

TABLE S1. Conventional MLST schemes used for *in silico* MLST.^a

Target	Sequence length
<u><i>Citrobacter freundii</i></u>	
arcA	435
aspC	513
clpX	567
dnaG	444
fadD	483
lysP	477
mdh	549
<u><i>Enterobacter cloacae</i></u>	
dnaA	442
fusA	646
gyrB	434
leuS	578
pyrG	259
rplB	607
rpoB	545
<u><i>Escherichia coli</i></u>	
adk	536
fumC	469
gyrB	460
icd	518
mdh	452
purA	478
recA	510
<u><i>Klebsiella oxytoca</i></u>	
gapA	450
infB	318
mdh	477
pgi	432
phoE	420
rpoB	501
tonB	405
<u><i>Klebsiella pneumoniae</i></u>	
gapA	450
infB	318
mdh	477
pgi	432
phoE	420
rpoB	501
tonB	414

MLST = multilocus sequence typing

a. MLST schemes were based on the publicly available PubMLST.org database (www.pubmlst.org)

TABLE S2. Whole genome sequences used for developing genus-, genetic complex- and species-specific wgMLST schemes: public database accession numbers and assembly characteristics.

Isolate	MLST ^a	BioSample	Assembly name	National Center for Biotechnology Information database				WGS project	Instit. Pasteur MLST database	Identification number	Level of assembly	Assembly characteristics									
				GenBank assembly	RefSeq assembly	GenBank sequence	RefSeq sequence					Sequence length	Contigs			Scaffolds			Gaps		
											Total	Unmapped	Number	N50	L50	Number	N50	L50	Spanned	Unspanned	
Citrobacter spp.																					
Citrobacter koseri ATCC BAA-895 ^b	NA	SAMN02003912	ASM1804v1	GCA_00011040.1	GF_00011040.1	CP008822.1	NC_009792.1	-	-	-	Complete genome, chromosome	4,720,402	-	-	-	-	-	-	-	-	-
Citrobacter amalonitidis LB4	NA	SAMN02226357	ASM71105v1	GCA_00073105.1	GF_00073105.1	-	-	JMK201	-	-	Complete genome, chromosome	5,273,145	-	110	115,086	15	-	-	-	-	-
Citrobacter farmetii GTC 1319	NA	SAMN0018686	ASM7473v1	GCA_00076473.1	GF_00076473.1	-	-	BBM001	-	-	Contig	4,529,495	-	31	240,203	9	-	-	-	-	-
Citrobacter freundii ATCC 8000 + MTCC 1658	Unknown ST, minor mismatch ^c	SAMN04269678	ASM31246v1	GCA_00031246.1	GF_00031246.1	-	-	ANV01	-	-	Contig	5,001,265	-	171	198,048	8	-	-	-	-	-
Citrobacter freundii Salkoff 7851	Unknown ST, minor mismatch ^c	SAMN0082765	ASM20876v1	GCA_00082765.1	GF_00082765.1	-	-	CACD01	-	-	Contig	4,904,641	4,904,566	363	60,237	27	357	60,237	27	6	0
Citrobacter freundii CFNH1	Unknown ST, minor mismatch ^c	SAMN0211384	ASM6485v1	GCA_0006485.1	GF_0006485.1	CP007557.1	NZ_CP007557.1	-	-	-	Complete genome, chromosome	5,099,034	-	-	-	-	-	-	-	-	-
Citrobacter freundii FDMARGOS_73	ST8	SAMN0235425	ASM78375v1	GCA_00078375.1	GF_00078375.1	-	-	JTB01	-	-	Contig	5,451,137	-	3	5,064,606	1	-	-	-	-	-
Citrobacter freundii GTC 09479	Unknown ST, minor mismatch ^c	SAMN02469850	Whole genome assembly	GCA_00034232.1	GF_00034232.1	-	-	ADM501	-	-	Contig	4,899,578	-	31	370,883	5	-	-	-	-	-
Citrobacter freundii GTC 09629	Unknown ST, minor mismatch ^c	SAMN02469849	Whole genome assembly	GCA_00038155.1	GF_00038155.1	-	-	AQUE1	-	-	Contig	5,053,892	-	79	240,358	8	-	-	-	-	-
Citrobacter freundii NBRC 12681	Unknown ST, minor mismatch ^c	SAMN0018684	ASM75973v1	GCA_00075973.1	GF_00075973.1	-	-	BBM01	-	-	Contig	4,920,734	-	48	288,133	7	-	-	-	-	-
Citrobacter freundii RL51	Unknown ST, minor mismatch ^c	SAMN02051916	Citrobacter assembly	GCA_00052816.1	GF_00052816.1	-	-	JKT01	-	-	Contig	4,937,688	-	88	158,049	9	-	-	-	-	-
Citrobacter ordellium KC168	Unknown ST, minor mismatch ^c	SAMN0222524	ASM7270v1	GCA_0002270.1	GF_0002270.1	FN64302.1	NC_013716.1	-	-	-	Complete genome, chromosome	5,346,659	-	-	-	-	-	-	-	-	-
