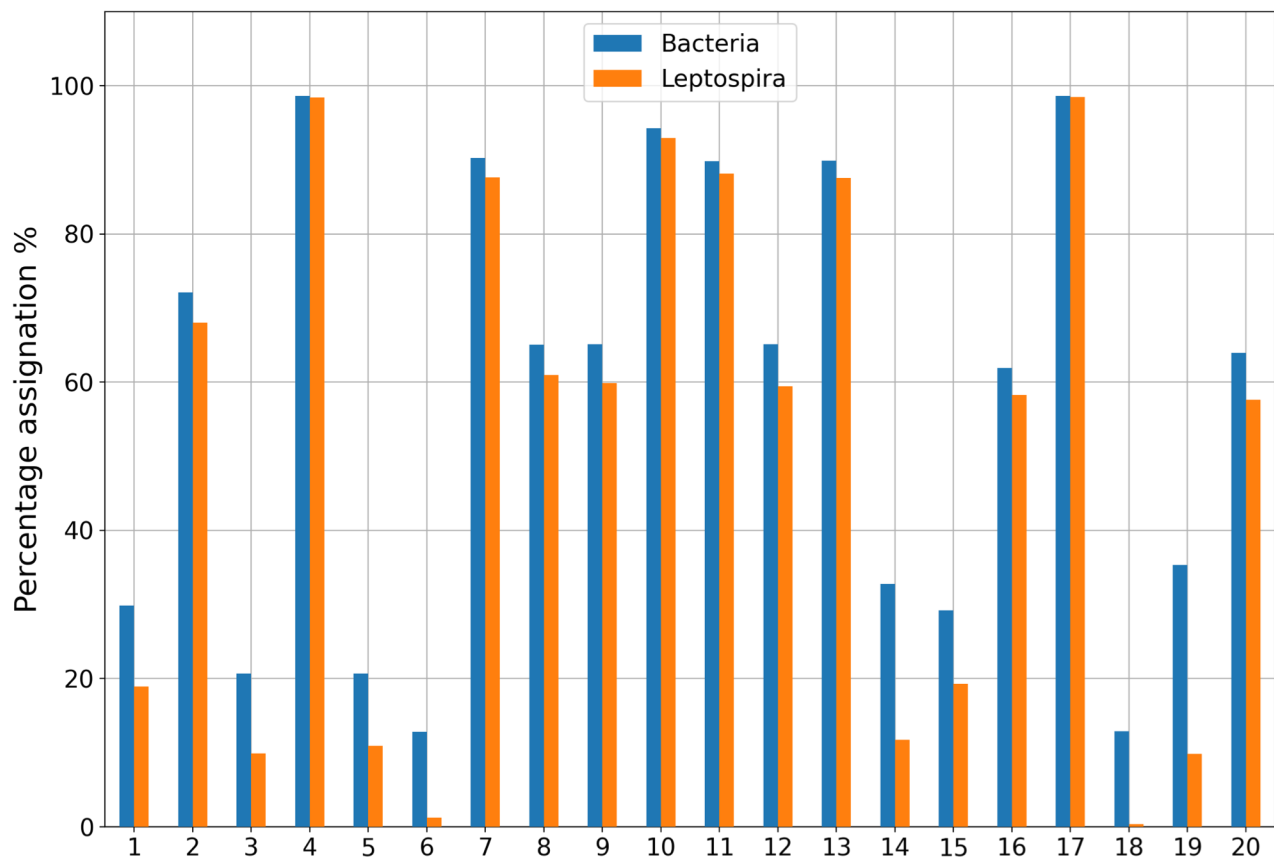
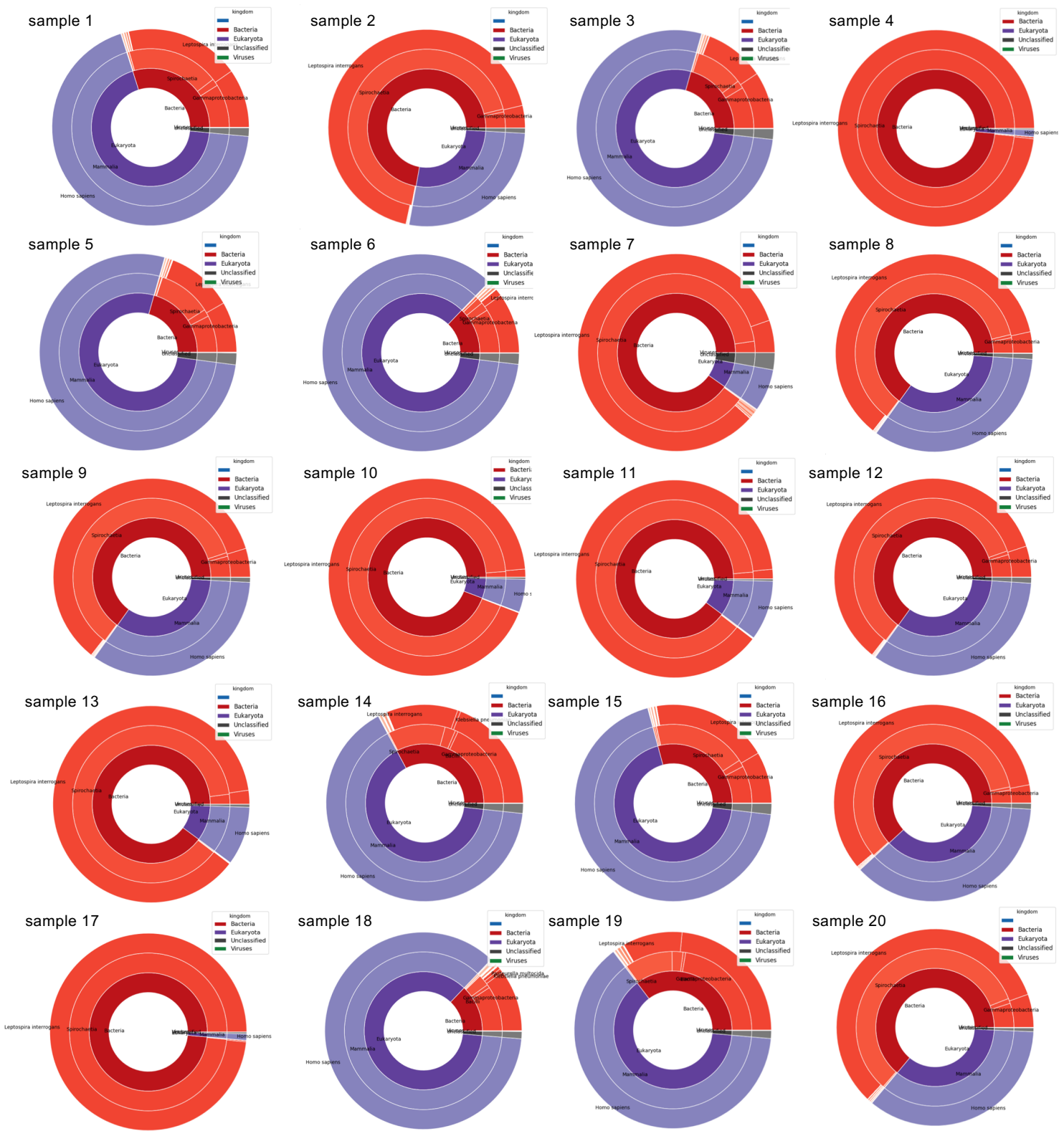
