

**Table S6** Small insertions and deletions in clone D relative to CFT073: allocation to lineage by virtual outgroup analysis. The *E. coli*/*Shigella* genomes used for the analysis are shown, with details of the blocks present in outgroup genomes and genomes under analysis, and also the final allocation and a measure of support level for that allocation.



Indel No.	Clone D <sup>a</sup>	CFT073 <sup>a</sup>	Lineage	type	site <sup>b</sup>	size	Locus_tag	Gene	Inferred ancestral <sup>c</sup>	Support level <sup>d</sup>	ED1a	536	S88	APEC O1	UTI89	E2348/69	ATCC8739	K-12	HS	SMS3-5	IA139	E24377A	SE11	55989	IA1	Sakai	UMN026	B4 Sb227	F5 8401	SS Ss046	D1 Sd197	B18 BS512	F2a 2457T	F2a 301
123	-	+	CFT073	ins	1129853	1	intergenic		-	++	/	-	/	/	-	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/
124	-	+	?	indel	1132746	1	intergenic		?	+/-	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/	
125	-	+	CFT073	ins	1141301	1	i02_1117		-	++++	/	-	/	/	/	-	-	-	-	-	/	/	/	/	/	-	-	/	-	/	-	/		
126	-	+	CFT073	ins	1203554	1	i02_1181	ycdW	-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
127	-	+	CFT073	ins	1232838	1	i02_1220		-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
128	-	+	CFT073	ins	1232865	1	i02_1220		-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
129	-	+	CFT073	ins	1232932	1	i02_1220		-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
130	-	+	CFT073	ins	1256746	1	i02_1247		-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
131	-	+	CFT073	ins	1256789	1	i02_1247		-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
132	-	+	CFT073	ins	1256798	1	i02_1247		-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
133	+	-	CFT073	del	1259736	1	i02_1250	pabC	+	++++	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+		
134	-	+	CFT073	ins	1259830	1	i02_1251	yceG	-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
135	-	+	CFT073	ins	1344697	1	i02_1357		-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
136	+	-	CFT073	del	1346650	12	intergenic		+	++++	+	+	+	+	+	/	/	/	/	/	+	/	/	/	+	/	/	/	/	/	/	/		
137	-	+	CFT073	ins	1358441	1	i02_1383		-	+++	/	/	-	-	-	/	/	/	/	/	/	/	/	/	-	/	/	/	/	/	/	/		
138	-	+	CFT073	ins	1358461	1	i02_1383		-	+++	/	/	-	-	-	/	/	/	/	/	/	/	/	/	-	/	/	/	/	/	/	/		
139	-	+	CFT073	ins	1358472	1	i02_1383		-	+++	/	/	-	-	-	/	/	/	/	/	/	/	/	-	/	/	/	/	/	/	/	/		
140	-	+	CFT073	ins	1358524	1	i02_1383		-	+++	/	/	-	-	-	/	/	/	/	/	/	/	/	-	/	/	/	/	/	/	/	/		
141	-	+	CFT073	ins	1358753	1	i02_1384		-	+++	/	/	-	-	-	/	/	/	/	/	/	/	/	-	/	/	/	/	/	/	/	/		
142	+	-	CFT073	del	1378275	1	i02_1415		+	++++	/	+	+	+	+	/	+	/	/	+	/	+	+	+	+	/	+	/	/	/	/			
143	+	-	CFT073	del	1378427	1	i02_1415		+	++++	/	+	+	+	+	/	+	/	/	+	/	+	+	+	+	/	+	/	/	/	/			
144	+	-	CFT073	del	1378444	1	i02_1415		+	++++	/	+	+	+	+	/	+	/	/	+	/	+	+	+	+	/	+	/	/	/	/			
145	+	-	CFT073	del	1378515	1	i02_1415		+	++++	/	+	+	+	+	/	+	/	/	+	/	+	+	+	+	/	+	/	/	/	/			
146	+	-	CFT073	del	1393522	1	i02_1430	sitA	+	++++	+	+	+	+	+	/	/	/	/	+	/	+	+	+	/	+	+	+	+	+	+			
147	+	-	CFT073	del	1393546	1	i02_1430	sitA	+	++++	+	+	+	+	+	/	/	/	/	+	/	+	+	+	/	+	+	+	+	+	+			





