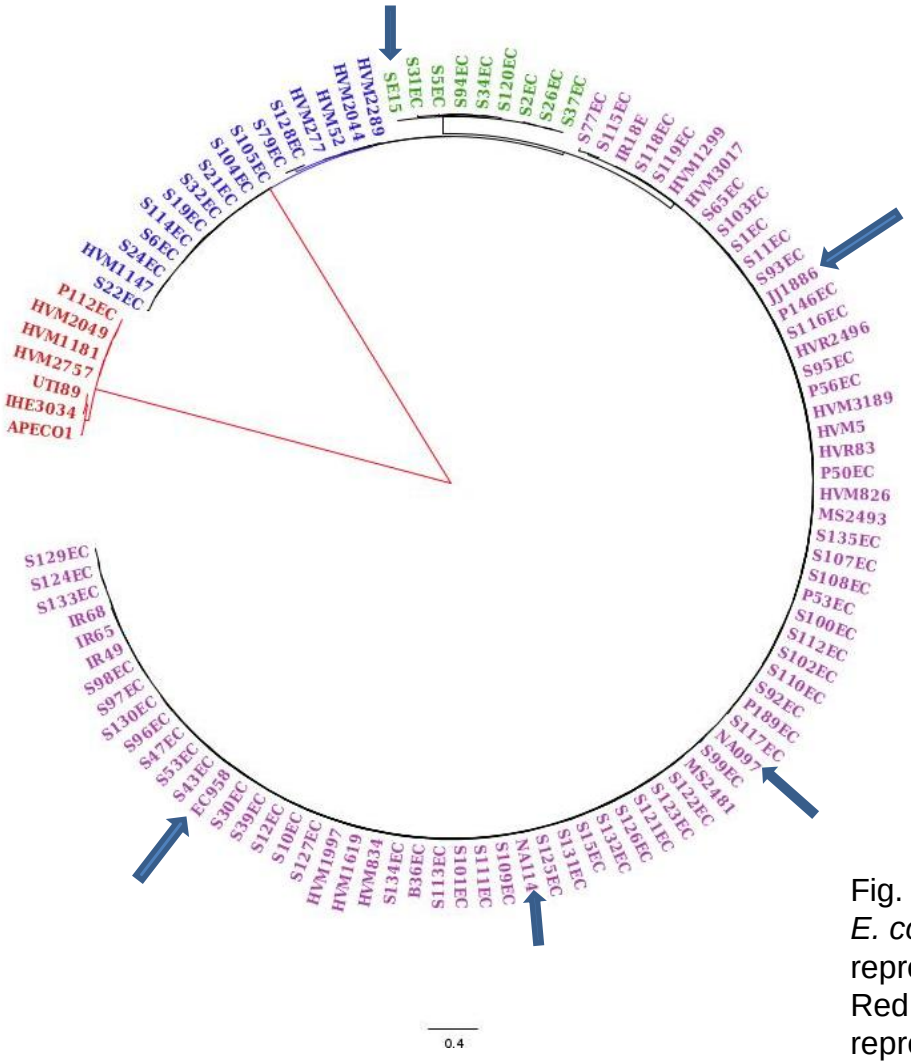

Fig. S1: Maximum Likelihood phylogenetic tree of 107 *E. coli* strains based on core genome SNPs. Green represents clade A, Blue clade B and Purple clade C. Red represents the outgroup members of ST95. Arrows represent the genomes that were used for BRIG analysis.

