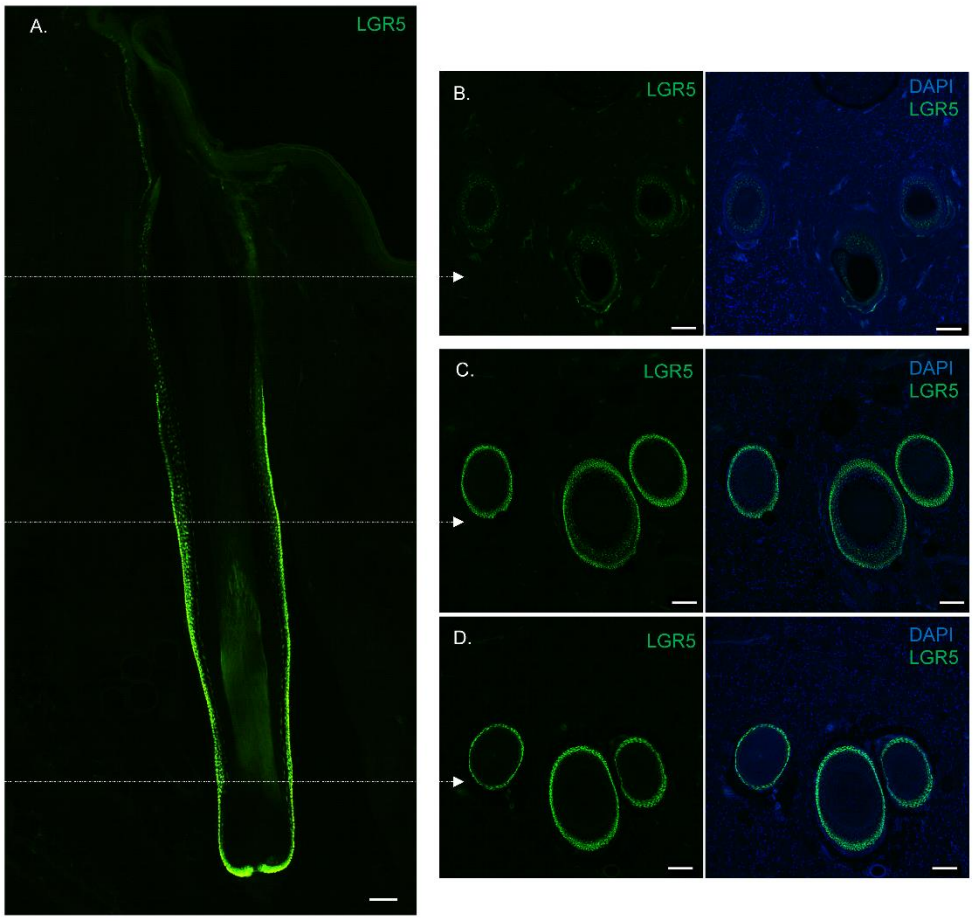
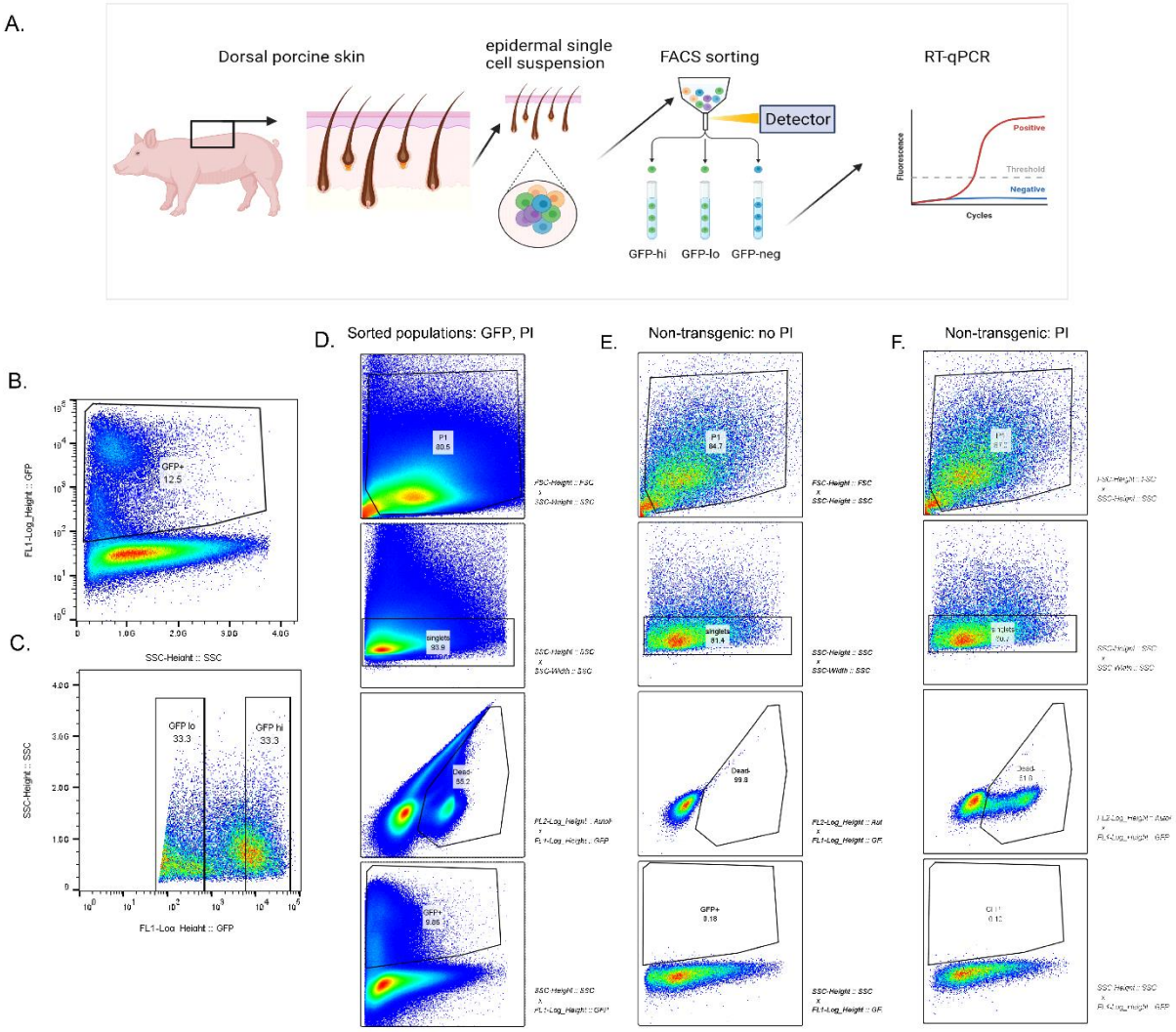
Gene	F (5'-3')	R (5'-3')
ACTB	ACTGCCGCATCCTCTTCCTC	CTCCTGCTTGCTGATCCACATC
GAPDH	ATCCTGGGCTACACTGAGGAC	AAGTGGTCGTTGAGGGCAATG
LGR4	GACCGTCGGGTAGATTGCTC	CCAGCCAATCGTAGCTCCTC
LGR5	CCTTGGCCCTGAACAAAATA	ATTTCTTTCCCAGGGAGTGG
LGR6	CAGGAGGACGGCTTCATGC	GAGCTCCGTGAGGTTGTTCA
CD34	GGTATCTGCCTGGAGCGAAA	GGGTCTTCGCCCAGCCTTT
SOX9	CGGTTCGAGCAAGAATAAGC	GTAATCCGGGTGGTCCTTCT
KRT5	CGACAACGTCAAGAAGCAGT	GAGAGGGTGTTTGTGACGAC
KRT15	GCGAGATGGAGTGCCAGAAC	TCCACTGACTCCTCGACGTT
KRT14	GGAGGTGAAGATCCGCGAC	TCTGCAGCACGACATTAGCG
CD200	TGTTCCAAGTTACTAATCAGGCTGAA	AGCCCATTAGCAACATGATACTCTTT
