**Supplemental Figure Legends**

Figure S1. (A) Representative examples of LTAg immunohistochemistry results in virus-negative MCC with wild-type *TP53* (ME00553, top) and virus-positive MCC with *TP53* mutation (ME00142, bottom). (B) Merkel cell polyomavirus copy number qPCR and *TP53* mutation status in MCC. Statistical comparisons are not performed because qPCR was a component in assigning MCPyV status. (C) MCPyV sequence in virus-positive/*TP53* mutant MCC with adequate DNA for whole genome sequencing. Red asterisks indicate predicted nonsense mutations. Black asterisks indicate predicted integration junctions with the host genome. Numbers along the top of the graphs indicate nucleotide position relative to MCPyV reference genome sequence HM011550.1. Viral gene regions are shown by colored bars along the bottom of the graph. (D) Annotated MCPyV genome coverage for tumor ME00580, with dashed boxes indicating areas of genome involved in integration, and gaps in genomic coverage corresponding to areas of viral genome predicted to be absent from the integration. A separate fragment of VP1 (blue dashed box) is integrated in an inverted orientation to the remainder of the genome. (E) Schematic of MCPyV integration for ME00580. Upper linear diagram demonstrates viral genome in relation to flanking host genome on chromosome 1 (at the listed hg19 genomic coordinates). Lower circular diagram demonstrates the viral genome with numbers indicating relevant nucleotide positions (per reference MCPyV genome sequence HM011550.1). Dashed gray semicircle denotes the major viral genome fragment involved in integration. Dashed blue box denotes the smaller genome fragment (inverted portion of VP1) also involved in the integration. NCCR: noncoding control region. T: 1st exon common to small T and large T antigens. ST: region specific to small T antigen. LT 2nd exon: large T antigen 2nd exon (specific to large T antigen). VP: viral protein.

Figure S2. *TP53* mutational status does not significantly correlate with MCC disease-specific survival or recurrence after controlling for MCPyV status.

Figure S3. (A) Differential expression patterns across 26 cancer-related genes in MCC. Tumors are organized by MCPyV status, 3-year disease-specific survival, and *CD8A* transcript expression. Genes are ordered by hierarchical clustering. The median value is used for genes with multiple amplicons. Inflammatory transcripts (dashed box) correlate with survival in virus-positive MCC. (B) Higher density of peritumoral granzyme-positive MCPyV by immunohistochemistry is significantly associated with longer recurrence-free survival. Merkel cell polyomavirus. DSS: disease-specific survival. DOD: died of disease.

.