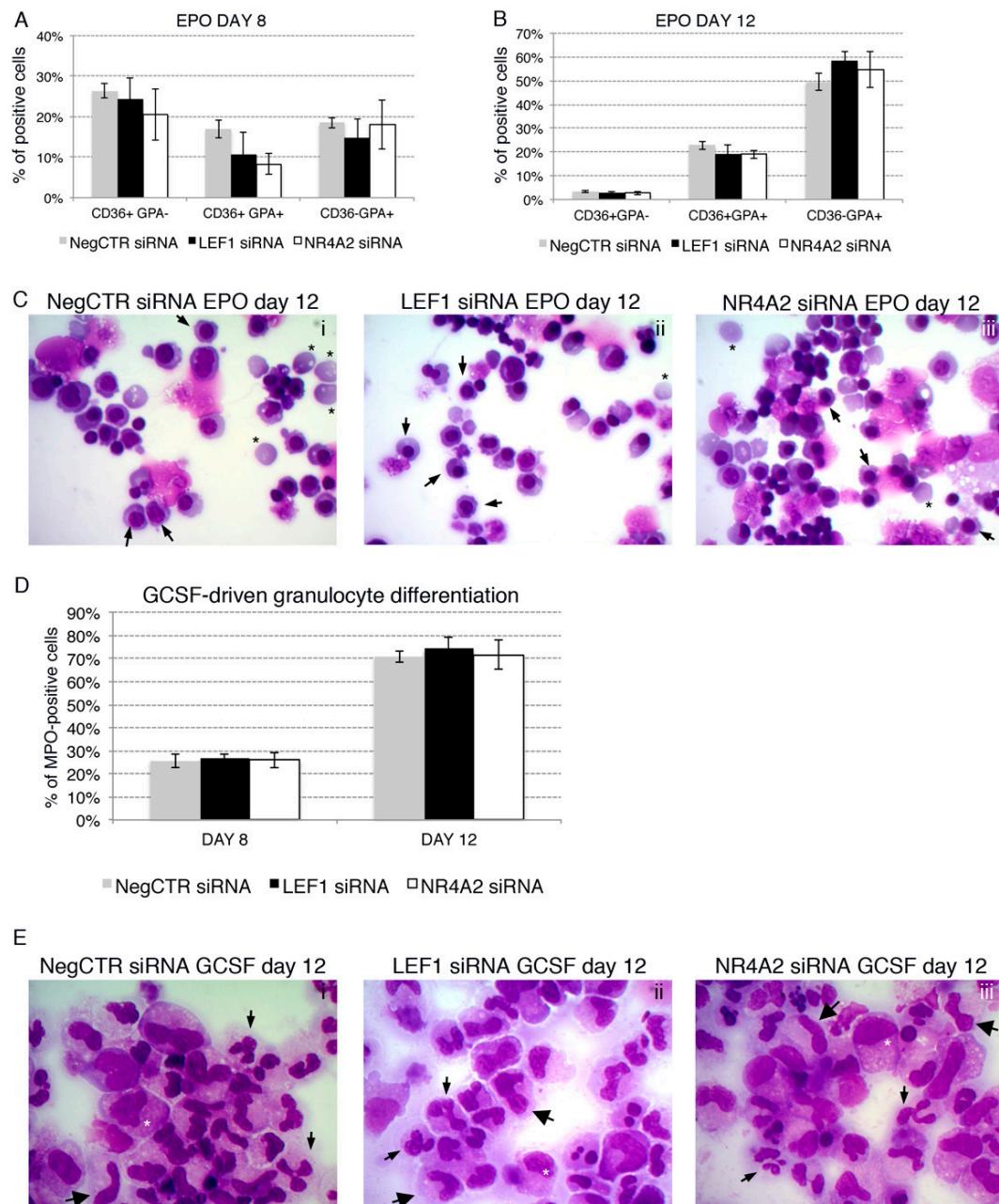


Figure S3. Effects of LEF1 and NR4A2 silencing on erythroid and granulocyte differentiation. (A,B) Flow cytometric analysis (mean \pm SEM; $n = 3$) of CD36 and glycophorin A (GPA) expression at day 8 (A) and day 12 (B) of EPO-driven erythroid unilineage culture post-nucleofection; (C) Morphological analysis of NegCTR siRNA (i), LEF1 siRNA (ii) and NR4A2 siRNA-transfected cells (iii) after May–Grünwald–Giemsa staining at day 8 of EPO-induced erythroid differentiation post-nucleofection in a representative experiment. Arrows indicate erythroblasts; asterisks indicate reticulocytes that have already extruded the nucleus. Magnification, $\times 1000$; (D) Flow cytometric detection (mean \pm SEM; $n = 3$) of the myeloperoxidase (MPO) marker at day 8 and day 12 of GCSF-driven granulocyte unilineage culture post-nucleofection; (E) Morphological analysis of NegCTR siRNA (i), LEF1 siRNA (ii) and NR4A2 siRNA-transfected cells (iii) after May–Grünwald–Giemsa staining at day 8 of GCSF-driven granulocyte differentiation post-nucleofection in a representative experiment. Thick arrows indicate band neutrophils; thin arrows indicate two-lobed neutrophils or mature neutrophils; white asterisks indicate promyelocytes. Magnification, $\times 1000$. Abbreviations: EPO, erythropoietin; GCSF, granulocyte colony stimulating factor.

Table S1. Ambion Silencer Select siRNA Sequences.

Target Transcript	RefSeq ID	Sequence (Sense)	Targeted Exon(s)	Ambion Silencer Select siRNA Product
LEF1	NM_001130713.2; NM_001130714.2; NM_001166119.1; NM_016269.4	5'-GUUGCUGAGUGUACUCUAAtt-3'	Exons 7,8	Silencer Select Pre-designed siRNA
NR4A2	NM_006186.3	5'-GGCGAACCCUGACUAUCAAtt-3'	Exon 6	Silencer Select Validated siRNA

Table S2. Differentially expressed genes between miR-34a-5p mimic and NegCTR mimic-transfected CD34+ cells.

Probeset ID	Gene Symbol	Gene Title	RefSeq Transcript ID	Fold Change miR-34a-5p Mimic vs. NegCTR Mimic-Transfected CD34+ Cells	p-Value miR-34a-5p Mimic vs. NegCTR Mimic-Transfected CD34+ Cells
11753714_a_at	HBE1	hemoglobin, epsilon 1	NM_005330	4.17	0.0023
