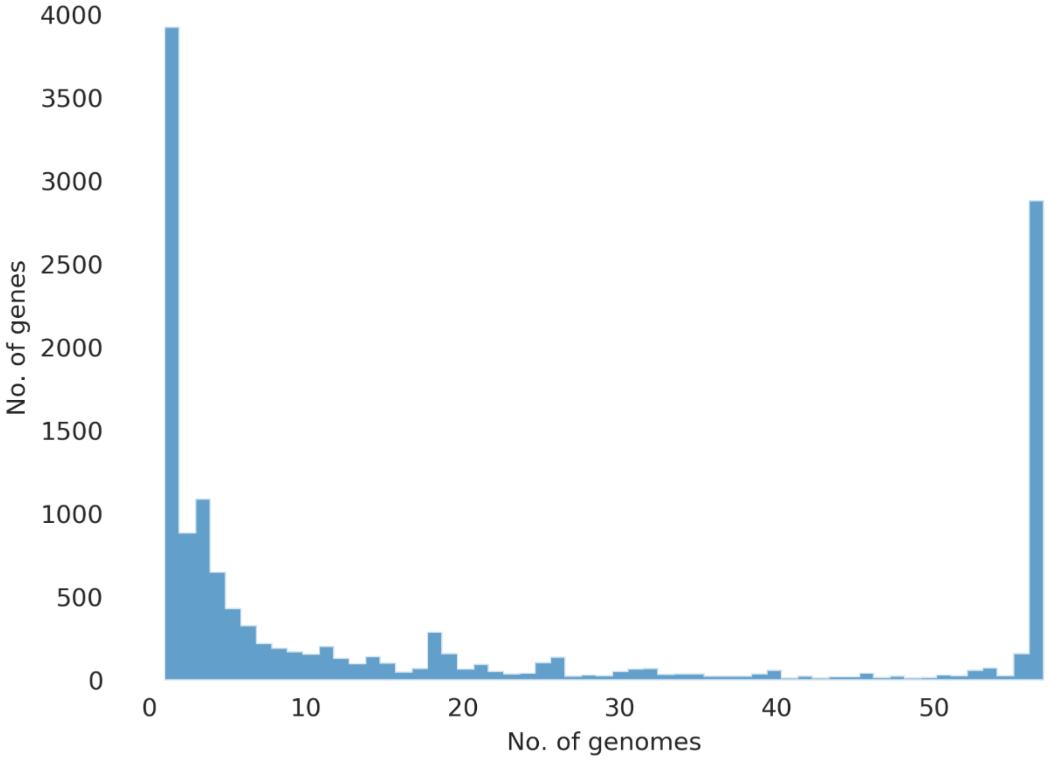
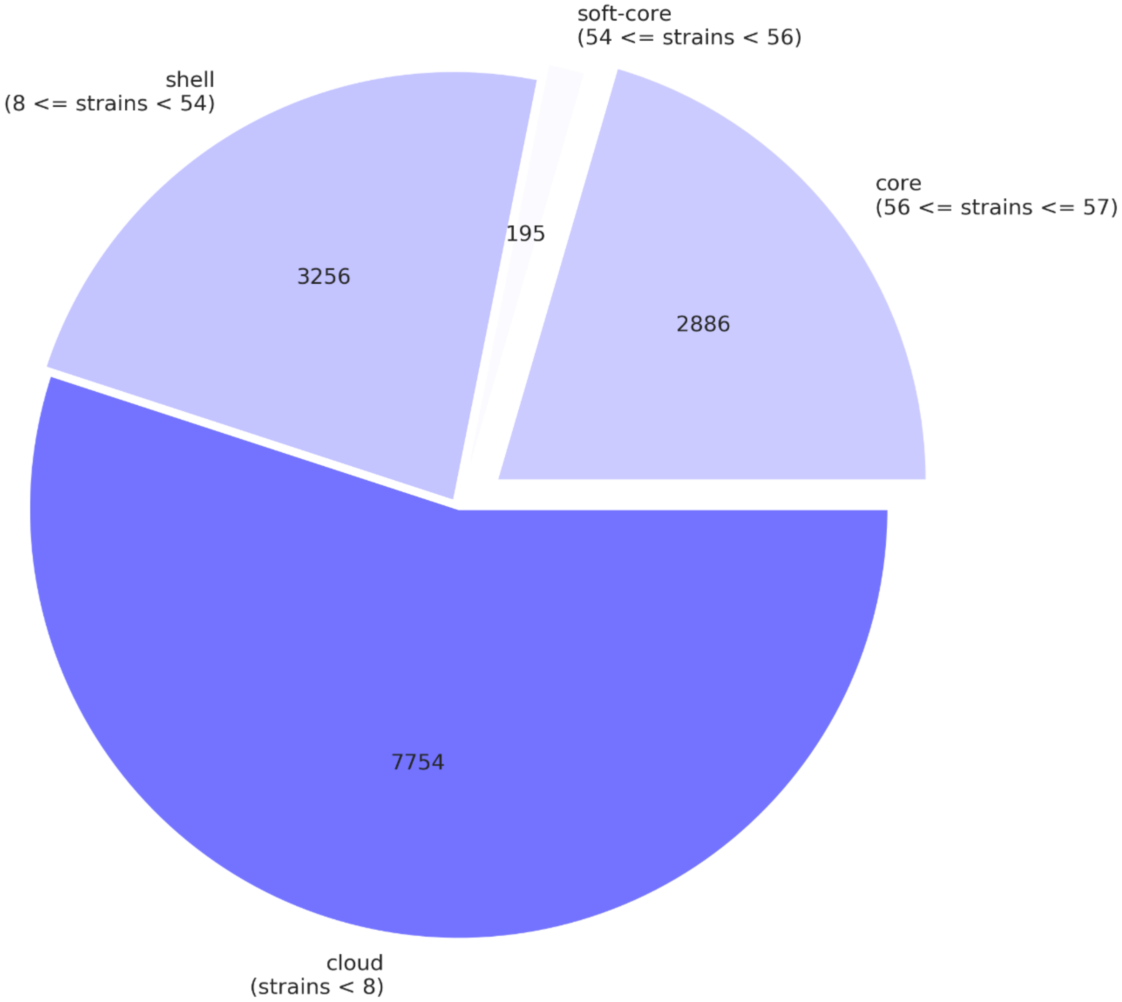
