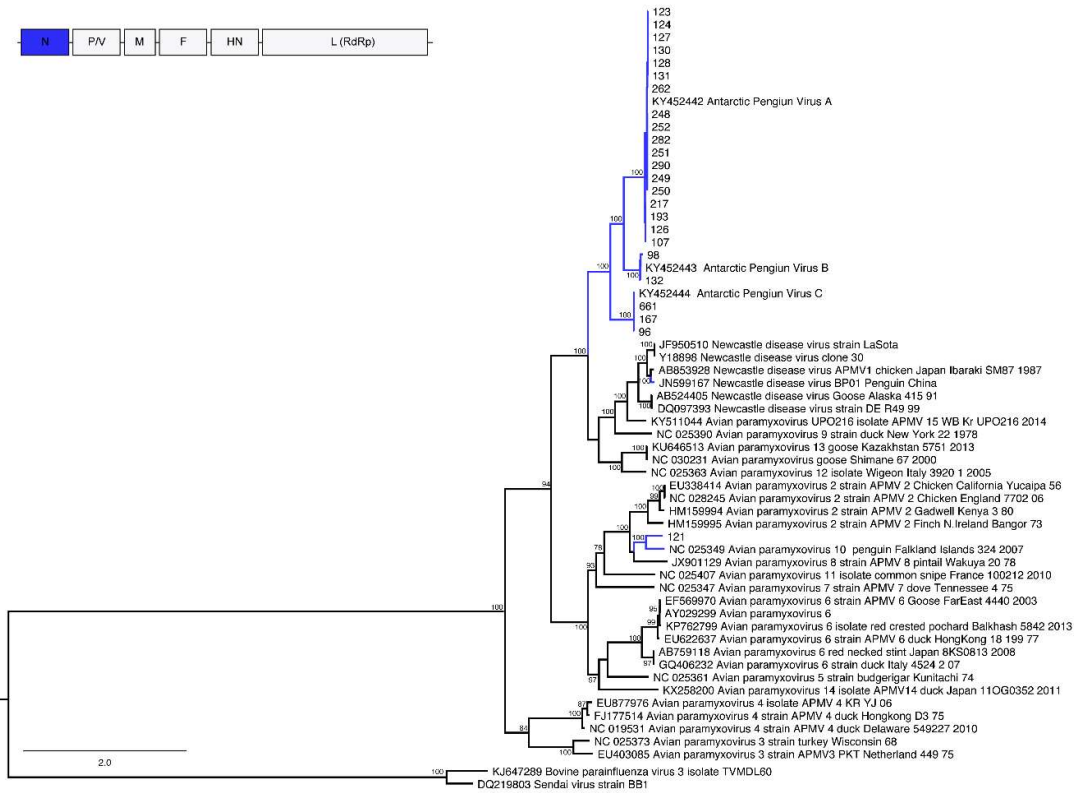


## **Antarctic penguins as reservoirs for a diversity of avian avulaviruses**

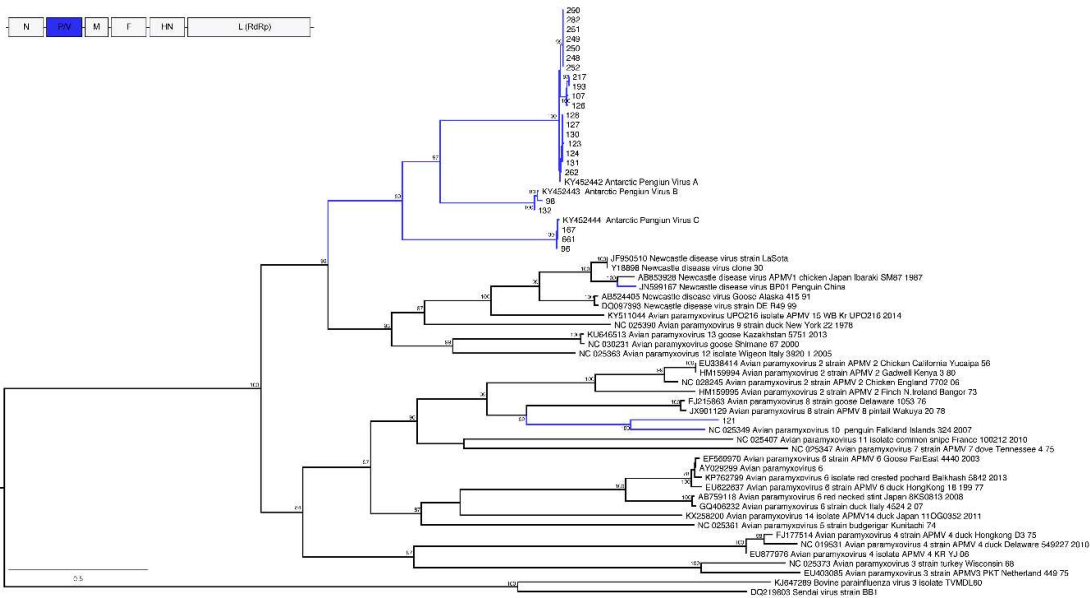
Michelle Wille, Malet Aban, Jing Wang, Nicole Moore, Songhua Shan, John Marshall, Daniel Gonzalez Acuña, Dhanasekaran Vijaykrishna, Jeff Butler, Jianning Wang, Richard Hall, David T. Williams, Aeron C. Hurt