11755537_s_at	HBG1 /// HBG2 /// LOC100653006 /// LOC100653319	hemoglobin, γ A /// hemoglobin, γ G /// uncharacterized LOC100653006 /// unchar	NM_000184 /// NM_000559 /// XR_132577 /// XR_132954	3.47	0.0013
11744478_s_at	HBG1 /// HBG2 /// LOC100653006 /// LOC100653319	hemoglobin, γ A /// hemoglobin, γ G /// uncharacterized LOC100653006 /// unchar	NM_000184 /// NM_000559 /// XR_132577 /// XR_132954	3.44	0.0006
11754267_x_at	HBA1 /// HBA2	hemoglobin, α 1 /// hemoglobin, α 2	NM_000517 /// NM_000558	3.40	0.0142
11715494_s_at	HBG1 /// HBG2 /// LOC100653006 /// LOC100653319	hemoglobin, γ A /// hemoglobin, γ G /// uncharacterized LOC100653006 /// unchar	NM_000184 /// NM_000559 /// XR_132577 /// XR_132954	3.31	0.0004
11729582_s_at	CA1	carbonic anhydrase I	NM_001128829 /// NM_001128830 /// NM_001128831 /// NM_001164830 /// NM_001738	3.06	0.0062
11758685_s_at	CEACAM8	carcinoembryonic antigen-related cell adhesion molecule 8	NM_001816	2.97	0.0371
11753823_a_at	S100A8	S100 calcium binding protein A8	NM_002964	2.85	0.0021
11758696_x_at	HBG1 /// HBG2 /// LOC100653006 /// LOC100653319	hemoglobin, γ A /// hemoglobin, γ G /// uncharacterized LOC100653006 /// unchar	NM_000184 /// NM_000559 /// XR_132577 /// XR_132954	2.77	0.0017
11720541_at	LGALS1	lectin, galactoside-binding-like	NM_014181	2.39	0.0111
11716523_at	S100A9	S100 calcium binding protein A9	NM_002965	2.37	0.0002
11729583_x_at	CA1	carbonic anhydrase I	NM_001128829 /// NM_001128830 /// NM_001128831 /// NM_001164830 /// NM_001738	2.27	0.0297
11758545_s_at	RHAG	Rh-associated glycoprotein	NM_000324	2.09	0.0305
11725897_at	TUBB1	tubulin, beta 1 class VI	NM_030773	2.06	0.0468
11756809_a_at	EFHC2	EF-hand domain (C-terminal) containing 2	NM_025184	2.06	0.0228
11758577_s_at	ELOVL7	ELOVL fatty acid elongase 7	NM_001104558 /// NM_024930	2.06	0.0038
11720608_a_at	S100B	S100 calcium binding protein B	NM_006272	2.05	0.0261
11751647_a_at	IL7R	interleukin 7 receptor	NM_002185	2.01	0.0058
11725632_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	NM_006186 /// NM_173171 /// NM_173172 /// NM_173173	-2.03	0.0245

