Table S1 Construction of EM used in this study sequenced by 16S rRNA

V3-V4 hypervariable regions on MiSeq Platform

|  |  |  |  |
| --- | --- | --- | --- |
| Phylum | Genus | Abundance, % | |
| Average | SD |
| *Firmicutes* | *Lactobacillus* | 84.021 | 12.309 |
| *Anoxybacillus* | 0.367 | 0.549 |
| *Lysinibacillus* | 0.207 | 0.314 |
| *Faecalibacterium* | 0.190 | 0.214 |
| *Roseburia* | 0.141 | 0.195 |
| *Phascolarctobacterium* | 0.115 | 0.184 |
| *Staphylococcus* | 0.078 | 0.127 |
| *Bacillus* | 0.092 | 0.115 |
| *Lachnospira* | 0.109 | 0.103 |
| *Brevibacillus* | 0.056 | 0.092 |
| *Streptococcus* | 0.057 | 0.080 |
| *Megamonas* | 0.059 | 0.056 |
| *Bacteroidetes* | *Bacteroides* | 1.374 | 1.887 |
| *Prevotella* | 0.130 | 0.218 |
| *Parabacteroides* | 0.131 | 0.200 |
| *Proteobacteria* | *Halomonas* | 0.680 | 1.108 |
| *Citrobacter* | 0.231 | 0.400 |
| *Ochrobactrum* | 0.180 | 0.296 |
| *Pseudomonas* | 0.139 | 0.239 |
| *Ralstonia* | 0.116 | 0.171 |
| *Sphingomonas* | 0.056 | 0.095 |
| *Agrobacterium* | 0.046 | 0.073 |
| *Acinetobacter* | 0.039 | 0.064 |
| *Acetobacter* | 5.297 | 9.169 |
| *[Thermi]* | *Meiothermus* | 0.853 | 1.444 |
| *Actinobacteria* | *Gordonia* | 0.193 | 0.307 |
| *Propionibacterium* | 0.109 | 0.169 |
| *Renibacterium* | 0.066 | 0.099 |
| Others/unassigned |  | 4.868 | 5.341 |