Article

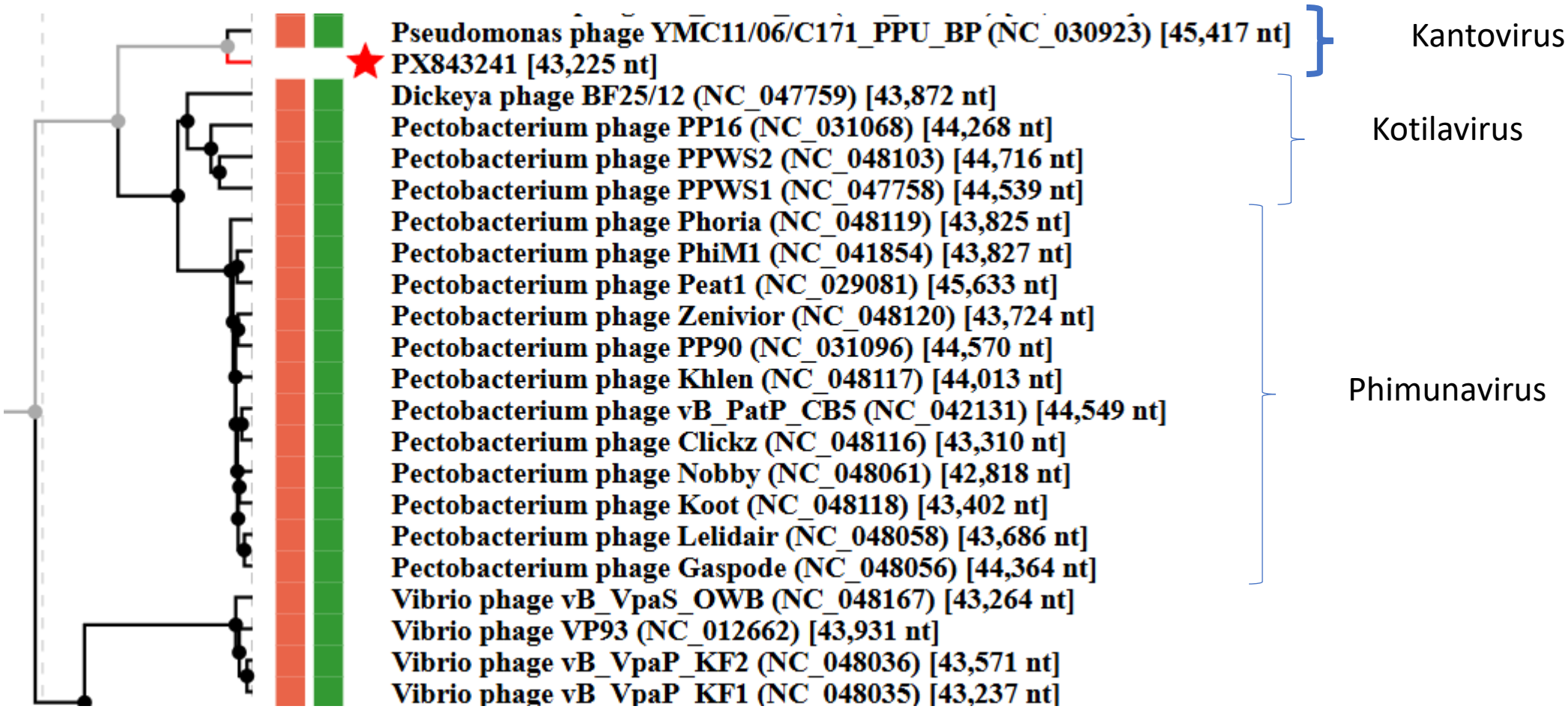
Antibacterial efficacy of *Pseudomonas aeruginosa* bacteriophages on a *Drosophila* infection model

Karel Petrzik [1,*], Sára Brázdová [1]

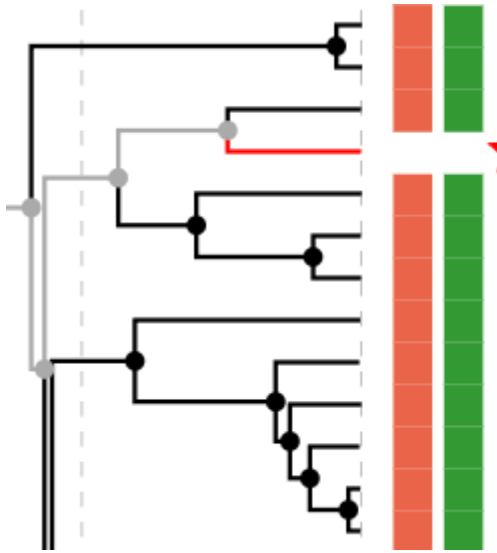
Supplementary material

1. ViPTree proteomic trees with distinct new viruses
2. Reconsctruction of N-J trees of large terminase proteins
3. Global genomic alignment with the closest viruses

1. ViPTree of the viruses, global genomic sequence identity to related viruses



PX843241 identity to YMC11 = 80.8%



Escherichia phage phiKT (NC_019520) [42,608 nt]
Escherichia phage PGT2 (NC_047890) [42,686 nt]
Pseudomonas phage VSW-3 (NC_041885) [40,556 nt]
PX843244 [40,737 nt]
Pseudomonas phage PollyC (NC_042104) [41,651 nt]
Pseudomonas phage Bf7 (NC_016764) [40,058 nt]
Pseudomonas phage Andromeda (NC_031014) [40,008 nt]
Xylella phage Paz (NC_022982) [43,869 nt]
Xylella phage Prado (NC_022987) [43,940 nt]
Xanthomonas phage XAJ24 (NC_047762) [44,862 nt]
Xanthomonas phage phi Xc10 (NC_047840) [44,597 nt]
Xanthomonas phage f30-Xaj (NC_030937) [44,262 nt]
Xanthomonas phage f20-Xaj (NC_030928) [43,851 nt]

Ermolevavirus
Napahaivirus
Polyceevirus
Bifseptvirus
Pazvirus
Pradovirus
Gujervirinae

