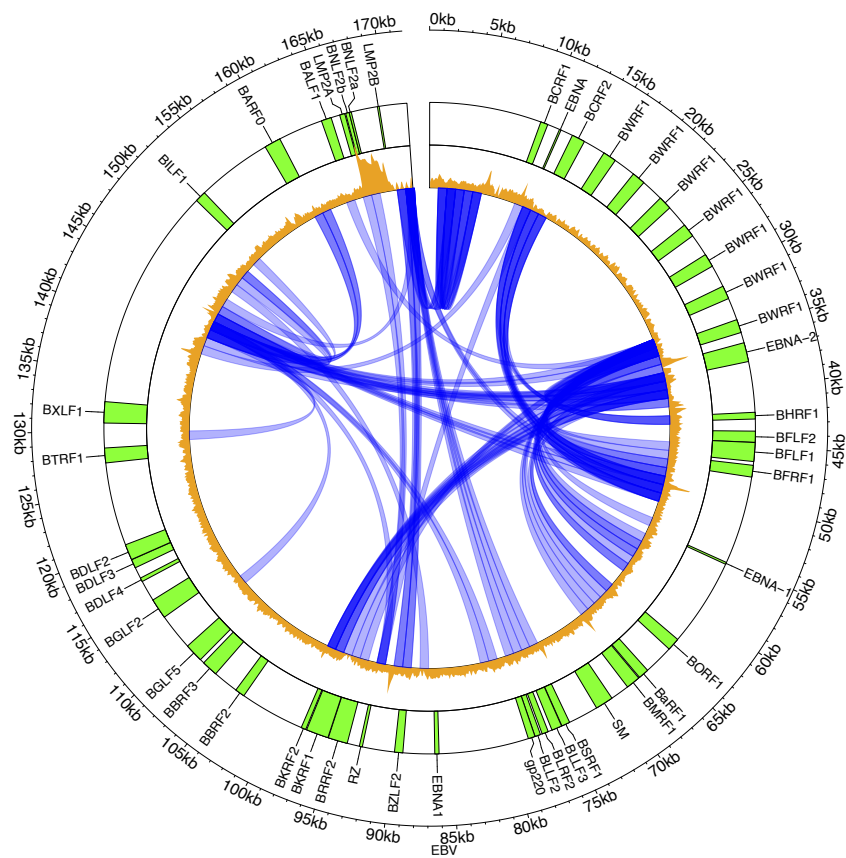
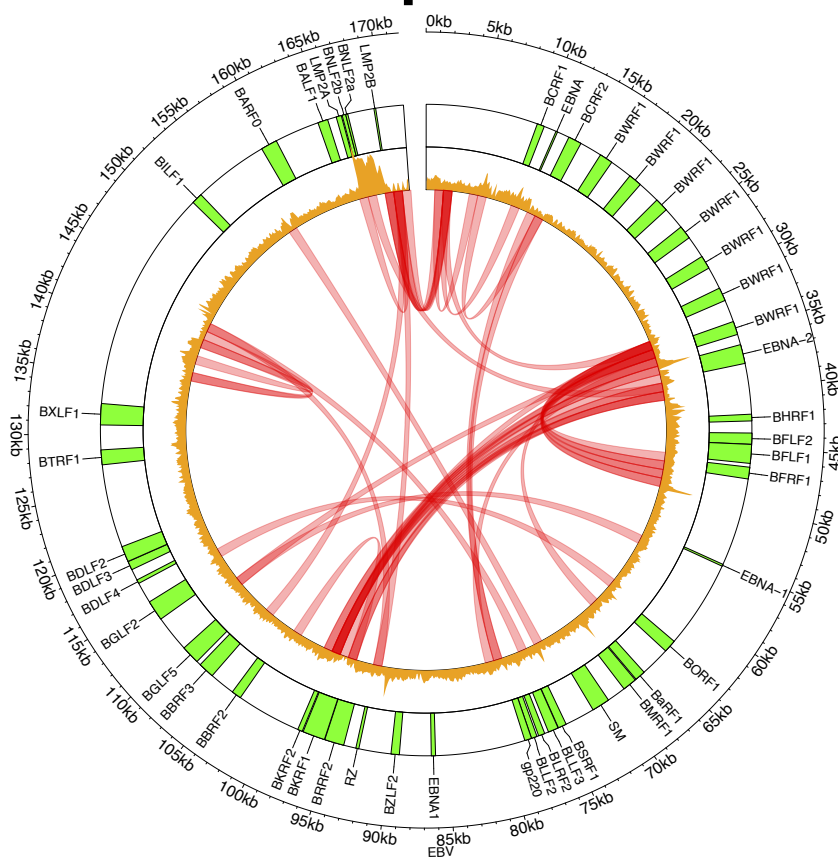


