

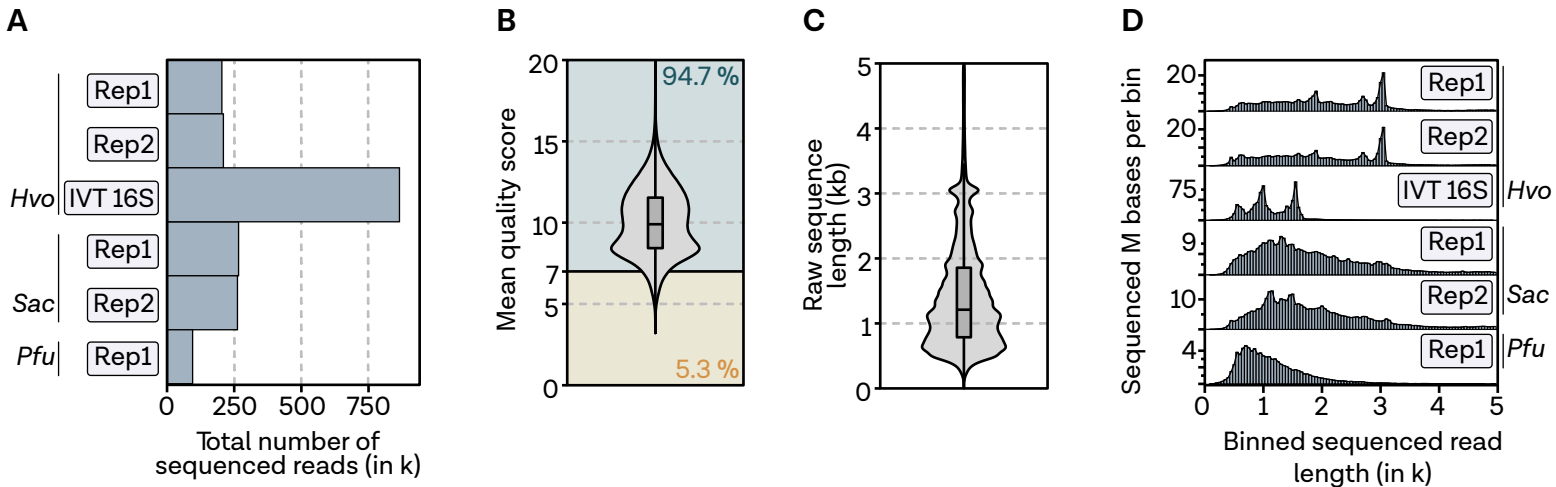


Fig. S2 | Quality control of sequenced cDNA reads.

A, Total number of sequenced reads shown for each library. **B**, Mixed violin/boxplot showing the distribution of the quality scores (mean_qscore_template) and the number of reads passing and failing the quality filter of 7. **C**, Distribution of raw sequence length for all libraries containing total RNA. **D**, Distribution of binned sequence read length (bin size 50 nt).