Table S1 List of signature genes (related to Figure 1)

Common HF-SC signature genes (v.s. HF-TAC)

Probe Set ID	Gene Symbol	Gene Title	qHF-SC-1
1429027_at	0610007N19Rik	RIKEN cDNA 0610007N19 gene, 0610007N19Rik	131.192588
1435464_at	1110003E01Rik	RIKEN cDNA 1110003E01 gene, 1110003E01Rik	459.023066
1454893_at	1110013L07Rik	RIKEN cDNA 1110013L07 gene, 1110013L07Rik	198.069232
1455288_at	1110036O03Rik	RIKEN cDNA 1110036O03 gene, 1110036O03Rik	704.177723
1436187_at	1110054M08Rik	RIKEN cDNA 1110054M08 gene, 1110054M08Rik	166.205275
1431786_s_at	1190003J15Rik	RIKEN cDNA 1190003J15 gene, 1190003J15Rik	5292.9276
1452609_at	1190005I06Rik	RIKEN cDNA 1190005I06 gene, 1190005I06Rik	292.853635
1456641_at	1190007F08Rik	RIKEN cDNA 1190007F08 gene, 1190007F08Rik	226.478324
1429065_at	1200009F10Rik	RIKEN cDNA 1200009F10 gene, 1200009F10Rik	168.096003
1428851_at	1300014I06Rik	RIKEN cDNA 1300014I06 gene, 1300014I06Rik	1496.9648
1456603_at	1500005K14Rik	RIKEN cDNA 1500005K14 gene, 1500005K14Rik	2579.9745
1426991_at	1810048J11Rik	RIKEN cDNA 1810048J11 gene, 1810048J11Rik	155.594842
1442129_at	1810058I24Rik	RIKEN cDNA 1810058I24 gene, 1810058I24Rik	256.375906
1430538_at	2210013O21Rik	RIKEN cDNA 2210013O21 gene, 2210013O21Rik	892.359045
1424968_at	2210023G05Rik	RIKEN cDNA 2210023G05 gene, 2210023G05Rik	177.623964
1428562_at	2210403K04Rik	RIKEN cDNA 2210403K04 gene, 2210403K04Rik	452.547108
1453008_at	2300002D11Rik	RIKEN cDNA 2300002D11 gene, 2300002D11Rik	761.795745
1428914_at	2310014D11Rik	RIKEN cDNA 2310014D11 gene, 2310014D11Rik	1307.00465
1424099_at	2310016C16Rik	RIKEN cDNA 2310016C16 gene, 2310016C16Rik	852.0807
1460344_at	2310033F14Rik	RIKEN cDNA 2310033F14 gene, 2310033F14Rik	198.429585
1453184_at	2310040C09Rik	RIKEN cDNA 2310040C09 gene, 2310040C09Rik	425.008452
1429505_at	2310076G13Rik	RIKEN cDNA 2310076G13 gene, 2310076G13Rik	314.67289
1417779_at	2310079N02Rik	RIKEN cDNA 2310079N02 gene, 2310079N02Rik	340.724779
1434581_at	2410066E13Rik	RIKEN cDNA 2410066E13 gene, 2410066E13Rik	181.422105
1428097_at	2510009E07Rik	RIKEN cDNA 2510009E07 gene, 2510009E07Rik	330.546377
1420465_s_at	2610016E04Rik	major urinary protein 1 /// major urinary protein 2 /// RI	116.874203
1454933_at	2610027C15Rik	RIKEN cDNA 2610027C15 gene, 2610027C15Rik	290.360024
1425913_a_at	2810022L02Rik	RIKEN cDNA 2810022L02 gene, 2810022L02Rik	300.698015
1417218_at	2810048G17Rik	RIKEN cDNA 2810048G17 gene, 2810048G17Rik	296.393408
1431424_at	2810055G20Rik	RIKEN cDNA 2810055G20 gene, 2810055G20Rik	308.296116
1423679_at	2810432L12Rik	RIKEN cDNA 2810432L12 gene, 2810432L12Rik	522.349612
1429089_s_at	2900026A02Rik	RIKEN cDNA 2900026A02 gene, 2900026A02Rik	816.282099
1435315_s_at	2900034E22Rik	RIKEN cDNA 2900034E22 gene, 2900034E22Rik	243.179956
1455091_at	3222402P14Rik	RIKEN cDNA 3222402P14 gene, 3222402P14Rik	579.142694
1428540_at	3321401G04Rik	RIKEN cDNA 3321401G04 gene, 3321401G04Rik	178.341631
1428861_at	4631422O05Rik	RIKEN cDNA 4631422O05 gene, 4631422O05Rik	1644.72242
1460463_at	4632413I24Rik	RIKEN cDNA 4632413I24 gene, 4632413I24Rik	858.687855
1416619_at	4632428N05Rik	RIKEN cDNA 4632428N05 gene, 4632428N05Rik	372.613465
1434591_at	4732460K03Rik	RIKEN cDNA 4732460K03 gene, 4732460K03Rik	107.45296
1455213_at	4930488E11Rik	RIKEN cDNA 4930488E11 gene /// thymosin beta-like, 49	227.991398
1416607_at	4931406C07Rik	RIKEN cDNA 4931406C07 gene, 4931406C07Rik	263.173
1447939_a_at	4933409K07Rik	RIKEN cDNA 4933409K07 gene /// predicted gene, EG545	177.536114
1428663_at	5133401H06Rik	RIKEN cDNA 5133401H06 gene, 5133401H06Rik	312.421655

Table S2 Histone marker occupancy (related to Figure 2)

Cell type	ChIP-seq	total-peaks	promoter-peaks	target-genes	target-transcripts
ES	H3K4me3	18294	12868	13597	16599
	H3K27me3	6101	3656	3048	3614
MEF	H3K4me3	16104	12342	12751	15667
	H3K27me3	6761	3123	2644	3114
NPC	H3K4me3	11620	10254	10046	12312
	H3K27me3	4773	1340	910	1059
qHF-SC	H3K4me3	10662	9643	10815	13255
	H3K79me2	23616	6654	6226	7806
	H3K27me3	6718	2076	1650	1959
aHF-SC	H3K4me3	10811	9819	10738	13117
	H3K79me2	25133	7658	7072	8840
	H3K27me3	8798	3071	2618	3135
HF-TAC	H3K4me3	9065	8534	9356	11345
	H3K79me2	23504	7650	7009	8750
	H3K27me3	8712	3369	2802	3372

