Table SI. Primers for RT-qPCR.

Transcript	**Primer**	**Sequence, 5'-3'**
β-actin	Forward	TCACCCACACTGTGCCCATCTACGA
	Reverse	CAGCGGAACCGCTCATTGCCAATGG
ANKRD1	Forward	CGGAGCATCTTATCGCCTGT
	Reverse	AGTCTCACCGCATCATGCAA
E-cadherin	Forward	TGCACCAACCCTCATGAGTG
	Reverse	GTCAGTATCAGCCGCTTTCAG
Endothelin-1	Forward	CAAACCAGGTCGGAGACCAT
	Reverse	GCTCGGTTGTGGGTCACATA
IL-6	Forward	CTTCGGTCCAGTTGCCTTCT
	Reverse	TGGAATCTTCTCCTGGGGGT
MMP-9	Forward	GGTGATTGACGACGCCTTTG
	reverse	CTGTACACGCGAGTGAAGGT
PLAU	forward	GATACGAACAGGCGAACTGTG
	reverse	TGCTGCCCTCCGAATTTCTT
UBE2T	forward	GCGAGCTCGTAGAAATATTAGGTG
	reverse	GAGAAATCGGATCTGAGGAGGT
Vimentin	forward	GCAAAGATTCCACTTTGCGT
	reverse	GAAATTGCAGGAGGAGATGC

ANKRD1, ankyrin repeat domain 1; IL-6, interleukin-6; MMP-9, matrix metalloproteinase-9; PLAU, plasminogen activator, urokinase; UBE2T, ubiquitin-conjugating enzyme E2 T.

Table SII. The genes with HR≥1.5 in KM-plotter analysis, identified among top 500 genes with upregulated expression in head and neck cancer tissues listed in GEPIA database.

Gene symbol	Gene name	HR	P-value
ADA	Adenosine Deaminase	1.5	0.014
AGTRAP	Angiotensin II Receptor Associated Protein	1.5	0.0083
ANO1	Anoctamin 1	1.73	$7.30x10^{-5}$
ARSI	Arylsulfatase Family Member I	1.5	0.0028
B4GALNT1	Beta-1,4-N-Acetyl-Galactosaminyltransferase 1	1.5	0.0027
BASP1	Brain Abundant Membrane Attached Signal Protein 1	1.59	0.00066
C16orf74	Chromosome 16 Open Reading Frame 74	1.78	0.00014
CXCL8	C-X-C Motif Chemokine Ligand 8	1.52	0.0048
DCBLD1	Discoidin, CUB And LCCL Domain Containing 1	1.51	0.0023
DKK1	Dickkopf WNT Signaling Pathway Inhibitor 1	2.12	$4.40x10^{-8}$
DUSP9	Dual Specificity Phosphatase 9	1.64	0.0038
ECT2	Epithelial Cell Transforming 2	1.56	0.01
FADS3	Fatty Acid Desaturase 3	1.76	$7.70x10^{-5}$
FAP	Fibroblast Activation Protein Alpha	1.59	0.00066
FN1	Fibronectin 1	1.5	0.0035
FOXD1	Forkhead Box D1	1.58	0.00073
FSCN1	Fascin Actin-Bundling Protein 1	1.81	0.00058
FST	Follistatin	1.65	0.0017
FSTL3	Follistatin Like 3	1.72	0.0015
GNA12	G Protein Subunit Alpha 12	1.57	0.0013
HIST2H2AA4	H2A Clustered Histone 19	1.55	0.0027
HMGA2	High Mobility Group AT-Hook 2	1.66	0.00057
IGF2BP2	Insulin Like Growth Factor 2 MRNA Binding Protein 2	2.01	$5.10x10^{-5}$
INHBA	Inhibin Subunit Beta A	1.66	0.00065
ITGA3	Integrin Subunit Alpha 3	1.73	0.00014
ITGA5	Integrin Subunit Alpha 5	1.63	0.00029
ITGA6	Integrin Subunit Alpha 6	1.7	$1.00x10^{-4}$
ITM2C	Integral Membrane Protein 2C	12.8	0.074
KLF7	KLF Transcription Factor 7	1.51	0.0028
LGALS1	Galectin 1	1.51	0.0027
LINC00958	Long Intergenic Non-Protein Coding RNA 958	1.56	0.001

