

Figure S1. Genomic organization of EserPV1, EserPV2, EserPV3 and RferPV1. Boxes correspond to the different open reading frames. Information on molecular mass in kDa and theoretical isoelectric point of the predicted proteins, as well as the nucleotide positions of the corresponding start and stop codons are included. Location of different putative regulatory elements and amino acid motifs listed in the inset is depicted.

Figure S2. E2BS pattern in Lambda+Mu-PVs. (A) Consensus putative E2 binding site (E2BS) sequences located within the NCR1 of Lambda+Mu-PVs **(B)** Consensus putative E2 binding site (E2BS) sequences located within the L2 gene of Lambda+Mu-PVs. Sequence variations are indicated in the legend. Nucleotide changes are highlighted in bold.

Figure S3. E2BS pattern in bat PVs. Consensus putative E2 binding site (E2BS) sequences located within the NCR1 of all bat PVs. Sequence variations are indicated in the legend. Nucleotide changes are highlighted in bold.

Figure S4. Bayesian nucleotide phylogenetic reconstruction for the E1-E2-L2-L1 concatenation. Branch lengths are drawn to scale, with the scale bar indicating the genetic distance in substitutions per site. Numbers above the branches indicate Bayesian posterior probabilities and ML bootstrap support values. Maximum values are indicated with an asterisk (*). Values below 0.50 and 50, respectively, are indicated with a dash (-). Colour code highlights the four PV crown groups: Red, Alpha+Omikron-PVs; green, Beta+Xi-PVs; blue, Delta+Zeta-PVs; ochre, Lambda+Mu-PVs. Viruses, whose detailed phylogenetic relationships could not be disentangled, are labelled in black. Silhouettes represent the infected host. Taxonomic classification of both hosts (host order) and viruses (PV genera) are included. Branches corresponding to bat PVs are highlighted with a grey dot. Branches corresponding to clades or PVs that contain an E2-L2 and may thus reflect individual recombination events region are highlighted with a black star. The novel bat PVs described here are highlighted with black arrows.

