Supplemental figure legends

Fig S1. Read coverage across the EBV genome showing high coverage of the BART/RPMS1 region of the genome. Y-axis represents the number of reads spanning each genomic position. Negative Y-axis values represent the number of reads spanning each genomic position in the antisense orientation.

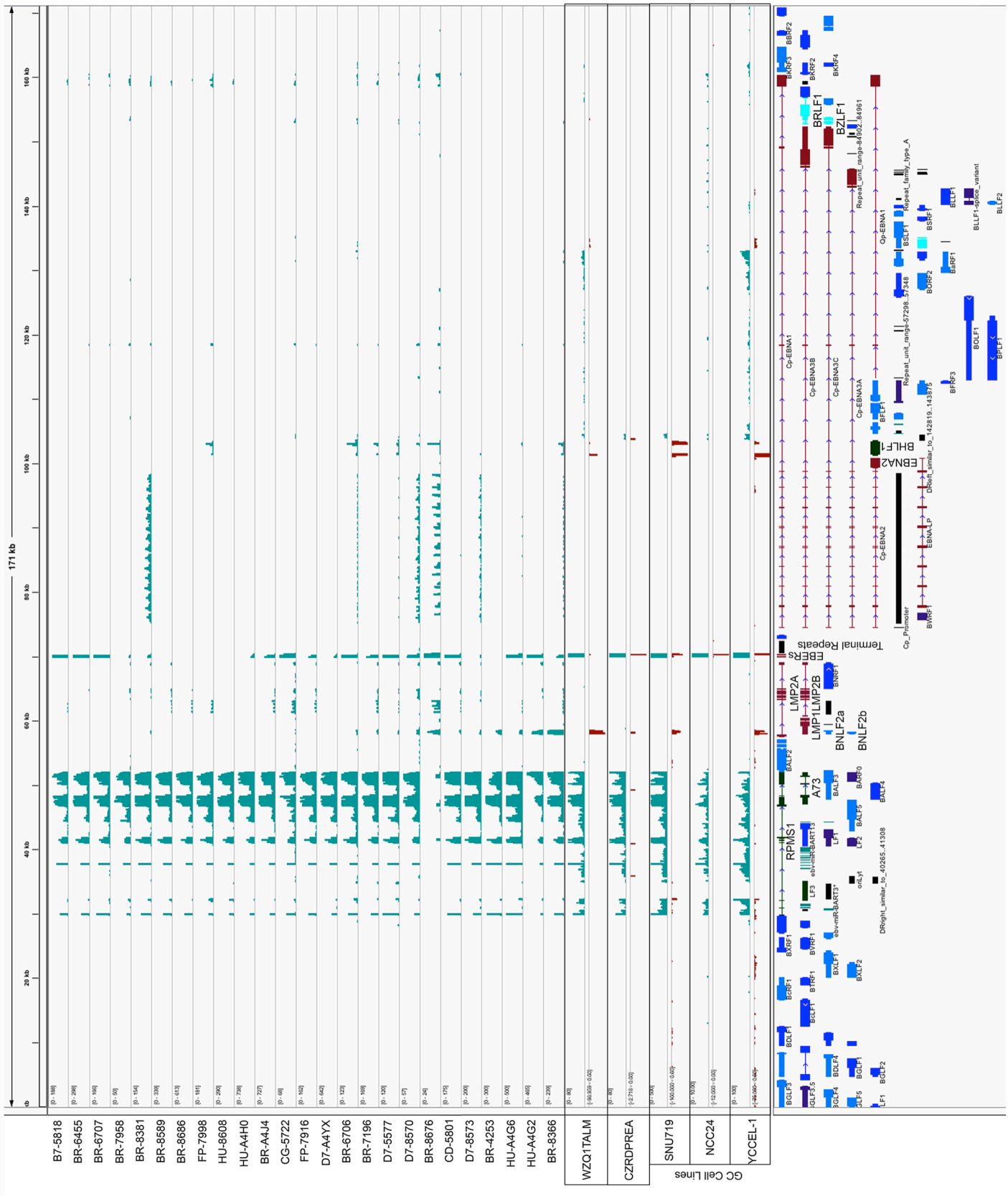
Fig S2. Genome browser view of the LMP2 locus for 25 EBV positive TCGA biopsies. Y-axis represents the number of reads spanning each genomic position. Since the first exons for the LMP2A and the LMP2B are located distally upstream, they are not included in the figure. Nevertheless, splicing to the LMP2A but not the LMP2B first exon is evident in some of the samples displaying higher LMP2 expression levels (data not shown).

