

Table SI. Short hairpin RNA sequence.

Gene	Target sequence
ALDH2_clone1 (TRCN0000026452)	5'-GCAGATCATTCGGTGG-3' AATTT
ALDH2_clone2 (TRCN0000026486)	5'-GCTGATAAGTACCACGGGAAA-3'

ALDH2, aldehyde dehydrogenase 2.

Table SII. Primer sequence.

Gene	Sequence
<i>ALDH2</i> -forward	5'-CAT GGA CGC ATC ACA CAG GG-3'
<i>ALDH2</i> -reverse	5'-CTT GCC ATT GTC CAG GGT CT-3'
<i>VEGFC</i> -forward	5'-GGC CAA CCT CAA CTC AAG GA-3'
<i>VEGFC</i> -reverse	5'-CTA TAC ACA CCT CCC GTG GC-3'
<i>ACTB</i> - forward	5'-AGA AAA TCT GGC ACC ACA CC-3'
<i>ACTB</i> - reverse	5'-AGA GGC GTA CAG GGA TAG CA-3'
<i>RELA</i> _ forward	5'-CCC ACG AGC TTG TAG GAA AGG-3'
<i>RELA</i> _ reverse	5'-GGA TTC CCA GGT TCT GGA AAC-3'
<i>Vegfc</i> -forward	5'-TTT GCC AAT CAC ACT TCC TGC-3'
<i>Vegfc</i> -reverse	5'-ACA CTG TGG TAA TGT TGC TGG-3'
<i>Actb</i> - forward	5'-CAG GTC ATC ACT ATT GGC AA-3'
<i>Actb</i> - reverse	5'-AGG TCT TTA CGG ATG TCA AC-3'

ALDH2, aldehyde dehydrogenase 2; VEGFC, Vascular Endothelial Growth Factor C; ACTB, Actin Beta; RELA, NF- κ B p65; vegfc, vascular endothelial growth factor c; actb, β -actin.

Table SIII. Antibody list.

Antibody	Supplier, cat. no.	Application	Dilution
ALDH2	Genetex, GTX101429	Western blot, immunohistochemistry	1:2,000, 1:200
Phosphorylated NF- κ B p65 (Ser536)	Cell Signaling, Inc., #3033	Western blot	1:1,000
NF- κ B p65	Santa Cruz Biotechnology, Inc., sc-8008	Western blot	1:200
β -actin	Sigma-Aldrich (Merck KGaA), A5441	Western blot	1:5,000
VEGFC	GeneTex, GTX52393	Inhibition	10-20 μ g/ml
Human IgG rabbit mAb	ABclonal, A19711	VEGFC Ab control	10-20 μ g/ml
VEGFC	GeneTex, GTX113574	IHC	1:1,000

Table SIV. Inhibitor and activator reagent list.

Reagent	Supplier, cat. no.	Function	Concentration
Alda-1	MedChemExpress, HY-18936	ALDH2 enzyme activator	20 μ M
Daidzin	MedChemExpress, HY-N0018	ALDH2 enzyme inhibitor	80-160 nM
Bay11-7082	MedChemExpress, HY-13453	NF κ B inhibitor	10-20 μ M
NAC	Sigma-Aldrich(Merck KGaA), A9165	Free radical scavengers	10 mM
H ₂ O ₂	Sigma-Aldrich(Merck KGaA), 31642	Non-radical ROS	80 μ M
Acetaldehyde	Sigma-Aldrich (Merck KGaA), #402788	Primary metabolite of ethanol	10 μ M

Table SV. Differentially expressed genes with enzyme annotation in head and neck cancer from dataset GSE6631.

Symbol	Regulation	Expression log ratio (tumor vs. normal)
TGM3	Down	-3.559
ADH7	Down	-2.250
COX7A1	Down	-1.845
ALDH3A1	Down	-1.839
MYH7	Down	-1.795
MYH2	Down	-1.748
TGM1	Down	-1.725
TNNI2	Down	-1.356
HPGD	Down	-1.339
GPX3	Down	-1.328
ANXA1	Down	-1.304
SULT2B1	Down	-1.294
LYZ	Down	-1.162
RRAD	Down	-1.161
ALOX12	Down	-1.145
GPD1L	Down	-1.106
RRAGD	Down	-1.099
MGLL	Down	-1.053
DNASE1L3	Down	-1.051
PGD	Down	-1.025
RNASE4	Down	-1.006
SELENBP1	Down	-0.974
GATM	Down	-0.905
AADAC	Down	-0.898
PTGDS	Down	-0.891
ACTC1	Down	-0.873
ENO3	Down	-0.859
ADH1B	Down	-0.851
TM7SF2	Down	-0.851
MGST2	Down	-0.835
CES2	Down	-0.833
RND3	Down	-0.828
PYGM	Down	-0.826
CYP2C18	Down	-0.819
ALDH9A1	Down	-0.812
COX6A2	Down	-0.807
FUT3	Down	-0.797
ALDH3A2	Down	-0.793
ALDH1A1	Down	-0.779
FUT6	Down	-0.772
TXN	Down	-0.770

