

## Supplemental Tables

16S <i>UB. ceftriaxensis</i> Specific primer									
	Sequence (5'->3')	Tem plate stran d	Len gth	St art	St op	T m	G C %	Self complem entarity	Self 3' complem entarity
Forward primer	GGCAAGCGTTAT CCGGAATG	Plus	20	51 1	53 0	59 .7	55	6	2
Reverse primer	GTAGTAGCGCCG AGGTTGAG	Minu s	20	60 5	58 6	60 .3	60	4	0
Internal oligo		Plus							
Product length						94			

**Suppl. Table 2: 16S primers to detect *UB. ceftriaxensis*.** 16S specific primers used for culturing experiments of *UB. ceftriaxensis*, constructed with NCBI primer blast.

	<i>UB. ceftriaxensis</i>	<i>P. distasonis</i>
Assembly size	2608799	4884146
Estimated genome completeness (%)	94.76	99.42
Estimated contamination (%)	2.45	0.38
N50	1925355	375178
Number of scaffolds	8	29
Average GC content (%)	51.67	44.95
Number of CDS	2386	4185
Number of rRNA genes	3	12
Number of tRNA genes	45	68

**Suppl. Table 3: Assembly statistics.** For the two bacterial genomes reconstructed from metagenomes in this study, assembly statistics a good quality.

Object	Length ( $\mu\text{m}$ )	Width ( $\mu\text{m}$ )
cell1	1.89	0.78
cell2	1.15	0.66

cell3	1.35	0.85
cell4	1.36	0.82
cell5	1.64	0.95
average	1.478	0.812

**Suppl. Table 5: Cell size of new species.** <sup>U</sup>*Borkfalki ceftriaxensis* size measurements based on FISH staining of fecal samples.

group	median AA percID	median NT percID	median percID 16S	minimum AA percID	minimum NT percID	minimum percID 16S
<b>all Ruminococcaceae</b>	60.71	59.33	88.81	51.67	54.32	83.67
<b>Ruminococcaceae main cluster</b>	65.40	64.94	90.36	61.66	61.68	88.33
<b>Ruminococcaceae main cluster + Eriseae</b>	61.03	58.09	88.46	55.67	54.32	83.67
<b>Ruminococcaceae main cluster + Discordiaceae</b>	54.23	57.54	87.09	51.67	55.10	85.00
<b>Eriseae</b>	71.73	69.56	94.57	70.71	68.42	91.61
<b>Discordiaceae</b>	63.27	60.68	86.11	60.02	58.89	85.93
<b>Eriseae + Discordiaceae</b>	58.66	58.55	87.82	55.43	57.80	83.89
<b>UB. ceftriaxensis + CAGs</b>	63.33	63.75	NA	61.60	61.94	NA
<b>UB. ceftriaxensis + CAGs + C.hongkongensis</b>	60.25	61.20	88.60	56.86	59.26	88.44
<b>UB. ceftriaxensis + C.hongkongensis</b>	56.86	59.86	88.60	56.86	59.86	88.44
<b>Ruminococcaceae main cluster + UB. ceftriaxensis + CAGs</b>	53.09	57.31	85.65	51.46	55.58	83.98
<b>Eriseae + UB. ceftriaxensis + CAGs</b>	55.05	56.76	86.62	53.73	55.01	83.38
<b>Discordiaceae + UB. ceftriaxensis + CAGs</b>	52.04	56.14	85.08	50.22	55.30	85.00
<b>Firmicutes within genus</b>	94.79	88.23	96.39	93.61	83.98	94.31
<b>Firmicutes within family</b>	70.90	67.92	91.56	45.25 (60.9)	53.25 (60.51)	84.44 (88.68)
<b>Firmicutes within class</b>	62.06	61.58	88.23	55.02	57.29	85.23

**Suppl. Table 9: Genetic similarity of taxonomic groups within Firmicutes.** Genetic distance among Firmicutes genomes within taxonomic groups indicated as median and minimum sequence identity of the the amino acid (AA) sequence of 40 conserved marker genes, the nucleotide similarity (NT) between 40 conserved marker genes and the 16S nucleotide sequence. In brackets the minimum sequence identity without the family Thermodesulfobiaceae is shown as it strongly deviates from all other families.

