

# Cooperative Recognition of Internationally Disseminated Ceftriaxone-resistant *Neisseria gonorrhoeae* Strain

## Technical Appendix

**Technical Appendix Table 1.** Whole genome assembly and fast quality control sequencing metrics.

| Assembly metrics |                       |                   |                      |                                     |                           |                        |                    |                   |                    |                          |                               |                       |
|------------------|-----------------------|-------------------|----------------------|-------------------------------------|---------------------------|------------------------|--------------------|-------------------|--------------------|--------------------------|-------------------------------|-----------------------|
| Strain           | Min contig length     | Max contig length | Mean contig length   | Standard deviation of contig length | Median contig length      | N50 contig length      | No. contigs        | No. contigs >=1kb | No. contigs in N50 | No. bases in all contigs | No. bases in contigs >=1kb    | GC Content of contigs |
| A7536            | 503                   | 153179            | 20434.6              | 27096.1                             | 9761                      | 46889                  | 107                | 95                | 15                 | 2186502                  | 2178363                       | 52.34%                |
| A7846            | 508                   | 170175            | 19717.04             | 27713.47                            | 8163                      | 47017                  | 111                | 93                | 15                 | 2188591                  | 2175598                       | 52.35%                |
| FC428            | 530                   | 205307            | 28134.55             | 36437.23                            | 13956                     | 60704                  | 78                 | 67                | 12                 | 2194495                  | 2186878                       | 52.31%                |
| FC460            | 530                   | 221468            | 20948.54             | 31872.34                            | 8474                      | 47483                  | 104                | 90                | 14                 | 2178648                  | 2169052                       | 52.49%                |
| H041             | 510                   | 337256            | 29213.03             | 49753.63                            | 7503                      | 86362                  | 72                 | 57                | 8                  | 2103338                  | 2092530                       | 52.64%                |
| F89              | 500                   | 260748            | 29941.97             | 45758.24                            | 9726                      | 73376                  | 72                 | 59                | 9                  | 2155822                  | 2146570                       | 52.40%                |
| A8806            | 510                   | 222588            | 33184.75             | 51000.25                            | 7449                      | 112376                 | 65                 | 57                | 7                  | 2157009                  | 2150822                       | 52.40%                |
| 47707            | 647                   | 208505            | 28633.58             | 45486.76                            | 7609                      | 76870                  | 77                 | 64                | 8                  | 2204786                  | 2193928                       | 52.34%                |
| FastQC Metrics   |                       |                   |                      |                                     |                           |                        |                    |                   |                    |                          |                               |                       |
| SE/PE            | Encoding              | No. Reads         | Total no. Base Pairs | Sequence length range               | Most abundant read length | No. reads for abundant | Estimated Coverage | Reference length  | Duplicate % R1     | Duplicate % R2           | No. overrepresented sequences |                       |
| PE               | Sanger / Illumina 1.9 | 6763774           | 777480038            | 35-151                              | 150                       | 2793366                | 360.96             | 2153922           | 63.98              | 62.11                    | 0                             |                       |
| PE               | Sanger / Illumina 1.9 | 3673072           | 435717067            | 35-151                              | 150                       | 1648675                | 202.29             | 2153922           | 57.22              | 55.61                    | 0                             |                       |
| PE               | Sanger / Illumina 1.9 | 6139112           | 1820565211           | 35-301                              | 300                       | 5438042                | 845.23             | 2153922           | 75.42              | 75.19                    | 0                             |                       |
| PE               | Sanger / Illumina 1.9 | 1278242           | 351830155            | 35-301                              | 300                       | 977031                 | 163.34             | 2153922           | 48.85              | 48.54                    | 0.22                          |                       |
| PE               | Sanger / Illumina 1.9 | 521860            | 156934157            | 85-301                              | 300                       | 497560                 | 72.86              | 2153922           | 9.9                | 7.17                     | 0                             |                       |
| PE               | Sanger / Illumina 1.9 | 529020            | 159081437            | 35-301                              | 300                       | 503799                 | 73.86              | 2153922           | 17.81              | 15.52                    | 0                             |                       |
| PE               | Sanger / Illumina 1.9 | 851030            | 255904621            | 46-301                              | 300                       | 811357                 | 118.81             | 2153922           | 11.23              | 8.54                     | 0                             |                       |
| PE               | Sanger / Illumina 1.9 | 697922            | 209832768            | 48-301                              | 300                       | 664719                 | 97.42              | 2153922           | 11.57              | 10.36                    | 0                             |                       |

**Technical Appendix Table 2.** Number of core SNVs among *Neisseria gonorrhoeae* isolates\*

| Isolate | FC428 | FC460 | A7536 | 47707 | A7846 | F89 | A8806 | H041 | FA1090 |
|---------|-------|-------|-------|-------|-------|-----|-------|------|--------|
| FC428   | 0     | 0     | 12†   | 12†   | 17†   | 275 | 305   | 292  | 307    |
| FC460   | 0     | 0     | 12†   | 12†   | 17†   | 275 | 305   | 292  | 307    |
| A7536   | 12†   | 12†   | 0     | 8     | 11    | 281 | 305   | 292  | 311    |
| 47707   | 12†   | 12†   | 8     | 0     | 5     | 281 | 305   | 292  | 309    |
| A7846   | 17†   | 17†   | 11    | 5     | 0     | 280 | 306   | 293  | 308    |
| F89     | 275   | 275   | 281   | 281   | 280   | 0   | 236   | 225  | 322    |
| A8806   | 305   | 305   | 305   | 305   | 306   | 236 | 0     | 17   | 352    |
| H041    | 292   | 292   | 292   | 292   | 293   | 225 | 17    | 0    | 339    |
| FA1090  | 307   | 307   | 311   | 309   | 308   | 322 | 352   | 339  | 0      |

\*SNV, single nucleotide variation.

†8 identical SNVs. Sample numbers listed in order as they appear in the phylogenetic tree of Figure 1.