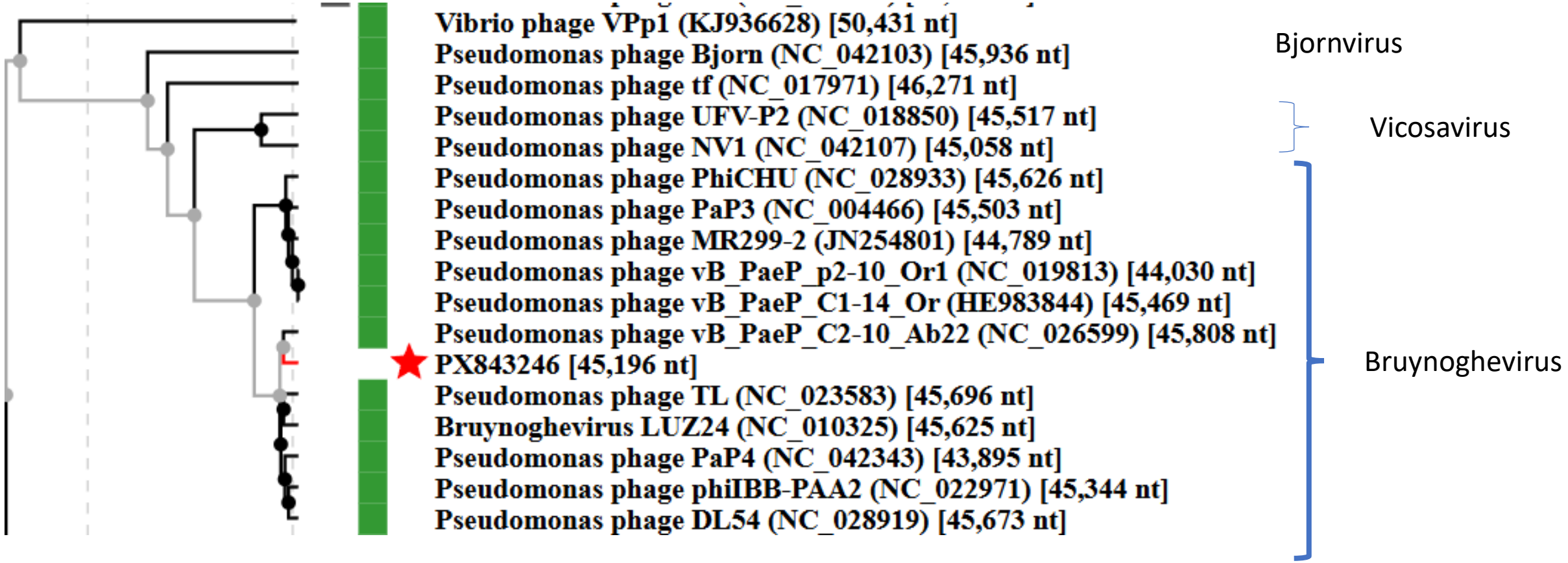
PX843244 identity to VSW-3 = 63.0%
to PollyC = 55.3%
to Bf7 = 55.4%



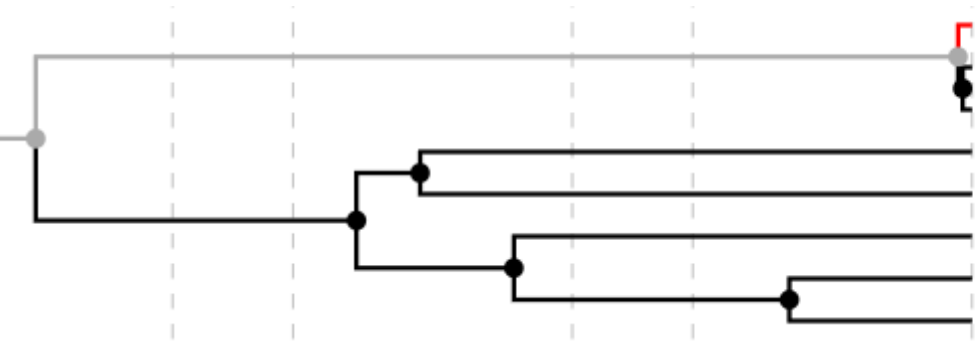
Pseudomonas phage Kaya (NC_069741) [43,067 nt]
Pseudomonas phage vB_PaeS-Yazdi-M (NC_069742) [42,439 nt]
Pseudomonas phage Guyu (NC_069743) [43,141 nt]
Xanthomonas phage vB_Xar_IVIA-DoCa1 (NC_069745) [43,553 nt]
Xanthomonas phage Samson (NC_069744) [43,314 nt]
Pseudomonas phage PaMx42 (NC_028879) [43,225 nt]
Pseudomonas phage vB_PaeS_SCUT-S3 (NC_072809) [42,622 nt]
Pseudomonas phage PSV3 (NC_069753) [39,019 nt]
Pseudomonas phage PSV3 (NC_069755) [43,315 nt]
Pseudomonas phage PSV3 (NC_069752) [40,244 nt]
Pseudomonas phage Kopi (NC_069746) [42,820 nt]
Pseudomonas phage Epa40 (NC_069747) [42,788 nt]
Stenotrophomonas phage vB_SmaS-DLP_1 (NC_069751) [42,887 nt]
Stenotrophomonas phage vB_SmaS-DLP_2 (NC_029019) [42,593 nt]
Pseudomonas phage UF_RH1 (NC_072810) [42,567 nt]
Pseudomonas phage 73 (NC_007806) [42,999 nt]
Pseudomonas phage BUCT-PX-5 (NC_069750) [42,828 nt]
PX843243 [42,816 nt]
Pseudomonas phage vB_PaeS_SCH_Ab26 (NC_024381) [43,056 nt]
PX843242 [42,855 nt]
Pseudomonas phage TehO (NC_069748) [43,015 nt]
Pseudomonas phage vB_PaeS_C1 (NC_069749) [43,133 nt]
Pseudomonas phage vB_Pae-Kakheti25 (NC_017864) [42,844 nt]

Septimatrevirus

PX843243 identity to BUCT-PX-5 = 96.4%
to phage 73 = 93.7%
to UF_RH1 = 93.0%
to Ab26 = 93.1%
PX84242 identity to Ab26 = 93.0%
to TehO = 92.3%
to BUCT-PX-5 = 93.9%



PX843246 identity to oldone = 91.1.%
to Ab22 = 90.9%
to TL = 88.3%
to LUZ24 = 84.0%