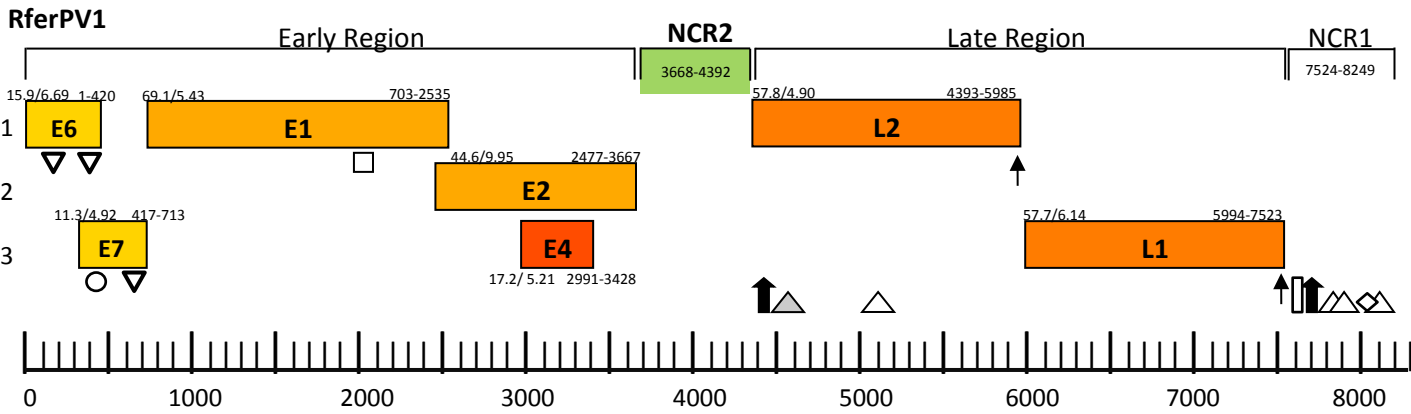
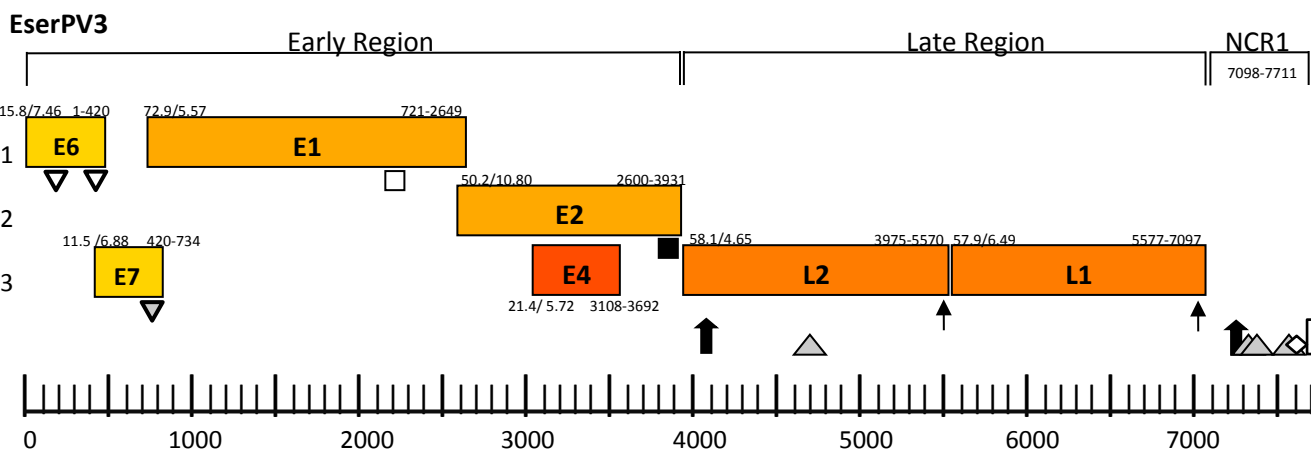
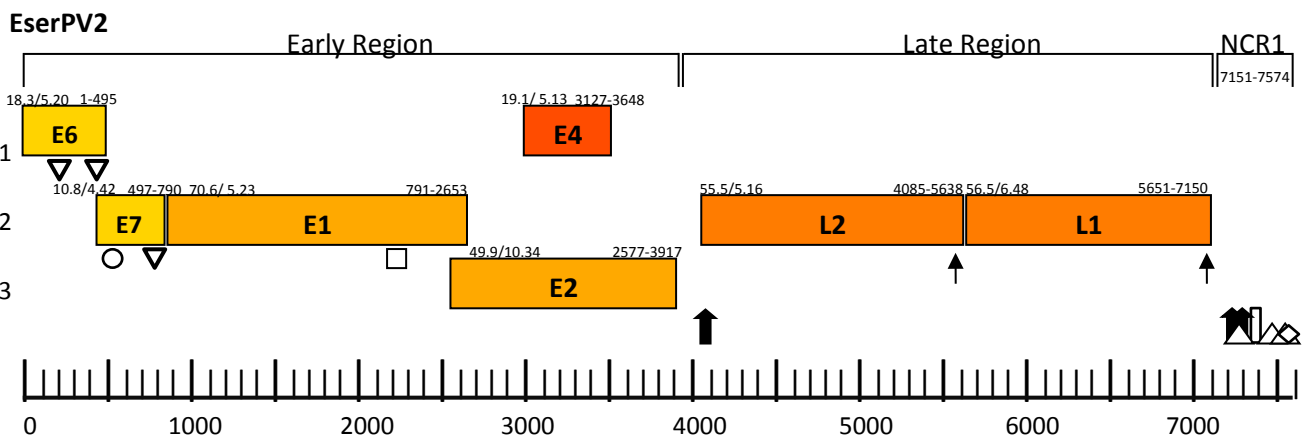
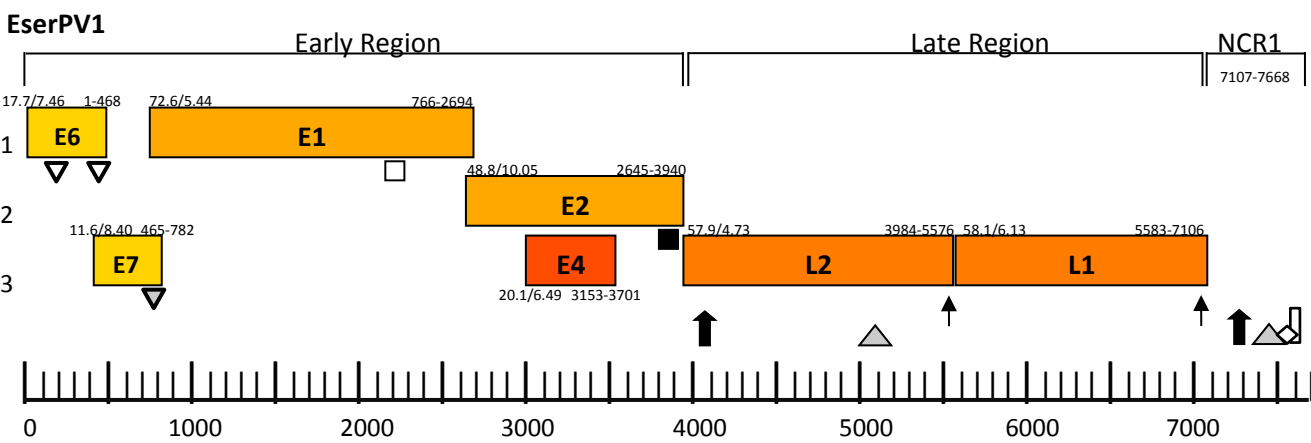
Figure S5. Phylogenetic positions assigned to E1, E2, L2 and L1 PV-like sequences. Colour code highlights the four PV crown groups: Red, Alpha+Omikron-PVs; green, Beta+Xi-PVs; blue, Delta+Zeta-PVs; ochre, Lambda+Mu-PVs. PV-like sequences were labelled according to the accession numbers provided by Baker and coworkers (2013). An additional tag was added to indicate the corresponding gene. Terminal taxa labelled in grey correspond to the PVs used to build the reference phylogeny. The colour of the bat PV-like sequences labels matches the PV crown group to which they belong.

