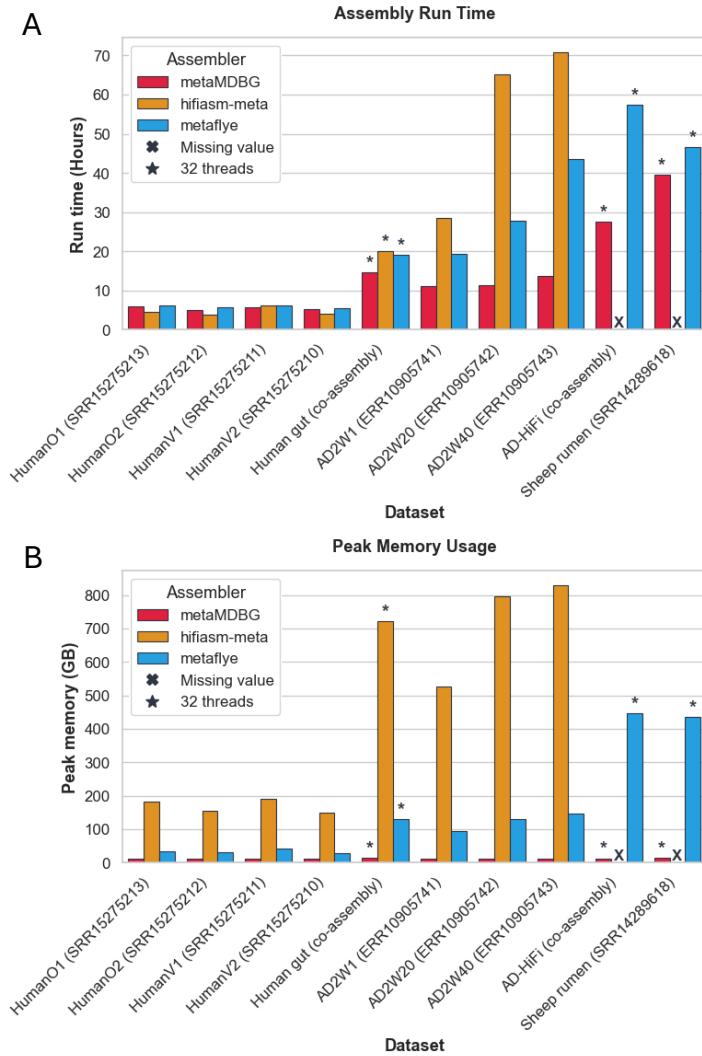


Supplementary Figures for the Report: High-quality metagenome assembly from long accurate reads with metaMDBG