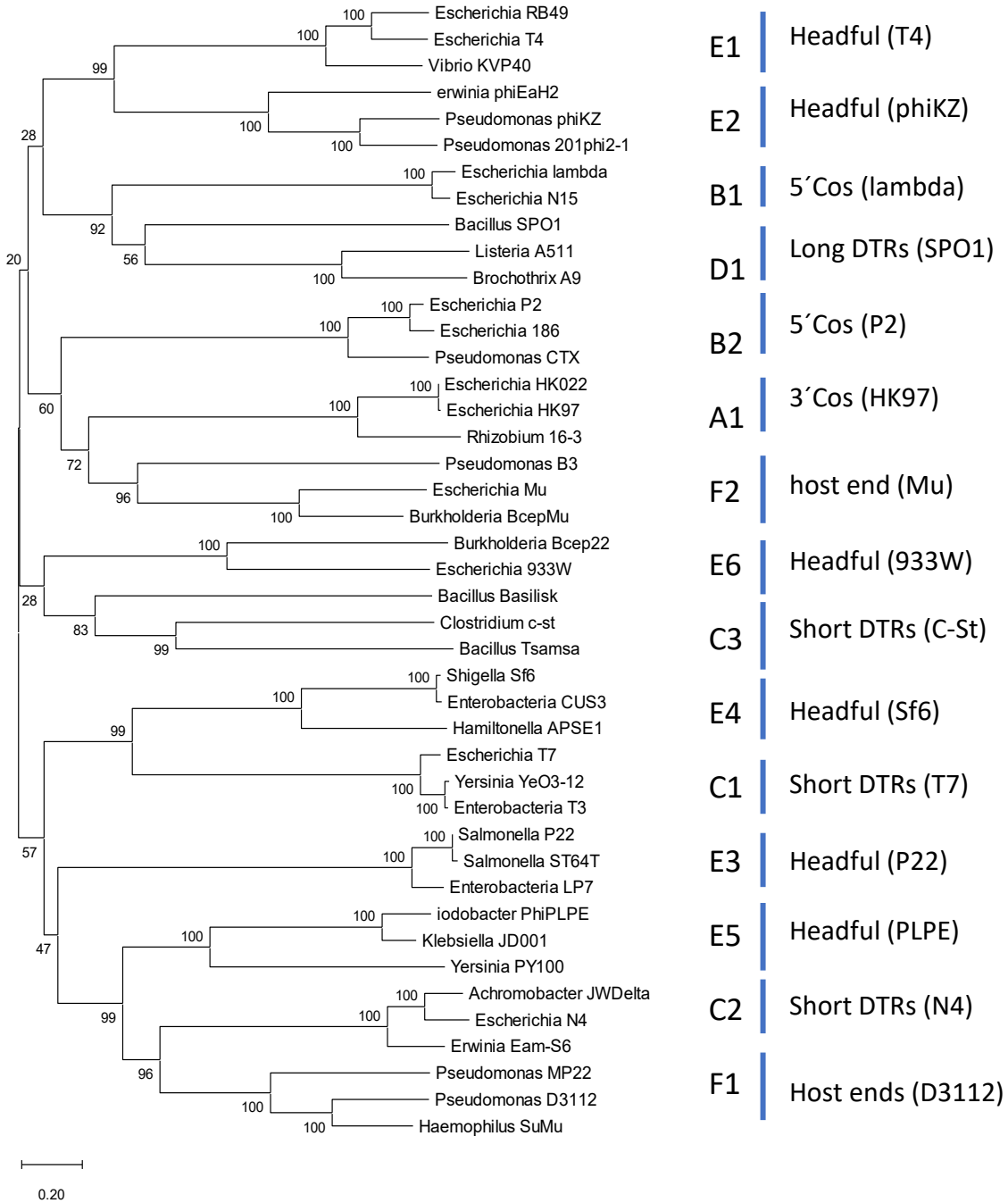


PX843245 [63,274 nt]
Pseudomonas phage phiR18 (NC_041964) [63,560 nt]
Pseudomonas phage KPP25 (NC_024123) [64,113 nt]
Rhizobium phage vB_RleS_L338C (NC_023502) [109,558 nt]
Pseudomonas phage SM1 (NC_041877) [93,191 nt]
Stenotrophomonas phage vB_SmaS_DLP_5 (NC_042082) [96
Vibrio phage SIO-2 (NC_016567) [81,184 nt]
Vibrio phage 1 (JF713456) [81,509 nt]

