Supplementary Material to "Gyrase Mutations are Associated with Variable Levels of Fluoroquinolone Resistance in *Mycobacterium tuberculosis*"

Supplementary Table 1: **Sequence and coordinates of the molecular inversion probes used for target sequence capture.**

Some probes are duplicates except for one SNP in one of the arms.

BRIDGE = AGATCGGAAGAGCGTCGTGTAGGGAAAGCTGAGCAAATGTTATCGAGGTC

# Probe name	Start	End Sequence
gyrB-gyrA_W_1_1	4973	5112 CAGGAAGAAAGATGTCCGACGCACG-(BRIDGE)-GGGTCCGCGCGACACCTACG
gyrB-gyrA_W_2_2	5113	5252 TTCGGATCGTGGCTGCCCAGA-(BRIDGE)-GCGCGGTTAGATGGGTAAAAACGAGG
gyrB-gyrA_W_3_1	5253	5392 ACCATCTCATTTGGGAGGTGGTCGAC-(BRIDGE)-AAAAGAAGGCCCAAGACGAATACGGCG
gyrB-gyrA_W_4_2	5393	5532 CGGCATACCGACCGTCGACGT-(BRIDGE)-AACGCGGTCGACGAGGCGAT
gyrB-gyrA_W_4_2a	5393	5532 CGGCATACTGACCGTCGACGT-(BRIDGE)-AACGCGGTCGACGAGGCGAT
gyrB-gyrA_W_5_1	5533	5672 CGAGATCAAGCGCGACGGGTACG-(BRIDGE)-GGTGATGACACAACTACATGCCGGC
gyrB-gyrA_W_6_2	5673	5812 GGAATACGACTTCGAAACCGTCGCC-(BRIDGE)-AGTGGTCTCAGGTTTATGAGAAGTCGGAACC
gyrB-gyrA_W_7_1	5813	5952 TCGGCAAGTGAACGCGCAGC-(BRIDGE)-CGCCGGCTGCAAGAGATGGC
gyrB-gyrA_W_8_2	5953	6092 TTCCGGCAAGGGCACCGGGC-(BRIDGE)-CGAATCCACTGCACCGCACAAAGT
gyrB-gyrA_W_9_1	6093	6232 GCTGACGTCGGTGGTGAACAAGTAC-(BRIDGE)-ACGAGGTGGAGATCGCGATGCA
gyrB-gyrA_W_10_2	6233	6372 CAGACCAAGACCAAGTTGGGCAACAC-(BRIDGE)-GCCAAGGACCGCAAGCTACTGAAG
gyrB-gyrA_W_10_2a	6233	6372 CAGACCAAGACCAAGTTGGGCAACAC-(BRIDGE)-GCCAAGGACCGCAAGCTATTGAAG
gyrB-gyrA_W_11_1	6373	6512 CGCGGCACGTAAGGCACGAG-(BRIDGE)-CGAGGTCAAATCGTTTGTGCAGAAGGTC
gyrB-gyrA_W_12_2	6513	6652 CGGTTCTGCAAAAAGCGGTCGC-(BRIDGE)-AGTTGGTGCGGCGTAAGAGCG
gyrB-gyrA_W_13_1	6653	6792 CCGGGATCCACGACGAGTTCGA-(BRIDGE)-GATTCGATGTTCCAGGCGATACTTCCGC
