Supplementary data

Table S1: *E. coli* ST457 collection metadata. The first part of the table contains data about our strains, the second part contains metadata of EnteroBase strains. Strains sequenced with PacBio are hihghligh in bold and accession numbers to obtained chromosomal sequence are 1517k (SAMN11130353), CE1628 (SAMN14966947), CE1803 (SAMN14966948). The background colours divide strains into clades - H25 North (red), H16 (orange), H6 (turquoise), H45 (purple), H25 South (blue), MC1 (light gray), MC2 (dark gray). The ID of EnteroBase strains is based on the name of Assembly barcode of downloaded fasta files and the original form of ESC_XX0000AA_AS is simplified into XX0000 form.

Strain ID	GenBank BioSample	Source	Source Details	Collection Year	Country	Location	Media (mg/L)
1508e	SAMN14840864	Poultry	Cloacal samples	2012	Paraguay	Luque	CEF 2
1514k	SAMN11130350	Poultry	Cloacal samples	2012	Paraguay	Villeta	COL 3.5
1515e	SAMN10698928	Poultry	Cloacal samples	2012	Paraguay	Villeta	CEF 2
1515k	SAMN11130351	Poultry	Cloacal samples	2012	Paraguay	Villeta	COL 3.5
1516e	SAMN11130341	Poultry	Cloacal samples	2012	Paraguay	Villeta	CEF 2
1516k	SAMN11130352	Poultry	Cloacal samples	2012	Paraguay	Villeta	COL 3.5
1517e	SAMN11130342	Poultry	Cloacal samples	2012	Paraguay	Villeta	CEF 2
1517k	SAMN11130353	Poultry	Cloacal samples	2012	Paraguay	Villeta	COL 3.5
1519e	SAMN14840960	Poultry	Cloacal samples	2012	Paraguay	Villeta	CEF 2
1521e	SAMN11130343	Poultry	Cloacal samples	2012	Paraguay	Villeta	CEF 2
1521k	SAMN11130357	Poultry	Cloacal samples	2012	Paraguay	VIlleta	COL 3.5
1523e	SAMN11130345	Poultry	Cloacal samples	2012	Paraguay	Nueva Italia	CEF 2
1527e	SAMN11130347	Poultry	Cloacal samples	2012	Paraguay	Nueva Italia	CEF 2
1527k	SAMN11130363	Poultry	Cloacal samples	2012	Paraguay	Nueva Italia	COL 3.5
EC0125	SAMN14931112	Clinical	UTI	2012	Australia	Wollongong	-
EC0382	SAMN14931113	Clinical	Unspecified	2012	Australia	SGH Sydney	-
CE1803A	SAMN14841025	Gulls	Cloacal samples	2012	Australia	Five Islands	CEF 2
CE1636	SAMN14841026	Gulls	Cloacal samples	2012	Australia	Five Islands	CEF 2
CE1564	SAMN14841027	Gulls	Cloacal samples	2012	Australia	Five Islands	CEF 2
CE1573	SAMN14841028	Gulls	Cloacal samples	2012	Australia	Five Islands	CEF 2
CE1600	SAMN14841029	Gulls	Cloacal samples	2012	Australia	Five Islands	CEF 2
CE1638	SAMN14841030	Gulls	Cloacal samples	2012	Australia	Five Islands	CEF 2
CE1590	SAMN14841031	Gulls	Cloacal samples	2012	Australia	Five Islands	CEF 2
CE1567	SAMN14841032	Gulls	Cloacal samples	2012	Australia	Five Islands	CEF 2
CE1628	SAMN14841033	Gulls	Cloacal samples	2012	Australia	Five Islands	CEF 2
CE1634	SAMN14841034	Gulls	Cloacal samples	2012	Australia	Five Islands	CEF 2
CE1619	SAMN14841035	Gulls	Cloacal samples	2012	Australia	Five Islands	CEF 2
CE1670	SAMN14841036	Gulls	Cloacal samples	2012	Australia	Five Islands	CEF 2
CE1715	SAMN14841037	Gulls	Cloacal samples	2012	Australia	Five Islands	CEF 2
CE1706	SAMN14841038	Gulls	Cloacal samples	2012	Australia	Five Islands	CEF 2
CE1683	SAMN14841039	Gulls	Cloacal samples	2012	Australia	Five Islands	CEF 2
CE1710	SAMN14841040	Gulls	Cloacal samples	2012	Australia	Five Islands	CEF 2
CE1731	SAMN14841041	Gulls	Cloacal samples	2012	Australia	Five Islands	CEF 2
CE1732A	SAMN14841042	Gulls	Cloacal samples	2012	Australia	Five Islands	CEF 2
CE1679	SAMN14841043	Gulls	Cloacal samples	2012	Australia	Five Islands	CEF 2
CE1994A	SAMN14841044	Gulls	Cloacal samples	2012	Australia	Montague Island	CEF 2
CE1833	SAMN14841045	Gulls	Cloacal samples	2012	Australia	Sydney	CEF 2
CE1848	SAMN14841046	Gulls	Cloacal samples	2012	Australia	Sydney	CEF 2
CE1818	SAMN14841047	Gulls	Cloacal samples	2012	Australia	Sydney	CEF 2
CE1865	SAMN14841048	Gulls	Cloacal samples	2012	Australia	Sydney	CEF 2
CE1957	SAMN14841049	Gulls	Cloacal samples	2012	Australia	Montague Island	CEF 2
CE2006	SAMN14841050	Gulls	Cloacal samples	2012	Australia	Montague Island	CEF 2
CE1886	SAMN14841051	Gulls	Cloacal samples	2012	Australia	Sydney	CEF 2
CE1963	SAMN14841052	Gulls	Cloacal samples	2012	Australia	Montague Island	CEF 2
CE1762	SAMN14841053	Gulls	Cloacal samples	2012	Australia	Sydney	CEF 2
CE1796	SAMN14841054	Gulls	Cloacal samples	2012	Australia	Sydney	CEF 2
CE1872	SAMN14841055	Gulls	Cloacal samples	2012	Australia	Sydney	CEF 2
CE1825	SAMN14841056	Gulls	Cloacal samples	2012	Australia	Sydney	CEF 2
CE1984	SAMN14841057	Gulls	Cloacal samples	2012	Australia	Montague Island	CEF 2
CE1765	SAMN14841058	Gulls	Cloacal samples	2012	Australia	Sydney	CEF 2
CE1814	SAMN14841059	Gulls	Cloacal samples	2012	Australia	Sydney	CEF 2
CE1917	SAMN14841060	Gulls	Cloacal samples	2012	Australia	Montague Island	CEF 2
CE2030	SAMN14841061	Gulls	Cloacal samples	2012	Australia	Montague Island	CEF 2
CE2042	SAMN14841062	Gulls	Cloacal samples	2012	Australia	Montague Island	CEF 2
CE1904	SAMN14841063	Gulls	Cloacal samples	2012	Australia	Montague Island	CEF 2
CE1966	SAMN14841064	Gulls	Cloacal samples	2012	Australia	Montague Island	CEF 2
CE1887	SAMN14841065	Gulls	Cloacal samples	2012	Australia	Sydney	CEF 2
CE2031A	SAMN14841066	Gulls	Cloacal samples	2012	Australia	Montague Island	CEF 2

Strain ID	Enterobase ID	Used source	Source Niche	Source Type	Source Details	Year	Country	Region	City
BA3207	AZ-TG60594	Poultry	Poultry	Avian	packaged whole turkey	2013	United States	Arizona	Flagstaff
CB7000	AG19-0248	Canine	Companion Animal	Canine	Urine (Canis familiaris)	2019	United States	Ohio	
CB7211	AUSMDU00026934	Human	Human	Human	Homo sapiens	2014	Australia		
DB2140	CVM N18EC1056	Poultry	Poultry	Avian	ground turkey	2018	United States	Iowa	
DB2269	CVM N18EC0492	Poultry	Poultry	Avian	Chicken Thighs	2018	United States	South Dakota	
FB3603	AUSMDU00008000	Human	Human	Human	Homo sapiens	2017	Australia		
FB5883	CN-593-D	Human	Human	Human		2018	China	Shanghai	Shanghai
FB7536	CN-441	Human	Human	Human		2017	China	Shanghai	Shanghai
FB9087	19GA08CB32	Poultry	Poultry	Avian	Whole Chicken	2019	United States	Georgia	
FB9797	16AR1251	Human	Human	Human	Homo sapiens	2016	New Zealand		
GA0711	AZ-TG-WCHI-2-2	Water	Environment	Water	Untreated wastewater	2014	United States	Arizona	
GA8976	MRSN388634	Clinical	Human	Human	Homo sapiens; Clinical	2016	United States		
GA9192	200628	Human	Human	Human	Human; Homo sapiens	2015	United Kingdom		
GA9323	204427	Human	Human	Human	Human; Homo sapiens	2016	United Kingdom		
GA9368	209671	Human	Human	Human	Human; Homo sapiens	2016	United Kingdom		
GB0145	P2.2	Swine	Livestock	Swine	Suine; Pork meat	2019	Brazil	Paraná	Londrina
HA3078	452	Poultry	Poultry	Avian		2014	China	Shandong	
HA7607	KOr019	Water	Environment	Water	river		Japan		
HA9232	1600430	Bovine	Livestock	Bovine	Faeces	2016	Luxembourg		
HA9243	1600431	Bovine	Livestock	Bovine	Faeces	2016	Luxembourg		
HA9247	1600759	Bovine	Livestock	Bovine	Faeces	2016	Luxembourg		
IA0789	9.1-R1	Human	Human	Human	Homo sapiens; human faeces	2008	Australia	New South Wales	Sydney
IA1961	B1700	Avian	Human	Human	Dacelo novaeguineae; Faeces	2011	Australia	Queensland	
IA1962	B093	Avian	Wild Animal	Air	Strepera graculina; Faeces	2001	Australia	New South Wales	
IA8721	14059134					2014	Italy		
JA0103	SCP20-70	Human	Human	Human	Homo sapiens		Netherlands		
JA0175	SCK33-56	Human	Human	Human	Homo sapiens		Netherlands		
LA1332	MOD1-EC3670	Poultry	Companion Animal	Air	feces Young Turkey,Meleagris gallopavo	2014	United States	South Carolina	
MA1963	NC_STEC34	Poultry	Poultry	Air	Chicken Fecal House 1 Front	2014	United States	Tennessee	
MA3450	FSIS1710886	Swine	Livestock	Swine	animal-swine-market swine	2017	United States	Indiana	
OA0813	EC-32	Artificial	Companion Animal	Air	artificial; artificial gut model	2015	United Kingdom		
OA0815	EC-34	Artificial	Companion Animal	Air	artificial; artificial gut model	2015	United Kingdom		
OA1337	ZTA15/00685EB1	Swine	Livestock	Air	Fattening pig caecal sample	2015	Spain		
PA1102	MER-67	Clinical	Human	Human	Homo sapiens; Age: 85; female; Blood	2015	Australia	Queensland	Brisbane
PA1693	20151357	Poultry	Poultry	Avian	Chicken; Feces		Vietnam		
QA5299	JML012	Human	Human	Human	feces; Homo sapiens	2015	Japan		
QA5359	JML078	Human	Human	Human	feces; Homo sapiens	2015	Japan		
QA5364	JML083	Human	Human	Human	feces; Homo sapiens	2015	Japan		
QA6402	9-024	Human	Human	Human	feces; Homo sapiens	2009	Japan		
QA7284	JML009	Human	Human	Human	feces; Homo sapiens	2015	Japan		
QA7342	JML100	Human	Human	Human	feces; Homo sapiens	2015	Japan		
RA2549	ARIMEC185-15	Human	Human	Human	stool; Homo sapiens	2015	Argentina		
RA4251	AC13136	Human			Breeder	2017	Germany		
RA5006	1034-14	Human	Human	Human	Homo sapiens; rectal swab	2014	Germany		
RA6708	INF9716R2E	Water	Environment	Water	Water/Influent	2016	United States	Colorado	
RA8202	NR0631	Human	Human	Human	Homo sapiens; Rectal swab	2014	United States	New York	New York
RA8205	35153	Human	Human	Human	Homo sapiens; stool	2014	United States	New York	New York
RA8206	35140	Human	Human	Human	Homo sapiens; stool	2014	United States	New York	New York
RA8209	35114	Human	Human	Human	Homo sapiens; stool	2014	United States	New York	New York
SA0179	PSU-0686	Canine	Companion Animal	Canine	Dog, (Canine)	2012	United States	New York	New York
SA4138	401636	Human	Human	Human	human; Homo sapiens	2017	United Kingdom		
SA4972	EcIB36	Human	Human	Human		2016	Bolivia	Cochabamba	Villa Tunari
SA9872	FSIS11811925	Swine	Livestock	Swine	animal-swine-market swine	2018	United States	Oklahoma	
TA7464	595625					2018	United Kingdom		
TA9995	FSIS11814329	Poultry	Poultry	Air	animal-chicken-young chicken	2018	United States	Georgia	
VA4049	1028085					2017	Mexico		
VA4091	CO1	Human	Human			2016	Ecuador	Pichincha	Quito
VA5574	14S03014-1	Bovine	Livestock	Bovine	bos taurus; feces	2014	Netherlands		
VA5580	14S03029-1	Bovine	Livestock	Bovine	bos taurus; feces	2014	Netherlands		
VA5582	14S03036-2	Bovine	Livestock	Bovine	bos taurus; feces	2014	Netherlands		
VA5681	14S05071-2	Bovine	Livestock	Bovine	bos taurus; feces	2014	Netherlands		
VA5694	15S00475-2	Bovine	Livestock	Bovine	bos taurus; feces	2015	Netherlands		
VA5695	15S00482-2	Bovine	Livestock	Bovine	bos taurus; feces	2015	Netherlands		
VA5961	UPCH_214	Human	Human	Human		2018	Peru		Lima
VA9753	FSIS11917410	Poultry	Poultry	Air	Animal-Turkey-Young Turkey	2019	United States	Michigan	
VA9780	ECOL-18-VL-SD-IA-0014	Canine	ND	Canine	Urine (Canine)	2018	United States	Iowa	
WA4304						2012	United States		
WA4383	12HE8	Clinical	Human	Human	Patient Blood; Homo sapiens	2012	China	Guangdong	
WA5506	JIE4016	Clinical	Human	Human	Homo sapiens; urine	2014	Australia	New South Wales	Sydney
WA5530	JIE3921	Clinical	Human	Human	Homo sapiens; urine	2013	Australia	New South Wales	Sydney
WA5541	JIE3711	Clinical	Human	Human	Homo sapiens; urine	2013	Australia	New South Wales	Sydney
WA5546	RPA22	Human	Human	Human	Homo sapiens	2009	Australia	New South Wales	Sydney
WA5552	SYD1232	Human	Human	Human	Homo sapiens	2015	Australia	New South Wales	Sydney
WA5591	JIE4096	Clinical	Human	Human	Homo sapiens; urine	2014	Australia	New South Wales	Sydney
WA7300	ERS2367440	Food	Food	ND	Human, Food	2016	Cambodia		
WA7349	ERS2367492	Food	Food	ND	Human, Food	2016	Cambodia		
XA6422	12HE7	Clinical	Human	Human	Patient Blood; Homo sapiens	2012	China	Unresolved	Unresolved
YA1066	14HE22	Clinical	Human	Human	Patient Blood; Homo sapiens	2014	China	Beijing	Beijing
ZA1576	FSIS11920379	Poultry	Poultry	Air	Animal-Turkey-Young Turkey	2019	United States	Indiana	
ZA5550	FSIS11921229	Poultry	Poultry	Air	Animal-Turkey-Young Turkey	2019	United States	Iowa	


