

Table S1: Primary organ failure upon admission to PICU and survival of patients by admission

<b>Primary Organ Failure</b>	<b>Number (%)</b>	<b>Survival (%)</b>
Neurological	14 (20.6)	14/14 (100)
Respiratory	21 (30.9)	19/21 (90.5)
Sepsis	27 (39.7)	27/27 (100)
Trauma/Surgical	6 (8.8)	5/6 (83.3)
TOTAL	68 (100)	65/68 (95.5)

Table S2: Antimicrobial usage for patients with microbiome profiles. Antibiotics are grouped by structural class. Inhibitors are Tazobactam and Clavulanic acid.

<b>Antimicrobial/Inhibitor</b>	<b>Patients (%)</b>
Aminoglycosides	10 (23.3)
Amphenicols	1 (2.3)
Cephalosporins	28 (65.1)
Glycopeptides	3 (7.0)
Lincosamides	8 (9.3)
Macrolides	11 (25.6)
Metronidazole	2 (4.7)
Penicillins	15 (34.9)
Quinolones	2 (4.7)
$\beta$ -lactam inhibitors	13 (30.2)

Table S3: Spearman's rank correlation ( $\rho$ ) of bacterial abundance to bile acid relative concentration measured from patient faecal samples. **Bold face** indicates significance  $p \leq 0.05$ , italic face indicates  $p$ -value  $0.05 < p \leq 0.1$ .  $n=15$  patient samples. Underlined Genera belong to the Lachnospiraceae

<b>Genus</b>	<b>p-value (tLCA)</b>	<b><math>\rho</math>[15] (tLCA)</b>	<b>p-value (DCA)</b>	<b><math>\rho</math>[15] (DCA)</b>
<i>Actinomyces</i>	<b>0.049</b>	<b>0.516</b>	0.564	0.162
<u><i>Agathobacter</i></u>	<i>0.071</i>	<i>0.480</i>	<b>0.006</b>	<b>0.671</b>
<i>Anaerovorax</i>	<b>0.005</b>	<b>0.681</b>	<b>0.004</b>	<b>0.700</b>
<i>Barnesiella</i>	<b>0.028</b>	<b>0.564</b>	<b>0.047</b>	<b>0.521</b>
<i>Collinsella</i>	<b>0.117</b>	<b>0.422</b>	<b>0.047</b>	<b>0.520</b>
<u><i>Coprococcus</i></u>	<i>0.067</i>	<i>0.484</i>	<b>0.046</b>	<b>0.522</b>
<u><i>Dorea</i></u>	<b>0.049</b>	<b>0.516</b>	0.124	0.415
<u><i>Anaerobutyricum hallii</i> group</u>	<b>0.044</b>	<b>0.527</b>	0.138	0.401
<i>Eubacterium oxidoreducens</i> group	0.129	0.410	<b>0.018</b>	<b>0.602</b>
<i>Faecalitalea</i>	<b>0.019</b>	<b>0.597</b>	0.185	0.362
<i>Gordonibacter</i>	<b>0.003</b>	<b>0.710</b>	0.143	0.397
<i>Incertae sedis</i>	<b>0.032</b>	<b>0.554</b>	0.111	0.429
<i>Odoribacter</i>	<b>0.026</b>	<b>0.572</b>	<i>0.085</i>	<i>0.459</i>
<i>Paraprevotella</i>	0.238	0.324	<b>0.019</b>	<b>0.595</b>
<i>Parasutterella</i>	<b>0.021</b>	<b>0.588</b>	0.427	0.222
<i>Pseudoflavonifractor</i>	<b>0.021</b>	<b>0.587</b>	0.209	0.344
<i>Romboutsia</i>	<b>0.018</b>	<b>0.600</b>	0.390	0.240
<i>Solobacterium</i>	<b>0.008</b>	<b>0.657</b>	0.125	0.414
<i>Sutterella</i>	0.306	0.284	<b>0.049</b>	<b>0.516</b>
<i>Turicibacter</i>	<b>0.008</b>	<b>0.653</b>	<b>0.037</b>	<b>0.542</b>

Table S4: Spearman's rank correlation ( $\rho$ ) between Lachnospiraceae bacteria counts and other bacterial counts in samples collected on days 8-10 of hospitalization. Eleven samples were collected from hospitalized children during days 8-10. Bacteria with negative correlations to are underlined. Values of  $p \leq 0.05$  are in **Bold**.

