

The rMLST and whole genome NEIGHBORNET analyses described in this paper can be replicated with the following steps:

1. Navigate to the *Campylobacter* database on PubMLST.org (<http://pubmlst.org/campylobacter/>).
2. Select the isolate database:

The screenshot shows the 'Campylobacter MLST Home Page'. On the left is a 'Navigation' sidebar with links for PubMLST, Software, and Recently updated. The main content area is titled 'Campylobacter MLST Home Page' and contains a tree of databases. A red box highlights 'PubMLST Isolate Database' under the 'Campylobacter jejuni/coli' category. Below this are sections for 'Database submissions' and 'Website and database managed by Keith Jolley'. On the right, a 'Citing the database' section provides citation information for the 'jejunii/coli' and 'Non-jejunii/coli' databases.

To replicate Figure 2b: rMLST analysis of 89 ST-21 complex isolates. The isolates can be selected using a list query.

3. Click 'List query':

The screenshot shows the 'Welcome to the Campylobacter jejuni/coli PubMLST database' page. At the top, there are navigation links like 'Query: Search | Browse | Profile/ST | List'. Below the welcome message, there are three main sections: 'Query database', 'Option settings', and 'General information'. In the 'Query database' section, the 'List query' option is selected and highlighted with a red box. Below this, there are sections for 'Breakdown', 'Export', 'Analysis', and 'Miscellaneous'.

4. Select 'isolate' as the search attribute, paste the following list in to the form and click 'Submit':

OXC6251	OXC6300	OXC6335	OXC6420	OXC6500	OXC6538	OXC6590	OXC6627
OXC6255	OXC6301	OXC6340	OXC6429	OXC6502	OXC6539	OXC6596	OXC6629
OXC6257	OXC6303	OXC6347	OXC6449	OXC6505	OXC6543	OXC6598	OXC6633
OXC6266	OXC6305	OXC6355	OXC6457	OXC6508	OXC6548	OXC6600	OXC6636
OXC6270	OXC6310	OXC6367	OXC6459	OXC6514	OXC6552	OXC6602	OXC6637
OXC6275	OXC6317	OXC6370	OXC6461	OXC6516	OXC6558	OXC6603	
OXC6277	OXC6324	OXC6379	OXC6464	OXC6519	OXC6562	OXC6604	
OXC6282	OXC6325	OXC6383	OXC6479	OXC6521	OXC6563	OXC6613	
OXC6285	OXC6326	OXC6384	OXC6483	OXC6524	OXC6564	OXC6615	
OXC6286	OXC6329	OXC6393	OXC6489	OXC6527	OXC6565	OXC6616	
OXC6289	OXC6331	OXC6394	OXC6493	OXC6530	OXC6571	OXC6619	
OXC6292	OXC6334	OXC6405	OXC6496	OXC6531	OXC6573	OXC6625	

