

Supplemental Table S1. Gene list of cluster C overexpressed in HNSCC

Symbol ¹	Gene description	Cytogenetic Location	Fold Change		
			Tumor ¹	wt p53- like ²	mt p53 ³
CRABP2	cellular retinoic acid binding protein 2	1q21.3	2.89	1.61	4.16
IL22RA1	interleukin 22 receptor	1p36.11	3.13	2.30	3.96
CDW52	CDW52 antigen (CAMPATH-1 antigen)	1p36	2.22	1.88	2.56
RARRES3	retinoic acid receptor responder (tazarotene induced) 3	11q23	3.31	2.43	4.18
APOL1	apolipoprotein L, 1	22q13.1	3.27	3.04	3.49
UBE2D4	ubiquitin-conjugating enzyme HBUCE1	7p13	2.78	2.66	2.90
APOL3	apolipoprotein L, 3	22q13.1	3.63	3.71	3.55
CGI-49	CGI-49 protein	1q44	2.07	2.23	1.91
SGCE	sarcoglycan, epsilon	7q21-q22	2.03	1.96	2.09
ALDH1A1	aldehyde dehydrogenase 1 family, member A1	9q21	6.32	2.21	10.43
NQO1	NAD(P)H dehydrogenase, quinone 1	16q22.1	2.51	2.26	2.76
ALP	alpha-actinin-2-associated LIM protein	4q35	2.36	2.12	2.60
FOXE1	forkhead box E1 (thyroid transcription factor 2)	9q22	2.06	1.91	2.21
CRIP1	cysteine-rich protein 1 (intestinal)	7q11.23	2.22	1.72	2.72
KCNJ8	potassium inwardly-rectifying channel, subfamily J, member 8	12p11.23	2.03	2.16	1.90
ISYNA1	myo-inositol 1-phosphate synthase A1	19p13.12	2.20	2.17	2.23
PIK3R3	phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma)	1pter-p32.1	2.32	1.86	2.77
EPS8	epidermal growth factor receptor pathway substrate 8	12q23-q24	2.52	3.29	1.75
SIM2	single-minded homolog 2 (Drosophila)	21q22.13	2.81	2.79	2.83
MAPK8IP1	mitogen-activated protein kinase 8 interacting protein 1	11p12-p11.2	2.15	2.15	2.16
CBX6	chromobox homolog 6	22q13.1	2.17	1.87	2.46
LAMP3	lysosomal-associated membrane protein 3	3q26.3-q27	3.09	2.27	3.91
MYO5B	myosin VB	18q21	2.49	2.01	2.97
TSPAN13	Tetraspanin 13	7p21.1	2.24	2.20	2.28
IMP-3	IGF-II mRNA-binding protein 3	7p11	1.97	1.91	2.03
HOXA13	homeo box A13	7p15-p14	2.01	1.69	2.33
TARBP1	TAR (HIV) RNA binding protein 1	1p	1.76	1.51	2.00
GBAS	glioblastoma amplified sequence	7p12	1.87	1.69	2.04
CEP1	centrosomal protein 1	9q33-q34	2.47	2.05	2.88
TAX1BP1	Tax1 (human T-cell leukemia virus type I) binding protein 1	7p15	2.00	2.08	1.91
HIBADH	3-hydroxyisobutyrate dehydrogenase	7p15.2	2.04	2.29	1.79
CLDN4	claudin 4	7q11.23	3.19	3.41	2.97
CLDN3	claudin 3	7q11.23	6.61	7.74	5.49
MDK	midkine (neurite growth-promoting factor 2)	11p11.2	2.53	2.35	2.72
KIAA1102	KIAA1102 protein	4p13	5.14	4.47	5.81
MEIS2	Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse)	15q13.2	2.24	1.81	2.66
NFIL3	nuclear factor, interleukin 3 regulated	9q22	1.94	1.85	2.03
LMO7	LIM domain only 7	13q21.33	3.47	2.69	4.26
HRASLS3	HRAS-like suppressor 3	11q12.3	2.11	1.96	2.27
RPS6KA5	ribosomal protein S6 kinase, 90kD, polypeptide 5	14q31-q32.1	2.35	1.75	2.94
RAB22A	RAB22A, member RAS oncogene family	20q13.32	2.37	1.72	3.02
DNM1	dynamitin 1	9q34	1.86	1.42	2.31
GPX4	glutathione peroxidase 4 (phospholipid hydroperoxidase)	19p13.3	1.76	1.31	2.20
BCAN	chondroitin sulfate proteoglycan BEHAB/brevican	1q31	5.83	2.78	8.87
NCOA3	nuclear receptor coactivator 3	20q12	1.78	1.56	2.00
CCND1	cyclin D1 (PRAD1; parathyroid adenomatosis 1)	11q13	2.38	1.73	3.04
GDA	guanine deaminase	9q21.11-21.33	4.80	3.18	6.43
CHK	choline kinase	11cen-q12.1	2.70	2.53	2.86
CCS	copper chaperone for superoxide dismutase	11q13	2.05	1.84	2.25
FBXL11	F-box and leucine-rich repeat protein 11	11q13.2	2.68	2.56	2.81
CIT	citron (rho-interacting, serine/threonine kinase 21)	12q	2.42	2.28	2.57

NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1 (51kD)	11q13	1.98	1.93	2.03
GPR56	G protein-coupled receptor 56	16q13	1.76	1.51	2.00
<i>Cluster C1</i>					
NOT56L	Not56 (D. melanogaster)-like protein	3q26.1-q26.33	1.83	1.65	2.01
OGFR	opioid growth factor receptor	20q13.3	1.85	1.55	2.16
HIST1H2AL	H2A histone family, member I	6p22-p21.3	2.08	1.57	2.60
IFI30	interferon, gamma-inducible protein 30	19p13.1	2.02	1.74	2.30
ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3	12q13	1.74	1.46	2.02
ELTD1	EGF-TM7-latrophilin-related protein	1p33-p32	1.77	1.41	2.13
LBP-32	LBP protein 32	2p25.2	2.27	1.96	2.58
IGFBP3	insulin-like growth factor binding protein 3	7p13-p12	33.12	15.91	50.34
HINT1	histidine triad nucleotide-binding protein	5q31.2	1.97	1.78	2.17
PIN1	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1	19p13	1.84	1.42	2.25
NUP214	nucleoporin 214kD (CAIN)	9q34.1	1.94	1.63	2.25
REA	B-cell associated protein	12p13	1.94	1.59	2.28
SULT1A1	phenol-preferring phenol sulfotransferase1	16p12.1	2.07	1.74	2.41
GCA	grancalcin, EF-hand calcium binding protein	2q24.3	2.11	1.60	2.61
CREG	cellular repressor of E1A-stimulated genes	1q24	2.60	2.03	3.16
P5CR2	pyrroline 5-carboxylate reductase isoform	1q42.13	1.65	1.26	2.03
SCHIP1	schwannomin interacting protein 1	3q26.1	2.14	1.60	2.69
C20orf99	chromosome 20 open reading frame 99	20p13-p12.2	1.92	1.45	2.38
RISC	serine carboxypeptidase 1	17q23.2	2.01	1.72	2.29
ALDH3A2	aldehyde dehydrogenase 3 family, member A2	17p11.2	1.74	1.36	2.11
RALGDS	ral guanine nucleotide dissociation stimulator	9q34	1.99	1.41	2.58
TSC1	tuberous sclerosis 1	9q34	1.72	1.44	2.00
PK2	pyruvate dehydrogenase kinase, isoenzyme 2	17q21.33	2.31	1.78	2.84
HDAC5	histone deacetylase 5	17q21	2.02	1.28	2.76
RABGAP1	RAB GTPase activating protein 1	9q33.2-q33.3	1.76	1.34	2.19
CALR	calreticulin	19p13.3-p13.2	2.21	1.39	3.03
SNCAIP	synuclein, alpha interacting protein (synphilin)	5q23.1-q23.3	1.80	1.23	2.37
ZNF297B	zinc finger protein 297B	9p24.1-q22.33	1.61	1.18	2.05
NFATC3	cytoplasmic nuclear factor of activated T-cells 3	16q13-q24	1.64	1.28	2.01
MAGEF1	MAGEF1 protein	3q13	2.94	1.80	4.08
F8	coagulation factor VIII	Xq28	2.06	1.43	2.70
SIRT7	silencing information regulator 2-like	17q25	1.68	1.26	2.09
SURF1	surfeit 1	9q33-q34	1.99	1.83	2.15
HEXA	hexosaminidase A (alpha polypeptide)	15q23-q24	1.88	1.70	2.07
GOLGA1	golgi autoantigen, golgin subfamily a, 1	9q34.11	2.02	1.78	2.27
GAA	acid alpha-glucosidase	17q25.2-q25.3	3.50	2.64	4.35
DAZAP2	DAZ associated protein 2	2q33-q34	2.01	1.63	2.39
MCCC1	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	3q27	3.02	2.17	3.88
DVL3	dishevelled, dsh homolog 3 (Drosophila)	3q27	2.18	1.62	2.75
ALDH3B2	aldehyde dehydrogenase 3 family, member B2	11q13	2.00	1.89	2.10
NCOA1	nuclear receptor coactivator 1	2p23	1.79	1.53	2.04
HOXD9	homeo box D9	2q31-q37	2.41	1.83	2.99
HOXD10	homeo box D10	2q31.1	2.31	2.01	2.62
PLA2G4B	phospholipase A2, group IVB (cytosolic)	15q11.2-q21.3	1.70	1.05	2.34
EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	1q42.1	2.65	1.46	3.84
MPHOSPH9	M-phase phosphoprotein 9	12q24.31	1.63	1.23	2.02
BDG29	BDG-29 proten	16q24.2	1.74	1.37	2.11
TFRC	transferrin receptor (p90, CD71)	3q26.2-qter	2.97	3.38	2.56
HSUP1	Similar to RPE-spondin	20q13.13	2.52	2.74	2.30
PTGES	prostaglandin E synthase	9q34.3	2.70	2.93	2.47
ADPRTL3	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)-like 3	3p22.2-p21.1	4.52	5.56	3.48