Figure S6. Phylogenetic positions assigned to the obtained partial E1 and L1 sequences. Colour code highlights the four PV crown groups: Red, Alpha+Omikron-PVs; green, Beta+Xi-PVs; blue, Delta+Zeta-PVs; ochre, Lambda+Mu-PVs. PV sequences were named after the bat species from which they were isolated (EserPV: *E. serotinus*; EisaPV: *E. isabellinus*), followed by the name of the primers with which they were obtained (FAP or CP) and a distinctive number. Branches corresponding to completely sequenced bat PVs are highlighted with a grey dot. The novel bat PVs described here are highlighted with black arrows. Branches corresponding to partial E1 and L1 sequences are highlighted with black dots. Black stars indicate the PVs or PV sequences which have been found in samples with coinfection.

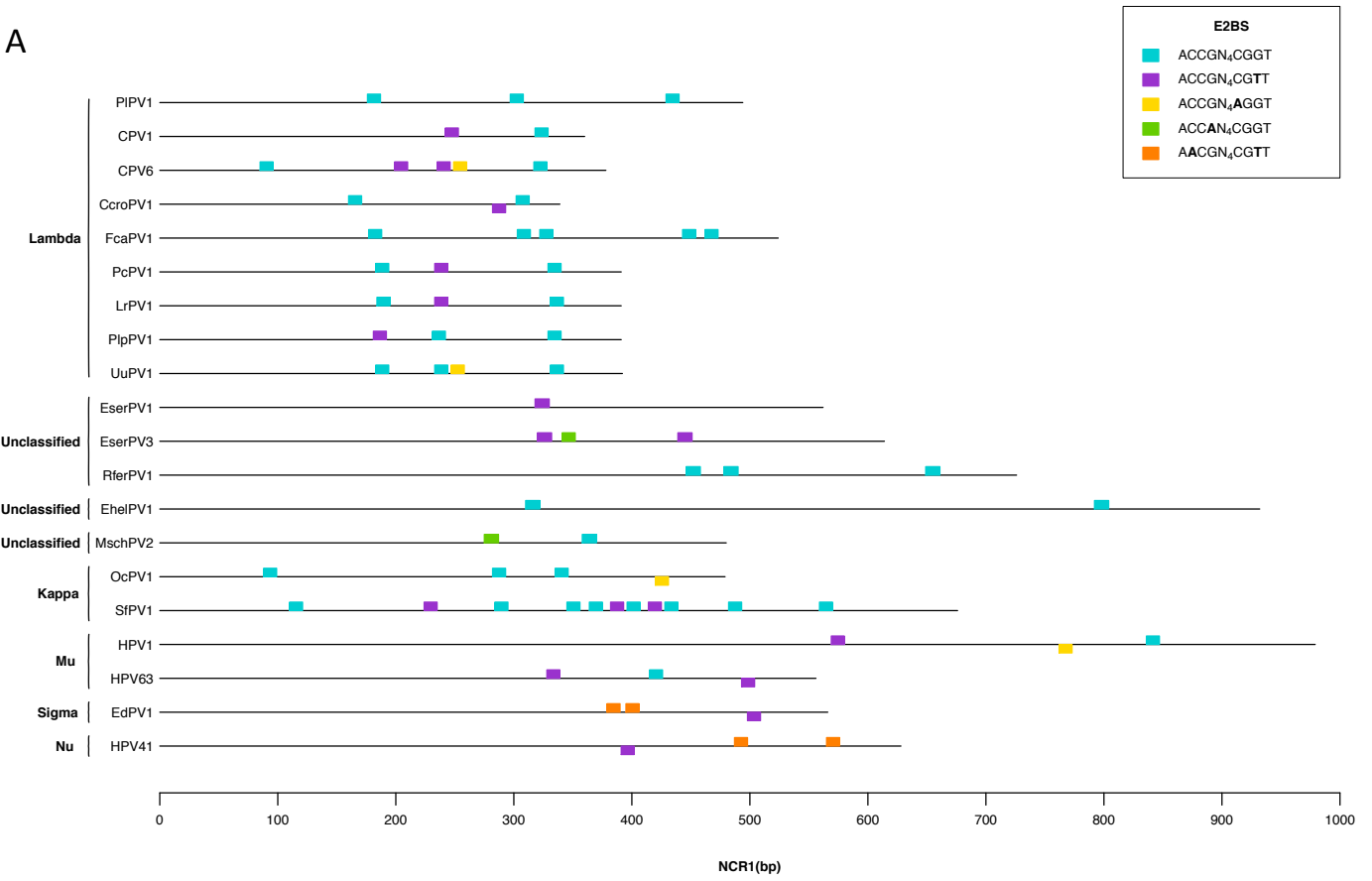
Figure S7. Best-known Maximum-Likelihood phylogenetic tree for the L2L1 concatenate. Branch lengths are drawn to scale, with the scale bar indicating the genetic distance in substitutions per site. Numbers above the branches indicate the ML bootstrap support values (nucleotide | amino acid). Maximum bootstrap support values are represented with an asterisk (*). Bootstrap support values below 50 are indicated with a dash (-). Colour code highlights the four PV crown groups: Red, Alpha+Omikron-PVs; green, Beta+Xi-PVs; blue,

Delta+Zeta-PVs; ochre, Lambda+Mu-PVs. Papillomaviruses, whose detailed phylogenetic relationships could not be disentangled, are labelled in black. Silhouettes represent the infected hosts. Taxonomic classification of both hosts (host order) and viruses (PV genera) are included. Branches corresponding to bat PVs are highlighted with a grey dot. Branches corresponding to clades or PVs that contain an E2-L2 region are highlighted with a black start. BCPVs, infecting *Bettongia penicillata*, are highlighted with a black arrow.

▼ CX₂CX₂₉CX₂C ▼ CX₂CX₃₀CX₂C ○ LXCXE □ GX₄GKS ■ LX₆LX₆LX₆L ↑ NLS ↑ POLYADENYLATION SITE □ TATA box ◇ E1BS △ E2BS ▲ E2BS*



A



B