Tree scale: 0.001
CB7211 Australia 2014 Human O11:H16
VA5694 Netherlands 2015 Bovine O11:H16
VA5695 Netherlands 2015 Bovine O11:H16
VA5681 Netherlands 2014 Bovine O11:H16
VA5580 Netherlands 2014 Bovine O11:H16
VA5582 Netherlands 2014 Bovine O11:H16
VA5574 Netherlands 2014 Bovine O11:H16
DB2140 USA 2018 Poultry O11:H25
VA9780 USA 2018 Canine ONT:H25
CB7000 USA 2019 Canine O11:H25
WA4304 USA 2012 O11:H25
BA3207 USA 2013 Poultry O11:H25
WA7300 Cambodia 2016 Food ONT:H25
HA3078 China 2014 Poultry O154:H25
FB7536 China 2017 Human O3:H25
WA4383 China 2012 Clinical O25:H25
XA6422 China 2012 Clinical O25:H25
GA8976 USA 2016 Clinical O11:H25
OA1337 Spain 2015 Swine O11:H25
HA9247 Luxembourg 2016 Bovine O11:H25
HA9241 Luxembourg 2016 Bovine ONT:H25
HA9232 Luxembourg 2016 Bovine O11:H25
GB0145 Brazil 2019 Swine O11:H25
FB5883 China 2018 Human O11:H25
MA3450 USA 2017 Swine ONT:H25
SA9872 USA 2018 Swine O11:H25
PA1693 Vietnam Poultry O11:H25
YA1066 China 2014 Clinical O11:H25
VA4091 Ecuador 2016 Human ONT:H25
VA4049 Mexico 2017 O166:H25
SA4972 Bolivia 2016 Human O157:H25
QA7342 Japan 2015 Human ONT:H25
FB3603 Australia 2017 Human O11:H25
WA7349 Cambodia 2016 Food O11:H25
SA4138 UK 2017 Human O11:H25
TA7464 UK 2018 O11:H25
RA8205 USA 2014 Human O11:H25
RA8200 USA 2014 Human O11:H25
RA8206 USA 2014 Human ONT:H25
RA8202 USA 2014 Human O11:H25
LA1332 USA 2014 Poultry ONT:H12
ZA1576 USA 2019 Poultry ONT:H51
HA7607 Japan Water O11:H6
QA7284 Japan 2015 Human O11:H6
ZA5550 USA 2019 Poultry ONT:H6
TA9995 USA 2018 Poultry O11:H6
DB2269 USA 2018 Poultry O11:H6
MA1963 USA 2014 Poultry O11:H6
VA9753 USA 2019 Poultry O11:H6
VA5961 Peru 2018 Human O11:H6
QA5359 Japan 2015 Human O11:H6
QA5364 Japan 2015 Human O11:H6
OA0813 UK 2015 Artificial O11:H6
OA0815 UK 2015 Artificial O11:H6
SA0179 USA 2012 Canine O11:H6
1521k Paraguay 2012 Poultry O11:H6
1521e Paraguay 2012 Poultry O11:H6
1508e Paraguay 2012 Poultry ONT:H6
1517e Paraguay 2012 Poultry O11:H6
1527k Paraguay 2012 Poultry ONT:H6
1517k Paraguay 2012 Poultry ONT:H6
1527e Paraguay 2012 Poultry O11:H6
1515e Paraguay 2012 Poultry ONT:H6
1523e Paraguay 2012 Poultry ONT:H6
1514k Paraguay 2012 Poultry ONT:H6
1516e Paraguay 2012 Poultry O11:H6
1519e Paraguay 2012 Poultry O11:H6
1515k Paraguay 2012 Poultry O11:H6
1516k Paraguay 2012 Poultry O11:H6
IA1962 Australia 2001 Avian O11:H25
WA5530 Australia 2013 Clinical O11:H25
CE1706 Australia 2012 Gulls O11:H25
WA5552 Australia 2015 Human ONT:H25
IA0789 Australia 2008 Human O11:H45
GA0711 USA 2014 Water O11:H45
WA5506 Australia 2014 Clinical O11:H45
CE1765 Australia 2012 Gulls O11:H45
WA5541 Australia 2013 Clinical ONT:H45
IA8721 Italy 2014 O11:H45
QA6402 Japan 2009 Human O11:H45
CE1567 Australia 2012 Gulls O11:H45
CE1825 Australia 2012 Gulls O11:H45
CE1886 Australia 2012 Gulls O11:H45
RA2549 Argentina 2015 Human O11:H25
CE1803A Australia 2012 Gulls O11:H25
CE1628 Australia 2012 Gulls O11:H25
IA1961 Australia 2011 Avian ONT:H25
CE1679 Australia 2012 Gulls O11:H25
CE1796 Australia 2012 Gulls O11:H25
CE1638 Australia 2012 Gulls O11:H25
CE1564 Australia 2012 Gulls O11:H25
CE1573 Australia 2012 Gulls O11:H25
CE1636 Australia 2012 Gulls ONT:H25
CE1715 Australia 2012 Gulls O11:H25
CE1634 Australia 2012 Gulls O11:H25
CE1710 Australia 2012 Gulls O11:H25
FB9797 New Zealand 2016 Human O11:H25
GA9323 UK 2016 Human O11:H25
GA9368 UK 2016 Human O11:H25
GA9192 UK 2015 Human O11:H25
FB9087 USA 2019 Poultry O11:H25
RA5006 Germany 2014 Human O11:H25
RA4251 Germany 2017 Human ONT:H25
RA6708 USA 2016 Water O11:H25
QA5299 Japan 2015 Human ONT:H25
CE1590 Australia 2012 Gulls O11:H25
CE1600 Australia 2012 Gulls O11:H25
CE1731 Australia 2012 Gulls O11:H25
CE1732A Australia 2012 Gulls O11:H25
CE1865 Australia 2012 Gulls O11:H25
CE1872 Australia 2012 Gulls O11:H25
CE1814 Australia 2012 Gulls O11:H25
CE1833 Australia 2012 Gulls O11:H25
CE1848 Australia 2012 Gulls O11:H25
CE1762 Australia 2012 Gulls O11:H25
CE1887 Australia 2012 Gulls O11/9:H25
JA0175 Netherlands Human O11:H25
JA0103 Netherlands Human O11:H25
PA1102 Australia 2015 Clinical O11:H25
CE1683 Australia 2012 Gulls O11:H25
CE1818 Australia 2012 Gulls O11:H25
CE1966 Australia 2012 Gulls O11:H25
WA5591 Australia 2014 Clinical ONT:H25
WA5546 Australia 2009 Human O11:H25
CE1670 Australia 2012 Gulls O11:H25
CE1619 Australia 2012 Gulls O11:H25
EC0382 Australia 2012 Clinical O11:H25
EC0125 Australia 2012 Clinical O11:H25
CE2006 Australia 2012 Gulls O11:H25
CE1984 Australia 2012 Gulls O11:H25
CE1917 Australia 2012 Gulls O11:H25
CE2030 Australia 2012 Gulls O11:H25
CE2031A Australia 2012 Gulls O11:H25
CE2042 Australia 2012 Gulls O11:H25
CE1963 Australia 2012 Gulls O11:H25
CE1994A Australia 2012 Gulls O11:H25
CE1957 Australia 2012 Gulls O11:H25
CE1904 Australia 2012 Gulls O11:H25

Figure S1: Phylogenetic analysis of *E. coli* ST457 and their characteristics

Five main clades are devided with colour - H16 (orange), H25 North (red), H6 (turquoise), H45 (purple) and H25 South (blue). Five strain are part of minor clades MC1 (BA3207 and WA4304) and MC2 (CB7000, DB2140, VA9780). The text columns contain name of the strain, country of isolation, year of isolation, source of isolation and serotype of the respected strain. The Australian Gull subset is distinguished with the text colour based on the location of the isolation: Montague island (green), Five Islands (purple) and Sydney (blue).

Pink squares indicates presence of virulence-associated genes (VAGs). All strains shared 27 VAGs: *chuSTUVWXY, entBCFS, espL1, fepABCD, fes, fimFGH, ompA* and *shuA* which are not part of the picture. The * represents cluster of several VAGs which showed identical profile (fim* - *fimCDEI*; gsp* - *gspCDEFGHI*; fyuA irp* ybt - *irp1, irp2, fyuA, ybtAEPQSTU*; iuc* - *iucBCD*; iro* - *iroBCDEN*; pap* - *papCHJK*; hly* - *hlyABCD*; agg* sat - *aspU, aag3ABCD, sat*; sfa* - *sfaBCDGHY, cnf1, focCD*). In some strains, the gene identity for *gspFHIJLM* was below 95% threshold but > 90%. Invasion-associated protein *aslA* was fruncated at the same position and half of it was detected within different contigs in four ST457 strains which formed a subclade within the H45 clade (98 - 182 SNPs among three of them, CE1706 > 1000 SNPs from others). As such *aslA* was expected to be non-functional in these four strains and marked as absent.

Purple squares represent detected resistance genes to antimicrobial and anticancer substances. Genes encoding resistance to beta-lactams (*bla*$_{\text{CMY-2}}$, *bla*$_{\text{DHA-1}}$, *bla*$_{\text{CTX-M-1;2,3;8;14;15;27;55;125}}$, *bla*$_{\text{TEM-1;135}}$, *bla*$_{\text{OXA-1;9}}$ – we excluded instrict *bla*$_{\text{EC}}$ detected in all strains), aminoglycosides (*aac(3)-IIa, aac(3)-IId, aac(3)-IVa, aac(3)-VIa, aac(6′)-Ib, aac(6′)-Ib4, aadA1, aadA2, aadA5, aph(3′′)-Ib, aph(3′)-IIa, aph(3′)-Ia, aph(4)-Ia, armA, rmtB1, aac(6′)-Ib-cr)*, sulphonamides (*sul1, sul2, sul3*), tetracyclines [*tet*(A), *tet*(B), *tet*(M), *tet*(X)], trimethoprim (*dfrA1, dfrA5, dfrA7, dfrA12, dfrA14, dfrA17*), amphenicols (*catA1, catA2, catB3, cmlA1, floR*), colistin (*mcr-*

1.1., mcr-2.1, mcr-5.1), macrolides [*erm*(B), *mph*(A), *mph*(E), *msr*(E)], fosfomycine (*fosA3, forA4*), quinolones (*oqxAB, aac(6′)-Ib-cr, qnrB4, qnrB19*), carbapenems ($bla_{\text{OXA-23}}$, $bla_{\text{IMP-4}}$, $bla_{\text{NDM-9}}$), lincosamides [*lnu*(F)] and rifampin (*arr-3*). Genes encoding resistance to bleomycin (*bleMBL, bleO, bleTn5*) which is mostly used in cancer treatment were detected.

Turquoise squares indicate precence of plasmid replicons as they were detected using PlasmidFinder database.

Table S2: Single nucleotide polymorphisms (SNPs) count heat map matrix for strains of the five main clades in tables H45; H16; H25 North; H6; H25 South. The heat maps are created using red (low SNP distance) - blue (high SNP distance) scale. The strains are represented by name, country and a number in line part, only number of the respected strain is present in the column part.

H45	**Country**		**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**
GA0711	**USA**	**1**	0	73	1322	662	655	80	1283	146	1318	691	1996	693	689	73
IA0789	**Australia**	**2**	73	0	1304	642	635	73	1265	139	1299	673	1976	673	670	66
IA1962	**Australia**	**3**	1322	1304	0	777	771	1322	150	1388	182	809	1404	808	805	1316
IA8721	**Italy**	**4**	662	642	777	0	97	661	739	727	773	131	1993	119	116	654
QA6402	**Japan**	**5**	655	635	771	97	0	654	732	719	766	91	1986	92	89	647
WA5506	**Australia**	**6**	80	73	1322	661	654	0	1284	94	1318	691	1995	692	689	21
WA5530	**Australia**	**7**	1283	1265	150	739	732	1284	0	1296	98	770	1364	769	766	1277
WA5541	**Australia**	**8**	146	139	1388	727	719	94	1296	0	1280	703	2061	758	701	33
WA5552	**Australia**	**9**	1318	1299	182	773	766	1318	98	1280	0	758	1390	804	755	1265
CE1567	**Australia**	**10**	691	673	809	131	91	691	770	703	758	0	2024	96	93	684
CE1706	**Australia**	**11**	1996	1976	1404	1993	1986	1995	1364	2061	1390	2024	0	2024	2021	1988
CE1886	**Australia**	**12**	693	673	808	119	92	692	769	758	804	96	2024	0	15	685
CE1825	**Australia**	**13**	689	670	805	116	89	689	766	701	755	93	2021	15	0	682
CE1765	**Australia**	**14**	73	66	1316	654	647	21	1277	33	1265	684	1988	685	682	0

H16	**Country**		**1**	**2**	**3**	**4**	**5**	**6**	**7**
CB7211	**Australia**	**1**	0	3690	3692	3693	3717	3716	3743
VA5574	**Netherlands**	**2**	3690	0	6	3	45	42	69
VA5580	**Netherlands**	**3**	3692	6	0	9	47	44	71
VA5582	**Netherlands**	**4**	3693	3	9	0	48	45	72
VA5681	**Netherlands**	**5**	3717	45	47	48	0	3	30
VA5694	**Netherlands**	**6**	3716	42	44	45	3	0	27
VA5695	**Netherlands**	**7**	3743	69	71	72	30	27	0

H25 North	Country		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
FB3603	Australia	1	0	1160	3070	1728	1164	7135	1748	1749	1749	1355	1767	1306	457	90	92	92	92	91	765	1393	92	1291	788	2918	1810	87	2918	1345
FB5883	China	2	1160	0	2561	1219	46	6627	1241	1242	1242	1152	1260	1103	1070	1164	1166	1166	1166	1165	1151	1190	1165	1387	884	2409	1303	1161	2409	1142
FB7536	China	3	3070	2561	0	1482	2565	5916	1509	1510	1510	2387	1528	2339	2979	3070	3072	3072	3072	3071	2723	2426	3072	2339	2430	1397	1698	3067	1397	2378
GA8976	USA	4	1728	1219	1482	0	1223	5778	111	112	112	1052	130	999	1639	1724	1726	1726	1726	1725	1594	1090	1726	1589	1088	1330	367	1721	1330	1038
GB0145	Brazil	5	1164	46	2565	1223	0	6631	1245	1246	1246	1156	1264	1107	1074	1168	1170	1170	1170	1169	1157	1194	1170	1391	888	2413	1307	1165	2413	1146
HA3078	China	6	7135	6627	5916	5778	6631	0	5778	5779	5779	6477	5797	6424	7047	7136	7138	7138	7138	7136	6648	6515	7137	6536	6495	6289	5855	7133	6289	6463
HA9232	Luxembourg	7	1748	1241	1509	111	1245	5778	0	1	1	1045	55	996	1659	1742	1744	1743	1744	1743	1615	1083	1744	1611	1108	1357	383	1739	1357	1035
HA9243	Luxembourg	8	1749	1242	1510	112	1246	5779	1	0	2	1046	56	997	1660	1743	1745	1744	1745	1744	1616	1084	1745	1612	1109	1358	384	1740	1358	1036
HA9247	Luxembourg	9	1749	1242	1510	112	1246	5779	1	2	0	1046	56	997	1656	1743	1745	1745	1745	1744	1616	1084	1745	1612	1109	1358	384	1740	1358	1036
MA3450	USA	10	1355	1152	2387	1052	1156	6477	1045	1046	1046	0	1064	79	1254	1361	1363	1362	1363	1362	1235	88	1363	1180	678	2236	1164	1357	2236	122
OA1337	Spain	11	1767	1260	1528	130	1264	5797	55	56	56	1064	0	1015	1678	1761	1763	1763	1763	1762	1634	1102	1763	1630	1127	1376	402	1758	1376	1054
PA1693	Vietnam	12	1306	1103	2339	999	1107	6424	996	997	997	79	1015	0	1218	1312	1314	1314	1314	1313	1187	117	1314	1154	652	2187	1116	1309	2187	69
QA7342	Japan	13	457	1070	2979	1639	1074	7047	1659	1660	1656	1254	1678	1218	0	465	467	466	467	467	784	1292	468	1180	699	2828	1719	462	2828	1256
RA8202	USA	14	90	1164	3070	1724	1168	7136	1742	1743	1743	1361	1761	1312	465	0	2	2	2	41	774	1399	42	1297	794	2918	1816	39	2918	1351
RA8205	USA	15	92	1166	3072	1726	1170	7138	1744	1745	1745	1363	1763	1314	467	2	0	4	2	43	776	1401	44	1299	796	2920	1818	41	2920	1353
RA8206	USA	16	92	1166	3072	1726	1170	7138	1743	1744	1745	1362	1763	1314	466	2	4	0	4	43	776	1400	44	1297	795	2920	1818	41	2920	1353
RA8209	USA	17	92	1166	3072	1726	1170	7138	1744	1745	1745	1363	1763	1314	467	2	2	4	0	43	776	1401	44	1299	796	2920	1818	41	2920	1353
SA4138	UK	18	91	1165	3071	1725	1169	7136	1743	1744	1744	1362	1762	1313	467	41	43	43	43	0	774	1400	1	1298	795	2919	1817	40	2919	1352
SA4972	Bolivia	19	765	1151	2723	1594	1157	6648	1615	1616	1616	1235	1634	1187	784	774	776	776	776	774	0	1273	775	1068	669	2585	1676	770	2585	1229
SA9872	USA	20	1393	1190	2426	1090	1194	6515	1083	1084	1084	88	1102	117	1292	1399	1401	1400	1401	1400	1273	0	1401	1218	716	2274	1202	1395	2274	160
TA7464	UK	21	92	1165	3072	1726	1170	7137	1744	1745	1745	1363	1763	1314	468	42	44	44	44	1	775	1401	0	1299	759	2920	1818	41	2920	1353
VA4049	Mexico	22	1291	1387	2339	1589	1391	6536	1611	1612	1612	1180	1630	1154	1180	1297	1299	1297	1299	1298	1068	1218	1299	0	604	2085	1672	1292	2085	1198
VA4091	Ecuador	23	788	884	2430	1088	888	6495	1108	1109	1109	678	1127	652	699	794	796	795	796	795	669	716	759	604	0	2278	1170	791	2278	695
WA4383	China	24	2918	2409	1397	1330	2413	6289	1357	1358	1358	2236	1376	2187	2828	2918	2920	2920	2920	2919	2585	2274	2920	2085	2278	0	1546	2915	0	2226
WA7300	Cambodia	25	1810	1303	1698	367	1307	5855	383	384	384	1164	402	1116	1719	1816	1818	1818	1818	1817	1676	1202	1818	1672	1170	1546	0	1813	1546	1155
WA7349	Cambodia	26	87	1161	3067	1721	1165	7133	1739	1740	1740	1357	1758	1309	462	39	41	41	41	40	770	1395	41	1292	791	2915	1813	0	2915	1348
XA6422	China	27	2918	2409	1397	1330	2413	6289	1357	1358	1358	2236	1376	2187	2828	2918	2920	2920	2920	2919	2585	2274	2920	2085	2278	0	1546	2915	0	2226
YA1066	China	28	1345	1142	2378	1038	1146	6463	1035	1036	1036	122	1054	69	1256	1351	1353	1353	1353	1352	1229	160	1353	1198	695	2226	1155	1348	2226	0

H6	**Country**		**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**	**18**	**19**	**20**	**21**	**22**	**23**	**24**	**25**	**26**	**27**	**28**	**29**
1508e	**Paraguay**	**1**	0	51	49	48	49	48	98	47	48	47	48	53	48	78	147	176	2059	135	242	235	1073	177	216	131	166	1098	177	2407	159
1514k	**Paraguay**	**2**	51	0	8	3	4	3	81	6	3	6	7	53	7	57	126	155	2011	114	221	214	1052	156	216	110	169	1077	157	2383	138
1515e	**Paraguay**	**3**	49	8	0	5	6	5	83	4	5	4	5	56	5	55	124	153	2009	112	219	212	1050	154	214	108	167	1075	154	2373	136
1515k	**Paraguay**	**4**	48	3	5	0	1	0	78	3	0	3	4	51	4	54	123	152	2008	111	218	211	1049	153	213	107	166	1074	154	2380	135
1516e	**Paraguay**	**5**	49	4	6	1	0	1	79	4	1	4	5	52	5	55	124	153	2009	112	219	212	1050	154	214	108	167	1075	155	2381	136
1516k	**Paraguay**	**6**	48	3	5	0	1	0	78	3	0	3	4	51	4	54	123	152	2008	111	218	211	1049	153	213	107	166	1074	154	2380	135
1517e	**Paraguay**	**7**	98	81	83	78	79	78	0	81	78	81	82	129	82	112	201	230	2086	189	296	289	1127	231	288	185	244	1152	228	2457	213
1517k	**Paraguay**	**8**	47	6	4	3	4	3	81	0	3	2	3	54	3	53	122	151	2007	110	217	210	1048	152	212	106	165	1073	153	2379	134
1519e	**Paraguay**	**9**	48	3	5	0	1	0	78	3	0	3	4	51	4	54	123	152	2008	111	218	211	1049	153	213	107	166	1074	154	2380	135
1521e	**Paraguay**	**10**	47	6	4	3	4	3	81	2	3	0	1	54	3	53	122	151	2007	110	217	210	1048	152	212	106	165	1073	153	2379	134
1521k	**Paraguay**	**11**	48	7	5	4	5	4	82	3	4	1	0	55	4	54	123	152	2008	111	218	211	1049	153	213	107	166	1074	154	2379	135
1523e	**Paraguay**	**12**	53	53	56	51	52	51	129	54	51	54	55	0	55	100	174	203	2059	162	269	262	1100	199	218	158	217	1079	205	2426	186
1527e	**Paraguay**	**13**	48	7	5	4	5	4	82	3	4	3	4	55	0	52	123	152	2008	111	218	211	1049	153	213	107	166	1073	154	2380	135
1527k	**Paraguay**	**14**	78	57	55	54	55	54	112	53	54	53	54	100	52	0	173	202	2058	161	268	261	1099	203	263	157	216	1124	204	2429	185
DB2269	**USA**	**15**	147	126	124	123	124	123	201	122	123	122	123	174	123	173	0	157	2040	24	199	191	1070	158	218	114	83	1094	175	2412	116
HA7607	**Japan**	**16**	176	155	153	152	153	152	230	151	152	151	152	203	152	202	157	0	2031	145	241	233	1061	149	195	105	162	1086	166	2431	131
LA1332	**USA**	**17**	2059	2011	2009	2008	2009	2008	2086	2007	2008	2007	2008	2059	2008	2058	2040	2031	0	2028	2087	2080	2944	1989	2082	1988	2045	2933	2015	2340	2014
MA1963	**USA**	**18**	135	114	112	111	112	111	189	110	111	110	111	162	111	161	24	145	2028	0	187	180	1058	146	206	102	71	1082	163	2400	104
OA0813	**UK**	**19**	242	221	219	218	219	218	296	217	218	217	218	269	218	268	199	241	2087	187	0	144	1101	207	303	199	232	1144	226	2489	201
OA0815	**UK**	**20**	235	214	212	211	212	211	289	210	211	210	211	262	211	261	191	233	2080	180	144	0	1148	200	284	192	225	1137	218	2480	194
QA5359	**Japan**	**21**	1073	1052	1050	1049	1050	1049	1127	1048	1049	1048	1049	1100	1049	1099	1070	1061	2944	1058	1101	1148	0	1062	1122	1016	1075	69	1055	3344	1044
QA5364	**Japan**	**22**	177	156	154	153	154	153	231	152	153	152	153	199	153	203	158	149	1989	146	207	200	1062	0	210	106	163	1051	132	2432	124
QA7284	**Japan**	**23**	216	216	214	213	214	213	288	212	213	212	213	218	213	263	218	195	2082	206	303	284	1122	210	0	166	223	1147	205	2480	192
SA0179	**USA**	**24**	131	110	108	107	108	107	185	106	107	106	107	158	107	157	114	105	1988	102	199	192	1016	106	166	0	119	1041	121	2388	88
TA9995	**USA**	**25**	166	169	167	166	167	166	244	165	166	165	166	217	166	216	83	162	2045	71	232	225	1075	163	223	119	0	1099	180	2420	121
VA5961	**Peru**	**26**	1098	1077	1075	1074	1075	1074	1152	1073	1074	1073	1074	1079	1073	1124	1094	1086	2933	1082	1144	1137	69	1051	1147	1041	1099	0	1045	3369	1069
VA9753	**USA**	**27**	177	157	154	154	155	154	228	153	154	153	154	205	154	204	175	166	2015	163	226	218	1055	132	205	121	180	1045	0	2448	149
ZA1576	**USA**	**28**	2407	2383	2373	2380	2381	2380	2457	2379	2380	2379	2379	2426	2380	2429	2412	2431	2340	2400	2489	2480	3344	2432	2480	2388	2420	3369	2448	0	2414
ZA5550	**USA**	**29**	159	138	136	135	136	135	213	134	135	134	135	186	135	185	116	131	2014	104	201	194	1044	124	192	88	121	1069	149	2414	0

