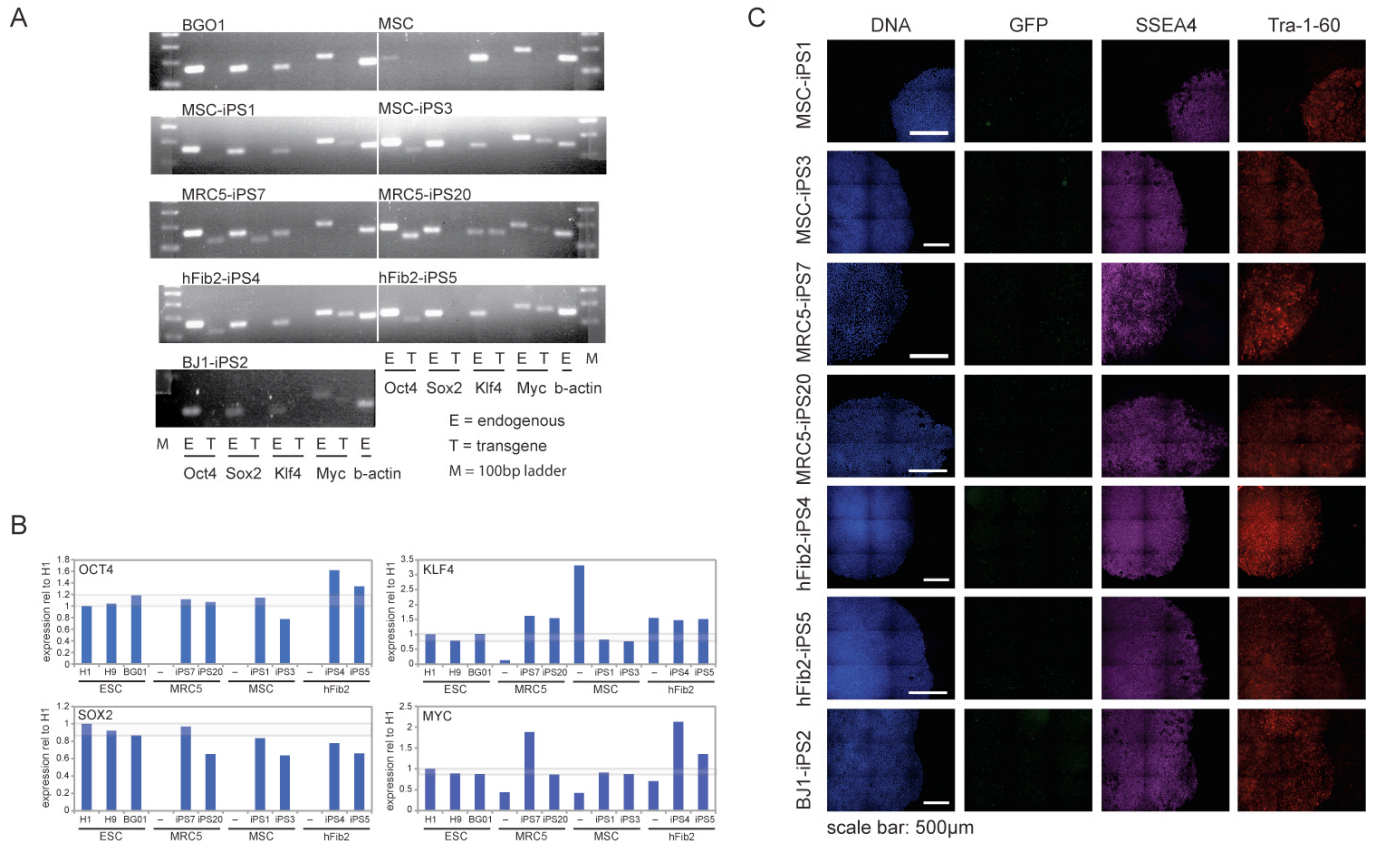


Supplementary Information

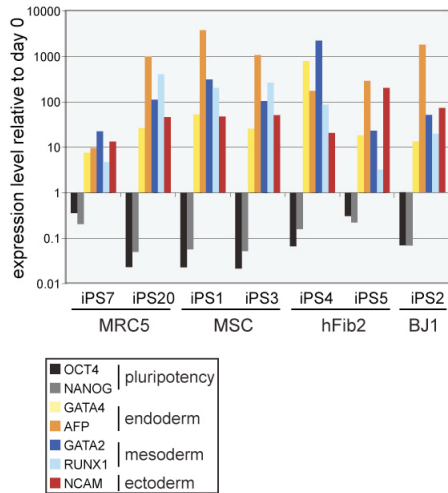
Large intergenic non-coding RNA-RoR modulates reprogramming of human induced pluripotent stem cells

Sabine Loewer, Moran N. Cabili, Mitchell Guttman, Yui-Han Loh, Kelly Thomas, In Hyun Park, Manuel Garber, Matthew Curran, Tamer Onder, Suneet Agarwal, Philip D. Manos, Sumon Datta, Eric S. Lander, Thorsten M. Schlaeger, George Q. Daley and John L. Rinn

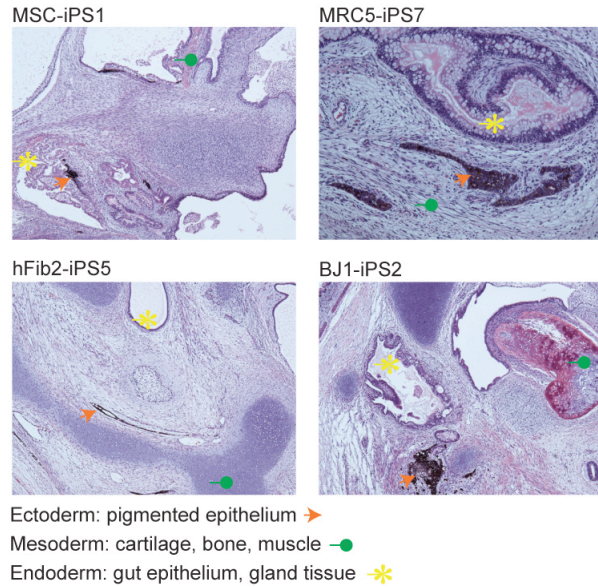


Supplementary Figure 1: Characterization of iPS cell lines used in this study. A) Semi-quantitative RT-PCR (30 cycles) to document silencing of retroviral transgenes in iPSC lines. BG01, MSC: ESC and fibroblast controls, respectively, for detection of pluripotency markers and absence of transgenes. B) qRT-PCR documents the total mRNA levels of reprogramming factor mRNAs of *OCT4*, *SOX2*, *KLF4*, and *MYC* in iPSC lines in comparison with the levels in ESC lines (H1, H9, BG01). mRNA levels are depicted relative to the levels in H1 ESCs. C) Fluorescence immunostaining shows upregulation of SSEA4 and Tra-1-60 surface markers, and absence of transgene expression as reflected by GFP in iPSCs. DNA was counterstained with Hoechst 33342.

A



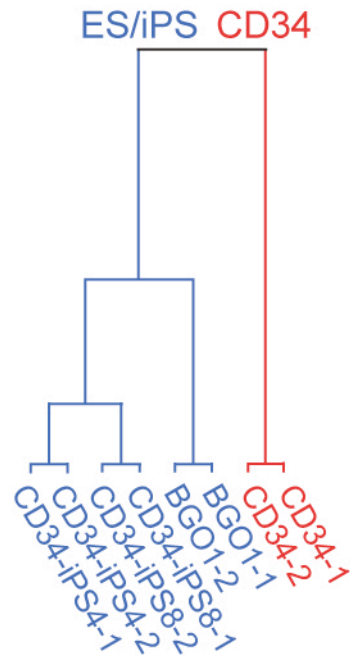
B



Supplementary Figure 2: Differentiation potential of fibroblast-derived iPSC lines. A) qRT-PCR to document the downregulation of pluripotency markers *OCT4* and *NANOG*, as well as upregulation of differentiation markers of all three germ layers on day 6 of EB differentiation relative to undifferentiated controls. B) Hematoxylin and Eosin (H+E) stained examples of teratomas showing tissues derived from all three germ layers obtained from iPSC injected into the femoral muscle of Rag2 γ c mice.

