A microfluidics-based in vitro model of the gastrointestinal human–microbe interface

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Changes in the human gastrointestinal microbiome are associated with several diseases. To infer causality, experiments in representative models are essential, but widely used animal models exhibit limitations. Here we present a modular, microfluidics-based model (HuMiX, human–microbial crosstalk), which allows co-culture of human and microbial cells under conditions representative of the gastrointestinal human–microbe interface. We demonstrate the ability of HuMiX to recapitulate in vivo transcriptional, metabolic and immunological responses in human intestinal epithelial cells following their co-culture with the commensal Lactobacillus rhamnosus GG (LGG) grown under anaerobic conditions. In addition, we show that the co-culture of human epithelial cells with the obligate anaerobe Bacteroides caccae and LGG results in a transcriptional response, which is distinct from that of a co-culture solely comprising LGG. HuMiX facilitates investigations of host–microbe molecular interactions and provides insights into a range of fundamental research questions linking the gastrointestinal microbiome to human health and disease.
The human microbiome is emerging as a key player governing human health and disease\(^1,2\). Recent high-resolution molecular analyses have linked microbial community disequilibria (dysbiosis), primarily in the gastrointestinal tract (GIT), to several idiopathic diseases, including diabetes\(^3\), obesity\(^4\), inflammatory bowel disease\(^5\), cancer\(^6\) and, most recently, neurodegenerative diseases\(^7\). However, a detailed understanding of the fundamental molecular mechanisms underlying host–microbe interactions and their potential impact on immune regulation, drug metabolism, nutrition and infection remain largely elusive\(^8,9\).

More specifically, patterns of association between distinct microorganisms, their traits and disease states resolved using ‘meta-omics’ do not allow direct causal inference, and thus experimental validation is essential\(^10\). For this, robust experimental models that allow the systematic manipulation of variables are required to test the multitude of hypotheses that arise from the generated high-dimensional data sets\(^10\).

Animal models used in human microbiome research are physiologically not representative\(^11\). In vitro models that mimic microbial processes along the GIT allow the simulation of luminal microbial communities\(^12,14\) and/or mucus-adherent microbiota\(^15,16\) but typically do not include provisions for assessing human host responses.

Host responses to GIT microbiota have traditionally been assessed following the exposure of cultured human cells to bacteria-free supernatants\(^17\) or through short-term direct-contact co-cultures involving, for example, Transwell systems\(^18\), microcarrier beads\(^19\) or mouse gut organoids models\(^20\). Recent advances in multi-layer microfluidics have led to the development of a gut-on-a-chip model that includes a provision for peristalsis\(^21\) and that has been used to study intestinal inflammation on a chip\(^22\). These human–microbial co-culture approaches are, however, limited in their scope because they only allow experiments with commensal and/or mutualistic microorganisms growing under aerobic conditions\(^21,22\).

To overcome these limitations, the recently introduced host–microbiota interaction (HMI) module, which interfaces with the in vitro simulator of the human intestinal microbial ecosystem model, incorporates a semi-permeable membrane between co-cultured human enterocytes and bacteria\(^23\). Through inclusion of a partitioning membrane between the human and microbial culture chambers, the HMI module allows the co-culture of intestinal cells with complex microbial communities under microaerophilic conditions\(^23\). This two-chamber design requires intermittent perfusion of the human cell culture medium to the apical surface of the epithelial cells, which is not representative of the continuous supply of nutrients to the basal membrane seen in vivo\(^24\)–\(^26\). The lack of multiplicity makes it difficult to include additional cell types of relevance to the GIT in the HMI module, for example, immune cells. Furthermore, it prevents the extraction of biomolecular fractions from the individual co-cultured cell contingents following specific experimental regimes and thereby renders the HMI module incompatible with downstream high-resolution molecular analyses. Although the HMI module currently is the most representative in vitro model of gastrointestinal host–microbial interactions, there still remains an unmet need for a modular, representative in vitro model of the gastrointestinal human–microbe interface.

Here we present a modular microfluidics-based human–microbial co-culture model, HuMiX, which overcomes the majority of the limitations of existing in vitro models and allows the partitioned yet proximal co-culture of representative human and microbial cells followed by downstream molecular analyses of the individual cell contingents. More specifically, we demonstrate the viable co-culture of differentiated human epithelial cells (Caco-2) with either a facultative anaerobe, *Lactobacillus rhamnosus* GG (LLG), grown solely under aerobic or anaerobic conditions, or grown in combination with an obligate anaerobe, *Bacteroides cacae*, under anaerobic conditions. Co-culture experiments were followed by detailed molecular analyses of the effects of the induced co-cultures on the physiology of human and bacterial cells. Comparison of our results with published in vitro and in vivo data sets demonstrates the ability of HuMiX to representatively mimic the gastrointestinal human–microbe interface.

**Results and Discussion**

**Design and characterisation of the HuMiX model.** To overcome the limitations of existing in vitro models\(^23\), we developed a modular microfluidics-based device, which allows the establishment of a model of the gastrointestinal human–microbe interface, named HuMiX (human-microbial crossstalk) (Fig. 1a–c).

The device consists of three co-laminar microchannels: a medium perfusion microchannel (henceforth referred to as the ‘perfusion microchannel’), a human epithelial cell culture microchannel (henceforth referred to as the ‘human microchannel’) and a microbial culture microchannel (henceforth referred to as the ‘microbial microchannel’); Fig. 1a,b; Supplementary Fig. 1a,b). Each microchamber has a dedicated inlet and outlet for the inoculation of cells as well as for the precise control of physicochemical parameters through the perfusion of laminar streams of dedicated culture media (Fig. 1d,e). Dedicated outlets provide means to collect eluates from the individual chambers for downstream characterisation (Fig. 1d; Supplementary Fig. 1a,b). By juxtaposing the human and microbial cell contingents at a distance of 0.5–1 mm across a separatory nanoporous membrane, the HuMiX model is representative of a healthy intact epithelial barrier\(^10\) (Supplementary Note 1). Furthermore, the model integrates oxygen sensors (optodes) for the real-time monitoring of the dissolved oxygen concentrations within the device (Fig. 1a,b,d; Supplementary Fig. 1c). Given the challenges associated with measuring transepithelial electrical resistance (TEER) on a chip\(^27\), a specially designed version of HuMiX, which allows the insertion of a commercial chopstick style electrode (STX2; Millipore), was fabricated to monitor TEER for the characterisation of cell growth and differentiation within the device (Fig. 1d; Supplementary Fig. 1d).

