

Zinc Finger Proteins in Head and Neck Squamous Cell Carcinomas: ZNF540 May Serve as a Biomarker

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Table S1. Number of patients' cases analyzed in the groups depending on the specific clinical parameters; *n* - number of cases.

ZNF		ZFP28	ZNF880	ZNF540	ZNF418	ZNF426	ZNF132
Parameter	Group	n	n	n	n	n	n
Age	< 61	258	258	258	258	258	258
	> 61	263	263	263	263	263	263
Gender	Female	137	137	137	137	137	173
	Male	385	385	385	385	385	385
Alcohol	Positive	348	348	348	348	348	348
	Negative	163	163	163	163	163	163
Smoking	No/Ex	333	333	333	333	333	333
	Yes	177	177	117	117	177	177
Cancer Stage	I + II	101	101	101	101	101	101
	III + IV	349	349	349	349	349	349
T stage	T1 + T2	185	185	185	185	185	185
	T3 + T4	274	274	274	274	274	274
N stage	N0 + N1	243	243	243	243	243	243
	N2 + N3	179	179	179	179	179	179
Grade	G1 + G2	368	368	368	368	368	368
	G3 + G4	132	132	132	132	132	132
Perineural Invasion	Positive	169	169	169	169	169	169
	Negative	195	195	195	195	195	195
Lymph Node Neck Dissection	Positive	422	422	422	422	422	422
	Negative	97	97	97	97	97	97
Angiolymphatic Invasion	Positive	125	125	125	125	125	125
	Negative	225	225	225	225	225	225
HPV p16 status	Positive	39	39	39	39	39	39
	Negative	73	73	73	73	73	73

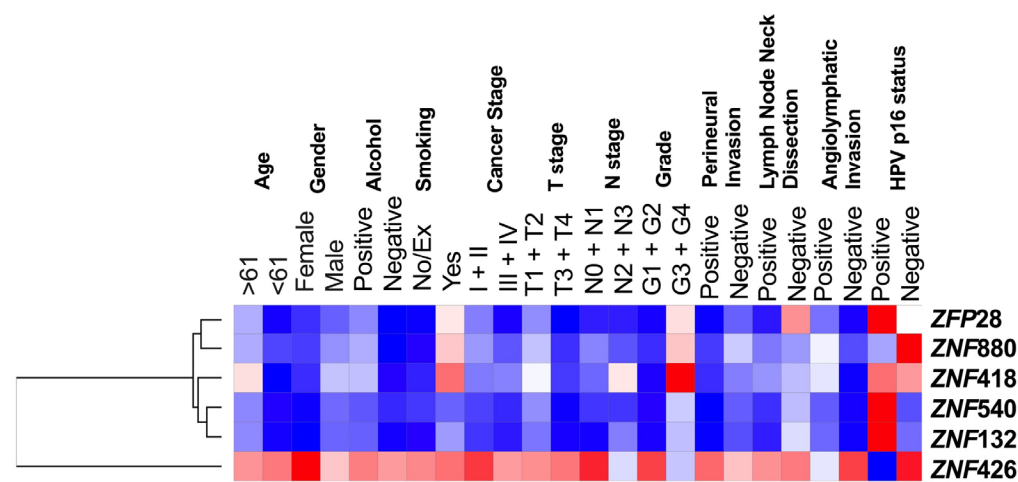


Figure S1. Heat map and clustering of mean expression levels of ZNFs depending on the specific clinical parameters.

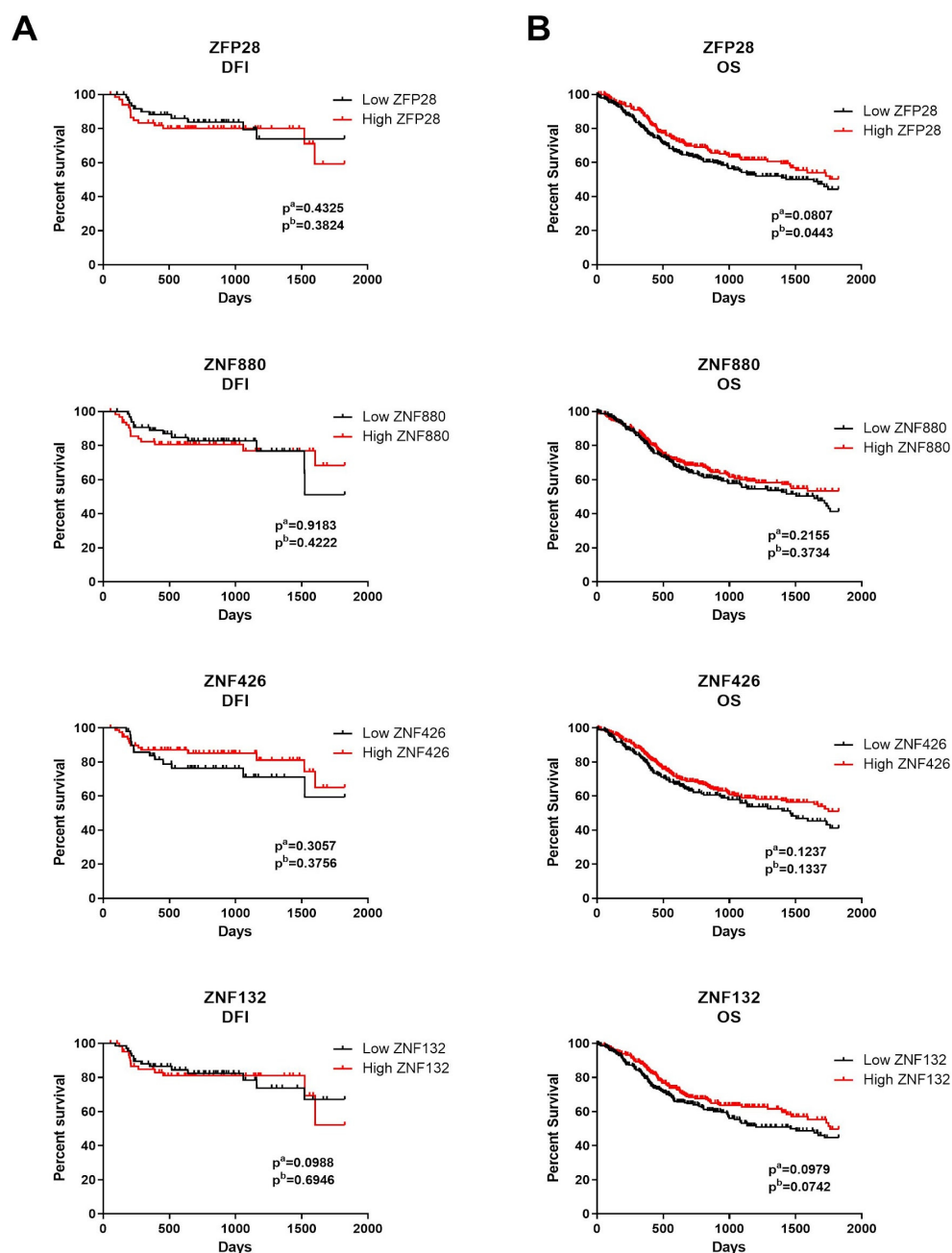


Figure S2. A) Disease-free interval (DFI) and B) overall survival (OS) of HNSCC patients depending on the *ZFP28*, *ZNF880*, *ZNF426* and *ZNF132* expression level, respectively. Results presented for 5 years observation, low and high subgroups of patients divided on the mean of expression; p^a - Long-rank (Mantel-Cox) test; p^b - Gehan-Breslow-Wilcoxon test; $p < 0.05$ considered significant.

Table S2. Collected genes assigned to pathways positively and negatively correlated with *ZFP28*, *ZNF880*, *ZNF540*, *ZNF418*, *ZNF426*, and *ZNF132*.

Positively correlated genes with ZFP28	
Defective CHST6 causes MCDC1	PRELP, KERA, LUM, OMD, OGN, CHST6, FMOD

Voltage gated Potassium channels	<i>KCNQ3, KCNQ1, KCNH2, KCND1, KCNG3, KCNH4, KCNK2, KCNA3, KCNA6, KCNAB2, KCNA5, KCNA2, KCNC3, KCNB2, CNKSR2</i>
Molecules associated with elastic fibers	<i>FBLN1, LTBP3, ELN, EFEMP2, ITGB3, MFAP4, FBLN5, EMILIN1, FBLN2, GDF5, FBN1, ITGA8</i>
Defective B4GALT1 causes B4GALT1-CDG (CDG-2d)	<i>PRELP, KERA, LUM, OMD, OGN, FMOD</i>
Defective ST3GAL3 causes MCT12 and EIEE15	<i>PRELP, KERA, LUM, OMD, OGN, FMOD</i>
Elastic fiber formation	<i>FBLN1, EFEMP2, ITGB3, EMILIN1, FBN1, ITGA8, LOXL3, LOXL4, LTBP3, ELN, DRP2, MFAP4, FBLN5, FBLN2, LOXL1, GDF5</i>
Collagen chain trimerization	<i>COL9A2, COL6A6, COL8A1, COL6A3, COL8A2, COL9A1, COL4A3, COL14A1, COL4A4, COL15A1, COL19A1</i>
Diseases associated with glycosaminoglycan metabolism	<i>PRELP, CHST14, GPC2, GPC3, OGN, SDC2, CHST6, VCAN, FMOD, KERA, LUM, OMD, PAPSS2, HSPG2, DCN</i>
Nuclear Receptor transcription pathway	<i>NR2F1, RARB, RORB, PGR, NR1D2, THRA, NR1I2, AR, NR5A2, NR2C2, ESRRG, NR3C2</i>
Post-transcriptional silencing by small RNAs	<i>AGO1, TNRC6C, TNRC6B</i>
Negatively correlated genes with ZFP28	
Transport of connexons to the plasma membrane	<i>TUBA4A, TUBB4B, TUBA1C, GJB2, TUBB6</i>
Prefoldin mediated transfer of substrate to CCT/TriC	<i>TUBA4A, TUBB4B, TUBA1C, TUBB6, CCT3</i>
Formation of the cornified envelope	<i>PKP3, KRT14, KRT16, PKP1, KRT17, JUP, KRT6A, KRT6B, KRT6C, KRT5, KLK8</i>
Microtubule-dependent trafficking of connexons from Golgi to the plasma membrane	<i>TUBA4A, TUBB4B, TUBA1C, TUBB6</i>
Neutrophil degranulation	<i>GSTP1, PKP1, FABP5, GM2A, ALDOA, PYCARD, S100A11, ATP6V1D, HMOX2, PA2G4, PYGL, S100A12, TUBB4B, JUP,</i>

