Supporting Information: Table S1: Overview of samples, characteristics and detection of Archaea.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Sample** | **Sample type** | **QPCR** | **Direct PCR** | **Nested PCR** | **FISH** |
| **Bacterial 16S rRNA gene copies per torso or m² floor** | **Bacterial 16S rRNA gene copies: standard deviation** | **Archaeal 16S rRNA gene copies per torso or m² floor** | **Archaea 16S rRNA gene copies: standard deviation** | **Percent archaeal 16S rRNA gene copies** | **Archaeal 16S rRNA gene PCR** | **Archaeal 16S rRNA gene library: clones/coverage1** | **Archaeal 16S rRNA gene nested-PCR** | **Archaeal 16S rRNA gene library (nested): clones/coverage1** |
| Hum\_01 | Human skin, wipe | 4,214,834 | 10% | 10,268 | 12% | 0.24% | negative | nd | **positive** | 42 / 90.5 | nd |
| Hum\_02 | Human skin, wipe | 1,334,029 | 4% | 12,223 | 21% | 0.91% | **positive** | nd | negative | nd | nd |
| Hum\_03 | Human skin, wipe | 491,439 | 11% | 938 | 31% | 0.19% | nd | nd | nd | nd | nd |
| Hum\_04 | Human skin, wipe | 25,363,739 | 48% | 7,488 | 8% | 0.03% | negative | nd | **positive** | 46 / 100 | nd |
| Hum\_05 | Human skin, wipe | 7,557,334 | 10% | 353 | 64% | 0.00% | nd | nd | nd | nd | nd |
| Hum\_06 | Human skin, wipe | 7,474,329 | 18% | 2,318 | 21% | 0.03% | negative | nd | negative | nd | nd |
| Hum\_07 | Human skin, wipe | 48,120,134 | 3% | 50,248 | 7% | 0.10% | **positive** | 53 / 98.1 | **positive** | nd | **positive** |
| Hum\_08 | Human skin, wipe | 167,256,499 | 6% | 6,278 | 21% | 0.00% | negative | nd | **positive** | 32 / 93.8 | nd |
| Hum\_09 | Human skin, wipe | 232,734 | 8% | 10,288 | 1% | 4.23% | nd | nd | nd | nd | nd |
| Hum\_10 | Human skin, wipe | 13,886,809 | 17% | 3,663 | 13% | 0.03% | negative | nd | **positive** | 44 / 97.7 | nd |
| Hum\_11 | Human skin, wipe | 1,218,714 | 16% | 668 | 79% | 0.05% | nd | nd | nd | nd | nd |
| Hum\_12 | Human skin, wipe | 52,859 | 21% | 998 | 86% | 1.85% | nd | nd | nd | nd | nd |
| Hum\_13 | Human skin, wipe | 163,199 | 11% | 238 | 173% | 0.15% | nd | nd | nd | nd | nd |
| Graz\_12 | Intensive care unit, BiSKit | nd | nd | 14,228 | 28% | nd | nd | nd | **positive** | 41 / 97.6 | nd |
| Graz\_13 | Intensive care unit, BiSKit | nd | nd | 1,112 | 63% | nd | nd | nd | **positive** | 48 / 97.9 | nd |
| Rgbg\_1 | Intensive care unit, wipe | 69,296 | 10% | 2,043 | 16% | 2.86% | **positive** | 45 / 100 | **positive** | nd | nd |
| Rgbg\_3 | Intensive care unit, wipe | 153,381 | 12% | 6,581 | 8% | 4.11% | **positive** | 39 / 97.4 | **positive** | nd | nd |
| Rgbg\_F | Intensive care unit, wipe | 62,180 | 12% | 2,498 | 17% | 3.86% | **positive** | 36 / 97.2 | **positive** | 45 /100 | nd |
| Rgbg\_1\_PMA | Intensive care unit, wipe, PMA2 | 65 | 19% | BDL | BDL | BDL | negative | nd | negative | nd | nd |
| Rgbg\_3\_PMA | Intensive care unit, wipe, PMA2 | 24,730 | 24% | 2,067 | 6% | 7.71% | **positive** | 41 / 95.1 | **positive** | nd | nd |
| Rgbg\_F\_PMA | Intensive care unit, wipe, PMA2 | 515 | 31% | BDL | BDL | BDL | negative | nd | negative | nd | nd |
| CR5 | Clean room ISO 5, BiSKit | 6,323,082 | 5% | 167,178 | 12% | 2.58% | negative | nd | **positive** | 37 / 86.5 | nd |
| CR8 | Clean room ISO 8, BiSKit | 2,707,996 | 2% | 92,074 | 16% | 3.29% | negative | nd | **positive** | 39 / 94.9 | nd |
| 1clones / coverage give the number of clones analyzed and the percent coverage after OTU grouping at 1% level |  |  |  |  |
| 2PMA = sample treated with propidium monoazide |  |  |  |  |  |  |  |  |  |
| nd = not determined |  |  |  |  |  |  |  |  |  |  |
| BDL = Below Detection Limit of qPCR, see Methods for details |  |  |  |  |  |  |  |  |  |