

1.420 1.440 1.460 1.480 1.500 1.520 1.540

gyrA_allele-270 TGCTATTTTACGCATGAGCCTGCGAAACCTGACCGGCCTCGATCGGAAAGAAATTTCGAAAGCTACAAAAACCTGATGGTAAATCATCGACTTTGTGGATATCCTCTCCAAACCCGAAACGCATTACCCAAATCATCC 1540

gyrA_allele-93 TGCTATTTTACGCATGAGCCTGCGAAACCTGACCGGCCTCGATCAGAAAGAAATTATCGAAAGCTACAAAAACCTGATGGTAAATCATCGACTTTGTGGATATCCTCTCCAAACCCGAAACGCATTACCCAAATCATCC 1540

gyrA_allele-496 TGCTATTTTACGCATGAGCCTGCGAAACCTGACCGGCCTCGATCAGAAAGAAATTATCGAAAGCTACAAAAACCTGATGGTAAATCATCGACTTTGTGGATATCCTCTCCAAACCCGAAACGCATTACCCAAATCATCC 1540

gyrA_allele-488 TGCTATTTTACGCATGAGCCTGCGAAACCTGACCGGCCTCGATCAGAAAGAAATTATCGAAAGCTACAAAAACCTGATGGTAAATCATCGACTTTGTGGATATCCTCTCCAAACCCGAAACGCATTACCCAAATCATCC 1540

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gyrA_allele-508 TGCTATTTTACGCATGAGCCTGCGAAACCTGACCGGCCTCGATCAGAAAGAAATTATCGAAAGCTACAAAAACCTGATGGTAAATCATCGACTTTGTGGATATCCTCTCCAAACCCGAAACGCATTACCCAAATCATCC 1540

FA1090_gyrA_allele-1 TGCTATTTTACGCATGAGCCTGCGAAACCTGACCGGCCTCGATCAGAAAGAAATTATCGAAAGCTACAAAAACCTGATGGTAAATCATCGACTTTGTGGATATCCTCTCCAAACCCGAAACGCATTACCCAAATCATCC 1540
Sequence logo **TGCTATTTTACGCATGAGCCTGCGAAACCTGACCGGCCTCGATCAGAAAGAAATTATCGAAAGCTACAAAAACCTGATGGTAAATCATCGACTTTGTGGATATCCTCTCCAAACCCGAAACGCATTACCCAAATCATCC**

1.560 1.580 1.600 1.620 1.640 1.660 1.680

gyrA_allele-270 GGACGAACTGGAAGAAATCAAACAACCTATGCGGACGAAAGCCGACGAAATCAACCCGTTGCGCGGCACATTGCCGATGAAGACCTGATTCGCACACGCGAAATGGTGGTACCCCTGACCCACGGCGGCTATATA 1680

gyrA_allele-93 GTGACGAACTGGAAGAAATCAAACAACCTATGCGGACGAAAGCCGACGAAATCAACCCGTTGCGCGGCACATTGCCGATGAAGACCTGATTCGCACACGCGAAATGGTGGTACCCCTGACCCACGGCGGCTATATA 1680

gyrA_allele-496 GTGACGAACTGGAAGAAATCAAACAACCTATGCGGACGAAAGCCGACGAAATCAACCCGTTGCGCGGCACATTGCCGATGAAGACCTGATTCGCACACGCGAAATGGTGGTACCCCTGACCCACGGCGGCTATATA 1680

gyrA_allele-488 GTGACGAACTGGAAGAAATCAAACAACCTATGCGGACGAAAGCCGACGAAATCAACCCGTTGCGCGGCACATTGCCGATGAAGACCTGATTCGCACACGCGAAATGGTGGTACCCCTGACCCACGGCGGCTATATA 1680

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gyrA_allele-508 GTGACGAACTGGAAGAAATCAAACAACCTATGCGGACGAAAGCCGACGAAATCAACCCGTTGCGCGGCACATTGCCGATGAAGACCTGATTCGCACACGCGAAATGGTGGTACCCCTGACCCACGGCGGCTATATA 1680

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Sequence logo **GTCACGAACTGGAAGAAATCAAACAACCTATGCGGACGAAAGCCGACGAAATCAACCCGTTGCGCGGCACATTGCCGATGAAGACCTGATTCGCACACGCGAAATGGTGGTACCCCTGACCCACGGCGGCTATATA**

