**Online supplementary file**

**Contents**

[STable 1a. Linear regression of association between *Neisseria subflava* MICs for azithromycin and ceftriaxone (log values) and consumption of macrolides and betalactams, respectively, limited to the two groups of MSM 2](#_Toc134805339)

[Table 1b. Linear regression of association between *Neisseria subflava* MICs for azithromycin and ceftriaxone (log values) and consumption of macrolides and betalactams, respectively, controlling for number of days since relevant antimicrobial was consumed. 2](#_Toc134805340)

[STable 2a. Zero inflated negative binomial regression of association between the abundance of macrolide, betalactam, fluoroquinolone and tetracycline resistance associated genes and the consumption of these classes of antimicrobials, limited to the two groups of MSM 3](#_Toc134805341)

[STable 2b. Zero inflated negative binomial regression of association between the abundance of macrolide, betalactam, fluoroquinolone and tetracycline resistance associated genes and the consumption of these classes of antimicrobials, controlling for number of days since relevant antimicrobial was consumed. 3](#_Toc134805342)

# STable 1a. Linear regression of association between *Neisseria subflava* MICs for azithromycin and ceftriaxone (log values) and consumption of macrolides and betalactams, respectively, limited to the two groups of MSM

|  |  |  |
| --- | --- | --- |
|  | Coef. (95% CI) | P-value |
| Azithromycin/macrolides | -0.10 (-1.23- 1.03) | 0.856 |
| Ceftriaxone/betalactams | -0.30 (-1.36- 0.77) | 0.572 |

# Table 1b. Linear regression of association between *Neisseria subflava* MICs for azithromycin and ceftriaxone (log values) and consumption of macrolides and betalactams, respectively, controlling for number of days since relevant antimicrobial was consumed.

|  |  |  |
| --- | --- | --- |
|  | Coef. (95% CI) | P-value |
| Azithromycin/macrolides | 3.37 (-4.83- 11.57) | 0.414 |
| Ceftriaxone/betalactams | -0.89 (-4.19- 2.41) | 0.590 |

# STable 2a. Zero inflated negative binomial regression of association between the abundance of macrolide, betalactam, fluoroquinolone and tetracycline resistance associated genes and the consumption of these classes of antimicrobials, limited to the two groups of MSM

|  |  |  |
| --- | --- | --- |
| Antimicrobial consumption/gene abundance | Coef. (95% CI) | P-value |
| Azithromycin/macrolides | 0.09 (-0.45- 0.63) | 0.740 |
| Ceftriaxone/betalactams | 0.19 (-0.69- 1.07) | 0.676 |
| Fluoroquinolone/fluoroquinolone | 0.14 (-1.12 -1.40) | 0.827 |
| Tetracycline/tetracycline | 0.42 (-0.24- 1.08) | 0.215 |

# STable 2b. Zero inflated negative binomial regression of association between the abundance of macrolide, betalactam, fluoroquinolone and tetracycline resistance associated genes and the consumption of these classes of antimicrobials, controlling for number of days since relevant antimicrobial was consumed.

|  |  |  |
| --- | --- | --- |
| Antimicrobial consumption/gene abundance | Coef. (95% CI) | P-value |
| Azithromycin/macrolides | 2.30 (-1.23- 5.83) | 0.202 |
| Ceftriaxone/betalactams | 2.07 (-0.84- 4.99) | 0.163 |
| Fluoroquinolone/fluoroquinolone | -2.65 (-6.03 -0.74) | 0.126 |
| Tetracycline/tetracycline | -3.21 (-11.4- 4.95) | 0.440 |