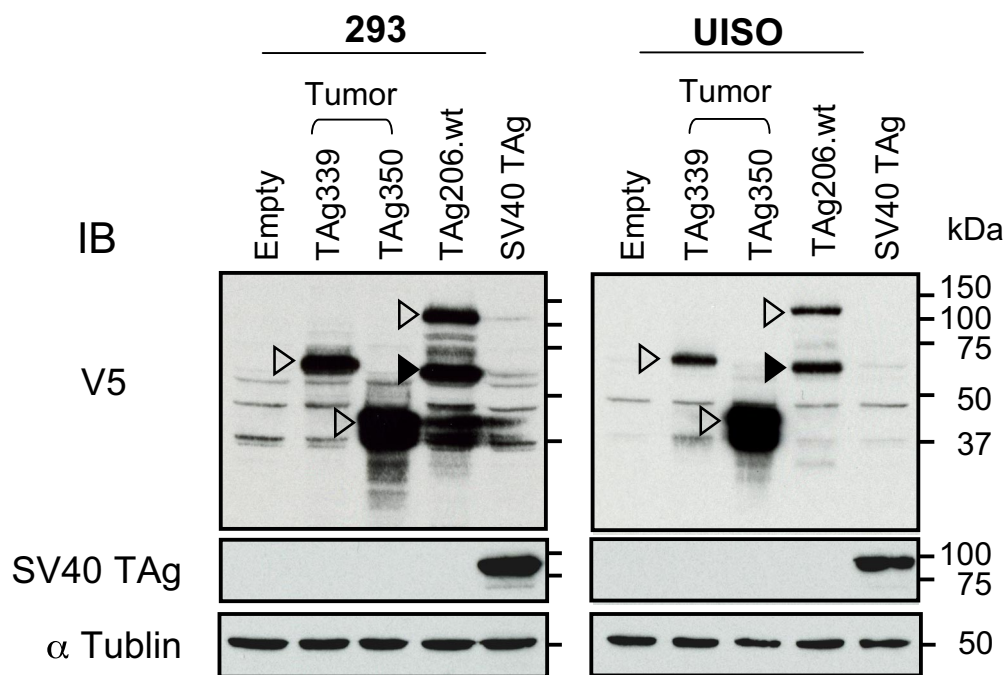


# Supporting Information

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**Fig. S1.** Expression of T Ag proteins in 293 and UIISO cell lines. Ten percent of cell lysate used for origin replication assay was subjected to immunoblot analysis to confirm T Ag protein expression. Open arrows indicate truncated tumor-derived LT or WT LT proteins. Closed arrows indicate T antigen protein isoforms.

**Table S1. MCV PCR detection in various cell lines**

Name	Origin	LT1	LT3	VP1	Summary
293	Human embryonic kidney	–	–	–	–
COS7	SV40-transfected African green monkey kidney	–	–	–	–
HT1080	Human fibrosarcoma	–	–	–	–
MCF7	Human breast cancer	–	–	–	–
UISO	MCC	–	–	–	–
MCC13	MCC	–	–	–	–
MCC26	MCC	–	–	–	–
MKL-1	MCC	+	+	+	+

One hundred nanograms of genomic DNA was amplified by using Taq DNA polymerase (Invitrogen) in a final volume of 50  $\mu$ l. The cycling condition was 3 min at 94°C, followed by 31 cycles each of 94°C for 45 s, 58°C for 30 s, and 72°C for 45 s, and final elongation of 15 min at 72°C. Three different primer sets for the T antigen locus (LT1 and LT3) and VP1 gene (VP1) were used to detect MCV (1).

1. Feng H, Shuda M, Chang Y, Moore PS (2008) Clonal integration of a polyomavirus in human Merkel cell carcinoma. *Science* 319:1096–1100.

