

Table 1. Regulation of candidate miR-210-target molecules in NESCs detected by microarray and IPA analyses

Gene Family	Gene symbol	Regulation	Fold change
Transcription regulator	ATN1	↓	0.36
	EGR2	→	ND
	ELL2	↓	0.49
	HDAC2	↑	3.61
	HOXA1	→	ND
	SREBF1	→	0.84
	STAT3	↑	2.01
	STAT6	↓	0.51
Growth factor	PGF	↑	7.19
Cytokine	IL11	↑	3.15
Kinase	ERBB2	↓	0.52
	MAP4K4	↓	0.45
	RPS6KA5	↑	2.53
Phosphatase	PTPN1	→	1.05
	PTPRF	↓	0.55
Peptidase	PLAU	↑	1.98
Transmembrane receptor	THBD	↑	2.84
Enzyme	GNA13	↑	1.9
	HMGCR	↑	1.93
	IRS2	↓	0.38
	MX1	↓	0.45
	PNPLA3	↑	2.3
	PPAT	↑	2.05

(Continued)

Gene Family	Gene symbol	Regulation	Fold change
Other	ANGPTL2	↑	1.96
	ANGPTL4	↑	2.77
	COL8A1	↓	0.51
	DAB2	↓	0.57
	EFEMP2	→	0.91
	IGFBP3	↓	0.41
	KRTAP4-12	→	1.25
	NF2	↓	0.57
	SKP2	↑	2.79
	SYNPO	↓	0.34
	THBS1	↓	0.47
	U2AF2	↓	0.42
Complex	Adaptor protein 1	→	NA*
	Collagen type IV	↓	NA*
	Stat1-Stat3	↑	NA*
	Stat3-Stat3	↑	NA*
Group	Fgfr	↓	NA*
	Mmp	↓	NA*
	PTPase	↓	NA*
	SRC	↓	NA*
	STAT	↓	NA*
	TGFBR	↑	NA*
	Thymidine kinase	↓	NA*
	Vegf	↑	NA*

*Complex and group were detected by IPA. Therefore the fold change data is not available.

IPA, Ingenuity pathways analysis; NA, not available; ND, not detected; NESCs, normal endometrial stromal cells.