

Supplementary figures



Figure S1: Amino acid sequence alignment of the GyrA homologs from *E. coli* (NCBI accession no. AAG57360.1), *S. Typhi* (NCBI accession no. AAO68297.1) and *S. Typhimurium* (NCBI accession no. AAL21173.1). The red box indicates the QRDR (Ala67-Gln106).

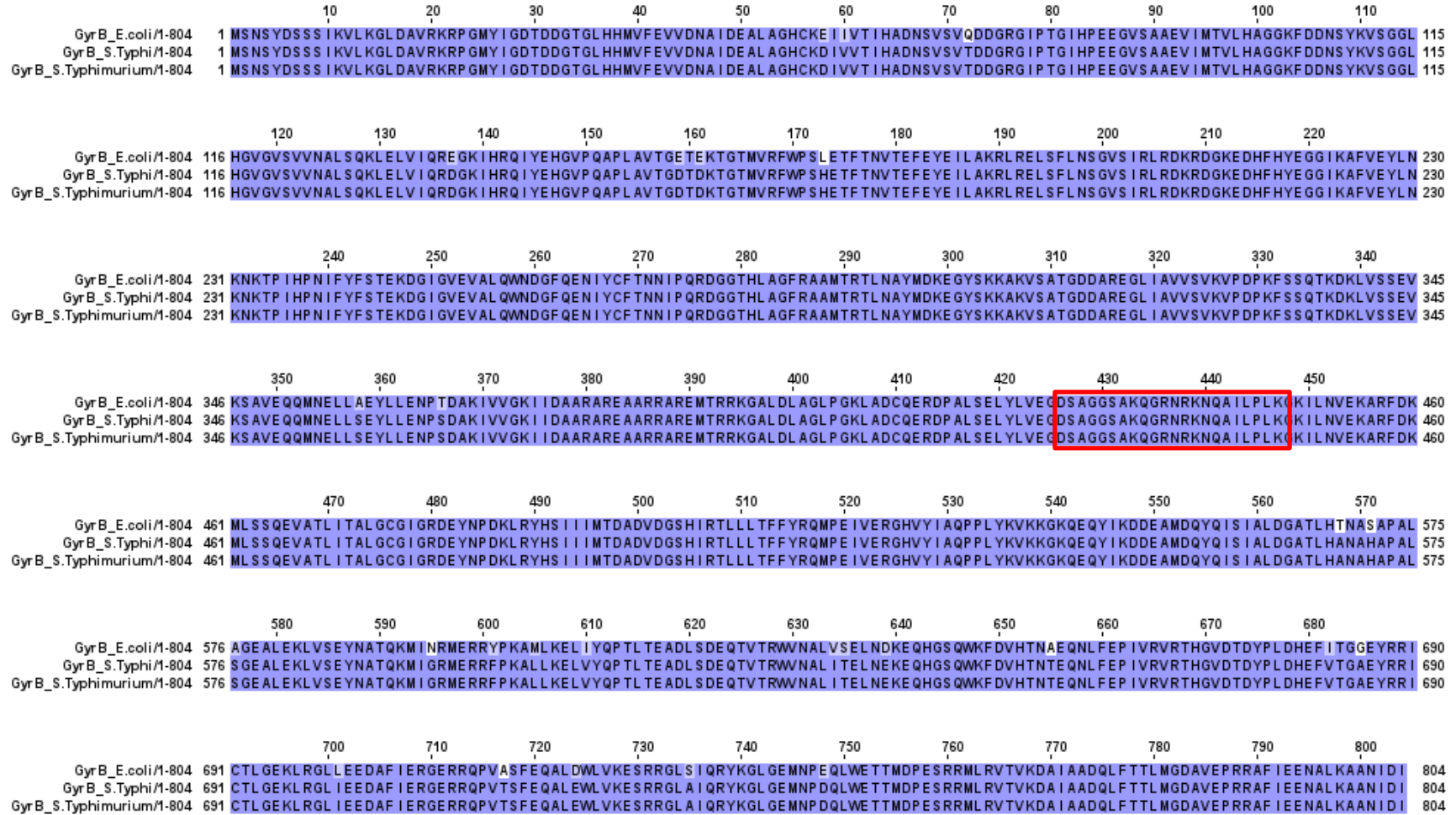


Figure S2: Amino acid sequence alignment of the GyrB homologs from *E. coli* (NCBI accession no. AAG58896.1), *S. Typhi* (NCBI accession no. AAO71180.1) and *S. Typhimurium* (NCBI accession no. AAL22694.1). The red box indicates the QRDR (Asp426-Lys447).