Supplementary Figures

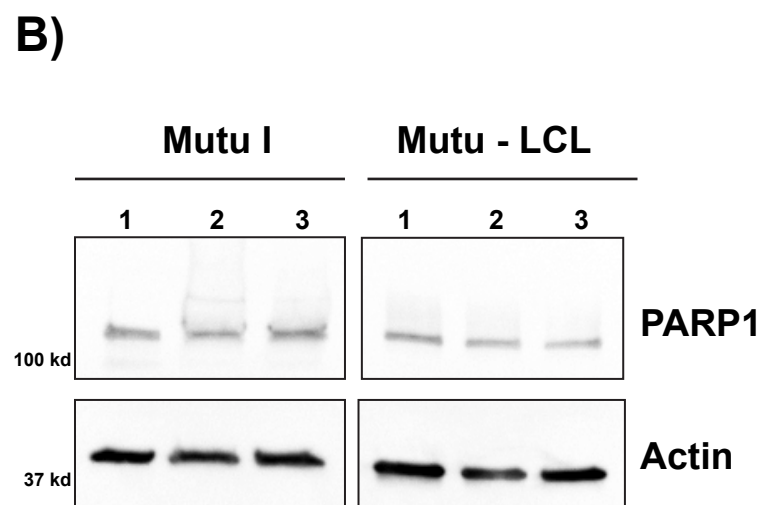
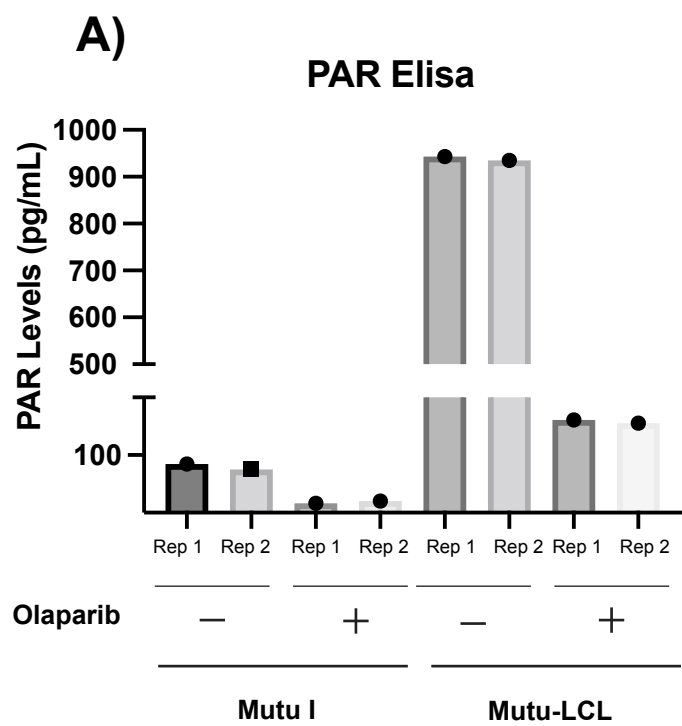
A) Control



B) Olaparib



Supplementary figure 1. CTCF binding profiles aligned to DNA-DNA contact maps. Circos graphs of all DNA-DNA contacts with significance of $< .05$ within the type III latency EBV genome (Mutu-LCL) derived from HiC matrices. A) circos graph represents the control (untreated genome, blue) and B) represents the type I genome with 2.5 μ M olaparib treatment (red). Darkness of arcs correspond to strength of DNA-DNA contact. CTCF ChIP-seq profile (orange) surrounds the circos graph in untreated (top) and olaparib treated (bottom) Mutu-LCL EBV genome.

