

Table S2. Differential abundance analysis reporting the significant variation at genus level.

Genus	Log2 Fold Change*	p-value	adjusted p-value
<i>Bifidobacterium</i>	2,7558	3,97 x 10 ⁻¹⁵	7,93 x 10 ⁻¹³
<i>Parasutterella</i>	3,0901	3,12 x 10 ⁻¹³	3,12 x 10 ⁻¹¹
<i>Mogibacterium</i>	-2,8128	3,07 x 10 ⁻¹¹	2,05 x 10 ⁻⁰⁹
<i>Oxalobacter</i>	5,8482	1,28 x 10 ⁻⁰⁷	6,39 x 10 ⁻⁰⁶
<i>Faecalibacterium</i>	-1,7174	2,49 x 10 ⁻⁰⁷	9,81 x 10 ⁻⁰⁶
<i>Lactobacillus</i>	1,1807	2,94 x 10 ⁻⁰⁷	9,81 x 10 ⁻⁰⁶
<i>Campylobacter</i>	1,372	1,22 x 10 ⁻⁰⁶	3,49 x 10 ⁻⁰⁵
<i>Collinsella</i>	-4,6674	5,23 x 10 ⁻⁰⁶	1.19 x 10 ⁻⁰⁴
<i>Oribacterium</i>	-2,1668	5,40 x 10 ⁻⁰⁶	1.19 x 10 ⁻⁰⁴
<i>Lachnobacterium</i>	-1,6558	1,57 x 10 ⁻⁰⁵	3.13 x 10 ⁻⁰⁴
<i>Fournierella</i>	-1,9893	1,73 x 10 ⁻⁰⁵	3.14 x 10 ⁻⁰⁴
<i>Mediterranea</i>	-3,8855	1,92 x 10 ⁻⁰⁵	3.19 x 10 ⁻⁰⁴
<i>Gemmiger</i>	-1,4709	3,03 x 10 ⁻⁰⁵	4.66 x 10 ⁻⁰⁴
<i>Cellulosilyticum</i>	2,7283	5,98 x 10 ⁻⁰⁵	8.54 x 10 ⁻⁰⁴
<i>Coproccoccus</i>	-1,9272	6,70 x 10 ⁻⁰⁵	8.93 x 10 ⁻⁰⁴
<i>Sutterella</i>	-1,3979	1.25 x 10 ⁻⁰⁴	1.54 x 10 ⁻⁰³
<i>Slackia</i>	-2,9637	1.32 x 10 ⁻⁰⁴	1.54 x 10 ⁻⁰³
<i>Alistipes</i>	1,0593	1.39 x 10 ⁻⁰⁴	1.54 x 10 ⁻⁰³
<i>Ruminococcus</i>	1,3224	3.81 x 10 ⁻⁰⁴	3.99 x 10 ⁻⁰³
<i>Lachnoclostridium</i>	0,60017	3.99 x 10 ⁻⁰⁴	3.99 x 10 ⁻⁰³
<i>Butyricicoccus</i>	-1,1101	4.33 x 10 ⁻⁰⁴	4.12 x 10 ⁻⁰³
<i>Fibrobacter</i>	1,1034	9.28 x 10 ⁻⁰⁴	8.44 x 10 ⁻⁰³
<i>Petrimonas</i>	3,8546	9.72 x 10 ⁻⁰⁴	8.45 x 10 ⁻⁰³
<i>Ruthenibacterium</i>	-1,535	1.62 x 10 ⁻⁰³	1.34 x 10 ⁻⁰²
<i>Parabacteroides</i>	0,77954	1.72 x 10 ⁻⁰³	1.34 x 10 ⁻⁰²
<i>Solitalea</i>	1,5431	1.74 x 10 ⁻⁰³	1.34 x 10 ⁻⁰²
<i>Corynebacterium</i>	-2,1777	1.93 x 10 ⁻⁰³	1.43 x 10 ⁻⁰²
<i>Lachnospira</i>	-1,3854	2.26 x 10 ⁻⁰³	1.58 x 10 ⁻⁰²
<i>Ruminiclostridium</i>	0,6677	2.30 x 10 ⁻⁰³	1.58 x 10 ⁻⁰²
<i>Phascolarctobacterium</i>	1,2654	3.38 x 10 ⁻⁰³	2.23 x 10 ⁻⁰²
<i>Anaerotruncus</i>	0,84996	3.57 x 10 ⁻⁰³	2.23 x 10 ⁻⁰²
<i>Enterorhabdus</i>	-1,8791	3.58 x 10 ⁻⁰³	2.23 x 10 ⁻⁰²
<i>Angelakisella</i>	0,78807	3.72 x 10 ⁻⁰³	2.25 x 10 ⁻⁰²
<i>Paraeggerthella</i>	-1,9912	3.96 x 10 ⁻⁰³	2.26 x 10 ⁻⁰²
<i>Oscillospira</i>	0,55307	3.99 x 10 ⁻⁰³	2.26 x 10 ⁻⁰²
<i>Peptococcus</i>	-1,0756	4.08 x 10 ⁻⁰³	2.26 x 10 ⁻⁰²
<i>Dorea</i>	-1,1646	5.70 x 10 ⁻⁰³	3.08 x 10 ⁻⁰²
<i>Taibaiella</i>	1,1028	7.73 x 10 ⁻⁰³	4.02 x 10 ⁻⁰²
<i>Anaerobium</i>	1,579	7.84 x 10 ⁻⁰³	4.02 x 10 ⁻⁰²
<i>Blautia</i>	-0,79387	8.87 x 10 ⁻⁰³	4.36 x 10 ⁻⁰²
<i>Filobacterium</i>	2,8164	8.95 x 10 ⁻⁰³	4.36 x 10 ⁻⁰²
<i>Bacteroides</i>	1,0571	9.57 x 10 ⁻⁰³	4.54 x 10 ⁻⁰²
<i>Rubrivirga</i>	2,8509	9.76 x 10 ⁻⁰³	4.54 x 10 ⁻⁰²

* changes in genus-level abundance refer to co-feed integration over time (T2 vs T0).