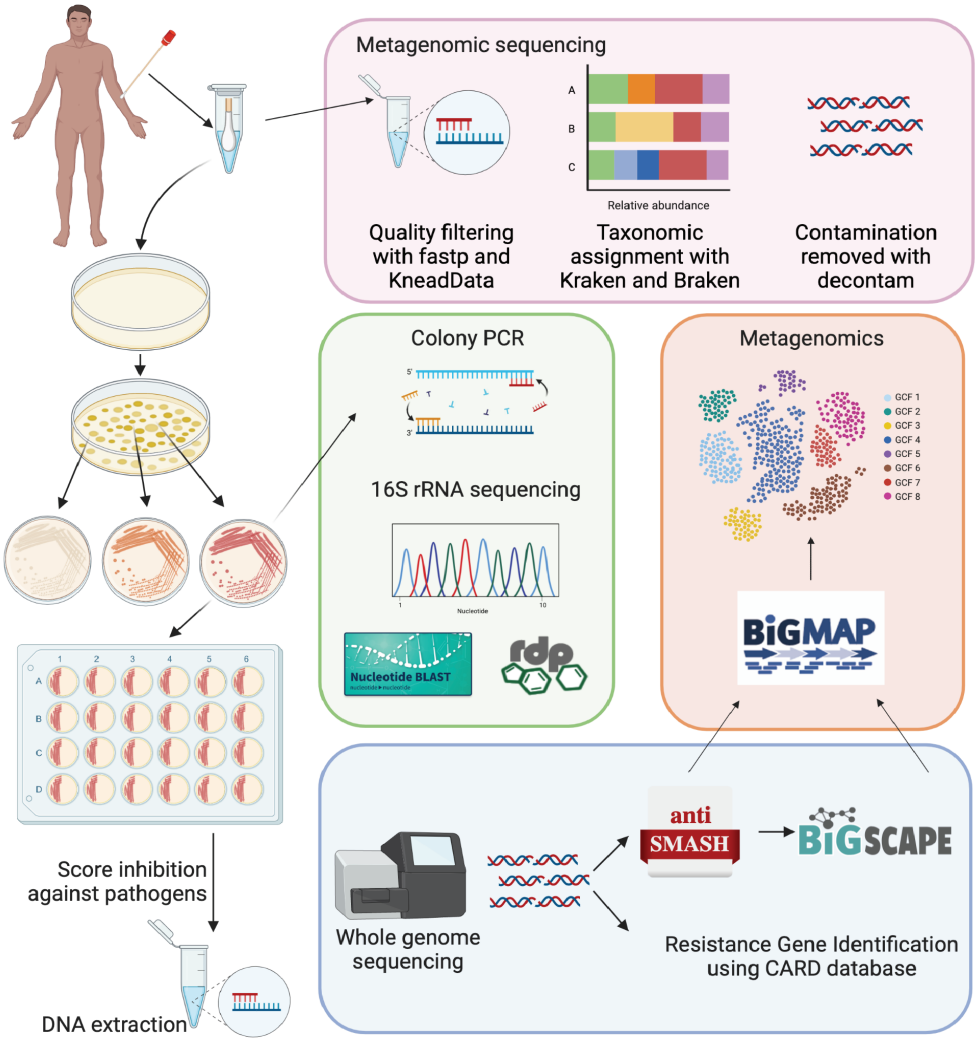

Figure 1. Comprehensive workflow for skin microbiome sampling and genomic analysis. We collected skin samples from each participant from eight different body sites for metagenomic sequencing. A set of skin samples was collected for strain isolation. For metagenomic sequencing, we performed microbiome DNA extractions, followed by quality filtering of raw reads using fastp and KneadData. Taxonomic assignment was achieved using Kraken2 and Bracken, and decontam was used to identify and remove contaminant DNA sequences. For strain isolation, we plated culture samples on selective media to isolate pure bacterial colonies. Strains were identified by 16S rRNA gene sequencing. We assessed these skin isolates for antimicrobial activity using a large-scale biological assay. We sequenced the whole genome for a subset of skin isolates. Genome assembly was performed and dereplicated to acquire distinct representative genomes. We annotated biosynthetic gene clusters and gene cluster families using antiSMASH/BiG-SCAPE and BiG-MAP for genomes and metagenomes, respectively. Lastly, we identified resistant genes using Resistance Gene Identifier (RGI) and the Comprehensive Antibiotic Resistance Gene (CARD) database.