

Figure S1. a. Amino acid alignment showing Bunya_RdRp conserved motifs A to E and premotif A within the RdRp of PpaBLV1-14 and selected bunyaviruses. DUGBA, Dugbe virus (accession number Q66431); RSVT, Rice stripe virus (Q85431); UUKS, Uukuniemi virus S23 (P33453); TSWV, Tomato spotted wilt virus (P28976); BUNYW, Bunyawera virus (P20470); BUNL8, La Crosse virus L78 (Q8JPR2); HANTV, Hantaan virus 76-118 (P23456). Gray boxes with numbers represent the number of positions deleted in the MUSCLE alignment. **b.** Amino acid alignment showing the conserved motifs of *Tenuivirus/Phlebovirus* nucleocapsid protein within PpaBLV11 and selected bunyaviruses. IWSTV, Iranian wheat stripe tenuivirus (Q7TBL7); UHBT, Urochloa hoja blanca tenuivirus (O11440); WYHV, Wheat yellow head virus (P84254); MSTV, Maize stripe tenuivirus (Q50HQ8); UUKV, Uukuniemi virus S23 (P22025); SFNV, Sandfly fever Naples virus (NC_006318); EnPLV1, Entoleuca phenui-like virus 1 (NC_055436); LeNSRV2, Lentinula edodes negative-strand RNA virus 2 (YP_010086263); GACLV4, Grapevine associated cogu-like virus 4 (QMP81965); LTV, Lihan tick virus (QFR36186). WFV1, Wuhan Fly Virus 1 (YP_009304999). Gray boxes with numbers represent the number of positions deleted in the MUSCLE alignment. The % of similarities are calculated based on Blosum62 score matrix with a threshold of 1.