ADH1A	Down	-0.763
CRYM	Down	-0.752
HS3ST1	Down	-0.749
CH25H	Down	-0.745
DDX3Y	Down	-0.713
CYP2J2	Down	-0.711
FMO2	Down	-0.703
EPHX2	Down	-0.685
HMGCS2	Down	-0.677
PLA2G2A	Down	-0.651
GSTA4	Down	-0.646
MYCBP2	Down	-0.641
RAB11A	Down	-0.639
ALDH3B2	Down	-0.625
BBOX1	Down	-0.624
CRY1	Down	-0.613
MAOA	Down	-0.610
DIO2	Down	-0.608
ALDH2	Down	-0.606
AMD1	Down	-0.600
CYP2E1	Down	-0.600
SMPDL3A	Down	-0.600
ACOX1	Down	-0.597
ACADM	Down	-0.593
CA3	Down	-0.584
DHRS3	Down	-0.582
MOXD1	Down	-0.568
ETFDH	Down	-0.559
TYRP1	Down	-0.558
DHCR24	Down	-0.555
ACADSB	Down	-0.545
RAB5A	Down	-0.542
MAOB	Down	-0.535
ASAH1	Down	-0.526
CBR3	Down	-0.521
OAT	Down	-0.513
AGL	Down	-0.512
PDZRN3	Down	-0.511
PMEL	Down	-0.508
ST6GALNAC2	Up	0.500
OAS2	Up	0.502
AGPS	Up	0.503
SMURF2	Up	0.506
GANAB	Up	0.514
MSH6	Up	0.514
MCM2	Up	0.519

GM2A	Up	0.520
ENO2	Up	0.527
B4GALT4	Up	0.532
CA9	Up	0.533
CAD	Up	0.540
CHPF	Up	0.541
PTDSS1	Up	0.541
UBE2L6	Up	0.542
LDHA	Up	0.543
MCM6	Up	0.545
HSP90AB1	Up	0.548
FTL	Up	0.549
PLTP	Up	0.552
WARS1	Up	0.552
ADA	Up	0.557
GCLC	Up	0.558
MCM7	Up	0.558
PLD3	Up	0.559
PLOD3	Up	0.561
RPN1	Up	0.564
FTH1	Up	0.572
GNS	Up	0.572
EXT1	Up	0.573
RHOC	Up	0.584
MCM4	Up	0.590
ODC1	Up	0.594
BIRC2	Up	0.600
PPT1	Up	0.606
LDHB	Up	0.607
MICAL2	Up	0.608
HSPA5	Up	0.611
MTHFD2	Up	0.615
FKBP9	Up	0.623
RAB31	Up	0.627
GMPS	Up	0.632
FEN1	Up	0.662
AKR1C3	Up	0.663
RHOB	Up	0.698
KIF14	Up	0.709
RSAD2	Up	0.725
TGM2	Up	0.727
P4HA1	Up	0.732
TOP2A	Up	0.733
CHST2	Up	0.737
GNAI1	Up	0.744
B4GALT2	Up	0.749

AKR1B1	Up	0.758
LOX	Up	0.765
MYO10	Up	0.784
UBE2C	Up	0.804
MYO5A	Up	0.806
TXNRD1	Up	0.817
UBE2S	Up	0.893
CA2	Up	0.901
PLOD2	Up	0.901
KYNU	Up	0.918
LOXL2	Up	0.928
RRAS2	Up	0.931
RFC4	Up	0.941
LPCAT1	Up	1.059
SULF1	Up	1.119
PFN2	Up	1.534

Table SVI. Ingenuity Pathway Analysis canonical pathways in head and neck cancer in the GSE6631 dataset.

