Table 5: Comparison of different tools for detection of antimicrobial resistance genes. We applied RGI[2], Abricate[3] (with the CARD database), AMRFinderPlus[4] and Resfinder[5] to the hybrid assemblies of 82 isolates of V. cholerae. RGI can detect the highest amount of genes and is uniquely able to use protein variant models to find gene variants. Abricate can detect gene loci at a higher completeness, being able to merge adjacent hits that were split in the underlying BLAST alignment. CholerAegon uses a combined approach, harnessing both RGI’s and Abricate’s advantages. RGI – Resistance Gene Identifier; COV – mean coverage of the reference gene sequence; EC parE – *Escherichia coli* parE conferring resistance to fluoroquinolones.

| AMR gene                  | RGI |           | Abricate |           | AMRFinderPlus |           | Resfinder |           |
|---------------------------|-----|-----------|----------|-----------|---------------|-----------|-----------|-----------|
|                           | # found | COV | # found | COV | # found | COV | # found | COV |
| APH(3')-Ib                | 74 | 97.08 | 74 | 100.00 | 74 | 99.11 | 74 | 100.00 |
| APH(6)-Id                 | 74 | 100.00 | 74 | 100.00 | 74 | 100.00 | 74 | 100.00 |
| CRP                       | 82 | 100.00 | 82 | 99.68 | 0 | – | 0 | – |
| Vibrio cholerae varG      | 79 | 95.90 | 79 | 100.00 | 79 | 100.00 | 0 | – |
| almG                      | 82 | 100.00 | 82 | 100.00 | 0 | – | 0 | – |
| catB9                     | 79 | 100.00 | 79 | 100.00 | 79 | 100.00 | 79 | 100.00 |
| dfrA1                     | 79 | 100.00 | 79 | 100.00 | 79 | 100.00 | 79 | 100.00 |
| floR                      | 74 | 99.94 | 74 | 100.00 | 74 | 99.96 | 74 | 99.92 |
| rsmA                      | 82 | 106.56 | 0 | – | 0 | – | 0 | – |
| sul2                      | 74 | 99.48 | 74 | 100.00 | 74 | 99.61 | 74 | 100.00 |
| EC parE                   | 82 | 99.37 | 0 | – | 0 | – | 0 | – |