Table S3 List of ESC bivalent genes resolved to H3K27me3 in qHF-SCs (r

RefSeq ID	Gene Name	ESC	qHF-SC
NM_001159638	0610012H03Rik	K4+27	K27
NM_029554	0610040J01Rik	K4+27	K27
NM_001163810	1700008P20Rik	K4+27	K27
NM_001085514	1700101E01Rik	K4+27	K27
NR_027899	1700109F18Rik	K4+27	K27
NM_001163145	1810041L15Rik	K4+27	K27
NR_027826	2610017I09Rik	K4+27	K27
NM_028277	2700045P11Rik	K4+27	K27
NM_001144992	2810459M11Rik	K4+27	K27
NR_015468	2900079G21Rik	K4+27	K27
NM_001145162	3110006E14Rik	K4+27	K27
NR_026733	3110039M20Rik	K4+27	K27
NM_177006	3110047P20Rik	K4+27	K27
NM_029008	4833403I15Rik	K4+27	K27
NM_029425	4833424O15Rik	K4+27	K27
NM_001081121	4931429I11Rik	K4+27	K27
NR_029437	4933406I18Rik	K4+27	K27
NM_198642	5031414D18Rik	K4+27	K27
NM_001032727	5730410E15Rik	K4+27	K27
NM_177854	6030405A18Rik	K4+27	K27
NM_001081227	6330403A02Rik	K4+27	K27
NM_001142965	6430704M03Rik	K4+27	K27
NR_029460	6530402F18Rik	K4+27	K27
NM_172419	9030612E09Rik	K4+27	K27
NR_030721	9130206I24Rik	K4+27	K27
NR_015562	9530036O11Rik	K4+27	K27
NR_015610	9530059O14Rik	K4+27	K27
NM_030728	9930013L23Rik	K4+27	K27
NR_027362	A930003O13Rik	K4+27	K27
NM_172399	A930038C07Rik	K4+27	K27
NM_007377	Aatk	K4+27	K27
NM_011510	Abcc8	K4+27	K27
NM_138955	Abcg4	K4+27	K27
NM_007424	Acan	K4+27	K27
NM_007384	Accn1	K4+27	K27
NM_009599	Ache	K4+27	K27
NM_007400	Adam12	K4+27	K27
NM_001024139	Adamts15	K4+27	K27
NM_172466	Adamts18	K4+27	K27
NM_175643	Adamts2	K4+27	K27
NM_001164785	Adamts20	K4+27	K27
NM_013906	Adamts8	K4+27	K27
NM_153534	Adcy2	K4+27	K27
NM_080435	Adcy4	K4+27	K27

Table S4A Chromatin states of Transcription Factor families (related to Figu

Sox family

RefSeq(s)	Gene(s)	ESC	NPC	MEF	HF-SC
NM_009233	Sox1	K4+27	K4	K27	K27
NM_011443	Sox2	K4	K4	K27	K27
NM_009237	Sox3	K4+27	K4	K27	K27
NM_009238	Sox4	K4+27	K4	K4	K4+79
NM_011444	Sox5	None	K4	K4	None
NM_001025560	Sox6	K4+27	K4	K4+27	K27
NM_011446	Sox7	K4+27	None	K4+27	K4
NM_011447	Sox8	K4+27	K4	K4+27	None
NM_011448	Sox9	K4+27	K4	K4	K4+79
NM_011437	Sox10	K4+27	None	K27	K27
NM_009234	Sox11	K4+27	K4	K4	K27
NM_011438	Sox12	K4	K4	K4	K4
NM_011439	Sox13	K4	K4	K4+27	K4
NM_011440	Sox14	K27	K27	K27	K27
NM_009235	Sox15	K4	None	None	None
NM_011441	Sox17	K4+27	K27	K27	K27
NM_009236	Sox18	K4+27	K27	K27	K27
NM_177753	Sox21	K4+27	K4	K4+27	K4+27
NM_173384	Sox30	K4+27	None	None	None

Lhx family

RefSeq(s)	Gene(s)	ESC	NPC	MEF	HF-SC
NM_008498	Lhx1	K4+27	K4	K4+27	K27
NM_010710	Lhx2	K4+27	K4	K4+27	K4+79
NM_001039653	Lhx3	K27	None	K27	K27
NM_010712	Lhx4	K4+27	K4+27	K4+27	K27
NM_008499	Lhx5	K27	K27	K27	K27
NM_008500	Lhx6	K27	K27	K4+27	K27
NM_010713	Lhx8	K4+27	K27	K27	K27
NM_010714	Lhx9	K4+27	None	K4+27	K27

Neurod family

RefSeq(s)	Gene(s)	ESC	NPC	MEF	HF-SC

Table S5

Table S5 List of HF-SC signature genes PcG-repressed (gain of the H3K

RefSeq ID	Gene Name	qHF-SC	HF-TAC	Genes highligted
NM_025831	1300014I06Rik	K4+79	K27	
NM_198649	Ablim3	K4+79	K27	
NM_009622	Adcy1	K4+79	K27	
NM_020332	Ank	K4+79	K27	
NM_016689	Aqp3	K4+79	K27	
NM_001048142	Bdnf	K4+79	K27	
NM_027112	Capns2	K4+79	K27	
NM_001111059	Cd34	K4+79	K27	
NM_009932	Col4a2	K4+79	K27	
NM_199473	Col8a2	K4+79	K27	
NM_010217	Ctgf	K4+79	K27	
NM_009911	Cxcr4	K4+79	K27	
NM_007722	Cxcr7	K4+79	K27	
NM_010330	Emb	K4+79	K27	
NM_172813	Enox1	K4+79	K27	
NM_201518	Flrt2	K4+79	K27	
NM_021458	Fzd3	K4+79	K27	
NM_008086	Gas1	K4+79	K27	
NM_145741	Gdf10	K4+79	K27	
NM_011824	Grem1	K4+79	K27	
NM_010437	Hivep2	K4+79	K27	
NM_001024720	Hmcn1	K4+79	K27	
NM_008393	Irx3	K4+79	K27	
NM_018826	Irx5	K4+79	K27	
NM_021359	Itgb6	K4+79	K27	
NR_027627	Kcnk2	K4+79	K27	
NM_001142731	Kctd1	K4+79	K27	
NM_008469	Krt15	K4+79	K27	
NM_010195	Lgr5	K4+79	K27	
NM_057173	Lmo1	K4+79	K27	
NM_022983	Lpar3	K4+79	K27	
NM_010733	Lrrn3	K4+79	K27	
NM_001081235	Mn1	K4+79	K27	
NM_001043355	Mtap6	K4+79	K27	
NM_008675	Nbl1	K4+79	K27	
NM_001164109	Nfatc1	K4+79	K27	
NM_001122953	Nfia	K4+79	K27	
NM_001164034	Ntf3	K4+79	K27	
NM_001081009	Parp8	K4+79	K27	
NM_016798	Pdlim3	K4+79	K27	
NM_019809	Pdlim5	K4+79	K27	
NM_001164593	Pdzrn4	K4+79	K27	
NM_001164594	Pdzrn4	K4+79	K27	
NM_011218	Ptprs	K4+79	K27	

