

**Table S2.** Oligonucleotides used in this study

| <b>Name</b>   | <b>Sequence (5' to 3')</b>                             |
|---|--|
| <b><i>lacZ</i> fusion constructions in <i>E. coli</i> and <i>H. pylori</i></b>            |  |
| <i>sabA</i> -1  | ATGAATTCCTCTAGCAATGTGTGG                               |
| <i>sabA</i> -3  | ATGGATCCCTTTTTCATAAAAGTTCCTT                           |
| <i>sabA</i> -Tf*  | GGTTAAAATACTCCAAAATCTTTTTTTTTTTTTGGAAATCCAATAAAATT     |
| <i>sabA</i> -Tr*  | AATTTATTGGATTTCAAAAAAAAAAAAAGATTTTGGAGTATTTTAACC       |
| P163-P165*, P167*   | AAGATGATTTTATCGTTACTTTTTTTTTTTTTGGAAATCCAATAATTTATAGTA |
| P162  | GTAACGATAAAATCATCTT                                    |
| <i>hypF</i> R   | GATCGTCGACGCCCCCTGTAACGAATA                            |
| <i>hypF</i> F   | GATCGGATCCGAAAGAATTTTCAGCCAT                           |
| <i>pyrGp</i> F  | GATCGTCGACGAAAGAATTTTCAGCCAT                           |
| <i>pyrGp</i> R  | GATCGGATCCGCCCCCTGTAACGAATA                            |
| <i>pyrG</i> 9Tf   | ACTGAAATTGTTTTTTTTGAAATCGCTT                           |
| <i>pyrG</i> 9Tf   | AAGCGATTTCAAAAAAAAAACAATTTTCAGT                        |
| Amut1-1F  | GCTTCACAGATACATAGTTACAGTACTC                           |
| Amut1-1R  | GAGTACTGTAACCTATGTATCTGTGAAGC                          |
| Amut1-2F  | TTATCGTTACACAGATCAACGCTTCACA                           |
| Amut1-2R  | TGTGAAGCGTTGATCTGTGTAACGATAA                           |
| Amut2-1F  | CTGATGATACAGTTCACAGGATGATTTTA                          |
| Amut2-1R  | TAAAATCATCCTGTGAACTGTATCATCAG                          |
| Amut2-2F  | GCTTTATTCCATTACATACTGATGATAC                           |
| Amut2-2R  | GTATCATCAGTATGTAATGGGAATAAAGC                          |
| <b>SM1109Δ<i>sabA</i>::<i>rpsLCAT</i> and T-variant constructions in <i>H. pylori</i></b> |  |
| LA-F  | AACCCCAAGCCCTCAAGATT                                   |
| LA-R  | GTGTTTAATCCATAGTTATAAAGCATCCTAAAACAAGAACGCATA          |
| RA-F  | CCCAGTTTGTGCGACTGATAAATGAAAAAGACAATTTTACTCT            |
| RA-R  | GGCAGTTGTCTATAATCGTTCTAA                               |
| <i>rpsLCAT</i> -F   | TTTGTGAGCTATGCGTTCCTGTTTTAGGATGCTTTATAACTATGGATT       |
| <i>rpsLCAT</i> -R   | AGAGTAAAATTGTCTTTTTTCATTTATCAGTGCGACAAACT              |
| P93   | AACCCCAAGCCCTCAAGATT                                   |
| P96   | GGCAGTTGTCTATAATCGTTCTAA                               |
| <b><i>hup</i> and <i>napA</i> deletion/insertion constructions</b>                        |  |
| <i>hup</i> -1   | CCCTTACCAAGCGATGGTGGGA                                 |
| <i>hup</i> -2   | TAGTGAAAAGTGTATTACGCCACGC                              |
| <i>hup</i> -3Km   | ACACAATCGCTCAAGACGTGTTCCGCTTTGTTTCATGTGG               |
| <i>hup</i> -4Km   | CTAATTCATGTCAGCCGTGAGTGCCTAAATTCAAAACCC                |
| <i>hup</i> -5   | GGGATTTTAATGGCTTGATTGTATCG                             |
| <i>hup</i> -in  | CTCTTTTGTGTTGTATTTACCCGC                               |
| <i>napA</i> 1F  | TTGATAATGGCAAGGAAGTGGA                                 |
| <i>napA</i> 1R  | TCAAGCCATAGCCGATAAGCT                                  |
| <i>napA</i> 2F  | CACGATCGCATCCGCTTGCA                                   |
| <i>napA</i> 2R  | TTACCGTAACTTATGCGGACGAT                                |
| <i>Kmup</i>   | CACGTCTTGAGCGATTGTGTAGG                                |
| <i>Kmdn</i>   | ACGGCTGACATGGGAATTAGCCA                                |
| <i>Km2</i>  | CGATTGTCTGTTGTGCC                                      |

\* Different variants of *sabA*-Tf and -Tr primers that harbor different length of the T tract were used. Here is one representative variant shown.

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| <b>Name</b>  | <b>Sequence (5' to 3')</b>      |
|--|---------------------------------|
| <b>5' RACE and Primer extension</b>                  |                                 |
| AB35   | GATTGGGTGGTGGCTGTTGTAGTTG       |
| J99-8  | GTTGTCTTCAGCGTGCAAGAGCG         |
| <i>sabA</i> -8                                       | CTTTTTCATAAAAAGTGTTCCTT         |
| <b>Sequencing <i>sabA</i> promoter</b>               |                                 |
| CL1  | GCAATGTGTGGCAGCAAC              |
| CL2  | CTAGCGGGTTTTGAGTATC             |
| P67  | TGGGTGGTGGCTGTTGTAGTTGTT        |
| P68  | CATTTTCATGGCGTTTGGTTTG          |
| <b>EMSA, Footprint and Surface plasmon resonance</b> |                                 |
| <i>sabA</i> -5                                       | CGTTCTTGTTTTAGTTTGGC            |
| Biotin- <i>sabA</i> -5                               | Biotin-CGTTCTTGTTTTAGTTTGGC     |
| <i>sabA</i> -8                                       | CTTTTTCATAAAAAGTGTTCCTT         |
| <b>FLA analysis – FAM primers</b>                    |                                 |
| FAM-F  | TATGCGTTCCTGTTTTAGTTT           |
| FAM-Rlong  | CTTTTTCATAAAAATGTTCCCTTAAAGTAAT |
| FAM-Rshort   | ATTACTTTAAGGAACATTTTATGAAAAAG   |
| <b>qPCR analysis</b>                                 |                                 |
| <i>sabA</i> -qP1F                                    | TGAACGAAAAATACGAGCAA            |
| <i>sabA</i> -qP1R                                    | CCGCATAAAGACTCCAAAA             |
| <i>sabA</i> -qP2F                                    | TTCGGTATTGGGTTTTTGGAG           |
| <i>sabA</i> -qP2R                                    | GCTTTAGTGGTAGCGTTTTGT           |
| <i>rrnA</i> -2F                                      | CTCCCTACGGGGGAAAGATT            |
| <i>rrnA</i> -2R                                      | GTAGGAGTCTGGACCGTGTC            |
| <i>ppk</i> -2F                                       | GCAAACCCAAAAAGGGAGTCA           |
| <i>ppk</i> -2R                                       | TGACCAATCCCACAAATCCC            |
| <i>gyrA</i> -1F                                      | GCTAGGATCGTGGGTGATGT            |
| <i>gyrA</i> -1R                                      | TGGCTTCAGTGTAAACGCATC           |