**Table 1** V4 primer sequence used for 16s RNA sequencing library preparation

|  |  |
| --- | --- |
| Forward Primer | Reverse Primer |
| 515F (Parada) | 806R (Apprill) |
| GTGYCAGCMGCCGCGGTAA | GGACTACNVGGGTWTCTAAT |

**Table 2** 16s sequencing results mapped bacterial communityat difference taxonomy classes with top associated bacteria

|  |  |  |
| --- | --- | --- |
| **Phylum** | **Number of OTUs** | **Percent of OTUs** |
| Firmicutes | 9,740 | 59.57% |
| Bacteroidetes | 4,199 | 25.68% |
| Proteobacteria | 687 | 4.20% |
| Actinobacteria | 477 | 2.92% |
| Unknown | 432 | 2.64% |
| Saccharibacteria | 276 | 1.69% |
| Tenericutes | 185 | 1.13% |
| Cyanobacteria | 130 | 0.80% |
| Verrucomicrobia | 67 | 0.41% |
| Deferribacteres | 64 | 0.39% |
| Patescibacteria | 29 | 0.18% |
| Acidobacteria | 25 | 0.15% |
| Planctomycetes | 19 | 0.12% |
| Epsilonbacteraeota | 15 | 0.09% |
| Chloroflexi | 3 | 0.02% |
| Chlamydiae | 1 | 0.01% |
| Deinococcus-Thermus | 1 | 0.01% |
| Fusobacteria | 1 | 0.01% |

**Table 3** List ofGut microbiota significantly changed by either AIN93M or PEITC diet at week 1 and week 4 for both WT and KO C57BL/6J mice

|  |  |
| --- | --- |
| AIN93M |  |
| Week 1 |  |
| Bacterial relative abundance decreased | Bacterial relative abundance increased |
| Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Prevotella | Bacteroidetes.Bacteroidia.Bacteroidales.(Odoribacteraceae).Odoribacter |
| Bacteroidetes.Bacteroidia.Bacteroidales.S24\_7 | Tenericutes.Mollicutes.Anaeroplasmatales.Anaeroplasmataceae.Anaeroplasma |
| TM7.TM7\_3.CW040.F16.g | Tenericutes.Mollicutes.Mycoplasmatales.Mycoplasmataceae |
| Week 4 |  |
| Bacterial relative abundance decreased | Bacterial relative abundance increased |
| Bacteroidetes.Bacteroidia.Bacteroidales.(Paraprevotellaceae).(Prevotella) | Bacteroidetes.Bacteroidia.Bacteroidales |
| Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Parabacteroides | Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Oscillospira |
| Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Prevotella | Proteobacteria.Deltaproteobacteria.Desulfovibrionales.Desulfovibrionaceae |
| Bacteroidetes.Bacteroidia.Bacteroidales.S24\_7 | Tenericutes.Mollicutes.Anaeroplasmatales.Anaeroplasmataceae.Anaeroplasma |
|  |  |
| PEITC |  |
| Week 1 |  |
| Bacterial relative abundance decreased | Bacterial relative abundance increased |
| Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Prevotella | Bacteroidetes.Bacteroidia.Bacteroidales |
| Bacteroidetes.Bacteroidia.Bacteroidales.S24\_7 | Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcus |
| TM7.TM7\_3.CW040.F16 |  |
| Week 4 |  |
| Bacterial relative abundance decreased | Bacterial relative abundance increased |
| Bacteroidetes.Bacteroidia.Bacteroidales.(Paraprevotellaceae).(Prevotella) | Acidobacteria.(Chloracidobacteria).RB41.Ellin6075 |
| Bacteroidetes.Bacteroidia.Bacteroidales.S24\_7 | Bacteroidetes.Bacteroidia.Bacteroidales |
|  | Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Oscillospira |
|  | Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcus |
|  | Tenericutes.Mollicutes.Mycoplasmatales.Mycoplasmataceae |
|  |  |

