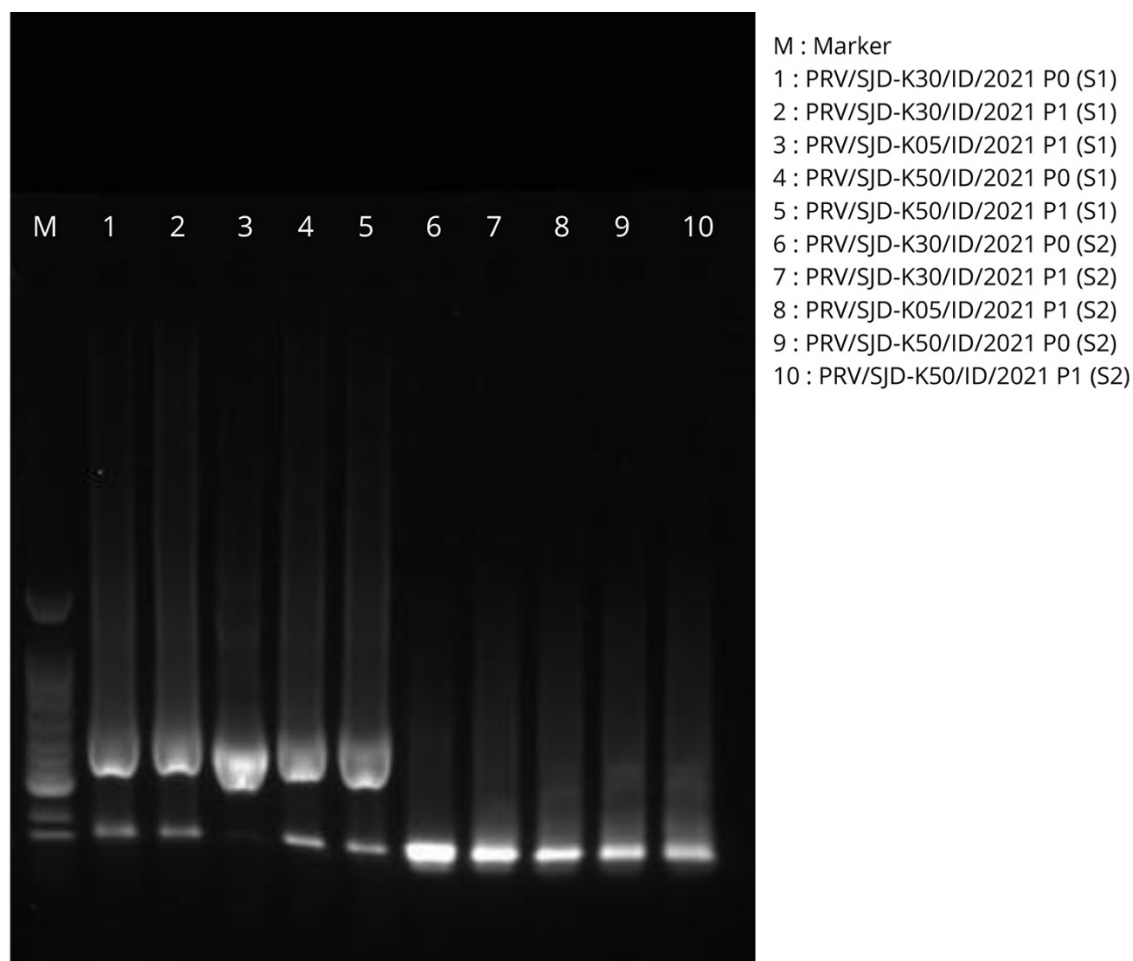
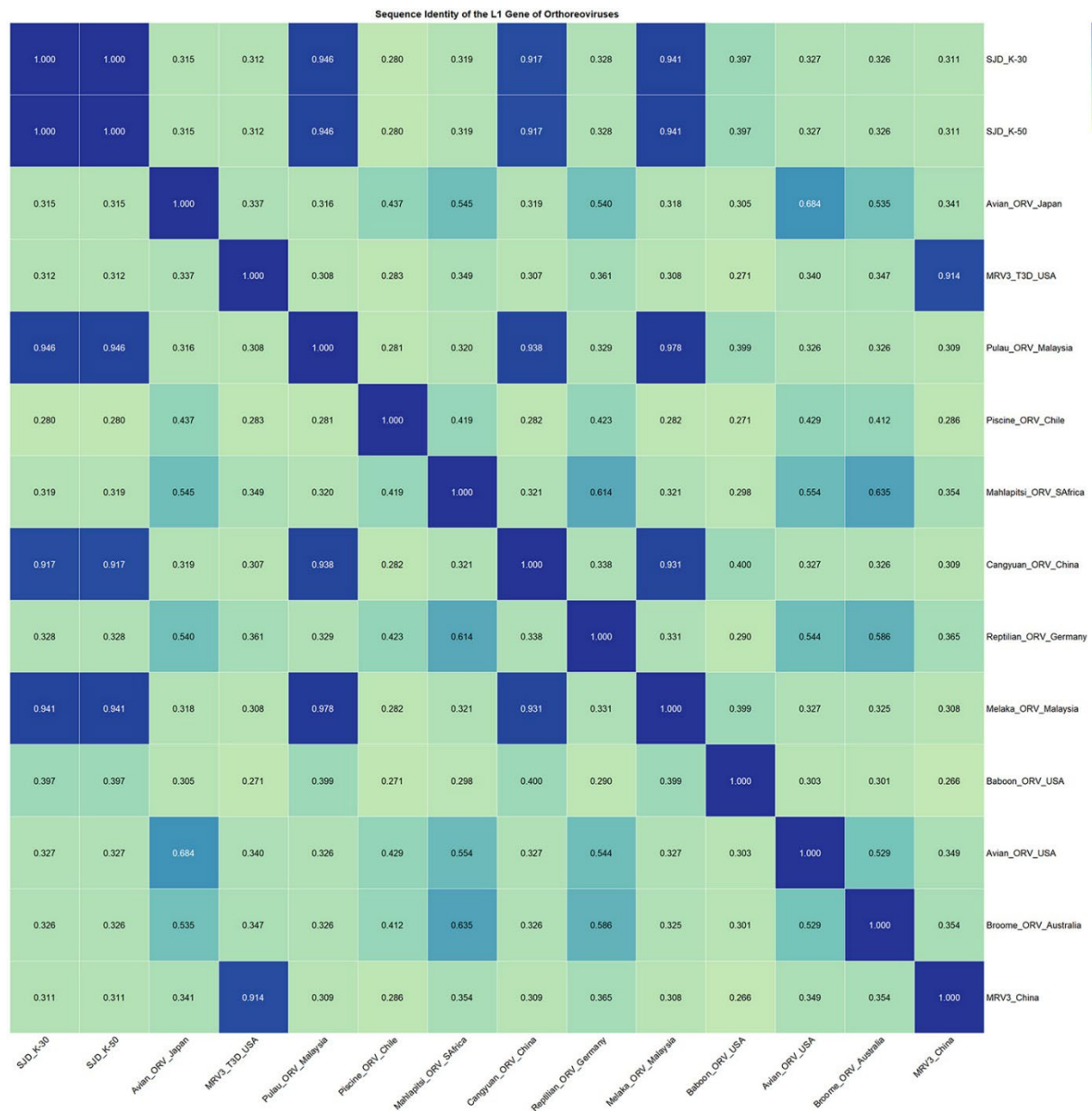


Identification of Zoonotic *Pteropine orthoreovirus* in *Rousettus amplexicaudatus* Fruit Bats, Indonesia

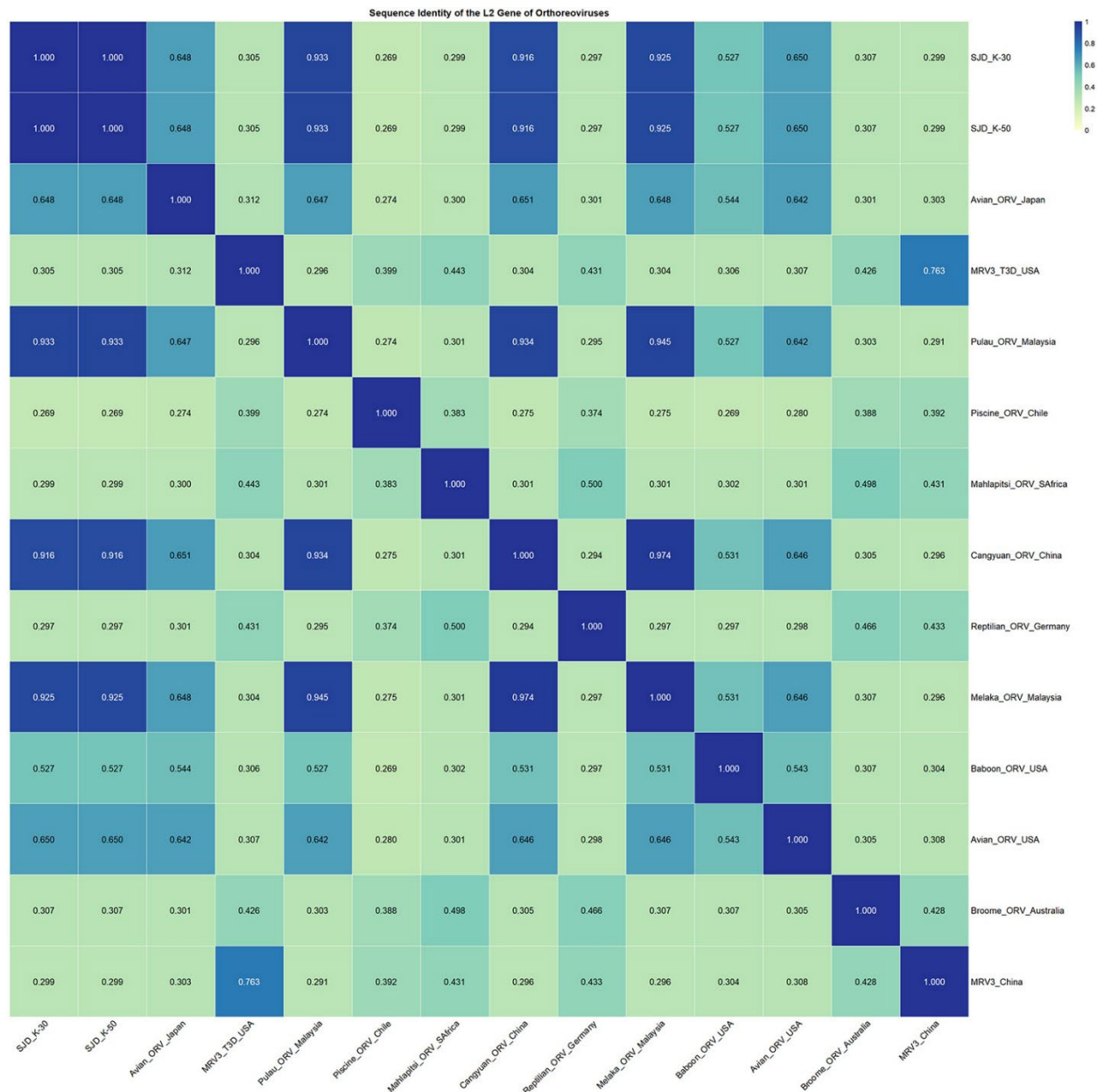
Appendix



