

Supplementary Tabel S1. Primer sequences for the investigated target genes and their silencing efficiency at three concentrations: C1, C2 and C3, after 24, respectively 48 hours.

[illegible]

Supplementary Table S2. Primer sequences for the investigated target genes

Gene	Primer forward	Primer reverse
E6HPV16	5'-GCATAAATCCCGAAAAGCAA-3'	5'-AGCGACCCAGAAAGTTACCA-3'
E7HPV16	5'-GCTCAGAGGAGGAGGATGAAATAG-3'	5'-TCCGGTTCTGCTTGCCAG-3'
GAPDH	5'-CCATCTTCCAGGAGCGAGATCCCT-3'	5'-TGAGCCCCAGCCTTCTTCATGGT-3'
PHF6	5'-GGAGAACCGAGACCGACTTC-3'	5'-GTCTCAAGAAATGCGGCAGG-3'
SF3B1	5'-AAAAGCATAGGCGGACCATGA-3'	5'-GGGGTTTTCCCTCCATCTGC-3'
FGF16	5'-CTGGAGATCTTCCCCAACGG-3'	5'-AACTCCAGGATTCCGAAGCG-3'
MAGEB17	5'-CCGGAAGTGAGGATCTTCGT-3'	5'-GGAGGTGGGCACCTTGATAC-3'
LINC02036	5'-AGCTCACCGGTAGCCTAGAA-3'	5'-ATATGGCTCAGCCGCATCTC-3'
EIF4G3	5'-ACAGAATGCAGGTCCAACCA-3'	5'-GGCCTCTGAAAAACGGAGA-3'
LINC02720	5'-AGCTCACCGGTAGCCTAGAA-3'	5'-ATATGGCTCAGCCGCATCTC-3'
EQTN	5'-TCCAAATGGCACTGAGTCTGA-3'	5'-AGTTGCATTGACAGTTTTATCGTT-3'
KCNJ3	5'-CTCACGCTTATGTTCCGGGT-3'	5'-GTGTCTGCCGAGATTTGAGC-3'
LGMN	5'-CACAGCTGCTACCCAGAGG-3'	5'-AACGCATACTCGTACGTGGG-3'
DDHD1	5'-ATTGTTTTAGGGGCCAGCAGA-3'	5'-AGTTGATCCCACTGCCATCT-3'
LINC01222	5'-AGCAGGGGTAACATTATGGGC-3'	5'-AGTCTTTGTAGGTCACCAACCC-3'
PSEN2	5'-AAGGGCCTCTGAGAATGCTG-3'	5'-CCACACCATGGCAGATGAGT-3'
CHMR3	5'-CTACCTGGAACAGGCCAACAC-3'	5'-TGCCAATAAGACTTGTGAGTTCCA-3'
ZFPM2	5'-TCCACAGAATTTGGGCCTGA-3'	5'-TGGATTCCTTCATCATCACCTTTG-3'
THEMIS	5'-CTGCCTATGAATTTCCAGGTCT-3'	5'-TGGTCCAATATGAATGGTCCTTGT-3'
CDK6	5'-CTGCAGGGAAAGAAAAGTGCAA-3'	5'-CTCCTCGAAGCGAAGTCCTC-3'
TRIM60	5'-TCCAACCTGCTCCAGGTCATC-3'	5'-AGGTTATAATACAGCGGTCATCCC-3'
LINC00936	5'-GCGTTTAAGGGGAGGACCC-3'	5'-GCGCGGCAAGTTCTAATCG-3'
GIPC2	5'-TCTCGCCGTCGGAGATCTTA-3'	5'-CCTCCTAAGAGTCTTCCATGTCA-3'
DCP2	5'-GGTAAAGCACAGGCAACCAC-3'	5'-TCCCTCATACTTTGATTCTTTCCT-3'
DLC1	5'-GCTCCTCGTTGTCTAGGTGG-3'	5'-TGAGGGTAAAGGAGATGGAAC-3'
SEMA5A-AS1	5'-CCTTGTGGCCACTACTGAACT-3'	5'-GTGGCATTCCTCCATAGGCTT-3'
CCDC138	5'-CTGCCCCGACGAGTATGATT-3'	5'-CCAAATCACCTGGGGAGGTT-3'
NRIP1	5'-ACACAGCCAGAAGATGCACA-3'	5'-AGGCTGTTGAAAAGTAGCTCTGA-3'
ARHGEF28	5'-CCATCGCTCCAGATGCGAAA-3'	5'-GCATAGATCATCATCTGCCCCG-3'
CLEC16A	5'-CAACCACCCTGAAAGCATGG-3'	5'-GGCCTGGTTATCCAATGACAC-3'
CDH17	5'-ATCGACCCACGTTTCTCCAG-3'	5'-CAGTCCTCTCTAGGAGATGAAGTTT-3'
ATXN10	5'-AGAGCAGCGGAACCGAGAA-3'	5'-GCAGGCAAGCTCAACAGCAT-3'
EPHA3	5'-TCACGGGTGTGGAGTACAGT-3'	5'-ACCAACCTTTTTCATGTCATCTGT-3'
LRRC4C	5'-GTAGTGACGGCAAGCTAGA-3'	5'-TCGCAGTAAAGAGAACCATTCTTC-3'
OR13F1	5'-TGGTTTGTGTGGACACCTCC-3'	5'-TGAGTAGCATTGGCATGGGG-3'