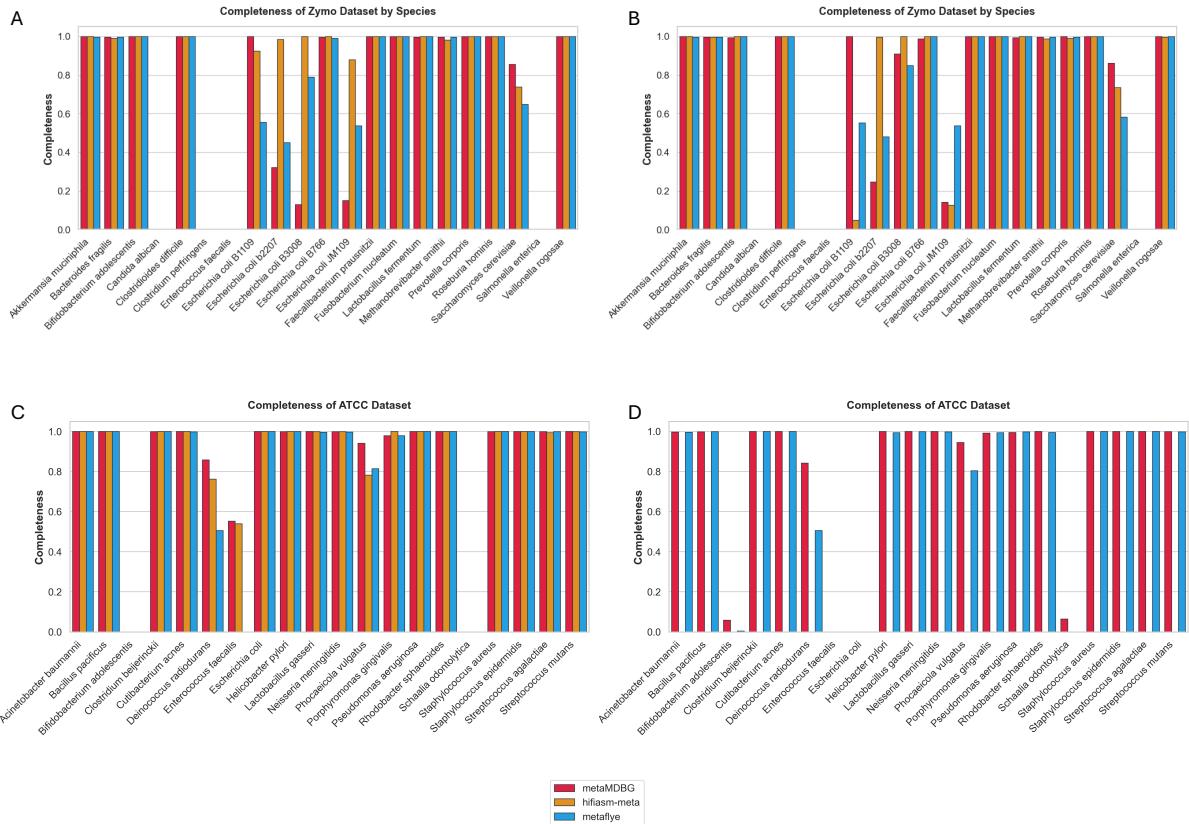
Brauckhoff, Tim Leon; Engeln, Eva Johanna; Freiwald, Johanna;

February 2, 2026



Supplementary Figure 1: Runtime and Memory usage. The run time (A) and the peak memory usage (B) for the real communities assemblies with a default of 16 threads was collected. For the co-assemblies and the sheep rumen sample 32 threads were used (marked with a star). Two assemblies of the real communities were not successfully performed for hifiasm-meta (marked with a cross). metaMDBG in red, hifiasm-meta in orange and metaFlye in blue.

