The HMI™ module: a new tool to study the Host-Microbiota Interaction in the human gastrointestinal tract *in vitro*

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Figure S1: computational fluid dynamics simulation of the module chamber under different shear forces. Color pathlines indicate the number of particle ID that will flow under different shear stresses. The experiment was designed to determine till which flow it was possible to obtain a homogenous flow. At low and medium shear stress no turbulence was observed and the flow was homogenous.

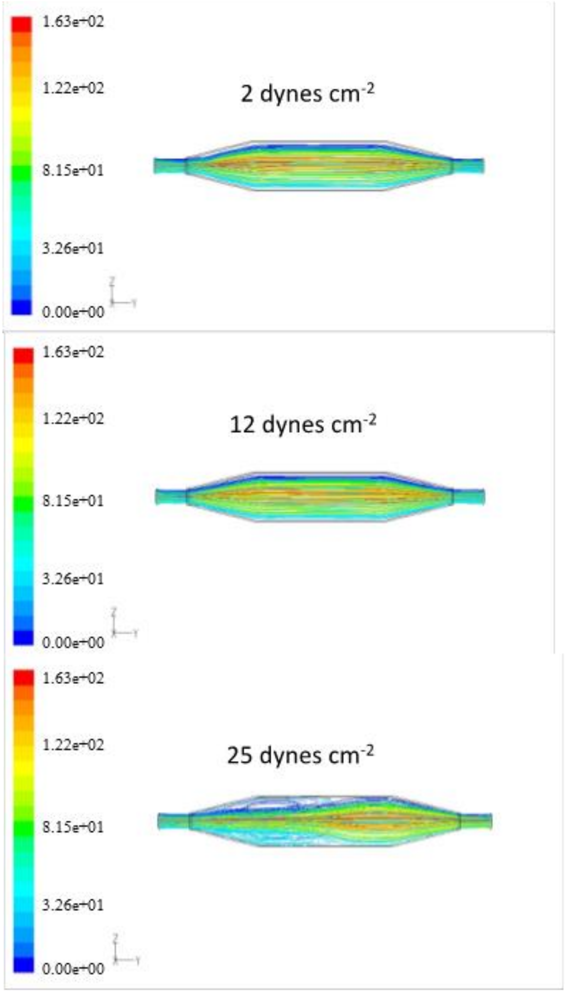

Figure S2: DGGE fingerprinting analysis for total bacteria. A = control period; B = treatment period. L = luminal samples; M = mucus sample. Clustering analysis was based on the Pearson product-moment correlation coefficient and the dendrogram was created by using UPGMA linkage.