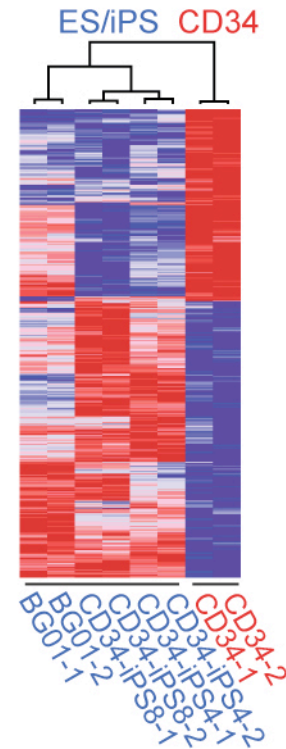
A

Unsupervised
hierarchical clustering

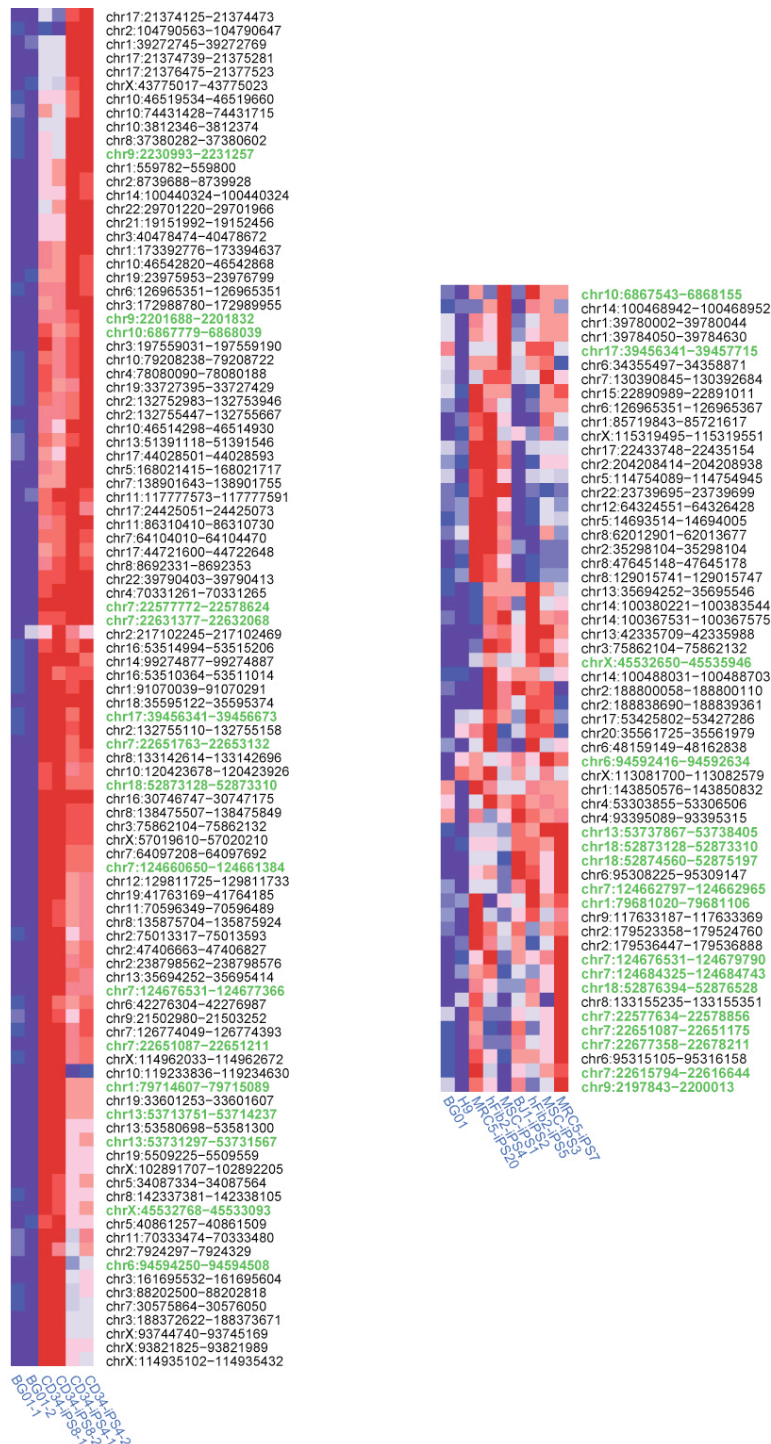


B

Supervised
hierarchical clustering



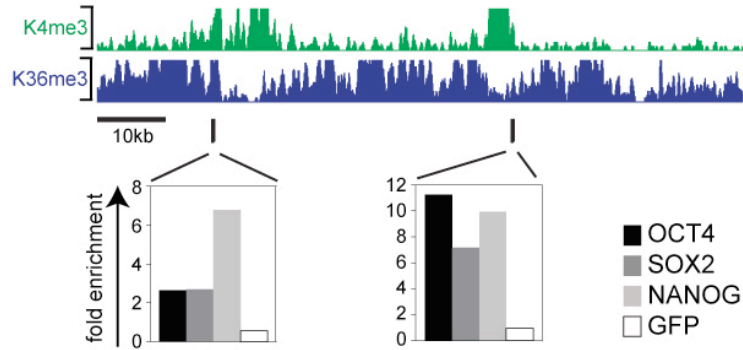
Supplementary Figure 4: Expression analysis of lincRNAs in CD34⁺-derived iPSCs. A) Unsupervised clustering of lincRNA expression segregates CD34⁺ cells (red) from ESCs and CD34⁺-derived iPSCs (blue). B) Supervised clustering analysis identifies 152 lincRNAs that were differentially expressed between ESCs/iPSCs and CD34⁺ cells (>2fold, FWER<0.05). Expression values are represented in shades of red and blue relative to being above (red) or below (blue) the median expression value across all samples (log scale 2, from -3 to +3).



Supplementary Figure 5: Heatmaps from Figure 2A showing lincRNAs with elevated expression in fibroblast-derived iPSCs (left) and CD34⁺-derived iPSCs relative to hESCs (>2fold, FWER<0.05). The chromosomal coordinates of differentially expressed lincRNA segments are indicated, and segments corresponding to the 10 overlapping iPSC-elevated lincRNAs are highlighted in green. Expression values are represented in shades of red and blue relative to being above (red) or below (blue) the median expression value across all samples (log scale 2, from -3 to +3).

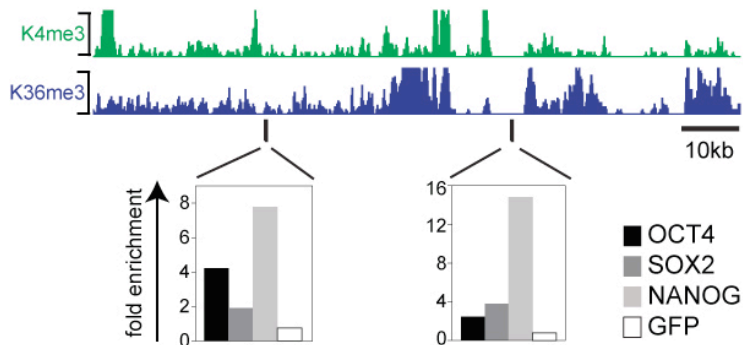
LincRNA-VLDLR H3K4-K36 domain

chr9:2197775-2288675



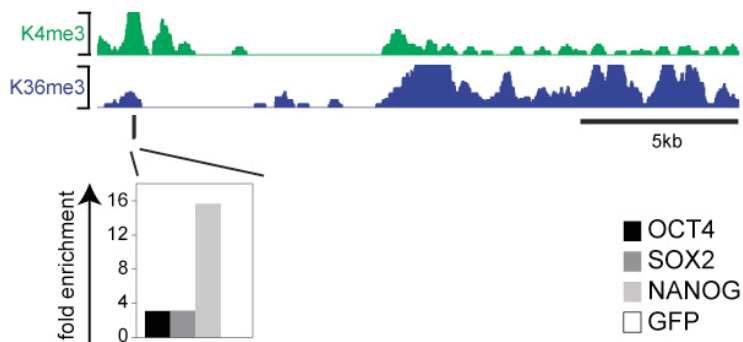
LincRNA-SFMBT2 H3K4-K36 domain

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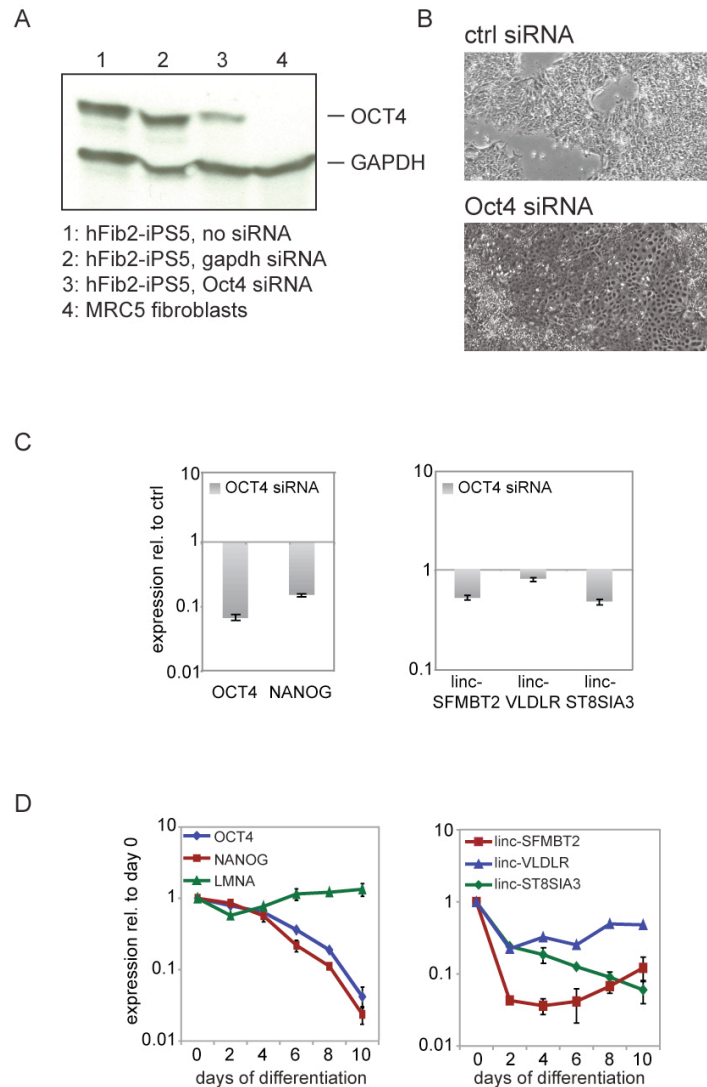


LincRNA-ST8SIA3 H3K4-K36 domain

chr18:52872000-52892000

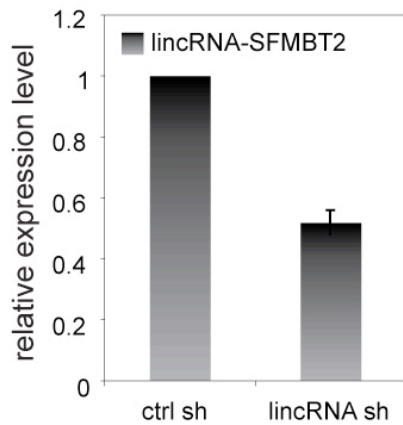


Supplementary Figure 6: ChIP analysis of iPSC-enriched lincRNA loci in BJ1-iPS2 cells. Top: lincRNA loci demarcated by histone H3K4me3 and H3K36me3 domains (green and blue, respectively). Bottom: ChIP in BJ1-iPS2 cells followed by qPCR analysis detects binding of OCT4, SOX2, and NANOG within lincRNA-SFMBT2, lincRNA-VLDLR, and lincRNA-ST8SIA3 regions. ChIP enrichment values are displayed normalized to a control region (chr12: 7,839,777- 7,839,966; hg18).

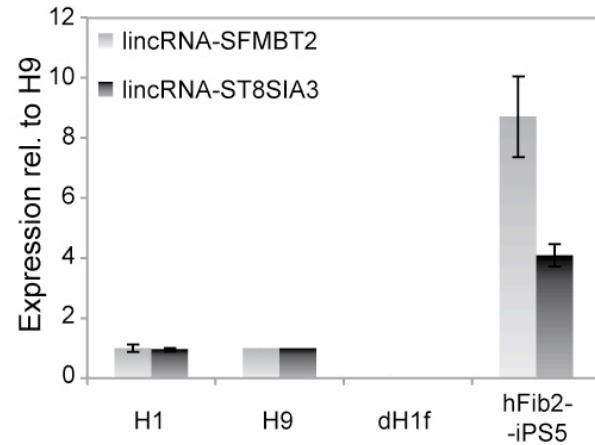


Supplementary Figure 7: Validation of siRNA mediated knock-down of OCT4 in hFib2-iPS5 cells and analysis of lincRNA expression upon differentiation of H9 cells. A) Western Blot showing reduction of OCT4 protein levels upon siRNA transfection. Lane 1: hFib2-iPS5 cells, no siRNA transfected; lane 2: hFib2-iPS5 cells, transfected with GAPDH control siRNA; lane 3: hFib2-iPS5 cells, transfected with OCT4 siRNA; lane 4: MRC5 fibroblasts as negative control. B) Cell morphology changes upon knock-down of OCT4 (right) compared to a control siRNA transfected sample (left). C) Changes in iPSC-enriched lincRNA levels upon siRNA-mediated knock-down of OCT4 in H9 ESCs. Left: qRT-PCR of *OCT4* and *NANOG* transcript levels upon depletion of OCT4. Right: qRT-PCR of iPSC-enriched lincRNA levels upon depletion of OCT4. Transcript levels are displayed relative to non-targeting control siRNAs (ctrl siRNA) (n=3, error bars +/-s.e.m). C) iPSC-enriched lincRNA expression during EB differentiation of H9 ESCs. Left: qRT-PCR analysis monitoring transcript levels of pluripotency markers (*OCT4* and *NANOG*) and the differentiation marker *LMNA* over a ten day differentiation time-course; right: qRT-PCR analysis of iPSC-enriched lincRNAs. RNA levels are depicted relative to undifferentiated cells (n=2, error bars +/-s.e.m).