Following the conceptualisation and engineering of the HuMiX model (Supplementary Note 1), we developed an optimised protocol for the co-culture of human epithelial cells with gastrointestinal microbes (Fig. 1e). The human cell line and bacterial isolates used for the co-culture experiments were originally obtained from the human large intestine and, together with the physical characteristics of the model (Supplementary Note 1), allowed the assembly of a model representing the human–microbe interface of the human colon. Nonetheless, given the modularity of the device and the flexibility of its set-up, other sections of the human GIT may also be modelled following appropriate modifications to the presented model (Supplementary Note 1). The protocol includes an extensive sterilisation and handling procedure that enables the culture of human epithelial cells (Caco-2) in antibiotic-free DMEM medium to allow their subsequent co-culture with bacteria in HuMiX. The Caco-2 cell line was chosen because it represents the most widely used model for the human gastrointestinal epithelial barrier, as it exhibits essential functional and physiological traits of the intestinal epithelium\(^25,28\). The differentiation of the epithelial cells was evaluated by measuring TEER of the Caco-2 cell monolayer (Fig. 2a) and through microscopic observation of the expression of the tight junction protein occludin (Fig. 2b).
Figure 1 | The HuMiX model. (a) Conceptual diagram of the HuMiX model for the representative co-culture of human epithelial cells with gastrointestinal microbiota. (b) Annotated exploded view of the HuMiX device. The device is composed of a modular stacked assembly of elastomeric gaskets (thickness: 700 μm) sandwiched between two polycarbonate (PC) enclosures, and each gasket defines a distinct spiral-shaped microchannel with the following characteristics: length of 200 mm, width of 4 mm and height of 0.5 mm, amounting to a total volume of 400 μl per channel. Semi-permeable membranes affixed to the elastomeric gaskets demarcate the channels. The pore sizes of the membranes were chosen for their intended functionality. A microporous membrane (pore diameter of 1 μm), which allows diffusion-dominant perfusion to the human cells, is used to partition the perfusion and human microchambers. A nanoporous membrane (pore diameter of 50 nm) partitions the human and microbial microchambers to prevent the infiltration of microorganisms, including viruses, into the human microchamber. (c) Photograph of the assembled HuMiX device (scale bar, 1 cm). (d) Diagram of the experimental set-up of the HuMiX model with provisions for the perfusion of dedicated oxic and anoxic culture media as well as the monitoring of the oxygen concentration and transepithelial electrical resistance. The oxygen concentration in the anoxic medium is maintained at 0.1% by continuously bubbling the medium with dinitrogen gas. (e) Diagrammatic overview of the HuMiX co-culture protocol.
Following the establishment of differentiated Caco-2 cell monolayers, we initiated co-cultures of these cells with LGG grown in anoxic DMEM medium (Supplementary Fig. 2a). LGG of the phylum Firmicutes was chosen, as it represents a commensal facultative anaerobic bacterium originally isolated from the human GIT29–31. Importantly, extensive data exist on its physiological impacts on mammalian mucosal tissues in vivo32–34. The developed co-culture protocol (Fig. 1e) first results in the establishment and maintenance of an epithelial cell monolayer. The Caco-2 cells adhere to the collagen-coated microporous membrane (Fig. 1a,e; Supplementary Note 1), proliferate and differentiate into confluent cell monolayers that form tight junctions between adjacent cells (Fig. 2a,b). The diffusion-based perfusion of the cell culture medium to the basal side of the Caco-2 cells through the microporous membrane mimics the intestinal blood supply and provides shear-free conditions accelerating the growth of the human cells35.

Co-culture with LGG was initiated after 7 days of epithelial cell culture (day 9 of the HuMiX co-culture protocol; Figs 1a,e and 2a,b). This first involved the introduction of anaerobically grown LGG cell suspensions into the microbial microchamber through the port on a three-way connector (Fig. 1d).

Following the co-culture, the modular device architecture allows access to individual cell contingents on disassembly, whereby one half of each of the cell contingents can be used for microscopic evaluation and the other half can be used for the extraction of intracellular biomolecules (DNA, RNA, proteins and metabolites) for subsequent high-resolution molecular analyses36. The viability of the co-cultured contingents was determined via live–dead staining and subsequent fluorescence microscopy, demonstrating that no apparent cytotoxic effects were induced in either cell contingent following their co-culture (Fig. 2c,d). RNA electropherograms confirmed that high-quality biomolecular fractions were obtained from the individual co-cultured contingents (Fig. 2e).

Due to the laminar flow profiles within the microchambers, eluate samples (Fig. 2f) can be recovered from each microchamber, thereby providing a means to continually monitor the effects of the co-culture on the individual co-cultured cell contingents through various analyses, such as the use of cytokine assays and metabolomic profiling. Visible differences in the eluates from the three proximal microchambers support the notion of distinct microenvironments in each of the microchambers (Fig. 2f).

Integrated oxygen sensors (optodes) allow continuous monitoring of the dissolved oxygen concentrations in the perfusion and microbial microchambers (Fig. 1e; Supplementary Fig. 1c). The simultaneous perfusion of oxic (21% dissolved O₂) and anoxic (0.1% O₂) media through the perfusion microchamber and the microbial microchamber, respectively, allowed the establishment and maintenance of an oxygen gradient representative of the in vivo situation (Fig. 2g). The measured
dissolved oxygen concentrations in the perfusion microchamber stabilised to 5.43 ± 0.137% for the final 12 h of co-culture between the Caco-2 cells and LGG, which is comparable to the actual recorded concentrations in human intestinal tissues, that is, 4.6% (ref. 37; Fig. 2g). The oxygen profiles in the microbial microchamber were characterised by a rapid decrease in the oxygen concentration (from 2.6 to ≤0.8% of dissolved oxygen), following an intermittent spike due to the introduction of small amounts of oxygen into the microbial microchamber during the inoculation process of LGG (Fig. 2g). The established anoxic conditions are analogous to those observed in vivo between the mucus layer and the luminal anaerobic zone (≤0.88%; ref. 38) and such oxygen concentrations have been reported to be favourable for the growth of diverse microbiota, including obligate anaerobes39. The gradient of oxygen in the HuMiX model was maintained through the continuous perfusion of anoxic media (0.1%) into the microbial microchamber and further shaped by the consumption of oxygen by Caco-2 cells and the facultative anaerobe LGG (Fig. 2g).

Through the consumption of oxygen, anaerobic niches are established in the microbial microchamber, which subsequently allow colonisation of the microbial microchamber by obligate anaerobes40. To showcase the ability of HuMiX to sustain culture of an obligate anaerobe, we initiated co-cultures using a simple microbial consortium comprising LGG in combination with B. caccae (Supplementary Figs 2b and 3). B. caccae was chosen as it represents an obligate anaerobic commensal that belongs to the phylum Bacteroidetes, the other dominant phylum apart from the Firmicutes (LGG) constituting the human GIT microbiome41. Both organisms were inoculated in equal starting proportions (optical density (OD) ~1) and co-cultured with Caco-2 cells for 24 h (Supplementary Fig. 2b). The consortium was sustained via continuous perfusion of anoxic DMEM medium. The consortium structure was determined using 16S rRNA gene amplicon sequencing after 24 h of co-culture, and the relative abundances of Bacteroides spp. and Lactobacillus spp. were found to be 69 and 31%, respectively (Fig. 2h). These results confirm the ability of the HuMiX model to support the growth of an obligate anaerobic microbial strain. Human cells still exhibited tight junctions (Supplementary Fig. 3a) and both contingents were viable (Supplementary Fig. 3b,c). It follows from these experiments that the inclusion of more complex communities into the HuMiX model is possible but goes beyond the scope of the reported proof-of-concept experiments.

Furthermore, to demonstrate the ability to incorporate other cell types within HuMiX, we cultured non-cancerous colonic cells, i.e., CCD-18Co, in the human microchamber (Supplementary Fig. 4a,b). In addition, to demonstrate that HuMiX can be used in a three-layered set-up for addressing specific research questions, we cultured primary CD4+ T cells in the perfusion microchamber of HuMiX (Supplementary Fig. 4c,d). The primary CD4+ T cells were cultured in the absence (Supplementary Fig. 4c,d) or presence of LGG (Supplementary Fig. 4e,f) over 48 h and did not exhibit any significant differences in terms of cell viability. These experiments highlight the potential of HuMiX to be used for investigating the cellular mechanisms involved in the interplay between GIT bacteria and different human cell types.