PODXL	podocalyxin-like	7q32-q33	4.16	3.56	4.76
GPR109B	G protein-coupled receptor 109B	12q24.31	3.12	2.94	3.30
USP11	ubiquitin specific protease 11	1q21	2.51	2.18	2.85
CDT1	DNA replication factor	16q24	2.07	1.76	2.38
EIF4G1	eukaryotic translation initiation factor 4 gamma, 1	3q27-qter	3.26	2.93	3.60
ANXA13	annexin A13	8q24.1-q24.2	2.24	2.04	2.44
ADA	adenosine deaminase	20q12-q13.11	2.26	2.16	2.36
PCCB	propionyl Coenzyme A carboxylase, beta polypeptide	3q21-q22 20q11.22-q11.23	2.95 2.76	2.73 2.56	3.16 2.96
C20orf104	chromosome 20 open reading frame 104 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	9q32-q33.3	2.71	2.46	2.97
PTGS1					
DHODH	dihydroorotate dehydrogenase	16q22	2.53	2.36	2.69
DOLPP1	Dolichyl pyrophosphate phosphatase 1	9q34.1	2.19	1.83	2.55
NEU1	sialidase 1 (lysosomal sialidase)	6p21.3	1.90	1.67	2.12
USP13	ubiquitin specific protease 13 (isopeptidase T-3)	3q26.2-q26.3	2.01	2.38	1.65
MSX1	msh homeo box homolog 1 (Drosophila)	4p16.3-p16.1	2.46	2.97	1.95
CYB561	cytochrome b-561	17q11-qter	2.18	2.59	1.77
TBX5	T-box 5 amyloid beta (A4) precursor protein-binding, family A, member 2 binding protein	12q24.1 20q11.22	2.00 1.96	2.33 2.01	1.67 1.91
APBA2BP					
HIST1H4C	H4 histone family, member G	6p21.3	2.73	3.25	2.21
HIST1H4B	H4 histone family, member I	6p21.3	1.96	2.21	1.70
HIST1H4E	H4 histone family, member J	6p21.3	1.90	2.01	1.79
SMC2L1	SMC2 structural maintenance of chromosomes 2-like 1 (yeast)	9q31.1	1.87	2.12	1.62
B4GALT5	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5	20q13.1-q13.2	2.03	1.95	2.11
ESPL1	extra spindle poles like 1 (S. cerevisiae)	12q	1.87	1.72	2.02
Cluster C2					
TRAP95	thyroid hormone receptor-associated protein, 95-kD subunit	19p13.3	2.93	3.71	2.16
BAG2	BCL2-associated athanogene 2	6p12.3-p11.2	4.43	5.79	3.06
RAMP2	receptor (calcitonin) activity modifying protein 2	17q12-q21.1	1.65	2.07	1.24
HOXB9	homeo box B9	17q21.3	2.18	2.67	1.70
TK1	thymidine kinase 1, soluble	17q23.2-q25.3	2.48	2.58	2.37
RECQL4	RecQ protein-like 4	8q24.3	2.21	2.43	1.98
CRIP2	cysteine-rich protein 2	14q32.3	2.54	2.81	2.27
EPHB2	EphB2	1p36.1-p35	2.02	2.44	1.61
OAZIN	Antizyme inhibitor 1	8q22.3	1.89	2.21	1.57
ATAD2	ATPase family, AAA domain containing 2	8q24.13	2.56	3.06	2.07
FBXO5	F-box only protein 5	6q25-q26	1.96	2.37	1.54
CDC45L	CDC45 cell division cycle 45-like (S. cerevisiae)	22q11.21	2.21	2.88	1.54
MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	20q13.1	2.71	3.39	2.03
ORC1L	origin recognition complex, subunit 1-like (yeast)	1p32	1.71	2.13	1.30
NASP	nuclear autoantigenic sperm protein (histone-binding)	1p34.1	1.87	2.40	1.34
KIF4A	kinesin family member 4A	Xq13.1	1.80	2.16	1.44
KIF2C	kinesin-like 6 (mitotic centromere-associated kinesin)	1p34.1	3.14	4.18	2.10
FBXL14	F-box and leucine-rich repeat protein 14	12p13.33	2.10	2.52	1.69
RNPS1	RNA binding protein S1, serine-rich domain	16p13.3	2.54	2.78	2.31
RNPC1	RNA-binding region (RNP1, RRM) containing 1	20q13.31	2.52	2.86	2.18
DDX11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11	12p11	2.45	2.86	2.04
CNAP1	chromosome condensation-related SMC-associated protein 1	12p13.3	2.64	2.88	2.40
UBE2C	ubiquitin-conjugating enzyme E2C	20q13.12	2.80	3.18	2.43
C20orf1	chromosome 20 open reading frame 1	20q11.2	2.42	2.84	2.00
RAI3	retinoic acid induced 3	12p13-p12.3	3.36	3.93	2.79
TBCD	tubulin-specific chaperone d	17q25.3	1.82	2.09	1.55
RPA3	replication protein A3 (14kD)	7p22	2.43	2.96	1.90
PTPRA	protein tyrosine phosphatase, receptor type, A	20p13	2.69	3.36	2.02