	<i>ANXA2, TOLLIP, PGAM1, PNP, AGPAT2, DYNLL1</i>
Gap junction trafficking	<i>TUBA4A, TUBB4B, GJB5, GJB6, TUBA1C, GJB3, CLTB, GJB2, TUBB6</i>
Gap junction assembly	<i>TUBA4A, TUBB4B, GJB5, GJB6, TUBA1C, GJB3, GJB2, TUBB6</i>
Gap junction trafficking and regulation	<i>TUBA4A, TUBB4B, GJB5, GJB6, TUBA1C, GJB3, CLTB, GJB2, TUBB6</i>
Carboxyterminal post-translational modifications of tubulin	<i>TUBA4A, TUBB4B, TUBA1C, TUBB6</i>
Keratinization	<i>PKP3, KRT14, KRT16, PKP1, KRT17, JUP, KRT6A, KRT6B, KRT6C, KRT5, KLK8</i>
Positively correlated genes with ZNF880	
Molecules associated with elastic fibers	<i>FBLN1, CD93, EFEMP2, EMILIN1, EMILIN2, FBN1, ITGA8, LTBP3, TGFB3, ELN, MFAP4, FBLN5, GDF5, FBLN2</i>
Elastic fiber formation	<i>FBLN1, CD93, EFEMP2, EMILIN1, EMILIN2, FBN1, ITGA8, LOXL3, LTBP3, TGFB3, ELN, MFAP4, FBLN5, GDF5, LOXL1, FBLN2</i>
Defective CHST6 causes MCDC1	<i>PRELP, KERA, LUM, OMD, OGN, CHST6, FMOD</i>
Collagen chain trimerization	<i>COL6A5, COL6A6, COL8A1, COL6A3, COL8A2, COL6A1, COL4A3, COL14A1, COL4A4, COL3A1, COL1A2, COL15A1, COL19A1</i>
Defective B3GALT1 causes Peters-plus syndrome (PpS)	<i>THSD7A, ADAMTS5, ADAMTS18, SEMA5A, ADAMTS3, ADAMTS2, ADAMTS9, ADAMTS8, ADAMTS10, ADAMTS12, ADAMTSL1, SPON1, CFP</i>
O-glycosylation of TSR domain-containing proteins	<i>THSD7A, ADAMTS5, ADAMTS18, SEMA5A, ADAMTS3, ADAMTS2, ADAMTS9, ADAMTS8, ADAMTS10, ADAMTS12, ADAMTSL1, SPON1, CFP, TMEM170B</i>
Defective B4GALT1 causes B4GALT1-CDG (CDG-2d)	<i>PRELP, KERA, LUM, OMD, OGN, FMOD</i>

Defective ST3GAL3 causes MCT12 and EIEE15	<i>PRELP, KERA, LUM, OMD, OGN, FMOD</i>
Diseases associated with glycosaminoglycan metabolism	<i>PRELP, SDC2, OGN, CHST6, VCAN, FMOD, GPC6, KERA, PSAP, LUM, OMD, PAPSS2, HSPG2, DCN</i>
Assembly of collagen fibrils and other multimeric structures	<i>COL6A5, COL6A6, COL8A1, COL6A3, COL8A2, PCOLCE, COL6A1, COL4A3, COL14A1, COL4A4, LOXL3, CTSS, COL3A1, COL1A2, COL15A1, LOXL1</i>
Negatively correlated genes with ZNF880	
Formation of the cornified envelope	<i>PKP3, KRT17</i>
Keratinization	<i>PKP3, KRT17</i>
RAS GTPase cycle mutants	<i>HRAS</i>
Defective factor XII causes hereditary angioedema	<i>F12</i>
Defective SERPING1 causes hereditary angioedema	<i>F12</i>
Activation of RAS in B cells	<i>HRAS</i>
RAS signaling downstream of NF1 loss-of-function variants	<i>HRAS</i>
SOS-mediated signalling	<i>HRAS</i>
Neutrophil degranulation	<i>PA2G4, GSTP1, S100A11</i>
Positively correlated genes with ZNF540	
Terminal pathway of complement	<i>C7, C5, C8G, CLU</i>
Phase 3 - rapid repolarization	<i>KCNE3, KCNQ1, KCNE2</i>
Interleukin receptor SHC signaling	<i>PIK3R3, IL5RA, CSF2RB, INPP5D, IL3RA, JAK3, IL2RG, CSF2RA, IL2</i>
Defective Base Excision Repair Associated with OGG1	<i>OGG1</i>
Voltage gated Potassium channels	<i>KCNA3, KCNA5, KCNAB2, KCNA2, KCNC3, KCNH8, KCNQ1, CNKSR2, KCND1, KCNH4, KCNAB3</i>

TNF receptor superfamily (TNFSF) members mediating non-canonical NF-κB pathway	<i>LTA, PDE4C, LTβ, CD40LG, TNFSF12, TNFRSF13C, MAP3K14</i>
Negatively correlated genes with ZNF540	
Insulin-like Growth Factor-2 mRNA Binding Proteins (IGF2BPs/IMPs/VICKZs) bind RNA	<i>IGF2BP2, ACTB, MYC, CD44</i>
Formation of the cornified envelope	<i>PKP3, PKP1, PI3, KRT6A, KRT6B, KRT6C, CDSN, KRT14, CAPN1, KRT16, FURIN, KRT17, JUP, LCE3D, KRT5, KLK8</i>
Transport of connexons to the plasma membrane	<i>TUBA4A, TUBB3, TUBA1C, GJB2, TUBB6</i>
Keratinization	<i>PKP3, PKP1, PI3, KRT6A, KRT6B, KRT6C, CDSN, KRT14, CAPN1, KRT16, FURIN, KRT17, JUP, LCE3D, KRT5, KLK8</i>
Prefoldin mediated transfer of substrate to CCT/TriC	<i>ACTG1, TUBA4A, TUBB3, TUBA1C, TUBB6, ACTB</i>
Signaling by MAPK mutants	<i>DUSP6, DUSP7</i>
RHO GTPases activate IQGAPs	<i>ACTG1, TUBA4A, TUBB3, TUBA1C, TUBB6, ACTB</i>
Type I hemidesmosome assembly	<i>KRT14, ITGB4, KRT5, PLEC, ITGA6</i>
Gap junction trafficking	<i>ACTG1, TUBA4A, TUBB3, GJB5, GJB6, GJB3, TUBA1C, GJB2, TUBB6, RAB11FIP5, ACTB</i>
Microtubule-dependent trafficking of connexons from Golgi to the plasma membrane	<i>TUBA4A, TUBB3, TUBA1C, TUBB6</i>
Positively correlated genes with ZNF418	
Defective B3GALTL causes Peters-plus syndrome (PpS)	<i>SSPO, THSD7A, THSD7B, ADAMTS5, SEMA5B, ADAMTSL2, ADAMTS18, ADAMTSL3, ADAMTS19, ADAMTS2, ADAMTS9, ADAMTS8, ADAMTS10, ADAMTSL1, ADAMTS16, SBSPON, SPON1, CFP</i>
O-glycosylation of TSR domain-containing proteins	<i>SSPO, THSD7A, THSD7B, ADAMTS5, SEMA5B, ADAMTSL2, ADAMTS18, ADAMTSL3, ADAMTS19, ADAMTS2, ADAMTS9, ADAMTS8, ADAMTS10,</i>

	<i>ADAMTSL1, ADAMTS16, SBSPON, SPON1, FMNL1, TMEM170B, CFP</i>
Voltage gated Potassium channels	<i>KCNQ4, KCNQ3, KCNQ1, KCND1, KCNK2, KCNA3, KCNA6, KCNAB1, KCNAB2, KCNA5, KCNB1, KCNC1, KCNA2, KCNC3, KCNH8, KCNA1, CNKSR2, KCNAB3</i>
Defective CHST6 causes MCDC1	<i>PRELP, KERA, LUM, OGN, OMD, CHST6, FMOD</i>
Molecules associated with elastic fibers	<i>FBLN1, CD93, EFEMP2, EMILIN1, FBN1, EMILIN2, ITGA8, LTBP3, TGFB3, ELN, MFAP4, FBLN5, GDF5, FBLN2</i>
cGMP effects	<i>ITPR1, PDE2A, PDE1A, PDE1B, PDE5A, KCNMB1, ALDH1A1, PDE9A, GIT2, PDE11A, PDE10A, MRVI1</i>
Defective B4GALT1 causes B4GALT1-CDG (CDG-2d)	<i>PRELP, KERA, LUM, OGN, OMD, FMOD</i>
Defective ST3GAL3 causes MCT12 and EIEE15	<i>PRELP, KERA, LUM, OGN, OMD, FMOD</i>
Collagen chain trimerization	<i>COL6A5, COL6A6, COL6A3, COL8A1, COL8A2, COL14A1, COL4A3, COL4A4, PZP, COL3A1, COL15A1, COL1A2, COL19A1</i>
Elastic fiber formation	<i>FBLN1, CD93, EFEMP2, EMILIN1, FBN1, EMILIN2, ITGA8, LOXL3, LOXL4, LTBP3, TGFB3, ELN, DRP2, MFAP4, FBLN5, GDF5, LOXL1, FBLN2</i>
Negatively correlated genes with ZNF418	
Transport of connexons to the plasma membrane	<i>TUBA4A, TUBB4B, TUBA1C, GJB2, TUBB6</i>
Formation of the cornified envelope	<i>KRT14, PKP3, KRT16, PI3, KRT17, JUP, PERP KRT6A, KRT6B</i>
Gap junction assembly	<i>TUBA4A, TUBB4B, GJB5, GJB6, TUBA1C, GJB3, GJB2, TUBB6</i>
Recruitment of NuMA to mitotic centrosomes	<i>TUBA4A, TUBB4B, TUBA1C, TUBG1, DYNLL1, TUBB6</i>
Gap junction trafficking	<i>TUBA4A, TUBB4B, GJB5, GJB6, TUBA1C, GJB3, GJB2, TUBB6</i>

Gap junction trafficking and regulation	<i>TUBA4A, TUBB4B, GJB5, GJB6, TUBA1C, GJB3, GJB2, TUBB6</i>
Microtubule-dependent trafficking of connexons from Golgi to the plasma membrane	<i>TUBA4A, TUBB4B, TUBA1C, TUBB6</i>
Keratinization	<i>KRT14, PKP3, KRT16, PI3, KRT17, JUP, PERP, KRT6A, KRT6B</i>
Carboxyterminal post-translational modifications of tubulin	<i>TUBA4A, TUBB4B, TUBA1C, TUBB6,</i>
Prefoldin mediated transfer of substrate to CCT/TriC	<i>TUBA4A, TUBB4B, TUBA1C, TUBB6</i>
Positively correlated genes with ZNF426	
Formation of the cornified envelope	<i>SPINK5, KRT6A, TGM1, DSP, KRT6B, KRT6C, TGM5, CDSN, LIPK, SPRR1A, SPRR1B, LIPM, RPTN, LIPN, KLK14, KLK13, KRT78, FLG2, SPRR3, KLK12, LCE3E, DSG1, PKP1, DSG3, SPRR2E, FLG, SPRR2F, SPRR2G, CAMK2D, SPRR2A, SPRR2B, DSC1, IVL, DSC2, SPRR2D, DSC3, PERP, LCE2C, LCE2B, KRT80, PPL, LCE2D</i>
Keratinization	<i>SPINK5, KRT6A, TGM1, DSP, KRT6B, KRT6C, TGM5, CDSN, LIPK, SPRR1A, SPRR1B, LIPM, RPTN, LIPN, KLK14, KLK13, KRT78, FLG2, SPRR3, KLK12, LCE3E, DSG1, PKP1, DSG3, SPRR2E, FLG, SPRR2F, SPRR2G, CAMK2D, SPRR2A, SPRR2B, DSC1, IVL, DSC2, SPRR2D, DSC3, PERP, LCE2C, LCE2B, KRT80, PPL, LCE2D</i>
Antigen processing: Ubiquitination & Proteasome degradation	<i>UBE4A, RBBP6, HECTD1, UBE2H, BTRC, PRMT9, UFL1, ANAPC1, CDH1, ITCH, LMO7, PJA2, KLHL11, UBA6, CUL5, UBE3C, GAN, AP1G1, RNF217, HERC3, KBTBD7, RNF111, TRIP12, UBR1, UBR2, PSME3, PPP2R5E, UBR4, NEDD4, NPEPPS, HACE1, FBXO11, LNPEP, FBXO30, LTN1</i>
JNK (c-Jun kinases) phosphorylation and activation mediated by activated human TAK1	<i>TAB3, NOD2, TAB2, TRAF6, MAP2K4, MAP3K7</i>

