Table S5:

Testing for distributional trend of ruminal microbiome (genus level) adhered to the six lignocellulosic forages during their rumen incubation (over 96 h with 24 h intervals) using orthogonal contrast analysis.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Forage** | **Genus** | **Trend** | **F value** | **Pr > F** |
| AP | Prevotella | Linear*d* | 7.88 | 0.0262 |
| Shuttleworthia | Quadratic | 6.68 | 0.0362 |
| Selenomonas | Linear*d* | 14.64 | 0.0065 |
| CR | Selenomonas | Quadratic | 6.73 | 0.0319 |
| DP | Un\_Succinivibrionaceae | Cubic | 5.58 | 0.0458 |
| Fibrobacter | Linear*i* | 11.89 | 0.0087 |
| Coprococcus | Cubic | 6.98 | 0.0296 |
| Selenomonas | Quadratic | 14.85 | 0.0049 |
| KS | Fibrobacter | Linear*i* | 6.92 | 0.0302 |
| Un\_S24-7 | Quadratic | 4.86 | 0.0334 |
| Un\_Veillonellaceae | Quadratic | 11.71 | 0.0091 |
| Lachnospira | Cubic | 8.49 | 0.0195 |
| Un\_Paraprevotellaceae | Cubic | 7.37 | 0.0264 |
| RS | Fibrobacter | Linear*i* | 8.37 | 0.0201 |
| Un\_S24-7 | Quadratic | 4.82 | 0.0500 |
| Un\_Veillonellaceae | Quadratic | 11.58 | 0.0093 |
| Ruminococcus | Cubic | 10.97 | 0.0107 |
| Coprococcus | Cubic | 7.04 | 0.0291 |
| Roseburia | Linear*d* | 5.13 | 0.0492 |
| SC | Butyrivibrio | Linear*d* | 14.89 | 0.0062 |
| Fibrobacter | Linear*i* | 6.32 | 0.0402 |
| Un\_S24-7 | Linear*i* | 6.52 | 0.0379 |
| Treponema | Cubic | 13.03 | 0.0086 |
| Un\_Veillonellaceae | Quadratic | 34.82 | 0.0006 |
| Un\_Paraprevotellaceae | Linear*i* | 13.75 | 0.0076 |
| Roseburia | Quadratic | 11.53 | 0.0115 |
| Bifidobacterium | Linear*d* | 5.69 | 0.0485 |
| Selenomonas | Linear*d* | 9.92 | 0.0162 |

Linear*i* ; linearly increased, Linear*d* ; linearly decreased, AP; camelthorn, CR; common reed, DP; date palm, KS; Kochia, RS; rice straw, and SC; Salicornia.