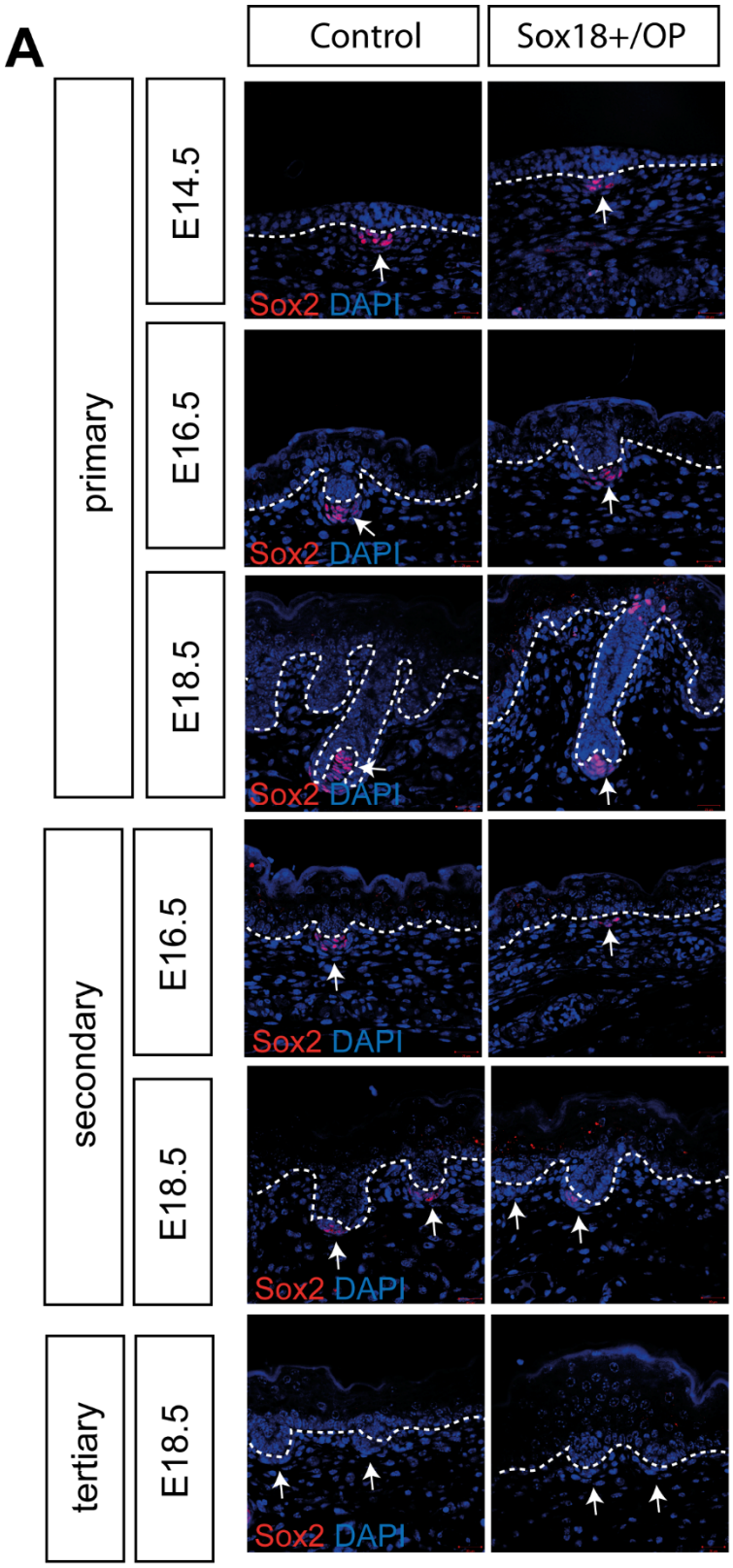
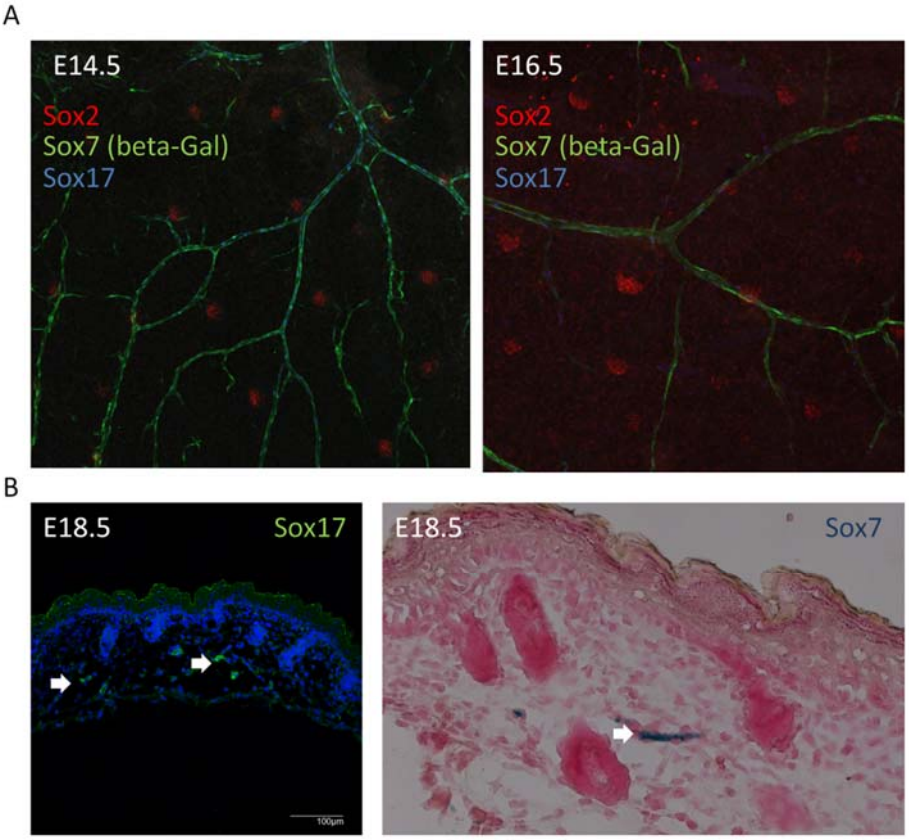
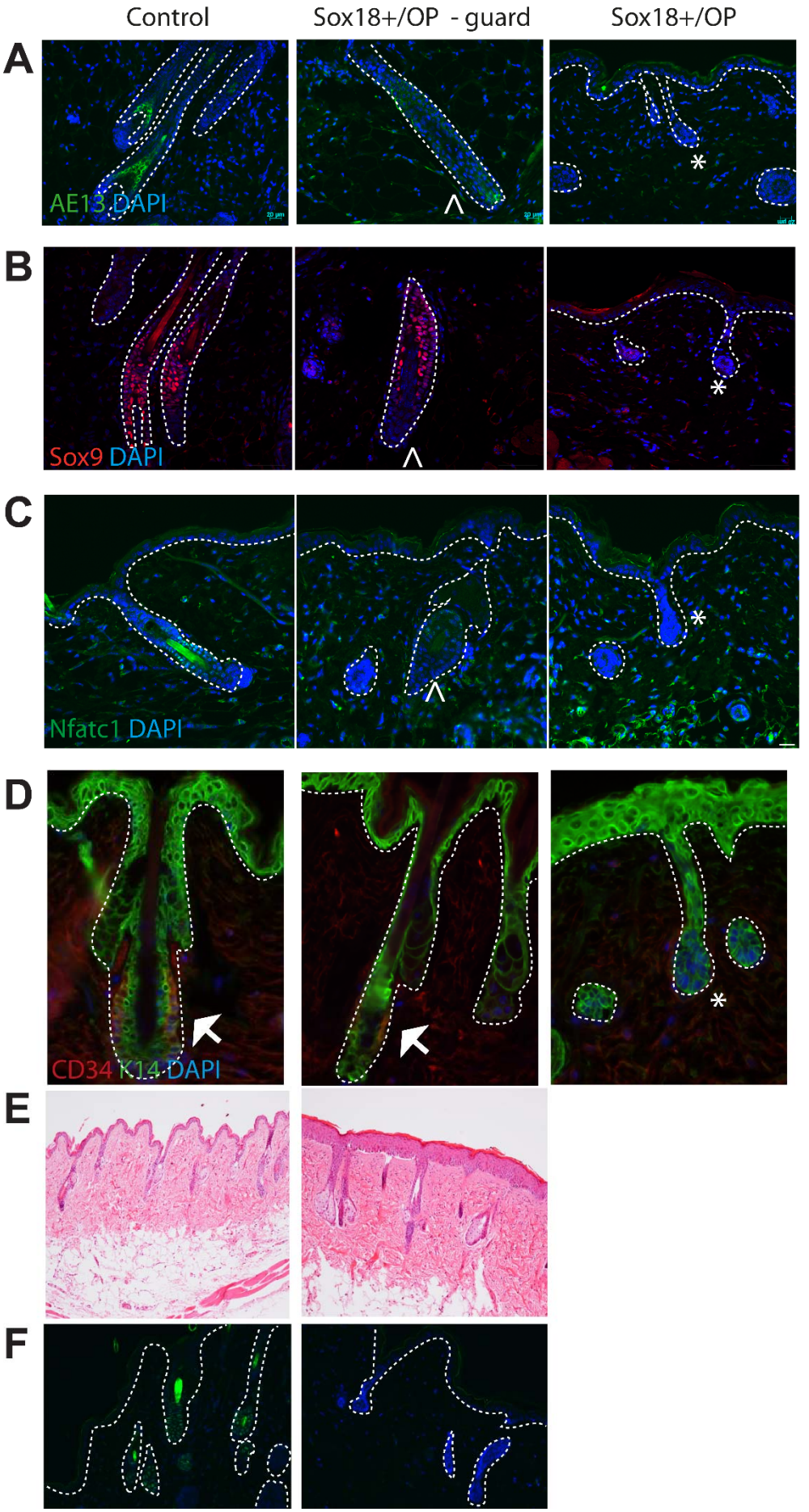


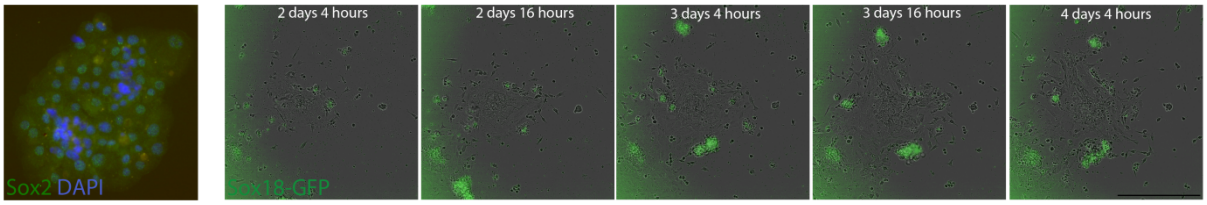
Supplemental Figure 1 : Primary and secondary hair DP development can be identified by Sox2 staining in control and Sox18$^{-/Op}$ skin. A) SOX2 (red) expression can be seen in early development of the primary hair follicle DP in both control and Sox18$^{-/Op}$ skin, at E14.5, E16.5 and E18.5 and in the developing secondary follicle at E16.5 and E18.5. As expected, at E18.5 no SOX2 expression was observed in the developing tertiary hair follicle DPs (arrows). All panels are counterstained with DAPI (blue), epidermal-dermal boundary indicated by dashed line, DP indicated by arrow.



