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Supplemental Data

A Two-Step Mechanism for Stem Cell Activation during Hair Regeneration

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Figure S1. Hair Germ and Bulge Cells Are Ultrastructurally Distinct.

Ultrastructural analyses reveal morphological distinctions between hair germ (HG) and bulge cells. HG cells display higher cytoplasmic density but possess fewer desmosomes (De). Areas boxed in red are magnified in insets. (A) Ultrastructure of hair follicle in late telogen. Bulge (Bu) and HG cells are highlighted in green and pink, respectively. Dotted line denotes the presence of the basement membrane. Cp, companion layer contiguous to bulge cells. DP, dermal papilla; HS, hair shaft; Der, dermis. Boxed areas B and C are shown below at higher magnification.(B) Bulge cells display numerous desmosomes (De), especially in their attachment to the companion layer. Boxed area enlarged in inset, showing intercellular junctions rich in desmosomes. (C) Hair germ cells possess fewer desmosomes. Boxed area is magnified in inset, showing intercellular junctions with scarcity of desmosomes.

Figure S2. The Epithelial Strand of P41 Catagen HFs Contains Cells Resembling the HG Cells of P43 Telogen HFs.

(A) Ultrastructural analysis of a late catagen HF. The epithelial strand (EpStr) connects the dermal papilla (DP) with the bulge stem cells that surround the old (club) hair (Cb). The strand is composed of an ultrastructurally heterogeneous population of cells. Black dashed line denotes the dermo-epithelial border. Double headed-arrow in (A) indicates the thick glassy membrane, composed of the basal lamina and a thick layer of collagen fibers. (B-C) The boxed area in (A) is enlarged in (B) and depicts apoptotic (Ap) cells as well as cells (denoted by an asterisk) that resemble the early telogen cells of the HG, shown in (C). These cells display an electro-dense cytoplasm and few desmosomes and they are attached to the basal lamina. Epithelial strand cells denoted by the black diamonds in (B) have a lighter cytoplasm and appear ultrastructurally distinct from HG cells. (D) Additional examples of apoptotic cells (Ap) in the EpStr of a catagen follicle. (E) Semi-thin section stained with toluidine blue of an early telogen HF. Dashed line indicates the basal lamina between HG and DP. (F) Intercellular junctions of epithelial strand cells (upper frame) resembling HG cells (lower frame). Both cells show a paucity of desmosomes. (G) HG cells facing the dermal sheath (DS) exhibit an abundance of hemidesmosomes (Hd). (H) By contrast, epithelial strand cells are attached to a convoluted basal lamina (bl) with very scarce hemidesmosomes.

Figure S3. The Kinetic of Hair Germ Activation in the Second Telogen to Anagen Transition Are Slower Than in the First Transition.

(A) The catagen retracting EpStr contains some Pcad(+) cells that are also positive for Sox9 (green). Data are reported as average ± SD. (B) 1d sequential pulses with BrdU at the end of the 2nd telogen show that within 5d (P75), nearly all the cells in the HG are proliferative and have initiated new follicle downgrowths. (C) Bulge cells become activated in anagen III. 1d BrdU pulse during the telogen to anagen transition (figure 2K) reveal that the bulge (CD34 in red) gets largely activated (BrdU incorporation in green) during Anagen III. Nuclei are marked with DAPI (blue).

Figure S4. Colony Initiation Ability of Bulge Cells Catches Up to Hair Germ Cells Over Time. (A) Over time the total number of single cells attached to the plate diminished over time, and it did so differently between the three populations. (B) Hair germ, Bulge and total *K14-H2BGFP* skin cells (all cells) were kept in culture for 14 days, and the total numbers of GFP epifluorescent cells were counted using a FACS analyzer. Note that since HG colonies initiate faster than bulge cells, the total number of cells over the two weeks is still greater for HG cultures than bulge cultures. (C) Representative pictures of colonies under regular or GFP fluorescence-sensitive lighting. In all graphs data are reported as average± STDEV. Representative examples of each experiment were used and each experiment was done at least in triplicates.

Figure S5. Cell Isolation From Morphologically Uniform Hair Follicles

Back skin of *K14H2BGFP* mice was carefully inspected on the dissecting scope to monitor the morphology and cycling stages of the hair follicles. (A-C) From left to right pictures show progressively higher magnification views of telogen back skin. (D) Back skin during catagen to telogen transition. Catagen hair follicles are easily recognized because of the appearance of long hair follicles and they are eliminated from the preparation. (E) Similarly, anagen hair follicles can also be quickly spotted with this whole mount preparation method because of their enlarged hair germs (arrows). (F) Back skin hair follicles of *LefRFP1/K14H2BGFP* mice at telogen. DP is RFP(+); keratinocytes are GFP(+).

Figure S6. Two-Step Sample Preparation

Back skin of telogen *Lef1RFP/K14H2BGFP* mice was first treated with collagenase. The collagenase-digested mixture (Supernatant 1) was further mechanically dissociated, trypsinized and analyzed by FACS. Supernatant 1 is enriched with DP cells (RFP+) and has very few GFP(+) keratinocytes. DP cells were further isolated by FACS on the basis RFP^{+}GFP^{-}CD45^{-}CD117^{-}Itgα7^{-} marker combinations (see Supplemental Figure 7 and Supplemental Experimental Procedures for further details). After removal of Supernatant 1, the remaining skin is further treated with trypsin. The trypsin-digested mixture (Supernatant 2) contains a high percentage of GFP(+) cells and is enriched with HG and bulge cells. These cells are isolated as described in Figure 3.

Figure S7. Sorting Strategy and Purification Efficiency of Dermal Papilla Cells

(A) Immunofluorescence skin section of 2nd telogen phase back skin from mice expressing *K14H2BGFP/Lef1RFP.* Note that GFP marks the keratinocytes of the epidermis and ORS, while RFP marks the DP and arrector pili muscle. The arrector pili muscle is also positive for smooth muscle actin (SMA) and integrin α7 (Itgα7) whereas the DP is not (upper right). Alkaline Phosphatase (AP) marks both the DP and the arrector pili muscle (bottom right). (B) Total skin cells (all cells) were dissociated as described in Supplemental Figure 6 and then cytospun onto a slide. Both DP cells and arrector pili muscle cells are present in the preparation, as shown. DP cells were purified by FACS for $RFP^+GFP^-CD45^-CD117^-Itg\alpha7^-$. (C) mRNAs were isolated from purified DP cells and the purity of the isolation was monitored by cytospin and immunolabeling for specific markers. Known DP markers such as AP, NCAM and Hhip were enriched at the mRNA level in the DP cells as compared to the total cell preparation (minus DP), whereas SMA and integrin $\alpha7$ are not detected by RT PCR of the DP preparation (left). Cytospin analysis shows the absence of SMA(+) smooth muscle cells in the preparation whereas all cells within the DP prep are positive for AP (right). Data are reported as average ± SD.

Figure S8. Effect of Noggin, FGF7 and FGF10 on Telogen Follicle *in vivo.*

WT (A, B, D) or *K14H2BGFP* transgenic CD1 mice (C) whose follicles were in early telogen were injected with beads soaked with BSA (A) or with the growth factors indicated in the panels (B, C, D), as described in Figure 7 and in Experimental Procedures. (A) Intradermal injection of BSA showed no effect on the early telogen dormant HG (in red) (additional example in Figure 7). (B) Intradermal injection of FGF7 resulted in precocious activation of cell cycling (Ki67 in green) in the HG and an increase in HG cell number (see also Figure 7 for additional data). (C) Intradermal injection of the BMP inhibitor Noggin led to an increase HG (in red) cell number and further downgrowth of the hair follicle. This effect appeared to be more robust than that of FGF7, but both were substantially different than the control BSA. (D-E) Intradermal injection of FGF10 also can leads to precocious activation of HG cells (in red) and induces them to proliferate (Ki67 in green). The effects of FGF10 were dosage dependent.

Figure S9. Model Depicting Signals Regulating HF Niche Activation.

The HF stem cell niche is maintained in an inhibitory growth state via BMPs produced both by the Bulge (Bu) and the Dermal Papilla (DP) cells at the beginning of the resting phase. During telogen, DP cells progressively enhance their expression of BMP inhibitors and FGF7. A number of so-called canonical WNTs are expressed by the HG, and the non-canonical Wnt5a is expressed by the DP.

Although it is not known which of these WNTs are essential, overall stabilization of β-catenin towards the end of telogen is known to be critical in transitioning HFs from telogen to anagen. Our data suggest that together with WNT factors, BMP inhibition and FGF7 activation act in concert to activate MAP kinase and β-catenin pathway cascades in the HG, thereby stimulating its proliferation and initiating a new hair follicle growth.

SUPPLEMENTAL EXPERIMENTAL PROCEDURES

Electron Microscopy

Samples were fixed in 2% glutaraldehyde, 4% PFA, and 2 mM $CaCl_2$ in 0.05 M sodium cacodylate buffer, pH 7.2, at r.t. for >1 h, postfixed in 1% osmium tetroxide, and processed for Epon embedding. Ultrathin sections (60–70 nm) were counterstained with uranyl acetate and lead citrate. Images were taken with a transmission electron microscope (Tecnai G2-12; FEI) equipped with a digital camera (model XR60; Advanced Microscopy Techniques, Corp.)

Histology and Immunolabeling

All the skin samples were fixed with Formaldehyde for 10-15’ at RT and the dilutions used in this paper are indicated here: Ncam (Immunotech, rat 1:50), CD34 (eBioscience, rat 1:50), Pcadherin (Fuchs lab rat 1:50, R&D, goat 1:100), Ki67 (NovoCastra, rabbit 1:300), beta-catenin (Sigma, mouse 1:100), NFATc1 (SantaCruz, mouse 1:100), Sox9 (SantaCruz, rabbit 1:100), Tcf3, Lef1 (Fuchs lab 1:100), Lhx2 (T. Jessell, Columbia, NYC rabbit 1:2000), BrdU (Abcam, rat 1:200), p44/42 MAP kinase (Cell Signaling, rabbit 1:100), Wif1 (R&D, goat 1:50), Prominin (eBioscience, rat 1:50), βgal (Sigma, mouse 1:5000), Ecadherin (Fuchs lab, rat 1:20), CD104-integrin β4 (BD, rat 1:100), SMA (NeoMarkers, mouse 1:100). For LacZ and AP reactions skin and cytospin sections were fixed with 0.1% gluteraldehyde. For thelacZ reaction sections were exposed to Xgal solution, for AP to BCIP/NBT solution.

Isolation of bulge, HG and DP cells

Subcutaneous fat was removed from the skins with a scalpel and the whole skin was placed dermis down on a HBSS solution containing 0.2% collagenase (Sigma) for 30’ at 37C . The tissue after collagenase treatment was enriched in DP cells, which were gently removed with a scalpel. The remaining tissue, containing HGs and bulges, was then treated with Trypsin (GIBCO) at 37°C for 30 minutes.