Indel No.	Clone D <sup>a</sup>	CFT073 <sup>a</sup>	Lineage	type	site <sup>b</sup>	size	Locus_tag	Gene	Inferred ancestral <sup>c</sup>	Support level <sup>d</sup>	ED1a	536	S88	APEC O1	UTI89	E2348/69	ATCC8739	K-12	HS	SMS3-5	IA39	E24377A	SE11	55989	IA1	Sakai	UMN026	B4 Sb227	F5 8401	SS Ss046	D1 Sd197	B18 BS512	F2a 2457T	F2a 301
198	-	+	CFT073	ins	2485913	2	i02_2500	yeiN	-	++++	-	-	-	-	-	-	-	-	-	-	-	-	/	-	-	-	-	-	-	-	-	-		
199	+	-	CFT073	del	2658778	1	i02_2665	yfcJ	+	++++	+	+	+	+	+	+	+	+	+	+	+	+	/	+	+	+	+	+	+	+	+	+		
200	+	-	CFT073	del	2658814	1	i02_2665	yfcJ	+	++++	+	+	+	+	+	+	+	+	+	+	+	+	/	+	+	+	+	+	+	+	+	+		
201	-	+	?	indel	2686052	1	i02_2693		?	+/-	/	/	/	/	/	/	/	/	-	/	/	/	/	/	/	/	/	/	/	/				
202	-	+	?	indel	2686086	1	i02_2693		?	+/-	/	/	/	/	/	/	/	/	-	/	/	/	/	/	/	/	/	/	/	/				
203	-	+	?	indel	2686164	18	i02_2693		?	+/-	/	/	/	/	/	/	/	/	+	/	/	/	/	/	/	/	/	/	/	/				
204	+	-	CFT073	del	2718016	1	i02_2714		+	++++	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+			
205	+	-	CFT073	del	2751344	1	i02_2746	cysK	+	++++	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+			
206	-	+	CFT073	ins	2751413	1	intergenic		-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				
207	-	+	CFT073	ins	2751487	1	intergenic		-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				
208	-	+	CFT073	ins	2752054	1	i02_2749	ptsI	-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				
209	+	-	clone D	ins	2852951	9	i02_2837	ppbC	-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	/	/	/	/	/				
210	-	+	CFT073	ins	2885705	1	i02_2869		-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				
211	-	+	CFT073	ins	2917217	1	intergenic		-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
212	-	+	CFT073	ins	2926828	1	rRNA_005	rrl	-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
213	+	-	CFT073	del	2927085	1	rRNA_005	rrl	+	++	+	+	+	+	+	+	-	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-		
214	+	-	CFT073	del	2927088	1	rRNA_005	rrl	+	++	+	+	+	+	+	+	-	-	+	+	-	-	-	-	-	-	-	-	-	-	-	-		
215	+	-	CFT073	del	2927224	13	rRNA_005	rrl	+	++	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
216	-	+	clone D	del	2927237	13	rRNA_005	rrl	+	++++	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+			
217	-	+	CFT073	ins	2927786	1	rRNA_005	rrl	-	++	-	+	-	-	-	-	+	+	-	-	+	-	+	-	+	+	+	+	-	-	+			
218	-	+	CFT073	ins	2928406	3	rRNA_005	rrl	-	++	-	+	-	-	-	+	+	+	-	+	+	-	+	+	-	-	+	+	-	+	+			
219	+	-	CFT073	del	2928408	3	rRNA_005	rrl	+	++	+	+	+	+	+	+	/	-	-	+	-	-	-	-	-	-	-	-	-	-	-			
220	-	+	CFT073	ins	2928417	1	rRNA_005	rrl	-	++	-	+	-	-	-	+	+	+	-	+	+	-	+	+	-	-	+	+	-	+	+			
221	-	+	clone D	del	2928977	2	intergenic		+	++++	/	/	+	+	/	/	+	+	+	+	+	+	/	/	/	+	/	/	/	/	/			
222	+	-	CFT073	del	2928978	16	intergenic		+	++	+	+	+	+	+	+	-	-	-	-	-	-	+	+	-	-	+	+	-	+	+			

