**Supplementary Figure Legends**

**Figure S1.** Representative microphotographs of samples showing different MCPyV RNA *in situ* hybridization (RNA-ISH) intensity (400X magnification). (A) Intensity score=0, no staining or less than 1 dot per 10 cells. (B) Intensity score=1, 1 to 3 dots per cell. (C) Intensity score=2, 4 to 9 dots per cell (few or no dot clusters). (D) Intensity score=3, 10 to 15 dots per cell (less than 10% in dot clusters). (E) Intensity score=4, greater than 15 dots per cell (more than 10% in dot clusters).

**Figure S2.** Read depth histograms across the Merkel cell polyomavirus (MCPyV) genome for two Merkel cell carcinoma (MCC) tumors. Known T antigen transcripts and viral proteins are represented on X axis. Estimated sequencing depth at MCPyV genome position is represented on Y axis. The most consistently detected region was at the 5’ end of large T antigen (LTAg) exon 2.

**Figure S3.** (A) Percentage of positive cells in MCPyV-positive tumors by RNA-ISH (n=42). (B) Photomicrograph of MCC/25 (Patient 12) with positive MCPyV RNA-ISH. The tumor (lymph node metastasis) was composed of a focal area of tumor cells surrounded by lymphocytes (green arrow). Tumor cells stain positively (red arrows) with punctate brown staining (400X magnification). (C) Comparison of percentage of positive cells by RNA-ISH and LTAg copy number by qPCR.