Supplemental Figures

Figure S1: **Sequencing Depth Summary.** *Number of sequences that aligned to (A) Phage and (B) Bacteria operational genomic units per sample and colored by study.*
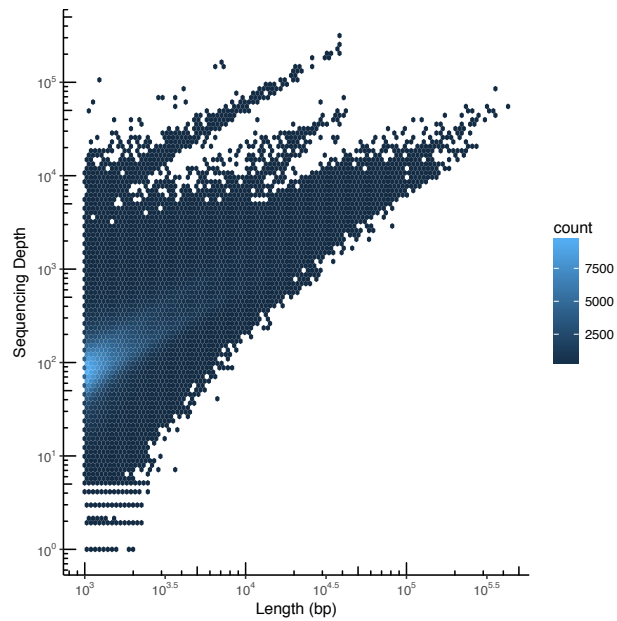
Figure S2: **Contig Summary Statistics.** *Scatter plot heat map with each hexagon representing the abundance of contigs. Contigs are organized by length on the x-axis and the number of aligned sequences on the y-axis.*
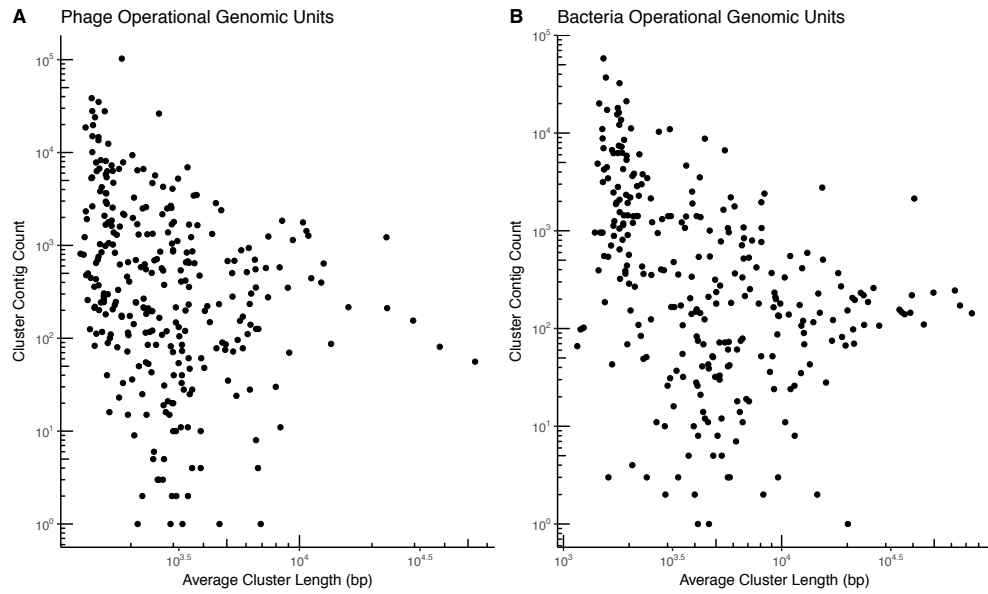
Figure S3: **Operational Genomic Unit Summary Statistics.** *Scatter plot with operational genomic unit clusters organized by average contig length within the cluster on the x-axis and the number of contigs in the cluster on the y-axis. Operational genomic units of (A) bacteriophages and (B) bacteria are shown.*
