**SUPPLEMENTARY TABLE**

**Supplementary table 1.** Impact of FS (FS) 10% [v/v] collected after 12 hours on gene expression in IPEC-J2 cells

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Target Family | Ingredients | Inulin  | Chicory root  | Chicory pulp | Rye bran | Soy hulls | Citrus pulp | p-value |
| *Mean* |  | *SEM* | *Mean* |  | *SEM* | *Mean* |  | *SEM* | *Mean* |  | *SEM* | *Mean* |  | *SEM* | *Mean* |  | *SEM* |
| Inflammation signalling pathway | ***AKT1*** | 1.00 b |  | 0.16 | 1.38 a  |  | 0.10 | 0.41 c |  | 0.23 | 1.07 ab |  | 0.07 | 1.17 ab |  | 0.03 | 1.12 ab |  | 0.08 | 0.0002 |
| ***MAPK14*** | 1.00 b |  | 0.11 | 1.32 a |  | 0.18 | 0.82 b |  | 0.09 | 0.84 b |  | 0.05 | 0.99 b |  | 0.05 | 0.89 b |  | 0.07 | 0.0002 |
| ***MARVELD2*** | 1.00 b |  | 0.03 | 1.15 a |  | 0.02 | 1.33 a |  | 0.11 | 0.91 b |  | 0.09 | 0.84 b |  | 0.02 | 1.07 b |  | 0.14 | 0.0002 |
| ***MyD88*** | 1.00 c |  | 0.09 | 1.22 ab |  | 0.11 | 0.76 cd |  | 0.14 | 1.09 abc |  | 0.07 | 1.37 a |  | 0.04 | 1.05 bc |  | 0.09 | 0.0002 |
| ***NF-kB1*** | 1.00 b |  | 0.19 | 0.91 b |  | 0.09 | 1.55 a |  | 0.21 | 1.00 b |  | 0.15 | 0.81 b |  | 0.04 | 0.93 b |  | 0.09 | 0.0002 |
| ***NF-kBIα*** | 1.00 ab |  | 0.18 | 1.13 ab |  | 0.07 | 0.31 c |  | 0.16 | 1.25 a |  | 0.18 | 0.96 ab |  | 0.04 | 0.81 b |  | 0.04 | 0.0002 |
| ***NOD1*** | 1.00 b |  | 0.11 | 1.05 b |  | 0.05 | 0.81 c |  | 0.08 | 0.88 bc |  | 0.03 | 1.03 b |  | 0.03 | 1.28 a |  | 0.03 | 0.0002 |
| ***PPARγ*** | 1.00 b |  | 0.36 | 0.89 b |  | 0.04 | 2.85 a |  | 0.51 | 0.87 b |  | 0.02 | 0.96 b |  | 0.04 | 1.17 b |  | 0.09 | 0.0002 |
| ***TLR2*** | 1.00 ab |  | 0.52 | 0.75 b |  | 0.52 | 0.66 b |  | 0.11 | 2.08 a |  | 0.32 | 0.93 ab |  | 0.20 | 0.78 ab |  | 0.43 | 0.0229 |
| ***TLR4*** | 1.00 a |  | 0.19 | 0.92 ab |  | 0.25 | 0.35 c |  | 0.09 | 0.55 abc |  | 0.18 | 0.51 abc |  | 0.16 | 0.45 bc |  | 0.12 | 0.0002 |
| Pro-inflammatory factors | ***COX2*** | 1.00 a |  | 0.38 | 1.46 a |  | 0.30 | 0.16 b |  | 0.08 | 0.84 ab |  | 0.36 | 1.13 a |  | 0.50 | 0.54 ab |  | 0.14 | 0.0003 |
| ***CXCL10*** | 1.00 |  | 0.42 | 0.61 |  | 0.32 | 0.68 |  | 0.06 | 0.35 |  | 0.06 | 0.71 |  | 0.39 | 0.06 |  | 0.03 | 0.2843 |
| ***DEFβ1*** | 1.00 b |  | 0.29 | 0.84 b |  | 0.05 | 2.18 a |  | 0.38 | 0.82 b |  | 0.11 | 0.80 b |  | 0.04 | 0.84 b |  | 0.07 | 0.0002 |
| ***DEFβ4a*** | 1.00 |  | 0.25 | 0.64 |  | 0.20 | 1.16 |  | 0.20 | 1.33 |  | 0.27 | 0.75 |  | 0.13 | 0.75 |  | 0.09 | 0.0683 |
| ***IL6*** | 1.00 ab |  | 0.18 | 0.89 b |  | 0.22 | 1.32 a |  | 0.21 | 1.27 a |  | 0.20 | 1.02 ab |  | 0.19 | 0.71 b |  | 0.10 | 0.0025 |
| ***IL8*** | 1.00 b |  | 0.39 | 0.99 b |  | 0.29 | 0.67 b |  | 0.11 | 2.14 a |  | 0.53 | 1.15 b |  | 0.03 | 0.72 b |  | 0.08 | 0.0002 |
| ***IL18*** | 1.00 b |  | 0.40 | 1.07 b |  | 0.21 | 2.33 a |  | 0.40 | 1.45 b |  | 0.21 | 1.31 b |  | 0.14 | 0.79 b |  | 0.07 | 0.0002 |
| ***ILRN1*** | 1.00 bc |  | 0.40 | 0.55 c |  | 0.05 | 2.73 a |  | 0.53 | 0.65 bc |  | 0.18 | 0.55 c |  | 0.03 | 1.58 b |  | 0.25 | 0.0002 |
| ***TNFα*** | 1.00 a |  | 0.24 | 0.89 ab |  | 0.18 | 0.54 c |  | 0.06 | 0.68 abc |  | 0.06 | 0.59 bc |  | 0.06 | 0.77 abc |  | 0.10 | 0.0022 |
| Intestinal barrier integrity | ***CASP3*** | 1.00 b |  | 0.31 | 0.93 b |  | 0.20 | 1.72 a |  | 0.30 | 1.35 ab |  | 0.41 | 1.00 b |  | 0.11 | 1.00 b |  | 0.15 | 0.0029 |
| ***CDH1*** | 1.00 b |  | 0.24 | 0.86 b |  | 0.08 | 1.86 a |  | 0.34 | 0.75 b |  | 0.12 | 0.61 b |  | 0.02 | 0.86 b |  | 0.08 | 0.0002 |
| ***Claudin-1*** | 1.00 b |  | 0.09 | 1.23 a |  | 0.14 | 0.90 bc |  | 0.04 | 0.96 bc |  | 0.15 | 0.85 bc |  | 0.02 | 0.74 c |  | 0.05 | 0.0002 |
| ***Claudin-3*** | 1.00 a |  | 0.15 | 0.84 a |  | 0.13 | 1.05 a |  | 0.12 | 0.55 b |  | 0.03 | 0.52 b |  | 0.03 | 0.76 ab |  | 0.05 | 0.0002 |
| ***Claudin-4*** | 1.00 b |  | 0.24 | 0.86 b |  | 0.10 | 2.00 a |  | 0.40 | 0.64 b |  | 0.08 | 0.54 b |  | 0.00 | 0.74 b |  | 0.02 | 0.0002 |
| ***EGFR*** | 1.00 ab |  | 0.12 | 1.15 a |  | 0.13 | 0.72 c |  | 0.05 | 0.72 c |  | 0.07 | 0.77 bc |  | 0.04 | 0.87 bc |  | 0.01 | 0.0002 |
| ***Occludin*** | 1.00 b |  | 0.24 | 0.97 b |  | 0.07 | 2.09 a |  | 0.34 | 0.79 b |  | 0.09 | 0.74 b |  | 0.05 | 1.14 b |  | 0.05 | 0.0002 |
| ***MUC1*** | 1.00 b |  | 0.40 | 0.87 b |  | 0.09 | 2.80 a |  | 0.51 | 0.62 b |  | 0.02 | 0.69 b |  | 0.02 | 1.27 b |  | 0.16 | 0.0002 |
| ***TGFβ1*** | 1.00 abc |  | 0.14 | 1.13 ab |  | 0.20 | 0.82 bc |  | 0.13 | 0.71 c |  | 0.04 | 0.70 c |  | 0.02 | 1.24 a |  | 0.13 | 0.0004 |
| ***VIL1*** | 1.00 a |  | 0.24 | 0.75 ab |  | 0.28 | 0.68 ab |  | 0.06 | 0.30 b |  | 0.10 | 0.72 ab |  | 0.18 | 0.91 ab |  | 0.12 | 0.0076 |
| ***ZO1*** | 1.00 ab |  | 0.07 | 1.07 ab |  | 0.07 | 1.03 ab |  | 0.05 | 0.96 ab |  | 0.08 | 0.94 b |  | 0.01 | 1.15 a |  | 0.07 | 0.0071 |

