The effect of supplementing pony diets with yeast on 2. The faecal microbiome

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**Supplementary material**

**Supplementary Figure S1 Significant taxa in the equine faeces for each diet identified by linear discriminant analysis effect size (LEfSe).** Each bar of the graph represents the effect size (LDA) for particular taxa (genus level or higher) in a certain group. The length of the bar represents a log10 transformed linear discriminant analysis (LDA) score. Any taxa coloured according to a variable (HF, HFY, HS and HSY diets) can be interpreted as that taxa relative abundance (RA) was significantly higher compared to the other groups (LDA score > 2). HF: high fibre without yeast, HFY: high fibre with yeast, HS: high starch without yeast, HSY: high starch with yeast; c\_: class, o\_: order, f\_: family, g\_: genus.



**Supplementary Figure S2 Distribution of sequences by phyla.**

Bacterial and Archaeal phyla relative abundance of sequences detected in equine faeces at level of 0.1 % or greater. HF: high fibre without yeast, HFY: high fibre with yeast, HS: high starch without yeast, HSY: high starch with yeast.