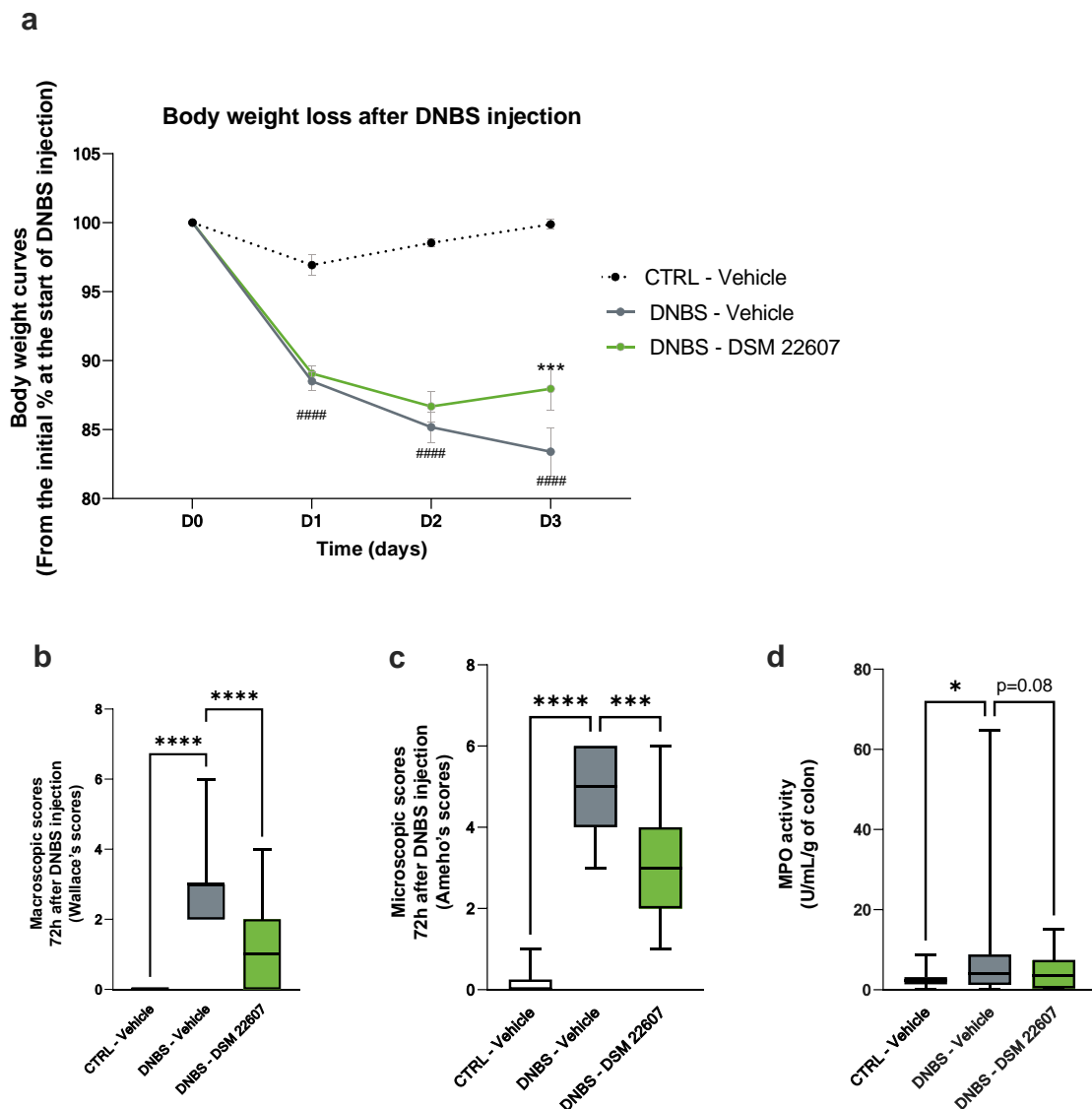


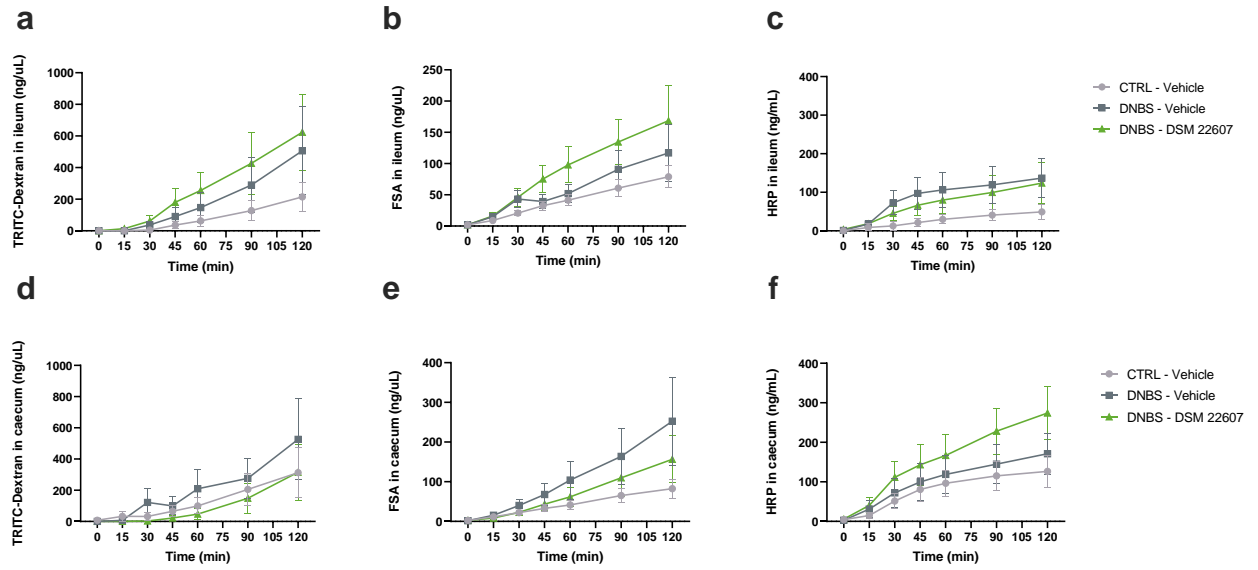
## Supplementary data



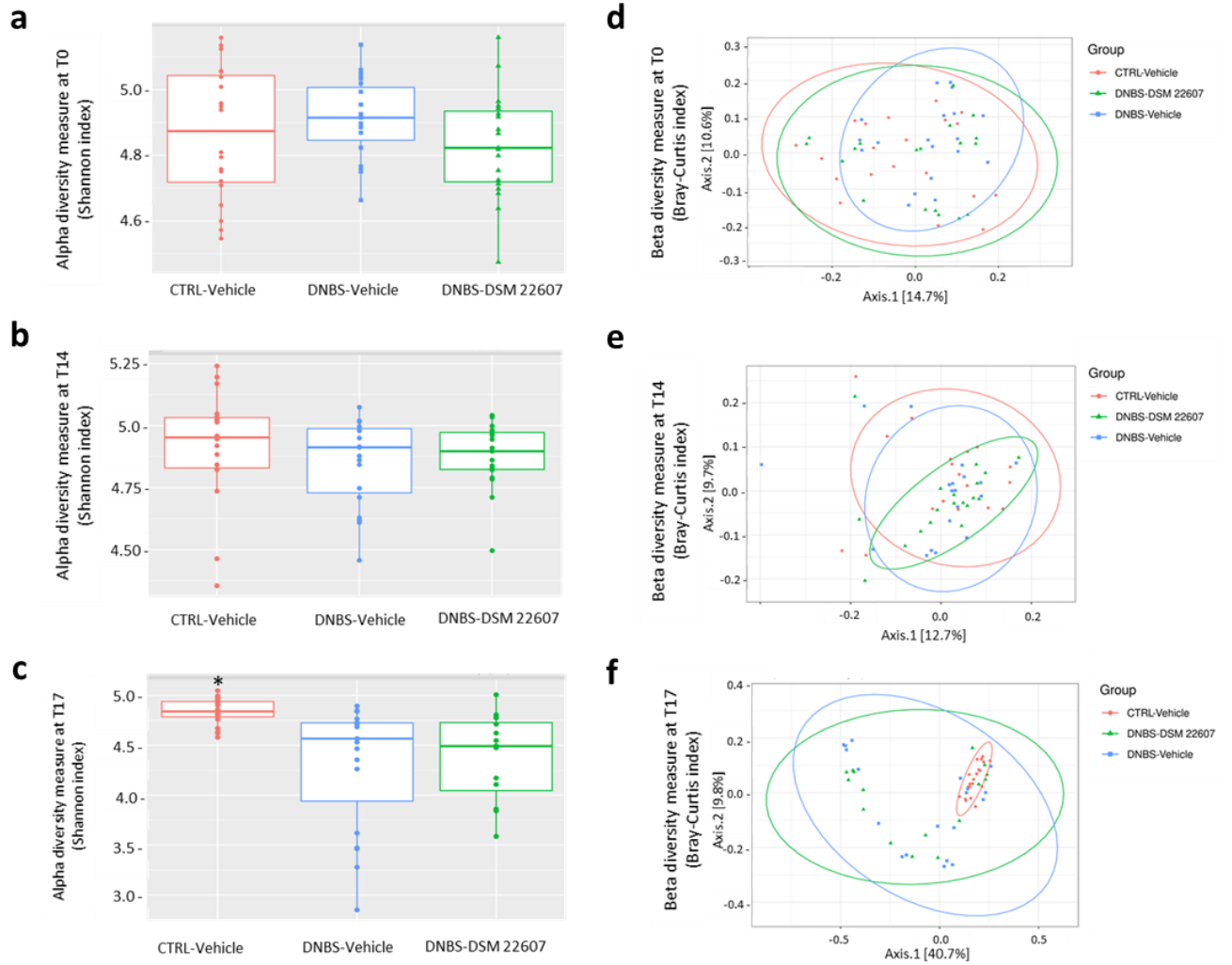
### Supplementary Figure 1. Beneficial effect of *C. minuta* on body weight gain and intestinal epithelium.