Indel No.	Clone D <sup>a</sup>	CFT073 <sup>a</sup>	Lineage	type	site <sup>b</sup>	size	Locus_tag	Gene	Inferred ancestral support level <sup>d</sup>	ED1a	536	S88	APEC O1	UTI89	E2348/69	ATCC8739	K-12	HS	SMS3-5	IAI39	E24377A	SE11	55989	IAI1	Sakai	UMN026	B4 Sb227	F5 8401	SS Ss046	D1 Sd197	B18 BS512	F2a 2457T	F2a 301
223	-	+	clone D	del	2928978	5	intergenic		+	++++	/	/	+	+	/	/	+	+	+	+	+	/	/	/	+	/	/	/	/	/	/	/	/
224	+	-	CFT073	del	2929090	13	intergenic		+	++	+	+	+	-	+	+	-	-	+	+	-	-	+	+	-	+	+	+	+	+	+	+	+
225	-	+	?	indel	2929104	13	intergenic		?	+/-	/	/	/	/	/	/	+	/	/	-	+	+	/	/	/	/	/	/	/	/	/	/	/
226	+	-	CFT073	del	2929226	20	intergenic		+	++	+	+	+	-	+	+	-	-	-	+	-	-	-	-	+	+	+	+	+	-	+	+	+
227	+	-	CFT073	del	2929450	1	rRNA_006	rrs	+	++++	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
228	+	-	CFT073	del	2929550	1	rRNA_006	rrs	+	++++	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
229	-	+	CFT073	ins	2930036	1	rRNA_006	rrs	-	++++	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
230	-	+	CFT073	ins	2930063	1	rRNA_006	rrs	-	++++	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
231	-	+	CFT073	ins	2930079	1	rRNA_006	rrs	-	++++	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
232	-	+	CFT073	ins	2930102	1	rRNA_006	rrs	-	++++	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
233	-	+	CFT073	ins	2930210	1	rRNA_006	rrs	-	++++	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
234	-	+	CFT073	ins	2930267	1	rRNA_006	rrs	-	++++	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
235	-	+	CFT073	ins	2930289	1	rRNA_006	rrs	-	++++	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
236	-	+	CFT073	ins	2930305	1	rRNA_006	rrs	-	++++	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
237	-	+	CFT073	ins	2930427	1	rRNA_006	rrs	-	++++	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
238	-	+	CFT073	ins	2930474	1	rRNA_006	rrs	-	++++	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
239	-	+	CFT073	ins	2930497	1	rRNA_006	rrs	-	++++	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
240	+	-	CFT073	del	2969602	1	i02_2955		+	++++	+	+	+	+	+	/	/	/	+	+	/	/	/	+	+	/	/	+	/	/	/	/	
241	+	-	CFT073	del	2969636	1	intergenic		+	++++	+	+	+	+	+	/	/	/	+	+	/	/	/	+	-	/	/	+	/	/	/	/	
242	-	+	CFT073	ins	2978621	1	intergenic		-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
243	-	+	CFT073	ins	2992303	1	i02_2981	alas	-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
244	-	+	CFT073	ins	3004393	1	i02_2995	norV	-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	/	-	-	-	-	-	-	-		
245	-	+	CFT073	ins	3038925	5	i02_3034		-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
246	-	+	CFT073	ins	3045109	2	intergenic		-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
247	-	+	clone D	del	3068496	15	i02_3065		+	++++	+	+	+	+	+	/	/	/	+	/	/	/	+	+	/	/	+	/	/	+	/	/	

