Supplementary material

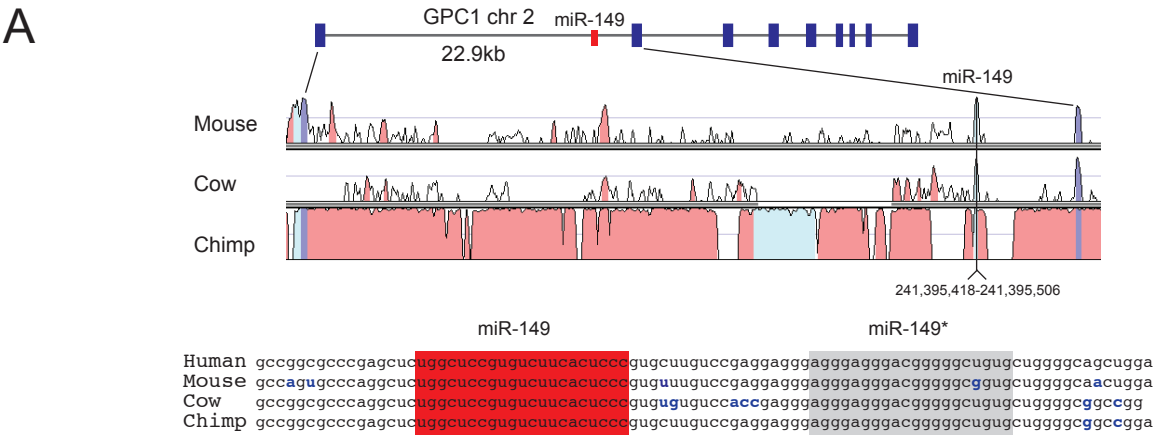
Fig. S1 (**A**) Schematic representation of the GPC1 gene locus, demonstrating the miR-149 coding sequence within intron 1 and its conservation among species (reference: human genome). (**B**) Predicted binding sites for miR-149 (in red) or miR-149* (in gray) in human FGFR1 and GPC1 3'UTRs. Point mutations (PM) of the selected predicted binding sites for miR-149 or miR-149* seed sequences in human FGFR1 or GPC1 3'UTRs are indicated in bold. (**C**) Chromatin State Segmentation track of the potential promoter regions of miR-149 in HUVECs cells (adaptation from ENCODE).

Fig. S2 PANTHER analysis of (**A**) miR-149 and (**B**) miR-149* predicted target genes in human based on biological pathways. Data are expressed as number of targets and their respective P values. P≤0.05. HUVECs transfected for 48 h with (**C**) CM, miR-149 or miR-149*, and (**D**) CI, I-miR-149 or I-miR-149*. qRT-PCR analysis of FGFR1 and GPC1. Data are expressed as relative expression to cell transfected with CM or CI and correspond to mean ± SEM of 3 experiments, P≤0.05. (**E**) Cell cycle analysis of HUVECs transfected as indicated in **C**, then cells were harvested and treated with BrdU for 1 h followed by BrdU detection and propidium iodide staining and analyzed by flow cytometry. Inserts correspond to dot plots that represent DNA content vs incorporation of BrdUrd (active phase S) into DNA. One representative experiment out of 3 with similar results is shown. (**F-H**) HUVECs were starved for 12 h and then treated with FGF2 (25 ng/mL) or non-treated for the indicated times. (**F**) qRT-PCR analysis of PAI-2 and Axl expression. Data are expressed as relative expression to non-treated cells and correspond to mean ± SEM of 3 experiments, P≤0.05. (**G**) Flow cytometry analysis of the GPC1 protein expression. Data are expressed as arbitrary fluorescence units to non-treated cells and correspond to one representative experiment out of 3 with similar results. (**H**) qRT-PCR analysis of FGFR1 expression. Data are expressed as relative expression to non-treated cells and correspond to mean ± SEM of 3 experiments, P≤0.05.