Values are means of triplicate well-measurements, with standard error of the mean.

Different superscripts denote significant difference (P<0.05).

The geometric mean of ribosomal protein L 13a (*RPL13a*), glyceraldehyde-3-phosphate dehydrogenase (*GAPDH*), peptidylprolyl isomerase A (*PPIA*) and tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein zeta (*YWHAZ*) was used to normalize samples.

Abbreviations: AKT1, serine/threonine-protein kinase 1; MAPK14, mitogen-activated protein kinase 14; MyD88, myeloid differentiation primary response 88; NF-kB, nuclear factor-kappa B; NF-kBIα, nuclear factor-kappa B inhibitor alpha; NOD1, nucleotide-binding oligomerization domain-containing protein 1; PPARγ, peroxisome proliferator-activated receptor gamma; TLR, toll-like receptor; CCL5, chemokine ligand 5; COX2, cyclooxygenase 2; CXCL10, C-X-C motif chemokine 10; DEFβ, defensin beta; EGFR, epidermal growth factor receptor; IFN, interferon; IL, interleukin; ILRN1, interleukin-1 receptor antagonist; MCP1, monocyte chemoattractant protein 1; TNFα, tumor necrosis factor alpha; CASP3, caspase 3; CDH1, E-cadherin; MARVELD2, tricellulin; MUC1, mucin 1; TGFβ1, transforming growth factor beta 1; VIL1, villin 1; ZO-1, zonula occludens-1.

**SUPPLEMENTARY FIGURE LEGEND**

**Supplementary figure 1.** Bacterial communities in the fermentation broth (12 hours of fermentation) of the ingredients screened via the *in vitro* batch fermentation model

1. *Clostridium* cluster IV abundance for the fructan-based ingredients
2. *Bifidobacterium* spp. abundance for the fructan-based ingredients
3. Butyryl-CoA : acetate-CoA transferase abundance for the fructan-based ingredients
4. *Clostridium* cluster IV abundance for the pectin-based ingredients
5. *Bifidobacterium* spp. abundance for the pectin-based ingredients
6. Butyryl-CoA : acetate-CoA transferase abundance for the pectin-based ingredients
7. Butyryl-CoA : acetate-CoA transferase abundance for the arabinoxylan-oligosaccharide-based ingredients
8. Butyryl-CoA : acetate-CoA transferase abundance for the other ingredients

*Mean values (n=3) ± SEM per bacterial group.*

*Different superscripts above columns indicate significant differences (P<0.05).*

*Total bacteria was selected as reference gene and was stable across treatment.*

**Abbreviations:** **a.u.,** arbitrary unit; **WDG,** wheat distillers grain.