Table S6A List of HF-TAC signature genes induced in HF-TACs from HF-S

RefSeq ID	Gene Name	qHF-SC	HF-TAC
NM_029639	1600029D21Rik	K4	K4+79
NM_197990	1700025G04Rik	K4	K4+79
NM_029368	1700029F09Rik	K4	K4+79
NM_001081085	2010317E24Rik	K4	K4+79
NM_001085493	2310030N02Rik	K4	K4+79
NM_028228	2610028A01Rik	K4	K4+79
NM_025642	2610039C10Rik	K4	K4+79
NM_025599	2610528E23Rik	K4	K4+79
NM_001037279	2700094K13Rik	K4	K4+79
NR_027866	5730408K05Rik	K4	K4+79
NM_153416	Aaas	K4	K4+79
NM_026179	Abhd5	K4	K4+79
NM_019673	Actl6a	K4	K4+79
NM_013464	Ahr	K4	K4+79
NM_009658	Akr1b3	K4	K4+79
NM_133237	Apcdd1	K4	K4+79
NM_027263	Apitd1	K4	K4+79
NM_181416	Arhgap11a	K4	K4+79
NM_027667	Arhgap19	K4	K4+79
NM_009791	Aspm	K4	K4+79
NM_011497	Aurka	K4	K4+79
NM_011496	Aurkb	K4	K4+79
NM_026505	Bambi	K4	K4+79
NM_013815	Baz1a	K4	K4+79
NM_054078	Baz2a	K4	K4+79
NM_201364	BC055324	K4	K4+79
NM_001122683	Bdh1	K4	K4+79
NM_001042527	Blm	K4	K4+79
NM_007557	Bmp7	K4	K4+79
NM_172578	C79407	K4	K4+79
NM_026613	Ccdc34	K4	K4+79
NM_027411	Ccdc99	K4	K4+79
NM_009828	Ccna2	K4	K4+79
NM_009829	Ccnd2	K4	K4+79
NM_007634	Ccnf	K4	K4+79
NM_009862	Cdc45l	K4	K4+79
NM_001025779	Cdc6	K4	K4+79
NM_013538	Cdca3	K4	K4+79
NM_026560	Cdca8	K4	K4+79
NM_007669	Cdkn1a	K4	K4+79
NM_026014	Cdt1	K4	K4+79
NM_007681	Cenpa	K4	K4+79
NM_173762	Cenpe	K4	K4+79
NM_021886	Cenph	K4	K4+79

Table S7

Table S7A List of HF-SC signature genes PcG-repressed in aHF-SCs and active

RefSeq ID	Gene Name	qHF-SC	aHF-SC
NM_001048142	Bdnf	K4+79	K27
NM_001164593	Pdzrn4	K4+79	K27
NM_001164034	Ntf3	K4+79	K27
NM_009622	Adcy1	K4+79	K4+27
NM_145741	Gdf10	K4+79	K4+27
NM_011824	Grem1	K4+79	K4+27
NM_001142731	Kctd1	K4+79	K4+27
NM_001164109	Nfatc1	K4+79	K4+27
NM_010455	Hoxa7	K4+79	K4+27
NM_001122758	Pcdh7	K4+79	K4+27
NM_007467	Aplp1	K4	K27
NM_053199	Cadm3	K4	K27
NM_008005	Fgf18	K4	K27
NM_001038613	Olfm1	K4	K27
NM_001083809	Slc43a1	K4	K27
NM_010484	Slc6a4	K4	K27
NM_178395	Zdhhc2	K4	K27
NM_019707	Cdh13	K4	K27
NM_019971	Pdgfc	K4	K27
NM_001162941	Mapre2	K4	K27
NM_001038612	Olfm1	K4	K27
NM_025451	Camk2n1	K4	K4+27
NM_009793	Camk4	K4	K4+27
NM_010279	Gfra1	K4	K4+27
NM_008115	Gfra2	K4	K4+27
NM_013589	Ltbp2	K4	K4+27
NM_019867	Ngef	K4	K4+27
NM_001081147	Oxtr	K4	K4+27
NM_148950	Pknox2	K4	K4+27
NM_027241	Polr3gl	K4	K4+27
NM_008858	Prkd1	K4	K4+27
NM_007706	Socs2	K4	K4+27
NM_177708	Rtn4rl1	K4	K4+27
NM_028804	Ccdc3	K4	K4+27
NM_018827	Crlf1	K4	K4+27
NM_028627	Psd	K4	K4+27
NM_198967	Tmtc1	K4	K4+27
NM_013602	Mt1	K4	K4+27