The DP-enriched fraction was washed with PBS, centrifuged and trypsinized for 5 minutes at 37°C. Subsequently, the cells were filtered with strainers (70 µm, then 40µm pores; BD Biosciences). The remaining skin cell suspension was collected and filtered through strainers (70µm, then 40µm pores; BD Biosciences).

For FACS analyses, single cell suspensions in 2% FCS in PBS were exposed for 15 minutes at 4°C to the appropriate conjugated antibodies. DP cells isolated from *LefRFP/K14H2BGFP* mice are RFP(+) GFP(-) Cy5(-) as depleted of fibroblastic, endothelial, muscle and melanocytic cells with a cocktail of the following antibodies. Integrin α7 (Kramer lab, rat 1:100), Cy5 anti-rat (Jackson, 1:100), CD45-biotinylated (Pharmingen 1:100), CD117-biotinylated (Pharmingen 1:100), CD34-biotinylated (eBioscience 1:100), SA-Cy5 (Jackson, 1:100). Hair germs were isolated from *LefRFP/K14H2BGFP* mice as RFP(-) GFP(+)Pcad^{Hi} CD34^{Neg}. Bulges were isolated from LefRFP/K14H2BGFP mice as RFP(-)GFP(+) Pcad^{lo}, CD34(+). (Pcad Biotinylated Fuchs lab, 1:100; SA Pcad Blue Invitrogen, 1:100; CD34-Alexa647 eBioscience 1:75)

RNA isolation and microarray analyses

Total RNAs from FACS cells were purified using the Absolutely RNA Microprep kit (Stratagene, La Jolla, California, United States), and quantified (Nanodrop, United States). Quality was assessed by RNA 6000 Pico Assay (Agilent Technologies, Palo Alto, California, United States). Two rounds of amplification/labeling were performed on 20 nanogram to obtain biotinylated cRNA (MessageAmp aRNA kit; Ambion, Austin, Texas, United States), and 10 µg labeled cRNA was hybridized 45 °C, 16 h to mouse genome array MOE430A2.0 (Affymetrix, Santa Clara, California, United States). Processed chips were read by an argon-ion laser confocal scanner (Genomics Core Facility, Sloan Kettering Cancer Center, New York, New York, United States). Scanned microarray images were imported into Gene Chip Operating Software (GCOS, Affymetrix) to generate signal values and absent/present calls for each probe-set using the MAS 5.0 statistical expression algorithm (.chp files). Each array was scaled to a target signal of 500 using all probe-sets and default analysis parameters. Signature gene lists for isolated hair germ and bulge cells at all 3 time points were compiled containing probesets that are $\geq$ 2-fold increased or $\leq$ 2-fold decreased. For functional gene annotation probeset lists were uploaded to the "Database for Annotation, Visualization and Integrated Discovery" (DAVID 2008) Web tool. To systematically analyze the level of gene expression changes in the hair germ and bulge between early, middle and late telogen fold changes were calculated with GCOS for P56 vs. P43 and P69 vs. P43 and plotted in Origin8 as a histogram at a bin width of 10.

For overlap comparisons of the hair germ/bulge signatures with previously acquired embryonic hair germ (Rhee et al., 2006), adult anagen/telogen bulge (Blanpain et al., 2004) and hair matrix microarrays (Rendl et al., 2005) present/absent calls and signal values of all probesets were aligned in excel and percentages of shared genes in the signature lists were calculated. Comparisons with multiple different cell populations are not possible with a single set of animals/FACS analysis. When made with multiple datasets, absolute signals cannot be relied upon with accuracy, but the trends are meaningful and consistent with known expression patterns. As judged by these comparisons, we learned that the P69 HG is more similar to the activated (anagen phase) bulge than to the other cell populations, while the P43 HG shows less similarity. These data suggest that as the germ progresses through telogen, it begins to acquire features consistent with an activated stem cell.

Semi-quantitative RT-PCR and real-time PCR

All primer pairs were designed to work at the same settings for real-time PCR using the LightCycler System (Roche, Basel, Switzerland), LightCycler 3.5 software and the LightCycler DNA

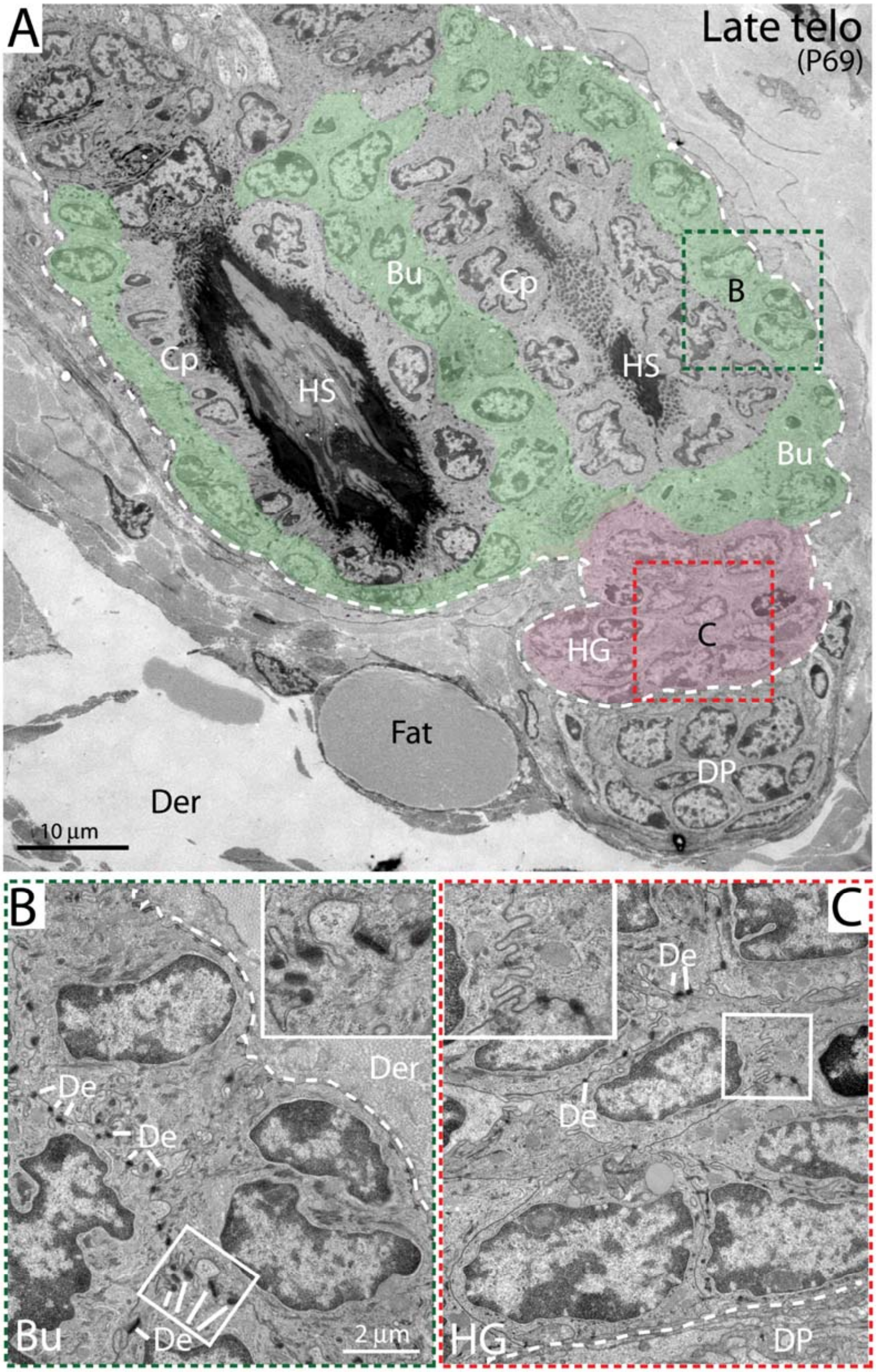
Master SYBR Green I reagents. Differences between samples and controls were calculated based on the 2-ΔΔCP method.

Total RNAs were purified from FACS-sorted cells as above, and after quantification with a NANO drop kit, equal amounts of RNAs were reverse transcribed using oligo(dT) primers (Superscript III First-Strand Synthesis System, Invitrogen). cDNAs were adjusted to equal levels by PCR amplification with primers to glyceraldehyde phosphate dehydrogenase (Gapdh). Real-time PCR amplification of genes of interest was performed using the LightCycler 480 (Roche) instrument and reagents. Differences between samples and controls were calculated based on the $2^{-\Delta\Delta CP}$ method and normalized to Gapdh (Rendl et al., 2008).

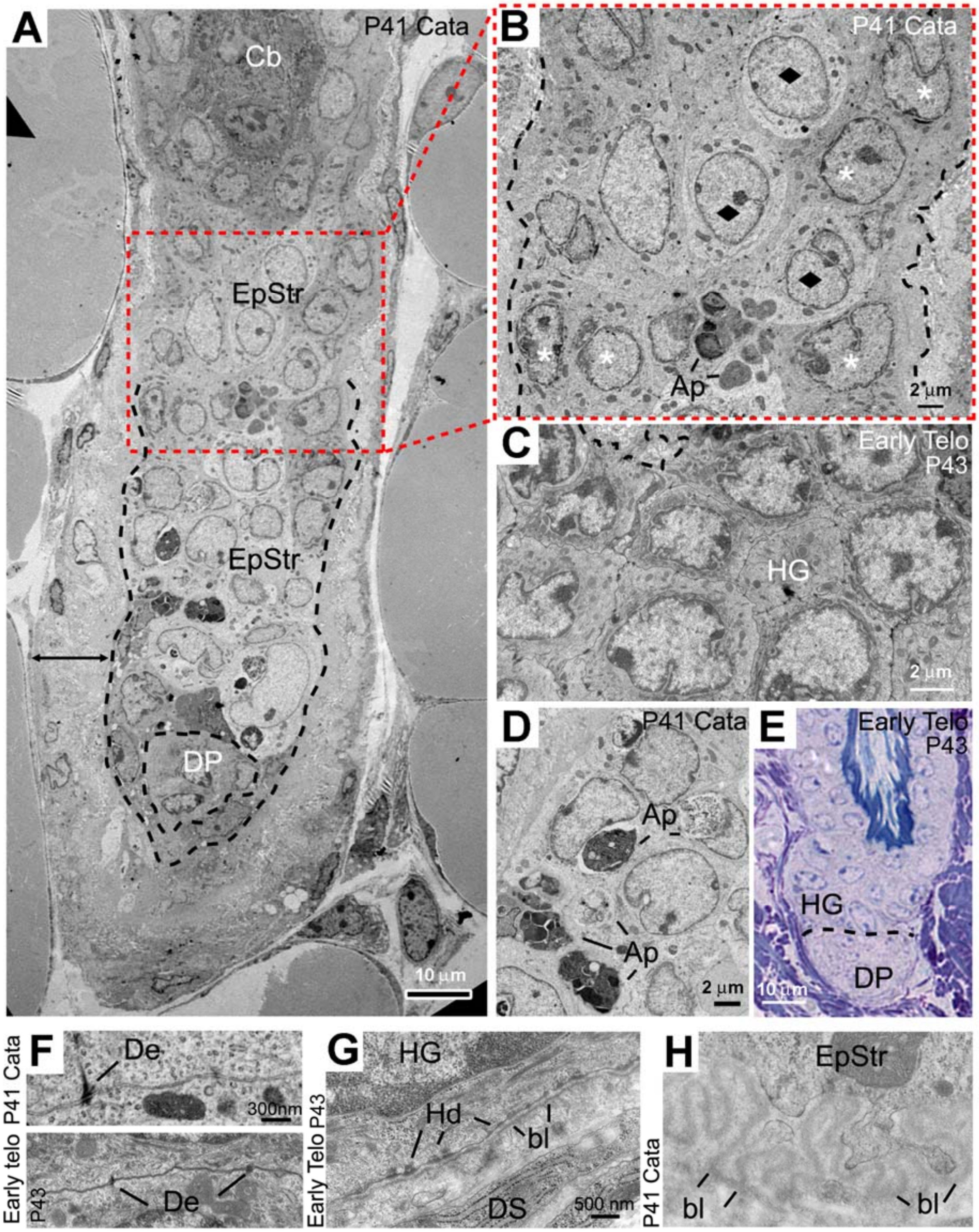
Growth Factor-Mediated Delivery Using Soaked Beads.