H25 South	Country		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55
EC0125	Australia	1	0	813	1	98	82	698	689	696	82	121	77	53	110	3076	123	100	100	37	45	115	104	103	102	103	103	104	116	29	24	142	53	116	104	103	83	22	97	97	49	106	22	21	22	98	90	107	21	98	21	22	22	26	43	98	22
CE1803A	Australia	2	813	0	813	807	791	1402	1393	1400	780	850	806	802	820	3786	834	809	810	792	800	812	801	800	811	800	812	801	813	808	797	841	802	813	813	812	780	803	806	806	804	815	803	802	803	807	787	816	802	807	802	803	846	807	798	807	803
EC0382	Australia	3	1	813	0	98	82	698	689	696	83	121	77	54	111	3077	123	100	101	38	46	115	104	103	102	103	103	104	116	30	25	142	54	116	104	103	83	23	97	97	50	106	23	22	23	98	90	107	22	98	22	23	23	27	44	98	23
FB9087	USA	4	98	807	98	0	76	691	682	689	77	135	91	87	104	3070	119	94	95	77	85	109	98	97	96	97	97	98	110	93	82	137	87	110	98	97	77	88	91	91	89	99	88	87	88	92	84	100	87	92	87	88	131	92	83	91	88
FB9797	New Zealand	5	82	791	82	76	0	673	664	671	61	119	75	71	89	3055	103	78	79	59	69	93	82	81	80	81	81	82	94	77	66	121	71	94	82	81	61	72	75	75	73	84	72	71	72	76	68	85	71	76	71	72	115	76	67	76	72
GA9192	UK	6	698	1402	698	691	673	0	9	8	677	735	691	687	705	3671	719	694	695	677	685	709	698	697	696	697	697	698	710	693	682	737	687	710	698	697	677	688	691	691	689	700	688	687	688	692	684	701	687	692	687	688	731	692	683	692	688
GA9323	UK	7	689	1393	689	682	664	9	0	15	668	726	682	678	696	3662	710	685	686	668	676	700	689	688	687	688	688	689	701	684	673	728	678	701	689	688	668	679	682	682	680	691	679	678	679	683	675	692	678	683	678	679	722	683	674	683	679
GA9368	UK	8	696	1400	696	689	671	8	15	0	675	733	689	685	703	3669	717	692	693	675	683	707	696	695	694	695	695	696	708	690	680	735	685	708	696	695	675	686	689	689	687	698	686	685	686	690	682	699	685	690	685	686	729	690	681	690	686
IA1961	Australia	9	82	780	83	77	61	677	668	675	0	120	76	71	90	3056	103	79	80	61	69	78	67	66	81	66	82	53	79	77	66	106	71	79	83	82	20	72	76	76	73	85	72	71	72	77	27	86	71	77	71	72	115	76	67	77	72
JA0103	Netherlands	10	121	850	121	135	119	735	726	733	120	0	48	110	148	3114	162	137	138	100	108	152	141	140	139	140	140	141	153	116	105	181	110	153	141	140	120	111	134	134	112	143	111	110	111	135	127	144	110	135	110	111	154	115	106	135	111
JA0175	Netherlands	11	77	806	77	91	75	691	682	689	76	48	0	66	104	3070	118	93	94	56	64	108	97	96	95	96	96	97	109	72	61	137	66	109	97	96	76	67	90	90	68	99	67	66	67	91	83	100	66	91	66	67	110	71	62	91	67
PA1102	Australia	12	53	802	54	87	71	687	678	685	71	110	66	0	99	3065	113	89	89	32	40	104	93	92	91	92	92	93	105	48	37	132	28	105	93	92	72	43	86	86	44	95	43	42	43	87	79	96	42	87	42	43	86	46	38	87	43
QA5299	Japan	13	110	820	111	104	89	705	696	703	90	148	104	99	0	3084	90	78	51	89	97	121	109	108	83	108	84	111	122	105	94	147	99	122	85	84	90	100	78	78	100	87	100	99	100	79	97	88	99	79	99	100	143	104	95	79	100
RA2549	Argentina	14	3076	3786	3077	3070	3055	3671	3662	3669	3056	3114	3070	3065	3084	0	3098	3072	3073	3054	3062	3088	3077	3076	3075	3076	3076	3077	3089	3071	3060	3012	3065	3089	3077	3076	3056	3066	3070	3070	3067	3079	3066	3065	3066	3071	3063	3080	3065	3071	3065	3066	3109	3070	3061	3071	3066
RA4251	Germany	15	123	834	123	119	103	719	710	717	103	162	118	113	90	3098	0	93	79	103	111	135	124	123	95	123	97	124	136	118	107	162	112	136	97	96	103	113	91	91	114	100	113	112	113	92	110	101	112	92	112	113	156	117	108	91	113
RA5006	Germany	16	100	809	100	94	78	694	685	692	79	137	93	89	78	3072	93	0	69	79	87	111	100	99	72	99	73	100	112	95	84	138	89	112	74	73	79	90	67	67	91	76	90	89	90	68	86	77	89	68	89	90	133	94	85	68	90
RA6708	USA	17	100	810	101	95	79	695	686	693	80	138	94	89	51	3073	79	69	0	79	87	112	101	100	73	100	74	101	113	95	84	140	89	113	75	74	80	90	68	68	91	77	90	89	90	69	87	78	89	69	89	90	133	94	85	69	90
WA5546	Australia	18	37	792	38	77	59	677	668	675	61	100	56	32	89	3054	103	79	79	0	10	94	83	82	81	82	82	83	95	32	21	123	32	95	83	82	62	27	76	76	20	85	27	26	27	77	69	86	26	77	26	27	70	31	10	77	27
WA5591	Australia	19	45	800	46	85	69	685	676	683	69	108	64	40	97	3062	111	87	87	10	0	102	91	90	89	90	90	91	103	40	29	130	40	103	91	90	70	35	84	84	28	93	35	34	35	85	77	94	34	85	34	35	78	39	18	85	35
CE1636	Australia	20	115	812	115	109	93	709	700	707	78	152	108	104	121	3088	135	111	112	94	102	0	67	66	113	66	114	99	3	110	99	32	104	3	115	114	78	105	108	108	106	117	105	104	105	109	85	118	104	109	104	105	105	109	100	109	105
CE1564	Australia	21	104	801	104	98	82	698	689	696	67	141	97	93	109	3077	124	100	101	83	91	67	0	1	102	1	103	88	68	99	88	95	93	68	104	103	67	94	97	97	95	106	94	93	94	98	74	107	93	98	93	94	94	98	89	98	94
CE1573	Australia	22	103	800	103	97	81	697	688	695	66	140	96	92	108	3076	123	99	100	82	90	66	1	0	101	0	102	87	67	98	87	94	92	67	103	102	66	93	96	96	94	105	93	92	93	97	73	106	92	97	92	93	93	97	88	97	93
CE1600	Australia	23	102	811	102	96	80	696	687	694	81	139	95	91	83	3075	95	72	73	81	89	113	102	101	0	101	3	102	114	97	86	141	91	114	4	3	81	92	55	55	93	64	92	91	92	56	88	65	91	56	91	92	92	96	87	54	92
CE1638	Australia	24	103	800	103	97	81	697	688	695	66	140	96	92	108	3076	123	99	100	82	90	66	1	0	101	0	102	87	67	98	87	94	92	67	103	102	66	93	96	96	94	105	93	92	93	97	73	106	92	97	92	93	93	97	88	97	93
CE1590	Australia	25	103	812	103	97	81	697	688	695	82	140	96	92	84	3076	97	73	74	82	90	114	103	102	3	102	0	103	115	98	87	142	92	115	5	4	82	93	56	56	94	65	93	92	93	57	89	66	92	57	92	93	136	97	88	54	93
CE1628	Australia	26	104	801	104	98	82	698	689	696	53	141	97	93	111	3077	124	100	101	83	91	99	88	87	102	87	103	0	100	99	88	128	93	100	104	103	53	94	97	97	95	106	94	93	94	98	60	107	93	98	93	94	94	98	89	98	94
CE1634	Australia	27	116	813	116	110	94	710	701	708	79	153	109	105	122	3089	136	112	113	95	103	3	68	67	114	67	115	100	0	111	100	29	105	0	116	115	79	106	109	109	107	118	106	105	106	110	86	119	105	110	105	106	106	110	101	110	106
CE1619	Australia	28	29	808	30	93	77	693	684	690	77	116	72	48	105	3071	118	95	95	32	40	110	99	98	97	98	98	99	111	0	19	139	48	111	99	98	78	19	92	92	44	101	19	18	19	93	85	102	18	93	18	19	19	23	38	93	19
CE1670	Australia	29	24	797	25	82	66	682	673	680	66	105	61	37	94	3060	107	84	84	21	29	99	88	87	86	87	87	88	100	19	0	128	37	100	88	87	67	14	81	81	33	90	14	13	14	82	74	91	13	82	13	14	14	18	27	82	14
CE1715	Australia	30	142	841	142	137	121	737	728	735	106	181	137	132	147	3012	162	138	140	123	130	32	95	94	141	94	142	128	29	139	128	0	132	29	143	142	107	134	136	136	135	145	134	133	134	137	114	146	133	137	133	134	134	138	129	137	134
CE1683	Australia	31	53	802	54	87	71	687	678	685	71	110	66	28	99	3065	112	89	89	32	40	104	93	92	91	92	92	93	105	48	37	132	0	105	93	92	72	43	86	86	44	95	43	42	43	87	79	96	42	87	42	43	43	47	38	87	43
CE1710	Australia	32	116	813	116	110	94	710	701	708	79	153	109	105	122	3089	136	112	113	95	103	3	68	67	114	67	115	100	0	111	100	29	105	0	116	115	79	106	109	109	107	118	106	105	106	110	86	119	105	110	105	106	106	110	101	110	106
CE1731	Australia	33	104	813	104	98	82	698	689	696	83	141	97	93	85	3077	97	74	75	83	91	115	104	103	4	103	5	104	116	99	88	143	93	116	0	1	83	94	57	57	95	66	94	93	94	58	90	67	93	58	93	94	94	98	89	56	94
CE1732A	Australia	34	103	812	103	97	81	697	688	695	82	140	96	92	84	3076	96	73	74	82	90	114	103	102	3	102	4	103	115	98	87	142	92	115	1	0	82	93	56	56	94	65	93	92	93	57	89	66	92	57	92	93	93	97	88	55	93
CE1679	Australia	35	83	780	83	77	61	677	668	675	20	120	76	72	90	3056	103	79	80	62	70	78	67	66	81	66	82	53	79	78	67	107	72	79	83	82	0	73	76	76	74	85	73	72	73	77	9	86	72	77	72	73	73	77	68	77	73
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CE1833	Australia	37	97	806	97	91	75	691	682	689	76	134	90	86	78	3070	91	67	68	76	84	108	97	96	55	96	56	97	109	92	81	136	86	109	57	56	76	87	0	0	88	29	87	86	87	1	83	30	86	1	86	87	87	91	82	1	87
CE1848	Australia	38	97	806	97	91	75	691	682	689	76	134	90	86	78	3070	91	67	68	76	84	108	97	96	55	96	56	97	109	92	81	136	86	109	57	56	76	87	0	0	88	29	87	86	87	1	83	30	86	1	86	87	87	91	82	1	87
CE1818	Australia	39	49	804	50	89	73	689	680	687	73	112	68	44	100	3067	114	91	91	20	28	106	95	94	93	94	94	95	107	44	33	135	44	107	95	94	74	39	88	88	0	97	39	38	39	89	81	98	38	89	38	39	39	43	26	89	39
CE1865	Australia	40	106	815	106	99	84	700	691	698	85	143	99	95	87	3079	100	76	77	85	93	117	106	105	64	105	65	106	118	101	90	145	95	118	66	65	85	96	29	29	97	0	96	95	96	30	92	1	95	30	95	96	96	99	91	30	96
CE1957	Australia	41	22	803	23	88	72	688	679	686	72	111	67	43	100	3066	113	90	90	27	35	105	94	93	92	93	93	94	106	19	14	134	43	106	94	93	73	0	87	87	39	96	0	1	0	88	80	97	1	88	1	2	2	4	33	88	2
CE2006	Australia	42	21	802	22	87	71	687	678	685	71	110	66	42	99	3065	112	89	89	26	34	104	93	92	91	92	92	93	105	18	13	133	42	105	93	92	72	1	86	86	38	95	1	0	1	87	79	96	0	87	0	1	1	5	32	87	1
CE1963	Australia	43	22	803	23	88	72	688	679	686	72	111	67	43	100	3066	113	90	90	27	35	105	94	93	92	93	93	94	106	19	14	134	43	106	94	93	73	0	87	87	39	96	0	1	0	88	80	97	1	88	1	2	2	4	33	88	2
CE1762	Australia	44	98	807	98	92	76	692	683	690	77	135	91	87	79	3071	92	68	69	77	85	109	98	97	56	97	57	98	110	93	82	137	87	110	58	57	77	88	1	1	89	30	88	87	88	0	84	31	87	2	87	88	88	92	83	2	88
CE1796	Australia	45	90	787	90	84	68	684	675	682	27	127	83	79	97	3063	110	86	87	69	77	85	74	73	88	73	89	60	86	85	74	114	79	86	90	89	9	80	83	83	81	92	80	79	80	84	0	93	79	84	79	80	80	84	75	84	80
CE1872	Australia	46	107	816	107	100	85	701	692	699	86	144	100	96	88	3080	101	77	78	86	94	118	107	106	65	106	66	107	119	102	91	146	96	119	67	66	86	97	30	30	98	1	97	96	97	31	93	0	96	31	96	97	97	100	92	31	97
CE1984	Australia	47	21	802	22	87	71	687	678	685	71	110	66	42	99	3065	112	89	89	26	34	104	93	92	91	92	92	93	105	18	13	133	42	105	93	92	72	1	86	86	38	95	1	0	1	87	79	96	0	87	0	1	1	5	32	87	1
CE1814	Australia	48	98	807	98	92	76	692	683	690	77	135	91	87	79	3071	92	68	69	77	85	109	98	97	56	97	57	98	110	93	82	137	87	110	58	57	77	88	1	1	89	30	88	87	88	2	84	31	87	0	87	88	88	92	83	2	88
CE1917	Australia	49	21	802	22	87	71	687	678	685	71	110	66	42	99	3065	112	89	89	26	34	104	93	92	91	92	92	93	105	18	13	133	42	105	93	92	72	1	86	86	38	95	1	0	1	87	79	96	0	87	0	1	1	5	32	87	1
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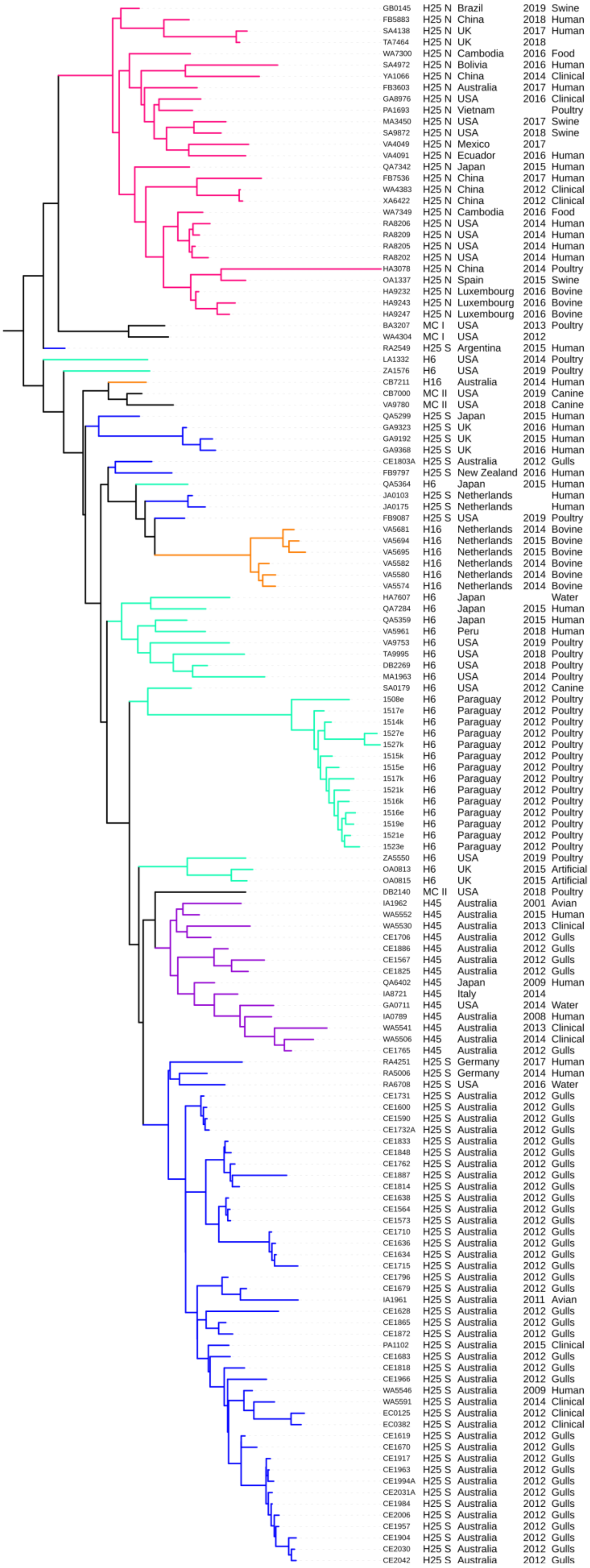
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TA7464 H25 N UK 2018
WA7300 H25 N Cambodia 2016 Food
SA4972 H25 N Bolivia 2016 Human
YA1066 H25 N China 2014 Clinical
FB3603 H25 N Australia 2017 Human
GA8976 H25 N USA 2016 Clinical
PA1693 H25 N Vietnam Poultry
MA3450 H25 N USA 2017 Swine
SA9872 H25 N USA 2018 Swine
VA4049 H25 N Mexico 2017
VA4091 H25 N Ecuador 2016 Human
QA7342 H25 N Japan 2015 Human
FB7536 H25 N China 2017 Human
WA4383 H25 N China 2012 Clinical
XA6422 H25 N China 2012 Clinical
WA7349 H25 N Cambodia 2016 Food
RA8206 H25 N USA 2014 Human
RA8209 H25 N USA 2014 Human
RA8205 H25 N USA 2014 Human
RA8202 H25 N USA 2014 Human
HA3078 H25 N China 2014 Poultry
OA1337 H25 N Spain 2015 Swine
HA9232 H25 N Luxembourg 2016 Bovine
HA9243 H25 N Luxembourg 2016 Bovine
HA9247 H25 N Luxembourg 2016 Bovine
BA3207 MC I USA 2013 Poultry
WA4304 MC I USA 2012
RA2549 H25 S Argentina 2015 Human
LA1332 H6 USA 2014 Poultry
ZA1576 H6 USA 2019 Poultry
CB7211 H16 Australia 2014 Human
CB7000 MC II USA 2019 Canine
VA9780 MC II USA 2018 Canine
QA5299 H25 S Japan 2015 Human
GA9323 H25 S UK 2016 Human
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RA4251 H25 S Germany 2017 Human
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CE1848 H25 S Australia 2012 Gulls
CE1762 H25 S Australia 2012 Gulls
CE1887 H25 S Australia 2012 Gulls
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CE1966 H25 S Australia 2012 Gulls
WA5546 H25 S Australia 2009 Human
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CE1619 H25 S Australia 2012 Gulls
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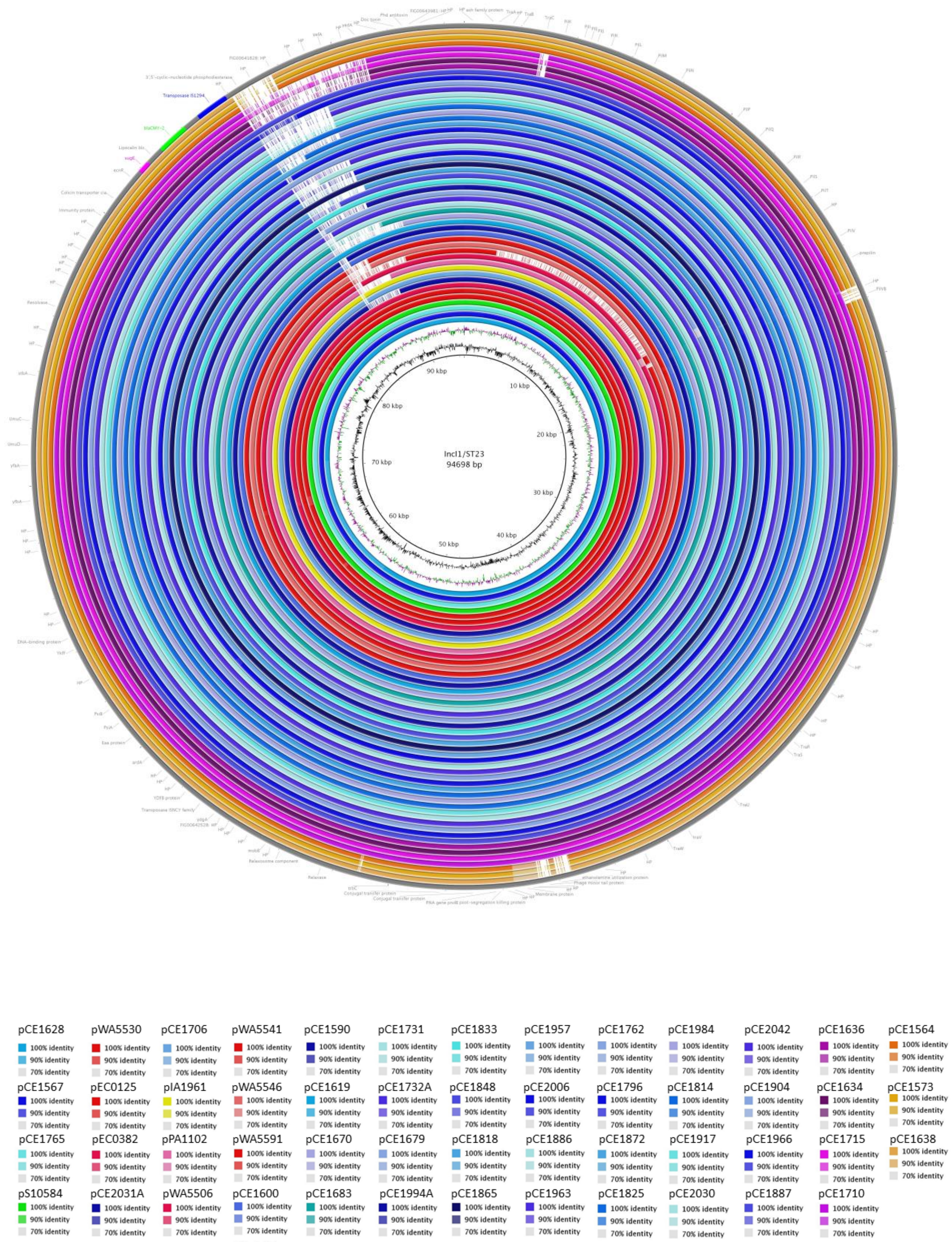
CE1963 H25 S Australia 2012 Gulls
CE1994A H25 S Australia 2012 Gulls
CE2031A H25 S Australia 2012 Gulls
CE1984 H25 S Australia 2012 Gulls
CE2006 H25 S Australia 2012 Gulls
CE1957 H25 S Australia 2012 Gulls
CE1904 H25 S Australia 2012 Gulls
CE2030 H25 S Australia 2012 Gulls
CE2042 H25 S Australia 2012 Gulls

