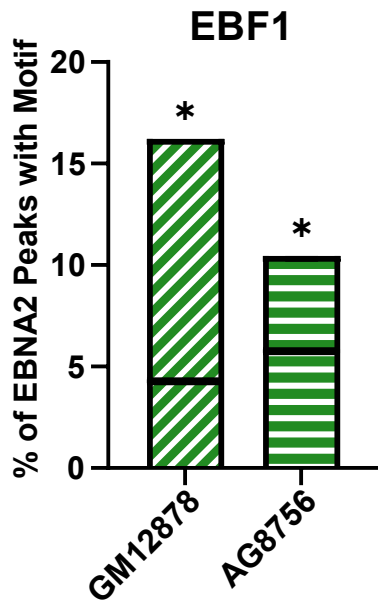
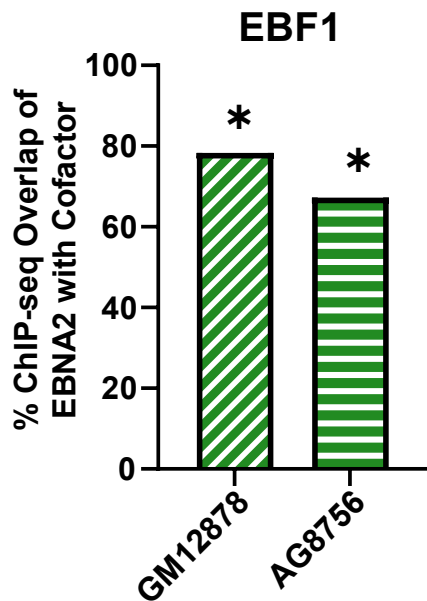


A: Predicted motif presence of EBF1



B: Validation: EBF1 ChIP-seq peak overlap



Additional File 9: Supplemental Figure 9. Identification of GM12878 and AG876 EBNA2 human cofactors. A) Frequency of occurrence of exemplary EBF1 motif in EBNA2 GM12878 (EBV-1) and AG876 (EBV-2) cell lines. The percent of peaks containing predicted binding sites for EBF1 is shown. Each bar represents percent foreground (i.e., the percent of actual peak DNA sequences containing a match to the motif). The horizontal black line within each bar depicts percent background (i.e., the percent of randomly selected genome sequences, matching GC content). Asterisks indicate significant motif enrichment ($P < 0.05$), as calculated by HOMER. B) Experimental validation of predicted EBNA2 co-occupancy with EBF1 in GM12878 (EBV-1) and AG876 (EBV-2) cell lines. Co-occupancy was assessed by EBF1 and EBNA2 ChIP-seq peak overlap. For each bar, the percent of each EBF1 peak set overlapping each EBNA2 ChIP-seq peak category is shown. Datasets with significant overlap between EBNA2 peak sets and EBF1 peaks (as calculated by RELI) are indicated with asterisks ($P < 0.05$).