Figure S1

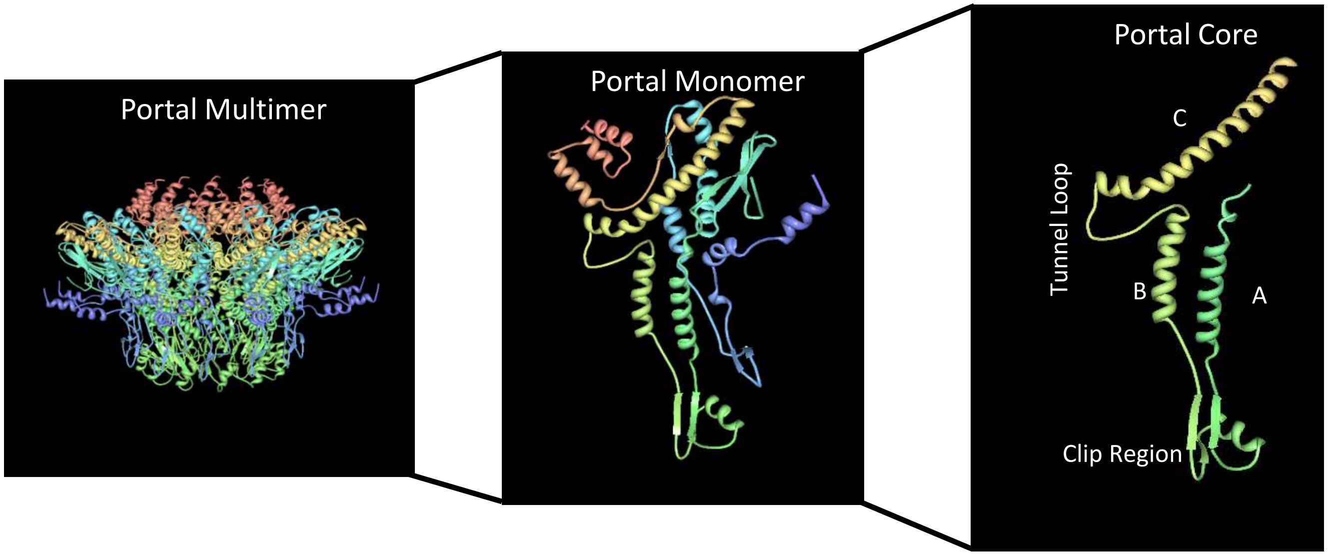

Fig. S1. The bacteriophage SPP1 portal protein. The three images are derived from crystallographic data used to determine structure of the SPP1 portal protein. The left panel represents the fully assembled portal dodecamer, the center panel shows one monomer of the portal multimer, and the right panel shows a highly conserved portal core region found in the ds DNA viruses. The core includes the major alpha helices, A, B, and C, and clip and tunnel loop regions thought to interact with ds DNA.

(1) PDB ID: 2JES, Lebedev A.A., Krause M.H., Isidro A.L., Vagin A.A., Orlova E.V., Turner J., Dodson E.J., Tavares P., Antson A.A. Structural framework for DNA translocation via the viral portal protein. EMBO J. 2007 Apr 4;26(7):1984-94.

(2) Images from the RCSB PDB (www.pdb.org) of PDB ID 2JES (Lebedev A.A., Krause M.H., Isidro A.L., Vagin A.A., Orlova E.V., Turner J., Dodson E.J., Tavares P., Antson A.A. Structural framework for DNA translocation via the viral portal protein. EMBO J. 2007 Apr 4;26(7):1984-94).

(3) Images of PDB ID 2JES (Lebedev A.A., Krause M.H., Isidro A.L., Vagin A.A., Orlova E.V., Turner J., Dodson E.J., Tavares P., Antson A.A. Structural framework for DNA translocation via the viral portal protein. EMBO J. 2007 Apr 4;26(7):1984-94) created with Protein Workshop (Moreland J.L., Gramada A., Buzko O.V., Zhang Q., Bourne P.E. (2005) The Molecular Biology Toolkit (MBT): a modular platform for developing molecular visualization applications. BMC Bioinformatics 6:21).