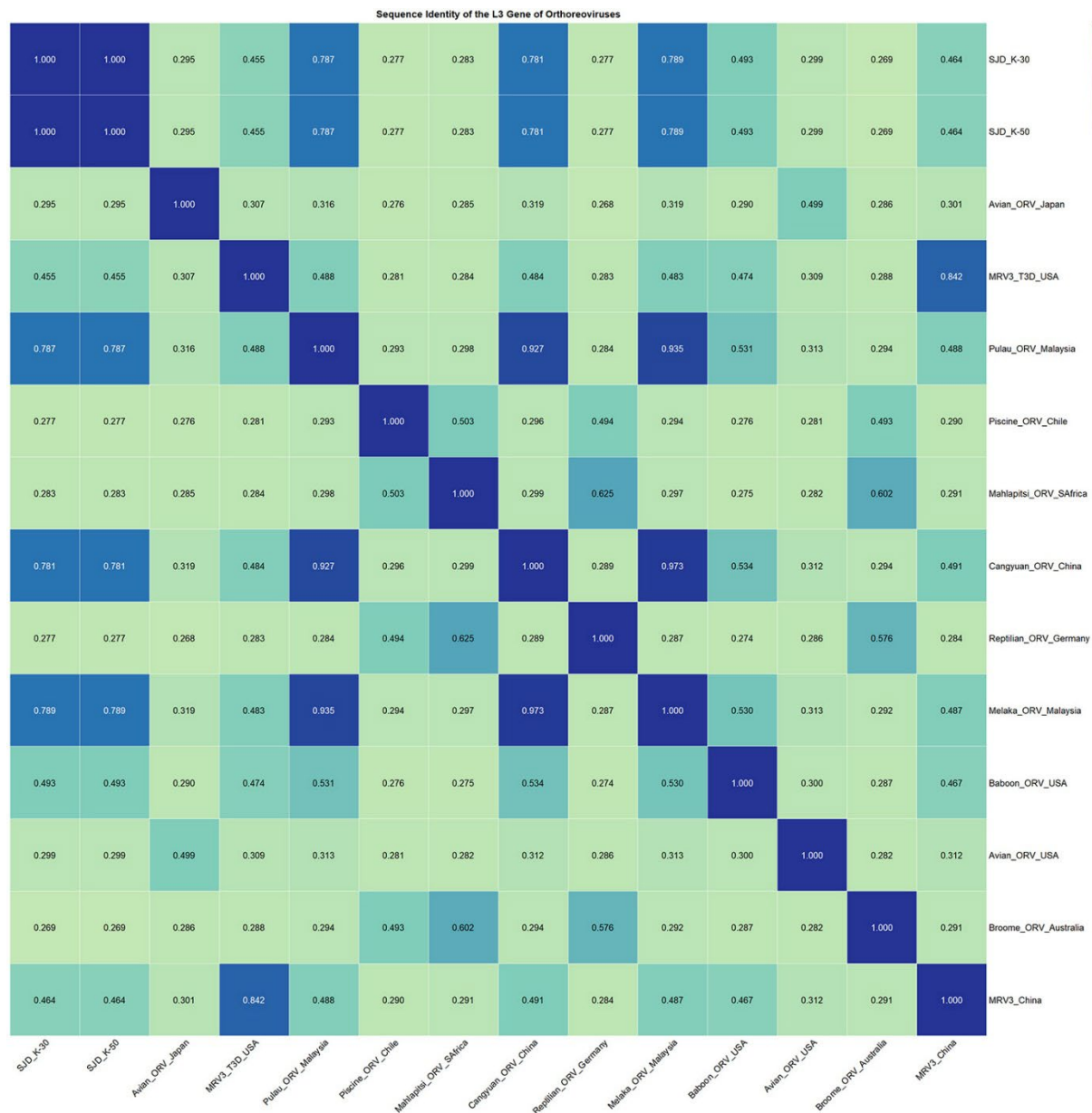
Appendix Figure 1. Reverse transcription PCR amplification results of the S1 and S2 genome segments from orthoreovirus isolates PRV/SJD-K30/ID/2021 and PRV/SJD-K50/ID/2021. PCR was performed as previously described (1) to confirm the presence of the S1 and S2 segments that were not completely recovered through next-generation sequencing analysis. Amplified products with the expected sizes were visualized by agarose gel electrophoresis. S, small.