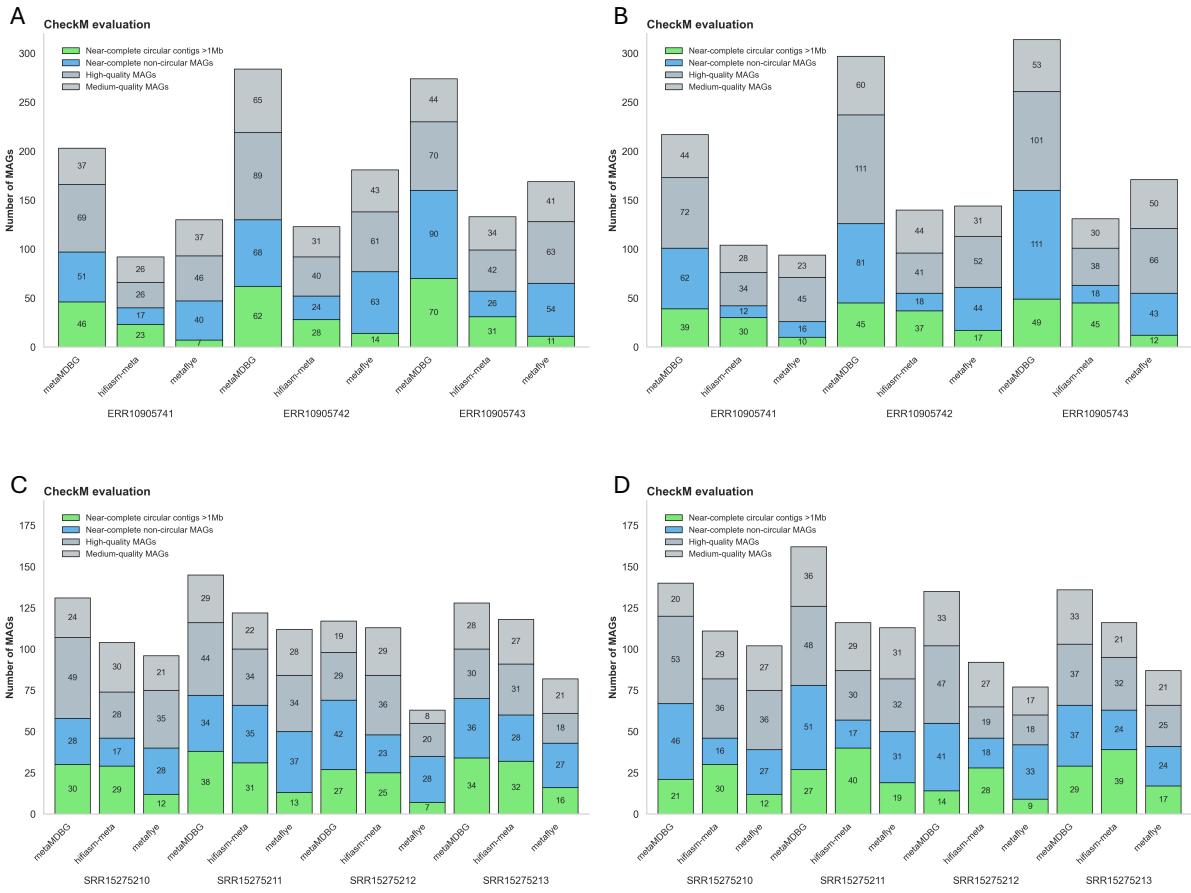
Results Benoit et al.



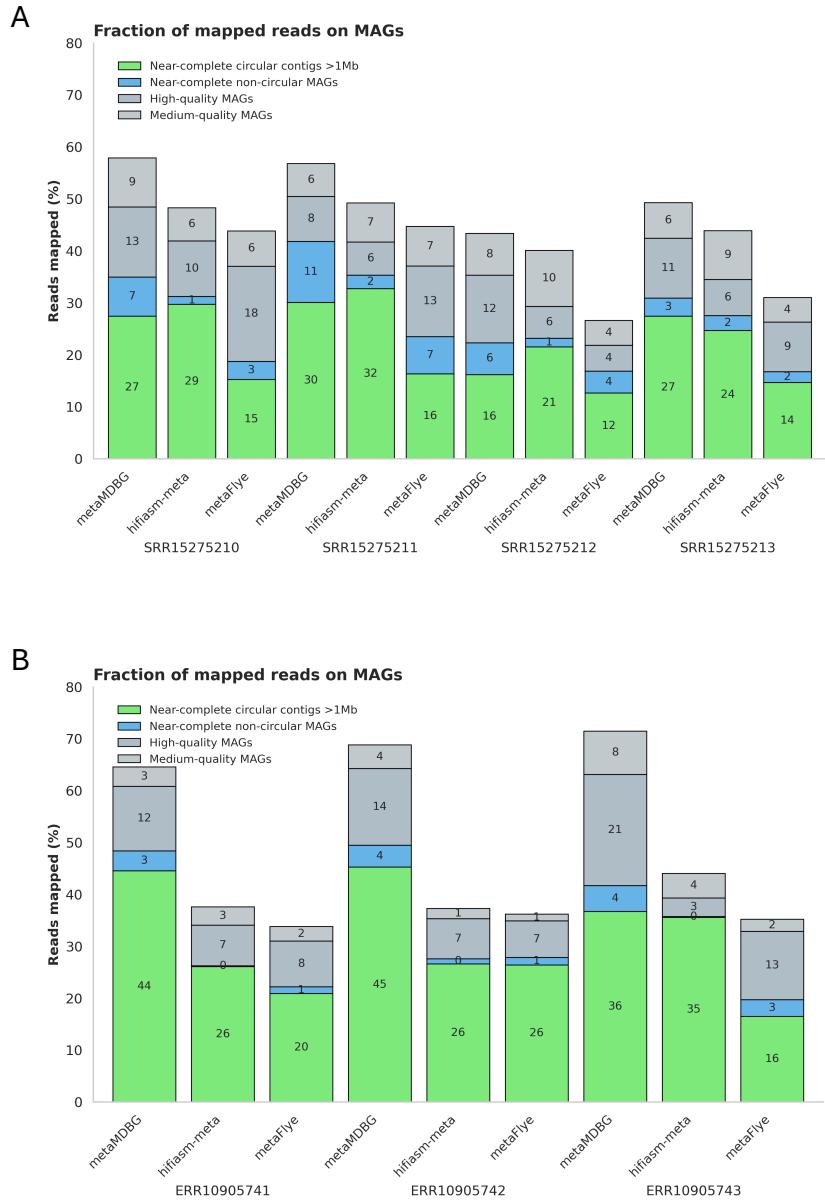
Supplementary Figure 2: Completeness mock communities. For the assembly of mock communities Zymo-HiFi (A and B) and ATCC (C and D) the results were compared to the reference and the completeness was computed with wfsmash. On the right (A and C) the completeness of Benoit et al. is shown whereas the left side (B and D) shows the reproduced results. metaMDBG in red, hifiasm-meta in orange and metaFlye in blue.

