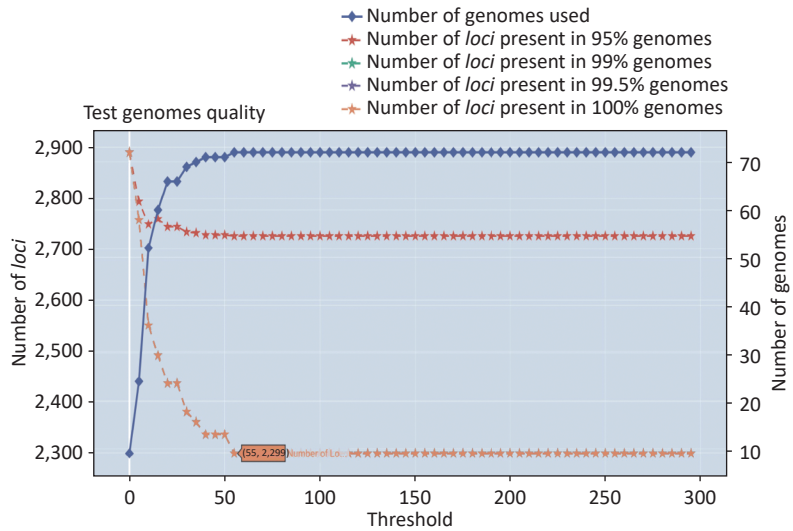
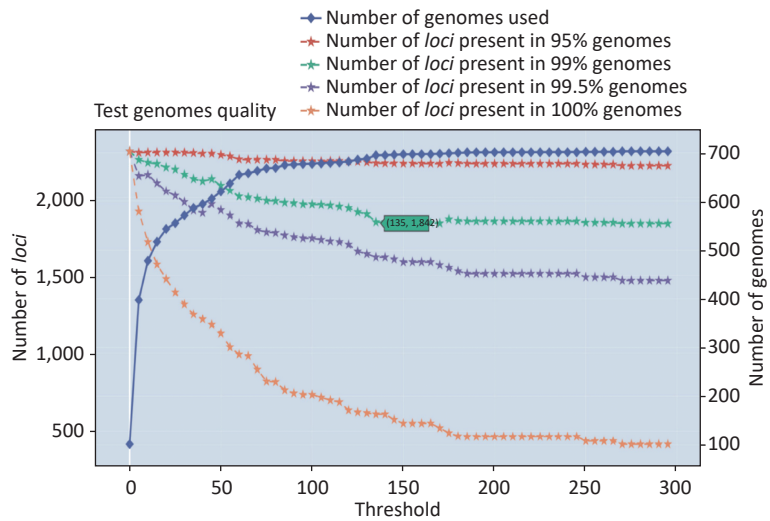
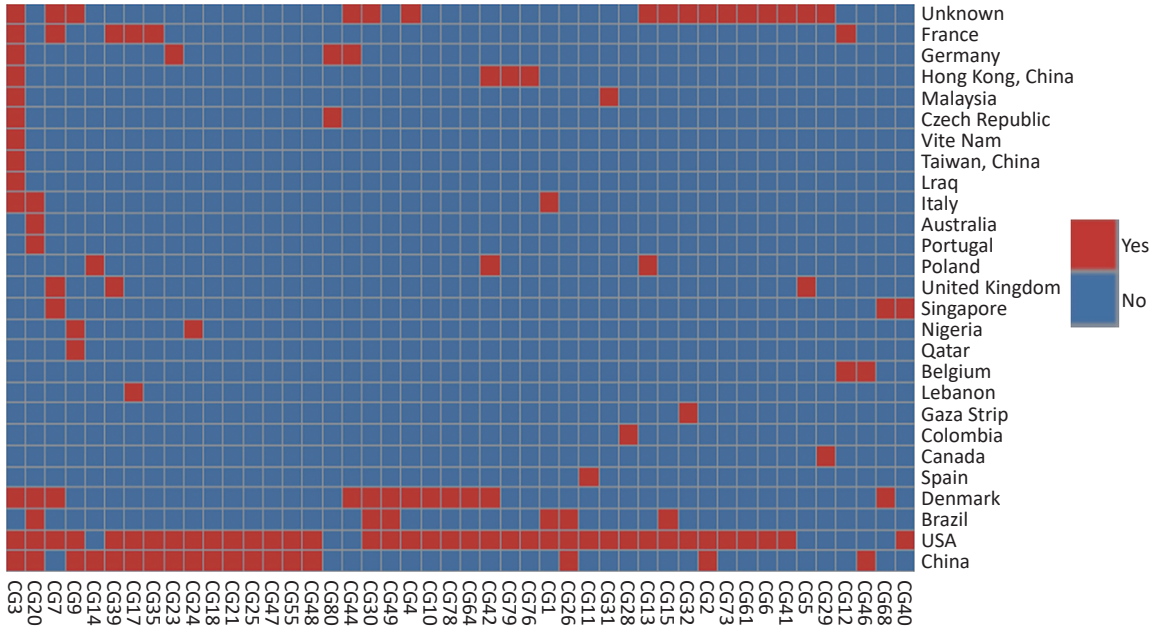


Supplementary Figure S1. Number of *loci* and number of strains at every exclusion threshold level for the 72 complete genomes that were used to create the cgMLST scheme.



Supplementary Figure S2. Number of *loci* and number of genomes at every exclusion threshold level for the 635 validation strains' genomes and 72 completed genomes that were used to construct the cgMLST scheme.



Supplementary Figure S3. Heatmap of 46 shared CGs in 26 countries or regions.

Supplementary Table S1. GenBank assembly accession of all *P. mirabilis* genomes removed during the establishment of the core genome Multilocus Sequence Typing (cgMLST) scheme

GenBank assembly accession	Reason for rejection
GCA_013344565.1	Poor assembly quality
GCA_001640165.1	Poor assembly quality
GCA_007004575.1	Poor assembly quality
GCA_019891935.1	Poor assembly quality
GCA_017146175.1	Poor assembly quality
GCA_017145995.1	Poor assembly quality
GCA_015889025.1	Poor assembly quality
GCA_015889005.1	Poor assembly quality
GCA_015888905.1	Poor assembly quality
GCA_900455245.1	Poor assembly quality
GCA_004570065.1	Poor assembly quality
GCA_017696325.1	Poor assembly quality
GCA_016073115.1	Poor assembly quality
GCA_015936865.1	Poor assembly quality
GCA_016074395.1	Poor assembly quality
GCA_016073395.1	Poor assembly quality
GCA_016073255.1	Poor assembly quality
GCA_016073075.1	Poor assembly quality
GCA_016073035.1	Poor assembly quality
GCA_016072795.1	Poor assembly quality
GCA_016072735.1	Poor assembly quality
GCA_016072675.1	Poor assembly quality
GCA_016072595.1	Poor assembly quality
GCA_015944595.1	Poor assembly quality
GCA_015936705.1	Poor assembly quality
GCA_018160295.1	Poor assembly quality
GCA_018160795.1	Poor assembly quality
GCA_018154235.1	Poor assembly quality
GCA_015936825.1	Poor assembly quality
GCA_018165975.1	Poor assembly quality
GCA_018165955.1	Poor assembly quality
GCA_018155945.1	Poor assembly quality
GCA_015940935.1	Poor assembly quality
GCA_015940825.1	Poor assembly quality
GCA_900455065.1	Poor assembly quality
GCA_018160775.1	Poor assembly quality
GCA_018159425.1	Poor assembly quality
GCA_018158755.1	Poor assembly quality
GCA_015940925.1	Poor assembly quality
GCA_010594645.1	Poor assembly quality
GCA_018087645.1	Poor assembly quality

GCA_017298035.1	Poor assembly quality
GCA_015940885.1	Poor assembly quality
GCA_010591355.1	Poor assembly quality
GCA_001028125.1	Poor assembly quality
GCA_004570665.1	CgMLST scheme validation process removed
GCA_004570195.1	CgMLST scheme validation process removed
GCA_004569205.1	CgMLST scheme validation process removed
GCA_004570055.1	CgMLST scheme validation process removed
GCA_004569255.1	CgMLST scheme validation process removed
GCA_004570115.1	CgMLST scheme validation process removed
GCA_004570105.1	CgMLST scheme validation process removed
GCA_002013325.1	CgMLST scheme validation process removed
GCA_901485075.1	CgMLST scheme validation process removed
GCA_006517445.1	CgMLST scheme validation process removed
GCA_017887605.1	CgMLST scheme validation process removed
GCA_001647515.1	CgMLST scheme validation process removed
GCA_000069965.1	Reference genome

Supplementary Table S2. All relevant information on the 695 *P. mirabilis* strains that were finally included in the analysis

Organism	Assembly	Strain	Assembly level	GenBank assembly accession	RefSeq assembly accession	BioSample	BioProject	Clonal groups (CGs)	Collection date	Geographic location	Host	Isolation source
Proteus mirabilis	MGBC000018		Scaffold	GCA_910574505.1	GCF_910574505.1	SAMEA8801261	PRJEB45232	CG205	2016	United Kingdom	Mus musculus	Stool
Proteus mirabilis	ERR414419-mag-bin.11		Contig	GCA_905204495.1	GCF_905204495.1	SAMEA7847754	PRJEB37358	CG204	Unknown	Spain	Homo sapiens	Gut
Proteus mirabilis	UHGG_MGYG-HGUT-02514		Scaffold	GCA_902387925.1	GCF_902387925.1	SAMEA5852019	PRJEB33885	CG43	Unknown	Sweden	Homo sapiens	Gut
Proteus mirabilis	36374_E01	NCTC4199	Complete Genome	GCA_900635965.1	GCF_900635965.1	SAMEA3222067	PRJEB6403	CG94	1933	United Kingdom	Rhesus macaques	Stool
Proteus mirabilis	40295_E02	NCTC13376	Contig	GCA_900455195.1	GCF_900455195.1	SAMEA3505363	PRJEB6403	CG73	1950/2006	Unknown	Unknown	Unknown
Proteus mirabilis	55884_G01	NCTC12441	Contig	GCA_900455055.1	GCF_900455055.1	SAMEA104200677	PRJEB6403	CG5	Unknown	United Kingdom	Homo sapiens	Cerebral abscess
Proteus mirabilis	58901_A01	NCTC12446	Contig	GCA_900455045.1	GCF_900455045.1	SAMEA104338381	PRJEB6403	CG39	1900/1990	United Kingdom	Unknown	Blood
Proteus mirabilis	52313_G01	NCTC60	Contig	GCA_900455025.1	GCF_900455025.1	SAMEA4552892	PRJEB6403	CG203	1900/1920	Unknown	Homo sapiens	Urine
Proteus mirabilis	52347_B01	NCTC6197	Contig	GCA_900454995.1	GCF_900454995.1	SAMEA4552894	PRJEB6403	CG44	1941	Unknown	Dog	Stool
Proteus mirabilis	IMG-taxon 2623620510 annotated assembly	NLAE-zl-G534	Contig	GCA_900113495.1	GCF_900113495.1	SAMN04487853	PRJEB17332	CG202	Unknown	Unknown	Unknown	Unknown
Proteus mirabilis	IMG-taxon 2654588119 annotated assembly	NLAE-zl-C285	Scaffold	GCA_900101725.1	GCF_900101725.1	SAMN05216484	PRJEB15761	CG201	Unknown	Unknown	Unknown	Unknown
Proteus mirabilis	PDT001114958.1		Contig	GCA_019735095.1	GCF_019735095.1	SAMN20862929	PRJNA288601	CG200	2019	USA	Homo sapiens	Unknown
Proteus mirabilis	PDT001114959.1		Contig	GCA_019724875.1	GCF_019724875.1	SAMN20862928	PRJNA288601	CG3	2019	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM1966082v1	PM58	Contig	GCA_019660825.1	GCF_019660825.1	SAMN20568155	PRJNA752009	CG18	2013	China	Homo sapiens	Urine
Proteus mirabilis	ASM1957223v1	pa1	Contig	GCA_019572235.1	GCF_019572235.1	SAMN20600707	PRJNA752529	CG3	2021	Iraq	Homo sapiens	Others
Proteus mirabilis	PDT000432664.2		Contig	GCA_019569915.1	GCF_019569915.1	SAMN07662963	PRJNA514245	CG199	2013	Germany	Homo sapiens	Skin
Proteus mirabilis	PDT001106425.1	Proteus_mirabilis_2021CK-01254	Contig	GCA_019507065.1	GCF_019507065.1	SAMN20675048	PRJNA288601	CG4	2017	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1944378v1	HNS2p	Complete Genome	GCA_019443785.1	GCF_019443785.1	SAMN14074717	PRJNA605713	CG22	2019	China	Swine	Tissue
Proteus mirabilis	PDT001090222.1	2021GO-0085	Contig	GCA_019258985.1	GCF_019258985.1	SAMN20244396	PRJNA288601	CG84	2021	USA	Homo sapiens	Swab
Proteus mirabilis	PDT001090225.1	2021GO-0082	Contig	GCA_019257545.1	GCF_019257545.1	SAMN20244393	PRJNA288601	CG84	2021	USA	Homo sapiens	Swab
Proteus mirabilis	PDT001086342.1	FSIS12139894	Contig	GCA_019198655.1	GCF_019198655.1	SAMN20152563	PRJNA701285	CG198	2021	USA	Chicken	Unknown
Proteus mirabilis	ASM1919264v1	6Pmi283	Complete Genome	GCA_019192645.1	GCF_019192645.1	SAMN19608370	PRJNA736086	CG28	2018	Colombia	Homo sapiens	Urine
Proteus mirabilis	PDT001078554.1		Contig	GCA_019060055.1	GCF_019060055.1	SAMN19658564	PRJNA514245	CG29	2017	Canada	Homo sapiens	Blood
Proteus mirabilis	ASM1905037v1	xz175	Contig	GCA_019050375.1	GCF_019050375.1	SAMN19797154	PRJNA739673	CG197	2019	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1897202v1	XH1653	Complete Genome	GCA_018972025.1	GCF_018972025.1	SAMN16824307	PRJNA679136	CG26	2015	China	Homo sapiens	Urine
Proteus mirabilis	ASM1896659v1	2021EL-00155	Contig	GCA_018966595.1	GCF_018966595.1	SAMN19672407	PRJNA288601	CG3	2021	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1896654v1	2021EL-00154	Contig	GCA_018966545.1	GCF_018966545.1	SAMN19672406	PRJNA288601	CG3	2021	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1891770v1	N96	Contig	GCA_018917705.1	GCF_018917705.1	SAMN19374036	PRJNA733006	CG83	2019	China	Macaca fascicularis	Stool
Proteus mirabilis	4337PV	4337PV	Contig	GCA_018861165.1	GCF_018861165.1	SAMN18746771	PRJNA722470	CG3	2019	Italy	Homo sapiens	Urine
Proteus mirabilis	ASM1847683v1	2021EL-00141	Contig	GCA_018476835.1	GCF_018476835.1	SAMN19243080	PRJNA288601	CG49	2021	USA	Homo sapiens	Urine
Proteus mirabilis	PDT001044764.1	2021GN-00004	Contig	GCA_018454805.1	GCF_018454805.1	SAMN19296569	PRJNA288601	CG73	2021	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM1844205v1	Survcare143	Scaffold	GCA_018442055.1	GCF_018442055.1	SAMN17372058	PRJNA692829	CG80	2018	Germany	Homo sapiens	Urine
Proteus mirabilis	ASM1844154v1	Survcare178	Scaffold	GCA_018441545.1	GCF_018441545.1	SAMN17372090	PRJNA692829	CG23	2018	Germany	Homo sapiens	Rectum
Proteus mirabilis	ASM1842231v1	Survcare357	Scaffold	GCA_018422315.1	GCF_018422315.1	SAMN17373036	PRJNA692829	CG3	2019	Germany	Homo sapiens	Swab
Proteus mirabilis	ASM1842201v1	Survcare372	Contig	GCA_018422015.1	GCF_018422015.1	SAMN17373050	PRJNA692829	CG3	2019	Germany	Homo sapiens	Blood
Proteus mirabilis	ASM1842165v1	Survcare401	Scaffold	GCA_018421655.1	GCF_018421655.1	SAMN17373069	PRJNA692829	CG3	2019	Germany	Homo sapiens	Rectum
Proteus mirabilis	ASM1837223v1		Contig	GCA_018372235.1	GCF_018372235.1	SAMN17801568	PRJNA698986	CG73	2016/2019	USA	Homo sapiens	Stool
Proteus mirabilis	ASM1837151v1		Contig	GCA_018371515.1	GCF_018371515.1	SAMN17801606	PRJNA698986	CG71	2016/2019	USA	Homo sapiens	Stool
Proteus mirabilis	ASM1833649v1	SNYG35	Complete Genome	GCA_018336495.1	GCF_018336495.1	SAMN13812099	PRJNA600292	CG27	2018	China	Chicken	Animals

Proteus mirabilis	ASM1833447v1	YNDJH6	Contig	GCA_018334475.1	GCF_018334475.1	SAMN18869229	PRJNA693126	CG39	2017	China	Chicken	Unknown
Proteus mirabilis	ASM1833445v1	SCRJC5FQ	Contig	GCA_018334455.1	GCF_018334455.1	SAMN18869232	PRJNA693126	CG3	2017	China	Chicken	Unknown
Proteus mirabilis	ASM1833442v1	SCDJC7FQ	Contig	GCA_018334425.1	GCF_018334425.1	SAMN18869233	PRJNA693126	CG39	2017	China	Chicken	Unknown
Proteus mirabilis	ASM1833441v1	HBSZC16FQ	Contig	GCA_018334415.1	GCF_018334415.1	SAMN18869235	PRJNA693126	CG24	2017	China	Swine	Unknown
Proteus mirabilis	ASM1833439v1	HBSZC14FQ	Contig	GCA_018334395.1	GCF_018334395.1	SAMN18869234	PRJNA693126	CG196	2017	China	Swine	Unknown
Proteus mirabilis	ASM1833437v1	HEDJC8FQ	Contig	GCA_018334375.1	GCF_018334375.1	SAMN18869236	PRJNA693126	CG27	2017	China	Chicken	Unknown
Proteus mirabilis	ASM1833435v1	SCSZC22FQ	Contig	GCA_018334355.1	GCF_018334355.1	SAMN18869227	PRJNA693126	CG11	2015	China	Swine	Unknown
Proteus mirabilis	ASM1833433v1	SCRJC4FQ	Contig	GCA_018334335.1	GCF_018334335.1	SAMN18869231	PRJNA693126	CG17	2017	China	Chicken	Unknown
Proteus mirabilis	ASM1833431v1	SCBCSZ5522	Contig	GCA_018334315.1	GCF_018334315.1	SAMN18869238	PRJNA693126	CG45	2015	China	Swine	Unknown
Proteus mirabilis	ASM1833429v1	HBRJC7FQ	Contig	GCA_018334295.1	GCF_018334295.1	SAMN18869241	PRJNA693126	CG46	2017	China	Chicken	Unknown
Proteus mirabilis	ASM1833425v1	SDDJ15	Contig	GCA_018334255.1	GCF_018334255.1	SAMN18869239	PRJNA693126	CG39	2016	China	Chicken	Unknown
Proteus mirabilis	ASM1833424v1	SCRJC7FQ	Contig	GCA_018334245.1	GCF_018334245.1	SAMN18869240	PRJNA693126	CG83	2017	China	Chicken	Unknown
Proteus mirabilis	ASM1833423v1	SCBCSZ55	Contig	GCA_018334235.1	GCF_018334235.1	SAMN18869237	PRJNA693126	CG45	2015	China	Swine	Unknown
Proteus mirabilis	ASM1833420v1	HEDJ122	Contig	GCA_018334205.1	GCF_018334205.1	SAMN18869228	PRJNA693126	CG17	2017	China	Chicken	Unknown
Proteus mirabilis	ASM1833419v1	SCRJC3FQ	Contig	GCA_018334195.1	GCF_018334195.1	SAMN18869230	PRJNA693126	CG3	2017	China	Chicken	Unknown
Proteus mirabilis	PDT001019331.1	2021GO-0002	Contig	GCA_018287555.1	GCF_018287555.1	SAMN19022495	PRJNA288601	CG48	2021	USA	Homo sapiens	Urine catheter
Proteus mirabilis	PDT001019336.1	2020GO-0201	Contig	GCA_018287495.1	GCF_018287495.1	SAMN19022491	PRJNA288601	CG32	2021	USA	Homo sapiens	Urine
Proteus mirabilis	PDT001012885.1	Proteus mirabilis	Contig	GCA_018184755.1	GCF_018184755.1	SAMEA6656532	PRJNA514245	CG49	2018	Denmark	Homo sapiens	Swab
Proteus mirabilis	PDT001013067.1	Proteus mirabilis	Contig	GCA_018184435.1	GCF_018184435.1	SAMEA6656821	PRJNA514245	CG7	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001013799.1	Proteus mirabilis	Contig	GCA_018183515.1	GCF_018183515.1	SAMEA6657653	PRJNA514245	CG20	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001012877.1	Proteus mirabilis	Contig	GCA_018181055.1	GCF_018181055.1	SAMEA6656524	PRJNA514245	CG44	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001013408.1	Proteus mirabilis	Contig	GCA_018180975.1	GCF_018180975.1	SAMEA6657228	PRJNA514245	CG3	2018	Denmark	Homo sapiens	Unknown
Proteus mirabilis	PDT001012879.1	Proteus mirabilis	Contig	GCA_018180755.1	GCF_018180755.1	SAMEA6656526	PRJNA514245	CG195	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001012883.1	Proteus mirabilis	Contig	GCA_018180295.1	GCF_018180295.1	SAMEA6656530	PRJNA514245	CG10	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001013769.1	Proteus mirabilis	Contig	GCA_018180095.1	GCF_018180095.1	SAMEA6657617	PRJNA514245	CG194	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001012876.1	Proteus mirabilis	Contig	GCA_018165995.1	GCF_018165995.1	SAMEA6656523	PRJNA514245	CG30	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001012881.1	Proteus mirabilis	Contig	GCA_018165935.1	GCF_018165935.1	SAMEA6656528	PRJNA514245	CG193	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001012882.1	Proteus mirabilis	Contig	GCA_018165915.1	GCF_018165915.1	SAMEA6656529	PRJNA514245	CG20	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001012884.1	Proteus mirabilis	Contig	GCA_018165875.1	GCF_018165875.1	SAMEA6656531	PRJNA514245	CG192	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001013111.1	Proteus mirabilis	Contig	GCA_018165475.1	GCF_018165475.1	SAMEA6656874	PRJNA514245	CG64	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001013132.1	Proteus mirabilis	Contig	GCA_018164115.1	GCF_018164115.1	SAMEA6656898	PRJNA514245	CG4	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001013264.1	Proteus mirabilis	Contig	GCA_018162175.1	GCF_018162175.1	SAMEA6657047	PRJNA514245	CG191	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001013293.1	Proteus mirabilis	Contig	GCA_018161895.1	GCF_018161895.1	SAMEA6657096	PRJNA514245	CG42	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001013313.1	Proteus mirabilis	Contig	GCA_018161675.1	GCF_018161675.1	SAMEA6657127	PRJNA514245	CG190	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001013401.1	Proteus mirabilis	Contig	GCA_018160475.1	GCF_018160475.1	SAMEA6657221	PRJNA514245	CG3	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001013419.1	Proteus mirabilis	Contig	GCA_018160315.1	GCF_018160315.1	SAMEA6657239	PRJNA514245	CG189	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001013415.1	Proteus mirabilis	Contig	GCA_018160275.1	GCF_018160275.1	SAMEA6657235	PRJNA514245	CG188	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001013426.1	Proteus mirabilis	Contig	GCA_018160135.1	GCF_018160135.1	SAMEA6657246	PRJNA514245	CG187	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001013442.1	Proteus mirabilis	Contig	GCA_018159935.1	GCF_018159935.1	SAMEA6657262	PRJNA514245	CG30	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001013464.1	Proteus mirabilis	Contig	GCA_018159695.1	GCF_018159695.1	SAMEA6657284	PRJNA514245	CG3	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001013503.1	Proteus mirabilis	Contig	GCA_018159215.1	GCF_018159215.1	SAMEA6657324	PRJNA514245	CG186	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001013499.1	Proteus mirabilis	Contig	GCA_018159195.1	GCF_018159195.1	SAMEA6657320	PRJNA514245	CG78	2018	Denmark	Homo sapiens	Urine

Proteus mirabilis	PDT001013530.1	Proteus mirabilis	Contig	GCA_018158815.1	GCF_018158815.1	SAMEA6657351	PRJNA514245	CG185	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001013533.1	Proteus mirabilis	Contig	GCA_018158735.1	GCF_018158735.1	SAMEA6657354	PRJNA514245	CG26	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001013551.1	Proteus mirabilis	Contig	GCA_018158435.1	GCF_018158435.1	SAMEA6657372	PRJNA514245	CG42	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001013556.1	Proteus mirabilis	Contig	GCA_018158335.1	GCF_018158335.1	SAMEA6657377	PRJNA514245	CG7	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001013603.1	Proteus mirabilis	Contig	GCA_018157635.1	GCF_018157635.1	SAMEA6657428	PRJNA514245	CG68	2018	Denmark	Unknown	Urine
Proteus mirabilis	PDT001013604.1	Proteus mirabilis	Contig	GCA_018157615.1	GCF_018157615.1	SAMEA6657429	PRJNA514245	CG68	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001013630.1	Proteus mirabilis	Contig	GCA_018157255.1	GCF_018157255.1	SAMEA6657458	PRJNA514245	CG184	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001013633.1	Proteus mirabilis	Contig	GCA_018157165.1	GCF_018157165.1	SAMEA6657461	PRJNA514245	CG42	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	PDT001013796.1	Proteus mirabilis	Contig	GCA_018154155.1	GCF_018154155.1	SAMEA6657648	PRJNA514245	CG183	2018	Denmark	Homo sapiens	Urine
Proteus mirabilis	ASM1813910v1	S74-3-2	Complete Genome	GCA_018139105.1	GCF_018139105.1	SAMN18781105	PRJNA722608	CG24	2018	China	Panthera tigris Amoyensis	Animals
Proteus mirabilis	ASM1813900v1	S62-3-2-2	Complete Genome	GCA_018139005.1	GCF_018139005.1	SAMN18781108	PRJNA722612	CG14	2018	China	Ailuropoda melanoleuca	Animals
Proteus mirabilis	ASM1813898v1	N639-2X	Complete Genome	GCA_018138985.1	GCF_018138985.1	SAMN18781106	PRJNA722609	CG93	2019	China	Paguma larvata	Paguma larvata
Proteus mirabilis	ASM1813894v1	N292	Complete Genome	GCA_018138945.1	GCF_018138945.1	SAMN18781111	PRJNA722615	CG19	2019	China	Saimiri sciureus	Others
Proteus mirabilis	ASM1806943v1	2020EL-00001	Contig	GCA_018069435.1	GCF_018069435.1	SAMN18510986	PRJNA288601	CG3	2019	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1806914v1	2020EL-00023	Contig	GCA_018069145.1	GCF_018069145.1	SAMN18511004	PRJNA288601	CG3	2019	USA	Homo sapiens	Swab
Proteus mirabilis	ASM1806910v1	2020EL-00022	Contig	GCA_018069105.1	GCF_018069105.1	SAMN18511003	PRJNA288601	CG3	2019	USA	Homo sapiens	Swab
Proteus mirabilis	ASM1806907v1	2020EL-00021	Contig	GCA_018069075.1	GCF_018069075.1	SAMN18511002	PRJNA288601	CG3	2019	USA	Homo sapiens	Swab
Proteus mirabilis	ASM1806906v1	2020EL-00020	Contig	GCA_018069065.1	GCF_018069065.1	SAMN18511001	PRJNA288601	CG3	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1806904v1	2020EL-00024	Contig	GCA_018069045.1	GCF_018069045.1	SAMN18511005	PRJNA288601	CG3	2019	USA	Homo sapiens	Swab
Proteus mirabilis	ASM1806902v1	2020EL-00026	Contig	GCA_018069025.1	GCF_018069025.1	SAMN18511007	PRJNA288601	CG3	2019	USA	Homo sapiens	Swab
Proteus mirabilis	ASM1806899v1	2020EL-00025	Contig	GCA_018068995.1	GCF_018068995.1	SAMN18511006	PRJNA288601	CG3	2019	USA	Homo sapiens	Swab
Proteus mirabilis	ASM1806898v1	2020EL-00028	Contig	GCA_018068985.1	GCF_018068985.1	SAMN18511009	PRJNA288601	CG3	2019	USA	Homo sapiens	Swab
Proteus mirabilis	ASM1806896v1	2020EL-00027	Contig	GCA_018068965.1	GCF_018068965.1	SAMN18511008	PRJNA288601	CG3	2019	USA	Homo sapiens	Swab
Proteus mirabilis	ASM1806894v1	2020EL-00029	Contig	GCA_018068945.1	GCF_018068945.1	SAMN18511010	PRJNA288601	CG3	2019	USA	Homo sapiens	Swab
Proteus mirabilis	ASM1806892v1	2020EL-00031	Contig	GCA_018068925.1	GCF_018068925.1	SAMN18511012	PRJNA288601	CG182	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1806890v1	2020EL-00030	Contig	GCA_018068905.1	GCF_018068905.1	SAMN18511011	PRJNA288601	CG3	2019	USA	Homo sapiens	Swab
Proteus mirabilis	ASM1806887v1	2020EL-00032	Contig	GCA_018068875.1	GCF_018068875.1	SAMN18511013	PRJNA288601	CG3	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1806884v1	2020EL-00034	Contig	GCA_018068845.1	GCF_018068845.1	SAMN18511015	PRJNA288601	CG3	2019	USA	Homo sapiens	Swab
Proteus mirabilis	ASM1806880v1	2020EL-00035	Contig	GCA_018068805.1	GCF_018068805.1	SAMN18511016	PRJNA288601	CG3	2019	USA	Homo sapiens	Swab
Proteus mirabilis	ASM1806860v1	2020EL-00047	Contig	GCA_018068605.1	GCF_018068605.1	SAMN18511027	PRJNA288601	CG181	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1806832v1	2020EL-00066	Contig	GCA_018068325.1	GCF_018068325.1	SAMN18511041	PRJNA288601	CG3	2019	USA	Homo sapiens	Swab
Proteus mirabilis	ASM1806808v1	2020EL-00081	Contig	GCA_018068085.1	GCF_018068085.1	SAMN18511056	PRJNA288601	CG3	2019	USA	Homo sapiens	Swab
Proteus mirabilis	ASM1806806v1	2020EL-00078	Contig	GCA_018068065.1	GCF_018068065.1	SAMN18511053	PRJNA288601	CG3	2020	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1806802v1	2020EL-00080	Contig	GCA_018068025.1	GCF_018068025.1	SAMN18511055	PRJNA288601	CG3	2019	USA	Homo sapiens	Swab
Proteus mirabilis	ASM1806800v1	2020EL-00082	Contig	GCA_018068005.1	GCF_018068005.1	SAMN18511057	PRJNA288601	CG3	2019	USA	Homo sapiens	Swab
Proteus mirabilis	ASM1806796v1	2020EL-00083	Contig	GCA_018067965.1	GCF_018067965.1	SAMN18511058	PRJNA288601	CG3	2019	USA	Homo sapiens	Swab
Proteus mirabilis	ASM1806792v1	2020EL-00086	Contig	GCA_018067925.1	GCF_018067925.1	SAMN18511061	PRJNA288601	CG3	2020	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1806772v1	2020EL-00098	Contig	GCA_018067725.1	GCF_018067725.1	SAMN18511071	PRJNA288601	CG75	2020	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1806767v1	2020EL-00100	Contig	GCA_018067675.1	GCF_018067675.1	SAMN18511073	PRJNA288601	CG6	2020	USA	Homo sapiens	Swab
Proteus mirabilis	ASM1806762v1	2020EL-00109	Contig	GCA_018067625.1	GCF_018067625.1	SAMN18511081	PRJNA288601	CG180	2020	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1806742v1	2020EL-00111	Contig	GCA_018067425.1	GCF_018067425.1	SAMN18511083	PRJNA288601	CG3	2020	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1790119v1	1035	Complete Genome	GCA_017901195.1	GCF_017901195.1	SAMN18593959	PRJNA719276	CG14	2018	China	Unknown	Others

Proteus mirabilis	ASM1769340v1	NvitL3-2V	Contig	GCA_017693405.1	GCF_017693405.1	SAMN15947955	PRJNA660265	CG82	2018	USA	Nasonia	L3 Larvae
Proteus mirabilis	ASM1769339v1	F2Hybrid-1H	Scaffold	GCA_017693395.1	GCF_017693395.1	SAMN15947342	PRJNA660265	CG82	2018	USA	Nasonia	L3 Larvae
Proteus mirabilis	ASM1769335v1	F2Hybrid-2H	Scaffold	GCA_017693355.1	GCF_017693355.1	SAMN15947597	PRJNA660265	CG82	2018	USA	Nasonia	L3 Larvae
Proteus mirabilis	ASM1769331v1	F2Hybrid-3H	Scaffold	GCA_017693315.1	GCF_017693315.1	SAMN15947724	PRJNA660265	CG82	2018	USA	Nasonia	L3 Larvae
Proteus mirabilis	ASM1769327v1	NvitL3-1V	Contig	GCA_017693275.1	GCF_017693275.1	SAMN15947872	PRJNA660265	CG82	2018	USA	Nasonia	L3 Larvae
Proteus mirabilis	ASM1769321v1	NgirL3-2G	Contig	GCA_017693215.1	GCF_017693215.1	SAMN15947205	PRJNA660265	CG82	2018	USA	Nasonia	L3 Larvae
Proteus mirabilis	ASM1769317v1	NgirL3-1G	Scaffold	GCA_017693175.1	GCF_017693175.1	SAMN15947202	PRJNA660265	CG82	2018	USA	Nasonia	L3 Larvae
Proteus mirabilis	ASM1730956v1	PM52812	Scaffold	GCA_017309565.1	GCF_017309565.1	SAMN16933299	PRJNA700516	CG3	2019	Czech Republic	Homo sapiens	Swab
Proteus mirabilis	ASM1717005v1	W1	Contig	GCA_017170055.1	GCF_017170055.1	SAMN10755195	PRJNA516144	CG79	2018	China: Hong Kong	Homo sapiens	Stool
Proteus mirabilis	ASM1717003v1	W3	Contig	GCA_017170035.1	GCF_017170035.1	SAMN10755197	PRJNA516144	CG79	2018	China: Hong Kong	Homo sapiens	Stool
Proteus mirabilis	ASM1717001v1	W2	Contig	GCA_017170015.1	GCF_017170015.1	SAMN10755196	PRJNA516144	CG79	2018	China: Hong Kong	Homo sapiens	Stool
Proteus mirabilis	ASM1716999v1	W4	Contig	GCA_017169995.1	GCF_017169995.1	SAMN10755198	PRJNA516144	CG79	2018	China: Hong Kong	Homo sapiens	Stool
Proteus mirabilis	ASM1716997v1	W5	Contig	GCA_017169975.1	GCF_017169975.1	SAMN10755199	PRJNA516144	CG79	2018	China: Hong Kong	Homo sapiens	Stool
Proteus mirabilis	ASM1716995v1	W6	Contig	GCA_017169955.1	GCF_017169955.1	SAMN10755200	PRJNA516144	CG79	2018	China: Hong Kong	Homo sapiens	Stool
Proteus mirabilis	ASM1716992v1	W7	Contig	GCA_017169925.1	GCF_017169925.1	SAMN10755201	PRJNA516144	CG79	2018	China: Hong Kong	Homo sapiens	Stool
Proteus mirabilis	ASM1716991v1	W8	Contig	GCA_017169915.1	GCF_017169915.1	SAMN10755202	PRJNA516144	CG79	2018	China: Hong Kong	Homo sapiens	Stool
Proteus mirabilis	ASM1716989v1	W9	Contig	GCA_017169895.1	GCF_017169895.1	SAMN10755203	PRJNA516144	CG79	2018	China: Hong Kong	Homo sapiens	Stool
Proteus mirabilis	ASM1716986v1	W12	Contig	GCA_017169865.1	GCF_017169865.1	SAMN10755206	PRJNA516144	CG79	2018	China: Hong Kong	Homo sapiens	Stool
Proteus mirabilis	ASM1716985v1	W10	Contig	GCA_017169855.1	GCF_017169855.1	SAMN10755204	PRJNA516144	CG79	2018	China: Hong Kong	Homo sapiens	Stool
Proteus mirabilis	ASM1716983v1	W11	Contig	GCA_017169835.1	GCF_017169835.1	SAMN10755205	PRJNA516144	CG79	2018	China: Hong Kong	Homo sapiens	Stool
Proteus mirabilis	ASM1716981v1	W13	Contig	GCA_017169815.1	GCF_017169815.1	SAMN10755207	PRJNA516144	CG79	2018	China: Hong Kong	Homo sapiens	Stool
Proteus mirabilis	ASM1716979v1	W14	Contig	GCA_017169795.1	GCF_017169795.1	SAMN10755208	PRJNA516144	CG3	2018	China: Hong Kong	Homo sapiens	Stool
Proteus mirabilis	ASM1716975v1	W18	Contig	GCA_017169755.1	GCF_017169755.1	SAMN10755212	PRJNA516144	CG81	2018	China: Hong Kong	Homo sapiens	Biopsy
Proteus mirabilis	ASM1716974v1	W15	Contig	GCA_017169745.1	GCF_017169745.1	SAMN10755209	PRJNA516144	CG79	2018	China: Hong Kong	Homo sapiens	Stool
Proteus mirabilis	ASM1716973v1	W17	Contig	GCA_017169735.1	GCF_017169735.1	SAMN10755211	PRJNA516144	CG81	2018	China: Hong Kong	Homo sapiens	Biopsy
Proteus mirabilis	ASM1716971v1	W16	Contig	GCA_017169715.1	GCF_017169715.1	SAMN10755210	PRJNA516144	CG79	2018	China: Hong Kong	Homo sapiens	Stool
Proteus mirabilis	ASM1716969v1	W19	Contig	GCA_017169695.1	GCF_017169695.1	SAMN10755213	PRJNA516144	CG76	2018	China: Hong Kong	Homo sapiens	Biopsy
Proteus mirabilis	ASM1716967v1	W20	Contig	GCA_017169675.1	GCF_017169675.1	SAMN10755214	PRJNA516144	CG76	2018	China: Hong Kong	Homo sapiens	Biopsy
Proteus mirabilis	ASM1716965v1	W22	Contig	GCA_017169655.1	GCF_017169655.1	SAMN10755216	PRJNA516144	CG76	2018	China: Hong Kong	Homo sapiens	Biopsy
Proteus mirabilis	ASM1716963v1	W21	Contig	GCA_017169635.1	GCF_017169635.1	SAMN10755215	PRJNA516144	CG76	2018	China: Hong Kong	Homo sapiens	Biopsy
Proteus mirabilis	ASM1716961v1	W23	Contig	GCA_017169615.1	GCF_017169615.1	SAMN10755217	PRJNA516144	CG42	2018	China: Hong Kong	Homo sapiens	Biopsy
Proteus mirabilis	ASM1716959v1	W24	Contig	GCA_017169595.1	GCF_017169595.1	SAMN10755218	PRJNA516144	CG42	2018	China: Hong Kong	Homo sapiens	Biopsy
Proteus mirabilis	ASM1716105v1	DY.F1.2	Complete Genome	GCA_017161055.1	GCF_017161055.1	SAMN13254342	PRJNA588591	CG27	2019	China	Swine	Stool
Proteus mirabilis	PDT000947578.1	2020GO-00172	Contig	GCA_017142915.1	GCF_017142915.1	SAMN17767353	PRJNA288601	CG32	2020	USA	Homo sapiens	Urine catheter
Proteus mirabilis	PDT000949973.1	Proteus_mirabilis_2021CK-00606	Contig	GCA_017119605.1	GCF_017119605.1	SAMN17815180	PRJNA288601	CG3	2020	USA	Homo sapiens	Blood
Proteus mirabilis	ASM1711679v1	SCQJJJ3	Contig	GCA_017116795.1	GCF_017116795.1	SAMN18017905	PRJNA693126	CG3	2020	China	Chicken	Unknown
Proteus mirabilis	ASM1711678v1	HYA2	Contig	GCA_017116785.1	GCF_017116785.1	SAMN18017904	PRJNA693126	CG22	2020	China	Chicken	Unknown
Proteus mirabilis	ASM1711452v1	PM53415	Contig	GCA_017114525.1	GCF_017114525.1	SAMN16933303	PRJNA700516	CG3	2019	Czech Republic	Homo sapiens	Swab
Proteus mirabilis	PDT000968707.1	Proteus_mirabilis_2021CK-00636	Contig	GCA_016974075.1	GCF_016974075.1	SAMN18006752	PRJNA288601	CG3	2020	USA	Homo sapiens	Blood
Proteus mirabilis	ASM1693973v1	PM52808	Complete Genome	GCA_016939735.1	GCF_016939735.1	SAMN16933297	PRJNA700516	CG3	2019	Czech Republic	Homo sapiens	Sputum
Proteus mirabilis	ASM1693971v1	PM52260	Complete Genome	GCA_016939715.1	GCF_016939715.1	SAMN16933295	PRJNA700516	CG3	2019	Czech Republic	Homo sapiens	Sputum
Proteus mirabilis	ASM1690586v1	PM45467	Contig	GCA_016905865.1	GCF_016905865.1	SAMN16933259	PRJNA700516	CG80	2018	Czech Republic	Homo sapiens	Swab

Proteus mirabilis	ASM1677235v1	C74	Complete Genome	GCA_016772355.1	GCF_016772355.1	SAMN12859943	PRJNA574564	CG22	2018	China	Chicken	Unknown
Proteus mirabilis	ASM1677233v1	C55	Complete Genome	GCA_016772335.1	GCF_016772335.1	SAMN12859940	PRJNA574562	CG22	2018	China	Chicken	Unknown
Proteus mirabilis	ASM1674621v1	QDGSZ34	Contig	GCA_016746215.1	GCF_016746215.1	SAMN17378675	PRJNA693126	CG27	2020	China	Chicken	Animals
Proteus mirabilis	ASM1674619v1	QDGSZ23	Contig	GCA_016746195.1	GCF_016746195.1	SAMN17378677	PRJNA693126	CG27	2020	China	Chicken	Unknown
Proteus mirabilis	ASM1674617v1	QDMD36	Contig	GCA_016746175.1	GCF_016746175.1	SAMN17378676	PRJNA693126	CG23	2020	China	Chicken	Unknown
Proteus mirabilis	ASM1674615v1	HYB3	Contig	GCA_016746155.1	GCF_016746155.1	SAMN17378678	PRJNA693126	CG19	2020	China	Chicken	Unknown
Proteus mirabilis	ASM1672590v1	FDAARGOS_1079	Complete Genome	GCA_016725905.1	GCF_016725905.1	SAMN16357248	PRJNA231221	CG92	Unknown	Germany	Unknown	Unknown
Proteus mirabilis	ASM1623935v1	PR00162	Contig	GCA_016239355.1	GCF_016239355.1	SAMN16982436	PRJNA475751	CG63	2018	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1623928v1	PR00169	Contig	GCA_016239285.1	GCF_016239285.1	SAMN16982439	PRJNA475751	CG73	2018	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1623926v1	PR00168	Contig	GCA_016239265.1	GCF_016239265.1	SAMN16982438	PRJNA475751	CG32	2018	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1623924v1	PR00167	Contig	GCA_016239245.1	GCF_016239245.1	SAMN16982437	PRJNA475751	CG32	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623922v1	PR00170	Contig	GCA_016239225.1	GCF_016239225.1	SAMN16982440	PRJNA475751	CG55	2018	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1623919v1	PR00172	Contig	GCA_016239195.1	GCF_016239195.1	SAMN16982442	PRJNA475751	CG41	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623917v1	PR00175	Contig	GCA_016239175.1	GCF_016239175.1	SAMN16982444	PRJNA475751	CG179	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623914v1	PR00171	Contig	GCA_016239145.1	GCF_016239145.1	SAMN16982441	PRJNA475751	CG40	2019	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1623912v1	PR00173	Contig	GCA_016239125.1	GCF_016239125.1	SAMN16982443	PRJNA475751	CG77	2019	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1623910v1	PR00177	Contig	GCA_016239105.1	GCF_016239105.1	SAMN16982446	PRJNA475751	CG79	2019	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1623908v1	PR00176	Contig	GCA_016239085.1	GCF_016239085.1	SAMN16982445	PRJNA475751	CG2	2019	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1623906v1	PR00178	Contig	GCA_016239065.1	GCF_016239065.1	SAMN16982447	PRJNA475751	CG62	2019	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1623904v1	PR00179	Contig	GCA_016239045.1	GCF_016239045.1	SAMN16982448	PRJNA475751	CG13	2019	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1623902v1	PR00180	Contig	GCA_016239025.1	GCF_016239025.1	SAMN16982449	PRJNA475751	CG78	2019	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1623900v1	PR00181	Contig	GCA_016239005.1	GCF_016239005.1	SAMN16982450	PRJNA475751	CG50	2019	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1623898v1	PR00183	Contig	GCA_016238985.1	GCF_016238985.1	SAMN16982452	PRJNA475751	CG17	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623896v1	PR00182	Contig	GCA_016238965.1	GCF_016238965.1	SAMN16982451	PRJNA475751	CG52	2019	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1623894v1	PR00185	Contig	GCA_016238945.1	GCF_016238945.1	SAMN16982454	PRJNA475751	CG77	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623892v1	PR00186	Contig	GCA_016238925.1	GCF_016238925.1	SAMN16982455	PRJNA475751	CG2	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623890v1	PR00184	Contig	GCA_016238905.1	GCF_016238905.1	SAMN16982453	PRJNA475751	CG2	2019	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1623888v1	PR00187	Contig	GCA_016238885.1	GCF_016238885.1	SAMN16982456	PRJNA475751	CG178	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623886v1	PR00188	Contig	GCA_016238865.1	GCF_016238865.1	SAMN16982457	PRJNA475751	CG65	2019	USA	Homo sapiens	Blood
Proteus mirabilis	ASM1623884v1	PR00189	Contig	GCA_016238845.1	GCF_016238845.1	SAMN16982458	PRJNA475751	CG47	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623882v1	PR00190	Contig	GCA_016238825.1	GCF_016238825.1	SAMN16982459	PRJNA475751	CG47	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623880v1	PR00193	Contig	GCA_016238805.1	GCF_016238805.1	SAMN16982462	PRJNA475751	CG2	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623878v1	PR00192	Contig	GCA_016238785.1	GCF_016238785.1	SAMN16982461	PRJNA475751	CG49	2019	USA	Homo sapiens	Blood
Proteus mirabilis	ASM1623875v1	PR00194	Contig	GCA_016238755.1	GCF_016238755.1	SAMN16982463	PRJNA475751	CG177	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623874v1	PR00191	Contig	GCA_016238745.1	GCF_016238745.1	SAMN16982460	PRJNA475751	CG6	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623872v1	PR00196	Contig	GCA_016238725.1	GCF_016238725.1	SAMN16982464	PRJNA475751	CG176	2019	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1623870v1	PR00198	Contig	GCA_016238705.1	GCF_016238705.1	SAMN16982466	PRJNA475751	CG175	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623867v1	PR00200	Contig	GCA_016238675.1	GCF_016238675.1	SAMN16982467	PRJNA475751	CG174	2019	USA	Homo sapiens	Tissue
Proteus mirabilis	ASM1623866v1	PR00197	Contig	GCA_016238665.1	GCF_016238665.1	SAMN16982465	PRJNA475751	CG173	2019	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1623864v1	PR00201	Contig	GCA_016238645.1	GCF_016238645.1	SAMN16982468	PRJNA475751	CG2	2019	USA	Homo sapiens	Tissue
Proteus mirabilis	ASM1623862v1	PR00202	Contig	GCA_016238625.1	GCF_016238625.1	SAMN16982469	PRJNA475751	CG32	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623860v1	PR00203	Contig	GCA_016238605.1	GCF_016238605.1	SAMN16982470	PRJNA475751	CG172	2019	USA	Homo sapiens	Urine

Proteus mirabilis	ASM1623858v1	PR00204	Contig	GCA_016238585.1	GCF_016238585.1	SAMN16982471	PRJNA475751	CG51	2019	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1623856v1	PR00205	Contig	GCA_016238565.1	GCF_016238565.1	SAMN16982865	PRJNA475751	CG3	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623852v1	PR00206	Contig	GCA_016238525.1	GCF_016238525.1	SAMN16982472	PRJNA475751	CG53	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623850v1	PR00209	Contig	GCA_016238505.1	GCF_016238505.1	SAMN16982474	PRJNA475751	CG171	2019	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1623847v1	PR00210	Contig	GCA_016238475.1	GCF_016238475.1	SAMN16982475	PRJNA475751	CG3	2019	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1623842v1	PR00207	Contig	GCA_016238425.1	GCF_016238425.1	SAMN16982473	PRJNA475751	CG32	2019	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1623840v1	PR00211	Contig	GCA_016238405.1	GCF_016238405.1	SRS4553229	PRJNA475751	CG3	2019	USA	Homo sapiens	CSF
Proteus mirabilis	ASM1623838v1	PR00215	Contig	GCA_016238385.1	GCF_016238385.1	SAMN16982479	PRJNA475751	CG25	2019	USA	Homo sapiens	Tissue
Proteus mirabilis	ASM1623836v1	PR00213	Contig	GCA_016238365.1	GCF_016238365.1	SAMN16982477	PRJNA475751	CG170	2019	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1623834v1	PR00212	Contig	GCA_016238345.1	GCF_016238345.1	SAMN16982476	PRJNA475751	CG54	2019	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1623832v1	PR00214	Contig	GCA_016238325.1	GCF_016238325.1	SAMN16982478	PRJNA475751	CG76	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623830v1	PR00216	Contig	GCA_016238305.1	GCF_016238305.1	SAMN16982480	PRJNA475751	CG35	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623828v1	PR00217	Contig	GCA_016238285.1	GCF_016238285.1	SAMN16982481	PRJNA475751	CG2	2019	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1623825v1	PR00220	Contig	GCA_016238255.1	GCF_016238255.1	SAMN16982484	PRJNA475751	CG7	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623823v1	PR00221	Contig	GCA_016238235.1	GCF_016238235.1	SAMN16982485	PRJNA475751	CG50	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623822v1	PR00218	Contig	GCA_016238225.1	GCF_016238225.1	SAMN16982482	PRJNA475751	CG2	2019	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1623820v1	PR00219	Contig	GCA_016238205.1	GCF_016238205.1	SAMN16982483	PRJNA475751	CG2	2019	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1623818v1	PR00222	Contig	GCA_016238185.1	GCF_016238185.1	SAMN16982486	PRJNA475751	CG15	2019	USA	Homo sapiens	Blood
Proteus mirabilis	ASM1623816v1	PR00223	Contig	GCA_016238165.1	GCF_016238165.1	SAMN16982487	PRJNA475751	CG75	2019	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1623814v1	PR00225	Contig	GCA_016238145.1	GCF_016238145.1	SAMN16982488	PRJNA475751	CG37	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623811v1	PR00226	Contig	GCA_016238115.1	GCF_016238115.1	SAMN16982489	PRJNA475751	CG74	2019	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1623808v1	PR00229	Contig	GCA_016238085.1	GCF_016238085.1	SAMN16982492	PRJNA475751	CG41	2019	USA	Homo sapiens	Tissue
Proteus mirabilis	ASM1623806v1	PR00231	Contig	GCA_016238065.1	GCF_016238065.1	SAMN16982494	PRJNA475751	CG30	2019	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1623804v1	PR00228	Contig	GCA_016238045.1	GCF_016238045.1	SAMN16982491	PRJNA475751	CG41	2019	USA	Homo sapiens	Tissue
Proteus mirabilis	ASM1623802v1	PR00227	Contig	GCA_016238025.1	GCF_016238025.1	SAMN16982490	PRJNA475751	CG74	2019	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1623800v1	PR00230	Contig	GCA_016238005.1	GCF_016238005.1	SAMN16982493	PRJNA475751	CG2	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623796v1	PR00232	Contig	GCA_016237965.1	GCF_016237965.1	SAMN16982495	PRJNA475751	CG53	2019	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1623794v1	PR00233	Contig	GCA_016237945.1	GCF_016237945.1	SAMN16982496	PRJNA475751	CG53	2019	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1623792v1	PR00239	Contig	GCA_016237925.1	GCF_016237925.1	SAMN16982498	PRJNA475751	CG169	2019	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM1623790v1	PR00240	Contig	GCA_016237905.1	GCF_016237905.1	SAMN16982499	PRJNA475751	CG168	2019	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1623788v1	PR00234	Contig	GCA_016237885.1	GCF_016237885.1	SAMN16982497	PRJNA475751	CG50	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623786v1	PR00245	Contig	GCA_016237865.1	GCF_016237865.1	SAMN16982502	PRJNA475751	CG72	2019	USA	Homo sapiens	Blood
Proteus mirabilis	ASM1623784v1	PR00246	Contig	GCA_016237845.1	GCF_016237845.1	SAMN16982503	PRJNA475751	CG167	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623782v1	PR00247	Contig	GCA_016237825.1	GCF_016237825.1	SAMN16982504	PRJNA475751	CG166	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623780v1	PR00241	Contig	GCA_016237805.1	GCF_016237805.1	SAMN16982500	PRJNA475751	CG73	2019	USA	Homo sapiens	Tissue
Proteus mirabilis	ASM1623778v1	PR00244	Contig	GCA_016237785.1	GCF_016237785.1	SAMN16982501	PRJNA475751	CG32	2019	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1623776v1	PR00248	Contig	GCA_016237765.1	GCF_016237765.1	SAMN16982505	PRJNA475751	CG40	2019	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1623774v1	PR00250	Contig	GCA_016237745.1	GCF_016237745.1	SAMN16982506	PRJNA475751	CG165	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623771v1	PR00252	Contig	GCA_016237715.1	GCF_016237715.1	SAMN16982508	PRJNA475751	CG1	2019	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1623768v1	PR00251	Contig	GCA_016237685.1	GCF_016237685.1	SAMN16982507	PRJNA475751	CG50	2019	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1623766v1	PR00253	Contig	GCA_016237665.1	GCF_016237665.1	SAMN16982509	PRJNA475751	CG164	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623764v1	PR00254	Contig	GCA_016237645.1	GCF_016237645.1	SAMN16982510	PRJNA475751	CG163	2019	USA	Homo sapiens	Urine

Proteus mirabilis	ASM1623762v1	PR00256	Contig	GCA_016237625.1	GCF_016237625.1	SAMN16982512	PRJNA475751	CG72	2019	USA	Homo sapiens	Blood
Proteus mirabilis	ASM1623760v1	PR00257	Contig	GCA_016237605.1	GCF_016237605.1	SAMN16982513	PRJNA475751	CG21	2019	USA	Homo sapiens	Bronch
Proteus mirabilis	ASM1623758v1	PR00259	Contig	GCA_016237585.1	GCF_016237585.1	SAMN16982874	PRJNA475751	CG162	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623756v1	PR00260	Contig	GCA_016237565.1	GCF_016237565.1	SAMN16982515	PRJNA475751	CG52	2019	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1623754v1	PR00255	Contig	GCA_016237545.1	GCF_016237545.1	SAMN16982511	PRJNA475751	CG71	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623752v1	PR00258	Contig	GCA_016237525.1	GCF_016237525.1	SAMN16982514	PRJNA475751	CG48	2019	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1623750v1	PR00262	Contig	GCA_016237505.1	GCF_016237505.1	SAMN16982517	PRJNA475751	CG161	2019	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1623747v1	PR00261	Contig	GCA_016237475.1	GCF_016237475.1	SAMN16982516	PRJNA475751	CG6	2019	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1623745v1	PR00264	Contig	GCA_016237455.1	GCF_016237455.1	SAMN16982519	PRJNA475751	CG160	2019	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1623743v1	PR00266	Contig	GCA_016237435.1	GCF_016237435.1	SAMN16982520	PRJNA475751	CG4	2019	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1623740v1	PR00263	Contig	GCA_016237405.1	GCF_016237405.1	SAMN16982518	PRJNA475751	CG52	2019	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1623738v1	PR00268	Contig	GCA_016237385.1	GCF_016237385.1	SAMN16982522	PRJNA475751	CG35	2019	USA	Homo sapiens	Tissue
Proteus mirabilis	ASM1623735v1	PR00267	Contig	GCA_016237355.1	GCF_016237355.1	SAMN16982521	PRJNA475751	CG6	2019	USA	Homo sapiens	Tissue
Proteus mirabilis	ASM1623731v1	PR00271	Contig	GCA_016237315.1	GCF_016237315.1	SAMN16982523	PRJNA475751	CG32	2019	USA	Homo sapiens	Tissue
Proteus mirabilis	ASM1623724v1	PR00274	Contig	GCA_016237245.1	GCF_016237245.1	SAMN16982524	PRJNA475751	CG63	2019	USA	Homo sapiens	Tissue
Proteus mirabilis	PDT000133644.1		Contig	GCA_016087455.1	GCF_016087455.1	SAMN05194532	PRJNA278886	CG32	2016	USA	Homo sapiens	Bronch
Proteus mirabilis	PDT000136649.1	CAV1120	Contig	GCA_016086495.1	GCF_016086495.1	SAMN03733684	PRJNA514245	CG6	2019	USA	Homo sapiens	Rectum
Proteus mirabilis	PDT000160694.1	M548	Contig	GCA_016085855.1	GCF_016085855.1	SAMEA1572904	PRJNA514245	CG159	Unknown	Unknown	Unknown	Unknown
Proteus mirabilis	PDT000160778.1	Proteus mirabilis (enterobacteria)	Contig	GCA_016085815.1	GCF_016085815.1	SAMEA1903562	PRJNA514245	CG70	Unknown	Unknown	Unknown	Unknown
Proteus mirabilis	PDT000160779.1	M590	Contig	GCA_016085795.1	GCF_016085795.1	SAMEA1903563	PRJNA514245	CG70	Unknown	Unknown	Unknown	Unknown
Proteus mirabilis	PDT000160833.1	M645	Contig	GCA_016085745.1	GCF_016085745.1	SAMEA1903616	PRJNA514245	CG69	Unknown	Unknown	Unknown	Unknown
Proteus mirabilis	PDT000160794.1	M572	Contig	GCA_016085735.1	GCF_016085735.1	SAMEA1903578	PRJNA514245	CG61	Unknown	Unknown	Unknown	Unknown
Proteus mirabilis	PDT000160798.1	M568	Contig	GCA_016085655.1	GCF_016085655.1	SAMEA1903582	PRJNA514245	CG61	Unknown	Unknown	Unknown	Unknown
Proteus mirabilis	PDT000160800.1	M566	Contig	GCA_016085615.1	GCF_016085615.1	SAMEA1903583	PRJNA514245	CG69	Unknown	Unknown	Unknown	Unknown
Proteus mirabilis	PDT000160832.1	M646	Contig	GCA_016085595.1	GCF_016085595.1	SAMEA1903619	PRJNA514245	CG15	Unknown	Unknown	Unknown	Unknown
Proteus mirabilis	PDT000160805.1	M547	Contig	GCA_016085575.1	GCF_016085575.1	SAMEA1903590	PRJNA514245	CG158	Unknown	Unknown	Unknown	Unknown
Proteus mirabilis	PDT000160801.1	M558	Contig	GCA_016085425.1	GCF_016085425.1	SAMEA1903585	PRJNA514245	CG157	Unknown	Unknown	Unknown	Unknown
Proteus mirabilis	PDT000160796.1	M570	Contig	GCA_016085315.1	GCF_016085315.1	SAMEA1903579	PRJNA514245	CG69	Unknown	Unknown	Unknown	Unknown
Proteus mirabilis	PDT000433411.1		Contig	GCA_016075815.1	GCF_016075815.1	SAMN05581783	PRJNA514245	CG4	2012	USA	Homo sapiens	Wound
Proteus mirabilis	PDT000434773.1	SMART449	Contig	GCA_016074875.1	GCF_016074875.1	SAMD00055768	PRJNA514245	CG1	2011	Italy	Homo sapiens	Unknown
Proteus mirabilis	PDT000444173.1	Proteus mirabilis	Contig	GCA_016073355.1	GCF_016073355.1	SAMEA4548072	PRJNA514245	CG3	Unknown	Unknown	Unknown	Unknown
Proteus mirabilis	PDT000444172.1	Proteus mirabilis	Contig	GCA_016073175.1	GCF_016073175.1	SAMEA4548071	PRJNA514245	CG3	Unknown	Unknown	Unknown	Unknown
Proteus mirabilis	PDT000444140.1	Proteus mirabilis	Contig	GCA_016073055.1	GCF_016073055.1	SAMEA4548045	PRJNA514245	CG3	Unknown	Unknown	Unknown	Unknown
Proteus mirabilis	PDT000443916.1	Proteus mirabilis	Contig	GCA_016072715.1	GCF_016072715.1	SAMEA4547877	PRJNA514245	CG156	Unknown	Unknown	Unknown	Unknown
Proteus mirabilis	PDT000444185.1	Proteus mirabilis	Contig	GCA_016072555.1	GCF_016072555.1	SAMEA4548078	PRJNA514245	CG3	Unknown	Unknown	Unknown	Unknown
Proteus mirabilis	PDT000538616.1	671-ESBLB	Contig	GCA_016068675.1	GCF_016068675.1	SAMN09460110	PRJNA514245	CG68	2017	Singapore	Homo sapiens	Swab
Proteus mirabilis	PDT000589415.1	CVM 45470	Contig	GCA_016065855.1	GCF_016065855.1	SAMN12619273	PRJNA561052	CG66	2019	USA	Unknown	Others
Proteus mirabilis	PDT000589436.1	CVM 45451	Contig	GCA_016065825.1	GCF_016065825.1	SAMN12619254	PRJNA561052	CG20	2019	USA	Unknown	Environment
Proteus mirabilis	PDT000590006.1	AUSMDU00003582	Contig	GCA_016065595.1	GCF_016065595.1	SAMN12342922	PRJNA514245	CG20	2015	Australia	Homo sapiens	Unknown
Proteus mirabilis	PDT000673189.1	Proteus mirabilis_014-E2-S01	Contig	GCA_015944635.1	GCF_015944635.1	SAMN11335435	PRJNA514245	CG3	2017	USA	Homo sapiens	Stool
Proteus mirabilis	PDT000673193.1	Proteus mirabilis_014-E1-U06	Contig	GCA_015944575.1	GCF_015944575.1	SAMN11335433	PRJNA514245	CG3	2017	USA	Homo sapiens	Urine
Proteus mirabilis	PDT000673195.1	Proteus mirabilis_014-E1-DxU	Contig	GCA_015944555.1	GCF_015944555.1	SAMN11335427	PRJNA514245	CG3	2017	USA	Homo sapiens	Urine

