Supplemental Information

Counteracting Activities of OCT4 and KLF4
during Reprogramming to Pluripotency

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Supplemental Data

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Supplemental References
**Figure S1, related to Figure 1. Oct4 overexpression impairs the proliferation of MEFs and NSCs**

20,000 cells were seeded on day 0, and Oct4 was induced by doxycycline treatment from day 1 onwards. Error bars correspond to the standard error of the mean (biological replicates, n = 4). Asterisks indicate the probability of a true null hypothesis according to a two-tailed, unpaired Student’s t-test: *, p < 0.05; **, p < 0.005.
Figure S2, related to Figure 3. Examples to illustrate score calculation
(A) Example of progression in gene expression that fulfills the defined criteria for
upregulation. (B) Example of progression in gene expression that does not fulfill the criteria
for downregulation.
Figure S3, related to Figure 3. Comparative transcriptome analysis of Oct4-induced somatic cells and controls

(A) Dendrogram displaying the results of an unsupervised hierarchical clustering based on the correlation of global gene expression profiles. (B) Direct comparison of individual samples. The number of differentially expressed genes (≥2-fold difference and signal ≥6 in at least one of the corresponding samples) is shown for each pair of samples and highlighted in shaded colors.
Figure S4, related to Figure 6. Expression of *Mgarp* mRNA in cells of the germline lineage at different developmental stages

The displayed data have been extracted from a microarray dataset previously published by our group (Sabour et al., 2011). Error bars correspond to the standard deviation of the mean (biological replicates, n = 2). EpiSC, epiblast stem cells.
Figure S5, related to Figure 6. Validation of viral *Mgarp* overexpression and sh*Mgarp* knockdown constructs

qRT-PCR for *Mgarp* mRNA in MEFs 3 days after infection with the different viral vectors. Error bars correspond to the standard deviation of the mean (technical replicates, n = 3). Tet-, tetracycline-inducible; TTA, tetracycline transactivator. See also Table S5.
Figure S6, related to Figure 6. Mitochondria number and membrane potential upon overexpression of Mgarp in MEFs

(A) Mitochondrial DNA (mtDNA) copy number after 7 days of Mgarp overexpression assessed by qPCR on total cellular DNA. Absolute copy numbers were estimated by normalization to the two presumable copies of genomic Actb per diploid cell. Error bars correspond to the standard deviation of the mean (technical replicates, n = 3). (B) Quantification of mitochondrial tetramethylrhodamine methyl ester (TMRM) staining by flow cytometry 3 days after Mgarp overexpression. Single, living cells were pre-selected by gating for scatter characteristics and DAPI permeability. The histogram shows the normalized distribution of TMRM fluorescence intensity across the analyzed cell populations, indicating mitochondrial membrane potential and activity. Also shown are representative pictures of TMRM-stained mitochondria (red), overlayed with nuclear Hoechst staining (blue). Scale bars, 25 µm. See also Table S5.
Figure S7, related to Figure 6. Proliferation rate, morphology, and Oct4 expression in ESCs upon overexpression and knockdown of Mgarp

(A) 20,000 ESCs were seeded on day 0. Error bars correspond to the standard error of the mean (biological replicates, n = 4). (B) Phase-contrast and Oct4-GFP reporter fluorescence images of representative ESC cultures. Scale bars, 250 µm.
Table S1, related to Figure 3. ESC-specific genes that were upregulated by OCT4 in the different somatic cell types

| Regulation in cell type | ESC-specific probes |
|-------------------------|---------------------|
| up in TO-MefS           | Gca, Kndc1, Vgf, Mme, Tpd5211, Zdhhc15, Tpd211, Vps41, Eml5, Stmn2, Flywch2, Chst8, Pthr1, S6glnac2, 4921528G01Rik, Tsc1, Ralgps2, Tek, Tdpl2, Is1, Rass7, Yipf2, 9432079M16Rik, Obfc1 |
| up in TO-NSCs           | Ryr1, Rnf125, Amigo2, Smtn2, Mapt, Kndc1, Col9a2, Bmf, Zfp423, Clcn2, Mi2, Lgals4, Pacsin1, Zfp423, 4921528G01Rik, 1190005f06Rik, Syt9, Hr, Phma2, Ralgps2, Vps41, Chst8, Arl5b, Mtmr14, LOC545238, Mpv171 |
| up in TO-BMCs           | Vgf |

Probes present in more than one cell type are set in bold font.
Table S2, related to Figure 3. Enriched gene ontology (GO) terms of OCT4-regulated genes in TO-MEF cells and corresponding p-values after Benjamini-Hochberg correction for multiple hypothesis testing.

| regulation in cell type | GO identifier | category* | ontology term                          | p-value      |
|-------------------------|---------------|-----------|----------------------------------------|--------------|
| up in TO-MEFs           | GO:0043005    | CC        | neuron projection                      | 2.15E-04     |
| down in TO-MEFs         | GO:0031012    | CC        | extracellular matrix                   | 2.04E-09     |
| down in TO-MEFs         | GO:0005578    | CC        | proteinaceous extracellular matrix     | 2.54E-08     |
| down in TO-MEFs         | GO:0044421    | CC        | extracellular region part              | 2.98E-08     |
| down in TO-MEFs         | GO:0044420    | CC        | extracellular matrix part              | 1.28E-06     |
| down in TO-MEFs         | GO:0005515    | MF        | protein binding                        | 7.48E-06     |
| down in TO-MEFs         | GO:0048513    | BP        | organ development                      | 9.86E-06     |
| down in TO-MEFs         | GO:0048856    | BP        | anatomical structure development       | 2.77E-05     |
| down in TO-MEFs         | GO:0030198    | BP        | extracellular matrix organization      | 3.06E-05     |
| down in TO-MEFs         | GO:0007275    | BP        | multicellular organismal development   | 3.11E-05     |
| down in TO-MEFs         | GO:0043062    | BP        | extracellular structure organization    | 3.29E-05     |
| down in TO-MEFs         | GO:0048731    | BP        | system development                     | 4.01E-05     |
| down in TO-MEFs         | GO:0032502    | BP        | developmental process                  | 9.62E-05     |
| down in TO-MEFs         | GO:0009888    | BP        | tissue development                     | 1.29E-04     |
| down in TO-MEFs         | GO:0048522    | BP        | positive regulation of cellular process| 2.65E-04     |
| down in TO-MEFs         | GO:0009653    | BP        | anatomical structure morphogenesis     | 2.74E-04     |
| down in TO-MEFs         | GO:0001944    | BP        | vasculature development                | 2.75E-04     |
| down in TO-MEFs         | GO:0042127    | BP        | regulation of cell proliferation       | 4.02E-04     |
| down in TO-MEFs         | GO:0001568    | BP        | blood vessel development               | 4.81E-04     |
| down in TO-MEFs         | GO:0005576    | CC        | extracellular region                   | 5.84E-04     |
| down in TO-MEFs         | GO:0005730    | CC        | nucleolus                              | 7.22E-04     |
| down in TO-MEFs         | GO:0009987    | BP        | cellular process                       | 8.24E-04     |

*CC, cellular component; MF, molecular function; BP, biological process.

Terms that also appeared in other cell types are set in bold font.
Table S3, related to Figure 3. Enriched gene ontology (GO) terms of OCT4-regulated genes in TO-NSC cells and corresponding p-values after Benjamini-Hochberg correction for multiple hypothesis testing

