**S4 Fig. Sequence properties of known polymycoviruses.** Schematic representation of the genomic organisation of **(a)** BdPmV-1 and **(b)** CcPmV-1. Each genome consist of five dsRNAs, each containing one ORF (grey boxes) flanked by 5'- and 3'-UTRs (black boxes). A comparative alignment of the 5'- and 3'-terminal sequences of **(c)** BdPmV-1 dsRNAs 1–5, **(d)** CcPmV-1 dsRNAs 1–5, **(e)** AltPmV-1 dsRNAs 2, 5 and 6, **(f)** BbPmV-1 dsRNAs 1–4 and **(g)** BbPmV-1 dsRNAs 1, 6 and 7. Asterisks signify identical nucleotides. AltPmV-1 dsRNA 6 does not share a similar 3'-terminal sequence with dsRNAs 2 or 5; however there is an internal sequence in its 3'-UTR with significant similarity to the 3'-terminus of dsRNAs 2 and 5, indicating a possible sequencing error. Virus names, acronyms, and GenBank accession numbers are listed in S3 Table.