Canonical pathway	Log(P-value)	Z-score	Molecules
Xenobiotic metabolism PXR signaling pathway	11.800	-3.357	ALDH1A1, ALDH2, ALDH3A1, ALDH3A2, ALDH3B2, ALDH9A1, CES2, CHST2, GSTA4, HS3ST1, HSP90AB1, MAOA, MAOB, MGST2, SULT2B1
Noradrenaline and adrenaline degradation	13.700	-3.162	ADH1A, ADH1B, ADH7, ALDH1A1, ALDH2, ALDH3A1, ALDH3A2, ALDH9A1, MAOA, MAOB
Serotonin degradation	10.600	-3.162	ADH1A, ADH1B, ADH7, ALDH1A1, ALDH2, ALDH3A1, ALDH3A2, ALDH9A1, MAOA, MAOB
Xenobiotic metabolism AHR signaling pathway	8.440	-3.000	ALDH1A1, ALDH2, ALDH3A1, ALDH3A2, ALDH3B2, ALDH9A1, GSTA4, HSP90AB1, MGST2
Ethanol degradation II	10.400	-2.828	ADH1A, ADH1B, ADH7, ALDH1A1, ALDH2, ALDH3A1, ALDH3A2, ALDH9A1
Putrescine degradation III	10.300	-2.646	ALDH1A1, ALDH2, ALDH3A1, ALDH3A2, ALDH9A1, MAOA, MAOB
Tryptophan degradation X (mammalian, via tryptamine)	9.610	-2.646	ALDH1A1, ALDH2, ALDH3A1, ALDH3A2, ALDH9A1, MAOA, MAOB
Dopamine degradation	9.040	-2.646	ALDH1A1, ALDH2, ALDH3A1, ALDH3A2, ALDH9A1, MAOA, MAOB
Xenobiotic metabolism CAR signaling pathway	9.580	-2.496	ALDH1A1, ALDH2, ALDH3A1, ALDH3A2, ALDH3B2, ALDH9A1, CHST2, FMO2, GSTA4, HS3ST1, HSP90AB1, MGST2, SULT2B1
Ethanol degradation IV	8.080	-2.449	ALDH1A1, ALDH2, ALDH3A1, ALDH3A2, ALDH9A1, TYRP1
Oxidative ethanol degradation III	8.700	-2.236	ALDH1A1, ALDH2, ALDH3A1, ALDH3A2, ALDH9A1, CYP2C18, CYP2E1, CYP2J2
Histamine degradation	6.790	-2.236	ALDH1A1, ALDH2, ALDH3A1, ALDH3A2, ALDH9A1
Fatty acid α -oxidation	6.790	-2.236	ALDH1A1, ALDH2, ALDH3A1, ALDH3A2, ALDH9A1
Nicotine degradation II	4.220	-2.236	ADH7, CYP2C18, CYP2E1, CYP2J2, FMO2
Superpathway of melatonin degradation	4.190	-2.236	CYP2C18, CYP2E1, CYP2J2, MAOA, MAOB

Table SVII. Univariate and multivariate analysis of overall survival in patients with head and neck cancer (n=106).

Characteristic	Univariate			Multivariate		
	HR	95% CI	P-value	HR	95% CI	P-value
Sex						
Male	1.73	(0.377, 7.94)	0.481	-	-	-
Female	1.00					
Age, years						
≥60	2.45	(0.736, 8.18)	0.144	-	-	-
<60	1.00					
T stage						
4	5.50	(0.660, 45.81)	0.115	3.00	(0.253, 20.85)	0.459
3	13.85	(1.249, 153.73)	0.032	9.52	(0.718, 126.40)	0.088
2	3.25	(0.337, 31.40)	0.308	1.788	(0.163, 19.43)	0.637
1	1.00			1.00		
N stage						
+	7.758	(2.091, 28.79)	0.002	6.71	(1.696, 26.72)	0.007
0	1.00			1.00		
AJCC stage						
III/IV	55.63	(0.515, 6008)	0.093	-	-	-
I/II	1.00					
ALDH2 expression						
High	0.216	(0.047, 0.988)	0.048	0.216	(0.043, 1.075)	0.061
Low	1.00			1.00		

HR, hazard ratio; CI, confidence interval; -, not applicable; AJCC, American Joint Committee on Cancer.

Table SVIII. Univariate and multivariate analysis of disease-free survival in patients with head and neck cancer (n=106).