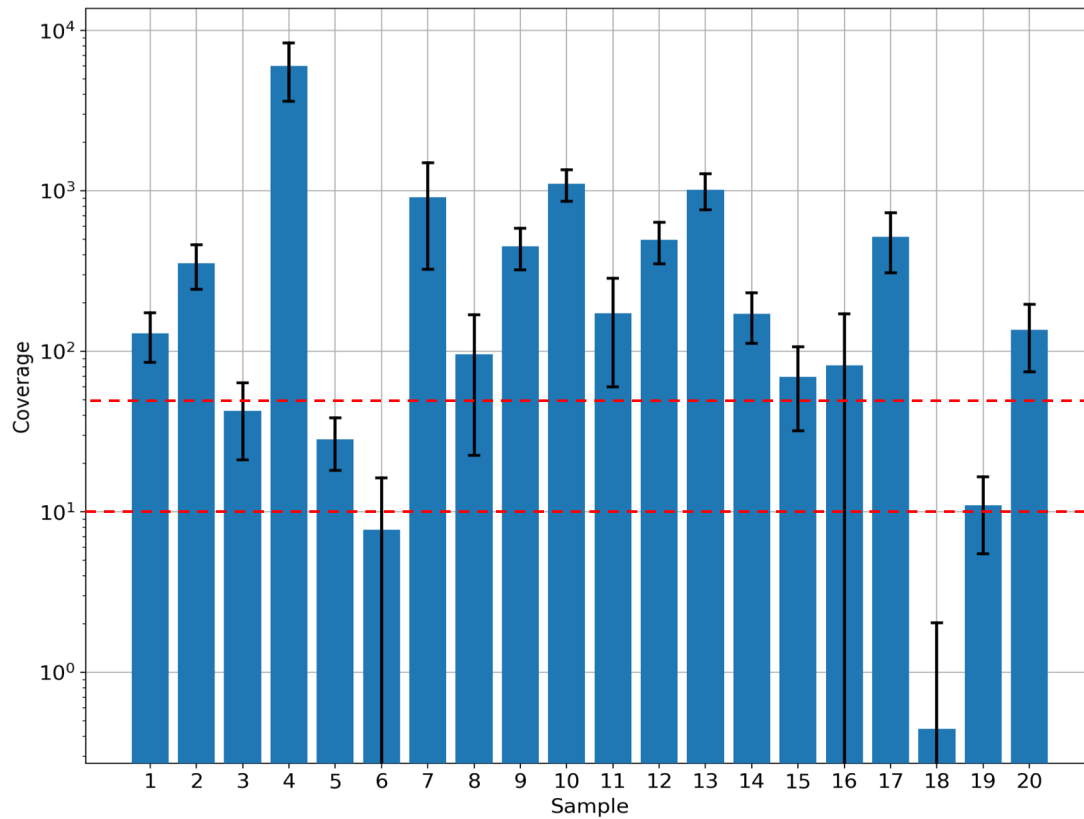