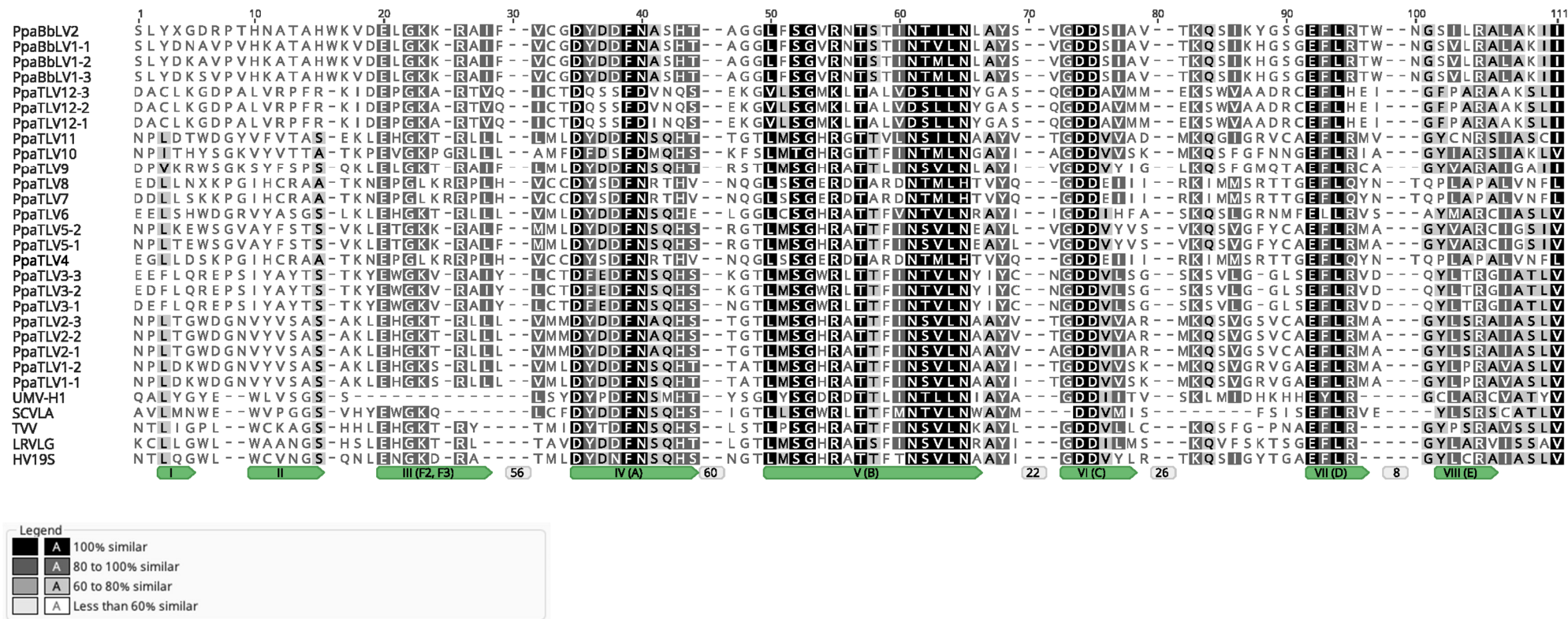


Figure S3. Conserved aa sequence motifs (I-VIII) of RdRp of totiviruses and botybirnaviruses in *P. palustris*. **PpaBbLV1-2** and **PpaTLV1-12**; **UMVH1**, Ustilago maydis virus H1 (NP_620728); **SCVLA**, Sacharomyces cerevisiae virus L-A (Q87025); **TVV**, Trichomonas vaginalis virus 3 (Q8V615); **LRVLG**, Leishmania RNA virus 1 (Q02382); **HV19S**, Helminthosporium victoriae virus 190S (O57044). Gray boxes with numbers represent the number of positions deleted in the MUSCLE alignment. The % of similarities are calculated based on Blossum62 score matrix with a threshold of 1.



Figure S4. Conserved aa sequence motifs (III-VII) of RdRp of narna-like viruses in *P. palustris* and ScNV-23S, Saccharomyces 23S RNA narnavirus (NP660177), ScNV-20S, Saccharomyces 20S RNA narnavirus (NP660178); PiRV4, Phytophthora infestans RNA virus 4 (YP009241365). Gray boxes with numbers represent the number of positions deleted in the MUSCLE alignment. The % of similarities are calculated based on Blosum62 score matrix with a threshold of 1.

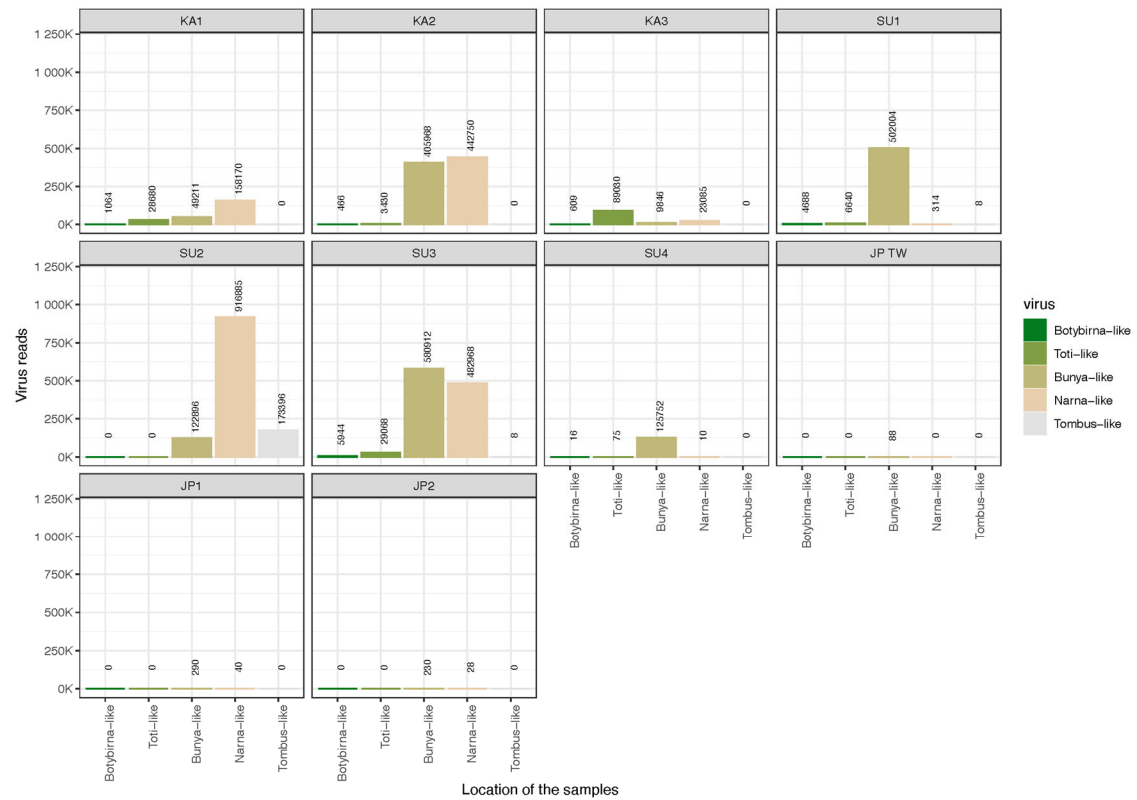


Figure S5. Contingency graphs showing the number of viral reads per virus group obtained in each RNA library.