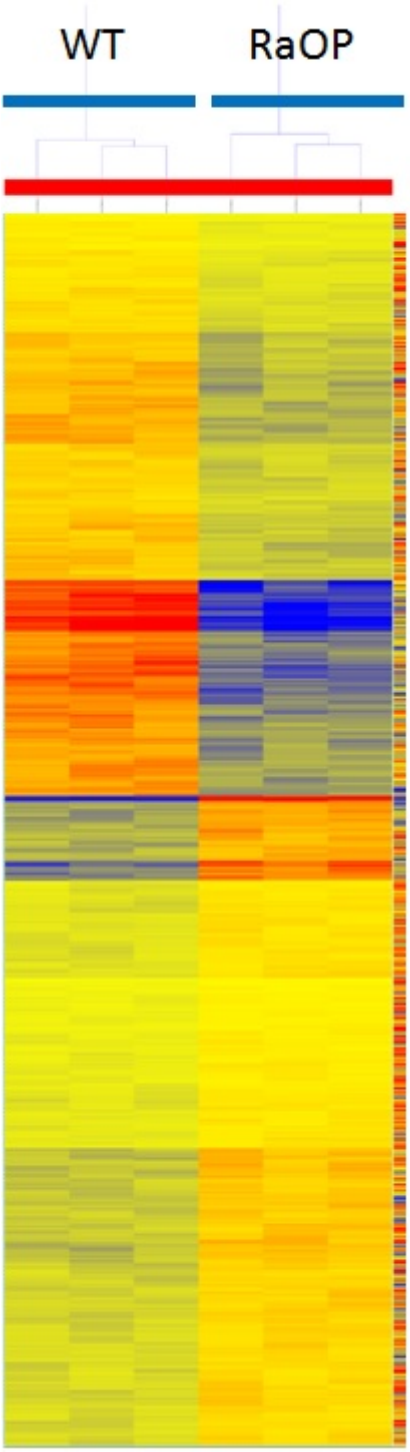
Supplemental Figure 2: *Sox18* expression in the dermal condensate is not associated with the expression of Sox7 and Sox17. A and B) Sox7-LacZ reporter mice were sacrificed at E14.5, E16.5 and E18.5. A) Whole mount Immunofluorescence of beta-galactosidase revealing Sox7 expression (green-cytoplasmic) combined with SOX17 (blue, nuclear) did not colocalize with dermal clusters as revealed by SOX2 (red) staining at E14.5 and E16.5. Sox7 and Sox17 could be visualized in vascular structures expectedly. B) At E18.5, sections were stained for SOX17 using immunofluorescence or histochemically stained with X-gal to reveal Sox7 related beta-galactosidase activity (blue) and counterstained with fast red.



Supplemental Figure 3. Decreased hair differentiation and lack of stem cell quiescence in guard hairs in *Sox18$^{+/OP}$* mice. A) AE13 (green) in P24 control and *Sox18$^{+/OP}$* (RaOP) skin, guard (^) and non-guard hair remnants (*) indicated on panel. B) Sox9 (red) in P24 skin control, *Sox18$^{+/OP}$* guard (^) and non-guard hair remnants (*) indicated on panel. C) Nfatc1 (green) in P22 skin control, *Sox18$^{+/OP}$* guard (^) and non-guard hair remnants (*) indicated on panel. D) CD34 (red) and K14 (green) in P24 skin control, *Sox18$^{+/OP}$* guard and non-guard hair remnants, white arrows indicate regions of CD34/Keratin14 co-staining. E-F) WT and RaOP skin at 1 year of age. E) Haematoxylin and eosin stain, F) Sox9 staining (green) A), B), C), D) and F) counterstained with DAPI (blue), epidermal-dermal boundary indicated by dashed line.



Supplemental Figure 4. Skin derived precursors (SKPs) isolated from neonatal dermis express Sox2 and Sox18. Left panel) Neonatal SKPs generated from wild-type mice were stained for SOX2 (green) and counterstained with DAPI (blue). (Other panels) Live imaging of neonatal SKPs generated from *Sox18*$^{+/GCre}$ mice showing GFP expression in forming spheres over time after culture (as indicated on each panel).



Supplemental Figure 5. Unsupervised hierarchical clustering of WT and Sox18+/OP SKPs. Gene expression analysis of Sox18+/OP (RaOP) and WT SKP spheres derived from littermates matched for sex allowed clear clustering of mutant and control mice.

Supplemental methods: Biotin labeled cRNA was produced using the Illumina® TotalPrep™ RNA Amplification (Ambion) as per supplier protocol. 50ng of starting total RNA was used and a 14 hour IVT reaction. cRNA samples was hybridized to Sentrix illumina_MouseWG-6 v2.0 Expression BeadChip overnight for 18 hours at 58^{o}C then scanned on a BeadStation 500 System using Beadscan software Version 3.5.31. Raw data was then imported into GenomeStudioV2010.2 for bead summarization and quality control assessment. Raw data files were submitted to Gene Express (accession number E-MEXP-3189). For data analysis, raw probe intensity data were imported into GeneSpring GX 11 and subsequent normalisation and significance analysis to identify differentially expressed probes were performed according to the default parameters used in the Guided workflow as outlined in the table below (adapted from GeneSpring GX 11 manual).