Citrobacter sedlakii NBRC 10572Z	NA	SAMN0018685	ASM75983v1	GCA_00075983.1	GF_00075983.1	-	-	BBM01	-	-	Contig	4,631,466	-	30	290,667	5	-	-	-	-	-
Citrobacter werkmanii NBRC 10572J	NA	SAMN0018685	ASM75975v1	GCA_00075975.1	GF_00075975.1	-	-	BBM01	-	-	Contig	4,947,997	-	30	427,597	5	-	-	-	-	-
Citrobacter youngae ATCC 29220	NA	SAMN02415922	ASM15597v1	GCA_00015597.1	GF_00015597.1	-	-	ABWL02	-	-	Scaffold	5,154,159	5,150,259	49	497,106	4	10	2,724,488	1	39	0
Enterobacteriaceae complex																					
Enterobacter cloacae subsp. cloacae ATCC 13047 ^b	ST1	SAMN02003901	ASM2556v1	GCA_0002556.1	GF_0002556.1	CP001918.1	NC_014121.1	-	-	-	Complete genome, chromosome	5,314,581	-	-	-	-	-	-	-	-	-
Enterobacter cloacae 34399	ST114	SAMN03067418	ASM81422v1	GCA_00081422.1	GF_00081422.1	CP010384.1	NZ_CP010384.1	-	-	-	Complete genome, chromosome	4,784,288	-	-	-	-	-	-	-	-	-
Enterobacter cloacae 34977	ST254	SAMN03067414	ASM81412v1	GCA_00081412.1	GF_00081412.1	CP010376.1	NZ_CP010376.1	-	-	-	Complete genome, chromosome	5,150,493	-	-	-	-	-	-	-	-	-
Enterobacter cloacae 35083	ST259	SAMN03067416	ASM81420v1	GCA_00081420.1	GF_00081420.1	CP010371.1	NZ_CP010371.1	-	-	-	Complete genome, chromosome	4,932,974	-	-	-	-	-	-	-	-	-
Enterobacter cloacae ECNH2	ST3	SAMN0211382	ASM72450v1	GCA_00072450.1	GF_00072450.1	CP008823.1	NZ_CP008823.1	-	-	-	Complete genome, chromosome	4,852,800	-	-	-	-	-	-	-	-	-
Enterobacter cloacae ECNH43	ST97	SAMN0211383	ASM73022v1	GCA_00073022.1	GF_00073022.1	CP008897.1	NZ_CP008897.1	-	-	-	Complete genome, chromosome	4,633,407	-	-	-	-	-	-	-	-	-
Enterobacter cloacae ECNH4	ST191	SAMN0281150	ASM78486v1	GCA_00078486.1	GF_00078486.1	CP009850.1	NZ_CP009850.1	-	-	-	Complete genome, chromosome	4,761,385	-	-	-	-	-	-	-	-	-
Enterobacter cloacae ECR901	ST97	SAMN0211384	ASM73027v1	GCA_00073027.1	GF_00073027.1	CP008905.1	NZ_CP008905.1	-	-	-	Complete genome, chromosome	4,621,385	-	-	-	-	-	-	-	-	-
Enterobacter cloacae ECRW51	ST2	SAMN0204307	ASM23997v1	GCA_00023997.1	GF_00023997.1	CP02886.1	NC_016814.1	-	-	-	Complete genome, chromosome	4,734,438	-	-	-	-	-	-	-	-	-
Enterobacter cloacae GGT036	ST432	SAMN03005138	ASM77015v1	GCA_00077015.1	GF_00077015.1	CP009756.1	NZ_CP009756.1	-	-	-	Complete genome, chromosome	4,848,754	-	-	-	-	-	-	-	-	-
Enterobacter cloacae subsp. cloacae ENKHU01	ST3	SAMN02003909	ASM2627v1	GCA_0002627.1	GF_0002627.1	CP00377.1	NC_018406.1	-	-	-	Complete genome, chromosome	4,726,562	-	-	-	-	-	-	-	-	-
Enterobacter cloacae subsp. dissolvens SDM1	ST736	SAMN02003921	ASM2376v3	GCA_0002376.3	GF_0002376.3	CP003678.1	NC_019879.1	-	-	-	Complete genome, chromosome	4,968,248	-	-	-	-	-	-	-	-	-
Escherichia spp.																					
Escherichia coli D42 ^b	ST114	SAMN0222727	ASM2712v1	GCA_0002712.1	GF_0002712.1	FN65476.1	NC_017826.1	-	-	-	Complete genome, chromosome	5,241,977	-	-	-	-	-	-	-	-	-
Escherichia coli 536	ST127	SAMN02604181	ASM1330v1	GCA_0001330.1	GF_0001330.1	CP00047.1	NC_008923.1	-	-	-	Complete genome, chromosome	4,938,520	-	-	-	-	-	-	-	-	-
Escherichia coli 568	ST678	SAMN0313829	ASM2624v1	GCA_0002624.1	GF_0002624.1	CU82145.2	NC_011748.1	-	-	-	Complete genome, chromosome	5,154,862	-	-	-	-	-	-	-	-	-
Escherichia coli ABU 83972	ST73	SAMN02003928	ASM14836v1	GCA_00014836.1	GF_00014836.1	CP001671.1	NC_017831.1	-	-	-	Complete genome, chromosome	5,131,397	-	-	-	-	-	-	-	-	-
Escherichia coli AFEC 01	ST95	SAMN02003424	ASM1484v1	GCA_0001484.1	GF_0001484.1	CP00468.1	NC_008963.1	-	-	-	Complete genome, chromosome	5,082,025	-	-	-	-	-	-	-	-	-