LYPD1	LY6/PLAUR Domain Containing 1	1.51	0.016
MAGED4	MAGE Family Member D4	1.54	0.0024
MET	MET Proto-Oncogene, Receptor Tyrosine Kinase	1.58	0.0019
MFAP2	Microfibril Associated Protein 2	1.55	0.0015
MMP13	Matrix Metallopeptidase 13	1.51	0.0081
MMP14	Matrix Metallopeptidase 14	1.52	0.011
MYO1B	Myosin IB	1.66	0.0038
NRG1	Neuregulin 1	2.39	0.057
NT5E	5'-Nucleotidase Ecto	1.54	0.0014
P4HA1	Prolyl 4-Hydroxylase Subunit Alpha 1	1.83	$1.40x10^{-5}$
P4HA2	Prolyl 4-Hydroxylase Subunit Alpha 2	1.62	0.0062
PLAU	Plasminogen Activator, Urokinase	1.72	0.00027
PLOD2	Procollagen-Lysine, 2-Oxoglutarate 5-Dioxygenase 2	1.72	0.0023
PMEPA1	Prostate Transmembrane Protein, Androgen Induced 1	1.61	0.0028
PXN	Paxillin	1.67	0.00036
RAB32	RAB32, Member RAS Oncogene Family	1.58	0.0026
RFC4	Replication Factor C Subunit 4	1.52	0.012
SCG5	Secretogranin V	1.55	0.0011
SERPINE1	Serpin Family E Member 1	1.93	$3.70x10^{-5}$
SERPINH1	Serpin Family H Member 1	1.66	0.00019
SFXN3	Sideroflexin 3	1.65	0.00038
STC2	Stanniocalcin 2	1.82	$1.50x10^{-5}$
TENM2	Teneurin Transmembrane Protein 2	1.54	0.0049
TGFBI	Transforming Growth Factor Beta 1	1.86	0.00034
TINAGL1	Tubulointerstitial Nephritis Antigen Like 1	1.54	0.002
TMEM92	Transmembrane Protein 92	1.58	0.00086
TNFAIP6	TNF Alpha Induced Protein 6	1.5	0.0033
TNFRSF12A	TNF Receptor Superfamily Member 12A	1.52	0.0023
TNFRSF6B	TNF Receptor Superfamily Member 6b	1.52	0.0026
TPST1	Tyrosylprotein Sulfotransferase 1	1.5	0.0028
UBE2T	Ubiquitin-Conjugating Enzyme E2 T	1.5	0.0061
WDR66	Cilia And Flagella Associated Protein 251	1.53	0.011
WNT7A	Wnt Family Member 7A	1.56	0.0012

GEPIA, gene expression profiling interactive analysis; KM-plotter, Kaplan-Meier plotter; HR, hazard ratio.

Table SIII. Stage plot results of top 10 genes showing the strongest correlation with head and neck cancer stage progression.

Gene symbol	Gene name	Stage F-value	P-value
UBE2T	Ubiquitin-conjugating enzyme 2T E	5.02	0.00193
C16orf74	Chromosome 16 Open Reading Frame 74	3.78	0.0105
PLOD2	Procollagen-Lysine,2-Oxoglutarate 5-Dioxygenase 2	3.64	0.0128
P4HA1	Prolyl 4-Hydroxylase Subunit Alpha-1	3.63	0.0129
STC2	Stanniocalcin 2	3.57	0.0139
FN1	Fibronectin 1	2.82	0.0384
RFC4	Replication Factor C Subunit 4	2.51	0.0583
MAGED4	Melanoma-Associated Antigen D4	2.12	0.0965
DCBLD1	Discoidin, CUB and LCCL Domain-containing 1	2.06	0.105
SCG5	Secretogranin V	2.01	0.111

Table SIV. GSEA results of UBE2T SAS cells vs. Control SAS cells.

Gene sets	NES	Nominal P-value
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	2.06	<0.0001
HALLMARK_MYC_TARGETS_V1	1.97	<0.0001
HALLMARK_OXIDATIVE_PHOSPHORYLATION	1.84	<0.0001
HALLMARK_KRAS_SIGNALING_UP	1.81	<0.0001
HALLMARK_FATTY_ACID_METABOLISM	1.72	<0.0001
HALLMARK_IL6_JAK_STAT3_SIGNALING	1.70	0.0046
HALLMARK_INTERFERON_GAMMA_RESPONSE	1.69	<0.0001
HALLMARK_TNFA_SIGNALING_VIA_NFKB	1.65	<0.0001
HALLMARK_UV_RESPONSE_UP	1.62	0.001
HALLMARK_MTORC1_SIGNALING	1.58	<0.0001

GSEA, gene set enrichment analysis; IL6, interleukin-6; JAK, Janus protein tyrosine kinase; MTORC1, mammalian target of rapamycin complex 1; NES, normalized enrichment score; NFKB, nuclear factor-κB; STAT3, signal transducer and activator of transcription 3; TNFA, tumor necrosis factor-α; UBE2T, ubiquitin-conjugating enzyme E2 T.