5. At the bottom of the page, click the 'Genome Comparator' button:

12883	OXC5548	UK	2011	2011-09-26	gastroenteritis human stool				2	1	5	3	2	1	5	19	ST-21 complex
12887	OXC5552	UK	2011	2011-09-26	gastroenteritis human stool				2	1	12	3	2	1	12	3769	ST-21 complex
12893	OXC5558	UK	2011	2011-09-22	gastroenteritis human stool				2	1	21	3	2	1	5	53	ST-21 complex
12897	OXC5562	UK	2011	2011-09-29	gastroenteritis human stool				2	1	1	3	2	1	5	21	ST-21 complex
12898	OXC5583	UK	2011	2011-09-30	gastroenteritis human stool				2	1	1	3	2	1	5	21	ST-21 complex
12899	OXC5584	UK	2011	2011-10-03	gastroenteritis human stool				2	1	1	3	2	1	5	21	ST-21 complex
12900	OXC5585	UK	2011	2011-10-03	gastroenteritis human stool				2	1	12	3	2	1	5	50	ST-21 complex
12906	OXC5571	UK	2011	2011-09-30	gastroenteritis human stool				2	1	12	3	2	1	5	50	ST-21 complex
12908	OXC5573	UK	2011	2011-09-30	gastroenteritis human stool				2	1	1	3	2	1	5	21	ST-21 complex
16049	OXC5251	UK	2011	2011-06-28	gastroenteritis human stool				2	1	1	3	2	1	5	21	ST-21 complex
16054	OXC5257	UK	2011	2011-06-30	gastroenteritis human stool				2	1	1	3	2	1	5	21	ST-21 complex
16063	OXC5286	UK	2011	2011-06-28	gastroenteritis human stool				2	1	12	3	2	1	5	50	ST-21 complex
16067	OXC5270	UK	2011	2011-07-04	gastroenteritis human stool				2	1	1	3	2	1	5	21	ST-21 complex
16072	OXC5275	UK	2011	2011-07-04	gastroenteritis human stool				2	1	1	3	2	1	5	21	ST-21 complex
16074	OXC5277	UK	2011	2011-07-04	gastroenteritis human stool				2	1	12	3	2	1	5	50	ST-21 complex
16079	OXC5282	UK	2011	2011-06-27	gastroenteritis human stool				2	1	21	3	2	1	5	53	ST-21 complex
16082	OXC5285	UK	2011	2011-06-28	gastroenteritis human stool				2	1	1	3	2	1	5	21	ST-21 complex
16083	OXC5286	UK	2011	2011-06-28	gastroenteritis human stool				2	1	12	3	2	1	5	50	ST-21 complex
16086	OXC5289	UK	2011	2011-06-30	gastroenteritis human stool				2	1	12	3	2	1	5	50	ST-21 complex
16089	OXC5292	UK	2011	2011-06-28	gastroenteritis human stool				2	1	12	3	2	1	5	50	ST-21 complex
16097	OXC5300	UK	2011	2011-07-11	gastroenteritis human stool				8	1	5	3	2	1	12	2135	ST-21 complex
16098	OXC6301	UK	2011	2011-07-12	gastroenteritis human stool				2	1	42	3	148	1	5	861	ST-21 complex
16100	OXC6303	UK	2011	2011-07-11	gastroenteritis human stool				2	1	5	3	2	1	5	19	ST-21 complex
16102	OXC6305	UK	2011	2011-07-11	gastroenteritis human stool				2	1	42	3	148	1	5	861	ST-21 complex
16107	OXC6310	UK	2011	2011-07-13	gastroenteritis human stool				2	1	1	3	2	1	5	21	ST-21 complex

Analysis tools:

Breakdown: Fields Two Field Codons Polymorphic sites Combinations Schemes/alleles Publications Sequence bin Tag status

Analysis: BURST **Genome Comparator**

Export: Dataset Presence/Absence Concatenate XJMA

Page: 1 2 3 4 > Last

- Expand the 'Typing' heading in the 'Schemes' selection and select 'Ribosomal MLST', then click 'Submit':

PubMLST Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Genome Comparator Toggle Show options

Please select the required isolate ids and loci for comparison - use ctrl or shift to make multiple selections. In addition to selecting individual loci, you can choose to include all loci defined in schemes by selecting the appropriate scheme description. Alternatively, you can enter the accession number for an annotated reference genome and compare using the loci defined in that.

Isolates: 10935) OXC6544, 12883) OXC6545, 12881) OXC6546, 12882) OXC6547, 12883) OXC6548, 12884) OXC6549, 12885) OXC6550, 12886) OXC6551

Loci: aae (CAMP0964), aat (CAMP1030), accA (CAMP0408), accB (CAMP1209), accC (CAMP1209), accD (CAMP0115), ackA (CAMP0635), acnB (CAMP0770)

Schemes: All loci, Typing, MLST, Ribosomal MLST (highlighted), eMLST (21 partial genes), Other schemes, Loci not in schemes

Reference genome: Enter accession number: or choose annotated genome: or upload Genbank/EMBL file: Browse...

Parameters / options: Min % identity: 70, Min % alignment: 50, BLASTN word size: 15, Use TBLASTX, Produce alignments (Clustal + XMFA), Include ref sequences in alignment, Align all loci (not only variable), Use tagged designations if available, Disable HTML output

Restrict included sequences by: Sequence method: Project:

Reset Submit

- The analysis job will be submitted to the server job queue. Click the job hyperlink to display the job viewer page. This will auto-refresh until the analysis is completed:

PubMLST Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Genome Comparator Toggle Show options

This analysis has been submitted to the job queue.
Please be aware that this job may take a long time depending on the number of comparisons and how busy the server is.
[Follow the progress of this job and view the output.](#)

Listings of variable, missing, matching and truncated loci, unique strains, and a NEIGHBORNET will be generated and displayed at the bottom of the page. Various output files are hyperlinked including the distance matrix used to generate the network. This can be loaded in to stand-alone Splitstree for further manipulation.