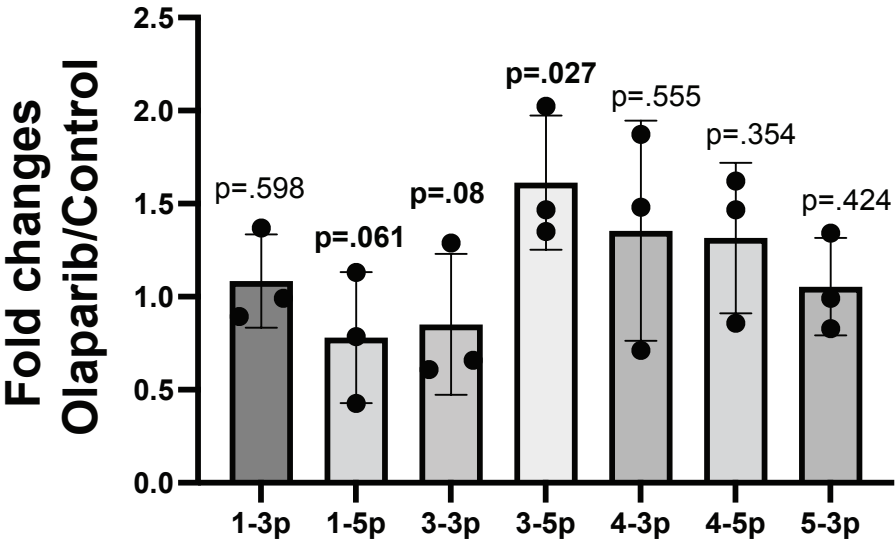


Supplemental figure 2. PAR ELISA. A) Biological duplicates of type I latency Mutu I or type III EBV latency LCL were collected before or after PARP inhibition (2.5uM olaparib for 72 hours). N=2, Mean. Source data are provided as a Source Data file. B) Three biological replicates of Mutu and Mutu-LCL were collected and immunoblotted for PARP1 protein levels as well as actin control. Source data are provided as a Source Data file.

Supplemental figure 3. Linearized depiction of chromatin loops across EBV genomes. A)

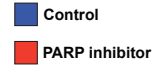
Linearized type I EBV genome (Mutu I) with arcs connecting DNA-DNA contacts derived from HiC matrices. Blue arcs represent chromatin loops that are more frequent in control genome, red arcs represent chromatin loops that are more frequently observed in the olaparib treated genome, and black arcs are loops that are unchanged between control and treatment. B) Linearized type III EBV genome (LCL) as described in A.

Expression levels BARTs

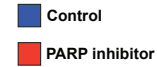


Supplemental figure 4. MicroRNA expression in LCL. RT-qPCR validation of seven randomly selected BART microRNAs, before and after PARP inhibition in LCL. Bar graph represents the average expression of three biological duplicates per treatment, each normalized to U6 snRNA, respectively. Data displayed as fold change of olaparib treated LCL over control (N=3, Mean $\pm$ SD). Treatment and control groups were compared by paired student's T-test assuming equal variance; ; (two-tailed). Source data are provided as a Source Data file

