

**Table S1. Primers used in this study.**

<b>Gene</b>	<b>Forward Primer</b>	<b>Reverse Primer</b>
<i>oct4</i>	AGTTGGCGTGGAGACTTTGC	CAGGGCTTTCATGTCCTGG
<i>nanog</i>	TTGCTTACAAGGGTCTGCTACT	ACTGGTAGAAGAATCAGGGCT
<i>sox2</i>	GCTCGCAGACCTACATGAAC	GCC TCGGACTTGACCACAG
<i>socs3</i>	CAAGAACCTACGCATCCAGTG	CCAGCTTGAGTACACAGTCGAA
<i>stat3</i>	TGGCACCTTGATTGAGAGTC	GCAGGAATCGGCTATATTGCT
<i>gp130</i>	ATCAGAGTGGGCAACAGAGAA	TGAGGAGACCTTCCCAAGGG
<i>lif-r</i>	ACCTCCTCCTTACTACTGAAGTG	TTCCGTCCTTGATTCTGTAGA
<i>klf2</i>	CTCAGCGAGCCTATCTTGCC	CACGTTGTTTAGGTCCTCATCC
<i>klf4</i>	TCCTTTCCAACCTCGCTAACCC	CGGATCGGATAGCTGAAGCTG
<i>pecam1</i>	ACGCTGGTGCTCTATGCAAG	TCAGTTGCTGCCCATTCATCA
<i>e-cadherin</i>	CAGGTCTCCTCATGGCTTTGC	CTTCCGAAAAGAAGGCTGTCC
<i>tbx3</i>	AGGAGCGTGTCTGTCAGGTT	GCCATTACCTCCCCAATTTT
<i>rex1</i>	CCCTCGACAGACTGACCCTAA	TCGGGGCTAATCTCACTTTCAT
<i>fgf5</i>	TGTGTCTCAGGGGATTGTAGG	AGCTGTTTTCTTGGAACTCTCTCC
<i>alp</i>	CAGTATGAATTGAATCGGAACAACC	CAGCAAGAAGAAGCCTTTGAGG
<i>dppa3/stella</i>	GACCCAATGAAGGACCCTGAA	GCTTGACACCGGGGTTTAG
<i>dazl</i>	ATGTCTGCCACAACCTTCTGAG	CTGATTTTCGTTTTCATCCATCCT
<i>stra8</i>	ACAACCTAAGGAAGGCAGTTTAC	GACCTCCTCTAAGCTGTTGGG
<i>nr0b1/dax1</i>	GGGCAGCATCTTATACAGCTTG	CACTCTGGGTACAGTAGGACAG
<i>fbxo15</i>	TCGTGGGACTGAGCACAACCTA	TGACAGATGAGCCTCTAACAAAC
<i>piwil2</i>	TTGGCCTCAAGCTCCTAGAC	GAACATGGACACCAAACCTACA
<i>gbx2</i>	CAACTTCGACAAAGCCGAGG	ACTCGTCTTTCCCTTGCCCT
<i>gdf3</i>	ATGCAGCCTTATCAACGGCTT	AGGCGCTTTCTCTAATCCCAG
<i>tdgf1</i>	CAGTGCGTTTGAATTTGGACC	GCACGAACTGGAAAGACCGA
<i>c-myc</i>	TCTCCATCCTATGTTGCGGTC	TCCAAGTAACTCGGTCATCATCT
<i>nodal</i>	GTGACCGGACAGAACTGGAC	GGAAAATGTCAATGGTGAGTGGG
<i>acvr2b</i>	ACCCCCAGGTGTACTTCTG	CATGGCCGTAGGGAGGTTTC
<i>gal</i>	GGCAGCGTTATCCTGCTAGG	CTGTTACAGGGTCCAACCTCT
<i>cldn6</i>	ATGGCCTCTACTGGTCTGCAA	GCCAACAGTGAGTCATACACCTT
<i>otx2</i>	TATCTAAAGCAACCGCCTTACG	AAGTCCATACCCGAAGTGGTC
<i>ebaf</i>	CCAACCGCACTGCCCTTAT	CGCGAAACGAACCAACTTGT
<i>lefty2</i>	CAGCCAGAATTTTCGAGAGGT	CAGTGCGATTGGAGCCATC
<i>foxa2</i>	CCCTACGCCAACATGAACTCG	GTTCTGCCGGTAGAAAGGGA
<i>eomes</i>	GGCCCCTATGGCTCAAATTCC	CCTGCCCTGTTTGGTGATG
<i>dkk1</i>	CTCATCAATTCCAACGCGATCA	GCCCTCATAGAGAACTCCCG
<i>gata6</i>	GGCAGTGTGAGTGGAGGTG	TGGTACGTTCCGTTTCAGCG
<i>sox17</i>	GATGCGGGATACGCCAGTG	CCACCACCTCGCCTTTCAC
<i>cer1</i>	CTCTGGGGAAGGCAGACCTAT	CCACAAACAGATCCGGCTT
<i>pitx2</i>	GCAGCCGTTGAATGTCTCTTC	GTCCGTGAACTCGACCTTTTTT
<i>acta2</i>	GTCCCAGACATCAGGGAGTAA	TCGGATACTTCAGCGTCAGGA

