### 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.