Results Benoit et al.

Reproduced assemblies

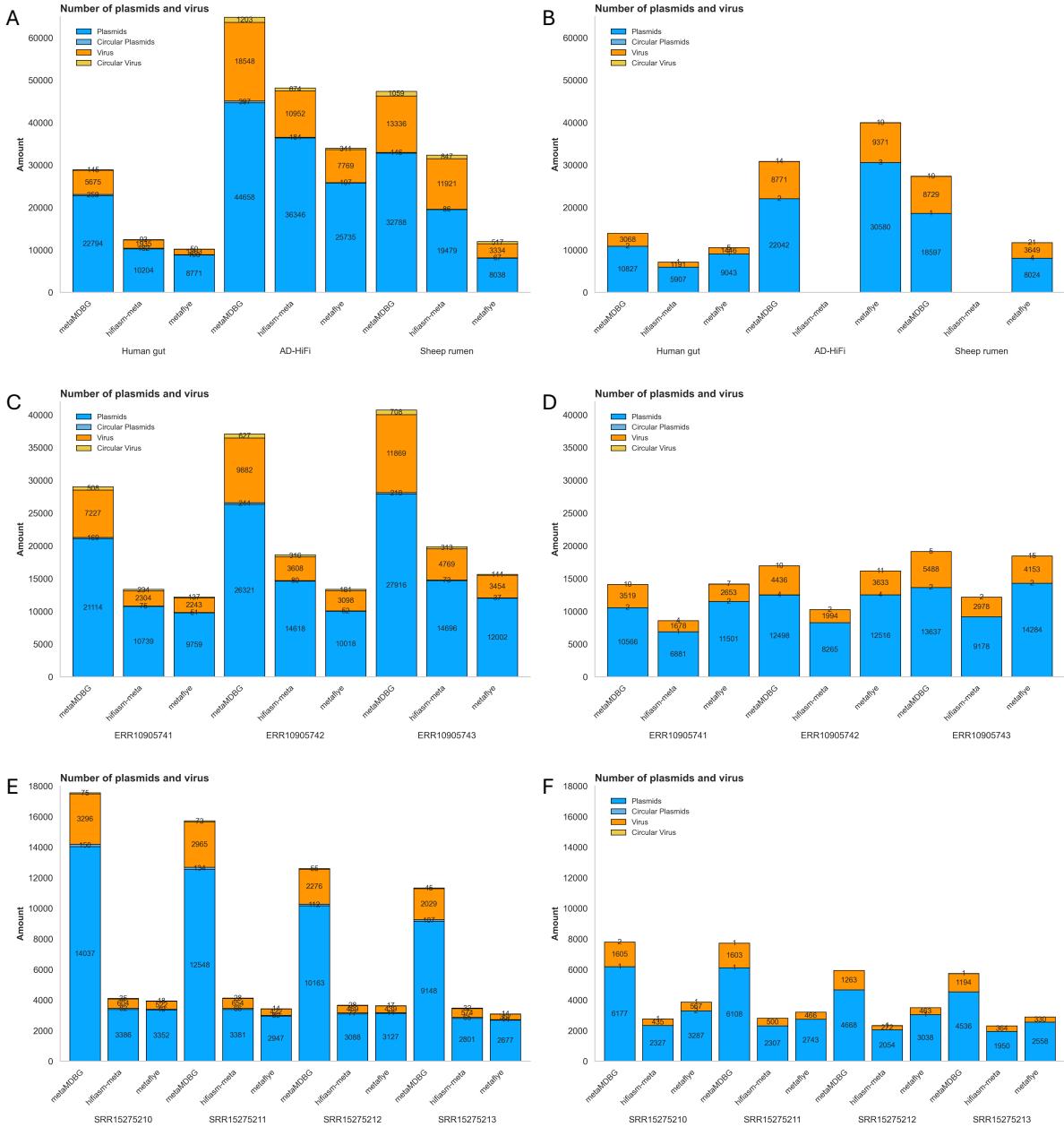


Supplementary Figure 3: CheckM evaluation. The single samples of the real communities of the human gut (A and B) and AD-HiFi (C and D) from Benoit et al. are shown on the right (A and C) and the reproduced results on the left (B and D). A MAG is considered ‘near-complete’ if its completeness is $\geq 90\%$ and contamination is $\leq 5\%$ (circularized - green, non-circularized - blue); ‘high quality’ if its completeness is $\geq 70\%$ and contamination is $\leq 10\%$ (dark gray); and ‘medium quality’ if its completeness is $\geq 50\%$ and contamination is $\leq 10\%$ (light gray).



Supplementary Figure 4: Percentage of mapped HiFi reads on MAGs. The single samples of the real communities human gut in Panel A and AD-HiFi in Panel B are shown dependent on the quality assessed with checkM. A MAG is considered ‘near-complete’ if its completeness is $\geq 90\%$ and contamination is $\leq 5\%$ (circularized - green, non-circularized - blue); ‘high quality’ if its completeness is $\geq 70\%$ and contamination is $\leq 10\%$ (dark gray); and ‘medium quality’ if its completeness is $\geq 50\%$ and contamination is $\leq 10\%$ (light gray).

