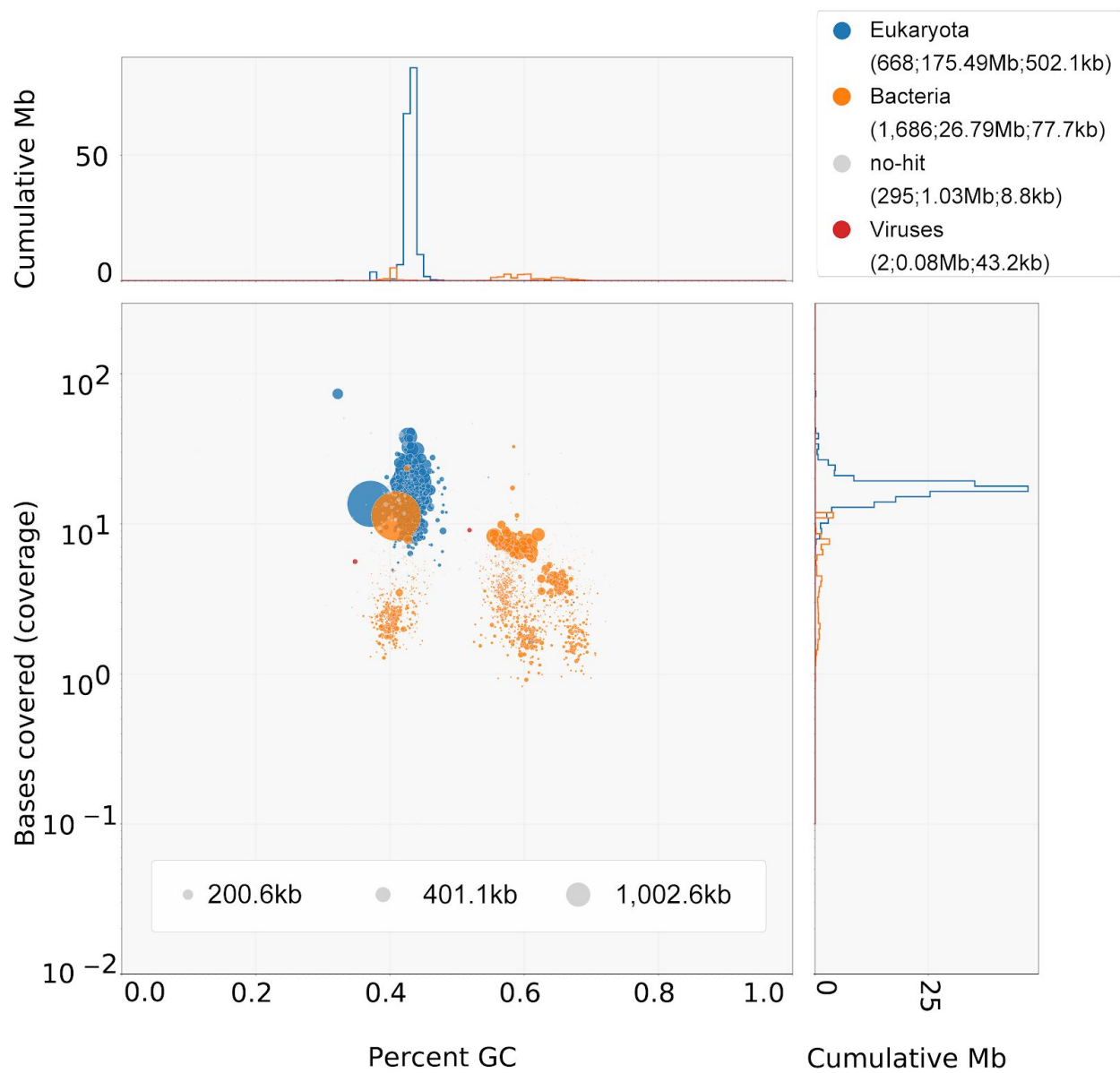**Figure S1.** Read length histograms of the raw (A, B) and trimmed (C, D) nanopore reads.

Figure S2. Blobplot showing the taxon-annotated GC content and coverage of the *C. cryptica* metagenome assembly. Legend format: "superkingdom (number of scaffolds; total scaffold length; scaffold N50 length)".