Intradermal protein solution injection: Recombinant human FGF7, FGF18, FGF10 and recombinant mouse Noggin were obtained from R&D Systems. Reconstitution of the proteins were performed in 0.1% BSA as per the manufacturer’s guidelines. For FGF7 dosage dependent assay 50μg/ml, 5μg/ml, or 0.5μg/ml of FGF7 were injected to the competent telogen back skin of adult mice using 30g syringe. For FGF10 dosage dependent assay 100μg/ml, 50μg/ml, or 5μg /ml of FGF10 were used. For noggin induced activation 0.5μg/ml noggin was used. To test the effect of FGF18, 100μg/ml of FGF18 was used. For beads injection: Affinity chromatography Affi-gel blue gel beads (Bio-Rad, Hercules, CA; 100 mm in Diameter) were washed in PBS. Then beads were re-suspended in equal volume of protein solution at 4°C for 30 min. Approximately 100 beads were introduced to the competent telogen skin of adult mice by means of a single puncture wound to the skin made by a 30 g syringe. To replenish proteins, subsequent doses of 10μl protein solution at respective concentration were microinjected to the site of the bead implantation every 24 h by means of a glass micro-needle until the tissue was harvested.

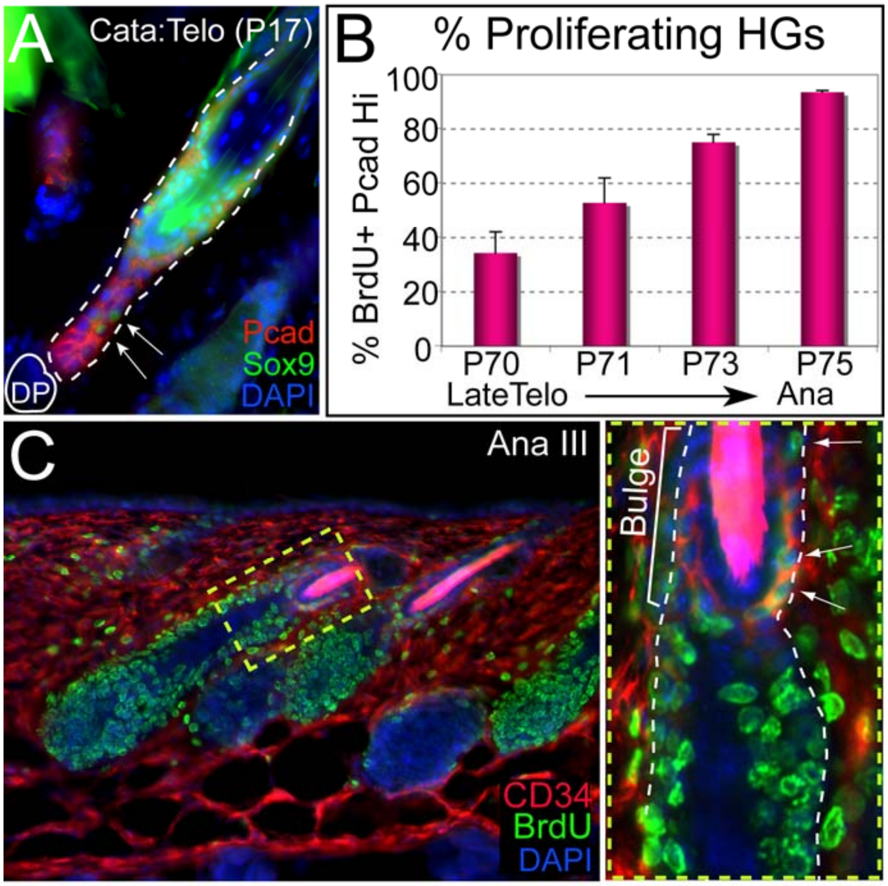
Supplemental Figure 1



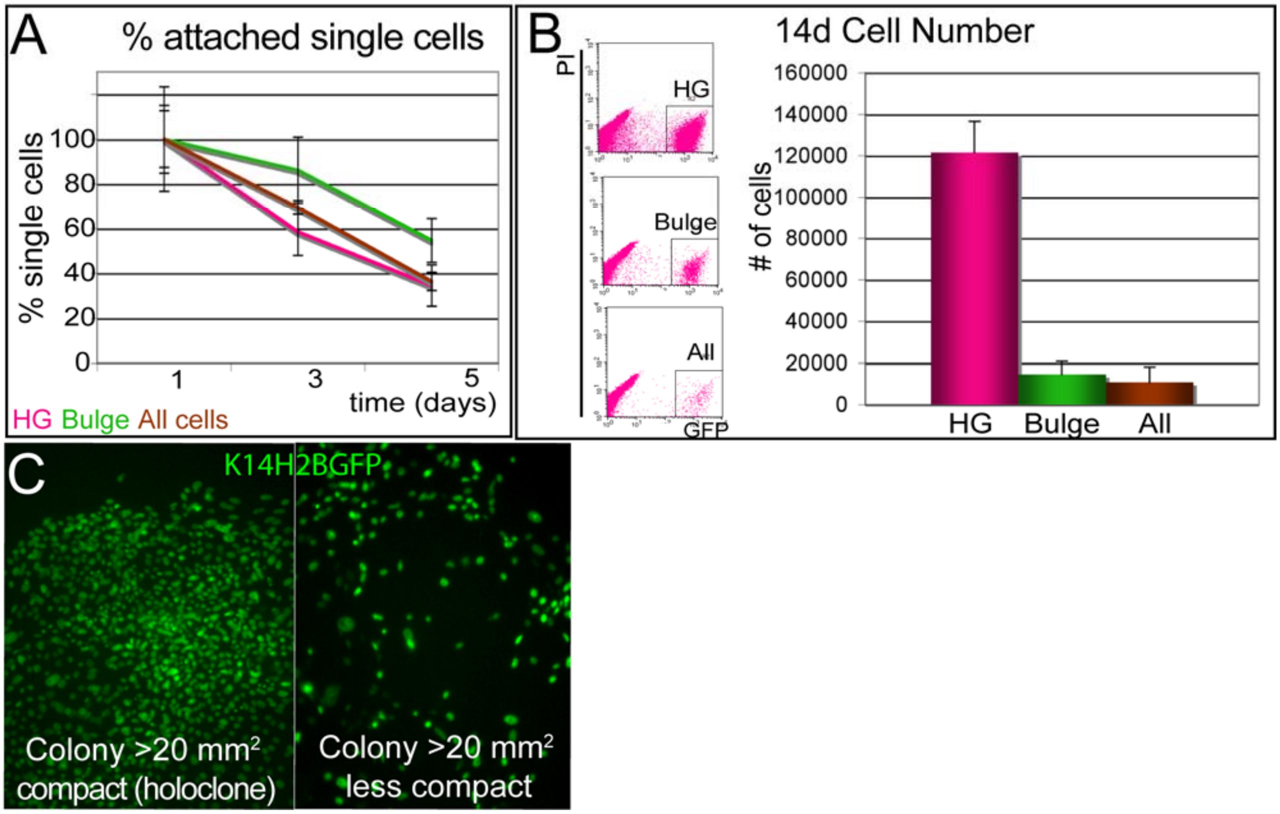
Supplemental Figure 2



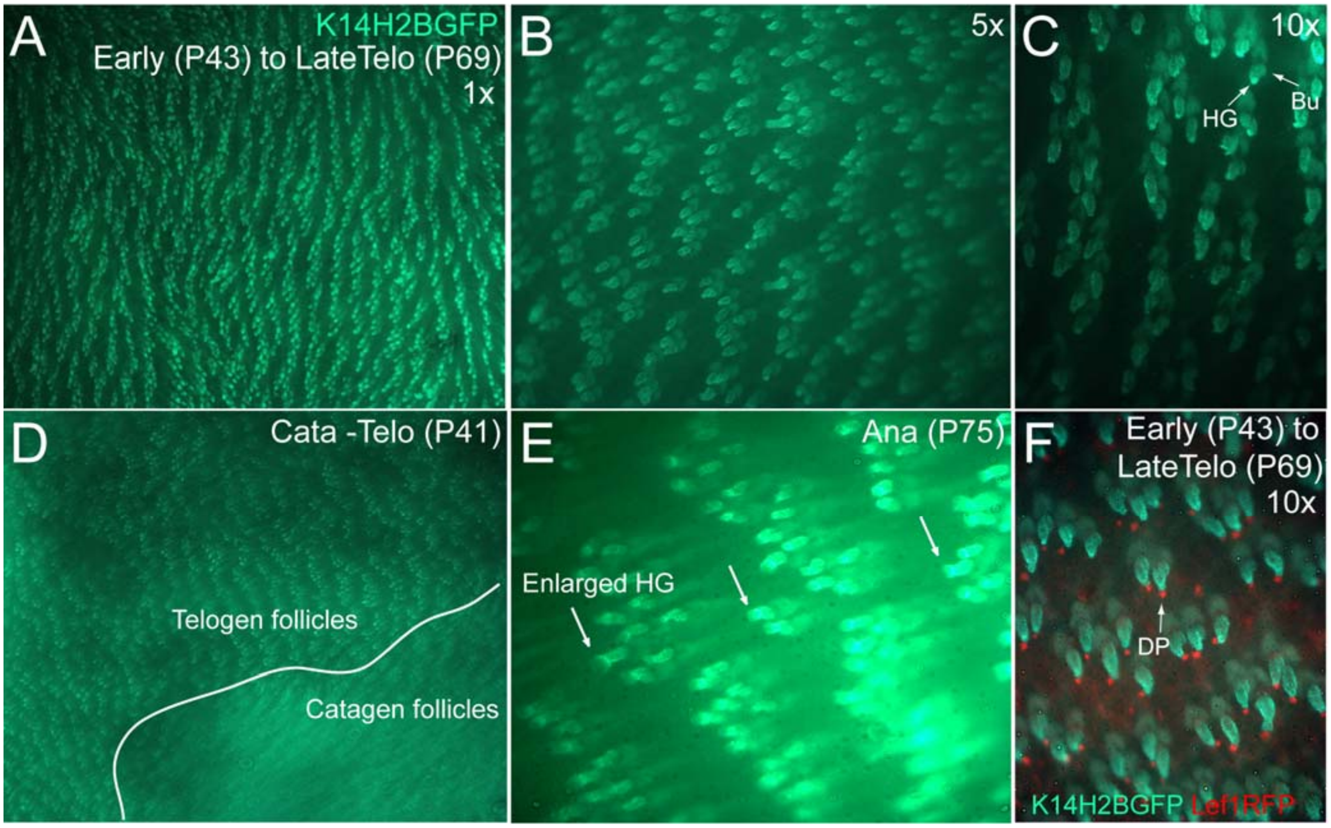
Supplemental Figure 3



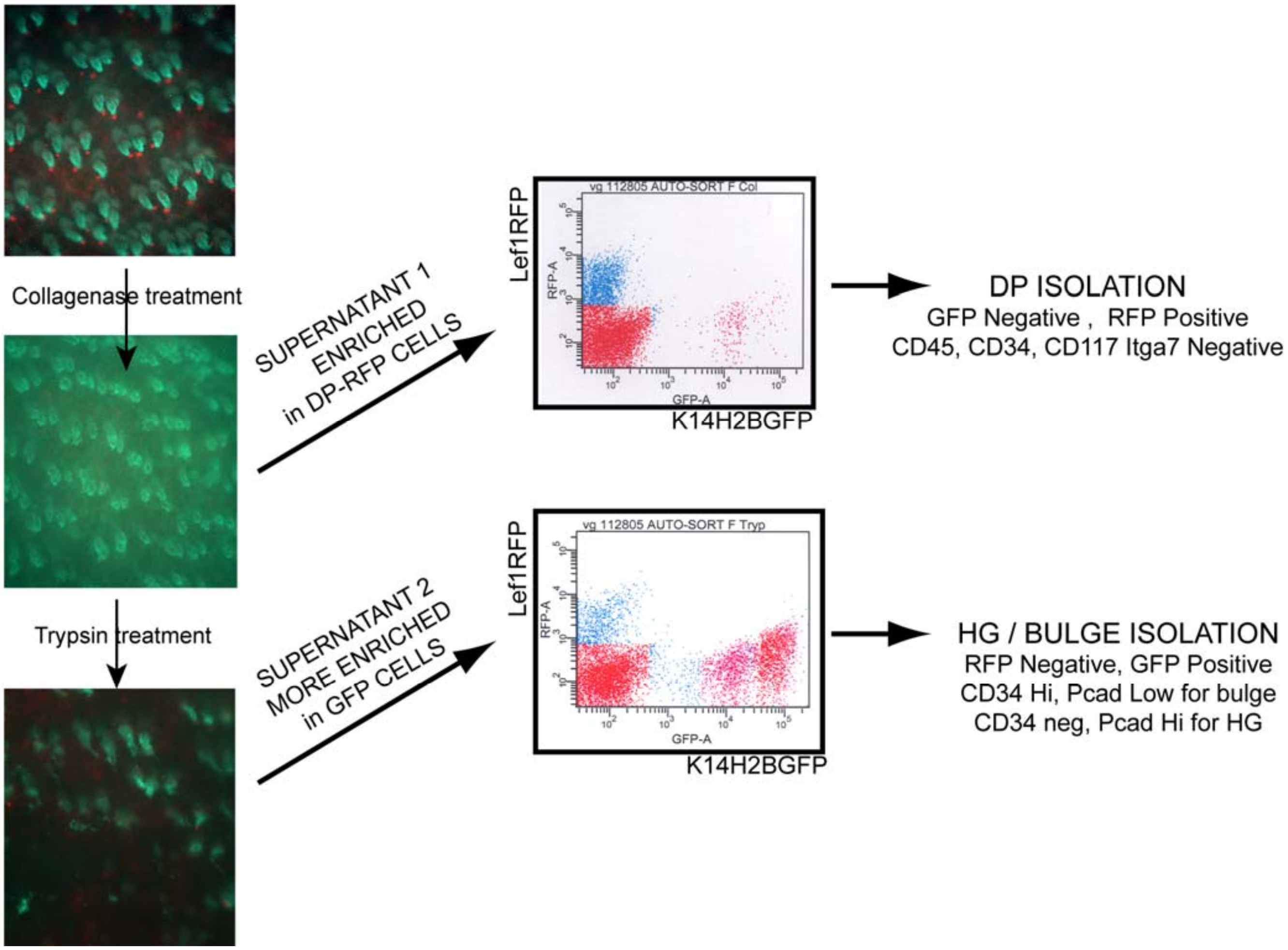
Supplementary Figure 4



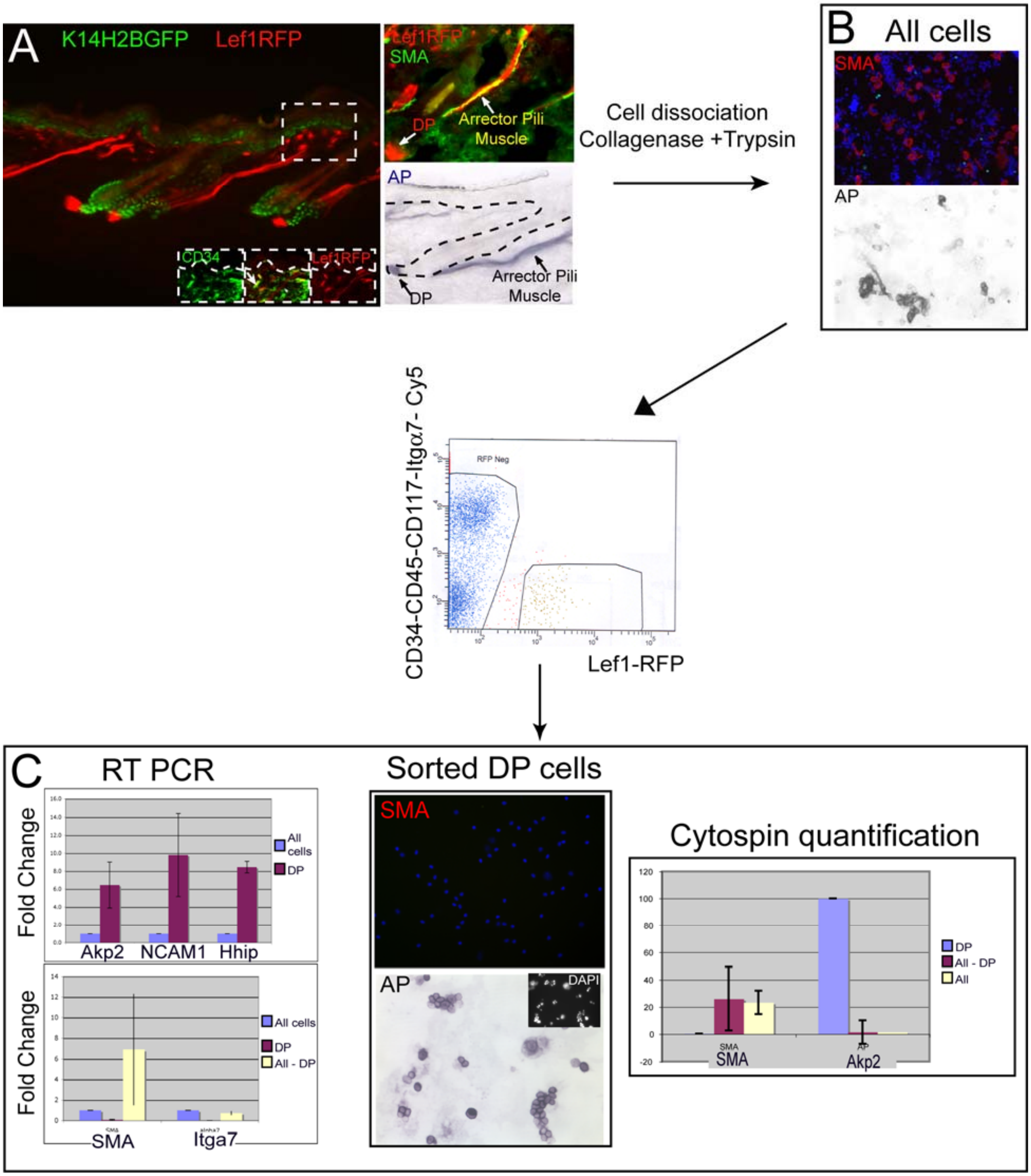
Supplemental Figure 5



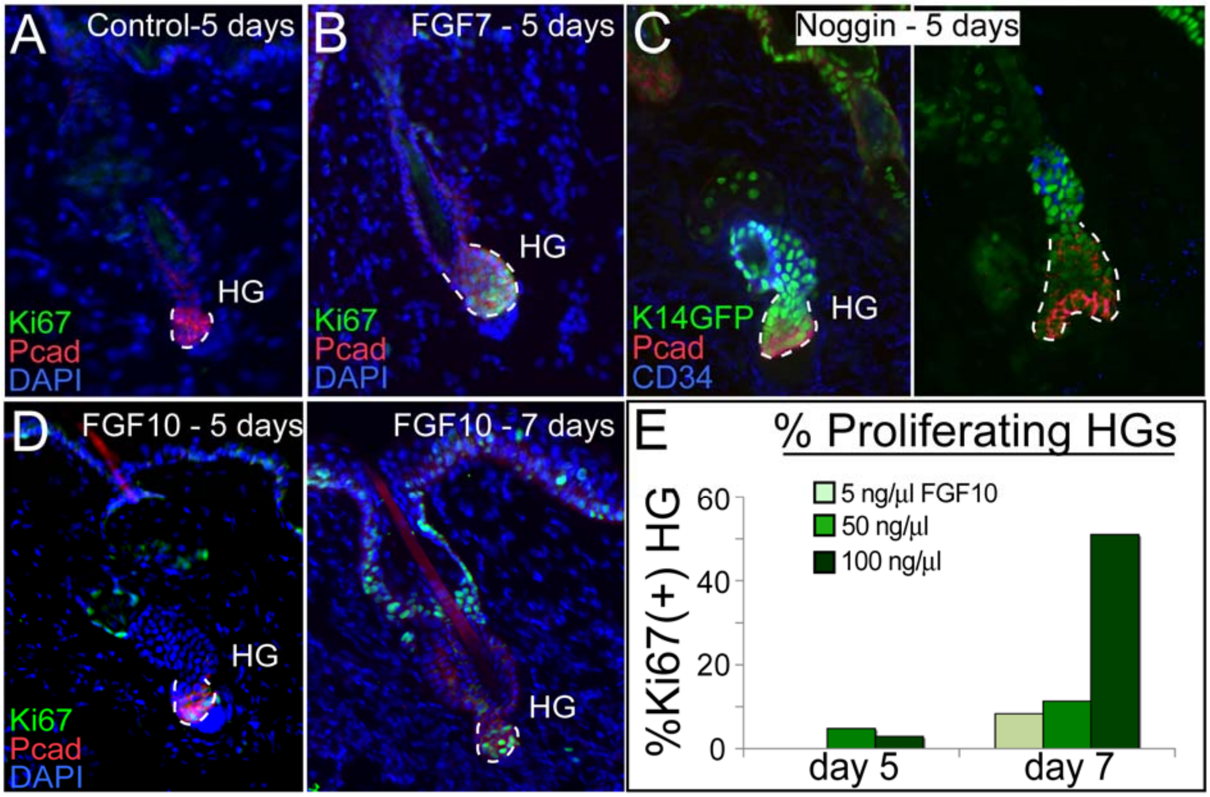
Supplementary Figure 6



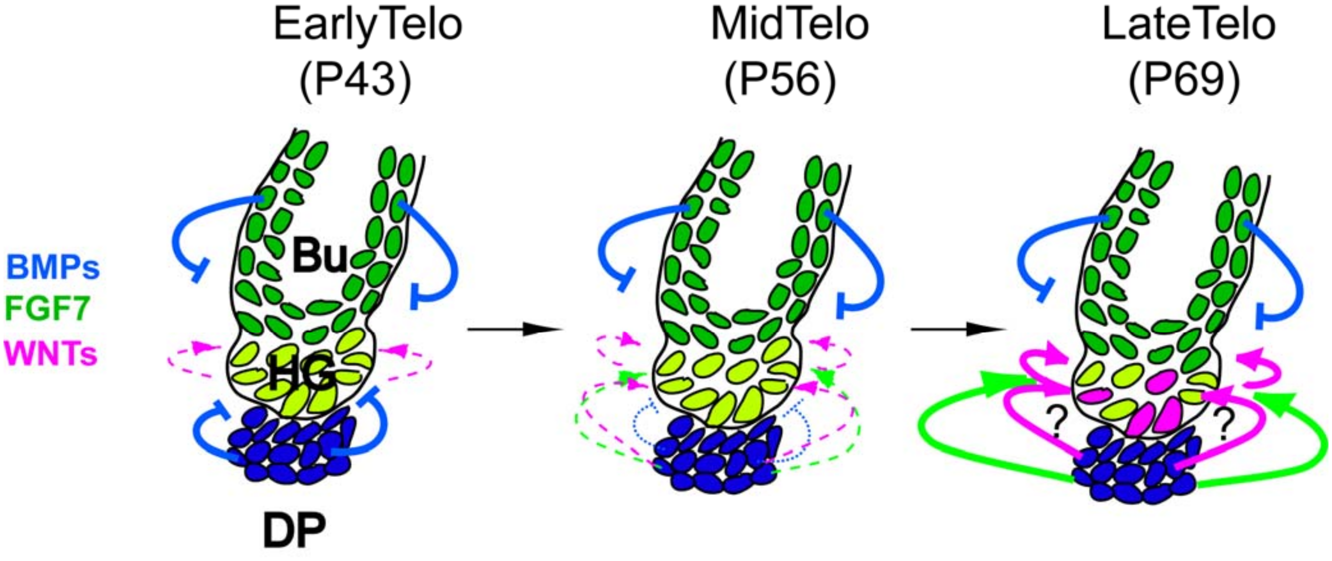
Supplementary Figure 7



Supplementary Figure 8



Model



Supplementary Table 1. Overlap between different bulge signatures.

Probe Set ID	Gene Title (annotation 03/19/2008)	Gene Symbol	Bulge vs HG	Bulge vs Epidermis/ORS
1444943_at	Transcribed locus	---	3.5	2.4
1455298_at	Transcribed locus	---	5.7	2.6