Escherichia coli AFEC 078	ST23	SAMN02003426	ASM33275v1	GCA_00033275.1	GF_00033275.1	CP004009.1	NC_020163.1	-	-	-	Complete genome, chromosome	4,798,435	-	-	-	-	-	-	-	-	-
Escherichia coli ATCC 8739	ST3021	SAMN02598405	ASM1938v1	GCA_0001938.1	GF_0001938.1	CP00046.1	NC_010468.1	-	-	-	Complete genome, chromosome	4,746,218	-	-	-	-	-	-	-	-	-
Escherichia coli B REL-006	ST93	SAMN02003921	ASM11798v1	GCA_00011798.1	GF_00011798.1	CP000819.1	NC_012967.1	-	-	-	Complete genome, chromosome	4,629,812	-	-	-	-	-	-	-	-	-
Escherichia coli RL21(D)C3	ST93	SAMN0222558	ASM959v1	GCA_0002258.1	GF_0002258.1	ABM4691.2	NC_012832.2	-	-	-	Complete genome, chromosome	4,556,947	-	-	-	-	-	-	-	-	-
Escherichia coli RL21(D)E3	ST93	SAMN02003478	ASM2269v1	GCA_0002269.1	GF_0002269.1	CP01509.3	NC_012971.2	-	-	-	Complete genome, chromosome	4,565,953	-	-	-	-	-	-	-	-	-
Escherichia coli BW2562	ST10	SAMN02003900	ASM2324v1	GCA_0002324.1	GF_0002324.1	CP001386.1	NC_012799.1	-	-	-	Complete genome, chromosome	4,578,159	-	-	-	-	-	-	-	-	-
Escherichia coli CF1073	ST73	SAMN02004094	ASM744v1	GCA_0000744.1	GF_0000744.1	AE014075.1	NC_004431.1	-	-	-	Complete genome, chromosome	5,231,428	-	-	-	-	-	-	-	-	-
Escherichia coli DH1	ST1060	SAMN02598470	ASM2363v1	GCA_0002363.1	GF_0002363.1	CP001637.1	NC_017825.1	-	-	-	Complete genome, chromosome	4,630,707	-	-	-	-	-	-	-	-	-
Escherichia coli DH1	ST1060	-	ASM27010v1	GCA_00027010.1	GF_00027010.1	AP012030.1	NC_017838.1	-	-	-	Complete genome, chromosome	4,621,340	-	-	-	-	-	-	-	-	-
Escherichia coli E2437A	ST1132	SAMN02004038	ASM1774v1	GCA_0001774.1	GF_0001774.1	CP008000.1	NC_009801.1	-	-	-	Complete genome, chromosome	4,979,619	-	-	-	-	-	-	-	-	-
Escherichia coli ED1a	ST452	SAMN0313823	ASM2620v1	GCA_0002620.1	GF_0002620.1	CU82162.2	NC_011745.1	-	-	-	Complete genome, chromosome	5,209,948	-	-	-	-	-	-	-	-	-
Escherichia coli ET11 H10407	ST48	SAMN0222727	ASM27047v1	GCA_00027047.1	GF_00027047.1	FN64944.1	NC_017833.1	-	-	-	Complete genome, chromosome	5,153,435	-	-	-	-	-	-	-	-	-
Escherichia coli H5	ST46	SAMN02003927	ASM1676v1	GCA_0001676.1	GF_0001676.1	CP008002.1	NC_009803.1	-	-	-	Complete genome, chromosome	4,643,638	-	-	-	-	-	-	-	-	-
Escherichia coli IA1	ST1128	SAMN0313820	ASM2626v1	GCA_0002626.1	GF_0002626.1	CU82160.2	NC_011741.1	-	-	-	Complete genome, chromosome	4,700,560	-	-	-	-	-	-	-	-	-
Klebsiella oxytoca																					
Klebsiella oxytoca KCTC 1680 ^b	ST28	SAMN02003930	ASM24032v1	GCA_00024032.1	GF_00024032.1	CP003218.1	NC_016812.2	-	-	-	Complete genome, chromosome	5,974,109	-	-	-	-	-	-	-	-	-
Klebsiella oxytoca 10-5248	ST53	SAMN02463997	PE_Kho_oxyl_10-5248_V1	GCA_00026958.1	GF_00026958.1	-	-	AKCF01	-	-	Contig	6,029,795	-	4	5,848,092	1	-	-	-	-	-
Klebsiella oxytoca 11492-1	ST36	SAMN02471877	K011492-1_1.0	GCA_00025915.1	GF_00025915.1	-	-	AIEM01	-	-	Contig	6,176,536	-	213	106,308	20	-	-	-	-	-
Klebsiella oxytoca E718	ST27	SAMN02003942	ASM27670v2	GCA_00027670.2	GF_00027670.2	CP003883.1	NC_018106.1	-	-	-	Complete genome, chromosome	6,097,032	-	-	-	-	-	-	-	-	-
Klebsiella oxytoca FDMARGOS_86	Unknown ST, minor mismatch ^c	SAMN02003945	ASM7389v1	GCA_0007389.1	GF_0007389.1	-	-	JTB01	-	-	Contig	6,477,598	-	5	6,071,363	1	-	-	-	-	-
Klebsiella oxytoca H19	ST62	SAMN0222646	ASM2450v1	GCA_0002450.1	GF_0002450.1	-	-	ARM01	-	-	Contig	5,860,821	-	88	192,319	10	-	-	-	-	-
Klebsiella oxytoca HKCP_L1	ST11	SAMN02081440	ASM36324																		