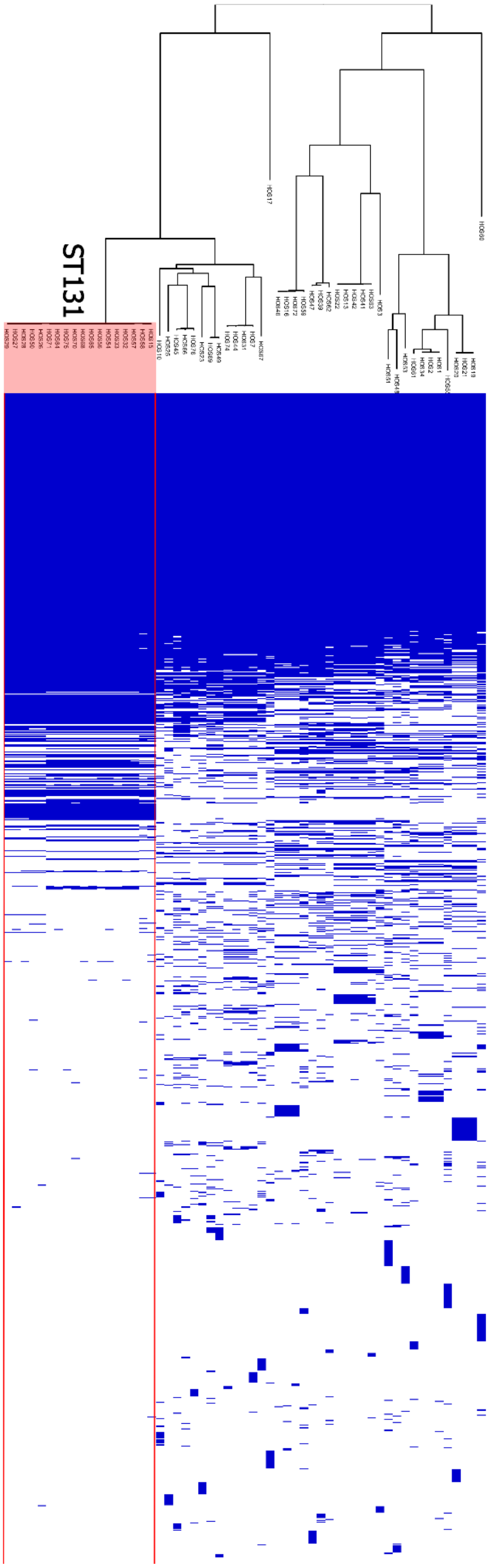