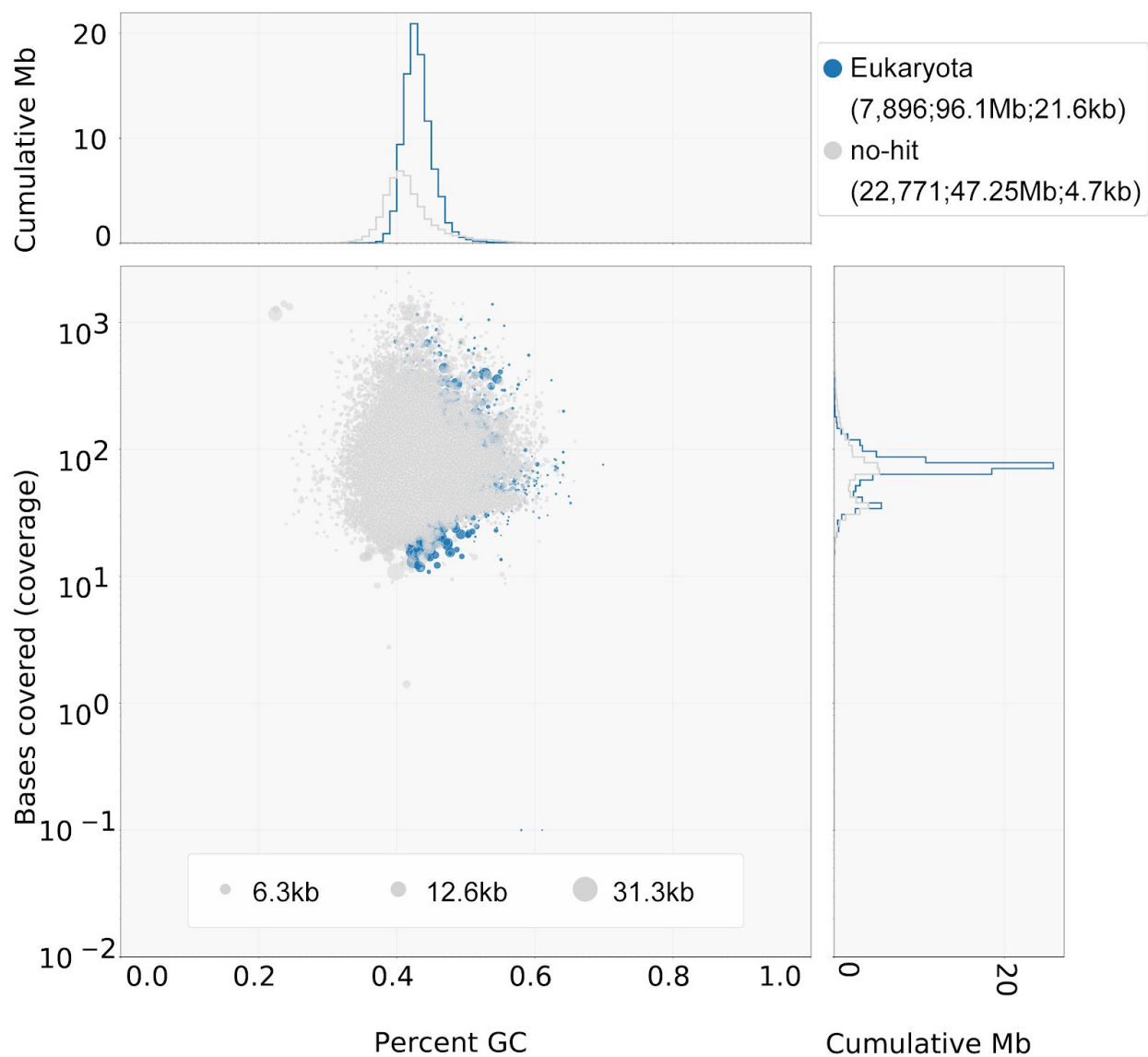
Figure S3. Blobplot showing the taxon-annotated GC content and coverage of the filtered *C. cryptica* ver. 1.0 assembly, after removing short (<1 kb) and contaminant scaffolds (taxonomic assignment to bacteria or viruses). Legend format: "superkingdom (number of scaffolds; total scaffold length; scaffold N50 length)".