| regulation in cell type | GO identifier | category* | ontology term | p-value |
|-------------------------|---------------|-----------|---------------|---------|
| down in TO-NSCs         | GO:0044424    | CC        | intracellular part | 4.63E-38 |
| down in TO-NSCs         | GO:0005622    | CC        | intracellular   | 5.74E-37 |
| down in TO-NSCs         | GO:0005634    | CC        | nucleus        | 3.32E-36 |
| down in TO-NSCs         | GO:0007049    | BP        | cell cycle     | 1.94E-35 |
| down in TO-NSCs         | GO:0043226    | CC        | organelle      | 1.23E-33 |
| down in TO-NSCs         | GO:0043229    | CC        | intracellular organelle | 1.29E-33 |
| down in TO-NSCs         | GO:0005694    | CC        | chromosome     | 8.09E-32 |
| down in TO-NSCs         | GO:0043229    | CC        | non-membrane–bounded organelle | 8.64E-31 |
| down in TO-NSCs         | GO:0043232    | CC        | intracellular non-membrane–bounded organelle | 8.64E-31 |
| down in TO-NSCs         | GO:0043231    | CC        | intracellular membrane–bounded organelle | 1.03E-30 |
| down in TO-NSCs         | GO:0043227    | CC        | membrane–bounded organelle | 1.17E-30 |
| down in TO-NSCs         | GO:0044422    | CC        | organelle part | 2.69E-30 |
| down in TO-NSCs         | GO:0044446    | CC        | intracellular organelle part | 2.78E-30 |
| down in TO-NSCs         | GO:0022403    | BP        | cell cycle phase | 6.61E-30 |
| down in TO-NSCs         | GO:0006259    | BP        | DNA metabolic process | 3.72E-29 |
| down in TO-NSCs         | GO:0022402    | BP        | cell cycle process | 3.96E-29 |
| down in TO-NSCs         | GO:0000278    | BP        | mitotic cell cycle | 7.65E-29 |
| down in TO-NSCs         | GO:0009887    | BP        | cellular process | 1.44E-27 |
| down in TO-NSCs         | GO:0000279    | BP        | M phase        | 2.93E-27 |
| down in TO-NSCs         | GO:0051301    | BP        | cell division  | 3.24E-27 |
| down in TO-NSCs         | GO:0044427    | CC        | chromosomal part | 4.41E-26 |
| down in TO-NSCs         | GO:0000280    | BP        | nuclear division | 3.78E-25 |
| down in TO-NSCs         | GO:0007067    | BP        | mitosis        | 3.78E-25 |
| down in TO-NSCs         | GO:0006087    | BP        | M phase of mitotic cell cycle | 8.04E-25 |
| down in TO-NSCs         | GO:0048285    | BP        | organelle fission | 1.69E-24 |
| down in TO-NSCs         | GO:0006260    | BP        | DNA replication | 2.35E-23 |
| down in TO-NSCs         | GO:0000775    | CC        | chromosome, centromeric region | 1.66E-20 |
| down in TO-NSCs         | GO:0044428    | CC        | nuclear part   | 3.40E-18 |
| down in TO-NSCs         | GO:0006139    | BP        | nucleobase, nucleoside, nucleotide, and nucleic acid metabolic process | 3.79E-15 |
| down in TO-NSCs         | GO:0000793    | CC        | condensed chromosome | 2.26E-14 |
| down in TO-NSCs         | GO:0044237    | BP        | cellular metabolic process | 3.31E-14 |
| down in TO-NSCs         | GO:0006281    | BP        | DNA repair     | 7.65E-14 |
| down in TO-NSCs         | GO:0034641    | BP        | cellular nitrogen compound metabolic process | 1.00E-13 |
| down in TO-NSCs         | GO:0006996    | BP        | organelle organization | 2.70E-13 |
| down in TO-NSCs         | GO:0000776    | CC        | kinetochore   | 4.59E-13 |
| down in TO-NSCs         | GO:0006874    | BP        | response to DNA damage stimulus | 8.34E-13 |
| down in TO-NSCs         | GO:0006807    | BP        | nitrogen compound metabolic process | 1.06E-12 |