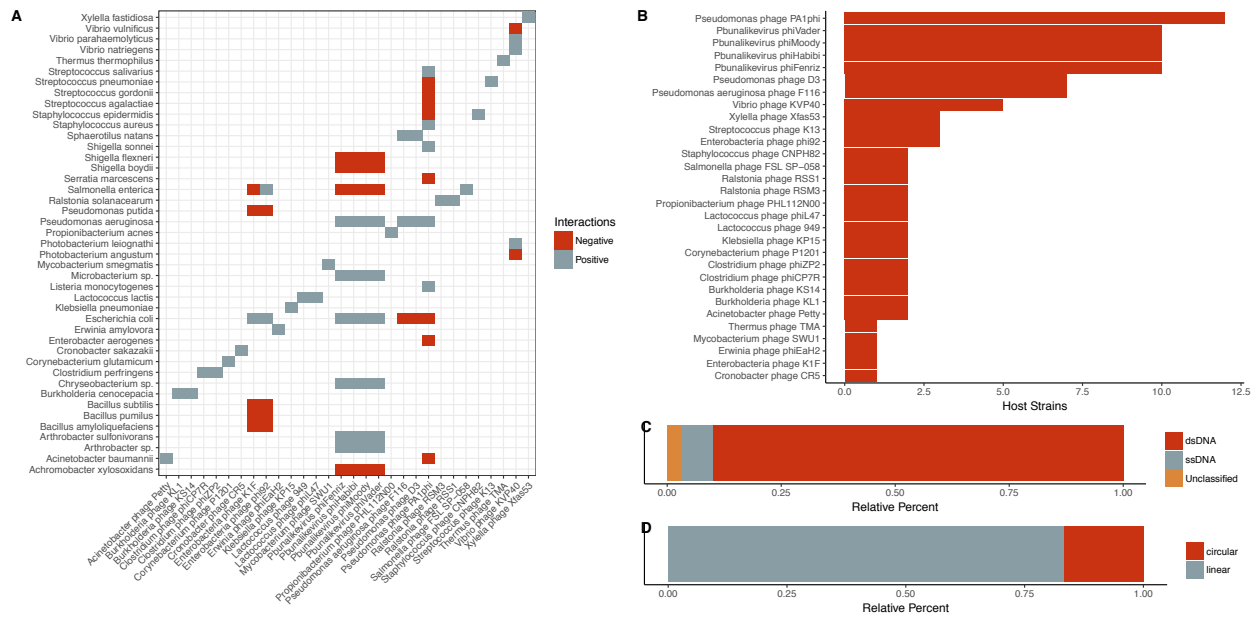
Figure S4: **Summary information of validation dataset used in the interaction predictive model.** *A) Categorical heat-map highlighting the experimentally validated positive and negative interactions. Only bacteria species are shown, which represent multiple reference strains. Phages are labeled on the x-axis and bacteria are labeled on the y-axis. B) Quantification of bacterial host strains known to exist for each phage. C) Genome strandedness and D) linearity of the phage reference genomes used for the dataset.*
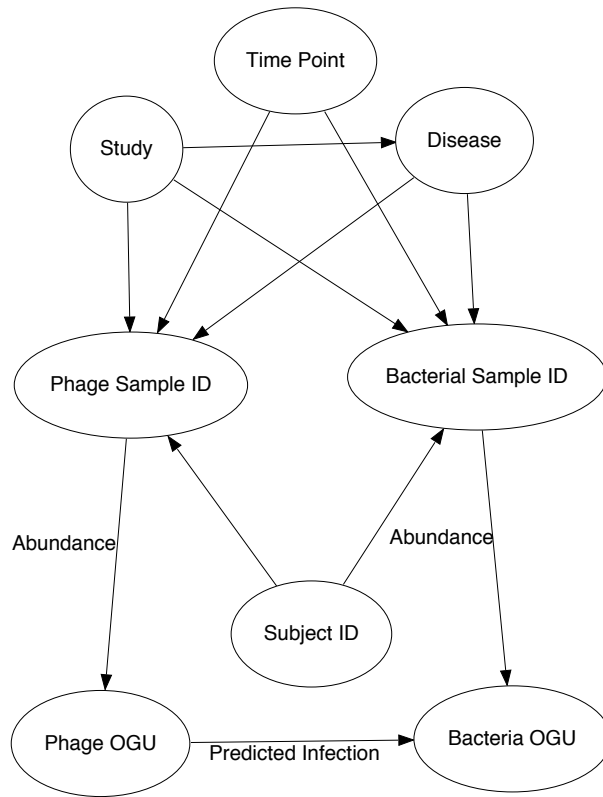
Figure S5: **Structure of the interactive network.** *Metadata relationships to samples (Phage Sample ID and Bacteria Sample ID) included the associated time point, the study, the subject the sample was taken