**Table S3 - Oligonucleotides used in this study, related to Figure STAR Methods.**

| Primer | Name | Sequence (5'->3') | Use |
|---|---|---|---|
| MTL01 | CCNA_03428-UP-F-less-hindiii | AGATAAGCTTcccgttttccggagcacgcgg | cloning |
| MTL02 | CCNA_03428-3xflag-1-R | cttgtagtcgccgtcgtggtccttgtagtcGCCGCTGCTGATCTCGCCGATCGCCGACAGATAG | cloning |
| MTL03 | CCNA_3428-3xflag-2-R | Ttacttgtcgtcgtcgtccttgtagtcgatgtcgtggtccttgtagtcgccgtcgtggtccttg | cloning |
| MTL04 | 3428dw-fuse-3xflag-F | aggacgacgacgacaagtaaGtttttcagcgtgcgtcggcgc | cloning |
| MTL05 | CCNA_03428-DW-R | AGATGCTAGCcgctgagcctcaaccatgcgggtc | cloning |
| MTL06 | FOR_UP331PNTPSPSTI | CCGGCTGGCGCCAAGCTTCTCTGCAGGAGCCGTTCTCTGGGATGTCG | cloning |
| MTL07 | CC3319TETDELUP-R | CGAGAAAGGGTGACGATTGAGTCGGCCATGGGGGCGTCTC | cloning |
| MTL08 | CC3319TETDELDW-F | GCAACGAGCCGATCGCTGATGAGATCTAGGTTTTTCAGCGTGCGTC | cloning |
| MTL09 | CC3319TETDELDW_SPEI-R | TAGAGGACTAGTATATTGGTAGGTCGTCGCCATTGTCC | cloning |
| MTL10 | CCNA_3428-F-NdeI | AGATCATATGGCCGACGACGCCATTCC | cloning |
| MTL11 | CCNA_3428_R_SacI | AGATGAGCTCCTAGATCTCGCCGATCGCCGAC | cloning |
| MTL12 | OL7_tet_F | CGGTATCGATAAGCTTGATATCG | cloning |
| MTL13 | OL8_tet_R | CTGCAGGAATTCAAGAAGTTCC | cloning |
| MTL14 | 455 CCNA_3428-F-NdeI | AGATCATATGGCCGACGACGCCATTCC | cloning |
| MTL15 | 456 CCNA_3428_R_SacI | AGATGAGCTCCTAGATCTCGCCGATCGCCGAC | cloning |
| MTL16 | GapR-F-BamHI | AGATGGATCCATGGCCGACGACGCCATTCC | cloning |
| MTL17 | GapR-R-NotI | AGATGCGGCCGCCTAGATCTCGCCGATCGCCGAC | cloning |
| MTL18 | ParC-F-BamHI-homology | CACAGAGAACAGATTGGTGGCAACGGATCCATGAACAAGCCTGTCCTTCCTCCC | cloning |
| MTL19 | ParC-R-NotI-homology | TGGTGGTGGTGGTGCTCGAGTGCTCATTTGGGACGGAACCGCTTGTTG | cloning |
| MTL20 | ParE-F-BamHI-homology | CACAGAGAACAGATTGGTGGCAACGGATCCATGTCCTCCTCCGATAAGATCCCCTC | cloning |
| MTL21 | ParE-R-NotI-homology | TGGTGGTGGTGGTGCTCGAGTGCCTACAAATCCAGATCCGCCGACG | cloning |
| MTL22 | GyraseA-F-BamHI-homology | CACAGAGAACAGATTGGTGGCAACGGATCCTTGAGCGACGATCACAACACCATC | cloning |
| MTL23 | GyraseA-R-NotI-homology | TGGTGGTGGTGGTGCTCGAGTGCTTACGGGGTCTCGTCCGCCCCGC | cloning |
| MTL24 | GyrB-F-BamHI-homology | CACAGAGAACAGATTGGTGGCAACGGATCCATGACCGAGAACACCGAAGACCAAG | cloning |
| MTL25 | GyrB-R-NotI-homology | TGGTGGTGGTGGTGCTCGAGTGCTTAGACGTCGACCTCGGCGTCG | cloning |
| MTL26 | Illumina PE adapter 1 | /5Phos/GATCGGAAGAGCGGTTCAGCAGGAATGCCGAG | high throughput sequencing |
| MTL27 | Illumina PE adapter 2 | ACACTCTTTCCCTACACGACGCTCTTCCGATCT | high throughput sequencing |
| MTL28 | Illumina PE PCR primer 1 | AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT | high throughput sequencing |
| MTL29 | Illumina PE PCR primer 2 | CAAGCAGAAGACGGCATACGAGATNNNNNNCGGTCTCGGCATTCCTGCTGAACCGCTCTTCCGATCT | high throughput sequencing |
| MTL30 | 16bp_f | CATTGCAATGCAGTCA | EMSA |
| MTL31 | 16bp_r | TGACTGCATTGCAATG | EMSA |
| MTL32 | 2830_20f | TTAAAATTAGCAGCAACAAT | EMSA |
| MTL33 | 2030_20r | ATTGTTGCTGCTAATTTTAA | EMSA |
| MTL34 | 2830_50f | CTCCACGTATCGATATTAAAATTAGCAGCAACAATACAATTACCCACCACC | EMSA |
| MTL35 | 2830_50r | GTGGTGGGTAATTGTATTGTTGCTGCTAATTTTAATATCGATACGTGGAG | EMSA |
| MTL36 | nuoA_150f | AGTCGCGTTCCTGTTCCCCTGGC | EMSA |
| MTL37 | nuoA_150r | CACTCCCATTCGAGGGCGCCCTTC | EMSA |
| MTL38 | 1084_210f | CCTGATGGCCGTACGCAATCATTG | EMSA |
| MTL39 | 1084_210r | GTTGATACACTCTGCGACCGCTGCAC | EMSA |
| MTL40 | 2830_300f | AGCCCCCCCTCTTTCGTTGACCTTGCAC | EMSA |
| MTL41 | 2030_300r | CGATCTGCTTGGTCATGTCGATGTCGGG | EMSA |
| MTL42 | Cori_2f | GAGCAATGCGACCGTTGATC | qRT-PCR |
| MTL43 | Cori_2r | CGGTTGCTTAACCACTTGCC | qRT-PCR |
| MTL44 | CCNA_01869f | TTCGTCTGGTTCTGGCTGTC | qRT-PCR |
| MTL45 | CCNA_01869r | CGTCAGCGTCTACGACTACC | qRT-PCR |
| MTL46 | 11bp_f | TTAAAATTAAA | crystal structue |
| MTL47 | 11bp_r | TTTAATTTTAA | crystal structue |
| MTL48 | GapR_up_KpnI | CTTAATTAATATGCATGGTACCGTCGCCAGCCATGGTTTGCTTTAG | cloning |
| MTL49 | GapR_down_NheI | GATCCCCCGGGCTGCAGCTAGCGGGATCCGGCGGCTTGGCGCGCAT | cloning |
| MTL50 | AT-rich site | 5´-Fluorescein-TTAAAATTAAA | fluorescence anisotropy |
| MTL51 | GC-rich site | 5´-Fluorescein-TGGGCGGGCGCCCGCCCA | fluorescence anisotropy |
| MTL52 | mixed bp site | 5´-Fluorescein-GTGAGTACTCAC | fluorescence anisotropy |