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.

<table>
<thead>
<tr>
<th>Gene Name</th>
<th>Gene Symbol</th>
<th>Mean</th>
<th>Mean</th>
<th>Mean</th>
<th>Mean</th>
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<td>Splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, Drosophila)</td>
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<td>Fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)</td>
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<td>Echinoderm microtubule associated protein like 2</td>
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<td>RAB35, member RAS oncogene family</td>
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<td>Value 2</td>
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<td>Nuclear factor I/X (CCAAT-binding transcription factor)</td>
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<td>Symbol</td>
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<td>Value 2</td>
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<td>Kruppel-like factor 13</td>
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Supplemental Table 3. Primers used in real time RT-PCR experiments.

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<tr>
<th>GENE</th>
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<tr>
<td>β-ACTIN</td>
<td>AGAAAATCTGGCACCACACC</td>
<td>GTCTCAAACATGATCTGGG</td>
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<tr>
<td>EGFR</td>
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<td>GCCCTTCGCACTTCTTTACAC</td>
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<tr>
<td>INVOLUCRIN</td>
<td>GGCCCTCAAGATCGTCTCATA</td>
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<td>KERATIN 1</td>
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<tr>
<td>KERATIN 10</td>
<td>GAAAAGCATGGGCAACTCACA</td>
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<tr>
<td>NOTCH 1</td>
<td>TGGGAGGAGGCAAGATTTTTG</td>
<td>CACTGGCATGACACACACA</td>
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<tr>
<td>FGFR3</td>
<td>CCCTGCTCTGGGTCAAAGAT</td>
<td>GCACTGAAGTGGCACCAGT</td>
</tr>
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<td>p53</td>
<td>AGGCCTTGGAACTCAAGGAT</td>
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<tr>
<td>FOXN1</td>
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<td>GCTTCCACCTTCTCGAACAC</td>
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<td>P63</td>
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<td>TCCACGTGACTGAGAGTTCAA</td>
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<td>MRCKa</td>
<td>ATTCGATCAGTGTATCTTTTCT</td>
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<td>36B4</td>
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<td>GCTTACCTTTTACTGCAAG</td>
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<td>Integrin a6</td>
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<tr>
<td>region A</td>
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<tr>
<td>FoxN1</td>
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<tr>
<td>region B</td>
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</table>
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.