I. Supplemental Figures

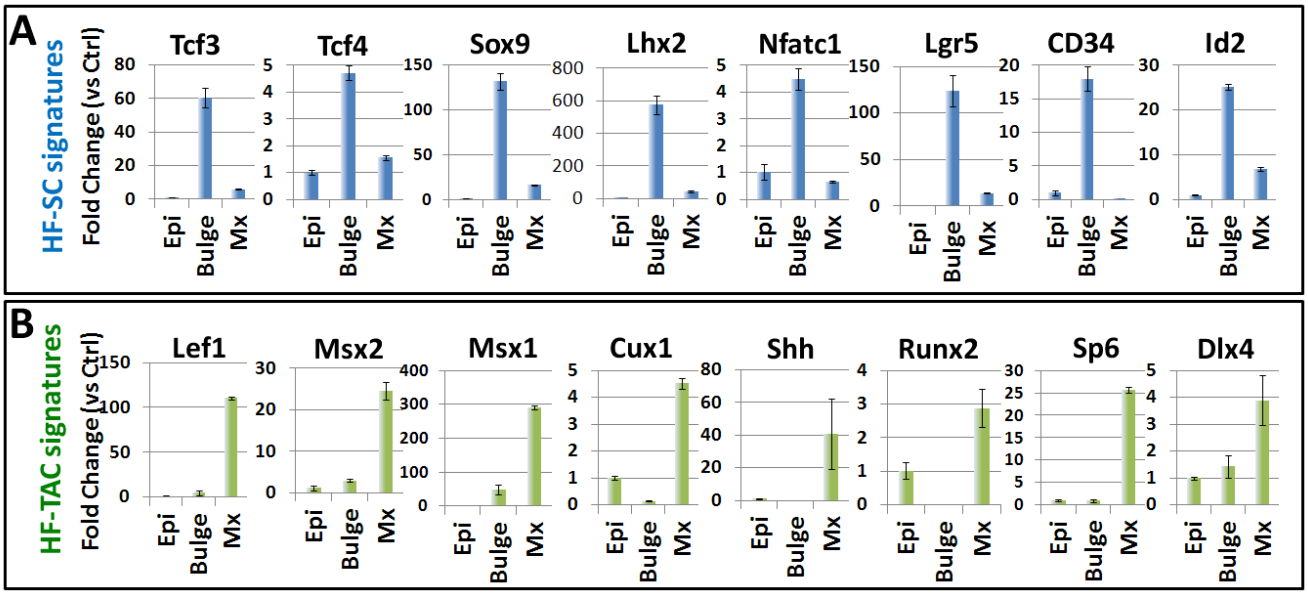

Figure S1. Confirmation of Key HF-SC and HF-TAC Signature Genes (Related to Figure 1). mRNAs were isolated from FACS-purified interfollicular epidermal cells (Epi), activated HF-SCs (Bulge) and matrix HF-TACs (Mx) and analyzed by real-time RT-PCRs to test the validity of our microarray data. We focused on well-established HF-SC **(A)** and HF-TAC **(B)** genes for our analyses. Fold changes were normalized to Epi mRNA (Epi=1), except for *Cd34, Shh, Runx2* and *Dlx4,* whose Epi value was zero, and hence were normalized to total epidermal basal cells (Epi+HF). Data are reported as average ± SD. n=3.

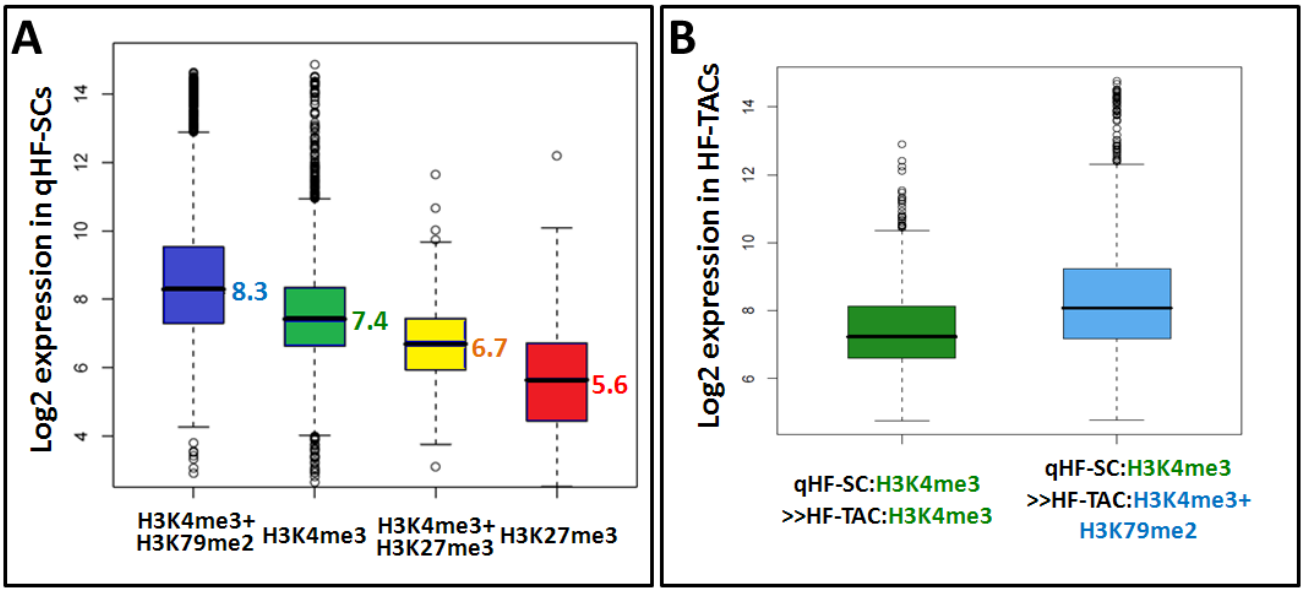

Figure S2. Comparative Analyses of Genes for Histone Modification Status and Gene Expression Levels (Related to Figure 4).

(**A**) The expression levels of genes marked by both H3K4me3 and H3K79me2 (primed and transcribed) are higher than those marked only by H3K4me3 (primed). mRNA expression levels in qHF-SCs are presented as Log2 expression, with the means listed (8.3 vs 7.4, $p<0.001$). Very few genes existed in a bivalent (poised) state (H3K4me3+H3K27me3) and these showed signs of higher expression than genes marked only by H3K27me3 (mean log2=6.7 vs 5.6, $p<0.001$). (**B**) The expression levels of HF-SC genes which gain the H3K79m2 mark in HF-TACs are greater than those displaying the single H3K4me3 mark in both populations. Log2 of mRNA expression levels are shown ($p<0.001$). Color coding is according to the system used in the main text.

