**Table S1:**

Reproducibility of label-free metaproteomics quantification of technical replicates estimated by Pearson correlation in RWS and TWS consortia replicates.

Replicate (RWS2\_T1\_C) was removed.

**RWS 1**

|  |  |  |
| --- | --- | --- |
|  | **RWS1-T1\_A** | **RWS1-T1\_B** |
| **RWS1-T1\_B** | 0.909 |  |
| **RWS1-T1\_C** | 0.890 | 0.927 |

|  |  |  |
| --- | --- | --- |
|  | **RWS1-T2\_A** | **RWS1-T2\_B** |
| **RWS1-T2\_B** | 0.930 |  |
| **RWS1-T2\_C** | 0.906 | 0.917 |

|  |  |  |
| --- | --- | --- |
|  | **RWS1-T3\_A** | **RWS1-T3\_B** |
| **RWS1-T3\_B** | 0.952 |  |
| **RWS1-T3\_C** | 0.944 | 0.953 |

|  |  |  |
| --- | --- | --- |
|  | **RWS1-T4\_A** | **RWS1-T4\_B** |
| **RWS1-T4\_B** | 0.764 |  |
| **RWS1-T4\_C** | 0.768 | 0.935 |

**TWS 1**

|  |  |  |
| --- | --- | --- |
|  | **TWS1-T1\_A** | **TWS1-T1\_B** |
| **TWS1-T1\_B** | 0.825 |  |
| **TWS1-T1\_C** | 0.918 | 0.834 |

**RWS2**

|  |  |  |
| --- | --- | --- |
|  | **RWS2-T1\_A** | **RWS2-T1\_B** |
| **RWS2-T1\_B** | 0.814 |  |
| **RWS2-T1\_C** | 0.447 | 0.462 |

|  |  |  |
| --- | --- | --- |
|  | **RWS2-T2\_A** | **RWS2-T2\_B** |
| **RWS2-T2\_B** | 0.911 |  |
| **RWS2-T2\_C** | 0.901 | 0.897 |

|  |  |  |
| --- | --- | --- |
|  | **RWS2-T3\_A** | **RWS2-T3\_B** |
| **RWS2-T3\_B** | 0.851 |  |
| **RWS2-T3\_C** | 0.746 | 0.714 |

|  |  |  |
| --- | --- | --- |
|  | **RWS2-T4\_A** | **RWS2-T4\_B** |
| **RWS2-T4\_B** | 0.861 |  |
| **RWS2-T4\_C** | 0.850 | 0.840 |

**TWS2**

|  |  |  |
| --- | --- | --- |
|  | **TWS2-T1\_A** | **TWS2-T1\_B** |
| **TWS2-T1\_B** | 0.924 |  |
| **TWS2-T1\_C** | 0.921 | 0.947 |
|  | **TWS1-T2\_A** | **TWS1-T2\_B** |
| **TWS1-T2\_B** | 0.934 |  |
| **TWS1-T2\_C** | 0.886 | 0.903 |

|  |  |  |
| --- | --- | --- |
|  | **TWS1-T3\_A** | **TWS1-T3\_B** |
| **TWS1-T3\_B** | 0.900 |  |
| **TWS1-T3\_C** | 0.939 | 0.895 |

|  |  |  |
| --- | --- | --- |
|  | **TWS1-T4\_A** | **TWS1-T4\_B** |
| **TWS1-T4\_B** | 0.902 |  |
| **TWS1-T4\_C** | 0.904 | 0.916 |

|  |  |  |
| --- | --- | --- |
|  | **TWS2-T2\_A** | **TWS2-T2\_B** |
| **TWS2-T2\_B** | 0.868 |  |
| **TWS2-T2\_C** | 0.872 | 0.929 |

|  |  |  |
| --- | --- | --- |
|  | **TWS2-T3\_A** | **TWS2-T3\_B** |
| **TWS2-T3\_B** | 0.928 |  |
| **TWS2-T3\_C** | 0.834 | 0.818 |

|  |  |  |
| --- | --- | --- |
|  | **TWS2-T4\_A** | **TWS2-T4\_B** |
| **TWS2-T4\_B** | 0.923 |  |
| **TWS2-T4\_C** | 0.931 | 0.926 |

