Figure S1. Protein expression level of the COPS subunits in HNSCC. Protein expression level of (A) COPS2, (B) COPS3, (C) COPS4, (D) COPS7A, (E) COPS7B and (F) COPS9 in normal oral tissues and HNSCC from the Human Protein Atlas Portal. COPS, COP9 signalosome 1x10^1.

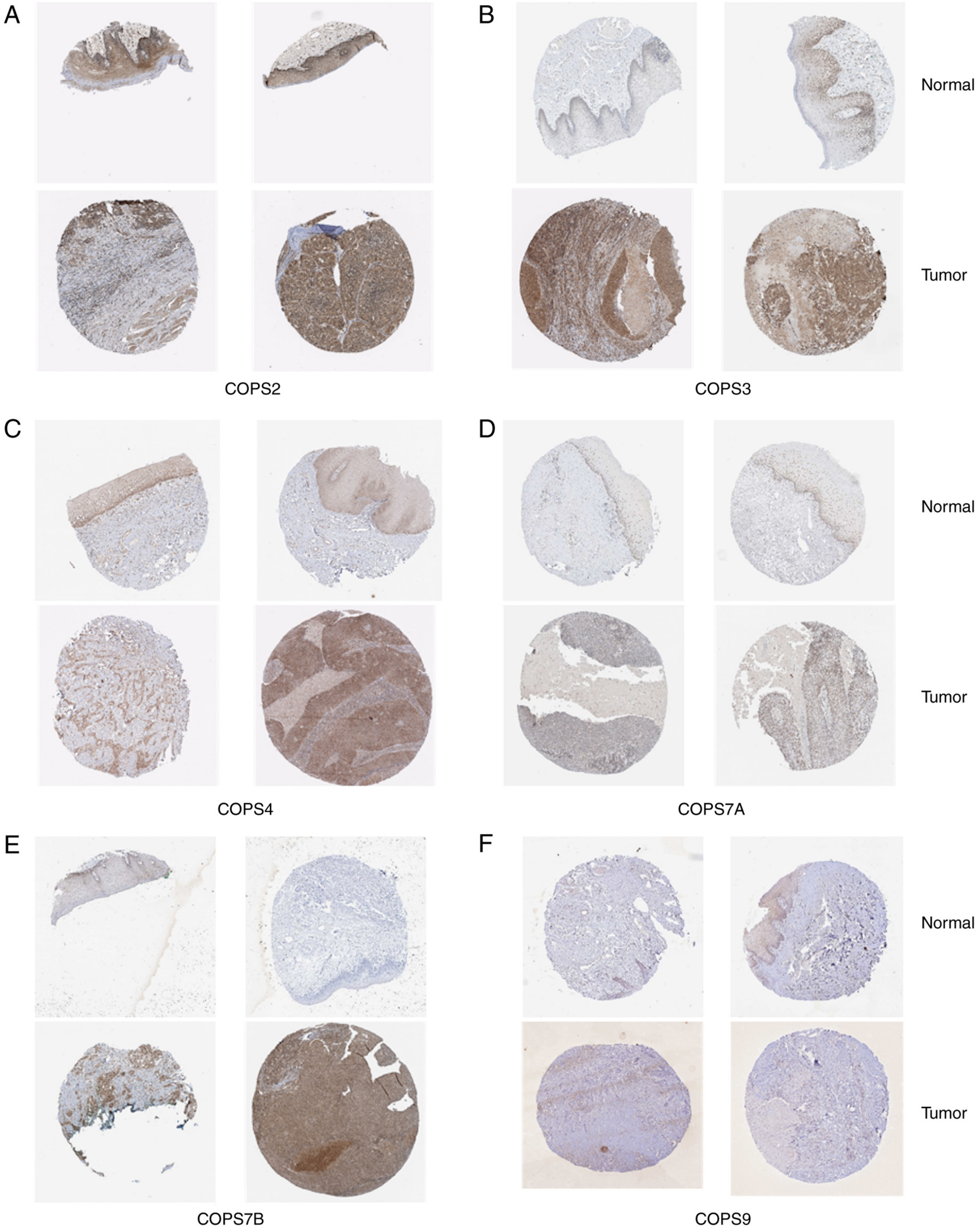

Table SI. Biological process terms of the COPS subunits from Gene Ontology functional enrichment analysis.

