Suppl. Table 1. Gene expression profiling of SK lesions.

Total RNA was prepared from four sporadic SK lesions from different patients and two age-matched normal epidermis. cRNA probes from each specimen were analyzed by hybridization to Affymetrix Human U133A 2.0 gene chips according to the manufacturer's recommendations. Affymetrix CEL files were loaded into the Resolver SE System (Rosetta Biosoftware) for data processing and normalization, applying the Affymetrix platform-specific error model. Intensity replicated profiles were then combined, through an error-weighted averaging, and compared to form ratio experiments where each gene is associated to an expression fold-change and a p-value that assesses the statistical significance of its modulation in the pathological versus the normal condition. Only genes with an absolute fold change greater than 10 and a p-value lower than 0.05 were considered as statistically significant (the p-value is derived from a two-sided error-weighted t-test available within the Resolver software). For the complete data set see Suppl. Table 2.

Gene Name	Gene Symbol	Mean Normal Skin	Mean SK	Mean N/SK
Zinc finger protein 36, C3H type-like 2	ZFP36L2	4.40	181.45	0.02
Splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, Drosophila)	SFRS8	3.70	73.73	0.05
Fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)	FGFR3*	23.40	334.85	0.07
Echinoderm microtubule associated protein like 2	EML2	3.00	52.75	0.06
RAB35, member RAS oncogene family	RAB35	3.60	64.58	0.06

Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	SEMA3F	5.45	78.43	0.07
Forkhead box N1	FOXN1*	4.35	86.98	0.05
Interleukin enhancer binding factor 3, 90kDa	ILF3	7.35	197.88	0.04
Major histocompatibility complex, class II, DR beta 4	HLA-DRB4	5.15	250.45	0.02
Nuclear factor I/X (CCAAT-binding transcription factor)	NFIX	4.45	77.03	0.06
Protocadherin gamma subfamily C, 3	PCDHGC3	2.90	81.08	0.04
Epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	EGFR	6.50	124.80	0.05
Hypothetical gene supported by AK054742; AK056642; BC009111	na	5.20	114.90	0.05
TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa	TAF6L	4.95	83.68	0.06
Rho GDP dissociation inhibitor (GDI) alpha	ARHGDIA	0.50	67.80	0.01
Ornithine decarboxylase antizyme inhibitor	OAZIN	2.60	52.95	0.05
Gelsolin (amyloidosis, Finnish type)	GSN	3.00	124.25	0.02
Nuclear mitotic apparatus protein 1	NUMA1	2.40	124.58	0.02
Microtubule-associated protein 1B	MAP1B	5.40	77.95	0.07
Uroplakin 1A	UPK1A	14.15	362.28	0.04
Osteoblast specific factor 2 (fasciclin I-like)	OSF-2	1.25	145.98	0.01
Hypothetical protein FLJ20619	FLJ20619	3.55	55.43	0.06
Plectin 1, intermediate filament binding protein 500kDa	PLEC1	1.15	179.35	0.01
Similar to RIKEN cDNA B230208J24	na	3.20	54.50	0.06
SH3-domain GRB2-like endophilin B2	SH3GLB2	25.70	378.03	0.07
Nasopharyngeal carcinoma susceptibility	LZ16	3.80	135.13	0.03

protein				
Hypothetical protein FLJ12598	FLJ12598	4.65	76.53	0.06
Kruppel-like factor 13	KLF13	2.65	58.28	0.05
Cytokine-like nuclear factor n-pac	N-PAC	2.25	60.88	0.04
Interleukin 17 receptor C	IL17RC	3.45	94.58	0.04
Hypothetical protein DKFZp762N1910	DKFZp762N1910	2.50	57.98	0.04

Supplemental Table 3. Primers used in real time RT-PCR experiments.

