

**Table S1: 16S rRNA gene amplicon sequencing metrics**

|  | Total  | A01  | A09  | A17  | B09  | B14  | B20  | C01   | C06   | C10   | D03   | D10  | D15  | E03   | E12   | E20  | F01  | F08  | F19  | G02   | G08   | G19  | H01  | H10   | H19   |
|--|--------|------|------|------|------|------|------|-------|-------|-------|-------|------|------|-------|-------|------|------|------|------|-------|-------|------|------|-------|-------|
| <b>Filtered reads</b>  | 235952 | 7249 | 7037 | 6857 | 8757 | 7918 | 9735 | 11633 | 15575 | 19687 | 11115 | 9642 | 6449 | 11729 | 11171 | 8737 | 5871 | 6768 | 7222 | 15518 | 10909 | 5048 | 5236 | 14053 | 12036 |
| <b># ASVs</b>  | 1056   | 157  | 176  | 194  | 181  | 181  | 187  | 280   | 289   | 356   | 185   | 220  | 169  | 279   | 229   | 207  | 129  | 147  | 148  | 293   | 207   | 125  | 147  | 276   | 262   |
| <b># SWARM OTUs</b>  | 921    | 155  | 173  | 190  | 176  | 177  | 183  | 274   | 280   | 346   | 178   | 214  | 161  | 271   | 222   | 202  | 126  | 146  | 145  | 282   | 203   | 125  | 146  | 268   | 257   |
| <b>% of reads assigned to 25 ubiquitous OTUs</b>                     |        | 63%  | 48%  | 41%  | 47%  | 48%  | 52%  | 48%   | 58%   | 52%   | 59%   | 44%  | 37%  | 41%   | 60%   | 51%  | 68%  | 56%  | 64%  | 42%   | 58%   | 59%  | 54%  | 43%   | 48%   |
| <b>% of reads assigned to 103 OTUs present in 24&gt;12 samples</b>   |        | 25%  | 32%  | 35%  | 34%  | 32%  | 29%  | 22%   | 21%   | 21%   | 17%   | 23%  | 23%  | 31%   | 23%   | 30%  | 22%  | 29%  | 23%  | 32%   | 27%   | 32%  | 31%  | 33%   | 28%   |
| <b>% of reads assigned to 556 OTUs present in 3 and less samples</b> |        | 2%   | 6%   | 7%   | 6%   | 6%   | 6%   | 7%    | 5%    | 8%    | 5%    | 8%   | 11%  | 7%    | 4%    | 4%   | 2%   | 7%   | 4%   | 5%    | 3%    | 3%   | 4%   | 6%    | 10%   |