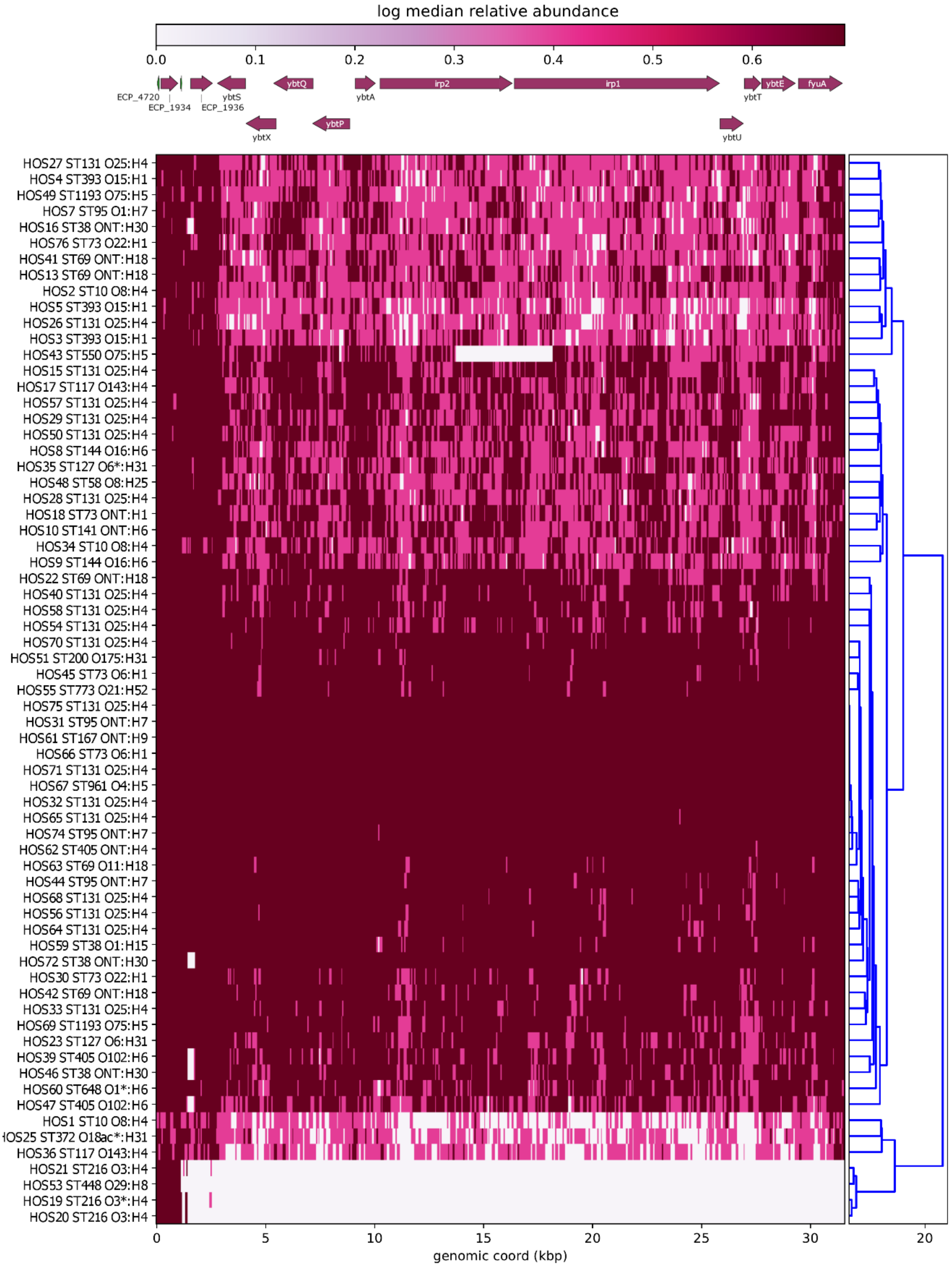
Supplementary Data 2. A) Frequency of genes versus the number of genomes depicting U shape graph with high number of singlets and core genes.