| GENE	FORWARD	REVERSE
β-ACTIN	AGAAAATCTGGCACCACACC	GTCTCAAACATGATCTGGG
EGFR	TCCCCGTAATTATGTGGTGAC	GCCCTTCGCACTTCTTACAC
INVOLUCRIN	GGCCCTCAGATCGTCTCATA	CACCCTCACCCCATTAAAGA
KERATIN 1	GTTCCAGCGTGAGGTTTGTT	TAAGGCTGGGACAAATCGAC
KERATIN 10	GAAAAGCATGGGCAACTCACA	TGTCGATCTGAAGCAGGATG
NOTCH 1	TTGGGAGGAGCAGATTTTTG	CACTGGCATGACACACAACA
FGFR3	CCACTGTCTGGGTCAAGGAT	GCACACTGAAGTGGCACAGT
p53	AGGCCTTGGAACTCAAGGAT	CTGAGTCAGGCCCTTCTGTC
FOXN1	TTCCCGTCAGCGAGATCTACA	GTTCTCCACCTTCTCGAAGCAC
P63	GGTGCCTCCACTATGATCCTTA	TCCACGTGACTGAGAGTTCAAT
MRCKa	ATTGCATCACTGTATCATTTCT	TGCTCTGTGGGGACCTTTCA
36B4	GCAATGTTGCCAGTGTCTGT	GCCTTGACCTTTTCAGCAAG
Integrin a6	ATAAATTTTGCACCCGAGAAGGAA	GTTGGAAGGGCTGTTTGTCACTGT
FoxN1 Promoter: region A	CACACCATCCTCACGATGAC	CTGGCTGTGTGACTTTGAGC
FoxN1 Promoter region B	TTCACTGGTCAGTCGGTCAG	GATCAGACCCCTGTGGAGAA
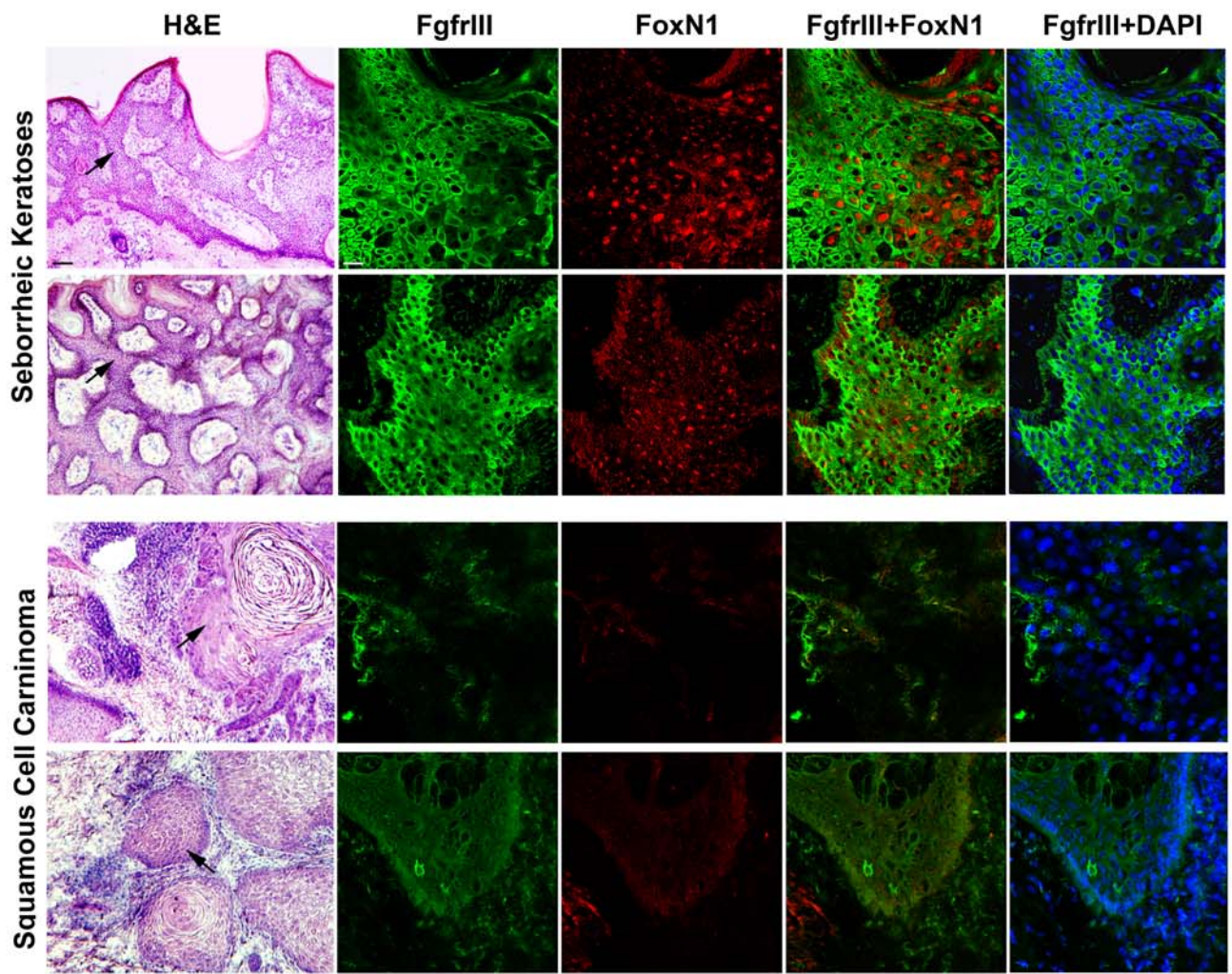
Figure S1

Suppl. Figure 1. Different expression levels of FOXN1 and FGFR3 in SK versus SCC tissue samples. Frozen sections from two additional surgically obtained SK and SCC tissue samples were stained with hematoxylin-eosin (left columns) and analyzed for expression of FOXN1 and FGFR3 (middle and right columns) similarly to those analyzed in Figure 2.
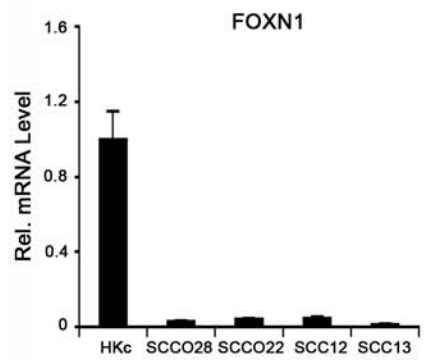
Figure S2

Suppl. Figure 2. FOXN1 expression is down-modulated in keratinocyte SCC cell lines. Primary human keratinocytes (HKC) were analyzed in parallel with keratinocyte-derived SCC cell lines (SCCO28, SCCO22, SCC12, and SCC13) by real time RT-PCR for FOXN1 and 36B4 for internal normalization. Error bars refer to SEM.
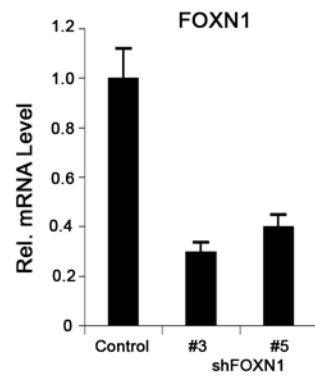
Figure S3

Suppl. Figure 3. FOXN1 knock-down efficiency by shRNA. Human keratinocytes were stably infected with two shRNA lentiviral constructs targeting FOXN1 expression. Total RNA was isolated 48h after infection and FOXN1 expression evaluated by RT-PCR with 36B4 for internal normalization. Error bars refer to SEM.