### **Supplementary Files:**

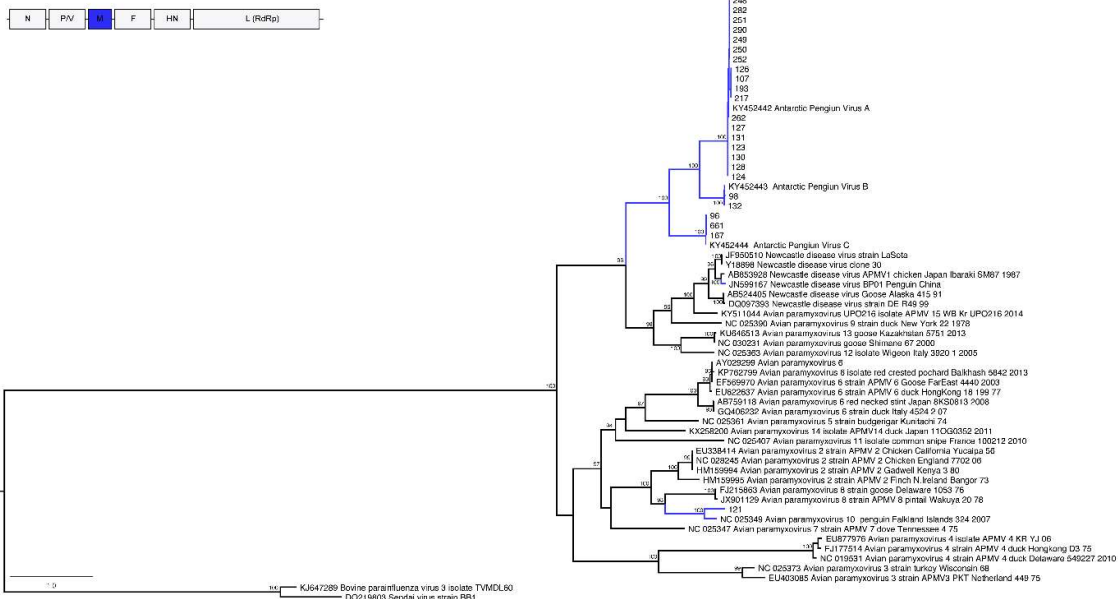
Figure S1-S7



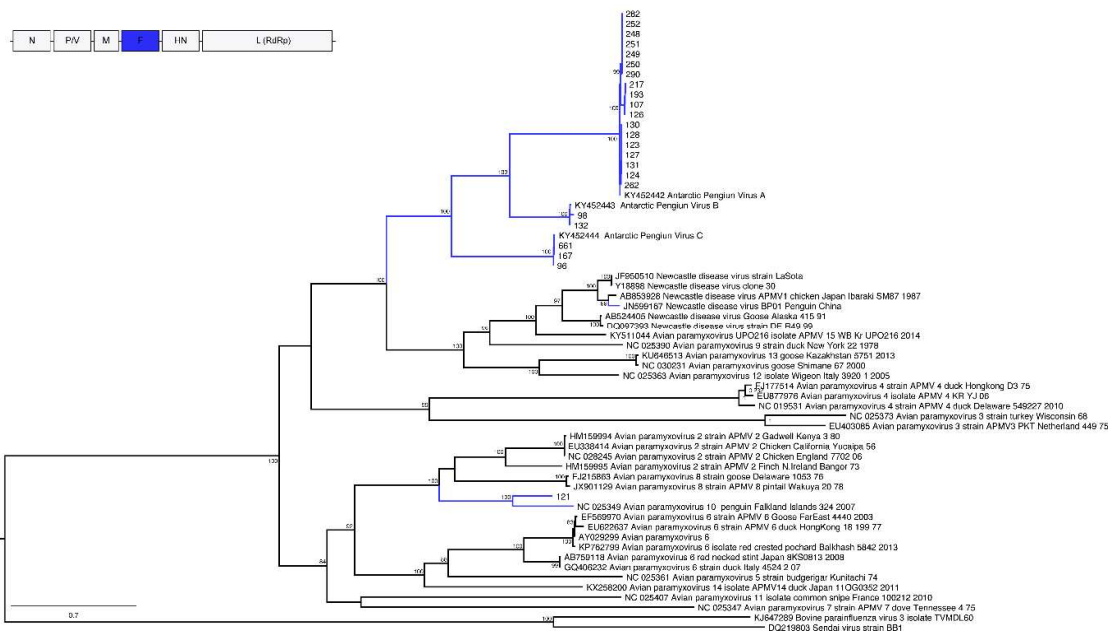
**Figure S1.** Maximum likelihood tree of the N gene of avian avulaviruses. Outgroup is Bovine Parainfluenza and Sendai Virus. Scale bar represents the number of substitutions per site. Blue branches/clades are those associated with penguins.