TABLE S3. Overview of target genes included in species-specific wgMLST- and cgMLST typing schemes^a

Microorganism	Name	Reference genome		Typing schemes							
		Target genes	Bases	Target genes included		Target genes excluded ^b		Bases included		Date created	SeqSphere+ version
				Core genome	Accessory genome	Whole genome	Core genome	Accessory genome	Whole genome		
<i>Citrobacter</i> spp.	<i>Citrobacter koseri</i> ATCC BAA-395	4,978	4,720,462	182	4,736	4,918	133,300	4,121,455	4,254,795	2015.02.09	2.3.0
<i>Enterobacter cloacae</i> complex	<i>Enterobacter cloacae</i> subsp. <i>cloacae</i> ATCC 13047	5,120	5,314,581	693	4,260	4,953	628,107	3,922,212	4,550,319	2015.03.10	2.3.0
<i>Escherichia coli</i>	<i>Escherichia coli</i> O42	4,793	5,241,977	2,764	1,785	4,549	2,735,270	1,615,200	4,350,470	2014.07.04	2.1.0
<i>Klebsiella oxydoxa</i>	<i>Klebsiella oxydoxa</i> KCTC 1686	5,340	5,974,109	3,068	2,200	5,268	3,099,178	2,016,620	5,115,798	2015.04.08	2.3.1
<i>Klebsiella pneumoniae</i>	<i>Klebsiella pneumoniae</i> NTUH-K2044	4,992	5,246,520	2,294	2,641	4,925	2,163,674	2,465,615	4,692,289	2014.07.18	2.1.0