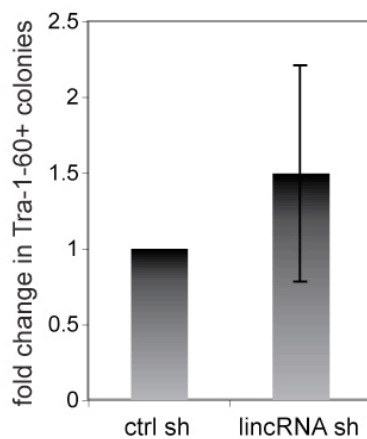
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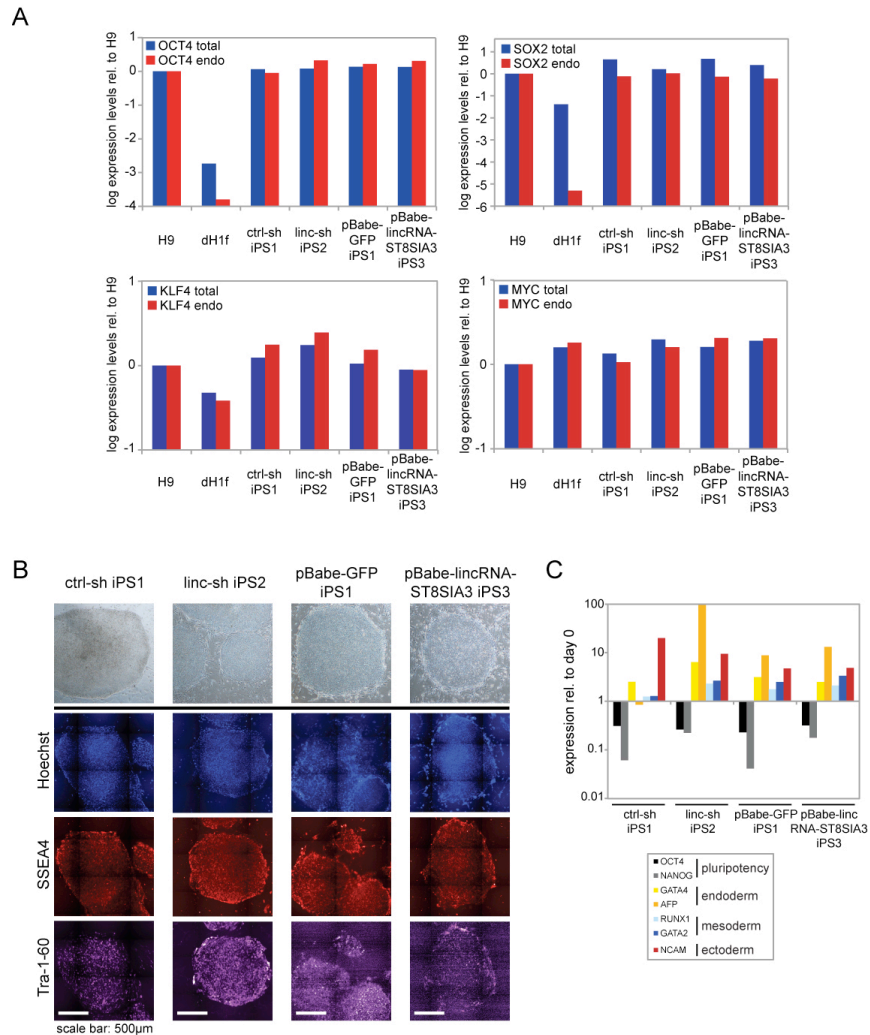
B



C

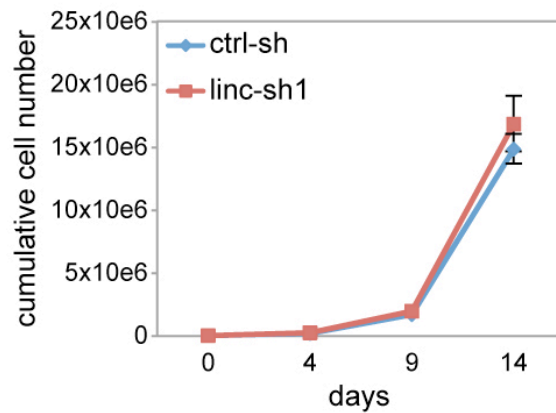


Supplementary Figure 8: Effect of lincRNA knock-down on reprogramming. A) qRT-PCR to document the efficiency of lincRNA-SFMBT2 knock-down following infection with shRNA-expressing lentivirus relative to a non-targeting control (n=4, error bar +/- s.e.m). B) qRT-PCR shows that lincRNA-SFMBT2 and lincRNA-ST8SIA3 are not expressed in dh1f fibroblasts prior to reprogramming (n=2, error bar +/- s.e.m.). Expression values are depicted relative to the levels in H9 cells. C) Quantification of iPSC colonies derived from dh1f cells upon knock-down of lincRNA-SFMBT2 relative to a non-targeting control (n=2, error bar +/- stdv).

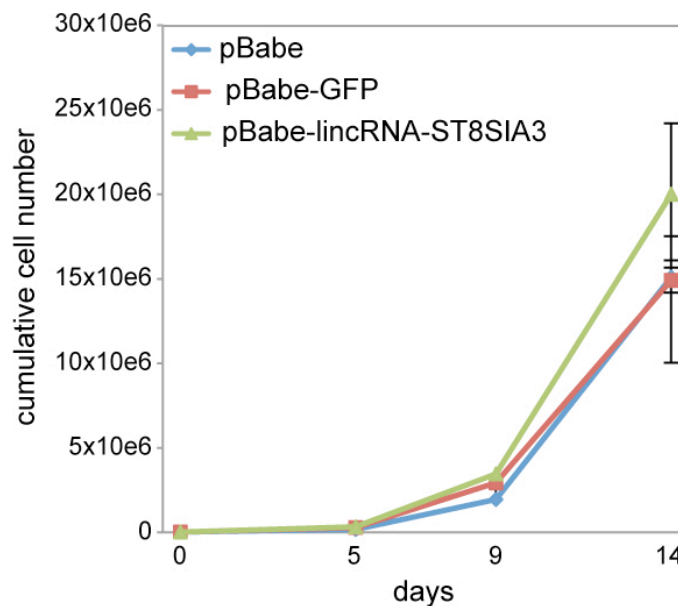


Supplementary Figure 9: Characterization of iPSCs derived from lincRNA-ST8SIA3 knock-down and overexpression reprogramming experiments. A) qRT-PCR to document the expression of reprogramming factor mRNAs; blue: total (transgenic and endogenous) levels of *OCT4*, *SOX2*, *KLF4*, and *MYC* mRNAs, red: endogenous levels of *OCT4*, *SOX2*, *KLF4*, and *MYC* mRNAs in H9 ESCs, dH1f fibroblasts, and fibroblast-derived iPSC lines derived from the non-targeting control-sh knock-down (ctrl-sh iPS1), the lincRNA-ST8SIA3 targeting knock-down (linc-sh iPS2), the control experiment with the GFP-expressing pBabe vector (pBabe-GFP iPS1), and the lincRNA-ST8SIA3 overexpression experiment (pBabe-lincRNA-ST8SIA3 iPS3). Expression levels are depicted relative to the levels in H9 ESCs (log scale). B) Top: Bright field images of iPSC colonies. Bottom: live-cell imaging of the same fibroblast-derived iPSC lines to document activation of the SSEA4 and Tra-1-60 cell surface markers. Hoechst 33342 was used as a DNA counter-stain. C) qRT-PCR to document downregulation of *OCT4* and *NANOG* mRNAs, as well as upregulation of differentiation markers *GATA4* and *AFP* (endoderm), *RUNX1* and *GATA2* (mesoderm), and *NCAM* (ectoderm) in day 6 EBs derived from ctrl-sh iPS1, linc-sh iPS2, pBabe-GFP iPS1, and pBabe-lincRNA-ST8SIA3 iPS3 cells. Expression values are represented relative to undifferentiated controls.

