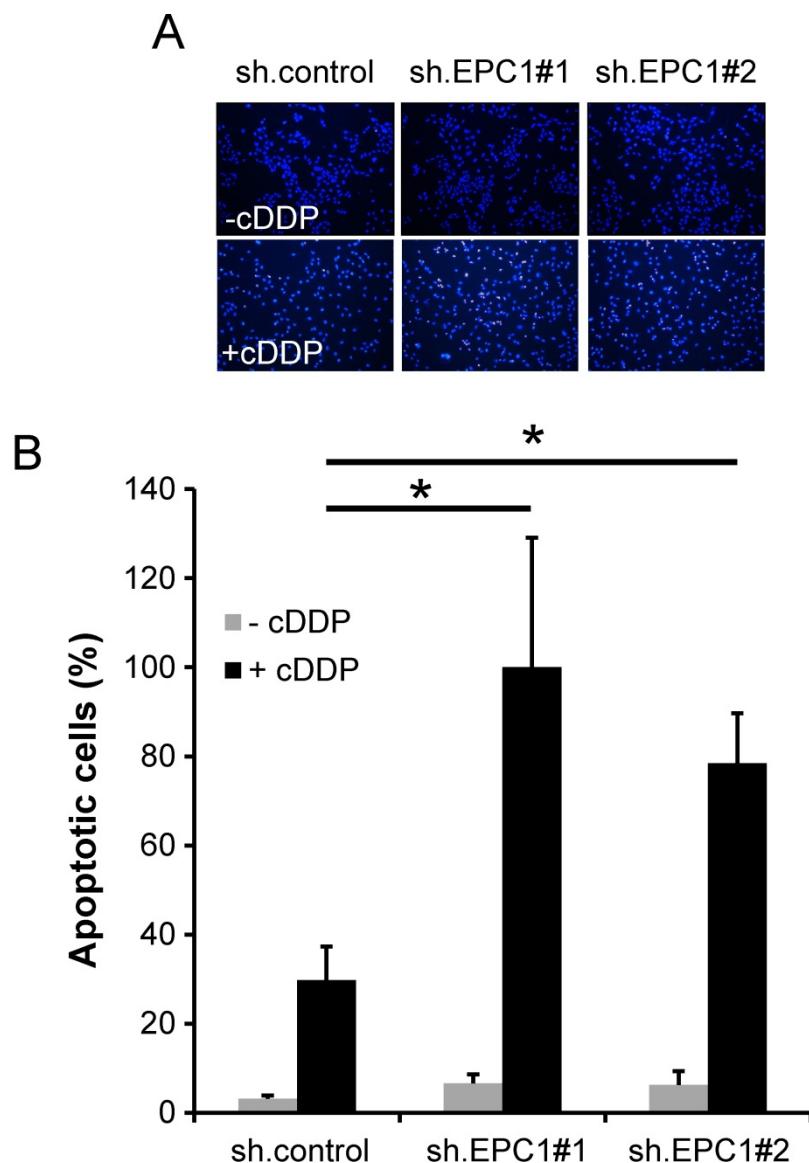


**Supplementary Table S1.** Primer sequences for mRNA expression analysis by PCR and for ChIP as well as generation of full-length EPC1 promoter construct