Proteus mirabilis	PDT000673145.1	Proteus mirabilis_014-E2-S02	Contig	GCA_015944535.1	GCF_015944535.1	SAMN11335436	PRJNA514245	CG3	2017	USA	Homo sapiens	Stool
Proteus mirabilis	PDT000673192.1	Proteus mirabilis_014-E1-U04	Contig	GCA_015944505.1	GCF_015944505.1	SAMN11335432	PRJNA514245	CG3	2017	USA	Homo sapiens	Urine
Proteus mirabilis	PDT000673188.1	Proteus mirabilis_014-E2-DxU	Contig	GCA_015944495.1	GCF_015944495.1	SAMN11335434	PRJNA514245	CG3	2017	USA	Homo sapiens	Urine
Proteus mirabilis	PDT000673190.1	Proteus mirabilis_014-E1-S04	Contig	GCA_015944445.1	GCF_015944445.1	SAMN11335430	PRJNA514245	CG3	2017	USA	Homo sapiens	Stool
Proteus mirabilis	PDT000673197.1	Proteus mirabilis_014-E1-S02	Contig	GCA_015944425.1	GCF_015944425.1	SAMN11335429	PRJNA514245	CG3	2017	USA	Homo sapiens	Stool
Proteus mirabilis	PDT000673196.1	Proteus mirabilis_014-E1-S01	Contig	GCA_015944385.1	GCF_015944385.1	SAMN11335428	PRJNA514245	CG3	2017	USA	Homo sapiens	Stool
Proteus mirabilis	PDT000673207.1	Proteus mirabilis_010-E1-U04	Contig	GCA_015944365.1	GCF_015944365.1	SAMN11335402	PRJNA514245	CG3	2017	USA	Homo sapiens	Urine
Proteus mirabilis	PDT000673202.1	Proteus mirabilis_010-E1-S04	Contig	GCA_015944345.1	GCF_015944345.1	SAMN11335399	PRJNA514245	CG3	2017	USA	Homo sapiens	Stool
Proteus mirabilis	PDT000673200.1	Proteus mirabilis_010-E1-DxU	Contig	GCA_015944265.1	GCF_015944265.1	SAMN11335397	PRJNA514245	CG3	2017	USA	Homo sapiens	Urine
Proteus mirabilis	PDT000712927.1	CVM 45678	Contig	GCA_015943445.1	GCF_015943445.1	SAMN14410619	PRJNA561052	CG58	2019	USA	Unknown	Unknown
Proteus mirabilis	PDT000716789.1		Contig	GCA_015940965.1	GCF_015940965.1	SAMN12911942	PRJNA514245	CG11	2013	Spain	Canis lupus familiaris	Unknown
Proteus mirabilis	PDT000716786.1		Contig	GCA_015940905.1	GCF_015940905.1	SAMN12911944	PRJNA514245	CG20	2014	Italy	Canis lupus familiaris	Unknown
Proteus mirabilis	PDT000716788.1		Contig	GCA_015940865.1	GCF_015940865.1	SAMN12911943	PRJNA514245	CG20	2014	Italy	Homo sapiens	Unknown
Proteus mirabilis	PDT000725315.1	2019GO-00001	Contig	GCA_015937185.1	GCF_015937185.1	SAMN14669191	PRJNA288601	CG3	2019	USA	Homo sapiens	Urine
Proteus mirabilis	PDT000799982.1	Proteus mirabilis (enterobacteria)	Contig	GCA_015929885.1	GCF_015929885.1	SAMN15688134	PRJNA288601	CG2	2020	USA	Homo sapiens	Urine
Proteus mirabilis	PDT000821565.1	Proteus_mirabilis_2020CK-00176	Contig	GCA_015929845.1	GCF_015929845.1	SAMN15907111	PRJNA288601	CG3	2020	USA	Homo sapiens	Urine
Proteus mirabilis	PDT000868691.1	2020GO-00074	Contig	GCA_015902305.1	GCF_015902305.1	SAMN16552558	PRJNA288601	CG56	2020	USA	Homo sapiens	Unknown
Proteus mirabilis	PDT000868692.1	2020GO-00073	Contig	GCA_015901445.1	GCF_015901445.1	SAMN16552557	PRJNA288601	CG49	2020	USA	Homo sapiens	Unknown
Proteus mirabilis	PDT000879472.1		Contig	GCA_015896365.1	GCF_015896365.1	SAMN15813765	PRJNA514245	CG9	2015	Qatar	Homo sapiens	Blood
Proteus mirabilis	PDT000881395.1	hkcpe42	Contig	GCA_015893265.1	GCF_015893265.1	SAMN15904711	PRJNA514245	CG3	2017	China: Hong Kong	Homo sapiens	Urine
Proteus mirabilis	ASM1574026v1	PR00129	Contig	GCA_015740265.1	GCF_015740265.1	SAMN12220771	PRJNA475751	CG3	2018	USA	Homo sapiens	Others
Proteus mirabilis	ASM1574023v1	PR00131	Contig	GCA_015740235.1	GCF_015740235.1	SAMN13622116	PRJNA475751	CG18	2018	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1574019v1	PR00134	Contig	GCA_015740195.1	GCF_015740195.1	SAMN13622119	PRJNA475751	CG67	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1574018v1	PR00133	Contig	GCA_015740185.1	GCF_015740185.1	SAMN13622118	PRJNA475751	CG67	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1574016v1	PR00132	Contig	GCA_015740165.1	GCF_015740165.1	SAMN13622117	PRJNA475751	CG155	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1574012v1	PR00135	Contig	GCA_015740125.1	GCF_015740125.1	SAMN13622120	PRJNA475751	CG49	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1574011v1	PR00136	Contig	GCA_015740115.1	GCF_015740115.1	SAMN13622121	PRJNA475751	CG17	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1574007v1	PR00138	Contig	GCA_015740075.1	GCF_015740075.1	SAMN13622123	PRJNA475751	CG39	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1574006v1	PR00139	Contig	GCA_015740065.1	GCF_015740065.1	SAMN13622124	PRJNA475751	CG154	2018	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM1574003v1	PR00142	Contig	GCA_015740035.1	GCF_015740035.1	SAMN13622127	PRJNA475751	CG31	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1574001v1	PR00140	Contig	GCA_015740015.1	GCF_015740015.1	SAMN13622125	PRJNA475751	CG50	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1573998v1	PR00141	Contig	GCA_015739985.1	GCF_015739985.1	SAMN13622126	PRJNA475751	CG49	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1573997v1	PR00143	Contig	GCA_015739975.1	GCF_015739975.1	SAMN13622128	PRJNA475751	CG153	2018	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1573996v1	PR00144	Contig	GCA_015739965.1	GCF_015739965.1	SAMN13622129	PRJNA475751	CG9	2018	USA	Homo sapiens	Blood
Proteus mirabilis	ASM1573993v1	PR00145	Contig	GCA_015739935.1	GCF_015739935.1	SAMN13622130	PRJNA475751	CG152	2018	USA	Homo sapiens	Blood
Proteus mirabilis	ASM1573989v1	PR00149	Contig	GCA_015739895.1	GCF_015739895.1	SAMN13622134	PRJNA475751	CG2	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1573988v1	PR00147	Contig	GCA_015739885.1	GCF_015739885.1	SAMN13622132	PRJNA475751	CG66	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1573985v1	PR00152	Contig	GCA_015739855.1	GCF_015739855.1	SAMN13622136	PRJNA475751	CG17	2018	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1573984v1	PR00148	Contig	GCA_015739845.1	GCF_015739845.1	SAMN13622133	PRJNA475751	CG4	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1573981v1	PR00150	Contig	GCA_015739815.1	GCF_015739815.1	SAMN13622135	PRJNA475751	CG4	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1573980v1	PR00155	Contig	GCA_015739805.1	GCF_015739805.1	SAMN13622139	PRJNA475751	CG151	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1573977v1	PR00153	Contig	GCA_015739775.1	GCF_015739775.1	SAMN13622137	PRJNA475751	CG150	2018	USA	Homo sapiens	Tissue

Proteus mirabilis	ASM1573973v1	PR00157	Contig	GCA_015739735.1	GCF_015739735.1	SAMN13622141	PRJNA475751	CG49	2018	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1573972v1	PR00156	Contig	GCA_015739725.1	GCF_015739725.1	SAMN13622140	PRJNA475751	CG41	2019	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1573969v1	PR00159	Contig	GCA_015739695.1	GCF_015739695.1	SAMN13622143	PRJNA475751	CG65	2018	USA	Homo sapiens	Tissue
Proteus mirabilis	ASM1573967v1	PR00158	Contig	GCA_015739675.1	GCF_015739675.1	SAMN13622142	PRJNA475751	CG2	2018	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1573966v1	PR00160	Contig	GCA_015739665.1	GCF_015739665.1	SAMN13622144	PRJNA475751	CG149	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1573961v1	PR00161	Contig	GCA_015739615.1	GCF_015739615.1	SAMN13622145	PRJNA475751	CG148	2018	USA	Homo sapiens	Tissue
Proteus mirabilis	ASM1572415v1	PR00003	Scaffold	GCA_015724155.1	GCF_015724155.1	SAMN10435811	PRJNA475751	CG147	2017	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1572414v1	PR00002	Scaffold	GCA_015724145.1	GCF_015724145.1	SAMN10435810	PRJNA475751	CG17	2017	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1572410v1	PR00005	Scaffold	GCA_015724105.1	GCF_015724105.1	SAMN10435813	PRJNA475751	CG1	2017	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1572409v1	PR00004	Scaffold	GCA_015724095.1	GCF_015724095.1	SAMN10435812	PRJNA475751	CG146	2017	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1572407v1	PR00007	Scaffold	GCA_015724075.1	GCF_015724075.1	SAMN10435815	PRJNA475751	CG145	2017	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572406v1	PR00006	Scaffold	GCA_015724065.1	GCF_015724065.1	SAMN10435814	PRJNA475751	CG17	2017	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572403v1	PR00008	Contig	GCA_015724035.1	GCF_015724035.1	SAMN10435816	PRJNA475751	CG54	2017	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1572402v1	PR00010	Contig	GCA_015724025.1	GCF_015724025.1	SAMN10435818	PRJNA475751	CG144	2017	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572398v1	PR00009	Contig	GCA_015723985.1	GCF_015723985.1	SAMN10435817	PRJNA475751	CG17	2017	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM1572397v1	PR00011	Scaffold	GCA_015723975.1	GCF_015723975.1	SAMN10435819	PRJNA475751	CG53	2017	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572396v1	PR00012	Contig	GCA_015723965.1	GCF_015723965.1	SAMN10435820	PRJNA475751	CG143	2017	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572394v1	PR00013	Contig	GCA_015723945.1	GCF_015723945.1	SAMN10435821	PRJNA475751	CG142	2017	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572390v1	PR00014	Contig	GCA_015723905.1	GCF_015723905.1	SAMN10435822	PRJNA475751	CG2	2017	USA	Homo sapiens	Tissue
Proteus mirabilis	ASM1572389v1	PR00015	Scaffold	GCA_015723895.1	GCF_015723895.1	SAMN10435823	PRJNA475751	CG17	2017	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572388v1	PR00017	Contig	GCA_015723885.1	GCF_015723885.1	SAMN10435825	PRJNA475751	CG2	2017	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572385v1	PR00016	Scaffold	GCA_015723855.1	GCF_015723855.1	SAMN10435824	PRJNA475751	CG4	2017	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572384v1	PR00020	Scaffold	GCA_015723845.1	GCF_015723845.1	SAMN10435828	PRJNA475751	CG54	2018	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1572382v1	PR00019	Scaffold	GCA_015723825.1	GCF_015723825.1	SAMN10435827	PRJNA475751	CG65	2017	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572378v1	PR00021	Contig	GCA_015723785.1	GCF_015723785.1	SAMN10435829	PRJNA475751	CG52	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572376v1	PR00022	Contig	GCA_015723765.1	GCF_015723765.1	SAMN10435830	PRJNA475751	CG65	2017	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM1572371v1	PR00023	Scaffold	GCA_015723715.1	GCF_015723715.1	SAMN10435831	PRJNA475751	CG141	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572370v1	PR00024	Scaffold	GCA_015723705.1	GCF_015723705.1	SAMN10435832	PRJNA475751	CG28	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572369v1	PR00026	Scaffold	GCA_015723695.1	GCF_015723695.1	SAMN10435834	PRJNA475751	CG30	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572368v1	PR00025	Contig	GCA_015723685.1	GCF_015723685.1	SAMN10435833	PRJNA475751	CG36	2018	USA	Homo sapiens	Tissue
Proteus mirabilis	ASM1572366v1	PR00027	Scaffold	GCA_015723665.1	GCF_015723665.1	SAMN10435835	PRJNA475751	CG140	2018	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1572363v1	PR00030	Scaffold	GCA_015723635.1	GCF_015723635.1	SAMN10435838	PRJNA475751	CG32	2018	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1572361v1	PR00028	Scaffold	GCA_015723615.1	GCF_015723615.1	SAMN10435836	PRJNA475751	CG60	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572360v1	PR00029	Scaffold	GCA_015723605.1	GCF_015723605.1	SAMN10435837	PRJNA475751	CG60	2018	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1572357v1	PR00031	Scaffold	GCA_015723575.1	GCF_015723575.1	SAMN10435839	PRJNA475751	CG52	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572356v1	PR00032	Scaffold	GCA_015723565.1	GCF_015723565.1	SAMN10435840	PRJNA475751	CG50	2018	USA	Homo sapiens	Blood
Proteus mirabilis	ASM1572352v1	PR00033	Scaffold	GCA_015723525.1	GCF_015723525.1	SAMN10435841	PRJNA475751	CG139	2018	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1572350v1	PR00035	Scaffold	GCA_015723505.1	GCF_015723505.1	SAMN10435843	PRJNA475751	CG2	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572349v1	PR00034	Contig	GCA_015723495.1	GCF_015723495.1	SAMN10435842	PRJNA475751	CG61	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572348v1	PR00037	Scaffold	GCA_015723485.1	GCF_015723485.1	SAMN10435844	PRJNA475751	CG17	2018	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1572346v1	PR00038	Scaffold	GCA_015723465.1	GCF_015723465.1	SAMN10435845	PRJNA475751	CG138	2018	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1572342v1	PR00039	Scaffold	GCA_015723425.1	GCF_015723425.1	SAMN10435846	PRJNA475751	CG137	2018	USA	Homo sapiens	Tissue

Proteus mirabilis	ASM1572341v1	PR00040	Contig	GCA_015723415.1	GCF_015723415.1	SAMN10435847	PRJNA475751	CG136	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572340v1	PR00042	Scaffold	GCA_015723405.1	GCF_015723405.1	SAMN10435848	PRJNA475751	CG49	2018	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1572338v1	PR00043	Scaffold	GCA_015723385.1	GCF_015723385.1	SAMN10435849	PRJNA475751	CG2	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572336v1	PR00044	Contig	GCA_015723365.1	GCF_015723365.1	SAMN11285113	PRJNA475751	CG65	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572333v1	PR00045	Contig	GCA_015723335.1	GCF_015723335.1	SAMN11285114	PRJNA475751	CG2	2018	USA	Homo sapiens	Tissue
Proteus mirabilis	ASM1572331v1	PR00047	Contig	GCA_015723315.1	GCF_015723315.1	SAMN11285116	PRJNA475751	CG63	2018	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1572330v1	PR00046	Contig	GCA_015723305.1	GCF_015723305.1	SAMN11285115	PRJNA475751	CG2	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572327v1	PR00048	Contig	GCA_015723275.1	GCF_015723275.1	SAMN11285117	PRJNA475751	CG135	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572326v1	PR00049	Contig	GCA_015723265.1	GCF_015723265.1	SAMN11285118	PRJNA475751	CG7	2018	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1572324v1	PR00051	Contig	GCA_015723245.1	GCF_015723245.1	SAMN11285120	PRJNA475751	CG134	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572321v1	PR00050	Contig	GCA_015723215.1	GCF_015723215.1	SAMN11285119	PRJNA475751	CG2	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572320v1	PR00052	Contig	GCA_015723205.1	GCF_015723205.1	SAMN11285121	PRJNA475751	CG1	2018	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1572317v1	PR00054	Contig	GCA_015723175.1	GCF_015723175.1	SAMN11285122	PRJNA475751	CG2	2018	USA	Homo sapiens	Tissue
Proteus mirabilis	ASM1572316v1	PR00055	Contig	GCA_015723165.1	GCF_015723165.1	SAMN11285123	PRJNA475751	CG64	2018	USA	Homo sapiens	Tissue
Proteus mirabilis	ASM1572313v1	PR00056	Contig	GCA_015723135.1	GCF_015723135.1	SAMN11285124	PRJNA475751	CG1	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572311v1	PR00058	Contig	GCA_015723115.1	GCF_015723115.1	SAMN11285126	PRJNA475751	CG2	2018	USA	Homo sapiens	Tissue
Proteus mirabilis	ASM1572310v1	PR00057	Contig	GCA_015723105.1	GCF_015723105.1	SAMN11285125	PRJNA475751	CG9	2018	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1572308v1	PR00059	Contig	GCA_015723085.1	GCF_015723085.1	SAMN11285127	PRJNA475751	CG52	2018	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1572306v1	PR00060	Contig	GCA_015723065.1	GCF_015723065.1	SAMN11285128	PRJNA475751	CG30	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572304v1	PR00061	Contig	GCA_015723045.1	GCF_015723045.1	SAMN11285129	PRJNA475751	CG17	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572301v1	PR00062	Contig	GCA_015723015.1	GCF_015723015.1	SAMN11285130	PRJNA475751	CG133	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572300v1	PR00063	Contig	GCA_015723005.1	GCF_015723005.1	SAMN11285131	PRJNA475751	CG17	2018	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1572298v1	PR00064	Contig	GCA_015722985.1	GCF_015722985.1	SAMN11285132	PRJNA475751	CG61	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572296v1	PR00065	Contig	GCA_015722965.1	GCF_015722965.1	SAMN11285133	PRJNA475751	CG2	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572293v1	PR00066	Contig	GCA_015722935.1	GCF_015722935.1	SAMN11285134	PRJNA475751	CG6	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572291v1	PR00067	Contig	GCA_015722915.1	GCF_015722915.1	SAMN11285135	PRJNA475751	CG7	2018	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1572289v1	PR00068	Contig	GCA_015722895.1	GCF_015722895.1	SAMN11285136	PRJNA475751	CG63	2018	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1572288v1	PR00069	Contig	GCA_015722885.1	GCF_015722885.1	SAMN11285137	PRJNA475751	CG62	2018	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1572283v1	PR00071	Contig	GCA_015722835.1	GCF_015722835.1	SAMN11285139	PRJNA475751	CG49	2018	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1572282v1	PR00072	Contig	GCA_015722825.1	GCF_015722825.1	SAMN11285140	PRJNA475751	CG2	2018	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1572278v1	PR00074	Contig	GCA_015722785.1	GCF_015722785.1	SAMN12220723	PRJNA475751	CG17	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572273v1	PR00076	Contig	GCA_015722735.1	GCF_015722735.1	SAMN12220725	PRJNA475751	CG30	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572272v1	PR00077	Contig	GCA_015722725.1	GCF_015722725.1	SAMN12220726	PRJNA475751	CG1	2018	USA	Homo sapiens	Tissue
Proteus mirabilis	ASM1572269v1	PR00078	Contig	GCA_015722695.1	GCF_015722695.1	SAMN12220727	PRJNA475751	CG61	2018	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1572268v1	PR00079	Contig	GCA_015722685.1	GCF_015722685.1	SAMN12220728	PRJNA475751	CG39	2018	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1572266v1	PR00080	Contig	GCA_015722665.1	GCF_015722665.1	SAMN12220729	PRJNA475751	CG132	2018	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1572264v1	PR00081	Contig	GCA_015722645.1	GCF_015722645.1	SAMN12220730	PRJNA475751	CG21	2018	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1572262v1	PR00083	Contig	GCA_015722625.1	GCF_015722625.1	SAMN12220731	PRJNA475751	CG7	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572258v1	PR00084	Contig	GCA_015722585.1	GCF_015722585.1	SAMN12220732	PRJNA475751	CG7	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572257v1	PR00086	Contig	GCA_015722575.1	GCF_015722575.1	SAMN12220733	PRJNA475751	CG32	2018	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1572251v1	PR00090	Contig	GCA_015722515.1	GCF_015722515.1	SAMN12220737	PRJNA475751	CG30	2018	USA	Homo sapiens	Blood
Proteus mirabilis	ASM1572250v1	PR00089	Contig	GCA_015722505.1	GCF_015722505.1	SAMN12220736	PRJNA475751	CG17	2018	USA	Homo sapiens	Tissue

