

Supplementary

Table S1. IMPACT2 patient information.

Sample Number	Patient Number	Gender	Age	Length of ICU Stay (days)	Overarching admission category	Admission from
QEH05	IMP2-05	F	45	19	Neurology	Other hospital
QEH06	IMP2-06	F	29	11	Hepatic	Other hospital
QEH08	IMP2-08	F	47	55	Transplant	Community
QEH09	IMP2-09	M	23	5	Burns	Community
QEH10	IMP2-10	M	41	13	Cardiovascular	Community
QEH11	IMP2-11	M	77	3	Cardiovascular	4 days on QEHB general ward
QEH13	IMP2-13	M	50	10	Neurology	10 days on QEHB general ward
QEH14	IMP2-14	F	57	14	Neurology	Other hospital
QEH15	IMP2-15	M	79	5	Cardiovascular	Community
QEH16	IMP2-16	M	80	7	Neurology	10 days on QEHB general ward
QEH19	IMP2-19	M	68	20	Trauma	Community
QEH20	IMP2-20	M	73	14	Oncology	Community
QEH21	IMP2-21	F	74	51	Trauma	Community
QEH23	IMP2-23	F	53	14	Cardiovascular	Community
QEH24	IMP2-24	M	20	16	Trauma	Community
QEH25	IMP2-25	F	61	24	Oncology	1 day on QEHB general ward
QEH26	IMP2-26	M	51	22	Gastroenterology	Other hospital
QEH28	IMP2-28	F	54	9	Elective surgery	Community
QEH29	IMP2-29	M	51	30	Neurology	Community
QEH30	IMP2-30	M	55	27	Respiratory	Community
QEH32	IMP2-32	M	56	17	Trauma	Community
QEH33	IMP2-33	M	25	8	Trauma	Community
QEH37	IMP2-37	M	44	16	Transplant	Community

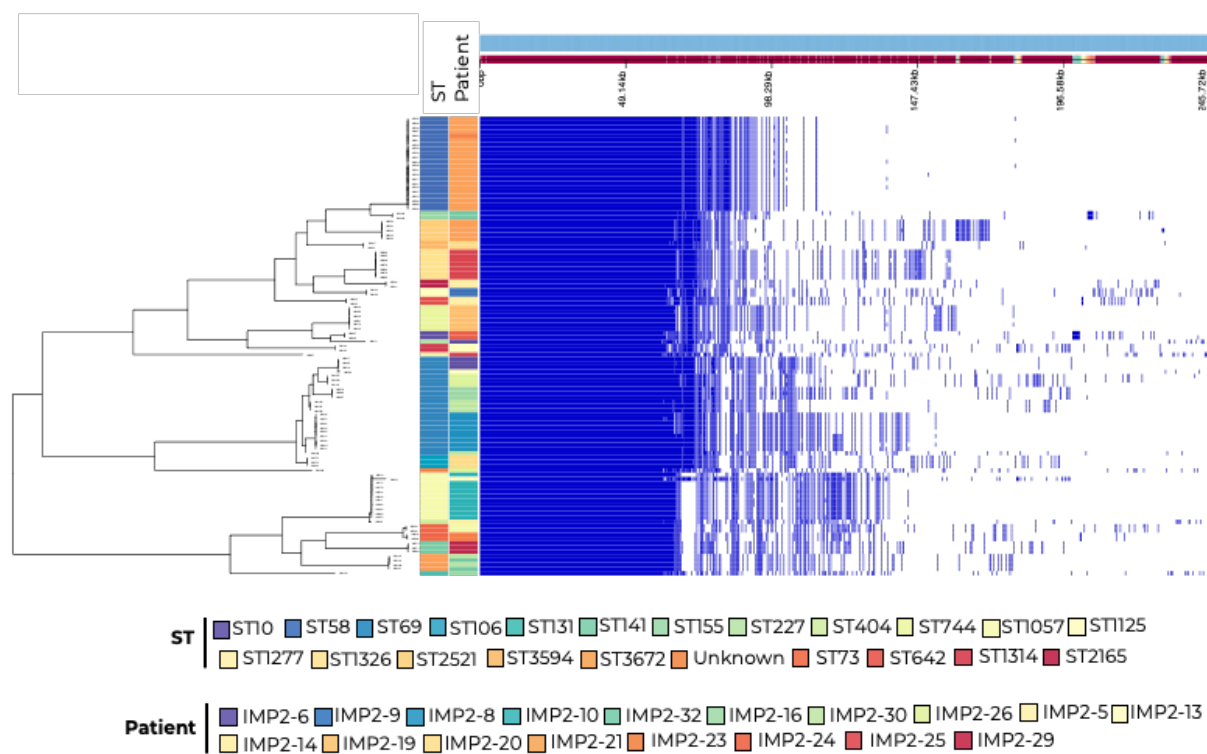
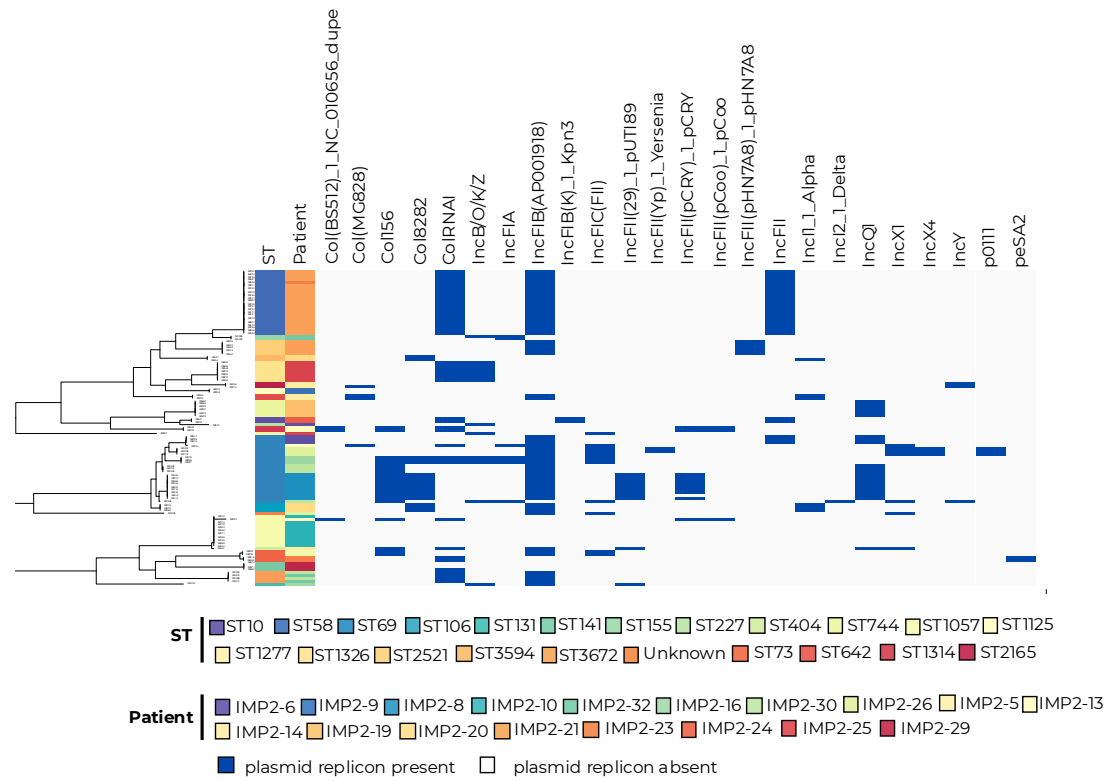


