|  |  |  |
| --- | --- | --- |
| **All****(n = 559)** | **All D0****(n = 243)** | **All D28****(n = 202)** |
| Proteobacteria48.88 ± 1.22 | Proteobacteria62.53 ± 1.55 | Firmicutes52.60 ± 1.95 |
| Firmicutes42.49 ± 1.25 | Firmicutes25.71 ± 1.41 | Proteobacteria39.12 ± 1.93 |
| Bacteroidota4.09 ± 0.27 | Bacteroidota5.35 ± 0.43 | Bacteroidota4.05 ± 0.44 |
| Actinobacteriota3.02 ± 0.27 | Actinobacteriota4.11 ± 0.47 | Actinobacteriota3.04 ± 0.48 |
| Deinococcota0.74 ± 0.18 | Deinococcota1.21 ± 0.38 | Deinococcota0.46 ± 0.16 |
| Fusobacteriota0.26 ± 0.12 | Fusobacteriota0.43 ± 0.25 | Fusobacteriota0.18 ± 0.09 |
| Verrucomicrobiota0.12 ± 0.01 | Patescibacteria0.16 ± 0.03 | Verrucomicrobiota0.14 ± 0.02 |
|  | Verrucomicrobiota0.13 ± 0.02 | Chloroflexi0.10 ± 0.03 |
|  | Chloroflexi0.10 ± 0.01 |  |

**Table S3.** Mean relative abundance plus or minus the standard error of the mean of taxonomic phyla representing > 0.1% of the overall microbial community across all samples at each of the sampling timepoints.