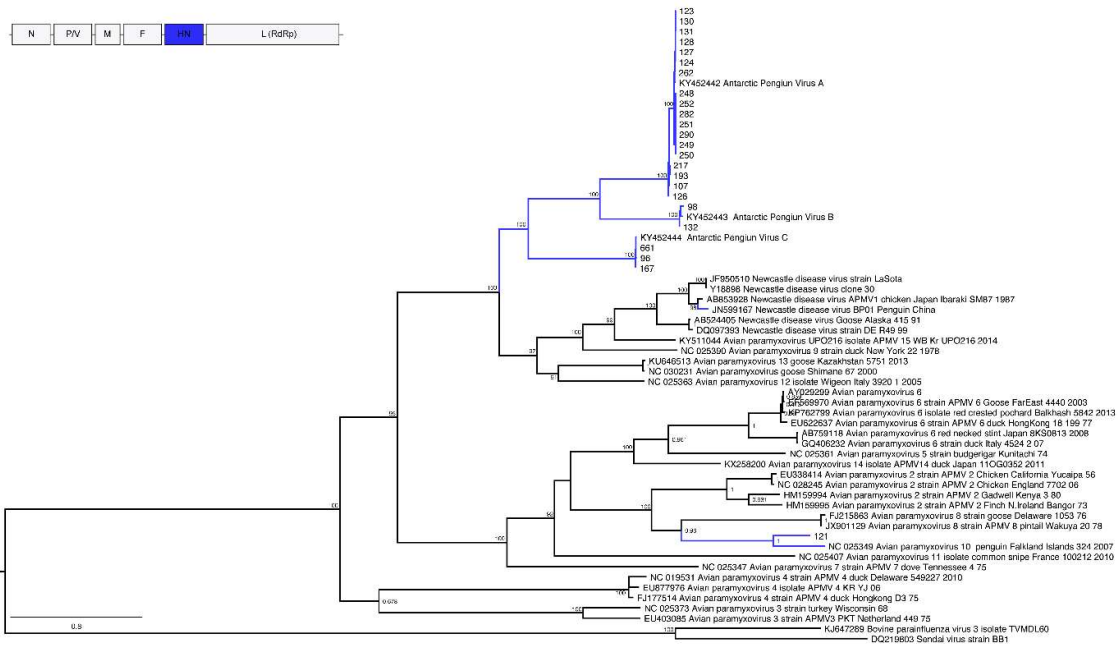
**Figure S2.** Maximum likelihood tree of the P gene of avian avulaviruses. Outgroup is Bovine Parainfluenza and Sendai Virus. Scale bar represents the number of substitutions per site. Blue branches/clades are those associated with penguins.



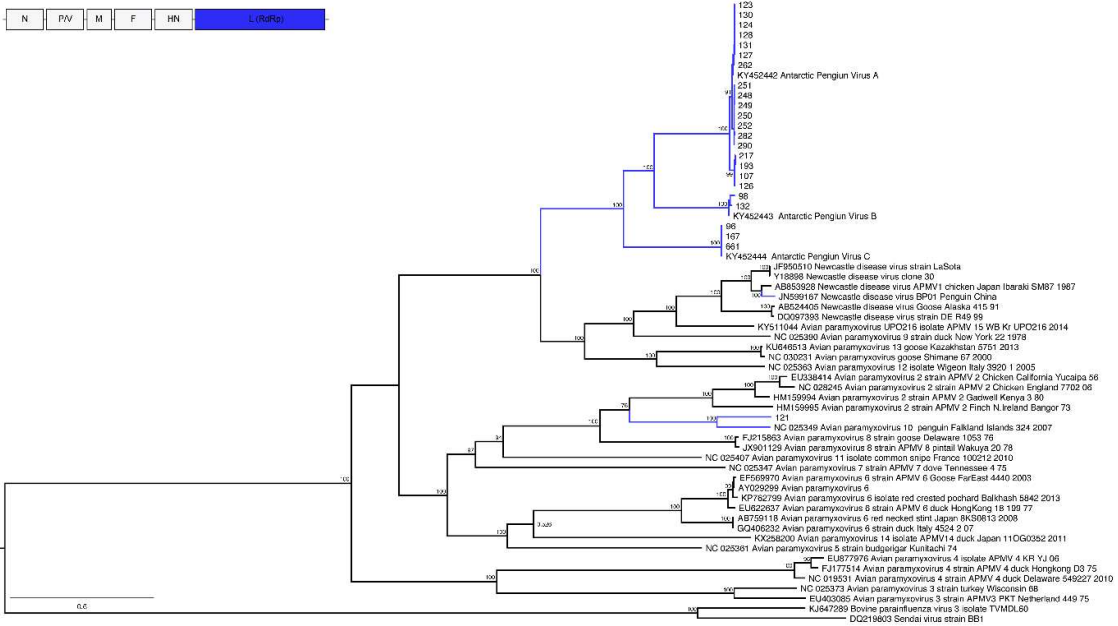
**Figure S3.** Maximum likelihood tree of the M gene of avian avulaviruses. Outgroup is Bovine Parainfluenza and Sendai Virus. Scale bar represents the number of substitutions per site. Blue branches/clades are those associated with penguins