| down in TO-NSCs         | GO:0000779    | CC        | condensed chromosome, centromeric region | 1.77E-12 |
| down in TO-NSCs         | GO:0005730    | CC        | nucleolus      | 1.82E-12 |
| down in TO-NSCs         | GO:00032991   | CC        | macromolecular complex | 1.83E-12 |
| down in TO-NSCs         | GO:0000777    | CC        | condensed chromosome kinetochore | 1.87E-12 |
| down in TO-NSCs         | GO:0031974    | CC        | membrane-enclosed lumen | 1.91E-12 |
| down in TO-NSCs         | GO:0044238    | BP        | primary metabolic process | 3.45E-11 |
| down in TO-NSCs         | GO:0005524    | MF        | ATP binding   | 8.84E-11 |
| down in TO-NSCs         | GO:0032559    | MF        | adenyl ribonucleotide binding | 9.80E-11 |
| down in TO-NSCs         | GO:0044260    | BP        | cellular macromolecule metabolic process | 1.03E-10 |
| down in TO-NSCs         | GO:0070013    | CC        | intracellular organelle lumen | 1.16E-10 |
| down in TO-NSCs         | GO:0043233    | CC        | organelle lumen | 1.33E-10 |
| down in TO-NSCs         | GO:0007059    | BP        | chromosome segregation | 1.98E-10 |
| down in TO-NSCs         | GO:0030554    | MF        | adenyl nucleotide binding | 3.11E-10 |
| down in TO-NSCs         | GO:0006152    | BP        | metabolic process | 3.10E-10 |
| down in TO-NSCs         | GO:0001883    | MF        | purine nucleoside binding | 4.28E-10 |
| down in TO-NSCs         | GO:0001882    | MF        | nucleoside binding | 4.52E-10 |
| down in TO-NSCs         | GO:0031981    | CC        | nuclear lumen | 6.72E-10 |
| down in TO-NSCs         | GO:0003824    | MF        | catalytic activity | 1.66E-09 |
| down in TO-NSCs         | GO:0016043    | BP        | cellular component organization | 1.96E-09 |
| regulation in cell type | GO identifier | category* | ontology term | p-value |
|-------------------------|---------------|-----------|---------------|---------|
| down in TO-NSCs         | GO:0043234    | CC        | protein complex | 1.97E-09 |
| down in TO-NSCs         | GO:0033554    | BP        | cellular response to stress | 8.02E-09 |
| down in TO-NSCs         | GO:0032555    | MF        | ribonucleotide binding | 1.37E-08 |
| down in TO-NSCs         | GO:0017076    | MF        | purine ribonucleotide binding | 1.37E-08 |
| down in TO-NSCs         | GO:0000166    | MF        | nucleotide binding | 3.66E-08 |
| down in TO-NSCs         | GO:0043170    | BP        | macromolecule metabolic process | 5.30E-08 |
| down in TO-NSCs         | GO:0006310    | BP        | DNA recombination | 1.45E-07 |
| down in TO-NSCs         | GO:0005657    | CC        | replication fork | 2.25E-07 |
| down in TO-NSCs         | GO:0022613    | BP        | ribonucleoprotein complex biogenesis | 2.25E-07 |
| down in TO-NSCs         | GO:0051276    | BP        | chromosome organization | 2.65E-07 |
| down in TO-NSCs         | GO:0006261    | BP        | DNA-dependent DNA replication | 4.35E-07 |
| down in TO-NSCs         | GO:0015630    | CC        | microtubule cytoskeleton | 6.46E-07 |
| down in TO-NSCs         | GO:0051716    | BP        | cellular response to stimulus | 4.98E-07 |
| down in TO-NSCs         | GO:0005819    | CC        | spindle | 6.05E-07 |
| down in TO-NSCs         | GO:0005635    | CC        | nuclear envelope | 8.18E-07 |
| down in TO-NSCs         | GO:0034660    | BP        | ncRNA metabolic process | 8.39E-07 |
| down in TO-NSCs         | GO:0005488    | MF        | binding | 1.36E-06 |
| down in TO-NSCs         | GO:0006270    | BP        | DNA replication initiation | 1.50E-06 |
