

Supplemental Material to:

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**Phospho- Δ Np63a/microRNA feedback regulation in
squamous carcinoma cells upon cisplatin exposure**

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Supplemental Methods

Preparation of the nuclear extracts and DNA/protein binding. 5×10^9 cells (~140mg of total protein) were incubated with control medium or 10 μ g/ml cisplatin for 12h and the nuclear pellets were prepared and further incubated at a 250:1 ratio with poly (deoxyinosinic-deoxycytidyllic) acid in 20mM HEPES-KOH (pH7.9), 1.5mM MgCl₂, 100mM NaCl, 0.1% (v/v) Nonidet P-40, and protease inhibitor mixture (Calbiochem) at room temperature for 10min, as described elsewhere.³¹ Resulting nuclear lysates were then incubated with MagnaBind streptavidin beads with the 25nmol bead-bound complementary double-stranded oligonucleotides (50bp) corresponding to the specific regions of the specific promoters for miR-181a-5p, miR-519a-3p, miR-374a-5p, miR-630 and miR-885-3p encompassing TP63 responsive element (Fig. 2, Fig. S1-S5). Double-stranded oligonucleotides were conjugated with MagnaBindTM streptavidin beads (Pierce).³¹ The concentration of conjugated DNA was 6fmol/ μ g of MagnaBind streptavidin beads.³¹ DNA/protein bead-bound complexes were washed with the binding buffer and bound proteins eluted using 100mM Tris-HCl (pH 7.3), 5mM EDTA, 0.05% SDS, and 8M urea at room temperature for 30min.³¹

iTRAQ labeling and fractionation by the strong cationic exchange (SCX) chromatography. For iTRAQ labeling, 200 μ g of eluted protein from large-scale DNA pull-downs were first subjected to gel-assisted digestion.²⁹ Trypsin digestion (20:1 (w/w) protein : trypsin) of gel samples were performed in 25mM TEABC at 37°C for 16h. Peptides were extracted from the gel using 50% acetonitril containing 5% (v/v) formic acid, vacuum dried, and reconstituted in 30 μ l of 25mM TEABC. To label peptides with the iTRAQ reagents (Applied Biosystems), one unit of labeling reagent (defined as the amount of reagent required to label 100 μ g of protein) was reconstituted in 70 μ l of ethanol. Products isolated from SCC-11 cells exposed to 10 μ g/ml cisplatin were labeled with

iTRAQ (115, 116 and 117), whereas products isolated from SCC-11M cells exposed to cisplatin were labeled with iTRAQ (113 and 114), respectively.²⁹ After incubation of specific mixes at room temperature for 1h, labeled peptides were pooled, resuspended in buffer A, and the specific mixes were fractionated by SCX chromatography on an Agilent HPLC system using a PolySulfoethyl A column.²⁹

Liquid chromatography (LC)/double mass spectrometry (MS/MS) analysis. Each SCX fraction were re-dissolved in 0.2% trifluoroacetic acid, desalted and separated on a C18 column with an 8 μ m emitter tip using 5-40% B (90% acetonitrile in 0.1% formic acid) gradient over 60min at 300nl/min. Eluting peptides were sprayed directly into an LTQ Orbitrap Velos mass-spectrometer (ThermoScientific) through an 1 μ m emitter tip at 1.6kV. Survey scans (full ms) were acquired from 350-1800 m/z with up to 10 peptide masses (precursor ions) individually isolated with a 1.2Da window and fragmented (MS/MS) using a collision energy of 45s and 30s dynamic exclusion.²⁹ Precursor and the fragment ions were analyzed at 30,000 and 7,500 respectively.

Data analysis. The MS/MS spectra were extracted and searched against the RefSeq 40 database and against the Swiss-Prot sequence database v54.2 using the MASCOT v2.2.1 program (Matrix Science) through Proteome Discoverer software (v1.1, Thermo Scientific). The peptides with a confidence threshold 5% False Discovery Rate (FDR) were identified based on a concatenated decoy database search). To calculate average protein ratios, the ratios of quantified unique iTRAQ peptides were weighted according to their peak intensities.²⁹ A protein's ratio is the median ratio of all unique peptides identifying the protein at a 5% FDR. The combination of two approaches was used to normalize the iTRAQ ratios: normalization by total protein (i.e. the average of all the ratios). Only proteins identified with ratios >1.25 or <0.75 were considered as potential targets.

Supplemental Legends

Figures 1-5. Schematic representation of the selected microRNA gene promoter sequences. Putative recognition sequences for tumor protein (TP) 53, TP63, sterol responsive element binding factor (SREBF), and nuclear factor (NF) -Y and other transcription factors are shown as bolded and shadowed boxes, while primers used for ChiP-PCR are underlined. Recognition sequences (responsive elements) defined using the web-based database: TFSEARCH: Searching Transcription Factor Binding Sites (version 1.3) (mbs.cbrc.jp/research/db/TFSEARCH.html). The following promoters depicted: S1 –miR-181a-5p; S2 – miR-519a-3p; S3- miR-374a-5p; S4 – miR-630; S5 – miR-885-3p.

Tables S1-S5. iTRAQ analysis of proteins bound to TP63 responsive element cognition sequence located in microRNA promoters induced by exposure of sensitive SCC-11 and resistant SCC-11M cells to cisplatin. Quantitative iTRAQ analysis was performed in triplicate. Protein complexes from the cells exposed to control medium were labeled with iTRAQ-113, or -114, while protein complexes from the cells exposed to cisplatin were labeled with iTRAQ-115, -116, or -117. Only proteins identified with iTRAQ ratios >1.3 or <0.7 were considered as potential differential interactors. S1 –miR-181a-5p; S2 – miR-519a-3p; S3- miR-374a-5p; S4 – miR-630; S5 – miR-885-3p.