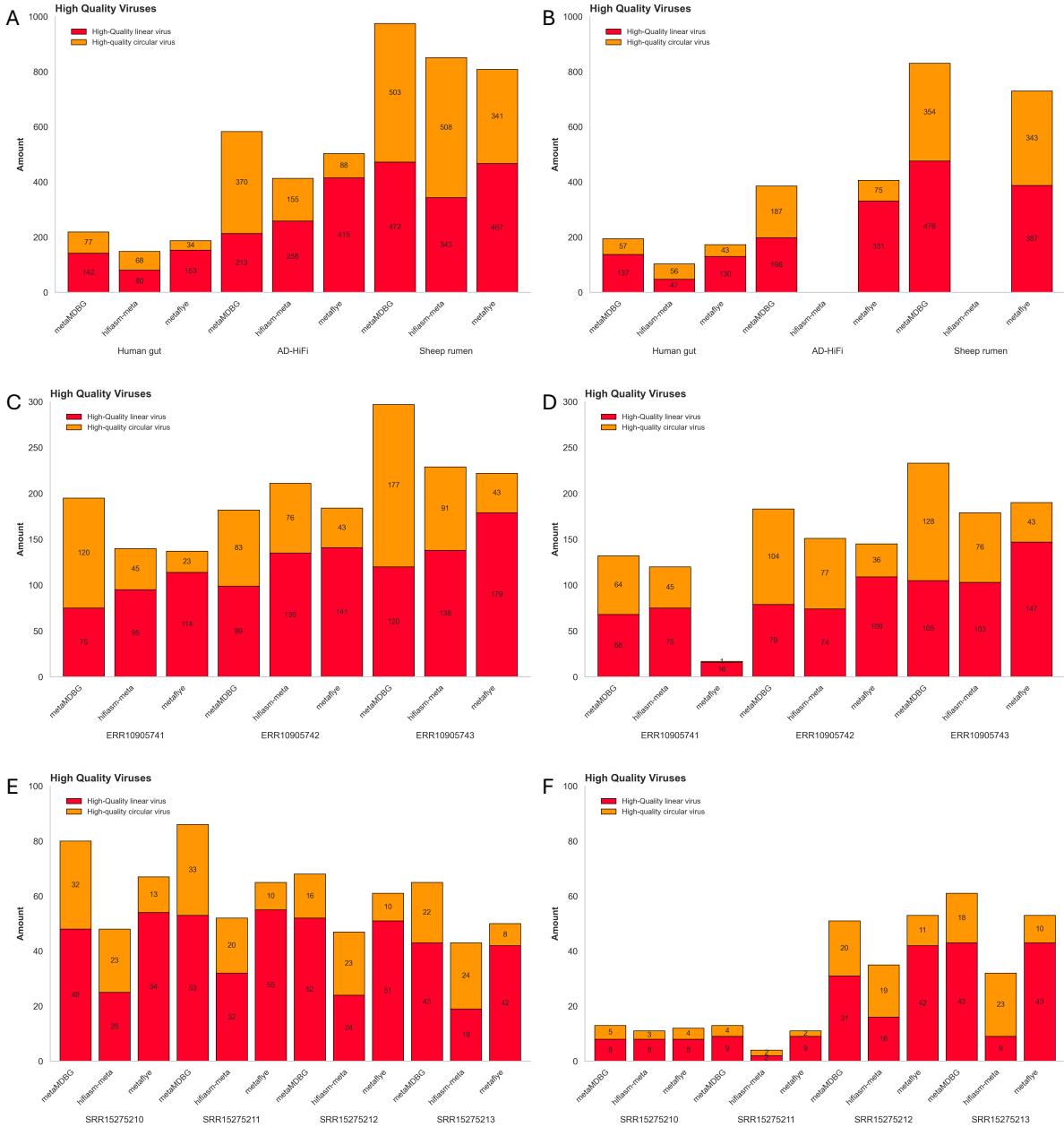
Results Benoit et al.



Supplementary Figure 5: Reconstruction of plasmids and viruses. The number of reconstructed plasmids and viruses for the real communities with viralVerify. The results from Benoit et al. are shown on the left (A, C, and E) and the reproduced results on the right (B, D, and F). Panels A and B show the co-assemblies and sheep rumen sample; C and D the AD-HiFi single samples; and E and F the Human gut single samples.

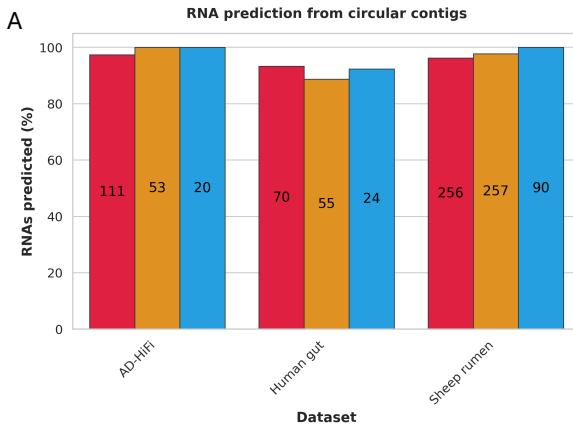
Results Benoit et al.

