Figure 5: Identification of novel skin species. (**A**) Searching NCBI SRA metagenomes with query genomes of skin isolates. Colors indicate metagenome sample types. (**B**) Assessing biological activity of Aestuariimicrobium LK1188 (first), Brevibacterium LK1337 (second), Corynebacterium LK952 (third), and Kocuria LK960 (fourth) using co-culture screening. Solid line indicates inhibition scores of skin isolates against Gram-positive pathogens (red), Gram-negative pathogens (blue) and fungal pathogens (green). Dotted line indicates the average inhibition score of all skin isolates tested in each corresponding genus against each pathogen type. Investigating novelty of BGC-ome of (**C**) Pairwise interaction between, in columns, LK952 (first), LK960 (second), LK1337 (third), and pathogen control (fourth) against fungal pathogens, in rows, *C. albicans* (first), *C. auris* (second), *T. asahii* (third), and *A. flavus* (fourth) (**D**) Corynebacterium LK952, (**E**) Kocuria LK960, and (**F**) Brevibacterium LK1337 to representative genomes from each genus. Colors indicate BGC type predicted in each species. X-axis indicates the average amino acid identity of a single BGC identified compared to the target genome. Y-axis indicates proportion of genes in identified BGC co-located in the target genome.