<b>FAM71D</b>	5'-AGCCCCACCTGTTGATTTTCAT-3'	5'-CAGTCCTCTCTAGGAGATGAAGTTT-3'
<b>LOC101928446</b>	5'-CCCAGGGATCCCCTGACATA-3'	5'-GAACCTGGGTGGGCCTTATT-3'
<b>PTGDR</b>	5'-GGGAGTAGGTGAGGCTTGAG-3'	5'-GTAAGCGCGATACTTGGGAG-3'
<b>GPR15</b>	5'-TGCTCTTTGGTGATGGACCC-3'	5'-CAGAGTTTGGGCTCGTAGCA-3'
<b>FABP6</b>	5'-GCCACACCATGACCAACAAG-3'	5'-ATCTGCACAGTGGCCTTGAA-3'
<b>MIR490</b>	5'-TGGAGGCCTTGCTGGTTTG-3'	5'-TCCTCCAGGTTGGTGCATCT-3'
<b>LRRC52</b>	5'-TGCTCTTTCCTGGACTTCGC-3'	5'-TGGCATTAGATCATCTGAGGGG-3'
<b>CHEK2P2</b>	5'-TGGTAGTGGATCCAAAGGCAT-3'	5'-GTCTTCATCCTGAAGCCACAGT-3'
<b>DSG2</b>	5'-TGCTGCTTCTCCTGATCTGC-3'	5'-GCAGCTTATTTTCATTTCTTGCT-3'
<b>KANK3</b>	5'-TGCGGCTTCAGGGTGC-3'	5'-GCAGGTTCTGATTACAGGGCA-3'
<b>EPCAM-DT</b>	TGGGGGATGAAGGGTGGTTA-3'	TTCTTGGCATATCAGGGGGA-3'
<b>STHG4</b>	GCCCAGCTGTTCAAAAACCC-3'	GCCCATTTTGGCTATGGTCG-3'
<b>PROKR2</b>	GTGACTCTCGATCCGGCTTC-3'	GCTGCCATGGTGATGTCTGT-3'
<b>LINC01718</b>	CTCCACAGCCTCGTGTGTTA-3'	TCGCTATGATTTCTCCGGC-3'
<b>CCDC134</b>	GCTGTTAGCCTGTTGGACCT-3'	TCCAAACCTCTTGAGCTGGC-3'
<b>IL1RAP</b>	ACTAGAACATCAGCAGGCCC-3'	ACCACAGAAGTGTCATCCTTTGA-3'
<b>FAT1</b>	CGGGCCAACCTTGCGATTTC-3'	GGAGCAGAAGCAGGAGCAAA-3'
<b>RHOH</b>	TTCTCCTTCACACACCAGTTGA-3'	CTTCTCCCTGCCCATCCAAG-3'
<b>MRPS30</b>	ATCAGCTGGTGTCAACCCTC-3'	GGGCATCTATAATCGAGGGCG-3'
<b>TTC33</b>	CCGCTTCTGTGGACTGTTCG-3'	ACCCAAAGGAAGCCATTCTGC-3'
<b>FAXC</b>	ACTCCTGGTCATTAGGAAACAGC-3'	GGAACACCATTGTTAGGTCTTGC-3'