Genera	Correlated Genera	$\rho$ [11]	p-value
<i>Agathobacter</i>	<i>Anaerobutyricum hallii</i> group	0.528	0.0950
<i>Anaerobutyricum hallii</i> group	<i>Ruminococcus</i>	0.544	0.0834
<i>Anaerobutyricum hallii</i> group	<i>Lachnoclostridium</i>	0.539	0.0874
<i>Anaerobutyricum hallii</i> group	<i>Enterococcus</i>	<b><u>-0.768</u></b>	<b><u>0.0058</u></b>
<i>Anaerobutyricum hallii</i> group	<i>Faecalibacterium</i>	<b>0.930</b>	<b>3.43e-05</b>
<i>Coprococcus</i>	<i>Anaerobutyricum hallii</i> group	<b>0.634</b>	<b>0.0361</b>
<i>Dorea</i>	<i>Enterococcus</i>	<u>-0.543</u>	<u>0.0840</u>
<i>Eisenbergiella</i>	<i>Ruminococcus</i>	0.553	0.0776
<i>Eisenbergiella</i>	<i>Lachnoclostridium</i>	<b>0.659</b>	<b>0.0273</b>
<i>Fusicatenibacter</i>	<i>Anaerobutyricum hallii</i> group	<b>0.830</b>	<b>0.0016</b>
<i>Hungatella</i>	<i>Ruminococcus</i>	<b>0.819</b>	<b>0.0021</b>
<i>Hungatella</i>	<i>Anaerobutyricum hallii</i> group	0.533	0.0911
<i>Hungatella</i>	<i>Lachnoclostridium</i>	<b>0.961</b>	<b>2.650E-06</b>
<i>Hungatella</i>	<i>Solobacterium</i>	0.562	0.0720
<i>Lachnoclostridium</i>	<i>Ruminococcus</i>	<b>0.861</b>	<b>6.631E-04</b>
<i>Lachnoclostridium</i>	<i>Escherichia-Shigella</i>	0.560	0.0730
<i>Lachnoclostridium</i>	<i>Enterococcus</i>	<u>-0.528</u>	<u>0.0947</u>
<i>Lachnoclostridium</i>	<i>Solobacterium</i>	0.539	0.0872
<i>Mediterraneibacter gnavus</i> group	<i>Ruminococcus</i>	<b>0.649</b>	<b>0.0306</b>
<i>Mediterraneibacter gnavus</i> group	<i>Anaerobutyricum hallii</i> group	<b>0.687</b>	<b>0.0194</b>
<i>Mediterraneibacter gnavus</i> group	<i>Enterococcus</i>	<u>-0.560</u>	<u>0.0731</u>
<i>Mediterraneibacter torques</i> group	<i>Ruminococcus</i>	<b>0.758</b>	<b>0.0068</b>
<i>Mediterraneibacter torques</i> group	<i>Anaerobutyricum hallii</i> group	<b>0.731</b>	<b>0.0106</b>
<i>Mediterraneibacter torques</i> group	<i>Lachnoclostridium</i>	0.527	0.0958
<i>Oribacterium</i>	<i>Bifidobacterium</i>	-0.547	0.0814
<i>Pseudobutyrvibrio</i>	<i>Ruminococcus</i>	0.560	0.0727
<i>Pseudobutyrvibrio</i>	<i>Bifidobacterium</i>	0.533	0.0913
<i>Pseudobutyrvibrio</i>	<i>Streptococcus</i>	<b>0.688</b>	<b>0.0192</b>
<i>Roseburia</i>	<i>Ruminococcus</i>	<b>0.654</b>	<b>0.0289</b>
<i>Roseburia</i>	<i>Anaerobutyricum hallii</i> group	<b>0.664</b>	<b>0.0257</b>
<i>Tyzzereella</i>	<i>Bacteroides</i>	0.558	0.0744
<i>Tyzzereella</i>	<i>Ruminococcus</i>	<b>0.642</b>	<b>0.0331</b>
<i>Tyzzereella</i>	<i>Escherichia-Shigella</i>	0.579	0.0619
<i>Tyzzereella</i>	<i>Anaerobutyricum hallii</i> group	<b>0.679</b>	<b>0.0216</b>
<i>Tyzzereella</i>	<i>Lachnoclostridium</i>	<b>0.760</b>	<b>0.0067</b>
<i>Tyzzereella</i>	<i>Enterococcus</i>	<b><u>-0.779</u></b>	<b><u>0.0047</u></b>
<i>Tyzzereella</i>	<i>Solobacterium</i>	<b>0.707</b>	<b>0.0150</b>