Figure S1. Mir-181a-5p promoter sequence

-2000 CTCG **AAATAA TTTAGAA** TAT AGAGCCTAAA G**TTTACTA** TC TTCTCT **GACA**
 CdxA CdxA CdxA ATF2
 -1950 **TTAG ATTAAT TGG** AAGCAAG AACACAGAGA TCCTATTTC CATTGTGGAG
 CdxA/Nkx2
 -1900 **GATTTAAACT GT** TAAGATA **TGAGGT** TTTAT CTT**TAACAAA** CTATGACTAT
 CdxA/POU3F1 AML1a SRY
 -1850 GATTAGCCCA AGG**AAAGAAA** **AAATAATTAA TCAC** TTT**ATT TATC** ATTGCT
 SRY CdxA/PBX1 CdxA
 -1800 ATTT**ATGTG TAAATAACAA** GACATTTAAT GTAA**CTTGTA TTGTTCAAG**
 XFD2/CdxA TP63
 -1750 T**GAATCAT** TA TAAGATTTT AAGAATTAA ATGTTAA**ATC AATTATA** GTT
 TFAP1 PBX1/CdxA
 -1700 AAGATTTTA TTCTAAGAAT GTAACAACCT TAGGATTAAG**TTAATTG** TAT
 Nkx2
 -1650 TCTTCCAAAG ACTTCTAGGA GAATATTTG G**AAAACAAAA GATAACATAG**
 SRY/RUNX1/CdxA
 -1600 TTATG**CCTTT TAATTATT** TG TAACTG**ACCT AGAG** CTTTGC TTACTGGTAG
 OCT1/CdxA TFAP1
 -1550 GC**CAAATG** CA TTTTGTGTTA AGGGAAAATA CAGAGCATGG AGTCTTTAT
 E-box
 -1500 CACAACATCC CTATTATACA AACGTTAG**CA GATGTAGCAA GAGATGAATA**
 E-box C/EBP β OCT1
 -1450 **GGCATGATTG AAAACATG** TG TATATTGACC**TGACACTAAT ACCACAAG** AG
 OCT1 TP53 TP63
 -1400 GCAGGCAACA GAA**CAGGAGT GATATGCTTG** CAGTC**GTAAT TGATAATGCA**
 TP63 POU4F2
 -1350 **AACAAATG** AA TCCTCAGTCT CATG**ATAATA** TTCTTCCAG CAGAACACAA
 E-box CdxA
 -1300 GAAATGCC**TA CTGATAAAAGC** ATTCTCTAG GGTTT**TATTC** **TGTGGGAGAA** A
 GATA-1 CdxA IKZF1
 -1250 ATTTGCTTCT TTCAAAAGAA T**AAACAAATG** CAAAATTTCAG ATACATCACT
 SOX5/SRY
 -1200 GTTTC**ATATT** CTGTGCCATT TTGTC**ACTTT AAAAT** TTACT TCCAGTTGAT
 CdxA TATA
 -1150 CTCTAGTCCC TGTTCTCTC AAAAAAAATC TGTTGAAGTT TTCATGAAA
 -1100 TAGTTGCT AAAAGGT**TAA ACAATTATTG GCTTAAAAT** **AATTCTAAGT**
 Sox-5/SRY/FOXM1 TATA CdxA/TFAP1
 -1050 **GACTGAAA** TG TAAGAATGTG TAAA**AATTG GGATACAT** AT TTCACTAACAA
 TFAP1 IKZF1/GATA-2
 -1000 TTTCGAGAGT AATTGCCATTG ACTTGAATAG ACCATTATCA CCTTCAAAGT
 -950 **AGCATTCCAA ATTA** TTGTGG GTTGTCCCTC CTA**CAGATAA TTACTCTATA**
 POU4F2 CdxA GATA1/OCT1/YY1
 -900 **ACCATATTAG ATG** CA**ACTTA AAT GTGTGAA ATAATGACTT** TCT**ATTCTGG**
 YY1 Nkx2 OCT1 CdxA/TP63
 -850 **TTTAGATACA TCCAAG** GTGA CTTTTGTTT AATTGATGGT AGAAAATTAT
 TP63
 -800 TGAAAAT**GGC TCTAAAAATA AATT** CAGTAG AG**TTCATAAT AATTT** TAAAAA
 MEF2/TATA OCT1/CdxA
 -750 TA**AGCATTAA TGATAAAACA** GTCTTAGAAA ATAAGACTAT GAAAAGAAC
 OCT1/GATA1
 -700 CCTCACCCAT CTAC**CCATAA AGAGATGT** TA GATGTTAGAT GTT**ATTTAAA**
 OCT1 CdxA
 -650 **ATAATAGGAA ATGAAC** GGTT TTGTAGCATA CATAGATTGT ATTTACCTT
 CdxA POU4F2
 -600 CACTGT**ATTC AT** GAACTCTT TGTGCCAT**AA ACTAA GA AAA ATG** TATTGAG
 CdxA SRY CdxA
 -550 CTGGTTCTT CACTTATAAT TTGTTCAGCA TTTTCTAAAT AAGATTGTT
 -500 TTAGGAAGTT ATACTAATTT TAAAACCTTA TTTTAGAATA AAATATAGTA
 -450 AATATATAAT GTAAATATAA ATGATATCAT CAATG**CCAAT TTGAGGAAAT**
 NF-Y C/EBP β /SRY

-400 **CTAAGGTAAT** TCTGTTT**AAT TT**CTGTATAA G**CTATATACA TAATGCTTGC**
 SRY/OCT1 CdxA XFD-1/TP63
 -350 **TTACTATACG** TGTAACAATA TT**AATTAT AAGATATTGT** TTGGATTTTA
 TP63 SOX5/CdxA CdxA/GATA3
 -300 TACCACAAAG TACTTTG**AAT ACAA**ATTGT CCCTGTCTT AACAGTGAGA
 CdxA/SRY
 -250 **TAATTCCAT**C TCTGGAACTA GC**CCAATATC GGCCATGTTT TTGCTTGATG**
 GATA1 NF-Y FOXM1/TP63/OCT1
 -200 **AAACAGG**TCC TTTCTCTCA TACAATGTGA TGTGGA**GGTT TGCCAAACTC**
 TP63/OCT1 C/EBP β