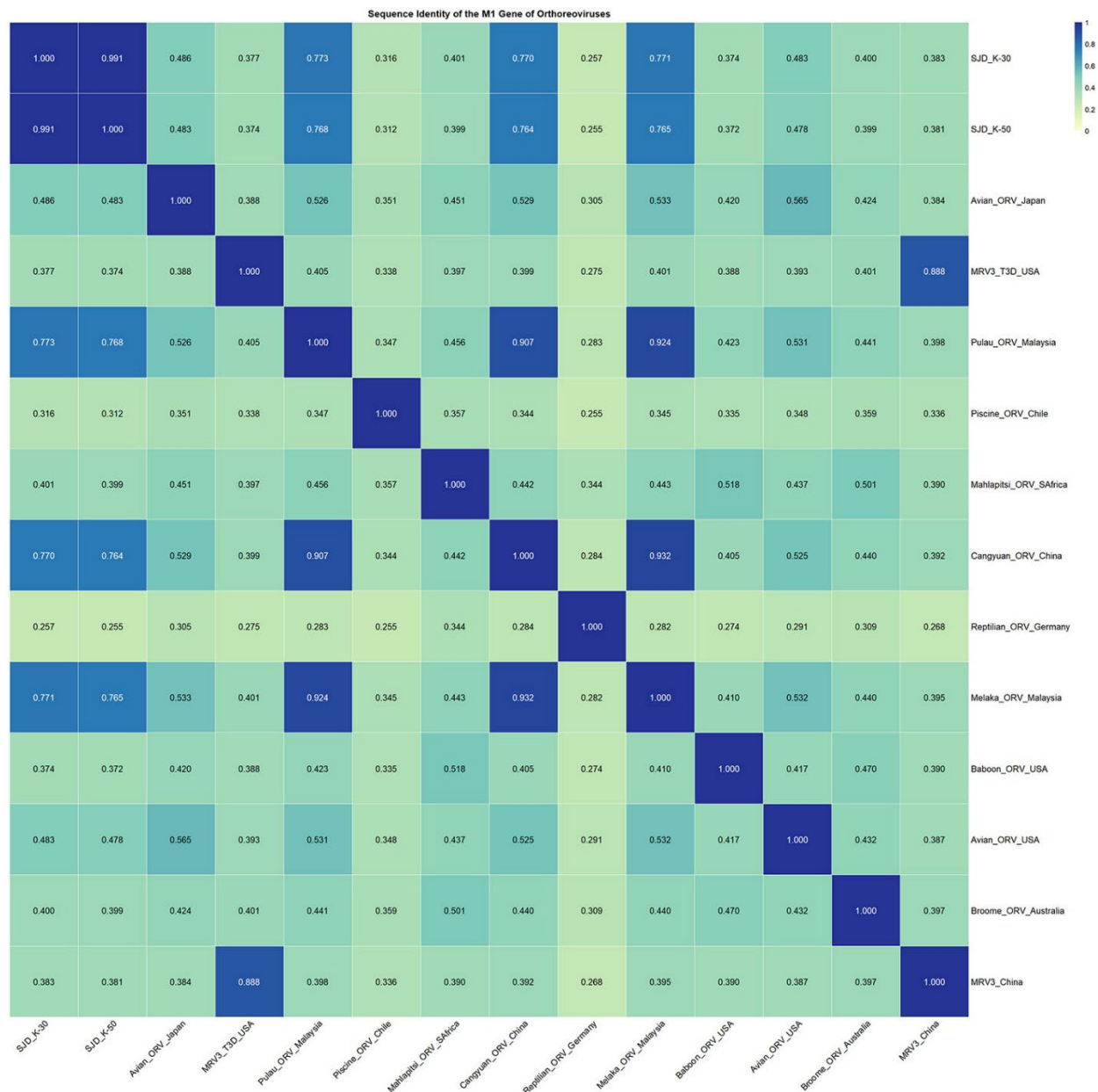
Appendix Figures 2. Heat map showing percentage of pairwise nucleotide sequence identities for L1 segment among orthoreovirus strains. Analysis includes the 2 bat-derived isolates identified in this study, PRV/SJD-K30/ID/2021 and PRV/SJD-K50/ID/2021, obtained from *Rousettus amplexicaudatus* in West Java, Indonesia. Reference sequences are avian, mammal, reptile, piscine, and bat orthoreoviruses retrieved from NCBI Virus (<https://www.ncbi.nlm.nih.gov/labs/virus/vssi>). Values in the squares represent pairwise nucleotide sequence identity (%). Color scale indicates degree of sequence similarity. L, large.



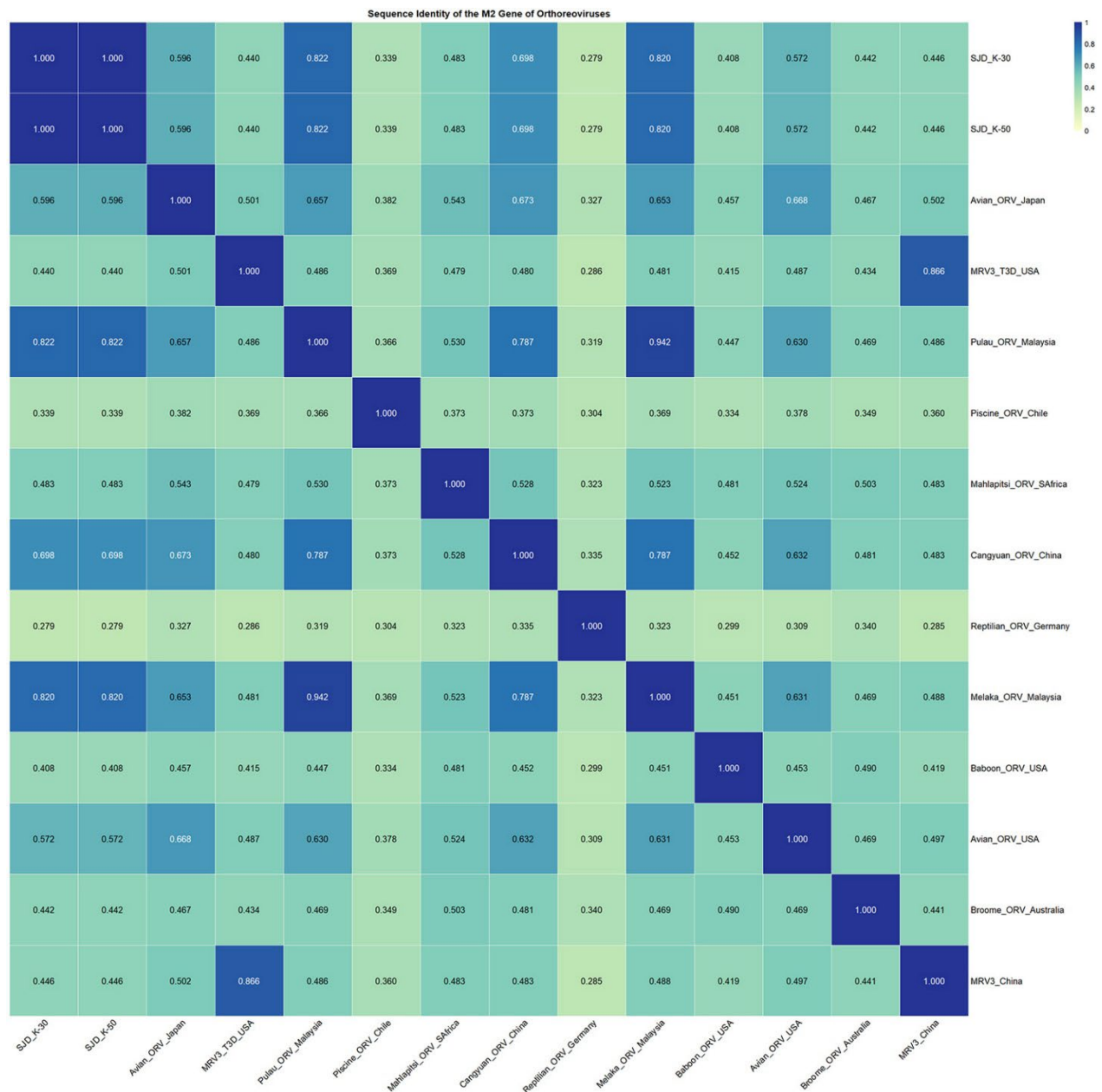
Appendix Figure 3. Heat map showing percentage of pairwise nucleotide sequence identities for L2 segment among orthoreovirus strains. Analysis includes the 2 bat-derived isolates identified in this study, PRV/SJD-K30/ID/2021 and PRV/SJD-K50/ID/2021, obtained from *Rousettus