activated TAK1 mediates p38 MAPK activation	TAB3, NOD2, TAB2, TRAF6, MAP3K7, MAPK14
Neutrophil degranulation	ANK3, PGM2, AMPD3, CDK12, ATP11A, ARG1, ATP11B, ACTR2, SEC24A, DSP, DYNC1H1, CEACAM6, NRAS, RAB6A, CDK13, BTRC, GSDMA, RBM12, MAPK1, CAP1, S100A12, QSOX1, ADAM10, RDX, FLG2, RAB10, SERPINB2, HRNR, IGF2R, HPSE, DSG1, PKP1, IQGAP1, CAB39, PTAFR, COPB1, CYFIP1, CXCR2, CD177, DDX3X, SERPINB12, VCL, DSC1, PRSS3, PAFAH1B2, ROCK1, UBR4, MAPK14
Interleukin-36 pathway	IL36RN, IL36B, IL1RL2, IL36A, IL1F10
RAS signaling downstream of NF1 loss-of-function variants	NRAS, KRAS
Small interfering RNA (siRNA) biogenesis	DICER1, AGO4, AGO3
Signaling by RAF1 mutants	BRAF, IQGAP1, CAMK2D, NRAS, VCL, KRAS, MAPK1
Negatively correlated genes with ZNF426	
SRP-dependent cotranslational protein targeting to membrane	RPL35A, RPS2, UBB, RPS19, SSR4, RPS5, SSR2, RPS15, RPS14, TFPT, RPL18, RPS11, RPL39, RPL19, SEC61B, RPL24, RPS20, RPL26, RPL22, RPS9, RPS27L, RPS27, RPL28, RPS24, RPL26L1, RPL13, RPL35, RPL38, RPL10, WBP1, RPL12, RPL34, RPLP1, RPL11, RPL30
Formation of a pool of free 40S subunits	RPL35A, RPS2, UBB, RPS19, RPS5, RPS15, RPS14, TFPT, RPL18, RPS11, RPL39, RPL19, RPL24, RPS20, RPL26, RPL22, RPS9, RPS27L, RPS27, RPL28, RPS24, RPL26L1, RPL13, RPL35, RPL38, RPL10, EIF3K, RPL12, RPL34, RPLP1, RPL11, RPL30
Selenocysteine synthesis	RPL35A, RPS2, UBB, RPS19, RPS5, EEFSEC, RPS15, RPS14, TFPT, RPL18, RPS11, RPL39, RPL19, RPL24, RPS20, RPL26, RPL22, RPS9, RPS27L, RPS27, RPL28, RPS24, RPL26L1, RPL13, RPL35, RPL38, RPL10, RPL12, RPL34, RPLP1, RPL11, RPL30

Eukaryotic Translation Termination	<i>RPL35A, RPS2, UBB, RPS19, RPS5, RPS15, RPS14, TFPT, RPL18, RPS11, RPL39, RPL19, RPL24, RPS20, RPL26, RPL22, RPS9, RPS27L, RPS27, RPL28, RPS24, RPL26L1, RPL13, RPL35, RPL38, RPL10, RPL12, RPL34, RPLP1, RPL11, RPL30</i>
L13a-mediated translational silencing of Ceruloplasmin expression	<i>RPL35A, RPS2, UBB, RPS19, RPS5, RPS15, RPS14, TFPT, RPL18, RPS11, RPL39, RPL19, RPL24, RPS20, RPL26, RPL22, RPS9, RPS27L, RPS27, RPL28, RPS24, RPL26L1, RPL13, RPL35, RPL38, RPL10, EIF3K, RPL12, RPL34, RPLP1, RPL11, RPL30</i>
Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	<i>RPL35A, RPS2, UBB, RPS19, RPS5, RPS15, RPS14, TFPT, RPL18, RPS11, RPL39, RPL19, RPL24, RPS20, RPL26, RPL22, RPS9, RPS27L, RPS27, RPL28, RPS24, RPL26L1, RPL13, RPL35, RPL38, RPL10, RPL12, RPL34, RPLP1, RPL11, RPL30</i>
Peptide chain elongation	<i>RPL35A, RPS2, UBB, RPS19, RPS5, RPS15, RPS14, TFPT, RPL18, RPS11, RPL39, RPL19, RPL24, RPS20, RPL26, RPL22, RPS9, RPS27L, RPS27, RPL28, RPS24, RPL26L1, RPL13, RPL35, RPL38, RPL10, RPL12, RPL34, RPLP1, RPL11, RPL30</i>
Viral mRNA Translation	<i>RPL35A, RPS2, UBB, RPS19, RPS5, RPS15, RPS14, TFPT, RPL18, RPS11, RPL39, RPL19, RPL24, RPS20, RPL26, RPL22, RPS9, RPS27L, RPS27, RPL28, RPS24, RPL26L1, RPL13, RPL35, RPL38, RPL10, RPL12, RPL34, RPLP1, RPL11, RPL30</i>
Mitochondrial translation elongation	<i>MRPS21, MRPL27, MRPL28, MRPL47, MRPS25, MRPS24, GADD45GIP1, MRPS26, CHCHD1, MRPL9, AIP, MRPL41, USF2, MRPL40, MRPL23, MRPL24, MRPL43, MRPS2, MRPL22, MRPL16, MRPL38, MRPL58, MRPS12, MRPS34, MRPS11, AURKAIP1, ERAL1, MRPL52, MRPL53, MRPL51, MRPL34, MRPL57, MRPL54, MRPL33, MRPL11, MRPL55</i>

Regulation of expression of SLITs and ROBOs	RPL35A, RPS2, ELOB, UBB, RPS19, RPS5, RPS15, RPS14, TFPT, RPL18, RPS11, RPL39, RPL19, RPL24, RNPS1, RPS20, RPL26, PSMD4, PSMB3, RPL22, PSMB1, MAGOH, PSMB4, RPS9, PSMB10, RBX1, RPS27L, SEM1, RPS27, RPL28, RPS24, RPL26L1, RPL13, RPL35, RPL38, RPL10, RPL12, RPL34, RPLP1, PSMC1, RPL11, RPL30, PSMC5, PSMA4, MAGOHB
Positively correlated genes with ZNF132	
Post-transcriptional silencing by small RNAs	AGO4, AGO1, TNRC6C, TNRC6B
Collagen chain trimerization	COL9A2, COL6A5, COL6A6, COL9A1, COL14A1, COL4A3, COL4A4, DENND4A, COL15A1, COL19A1
Nuclear Receptor transcription pathway	NR2F1, RARB, NR1D2, RORB, NR1I2, AR, NR5A2, NR2C2, ESRRG, NR3C2
Competing endogenous RNAs (ceRNAs) regulate PTEN translation	AGO4, CNOT6L, AGO1, TNRC6C, TNRC6B
Voltage gated Potassium channels	KCNA3, KCNAB1, KCNA5, KCNAB2, KCNA2, KCNB2, KCNC3, CNKSR2, KCND1, KCNH4,
Molecules associated with elastic fibres	LTBP3, ELN, MFAP4, SMCHD1, FBLN5, FBLN2, GDF5, ITGA8
FGFR2 ligand binding and activation	FGFR2, FGF18, FGF7, FGF2
XAV939 stabilizes AXIN	TNKS
Negatively correlated genes with ZNF132	
Prefoldin mediated transfer of substrate to CCT/TriC	ACTG1, TUBA4A, TUBB3, PFDN2, TUBB4B, TUBB2A, TUBA1C, CCT7, TUBB6, CCT3, ACTB
Transport of connexons to the plasma membrane	TUBA4A, TUBB3, TUBB4B, TUBB2A, TUBA1C, GJB2, TUBB6
Microtubule-dependent trafficking of connexons from Golgi to the plasma membrane	TUBA4A, TUBB3, TUBB4B, TUBB2A, TUBA1C, TUBB6
Neutrophil degranulation	NAPRT, FABP5, TRAPPC1, PYCARD, ALDOA, S100A11, PA2G4, NME2, RHOG, S100A12, TUBB4B, JUP, SLPI, IMPDH1,

	<i>TOLLIP, PSMD13, PGAM1, ERP44, PSMB7, PKM, CST3, GSTP1, PKP1, PPIA, ATP6V1D, HMOX2, PYGL, ANXA2, PNP, DYNLL1</i>
RHO GTPases activate IQGAPs	<i>ACTG1, TUBA4A, TUBB3, TUBB4B, TUBB2A, TUBA1C, TUBB6, ACTB</i>
Formation of the cornified envelope	<i>PKP3, PKP1, PI3, KRT6A, SPINK6, KRT6B, SPRR2G, KRT6C, CDSN, SPRR1B, KRT14, KRT16, KRT17, JUP, LCE3D, KLK8, LCE3E</i>
Gap junction trafficking	<i>GJB5, GJB6, GJB3, CLTB, TUBB6, ACTG1, TUBA4A, TUBB3, TUBB4B, TUBB2A, TUBA1C, GJB2, ACTB</i>
Formation of tubulin folding intermediates by CCT/TriC	<i>TUBA4A, TUBB3, TUBB4B, TUBB2A, TUBA1C, CCT7, TUBB6, CCT3</i>
Gap junction trafficking and regulation	<i>GJB5, GJB6, GJB3, CLTB, TUBB6, ACTG1, TUBA4A, TUBB3, TUBB4B, TUBB2A, TUBA1C, GJB2, ACTB</i>
Post-chaperonin tubulin folding pathway	<i>TUBA4A, TUBB3, TUBB4B, TUBB2A, TUBA1C, TUBB6</i>

Table S3. Involvement of *ZNFs* transcripts in cellular processes based on GSEA analysis in HNSCC patients. Normalized enrichment scores for GSEA analysis of MSigDB gene sets for oncogenic and hallmark genes sets in the group of patients with low and high expression levels of specified *ZNFs*. Only results set with $p \leq 0.05$ and $FDR \leq 0.25$ were shown. NES (normalized enrichment score), p-val (nominal p-value) and FDR q-val (false discovery rate).