Figure S2. Mir-519a-3p promoter sequence

-2000 **GTTTTGTTTG GTTGGTTATT TTT**GAGACAA **GGTCTGGCTC TGTCATCCAG**
 SRY/FOXM1 C/EBP/CdxA ZBTB6 TP63
 -1950 **GCTGGAGTGT** AGTGGTGTGA TCTCAGCTCA CTGCAACCTC CACCCCCGAC
 -1900 CTAAGCCTAC TGAATTA **GTG TCTACAGGCA CGCACTACCA CACCTGG**CTC
 SREBF TP63
 -1850 ACTTTTGTAT TTTTGTA**CA CATGGGGTTT CACATG** ATTG CGGGGGCTGG
 E-box TP53
 -1800 TCTCAAAC**C CTGTGCTCAG GTGATCCTCC** CATCACGGCC TCCT**AAAGTG**
 TP63 USF SREBF Nkx2
 -1750 **CTGGAATTAG AGGTG**TGAGC CGCCACGC**CC CACCTGT**ACT TGTGTATCTC
 POU3F1 USF
 -1700 TGTT**CAAATG** TTACTGAGGA GCTTTTACAG **CGTAACCTGT GGTCTATCCT**
 E-box
 -1650 GGAA**AATGTT TGTGTGTGAG ACAATGTACA** TTCTCAACA TCTTAGATTG
 FOXD3 C/EBP
 -1600 CAGTTTGGAT GCTCCGT**CA GGACTGTGTG TCCCTG**TGCT GGGACT**CAAG**
 TP63 E-box
 -1550 **TG**AACACTGG GCTCTCCATC CATTGCTGTT GTCTAGAAAT CCAGC**CCAAT**
 NF-Y
 -1500 TCTCTTGGGT **AAATAT**GAGG TATGTGTAGT AGGCATTGCT TTTTCTTCT
 CdxA
 -1450 GGAGACAAAG CT**CAGGAGGA TTGCCCCTG** AT**AAACAAA**G CTAACCTGCT
 TP63 SRY
 -1400 GATTCTTGGA AGCAAGGAAC TGGAGATGGT CCTTTAGGG GTTTATATTC
 -1350 TGGATTCCAG AAAACATGCA AA**CAGGACCA ATAATGCGT** GCTTATTCTT
 PBX1/TP63
 -1300 GTGTCTGTTT TAACCTGGTC AAGGAAAATT CCAACAAAAA ATCCACGATG
 -1250 CTGGAG**CATG AAGATCTCAG** G**CTGTGTCCC TCTAGAGGGA AGCGCTTCT**
 TP53
 -1200 GTGTCTG**AA AGAAAAGAAA AT**GGTTCCCT TTAGAGTGTGTT ACGCTTGAG
 SRY/ RUNX1
 -1150 AAAAGCATCG CTGATCTTGG TAACACATT GCAGAGAATG **CTTATAATCA**
 OCT1
 -1100 **GACG**TGGATG ATGTTGAAGT TTTGC**GTGG TTTGTTTG TTTT**TTTCC
 OCT1 FOXD3 FOXD3
 -1050 TAGACAGGGT GTCTGCTGCC **CAACTG**AGAG TGCGGTGGCA CTTCCAACCT
 E-box
 -1000 AGACCTCTTG GGT**TTAAGTG** GCCCTCTATT TT**GGGATAGA GT**CTTGCTCT
 Nkx2 IKZF1
 -950 GTGGCC**CTGG CTGGAGTGCA GTGTCAGG**AA CTCTGCTCAC TGCGACCTCT
 TP63
 -900 **GCCTCCTAGG TTCAAGCGAT** TCTCTTGCTT CAGCCTCCTG **AGCAGCTGGG**
 Ik-2/E-box
 -850 **ATTA**CGGGCA TGTGCCACCA TGCCTGGCTA ATTTTTGTAT TTTTTATTAT
 -800 TT**ATTTAT**TT **ATTTAT**TTT GAGACAGAGT **CTCGCTCTGT CACCCAGGCT**

CdxA **CdxA**
 -750 **GAAAGTG**CAGT GGTGCGATCT TGGCTCACCG CAACCTCTAC CTCCCACCTC
Nkx2
 -700 AGCCTCC**TGA ACAGCTGTCT** C**CAGGCGTGC ACCACCACAC CTGG**CTAACT
MyoD/E-box **TP63** **E-box**
 -650 TCTGTATTG TTTTACAGT**C ATGGTTTCAC CATG**TTGCC GGGCTCATCT
TP53
 -600 TGAACCTCTG AGC**TCAAGTG** **ATCCTCCC**GC CTCAGCCTCC TAAAGTGCTG
Nkx2/E-box/SREBF
 -550 TGAGCCACCG TGTCCCAACA GTACTTGTTG GTTTCCGTT AAATTGTATT
 -500 GAGGAGCTTT TACAGCATAG CCTGTGGTCT CTCCGGG**AGA ATGTTTTGT**
FOXD3
 -450 TTACGACAAT GTATATTCTT CAACATCGTA GATTCCATTT TGGATGCCCT
 -400 **CATTGGGACT GT**GTGTC**CCT G**TACTGGAAC **TCAAG**TGAA**C ACTTG**GCTCA
IKZF1 **TP63/Nkx2** **E-box**

Figure S3. Mir-374a-5p promoter sequence

-2250 TTATCGAAGA GACTTCTAGA ATTAGTTATT TGTCAAAAGA TTTGAACATT
 -2200 ATAA**AGAATT GGCATATTTA CTTT**TCAA**AA AATT**AATGTC AGTTTTGTA
OCT1/FOXM1 **CdxA**
 -2150 **CCCAGTC****ATT TAG**GTACTTA **AAAAAA****ATGT** TTTTGCTTT TTTTTTTTG
CdxA **TATA** **FOXM1**
 -2100 **CTGACTCCAT TTGTAAA**TGA ATGAATGATA TCTCTGTGGG GTTTTTTGT
TFAP1 **YY1**
 -2050 **TTTTGTTTT TTC**TGAGA**CA GGCTCTCCCC CTG**TCGCCTA GG**CTGGAGTA**
FOXD3 **TP63** **TP63**
 -2000 **CAGTGGCGTG** **ATTATG**GCTC ACTGAAGCCT **CCAAT**TCCAG GGCTCCAGAG
TP63 **SREBF** **NF-Y**
 -1950 ATCCTCCTAC CTCAGCCT**CC TGAGTAGCGG GAGTACAGG TGTGTGCC**ACC
TP63 **E-box/TCF3**
 -1900 **ATGTCCAGCT AATT**TTAAA TTTTTTTGT **AGAGATGGAGT** TTTGCCATGT
GATA1
 -1850 TGCT**CAGGCT TGTCTGAAC TCCTGG**GC**TC AAGTGATT**TT CCACCCGG
TP63 **Nkx2** **SREBF**
 -1800 CT**CCCCAAAA** **TGCTGGGATT ACAGGGGTGA GCCACCATA**C**CTGG**CCGATA
STAT **IKZF1** **TP63**
 -1750 **TCTTTGTTTT** GTGATACAGT TCTCTGATTA TTAGTGAGGC TGGACTTTA
FOXM1
 -1700 GAT**CTTAATT AC**TAGC**TCTT ATTTCTT**TT GTGAATTATT CAATTGTGC
Nkx2 **FOXM1**
 -1650 CTGAATGTT**A TTTG**TAAGTT **GAAATG**TCG TTTGTTGCAG ATATGCTCCC
CdxA **E-box**
 -1600 **AGTAATATTG GTTG** CCATTG **AGTCTGAAGA A**ATGTTGCA ATTCAAATA
CdxA **FOXM1** **C/EBP β**
 -1550 TAACTGCTGT GTGGATACAT GTCTGGTTCT T**GGTAGCCAT TTTGAGATA**AA
YY1
 -1500 **CATTTG**TCTG ACCTCTATCT TATTTTGTT TTTATTTTA GAGTGGAGGT
E-box
 -1450 CTG**CCATG CTGGTCTCGA ACTCCTGGGC** TCAAGCAATC TTTCTGCCTC
TP53
 -1400 CGCCTCCCAA AG**TGCTGGGA TTAC**AGGCAT AAGCCACCTT ACCCAGCCTT
IKZF1
 -1350 GTC**TGACCTT TAAACA**AAA TCCATTCTT TTTATCTAAA AGGAAAGCAC
NR2F2
 -1300 TTTTGAGTAC TGTACAACAG TGGTGCTTCC TGGCC**CTGGG CATGGGGAGA**
TP63/MZF1
 -1250 **AGACAGG**GCA ACATTTG**TC CCTAATGAGA A**ACTAATTAA GACAAGAAC
TP63 **OCT1**
 -1200 **AAAACA**CGGG TCCCTCTCC CCCAT**CCAAT** CAGGGACTGG TCTTATTTA
SRY **NF-Y**