Sup. Fig. 1 : Proportion of reads of the 20 samples assigned to bacteria genomes (blue bars) and proportion of reads assigned specifically to the *Leptospiraceae* family (orange bars).

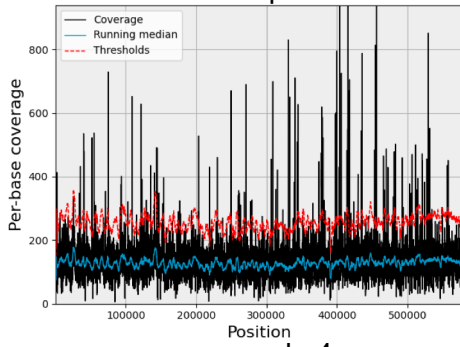


Sup. Fig 2 : Taxonomic assignment of the reads of the 20 samples by Kraken2

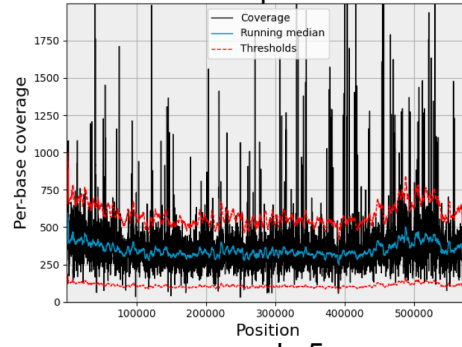


Sup. Fig. 3 : Coverage depth of the *L. interrogans* core genome across samples. The coverage depth on average for all samples is above 50X (top dashed red line) in most samples (sample 3 coverage equal 42X). Sample 5 and 6 have low coverage of 28X and 8X. Sample 18 coverage is below 1X. Black bars give the ± 1 standard deviation.