from, and the associated disease. Infectious interactions were recorded between phage and bacteria operational genomic units (OGUs). Sequence count abundance for each OGU within each sample was also recorded.*
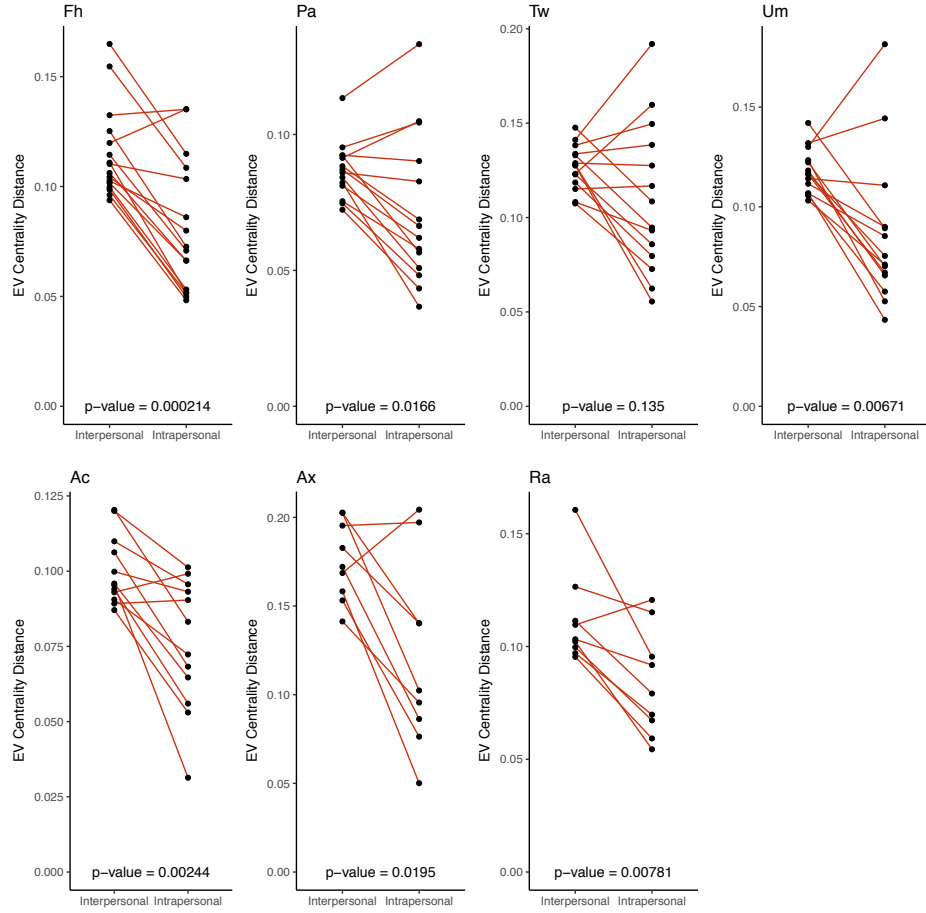
Figure S6: **Intrapersonal vs Interpersonal Dissimilarity of the Skin.** *Quantification of skin network dissimilarity within the same subject and anatomical location over time (intrapersonal) and the mean dissimilarity between the subject of interest and all other subjects at the same time and the same anatomical location (interpersonal), separated by each anatomical site (forehead [Fh], palm [Pa], toe web [Tw], umbilicus [Um], antecubital fossa [Ac], axilla [Ax], and retroauricular crease [Ra]). P-value was calculated using a paired Wilcoxon test.*