-1150 AAT **ATTTCTG** AGTGGTCTGA GGGAGGATAT GGGCAATAT **T GAAGTC** TCCA
 CdxA
 -1100 C**ATTTAT**ACA TACTGTTAAA TGCTT**TGGGG AT** GTGAAATG CTAATAGGAA
 CdxA
 -1050 **CAGGCTAGCA TGTGAGAAGG CACCATGAGT GGGCTA** ATTG GCAGAAAGGA
 TP53 **p300**
 -1000 ACAGTGTATA GGCAAGAGCA GTGAAATAAC TTTAGGGGAA AATAGTATGT
 -950 TAAGCTTATT AAATAACAGC CTCATAGAGA CATTGGGTCC CAAACAGTG
 -900 ATCTCAGTAT **AACTGTCAAC AACTTGC TGA TGTATCAGC CCTATTTGCT**
 ATF2 **FOXM1**
 -850 GGTCAGAGAC AAAAAGCCA GTAAAAACCT AGGTA**TTATT AAGAAAGGT**A
 CdxA **C/EBP β**
 -800 TGAGGCACAG AAAATGCCA TCTTATCTT **GTATAAAA**CC ATCTGAACCA
 TATA
 -750 AATAACTATT **ACAGTAATAA TCTT**GCCTCA AGGAGTCTGT TACTATCACT
 OCT1
 -700 **CACATGATT TGAAAAGGGA GTGGGCA**GAG TGTGTTATCT CTCTGTTCA
 USF **C/EBP β** **p300**
 -650 TTTTCTTGT TTATAATACA TAG**GGTGAATT AGATATT**CTC AAAGGTCTTG
 OCT1
 -600 GAGGGGTCTA ATTCTGG**TTT CCTGAAA**TG AATGTTATTT CTAGTTAGA
 STAT **FOXD3**
 -550 GAATC**TGTTT AATTATGT**TT ATTAAATAAA CTTTTCTAAC TTATTCCTAC
 OCT1

Figure S4. Mir-630 promoter sequence

-1700 GTTGAGTGT CATAAA**TCCA CGTG**TTCCTG TTGCAACAAA TACCCAAAAA
 Nkx2
 -1650 TTGTGTGTGC ACTTCCTAAT ACCAGTCTTC ACCCATGGAG GAACAGTGCT
 -1600 TTTAGAGAT GCTTCTATT TCAATGTTGG CATACTG**CCT GAGGGTATTG**
 TP63
 -1550 **CAGTTG**TGGG TGCATTCCT AATTGTATG ATCAAGATGA ACTGGCCCTT
 E-box
 -1500 **TTCTACTTCC AAG**CTTTAA CAG**ATACCAC CATATTTGAC A**GAATTCCCA
 TP63
 -1450 GAGTGAATTG CTTGTGTTAT TAGTAGAT**TC AGTG**CCCCCA GCTGGGATAG
 Nkx2
 -1400 G**CAAGCCATG ACAGCTTCCC TG**TTTCACCT ACAGAAGTCT TATCTGAGGG
 TP63
 -1350 GATCTATTCA AGTAAGCAC**C ATGGTCTCCA TGTCTTCAGG** TCAGTTTCAT
 TP53
 -1300 T**GTCTTTGA AAAGT**GCATG CTT**CATTTGA ACAATTTCATT C**AGCAGCAGA
 C/EBP β **E-box** **SOX5**
 -1250 TGGACTTTC **ATGTGATTAAA ATAAA**TTTT GATCAAAGC T**CAGGACACA**
 POU3F1 **TP53**
 -1200 **AACCACAGG**T GTAAAATTGA GTAGCATATA ATATCAGACT AAATTATCTG
 TP53
 -1150 TAATTTCCA CAACCCAGAT TGTATGTGTT TTATGTGTT TTAAATAAAAT
 -1100 ATGTTAG**ATA CACGTGTATA** CATACACCCA TATACAACAG ATCCAAGACT
 N-MYC/USF
 -1050 GG**CTGACTTC ATTTGAAATG GTT**GAATCTG CTG**TGTAATA AAGTG**GTTCA
 TFAP1 **POU3F2** **OCT1**
 -1000 AC**CATGATTA GGACATG**AAA TTTAGTAGAA GAGGGAA**AAAG GAGTTAATG**T
 TP53 **p300**
 -950 **AACAAAT**TAT TTTAGCTACA AACCCCGGTA ATAGAGC**ACT TGGGGGAT**GG
 SRY **MZF1**
 -900 GATGGGGTGG GTGGTGAGA CAATG**CCAAT** TGTAAATTGA TTAAATGCTC
 NF-Y
 -850 CTAACCCTGT AATTTGTGC ATAGAGCACC CTATGCTGTG GA**AATAACTG**