Description	P-value	Gene count	Gene ratio
Protein ubiquitination involved in ubiquitin-dependent protein catabolic process	9.90x10^{-17}	14	29.166
Protein neddylation	1.03x10^{-15}	8	16.666
Regulation of sequence-specific DNA binding transcription factor activity	2.82x10^{-13}	8	16.666
Protein ubiquitination	2.97x10^{-13}	15	31.250
Proteasome-mediated ubiquitin-dependent protein catabolic process	1.18x10^{-10}	11	22.916
Fc-epsilon receptor signaling pathway	8.81x10^{-10}	10	20.833
Ubiquitin-dependent protein catabolic process	1.07x10^{-09}	10	20.833
SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	4.50x10^{-09}	6	12.500
Regulation of transcription from RNA polymerase II promoter in response to hypoxia	1.03x10^{-08}	6	12.500
Viral process	8.06x10^{-08}	10	20.833
Nucleotide-excision repair, preincision complex stabilization	2.60x10^{-07}	5	10.416
G_1/S transition of mitotic cell cycle	2.91x10^{-07}	7	14.583
Nucleotide-excision repair, DNA duplex unwinding	3.18x10^{-07}	5	10.416
Nucleotide-excision repair, DNA damage recognition	3.84x10^{-07}	5	10.416
Nucleotide-excision repair, DNA incision, 3'-to lesion	3.84x10^{-07}	5	10.416
Protein polyubiquitination	5.40x10^{-07}	8	16.666
Nucleotide-excision repair, preincision complex assembly	1.02x10^{-06}	5	10.416
Intrinsic apoptotic signaling pathway	1.17x10^{-06}	5	10.416
Global genome nucleotide-excision repair	1.53x10^{-06}	5	10.416
Nucleotide-excision repair, DNA incision, 5'-to lesion	2.79x10^{-06}	5	10.416
Nucleotide-excision repair, DNA incision	3.11x10^{-06}	5	10.416
Histone H2A monoubiquitination	3.89x10^{-06}	4	8.333
Positive regulation of cyclase activity	2.10x10^{-05}	3	6.250
JUN phosphorylation	4.20x10^{-05}	3	6.250
DNA damage response, detection of DNA damage	1.21x10^{-04}	4	8.333
Regulation of circadian rhythm	3.04x10^{-04}	4	8.333
UV-damage excision repair	3.80x10^{-04}	3	6.250
Regulation of ossification	3.80x10^{-04}	3	6.250
Positive regulation of transcription, DNA-templated	4.05x10^{-04}	8	16.666
Rhythmic process	4.05x10^{-04}	4	8.333
Cell cycle arrest	5.43x10^{-04}	5	10.416
NIK/NF-κb signaling	7.31x10^{-04}	4	8.3333
Response to muscle stretch	8.23x10^{-04}	3	6.250
Transcription-coupled nucleotide-excision repair	1.00x10^{-03}	4	8.3333
Wnt signaling pathway	2.00x10^{-03}	5	10.416
Transforming growth factor β receptor signaling pathway	2.00x10^{-03}	4	8.333
Cellular response to DNA damage stimulus	2.00x10^{-03}	5	10.416
Transcription from RNA polymerase II promoter	2.00x10^{-03}	7	14.583
Protein monoubiquitination	3.00x10^{-03}	3	6.250
Cellular protein modification process	3.00x10^{-03}	4	8.333
Activation of MAPK activity	3.00x10^{-03}	4	8.333
Lipopolysaccharide-mediated signaling pathway	3.00x10^{-03}	3	6.250
Negative regulation of cell proliferation	4.00x10^{-03}	6	12.500
Peptidyl-serine phosphorylation	5.00x10^{-03}	4	8.333
Positive regulation of neuron apoptotic process	6.00x10^{-03}	3	6.250
Regulation of transcription from RNA polymerase II promoter	6.00x10^{-03}	6	12.500
Cellular response to hormone stimulus	6.00x10^{-03}	3	6.250
Response to camp	7.00x10^{-03}	3	6.250
JNK cascade	8.00x10^{-03}	3	6.250
Cardiac neural crest cell development involved in heart development	8.00x10^{-03}	2	4.166
MAPK import into nucleus	8.00x10^{-03}	2	4.166
Cellular response to calcium ion	8.00x10^{-03}	3	6.250

Table SI. Continued.

Description	P-value	Gene count	Gene ratio
Negative regulation of canonical Wnt signaling pathway	9.00x10^{-03}	4	8.333
Response to epidermal growth factor	1.00x10^{-02}	2	4.166
Regulation of Golgi inheritance	1.10x10^{-02}	2	4.166
Response to stress	1.20x10^{-02}	3	6.250
Caveolin-mediated endocytosis	1.30x10^{-02}	2	4.166
Positive regulation of transcription from RNA polymerase II promoter	1.50x10^{-02}	8	16.66
Trachea formation	1.60x10^{-02}	2	4.166
Cell cycle	2.00x10^{-02}	4	8.333
Regulation of stress-activated MAPK cascade	2.10x10^{-02}	2	4.166
Regulation of early endosome to late endosome transport	2.10x10^{-02}	2	4.166
Response to toxic substance	2.20x10^{-02}	3	6.250
Bergmann glial cell differentiation	2.40x10^{-02}	2	4.166
Outer ear morphogenesis	2.40x10^{-02}	2	4.166
MAPK cascade	3.30x10^{-02}	4	8.333
Protein phosphorylation	3.30x10^{-02}	5	10.416
Lung morphogenesis	3.40x10^{-02}	2	4.166
Interleukin-1-mediated signaling pathway	3.70x10^{-02}	2	4.166
JAK-STAT cascade involved in growth hormone signaling pathway	3.90x10^{-02}	2	4.166
Positive regulation of telomere capping	4.20x10^{-02}	2	4.166
Regulation of cell cycle	4.40x10^{-02}	3	6.250
Response to light stimulus	4.50x10^{-02}	2	4.166
Positive regulation of myoblast fusion	4.50x10^{-02}	2	4.166
Response to corticosterone	4.70x10^{-02}	2	4.166
Face development	4.70x10^{-02}	2	4.166
Response to drug	4.80x10^{-02}	4	8.333
Regulation of cytoskeleton organization	5.00x10^{-02}	2	4.166

COPS, COP9 signalosome.