A

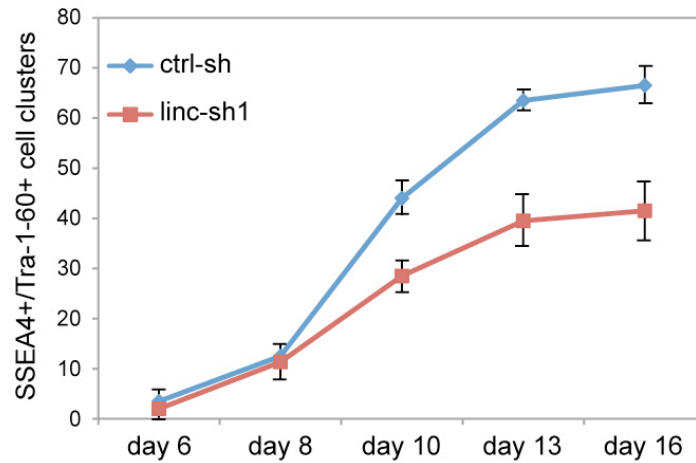


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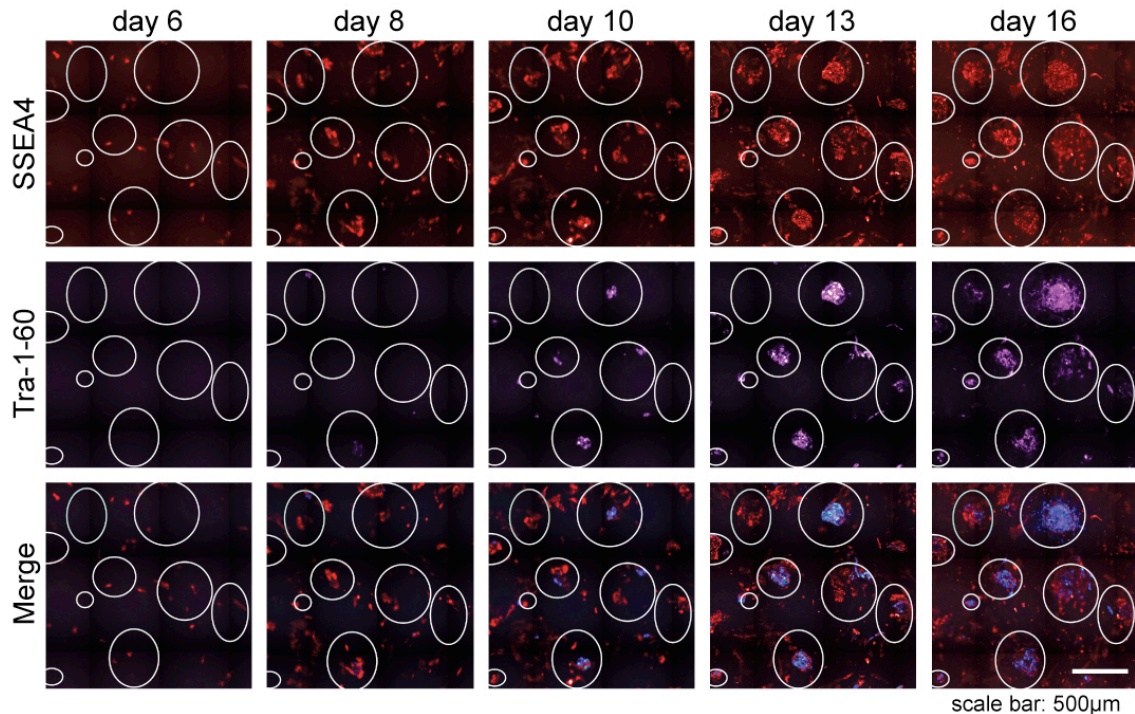


Supplementary Figure 10: Knock-down or overexpression of lincRNA-ST8SIA3 in dH1f fibroblasts does not affect cell growth. A) Cumulative cell numbers measured over a 14 day time-course after infection of dH1f with a non-targeting control-shRNA expressing virus (ctrl-sh) and a lincRNA-ST8SIA3 targeting virus (linc-sh1). No statistically significant difference in cell growth could be observed ($n=4$, error bars \pm s.e.m.; $P=0.92$). B) Cumulative cell numbers measured over a 14 day time-course after infection of dH1f with empty pBabe virus, pBabe-GFP, or lincRNA-ST8SIA3 overexpression virus (pBabe-lincRNA-ST8SIA3). No statistically significant difference in cell growth could be observed ($n=2$, error bars \pm s.e.m.; $P=0.79$ (compared with pBabe) and 0.81 (compared with pBabe-GFP)). Statistics were performed using Student's t-test.

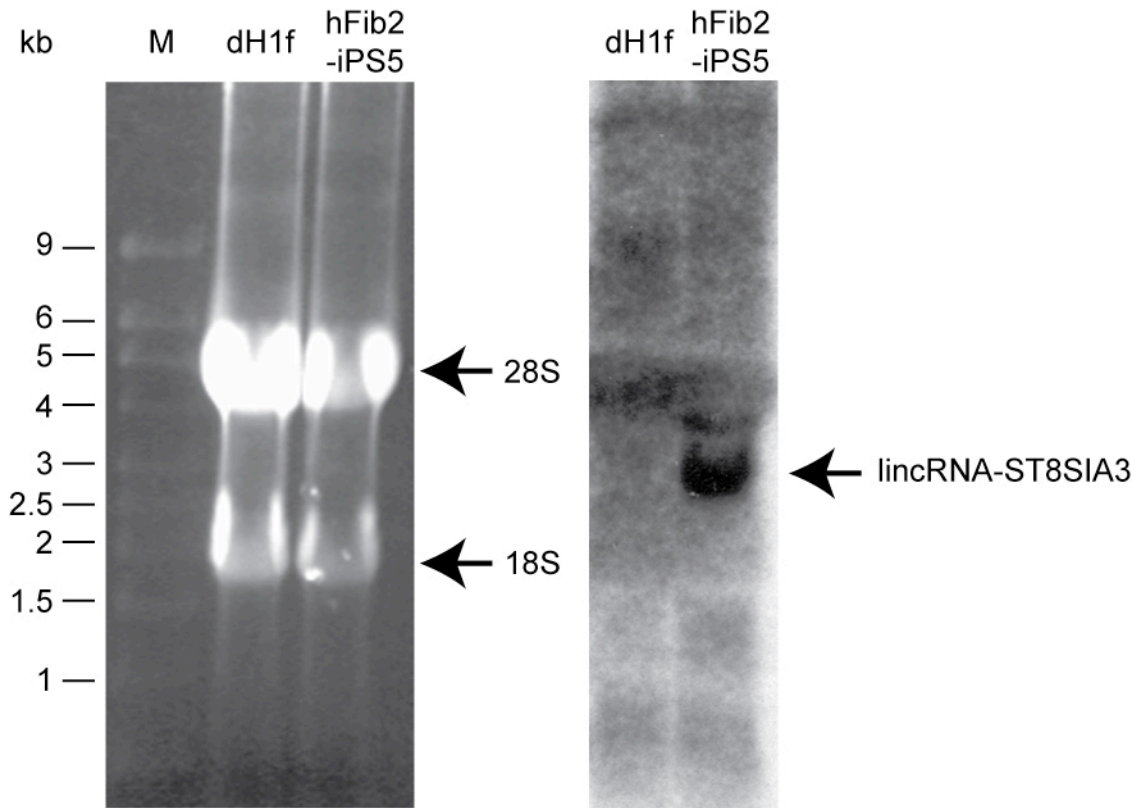
A



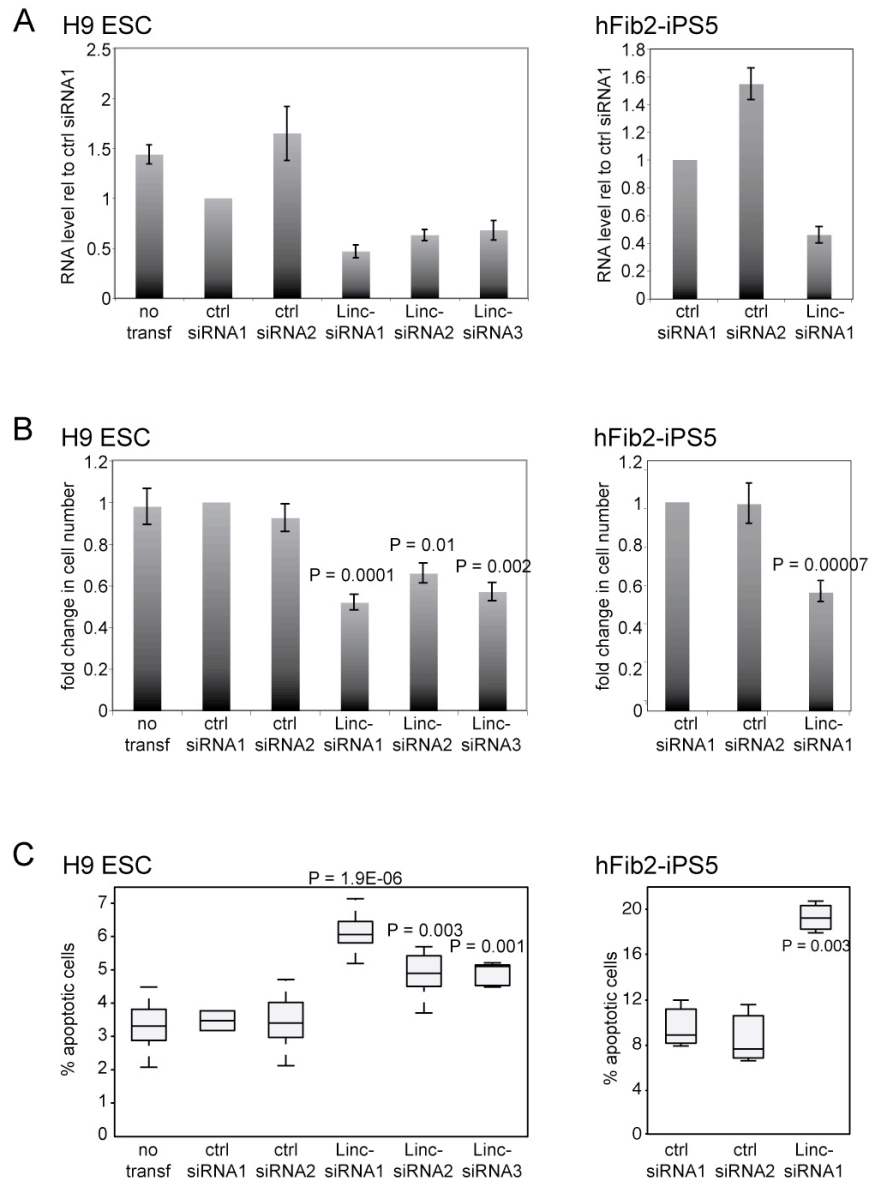
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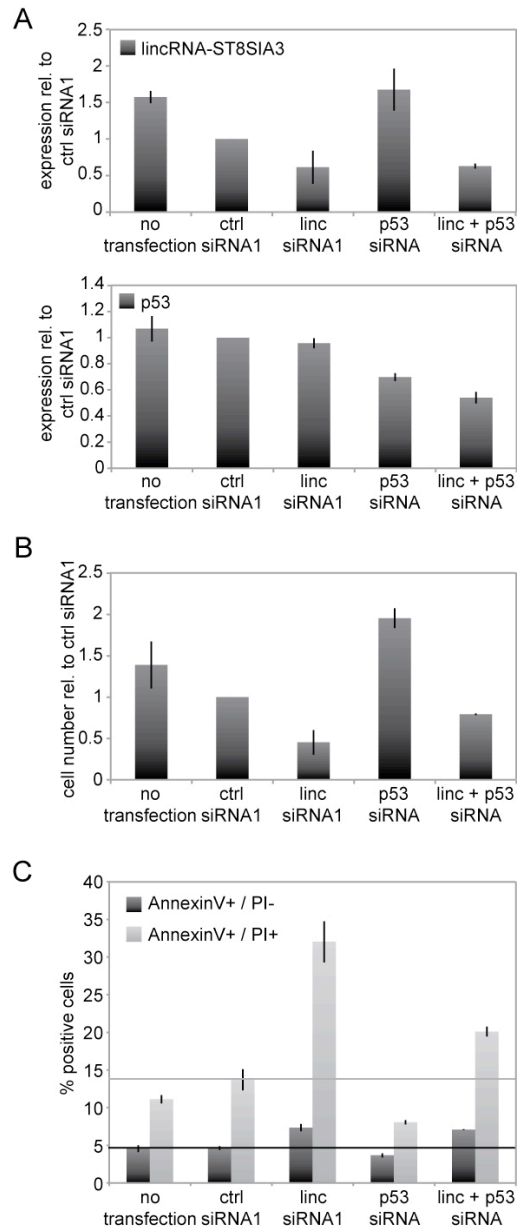
Supplementary Figure 11: Live-cell imaging to follow the kinetics of reprogramming. A) Quantification of SSEA4+/Tra-1-60+ cell clusters from day 6 to day 16 of reprogramming in the control (ctrl-sh) and lincRNA-ST8SIA3 knock-down (linc-sh1) sample. Four regions per 6well (each region with an area of 53.21mm²) were quantified for each control and linc-sh1, and average numbers of cell clusters per area are plotted on the y-axis. Error bars represent +/- stdv. B) Representative subregion of SSEA4 (red) and Tra1-60 (purple) stained reprogramming cells. White circles mark SSEA4+/Tra-1-60+ cell clusters identified on day 16.