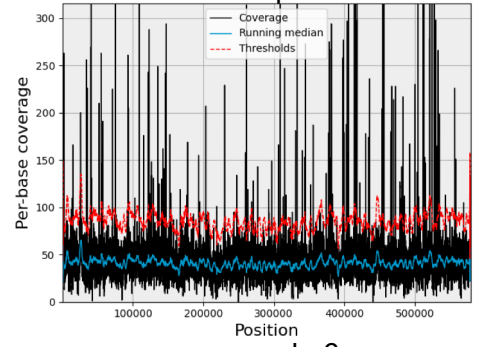
sample 1



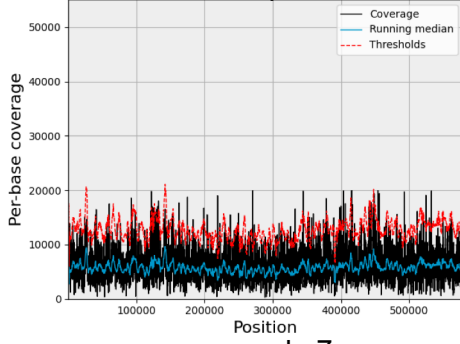
sample 2



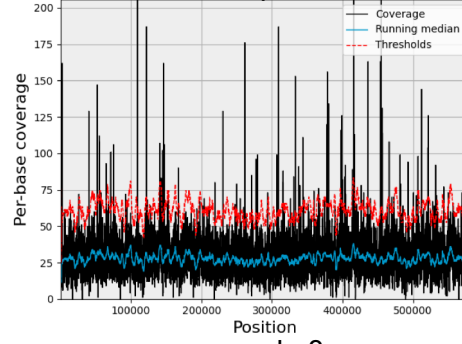
sample 3



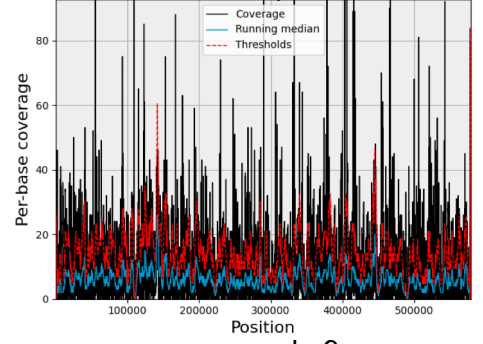
sample 4



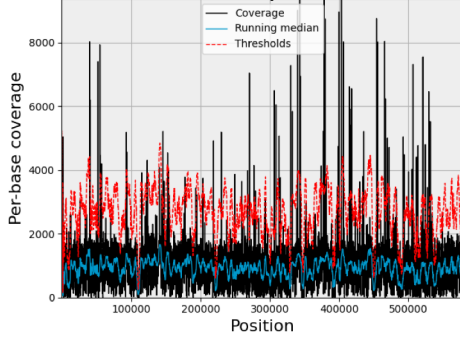
sample 5



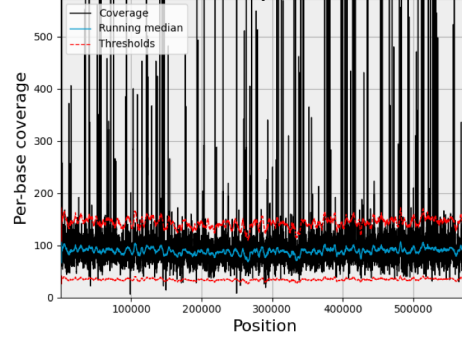
sample 6



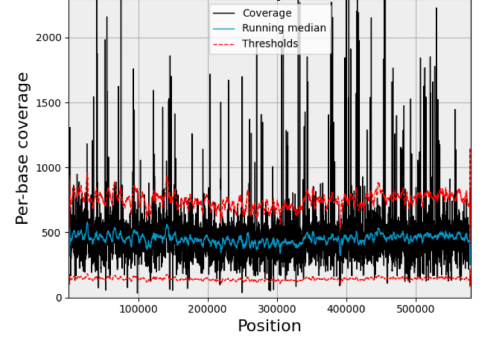
sample 7