| down in TO-NSCs         | GO:0042254    | BP        | ribosome biogenesis | 3.35E-06 |
| down in TO-NSCs         | GO:0034621    | BP        | cellular macromolecular complex subunit organization | 5.73E-06 |
| down in TO-NSCs         | GO:0032983    | CC        | protein-DNA complex | 9.64E-06 |
| down in TO-NSCs         | GO:0005737    | CC        | cytoplasm | 1.35E-05 |
| down in TO-NSCs         | GO:0009058    | BP        | biosynthetic process | 1.37E-05 |
| down in TO-NSCs         | GO:0005643    | CC        | nuclear pore | 1.81E-05 |
| down in TO-NSCs         | GO:0006323    | BP        | DNA packaging | 1.91E-05 |
| down in TO-NSCs         | GO:0034470    | BP        | ncRNA processing | 2.51E-05 |
| down in TO-NSCs         | GO:0006695    | BP        | cholesterol biosynthetic process | 2.52E-05 |
| down in TO-NSCs         | GO:0003677    | MF        | DNA binding | 2.84E-05 |
| down in TO-NSCs         | GO:0016126    | BP        | sterol biosynthetic process | 3.26E-05 |
| down in TO-NSCs         | GO:0006364    | BP        | rRNA processing | 5.03E-05 |
| down in TO-NSCs         | GO:0016072    | BP        | rRNA metabolic process | 5.75E-05 |
| down in TO-NSCs         | GO:0044085    | BP        | cellular component biogenesis | 5.75E-05 |
| down in TO-NSCs         | GO:0044430    | CC        | cytoskeletal part | 7.35E-05 |
| down in TO-NSCs         | GO:0003676    | MF        | nucleic acid binding | 9.50E-05 |
| down in TO-NSCs         | GO:0044249    | BP        | cellular biosynthetic process | 1.19E-04 |
| down in TO-NSCs         | GO:0034622    | BP        | cellular macromolecular complex assembly | 1.69E-04 |
| down in TO-NSCs         | GO:0046930    | CC        | pore complex | 1.82E-04 |
| down in TO-NSCs         | GO:0016740    | MF        | transferase activity | 1.86E-04 |
| down in TO-NSCs         | GO:0007017    | BP        | microtubule-based process | 1.87E-04 |
| down in TO-NSCs         | GO:0006396    | BP        | RNA processing | 2.29E-04 |
| down in TO-NSCs         | GO:0044454    | CC        | nuclear chromosome part | 3.19E-04 |
| down in TO-NSCs         | GO:0043933    | BP        | macromolecular complex subunit organization | 3.27E-04 |
| down in TO-NSCs         | GO:0012505    | CC        | endomembrane system | 3.67E-04 |
| down in TO-NSCs         | GO:0016462    | MF        | pyrophosphatase activity | 3.97E-04 |
| down in TO-NSCs         | GO:0016818    | MF        | hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides | 3.98E-04 |
| down in TO-NSCs         | GO:0003887    | MF        | DNA-directed DNA polymerase activity | 4.10E-04 |
| down in TO-NSCs         | GO:0009262    | BP        | deoxyribonucleotide metabolic process | 4.52E-04 |
| down in TO-NSCs         | GO:0000228    | CC        | nuclear chromosome | 5.10E-04 |
| down in TO-NSCs         | GO:0016817    | MF        | hydrolase activity, acting on acid anhydrides | 5.34E-04 |
| down in TO-NSCs         | GO:0034061    | MF        | DNA polymerase activity | 7.80E-04 |
| down in TO-NSCs         | GO:0031967    | CC        | organelle envelope | 8.63E-04 |
| regulation in cell type | GO identifier | category | ontology term | p-value   |
|-------------------------|---------------|----------|---------------|-----------|
| down in TO-NSCs         | GO:0031975    | CC       | envelope      | 8.89E-04  |
| down in TO-NSCs         | GO:0000785    | CC       | chromatin     | 8.90E-04  |
| down in TO-NSCs         | GO:0005856    | CC       | cytoskeleton  | 9.25E-04  |