Weight loss following DNBS injection until euthanasia (a); macroscopic (b) and microscopic (c) scores after DNBS injection; myeloperoxidase (MPO) activity in the colon (d). CTRL-Vehicle (N=26; white); DNBS-Vehicle (N=29; dark grey); DNBS-DSM 22607 (N=31; green). Data are means and SEM.

Results of Original FDR method of Benjamini and Hochberg multiple comparison tests comparing the DNBS-Vehicle group to the three other groups. For macroscopic and microscopic scores, results of Kruskal Wallis test with a Dunn's multiple comparisons test comparing the DNBS-Vehicle group to the three other groups.

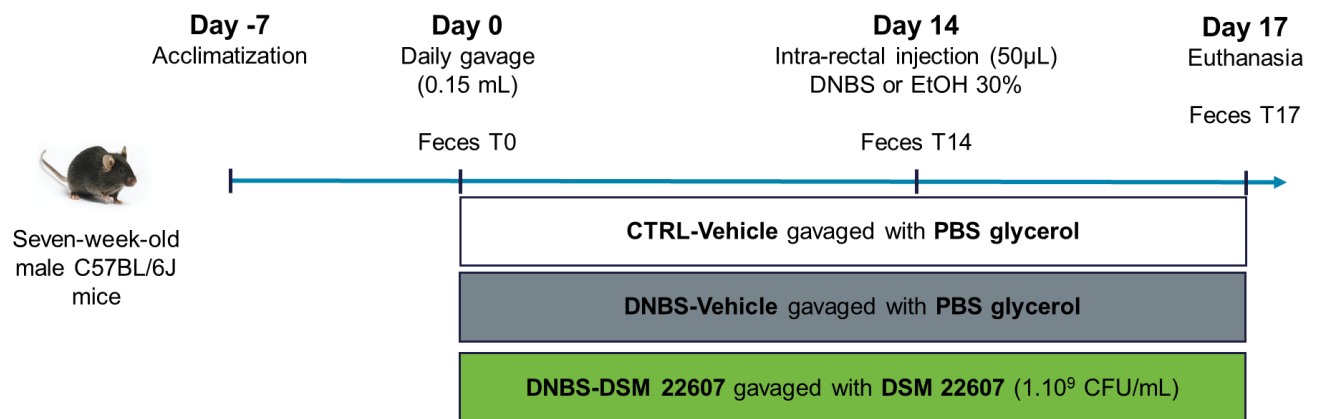


**Supplementary Figure 2. *C. minuta* showed contrasting effects on *in vitro* permeability assay.** Analysis of paracellular permeability in the ileum by measuring TRITC-dextran (a) and FSA (b). Transcellular pathway was evaluated by measuring HRP in the ileum (c). Same was done in the caecum for paracellular (d and e) and transcellular pathway (f). CTRL-Vehicle (N=9; light grey); DNBS-Vehicle (N=12; dark grey); DNBS-DSM 22607 (N=12; green). Data are means and SEM.



