

Supplementary Table S2. Whole-genome sequencing and assembly statistics of *A. baumannii* clinical isolates included in the study.

| Isolate ID | Avg. Coverage | Read Count | Avg. Read Length (bp) | Assembly Base Count | Contig Count | N50 (bp) | Avg. Contig Length (bp) | Max. Contig Length (bp) | Min. Contig Length (bp) |
|-------------------|----------------------|-------------------|------------------------------|----------------------------|---------------------|-----------------|--------------------------------|--------------------------------|--------------------------------|
| 52944 | 70 | 1463594 | 187 | 3891392 | 530 | 14092 | 7342 | 70468 | 177 |
| 61317 | 95 | 1691750 | 219 | 4051914 | 380 | 25362 | 10662 | 80799 | 205 |
| 61979 | 94 | 1845066 | 198 | 3868427 | 461 | 19131 | 8391 | 70400 | 192 |
| 63231 | 75 | 1724710 | 170 | 3815419 | 535 | 14782 | 7131 | 61611 | 161 |
| 63485 | 97 | 1917776 | 196 | 3851357 | 498 | 17254 | 7733 | 49801 | 185 |
| 66116 | 78 | 1500004 | 203 | 3987347 | 251 | 40792 | 15885 | 134420 | 193 |
| 67098 | 99 | 2007834 | 193 | 3972821 | 240 | 39022 | 16553 | 156766 | 181 |
| 67510 | 109 | 2194376 | 194 | 4028273 | 457 | 20511 | 8814 | 81834 | 192 |
| 67745 | 105 | 1940996 | 211 | 3909264 | 560 | 15794 | 6980 | 63303 | 201 |
| 20189365 | 99 | 1845870 | 210 | 3894930 | 534 | 16364 | 7293 | 78534 | 201 |
| 20216722 | 118 | 2337936 | 197 | 3916738 | 446 | 19712 | 8781 | 88433 | 185 |
| 182122 | 103 | 1887198 | 213 | 3795841 | 281 | 27542 | 13508 | 70036 | 201 |
| 71838 | 119 | 2417018 | 191 | 3719202 | 486 | 14260 | 7652 | 57637 | 181 |
| 206182 | 117 | 2221686 | 204 | 3996890 | 423 | 20656 | 9448 | 73002 | 193 |
| 71813 | 93 | 2084788 | 173 | 3748797 | 390 | 19198 | 9612 | 65033 | 161 |
| 278860 | 89 | 1591158 | 217 | 3868684 | 421 | 18972 | 9189 | 72810 | 205 |
| 300736 | 104 | 1903622 | 212 | 3969551 | 421 | 22412 | 9428 | 72848 | 201 |
| 10042 | 69 | 1496268 | 180 | 3863634 | 391 | 22219 | 9881 | 81949 | 169 |

Raw sequence and assembly data retrieved from SeqSphere v.7.0.4 software, before and after *de novo* genome assembly using Velvet.