Table S2. Primer sequences

Primer	Sequence
DNA sequencing of control tissues	
MCV.LT.P1.F1	AGTCATTGCTCCTCTGCT
MCV.LT.P1.R1	ATTGGGTGTGCTGGATTCTC
MCV.LT.P1.F2.HindIII	CCAAGCTTTTCTCCTCTGCTSTTTCTG
MCV.LT.P1.R2	TTGGTGGTCTCCTCTCTGCT
MCV.LT.P2.F1	TGGGTATGGGTCTTCTCAG
MCV.LT.P2.R1	GCTTGTTGGCAAATGGTTTT
MCV.LT.P2.F2	GCTTCAGACTCCAGTCCAG
MCV.LT.P2.R2	TGGCAAATGGTTTTCTGAGAT
MCV.LT.P3.F1	CCATTTCTTGCCAAAAGTG
MCV.LT.P3.R1	GCCCCAGAAAAACAAACACA
MCV.LT.P3.F2	CAGATCTCGCCTCAAACCTC
MCV.LT.P3.R2.XhoI	CCGCTCGAGTGAAGCAGATGCCTTTATTGA
DNA replication assay	
Ori.5074.Xho(S)	CTCGAGAGCAATTTACCAATATTGGCC
Ori.270.EcoV(AS)	GATATCGCCATAACAATTAGGAGCAATCT
RACE analysis of T antigen*	
GeneRacer 5' primer	CGACTGGAGCACGAGGACACTGA
GeneRacer 5' nested primer	GGACACTGACATGGACTGAAGGAGTA
GeneRacer 3' primer	GCTGTCAACGATACGCTACGTAACG
GeneRacer 3' nested primer	CGCTACGTAACGGCATGACAGTG
M1L	TTCTCTTGCAATTTTGAAGGGGACTTAC
M3	TTTCAGGCATCTTATCACTCC
M2L	AGCAGGCATGCCTGTGAATTAGGATGTA
M4	TTTTTGCTTACCTTCTGCACT
350.RACE.F	TTTCCTTGGGAAGAATATGGAACCTTAAAGGA
350.RACE.R	TAATACAAGCGCACTTAGAATCTCTAAGTTGCT
350.t.nested.F	GCTAGATTTTGCAAGGCTCTG
350.contig.1R	CCAGGACCTCTGCAAAATCT
350.contig.2R	ATATAGGGGCTCGTCAACC
350.contig.3R	GGGAGGAAAGTGATTCACTG
350.contig.4R	AAATGGCAAACAACCTACTGTT
350.contig.5R	GAGCCTTGTGAGGTTTGAAG
350.contig.6R	GCAGCAAAGCTTGTTTTTCC
350.contig.7R	TGTATCAGGCAAGCACAAA
350.contig.8R	TTACCCAAAGCCTCTGTGG
350.contig.9R	TCAGACAGGCTCTCAGACTCC
350.FLT.XhoI.R	CCGCTCGAGCGTGGGCTATTAGACAGGCTCT
350.FLT.KpnI.F1	GGGGTACCCAGCTCATTTGCTCTCTGCT
350.FLT.KpnI.F2	GGGGTACCCAGCTCATTTGCTCTCTGCTGTTTCT
Cloning of MCV T antigen	
MCV.EcoRV(S)	CCGATATCATGGATTTAGTCTCTAAATAGG
MCV.XhoI(AS)	GGGCTCGAGTATTGAGAAAAAGTACCAGAATCTTGGG
MCV.350.XhoI(S)	GGGCTCGAGTAATCTGAAAAGTACCAGAATCTTGGG
MCV.339.EcoRV(AS)	CCGATATCATGGATTTAGTCTCTAAACAGG
MCV.339.XhoI(AS)	GGGCTCGAGTACATAGCATTCTGTCTCTGGTCAT
Probes in Northern blotting	
MCV350(196–429).S	ATGGATTTAGTCTCTAAATAGGAAAG
MCV350(196–429).AS	CTCATCAAACATAGAGAAGTACC
MCV350(430–756).S	GTTAGTACAAAATTTCTTGGGAAG
MCV350(430–756).AS	CTAGAAAAGGTGCAGATGCAGTAAGC
MCV350(861–1622).S	CACAGCCAGAGCTCTCTCTGGG
MCV350(861–1622).AS	GGTGAAGGAGGAGGATATGTATTCC
MCV350(1623–2777).S	GGAGTGAATAAGATGCCTGAAATG
MCV350(1623–2777).AS	GCATTTCTGTCTGGTCAATTTCCAGC
MCV350(2778–3080).S	GCAAATCTAAGAGATTCCCTGGATC
MCV350(2778–3080).AS	TTATTGAGAAAAAGTACCAGAATCTTGGG
LXCXE mutagenesis	
MCV.T.E216K(S)	GGATCTCTTCTGCGATAAATCACTTCTCTCC
MCV.T.E216K(AS)	GGAGGAAAGTATTTATCGCAGAAGAGATCC

\*RACE results identify the following splicing sites (Fig. 1) according to the MCV prototype (EU375803): T1 exon 1 (196–429), exon 2 (861–3080); T2 exon 1 (196–777), exon 2 (861–3080); T3 exon 1 (196–777), exon 2 (861–1622), exon 3 (2778–3080); T4 exon 1 (196–429), exon 2 (861–1622), exon 3 (2778–3080).