Fig. S2. *E. coli* core gene alignment phylogeny with Panaroo core gene presence absence profile in navy displayed alongside patient number and *E. coli* ST.

a)



b)

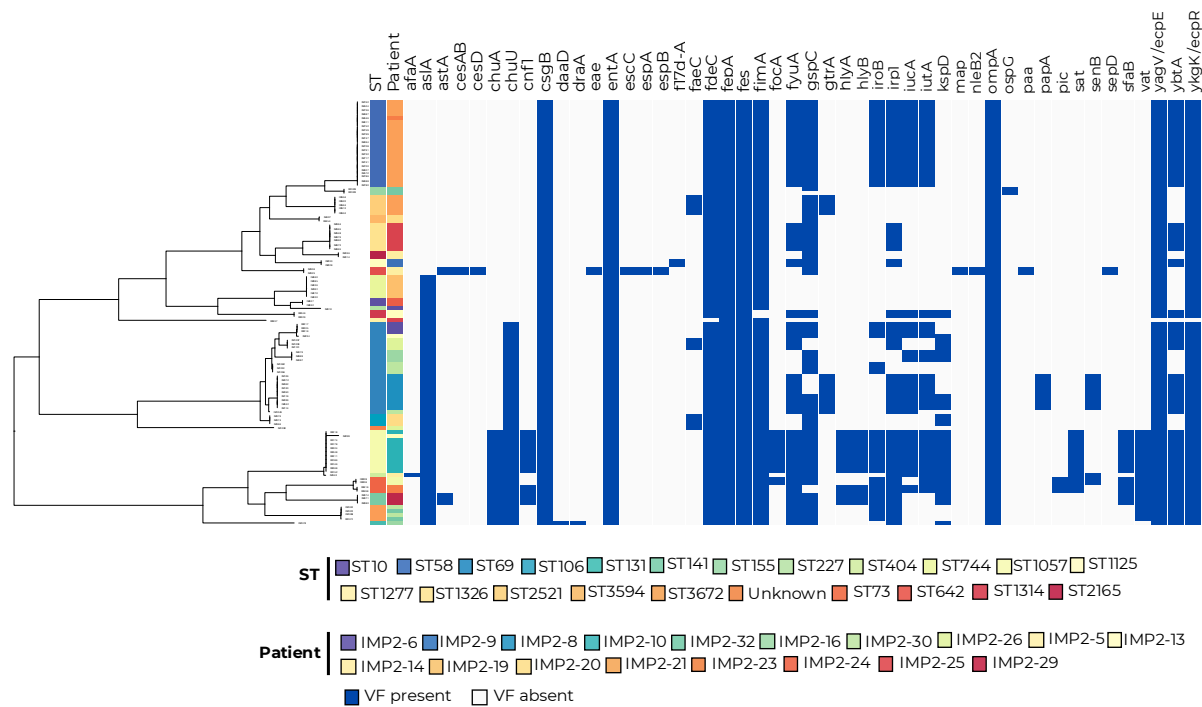


Fig. S3. A) Plasmid replicon profile and b) virulence factor profile for all colonising *E. coli* displayed alongside ST and patient number. Plasmid replicon/virulence gene presence (navy) and absence (grey) are indicated. A selection of virulence genes are displayed here, representing those normally seen in pathogenic *E. coli*.

Table S4 SNP difference matrix of ST69 strains*

Isolate	Patient	IM476	IM487	IM889	IM234	IM1093	IM1097	IM1101	IM1049	IM1051	IM1056	IM1062	IM005	IM016	IM017	IM039	IM042	IM050	IM062	IM072	IM106	IM114	IM116	IM120
IM476	IMP2-16	0	0	0	7651	6049	6050	6045	6766	4701	4700	4701	7563	7566	7563	8095	8093	8096	8096	8095	8097	8097	8096	8095
IM487	IMP2-16	0	0	0	7651	6049	6050	6045	6766	4701	4700	4701	7563	7566	7563	8095	8093	8096	8096	8095	8097	8097	8096	8095
IM889	IMP2-16	0	0	0	7651	6049	6050	6045	6766	4701	4700	4701	7563	7566	7563	8095	8093	8096	8096	8095	8097	8097	8096	8095
IM234	IMP2-13	7651	7651	7651	0	6566	6567	6562	8201	6044	6043	6044	406	409	406	7834	7832	7835	7835	7834	7836	7836	7835	7834
IM1093	IMP2-26	6049	6049	6049	6566	0	13	4	6076	3957	3956	3957	6299	6302	6299	6370	6368	6371	6371	6370	6372	6372	6371	6370
IM1097	IMP2-26	6050	6050	6050	6567	13	0	9	6077	3958	3957	3958	6300	6303	6300	6371	6369	6372	6372	6371	6373	6373	6372	6371
IM1101	IMP2-26	6045	6045	6045	6562	4	9	0	6072	3953	3952	3953	6295	6298	6295	6366	6364	6367	6367	6366	6368	6368	6367	6366
IM1049	IMP2-30	6766	6766	6766	8201	6076	6077	6072	0	2363	2362	2363	7929	7932	7929	1691	1689	1692	1692	1691	1693	1698	1692	1693
IM1051	IMP2-30	4701	4701	4701	6044	3957	3958	3953	2363	0	1	0	5798	5801	5798	3782	3780	3783	3783	3782	3784	3784	3783	3782
IM1056	IMP2-30	4700	4700	4700	6043	3956	3957	3952	2362	1	0	1	5797	5800	5797	3781	3779	3782	3782	3781	3783	3783	3782	3781
IM1062	IMP2-30	4701	4701	4701	6044	3957	3958	3953	2363	0	1	0	5798	5801	5798	3782	3780	3783	3783	3782	3784	3784	3783	3782
IM005	IMP2-6	7563	7563	7563	406	6299	6300	6295	7929	5798	5797	5798	0	3	0	7581	7579	7582	7582	7581	7583	7583	7582	7581
IM016	IMP2-6	7566	7566	7566	409	6302	6303	6298	7932	5801	5800	5801	3	0	3	7584	7582	7585	7585	7584	7586	7586	7585	7584
IM017	IMP2-6	7563	7563	7563	406	6299	6300	6295	7929	5798	5797	5798	0	3	0	7581	7579	7582	7582	7581	7583	7583	7582	7581
IM039	IMP2-8	8095	8095	8095	7834	6370	6371	6366	1691	3782	3781	3782	7581	7584	7581	0	4	3	3	4	4	9	3	4
IM042	IMP2-8	8093	8093	8093	7832	6368	6369	6364	1689	3780	3779	3780	7579	7582	7579	4	0	5	5	6	6	11	5	6
IM050	IMP2-8	8096	8096	8096	7835	6371	6372	6367	1692	3783	3782	3783	7582	7585	7582	3	5	0	0	1	1	8	4	1
IM062	IMP2-8	8096	8096	8096	7835	6371	6372	6367	1692	3783	3782	3783	7582	7585	7582	3	5	0	0	1	1	8	4	1
IM072	IMP2-8	8095	8095	8095	7834	6370	6371	6366	1691	3782	3781	3782	7581	7584	7581	4	6	1	1	0	2	9	5	2
IM106	IMP2-8	8097	8097	8097	7836	6372	6373	6368	1693	3784	3783	3784	7583	7586	7583	4	6	1	1	2	0	9	5	2
IM114	IMP2-8	8097	8097	8097	7836	6372	6373	6368	1698	3784	3783	3784	7583	7586	7583	9	11	8	8	9	9	0	10	9
IM116	IMP2-8	8096	8096	8096	7835	6371	6372	6367	1692	3783	3782	3783	7582	7585	7582	3	5	4	4	5	5	10	0	5
IM120	IMP2-8	8095	8095	8095	7834	6370	6371	6366	1693	3782	3781	3782	7581	7584	7581	4	6	1	1	2	2	9	5	0