gyrB-gyrA_W_14_2	6793	6932 CGAGAACGGGCATGTGTTTTTGGCAC-(BRIDGE)-TATCGGCAAGCTGCGCTACCACA
gyrB-gyrA_W_15_1	6933	7072 GGAAGACGGCATTCAGCGGTACAAG-(BRIDGE)-AACCGCCGCTGTACAAACTCAAGTG
gyrB-gyrA_W_16_2	7073	7212 ATGGGCGAGGACGTCGACGC-(BRIDGE)-GGTCTAGGTGAAATGGACGCTAAGGAGTTG
gyrB-gyrA_W_17_1	7213	7352 TCGCTCGACCGGATCGAACCG-(BRIDGE)-GCGGCGCAGCTTTATCACCCG
gyrB-gyrA_W_17_1a	7213	7352 TCGCTCGACCGGATCGAACCG-(BRIDGE)-GCGGCGCAGTTTTATCACCCG
gyrB-gyrA_W_18_2	7353	7492 TGCTCTATGCAATGTTCGATTCCGGCTT-(BRIDGE)-GTTGACATCGAGCAGGAGATGCAGC
gyrB-gyrA_W_18_2a	7353	7492 TGCTCTATGCAATGTTCGATTCCGGCTT-(BRIDGE)-GTTGACATCCAGCAGGAGATGCAGC
gyrB-gyrA_W_19_1	7493	7632 GCTGCGCTACCCGCTGGTGG-(BRIDGE)-CCGCCCGGACCGCAGCCACG
gyrB-gyrA_W_20_2	7633	7772 AGGAGACAGTCGATTTCATCCCTAACTACGAC-(BRIDGE)-ACGGCCAGGGCAACTTCGGC
gyrB-gyrA_W_21_1	7773	7912 GCCGACGCGGTGTTCTGGGC-(BRIDGE)-GGCCGGGTGCAAGAGCCGAC
gyrB-gyrA_W_22_2	7913	8052 CAAAACTGGCCGCGGCTCCA-(BRIDGE)-GCTGGAGAATCACGACGCCGAC
gyrB-gyrA_W_22_2a	7913	8052 CAAAACTAGCCGCGGCTCCA-(BRIDGE)-GCTGGAGAATCACGACGCCGAC
gyrB-gyrA_W_23_1	8053	8192 TCCGAGACGGCAAGCTGGCC-(BRIDGE)-TTCGAATGCGCGGAGTTGTTGAGG
gyrB-gyrA_W_23_1a	8053	8192 TCGGAGACGGCAAGCTGGCC-(BRIDGE)-TTCGAATGCGCGGAGTTGTTGAGG
gyrB-gyrA_W_24_2	8193	8332 GCAGACCAGCTTTGGCGCCAA-(BRIDGE)-GGCATTTCCAACATTGAGGACCAGTCTAGC
gyrB-gyrA_W_24_2a	8193	8332 GCAGACCAGCTTCGGCGCCAA-(BRIDGE)-GGCATTTCCAACATTGAGGACCAGTCTAGC
gyrB-gyrA_W_25_1	8333	8472 GGCAAACGAGCGAGCCCACATTC-(BRIDGE)-CATGCTAGCGATCGTCGACGGGG
gyrB-gyrA_W_26_2	8473	8612 CCAGGCCCAGGCAATCCTGGAC-(BRIDGE)-TGCGCGGCCTGGTTAAAGCG
gyrB-gyrA_W_27_1	8613	8752 ATCGTGCGCGACGAACTCGC-(BRIDGE)-ATGCAGTTGCGGCGCCTGGC
