

Supplementary File

Molecular and phylogenetic characterisation of a highly divergent novel parvovirus (Psittaciform chaphamaparvovirus 2) in Australian *Neophema* parrots

Subir Sarker^{a*}

^a Department of Physiology, Anatomy and Microbiology, School of Life Sciences, La Trobe University, Bundoora, VIC 3086, Australia

*** Author for correspondence:** Dr Subir Sarker, Department of Physiology, Anatomy and Microbiology, School of Life Sciences, La Trobe University, Bundoora, VIC 3086, Australia, email: s.sarker@latrobe.edu.au; phone: +61 3 9479 2317; fax: +61 3 9479 1222.

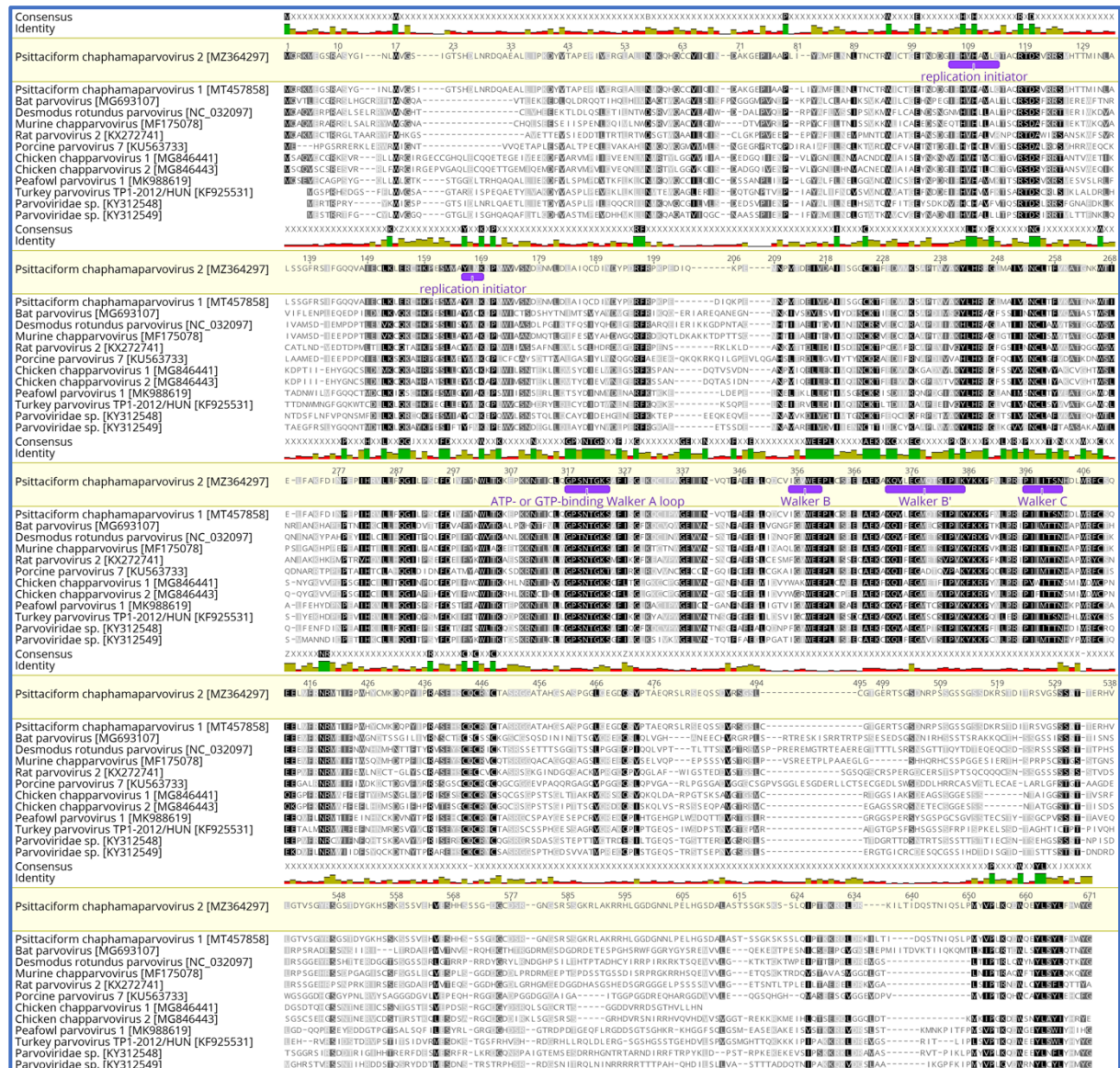


Figure S1. Alignment of the amino acid sequences of the complete NS1 gene under the genus *Chaphamaparvovirus* using MAFFT in Geneious (version 10.2.2) to show the genetic variation between Psittaciform