

Supplemental Materials

Table S1. Pairwise comparison of bacterial composition at phylum level across the diet groups

| Taxon 1 | Taxon 2 | Correlation | p-value |
|--------------------------------|-------------------------------------|--------------------|----------------|
| <i>Adlercreutzia</i> | <i>Bacteroides acidifaciens</i> | -0.5019 | 0.0198 |
| <i>Adlercreutzia</i> | <i>Mogibacteriaceae</i> (I) | -0.4819 | 0.0099 |
| <i>Adlercreutzia</i> | <i>Muribaculaceae</i> | -0.4097 | 0.0297 |
| <i>Akkermansia muciniphila</i> | <i>Bacteroidales</i> | 0.4769 | 0.0198 |
| <i>Akkermansia muciniphila</i> | <i>Bacteroides acidifaciens</i> | 0.4489 | 0.0297 |
| <i>Akkermansia muciniphila</i> | F16 | -0.5229 | 0.0099 |
| <i>Akkermansia muciniphila</i> | rc4 4 | 0.4385 | 0.0198 |
| <i>Allobaculum</i> | <i>Anaerotruncus</i> | -0.5972 | 0.0099 |
| <i>Allobaculum</i> | <i>Bacteroidales</i> | 0.4989 | 0.0099 |
| <i>Allobaculum</i> | <i>Bacteroides</i> | -0.6901 | 0.0099 |
| <i>Allobaculum</i> | <i>Bacteroides acidifaciens</i> | 0.6969 | 0.0099 |
| <i>Allobaculum</i> | <i>Butyricicoccus pullicaecorum</i> | 0.6164 | 0.0099 |
| <i>Allobaculum</i> | <i>Christensenellaceae</i> | -0.6602 | 0.0099 |
| <i>Allobaculum</i> | <i>Clostridiales</i> (II) | -0.6417 | 0.0198 |
| <i>Allobaculum</i> | <i>Clostridium methylpentosum</i> | -0.665 | 0.0099 |
| <i>Allobaculum</i> | <i>Coproccoccus</i> | -0.6128 | 0.0099 |
| <i>Allobaculum</i> | <i>Desulfovibrionaceae</i> | -0.5851 | 0.0099 |
| <i>Allobaculum</i> | <i>Lactobacillus</i> | 0.5286 | 0.0198 |
| <i>Allobaculum</i> | <i>Mogibacteriaceae</i> (II) | 0.4387 | 0.0198 |
| <i>Allobaculum</i> | <i>Mucispirillum schaedleri</i> | -0.6859 | 0.0099 |
| <i>Allobaculum</i> | <i>Muribaculaceae</i> | 0.6225 | 0.0198 |
| <i>Allobaculum</i> | <i>Oscillospira</i> | -0.8149 | 0.0099 |
| <i>Allobaculum</i> | <i>Peptococcaceae</i> | -0.6891 | 0.0099 |
| <i>Allobaculum</i> | rc4 4 | 0.6133 | 0.0099 |
| <i>Allobaculum</i> | RF32 | 0.5875 | 0.0099 |
| <i>Allobaculum</i> | RF39 | 0.4504 | 0.0099 |
| <i>Allobaculum</i> | <i>Rikenellaceae</i> | 0.7471 | 0.0099 |
| <i>Allobaculum</i> | <i>Ruminococcaceae</i> (I) | -0.7728 | 0.0198 |
| <i>Allobaculum</i> | <i>Ruminococcaceae</i> (II) | -0.6007 | 0.0297 |
| <i>Allobaculum</i> | <i>Ruminococcus gnavus</i> | -0.7664 | 0.0099 |
| <i>Allobaculum</i> | <i>Sutterella</i> | 0.7814 | 0.0099 |
| <i>Anaerotruncus</i> | <i>Allobaculum</i> | -0.5972 | 0.0099 |
| <i>Anaerotruncus</i> | <i>Bacteroides</i> | 0.6121 | 0.0099 |

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| Taxon 1 | Taxon 2 | Correlation | p-value |
|----------------------|-------------------------------------|--------------------|----------------|
| <i>Anaerotruncus</i> | <i>Bacteroides acidifaciens</i> | -0.4836 | 0.0396 |
| <i>Anaerotruncus</i> | <i>Bilophila</i> | 0.7033 | 0.0099 |
| <i>Anaerotruncus</i> | <i>Christensenellaceae</i> | 0.695 | 0.0099 |
| <i>Anaerotruncus</i> | <i>Clostridiales (II)</i> | 0.6543 | 0.0297 |
| <i>Anaerotruncus</i> | <i>Clostridium methylpentosum</i> | 0.6913 | 0.0099 |
| <i>Anaerotruncus</i> | <i>Lactococcus</i> | 0.4505 | 0.0198 |
| <i>Anaerotruncus</i> | <i>Mucispirillum schaedleri</i> | 0.6487 | 0.0099 |
| <i>Anaerotruncus</i> | <i>Oscillospira</i> | 0.7022 | 0.0099 |
| <i>Anaerotruncus</i> | <i>Parabacteroides gordonii</i> | 0.5829 | 0.0198 |
| <i>Anaerotruncus</i> | <i>Peptococcaceae</i> | 0.7029 | 0.0099 |
| <i>Anaerotruncus</i> | <i>rc4 4</i> | -0.4664 | 0.0099 |
| <i>Anaerotruncus</i> | <i>RF32</i> | -0.5394 | 0.0099 |
| <i>Anaerotruncus</i> | <i>Rikenellaceae</i> | -0.5739 | 0.0396 |
| <i>Anaerotruncus</i> | <i>Ruminococcaceae (I)</i> | 0.5555 | 0.0396 |
| <i>Anaerotruncus</i> | <i>Ruminococcaceae (II)</i> | 0.6048 | 0.0297 |
| <i>Anaerotruncus</i> | <i>Ruminococcus gnavus</i> | 0.6821 | 0.0099 |
| <i>Anaerotruncus</i> | <i>Streptococcus</i> | 0.5456 | 0.0099 |
| <i>Anaerotruncus</i> | <i>Sutterella</i> | -0.622 | 0.0099 |
| <i>Bacteroidales</i> | <i>Akkermansia muciniphila</i> | 0.4769 | 0.0198 |
| <i>Bacteroidales</i> | <i>Allobaculum</i> | 0.4989 | 0.0099 |
| <i>Bacteroidales</i> | <i>Bacteroides acidifaciens</i> | 0.6714 | 0.0099 |
| <i>Bacteroidales</i> | <i>Butyricicoccus pullicaecorum</i> | 0.5549 | 0.0099 |
| <i>Bacteroidales</i> | <i>Clostridiales (II)</i> | -0.6171 | 0.0396 |
| <i>Bacteroidales</i> | <i>Lactococcus</i> | -0.4184 | 0.0099 |
| <i>Bacteroidales</i> | <i>Mucispirillum schaedleri</i> | -0.5242 | 0.0099 |
| <i>Bacteroidales</i> | <i>Muribaculaceae</i> | 0.7358 | 0.0099 |
| <i>Bacteroidales</i> | <i>rc4 4</i> | 0.472 | 0.0099 |
| <i>Bacteroidales</i> | <i>RF32</i> | 0.5945 | 0.0099 |
| <i>Bacteroidales</i> | <i>Rikenellaceae</i> | 0.5491 | 0.0099 |
| <i>Bacteroidales</i> | <i>Sutterella</i> | 0.6197 | 0.0099 |
| <i>Bacteroides</i> | <i>Allobaculum</i> | -0.6901 | 0.0099 |
| <i>Bacteroides</i> | <i>Anaerotruncus</i> | 0.6121 | 0.0099 |
| <i>Bacteroides</i> | <i>Bacteroides acidifaciens</i> | -0.7297 | 0.0099 |
| <i>Bacteroides</i> | <i>Bilophila</i> | 0.5469 | 0.0396 |

Table S1. Pairwise comparison of bacterial composition at phylum level across the diet groups

| Taxon 1 | Taxon 2 | Correlation | p-value |
|---------------------------------|-------------------------------------|--------------------|----------------|
| <i>Bacteroides</i> | <i>Butyricicoccus pullicaecorum</i> | -0.5548 | 0.0099 |
| <i>Bacteroides</i> | <i>Christensenellaceae</i> | 0.6673 | 0.0099 |
| <i>Bacteroides</i> | <i>Clostridium methylpentosum</i> | 0.5067 | 0.0099 |
| <i>Bacteroides</i> | <i>Lactococcus</i> | 0.4501 | 0.0297 |
| <i>Bacteroides</i> | <i>Mogibacteriaceae</i> (II) | -0.4732 | 0.0396 |
| <i>Bacteroides</i> | <i>Mucispirillum schaedleri</i> | 0.626 | 0.0099 |
| <i>Bacteroides</i> | <i>Oscillospira</i> | 0.7179 | 0.0297 |
| <i>Bacteroides</i> | <i>Peptococcaceae</i> | 0.7086 | 0.0297 |
| <i>Bacteroides</i> | <i>rc4 4</i> | -0.7371 | 0.0198 |
| <i>Bacteroides</i> | <i>RF32</i> | -0.5772 | 0.0198 |
| <i>Bacteroides</i> | <i>Rikenellaceae</i> | -0.6628 | 0.0099 |
| <i>Bacteroides</i> | <i>Ruminococcus gnavus</i> | 0.737 | 0.0099 |
| <i>Bacteroides</i> | <i>Streptococcus</i> | 0.4986 | 0.0198 |
| <i>Bacteroides</i> | <i>Sutterella</i> | -0.7186 | 0.0099 |
| <i>Bacteroides acidifaciens</i> | <i>Adlercreutzia</i> | -0.5019 | 0.0198 |
| <i>Bacteroides acidifaciens</i> | <i>Akkermansia muciniphila</i> | 0.4489 | 0.0297 |
| <i>Bacteroides acidifaciens</i> | <i>Allobaculum</i> | 0.6969 | 0.0099 |
| <i>Bacteroides acidifaciens</i> | <i>Anaerotruncus</i> | -0.4836 | 0.0396 |
| <i>Bacteroides acidifaciens</i> | <i>Bacteroidales</i> | 0.6714 | 0.0099 |
| <i>Bacteroides acidifaciens</i> | <i>Bacteroides</i> | -0.7297 | 0.0099 |
| <i>Bacteroides acidifaciens</i> | <i>Bilophila</i> | -0.474 | 0.0396 |
| <i>Bacteroides acidifaciens</i> | <i>Butyricicoccus pullicaecorum</i> | 0.5836 | 0.0099 |
| <i>Bacteroides acidifaciens</i> | <i>Christensenellaceae</i> | -0.4859 | 0.0099 |
| <i>Bacteroides acidifaciens</i> | <i>Clostridiales</i> (I) | -0.5447 | 0.0495 |
| <i>Bacteroides acidifaciens</i> | <i>Clostridiales</i> (II) | 1 | 0.0297 |
| <i>Bacteroides acidifaciens</i> | <i>Clostridium methylpentosum</i> | -0.6347 | 0.0099 |
| <i>Bacteroides acidifaciens</i> | <i>Desulfovibrionaceae</i> | -0.4005 | 0.0099 |
| <i>Bacteroides acidifaciens</i> | <i>F16</i> | -0.5527 | 0.0099 |
| <i>Bacteroides acidifaciens</i> | <i>Lachnospiraceae</i> (I) | -0.6692 | 0.0297 |
| <i>Bacteroides acidifaciens</i> | <i>Lactococcus</i> | -0.6788 | 0.0099 |
| <i>Bacteroides acidifaciens</i> | <i>Mogibacteriaceae</i> (II) | 0.7584 | 0.0099 |
| <i>Bacteroides acidifaciens</i> | <i>Mucispirillum schaedleri</i> | -0.6543 | 0.0099 |
| <i>Bacteroides acidifaciens</i> | <i>Muribaculaceae</i> | 0.7002 | 0.0297 |
| <i>Bacteroides acidifaciens</i> | <i>Oscillospira</i> | -0.6911 | 0.0297 |