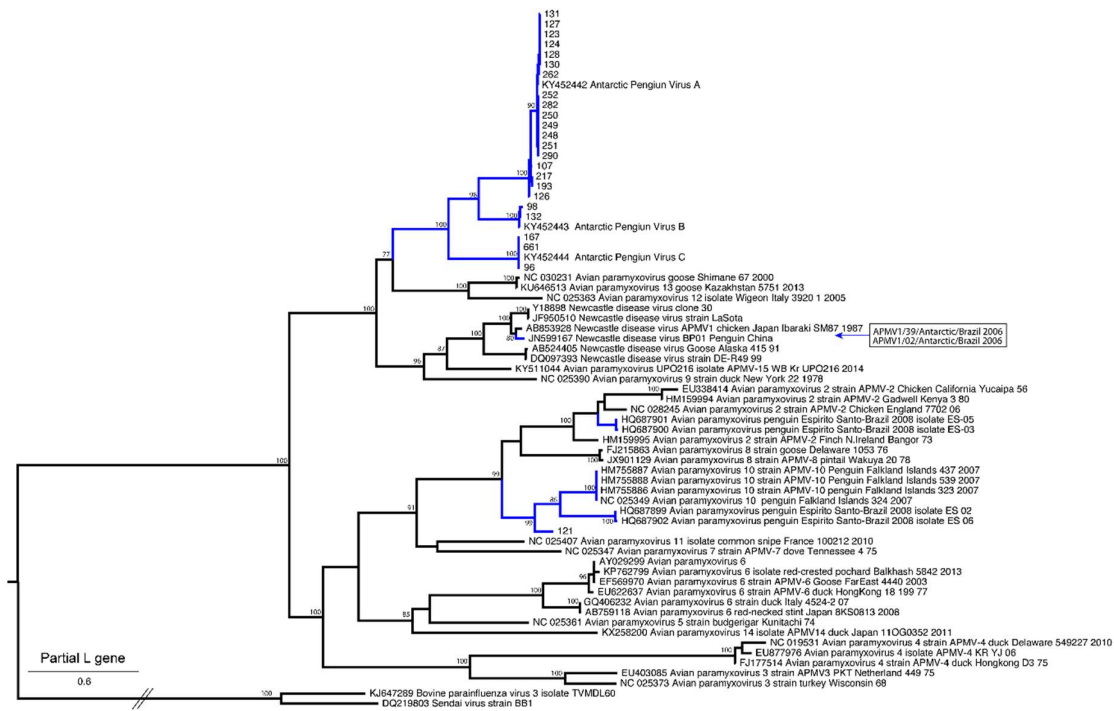
**Figure S4.** Maximum likelihood tree of the F gene of avian avulaviruses. Outgroup is Bovine Parainfluenza and Sendai Virus. Scale bar represents the number of substitutions per site. Blue branches/clades are those associated with penguins



**Figure S5.** Maximum likelihood tree of the HN gene of avian avulaviruses. Outgroup is Bovine Parainfluenza and Sendai Virus. Scale bar represents the number of substitutions per site. Blue branches/clades are those associated with penguins



**Figure S6.** Maximum likelihood tree of the L gene of avian avulaviruses. Outgroup is Bovine Parainfluenza and Sendai Virus. Scale bar represents the number of substitutions per site. Blue branches/clades are those associated with penguins



**Figure S7.** Maximum likelihood of partial L gene of avian avulaviruses. Utilization of partial L gene allows for the inclusion of AAvV-10 and AAvV -2 from penguins in Brazil. Approximate position of AAvV -1 from Antarctica are shown, but not included as available sequences are from the F gene. Outgroup is Bovine Parainfluenza and Sendai Virus. Scale bar represents the number of substitutions per site. Blue branches/clades are those associated with penguin.