Table SV. List of 62 DEGs upregulated more than 3.0-fold in UBE2T SAS cells vs. Control SAS cells.

		Expression level log2(TPM+1)			
Gene Identifier	**Ensemble ID**	**NC_1**	**NC_2**	**UBE2T_1**	**UBE2T_2**
ALOX5AP	ENSG00000132965	0.7178699	0.9993426	2.7623286	2.6654954
ANKRD1	ENSG00000148677	4.695823	5.33594	6.7235913	6.697821
ANO2	ENSG00000047617	2.7596478	3.3816879	5.382657	5.3583055
BACE2	ENSG00000182240	0.7073071	0.9158071	2.558877	2.644311
CAPSL	ENSG00000152611	0.3884942	0.8216217	2.4955034	2.7364442
CDH11	ENSG00000140937	0.3334015	0.4879215	2.8864522	2.9246304
CHN1	ENSG00000128656	1.9297448	2.460602	3.959442	3.9606454
CSF2	ENSG00000164400	2.3081574	3.0571268	5.343888	5.346417
CXCL1	ENSG00000163739	1.2050318	1.5381256	4.3657136	4.3920074
DAW1	ENSG00000123977	3.7121882	4.579878	5.951195	5.9312344
ECSCR	ENSG00000249751	2.1829805	2.8634233	4.534851	4.5626116
EDIL3	ENSG00000164176	1.3319232	1.8040282	3.1102366	3.2384324
EDN1	ENSG00000078401	1.363468	1.5760233	3.3225675	3.1704574
GJA1	ENSG00000152661	0.6005657	0.8955959	5.082703	5.158631
GSG1	ENSG00000111305	0.9041107	1.4594278	2.955711	2.9257584
HHAT	ENSG00000054392	1.4710141	1.8755703	4.268314	4.33598
HSD11B1	ENSG00000117594	4.2269077	5.0969095	7.3550453	7.327537
IGFL1	ENSG00000188293	2.9462502	3.3641484	5.482359	5.3482456
IL32	ENSG00000008517	2.8526955	3.388186	4.9799056	4.9011755
IL6	ENSG00000136244	0.7130638	1.1922693	3.094498	3.0411346
KRT81	ENSG00000205426	5.935103	6.830429	8.479475	8.507409
KRT86	ENSG00000170442	2.384861	3.118648	4.568863	4.604279
KRTAP2-3	ENSG00000212724	5.249469	5.7748847	7.1854763	7.312811
LINC00601	ENSG00000235180	1.7514783	2.8383687	4.0925775	3.8191571
LOX	ENSG00000113083	2.8349707	3.6084135	4.878864	4.9239645
LYPD1	ENSG00000150551	2.7977455	4.0189567	5.56027	5.7980657
MAOA	ENSG00000189221	2.8558064	3.6994224	6.025945	5.9751167
MMP9	ENSG00000100985	0.7711058	1.2144533	3.1434715	3.265
NEFL	ENSG00000277586	1.6817783	2.3697867	4.0942397	4.005871

