

R1RV

MGQTTSSPLGLTSHFKDVRERAYRLSVEVRKGMVTFNTEWPSFNI GWPSEGTDL SIVSAVEDIVFRPRDG-HPDQVPII VVKDLIRHPLPWLKSFPPSQKVP---VMVAKAGRSRPREVAPPTAPLYV LQGGSEEEIIFP (146)
PERV-C
Gag begin
LPPYRLVPPPQAPLPPSLVLEPLPAELPPAPLLPPPQSGQNVQPAPSSGPAHNRRLQRHPPLEADSTV LPLRAVGPVARGD-QLFHYWPFATSDLYNWRSNQAFSDNPKDLINLLETVLFHQPTWDDCQQLLQVL (292)
PERV-C
FTTEERERI IQEARKLIPGPTGIPTTIPAAIDVAFPMRSRPEWDYNMAEGKERLQVYRQALLAGLAAAARWPTNLAKVREVIQGATEPPSVFLERLMEAFRRYTPDPASEGQRASVAMAFIQSALDIRKRLRLEGLQDVTLLQDL (438)
PERV-C
VKEAENVYHKRETEEEKRKEKEREERDRKREKNLTRLAAVVN-----EKGQEQTSRAKRSNGLNRTPLDKDQCSYCKEKGHWARECPKLRKNGSSKVLAEEDD*RG-GSEPLPEPRVLEVEWRPVEFLVD (584)
PERV-C
Gag end | Pol begin
TGAQHSVLLLEPAGPVSHKSWVIGATGHQQYSWTRTRTVDLGKRVTHSFLVIPCPCAPLLGRDLLTKMGAQISFT---PEVTQGERMATALTIRLDEHRLFEEQGAETHINDWLNKYPGAWAEMAGTGLAVERPPVIELKAT (730)
PERV-C
STPVAIRQYPMTEAREGIRPHIQRLLQGGILVRCQSPWNTPLPVKPKGTGDYHPVQDLREVNKRVDIHTPTVNPYNLSSLPDHWVYVTLVDLKDFFCFLRLHPSSRNIFAFWEWRDPSGTQTLTWLRLPKGFKNSPTLDFE (876)
PERV-C
ALHQDLAHFCASHQESSPIYSKGMQ----- (1022)
PERV-C
KKALLSAPALALPDVTKPFTLVYDERKGVARGVLTQTLPWRPVAYL SKKLDPIASGWPVCLKAATAVAI LVDKADKLTGQNTIT IAPHALENIVRQPPDRWMTNARMITQYQSLLLTERITFPAAALNPATLLPEETDEPVTH (1168)
PERV-C
DCHQLLIEETGVRKLDIDILPTEGLVTFWTDGSSVYVEGKRMAGAAVVDGTRT I WASSLPEGTSQAQKELMALTALRLADGKSNINYDSRYAFATAHVHGAIYKQGLLTSAGREIKNKEEILSLEALHLPKRLAIHCPGHQ (1314)
PERV-C
KAKDPISRGNMADRVAQAAQVNLPIIETPKAPEPGRQVTLDEWQEKIKKIDQFSETPERTCYTSDGKEILPHKEGLEVVQQLIHLRHLGTHLQQLVVRTSPYHVLRLPGVADSVVHKVPCQLVNPANSRIPPKGRRLRGSHPG (1460)
PERV-C
SYWEVDFTVEVKPARYGRYLLVFDVTFSGWVKAFTPKKETAQMVAKKILEDFPRFGVPKVIGSDNGPAFVAQVSQLAKILGLDWLHCAIRPQSSGQVERM (1563)
PERV-C
AHWEVDFTVEVKPAKYKNYLLVFDVTFSGWVEAFTPKKETSIVVAKKILEEIPFRFGIPKVIGSDNGPAFVAQVSQLAKILGLDWLHCAIRPQSSGQVERM

M1RV

PTNLAKVREVLQRVPEPPSMFLEGLIETRYRYTPDPDSDGQAAVAMAFIQGSAPDIKKNLQRLLEGLQDQALQDLVKEKTEVFKHRETEEEKEREKREAEERDRDRHRQERNLTRLAAVGERDRDRAGRPQQNGLNGRPP (146)
MDEV
PGIRDEERRRPLDKDQAYCKEKGHWARDCTPPKGRAPKVLAEEDD*RGWSDPLPEPRVTLIVEGTLMDLFDVDTGAHVSLSKQLKGLKKNKTTVIGA----- (292)
MDEV
Gag end | Pol begin
AQQVFTSEGPVSWGKAPLACLVLSTEEYRLHEEQPKGAAPLDWVTFAPNVAEQMGLAKQVPPVVVELKADATPISVRYQPMKSEKEGIRPHIRRLDQGILVACQSPWNTPLPVKPKGTNDYRPVQDLREVNKRVDIHI (438)
MDEV
PTVPNPYNLSSLPERTVYVTLVDLKDADFCLRLHPSQLLFAFEWRDEGGQTGLTWLRLPQGFKNSTPLFDEALHRDLAPFRAQNPQLTLLQYVDDLLIAASKELCQQTERRLTELNGLYRSAKKAQICQTEVLYLGYT (584)
MDEV
LREGKRWLTEARKKSVTRIPPTPRQVREFLGTAGFCRLRIPGFATLAAPLYPLTKEGGEFVWPEHQAEDFKIKALLSAPALALPDLTKPFTLYVDERAGVAGQVLTQTLGPWKRVAYL SKKLDPVASGWPCLKAITAVAL (730)
MDEV
LVKDDAKLTGQQVTIVAPHALGSII RQPPDRWMTTARMTHYQSLPLTELSFAPPAILNPATLLPETEDSSPHHCADILAEETGTRDRDQWAGSPTWYTDGSWFVVEGKRRAGA AVDGKRV I WASSLPEGTSQAQKAE LVA (876)
MDEV
LTIQAPRLAEGKNINYDSRYAFATAHIGAIYRQRGLLTSAGKD IKNKEEMLSLLEAHLPAKVAI IHCPCGKQGREAVAKGNQADLVAQTAQGTMI LAARES KDYNNIRETSFRYTDQHNDAMDGLGLIRHTPYGISQTEDR (1022)
MDEV
DLT-PEEG- IKFVGLHQFTHLGVEMMRLIKSRVQVNLKSAVQKINSKACAFNTATKYKEPKGRQDRPGVYWEVDFTVEVKPMYKNYLLVFDVTFSGWVEAFTPKTETAQIVAKKIFEEILPRYGVKPVIGSDNGPA (1168)
MDEV
FVTQVSQGLATQLGVKWLHCAIRPQSSGQVERM (1202)
MDEV
FVAQVSQLATQLGIDWKLHCAIRPQSSGQVERM

Fig. S1. Alignments of bat gammaretroviruses with their closest relatives. R1RV was aligned with its closest relative – PERV-C, while M1RV was aligned with MDEV. Asterisks represent shared amino acids in both genomes and dashes denote deletions. Gag and Pol positions are indicated.