

**(Supplementary Text File)**

**Possible HPV38 contamination of endometrial cancer RNA-Seq samples  
in The Cancer Genome Atlas database**

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**Table S1. Detailed information on RNA-Seq samples used in this study.** Information about each sample was obtained from the Cancer Genomics Hub.

**Table S2. Detailed information on viral presence in various cancers.** For each cancer RNA-Seq sample represented by “TCGA barcode”, shown are the type, virus name, and the number of unique and high-quality reads that were mapped to the indicated virus sequence.

**Table S3. RNA-Seq and corresponding WXS samples with EBV, HHV6B, and CMV sequences from literature.** For each sample (rows) for which EBV, HHV6B, or CMV sequences were detected (26), shown are the TCGA barcodes, cancer type, and the number of reads matching the indicated virus in RNA-Seq and corresponding WXS data.