Characteristic	Univariate			Multivariate		
	HR	95% CI	P-value	HR	95% CI	P-value
Sex						
Male	1.304	(0.294, 5.778)	0.727	-	-	-
Female	1.00					
Age, years						
≥60	1.389	(0.535, 3.611)	0.500	-	-	-
<60	1.00					
T stage						
4	1.836	(0.551, 6.119)	0.322	-	-	-
3	3.281	(0.598, 18.009)	0.171	-	-	-
2	0.769	(0.171, 3.450)	0.731	-	-	-
1	1.00					
N stage						
+	3.932	(1.489, 10.383)	0.006	2.64	(0.885, 7.87)	0.082
0	1.00			1.00		
AJCC stage						
III/IV	6.503	(1.484, 28.493)	0.013	6.71	(0.710, 18.686)	0.121
I/II	1.00			1.00		
ALDH2 expression						
High	0.211	(0.060, 0.742)	0.015	0.192	(0.053, 0.694)	0.012
Low	1.00			1.00		

HR, hazard ratio; CI, confidence interval; -, not applicable; AJCC, American Joint Committee on Cancer.

Table SIX. Upstream regulator Ingenuity Pathway Analysis of TW2.6/shALDH2 cells.

Upstream regulator	Molecule type	P-value of overlap	Target molecules in dataset
TNF	Cytokine	2.97×10^{-14}	ABCC3, ADGRG6, ADM, ALDH2, ARHGEF10L, ARHGEF5, BST2, C3, CCND2, CD44, CD74, CDH11, CDH2, CDKN1A, CFB, CHI3L1, CRHR1, CXCL16, CXCL8, CXCL9, DPP4, DUSP1, DUSP5, F3, FOS, FST, GPR176, HBEGF, HCAR3, HLA-, HMOX1, IDO1, IFI27, IFIT1, IL20RB, IL4R, IL6, IRAK3, JUN, KRT15, KRT34, KYNU, LAMA3, LBP, LCN2, LTBP2, LYN, MMP1, MT-CYB, NLRP7, OAS1, OASL, OCLN, P2RY6, PDPN, PHGDH, PLAAT4, PLSCR1, PPP1R15A, PRDM1, PSME2, RASGRF1, RGS2, RHOB, RND3, RXRA, S100A8, S100A9, SAA1, SELE, SERPINB2, SERPINE1, SLC8A1, SNAI1, SOCS1, SOD2, SREBF1, TAPBP, TCIM, TFAP2A, TGFBR2, TIAM2, TIE1, TLR4, TNFRSF1B, TNFSF10, TNFSF11, UBQLN2, VCAM1, VEGFC, WNT5A
CG	Complex	6.91×10^{-14}	ABTB2, ANGPTL4, ARID5B, BDNF, BRCA1, BRCA2, C1RL, CCNE2, CDH2, CFB, CREB5, CRYBG1, CXCL8, DUSP1, E2F8, ELK3, EPB41L4B, ESM1, ESR2, ETV1, F3, FAT4, FILIP1L, FJX1, FLRT2, FOS, FOSL1, FST, GADD45B, GYS1, HAS2, HSD17B6, HSD3B1, IL13RA2, IL18R1, IL1R2, IL1RL1, IL20, ITGA3, JUN, KRT34, MARCHF3, MMP1, NAT9, PLPP3, PRICKLE2, RASAL2, RGS2, RGS4, RUNX1, SLC2A12, SMARCA1, STEAP1, TMX4, TNFRSF1B, TNFSF11, TRIB3, TRIM22, UNG, UPP1, VCAM1, VEGFC
TP63	Transcription regulator	3.97×10^{-12}	ACTL6A, ADM, AJUBA, BDKRB2, BRCA1, BST2, CASP3, CCND2, CD82, CDH2, CDKN1A, CGN, CITED2, CSTA, CXCL8, DKK1, DLL1, DST, EDN2, ENG, F3, FOS, FOSL1, FST, GPX2, GRHL2, HBEGF, ID3, IGFBP7, IL1RAP, IL6, ITGA3, ITGB4, ITGB8, JUN, KRT6B, LCN2, LYN, MIR205HG, MPZL2, PTHLH, PTPRU, S100A2, S100A8, S100A9, SERPINB2, SERPINE1, SNAI1, TGFBR2, TINAGL1, TMBIM6, TNFSF10, TNS4, UGT1A9 (includes others), VNN1, WNT4, WNT5A, ZEB1