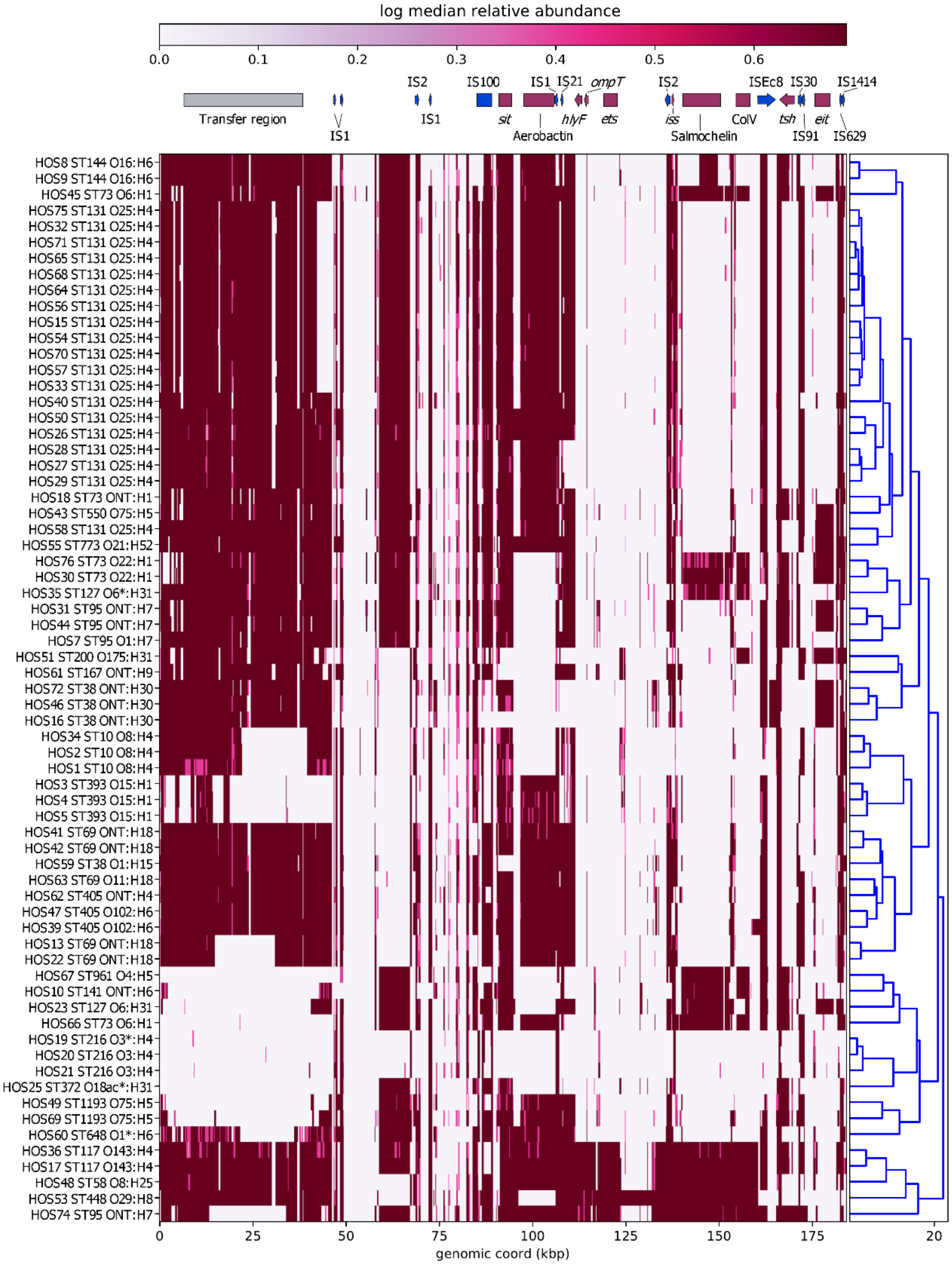
Supplementary Data 2. B) The pie chart of the breakdown of genes and the number of isolates they are presented in, showing relative abundance of each group of genes with vast majority to be cloud genes (genes which are present in less than 8 samples).