Supplementary Figure 12: Northern Blot of lincRNA-ST8SIA3 in dH1f and hFib2-iPS5 cells detects a 2.6kb band. Left: ethidium bromide stained agarose gel to show 28S and 18S ribosomal RNA loading controls, as well as the position of RNA marker bands. Right: Blot of lincRNA-ST8SIA3 using a specific probe (see Supplementary Methods) confirms its 2.6kb length.



Supplementary Figure 13: siRNA-mediated knock-down of lincRNA-ST8SIA3 affects ESC and iPSC growth. A) qRT-PCR validation of three lincRNA-ST8SIA3-targeting siRNAs (Linc-siRNA1, -siRNA2, -siRNA3) compared with two non-targeting controls (ctrl siRNA1 and ctrl siRNA2) as well as non-transfected cells in H9 ESCs (left) and hFib2-iPS5 cells (right). RNA levels are depicted relative to the levels in cells transfected with ctrl siRNA1 ($n \geq 3$, error bar \pm s.e.m.). B) Cell growth of H9 ESCs (left) and hFib2-iPS5 cells (right) upon knock-down of lincRNA-ST8SIA3 compared to non-targeting controls as measured by total cell numbers 72h post-transfection. Cell numbers are depicted relative to the control (ctrl siRNA1). C) Percentage of early apoptotic cells (AnnexinV⁺/Propidium iodide⁻) measured by flow cytometry in non-transfected cells, cells transfected with non-targeting control siRNAs, and lincRNA-ST8SIA3-targeting siRNAs in H9 ESCs (left) and hFib2-iPS5 cells (right). Boxes represent the 25th to 75th percentiles of the data, the central line marks median values. Whiskers extend to the most extreme data points. Statistical analysis was performed using Student's t-test.



Supplementary Figure 14: siRNA-mediated knock-down of p53 partially rescues growth deficiency and elevated cell death of H9 cells caused by lincRNA-ST8SIA3 knock-down. A) qRT-PCR documents the efficiency of lincRNA-ST8SIA3 (top) and p53 (bottom) knock-down 72h after siRNA transfection. Expression values are depicted relative to the non-targeting control (ctrl siRNA 1); n=2, error bars +/-s.e.m. B) Relative cell numbers 72h post-transfection in non-transfected cells, or cells transfected with lincRNA-ST8SIA3 targeting siRNA (linc siRNA 1), p53-targeting siRNA (p53 siRNA), or both compared with control-transfected cells (ctrl siRNA 1); n=2, error bars +/-s.e.m. C) Flow cytometric analysis of early apoptotic (AnnexinV+/PI-) and late apoptotic/necrotic (AnnexinV+/PI+) cells 72h following knock-down of lincRNA-ST8SIA3, p53, or both, compared with the non-targeting control and untransfected cells; n=2, error bars +/-s.e.m.

References

1. Subramanian, A. et al. Gene set enrichment analysis: a knowledge-based approach for interpreting genome-wide expression profiles. *Proc Natl Acad Sci U S A* **102**, 15545-50 (2005).
2. Assou, S. et al. A meta-analysis of human embryonic stem cells transcriptome integrated into a web-based expression atlas. *Stem Cells* **25**, 961-73 (2007).
3. Lowry, W.E. et al. Generation of human induced pluripotent stem cells from dermal fibroblasts. *Proc Natl Acad Sci U S A* **105**, 2883-8 (2008).

Supplementary Table 1: Differentially expressed lincRNAs

A) ES-fibroIPS-fibro_comparison

lincRNAs upregulated in ES and fibro-iPS lincRNAs upregulated in fibroblasts

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chr7:22570350-22689975	chr3:157938400-157953775
chr7:25945000-25956500	chr3:157960475-158021825
chr7:108969225-109059825	chr3:158438000-158454000
chr7:124660350-124687075	chr3:196904200-196928625
chr7:125351475-125521800	chr7:22860450-22876975
chr7:129188850-129205475	chr7:30552675-30585400
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chr18:31720150-31782325	chr7:78921550-78942375
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B) ES-CD34iPS-CD34_comparison

lincRNAs upregulated in ES and CD34-iPS lincRNAs upregulated in CD34+ cells

chr3:13068175-13122525	chr3:157960475-158021825
chr3:88233150-88258600	chr3:172974575-173014100
chr3:157960475-158021825	chr3:195671625-195688075
chr3:188363175-188375850	chr7:30552675-30585400
chr7:22570350-22689975	chr7:126777625-126793150
chr7:105333950-105351950	chr18:72307325-72331925
chr7:124660350-124687075	chr2:74047225-74063900
chr18:31270875-31282100	chr2:111676650-111726950
chr18:31720150-31782325	chr20:30614850-30628550
chr18:52872300-52882675	chr20:36470500-36515575
chr2:47401150-47414050	chr17:7716675-7728025
chr2:64323075-64376900	chr17:21373950-21390575
chr2:77174650-77185275	chr14:80937850-80948425
chr2:85039975-85050950	chr14:80950175-80970975
chr2:152335500-152361525	chr6:6628525-6646600
chr2:179511550-179537625	chr6:29809950-29822800
chr2:216182125-216421975	chr6:167309700-167331675
chr2:216373475-216392050	chr1:23477400-23492375
chr20:56824850-56837175	chr1:39776600-39792825
chr17:39456275-39467525	chr1:206037850-206063200
chr17:67895375-68098675	chr1:206037900-206108750
chr14:47751025-47794125	chr21:2585665-25874075
chr14:70858200-70993750	chr21:2668020-26712875
chr14:99267075-99297500	chr21:2785925-27869625
chr1:9129450-9164075	chr21:2892745-28941150
chr1:65291650-65304400	chr21:2901957-29035625
chr1:172235150-172257650	chr21:2947217-29486175
chr1:173389275-173428400	chr21:2948882-29522825
chr1:203671525-203684250	chr21:2968805-29711875
chr1:203936725-203948900	chr21:2971672-29731300
chr1:212579525-212590200	chr21:2974940-29813925
chr1:245184075-245194450	chr21:3537187-35411225
chr6:14814750-14856150	chr10:120025775-120037250
chr6:30364275-30401550	chr5:43102225-43120425
chr6:40412925-40431825	chr5:77321525-77331525
chr6:44149375-44170550	chr16:3113750-3124850
chr6:48152775-48178175	chr13:49505400-49519275
chr6:86438525-86452775	chr13:49555700-49595650
chr6:94572500-94596150	chr11:72124275-72140250
chr6:114829475-114849375	chr4:53272125-53310900
chr6:139002750-139061900	chr19:32954225-32988950
chr21:39892800-39905250	chr19:41757025-41772825
chr10:6819700-6929500	chr8:125541150-125555450
chr10:29739925-29758500	chr8:129111400-129188100
chr10:46514400-46569425	chr12:131170325-131183625
chr10:64906075-64942725	chrX:62560050-62574175
chr10:79193175-79209400	chrX:112927350-113120025

chr10:118576375-118598450
chr10:119231725-119242550
chr5:12679825-12772900
chr5:25421700-25481600
chr5:74363725-74384025
chr5:173065450-173083600
chr16:53502500-53517100
chr13:39913400-39927450
chr13:42303950-42340125
chr13:47348925-47379300
chr13:53572000-53599550
chr13:53710800-53826900
chr13:55006675-55050350
chr13:90799275-90818300
chr22:29695900-29706450
chr9:2197775-2288675
chr9:2746150-2763400
chr9:21481050-21587675
chr9:23587325-23674450
chr9:36392125-36402600
chr11:27179825-27196825
chr11:70203250-70246225
chr11:70284600-70344900
chr11:70569675-70613500
chr11:86297350-86316725
chr11:121514300-121572575
chr11:127925850-127944925
chr11:130235450-130250500
chr15:22809575-22841625
chr15:22809575-22919700
chr15:49996975-50010800
chr15:79937400-79947500
chr4:235050-250725
chr4:15266300-15304725
chr4:15848275-15885050
chr4:21970900-21980925
chr4:53272125-53310900
chr4:93394800-93411650
chr19:52838475-52873175
chr8:37377750-37470000
chr8:90795725-90810750
chr8:115369100-115387225
chr8:133140825-133161650
chr8:135860125-135912450
chr8:138457025-138490825
chr12:45330500-45384750
chr12:64277400-64357675
chr12:74301700-74547775
chr12:78463525-78491000

chrX:45482950-45595350
chrX:57018625-57030000
chrX:73336425-73429775
chrX:93707725-93920325
chrX:102886975-102898350
chrX:112927350-113120025
chrX:114965050-114983975
chrX:130653175-130673725
chrX:130702275-130791225