Supplementary Table S3: Cell cycle and total apoptosis distribution in silenced or unsilenced CaSki cells with shRNAs












shRNAs	24 hours				48 hours			
				Total apoptosis				Total apoptosis
	%G1	%G2+M	% S	Q2+Q4	%G1	%G2+M	% S	Q2+Q4
<b>shRNAE6</b>	62.6	1.8	35.5	1,7+ 14,9 = 16,6%	53.1	0.3	46.6	10,7 +42=52,7%
<b>shRNAE7</b>	62.6	0.3	37.1	12,8+ 2,5=15,3%	56	4	40	24,2 +12,9=37,1%
<b>shjRNA23</b>	57.3	2.5	40.2	10,2+ 22,3=32,5%	69.4	17.5	14.1	19 +48,2=67,2%
<b>Control</b>	55	10.8	34.2	1.5+0.3=1.8%	53.5	0.5	46	8.5+1.3=9.8%








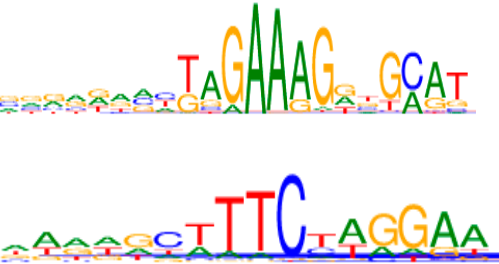


Supplementary Table S4: Time dependent percentage of silencing with shRNAs











shRNA	Percentage (%) of silencing /		Percentage (%) of silencing /	
	24 hours		48 hours	
<b>shjRNA23</b>	<b>E6</b>	79.51	43.18	
	<b>E7</b>	66.66	30.26	
<b>shE6RNA</b>		80.45	55.71	
<b>shE7RNA</b>		63.27	49.83	










Table S5. Significantly enriched motifs and associated transcription factors

Genes	Motifs	Stamp E-value	Transcriptional factors
shE6RNA			
MAGEB17		2.5e-09	BATF::JUN
LINC02036		2.1e-09	ZCSAN16
EIF4G3		2.4e-09	HOXA13_MEIS1
LINC01222		3.7e-09	Homeobox protein Nkx-2.5
PSEN2		2.2e-08	ZBTB40
CHRM3		2.8e-08	ZNF223
shE7RNA			
FGF16		1.8e-09	TATA box binding protein
PHF6		1.3e-07	Pituitary-specific positive transcription factor 1
SF3B1		2.2e-09	NFAT5



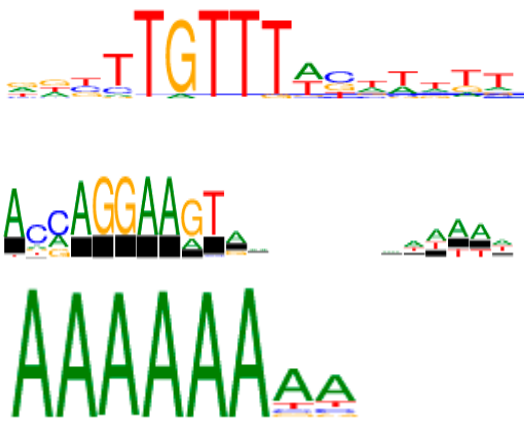


OR13F1		3.9e-10	TFEB
EPHA3		2.0e-07	TATA-box-binding protein
ATXN10		1.1e-07	STAT5B
LRRC4C		8.9e-10	Bhlha15
RSBN1L		7.8e-09	TATA-box-binding protein
MRPS30		6.5e-09	Forkhead box protein O1
C16orf78 (STPG4)		1.9e-08	ZNF596
ZNF585A		9.4e-07	ZNF134
shj23RNA			
ZFPM2		4.8e-07	FOXJ2_PITX1, FOXJ2::PITX1
THEMIS		9.4e-06	FOXB1
CDK6		2.2e-07	Homeobox protein Nkx-2.5

TRIM60		3.4e-08	ALX1
LINC00936		1.3e-07	FOXJ2_PITX1, FOXJ2::PITX1
GIPC2		1.8e-06	FOXJ2_PITX1, FOXJ2::PITX1
DCP2		6.4e-07	Zinc finger protein 217
DLC1		1.5e-07	NFYA
SEMA5A- AS1		6.8e-08	POU6F1, T093398_1.02
CCDC138		5.8e-06	NR1D1
NRIP1		2.3e-08	ZNF184 +  BCL6 (transcriptional repressor which has emerged as a critical regulator of germinal centers (GC))
ARHGEF28		3.6e-09	SOX15
CLEC16A		8.8e-09	ATF4

