SUPPLEMENTARY TABLE AND FIGURE LEGENDS

Supplementary Table 1. TaqMan primer-probe sets used in study.

Supplementary Table 2. Microarray analysis demonstrating differential expression of mRNA's from transgenic compared to nontransgenic keratinocytes. Increased expression of SELENBP1, SELENBP2, and NDRG1 was not statistically significant at $p<0.05$, $n=3$ independent cultures, yet enhanced expression of these mRNA's was subsequently validated by real-time RT-PCR and Western analysis.

Supplementary Figure 1. Increased angiogenesis in transgenic papillomas and cancers. Increase in microvessels, revealed by MECA-32 immunohistochemistry (green), in DPM transgenic papillomas (Panel B) and squamous carcinomas (Panel D) versus nontransgenic papillomas (Panel A) and squamous cancers (Panel C). Counterstaining was done with a keratin-14 antibody (Panels A-D, red fluorescence). Images were obtained with 100X magnification.

Supplementary Figure 2. Diminution in proliferation in transgenic papillomas. In-vivo BrdU labeling (green fluorescence) in nontransgenic (Panel A) and transgenic (Panel B) papillomas. There was a diffuse increase in BrdU positive nontransgenic epidermal keratinocytes with frequent positive suprabasal cells (arrowheads, Panel A). Proliferation was markedly decreased in transgenic papillomas with only rare positive suprabasal cells (arrowheads, Panel B). Keratin-14 (red fluorescence) was used as a counterstain. Magnification was 200X.

Supplementary Figure 3. Decrease in proliferation markers in transgenic papillomas. Real-time TaqMan RT–PCR analysis of the proliferation markers Ki67 and cyclin D1 from total RNA indicate a significant decrement in transgenic papillomas (HIF-1αDPM) compared to nontransgenic (NTG) counterparts. Error bars represent mean ± SEM. Results are representative of three independent experiments. (*$P < 0.05$, t-test).

Supplementary Figure 4. Shift of transgenic skin NDRG1 expression to the proliferative compartment. Immunofluorescence demonstrates redirection of NDRG1 expression to the basal transgenic epidermal keratinocytes (Panels B and D, green fluorescence), with marked accumulation and localization to the perinuclear compartment (arrowheads, Panel B). In contrast, there is low-level NDRG1 expression in the differentiated suprabasal and granular layers of nontransgenic epidermal back skin (Panels A and C). Activation of hair follicle proliferation and intraepidermal proliferation and differentiation by TPA (Panels C and D) uncovers latent NDRG1 expression in the hair follicle inner root sheath (Panel C, arrowhead) and enhances granular layer expression as well, where NDRG1 is also localized to the perinuclear compartment (arrow, Panel C). TPA/hair follicle activation also highlights NDRG1 expression in the proliferative outer root epidermal cell layer compartment as well (arrowheads, Panel D). Keratin-14 counterstain (red fluorescence) in Panels A-D. Magnification in Panels A and B is 400X, and 200X in Panels C and D.