cgMLST = core genome multilocus sequence typing; wgMLST = whole genome multilocus sequence typing

a. cgMLST schemes included only the core genome targets; wgMLST schemes included all whole genome targets

b. Based on reference genome filters

TABLE S4. Summary of assembly characteristics of 1,827 ESBL-E isolates.^a

Parameter	Mean	Median	Minimum	Maximum
Reads				
Number, <i>n</i>	2,500,805	2,451,808	530,780	9,760,870
Number matched, <i>n</i>	2,212,150	2,203,775	519,703	7,884,490
Number non-matched, <i>n</i>	288,655	83,092	7,385	1,876,380
Percentage reads used, %	90.8%	96.2%	61.5%	99.2%
Mean length (base count), <i>n</i>	142	149	92	243
Mean length matched (base count), <i>n</i>	144	152	93	247
Mean length non-matched (base count), <i>n</i>	86	92	11	180
Total base count, <i>n</i>	325,313,458	307,929,108	94,871,782	1,073,062,634
Total base count matched, <i>n</i>	298,988,597	271,970,730	94,013,404	1,061,919,732
Total base count non-matched, <i>n</i>	26,324,861	5,039,174	661,973	177,356,775
Scaffolds				
Number, <i>n</i>	125	115	23	644
Mean length (mean base count), <i>n</i>	48,892	44,631	8,763	200,940
N50 (base count), <i>n</i>	163,804	147,658	16,990	997,471
Minimum length (base count), <i>n</i>	530	513	500	933
Maximum length (base count), <i>n</i>	433,762	388,849	76,938	2,146,409
Consensus base count, <i>n</i>	5,160,832	5,135,666	3,746,759	6,657,910
Coverage				
Coverage (mean depth), <i>n</i>	63	60	20	224
Coverage matched, <i>n</i>	58	53	19	221
Breadth-of-coverage (% of expected size), %				
Minimum reference genome size ^b	111%	111%	98%	125%
Maximum reference genome size ^b	97%	97%	87%	113%

ESBL-E = extended-spectrum beta-lactamase-producing *Enterobacteriaceae*; N50 = largest scaffold length *N*, such that 50% of the assembled genome size is contained in scaffolds with a length of at least *N*; wgMLST = whole genome multilocus sequence typing

a. Including *n*=8 isolates that were sequenced in duplicate.

b. Species-specific minimum and maximum reference genome sizes were based on the assembled genomes used to create species-specific wgMLST schemes (see Table S2).

TABLE S5. Presence of core genome, accessory genome and whole genome target genes for 1,798 ESBL-E isolates.