Indel No.	Clone D <sup>a</sup>	CFT073 <sup>a</sup>	Lineage	type	site <sup>b</sup>	size	Locus_tag	Gene	Inferred ancestral <sup>c</sup>	Support level <sup>d</sup>	ED1a	536	S88	APEC O1	UT189	E2348/69	ATCC8739	K-12	HS	SMS3-5	IA39	E24377A	SE11	55989	IA1	Sakai	UMN026	B4 Sb227	F5 8401	SS Ss046	D1 Sd197	B18 BS512	F2a 2457T	F2a 301
248	-	+	CFT073	ins	3082607	1	i02_3076	ygcX	-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
249	-	+	CFT073	ins	3082619	1	i02_3076	ygcX	-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
250	+	-	CFT073	del	3100943	1	i02_3096	fucK	+	++++	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	
251	+	-	CFT073	del	3134313	1	i02_3121		+	+++	/	+	+	+	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/	
252	+	-	CFT073	del	3134331	1	i02_3121		+	+++	/	+	+	+	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/		
253	+	-	CFT073	del	3261304	1	i02_3238		+	++++	+	+	+	+	+	/	/	/	+	+	/	/	/	+	/	/	+	/	/	+	/	+		
254	+	-	CFT073	del	3261317	1	i02_3238		+	++++	+	+	+	+	+	/	/	/	+	+	/	/	/	+	/	/	+	/	/	+	/	+		
255	+	-	CFT073	del	3261350	2	i02_3238		+	++++	+	+	+	+	+	/	/	/	+	+	/	/	/	+	/	/	+	/	+	/	+			
256	+	-	CFT073	del	3261357	1	i02_3238		+	++++	+	+	+	+	+	/	/	/	+	+	/	/	/	+	/	/	+	/	+	/	+			
257	+	-	CFT073	del	3296532	12	i02_3275		+	+	/	/	+	+	/	/	/	/	/	+	/	/	/	/	/	/	/	/	/	/	/			
258	-	+	?	indel	3298504	1	intergenic		?	+/-	/	+	-	-	+	/	/	/	-	/	/	/	/	+	/	/	/	/	/	/	/			
259	+	-	CFT073	del	3300102	1	intergenic		+	+++	/	+	+	+	+	/	/	/	+	/	/	/	/	+	/	/	/	/	/	/	/			
260	-	+	clone D	del	3300420	1	i02_3284		+	+++	/	+	+	+	+	/	/	/	-	/	/	/	/	+	/	/	/	/	/	/	/			
261	+	-	CFT073	del	3302284	1	i02_3287		+	++++	+	+	+	+	+	/	/	/	+	+	+	/	+	+	-	+	+	+	+	+	+			
262	+	-	?	indel	3303805	8	i02_3289		?	+/-	/	/	-	/	+	/	/	/	+	+	/	/	/	-	+	/	+	+	+	/	+			
263	+	-	CFT073	del	3307276	1	i02_3294		+	++++	/	/	/	/	+	/	/	+	/	+	/	/	+	/	/	+	-	+	+	+	+	+		
264	-	+	clone D	del	3311423	5	intergenic		+	+++	+	/	/	/	/	/	/	/	/	/	/	/	/	+	/	+	+	+	/	/	/			
265	-	+	clone D	del	3326445	1	intergenic		+	++++	+	/	/	/	/	/	/	/	/	-	-	/	/	+	/	/	+	+	+	/	+			
266	+	-	CFT073	del	3336055	1	i02_3326		+	++	+	/	/	/	+	/	/	/	/	/	/	/	/	/	+	/	/	/	/	/	/			
267	+	-	CFT073	del	3336093	1	i02_3326		+	++	+	/	/	/	+	/	/	/	/	/	/	/	/	/	+	/	/	/	/	/	/			
268	+	-	CFT073	del	3336107	1	i02_3326		+	++	+	/	/	/	+	/	/	/	/	/	/	/	/	+	/	/	/	/	/	/				
269	+	-	CFT073	del	3336128	1	i02_3326		+	++	+	/	/	/	+	/	/	/	/	/	/	/	/	+	/	/	/	/	/	/				
270	+	-	CFT073	del	3336135	1	i02_3326		+	++	+	/	/	/	+	/	/	/	/	/	/	/	/	+	/	/	/	/	/	/				
271	+	-	CFT073	del	3336142	1	i02_3326		+	++	+	/	/	/	+	/	/	/	/	/	/	/	/	+	/	/	/	/	/	/				
272	+	-	CFT073	del	3336159	1	i02_3326		+	++	+	/	/	/	+	/	/	/	/	/	/	/	/	+	/	/	/	/	/	/				