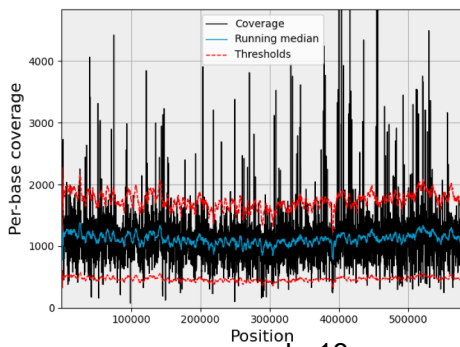
sample 8



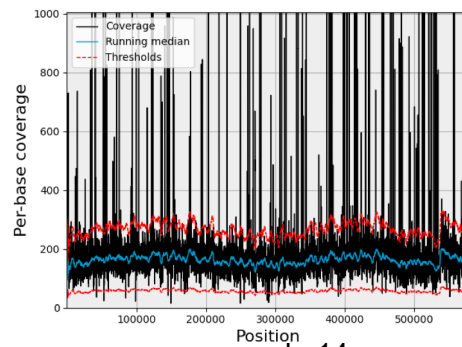
sample 9



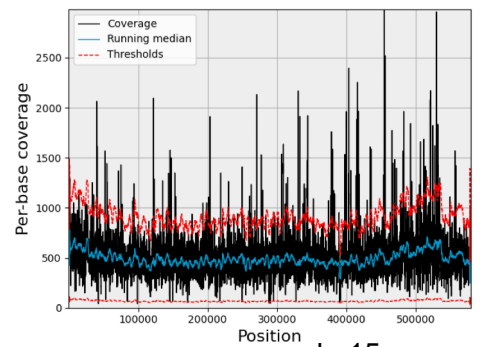
sample 10



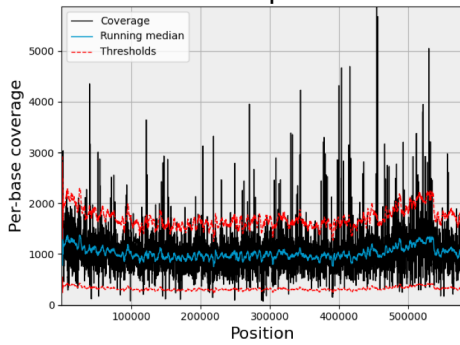
sample 11



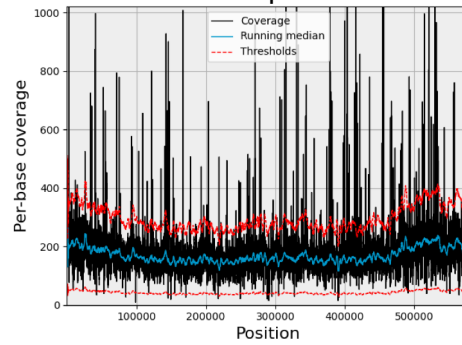
sample 12



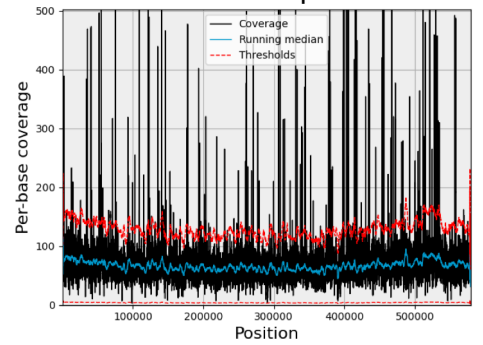
sample 13



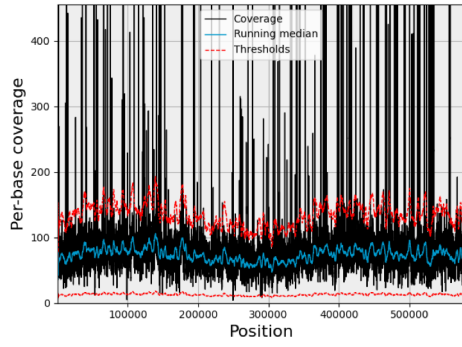