In summary, HuMiX exhibits the following essential characteristics: (1) modular microfluidic device architecture consisting of three microchambers engineered to facilitate the proximal co-culture of human and microbial cells; (2) ability to perfuse the device with dedicated culture media to allow the establishment of aerobic conditions for human cell culture and anaerobic conditions for GIT bacteria; (3) real-time monitoring of oxygen concentrations; (4) easy access to the individual cell contingents following specific experimental regimes; and (5) compatibility with end point microscopic assays as well as high-resolution multi-omic analyses.

HuMiX recapitulates in vivo responses. Given the demonstrated ability to establish conditions representative of the human GIT in HuMiX, we conducted further validation experiments to assess the human cellular responses with respect to different co-culture conditions in HuMiX. LGG has been widely used in several human clinical trials aimed at understanding the efficacy of probiotic treatments in humans32,33. More specifically, gene expression differences have been documented in human intestinal mucosal biopsy samples after the administration of LGG to either healthy subjects32 or as a therapeutic supplement for male individuals suffering from esophagitis33. Therefore, to validate our in vitro co-culture approach, we performed detailed experiments involving the co-culture of Caco-2 cells maintained under aerobic conditions with LGG cultured under anaerobic conditions (Supplementary Fig. 2a) and compared the resulting Caco-2 gene expression data with reference data from clinical studies32,33. For this, total RNA was first extracted from Caco-2 cells following their co-culture with LGG grown under anaerobic conditions as well as their corresponding LGG-free controls (anoxic medium was perfused through the microbial microchamber, but no bacteria were inoculated, Supplementary Fig. 2a). The RNA was then subjected to DNA microarray-based messenger RNA and microRNA (miRNA) profiling.

Overall, we identified 208 genes that were differentially expressed following co-culture with LGG grown under anaerobic conditions (fold change (FC) >1.5 and equivalently with swapped conditions for decreased expression, P<0.01, empirical Bayes moderated t-statistic (BtS); Fig. 3a; Supplementary Fig. 5a; Supplementary Table 1). Given the lack of detail regarding the identities of the majority of genes found to be differentially expressed in vivo, we limited our subsequent analyses and discussions to genes that were explicitly highlighted in the in vivo clinical studies and that showed statistically significant differences in our study (Table 1). Among the top differentially expressed genes, we validated the gene expression of four genes—cdc2, p13, egr1 and mt2a—using quantitative PCR with reverse transcription (RT–qPCR) analyses. The RT–qPCR results showed differential expression patterns analogous to those observed in the micro-array data (Supplementary Fig. 5b).

The transcriptomic results exhibit a high level of concordance between the LGG-treated human mucosal in vivo transcriptomic data and the differentially expressed gene sets identified through the comparison of HuMiX-based co-cultures with LGG grown under anaerobic conditions compared with the corresponding LGG-free controls32,33 (Table 1; Supplementary Fig. 5a). The co-culture involving LGG in HuMiX resulted in the up- and downregulation of 127 and 81 genes in the Caco-2 cells, respectively (Supplementary Table 1; FC>1.5 and P<0.01, BtS). Importantly, the co-culture of Caco-2 with LGG resulted in the differential expression of eight genes (egr1, ccl2, scl9a1, ubd, cxcx4, mybl2, pim1 and cyp1a1 (Table 1; Supplementary Fig. 5a: Supplementary Note 2; P<0.05, BtS)), which had also been found to be differentially expressed in human intestinal biopsy samples after the administration of LGG32,33. In addition to the genes described above, we also identified four (elf3, cdk9, gadd45b and pilrb) genes, previously highlighted as responsive to LGG in human subjects32,33 (Table 1), but the expression of these genes was found to be disparate when comparing our results to the in vivo expression data (Table 1). The highlighted differences in the expression of these four genes are likely due to the reduced complexity of the microenvironment, the human epithelial cells
parameter used was the metabolites. Ranking was based on the Caco-2 cells co-cultured with LGG growing under anaerobic conditions compared with their corresponding LGG-free controls (initiation of co-culture with LGG. Eluate samples were obtained from the perfusion microchamber (distance metric was performed to determine the ordering of the genes. (germ-free piglets34. In accordance with the findings from the response to the primocolonisation by LGG was conducted in systemic in vivo an already mature GIT microbiome. At present, the only primocolonisation of germ-free animals than its introduction into (Supplementary Note 3). The threshold parameters used were FC > 2 and P < 0.01, as determined using the empirical Bayes moderated t-statistic65. Ranking was based on the p-values calculated using the log-fold changes and P values (BtS). An average linkage hierarchical clustering with the Euclidean distance metric was performed to determine the ordering of the genes. (b) Extracellular CCL20/MIP3A and IL-8 cytokine levels before and 24 h after the initiation of co-culture with LGG. Eluate samples were obtained from the perfusion microchamber (n = 3). (c) Heat map of intracellular metabolites from Caco-2 cells co-cultured with LGG growing under anaerobic conditions compared with their corresponding LGG-free controls (n = 3). The threshold parameter used was P < 0.1 (StT). An average linkage hierarchical clustering with the Euclidean distance metric was performed to determine the ordering of the metabolites.

and the microbiota used in our proof-of-concept experiments compared with the in vivo situation. In addition, we found a high degree of concordance in responsive pathways (for example, interferon response, calcium signalling and ion homeostasis) in Caco-2 cells following their co-culture with LGG grown under anaerobic conditions when compared to the available in vivo mucosal transcriptomic data32,33 (Supplementary Tables 2 and 3; Supplementary Note 3).

The inoculation of HuMiX with LGG is more similar to the primocolonisation of germ-free animals than its introduction into an already mature GIT microbiome. At present, the only systematic in vivo study highlighting the host transcriptomic response to the primocolonisation by LGG was conducted in germ-free piglets34. In accordance with the findings from the latter study, our data also highlight a differential expression in eight genes (all P < 0.03, BrS; Table 1; Supplementary Note 4), which also exhibited an altered transcriptional response in mucosal tissues of gnotobiotic piglets 24 h after their inoculation with LGG34.