amplexicaudatus* in West Java, Indonesia. Reference sequences are avian, mammal, reptile, piscine, and bat orthoreoviruses retrieved from NCBI Virus (<https://www.ncbi.nlm.nih.gov/labs/virus/vssi>). Values in the squares represent pairwise nucleotide sequence identity (%). Color scale indicates degree of sequence similarity. L, large.



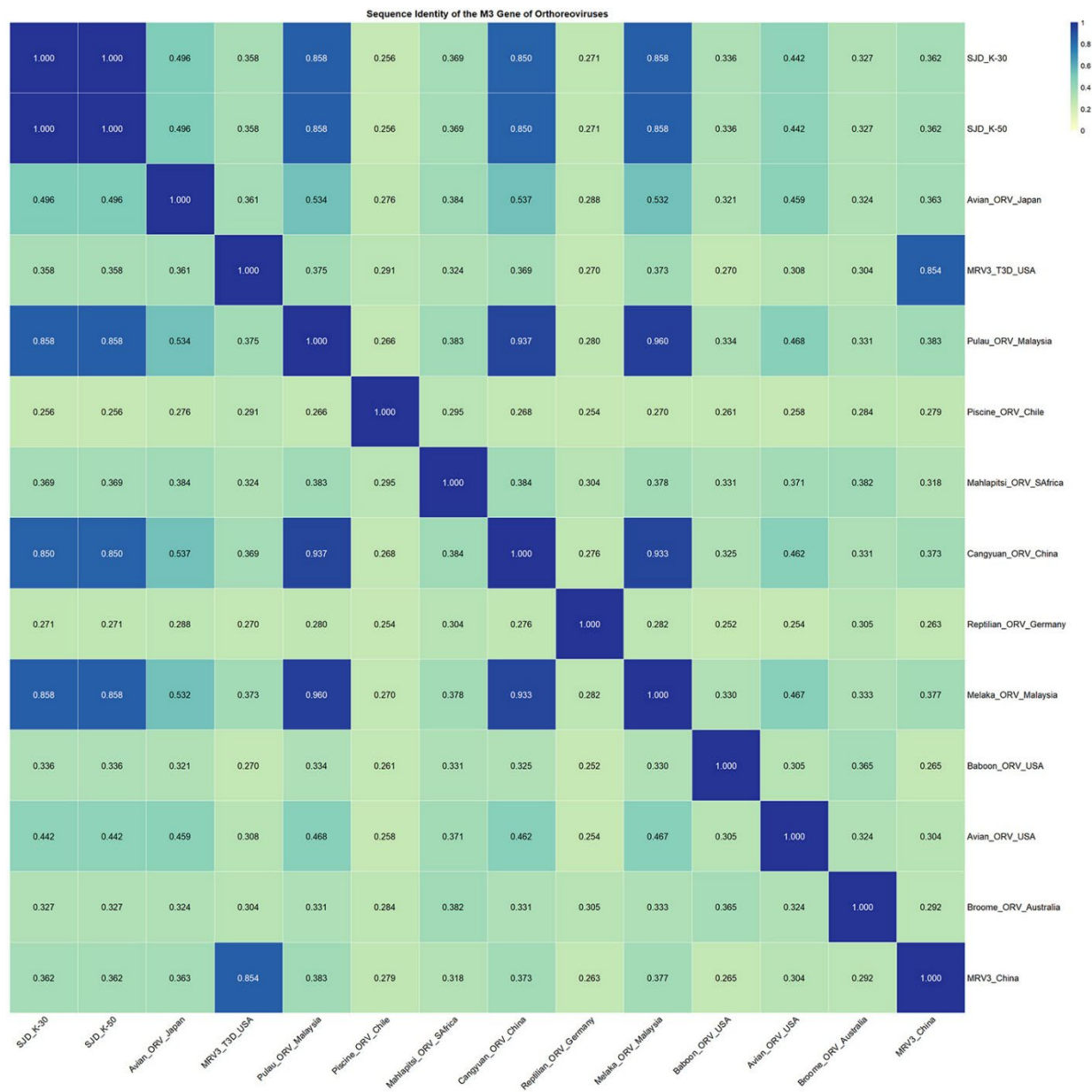
Appendix Figure 4. Heat map showing percentage of pairwise nucleotide sequence identities for L3 segment among orthoreovirus strains. Analysis includes the 2 bat-derived isolates identified in this study, PRV/SJD-K30/ID/2021 and PRV/SJD-K50/ID/2021, obtained from *Rousettus amplexicaudatus* in West Java, Indonesia. Reference sequences are avian, mammal, reptile, piscine, and bat orthoreoviruses retrieved from NCBI Virus (<https://www.ncbi.nlm.nih.gov/labs/virus/vssi>). Values in the squares represent pairwise nucleotide sequence identity (%). Color scale indicates degree of sequence similarity. L, large.