1451930_at	CDNA clone MGC:27981 IMAGE:3596365	---	2.3	2.7
1435221_at	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230341P20 product:inferred: forkhead box P1, full insert sequence	---	6.1	2.9
1438802_at	Transcribed locus	---	3.2	5.3
1449625_at	---	---	9.2	5.4
1455961_at	Transcribed locus	---	9.2	13.7
1448021_at	Transcribed locus	---	7.5	14.6
1456603_at	RIKEN cDNA 1500005K14 gene	1500005K14Rik	9.2	8.3
1436839_at	RIKEN cDNA 2010109K11 gene	2010109K11Rik	2.0	5.1
1449357_at	RIKEN cDNA 2310030G06 gene	2310030G06Rik	4.6	2.6
1420113_s_at	RIKEN cDNA 2410022L05 gene	2410022L05Rik	4.0	2.3
1451634_at	RIKEN cDNA 2810051F02 gene	2810051F02Rik	4.6	3.9
1423679_at	RIKEN cDNA 2810432L12 gene	2810432L12Rik	3.0	3.0
1428585_at	actinin, alpha 1	Actn1	6.1	4.1
1451932_a_at	ADAMTS-like 4	Adamtsl4	24.3	6.9
1420679_a_at	androgen-induced 1	Aig1	2.5	2.4
1418979_at	aldo-keto reductase family 1, member C14	Akr1c14	5.7	16.5
1423364_a_at	thymoma viral proto-oncogene 1 interacting protein	Aktip	2.8	2.3
1437767_s_at	thymoma viral proto-oncogene 1 interacting protein	Aktip	2.3	2.7
1426300_at	activated leukocyte cell adhesion molecule	Alcam	2.5	4.6
1451461_a_at	aldolase 3, C isoform	Aldoc	4.6	4.3
1454890_at	angiomotin	Amot	2.0	3.0
1455090_at	angiopoietin-like 2	Angptl2	4.9	3.6
1450627_at	progressive ankylosis	Ank	7.0	3.1
1430776_s_at	ankyrin repeat domain 24	Ankrd24	2.0	2.5
1435857_s_at	amyloid beta (A4) precursor-like protein 1	Aplp1	2.6	3.1
1421889_a_at	amyloid beta (A4) precursor-like protein 2	Aplp2	3.5	2.1
1432344_a_at	amyloid beta (A4) precursor-like protein 2	Aplp2	2.3	3.7
1420621_a_at	amyloid beta (A4) precursor protein	App	2.5	2.7
1426743_at	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2	Appl2	4.9	2.9

1450460_at	aquaporin 3	Aqp3	3.5	2.3
1422008_a_at	aquaporin 3	Aqp3	4.3	4.5
1418818_at	aquaporin 5 /// similar to aquaporin 5	Aqp5 /// LOC100046616	26.0	29.8