v-Myb

-800 **TT**CTTAGATT TCATTGTAAC**C TGGACTGTT CAGG**TTGCCCA GAGGGAAAGA
TP63

-750 **ACATTCC**TAA TTCTAATAAA ATAAA**CTTT**TTTGTAT TCCATTAGTT
HSF1

-700 **ACCTATGTTT ATT**TTTATAG TTAAAAAAATG ACTAAAGGTG GCTAATAGCC
FOXM1

-650 ACCCGTATTAT TGTGCCTTAT TCACTGTTCC CACTTAATAT AAAATGTCAA

-600 AAATTGGTTG TTTCTTGCA GGGAACTGTG AATGAGCCCA **TTCCCCAAC**
STAT

-550 ATTTAACTT**G GTTAATGAAG CT**TTCAGAGC ATTTTCTGAA AGATTTCAA
OCT1

-500 TTTCTGCATC TCAGA**TATTG AATTTAAATT GTTTGT**GTTG TAACAGTGAT
POU3F1 FOXD3

-450 ACAAAAATGT TCAATAGCTC TTTGAATGCC ACTTT**TTTA AA**GAAAATAC
TATA

-400 **TTTAAAAA**GTC ATTCTTAGCT AACCTCAAAA CTCCTTACA TTACTTTCAT
TATA

-350 TTTAGCTCAC TCTTAAAGCT GATACTGTTA TATAGGGATG AAGGGAGAGT

-300 TTTCTTAAAG AAGGTCCCAA AGTTGAAGAT CGTTGTCAT TGATACTCTG

-250 GC**CAAGTCCA GGTTTAGGA CATG**TTAATT TACTCTTATT TGGATCTGTA
TP53

Figure S5. Mir-885-3p promoter sequence

-2350 AGACTGGGTT **CCAAT**CCCAA CTCTACTCCT TAGCCAGGGA CCCCAACAA
NF-Y

-2300 GCTTCCCCCC CTTTCTGATT ATAGCCCCAG CTCATGAG**GT TGTGTTGAAA**
C/EBP β

-2250 **TCT**GGAACCT CCAGAAATGT CCA**TTTCGCC** CTCTCATCCT TCATCT**CAAA**
E2F E-box

-2200 **TG**TCTCCCCT TTCCCACCTC TCTGGGCTAC CCCCTTCCTC TTCATCATCC

-2150 AACTCCTCCC TACCTTCAG**C CTGCAGCAGC CTGCCTCCCC CAGGGGGTGT**
TP63 c-Rel

-2100 **TCC**TTGATTA GTTTCTTCCC CAGTGTTC TG AACTCCCTGC ATAACAGC**CA**

-2050 **TTTG**GAT**GCT CATTTTATG** **CA**CAACCAGA CACCATGGGC CCTTTACATC
E-box OCT1

-2000 **ACGGGGGA**GG CCTTGC**TGGG CCTTCCA**GTC TGATGATC**CT TGAGGAACAA**
MZF1 c-Rel TP63

-1950 **CACAGAGAGA CCAGG**CTGGG GG**CATTTGTG GTGT**CGTTAT GGTGGTTGAG
TP63 E-box ATF2

-1900 AAAGCCCTAG TGTCATCTCA TGCACTGTTT CAGCTTAGAA GAGGGCAGGA

-1850 AACACTCCGC TCTGGT**CAGT TG**GTCCAACC ATGCTTGGCC TGTGACCCCTG
E-box

-1800 GACAGGTCCC TTCACCTCTC TGAGCCTCTG TGTCTGTGTC AGTGCAATGG

-1750 GGAAGCTGGT GAGGCCTCCA CTGCCTGCC **CACATGGCTG TTGTGGGAC**
E-box/TP53/c-Myb/MZF1

-1700 **CACAGGCATG** **CACACGTG**TG ACTGTCCTTT GC**AAACAAA**C CCTGCGGTTG
TP53 USF/E-box SRY

-1650 TGAGGTGCTG TATGGTGTGG AAGGAATGTG G**CATCTG**GAG GCAGAATGCC
E-box

-1600 CAGGTTCCAG CCCTCCAACA GCTCCCAC TG GCCCTCTGC CCCTCAGAAC

-1550 CTCAGTTCC C**CATCTGACA AGTG**AGGGCA GACCAGCCTT CAGAAAGACT
E-box/Nkx2

-1500 CAA**TGACCT CA**ACACT**CAG GGCACCAAGG AAATCATCAA AACCATG**CAG
ATF2 TP53

-1450 **GT**TTCCCCCTA CCTTCCTACC CTC**CAGGGAC GGACAGG**CAG ACACGAGGCC
TCF3 TP53/TP63

-1400 ATGTCTGGTG TATCT**TCAAA CGGG**ACAGAG TAAA**AATATT CAGAAATTG**C
v-Myb Oct-1/C/EBP β

-1350 AACTCATAT GTCTGCAGGG C**CAGGTAGGG AGAGCACATG**TCCTTGGCC

TP53 C/EBP β **E2F**
E-box **NF-Y**

-1300 AAACCA **CAGC TG** CTTCCCTGT TGCTGCCTGC AGAAGCGCCA GC **CCAAT** CTG
-1250 ACCTCAGTGC TCACTTTGCA AGAGGAGCCA GAAATCCAGA TTTCCCTGTA
-1200 CCAGCTCTCA ATGTTAAGT ATTGGCAAGA AATTCCCACA TTTAAGGTC
-1150 CCTATGGGTC **AAGCCA CATA TG** GGTGGGAC CTAGAGTGCA AACTCTGACC
E-box

-1100 TAGGCCTATT TTTAGCTTT GTATTTAAG ATAATTCAA ACTTCAGAA
-1050 AAGTTGCAAG GATGGCACAA AGAATACGGG CATGCCCTC ACTCTGATTC
-1000 GGCTGTTGCT AACCTTTGC CGTCTTGCT CTCTGACAAA TCTCACTCTC
-950 CTCCTCATCA TGCAGATGTG ATGGCCTTCT CCCGCTAGAC ACTG **CAGGTG**
E-box

-900 TGTCTCCCAA GAG **CAAGGGT ATTCTCATG** C ATAACCACAA CACAGCCATC
TP53

-850 AATTCAAGGAA ACTTGACATT GATTGGTAC TGTTACCTGC **TGTGCCATCC**
-800 **ATATTCACAT TCTGCCAAT** GTG **CCTGCAG CGTTCTCCAG** **GCCAGGATC**
ATF2/E-box/NF-Y **TP63**

-750 **ATGTGGGTC CTGCATGCCA CTTG** GATGTC CTGCCTCTT GGTCTCCTGC
E-box/TP53 **E-box**

-700 ATGGAGCAGC GCCTCATCTT TTCATTGTCT TCATGGAAAG CCAGTGTGTTT
-650 TAAACCCCTC CTAGGTCACTG AACTTCCGTG AGAGTTCCAC **TAAAGCAGTG**
-600 ACCCCTCTTA TAAGGAACAG ATGCCAGAC TCCTC **ATCTT GCAACATTC**
C/EBP β

-550 AGGGGATTCA ATGATCCCTA GAGGACCCCTG GTCCTATCCC AATTGCGAGC
-500 **TGGGGAA** ACT GAGACCCAGA GCAGAAGTGT AAGGCCAAC AGAGGGCAGG
MZF1

