



**Fig. 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. **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). Investigating novelty of BGC-ome of **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.