*Isolates with less than 13 SNPs different are highlighted in red. Patient number is displayed alongside SNP differences. White and grey banding is used to display different patients by rows. Only IMP2-6 and IMP2-8 had overlapping ICU stays.

Table S5 SNP difference matrix of ST58 strains*

Isolate	Patient	IM504	IM572	IM646	IM688	IM694	IM708	IM717	IM732	IM736	IM741	IM747	IM752	IM759	IM762	IM780	IM786	IM791	IM799	IM807	IM811	IM687	IM700
IM504	IMP2-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
IM572	IMP2-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
IM708	IMP2-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
IM688	IMP2-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
IM694	IMP2-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
IM717	IMP2-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
IM732	IMP2-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
IM736	IMP2-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
IM741	IMP2-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
IM646	IMP2-23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
IM747	IMP2-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
IM752	IMP2-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
IM759	IMP2-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
IM762	IMP2-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
IM780	IMP2-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
IM786	IMP2-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
IM791	IMP2-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
IM799	IMP2-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
IM807	IMP2-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
IM811	IMP2-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
IM687	IMP2-21	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	2
IM700	IMP2-21	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	0

*Isolates with 0 SNPs different are highlighted in yellow. Patient number is displayed alongside SNP differences. White and grey banding is used to display different patients by rows. IM646 was isolated a day after IM741.

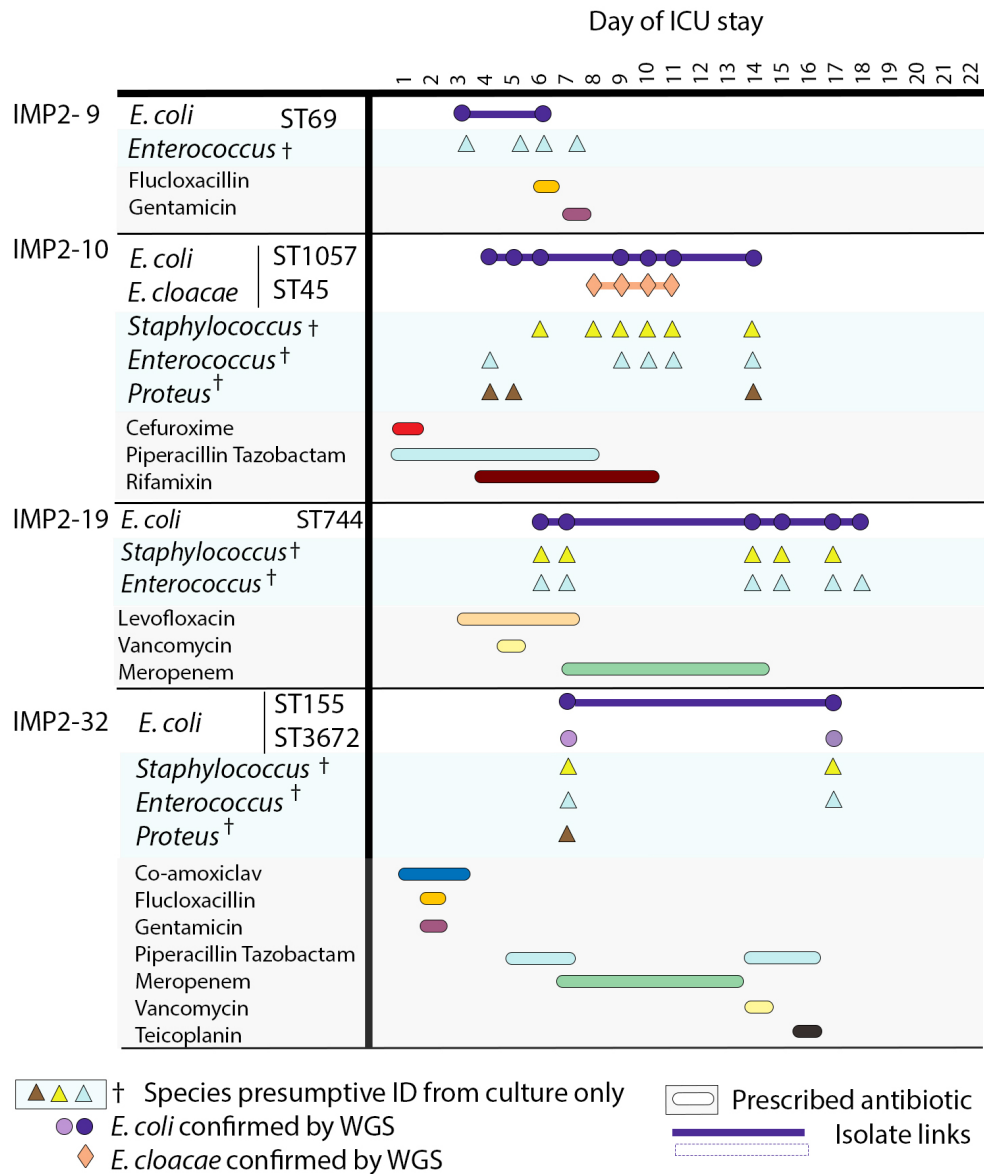


Fig. S6 Colonising isolates in patients where *E. coli* colonisation was stable during inpatient stay. All species confirmed using WGS are displayed alongside species presumptively identified using culture plates only. Antibiotics prescribed during a patient stay is displayed below. Patients were in the ICU at differing times but for the purpose of this figure the timeline is the inpatient stay day number. In cases where STs are the same they are shown on this figure as the same colour when they occurred in the same patient, but these colours cannot be compared across patients. Isolate links demonstrated with a solid line where colonisation occurs. A dashed line is used where this ST strain is interrupted by another ST.