C) ES-fibroIPS_comparison

lincRNAs upregulated in fibro-iPS	lincRNAs upregulated in ES
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chr7:22570350-22689975	chr3:37389200-37409700
chr7:124660350-124687075	chr3:196904200-196928625
chr7:130178825-130451400	chr18:46799075-46810100
chr7:130380300-130441050	chr2:134596475-134694600
chr18:52872300-52882675	chr2:177854175-177922425
chr2:179511550-179537625	chr1:113301525-113321425
chr17:39456275-39467525	chr1:154326000-154341900
chr14:100364750-100405275	chr1:191490425-191504575
chr14:100459225-100603275	chr6:21775750-21969750
chr6:48152775-48178175	chr6:21775750-22268800
chr6:94572500-94596150	chr6:21991500-22268800
chr6:95307575-95320325	chr6:22082150-22268675
chr1:39776600-39792825	chr6:22216575-22268800
chr1:79669875-79726875	chr6:80305150-80328275
chr1:85705400-85746650	chr6:114868875-114889350
chr10:6819700-6929500	chr6:155200400-155227200
chr13:42303950-42340125	chr21:2585665-25874075
chr13:53710800-53826900	chr21:2668020-26712875
chr22:23738700-23794025	chr21:2785925-27869625
chr9:2197775-2288675	chr21:2892745-28941150
chr9:117628000-117640825	chr21:2901957-29035625
chr15:22809575-22919700	chr21:2947217-29486175
chr4:53272125-53310900	chr21:2948882-29522825
chr4:93394800-93411650	chr21:2968805-29711875
chr12:64277400-64357675	chr21:2971672-29731300
chrX:45482950-45595350	chr21:2974940-29813925
chrX:112927350-113120025	chr21:3537187-35411225
chrX:115315750-115327875	chr5:87601475-87624775
	chr5:94014600-94029225
	chr5:102119525-102221625
	chr5:115659375-115672450
	chr5:127413650-127433475
	chr5:147366150-147380650
	chr16:25178750-25189800
	chr13:44814075-44848225
	chr13:53710800-53826900
	chr22:16799450-16847225
	chr22:23738700-23794025
	chr11:27179825-27196825
	chr11:64946775-64971250
	chr11:86297350-86316725
	chr15:22809575-22841625
	chr15:22809575-22919700
	chr15:48435425-48449025
	chr15:49996975-50010800
	chr15:86833575-86843600
	chr4:15848275-15885050

chr19:52805475-52829200
chr8:6541450-6552025
chr8:28599675-28613975
chr8:52950675-52973175
chr8:102256850-102268925
chr8:124541550-124568875
chr8:128891450-128984025
chr12:64452900-64492900
chr12:131170325-131183625
chrX:73081400-73149600
chrX:93707725-93920325
chrX:112927350-112984650
chrX:112927350-113120025

D) ES-CD34iPS_comparison

lincRNAs upregulated in CD34-iPS

chr3:88191225-88208250
chr3:172974575-173014100
chr3:188363175-188375850
chr7:22570350-22689975
chr7:30552675-30585400
chr7:64088850-64099775
chr7:124660350-124687075
chr18:35328475-35629325
chr18:35592575-35629325
chr18:52872300-52882675
chr2:47401150-47414050
chr2:217089600-217121725
chr14:99267075-99297500
chr17:21373950-21390575
chr17:39456275-39467525
chr6:94572500-94596150
chr1:79669875-79726875
chr1:173389275-173428400
chr21:2585665-25874075
chr21:2668020-26712875
chr21:2785925-27869625
chr21:2892745-28941150
chr21:2901957-29035625
chr21:2947217-29486175
chr21:2948882-29522825
chr21:2968805-29711875
chr21:2971672-29731300
chr21:2974940-29813925
chr21:3537187-35411225
chr10:6819700-6929500
chr10:46514400-46569425
chr10:79193175-79209400
chr10:119231725-119242550
chr16:53502500-53517100
chr13:51388950-51400950
chr13:53572000-53599550
chr13:53710800-53826900
chr22:29695900-29706450
chr11:70284600-70344900
chr11:70569675-70613500
chr11:86297350-86316725
chr9:2197775-2288675
chr9:21481050-21587675
chr19:41757025-41772825
chr8:37377750-37470000
chr8:135860125-135912450
chr8:138457025-138490825

lincRNAs upregulated in ES

chr3:88233150-88258600
chr3:157960475-158021825
chr7:30552675-30585400
chr7:86800800-86810825
chr7:104403400-104440275
chr7:105333950-105351950
chr7:126777625-126793150
chr7:129188850-129205475
chr7:130178825-130451400
chr18:70409300-70433425
chr18:72307325-72331925
chr2:7918700-7954175
chr2:70121450-70165275
chr2:77174650-77185275
chr2:85039975-85050950
chr2:111676650-111726950
chr2:138962200-138974800
chr2:152335500-152361525
chr2:177854175-177922425
chr2:224209950-224295925
chr20:36470500-36515575
chr20:56824850-56837175
chr14:20977125-20993325
chr14:47751025-47794125
chr14:57814000-57830600
chr14:100425525-100457175
chr6:3944675-3963450
chr6:30364275-30401550
chr6:44149375-44170550
chr6:74040350-74054750
chr6:114829475-114849375
chr6:139002750-139061900
chr6:167309700-167331675
chr1:41728875-41743675
chr1:203936725-203948900
chr1:206037850-206063200
chr1:206037900-206108750
chr1:212579525-212590200
chr21:3537187-35411225
chr21:39892800-39905250
chr10:6663500-6677950
chr10:64906075-64942725
chr10:118576375-118598450
chr5:12679825-12772900
chr5:25421700-25481600
chr5:43102225-43120425
chr16:3113750-3124850

chrX:45482950-45595350
chrX:57018625-57030000
chrX:93707725-93920325
chrX:102886975-102898350
chrX:114919750-114943350

chr16:72904500-72918375
chr13:39913400-39927450
chr13:47348925-47379300
chr22:16799450-16847225
chr22:30445350-30475775
chr15:22809575-22841625
chr15:22809575-22919700
chr15:49996975-50010800
chr15:79937400-79947500
chr11:70284600-70344900
chr11:70569675-70613500
chr11:121514300-121572575
chr9:23587325-23674450
chr4:15266300-15304725
chr4:53272125-53310900
chr4:76853725-76868150
chr4:103556475-103569975
chr4:120611850-120623600
chr19:52838475-52873175
chr8:6541450-6552025
chr8:90684400-90697825
chr8:135860125-135912450
chr12:64277400-64357675
chrX:62560050-62574175
chrX:73336425-73429775
chrX:112927350-113120025
chrX:115315750-115327875
chrX:130702275-130791225

E) iPSC-enriched lincRNAs that overlap between fibro-iPS and CD34-iPS

chr10:6819700-6929500

chr7:22570350-22689975

chr7:124660350-124687075

chr18:52872300-52882675

chr13:53710800-53826900

chr9:2197775-2288675

chr17:39456275-39467525

chr1:79669875-79726875

chr6:94572500-94596150

chrX:45482950-45595350

Supplementary Table 2: Reprogramming experiments - iPSC colony counts

LincRNA-ST8SIA3 knock-down

	Experiment 1	Experiment 2	Experiment 3	Experiment 4
ctrl-sh	27	28	14	168
linc-sh1	3	7	0	29
linc-sh2	11	19	3	116

LincRNA-ST8SIA3 overexpression

	Experiment 1	Experiment 2	Experiment 3	Experiment 4	Experiment 5
pBabe	98	85	168	26	14
pBabe-GFP	61	55	123	26	15
pBabe-L18	219	202	190	83	40

Supplementary Table 3

Genes deregulated upon lincRNA-ST8SIA3 knock-down

A) Differentially expressed genes

Genes up in knock-down	Genes down in knock-down
AACSL	ATP10D
ABCA1	C13orf18
ABCB7	chd7
Abi1	Chst9
Acox2	CUZD1
Acpl2	Dsel
Actg2	EXPH5
actn3	FAM126A
AIG1	FAR2
akap2	FRZB
akap8l	Gli3
Akna	gtf2a1l
ALG13	gxylt2
alkbh6	IFIH1
ALS2	LOC100128626
ANAPC13	Lpl
ANAPC16	MET
ANTXR1	MGAT4A
ARHGAP27	MYRIP
armc8	Npy1r
arrdc3	PANX1
asap1	PECI
Atp1a2	PLOD2
Atpaf1	PPP1R2P4
b4galt2	RAP2A
bbs7	Serpinb3
BEX2	serpinb4
BLOC1S3	Sfrp1
bmp7	snx7
C12orf60	SOX11
C13orf1	SPIRE1
c14orf1	STAU2
C14orf118	stc1
C17orf56	STON1
C17orf68	STON1-GTF2A1L
C19orf12	TIFA
C1orf226	TMEM106C
C2orf56	Tmem178
C2orf56	UBE2J1
C2orf74	UGT3A1
C2orf88	UGT8
c3orf64	ZNF664
C4orf38	

C5orf28
C5orf41
C6orf35
C7orf57
c8orf40
cabcl
CACNA2D2
CALD1
CAMK2D
CARS2
CASP8
CBFA2T2
cbr4
CBWD2
cbx4
CCDC50
CDH11
CECR1
Cel
CH25H
CLDN20
CNN1
CNOT6
Col16a1
COL1A2
cpt2
CREB5
cxorf38
CYP1B1
CYP3A5
DAAM1
DBT
dcaf7
DDX25
DDX3Y
DKFZP586B0319
Dnajc16
Dnajc21
dnal1
Dnase1l1
DNMT3A
Dock5
DPEP3
EEF1A1
EEF1A1P24
EEF1A1P5
EEF1A1P9
EFNA5
Eif5a2

ELAVL1
eml4
Enpp1
Enpp5
EPHA7
EPPK1
ERRFI1
Esyt2
ESYT3
ETV5
EXOC3L
EXOC6B
FAM110B
Fam116a
FAM200B
fam20a
Fam71f1
fam73a
FASTKD2
Fbxl20
fbxo27
fdxr
FLJ25613
flvcr1
FNBP4
Fntb
FSD1L
Galnt6
Gatad2b
GLS
gltP
GLTPP1
Gnpnat1
Golim4
GPCPD1
Gpld1
Gpr143
GREM1
gstk1
Hdac8
HECW1
herc4
Hist1h2ab
Hist1h2ad
Hist1h2ae
HIST1H2BK
HIST1H3A
HIST1H3B
HIST1H3C

HIST1H3D
HIST1H3E
HIST1H3F
hist1h3g
HIST1H3H
Hist1h3i
HIST1H3J
HIST2H3A
hist2h3c
HIST2H3D
hnrpII
HS6ST2
HSD17B12
hsd17b14
Hsp90b1
ID2
ids
Insm1
IPO7
Ipw
irak1bp1
isyna1
itga6
Jph4
Jun
KCNK12
KCTD1
KIAA0232
KIAA1217
KIF5C
Klf4
klf6
KLHDC5
LGALS1
LMCD1
Imna
Lnx1
LOC100129240
LOC100132111
LOC100133398
LOC100133772
LOC100271832
LOC151878
LOC283174
LOC285401
LOC286467
LOC401317
LOC440434
LOC642031

LOC642587
LOC645100
LOC647859
LOC729143
Lrrn4
Lyplal1
MAGI2
MALAT1
MAPK1
Mbn1
MCART1
mcl1
Med13l
MED17
MEGF6
MFF
MGC16121
MGC9913
MID1
MIDN
Mir21
MPHOSPH9
Mrip
mrps11
Mtmr9
mxra7
Myo10
MYO1E
myoz2
NAP1L1
NAV2
NCRNA00081
Ncrna00086
NCRNA00087
NCRNA00230B
nfatc1
NFYB
ngly1
NLN
NOX1
npepps
NPY
nr2c1
Nup214
Ocln
Osbp16
OSBPL7
OSGIN2
P2RY14