ZFP28 LOW						
HALLMARK						
Process	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
HALLMARK_MYC_TARG ETS_V1	188	-0.7033593	-1.9591562	0	0.0325078 37	0.031
ONCOGENIC						
Process	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
SINGH_KRAS_DEPENDE NCY_SIGNATURE	20	-0.7966735	-1.7382913	0.0119284 3	0.0943668 9	0.245
RB_P107_DN.V1_DN	111	0.4110926 7	-1.6093328	0.0184049 08	0.1488007 8	0.502
ZFP28 HIGH						
HALLMARK						
Process	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val

No process			-			
ONCOGENIC						
Process	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
ESC_V6.5_UP_EARLY.V1_UP	153	0.41845626	1.7548374	0	0.062050827	0.245
BRCA1_DN.V1_DN	123	0.411691	1.68942	0	0.07300265	0.367
MTOR_UP.V1_DN	170	0.45409486	1.820618	0	0.08531365	0.139
BRCA1_DN.V1_UP	122	0.5070129	1.888495	0	0.09420856	0.075
IL2_UP.V1_DN	172	0.48583123	1.8270137	0	0.09847495	0.131
KRAS.PROSTATE_UP.V1_UP	126	0.5140462	1.9229596	0	0.112964265	0.045
STK33_DN	237	0.41059783	1.7932984	0.0019193857	0.063047	0.179
MTOR_UP.N4.V1_DN	154	0.53650737	1.7974787	0.0019379845	0.07784095	0.176
STK33_SKM_DN	235	0.41189855	1.7352247	0.0019417476	0.06588144	0.272
IL21_UP.V1_DN	166	0.4507301	1.7976047	0.001984127	0.09052824	0.176
BMI1_DN_MEL18_DN.V1_DN	137	0.5041968	1.878085	0.002008032	0.07285083	0.086
PRC1_BMI_UP.V1_UP	168	0.43189573	1.7296886	0.0020283975	0.06564677	0.284
IL15_UP.V1_DN	164	0.4607605	1.7774625	0.0020491802	0.061206225	0.201
KRAS.BREAST_UP.V1_DN	129	0.48597175	1.7937435	0.0020703934	0.07078621	0.179
EGFR_UP.V1_DN	166	0.3919127	1.5847212	0.0037664783	0.072305344	0.579
STK33_NOMO_DN	237	0.40316385	1.673443	0.0039138943	0.06845865	0.4
GCNP_SHH_UP_EARLY.V1_DN	157	0.39341584	1.6434138	0.006024096	0.06798053	0.466
CRX_NRL_DN.V1_UP	129	0.3669617	1.5494833	0.006024096	0.08243801	0.624
RAPA_EARLY_UP.V1_UP	153	0.37599713	1.5618075	0.00625	0.081019804	0.608
JNK_DN.V1_UP	170	0.43698993	1.6787323	0.0062761507	0.07056176	0.39
PTEN_DN.V2_DN	125	0.3897153	1.6050193	0.007797271	0.072676644	0.539
CTIP_DN.V1_UP	120	0.45687774	1.7085323	0.007952286	0.06766376	0.324
P53_DN.V2_DN	141	0.3707659	1.5477594	0.007984032	0.08199287	0.628
E2F3_UP.V1_UP	171	0.45879358	1.7036487	0.008016032	0.067471534	0.339
CYCLIN_D1_KE_V1_DN	184	0.4035997	1.6490792	0.00814664	0.06719784	0.456

VEGF_A_UP.V1_UP	185	0.4647047 5	1.7566174	0.0082135 53	0.0661240 2	0.241
JNK_DN.V1_DN	174	0.4551533 5	1.781058	0.0082304 52	0.0650641 84	0.198
KRAS.AMP.LUNG_UP.V1_UP	130	0.4413422	1.6418837	0.0085106 38	0.0669324 4	0.474
NOTCH_DN.V1_UP	169	0.3896639	1.5877337	0.0100401 6	0.0753139 5	0.572
KRAS.KIDNEY_UP.V1_UP	136	0.5521734	1.7655439	0.0101010 1	0.0659581 35	0.226
CAHOY_ASTROCYTIC	97	0.4089668 7	1.586903	0.0117416 83	0.0741150 16	0.573
KRAS.600.LUNG.BREAST_UP.V1_DN	265	0.3849388 7	1.5926368	0.0120724 35	0.0740883 05	0.564
NOTCH_DN.V1_DN	170	0.4097423 3	1.6532688	0.0121457 49	0.0689974 8	0.44
PRC2_SUZ12_UP.V1_DN	169	0.3727078 4	1.5814753	0.0121951 215	0.0727754 3	0.581
CAHOY_NEURONAL	94	0.4629674	1.6626521	0.0125523 01	0.0688600 5	0.422
ATF2_UP.V1_DN	170	0.4627025 4	1.6836009	0.0138888 89	0.0705396 3	0.378
ESC_V6.5_UP_LATE.V1_U P	170	0.4376104 2	1.6751012	0.0140280 565	0.0698170 6	0.396
JAK2_DN.V1_UP	170	0.3821609 6	1.6006777	0.0144032 92	0.0721480 85	0.548
PTEN_DN.V1_UP	168	0.4153383 4	1.6022748	0.0145228 22	0.0726898 5	0.546
KRAS.AMP.LUNG_UP.V1_DN	126	0.4327225 4	1.6655899	0.0145530 14	0.0697021 1	0.415
PRC1_BMI_UP.V1_DN	171	0.3846945 2	1.6185759	0.0151187 91	0.0696189 9	0.519
ATF2_S_UP.V1_DN	176	0.4736425 3	1.7452166	0.0158102 77	0.0644399 15	0.259
CAHOY_OLIGODENDRO CUTIC	85	0.3955319	1.5262989	0.0158415 85	0.0884138 4	0.654
KRAS.300_UP.V1_UP	136	0.4705382 3	1.6887871	0.0161616 17	0.0704136	0.369
RAPA_EARLY_UP.V1_DN	173	0.3436187	1.4682466	0.0164609 05	0.1127429 7	0.766
LTE2_UP.V1_UP	176	0.3924641 6	1.5957209	0.0191570 87	0.0735072 5	0.555
NRL_DN.V1_UP	129	0.3494967 2	1.460184	0.0196078 44	0.1167268 46	0.792
KRAS.600_UP.V1_UP	261	0.4583389	1.7088232	0.0202020 2	0.0710207	0.323
IL21_UP.V1_UP	172	0.3773899 7	1.5468907	0.0204081 63	0.0809231 6	0.628
BMI1_DN.V1_DN	128	0.4168698	1.6061801	0.0204498 97	0.0740148 4	0.539
MEL18_DN.V1_DN	137	0.4547810 3	1.6491336	0.0214007 78	0.0692977 7	0.456
DCA_UP.V1_DN	162	0.3440123 2	1.4968454	0.0217391 3	0.1015385 5	0.709

PTEN_DN.V1_DN	167	0.3903067 7	1.5519207	0.0220883 53	0.0827004 5	0.62
AKT_UP.V1_DN	179	0.4300792 5	1.6620604	0.0221327 97	0.0668407 9	0.424
CSR_LATE_UP.V1_DN	131	0.4277939	1.6382835	0.0222672 06	0.0667448	0.484
PRC2_SUZ12_UP.V1_UP	172	0.3692439 5	1.5611689	0.0223123 73	0.0797157 1	0.608
ATF2_S_UP.V1_UP	177	0.3251966 8	1.4505827	0.0233009 7	0.1218537 54	0.801
KRAS.50_UP.V1_UP	47	0.5456285	1.7176628	0.0244897 96	0.0704534 05	0.309
LEF1_UP.V1_UP	186	0.4447504 3	1.6381508	0.0245398 77	0.0650278 5	0.484
PKCA_DN.V1_DN	146	0.3615935 7	1.5272518	0.0248962 66	0.0893807 6	0.653
KRAS.600.LUNG.BREAST_UP.V1_UP	267	0.4079109 4	1.6299127	0.0256410 26	0.0676913 1	0.504
PIGF_UP.V1_DN	178	0.3852282 5	1.5867903	0.0268041 23	0.0726241 5	0.573
WNT_UP.V1_UP	169	0.3448856	1.4814402	0.0270270 28	0.1062937	0.739
P53_DN.V2_UP	142	0.421922	1.6280116	0.0276008 49	0.0667542 7	0.506
CTIP_DN.V1_DN	118	0.3786531 4	1.4894131	0.0280561 13	0.1030402 7	0.729
PRC2_EED_UP.V1_UP	174	0.3539562 8	1.4734133	0.0309477 77	0.1105945 6	0.753
ATF2_UP.V1_UP	181	0.3429885 2	1.4673829	0.0336134 47	0.1117243 84	0.767
SRC_UP.V1_UP	148	0.3920020 8	1.5065879	0.0366598 78	0.0964695 2	0.69
RELA_DN.V1_DN	127	0.3881461 3	1.5236872	0.0386178 87	0.0885104 5	0.659
KRAS.BREAST_UP.V1_UP	128	0.4019797 4	1.538174	0.04	0.0843254 3	0.64
CYCLIN_D1_UP.V1_DN	179	0.3274572 5	1.4013363	0.0459081 83	0.1487338 4	0.851
ERBB2_UP.V1_UP	179	0.3773266	1.5130033	0.0476190 5	0.0937429 1	0.68
DCA_UP.V1_UP	166	0.3245589	1.3904004	0.0499002	0.1525173 5	0.861
ZNF132 LOW						
HALLMARK						
Process	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
No process				-		
ONCOGENIC						
Process	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
No process				-		
ZNF132 HIGH						
HALLMARK						
Process	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val

No process				-		
ONCOGENIC						
Process	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
IL2_UP.V1_DN	172	0.48074335	1.8123108	0.0019305019	0.22845033	0.141
ZNF418 LOW						
HALLMARK						
Process	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
HALLMARK_MYC_TARG ETS_V1	188	0.70635825	1.9595909	0.0019607844	0.024626149	0.034
HALLMARK_MYC_TARG ETS_V2	58	0.6444798	1.6591418	0.06346154	0.24339326	0.359
ONCOGENIC						
Process	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
SINGH_KRAS_DEPENDE NCY_SIGNATURE	20	0.7439315	1.6562297	0.033398822	0.13443983	0.398
RB_P107_DN.V1_DN	111	0.3821421	1.5333258	0.03285421	0.17947969	0.641
ZNF418 HIGH						
HALLMARK						
Process	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
HALLMARK_KRAS_SIGN ALING_UP	193	-0.5189731	-1.8128397	0.0019493178	0.2462509	0.126
HALLMARK_COAGULAT ION	136	-0.49198148	-1.767163	0.009633912	0.19013539	0.183
HALLMARK_IL2_STAT5_ SIGNALING	194	-0.4797305	-1.759137	0.009823183	0.14186552	0.199
HALLMARK_COMPLEME NT	195	-0.46599516	-1.6740719	0.027027028	0.16059901	0.32
ONCOGENIC						
Process	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
KRAS.PROSTATE_UP.V1_ UP	126	0.58782035	-2.2336104	0	0	0
KRAS.AMP.LUNG_UP.V1_ UP	130	0.54051894	-2.0606806	0	0.001913292	0.005
PTEN_DN.V1_UP	168	-0.5262224	-2.0632331	0	0.002232174	0.005
IL2_UP.V1_DN	172	-0.5585994	-2.1607866	0	0.002267471	0.002
KRAS.600_UP.V1_UP	261	-0.5446241	-2.0659223	0	0.002372522	0.004
IL15_UP.V1_DN	164	-0.5035248	-1.9823798	0	0.0025143845	0.021
KRAS.AMP.LUNG_UP.V1_ DN	126	-0.546705	-2.1095316	0	0.0025592665	0.003