Kochitakasuvirus

Delepquintavirus

PX843245 identity to R18 = 92.7%
to KPP25 = 93.6%



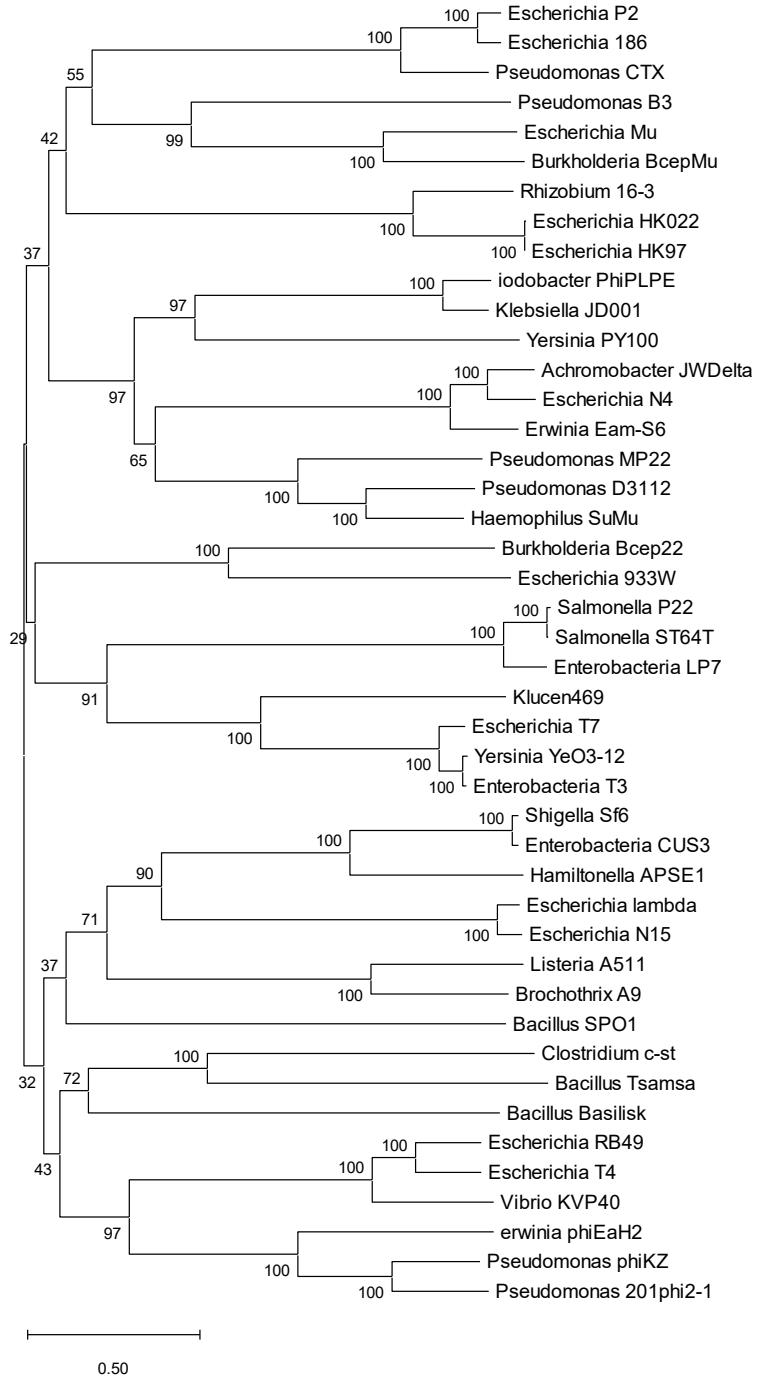
E1	Headful (T4)
E2	Headful (phiKZ)
B1	5´Cos (lambda)
D1	Long DTRs (SPO1)
B2	5´Cos (P2)
A1	3´Cos (HK97)
F2	host end (Mu)
E6	Headful (933W)
C3	Short DTRs (C-St)
E4	Headful (Sf6)
C1	Short DTRs (T7)
E3	Headful (P22)
E5	Headful (PLPE)
C2	Short DTRs (N4)
F1	Host ends (D3112)

2. Reconstruction of N-J tree of large terminase proteins

The tree was generated in MEGA12, ClustalW alignment with BLOSOM protein weight matrix; N-J tree with poison correction model; bootstrap values are for 1000 trials.

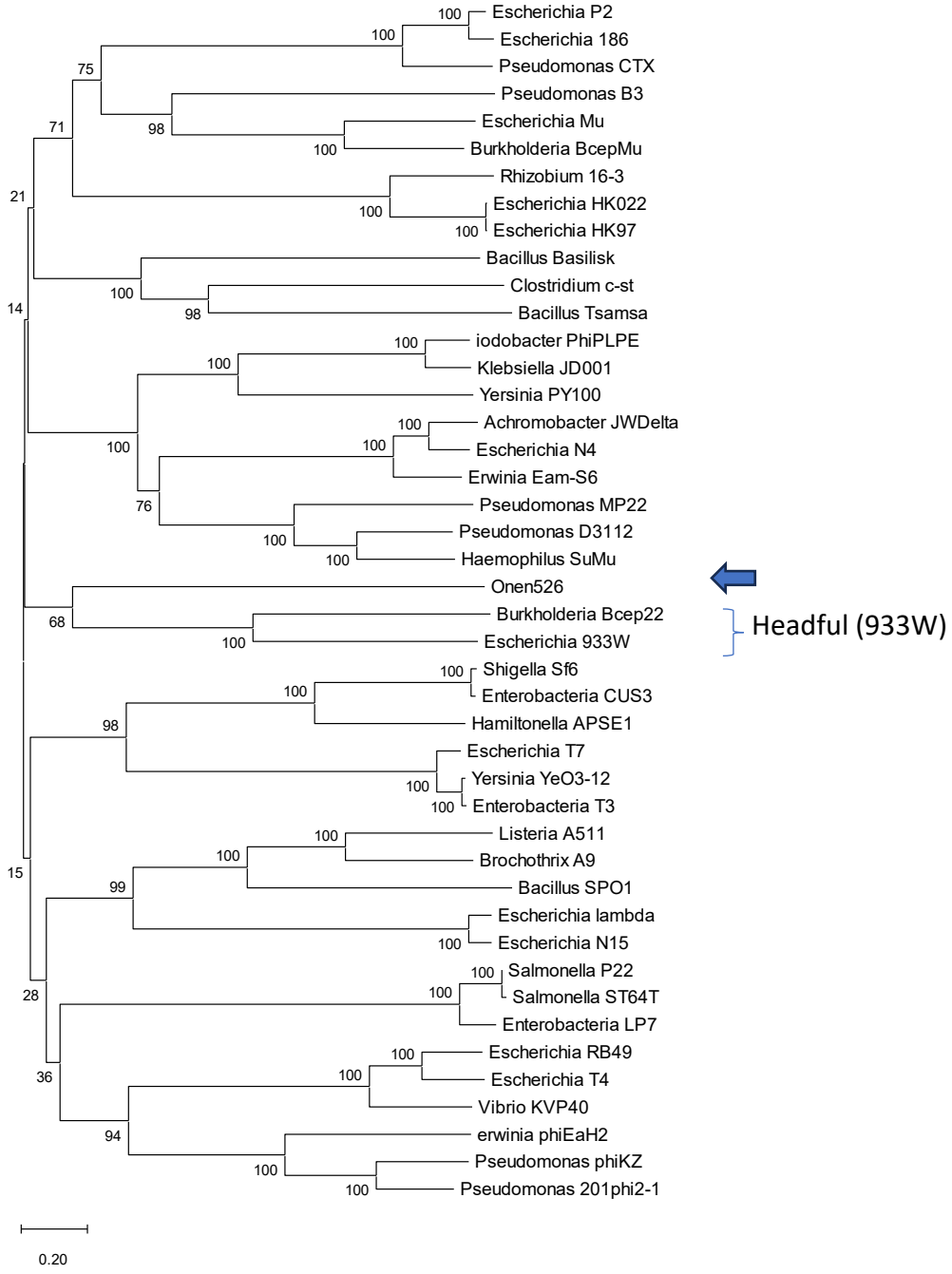
Sequences as published in Merill et al. 2016 are used.