This is the NEIGHBORNET annotated in Figure 2b.

To replicate Figure 2c: 1643 locus analysis of ten isolates belonging to the ST-21 complex rMLST strain 3.

8. Return to the list query page as in step 3, select 'isolate' as the search attribute, paste the following list in to the form and click 'Submit':

OXC6266
OXC6286
OXC6292
OXC6331
OXC6347
OXC6449
OXC6457
OXC6531
OXC6571
OXC6615

Query: Search | Browse | Profile/ST | List
 Breakdown: Isolate fields | Scheme/alleles | Publications
 Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Toggle: Field help: Go

Query *Campylobacter jejuni/coli* PubMLST database matching a field against a list

Please select attribute
 isolate

Enter your list of attribute values below (one per line)

OXC6292
 OXC6331
 OXC6347
 OXC6449
 OXC6457
 OXC6531
 OXC6571
 OXC6615

Display/sort options
 Order by: id ascending
 Display: 25 records per page

Reset Submit

9. At the bottom of the page, click the 'Genome Comparator' button:

OXC6449
 OXC6457
 OXC6531
 OXC6571

Reset Submit

10 records returned. Click the hyperlinks for detailed information.

Isolate fields							MLST											
id	isolate	aliases	country	year	isolation date	disease	source	epidemiology	penner	aspA	pinA	gtaA	plyA	pmw	ctx	uncA	ST	clonal complex
12906	OXC6571		UK	2011	2011-09-30	gastroenteritis	human stool			2	1	12	3	2	1	5	50	ST-21 complex
16053	OXC6266		UK	2011	2011-06-28	gastroenteritis	human stool			2	1	12	3	2	1	5	50	ST-21 complex
16083	OXC6286		UK	2011	2011-06-28	gastroenteritis	human stool			2	1	12	3	2	1	5	50	ST-21 complex
16089	OXC6292		UK	2011	2011-06-28	gastroenteritis	human stool			2	1	12	3	2	1	5	50	ST-21 complex
16128	OXC6331		UK	2011	2011-07-18	gastroenteritis	human stool			2	1	12	3	2	1	5	50	ST-21 complex
16144	OXC6347		UK	2011	2011-07-28	gastroenteritis	human stool			2	1	12	3	2	1	5	50	ST-21 complex
16242	OXC6449		UK	2011	2011-08-19	gastroenteritis	human stool			2	1	12	3	2	1	5	50	ST-21 complex
16249	OXC6457		UK	2011	2011-08-22	gastroenteritis	human stool			2	1	12	3	2	1	5	50	ST-21 complex
16323	OXC6531		UK	2011	2011-09-19	gastroenteritis	human stool			2	1	12	3	2	1	5	50	ST-21 complex
16365	OXC6615		UK	2011	2011-10-16	gastroenteritis	human stool			2	1	12	3	2	1	5	50	ST-21 complex

Analysis tools:

Breakdown: Fields Two Field Codons Polymorphic sites Combinations Scheme/alleles Publications Sequence bin Tag status

Analysis: BURST **Genome Comparator**

Export: Dataset Presence/Absence Concatenate XMFA

10. Expand the 'Other schemes' heading in the 'Schemes' selection and select '1643 Gundogdu loci'. Alignments of alleles from variable loci can be obtained for this and all other Genome Comparator datasets by checking the box next to 'Produce alignments (Clustal + XMFA)'. Click 'Submit':

Query: Search | Browse | Profile/ST | List
 Breakdown: Isolate fields | Scheme/alleles | Publications
 Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Toggle: Show options

Genome Comparator

Please select the required isolate ids and loci for comparison - use ctrl or shift to make multiple selections. In addition to selecting individual loci, you can choose to include all loci defined in schemes by selecting the appropriate scheme description. Alternatively you can enter the accession number for an annotated reference genome and compare using the loci defined in that.