GLI1	Transcription regulator	3.06×10^{-10}	ABCC3, ABCG1, AHNAK, AHNAK2, AKR1C1/AKR1C2, AKR1C3, ANKRD22, ANO1, ANXA6, ASPM, ATF3, C1orf116, CAV2, CCSAP, CD44, CDKN1A, CEACAM6, CHI3L1, CSRNP1, CXCL8, DUSP5, EPB41L4B, FOS, FOXA2, GADD45B, HSD17B6, HUS1, ID1, ID3, IGFBP7, IL1R2, IMPA2, ITGA3, ITGB4, KLK6, KLRC3, KRT15, LY6G6D, MALL, MAPK11, MICAL2, MTURN, NIPAL2, OVOL1, PCDH7, PLXDC1, POLD4, PTCH1, RIN2, RPS6KA1, RXRA, S100A2, S100A9, SCARA3, SCD, SCD5, SERPINA1, SERTAD4, SLC16A9, SLC1A3, SNAI1, SYNE1, TBX3, TIMP2, TNS4, TRIM15, TSPAN1, TTC13, UBALD2, VEGFC, WNT5A
TGFB1	Growth factor	3.95×10^{-10}	ADAM12, AKR1C1/AKR1C2, ANGPTL4, ANKRD1, ASPM, ASPN, ATF3, BGN, BRIP1, CASP3, CCN2, CCND2, CCNE2, CD44, CDH11, CDH2, CDKN1A, CELSR2, CHI3L1, CITED2, CLDN1, CXCL8, DDIT3, ELK3, ENG, ESR2, F3, FOS, FOSL1, FST, FURIN, HAS2, HBEGF, HKDC1, HMOX1, HSPA5, ID1, IL13RA2, IL1RL1, IL6, ITGA3, ITGB2, JUN, LCN2, LTBP2, MAPK8IP3, MLXIP, MLXIPL, MMP1, MYBL2, NEK2, OCLN, PECAM1, PRSS3, PTHLH, RFC4, RHOB, SCD, SERPINA1, SERPINA3, SERPINE1, SNAI1, SPOCK1, STAT3, TBX3, TFAP2A, TGFB1, TGFB2, TLR4, TSPAN7, VCAN, WNT5A, ZEB1
P38 MAPK	Kinase	5.15×10^{-9}	ATF3, CCN2, CCNE1, CD44, CD70, CD82, CDKN1A, CRHR1, CXCL8, CXCL9, CYP19A1, F3, FADD, FOS, FST, GJA1, HMOX1, HSPA5, IL6, ITGB4, ITGB8, JUN, LAMA3, MMP1, PLA2G4A, RND3, RRAD, SELE, SERPINE1, SNAI1, TNFSF10, VCAM1, VDR, ZMAT3
SMARCA4	Transcription regulator	1.07×10^{-8}	AHNAK, AIM2, ALDH2, ANO1, APOBEC3G, ARHGDI5, ASNS, ATR, CCN2, CD163L1, CD44, CD52, CD74, CDH2, CDKN1A, CEACAM6, CLDN1, CP, CRIM1, CRYBG1, CXCL8, DLL1, EPHA1, EPHA4, F3, FAM167A, FGFBP1, FMO2, FOS, GPR158, GPR83, GSG1, HK1, HKDC1, HLA-B, HS3ST1, ID3, IFIT1, IGFBP4, IGFBP7, IL20RB, ITGA3, JUN, KRT15, LAMA3, MC4R, MGP, MMP1, MMP7, NECTIN1, NPFFR2, PFKL, PLPP3, PSME2, PTHLH, RGS2, S100A2, SEL1L3, SEMA7A, SERPINB2, SLC43A3, SNAI1, SPINK1, STAMBPL1, TACSTD2, TAPBPL, TCIM, TREM1, TREM2, TRIM15, TRIM36
SBDS	Ribosome maturation protein	2.2×10^{-8}	AKR1C1/AKR1C2, AKR1C3, CCN2, CHAC1, COL27A1, DDIT3, DNAJB1, ERBB3, FBXL16, FOS, GABRE, GADD45B, HSPA5, ID1, IGFBP7, IL4R, MYD88, OPN3, PCDH7, PPP1R15A, PPP2R2C, RGS4, TRIB3