1451340_at	AT rich interactive domain 5A (Mrf1 like)	Arid5a	2.5	2.2
1415780_a_at	armadillo repeat containing, X-linked 2	Armcx2	2.8	4.2
1460359_at	armadillo repeat containing, X-linked 3 /// hypothetical protein LOC100044266	Armcx3 /// LOC100044266	2.8	2.5
1423061_at	armadillo repeat gene deleted in velo-cardio-facial syndrome	Arvcf	3.7	3.0
1448421_s_at	asporin	Aspn	19.7	4.8
1416652_at	asporin	Aspn	13.9	5.9
1448211_at	ATPase, H+ transporting, lysosomal V0 subunit E2	Atp6v0e2	7.0	8.1
1460294_at	ATPase, aminophospholipid transporter-like, class I, type 8A, member 2	Atp8a2	7.0	23.0
1420776_a_at	AU RNA binding protein/enoyl-coenzyme A hydratase	Auh	2.6	2.7
1424680_at	expressed sequence BB146404	BB146404	8.6	8.4
1434943_at	cDNA sequence BC023055	BC023055	2.3	2.7
1456005_a_at	BCL2-like 11 (apoptosis facilitator)	Bcl2l11	3.7	2.3
1422169_a_at	brain derived neurotrophic factor	Bdnf	42.2	5.6
1451780_at	B-cell linker	Blnk	5.7	3.8
1450759_at	bone morphogenetic protein 6	Bmp6	24.3	14.5
1426869_at	biregional cell adhesion molecule-related/down-regulated by oncogenes (Cdon) binding protein	Boc	3.0	4.0
1448687_at	C1q domain containing 2	C1qdc2	5.7	2.1
1439422_a_at	C1q domain containing 2	C1qdc2	2.6	2.6
1417393_a_at	C1q domain containing 2	C1qdc2	4.0	2.7
1455264_at	C1q domain containing 2	C1qdc2	5.3	2.9
1451620_at	C1q-like 3	C1ql3	274.4	25.4
1422815_at	complement component 9	C9	5.7	2.4
1421297_a_at	calcium channel, voltage-dependent, L type, alpha 1C subunit	Cacna1c	84.4	10.6
1417378_at	cell adhesion molecule 1	Cadm1	4.3	3.1
1417377_at	cell adhesion molecule 1	Cadm1	3.2	3.8
1417376_a_at	cell adhesion molecule 1	Cadm1	4.9	3.8
1424768_at	caldesmon 1	Cald1	5.7	4.3
1424770_at	caldesmon 1	Cald1	5.7	12.0
1424769_s_at	caldesmon 1	Cald1	7.5	12.0
1418608_at	calmodulin-like 3	Calml3	16.0	6.2
1450429_at	calpain 6	Capn6	4.0	2.7
1451398_at	carbonyl reductase 4 /// similar to carbonic reductase 4	Cbr4 /// LOC100046395	2.6	2.0