SHH	CAGTTTATCCCCAACGTGGC	CCACTGGTTCATCACGGAGA
TCF4	TGCCTTAGGGACGGACAAAG	ATAGTTCCTGGACGGGCTTG
WNT3A	GCGACTTCCTCAAGGACAAG	GGTCACGTGTACCGAAGGAT
LRIG1	GACGCGGAGCCTAAACCTAA	CTCCACGCTGCGAATCCTAT
HOPX	GGAGGAGACCCAGAAATGGTT	TCTTGGTGGAAGGAAGCAGC
KI67	GGACCAGGCACAATGGATGG	CAGCTTTTGTCGAAGCGTCC

Table S1. Genes and primer sequences used in RT-qPCR analyses

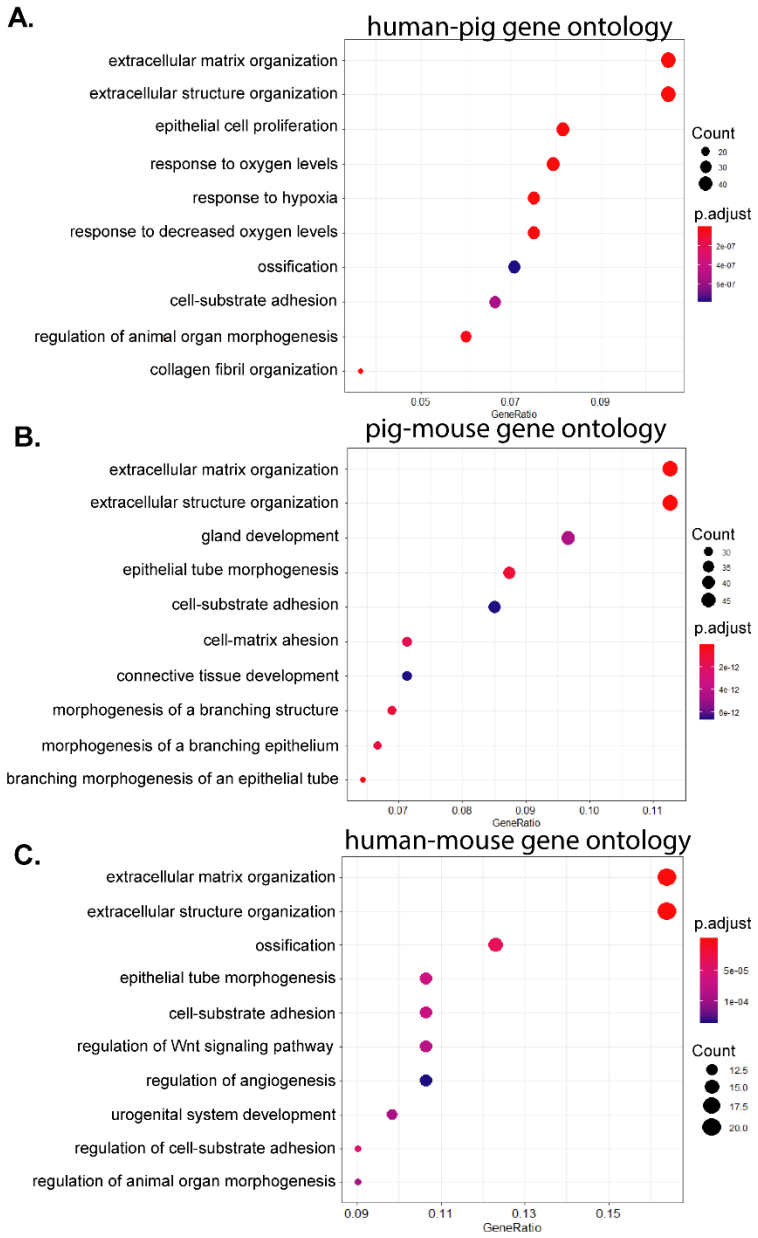
Supplementary figures



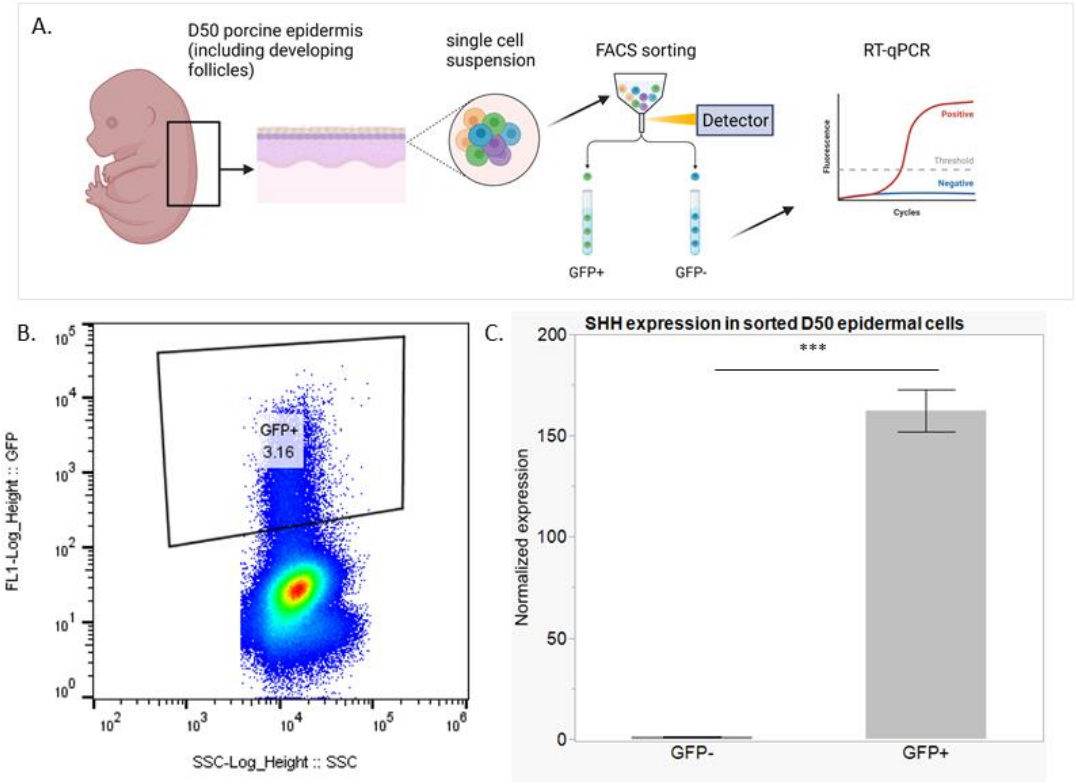
Supplementary Figure 1. Cross section of porcine hair follicle shows that LGR5 is expressed at a high level in the outer root sheath, and low level in the inner root sheath. H-J) Cross sections of hair