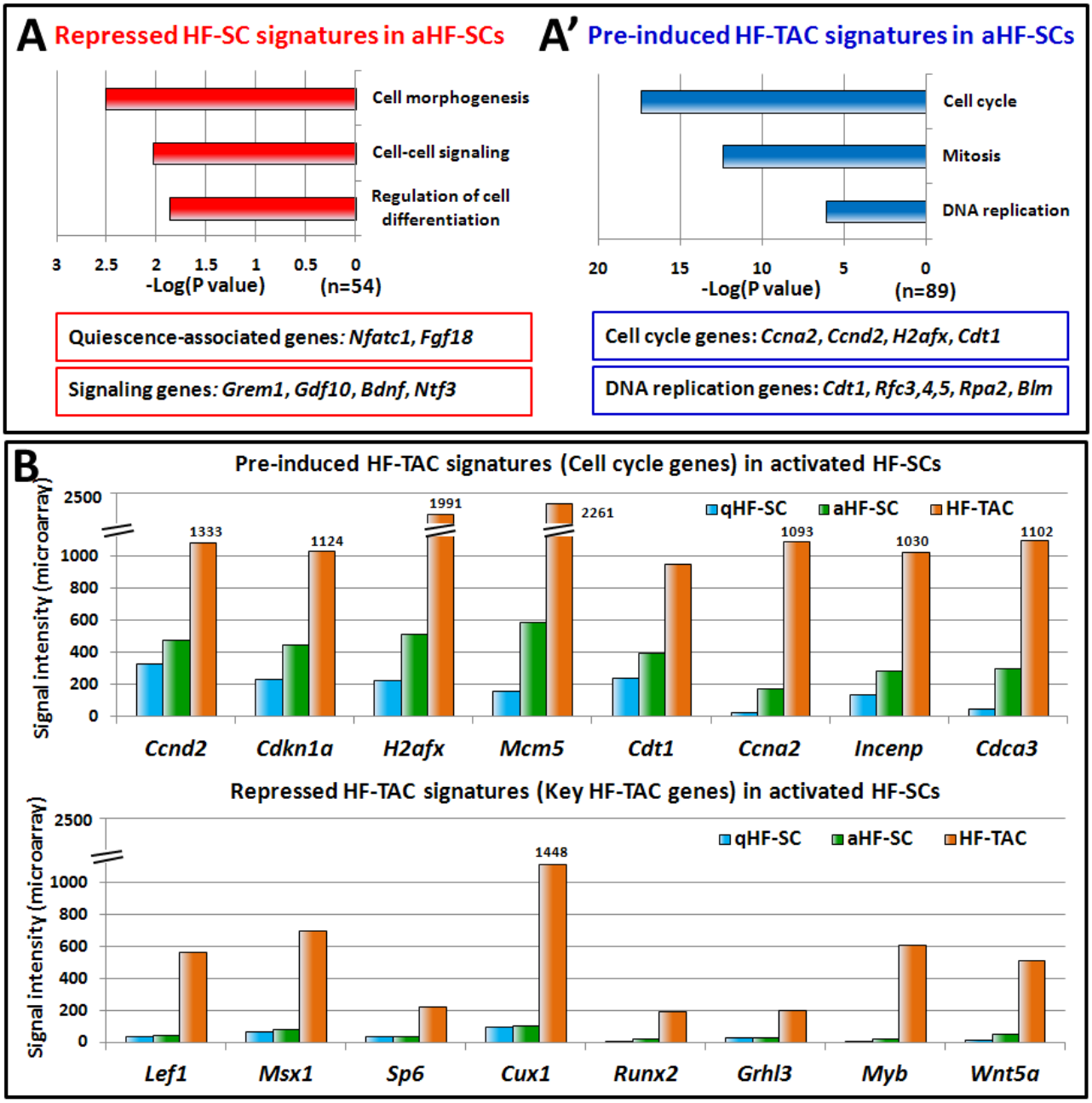

Figure S3. Cell Cycle Genes Are Pre-induced While Key HF-TAC Genes Remain Silenced in aHF-SCs (Related to Figure 6).

(**A**) Gene ontology analysis and representative examples of repressed HF-SC signatures (left) and pre-induced HF-TAC signatures (right) in aHF-SCs. Note that a small number of HF-SC signature genes become PcG-repressed and that some cell cycle genes (more highly expressed in HF-TACs), become pre-induced in aHF-SCs. (**B**) Signal intensities of HF-TAC mRNAs whose genes either become pre-induced (top) or retain repression (bottom) during the transition from HF-SC quiescence

to activation. Note that pre-induced cell cycle genes in aHF-SCs are primed and transcribed by ~2X, although their levels are considerably higher in HF-TACs. By contrast, genes that are PcG-repressed display much tighter control, remaining silent in both quiescent and activated HF-SCs. Notably, many of these PcG-repressed genes in HF-SCs are known to play a role in hair lineage determination and differentiation.

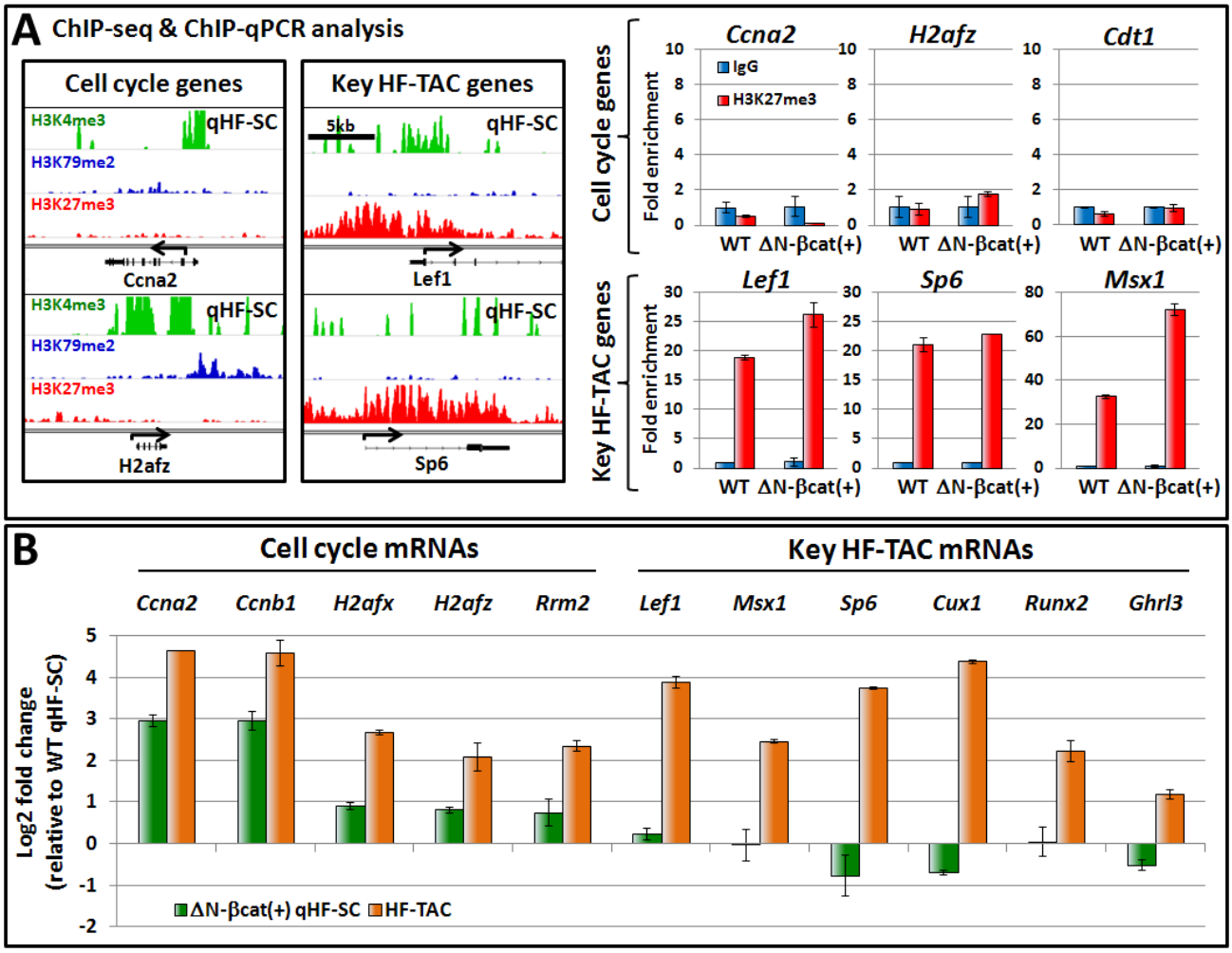

Figure S4. Elevated β-catenin in Quiescent HF-SCs Is Not Sufficient to Relieve PcG-mediated Repression of Key HF-TAC Genes (Related to Figure 6).