Caco-2 cells are known to secrete distinct cytokines analogous to immune cells when they are challenged with different microbial stimuli. More specifically, the secretion of the pro-inflammatory cytokines interleukin-8 (IL-8) and CCL20 by Caco-2 cells following direct co-culture with microbial strains42,43 or the application of cell-free microbial supernatants and/or other microbial products is well established44. Consequently, they represent a good model for assessing the specific immunological responses to different microorganisms and their products18. To test for similar responses in Caco-2 cells when co-cultured in HuMiX, we sampled eluate from the perfusion microchamber (which is in contact with the basal side of the Caco-2 cells) before and 24 h after co-culture with LGG grown under anaerobic conditions, and we screened for immunological markers, including IL-8 and CCL20 (Fig. 3b). No statistically significant increase (paired Student’s t-test (StT); P < 0.3) but an apparent slight decrease (Fig. 3b) in the pro-inflammatory cytokines released by the human epithelial cells was observed when they were co-cultured for 24 h with LGG. This observation (Fig. 3b)
is in agreement with previous findings, suggesting a subtle anti-inflammatory effect by LGG on human epithelial cells. In addition to the highlighted cytokine and transcriptional responses of Caco-2 cells, the proximal co-culture of host and microbial cells has the potential to elucidate the complex molecular crosstalk that may induce metabolic changes in the host and microbial cells. Hence, to demonstrate the potential of HuMiX for investigating metabolic interactions between human
and microbial cells and for assessing the impact of co-culture on human cellular metabolism, we conducted metabolomic analyses of the intracellular metabolite fractions from the Caco-2 cells when these were co-cultured with LGG growing under anaerobic conditions (Fig. 3c). After 24 h of co-culture, of the 313 metabolites detected, 214 (14 of which were statistically significant ($P < 0.1$, S/WT)) were more and 99 (5 of which were statistically significant ($P < 0.1$, S/WT)) were less abundant in the co-cultured Caco-2 intracellular metabolite fractions when compared with their levels in the corresponding controls (Supplementary Table 4). Sixty-eight per cent of metabolites could not be identified using available metabolite databases. Five unknown metabolites that were present in control samples were not detected in the Caco-2 metabolite fractions following co-culture. The intracellular levels of certain tricarboxylic acid cycle intermediates increased. In particular, the intracellular concentrations of fumaric acid ($FC > 3$, $P < 0.05$, S/WT), citric acid ($FC > 6$, $P < 0.05$, S/WT) and isocitric acid ($FC > 6$, $P < 0.07$, S/WT; Fig. 3c) increased significantly (Supplementary Table 4). Interestingly, the increase in tricarboxylic acid cycle intermediates agrees with the previous observations of similar increases in the blood serum of germ-free mice upon their conventionalisation.\(^{45}\)

Furthermore, the apparent decrease in intracellular concentrations of urea ($FC > 2$, $P < 0.2$, S/WT; Supplementary Table 4) after inoculation with LGG was analogous to the earlier reports describing the induced metabolic changes following the conventionalisation of germ-free mice.\(^{45}\) Our transcriptomic data further revealed that the $cps1$ gene was downregulated in Caco-2 cells following their co-culture with LGG grown under anaerobic conditions (Fig. 5a; Supplementary Fig. 8; $FC > 1.4$, $P < 0.05$, BrS). The CPS1 protein is the first and rate-limiting step of the urea cycle that converts ammonia to carbamoyl phosphate. CPS1 has previously been found to be expressed in intestinal epithelial cells.\(^{46}\) and our results suggest that microbiome-mediated modulation of ureagenesis may occur in the GIT.

Analogous to the experiments involving Caco-2 cells, we also conducted a metabolomic investigation of the intracellular LGG metabolite fractions after co-culture with Caco-2 cells and compared the results with those derived from mono-cultured LGG to further investigate crosstalk between the Caco-2 cells and LGG. Interestingly, 170 intracellular metabolites (representing 47% of all metabolites detected) were reduced or even undetectable after the co-culture with Caco-2 cells ($P < 0.05$, S/WT; Supplementary Fig. 6; Supplementary Table 5). Furthermore, the CPS1 gene was downregulated in Caco-2 cells following their co-culture with LGG grown under anaerobic conditions.

### Table 4

| Metabolite          | Measured intensity | No match | Match (Supplementary Table 4) |
|---------------------|--------------------|----------|------------------------------|
| Glutaric acid       | No match: 1,913    |          |                              |
| 2-Oxoglutaric acid  | Unknown: 1,913     |          |                              |
| Succinic acid       | No match: 1,435.90 |          |                              |
| Lactic acid         | No match: 1,465.76 |          |                              |
| 2-Hydroxybutyric acid| No match: 2,534.86 |          |                              |

**Figure 4 | Transcriptional and metabolic changes induced in human cells following their co-culture with LGG and $B. caccae$.** (a) Heat map highlighting the top 30 differentially expressed genes and miRNAs in Caco-2 cells co-cultured with either LGG alone or LGG and $B. caccae$ growing under anaerobic conditions compared with their bacteria-free controls ($n = 3$). The threshold parameters used were $FC > 2$ and $P < 0.01$, as determined using the empirical Bayes moderated $t$-statistic.\(^{45}\) Ranking was based on the $z$-values calculated using the log-fold changes and $P$ values (BS). An average linkage hierarchical clustering with the Euclidean distance metric was performed to determine the ordering of the genes. (b) Venn diagram comparing the gene expression patterns obtained when Caco-2 cells were co-cultured with LGG or with a consortium of LGG and $B. caccae$ growing under anaerobic conditions. The threshold parameters used were $FC > 1.5$ and $P < 0.01$ (BS). (c) Heat map of intracellular metabolites from Caco-2 cells co-cultured with LGG and $B. caccae$ growing under anaerobic conditions in comparison with monocultures of Caco-2 cells for which anaerobic medium was perfused through the microbial microchamber. The threshold parameter used was $P < 0.1$ (S/WT). An average linkage hierarchical clustering with the Euclidean distance metric was performed to determine the ordering of the metabolites.
The distance metric was performed to determine the ordering of the genes. The threshold parameters used were based on the $p$-values calculated using log-fold changes and $P$-values ($\leq 0.05$; Supplementary Table 5). Interestingly, following the inclusion of $B$. caccae, only 6 genes (slc9a1, elf3, myb12, gadd45b, igfbp2 and gsta1) out of the previously highlighted 19 genes (Table 1) which showed differential gene expression under an LGG anaerobic co-culture regime as well as in the in vivo human clinical studies, were identified to be differentially expressed in the Caco-2 cells. However, three additional Caco-2 genes ($ndrg3$, $hmgs2$ and $cryb1$), all FC $>1.5$, $P < 0.08$; Supplementary Note 5) earlier highlighted in human clinical trials to be differentially expressed after LGG administration were found to be differentially expressed only after co-culturing with LGG and $B$. caccae, which suggests that consortium-driven synergistic mechanisms are likely at play (Supplementary Table 6). Overall, we found that 1,638 human genes exhibited differential expression specifically when Caco-2 cells were co-cultured with LGG and $B$. caccae compared with 856 genes that were differentially expressed by Caco-2 cells when solely co-cultured with LGG (Fig. 4b; $P < 0.01$, BS). One hundred and eleven genes showed a similar expression pattern under both co-culture conditions (Fig. 4b; $P < 0.01$, BS).

Furthermore, we analysed the intracellular metabolite fractions of the Caco-2 cells to determine the induced effects as a result of the co-culture regimes involving LGG and $B$. caccae (Fig. 4c). Analogous to the transcriptional response, the intracellular metabolite fractions of the Caco-2 cells were significantly altered in response to the consortium co-culture as compared with the cells co-cultured solely with LGG (Fig. 3c; Supplementary Table 7). Our results demonstrate that the HuMiX model is capable of capturing transcriptional and metabolic responses of the human epithelial cells in response to changes in the composition of the co-cultured microorganisms.