Supplementary Data 2. C) Pangenome gene presence/absence map highlighting similarities between EXPEC STs. All genomes annotated by Prokka, analysed by Roary, and visualised by Phandango.



Supplementary Data 6: Short-read mapping to PAI IV_{536}/HPI. Tree to the left of heatmap were constructed by hierarchical clustering using Euclidean agglomeration method.



Supplementary Data 8: Short-read mapping to colV plasmid pAPEC-O2-ColV. Tree to the left of heatmap were constructed by hierarchical clustering using Euclidean agglomeration method

Supplementary Data 9: Table cataloguing SNPs in serial patients

SNP analysis of serial isolates. Coloured amino acid changes signify negative values for substitutions using BLOSUM64 matrix [reference]. Green = -1 or -2 Red = -3 or -4

Isolate	**ST/Serotype**	**Diagnosis**	**Time difference from initial (days)**	
HOS1	ST10/O8:H4	Cystitis	-	
HOS2	ST10/O8:H4	Pyelonephritis	63	
HOS34	ST10/O8:H4	Pyelonephritis	78	
SNP Analysis				
Gene	**SNP or variation**	**Amino acid change**	**Recurrent infection**	**Different Patient**
speC	G->T	H333Q	✓	✓
gspI	G->C	H67Q	✓	✓
irp1	T->G	D2717A	✓	✓
ybtS	C->G	P184A	✓	✓
	CA->GC	A189G	✓	✓
astA	G->T	G103V	✓	✓
aroC	C->T	G152E	✓	✓
menD	C->T	D412N	✓	✓
hyfD	T->G	L374V	✓	✓
fadH	C->A	Silent I98	✓	✓
astD	C->T	Silent A37	✓	✓
rnhB	C->A	R98L	✓	✓
hrpB	C->T	G644E	✓	✓
traC	G->T	G493W	✓	✓
	G->C	E494Q	✓	✓
recC	G->T	S794C	✓	✓
	G->T	H793N	✓	✓
mfd	G->T	A432D	✓	
zntA	A->G	V411A	✓	✓
ugpC	C->A	L297M	✓	✓
modB	T->G	Silent L208	✓	✓
lsrA	A->G	E296G	✓	✓
	G->C	Silent A306		✓
drrB	G->T	T99N	✓	✓
chemotaxis YjcZ-like protein	G->T	Silent P172	✓	✓
YdbH family protein	A->G	L103P	✓	
	G->A	Silent S96	✓	✓
mobA	T->G	S252A		✓
14 bp insertion between partial *btuC* and hypothetical	A-> ACCTCAGTTGATTTG		✓	
Between two tRNA-Gly	TAAG->CAAA		✓	
Between *yjjG* and *prfC*	A->G		✓	
Between *sodC2* and scaffold break	A->G			✓
Between *paaD* and contig break	C->T			✓
Between tRNA-Arg and scaffold break	G->A			✓
Isolate	**ST/Serotype**	**Diagnosis**	**Time difference from initial (days)**	**Total SNPs**