-450 **GGCAGGGCGG** AAGCCAGACC CCAGCTCTGG GCTCTCCTG TAGCCCCAT
Sp1

-400 **G CAGGAGCCT GCCTCCTTG** AGTAACCTCC ACTGGAAAT GCAGGACTAG
TP63

-350 ACTAGATGCC ATCAATGTGG CAGTGGAAAGG GGCTGGAGCC AGGGGGCCAG
-300 GATGGCGGGG CTGTCTCAA AAAACAGCAA GGCCTGGCTC CAGCAGGCC
-250 GATGGCTCAA CCCCCGCGAG ACCCCGACAC ACCCTCCTCC CTTCCCCCTG
-200 CCAGCCAGAG CACTAACAGC ATGAGGTAT GCAGGACATC GGTAAACCT
-150 CTTGGGACTC TGCCCACATC CCAGGACCTG CTGCCAACCC CAC **CATGCAG**
TP53

-100 **AAGGCCAGGC ATG** GGAGAGC CGGACCTGCC ACCACTGCC CCGTCTCCAG
TP53

Description	Accession	MW [kDa]	5: 114/111	4: 113	5: 115/1	1: 115/1	1: 116/1	1: 116/1	1: 15/11	1: 117/1	1: 117/1	pI	Coverage	#PS	Pept.	Score A3	coverage A	PSM	Tides
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Table S1. Proteins interacting with the miR-181a-5p promoter sequence in SCC cells (11/11M) upon cisplatin exposure

tumor protein p63 [Homo sapiens], TP63	169234657	67.9	0.989	21	8.854	10	7.648	14	1.00	8.408	11	6.64	38.03	19	7	1528.45	53.03	31	12
histone deacetylase 4 [Homo sapiens], HDAC4	153085395	117.6	0.958	19	2.634	15	2.625	12	0.80	2.503	9	4.93	47.31	28	5	1295.89	47.31	15	5
nuclear transcription factor Y subunit alpha [Homo sapiens], NFYA	56417679	21.5	0.971	8	1.970	8	1.729	8	0.86	1.669	8	4.94	21.58	16	3	368.26	17.37	7	2
C-terminal-binding protein 1 isoform 1 [Homo sapiens], CTBP1	4557497	48.5	1.205	2	1.781	2	1.678	2	1.15	1.514	2	5.41	8.82	4	2	147.51	8.82	2	2
zinc finger and BTB domain-containing protein 2 [Homo sapiens], ZBTB2	24308241	61.0	0.909	4	1.718	4	1.527	4	0.97	1.611	4	4.98	11.16	5	8	542.97	9.13	15	6
SIN3 homolog B, transcription regulator [Homo sapiens], SIN3B	84569981	40.8	1.089	3	1.492	3	1.439	3	1.12	1.418	3	4.81	6.56	5	1	84.39	6.56	2	1
basic helix-loop-helix family, member e41 [Homo sapiens], SHARP1 (BHLHE41)	19684064	53.6	1.093	1	1.473	1	1.411	1	1.15	1.401	1	10.36	10.14	1	1	19.34	5.79	1	1
CCAAT/enhancer binding protein, beta [Homo sapiens], C/EBPbeta	119596035	40.1	1.137	8	1.446	8	1.280	8	0.93	1.503	8	8.22	13.24	13	7	243.76	9.00	5	5
methyl-CpG-binding protein 2 isoform 1 [Homo sapiens], MECP2	4826830	53.4	1.085	4	1.419	4	1.673	4	0.97	1.511	4	4.98	11.16	4	4	542.97	9.13	15	6
CCCTC-binindg transcriptional repressor, isoform 1 [Homo sapiens], CTCF	5729790	80.8	1.048	13	1.303	14	1.319	14	1.97	1.302	14	6.07	12.45	12	7	354.67	11.45	24	9
Y-box binding protein 1 [Homo sapiens], YBX1	116283293	20.6	1.099	2	1.251	2	1.224	2	0.81	1.235	2	5.96	1.73	3	1	38.38	1.73	1	1
sex-determining region Y protein [Homo sapiens], SRY	383087989	23.6	0.905	18	1.217	57	1.380	17	1.18	1.263	17	8.84	32.74	14	16	2217.01	29.89	48	14
histone acetyltrasferase KAT5 isoform 1 [Homo sapiens], KAT5	36287069	59.6	1.078	9	0.591	10	0.648	10	1.00	0.408	9	6.64	38.03	9	4	1926.45	38.03	34	9
CREB-regulated transcription activator 2 [Homo sapiens], CRTC2	32171215	77.5	0.916	29	0.581	29	0.625	29	0.80	0.503	29	4.93	47.31	28	5	535.89	47.31	15	5
histone-arginine methyltransferase [Homo sapiens] CARM1	40288288	66.5	1.135	4	0.322	4	0.348	4	0.81	0.236	4	8.35	13.43	6	5	367.22	11.51	11	4

Description	Accession	MW [kDa]	5: 114/114	4: 113	5: 115/115	5: 113	116/116	6: 113	115/115	117/117	7: 113	pI	Covered	# PSM	Pept.	Score A3	Average	SM A3tides
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Table SII. Proteins interacting with the miR-519-3p promoter sequence in SCC cells (11/11M) upon cisplatin exposure

tumor protein p63 [Homo sapiens], TP63	169234657	67.9	1.046	11	6.854	10	7.248	9	1.00	6.528	11	5.64	18.03	10	4	428.45	13.03	7	3
histone deacetylase 1 [Homo sapiens], HDAC1	13128860	57.9	1.040	9	2.634	5	2.625	7	0.80	2.503	9	7.93	17.31	8	3	205.89	11.31	11	5
SIN3 homolog B, transcription regulator [Homo sapiens], SIN3B	84569981	40.8	1.160	5	2.449	5	2.145	5	0.89	2.116	5	5.29	23.94	8	2	194.50	23.94	3	2
nuclear transcription factor Y subunit alpha [Homo sapiens], NFYA	56417679	21.4	1.019	9	1.851	9	1.801	9	1.08	1.801	9	5.33	28.05	10	4	486.50	28.05	9	4
BTG3 associated nuclear protein SMAR1 isoform a [Homo sapiens], BANP	17986266	55.3	1.016	5	1.807	5	1.406	5	0.89	1.612	5	5.29	23.94	8	2	194.50	23.94	3	2
forkhead box D3 [Homo sapiens], FOXD3	6912372	52.5	0.931	1	1.731	1	1.641	1	1.15	1.440	1	10.36	10.14	1	1	19.34	5.79	1	1
C-terminal-binding protein 1 [Homo sapiens], CTBP1	4557497	48.1	0.538	1	1.476	1	1.208	1	1.13	1.515	1	11.41	11.72	2	1	78.53	11.72	1	1
sex-determining region Y protein [Homo sapiens], SRY	383087989	23.6	0.943	1	1.397	1	1.208	1	0.90	1.309	1	5.76	1.86	2	1	62.89	1.86	1	1
basic helix-loop-helix family, member e41 [Homo sapiens], SHARP1 (BHLHE41)	19684064	53.6	1.243	2	1.368	2	1.485	2	0.97	1.216	2	6.33	16.56	52	6	764.68	16.56	24	6
CCCTC-binding transcriptional repressor, isoform 1 [Homo sapiens], CTCF	5729790	80.8	1.043	13	1.311	14	1.219	14	1.10	1.302	14	6.07	16.97	50	8	570.77	15.51	21	7
CCAAT/enhancer binding protein, beta [Homo sapiens], C/EBPbeta	119596035	40.1	1.079	5	1.245	5	1.370	5	0.85	1.216	5	5.64	5.48	8	3	425.91	5.48	5	3
zinc finger and BTB domain-containing protein 2 [Homo sapiens], ZBTB2	24308241	61.2	0.755	2	1.232	2	1.425	2	1.03	1.399	2	6.80	5.94	4	2	108.46	5.94	2	2
CREB-regulated transcription activator 2 [Homo sapiens], CRTC2	32171215	77.5	0.916	29	0.681	29	0.625	29	0.80	0.713	29	4.93	47.31	38	5	535.89	47.31	15	5
histone acetyltransferase KAT2B [Homo sapiens], KAT2B	40805843	91.1	0.961	1	0.377	1	0.550	1	0.98	0.413	1	6.33	3.49	3	2	67.48	3.49	2	2