CCNB2	cyclin B2	15q21.2	2.62	2.81	2.43
CPSF5	cleavage and polyadenylation specific factor 5, 25 kD subunit	16q12.2	1.71	2.01	1.42
ARAP3	ARF-GAP, RHO-GAP, ankyrin repeat and plekstrin homology domains-containing protein 3	5q31.3	2.00	2.44	1.56
C20orf24	chromosome 20 open reading frame 24	20q11.23	2.50	2.91	2.09
GLE1L	GLE1 RNA export mediator-like (yeast)	9q34.13	2.05	2.08	2.02
POLE3	polymerase (DNA directed), epsilon 3 (p17 subunit)	9q33	2.01	2.09	1.92
MCM2	MCM2 minichromosome maintenance deficient 2, mitotin (S. cerevisiae)	3q21	2.17	2.40	1.93
HSPC176	Hematopoietic stem/progenitor cells 176	16q24.3	1.92	2.03	1.80
TROAP	trophinin associated protein (tastin)	12q13.12	1.83	2.13	1.53
Cluster C3					
BAT8	HLA-B associated transcript 8	6p21.3	1.99	2.05	1.93
DEK	DEK oncogene (DNA binding)	6p23	2.17	1.99	2.36
ZNF266	zinc finger protein 266	19p13.2	2.00	1.91	2.10
TOPBP1	topoisomerase (DNA) II binding protein	3q22.2	2.23	1.97	2.49
ITPKA	inositol 1,4,5-trisphosphate 3-kinase A	15q14-q21	2.48	2.13	2.83
UBXD5	Socius	1p36.11	2.03	2.11	1.96
ALDH5A1	aldehyde dehydrogenase 5 family, member A1	6p22	2.03	2.18	1.88
AKNA	AT-hook transcription factor AKNA	9q32	2.29	2.50	2.08
ARL6IP	ADP-ribosylation factor-like 6	16p12-p11.2	2.12	2.31	1.93
PRIM1	primase, polypeptide 1 (49kD)	12q13	2.34	2.85	1.83
IFIT1	interferon-induced protein 56	10q25-q26	2.10	2.28	1.91
PPAP2C	phosphatidic acid phosphatase type 2C	19p13	4.29	4.01	4.56
FARP1	FERM, RhoGEF, and pleckstrin domain protein 1	13q32.2	2.55	2.57	2.52
MAL2	mal, T-cell differentiation protein 2	8q23	3.68	3.67	3.69
ETV1	ets variant gene 1	7p21.3	4.10	4.33	3.88
VPS45A	vacuolar protein sorting 45A (yeast)	1q21-q22	2.09	1.73	2.44