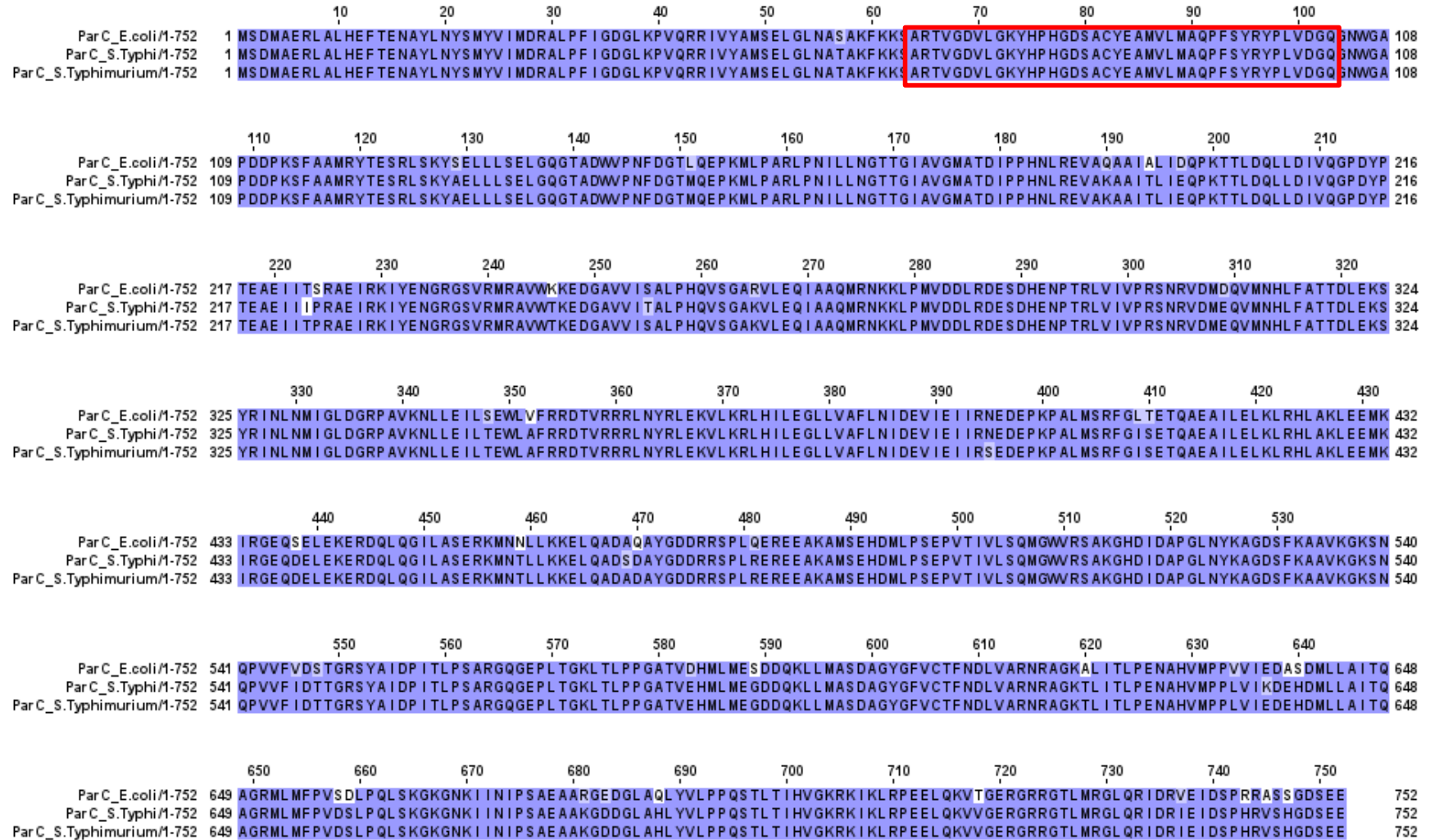


Figure S3: Amino acid sequence alignment of the ParC homologs from *E. coli* (NCBI accession no. AAG58155.1), *S. Typhi* (NCBI accession no. AAO70639.1) and *S. Typhimurium* (NCBI accession no. AAL22048.1). The red box indicates the QRDR (Ala64 to Gln103).