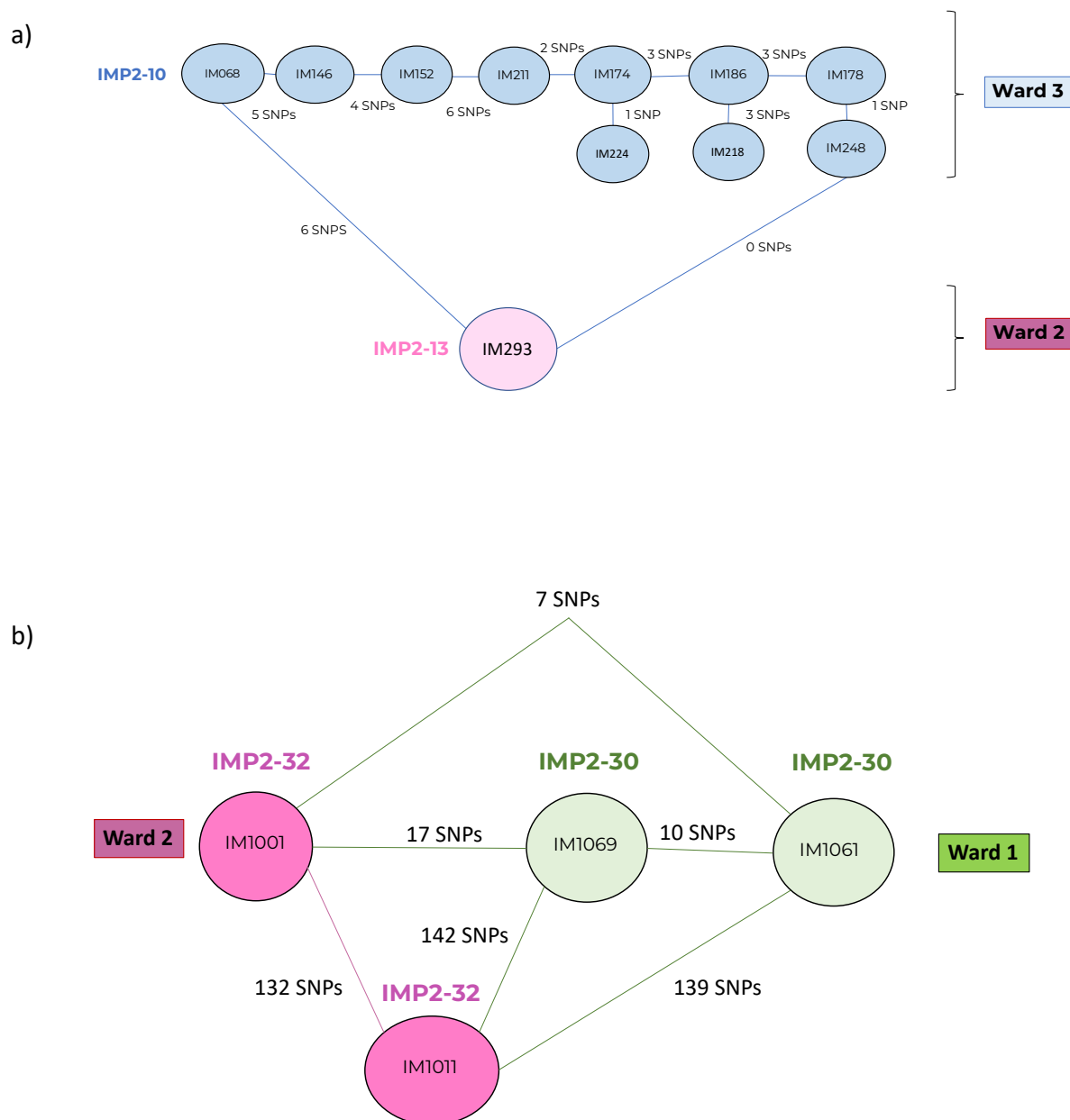


Fig. S7 - Colonisation of different patients with the same *E. coli* strain of a) ST1057 and b) ST3672. IM number refers to isolate number and IMP2 number is patient number. SNP differences and ward location (Ward 1 /Ward 2 /Ward 3) are displayed. Ward name where the patient was staying at the time of isolation is linked to the colour of isolate from the ward (Ward 1: Green, Ward 2: Pink, Ward 3: Blue). IM293 was isolated 29 days after IM068. IM1001 and IM1011 were isolated 23 and 33 days after IM1069 respectively.