*CC, cellular component; MF, molecular function; BP, biological process.
Terms that also appeared in other cell types are set in bold font.
Table S4, related to Figure 3. Enriched gene ontology (GO) terms of OCT4-regulated genes in TO-BMC cells and corresponding p-values after Benjamini-Hochberg correction for multiple hypothesis testing

| regulation in cell type | GO identifier | category | ontology term                  | p-value  |
|-------------------------|---------------|----------|--------------------------------|----------|
| down in TO-BMCs         | GO:0050896    | BP       | response to stimulus           | 2.48E-08 |
| down in TO-BMCs         | GO:0002376    | BP       | immune system process          | 6.16E-08 |
| down in TO-BMCs         | GO:0006955    | BP       | immune response                | 9.30E-08 |
| down in TO-BMCs         | GO:0009605    | BP       | response to external stimulus  | 1.09E-07 |
| down in TO-BMCs         | GO:0005576    | CC       | extracellular region           | 5.75E-07 |
| down in TO-BMCs         | GO:0006952    | BP       | defense response               | 8.35E-06 |
| down in TO-BMCs         | GO:0009611    | BP       | response to wounding           | 1.63E-05 |
| down in TO-BMCs         | GO:0006950    | BP       | response to stress             | 3.77E-05 |
| down in TO-BMCs         | GO:0009607    | BP       | response to biotic stimulus    | 7.70E-05 |
| down in TO-BMCs         | GO:0007599    | BP       | hemostasis                     | 1.31E-04 |
| down in TO-BMCs         | GO:0051707    | BP       | response to other organism     | 1.43E-04 |
| down in TO-BMCs         | GO:0007596    | BP       | blood coagulation              | 1.45E-04 |
| down in TO-BMCs         | GO:0050817    | BP       | coagulation                    | 1.45E-04 |
| down in TO-BMCs         | GO:0042060    | BP       | wound healing                  | 2.69E-04 |
| down in TO-BMCs         | GO:0050878    | BP       | regulation of body fluid levels| 5.15E-04 |