Proteus mirabilis	ASM1572247v1	PR00092	Contig	GCA_015722475.1	GCF_015722475.1	SAMN12220739	PRJNA475751	CG23	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572246v1	PR00091	Contig	GCA_015722465.1	GCF_015722465.1	SAMN12220738	PRJNA475751	CG7	2018	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1572244v1	PR00094	Contig	GCA_015722445.1	GCF_015722445.1	SAMN12220741	PRJNA475751	CG60	2018	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1572241v1	PR00093	Contig	GCA_015722415.1	GCF_015722415.1	SAMN12220740	PRJNA475751	CG131	2018	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1572240v1	PR00097	Contig	GCA_015722405.1	GCF_015722405.1	SAMN12220744	PRJNA475751	CG130	2018	USA	Homo sapiens	CSF
Proteus mirabilis	ASM1572237v1	PR00095	Contig	GCA_015722375.1	GCF_015722375.1	SAMN12220742	PRJNA475751	CG59	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572235v1	PR00096	Contig	GCA_015722355.1	GCF_015722355.1	SAMN12220743	PRJNA475751	CG32	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572234v1	PR00098	Contig	GCA_015722345.1	GCF_015722345.1	SAMN12220745	PRJNA475751	CG49	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572232v1	PR00101	Contig	GCA_015722325.1	GCF_015722325.1	SAMN12220748	PRJNA475751	CG53	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572229v1	PR00099	Contig	GCA_015722295.1	GCF_015722295.1	SAMN12220746	PRJNA475751	CG129	2018	USA	Homo sapiens	Tissue
Proteus mirabilis	ASM1572228v1	PR00100	Contig	GCA_015722285.1	GCF_015722285.1	SAMN12220747	PRJNA475751	CG23	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572226v1	PR00102	Contig	GCA_015722265.1	GCF_015722265.1	SAMN12220749	PRJNA475751	CG51	2018	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1572223v1	PR00103	Contig	GCA_015722235.1	GCF_015722235.1	SAMN12220750	PRJNA475751	CG30	2018	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1572221v1	PR00104	Contig	GCA_015722215.1	GCF_015722215.1	SAMN12220751	PRJNA475751	CG30	2018	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1572220v1	PR00105	Contig	GCA_015722205.1	GCF_015722205.1	SAMN12220752	PRJNA475751	CG59	2018	USA	Homo sapiens	Blood
Proteus mirabilis	ASM1572218v1	PR00106	Contig	GCA_015722185.1	GCF_015722185.1	SAMN12220753	PRJNA475751	CG42	2018	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1572216v1	PR00107	Contig	GCA_015722165.1	GCF_015722165.1	SAMN12220754	PRJNA475751	CG48	2018	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1572214v1	PR00109	Contig	GCA_015722145.1	GCF_015722145.1	SAMN12220756	PRJNA475751	CG2	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572211v1	PR00108	Contig	GCA_015722115.1	GCF_015722115.1	SAMN12220755	PRJNA475751	CG128	2018	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1572210v1	PR00110	Contig	GCA_015722105.1	GCF_015722105.1	SAMN12220757	PRJNA475751	CG42	2018	USA	Homo sapiens	Blood
Proteus mirabilis	ASM1572208v1	PR00113	Contig	GCA_015722085.1	GCF_015722085.1	SAMN12220760	PRJNA475751	CG17	2018	USA	Homo sapiens	Tissue
Proteus mirabilis	ASM1572206v1	PR00111	Contig	GCA_015722065.1	GCF_015722065.1	SAMN12220758	PRJNA475751	CG127	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572202v1	PR00117	Contig	GCA_015722025.1	GCF_015722025.1	SAMN12220763	PRJNA475751	CG58	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572201v1	PR00112	Contig	GCA_015722015.1	GCF_015722015.1	SAMN12220759	PRJNA475751	CG58	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572200v1	PR00115	Contig	GCA_015722005.1	GCF_015722005.1	SAMN12220761	PRJNA475751	CG126	2018	USA	Homo sapiens	Blood
Proteus mirabilis	ASM1572198v1	PR00116	Contig	GCA_015721985.1	GCF_015721985.1	SAMN12220762	PRJNA475751	CG57	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572194v1	PR00119	Contig	GCA_015721945.1	GCF_015721945.1	SAMN12220765	PRJNA475751	CG32	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572193v1	PR00118	Contig	GCA_015721935.1	GCF_015721935.1	SAMN12220764	PRJNA475751	CG17	2018	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1572192v1	PR00120	Contig	GCA_015721925.1	GCF_015721925.1	SAMN12220766	PRJNA475751	CG39	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572189v1	PR00125	Contig	GCA_015721895.1	GCF_015721895.1	SAMN12220769	PRJNA475751	CG57	2018	USA	Homo sapiens	Sputum
Proteus mirabilis	ASM1572188v1	PR00121	Contig	GCA_015721885.1	GCF_015721885.1	SAMN13622115	PRJNA475751	CG125	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1572184v1	PR00124	Contig	GCA_015721845.1	GCF_015721845.1	SAMN12220768	PRJNA475751	CG2	2018	USA	Homo sapiens	Wound
Proteus mirabilis	ASM1572182v1	PR00123	Contig	GCA_015721825.1	GCF_015721825.1	SAMN12220767	PRJNA475751	CG56	2018	USA	Homo sapiens	Blood
Proteus mirabilis	ASM1572180v1	PR00126	Contig	GCA_015721805.1	GCF_015721805.1	SAMN12220770	PRJNA475751	CG124	2018	USA	Homo sapiens	Urine
Proteus mirabilis	ASM1569402v1	PmBJ020-1	Complete Genome	GCA_015694025.1	GCF_015694025.1	SAMN16816162	PRJNA678945	CG20	2017	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1569400v1	PmBJ023-2	Complete Genome	GCA_015694005.1	GCF_015694005.1	SAMN16816163	PRJNA678945	CG20	2017	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1569398v1	PmBJ024-1	Complete Genome	GCA_015693985.1	GCF_015693985.1	SAMN16816180	PRJNA678945	CG20	2017	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1569396v1	PmBJ012-2	Complete Genome	GCA_015693965.1	GCF_015693965.1	SAMN16816126	PRJNA678945	CG20	2017	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1569386v1	PmBJ015-2	Complete Genome	GCA_015693865.1	GCF_015693865.1	SAMN16816155	PRJNA678945	CG20	2017	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1566625v1	PmBJ004-1	Contig	GCA_015666255.1	GCF_015666255.1	SAMN16816112	PRJNA678945	CG20	2017	China	Homo sapiens	Urine
Proteus mirabilis	ASM1556068v1	1001254B_151014_E5	Scaffold	GCA_015560685.1	GCF_015560685.1	SAMN15532486	PRJNA637878	CG123	2015	USA	Homo sapiens	Stool
Proteus mirabilis	ASM1555035v1	1001295B_180824_A3	Scaffold	GCA_015550355.1	GCF_015550355.1	SAMN15533164	PRJNA637878	CG39	2018	USA	Homo sapiens	Stool

Proteus mirabilis	ASM1523531v1	19428wB5_irhom_Sw	Contig	GCA_015235315.1	GCF_015235315.1	SAMN16540192	PRJNA671681	CG7	2018	United Kingdom	Mus musculus	Others
Proteus mirabilis	ASM1516901v1	Yak 2019	Complete Genome	GCA_015169015.1	GCF_015169015.1	SAMN16521237	PRJNA670828	CG26	2019	China	Yak	Unknown
Proteus mirabilis	ASM1493158v1	ChSC1905	Complete Genome	GCA_014931585.1	GCF_014931585.1	SAMN13870809	PRJNA601609	CG17	2019	China	Swine	Unknown
Proteus mirabilis	ASM1484311v1	S012	Complete Genome	GCA_014843115.1	GCF_014843115.1	SAMN15770595	PRJNA656064	CG26	2017	China	retail chicken	Cell culture
Proteus mirabilis	ASM1471226v1	PC1	Contig	GCA_014712265.1	GCF_014712265.1	SAMN16176564	PRJNA663658	CG3	2016	China	Swine	Swab
Proteus mirabilis	ASM1432428v1	SCDJC7	Contig	GCA_014324285.1	GCF_014324285.1	SAMN08991222	PRJNA453830	CG39	2017	China	Chicken	Swab
Proteus mirabilis	ASM1421267v1	5pro	Scaffold	GCA_014212675.1	GCF_014212675.1	SAMN15786798	PRJNA656522	CG55	2016	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1421266v1	15bian	Scaffold	GCA_014212665.1	GCF_014212665.1	SAMN15786799	PRJNA656522	CG55	2016	China	Homo sapiens	Urine
Proteus mirabilis	ASM1421265v1	16pro	Scaffold	GCA_014212655.1	GCF_014212655.1	SAMN15786800	PRJNA656522	CG55	2017	China	Homo sapiens	Wound
Proteus mirabilis	ASM1421263v1	20bian	Scaffold	GCA_014212635.1	GCF_014212635.1	SAMN15786801	PRJNA656522	CG35	2017	China	Homo sapiens	Urine
Proteus mirabilis	ASM1421261v1	22bian	Scaffold	GCA_014212615.1	GCF_014212615.1	SAMN15786802	PRJNA656522	CG122	2017	China	Homo sapiens	Urine
Proteus mirabilis	ASM1421256v1	37pro	Scaffold	GCA_014212565.1	GCF_014212565.1	SAMN15786803	PRJNA656522	CG2	2018	China	Homo sapiens	Wound
Proteus mirabilis	ASM1421255v1	23266	Contig	GCA_014212555.1	GCF_014212555.1	SAMN15786805	PRJNA656522	CG3	2018	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1421254v1	41bian	Contig	GCA_014212545.1	GCF_014212545.1	SAMN15786804	PRJNA656522	CG121	2018	China	Homo sapiens	Wound
Proteus mirabilis	ASM1421253v1	23809	Scaffold	GCA_014212535.1	GCF_014212535.1	SAMN15786806	PRJNA656522	CG120	2018	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1421250v1	131597	Contig	GCA_014212505.1	GCF_014212505.1	SAMN15786807	PRJNA656522	CG119	2018	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1335879v1	HN2p	Complete Genome	GCA_013358795.1	GCF_013358795.1	SAMN13254340	PRJNA588589	CG22	2019	China	Swine	Stool
Proteus mirabilis	ASM1335758v1	MPE0346	Complete Genome	GCA_013357585.1	GCF_013357585.1	SAMN14937971	PRJNA633229	CG3	2018	China	Malayan pangolin	Unknown
Proteus mirabilis	ASM1335756v1	MPE5203	Complete Genome	GCA_013357565.1	GCF_013357565.1	SAMN14930855	PRJNA633018	CG25	2018	China	Homo sapiens	Unknown
Proteus mirabilis	ASM1335754v1	MPE5139	Complete Genome	GCA_013357545.1	GCF_013357545.1	SAMN14930506	PRJNA633016	CG3	2019	China	Homo sapiens	Stool
Proteus mirabilis	ASM1335752v1	MPE4069	Complete Genome	GCA_013357525.1	GCF_013357525.1	SAMN14916645	PRJNA632650	CG3	2019	China	Caracal caracal	Stool
Proteus mirabilis	ASM1335750v1	MPE0027	Complete Genome	GCA_013357505.1	GCF_013357505.1	SAMN14910118	PRJNA632465	CG3	2018	China	Panthera tigris Amoyensis	Stool
Proteus mirabilis	ASM1335748v1	MPE0156	Complete Genome	GCA_013357485.1	GCF_013357485.1	SAMN14909848	PRJNA632462	CG24	2018	China	Ailuropoda melanoleuca	Unknown
Proteus mirabilis	ASM1335746v1	M3-1-17	Complete Genome	GCA_013357465.1	GCF_013357465.1	SAMN14909661	PRJNA632453	CG24	2018	China	Cacatua galerita	Stool
Proteus mirabilis	ASM1335744v1	S74-1(++)-2	Complete Genome	GCA_013357445.1	GCF_013357445.1	SAMN14896267	PRJNA631894	CG24	2018	China	Panthera tigris Amoyensis	Unknown
Proteus mirabilis	ASM1335742v1	MPE0767	Complete Genome	GCA_013357425.1	GCF_013357425.1	SAMN14938214	PRJNA633229	CG23	2018	China	Malayan pangolin	Animals
Proteus mirabilis	ASM1335740v1	MPE0734	Complete Genome	GCA_013357405.1	GCF_013357405.1	SAMN14938213	PRJNA633229	CG23	2018	China	Malayan pangolin	Animals
Proteus mirabilis	ASM1334325v1	L90-1	Complete Genome	GCA_013343255.1	GCF_013343255.1	SAMN13037561	PRJNA577780	CG3	2016	China	Homo sapiens	Unknown
Proteus mirabilis	ASM1325607v1	YPM35	Complete Genome	GCA_013256075.1	GCF_013256075.1	SAMN15002272	PRJNA634613	CG8	2017	China	Unknown	Gut
Proteus mirabilis	ASM1325576v1	JPM24	Complete Genome	GCA_013255765.1	GCF_013255765.1	SAMN15002270	PRJNA634613	CG14	2017	China	Chicken	Gut
Proteus mirabilis	ASM1318471v1	PM380	Scaffold	GCA_013184715.1	GCF_013184715.1	SAMN14389037	PRJNA612943	CG3	2019	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1318469v1	PM431	Scaffold	GCA_013184695.1	GCF_013184695.1	SAMN14389038	PRJNA612943	CG3	2019	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1318467v1	PM906	Scaffold	GCA_013184675.1	GCF_013184675.1	SAMN14389039	PRJNA612943	CG3	2019	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1318465v1	PM187	Scaffold	GCA_013184655.1	GCF_013184655.1	SAMN14389040	PRJNA612943	CG3	2019	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1318426v1	PmirS	Contig	GCA_013184265.1	GCF_013184265.1	SAMN10846777	PRJNA517864	CG3	2015	France	Homo sapiens	Bronch
Proteus mirabilis	ASM1251651v1	STP3	Complete Genome	GCA_012516515.1	GCF_012516515.1	SAMN14558572	PRJNA623736	CG22	2019	China	Swine	Tissue
Proteus mirabilis	ASM1236025v1	PmirR	Contig	GCA_012360255.1	GCF_012360255.1	SAMN13110952	PRJNA579393	CG3	2015	France	Homo sapiens	Bronch
Proteus mirabilis	ASM1203051v1	UMB1310	Contig	GCA_012030515.1	GCF_012030515.1	SAMN14478486	PRJNA316969	CG30	Unknown	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM1203031v1	UMB0038	Contig	GCA_012030315.1	GCF_012030315.1	SAMN14478477	PRJNA316969	CG30	Unknown	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM1160420v1	XH1553	Contig	GCA_011604205.1	GCF_011604205.1	SAMN14363851	PRJNA612157	CG3	2013	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1160415v1	XH1567	Contig	GCA_011604155.1	GCF_011604155.1	SAMN14363865	PRJNA612157	CG3	2013	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1160414v1	XH1556	Contig	GCA_011604145.1	GCF_011604145.1	SAMN14363854	PRJNA612157	CG3	2013	China	Homo sapiens	Sputum

Proteus mirabilis	ASM1160413v1	XH1565	Contig	GCA_011604135.1	GCF_011604135.1	SAMN14363863	PRJNA612157	CG3	2013	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1160412v1	XH1566	Contig	GCA_011604125.1	GCF_011604125.1	SAMN14363864	PRJNA612157	CG3	2013	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1160410v1	XH1559	Contig	GCA_011604105.1	GCF_011604105.1	SAMN14363857	PRJNA612157	CG3	2013	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1160408v1	XH1561	Contig	GCA_011604085.1	GCF_011604085.1	SAMN14363859	PRJNA612157	CG3	2013	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1160405v1	XH1555	Contig	GCA_011604055.1	GCF_011604055.1	SAMN14363853	PRJNA612157	CG3	2013	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1160404v1	XH1560	Contig	GCA_011604045.1	GCF_011604045.1	SAMN14363858	PRJNA612157	CG3	2013	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1160402v1	XH1557	Contig	GCA_011604025.1	GCF_011604025.1	SAMN14363855	PRJNA612157	CG3	2013	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1160301v1	XH1552	Contig	GCA_011603015.1	GCF_011603015.1	SAMN14363850	PRJNA612157	CG3	2013	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1160299v1	XH1558	Contig	GCA_011602995.1	GCF_011602995.1	SAMN14363856	PRJNA612157	CG3	2013	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1160298v1	XH1551	Contig	GCA_011602985.1	GCF_011602985.1	SAMN14363849	PRJNA612157	CG3	2014	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1160295v1	XH1554	Contig	GCA_011602955.1	GCF_011602955.1	SAMN14363852	PRJNA612157	CG3	2013	China	Homo sapiens	Urine
Proteus mirabilis	ASM1160294v1	XH1549	Contig	GCA_011602945.1	GCF_011602945.1	SAMN14363847	PRJNA612157	CG3	2014	China	Homo sapiens	Urine
Proteus mirabilis	ASM1160290v1	XH1550	Contig	GCA_011602905.1	GCF_011602905.1	SAMN14363848	PRJNA612157	CG3	2014	China	Homo sapiens	Urine
Proteus mirabilis	ASM1160289v1	XH1548	Contig	GCA_011602895.1	GCF_011602895.1	SAMN14363846	PRJNA612157	CG3	2013	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1160288v1	XH1563	Contig	GCA_011602885.1	GCF_011602885.1	SAMN14363861	PRJNA612157	CG3	2013	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1160286v1	XH1547	Contig	GCA_011602865.1	GCF_011602865.1	SAMN14363845	PRJNA612157	CG3	2013	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1160282v1	XH1562	Contig	GCA_011602825.1	GCF_011602825.1	SAMN14363860	PRJNA612157	CG3	2013	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1160278v1	XH1564	Contig	GCA_011602785.1	GCF_011602785.1	SAMN14363862	PRJNA612157	CG3	2013	China	Homo sapiens	Sputum
Proteus mirabilis	ASM1138304v1	XH1569	Complete Genome	GCA_011383045.1	GCF_011383045.1	SAMN14331403	PRJNA611104	CG21	2020	China	Homo sapiens	Urine
Proteus mirabilis	ASM1138302v1	XH1568	Complete Genome	GCA_011383025.1	GCF_011383025.1	SAMN14331295	PRJNA611096	CG91	2019	China	Homo sapiens	Body fluid
Proteus mirabilis	ASM1136508v1	PmSDC32	Contig	GCA_011365085.1	GCF_011365085.1	SAMN10754624	PRJNA515404	CG46	2018	China	Gallus gallus	Unknown
Proteus mirabilis	ASM1114967v1	PmBR607	Complete Genome	GCA_011149675.1	GCF_011149675.1	SAMN12995602	PRJNA576511	CG20	2015	Brazil	Homo sapiens	Urine
Proteus mirabilis	ASM1107810v1	M-12	Scaffold	GCA_011078105.1	GCF_011078105.1	SAMN14134907	PRJNA607405	CG3	2018	China	Chicken	Unknown
Proteus mirabilis	ASM1106712v1	PrK 34/57	Contig	GCA_011067125.1	GCF_011067125.1	SAMN14252151	PRJNA506729	CG118	2003	Czech Republic	Homo sapiens	Cell culture
Proteus mirabilis	ASM1104585v1	ZA25	Complete Genome	GCA_011045855.1	GCF_011045855.1	SAMN13738061	PRJNA599042	CG19	2018	China	Unknown	Swab
Proteus mirabilis	ASM1104557v1	1701092	Complete Genome	GCA_011045575.1	GCF_011045575.1	SAMN12558915	PRJNA559775	CG18	2017	China	Unknown	Gut
Proteus mirabilis	ASM1069286v1	CC15031	Complete Genome	GCA_010692865.1	GCF_010692865.1	SAMN14074148	PRJNA596082	CG17	2017	China	Dog	Gut
Proteus mirabilis	ASM1059809v1	AS012308	Scaffold	GCA_010598095.1	GCF_010598095.1	SAMN12250627	PRJNA553678	CG54	2015	USA	Homo sapiens	Lung
Proteus mirabilis	ASM1059800v1	AS012310	Scaffold	GCA_010598005.1	GCF_010598005.1	SAMN12250629	PRJNA553678	CG53	2015	USA	Homo sapiens	Lung
Proteus mirabilis	ASM1059788v1	AS012318	Scaffold	GCA_010597885.1	GCF_010597885.1	SAMN12250637	PRJNA553678	CG52	2016	USA	Homo sapiens	Lung
Proteus mirabilis	ASM1059772v1	AS012328	Scaffold	GCA_010597725.1	GCF_010597725.1	SAMN12250647	PRJNA553678	CG42	2015	USA	Homo sapiens	Lung
Proteus mirabilis	ASM1059574v1	AS012362	Scaffold	GCA_010595745.1	GCF_010595745.1	SAMN12250681	PRJNA553678	CG51	2016	USA	Homo sapiens	Lung
Proteus mirabilis	ASM1059474v1	AS012355	Scaffold	GCA_010594745.1	GCF_010594745.1	SAMN12250674	PRJNA553678	CG17	2016	USA	Homo sapiens	Lung
Proteus mirabilis	ASM1059468v1	AS012360	Scaffold	GCA_010594685.1	GCF_010594685.1	SAMN12250679	PRJNA553678	CG32	2015	USA	Homo sapiens	Lung
Proteus mirabilis	ASM1059466v1	AS012363	Scaffold	GCA_010594665.1	GCF_010594665.1	SAMN12250682	PRJNA553678	CG50	2015	USA	Homo sapiens	Lung
Proteus mirabilis	ASM1059462v1	AS012367	Scaffold	GCA_010594625.1	GCF_010594625.1	SAMN12250686	PRJNA553678	CG35	2015	USA	Homo sapiens	Lung
Proteus mirabilis	ASM1059460v1	AS012370	Scaffold	GCA_010594605.1	GCF_010594605.1	SAMN12250689	PRJNA553678	CG2	2016	USA	Homo sapiens	Lung
Proteus mirabilis	ASM1059440v1	AS012382	Scaffold	GCA_010594405.1	GCF_010594405.1	SAMN12250701	PRJNA553678	CG6	2015	USA	Homo sapiens	Lung
Proteus mirabilis	ASM1059140v1	AS012407	Scaffold	GCA_010591405.1	GCF_010591405.1	SAMN12250726	PRJNA553678	CG2	2016	USA	Homo sapiens	Lung
Proteus mirabilis	ASM1059108v1	AS012423	Scaffold	GCA_010591085.1	GCF_010591085.1	SAMN12250742	PRJNA553678	CG117	2016	USA	Homo sapiens	Lung
Proteus mirabilis	ASM1059084v1	AS012436	Scaffold	GCA_010590845.1	GCF_010590845.1	SAMN12250755	PRJNA553678	CG32	2015	USA	Homo sapiens	Lung
Proteus mirabilis	ASM1059080v1	AS012439	Scaffold	GCA_010590805.1	GCF_010590805.1	SAMN12250758	PRJNA553678	CG6	2015	USA	Homo sapiens	Lung

