**Supplemental Table. Antibacterial susceptibilitya patterns by whole genome sequencing (WGS) group.**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **WGS group** | **Levofloxacin** | **Clindamycin** | **Doxycycline** | **Minocycline** | **Trimethoprim/Sulfa-methoxazole** | **Vancomycin** | **Mupirocin** | **Rifampin** |
| **% susceptible (number of tested isolates)** |
| **1** | 100% (10) | 100% (10) | 100% (10) | 100% (10) | 100% (10) | 100% (10) | 100% (10) | 100% (10) |
| **2** | 100% (4) | 100% (4) | 100% (4) | 100% (4) | 100% (4) | 100% (4) | 100% (4) | 100% (4) |
| **3** | 100% (4) | 100% (4) | 100% (4) | 100% (4) | 100% (4) | 100% (4) | 100% (4) | 100% (4) |
| **4** | 100% (4) | 75% (3)b | 75% (3)c | 100% (4) | 100% (4) | 100% (4) | 100% (4) | 100% (4) |
| **5** | 100% (4) | 0% (0) | 100% (4) | 100% (4) | 100% (4) | 100% (4) | 100% (4) | 100% (4) |
| **6** | 100% (3) | 100% (3) | 100% (3) | 100% (3) | 100% (3) | 100% (3) | 100% (3) | 100% (3) |
| **7** | 100% (2) | 0% (0) | 100% (2) | 100% (2) | 100% (2) | 100% (2) | 100% (2) | 100% (2) |
| **8** | 100% (2) | 0% (0) | 100% (2) | 100% (2) | 100% (2) | 100% (2) | 100% (2) | 100% (2) |
| **9** | 100% (2) | 100% (2) | 0% (0) | 50% (1)d | 100% (2) | 100% (2) | 100% (2) | 100% (2) |
| **10** | 100% (2) | 100% (2) | 100% (2) | 100% (2) | 100% (2) | 100% (2) | 100% (2) | 100% (2) |
| **11** | 100% (2) | 100% (2) | 100% (2) | 100% (2) | 100% (2) | 100% (2) | 100% (2) | 100% (2) |
| **Un-related** | 96% (27) | 89% (25) | 96% (27) | 96% (27) | 100% (28) | 100% (28) | 96% (27) | 100% (25) |
| **Not typed** | 100% (1) | 100% (1) | 100% (1) | 100% (1) | 100% (1) | 100% (1) | 100% (1) | 100% (1) |
| **Total** | 99% (67) | 82% (56) | 94% (64) | 97% (66) | 100% (68) | 100% (68) | 99% (67) | 100% (68) |

aSusceptibility testing was done by agar dilution.

bIsolate 40 tested clindamycin susceptible.

cIsolate 12 tested doxycycline intermediate.

dIsolate 16 tested minocycline susceptible and isolate 20 intermediate.