| | Skin | | Stool |
|---|------|-------------|--|
| Bacilli; Staphylococcus_sp - | 38.9 | 0 | 0 |
| Bacilli; Streptococcus_suis - | 2.8 | 27.5 | 0 |
| Betaproteobacteria; Bordetella_petrii - | 0 | 0 | 19.4 |
| Betaproteobacteria; Bordetella_sp - | 0 | 0 | 17.3 |
| Bacilli; Jeotgalibaca_PTS2502 - | 0 | 15.6 | 0 |
| Bacilli; Staphylococcus_aureus - | 12.6 | 0 | 0 |
| Betaproteobacteria; Bordetella_pseudohinzii - | 0 | 0 | 9.2 |
| Bacteroidia; Bacteroides_thetaiotaomicron - | 0 | 0 | 8 |
| Actinomycetes; Pimelobacter_simplex - | 7.9 | 0 | 0 |
| Betaproteobacteria; Neisseria_meningitidis - | 0 | 7.7 | 0 |
| Clostridia; Clostridium_aceticum - | 0 | 0 | 6.8 |
| Bacteroidia; Phocaeicola_dorei - | 6.3 | 0 | 0.4 |
| Gammaproteobacteria; Haemophilus_ducreyi - | 0 | 6.7 | 0 |
| Bacilli; Streptococcus_sp - | 1.4 | 4.4 | 0 |
| Betaproteobacteria; Bordetella_pertussis - | 0 | 0 | 5.8 |
| Bacilli; Jeotgalibaca_sp - | 0 | 4.4 | 0 |
| Gammaproteobacteria; Acinetobacter_TTH0-4 - | 4 | 0 | 0 |
| Actinomycetes; Propionibacterium_freudenreichii - | 3.6 | 0 | 0 |
| Bacteroidia; Porphyromonas_gingivalis - | 0 | 3.6 | 0 |
| Bacilli; Staphylococcus_epidermidis - | 3.4 | 0 | 0 |
| Bacteroidia; Bacteroides_fragilis - | 0 | 0 | 3.3 |
| Bacilli; Streptococcus_pneumoniae - | 2.5 | 0.5 | 0 |
| Clostridia; Clostridium_sp - | 0 | 0 | 2.9 |
| Bacilli; Staphylococcus_warneri - | 2.9 | 0 | 0 |
| Bacilli; Streptococcus_dysgalactiae - | 2.8 | 0 | 0 |
| Actinomycetes; Micrococcus_luteus - | 2.5 | 0 | 0 |
| Clostridia; Clostridium_pasteurianum - | 0 | 0 | 2.5 |
| Clostridia; Clostridium_scatologenes - | 0 | 0 | 2.3 |
| Bacilli; Streptococcus_pyogenes - | 1.8 | 0.5 | 0 |
| Betaproteobacteria; Neisseria_sp - | 0 | 2.2 | 0 |
| Clostridia; Clostridium_botulinum - | 0 | 0 | 2.1 |
| Bacilli; Marinilactibacillus_15R - | 0 | 2.1 | 0 |
| Bacilli; Staphylococcus_schleiferi - | 1.9 | 0 | 0 |
| Unclassified; Unclassified_sp - | 0.5 | 0.6 | 0.8 |
| Clostridia; Clostridioides_difficile - | 0 | 1.9 | 0 |
| Remaining taxa (926) - | 4.2 | 22.3 | 19.1 |
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% Read Abundance

10.0