follicles show distribution of GFP in correspondence with dashed white line. Scale bar represents 200 μM (A-C) or 100 μM (D-J).



Supplementary Figure 2. Representative flow cytometry gating strategy and controls. A) Schematic depicting process of cell isolation and fluorescence activated cell sorting (FACS), created with BioRender. GFP+ cells were split into GFP-high or GFP-low (B-C). Gating strategies determined as follows: D) Transgenic LGR5-H2B-GFP porcine epidermis stained with propidium iodide (PI) for live-dead, E) non-transgenic porcine epidermis with no PI, F) non-transgenic porcine epidermis with PI.



Supplementary Figure 3. Related to figure 4. Shared upregulated gene ontology pathways of upregulated genes in LGR5-high cells, compared pairwise across human, mouse and pig datasets.



Supplementary Figure 4: SHH expression in porcine LGR5+ D50 epidermis. A) Schematic depicting cell isolation, sorting, and RT-qPCR analysis processes, created with BioRender. B) Representative fluorescence activated cell sorting plot representing GFP+ population from D80 fetus. C) RT-qPCR relative expression of SHH of LGR5-GFP+ vs LGR5-GFP- sorted cells. Samples were normalized using a ddCT analysis to GAPDH and ACTB and then to the GFP- sample. Student's t-test *** indicates P=0.02, n=2 pigs.