(**A**) Comparative analysis of chromatin status for HF-TAC genes in WT and ΔN-βcat(+) qHF-SCs. (**left**) ChIP-seq signal tracks reveal the activation/repression status of non-PcG-regulated cell cycle and PcG-regulated HF-TAC genes in WT qHF-SCs. (**right**) ChIP-qPCR analysis reveal the H3K27me3 status of the same genes in WT and in ΔN-βact(+) qHF-SCs. IgG Abs were used as a non-specific IP control. ChIP signals were normalized against a *Gapdh*-promoter ChIP (input vs IP). Note that PcG-repressed key HF-TAC regulators were not relieved from PcG-mediated repression by sustained β-catenin signaling in qHF-SCs. (**B**) RT-PCR to measure relative levels (log2) of HF-TAC signature mRNAs contrasted with ΔN-βact(+) qHF-SCs or matrix HF-TACs vs WT qHF-SCs. Note that

although non-PcG regulated cell cycle genes are much more highly expressed in ΔN-βact(+) than WT qHF-SCs, this is not the case for PcG-repressed HF-TAC genes.

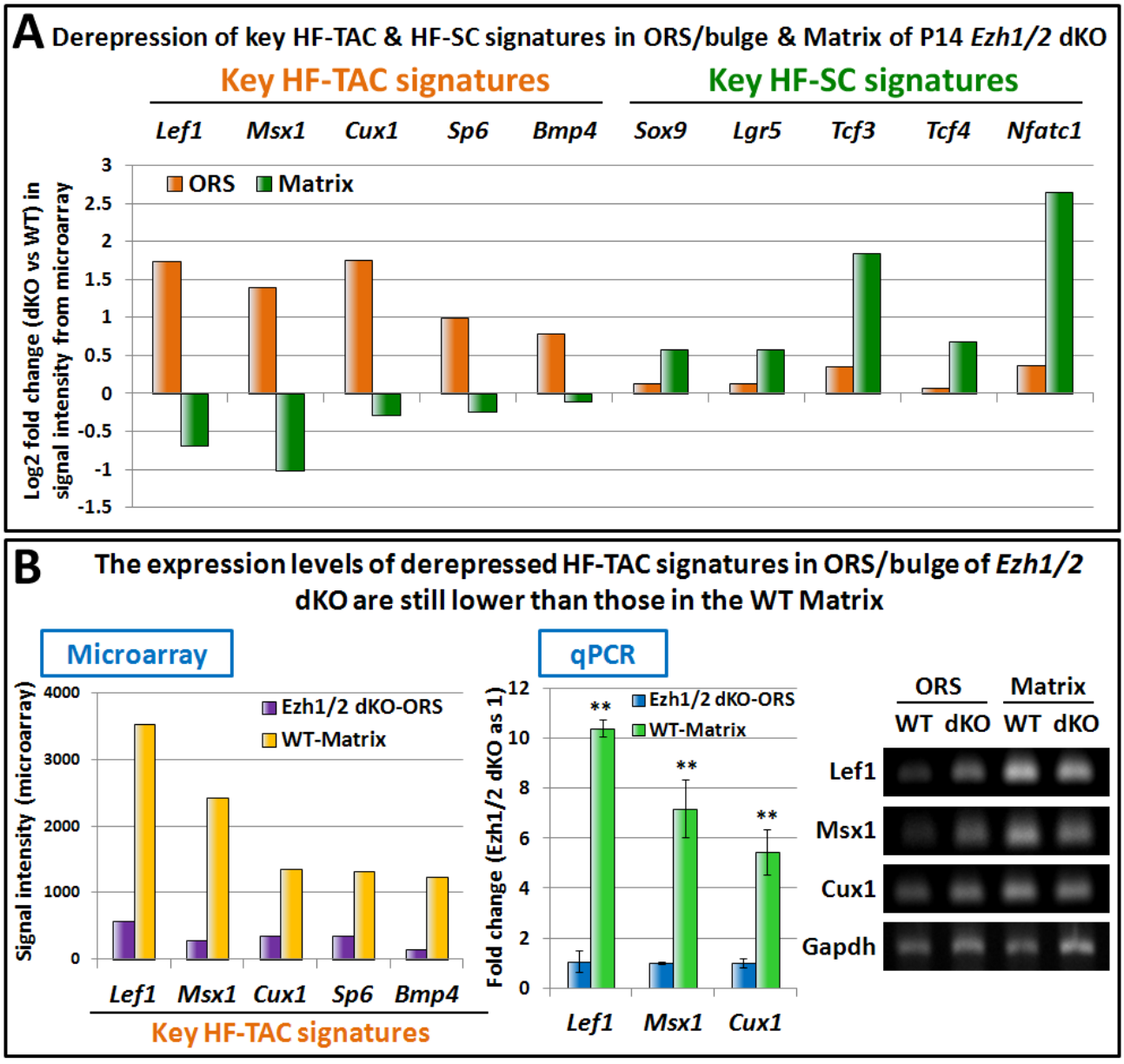

Figure S5. PcG-Regulated Signature Genes Are Ectopically Activated in *Ezh1/2* dKO HF Populations, but Their Levels Are Markedly Lower than Their Normal Activation Levels in the Lineage (Related to Figure 6).

(**A**) Log2 of fold changes (*Ezh1/2* dKO vs WT) in microarray signal intensities of the key HF-TAC and HF-SC signature mRNAs from ORS/bulge and matrix cells in P14 wild-type (WT) and *Ezh1/2* dKO (dKO) engrafted skins. Note that in the absence of EZH1/2, key HF-TAC genes were precociously activated in ORS/bulge, and conversely, key HF-SC signature genes sustained expression later in the lineage than normal. (**B**) The precocious expression of key HF-TAC signature genes in *Ezh1/2* dKO

ORS/bulge cells was significantly lower than in the WT matrix, where these genes are normally activated. Microarray intensities of key HF-TAC signature mRNAs in *Ezh1/2* dKO ORS/bulge and WT matrix (**left**). Fold changes (*Ezh1/2* dKO vs WT) in mRNA expression were analyzed by RT-qPCR. Quantifications are shown (**middle**) along with the gel images of amplified cDNA (**right**). Expression levels were normalized against Gapdh mRNA, and fold changes are presented as *Ezh1/2* dKO-ORS mRNA equal to 1. Data are reported as average ± SD. n=3. **, $p<0.01$.