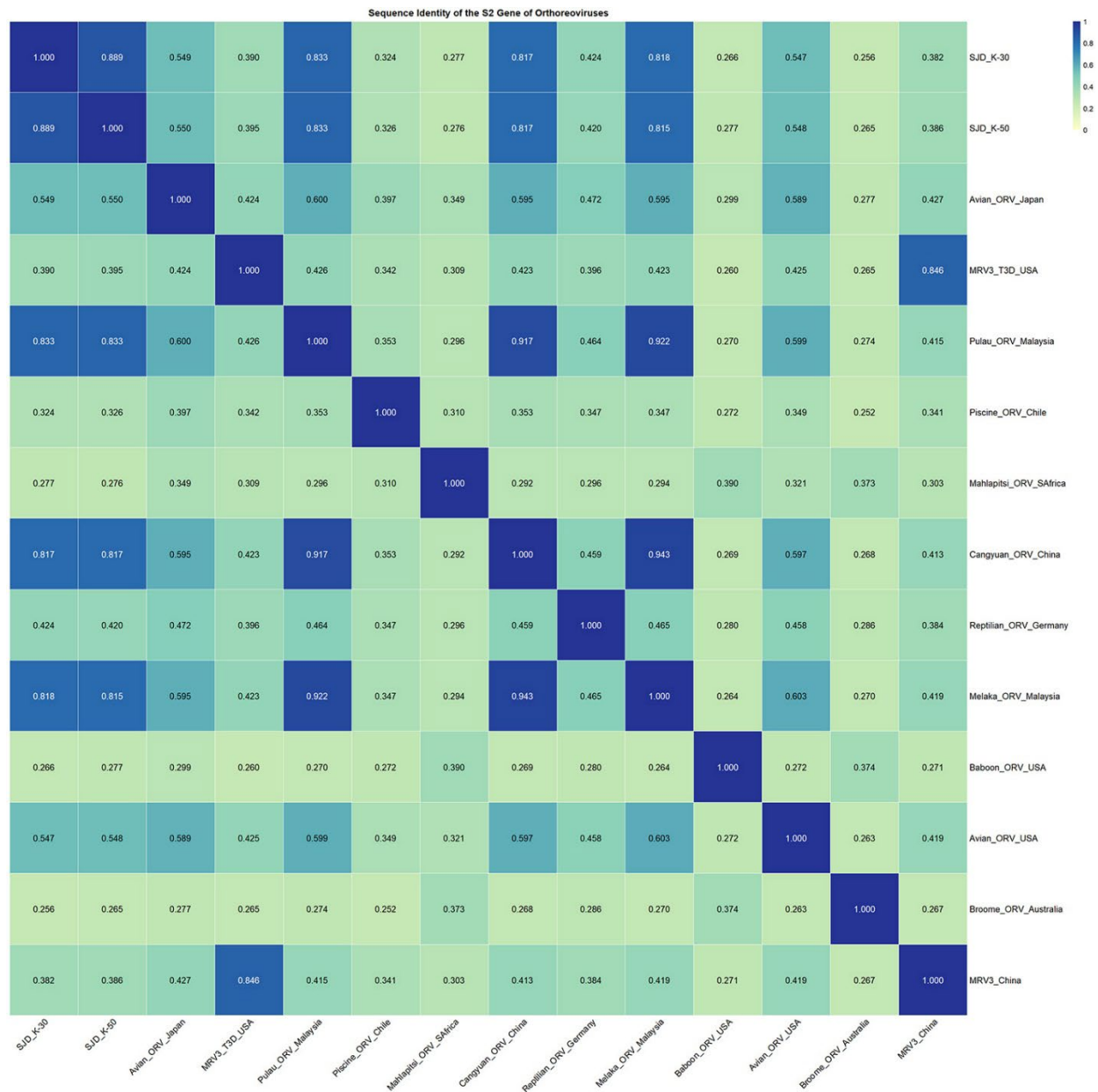
Appendix Figure 5. Heat map showing percentage of pairwise nucleotide sequence identities for M1 segment among orthoreovirus strains. Analysis includes the 2 bat-derived isolates identified in this study, PRV/SJD-K30/ID/2021 and PRV/SJD-K50/ID/2021, obtained from *Rousettus amplexicaudatus* in West Java, Indonesia. Reference sequences are avian, mammal, reptile, piscine, and bat orthoreoviruses retrieved from NCBI Virus (<https://www.ncbi.nlm.nih.gov/labs/virus/vssi>). Values in the squares represent pairwise nucleotide sequence identity (%). Color scale indicates degree of sequence similarity. M, medium.