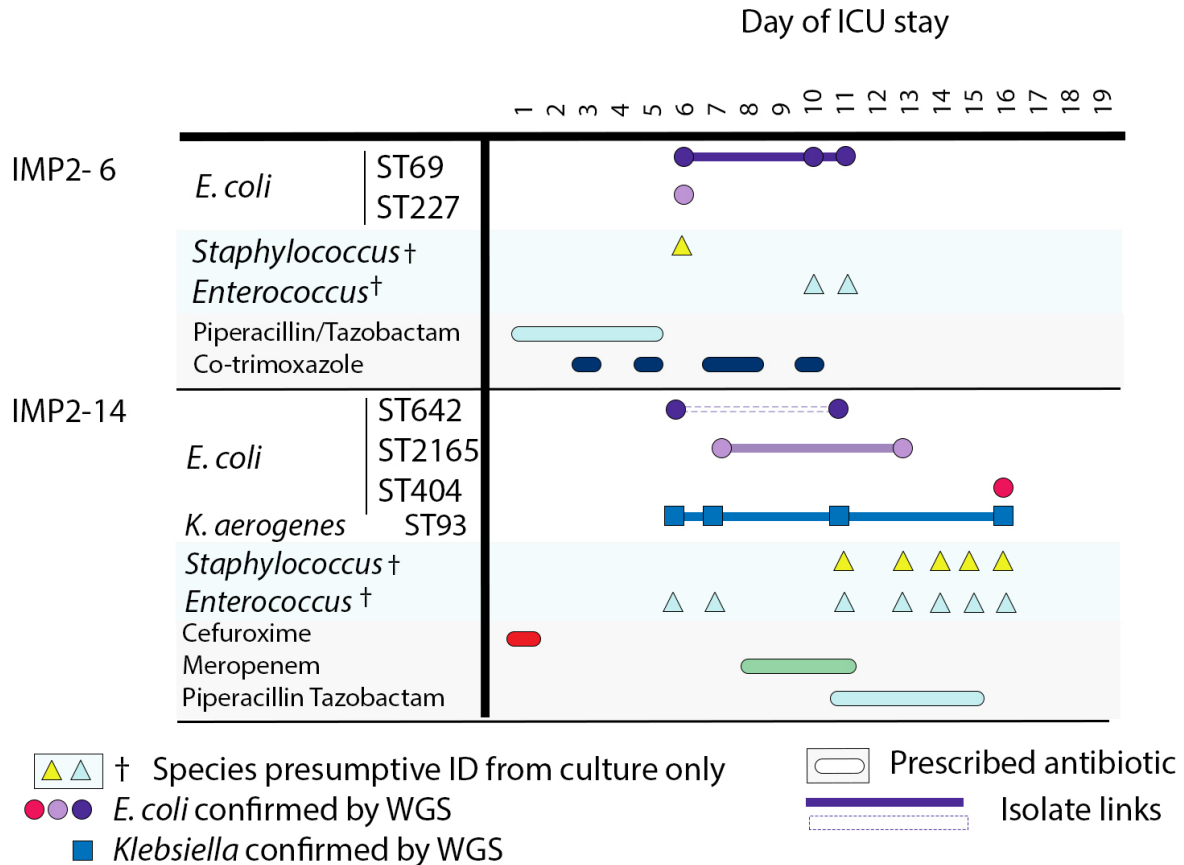


Fig. S8 Fluctuating colonisation in ICU patients. All species confirmed using WGS are displayed alongside species presumptively identified using culture plates only. Antibiotics prescribed during a patient stay is displayed below. Patients were in the ICU at differing times but for the purpose of this figure the timeline is the inpatient stay day number. In cases where STs are the same they are shown on this figure as the same colour when they occurred in the same patient, but these colours cannot be compared across patients. Isolate links demonstrate with a solid line where colonisation occurs with a solid line and where this ST strain is interrupted by another ST, a dashed line is used.

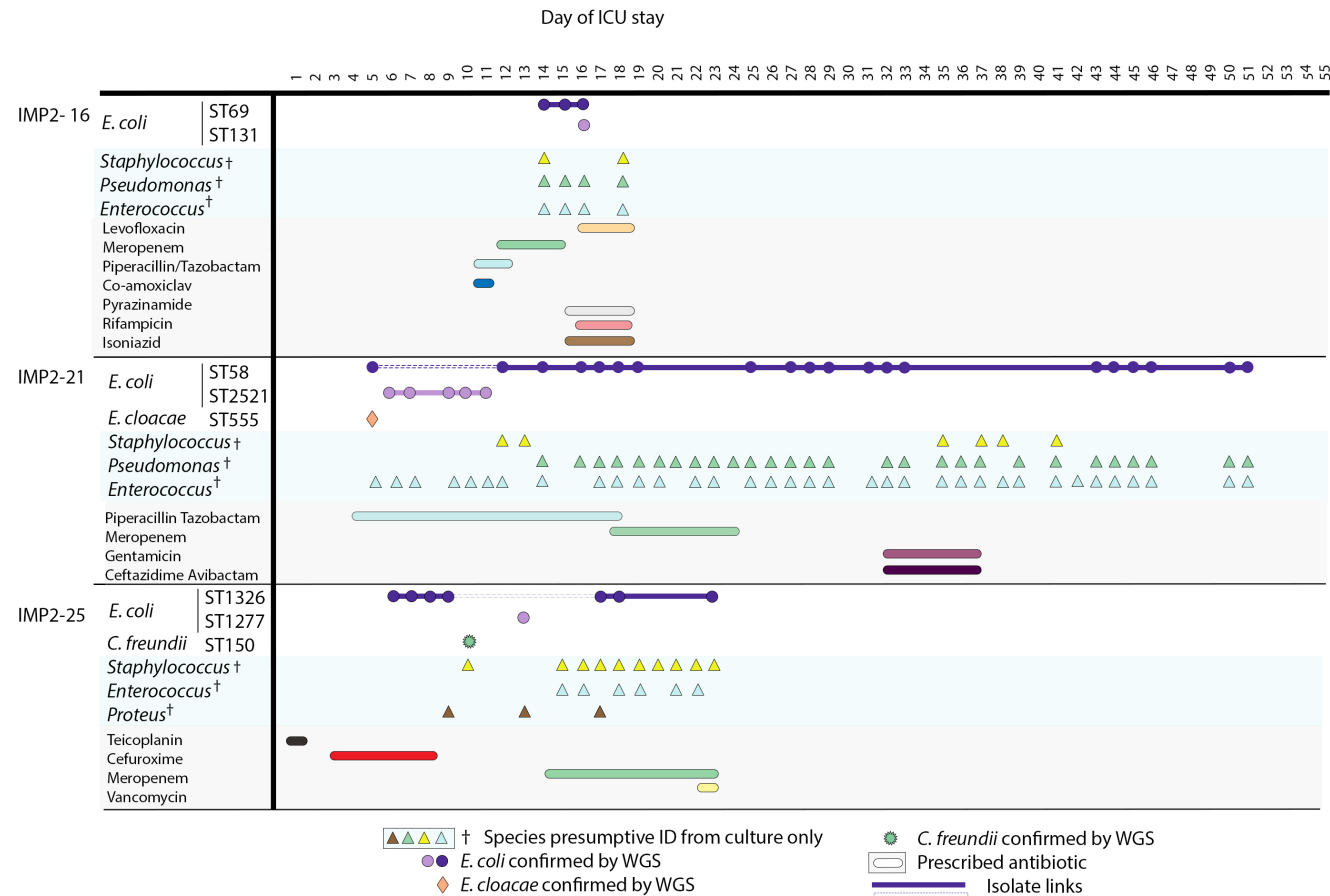


Fig. S9 Colonising isolate timeline where the patient acquired a new *E. coli* ST during their stay. All species confirmed using WGS are displayed alongside species presumptively identified using culture plates only. Antibiotics prescribed during a patient stay is displayed below. Patients were in the ICU at differing times but for the purpose of this figure the timeline is the inpatient stay day number. In cases where STs are the same they are shown on this figure as the same colour when they occurred in the same patient, but these colours cannot be compared across patients. Isolate links demonstrate with a solid line where colonisation occurs with a solid line and where this ST strain is interrupted by another ST, a dashed line is used.