Packaging mechanisms, cluster numbers, and physical ends are marked.



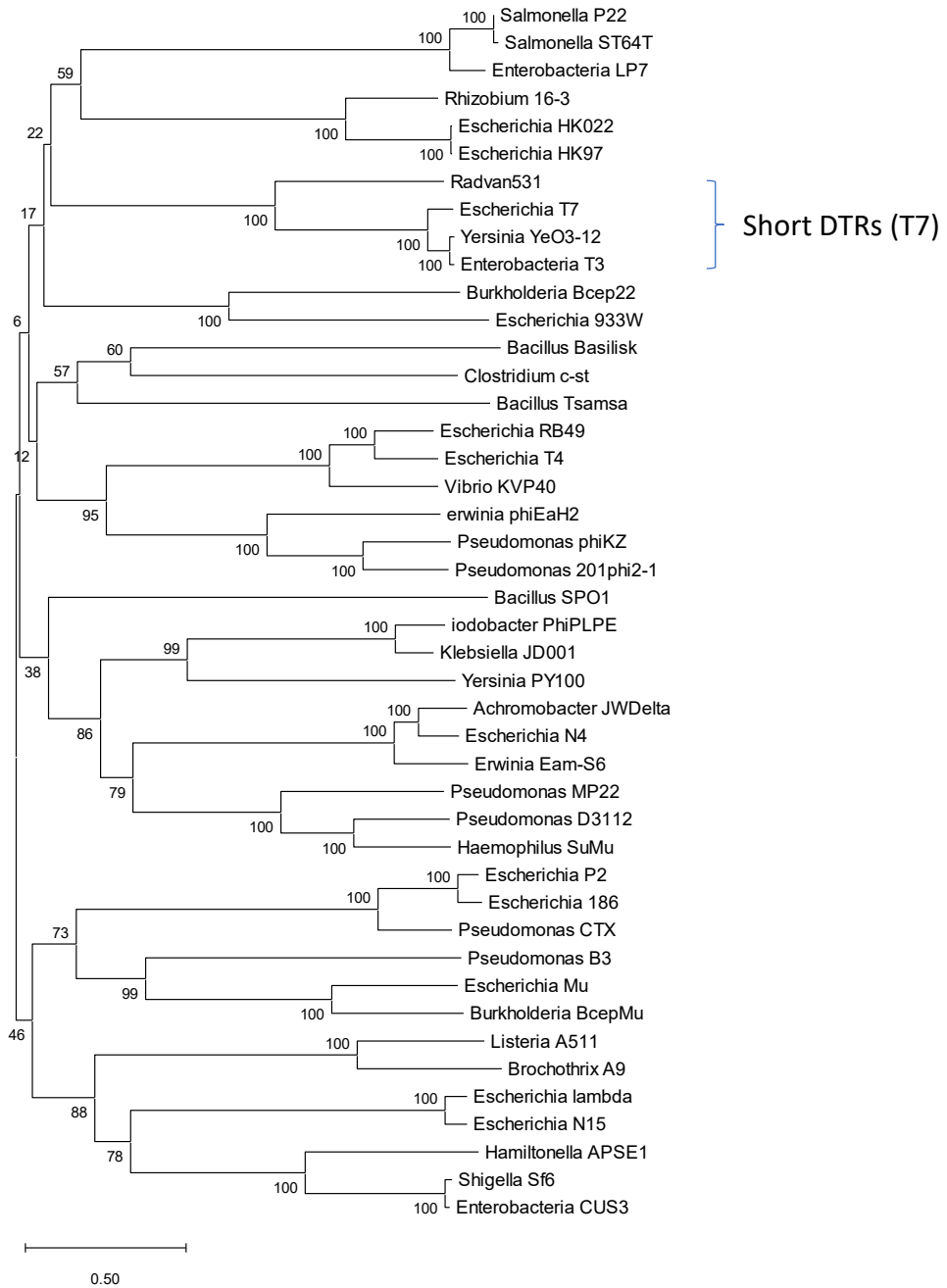
Klucen469 large terminase clustering

Short DTRs (T7)



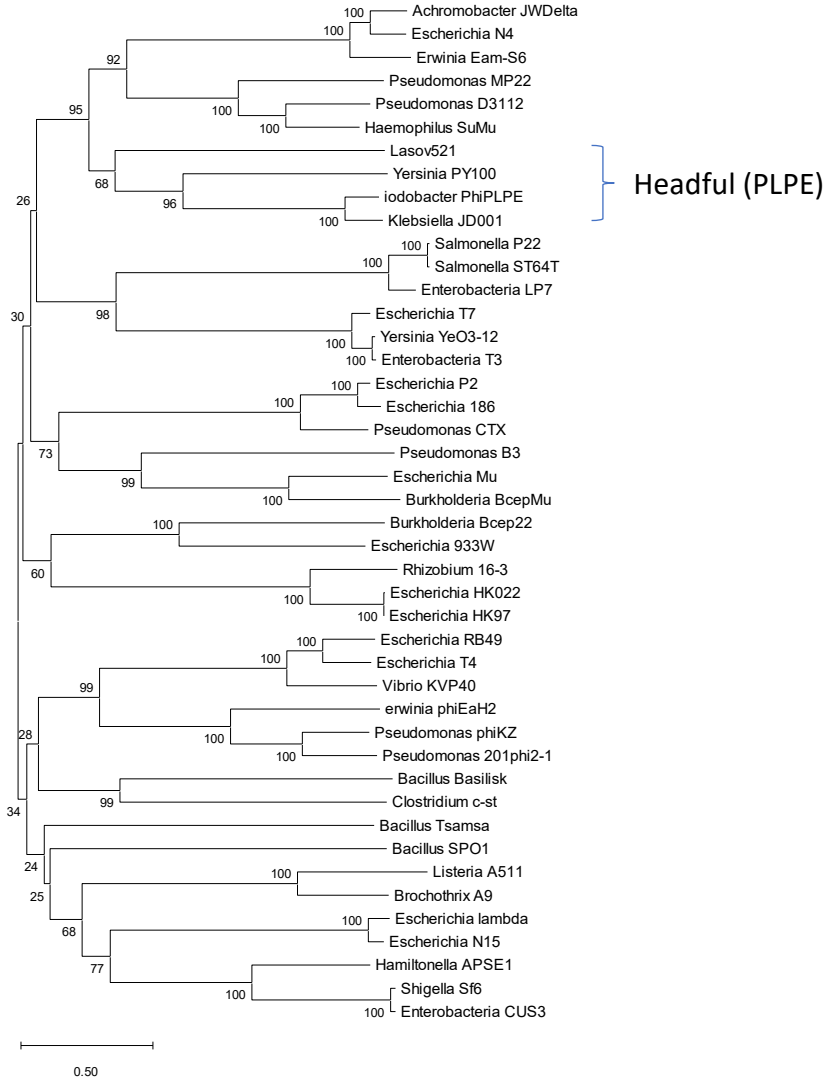
Headful (933W)

