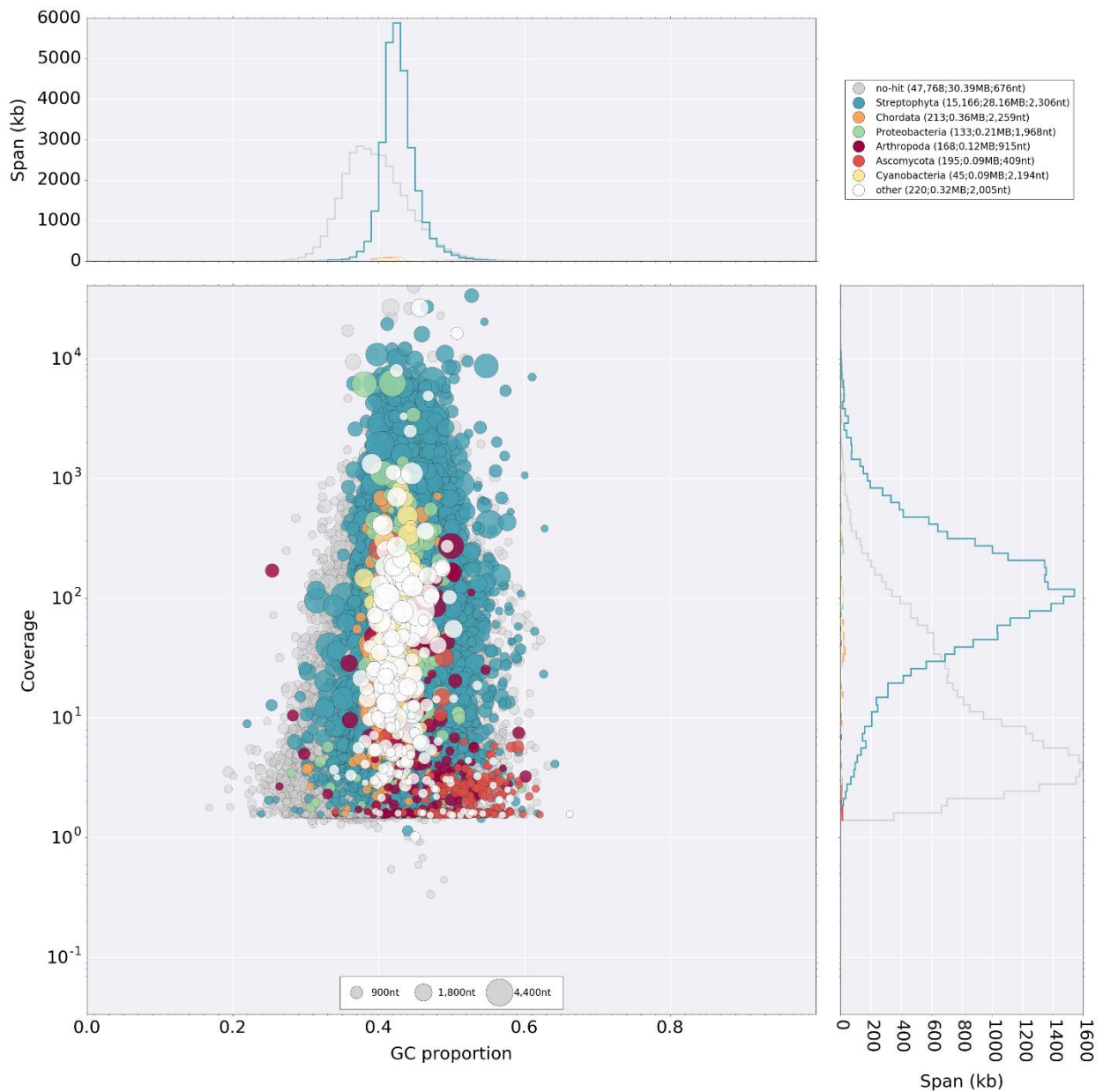**Supplementary fig. S2. Blobtools analysis of the transcriptome. (A)** Mapping of reads to sequences from different organism classes, linked to GC contents. **(B)** Summary of results. Note that these results are based on raw reads, not on assembled contigs.

A

B