| | | | | | | | | | | |
|--------------------------|-----|---|-----|-----|-----|-----|-----|-----|-----|-----|
| | | 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 | |
| ParE_E.coli/1-630 | 1 | MTQTYNADAIEVLTGLEPVRRRPGMYTDTTRPNHLGQEVIDNSVDEALAGHAKRVDVILHADQSLEVIDDGRGMPVDIHPEEGVPAVELI | | | | | | | | 90 |
| ParE_S.Typhi/1-630 | 1 | MTQTYNADAIEVLTGLEPVRRRPGMYTDTTRPNHLGQEVIDNSVDEALAGHAKRVDVILHADQSLEVIDDGRGMPVDIHPEEGVPAVELI | | | | | | | | 90 |
| ParE_S.Typhimurium/1-630 | 1 | MTQTYNADAIEVLTGLEPVRRRPGMYTDTTRPNHLGQEVIDNSVDEALAGHAKRVDVILHADQSLEVIDDGRGMPVDIHPEEGVPAVELI | | | | | | | | 90 |
| | | 100 | 110 | 120 | 130 | 140 | 150 | 160 | 170 | |
| ParE_E.coli/1-630 | 91 | LCRLHAGGKFSNKNYQFSGGLHGVGISVVNALS KRVEVXNVRRDGQVYNI AFENG EKVQDLQVVGNCGKRNTGTSVHFWDPTFFDSPRFS | | | | | | | | 180 |
| ParE_S.Typhi/1-630 | 91 | LCRLHAGGKFSNKNYQFSGGLHGVGISVVNALS KRVEVTVRRDGQVYNI AFENG EKVQDLQVVGTGCKRNTGTSVHFWDPTFFDSPRFS | | | | | | | | 180 |
| ParE_S.Typhimurium/1-630 | 91 | LCRLHAGGKFSNKNYQFSGGLHGVGISVVNALS KRVEVTVRRDGQVYNI AFENG EKVQDLQVVGTGCKRNTGTSVHFWDPTFFDSPRFS | | | | | | | | 180 |
| | | 190 | 200 | 210 | 220 | 230 | 240 | 250 | 260 | |
| ParE_E.coli/1-630 | 181 | VSRLTHVLKAKAVLCPGVEITFKDEINNTEQRWCYQDGLNDYLAEAVNGLPTLPEKPFIGNFAGDTEAVDWALLWLPEGGELLTESYVNL | | | | | | | | 270 |
| ParE_S.Typhi/1-630 | 181 | VSRLMHVLKAKAVLCPGVEITFKDEVNNSEQRWCYQDGLNDYLGEAVNGLPTLPEKPFIGNFNGETEAVDWALLWLPEGGELLTESYVNL | | | | | | | | 270 |
| ParE_S.Typhimurium/1-630 | 181 | VSRLMHVLKAKAVLCPGVEITFKDEVNNSEQRWCYQDGLNDYLGEAVNGLPTLPEKPFIGNFNGETEAVDWALLWLPEGGELLTESYVNL | | | | | | | | 270 |
| | | 280 | 290 | 300 | 310 | 320 | 330 | 340 | 350 | |
| ParE_E.coli/1-630 | 271 | IPTMQGGTHVNGLRQGLLDAMREFCEYRNILPRGVKLSAEDIWDRCAVYLSVKMQDPQFAGQTKERLSSRQCAAFVSGVVKDAFSLWLNQ | | | | | | | | 360 |
| ParE_S.Typhi/1-630 | 271 | IPTMQGGTHVNGLRQGLLDAMREFCEYRNILPRGVKLSAEDIWDRCAVYLSVKMQDPQFAGQTKERLSSRQCAAFVSGVVKDAFSLWLNQ | | | | | | | | 360 |
