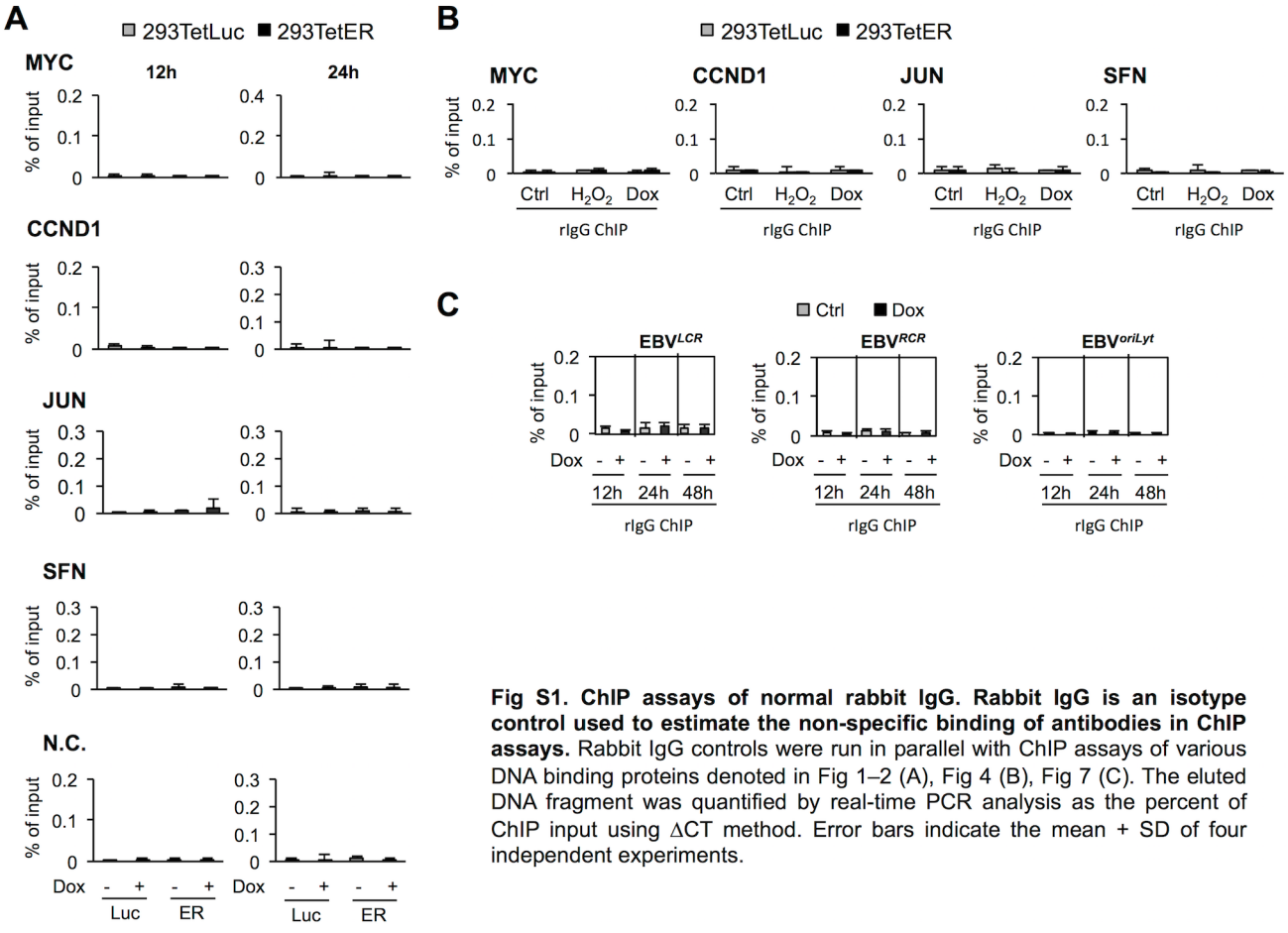

Fig S1. ChIP assays of normal rabbit IgG. Rabbit IgG is an isotype control used to estimate the non-specific binding of antibodies in ChIP assays. Rabbit IgG controls were run in parallel with ChIP assays of various DNA binding proteins denoted in Fig 1–2 (A), Fig 4 (B), Fig 7 (C). The eluted DNA fragment was quantified by real-time PCR analysis as the percent of ChIP input using ΔCT method. Error bars indicate the mean + SD of four independent experiments.