HOS3	ST393/O15:H1	Cystitis	-	-
HOS4	ST393/O15:H1	Pyelonephritis	284	13
HOS5	ST393/O15:H1	Pyelonephritis	412 (128 after recurrent 1)	19
SNP Analysis				
Gene	**SNP or variation**	**Amino acid change**	**Recurrent infection I**	**Recurrent infection 2**
fecA	G->A	E124D	✓	
allC	A->G	I148T	✓	
galE	G->GA	Addition of E39 causing fusion with *capD*	✓	✓
fimH	G->A	A23V		✓
*rfaL**	T->TGGTTAC	Insertion of G and Y at 287		✓
ybiB	T->C	S227G	✓	
folC	A->T	Silent V93	✓	✓
argH	T->C	Silent A61	✓	✓
cysH	GCGCACAGCAGAA->G	Deletion of R, T, A and Q at 149-152	✓	
gpsA	C->T	T135M	✓	
udp	C->T	Q166STOP causing 9.9 kDa truncation		✓
mukF	A->C	F401V	✓	✓
	CGT->GTG	T394H	✓	✓
*ompF**	C->CT	Causing addition of 13.7 kDa		✓
BapA prefix-like domain-containing protein	C->G	STOP6042Y causing fusion with hypothetical protein	✓	✓
Autotransporter*	GAT->G	Deletion causing truncation of 39.3 kDa		✓
Between *yqjH* and tRNA-Met	G->C		✓	
Between *Alaa* and *LrhA*	T->C		✓	
Small contig, possibly within fibronectin type III protein	G->A			✓
	T->G			✓
	C->T			✓
Between *fimA* and *fimE*	T->TCC			✓
Between *gldA* and *yiijF**	TTACC->ATACG			✓
	T->C			✓
	TC->GA			✓
	A->C			✓
Isolate	**ST/Serotype**	**Diagnosis**	**Time difference from initial (days)**	**Total SNPs**
HOS8	ST144/O16:H6	Cystitis	-	-
HOS9	ST144/O16:H6	Cystitis	0	5
SNP Analysis				
Gene	**SNP or variation**	**Amino acid change**		
tnpB	C->T	G11R		
	C->T	Silent L116		
cysJ	C->G	V371L		
hofM	C->G	Silent A232		
ves	C->G	G7R		

Isolate	ST/Serotype	Diagnosis	Time difference from initial (days)	Total SNPs
HOS26	ST131/O25:H4	Cystitis	-	-
HOS27	ST131/O25:H4	Urosepsis	181	53
HOS28	ST131/O25:H4	Urosepsis	282 (101 after recurrent infection 1)	61
HOS29	ST131/O25:H4	Urosepsis	285 (3 after recurrent infection 2)	62
HOS50	ST131/O25:H4	Pyelonephritis	27 before initial presentation	21

SNP Analysis

Gene	SNP or variation	Amino acid change	Recurrent infection 1	Recurrent infection 2	Recurrent infection 3	Different Patient
kpsM	G->T	R18L	✓	✓	✓	✓
speC	C->T	A385	✓	✓	✓	✓
cyaA	T->C	V315A	✓	✓	✓	✓
narI	T->G	M128L	✓	✓	✓	✓
	G->C	A124G	✓	✓	✓	✓
iutA	C->T	G419D	✓	✓	✓	
*iucC**	A->G	Silent H38	✓	✓	✓	
	GGC->TGT	A25T	✓	✓	✓	
	C->A	Silent T16	✓	✓	✓	
	A->C	H12Q	✓	✓	✓	
	T->G	M9L	✓	✓	✓	
	C->A	E8D	✓	✓	✓	
	A->G	Silent C5	✓	✓	✓	
*sitC**	T->C	Silent K279	✓	✓	✓	
	C->T	Silent V230	✓	✓	✓	
	T->G	I177L	✓	✓	✓	
	G->A	Silent S115	✓	✓	✓	
	G->A	Silent G95	✓	✓	✓	
	A->G	Silent T86	✓	✓	✓	
	A->C	L85R	✓	✓	✓	
	T->A	Silent A75	✓	✓	✓	
	G->A	Silent L46	✓	✓	✓	
*sitB**	T->A	Silent A264	✓	✓	✓	
	C->T	Silent L234	✓	✓	✓	
	C->T	Silent T199	✓	✓	✓	
	G->A	Silent T171		✓	✓	
	C->G	Silent Q179	✓	✓	✓	
	C->T	D134N	✓	✓	✓	
	C->T	Silent Q121	✓	✓	✓	
	C->A	Q88D	✓	✓	✓	
	G->A	Silent L75	✓	✓	✓	
	T->C	Silent T71	✓	✓	✓	