<i>egr1</i>	TCGGCTCCTTTCCTCACTCA	CTCATAGGGTTGTTGCTCGG
<i>gapdh</i>	AGGTCGGTGTGAACGGATTTG	TGTAGACCATGTAGTTGAGGTCA
<i>b-actin</i>	GAAATCGTGCGTGACATCAAAG	TGTAGTTTCATGGATGCCACAG

**Table S2**

**Colony counts of ALP-positive CDEs (cells seeded at  $10^5$  unless otherwise noted)**

CDE	CDE- $\mu$ P	CDE- $\mu$ P <sub>LIF</sub>
0	11	28
3	24	32
6 (seeded @ $7.5 \times 10^4$ )	26	44
7	28	59
8		70

**Colony counts of ALP-positive 129S2C1a (cells seeded at  $10^5$  unless otherwise noted)**

129S2C1a	129S2C1a- $\mu$ P	129S2C1a- $\mu$ P <sub>LIF</sub>
0	57	301
1	166	433
8	176	455
		108 (seeded @ $5 \times 10^4$ )

**Figure S1**

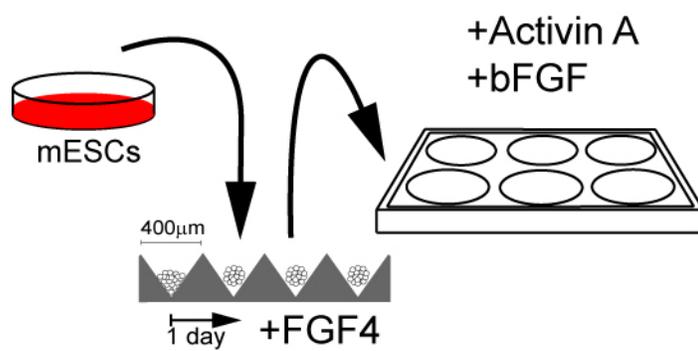
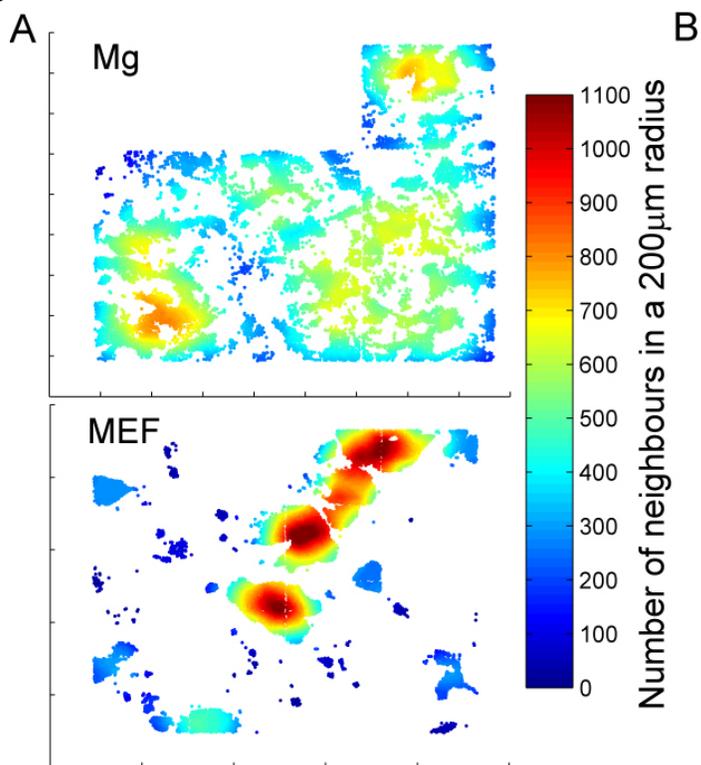
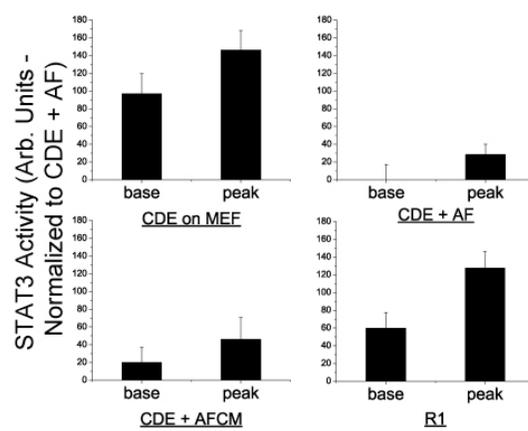


