

Suppl. Table 1 Genome sequencing of fecal *Streptococcus* isolates

Strain code	Taxonomy	Coverage	contig nb	max contig length [Mb]	sum contigs [Mb]	Consensus Concordance	comment
SgS1	<i>Streptococcus gallolyticus S1</i>	173x	1	2.05	2.05	99.9997	sick child
SgS3	<i>Streptococcus gallolyticus S3</i>	176x	2	1.8	2.13	99.9991	sick child
SiS5	<i>Streptococcus infantarius N2</i>	163x	1	1.81	1.81	99.9997	sick child
SbS6	<i>Streptococcus bovis N1</i>	110x	3	1.5	1.85	99.9985	healthy child

Suppl. Table 2 Borderline difference in fecal microbiota composition between placebo and phage recipients T, but not M in the acute phase of proven ETEC diarrhea

Comparison	Day_of hospitalization	No of samples	P (Permanova)	R ² ; Explained variance
P vs. M	D1	11;9	0.38	
	D2	11;9	0.55	
	D3	11;9	0.99	
	D4	11;7	0.08	
	D5	7;4	0.13	
	D21	7;7	0.74	
P vs. T	D1	11;10	0.05	17%
	D2	11;9	0.05	24%*
	D3	11;10	0.13	
	D4	11;9	0.37	
	D5	7;4	0.96	
	D21	7;7	0.31	

*difference contributed by *Bifidobacterium* and *Streptococcus* as shown by LEfSe analysis

Supplementary Table 3 Candidate virulence genes in *S. lutetiensis* strain 0033 and *S. infantarius* strain S5

Strain 0033 gene number	Present in S5	Annotation in 0033 (Jin et al. 2013)	Alternative comments
KE3_0855	-	Pilin gene inverting-related protein	
KE3_0863	-	Pilin gene inverting-related protein	
KE3_0878	-	Pilin gene inverting-related protein	
KE3_0857	-	Putative laminin adhesion	
KE3_0728	+	Fibronectin/fibrinogen binding protein	dihydroorotate dehydrogenase
KE3_1942	+	Putative pilus subunit protein	No domain detected
KE3_1943	+	Putative pilus subunit protein	LPTXG cell wall anchor
KE3_1766	+	Sortase A	
KE3_1047	+	Exfoliative toxin A/B	Tellurite resistance/ dicarboxylate transporter
KE3_0590	+	Hemolysin A	Cell division protein FtsJ
KE3_1574	+	Hemolysis inducing protein	SdpI multipass integral membrane protein
KE3_1645	+	Putative hemolysin	Mg ²⁺ /Co ²⁺ transporter
KE3_1380	+	Putative surface adhesion	ABC-type Zn ²⁺ transporter

Supplementary Table 4 Dirichlet Multinomial Mixtures analysis parameters describing the weights of each partition (π) and the variability of the communities in each partition (θ). A low θ means a high variability

Partition	θ	π
P1	5.6869	0.11
P2	12.7678	0.2
P3	9.0694	0.29
P4	2.3953	0.41

Supplementary Table 5 Genera frequencies of the Dirichlet Multinomial Mixtures analysis

Rank	All	P1	P2	P3	P4	Percentage Difference	Cumulative Fraction	Genus
1	40.2	33.8- 46.6 -64.3	44.1- 58.2 -76.8	66.2- 90.6 -124.1	12.8- 16.0 -20.1	37	37	<i>Bifidobacterium</i>
2	31.7	11.0- 16.0 -23.2	26.0- 34.4 -45.4	02.9- 04.0 -05.4	53.5- 68.5 -87.7	31	68	<i>Streptococcus</i>
3	05.0	01.1- 02.1 -03.8	00.5- 00.8 -01.4	00.9- 01.3 -01.9	03.6- 04.9 -06.6	4	72	<i>Escherichia</i>
4	01.9	05.3- 07.7 -11.3	00.2- 00.4 -00.8	00.1- 00.2 -00.5	00.1- 00.3 -00.8	4	76	<i>Dorea</i>
5	01.9	04.0- 06.0 -09.2	00.1- 00.2 -00.5	00.1- 00.3 -00.6	00.4- 00.8 -01.5	3	79	<i>Blautia</i>
6	03.7	01.0- 01.8 -03.4	01.4- 02.0 -02.9	00.8- 01.2 -01.8	00.7- 01.2 -02.0	3	82	<i>Lactobacillus</i>
7	02.4	02.2- 03.6 -05.7	00.5- 00.8 -01.4	00.4- 00.6 -01.0	00.2- 00.4 -01.0	2	85	<i>Collinsella</i>
8	02.1	00.8- 01.6 -03.1	00.4- 00.7 -01.2	00.3- 00.5 -00.9	00.6- 01.1 -01.9	2	86	<i>Enterococcus</i>
9	00.6	01.2- 02.1 -03.8	00.0- 00.0 -01.1	00.0- 00.1 -00.3	00.0- 00.0 -04.3	1	88	<i>Ruminococcus</i>
10	00.7	01.1- 01.9 -03.5	00.0- 00.1 -00.4	00.0- 00.1 -00.3	00.0- 00.1 -00.6	1	89	<i>Faecalibacterium</i>

Percentage relative abundance of the first 10 out of 35 genera in the estimate of the mean of the reference single Dirichlet component, All; and the four Dirichlet mixture components, P1-P4 fitted to the Twins data. For the mixture components the upper and lower 95% credible intervals are also given in the format (lower-**estimate** (in bold)-upper). Genera are ranked in order of their contribution to the total mean difference to the reference across components, Percentage Difference. The cumulative fraction of this difference accounted for is also given.