

Supplementary Table S1. Clinicopathological characteristics of patients with squamous cell carcinoma and basal cell carcinoma

Characteristics	SCC (n = 70)	BCC (n = 146)
Age, median (range, years)	77 (33–96)	71 (29–98)
Sex		
Female	34 (48.6%)	86 (58.9%)
Male	36 (51.4%)	60 (41.1%)
Tumor size, mean (range, cm)*	2.3 (0.2–14.0)	1.1 (0.2–5.0)
Location		
Scalp	7 (10.0%)	7 (4.8%)
Face	38 (54.3%)	116 (79.4%)
Neck	1 (1.4%)	2 (1.4%)
Upper extremity	7 (10.0%)	1 (0.7%)
Lower extremity	11 (15.7%)	3 (2.1%)
Trunk	6 (8.6%)	11 (7.5%)
Urogenital region	0 (0%)	6 (4.1%)
Ulceration		
Not identified	49 (70.0%)	128 (87.7%)
Present	21 (30.0%)	18 (12.3%)
Perineural invasion		
Not identified	66 (94.3%)	142 (97.3%)
Present	4 (5.7%)	4 (2.7%)
Local recurrence		
No	64 (91.4%)	142 (97.3%)
Yes	6 (8.6%)	4 (2.7%)
Lymph node metastasis		
No	66 (94.3%)	146 (100%)
Yes	4 (5.7%)	0 (0%)
Histological subtype		
Nodular		88 (60.2%)
Superficial		11 (7.5%)
Micronodular		8 (5.5%)
Infiltrating		2 (1.4%)
Sclerosing/morphoeic		1 (0.7%)
Basosquamous		2 (1.4%)
Fibroepithelial		1 (0.7%)
BCC with adnexal differentiation		3 (2.1%)
Mixed		30 (20.5%)

Histological grade		
G1 (well differentiated)	52 (74.3%)	
G2 (moderately differentiated)	15 (21.4%)	
G3 (poorly differentiated)	3 (4.3%)	
Level of invasion		
Papillary dermis	16 (22.8%)	12 (8.2%)
Reticular dermis	34 (48.6%)	101 (69.2%)
Subcutis	14 (20.0%)	20 (13.7%)
Skeletal muscle	6 (8.6%)	13 (8.9%)

* Tumor size; 11 cases of SCC and 33 cases of BCC were missing data.

Abbreviations: BCC, basal cell carcinoma; SCC, squamous cell carcinoma.

Supplementary Table S2. Biological functions involving a set of genes potentially related to SSBP2 in squamous cell carcinoma derived by Gene Ontology enrichment analysis

GO category	Term	Genes	Fold enrichment
MF	Actin filament binding (GO:0051015)	<i>MYO10, MYO9A, MYOM3</i>	7.48
	Actin binding (GO:0003779)	<i>MYO10, KLHL3, PDLIM5, MYO9A</i>	6.51
	Transcription coactivator activity (GO:0003713)	<i>NCOA1, KAT6B, SUB1</i>	6.30
	Metal ion binding (GO:0046872)	<i>ZFYVE16, KAT6B, JMJD1C, WDFY2, PDLIM5, JAK2, MYO9A, FOXP2, BPTF</i>	1.87
	Protein binding (GO:0005515)	<i>OTCH3, GALT, UBA6, JMJD1C, PTPN22, NR3C1, FAM124B, APBB2, JAK2, FNIP1, PDLIM5, BPTF, NCOA1, CAST, MYO10, KLHL3, MYO9A, KRT74, FOXP2, SHISA6, ZFYVE16, KAT6B, SUB1, STRAP, SNRPF, WDFY2, FAM50A</i>	1.19
CC	Early endosome (GO:0005769)	<i>ZFYVE16, APBB2, WDFY2</i>	5.86
	Chromatin (GO:0000785)	<i>NCOA1, JMJD1C, NR3C1, FOXP2, BPTF</i>	2.87
	Cytosol (GO:0005829)	<i>NCOA1, CAST, NOTCH3, GALT, MYO10, UBA6, HSD17B4, KLHL3, PTPN22, NR3C1, MYO9A, KRT74, ZFYVE16, CDC42EP5, STRAP, SNRPF, JAK2, FNIP1, PDLIM5</i>	2.08
	Nucleoplasm (GO:0005654)	<i>NCOA1, NOTCH3, FAM124B, KAT6B, SUB1, JMJD1C, SNRPF, JAK2, NR3C1, BPTF, FAM50A</i>	1.68
	Cytoplasm (GO:0005737)	<i>CAST, GALT, UBA6, PTPN22, NR3C1, MYO9A, KRT74, CDC42EP5, STRAP, APBB2, JAK2, FNIP1, PDLIM5, BPTF</i>	1.50
BP	Chromatin organization (GO:0006325)	<i>JMJD1C, JAK2, NR3C1, FAM50A</i>	8.22
	Negative regulation of transcription from RNA polymerase II promoter	<i>NOTCH3, STRAP, APBB2, FNIP1, NR3C1, FOXP2, BPTF</i>	4.05

(GO:0000122)		
Positive regulation of transcription from RNA polymerase II promoter	<i>NCOA1, NOTCH3, KAT6B, APBB2, JAK2, NR3C1, BPTF</i>	3.31
(GO:0045944)		
Regulation of transcription, DNA-templated	<i>KAT6B, JMJD1C, APBB2, NR3C1, BPTF</i>	2.92
(GO:0006355)		

Abbreviations: BP, biological process; CC, cellular component; MF, molecular function; SSBP2, single-stranded DNA binding protein 2.