Primer name	Sequence
<b>E2F1-fwd</b>	ACCAGGGTTCCAGAGATGC
<b>E2F1-rev</b>	CACCACACAGACTCCTCCC
<b>EPC1-fwd</b>	AGCCGATCTTATCCGACCGAA
<b>EPC1-rev</b>	TCCAAGGCCAGTTGCCAGTT
<b>EZH2-fwd</b>	TATTCAAGGGGGCTCCAAAAA
<b>EZH2-rev</b>	TGGATGGCTCTCTGCGAAA
<b>EED-fwd</b>	TGCTGGAAACCTGGCAAGAT
<b>EED-rev</b>	AGCGCCAAATACTGGCATCA
<b>p27-fwd</b>	TTCATCAAGCAGTGATGTATCTGA
<b>p27-rev</b>	AAGAAGCCTGGCCTCAGAAG
<b>Bax-fwd</b>	CACCAGCTCTGAGCAGATCAT
<b>Bax-rev</b>	GCGGCAATCATCCTCTGCAG
<b>Bim-fwd</b>	TCTGTTGCCAGCCTGCATTGAT
<b>Bim-rev</b>	ATGGGAAAGCCTGCAACCAGAA
<b>Bcl-2-fwd</b>	CGTACAGTTCCACAAAGG
<b>Bcl-2-rev</b>	ATGTGTGTGGAGAGCGTC
<b>BIRC5-fwd</b>	TGCAAAGGAAACCAACAA
<b>BIRC5-rev</b>	TCAATCCATGGCAGCCAG
<b>GAPDH-fwd</b>	GTCATCCCTGAGCTGAAC
<b>GAPDH-rev</b>	CTCCTTGGAGGCCATGTG
<b>EPC1-P1-fwd</b>	GAGCGCACAGTGGAGTTTA
<b>EPC1-P1-rev</b>	GCCCGAAACGACAGTTACTC
<b>EPC1-P2-fwd</b>	AGCATCTGCCCTAATTCACT
<b>EPC1-P2-rev</b>	CTCACTTCTCACGCTCGCT
<b>EPC1-P3-fwd</b>	AACCGATGCCACCCATCTAT
<b>EPC1-P3-rev</b>	TCAAAGAGACTGCGGCTTCA
<b>EZH2-P-fwd</b>	CCCTCCACAAATGTGGATCT
<b>EZH2-P-rev</b>	CCAGCCTGAATATGATCACC
<b>EPC1-Prom-fwd</b>	GAGGTACCAAGCTAGTGACAGCTCATATCA
<b>EPC1-Prom-rev</b>	GAAAGCTTCTCAGGCGCAGCAGATAACCTCT
<b>p27 ChIP fwd</b>	GGCCTCCCCCGCAGACCAC
<b>p27 ChIP rev</b>	GTTCCGCCACCTCCCCTCGTTCC
<b>Bcl-2 ChIP fwd</b>	CTTCCCAATGAATCAGGAGTCG
<b>Bcl-2 ChIP rev</b>	GCGTCCTGCCTTCATTATCCA

**Supplementary Table S2.** Interacting residues of E2F1 and EPC1 in interaction pose A and B

Residues forming H-bond (A: E2F1 & B: EPC1)	Domains of E2F1
<b>Interaction pose A</b>	
A:ARG85:HN - B:GLU49:OE1	Cyclin A/CDK2 binding
A:ARG91:HE - B:ARG36:O	Cyclin A/CDK2 binding
A:ARG91:HH11 - B:GLU93:O	Cyclin A/CDK2 binding
A:ARG91:HH21 - B:SER33:O	Cyclin A/CDK2 binding
A:ARG91:HH22 - B:PHE94:O	Cyclin A/CDK2 binding
A:ARG109:HN - B:ALA84:O	DNA binding
A:GLY110:HN - B:ALA84:O	DNA binding
A:ALA379:HN - B:LYS129:O	Transactivation
B:MET1:HT1 - A:GLU280:O	Marked box
B:ASN35:HD22 - A:GLU354:O	Marked box
B:TYR85:HH - A:ASP436:OD1	Transactivation
B:SER88:HG - A:GLY106:O	Cyclin A/CDK2 binding
<b>Interaction pose B</b>	
A:TYR100:HH - B:ARG461:O	Cyclin A/CDK2 binding
A:SER104:HG - B:GLY460:O	Cyclin A/CDK2 binding
A:ARG111:HH21 - B:TYR412:OH	Cyclin A/CDK2 binding
A:ARG422:HH12 - B:CYS451:O	Transactivation
B:TYR412:HH - A:ASP423:OD1	Transactivation
B:ARG439:HH21 - A:SER121:O	Cyclin A/CDK2 binding
B:ARG450:HH11 - A:GLU419:OE1	Transactivation
B:VAL465:HN - A:GLU103:OE1	Cyclin A/CDK2 binding
B:ARG469:HH12 - A:LEU351:O	Marked box
B:ASN499:HD21 - A:ARG109:O	Cyclin A/CDK2 binding
B:ASN499:HD21 - A:GLY110:O	Cyclin A/CDK2 binding



**Supplementary Figure S1 related to Figure 4.** EPC1 suppresses cisplatin (cDDP) induced apoptosis. **(A)** Representative photomicrographs of Hoechst 33342 stained (1 µg/ml) SK-Mel-147 cells expressing indicated shRNAs in the presence or absence of cDDP (30 µM). Cells exposed to cDDP exhibit characteristic chromatin condensation. **(B)** The bar graph represents the percentages of apoptotic cells relative to the sh.EPC1#1/+cDDP group. Quantification of apoptosis was determined by counting the number of apoptotic cells from four randomly chosen fields of view per condition with a minimum number of 500 cells scored in each. Data are presented as the mean with standard deviation in an experiment representative of several independent others. Asterisks indicate P values of <0.01.