IL21_UP.V1_DN	166	- 0.4954881 4	-2.0160117	0	0.0025682 386	0.014
BRCA1_DN.V1_DN	123	- 0.4788843 4	-1.9826748	0	0.0026820 102	0.021
CTIP_DN.V1_UP	120	- 0.5453158 6	-2.0308762	0	0.0027760 696	0.011
BMI1_DN_MEL18_DN.V1_DN	137	- 0.5415358 5	-2.0172582	0	0.0028250 625	0.014
BRCA1_DN.V1_UP	122	-0.5335266	-1.9853559	0	0.0028735 823	0.021
KRAS.BREAST_UP.V1_DN	129	-0.5525263	-2.069255	0	0.0029656 522	0.004
ATF2_S_UP.V1_DN	176	-0.5485492	-1.9883087	0	0.0030135 585	0.02
JNK_DN.V1_UP	170	- 0.5121705 5	-2.0174675	0	0.0031389 585	0.014
JNK_DN.V1_DN	174	-0.5023681	-1.9893346	0	0.0031606 69	0.019
PTEN_DN.V1_DN	167	-0.4804555	-1.9537499	0	0.0040733 814	0.034
ATF2_UP.V1_DN	170	-0.5226324	-1.9297507	0	0.0047080 237	0.044
PRC2_SUZ12_UP.V1_DN	169	- 0.4456909 3	-1.9306606	0	0.0049695 81	0.044
DCA_UP.V1_UP	166	- 0.4411171 7	-1.8949682	0	0.0060598 324	0.065
NOTCH_DN.V1_DN	170	- 0.4711827 3	-1.9080054	0	0.0061417 907	0.058
CSR_LATE_UP.V1_DN	131	-0.490256	-1.8905959	0	0.0061941 384	0.068
CYCLIN_D1_KE_.V1_DN	184	-0.4626264	-1.8963137	0	0.0062055 78	0.064
P53_DN.V2_DN	141	- 0.4431821 7	-1.8760443	0	0.0062493 46	0.078
KRAS.600.LUNG.BREAST_UP.V1_DN	265	- 0.4553523 4	-1.8769166	0	0.0064332 52	0.077
MEL18_DN.V1_DN	137	- 0.5128081 4	-1.8598994	0	0.0064573 325	0.093
BMI1_DN.V1_DN	128	-0.4769156	-1.8621953	0	0.0066023 23	0.089
KRAS.600.LUNG.BREAST_UP.V1_UP	267	- 0.4585180 6	-1.878191	0	0.0066334 005	0.076

PRC1_BMI_UP.V1_UP	168	- 0.4556695 8	-1.8787928	0	0.0067874 98	0.076
ALK_DN.V1_UP	131	- 0.4485801 5	-1.862391	0	0.0068153 017	0.089
NOTCH_DN.V1_UP	169	- 0.4447054 3	-1.8454466	0	0.0078503 02	0.114
RAPA_EARLY_UP.V1_UP	153	- 0.4391221 7	-1.8330141	0	0.0085852 37	0.134
ATF2_S_UP.V1_UP	177	-0.4099953	-1.8184426	0	0.0089427 04	0.147
PKCA_DN.V1_DN	146	- 0.4258873 8	-1.812706	0	0.0089724 48	0.154
MTOR_UP.N4.V1_DN	154	-0.5231579	-1.8121986	0	0.0089766 97	0.157
STK33_SKM_DN	235	- 0.4308254 4	-1.8206153	0	0.0090484 03	0.147
PIGF_UP.V1_DN	178	- 0.4418476 8	-1.8210858	0	0.0092037 77	0.146
GCNP_SHH_UP_EARLY.V1_DN	157	-0.4275579	-1.7971119	0	0.0094209 695	0.174
ESC_V6.5_UP_EARLY.V1_UP	153	-0.4347706	-1.7997797	0	0.0094393 45	0.174
ESC_V6.5_UP_LATE.V1_UP	170	-0.4712934	-1.800405	0	0.0095204 94	0.173
CAHOY_OLIGODENDRO CUTIC	85	-0.4540185	-1.7867582	0	0.0098487 38	0.183
CRX_DN.V1_UP	125	- 0.4185486 7	-1.7739898	0	0.0102780 94	0.204
PRC2_EED_UP.V1_UP	174	- 0.4293600 6	-1.7749729	0	0.0104913 1	0.201
PDGF_UP.V1_DN	117	- 0.4557432 8	-1.7648411	0	0.0111190 64	0.214
JAK2_DN.V1_UP	170	-0.4131979	-1.74807	0	0.0118345 14	0.238
NRL_DN.V1_DN	121	-0.4069717	-1.7369152	0	0.0127949 22	0.252
STK33_DN	237	-0.3901516	-1.7097195	0	0.0152777 04	0.306
CRX_NRL_DN.V1_UP	129	-0.4063586	-1.7099057	0	0.0154621 78	0.306
ESC_J1_UP_EARLY.V1_UP	151	- 0.3971042 3	-1.6955601	0	0.0174772 5	0.33

PRC1_BMI_UP.V1_DN	171	- 0.3952423 3	-1.6849236	0	0.0182382 11	0.34
PRC2_SUZ12_UP.V1_UP	172	- 0.4196659 6	-1.781849	0.0019305 019	0.0099062 64	0.188
GCNP_SHH_UP_LATE.V1_DN	168	-0.3615609	-1.603944	0.0019801 98	0.0326330 55	0.504
ATM_DN.V1_UP	140	-0.4430142	-1.821271	0.0019920 32	0.0094229 14	0.146
CAHOY_ASTROCYTIC	97	- 0.4490713 8	-1.7352251	0.002	0.0128575 92	0.256
MTOR_UP.V1_DN	170	-0.4528975	-1.843926	0.0020161 29	0.0076325 005	0.116
KRAS.LUNG.BREAST_UP.V1_DN	132	- 0.4420526 3	-1.714924	0.0020161 29	0.0149397 63	0.295
LTE2_UP.V1_UP	176	- 0.4268371 2	-1.7637072	0.0020283 975	0.0110000 88	0.215
AKT_UP.V1_DN	179	- 0.4774854 2	-1.8606879	0.0020325 202	0.0066007 213	0.092
WNT_UP.V1_UP	169	- 0.3980391 6	-1.7108196	0.0020408 162	0.0156081 66	0.306
AKT_UP_MTOR_DN.V1_DN	177	-0.3926892	-1.7162569	0.0020618 557	0.0148129 25	0.292
P53_DN.V2_UP	142	-0.4796643	-1.9070125	0.0020661 156	0.0060424 78	0.059
STK33_NOMO_DN	237	-0.41628	-1.7516512	0.0020661 156	0.0118378 07	0.231
YAP1_DN	40	- 0.4751294 6	-1.6658838	0.0039062 5	0.0207450 37	0.377
ATF2_UP.V1_UP	181	- 0.3978132 6	-1.6852853	0.0039840 64	0.0182959 87	0.339
DCA_UP.V1_DN	162	- 0.3854321 5	-1.6451837	0.0039840 64	0.0250376 9	0.423
P53_DN.V1_DN	186	- 0.4907344 6	-1.8404187	0.004	0.0077967 57	0.119
ATM_DN.V1_DN	140	- 0.4435315 7	-1.7871188	0.004	0.0099375 15	0.181
KRAS.LUNG_UP.V1_UP	130	- 0.4469970 8	-1.7470609	0.004	0.0117216 58	0.238
ALK_DN.V1_DN	128	-0.4361652	-1.7480787	0.004	0.0120111 49	0.238
KRAS.300_UP.V1_UP	136	-0.5224938	-1.9025966	0.0040567 95	0.0059404 033	0.061

KRAS.KIDNEY_UP.V1_UP	136	-0.5694077	-1.8627278	0.0040567 95	0.0069631 99	0.088
CTIP_DN.V1_DN	118	-0.4513732	-1.8069801	0.0040650 405	0.0090116 36	0.163
RELA_DN.V1_DN	127	- 0.4636906 7	-1.8220394	0.0040650 405	0.0095281 49	0.145
IL21_UP.V1_UP	172	- 0.4265453 5	-1.7337606	0.0041322 31	0.0127724 53	0.256
WNT_UP.V1_DN	163	- 0.4234851 3	-1.7570467	0.0041493 78	0.0114248 5	0.225
SNF5_DN.V1_UP	158	- 0.4983180 2	-1.8134499	0.0041580 04	0.0090950 88	0.153
BCAT.100_UP.V1_UP	46	- 0.4880093 3	-1.6691583	0.0042918 455	0.0205770 64	0.374
NRL_DN.V1_UP	129	- 0.3835801 8	-1.603741	0.0058252 425	0.0323077 48	0.504
PTEN_DN.V2_DN	125	- 0.3951398 7	-1.6186128	0.0059405 942	0.0294070 2	0.469
KRAS.KIDNEY_UP.V1_DN	126	-0.4665823	-1.8453215	0.0059880 24	0.0076322 39	0.114
E2F1_UP.V1_DN	174	-0.4417965	-1.7285908	0.0061349 69	0.0131946 51	0.264
KRAS.BREAST_UP.V1_UP	128	- 0.4743098 6	-1.8105708	0.0062240 665	0.0090029 86	0.159
CAHOY_ASTROGLIAL	92	-0.5051626	-1.7940445	0.0062630 48	0.0096181 42	0.176
LEF1_UP.V1_UP	186	- 0.4940197 8	-1.8104372	0.0062893 08	0.0088648 3	0.16
VEGF_A_UP.V1_UP	185	-0.4793994	-1.8289244	0.0078895 46	0.0088734 96	0.137
PTEN_DN.V2_UP	129	- 0.4309052 5	-1.6312122	0.0103305 78	0.0268991 92	0.449
CRX_DN.V1_DN	128	-0.3943917	-1.5623249	0.0104602 51	0.0409993 38	0.581
KRAS.50_UP.V1_UP	47	-0.557791	-1.7746135	0.0105042 02	0.0103380 56	0.201
KRAS.600_UP.V1_DN	264	-0.413695	-1.6921346	0.0119521 92	0.0177759 51	0.335
CYCLIN_D1_UP.V1_DN	179	- 0.3625586 6	-1.5663463	0.0121703 86	0.0401359 87	0.576
E2F3_UP.V1_UP	171	- 0.4459795 4	-1.6856071	0.0134357 01	0.0184487 57	0.339

