

Figure S2. Long-read MinION results: read length distribution and other statistics

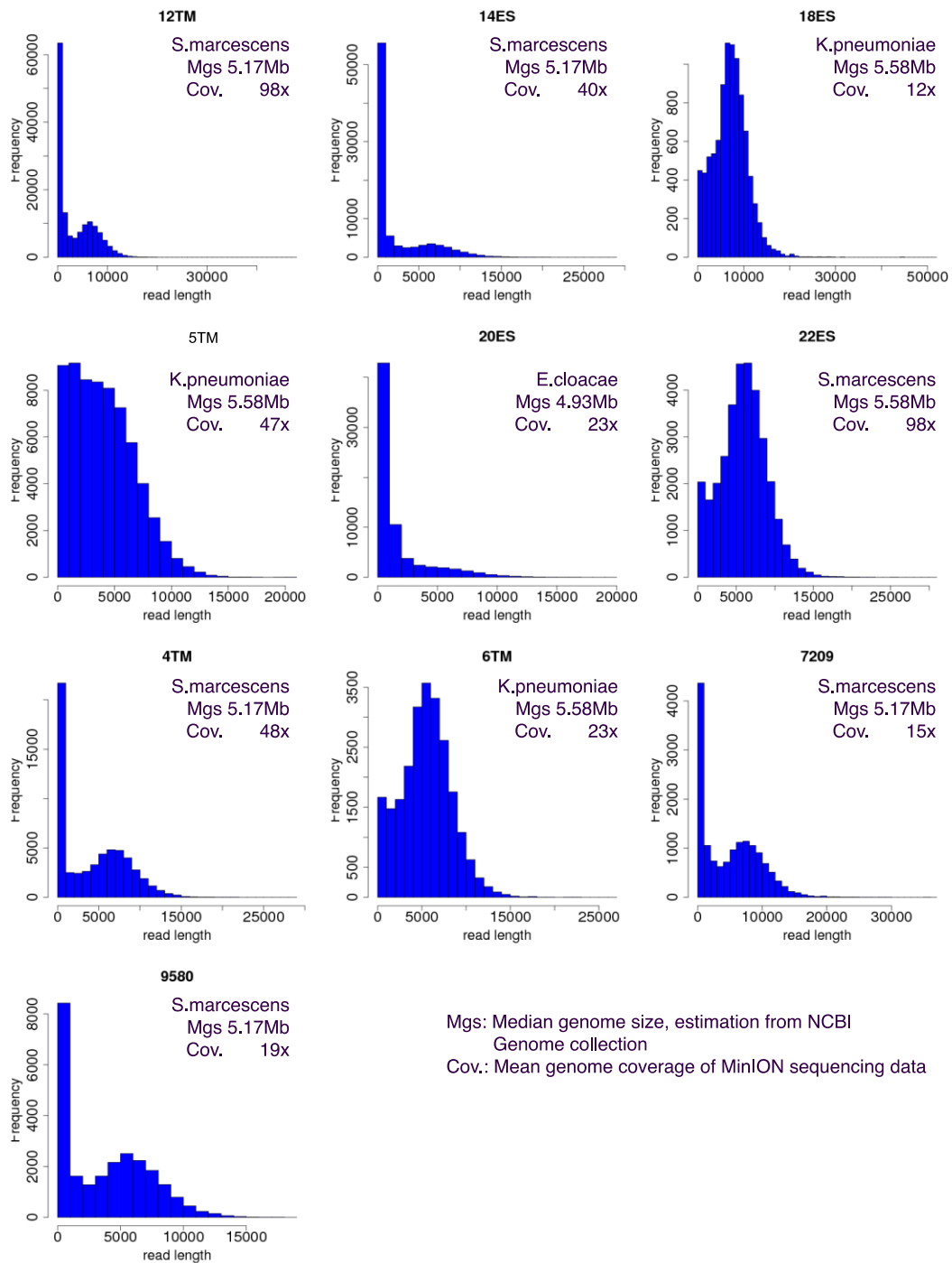


Table S2. Summary of MinION sequencing assemblies (n=10 isolates)

Sample	Species/ST	Coverage	Assembly size (bp)	# contigs	Mean contig size (bp)	Max contig size (bp)	Min contig size (bp)	NDM-1 contig information			
								NDM-1 contig	Length (bp)	Circularised	Overlapping size
7209	<i>S. marcescens</i>	15	5638452	14	402747	1662736	11772	tig00000046	93134	yes	5541
9580	<i>S. marcescens</i>	19	5643686	13	434130	1179329	57857	tig00000056	115471	yes	9857
12TM	<i>S. marcescens</i>	98	5509644	3	1836548	5285959	94286	tig00000069	129399	yes	10353
14ES	<i>S. marcescens</i>	40	5331861	6	888644	3599641	6400	NA (<i>bla</i> _{NDM} - negative)	NA	NA	NA
18ES	<i>K. pneumoniae</i> ST307	12	5714026	10	571403	1478046	112277	tig00000042	118336	yes	7904
5TM	<i>K. pneumoniae</i>	47	6016823	11	546984	3036277	7956	tig00000073	130514	yes	10108

	New ST										
20ES	<i>E. cloacae</i> ST254	23	5617583	19	295662	3105465	5075	tig00000068	120312	yes	9546
22ES	<i>E. cloacae</i> ST90	98	5346364	13	411259	2478567	4970	tig00000109	111157	yes	10764
4TM	<i>S. marcescens</i>	48	5522902	5	1104580	4325511	16158	tig00000109	130921	yes	11874
6TM	<i>K. pneumoniae</i> New ST	23	6015958	13	462766	2460992	6608	tig00000045	128459	yes	8381