Reproduced assemblies

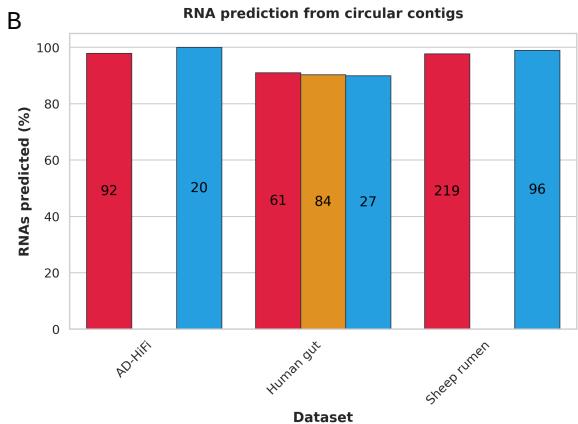


Supplementary Figure 6: High quality viruses. The number of high-quality viruses identified in the real community assemblies with checkV. The results from Benoit et al. are shown on the left (A, C, and E) and the reproduced results on the right (B, D, and F). Panels A and B show the co-assemblies and sheep rumen sample; C and D the AD-HiFi single samples; and E and F the Human gut single samples.

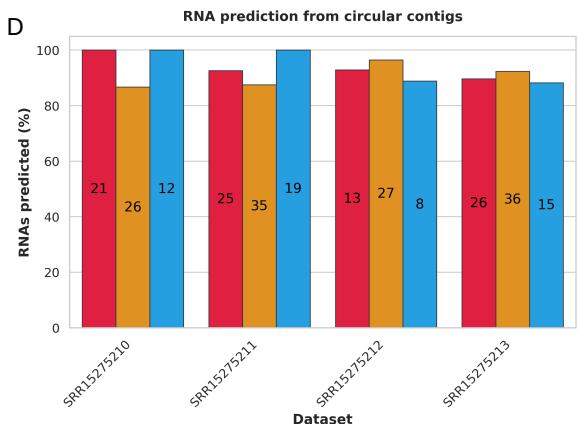
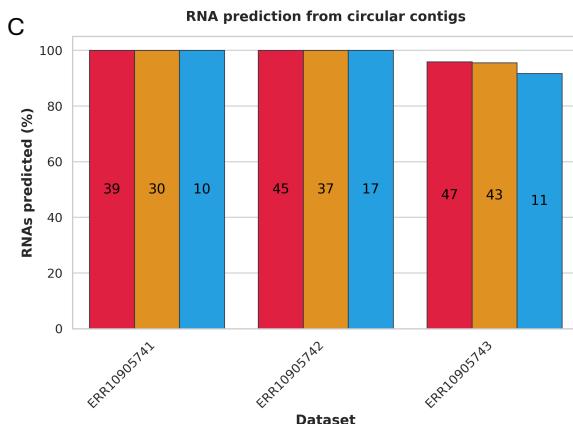
Results Benoit et al.



Reproduced assemblies



Reproduced assemblies – Single samples



■ metaMDBG
■ hifiasm-met
■ metaflye

Supplementary Figure 7: Fraction of near-complete circular contigs with RNA genes.
tRNA and rRNA genes were predicted using Infernal and Barrnap. A and B show the results for the human gut and AD-HiFi co-assemblies as well as the sheep rumen dataset. The results of Benoit et al. are in Panel A, the reproduced results are in Panel B. C and D show the reproduced results for single samples of human gut (C) and AD-HiFi (D). metaMDBG in red, hifiasm-met in orange and metaFlye in blue.