**HuMiX-based co-cultures with a bacterial consortium.** To evaluate the effect of a bacterial consortium on Caco-2 cells, $B$. caccae and LGG were both placed in co-culture with Caco-2 cells, whereby the bacterial consortium was maintained under anaerobic conditions (Supplementary Fig. 2b). The addition of $B$. caccae lead to a significant change in the transcriptional response of the Caco-2 cells in comparison with the response when Caco-2 cells were co-cultured solely with only LGG (Fig. 4a).

fumaric acid was one of the metabolites under the detection limit after co-culture with Caco-2 cells ($P < 0.05$; Supplementary Table 5). The concomitant increase in the intracellular fumaric acid concentration in the Caco-2 cells (Fig. 3c) suggests possible cross-feeding of this metabolite between the Caco-2 and LGG cells. Furthermore, this suggests that the catalytic activity of the enzyme succinate dehydrogenase might be differently regulated in bacteria compared with human cells following their co-culture. Most of the metabolites detected (77%) did not result in a direct match in the available databases (Supplementary Fig. 6a). Interestingly, 51 of those metabolites were only discovered in the mono-cultured LGG but were not discovered in the intracellular LGG metabolite fraction after co-culture with Caco-2 cells ($P < 0.05$, S/T; Supplementary Table 5). Intriguingly, three unknown (no match) metabolites were detectable in the intracellular LGG pool only after the co-culture with Caco-2 cells ($P < 0.05$, S/T; Supplementary Table 5). These results suggest significant shifts in LGG metabolism owing to extensive cross-feeding with the human epithelial cells. Our results further confirm that despite the presence of a partitioning nanoporous membrane between the epithelial cells and LGG in the HuMiX model, there exists an efficient crosstalk between the human and microbial cells, as demonstrated by the specific physiological responses in both human epithelial and bacterial cells following their co-culture in HuMiX.

**Anaerobic or aerobic bacterial co-affects human transcriptome.** Since HuMiX offers the possibility to co-culture human cells with bacteria growing under anaerobic conditions (that is, mimicking the conditions in the GIT), we explored the potential benefits of such co-cultures in contrast to traditional co-culture approaches that maintain bacteria under aerobic conditions, which are...
likely to induce non-representative changes in bacterial metabolism\cite{31} and consequential effects in human cells. For this, we compared the gene expression patterns of Caco-2 cells following 24 h of co-culture with LGG grown under anaerobic conditions ($\leq 0.8\%$ dissolved oxygen) or aerobic conditions (21%\%; Fig. 5a,b; Supplementary Fig. 2c, Supplementary Table 8).

The generic Caco-2 response to co-culture with LGG was first determined by focusing on the genes that exhibited similar expression patterns under both LGG culture conditions compared with their respective LGG-free controls (Supplementary Fig. 2a,c; Supplementary Fig. 7). Ninety-four genes exhibited differential expression under either of the two co-culture conditions (Fig. 5b; Supplementary Fig. 7; P < 0.01, BtS). Conversely, genes that were differentially expressed under either condition were determined to be specific to one of the two conditions, that is, LGG grown under anaerobic conditions or aerobic conditions. Overall, we identified 492 human genes that exhibited differential expression specifically when Caco-2 cells were co-cultured with LGG growing under anaerobic conditions, whereas 20 genes were specifically expressed by Caco-2 cells co-cultured with aerobically growing LGG (Fig. 5a,b; Supplementary Table 8). The differential expression of cancer-related genes in cancer-derived Caco-2 cells was determined by focusing on the genes that exhibited similar expression patterns under both LGG culture conditions (Supplementary Fig. 8; Table 1). The differential expression of cancer-related genes in cancer-derived Caco-2 cells was only differentially expressed in the presence of LGG, while 20 genes were specifically expressed by Caco-2 cells co-cultured with LGG growing under anaerobic conditions, whereas 20 genes were specifically expressed by Caco-2 cells co-cultured with aerobically growing LGG (Fig. 5a,b; Supplementary Table 8).

Among the top differentially expressed genes in Caco-2 cells when co-cultured with LGG grown under anaerobic conditions, we identified four human genes (ccl2 \(P < 0.001\), egr1 \(P < 0.005\), ubd \(P < 0.05\) and slc9a1 \(P < 0.05\)) that exhibited expression patterns identical to those observed in mucosal biopsy samples obtained from healthy human subjects following the administration of the probiotic LGG (Fig. 5a; Supplementary Fig. 8; Table 1; Supplementary Table 8, all FC > 1.5, BtS). Intriguingly, when the Caco-2 cells were co-cultured with LGG growing under aerobic conditions instead, these genes were either up- or downregulated in one co-culture versus control pair situation, and exhibited the opposite trend in the other scenario (Fig. 5a; Supplementary Fig. 8). Among the genes that presented such opposing expression patterns, we identified a number of genes that play important roles in the regulation of inflammatory responses, maintenance and regulation of epithelial barrier function, mediation of host–microbe interactions, and regulation of cancer-related pathways (Supplementary Fig. 8; Supplementary Note 6). In addition, we found four genes (ccsr4, pim1, cypl1a1 and myb12, \(P < 0.05\), BtS), which had previously been identified in human clinical trials to be differentially expressed in the presence of LGG\cite{32,33}; to exhibit a more generic response to co-culture with LGG, that is, similar expression in Caco-2 cells when co-cultured with LGG under either condition (Supplementary Fig. 7; Table 1). The differential expression of cancer-related genes in cancer-derived Caco-2 cells following their co-culture with LGG is interesting and further investigations are required to determine whether this is a generic response by human epithelial cells or whether this is limited to cancer-derived cells. In all of the presented results, as the gene expression profiles of the co-cultured cells have been compared with mono-cultured Caco-2 cells, the effects observed are attributable to the influence of the co-cultured bacteria on the Caco-2 cells.

To further define the effects of LGG on Caco-2 cells when LGG was grown in two distinct oxygen conditions, a pathway enrichment analysis was conducted this time using only the Caco-2 genes that exhibited contrasting gene expression patterns (the threshold parameters used were FC > 1.5 and \(P < 0.05\), BtS; Supplementary Table 9). The pathways that exhibited differential expression based on the contrasting gene expression patterns were linked to gut motility, immune response, cell cycle, cell adhesion, apoptosis, cytoskeleton remodelling, lipid metabolism regulation, signal transduction and developmental signalling pathways (Supplementary Table 9; Supplementary Note 6). An additional data-driven pathway analysis using the gene ontology database revealed that the top enriched pathways exhibiting contrasting gene expression patterns under anaerobic or aerobic conditions were related to metabolism (more specifically, lipid, protein and carbohydrate metabolism), cellular homeostasis, amino-acid transport and particularly adaptive immune responses (Supplementary Table 10; Supplementary Note 6).

Given the pivotal role of anaerobic conditions in the GIT for the maintenance of the GIT microbiota composition\cite{47}, host–microbe mutualistic interactions\cite{48} and possibly dysbiosis\cite{49}, the obtained results represent an important validation of the HuMiX approach for representative studies of host–microbe interactions. On the basis of these results, the existing models, which typically involve the co-culturing of bacteria and human cells under aerobic conditions, induce a partial and partly non-representative transcriptional response in Caco-2 cells and this highlights the importance of maintaining anaerobic culture conditions when co-culturing GIT bacteria with human cells. The ability to maintain bacteria under anaerobic conditions therefore represents an essential functionality of the HuMiX model.

**Discovery-driven investigations of host-microbe interactions.** Although the primary purpose of our experimental work was to validate the HuMiX model in relation to already existing knowledge primarily from in vivo studies, our multi-omic data also potentially allow novel insights in the context of host–microbe molecular interactions. More specifically, the opportunity to comprehensively mimic and probe the individual cell contingents using high-resolution molecular analyses provides an unprecedented opportunity to study the effects of live bacterial cells growing under representative environmental conditions in close proximity to human cells. Here we describe interesting observations obtained following the co-culture of Caco-2 cells with LGG or with the LGG and *B. caccae* consortium when these were maintained under anaerobic conditions.