Proteus mirabilis	ASM1059075v1	AS012444	Scaffold	GCA_010590755.1	GCF_010590755.1	SAMN12250763	PRJNA553678	CG116	2015	USA	Homo sapiens	Lung
Proteus mirabilis	ASM1059042v1	AS012459	Scaffold	GCA_010590425.1	GCF_010590425.1	SAMN12250778	PRJNA553678	CG50	2015	USA	Homo sapiens	Lung
Proteus mirabilis	ASM1059038v1	AS012462	Scaffold	GCA_010590385.1	GCF_010590385.1	SAMN12250781	PRJNA553678	CG2	2015	USA	Homo sapiens	Lung
Proteus mirabilis	ASM1058815v1	AS012495	Scaffold	GCA_010588155.1	GCF_010588155.1	SAMN12250814	PRJNA553678	CG50	2016	USA	Homo sapiens	Lung
Proteus mirabilis	ASM1044267v1	N18-00201	Complete Genome	GCA_010442675.1	GCF_010442675.1	SAMN13936255	PRJNA603518	CG90	2018	Canada	Homo sapiens	Urine
Proteus mirabilis	ASM990701v1	C4	Contig	GCA_009907015.1	GCF_009907015.1	SAMN13830006	PRJNA600702	CG9	2015	Nigeria	Homo sapiens	Urine
Proteus mirabilis	ASM982905v1	18QD2AZ3W	Contig	GCA_009829055.1	GCF_009829055.1	SAMN13531401	PRJNA594823	CG3	2018	China	Pig	Stool
Proteus mirabilis	ASM982169v1	SC89	Scaffold	GCA_009821695.1	GCF_009821695.1	SAMN11928066	PRJNA545690	CG3	Unknown	Unknown	Chicken	Unknown
Proteus mirabilis	ASM982167v1	SC90	Contig	GCA_009821675.1	GCF_009821675.1	SAMN11928067	PRJNA545690	CG3	Unknown	Unknown	Chicken	Unknown
Proteus mirabilis	ASM982161v1	SC93	Scaffold	GCA_009821615.1	GCF_009821615.1	SAMN11928070	PRJNA545690	CG3	Unknown	Unknown	Chicken	Unknown
Proteus mirabilis	ASM980671v1	SCBX1.1	Complete Genome	GCA_009806715.1	GCF_009806715.1	SAMN13509247	PRJNA594246	CG9	2019	China	Swine	Others
Proteus mirabilis	ASM974925v1	L76	Contig	GCA_009749255.1	GCF_009749255.1	SAMN10219240	PRJNA495102	CG3	2016	China	Homo sapiens	Stool
Proteus mirabilis	ASM974924v1	L90	Contig	GCA_009749245.1	GCF_009749245.1	SAMN10219264	PRJNA495102	CG3	2016	China	Homo sapiens	Stool
Proteus mirabilis	ASM974922v1	L71	Contig	GCA_009749225.1	GCF_009749225.1	SAMN10219241	PRJNA495099	CG3	2016	China	Homo sapiens	Stool
Proteus mirabilis	ASM974918v1	L44	Contig	GCA_009749185.1	GCF_009749185.1	SAMN10218954	PRJNA495099	CG3	2016	China	Homo sapiens	Stool
Proteus mirabilis	ASM974917v1	L49	Contig	GCA_009749175.1	GCF_009749175.1	SAMN10219204	PRJNA495102	CG3	2016	China	Homo sapiens	Stool
Proteus mirabilis	ASM974908v1	L52	Contig	GCA_009749085.1	GCF_009749085.1	SAMN10219238	PRJNA495104	CG3	2016	China	Homo sapiens	Stool
Proteus mirabilis	ASM971874v1	BIOML-A3	Scaffold	GCA_009718745.1	GCF_009718745.1	SAMN11946305	PRJNA544527	CG24	2014	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM968466v1	ENT1157	Complete Genome	GCA_009684665.1	GCF_009684665.1	SAMN11567705	PRJNA540912	CG16	2014	Singapore	Homo sapiens	Urine
Proteus mirabilis	ASM968463v1	ENT1301	Chromosome	GCA_009684635.1	GCF_009684635.1	SAMN11567707	PRJNA540912	CG115	2014	Singapore	Homo sapiens	Urine
Proteus mirabilis	ASM968459v1	ENT1224	Chromosome	GCA_009684595.1	GCF_009684595.1	SAMN11567706	PRJNA540912	CG16	2014	Singapore	Homo sapiens	Urine
Proteus mirabilis	ASM942904v2	CRE14IB	Complete Genome	GCA_009429045.2	GCF_009429045.2	SAMN13082492	PRJNA578857	CG15	2019	Italy	Homo sapiens	Urine catheter
Proteus mirabilis	ASM918460v1	PmBR19	Contig	GCA_009184605.1	GCF_009184605.1	SAMN12995601	PRJNA576511	CG26	2015	Brazil	Homo sapiens	Urine
Proteus mirabilis	ASM918373v1	PmBR614	Contig	GCA_009183735.1	GCF_009183735.1	SAMN12995603	PRJNA576511	CG30	2015	Brazil	Homo sapiens	Urine
Proteus mirabilis	ASM918370v1	PmBR618	Contig	GCA_009183705.1	GCF_009183705.1	SAMN12995604	PRJNA576511	CG20	2015	Brazil	Homo sapiens	Urine
Proteus mirabilis	ASM918368v1	PmBR595	Contig	GCA_009183685.1	GCF_009183685.1	SAMN12995605	PRJNA576511	CG49	2015	Brazil	Homo sapiens	Urine
Proteus mirabilis	ASM870519v1	K817	Complete Genome	GCA_008705195.1	GCF_008705195.1	SAMN12770272	PRJNA506729	CG14	2002	Poland	Homo sapiens	Cell culture
Proteus mirabilis	ASM863065v1	S1959	Complete Genome	GCA_008630655.1	GCF_008630655.1	SAMN12734738	PRJNA506729	CG13	1987	Poland	Homo sapiens	Cell culture
Proteus mirabilis	ASM819560v1	CRPM10	Complete Genome	GCA_008195605.1	GCF_008195605.1	SAMN12636071	PRJNA562190	CG89	2018	China	Homo sapiens	Urine
Proteus mirabilis	ASM804189v1	VAC	Complete Genome	GCA_008041895.1	GCF_008041895.1	SAMN12566310	PRJNA521327	CG12	2016	France	Unknown	Rectum
Proteus mirabilis	ASM719765v1	CRPM1	Scaffold	GCA_007197655.1	GCF_007197655.1	SAMN12258067	PRJNA554225	CG26	2018	China	Homo sapiens	Urine
Proteus mirabilis	ASM719762v1	CRPM11	Scaffold	GCA_007197625.1	GCF_007197625.1	SAMN12259022	PRJNA554227	CG48	2018	China	Homo sapiens	Sputum
Proteus mirabilis	ASM709709v1	Pm1LENAR	Contig	GCA_007097095.1	GCF_007097095.1	SAMN12216147	PRJNA434210	CG39	2013	France	Homo sapiens	Unknown
Proteus mirabilis	ASM701228v1	CLPM181223	Chromosome	GCA_007012285.1	GCF_007012285.1	SAMN12215362	PRJNA552673	CG47	2018	China	Duck	Others
Proteus mirabilis	ASM651768v1	4748	Contig	GCA_006517685.1	GCF_006517685.1	SAMN09272520	PRJNA473355	CG30	2017	Brazil	Homo sapiens	Swab
Proteus mirabilis	ASM650808v1	BOC1	Contig	GCA_006508085.1	GCF_006508085.1	SAMN09519131	PRJNA478568	CG35	2016	France	Homo sapiens	Bronch
Proteus mirabilis	ASM457078v1	160A10	Contig	GCA_004570785.1	GCF_004570785.1	SAMN10883387	PRJNA521327	CG17	2018	France	Homo sapiens	Urine
Proteus mirabilis	ASM457077v1	S4	Contig	GCA_004570775.1	GCF_004570775.1	SAMN10883394	PRJNA521327	CG12	1996	France	Homo sapiens	Unknown
Proteus mirabilis	ASM457076v1	CNR20130297	Contig	GCA_004570765.1	GCF_004570765.1	SAMN10883395	PRJNA521327	CG46	2013	Belgium	Homo sapiens	Unknown
Proteus mirabilis	ASM457074v1	172J1	Contig	GCA_004570745.1	GCF_004570745.1	SAMN10883390	PRJNA521327	CG12	2018	France	Homo sapiens	Urine
Proteus mirabilis	ASM457071v1	175H8	Contig	GCA_004570715.1	GCF_004570715.1	SAMN10883391	PRJNA521327	CG12	2018	France	Homo sapiens	Urine
Proteus mirabilis	ASM457070v1	188J6	Contig	GCA_004570705.1	GCF_004570705.1	SAMN10883392	PRJNA521327	CG12	2018	France	Homo sapiens	Urine

Proteus mirabilis	ASM457064v1	130688346-L100	Contig	GCA_004570645.1	GCF_004570645.1	SAMN10883399	PRJNA521327	CG12	2016	France	Homo sapiens	Unknown
Proteus mirabilis	ASM457059v1	irhom_Sw	Contig	GCA_004570595.1	GCF_004570595.1	SAMN11126836	PRJNA527079	CG7	2018	United Kingdom	Mus musculus	Swab
Proteus mirabilis	ASM457027v1	130608239-L92	Contig	GCA_004570275.1	GCF_004570275.1	SAMN10883400	PRJNA521327	CG12	2016	France	Homo sapiens	Unknown
Proteus mirabilis	ASM457023v1	CNR20160877	Contig	GCA_004570235.1	GCF_004570235.1	SAMN10883402	PRJNA521327	CG12	2016	Belgium	Homo sapiens	Urine
Proteus mirabilis	ASM457022v1	168F7	Contig	GCA_004570225.1	GCF_004570225.1	SAMN10883388	PRJNA521327	CG12	2018	France	Homo sapiens	Urine
Proteus mirabilis	ASM457021v1	172C2	Contig	GCA_004570215.1	GCF_004570215.1	SAMN10883389	PRJNA521327	CG12	2018	France	Homo sapiens	Blood
Proteus mirabilis	ASM457017v1	CNR20160679	Contig	GCA_004570175.1	GCF_004570175.1	SAMN10883401	PRJNA521327	CG12	2016	Belgium	Homo sapiens	respiratory sample
Proteus mirabilis	ASM457014v1	CNR20160617	Contig	GCA_004570145.1	GCF_004570145.1	SAMN10883403	PRJNA521327	CG12	2016	Belgium	Homo sapiens	Urine
Proteus mirabilis	ASM457007v1	130B9	Contig	GCA_004570075.1	GCF_004570075.1	SAMN10883386	PRJNA521327	CG12	2017	France	Homo sapiens	Unknown
Proteus mirabilis	ASM456924v1	BCT11	Contig	GCA_004569245.1	GCF_004569245.1	SAMN10883407	PRJNA521327	CG12	2017	France	Homo sapiens	Urine
Proteus mirabilis	ASM452250v1	PMS-MEIH	Contig	GCA_004522505.1	GCF_004522505.1	SAMN10820088	PRJNA517134	CG17	2018	Lebanon	Homo sapiens	Unknown
Proteus mirabilis	ASM434758v1	PmOXA23-13	Contig	GCA_004347585.1	GCF_004347585.1	SAMN10038495	PRJNA490489	CG12	2018	France	Homo sapiens	Others
Proteus mirabilis	ASM417939v1	071H3	Scaffold	GCA_004179395.1	GCF_004179395.1	SAMN10840742	PRJNA517688	CG7	2018	France	Homo sapiens	Unknown
Proteus mirabilis	ASM414585v1	GEN000048	Scaffold	GCA_004145855.1	GCF_004145855.1	SAMN10847446	PRJNA517917	CG114	2016	France	Homo sapiens	Unknown
Proteus mirabilis	ASM414539v1	071H2	Scaffold	GCA_004145395.1	GCF_004145395.1	SAMN10840741	PRJNA517688	CG7	2018	France	Homo sapiens	Unknown
Proteus mirabilis	ASM397748v1	GCID_CRE_0016	Contig	GCA_003977485.1	GCF_003977485.1	SAMN10527292	PRJNA508509	CG113	Unknown	Egypt	Unknown	Unknown
Proteus mirabilis	ASM385621v1	PmDJ107	Contig	GCA_003856215.1	GCF_003856215.1	SAMN10458224	PRJNA506344	CG39	2017	China	Chicken	Unknown
Proteus mirabilis	ASM385619v1	PmSN55	Contig	GCA_003856195.1	GCF_003856195.1	SAMN10458210	PRJNA506341	CG20	2017	China	Chicken	Unknown
Proteus mirabilis	ASM385617v1	PmBC55	Contig	GCA_003856175.1	GCF_003856175.1	SAMN10458081	PRJNA506328	CG45	2017	China	Swine	Unknown
Proteus mirabilis	ASM385563v1	PmSC1111	Complete Genome	GCA_003855635.1	GCF_003855635.1	SAMN10458171	PRJNA506338	CG11	2017	China	Swine	Unknown
Proteus mirabilis	ASM385561v1	PmBC1123	Complete Genome	GCA_003855615.1	GCF_003855615.1	SAMN10458127	PRJNA506335	CG10	2017	China	Swine	Unknown
Proteus mirabilis	ASM368808v1	998368	Contig	GCA_003688085.1	GCF_003688085.1	SAMN10252255	PRJNA497260	CG20	2017	Portugal	Homo sapiens	Unknown
Proteus mirabilis	ASM368778v1	1023322	Contig	GCA_003687785.1	GCF_003687785.1	SAMN10252249	PRJNA497260	CG3	2017	USA	Unknown	Unknown
Proteus mirabilis	ASM358350v1	PMWJ	Scaffold	GCA_003583505.1	GCF_003583505.1	SAMN09976767	PRJNA489384	CG3	2018	Unknown	Homo sapiens	CSF
Proteus mirabilis	ASM332294v1	GER_MD10_1505_Pmi_049	Contig	GCA_003322945.1	GCF_003322945.1	SAMN08519252	PRJNA433857	CG44	2015	Germany	Canis lupus familiaris	Stool
Proteus mirabilis	ASM320411v1	AR_0029	Complete Genome	GCA_003204115.1	GCF_003204115.1	SAMN04014870	PRJNA292901	CG9	Unknown	Unknown	Unknown	Unknown
Proteus mirabilis	ASM319430v1	CCUG 70746	Chromosome	GCA_003194305.1	GCF_003194305.1	SAMN07602702	PRJNA401330	CG43	2013	Sweden	Homo sapiens	Stool
Proteus mirabilis	ASM318570v1	11985-2-3	Contig	GCA_003185705.1	GCF_003185705.1	SAMN09270740	PRJNA473071	CG112	2017	United Kingdom	Estuarine mud	Environment
Proteus mirabilis	ASM317649v1	TUM4660	Contig	GCA_003176495.1	GCF_003176495.1	SAMD00115707	PRJDB6851	CG111	2008	Unknown	Homo sapiens	Unknown
Proteus mirabilis	ASM317549v1	TUM11571	Contig	GCA_003175495.1	GCF_003175495.1	SAMD00115676	PRJDB6851	CG6	2012	Unknown	Homo sapiens	Unknown
Proteus mirabilis	ASM317547v1	TUM11570	Contig	GCA_003175475.1	GCF_003175475.1	SAMD00115675	PRJDB6851	CG6	2012	Unknown	Homo sapiens	Unknown
Proteus mirabilis	ASM317545v1	TUM11569	Contig	GCA_003175455.1	GCF_003175455.1	SAMD00115674	PRJDB6851	CG6	2012	Unknown	Homo sapiens	Unknown
Proteus mirabilis	ASM317543v1	TUM11568	Contig	GCA_003175435.1	GCF_003175435.1	SAMD00115673	PRJDB6851	CG6	2012	Unknown	Homo sapiens	Unknown
Proteus mirabilis	ASM317541v1	TUM11567	Contig	GCA_003175415.1	GCF_003175415.1	SAMD00115672	PRJDB6851	CG6	2012	Unknown	Homo sapiens	Unknown
Proteus mirabilis	ASM317169v1	LBUEL-H11	Scaffold	GCA_003171695.1	GCF_003171695.1	SAMN09222159	PRJNA471902	CG1	2015	Brazil	Homo sapiens	respiratory sample
Proteus mirabilis	ASM311489v2	MH13-009N	Contig	GCA_003114895.2	GCF_003114895.2	SAMD00112926	PRJDB6655	CG3	2013	Viet Nam	Homo sapiens	Unknown
Proteus mirabilis	ASM307558v1	AR_0377	Contig	GCA_003075585.1	GCF_003075585.1	SAMN07291520	PRJNA316321	CG32	Unknown	Unknown	Unknown	Unknown
Proteus mirabilis	ASM307393v1	AR379	Complete Genome	GCA_003073935.1	GCF_003073935.1	SAMN07291522	PRJNA316321	CG88	Unknown	Unknown	Homo sapiens	Unknown
Proteus mirabilis	ASM305184v1	K1609	Chromosome	GCA_003051845.1	GCF_003051845.1	SAMN08798891	PRJNA445791	CG110	2000	Poland	Homo sapiens	Unknown
Proteus mirabilis	ASM303094v1	K670	Chromosome	GCA_003030945.1	GCF_003030945.1	SAMN08798946	PRJNA445794	CG42	2000	Poland	Homo sapiens	Unknown
Proteus mirabilis	ASM302474v1	PmPHI	Contig	GCA_003024745.1	GCF_003024745.1	SAMN08541515	PRJNA434210	CG109	2012	France	Homo sapiens	Unknown
Proteus mirabilis	ASM294523v1		Complete Genome	GCA_002945235.1	GCF_002945235.1	SAMN08463802	PRJNA432858	CG87	2014	China	Homo sapiens	Urine