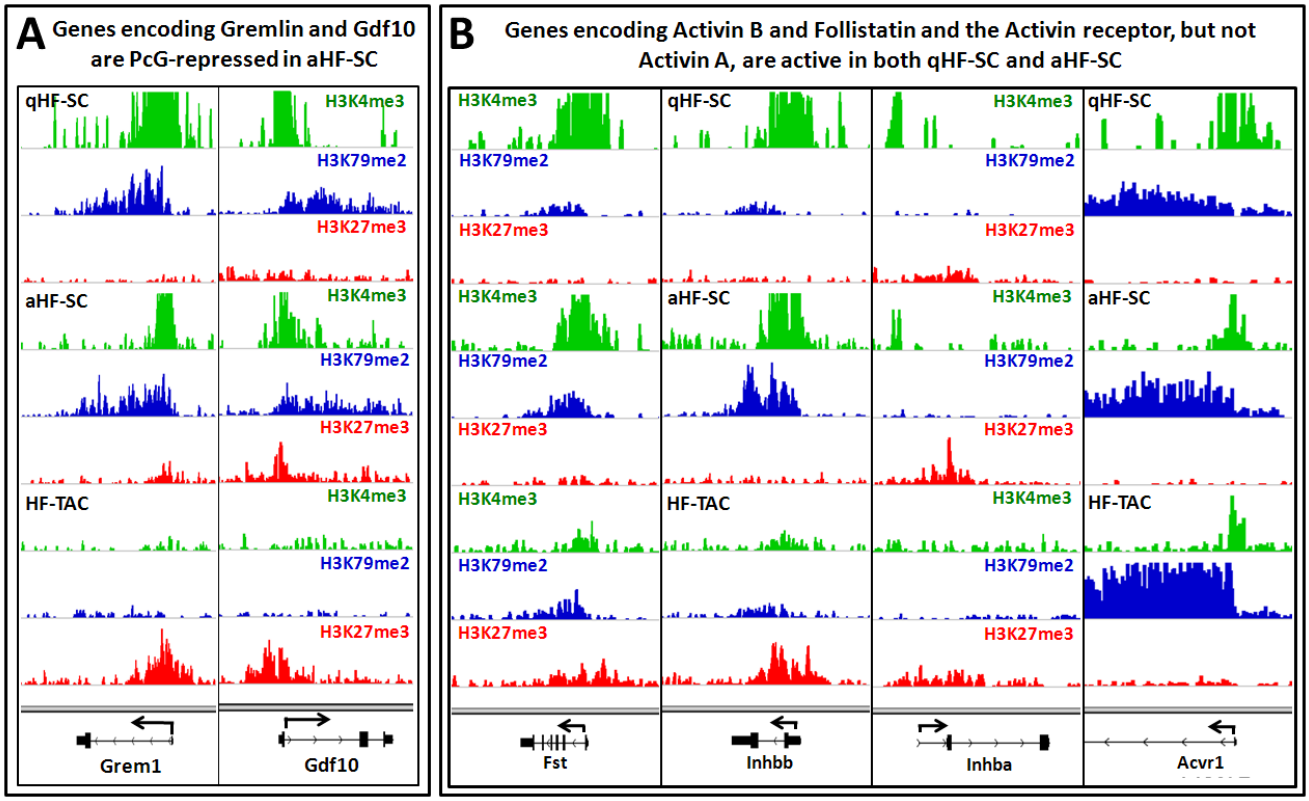

Figure S6. Genes Encoding Gremlin and Gdf10 Are Active in qHF-SC and PcG-repressed in aHF-SC, While Genes Encoding Activin B and Follistatin and the Activin Receptor, but Not Activin A, Are Active in Both qHF-SC and aHF-SC. (Related to Figure 7).

(A) ChIP-seq signal tracks are shown for *Grem1* and *Gdf10* genes in chromatin from qHF-SCs, aHF-SCs, and HF-TACs. All tracks are set with the same scale. Note that PcG repression of *Grem1* and *Gdf10* in aHF-SC suggests that their functional significance wanes once HF-SCs are activated. **(B)** ChIP-seq signal tracks of Activin signaling, including *Follistatin (Fst), Activin B (Inhbb), Activin A (Inhba),* and *Activin receptor (Acvr1)* are shown for chromatin isolated from qHF-SCs, aHF-SCs, and HF-TACs. All tracks were set on the same scale. Note that Activin B and its receptors are both expressed in HF-SCs, reflecting cell-autonomous regulation.

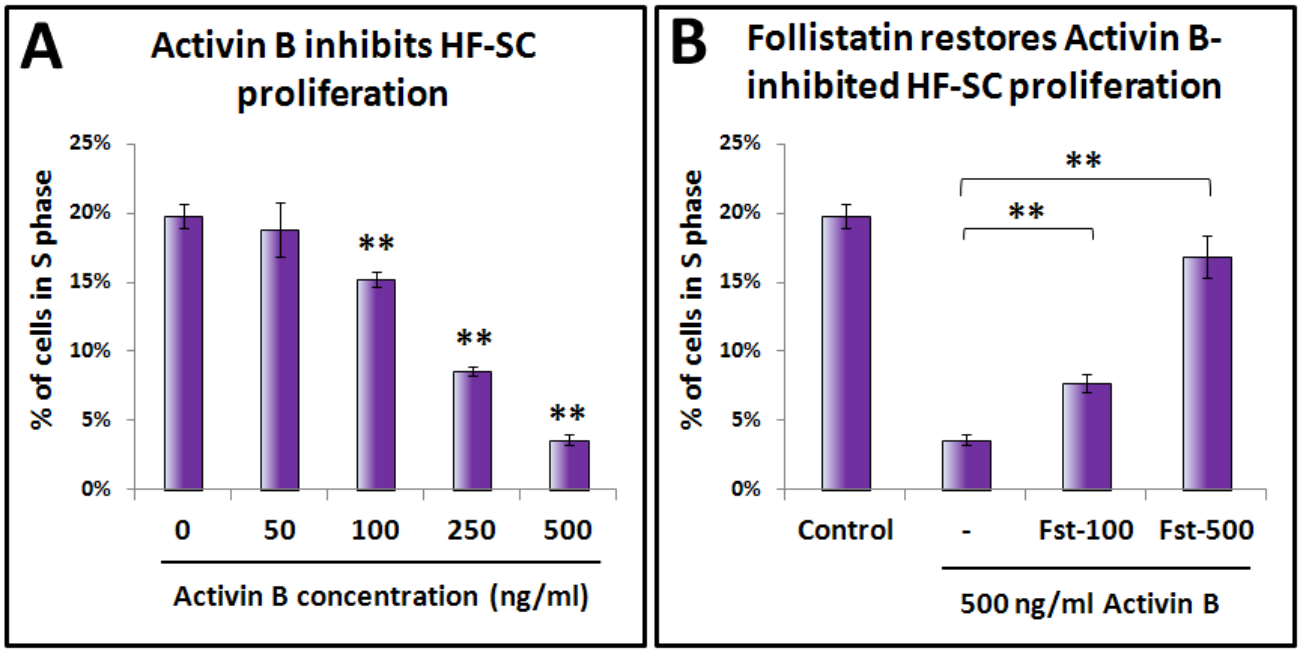

Figure S7. Activin B Inhibits HF-SC Proliferation While Follistatin Counterbalances This Inhibition (Related to Figure 7).