**Table 4** List ofGut microbiota significantly changed due to genotype at week 1.

|  |  |
| --- | --- |
| Week 1-AIN93M |  |
| Bacterial relative abundance decreased in KO samples | Bacterial relative abundance increased in KO samples |
| Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Lactococcus | Actinobacteria.Coriobacteriia.Coriobacteriales.Coriobacteriaceae.Adlercreutzia |
| Firmicutes.Clostridia.Clostridiales.Lachnospiraceae | Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae.Rikenella |
| Proteobacteria.Deltaproteobacteria.Desulfovibrionales.Desulfovibrionaceae.Bilophila | Cyanobacteria.4C0d\_2.YS2 |
|  | Tenericutes.Mollicutes.Mycoplasmatales.Mycoplasmataceae |
|  |  |
| Week 1-PEITC |  |
| Bacterial relative abundance decreased in KO samples | Bacterial relative abundance increased in KO samples |
| Actinobacteria.Coriobacteriia.Coriobacteriales.Coriobacteriaceae.Olsenella | Actinobacteria.Coriobacteriia.Coriobacteriales.Coriobacteriaceae.Adlercreutzia |
| Bacteroidetes.Bacteroidia.Bacteroidales.S24\_7 | Cyanobacteria.4C0d\_2.YS2 |
| Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus | Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Coprococcus |
| Firmicutes.Clostridia.Clostridiales.Clostridiaceae.Clostridium | Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcus |
| Firmicutes.Clostridia.Clostridiales.Dehalobacteriaceae.Dehalobacterium | Tenericutes.Mollicutes.Mycoplasmatales |
| Firmicutes.Erysipelotrichi.Erysipelotrichales.Erysipelotrichaceae.Allobaculum |  |
| Proteobacteria.Betaproteobacteria.Burkholderiales.Alcaligenaceae.Sutterella |  |
| Proteobacteria.Deltaproteobacteria.Desulfovibrionales.Desulfovibrionaceae |  |

**Table 5** List ofGut microbiota significantly changed due to genotype at week 4.

|  |  |
| --- | --- |
| Week 4-AIN93M |  |
| Bacterial relative abundance decreased in KO samples | Bacterial relative abundance increased in KO samples |
| Actinobacteria.Coriobacteriia.Coriobacteriales.Coriobacteriaceae.Olsenella | Actinobacteria.Coriobacteriia.Coriobacteriales.Coriobacteriaceae.Adlercreutzia |
| Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae.AF12 | Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae.Rikenella |
| Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus | Cyanobacteria.4C0d\_2.YS2 |
| Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Lactococcus | Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium |
| Firmicutes.Clostridia.Clostridiales.Clostridiaceae.Clostridium | Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcus |
| Firmicutes.Clostridia.Clostridiales.Dehalobacteriaceae.Dehalobacterium | Tenericutes.Mollicutes.Mycoplasmatales.Mycoplasmataceae |
| Firmicutes.Clostridia.Clostridiales.Lachnospiraceae | TM7.TM7\_3.CW040.F16.Unclassified\_g |
| Firmicutes.Clostridia.Clostridiales.Peptostreptococcaceae |  |
| Tenericutes.Mollicutes |  |
|  |  |
| Week 4-PEITC |  |
| Bacterial relative abundance decreased in KO samples | Bacterial relative abundance increased in KO samples |
| Actinobacteria.Coriobacteriia.Coriobacteriales.Coriobacteriaceae.Olsenella | Actinobacteria.Coriobacteriia.Coriobacteriales.Coriobacteriaceae.Adlercreutzia |
| Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae | Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae.Rikenella |
| Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus | Cyanobacteria.4C0d\_2.YS2 |
| Firmicutes.Clostridia.Clostridiales.Lachnospiraceae | Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcus |
| Proteobacteria.Betaproteobacteria.Burkholderiales.Alcaligenaceae.Sutterella |  |
| Tenericutes.Mollicutes.Anaeroplasmatales.Anaeroplasmataceae.Anaeroplasma |  |
| Tenericutes.Mollicutes.RF39 |  |