PABPC1L
PALM2
PALM2-AKAP2
PAPPA
PAPPAS
Pcdh19
PCLO
pcm1
Pde4b
PDE4D
PIAS2
PICALM
PIP5K1A
pitpna
PKMYT1
PLBD2
POLR3C
POMP
POU2F3
PPM1A
PRODH
Prr24
pten
PTENP1
Ptpn23
rab21
RABGGTB
Ran
Ranbp2
Rasgrp2
Rbm46
REV3L
RFK
Rhebl1
RNY1
RNY3
RNY4
RNY4P19
RNY4P7
RNY5P10
RPL37A
Rps6kl1
Scai
SCFD2
SCG5
Scyl3
SEC22B
Sec61a2
selt

Sema4a
SEMA6A
sf3b1
sfrs18
SGK223
SGSM3
Sh3kbp1
SLC11A2
SLC16A5
SLC16A9
SLC19A2
slc25a16
SLC2A3
SLC2A4RG
SLC35A3
SLC38A7
SLMAP
SMAD3
smek2
SMYD2
SNORD113-1
SNORD113-2
SNORD113-3
SNORD113-4
SNORD113-5
SNORD113-6
SNORD113-7
SNORD113-8
SNORD113-9
SNORD114-1
SNORD114-10
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SNORD114-20
SNORD114-21
SNORD114-22
SNORD114-23
SNORD114-24
SNORD114-25
SNORD114-26
SNORD114-27

SNORD114-28
SNORD114-29
SNORD114-3
SNORD114-30
SNORD114-31
SNORD114-4
SNORD114-5
SNORD114-6
SNORD114-7
SNORD114-8
SNORD114-9
SNRPN
sntb2
SNURF
Snx30
Socs4
SORBS1
SPOPL
spred1
SPTBN1
sqstm1
SRI
ssu72
ST6GAL2
STK11
STX17
SULT1A3
SULT1A4
Syt11
SYTL2
TCEA1
TCEA1P2
Tceal7
Tcf7l2
TCIRG1
TCTN3
Tecpr1
TFAP2C
tgfbr1
Tmem43
TNC
TNFAIP8
TNFAIP8
TNRC18B
TNS1
Tpcn2
trim2
TRIO
TTC28

ube2b
UBR1
UBR3
Uevld
USP22
USP4
usp53
Utf1
VGF
vil1
vps37b
Vps41
Wdhd1
WDR35
Wif1
ZBTB10
ZFP36
znf277
ZNF658
ZNF682
ZNF83



B) Gene Set Enrichment Analysis

Gene Sets enriched in lincRNA-ST8SIA3 knock-down

<i>NAME</i>	<i>SIZE</i>	<i>ES</i>	<i>NES</i>	<i>NOM p-val</i>	<i>FDR q-val</i>	<i>FWER p-val</i>	<i>RANK AT MAX LEADING EDGE</i>
KANNAN_P53_UP	36	0.6855854	2.2099452	0	0	0	3587 tags=50%, list=18%, signal=61%
OXSTRESS_BREASTCA_UP	28	0.68489933	2.0290132	0	0.02775887	0.05	2147 tags=43%, list=11%, signal=48%
HDACI_COLON_TSA2HRS_UP	60	0.53059876	1.9356368	0	0.04733173	0.17	5199 tags=47%, list=26%, signal=63%
HDACI_COLON_SUL12HRS_UP	26	0.6856895	1.9478719	0	0.05199197	0.14	2453 tags=27%, list=12%, signal=31%
CORDERO_KRAS_KD_VS_CONTROL_UP	75	0.5086824	1.908135	0	0.06252702	0.26	4048 tags=45%, list=20%, signal=57%
UVB_NHEK3_C3	17	0.6352384	1.8264904	0	0.11714856	0.58	2078 tags=24%, list=10%, signal=26%
HDACI_COLON_SUL16HRS_UP	42	0.554931	1.842247	0	0.11921456	0.47	1637 tags=14%, list=8%, signal=16%
HDACI_COLON_CURSUL_UP	42	0.5412102	1.831326	0	0.11951414	0.56	2453 tags=21%, list=12%, signal=24%
CROONQUIST_IL6_STROMA_UP	39	0.5643391	1.7390693	0	0.17592216	0.9	1433 tags=26%, list=7%, signal=28%
HSA00051_FRUCTOSE_AND_MANNANOSE_METABOLISM	42	0.51609683	1.7583388	0	0.17687044	0.87	6230 tags=48%, list=31%, signal=69%
GAMMA_ESR_WS_UNREG	29	0.5693539	1.7417186	0	0.1829188	0.9	2533 tags=28%, list=13%, signal=32%
HDACI_COLON_CUR12HRS_UP	21	0.61049736	1.7476523	0.01724138	0.18395676	0.89	2453 tags=24%, list=12%, signal=27%
HDACI_COLON_BUT24HRS_UP	70	0.50772095	1.7792326	0	0.1861808	0.75	5004 tags=46%, list=25%, signal=61%
4NQO_ESR_WS_UNREG	36	0.5860095	1.770935	0.01694915	0.19109344	0.83	2393 tags=28%, list=12%, signal=31%
MTA3PATHWAY	15	0.6518004	1.7129923	0	0.19236505	0.96	1983 tags=27%, list=10%, signal=30%
HSA04115_P53_SIGNALING_PATHWAY	68	0.48712826	1.7583611	0	0.19294956	0.87	4215 tags=35%, list=21%, signal=45%
MCALPAINPATHWAY	24	0.60301137	1.7241952	0	0.1969163	0.93	3299 tags=38%, list=16%, signal=45%
DEATHPATHWAY	33	0.5064673	1.7170511	0	0.1984698	0.96	4997 tags=48%, list=25%, signal=64%

Gene Sets enriched in control

<i>NAME</i>	<i>SIZE</i>	<i>ES</i>	<i>NES</i>	<i>NOM p-val</i>	<i>FDR q-val</i>	<i>FWER p-val</i>	<i>RANK AT MAX LEADING EDGE</i>
BRENTANI_IMMUNE_FUNCTION	52	-0.5442895	-2.103492	0	0	0	5744 tags=58%, list=29%, signal=81%
CITED1_KO_HET_UP	27	-0.5451648	-1.787516	0	0.11554463	0.68	1863 tags=33%, list=9%, signal=37%
HSA03050_PROTEASOME	22	-0.6002818	-1.775813	0	0.12125231	0.72	6971 tags=86%, list=35%, signal=132%
HSA04950_MATURITY_ONSET_DIABETES_OF_THE_YO	20	-0.5684359	-1.790119	0	0.12600382	0.67	4763 tags=60%, list=24%, signal=79%
GPCRS_CLASS_A_RHODOPSIN_LIKE	136	-0.4255976	-1.80731	0	0.1272712	0.6	2377 tags=27%, list=12%, signal=31%
GPCRDB_CLASS_A_RHODOPSIN_LIKE	175	-0.4301317	-1.817794	0	0.13727143	0.54	3702 tags=36%, list=18%, signal=44%
HUMAN_TISSUE_THYMUS	16	-0.6413668	-1.74808	0	0.1406226	0.82	3795 tags=63%, list=19%, signal=77%
GH_HYPOPHYSECTOMY_RAT_DN	15	-0.6169487	-1.737384	0	0.14207716	0.87	303 tags=13%, list=2%, signal=14%
ANDROGEN_AND_ESTROGEN_METABOLISM	23	-0.5665722	-1.753078	0.04	0.1472102	0.82	3028 tags=39%, list=15%, signal=46%
POMEROY_MD_TREATMENT_GOOD_VS_POOR_UP	29	-0.5653929	-1.821171	0	0.16306625	0.53	2324 tags=28%, list=12%, signal=31%
HSA04080_NEUROACTIVE_LIGAND_RECEPTOR_INTER	250	-0.4003365	-1.837287	0	0.17557299	0.45	3536 tags=32%, list=18%, signal=38%