(4) The RCSB PDB can be found at www.pdb.org (Berman H.M., Westbrook J., Feng Z., Gilliland G., Bhat T.N., Weissig H., Shindyalov I.N., Bourne P.E. (2000). The Protein Data Bank Nucleic Acids Research, 28:235-242) and www.wwpdb.org (Berman H.M., Henrick K., Nakamura H. (2003). Announcing the worldwide Protein Data Bank Nature Structural Biology 10 (12):98).

Figure S2

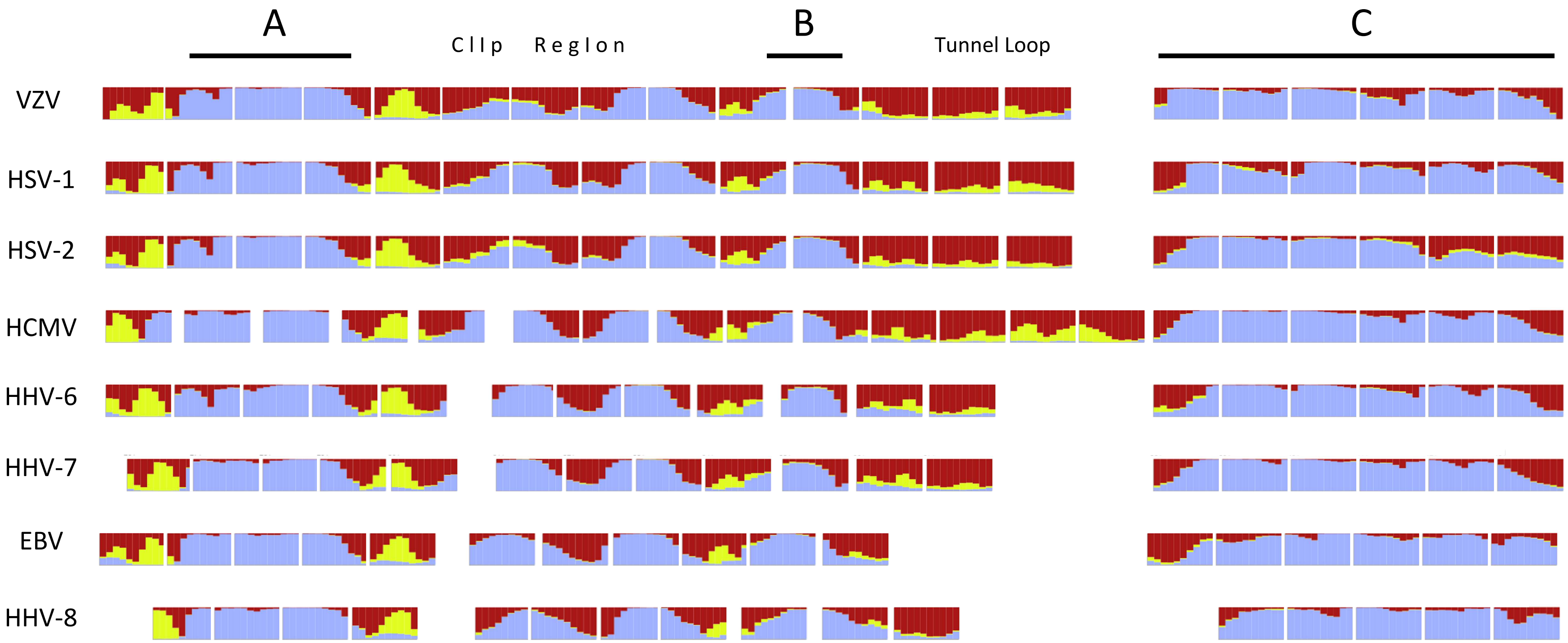

Fig. S2. The conserved core of Herpesvirus family portal proteins. The Raptor X webserver was used to structurally model the core portal protein region for the 8 human herpesviruses. This approximated core ranged from 160 to 200 amino acids. Core regions are indicated at the top of the figure and correspond to those labeled in the last panel of Fig. S1. Key: alpha helix (light blue), beta sheet (red), or loop / unstructured (yellow).

(1) Morten Källberg, Haipeng Wang, Sheng Wang, Jian Peng, Zhiyong Wang, Hui Lu & Jinbo Xu. Template-based protein structure modeling using the RaptorX web server. Nature Protocols 7, 1511–1522, 2012.