	C->T	Silent G62	✓	✓	✓	
	GCC->ACT	G32S	✓	✓	✓	
*sitA**	T->C	Silent G110	✓	✓	✓	
	G->A	Silent A109	✓	✓	✓	
	C->A	Silent L96	✓	✓	✓	
	A->C	Silent P90	✓	✓	✓	
	A->G	Silent G74	✓	✓	✓	
	C->T	Silent A71	✓	✓	✓	
*flgK**	GCAATGGCGTCTACGTTTCTGGTGTGCA->G	Deletion of N, G, V, Y, V, S, G, V and Q at 55		✓	✓	
TerC family protein	G->A	Silent V36		✓	✓	
irp2	C->T	G201E		✓	✓	✓
moeA	G->T	R268L	✓	✓	✓	✓
galF	T->C	Silent R118				✓
aceK	C->T	Silent N550	✓			
prpE	T->C	Silent K587	✓			
nrdD	C->T	G389S	✓	✓	✓	✓
putative DNA-binding transcriptional regulator	T->G	E69D	✓	✓	✓	✓
dinG	T->A	I318L	✓	✓	✓	✓
uroporphyrinogen-III C-methyltransferase*	CGGTGCA->C	Deletion of P and A at 389			✓	
mdtK	T->C	Silent R302	✓	✓	✓	
hycC	T->G	S585A		✓	✓	✓
traC	A->G	S550P		✓	✓	
glp	C->A	Silent V107	✓	✓	✓	✓
ycdY	T->C	M58R	✓	✓	✓	✓
ag43/flu	A->G	Silent G752	✓	✓	✓	✓
sixA	A->G	Silent A117	✓	✓	✓	✓
yjbH domain-containing protein	G->A	Silent E52		✓	✓	
yaiW	T->C	Q24R		✓	✓	
gpH	G->T	Silent A716		✓	✓	✓
	G->C	R715G		✓	✓	✓
	A->C	C713G		✓	✓	✓
Hypothetical protein WLH_00908	G->T	G129V		✓	✓	
Between partial *mpi* and *dpK*	GGCGC->TGCAT		✓			
Between *AraH* and *otsB*	C->T		✓			

Between *wrbA* and MBL fold metallo-hydrolase	C->T		✓	✓	✓	✓
Between *SitC* and scaffold break	T->C		✓	✓	✓	
	A->T		✓	✓	✓	
Between replication protein rep and scaffold break	T->C			✓	✓	✓
Between *caiE* and scaffold break	A->C				✓	

Isolate	**ST/Serotype**	**Diagnosis**	**Time difference from initial (days)**	**Total SNPs**
HOS41	ST69/ONT:H18	Urosepsis	-	-
HO542	ST69/ONT:H18	Urosepsis		12

SNP Analysis

Gene	**SNP or variation**	**Amino acid change**	**Recurrent infection**
ybtT	C->A	R133L	
	C->G	E132Q	
	C->T	R128H	
lpxM	C->G	Silent L70	
	A->C	STOP73C causing fusion with *ipxM*	
sipD	C->A	N4K	
cvrA	T->G	R337S	
hypothetical protein	A->G	Silent I170	
hypothetical protein	CA->AG	M1A	
Between *yjjV* and scaffold break	C->A		
Between tRNA-Lys and *nadA*	G->A		
Between DUF905 domain-containing protein and *parB*	A->G		
Between hypothetical protein and scaffold break	T->C		