Supplemental Tables

Table S1. Counts for human and virus mapped RNA-seq reads for TCGA tumor and normal specimens. Virus data is displayed here if at least one viral read was detected in at least one sample.

Table S2. Counts for human and virus mapped WXS reads for TCGA tumor specimens. Virus data is displayed here if at least one viral read was detected in at least one sample.

Table S3. Counts for human and virus mapped RNA-seq reads for CCLE GC cell lines. Virus data is displayed here if at least one viral read was detected in at least one sample.



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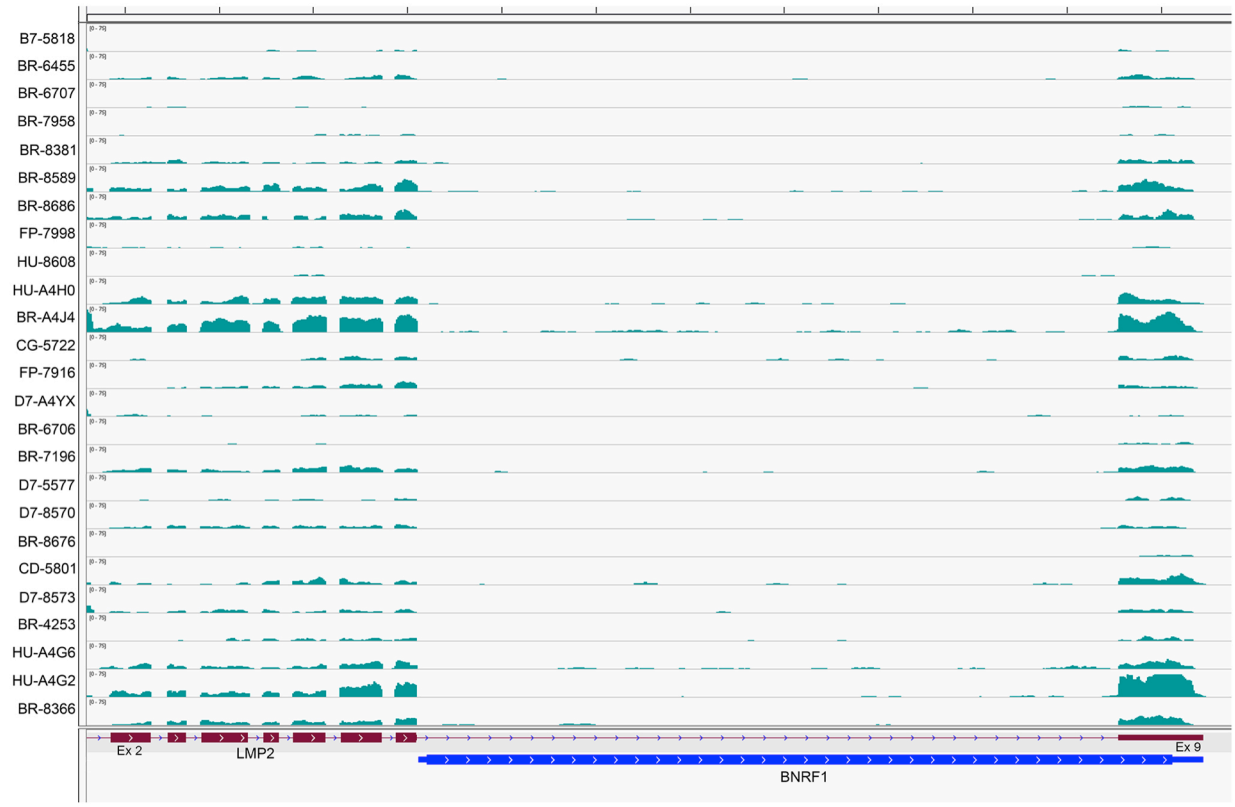

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