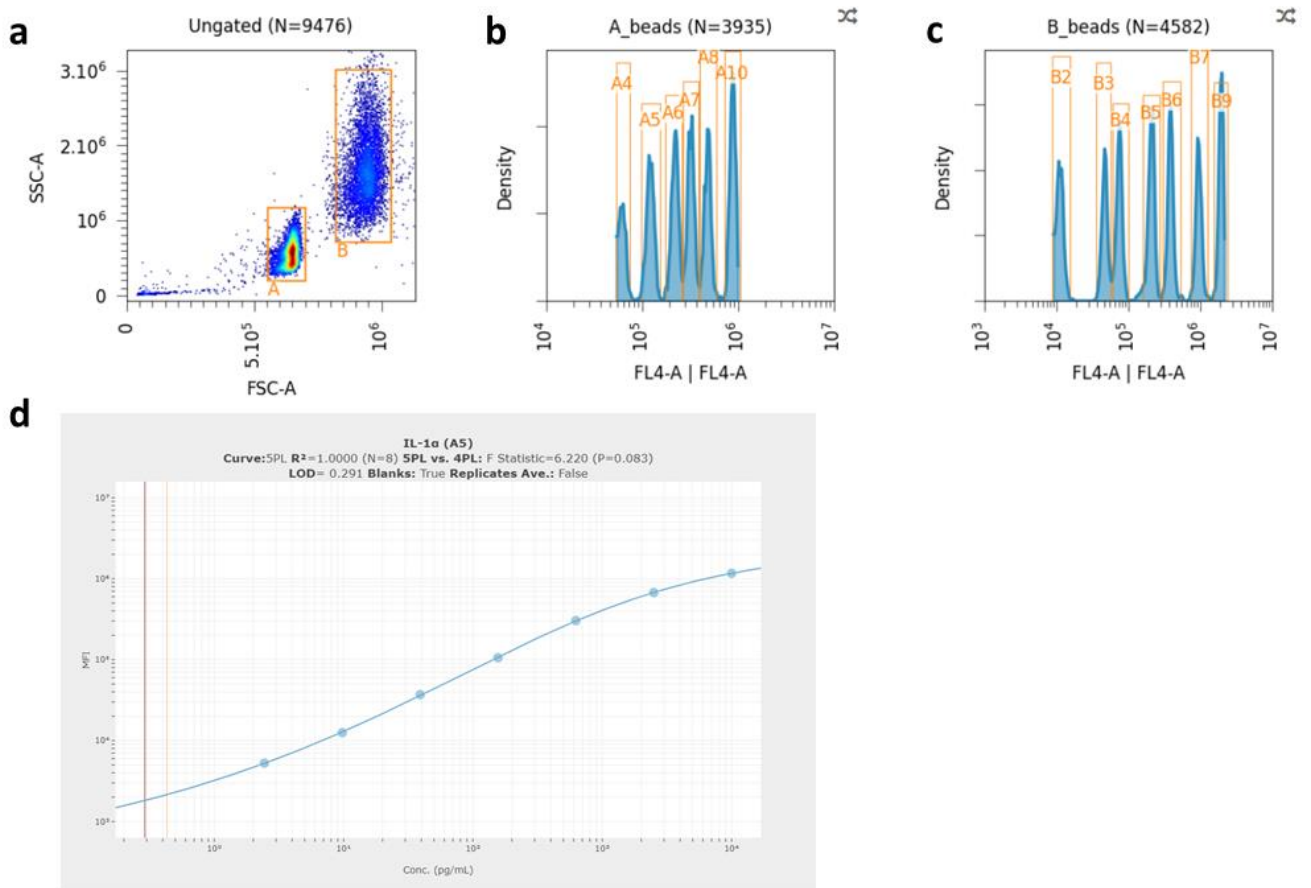
**Supplementary Figure 3. Alpha-diversity (Shannon index) and beta-diversity (Bray-curtis index) among time points and treatments.**

Boxplot of Shannon diversity at T0 (a), T14 (b) and T17 (c); MultiDimensional Scaling of beta diversity at T0 (d), T14 (e) and T17 (f). CTRL-Vehicle (N=20; red); DNBS-Vehicle (N=19; blue); DNBS-DSM 22607 (N=19; green).



**Supplementary Figure 4: DNBS protocol in C57BL/6J mice.**

Gavages, intra-rectal injections, feces sampling for 16S microbiota sequencing and colon collection for transcriptomic analysis



**Supplementary Figure 5. LegendPlex analysis method.**

Forward scatter vs. side scatter was used to identify A and B bead populations (a). A-beads and B-beads classification channel mono-variate histograms were used to identify A and B bead IDs (b and c). For each analyte in your LEGENDplex™ assay, the software fits a 5-PL curve to the uploaded FCS standard curve files using logistic regression curve fitting algorithms (d). These curves were then used to calculate analyte concentrations in the uploaded experimental samples.