	Core genome targets		Accessory genome targets		Whole genome targets	
	n	%	n	%	n	%
<u><i>Citrobacter</i> spp. (n = 41)</u>						
Mean	178	97.9	264	5.6	442	9.0
Median	179	98.4	164	3.5	342	7.0
Minimum	169	92.9	153	3.2	326	6.6
Maximum	180	98.9	4,284	90.5	4,463	90.8
<u><i>Enterobacter cloacae</i> complex (n = 121)</u>						
Mean	679	98.0	450	10.6	1,129	22.8
Median	681	98.3	406	9.5	1,088	22.0
Minimum	651	93.9	337	7.9	1,008	20.4
Maximum	689	99.4	890	20.9	1,567	31.6
<u><i>Escherichia coli</i> (n = 1,351)</u>						
Mean	2,728	98.7	856	48.0	3,584	78.8
Median	2,733	98.9	817	45.8	3,547	78.0
Minimum	2,504	90.6	646	36.2	3,321	73.0
Maximum	2,755	99.7	1,232	69.0	3,970	87.3
<u><i>Klebsiella oxytoca</i> (n = 18)</u>						
Mean	3,020	98.4	1,409	64.0	4,429	84.1
Median	3,023	98.5	1,516	68.9	4,535	86.1
Minimum	2,963	96.6	513	23.3	3,539	67.2
Maximum	3,059	99.7	1,874	85.2	4,916	93.3
<u><i>Klebsiella pneumoniae</i> (n = 267)</u>						
Mean	2,259	98.9	2,134	80.8	4,393	89.2
Median	2,265	99.2	2,165	82.0	4,430	89.9
Minimum	2,139	93.7	1,588	60.1	3,837	77.9
Maximum	2,282	99.9	2,285	86.5	4,551	92.4

ESBL-E = extended-spectrum beta-lactamase-producing *Enterobacteriaceae*

TABLE S6. Summary statistics of the distributions of genetic distance for 950,275 pairwise comparisons of ESBL-E isolates: core genome, accessory genome and whole genome

	Pairwise comparisons	Number of alleles compared			Number of different alleles			Proportion of different alleles (= genetic distance)	
		n	Median	Range	Median	Range	Median	Range	
<u>Core genome</u>									
<i>Citrobacter</i> spp.	820	177	[164 - 180]	109	[0 - 177]	0.609 ^{a,d}	[0.000 - 0.994]		
<i>Enterobacter cloacae</i> complex	7,260	674	[629 - 688]	598	[0 - 672]	0.892 ^{a,d}	[0.000 - 0.987]		
<i>Escherichia coli</i>	906,531	2,705	[2,325 - 2,755]	2,593	[0 - 2,684]	0.964 ^{a,d}	[0.000 - 0.985]		
<i>Klebsiella oxytoca</i>	153	2,984	[2,899 - 3,044]	2,893	[2 - 3,004]	0.965 ^{a,d}	[0.001 - 0.996]		
<i>Klebsiella pneumoniae</i>	35,511	2,245	[2,027 - 2,281]	1,895	[0 - 2,232]	0.844 ^{a,d}	[0.000 - 0.998]		
<u>Accessory genome</u>									
<i>Citrobacter</i> spp.	820	146	[74 - 173]	106	[0 - 171]	0.748 ^{b,d}	[0.000 - 1.000]		
<i>Enterobacter cloacae</i> complex	7,260	311	[220 - 886]	277	[0 - 687]	0.943 ^{b,d}	[0.000 - 1.000]		
<i>Escherichia coli</i>	906,531	660	[432 - 1,206]	594	[0 - 922]	0.969 ^{b,d}	[0.000 - 0.998]		
<i>Klebsiella oxytoca</i>	153	1,387	[344 - 1,800]	1,062	[0 - 1,604]	0.995 ^{b,d}	[0.000 - 1.000]		
<i>Klebsiella pneumoniae</i>	35,511	2,044	[1,335 - 2,244]	1,820	[0 - 1,962]	0.899 ^{b,d}	[0.000 - 0.997]		
<u>Whole genome</u>									
<i>Citrobacter</i> spp.	820	325	[246 - 348]	215	[0 - 343]	0.659 ^c	[0.000 - 0.997]		
<i>Enterobacter cloacae</i> complex	7,260	984	[872 - 1,561]	884	[0 - 1,314]	0.911 ^c	[0.000 - 0.989]		
<i>Escherichia coli</i>	906,531	3,359	[2,922 - 3,938]	3,175	[0 - 3,538]	0.966 ^c	[0.000 - 0.986]		
<i>Klebsiella oxytoca</i>	153	4,341	[3,276 - 4,813]	3,905	[2 - 4,399]	0.974 ^c	[0.000 - 0.996]		
<i>Klebsiella pneumoniae</i>	35,511	4,288	[3,489 - 4,520]	3,727	[0 - 3,938]	0.870 ^c	[0.000 - 0.997]		