*CC, cellular component; MF, molecular function; BP, biological process.
Terms that also appeared in other cell types are set in bold font.
| primer          | sequence                                                                 |
|----------------|---------------------------------------------------------------------------|
| Oct4 qRT-PCRfw | 5'-GGC TAG AGA AGG ATG TGG TTC GAG-3'                                   |
| Oct4 qRT-PCRev | 5'-CCT GGG AAA GGT GTC CCT GTA G-3'                                     |
| Parml qRT-PCRfw| 5'-GAG TCA TCG CGG TAG TGT TGAC-3'                                     |
| Parml qRT-PCRev| 5'-GCG TGCC AGG AGC TTG CCA TA-3'                                      |
| Mgarq qRT-PCRfw| 5'-AAA GAA CAA ACA AAG GCG GAG TGG-3'                                  |
| Mgarq qRT-PCRev| 5'-GAG ACT TCC TCG GCT TCG GAC-3'                                     |
| Scl24a3 qRT-PCRfw| 5'-TGG GCC TCC ACC TCC GTG-3'                                          |
| Scl24a3 qRT-PCRev| 5'-TCC AAG GAT GGG ACG AAG TGC-3'                                     |
| Tmem53 qRT-PCRfw| 5'-AGG CTG GAG GGA CAA GAT CTC-3'                                     |
| Tmem53 qRT-PCRev| 5'-GGG ATG CCC AAG GAC TCA GA-3'                                      |
| Adorab2 qRT-PCRfw| 5'-CGT CCC GCT GAT GTA TAA AGG TT-3'                                   |
| Adorab2 qRT-PCRev| 5'-AGG CAA GGA CCC AGA GGA CA-3'                                      |
| Kank4 qRT-PCRfw | 5'-GAA CCT GGC TGA CGG AAG TG-3'                                       |
| Kank4 qRT-PCRev | 5'-TGG ACA ATG CCG GAG TTA GAG TGG-3'                                  |
| Gap43 qRT-PCRfw | 5'-GCA GAA AGC AGC CAA GAT CTA G-3'                                    |
| Gap43 qRT-PCRev | 5'-TCC TGT CGG GAA CTT TCC TT-3'                                       |
| Gadd45q qRT-PCRfw| 5'-ACG AGT CCG CCA AAC GTG TCG-3'                                     |
| Gadd45q qRT-PCRev| 5'-GGG CTA TGT CGC CCT CAT CT-3'                                      |
| Gadd45q qRT-PCfw | 5'-CCA ATG TGT CGC TCG TGG AT-3'                                       |
| Gadd45q qRT-PCRev| 5'-GCG TCC TTC GCC AAT AGT GA-3'                                      |
| Oct4 methylation 1st | 5'-TGT TTT TTA TTA ATT TAG GGG G-3'                                    |
| Oct4 methylation 2nd | 5'-ATC CCC AAT ACC TCT AAT AAG ACC-3'                                   |
| Oct4 methylation 3rd | 5'-GAG TTA GAG GTT AAG GTT AGA GGG-3'                                   |
| Nanog methylation 1st | 5'-TTT GTA GGT GGG ATT AAT TGG TAA-3'                                   |
| Nanog methylation 2nd | 5'-AAAA AAA TTA ACA ACA ACC AAA A-3'                                   |
| Nanog methylation 3rd | 5'-TTT GTA GGT GGG ATT AAT TGT GAA-3'                                   |
| Nanog methylation 4th | 5'-AAAA AAA ACA AAA CAC CAA CCA CAA AAT-3'                              |
| Gfp genotyping fw | 5'-GGGA AAA TTA GGG GTA TCC AC-3'                                     |
| Gfp genotyping rev | 5'-GTT TTA ATG GGC TTC TTC TGG GAG-3'                                  |
| Mgarpa ChIPfw | 5'-AGG CTT GTG GAC TCG AAG CCA GTG-3'                                   |
| Mgarpa ChIPrev | 5'-GCC TCT GTG TCT GTG GCC TGC-3'                                      |
| Mgarb ChIPfw | 5'-GCT CTA ACT CTG GTT GGT CTG AGC-3'                                   |
| Mgarb ChIPrev | 5'-GCT TGT AGT GTA GAG TCG TCA GCC TCC TC-3                             |
| Mgarc ChIPfw | 5'-GCG TCC AGG TTC CGG TGC TTC TGG CAT-3                                |
| Mgarc ChIPrev | 5'-ACCCAA ACA CAC TGCC TTC TTC ACG A-3                                  |
| Mgar d ChIPfw | 5'-ATG AGT TGG CAG GGA GAA CCT TTG GGC-3                                |
| Mgar d ChIPrev | 5'-AGG TTA GGG CCC TCA CCC TCG TAA-3                                   |
| Mgar e ChIPfw | 5'-TGG AGA CCA GCA ATG CTG AGG ACC A-3                                  |
| Mgar e ChIPrev | 5'-GAG CAG AGA AAT CGT GGT CGC GCA-3                                   |
| Mgar f ChIPfw | 5'-ATG CTT GAT GTA TGC TGC TCA GCC CCA-3                                |
| Mgar f ChIPrev | 5'-GGC ATC GCC AGG GGG AAA CTT TAC-3                                   |
| Mgar g ChIPfw | 5'-GCC TCC CCA GGA AGA GGT AGC GGG-3                                  |
| Mgar g ChIPrev | 5'-CTC CCT CTG AGC CTG GTG TGC TCG-3                                   |
| Mgar h ChIPfw | 5'-AGG AGA TAC ATG GCC AGA TGC-3                                       |
| Mgar h ChIPrev | 5'-AGG GAT GGA TGG GTA GGA AAT GGG CTC A-3                              |
| Mgar i ChIPfw | 5'-ACA GAG AGG GTG GCC CCC GTG TCG-3                                   |
| Mgar i ChIPrev | 5'-GCC CCC TCT TCC AGG CCT TCC CTA-3                                   |
| Mgar j ChIPfw | 5'-AGA GGA GTG GGA GGG AGA AGA TGC-3                                   |
| Mgar j ChIPrev | 5'-GCC AGC TCT TTT TCT TTT TAT CCA A-3                                  |
| Mgar k ChIPfw | 5'-GCA GAA GGA CTG AGT AGT GGT TGC-3                                   |
| Mgar k ChIPrev | 5'-GCT CAG GAC CCA CGT AGT GGG AGA A-3                                  |
| Mgar l ChIPfw | 5'-GGG CTG TGG TGA TGG CTT GGA TGC-3                                   |
| Mgar l ChIPrev | 5'-TGC TCT CCT TGC TGC TGC TGC A-3                                     |
| rDNA-28S ChIPfw | 5'-CTG GTG ATG ATT AGG GGG AAG GAC-3                                 |
| rDNA-28S ChIPrev | 5'-GGC CCC AAG ACC TCT AAT CAT-3                                     |
| Oct4 ChIPfw | 5'-GGT GAG ACT TCC GGC CAG ACC A-3                                     |
| Oct4 ChIPrev | 5'-GCC AGC GAA CTA TCA TGC ACC ACC-3                                   |
| primer          | sequence                                             |
|----------------|------------------------------------------------------|
| Cdh1 ChIP fw.  | 5'-CCA TGT CTC CGT GGG TCA GAG CAC-3'                |
| Cdh1 ChIP rev. | 3'-GTA TGC TAG TTG GTG GCA TGG GGC                 |
| mtDNA qPCR fw. | 5'-ACA TTC CTA TGG ATC CGA GC-3'                    |
| mtDNA qPCR rev.| 3'-GAT GAT GGC AAG GGT GAT AG-3'                    |
| Actb qPCR fw.  | 5'-CCC TAC AGT GCT GTG GGT TT-3'                    |
| Actb qPCR rev. | 3'-GAT GAT GGC AAG GGT GAT AG-3'                    |
| shMgrap #1     | 5'-AGA CAC TGC TGT AAC GGA AGC TGA A-3'             |
| shMgrap #2     | 3'-CAA AGC AAG TGA GAC GTA CAG AAC A-3'             |
| shRNA control  | 5'-GTT CAG ATG TGC GGC GAG T-3'                     |