sample 14



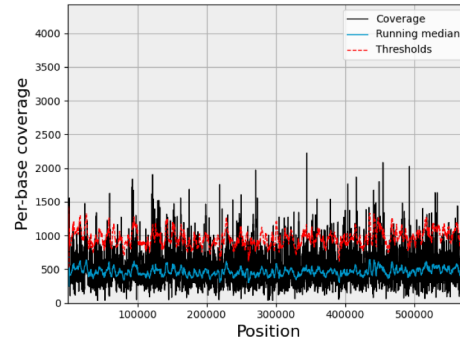
sample 15



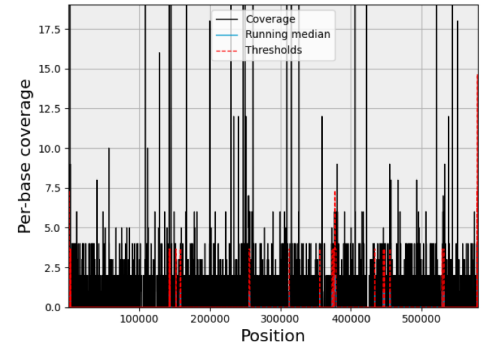
sample 16



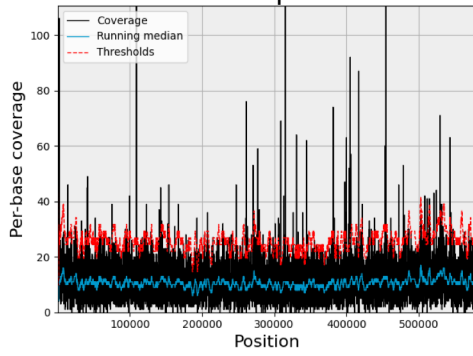
sample 17



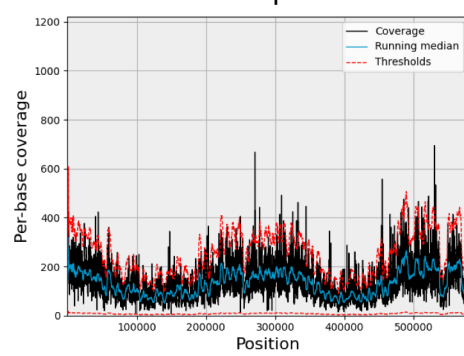
sample 18



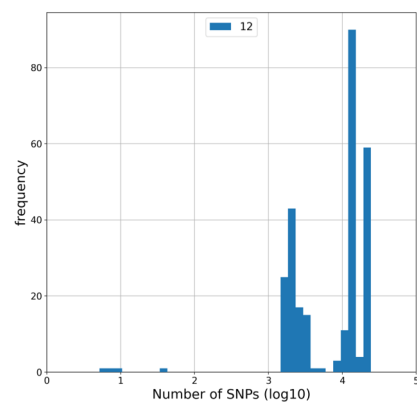
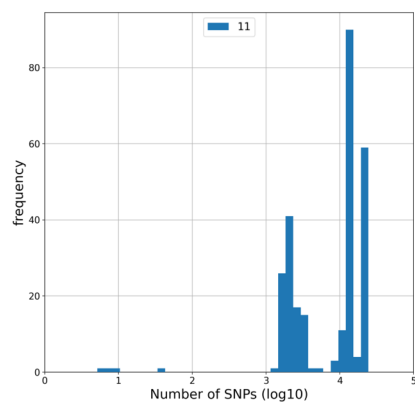
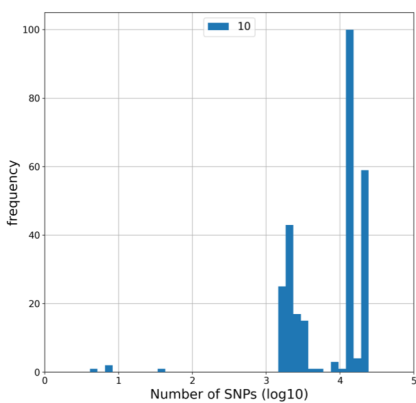
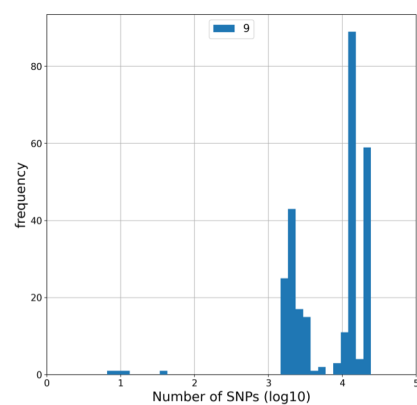
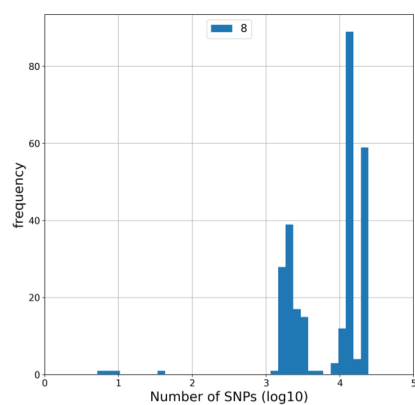
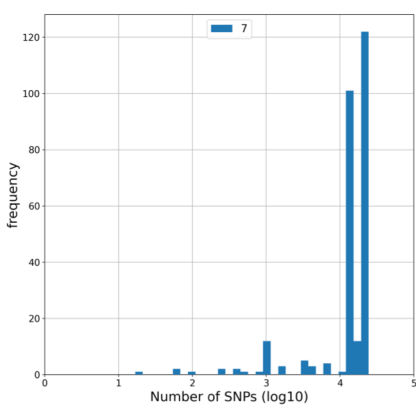
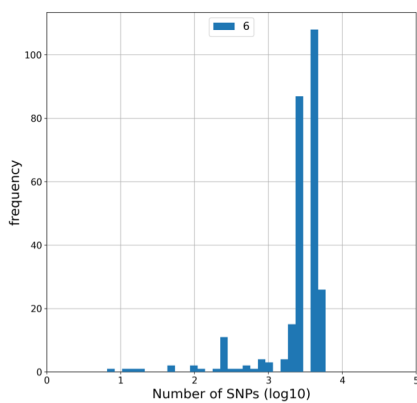
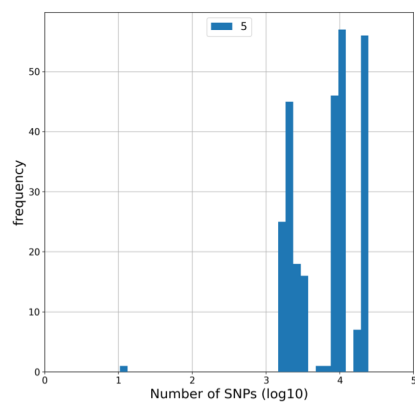
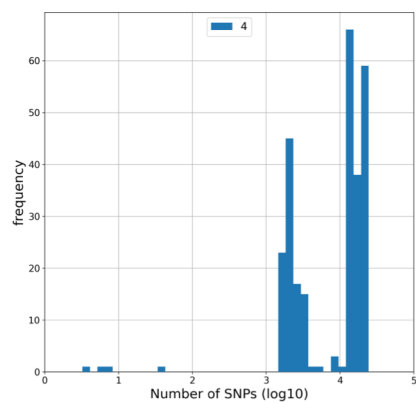
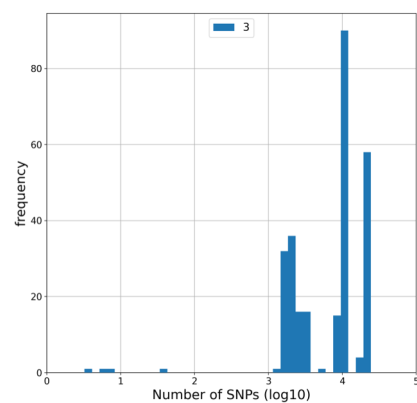
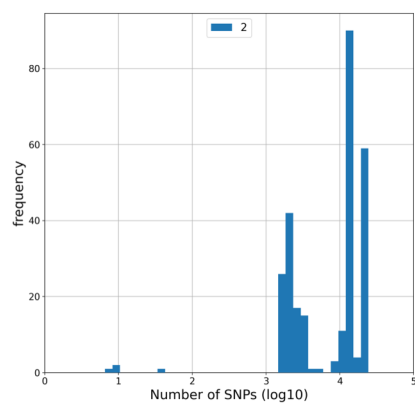
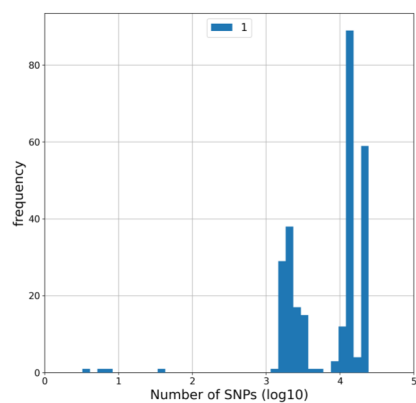
sample 19

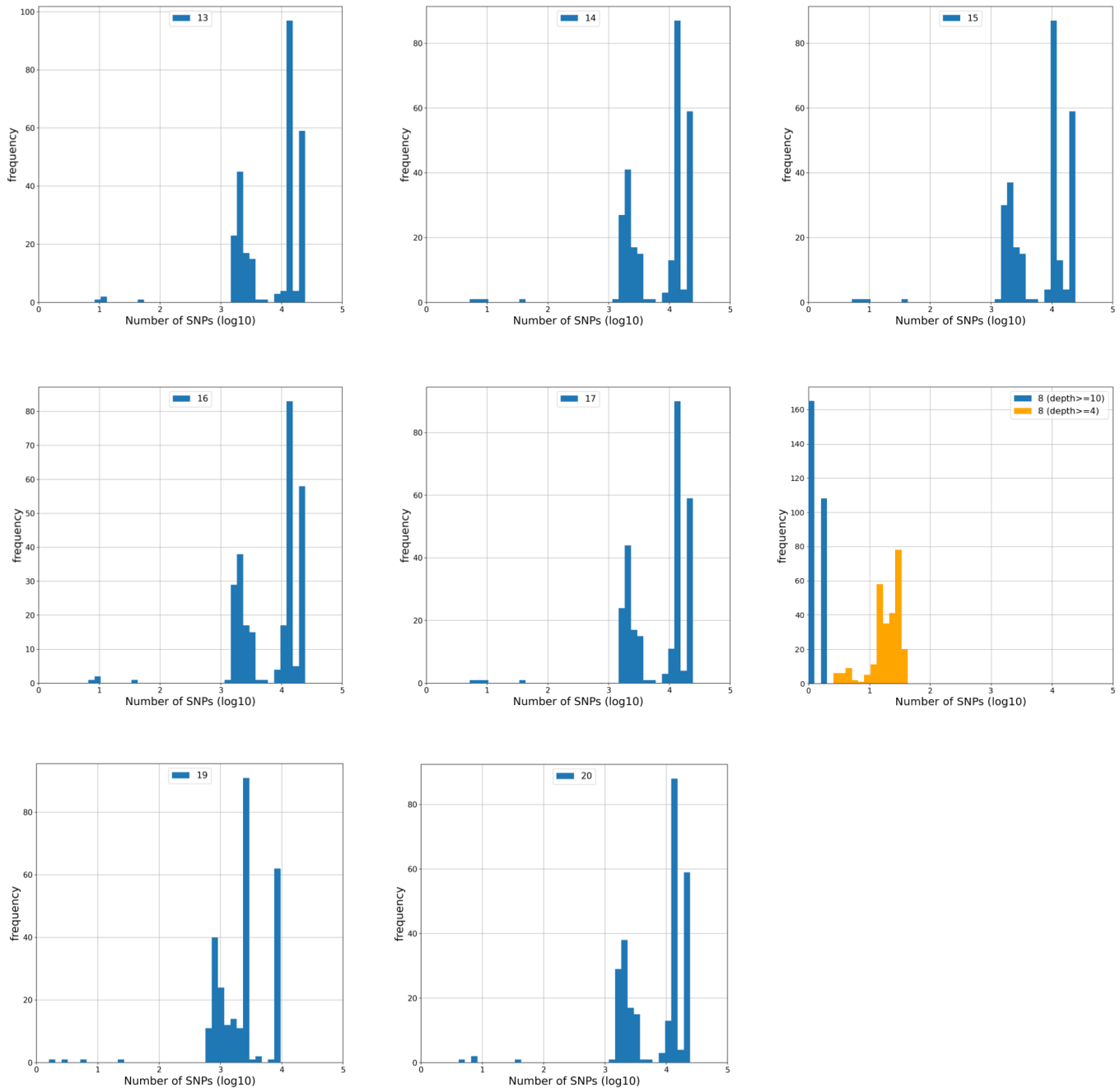


sample 20



Sup. Fig. 4 : Depth coverage of the 20 samples across the *L. interrogans* core genome





Sup. Fig. 5 : Histogram of SNP counts found in the 20 samples across all 273 genomes.

For each of the 20 samples, we called variants using the 273 references of *Leptospira* (sup. Table 2) independently. For each genome, we obtained a set of SNPs that were filtered out to remove low quality variants (frequency below 10, uneven strand balance). Reference genomes distant from a sample led to thousands of SNPs while closely-related genomes led to less than 10 SNPs. Minimizing the count gives the closet genome to a given sample. Number of SNPs found in the 20 samples across all 273 genomes. Most genomes have more than 10,000 SNPs while only a few exhibit SNPs below 100.