| | | | Repeats | | Repeats |
|----------------------|-------------------------------|--------------------------|-------------------|--------------------------|---------------------------|
| Strain | Pathology ^a | modA allele ^c | AGCC ^b | modB allele ^c | CCCAA ^b |
| FA1090 | DGI | modA13 | 19 (ON) | modB1 | 12 (ON) |
| 01G1052 | MI | modA13 | 15 (OFF) | modB1 | 16 (OFF) |
| 01G1370 ^d | MI | modA13 | 13 (ON) | NA | NA |
| 01G0957 | DGI | modA12 | 13 (ON) | modB1 | 16 (OFF) |
| 90/G747 | DGI | modA13 | 17 (OFF) | modB1 | 8 (OFF) |
| 94G163 | MI | modA13 | 17 (OFF) | modB1 | 31 (OFF) |
| 98G1131 | DGI | modA12 | 20 (OFF) | modB1 | 20 (OFF) |
| 00G0794 ^d | MI | modA12 | 33 (OFF) | modB1 | 8 (OFF) |
| 01D064 | MI | modA12 | 17 (OFF) | modB1 | 21 (ON) |
| 02D004 | DGI | modA12 | 26 (OFF) | modB1 | 17(OFF) |
| 02D156 | DGI | modA12 | 15 (OFF) | modB1 | 2 (OFF) |
| 02W001 | DGI | modA13 | 10 (ON) | modB1 | 19 (OFF) |
| 98D159 | DGI | modA12 | 27 (OFF) | modB1 | 16 (OFF) |
| 97D040 | DGI | modA12 | 20 (OFF) | modB1 | 12 (ON) |
| 97D059 | MI | modA12 | 24 (OFF) | modB1 | 2 (OFF) |
| 96D551 | MI | modA12 | 25 (ON) | modB1 | 16 (OFF) |
| 1291 | UG | modA13 | 15 (OFF) | modB1 | 7 (OFF) |
| MS11 | UG | modA13 | 26 (OFF) | modB1 | 8 (OFF) |

Table S2. *Mod* alleles and repeat numbers for *N. gonorrhoeae* clinical isolate strains

^a DGI: disseminated gonococcal infection clinical isolates, MI: asymptomatic carriage or mucosal gonorrhoeae infection clinical isolates, UG: uncomplicated gonorrhoeae

^b Number and expression state of repeats within the *mod* gene; in-frame (ON) or out-of-frame (OFF)

^c A strain was defined as having the *modA13* allele if the DNA recognition region was \geq 95% identical at the nucleotide level to the *modA13* gene of *N. gonorrhoeae* strain FA1090 (NGO0641), and as *modA12* allele if the DNA recognition region was \geq 95% identical at the nucleotide level to the *modA12* gene of *N. meningitidis* strain Z2491 (NMA1589/90). A strain was defined as having the *modB1* allele if the DNA recognition region was \geq 95% identical at the nucleotide level to the nucleotide level to the *modA12* gene of *N. meningitidis* strain Z2491 (NMA1589/90). A strain was defined as having the *modB1* allele if the DNA recognition region was \geq 95% identical at the nucleotide level to the *modB1* gene of *N. gonorrhoeae* strain FA1090 (NGO0545), see Figure 1.

NA- *modB* gene not present,

^d 750 bp in-frame deletion in *res*

ND: not determined

Refer to Figure 1 and to the text