ERBB2_UP.V1_UP	179	- 0.4132729 5	-1.6339794	0.0138888 89	0.0267401 82	0.441
ESC_J1_UP_LATE.V1_UP	175	- 0.4385607 2	-1.6900861	0.0141987 83	0.0179455 76	0.337
EGFR_UP.V1_DN	166	- 0.3833370 2	-1.5711657	0.0160320 64	0.0393627 43	0.568
LEF1_UP.V1_DN	177	- 0.3924903 6	-1.5994887	0.0160965 79	0.0330168 57	0.515
TGFB_UP.V1_DN	179	- 0.3465488 6	-1.496096	0.0163599 18	0.0587686 37	0.694
IL15_UP.V1_UP	171	- 0.3697301 7	-1.5903349	0.0181086 51	0.0349560 86	0.535
PDGF_ERK_DN.V1_UP	132	- 0.3149544 3	-1.4084008	0.0184049 08	0.0912412 26	0.83
KRAS.PROSTATE_UP.V1_DN	135	-0.4369884	-1.6348603	0.0187891 44	0.0268607 85	0.441
RPS14_DN.V1_UP	184	-0.5615499	-1.7861389	0.0205761 32	0.0097207 865	0.183
RAPA_EARLY_UP.V1_DN	173	-0.3509905	-1.5225507	0.0210325 05	0.0504562 33	0.668
SRC_UP.V1_UP	148	- 0.4106425 3	-1.5412781	0.0216535 44	0.0463671 65	0.631
CSR_EARLY_UP.V1_DN	111	-0.4124138	-1.5780567	0.0230326 3	0.0377973 73	0.556
RAF_UP.V1_DN	177	- 0.4099345 2	-1.5448812	0.0261569 41	0.0457649 12	0.624
CAHOY_NEURONAL	94	-0.4488035	-1.6332852	0.0275590 55	0.0265922 1	0.442
RELA_DN.V1_UP	145	-0.3550513	-1.4845804	0.0278884 47	0.0624891 3	0.712
NFE2L2.V2	411	- 0.3621511 5	-1.5801932	0.0293542 07	0.0374653 8	0.55
BCAT_GDS748_UP	46	- 0.4427966 5	-1.5236131	0.0325203 24	0.0505429	0.663
PKCA_DN.V1_UP	150	- 0.3561986 4	-1.5045141	0.0325203 24	0.0564100 78	0.688
IL2_UP.V1_UP	173	- 0.3828537 8	-1.5565723	0.0330578 5	0.0427576 68	0.596
KRAS.300_UP.V1_DN	131	- 0.3958276 5	-1.537856	0.0354330 73	0.0461647 36	0.64

RB_P130_DN.V1_UP	116	- 0.4175897 5	-1.5385842	0.0390143 73	0.0467800 35	0.639
CYCLIN_D1_UP.V1_UP	178	-0.332474	-1.413482	0.0462776 65	0.0895022 9	0.821
KRAS.LUNG.BREAST_UP. V1_UP	135	- 0.4054509 7	-1.5378803	0.0476190 5	0.0465921 87	0.64
SRC_UP.V1_DN	152	- 0.3073923 6	-1.3628328	0.0483870 95	0.1134706 2	0.886
KRAS.DF.V1_DN	183	- 0.3338904 7	-1.3887444	0.0499002	0.0997421 15	0.848
HOXA9_DN.V1_UP	171	- 0.4506379 7	-1.5686555	0.05	0.0396810 17	0.571
ZNF426 LOW						
HALLMARK						
Process	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
HALLMARK_DNA_REPAIR	140	0.5191116	1.8323119	0.0120481 92	0.0723354 2	0.125
HALLMARK_OXIDATIVE _PHOSPHORYLATION	182	0.6202922	1.8700818	0.0141414 14	0.0921936 1	0.089
ONCOGENIC						
Process	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
CAMP_UP.V1_UP	180	0.4031805 7	1.7084215	0.0019157 088	0.1711983 5	0.302
ZNF426 HIGH						
HALLMARK						
Process	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
HALLMARK_TGF_BETA_ SIGNALING	54	- 0.6055429 6	-1.8469702	0.0041493 78	0.1681964 2	0.092
HALLMARK_PROTEIN_S ECRETION	95	-0.5346111	-1.7968848	0.0060851 93	0.1318925 8	0.138
HALLMARK_UV_RESPO NSE_DN	137	-0.5330411	-1.7297308	0.0085106 38	0.1195591 7	0.225
HALLMARK_ANDROGE N_RESPONSE	96	- 0.4759889 5	-1.7401007	0.0101214 57	0.1433816	0.212
HALLMARK_ESTROGEN_ RESPONSE_EARLY	192	-0.4221948	-1.6895446	0.0143737 17	0.1272883 4	0.281
ONCOGENIC						
Process	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
TBK1.DF_DN	257	- 0.5727204 7	-1.9589195	0	0.0135269 73	0.027
EIF4E_DN	90	-0.6262681	-2.0373917	0	0.0147034 09	0.011

PIGF_UP.V1_UP	177	- 0.5848549 6	-1.9663792	0.0039920 16	0.0177753 98	0.023
ZNF540 LOW						
HALLMARK						
Process	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
No process				-		
ONCOGENIC						
Process	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
CSR_EARLY_UP.V1_UP	136	0.5592234	1.8651284	0.0038387 715	0.0682257 6	0.091
SINGH_KRAS_DEPENDENCY_SIGNATURE	20	0.7738371 5	1.7358071	0.0273437 5	0.1337076 6	0.248
ZNF540 HIGH						
HALLMARK						
Process	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
No process				-		
ONCOGENIC						
Process	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
KRAS.BREAST_UP.V1_DN	129	- 0.4814613 2	-1.7783498	0	0.0944923 3	0.185
KRAS.PROSTATE_UP.V1_UP	126	- 0.4769507 6	-1.8134872	0	0.1069939 7	0.147
PRC2_SUZ12_UP.V1_DN	169	- 0.4020540 7	-1.7224718	0	0.1135172 55	0.274
IL2_UP.V1_DN	172	- 0.4830475 2	-1.8390303	0	0.1159102 25	0.117
CTIP_DN.V1_UP	120	- 0.5135624 4	-1.8974354	0.0020283 975	0.1073156 3	0.064
KRAS.AMP.LUNG_UP.V1_DN	126	-0.4467045	-1.7455815	0.0038167 94	0.1149683 4	0.231
MTOR_UP.N4.V1_DN	154	-0.512408	-1.7972623	0.0041152 26	0.0960128 1	0.166
CRX_DN.V1_UP	125	- 0.3750447 6	-1.6064051	0.0057471 264	0.1434885 1	0.485
DCA_UP.V1_DN	162	- 0.3592804 7	-1.5646865	0.0059055 12	0.109942	0.574
KRAS.AMP.LUNG_UP.V1_UP	130	- 0.4562855 4	-1.6898639	0.0059523 81	0.1108542 1	0.319
BRCA1_DN.V1_UP	122	- 0.4723107 8	-1.7444317	0.0061349 69	0.0997546 3	0.231

IL15_UP.V1_DN	164	- 0.4375225 6	-1.6933297	0.0061983 47	0.1178577 24	0.312
P53_DN.V2_DN	141	- 0.3883070 6	-1.636611	0.0062761 507	0.1571774 8	0.423
ATF2_S_UP.V1_UP	177	-0.3585978	-1.5911301	0.0079840 32	0.1387612 1	0.515
BMI1_DN.MEL18_DN.V1_DN	137	- 0.4618326 7	-1.7192783	0.0081799 59	0.1036663 9	0.279
STK33_DN	237	- 0.3630344 3	-1.6009351	0.0081799 59	0.1347217 3	0.493
PTEN_DN.V1_UP	168	- 0.4036195 3	-1.5676091	0.0102459 015	0.1148764 5	0.566
BRCA1_DN.V1_DN	123	-0.3892924	-1.6127898	0.0102880 66	0.1547033 6	0.473
PRC1_BMI_UP.V1_DN	171	-0.3623015	-1.5305016	0.0119284 3	0.1232848 6	0.648
KRAS.600.LUNG.BREAST_UP.V1_DN	265	- 0.3946220 3	-1.6206548	0.012	0.1523793	0.454
IL21_UP.V1_DN	166	- 0.3994833 8	-1.6069379	0.014	0.1512433 1	0.482
PRC2_SUZ12_UP.V1_UP	172	- 0.3681104 8	-1.5815599	0.0140280 565	0.1293786 9	0.527
ESC_V6.5_UP_EARLY.V1_UP	153	- 0.3616122 6	-1.5080565	0.0159045 72	0.1250300 7	0.688
CSR_EARLY_UP.V1_DN	111	-0.4237799	-1.6317422	0.0164609 05	0.1518801 9	0.435
STK33_SKM_DN	235	-0.3678678	-1.5844793	0.0166320 17	0.1327713 7	0.526
SRC_UP.V1_UP	148	- 0.4201329 4	-1.5690321	0.0176125 24	0.1220587 3	0.562
CRX_NRL_DN.V1_UP	129	- 0.3711030 2	-1.5689805	0.0179640 73	0.1177792 85	0.562
NOTCH_DN.V1_DN	170	- 0.3899374 6	-1.5779254	0.0183299 39	0.1223932 65	0.534
JAK2_DN.V1_UP	170	- 0.3624685 4	-1.4954052	0.0197238 66	0.1306938 1	0.713
MTOR_UP.V1_DN	170	- 0.3913824 3	-1.6027552	0.0205338 8	0.1389874 8	0.488
JNK_DN.V1_UP	170	- 0.4009769 3	-1.5703297	0.0206185 56	0.1251537 7	0.557

STK33_NOMO_DN	237	-	0.3633149	-1.5206835	0.0228215 77	0.1278755	0.668
E2F3_UP.V1_UP	171	-	-0.4123802	-1.5503093	0.0271844 66	0.1110032 6	0.608
LEF1_UP.V1_DN	177	-	-0.3852115	-1.5596665	0.0283975 66	0.1102901 55	0.581
PRC1_BMI_UP.V1_UP	168	-	-0.361633	-1.4804169	0.0283975 66	0.1334447 9	0.738
BMI1_DN.V1_DN	128	-	-0.4102482	-1.5902628	0.0289256 2	0.1330046 8	0.516
CAHOY_OLIGODENDRO CUTIC	85	-	0.3670738	-1.4753858	0.0304259 64	0.1319194 9	0.743
RAPA_EARLY_UP.V1_UP	153	-	0.3568580	-1.4766347	0.0316831 7	0.1337290 1	0.742
P53_DN.V2_UP	142	-	0.3935677	-1.5785142	0.0322580 64	0.1271423 5	0.534
PTEN_DN.V1_DN	167	-	-0.3780826	-1.5146405	0.0356435 63	0.1257368 6	0.679
ATM_DN.V1_UP	140	-	-0.3551041	-1.4652463	0.0362903 2	0.1348755 8	0.759
DCA_UP.V1_UP	166	-	0.3299048	-1.4171975	0.0363636 35	0.1565429	0.82
ALK_DN.V1_DN	128	-	0.3735321	-1.482125	0.0368932 04	0.1349897 4	0.735
KRAS.LUNG.BREAST_UP. V1_DN	132	-	0.3781921	-1.4714079	0.0398406 4	0.1323610 7	0.748
PIGF_UP.V1_DN	178	-	0.3652449	-1.4974983	0.0417495 03	0.1313449 3	0.708
GCNP_SHH_UP_EARLY.V 1_DN	157	-	0.3449003	-1.436735	0.0443037 97	0.1480858	0.803
KRAS.300_UP.V1_DN	131	-	0.3874197	-1.483671	0.0454545 47	0.13633	0.73
JNK_DN.V1_DN	174	-	0.3863625	-1.5199273	0.0473251 04	0.1249660 5	0.67
ZNF880 LOW							
HALLMARK							
Process	SIZE	ES	NES	NOM p- val	FDR q-val	FWER p- val	
HALLMARK_MYC_TARG ETS_V1	188	0.7553346	2.1108708	0	0.0019721 505	0.005	
ONCOGENIC							
Process	SIZE	ES	NES	NOM p- val	FDR q-val	FWER p- val	

