Reducing agent can be omitted in the incubation medium of the batch *in vitro* fermentation model of the pig intestines

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**Supplementary Table S1**Sampling completeness anddiversity indexes for16S rRNA genes in clone libraries from broth collected after 24 h of fermentation of four ingredients (casein, soybean proteins, cellulose, potato starch) and blank of fermentation by pig fecal bacteria according to the incubation media: with Na2S or cysteine-HCl (Cys) or control (Ctrl) without reducing agent (n = 2). Sampling completeness was assessed at the genus level by Good's coverage index (%). Chao index and inverted Simpson index have been used for population richness estimation and for alpha diversity estimation, respectively. Species evenness was deduced from Simpson index values.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Casein | Soybean proteins | Cellulose | Potato starch | Blank |  |
| Index | Cys | Na2S | Ctrl | Cys | Na2S | Ctrl | Cys | Na2S | Ctrl | Cys | Na2S | Ctrl | Cys | Na2S | Ctrl | SEM |
| Good’s coverage | 99.2% | 99.2% | 99.3% | 99.3% | 99.3% | 99.2% | 99.0% | 99.2% | 99.1% | 99.3% | 99.4% | 99.3% | 99.2% | 99.0% | 99.2% | 0.025 |
| Chao | 78.9 | 73.9 | 68.7 | 71.6 | 67.9 | 73.2 | 90.4 | 76.0 | 76.4 | 69.4 | 69.0 | 75.6 | 74.2 | 84.6 | 77.8 | 1.423 |
| Inverse Simpson’s  | 10.5 | 10.4 | 10.3 | 7.87 | 7.80 | 7.25 | 10.5 | 9.74 | 9.95 | 7.12 | 9.15 | 8.53 | 11.0 | 10.5 | 10.9 | 0.260 |
| Simpson evenness | 0.173 | 0.178 | 0.184 | 0.134 | 0.144 | 0.128 | 0.173 | 0.175 | 0.174 | 0.126 | 0.160 | 0.141 | 0.185 | 0.169 | 0.176 | 0.004 |

**Supplementary Figure S1** Rarefaction curves for 16S rRNA genes (at the genus level) from broth collected after 24 h of fermentation of four ingredients (casein, soybean proteins, cellulose, potato starch) and blank of fermentation by pig fecal bacteria according to the incubation media: with Na2S or cysteine-HCl (Cys) or control (Ctrl) without reducing agent (n = 2).