Table SII. Cellular component terms of the COPS subunits from Gene Ontology functional enrichment analysis.

Description	P-value	Gene count	Gene ratio
SCF ubiquitin ligase complex	$2.51\text{x}10^{-19}$	12	25.000
Nucleoplasm	$2.28\text{x}10^{-13}$	30	62.500
Cullin-RING ubiquitin ligase complex	$1.02\text{x}10^{-11}$	6	12.500
Cul3-RING ubiquitin ligase complex	$3.14\text{x}10^{-10}$	8	16.666
Cytosol	$1.05\text{x}10^{-09}$	28	58.333
VCB complex	$1.24\text{x}10^{-09}$	5	10.416
Cul4B-RING E3 ubiquitin ligase complex	$1.50\text{x}10^{-07}$	4	8.333
Cul5-RING ubiquitin ligase complex	$5.23\text{x}10^{-07}$	4	8.333
Cul4A-RING E3 ubiquitin ligase complex	$1.78\text{x}10^{-06}$	4	8.333
Cul2-RING ubiquitin ligase complex	$3.26\text{x}10^{-06}$	4	8.333
Cul4-RING E3 ubiquitin ligase complex	$9.98\text{x}10^{-06}$	4	8.333
Cul7-RING ubiquitin ligase complex	$6.20\text{x}10^{-05}$	3	6.250
Nucleus	$4.13\text{x}10^{-04}$	26	54.166
Nuclear SCF ubiquitin ligase complex	$5.00\text{x}10^{-03}$	2	4.166
Parkin-FBXW7-Cul1 ubiquitin ligase complex	$8.00\text{x}10^{-03}$	2	4.166
Elongin complex	$2.20\text{x}10^{-02}$	2	4.166
Midbody	$4.20\text{x}10^{-02}$	3	6.250
Pseudopodium	$4.20\text{x}10^{-02}$	2	4.166

COPS, COP9 signalosome.

Table SIII. Molecular function terms of the COPS subunits from Gene Ontology functional enrichment analysis.

Description	P-value	Gene count	Gene ratio
Ubiquitin-protein transferase activity	8.75×10^{-18}	18	37.500
Ubiquitin protein ligase binding	8.87×10^{-16}	16	33.333
Ubiquitin protein ligase activity	2.56×10^{-15}	14	29.166
MAP kinase activity	2.64×10^{-10}	6	12.500
Protein binding	5.22×10^{-08}	43	89.583
NEDD8 transferase activity	8.08×10^{-08}	4	8.333
Cullin family protein binding	7.21×10^{-06}	4	8.333
Transcription factor binding	1.25×10^{-05}	8	16.666
JUN kinase activity	2.27×10^{-05}	3	6.250
Transcription factor activity, RNA polymerase II core promoter proximal region sequence-specific binding	3.44×10^{-05}	4	8.333
Kinase activity	5.35×10^{-04}	6	12.500
Transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding	4.00×10^{-03}	5	10.416
NEDD8 activating enzyme activity	5.00×10^{-03}	2	4.166
Damaged DNA binding	1.30×10^{-02}	3	6.250
RNA polymerase II core promoter proximal region sequence-specific DNA binding	1.60×10^{-02}	5	10.416
ATP binding	2.00×10^{-02}	10	20.833
MAP kinase kinase activity	3.30×10^{-02}	2	4.166
Phosphotyrosine binding	3.60×10^{-02}	2	4.166
Protein heterodimerization activity	4.00×10^{-02}	5	10.416

COPS, COP9 signalosome.

Table SIV. Pathways from Kyoto Encyclopedia of Genes and Genomes analysis of the COPS subunits.

Description	P-value	Gene count	Gene ratio
Ubiquitin mediated proteolysis	$4.83\text{x}10^{-29}$	23	47.916
Osteoclast differentiation	$1.00\text{x}10^{-09}$	11	22.916
Renal cell carcinoma	$4.43\text{x}10^{-08}$	8	16.666
Hepatitis B	$4.82\text{x}10^{-08}$	10	20.833
Pathways in cancer	$5.75\text{x}10^{-08}$	14	29.166
Pertussis	$1.09\text{x}10^{-07}$	8	16.666
Salmonella infection	$2.21\text{x}10^{-07}$	8	16.666
Colorectal cancer	$7.83\text{x}10^{-07}$	7	14.583
Chagas disease (American trypanosomiasis)	$1.05\text{x}10^{-06}$	8	16.666
Toll-like receptor signaling pathway	$1.19\text{x}10^{-06}$	8	16.666
TNF signaling pathway	$1.27\text{x}10^{-06}$	8	16.666
Prolactin signaling pathway	$1.76\text{x}10^{-06}$	7	14.583
Herpes simplex infection	$4.29\text{x}10^{-06}$	9	18.750
Wnt signaling pathway	$6.99\text{x}10^{-06}$	8	16.666
GnRH signaling pathway	$7.59\text{x}10^{-06}$	7	14.583
HIF-1 signaling pathway	$1.03\text{x}10^{-05}$	7	14.583
NOD-like receptor signaling pathway	$1.07\text{x}10^{-05}$	6	12.500
Choline metabolism in cancer	$1.39\text{x}10^{-05}$	7	14.583
Shigellosis	$2.06\text{x}10^{-05}$	6	12.500
Fc epsilon RI signaling pathway	$2.77\text{x}10^{-05}$	6	12.500
Neurotrophin signaling pathway	$3.71\text{x}10^{-05}$	7	14.583
FoxO signaling pathway	$6.91\text{x}10^{-05}$	7	14.583
Progesterone-mediated oocyte maturation	$9.13\text{x}10^{-05}$	6	12.500
ErbB signaling pathway	$9.13\text{x}10^{-05}$	6	12.500
Nucleotide excision repair	$1.07\text{x}10^{-04}$	5	10.416
Type II diabetes mellitus	$1.16\text{x}10^{-04}$	5	10.416
T cell receptor signaling pathway	$1.77\text{x}10^{-04}$	6	12.500
Retrograde endocannabinoid signaling	$1.85\text{x}10^{-04}$	6	12.500
Toxoplasmosis	$2.77\text{x}10^{-04}$	6	12.500
Influenza A	$2.91\text{x}10^{-04}$	7	14.583
MAPK signaling pathway	$3.35\text{x}10^{-04}$	8	16.666
Pancreatic cancer	$3.79\text{x}10^{-04}$	5	10.416
Sphingolipid signaling pathway	$4.14\text{x}10^{-04}$	6	12.500
Epithelial cell signaling in Helicobacter pylori infection	$4.26\text{x}10^{-04}$	5	10.416
Epstein-Barr virus infection	$4.47\text{x}10^{-04}$	6	12.500
B cell receptor signaling pathway	$4.77\text{x}10^{-04}$	5	10.416
Leishmaniasis	$5.32\text{x}10^{-04}$	5	10.416
Circadian rhythm	$5.81\text{x}10^{-04}$	4	8.333
cAMP signaling pathway	$5.82\text{x}10^{-04}$	7	14.583
Hepatitis C	$6.64\text{x}10^{-04}$	6	12.500
TGF-beta signaling pathway	$1.00\text{x}10^{-03}$	5	10.416
Protein processing in endoplasmic reticulum	$2.00\text{x}10^{-03}$	6	12.500
Tuberculosis	$2.00\text{x}10^{-03}$	6	12.500
Oocyte meiosis	$3.00\text{x}10^{-03}$	5	10.416
VEGF signaling pathway	$4.00\text{x}10^{-03}$	4	8.333
Focal adhesion	$5.00\text{x}10^{-03}$	6	12.500
Dopaminergic synapse	$5.00\text{x}10^{-03}$	5	10.416
RIG-I-like receptor signaling pathway	$6.00\text{x}10^{-03}$	4	8.333
Insulin signaling pathway	$6.00\text{x}10^{-03}$	5	10.416
Oxytocin signaling pathway	$8.00\text{x}10^{-03}$	5	10.416
Prion diseases	$1.40\text{x}10^{-02}$	3	6.250
Inflammatory mediator regulation of TRP channels	$1.50\text{x}10^{-02}$	4	8.333

Table SIV. Continued.

Description	P-value	Gene count	Gene ratio
Estrogen signaling pathway	$1.60\text{x}10^{-02}$	4	8.333
Viral carcinogenesis	$2.30\text{x}10^{-02}$	5	10.416
Cell cycle	$2.80\text{x}10^{-02}$	4	8.333
Ras signaling pathway	$3.20\text{x}10^{-02}$	5	10.416
Non-alcoholic fatty liver disease	$4.70\text{x}10^{-02}$	4	8.333
Amphetamine addiction	$4.90\text{x}10^{-02}$	3	6.250

COPS, COP9 signalosome.

Table SV. Gene Set Enrichment analysis of high expression of COPS5 using Hallmark annotation.

Name	Counts	Es	Nes	Nom P-value	FDR q-value	Fwer P-value
HALLMARK_DNA_REPAIR	148	-0.778	-2.332	0	0	0
HALLMARK_UV_RESPONSE_UP	156	-0.651	-2.310	0	0	0
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	110	-0.783	-2.244	0	0	0
HALLMARK_MTORC1_SIGNALING	198	-0.724	-2.216	0	2.88x10^{-04}	1.00x10^{-03}
HALLMARK_MYC_TARGETS_V1	197	-0.851	-2.211	0	2.30x10^{-04}	1.00x10^{-03}
HALLMARK_GLYCOLYSIS	197	-0.638	-2.168	0	4.53x10^{-04}	2.00x10^{-03}
HALLMARK_PI3K_AKT_MTOR_SIGNALING	104	-0.703	-2.137	0	8.70x10^{-04}	5.00x10^{-03}
HALLMARK_G2M_CHECKPOINT	192	-0.804	-2.129	0	9.05x10^{-04}	6.00x10^{-03}
HALLMARK_MYC_TARGETS_V2	58	-0.859	-2.128	0	8.04x10^{-04}	6.00x10^{-03}
HALLMARK_P53_PATHWAY	197	-0.613	-2.118	0	7.24x10^{-04}	6.00x10^{-03}
HALLMARK_E2F_TARGETS	197	-0.824	-2.116	0	6.58x10^{-04}	6.00x10^{-03}
HALLMARK_PROTEIN_SECRETION	95	-0.766	-2.109	0	9.84x10^{-04}	8.00x10^{-03}
HALLMARK_ADIPOGENESIS	194	-0.655	-2.108	0	9.08x10^{-04}	8.00x10^{-03}
HALLMARK_HEME_METABOLISM	197	-0.605	-2.071	0	1.00x10^{-03}	1.10x10^{-02}
HALLMARK_OXIDATIVE_PHOSPHORYLATION	184	-0.731	-2.055	0	1.00x10^{-03}	1.30x10^{-02}
HALLMARK_APOPTOSIS	160	-0.599	-2.054	0	1.00x10^{-03}	1.30x10^{-02}
HALLMARK_MITOTIC_SPINDLE	198	-0.701	-1.976	0	3.00x10^{-03}	2.30x10^{-02}
HALLMARK_PEROXISOME	104	-0.593	-1.961	0	3.00x10^{-03}	2.90x10^{-02}
HALLMARK_ESTROGEN_RESPONSE_LATE	197	-0.510	-1.921	0	5.00x10^{-03}	5.30x10^{-02}
HALLMARK_FATTY_ACID_METABOLISM	157	-0.587	-1.919	3.00x10^{-03}	5.00x10^{-03}	5.30x10^{-02}
HALLMARK_APICAL_JUNCTION	194	-0.553	-1.875	4.00x10^{-03}	8.00x10^{-03}	7.70x10^{-02}
HALLMARK_SPERMATOGENESIS	135	-0.516	-1.864	2.00x10^{-03}	8.00x10^{-03}	8.10x10^{-02}
HALLMARK_HYPOXIA	191	-0.527	-1.849	5.00x10^{-03}	9.00x10^{-03}	8.50x10^{-02}
HALLMARK_ANDROGEN_RESPONSE	96	-0.587	-1.824	0	1.20x10^{-02}	1.00x10^{-01}
HALLMARK_COMPLEMENT	199	-0.533	-1.811	1.40x10^{-02}	1.30x10^{-02}	1.10x10^{-01}
HALLMARK_TGF_β_SIGNALING	54	-0.647	-1.808	1.40x10^{-02}	1.30x10^{-02}	1.12x10^{-01}
HALLMARK_WNT_β_CATENIN_SIGNALING	42	-0.614	-1.791	2.00x10^{-03}	1.50x10^{-02}	1.24x10^{-01}
HALLMARK_NOTCH_SIGNALING	32	-0.614	-1.790	6.00x10^{-03}	1.40x10^{-02}	1.24x10^{-01}
HALLMARK_IL2_STAT5_SIGNALING	196	-0.511	-1.779	2.10x10^{-02}	1.50x10^{-02}	1.31x10^{-01}
HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY	47	-0.601	-1.772	1.90x10^{-02}	1.50x10^{-02}	1.34x10^{-01}
HALLMARK_XENOBIOTIC_METABOLISM	199	-0.473	-1.751	9.00x10^{-03}	1.80x10^{-02}	1.54x10^{-01}
HALLMARK_TNFA_SIGNALING_VIA_NFKB	198	-0.531	-1.691	4.70x10^{-02}	2.80x10^{-02}	2.15x10^{-01}
HALLMARK_ESTROGEN_RESPONSE_EARLY	195	-0.474	-1.668	2.20x10^{-02}	3.30x10^{-02}	2.35x10^{-01}
HALLMARK_CHOLESTEROL_HOMEOSTASIS	74	-0.510	-1.657	2.90x10^{-02}	3.50x10^{-02}	2.51x10^{-01}
HALLMARK_INTERFERON_γ_RESPONSE	199	-0.607	-1.649	4.80x10^{-02}	3.50x10^{-02}	2.57x10^{-01}
HALLMARK_INTERFERON_α_RESPONSE	95	-0.711	-1.643	4.80x10^{-02}	3.50x10^{-02}	2.64x10^{-01}
HALLMARK_BILE_ACID_METABOLISM	112	-0.466	-1.627	3.80x10^{-02}	3.80x10^{-02}	2.82x10^{-01}
HALLMARK_PANCREAS_β_CELLS	40	-0.492	-1.583	1.40x10^{-02}	4.70x10^{-02}	3.32x10^{-01}

ES, enrichment score; FDR, false discovery rate; FWER, family-wise error rate; NES, normalized enrichment score; NOM, nominal.

Table SVI. Gene Set Enrichment Analysis of high expression of COPS6 using Hallmark annotation.

Name	Counts	Es	Nes	Nom P-value	FDR q-value	Fwer P-value
HALLMARK_DNA_REPAIR	148	-0.782	-2.314	0	0	0
HALLMARK_UV_RESPONSE_UP	156	-0.645	-2.277	0	0	0
HALLMARK_MYC_TARGETS_V1	197	-0.855	-2.255	0	0	0
HALLMARK_OXIDATIVE_PHOSPHORYLATION	184	-0.793	-2.201	0	0	0
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	110	-0.764	-2.199	0	0	0
HALLMARK_ADIPOGENESIS	194	-0.700	-2.193	0	0	0
HALLMARK_MTORC1_SIGNALING	198	-0.712	-2.190	0	0	0
HALLMARK_P53_PATHWAY	197	-0.622	-2.158	0	4.23x10^{-04}	1.00x10^{-03}
HALLMARK_GLYCOLYSIS	197	-0.643	-2.150	0	3.76x10^{-04}	1.00x10^{-03}
HALLMARK_FATTY_ACID_METABOLISM	157	-0.654	-2.105	0	5.44x10^{-04}	3.00x10^{-03}
HALLMARK_PEROXISOME	104	-0.643	-2.078	0	7.48x10^{-04}	5.00x10^{-03}
HALLMARK_XENOBIOTIC_METABOLISM	199	-0.563	-2.048	2.00x10^{-03}	2.00x10^{-03}	1.20x10^{-02}
HALLMARK_E2F_TARGETS	197	-0.823	-2.046	0	1.00x10^{-03}	1.20x10^{-02}
HALLMARK_PI3K_AKT_MTOR_SIGNALING	104	-0.684	-2.043	0	1.00x10^{-03}	1.20x10^{-02}
HALLMARK_HEME_METABOLISM	197	-0.603	-2.030	0	2.00x10^{-03}	1.40x10^{-02}
HALLMARK_MYC_TARGETS_V2	58	-0.841	-2.026	2.00x10^{-03}	2.00x10^{-03}	1.50x10^{-02}
HALLMARK_APOPTOSIS	160	-0.602	-2.012	0	2.00x10^{-03}	1.80x10^{-02}
HALLMARK_ESTROGEN_RESPONSE_LATE	197	-0.545	-2.010	2.00x10^{-03}	2.00x10^{-03}	1.80x10^{-02}
HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY	47	-0.680	-2.005	2.00x10^{-03}	2.00x10^{-03}	1.80x10^{-02}
HALLMARK_CHOLESTEROL_HOMEOSTASIS	74	-0.619	-1.990	2.00x10^{-03}	2.00x10^{-03}	2.10x10^{-02}
HALLMARK_G$_2$M_CHECKPOINT	192	-0.751	-1.987	0	2.00x10^{-03}	2.10x10^{-02}
HALLMARK_MITOTIC_SPINDLE	198	-0.704	-1.949	0	3.00x10^{-03}	2.80x10^{-02}
HALLMARK_WNT_β_CATENIN_SIGNALING	42	-0.659	-1.902	0	5.00x10^{-03}	5.80x10^{-02}
HALLMARK_PROTEIN_SECRETION	95	-0.687	-1.883	4.00x10^{-03}	6.00x10^{-03}	6.10x10^{-02}
HALLMARK_SPERMATOGENESIS	135	-0.517	-1.839	0	9.00x10^{-03}	8.90x10^{-02}
HALLMARK_HYPOXIA	191	-0.540	-1.840	1.10x10^{-02}	9.00x10^{-03}	8.90x10^{-02}
HALLMARK_BILE_ACID_METABOLISM	112	-0.540	-1.834	3.00x10^{-03}	9.00x10^{-03}	8.90x10^{-02}
HALLMARK_ANDROGEN_RESPONSE	96	-0.593	-1.810	4.00x10^{-03}	1.10x10^{-02}	1.08x10^{-01}
HALLMARK_APICAL_JUNCTION	194	-0.533	-1.767	6.00x10^{-03}	1.60x10^{-02}	1.34x10^{-01}
HALLMARK_NOTCH_SIGNALING	32	-0.598	-1.697	9.00x10^{-03}	2.70x10^{-02}	2.04x10^{-01}
HALLMARK_IL2_STAT5_SIGNALING	196	-0.495	-1.675	2.20x10^{-02}	3.10x10^{-02}	2.29x10^{-01}
HALLMARK_ESTROGEN_RESPONSE_EARLY	195	-0.481	-1.657	3.20x10^{-02}	3.40x10^{-02}	2.44x10^{-01}
HALLMARK_COMPLEMENT	199	-0.499	-1.641	4.40x10^{-02}	3.70x10^{-02}	2.62x10^{-01}
HALLMARK_APICAL_SURFACE	43	-0.476	-1.545	3.20x10^{-02}	6.50x10^{-02}	3.79x10^{-01}

ES, enrichment score; FDR, false discovery rate; FWER, family-wise error rate; NES, normalized enrichment score; NOM, nominal.

Table SVII. Gene Set Enrichment Analysis of high expression of COPS8 in Hallmark annotation.