Isolates
 12899 OXC6564
 12900 OXC6565
 12901 OXC6566
 12902 OXC6567
 12903 OXC6568
 12904 OXC6569
 12905 OXC6570
 12906 OXC6571

Locs
 aas (CAMP0864)
 aat (CAMP1030)
 aca (CAMP0400)
 accb (CAMP1209)
 accc (CAMP1208)
 acd (CAMP0115)
 adA (CAMP0635)
 acb (CAMP0770)

Schemes
 All loci
 Typing
 Other schemes
 1643 Gundogdu loci
 Loci not in schemes

Reference genome
 Enter accession number:
 or choose annotated genome:
 or upload Genbank/EMBL file:

Parameters / options
 Min % identity: 70
 Min % alignment: 50
 BLASTN word size: 15
 Make tblASTN
 Produce alignments (Clustal + XMFA)
 Include ref sequences in alignment
 Align all loci (not only variable)
 Use tagged designations if available
 Disable HTML output

Restrict included sequences by
 Sequence method: Project

Reset Submit

11. The analysis job will be submitted to the server job queue. Click the job hyperlink to display the job viewer page. This will auto-refresh until the analysis is completed:

PubMLST Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Schemalleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Genome Comparator Toggle
Show options

This analysis has been submitted to the job queue.
Please be aware that this job may take a long time depending on the number of comparisons and how busy the server is.
Follow the progress of this job and view the output.

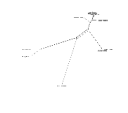
Listings of variable, missing, matching and truncated loci, unique strains, and a NEIGHBORNET will be generated and displayed at the bottom of the page. Various output files including a hyperlink to the distance matrix used to generate the network and a hyperlink to the alignments will also be displayed.

CAMP1250 (psdD)	T	T	T	T	T	32	79	T	T	T
CAMP1252 (maf4)	T	T	T	T	T	25	new#1	T	T	T
CAMP1256 (Cj1340c)	X	X	X	X	X	38	T	X	X	32
CAMP1257 (maf9)	X	X	X	X	X	new#1	T	X	X	new#2
CAMP1340 (Cj1429c)	12	12	12	12	T	new#1	X	X	X	new#1
CAMP1460 (Cj1564)	X	X	X	X	X	X	X	T	T	X
CAMP1572 (Cj1677)	new#1	new#1	new#1	new#1	new#1	new#2	new#3	new#4	T	new#2
CAMP1631 (ndpA)	4	3	4	2	T	new#1	new#2	new#3	new#4	new#5

Unique strains: 10

Strain 1	Strain 2	Strain 3	Strain 4	Strain 5	Strain 6	Strain 7	Strain 8	Strain 9	Strain 10
16242 (OXC6449)	16128 (OXC6331)	16365 (OXC6615)	12906 (OXC6571)	16323 (OXC6531)	16063 (OXC6266)	16144 (OXC6347)	16249 (OXC6457)	16083 (OXC6286)	16089 (OXC6292)

- Main output file
 - Distance matrix (Nexus format) - Suitable for loading in to SplitsTree. Distances between taxa are calculated as the number of loci with different allele sequences
 - Splits graph (Neighbour-net, PNG format)



(click to enlarge)

- Splits graph (Neighbour-net, SVG format) - This can be edited in Inkscape or other vector graphics editors
- Alignments
- Alignment stats
- Extracted sequences (XMPA format)

This page will reload in 1 minute and 10 seconds. You can refresh it any time, or bookmark it and close your browser if you wish.
Please note that job results will remain on the server for 7 days.

This is the NeighborNet annotated in Figure 2c.

To replicate Figure 2d: 1643 locus analysis of five closely-related strain 3 isolates.

12. Repeat the previous analysis using the following isolate list:

OXC6266

OXC6286

OXC6292

OXC6571

OXC6615

Use the '1643 Gundogdu loci' scheme in Genome Comparator as before.

The resulting NeighborNet is annotated in Figure 2d:

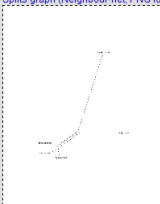
CAMP1236 (maf1)	T	T	T	T	T
CAMP1243 (Cj1325)	new#1	new#1	T	T	T
CAMP1250 (pseD)	T	T	T	T	T
CAMP1252 (maf4)	T	T	T	T	T

Unique strains

Unique strains: 5

Strain 1	Strain 2	Strain 3	Strain 4	Strain 5
16385 (OXC6615)	16089 (OXC6292)	16083 (OXC6286)	12906 (OXC6571)	16063 (OXC6266)

- [Main output file](#)
- [Distance matrix \(Nexus format\)](#) - Suitable for loading in to [SplitsTree](#). Distances between taxa are calculated as the number of loci with different allele sequences
- [Splits graph \(Neighbour-net PNG format\)](#)



(click to enlarge)

- [Splits graph \(Neighbour-net SVG format\)](#) - This can be edited in [inkscape](#) or other vector graphics editors

Please note that job results will remain on the server for 7 days.