Onen526 and Onen484 large terminase clustering – probably headful



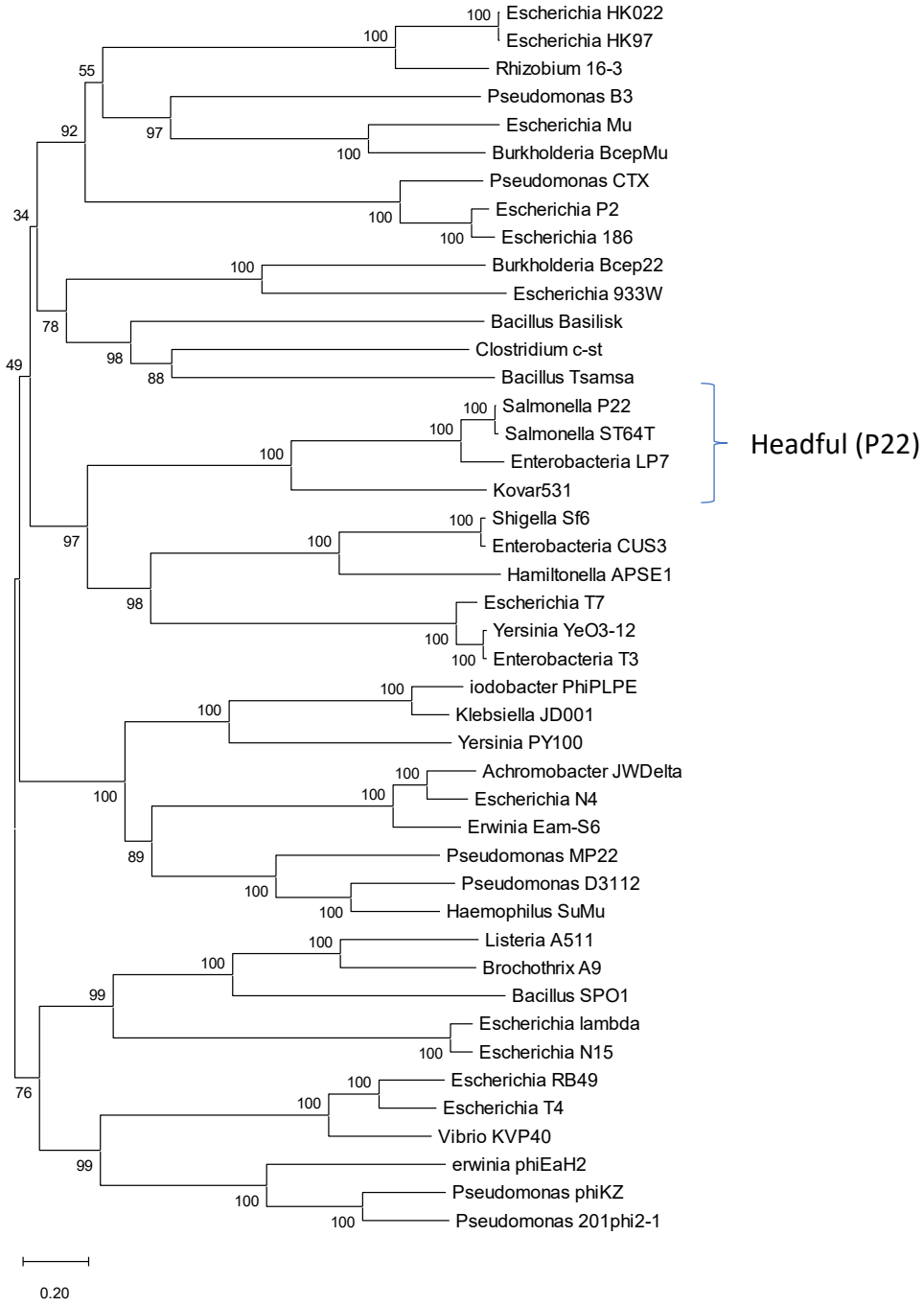
Short DTRs (T7)

Radvan531 large terminase clustering – probably short DTRs



Headful (PLPE)

Lasov521 large terminase clustering



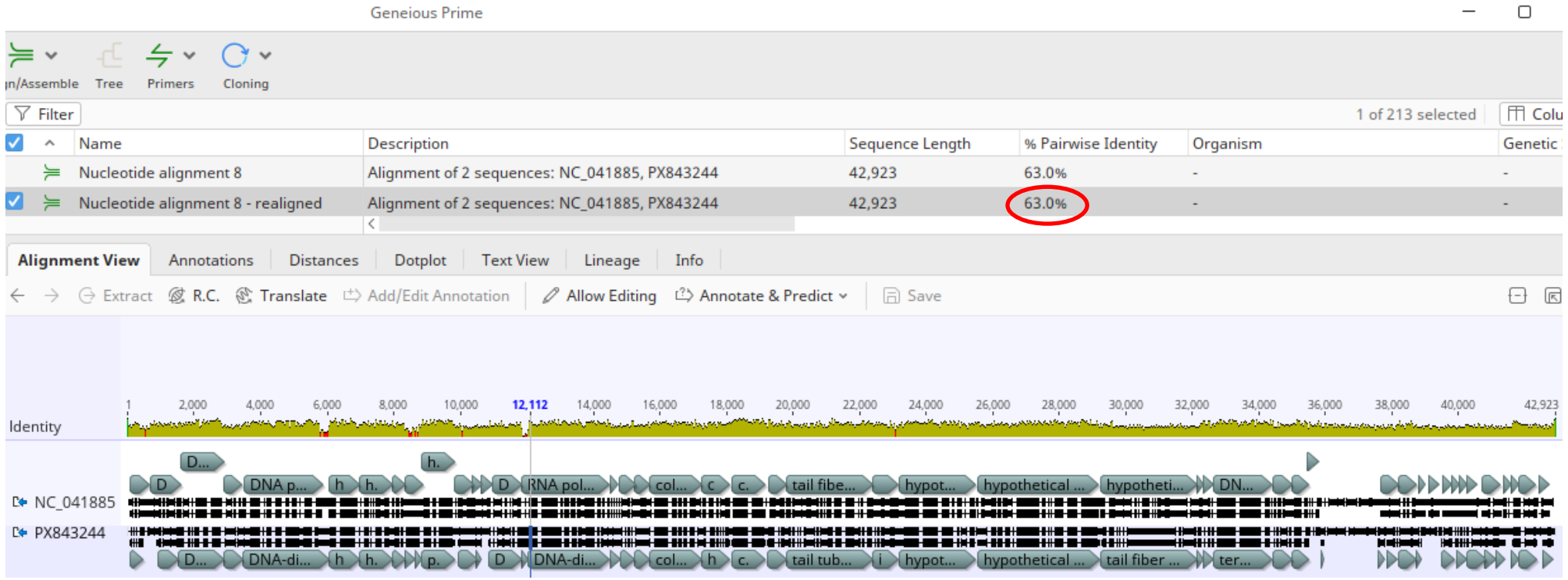
Headful (P22)