ChIP Signal



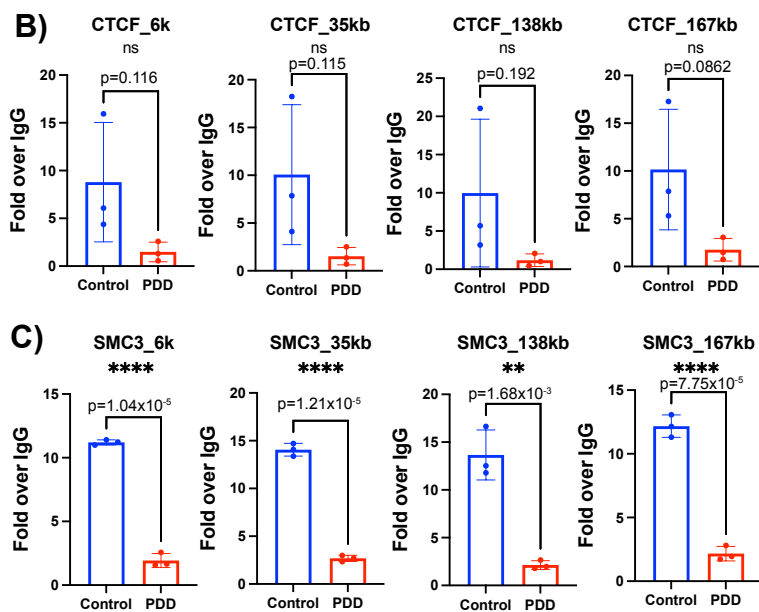
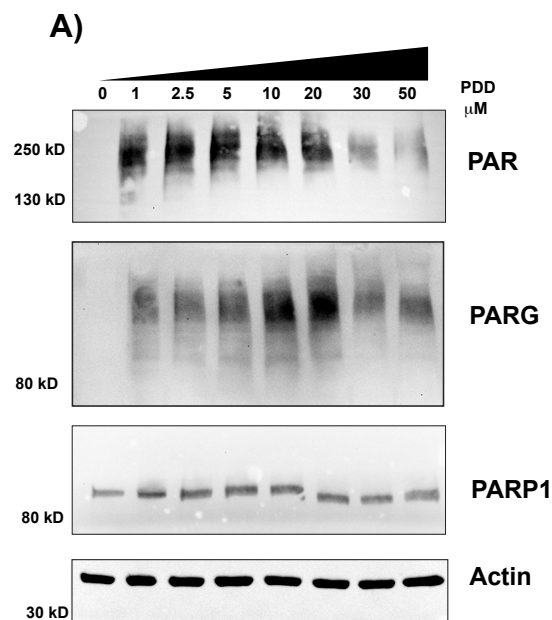
ChIP Signal



A horizontal number line with major tick marks every 10,000 units, labeled from 10,000 to 170,000.