Figure S1. A ‘Click by Click Guide’ to NEIGHBOR-NET analysis using BIGSDB as implemented on pubMLST.org.

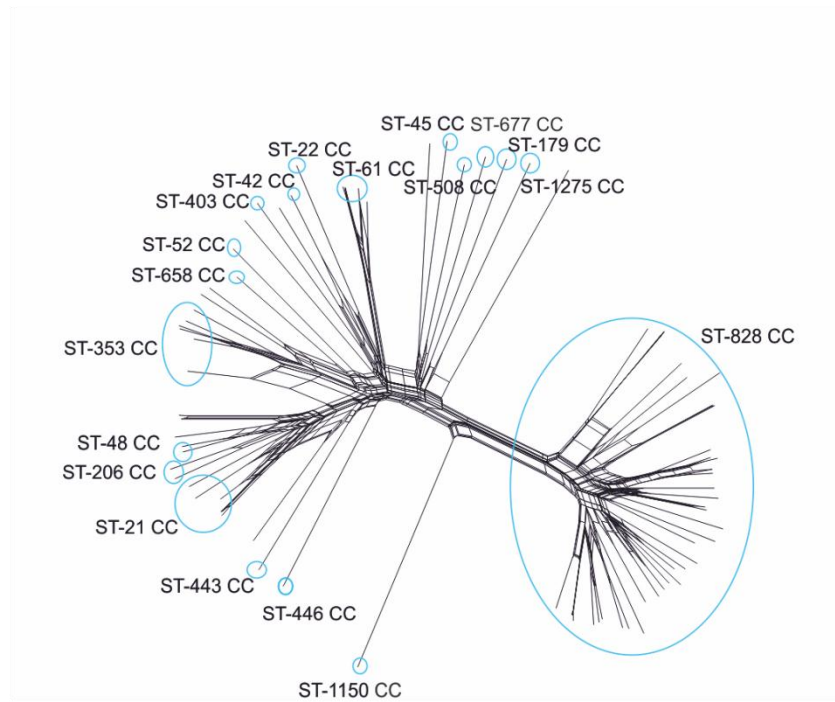


Figure S2. NEIGHBORNET phylogeny for rMLST alleles from 83 *Campylobacters* isolated from various host species from Europe, Canada and USA over more than a decade, labelled by clonal complex.

Locus	No of new alleles identified in 379 isolates	No of isolates
BACT000001 (<i>rpsA</i>)	48	87
BACT000002 (<i>rpsB</i>)	15	43
BACT000003 (<i>rpsC</i>)	13	33
BACT000004 (<i>rpsD</i>)	17	34
BACT000005 (<i>rpsE</i>)	14	17
BACT000006 (<i>rpsF</i>)	6	11
BACT000007 (<i>rpsG</i>)	13	21
BACT000008 (<i>rpsH</i>)	6	8
BACT000009 (<i>rpsI</i>)	8	10
BACT000010 (<i>rpsJ</i>)	4	14
BACT000011 (<i>rpsK</i>)	4	4
BACT000012 (<i>rpsL</i>)	11	18
BACT000013 (<i>rpsM</i>)	4	6
BACT000014 (<i>rpsN</i>)	4	6
BACT000015 (<i>rpsO</i>)	8	24
BACT000016 (<i>rpsP</i>)	4	9
BACT000017 (<i>rpsQ</i>)	2	2
BACT000018 (<i>rpsR</i>)	4	6
BACT000019 (<i>rpsS</i>)	4	6
BACT000020 (<i>rpsT</i>)	4	8
BACT000021 (<i>rpsU</i>)	4	4
BACT000030 (<i>rplA</i>)	15	16
BACT000031 (<i>rplB</i>)	26	45
BACT000032 (<i>rplC</i>)	19	34
BACT000033 (<i>rplD</i>)	17	35
BACT000034 (<i>rplE</i>)	11	19
BACT000035 (<i>rplF</i>)	13	15
BACT000036 (<i>rplL</i>)	12	21
BACT000038 (<i>rplI</i>)	19	32
BACT000039 (<i>rplJ</i>)	15	22
BACT000040 (<i>rplK</i>)	8	21
BACT000042 (<i>rplM</i>)	9	44
BACT000043 (<i>rplN</i>)	4	45
BACT000044 (<i>rplO</i>)	9	17
BACT000045 (<i>rplP</i>)	7	11
BACT000046 (<i>rplQ</i>)	6	9
BACT000047 (<i>rplR</i>)	15	25
BACT000048 (<i>rplS</i>)	3	3
BACT000049 (<i>rplT</i>)	15	39
BACT000050 (<i>rplU</i>)	8	11
BACT000051 (<i>rplV</i>)	8	11
BACT000052 (<i>rplW</i>)	7	9

