**Supplementary File – for Online Publication Only**

**Supplementary Table S1:** Oligonucleotide primers used for real-time quantitative PCR

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| --- | --- | --- | --- |
| **Target** | **rrs gene primer sequence** | **Product size** | **Reference** |
| *Fibrobacter succinogenes* | F 5'-GTTCGGAATTACTGGGCGTAAA-3'  R 5'-CGCCTGCCCCTGAACTATC-3' | 121 | Denman and Mc Sweeney, 2006 |
| *Ruminococcus flavefaciens* | F 5'-CGAACGGAGATAATTTGAGTTTACTTAGG-3'  R 5'-CGGTCTCTGTATGTTATGAGGTATTACC-3' | 132 | Denman and Mc Sweeney, 2006 |
| *Selenomonas ruminantium* | F 5'-CAATAAGCATTCCGCCTGGG-3'  R 5'-TTCACTCAATGTCAAGCCCTGG-3' | 82 | Stevenson and Weimer, 2007 |
| General bacteria | F 5'-AGCAGCCGCGGTAAT-3'  R 5'-CAGGGTATCTAATCCTGTT-3' | 280 | Edwards et al., 2007b |



**Supplementary Figure S1**: Experimental design. During adaptation and Resting Periods (RPs), wethers were fed the resting periods diets (20:80, concentrate:hay). During Acidosis Challenges (ACs), wethers were fed the acidosis challenges diets (60:40, concentrate:hay). The shifts from RPs to ACs and ACs to RPs were done without any transition period.



**Supplementary Figure S2**: Daily mean ruminal pH during the trial. The pH was recorded continuously during 105 days using indwelling pH sensors. Values are means of 6 animals per group.

Plain line: Yeast supplemented group (n=6), dotted line: Control group (n=6).

Grey blocks represents each acidosis challenge period during which wethers were fed 60:40, concentrate:hay. During the resting periods animals were fed 20:80, concentrate:hay.

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**Supplementary Figure S3**: Evolution of the Simpson diversity index during the trial.

Plain line: Yeast supplemented group (n=6), dotted line: Control group (n=6).

Grey blocks indicates each acidosis challenge period during which animals were fed 60:40, concentrate:hay. During the resting periods animals were fed 20:80, concentrate:hay.