Name	Counts	Es	Nes	Nom P-value	FDR q-value	Fwer P-value
HALLMARK_UV_RESPONSE_UP	156	-0.627	-2.268	0	1.00x10^{-03}	1.00x10^{-03}
HALLMARK_APOPTOSIS	160	-0.643	-2.252	0	5.47x10^{-04}	1.00x10^{-03}
HALLMARK_GLYCOLYSIS	197	-0.657	-2.243	0	3.64x10^{-04}	1.00x10^{-03}
HALLMARK_APICAL_JUNCTION	194	-0.649	-2.231	0	2.73x10^{-04}	1.00x10^{-03}
HALLMARK_DNA_REPAIR	148	-0.740	-2.213	0	6.30x10^{-04}	2.00x10^{-03}
HALLMARK_HYPOXIA	191	-0.620	-2.205	0	5.25x10^{-04}	2.00x10^{-03}
HALLMARK_ANDROGEN_RESPONSE	96	-0.694	-2.170	0	4.50x10^{-04}	2.00x10^{-03}
HALLMARK_ADIPOGENESIS	194	-0.660	-2.169	0	3.94x10^{-04}	2.00x10^{-03}
HALLMARK_MITOTIC_SPINDLE	198	-0.761	-2.165	0	4.64x10^{-04}	2.00x10^{-03}
HALLMARK_HEME_METABOLISM	197	-0.620	-2.148	0	6.23x10^{-04}	2.00x10^{-03}
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	110	-0.747	-2.140	0	7.66x10-^{04}	3.00x10^{-03}
HALLMARK_PROTEIN_SECRETION	95	-0.773	-2.138	2.00x10^{-03}	7.02x10^{-04}	3.00x10^{-03}
HALLMARK_IL2_STAT5_SIGNALING	196	-0.599	-2.134	2.00x10^{-03}	9.01x10^{-04}	5.00x10^{-03}
HALLMARK_UV_RESPONSE_DN	137	-0.704	-2.133	0	8.36x10^{-04}	5.00x10^{-03}
HALLMARK_PI3K_AKT_MTOR_SIGNALING	104	-0.684	-2.117	2.00x10^{-03}	1.00x10^{-03}	5.00x10^{-03}
HALLMARK_G2M_CHECKPOINT	192	-0.765	-2.113	0	9.97x10^{-04}	5.00x10^{-03}
HALLMARK_WNT_β_CATENIN_SIGNALING	42	-0.718	-2.100	0	9.38x10^{-04}	5.00x10^{-03}
HALLMARK_MTORC1_SIGNALING	198	-0.677	-2.095	0	9.47x10^{-04}	5.00x10^{-03}
HALLMARK_TGF_β_SIGNALING	54	-0.752	-2.073	0	1.00x10^{-03}	7.00x10^{-03}
HALLMARK_E2F_TARGETS	197	-0.784	-2.060	0	1.00x10^{-03}	7.00x10^{-03}
HALLMARK_KRAS_SIGNALING_UP	195	-0.569	-2.047	2.00x10^{-03}	9.95x10^{-04}	7.00x10^{-03}
HALLMARK_MYC_TARGETS_V1	197	-0.769	-2.044	0	9.50x10^{-04}	7.00x10^{-03}
HALLMARK_P53_PATHWAY	197	-0.598	-2.043	0	9.55x10^{-04}	8.00x10^{-03}
HALLMARK_NOTCH_SIGNALING	32	-0.689	-2.025	0	1.00x10^{-03}	1.30x10^{-02}
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	197	-0.713	-2.014	0	2.00x10^{-03}	1.60x10^{-02}
HALLMARK_FATTY_ACID_METABOLISM	157	-0.595	-2.001	0	2.00x10^{-03}	2.00x10^{-02}
HALLMARK_ANGIOGENESIS	36	-0.719	-2.001	0	2.00x10^{-03}	2.10x10^{-02}
HALLMARK_COMPLEMENT	199	-0.596	-1.992	6.00x10^{-03}	2.00x10^{-03}	2.30x10^{-02}
HALLMARK_OXIDATIVE_PHOSPHORYLATION	184	-0.671	-1.987	1.20x10^{-02}	2.00x10^{-03}	2.30x10^{-02}
HALLMARK_XENOBIOTIC_METABOLISM	199	-0.531	-1.967	0	2.00x10^{-03}	2.70x10^{-02}
HALLMARK_TNFA_SIGNALING_VIA_NFKB	198	-0.615	-1.951	6.00x10^{-03}	3.00x10^{-03}	3.10x10^{-02}
HALLMARK_SPERMATOGENESIS	135	-0.520	-1.940	0	3.00x10^{-03}	3.30x10^{-02}
HALLMARK_HEDGEHOG_SIGNALING	35	-0.655	-1.934	0	3.00x10^{-03}	3.60x10^{-02}
HALLMARK_PEROXISOME	104	-0.579	-1.926	2.00x10^{-03}	3.00x10^{-03}	4.00x10^{-02}
HALLMARK_ESTROGEN_RESPONSE_EARLY	195	-0.534	-1.919	4.00x10^{-03}	3.00x10^{-03}	4.30x10^{-02}
HALLMARK_IL6_JAK_STAT3_SIGNALING	86	-0.609	-1.886	8.00x10^{-03}	4.00x10^{-03}	6.30x10^{-02}
HALLMARK_INFLAMMATORY_RESPONSE	198	-0.584	-1.884	6.00x10^{-03}	4.00x10^{-03}	6.40x10^{-02}
HALLMARK_ESTROGEN_RESPONSE_LATE	197	-0.493	-1.841	4.00x10^{-03}	6.00x10^{-03}	8.50x10^{-02}
HALLMARK_PANCREAS_β_CELLS	40	-0.563	-1.838	0	6.00x10^{-03}	8.90x10^{-02}
HALLMARK_MYC_TARGETS_V2	58	-0.741	-1.825	2.00x10^{-03}	6.00x10^{-03}	9.40x10^{-02}
HALLMARK_COAGULATION	138	-0.538	-1.819	8.00x10^{-03}	7.00x10^{-03}	9.90x10^{-02}
HALLMARK_ALLOGRAFT_REJECTION	199	-0.574	-1.743	4.00x10^{-02}	1.40x10^{-02}	1.69x10^{-01}
HALLMARK_BILE_ACID_METABOLISM	112	-0.500	-1.740	1.10x10^{-02}	1.40x10^{-02}	1.71x10^{-01}
HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY	47	-0.579	-1.732	1.10x10^{-02}	1.50x10^{-02}	1.75x10^{-01}
HALLMARK_CHOLESTEROL_HOMEOSTASIS	74	-0.537	-1.725	1.50x10^{-02}	1.50x10^{-02}	1.86x10^{-01}
HALLMARK_APICAL_SURFACE	43	-0.496	-1.645	1.50x10^{-02}	2.70x10^{-02}	2.69x10^{-01}
HALLMARK_KRAS_SIGNALING_DN	195	-0.386	-1.575	2.40x10^{-02}	4.20x10^{-02}	3.51x10^{-01}