CDH17		1.5e-06	POU6F1
FAM71D		3.0e-07	NKX2-8
LINC02720		1.1e-09	ZNF324
PTGDR		2.5e-10	NEUROD1
GPR15		4.2e-12	Histone-lysine N-methyltransferase PRDM9
FABP6		1.9e-06	ZNF304
MIR490		1.6e-08	EKLF, Erythroid krueppel-like transcription factor, HBFQTL6, INLU, KLF1_R328H_R2, Krueppel-like factor 1
LRRC52		2.4e-11	ZNF280D
CHEK2P2		4.1e-11	GLI3
DSG2		1.6e-08	EKLF, Erythroid krueppel-like transcription factor, HBFQTL6, INLU, KLF1_R328H_R2,

			Krueppel-like factor 1
KANK3		2.4e-10	ZNF182
LOC101927043		3.8e-09	CEBPG
C2orf61		8.9e-08	Wilms tumor protein
PROKR2		3.0e-10	ZBTB14
LINC01718		2.5e-10	ZNF627
CCDC134	 	2.9e-13	ZNF384
		8.8e-10	ELF3
IL1RAP	 	1.6e-06	Zinc finger protein 217
		1.5e-07	Octamer-Binding Transcription Factor 1



FAT1		3.1e-08	Forkhead box protein O1
RHOH		4.8e-08	NFATC4
MRPS30		1.9e-10	FOXO1
		5.0e-10	ELF3
		4.7e-08	ZNF384
TTC33		3.7e-09	ZNF232
FAXC		5.2e-08	SOX8

Supplementary Table S6. Common molecular targets for identified factors

Name of identified factors	Total number of common targets	Name of targeted molecular factors
DCP2, EIF4G3, PHF6, SF3B1	1	PLEKHA4
DCP2, GPR15, PHF6	1	miR-217-5p
DCP2, PHF6, SF3B1	2	CCNF, RAF1
DCP2, EIF4G3, SF3B1	1	YWHAG
EIF4G3, PHF6, SF3B1	7	MYCN, NAA40, NTRK1, PRKN, STAU1, TRIM67, ESR1
DCP2, GPR15	3	miR-148a-3p, miR-6740-3p, miR-20a-3p

GPR15, PHF6	8	miR-555, miR-4475, miR-143-3p, miR-2682-5p, miR-6758-5p, miR-6841-3p, miR-4780, miR-455-3p.
GPR15, SF3B1	1	miR-1243
EIF4G3, GPR15	4	miR-3924, miR-6868-3p, miR-4666a-5p, miR-1237-3p
DCP2, PHF6	9	SUFU, COIL, HNRNPA2B1, miR-3613-3p, miR-5094, miR-1283, miR-3117-5p, miR-4689, miR-377-3p
DCP2, SF3B1	10	PRPF40A, SRP9, SGF29, HDLBP, FANCD2, RBM8A, miR-330-3p, miR-5089-3p, miR-124-5p,
DCP2, EIF4G3	4	SNCA, DDX6, PSMC3, miR-4691-5p
PHF6, SF3B1	50	TRIM31, SNRNP200, RPL10, MAP1LC3B, MAGOH, ZRANB1, CAND1, UFL1, CUL3, BRD4, BRD7, H4C1, CHD4, NUPR1, LARP7, DDRGK1, RNF113A, PRPF8, EP300, RALY, NR2C2, H1-4, RPLP0, TP53BP1, ZBTB2, RECQL4, HSPA1A/HSPA1B, FBXW7, RPS8, KLF16, CHD3, HNRNPC, MYC, PHB1, CMTR1, RPL13, BIRC3, MEPCE, CSNK1A1, MECOM, RC3H1, RNF4, SMURF1, RC3H2, FZR1, STIP1, miR-452-5p, miR-193a-3p, miR-3611, miR-4477b
EIF4G3, PHF6	9	ESR2, CTR9, DYRK1A, RPL4, MRFAP1L1, HNRNPL, miR-6802-3p, miR-1278, miR-1301-5p
EIF4G3, SF3B1	16	VIRMA, YES1, EIF4A2, HSPA8, RPL19, GRWD1, SIRT7, FUS, EIF4E, BAP1, USP10, A1BG, LGR4, NCBP1, KIF23, miR-106a-3p
PHF6	1	SF3B1