TMOD1	tropomodulin	9q22.3	1.90	1.58	2.21
RAE1	RAE1 RNA export 1 homolog (S. pombe)	20q13.31	2.35	2.37	2.32
VPS41	vacuolar protein sorting 41 (yeast)	7p14-p13	1.99	1.91	2.07
IVD	isovaleryl Coenzyme A dehydrogenase	15q14-q15	2.47	2.38	2.56
CIA30	CGI-65 protein	15q11.2-q21.3	2.78	2.93	2.63
SEMA4D	semaphorin 4D	9q22-q31	9.55	9.23	9.87
TNXB	tenascin XB	6p21.3	15.95	13.79	18.11
C20orf11	chromosome 20 open reading frame 11	20q13.33	2.15	2.11	2.20
KEAP1	Kelch-like ECH-associated protein 1	19p13.2	2.26	2.17	2.35
ANKT	nucleolar protein ANKT	15q13.3	2.53	2.26	2.80
TOP2A	topoisomerase (DNA) II alpha (170kD)	17q21-q22	2.13	2.10	2.16
RFC4	replication factor C 4	3q27	2.00	2.00	2.01
DHX35	DEAD/H box polypeptide 35	20pter-q12	1.92	2.05	1.80
PIGT	Phosphatidylinositol glycan, class T	20q12-q13.12	2.10	1.95	2.25
ERGIC3	ERGIC and golgi 3	20pter-q12	1.99	2.10	1.87
TAF7	TAF7 RNA polymerase II, 55 kD	5q31	2.11	2.06	2.16
F8A1	coagulation factor VIII-associated protein	Xq28	2.16	2.07	2.24
SEN2	senrin-specific protease	3q27.2	2.06	1.82	2.30
GOLGA1	golgi autoantigen, golgin subfamily a, 1	9q34.11	2.02	1.78	2.27
TIMP2	tissue inhibitor of metalloproteinase 2	17q25	4.73	5.39	4.07
IL10RB	interleukin 10 receptor, beta	21q22.11	2.08	2.10	2.07
NEK2	NIMA-related kinase 2	1q32.2-q41	2.20	2.03	2.37
TNFAIP2	TNF, alpha-induced protein 2	14q32	9.21	11.33	7.09
PPGB	protective protein for beta-galactosidase	20q13.1	2.02	2.21	1.83
OVCA2	ovarian cancer gene-2 protein	17p13.3	1.97	1.84	2.10
HOXB7	homeo box B7	17q21-q22	2.17	2.08	2.27
SDR1	short-chain dehydrogenase/reductase 1	1p36.1	4.71	5.27	4.14
APIP	APAF1 interacting protein	11p13	2.01	2.17	1.84