**Co-cultured microorganisms alter expression of miRNAs linked to colorectal cancer in Caco-2 cells.** Following co-culture with LGG or LGG with *B. caccae* grown under anaerobic conditions, miRNA profiling highlighted differential regulation of a vast number of miRNAs (mir483-3p, mir1229-3p, mir92b, mir1915, mir30b-5p, mir4521, mir193a-5p, mir125a-5p and mir141-3p) linked to colorectal cancer (Fig. 6). Notably, many of these have been recently added to the panels of biomarkers for diagnosis and prognosis of gastrointestinal cancers\cite{50-54}. Many of these miRNAs were only differentially expressed in the presence of LGG, while the expression of others was altered by the presence of *B. caccae* in the consortium. Despite the fact that Caco-2 cells are cancer-derived, our results demonstrate that the presence of different bacteria leads to a differential regulation of the expression of these cancer-related miRNAs. These results underpin the notion that HuMiX may prove valuable as a screening tool for identifying and validating biomarker signatures (Supplementary Note 7) and for testing microbiome-based therapeutic interventions, for example, in the context of colorectal cancer.

**LGG induces the accumulation of GABA in epithelial cells.** The intracellular accumulation of GABA (4-aminobutanoic acid) in Caco-2 cells following co-culture with LGG grown under anaerobic conditions (Fig. 3c, FC = 2.18, \(P < 0.06\), SfS; Supplementary Note 8) is similar to previous observations in pulmonary epithelial cells\cite{55}, in which GABA was found to subsequently contribute to the relaxation of smooth muscle tone\cite{56}. ccl2 (FC > 1.5, \(P < 0.001\), BtS), which was ranked among the top 10 differentially expressed genes in our co-culture experiments (Table 1) as well as in vivo transcriptomic data.
forms of glutamic acid decarboxylase that catalyses the production of GABA and to contribute to the regulation of the GABAergic neurotransmission. This may allow detailed investigations of the molecular mechanisms governing the gut–brain axis in the future.

Potential local and systemic effects of GABA administration have been shown to interact with GABA and to contribute to the regulation of the GABAergic response in neurons. In addition, the expression of the gad1 gene was slightly upregulated following the co-culture of Caco-2 cells with LGG grown under anaerobic conditions. The mechanism of GABA accumulation in the Caco-2 cells in our experiments and its potential local and systemic effects in vivo are important research questions for future HuMiX-based investigations but go beyond the scope of the present study. Given its modularity and flexibility for inclusion of additional cell types, the HuMiX model may allow detailed investigations of the molecular mechanisms governing the gut–brain axis in the future.

**Conclusion.** Our detailed experimental results demonstrate that HuMiX is a representative model of the gastrointestinal human–microbe interface, as individual transcriptional responses from human epithelial cells co-cultured with LGG inside HuMiX are in agreement with in vivo data. HuMiX also allows discovery-based studies particularly in relation to proving causal relationships between gastrointestinal microbiota and human diseases. Although HuMiX was developed with a focus on host–microbe interactions, it may find applications in a number of other domains including drug screening, drug discovery, drug delivery as well as in pharmacokinetics and nutritional study. The ability to co-culture human and microbial cells in a controlled manner and perform systematic investigations of such co-cultures opens up numerous avenues for basic and applied research in the context of the human microbiome in the future.

**Methods**

**Fabrication and assembly of the HuMiX device.** The HuMiX device is comprised of two polycarbonate (PC) enclosures, which sandwich silicone rubber gaskets, which are themselves attached to semi-permeable PC membranes (Fig. 1b). Anaerobic bacteria-free control

Normalised expression

| Normalised expression | Anaerobic bacteria-free control | Anaerobic LGG co-culture | Anaerobic co-culture with LGG + B. caccae |
|-----------------------|---------------------------------|--------------------------|------------------------------------------|
| −1                    |                                 |                          |                                          |
| 0                     |                                 |                          |                                          |
| 1                     |                                 |                          |                                          |

**Figure 6 | Co-culture regime-specific miRNA expression.** Heat map of the top 30 statistically significant differentially expressed genes in Caco-2 cells when comparing their expression after co-culture with LGG, LGG and B. caccae and their corresponding bacteria-free controls. The threshold parameters used were FC >1.5 and P < 0.05 (BH). An average linkage hierarchical clustering with the Euclidean distance metric was performed to determine the ordering of the genes.

Coating of the membranes and permeability assays. After autoclaving, the 1-μm pore size PC membranes were exposed to ultraviolet for 10–20 min under a laminar flow bench before assembly.

Sterilisation of the HuMiX device. A robust sterilisation procedure was developed and optimised to completely avoid both fungal and bacterial contamination in any of the microchambers. All the parts (enclosures, gaskets, screws, nuts, syringe needles, peristaltic pump tubings, media bottles, etc.) were autoclaved at 110 °C for 60 min. Before assembly of the microchambers, the PC enclosures were thoroughly cleaned with 70% v/v ethanol and air dried for 30 min under sterile conditions. The thickness of the mucin layer was measured using confocal laser scanning microscopy by embedding 4 kDa fluorescein isothiocyanate-conjugated dextran (Sigma-Aldrich) solution for 1 h. Excess solution was removed after the coating procedure and the membranes were air dried for 30 min under sterile conditions. The thickness of the mucin layer was measured using confocal laser scanning microscopy by embedding 4 kDa fluorescein isothiocyanate-conjugated dextran (Sigma-Aldrich) solution for 1 h.
Maintenance of cells and microbial cultures. The human epithelial colorectal cell line Caco-2 (DSMZ: ACC169) and non-cancerous colonic cell line CDD-18Co (ATCC: CRL-1630) were maintained at 37°C with 5% CO₂ in air, 200 r.p.m., D-MEM supplemented with 20% FBS (Life Technologies) and 1% penicillin–streptomycin (Sigma-Aldrich) until use and viability (Supplementary Fig. 4a,b). The human epithelial colorectal cell line Caco-2 (DSMZ: ACC169) was cultured in anoxic DMEM medium supplemented with 20% FBS without antibiotics in a shaking incubator at 37°C and 200 r.p.m. B. caccae (DSMZ: 19024) was cultured in aerobic DMEM medium supplemented with 20% FBS and haeme or HBIM medium. Subsequently, the inoculation of the microbial cells into HuMiX device, the microbial suspensions were pelleted and washed with 0.9% NaCl before suspending them in 5 ml fresh anoxic DMEM medium.