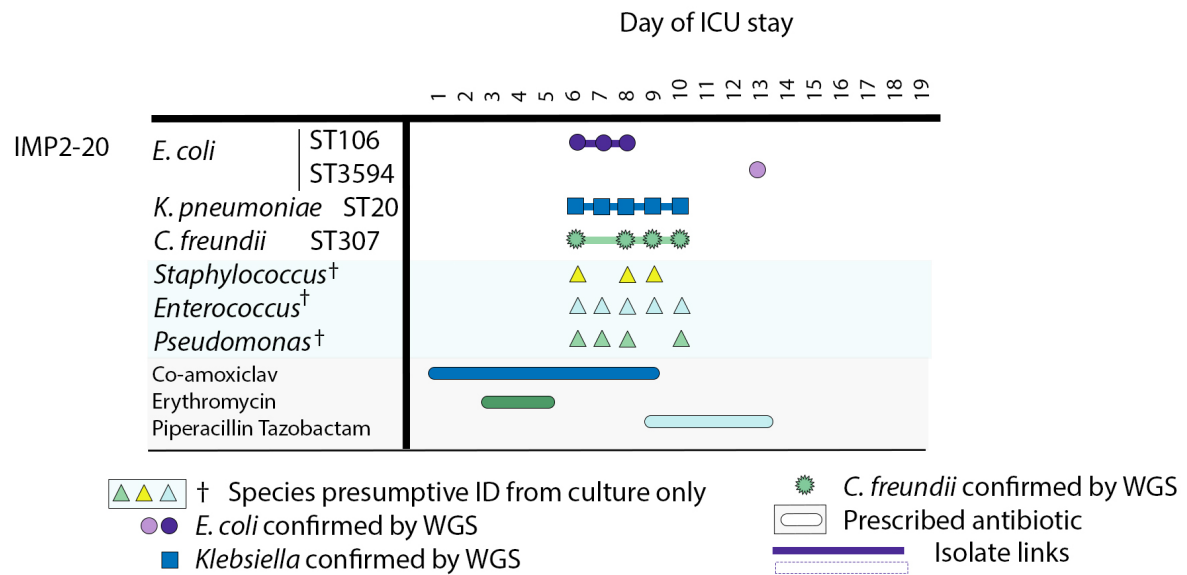


Fig. S10 IMP2-20 timeline where an acquired *E. coli* appeared to overgrow other initial colonising species. All species confirmed using WGS are displayed alongside species presumptively identified using culture plates only. Antibiotics prescribed during a patient stay is displayed below. Patients were in the ICU at differing times but for the purpose of this figure the timeline is the inpatient stay day number. In cases where STs are the same they are shown on this figure as the same colour when they occurred in the same patient, but these colours cannot be compared across patients. Isolate links demonstrate with a solid line where colonisation occurs with a solid line and where this ST strain is interrupted by another ST, a dashed line is used.

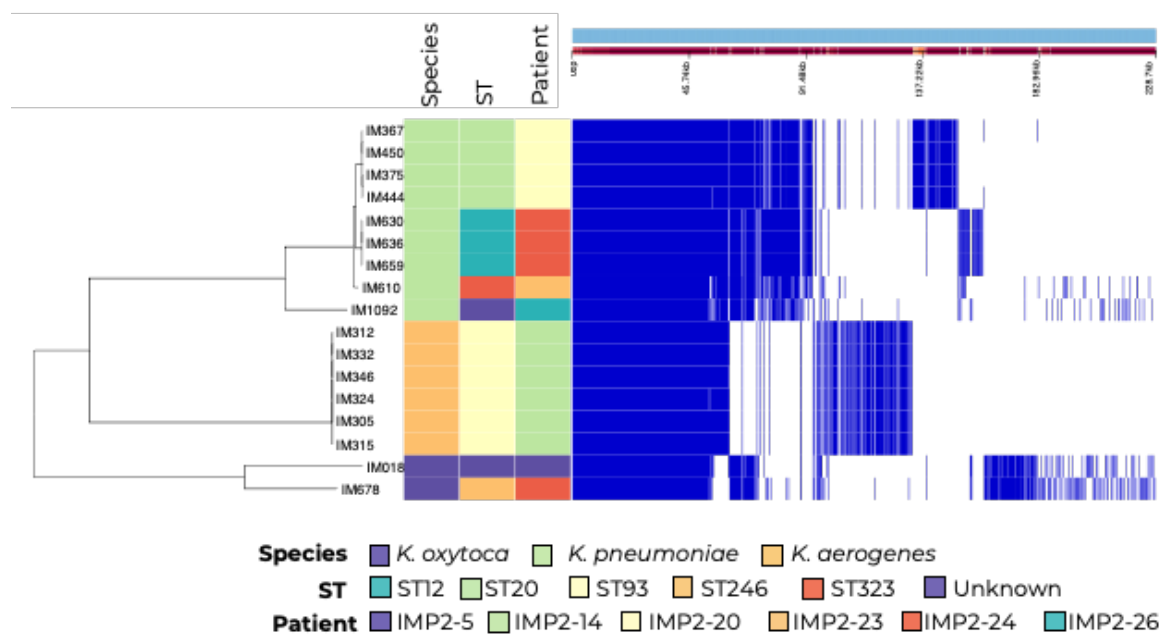
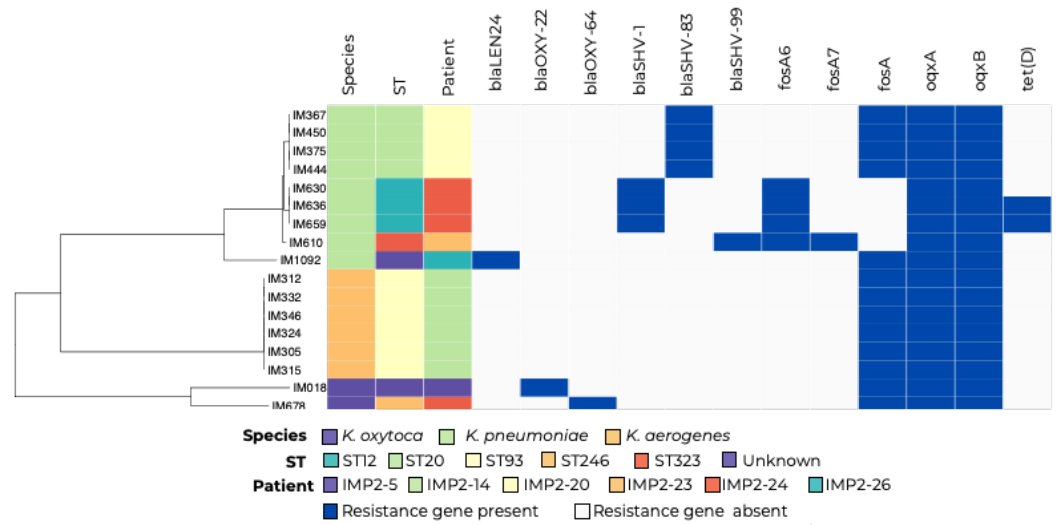
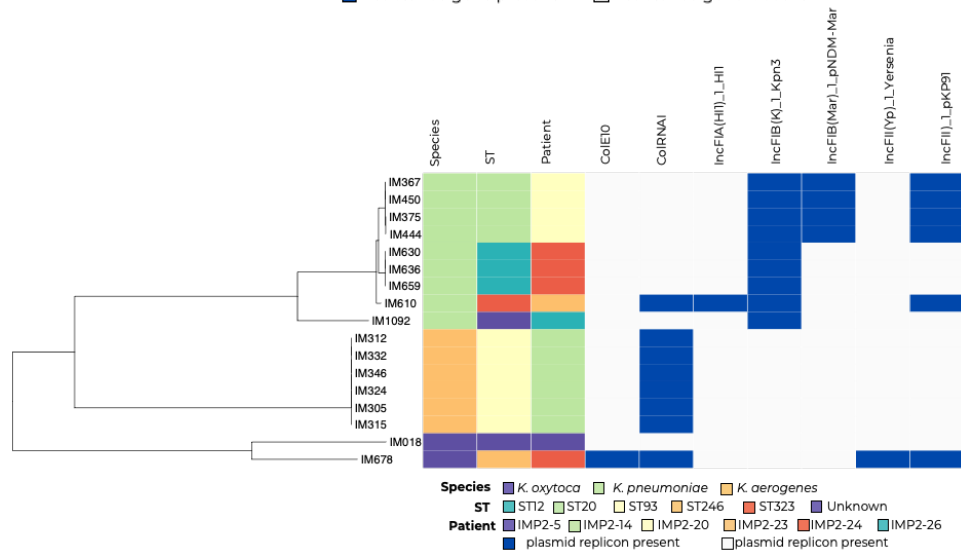