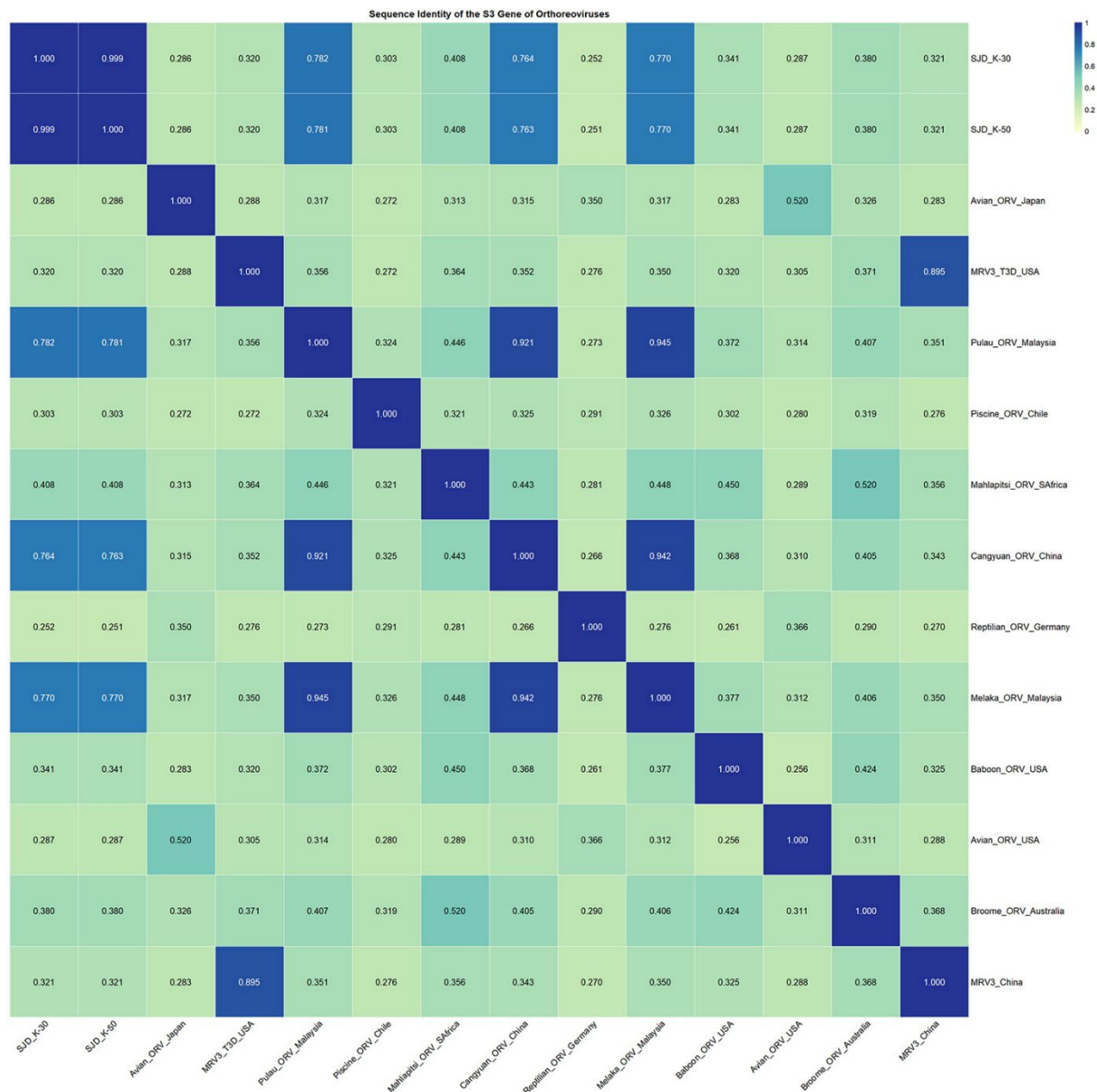
Appendix Figure 6. Heat map showing percentage of pairwise nucleotide sequence identities for M2 segment among orthoreovirus strains. Analysis includes the 2 bat-derived isolates identified in this study, PRV/SJD-K30/ID/2021 and PRV/SJD-K50/ID/2021, obtained from *Rousettus amplexicaudatus* in West Java, Indonesia. Reference sequences are avian, mammal, reptile, piscine, and bat orthoreoviruses retrieved from NCBI Virus (<https://www.ncbi.nlm.nih.gov/labs/virus/vssi>). Values in the squares represent pairwise nucleotide sequence identity (%). Color scale indicates degree of sequence similarity. M, medium.