HTATIP2	HIV-1 Tat interactive protein 2, 30 kD	11p15.1	2.54	2.46	2.62
PORIMIN	pro-oncosis receptor inducing membrane injury gene	11q22.1	1.97	2.10	1.84
C20orf35	chromosome 20 open reading frame 169	20q13.12	1.85	2.04	1.65
CLDN7	claudin 7	17p13	8.62	10.67	6.56
CGN	cingulin	1q21	2.42	2.90	1.93
TACSTD1	tumor-associated calcium signal transducer 1	4q	6.35	8.27	4.43
FLOT1	flotillin 1	6p21.3	2.63	2.71	2.56
ELF3	E74-like factor 3 (ets domain transcription factor, epithelial-specific)	1q32.2	7.49	7.98	6.99
CD151	CD151 antigen	11p15.5	11.53	13.49	9.57
SULT1A4	Sulfotransferase family, cytosolic, 1A, phenol-preferring, member 4	16p11.2	2.07	1.99	2.15
PPIB	peptidylprolyl isomerase B (cyclophilin B)	15q21-q22	2.35	2.34	2.35
SLC12A7	solute carrier family 12 (potassium/chloride transporters), member 7	5p15	2.10	2.03	2.17
AARS	alanyl-tRNA synthetase	16q22	2.28	2.13	2.44
SEZ6L2	Seizure related 6 homolog (mouse)-like 2	16p11.2	3.23	3.03	3.44
GABARAPL1	GABA(A) receptor-associated protein like 1	12p13.31	2.31	2.25	2.37
ATP9A	ATPase, Class II, type 9A	20q13.11-13.2	2.56	2.86	2.25
PIM1	pim-1 oncogene	6p21.2	2.05	2.25	1.84
TNP1	transition protein 1 (during histone to protamine replacement)	16p13.13	2.03	2.18	1.88
DPP7	dipeptidylpeptidase 7	9q34.3	2.59	2.56	2.61
SPOCK1	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1	5q31	2.07	1.70	2.44
FOXM1	forkhead box M1	12p13	2.52	2.47	2.57
PMS2	PMS2 postmeiotic segregation increased 2 (S. cerevisiae)	7p22	2.05	1.78	2.31
SLC27A2	fatty-acid-Coenzyme A ligase, very long-chain 1	15q21.2	1.98	2.42	1.54
GATA2	GATA binding protein 2	3q21	2.48	2.88	2.07
EPB41L4B	EHM2 gene	9q22.1-q22.3	2.04	1.91	2.17
BLMH	bleomycin hydrolase	17q11.2	2.13	2.29	1.96
CYBA	cytochrome b-245, alpha polypeptide	16q24	10.55	14.32	6.78
CTSH	cathepsin H	15q24-q25	4.55	5.42	3.68
ALDH1A3	aldehyde dehydrogenase 1 family, member A3	15q26	2.65	2.90	2.39
KHK	ketohexokinase (fructokinase)	2p23.3-p23.2	2.15	2.56	1.75
LCN2	lipocalin 2 (oncogene 24p3)	9q34	2.97	3.30	2.65
KLRC2	killer cell lectin-like receptor subfamily C, member 2	12p13	2.04	2.82	1.25
CED-6	CED-6 protein	2q32.3-q33	2.25	2.56	1.93

Shown are gene list and fold change in cluster C over-expressed in Head and Neck Squamous Cell Carcinoma (HNSCC).

¹ Order of gene refers to the order in the tree. Shown in bold are three subclusters C1, C2 and C3 of cluster C.

² fold change = average of 10 HNSCC vs. average of 4 Human Normal Keratinocytes (HKC)

³ fold change = average of 5 HNSCC of wild type (wt) p53-like vs. average of 4 HKC

⁴ fold change = average of 5 HNSCC of mutant (mt) p53 vs. average of 4 HKC