| ParE_S.Typhimurium/1-630 | 271 | IPTMQGGTHVNGLRQGLLDAMREFCEYRNILPRGVKLSAEDIWDRCAVYLSVKMQDPQFAGQTKERLSSRQCAAFVSGVVKDAFSLWLNQ | | | | | | | | 360 |
| | | 370 | 380 | 390 | 400 | 410 | 420 | 430 | 440 | |
| ParE_E.coli/1-630 | 361 | NVQAAELLAEMAISQAQRRLRAAKKVVRKKLTS GPALPGKLADCTAQDLNRTFLVEQDSAGGS AKQARDREYQAIMPLKIKILNTWEV | | | | | | | | 450 |
| ParE_S.Typhi/1-630 | 361 | NVQAAEQLAEMAISQAQRRLRAAKKVVRKKLTS GPALPGKLADCTAQDLNRTFLVEQDSAGGS AKQARDREYQAIMPLKIKILNTWEV | | | | | | | | 450 |
| ParE_S.Typhimurium/1-630 | 361 | NVQAAEQLAEMAISQAQRRLRAAKKVVRKKLTS GPALPGKLADCTAQDLNRTFLVEQDSAGGS AKQARDREYQAIMPLKIKILNTWEV | | | | | | | | 450 |
| | | 460 | 470 | 480 | 490 | 500 | 510 | 520 | 530 | |
| ParE_E.coli/1-630 | 451 | SSDEVLASQEVHDISVAIGIDPDSDDLSQLRYGKICILADADSDGLHIATLLCALFVKHFRALVKHGHVYVALPPLYRIDLGKEVYYALT | | | | | | | | 540 |
| ParE_S.Typhi/1-630 | 451 | SSDEVLASQEVHDISVAIGIDPDSDDLSQLRYGKICILADADSDGLHIATLLCALFVRHFRALVKHGHVYVALPPLYRIDLGKEVYYALT | | | | | | | | 540 |
| ParE_S.Typhimurium/1-630 | 451 | SSDEVLASQEVHDISVAIGIDPDSDDLSQLRYGKICILADADSDGLHIATLLCALFVRHFRALVKHGHVYVALPPLYRIDLGKEVYYALT | | | | | | | | 540 |
| | | 550 | 560 | 570 | 580 | 590 | 600 | 610 | 620 | |
| ParE_E.coli/1-630 | 541 | EEKEGVLEQLKRKKGKPNVQRFKGLGEMNPMQLRETTLPNTRRLVQLTISDEDDQRTNAMMDMLLAKKRSEDRRNWLQEKGDMAEIEV | | | | | | | | 630 |
| ParE_S.Typhi/1-630 | 541 | EEKAGVLEQLKRKKGKPNVQRFKGLGEMNPMQLRETTLPNTRRLVQLTISDEDDQRTNAMMDMLLAKKRSEDRRNWLQEKGDADLDV | | | | | | | | 630 |
| ParE_S.Typhimurium/1-630 | 541 | EEKAGVLEQLKRKKGKPNVQRFKGLGEMNPMQLRETTLPNTRRLVQLTISDEDDQRTNAMMDMLLAKKRSEDRRNWLQEKGDADLDV | | | | | | | | 630 |

Figure S4: Amino acid sequence alignment for the ParE homologs from *E. coli* (NCBI accession no. AAG58169.1), *S. Typhi* (NCBI accession no. AAO70645.1) and *S. Typhimurium* (NCBI accession no. AAL22055.1). The red box indicates the QRDR (Asp420-Lys441).