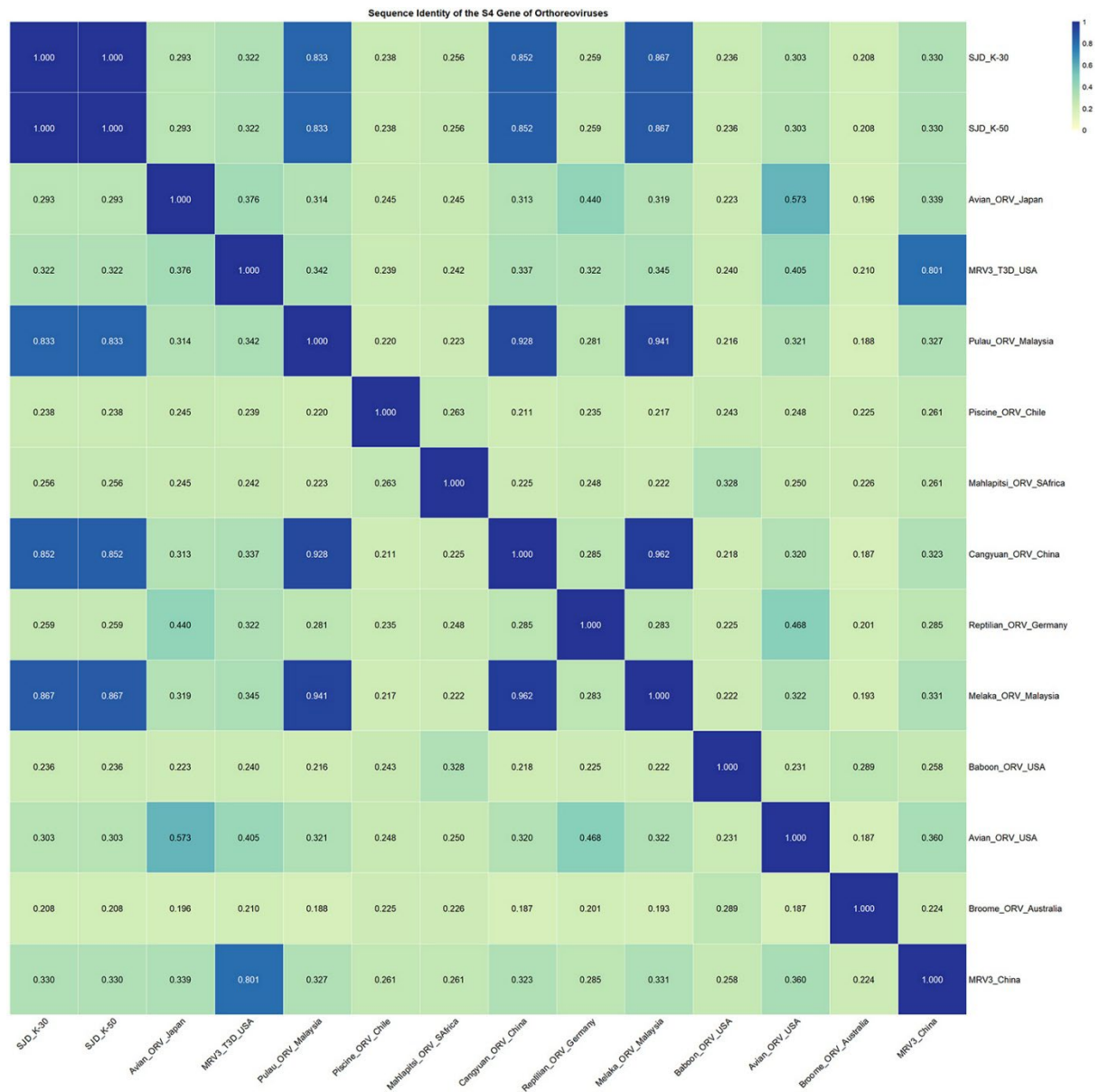
Appendix Figure 7. Heat map showing percentage of pairwise nucleotide sequence identities for M3 segment among orthoreovirus strains. Analysis includes the 2 bat-derived isolates identified in this study, PRV/SJD-K30/ID/2021 and PRV/SJD-K50/ID/2021, obtained from *Rousettus amplexicaudatus* in West Java, Indonesia. Reference sequences are avian, mammal, reptile, piscine, and bat orthoreoviruses retrieved from NCBI Virus (<https://www.ncbi.nlm.nih.gov/labs/virus/vssi>). Values in the squares represent pairwise nucleotide sequence identity (%). Color scale indicates degree of sequence similarity. M, medium.



Appendix Figure 8. Heat map showing percentage of pairwise nucleotide sequence identities for S2 segment among orthoreovirus strains. Analysis includes the 2 bat-derived isolates identified in this study, PRV/SJD-K30/ID/2021 and PRV/SJD-K50/ID/2021, obtained from *Rousettus amplexicaudatus* in West Java, Indonesia. Reference sequences are avian, mammal, reptile, piscine, and bat orthoreoviruses retrieved from NCBI Virus (<https://www.ncbi.nlm.nih.gov/labs/virus/vssi>). Values in the squares represent pairwise nucleotide sequence identity (%). Color scale indicates degree of sequence similarity. S, small.



Appendix Figure 9. Heat map showing percentage of pairwise nucleotide sequence identities for S3 segment among orthoreovirus strains. Analysis includes the 2 bat-derived isolates identified in this study, PRV/SJD-K30/ID/2021 and PRV/SJD-K50/ID/2021, obtained from *Rousettus amplexicaudatus* in West Java, Indonesia. Reference sequences are avian, mammal, reptile, piscine, and bat orthoreoviruses retrieved from NCBI Virus (<https://www.ncbi.nlm.nih.gov/labs/virus/vssi>). Values in the squares represent pairwise nucleotide sequence identity (%). Color scale indicates degree of sequence similarity. S, small.



Appendix Figure 10. Heat map showing percentage of pairwise nucleotide sequence identities for S4 segment among orthoreovirus strains. Analysis includes the 2 bat-derived isolates identified in this study, PRV/SJD-K30/ID/2021 and PRV/SJD-K50/ID/2021, obtained from *Rousettus amplexicaudatus* in West Java, Indonesia. Reference sequences are avian, mammal, reptile, piscine, and bat orthoreoviruses retrieved from NCBI Virus (<https://www.ncbi.nlm.nih.gov/labs/virus/vssi>). Values in the squares represent pairwise nucleotide sequence identity (%). Color scale indicates degree of sequence similarity. S, small.

Reference

1. Takemae H, Basri C, Mayasari NLPI, Tarigan R, Shimoda H, Omatsu T, et al. Isolation of *Pteropine orthoreovirus* from *Pteropus vampyrus* in Garut, Indonesia. *Virus Genes*. 2018;54:823–7.
[PubMed https://doi.org/10.1007/s11262-018-1603-y](https://doi.org/10.1007/s11262-018-1603-y)