Fig. S11 *Klebsiella* core gene alignment phylogeny with Panaroo core gene presence absence profile, patient number and *E. coli* ST displayed alongside. Blue is core gene presence and white is core gene absence. Phylogenetic tree is midpoint rooted with increasing nodes.

a)



b)



c)

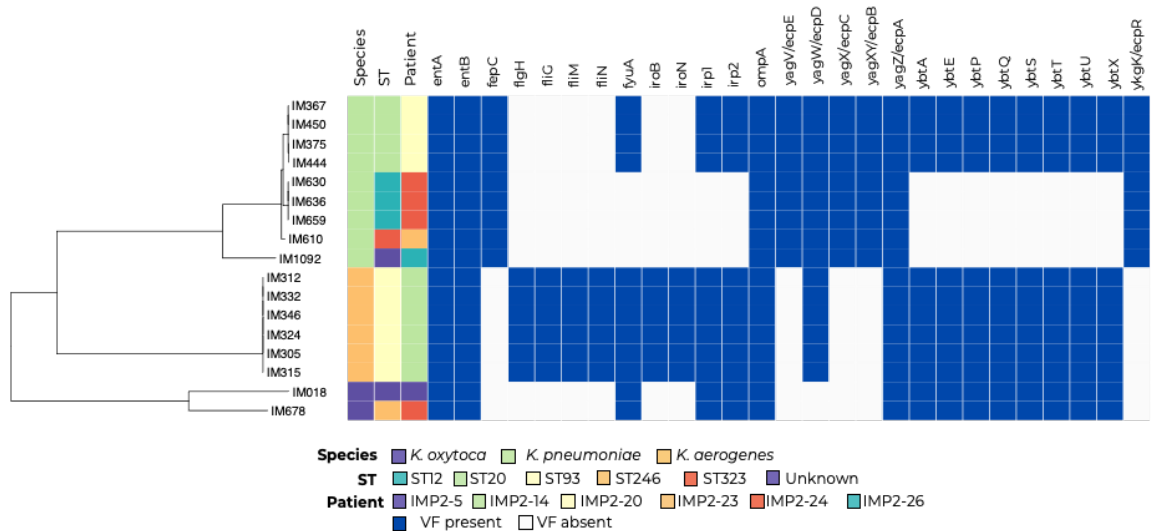


Fig. S12 a) Resistance profile, b) Plasmid replicon profile and c) virulence gene profile for all colonising *Klebsiella* displayed alongside ST and patient number. Navy indicates resistance/plasmid replicon gene presence and grey resistance/plasmid replicon gene absence. Phylogeny is midpoint rooted with increasing nodes.

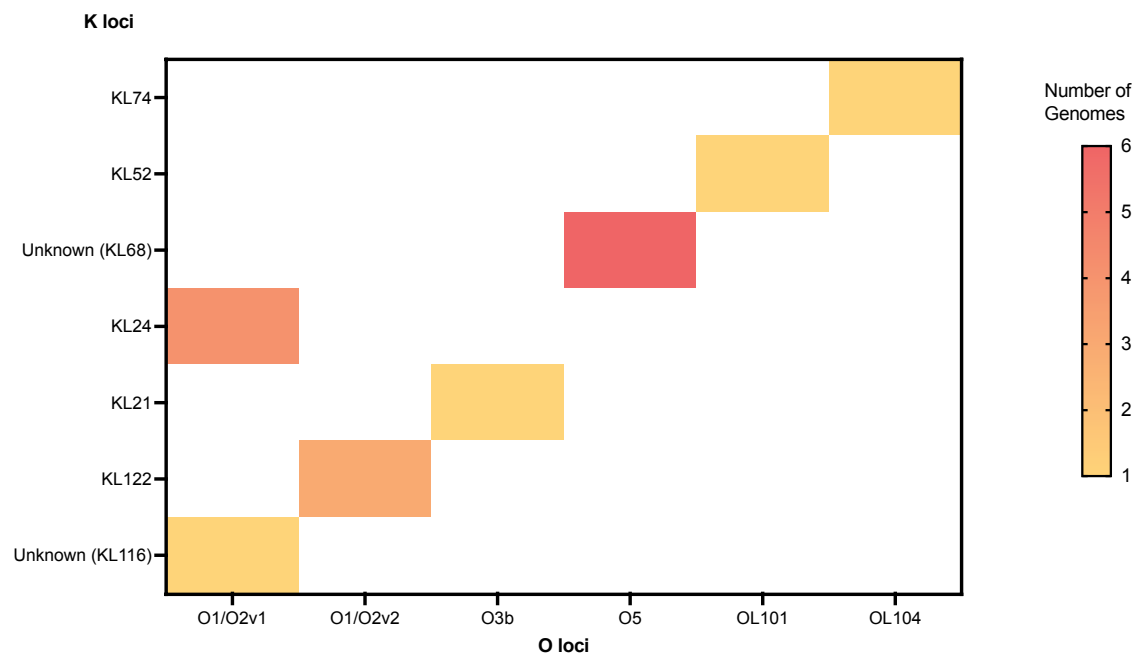
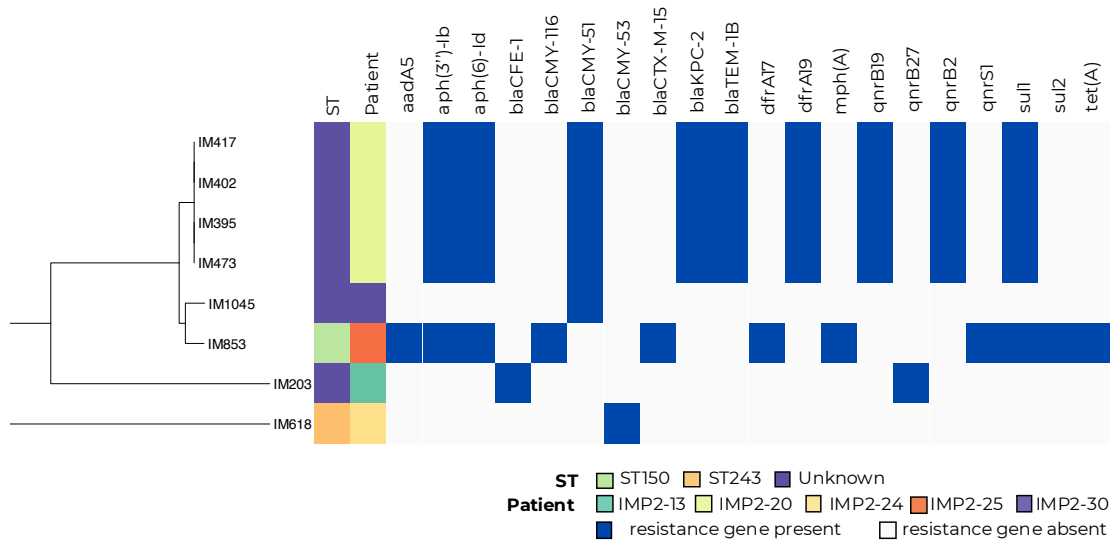