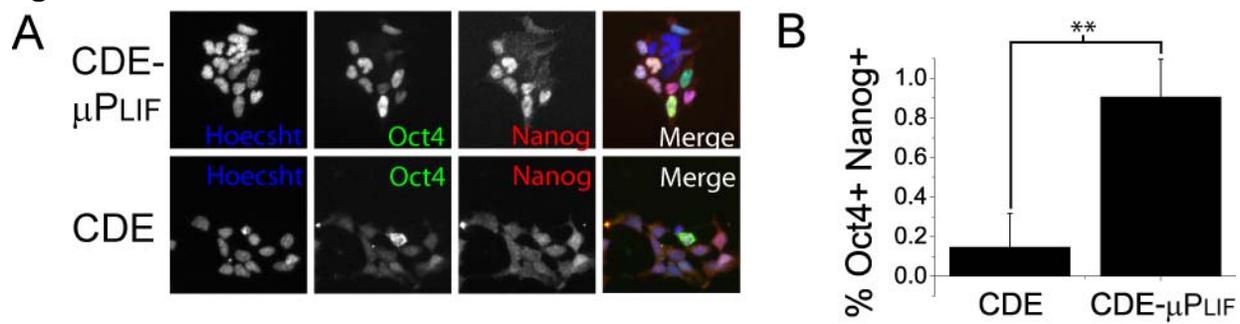
Figure S2



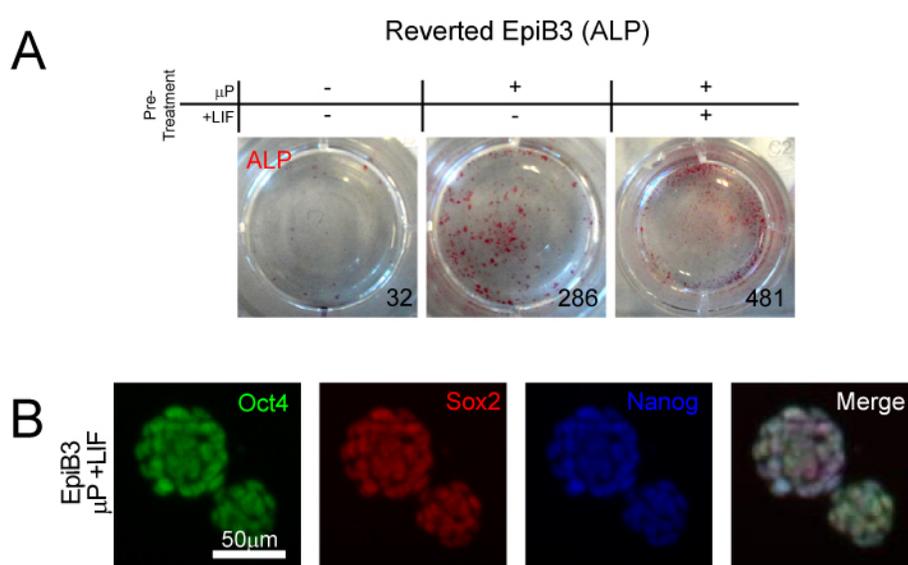
**B**



**Figure S3**



**Figure S4**



**Figure S1. Protocol for generation of CDEs.** CDEs were derived from mESCs by size-controlled aggregation using microwells followed by culture in the microwells in the presence of 10ng/ml FGF4 for 1 day and then seeding onto Matrigel-coated plates in 20ng/ml Activin A and 20ng/ml bFGF.