Proteus mirabilis	ASM294449v1	BC11-24	Complete Genome	GCA_002944495.1	GCF_002944495.1	SAMN08450188	PRJNA432494	CG8	2016	China	Pig	Liver
Proteus mirabilis	ASM293621v2	CRK0329	Contig	GCA_002936215.2	GCF_002936215.2	SAMN08513478	PRJNA433394	CG108	2016	USA	Homo sapiens	Body fluid
Proteus mirabilis	ASM286110v1	UMB0315	Contig	GCA_002861105.1	GCF_002861105.1	SAMN08193712	PRJNA316969	CG2	2015	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM241744v1	PM005	Contig	GCA_002417445.1	GCF_002417445.1	SAMN06106876	PRJNA355910	CG107	2013	South Africa	Homo sapiens	Unknown
Proteus mirabilis	ASM236464v1		Scaffold	GCA_002364645.1	GCF_002364645.1	SAMN06451193	PRJNA348753	CG7	Unknown	USA	Homo sapiens	Environment
Proteus mirabilis	ASM231089v1	T18	Complete Genome	GCA_002310895.1	GCF_002310895.1	SAMN05715220	PRJNA340922	CG3	2014	China	Homo sapiens	Urine
Proteus mirabilis	ASM231087v1	T21	Complete Genome	GCA_002310875.1	GCF_002310875.1	SAMN05715221	PRJNA340922	CG3	2013	China	Homo sapiens	Sputum
Proteus mirabilis	ASM226538v1	PM185	Contig	GCA_002265385.1	GCF_002265385.1	SAMN07376741	PRJNA395387	CG6	2016	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM226535v1	PM187	Scaffold	GCA_002265355.1	GCF_002265355.1	SAMN07376756	PRJNA395387	CG106	2016	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM220614v2	FDAARGOS_284	Contig	GCA_002206145.2	GCF_002206145.2	SAMN06173297	PRJNA231221	CG105	2014	USA	Homo sapiens	Others
Proteus mirabilis	ASM219740v1	AR_0156	Complete Genome	GCA_002197405.1	GCF_002197405.1	SAMN04014997	PRJNA292902	CG7	Unknown	Unknown	Unknown	Unknown
Proteus mirabilis	ASM218023v1	AR_0155	Complete Genome	GCA_002180235.1	GCF_002180235.1	SAMN04014996	PRJNA292902	CG6	Unknown	Unknown	Homo sapiens	Unknown
Proteus mirabilis	ASM218011v1	AR_0159	Complete Genome	GCA_002180115.1	GCF_002180115.1	SAMN04015000	PRJNA292902	CG5	Unknown	Unknown	Unknown	Unknown
Proteus mirabilis	ASM205568v1	AR_0059	Complete Genome	GCA_002055685.1	GCF_002055685.1	SAMN04014900	PRJNA292904	CG4	Unknown	Unknown	Unknown	Unknown
Proteus mirabilis	ASM186732v1	1091	Contig	GCA_001867325.1	GCF_001867325.1	SAMN05513636	PRJNA337898	CG12	2015	Belgium	Homo sapiens	Blood
Proteus mirabilis	ASM185818v1	T1C	Contig	GCA_001858185.1	GCF_001858185.1	SAMN05383975	PRJNA328901	CG104	2013	Malaysia	Homo sapiens	Others
Proteus mirabilis	ASM165384v1	PM_178	Contig	GCA_001653845.1	GCF_001653845.1	SAMN04901710	PRJNA319626	CG3	2013	Malaysia	Homo sapiens	Urine
Proteus mirabilis	ASM165383v1	PM_125	Contig	GCA_001653835.1	GCF_001653835.1	SAMN04901708	PRJNA319626	CG3	2013	Malaysia	Homo sapiens	Urine
Proteus mirabilis	ASM164375v1	Wood	Contig	GCA_001643755.1	GCF_001643755.1	SAMN02900469	PRJNA254158	CG103	2010	USA	Homo sapiens	Others
Proteus mirabilis	ASM164098v1	AOUC-001	Complete Genome	GCA_001640985.1	GCF_001640985.1	SAMN04849770	PRJNA318385	CG3	2013	Italy	Homo sapiens	Blood
Proteus mirabilis	ASM161979v1	M16	Contig	GCA_001619795.1	GCF_001619795.1	SAMN04390157	PRJNA308262	CG102	2011	Malaysia	Unknown	Environment
Proteus mirabilis	ASM161730v1	GB11	Scaffold	GCA_001617305.1	GCF_001617305.1	SAMN04395120	PRJNA308382	CG11	2012	China	Homo sapiens	Urine
Proteus mirabilis	ASM161729v1	GB08	Contig	GCA_001617295.1	GCF_001617295.1	SAMN04395118	PRJNA308381	CG3	2012	China	Homo sapiens	Urine
Proteus mirabilis	ASM160470v1	C02011	Contig	GCA_001604705.1	GCF_001604705.1	SAMN03418023	PRJNA278352	CG101	2002	China	Homo sapiens	Others
Proteus mirabilis	ASM155352v1	GED7834	Scaffold	GCA_001553525.1	GCF_001553525.1	SAMN03948578	PRJNA272095	CG41	Unknown	Unknown	Homo sapiens	Others
Proteus mirabilis	ASM146302v1	50664164	Contig	GCA_001463025.1	GCF_001463025.1	SAMN04158302	PRJNA295003	CG24	2012	Norway	Homo sapiens	Urine
Proteus mirabilis	ASM146247v1	PM655	Contig	GCA_001462475.1	GCF_001462475.1	SAMN03154481	PRJNA266008	CG40	2013	Ireland	Homo sapiens	Urine
Proteus mirabilis	ASM146238v1	PM593	Contig	GCA_001462385.1	GCF_001462385.1	SAMN03154486	PRJNA266009	CG39	2013	Ireland	Homo sapiens	Swab
Proteus mirabilis	ASM144844v1	NO-051/03	Contig	GCA_001448445.1	GCF_001448445.1	SAMN03840807	PRJNA289042	CG3	2003	Italy	Homo sapiens	Skin
Proteus mirabilis	ASM128156v1	CYPV1	Complete Genome	GCA_001281565.1	GCF_001281565.1	SAMN03968923	PRJNA292343	CG3	2012	China: Taiwan	Homo sapiens	Sputum
Proteus mirabilis	ASM128154v1	CYPM1	Complete Genome	GCA_001281545.1	GCF_001281545.1	SAMN03968924	PRJNA292344	CG3	2012	China: Taiwan	Homo sapiens	Urine
Proteus mirabilis	ASM107710v1	646_PMIR	Scaffold	GCA_001077105.1	GCF_001077105.1	SAMN03197847	PRJNA267549	CG30	Unknown	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM107675v1	430_PMIR	Scaffold	GCA_001076755.1	GCF_001076755.1	SAMN03197624	PRJNA267549	CG38	Unknown	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM107671v1	429_PMIR	Scaffold	GCA_001076715.1	GCF_001076715.1	SAMN03197622	PRJNA267549	CG38	Unknown	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM107670v1	418_PMIR	Scaffold	GCA_001076705.1	GCF_001076705.1	SAMN03197609	PRJNA267549	CG100	Unknown	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM107669v1	373_PMIR	Scaffold	GCA_001076695.1	GCF_001076695.1	SAMN03197564	PRJNA267549	CG37	Unknown	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM106685v1	672_PMIR	Contig	GCA_001066855.1	GCF_001066855.1	SAMN03197875	PRJNA267549	CG99	Unknown	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM106591v1	68_PMIR	Contig	GCA_001065915.1	GCF_001065915.1	SAMN03197882	PRJNA267549	CG35	Unknown	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM106508v1	47_PMIR	Scaffold	GCA_001065085.1	GCF_001065085.1	SAMN03197664	PRJNA267549	CG35	Unknown	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM106437v1	292_PMIR	Scaffold	GCA_001064375.1	GCF_001064375.1	SAMN03197486	PRJNA267549	CG36	Unknown	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM106410v1	25_PMIR	Scaffold	GCA_001064105.1	GCF_001064105.1	SAMN03197440	PRJNA267549	CG98	Unknown	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM106357v1	51_PMIR	Contig	GCA_001063575.1	GCF_001063575.1	SAMN03197703	PRJNA267549	CG35	Unknown	USA	Homo sapiens	Unknown

Proteus mirabilis	ASM106320v1	360_PMIR	Scaffold	GCA_001063205.1	GCF_001063205.1	SAMN03197551	PRJNA267549	CG21	Unknown	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM106303v1	232_PMIR	Scaffold	GCA_001063035.1	GCF_001063035.1	SAMN03197423	PRJNA267549	CG4	Unknown	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM106274v1	1330_PMIR	Scaffold	GCA_001062745.1	GCF_001062745.1	SAMN03197311	PRJNA267549	CG3	Unknown	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM106265v1	1313_PMIR	Scaffold	GCA_001062655.1	GCF_001062655.1	SAMN03197290	PRJNA267549	CG34	Unknown	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM106238v1	1230_SSON	Contig	GCA_001062385.1	GCF_001062385.1	SAMN03197195	PRJNA267549	CG97	Unknown	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM106213v1	1166_PMIR	Scaffold	GCA_001062135.1	GCF_001062135.1	SAMN03197123	PRJNA267549	CG34	Unknown	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM106159v1	1326_PMIR	Scaffold	GCA_001061595.1	GCF_001061595.1	SAMN03197306	PRJNA267549	CG3	Unknown	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM106083v1	1293_PMIR	Scaffold	GCA_001060835.1	GCF_001060835.1	SAMN03197265	PRJNA267549	CG34	Unknown	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM106076v1	127_PMIR	Scaffold	GCA_001060765.1	GCF_001060765.1	SAMN03197238	PRJNA267549	CG96	Unknown	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM106035v1	1150_PMIR	Scaffold	GCA_001060355.1	GCF_001060355.1	SAMN03197106	PRJNA267549	CG33	Unknown	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM106032v1	1134_PMIR	Scaffold	GCA_001060325.1	GCF_001060325.1	SAMN03197088	PRJNA267549	CG33	Unknown	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM106028v1	1114_PMIR	Scaffold	GCA_001060285.1	GCF_001060285.1	SAMN03197068	PRJNA267549	CG2	Unknown	USA	Homo sapiens	Unknown
Proteus mirabilis	ASM97266v1	25933 GTA	Contig	GCA_000972665.1	GCF_000972665.1	SAMN03437553	PRJNA254477	CG95	2013	Canada	Unknown	Others
Proteus mirabilis	ASM78401v2	FDAARGOS_60	Complete Genome	GCA_000784015.2	GCF_000784015.2	SAMN02934509	PRJNA231221	CG2	2013	USA	Homo sapiens	Swab
Proteus mirabilis	ASM78387v2	FDAARGOS_67	Complete Genome	GCA_000783875.2	GCF_000783875.2	SAMN02934516	PRJNA231221	CG1	2013	USA	Homo sapiens	Wound
Proteus mirabilis	ASM78359v2	FDAARGOS_80	Complete Genome	GCA_000783595.2	GCF_000783595.2	SAMN02934535	PRJNA231221	CG86	2013	USA	Homo sapiens	Swab
Proteus mirabilis	ASM78357v2	FDAARGOS_81	Complete Genome	GCA_000783575.2	GCF_000783575.2	SAMN02934536	PRJNA231221	CG49	2013	USA	Homo sapiens	Urine
Proteus mirabilis	ASM78346v2	FDAARGOS_85	Contig	GCA_000783465.2	GCF_000783465.2	SAMN02934539	PRJNA231221	CG30	2013	USA	Homo sapiens	Urine catheter
Proteus mirabilis	ASM77076v1	Pm-Oxa48	Contig	GCA_000770765.1	GCF_000770765.1	SAMN03140307	PRJNA264732	CG32	2012	Gaza Strip	Homo sapiens	Urine
Proteus mirabilis	ASM75548v1	ATCC 7002	Scaffold	GCA_000755485.1	GCF_000755485.1	SAMN02870743	PRJNA244573	CG2	Unknown	Unknown	Unknown	Unknown
Proteus mirabilis	ASM44442v1	BB2000	Complete Genome	GCA_000444425.1	GCF_000444425.1	SAMN02603303	PRJNA183065	CG85	Unknown	USA	Homo sapiens	Others
Proteus mirabilis	PM version 1	PR03	Contig	GCA_000372565.1	GCF_000372565.1	SAMN02469777	PRJNA185396	CG31	2009	Malaysia	Homo sapiens	Blood
Proteus mirabilis	Version 1 for Proteus mirabilis C05028 genome	C05028	Scaffold	GCA_000313255.1	GCF_000313255.1	SAMN02470975	PRJNA178083	CG3	2005	China	Homo sapiens	Stool
Proteus mirabilis	Prot_mira_WGLW4_V1	WGLW4	Scaffold	GCA_000297835.1	GCF_000297835.1	SAMN02463960	PRJNA169467	CG30	Unknown	Unknown	Unknown	Unknown
Proteus mirabilis	Prot_mira_WGLW6_V1	WGLW6	Scaffold	GCA_000297815.1	GCF_000297815.1	SAMN02463961	PRJNA169468	CG29	Unknown	Unknown	Unknown	Unknown
Proteus mirabilis	ASM16075v1	ATCC 29906	Scaffold	GCA_000160755.1	GCF_000160755.1	SAMN00001486	PRJNA31523	CG13	Unknown	Unknown	Homo sapiens	Unknown

Supplementary Table S3. Distribution of 159 unique clonal groups (CGs) in 16 countries or regions

Clonal group (CGs)	Geographic location																
	USA	China	Denmark	France	Hong kong, China	Czech Republic	Germany	United Kingdom	Poland	Canada	Singapore	Malaysia	Spain	Egypt	Sweden	South Africa	Unknown
CG99	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG98	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG97	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG96	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG86	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG85	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG200	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG198	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG182	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG181	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG180	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG179	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG178	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG177	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG176	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG175	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG174	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG173	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG172	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG171	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG170	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG169	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG168	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG167	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG166	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG165	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG164	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG163	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG162	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG161	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG160	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG155	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG154	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG153	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG152	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG151	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG150	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG149	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

CG148	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG147	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG146	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG145	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG144	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG143	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG142	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG141	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG140	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG139	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG138	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG137	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG136	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG135	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG134	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG133	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG132	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG131	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG130	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG129	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG128	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG127	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG126	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG125	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG124	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG123	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG117	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG116	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG108	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG106	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG105	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG103	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG100	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG50	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG52	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG82	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG53	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG65	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG84	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG77	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG75	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG74	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

CG72	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG71	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG67	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG66	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG63	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG62	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG60	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG59	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG58	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG57	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG56	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG54	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG51	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG38	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG37	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG36	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG34	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG33	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG94	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
CG205	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
CG112	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
CG204	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
CG107	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
CG43	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
CG16	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
CG115	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
CG110	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
CG104	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
CG102	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
CG81	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
CG92	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
CG199	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
CG114	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
CG109	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
CG113	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
CG195	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
CG194	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
CG193	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
CG192	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
CG191	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
CG190	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
CG189	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0

CG188	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
CG187	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
CG186	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
CG185	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
CG184	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
CG183	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
CG118	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
CG93	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG91	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG89	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG87	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG197	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG196	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG122	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG121	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG120	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG119	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG101	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG22	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG27	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG83	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG45	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG19	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CG95	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
CG90	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
CG88	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
CG203	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
CG202	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
CG201	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
CG159	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
CG158	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
CG157	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
CG156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
CG111	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
CG70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
CG69	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1

Note."1" means that a clonal group exists in a certain country or region, and "0" means it does not exist.

Supplementary Table S4. Distribution of the subtypes of 64 virulence gene types among the 205 clonal groups (CGs)

Virulence gene	Clonal groups (CGs)																																																
	CG2	CG	CG6	CG14	CG7	CG	CG1	CG12	CG10	CG9	CG9	CG9	CG9	CG9	CG9	CG9	CG9	CG9	CG9	CG	CG8	CG8	CG8	CG8	CG8	CG8	CG8	CG8	CG8	CG8	CG	CG7	CG7	CG7	CG7	CG7	CG7	CG7	CG7	CG7	CG	CG6	CG6	CG6	CG6	CG6	CG6	CG6	CG6	CG6
	0	6	7	1	0	3	7	0	6	9	8	7	6	5	4	3	2	1	0	9	9	8	7	6	5	4	3	2	1	0	8	9	8	7	6	5	4	3	2	1	7	9	8	6	5	4	3	2	1	0
astA	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cap8E	0	0	1	0	0	1	1	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
cheB	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
cheW	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
cheY	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
cheZ	1	1	1	0	1	0	0	1	0	0	0	0	1	0	0	0	0	0	1	0	0	1	0	0	0	1	1	0	0	0	0	0	0	1	0	1	1	0	0	0	0	1	0	0	0	0	1	0	0	1
chuT	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
chuU	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
chuV	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
chuW	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
chuX	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
clpP	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cnf1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
flgC	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
flgG	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
flgH	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
flgI	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
flhA	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
flhC	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
flhD	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliA	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliG	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliI	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliM	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliN	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliP	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliQ	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
fliZ	1	1	0	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
galU	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
gmhA/lpcA	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
gtrB	1	0	1	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
hcp-2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	1	1
hlyA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
hlyB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
hlyC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
hlyD	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
htpB	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
ipaH1.4	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

katA	0	0	0	1	0	1	1	0	0	0	0	0	1	1	0	0	1	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	1	0	0	0	1	0	1	0	0	0	1	0	0	0	0	1	0	1
kdsA	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
lpxC	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
lpxD	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
luxS	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
motA	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ompA	1	1	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
papB	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papC	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papD	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papE	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papF	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papG	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papH	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papI	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papJ	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papK	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
pilU	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rfaD	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
rfaE	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
shuX	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
shuY	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sodB	1	1	0	0	1	1	1	0	1	1	1	1	0	0	1	0	1	1	0	1	0	1	1	1	0	1	0	0	0	1	0	0	0	0	1	1	0	1	1	1	1	1	1	1	1	1	1	0	1	1
ureG	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
vipB/mglB	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	1	1
yopJ/yopP	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Supplementary Table S4 continued

Virulence gene	Clonal groups (CGs)																																																	
	CG59	CG58	CG57	CG56	CG55	CG54	CG53	CG52	CG51	CG50	CG5	CG49	CG48	CG47	CG46	CG45	CG44	CG43	CG42	CG41	CG40	CG4	CG39	CG38	CG37	CG36	CG35	CG34	CG33	CG32	CG31	CG30	CG29	CG28	CG27	CG26	CG25	CG24	CG23	CG22	CG21	CG205	CG204	CG203	CG202	CG201	CG200	CG2	CG199	CG198	CG197
astA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cap8E	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cheB	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
cheW	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
cheY	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
cheZ	0	0	1	0	1	0	0	0	1	1	0	0	0	1	1	1	1	0	1	0	1	1	1	0	0	0	1	1	1	1	0	1	0	1	0	0	0	1	1	1	0	0	0	1	1	0	1	0	0	1	0
chuT	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
chuU	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
chuV	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
chuW	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
chuX	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0

clpP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cnf1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
flgC	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1
flgG	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
flgH	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
flgI	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
flhA	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
flhC	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
flhD	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliA	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliG	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliI	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliM	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliN	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliP	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliQ	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
fliZ	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
galU	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
gmhA/lpcA	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
gtrB	0	0	0	0	0	0	0	0	0	1	0	0	1	0	1	1	0	1	1	0	0	0	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0
hcp-2	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	1	1	1	1
hlyA	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
hlyB	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
hlyC	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
hlyD	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
htpB	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
ipaH1.4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
katA	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	1	0	0	0	1
kdsA	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
lpxC	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
lpxD	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
luxS	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
motA	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ompA	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
papB	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papD	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papF	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papH	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papI	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

papJ	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papK	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
pilU	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rfaD	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
rfaE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
shuX	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
shuY	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sodB	1	1	1	0	0	1	1	1	1	1	1	1	0	0	1	1	1	1	1	1	0	1	0	1	0	1	1	0	1	1	1	1	1	1	1	1	0	1	0	0	1	0	0	0	1	1	1	1	0	0	1
ureG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
vipB/mglB	1	1	1	0	1	1	0	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1
yopJ/yopP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Supplementary Table S4 continued