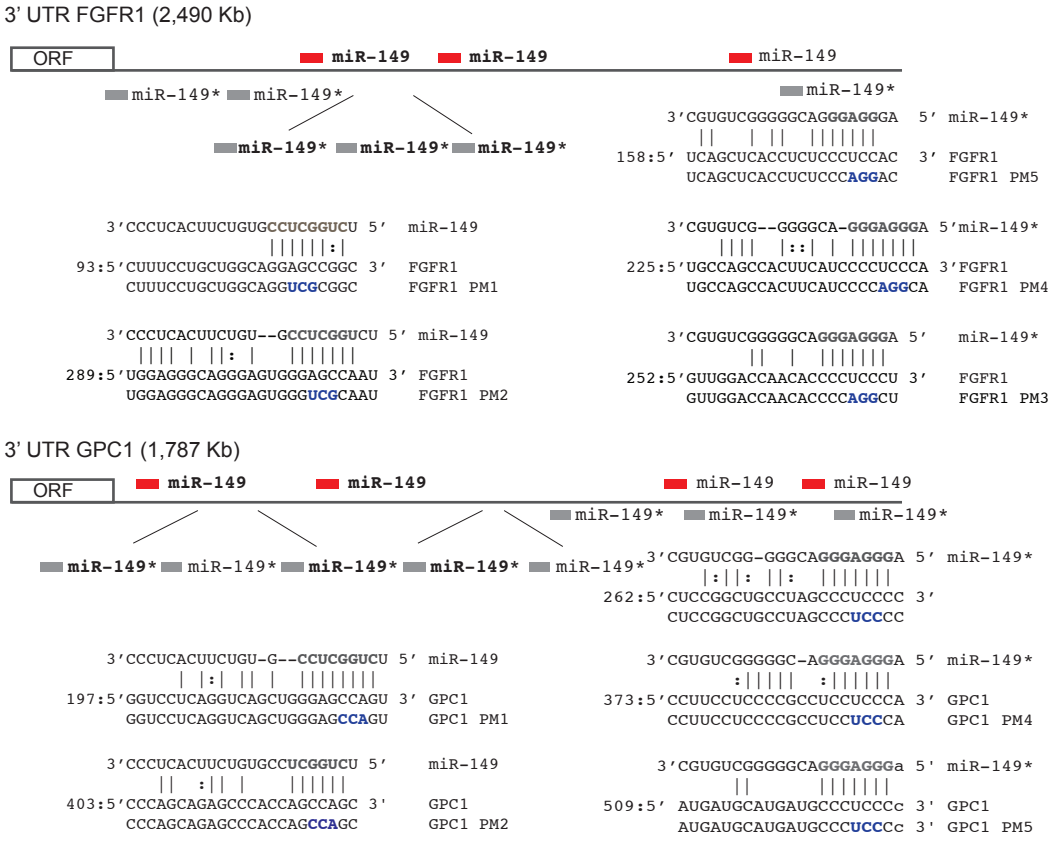
Table 1. Predicted targets for miR-149 and miR-149* involved in angiogenesis. Positive regulators of angiogenesis are indicated in red, negative in blue, positive/negative in black, unknown in grey and expressed in endothelial cells in italic.

