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Supplemental Figure 1. Molecular characterization of SCC tumors and cell lines. (A) Western blot analysis of indicated proteins in murine SCC tumors. Ribosomal S6 serves as a loading control. (B) PCR analysis for loss of *Wild-type* p53 in murine SCC tumors. N= no DNA, G= genomic DNA, T= Tumor DNA. *Wild-type* allele PCR product is 450 base pairs; *null* allele PCR product is 650 base pairs. Note reduced WT band in tumor 1423, suggesting LOH. (C) Western blot analysis of p53 protein in Human SCC cell lines using DO-1 antibody recognizing an epitope between amino acids 11 and 25. Ribosomal S6 serves as a loading control. Known p53 mutations are indicated. LOH = loss of heterozygousity. F.S. = frameshift mutation.



В

Α

С



p63^{L/L} K14-CreER

Supplemental Figure 2. Excision of *p***63 in murine SCC.** (A) Schematic of generation of the *p*63^{Brdm3} allele. Cremediated recombination results in excision of exons 5, 6, and 7, which encode the majority of the DNA-binding domain (red). PCR of genomic DNA with primers in exons 4 and 8 result in a 240bp product only in the recombined allele, as seen in Figure 2B. (B) Regression of cutaneous *p*63^{L/L} *K*14-CreER tumor following tamoxifen treatment as described in Figure 2D. (C) Progression of *p*63^{+/+} *K*14-CreER oral SCC tumor (left) versus regression *of p*63^{L/L} *K*14-CreER tumor (right) following tamoxifen treatment as in Figure 2D. Scale bar = 0.5cm



p-value: 2.66x10⁻⁴, Fold Change: 1.449

Supplemental Figure 3. Microarray identification of FGFR2 in SCC. (A) Growth of orthotopic tumors with varying numbers of viable CD31^{neg} CD45^{neg} cells (n=2 per set). Tumor and stromal cells were not separated during FACS sorting, and cell number represents total number of tumor and stromal cells injected. (B) Tumor growth of $p63^{L/L} K14$ -*CreER* orthotopic tumors following tamoxifen (n=12) or vehicle (n=14) treatment. Tumor volume is normalized to size prior to first treatment. p<0.0001 as assessed by multiple measures ANOVA. Error bars +/- SEM. (C) Tumor growth of $p63^{L/L}$ orthotopic tumors following tamoxifen (n=6) or vehicle (n=6) treatment. Tumor volume is normalized to size prior to first treatment. p-value is not significant as assessed by multiple measures ANOVA. Error bars +/- SEM. (D) Gene rank analysis of FGFR2 overexpression in Oncomine microarray datasets. Numbers refer to citations for primary data found in Supplemental References. (E) Representative FGFR2 and p63 levels in Esophagus compared to Esophageal SCC from the "*Su Esophagus 2*" dataset (Ref. 28). Wiskers indicate 95th percentile of data. p-values calculated by Students's t-test.

p-value: 4.59x10⁻¹⁶, Fold Change: 3.032



Supplemental Figure 4. Direct functional regulation of *Fgfr2* **by p63. (A) QRT-PCR of mRNA levels of indicated genes in** *p***63-intact (n=3) or** *p***63-ablated (n=3) autochthonous tumors on day 6 after tamoxifen or vehicle treatment, respectively. *p<0.05. Error bars represent +/- SEM. (B) Western blot analysis of murine B9 SCC cells following immunoprecipitation with the α-p63 H129 antibody or control IgG antibody (left) or FLAG-epitope tagged wild-type ΔNp63α (WT) or DNA-binding deficient ΔNp63α (R304W) following immunoprecipitation with α-FLAG M2 antibody (right). Blots probed with α-p63 4A4 antibody. (C) Quantitative Real-Time PCR of mRNA levels of** *p***63, and** *FGFR2* **mRNA after p63 knock down in human HNSCC cells 72 hours following lentiviral-mediated knock-down of** *p***63 (sh***p***63) or infection with control shRNA (Vector). *p<0.05, **p<0.01, ***p<0.001 as assessed by student's unpaired t-test. Error bars indicate +/- SEM. (D) FGFR2 is required for colony formation of HNSCC cells. Quantification Human HNSCC cells plated on plastic 72 hours after infection with control lentivirus, or lentivirus expressing p63 or FGFR2-directed shRNAs. **p<0.01, ***p<0.001 as assessed by students unpaired t-test. Error bars represent +/- SEM of 3 biological replicates. (E) Selective induction of FGFR2 by ΔNp63α requires DNA binding. Expression of FGFR2 in human HaCAT cells following stable expression of GFP, or FLAG-tagged wild type (WT) or R304W mutant (RW) ΔNp63α or TAp63α. Arrow indicates TAp63α; arrowhead indicates ΔNp63α. GAPDH serves as a loading control.**



Supplemental Figure 5. Activation of p63-Fgfr2-Fgf7 axis in SCC and hair follicles. (A) Up-regulation of *p*63 and *Fgfr2* in Human SCC tumors versus cell lines. Relative mRNA expression was determined by QRT-PCR in human HNSCC cell lines (n=7) and tumors (n=18). Bar indicates mean value. *p<0.05 as assessed by students unpaired t-test. (B) Immunofluorescent staining of murine skin (top) or SCC tumors (bottom) with indicated antibodies. K14= Keratin 14, SMA = Smooth Muscle Actin. Hoechst dye (blue) identifies nuclei. Arrowheads indicate blood vessels. Scale bar = 25μ m. (C) Relative mRNA expression Fgfr2 IIIb ligands in murine SCC tumors. Error bars +/- SEM. (D) Immunofluorescent staining of murine hair follicles in telogen with indicated antibodies. DP = Dermal papilla. HS = Hair Shaft. Scale bar = 25μ m (E) Immunofluorescent staining of murine SCC tumors with indicated antibodies. Scale bar = 25μ m.