gyrB-gyrA_W_28_2	8753	8892 GGGATACGCCAAGCGCACCAAGA-(BRIDGE)-CGAAATCGTGGACAGGCACGGC
gyrB-gyrA_W_29_1	8893	9032 CTTCACCACCCAGGGACGGGTTTAT-(BRIDGE)-CCGATCTGTATCGCAGCCAGAAACG
gyrB-gyrA_W_29_1a	8893	9032 CTTCACCACCCAGGGACGGGTTTAT-(BRIDGE)-CCGACCTGTATCGCAGCCAGAAACG
gyrB-gyrA_W_30_2	9033	9172 ACCGACGCCCCGTACCTGGT-(BRIDGE)-CGGGCCAAGGCCTACGACTTGC
gyrB-gyrA_W_31_1	9173	9312 GTGTTCGGCCGGCGACGACC-(BRIDGE)-GCTGGCCACTCGCAACGGGC
gyrB-gyrA_W_31_1a	9173	9312 GTGTTCGGCCGACGACGACC-(BRIDGE)-GCTGGCCACTCGCAACGGGC
gyrB-gyrA_W_32_2	9313	9452 GCTGCTGTCGCTGAACGTCGTG-(BRIDGE)-TGCTGCTGGTCTCGGCCAACG
gyrB-gyrA_W_33_1	9453	9592 CGGCGCGGCAGGTTGGTTGG-(BRIDGE)-CGTGAAGGCACCTATCTGCTGGTGG
gyrB-gyrA_W_34_2	9593	9732 TGAATCTGGGCGAGGGCGACA-(BRIDGE)-GGCGTTGATTGTCGACGACGACA
gyrB-gyrA_W_35_1	9733	9872 CGTAGCGATCTGAGGAGGAATCGGG-(BRIDGE)-CACTGTTGGCCATCGCGCGC
gyrB-gyrA_W_36_2	9873	10012 CACATCGGGCAGCGACCGGG-(BRIDGE)-CAGCTAGGCTCGGCAGCCGG
gyrB-gyrA_C_1_2	5023	5162 TCTCAGGCCGGGACCGGAGC-(BRIDGE)-CGGGCGCCAGGGCCGATCTT
gyrB-gyrA_C_2_1	5163	5302 GGTCGCACACCACTGTACCGTGAT-(BRIDGE)-TTCGAGAATGGTGATAGACGCAGCGC
gyrB-gyrA_C_3_2	5303	5442 TTGCGGACGGCCTCCAGCCC-(BRIDGE)-ACTACGTTCACTGTGGTTGCATAACCGG
gyrB-gyrA_C_4_1	5443	5582 GACACCGCCATCCTCAAGCAGC-(BRIDGE)-CATACGCGTCCGAGTCGAACTTGC
gyrB-gyrA_C_5_2	5583	5722 CGCCGTGCAGACCACCAGATATCG-(BRIDGE)-CCCTTGCTTGAGGCCCAGGGG
gyrB-gyrA_C_6_1	5723	5862 CCCGTCTTCTTGGTCGGCGC-(BRIDGE)-AGGTTGATGGTCAGCCCCTTGTTGA
gyrB-gyrA_C_7_2	5863	6002 CTTGGGTCACCCTCTCGTCGGTC-(BRIDGE)-CCGGATAGTGAAAGGTGCGGCTCT
gyrB-gyrA_C_8_1	6003	6142 GTTTCACGAAGTCCACCAGGCCAC-(BRIDGE)-CACCGACTCCGAATACCCGGCG
gyrB-gyrA_C_9_2	6143	6282 TGTTGATGGTGTTGGCGAAGGTGTG-(BRIDGE)-TCACCGGTGAGGTTGGGGTCC