**Figure S2. CDEs cultured on MEFs demonstrate an increase in local cell density and increase in LIF responsiveness.** A) Choropleth map of the number of neighbours in 200mm radius in Matrigel (Mg)-coated plates(top panel) vs. MEF co-culture (bottom panel) B) Quantification of pSTAT3 staining in CDEs cultured on MEFs (MEF), CDEs cultured on Mg in AF media alone (AF), CDEs cultured on Mg in MEF-conditioned AF media (AF<sub>CM</sub>), and R1 mESCs (R1). Data represented as mean ± S.D. (n=4).

**Figure S3. Staining for Oct4 and Nanog predicts reversion frequency at 2 days following seeding.** A) Micropatterned CDEs treated with LIF were plated into 2iL media (CDE- $\mu$ P<sub>LIF</sub>) and stained for Oct4 and Nanog after 2 days B) Quantification of Oct4/Nanog double positive cells. Data represented as mean ± S.D. (n=4) \*\*p<0.01 as determined by two-sample t-test assuming equal variance.

**Figure S4. Reversion of another embryo-derived EpiSC line, EpiB3.** A) ALP staining of embryo-derived EpiB3 cells in 2iL following treatment with (+) or without (-) micropatterning ( $\mu$ P) and LIF. Colony counts listed in inset. B) Staining of revertant cells generated by  $\mu$ P<sub>LIF</sub>-treated EpiB3s demonstrates robust expression of Oct4, Sox2 and Nanog.

## Supplementary Experimental Procedures

### *qRT-PCR*

RNA was isolated using the RNeasy RNA isolation kit (Qiagen). Complimentary DNA (cDNA) was obtained from the RNA using SuperScript™ III Reverse Transcriptase (Invitrogen). cDNA was then loaded into 384-well plates (Applied Biosystems) along with primers (Supp. Table 1), and 2x Fast start SYBR green master mix (Roche). PCR was run for 40 cycles at 92°C, 60°C, and 72°C for 30s, 30s, and 15s, respectively on the ABI 7900HT Fast System (Applied Biosystems). Primer sequences were obtained from Primer Bank<sup>1</sup> or designed with Primer 3<sup>2</sup>. Data was normalized to a  $\beta$ -actin or GAPDH housekeeping control.

### *Immunocytochemistry*

Prior to imaging, cells were fixed in 3.7% formaldehyde for 10 minutes at 37°C, permeabilized in methanol for 2 minutes at room temperature, and blocked in 10% fetal bovine serum (FBS) in PBS overnight at 4°C. Primary antibodies were then added and left overnight at 4°C. Antibodies for phospho-STAT3 (Cell Signal Technologies), Oct3/4 (BD biosciences), Nanog (eBiosciences), and Sox2 (R&D), and H3K27me3 (Millipore) were all used at a 1:200 dilution. Alexa-Fluor™ (Invitrogen) secondary antibodies and Hoechst dye were added for 1 hour at room temperature diluted at 1:200 and 1:100, respectively. Stained cells were then imaged and fluorescence intensity was quantified using the Cellomics ArrayScan VTI high content screening platform (Thermo Fisher). Normalization was performed by first taking data from single-stained (e.g. Oct4 only) cells and measuring a bleed-through curve to determine the extent of background in the

channel of interest (e.g. pSTAT3). Compensation was then performed to eliminate the background from other channels.

#### *Alkaline Phosphatase Staining*

To identify alkaline phosphatase (ALP) positive colonies, cells were fixed in 10% formaldehyde for 45m at room temperature then washed 3 times in PBS. Fixed cells were then incubated in a mix of Fast Red Violet LB salt (Sigma), Naphthol AS-MX (Sigma), N,N-dimethylformamide (Sigma), and 0.1mM pH=8.3 Tris-HCl Buffer for 45m at room temperature in the dark. Cells were washed with PBS and kept in PBS for imaging or colony counting. Alternatively, following fixation, the Vector® Red Alkaline Phosphatase Substrate Kit I (VectorLabs) was used as described in the kit protocol.

## References

1. A. Spandidos, X. Wang, H. Wang and B. Seed, *Nucleic Acids Res*, 38. D792-9.
2. S. Rozen and H. Skaletsky, *Methods Mol Biol*, 2000, 132. 365-86.