Supplementary Table 4: Primer, cloning, northern probe, siRNA, shRNA sequences

A) Primer sequences

Name	sequence	purpose
lincRNA-VLDLR_FOR	AGCAGTCACATTCATCGCAC	qRT-PCR
lincRNA-VLDLR_REV	GAGGAATAGGTGCGAACTGC	qRT-PCR
lincRNA-SFMBT2_FOR	TCCCCTGAGAGAACATCGTC	qRT-PCR
lincRNA-SFMBT2_REV	AGCACGCTATTGGAGGAATG	qRT-PCR
lincRNA-ST8SIA3_FOR	CTCAGTGGGGAAGACTCCAG	qRT-PCR
lincRNA-ST8SIA3_REV	AGGAAGCCTGAGAGTTGGC	qRT-PCR, 3,'RACE
lincRNA-LSM12_FOR	GTTATCCAACAACAGCAGCCGCAT	qRT-PCR
lincRNA-LSM12_REV	TGGGAATGACATCAGTGAGCTGGA	qRT-PCR
lincRNA-LPHN2_FOR	AGGCAGGACCTGTGGGTAG	qRT-PCR
lincRNA-LPHN2_REV	AACTGCTTTACACACCTTGCC	qRT-PCR
lincRNA-mir297_FOR	ACAGGGCTATGGAGTCATGG	qRT-PCR
lincRNA-mir297_REV	ATGGAACCTCTGACATCAACG	qRT-PCR
lincRNA-GRM8_FOR	ACCACCTCTAGGCATTCTGGACAA	qRT-PCR
lincRNA-GRM8_REV	AAGGCAGCAGCTTCCAATCATGTG	qRT-PCR
lincRNA-MANEA_FOR	AACCTGAACTCCACATGGCATCA	qRT-PCR
lincRNA-MANEA_REV	AATGCACAGGACTCAGCACAGGA	qRT-PCR
lincRNA-ZNF673_FOR	TAGAGGCAGAGTGTAAAGCATGCCA	qRT-PCR
lincRNA-ZNF673_REV	TTTCAGCGGCTTTATGGTCTGTGC	qRT-PCR
lincRNA-IL6_FOR	AGGCATCTTGGCATGAACCAAACC	qRT-PCR
lincRNA-IL6_REV	TATGCTAGGATTGAGGCAGCACCT	qRT-PCR
b-ACTIN_FOR	GGCACCCAGCACAAATGAAGATCAA	qRT-PCR
b-ACTIN_REV	TAGAAGCATTTGCGGTGGACGATG	qRT-PCR
GAPDH_FOR	CATGTTTCGTCATGGGTGTGAACCA	qRT-PCR
GAPDH_REV	AGTGATGGCATGGACTGTGGTCAT	qRT-PCR
OCT4_FOR	TATGCAAAGCAGAAACCCCTCGTGC	qRT-PCR
OCT4_REV	TTCCGGGCACTGCAGGAACAAATTC	qRT-PCR
NANOG_FOR	TCCAGCAGATGCAAGAACTCTCCA	qRT-PCR
NANOG_REV	CACACCATTGCTATTCTTCGGCCA	qRT-PCR
LAMIN-A/C_FOR	TGAGAACAGGCTGCAGACCATGAA	qRT-PCR
LAMIN-A/C_REV	CAAACCTCACGCTGCTTCCCATTGT	qRT-PCR
RUNX1_FOR	CCCTAGGGGATGTTCCAGAT	qRT-PCR
RUNX1_REV	TGAAGCTTTTCCCTCTTCCA	qRT-PCR
AFP_FOR	AGCTTGGTGGTGGATGAAAC	qRT-PCR
AFP_REV	CCCTCTCAGCAAAGCAGAC	qRT-PCR
GATA4_FOR	CTAGACCGTGGGTTTTGCAT	qRT-PCR
GATA4_REV	TGGGTTAAGTGCCCTGTAG	qRT-PCR
NCAM_FOR	ATGGAAACTCTATTAAGTGAACCTG	qRT-PCR
NCAM_REV	TAGACCTCATACTCAGCATTCCAGT	qRT-PCR
GATA2_FOR	CACAACATACATGGAACCCGCGCAGCT	qRT-PCR
GATA2_REV	TGCAACAAGTGTGGCGGCACATCT	qRT-PCR
P53_FOR	TTC AGA TCC GTG GGC GTG AG	qRT-PCR
P53_REV	ATG GCG GGA GGT AGA CTG AC	qRT-PCR
382_lincRNA_VLDLR_FOR	AGACGCAGGTAACGCCAGGCAACGT	ChIP
383_lincRNA_VLDLR_REV	GGCAGCTGAGAGGATGAAAAGGCCT	ChIP
386_lincRNA_VLDLR_FOR	CCTCACCAACCAGTCTTTTGAAGGA	ChIP
387_lincRNA_VLDLR_REV	CCCTCTTGGACCTGGTTAACGTGAC	ChIP
360_lincRNA_SFMBT2_FOR	ACAGGCTTGAACCAAGATTGTGGG	ChIP
361_lincRNA_SFMBT2_REV	CTCCTAAACAGCTGCTTCGTCTGCA	ChIP
372_lincRNA_SFMBT2_FOR	CAGCCCAGTAAGGTGGATCAGAAGT	ChIP
373_lincRNA_SFMBT2_REV	CCAGGCTTGCCAACCTTCTACTCCTT	ChIP
594_lincRNA_ST8SIA3_FOR	GTGGTGGAAATGTCATCAGTTAAGGCG	ChIP
594_lincRNA_ST8SIA3_REV	TCTAGGAGTCCACCTCATAAGCAC	ChIP
ChIP_control_FOR	GAGGTCTCGTATTTGCTGCATCGTA	ChIP
ChIP_control_REV	GCTAATTTCCCTTCTCCACCCCAACCA	ChIP
Primers for detection of endogenous/transgenic/total OCT4, SOX2, KLF4, MYC: see ⁸ and ²		
lincRNA-ST8SIA3_Northern_FOR	TTCTTCCAGGTCTCAGGAATGGGA	Northern Blot
lincRNA-ST8SIA3-Northern_REV	AGGCATGAGGAGTCATTGAAGGT	Northern Blot
lincRNA-ST8SIA3_cDNA_FOR	GGTGAATAAACAGCCATGTTGCTCACA	cDNA cloning
lincRNA-ST8SIA3_cDNA_REV	TTTATTTTTTGGAGAACTGTCATACCGTTTCC	cDNA cloning

B) LincRNA-ST8SIA3/lincRNA-RoR cDNA sequence

GGTGAATAAACAGCCATGTTGCTCACACAAAGCCTGTTTGGTGGTCTCTTCACACGGACGC
TCATGAAATTTGGTGATGTGACTCGGATAGGGGGACCTCCCTTGGGAGATCAGTACCCGTGC
CTCCTGCTCTTTGCTCCGTGAGAAAGATCCACCTACAACCTCAGGTCCTTAGACCAACCAGC
CCAAGAAACATCTACCAATTTCAAATCCAGACCCCACTGGAATCGGACTGTCCAACCTCAC
CTGACAGCCACTCCCACAGCCGCTGGAACCTGGCCCAAGGCTCTCTGACTCCTTCCCAGAT
CTTCTTGGCTTAGCGGCTGAAGACTGACGCTGCCCGATCGCCTCGGAAGCCCCCTAGACCA
TCACGGACGCCGAGCTTCGGGTAACCTCACAGTGAAGAAACACAACCTACAGATTTCTACC
TGGTGCATGGCCATCGCTCATGAAGACTACAACCTCCAGCTTCCTTTGAGAAAAAGAGGAC
TTGATGGCATTGTCGCTAAGTAAGAAATAATGTGTGTGACTTCAGGGTTGCCCCCTTAAAGG
GAGGGGACATTTTCCATCCTGCTGTTTCCAGAGTATGGATGTGATGAGAGACATCTTGGATGAT
GCAGAGGAGGTGAACACCCCAAGGACAATGAAACCACAGGAGAGAAAGAGCCTGCGCTGGC
CCATCTAGCACAGCCACTGGACACAGGGACCACCTGCCTCTGCACTCTTATGGAAGGAGGA
AATCTAACTTTCCAGTTTAAAGGCACTGTTACTTTGGGCTCCTGTTACATAACTGTGGCAGAA
TGAAGGTTCAACATGGAAACTGGCAATGTTGAAGAAACATAAAGTTTATTGCTTGAATATCT
GAAGTTGTGGACTCAATCTCATACTGCTCCACTTATGAGTTATAGTTCTTCCAGGTCTCAGG
AATGGGATCAGCAGGTCTCAGGGTGTACTCTCCTGGATCTCTCACCAGCCACCTCAAACCA
GCTGCCATAGCCTGTCCACTTCCACTCCAATCTTCTCTTCCCTTCATCACCTCCCTTGCACACC
CTGATAACCTCGAAAGAGAATCTTCCCAAGGCTCTGTTCCAAACACATCGCCACTCTGCTTA
GAACCTTCAATGACTCCTCATGGCCTAGGAGGTTTCTCTCCCATCTGGATCCAGCTGACGTT
CCCAGCACCTTCTCCTGACTCCTGTCTTTTCTTGAACCAGTTCTGCCCAACAAGGAGGAAAG
GGCTGACAGAGTGAAAGTCCCAGGGCATGTGGGAATGTGACTCTTTTCACTTTAAATTCTAT
GACTGGAAAGTTTTGGGCAGAGTTGGACATGTGCACTTAGCTTCCAGAAGACAGAATCCTTT
TAAAAGAGTCAGAGAAAACACTGGCTTCTGCCATGACATGAGATACAGACAGGAGAGTTG
GGAAGCTTTTTAAAGATGGCACTATGACTACAATCACAGAACTCTCCATGAGGAAGTAAAA
GAAAGCACCTGCAACACTCCAGCTATGCAGACCACTCTGTAATGGGCTCAGATCTGGACAG
GTGTGTGGAAAGGTGGGTCAACAGGTCAGGCGTCACAGACTTGGAAACATTCATGGTGGAAA
AGAAAAAGCCCCAAAGAAGAGACTTCAGGATAAATGAGAAAATACTCAAGACAGCAAAAAGTC
TCTTTTAGAAATGTTGGAGAAAGAACACTTAATGTCAGGAGTTACTGTTGATTGATGGCCTTA
CTGTGTAGCAGGTGAGAAACCCATTGTTTCAAGTTCCCTAAAGTCACCCTATTCTCCAATCATC
CTATGGAGGGGGAACCATGATGGTTATCCCCATCTTATAAATAAAGCAACAGAGGCTTAGAA
GGACGAACTTTTTTCTCAAGGTTACCCAGATCATTTTGCAGAAGTCCCTAGATTTGAATCAT
GCTCTTGCTTTGAGGTTAAAGACACAGGGGAAGTCAACTCCTTATCTCCTATATCCTGAATA
GGGAAAACCAAACATTGTCAAGAGGAGAGGAAGCCTGAGAGTTGGCATGAATCAGAGTGCT
GGGAGTCTGGAGTCTTCCCACTGAGTTGATGATGGAACAGTAGAGTGGGGCCTGAGCCC
CGTTAGGGCATGAGCTGCTGAATGATTCATGTGAACACCATGCACATGGGAGTGAGGTTTT
GAGCAGTGTGCCACAGGAGCCTACCCTCAGGCCCCACCATAAAAATGTAGGGCCAGTCCTAC
ATTTTATCAATGACTTGCCTGAACACAGAAAATGTGGATACAACCAAAGGTAACAATCCAAT
TAAAAAATGGACAAAAAATTTGAATAAACATTTCTCAAAGAAGATATACAAATGATCAAAAA
GCATATGAAAAAATGCTCAACATCGCTAATTGTAAGAGAAATGCAAATCAAACTATAATGAG
ATACCACCTTATATTGATTAGGAAGACTGCTATAAAAATAGTAAACAAACAAACAAACAAAGT
AAGTCTTGGGAGGATGCAGAGAAATTAATTTTTGTGCACTGTTAGTGGGAATGTAAAT
GGTGCAGCTGTTACGGGAAACGGTATGACAGTTCCTCAAAAAATAAAA

C) siRNA and shRNA sequences

siRNAs

<i>NAME</i>	<i>SEQUENCE</i>
OCT4	AGCAGCTTGGGCTCGAGAA
Ctrl siRNA1	AllStars Negative Control siRNA (Qiagen #1027280)
Ctrl siRNA2	siGENOME Non-targeting siRNA #1 (Dharmacon #D-001210-01-05)
GAPDH control siRNA	siGENOME GAPDH Control siRNA (Dharmacon #D-001140-01)
LincRNA-ST8SIA3 siRNA1	GGAGAGGAAGCCTGAGAGT
LincRNA-ST8SIA3 siRNA2	GGTTAAAGACACAGGGGAA
LincRNA-ST8SIA3 siRNA3	CTTCAGGATAAATGAGAAA
LincRNA-ST8SIA3 siRNA 4	CCTGAGAGTTGGCATGAAT
si-p53	siGENOME SMARTpool (Dharmacon)

shRNA Constructs

<i>NAME</i>	<i>SEQUENCE</i>
incRNA-ST8SIA3/lincRNA-RoR /linc-sh1 (sense oligo)	CCGGAAGCCTGAGAGTTGGCATGAATTCAAGAGATTCATGCCAACTCTCAGGCTTTTTTTTG
lincRNA-ST8SIA3/lincRNA-RoR/linc-sh2 (sense oligo)	CCGGGAGAGGAAGCCTGAGAGTCTCGAGACTCTCAGGCTTCCTCTCCTTTTTG
lincRNA-SFMBT2 (sense oligo)	ccggAAGGCTAGAAACCCCATCTGTTCAAGAGACAGATGGGGGTTTCTAGCCTTtttttg