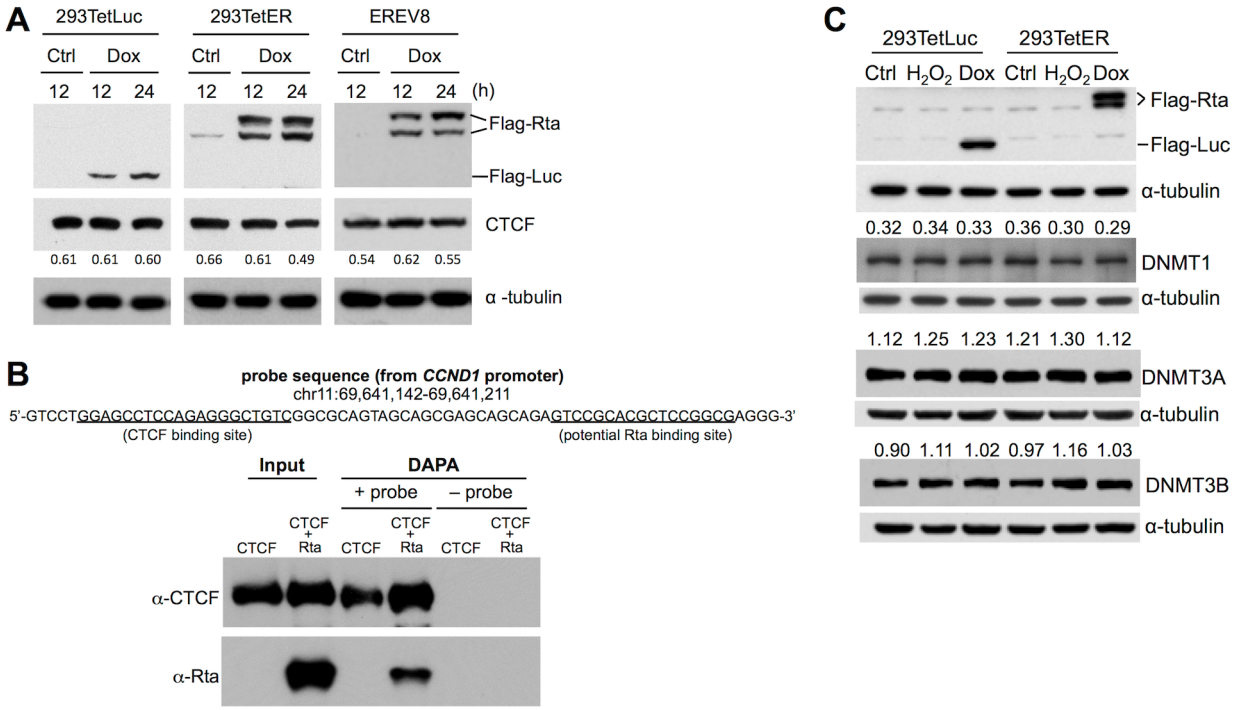

Fig S2. Direct binding of EBV Rta into DNA does not interfere with CTCF occupancy. (A) Protein extracts of untreated (Ctrl) and Dox-treated (Dox) 293TetLuc, 293TetER, and EREV8 cells at indicated time points were harvested and subjected to western blot analysis for CTCF and Flag-Luc/Rta expression. Numeric values beneath each band denote fractions of intensity normalized with α-tubulin. (B) DNA affinity precipitation assay (DAPA) of CTCF and Rta. Nuclear extracts of CTCF- or CTCF plus Rta-overexpressed 293T cells were harvested and subjected to DAPA analysis by incubating with (+) or without (–) DNA probes. CTCF and Rta proteins in the inputs (1/30) or DAPA precipitates were detected using a western blot assay. (C) Protein extracts harvested from untreated (Ctrl), 500 μM H_2O_2, or 50 ng/ml Dox-treated 293TetLuc and 293TetER cells were subjected to western blot analysis using antibodies of Flag, DNMT1, DNMT3A, DNMT3B, and α-tubulin. Numeric values above each band denote fractions of intensity normalized with α-tubulin.

