

**Supplemental Table S3.** Lineage-associated Gene Expression Validation: Microarray-Q-RT-PCR Correlation.Spearman's  $\rho=0.483$ ,  $p=0.0004$ Kendall's  $\tau=0.35$ ,  $p=0.0002$ **A. eMSC Lineage In Vivo****eMSC FACS.control vs eSF FACS.control**

Gene symbol	Array FC	Q-RT-PCR FC
ANGPT2	25.5	276.9
BMP8A	5.8	94.7
CDH6	14.3	234.4
FRZB	8.3	15.6
GJA4	8.4	798.1
HEYL	4.5	8.8
HIGD1B	14.8	2081.6
IL6R	2.5	2.1
JAG1	8.3	21.0
MCAM	11.2	145.6
NOTCH1	2.6	3.6
PDE1A	8.7	39.2
PDE3A	7.6	5.1
RGS5	39.2	17.1
SLIT2	6.2	28.7
SLIT3	2.9	7.7

**B. eSF Lineage In Vivo****eSF FACS.control vs eMSC FACS.control**

Gene symbol	Array FC	Q-RT-PCR FC
DIO2	4.0	3.8
FGF7	4.0	8.3
FGF9	4.9	121.0
PDGFD	4.5	6.2
ROBO2	3.0	290.7
WNT2	3.9	6.2
WNT5A	2.9	3.5

**C. eSF Lineage In Vitro****eSF Late.control vs eMSC FACS.control**

Gene symbol	Array FC	Q-RT-PCR FC
CALB2	5.1	2.9
CDH2	8.7	6.7

FGF7	7.5	17.6
FGF9	3.4	163.2
GJA1	6.9	3.3
GREB1L	2.2	15.3
IL13RA1	3.0	5.5
IL13RA2	2.1	15.5
LCP1	2.0	2.4
LOX	21.6	11.1
MME	8.6	2.5
PDGFC	6.3	12.1
PDGFD	5.2	6.3
PDGFRA	7.3	5.6
ROBO2	3.2	193.6
TOX	2.9	5.4
TRIP11	2.7	2.8
VEGFC	4.3	9.9

#### D. eMSC Differentiation In Vitro

##### eMSC Late.control vs eMSC FACS.control

Gene symbol	Array FC	Q-RT-PCR FC
ASAM	3.8	11.1
CDH2	7.4	16.1
FGF7	6.2	8.9
FGF9	4.1	212.0
GJA1	5.9	12.3
LOX	19.3	6.0
PDGFD	4.5	8.5
TOX	3.5	14.9
VEGFC	4.2	27.2

##### eMSC Late.control vs eSF FACS.control

Gene symbol	Array FC	Q-RT-PCR FC
CXCL2	-2.9	-21.007
HEYL	-2.7	-305.345
IL8	-2.1	-30.138
SLIT3	-2.8	-8.446

eMSC = endometrial mesenchymal stem cells; eSF = endometrial stromal fibroblasts; control = no endometriosis; FC= fold change; Q-RT-PCR= quantitative reverse transcription polymerase chain reaction.