SINGH_KRAS_DEPENDENCY_SIGNATURE	20	0.7726228	1.7392375	0.022132797	0.0793264	0.25
ZNF880 HIGH						
HALLMARK						
Process	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
HALLMARK_KRAS_SIGNALLING_UP	193	- 0.53431296	-1.8807771	0.0019417476	0.13277923	0.073
HALLMARK_IL2_STAT5_SIGNALING	194	-0.492885	-1.8228027	0.008016032	0.08579951	0.128
HALLMARK_COAGULATION	136	- 0.50367165	-1.8331504	0.009505703	0.11030985	0.114
HALLMARK_WNT_BETA_CATENIN_SIGNALING	42	- 0.48259205	-1.6514124	0.017578125	0.19889294	0.353
HALLMARK_KRAS_SIGNALLING_DN	188	-0.3903482	-1.6159383	0.02053388	0.15808839	0.408
HALLMARK_APICAL_SURFACE	43	- 0.43622726	-1.5511712	0.022680413	0.18224429	0.515
HALLMARK_UV_RESPONSE_DN	137	- 0.50507885	-1.6149762	0.032945737	0.14073399	0.408
HALLMARK_BILE_ACID_METABOLISM	112	-0.3690332	-1.4684645	0.036659878	0.20230177	0.674
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	194	-0.6100307	-1.671884	0.047244094	0.21426366	0.324
ONCOGENIC						
Process	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
BRCA1_DN.V1_UP	122	-0.5570718	-2.0580592	0	0.0020800577	0.006
JNK_DN.V1_UP	170	-0.5336213	-2.1285303	0	0.002087807	0.002
IL21_UP.V1_DN	166	- 0.51926875	-2.0645976	0	0.0023379507	0.005
KRAS.600_UP.V1_UP	261	-0.5205863	-1.966695	0	0.0026885504	0.019
KRAS.PROSTATE_UP.V1_UP	126	- 0.56847614	-2.0996742	0	0.0027082842	0.004
BMI1_DN.V1_DN	128	- 0.50684017	-1.9754233	0	0.0027929503	0.019
JNK_DN.V1_DN	174	-0.4984375	-1.976734	0	0.0030077924	0.019
PTEN_DN.V1_UP	168	- 0.50598216	-1.9572101	0	0.0031016576	0.024
KRAS.KIDNEY_UP.V1_UP	136	-0.5996813	-1.958878	0	0.0031779842	0.023

P53_DN.V1_DN	186	- 0.5336485 5	-1.9778731	0	0.0032584 418	0.019
IL15_UP.V1_DN	164	- 0.5101144 3	-2.0009875	0	0.0035245 91	0.018
MEL18_DN.V1_DN	137	-0.5422305	-1.9807446	0	0.0035546 639	0.019
CYCLIN_D1_KE_.V1_DN	184	-0.4780042	-1.982091	0	0.0039101 304	0.019
BMI1_DN_MEL18_DN.V1_DN	137	-0.5401704	-2.0023165	0	0.0039651 645	0.018
NOTCH_DN.V1_DN	170	- 0.5313173 5	-2.142779	0	0.0041756 14	0.002
ATF2_UP.V1_DN	170	-0.5211129	-1.9302804	0	0.0042912 527	0.035
KRAS.300_UP.V1_UP	136	- 0.5279162 5	-1.9322002	0	0.0044714 063	0.035
ATF2_S_UP.V1_DN	176	-0.5439721	-2.003248	0	0.0045316 17	0.018
STK33_SKM_DN	235	- 0.4520553 4	-1.9254154	0	0.0045759 07	0.038
CTIP_DN.V1_UP	120	-0.5206223	-1.9216428	0	0.0046287 04	0.04
IL2_UP.V1_DN	172	- 0.5404334 7	-2.009067	0	0.0050823 945	0.018
LTE2_UP.V1_UP	176	- 0.4589202 7	-1.89521	0	0.0055797 915	0.048
MTOR_UP.N4.V1_DN	154	- 0.5356571 7	-1.8682472	0	0.0056409 477	0.069
P53_DN.V2_DN	141	- 0.4460598 8	-1.8683933	0	0.0057789 14	0.069
BRCA1_DN.V1_DN	123	- 0.4636072 2	-1.8856051	0	0.0058287 18	0.059
KRAS.50_UP.V1_UP	47	- 0.5894888 6	-1.8632555	0	0.0058599 375	0.076
CAHOY_OLIGODENDRO CUTIC	85	-0.4713739	-1.8782787	0	0.0059171 855	0.064
ATM_DN.V1_DN	140	- 0.4626047 3	-1.8887779	0	0.0060668 77	0.056
VEGF_A_UP.V1_UP	185	-0.5057899	-1.8879248	0	0.0061673 37	0.057
KRAS.600.LUNG.BREAST_ UP.V1_DN	265	- 0.4476342 5	-1.8423011	0	0.0062971 28	0.094

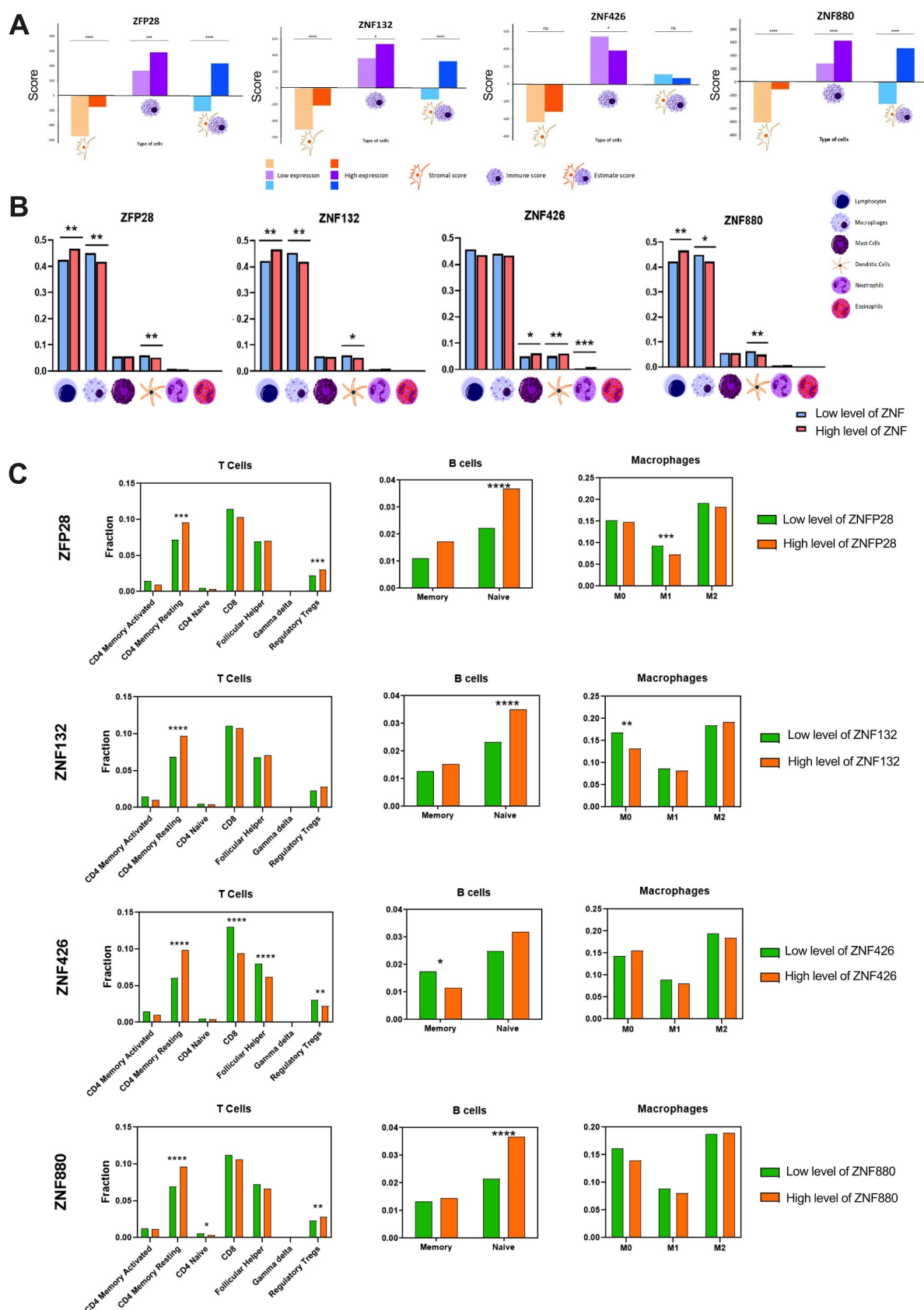
PRC1_BMI_UP.V1_UP	168	-0.4602045	-1.890119	0	0.0063196 64	0.056
JAK2_DN.V1_UP	170	- 0.4413165 5	-1.8521793	0	0.0063638 673	0.087
ESC_V6.5_UP_EARLY.V1_UP	153	- 0.4383237 7	-1.8425586	0	0.0064076 055	0.094
MTOR_UP.V1_DN	170	- 0.4605473 3	-1.844177	0	0.0065484 666	0.094
AKT_UP.V1_DN	179	- 0.4779144 2	-1.8311363	0	0.0069455 355	0.107
PKCA_DN.V1_DN	146	-0.4262535	-1.826998	0	0.0069882 134	0.11
PRC2_SUZ12_UP.V1_DN	169	- 0.4322900 5	-1.8212489	0	0.0076670 74	0.122
GCNP_SHH_UP_EARLY.V1_DN	157	- 0.4346948 6	-1.8087583	0	0.0081803 28	0.137
KRAS.AMP.LUNG_UP.V1_DN	126	- 0.4673130 2	-1.7980953	0	0.0085180 355	0.147
KRAS.AMP.LUNG_UP.V1_UP	130	- 0.4840309 3	-1.7991425	0	0.0086548 03	0.147
RAPA_EARLY_UP.V1_UP	153	- 0.4360724 7	-1.7919617	0	0.0090059 6	0.157
PRC2_EED_UP.V1_UP	174	- 0.4247905 6	-1.7809367	0	0.0090641 69	0.177
KRAS.BREAST_UP.V1_DN	129	- 0.4875043 6	-1.7870405	0	0.0090923 69	0.168
CAHOY_ASTROCYTIC	97	- 0.4509476 4	-1.7721968	0	0.0095814 84	0.19
CYCLIN_D1_UP.V1_DN	179	-0.3866293	-1.6980233	0	0.0172555 28	0.326
ATF2_S_UP.V1_UP	177	-0.3779935	-1.6573681	0	0.0228551 76	0.405
KRAS.600.LUNG.BREAST_UP.V1_UP	267	- 0.4416869 6	-1.7998439	0.0019157 088	0.0088107 86	0.147
AKT_UP_MTOR_DN.V1_DN	177	- 0.3756764 8	-1.6380923	0.0019379 845	0.0256490 6	0.441
ESC_J1_UP_LATE.V1_UP	175	- 0.4764093 5	-1.8625531	0.0019417 476	0.0056971 614	0.076
CTIP_DN.V1_DN	118	- 0.4527053 2	-1.817208	0.0019455 253	0.0076750 21	0.126