chaphamaparvovirus 2 (PsChPV-2) and other selected parvoviruses. PsChPV-2 was highlighted with yellow background. The top graph represents the mean pairwise sequence identity over all pairs in the column (green: 100% identity; mustard: $\geq 30\%$ and $< 100\%$ identity; red: $< 30\%$ identity).

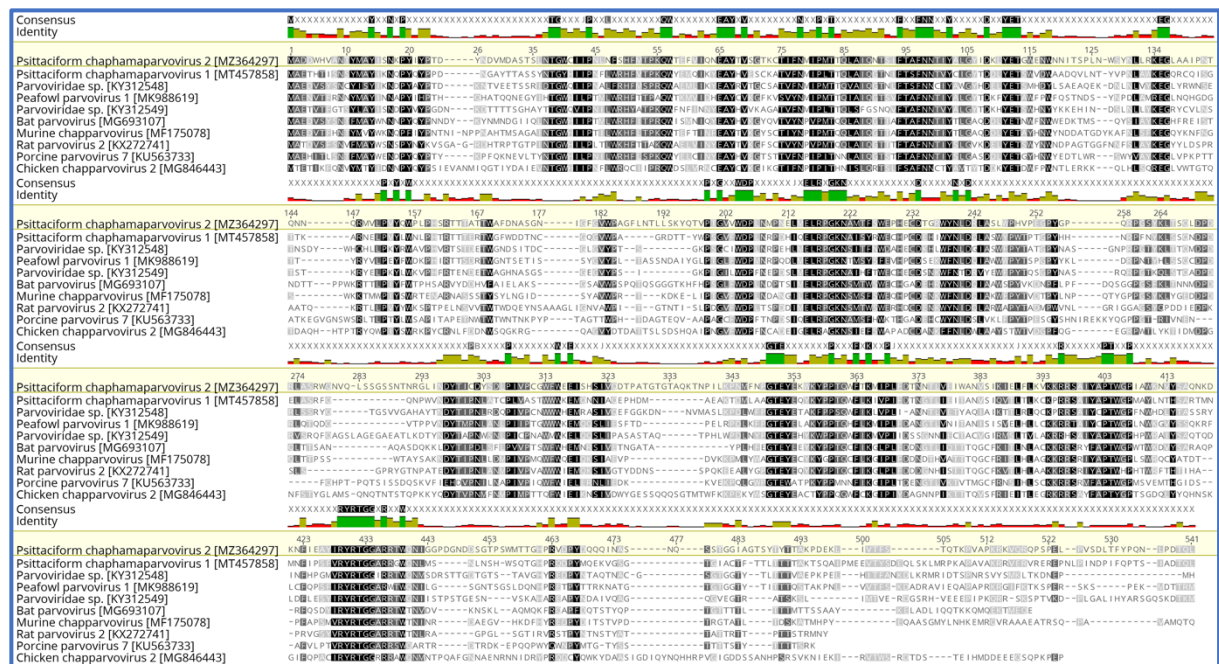


Figure S2. Alignment of the amino acid sequences of the complete VP1 gene under the genus *Chaphamaparvovirus* using MAFFT in Geneious (version 10.2.2) to show the genetic variation between Psittaciform chaphamaparvovirus 2 (PsChPV-2) and other selected parvoviruses. PsChPV-2 was highlighted with yellow background. The top graph represents the mean pairwise sequence identity over all pairs in the column (green: 100% identity; mustard: $\geq 30\%$ and $< 100\%$ identity; red: $< 30\%$ identity).