ES, enrichment score; FDR, false discovery rate; FWER, family-wise error rate; NES, normalized enrichment score; NOM, nominal.

Table SVIII. CERES score of the COPS subunits in the head and neck squamous cell carcinoma cell lines.

	CERES SCORE									
Cell line	COPS1	COPS2	COPS3	COPS4	COPS5	COPS6	COPS7A	COPS7B	COPS8	COPS9
SCC9	-1.28934	-0.66186	-1.22417	-1.24944	-1.16996	-1.74139	-0.06412	-0.0028	-1.21462	-0.43712
BICR31	-1.00316	-0.64892	-1.38969	-0.99958	-1.18269	-1.57543	-0.32725	0.334408	-0.90385	-0.27625
SCC4	-1.04122	-0.68956	-1.13561	-0.98027	-1.10797	-1.00064	-0.03847	0.115902	-0.72334	-0.02167
BICR6	-1.37128	-0.88969	-1.45932	-1.18533	-1.42743	-1.65818	-0.0239	0.158193	-1.22956	-0.41849
HSC2	-0.97339	-0.49881	-1.05116	-0.97342	-1.34365	-1.55188	-0.08035	0.241614	-1.01897	-0.17959
SNU46	-1.02281	-0.26952	-1.64207	-1.42176	-0.75256	-1.46351	0.19913	0.387861	-1.19944	-0.02277
BICR16	-1.27399	-0.65448	-0.90978	-1.5647	-1.31868	-1.5756	-0.66187	0.276205	-1.16554	-0.12389
CAL33	-1.33496	-0.82783	-1.26041	-1.24421	-1.22647	-1.96546	-0.25247	0.100612	-1.01106	-0.3496
BHY	-1.1153	-0.68258	-1.19977	-1.16481	-1.4294	-1.68529	-0.11417	0.147281	-1.16541	-0.3494
SNU1076	-1.15394	-0.47483	-1.17187	-1.29453	-1.19382	-1.76827	-0.20979	0.097881	-1.21114	-0.32702
PECAPJ34 CLONEC12	-0.90251	-0.81858	-1.0207	-1.07345	-1.19684	-1.5041	0.100057	0.069725	-0.78916	-0.60219
SNU1041	-1.19455	-0.89721	-1.12502	-1.25261	-1.40313	-1.83789	0.000802	0.216124	-1.12394	-0.23212
PECAPJ15	-1.22508	-0.8439	-1.255	-1.43533	-1.5806	-1.30705	-0.0195	0.167109	-1.00942	-0.38314
YD8	-1.03407	-0.83597	-1.12926	-0.93722	-1.30552	-1.60048	-0.37294	0.269899	-1.33473	-0.21245
SNU1066	-1.34675	-1.0735	-1.39344	-1.66302	-1.31321	-1.50439	-0.51127	0.130286	-1.18701	-0.53291
PECAPJ41 CLONED2	-1.13937	-0.77267	-1.15171	-1.0099	-0.87715	-1.30251	-0.22419	0.077994	-0.96826	-0.60421
PECAPJ49	-1.03551	-0.81406	-1.18803	-1.12162	-0.97153	-1.76352	-0.15102	0.125814	-0.95677	-0.23279
A253	-1.20051	-0.9579	-1.2889	-1.46499	-1.1688	-1.63601	-0.24868	0.229367	-1.02174	-0.21491
YD38	-1.14614	-0.93706	-1.03643	-1.03843	-1.37084	-1.71803	-0.20689	0.340158	-0.77187	0.011194
BICR56	-1.24409	-0.76651	-1.25522	-1.35289	-1.39892	-1.72609	-0.26801	0.15419	-1.26355	-0.57121
HSC3	-1.17914	-1.23168	-1.17379	-1.09276	-1.59412	-1.87178	-0.32912	0.376717	-0.95882	-0.21834

COPS, COP9 signalosome.