1424407_s_at	chromobox homolog 6	Cbx6	2.1	7.3
1419188_s_at	chemokine (C-C motif) ligand 27 /// similar to chemokine (C-C motif) ligand 27	Ccl27 /// LOC100039863 /// LOC100039939 /// LOC100040048	6.5	2.7
1430375_a_at	chemokine (C-C motif) ligand 27 /// similar to chemokine (C-C motif) ligand 27	Ccl27 /// LOC100039863 /// LOC100039939 /// LOC100040048	4.9	4.0
1416072_at	CD34 antigen	Cd34	4096.0	20.4
1422642_at	CDC42 effector protein (Rho GTPase binding) 3	Cdc42ep3	2.5	2.5
1450700_at	CDC42 effector protein (Rho GTPase binding) 3	Cdc42ep3	2.1	3.7
1449152_at	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	Cdkn2b	2.8	3.8
1423233_at	CCAAT/enhancer binding protein (C/EBP), delta	Cebpd	2.8	4.9
1427384_at	chromodomain helicase DNA binding protein 6	Chd6	2.6	2.6
1452207_at	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	Cited2	8.0	4.9
1448316_at	CKLF-like MARVEL transmembrane domain containing 3 /// similar to CKLF-like MARVEL transmembrane domain containing 3	Cmtm3 /// LOC100046883	2.6	8.6
1427964_at	CKLF-like MARVEL transmembrane domain containing 8	Cmtm8	4.0	2.8
1455494_at	collagen, type I, alpha 1	Col1a1	2.3	4.9
1450857_a_at	collagen, type I, alpha 2	Col1a2	3.7	8.1
1423110_at	collagen, type I, alpha 2	Col1a2	4.0	37.5
1427884_at	collagen, type III, alpha 1	Col3a1	6.1	6.7
1427883_a_at	collagen, type III, alpha 1	Col3a1	3.7	36.6
1424051_at	collagen, type IV, alpha 2	Col4a2	2.1	3.4
1450625_at	collagen, type V, alpha 2	Col5a2	9.8	8.7
1422437_at	collagen, type V, alpha 2	Col5a2	5.7	11.5
1448590_at	collagen, type VI, alpha 1	Col6a1	17.1	6.7
1452250_a_at	collagen, type VI, alpha 2	Col6a2	29.9	17.9
1460693_a_at	collagen, type IX, alpha 3	Col9a3	42.2	77.7
1418455_at	coatomer protein complex, subunit zeta 2	Copz2	2.6	2.8
1424218_a_at	cAMP responsive element binding protein 3-like 4	Creb3l4	5.7	7.1
1416326_at	cysteine-rich protein 1 (intestinal)	Crip1	3.2	5.6
1423353_at	cysteine-rich secretory protein LCCL domain containing 1	Crispld1	2.6	2.8
1416455_a_at	crystallin, alpha B	Cryab	52.0	5.7
1434369_a_at	crystallin, alpha B	Cryab	11.3	9.8
1423341_at	chondroitin sulfate proteoglycan 4	Cspg4	2.1	5.6
1416953_at	connective tissue growth factor	Ctgf	7.0	9.5

1451019_at	cathepsin F	Ctsf	4.3	2.7
1417868_a_at	cathepsin Z	Ctsz	2.3	3.2
1418456_a_at	chemokine (C-X-C motif) ligand 14	Cxcl14	4.6	3.1
1418457_at	chemokine (C-X-C motif) ligand 14	Cxcl14	7.0	5.0
1454268_a_at	cytochrome b-245, alpha polypeptide	Cyba	2.8	23.7
1422257_s_at	cytochrome P450, family 2, subfamily b, polypeptide 10	Cyp2b10	3.0	3.7
1425645_s_at	cytochrome P450, family 2, subfamily b, polypeptide 10	Cyp2b10	3.0	3.9
1451787_at	cytochrome P450, family 2, subfamily b, polypeptide 10	Cyp2b10	4.0	4.2
1419040_at	cytochrome P450, family 2, subfamily d, polypeptide 22	Cyp2d22	3.2	6.4
1450839_at	DNA segment, human D4S114	D0H4S114	21.1	5.9
1456481_at	DNA segment, Chr 9, ERATO Doi 280, expressed	D9Ertd280e	3.7	3.9
1423805_at	disabled homolog 2 (Drosophila)	Dab2	8.0	3.8
1420498_a_at	disabled homolog 2 (Drosophila)	Dab2	14.9	16.4
1423790_at	death-associated protein	Dap	3.5	3.2
1451112_s_at	death-associated protein	Dap	2.5	3.8
1451453_at	death-associated kinase 2	Dapk2	6.5	3.9
1450863_a_at	doublecortin-like kinase 1	Dclk1	9.2	5.1
1424271_at	doublecortin-like kinase 1	Dclk1	19.7	8.3
1451289_at	doublecortin-like kinase 1	Dclk1	207.9	10.2
1439332_at	DNA-damage-inducible transcript 4-like	Ddit4l	4.6	5.6
1423346_at	degenerative spermatocyte homolog 1 (Drosophila)	Degs1	2.8	2.1
1417312_at	dickkopf homolog 3 (Xenopus laevis)	Dkk3	3.7	13.4
1448669_at	dickkopf homolog 3 (Xenopus laevis)	Dkk3	3.0	14.4
1427411_s_at	deleted in lymphocytic leukemia, 2	Dleu2	2.6	2.1
1427410_at	deleted in lymphocytic leukemia, 2	Dleu2	2.8	2.8
1426465_at	discs, large homolog-associated protein 4 (Drosophila)	Dlgap4	3.2	4.0
1449863_a_at	distal-less homeobox 5	Dlx5	2.8	2.1
1417307_at	dystrophin, muscular dystrophy	Dmd	2.5	2.8
1448665_at	dystrophin, muscular dystrophy	Dmd	3.0	2.9
1434944_at	dystrophia myotonica-protein kinase	Dmpk	3.5	8.5
1434196_at	DnaJ (Hsp40) homolog, subfamily A, member 4 /// similar to DnaJ (Hsp40) homolog, subfamily A, member 4	Dnaja4 /// LOC100048331	2.8	4.4
1460372_at	dual oxidase maturation factor 1	Duoxa1	3.0	7.0
1431422_a_at	dual specificity phosphatase 14	Dusp14	4.6	2.1
1427318_s_at	dysferlin /// fer-1-like 3, myoferlin (C. elegans)	Dysf /// Fer1l3	3.0	2.8
1448613_at	extracellular matrix protein 1	Ecm1	5.3	5.7
1418723_at	endothelial differentiation, lysophosphatidic acid G-protein-	Edg7	2.5	3.3

	coupled receptor 7			
1449365_at	endothelial differentiation, sphingolipid G-protein-coupled receptor, 8	Edg8	3.7	2.4
1427367_at	EF-hand calcium binding domain 4A	Efcab4a	5.3	4.3
1422302_s_at	ferritin light chain 1 /// ferritin light chain 2 /// ferritin light chain 1 pseudogene /// predicted gene, EG665937	EG665937 /// Ftl1 /// Ftl2 /// mCG_17237	6.5	3.0
1419332_at	EGF-like-domain, multiple 6	Egfl6	8.0	5.5
1421883_at	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	Elavl2	4.9	17.5
1415856_at	embigin	Emb	2.1	2.5
1417104_at	epithelial membrane protein 3	Emp3	3.7	2.8
1424801_at	enabled homolog (Drosophila)	Enah	2.8	3.0
1450061_at	ectodermal-neural cortex 1	Enc1	5.7	7.4
1420965_a_at	ectodermal-neural cortex 1	Enc1	9.8	10.1
1419276_at	ectonucleotide pyrophosphatase/phosphodiesterase 1	Enpp1	2.5	3.3
1427807_at	predicted gene, ENSMUSG00000060559	ENSMUSG00000060559	2.8	2.2
1450380_at	ependymin related protein 1 (zebrafish)	Epdr1	8.0	9.8
1422438_at	epoxide hydrolase 1, microsomal	Ephx1	2.0	3.0
1422824_s_at	epidermal growth factor receptor pathway substrate 8	Eps8	6.5	6.3
1422823_at	epidermal growth factor receptor pathway substrate 8 /// similar to Epidermal growth factor receptor kinase substrate 8	Eps8 /// LOC632638	7.0	4.2
1452280_at	FERM, RhoGEF (Arhgef) and pleckstrin domain protein 1 (chondrocyte-derived) /// similar to FERMRhoGEF (Arhgef) and pleckstrin domain protein 1	Farp1 /// LOC100045542	16.0	6.0
1451119_a_at	fibulin 1	Fbln1	2.0	4.3
1422831_at	fibrillin 2	Fbn2	18.4	5.9
1427155_at	FCH and double SH3 domains 1	Fchsd1	2.5	3.5
1434180_at	fermitin family homolog 2 (Drosophila)	Fermt2	4.3	4.4
1456014_s_at	fermitin family homolog 3 (Drosophila)	Fermt3	18.4	2.6
1450869_at	fibroblast growth factor 1	Fgf1	2.8	2.6
1423136_at	fibroblast growth factor 1	Fgf1	5.7	4.6
1449545_at	fibroblast growth factor 18	Fgf18	548.7	6.5
1417872_at	four and a half LIM domains 1	Fhl1	9.8	3.1
1426750_at	filamin, beta	Flnb	6.5	5.9
1419485_at	forkhead box C1	Foxc1	9.8	3.6

1419486_at	forkhead box C1	Foxc1	8.0	3.9
1455242_at	forkhead box P1	Foxp1	7.5	2.4
1435222_at	forkhead box P1	Foxp1	4.6	2.5
1421141_a_at	forkhead box P1	Foxp1	4.9	2.9
1421140_a_at	forkhead box P1	Foxp1	4.9	3.1
1421142_s_at	forkhead box P1	Foxp1	5.3	3.6
1421365_at	follistatin	Fst	3.5	3.7
1448259_at	follistatin-like 1	Fstl1	7.5	15.1
1416221_at	follistatin-like 1	Fstl1	6.1	17.6
1418364_a_at	ferritin light chain 1	Ftl1	5.3	3.2
1418532_at	frizzled homolog 2 (Drosophila)	Fzd2	11.3	5.5
1418533_s_at	frizzled homolog 2 (Drosophila)	Fzd2	7.0	8.4
1418534_at	frizzled homolog 2 (Drosophila)	Fzd2	8.0	15.7
1449730_s_at	frizzled homolog 3 (Drosophila)	Fzd3	3.7	2.7
1450135_at	frizzled homolog 3 (Drosophila)	Fzd3	4.0	4.9
1450044_at	frizzled homolog 7 (Drosophila)	Fzd7	8.6	3.4
1416419_s_at	gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1	Gabarapl1	2.0	2.1
1424007_at	growth differentiation factor 10	Gdf10	59.7	28.6
1424076_at	glycerophosphodiester phosphodiesterase domain containing 1	Gdpd1	39.4	2.4
1417594_at	G kinase anchoring protein 1	Gkap1	4.3	2.6
1422504_at	glycine receptor, beta subunit	Glrb	7.0	3.7
1419316_s_at	guanine nucleotide binding protein (G protein), beta polypeptide 1-like /// similar to mKIAA1645 protein	Gnb1l /// LOC100044103	2.5	4.0
1419689_at	glypican 6 /// similar to Glypican 6	Gpc6 /// LOC100045283	4.9	3.5
1419688_at	glypican 6 /// similar to Glypican 6	Gpc6 /// LOC100045283	9.8	4.4
1426462_at	gephyrin	Gphn	4.6	3.2
1426463_at	gephyrin	Gphn	4.0	3.4
1423091_a_at	glycoprotein m6b	Gpm6b	2.3	5.0
1450881_s_at	G protein-coupled receptor 137B	Gpr137b	2.5	2.2
1439255_s_at	G protein-coupled receptor 137B /// G protein-coupled receptor 137B, pseudogene /// similar to Gpr137b protein	Gpr137b /// Gpr137b-ps /// LOC100044979	4.6	2.3
1417673_at	growth factor receptor bound protein 14	Grb14	8.6	3.0
1425357_a_at	gremlin 1	Grem1	9.2	19.7
1427676_a_at	glutamate receptor, ionotropic, kainate 1	Grik1	32.0	4.8
1421350_a_at	glutamate receptor interacting protein 1	Grip1	8.0	2.8
1435951_at	glutamate receptor interacting protein 1	Grip1	6.5	4.9