Indel No.	Clone D <sup>a</sup>	CFT073 <sup>a</sup>	Lineage	type	site <sup>b</sup>	size	Locus_tag	Gene	Inferred ancestral support level <sup>d</sup>	ED1a	536	S88	APEC O1	UTI89	E2348/69	ATCC8739	K-12	HS	SMS3-5	IAI39	E24377A	SE11	55989	IAI1	Sakai	UMN026	B4 Sb227	F5 8401	SS Ss046	D1 Sd197	B18 BS512	F2a 2457T	F2a 301
273	+	-	CFT073	del	3336176	1	i02_3326		+	++	+	/	/	/	+	/	/	/	/	/	/	/	/	/	/	+	/	/	/	/	/	/	/
274	+	-	CFT073	del	3336181	1	i02_3326		+	++	+	/	/	/	+	/	/	/	/	/	/	/	/	/	/	+	/	/	/	/	/	/	/
275	+	-	CFT073	del	3336202	1	i02_3326		+	++	+	/	/	/	+	/	/	/	/	/	/	/	/	/	+	/	/	/	/	/	/	/	
276	+	-	CFT073	del	3336311	1	i02_3326		+	++	+	/	/	/	+	/	/	/	/	/	/	/	/	/	+	/	/	/	/	/	/	/	
277	-	+	CFT073	ins	3337181	1	i02_3328		-	++	-	/	/	/	/	/	/	/	/	/	/	/	/	-	/	/	/	/	/	/	/		
278	-	+	CFT073	ins	3337246	1	i02_3328		-	++	-	/	/	/	/	/	/	/	/	/	/	/	/	-	/	/	/	/	/	/	/		
279	-	+	CFT073	ins	3337294	1	i02_3328		-	++	-	/	/	/	/	/	/	/	/	/	/	/	/	-	/	/	/	/	/	/	/		
280	-	+	clone D	del	3344259	1	intergenic		+	++	+	/	/	/	/	/	/	/	/	/	/	/	/	+	/	/	/	/	/	/	/		
281	-	+	CFT073	ins	3344306	2	intergenic		-	++	-	/	/	/	/	/	/	/	/	/	/	/	/	-	/	/	/	/	/	/	/		
282	-	+	CFT073	ins	3344350	2	intergenic		-	++	-	/	/	/	/	/	/	/	/	/	/	/	/	-	/	/	/	/	/	/	/		
283	-	+	CFT073	ins	3344364	1	intergenic		-	++	-	/	/	/	/	/	/	/	/	/	/	/	/	-	/	/	/	/	/	/	/		
284	-	+	CFT073	ins	3344381	1	intergenic		-	++	-	/	/	/	/	/	/	/	/	/	/	/	/	-	/	/	/	/	/	/	/		
285	+	-	CFT073	del	3348189	1	i02_3340		+	+++	/	+	/	/	+	/	/	+	/	+	/	+	/	+	/	/	/	/	+	+	+		
286	+	-	CFT073	del	3348569	1	intergenic		+	+++	/	/	/	/	+	/	/	+	/	+	/	+	/	-	/	/	+	/	/	/	/	/	
287	+	-	CFT073	del	3349813	1	intergenic		+	+++	/	/	/	/	+	/	/	+	/	+	/	+	/	+	/	/	/	/	/	/	/	/	
288	+	-	?	indel	3350480	5	intergenic		?	+/-	/	/	-	/	+	/	/	/	/	/	/	/	/	-	/	/	/	/	/	/	/		
289	-	+	?	indel	3350750	14	intergenic		?	+/-	/	/	/	/	/	/	/	/	/	/	/	/	/	-	/	/	/	/	/	/	/		
290	-	+	CFT073	ins	3350827	7	i02_3344		-	+	/	/	/	/	/	/	/	-	/	/	/	/	-	/	/	/	/	/	/	/			
291	+	-	?	indel	3350918	6	intergenic		?	+/-	/	/	/	/	/	/	/	/	/	/	/	/	/	+	/	/	/	/	/	/	/		
292	+	-	?	indel	3359351	1	intergenic		?	+/-	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/		
293	+	-	CFT073	del	3364637	1	i02_3359		+	++++	+	+	+	+	/	/	+	+	-	+	+	/	+	-	/	/	+	+	/	/			
294	-	+	clone D	del	3364699	1	i02_3359		+	++	+	-	+	-	+	/	/	-	+	+	+	+	/	+	+	+	+	+	-	/			
295	-	+	CFT073	indel	3367923	1	i02_3364		?	+/-	/	/	/	/	/	/	/	/	/	/	/	/	+	/	/	/	-	/	/	/			
296	+	-	clone D	ins	3387223	1	intergenic		-	++	-	-	+	+	/	/	/	-	-	/	/	/	-	/	/	/	-	/	/	/			
297	-	+	CFT073	ins	3387673	1	intergenic		-	++++	-	-	-	-	-	/	/	/	-	-	/	/	/	-	/	/	/	-	/	/			