NEUROG1	Transcription regulator	2.23×10 ⁻⁸	AMIGO2, C3, CCND2, CD82, CEMIP, CYSLTR2, DSP, FABP3, GAS2, H4C6, HAS2, IL6, LCP1, P4HA2, SCG2, SLC43A3, SPOCK1, TRIM22, TSPAN7
JUN	Transcription regulator	4.28×10 ⁻⁸	ANKRD1, ASNS, ATF3, CCN2, CD44, CDH11, CDH2, CDKN1A, CXCL8, CYP19A1, DKK1, DUSP1, DUSP5, FLG, FOSL1, FOXA2, GJA1,- HLA-B, HMOX1, IL6, ITGB4, ITGB8, JUN, MMP1, MMP7, NR4A1, PADI3, PADI4, POLI, SAA1, SERPINE1, SLC38A2, SOD2, VAV3, VEGFC, ZEB1
IFNG	Cytokine	1.57×10 ⁻⁷	AIM2, APOL1, ATF3, BST2, C3, CASP3, CDH2, CDKN1A, CHAC1, CP, CXCL16, CXCL8, CXCL9, CYSLTR2, DDX60, DEFB1, DKK1, DPP4, ERAP2, HLA-A, HLA-B, HLA-G, HSPA1A/HSPA1B, IDO1, IFI27, IFIT1, IFIT2, IGFBP4, IL27, IL6, KRT15, LGALS9, MMP1, MYD88, NFE2L3, OAS1, OASL, OCLN, PDCD1LG2, PLAAT4, PLSCR1, PTAFR, RAB36, RSPH14, SAMD9, SELE, SNAI1, SOCS1, SOD2, SREBF2, TLR4, TNFRSF1B, TNFSF10, TRIM22, VCAM1
EZH2	Transcription regulator	1.63×10 ⁻⁷	ARHGDI1B, C15orf48, C3, CCND2, CCNE2, CD82, CDH2, CDKN1A, CEMIP, CHRM3, CXCL8, DAB2IP, DKK1, DUSP5, EP300, EPHA1, FHOD3, GDF15, IL6, KIAA1217, LCN2, LIN28B, MAPK15, MMP7, MPZL2, NEUROD1, PLA2G4A, PLAAT4, RUNX1, SAA1, SELENON, SERPINA1, SLC1A3, SNAI1, TBX3, TGFB1, TGFB2, TIMP2, ZEB1

Table SX. Canonical pathways Ingenuity Pathway Analysis of TW2.6/shALDH2 cells.

Canonical pathway	-log(P-value)	Ratio	Z-score	Molecules
Myelination signaling pathway	1.7900	0.1060	3.4300	ACVR2B, ADGRG6, APC, ARHGAP8/PRR5-ARHGAP8, BDNF, CREB3, CREB5, DLC1, EP300, ERBB3, FOS, FRK, ITGA3, ITGB2, ITGB4, ITGB8, JUN, LAMA1, LAMA3, LAMA5, LGI4, LYN, NFATC2, PLP1, PPP3CB, PRKACB, SCD, SLC16A1, SMAD6, SRC, SREBF1, SREBF2, WNT4, WNT5A
STAT3 pathway	1.4500	0.1190	2.8280	CDKN1A, IL10RB, IL13RA2, IL18R1, IL1R2, IL1RL1, IL20RB, IL4R, IL9R, MAP3K11, MAPK11, SOCS1, SRC, STAT3, TGFBR1, TGFBR2
NF-κB signaling	0.0000	0.0408	2.3240	BCL10, EP300, FADD, IL1R2, IRAK3, MAP3K14, MAP3K8, MYD88, PRKACB, TGFBR1, TGFBR2, TLR4, TLR6, TNFRSF1B, TNFSF11
Neurovascular coupling signaling pathway	1.3300	0.1050	2.2940	ABHD3, BDKRB2, CACNA1B, CACNG2, CACNG7, CHRM3, GABRB1, GABRE, GABRG1, GABRR1, GJA1, GUCY1A1, KCNJ15, PLA2G12A, PLA2G4A, PLA2R1, PLAAT4, PLCB1, PPP1R12B, PRKACB, RYR2, SLC16A1, SLC1A3
Antiproliferative role of TOB in T cell signaling	0.0000	0.0222	2.2360	CCNE1, CCNE2, RPS6KA1, TGFBR1, TGFBR2
PXR/RXR activation	1.0700	0.1270	2.1210	ABCC3, CES2, FOXA2, IL6, PRKACB, RXRA, SCD, UGT1A9
GP6 signaling Pathway	0.3960	0.0813	2.1210	COL27A1, COL4A5, COL4A6, FYB1, ITGA2B, LAMA1, LAMA3, LAMA5, LYN, VAV3