1415812_at	gelsolin	Gsn	2.5	2.8
1449169_at	hyaluronan synthase 2	Has2	3.7	4.0
1449024_a_at	hexosaminidase A	Hexa	2.8	5.6
1460180_at	hexosaminidase B	Hexb	8.6	4.3
1437874_s_at	hexosaminidase B	Hexb	4.9	9.4
1415999_at	hairy/enhancer-of-split related with YRPW motif 1	Hey1	13.9	30.5
1421426_at	Hedgehog-interacting protein	Hhip	26.0	3.8
1422155_at	histone cluster 2, H3c2	Hist2h3c2	5.7	3.4
1450780_s_at	high mobility group AT-hook 2	Hmga2	2.6	2.3
1424367_a_at	homer homolog 2 (Drosophila)	Homer2	10.6	6.7
1451776_s_at	HOP homeobox	Hopx	4.6	2.2
1455626_at	homeo box A9	Hoxa9	3.5	2.3
1418415_at	homeo box B5	Hoxb5	3.0	4.3
1451660_a_at	homeo box B6	Hoxb6	6.1	2.4
1452412_at	homeo box C8	Hoxc8	2.1	2.3
1431099_at	homeo box D8	Hoxd8	27.9	7.4
1419126_at	homeo box D9	Hoxd9	26.0	6.8
1448812_at	hippocalcin-like 1	Hpcal1	3.2	2.6
1419905_s_at	hydroxyprostaglandin dehydrogenase 15 (NAD)	Hpgd	3.7	4.5
1434642_at	hydroxysteroid (17-beta) dehydrogenase 11	Hsd17b11	8.6	3.0
1449010_at	heat shock protein 4 like	Hspa4l	2.1	2.4
1417013_at	heat shock protein 8	Hspb8	2.5	2.3
1453596_at	inhibitor of DNA binding 2	Id2	3.5	8.5
1422537_a_at	inhibitor of DNA binding 2	Id2	48.5	8.9
1435176_a_at	inhibitor of DNA binding 2	Id2	5.3	9.6
1416630_at	inhibitor of DNA binding 3	Id3	4.6	3.7
1423260_at	inhibitor of DNA binding 4 /// similar to Id4	Id4 /// LOC100045546	2.1	2.6
1423259_at	inhibitor of DNA binding 4 /// similar to Id4	Id4 /// LOC100045546	3.0	3.3
1450048_a_at	isocitrate dehydrogenase 2 (NADP+), mitochondrial	Idh2	2.1	2.0
1419647_a_at	immediate early response 3	Ier3	2.1	3.1
1418929_at	intraflagellar transport 57 homolog (Chlamydomonas)	Ift57	8.6	8.7
1419286_s_at	intraflagellar transport 81 homolog (Chlamydomonas)	Ift81	2.8	4.0
1452114_s_at	insulin-like growth factor binding protein 5	Igfbp5	7.0	5.8
1417505_s_at	interleukin 11 receptor, alpha chain 1 /// interleukin 11 receptor, alpha chain 2 /// similar to interleukin 11 receptor, alpha chain 2	Il11ra1 /// Il11ra2 /// LOC100038993	3.5	2.3
1451535_at	interleukin 31 receptor A	Il31ra	7.0	13.3
1423274_at	integrator complex subunit 6	Ints6	2.8	2.9

1452327_at	IQ motif and Sec7 domain 1	Iqsec1	2.5	3.2
1423608_at	integral membrane protein 2A	Itm2a	2.8	11.7
1450350_a_at	Jun dimerization protein 2	Jundm2	2.3	3.2
1449158_at	potassium channel, subfamily K, member 2	Kcnk2	29.9	15.4
1424848_at	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	Kcnma1	17.1	3.1
1422945_a_at	kinesin family member 5C	Kif5c	9.8	9.9
1460678_at	kelch domain containing 2	Klhdc2	4.6	2.0
1435086_s_at	kelch domain containing 2	Klhdc2	3.7	2.3
1426481_at	kelch-like 22 (Drosophila)	Klhl22	2.1	5.5
1427378_at	keratin 75	Krt75	24.3	3.1
1419619_at	keratin 80	Krt80	3.0	2.2
1419573_a_at	lectin, galactose binding, soluble 1	Lgals1	3.5	3.9
1455439_a_at	lectin, galactose binding, soluble 1	Lgals1	3.7	5.4
1424594_at	lectin, galactose binding, soluble 7	Lgals7	3.5	5.2
1450988_at	leucine rich repeat containing G protein coupled receptor 5	Lgr5	4.6	13.4
1418317_at	LIM homeobox protein 2	Lhx2	6.5	12.9
1418478_at	LIM domain only 1	Lmo1	3.2	3.3
1455056_at	LIM domain only 7	Lmo7	3.0	3.2
1425779_a_at	T-box 1 /// similar to T-box 1	LOC100044104 /// Tbx1	4.9	8.5
1419717_at	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E /// hypothetical protein LOC100044162	LOC100044162 /// Sema3e	16.0	7.5
1417580_s_at	selenium binding protein 1 /// hypothetical protein LOC100044204	LOC100044204 /// Selenbp1	4.9	3.3
1450699_at	selenium binding protein 1 /// hypothetical protein LOC100044204	LOC100044204 /// Selenbp1	7.0	3.4
1450928_at	similar to Id4	LOC100045546	2.6	4.4
1456140_at	similar to OPR	LOC100045988	274.4	2.5
1420401_a_at	receptor (calcitonin) activity modifying protein 3 /// similar to receptor activity modifying protein 3	LOC100046186 /// Ramp3	2.8	2.6
1418932_at	nuclear factor, interleukin 3, regulated /// similar to NFIL3/E4BP4 transcription factor	LOC100046232 /// Nfil3	3.7	9.6
1421998_at	torsin family 3, member A /// similar to ADIR1	LOC100047963 /// Tor3a	2.6	2.3
1418505_at	nudix (nucleoside diphosphate linked moiety X)-type motif 4 /// similar to Nudt4 protein	LOC100048122 /// Nudt4	5.3	3.2
1424460_s_at	lysophosphatidylcholine acyltransferase 1	Lpcat1	4.3	3.2
1433842_at	leucine rich repeat (in FLII) interacting protein 1	Lrrfip1	2.3	2.5

1437477_at	leucine rich repeat (in FLII) interacting protein 1	Lrrfip1	3.5	2.5
1418061_at	latent transforming growth factor beta binding protein 2	Ltbp2	19.7	18.4
1438312_s_at	latent transforming growth factor beta binding protein 3	Ltbp3	2.5	3.3
1418049_at	latent transforming growth factor beta binding protein 3	Ltbp3	2.8	3.6
1451490_at	lysophospholipase-like 1	Lyplal1	4.6	3.9
1460335_at	LysM, putative peptidoglycan-binding, domain containing 3	Lysmd3	2.3	2.2
1428847_a_at	microtubule-actin crosslinking factor 1	Macf1	3.2	3.2
1423284_at	MANSC domain containing 1	Mansc1	9.2	6.0
1449630_s_at	MAP/microtubule affinity-regulating kinase 1	Mark1	21.1	3.2
1452864_at	mediator of RNA polymerase II transcription, subunit 12 homolog (yeast)-like	Med12l	24.3	2.8
1420911_a_at	milk fat globule-EGF factor 8 protein	Mfge8	6.5	8.3
1422025_at	microphthalmia-associated transcription factor	Mitf	3.2	4.2
1455214_at	microphthalmia-associated transcription factor	Mitf	5.3	7.6
1428835_at	myosin, heavy polypeptide 14	Myh14	6.5	2.6
1450468_at	myocilin	Myoc	9.8	12.8
1448428_at	neuroblastoma, suppression of tumorigenicity 1	Nbl1	2.5	3.2
1420760_s_at	N-myc downstream regulated gene 1	Ndrg1	4.6	3.0
1450976_at	N-myc downstream regulated gene 1	Ndrg1	5.3	3.4
1423413_at	N-myc downstream regulated gene 1	Ndrg1	2.6	4.8
1448154_at	N-myc downstream regulated gene 2	Ndrg2	5.3	3.0
1436188_a_at	N-myc downstream regulated gene 4	Ndrg4	2.3	3.2
1426615_s_at	N-myc downstream regulated gene 4	Ndrg4	2.0	3.4
1418947_at	NIMA (never in mitosis gene a)-related expressed kinase 3	Nek3	5.3	3.7
1417879_at	neuron derived neurotrophic factor	Nenf	4.3	2.1
1425761_a_at	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	Nfatc1	3.7	2.3
1417621_at	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	Nfatc1	9.2	2.4
1416473_a_at	neighbor of Punc E11	Nope	39.4	9.0
1416474_at	neighbor of Punc E11	Nope	34.3	11.7
1434877_at	neuronal pentraxin 1	Nptx1	7.0	3.3
1448758_at	nuclear receptor binding factor 2	Nrbf2	2.5	2.5
1434709_at	neuron-glia-CAM-related cell adhesion molecule	Nrcam	17.1	7.5
1424882_a_at	5'-nucleotidase domain containing 2	Nt5dc2	2.1	4.9