Fig. S13 K and O loci of all *Klebsiella* isolates as allocated by Kleborate. Number of genomes with the specific K and O loci combination demonstrated by colour gradient.

a)



b)

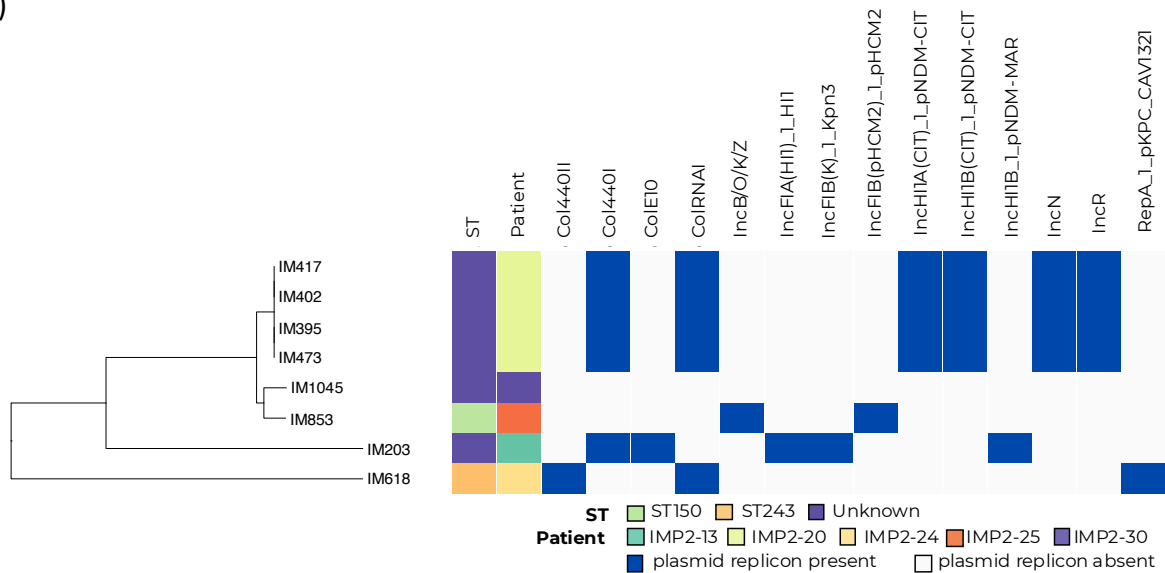


Fig. S14 a) Acquired resistance gene profile and **b)** Plasmid replicon profile for all colonising *C. freundii* displayed next to ST and patient number. There were 8 colonising *Citrobacter freundii* identified in this study, six of which could not be assigned a sequence type. Navy indicates resistance gene/plasmid replicon presence and grey resistance gene/plasmid replicon absence. Phylogeny is midpoint rooted with increasing nodes.

Table S6 – *Enterobacter cloacae* characteristics

Isolate	Patient	Day	ST	Patient	Resistance Genes	Plasmid Replicons
IM157	IMP2-10	7	45	IMP2-10	<i>bla</i> _{ACT-15f} , <i>mdf</i> (A), <i>oqx</i> A, <i>oqx</i> B	Col440I, ColRNAI, IncR
IM212	IMP2-10	8	45	IMP2-10	<i>bla</i> _{ACT-15f} , <i>mdf</i> (A), <i>oqx</i> A, <i>oqx</i> B	Col440I, ColRNAI, IncR
IM217	IMP2-10	10	45	IMP2-10	<i>bla</i> _{ACT-15f} , <i>mdf</i> (A), <i>oqx</i> A, <i>oqx</i> B	Col440I, ColRNAI, IncR
IM223	IMP2-10	9	45	IMP2-10	<i>bla</i> _{ACT-15f} , <i>mdf</i> (A), <i>oqx</i> A, <i>oqx</i> B	Col440I, ColRNAI, IncR
IM1026	IMP2-37	11	50	IMP2-37	<i>bla</i> _{ACT-15f} , <i>fos</i> A, <i>oqx</i> A, <i>oqx</i> B	IncFIB(pB171)_1_pB171
IM1031	IMP2-37	14	50	IMP2-37	<i>bla</i> _{ACT-15f} , <i>fos</i> A, <i>oqx</i> A, <i>oqx</i> B	-
IM1071	IMP2-37	15	50	IMP2-37	<i>bla</i> _{ACT-15f} , <i>fos</i> A, <i>oqx</i> A, <i>oqx</i> B	-
IM1072	IMP2-37	16	50	IMP2-37	<i>bla</i> _{ACT-15f} , <i>fos</i> A, <i>oqx</i> A, <i>oqx</i> B	-
IM993	IMP2-33	7	50	IMP2-33	<i>bla</i> _{ACT-15f} , <i>fos</i> A, <i>oqx</i> A, <i>oqx</i> B	IncFIB(pENTAS01)_1_pENTAS01, IncFII(pECLA)_1_pECLA
IM998	IMP2-33	7	50	IMP2-33	<i>bla</i> _{ACT-15f} , <i>fos</i> A, <i>oqx</i> A, <i>oqx</i> B	Col440I, ColRNAI, IncR
IM999	IMP2-33	7	50	IMP2-33	<i>bla</i> _{ACT-15f} , <i>fos</i> A, <i>oqx</i> A, <i>oqx</i> B	Col440I, ColRNAI, IncR
IM585	IMP2-24	9	133	IMP2-24	<i>bla</i> _{ACT-7f} , <i>fos</i> A, <i>oqx</i> A, <i>oqx</i> B	-
IM670	IMP2-24	16	133	IMP2-24	<i>bla</i> _{ACT-7f} , <i>fos</i> A, <i>oqx</i> A, <i>oqx</i> B	IncFIA(HI1)_1_HI1, IncFIB(pECLA)_1_pECLA, IncFII(pECLA)_1_pECLA
IM676	IMP2-24	13	133	IMP2-24	<i>bla</i> _{ACT-7f} , <i>fos</i> A, <i>oqx</i> A, <i>oqx</i> B	-
IM508	IMP2-21	4	555	IMP2-21	<i>bla</i> _{ACT-9f} , <i>fos</i> A, <i>oqx</i> A, <i>oqx</i> B	Col440II, Col440I
IM227	IMP2-13	8	1704	IMP2-13	<i>bla</i> _{ACT-6f} , <i>mdf</i> (A), <i>oqx</i> A, <i>oqx</i> B	Col440II, Col440I
IM1065	IMP2-30	27	-	IMP2-30	<i>bla</i> _{ACT-6f} , <i>fos</i> A	Col440I, ColRNAI, IncR
IM233	IMP2-13	6	-	IMP2-13	<i>bla</i> _{ACT-14f} , <i>fos</i> A, <i>oqx</i> A, <i>oqx</i> B	Col440II, Col440I

E. cloacae did not carry many resistance genes, with all carrying the AmpC β -lactamase *bla*_{ACT} and other resistance genes that are normally found on the chromosome of *Enterobacter*.