fw., forward; rev., reverse.
Table S6, related to Figures 1, 2, and 7. Antibody information

| antigen | host and clonality | clone / specification | manufacturer              | dilution |
|---------|--------------------|-----------------------|---------------------------|----------|
| OCT4    | goat polyclonal    | N19 sc-8628           | Santa Cruz Biotechnology  | 1 : 1000 |
| GAPDH   | mouse monoclonal   | AM4300                | Ambion                    | 1 : 10,000 |
| NANOG   | rabbit polyclonal  | REC-RCAB0002P-F       | Cosmo Bio                 | 1 : 1000 |
| SSEA-1  | mouse monoclonal   | MC-480                | Millipore                 | 1 : 100   |
| TUBB3   | mouse monoclonal   | TUJ1 MMS-435P         | Covance                   | 1 : 1000 |
| ACTA2   | mouse monoclonal   | 1A4                   | Dako                      | 1 : 100   |
| SOX17   | goat polyclonal    | AF1924                | R&D Systems               | 1 : 100   |
| KLF4    | goat polyclonal    | AF3158                | R&D Systems               | 1 : 1000 |
Supplemental References

Sabour, D., Araúzo-Bravo, M.J., Hübner, K., Ko, K., Greber, B., Gentile, L., Stehling, M., and Schöler, H.R. (2011). Identification of genes specific to mouse primordial germ cells through dynamic global gene expression. Human molecular genetics 20, 115-125.