**Table S2: Diversity index based on OTUs and proteins detected by metaproteomics in RWS and TWS samples**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | 16S rRNA | | Metaproteomics | | | |
|  | Richness (OTUs) | Shannon index | Richness  (Protein groups) | | | Shannon index |
| RWS-1\* T1 | 166 | 7.97 | 3016 | 3936 | 7149 | 3.65 |
| RWS-1 T2 | 175 | 5.63 | 2524 | 4.00 |
| RWS-1 T3 | 176 | 4.29 | 2389 | 3.68 |
| RWS-1 T4 | 182 | 5.90 | 2463 | 3.63 |
| RWS-2\* T1 | 172 | 5.15 | 2329 | 4777 | 3.50 |
| RWS-2 T2 | 177 | 5.19 | 2741 | 3.56 |
| RWS-2 T3 | 179 | 6.51 | 2241 | 3.62 |
| RWS-2 T4 | 176 | 5.99 | 2617 | 3.68 |
| TWS-1 T1 | 101 | 2.79 | 3142 | 4802 | 6682 | 3.34 |
| TWS-1 T2 | 103 | 2.07 | 3155 | 3.17 |
| TWS-1 T3 | 134 | 2.04 | 2890 | 3.07 |
| TWS-1 T4 | 134 | 2.06 | 2606 | 2.92 |
| TWS-2 T1 | 120 | 2.92 | 3784 | 5724 | 3.58 |
| TWS-2 T2 | 115 | 3.11 | 3159 | 3.44 |
| TWS-2 T3 | 128 | 2.66 | 2878 | 3.31 |
| TWS-2 T4 | 134 | 2.95 | 2742 | 3.21 |

Note: \*1 and 2 indicate the biological replicate bioreactors.

**Table S3.** PERMANOVA analysis of taxa abundance deduced from metaproteomic data (at the genus level) on RWS and TWS, based on Euclidean distance, using inoculum source (“inoculum”: RWS or TWS) and incubation time (T1-T2-T3-T4 points) and the interaction between them (Inoculum:Incubation time) as factors. The degrees of freedom (Df), sequential sum of squares (SumOfSquares), R-squared (R2) and p-values based in 9999 permutations Pr(>F).

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Factors** | **Df** | **SumsOfSqs** | **R2** | **Pr(>F)** |  |
| **Inoculum** | 1 | 102.6339 | 0.6214 | 0.0001 | \*\*\* |
| **Inc. Time** | 3 | 33.3990 | 0.2022 | 0.0049 | \*\* |
| **Inoculum: Inc. Time** | 3 | 8.6703 | 0.0524 | 0.3779 |  |
| **Residual** | 8 | 20.4584 | 0.1238 |  |  |
| **Total** | 15 | 165.1618 | 1.0000 |  |  |

**Table S4.** PERMANOVA analysis of metaproteomics data of CAZyme families abundance on RWS and TWS. Analysis is based on Euclidean distance, using inoculum source (“inoculum”: RWS or TWS) and incubation time (T1-T2-T3-T4 points) and the interaction between them (Inoculum:Incubation time”) as factors. The degrees of freedom (Df), sequential sum of squares (SumOfSquares), R-squared (R2) and p-values based in 9999 permutations Pr(>F).

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Factors** | **Df** | **SumsOfSqs** | **R2** | **Pr(>F)** |  |
| **Inoculum** | 1 | 96.99791 | 0.252 | 0.0001 | \*\*\* |
| **Inc. Time** | 3 | 108.91534 | 0.284 | 0.0060 | \*\* |
| **Inoculum:Inc. Time** | 3 | 42.13673 | 0.110 | 0.7037 |  |
| **Residual** | 8 | 135.90328 | 0.354 |  |  |
| **Total** | 15 | 383.95326 | 1.000 |  |  |

**Table S5:** Comparative analysis of main bacterial GH families targeting plant cell wall degradation found in this study and in other omics studies concerning bovine rumen and termite hindgut microbiomes.