Species	Current family	Suggested family	Supported 40AA	Supported 40nt	Supported 16S	
<b>Hungatella hathewayi</b>	Clostridiaceae	Lachnospiraceae	Y	Y	Y	<b>Reassign family</b>
<b>Heliobacterium modesticaldum</b>	Heliobacteriaceae	Peptococcaceae	Y	?	Y	
<b>Bavariicoccus seileri</b>	Enterococcaceae	Carnobacteriaceae	Y	Y	Y	
<b>Sharpea azabuensis</b>	Lactobacillaceae	Erysipelotrichaceae	Y	Y	Y	
<b>Alkaliphilus transvaalensis</b>	Clostridiaceae	Peptostreptococcaceae	Y	Y	Y	
<b>Clostridium aceticum</b>	Clostridiaceae	Peptostreptococcaceae	Y	Y	Y	
<b>Butyricicoccus pullicaecorum</b>	Clostridiceae	Ruminococcaceae/ or Oscillospiraceae	Y	Y	Y	
<b>Coprothermobacter platensis</b>	Thermodesulfobiaceae	?	Y	Y	Y	<b>Create new family</b>
<b>Clostridium cellulyticum</b>	Ruminococcaceae	Erisaceae	Y	Y	Y	
<b>Clostridium josui</b>	Ruminococcaceae	Erisaceae	Y	Y	Y	
<b>Pseudobacteroides cellulosolvens</b>	Ruminococcaceae	Erisaceae	Y	Y	Y	
<b>Ruminoclostridium thermocellum</b>	Ruminococcaceae	Erisaceae	Y	Y	Y	
<b>Acetivibrio cellulyticus</b>	Ruminococcaceae	Erisaceae	Y	Y	Y	
<b><i>Ruminococcaceae bacterium</i> AB4001</b>	Ruminococcaceae	Discordiaceae	Y	Y	Y	
<b><i>Ruminococcaceae bacterium</i> AE2021</b>	Ruminococcaceae	Discordiaceae	Y	Y	Y	
<b><i>Mageeibacillus indolicus</i></b>	Ruminococcaceae	Discordiaceae	Y	Y	Y	
<b>Caldisalibacter kiritimatiensis</b>	Clostridiaceae	?	Y	Y	Y	
<b>Clostridiisalibacter paucivorans</b>	Clostridiaceae	?	Y	Y	Y	

<b>Caloranaerobacter azorensis</b>	Clostridiaceae	?	Y	Y	Y	
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**Suppl. Table 10: Restructured Firmicutes phylogeny.** Proposed changes to current Firmicutes taxonomy, based on 40 marker genes (AA or nt sequence) or 16S rRNA gene based maximum likelihood phylogenies.

ARG	p-value	Enrichment	PostHoc test	2nd-AB - 1st-AB	post-AB - 1st-AB	pre-AB - 1st-AB	post-AB - 2nd-AB	pre-AB - 2nd-AB	pre-AB - post-AB
		0.001077	pre-AB = 2nd-AB >> post-AB > 1st-AB	q-val	0.066806723	0.042857143	0.068571429	0.00140056	0.904761905
			p-val	0.035714286	0.014285714	0.057142857	0.000233427	0.904761905	0.044537815
PPG	p-value	Enrichment	PostHoc test	2nd-AB - 1st-AB	post-AB - 1st-AB	pre-AB - 1st-AB	post-AB - 2nd-AB	pre-AB - 2nd-AB	pre-AB - post-AB
	0.037756	1st-AB = pre-AB = post-AB > 2nd-AB	q-val	0.685714286	0.685714286	0.857142857	0.026610644	0.095238095	0.260504202
			p-val	0.571428571	0.521428571	0.857142857	0.004435107	0.031746032	0.130252101

**Suppl. Table 12: Significant changes in overall PPG and ARG potential between antibiotic treatments.** Kruskal-Wallis test and posthoc test on the total ARG (antibiotic resistance gene) and PPG (putative pathogenicity gene) abundance between different phases in HD.S1 time series. 1st-AB refers to the first response stage samples after Ceftriaxone treatment (n=2) and 2nd-AB referring to the second response stage of the community (n=5), pre-AB (n=4) and post-AB (n=13) samples being all other HD.S1 samples. Enrichment columns shows the median class abundance for each feature sorted descending, with "=" indicating no significant difference between adjacent labels and "<", "<<", "<<<" indicating a significant difference at q<0.1, 0.05, 0.01, respectively, in a post-hoc test.