KRAS.BREAST_UP.V1_UP	128	- 0.4913867 4	-1.8869253	0.0019493 178	0.0059792 15	0.058
PRC2_SUZ12_UP.V1_UP	172	-0.39345	-1.6650878	0.0019493 178	0.0215650 03	0.394
PDGF_UP.V1_DN	117	- 0.4465543 3	-1.788049	0.0019531 25	0.0091296 95	0.166
PTEN_DN.V1_DN	167	- 0.4717122 3	-1.872992	0.0019607 844	0.0055950 647	0.067
ESC_V6.5_UP_LATE.V1_U P	170	- 0.4787799 4	-1.813443	0.0019880 715	0.0078247 13	0.128
STK33_NOMO_DN	237	-0.4136329	-1.7405137	0.0019920 32	0.0124952 6	0.24
NOTCH_DN.V1_UP	169	- 0.4144337 5	-1.7255309	0.002	0.0138906 07	0.274
STK33_DN	237	- 0.3918237 7	-1.713288	0.0020120 724	0.0149179 7	0.288
LEF1_UP.V1_UP	186	- 0.5129769 4	-1.8779308	0.0020202 02	0.0057199 458	0.064
E2F1_UP.V1_DN	174	- 0.4214429 3	-1.6897892	0.0020202 02	0.0185179 75	0.343
DCA_UP.V1_UP	166	-0.4088643	-1.7393749	0.0020283 975	0.0124191 595	0.241
KRAS.KIDNEY_UP.V1_DN	126	- 0.4476407 2	-1.7195729	0.0020491 802	0.0142843 42	0.281
RELA_DN.V1_DN	127	- 0.4728921 4	-1.8196473	0.0020576 13	0.0076421 61	0.123
IL21_UP.V1_UP	172	- 0.4336121 7	-1.7476187	0.0020618 557	0.0119441 98	0.231
ATM_DN.V1_UP	140	-0.4321151	-1.7387314	0.0020876 827	0.0122741 84	0.242
CAHOY_ASTROGLIAL	92	-0.5239279	-1.8736614	0.0039840 64	0.0057402 295	0.067
PTEN_DN.V2_UP	129	- 0.4677861 6	-1.7916532	0.0040241 447	0.0088360 37	0.157
KRAS.PROSTATE_UP.V1_ DN	135	- 0.4753490 4	-1.7864103	0.0040241 447	0.0089549 19	0.169
LEF1_UP.V1_DN	177	-0.4180833	-1.6887565	0.0040241 447	0.0182356 63	0.345
PRC1_BMI_UP.V1_DN	171	- 0.3876536 2	-1.6065522	0.0040241 447	0.0306880 9	0.496

CRX_DN.V1_UP	125	- 0.3980547 2	-1.689496	0.0040567 95	0.0183196 53	0.345
P53_DN.V2_UP	142	-0.452817	-1.7841852	0.0059055 12	0.0090549 73	0.174
KRAS.600_UP.V1_DN	264	-0.4198844	-1.7122804	0.0059405 942	0.0148291 57	0.291
IL15_UP.V1_UP	171	- 0.3692649 3	-1.5682822	0.0060120 24	0.0382637 6	0.57
ESC_V6.5_UP_EARLY.V1_DN	153	-0.4833999	-1.803128	0.0060362 173	0.0086085 12	0.142
WNT_UP.V1_DN	163	- 0.4252768 8	-1.7544483	0.0060728 746	0.0112338 05	0.218
EGFR_UP.V1_DN	166	-0.40838	-1.6716326	0.0060975 607	0.0207476 65	0.383
CRX_NRL_DN.V1_UP	129	-0.3736479	-1.5742764	0.0061728 396	0.0368991	0.549
CSR_LATE_UP.V1_DN	131	- 0.4584121 4	-1.7828397	0.0078277 89	0.0090724 29	0.176
GCNP_SHH_UP_LATE.V1_DN	168	- 0.3321255 7	-1.4565773	0.0098814 23	0.0661324 3	0.769
KRAS.LUNG.BREAST_UP.V1_DN	132	-0.4208828	-1.64033	0.0099403 58	0.0254948 92	0.438
ESC_J1_UP_EARLY.V1_UP	151	- 0.3817539 5	-1.6222422	0.0099601 6	0.0278407 58	0.469
RAF_UP.V1_DN	177	- 0.4467896 2	-1.7229601	0.0113852	0.0142087 47	0.278
NRL_DN.V1_UP	129	- 0.3711713 9	-1.55595	0.0116731 515	0.0400114 02	0.587
KRAS.LUNG_UP.V1_UP	130	-0.4630544	-1.7793784	0.0119521 92	0.0090586 25	0.18
RAPA_EARLY_UP.V1_DN	173	- 0.3638496 7	-1.5795484	0.0120724 35	0.0366130 17	0.544
PKCA_DN.V1_UP	150	- 0.3628052 5	-1.5431333	0.0121212 12	0.0419527 9	0.613
RPS14_DN.V1_UP	184	-0.5755643	-1.9073397	0.0135922 33	0.0048498 15	0.042
WNT_UP.V1_UP	169	- 0.3715554 5	-1.5699593	0.0141700 4	0.0380317 98	0.565
SNF5_DN.V1_DN	147	- 0.4087349 5	-1.6342388	0.0157790 93	0.0261701 08	0.448
RELA_DN.V1_UP	145	- 0.3713486 2	-1.541634	0.0159680 64	0.0419874 97	0.617

ERBB2_UP.V1_UP	179	- 0.4077924 5	-1.6321173	0.0179640 73	0.0263481 03	0.451
BCAT.100_UP.V1_DN	28	-0.4691471	-1.5784229	0.0179640 73	0.0364797 5	0.544
ALK_DN.V1_DN	128	- 0.4031704 4	-1.586379	0.0180722 88	0.0350074 5	0.525
PTEN_DN.V2_DN	125	- 0.3824116 6	-1.5513586	0.0191204 59	0.0402142 44	0.594
ATF2_UP.V1_UP	181	-0.3634727	-1.5213069	0.0198019 8	0.0458936 9	0.658
DCA_UP.V1_DN	162	- 0.3369641 6	-1.4625524	0.0199600 8	0.0644632	0.754
SNF5_DN.V1_UP	158	-0.4820875	-1.7539169	0.0207468 89	0.0110897 15	0.218
CRX_DN.V1_DN	128	- 0.3721545 3	-1.5050715	0.0215686 28	0.0498792 86	0.682
ALK_DN.V1_UP	131	- 0.3787124 2	-1.550308	0.0219560 88	0.0400530 47	0.597
KRAS.300_UP.V1_DN	131	-0.4152209	-1.5910677	0.0221774 19	0.0341065 5	0.521
STK33_SKM_UP	238	-0.4503159	-1.6263297	0.0224489 8	0.0272794 35	0.46
HOXA9_DN.V1_UP	171	- 0.4852942 2	-1.6817813	0.0227743 28	0.0190992 93	0.357
E2F3_UP.V1_UP	171	- 0.4181543 3	-1.5769879	0.0242537 32	0.0365063 44	0.545
RAF_UP.V1_UP	182	- 0.3883815 7	-1.5095226	0.026	0.0489747 9	0.678
KRAS.LUNG.BREAST_UP. V1_UP	135	- 0.4309287 4	-1.6563247	0.0266666 67	0.0227310 23	0.407
CAHOY_NEURONAL	94	- 0.4599901 4	-1.655503	0.0278884 47	0.0226487 33	0.408
NFE2L2.V2	411	- 0.3550576 3	-1.5227377	0.0301810 86	0.0457826 6	0.656
SRC_UP.V1_UP	148	- 0.4105423 4	-1.5533906	0.0307101 72	0.0404956 23	0.593
P53_DN.V1_UP	184	-0.3905705	-1.5518457	0.0336633 66	0.0405067 2	0.594
NRL_DN.V1_DN	121	- 0.3390013 3	-1.458594	0.0368852 47	0.0656651 6	0.76

BCAT_GDS748_UP	46	- 0.4579789 3	-1.5607423	0.0370370 37	0.0393232 55	0.577
CAMP_UP.V1_DN	186	- 0.4055335 2	-1.5637769	0.0376237 63	0.0390709 15	0.574
BCAT.100_UP.V1_UP	46	- 0.4525393 2	-1.524421	0.0391752 57	0.0462370 78	0.656
KRAS.DF.V1_UP	182	- 0.3839599 8	-1.5589074	0.0418326 7	0.0395311 9	0.579
KRAS.DF.V1_DN	183	-0.3370468	-1.4191353	0.0419161 7	0.0810763 54	0.824
TGFB_UP.V1_DN	179	- 0.3216399 6	-1.3935256	0.0425101 22	0.0911034 9	0.861
SRC_UP.V1_DN	152	-0.3125242	-1.4091281	0.0434782 6	0.0852913 7	0.841
PIGF_UP.V1_DN	178	- 0.3736156 8	-1.500715	0.0449897 76	0.0514219	0.694
CYCLIN_D1_UP.V1_UP	178	- 0.3406034 4	-1.433372	0.0492813 14	0.0752866 6	0.804
PRC2_EZH2_UP.V1_UP	180	- 0.3976676 8	-1.5231307	0.05	0.0461528 93	0.656



and macrophages; *ns* - not significant; * $p \leq 0.05$; ** $p \leq 0.01$; *** $p \leq 0.001$; **** $p \leq 0.0001$ considered as significant.

Table S4. Expression level of *ZNF540* depending on clinical-pathological parameters in HNSCC patients from GSE65858; Mann-Whitney U test or one-way ANOVA, $p < 0.05$ considered as significant.

Parameter	Group	Mean \pm SEM	P-val	Cases
Age	<60	6.448 \pm 0.01302	0.3211	157
	>60	6.449 \pm 0.01304		113
Gender	Female	6.469 \pm 0.02326	0.2616	47
	Male	6.444 \pm 0.01016		223
Alcohol	Positive	6.444 \pm 0.009569	0.2698	239
	Negative	6.487 \pm 0.03356		31
Smoking	Positive	6.439 \pm 0.009893	0.0418	222
	Negative	6.491 \pm 0.02489		48
UICC Stage	I + II	6.431 \pm 0.01561	0.8075	55
	III + IV	6.453 \pm 0.01100		215
T stage	T1 + T2	6.454 \pm 0.01377	0.4456	115
	T3 + T4	6.445 \pm 0.01264		155
N stage	N0	6.432 \pm 0.01287	0.6297	94
	N1+N2+N3	6.457 \pm 0.01251		176
Localization	Oral cavity	6.423 \pm 0.01353	> 0.05	83
	Hypopharynx	6.404 \pm 0.01454		33
	Larynx	6.416 \pm 0.01448		48
	Oropharynx	6.498 \pm 0.01893		102