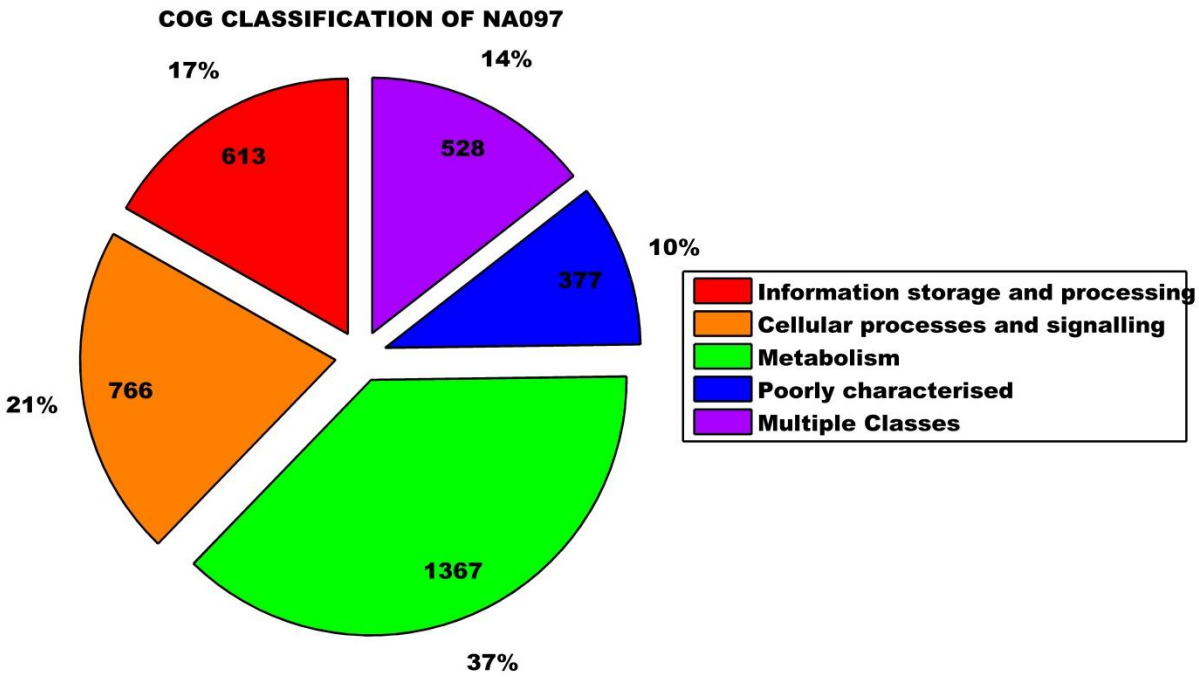

Fig. S2: COG functional classification of the annotated draft genome of NA097 from CDD database.

Table S1: Status table for UPEC specific virulence factors within the compared strains of ST131 *E. coli* as per the parameters described earlier.

S. no	VF	VFDB/ GenBank ID	EC958	SE15	NA097	NA114	JJ1886
1.	fimB	VFG0871	-	+	-	-	-
2.	draC	VFG0944	+	-	+	-	-
3.	draB	VFG0943	+	-	+	-	-
4.	draA	VFG0942	+	-	+	-	-
5.	draP	VFG0946	+	-	+	-	-
6.	draD	VFG0945	+	-	+	-	-
7.	papF	VFG0889	-	-	-	+	-
8.	papB	VFG0881	-	-	-	+	-
9.	papD	VFG0885	-	-	-	+	-
10.	papC	VFG0884	-	-	-	+	-
11.	papG	VFG0890	-	-	-	+	-
12.	papH	VFG0883	-	-	-	+	-
13.	papK	VFG0887	-	-	-	+	-
14.	papJ_2	VFG0897	-	-	-	+	-
15.	TRAT1	gi20095235	+	+	+	+	+
16.	entE	VFG0932	+	+	+	+	+
17.	entB	VFG0933	+	+	+	+	+
18.	chuT	VFG0918	+	+	+	+	+
19.	entA	VFG0934	+	+	+	+	+
20.	fimI	VFG0874	+	+	+	+	+
21.	papI_2	VFG0891	+	-	+	+	+
22.	chuS	VFG0916	+	+	+	+	+
23.	entD	VFG0929	+	+	+	+	+
24.	fepA	VFG0923	+	+	-	+	+
25.	fimC	VFG0875	+	+	+	+	+
26.	fepD	VFG0926	+	+	+	+	+
27.	chuA	VFG0917	+	+	+	+	+
28.	chuX	VFG0920	+	+	+	+	+
29.	iutA	VFG0936	-	-	+	+	+
30.	iucA	VFG0940	+	-	+	+	+
31.	entC	VFG0931	+	+	+	+	+
32.	fimA	VFG0873	+	+	+	+	+
33.	ompA	VFG1443	+	+	+	+	+
34.	fimE	VFG0872	+	+	+	+	+
35.	kpsM	VFG1450	+	+	+	+	+
36.	fimG	VFG0878	+	+	+	+	+
37.	ibeB	VFG1441	+	+	+	+	+
38.	sat	VFG0902	+	-	+	+	+

39.	aslA	VFG1444	+	+	+	+	+
40.	iucD	VFG0937	+	-	+	+	+
41.	kpsD	VFG1448	+	+	+	+	+
42.	fimF	VFG0877	+	+	+	+	+
43.	iucC	VFG0938	+	-	+	+	+
44.	ibeC	VFG1440	+	+	+	+	+
45.	fimD	VFG0876	+	+	+	+	+
46.	iucB	VFG0939	+	-	+	+	+
47.	Usp	gi7416048	+	+	+	+	+
48.	traJ	VFG1445	+	+	+	+	+
49.	fimH	VFG0879	+	+	+	+	+
50.	chuY	VFG0921	+	+	+	+	+
51.	entF	VFG0930	+	+	+	+	+
52.	fepC	VFG0925	+	+	+	+	+
53.	chuU	VFG0922	+	+	+	+	+
54.	fepB	VFG0924	+	+	+	+	+
55.	chuW	VFG0919	+	+	+	+	+

