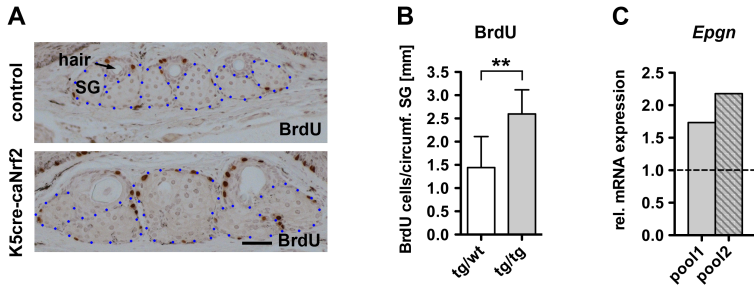
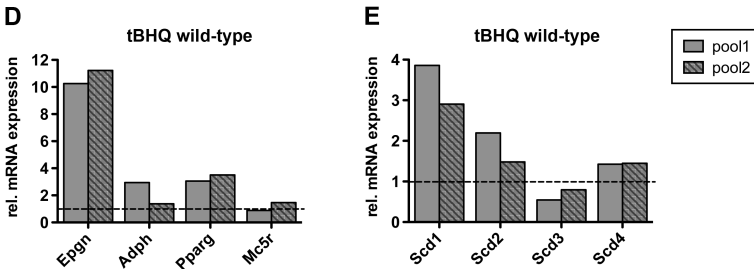


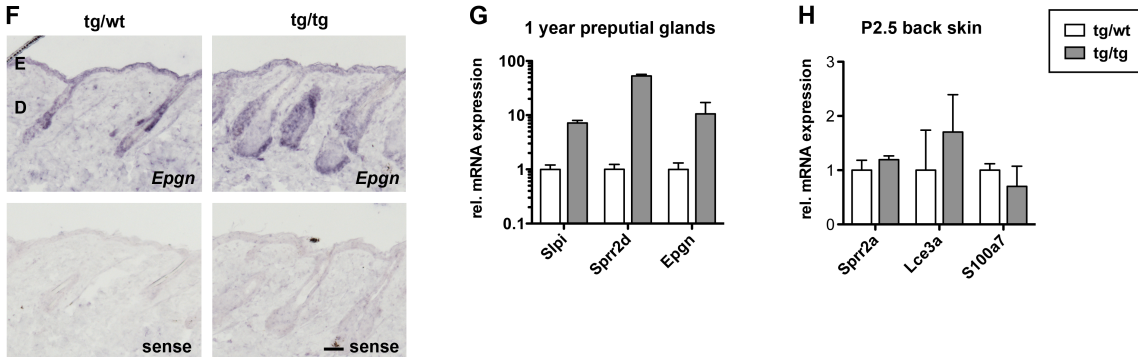
K5cre-caNrf2 mice



tBHQ wt mice



K5cre-CMVcaNrf2 mice



Supporting Information Fig S6: Nrf2 activation increases sebocyte proliferation by induction of epigen expression and affects sebocyte differentiation

(A) BrdU staining of transverse tail skin sections of control and K5cre-caNrf2 mice. Note the increase in BrdU positive peripheral sebocyte progenitors (indicated by blue dots) and ORS of the hair follicles in K5cre-caNrf2 mice. Scale bar: 100µm. (B) Quantification of BrdU positive sebocyte progenitor cells per circumference of the sebaceous gland in control (tg/wt) and K5cre-caNrf2 (tg/tg) mice (N=5/6, **P=0.0043). Measurements were performed on serial sections, and the SG circumferences at the largest extent were used for the statistical analysis. Values are shown as the mean with SD. P-values were calculated by Mann-Whitney-U test. (C) qRT-PCR of *Epgn* relative to *Gapdh* using

RNAs from skin of control (tg/wt) and K5cre-caNrf2 (tg/tg) mice. Expression of tg/wt mice was arbitrarily set as 1. Results obtained with RNAs pooled from two to three mice from two independent litters (pool1 and pool2) are shown. **(D,E)** qRT-PCR of *Epgn*, *Adph*, *Pparg*, *Mc5r* (D) and *Scd1*, 2, 3, 4 (E) relative to *Gapdh* using RNAs from back skin of tBHQ-treated and vehicle-treated wt mice. Results obtained with RNAs pooled from three mice from two independent litters (pool1 and pool2) are shown. Expression in vehicle-treated mice was arbitrarily set as 1, indicated by dashed line. **(F)** *In-situ* hybridization on 8w old tg/wt and tg/tg back skin sections using *Epgn* sense (upper panel) and antisense probes (lower panel). Note strong staining in interfollicular epidermis and pilosebaceous unit on tg/wt and tg/tg section hybridized with the *Epgn* antisense probe. Scale bar: 50 μ m. **(G)** qRT-PCR of *Slpi*, *Sprp2d*, and *Epgn* relative to *Gapdh* using RNA from isolated preputial glands of 1 year-old tg/tg and tg/wt mice. Expression in tg/wt mice was arbitrarily set as 1. All genes show elevated expression levels in preputial glands of tg/tg mice compared to tg/wt mice (N=4/3). Values are shown as the mean with SD. **(H)** qRT-PCR of *Sprp2a*, *Lce3a*, and *S100a6* relative to *Gapdh* using RNA from isolated preputial glands of P2.5 tg/tg and tg/wt mice. Expression in tg/wt mice was arbitrarily set as 1 (N=3). Values are shown as the mean with SD.