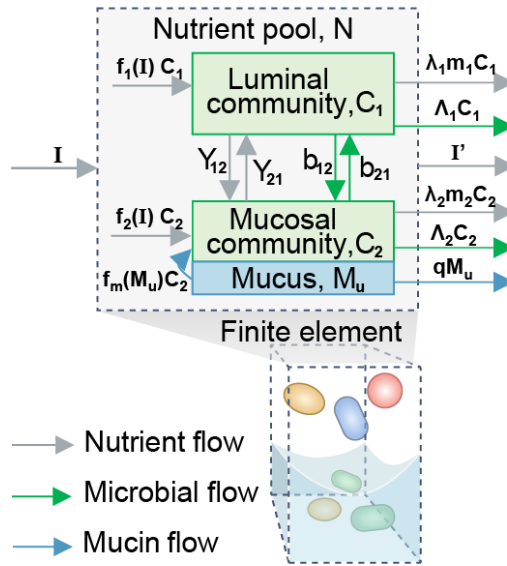


508 **Supplementary Information**

509

510 A mathematical model describing the MLI ecosystem based on mass-flow:



511

512 In order to describe the gut ecosystem, a finite element is taken from the MLI. This finite element  
 513 includes a luminal microbial community (size:  $C_2$ ), a mucosal microbial community (size:  $C_1$ ), a nutrient  
 514 pool of the gut lumen (size:  $N$ ), and a nutrient pool of the mucus (size:  $M_u$ ).

515 Other parameters shown in the figure are:

- 516 •  $I$ , constant input of nutrient per unit time
- 517 •  $I'$ , un-used nutrient per unit time (parts that are not involved in metabolism)
- 518 •  $f_i(I)$ , functional response of community  $i$  to nutrient availability
- 519 •  $\lambda_i$ , fraction of nutrient lost from community  $i$
- 520 •  $m_i$ , release of nutrient from community  $i$  due to metabolism & mortality

- 521 •  $Y_{ij}$  syntrophic interactions in which  $C_i$  provides nutrients to  $C_j$
- 522 •  $\Lambda_i$ , fraction of bacterial loss due to continuous flow in community i
- 523 •  $\Lambda$ , total bacterial loss due to continuous flow
- 524 •  $b_{ij}$ , bacterial dispersal from  $C_i$  to  $C_j$

525 where,  $i, j \in [1, 2], i \neq j$

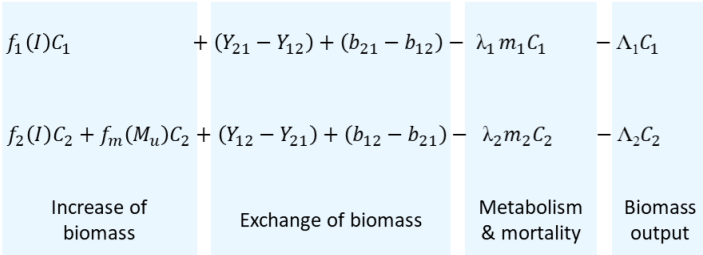
526

527 System dynamics can be described using the following equation:

i. Bacterial communities: biomass dynamics

$$\frac{dC_1}{dt} = f_1(I)C_1 + (Y_{21} - Y_{12}) + (b_{21} - b_{12}) - \lambda_1 m_1 C_1 - \Lambda_1 C_1 \quad (1)$$

$$\frac{dC_2}{dt} = f_2(I)C_2 + f_m(M_u)C_2 + (Y_{12} - Y_{21}) + (b_{12} - b_{21}) - \lambda_2 m_2 C_2 - \Lambda_2 C_2 \quad (2)$$



ii. Nutrient pool dynamics

$$\frac{dN}{dt} = I - I' - \lambda_1 m_1 C_1 - \Lambda_1 C_1 - \lambda_2 m_2 C_2 - \Lambda_2 C_2 \quad (3)$$

528

iii. Growth of microbial communities

Assume logistic growth of both communities

$$\text{Increase of biomass} \quad f_1(I)C_1 - \lambda_1 m_1 C_1 = r_1 C_1 \left(1 - \frac{C_1}{K_1}\right) \quad (4)$$

$$\text{metabolism \& mortality:} \quad f_2(I)C_2 + f_m(M_u)C_2 - \lambda_2 m_2 C_2 = r_2 C_2 \left(1 - \frac{C_2}{K_2}\right) \quad (5)$$

Where,  $r_i$  intrinsic rate of natural growth;  $K_i$  carrying capacity of the system

$$\text{At equilibrium:} \quad \frac{dC_i}{dt} = 0 \quad (6)$$

$$\text{hence} \quad C_i^* = K_i \frac{r_i - \Lambda_i \pm \sqrt{(r_i - \Lambda_i)^2 + 4 \frac{r_i}{K_i} (\Delta Y_{ij} + \Delta b_{ij})}}{2r_i} \quad (7)$$

529

530

531 Thus, if assume logistic growth of both mucosal and luminal communities, an equilibrium may be  
532 achieved in relation to ecosystem carrying capacity (nutrients from food and mucus), intrinsic rate of  
533 growth (microbial community activities), bacterial loss ratio (bowel movement), as well as syntrophic  
534 interactions and bacterial dispersal between the two communities. Assumptions/parameters need to be  
535 improved/determined by experiments. Metaproteomics will be an adequate tool for obtaining the data.