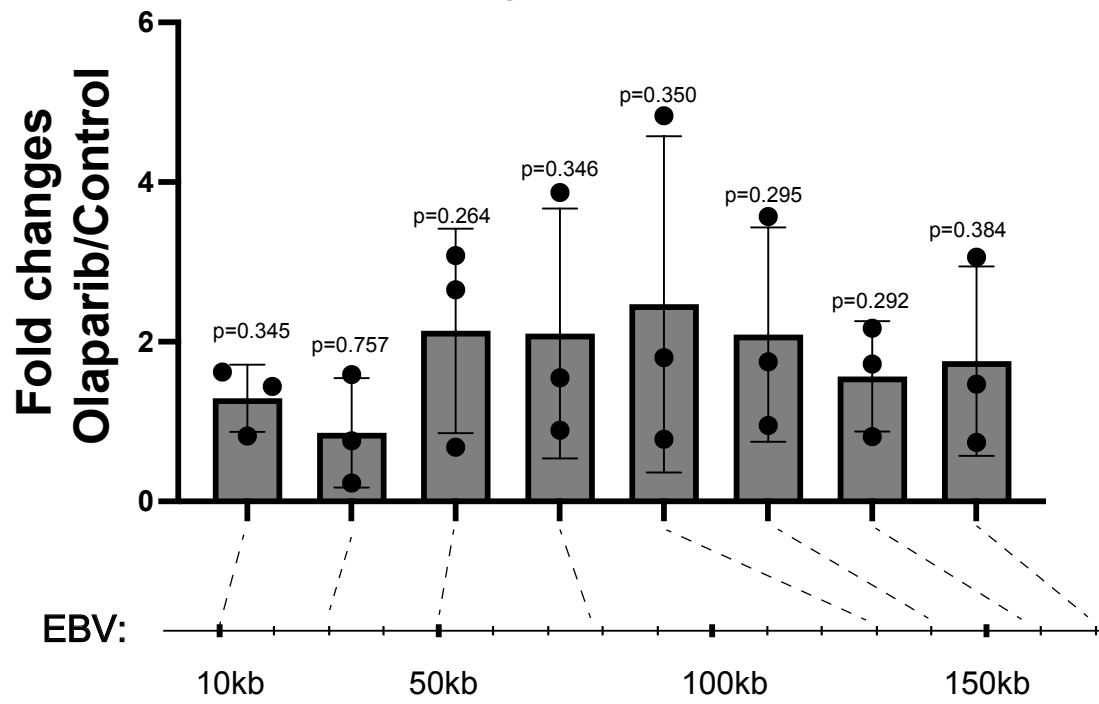
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 oriLy1.1
 Fp.1.1 BORF1.1
 BSRF1.1
 BZLF2.1
 BBRF1.1
 BGLF1.1
 BTRF1.1
 LF3.1
 A73.1
 LMP-2A.4
 DS.1
 BWRF1.4
 BWRF1.8
 BRF1.1
 BOLF1.1
 BLLF3.1
 BZLF1.1
 BBRF2.1
 BDLF4.1
 BXL2.1
 LF2.1
 BALF2.1
 LMP-2A.2
 BWRF1.3
 BWRF1.7
 BHRF1.31
 Op.1
 BOLF2.1
 BLLF1.1
 BZLF2.2
 BBRF3.1
 BDLF2.1
 BXL1.1
 LF1.1
 BALF1.1
 LMP-2B.3
 Cp.1.1
 BWRF1.5
 BHLF1.1
 BHRF1.3
 BRF1.1
 BOLF2.1
 BLLF1.1
 BZLF2.2
 BBRF3.1
 BDLF1.1
 BXL1.1
 LF1.1
 BALF1.1
 BNRF1.1
 EBNA-2.2
 BFRF3.1
 BOLF2.1
 BLLF1.1
 BZLF2.2
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 BDLF1.1
 BXL1.1
 LF1.1
 BALF1.1
 EBER1.1
 BHRF1.1
 BOLF2.1
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 BXL1.1
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 EBER2.1
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 LF1.1
 BALF1.1
 EBNA-2.1
 BOLF2.1

Supplemental figure 5. Mutu-LCL CTCF and RAD21 binding profiles overlaid with and without PARP inhibition. Read counts from respective ChIP-seq assays were first normalized to the number of reads from input chromatin collected before antibody immunoprecipitation. Normalized reads from CTCF or RAD21 ChIP-seq, before (blue) and after PARP inhibition (red), are aligned together along the EBV genome, viewed in equal scale.



Supplemental figure 6. CTCF and cohesin ChIP-qPCR with PARG inhibition. A) Immunoblot of poly(ADP-ribose) (PAR), PARG, PARP1, and actin control in Mutu-LCL at increasing concentration of the PARG inhibitor PDD 00017273. Displayed data is representative of three independent assays. Source data are provided as a Source Data file. B-C) ChIP-qPCR of CTCF or cohesin component SMC3 at previously assessed CTCF/cohesin colocalization sites in Mutu-LCL before and after treatment with 2.5 mM of the PARG inhibitor PDD 00017273. Data presented is an average of three independent assays (N=3, Mean $\pm$ SD). Treatment and control groups were compared by paired student's T-test assuming equal variance; ; (two-tailed). (*= $p \leq .05$, **= $p \leq .01$, ***= $p \leq .001$, ****= $p \leq .0001$). Source data are provided as a Source Data file.

ChIP PARP1



Supplemental figure 7. PARP1 chromatin binding in Mutu-LCL. ChIP-qPCR of PARP1 binding at previously assessed cohesin/CTCF colocalization sites in Mutu-LCL, as well as four additional PARP1 binding sites along the EBV genome, with and without 2.5uM olaparib treatment. ChIP data was normalized to input chromatin. Data presented is an average of three independent experiments, displayed as fold change of treatment over control. Groups were compared by paired student's T-test assuming equal variance; ; (two-tailed). Source data are provided as a Source Data file