# Probe name	Start	End Sequence
gyrB-gyrA_C_10_1	6283	6422 GGCCAGGCCTTCCCGGATATCG-(BRIDGE)-AGTGGGTCAGCTGTTCGTTACAGACC
gyrB-gyrA_C_11_2	6423	6562 GTCGGTGGGGTTGGCTTCAAACC-(BRIDGE)-CTTGCCGGGCAATCCACCGATG
gyrB-gyrA_C_12_1	6563	6702 CGTGGAACGGCAATCGGCCAG-(BRIDGE)-ACATTGATGATCTTGCCGCGCAGC
gyrB-gyrA_C_13_2	6703	6842 CGGTCGATGCGCGCTTTCTCC-(BRIDGE)-CATCGGCGTCGGCCATCAGC
gyrB-gyrA_C_14_1	6843	6982 CAGCGTGGAAATATGTTGGCCGTCAA-(BRIDGE)-TGCGAATTCCGGGTCACTGCG
gyrB-gyrA_C_14_1a	6843	6982 CAGCGTGGAAATATGTTGGCCGTCAA-(BRIDGE)-TGCGAATTCCGGGTCGCTGCG
gyrB-gyrA_C_15_2	6983	7122 TCGCGCTCGCGGTCGGAGTA-(BRIDGE)-GGATCCATGGTGGTCTCCCACAACTC
gyrB-gyrA_C_16_1	7123	7262 ACTTGACGCAACACACGAACCGAG-(BRIDGE)-CATCCAGGAACCGAACATCCTTGGCG
gyrB-gyrA_C_17_2	7263	7402 CAATCGAACGCAGGGTTGCGTTAGA-(BRIDGE)-CTCATCGCATAGTCGATGTAGCTGCGC
gyrB-gyrA_C_18_1	7403	7542 GCGCGCGGCCGACGATCACG-(BRIDGE)-TGGTCTCGGCAACCGACCGG
gyrB-gyrA_C_19_2	7543	7682 CGTGCGGGTGGTAGTTGCCCA-(BRIDGE)-CATCGCCGCCGGTGGGTCAT
gyrB-gyrA_C_19_2a	7543	7682 CGTGCGGGTGGTAGTTGCCCA-(BRIDGE)-CATCCCCGCCGGTGGGTCAT
gyrB-gyrA_C_19_2b	7543	7682 CGTGCGGGTGGTAGTTGCCCA-(BRIDGE)-CATCGTCGCCGGTGGGTCAT
gyrB-gyrA_C_20_1	7683	7822 CAGCCGGGCTTCGGTGTACCT-(BRIDGE)-AGCAGGTTGGGGAACCGGCT
gyrB-gyrA_C_21_2	7823	7962 TGCCGCCTGACCCGTTGGCC-(BRIDGE)-CCATGACCGCGGCCAGGGTC
gyrB-gyrA_C_22_1	7963	8102 GTCCGGGCCTTTAACCCGCC-(BRIDGE)-GGTACGACCGCGGGAATCCTCT
gyrB-gyrA_C_23_2	8103	8242 GGCAACTCGGTGATCACCAGCGA-(BRIDGE)-ATGCGTAAACCGACCCGATCGCT
gyrB-gyrA_C_24_1	8243	8382 GCATCGCGCTTGATCTCGATGACG-(BRIDGE)-GCTGGTCCAGCCGCAGCGTG
gyrB-gyrA_C_25_2	8383	8522 AGTTGGTGGTCAACGTAATAGCGGATCA-(BRIDGE)-CAGTGCAATGACCTCGTCCAGCG
gyrB-gyrA_C_26_1	8523	8662 ACGGTCTCCGACGCCCGGAT-(BRIDGE)-TCGTCGATGATGCGCTGGCG
gyrB-gyrA_C_27_2	8663	8802 CTCGGCCTCGATTTTGGCCAGG-(BRIDGE)-CCGCGATGATCCGGGTACGC
gyrB-gyrA_C_28_1	8803	8942 CGTCGCTGACGTCTCCGTCGG-(BRIDGE)-CGCACCCTGCACGCCCTTGC
gyrB-gyrA_C_28_1a	8803	8942 CGTCGCTGACGTCTCCGTCGG-(BRIDGE)-CGCACCCTGCAC**T**CCCTTGC
gyrB-gyrA_C_29_2	8943	9082 CGACGATGTCGTCCTGCTTCAACCC-(BRIDGE)-TGCCCGCGCGCCGTCCGGGA
gyrB-gyrA_C_30_1	9083	9222 GGCTAACAGGTTGGCCACGTGC-(BRIDGE)-CGAAGTCGGTCAGCTTGGACTTTTTCAC
gyrB-gyrA_C_31_2	9223	9362 TCCGCCCGAGCGATTGGAGT-(BRIDGE)-GTCGGTCGCCGAGAACCTGATGG
gyrB-gyrA_C_32_1	9363	9502 CCCATTGGCCGCAGCGCCTC-(BRIDGE)-CGTTTCGCATAGCCCCCTGACG
gyrB-gyrA_C_33_2	9503	9642 ACCGGGTATTCCTCGATCGCGGTA-(BRIDGE)-CGCCGGAAGTGACGGCATACAG
gyrB-gyrA_C_34_1	9643	9782 CGCGGTGCGGATCACGCCAC-(BRIDGE)-GGCATTATCGTCGCCACTTTCTTCGG
gyrB-gyrA_C_35_2	9783	9922 TCTGCGCCGTTGGCGTCCAC-(BRIDGE)-TGCAGTCACCCCGACTCCTAACAC