Indel No.	Clone D <sup>a</sup>	CFT073 <sup>a</sup>	Lineage	type	site <sup>b</sup>	size	Locus_tag	Gene	Inferred ancestral support level <sup>d</sup>	ED1a	536	S88	APEC O1	UTI89	E2348/69	ATCC8739	K-12	HS	SMS3-5	IAI39	E24377A	SE11	55989	IAI1	Sakai	UMN026	B4 Sb227	F5 8401	SS Ss046	D1 Sd197	B18 BS512	F2a 2457T	F2a 301
298	+	-	CFT073	del	3389261	1	i02_3380	gspL	+	++++	+	+	+	+	/	/	+	+	+	+	+	+	/	+	/	/	+	+	/	/	/		
299	-	+	CFT073	ins	3415674	5	i02_3402	yghO	-	++++	-	-	-	-	-	+	/	+	-	-	-	-	/	-	/	/	/	/	/	/	/		
300	-	+	clone D	del	3415911	1	intergenic		+	++	+	+	+	+	+	/	+	-	-	-	-	/	-	/	+	/	/	/	/	/	/		
301	-	+	CFT073	ins	3450140	1	i02_3439	yqhG	-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	/	/	/			
302	-	+	CFT073	ins	3525549	1	i02_3514		-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
303	-	+	CFT073	ins	3525566	1	i02_3514		-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
304	+	-	CFT073	del	3561339	1	i02_3550	yqjF	+	++++	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+		
305	-	+	CFT073	ins	3562225	2	i02_3551	yqjG	-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
306	-	+	CFT073	ins	3567159	1	i02_3557		-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
307	-	+	CFT073	ins	3629787	1	i02_3621	hflB	-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				
308	+	-	CFT073	del	3704908	3	i02_3698		+	++++	+	+	+	+	+	/	/	/	/	/	/	/	/	/	/	/	/	/	/	/			
309	+	-	CFT073	del	3726492	1	rRNA_008	rrl	+	++++	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+				
310	-	+	CFT073	ins	3728030	1	rRNA_008	rrl	-	++	-	+	-	-	-	+	+	-	-	+	-	+	+	-	+	+	-	-	+				
311	-	+	CFT073	ins	3728661	1	rRNA_008	rrl	-	++	-	+	+	-	+	-	+	+	-	-	+	+	+	+	+	+	+	+	+				
312	-	+	CFT073	ins	3729221	2	intergenic		-	++	-	-	+	-	+	-	+	+	+	+	+	-	-	-	-	-	-	-	-	-			
313	+	-	CFT073	del	3729227	11	intergenic		+	++++	+	+	+	+	+	+	/	/	/	/	/	/	/	/	/	/	/	/	/				
314	-	+	CFT073	ins	3809580	1	i02_3825	yhfZ	-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-					
315	-	+	clone D	del	3913324	6	i02_3927	ftsY	+	++	+	+	+	+	+	-	+	+	+	+	+	+	+	-	/	+	+	+	+				
316	+	-	CFT073	del	3933212	1	i02_3950		+	++++	/	/	+	+	/	/	/	/	+	/	/	/	/	+	/	/	/	/	/				
317	-	+	CFT073	ins	4141078	2	intergenic		-	++++	-	-	-	-	-	-	/	/	/	-	/	/	/	/	/	/	/	/					
318	+	-	clone D	ins	4145486	1	intergenic		-	++	-	/	-	-	+	/	/	/	-	/	/	/	/	+	/	/	-	-	/				
319	+	-	clone D	ins	4145592	1	intergenic		-	+++	/	-	/	/	+	/	/	/	-	/	/	/	/	/	/	-	-	/	/				
320	-	+	?	indel	4145717	1	intergenic		?	+/-	/	/	/	/	/	/	/	/	/	+	/	/	/	-	/	+	+	+	/				
321	-	+	CFT073	ins	4196764	1	i02_4207	dgoA	-	++++	-	-	-	-	-	-	-	-	-	-	-	-	-	/	-	-	/	/					
322	-	+	CFT073	ins	4199528	1	i02_4210		-	++++	-	-	-	-	-	-	/	/	/	-	/	/	/	-	/	/	/	/	/				