Figure S2: Phylogeny of accessory genome of *E. coli* ST457 collection. The branches colours are used respecting the colour of clades in core genome phylogeny - H16 (orange), H25 North (red), H6 (turquoise), H45 (purple) and H25 South (blue) to highlight to which extent the accessory clades coping the core genome clades. The metadata consists of strain name, clade of core genome in which the respected strain belongs, country of origin, year and source of origin.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20 kbp
30 kbp
40 kbp
50 kbp
60 kbp
70 kbp
80 kbp
90 kbp
FIG00643981: HP
HP
HP
ash family protein
TraA
HP
TraB
TraC
PilK
PilI
PilJ
PilL
PilM
PilN
PilP
PilQ
PilR
PilS
PilT
HP
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prepilin
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PilVB
Phd antitoxin
Doc toxin
HP
YkfA
HP
HP
vafA
HP
HP
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3',5'-cyclic-nucleotide phosphodiesterase
HP
Transposase IS1294
blaCMY-2
Lipocalin blc
sugE
ecnR
Colicin transporter cia
Immunity protein
HP
HP
HP
HP
HP
HP
HP
Resolvase
HP
HP
stbA
UmuC
UmuD
yfbA
yfbA
HP
HP
HP
HP
HP
DNA-binding protein
YkfF
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PsiB
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ardA
HP
HP
HP
YDFB protein
Transposase ISNCY family
ydgA
FIG00642528: HP
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HP
HP
mobB
HP
Relaxosome component
Relaxase
trbC
Conjugal transfer protein
Conjugal transfer protein
RNA gene pndB post-segregation killing protein
HP
HP
Membrane protein
HP
HP
Phage minor tail protein
ethanolamine utilization protein
HP
HP
TraW
traV
TraU
TraS
TraR
HP
HP
HP
HP
HP
HP
pCE1628 100% identity 90% identity 70% identity
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pCE1963 100% identity 90% identity 70% identity
pCE1825 100% identity 90% identity 70% identity
pCE2030 100% identity 90% identity 70% identity
pCE1887 100% identity 90% identity 70% identity
pCE1710 100% identity 90% identity 70% identity

Figure S3: BRIG comparison of all IncI1/ST23, Inc/ST315 and IncI1/ST314 plasmids from this study carrying *bla*$_{\text{CMY-2}}$ (lime). The strains with these plasmids coming from gulls (blue ST23, purple ST315 and orange ST314), human and clinical strains (red and pink), *Dacelo novaguineae* (yellow) and a single plasmid IncI1/ST265 (pS10584) coming from *Salmonella enterica* strain SJTUF10584 (green) from Shanghai. The plasmid labels are organized from the iner circle into columns.