Supporting Table S1. List of primers used in the present study

Primers for real-time RT-PCR analysis			
Gene Name		Primer sequence (5' → 3')	PCR
CCDC86	Forward	AAGTGAGGAGGCACCAAAGT	137 bp
	Reverse	CGGGGTAAGGCTCTGGTGAT	
CCND1	Forward	CAAGGCCTGAACCTGAGGAG	171 bp
	Reverse	CTTGGGGTCCATGTTCTGCT	
DHCR7	Forward	ACAGAACCGCATCTCAAGGG	135 bp
	Reverse	AGCTGTACTGGTCACAAGCC	
DHCR24	Forward	ATGCACTCCGTCCGAAAACT	126 bp
	Reverse	TCGAAACGCAGCTTGACGTA	
ERI3	Forward	AGGAGAGTTTTAGATGCTTCTGG	113 bp
	Reverse	AATAAGTGGGAGCCCAGCAC	
FAM84B	Forward	GCCGAGCCTACACCTTCAAA	94 bp
	Reverse	CTACCCGCGGAGAGGTGAAG	
GAPDH	Forward	CAAGAAGGTGGTGAAGCAGG	91 bp
	Reverse	GCTGTTGAAGTCAGAGGAGACC	
JUN	Forward	GTGCCGAAAAAGGAAGCTGG	175 bp
	Reverse	CTGCGTTAGCATGAGTTGGC	
MYC	Forward	AGCATACATCCTGTCCGTCC	226 bp
	Reverse	CTCAGCCAAGGTTGTGAGGT	
SFN	Forward	GCCCCTGCTGCCTCTGATCG	170 bp
	Reverse	ACACCCAGCAGACATGCTTTCCC	
TRIB1	Forward	TCGCTCGCTCTCATACACG	121 bp
	Reverse	GAGCCACGAAGCAAATGCAC	
EBV_BHLF1	Forward	CGCAACAGTGCCACCAAC	73 bp
	Reverse	CAGGACCTGGCGGTAGTG	
EBV_BHRF1	Forward	GATTCATCAACAGGGCGG	89 bp
	Reverse	GTCCAGCAAGAAACAAAGTCC	
EBV_BKRF4	Forward	GGACGTGAGTGACACTGA	157 bp
	Reverse	GCTCTCGCTGTAGTCAGA	
EBV_LMP1	Forward	GGGTCGTCATCATCTCCACC	59 bp
	Reverse	CCACACCTTCCTACGCTGC	
EBV_LMP2A	Forward	CGTGAATCTAATGAAGAGCCC	81 bp
	Reverse	TGGTTGATAGTCCGAGTGACG	
EBV_Zta (BZLF1)	Forward	GAGTCAACATCCAGGCTTGG	96 bp
	Reverse	GCAGCACTACCGTGAGGTG	
Primers for ChIP assay and DNA methylation analysis			
Gene Name		Primer sequence (5' → 3')	PCR
MYC	Forward	CCGGTTTTCGGGGCTTTATC	273 bp
	Reverse	GCTCGGGTGTTGTAAGTTCC	
CCND1	Forward	ACAACAGTAACGTCACACGGAC	228 bp
	Reverse	TTCCATGGCTGGGGCTCTTC	
JUN	Forward	CGAAAGAACCAGGATTCCCGA	234 bp
	Reverse	CACTCGCATAAAGTCACGCAG	
SFN	Forward	TTTATGGGCTCTGTCGAGGC	263 bp
	Reverse	TTCCGGCTCTGCAGTAAAGG	
Negative control	Forward	TATGTGGAGCGGCTTCTCGG	148 bp
	Reverse	GCTCAGATCCTGCAGGTACAA	
EBV_LCR	Forward	TCCCTACTCTCCACGGGATG	208 bp
	Reverse	GCTGGGGGTGTCAACAAAGA	
EBV_RCR	Forward	GGAAGAGTACCCCAGTGACG	165 bp
	Reverse	TGTTGGGTAGATGGCGAGAC	
EBV_*oriLyt*	Forward	TAGAGGTCCGCGAGATTTGG	213 bp
	Reverse	AGGAACCTAGCTGAATCCTACCT	
Primers for determination of intracellular viral genome copies			
Gene Name		Primer sequence (5' → 3')	PCR
EBV_DNA Pol (BALF5)	Forward	CGGAGTTGTTATCAAAGAGGC	135 bp
	Reverse	CGAGAAAGACGGAGATGGC	