

Resource Summary Report

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Script R1: Virome Contig and Sequencing Statistics

DOI:10.17504/protocols.io.eh5bb86

Type: Protocol

Proper Citation

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Protocol Information

URL: <https://dx.doi.org/10.17504/protocols.io.eh5bb86>

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Group: VERVE Net, Club Grice

Summary: This protocol outlines the analysis used to plot contig coverage statistics, as well as sequence count and length stats. We begin with visualizing contig length vs coverage. We then visualize the distributions of sequence counts per sample as a probability density plot (similar idea as a histogram), and then do the same for median sequence length. Based on the methods from the following publication: Hannigan, Geoffrey D., et al. "The Human Skin Double-Stranded DNA Virome: Topographical and Temporal Diversity, Genetic Enrichment, and Dynamic Associations with the Host Microbiome." mBio 6.5 (2015): e01578-15.

Associated Publications: Kindler L, Stoliartchouk A, Teytelman L, Hurwitz BL, Method-centered digital communities on protocols.io for fast-paced scientific innovation. F1000Research doi: [10.12688/f1000research.9453.2](https://doi.org/10.12688/f1000research.9453.2)

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