Indel No.	Clone D <sup>a</sup>	CFT073 <sup>a</sup>	Lineage	type	site <sup>b</sup>	size	Locus_tag	Gene	Inferred ancestral <sup>c</sup>	Support level <sup>d</sup>	ED1a	536	S88	APEC_O1	UTI89	E2348/69	ATCC8739	K-12	HS	SMS3-5	IAI39	E24377A	SE11	55989	IAI1	Sakai	UMN026	B4_Sb227	F5_8401	SS_Ss046	D1_Sd197	B18_BS512	F2a_2457T	F2a_301
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<sup>a</sup> "+" indicates the block present, "-" indicates the block absent, "/" indicates the block and nearby sequence absent.

<sup>b</sup> Using the clone D\_i2 genome as reference. For indels the base indicated is the base before the insertion or deletion.

<sup>c</sup> Presence or absence of indel block in clone D/CFT073 ancestor as inferred from outgroup analysis.

<sup>d</sup> Level of support for allocation of indel blocks as given in previous column.

"++++" agreement is high-8 or more outgroup strains with expected type and at most 2 with the opposite, and ED1a agrees or site not present

"+++" agreement good-4 or more outgroup strains with expected type and at most 2 with the opposite, and ED1a agrees or site not present

"++" agreement in ED1a regardless of situation with other outgroup strains

"+" no conflict but very limited support as either the block and nearby sequence absent in ED1a, and/or outgroup support less than given above

"+/-" no conflict but no support (the block and its nearby sequence not present in any outgroup OR both alternative lineages supported equally).