1426887_at	nudix (nucleoside diphosphate linked moiety X)-type motif 11	Nudt11	12.1	3.2
1420718_at	odd Oz/ten-m homolog 2 (Drosophila)	Odz2	3.2	4.8
1419108_at	oligophrenin 1	Ophn1	3.5	2.4
1427228_at	palladin, cytoskeletal associated protein	Palld	2.6	3.5
1426910_at	PRKC, apoptosis, WT1, regulator	Pawr	2.3	2.5
1418713_at	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 1	Pcbd1	4.6	2.8
1417526_at	poly(rC) binding protein 3	Pcbp3	3.7	3.0
1449178_at	PDZ and LIM domain 3	Pdlim3	157.6	14.3
1417689_a_at	PDZK1 interacting protein 1	Pdzk1ip1	4.6	2.4
1455477_s_at	PDZK1 interacting protein 1	Pdzk1ip1	3.7	2.7
1416846_a_at	PDZ domain containing RING finger 3	Pdzrn3	13.9	5.9
1417355_at	paternally expressed 3	Peg3	11.3	2.6
1433924_at	Paternally expressed 3	Peg3	14.9	8.9
1418209_a_at	profilin 2	Pfn2	9.8	4.1
1418210_at	profilin 2	Pfn2	9.8	5.5
1437062_s_at	phytanoyl-CoA hydroxylase interacting protein-like	Phyhipl	4.3	7.8
1420411_a_at	phosphatidylinositol 4-kinase type 2 beta	Pi4k2b	2.3	3.0
1416489_at	phosphatidylinositol 4-kinase type 2 beta	Pi4k2b	2.5	3.6
1425514_at	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)	Pik3r1	7.0	3.3
1460210_at	polycystic kidney disease 1 homolog	Pkd1	3.0	5.8
1417753_at	polycystic kidney disease 2	Pkd2	2.0	3.5
1449799_s_at	plakophilin 2	Pkp2	16.0	10.1
1415806_at	plasminogen activator, tissue	Plat	2.3	2.5
1451753_at	plexin A2	Plxna2	13.9	3.6
1417133_at	peripheral myelin protein	Pmp22	13.0	16.4
1423371_at	polymerase (DNA-directed), epsilon 4 (p12 subunit)	Pole4	2.5	2.5
1422619_at	phosphatidic acid phosphatase 2a	Ppap2a	8.0	11.4
1422620_s_at	phosphatidic acid phosphatase 2a	Ppap2a	9.2	11.8
1448908_at	phosphatidic acid phosphatase type 2B	Ppap2b	2.1	3.0
1434099_at	Peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	Ppargc1a	9.2	2.4
1460336_at	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	Ppargc1a	2.8	2.5
1456395_at	peroxisome proliferative activated receptor, gamma, coactivator 1	Ppargc1a	5.7	3.0

	alpha			
1428351_at	protein phosphatase 1M	Ppm1m	3.5	2.0
1433691_at	protein phosphatase 1, regulatory (inhibitor) subunit 3C	Ppp1r3c	147.0	15.5
1428265_at	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform	Ppp2r1b	2.0	2.6
1455958_s_at	PTC7 protein phosphatase homolog (S. cerevisiae)	Pptc7	2.0	2.4
1424906_at	PQ loop repeat containing	Pqlc3	2.3	2.1
1422673_at	protein kinase C, mu	Prkcm	11.3	5.9
1416844_at	protein arginine N-methyltransferase 2	Prmt2	2.1	2.1
1453578_at	phosphotriesterase related	Pter	3.7	2.3
1422324_a_at	parathyroid hormone-like peptide	Pthlh	8.6	4.4
1448254_at	pleiotrophin	Ptn	3.5	3.5
1416211_a_at	pleiotrophin	Ptn	4.0	6.8
1456315_a_at	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a	Ptpla	2.5	5.3
1423277_at	protein tyrosine phosphatase, receptor type, K	Ptprk	6.1	3.7
1423278_at	protein tyrosine phosphatase, receptor type, K	Ptprk	5.3	5.2
1451690_a_at	poliovirus receptor-related 4	Pvrl4	4.3	3.3
1450541_at	plasmacytoma variant translocation 1	Pvt1	7.5	2.4
1452324_at	plasmacytoma variant translocation 1	Pvt1	5.7	10.2
1417829_a_at	RAB15, member RAS oncogene family	Rab15	2.1	3.6
1443856_at	rabaptin, RAB GTPase binding effector protein 1	Rabep1	3.2	2.0
1417400_at	retinoic acid induced 14	Rai14	2.1	3.0
1417481_at	receptor (calcitonin) activity modifying protein 1	Ramp1	55.7	27.5
1449027_at	ras homolog gene family, member U	Rhou	3.7	2.4
1449028_at	ras homolog gene family, member U	Rhou	4.3	2.7
1434628_a_at	rhophilin, Rho GTPase binding protein 2	Rhpn2	4.6	4.8
1435105_at	ring finger protein 208	Rnf208	2.5	2.8
1419814_s_at	S100 calcium binding protein A1	S100a1	4.3	3.3
1424542_at	S100 calcium binding protein A4	S100a4	14.9	22.4
1421375_a_at	S100 calcium binding protein A6 (calcyclin)	S100a6	4.6	3.6
1427020_at	scavenger receptor class A, member 3	Scara3	2.6	9.5
1420764_at	scrapie responsive gene 1	Scrg1	2.5	6.7
1453486_a_at	signal peptide, CUB domain, EGF-like 2	Scube2	9.2	2.3

1417011_at	syndecan 2	Sdc2	4.0	2.6
1448545_at	syndecan 2	Sdc2	3.5	2.7
1450027_at	syndecan 3	Sdc3	3.5	2.2
1450941_at	syndecan binding protein	Sdcbp	2.8	3.1
1419478_at	secreted and transmembrane 1B	Sectm1b	2.8	2.6
1449451_at	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 11	Serpinb11	9.8	6.2
1448395_at	secreted frizzled-related protein 1	Sfrp1	2.3	6.1
1460337_at	SH3-domain kinase binding protein 1	Sh3kbp1	29.9	4.8
1431592_a_at	SH3-domain kinase binding protein 1	Sh3kbp1	7.0	6.2
1455149_at	SH3 domain containing ring finger 1	Sh3rf1	4.3	3.4
1416832_at	solute carrier family 39 (metal ion transporter), member 8	Slc39a8	4.0	2.5
1421346_a_at	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	Slc6a6	2.1	2.7
1427086_at	slit homolog 3 (Drosophila)	Slit3	5.3	3.7
1423389_at	MAD homolog 7 (Drosophila)	Smad7	3.5	2.7
1448321_at	SPARC related modular calcium binding 1	Smoc1	11.3	6.8
1417300_at	sphingomyelin phosphodiesterase, acid-like 3B	Smpdl3b	2.3	3.1
1417788_at	synuclein, gamma	Sncg	68.6	29.4
1424950_at	SRY-box containing gene 9	Sox9	4.0	3.6
1451538_at	SRY-box containing gene 9	Sox9	3.2	4.9
1448664_a_at	SPEG complex locus	Speg	5.7	13.4
1424876_s_at	spastic paraplegia 20, spartin (Troyer syndrome) homolog (human)	Spg20	3.0	2.4
1451520_at	spastic paraplegia 20, spartin (Troyer syndrome) homolog (human)	Spg20	3.7	2.7
1422106_a_at	splA/ryanodine receptor domain and SOCS box containing 2	Spsb2	2.6	2.6
1420641_a_at	sulfide quinone reductase-like (yeast)	Sqrdl	2.6	2.7
1448743_at	synovial sarcoma, X breakpoint 2 interacting protein	Ssx2ip	3.5	4.0
1419420_at	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5	St6galnac5	2.8	8.1
1420377_at	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	St8sia2	6.1	8.3
1434442_at	starch binding domain 1	Stbd1	2.8	3.3
1423038_at	syntaxin 6	Stx6	3.5	2.2
1430388_a_at	sulfatase 2	Sulf2	10.6	4.0
1423258_at	synaptotagmin IX	Syt9	10.6	2.6
1425745_a_at	transforming, acidic coiled-coil containing protein 2	Tacc2	2.1	2.5
1424918_at	TBC1 domain family, member 19	Tbc1d19	3.5	2.7

1424634_at	transcription elongation factor A (SII)-like 1	Tceal1	5.7	3.4
1450117_at	transcription factor 3	Tcf3	4.3	5.5
1429427_s_at	transcription factor 7-like 2, T-cell specific, HMG-box	Tcf7l2	2.6	2.4
1423340_at	transcription factor AP-2 beta	Tcfap2b	2.5	2.7
1418484_at	tektin 2	Tekt2	13.0	15.1
1427055_at	thioesterase superfamily member 4	Them4	4.3	2.3
1449621_s_at	thrombospondin, type I, domain 1	Thsd1	13.9	11.3
1418205_at	thrombospondin, type I, domain 1	Thsd1	21.1	13.7
1460287_at	tissue inhibitor of metalloproteinase 2	Timp2	5.3	7.6
1433662_s_at	tissue inhibitor of metalloproteinase 2	Timp2	9.2	8.9
1454677_at	tissue inhibitor of metalloproteinase 2	Timp2	7.0	9.3
1457676_at	toll-interleukin 1 receptor (TIR) domain-containing adaptor protein	Tirap	3.2	2.3
1452666_a_at	transmembrane and coiled-coil domains 2	Tmcc2	4.0	76.8
1428074_at	transmembrane protein 158	Tmem158	2.1	4.4
1426628_at	transmembrane protein 34	Tmem34	2.5	3.0
1423851_a_at	transmembrane protein 46	Tmem46	9.2	14.6
1423852_at	transmembrane protein 46	Tmem46	6.5	17.0
1449033_at	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	Tnfrsf11b	10.6	7.7
1419283_s_at	tensin 1	Tns1	4.3	2.9
1423721_at	tropomyosin 1, alpha	Tpm1	3.2	3.2
1421733_a_at	protein-tyrosine sulfotransferase 1	Tpst1	2.0	4.0
1417027_at	tripartite motif protein 2	Trim2	3.2	2.3
1455315_at	transformation related protein 53 inducible protein 13	Trp53i13	2.1	2.8
1417545_at	transient receptor potential cation channel, subfamily V, member 4	Trpv4	2.0	17.9
1432417_a_at	tetraspanin 2	Tspan2	9.2	3.0
1424567_at	tetraspanin 2	Tspan2	26.0	6.5
1424568_at	tetraspanin 2	Tspan2	36.8	7.4
1427284_a_at	tocopherol (alpha) transfer protein	Ttpa	4.0	7.3
1427347_s_at	tubulin, beta 2a	Tubb2a	4.0	3.4
1452679_at	tubulin, beta 2b	Tubb2b	4.0	4.1
1416689_at	tuftelin 1	Tuft1	2.3	2.5
1416308_at	UDP-glucose dehydrogenase	Ugdh	2.6	2.1
1426399_at	von Willebrand factor A domain containing 1	Vwa1	5.3	3.1
1448146_at	WW domain containing E3 ubiquitin protein ligase 2	Wwp2	6.5	5.3
1448145_at	WW domain containing E3 ubiquitin protein ligase 2	Wwp2	6.1	6.7

1420944_at	zinc finger protein 185	Zfp185	2.6	2.5
1417240_at	zyxin	Zyx	2.1	3.0

Supplemental Table 1. Refining the Bulge Signature: Genes Upregulated in the Bulge When Compared Against Both Epidermal and Hair Lineages

Comparisons between our previous telogen bulge signature determined by comparing the bulge to basal epidermis/upper ORS cells (Blanpain et al., 2004; Lowry et al., 2005; Tumbar et al., 2004) and our new signature derived by comparing the bulge to HG. Interestingly, ~50% of upregulated genes were common to both bulge signatures. Included in the telogen bulge signature after refinement against two skin lineages were *Bmp6,* FGF18 and NFATc1 involved in SC quiescence; essential SC transcription factors Lhx2, Sox9 and Tcf3; and key SC markers Lgr5, CD34 and S100A6. Affymetrix P value cut off is 0.0075.