

a)

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NM01      TGTATGTTTATTAAATTCTAAATCAATAATAATATTTCCCAATCAGAGCTT
NM11      TGTATGTTTATTAAATTCTAAATCAATAATAATATTTCCCAATCAGAGCTT
NM12      TGTATGTTTATTAAATTCTAAATCAATAATAATATTTCCCAATCAGAGCTT
NM13      TGTATGTTTATTAAATTCTAAATCAATAATAATATTTCCCAATCAGAGCTT
NM16      TGTATGTTTATTAAATTCTAAATCAATAATAATATTTCCCAATCAGAGCTT
NM18      TGTATGTTTATTAAATTCTAAATCAATAATAATATTTCCCAATCAGAGCTT
NM20      TGTATGTTTATTAAATTCTAAATCAATAATAATATTTCCCAATCAGAGCTT
NM25      TGTATGTTTATTAAATTCTAAATCAATAATAATATTTCCCAATCAGAGCTT
DuyDNT    TGTATGTTTATTAAATTCTAAATCAATAATAATATTTCCCAATCAGAGCTT
MC58      TGTATGTTTATTAAATTCTAAATCAATAATAATATTTCCCA-----

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b)

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NM01      GTTAGTACAAAGACCTTGTGTTTCTTTTTAACCAATATTTTCATATATATC
NM11      GTTAGTACAAAGACCTTGTGTTTCTTTTTAACCAATATTTTCATATATATC
NM12      GTTAGTACAAAGACCTTGTGTTTCTTTTTAACCAATATTTTCATATATATC
NM13      GTTAGTACAAAGACCTTGTGTTTCTTTTTAACCAATATTTTCATATATATC
NM16      GTTAGTACAAAGACCTTGTGTTTCTTTTTAACCAATATTTTCATATATATC
NM18      GTTAGTACAAAGACCTTGTGTTTCTTTTTAACCAATATTTTCATATATATC
NM20      GTTAGTACAAAGACCTTGTGTTTCTTTTTAACCAATATTTTCATATATATC
NM25      GTTAGTACAAAGACCTTGTGTTTCTTTTTAACCAATATTTTCATATATATC
DuyDNT    GTTAGTACAAAGACCTTGTGTTTCTTTTTAACCAATATTTTCATATATATC
MC58      -----TTAACCAATATTTTCATATATATC

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Supplementary Figure 1. A sequence alignment of the nine chloramphenicol resistant and intermediate strains and the MC58 reference genome, showing the a) upstream and b) downstream flanking regions of the *catP* insertion which match the previously-reported insertion.