Description	Accession	MW [kDa]	114/1	114/1	115/1	115/1	116/1	116/1	115/11	117/1	7/113	pI	Coverage	PSM	Peptides	Score A3	Average	SM A	Peptides A3
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Table SIII. Proteins interacting with the miR-374a-5p promoter sequence in SCC cells (11/11M) upon cisplatin exposure

tumor protein p63 [Homo sapiens], TP63	169234657	67.9	0.985	50	7.518	51	7.744	51	0.87	8.841	51	5.59	53.03	103	7	1528.96	53.03	46	6
forkhead box D3 [Homo sapiens], FOXD3	6912372	52.6	1.153	17	1.726	17	2.042	17	0.85	1.351	17	5.38	47.45	27	6	528.50	40.88	11	5
sex-determining region Y protein [Homo sapiens], SRY	383087989	23.6	0.800	12	1.587	12	1.386	12	1.14	1.728	12	8.24	7.16	21	4	384.84	7.16	9	4
transcription factor AP-4 (activating enhancer binding protein 4) [Homo sapiens], TFAP4	4507447	43.2	0.956	1	1.558	1	1.290	1	0.90	1.352	1	6.80	1.25	2	1	46.78	1.25	1	1
CCAAT/enhancer binding protein, beta [Homo sapiens], C/EBPbeta	119596035	40.6	1.053	27	1.556	28	1.546	28	1.01	1.750	28	8.02	27.58	70	9	1373.71	26.32	34	8
forkhead box M1 isoform 1 [Homo sapiens], FOXM1	42544167	93.1	0.976	10	1.526	10	1.559	10	0.98	1.695	10	4.88	26.27	10	4	161.57	13.56	5	2
nuclear transcription factor Y subunit alpha, isoform 1 [Homo sapiens], NFYA	4505389	39.5	0.971	8	1.497	8	1.273	8	0.86	1.546	8	4.94	21.58	16	3	368.26	17.37	7	2
YY1 transcription factor [Homo sapiens], YY1	4507955	51.1	1.023	38	1.385	38	1.262	38	0.96	1.480	38	11.62	29.41	69	7	948.85	29.41	33	7
histone deacetylase 2 [Homo sapiens], HDAC2	46623327	137.9	1.084	21	1.350	21	1.531	21	0.88	1.558	21	6.98	27.53	33	7	579.47	25.00	17	6
CCCTC-binding transcriptional repressor, isoform 1 [Homo sapiens], CTCF	5729790	83.8	1.197	1	1.309	1	1.451	1	0.90	1.296	1	7.20	2.59	2	1	31.94	2.59	1	1
general transcription factor IIB [Homo sapiens], GTF2B	4504193	38.8	1.229	2	0.744	2	0.638	2	0.89	0.594	2	9.76	10.88	2	2	57.71	6.22	1	1
CREB-regulated transcription coactivator 2 [Homo sapiens], CTRC2	32171215	77.6	1.088	4	0.460	4	0.427	4	1.15	0.383	4	6.05	7.41	7	2	266.39	7.41	4	2
Sp1 transcription factor [Homo sapiens], Sp1	38372901	90.8	1.317	1	0.403	1	0.557	1	0.84	0.459	1	6.18	3.95	2	2	109.86	2.40	1	1
Cbp/p300-interacting transactivator 2, isoform 1 [Homo sapiens], CITED2	19923343	31.6	1.004	16	0.372	16	0.310	16	1.16	0.421	16	8.53	11.13	21	11	417.44	8.40	12	8
transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha) [Homo sapiens], TFAP2A	109389358	45.3	1.049	1	0.219	1	0.293	1	0.94	0.258	1	7.75	3.01	2	1	51.61	3.01	1	1

Description	Accession	MW [kDa]	A5: 114/113	S: 114/111	A5: 115/111	S: 115/111	A5: 116/113	S: 116/111	A5: 117/113	S: 117/113	pI	Covered	Σ PSMs	Peptides	Score A3	Coverage A3	PSM A3	Peptides A
Table SIV. Proteins interacting with the miR-630 promoter sequence in SCC cells (11/11M) upon cisplatin exposure																		

