Rapid Nanopore Sequencing of Plasmids and Resistance Gene Detection in Clinical Isolates

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Supplementary Material

Table S1: Resistance Gene Annotation in KPNIH1 assemblies

		Assembly:			
Plasmid	**Accession Number**	**Reference Sequence (% Identity)**	**Draft MinION (% Identity)**	**Polished MinION (% Identity)**	**Polished MinION+ MiSeq (% Identity)**
pKPN-498	NZ_CP008829	*aadA2* (100)	+ (99.6)	+ (99.1)	+ (99.4)
		aph(3')-Ia (100)	+ (99.4)	+ (99.5)	+ (100)
		mph(A) (100)	+ (99.2)	+ (98.9)	+ (99.6)
		catA1 (99.9)	+ (99.4)	+ (98.5)	+ (99.9)
		sul1 (100)	+ (99.8)	+ (99.7)	+ (100)
		dfrA12 (100)	+ (99.4)	+ (99.4)	+ (100)
pKpQIL-6e6	NZ_CP008830	*blaKPC-3* (100)	+(99.7)	+(99.3)	+(99.9)
		blaOXA-9 (99.9)	+ (99.3)	+ (99.1)	+ (99.5)
		blaTEM-1A (99.9)	+ (99.5)	+ (99.5)	+ (99.7)
pAAC154-a50	NZ_CP008828	*aac(6')-Ib* (100)	+ (99.7)	+ (99.7)	+ (99.8)
		aac(6')Ib-cr (99.4)	+ (99.0)	+ (99.0)	+ (99.2)

Draft and polished MinION assemblies generated from MinION reads only with Canu, and Canu and Racon, respectively. Polished MinION + MiSeq assembly is a MinION assembly polished with MiSeq reads using Pilon.

Table S2: Resistance Gene Annotation in ECESBL-1 Assemblies

Contig Name	**Resistance Gene**	**Draft MinION Assembly (% Identity)**	**Finished MinION + MiSeq Assembly (% Identity)**	**SPAdes MiSeq Assembly (% Identity)**
Contig 8	*strA*	+ (99.3)	+ (100)	+ (100)
	strB	+ (99.3)	+ (100)	+ (100)
	aadA5	+ (99.2)	+ (100)	+ (100)
	aac(3)-IId	+ (99.3)	+ (99.9)	+ (99.9)
	bla_{TEM-1B}	+ (99.7)	+ (100)	+ (100)
	mph(A)	+ (98.3)	+ (100)	+ (100)
	erm(B)	+ (99.7)	+ (99.9)	-
	sul1	+ (99.7)	+ (100)	+ (100)
	sul2	+ (99.3)	+ (100)	+ (100)
	tet(B)	+ (99.6)	+ (100)	+ (100)
	dfrA17	-	+ (100)	+ (100)
Contig 91	bla_{CMY-42}	+ (99.0)	+ (100)	+ (100)

Draft MinION assembly was generated from MinION reads using canu. Finished assemblies were generated from MinION reads and polished with MiSeq reads. SPAdes assemblies were generated from whole-genome shotgun MiSeq reads only.

Table S3: Resistance Gene Annotation in KPESBL-1 Assemblies

Contig Name	Resistance Gene	Draft MinION Assembly (% Identity)	Finished MinION + MiSeq Assembly (% Identity)	SPAdes MiSeq Assembly (% Identity)
Contig 8	*bla*$_{SHV}$	+ (99.0)	+ (100)	+ (100)
Contig 14	*aadA1*	aadA24 (92.8)	+ (100)	+ (100)
	aadA2	+ (99.1)	+ (100)	+ (100)
	aac(3)-IVa	+ (98.4)	+ (99.9)	+ (99.9)
	aph(4)-Ia	+ (99.8)	+ (100)	+ (100)
	aac(6')-1b	+ (99.3)	+ (100)	+ (100)
	aac(6')-1b	+ (98.8)	+ (99.0)	-
	aac(6')1b-cr	+ (98.8)	+ (99.4)	+ (99.4)
	aac(6')1b-cr	+ (98.2)	+ (98.3)	-
	cmlA1	+ (99.1)	+ (99.9)	+ (99.9)
	sul3	+ (98.5)	+ (100)	+ (100)
Contig 17	*aadA2*	+ (98.5)	+ (100)	-
	mph(A)	+ (99.5)	+ (100)	+ (100)
	catA1	+ (98.2)	+ (99.9)	+ (99.9)
	sul1	+ (98.4)	+ (100)	+ (100)
	dfrA12	+ (98.8)	+ (100)	-

Draft MinION assembly was generated from MinION reads using Canu. Finished assemblies were generated from MinION reads and polished with MiSeq reads. SPAdes assemblies were generated from whole-genome shotgun MiSeq reads only.

Table S4. Individual plasmid coverage by MinION assemblies from reads subsest.