Plasmids sharing identical structure (no gaps) and at least 90% identity of all regions with our reference IncI1/ST23 plasmid (CE1628, gull, Five Islands, GenBank MT468652) came from humans from Wollongong hospital (EC0125) and from Syndey (EC0382 and WA5530), gulls from Sydney (CE1765, CE1833, CE1865, CE1762, CE1872, CE1814, CE1887) and Five Islands (CE1619, CE1567) and *Salmonella enterica* strain SJTUF10584 (pS10584). This reveals that these identical plasmids were found in 58% (7/12) of Sydney gulls, 16% of Five Islands gulls (3/19) and none of Montague island gulls.

Table S3: MIC values to 24 different antibiotics or their combinations for CE1628 strain which carried *bla*$_{\text{OXA-23}}$ within its chromosome. The resistance/susceptibility was determined using CLSI breakpoints. NA is used when the breakpoint was not available for the respected antibiotics.

ATB	**CE1628 MIC (mg/L)**	**CLSI**
Ampicilin	>128	Resistant
Ampiclin-sulbactam	32	Resistant
Cefazolin	>16	Intermediate
Cefuroxime	64	Resistant
Piperacilin	32	Susceptible
Piperacillin-tazobactam	2	Susceptible
Cefotaxime	>8	Resistant
Cefaclor	16	Susceptible
Cefprozil	64	Resistant
Cefepime	1	Susceptible
Cefoperazone-sulbactam	16	NA
Meropenem	<0.125	Susceptible
Ertapenem	1	Intermediate
Aztreonam	8	Intermediate
Netilmicin	0.25	Susceptible
Tobramycin	0.5	Susceptible
Gentamicin	0.5	Susceptible
Amikacin	<0.5	Susceptible
Tigecycline	0.125	NA
Colistin	0.25	Susceptible
Sulfomethoxazol-trimethoprim	0.25	Susceptible
Ciprofloxacin	<0.063	Susceptible
Chloramphenicol	4	Susceptible
Tetracyclin	1	Susceptible

Table S4: Genetic regions detected in at least 95% of our *E. coli* ST457 strains and not present in a reference genome of *E. coli* K-12 substrain (MG1655) using RAST annotation and position in CE1628 chromosome (SAMN14966947).

Cluster	RAST annotation	Position
AA	Putative sugar kinase, PfkB family protein	3626..4588
	ABC transporter, permease protein (cluster 2, ribose/xylose/arabinose/galactose)	4610..5599
	Putative ribose/galactose/methyl galactoside import ATP-binding protein 1	5600..7099
	ABC transporter, substrate-binding protein (cluster 2, ribose/xylose/arabinose/galactose)	7160..8050
	Tagatose-1,6-bisphosphate aldolase GatY	8086..8940
	Aga operon transcriptional repressor, DeoR family	9297..10112
AC	RelE-like translational repressor toxin	117831..118148
	Antitoxin to RelE-like translational repressor toxin	118207..118503
AD	putative membrane protein	147584..148189
	hypothetical protein	148192..149184
	Phosphate ABC transporter, substrate-binding protein PstS	149210..150715
AE	Putative DNA processing chain A	162419..163621
	ATP-dependent DNA helicase RecQ	163621..165717
AF	FIG00643143: hypothetical protein	198036..198344
AG	HicB-like protein	208916..209275
	HicA-like protein	209272..209547
AH	Arsenical resistance operon repressor	234432..234752
	Uncharacterized membrane protein, YraQ family	234859..235860
AI	Hemin transport protein HmuS	239219..240247
	TonB-dependent hemin, ferrichrome receptor	240296..242278
	hypothetical protein	242647..242808
	Periplasmic hemin-binding protein	242962..243876
	Radical SAM family protein HutW, similar to coproporphyrinogen III oxidase, oxygen-independent, associated with heme uptake	243896..245233
	Putative heme iron utilization protein	245246..245740
	Flavin reductase (EC 1.5.1.30)	245740..246363
	Hemin ABC transporter, permease protein	246412..247404
	ABC-type hemin transport system, ATPase component	247401..248171
AK	Transcriptional regulator, AraC family	344711..345526
	Xyloside transporter XynT	345752..347152
	Putative glycosyl hydrolase of unknown function	347163..349142

AK	(DUF1680)	
	Prophage Lp2 protein 6	350339..351418
AL	hypothetical protein	353105..354400
AM	Per-activated serine protease autotransporter enterotoxin EspC / autotransporter domain, T5aSS type secretion	359967..363776
	hypothetical protein	363948..364466
	Protein fanG precursor	364459..364980
	Protein fanF precursor	364994..365965
	Chaperone protein fanE precursor	365995..366690
	hypothetical protein	366683..369040
	hypothetical protein	369112..369639
	hypothetical protein	370382..370888
	HTH-type transcriptional regulator gadW	371080..371910
AN	putative lipoprotein	379271..379954
	hypothetical protein	379998..384413
AP	protein of unknown function DUF1498	436052..436732
	ROK family sugar kinase or transcriptional regulator	436713..437645
	Fructose-bisphosphate aldolase class II homolog	437693..438553
	Fructose-bisphosphate aldolase class II (EC 4.1.2.13) homolog	438634..439485
	PTS system, IIC component	439497..440588
	PTS system, IIB component	440613..440927
	PTS system, IIA component	440945..441415
	Transcription antiterminator, BglG family	441442..442995
AR	RelE-like translational repressor toxin	470535..470813
	Antitoxin to RelE-like translational repressor toxin	470826..471149
AS	hypothetical protein	480204..481643
	hypothetical protein	481922..483205
AT	Maltose-6'-phosphate glucosidase	493295..494617
AV	hypothetical protein	534486..536984
	hypothetical protein	537144..537257
AW	hypothetical protein	542238..543308
	adhesin	543319..545841
	fimbrial chaperone protein	545866..546597
	adhesin	546645..547217
AX	hypothetical protein	629581..631608
	hypothetical protein	631980..632534
AY	hypothetical protein	638555..639457
AZ	FIG00638425: hypothetical protein	641660..642157
	hypothetical protein	642154..643002
BA	hypothetical protein	655306..656202
	Cytosine/purine/uracil/thiamine/allantoin permease family protein	656280..657503

BA	Amidase	657529..657918
	Carbamate kinase	657935..658891
	Uncharacterized protein YahG	658884..660308
	Membrane protein FdrA	660305..661864
	Isochorismatase	662825..663493
BB	Tripartite tricarboxylate transporter TctA family	665620..667110
	Tripartite tricarboxylate transporter TctB family	667123..667629
	2-dehydro-3-deoxyphosphogalactonate aldolase	668645..669274
	2-dehydro-3-deoxygalactonokinase	669264..670268
	D-galactonate regulator, IclR family	670292..671059
BD	hypothetical protein	733701..735515
BE	toxin	736869..737243
BF	Hsp90xo protein	744143..745978
	hypothetical protein	745980..748286
BG	Putative glycoporin	754779..756173
BH	hypothetical protein	783029..783655
	hypothetical protein	783778..784452
BI	Nucleoside-specific channel-forming protein Tsx precursor	798027..798887
	5'-nucleotidase (EC 3.1.3.5)	798966..800585
	5'-nucleotidase (EC 3.1.3.5)	800626..802176
	hypothetical protein	802409..803536
	5'-nucleotidase (EC 3.1.3.5)	803669..805222
BJ	Mannonate dehydratase	831502..832716
	L-galactonate transporter	832783..834066
BK	Ribokinase (EC 2.7.1.15)	865287..866504
	hypothetical protein	866506..868005
	hypothetical protein	867998..870652
	hypothetical protein	870683..871333
BM	Shikimate 5-dehydrogenase I gamma (EC 1.1.1.25)	908285..909097
	L-sorbose 1-phosphate reductase	909090..910319
	PTS system, sorbose-specific IID component	910371..911195
	PTS system, sorbose-specific IIC component	911206..912003
	PTS system, sorbose-specific IIB component	912069..912563
	PTS system, sorbose-specific IIA component	912563..912970
	Sorbitol-6-phosphate 2-dehydrogenase	912980..913786
	Sorbitol operon regulator SorC	913856..914803
BN	Putative stomatin/prohibitin-family membrane protease subunit aq_911	916825..917952
	Uncharacterized protein YcgL	917958..918749
	hypothetical protein	918763..919218
	hypothetical protein	919215..919922
	Phage tail fiber protein H	919919..921499
	Phage tail formation protein I	921502..922218
	Phage baseplate assembly protein J	922211..923326

BN	Phage baseplate assembly protein	922211..923326
	Phage baseplate assembly protein V	923775..924476
	Phage tail formation protein D	924486..925526
	Phage Tail Protein X	925514..925723
	Phage tail protein U	925723..926676
	Phage tail length tape-measure protein T	926676..929051
	hypothetical protein	929153..929281
	Phage tail protein E	929241..929558
	Phage tail tube protein FII	929609..930133
	Phage tail sheath protein FI	930133..931557
	hypothetical protein	931547..931744
	hypothetical protein	931741..932196
	Putative inner membrane protein	932341..932655
	Phage lytic murein transglycosylase	932668..933273
	Putative inner membrane protein	933276..933563
	hypothetical protein	934101..934448
BO	hypothetical protein	1081708..1081842
	Mobile element protein	1081949..1082209
	Transposase	1082302..1082730
	hypothetical protein	1082873..1083586
	Inner membrane protein YjeO	1083583..1083900
BP	TRAP-type C4-dicarboxylate transport system, periplasmic component	1124454..1125425
	TRAP-type C4-dicarboxylate transport system, large permease component	1125478..1126779
	TRAP-type transport system, small permease component, predicted N-acetylneuraminate transporter	1126822..1127298
	Succinate dehydrogenase flavoprotein subunit	1127319..1129400
	Acetyl-CoA:acetoacetyl-CoA transferase alpha subunit	1129397..1130938
	3-hydroxybutyryl-CoA dehydratase	1130948..1131724
	Oxidoreductase, short-chain dehydrogenase/reductase family	1132586..1133377
BR	RelB/StbD replicon stabilization protein (antitoxin to RelE/StbE)	1167572..1167814
	mRNA interferase RelE	1167804..1168094
BT	Type I restriction-modification system, restriction subunit R (EC 3.1.21.3)	1260149..1260811
	Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72)	1260808..1260984
	hypothetical protein	1261029..1262195
	hypothetical protein	1262392..1262679
	hypothetical protein	1262666..1262968
BU	Putative cryptic D-serine deaminase (EC 4.3.1.18)	1266640..1267860
	N-acyl-D-amino-acid deacylase	1268061..1269503

BU	RidA/YER057c/UK114 superfamily protein	1269513..1269902
	sodium-solute symporter, putative	1270005..1271474
	Transcriptional regulator of RpiR family in catabolic operon	1271484..1272347
BW	hypothetical protein	1385799..1385936
	hypothetical protein	1386118..1386879
	Arylsulfatase	1386899..1388392
	hypothetical protein	1388522..1389766
BX	alpha-xylosidase	1392207..1394246
	Putative Na+/galactoside symporter STM0042	1394286..1395659
BY	FIG00641998: hypothetical protein	1425867..1426316
	hypothetical protein	1426352..1426951
BZ	FIG00642063: hypothetical protein	1446419..1446571
	Mobile element protein	1446626..1446748
	hypothetical protein	1446876..1447724
	FIG00641699: hypothetical protein	1447731..1448153
CA	hypothetical protein	1452764..1453333
CC	Uncharacterized protein YadD	1524729..1525661
CD	SAM-dependent methyltransferase YafE (UbiE paralog)	1608842..1609612
CF	Protein with similarity to RtcB	1627140..1628279
CG	hypothetical protein	1628898..1629461
CI	putative NADH-dependent flavin oxidoreductase	1667232..1668374
	Dienelactone hydrolase and related enzymes	1668619..1669539
	Transcriptional regulator, LysR family	1669633..1670622
	Oxidoreductase, aldo/keto reductase family	1671747..1672736
	Oxidoreductase, aldo/keto reductase family	1672763..1673614
CJ	Putative adhesin	1674180..1678433
CK	Oxidoreductase, aldo/keto reductase family	1679659..1680528
CL	hypothetical protein	1767310..1767765
CM	hypothetical protein	1783133..1784578
CN	ParD protein (antitoxin to ParE)	1790888..1791130
	ParE toxin protein	1791123..1791404
CP	hypothetical protein	1809179..1809334
	FIG00639058: hypothetical protein	1809443..1810000
	FIG00639058: hypothetical protein	1810006..1810287
	hypothetical protein	1810343..1810885
	hypothetical protein	1810869..1811180
CR	hypothetical protein	1880215..1880418
	putative lipoprotein	1880415..1880837
	adhesin/invasin-like protein [similarity]	1880891..1881907
	FIG00640270: hypothetical protein	1882005..1882127
	hypothetical protein	1882273..1882635
CT	YVTN beta-propeller repeat-containing protein	2074053..2075930
CU	FIG00640465: hypothetical protein	2084189..2084626