Supplementary material Fig. 1

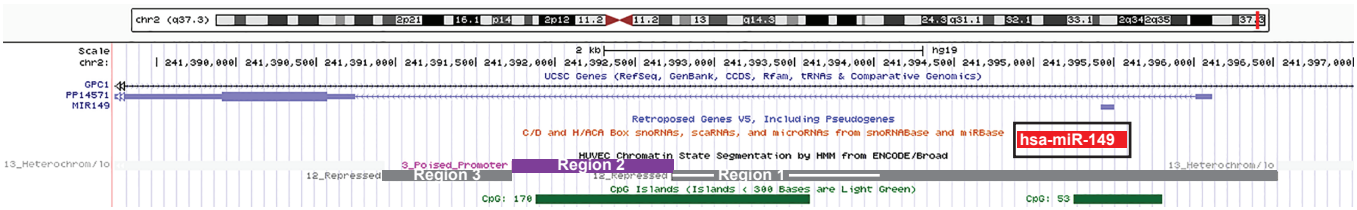
A



B

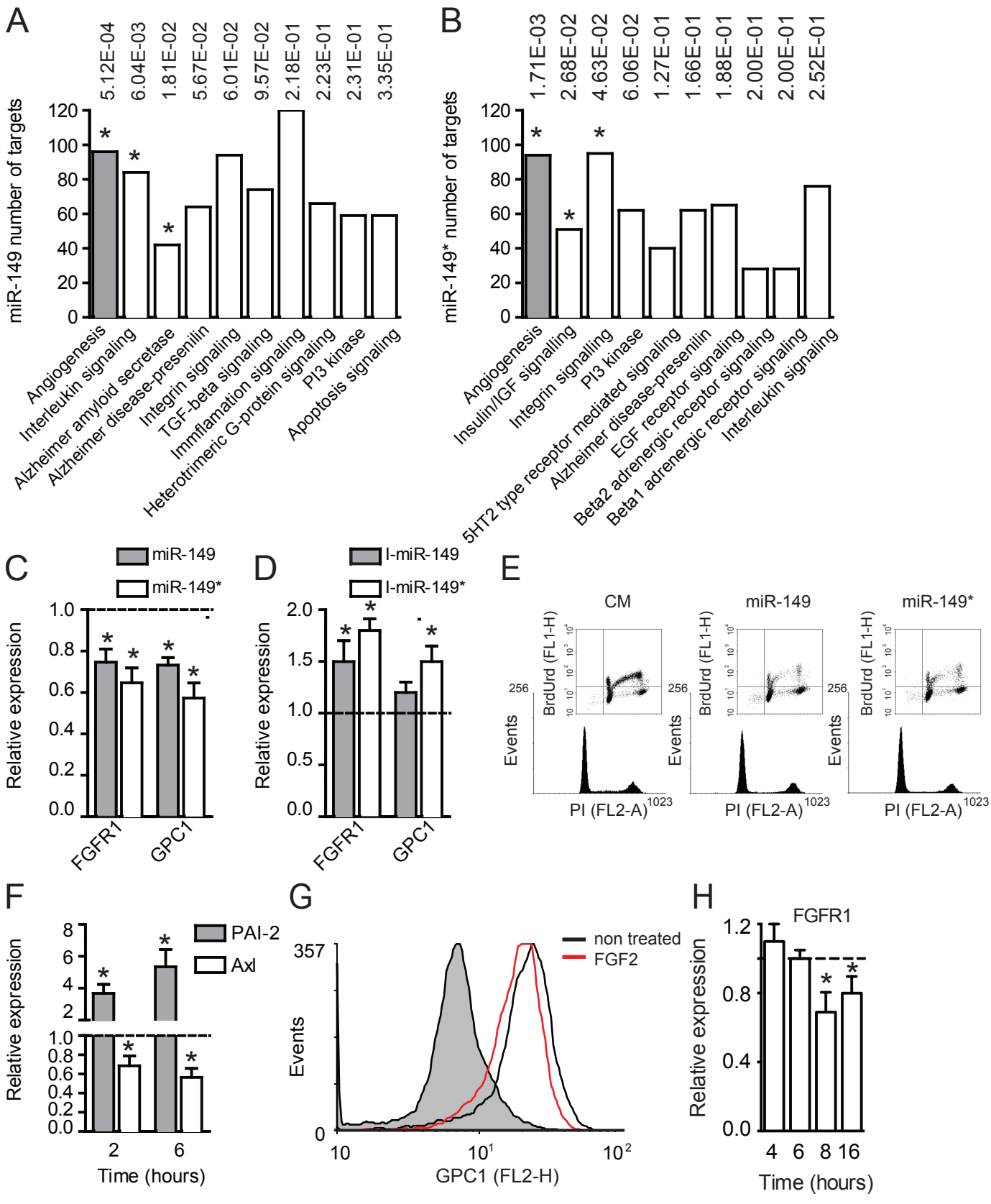


C



Region 1: repressed promoter
Region 2: poised promoter
Region 3: repressed promoter

Supplementary material Fig.2



Supplementary material Table 1

miR-149 targets (36)	miR-149-miR-149*targets (61)		miR-149* targets (34)
FGF1	*PRKCA*	*FGFR1*	*WNT2*
DOK1	*EFNB1*	APC2	*PAK1*
HSH2D	PI4KB	*MAPKAPK2*	SH2D4B
PKD2	*GRB2*	DVL1	*RHOC*
FZD3	*PTK2*	*WNT7B*	AKT2
STAT1	*PKD1*	PRKACA	*PIK3CG*
PLCG1	AXIN2	*FRS2*	*PLD2*
JAG1	*RAF1*	*EFNB2*	*BIRC5*
PDGFC	CRYAA	PDGFRB	*PRKD2*
MAP3K1	PRKD3	*WNT5A*	*NOS3*
TEK	*WNT5B*	MAPKAPK3	*PIK3C2B*
VEGFR2	*PTPRB*	MAP2K4	*NCK2*
CTNNB1	*FZD5*	*RHOB*	KRAS
PAK3	*NOTCH1*	*WNT10A*	EPHA3
AKT3	F7	MAPK4	FRS3
HN1	CRKL	*MAPK3*	*DLL4*
PLA2G4C	GRAP	*SRC*	*PIK3R2*
ANGPT1	NOS1	*GSK3B*	*GSK3A*
PTPN6	*STAT3*	*AKT1*	*WNT7A*
ETS1	ARHGAP1	*PAK2*	*PRKCG*
PLD1	PLA2G4F	*ANGPT2*	*VEGFA*
MAPK1	*RHOA*	*PIK3C2A*	AXIN1
MAPK6	*RBPJL*	PIK3CD	*NOTCH4*
GRB14	*EPHB3*	FZD1	*PDGFB*
PRKCZ	*PXN*	PTPN11	*WNT1*
LPXN	*EPHB2*	*NOTCH3*	*WNT10B*
NR1I2	PIK3R3	*ITGB3*	*PRKCI*
FOS	*NOTCH2*		FZD8
MAPK14	*GRB7*		*FLT4*
PDGFD	SH2D4A		*HRAS*
FGF2	*PRKCE*		SHC1
DLL1	*JUN*		F3
PIK3R1	PDGFRA		*DVL2*
BAD	*TGFB1I1*		*DVL3*
SFRP1			
CRK			