NGF	ENSG00000134259	1.4406396	2.1250641	3.6721816	3.7435563
NNMT	ENSG00000166741	3.4475274	4.213741	6.6662846	6.650917
NTF3	ENSG00000185652	1.2921809	1.695057	3.7027931	3.6075027
PLAU	ENSG00000122861	6.853114	7.5155826	9.164218	9.1817
PRSS23	ENSG00000150687	4.4808393	5.319453	6.473401	6.5180707
PTPRR	ENSG00000153233	1.1634018	1.5176588	3.0029163	2.9704752
PTX3	ENSG00000163661	1.5795472	2.3706164	5.263225	5.3044662
QPCT	ENSG00000115828	2.923895	3.7738793	4.911306	5.0358806
RARRES3	ENSG00000133321	1.8435555	1.4202232	3.3704634	3.228167
RGS4	ENSG00000117152	1.2157208	1.5903273	3.5590212	3.5230124
S100A3	ENSG00000188015	2.2041125	2.7765667	4.574708	4.4639
SAA1	ENSG00000173432	0.720086	1.1282854	4.407286	4.446394
SCG2	ENSG00000171951	0.8269953	1.2149825	3.5498767	3.5661268
SCG5	ENSG00000166922	0.6802306	1.1752195	2.9864101	3.0804868
SEC22B	ENSG00000265808	6.4196014	7.2603292	8.411599	8.459354
SERPINB2	ENSG00000197632	7.373833	8.321218	9.497752	9.539339
SERPINE2	ENSG00000135919	1.7414718	2.3499656	3.7190247	3.7754853
SERTAD4	ENSG00000082497	3.0555203	3.6977043	4.9646945	5.0458717
SERTAD4-AS1	ENSG00000203706	1.104868	1.6639359	3.1350276	3.2596169
SH2D1B	ENSG00000198574	1.3076029	1.7929637	3.2658334	3.3892648
SRGN	ENSG00000122862	2.033796	2.9656997	5.77917	5.7931857
STK32B	ENSG00000152953	1.0681258	1.5671375	3.0879133	2.9408674
SYT14	ENSG00000143469	1.187333	1.6410606	3.005452	3.1466615
TDO2	ENSG00000151790	0.0824191	0.0392464	2.3245203	2.207478
TM4SF1	ENSG00000169908	4.2345967	4.871212	6.216637	6.166579
TMEM200A	ENSG00000164484	4.2664967	5.027463	6.433199	6.456367
TNFSF18	ENSG00000120337	1.165601	1.7283058	3.1350276	3.1957028
TPM1	ENSG00000140416	4.023439	4.7425375	5.9895105	6.0408244
TSPAN2	ENSG00000134198	1.8822137	2.4930134	3.83003	3.9069123
UBE2T	ENSG00000077152	6.399833	7.350524	13.342574	13.258359
UPK1B	ENSG00000114638	0.7193666	0.935751	2.889159	3.0566688
VIM	ENSG00000026025	5.299855	6.2110023	8.863347	8.852269
WNT5B	ENSG00000111186	2.4544556	3.0220776	4.5034623	4.5387707

DEGs, differentially expressed genes; ALOX5AP, arachidonate 5-lipoxygenase activating protein; ANKRD1, ankyrin repeat domain 1; ANO2, anoctamin 2; BACE2, β-site APP-cleaving enzyme 2; CAPSL, calcyphosine-like; CDH11,

cadherin-11; CHN1, chimerin 1; CSF2, colony-stimulating factor 2; CXCL1, C-X-C motif chemokine ligand 1; DAW1, dynein assembly factor with WD repeats 1; ECSCR, endothelial cell-specific chemotaxis receptor; EDIL3, EGF-like repeat and discoidin I-like domain-containing protein 3; EDN1, endothelin 1; GJA1, gap junction protein alpha-1; GSG1, germ cell-specific gene 1; HHAT, Hedgehog acyltransferase; HSD11B1, hydroxysteroid 11-βdehydrogenase 1; IGFL1, insulin growth factor-like family member 1; IL, interleukin; KRT, keratin; KRTAP2-3, keratin-associated protein 2-3; LINC00601, long intergenic non-protein coding RNA 601; LOX, lysyl oxidase; LYPD1, Ly6/PLAUR domain-containing protein 1; MAOA, monoamine oxidase A; MMP9, matrix metalloproteinase-9; NEFL, neurofilament light chain; NGF, nerve growth factor; NNMT, nicotinamide N-methyltransferase; NTF3, neurotrophin 3; PLAU, plasminogen activator, urokinase; PRSS23, serine protease 23; PTPRR, protein tyrosine phosphatase receptor type R; PTX3, pentraxin 3; QPCT, glutaminyl-peptide cyclotransferase; RARRES3, retinoic acid receptor responder 3; RGS4, regulator of G protein signaling 4; S100A3, S100 calcium-binding protein A3; SAA1, serum amyloid A1; SCG, secretogranin; SEC22B, SEC22 homolog B, vesicle trafficking protein; SERPINB2, serpin family B member 2; SERPINE2, serpin family E member 2; SERTAD4, SERTA domain-containing protein 4; SERTAD4-AS1, SERTAD4 antisense RNA 1; SH2D1B, SH2 domain-containing protein 1B; SRGN, serglycin; STK32B, serine/threonine kinase 32B; SYT14, synaptotagmin-14; TDO2, tryptophan 2,3-dioxygenase; TM4SF1, transmembrane 4 L six family member 1; TMEM200A, transmembrane protein 200A; TNFSF18, tumor necrosis factor (ligand) superfamily, member 18; TPM1, tropomyosin 1; TSPAN2, tetraspanin 2; UBE2T, ubiquitin-conjugating enzyme E2 T; UPK1B, uroplakin 1B; VIM, vimentin; WNT5B, Wnt family member 5B.