1.700 1.720 1.740 1.760 1.780 1.800 1.820

gyrA_allele-270 AAAACCCAGCCGACCAACCGACTATCAGGCTCAGCGTCGCGGGGGCGCGCAACAGGGCGGCTGCCACCAAGAGCAAGACTTTATCGAAACCCCTGTTGTTGCCAACACGCAATGATGATGTTTTACCAACCT 1820

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gyrA_allele-508 AAAACCCAGCCGACCAACCGACTATCAGGCTCAGCGTCGCGGGGGCGCGCAACAGGGCGGCTGCCACCAAGAGCAAGACTTTATCGAAACCCCTGTTGTTGCCAACACGCAATGATGATGTTTTACCAACCT 1820

FA1090_gyrA_allele-1 AAAACCCAGCCGACCAACCGACTATCAGGCTCAGCGTCGCGGGGGCGCGCAACAGGGCGGCTGCCACCAAGAGCAAGACTTTATCGAAACCCCTGTTGTTGCCAACACGCAATGATGATGTTTTACCAACCT 1820
Sequence logo **AAAACCCAGCCGACCAACCGACTATCAGGCTCAGCGTCGCGGGGGCGCGCAACAGGGCGGCTGCCACCAAGAGCAAGACTTTATCGAAACCCCTGTTGTTGCCAACACGCAATGATGATGTTTTACCAACCT**

1.840 1.860 1.880 1.900 1.920 1.940 1.960

gyrA_allele-270 CGGCAAGTGCCACTGGATTAAAGTTTACAAACTGCCGAAGGCGGACGCAACAGCGCGGCGCTCCGATTAAACAACGTATCCAGTGGAAAGAGGCGAAAAGTCAAGCGGATTCGGCAGTACGCGAGTTCCCGAAG 1960

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FA1090_gyrA_allele-1 CGGCAAGTGCCACTGGATTAAAGTTTACAAACTGCCGAAGGCGGACGCAACAGCGCGGCGCTCCGATTAAACAACGTATCCAGTGGAAAGAGGCGAAAAGTCAAGCGGATTCGGCAGTACGCGAGTTCCCGAAG 1960
Sequence logo **CGGCAAGTGCCACTGGATTAAAGTTTACAAACTGCCGAAGGCGGACGCAACAGCGCGGCGCTCCGATTAAACAACGTATCCAGTGGAAAGAGGCGAAAAGTCAAGCGGATTCGGCAGTACGCGAGTTCCCGAAG**

1.980 2.000 2.020 2.040 2.060 2.080 2.100

gyrA_allele-270 ACCAATACGTCTTCTTCCGCCACCGCGCAAGGATGGTGAAGAAAGTCCAACCTTCCGCTTTAAAAACGTCCGCGCCCAAGGCATTAAAGCCATCGCACTCAAAGAAGGCGACTACCTCGTCCGCGCTGCGCAAACAGGC 2100

gyrA_allele-93 ACCAATACGTCTTCTTCCGCCACCGCGCAAGGATGGTGAAGAAAGTCCAACCTTCCGCTTTAAAAACGTCCGCGCCCAAGGCATTAAAGCCATCGCACTCAAAGAAGGCGACTACCTCGTCCGCGCTGCGCAAACAGGC 2100

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gyrA_allele-508 ACCAATACGTCTTCTTCCGCCACCGCGCAAGGATGGTGAAGAAAGTCCAACCTTCCGCTTTAAAAACGTCCGCGCCCAAGGCATTAAAGCCATCGCACTCAAAGAAGGCGACTACCTCGTCCGCGCTGCGCAAACAGGC 2100

FA1090_gyrA_allele-1 ACCAATACGTCTTCTTCCGCCACCGCGCAAGGATGGTGAAGAAAGTCCAACCTTCCGCTTTAAAAACGTCCGCGCCCAAGGCATTAAAGCCATCGCACTCAAAGAAGGCGACTACCTCGTCCGCGCTGCGCAAACAGGC 2100
Sequence logo **ACCAATACGTCTTCTTCCGCCACCGCGCAAGGATGGTGAAGAAAGTCCAACCTTCCGCTTTAAAAACGTCCGCGCCCAAGGCATTAAAGCCATCGCACTCAAAGAAGGCGACTACCTCGTCCGCGCTGCGCAAACAGGC**