(**A**) Activin B inhibits HF-SC proliferation in a dose-dependent fashion. (**B**) Follistatin antagonizes Activin B-mediated inhibitory effect in a dose-dependent fashion. HF-SCs were cultured with indicated concentrations of Activin B, and in the presence of 500 ng/ml Activin B, cells were treated with or without 100 (Fst-100) and 500 ng/ml (Fst-500) of Follistatin, respectively. In all graphs, data are reported as average ± SD; **, $p<0.01$.

II. Supplemental Tables (All in supplemental Excel files)

Table S1 List of signature genes (Related to Figure 1)

Table S2 Histone marker occupancy (Related to Figure 2)

Table S3 List of ESC bivalent genes resolved to H3K27me3 in qHF-SCs (Related to Figure 2)

Table S4 List of (A) Chromatin states of transcription factor families (B) HF-SC signature genes resolved from a bivalent state in ESCs (Related to Figure 3)

Table S5 List of HF-SC signature genes PcG-repressed (gain of the H3K27me3 mark) in HF-TACs (Related to Figure 4)

Table S6 List of (A) HF-TAC signature genes induced in HF-TACs from HF-SCs (B) HF-TAC signature genes derepressed in HF-TACs from an H3K27me3 marked state in HF-SCs (Related to Figure 5)

Table S7 List of (A) HF-SC signature genes PcG-repressed in aHF-SCs and active in qHF-SCs (B) HF-TAC signature genes transcribed at low levels (pre-induced) in aHF-SCs and silent but not PcG-repressed in qHF-SCs (Related to Figure 6). Note that genes e.g. *Nfatc1* and *Fgf18,* are on PcG-repressed list; their role in HF-SC quiescence is established.

III. Supplemental Experimental Procedures

Antibody Information

The following antibodies (Abs) were used for ChIP-seq: H3K4me3 (Abcam, ab1012), H3K27me3 (Millipore, 07-449), H3K79me2 (Abcam, ab3594). The following Abs were used for FACS: integrin α6 (eBiosciences, APC-conjugated, 17-0495; PE-conjugated, 12-0495), CD34 (eBiosciences, Alexa Fluor 647-conjugated, 51-0341; Alexa Fluor 700-conjugated, 56-0341), Sca-1 (eBiosciences, PerCP-

Cy5.5-conjugated, 45-5981), ephrinB1 (R&D Systems, Biotinylated Abs, BAF473), Streptavidin-PE (R&D Systems, F0040).

Florescence-Activated Cell Sorting

To prepare samples for FACS, we incubated 12-15 CD-1 mouse back skins with trypsin at 37°C for 35-45 minutes to detach and generate single cell suspensions of the epidermal and HF cells. FACS purifications of telogen HF-SCs from P52-60 mice and anagen HF-SCs and matrix HF-TACs from P28-30 mice were performed on a FACS Aria system equipped with FACS DiVa software (BD Biosciences). Cells were gated for single events and for viability and then sorted based on surface expression of integrin α6 and CD34 (telogen bulge SCs), or on the basis of GFP and surface expression of integrin α6 and CD34 (anagen bulge) or GFP and surface expression of ephrinB1 (HF-TACs) and negatively for Sca-1 to remove upper ORS cells. See Figure 1C for further details. Cells were collected into either Trizol LS reagent (Invitrogen) for RNA purification and microarray analysis, or pre-coated 15-ml Flacon tubes for ChIP-seq.

Microarray Analysis

For each FACS-purified population of HF-cells, mRNAs were purified and provided to the Genomics Core Facility at Memorial Sloan Ketering Institute (MSKI) for quality control, quantification, reverse transcription, labeling and hybridization to MOE430 2.0 microarray chips (Affymetrix). Arrays were then scanned according to the manufacturer's specifications for Affymetrix MOE430 2.0 chips. After subtracting for background, probe signals were normalized using Gene Pattern (Broad Institution). The entire procedure was repeated in duplicate for each sample to produce two independent datasets per mRNA sample. After eliminating probe signals with a value <100 or called absent, signature genes were then selected as remaining probes that were elevated at least two times ($p<0.02$) in HF-SC populations relative to HF-TACs as follows: a) Common HF-SC signature: ≥2X in both telogen and anagen bulge over matrix; b) Quiescent HF-SC signature: ≥2X in telogen bulge vs matrix and not shared in the list of anagen bulge vs matrix; c) Active HF-SC signature: ≥2X in anagen bulge over

matrix and not shared in the list of anagen bulge vs matrix; d) HF-TA signature: ≥2X in matrix over telogen or anagen bulge. These signature genes were hierarchically clustered based on their expression correlation co-efficiencies, and the resulting clusters are shown as a heatmap in Figure 3. Microarray raw data have been submitted to http://www.ncbi.nlm.nih.gov/geo.

Reverse Transcription and Real-time PCR confirmation

Total RNAs from FACS-sorted cells described above were purified with the RNeasy Micro Kit (Qiagen) and reverse transcribed (Invitrogen). cDNAs were amplified with primers in SYBR Green quantitative PCR assay on the Applied Biosystems 7900HT Fast Real-Time PCR system. Expression levels were normalized to PCR amplification with primers to GAPDH. Primers were designed using Primer 3 online software to amplify regions spanning ~100-120 nucleotides and encompassing exon/intron boundaries.

Cell Culture & Growth Factor Treatment

HF-SCs were isolated from P52-60 *K14-H2BGFP* mice and cultured and expanded as described (Blanpain et al, 2004). After two passages, SCs were seeded onto 24-well plates with mitomycin C-treated J2 3T3 mouse fibroblast feeders. On day 2 after seeding, SCs were treated with the desired growth factors for 6 days and then EdU-pulsed (10 μM) for 1 hour to label S-phase cells prior to harvesting for FACS analysis. Treatment conditions were: Control (PBS/4 μM HCl), BMP6 (R&D Systems, 400 ng/ml), Noggin (R&D Systems, 1000 ng/ml), Gremlin (R&D Systems, 500 & 1000 ng/ml), Gdf10 (R&D Systems, 500 & 1000 ng/ml), Activin B (R&D Systems, 50, 100, 250 & 500 ng/ml), Follistatin (R&D Systems, 100 & 500 ng/ml), as indicated. Incorporated EdU was detected using Click-iT EdU Flow Cytometry Assay Kit (Invitrogen). Statistical analyses were determined by the student *t-test*.