ESBL-E = extended-spectrum beta-lactamase-producing *Enterobacteriaceae*

- a. Difference in median genetic distance between species, core genome: Kruskal-Wallis Chi-square: 22,685; p<0.0005
b. Difference in median genetic distance between species, accessory genome: Kruskal-Wallis Chi-square: 15,980; p<0.0005
c. Difference in median genetic distance between species, whole genome: Kruskal-Wallis Chi-square: 20,867; p<0.0005
d. Difference in median genetic distance between core and accessory genome: Sign test p<0.0005

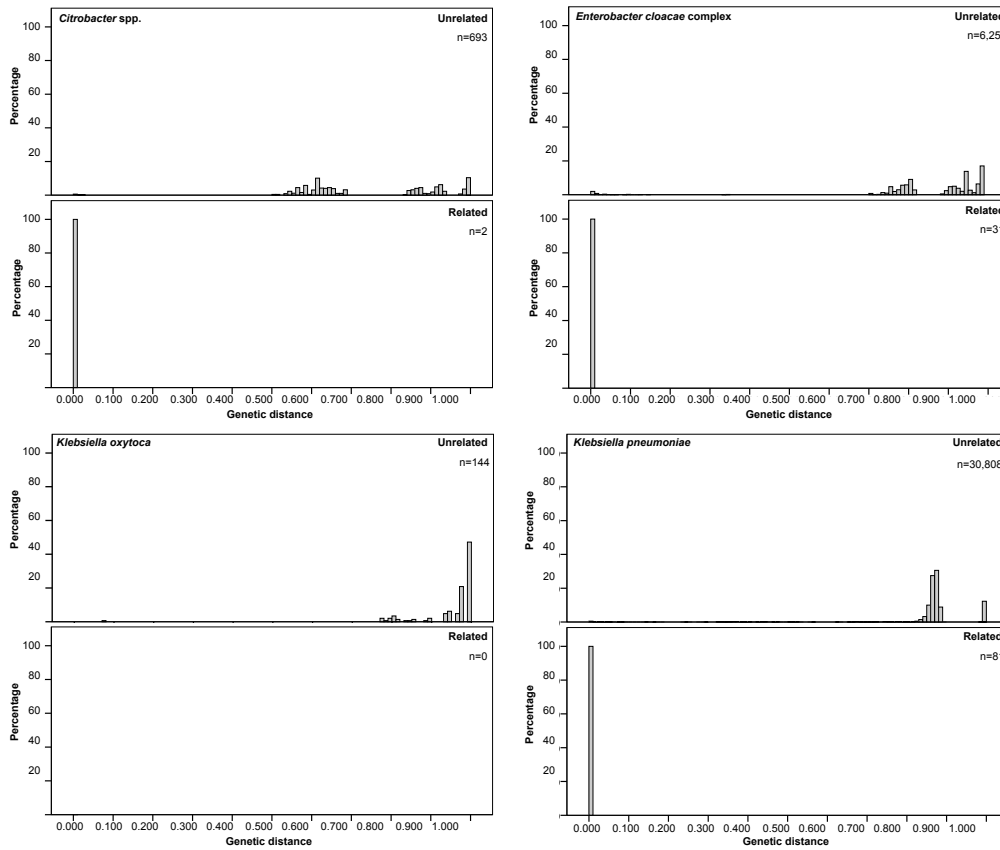


FIGURE S1. Distribution of whole genome multilocus sequence typing (wgMLST)-based genetic distance for pairwise comparisons of epidemiologically related and unrelated extended-spectrum beta-lactamase (ESBL)-producing *Citrobacter* spp., *Enterobacter cloacae* complex, *Klebsiella oxytoca*, and *Klebsiella pneumoniae* isolates. Epidemiologically related isolates were defined as being obtained from the same patient, belonging to the same sequence type (ST), and cultured within a time window of 30 days. Epidemiologically unrelated isolates were defined as being obtained from patients without a known epidemiological link. The strain collection did not include a pair of epidemiologically related ESBL-producing *Klebsiella oxytoca* isolates.