S2: Relative abundance of bacterial taxa showing significant (or trend) diet effect in the caecum, right ventral colon and faeces of horses fed the diets H (100% hay) and B (56% hay + 44% barley) and receiving (S) or not (NoS) a yeast/microalgae supplementation

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | H diet | | B diet | |  | S.e. | | Diet effect,  P-value |
| Bacterial taxa (Phylum>Class>Family) | NoS | S | NoS | S |  | NoS | S |
| **Caecum** (n=18) |  |  |  |  |  |  |  |  |
| **Bacteroidetes** | 56.1 a | 55.1 a | 44.1 b | 39.6 b |  | 4.6 | 5.8 | **0.024** |
| **Bacteroidia** (Bacteroidetes) | 55.9 a | 54.6 a | 43.4 b | 39.2 b |  | 4.7 | 5.8 | **0.022** |
| **Prevotellaceae** (Bacteroidetes>Bacteroidia) | 29.4 a | 30.5 a | 24.3 b | 22.1 b |  | 2.5 | 3.1 | **0.038** |
| ***Prevotellaceae UCG003*** (Bacteroidetes>Bacteroidia>Prevotellaceae) | 7.90 a | 7.96 a | 3.79 b | 4.75 b |  | 0.75 | 0.95 | **0.002** |
| **Rikenellaceae** (Bacteroidetes>Bacteroidales) | 5.85 a | 4.73 a | 3.37 b | 1.51 b |  | 0.89 | 1.12 | **0.027** |
| ***Rikenellaceae RC9 gut*** (Bacteroidetes>Bacteroidales>Rikenellaceae) | 5.32 a | 4.41 a | 3.07 b | 1.31 b |  | 0.97 | 1.22 | **0.046** |
| **Veillonellaceae** (Firmicutes>Negativicutes) | 0.83 b | 0.69 b | 5.59 a | 6.37 a |  | 1.12 | 1.36 | **0.001** |
| ***Streptococcus*** (Firmicutes>Bacilli>Streptococcaceae) | 0.06 B | 0.07 B | 0.13 A | 0.24 A |  | 0.05 | 0.06 | 0.058 |
| ***Clostridium sensu stricto*** (Firmicutes>Clostridia>Clostridiaceae 1) | 0.01 b | 0.01 b | 0.15 a | 0.11 a |  | 0.04 | 0.05 | **0.012** |
| **Clostridiales vadin BB60** (Firmicutes>Clostridia) | 0.45 A | 0.32 A | 0.28 B | 0.04 B |  | 0.12 | 0.14 | 0.062 |
| **Clostridiales family XIII** (Firmicutes>Clostridia) | 0.42 a | 0.52 a | 0.16 b | 0.38 b |  | 0.06 | 0.08 | **0.007** |
| ***Anaerovorax*** (Firmicutes>Clostridia>Clostr. family XIII) | 0.23 a | 0.29 a | 0.07 b | 0.12 b |  | 0.04 | 0.05 | **0.003** |
| ***Family XIII Clostridiales UCG001***(Firmicutes>Clostridia>Clostr. family XIII) | 0.03 A | 0.02 A | 0.01 B | 0.01 B |  | 0.01 | 0.01 | 0.084 |
| ***Eubacterium ruminantium group*** (Firmicutes>Clostridia>Lachnospiraceae) | 0.62 a | 0.75 a | 0.28 b | 0.25 b |  | 0.07 | 0.09 | **0.0004** |
| ***Eubacterium ventriosum group*** (Firmicutes>Clostridia>Lachnospiraceae) | 0.10 a | 0.11 a | 0.02 b | 0.01 b |  | 0.01 | 0.01 | **<.0001** |
| ***Lachnoclostridium*** (Firmicutes>Clostridia>Lachnospiraceae) | 0.52 a | 0.51 a | 0.31 b | 0.24 b |  | 0.04 | 0.05 | **0.0001** |
| ***Lachnospira*** (Firmicutes>Clostridia>Lachnospiraceae) | 0.06 a | 0.05 a | 0.02 b | 0.01 b |  | 0.01 | 0.02 | **0.035** |
| ***Lachnospiraceae NC2004*** (Firmicutes>Clostridia>Lachnospiraceae) | 0.60 A | 0.85 A | 0.38 B | 0.38 B |  | 0.14 | 0.17 | 0.051 |
| ***Lachnospiraceae NK4A136*** (Firmicutes>Clostridia>Lachnospiraceae) | 3.84 a | 3.43 a | 2.60 b | 2.00 b |  | 0.52 | 0.66 | **0.043** |
| ***Lachnospiraceae UCG001*** (Firmicutes>Clostridia>Lachnospiraceae) | 0.05 A | 0.08 A | 0.03 B | 0.01 B |  | 0.02 | 0.03 | 0.084 |
| ***Lachnospiraceae UCG005*** (Firmicutes>Clostridia>Lachnospiraceae) | 0.47 a | 0.49 a | 0.25 b | 0.28 b |  | 0.08 | 0.09 | **0.005** |
| ***Oribacterium*** (Firmicutes>Clostridia>Lachnospiraceae) | 0.32 a | 0.24 a | 0.16 b | 0.12 b |  | 0.04 | 0.05 | **0.009** |
| **Ruminococcaceae** (Firmicutes>Clostridia) | 13.4 a | 14.9 a | 9.6 b | 13.0 b |  | 1.5 | 1.9 | **0.029** |
| ***Faecalibacterium*** (Firmicutes>Clostridia>Ruminococcaceae) | 0.20 a | 0.20 a | 0.04 b | 0.03 b |  | 0.06 | 0.07 | **0.025** |
| ***Ruminococcaceae UCG014*** (Firmicutes>Clostridia>Ruminococcaceae) | 1.61 a | 2.08 a | 0.64 b | 0.43 b |  | 0.14 | 0.17 | **<.0001** |
| ***Ruminococcus*** (Firmicutes>Clostridia>Ruminococcaceae) | 2.18 a | 3.49 a | 1.63 b | 2.28 b |  | 0.37 | 0.46 | **0.036** |
| ***Saccharofermentans*** (Firmicutes>Clostridia>Ruminococcaceae) | 0.46 a | 0.62 a | 0.32 b | 0.25 b |  | 0.08 | 0.10 | **0.025** |
| **Proteobacteria** | 2.19 b | 1.66 b | 17.61 a | 8.26 a |  | 2.88 | 3.58 | **0.006** |
| **Gammaproteobacteria** (Proteobacteria) | 0.35 b | 0.39 b | 15.62 a | 6.70 a |  | 3.06 | 3.81 | **0.009** |
| **Succinivibrionaceae** (Proteobacteria>Gammaproteobacteria) | 0.13 b | 0.00 b | 14.99 a | 4.75 a |  | 3.37 | 4.21 | **0.022** |
| **Oxalobacteraceae** (Proteobacteria>Betaproteobacteria) | 0.09 a | 0.05 a | 0.04 b | 0.01 b |  | 0.02 | 0.03 | **0.046** |
| **Fibrobacteres** | 1.93 A | 1.50 A | 1.33 B | 0.49 B |  | 0.62 | 0.78 | 0.096 |
| ***Fibrobacter*** (Fibrobacteres>Fibrobacteria>Fibrobacteraceae) | 1.93 A | 1.50 A | 1.33 B | 0.49 B |  | 0.62 | 0.78 | 0.096 |
| **Tenericutes** | 0.25 a | 0.26 a | 0.17 b | 0.04 b |  | 0.06 | 0.07 | **0.043** |
| ***Anaeroplasma*** (Tenericutes>Mollicutes>Anaeroplasmataceae) | 0.21 a | 0.21 a | 0.13 b | 0.01 b |  | 0.05 | 0.06 | **0.030** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | H diet | | B diet | |  | S.e. | | Diet effect,  P-value |