Supplemental Figure 6. AZD4547 treatment of SCC cells and tumors. (A) Quantitative Real-Time PCR of mRNA levels of *FGFR2* mRNA in human HNSCC cell lines and HNSCC primary tumors. mRNA levels were normalized to β -*actin.* Error Bars +/- SEM. (B) AZD4547 does not inhibit EGF-mediated signaling. Cells were serum-starved and pre-treated for 1 hour with indicated dose of AZD4547, followed by a 15-minute stimulation with indicated ligand. Protein levels were assessed by western blotting with indicated antibodies. (C) Growth of HNSCC cells following AZD4547 treatment. Cell growth at indicated doses of AZD4547 was assessed using Cell-TiterGlo after 3 days of treatment. Note 1135 and B9 are murine SCC cell lines. Error Bars +/- SEM. (D) Kaplin-Meyer curve of mice bearing DMBA-induced SCC tumors treated daily oral AZD4547 (12.5mg/kg, n=7) or vehicle control (n=6). Tumors were considered to have progressed when they reached 150% original volume. P-value calculated using log-rank test.

Real-Time PCR		
Mouse	Forward Primer (5'-3')	Reverse Primer (5'-3')
Total p63	CTGTACTGCCAGATTGCGAA	CTCATTGAACTCACGGCTCA
ΔNp63	GGAAAACAATGCCCAGACTC	GTGGAATACGTCCAGGTGGC
ТАр63	TTACAGATCTGCCATGTCGC	CCCAGATATGCTGGAAGACC
Fgfrl	CAACCGTGTGACCAAAGTGG	TCCGACAGGTCCTTCTCCG
Fgfr2 IIIb	GCTGGCTCTGTTCAATGTGACGG	CTCACAGGCGCTTGCTGTTTGG
Fgfr2 IIIc	GTGGTTGCCCCCGGGGAATCG	GGTGTGGTGACCGTTCAACGACA
Fgfr3	CCACCGACAAGGAGCTAGAGG	CGGTGACAGGCTTGGCAGTA
Fgfr4	CATGCAGTGCCTGCCGGGAA	TGTTGGTGGCGCAGCCGAAT
Egfr	GTTCAGGCCAACGACCGCCA	ACTGCCATCAGCGGGGACCT
β4 Integrin	TGTGTTCCAGGTGTTTGAGC	CAATGGTGTAGTCGCTGGTG
α6 Integrin	AGCCCCAGGGACTTACAACT	GGGCACGAGACTTTCATCAT
Coll7al	GGAAGTCGGTTGGAGAAGCA	CCTCGGATGCTTCCACTTGA
Fgfl	CGGCTCGCAGACACCAAATGAGG	GGCCTGAGGGTTAGCGCAGC
Fgf7	CAGAACAAAAGTCAAGGAGCAACCG	GTCGCTCGGGGGCTGGAACAG
Fgf10	CTGTCCGTACAGTGTCCTGGAGATA	CCCAGCCCCCACCACAACAT
β -actin	ATGAGCTGCCTGACGGCCAGGTCATC	TGGTACCACCAGACAGCACTGTGTTG
Etv4	GCTGCGCCCGGAAAACAAGC	GCGGAGGCAGAGACCTGAGGT
Egrl	ACCTGACCACAGAGTCCTTTTC	GTCGGAGGATTGGTCATGCT
Pld1	AGAGTAAAATGGAGCACCGCT	GAATGGGATGCACCCTTCCT
Human	Forward Primer (5'-3')	Reverse Primer (5'-3')
ΔNp63	GGAAAACAATGCCCAGACTCA	TGTTCAGGAGCCCCAGGTT
ΔNp63 probe	TTAGTGAGCCACAGTACAC	
Human	Purchased from Applied Biosystems	
β -actin	Hs99999903_m1	
FGFR2	Hs00256382_m1	
	Chromatin Immunoprecip	itation
Mouse	Forward Primer (5'-3')	Reverse Primer (5'-3')
Fgfr2	CCACCCTCCACCCCCTACGG	CGTCATGAGGCCTTCTGGGGA
-2.4 Kb		
Fgfr2	CCCCCTCAGCCACAGTGGGT	GCCICITGIGGCGCICCCAG
-12.5 KD		
PlaI	ACCICGGIAAGCAACCCIIG	GGAAGCIGGGCIAAACGACI
$\pm 13.3 \text{ K0}$		CAAGTCGTTCCCAGCTCCTC
65 Kh	OCUAUCEICAAACUUAAAIC	GAAGIOGITECEAGETEETE
-0.3 KU		
Genomic DNA PCR primers		
Mouse	Forward Primer	Reverse Primer
p63 ^{Brdm3}	CAGAGGAGGCAACACAGGATAGA	CCGGGGGATCCGAATTCATCGA
loading	CAATGGTAGGCTCACTCTGGGAGATGATA	AACACACACTGGCAGGACTGGCTAGG

Supplemental Table 1: Sequences for primers used in this study

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