CV	hypothetical protein	2123470..2124183
	Demethylmenaquinone methyltransferase-like protein	2124447..2125133
	hypothetical protein	2125146..2126159
	Oxidoreductase, short-chain dehydrogenase/reductase family	2126171..2126926
	Altronate hydrolase	2126941..2127252
	Altronate dehydratase	2127252..2128448
	TRAP transporter solute receptor, unknown substrate 8	2128476..2129444
	TRAP dicarboxylate transporter, DctQ subunit, unknown substrate 8	2129504..2129965
	TRAP dicarboxylate transporter, DctM subunit, unknown substrate 8	2129965..2131275
CW	RtcB-like protein	2143004..2144401
	hypothetical protein	2144607..2144759
	Urocanate hydratase	2145159..2146856
	Cytosine/purine/uracil/thiamine/allantoin permease family protein	2147020..2148429
	Conserved hypothetical protein (perhaps related to histidine degradation	2148431..2149021
	Imidazolonepropionase	2149018..2150229
	Formiminoglutamase	2150229..2151179
	Histidine ammonia-lyase	2151230..2152900
	Transcriptional regulator, LysR family	2153171..2154076
	Cob(I)alamin adenosyltransferase	2154110..2154712
	Fumarate hydratase class I	2154722..2156374
	Putative symport protein	2156482..2157762
	hypothetical protein	2157923..2158240
	DNA for 3-methylaspartate ammonia-lyase, glutamate mutase	2158237..2159607
	Methylaspartate ammonia-lyase	2159611..2160852
	Methylaspartate mutase, E subunit	2160852..2162297
	Uncharacterized protein GlmL	2162316..2163704
	Methylaspartate mutase, S subunit	2163704..2164153
	hypothetical protein	2164700..2165122
	hypothetical protein	2165203..2166147
CX	Prevent host death protein, Phd antitoxin	2226987..2227427
	hypothetical protein	2227427..2227708
CZ	Antitoxin to RelE-like translational repressor toxin	2272580..2272909
	RelE-like translational repressor toxin	2272899..2273285
DA	hypothetical protein	2301648..2303450
DC	Molybdate metabolism regulator	2348701..2352501
DD	Integrase	2363694..2365001

DD	5-methylcytosine-specific restriction enzyme A (EC 3.1.21.)	2365130..2365855
	hypothetical protein	2365933..2366280
	Putative transcription regulator	2366391..2366855
	resolvase	2367022..2367573
	hypothetical protein	2367754..2367876
	hypothetical protein	2369338..2369520
	hypothetical protein	2369667..2370386
	hypothetical protein	2370398..2370643
	hypothetical protein	2370809..2371048
DE	FIG00638046: hypothetical protein	2389168..2389464
	Transcriptional regulator	2389466..2389717
DG	Helix-turn-helix motif	2415956..2416246
	Phage protein	2416236..2416574
DO	Transcriptional regulator, AraC family	3005628..3006641
	hypothetical protein	3006694..3007092
DP	Transcriptional regulator, GntR family	3009450..3010148
	FIG00639603: hypothetical protein	3010195..3010338
	PTS system, cellobiose-specific IIB component	3010347..3010658
	PTS system, cellobiose-specific IIC component	3010772..3011629
	PTS system, cellobiose-specific IIC component	3011696..3012094
	PTS system, cellobiose-specific IIA component	3012122..3012433
	Outer membrane porin	3012489..3014162
	6-phospho-beta-glucosidase	3014187..3015626
DQ	Uncharacterized GGDEF domain protein YneF	3024064..3025482
DR	Type-1 fimbrial protein, A chain	3044366..3044929
	chaperone FimC	3045292..3046002
	Outer membrane usher protein FimD	3046044..3048695
DS	Toxin HigB	3115551..3115829
DT	Outer membrane porin OmpD	3122125..3123225
	hypothetical protein	3123395..3124654
DV	Putative alkyl/aryl-sulfatase YjcS	3138892..3140868
	hypothetical protein	3140963..3142012
DY	Multidrug resistance transporter, Bcr/CflA family	3264356..3265519
	Efflux transport system, outer membrane factor (OMF) lipoprotein	3265528..3266901
	RND efflux system, inner membrane transporter	3266905..3270012
	RND efflux system, membrane fusion protein	3270012..3271133
	Transcriptional regulator, AcrR family	3271282..3271848
DZ	FIG00640233: hypothetical protein	3295641..3295949
	hypothetical membrane protein	3295959..3296981
ED	ABC transporter, substrate-binding protein (cluster 8, B12/iron complex)	3375281..3376303
	ABC transporter, permease protein (cluster 8,	3376303..3377283

ED	B12/iron complex)	
	ABC transporter, ATP-binding protein (cluster 8, B12/iron complex)	3377280..3378038
	Orf2	3378048..3378860
	Molybdenum transport system protein ModD	3378857..3379711
	Putative TonB dependent outer membrane receptor	3379737..3381707
EE	FIG00640682: hypothetical protein	3386524..3386685
	hypothetical protein	3387024..3388460
EG	Uncharacterized protein STM4317	3473624..3473917
	Acetyltransferase	3473914..3474408
EI	Transcriptional regulator STM2195	3704379..3704768
	L-serine dehydratase, beta subunit (EC 4.3.1.17) / L-serine dehydratase, alpha subunit	3704770..3706122
	hypothetical protein	3706131..3706253
	Phosphoserine phosphatase	3706333..3707220
	Uncharacterized MFS-type transporter STM2198	3707253..3708575
EJ	Uncharacterized dehydratase STM2273	3801510..3802712
	Uncharacterized MFS-type transporter	3802725..3804053
	Transcriptional regulator STM2275, GntR family	3804291..3804989
EK	Uncharacterized MFS-type transporter	3814910..3816100
	Transcriptional regulator STM2281, LysR family	3816252..3817151
EL	Na+/H+ antiporter NhaC	3885540..3886979
	Cystathionine beta-lyase	3886976..3888193
EM	ATP-binding protein	3915179..3916537
	hypothetical protein	3916521..3917180
EP	RatA homolog	4205692..4213767
	SinI homolog	4213877..4214869
	adherence and invasion outermembrane protein (Inv,enhances Peyer's patches colonization)	4214925..4217099
ER	Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1)"	4360629..4361963
	hypothetical protein	4362051..4362482
ES	hypothetical protein	4404126..4404899
ET	Molybdate-binding domain of ModE	4418809..4419237
EU	Hydroxyaromatic non-oxidative decarboxylase protein D (EC 4.1.1.-)	4423272..4423508
	Hydroxyaromatic non-oxidative decarboxylase protein C	4423519..4424946
	Hydroxyaromatic non-oxidative decarboxylase protein B (EC 4.1.1.-)	4424946..4425539
	Transcriptional regulator, MarR family	4425686..4426093
EV	Hok/Gef-like protein	4437399..4437551
EW	Fructokinase	4453774..4454691
	Sucrose outer membrane porin	4454862..4456379

EW	PTS system, sucrose-specific IIB component (EC 2.7.1.211) / PTS system, sucrose-specific IIC component	4456440..4457810
	Sucrose-6-phosphate hydrolase	4457816..4459219
	Sucrose operon repressor ScrR, LacI family	4459245..4460252
EX	LemA PROTEIN	4461181..4461783
	hypothetical protein	4461797..4462690
	hypothetical protein	4462705..4463853
EY	D-3-phosphoglycerate dehydrogenase	4505746..4506693
	D-arabinose-5-phosphate isomerase	4506765..4507361
	Cystathionine beta-lyase MalY (EC 4.4.1.8) Maltose regulon modulator	4507364..4508539
	PTS system, maltose and glucose-specific IIC component / PTS system, maltose and glucose-specific IIB	4508539..4510119
	Beta-glucoside bgl operon antiterminator, BglG family	4510151..4510975
	FIG00643868: hypothetical protein	4511110..4511223
FC	General secretion pathway protein K	4764842..4765819
	General secretion pathway protein J	4765816..4766421
	General secretion pathway protein I	4766418..4766789
	General secretion pathway protein H	4766786..4767349
	General secretion pathway protein G	4767353..4767808
	General secretion pathway protein F	4767825..4769048
	General secretion pathway protein E	4769048..4770541
	General secretion pathway protein D	4770541..4772601
FI	Alpha-fimbriae tip adhesin	4924270..4925349
	Alpha-fimbriae usher protein	4925346..4928030
	Alpha-fimbriae major subunit	4928121..4928621
	hypothetical protein	4928651..4929367
	hypothetical protein	4929449..4929577
FJ	PTS system, N-acetylgalactosamine-specific IIC component	4963482..4964261
	PTS system, N-acetylgalactosamine-specific IID component	4964251..4965129
	PTS system, N-acetylgalactosamine-specific IIA component, PTS system, galactosamine-specific IIA	4965147..4965581
	N-acetylgalactosamine-6-phosphate deacetylase	4965578..4966711
FK	hypothetical protein	5050200..5050994

Table S5: Genetic regions shared by chromosomes of our three PacBio sequences (CE1628, CE1803A and 1517k) and not present in a reference genome of *E. coli* K-12 substrain (MG1655) which were detected in less than 95% of *E. coli* ST457 strains.

Cluster	**Rast annotation**	**Position**
AB	Leader peptidase HopD	57296..57763
AJ	Small inner membrane protein, YmgF family	292942..293109
AJ	Mobile element protein	293289..293420
	Small inner membrane protein, YmgF family	293425..293592
	hypothetical protein	293717..293893
	Small inner membrane protein, YmgF family	293909..294076
AO	O-antigen ligase	402968..404221
	Beta-1,3-glucosyltransferase	404267..405250
	UDP-galactose:(galactosyl) LPS alpha1,2-galactosyltransferase WaaW	405332..406360
AQ	Type III secretion chaperone protein for YopD (SycD)	451870..452367
	FIG00643201: hypothetical protein	452377..452559
	cell invasion protein SipB	452615..454396
	FIG00637902: hypothetical protein	454409..455560
	putative type III effector protein SipD	455604..456953
	Invasion protein iagA	457156..458853
	adherence and invasion outermembrane protein (Inv,enhances Peyer's patches colonization)	458905..468870
AU	hypothetical protein	530110..532518
	hypothetical protein	532819..533274
	hypothetical protein	533279..534016
BC	Transposase InsG for insertion sequence element IS4	713785..715113
BL	no annotation	888670 - 894170
BQ	hypothetical protein	1137539..1138696
	hypothetical protein	1138729..1140222
BS	hypothetical protein	1204773..1205552
	hypothetical protein	1205621..1205998
	Putative superfamily I DNA helicases	1206324..1209839
	putative restriction endonuclease	1209902..1210957
	hypothetical protein	1211142..1212179
	Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72)	1212423..1213922
	Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72)	1213928..1215418
	Type I restriction-modification system, specificity subunit S	1215419..1216585
	Type I restriction-modification system,	1216587..1219649

BS	restriction subunit R (EC 3.1.21.3)	
	Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72)	1219730..1221637
	hypothetical protein	1221634..1223367
BV	hypothetical protein	1351354..1351617
CB	Mobile element protein	1506064..1507044
CE	Transposase and inactivated derivatives	1622296..1622793
CH	Integrase	1637846..1639060
	hypothetical protein	1639306..1639419
	Transcriptional regulator, AlpA like	1639488..1639691
	hypothetical protein	1639691..1640122
	AntA/AntB antirepressor domain protein	1640135..1640968
	hypothetical protein	1640961..1641143
	Phage terminase, small subunit	1641281..1641397
	Fructokinase (EC 2.7.1.4)	1641799..1641993
	FIG01068751: hypothetical protein	1641986..1642204
	FIG00641311: hypothetical protein	1642197..1642391
	FIG00643307: hypothetical protein	1642388..1642651
	hypothetical protein	1642648..1642869
	FIG00641080: hypothetical protein	1642862..1643464
	hypothetical protein	1643475..1643816
	FIG00640442: hypothetical protein	1643809..1644180
	DNA primase, phage associated	1644167..1646923
	FIG00642382: hypothetical protein	1647212..1647325
	FIG00641614: hypothetical protein	1647508..1647669
	hypothetical protein	1647686..1648147
	Phage DNA transfer protein	1648141..1648818
	Phage DNA transfer protein	1648818..1650239
	Phage DNA transfer protein	1650239..1652344
	hypothetical protein	1652363..1652752
	hypothetical protein	1652853..1653035
	Abortive infection bacteriophage resistance protein	1653588..1654550
	hypothetical protein	1654552..1655007
	hypothetical protein	1655267..1655554
	hypothetical protein	1655554..1655664
	FIG00639659: hypothetical protein	1656156..1656290
CO	Mobile element protein	1793431..1793619
	hypothetical protein	1793808..1793987
	Putative transposase InsQ for insertion sequence element IS609	1794025..1795173
CQ	Toxin HigB	1873948..1874250
CS	hypothetical protein	2029119..2029208
CY	Putative inner membrane protein	2252196..2252312
	Mobile element protein	2252410..2253390
DB	Mobile element protein	2314265..2315290