Table S2: Status table of resistance associated genes as obtained from ARDB based on parameters as mentioned above within the compared strains

	Resistance	Resistance class	EC958	SE15	NA097	NA114	JJ1886
1.	blaCTXM-15	Beta lactam	+	-	+	+	+
2.	BlaTEM-1.	Beta lactam	+	-	+	-	+
3.	OXA-1	Beta lactam	+	-	+	+	+
4.	CMY-23	Beta lactam	+	-	-	-	-
5.	AadA4	Aminoglycoside	+	-	+	+	-
6.	AAC(6')-Ib-cr	Fluoroquinolones	+	-	+	+	+
7.	AAC(3)-IIc	Aminoglycoside	-	-	+	-	-
8.	acrD	Eflux	+	+	+	+	+
9.	acrA.	Eflux	+	+	+	+	+
10.	acrF	Eflux	+	+	+	+	+
11.	acrB	Eflux	+	+	+	+	+
12.	acrE	Eflux	+	+	+	+	+
13.	APH(6)-Id	Aminoglycoside	-	-	+	-	-
14.	APH(3")-Ib	Aminoglycoside	+	+	+	+	+
15.	StrA	Streptomycin	-	-	+	-	-
16.	sul2	Sulphonamides	-	-	+	-	-
17.	Sul1	Sulphonamides	+	-	+	+	-
18.	dfrA17	trimethoprim	+	-	+	+	-
19.	catB2	Phenolics	-	-	+	-	-
20.	tetC*	Tetracyclines	+	-	+	+	-
21.	mdtK	MDR efflux	+	+	+	+	+
22.	mdtH	MDR efflux	+	+	+	+	+
23.	mdtF	MDR efflux	+	+	+	+	+
24.	mdtB	MDR efflux	+	+	+	+	+
25.	mdtD	MDR efflux	+	+	+	+	+
26.	mdtG	MDR efflux	+	+	+	+	+
27.	mdtL	MDR efflux	+	+	+	+	+

28.	mdtA	MDR efflux	+	+	+	+	+
29.	mdtE	MDR efflux	+	+	+	+	+
30.	mdtC	MDR efflux	+	+	+	+	+
31.	emrA	MDR efflux	+	+	+	+	+
32.	emrY	MDR efflux	+	+	+	-	+
33.	emrK	MDR efflux	+	+	+	+	+
34.	emrD	MDR efflux	+	+	+	+	+
35.	asmA	Bile resistance	+	+	+	+	+
36.	ompF	MDR	+	+	+	+	+
37.	ECs3903	Fluoroquinolones	+	+	+	+	+
38.	ECs2138	MAR regulator	+	+	+	+	+
39.	ECs1739	Polymixin B/aminoglycoside/ EDTA	+	+	+	+	+
40.	ECs5045	Drug induced oxidative stress	+	+	+	+	+
41.	ECs5044	Drug induced oxidative stress	+	+	+	+	+
42.	parE	Fluoroquinolones	+	+	+	+	+
43.	PhoQ	Antimicrobial Peptide resistance	+	+	+	+	+
44.	EvgA	Acid	+	+	+	+	+
45.	cpxA	Drug induced oxidative stress	+	+	+	+	+
46.	rpoB	Rifamycin	+	+	+	+	+
47.	folP	Sulphonamides	+	+	+	+	+
48.	tolC	MDR efflux	+	+	+	+	+
49.	elongation|factor|Tu	Kirromycin	-	+	+	+	+
50.	gyrA	Fluoroquinolones	+	+	+	+	+
51.	EnvR	acrAB repressor	+	+	+	+	+
52.	envZ	MDR	+	+	+	+	+
53.	uppP	Bacitracin	+	+	+	+	+
54.	yjiO	MDR	+	+	+	+	+
55.	rpoB	Rifamycin	+	+	+	+	+
56.	yfbG	polymyxin	-	+	+	+	+

57.	EvgA	Acid	+	+	+	+	+
58.	gadX	Acid	+	+	+	+	+
59.	mph(A)|protein	Macrolide	+	-	+	+	-
60.	CRP	MDR	+	+	+	+	+
61.	Multidrug resistance protein B	Multi drug resistance	+	+	+	+	+
62.	RobA	Multi drug resistance	+	+	+	+	+
63.	MdfA	Multi drug resistance	+	+	+	+	+
64.	CpxR	Drug induced oxidative stress	+	+	+	+	+
65.	mcrB	Bacteriophage resistance	+	+	+	+	+
66.	DLP12	MDR	+	+	+	+	+
67.	baeR.|Sensor|BaeS	Multi drug exporter	+	+	+	+	+