

Figure S1, related to Figure 4: Staining of Smo protein in mouse *Ptch*^{+/-} Basal Cell Carcinoma.

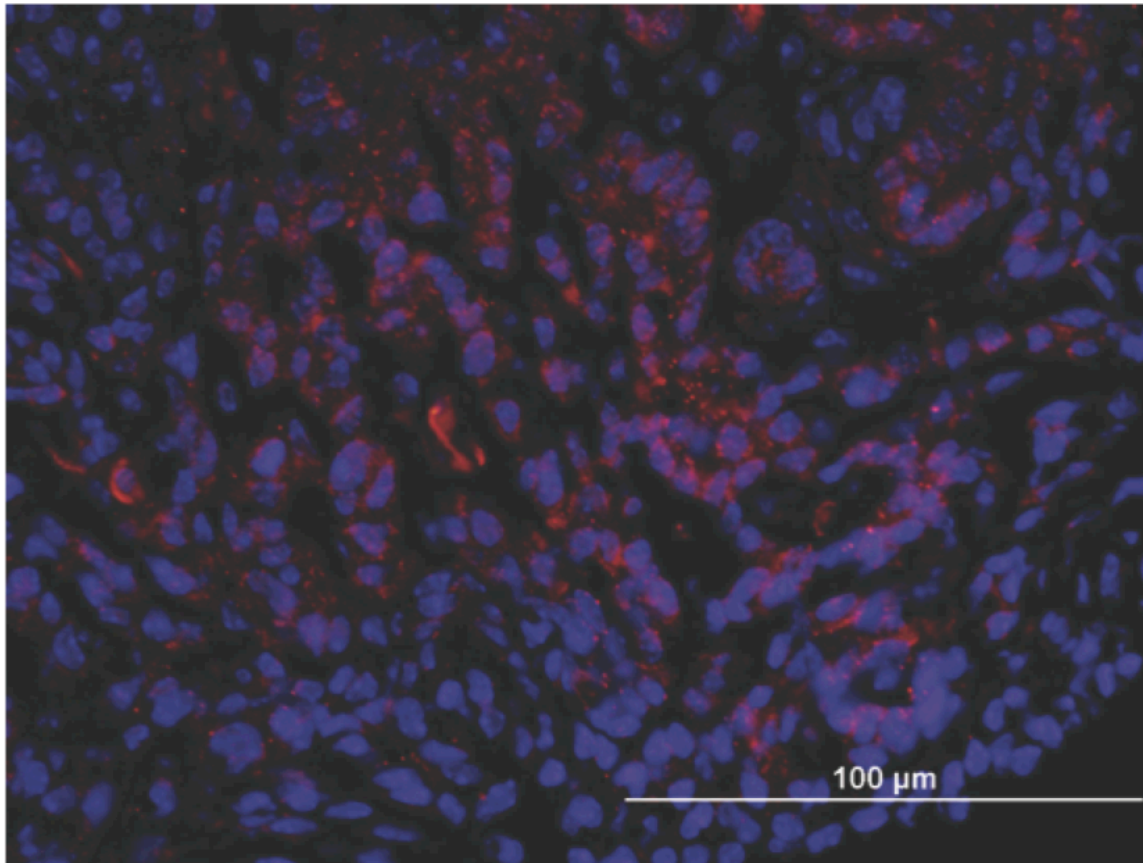


Table S1: top 100 genes ranked by number of differentially correlated other genes when comparing tail skin and dorsal skin

Table S2: All genes whose expression is significantly correlated with *Krt16* in TPA time course data. Correlation minimum of +/- 0.8 was set by calculating the 5% Genome-Wide Error Rate

Table S3: Genes whose expression shows significant differential correlation with expression of *Krt16* expression, when comparing tail (Class_A) vs. dorsal (class_B).

Table S4: Genes whose expression are significantly correlated with expression of *Krt16* in tail skin.

Table S5: Genes whose expression are significantly correlated with expression of *Krt17* in tail skin.

Table S6: Hubs of frequent differential correlation during tumorigenesis.

After calculating differential correlation for expression values reported by all microarray probes when comparing normal tail skin and papillomas, each probeset was ranked by the number other probesets with which it was significantly differentially correlated.

Supplementary Methods

Scripts to reproduce all results, tables, and analysis figures in this manuscript can be obtained at:

http://davidquigley.com/publications/2016/quigley_et_al_CellReports_2016.zip