Isolate	Plasmid	Length (bp)	200	500	1000	2000	5000
KPNIH1	pKPN-498	243824	0.0%	14.1%	87.6%	99.9%	99.9%
KPNIH1	pKpQIL-6e6	113639	63.8%	99.1%	100.0%	100.0%	100.0%
KPNIH1	pAAC154-a50	15096	0.0%	0.0%	100.0%	100.0%	100.0%
ECESBL-1	ctg_8	110096	90.3%	100.0%	100.0%	100.0%	100.0%
ECESBL-1	ctg_91	48584	24.9%	97.7%	100.0%	100.0%	100.0%
ECESBL-1	ctg_94	6648	0.0%	0.0%	0.0%	0.0%	100.0%
ECESBL-1	ctg_41	3174	0.0%	0.0%	0.0%	100.0%	0.0%
ECESBL-1	ctg_83	2101	0.0%	0.0%	0.0%	66.2%	0.0%
KPESBL-1	ctg_17	207553	0.0%	0.0%	0.0%	0.2%	100.0%
KPESBL-1	ctg_14	47948	100.0%	100.0%	100.0%	100.0%	100.0%
KPESBL-1	ctg_8	43380	100.0%	100.0%	100.0%	100.0%	100.0%

Figure S1. Heatmap representation of plasmid coverage.

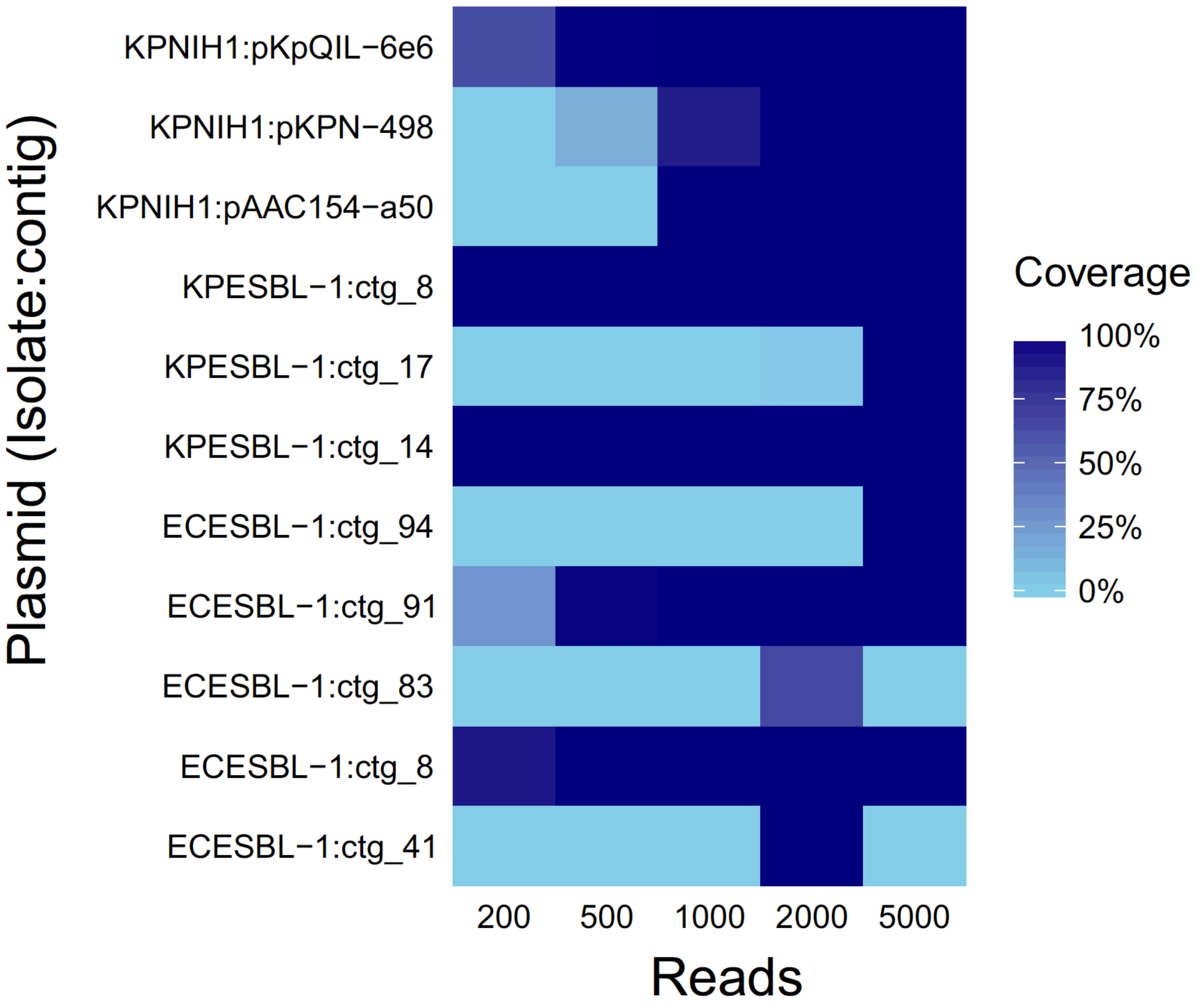

Figure S1: Proportion of reference covered by draft assembly is represented for all plasmids for random subsets of 200, 500, 1000, 2000, and 5000 reads.