DF	orf; Unknown function	2401963..2402109
	orf; Unknown function	2402291..2402437
	orf; Unknown function	2402619..2402765
DH	N-acetyl-alpha-D-glucosaminyl-diphospho-ditrans, octacis-undecaprenol 4-epimerase	2442276..2443271
DI	hypothetical protein	2444780..2446015
	Glycosyl transferase, group 2 family protein	2446024..2446749
	hypothetical protein	2446746..2447981
	hypothetical protein	2447983..2449050
	UDP-glucose 4-epimerase	2449071..2450087
	Mannosyltransferase	2450156..2451163
	GDP-mannose 4,6-dehydratase	2451174..2452295
	GDP-L-fucose synthetase	2452299..2453264
	GDP-mannose mannosyl hydrolase	2453267..2453722
	Mannose-1-phosphate guanylyltransferase (EC 2.7.7.13) / Mannose-6-phosphate isomerase	2453734..2455119
	Colanic acid biosynthesis glycosyl transferase WcaE	2455203..2455949
	Phosphomannomutase (EC 5.4.2.8) => Colanic acid	2455974..2457344
DJ	FIG00639501: hypothetical protein	2469038..2469166
DK	Antirestriction protein klcA	2482161..2482640
	UPF0380 proteins YafZ and homologs	2482722..2483543
	hypothetical protein	2483633..2483767
	hypothetical protein	2483764..2484174
	hypothetical protein	2484190..2484873
	Patatin	2485009..2486079
	Uncharacterized protein YjcZ paralog	2486076..2486981
	Clamp-binding protein paralog	2486978..2489374
	hypothetical protein	2490548..2491699
	hypothetical protein	2491727..2491873
	Mobile element protein	2493627..2494148
	Putative transposase InsK for insertion sequence element IS150	2494145..2494996
	hypothetical protein	2495539..2496141
	hypothetical protein	2496235..2496441
	FIG00639191: hypothetical protein	2498836..2499036
	hypothetical protein	2499236..2499805
	hypothetical protein	2500065..2500466
	FIG00638721: hypothetical protein	2500454..2500861
	Transposase	2501667..2502524
	Gamma-glutamyltranspeptidase (EC 2.3.2.2) Glutathione hydrolase (EC 3.4.19.13)	2502859..2503026
	Gamma-glutamyltranspeptidase (EC 2.3.2.2) Glutathione hydrolase (EC 3.4.19.13)	2503017..2503130
	Puative phophotriesterase	2503170..2504204

DK	Putative inner membrane protein	2504207..2505172
	hypothetical protein	2505229..2505987
	Putative ribokinase	2506001..2507215
	Transposase	2507411..2507527
	FIG00640053: hypothetical protein	2507634..2507771
	Aspartate ammonia-lyase	2508759..2510159
	Anaerobic C4-dicarboxylate transporter	2510382..2511680
	Aspartate racemase	2511739..2512458
	LysR-family transcriptional regulator YjiE	2512798..2513697
	hypothetical protein	2513967..2514101
	Transposase, IS200 family	2514612..2514731
	D-galactonate transporter	2515050..2516342
	Galactonate dehydratase	2516462..2517610
	2-dehydro-3-deoxyphosphogalactonate aldolase	2517607..2518224
	2-dehydro-3-deoxygalactonokinase	2518208..2519086
	D-Galactonate repressor DgoR	2519083..2519772
	Mobile element protein	2520125..2520457
	hypothetical protein	2520571..2520741
	Transposase InsN for insertion sequence element IS911	2521004..2521315
	Transposase InsO for insertion sequence element IS911	2521504..2522181
	hypothetical protein	2522401..2522535
	Insertion element IS401 (Burkholderia multivorans) transposase	2522617..2522838
	hypothetical protein	2523219..2523356
	Uncharacterized MFS-type transporter	2523787..2525181
	Transcriptional regulator CKO_02662, LacI family	2525286..2526317
	Inosine-uridine preferring nucleoside hydrolase	2526277..2527311
	Mg(2+)-transport-ATPase-associated protein MgtC	2527375..2528088
	Mobile element protein	2528245..2528844
	Transposase	2528899..2529792
	Transposase	2529840..2530382
	Transposase	2530379..2530657
	hypothetical protein	2531103..2531381
	Isoaspartyl aminopeptidase	2531719..2532750
	hypothetical protein	2533077..2533226
	Retron-type RNA-directed DNA polymerase	2533274..2533720
	hypothetical protein	2534082..2534216
	Anaerobic C4-dicarboxylate transporter DcuC	2534385..2535746
	Tripeptide aminopeptidase	2535743..2536999
	Aspartate ammonia-lyase	2537865..2539265
	Anaerobic C4-dicarboxylate transporter DcuA	2539421..2540755
	L-asparaginase	2541243..2542289
	hypothetical protein	2542619..2542744
	Fumarate respiration two-component response regulator DcuR	2542883..2543608

DK	regulatory protein GntR, HTH:GntR-like	2544587..2545243
	Anaerobic C4-dicarboxylate transporter	2545398..2546714
	Anaerobic C4-dicarboxylate transporter DcuB	2546830..2548146
	Argininosuccinate lyase	2548211..2549587
	Polyketide synthase modules and related proteins	2550246..2550635
	hypothetical protein	2550897..2551031
	Co-activator of prophage gene expression IbrA	2551021..2552253
	Co-activator of prophage gene expression IbrB	2552238..2552882
	hypothetical protein	2553137..2553253
	Colicin I receptor	2553253..2555400
DL	Invasin	2572779..2573528
	iron aquisition outermembrane yersiniabactin receptor (FyuA,Psn,pesticin receptor), Outer membrane receptor for ferric siderophore	2574179..2576200
	iron aquisition 2,3-dihydroxybenzoate-AMP ligase (EC 2.7.7.58,Irp5) 2,3-dihydroxybenzoate-AMP ligase (EC 2.7.7.58) of siderophore biosynthesis	2576331..2577908
	Iron aquisition yersiniabactin synthesis enzyme YbtT Thioesterase in siderophore biosynthesis gene cluster	2577912..2578715
	Yersiniabactin synthetase, thiazolinyl reductase component Irp3, Thiazolinyl imide reductase in siderophore biosynthesis gene cluster	2578712..2579812
	iron aquisition yersiniabactin synthesis enzyme (Irp1,polyketide synthetase), Siderophore biosynthesis non-ribosomal peptide synthetase modules	2579809..2589300
	iron aquisition yersiniabactin synthesis enzyme (Irp2) Siderophore biosynthesis non-ribosomal peptide synthetase modules	2589388..2595495
	iron aquisition regulator (YbtA,AraC-like,required for transcription of FyuA/psn,Irp2)	2595686..2596645
	Iron siderophore ABC transporter, permease/ATP-binding protein YbtP	2596812..2598614
	Iron siderophore ABC transporter, permease/ATP-binding protein YbtQ	2598601..2600403
	Putative signal transducer	2600396..2601676
	Salicylate synthetase (EC 5.4.4.2)(EC 4.2.99.21) Salicylate synthetase (EC 5.4.4.2)(EC 4.2.99.21) of siderophore biosynthesis	2601704..2603008
	Integrase	2603202..2604245
DM	Mobile element protein	2701154..2702134
DN	2-oxoglutarate/malate translocator	2860920..2862320
	D-3-phosphoglycerate dehydrogenase	2862356..2863315
	probable beta-D-galactosidase	2863326..2863805

DN	L-fuco-beta-pyranose dehydrogenase	2863818..2864561
DU	Mobile element protein	3135549..3136529
DW	Mobile element protein	3176170..3176691
	Putative transposase InsK for insertion sequence element IS150	3176688..3177539
DX	regulatory protein for 2-phenylethylamine catabolism	3196463..3196654
EA	Transposase InsG for insertion sequence element IS4	3328295..3329623
EB	Small inner membrane protein, YmgF family	3353580..3353714
EC	FIG00641724: hypothetical protein	3367370..3367600
EF	Transposase InsN for insertion sequence element IS911	3404823..3405134
	Transposase InsO for insertion sequence element IS911	3405323..3406000
EH	Mobile element protein	3687986..3689011
EN	Phage integrase, Phage P4-associated	3973432..3974622
	hypothetical protein	3974942..3975055
	hypothetical protein	3975890..3976045
	Transposase InsF for insertion sequence IS3	3976042..3976473
	Transposase InsF for insertion sequence IS3	3976505..3976885
	Transposase InsE for insertion sequence IS3E	3976882..3977181
	hypothetical protein	3977358..3979718
	hypothetical protein	3980362..3981378
	ATP-dependent helicase	3981860..3984058
	ATP/GTP-binding protein	3984055..3985371
	probable membrane protein YPO2297	3985375..3987684
	hypothetical protein	3988153..3988311
	hypothetical protein	3988319..3988438
	hypothetical protein	3988486..3988725
	Mobile element protein	3988920..3989213
	Mobile element protein	3989524..3989670
	Putative transport protein	3989959..3991248
	Oxidoreductase, zinc-binding dehydrogenase family (EC 1.1.1.-)	3991220..3992245
	hypothetical protein	3992493..3992636
	Transposase	3992801..3993607
	Insertion element IS600 (Shigella sonnei) transposase	3993643..3993945
	hypothetical protein	3994335..3994457
	hypothetical protein	3994515..3994652
	Transposase	3994805..3995287
	Transposase	3995284..3995472
	Mobile element protein	3995772..3996512
	hypothetical protein	3996519..3997448
	Mobile element protein	3997523..3997861
	hypothetical protein	3997855..3998142
	hypothetical protein	3998234..3998347
	Putative Heme-regulated two-component response	3998826..3999260

EN	regulator	
	Transcriptional regulator STM1541, GntR family	3999308..3999979
	Mobile element protein	4000193..4000447
	Mobile element protein	4000398..4000976
	Transposase InsO for insertion sequence element IS911	4001034..4001711
	Transposase InsN for insertion sequence element IS911	4001900..4002211
	Uncharacterized protein YeeT	4002273..4002452
	YeeU protein (antitoxin to YeeV)	4002736..4002936
	FIG00639775: hypothetical protein	4003474..4003992
	hypothetical protein	4004052..4011971
	hypothetical protein	4011996..4012616
	Type 1 fimbriae regulatory protein, FimB/FimE family	4012934..4013563
EO	Putative transposase InsQ for insertion sequence element IS609	4056484..4056906
	Putative transposase InsQ for insertion sequence element IS609	4057045..4057290
	Putative transposase InsQ for insertion sequence element IS609	4057372..4057632
	hypothetical protein	4057670..4057849
	Mobile element protein	4058038..4058241
EQ	Transposase InsG for insertion sequence element IS4	4317727..4319055
EZ	Predicted regulator of STY3230 transporter operon	4624531..4624962
	Substrate-specific component STY3230 of queuosine-regulated ECF transporter	4624985..4625563
	Transmembrane component STY3231 of energizing module of queuosine-regulated ECF transporter	4625564..4626271
	ATPase component STY3232 of energizing module of queuosine-regulated ECF transporter	4626259..4626936
	ATPase component STY3233 of energizing module of queuosine-regulated ECF transporter	4626930..4627607
FA	hypothetical protein	4645977..4646708
FB	FIG00640004: hypothetical protein	4741484..4741609
	D-arabinose-5-phosphate isomerase (EC 5.3.1.13)	4742127..4743110
	Capsular polysaccharide export system inner membrane protein KpsE	4743182..4744330
	Capsular polysaccharide export system periplasmic protein KpsD	4744354..4746030
	3-deoxy-manno-octulosonate cytidylyltransferase	4746040..4746780
	Capsular polysaccharide export system protein KpsC	4746777..4748804
	Capsular polysaccharide export system protein KpsS	4748839..4750080
	Capsular polysaccharide ABC transporter, ATP-binding protein KpsT	4760607..4761299
	Capsular polysaccharide ABC transporter,	4761296..4762072

FB	permease protein KpsM	
FD	AMP-binding enzyme, associated with serine palmitoyltransferase	4791023..4792744
	Nucleoside-diphosphate-sugar epimerase	4792741..4793655
	Acyl carrier protein Acyl carrier protein associated with serine palmitoyltransferase	4793687..4793935
	Serine palmitoyltransferase	4793935..4795107
	Permease, YjgP/YjgQ family	4795142..4796221
	Permease Ygh-P1, YjgP/YjgQ family	4796218..4797288
	Transcriptional regulator, YtfJ-family	4797319..4797879
	Conserved hypothetical TPR repeat protein, clustered with yghQ	4797891..4798715
FE	hypothetical protein	4826337..4827254
	hypothetical protein	4827436..4827783
FF	Transcriptional regulator STM3084, GntR family	4830325..4831074
	D-mannonate oxidoreductase	4831397..4832869
	L-galactonate-5-dehydrogenase	4832866..4833882
	Malate dehydrogenase	4833893..4834903
	TRAP-type C4-dicarboxylate transport system, periplasmic component	4834976..4835959
	TRAP-type C4-dicarboxylate transport system, small permease component	4836000..4836482
	TRAP-type C4-dicarboxylate transport system, large permease component	4836493..4837797
FG	hypothetical phosphosugar isomerases	4848603..4849490
	ABC transporter, substrate-binding protein (cluster 8, B12/iron complex)	4849487..4850434
	Iron compound ABC transporter, permease protein	4850445..4851494
	Iron compound ABC transporter, permease protein	4851491..4852474
	Iron compound ABC transporter, ATP-binding protein	4852471..4853280
	Putative iron compound receptor	4853654..4855795
FH	Putative arylsulfate sulfotransferase	4864421..4866217
	Periplasmic thiol:disulfide interchange protein, DsbA-like	4866235..4866903
	Inner membrane thiol:disulfide oxidoreductase, DsbB-like"	4866918..4867589