

Table S2. Region-specific microbial colonization in the SHIME[®]. Average (\pm SD) levels (log (cells/mL)) of different bacterial families encountered in all proximal colon (PC) and distal colon (DC) vessels during the last week of the control period (n=9). The p-value has been indicated in bold when significant differences ($p < 0.05$) were obtained between the different colon regions. In addition, the intensity of the shading correlates with the absolute abundance, normalized for each of the different families (i.e., within each row).

Phylum	Family	Abundance				p-value
		PC		DC		
		Average	SD	Average	SD	
Actinobacteria	<i>Bifidobacteriaceae</i>	8.21	0.10	8.43	0.16	0.0057
	<i>Coriobacteriaceae</i>	6.66	0.08	6.82	0.20	0.0862
	<i>Microbacteriaceae</i>	7.40	0.84	7.55	0.65	0.3365
	<i>Micrococcaceae</i>	7.06	0.25	7.22	0.15	0.0604
Bacteroidetes	<i>Bacteroidaceae</i>	8.59	0.22	8.74	0.10	0.0319
	<i>Bacteroidia_unclassified</i>	<LOQ	0.00	6.26	0.13	0.0000
	<i>Barnesiellaceae</i>	<LOQ	0.00	5.99	0.11	0.0000
	<i>Marinifilaceae</i>	<LOQ	0.00	6.25	0.14	0.0000
	<i>Prevotellaceae</i>	6.27	0.74	6.20	0.32	0.4344
	<i>Rikenellaceae</i>	5.47	1.83	6.83	0.10	0.0042
	<i>Tannerellaceae</i>	6.79	0.41	7.57	0.10	0.0000
Epsilonbacteraeota	<i>Campylobacteraceae</i>	5.29	2.67	5.23	2.85	0.6857
Firmicutes	<i>Acidaminococcaceae</i>	7.15	0.18	7.45	0.14	0.0009
	<i>Bacillaceae</i>	5.92	0.15	<LOQ	2.84	0.0019
	<i>Christensenellaceae</i>	<LOQ	0.00	6.37	0.16	0.0000
	<i>Clostridiaceae_1</i>	5.96	0.59	5.17	2.64	0.0333
	<i>Defluviitaleaceae</i>	<LOQ	0.00	6.10	0.29	0.0000
	<i>DTU014_fa</i>	<LOQ	0.00	5.69	2.54	0.0001
	<i>Enterococcaceae</i>	6.44	3.18	6.47	3.18	0.9890
	<i>Erysipelotrichaceae</i>	<LOQ	0.00	6.12	0.22	0.0000
	<i>Eubacteriaceae</i>	<LOQ	0.00	6.75	0.13	0.0000
	<i>Family_XIII</i>	<LOQ	0.00	6.67	0.16	0.0000
	<i>Firmicutes_unclassified</i>	5.13	2.79	5.30	2.86	0.9607
	<i>Lachnospiraceae</i>	8.38	0.17	8.79	0.07	0.0000
	<i>Paenibacillaceae</i>	5.55	3.00	<LOQ	2.68	0.8769
	<i>Planococcaceae</i>	6.11	0.22	5.44	1.83	0.0621
	<i>Ruminococcaceae</i>	6.63	0.33	7.68	0.11	0.0000
<i>Veillonellaceae</i>	9.16	0.04	9.20	0.10	0.3927	
Lentisphaerae	<i>vadinBE97</i>	<LOQ	0.00	6.50	0.21	0.0000
	<i>Victivallaceae</i>	<LOQ	0.00	6.59	0.34	0.0000
Proteobacteria	<i>Burkholderiaceae</i>	6.60	0.36	6.81	0.15	0.0373
	<i>Desulfovibrionaceae</i>	6.27	2.66	7.67	0.13	0.0030
	<i>Enterobacteriaceae</i>	7.91	0.54	7.23	0.42	0.0312
	<i>Pseudomonadaceae</i>	7.12	0.68	7.16	0.26	0.0572
	<i>uncultured</i>	6.41	3.41	6.19	2.04	0.0848
Synergistetes	<i>Synergistaceae</i>	<LOQ	0.00	5.38	2.99	0.0225
Verrucomicrobia	<i>Akkermansiaceae</i>	<LOQ	0.00	6.45	0.60	0.0000
	<i>Puniceicoccaceae</i>	<LOQ	0.00	6.01	0.38	0.0000