BACT000053 (rplX)	1	4
BACT000056 (rpmA)	11	15
BACT000057 (rpmB)	2	6
BACT000058 (rpmC)	1	1
BACT000060 (rpmE)	0	0
BACT000061 (rpmF)	3	7
BACT000062 (rpmG)	6	9
BACT000063 (rpmH)	3	3
BACT000064 (rpmI)	5	12
BACT000065 (rpmJ)	3	3
TOTAL	478	

Table S1. rMLST loci at which novel alleles were identified in a group of 376 *Campylobacter* isolates causing human disease.

Locus	No of patients	Function	Patient 1	Patient 2	Patient 3	Patient 4	Patient 5	Patient 6	Patient 7	Patient 8	Patient 9	Patient 10	Patient 11	Patient 12	Patient 13	Patient 14	Patient 15	Patient 16	Patient 17			
			6266 6292	6269 6295	6271 6273	6298 6299	6320 6336	6328 6345 6377	6331 6347	6333 6388	6382 6462	6391 6392	6433 6435	6442 6443	6471 6472	6484 6485	6554 6555	6550	6566 6575	6542 6595	6610	
CAMP0044 (Cj0045c)	9	putative iron binding protein	18	70*		67	66*	65*	39	74*	64	75*	52	75*	7	76*				77*	77*	50
CAMP1223 (Cj1305c)	9	hypothetical protein	23	40				104	105*													
CAMP1224 (Cj1306c)	9	hypothetical protein	63	54				X	X			17	56	66	54	1						
CAMP0631 (cipA)	5	invasion protein CipA					2*	3*	9*	8*		7*	4									
CAMP0575 (Cj0617)	4	hypothetical protein										24	26*			18*	30					
CAMP1413 (Cj1506c)	4	putative MCP-type signal transduction protein	97	1										79	25			23	77			
CAMP1228 (Cj1310c)	4	hypothetical protein	62	64*	8	65*		47	66	X	X											
CAMP1213 (Cj1295)	3	conserved hypothetical protein			1	80*						1	1	80*								
CAMP1214 (Cj1296)	3	hypothetical protein																		11*	7	
² CAMP1236 (maf1)	3	motility accessory factor												52	53					8	8	12*
² CAMP1250 (pseD)	3	pseD protein												84	X					14	14	11
² CAMP1252 (maf4)	3	motility accessory factor												20	20	18	25	13				
² CAMP1253 (pseE)	3	pseE protein												53	52					14	14	11
² CAMP1257 (maf6)	3	motility accessory factor												58	128	119	120			45	42	42
CAMP0254 (cheV)	2	chemotaxis protein	1	80										X	X					X	X	X
CAMP0637 (Cj0691)	2	hypothetical protein						54	42													
CAMP0751 (Cj0816)	2	hypothetical protein																				
CAMP0974 (cjel)	2	restriction modification enzyme								8	11*	11*										
CAMP1031 (Cj1110c)	2	putative MCP-type signal transduction protein		41	81					41	78	41										
¹ CAMP1258 (maf7)	2	motility accessory factor												52	100*	103*	82					
CAMP1331 (Cj1420c)	2	putative methyltransferase												15	65*							18
CAMP1256 (Cj1340c)	2	hypothetical protein														97	100					27
CAMP0010 (rnhB)	1	probable ribonuclease HII		18	57																	28
CAMP0019 (Cj0019c)	1	putative MCP-domain signal transduction protein																				24
CAMP0052 (fliM)	1	flagellar motor switch protein FliM																				72
CAMP0068 (cdtB)	1	cytotolethal distending toxin B		1	26																	72
CAMP0157 (Cj0170)	1	hypothetical protein																				71
CAMP0167 (tonB1)	1	putative TonB-dependent outer membrane receptor																				
CAMP0202 (nrdF)	1	mononucleotide-di-phosphate reductase subunit beta		30	84																	
CAMP0208 (cynT)	1	carbonic anhydrase		23	51																	
CAMP0219 (Cj0249)	1	hypothetical protein																				
CAMP0252 (cheW)	1	chemotaxis protein																				
CAMP0253 (cheA)	1	chemotaxis histidine kinase																				
CAMP0363 (gatC)	1	gamma-glutamyl-tRNA amidotransferase subunit C																				