Virulence gene	Clonal groups (CGs)																																																		
	CG1 96	CG1 95	CG1 94	CG1 93	CG1 92	CG1 91	CG1 90	CG 19	CG1 89	CG1 88	CG1 87	CG1 86	CG1 85	CG1 84	CG1 83	CG1 82	CG1 81	CG1 80	CG 18	CG1 79	CG1 78	CG1 77	CG1 76	CG1 75	CG1 74	CG1 73	CG1 72	CG1 71	CG1 70	CG1 69	CG1 68	CG1 67	CG1 66	CG1 65	CG1 64	CG1 63	CG1 62	CG1 61	CG1 60	CG 16	CG1 59	CG1 58	CG1 57	CG1 56	CG1 55	CG1 54	CG1 53	CG1 52	CG1 51	CG1 50	CG 15	CG1 49
astA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cap8E	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	1	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
cheB	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
cheW	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
cheY	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
cheZ	0	1	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	1	0	1	0	0	1	0	0	0	0	1	1	0	0	0	1	0	1	0	0	0	0	1	1	0	1	0	0	0	0	0	1	0	1	1
chuT	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
chuU	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
chuV	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
chuW	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
chuX	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
clpP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cnf1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
flgC	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1
flgG	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
flgH	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
flgI	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
flhA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
flhC	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
flhD	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliA	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliG	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliI	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliM	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliN	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliP	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliQ	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0

fliZ	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
galU	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
gmhA/lpc																																																				
A	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
gtrB	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
hcp-2	1	1	0	1	1	0	1	1	1	1	1	1	0	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	0	1	1	1	1	1	1	1	0	1	1	0	1	1
hlyA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
hlyB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
hlyC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
hlyD	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
htpB	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
ipaH1.4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
katA	1	0	1	0	0	0	0	0	0	0	1	0	1	0	1	0	0	1	1	1	0	0	0	0	0	0	1	1	1	0	0	1	1	1	0	0	0	0	0	0	0	0	0	1	1	1	0	0	1	1	0	0
kdsA	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
lpxC	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
lpxD	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
luxS	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
motA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ompA	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
papB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papD	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papF	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papH	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papI	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papJ	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papK	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
pilU	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rfaD	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
rfaE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
shuX	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
shuY	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sodB	1	0	1	1	0	1	1	1	0	0	1	1	1	1	1	1	1	0	1	0	0	0	1	1	0	1	1	0	0	0	1	1	1	1	1	0	0	1	1	1	1	0	1	1	1	1	1	0	1	0	0	1
ureG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
vipB/mgl																																																				
B	1	1	0	1	1	1	1	1	1	1	1	1	0	1	1	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	0	1	1
yopJ/yop																																																				
P	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Supplementary Table S4 continued

Virulence gene	Clonal groups (CGs)																																																										
	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG	C
	48	47	46	45	44	43	42	40	14	39	38	37	36	35	34	33	32	31	30	13	29	28	27	26	25	24	23	22	21	12	19	18	17	16	15	14	13	12	11	10	11	09	08	07	05	04	03	02	01	00	10	G1
astA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cap8E	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	1	0	1	0	0	0
cheB	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
cheW	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
cheY	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
cheZ	0	1	1	1	0	0	0	1	0	0	1	1	1	0	0	1	0	0	0	0	0	1	0	0	0	0	0	1	0	1	0	1	1	0	0	1	0	0	1	1	0	0	1	0	1	0	0	1	0	0	0	1
chuT	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
chuU	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
chuV	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
chuW	0	1	1	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
chuX	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
clpP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cnf1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
flgC	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1
flgG	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
flgH	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
flgI	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
flhA	0	1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
flhC	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
flhD	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliA	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliG	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliI	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliM	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliN	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliP	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
fliQ	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
fliZ	1	0	0	1	1	1	1	1	0	1	1	0	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1
galU	1	0	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1
gmhA/lpcA	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
gtrB	0	0	0	0	0	0	0	0	1	0	0	0	1	0	1	1	0	0	1	1	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0	0	1
hcp-2	1	1	1	0	1	1	1	1	1	1	1	1	0	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
hlyA	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
hlyB	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
hlyC	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
hlyD	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
htpB	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
ipaH1.4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

katA	0	0	0	1	0	1	0	0	0	1	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	1	0	1	1	0	1	0	0	1	0	0	0	0	0	1	0	0	1	0	0	0	1	1	1	1
kdsA	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
lpxC	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
lpxD	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
luxS	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
motA	0	1	1	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
ompA	1	0	0	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1
papB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
papC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papD	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papF	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papH	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papI	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papJ	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
papK	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
pilU	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rfaD	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
rfaE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
shuX	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
shuY	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sodB	0	0	0	1	1	1	0	1	1	1	1	0	0	1	1	0	1	0	1	1	1	0	1	0	0	0	0	1	0	0	1	1	0	0	1	1	0	1	0	0	0	1	1	1	0	0	0	1	1	1	1	1
ureG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
vipB/mglB	1	1	1	0	1	1	0	1	1	1	1	1	0	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
yopJ/yop																																																				
P	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Note. "1" means that a clonal group exists in a certain country or region, and "0" means it does not exist.

Supplementary Table S5. Distribution of the subtypes of 156 antibiotic resistance genes among the 205 clonal groups (CGs)

	Clonal groups (CGs)																																																					
Resistance gene	CG	CG2	CG2	CG3	CG	CG4	CG4	CG8	CG1	CG	CG	CG	CG6	CG6	CG4	CG2	CG1	CG1	CG	CG1	CG3	CG7	CG3	CG4	CG5	CG3	CG2	CG5	CG8	CG2	CG2	CG2	CG5	CG	CG2	CG6	CG7	CG8	CG8	CG8	CG	CG7	CG7	CG7	CG7	CG7	CG7	CG7	CG7	CG6	CG6	CG6
	3	0	9	2	6	9	1	0	2	7	4	1	1	8	8	8	1	07	2	7	0	9	9	2	0	5	4	2	2	2	3	6	3	9	7	5	3	4	3	1	8	8	7	6	5	4	2	1	0	9	7	6
AAC(2')-IIa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(3)-IId	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(3)-IIe	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(3)-IV	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	1	1	1	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0
AAC(3)-Ia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(3)-Id	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-IIa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-IIc	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-Ian	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-Ib-cr	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	1	0	0	0	1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-Ib10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-Ib7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-Ib9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-II	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANT(2'')-Ia	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANT(3'')-IIa	1	0	1	1	1	0	0	0	1	0	1	0	0	0	0	0	1	0	0	1	0	0	1	0	0	0	1	0	0	1	1	0	0	1	1	1	0	0	1	0	1	1	0	0	1	1	0	0	0	0	0	0	0
APH(3'')-Ib	1	0	1	0	0	0	0	1	1	0	0	0	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
APH(3')-IIa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
APH(3')-Ia	1	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0
APH(3')-VI	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
APH(3')-VIa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
APH(4)-Ia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	1	1	1	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0
APH(6)-Id	1	0	1	0	0	0	0	1	1	0	0	0	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
CARB-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
CMY-59	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CRP	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
CTX-M-1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-121	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-89	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DHA-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0

EreA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Erm(42)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ErmB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Escherichia_coli_mdfA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FosA3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
H-NS	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
IMP-27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
KPC-1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
KPC-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
KPC-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Klebsiella_pneumoniae_KpnE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MCR-4.3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MCR-9	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NDM-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
NDM-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NDM-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OXA-1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
OXA-10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OXA-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OXA-23	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OXA-48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OXA-58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OXA-9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PER-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QepA2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QnrA1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QnrB17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QnrB5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QnrB58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QnrD1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
QnrD2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QnrS1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SAT-1	1	0	1	1	1	0	0	0	1	0	1	0	0	0	0	0	0	0	1	0	0	1	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0
SCO-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SHV-105	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SHV-134	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SHV-187	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-1	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
TEM-104	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-122	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-131	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

TEM-141	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-150	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-79	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-92	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tet(X4)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VEB-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VIM-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VIM-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA2	0	1	1	0	0	0	0	0	0	0	1	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	1	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0
aadA3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA5	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA8b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
acrB	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
aphA15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
armA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arr-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arr-3	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	1	0	0	0	1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
catA4	1	1	1	1	1	1	1	1	1	0	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	0	1	1	1	1	0	1	1	1	1	1	0	1	1	1	0	0
catB11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catB2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catB3	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
catI	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
catII	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catII_from_Escherichia_coli_																																																						
K-12	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cfrA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
cmlA1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
cmlA5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cmlA6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
cpxA	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
determinant_of_bleomycin_r																																																						
esistance	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
dfrA1	1	0	1	1	1	0	0	0	1	0	1	0	0	0	0	0	1	0	0	1	0	0	1	0	0	0	1	0	0	1	1	0	0	1	0	0	0	0	1	0	1	0	0	0	0	1	0	0	0	0	0	0
dfrA10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

dfrA16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
dfrA17	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA19	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
emrR	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0
floR	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	1	1	0	0	0	0	0	0	0	0	1	0	0	1	1	1	0	0	0	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0
linG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
lnuF	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0
lnuG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
mphA	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
mphE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0
msbA	0	0	0	1	1	0	1	0	1	1	1	1	1	0	1	1	1	1	1	0	0	1	1	1	1	0	0	1	1	0	1	1	1	0	0	1	1	1	1	1	1	1	1	0	0	1	0	0	0	1	1	1
msrE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0
oqxA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
oqxB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
qacH	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
rmtB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rosA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
rosB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sul1	1	1	1	1	0	0	0	1	0	0	1	0	0	0	1	1	1	1	0	0	0	0	0	0	0	0	1	0	0	1	1	1	0	1	1	0	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0
sul2	1	0	1	0	0	0	0	1	1	0	0	0	0	0	1	1	1	1	0	1	0	0	0	0	0	0	0	0	0	1	1	1	0	1	0	1	0	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0
sul3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
tet(A)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet(B)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet(C)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet(D)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet(G)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet(H)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet(J)	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1
tet(Y)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tetM	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ugd	0	0	1	1	1	1	1	1	1	0	1	1	0	1	1	1	1	1	1	0	1	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	0	1	1	1	1	0	1	1	0	1	1	1
vanRA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Supplementary Table S5 continued

	Clonal groups (CGs)																																																			
Resistance gene	CG 63	CG 62	CG 60	CG 59	CG 58	CG 57	CG 56	CG 55	CG 54	CG 51	CG 5	CG 47	CG 46	CG 45	CG 44	CG 43	CG 40	CG 38	CG 37	CG 36	CG 34	CG 33	CG 31	CG 25	CG 21	CG 19	CG 18	CG 16	CG 15	CG 14	CG 13	CG 10	CG 64	CG2 05	CG2 04	CG 94	CG2 03	CG2 02	CG2 01	CG2 00	CG1 99	CG1 98	CG1 97	CG1 96	CG1 95	CG1 94	CG1 93	CG1 92	CG1 91	CG1 90	CG1 89	CG1 88
AAC(2')-IIa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(3)-IId	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

AAC(3)-IIe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(3)-IV	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(3)-Ia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(3)-Id	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-IIa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-IIc	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-Ian	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-Ib-cr	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	1	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-Ib10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
AAC(6')-Ib7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-Ib9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-II	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANT(2'')-Ia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0
ANT(3'')-IIa	0	0	1	0	0	0	1	0	0	0	0	0	1	1	0	1	1	0	0	0	0	0	0	0	0	1	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1
APH(3'')-Ib	0	0	0	0	0	0	0	0	0	0	1	1	0	1	0	1	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0
APH(3')-IIa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
APH(3')-Ia	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	1	0	1	0	0	0	1	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
APH(3')-VI	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
APH(3')-VIa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
APH(4)-Ia	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
APH(6)-Id	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	1	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0
CARB-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CMY-59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CRP	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
CTX-M-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-121	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-89	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DHA-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
EreA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Erm(42)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ErmB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Escherichia_coli_mdfA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FosA3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
H-NS	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1

IMP-27	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
KPC-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
KPC-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
KPC-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Klebsiella_pneumoniae_Kpn E	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
MCR-4.3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MCR-9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NDM-1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
NDM-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NDM-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OXA-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OXA-10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OXA-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OXA-23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OXA-48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OXA-58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OXA-9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PER-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QepA2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QnrA1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
QnrB17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QnrB5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QnrB58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QnrD1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	0
QnrD2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QnrS1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SAT-1	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0	0
SCO-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SHV-105	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SHV-134	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SHV-187	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	1	0	0	0
TEM-104	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-122	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-131	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-141	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-150	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-79	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-92	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Tet(X4)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VEB-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
VIM-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VIM-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA2	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	1	0	0	0	0	0	0	0	1	0	1	1	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
aadA3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA8b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
acrB	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
aphA15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
armA	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arr-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arr-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	1	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catA4	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
catB11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
catB2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catB3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catI	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
catII	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catII_from_Escherichia_col																																																				
i_K-12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cfrA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cmlA1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cmlA5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cmlA6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cpxA	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
determinant_of_bleomyci																																																				
n_resistance	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
dfrA1	0	0	1	0	0	0	0	0	0	0	1	0	0	1	0	0	1	1	0	0	0	0	0	0	0	1	1	0	1	0	0	1	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	1	0
dfrA10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA12	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	1	0	0	0	0	0	0	0	0	0	1	1	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

dfrA5	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
dfrA7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
emrR	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
floR	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	1	0	0	0	0	0	0	0	1	0	1	1	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
linG	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
lnuF	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
lnuG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
mphA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
mphE	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
msbA	0	1	0	0	1	1	0	1	0	0	1	0	1	1	1	0	1	1	0	1	1	1	1	1	0	1	0	0	1	1	1	0	1	1	1	1	1	0	0	1	1	0	1	0	1	0	1	1	1	1	1	1
msrE	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
oqxA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
oqxB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
qacH	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rmtB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rosA	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rosB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sul1	0	0	0	0	0	0	0	1	0	0	1	0	1	1	0	1	1	1	0	0	0	0	0	1	0	1	1	0	0	1	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	1	1	0
sul2	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	1	0	1	0	0	0	0	0	1	0	1	1	0	0	1	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0
sul3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet(A)	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0
tet(B)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
tet(C)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet(D)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet(G)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet(H)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet(J)	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1
tet(Y)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tetM	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ugd	0	0	1	1	1	1	0	1	1	0	0	1	1	0	0	0	0	0	1	1	1	1	1	1	0	0	0	1	0	1	1	1	0	1	1	0	0	1	1	1	1	1	1	1	1	1	1	1	0	0	1	0
vanRA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Supplementary Table S5 continued

Resistance gene	Clonal groups (CGs)																																																			
	CG187	CG186	CG185	CG184	CG183	CG93	CG182	CG181	CG180	CG92	CG179	CG178	CG177	CG176	CG175	CG174	CG173	CG172	CG171	CG170	CG169	CG168	CG167	CG166	CG165	CG164	CG163	CG162	CG161	CG160	CG159	CG158	CG157	CG156	CG155	CG154	CG153	CG152	CG151	CG150	CG149	CG148	CG147	CG146	CG145	CG144	CG143	CG142	CG141	CG140	CG139	CG138
AAC(2')-IIa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(3)-IId	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(3)-IIe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(3)-IV	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(3)-Ia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(3)-Id	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-IIa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

AAC(6')-IIc	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-Ian	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-Ib-cr	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-Ib10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-Ib7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-Ib9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-II	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANT(2'')-Ia	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
ANT(3'')-IIa	0	0	0	0	0	0	1	1	1	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
APH(3'')-Ib	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
APH(3')-IIa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
APH(3')-Ia	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
APH(3')-VI	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
APH(3')-VIa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
APH(4)-Ia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
APH(6)-Id	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CARB-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CMY-59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CRP	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
CTX-M-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-121	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-89	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DHA-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
EreA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Erm(42)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ErmB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Escherichia_coli_mdfA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FosA3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
H-NS	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1
IMP-27	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
KPC-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
KPC-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
KPC-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Klebsiella_pneumoniae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

_KpnE																																																					
MCR-4.3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MCR-9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NDM-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NDM-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NDM-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OXA-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OXA-10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OXA-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OXA-23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OXA-48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OXA-58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OXA-9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PER-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QepA2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QnrA1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QnrB17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QnrB5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QnrB58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QnrD1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
QnrD2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QnrS1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SAT-1	0	0	0	0	0	0	1	1	1	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
SCO-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SHV-105	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SHV-134	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SHV-187	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
TEM-104	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-122	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-131	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-141	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-150	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-79	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-92	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tet(X4)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VEB-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VIM-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VIM-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

aadA15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
aadA3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA8b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
acrB	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
aphA15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
armA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arr-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arr-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catA4	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	0	0	1	1	1	1	0	1	0	1
catB11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catB2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catB3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catI	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catII	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catII_from_Escherichia_																																																				
coli_K-12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cfrA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cmlA1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cmlA5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cmlA6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cpxA	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
determinant_of_bleom																																																				
ycin_resistance	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
dfrA10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
emrR	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
floR	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
linG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

lnuF	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
lnuG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
mphA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
mphE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
msbA	0	0	1	1	1	0	0	1	0	0	0	1	1	1	1	1	1	1	0	0	1	1	1	1	1	1	1	0	1	1	0	1	0	0	1	0	1	1	0	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1
msrE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
oqxA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
oqxB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
qacH	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rmtB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rosA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
rosB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sul1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
sul2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sul3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet(A)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet(B)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet(C)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet(D)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet(G)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
tet(H)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
tet(J)	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	0	1	1	1	1	1	1	1	0	0	1	1	1	1	0	1	1	1
tet(Y)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tetM	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ugd	0	1	1	0	0	1	0	1	0	1	1	1	1	1	0	1	0	1	1	1	1	1	0	0	1	0	1	1	1	0	1	1	0	0	0	1	1	1	1	1	1	0	1	1	1	1	1	1	0	0	1	1	1	0	0	1	1
vanRA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Supplementary Table S5 continued

Resistance gene	Clonal groups (CGs)																																															
	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG	CG1	CG1	CG1	CG	CG1	CG	CG1	CG1	CG1	CG1	CG	CG1	CG1	CG	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG1	CG	CG	CG	CG	CG	CG	CG
	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	91	18	17	16	90	15	89	14	13	12	11	88	10	09	87	08	06	05	04	03	02	01	00	99	98	97	96	95	86	85
AAC(2')-IIa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(3)-IId	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(3)-IIe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(3)-IV	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(3)-Ia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(3)-Id	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-IIa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-IIc	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-Ian	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-Ib-cr	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-Ib10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-Ib7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

AAC(6')-Ib9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAC(6')-II	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANT(2'')-Ia	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANT(3'')-IIa	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0
APH(3'')-Ib	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0
APH(3')-IIa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
APH(3')-Ia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
APH(3')-VI	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
APH(3')-VIa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
APH(4)-Ia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
APH(6)-Id	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0
CARB-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CMY-59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CRP	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
CTX-M-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-121	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-89	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTX-M-9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DHA-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
EreA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Erm(42)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ErmB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Escherichia_coli_mdfA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FosA3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
H-NS	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
IMP-27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
KPC-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
KPC-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
KPC-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Klebsiella_pneumoniae_Kpn E	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MCR-4.3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MCR-9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NDM-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NDM-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

NDM-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OXA-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OXA-10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OXA-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OXA-23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OXA-48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OXA-58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
OXA-9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PER-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QepA2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QnrA1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QnrB17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QnrB5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QnrB58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QnrD1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
QnrD2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QnrS1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SAT-1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0
SCO-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SHV-105	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SHV-134	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SHV-187	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0
TEM-104	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-122	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-131	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-141	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-150	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-79	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEM-92	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tet(X4)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VEB-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VIM-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VIM-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA14	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

aadA7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA8b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
acrB	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1
aphA15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
armA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arr-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arr-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catA4	0	0	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	1	1	1	1	1	1	1
catB11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catB2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catB3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catI	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
catII	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catII_from_Escherichia_coli_K-12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cfrA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cmlA1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cmlA5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cmlA6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cpxA	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1
determinant_of_bleomycin_resistance	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
dfrA10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
emrR	1	1	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
floR	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	1	0	1	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
linG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
lnuF	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
lnuG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
mphA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
mphE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
msbA	1	1	1	1	1	1	1	1	0	1	1	1	0	0	1	1	0	1	0	1	1	0	1	1	1	0	1	1	1	0	0	1	0	1	1	0	1	0	1	0	1	1	1	1	1	1	1	1	1

msrE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
oqxA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
oqxB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
qacH	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rmtB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rosA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rosB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sul1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	1	1	0	0	1	0	0	0	1	0	0	1	0	0	0	1	1	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0
sul2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
sul3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet(A)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet(B)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet(C)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet(D)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet(G)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet(H)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
tet(J)	0	0	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1
tet(Y)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tetM	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ugd	1	0	1	0	1	1	0	1	1	1	1	0	0	1	0	1	0	1	1	0	0	1	1	1	0	0	1	1	0	0	1	0	1	0	1	1	1	0	0	0	0	0	1	1	0	1	0	1	1
vanRA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Note. "1" means that a clonal group exists in a certain country or region, and "0" means it does not exist.