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| <i>Bacteroides acidifaciens</i> | <i>Peptococcaceae</i> | -0.7333 | 0.0099 |
| <i>Bacteroides acidifaciens</i> | <i>rc4 4</i> | 0.802 | 0.0099 |
| <i>Bacteroides acidifaciens</i> | <i>RF32</i> | 0.9205 | 0.0099 |
| <i>Bacteroides acidifaciens</i> | <i>Rikenellaceae</i> | 0.8036 | 0.0099 |
| <i>Bacteroides acidifaciens</i> | <i>Ruminococcus gnavus</i> | -0.7898 | 0.0198 |
| <i>Bacteroides acidifaciens</i> | <i>Streptococcus</i> | -0.5349 | 0.0099 |
| <i>Bacteroides acidifaciens</i> | <i>Sutterella</i> | 0.8574 | 0.0099 |
| <i>Bilophila</i> | <i>Anaerotruncus</i> | 0.7033 | 0.0099 |
| <i>Bilophila</i> | <i>Bacteroides</i> | 0.5469 | 0.0396 |
| <i>Bilophila</i> | <i>Bacteroides acidifaciens</i> | -0.474 | 0.0396 |
| <i>Bilophila</i> | <i>rc4 4</i> | -0.4771 | 0.0099 |
| | <i>Ruminococcus</i> | | |
| <i>Bilophila</i> | <i>(Lachnospiraceae)</i> | 0.406 | 0.0396 |
| <i>Bilophila</i> | <i>Streptococcus</i> | 0.4858 | 0.0198 |
| <i>Bilophila</i> | <i>Sutterella</i> | -0.5135 | 0.0099 |
| <i>Butyricicoccus pullicaecorum</i> | <i>Allobaculum</i> | 0.6164 | 0.0099 |
| <i>Butyricicoccus pullicaecorum</i> | <i>Bacteroidales</i> | 0.5549 | 0.0099 |
| <i>Butyricicoccus pullicaecorum</i> | <i>Bacteroides</i> | -0.5548 | 0.0099 |
| <i>Butyricicoccus pullicaecorum</i> | <i>Bacteroides acidifaciens</i> | 0.5836 | 0.0099 |
| <i>Butyricicoccus pullicaecorum</i> | <i>Christensenellaceae</i> | -0.5198 | 0.0099 |
| <i>Butyricicoccus pullicaecorum</i> | <i>Clostridiales (II)</i> | -0.7977 | 0.0198 |
| <i>Butyricicoccus pullicaecorum</i> | <i>Clostridium methylpentosum</i> | -0.633 | 0.0099 |
| <i>Butyricicoccus pullicaecorum</i> | <i>Dehalobacterium</i> | -0.6866 | 0.0495 |
| <i>Butyricicoccus pullicaecorum</i> | <i>Mucispirillum schaedleri</i> | -0.5751 | 0.0099 |
| <i>Butyricicoccus pullicaecorum</i> | <i>Muribaculaceae</i> | 0.5862 | 0.0198 |

Table S1. Pairwise comparison of bacterial composition at phylum level across the diet groups

| Taxon 1 | Taxon 2 | Correlation | p-value |
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| <i>Butyricicoccus pullicaecorum</i> | <i>Oscillospira</i> | -0.62 | 0.0198 |
| <i>Butyricicoccus pullicaecorum</i> | <i>Parabacteroides gordonii</i> | -0.4809 | 0.0198 |
| <i>Butyricicoccus pullicaecorum</i> | <i>Peptococcaceae</i> | -0.5492 | 0.0099 |
| <i>Butyricicoccus pullicaecorum</i> | <i>rc4 4</i> | 0.436 | 0.0198 |
| <i>Butyricicoccus pullicaecorum</i> | <i>RF32</i> | 0.6163 | 0.0099 |
| <i>Butyricicoccus pullicaecorum</i> | <i>RF39</i> | 0.6112 | 0.0099 |
| <i>Butyricicoccus pullicaecorum</i> | <i>Rikenellaceae</i> | 0.6001 | 0.0198 |
| <i>Butyricicoccus pullicaecorum</i> | <i>Ruminococcaceae (I)</i> | -0.6007 | 0.0198 |
| <i>Butyricicoccus pullicaecorum</i> | <i>Ruminococcaceae (II)</i> | -0.6147 | 0.0198 |
| <i>Butyricicoccus pullicaecorum</i> | <i>Ruminococcus gnavus</i> | -0.6088 | 0.0099 |
| <i>Butyricicoccus pullicaecorum</i> | <i>Sutterella</i> | 0.653 | 0.0099 |
| <i>Christensenellaceae</i> | <i>Allobaculum</i> | -0.6602 | 0.0099 |
| <i>Christensenellaceae</i> | <i>Anaerotruncus</i> | 0.695 | 0.0099 |
| <i>Christensenellaceae</i> | <i>Bacteroides</i> | 0.6673 | 0.0099 |
| <i>Christensenellaceae</i> | <i>Bacteroides acidifaciens</i> | -0.4859 | 0.0099 |
| <i>Christensenellaceae</i> | <i>Butyricicoccus pullicaecorum</i> | -0.5198 | 0.0099 |
| <i>Christensenellaceae</i> | <i>Clostridium methylpentosum</i> | 0.7227 | 0.0099 |
| <i>Christensenellaceae</i> | <i>Coproccoccus</i> | 0.5055 | 0.0396 |
| <i>Christensenellaceae</i> | <i>Dehalobacterium</i> | 0.7359 | 0.0495 |
| <i>Christensenellaceae</i> | <i>Dorea</i> | 0.4754 | 0.0099 |
| <i>Christensenellaceae</i> | <i>Lactococcus</i> | 0.4332 | 0.0198 |
| <i>Christensenellaceae</i> | <i>Mucispirillum schaedleri</i> | 0.6366 | 0.0099 |
| <i>Christensenellaceae</i> | <i>Oscillospira</i> | 0.7229 | 0.0198 |
| <i>Christensenellaceae</i> | <i>Parabacteroides gordonii</i> | 0.4699 | 0.0198 |

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| <i>Christensenellaceae</i> | <i>Peptococcaceae</i> | 0.6144 | 0.0099 |
| <i>Christensenellaceae</i> | <i>rc4 4</i> | -0.4383 | 0.0099 |
| <i>Christensenellaceae</i> | <i>RF32</i> | -0.5837 | 0.0099 |
| <i>Christensenellaceae</i> | <i>Rikenellaceae</i> | -0.6868 | 0.0099 |
| <i>Christensenellaceae</i> | <i>Ruminococcaceae (II)</i> | 0.5596 | 0.0297 |
| <i>Christensenellaceae</i> | <i>Ruminococcus gnavus</i> | 0.6767 | 0.0099 |
| <i>Christensenellaceae</i> | <i>Streptococcus</i> | 0.4039 | 0.0099 |
| <i>Christensenellaceae</i> | <i>Sutterella</i> | -0.6203 | 0.0099 |
| <i>Clostridiales (I)</i> | <i>Bacteroides acidifaciens</i> | -0.5447 | 0.0495 |
| <i>Clostridiales (I)</i> | <i>Sutterella</i> | -0.4444 | 0.0495 |
| <i>Clostridiales (II)</i> | <i>Allobaculum</i> | -0.6417 | 0.0198 |
| <i>Clostridiales (II)</i> | <i>Anaerotruncus</i> | 0.6543 | 0.0297 |
| <i>Clostridiales (II)</i> | <i>Bacteroidales</i> | -0.6171 | 0.0396 |
| <i>Clostridiales (II)</i> | <i>Bacteroides acidifaciens</i> | 1 | 0.0297 |
| <i>Clostridiales (II)</i> | <i>Butyricicoccus pullicaecorum</i> | -0.7977 | 0.0198 |
| <i>Clostridiales (II)</i> | <i>Mucispirillum schaedleri</i> | 0.6475 | 0.0396 |
| <i>Clostridiales (II)</i> | <i>rc4 4</i> | -0.6854 | 0.0198 |
| <i>Clostridiales (II)</i> | <i>RF32</i> | -0.6371 | 0.0297 |
| <i>Clostridiales (II)</i> | <i>RF39</i> | -0.6351 | 0.0198 |
| <i>Clostridiales (II)</i> | <i>Rikenellaceae</i> | -0.7392 | 0.0396 |
| <i>Clostridiales (II)</i> | <i>Streptococcus</i> | 0.6597 | 0.0198 |
| <i>Clostridiales (II)</i> | <i>Sutterella</i> | -0.8571 | 0.0198 |
| <i>Clostridium colinum</i> | <i>Roseburia</i> | 0.7085 | 0.0099 |
| <i>Clostridium hathewayi</i> | <i>Desulfovibrionaceae</i> | 0.5141 | 0.0099 |
| <i>Clostridium hathewayi</i> | <i>Muribaculaceae</i> | -0.5008 | 0.0198 |
| <i>Clostridium (I)</i> | <i>Muribaculaceae</i> | -0.442 | 0.0198 |
| <i>Clostridium (II)</i> | <i>Dorea</i> | -0.4974 | 0.0099 |
| | <i>Ruminococcus</i> | | |
| <i>Clostridium (II)</i> | <i>(Ruminococcaceae)</i> | 0.6413 | 0.0099 |
| <i>Clostridium methylpentosum</i> | <i>Allobaculum</i> | -0.665 | 0.0099 |
| <i>Clostridium methylpentosum</i> | <i>Anaerotruncus</i> | 0.6913 | 0.0099 |
| <i>Clostridium methylpentosum</i> | <i>Bacteroides</i> | 0.5067 | 0.0099 |
| <i>Clostridium methylpentosum</i> | <i>Bacteroides acidifaciens</i> | -0.6347 | 0.0099 |
| <i>Clostridium methylpentosum</i> | <i>Butyricicoccus pullicaecorum</i> | -0.633 | 0.0099 |