Kovar531 large terminase clustering

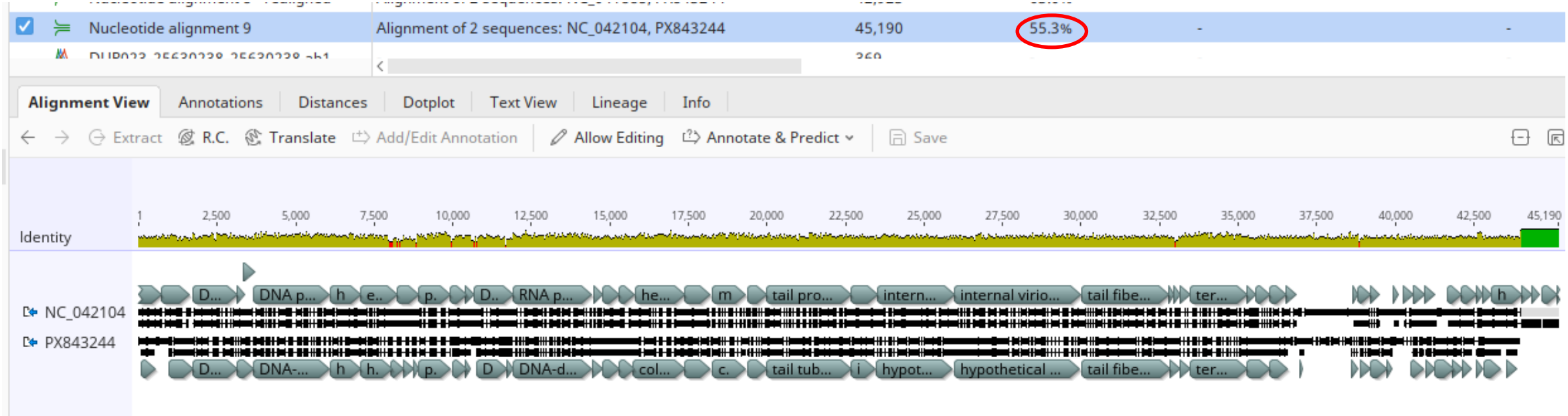
3. Global genomic alignment with the closest viruses

The sequences orientation and the starting point were corrected and sequences were aligned with the Global Alignment with Free End Gaps algorithm from the Geneious Prime v. 2025.2.2. software with a Cost Matrix of 65 % similarity, a Gap Opening Penalty of12, and a Gap Extension Penalty of 3 (default setting).

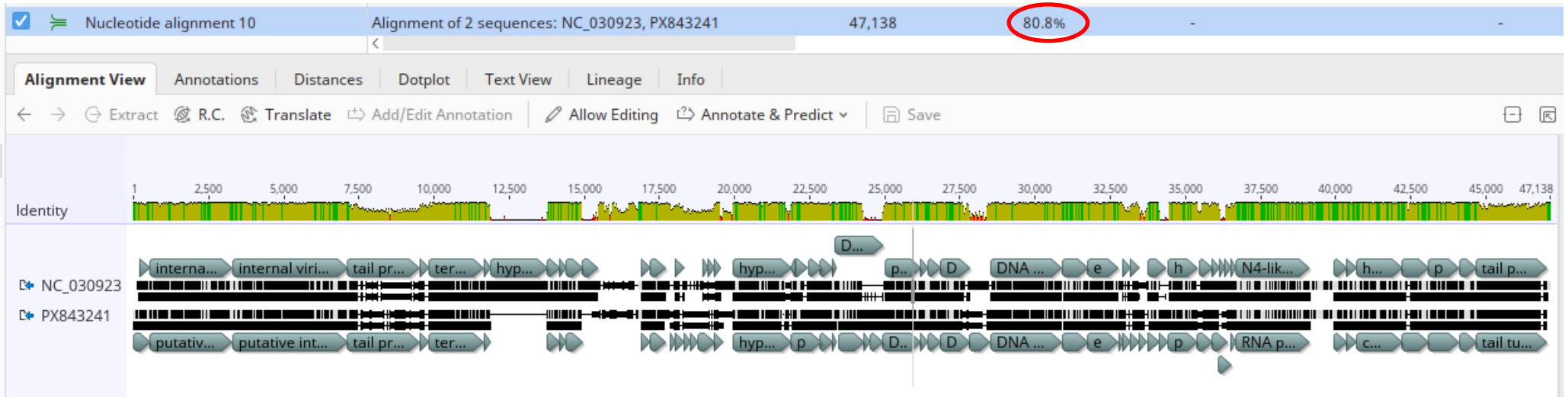
PX843244 (Radvan531) vz NC_041885 (VSW3) **63% sekvence identity**



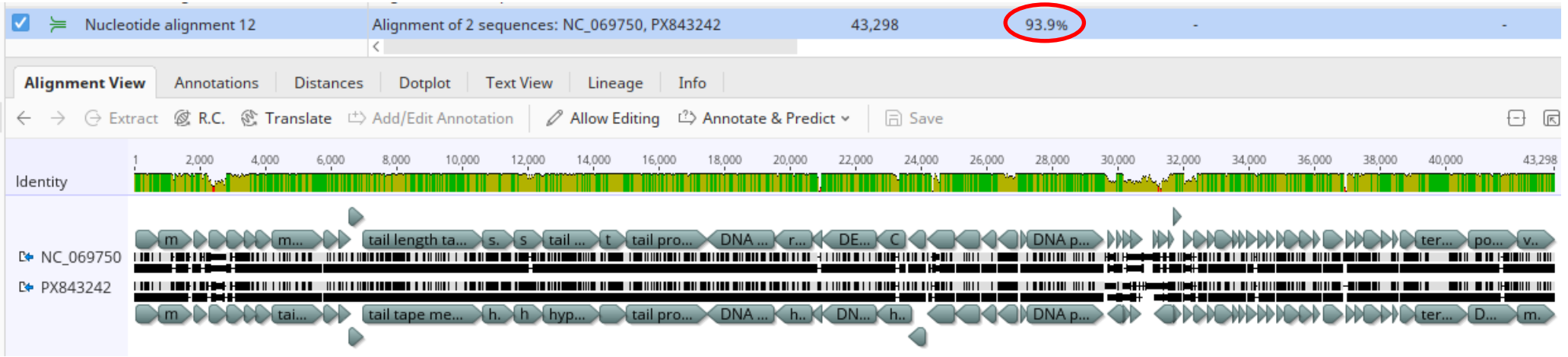
PX843244 (Radvan531) vz NC_042104 (pollyC) – **sequence identity 55.3%**



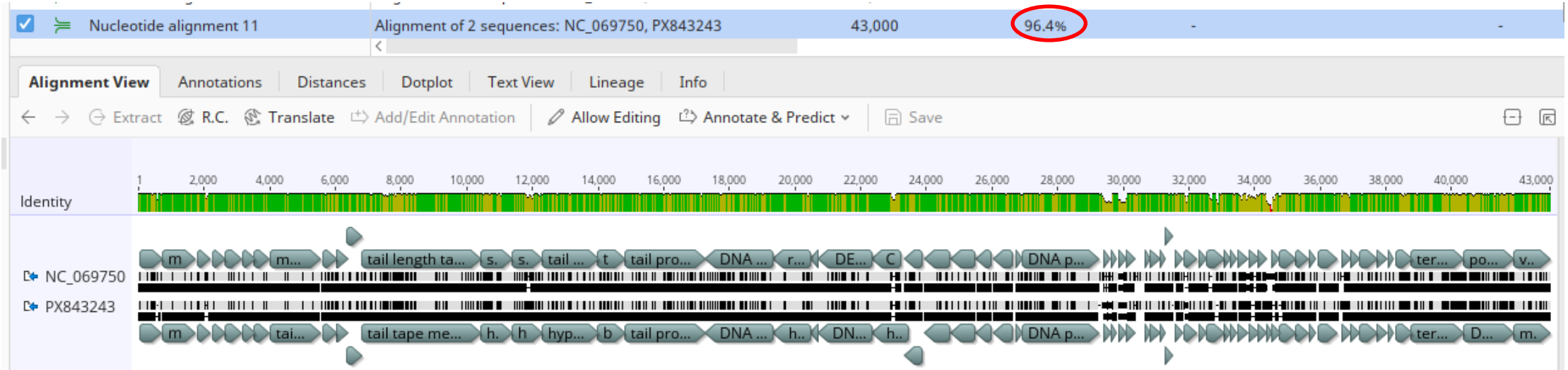
PX843241 (Klucen469) with NC_030923 (YMC11) – **sequence identity 80.8%**



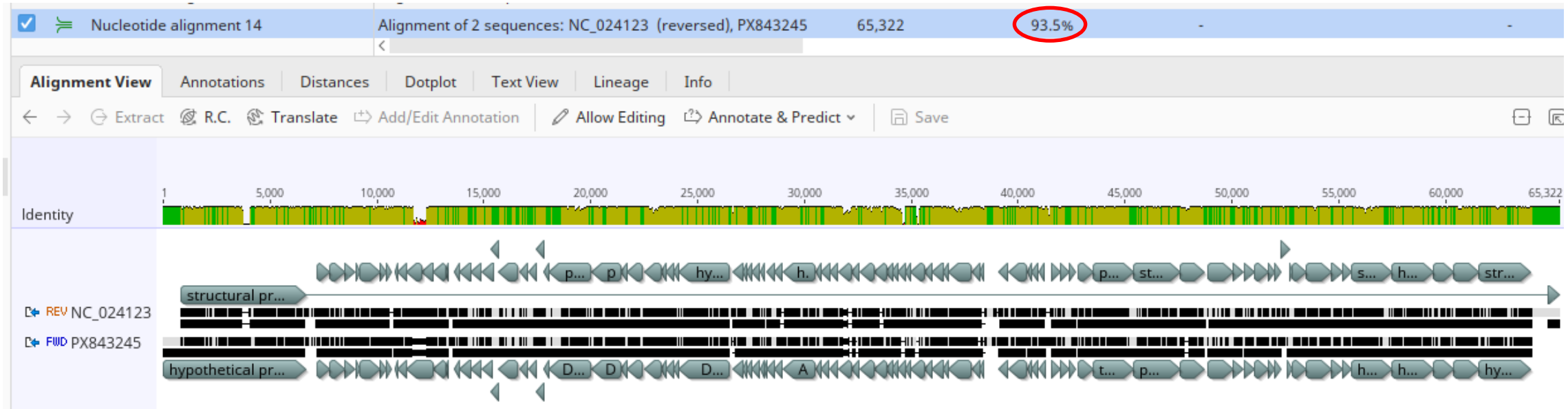
PX843242 (Onen484) with NC_069750 (BUCT-Px-5) – **sequence identity 93.9%**



PX843243 (Onen526) with NC_069750 (BUCT-Px-5) – **sequence identity 96.4% (strain of BUCT-Px-5)**



PX843245 (Lasov521) with NC_024123 (KPP25) – **sequence identity 93.5%**



PX843246 (Kovar531) with MT119371 (oldone) – **sequence identity 91.1%**

