

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 | dynamamin 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 (<i>D. melanogaster</i>)-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 | granulocytin, 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 |
| PDK2 | 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 (<i>Drosophila</i>) | 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 | 2.73 | 3.16 |
| 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 | 12q24.1 | 2.00 | 2.33 | 1.67 |
| APBA2BP | amyloid beta (A4) precursor protein-binding, family A, member 2 binding protein | 20q11.22 | 1.96 | 2.01 | 1.91 |
| 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 |
| <i>Cluster C2</i> | | | | | |
| 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 (RNPI, 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 |
| <i>Cluster C3</i> | | | | | |
| 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 | sentrin-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 |
| PP1B | 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