Table S1. Homology between the respective E9, A20 and D4 proteins of MCV and VV.

	Identity	Similarity
E9	53 %	72 %
A20	30 %	71 %
D4	55 %	82 %

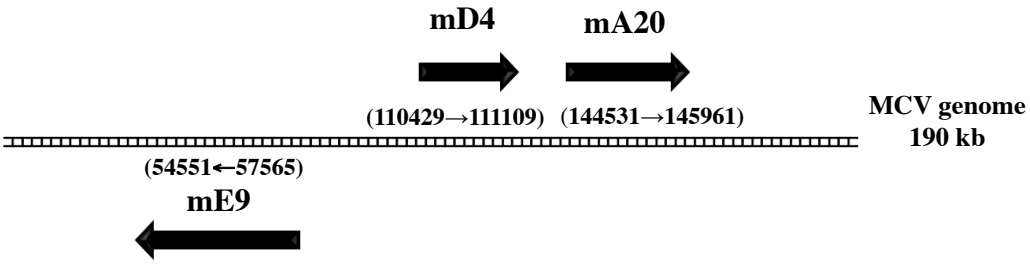

FIG S1 The location of D4, A20 and E9 genes on the MCV genome. Indicated are the orientations (arrows) and the locations of the nucleotide coding regions (numbers) for the mD4 and mA20 processivity factors and the mE9 DNA polymerase on the MCV genome.

A

```
mD4    1 MLRERALRAAPHVLRYHEDWEPVAEPLADAYAEVAPWLLRDRTEPAPERFFRQLELPLRD
vD4    1 MNSVTVSH-APYTITYHDDWEPVMSQLVEFYNEVASWLLRDETSPIPDKFFIQLKQPLRN

mD4   61 KRVCIVGIDPYPEGATGVPFESPDFSKKTARALAAAAARAAEHGGCRRVSAYRNYDFRGV
vD4   60 KRVCVCGIDPYPKDGTGVPFESPNFTKKSIKEIASSISRLTG------VIDYKGYNLNII

mD4  121 QGVLAWNYYLSCRRGETKSHAMHWERIARMLLAHIARFVRVFYFLGRSDFGGVRAKLTAP
vD4  114 DGVIPWNYYLSCKLGETKSHAIYWDKISKLLLQHITKHVSVLYCLGKTDFSNIRAKLESP

mD4  181 VTLLVGYHPAARGGQFESERTLEILNVLLELHGLAPVDWAQGFVPL 226
vD4  174 VTTIVGYHPAARDRQFEKDRSFEIINVLLELDNKAPINWAQGFIY 218
```

B

FIG S2 (A) Alignment of mD4 and vD4. Identical amino acids are shaded. Missing amino acids are denoted by dashes. The C-terminal residues 167-180 and 191-206 of vD4 (underlined) are important for interacting with vA20. (B) Superimposition of mD4 predicted structure onto vD4 crystal structure. mD4 structure was generated by homology modeling using the SWISS-MODEL (1).

REFERENCE

1. **Arnold K, Bordoli L, Kopp J, Schwede T.** 2006. The SWISS-MODEL workspace: a web-based environment for protein structure homology modelling. Bioinformatics **22:**195-201.