**Table S1: Most abundant genera on the skin metagenomic datasets**

Relative distribution of the 16 most detected genera in the skin metagenomes using the Lowest common ancestor approach.Data were normalized with the total of annotated sequences. + symbolize the detection in rrs- based studies, - the absence ; then the publication associated.

|  |  |  |  |
| --- | --- | --- | --- |
| genus | Relative frequency in individual n°1 (%) | Relative frequency in individual n°2 (%) | Detection in *rrs*-based studies |
| Corynebacterium | 38,98 ±1,69 | 31,83 ±4,85 | + | [3] |
| Propionibacterium | 7,92 ±0,98 | 38,37 ±5,05 | + | [3] |
| Staphylococcus | 33,3 ±3,66 | 13,42 ±0,98 | + | [3] |
| Brevibacterium | 0,57 ±0,50 | 0,1 ±0,06 | + | [6] |
| Rothia | 0,43 ±0,01 | 0,06 ±0,00 | + | [6] |
| Malassezia | 0,28 ±0,08 | 0,41 ±0,14 |  + Eukaryote |   |
| Cupriavidus | 0,36 ±0,36 | 0 ±0,00 | - |   |
| Streptococcus | 0,32 ±0,19 | 0,2 ±0,05 | + | [3] |
| Anaerococcus | 0,2 ±0,04 | 0,08 ±0,02 | + | [3] |
| Micrococcus | 0,2 ±0,08 | 0,08 ±0,02 | + | [3] |
| Kocuria | 0,17 ±0,02 | 0,06 ±0,01 | + | [6] |
| Cyanothece | 0,02 ±0,02 | 0,17 ±0,04 | - |   |
| Eremococcus | 0,14 ±0,00 | 0 ±0,00 | + | [6] |
| Coprobacillus | 0,03 ±0,01 | 0,14 ±0,03 | - |   |
| Arthrobacter | 0,13 ±0,07 | 0,03 ±0,02 | - |   |
| Actinomyces | 0,1 ±0,01 | 0,07 ±0,01 | + | [3] |

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