HuMiX co-cultures involving Caco-2 cells. Before inoculation of the Caco-2 cells into the HuMiX device, the tubes (peristaltic pump tubes as well as the tubes to be later connected to the HuMiX devices) were connected to 0.5-ml serum bottles (Glasgerätebau Ochs) containing the culture media (Fig. 1d). The HuMiX device was then integrated into the tubing set-up by attaching the elastomeric tubing to the connectors of the HuMiX device. To prime the HuMiX device, DMEM medium supplemented with 20% FBS was perfused at 1.5 ml min⁻¹ through all the channels of the HuMiX device using a programmable 205CA peristaltic pump (Watson Marlow). After the priming of the HuMiX device, the tubing set-up was moved to a laminar flow bench and inoculated with human epithelial cells (Caco-2 by injecting a 1-ml cell suspension (6 × 10⁵ cells per ml) into the human microchamber using a sterile syringe (Becton Dickinson) via a Discofax three-way adaptor (B. Braun). Subsequently, the HuMiX device was incubated at 37°C without flow for 2 h to allow attachment of the cells to the collagen-coated microporous membrane. After 2 h, the Caco-2 cells were perfused at their basal side via the perfusion microchamber with DMEM medium supplemented with 20% FBS at a flow rate of 25 ml min⁻¹. Perfusion through the microchamber was simultaneously initiated. If the Caco-2 cells were less to be co-cultured with LGG or LGG and B. caccae grown under anaerobic conditions, perfusion with aerobic DMEM medium was carried out at the same flow rate of 25 ml min⁻¹. Anoxic DMEM medium was obtained by constantly bubbling the medium with nitrogen gas through a sterile oxygen needle placed inside the medium bottle (B. Braun). For each microchamber prepared in this condition (LGG grown under either anaerobic or aerobic conditions, Supplementary Fig. 2a,c), human epithelial cells were introduced into the microbial microchamber on day 7 following the initiation of the Caco-2 cell culture. At day 7, the Caco-2 cells were found to have formed tight junctions (Fig. 2b) and the cell number (~1 × 10⁶) reached a value above 90% of the confluent state. LGG or LGG and B. caccae cell suspensions were then introduced into the microbial microchamber using a Discofax two-way adaptor in a 1-ml suspension (OD ~1) and later perfused with anoxic or aerobic DMEM medium at 25 ml min⁻¹. Following 24 h of co-culture, the devices were disassembled and the human and microbial gaskets were separated. For further detailed analyses, the gaskets were divided into three parts, whereby half of the cell-covered membranes were used for extraction of the intracellular metabolites, DNA, RNA and proteins using a comprehensive bioluminescence extraction protocol. The other two quarters were used for live–dead staining or LGG (Supplementary Fig. 4c,d) or cultured in the presence of LGG (Supplementary Fig. 4e,f) was determined using the LIVE/DEAD fixable near IR cell kit (Molecular Probes) and flow cytometry.

Oxygen sensing. The integrated optical sensors (optodes) allowed for continuous, non-invasive and non-cytotoxic detection of oxygen levels in the HuMiX device (Fig. 1a; Supplementary Fig. 1c). The 5-mm diameter optodes (sensitivity of up to 0.03% of O₂) were bonded into the 1.2-mm deep machined pockets by using a UV-curable adhesive (PreSens) or B. caccae cell suspensions were affixed to both PC enclosures 20 mm adjacent to the inlets and outlets of the perfusion microchamber and microbial microchamber, respectively (Fig. 1a; Supplementary Fig. 1a). For microbial staining and visualisation, one quarter of the membranes was stained using the L7007 BacLight microbial viability kit (Molecular Probes). The oxygen concentration was measured every 15 min using an OXY-4 trace oxygen transmitter/recorder (PreSens) and logged using the oxy4v2_41FB software (PreSens) using a connected personal computer.

Epithelial barrier measurements. As detailed above, a dedicated HuMiX-TEER device was fabricated to allow measurement of TEER using a STX2 electrode connected to a Millécill ERS-2 Epithelial Volt-Ohm Meter during cell culture trials in HuMiX (Millipore; Supplementary Fig. 1d). For this, double-electrode pairs of the STX2 electrodes were introduced into the perfusion and microbial microchambers, respectively. Before inoculation of the human cells, TEER values were recorded to determine the background resistance of the HuMiX device after all the channels were filled with DMEM medium. The background TEER was subtracted from the readings subsequently to infer the growth curve of Caco-2 cells by following the increase in resistance. As the insertion of chopstick electrodes through the side ports can lead to contamination of the experiment, the TEER measurements were conducted as an end point assay and related to epithelial barrier function ascertained following immunostaining and fluorescence microscopic analyses. The HuMiX-TEER device was in particular used to determine the optimal point in time when the cells had differentiated for the subsequent immunostaining of bacteria into the adipose. As a reference, Candida albicans (C. albicans) was inoculated in the standard Transwell systems and supplied with antibiotic-free DMEM medium analogous to the cultivation conditions in HuMiX. Here again, the background TEER was also measured in Transwell inserts before inoculation with Caco-2 cells and later subtracted from the actual TEER readings.

Cytokine profiling of eluate samples. To assess possible immunological responses of the epithelial cells to the co-cultured bacteria, 150 – 200 µl of eluate samples was collected from the perfusion microchamber, flash-frozen and preserved at ~ 80°C until further analysis. A measure of 50 µl of the eluates collected from the perfusion microchamber before and after inoculation with LGG was analysed for eight different cytokines using a Human Premixed Multi-Analyte Assay Kit (Luminex Systems, Europe; UK) in combination with the Luminex MAGPIX (Luminex) according to the manufacturers’ instructions. The kit allowed screening for the following human cytokines of interest: CXCL8/L-8, CCL20/MIP-3 alpha, GM-CSF, IL-1 beta, IL-6, IL-10, IL-12p70 and TNF-alpha. Only CCL20 and IL-8 were detectable in the samples.

Sampling of cellular material post culture. Twenty-four hours after the initiation of co-culture of Caco-2 cells with LGG or LGG and B. caccae, perfusion of the device was stopped and the device was disassembled using a manual screwdriver. The gasket–membrane assemblies bearing the cells (Caco-2 or LGG or LGG and B. caccae) were then cut into two halves: one half was used for comprehensive bioluminescence extractions and the other half for microscopic inspection.

Live-dead analyses. Live-dead staining was performed for determining Caco-2 and bacterial cell viability. The Calbiochem kit (Millipore) was used on the microporous membranes containing the Caco-2 cells, whereas the BacLight microbial viability kit (Molecular Probes) was applied to the nanoporous membranes containing LGG or LGG and B. caccae. Before staining the membrane-bound Caco-2 cells, the membranes were separated from the gaskets using 200 µl of a staining buffer from the ‘TEER’ chamber, then applied to one quarter of the membranes and incubated at 37°C for 15 min. After perfusion and visualisation, one quarter of the membranes was stained using the L7007 BacLight microbial viability kit (Molecular Probes). A measure of 200 µl of staining solution was prepared as per the manufacturer’s recommendations and applied to the gaskets followed by incubation at 37°C for 5 min. After removal of the staining buffer, the unstained samples were removed by washing of the membrane-bound human and microbial cells with 1 × PBS.
solution at pH 7.2. The stained cells on the membranes were then fixed in a 4% paraformaldehyde (PFA)/1 × PBS solution for 10 min at room temperature in the dark. After an additional wash in 1 × PBS, the fixed membranes were mounted on microscope slides using ProLong Gold anti-fading mounting medium (Life Technologies, Europe). The microscope slides were then allowed to dry overnight at room temperature in the dark and observed at appropriate excitation wavelengths using a Zeiss 710 Meta confocal laser scanning microscope to evaluate the morphology and viability of the cells.