Table S2. Cont.

Probeset ID	Gene Symbol	Gene Title	RefSeq Transcript ID	Fold Change miR-34a-5p Mimic vs. NegCTR Mimic-Transfected CD34+ Cells	p-Value miR-34a-5p Mimic vs. NegCTR Mimic-Transfected CD34+ Cells
11729641_a_at	TPD52	tumor protein D52	NM_001025252 /// NM_001025253 /// NM_005079	-2.06	0.0036
11715245_s_at	IGLL1	immunoglobulin lambda-like polypeptide 1	NM_020070 /// NM_152855	-2.15	0.0303
11718479_x_at	STAR	steroidogenic acute regulatory protein	NM_000349 /// NM_001007243	-2.17	0.0057
11720051_at	SPOCK1	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1	NM_004598	-2.17	0.0183
11718477_a_at	STAR	steroidogenic acute regulatory protein	NM_000349 /// NM_001007243	-2.24	0.0164
11726333_s_at	LEF1	lymphoid enhancer-binding factor 1	NM_001130713 /// NM_001130714 /// NM_001166119 /// NM_016269	-2.29	0.0042
11723339_at	CTSG	cathepsin G	NM_001911	-2.29	0.0436
11745205_s_at	TPD52	tumor protein D52	NM_001025252 /// NM_001025253 /// NM_005079	-2.59	0.0027
11715306_s_at	AREG /// AREGB	amphiregulin /// amphiregulin B	NM_001657 /// XM_001125684	-2.61	0.0045
11727965_at	ELANE	elastase, neutrophil expressed	NM_001972	-2.65	0.0095
11754659_x_at	TPD52	tumor protein D52	NM_001025252 /// NM_001025253 /// NM_005079	-2.69	0.0079
11729643_s_at	TPD52	tumor protein D52	NM_001025252 /// NM_001025253 /// NM_005079	-2.89	0.0069
11756600_a_at	TPD52	tumor protein D52	NM_001025252 /// NM_001025253 /// NM_005079	-2.93	0.0047
11728026_x_at	IGLL1	immunoglobulin lambda-like polypeptide 1	NM_020070 /// NM_152855	-3.22	0.0157
11734171_at	PRTN3	proteinase 3	NM_002777	-3.81	0.0004