Supplementary Table 2: Parameters used to call variants from MIP read data**.**

Program	***Version***	***Parameters***
megablast (used by MIPCleaner)	2.2.14	-p 90 -W 10 -e 1e-1 -X16 –JF –m8 –FF -v9000000 -b9000000
Bowtie	0.12.7	-q -k 2 -l 20 -m 5 --best –strata (with the additional filtering out of alignments with NM:i:x tags having x>5)
samtools	0.1.18	mpileup -u -R -B -q0 -Q0 -C0 -d1000000
bcftools	0.1.18	view -vg -p0.05
vcfutils.pl	0.1.18	varFilter -d 10 -a 5 -D1000000 -W10 -10 -20 -30 -40 -e0
Stampy	1.0.23	Default
Platypus	0.5.2	Default. Filtered variants with platypusfilter='badreads' or quality≤30 or purity <40%.

Supplementary Table 3: Isolate status at lineage defining SNPs listed in Coll *et. al.* (PMID 25176035) or Feuerriegel *et. al.* (PMID 24458512). Additionally the Euro-American X-type SNP Q139H_embB was not present in any isolate.

Isolate ID	T608N_embA_EuA_T2	V981L_embC_EuA_T_H_X	L16R_gid_EuA_LAM	G247S_gyrA_EuA_LAM9_T5	R463L_katG_EuA	T80A_gyrA_EuA_T2	V18A_ndh_EuA_S_T1	C492T_rrs_EuA_LAM3	E92D_gid_Beijing	G88A_promoter_ahpC_CAS	P913S_embA_EAI	V206M_embA_EAI3to6	E378A_embB_EAI_bovis_africanium_ethiop	H481Q_iniA_EAI_bovis_africanium_ethiop	T270I_embC_africanium	N394D_embC_EAI	A384V_gyrA_EAI	M330I_gyrB_EAI	R738Q_embC_CAS	R567H_embC_CAS	V104M_embC_CAS	C61T_promoter_rpoB_CAS	sum
601	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
602	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
604	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
606	0	1	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	3
701	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
702	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2
703	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
704	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
705	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
706	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
707	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
708	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
709	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
710	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
712	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
713	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
714	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
715	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2
716	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
717	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
719	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

720	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
722	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
724	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
726	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2
727	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
728	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
729	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
731	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
732	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
733	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
734	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
735	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
736	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
737	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
738	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
739	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
740	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
741	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
742	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
744	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2
747	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
748	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
749	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
750	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
751	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
752	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
753	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
754	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
755	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
756	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1

757	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
759	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
764	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
765	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
766	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
767	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
768	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
770	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
771	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
772	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
777	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
778	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2
779	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
781	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
782	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2
783	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
784	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2
785	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
786	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
787	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
788	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
789	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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799	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
800	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2
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807	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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810	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
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815	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
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843	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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1108	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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1126	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
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1217	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
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1276	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
1307	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
1315	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
1321	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
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1339	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
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1369	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
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2236	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
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2314	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2315	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
2316	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1

2326	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2334	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2338	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
2351	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
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2366	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
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2430	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
2434	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
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2459	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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2462	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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2481	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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2483	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2489	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2

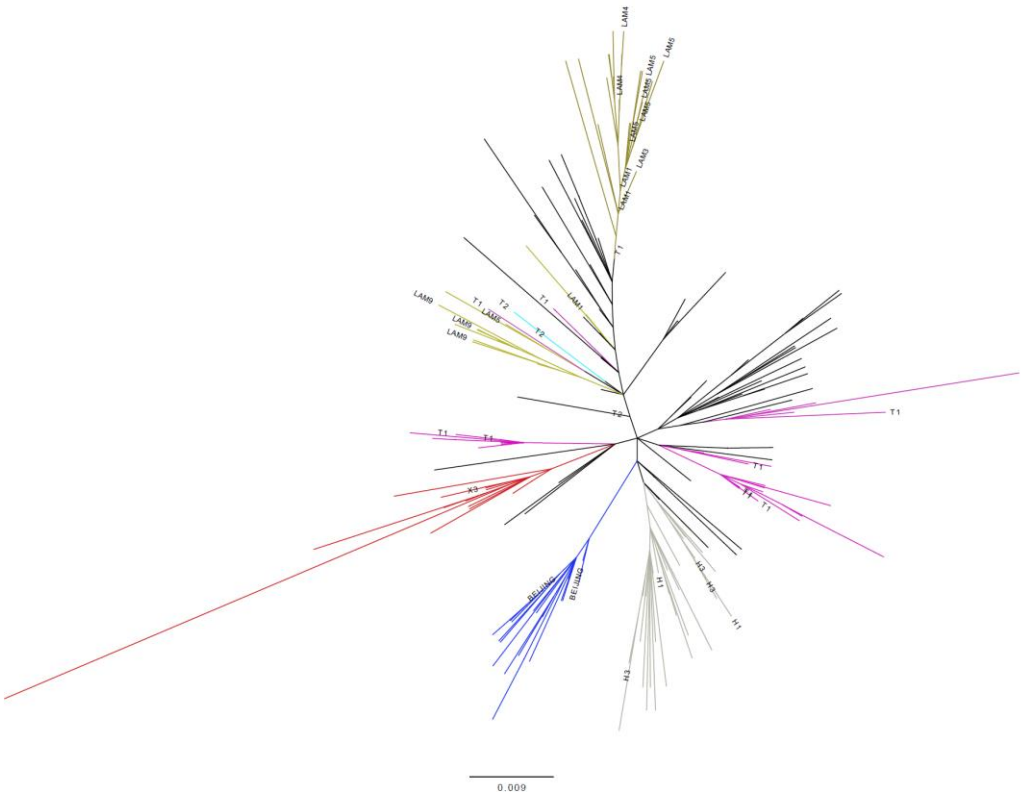
2493	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2
2496	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2497	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2506	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2507	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2
2510	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
2519	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2578	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
2592	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SUM	5	68	87	45	27	4	0	7	26	0	0	0	0	0	0	0	0	0	0	0	0	0	