CAMP0573 (pstA)	1	putative phosphate transport system permease protein																				
CAMP0586 (Cj0628)	1	putative lipoprotein																				
CAMP0624 (kdpB)	1	potassium-transporting ATPase subunit B																				
CAMP0687 (Cj0741)	1	hypothetical protein																				
CAMP0714 (tpx)	1	thiol peroxidase																				
CAMP0749 (Cj0814)	1	hypothetical protein																				
CAMP0750 (Cj0815)	1	hypothetical protein																				
CAMP0803 (Cj0874c)	1	putative cytochrome C																				
CAMP0822 (aroA)	1	l-phenylalanine 1-carboxyvinyltransferase																				
CAMP0849 (cheR)	1	putative MCP protein methyltransferase																				
CAMP0851 (rpiB)	1	ribose 5-phosphate isomerase																				
CAMP0898 (Cj0975)	1	putative outer-membrane protein		24	27																	
CAMP0899 (Cj0976)	1	putative methyltransferase		54	85																	
CAMP0950 (gyrA)	1	DNA gyrase subunit A																				
CAMP1064 (neuA1)	1	two-domain bifunctional protein																				
CAMP1097 (Cj1178c)	1	highly acidic protein																				
CAMP1108 (cetB)	1	bipartate energy taxis response protein cetB																				
CAMP1109 (cetA)	1	bipartate energy taxis response protein cetA																				
CAMP1123 (atpB)	1	FOF1 ATP synthase subunit A		23	67																	
CAMP1124 (radA)	1	DNA repair protein radA																				
CAMP1143 (Cj1224)	1	putative iron-binding protein																				
CAMP1165 (uvrC)	1	excinuclease ABC subunit C																				
CAMP1181 (racS)	1	two-component sensor (histidine kinase)																				
CAMP1243 (Cj1325)	1	putative methyltransferase																				
CAMP1255 (flaA)	1	flagellin																				
CAMP1283 (Cj1367c)	1	putative nucleotidyltransferase		20	136																	
CAMP1396 (ccoQ)	1	cb-type cytochrome C oxidase subunit IV		13	1																	
CAMP1422 (Cj1516)	1	putative periplasmic oxidoreductase																				
CAMP1442 (Cj1542)	1	putative allophanate hydrolase subunit 1																				
CAMP1510 (chuA)*	1	haem uptake system outer membrane receptor																				
CAMP1527 (Cj1631c)	1	conserved hypothetical protein																				
CAMP1572 (Cj1677)	1	putative lipoprotein																				
CAMP1581 (secY)	1	preprotein translocase subunit SecY																				
CAMP1631 (kdpA)*	1	dogene (potassium-transporting ATPase A sub	3*	2*																		

* involves change in homopolymeric tract length of assigned allele as compared to consensus for this ORF in strain 11166

X allele unassigned due to paralogous sequence

¹ Member of 617 family of variable genes (24).

² Member of 1318 family of variable genes (24).

Table S2. Allele numbers at loci where polymorphisms were identified between samples of the same sequence type, obtained from the same patient.

	Isolates	No of matching loci	No of variable loci	Percent matching
13	6471 / 6471R	1478	1	99.93
13	6472 / 6472R	1478	1	99.93
14	6484 / 6484R	1552	2	99.87
14	6485 / 6485R	1557	1	99.94
16	6566 / 6566R	1583	2	99.87
16	6575 / 6575R	1586	7	99.56
17	6595 / 6595R	1533	3	99.80
17	6610 / 6610R	1530	1	99.93
NA	6576 / 6576R	1455	6	99.59
NA	6578 / 6578R	1584	2	99.87

Table S3. Variation detected between repeated samples.