tumor protein p63 [Homo sapiens], TP63	169234657	67.9	0.987	21	7.369	21	6.753	21	0.81	6.999	21	6.16	50.05	20	8	1529.55	49.01	19	7
nuclear transcription factor Y, beta [Homo sapiens], NFYB	5453780	25.6	1.035	10	2.724	10	2.350	10	0.84	0.272	10	8.29	15.35	16	4	407.44	182.40	12	4
CREB-regulated transcription coactivator 2 [Homo sapiens], CRTC2	32171215	77.5	0.753	6	2.171	6	2.078	6	0.90	2.463	6	8.66	3.02	12	2	221.79	1.51	5	1
DNA damage-inducible transcript 3 [Homo sapiens], DDIS3	304282231	20.3	0.974	2	2.107	2	1.971	2	1.00	2.142	2	4.92	1.25	20	3	285.28	1.00	9	2
heat shock transcription factor 1 [Homo sapiens], HSF1	15779147	59.5	0.974	2	1.865	2	1.471	2	1.00	1.544	2	4.92	1.25	2	3	285.28	1.00	9	2
transcription factor Sp1, isoform a [Homo sapiens], SP1	38372901	92.4	0.953	7	1.724	7	1.325	7	0.93	1.537	7	6.92	10.61	13	2	173.50	10.61	6	2
transcription factor AP-2alpha, isoform a [Homo sapiens], TFAP2A	4507441	48.5	1.053	27	1.596	28	1.246	28	1.01	1.250	28	8.02	27.58	30	9	1373.71	26.32	34	8
v-myb myeloblastosis virus oncogene homolog [Homo sapiens], c-MYB	71682821	69.8	0.916	1	1.538	1	1.411	1	0.83	1.352	1	7.01	49.03	1	1	3911.15	38.41	1	1
general transcription factor IIB [Homo sapiens], GTF2B	18088837	36.5	0.953	6	1.417	6	1.380	6	0.90	1.463	6	8.66	3.02	12	2	221.79	1.51	5	1
histone acetyltransferase, KAT2B [Homo sapiens], KAT2B	40805843	94.6	0.982	1	1.392	1	1.473	1	1.02	1.432	1	4.67	6.79	5	6	712.45	6.56	3	2
Cbp/p300-interacting transactivator 2 isoform 1 [Homo sapiens], CITED2	19923343	31.6	0.968	1	1.358	1	1.276	1	1.15	1.276	1	6.13	3.15	2	1	66.61	3.15	1	1
TATA-binding protein-like protein 1 [Homo sapiens], TBPL1	358439409	21.6	0.905	3	1.247	3	1.329	3	1.10	1.555	3	5.12	5.14	4	2	84.19	2.86	1	1
activating transcription factor 2 [Homo sapiens], ATF2	120660330	57.8	0.933	2	1.228	2	1.248	2	0.81	1.530	2	7.03	51.92	4	4	5402.07	51.92	4	4
C-terminal-binding protein 1 isoform 1 [Homo sapiens], CTBP1	4557497	48.3	0.913	1	0.525	1	0.428	1	0.90	0.562	1	9.28	35.37	4	2	148.28	35.37	3	2
histone deacetylase 1 [Homo sapiens], HDAC1	49456395	53.6	0.904	16	0.347	16	0.390	16	1.16	0.472	16	8.53	11.13	16	11	417.44	8.40	12	8
histone-lysine N-methyltransferase EZH2 isoform b [Homo sapiens], EZH2	23510384	78.3	0.913	11	0.327	11	0.353	11	1.02	0.343	11	6.32	10.25	10	8	549.55	9.21	9	7
SIN3 homolog B, transcription regulator [Homo sapiens], SIN3B	84569981	40.8	1.189	4	0.315	3	0.344	3	1.12	0.379	3	4.81	6.56	5	1	84.39	6.56	2	1
CCCTC-binding transcriptional repressor, isoform 1 [Homo sapiens], CTCF	5729790	80.8	0.948	3	0.280	14	0.319	14	1.97	0.302	14	6.07	12.45	12	7	354.67	11.45	24	9

Description	Accession	MW [kDa]	A5: 114/113	S5: 114/111	A5: 115/113	S5: 115/111	A5: 116/113	S5: 116/111	115/116	A5: 117/113	S5: 117/113	pI	Coverage	PSMs	Peptides	Score A3	Coverage A3	PSM A3	Peptides A
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Table SV. Proteins interacting with the miR-885-3p promoter sequence in SCC cells (11/11M) upon cisplatin exposure

tumor protein p63 [Homo sapiens], TP63	169234657	67.9	1.009	11	6.371	11	7.278	11	1.19	7.146	11	6.36	1.79	12	11	121.89	1.81	11	10
histone acetyltransferase, EP300 [Homo sapiens], KAT3B	50345997	271.3	1.013	1	2.757	1	2.828	1	1.02	2.328	1	5.76	5.33	2	2	108.85	5.39	3	2
Cbp/p300-interacting transactivator 2 isoform 1 [Homo sapiens], CITED2	19923343	31.6	1.018	1	2.135	1	2.086	1	0.97	2.065	10	6.62	22.65	1	1	504.31	18.58	1	1
CREB-regulated transcription coactivator 2 [Homo sapiens], CRTC2	32171215	77.5	0.908	6	1.942	6	1.813	6	1.16	1.629	6	7.96	8.82	7	4	137.17	8.82	4	4
TATA-binding protein-like protein 1 [Homo sapiens], TBPL1	358439409	20.5	0.976	24	1.931	24	1.558	24	1.00	1.719	24	7.55	16.96	42	11	1010.36	14.80	18	8
c-Rel homolog [Homo sapiens], c-REL	219518044	65.4	1.149	5	1.833	5	1.609	5	0.87	1.420	5	5.40	15.43	35	7	655.12	15.43	17	7
transcription factor Sp3, isoform 1 [Homo sapiens], SP3	38373693	88.5	0.929	16	1.794	15	1.750	15	1.08	1.649	16	5.66	17.84	48	14	1042.57	14.71	20	10
transcription factor AP2alpha, isoform a [Homo sapiens], TFAP2A	4507441	49.5	1.071	6	1.766	6	1.676	6	1.07	1.685	6	8.18	4.86	6	2	50.73	2.16	1	1
general transcription factor 2B [Homo sapiens], GTF2B	4504193	36.6	0.991	4	1.573	4	1.629	4	0.91	1.675	4	8.60	3.06	7	3	186.38	2.46	3	2
activating transcription factor 2 [Homo sapiens], ATF2	120660330	56.5	0.988	40	1.351	40	1.376	40	0.92	1.331	40	9.38	15.32	72	16	1292.39	13.47	36	13
DNA-damage-inducible transcript 3 [Homo sapiens], DDIT3	304282231	20.6	0.915	6	1.311	6	1.343	6	0.86	1.372	6	5.19	17.05	8	5	200.39	17.05	5	5
nuclear transcription factor Y, beta [Homo sapiens], NFYB	5453780	22.7	0.908	5	1.299	5	1.337	5	0.95	1.510	5	6.34	27.78	9	1	1590.80	27.78	4	1
histone-lysine N-methyltransferase EZH2 isoform a [Homo sapiens], EZH2	21361095	83.3	0.913	11	0.567	11	0.653	11	1.02	0.430	11	6.32	10.25	10	8	549.55	9.21	9	7
histone deacetylase 4 [Homo sapiens], HDAC4	153085395	117.6	0.753	6	0.337	6	0.278	6	0.90	0.463	6	8.66	3.02	12	2	221.79	1.51	5	1
C-terminal-binding protein 1 isoform 1 [Homo sapiens], CTBP1	4557497	48.3	1.091	1	0.257	1	0.283	1	0.90	0.328	1	9.28	35.37	4	2	148.28	35.37	3	2
SIN3 homolog B, transcription regulator [Homo sapiens], SIN3B	84569981	40.8	0.989	6	0.239	4	0.214	4	0.92	0.279	4	4.81	8.16	5	2	45.39	8.16	4	2