Supplementary Table 4: Isolates with more than one *gyr* mutation and their moxifloxacin and ofloxacin MICs. *These two mutations were exactly co-linear

ID	Mutation number	MXF MIC	OFX MIC	mutations
181	2	0.125	<1	gyrB_I310M*, gyrB_S700T*
1167	2	1	4	gyrA_D94Y, gyrA_P102S
1370	2	1	4	gyrA_D94Y, gyrA_T267I
1578	2	4	4	gyrA_A90V, gyrB_V340L
1914	2	4	6	gyrA_D94G, gyrB_V340L
2029	3	8	>10	gyrA_D94Y, gyrB_I310M
2044	2	>8	>10	gyrA_D94G, gyrB_N538T
2049	2	>8	>10	gyrA_D94N, gyrB_N538T
2600	3	1	<1	gyrB_I310M*, gyrB_S700T*, gyrB_R485H
2772	2	<0.125	<1	gyrB_I310M*, gyrB_S700T*
3139	2	<0.125	<1	gyrB_I310M*, gyrB_S700T*
150	2	4	2	gyrA_S91P, gyrA_D94G
272	2	0.25	<1	gyrB_I310M*, gyrB_S700T*
492	2	0.25	<1	gyrB_V340L, gyrB_A453S
949	3	1	2	gyrA_D94A, gyrB_I310M*, gyrB_S700T*
950	2	4	2	gyrA_D94G, gyrB_V340L
951	5	<0.125	2	gyrA_A90V, gyrB_I310M*, gyrB_S700T*, gyrB_R485C, gyrB_E78K
1279	2	1	4	gyrA_A90V, gyrB_V340L
1280	2	1	4	gyrA_A90V, gyrB_V340L
1281	2	1	4	gyrA_D94A, gyrA_T267I
1293	3	1	4	gyrA_A90V, gyrB_I310M*, gyrB_S700T*
1316	3	1	4	gyrA_A90V, gyrB_I310M*, gyrB_S700T*
1444	2	1	4	gyrA_A90V, gyrB_V340L
1570	2	4	4	gyrA_A90V, gyrB_V340L

1770	2	4	6	gyrB_I310M*, gyrB_S700T*
1811	2	4	6	gyrA_D94G, gyrA_R392C
2017	2	4	>10	gyrA_D94G, gyrB_V340L
2028	2	8	>10	gyrA_D94G, gyrB_N538T
2135	2	0.25	<1	gyrB_I310M*, gyrB_S700T*
3092	2	<0.125	<1	gyrB_I310M*, gyrB_S700T*
3202	2	<0.125	<1	gyrB_I310M*, gyrB_S700T*
3431	2	<0.125	<1	gyrB_I310M*, gyrB_S700T*
2170	2	0.25	<1	gyrB_I310M*, gyrB_S700T*
899	2	0.5	2	gyrA_D94A, gyrB_V340L

Supplementary Figure 1: Isolate neighbor joining tree. Subtree branches were colored if a neighbor had a fingerprint from MIRU or spoligotyping as follows: LAM: olive, T1: purple, X: red, Beijing: dark blue, H: grey, T2: light blue, unknown: black.


LAM4
LAM5
LAM5
LAM5