**Fluorescence microscopic analysis of co-cultured cell contingents.** Apart from live–dead staining, the membrane-bound human and microbial cells were also stained with specific dyes and analysed by fluorescence microscopy. For the detection of occludin, a quarter of the microporous membranes covered by the Caco-2 cells were fixed in a 4% (v/v) PFA/PBS solution for 10 min at room temperature, washed with 1 × PBS and then blocked for 15 min with 5% bovine serum albumin (BSA; Sigma–Aldrich) in 1 × PBS. The cells were then stained with anti-Occludin mAb Mouse Alexa Fluor 488 conjugate (Life Technologies, Europe) diluted 1/200 in 1% (v/v) BSA/PBS solution for 30 min at room temperature in the dark. Subsequently, the membrane-bound cells were washed three times with 1 × PBS to SuperFrost Plus microscope slides (Menzel) and subsequently labelled antibodies. For staining the Caco-2 cell nuclei, 200 μl of Hoechst stain (Life Technologies, Europe) diluted 1:1,000 in 1% (v/v) BSA/PBS solution was applied to the cells and incubated for 2 min at room temperature in the dark. After three consecutive washes in 1 × PBS, excess solution was removed and the membranes were mounted on a microscope slide using ProLong Antifade Reagent (Life Technologies, Europe). The microscope slides were then allowed to dry overnight at room temperature in the dark and observed at appropriate excitation wavelengths using a Zeiss 710 Meta confocal laser scanning microscope to visualise cell nuclei and tight junctions.

The membrane-bound LGG or LGG and B. caccae cells were fixed by applying a 4% (v/v) PFA/PBS solution at room temperature for 10 min. After three washes in 1 × PBS to remove excess fixing solution, the membranes were mounted on microscope slides using the ProLong Antifade Reagent (Life Technologies, Europe) and the cells were visualised using a Zeiss 710 Meta confocal microscope.

**Microscopic image processing.** Confocal image z-stacks were acquired using the Zeiss Zen Black software suite. Z-stacks were processed using Imaris 8 (Bitplane AG) coupled with the AutoQuant suite (x 3.0.0, Media Cybernetics) for background correction.

**Biomolecular extractions.** For biomolecular extractions on the adherent Caco-2 cells, the gasket–membrane assemblies were first washed in a 0.9% (w/v) NaCl solution. The cells were then immediately treated with 800 μl of an ice-cold 1:1 methanol:water (v/v) solution. Subsequently, the cells were disrupted and detached from the membranes using a plastic scraper (VWR). The methanol:water suspension containing cells was then placed into a 2-ml sample tube and 400 μl of ice-cold chloroform were added. The mixture was vortexed and centrifuged at 14,000 r.p.m. (21,475 g) for 5 min to separate the polar and non-polar metabolite phases and to concentrate the interference pellets that were subsequently used for the extraction of biomacromolecules (RNA, DNA and proteins)36. The Caco-2 interphase pellets were then processed using the Qiagen AllPrep DNA/RNA/Protein Mini Kit (Qiagen). Complementary DNA (cDNA) synthesis was carried out on the extracted RNA using the SuperScript III First-Strand Synthesis System (Life Technologies, Europe). Equal amounts of cDNA were amplified in combination with sequence-specific forward and reverse primers (Eurogentec). The amplification reaction took place in a total volume of 20 μl of reaction mixture, whereby primers (Supplementary Table 11) were added at a concentration of 10 μM, 10 μl of iQ SYBR Green Supermix (Bio-Rad) and the remaining volume was adjusted for the cDNA amount with water. To normalise the messenger RNA expression for each analysed sample, the human house-keeping gene L27 was amplified using the same reaction conditions. Real-time PCR was carried out on a LightCycler 480 Real-Time PCR System (Roche) using a denaturation step of 95 °C for 3 min followed by 45 cycles of 95 °C for 30 s, 60 °C for 30 s and 72 °C for 20 s, respectively. Cq values were obtained using automatic baseline and threshold settings provided by the LightCycler 480 Software, Version 1.5. Data were analysed and normalised using the ‘advanced relative quantification’ method. Individual targets were analysed in three biological replicates and represented as a mean. Statistical significance was calculated using a paired Student’s t-test.

**Data analyses.** The microarray gene expression data were pre-processed using the GC-RMA procedure for background correction, quantile normalisation and probe replicate summarisation implemented in the germa R-package62. All statistical analyses were performed in the R Statistical Programming Environment63 and all differential expression analyses were carried out using the R-package limma64. Differential expression of genes between anaerobic co-cultures, aerobic co-cultures and their corresponding control samples was analysed using the empirical Bayes moderated t-statistic65. To account both for significance and effect size, the final ranking of genes was determined using the π-value, a statistic combining the P value significance and logarithmic FC (log FC) into a single score66. Only genes with known functional annotations were considered for further analysis. Genes were considered differentially altered between anaerobic and aerobic conditions under the different experimental conditions (Supplementary Fig. 3) were identified and scored as follows: first, the π-value for differential expression between co-culture and control samples was determined for each gene as described above, once for anaerobic samples and once for aerobic samples. Next, the genes in the two π-value sets were determined analogously, only changing the above procedure by filtering such that only genes were retained for which the sign of the log-FC was the same for anaerobic and aerobic samples. The final ranking for these genes was obtained from the sum of ranks for the two π-value rankings (that is, sorting the genes by decreasing π-values for both anaerobic and aerobic samples and summing up the ranks for each gene). Genes with shared expression profiles were determined analogously, only changing the above procedure by filtering such that only genes were retained for which the sign of the log FC was the same for anaerobic and aerobic samples.

For the analysis of altered cellular pathways, the GeneGo MetaCore software suite was used with the differential expression statistics from the empirical Bayes moderated t-statistic as input data. The pathways were pre-filtered using a P value significance threshold (P < 0.05) before applying the GeneGO analysis. To investigate the global gene expression alterations in biological processes of the...
gene ontology (GO) database, we determined all GO processes covered by at least 10 genes in the microarray data set and computed the median gene expression levels across process members for each of these GO processes. Significantly altered processes were then determined by applying the empirical Bayes moderated t-statistic again.

Finally, to visualize the expression of the genes or levels of the metabolites in the different experimental conditions, heat maps and dendrogram visualisations were generated using the gplots R-package (http://cran.r-project.org/web/packages/gplots) and an average linkage hierarchical clustering with the Euclidean distance metric to determine the ordering of the genes and metabolites. Gene expression measurements were converted to Z-scores and visualised by a colour gradient, where blue colours represent lower Z-scores and yellow colours stand for higher Z-scores (the colour darkness in each heat map is proportional to the absolute Z-score). A different colour scheme was used for the metabolite plots (light blue and pink). All box plots were created using the standard R boxplot function.

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Author contributions

P.S., M.E., F.Z. and P.W. conceptualized the HuMiX model. P.S., J.V.F., M.S.D., K.G., A.F., M.N., M.E., C.S.-D., F.Z. and P.W. developed the experimental plan. P.S. and M.E. prototyped the device. P.S., J.V.F., M.N., K.G. and A.F. conducted the co-culture experiments. C.J. conducted metabolite analyses. P.S., J.V.F., E.G. and P.W. analysed the data. P.S., J.V.F. and P.W. wrote the manuscript. All authors commented on and approved the final version of the manuscript.

Additional information

Accession codes: The metabonomic data have been deposited in the MetaboLights database under the accession code MTBLS328. The transcriptomic data have been deposited in the Gene Expression Omnibus (GEO) database under accession code GSE79383.

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Competing financial interests: The authors have a corresponding patent application (WO/2013/144253), which is currently pending.

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