**Table S4:** OTUs which were significantly changed at each time point between cages (P < 0.05, corrected for multiple testing), see Figure S3 for more detail.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Time point | OTU | Genus (Family) | Rangea | Cage difference |
| Week 5 | 001 | *Clostridium* *XI* (*Peptostreptococcaceae*) | 30-55% | 1 > Allb |
| 017 | *Bacteroides* | 10-15% | 3 > All |
| 032 | *Subdoligranulum* | 5-6% | 3 > All |
| Week 7 | 002 | *Meniscus* | 20-50% | 4 >3  5 > 3  6 > 1,2,3,4 & 5 |
| 009 | *Hallella* | 6-10% | 5 > All |
| 026 | *Marvinbryantia* | 5-6% | 2 > All |
| 104 | *Clostridium IV* (*Ruminococcaceae*) | 1-2% | 1 > 2,3,4 & 5  6 > 3,4 & 5 |
| 197 | *Meniscus* | 2.5-3% | 6 > All |
| Week 10 | 019 | *Meniscus* | 1.5-3% | 1 > 2 & 4  3 > 2,4 & 5  6 > 2,4 & 5 |
| 037 | *Oscillibacter* | 2-5% | 2 > 1,4,5 & 6  3 > 1,4 & 5 |
| 278 | *Coprococcus* | 5-6% | 1 > All |
| Week 14 | 002 | *Meniscus* | 10-20% | 1 > 2,3,4 & 6  5 > 2,3,4 & 6 |
| 003 | *Meniscus* | 10-25% | 1 > 2  5 > 2  6 > 2,3 & 4 |
| 004 | *Prevotella* | 2-8% | 2 > All  3 > 4 & 6 |
| 016 | *Parasporobacterium* | 2-3% | 6 > All |
| 019 | *Meniscus* | 2-5% | 1 > 2  3 > 2  5 > 4  6 > 1,2,3 & 4 |
| 045 | *Meniscus* | 0.5-1.5% | 1 > 3,4 & 6  2 > 3,4,5 & 6 |
| 047 | *Tannerella* | 0.5%  1.5-2.5% | 2 > 1,3,4,5 & 6  3 > 1,4,5 & 6 |
| 155 | *Butyrivibrio* | 1.4% | 6 > 1,2,3,4 & 5 |

Footnote a The range describes how large the change was between the samples.

b In this example cage 1 is enriched when compared to all other cages in OTU001