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| <i>Clostridium methylpentosum</i> | <i>Christensenellaceae</i> | 0.7227 | 0.0099 |
| <i>Clostridium methylpentosum</i> | <i>Desulfovibrionaceae</i> | 0.4204 | 0.0099 |
| <i>Clostridium methylpentosum</i> | <i>Lactococcus</i> | 0.4939 | 0.0198 |
| <i>Clostridium methylpentosum</i> | <i>Mucispirillum schaedleri</i> | 0.5571 | 0.0099 |
| <i>Clostridium methylpentosum</i> | <i>Muribaculaceae</i> | -0.5136 | 0.0495 |
| <i>Clostridium methylpentosum</i> | <i>Oscillospira</i> | 0.6992 | 0.0099 |
| <i>Clostridium methylpentosum</i> | <i>Parabacteroides gordonii</i> | 0.5318 | 0.0495 |
| <i>Clostridium methylpentosum</i> | <i>Peptococcaceae</i> | 0.573 | 0.0297 |
| <i>Clostridium methylpentosum</i> | <i>rc4 4</i> | -0.4652 | 0.0099 |
| <i>Clostridium methylpentosum</i> | <i>RF32</i> | -0.5764 | 0.0099 |
| <i>Clostridium methylpentosum</i> | <i>RF39</i> | -0.4129 | 0.0495 |
| <i>Clostridium methylpentosum</i> | <i>Rikenellaceae</i> | -0.7087 | 0.0099 |
| <i>Clostridium methylpentosum</i> | <i>Ruminococcaceae (II)</i> | 0.5615 | 0.0396 |
| <i>Clostridium methylpentosum</i> | <i>Ruminococcus gnavus</i> | 0.6431 | 0.0099 |
| <i>Clostridium methylpentosum</i> | <i>Streptococcus</i> | 0.5758 | 0.0099 |
| <i>Clostridium methylpentosum</i> | <i>Sutterella</i> | -0.6956 | 0.0099 |
| <i>Coprococcus</i> | <i>Allobaculum</i> | -0.6128 | 0.0099 |
| <i>Coprococcus</i> | <i>Christensenellaceae</i> | 0.5055 | 0.0396 |
| <i>Coprococcus</i> | <i>Desulfovibrionaceae</i> | 0.6027 | 0.0198 |
| <i>Coprococcus</i> | <i>Dorea</i> | 0.4412 | 0.0297 |
| <i>Coprococcus</i> | <i>Mucispirillum schaedleri</i> | 0.5846 | 0.0297 |
| <i>Coprococcus</i> | <i>Rikenellaceae</i> | -0.4904 | 0.0495 |
| | <i>Ruminococcus</i> | | |
| <i>Coprococcus</i> | <i>(Lachnospiraceae)</i> | 0.4657 | 0.0396 |
| <i>Coprococcus</i> | <i>Sutterella</i> | -0.5118 | 0.0198 |
| <i>Dehalobacterium</i> | <i>Butyricicoccus pullicaecorum</i> | -0.6866 | 0.0495 |
| <i>Dehalobacterium</i> | <i>Christensenellaceae</i> | 0.7359 | 0.0495 |
| <i>Dehalobacterium</i> | <i>Streptococcus</i> | 0.6254 | 0.0495 |
| <i>Desulfovibrionaceae</i> | <i>Allobaculum</i> | -0.5851 | 0.0099 |
| <i>Desulfovibrionaceae</i> | <i>Bacteroides acidifaciens</i> | -0.4005 | 0.0099 |
| <i>Desulfovibrionaceae</i> | <i>Clostridium hathewayi</i> | 0.5141 | 0.0099 |
| <i>Desulfovibrionaceae</i> | <i>Clostridium methylpentosum</i> | 0.4204 | 0.0099 |
| <i>Desulfovibrionaceae</i> | <i>Coprococcus</i> | 0.6027 | 0.0198 |
| <i>Desulfovibrionaceae</i> | <i>Mucispirillum schaedleri</i> | 0.524 | 0.0099 |

Table S1. Pairwise comparison of bacterial composition at phylum level across the diet groups

| Taxon 1 | Taxon 2 | Correlation | p-value |
|-----------------------------|---------------------------------|--------------------|----------------|
| <i>Desulfovibrionaceae</i> | <i>Oscillospira</i> | 0.5906 | 0.0297 |
| <i>Desulfovibrionaceae</i> | RF39 | -0.4195 | 0.0297 |
| <i>Desulfovibrionaceae</i> | <i>Rikenellaceae</i> | -0.4792 | 0.0099 |
| <i>Desulfovibrionaceae</i> | <i>Ruminococcaceae</i> (I) | 0.8177 | 0.0198 |
| <i>Desulfovibrionaceae</i> | <i>Ruminococcaceae</i> (II) | 0.5364 | 0.0198 |
| <i>Desulfovibrionaceae</i> | <i>Ruminococcus gnavus</i> | 0.4909 | 0.0198 |
| <i>Dorea</i> | <i>Christensenellaceae</i> | 0.4754 | 0.0099 |
| <i>Dorea</i> | <i>Clostridium</i> (II) | -0.4974 | 0.0099 |
| <i>Dorea</i> | <i>Coproccoccus</i> | 0.4412 | 0.0297 |
| <i>Dorea</i> | <i>Mucispirillum schaedleri</i> | 0.5073 | 0.0099 |
| <i>Dorea</i> | <i>Oscillospira</i> | 0.4715 | 0.0495 |
| <i>Dorea</i> | <i>Peptococcaceae</i> | 0.5028 | 0.0297 |
| <i>Dorea</i> | RF32 | -0.4313 | 0.0099 |
| <i>Dorea</i> | <i>Rikenellaceae</i> | -0.4171 | 0.0198 |
| <i>Dorea</i> | <i>Ruminococcus gnavus</i> | 0.4663 | 0.0396 |
| <i>Dorea</i> | <i>Sutterella</i> | -0.4438 | 0.0297 |
| <i>Enterobacteriaceae</i> | <i>Ruminococcaceae</i> (II) | 0.4495 | 0.0099 |
| | <i>Ruminococcus</i> | | |
| <i>Enterobacteriaceae</i> | (<i>Ruminococcaceae</i>) | 0.447 | 0.0198 |
| <i>Erysipelotrichaceae</i> | <i>Lachnospiraceae</i> (II) | -0.5727 | 0.0495 |
| <i>Erysipelotrichaceae</i> | <i>Ruminococcaceae</i> (I) | -0.5415 | 0.0396 |
| F16 | <i>Akkermansia muciniphila</i> | -0.5229 | 0.0099 |
| F16 | <i>Bacteroides acidifaciens</i> | -0.5527 | 0.0099 |
| F16 | <i>Lactobacillus</i> | -0.4591 | 0.0099 |
| F16 | <i>Muribaculaceae</i> | -0.501 | 0.0099 |
| <i>Lachnospiraceae</i> (I) | <i>Bacteroides acidifaciens</i> | -0.6692 | 0.0297 |
| <i>Lachnospiraceae</i> (I) | rc4 4 | -0.5018 | 0.0099 |
| <i>Lachnospiraceae</i> (II) | <i>Erysipelotrichaceae</i> | -0.5727 | 0.0495 |
| <i>Lachnospiraceae</i> (II) | rc4 4 | -0.5261 | 0.0396 |
| | <i>Ruminococcus</i> | | |
| <i>Lachnospiraceae</i> (II) | (<i>Lachnospiraceae</i>) | 0.5788 | 0.0099 |
| <i>Lactobacillus</i> | <i>Allobaculum</i> | 0.5286 | 0.0198 |
| <i>Lactobacillus</i> | F16 | -0.4591 | 0.0099 |
| <i>Lactobacillus</i> | <i>Oscillospira</i> | -0.6672 | 0.0198 |

Table S1. Pairwise comparison of bacterial composition at phylum level across the diet groups

| Taxon 1 | Taxon 2 | Correlation | p-value |
|---------------------------------|-----------------------------------|--------------------|----------------|
| <i>Lactobacillus</i> | <i>Ruminococcus gnavus</i> | -0.5506 | 0.0297 |
| | <i>Ruminococcus</i> | | |
| <i>Lactobacillus</i> | (<i>Ruminococcaceae</i>) | -0.6606 | 0.0198 |
| <i>Lactobacillus</i> | <i>Sutterella</i> | 0.4253 | 0.0396 |
| <i>Lactococcus</i> | <i>Anaerotruncus</i> | 0.4505 | 0.0198 |
| <i>Lactococcus</i> | <i>Bacteroidales</i> | -0.4184 | 0.0099 |
| <i>Lactococcus</i> | <i>Bacteroides</i> | 0.4501 | 0.0297 |
| <i>Lactococcus</i> | <i>Bacteroides acidifaciens</i> | -0.6788 | 0.0099 |
| <i>Lactococcus</i> | <i>Christensenellaceae</i> | 0.4332 | 0.0198 |
| <i>Lactococcus</i> | <i>Clostridium methylpentosum</i> | 0.4939 | 0.0198 |
| <i>Lactococcus</i> | <i>Mucispirillum schaedleri</i> | 0.5349 | 0.0099 |
| <i>Lactococcus</i> | <i>Muribaculaceae</i> | -0.6427 | 0.0198 |
| <i>Lactococcus</i> | rc4 4 | -0.4528 | 0.0099 |
| <i>Lactococcus</i> | RF32 | -0.5218 | 0.0099 |
| <i>Lactococcus</i> | <i>Rikenellaceae</i> | -0.5777 | 0.0099 |
| <i>Lactococcus</i> | <i>Ruminococcus gnavus</i> | 0.4753 | 0.0099 |
| <i>Lactococcus</i> | <i>Streptococcus</i> | 0.4863 | 0.0099 |
| <i>Lactococcus</i> | <i>Sutterella</i> | -0.5508 | 0.0099 |
| <i>Mogibacteriaceae</i> (I) | <i>Adlercreutzia</i> | -0.4819 | 0.0099 |
| <i>Mogibacteriaceae</i> (II) | <i>Allobaculum</i> | 0.4387 | 0.0198 |
| <i>Mogibacteriaceae</i> (II) | <i>Bacteroides</i> | -0.4732 | 0.0396 |
| <i>Mogibacteriaceae</i> (II) | <i>Bacteroides acidifaciens</i> | 0.7584 | 0.0099 |
| <i>Mogibacteriaceae</i> (II) | <i>Muribaculaceae</i> | 0.6559 | 0.0099 |
| <i>Mogibacteriaceae</i> (II) | rc4 4 | 0.5009 | 0.0099 |
| <i>Mogibacteriaceae</i> (II) | RF32 | 0.4702 | 0.0099 |
| <i>Mogibacteriaceae</i> (II) | <i>Rikenellaceae</i> | 0.5896 | 0.0297 |
| <i>Mogibacteriaceae</i> (II) | <i>Ruminococcus gnavus</i> | -0.4378 | 0.0198 |
| <i>Mogibacteriaceae</i> (II) | <i>Sutterella</i> | 0.5853 | 0.0099 |
| <i>Mucispirillum schaedleri</i> | <i>Allobaculum</i> | -0.6859 | 0.0099 |
| <i>Mucispirillum schaedleri</i> | <i>Anaerotruncus</i> | 0.6487 | 0.0099 |
| <i>Mucispirillum schaedleri</i> | <i>Bacteroidales</i> | -0.5242 | 0.0099 |
| <i>Mucispirillum schaedleri</i> | <i>Bacteroides</i> | 0.626 | 0.0099 |
| <i>Mucispirillum schaedleri</i> | <i>Bacteroides acidifaciens</i> | -0.6543 | 0.0099 |
| <i>Mucispirillum schaedleri</i> | <i>Butyricoccus pullicaecorum</i> | -0.5751 | 0.0099 |

Table S1. Pairwise comparison of bacterial composition at phylum level across the diet groups

| Taxon 1 | Taxon 2 | Correlation | p-value |
|---------------------------------|-------------------------------------|--------------------|----------------|
| <i>Mucispirillum schaedleri</i> | <i>Christensenellaceae</i> | 0.6366 | 0.0099 |
| <i>Mucispirillum schaedleri</i> | <i>Clostridiales (II)</i> | 0.6475 | 0.0396 |
| <i>Mucispirillum schaedleri</i> | <i>Clostridium methylpentosum</i> | 0.5571 | 0.0099 |
| <i>Mucispirillum schaedleri</i> | <i>Coprococcus</i> | 0.5846 | 0.0297 |
| <i>Mucispirillum schaedleri</i> | <i>Desulfovibrionaceae</i> | 0.524 | 0.0099 |
| <i>Mucispirillum schaedleri</i> | <i>Dorea</i> | 0.5073 | 0.0099 |
| <i>Mucispirillum schaedleri</i> | <i>Lactococcus</i> | 0.5349 | 0.0099 |
| <i>Mucispirillum schaedleri</i> | <i>Muribaculaceae</i> | -0.5718 | 0.0495 |
| <i>Mucispirillum schaedleri</i> | <i>Oscillospira</i> | 0.775 | 0.0099 |
| <i>Mucispirillum schaedleri</i> | <i>Parabacteroides gordonii</i> | 0.4165 | 0.0396 |
| <i>Mucispirillum schaedleri</i> | <i>Peptococcaceae</i> | 0.6764 | 0.0198 |
| <i>Mucispirillum schaedleri</i> | <i>rc4 4</i> | -0.504 | 0.0297 |
| <i>Mucispirillum schaedleri</i> | <i>RF32</i> | -0.5706 | 0.0099 |
| <i>Mucispirillum schaedleri</i> | <i>RF39</i> | -0.4558 | 0.0297 |
| <i>Mucispirillum schaedleri</i> | <i>Rikenellaceae</i> | -0.624 | 0.0099 |
| <i>Mucispirillum schaedleri</i> | <i>Ruminococcaceae (I)</i> | 0.7894 | 0.0495 |
| <i>Mucispirillum schaedleri</i> | <i>Ruminococcus gnavus</i> | 0.7156 | 0.0099 |
| <i>Mucispirillum schaedleri</i> | <i>Streptococcus</i> | 0.4798 | 0.0099 |
| <i>Mucispirillum schaedleri</i> | <i>Sutterella</i> | -0.749 | 0.0099 |
| <i>Muribaculaceae</i> | <i>Adlercreutzia</i> | -0.4097 | 0.0297 |
| <i>Muribaculaceae</i> | <i>Allobaculum</i> | 0.6225 | 0.0198 |
| <i>Muribaculaceae</i> | <i>Bacteroidales</i> | 0.7358 | 0.0099 |
| <i>Muribaculaceae</i> | <i>Bacteroides acidifaciens</i> | 0.7002 | 0.0297 |
| <i>Muribaculaceae</i> | <i>Butyricicoccus pullicaecorum</i> | 0.5862 | 0.0198 |
| <i>Muribaculaceae</i> | <i>Clostridium hathewayi</i> | -0.5008 | 0.0198 |
| <i>Muribaculaceae</i> | <i>Clostridium (I)</i> | -0.442 | 0.0198 |
| <i>Muribaculaceae</i> | <i>Clostridium methylpentosum</i> | -0.5136 | 0.0495 |
| <i>Muribaculaceae</i> | <i>F16</i> | -0.501 | 0.0099 |
| <i>Muribaculaceae</i> | <i>Lactococcus</i> | -0.6427 | 0.0198 |
| <i>Muribaculaceae</i> | <i>Mogibacteriaceae (II)</i> | 0.6559 | 0.0099 |
| <i>Muribaculaceae</i> | <i>Mucispirillum schaedleri</i> | -0.5718 | 0.0495 |
| <i>Muribaculaceae</i> | <i>rc4 4</i> | 0.6779 | 0.0198 |
| <i>Muribaculaceae</i> | <i>RF32</i> | 0.7999 | 0.0099 |
| <i>Muribaculaceae</i> | <i>Rikenellaceae</i> | 0.6916 | 0.0297 |

Table S1. Pairwise comparison of bacterial composition at phylum level across the diet groups

| Taxon 1 | Taxon 2 | Correlation | p-value |
|---------------------------------|-------------------------------------|--------------------|----------------|
| <i>Muribaculaceae</i> | <i>Ruminococcus gnavus</i> | -0.7735 | 0.0099 |
| <i>Muribaculaceae</i> | <i>Sutterella</i> | 0.8523 | 0.0099 |
| <i>Oscillospira</i> | <i>Allobaculum</i> | -0.8149 | 0.0099 |
| <i>Oscillospira</i> | <i>Anaerotruncus</i> | 0.7022 | 0.0099 |
| <i>Oscillospira</i> | <i>Bacteroides</i> | 0.7179 | 0.0297 |
| <i>Oscillospira</i> | <i>Bacteroides acidifaciens</i> | -0.6911 | 0.0297 |
| <i>Oscillospira</i> | <i>Butyricicoccus pullicaecorum</i> | -0.62 | 0.0198 |
| <i>Oscillospira</i> | <i>Christensenellaceae</i> | 0.7229 | 0.0198 |
| <i>Oscillospira</i> | <i>Clostridium methylpentosum</i> | 0.6992 | 0.0099 |
| <i>Oscillospira</i> | <i>Desulfovibrionaceae</i> | 0.5906 | 0.0297 |
| <i>Oscillospira</i> | <i>Dorea</i> | 0.4715 | 0.0495 |
| <i>Oscillospira</i> | <i>Lactobacillus</i> | -0.6672 | 0.0198 |
| <i>Oscillospira</i> | <i>Mucispirillum schaedleri</i> | 0.775 | 0.0099 |
| <i>Oscillospira</i> | <i>Peptococcaceae</i> | 0.7573 | 0.0495 |
| <i>Oscillospira</i> | <i>rc4 4</i> | -0.7207 | 0.0198 |
| <i>Oscillospira</i> | <i>RF32</i> | -0.5912 | 0.0099 |
| <i>Oscillospira</i> | <i>RF39</i> | -0.6057 | 0.0297 |
| <i>Oscillospira</i> | <i>Rikenellaceae</i> | -0.7144 | 0.0198 |
| <i>Oscillospira</i> | <i>Ruminococcus gnavus</i> | 0.8118 | 0.0198 |
| <i>Oscillospira</i> | <i>Streptococcus</i> | 0.6218 | 0.0198 |
| <i>Oscillospira</i> | <i>Sutterella</i> | -0.845 | 0.0099 |
| <i>Parabacteroides gordonii</i> | <i>Anaerotruncus</i> | 0.5829 | 0.0198 |
| <i>Parabacteroides gordonii</i> | <i>Butyricicoccus pullicaecorum</i> | -0.4809 | 0.0198 |
| <i>Parabacteroides gordonii</i> | <i>Christensenellaceae</i> | 0.4699 | 0.0198 |
| <i>Parabacteroides gordonii</i> | <i>Clostridium methylpentosum</i> | 0.5318 | 0.0495 |
| <i>Parabacteroides gordonii</i> | <i>Mucispirillum schaedleri</i> | 0.4165 | 0.0396 |
| <i>Peptococcaceae</i> | <i>Allobaculum</i> | -0.6891 | 0.0099 |
| <i>Peptococcaceae</i> | <i>Anaerotruncus</i> | 0.7029 | 0.0099 |
| <i>Peptococcaceae</i> | <i>Bacteroides</i> | 0.7086 | 0.0297 |
| <i>Peptococcaceae</i> | <i>Bacteroides acidifaciens</i> | -0.7333 | 0.0099 |
| <i>Peptococcaceae</i> | <i>Butyricicoccus pullicaecorum</i> | -0.5492 | 0.0099 |
| <i>Peptococcaceae</i> | <i>Christensenellaceae</i> | 0.6144 | 0.0099 |
| <i>Peptococcaceae</i> | <i>Clostridium methylpentosum</i> | 0.573 | 0.0297 |
| <i>Peptococcaceae</i> | <i>Dorea</i> | 0.5028 | 0.0297 |

Table S1. Pairwise comparison of bacterial composition at phylum level across the diet groups

| Taxon 1 | Taxon 2 | Correlation | p-value |
|-----------------------|-------------------------------------|--------------------|----------------|
| <i>Peptococcaceae</i> | <i>Mucispirillum schaedleri</i> | 0.6764 | 0.0198 |
| <i>Peptococcaceae</i> | <i>Oscillospira</i> | 0.7573 | 0.0495 |
| <i>Peptococcaceae</i> | <i>rc4 4</i> | -0.716 | 0.0099 |
| <i>Peptococcaceae</i> | RF32 | -0.6533 | 0.0099 |
| <i>Peptococcaceae</i> | <i>Rikenellaceae</i> | -0.6968 | 0.0198 |
| <i>Peptococcaceae</i> | <i>Ruminococcus gnavus</i> | 0.7785 | 0.0099 |
| | <i>Ruminococcus</i> | | |
| <i>Peptococcaceae</i> | (<i>Lachnospiraceae</i>) | 0.4304 | 0.0495 |
| <i>Peptococcaceae</i> | <i>Streptococcus</i> | 0.6544 | 0.0099 |
| <i>Peptococcaceae</i> | <i>Sutterella</i> | -0.6967 | 0.0198 |
| <i>rc4 4</i> | <i>Akkermansia muciniphila</i> | 0.4385 | 0.0198 |
| <i>rc4 4</i> | <i>Allobaculum</i> | 0.6133 | 0.0099 |
| <i>rc4 4</i> | <i>Anaerotruncus</i> | -0.4664 | 0.0099 |
| <i>rc4 4</i> | <i>Bacteroidales</i> | 0.472 | 0.0099 |
| <i>rc4 4</i> | <i>Bacteroides</i> | -0.7371 | 0.0198 |
| <i>rc4 4</i> | <i>Bacteroides acidifaciens</i> | 0.802 | 0.0099 |
| <i>rc4 4</i> | <i>Bilophila</i> | -0.4771 | 0.0099 |
| <i>rc4 4</i> | <i>Butyricicoccus pullicaecorum</i> | 0.436 | 0.0198 |
| <i>rc4 4</i> | <i>Christensenellaceae</i> | -0.4383 | 0.0099 |
| <i>rc4 4</i> | <i>Clostridiales</i> (II) | -0.6854 | 0.0198 |
| <i>rc4 4</i> | <i>Clostridium methylpentosum</i> | -0.4652 | 0.0099 |
| <i>rc4 4</i> | <i>Lachnospiraceae</i> (I) | -0.5018 | 0.0099 |
| <i>rc4 4</i> | <i>Lachnospiraceae</i> (II) | -0.5261 | 0.0396 |
| <i>rc4 4</i> | <i>Lactococcus</i> | -0.4528 | 0.0099 |
| <i>rc4 4</i> | <i>Mogibacteriaceae</i> (II) | 0.5009 | 0.0099 |
| <i>rc4 4</i> | <i>Mucispirillum schaedleri</i> | -0.504 | 0.0297 |
| <i>rc4 4</i> | <i>Muribaculaceae</i> | 0.6779 | 0.0198 |
| <i>rc4 4</i> | <i>Oscillospira</i> | -0.7207 | 0.0198 |
| <i>rc4 4</i> | <i>Peptococcaceae</i> | -0.716 | 0.0099 |
| <i>rc4 4</i> | RF32 | 0.7551 | 0.0099 |
| <i>rc4 4</i> | <i>Rikenellaceae</i> | 0.6339 | 0.0099 |
| <i>rc4 4</i> | <i>Ruminococcaceae</i> (I) | -0.5975 | 0.0396 |
| <i>rc4 4</i> | <i>Ruminococcus gnavus</i> | -0.6217 | 0.0099 |
| <i>rc4 4</i> | <i>Streptococcus</i> | -0.489 | 0.0099 |

Table S1. Pairwise comparison of bacterial composition at phylum level across the diet groups

| Taxon 1 | Taxon 2 | Correlation | p-value |
|----------------------|-------------------------------------|--------------------|----------------|
| <i>rc4 4</i> | <i>Sutterella</i> | 0.7031 | 0.0099 |
| <i>RF32</i> | <i>Allobaculum</i> | 0.5875 | 0.0099 |
| <i>RF32</i> | <i>Anaerotruncus</i> | -0.5394 | 0.0099 |
| <i>RF32</i> | <i>Bacteroidales</i> | 0.5945 | 0.0099 |
| <i>RF32</i> | <i>Bacteroides</i> | -0.5772 | 0.0198 |
| <i>RF32</i> | <i>Bacteroides acidifaciens</i> | 0.9205 | 0.0099 |
| <i>RF32</i> | <i>Butyricicoccus pullicaecorum</i> | 0.6163 | 0.0099 |
| <i>RF32</i> | <i>Christensenellaceae</i> | -0.5837 | 0.0099 |
| <i>RF32</i> | <i>Clostridiales (II)</i> | -0.6371 | 0.0297 |
| <i>RF32</i> | <i>Clostridium methylpentosum</i> | -0.5764 | 0.0099 |
| <i>RF32</i> | <i>Dorea</i> | -0.4313 | 0.0099 |
| <i>RF32</i> | <i>Lactococcus</i> | -0.5218 | 0.0099 |
| <i>RF32</i> | <i>Mogibacteriaceae (II)</i> | 0.4702 | 0.0099 |
| <i>RF32</i> | <i>Mucispirillum schaedleri</i> | -0.5706 | 0.0099 |
| <i>RF32</i> | <i>Muribaculaceae</i> | 0.7999 | 0.0099 |
| <i>RF32</i> | <i>Oscillospira</i> | -0.5912 | 0.0099 |
| <i>RF32</i> | <i>Peptococcaceae</i> | -0.6533 | 0.0099 |
| <i>RF32</i> | <i>rc4 4</i> | 0.7551 | 0.0099 |
| <i>RF32</i> | <i>Rikenellaceae</i> | 0.862 | 0.0099 |
| <i>RF32</i> | <i>Ruminococcus gnavus</i> | -0.588 | 0.0099 |
| <i>RF32</i> | <i>Streptococcus</i> | -0.6317 | 0.0099 |
| <i>RF32</i> | <i>Sutterella</i> | 0.7779 | 0.0099 |
| <i>RF39</i> | <i>Allobaculum</i> | 0.4504 | 0.0099 |
| <i>RF39</i> | <i>Butyricicoccus pullicaecorum</i> | 0.6112 | 0.0099 |
| <i>RF39</i> | <i>Clostridiales (II)</i> | -0.6351 | 0.0198 |
| <i>RF39</i> | <i>Clostridium methylpentosum</i> | -0.4129 | 0.0495 |
| <i>RF39</i> | <i>Desulfovibrionaceae</i> | -0.4195 | 0.0297 |
| <i>RF39</i> | <i>Mucispirillum schaedleri</i> | -0.4558 | 0.0297 |
| <i>RF39</i> | <i>Oscillospira</i> | -0.6057 | 0.0297 |
| <i>RF39</i> | <i>Ruminococcaceae (I)</i> | 1 | 0.0297 |
| <i>RF39</i> | <i>Ruminococcus gnavus</i> | -0.4498 | 0.0099 |
| <i>Rikenellaceae</i> | <i>Allobaculum</i> | 0.7471 | 0.0099 |
| <i>Rikenellaceae</i> | <i>Anaerotruncus</i> | -0.5739 | 0.0396 |
| <i>Rikenellaceae</i> | <i>Bacteroidales</i> | 0.5491 | 0.0099 |

Table S1. Pairwise comparison of bacterial composition at phylum level across the diet groups

| Taxon 1 | Taxon 2 | Correlation | p-value |
|----------------------------|-------------------------------------|--------------------|----------------|
| <i>Rikenellaceae</i> | <i>Bacteroides</i> | -0.6628 | 0.0099 |
| <i>Rikenellaceae</i> | <i>Bacteroides acidifaciens</i> | 0.8036 | 0.0099 |
| <i>Rikenellaceae</i> | <i>Butyricicoccus pullicaecorum</i> | 0.6001 | 0.0198 |
| <i>Rikenellaceae</i> | <i>Christensenellaceae</i> | -0.6868 | 0.0099 |
| <i>Rikenellaceae</i> | <i>Clostridiales (II)</i> | -0.7392 | 0.0396 |
| <i>Rikenellaceae</i> | <i>Clostridium methylpentosum</i> | -0.7087 | 0.0099 |
| <i>Rikenellaceae</i> | <i>Coprococcus</i> | -0.4904 | 0.0495 |
| <i>Rikenellaceae</i> | <i>Desulfovibrionaceae</i> | -0.4792 | 0.0099 |
| <i>Rikenellaceae</i> | <i>Dorea</i> | -0.4171 | 0.0198 |
| <i>Rikenellaceae</i> | <i>Lactococcus</i> | -0.5777 | 0.0099 |
| <i>Rikenellaceae</i> | <i>Mogibacteriaceae (II)</i> | 0.5896 | 0.0297 |
| <i>Rikenellaceae</i> | <i>Mucispirillum schaedleri</i> | -0.624 | 0.0099 |
| <i>Rikenellaceae</i> | <i>Muribaculaceae</i> | 0.6916 | 0.0297 |
| <i>Rikenellaceae</i> | <i>Oscillospira</i> | -0.7144 | 0.0198 |
| <i>Rikenellaceae</i> | <i>Peptococcaceae</i> | -0.6968 | 0.0198 |
| <i>Rikenellaceae</i> | <i>rc4 4</i> | 0.6339 | 0.0099 |
| <i>Rikenellaceae</i> | <i>RF32</i> | 0.862 | 0.0099 |
| <i>Rikenellaceae</i> | <i>Ruminococcaceae (I)</i> | -0.729 | 0.0396 |
| <i>Rikenellaceae</i> | <i>Ruminococcaceae (II)</i> | -0.7436 | 0.0396 |
| <i>Rikenellaceae</i> | <i>Ruminococcus gnavus</i> | -0.784 | 0.0099 |
| <i>Rikenellaceae</i> | <i>Streptococcus</i> | -0.4309 | 0.0495 |
| <i>Rikenellaceae</i> | <i>Sutterella</i> | 0.7562 | 0.0099 |
| <i>Roseburia</i> | <i>Clostridium colinum</i> | 0.7085 | 0.0099 |
| <i>Ruminococcaceae (I)</i> | <i>Allobaculum</i> | -0.7728 | 0.0198 |
| <i>Ruminococcaceae (I)</i> | <i>Anaerotruncus</i> | 0.5555 | 0.0396 |
| <i>Ruminococcaceae (I)</i> | <i>Butyricicoccus pullicaecorum</i> | -0.6007 | 0.0198 |
| <i>Ruminococcaceae (I)</i> | <i>Desulfovibrionaceae</i> | 0.8177 | 0.0198 |
| <i>Ruminococcaceae (I)</i> | <i>Erysipelotrichaceae</i> | -0.5415 | 0.0396 |
| <i>Ruminococcaceae (I)</i> | <i>Mucispirillum schaedleri</i> | 0.7894 | 0.0495 |
| <i>Ruminococcaceae (I)</i> | <i>rc4 4</i> | -0.5975 | 0.0396 |
| <i>Ruminococcaceae (I)</i> | <i>RF39</i> | 1 | 0.0297 |
| <i>Ruminococcaceae (I)</i> | <i>Rikenellaceae</i> | -0.729 | 0.0396 |
| | <i>Ruminococcus</i> | | |
| <i>Ruminococcaceae (I)</i> | <i>(Lachnospiraceae)</i> | 0.4986 | 0.0396 |

Table S1. Pairwise comparison of bacterial composition at phylum level across the diet groups

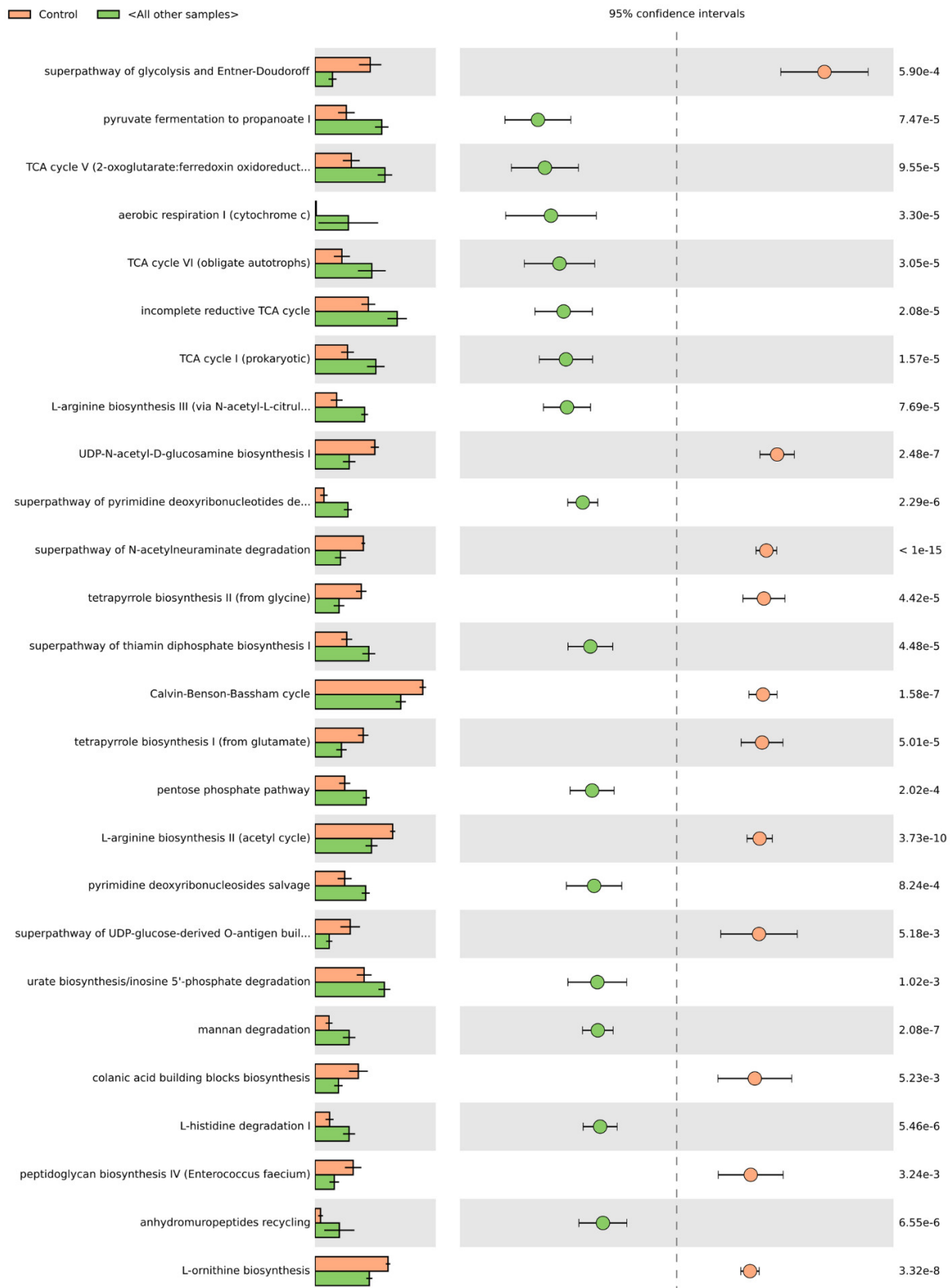
| Taxon 1 | Taxon 2 | Correlation | p-value |
|-----------------------------|-------------------------------------|--------------------|----------------|
| <i>Ruminococcaceae</i> (I) | <i>Streptococcus</i> | 0.6585 | 0.0297 |
| <i>Ruminococcaceae</i> (I) | <i>Sutterella</i> | -0.6546 | 0.0396 |
| <i>Ruminococcaceae</i> (II) | <i>Allobaculum</i> | -0.6007 | 0.0297 |
| <i>Ruminococcaceae</i> (II) | <i>Anaerotruncus</i> | 0.6048 | 0.0297 |
| <i>Ruminococcaceae</i> (II) | <i>Butyricicoccus pullicaecorum</i> | -0.6147 | 0.0198 |
| <i>Ruminococcaceae</i> (II) | <i>Christensenellaceae</i> | 0.5596 | 0.0297 |
| <i>Ruminococcaceae</i> (II) | <i>Clostridium methylpentosum</i> | 0.5615 | 0.0396 |
| <i>Ruminococcaceae</i> (II) | <i>Desulfovibrionaceae</i> | 0.5364 | 0.0198 |
| <i>Ruminococcaceae</i> (II) | <i>Enterobacteriaceae</i> | 0.4495 | 0.0099 |
| <i>Ruminococcaceae</i> (II) | <i>Rikenellaceae</i> | -0.7436 | 0.0396 |
| <i>Ruminococcaceae</i> (II) | <i>Sutterella</i> | -0.5098 | 0.0495 |
| <i>Ruminococcus gnavus</i> | <i>Allobaculum</i> | -0.7664 | 0.0099 |
| <i>Ruminococcus gnavus</i> | <i>Anaerotruncus</i> | 0.6821 | 0.0099 |
| <i>Ruminococcus gnavus</i> | <i>Bacteroides</i> | 0.737 | 0.0099 |
| <i>Ruminococcus gnavus</i> | <i>Bacteroides acidifaciens</i> | -0.7898 | 0.0198 |
| <i>Ruminococcus gnavus</i> | <i>Butyricicoccus pullicaecorum</i> | -0.6088 | 0.0099 |
| <i>Ruminococcus gnavus</i> | <i>Christensenellaceae</i> | 0.6767 | 0.0099 |
| <i>Ruminococcus gnavus</i> | <i>Clostridium methylpentosum</i> | 0.6431 | 0.0099 |
| <i>Ruminococcus gnavus</i> | <i>Desulfovibrionaceae</i> | 0.4909 | 0.0198 |
| <i>Ruminococcus gnavus</i> | <i>Dorea</i> | 0.4663 | 0.0396 |
| <i>Ruminococcus gnavus</i> | <i>Lactobacillus</i> | -0.5506 | 0.0297 |
| <i>Ruminococcus gnavus</i> | <i>Lactococcus</i> | 0.4753 | 0.0099 |
| <i>Ruminococcus gnavus</i> | <i>Mogibacteriaceae</i> (II) | -0.4378 | 0.0198 |
| <i>Ruminococcus gnavus</i> | <i>Mucispirillum schaedleri</i> | 0.7156 | 0.0099 |
| <i>Ruminococcus gnavus</i> | <i>Muribaculaceae</i> | -0.7735 | 0.0099 |
| <i>Ruminococcus gnavus</i> | <i>Oscillospira</i> | 0.8118 | 0.0198 |
| <i>Ruminococcus gnavus</i> | <i>Peptococcaceae</i> | 0.7785 | 0.0099 |
| <i>Ruminococcus gnavus</i> | <i>rc4 4</i> | -0.6217 | 0.0099 |
| <i>Ruminococcus gnavus</i> | <i>RF32</i> | -0.588 | 0.0099 |
| <i>Ruminococcus gnavus</i> | <i>RF39</i> | -0.4498 | 0.0099 |
| <i>Ruminococcus gnavus</i> | <i>Rikenellaceae</i> | -0.784 | 0.0099 |
| <i>Ruminococcus gnavus</i> | <i>Streptococcus</i> | 0.5417 | 0.0099 |
| <i>Ruminococcus gnavus</i> | <i>Sutterella</i> | -0.7761 | 0.0099 |

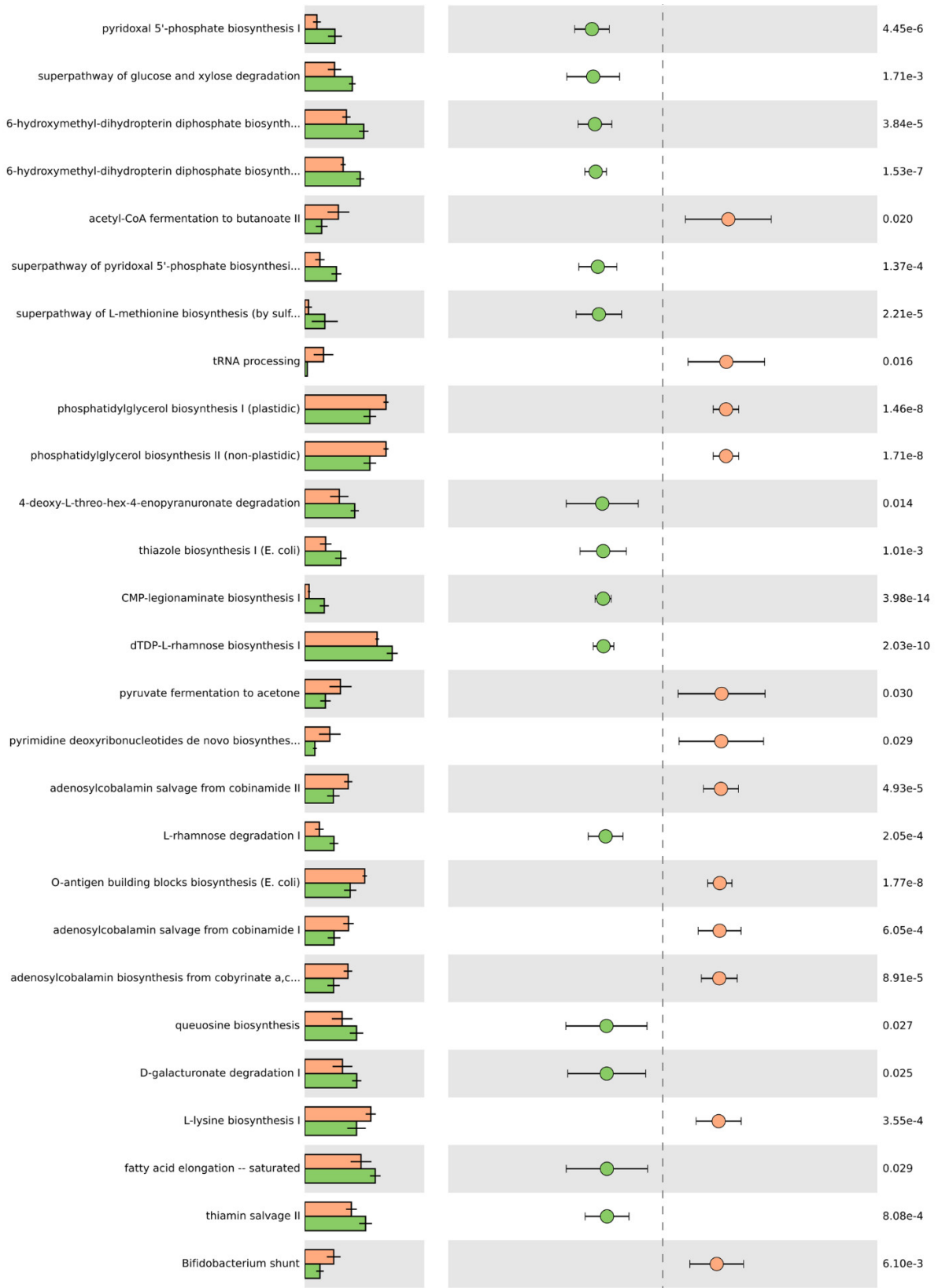
Table S1. Pairwise comparison of bacterial composition at phylum level across the diet groups

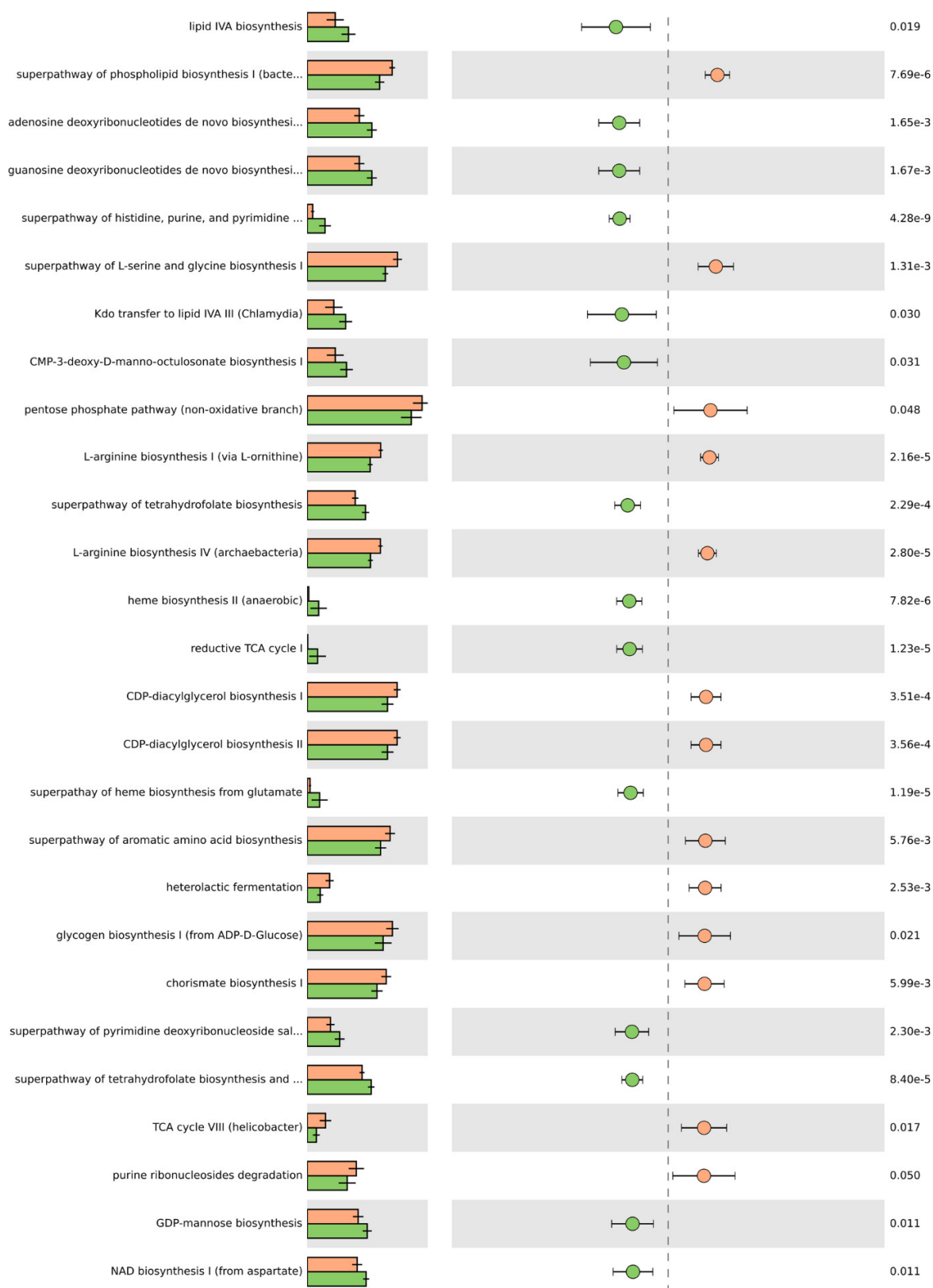
| Taxon 1 | Taxon 2 | Correlation | p-value |
|---------------------------------------------------|-----------------------------------|--------------------|----------------|
| <i>Ruminococcus</i> (<i>Lachnospiraceae</i>) | <i>Bilophila</i> | 0.406 | 0.0396 |
| <i>Ruminococcus</i> (<i>Lachnospiraceae</i>) | <i>Coprococcus</i> | 0.4657 | 0.0396 |
| <i>Ruminococcus</i> (<i>Lachnospiraceae</i>) | <i>Lachnospiraceae</i> (II) | 0.5788 | 0.0099 |
| <i>Ruminococcus</i> (<i>Lachnospiraceae</i>) | <i>Peptococcaceae</i> | 0.4304 | 0.0495 |
| <i>Ruminococcus</i> (<i>Lachnospiraceae</i>) | <i>Ruminococcaceae</i> (I) | 0.4986 | 0.0396 |
| <i>Ruminococcus</i> (<i>Ruminococcaceae</i>) | <i>Clostridium</i> (II) | 0.6413 | 0.0099 |
| <i>Ruminococcus</i> (<i>Ruminococcaceae</i>) | <i>Enterobacteriaceae</i> | 0.447 | 0.0198 |
| <i>Ruminococcus</i> (<i>Ruminococcaceae</i>) | <i>Lactobacillus</i> | -0.6606 | 0.0198 |
| <i>Streptococcus</i> | <i>Anaerotruncus</i> | 0.5456 | 0.0099 |
| <i>Streptococcus</i> | <i>Bacteroides</i> | 0.4986 | 0.0198 |
| <i>Streptococcus</i> | <i>Bacteroides acidifaciens</i> | -0.5349 | 0.0099 |
| <i>Streptococcus</i> | <i>Bilophila</i> | 0.4858 | 0.0198 |
| <i>Streptococcus</i> | <i>Christensenellaceae</i> | 0.4039 | 0.0099 |
| <i>Streptococcus</i> | <i>Clostridiales</i> (II) | 0.6597 | 0.0198 |
| <i>Streptococcus</i> | <i>Clostridium methylpentosum</i> | 0.5758 | 0.0099 |
| <i>Streptococcus</i> | <i>Dehalobacterium</i> | 0.6254 | 0.0495 |
| <i>Streptococcus</i> | <i>Lactococcus</i> | 0.4863 | 0.0099 |
| <i>Streptococcus</i> | <i>Mucispirillum schaedleri</i> | 0.4798 | 0.0099 |
| <i>Streptococcus</i> | <i>Oscillospira</i> | 0.6218 | 0.0198 |
| <i>Streptococcus</i> | <i>Peptococcaceae</i> | 0.6544 | 0.0099 |
| <i>Streptococcus</i> | <i>rc4 4</i> | -0.489 | 0.0099 |
| <i>Streptococcus</i> | <i>RF32</i> | -0.6317 | 0.0099 |
| <i>Streptococcus</i> | <i>Rikenellaceae</i> | -0.4309 | 0.0495 |
| <i>Streptococcus</i> | <i>Ruminococcaceae</i> (I) | 0.6585 | 0.0297 |
| <i>Streptococcus</i> | <i>Ruminococcus gnavus</i> | 0.5417 | 0.0099 |
| <i>Streptococcus</i> | <i>Sutterella</i> | -0.5752 | 0.0099 |
| <i>Sutterella</i> | <i>Allobaculum</i> | 0.7814 | 0.0099 |

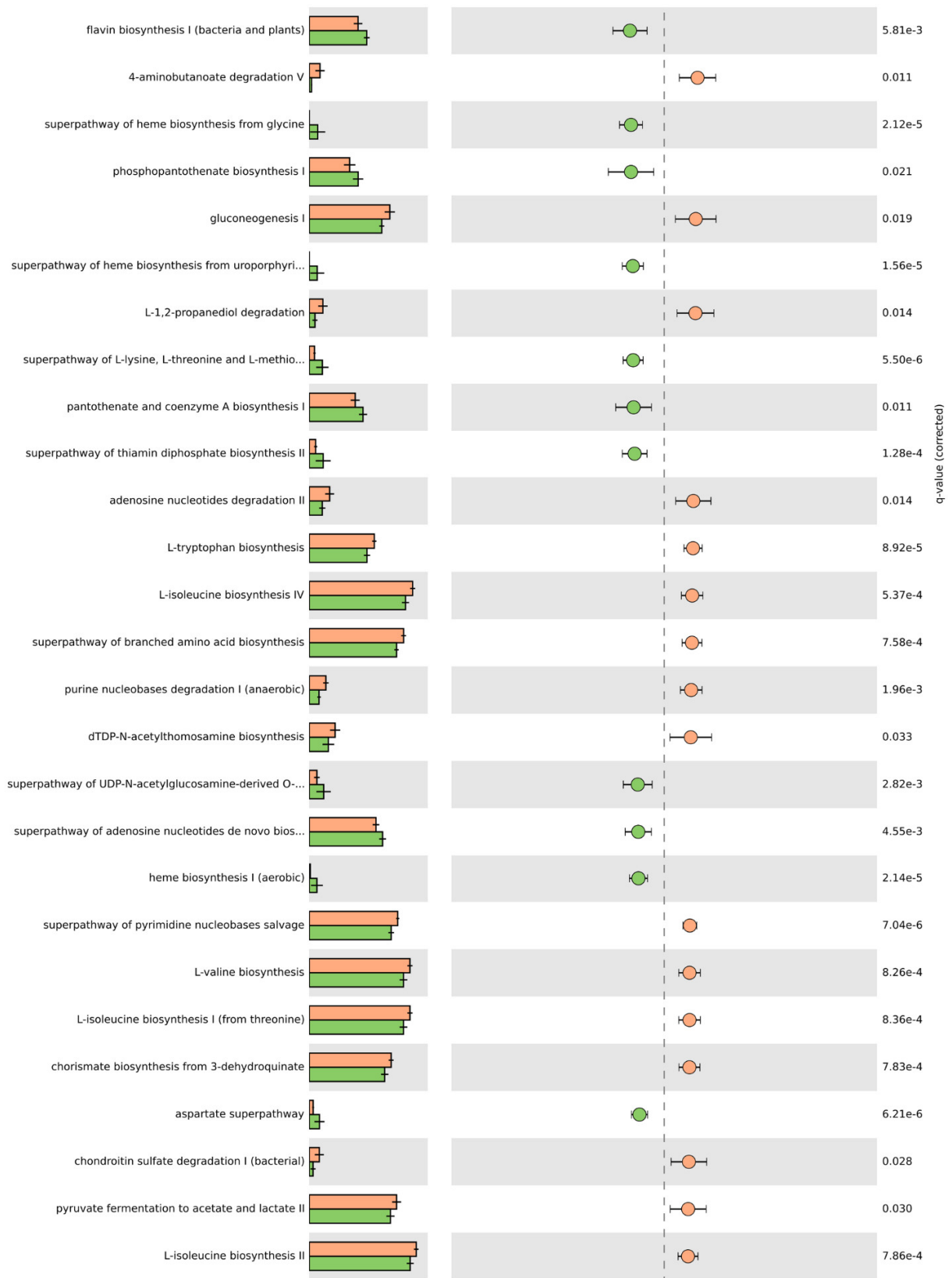
Table S1. Pairwise comparison of bacterial composition at phylum level across the diet groups

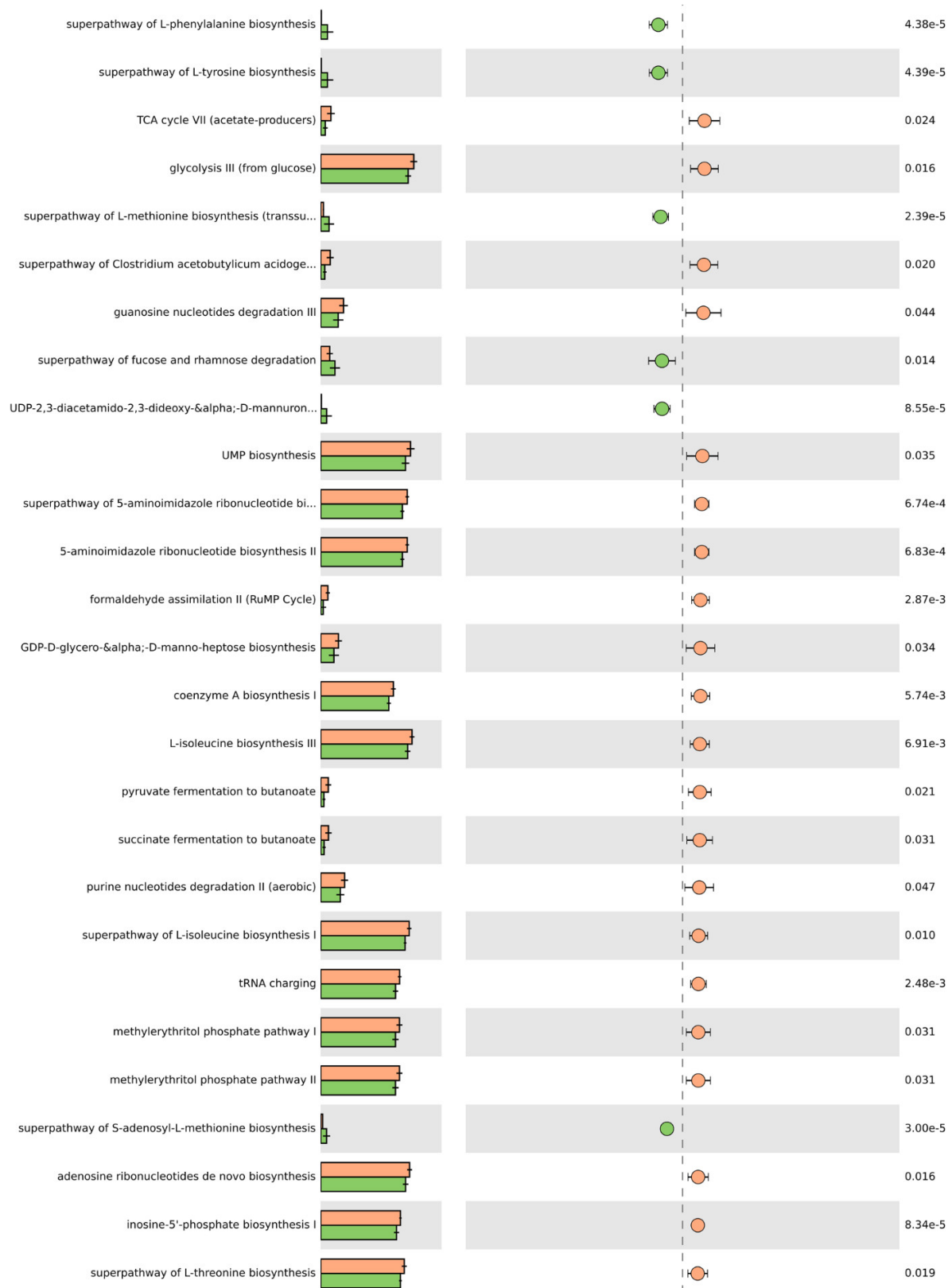
| Taxon 1 | Taxon 2 | Correlation | p-value |
|-------------------|-------------------------------------|--------------------|----------------|
| <i>Sutterella</i> | <i>Anaerotruncus</i> | -0.622 | 0.0099 |
| <i>Sutterella</i> | <i>Bacteroidales</i> | 0.6197 | 0.0099 |
| <i>Sutterella</i> | <i>Bacteroides</i> | -0.7186 | 0.0099 |
| <i>Sutterella</i> | <i>Bacteroides acidifaciens</i> | 0.8574 | 0.0099 |
| <i>Sutterella</i> | <i>Bilophila</i> | -0.5135 | 0.0099 |
| <i>Sutterella</i> | <i>Butyricicoccus pullicaecorum</i> | 0.653 | 0.0099 |
| <i>Sutterella</i> | <i>Christensenellaceae</i> | -0.6203 | 0.0099 |
| <i>Sutterella</i> | <i>Clostridiales (I)</i> | -0.4444 | 0.0495 |
| <i>Sutterella</i> | <i>Clostridiales (II)</i> | -0.8571 | 0.0198 |
| <i>Sutterella</i> | <i>Clostridium methylpentosum</i> | -0.6956 | 0.0099 |
| <i>Sutterella</i> | <i>Coprococcus</i> | -0.5118 | 0.0198 |
| <i>Sutterella</i> | <i>Dorea</i> | -0.4438 | 0.0297 |
| <i>Sutterella</i> | <i>Lactobacillus</i> | 0.4253 | 0.0396 |
| <i>Sutterella</i> | <i>Lactococcus</i> | -0.5508 | 0.0099 |
| <i>Sutterella</i> | <i>Mogibacteriaceae (II)</i> | 0.5853 | 0.0099 |
| <i>Sutterella</i> | <i>Mucispirillum schaedleri</i> | -0.749 | 0.0099 |
| <i>Sutterella</i> | <i>Muribaculaceae</i> | 0.8523 | 0.0099 |
| <i>Sutterella</i> | <i>Oscillospira</i> | -0.845 | 0.0099 |
| <i>Sutterella</i> | <i>Peptococcaceae</i> | -0.6967 | 0.0198 |
| <i>Sutterella</i> | <i>rc4 4</i> | 0.7031 | 0.0099 |
| <i>Sutterella</i> | <i>RF32</i> | 0.7779 | 0.0099 |
| <i>Sutterella</i> | <i>Rikenellaceae</i> | 0.7562 | 0.0099 |
| <i>Sutterella</i> | <i>Ruminococcaceae (I)</i> | -0.6546 | 0.0396 |
| <i>Sutterella</i> | <i>Ruminococcaceae (II)</i> | -0.5098 | 0.0495 |
| <i>Sutterella</i> | <i>Ruminococcus gnavus</i> | -0.7761 | 0.0099 |
| <i>Sutterella</i> | <i>Streptococcus</i> | -0.5752 | 0.0099 |

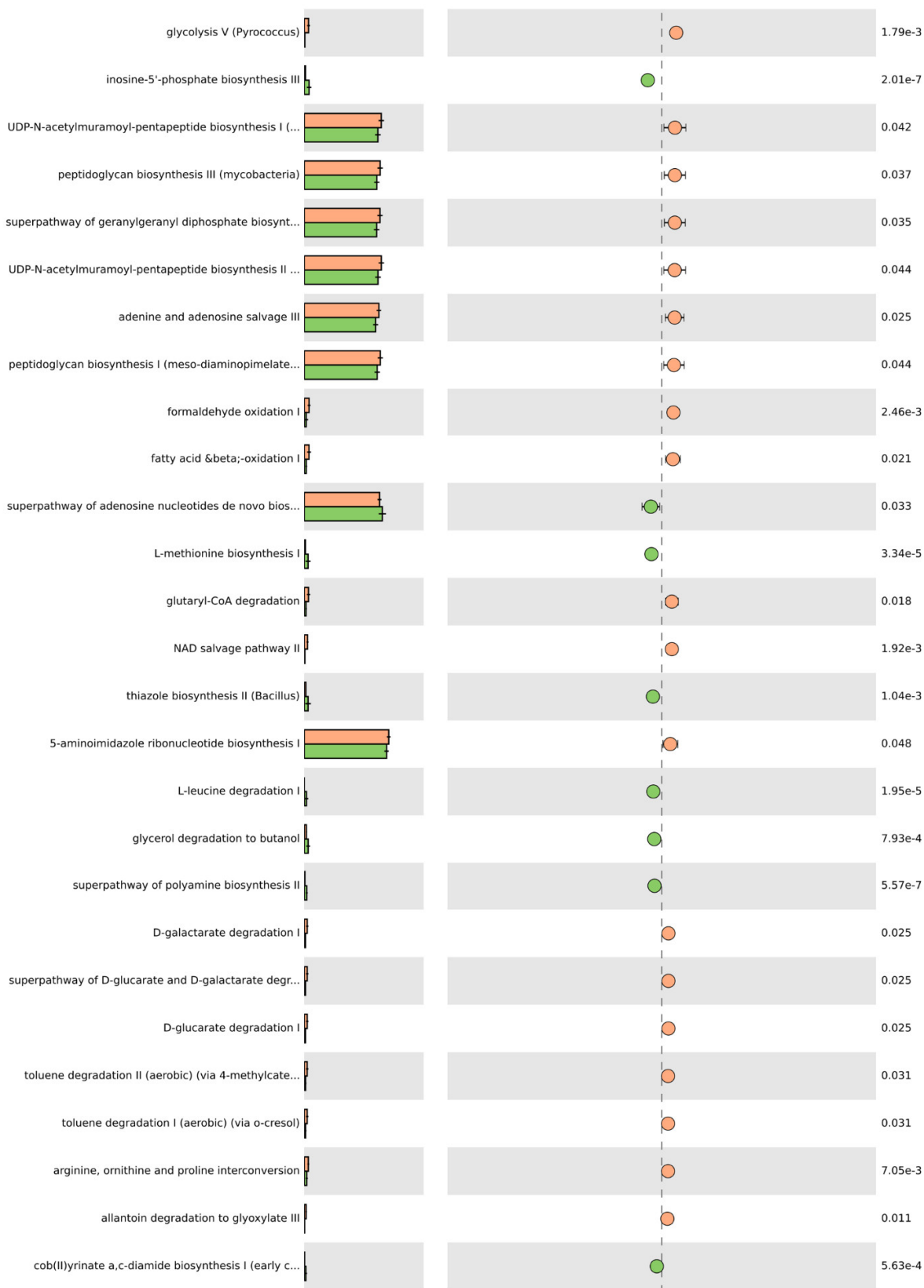












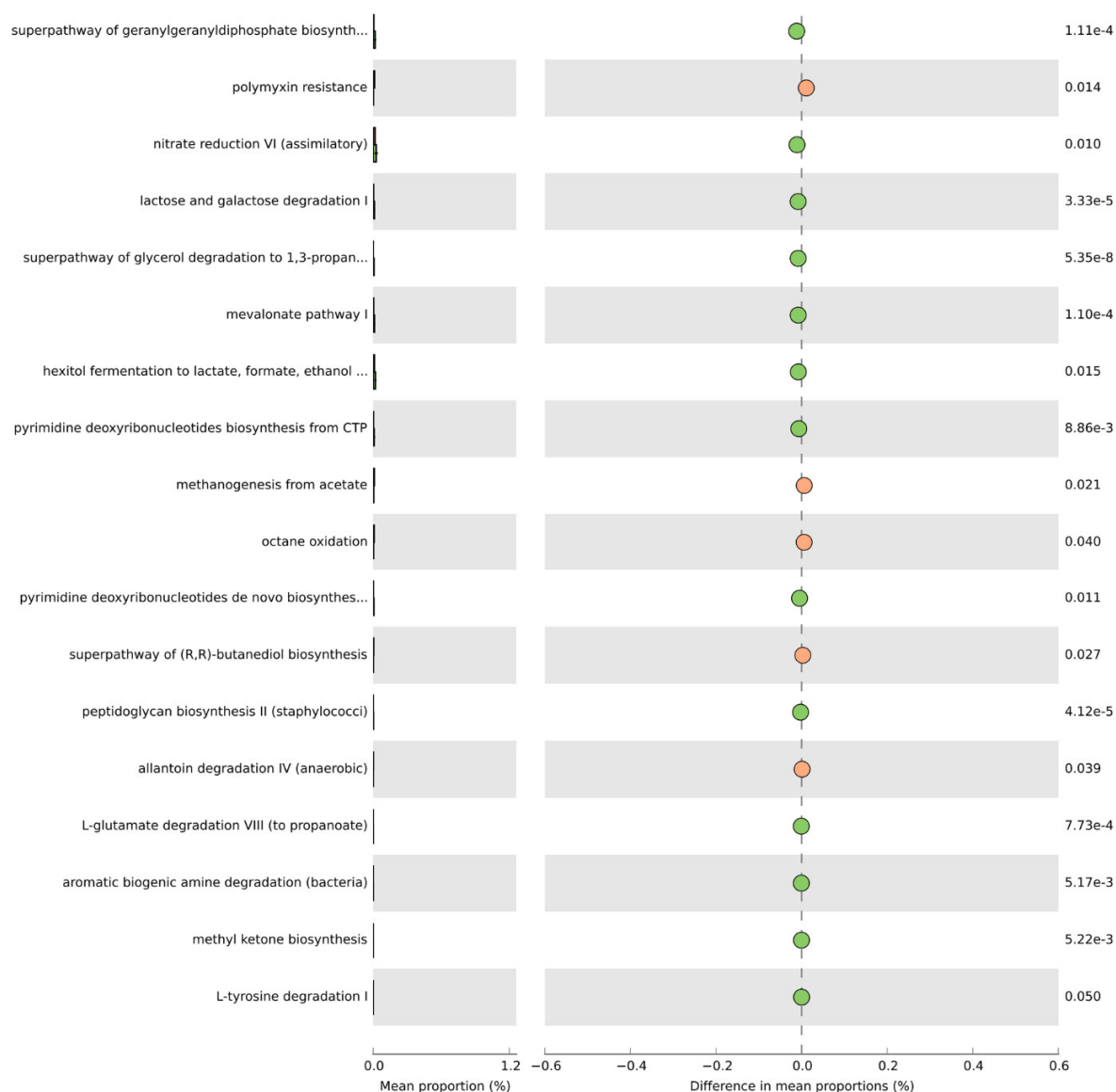


Figure S1. PICRUST2 results indicating differential pathways between the pulse-free and pulse-supplemented diet groups. 179 significant pathways are presented here in the Extended error bar plot indicating the mean proportion of pathways assigned to each group, difference between them, and corrected p -value (q -value) of each: pulse-free diet (*Control*) is indicated in beige, while pulse-based diet samples (*All other samples*)—in green: