

Resource Summary Report

Generated by [dkNET](#) on Sep 3, 2026

Script R5: Virome Alpha Diversity

DOI:10.17504/protocols.io.eimbcc6

Type: Protocol

Proper Citation

HANNIGAN GD, GRICE EA, ET AL. 2016. Script R5: Virome Alpha Diversity. protocols.io dx.doi.org/10.17504/protocols.io.eimbcc6

Protocol Information

URL: <https://dx.doi.org/10.17504/protocols.io.eimbcc6>

Authors: HANNIGAN GD, GRICE EA, ET AL.

Group: VERVE Net, Club Grice

Summary: This protocol outlines our alpha diversity analyses of the virome (from PHACCS) and whole metagenome (from MetaPhlan OTU table). We start by comparing the virome and whole metagenome alpha diversity values, and then look at the differences in virome and whole metagenome diversity between skin sites. 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)

Affiliations: DEPARTMENT OF DERMATOLOGY UNIVERSITY OF PENNSYLVANIA, DEPARTMENT OF DERMATOLOGY UNIVERSITY OF PENNSYLVANIA, DEPARTMENT OF DERMATOLOGY UNIVERSITY OF PENNSYLVANIA

External URL: <http://mbio.asm.org/content/6/5/e01578-15.full>

Version: 1

Publication Date: 2016

Proper Citation: HANNIGAN GD, GRICE EA, ET AL. 2016. Script R5: Virome Alpha Diversity. protocols.io dx.doi.org/10.17504/protocols.io.eimbcc6

Record Creation Time: 20210329T220537+0000

Record Last Update: 20210329T221042+0000

Data and Source Information

Source: