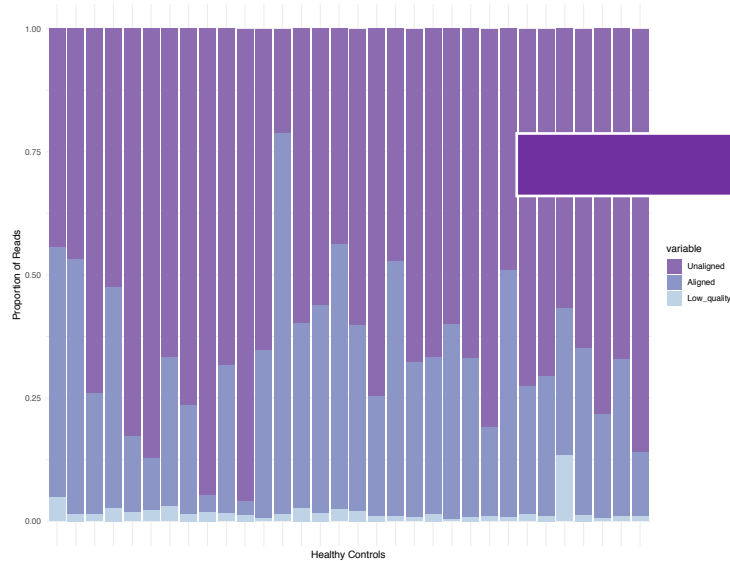


Questions and Goals

- In our hands, how much of the skin microbiome is dark matter?
- **What are the genus and species-level holes in the database that we can fill with publicly available reference genomes?**
- What are the strain level holes in the database that we need to fill by culturing and sequencing?

Identifying missing microbial taxa



363,525,943 reads
BLASTn to HTGs,
viral, EST_others,
and nt databases

Retain top hit from
each sequence >50
coverage and >90%
identity