| Bacterial taxa (Phylum>Class>Family) | NoS | S | NoS | S |  | NoS | S |
| **RV Colon** (n=22) |  |  |  |  |  |  |  |  |
| **Bacteroidetes** | 42.3 A | 35.2 A | 26.4 B | 32.7 B |  | 5.9 | 6.5 | 0.092 |
| **Bacteroidia** (Bacteroidetes) | 41.9 A | 35.0 A | 26.1 B | 32.3 B |  | 5.9 | 6.5 | 0.087 |
| **Bacteroidales RF16** (Bacteroidetes) | 3.44 A | 4.42 A | 2.28 B | 1.37 B |  | 1.37 | 1.50 | 0.097 |
| ***Prevotellaceae UCG001*** (Bacteroidetes>Bacteroidia>Prevotellaceae) | 4.07 a | 4.13 a | 1.29 b | 2.14 b |  | 0.70 | 0.77 | **0.003** |
| ***Prevotellaceae UCG003*** (Bacteroidetes>Bacteroidia>Prevotellaceae) | 5.35 a | 4.32 a | 1.59 b | 2.79 b |  | 1.03 | 1.14 | **0.017** |
| ***Prevotellaceae UCG004*** (Bacteroidetes>Bacteroidia>Prevotellaceae) | 1.83 A | 1.17 A | 0.99 B | 1.01 B |  | 0.33 | 0.35 | 0.061 |
| ***Rikenellaceae hoa-507d05 gut*** (Bacteroidetes>Bacteroidia>Rikenellaceae) | 0.35 A | 0.25 A | 0.19 B | 0.20 B |  | 0.06 | 0.06 | 0.094 |
| ***Anaerovibrio*** (Firmicutes>Negativicutes>Veillonellaceae) | 0.57 b | 0.33 b | 1.52 a | 3.13 a |  | 0.57 | 0.62 | **0.002** |
| ***Streptococcus*** (Firmicutes>Bacilli>Streptococcaceae) | 0.02 B | 0.06 B | 0.59 A | 0.13 A |  | 0.16 | 0.18 | 0.073 |
| **Clostridialesvadin BB60** (Firmicutes>Clostridia) | 1.46 a | 0.68 a | 0.42 b | 0.24 b |  | 0.31 | 0.34 | **0.018** |
| **Christensenellaceae** (Firmicutes>Clostridia) | 1.87 B | 3.54 B | 4.42 A | 4.27 A |  | 0.91 | 1.00 | 0.052 |
| ***Christensenellaceae R7*** (Firmicutes>Clostridia>Christensenellaceae) | 1.74 b | 3.39 b | 4.36 a | 4.20 a |  | 0.91 | 0.99 | **0.042** |
| ***Family XIII Clostridiales*** (Fimicutes>Clostridia) | 0.13 B | 0.16 B | 0.20 A | 0.26 A |  | 0.04 | 0.05 | 0.062 |
| ***Mogibacterium*** (Fimicutes>Clostridia>Family XIII Clostr.) | 0.05 B | 0.06 B | 0.15 A | 0.12 A |  | 0.05 | 0.05 | 0.075 |
| ***Blautia*** (Fimicutes>Clostridia>Lachnospiraceae) | 1.16 a | 1.14 a | 0.33 b | 0.53 b |  | 0.28 | 0.31 | **0.014** |
| ***Butyrivibrio*** (Fimicutes>Clostridia>Lachnospiraceae) | 0.0 B | 0.09 B | 0.22 A | 1.12 A |  | 0.31 | 0.34 | 0.083 |
| ***Eubacterium ruminantium group*** (Fimicutes>Clostridia>Lachnospiraceae) | 0.57 A | 0.47 A | 0.25 B | 0.26 B |  | 0.13 | 0.14 | 0.052 |
| ***Lachnospiraceae NK4A136*** (Fimicutes>Clostridia>Lachnospiraceae) | 3.21 a | 2.21 a | 0.91 b | 1.93 b |  | 0.57 | 0.63 | **0.032** |
| ***Lachnospiraceae UCG005*** (Fimicutes>Clostridia>Lachnospiraceae) | 0.28 a | 0.31 a | 0.05 b | 0.15 b |  | 0.07 | 0.08 | **0.009** |
| **Peptococcaceae** (Firmicutes>Clostridia) | 0.16 A | 0.14 A | 0.12 B | 0.07 B |  | 0.05 | 0.05 | 0.091 |
| ***Faecalibacterium*** (Firmicutes>Clostridia>Ruminococcaceae) | 0.34 a | 0.08 a | 0.03 b | 0.02 b |  | 0.08 | 0.09 | **0.028** |
| ***Ruminococcaceae NK4A214*** (Firmicutes>Clostridia>Ruminococcaceae) | 1.24 B | 1.27 B | 2.70 A | 1.40 A |  | 0.49 | 0.54 | 0.094 |
| ***Saccharofermentans*** (Firmicutes>Clostridia>Ruminococcaceae) | 0.59 a | 0.31 a | 0.16 b | 0.16 b |  | 0.12 | 0.13 | **0.038** |
| **Betaproteobacteria** (Proteobacteria) | 0.26 A | 0.17 A | 0.17 B | 0.15 B |  | 0.05 | 0.06 | 0.056 |
| **Oxalobacteraceae** (Proteobacteria>Betaproteobacteria) | 0.14 a | 0.08 a | 0.08 b | 0.05 b |  | 0.04 | 0.04 | **0.028** |
| **Succinivibrionaceae** (Proteobacteria>Gammaproteobacteria) | 0.09 b | 0.05 b | 4.58 a | 2.19 a |  | 1.26 | 1.40 | **0.020** |
| ***Anaeroplasma*** (Tenericutes>Mollicutes>Anaeroplasmataceae) | 0.20 a | 0.14 a | 0.04 b | 0.05 b |  | 0.03 | 0.03 | **0.0005** |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | H diet | | B diet | |  | S.e. | | Diet effect,  P-value |
| Bacterial taxa (Phylum>Class>Family) | NoS | S | NoS | S |  | NoS | S |
| **Faeces** (n=22) |  |  |  |  |  |  |  |  |
| **Bacteroidales S24-7** (Bacteroidetes>Bacteroidia) | 7.53 a | 9.16 a | 1.63 b | 2.94 b |  | 0.91 | 1.02 | **<.0001** |
| **Bacteroidetes VC2.1 Bac22** (Bacteroidetes) | 0.61 a | 0.48 a | 0.24 b | 0.29 b |  | 0.12 | 0.13 | **0.023** |
| ***Rikenellaceae hoa-507d05 gut*** (Bacteroidetes>Bacteroidia>Rikenellaceae) | 1.15 a | 1.15 a | 0.31 b | 0.39 b |  | 0.16 | 0.18 | **0.0003** |
| ***Christensenellaceae R7*** (Firmicutes>Clostridia>Christensenellaceae) | 2.42 b | 2.87 b | 5.50 a | 5.15 a |  | 1.09 | 1.21 | **0.042** |
| ***Clostridium sensu stricto*** (Firmicutes>Clostridia>Clostridiaceae 1) | 0.06 b | 0.05 b | 0.18 a | 0.11 a |  | 0.03 | 0.04 | **0.025** |
| ***Eubacterium nodatum group*** (Firmicutes>Clostridia>Clostr. Family XIII) | 0.08 a | 0.08 a | 0.02 b | 0.04 b |  | 0.02 | 0.02 | **0.014** |
| ***Family XIII Clostridiales AD3011*** (Firmicutes>Clostridia>Clostr. Family XIII) | 0.17 A | 0.21 A | 0.13 B | 0.18 B |  | 0.04 | 0.04 | 0.088 |
| ***Family XIII Clostridiales UCG001*** (Firmicutes>Clostridia>Clostr. Family XIII) | 0.03 a | 0.07 a | 0.02 b | 0.03 b |  | 0.01 | 0.01 | **0.013** |
| ***Mogibacterium*** (Firmicutes>Clostridia>Clostridiales Family XIII) | 0.13 b | 0.17 b | 0.27 a | 0.39 a |  | 0.09 | 0.09 | **0.036** |
| **Clostridiales vadin BB60** (Firmicutes>Clostridia) | 0.08 a | 0.27 a | 0.05 b | 0.11 b |  | 0.04 | 0.04 | **0.035** |
| **Lachnospiraceae** (Firmicutes>Clostridia) | 30.1 a | 26.6 a | 17.4 b | 19.1 b |  | 2.8 | 3.1 | **0.002** |
| ***Acetitomaculum*** (Firmicutes>Clostridia>Lachnospiraceae) | 0.22 a | 0.27 a | 0.07 b | 0.08 b |  | 0.07 | 0.08 | **0.044** |
| ***Butyrivibrio*** (Firmicutes>Clostridia>Lachnospiraceae) | 0.02 A | 0.03 A | 0.00 B | 0.01 B |  | 0.01 | 0.01 | 0.065 |
| ***Lachnospiraceae AC2044*** (Firmicutes>Clostridia>Lachnospiraceae) | 7.87 a | 5.69 a | 1.90 b | 3.35 b |  | 0.88 | 0.99 | **0.0006** |
| ***Lachnospiraceae FCS020*** (Firmicutes>Clostridia>Lachnospiraceae) | 0.19 a | 0.20 a | 0.11 b | 0.10 b |  | 0.03 | 0.03 | **0.004** |
| ***Lachnospiraceae NK4A136*** (Firmicutes>Clostridia>Lachnospiraceae) | 6.13 a | 4.84 a | 1.83 b | 2.09 b |  | 0.55 | 0.61 | **<.0001** |
| ***Candidatus Soleaferrea*** (Firmicutes>Clostridia>Ruminococcaceae) | 0.30 B | 0.38 B | 0.34 A | 0.63 A |  | 0.07 | 0.08 | 0.075 |
| ***Ruminococcaceae NK4A214*** (Firmicutes>Clostridia>Ruminococcaceae) | 2.95 b | 2.30 b | 4.82 a | 4.83 a |  | 0.61 | 0.68 | **0.008** |
| ***Ruminococcaceae UCG002*** (Firmicutes>Clostridia>Ruminococcaceae) | 0.97 b | 1.44 b | 1.52 a | 2.98 a |  | 0.30 | 0.33 | **0.005** |
| ***Ruminococcaceae UCG007*** (Firmicutes>Clostridia>Ruminococcaceae) | 0.07 b | 0.09 b | 0.36 a | 0.19 a |  | 0.06 | 0.07 | **0.010** |
| ***Ruminococcus*** (Firmicutes>Clostridia>Ruminococcaceae) | 3.21 a | 3.43 a | 1.63 b | 2.23 b |  | 0.42 | 0.46 | **0.006** |
| **Deltaproteobacteria** (Proteobacteria) | 0.32 a | 0.51 a | 0.09 b | 0.17 b |  | 0.06 | 0.07 | **0.0009** |
| ***Desulfovibrio*** (Proteobacteria>Deltaproteobacteria>Desulfovibrionaceae) | 0.21 a | 0.22 a | 0.05 b | 0.15 b |  | 0.03 | 0.03 | **0.0009** |
| **Spirochaetales PL-11B10** (Spirochaetae>Spirochaetes) | 0.13 b | 0.19 b | 0.82 a | 1.10 a |  | 0.32 | 0.36 | **0.028** |
| **Coriobacteriia** (Actinobacteria) | 0.21 A | 0.23 A | 0.12 B | 0.19 B |  | 0.03 | 0.04 | 0.085 |
| ***Anaeroplasma*** (Tenericutes>Mollicutes>Anaeroplasmataceae) | 0.06 A | 0.05 A | 0.03 B | 0.02 B |  | 0.01 | 0.01 | 0.069 |