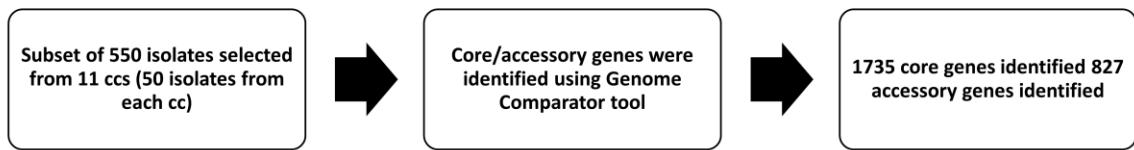
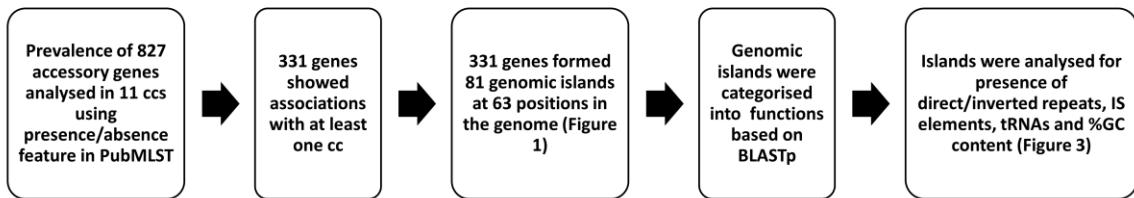


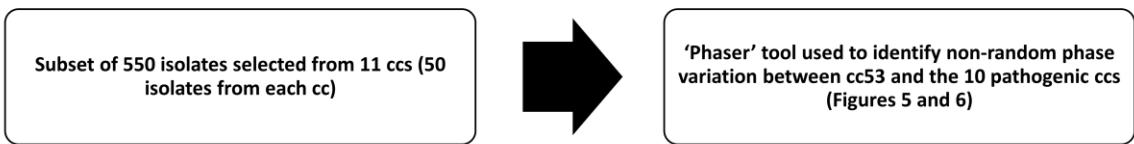
Analysis 1: Identification of core and accessory genomes in 11 clonal complexes of *N. meningitidis*



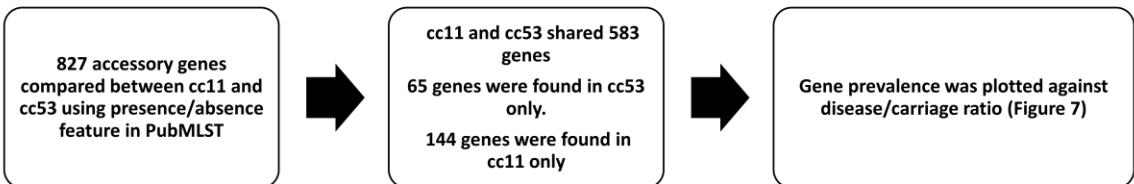
Analysis 2: Prevalence of genomic islands in 11 clonal complexes of *N. meningitidis*



Analysis 3: Identification of non-random phase variation in *N. meningitidis*

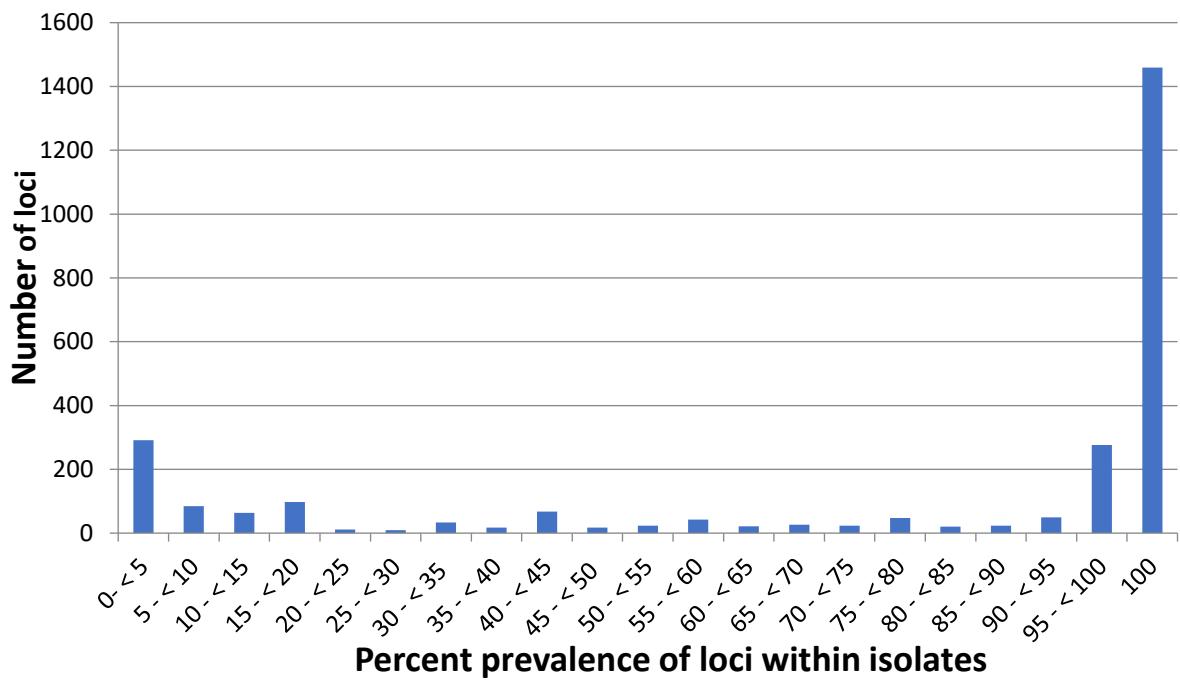


Analysis 4: Direct comparison of hyper-virulent cc11 and cc53



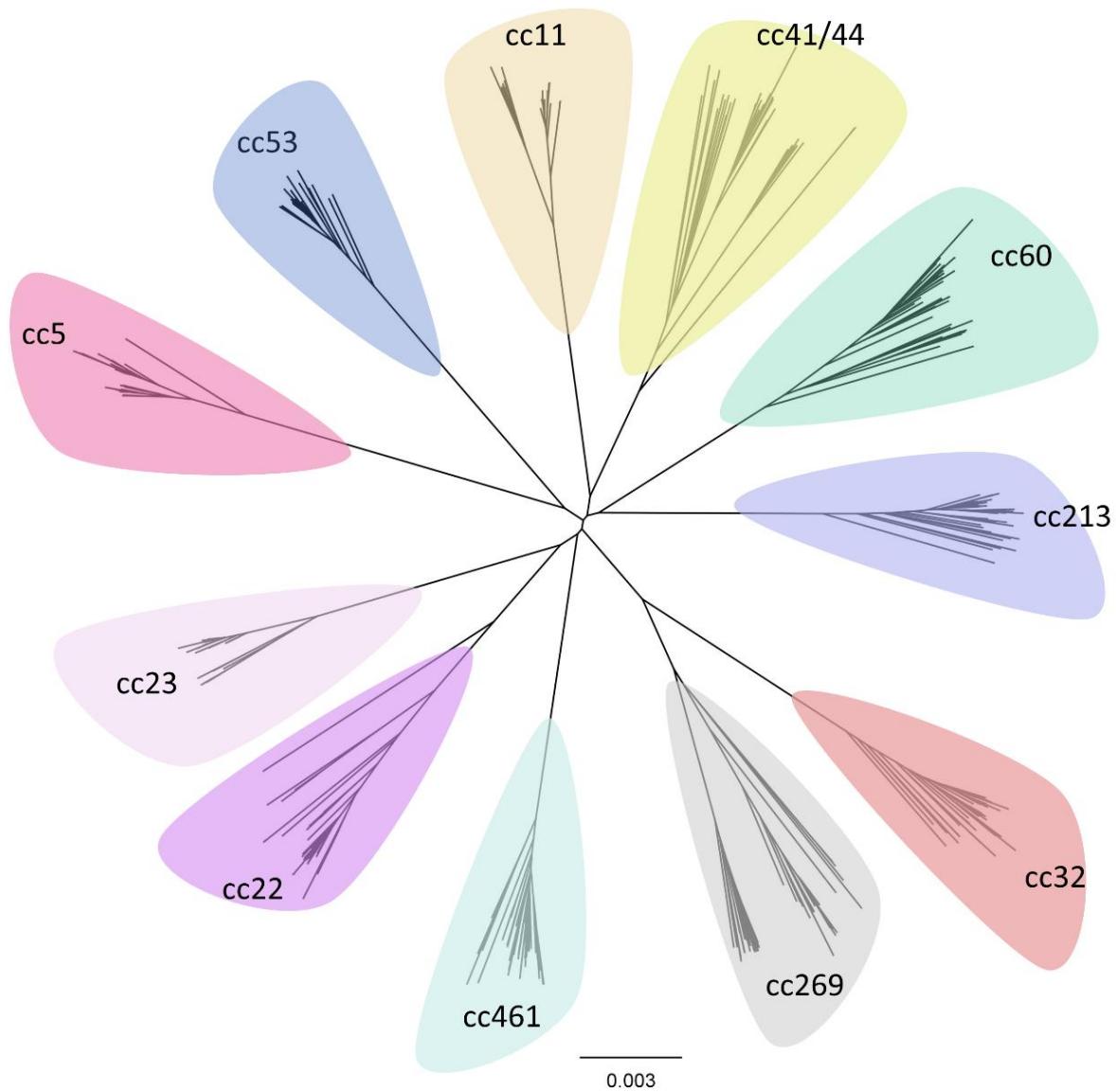
Supplementary Figure 1. Summary of methodology used in this study.

The five different analysis pipelines used in this study are summarised including the species, number of isolates, and clonal complexes analysed.

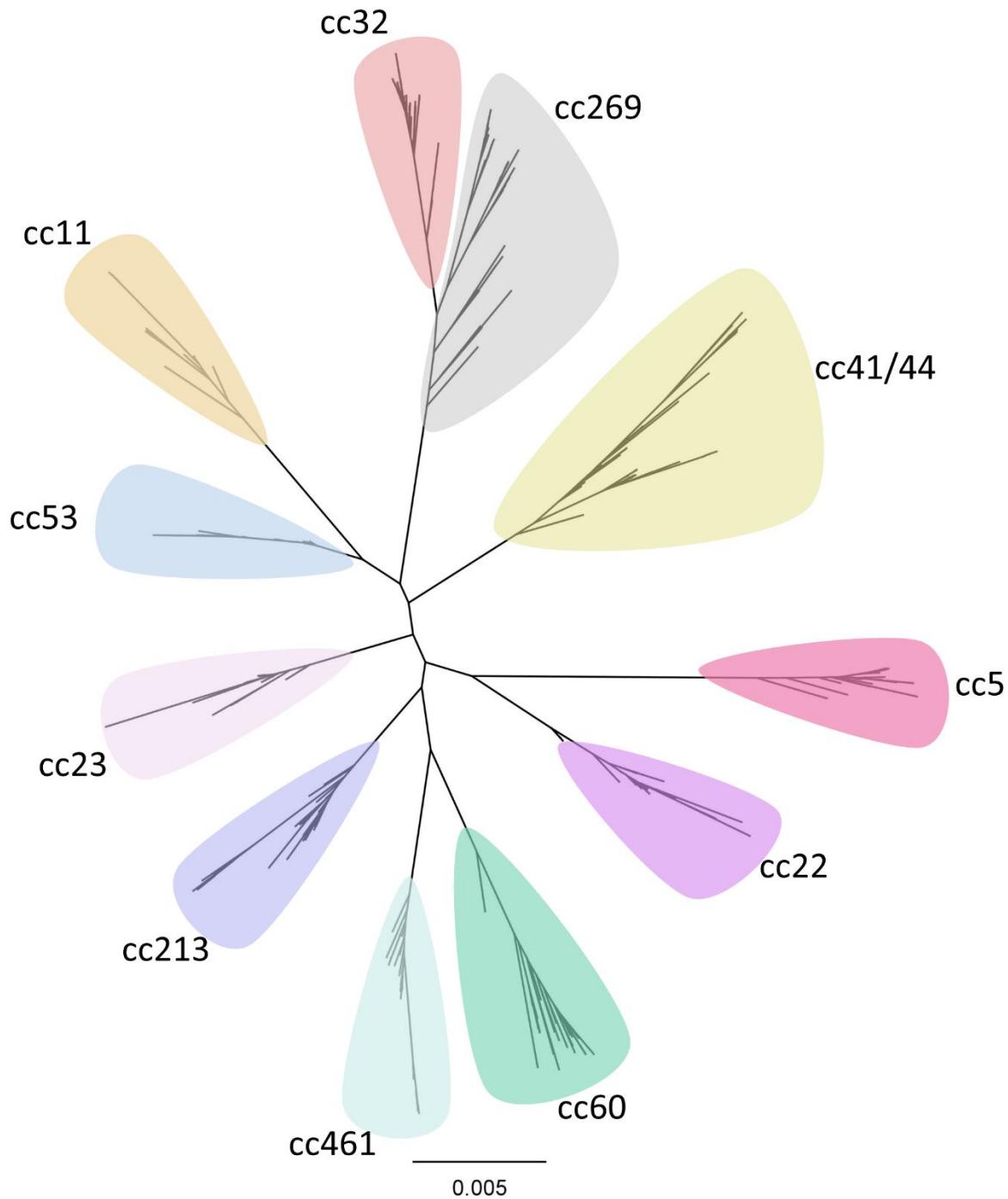


Supplementary Figure 2.

Locus presence frequency of pangenome of *N. meningitidis* consisting of 2562 genes in 550 whole genome sequences.

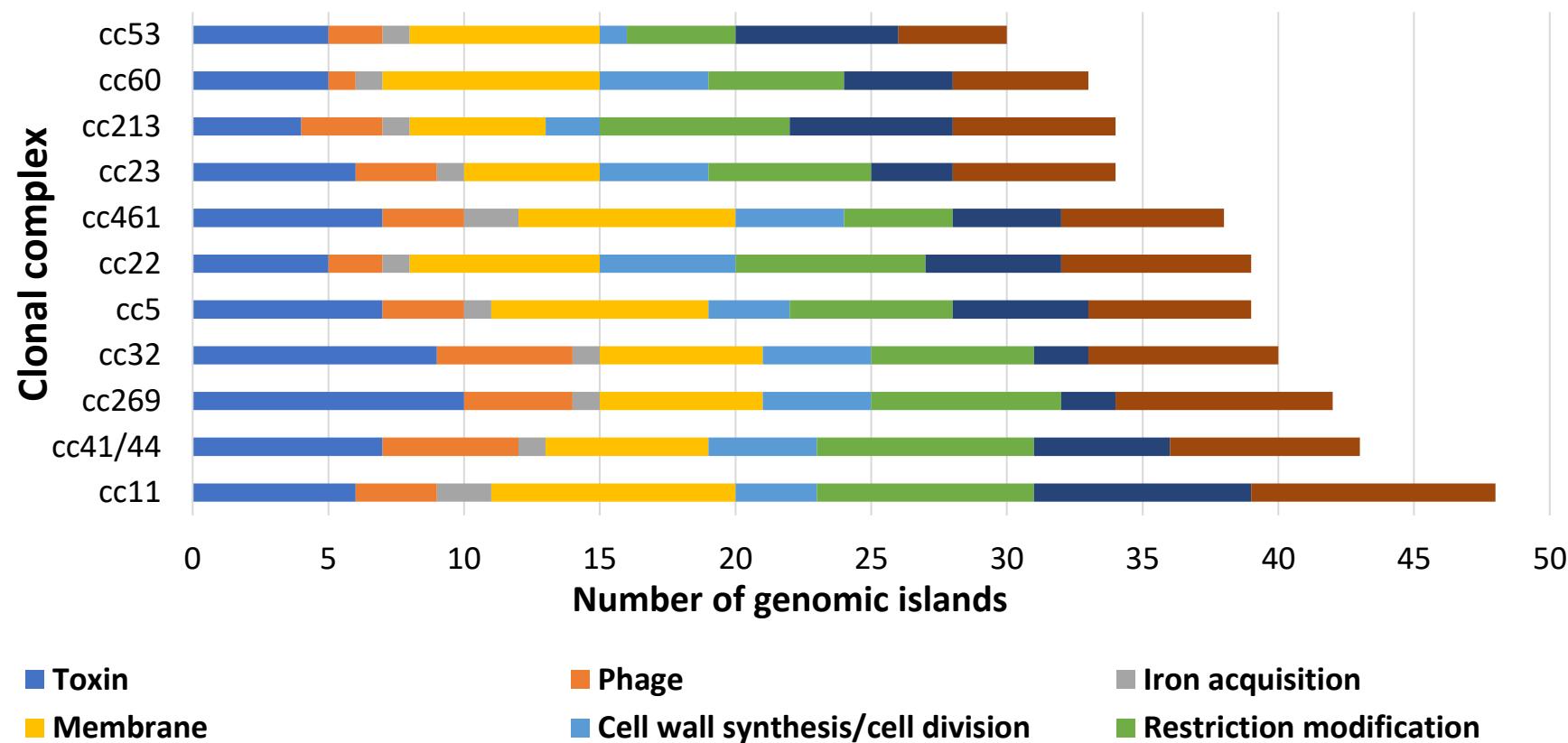


Supplementary Figure 3A. Evolutionary tree of *N. meningitidis* based on concatenated sequences from the 1735 genes that make up that core genome.
The tree was generated from 550 isolates from 11 clonal complexes using the Neighbour-Joining method with the Tamura-Nei genetic distance model. Each of the 11 clonal complexes is shown in a different colour.



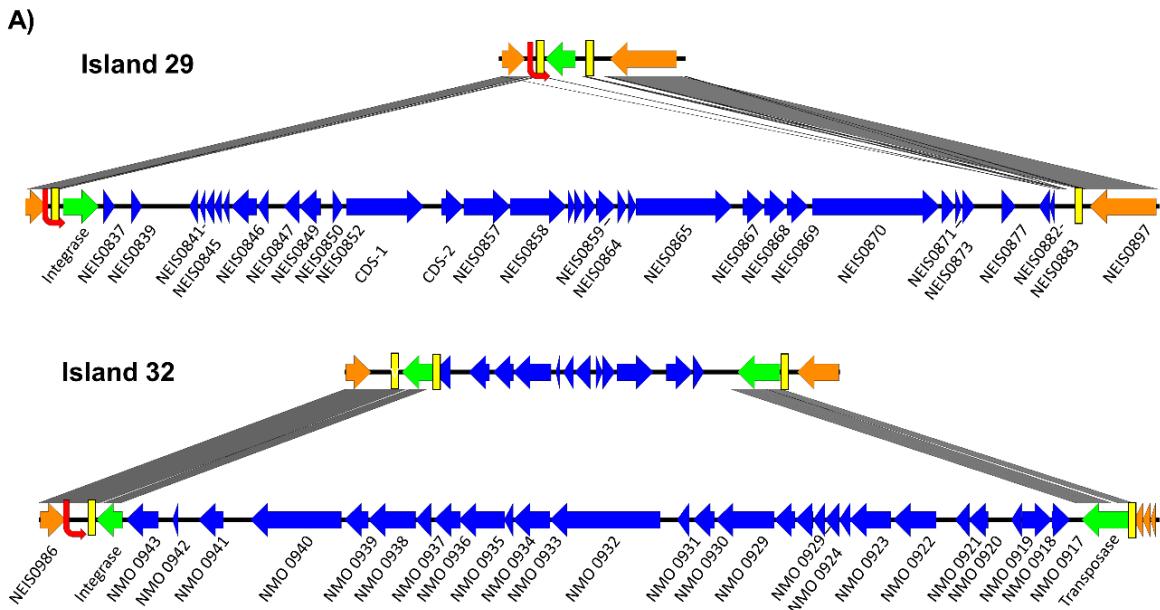
Supplementary Figure 3B. Evolutionary tree of *N. meningitidis* based on concatenated sequences from the 827 genes that make up the pan-accessory genome.

The tree was generated from 550 isolates from 11 clonal complexes using the Neighbor-Joining method with the Tamura-Nei genetic distance model. Each of the 11 clonal complexes is shown in a different colour.



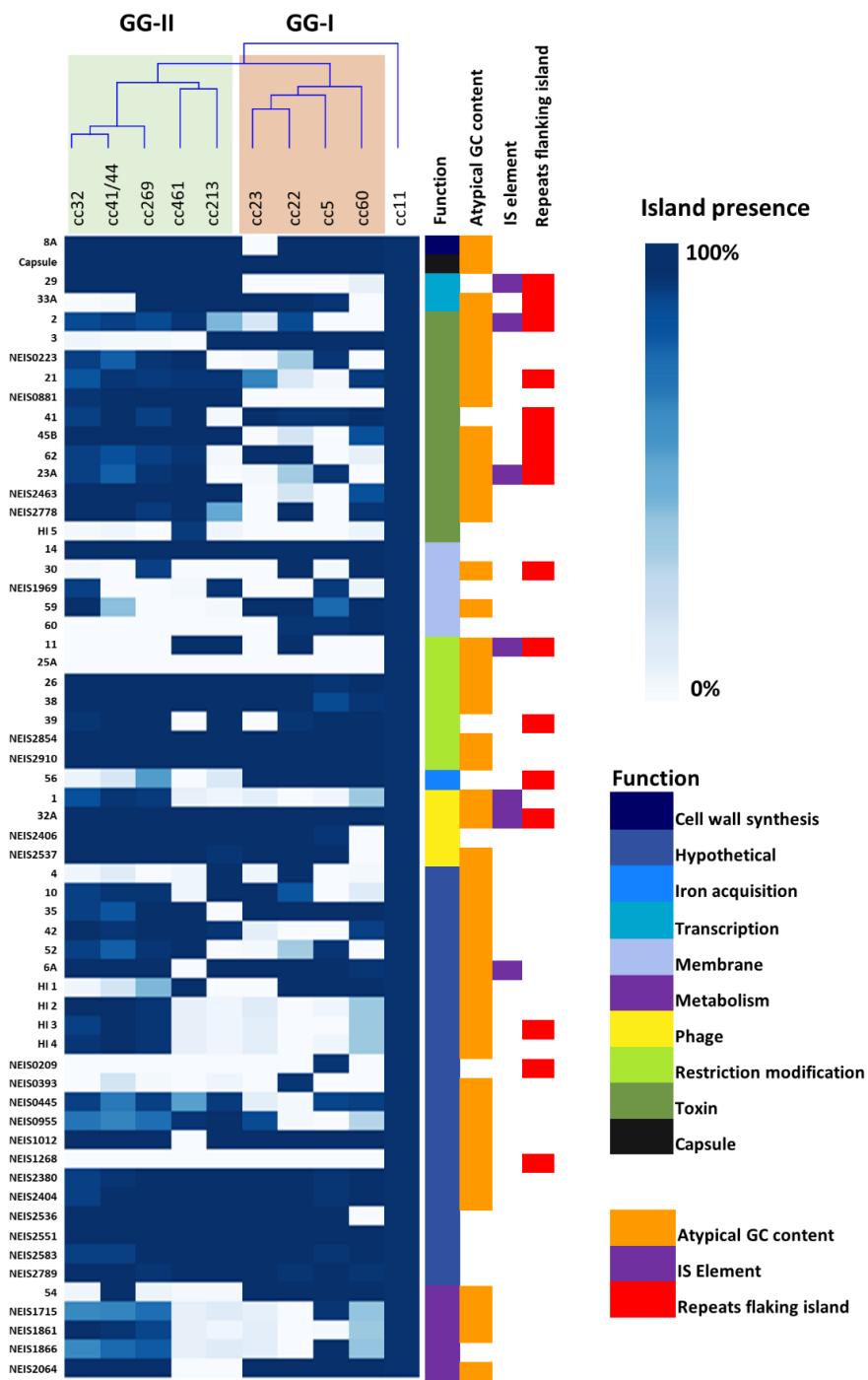
Supplementary Figure 4. Frequency of the 81 genomic islands amongst the 11 clonal complexes, by function.

Each functional category has been assigned a separate colour. If a GI was present in greater than 80% of isolates in a cc, it was counted as present.



Supplementary Figure 5. Genomic islands that show evidence of a mechanism of horizontal transfer.

Genes within the island are depicted by blue arrows, green arrows represent transposable genetic elements, and the orange arrows represent the core genes flanking the island. tRNAs are depicted by red arrows. Direct repeats are shown in yellow boxes. The shaded grey regions between islands show regions of homology.



Supplementary Figure 6. Heatmap of hypervirulent associated genes (HVAGs) in 11 clonal complexes.

Each functional category has been assigned a different colour. Clonal complexes are hierarchically clustered based on the presence of the pathogen associated islands and a corresponding dendrogram was generated. Genomic islands and single genes have been clustered according to putative function. Where a GI has been assigned a number, it has been listed next to the island. Island comprising hypothetical genes have been denoted as HI. Genomic islands with atypical GC content are coloured in orange, islands associated with an IS element are coloured in purple, and islands with flanking repeats are denoted in red. A dendrogram has been used to cluster clonal complexes into genogroup I (GG-I, orange) and II (GG-II, green).

Supplementary Table 1. Isolates used in this study from PubMLST.

| PubMLST ID | Isolate name | Country of isolation | Collection date | Clonal complex |
|------------|--------------|----------------------|-----------------|------------------|
| 7 | 7891 | Finland | 1975 | ST-5 complex |
| 24 | S4355 | Denmark | 1974 | ST-5 complex |
| 30 | 14 | Germany | 1999 | ST-53 complex |
| 82 | 11-004 | China | 1984 | ST-5 complex |
| 84 | IAL2229 | Brazil | 1976 | ST-5 complex |
| 120 | F4698 | Saudi Arabia | 1987 | ST-5 complex |
| 128 | F6124 | Chad | 1988 | ST-5 complex |
| 210 | H1964 | UK | 1987 | ST-5 complex |
| 237 | H44/76 | Norway | 1976 | ST-32 complex |
| 238 | 153 | China | 1966 | ST-5 complex |
| 239 | 154 | China | 1966 | ST-5 complex |
| 240 | MC58 | UK | 1983 | ST-32 complex |
| 299 | 80049 | China | 1963 | ST-5 complex |
| 314 | D1 | Mali | 1989 | ST-11 complex |
| 340 | 196/87 | Norway | 1987 | ST-32 complex |
| 343 | 500 | Italy | 1984 | ST-11 complex |
| 349 | 38VI | USA | 1964 | ST-11 complex |
| 369 | M597 | Israel | 1988 | ST-11 complex |
| 391 | 90/18311 | UK [Scotland] | 1990 | ST-11 complex |
| 400 | BZ 83 | The Netherlands | 1984 | ST-32 complex |
| 403 | BZ 147 | The Netherlands | 1963 | ST-41/44 complex |
| 408 | BZ 169 | The Netherlands | 1985 | ST-32 complex |
| 409 | BZ 198 | The Netherlands | 1986 | ST-41/44 complex |
| 415 | EG 329 | Germany | 1985 | ST-32 complex |
| 419 | NG 6/88 | Norway | 1988 | ST-269 complex |

| PubMLST ID | Isolate name | Country of isolation | Collection date | Clonal complex |
|-------------------|---------------------|-----------------------------|------------------------|-----------------------|
| 420 | NG F26 | Norway | 1988 | ST-269 complex |
| 421 | NG H15 | Norway | 1988 | ST-41/44 complex |
| 427 | NG E30 | Norway | 1988 | ST-41/44 complex |
| 428 | NG H36 | Norway | 1988 | ST-41/44 complex |
| 430 | NG 080 | Norway | 1981 | ST-32 complex |
| 431 | NG144/82 | Norway | 1982 | ST-32 complex |
| 434 | NG PB24 | Norway | 1985 | ST-32 complex |
| 441 | 8680 | Chile | 1987 | ST-32 complex |
| 451 | 14/1455 | Russia | 1970 | ST-5 complex |
| 468 | BRAZ10 | Brazil | 1976 | ST-11 complex |
| 507 | MA-5756 | Spain | 1985 | ST-11 complex |
| 597 | 92001 | China | 1992 | ST-5 complex |
| 644 | L93/4286 | UK [England] | 1993 | ST-11 complex |
| 645 | 204/92 | Cuba | 1992 | ST-32 complex |
| 646 | 400 | Austria | 1991 | ST-41/44 complex |
| 647 | AK50 | Greece | 1992 | ST-41/44 complex |
| 648 | M-101/93 | Iceland | 1993 | ST-41/44 complex |
| 649 | 50/94 | Norway | 1994 | ST-41/44 complex |
| 650 | M40/94 | Chile | 1994 | ST-41/44 complex |
| 651 | 931905 | The Netherlands | 1993 | ST-41/44 complex |
| 652 | N45/96 | Norway | 1996 | ST-41/44 complex |
| 653 | 91/40 | New Zealand | 1991 | ST-41/44 complex |
| 659 | A22 | Norway | 1986 | ST-22 complex |
| 660 | 71/94 | Norway | 1994 | ST-23 complex |
| 662 | 2837 | UK | 1997 | ST-11 complex |
| 665 | 2845 | UK | 1997 | ST-11 complex |
| 666 | 2843 | UK | 1997 | ST-11 complex |
| 667 | 2842 | UK | 1997 | ST-11 complex |

| PubMLST ID | Isolate name | Country of isolation | Collection date | Clonal complex |
|-------------------|---------------------|-----------------------------|------------------------|-----------------------|
| 669 | 2846 | UK | 1997 | ST-11 complex |
| 670 | 2840 | UK | 1997 | ST-11 complex |
| 671 | 2844 | UK | 1997 | ST-11 complex |
| 672 | 2847 | UK | 1997 | ST-11 complex |
| 684 | 0259/93 | Czech Republic | 1993 | ST-11 complex |
| 698 | FAM18 | USA | 1983 | ST-11 complex |
| 939 | 0022/93 | Czech Republic | 1993 | ST-11 complex |
| 940 | 0023/93 | Czech Republic | 1993 | ST-11 complex |
| 942 | 0025/93 | Czech Republic | 1993 | ST-11 complex |
| 946 | 0033/93 | Czech Republic | 1993 | ST-11 complex |
| 948 | 0035/93 | Czech Republic | 1993 | ST-11 complex |
| 949 | 0036/93 | Czech Republic | 1993 | ST-11 complex |
| 950 | 0037/93 | Czech Republic | 1993 | ST-11 complex |
| 952 | 0039/93 | Czech Republic | 1993 | ST-11 complex |
| 954 | 0042/93 | Czech Republic | 1993 | ST-11 complex |
| 955 | 0043/93 | Czech Republic | 1993 | ST-11 complex |
| 957 | 0045/93 | Czech Republic | 1993 | ST-11 complex |
| 958 | 0046/93 | Czech Republic | 1993 | ST-11 complex |
| 968 | 0061/93 | Czech Republic | 1993 | ST-22 complex |
| 969 | 0062/93 | Czech Republic | 1993 | ST-32 complex |
| 972 | 0066/93 | Czech Republic | 1993 | ST-53 complex |
| 973 | 0067/93 | Czech Republic | 1993 | ST-41/44 complex |
| 975 | 0069/93 | Czech Republic | 1993 | ST-41/44 complex |
| 977 | 0071/93 | Czech Republic | 1993 | ST-41/44 complex |
| 978 | 0073/93 | Czech Republic | 1993 | ST-11 complex |
| 979 | 0074/93 | Czech Republic | 1993 | ST-11 complex |
| 982 | 0079/93 | Czech Republic | 1993 | ST-11 complex |
| 984 | 0083/93 | Czech Republic | 1993 | ST-53 complex |
| 991 | 0091/93 | Czech Republic | 1993 | ST-41/44 complex |

| PubMLST ID | Isolate name | Country of isolation | Collection date | Clonal complex |
|-------------------|---------------------|-----------------------------|------------------------|-----------------------|
| 992 | 0093/93 | Czech Republic | 1993 | ST-11 complex |
| 993 | 0095/93 | Czech Republic | 1993 | ST-11 complex |
| 994 | 0096/93 | Czech Republic | 1993 | ST-11 complex |
| 1168 | BM33 | Greece | 1996 | ST-32 complex |
| 1169 | BM45 | Greece | 1996 | ST-11 complex |
| 1170 | BM45a | Greece | 1996 | ST-11 complex |
| 1178 | W72 | Greece | 1997 | ST-11 complex |
| 1179 | W72a | Greece | 1997 | ST-11 complex |
| 1180 | W72b | Greece | 1997 | ST-11 complex |
| 1181 | W138 | Greece | 1998 | ST-11 complex |
| 1212 | 0099/93 | Czech Republic | 1993 | ST-11 complex |
| 1570 | 0101/93 | Czech Republic | 1993 | ST-11 complex |
| 1571 | 0102/93 | Czech Republic | 1993 | ST-11 complex |
| 1572 | 0103/93 | Czech Republic | 1993 | ST-11 complex |
| 1573 | 0104/93 | Czech Republic | 1993 | ST-11 complex |
| 1578 | 0109/93 | Czech Republic | 1993 | ST-11 complex |
| 1585 | 0117/93 | Czech Republic | 1993 | ST-41/44 complex |
| 1588 | 0120/93 | Czech Republic | 1993 | ST-41/44 complex |
| 1597 | 0206/93 | Czech Republic | 1993 | ST-53 complex |
| 1601 | 0211/93 | Czech Republic | 1993 | ST-269 complex |
| 1603 | 0213/93 | Czech Republic | 1993 | ST-41/44 complex |
| 1604 | 0214/93 | Czech Republic | 1993 | ST-41/44 complex |
| 1605 | 0215/93 | Czech Republic | 1993 | ST-41/44 complex |
| 1606 | 0216/93 | Czech Republic | 1993 | ST-41/44 complex |
| 1607 | 0217/93 | Czech Republic | 1993 | ST-41/44 complex |
| 1615 | 0225/93 | Czech Republic | 1993 | ST-41/44 complex |
| 1616 | 0226/93 | Czech Republic | 1993 | ST-41/44 complex |
| 1617 | 0227/93 | Czech Republic | 1993 | ST-41/44 complex |
| 1618 | 0228/93 | Czech Republic | 1993 | ST-41/44 complex |

| PubMLST ID | Isolate name | Country of isolation | Collection date | Clonal complex |
|-------------------|---------------------|-----------------------------|------------------------|-----------------------|
| 1633 | 0244/93 | Czech Republic | 1993 | ST-41/44 complex |
| 1639 | 0252/93 | Czech Republic | 1993 | ST-53 complex |
| 1640 | 0253/93 | Czech Republic | 1993 | ST-41/44 complex |
| 1642 | 0255/93 | Czech Republic | 1993 | ST-41/44 complex |
| 1645 | 0258/93 | Czech Republic | 1993 | ST-41/44 complex |
| 1649 | 0269/93 | Czech Republic | 1993 | ST-53 complex |
| 1654 | 0277/93 | Czech Republic | 1993 | ST-53 complex |
| 1656 | 0280/93 | Czech Republic | 1993 | ST-41/44 complex |
| 1949 | 0306/93 | Czech Republic | 1993 | ST-22 complex |
| 1955 | 0011/93 | Czech Republic | 1993 | ST-41/44 complex |
| 1958 | 0307/93 | Czech Republic | 1993 | ST-41/44 complex |
| 2077 | 153 | Germany | 1999 | ST-60 complex |
| 2216 | 0190/93 | Czech Republic | 1993 | ST-269 complex |
| 2220 | 0312/93 | Czech Republic | 1993 | ST-22 complex |
| 2222 | 0314/93 | Czech Republic | 1993 | ST-53 complex |
| 2233 | 0531/93 | Czech Republic | 1993 | ST-32 complex |
| 8139 | 0320/93 | Czech Republic | 1993 | ST-41/44 complex |
| 8144 | 0325/93 | Czech Republic | 1993 | ST-41/44 complex |
| 8156 | 0342/93 | Czech Republic | 1993 | ST-41/44 complex |
| 8164 | 0404/93 | Czech Republic | 1993 | ST-41/44 complex |
| 8168 | 0409/93 | Czech Republic | 1993 | ST-41/44 complex |
| 8169 | 0410/93 | Czech Republic | 1993 | ST-53 complex |
| 8171 | 0412/93 | Czech Republic | 1993 | ST-41/44 complex |
| 8173 | 0414/93 | Czech Republic | 1993 | ST-41/44 complex |
| 8176 | 0421/93 | Czech Republic | 1993 | ST-41/44 complex |
| 8177 | 0422/93 | Czech Republic | 1993 | ST-53 complex |
| 8181 | 0426/93 | Czech Republic | 1993 | ST-53 complex |
| 9756 | 275 | Germany | 2000 | ST-22 complex |
| 10705 | N 25/99 | Norway | 1999 | ST-41/44 complex |

| PubMLST ID | Isolate name | Country of isolation | Collection date | Clonal complex |
|-------------------|---------------------|-----------------------------|------------------------|-----------------------|
| 10735 | N 56/99 | Norway | 1999 | ST-41/44 complex |
| 10756 | 8/00 | Norway | 2000 | ST-41/44 complex |
| 10758 | 10/00 | Norway | 2000 | ST-41/44 complex |
| 10812 | 64/00 | Norway | 2000 | ST-41/44 complex |
| 10830 | MK 66/96 | Norway | 1996 | ST-41/44 complex |
| 10837 | MK 75/96 | Norway | 1996 | ST-41/44 complex |
| 14480 | M5178 | USA | 1998 | ST-32 complex |
| 15249 | 0379/93 | Czech Republic | 1993 | ST-32 complex |
| 15313 | 0469/93 | Czech Republic | 1993 | ST-32 complex |
| 18968 | M10 240474 | UK [England] | 2010 | ST-269 complex |
| 19023 | M10 240473 | UK [England] | 2010 | ST-269 complex |
| 19028 | M10 240485 | UK [England] | 2010 | ST-269 complex |
| 19029 | M10 240487 | UK [England] | 2010 | ST-269 complex |
| 19030 | M10 240489 | UK [England] | 2010 | ST-461 complex |
| 19031 | M10 240490 | UK [England] | 2010 | ST-269 complex |
| 19260 | WUE 2594 | Germany | 1991 | ST-5 complex |
| 19264 | M04-240196 | UK | 2004 | ST-269 complex |
| 19265 | M01-240355 | UK | 2001 | ST-213 complex |
| 19359 | M13399 | Unknown | 2005 | ST-269 complex |
| 19362 | CU385 | Unknown | 1980 | ST-32 complex |
| 19366 | M10699 | USA | 2003 | ST-32 complex |
| 19368 | M13220 | Philippines | 2005 | ST-5 complex |
| 19372 | M15293 | USA | 2006 | ST-32 complex |
| 19958 | M10 240476 | UK [England] | 2010 | ST-213 complex |
| 19959 | M10 240499 | UK [England] | 2010 | ST-269 complex |
| 19962 | M10 240503 | UK [England] | 2010 | ST-23 complex |
| 19963 | M10 240505 | UK [England] | 2010 | ST-23 complex |
| 19964 | M10 240507 | UK [England] | 2010 | ST-23 complex |
| 19969 | M10 240515 | UK [England] | 2010 | ST-269 complex |

| PubMLST ID | Isolate name | Country of isolation | Collection date | Clonal complex |
|-------------------|---------------------|-----------------------------|------------------------|-----------------------|
| 19970 | M10 240520 | UK [England] | 2010 | ST-23 complex |
| 19973 | M10 240525 | UK [England] | 2010 | ST-32 complex |
| 19974 | M10 240527 | UK [England] | 2010 | ST-269 complex |
| 19975 | M10 240528 | UK [England] | 2010 | ST-269 complex |
| 19976 | M10 240530 | UK [England] | 2010 | ST-23 complex |
| 19977 | M10 240531 | UK [England] | 2010 | ST-23 complex |
| 19979 | M10 240534 | UK [England] | 2010 | ST-23 complex |
| 19980 | M10 240536 | UK [England] | 2010 | ST-23 complex |
| 19981 | M10 240540 | UK [England] | 2010 | ST-23 complex |
| 19982 | M10 240546 | UK [England] | 2010 | ST-213 complex |
| 19983 | M10 240547 | UK [England] | 2010 | ST-32 complex |
| 19986 | M10 240550 | UK [England] | 2010 | ST-269 complex |
| 19987 | M10 240553 | UK [Wales] | 2010 | ST-269 complex |
| 19991 | M10 240566 | UK [England] | 2010 | ST-213 complex |
| 19992 | M10 240568 | UK [England] | 2010 | ST-213 complex |
| 19995 | M10 240572 | UK [England] | 2010 | ST-269 complex |
| 19996 | M10 240578 | UK [England] | 2010 | ST-32 complex |
| 19998 | M10 240580 | UK [England] | 2010 | ST-23 complex |
| 20000 | M10 240582 | UK [England] | 2010 | ST-32 complex |
| 20006 | M10 240590 | UK [England] | 2010 | ST-23 complex |
| 20007 | M10 240591 | UK [England] | 2010 | ST-461 complex |
| 20009 | M10 240595 | UK [England] | 2010 | ST-213 complex |
| 20012 | M10 240602 | UK [England] | 2010 | ST-269 complex |
| 20015 | M10 240606 | UK [England] | 2010 | ST-213 complex |
| 20017 | M10 240611 | UK [England] | 2010 | ST-32 complex |
| 20018 | M10 240612 | UK [England] | 2010 | ST-269 complex |
| 20019 | M10 240613 | UK [England] | 2010 | ST-269 complex |
| 20021 | M10 240616 | UK [England] | 2010 | ST-22 complex |
| 20022 | M10 240617 | UK [England] | 2010 | ST-213 complex |

| PubMLST ID | Isolate name | Country of isolation | Collection date | Clonal complex |
|-------------------|---------------------|-----------------------------|------------------------|-----------------------|
| 20023 | M10 240618 | UK [England] | 2010 | ST-60 complex |
| 20024 | M10 240619 | UK [England] | 2010 | ST-213 complex |
| 20025 | M10 240621 | UK [Wales] | 2010 | ST-213 complex |
| 20027 | M10 240623 | UK [England] | 2010 | ST-269 complex |
| 20028 | M10 240624 | UK [England] | 2010 | ST-269 complex |
| 20029 | M10 240626 | UK [England] | 2010 | ST-269 complex |
| 20030 | M10 240627 | UK [England] | 2010 | ST-32 complex |
| 20031 | M10 240631 | UK [England] | 2010 | ST-269 complex |
| 20032 | M10 240632 | UK [England] | 2010 | ST-23 complex |
| 20033 | M10 240633 | UK [England] | 2010 | ST-23 complex |
| 20036 | M10 240638 | UK [England] | 2010 | ST-269 complex |
| 20039 | M10 240641 | UK [England] | 2010 | ST-22 complex |
| 20041 | M10 240643 | UK [England] | 2010 | ST-23 complex |
| 20042 | M10 240644 | UK [England] | 2010 | ST-22 complex |
| 20043 | M10 240645 | UK [England] | 2010 | ST-269 complex |
| 20044 | M10 240649 | UK [England] | 2010 | ST-269 complex |
| 20046 | M10 240651 | UK [England] | 2010 | ST-213 complex |
| 20047 | M10 240652 | UK [England] | 2010 | ST-269 complex |
| 20050 | M10 240661 | UK [England] | 2010 | ST-269 complex |
| 20052 | M10 240665 | UK [England] | 2010 | ST-213 complex |
| 20056 | M10 240670 | UK [England] | 2010 | ST-269 complex |
| 20064 | M10 240682 | UK [Northern Ireland] | 2010 | ST-269 complex |
| 20067 | M10 240685 | UK [England] | 2010 | ST-23 complex |
| 20068 | M10 240687 | UK [England] | 2010 | ST-60 complex |
| 20071 | M10 240693 | UK [England] | 2010 | ST-60 complex |
| 20074 | M10 240700 | UK [England] | 2010 | ST-23 complex |
| 20075 | M10 240701 | UK [England] | 2010 | ST-213 complex |
| 20077 | M10 240703 | UK [England] | 2010 | ST-213 complex |

| PubMLST ID | Isolate name | Country of isolation | Collection date | Clonal complex |
|-------------------|---------------------|-----------------------------|------------------------|-----------------------|
| 20078 | M10 240704 | UK [England] | 2010 | ST-269 complex |
| 20081 | M10 240708 | UK [England] | 2010 | ST-269 complex |
| 20082 | M10 240709 | UK [England] | 2010 | ST-269 complex |
| 20083 | M10 240711 | UK [England] | 2010 | ST-269 complex |
| 20084 | M10 240712 | UK [England] | 2010 | ST-213 complex |
| 20085 | M10 240713 | UK [England] | 2010 | ST-269 complex |
| 20086 | M10 240716 | UK [England] | 2010 | ST-461 complex |
| 20087 | M10 240717 | UK [England] | 2010 | ST-213 complex |
| 20088 | M10 240718 | UK [England] | 2010 | ST-60 complex |
| 20089 | M10 240719 | UK [England] | 2010 | ST-32 complex |
| 20090 | M10 240720 | UK [England] | 2010 | ST-269 complex |
| 20095 | M10 240728 | UK [England] | 2010 | ST-269 complex |
| 20096 | M10 240729 | UK [England] | 2010 | ST-269 complex |
| 20099 | M10 240732 | UK [England] | 2010 | ST-23 complex |
| 20101 | M10 240737 | UK [England] | 2010 | ST-22 complex |
| 20102 | M10 240742 | UK [England] | 2010 | ST-213 complex |
| 20103 | M10 240743 | UK [England] | 2010 | ST-269 complex |
| 20104 | M10 240745 | UK [England] | 2010 | ST-23 complex |
| 20110 | M10 240751 | UK [England] | 2010 | ST-213 complex |
| 20111 | M10 240752 | UK [England] | 2010 | ST-269 complex |
| 20112 | M10 240753 | UK [England] | 2010 | ST-32 complex |
| 20114 | M10 240756 | UK [England] | 2010 | ST-22 complex |
| 20119 | M10 240766 | UK [England] | 2010 | ST-269 complex |
| 20120 | M10 240767 | UK [Wales] | 2010 | ST-32 complex |
| 20121 | M10 240768 | UK [England] | 2010 | ST-269 complex |
| 20122 | M10 240770 | UK [England] | 2010 | ST-269 complex |
| 20124 | M10 240772 | UK [England] | 2010 | ST-269 complex |
| 20126 | M10 240774 | UK [Wales] | 2010 | ST-269 complex |
| 20128 | M10 240776 | UK [England] | 2010 | ST-23 complex |

| PubMLST ID | Isolate name | Country of isolation | Collection date | Clonal complex |
|-------------------|---------------------|-----------------------------|------------------------|-----------------------|
| 20129 | M10 240777 | UK [England] | 2010 | ST-23 complex |
| 20130 | M10 240778 | UK [Wales] | 2010 | ST-213 complex |
| 20131 | M10 240779 | UK [England] | 2010 | ST-269 complex |
| 20132 | M10 240781 | UK [England] | 2010 | ST-22 complex |
| 20133 | M10 240783 | UK [England] | 2010 | ST-269 complex |
| 20135 | M10 240786 | UK [England] | 2010 | ST-23 complex |
| 20136 | M10 240787 | UK [England] | 2010 | ST-23 complex |
| 20138 | M10 240789 | UK [Wales] | 2010 | ST-269 complex |
| 20139 | M10 240790 | UK [England] | 2010 | ST-32 complex |
| 20141 | M10 240794 | UK [England] | 2010 | ST-32 complex |
| 20143 | M10 240798 | UK [England] | 2010 | ST-23 complex |
| 20144 | M10 240799 | UK [England] | 2010 | ST-213 complex |
| 20146 | M10 240804 | UK [England] | 2010 | ST-23 complex |
| 20159 | M10 240822 | UK [England] | 2010 | ST-22 complex |
| 20161 | M10 240824 | UK [England] | 2010 | ST-32 complex |
| 20162 | M10 240825 | UK [England] | 2010 | ST-60 complex |
| 20164 | M11 240000 | UK [England] | 2011 | ST-23 complex |
| 20165 | M11 240001 | UK [England] | 2011 | ST-461 complex |
| 20169 | M11 240005 | UK [England] | 2011 | ST-23 complex |
| 20170 | M11 240006 | UK [Wales] | 2011 | ST-32 complex |
| 20171 | M11 240007 | UK [England] | 2011 | ST-23 complex |
| 20176 | M11 240013 | UK [England] | 2011 | ST-32 complex |
| 20177 | M11 240014 | UK [England] | 2011 | ST-461 complex |
| 20179 | M11 240016 | UK [Wales] | 2011 | ST-32 complex |
| 20183 | M11 240021 | UK [England] | 2011 | ST-32 complex |
| 20189 | M11 240027 | UK [England] | 2011 | ST-60 complex |
| 20190 | M11 240028 | UK [England] | 2011 | ST-60 complex |
| 20191 | M11 240029 | UK [England] | 2011 | ST-22 complex |
| 20193 | M11 240031 | UK [England] | 2011 | ST-23 complex |

| PubMLST ID | Isolate name | Country of isolation | Collection date | Clonal complex |
|-------------------|---------------------|-----------------------------|------------------------|-----------------------|
| 20197 | M11 240036 | UK [Wales] | 2011 | ST-23 complex |
| 20198 | M11 240037 | UK [England] | 2011 | ST-32 complex |
| 20203 | M11 240042 | UK [England] | 2011 | ST-461 complex |
| 20204 | M11 240043 | UK [England] | 2011 | ST-23 complex |
| 20207 | M11 240046 | UK [England] | 2011 | ST-213 complex |
| 20209 | M11 240048 | UK [England] | 2011 | ST-60 complex |
| 20210 | M11 240050 | UK [England] | 2011 | ST-213 complex |
| 20211 | M11 240052 | UK [Wales] | 2011 | ST-461 complex |
| 20220 | M11 240061 | UK [England] | 2011 | ST-213 complex |
| 20224 | M11 240065 | UK [England] | 2011 | ST-23 complex |
| 20233 | M11 240074 | UK [Wales] | 2011 | ST-213 complex |
| 20238 | M11 240082 | UK [England] | 2011 | ST-32 complex |
| 20239 | M11 240083 | UK [England] | 2011 | ST-461 complex |
| 20245 | M11 240096 | UK [England] | 2011 | ST-23 complex |
| 20250 | M11 240109 | UK [England] | 2011 | ST-32 complex |
| 20252 | M11 240111 | UK [England] | 2011 | ST-213 complex |
| 20254 | M11 240113 | UK [England] | 2011 | ST-213 complex |
| 20256 | M11 240116 | UK [England] | 2011 | ST-23 complex |
| 20257 | M11 240117 | UK [England] | 2011 | ST-60 complex |
| 20259 | M11 240121 | UK [England] | 2011 | ST-213 complex |
| 20264 | M11 240126 | UK [England] | 2011 | ST-23 complex |
| 20270 | M11 240134 | UK [England] | 2011 | ST-213 complex |
| 20271 | M11 240137 | UK [England] | 2011 | ST-213 complex |
| 20275 | M11 240147 | UK [England] | 2011 | ST-213 complex |
| 20281 | M11 240157 | UK [England] | 2011 | ST-23 complex |
| 20286 | M11 240166 | UK [England] | 2011 | ST-23 complex |
| 20287 | M11 240167 | UK [England] | 2011 | ST-60 complex |
| 20292 | M11 240175 | UK [England] | 2011 | ST-32 complex |
| 20295 | M11 240181 | UK [England] | 2011 | ST-213 complex |

| PubMLST ID | Isolate name | Country of isolation | Collection date | Clonal complex |
|-------------------|---------------------|-----------------------------|------------------------|-----------------------|
| 20297 | M11 240183 | UK [England] | 2011 | ST-32 complex |
| 20302 | M11 240192 | UK [Wales] | 2011 | ST-23 complex |
| 20306 | M11 240206 | UK [England] | 2011 | ST-461 complex |
| 20309 | M11 240210 | UK [England] | 2011 | ST-23 complex |
| 20313 | M11 240214 | UK [England] | 2011 | ST-461 complex |
| 20314 | M11 240215 | UK [England] | 2011 | ST-23 complex |
| 20315 | M11 240216 | UK [England] | 2011 | ST-23 complex |
| 20317 | M11 240227 | UK [England] | 2011 | ST-23 complex |
| 20318 | M11 240231 | UK [England] | 2011 | ST-22 complex |
| 20328 | M11 240246 | UK [England] | 2011 | ST-60 complex |
| 20335 | M11 240258 | UK [England] | 2011 | ST-23 complex |
| 20337 | M11 240261 | UK [England] | 2011 | ST-22 complex |
| 20338 | M11 240262 | UK [England] | 2011 | ST-5 complex |
| 20339 | M11 240263 | UK [England] | 2011 | ST-23 complex |
| 20341 | M11 240266 | UK [England] | 2011 | ST-213 complex |
| 20342 | M11 240268 | UK [England] | 2011 | ST-213 complex |
| 20346 | M11 240277 | UK [England] | 2011 | ST-23 complex |
| 20347 | M11 240278 | UK [England] | 2011 | ST-23 complex |
| 20350 | M11 240282 | UK [England] | 2011 | ST-213 complex |
| 20351 | M11 240283 | UK [England] | 2011 | ST-23 complex |
| 20353 | M11 240285 | UK [England] | 2011 | ST-32 complex |
| 20357 | M11 240290 | UK [England] | 2011 | ST-213 complex |
| 20361 | M11 240296 | UK [England] | 2011 | ST-32 complex |
| 20362 | M11 240297 | UK [England] | 2011 | ST-213 complex |
| 20363 | M11 240298 | UK [England] | 2011 | ST-23 complex |
| 20365 | M11 240302 | UK [England] | 2011 | ST-22 complex |
| 20372 | M11 240312 | UK [England] | 2011 | ST-23 complex |
| 20373 | M11 240313 | UK [England] | 2011 | ST-23 complex |
| 20382 | M11 240324 | UK [England] | 2011 | ST-32 complex |

| PubMLST ID | Isolate name | Country of isolation | Collection date | Clonal complex |
|-------------------|---------------------|-----------------------------|------------------------|-----------------------|
| 20389 | M11 240337 | UK [England] | 2011 | ST-213 complex |
| 20391 | M11 240339 | UK [England] | 2011 | ST-60 complex |
| 20393 | M11 240342 | UK [England] | 2011 | ST-32 complex |
| 20395 | M11 240344 | UK [England] | 2011 | ST-213 complex |
| 20398 | M11 240348 | UK [England] | 2011 | ST-213 complex |
| 20399 | M11 240349 | UK [England] | 2011 | ST-22 complex |
| 20403 | M11 240356 | UK [England] | 2011 | ST-32 complex |
| 20409 | M11 240366 | UK [Northern Ireland] | 2011 | ST-32 complex |
| 20422 | M11 240387 | UK [England] | 2011 | ST-22 complex |
| 20427 | M11 240392 | UK [England] | 2011 | ST-32 complex |
| 20428 | M11 240394 | UK [England] | 2011 | ST-60 complex |
| 20438 | M11 240406 | UK [England] | 2011 | ST-32 complex |
| 20441 | M11 240412 | UK [England] | 2011 | ST-60 complex |
| 20457 | M11 240440 | UK [England] | 2011 | ST-60 complex |
| 20477 | H44/76 | Norway | 1976 | ST-32 complex |
| 20564 | Nm6938 | Canada | 2001 | ST-22 complex |
| 20565 | Nm2732 | Canada | 2007 | ST-22 complex |
| 20741 | M09 240064 | UK | 2013 | ST-60 complex |
| 20753 | M09 240242 | UK | 2013 | ST-461 complex |
| 20759 | M09 240296 | UK | 2013 | ST-213 complex |
| 20763 | M09 240440 | UK | 2013 | ST-213 complex |
| 20769 | M09 240659 | UK | 2013 | ST-213 complex |
| 20771 | M09 240681 | UK | 2013 | ST-213 complex |
| 20790 | M10 240127 | UK | 2013 | ST-60 complex |
| 20793 | M10 240140 | UK | 2013 | ST-461 complex |
| 20899 | M05 240362 | UK | 2013 | ST-60 complex |
| 20900 | M05 240370 | UK | 2013 | ST-60 complex |
| 20903 | M05 241347 | UK | 2013 | ST-22 complex |

| PubMLST ID | Isolate name | Country of isolation | Collection date | Clonal complex |
|-------------------|---------------------|-----------------------------|------------------------|-----------------------|
| 20904 | M05 241348 | UK | 2013 | ST-22 complex |
| 20912 | M05 241259 | UK | 2013 | ST-213 complex |
| 20921 | M03 240607 | UK | 2013 | ST-213 complex |
| 20922 | M03 240609 | UK | 2013 | ST-213 complex |
| 20923 | M03 240829 | UK | 2013 | ST-213 complex |
| 20924 | M03 240830 | UK | 2013 | ST-213 complex |
| 20925 | M03 241030 | Ireland | 2013 | ST-213 complex |
| 20926 | M03 241054 | Ireland | 2013 | ST-213 complex |
| 20971 | M08 240422 | Isle of Man | 2008 | ST-60 complex |
| 20972 | M08 240423 | Isle of Man | 2013 | ST-60 complex |
| 21092 | M11 240443 | UK [England] | 2011 | ST-461 complex |
| 21112 | M11 240471 | UK [England] | 2011 | ST-60 complex |
| 21132 | M11 240497 | UK [England] | 2011 | ST-22 complex |
| 21139 | M11 240508 | UK [England] | 2011 | ST-22 complex |
| 21156 | M11 240716 | UK [England] | 2011 | ST-22 complex |
| 21175 | M11 240741 | UK [England] | 2011 | ST-22 complex |
| 21193 | M11 240780 | UK [England] | 2011 | ST-22 complex |
| 21228 | M11 240988 | UK [England] | 2011 | ST-461 complex |
| 21246 | M11 241031 | UK [England] | 2011 | ST-461 complex |
| 21271 | M11 241064 | UK [England] | 2011 | ST-22 complex |
| 21280 | M11 241075 | UK [Wales] | 2011 | ST-60 complex |
| 21290 | M12 240008 | UK [England] | 2012 | ST-22 complex |
| 21300 | M12 240019 | UK [England] | 2012 | ST-461 complex |
| 21349 | M12 240088 | UK [England] | 2012 | ST-22 complex |
| 21352 | M12 240093 | UK [England] | 2012 | ST-60 complex |
| 21371 | M12 240121 | UK [England] | 2012 | ST-22 complex |
| 21380 | M12 240132 | UK [England] | 2012 | ST-22 complex |
| 21396 | M12 240158 | UK [England] | 2012 | ST-60 complex |
| 21432 | M12 240222 | UK [England] | 2012 | ST-60 complex |

| PubMLST ID | Isolate name | Country of isolation | Collection date | Clonal complex |
|-------------------|---------------------|-----------------------------|------------------------|-----------------------|
| 21454 | M12 240251 | UK [England] | 2012 | ST-22 complex |
| 21576 | SA_serogroup W_NM4 | South Africa | 2012 | ST-22 complex |
| 26067 | 959000095 | Sweden | 1995 | ST-22 complex |
| 26253 | T97 | UK | 2011 | ST-53 complex |
| 26263 | V259 | UK | 2011 | ST-53 complex |
| 26264 | V302 | UK | 2012 | ST-60 complex |
| 26267 | T98 | UK | 2011 | ST-53 complex |
| 26271 | BB66 | UK | 2012 | ST-53 complex |
| 26273 | BB58 | UK | 2012 | ST-22 complex |
| 26274 | v191 | UK | 2012 | ST-53 complex |
| 26275 | BB242 | UK | 2012 | ST-22 complex |
| 26278 | BB122 | UK | 2012 | ST-60 complex |
| 26283 | R121 | UK | 2011 | ST-53 complex |
| 26287 | V129 | UK | 2011 | ST-22 complex |
| 26297 | T36 | UK | 2011 | ST-60 complex |
| 26303 | T287 | UK | 2011 | ST-22 complex |
| 26306 | R279 | UK | 2011 | ST-60 complex |
| 26308 | x268 | UK | 2012 | ST-60 complex |
| 26314 | z54 | UK | 2012 | ST-60 complex |
| 26320 | R136 | UK | 2011 | ST-53 complex |
| 26325 | x83 | UK | 2012 | ST-53 complex |
| 26326 | T304 | UK | 2011 | ST-53 complex |
| 26327 | R122 | UK | 2011 | ST-60 complex |
| 26329 | BB130 | UK | 2012 | ST-60 complex |
| 26332 | BB111 | UK | 2012 | ST-461 complex |
| 26336 | v216 | UK | 2012 | ST-53 complex |
| 26344 | R243 | UK | 2011 | ST-53 complex |
| 26349 | BB279 | UK | 2012 | ST-60 complex |

| PubMLST ID | Isolate name | Country of isolation | Collection date | Clonal complex |
|-------------------|---------------------|-----------------------------|------------------------|-----------------------|
| 26350 | T3 | UK | 2011 | ST-53 complex |
| 26352 | BB36 | UK | 2012 | ST-60 complex |
| 26355 | R263 | UK | 2011 | ST-53 complex |
| 26360 | R221 | UK | 2011 | ST-60 complex |
| 26365 | z191 | UK | 2012 | ST-53 complex |
| 26370 | R129 | UK | 2011 | ST-22 complex |
| 26372 | V304 | UK | 2012 | ST-53 complex |
| 26381 | R210 | UK | 2011 | ST-22 complex |
| 26382 | X136 | UK | 2011 | ST-53 complex |
| 26383 | R216 | UK | 2011 | ST-53 complex |
| 26390 | BB210 | UK | 2012 | ST-22 complex |
| 26394 | T121 | UK | 2011 | ST-53 complex |
| 26399 | R155 | UK | 2011 | ST-53 complex |
| 26402 | R83 | UK | 2011 | ST-53 complex |
| 26406 | T122 | UK | 2011 | ST-60 complex |
| 26408 | BB287 | UK | 2012 | ST-22 complex |
| 26409 | R222 | UK | 2011 | ST-60 complex |
| 26411 | R36 | UK | 2011 | ST-60 complex |
| 26414 | R4 | UK | 2011 | ST-60 complex |
| 26415 | T191 | UK | 2011 | ST-53 complex |
| 26418 | x222 | UK | 2012 | ST-60 complex |
| 26419 | T119 | UK | 2011 | ST-53 complex |
| 26425 | R256 | UK | 2011 | ST-60 complex |
| 26432 | T210 | UK | 2011 | ST-22 complex |
| 26434 | T302 | UK | 2011 | ST-60 complex |
| 26444 | R97 | UK | 2011 | ST-53 complex |
| 26445 | Z119 | UK | 2012 | ST-53 complex |
| 26450 | BB159 | UK | 2012 | ST-60 complex |
| 26451 | r119 | UK | 2011 | ST-53 complex |

| PubMLST ID | Isolate name | Country of isolation | Collection date | Clonal complex |
|-------------------|---------------------|-----------------------------|------------------------|-----------------------|
| 26457 | R191 | UK | 2011 | ST-53 complex |
| 26464 | Z221 | UK | 2012 | ST-60 complex |
| 26466 | X119 | UK | 2012 | ST-53 complex |
| 26474 | T216 | UK | 2011 | ST-53 complex |
| 26476 | R58 | UK | 2011 | ST-22 complex |
| 26498 | T279 | UK | 2011 | ST-60 complex |
| 26500 | BB83 | UK | 2012 | ST-53 complex |
| 26515 | BB54 | UK | 2012 | ST-60 complex |
| 26518 | v119 | UK | 2012 | ST-53 complex |
| 26519 | T53 | UK | 2011 | ST-60 complex |
| 26522 | x121 | UK | 2012 | ST-53 complex |
| 26529 | BB228 | UK | 2012 | ST-53 complex |
| 26530 | V210 | UK | 2012 | ST-22 complex |
| 26839 | 12005_2011 | Ireland | 2011 | ST-461 complex |
| 26847 | 12018_2011 | Ireland | 2011 | ST-461 complex |
| 26888 | 12029_2012 | Ireland | 2012 | ST-22 complex |
| 26900 | 12004_2013 | Ireland | 2013 | ST-22 complex |
| 26922 | 10215v3 | UK | 2013 | ST-22 complex |
| 26923 | 10215v4 | UK | 2013 | ST-22 complex |
| 27782 | M12 240347 | UK [England] | 2012 | ST-461 complex |
| 27814 | M12 240704 | UK [England] | 2012 | ST-461 complex |
| 27839 | M12 240763 | UK [England] | 2012 | ST-461 complex |
| 27843 | M12 240778 | UK [England] | 2012 | ST-461 complex |
| 27849 | M12 240787 | UK [Wales] | 2012 | ST-461 complex |
| 27864 | M12 240819 | UK [England] | 2012 | ST-461 complex |
| 27871 | M12 240844 | UK [England] | 2012 | ST-461 complex |
| 27887 | M12 240873 | UK [Wales] | 2012 | ST-461 complex |
| 27907 | M13 240006 | UK [England] | 2013 | ST-461 complex |
| 27914 | M13 240021 | UK [England] | 2013 | ST-461 complex |

| PubMLST ID | Isolate name | Country of isolation | Collection date | Clonal complex |
|-------------------|---------------------|-----------------------------|------------------------|-----------------------|
| 27927 | M13 240045 | UK [England] | 2013 | ST-461 complex |
| 27933 | M13 240057 | UK [England] | 2013 | ST-461 complex |
| 27934 | M13 240063 | UK [England] | 2013 | ST-461 complex |
| 27938 | M13 240074 | UK [England] | 2013 | ST-461 complex |
| 27941 | M13 240078 | UK [England] | 2013 | ST-461 complex |
| 28017 | M13 240248 | UK [England] | 2013 | ST-461 complex |
| 28043 | M13 240406 | UK [England] | 2013 | ST-461 complex |
| 29291 | 15003 | South Africa | 2004 | ST-5 complex |
| 29304 | 27937 | South Africa | 2010 | ST-5 complex |
| 29312 | 5957 | South Africa | 2006 | ST-53 complex |
| 29434 | 139 | South Africa | 2005 | ST-5 complex |
| 30269 | M99 243594 | UK | 1999 | ST-5 complex |
| 30466 | NMA510612 | China | 2006 | ST-5 complex |
| 30697 | 12011-10 | Ireland | 2010 | ST-461 complex |
| 30708 | 12021-13 | Ireland | 2013 | ST-461 complex |
| 30760 | M14.1 | Ireland | 2013 | ST-461 complex |
| 31208 | NM10853 | UK [England] | 2013 | ST-53 complex |
| 31215 | LIM534 | France | 2006 | ST-5 complex |
| 34572 | 75643 | Brazil | 1975 | ST-5 complex |
| 34573 | 75689 | Brazil | 1975 | ST-5 complex |
| 34578 | 88050 | Chad | 1988 | ST-5 complex |
| 34583 | 96023 | Niger | 1996 | ST-5 complex |
| 34584 | 96024 | Niger | 1996 | ST-5 complex |
| 34587 | 97008 | Niger | 1997 | ST-5 complex |
| 34589 | 97018 | Mali | 1997 | ST-5 complex |
| 34590 | 97020 | Mali | 1997 | ST-5 complex |
| 34594 | 98005 | Niger | 1998 | ST-5 complex |
| 34595 | 98008 | France | 1998 | ST-461 complex |
| 34597 | 2000063 | Niger | 2000 | ST-5 complex |

| PubMLST ID | Isolate name | Country of isolation | Collection date | Clonal complex |
|-------------------|---------------------|-----------------------------|------------------------|-----------------------|
| 34598 | 2000080 | Algeria | 2000 | ST-5 complex |
| 34599 | 2001212 | Burkina Faso | 2001 | ST-5 complex |
| 34600 | 2002007 | Niger | 2002 | ST-5 complex |
| 34604 | 2003022 | Niger | 2003 | ST-5 complex |
| 34606 | 2004085 | Niger | 2004 | ST-5 complex |
| 34607 | 2004090 | Niger | 2004 | ST-5 complex |
| 34610 | 2007056 | Burkina Faso | 2007 | ST-5 complex |
| 34654 | NM3642 | Bangladesh | 2003 | ST-5 complex |
| 34655 | NM3652 | Bangladesh | 2006 | ST-5 complex |
| 34663 | NM604 | USA | 2000 | ST-5 complex |
| 34665 | NM607 | USA | 2001 | ST-5 complex |
| 34805 | ERR051676 | Ghana | 2008 | ST-5 complex |
| 34806 | ERR051677 | Ghana | 2009 | ST-5 complex |
| 34807 | ERR051678 | Ghana | 2009 | ST-5 complex |
| 34808 | ERR052799 | Burkina Faso | 2006 | ST-5 complex |
| 34809 | ERR052812 | Burkina Faso | 2006 | ST-5 complex |
| 34810 | ERR052817 | Burkina Faso | 2006 | ST-5 complex |
| 34811 | ERR052816 | Burkina Faso | 2007 | ST-5 complex |
| 34812 | ERR052813 | Burkina Faso | 2006 | ST-5 complex |
| 35330 | 12.1192.H | UK [Scotland] | 2012 | ST-461 complex |
| 35345 | 13.2973.F | UK [Scotland] | 2013 | ST-461 complex |
| 35346 | 13.3065.D | UK [Scotland] | 2013 | ST-461 complex |
| 35427 | M13 240534 | UK [England] | 2013 | ST-461 complex |
| 35436 | M13 240554 | UK [England] | 2013 | ST-461 complex |
| 35448 | M13 240581 | UK [England] | 2013 | ST-461 complex |
| 35480 | M13 240644 | UK [England] | 2013 | ST-461 complex |
| 35577 | M14 240083 | UK [Northern Ireland] | 2014 | ST-461 complex |
| 35580 | M14 240088 | UK [England] | 2014 | ST-461 complex |

| PubMLST ID | Isolate name | Country of isolation | Collection date | Clonal complex |
|-------------------|---------------------|-----------------------------|------------------------|-----------------------|
| 35612 | M14 240133 | UK [Wales] | 2014 | ST-461 complex |
| 36135 | 12010_2012 | Ireland | 2012 | ST-53 complex |
| 38889 | P27 | Italy | 2012 | ST-53 complex |
| 38943 | P106 | Italy | 2013 | ST-53 complex |
| 38946 | P109 | Italy | 2013 | ST-53 complex |
| 38953 | P117 | Italy | 2013 | ST-53 complex |

Supplementary Table 2. Genomic islands from the pan-accessory genome of *N. meningitidis* identified in this study.

| Island number/function | NEIS Code | BLASTP ID | GC% | GC percent different from mean | Closest non-Neisseria hit (ID and origin) | BLASTP %ID of non-Neisseria hit | Repeats flanking island | tRNA | Reference |
|--|-----------|--|-------|--------------------------------|--|---------------------------------|-------------------------|------|--|
| Island 1 (MDA-φ) Phage | | IS110 | | | | | DR | No | Proximal core gene is <i>pilA</i> (NEIS0021) (Bille et al., 2008) |
| | NEIS0023 | Zonular occludens toxin (Zot) family protein | 44.53 | Yes | Hypothetical protein - <i>Helicobacter pylori</i> | 99% | | | |
| | NEIS0024 | Putative integral membrane protein | 44.91 | Yes | Hypothetical protein - <i>Kingella sp.</i> | 45% | | | |
| | NEIS0025 | T cell/B cell stimulating protein TspB | 47.69 | Yes | None | | | | |
| | NEIS0027 | Membrane protein (<i>Neisseria meningitidis</i>) | 43.67 | Yes | Hypothetical protein - <i>Helicobacter pylori</i> | 96% | | | |
| | NEIS0028 | Membrane protein (<i>N. meningitidis</i>) | 54.63 | Yes | Membrane protein - <i>Proteobacteria</i> | 93% | | | |
| | NEIS0029 | Hypothetical protein | 53.84 | No | Hypothetical protein - <i>Kingella kingae</i> | 51% | | | |
| | NEIS0030 | Hypothetical protein | 53.58 | No | Hypothetical protein - <i>Helicobacter pylori</i> | 97% | | | |
| | NEIS0031 | Replication initiation factor (<i>N. meningitidis</i>) | 52.23 | No | None | | | | |
| Island 2 (Bacteriocin encoding GI-BGI 1) Toxin | | IS1016 | | | | | | | Proximal core gene is <i>pykA</i> (NEIS0074) (Allunans et al., 2008) |
| | NEIS0080 | Bacteriocin transporter (<i>N. meningitidis</i>) | 38.4 | Yes | Hypothetical protein - <i>Simonsiella muelleri</i> | 76% | IR | No | |
| | NEIS0081 | Hypothetical protein (<i>N. meningitidis</i>) | 33.77 | Yes | Hypothetical protein - <i>Simonsiella muelleri</i> | 70% | | | |
| | NEIS0083 | Multispecies membrane protein (<i>Neisseria</i>) | 22.87 | Yes | NADH dehydrogenase - <i>Leptospira santarosai</i> | 40% | | | |
| | NEIS0084 | Membrane protein (<i>Neisseria meningitidis</i>) | 26.81 | Yes | None | | | | |
| | NEIS0085 | Colicin V secretion protein (<i>Neisseria</i>) | 37.44 | Yes | Transporter protein - <i>Acinetobacter sp</i> | 47% | | | |

| | | | | | | | | | |
|---|----------|---|-------|-----|--|-----|----|----|---|
| | NEIS0086 | Colicin V processing peptidase (<i>Neisseria meningitidis</i>) Phase variable | 34.24 | Yes | Colicin V processing peptidase - <i>Acinetobacter sp</i> | 56% | | | |
| | NEIS0089 | Hypothetical protein | 34.69 | Yes | None | | | | |
| | | IS1016 | | | | | | | |
| Island 3 (Abi-like) Metabolism | NEIS0169 | Abi-like family protein (bacteriocin self-immunity protein) | 35.41 | Yes | CAAX protease - <i>Mesonia mobilis</i> | 80% | No | No | Proximal core gene is <i>lpxA</i> (NEIS0168) (Kjos et al., 2010) |
| Island 4 Hypothetical | NEIS0193 | Hypothetical protein(<i>Neisseria meningitidis</i>) | 28.72 | Yes | Hypothetical protein - <i>Bibersteinia trehalosi</i> | 34% | No | No | Proximal core gene is <i>lpxB</i> (NEIS0191) |
| Island 5 (Pgl-1) Membrane | NEIS2516 | Hypothetical protein | 50 | No | Glycosyltransferase <i>N. gonorrhoeae</i> (all other hits are for <i>Neisseria</i>) | 86% | IR | No | Proximal core gene is <i>pglA</i> (NEIS0213) (Dinh et al., 1994, Yan, 2013) |
| | NEIS0214 | Major Facilitator Superfamily transporter (<i>Neisseria meningitidis</i>) | 60.34 | Yes | MFS transporter - <i>Kingella dentrificans</i> | 58% | | | |
| | NEIS0215 | bile acid:sodium symporter(<i>Neisseria meningitidis</i>) | 57.26 | Yes | bile acid:sodium symporter - <i>Alysilla crassa</i> | 80% | DR | | |
| Island 6A (SMI1/KNR4) Cell wall synthesis | NEIS0231 | SMI1 / KNR4 family protein (cell division co-ordination) | 45.93 | Yes | SMI1 / KNR4 family protein - <i>Chryseobacterium sp</i> | 53% | No | No | Proximal core gene is NEIS0230 (Basmaji et al., 2006) |
| | NEIS0232 | Hypothetical protein | 30.56 | Yes | pyruvate, phosphate dikinase - <i>Propionibacterium acnes</i> | 40% | | | |
| | NEIS0233 | Hypothetical protein | 27.5 | Yes | Immunity protein 47 family protein - <i>Serratia symbiotica</i> | 36% | | | |
| | CDS | septum formation inhibitor Maf | 36.6 | Yes | Transposase - <i>Kingella kingae</i> | 92% | | | |
| | | IS1595 | | | | | | | |
| Island 6B Membrane | CDS | Membrane protein | 41.67 | Yes | Membrane protein - <i>Actinobacillus muris</i> | 42% | No | No | See above |
| | CDS | IS5 | | | | | | | |

| | | | | | | | | | |
|--|----------|--|-------|-----|---|-----|----|----|---|
| Island 7A Restriction Modification | NEIS2477 | putative type II restriction endonuclease DpnC (dam replacing protein) | 42.8 | Yes | Hypothetical protein - <i>Eikenella corrodens</i> | 60% | No | No | Proximal core gene is NEIS0326 (Jolley et al., 2004) |
| Island 7B Metabolism | NEIS2475 | Zn-dependent protease with chaperone function | 54 | No | deoxyribonuclease HsdR - <i>Stenoxybacter acetivorans</i> | 54% | No | No | Proximal core gene is NEIS0326 |
| Island 8A (NmFic) Cell wall synthesis | NEIS0249 | adenosine monophosphate-protein transferase NmFic (Neisseria) | 46.01 | Yes | Fic Family protein - <i>Aggregatibacter sp</i> | 85% | No | No | Proximal core gene is NEIS0258 (Stanger et al., 2016) |
| | NEIS0250 | Hypothetical protein | 39.77 | Yes | Hypothetical protein – <i>Vibrio gazogenes</i> | 51% | | | |
| Island 8B Membrane | NEIS2517 | Putative permease | 35.97 | Yes | permease - <i>Dickeya zeae</i> | 48% | No | No | Proximal core gene is NEIS0258 |
| Island 9 Cell wall synthesis | NEIS2518 | HKD family nuclease | 33.93 | Yes | Hypothetical protein - <i>Vibrio harveyi</i> | 47% | No | No | Proximal core gene is NEIS0251 |
| Island 10 Membrane | NEIS0267 | Membrane protein | 22.22 | Yes | Membrane protein <i>Kingella kingae</i> | 43% | No | No | Proximal core gene is NEIS0265 |
| Island 11 Restriction modification | NEIS0295 | Modification methylase HgaIA | 38.32 | Yes | restriction endonuclease Eco57I <i>Flavobacterium psychrophilum</i> | 63% | IR | No | Proximal core gene is NEIS0294 (Claus et al., 2000) |
| | CDS | Hin4II restriction endonuclease | 34.83 | Yes | hypothetical protein <i>Brachyspira hyodysenteriae</i> | 47% | | | |
| | NEIS0298 | Hypothetical protein | 33.33 | Yes | Hypothetical protein <i>Gilliamella apicola</i> | 51% | | | |
| | | IS5 | | | | | | | |
| Island 12 (Dam) Restriction modification | NEIS0327 | DNA adenine methylase | 41.08 | Yes | DNA adenine methylase - <i>Kingella oralis</i> | 68% | No | No | Proximal core gene is NEIS0326 (Jolley et al., 2004) |
| | NEIS0328 | modification methylase DpnIIB | 39.8 | Yes | DNA methylase N-4 <i>Kingella oralis</i> | 78% | | | |
| | NEIS0329 | hypothetical protein | 34.95 | Yes | Hypothetical protein - <i>AlysIELLA crassa</i> | 72% | | | |
| Island 13 Hypothetical | NEIS2506 | Hypothetical protein | 29.44 | Yes | Hypothetical protein - <i>Aggregatibacter aphrophilus</i> | 52% | No | No | Proximal core gene is NEIS0367 |

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|---|----------|--|-------|-----|--|-----|----|----|----|--|
| Island 14 (PgII) Membrane | NEIS0380 | PgII | 53.61 | No | None | | | No | No | Proximal gene NEIS0381 (tyrosyl-tRNA synthetase) (Warren et al., 2004) |
| Island 15A (BGI-2) Toxin | CDS | Initiator RepB protein | 36.34 | Yes | Initiator RepB protein - <i>Moraxella bovoculi</i> | 70% | No | No | | Proximal core gene is NEIS0388 |
| | | | 0 | Yes | | | | | | |
| | CDS | Cupin Superfamily protein | 32.74 | Yes | Cupin - <i>Acinetobacter baumannii</i> | 52% | | | | |
| | CDS | Cupin Superfamily protein | 36.86 | Yes | Cupin - <i>Simonsiella muelleri</i> | 68% | | | | |
| | NEIS0891 | Cupin | 32.58 | | cupin - <i>Simonsiella muelleri</i> | 65% | | | | |
| | CDS | Bacteriocin transporter | 39.29 | Yes | hypothetical protein - <i>Acinetobacter guillouiae</i> | 34% | | | | |
| | NEIS0890 | Membrane protein | 18.1 | Yes | Organic cation transporter like protein - <i>Papilio polytes</i> | 29% | | | | |
| | NEIS0889 | Membrane protein | 46.13 | Yes | hypothetical protein - <i>Oceanospirillum maris</i> | 41% | | | | |
| | CDS | Bacteriocin transporter | 39.4 | Yes | hypothetical protein - <i>Acinetobacter guillouiae</i> | 34% | | | | |
| | CDS | putative bacteriocin processing protease | 45.21 | Yes | ABC transporter - <i>Burkholderia ubonensis</i> | 52% | | | | |
| | | | 0 | Yes | | | | | | |
| Island 15B (CRISPR Cas9) Restriction modification | IS1016 | | | | | | | | | |
| | NEIS2568 | CRISPR protein Cas2 | 44.34 | Yes | subtype II CRISPR-associated endonuclease Cas1- <i>Pastuerella multocida</i> | 64% | DR | No | | Proximal core gene is NEIS0385 (Zhang et al., 2011) |
| | NEIS2567 | CRISPR protein Cas1 | 49.73 | No | type II CRISPR RNA-guided endonuclease Cas - <i>Actinobacillus minor</i> | 68% | | | | |
| | CDS | CRISPR protein Cas9 | 48.72 | Yes | CRISPR protein Cas9 - <i>Actinobacillus minor</i> | 67% | | | | |
| | | IS1106 | | | | | IR | | | |
| Island 16 Iron Acquisition | NEIS0387 | TonB-dependent receptor | 55.38 | Yes | TonB-dependent receptor - <i>Morococcus cerebrosus</i> | 84% | IR | | | Proximal core gene is NEIS0386 |
| | NEIS0388 | esterase | 56.48 | Yes | Esterase - <i>Morococcus cerebrosus</i> | 55% | | | | |

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|------------------------------------|----------|---|-------|-----|---|-----|----|----|---|
| | | | | | | | | | |
| Island 17 (Pgl-2) Metabolism | NEIS0398 | haloacid dehalogenase | 50.51 | No | haloacid dehalogenase - <i>Pseudoalteromonas sp.</i> | 45% | No | No | Proximal core gene is NEIS0397 in the pilin glycan biosynthesis locus (Kahler et al., 2001) |
| Island 18A (PglB1) Membrane | NEIS0399 | PglB1 | 50.79 | No | UDP-N-acetylgalactosaminyltransferase - <i>Pseudomonadaceae</i> | 58% | No | No | Proximal core gene is NEIS0398 (Kahler et al., 2001) |
| Island 18B (PglB2) Membrane | NEIS2838 | PglB2 | 50.79 | No | UDP-N-acetylgalactosaminyltransferase - <i>Pseudomonadaceae</i> | | | | |
| Island 19 (PglH) Membrane | NEIS0400 | glycosyltransferase family 1 (PglH) | 52 | No | None | | No | No | Proximal core gene is NEIS0399 (Power et al., 2003); (Hadjineophytou et al., 2019) |
| Island 20 (PglG) Membrane | NEIS0401 | glycosyl transferase 4-like domain protein (PglG) | 56.16 | Yes | None | | No | No | Proximal core gene is NEIS0400 (Power et al., 2003); (Hadjineophytou et al., 2019) |
| Island 21A (TpsA/B) Toxin | NEIS0443 | Hemin transporter TpsB | 45.96 | Yes | None | | IR | No | Proximal core gene is NEIS0441 (Arenas et al., 2013) |
| | CDS | hemagglutinin/hemolysin-related protein TpsA | 48.64 | Yes | pre-toxin domain with VENN motif family protein- <i>Morococcus cerebrosus</i> | 96% | | | |
| Island 21B (CDI) Toxin | NEIS0453 | Hypothetical protein | 30.47 | Yes | Hypothetical protein - <i>Enterobacteriaceae</i> | 37% | | | |
| | NEIS0454 | Hypothetical protein | 32.23 | Yes | Hypothetical protein - <i>Bacillus sp.</i> | | | | |
| Island 21C (CDI) | CDS | hemagglutinin | 35.19 | Yes | Hemagglutinin - <i>Morococcus cerebrosus</i> | | | | |

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|---|----------|--|-------|-----|--|-----|----|----|--|
| Toxin | NEIS2490 | Chain A, The Crystal Structure Of An Immunity Protein Nmb0503 | 25.69 | Yes | Hypothetical protein - <i>Morococcus cerebrosus</i> | 99% | | | |
| Island 21D (CDI) Toxin | CDS | hemagglutinin | 47.86 | Yes | None | | | | |
| | NEIS2472 | Chain A, The Crystal Structure Of Functionally Unknown Protein From <i>Neisseria Meningitidis</i> Mc58 | 28.1 | Yes | hypothetical protein, partial - <i>Photorhabdus luminescens</i> | 37% | | | |
| | | | 0 | Yes | | | | | |
| | | | 0 | Yes | | | | | |
| | NEIS2471 | hypothetical protein NM96060_2231 | 30.13 | Yes | hypothetical protein - <i>Enterobacter lignolyticus</i> | 32% | | | |
| Island 21E (CDI) Toxin | CDS | pre-toxin domain with VENN motif family protein | 48.8 | Yes | None | | | | |
| | NEIS0449 | Hypothetical protein | 31.82 | Yes | MULTISPECIES: 3'-5' exoribonuclease - <i>Bacillus cereus</i> group | 55% | | | |
| | CDS | pre-toxin domain with VENN motif family protein | 54.55 | Yes | None | | | | |
| Island 22 (FrpD/C) Iron acquisition | NEIS0456 | pre-toxin domain with VENN motif family protein | 43.55 | Yes | pre-toxin domain with VENN motif family protein - <i>Acinetobacter baumannii</i> | 51% | | | |
| | NEIS0526 | FrpC Operon Protein FrpD | 38.97 | Yes | None | | DR | No | Proximal core gene is NEIS0524 (Prochazkova et al., 2005, Thompson et al., 1993) |
| | NEIS0527 | Iron regulated FrpA/C | 45.5 | Yes | None | | IR | No | |
| Island 23A (MGI-2) Toxin | NEIS0586 | MafB1_MGI-2 | 49.21 | Yes | None | | IR | | Proximal core gene is <i>ntpA</i> (NEIS0585) (Jamet et al., 2015); |
| | NEIS0587 | Hypothetical protein | 28.39 | Yes | O-succinylbenzoic acid--CoA ligase - <i>Cyclobacteriaceae bacterium</i> | 28% | | | |
| | NEIS0588 | Putative lipoprotein | 43.92 | Yes | None | | | | |
| | NEIS0589 | MafI1_MGI-2 (PUBMLST) | 25.69 | Yes | Barnase inhibitor <i>Coromonas testosterone</i> | 34% | | | |

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|--------------------------------|----------|---|-------|------------|---|--------|--|--|
| | NEIS0591 | Hypothetical protein | 31.9 | Yes | None | | | |
| | NEIS0592 | Putative immunity protein | 25.93 | Yes | Immunity protein – <i>Kingella negevensis</i> | 93.75% | | |
| | NEIS0593 | HNH endonuclease | 44.31 | Yes Yes | HNH endonuclease – <i>Acinetobacter baumanii</i> | 70.13% | | |
| | | | | | | | | |
| | NEIS0594 | Hypothetical protein | 32.04 | Yes | Hypothetical protein – <i>Morococcus cerobrosus</i> | 65% | | |
| | NEIS0595 | Hypothetical protein | 33.08 | Yes | None | | | |
| | NEIS0596 | MafA – MGI -2 | 59.13 | Yes | None | | | |
| | NEIS0597 | MafB – Found in both MGI-1 and MGI-2 | 52.4 | No | None | | | |
| | NEIS0598 | Hypothetical protein | 33.96 | Yes | Hypothetical protein – <i>Kingella potus</i> | 58.33% | | |
| | NEIS0601 | MafS2 – MGI11 or MGI-2 | 44.99 | No | None | | | |
| | NEIS0602 | Hypothetical protein | 35.19 | Yes | None | | | |
| | NEIS0603 | Hypothetical protein | 39.87 | Yes | None | | | |
| | NEIS0604 | Suppressor of fused family protein (SUFU) | 59.27 | Yes | SUFU protein – <i>Leptospira licerasiae</i> | 44% | | |
| | NEIS0605 | Suppressor of fused family protein (SUFU) | 38.3 | Yes | SUFU protein – <i>Kingella sp</i> | | | |
| | NEIS0606 | Hypothetical protein | 52.78 | Yes | None | | | |
| | NEIS0607 | Hypothetical protein | 25.37 | Yes | None | | | |
| | NEIS0608 | Hypothetical protein | 30.26 | Yes | Nona | | | |
| | | IS1016 | | | | | | |
| Island 23B (MGI-2) Toxin | NEIS0586 | MafB1 MGI-2 | 49.21 | Yes | None | | | |
| | NEIS0591 | Hypothetical protein | 31.44 | Yes | None | | | |
| | NEIS0592 | Putative immunity protein | 25.93 | Yes | Immunity protein – <i>Kingella negevensis</i> | 93.75% | | |
| | NEIS0593 | HNH endonuclease | 44.31 | Yes Yes | HNH endonuclease – <i>Acinetobacter baumanii</i> | 70.13% | | |
| | NEIS0594 | Hypothetical protein | 32.04 | Yes | Hypothetical protein – <i>Morococcus cerobrosus</i> | 65% | | |

Proximal core gene is *ntpA* (NEIS0585) (Jamet et al., 2015);

| | | | | | | | | | |
|---|----------|--|-------|-----|--|-----|----|----|---|
| | NEIS0595 | Hypothetical protein | 33.08 | Yes | None | | | | |
| | NEIS0596 | MafA – MGI -2 | 59.13 | Yes | None | | | | |
| | NEIS0597 | MafB – Found in both MGI-1 and MGI-2 | 52.4 | No | None | | | | |
| | NEIS0598 | Hypothetical protein | 33.96 | Yes | Hypothetical protein – <i>Kingella potus</i> | | | | |
| | NEIS2694 | Hypothetical protein | 35.57 | Yes | None | | | | |
| | NEIS1791 | Hypothetical protein | 32.51 | Yes | Hypothetical protein - <i>Vibrio splendicus</i> | 38% | | | |
| | NEIS1792 | Hypothetical protein | 34.62 | Yes | Hypothetical protein - <i>Tolumonas sp.</i> | 58% | | | |
| | NEIS1800 | MafB- MGI-1 | 45.87 | No | None | | | | |
| | NEIS1795 | Hypothetical protein | 32.19 | Yes | | | | | |
| | | IS1016 | | | | | | | |
| Island 24 Membrane | NEIS0632 | lipoprotein | 52.33 | No | Hypothetical protein – <i>Dyella japonica</i> | 44% | No | No | Proximal gene is NEIS0631 |
| | | | 0 | | | | | | |
| Island 25A (Vsr-1) Restriction modification | NEIS0678 | HpaII very short patch repair endonuclease | 45.86 | Yes | <i>Aggregatibacter actinomycetemcomitans</i> | 95% | No | No | Proximal core gene is <i>rplT</i> (NEIS0675) (Claus et al., 2000) |
| | CDS-1 | putative modification methylase NmeDI | 41.43 | Yes | Modification methylase – <i>Morococcus cerebrosus</i> | 99% | | | |
| | NEIS0680 | type II restriction endonuclease NmeDIP | 42.99 | Yes | Restriction endonuclease NmeDIP - <i>Morococcus cerebrosus</i> | 99% | | | |
| Island 25B Restriction modification | CDS-1 | Unnamed protein product (top hit) | 32.2 | Yes | Restriction endonuclease subunit M - <i>Kingella kingae</i> | 80% | No | No | As above |
| | CDS-2 | Unnamed protein product (top hit) | 27.74 | Yes | Restriction endonuclease subunit M - <i>Kingella kingae</i> | 80% | | | |
| Island 25C Restriction modification | NEIS2377 | modification methylase HgaI-1,restriction endonuclease | 33.62 | Yes | Restriction endonuclease subunit M - <i>Alys iella crassa</i> | 75% | | | As above |
| | NEIS2378 | type II restriction enzyme HgaI | 31.02 | Yes | Restriction endonuclease – <i>Alys iella crassa</i> | 79% | | | |
| | NEIS2379 | N-6 adenine-specific DNA methylase | 32.72 | Yes | DNA methyltransferase - <i>Alys iella crassa</i> | 85% | | | |
| Island 26 | NEIS0771 | DNA methyltransferase | 33.58 | Yes | DNA methyltransferase <i>Haemophilus influenzae</i> | 88% | | | |

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|---------------------------|----------|--|-------|-----|--|------|----|--------------------------------|---|
| Restriction modification | NEIS0772 | type II restriction endonuclease | 31.59 | Yes | restriction endonuclease - <i>Paenibacillus sophorae</i> | 82% | | | Proximal core gene is <i>hldA</i> (NEIS0769) (Shih et al., 2001) |
| Island 27A Hypothetical | NEIS0796 | Hypothetical protein | 26.28 | Yes | None | 100% | | | Proximal core gene is NEIS0795 |
| Island 27B Hypothetical | NEIS2392 | Hypothetical protein | 38.1 | Yes | Hypothetical protein - <i>Chryseobacterium gallinarum</i> | 62% | | | See above |
| | NEIS0798 | Hypothetical protein | 42.49 | Yes | Hypothetical protein - <i>Moraxella caprae</i> | 47% | | | |
| | NEIS0800 | Hypothetical protein | 35.52 | Yes | hypothetical protein - <i>AlysIELLA crassa</i> | 41% | | | |
| | NEIS0801 | Membrane protein | 46.99 | Yes | RHS repeat-associated core domain protein - <i>Alcanivorax pacificus</i> | 63% | | | |
| Island 28 (PilX) Membrane | NEIS0831 | type IV pilin PilX | 42.74 | Yes | None | 100% | | | Proximal core gene is <i>pilK</i> (NEIS0830) (Helaine et al., 2005) |
| | NEIS0832 | branched-chain amino acid ABC transporter permease | 50.35 | No | branched-chain amino acid ABC transporter permease - <i>Morococcus cerbosus</i> | 83% | | | |
| Island 29 Phage | NEIS0836 | Phage integrase | 55.89 | Yes | Hypothetical protein - <i>Eikenella sp.</i> | 39% | IR | Yes (2 tRNAs before integrase) | Proximal core gene is NEIS0835 |
| | NEIS0837 | mRNA interferase PemK | 49.87 | No | Hypothetical protein - <i>Haemophilus parasuis</i> | 64% | | | |
| | NEIS0838 | Hypothetical protein | 58.2 | Yes | ABC transporter permease - <i>Bifidobacterium cuniculi</i> | 39% | | | This locus is not the core locus <i>ldhA</i> described by Sigurlasdottir et al. (Sigurlasdottir et al., 2019) |
| | NEIS0839 | DUF4760 domain protein | 47.62 | Yes | DUF4760 domain protein - <i>Moraxella caprae</i> | 62% | | | |
| | NEIS0840 | DNA binding protein | 52.94 | No | Hypothetical protein - <i>Eikenella sp.</i> | 60% | | | |
| | NEIS0841 | Lactate dehydrogenase | 54.39 | Yes | D-isomer specific 2-hydroxyacid dehydrogenase - <i>Amycolatopsis decaplanina</i> | 43% | | | |
| | NEIS0842 | Hypothetical protein | 46.88 | Yes | Hypothetical protein - <i>Eikenella corrodens</i> | 63% | | | |

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|--|----------|---------------------------|-------|-----|--|--------------------|--|--|--|
| | NEIS0843 | Hypothetical protein | 50.34 | No | Hyothetical protein - <i>Nonomuraea coxensis</i> | 33% (e-value of 3) | | | |
| | NEIS0844 | Hypothetical protein | 55.56 | Yes | Dystonin like protein - <i>Pygoscelis adeliae</i> | 30% | | | |
| | NEIS0845 | Hypothetical protein | 53.7 | No | LSM domain containing protein - <i>Cryptosporidium muris</i> | 45% | | | |
| | NEIS0846 | Hypothetical protein | 47.02 | Yes | Hypothetical protein - <i>Microvirgula aerodenitrificans</i> | 44% | | | |
| | NEIS0847 | Hypothetical protein | 47.22 | Yes | Methyltransferase small domain protein - <i>Snodgrassella alvi</i> | 59% | | | |
| | NEIS0848 | Hypothetical protein | 42.79 | Yes | Hypothetical protein - <i>Haemophilus ducreyi</i> | | | | |
| | NEIS0849 | Hypothetical protein | 45.9 | Yes | Hypothetical protein - <i>Kingella deritrophicans</i> | 38% | | | |
| | NEIS0850 | Transcriptional regulator | 54.25 | No | Repressor - <i>Kingella oralis</i> | 55% | | | |
| | NEIS0852 | Hypothetical protein | 50.86 | No | Thiol reductase thioredoxin - <i>Porphyromonas</i> | 35% | | | |
| | NEIS0853 | Primase | 48.3 | Yes | Hypothetical protein - <i>Simonsiella muelleri</i> | 43% | | | |
| | NEIS0854 | Hypothetical protein | 45.71 | Yes | Al hits are for Neisseria | 100% | | | |
| | NEIS0855 | Hypothetical protein | 48.32 | Yes | Hypothetical protein - <i>Pseudomonas nitroducens</i> | 68% | | | |
| | NEIS0856 | Hypothetical protein | 53.73 | No | Hypothetical protein - <i>Chitinilyticum aquatile</i> | 45% | | | |
| | NEIS0857 | Phage portal protein | 57.01 | Yes | Hypothetical protein - <i>Pseudohodoferax sp.</i> | 54% | | | |
| | NEIS0858 | Peptidase | 53.88 | No | Capsid protein - <i>Thioalkalivibrio sp.</i> | 45% | | | |
| | NEIS0859 | Hypothetical protein | 54.39 | Yes | Hypothetical protein - <i>Fischerella sp.</i> | 30% | | | |
| | NEIS0860 | Hypothetical protein | 51.16 | No | Hypothetical protein - <i>Nitrafractor salsuginis</i> | 34% | | | |
| | NEIS0861 | Hypothetical protein | 52.91 | No | alpha -2 - macroglobulin - <i>Shewanella algae</i> | 33% | | | |
| | NEIS0862 | Phage tail protein | 48.75 | Yes | Phage tail protein - <i>Alysiella crassa</i> | 49% | | | |
| | NEIS0863 | Hypothetical protein | 49.68 | No | Hypothetical protein - <i>Acromobacter sp.</i> | 48% | | | |
| | NEIS0864 | Hypothetical protein | 49.82 | No | Phage protein - <i>Pseudomonas aeruginosa</i> | 43% | | | |

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|--------------------|----------|--|-------|-----|---|-----|----|----|--------------------------------|
| | NEIS0865 | Phage tail protein | 53.18 | No | Hypothetical protein - <i>Conchiformibius kuhniae</i> | 40% | | | |
| | NEIS0866 | Phage minor tail family protein | 50 | No | Minor tail family protein - <i>Pseudomonas protegens</i> | 43% | | | |
| | NEIS0867 | tail protein | 56.43 | Yes | Tail protein - <i>Simonsiella muelleri</i> | 64% | | | |
| | NEIS0868 | alkaline phosphatase | 55.56 | Yes | Alkaline phosphatase - <i>Vitreoscilla sp.</i> | 54% | | | |
| | NEIS0869 | Phage tail assembly protein | 55.74 | Yes | Phage tail assembly protein - <i>Conchiformibius kuhniae</i> | 55% | | | |
| | NEIS0870 | Hypothetical protein | 51.83 | No | Hypothetical protein - <i>Acinetobacter gyllenbergsii</i> | 24% | | | |
| | NEIS0871 | Hypothetical protein | 44.97 | Yes | Hypothetical protein - <i>Plesiocystic pacifica</i> | 28% | | | |
| | NEIS0872 | membrane protein | 48.31 | Yes | Hypothetical protein - <i>Kingella kingae</i> | 40% | | | |
| | NEIS0873 | Hypothetical protein | 51.82 | No | Hypothetical protein - <i>Conchiformibius kuhniae</i> | 35% | | | |
| | NEIS0877 | ATP-Binding protein | 55.7 | Yes | ATP-Binding protein - <i>Moraxella bovoculi</i> | 59% | | | |
| | NEIS0878 | Phage associated membrane protein | 52.55 | No | Hypothetical protein - <i>Kingella oralis</i> | 34% | | | |
| Island 30 Membrane | | IS5 | 51.53 | No | DDE transposase - <i>Eikenella corrodens</i> | 98% | IR | No | Proximal core gene is NEIS0422 |
| | CDS-1 | Hypothetical protein | 53.05 | No | None | | | | |
| | NEIS0887 | Hemolysin D family secretion protein | 36.9 | Yes | Transporter - <i>Acinetobacter nosocomialis</i> | 44% | | | |
| | NEIS0888 | ABC transporter | 40.3 | Yes | ABC transporter - <i>Acinetobacter baumannii</i> | 54% | | | |
| | NEIS0889 | membrane protein | 44.64 | Yes | Hypothetical protein - <i>Oceanospirillum maris</i> | 35% | | | |
| | NEIS0890 | Membrane protein | 19.76 | Yes | Organic cation transporter like protein-F150 <i>Papilio polytes</i> | 29% | | | |
| | NEIS0891 | Cupin family protein | 32.03 | Yes | Cupin - <i>Simonsiella muelleri</i> | 58% | | | |
| | NEIS0892 | Hypothetical protein | 27.35 | Yes | None | | | | |
| | NEIS0893 | ParB (chromosome partitioning protein) | 35.29 | Yes | ParB protein - <i>Haemophilus influenzae</i> | 69% | | | |
| | | IS5 | 53.46 | No | DDE transposase - <i>Helicobacter pylori</i> | 96% | | | |

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|-----------------------------------|----------|--|-------|-----|--|------|----|-----|--------------------------------|
| Island 31A Metabolism | CDS-1 | Transcriptional regulator | 51.59 | No | WYL domain containing protein - <i>Gammaproteobacteria</i> | 44% | No | No | Proximal core gene is NEIS0938 |
| Island 31B Cell wall synthesis | | IS200 | | | | | | | See above |
| | NEIS0940 | ATP-dependent helicase | 28.42 | Yes | DNA helicase - <i>Rhodivulum sulfidophilum</i> | 44% | | | |
| Island 31C Hypothetical | NEIS2397 | FunZ family protein | 28.38 | Yes | FunZ protein - <i>Klebsiella oxytoca</i> | 59% | No | No | See above |
| Island 32A (P2-like) Phage | | | | | | | IR | No | Proximal core gene is NEIS0986 |
| | NEIS2552 | Putative phage associated protein | 57.28 | Yes | Putative phage associated protein - <i>Morococcus cerebrosus</i> | 69% | | | |
| | NEIS0989 | Putative phage integrase | 54.35 | Yes | Putative phage integrase - <i>Morococcus cerebrosus</i> | 69% | | | |
| | NEIS0992 | Putative phage integrase | 62.33 | Yes | Putative phage integrase | 37% | | | |
| | NEIS0993 | Phage protein | 54.41 | Yes | Hypothetical protein - <i>Kingella kingae</i> | 70% | | | |
| | NEIS0995 | DNA phage binding protein | 53.69 | No | DNA phage binding protein - <i>Alysilla crassa</i> | 71% | | | |
| | NEIS0996 | BcepMu gp16 family phage associated protein | 51.92 | No | Hypothetical protein - <i>Simonsiella muelleri</i> | 78% | | | |
| | NESI0997 | Phage repressor | 41.27 | Yes | Transcriptional regulator - <i>Actinobacillus capsulatus</i> | 45% | | | |
| | NEIS0998 | Hypothetical protein | 41.46 | Yes | SAM-dependent methyltransferase - <i>Steptococcus castoreus</i> | 25% | | | |
| | NEIS0999 | Hypothetical protein | 44.09 | Yes | None | 100% | | | |
| | NEIS1000 | Hypothetical protein | 37.94 | Yes | Hypothetical protein - <i>Peptoclostridium difficile</i> | 98% | | | |
| | NEIS1001 | Membrane protein | 32.51 | Yes | Hypothetical protein - <i>Haemophilus sp.</i> | 47% | | | |
| | NEIS1002 | Hypothetical protein | 56.75 | Yes | Peptidoglycan domain protein - <i>Morococcus cerebrosus</i> | 92% | | | |
| Island 32B | | Bacteriophage transposase | | | | | IR | Yes | See above |
| | CDS-1 | Phage protein - Integrase NMO_0917 | 57.37 | Yes | Integrase - <i>Pseudomonas sp.</i> | 45% | | | |
| | CDS-2 | putative phage associated conserved protein NMO_0918 | 56.62 | Yes | Hypothetical protein - <i>Burkholderia cenocepacia</i> | 42% | | | |

| | | | | | | | | | |
|--|--------|--|-------|-----|--|-----|--|--|--|
| | CDS-3 | putative phage associated membrane protein NMO_0919 | 43.8 | Yes | None | | | | |
| | CDS-4 | Rha family transcriptional regulator NMO_0920 | 57.65 | Yes | Hypothetical protein - <i>Eikenella corrodens</i> | 66% | | | |
| | CDS-5 | putative bacteriophage transcriptional regulator NMO_0921 | 54.68 | Yes | DNA binding protein - <i>Morococcus cerebrosus</i> | 89% | | | |
| | CDS-6 | ATPases with chaperone activity ATP-binding subunit NMO_0922 | 57.27 | Yes | 2-oxoacid:acceptor oxoreductase - <i>Alysella crassa</i> | 54% | | | |
| | CDS-7 | Isocitrate/isopropylmalate dehydrogenase NMO_0923 | 56.83 | Yes | Hypothetical protein <i>Morococcus cerebrosus</i> | 95% | | | |
| | CDS-8 | putative phage associated hypothetical protein NMO_0924 | 51.11 | No | Hypothetical protein <i>Kingella oralis</i> | 45% | | | |
| | CDS-9 | putative phage associated hypothetical protein NMO_0925 | 57.82 | Yes | Hypothetical protein <i>Eikenella corrodens</i> | 68% | | | |
| | CDS-10 | putative phage associated hypothetical protein NMO_0926 | 55.56 | Yes | Hypothetical protein <i>Morococcus cerebrosus</i> | 91% | | | |
| | CDS-11 | putative phage associated protein NMO_0927 | 58.45 | Yes | Hypothetical protein <i>Kingella kingae</i> | 72% | | | |
| | CDS-12 | putative phage associated protein NMO_0928 | 55.02 | Yes | Hypothetical protein <i>Kingella kingae</i> | 68% | | | |
| | CDS-13 | putative phage major tail sheath protein NMO_0929 | 56.77 | Yes | phage tail protein <i>Morococcus cerebrosus</i> | 88% | | | |
| | CDS-14 | Phage tail tube protein FII NMO_0930 | 50.78 | No | tail protein <i>Morococcus cerebrosus</i> | 95% | | | |
| | CDS-15 | putative phage associated hypothetical protein NMO_0931 | 52.19 | No | Hypothetical protein <i>Kingella kingae</i> | 56% | | | |
| | CDS-16 | Phage-related tail protein NMO_0932 | 54.86 | Yes | Phage tail tape measure protein <i>Moraxella caprae</i> | 43% | | | |

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|--------------------------------------|----------|--|-------|-----|---|------|-------|----|--------------------------|
| | CDS-17 | putative phage tail assembly protein NMO_0933 | 57.4 | Yes | tail protein <i>Morococcus cerebrosus</i> | 88% | | | |
| | CDS-18 | putative phage tail protein NMO_0934 | 54.34 | Yes | membrane protein <i>Kingella kingae</i> | 80% | | | |
| | CDS-19 | putative bacteriophage regulatory protein NMO_0935 | 53.24 | No | Hypothetical protein <i>Morococcus cerebrosus</i> | 88% | | | |
| | CDS-20 | Phage P2 baseplate assembly protein gpV NMO_0936 | 56.76 | Yes | Phage baseplate protein <i>Morococcus cerebrosus</i> | 87% | | | |
| | CDS-21 | Phage baseplate assembly protein W NMO_0937 | 54.5 | Yes | Phage baseplate protein <i>Morococcus cerebrosus</i> | 92% | | | |
| | CDS-22 | putative phage-related baseplate assembly protein NMO_0938 | 57.58 | Yes | Baseplate assembly protein <i>Alysiella crassa</i> | 63% | | | |
| | CDS-23 | Bacteriophage P2-related tail formation protein NMO_0939 | 57.17 | Yes | Tail fiber protein - <i>Morococcus cerebrosus</i> | 79% | | | |
| | CDS-24 | putative phage tail fibre protein NMO_0940 | 59.53 | Yes | None | | | | |
| | CDS-25 | putative phage fibre-spike protein NMO_0941 | 56.22 | Yes | Hypothetical protein - <i>Kingella kingae</i> | 50% | | | |
| | CDS-26 | putative phage associated hypothetical protein NMO_0942 | 42.96 | Yes | None | | | | |
| | | putative phage associated type II DNA-methyltransferase NMO_0943 | 50.64 | No | DNA methyltransferase - <i>Morococcus cerebrosus</i> | 95% | | | |
| | | Bacteriophage transposase | | | | | | | |
| Island 33A (IHT-E)(PNM2) Phage | NEIS1041 | ABC transporter, ATP binding | 58.74 | Yes | ABC transporter permease – <i>Morococcus cerebrosus</i> | 92% | IR/DR | No | (Masignani et al., 2001) |
| | NEIS1042 | Hypothetical protein | 46.67 | Yes | None | 100% | | | |
| | NEIS1044 | Transcriptional regulator/DNA binding protein | 38.89 | Yes | Putative DNA binding protein (fragment) - <i>Peptoclostridium difficile</i> | 99% | | | |

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|------------------------|----------|---|-------|-----|--|-----|-------|----|---|
| | NEIS1045 | transcriptional regulator/DNA binding protein | 38.49 | Yes | XRE family transcriptional regulator - <i>Alysella crassa</i> | 60% | | | Proximal core gene is NEIS1040 (Joseph et al., 2011) |
| | NEIS1046 | Phage transposase | 54.34 | Yes | Putative phage transposase - <i>Snodgrasella alvi</i> | 51% | | | |
| | NEIS1048 | Phage transposase | 50.82 | No | XRE family transcriptional regulator - <i>Citrobacter freundii</i> | 45% | | | |
| | NEIS1049 | Hypothetical protein | 48.45 | Yes | None | | | | |
| | NEIS1050 | Hypothetical protein | 44.44 | Yes | Hypothetical protein - <i>Peptoclostridium difficile</i> | 97% | | | |
| | NEIS1051 | Hypothetical protein | 52.87 | No | None | | | | |
| | NEIS1052 | Hypothetical protein | 52.38 | No | None | | | | |
| | NEIS1053 | Hypothetical protein | 35.53 | Yes | None | | | | |
| | NEIS1054 | Host nuclease inhibitor (gam) | 52.22 | No | Host nuclease inhibitor (gam) - <i>Kingella oralis</i> | 51% | | | |
| | NEIS1055 | transposase | 51.35 | No | None | | | | |
| | NEIS1057 | Phage tail protein | 61.68 | Yes | Phage tail protein - <i>Kingella kingae</i> | 59% | | | |
| | NEIS1058 | tail protein | 58.21 | Yes | Phage tail fibre protein - <i>Haemophilus aegypticus</i> | 59% | | | |
| | NEIS1059 | Hypothetical protein | 59.24 | Yes | Hypothetical protein - <i>Haemophilus haemolyticus</i> | 59% | | | |
| | NEIS1060 | DNA helicase UrvD | 58.92 | Yes | DNA helicase UrvD - <i>Haemophilus influenzae</i> | 74% | | | |
| | NEIS1062 | ABC transporter, ATP binding | 52.27 | No | ABC transporter, ATP binding - <i>Kingella oralis</i> | 77% | | | |
| | | Transposase | | | | | IR/DR | No | |
| Island 33B (MuMenB) | NEIS2412 | Hypothetical protein | 35.53 | Yes | Hypothetical protein - <i>Kingella kingae</i> | 42% | | | (Massignani et al., 2001) |
| | NEIS2413 | Phage protein | 56.28 | Yes | Phage protein - <i>Avibacterium paragallinarum</i> | 71% | | | |
| | NEIS2414 | Mu bacteriophage protein gp29 | 56.21 | Yes | Mu bacteriophage protein gp29 - <i>Kingella kingae</i> | 64% | | | |
| | NEIS2415 | Phage head morphogenesis protein | 48.84 | Yes | Phage head morphogenesis protein - <i>Kingella kingae</i> | 66% | | | |
| | NESI2416 | Bacteriophage Mu I protein GP32 | 54.14 | No | Hypothetical protein - <i>Kingella kingae</i> | 74% | | | |
| | NEIS2417 | Hypothetical protein | 57.76 | Yes | Hypothetical protein - <i>Kingella kingae</i> | 56% | | | |

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|------------------------------|----------|--|-------|-----|---|-----|----|----|--------------------------------|
| | NEIS2418 | Hypothetical protein | 58.39 | Yes | Hypothetical protein - <i>Kingella kingae</i> | 72% | | | |
| | NESI2419 | Mu-like prophage FlmU protein gp37 | 57.41 | Yes | Hypothetical protein - <i>Kingella kingae</i> | 64% | | | |
| | NEIS2420 | Hypothetical protein | 54.55 | Yes | Hypothetical protein - <i>Kingella kingae</i> | 62% | | | |
| | NEIS2421 | tail sheath protein | 57.09 | Yes | Tail sheath protein - <i>Kingella kingae</i> | 73% | | | |
| | NEIS2422 | Phage tail protein | 51.85 | No | Phage tail protein - <i>Kingella kingae</i> | 79% | | | |
| | NEIS2423 | Hypothetical protein | 59.29 | Yes | Hypothetical protein - <i>Kingella kingae</i> | 51% | | | |
| | NEIS2424 | lipoprotein | 38.81 | Yes | Transporter - <i>Photobacterium ganghwense</i> | 25% | | | |
| | NEIS2425 | PRTRC system protein F | 53.13 | No | Hypothetical protein - <i>Kingella oralis</i> | 41% | | | |
| | NEIS2426 | Phage morphogenesis protein | 58.39 | Yes | Phage morohogenesis protein - <i>Kingella kingae</i> | 54% | | | |
| | NEIS2427 | Phage tail protein | 57.85 | Yes | Tail protein - <i>Kingella kingaae</i> | 72% | | | |
| | NEIS2428 | Baseplate assembly protein | 56.35 | Yes | Baseplate assembly protein - <i>Haemophilus parasuis</i> | 58% | | | |
| | NEIS2429 | Hypothetical protein | 58.62 | Yes | Hypothetical proten - <i>Kingella kingae</i> | 70% | | | |
| | NEIS2430 | Hypothetical protein | 52.48 | No | Hypothetical protein - <i>Haemophilus influenzae</i> | 59% | | | |
| | NEIS2431 | Hypothetical protein | 45.14 | Yes | Hypothetical protein - <i>Gallibacterium anatis</i> | 68% | | | |
| Island 34 Membrane | NEIS1074 | Amino acid permease | 55.78 | Yes | Hypothetical protein - <i>Morococcus cerbosus</i> | 36% | No | No | Proximal core gene is NEIS1073 |
| Island 35 Membrane | NEIS1082 | lipoprotein | 42.62 | Yes | hypothetical protein - <i>Marinobacterium rhizophilum</i> | 36% | No | No | Proximal core gene is NEIS1081 |
| | NEIS1083 | Hypothetical protein | 36.72 | Yes | Hypothetical protein - <i>Pasteurella multocida</i> | 40% | | | |
| Island 36 (HlyC) Toxin | NEIS2434 | hemolysin-activating lysine-acyltransferase HlyC | 47.01 | Yes | HlyC - <i>Acinetobacter guillouiae</i> | 46% | IR | No | Proximal core gene is NEIS1108 |
| | NEIS2435 | Hypothetical protein | 38.27 | Yes | Hypothetical protein - <i>Cardiobacterium hominis</i> | 33% | | | |

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|---|----------|---|-------|-----|--|-----|----|----|--|
| | NEIS2436 | Lipoprotein | 47.2 | Yes | Hypothetical protein - <i>Haemophilus influenza</i> | 41% | | | |
| | NEIS2437 | Lipoprotein | 44.9 | Yes | Hypothetical protein - <i>Haemophilus influenza</i> | 36% | | | |
| | NEIS2438 | Hemagglutinin | 50.6 | No | Hemagglutinin - <i>Haemophilus haemolyticus</i> | 40% | | | |
| Island 37A Metabolism | NEIS1117 | Beta-lactamase fold protein | 50.37 | No | Hypothetical protein - <i>Eikenella corrodens</i> | 87% | IR | No | Proximal core gene is NEIS1116 which is the site for the T4SS islands in lineage 5 (Harrison et al., 2015) |
| | NEIS1118 | MarR family transcriptional regulator | 52.44 | No | MarR family transcriptional regulator - <i>Eikenella corrodens</i> | 96% | | | |
| | CDS-1 | prokaryotic cytochrome b561 family protein | 52.44 | No | cytochrome B561 - <i>Cardiobacterium valvarum</i> | 62% | | | |
| | NEIS1121 | NADH dehydrogenase | 51.32 | No | cytochrome B561 - <i>Cardiobacterium valvarum</i> | 55% | | | |
| | NEIS1122 | antibiotic biosynthesis monooxygenase | 53.55 | No | polysaccharide biosynthesis protein - <i>Phaeobacter gallaeciensis</i> | 60% | | | |
| | CDS-2 | Hypothetical protein | 53.01 | No | DNA binding response regulator | 27% | | | |
| | | IS630 | | | | | | | |
| Island 37B Restriction modification | CDS-1 | restriction endonuclease subunit M | 51.39 | No | type I restriction-modification protein subunit M - <i>M.catarrhalis</i> | 87% | No | No | See above |
| | CDS-2 | N-6 DNA Methylase family protein | 50.21 | No | type I restriction-modification protein subunit M - <i>M.catarrhalis</i> | 74% | | | |
| | CDS-3 | type I restriction-modification system DNA-methyltransferase | 43.55 | Yes | Hypothetical protein - <i>Gallibacterium anatis</i> | 77% | | | |
| | CDS-4 | myosin VC domain protein | 50 | No | type I restriction-modification protein subunit M - <i>M.catarrhalis</i> | 51% | | | |
| Island 38 Restriction modification | NEIS1158 | type I restriction enzyme system modification protein" | 41.28 | Yes | DNA methyltransferase <i>Cardiobacterium hominis</i> | 89% | No | No | Proximal core gene is NEIS1157 |
| Island 39 (ModB) Restriction modification | NEIS1193 | type III restriction-modification system endonuclease protein" | 48.37 | Yes | type III restriction-modification system endonuclease - <i>Mannheimia succiniciproducens</i> | 73% | DR | No | Proximal core gene is NEIS1195 (<i>mip</i>) (Srikhanta et al., 2009) |
| | NEIS1194 | Type III restriction/modification system methyltransferase (ModB) | 45.11 | Yes | type III restriction endonuclease subunit M - <i>Haemophilus influenza</i> | 66% | | | |

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|--|----------|---|-------|-----|---|-----|----|----|--|
| Island 40 Metabolism | NEIS1225 | CAAX amino protease | 41.45 | Yes | CAAX amino protease - <i>Morococcus cerebrosus</i> | 94% | No | No | Proximal core gene is NEIS1223 |
| Island 41A Toxin | NEIS1357 | addiction module protein | 50.62 | No | Addicton module protein - <i>Alysiella crassa</i> | 77% | IR | No | Proximal core gene is <i>fis</i> (NEIS1353) (Lehnher et al., 1993) |
| Island 41B Metabolism | NEIS1358 | peptidase | 53.47 | No | Hypothetical protein - <i>Moraxella boevrei</i> | 32% | | | |
| Island 42 Hypothetical | NEIS1424 | hypothetical protein | 47.58 | Yes | Hypothetical protein - <i>Kingella sp.</i> | 59% | No | No | Proximal core gene is NEIS1423 |
| Island 43 Restriction modification | NEIS1519 | Type II restriction nuclease | 44.57 | Yes | Type II restriction endonuclease - <i>Methylococcus capsulatus</i> | 58% | IR | No | Proximal core gene is NEIS1518 |
| | NEIS1520 | C-5 cytosine-specific DNA methylase | 42.89 | Yes | DNA methyltransferase - <i>Methylococcus capsulatus</i> | 70% | | | |
| Island 44 GpxA Metabolism | NEIS1547 | glutathione peroxidase GpxA | 48.5 | Yes | Glutathione peroxidase - <i>Kingella sp.</i> | 71% | No | No | Proximal core gene is NEIS1546 (Moore and Sparling, 1995) |
| Island 45 Toxin | NEIS1583 | excinuclease ATPase subunit | 52.79 | No | Excinuclease - <i>Conchiformibius steedae</i> | 55% | No | No | Proximal core gene is NEIS1582 (Liu et al., 2008) |
| | NEIS1584 | Death on curing protein, Doc toxin, partial | 42.64 | Yes | DNA-binding protein - <i>Serratia marcescens</i> | 60% | IR | No | |
| | NEIS1585 | prevent-host-death protein | 39.36 | Yes | Prevent-host-death protein - <i>Serratia marcescens</i> | 52% | | | |
| Island 46 Hypothetical | NEIS1626 | Hypothetical protein | 31.71 | Yes | Hypothetical protein - <i>Streptococcus sp.</i> | 99% | No | No | Proximal core gene is NEIS1625 |
| Island 47 (IHT-C) Toxin | NEIS2495 | Virulence associated protein VapD (CRISPR associated protein) | 39.95 | Yes | VapD - <i>Kingella dentrificans</i> | 91% | IR | No | Proximal gene is <i>tspB</i> (NEIS1715) |
| | NEIS2496 | Hypothetical protein | 39.13 | Yes | acetyl-CoA carboxylase carboxyl transferase subunit alpha – <i>Methylibium sp</i> | 34% | | | |
| | NEIS2497 | Hypothetical protein | 40 | Yes | None | | | | |
| | NEIS2470 | Hypothetical protein | 34.74 | Yes | None | | | | |

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|---|----------|--|-------|-----|---|-----|----|----|---|
| | NEIS2498 | Fic family protein | 43.96 | Yes | Fic family protein - <i>Actinobacillus sp</i> | 64% | | | (Tettelin et al., 2000) |
| | NEIS2499 | Hypothetical protein | 40.83 | Yes | Hypothetical protein - <i>Actinobacillus ureae</i> | 83% | | | |
| | NEIS2500 | HipA family protein | 42.34 | Yes | Phosphatidylinositol kinase - <i>Polaromonas sp</i> | 33% | | | |
| | NEIS2501 | hemin transporter | 47.99 | Yes | Hemin transporter - <i>Kingella sp.</i> | 76% | | | |
| | NEIS2502 | HlyC protein (RTX toxin) | 45.32 | Yes | Hypothetical protein - <i>Acinetobacter sp.</i> | 46% | | | |
| | NEIS2503 | lipoprotein | 37.14 | Yes | Hypothetical protein - <i>Histophilus somni</i> | 50% | | | |
| | NEIS2504 | Hypothetical protein | 31.67 | Yes | Hypothetical protein - <i>Neisseria flavescens</i> | 28% | | | |
| | NEIS2505 | Hemagglutinin | 37.57 | Yes | Hemagglutinin - <i>N. lactamica</i> | 82% | | | |
| | CDS-1 | Hemagglutinin | 46.19 | Yes | Hemagglutinin - <i>N. lactamica</i> | 92% | | | |
| Island 48 Hypothetical | NEIS1695 | hypothetical protein | 44.65 | Yes | Cell division protein - <i>Campylobacter fetus</i> | 43% | No | No | Proximal core gene is NEIS1694 |
| Island 49A VanX Cell wall synthesis | NEIS1730 | Putative integral membrane protein | 37.68 | Yes | Membrane protein - <i>Xenorhabdus bovienii</i> | 63% | No | No | Proximal core gene NEIS1729 (Deghorain et al., 2007, Joseph et al., 2010) |
| | NEIS1731 | ddpX D-alanyl-D-alanine dipeptidase (VanX) | 42.01 | Yes | Putative D-alanyl-D-alanine dipeptidase - <i>Xenorhabdus cabanillasii</i> | 46% | | | |
| Island 49B Membrane | NEIS2488 | YfcA inner membrane protein | 49.68 | No | Membrane protein - <i>Acinetobacter calcoaceticus</i> | 70% | No | No | As above |
| Island 50 Hypothetical | NEIS1801 | hypothetical protein | 33.95 | Yes | hypothetical protein - <i>Kiloniella laminariae</i> | 27% | No | No | Proximal region is Island 23 preceded by NEIS1788 |
| Island 51 Membrane | NEIS1802 | lipoprotein | 26.11 | Yes | hypothetical protein - <i>Aneurinibacillus migulanus</i> | 38% | No | No | Proximal region is NEIS1801 (Island 50) |
| Island 52 Hypothetical | NEIS1803 | hypothetical protein | 38.69 | Yes | hypothetical protein - <i>Rothia dentocariosa</i> | 41% | No | No | Proximal region is NEIS1802 (Island 51) |

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|--|---------------------------------|---|-------|-----|---|-----|-------|----|--|
| Island 53 Toxin | NEIS2370 | Immunity protein | 31.95 | Yes | None | | No | No | Proximal core gene is NEIS1853 |
| Island 54 Metabolism | NEIS1886 | Helicase | 39.55 | Yes | Helicase - <i>Methylomicrobium agile</i> | 61% | No | No | Proximal core gene is NEIS1885 |
| Island 55 Hypothetical | NEIS1940 | Hypothetical protein | 25.64 | Yes | hypothetical protein - <i>Ralstonia solanacearum</i> | 55% | No | No | Proximal core gene is NEIS1939 |
| | NEIS1941 | Hypothetical protein | 40.03 | Yes | hypothetical protein, partial - <i>Cardiobacterium hominis</i> | 61% | | | |
| Island 56 (HpuA/B) Iron acquisition | NEIS1946 (<i>hpuA</i>) | hemoglobin receptor component HpuA | 52.53 | No | None | | IR/DR | No | Proximal core gene is NEIS1945 (Lewis et al., 1997) |
| | NEIS1947 (<i>hpuB</i>) | hemoglobin-haptoglobin utilization protein HpuB | 55.03 | Yes | hemoglobin-haptoglobin utilization protein - <i>Morococcus cerebrosus</i> | 78% | | | |
| Island 57 (MspA) Membrane | CDS | immunoglobulin A1 protease | 52.87 | No | None | | DR | No | Proximal core gene is NEIS1973 |
| | NEIS1974 | MspA | 56.94 | Yes | Hypothetical protein - <i>Helicobacter pylori</i> | 99% | | | (Turner et al., 2006) |
| Island 58 (Vsr-2) Restriction modification | NEIS1990 | patch repair protein (Vsr) | 37.73 | Yes | Very short patch repair protein - <i>Actinobacillus suis</i> | 66% | No | No | Proximal core gene is NEIS1987 (Bazleкова et al., 2017) |
| | NEIS1991 | GHKL domain containing protein | 36.9 | Yes | Molecular chaperone - <i>Chlenobacter oris</i> | 57% | | | |
| | NEIS1992 | cytosine-specific DNA methylase | 40.72 | Yes | Modification methylase - <i>Haemophilus influenzae</i> | 79% | | | |
| Island 59 (LgtG) Membrane | NEIS2011 | glycosyltransfersase family 1 (LgtG) | 56.37 | Yes | None | | No | No | Proximal core gene is NEIS2010 (Banerjee et al., 1998) (Kahler et al., 2005) |
| Island 60 (Lpt6) Membrane | NEIS2012 | lipopolysaccharide inner-core distal heptose 6-phosphoethanolamine transferase (Lpt6) | 53.96 | No | Membrane protein - <i>Haemophilus influenzae</i> | 69% | No | No | See above (Wright et al., 2004, Kahler et al., 2005) |
| Island 61 Restriction modification | (Preceded by NEIS2062) CDS-1 | Restriction endonuclease | 42.03 | Yes | Modification methylase - <i>Haemophilus influenzae</i> | 77% | No | No | Proximal core gene is NEIS2061 |

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|------------------------------------|----------|--|-------|-----|---|--------|-------|----|---|
| | CDS -2 | Restriction endonuclease | 37.74 | Yes | Restriction endonuclease - <i>Haemophilus influenzae</i> | 67% | | | |
| Island 62 (MGI-3 MafI) Toxin | NEIS2085 | MafI immunity protein | 25.47 | Yes | Hypothetical protein - <i>Eikenella corrodens</i> | 45% | IR/DR | No | Proximal gene for this <i>maf</i> locus is 2082 (Jamet et al., 2015) |
| Island 63 (modD) | NEIS2364 | Type II Restriction Modification Enzyme | 49.7 | No | DNA methyltransferase – <i>Bergeriella denitfificans</i> | 69.88% | No | No | (Seib et al., 2011) |

REFERENCES for Supplementary Table 2

- ALLUNANS, J., KRISTIANSEN, K. I., ASSALKHOU, R. & BJORAS, M. 2008. Bacteriocins (meningocins) in Norwegian isolates of *Neisseria meningitidis*: possible role in the course of a meningococcal epidemic. *APMIS*, 116, 333-44.
- ARENAS, J., SCHIPPER, K., VAN ULSEN, P., VAN DER ENDE, A. & TOMMASSEN, J. 2013. Domain exchange at the 3' end of the gene encoding the fratricide meningococcal two-partner secretion protein A. *BMC Genomics*, 14, 622.
- BANERJEE, A., WANG, R., ULJON, S. N., RICE, P. A., GOTSCHLICH, E. C. & STEIN, D. C. 1998. Identification of the gene (*lgtG*) encoding the lipooligosaccharide beta chain synthesizing glucosyl transferase from *Neisseria gonorrhoeae*. *Proc Natl Acad Sci U S A*, 95, 10872-7.
- BASMAJI, F., MARTIN-YKEN, H., DURAND, F., DAGKESSAMANSKAIA, A., PICHEREAUX, C., ROSSIGNOL, M. & FRANCOIS, J. 2006. The 'interactome' of the Knr4/Smi1, a protein implicated in coordinating cell wall synthesis with bud emergence in *Saccharomyces cerevisiae*. *Mol Genet Genomics*, 275, 217-30.
- BAZLEKOWA, M., ADAMCZYK-POPLAWSKA, M. & KWIATEK, A. 2017. Characterization of Vsr endonucleases from *Neisseria meningitidis*. *Microbiology (Reading)*, 163, 1003-1015.
- BILLE, E., URE, R., GRAY, S. J., KACZMARSKI, E. B., MCCARTHY, N. D., NASSIF, X., MAIDEN, M. C. & TINSLEY, C. R. 2008. Association of a bacteriophage with meningococcal disease in young adults. *PLoS One*, 3, e3885.
- CLAUS, H., FRIEDRICH, A., FROSCH, M. & VOGEL, U. 2000. Differential distribution of novel restriction-modification systems in clonal lineages of *Neisseria meningitidis*. *Journal of Bacteriology*, 182, 1296-1303.
- DEGHORAIN, M., GOFFIN, P., FONTAINE, L., MAINARDI, J. L., DANIEL, R., ERRINGTON, J., HALLET, B. & HOLS, P. 2007. Selectivity for D-lactate incorporation into the peptidoglycan precursors of *Lactobacillus plantarum*: role of Aad, a VanX-like D-alanyl-D-alanine dipeptidase. *J Bacteriol*, 189, 4332-7.
- DINH, T., PAULSEN, I. T. & SAIER, M. 1994. A family of extracytoplasmic proteins that allow transport of large molecules across the outer membranes of gram-negative bacteria. *Journal of Bacteriology*, 176, 3825-3831.
- HADJINEOPHYTOU, C., ANONSEN, J. H., WANG, N., MA, K. C., VIBURIENE, R., VIK, A., HARRISON, O. B., MAIDEN, M. C. J., GRAD, Y. H. & KOOMEY, M. 2019. Genetic determinants of genus-level glycan diversity in a bacterial protein glycosylation system. *PLoS Genet*, 15, e1008532.
- HARRISON, O. B., BRAY, J. E., MAIDEN, M. C. & CAUGANT, D. A. 2015. Genomic Analysis of the Evolution and Global Spread of Hyper-invasive Meningococcal Lineage 5. *EBioMedicine*, 2, 234-243.
- HELAINE, S., CARBONNELLE, E., PROUVENSIER, L., BERETTI, J. L., NASSIF, X. & PELICIC, V. 2005. PilX, a pilus-associated protein essential for bacterial aggregation, is a key to pilus-facilitated attachment of *Neisseria meningitidis* to human cells. *Mol Microbiol*, 55, 65-77.
- JAMET, A., JOUSSET, A. B., EUPHRASIE, D., MUKORAKO, P., BOUCHARLAT, A., DU COUSSO, A., CHARBIT, A. & NASSIF, X. 2015. A new family of secreted toxins in pathogenic *Neisseria* species. *PLoS Pathog*, 11, e1004592.
- JOLLEY, K. A., SUN, L., MOXON, E. R. & MAIDEN, M. C. 2004. Dam inactivation in *Neisseria meningitidis*: prevalence among diverse hyperinvasive lineages. *BMC microbiology*, 4, 1-7.
- JOSEPH, B., SCHNEIKER-BEKEL, S., SCHRAMM-GLÜCK, A., BLOM, J., CLAUS, H., LINKE, B., SCHWARZ, R. F., BECKER, A., GOESMANN, A. & FROSCH, M. 2010. Comparative genome biology of a serogroup B carriage and disease strain supports a polygenic nature of meningococcal virulence. *Journal of bacteriology*, 192, 5363-5377.

- JOSEPH, B., SCHWARZ, R. F., LINKE, B., BLOM, J., BECKER, A., CLAUS, H., GOESMANN, A., FROSCH, M., MULLER, T., VOGEL, U. & SCHOEN, C. 2011. Virulence evolution of the human pathogen *Neisseria meningitidis* by recombination in the core and accessory genome. *PLoS One*, 6, e18441.
- KAHLER, C. M., DATTA, A., TZENG, Y. L., CARLSON, R. W. & STEPHENS, D. S. 2005. Inner core assembly and structure of the lipooligosaccharide of *Neisseria meningitidis*: capacity of strain NMB to express all known immunotype epitopes. *Glycobiology*, 15, 409-19.
- KAHLER, C. M., MARTIN, L. E., TZENG, Y.-L., MILLER, Y. K., SHARKEY, K., STEPHENS, D. S. & DAVIES, J. K. 2001. Polymorphisms in pilin glycosylation locus of *Neisseria meningitidis* expressing class II pili. *Infection and immunity*, 69, 3597-3604.
- KJOS, M., SNIPEN, L., SALEHIAN, Z., NES, I. F. & DIEP, D. B. 2010. The abi proteins and their involvement in bacteriocin self-immunity. *J Bacteriol*, 192, 2068-76.
- LEHNHERR, H., MAGUIN, E., JAFRI, S. & YARMOLINSKY, M. B. 1993. Plasmid addiction genes of bacteriophage P1: doc, which causes cell death on curing of prophage, and phd, which prevents host death when prophage is retained. *J Mol Biol*, 233, 414-28.
- LEWIS, L. A., GRAY, E., WANG, Y. P., ROE, B. A. & DYER, D. W. 1997. Molecular characterization of hpuAB, the haemoglobin–haptoglobin-utilization operon of *Neisseria meningitidis*. *Molecular microbiology*, 23, 737-749.
- LIU, M., ZHANG, Y., INOUYE, M. & WOYCHIK, N. A. 2008. Bacterial addiction module toxin Doc inhibits translation elongation through its association with the 30S ribosomal subunit. *Proc Natl Acad Sci U S A*, 105, 5885-90.
- MASIGNANI, V., GIULIANI, M. M., TETTELIN, H., COMANDUCCI, M., RAPPOLI, R. & SCARLATO, V. 2001. Mu-like prophage in serogroup B *Neisseria meningitidis* coding for surface-exposed antigens. *Infection and immunity*, 69, 2580-2588.
- MOORE, T. & SPARLING, P. F. 1995. Isolation and identification of a glutathione peroxidase homolog gene, gpxA, present in *Neisseria meningitidis* but absent in *Neisseria gonorrhoeae*. *Infection and immunity*, 63, 1603-1607.
- POWER, P. M., RODDAM, L. F., RUTTER, K., FITZPATRICK, S. Z., SRIKHANTA, Y. N. & JENNINGS, M. P. 2003. Genetic characterization of pilin glycosylation and phase variation in *Neisseria meningitidis*. *Mol Microbiol*, 49, 833-47.
- PROCHAZKOVA, K., OSICKA, R., LINHARTOVA, I., HALADA, P., SULC, M. & SEBO, P. 2005. The *Neisseria meningitidis* outer membrane lipoprotein FrpD binds the RTX protein FrpC. *J Biol Chem*, 280, 3251-8.
- SEIB, K. L., PIGOZZI, E., MUZZI, A., GAWTHORNE, J. A., DELANY, I., JENNINGS, M. P. & RAPPOLI, R. 2011. A novel epigenetic regulator associated with the hypervirulent *Neisseria meningitidis* clonal complex 41/44. *Faseb Journal*, 25, 3622-3633.
- SHIH, G. C., KAHLER, C. M., CARLSON, R. W., RAHMAN, M. M. & STEPHENS, D. S. 2001. gmhX, a novel gene required for the incorporation of L-glycero-D-manno-heptose into lipooligosaccharide in *Neisseria meningitidis*. *Microbiology (Reading)*, 147, 2367-2377.
- SIGURLASDOTTIR, S., WASSING, G. M., ZUO, F., ARTS, M. & JONSSON, A. B. 2019. Deletion of D-Lactate Dehydrogenase A in *Neisseria meningitidis* Promotes Biofilm Formation Through Increased Autolysis and Extracellular DNA Release. *Front Microbiol*, 10, 422.
- SRIKHANTA, Y. N., DOWIDEIT, S. J., EDWARDS, J. L., FALSETTA, M. L., WU, H. J., HARRISON, O. B., FOX, K. L., SEIB, K. L., MAGUIRE, T. L., WANG, A. H., MAIDEN, M. C., GRIMMOND, S. M., APICELLA, M. A. & JENNINGS, M. P. 2009. Phasevarions mediate random switching of gene expression in pathogenic *Neisseria*. *PLoS Pathog*, 5, e1000400.
- STANGER, F. V., BURMANN, B. M., HARMS, A., ARAGAO, H., MAZUR, A., SHARPE, T., DEHIO, C., HILLER, S. & SCHIRMER, T. 2016. Intrinsic regulation of FIC-domain AMP-transferases by oligomerization and automodification. *Proc Natl Acad Sci U S A*, 113, E529-37.

- TETTELIN, H., SAUNDERS, N. J., HEIDELBERG, J., JEFFRIES, A. C., NELSON, K. E., EISEN, J. A., KETCHUM, K. A., HOOD, D. W., PEDEN, J. F. & DODSON, R. J. 2000. Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58. *Science*, 287, 1809-1815.
- THOMPSON, S. A., WANG, L. L., WEST, A. & SPARLING, P. F. 1993. *Neisseria meningitidis* produces iron-regulated proteins related to the RTX family of exoproteins. *J Bacteriol*, 175, 811-8.
- TURNER, D. P., MARIETOU, A. G., JOHNSTON, L., HO, K. K., ROGERS, A. J., WOOLDRIDGE, K. G. & ALA'ALDEEN, D. A. 2006. Characterization of MspA, an immunogenic autotransporter protein that mediates adhesion to epithelial and endothelial cells in *Neisseria meningitidis*. *Infect Immun*, 74, 2957-64.
- WARREN, M. J., RODDAM, L. F., POWER, P. M., TERRY, T. D. & JENNINGS, M. P. 2004. Analysis of the role of pgII in pilin glycosylation of *Neisseria meningitidis*. *FEMS Immunology & Medical Microbiology*, 41, 43-50.
- WRIGHT, J. C., HOOD, D. W., RANDLE, G. A., MAKEPEACE, K., COX, A. D., LI, J., CHALMERS, R., RICHARDS, J. C. & MOXON, E. R. 2004. lpt6, a gene required for addition of phosphoethanolamine to inner-core lipopolysaccharide of *Neisseria meningitidis* and *Haemophilus influenzae*. *J Bacteriol*, 186, 6970-82.
- YAN, N. 2013. Structural advances for the major facilitator superfamily (MFS) transporters. *Trends in biochemical sciences*, 38, 151-159.
- ZHANG, D., IYER, L. M. & ARAVIND, L. 2011. A novel immunity system for bacterial nucleic acid degrading toxins and its recruitment in various eukaryotic and DNA viral systems. *Nucleic Acids Res*, 39, 4532-52.

Supplementary Table 3. List of strains from PubMLST database used in the Phaser analysis.

| PubMLST ID | Isolate name | Country of isolation | Collection date | Serogroup group | Sequence Type | Clonal Complex |
|------------|--------------|----------------------|-----------------|-----------------|---------------|------------------|
| 7 | 7891 | Finland | 1975 | A | 5 | ST-5 complex |
| 24 | S4355 | Denmark | 1974 | A | 5 | ST-5 complex |
| 30 | 14 | Germany | 1999 | cnl | 53 | ST-53 complex |
| 82 | 11-004 | China | 1984 | A | 5 | ST-5 complex |
| 84 | IAL2229 | Brazil | 1976 | A | 5 | ST-5 complex |
| 128 | F6124 | Chad | 1988 | A | 5 | ST-5 complex |
| 210 | H1964 | UK | 1987 | A | 5 | ST-5 complex |
| 237 | H44/76 | Norway | 1976 | B | 32 | ST-32 complex |
| 238 | 153 | China | 1966 | A | 5 | ST-5 complex |
| 239 | 154 | China | 1966 | A | 6 | ST-5 complex |
| 240 | MC58 | UK | 1983 | B | 74 | ST-32 complex |
| 340 | 196/87 | Norway | 1987 | C | 32 | ST-32 complex |
| 343 | 500 | Italy | 1984 | C | 11 | ST-11 complex |
| 349 | 38VI | USA | 1964 | B | 11 | ST-11 complex |
| 369 | M597 | Israel | 1988 | C | 11 | ST-11 complex |
| 391 | 90/18311 | UK [Scotland] | 1990 | C | 11 | ST-11 complex |
| 400 | BZ 83 | The Netherlands | 1984 | B | 34 | ST-32 complex |
| 403 | BZ 147 | The Netherlands | 1963 | B | 48 | ST-41/44 complex |
| 408 | BZ 169 | The Netherlands | 1985 | B | 32 | ST-32 complex |

| Isolate ID | Strain name | Country of isolation | Collection date | Serogroup group | Sequence Type | Clonal Complex |
|------------|-------------|----------------------|-----------------|-----------------|---------------|------------------|
| 409 | BZ 198 | The Netherlands | 1986 | B | 41 | ST-41/44 complex |
| 415 | EG 329 | Germany | 1985 | B | 32 | ST-32 complex |
| 419 | NG 6/88 | Norway | 1988 | B | 13 | ST-269 complex |
| 430 | NG 080 | Norway | 1981 | B | 32 | ST-32 complex |
| 431 | NG144/82 | Norway | 1982 | B | 32 | ST-32 complex |
| 434 | NG PB24 | Norway | 1985 | B | 32 | ST-32 complex |
| 441 | 8680 | Chile | 1987 | B | 32 | ST-32 complex |
| 451 | 14/1455 | Russia | 1970 | A | 5 | ST-5 complex |
| 468 | BRAZ10 | Brazil | 1976 | C | 11 | ST-11 complex |
| 507 | MA-5756 | Spain | 1985 | C | 11 | ST-11 complex |
| 597 | 92001 | China | 1992 | A | 7 | ST-5 complex |
| 644 | L93/4286 | UK [England] | 1993 | C | 11 | ST-11 complex |
| 645 | 204/92 | Cuba | 1992 | B | 33 | ST-32 complex |
| 646 | 400 | Austria | 1991 | B | 40 | ST-41/44 complex |
| 647 | AK50 | Greece | 1992 | B | 41 | ST-41/44 complex |
| 648 | M-101/93 | Iceland | 1993 | B | 41 | ST-41/44 complex |
| 649 | 50/94 | Norway | 1994 | B | 45 | ST-41/44 complex |
| 650 | M40/94 | Chile | 1994 | B | 41 | ST-41/44 complex |
| 651 | 931905 | The Netherlands | 1993 | B | 41 | ST-41/44 complex |
| 652 | N45/96 | Norway | 1996 | B | 41 | ST-41/44 complex |
| 653 | 91/40 | New Zealand | 1991 | B | 42 | ST-41/44 complex |
| 660 | 71/94 | Norway | 1994 | Y | 23 | ST-23 complex |
| 662 | 2837 | UK | 1997 | C | 50 | ST-11 complex |
| 670 | 2840 | UK | 1997 | C | 50 | ST-11 complex |

| Isolate ID | Strain name | Country of isolation | Collection date | Serogroup group | Sequence Type | Clonal Complex |
|------------|-------------|----------------------|-----------------|-----------------|---------------|------------------|
| 671 | 2844 | UK | 1997 | C | 50 | ST-11 complex |
| 672 | 2847 | UK | 1997 | C | 50 | ST-11 complex |
| 684 | 0259/93 | Czech Republic | 1993 | C | 11 | ST-11 complex |
| 698 | FAM18 | USA | 1983 | C | 11 | ST-11 complex |
| 972 | 0066/93 | Czech Republic | 1993 | E | 53 | ST-53 complex |
| 984 | 0083/93 | Czech Republic | 1993 | E | 53 | ST-53 complex |
| 1168 | BM33 | Greece | 1996 | B | 33 | ST-32 complex |
| 1169 | BM45 | Greece | 1996 | C | 11 | ST-11 complex |
| 1178 | W72 | Greece | 1997 | C | 211 | ST-11 complex |
| 1181 | W138 | Greece | 1998 | B | 11 | ST-11 complex |
| 1597 | 0206/93 | Czech Republic | 1993 | E | 122 | ST-53 complex |
| 1639 | 0252/93 | Czech Republic | 1993 | E | 53 | ST-53 complex |
| 1649 | 0269/93 | Czech Republic | 1993 | E | 53 | ST-53 complex |
| 1654 | 0277/93 | Czech Republic | 1993 | cnl | 123 | ST-53 complex |
| 1955 | 0011/93 | Czech Republic | 1993 | B | 740 | ST-41/44 complex |
| 2216 | 0190/93 | Czech Republic | 1993 | B | 998 | ST-269 complex |
| 2222 | 0314/93 | Czech Republic | 1993 | cnl | 124 | ST-53 complex |
| 2233 | 0531/93 | Czech Republic | 1993 | B | 1015 | ST-32 complex |
| 2281 | M7089 | USA | 2000 | W | 11 | ST-11 complex |
| 2290 | M7124 | Saudi Arabia | 2000 | W | 11 | ST-11 complex |
| 4145 | 0148/00 | Czech Republic | 2000 | B | 2994 | ST-11 complex |
| 5171 | 0085/00 | Czech Republic | 2000 | B | 3537 | ST-11 complex |
| 6986 | 0131/95 | Czech Republic | 1995 | B | 4993 | ST-11 complex |
| 7891 | 0179/04 | Czech Republic | 2004 | B | 5756 | ST-11 complex |
| 7892 | 0263/04 | Czech Republic | 2004 | B | 5757 | ST-11 complex |

| Isolate ID | Strain name | Country of isolation | Collection date | Serogroup group | Sequence Type | Clonal Complex |
|------------|-------------|----------------------|-----------------|-----------------|---------------|------------------|
| 8169 | 0410/93 | Czech Republic | 1993 | cnl | 53 | ST-53 complex |
| 8177 | 0422/93 | Czech Republic | 1993 | cnl | 53 | ST-53 complex |
| 8181 | 0426/93 | Czech Republic | 1993 | cnl | 53 | ST-53 complex |
| 8682 | 0030/01 | Czech Republic | 2001 | B | 11 | ST-11 complex |
| 10436 | 0290/94 | Czech Republic | 1994 | W | 247 | ST-11 complex |
| 10479 | 0233/96 | Czech Republic | 1996 | B | 11 | ST-11 complex |
| 10487 | 0288/96 | Czech Republic | 1996 | B | 11 | ST-11 complex |
| 10499 | 0467/96 | Czech Republic | 1996 | B | 11 | ST-11 complex |
| 10500 | 0492/96 | Czech Republic | 1996 | B | 11 | ST-11 complex |
| 10705 | N 25/99 | Norway | 1999 | B | 44 | ST-41/44 complex |
| 10735 | N 56/99 | Norway | 1999 | B | 45 | ST-41/44 complex |
| 10756 | 8/00 | Norway | 2000 | B | 43 | ST-41/44 complex |
| 10758 | 10/00 | Norway | 2000 | B | 110 | ST-41/44 complex |
| 10812 | 64/00 | Norway | 2000 | B | 146 | ST-41/44 complex |
| 11389 | 2379 | South Africa | 2005 | B | 6697 | ST-41/44 complex |
| 13420 | 0106/07 | Czech Republic | 2007 | B | 11 | ST-11 complex |
| 14480 | M5178 | USA | 1998 | B | 32 | ST-32 complex |
| 14627 | M20918 | USA | 2009 | A | 47,897,980 | ST-5 complex |
| 14765 | 0002/93 | Czech Republic | 1993 | C | 11 | ST-11 complex |
| 15032 | 0186/93 | Czech Republic | 1993 | C | 11 | ST-11 complex |
| 15035 | 0188/93 | Czech Republic | 1993 | C | 11 | ST-11 complex |
| 15152 | 0263/93 | Czech Republic | 1993 | discrepancy | 11 | ST-11 complex |
| 15154 | 0264/93 | Czech Republic | 1993 | C | 11 | ST-11 complex |
| 15174 | 0284/93 | Czech Republic | 1993 | C | 11 | ST-11 complex |
| 15176 | 0287/93 | Czech Republic | 1993 | C | 11 | ST-11 complex |

| Isolate ID | Strain name | Country of isolation | Collection date | Serogroup group | Sequence Type | Clonal Complex |
|------------|-------------|----------------------|-----------------|-----------------|---------------|------------------|
| 15238 | 0343/93 | Czech Republic | 1993 | C | 11 | ST-11 complex |
| 15242 | 0351/93 | Czech Republic | 1993 | C | 11 | ST-11 complex |
| 15249 | 0379/93 | Czech Republic | 1993 | B | 118 | ST-32 complex |
| 15261 | 0400/93 | Czech Republic | 1993 | C | 11 | ST-11 complex |
| 15313 | 0469/93 | Czech Republic | 1993 | B | 118 | ST-32 complex |
| 15315 | 0489/93 | Czech Republic | 1993 | C | 11 | ST-11 complex |
| 15316 | 0490/93 | Czech Republic | 1993 | C | 11 | ST-11 complex |
| 15319 | 0500/93 | Czech Republic | 1993 | C | 11 | ST-11 complex |
| 15325 | 0512/93 | Czech Republic | 1993 | C | 11 | ST-11 complex |
| 15330 | 0520/93 | Czech Republic | 1993 | C | 11 | ST-11 complex |
| 15336 | 0529/93 | Czech Republic | 1993 | C | 11 | ST-11 complex |
| 15342 | 0535/93 | Czech Republic | 1993 | C | 11 | ST-11 complex |
| 15344 | 0538/93 | Czech Republic | 1993 | C | 11 | ST-11 complex |
| 15623 | 0091/04 | Czech Republic | 2004 | B | 5756 | ST-11 complex |
| 15630 | 0140/04 | Czech Republic | 2004 | B | 5756 | ST-11 complex |
| 18968 | M10 240474 | UK [England] | 2010 | B | 269 | ST-269 complex |
| 18969 | M10 240478 | UK [England] | 2010 | B | 1194 | ST-41/44 complex |
| 19023 | M10 240473 | UK [England] | 2010 | B | 1161 | ST-269 complex |
| 19024 | M10 240480 | UK [England] | 2010 | B | 1194 | ST-41/44 complex |
| 19026 | M10 240482 | UK [England] | 2010 | B | 3754 | ST-41/44 complex |
| 19027 | M10 240484 | UK [England] | 2010 | B | 1097 | ST-41/44 complex |
| 19028 | M10 240485 | UK [England] | 2010 | B | 275 | ST-269 complex |
| 19029 | M10 240487 | UK [England] | 2010 | B | 1049 | ST-269 complex |
| 19030 | M10 240489 | UK [England] | 2010 | B | 461 | ST-461 complex |
| 19031 | M10 240490 | UK [England] | 2010 | B | 1161 | ST-269 complex |

| Isolate ID | Strain name | Country of isolation | Collection date | Serogroup group | Sequence Type | Clonal Complex |
|------------|-------------|----------------------|-----------------|-----------------|---------------|------------------|
| 19032 | M10 240498 | UK [Wales] | 2010 | B | 41 | ST-41/44 complex |
| 19260 | WUE 2594 | Germany | 1991 | A | 5 | ST-5 complex |
| 19261 | alpha710 | Germany | 2012 | B | 136 | ST-41/44 complex |
| 19263 | NZ-05/33 | New Zealand | 2005 | B | 42 | ST-41/44 complex |
| 19264 | M04-240196 | UK | 2004 | B | 269 | ST-269 complex |
| 19265 | M01-240355 | UK | 2001 | B | 213 | ST-213 complex |
| 19266 | M01-240149 | UK | 2001 | B | 41 | ST-41/44 complex |
| 19359 | M13399 | Unknown | 2005 | B | 2976 | ST-269 complex |
| 19362 | CU385 | Unknown | 1980 | B | 33 | ST-32 complex |
| 19366 | M10699 | USA | 2003 | B | 32 | ST-32 complex |
| 19367 | M11791 | USA | 2003 | Y | 23 | ST-23 complex |
| 19368 | M13220 | Philippines | 2005 | A | 7 | ST-5 complex |
| 19370 | M14900 | USA | 2006 | Y | 1625 | ST-23 complex |
| 19372 | M15293 | USA | 2006 | NG | 32 | ST-32 complex |
| 19378 | M18575 | Burkina Faso | 2003 | A | 2859 | ST-5 complex |
| 19958 | M10 240476 | UK [England] | 2010 | B | 9812 | ST-213 complex |
| 19959 | M10 240499 | UK [England] | 2010 | B | 275 | ST-269 complex |
| 19960 | M10 240500 | UK [England] | 2010 | B | 41 | ST-41/44 complex |
| 19961 | M10 240502 | UK [England] | 2010 | B | 340 | ST-41/44 complex |
| 19962 | M10 240503 | UK [England] | 2010 | Y | 23 | ST-23 complex |
| 19963 | M10 240505 | UK [England] | 2010 | Y | 1655 | ST-23 complex |
| 19964 | M10 240507 | UK [England] | 2010 | Y | 183 | ST-23 complex |
| 19967 | M10 240512 | UK [England] | 2010 | B | 41 | ST-41/44 complex |
| 19969 | M10 240515 | UK [England] | 2010 | B | 269 | ST-269 complex |
| 19970 | M10 240520 | UK [England] | 2010 | Y | 1655 | ST-23 complex |

| Isolate ID | Strain name | Country of isolation | Collection date | Serogroup group | Sequence Type | Clonal Complex |
|------------|-------------|----------------------|-----------------|-----------------|---------------|------------------|
| 19971 | M10 240521 | UK [England] | 2010 | B | 3802 | ST-41/44 complex |
| 19972 | M10 240522 | UK [England] | 2010 | B | 41 | ST-41/44 complex |
| 19973 | M10 240525 | UK [England] | 2010 | B | 2931 | ST-32 complex |
| 19974 | M10 240527 | UK [England] | 2010 | B | 269 | ST-269 complex |
| 19975 | M10 240528 | UK [England] | 2010 | B | 7833 | ST-269 complex |
| 19976 | M10 240530 | UK [England] | 2010 | Y | 9813 | ST-23 complex |
| 19977 | M10 240531 | UK [England] | 2010 | Y | 1655 | ST-23 complex |
| 19978 | M10 240532 | UK [England] | 2010 | B | 41 | ST-41/44 complex |
| 19979 | M10 240534 | UK [England] | 2010 | Y | 1655 | ST-23 complex |
| 19980 | M10 240536 | UK [England] | 2010 | Y | 1655 | ST-23 complex |
| 19981 | M10 240540 | UK [England] | 2010 | Y | 9814 | ST-23 complex |
| 19982 | M10 240546 | UK [England] | 2010 | B | 213 | ST-213 complex |
| 19983 | M10 240547 | UK [England] | 2010 | B | 749 | ST-32 complex |
| 19984 | M10 240548 | UK [England] | 2010 | B | 340 | ST-41/44 complex |
| 19985 | M10 240549 | UK [Wales] | 2010 | B | 41 | ST-41/44 complex |
| 19986 | M10 240550 | UK [England] | 2010 | B | 1163 | ST-269 complex |
| 19987 | M10 240553 | UK [Wales] | 2010 | B | 1161 | ST-269 complex |
| 19988 | M10 240556 | UK [England] | 2010 | B | 9815 | ST-41/44 complex |
| 19989 | M10 240558 | UK [Wales] | 2010 | B | 1992 | ST-41/44 complex |
| 19991 | M10 240566 | UK [England] | 2010 | B | 213 | ST-213 complex |
| 19992 | M10 240568 | UK [England] | 2010 | B | 213 | ST-213 complex |
| 19994 | M10 240570 | UK [England] | 2010 | B | 5357 | ST-41/44 complex |
| 19995 | M10 240572 | UK [England] | 2010 | B | 1161 | ST-269 complex |
| 19996 | M10 240578 | UK [England] | 2010 | B | 34 | ST-32 complex |
| 19998 | M10 240580 | UK [England] | 2010 | Y | 1655 | ST-23 complex |

| Isolate ID | Strain name | Country of isolation | Collection date | Serogroup group | Sequence Type | Clonal Complex |
|------------|-------------|-----------------------|-----------------|-----------------|---------------|------------------|
| 20000 | M10 240582 | UK [England] | 2010 | B | 34 | ST-32 complex |
| 20002 | M10 240585 | UK [England] | 2010 | B | 46 | ST-41/44 complex |
| 20003 | M10 240586 | UK [England] | 2010 | B | 485 | ST-41/44 complex |
| 20004 | M10 240587 | UK [England] | 2010 | B | 9879 | ST-41/44 complex |
| 20005 | M10 240589 | UK [England] | 2010 | B | 40 | ST-41/44 complex |
| 20006 | M10 240590 | UK [England] | 2010 | Y | 23 | ST-23 complex |
| 20007 | M10 240591 | UK [England] | 2010 | B | 461 | ST-461 complex |
| 20008 | M10 240592 | UK [England] | 2010 | B | 6782 | ST-41/44 complex |
| 20009 | M10 240595 | UK [England] | 2010 | B | 213 | ST-213 complex |
| 20010 | M10 240597 | UK [England] | 2010 | B | 41 | ST-41/44 complex |
| 20011 | M10 240598 | UK [England] | 2010 | B | 41 | ST-41/44 complex |
| 20012 | M10 240602 | UK [England] | 2010 | B | 1161 | ST-269 complex |
| 20013 | M10 240604 | UK [Northern Ireland] | 2010 | B | 8384 | ST-41/44 complex |
| 20014 | M10 240605 | UK [England] | 2010 | B | 41 | ST-41/44 complex |
| 20015 | M10 240606 | UK [England] | 2010 | B | 213 | ST-213 complex |
| 20017 | M10 240611 | UK [England] | 2010 | B | 749 | ST-32 complex |
| 20018 | M10 240612 | UK [England] | 2010 | B | 269 | ST-269 complex |
| 20019 | M10 240613 | UK [England] | 2010 | B | 1161 | ST-269 complex |
| 20021 | M10 240616 | UK [England] | 2010 | W | 1224 | ST-22 complex |
| 20022 | M10 240617 | UK [England] | 2010 | B | 213 | ST-213 complex |
| 20023 | M10 240618 | UK [England] | 2010 | E | 2435 | ST-60 complex |
| 20024 | M10 240619 | UK [England] | 2010 | B | 213 | ST-213 complex |
| 20025 | M10 240621 | UK [Wales] | 2010 | B | 213 | ST-213 complex |
| 20027 | M10 240623 | UK [England] | 2010 | B | 1161 | ST-269 complex |
| 20028 | M10 240624 | UK [England] | 2010 | B | 275 | ST-269 complex |

| Isolate ID | Strain name | Country of isolation | Collection date | Serogroup group | Sequence Type | Clonal Complex |
|------------|-------------|-----------------------|-----------------|-----------------|---------------|------------------|
| 20029 | M10 240626 | UK [England] | 2010 | B | 4401 | ST-269 complex |
| 20030 | M10 240627 | UK [England] | 2010 | B | 6083 | ST-32 complex |
| 20031 | M10 240631 | UK [England] | 2010 | C | 467 | ST-269 complex |
| 20032 | M10 240632 | UK [England] | 2010 | Y | 1655 | ST-23 complex |
| 20033 | M10 240633 | UK [England] | 2010 | Y | 1655 | ST-23 complex |
| 20034 | M10 240634 | UK [Northern Ireland] | 2010 | B | 42 | ST-41/44 complex |
| 20036 | M10 240638 | UK [England] | 2010 | B | 275 | ST-269 complex |
| 20039 | M10 240641 | UK [England] | 2010 | W | 184 | ST-22 complex |
| 20041 | M10 240643 | UK [England] | 2010 | Y | 23 | ST-23 complex |
| 20042 | M10 240644 | UK [England] | 2010 | Y | 3651 | ST-22 complex |
| 20043 | M10 240645 | UK [England] | 2010 | B | 283 | ST-269 complex |
| 20044 | M10 240649 | UK [England] | 2010 | B | 275 | ST-269 complex |
| 20046 | M10 240651 | UK [England] | 2010 | B | 9881 | ST-213 complex |
| 20047 | M10 240652 | UK [England] | 2010 | B | 275 | ST-269 complex |
| 20049 | M10 240659 | UK [England] | 2010 | B | 41 | ST-41/44 complex |
| 20050 | M10 240661 | UK [England] | 2010 | B | 1161 | ST-269 complex |
| 20051 | M10 240662 | UK [England] | 2010 | B | 9882 | ST-41/44 complex |
| 20052 | M10 240665 | UK [England] | 2010 | B | 213 | ST-213 complex |
| 20055 | M10 240669 | UK [England] | 2010 | B | 1992 | ST-41/44 complex |
| 20056 | M10 240670 | UK [England] | 2010 | B | 269 | ST-269 complex |
| 20058 | M10 240674 | UK [England] | 2010 | B | 41 | ST-41/44 complex |
| 20064 | M10 240682 | UK [Northern Ireland] | 2010 | B | 269 | ST-269 complex |
| 20067 | M10 240685 | UK [England] | 2010 | Y | 1655 | ST-23 complex |
| 20068 | M10 240687 | UK [England] | 2010 | B | 60 | ST-60 complex |

| Isolate ID | Strain name | Country of isolation | Collection date | Serogroup group | Sequence Type | Clonal Complex |
|------------|-------------|----------------------|-----------------|-----------------|---------------|----------------|
| 20071 | M10 240693 | UK [England] | 2010 | B | 1430 | ST-60 complex |
| 20074 | M10 240700 | UK [England] | 2010 | Y | 6463 | ST-23 complex |
| 20075 | M10 240701 | UK [England] | 2010 | B | 213 | ST-213 complex |
| 20077 | M10 240703 | UK [England] | 2010 | B | 9884 | ST-213 complex |
| 20078 | M10 240704 | UK [England] | 2010 | B | 269 | ST-269 complex |
| 20081 | M10 240708 | UK [England] | 2010 | B | 1195 | ST-269 complex |
| 20082 | M10 240709 | UK [England] | 2010 | B | 479 | ST-269 complex |
| 20083 | M10 240711 | UK [England] | 2010 | B | 275 | ST-269 complex |
| 20084 | M10 240712 | UK [England] | 2010 | B | 213 | ST-213 complex |
| 20085 | M10 240713 | UK [England] | 2010 | B | 9829 | ST-269 complex |
| 20086 | M10 240716 | UK [England] | 2010 | B | 461 | ST-461 complex |
| 20087 | M10 240717 | UK [England] | 2010 | B | 9830 | ST-213 complex |
| 20088 | M10 240718 | UK [England] | 2010 | B | 9885 | ST-60 complex |
| 20089 | M10 240719 | UK [England] | 2010 | B | 34 | ST-32 complex |
| 20090 | M10 240720 | UK [England] | 2010 | B | 479 | ST-269 complex |
| 20095 | M10 240728 | UK [England] | 2010 | B | 9840 | ST-269 complex |
| 20096 | M10 240729 | UK [England] | 2010 | B | 1049 | ST-269 complex |
| 20099 | M10 240732 | UK [England] | 2010 | Y | 23 | ST-23 complex |
| 20101 | M10 240737 | UK [England] | 2010 | W | 1281 | ST-22 complex |
| 20102 | M10 240742 | UK [England] | 2010 | B | 8955 | ST-213 complex |
| 20103 | M10 240743 | UK [England] | 2010 | B | 269 | ST-269 complex |
| 20104 | M10 240745 | UK [England] | 2010 | Y | 1655 | ST-23 complex |
| 20110 | M10 240751 | UK [England] | 2010 | B | 213 | ST-213 complex |
| 20111 | M10 240752 | UK [England] | 2010 | B | 1161 | ST-269 complex |
| 20112 | M10 240753 | UK [England] | 2010 | B | 34 | ST-32 complex |

| Isolate ID | Strain name | Country of isolation | Collection date | Serogroup group | Sequence Type | Clonal Complex |
|------------|-------------|----------------------|-----------------|-----------------|---------------|----------------|
| 20114 | M10 240756 | UK [England] | 2010 | W | 2114 | ST-22 complex |
| 20119 | M10 240766 | UK [England] | 2010 | B | 479 | ST-269 complex |
| 20120 | M10 240767 | UK [Wales] | 2010 | B | 34 | ST-32 complex |
| 20121 | M10 240768 | UK [England] | 2010 | B | 2873 | ST-269 complex |
| 20122 | M10 240770 | UK [England] | 2010 | B | 1195 | ST-269 complex |
| 20124 | M10 240772 | UK [England] | 2010 | B | 1161 | ST-269 complex |
| 20126 | M10 240774 | UK [Wales] | 2010 | B | 1161 | ST-269 complex |
| 20128 | M10 240776 | UK [England] | 2010 | Y | 1655 | ST-23 complex |
| 20129 | M10 240777 | UK [England] | 2010 | Y | 23 | ST-23 complex |
| 20130 | M10 240778 | UK [Wales] | 2010 | B | 9187 | ST-213 complex |
| 20131 | M10 240779 | UK [England] | 2010 | B | 269 | ST-269 complex |
| 20132 | M10 240781 | UK [England] | 2010 | Y | 3651 | ST-22 complex |
| 20133 | M10 240783 | UK [England] | 2010 | B | 1161 | ST-269 complex |
| 20135 | M10 240786 | UK [England] | 2010 | Y | 9831 | ST-23 complex |
| 20136 | M10 240787 | UK [England] | 2010 | Y | 1655 | ST-23 complex |
| 20138 | M10 240789 | UK [Wales] | 2010 | B | 283 | ST-269 complex |
| 20139 | M10 240790 | UK [England] | 2010 | B | 259 | ST-32 complex |
| 20141 | M10 240794 | UK [England] | 2010 | B | 32 | ST-32 complex |
| 20143 | M10 240798 | UK [England] | 2010 | Y | 1655 | ST-23 complex |
| 20144 | M10 240799 | UK [England] | 2010 | B | 213 | ST-213 complex |
| 20146 | M10 240804 | UK [England] | 2010 | Y | 1655 | ST-23 complex |
| 20149 | M10 240808 | UK [England] | 2010 | B | 1092 | ST-269 complex |
| 20153 | M10 240814 | UK [Wales] | 2010 | B | 1161 | ST-269 complex |
| 20159 | M10 240822 | UK [England] | 2010 | W | 1224 | ST-22 complex |
| 20161 | M10 240824 | UK [England] | 2010 | B | 32 | ST-32 complex |

| Isolate ID | Strain name | Country of isolation | Collection date | Serogroup group | Sequence Type | Clonal Complex |
|------------|-------------|----------------------|-----------------|-----------------|---------------|----------------|
| 20162 | M10 240825 | UK [England] | 2010 | B | 9818 | ST-60 complex |
| 20164 | M11 240000 | UK [England] | 2011 | Y | 23 | ST-23 complex |
| 20165 | M11 240001 | UK [England] | 2011 | B | 1946 | ST-461 complex |
| 20169 | M11 240005 | UK [England] | 2011 | Y | 23 | ST-23 complex |
| 20170 | M11 240006 | UK [Wales] | 2011 | B | 8049 | ST-32 complex |
| 20171 | M11 240007 | UK [England] | 2011 | Y | 1655 | ST-23 complex |
| 20176 | M11 240013 | UK [England] | 2011 | B | 9890 | ST-32 complex |
| 20177 | M11 240014 | UK [England] | 2011 | B | 9891 | ST-461 complex |
| 20179 | M11 240016 | UK [Wales] | 2011 | B | 1096 | ST-32 complex |
| 20183 | M11 240021 | UK [England] | 2011 | B | 259 | ST-32 complex |
| 20189 | M11 240027 | UK [England] | 2011 | B | 60 | ST-60 complex |
| 20190 | M11 240028 | UK [England] | 2011 | B | 60 | ST-60 complex |
| 20191 | M11 240029 | UK [England] | 2011 | W | 1286 | ST-22 complex |
| 20193 | M11 240031 | UK [England] | 2011 | Y | 1655 | ST-23 complex |
| 20197 | M11 240036 | UK [Wales] | 2011 | Y | 1655 | ST-23 complex |
| 20198 | M11 240037 | UK [England] | 2011 | B | 34 | ST-32 complex |
| 20203 | M11 240042 | UK [England] | 2011 | B | 1946 | ST-461 complex |
| 20204 | M11 240043 | UK [England] | 2011 | Y | 9842 | ST-23 complex |
| 20207 | M11 240046 | UK [England] | 2011 | B | 213 | ST-213 complex |
| 20209 | M11 240048 | UK [England] | 2011 | B | 60 | ST-60 complex |
| 20210 | M11 240050 | UK [England] | 2011 | B | 213 | ST-213 complex |
| 20211 | M11 240052 | UK [Wales] | 2011 | B | 461 | ST-461 complex |
| 20220 | M11 240061 | UK [England] | 2011 | B | 9833 | ST-213 complex |
| 20224 | M11 240065 | UK [England] | 2011 | Y | 1655 | ST-23 complex |
| 20233 | M11 240074 | UK [Wales] | 2011 | B | 213 | ST-213 complex |

| Isolate ID | Strain name | Country of isolation | Collection date | Serogroup group | Sequence Type | Clonal Complex |
|------------|-------------|----------------------|-----------------|-----------------|---------------|----------------|
| 20238 | M11 240082 | UK [England] | 2011 | B | 290 | ST-32 complex |
| 20239 | M11 240083 | UK [England] | 2011 | B | 461 | ST-461 complex |
| 20245 | M11 240096 | UK [England] | 2011 | Y | 1655 | ST-23 complex |
| 20250 | M11 240109 | UK [England] | 2011 | B | 2931 | ST-32 complex |
| 20252 | M11 240111 | UK [England] | 2011 | B | 213 | ST-213 complex |
| 20254 | M11 240113 | UK [England] | 2011 | B | 2666 | ST-213 complex |
| 20256 | M11 240116 | UK [England] | 2011 | Y | 1655 | ST-23 complex |
| 20257 | M11 240117 | UK [England] | 2011 | B | 9821 | ST-60 complex |
| 20259 | M11 240121 | UK [England] | 2011 | B | 213 | ST-213 complex |
| 20264 | M11 240126 | UK [England] | 2011 | Y | 23 | ST-23 complex |
| 20270 | M11 240134 | UK [England] | 2011 | B | 213 | ST-213 complex |
| 20271 | M11 240137 | UK [England] | 2011 | B | 213 | ST-213 complex |
| 20275 | M11 240147 | UK [England] | 2011 | B | 213 | ST-213 complex |
| 20281 | M11 240157 | UK [England] | 2011 | Y | 10138 | ST-23 complex |
| 20286 | M11 240166 | UK [England] | 2011 | Y | 23 | ST-23 complex |
| 20287 | M11 240167 | UK [England] | 2011 | B | 9327 | ST-60 complex |
| 20292 | M11 240175 | UK [England] | 2011 | B | 33 | ST-32 complex |
| 20295 | M11 240181 | UK [England] | 2011 | B | 213 | ST-213 complex |
| 20297 | M11 240183 | UK [England] | 2011 | B | 32 | ST-32 complex |
| 20302 | M11 240192 | UK [Wales] | 2011 | Y | 1655 | ST-23 complex |
| 20306 | M11 240206 | UK [England] | 2011 | B | 461 | ST-461 complex |
| 20309 | M11 240210 | UK [England] | 2011 | Y | 23 | ST-23 complex |
| 20313 | M11 240214 | UK [England] | 2011 | B | 1946 | ST-461 complex |
| 20314 | M11 240215 | UK [England] | 2011 | Y | 1655 | ST-23 complex |
| 20315 | M11 240216 | UK [England] | 2011 | Y | 1655 | ST-23 complex |

| Isolate ID | Strain name | Country of isolation | Collection date | Serogroup group | Sequence Type | Clonal Complex |
|------------|-------------|----------------------|-----------------|-----------------|---------------|----------------|
| 20317 | M11 240227 | UK [England] | 2011 | Y | 6463 | ST-23 complex |
| 20318 | M11 240231 | UK [England] | 2011 | W | 184 | ST-22 complex |
| 20328 | M11 240246 | UK [England] | 2011 | E | 60 | ST-60 complex |
| 20335 | M11 240258 | UK [England] | 2011 | Y | 23 | ST-23 complex |
| 20337 | M11 240261 | UK [England] | 2011 | W | 184 | ST-22 complex |
| 20338 | M11 240262 | UK [England] | 2011 | A | 4789 | ST-5 complex |
| 20339 | M11 240263 | UK [England] | 2011 | Y | 1655 | ST-23 complex |
| 20341 | M11 240266 | UK [England] | 2011 | B | 213 | ST-213 complex |
| 20342 | M11 240268 | UK [England] | 2011 | B | 213 | ST-213 complex |
| 20346 | M11 240277 | UK [England] | 2011 | Y | 1655 | ST-23 complex |
| 20347 | M11 240278 | UK [England] | 2011 | Y | 1655 | ST-23 complex |
| 20350 | M11 240282 | UK [England] | 2011 | B | 213 | ST-213 complex |
| 20351 | M11 240283 | UK [England] | 2011 | Y | 23 | ST-23 complex |
| 20353 | M11 240285 | UK [England] | 2011 | B | 33 | ST-32 complex |
| 20357 | M11 240290 | UK [England] | 2011 | B | 9895 | ST-213 complex |
| 20361 | M11 240296 | UK [England] | 2011 | B | 34 | ST-32 complex |
| 20362 | M11 240297 | UK [England] | 2011 | B | 213 | ST-213 complex |
| 20363 | M11 240298 | UK [England] | 2011 | Y | 1655 | ST-23 complex |
| 20365 | M11 240302 | UK [England] | 2011 | W | 184 | ST-22 complex |
| 20382 | M11 240324 | UK [England] | 2011 | C | 32 | ST-32 complex |
| 20389 | M11 240337 | UK [England] | 2011 | B | 213 | ST-213 complex |
| 20391 | M11 240339 | UK [England] | 2011 | B | 60 | ST-60 complex |
| 20393 | M11 240342 | UK [England] | 2011 | B | 32 | ST-32 complex |
| 20395 | M11 240344 | UK [England] | 2011 | B | 213 | ST-213 complex |
| 20398 | M11 240348 | UK [England] | 2011 | B | 213 | ST-213 complex |

| Isolate ID | Strain name | Country of isolation | Collection date | Serogroup group | Sequence Type | Clonal Complex |
|------------|-------------|-----------------------|-----------------|-----------------|---------------|----------------|
| 20399 | M11 240349 | UK [England] | 2011 | W | 22 | ST-22 complex |
| 20403 | M11 240356 | UK [England] | 2011 | B | 32 | ST-32 complex |
| 20409 | M11 240366 | UK [Northern Ireland] | 2011 | B | 33 | ST-32 complex |
| 20422 | M11 240387 | UK [England] | 2011 | W | 184 | ST-22 complex |
| 20427 | M11 240392 | UK [England] | 2011 | B | 290 | ST-32 complex |
| 20428 | M11 240394 | UK [England] | 2011 | B | 5103 | ST-60 complex |
| 20438 | M11 240406 | UK [England] | 2011 | B | 32 | ST-32 complex |
| 20441 | M11 240412 | UK [England] | 2011 | B | 1430 | ST-60 complex |
| 20457 | M11 240440 | UK [England] | 2011 | B | 60 | ST-60 complex |
| 20477 | H44/76 | Norway | 1976 | B | 32 | ST-32 complex |
| 20564 | Nm6938 | Canada | 2001 | W | 22 | ST-22 complex |
| 20565 | Nm2732 | Canada | 2007 | W | 22 | ST-22 complex |
| 20740 | M09 240044 | UK | 2013 | B | 32 | ST-32 complex |
| 20741 | M09 240064 | UK | 2013 | B | 7788 | ST-60 complex |
| 20753 | M09 240242 | UK | 2013 | B | 461 | ST-461 complex |
| 20759 | M09 240296 | UK | 2013 | B | 213 | ST-213 complex |
| 20763 | M09 240440 | UK | 2013 | B | 2388 | ST-213 complex |
| 20769 | M09 240659 | UK | 2013 | B | 213 | ST-213 complex |
| 20771 | M09 240681 | UK | 2013 | B | 213 | ST-213 complex |
| 20790 | M10 240127 | UK | 2013 | B | 60 | ST-60 complex |
| 20793 | M10 240140 | UK | 2013 | B | 461 | ST-461 complex |
| 20899 | PM83TS | UK | 2013 | B | 60 | ST-60 complex |
| 20900 | PM83B | UK | 2013 | B | 60 | ST-60 complex |
| 20903 | PM27TS | UK | 2013 | | 1281 | ST-22 complex |
| 20904 | PM27B | UK | 2013 | W | 1281 | ST-22 complex |

| Isolate ID | Strain name | Country of isolation | Collection date | Serogroup group | Sequence Type | Clonal Complex |
|------------|-------------|----------------------|-----------------|-----------------|---------------|----------------|
| 20912 | PM22B | UK | 2013 | B | 2100 | ST-213 complex |
| 20921 | PM18CSF | UK | 2013 | B | 213 | ST-213 complex |
| 20922 | PM18TS | UK | 2013 | B | 213 | ST-213 complex |
| 20923 | PM19TS | UK | 2013 | B | 213 | ST-213 complex |
| 20924 | PM19B | UK | 2013 | B | 213 | ST-213 complex |
| 20925 | PM24TS | Ireland | 2013 | B | 5482 | ST-213 complex |
| 20926 | PM24B | Ireland | 2013 | B | 5482 | ST-213 complex |
| 20971 | PM84CSF | Isle of Man | 2008 | B | 60 | ST-60 complex |
| 20972 | PM84TS | Isle of Man | 2013 | B | 60 | ST-60 complex |
| 21092 | M11 240443 | UK [England] | 2011 | B | 461 | ST-461 complex |
| 21112 | M11 240471 | UK [England] | 2011 | B | 60 | ST-60 complex |
| 21132 | M11 240497 | UK [England] | 2011 | W | 1281 | ST-22 complex |
| 21139 | M11 240508 | UK [England] | 2011 | W | 184 | ST-22 complex |
| 21156 | M11 240716 | UK [England] | 2011 | W | 3795 | ST-22 complex |
| 21175 | M11 240741 | UK [England] | 2011 | W | 1286 | ST-22 complex |
| 21193 | M11 240780 | UK [England] | 2011 | W/Y | 3651 | ST-22 complex |
| 21228 | M11 240988 | UK [England] | 2011 | B | 461 | ST-461 complex |
| 21246 | M11 241031 | UK [England] | 2011 | B | 461 | ST-461 complex |
| 21271 | M11 241064 | UK [England] | 2011 | Y | 3651 | ST-22 complex |
| 21280 | M11 241075 | UK [Wales] | 2011 | B | 60 | ST-60 complex |
| 21290 | M12 240008 | UK [England] | 2012 | W | 184 | ST-22 complex |
| 21300 | M12 240019 | UK [England] | 2012 | B | 461 | ST-461 complex |
| 21349 | M12 240088 | UK [England] | 2012 | W | 1224 | ST-22 complex |
| 21352 | M12 240093 | UK [England] | 2012 | E | 4146 | ST-60 complex |
| 21371 | M12 240121 | UK [England] | 2012 | W | 184 | ST-22 complex |

| Isolate ID | Strain name | Country of isolation | Collection date | Serogroup group | Sequence Type | Clonal Complex |
|------------|--------------------|----------------------|-----------------|-----------------|---------------|----------------|
| 21380 | M12 240132 | UK [England] | 2012 | W | 184 | ST-22 complex |
| 21396 | M12 240158 | UK [England] | 2012 | B | 10287 | ST-60 complex |
| 21432 | M12 240222 | UK [England] | 2012 | B | 10292 | ST-60 complex |
| 21454 | M12 240251 | UK [England] | 2012 | W | 1281 | ST-22 complex |
| 21576 | SA_serogroup W_NM4 | South Africa | 2012 | W | 184 | ST-22 complex |
| 26067 | 959000095 | Sweden | 1995 | W | 22 | ST-22 complex |
| 26253 | T97 | UK | 2011 | cnl | 53 | ST-53 complex |
| 26263 | V259 | UK | 2011 | cnl | 53 | ST-53 complex |
| 26264 | V302 | UK | 2012 | E | 60 | ST-60 complex |
| 26267 | T98 | UK | 2011 | cnl | 53 | ST-53 complex |
| 26271 | BB66 | UK | 2012 | cnl | 53 | ST-53 complex |
| 26273 | BB58 | UK | 2012 | W | 184 | ST-22 complex |
| 26274 | v191 | UK | 2012 | cnl | 53 | ST-53 complex |
| 26275 | BB242 | UK | 2012 | W | 22 | ST-22 complex |
| 26278 | BB122 | UK | 2012 | E | 10454 | ST-60 complex |
| 26283 | R121 | UK | 2011 | cnl | 2441 | ST-53 complex |
| 26287 | V129 | UK | 2011 | W | 22 | ST-22 complex |
| 26297 | T36 | UK | 2011 | E | 10457 | ST-60 complex |
| 26303 | T287 | UK | 2011 | Y | 114 | ST-22 complex |
| 26306 | R279 | UK | 2011 | E | 60 | ST-60 complex |
| 26308 | x268 | UK | 2012 | E | 10343 | ST-60 complex |
| 26314 | z54 | UK | 2012 | E | 4146 | ST-60 complex |
| 26320 | R136 | UK | 2011 | cnl | 53 | ST-53 complex |
| 26325 | x83 | UK | 2012 | cnl | 53 | ST-53 complex |
| 26326 | T304 | UK | 2011 | cnl | 53 | ST-53 complex |

| Isolate ID | Strain name | Country of isolation | Collection date | Serogroup group | Sequence Type | Clonal Complex |
|------------|-------------|----------------------|-----------------|-----------------|---------------|----------------|
| 26327 | R122 | UK | 2011 | E | 10454 | ST-60 complex |
| 26329 | BB130 | UK | 2012 | E | 4146 | ST-60 complex |
| 26332 | BB111 | UK | 2012 | B | 461 | ST-461 complex |
| 26336 | v216 | UK | 2012 | cnl | 53 | ST-53 complex |
| 26344 | R243 | UK | 2011 | cnl | 53 | ST-53 complex |
| 26349 | BB279 | UK | 2012 | E | 60 | ST-60 complex |
| 26350 | T3 | UK | 2011 | cnl | 53 | ST-53 complex |
| 26352 | BB36 | UK | 2012 | E | 10457 | ST-60 complex |
| 26355 | R263 | UK | 2011 | cnl | 53 | ST-53 complex |
| 26360 | R221 | UK | 2011 | E | 466 | ST-60 complex |
| 26365 | z191 | UK | 2012 | cnl | 53 | ST-53 complex |
| 26370 | R129 | UK | 2011 | W | 22 | ST-22 complex |
| 26372 | V304 | UK | 2012 | cnl | 53 | ST-53 complex |
| 26381 | R210 | UK | 2011 | X | 5799 | ST-22 complex |
| 26382 | X136 | UK | 2011 | cnl | 53 | ST-53 complex |
| 26383 | R216 | UK | 2011 | cnl | 53 | ST-53 complex |
| 26390 | BB210 | UK | 2012 | X | 5799 | ST-22 complex |
| 26394 | T121 | UK | 2011 | cnl | 2441 | ST-53 complex |
| 26399 | R155 | UK | 2011 | cnl | 53 | ST-53 complex |
| 26402 | R83 | UK | 2011 | cnl | 53 | ST-53 complex |
| 26406 | T122 | UK | 2011 | E | 10454 | ST-60 complex |
| 26408 | BB287 | UK | 2012 | Y | 114 | ST-22 complex |
| 26409 | R222 | UK | 2011 | E | 10343 | ST-60 complex |
| 26411 | R36 | UK | 2011 | E | 10457 | ST-60 complex |
| 26414 | R4 | UK | 2011 | E | 60 | ST-60 complex |

| Isolate ID | Strain name | Country of isolation | Collection date | Serogroup group | Sequence Type | Clonal Complex |
|------------|-------------|----------------------|-----------------|-----------------|---------------|----------------|
| 26415 | T191 | UK | 2011 | cnl | 53 | ST-53 complex |
| 26418 | x222 | UK | 2012 | E | 10343 | ST-60 complex |
| 26419 | T119 | UK | 2011 | cnl | 53 | ST-53 complex |
| 26425 | R256 | UK | 2011 | E | 466 | ST-60 complex |
| 26432 | T210 | UK | 2011 | X | 5799 | ST-22 complex |
| 26434 | T302 | UK | 2011 | E | 60 | ST-60 complex |
| 26444 | R97 | UK | 2011 | cnl | 53 | ST-53 complex |
| 26445 | Z119 | UK | 2012 | cnl | 53 | ST-53 complex |
| 26450 | BB159 | UK | 2012 | E | 4146 | ST-60 complex |
| 26451 | r119 | UK | 2011 | cnl | 53 | ST-53 complex |
| 26457 | R191 | UK | 2011 | cnl | 53 | ST-53 complex |
| 26464 | Z221 | UK | 2012 | E | 466 | ST-60 complex |
| 26466 | X119 | UK | 2012 | cnl | 53 | ST-53 complex |
| 26474 | T216 | UK | 2011 | cnl | 53 | ST-53 complex |
| 26476 | R58 | UK | 2011 | W | 184 | ST-22 complex |
| 26498 | T279 | UK | 2011 | E | 60 | ST-60 complex |
| 26500 | BB83 | UK | 2012 | cnl | 53 | ST-53 complex |
| 26515 | BB54 | UK | 2012 | E | 4146 | ST-60 complex |
| 26518 | v119 | UK | 2012 | cnl | 53 | ST-53 complex |
| 26519 | T53 | UK | 2011 | E | 10454 | ST-60 complex |
| 26520 | T4 | UK | 2011 | E | 60 | ST-60 complex |
| 26522 | x121 | UK | 2012 | cnl | 2441 | ST-53 complex |
| 26529 | BB228 | UK | 2012 | cnl | 53 | ST-53 complex |
| 26530 | V210 | UK | 2012 | X | 5799 | ST-22 complex |
| 26839 | 12005_2011 | Ireland | 2011 | B | 8949 | ST-461 complex |

| Isolate ID | Strain name | Country of isolation | Collection date | Serogroup group | Sequence Type | Clonal Complex |
|------------|-------------|----------------------|-----------------|-----------------|---------------|----------------|
| 26847 | 12018_2011 | Ireland | 2011 | B | 1946 | ST-461 complex |
| 26888 | 12029_2012 | Ireland | 2012 | B | 10548 | ST-22 complex |
| 26900 | 12004_2013 | Ireland | 2013 | W | 22 | ST-22 complex |
| 26922 | 10215v3 | UK | 2013 | W | 22 | ST-22 complex |
| 26923 | 10215v4 | UK | 2013 | | 11141 | ST-22 complex |
| 26954 | 80241v5 | UK | 2013 | W | 184 | ST-22 complex |
| 26955 | 80305v4 | UK | 2013 | W | 184 | ST-22 complex |
| 26956 | 80305v5 | UK | 2013 | W | 184 | ST-22 complex |
| 26976 | 90104v5 | UK | 2013 | W | 3651 | ST-22 complex |
| 26985 | 90130v1 | UK | 2013 | W | 184 | ST-22 complex |
| 27782 | M12 240347 | UK [England] | 2012 | B | 461 | ST-461 complex |
| 27814 | M12 240704 | UK [England] | 2012 | B | 7261 | ST-461 complex |
| 27839 | M12 240763 | UK [England] | 2012 | B | 1946 | ST-461 complex |
| 27843 | M12 240778 | UK [England] | 2012 | B | 1946 | ST-461 complex |
| 27849 | M12 240787 | UK [Wales] | 2012 | B | 1946 | ST-461 complex |
| 27864 | M12 240819 | UK [England] | 2012 | B | 461 | ST-461 complex |
| 27871 | M12 240844 | UK [England] | 2012 | B | 8223 | ST-461 complex |
| 27887 | M12 240873 | UK [Wales] | 2012 | B | 10705 | ST-461 complex |
| 27907 | M13 240006 | UK [England] | 2013 | B | 461 | ST-461 complex |
| 27914 | M13 240021 | UK [England] | 2013 | B | 461 | ST-461 complex |
| 27927 | M13 240045 | UK [England] | 2013 | B | 1946 | ST-461 complex |
| 27933 | M13 240057 | UK [England] | 2013 | B | 5983 | ST-461 complex |
| 27934 | M13 240063 | UK [England] | 2013 | B | 461 | ST-461 complex |
| 27938 | M13 240074 | UK [England] | 2013 | B | 461 | ST-461 complex |
| 27941 | M13 240078 | UK [England] | 2013 | B | 1946 | ST-461 complex |

| Isolate ID | Strain name | Country of isolation | Collection date | Serogroup group | Sequence Type | Clonal Complex |
|------------|-------------|----------------------|-----------------|-----------------|---------------|----------------|
| 28017 | M13 240248 | UK [England] | 2013 | B | 1946 | ST-461 complex |
| 28043 | M13 240406 | UK [England] | 2013 | B | 1946 | ST-461 complex |
| 29291 | 15003 | South Africa | 2004 | A | 7 | ST-5 complex |
| 29304 | 27937 | South Africa | 2010 | A | 7 | ST-5 complex |
| 29312 | 5957 | South Africa | 2006 | cnl | 53 | ST-53 complex |
| 29434 | 139 | South Africa | 2005 | A | 7 | ST-5 complex |
| 29469 | 2730 | UK | 2014 | A | 5 | ST-5 complex |
| 30269 | M99 243594 | UK | 1999 | A | 5 | ST-5 complex |
| 30466 | NMA510612 | China | 2006 | A | 7 | ST-5 complex |
| 30697 | 12011-10 | Ireland | 2010 | B | 461 | ST-461 complex |
| 30708 | 12021-13 | Ireland | 2013 | B | 7261 | ST-461 complex |
| 31208 | NM10853 | UK [England] | 2013 | cnl | 53 | ST-53 complex |
| 31215 | LIM534 | France | 2006 | A | 4789 | ST-5 complex |
| 34572 | 75643 | Brazil | 1975 | A | 5 | ST-5 complex |
| 34573 | 75689 | Brazil | 1975 | A | 5 | ST-5 complex |
| 34578 | 88050 | Chad | 1988 | A | 5 | ST-5 complex |
| 34583 | 96023 | Niger | 1996 | A | 5 | ST-5 complex |
| 34584 | 96024 | Niger | 1996 | A | 5 | ST-5 complex |
| 34587 | 97008 | Niger | 1997 | A | 5 | ST-5 complex |
| 34589 | 97018 | Mali | 1997 | A | 580 | ST-5 complex |
| 34590 | 97020 | Mali | 1997 | A | 580 | ST-5 complex |
| 34594 | 98005 | Niger | 1998 | A | 5 | ST-5 complex |
| 34595 | 98008 | France | 1998 | discrepancy | 461 | ST-461 complex |
| 34597 | 2000063 | Niger | 2000 | A | 7 | ST-5 complex |
| 34598 | 2000080 | Algeria | 2000 | A | 7 | ST-5 complex |

| Isolate ID | Strain name | Country of isolation | Collection date | Serogroup group | Sequence Type | Clonal Complex |
|------------|-------------|----------------------|-----------------|-----------------|---------------|----------------|
| 34599 | 2001212 | Burkina Faso | 2001 | A | 7 | ST-5 complex |
| 34600 | 2002007 | Niger | 2002 | A | 7 | ST-5 complex |
| 34604 | 2003022 | Niger | 2003 | A | 7 | ST-5 complex |
| 34606 | 2004085 | Niger | 2004 | A | 7 | ST-5 complex |
| 34607 | 2004090 | Niger | 2004 | A | 7 | ST-5 complex |
| 34610 | 2007056 | Burkina Faso | 2007 | A | 2859 | ST-5 complex |
| 34654 | NM3642 | Bangladesh | 2003 | A | 4789 | ST-5 complex |
| 34655 | NM3652 | Bangladesh | 2006 | A | 8428 | ST-5 complex |
| 34663 | NM604 | USA | 2000 | A | 7 | ST-5 complex |
| 34665 | NM607 | USA | 2001 | A | 7 | ST-5 complex |
| 34808 | ERR052799 | Burkina Faso | 2006 | A | 2859 | ST-5 complex |
| 34811 | ERR052816 | Burkina Faso | 2007 | A | 2859 | ST-5 complex |
| 34818 | ERR052800 | Burkina Faso | 2006 | A | 2859 | ST-5 complex |
| 34822 | ERR052787 | Burkina Faso | 2006 | A | 2859 | ST-5 complex |
| 34825 | ERR052767 | Ghana | 2004 | A | 7 | ST-5 complex |
| 34836 | ERR052737 | Ghana | 2001 | A | 7 | ST-5 complex |
| 34837 | ERR052779 | Ghana | 2004 | A | 7 | ST-5 complex |
| 35330 | 12.1192.H | UK [Scotland] | 2012 | B | 1946 | ST-461 complex |
| 35345 | 13.2973.F | UK [Scotland] | 2013 | B | 461 | ST-461 complex |
| 35346 | 13.3065.D | UK [Scotland] | 2013 | B | 461 | ST-461 complex |
| 35427 | M13 240534 | UK [England] | 2013 | B | 1946 | ST-461 complex |
| 35436 | M13 240554 | UK [England] | 2013 | B | 461 | ST-461 complex |
| 35448 | M13 240581 | UK [England] | 2013 | B | 1946 | ST-461 complex |
| 35480 | M13 240644 | UK [England] | 2013 | B | 461 | ST-461 complex |

| Isolate ID | Strain name | Country of isolation | Collection date | Serogroup group | Sequence Type | Clonal Complex |
|-------------------|--------------------|-----------------------------|------------------------|------------------------|----------------------|-----------------------|
| 35577 | M14 240083 | UK [Northern Ireland] | 2014 | B | 11865 | ST-461 complex |
| 35580 | M14 240088 | UK [England] | 2014 | B | 461 | ST-461 complex |
| 35612 | M14 240133 | UK [Wales] | 2014 | B | 1946 | ST-461 complex |
| 35713 | M14 240317 | UK [England] | 2014 | B | 1946 | ST-461 complex |
| 36135 | 12010_2012 | Ireland | 2012 | cnl | 53 | ST-53 complex |
| 38889 | P27 | Italy | 2012 | cnl | 53 | ST-53 complex |
| 38943 | P106 | Italy | 2013 | cnl | 53 | ST-53 complex |
| 38946 | P109 | Italy | 2013 | cnl | 53 | ST-53 complex |
| 38953 | P117 | Italy | 2013 | cnl | 53 | ST-53 complex |
| 38954 | P118 | Italy | 2013 | cnl | 11167 | ST-53 complex |
| 38956 | P120 | Italy | 2013 | cnl | 11133 | ST-53 complex |

Supplementary Table 4. List of 144 putative hypervirulence associated genes (HVAGs).

| NEIS code | BLASTp ID | Length (bp) | GC percentage | Genomic Island # | Function | Reference |
|-----------|---|-------------|---------------|------------------|---------------------|-------------------------|
| NEIS0023 | Putative zonular occludens toxin-like protein | 1188 | 44.53 | 1 (MDA φ) | Phage | (Bille et al., 2008) |
| NEIS0024 | Integral membrane protein | 285 | 44.91 | | | |
| NEIS0025 | TspB protein | 1560 | 47.69 | | | |
| NEIS0027 | Integral membrane protein | 303 | 43.67 | | | |
| NEIS0028 | Integral membrane protein | 231 | 54.63 | | | |
| NEIS0029 | Hypothetical protein | 201 | 53.84 | | | |
| NEIS0030 | Hypothetical protein | 312 | 53.58 | | | |
| NEIS0031 | phage replication initiation factor | 1209 | 52.23 | | | |
| NEIS0080 | Bacteriocin transporter | 237 | 38.4 | 2 (BGI-1) | Toxin | (Allunans et al., 2008) |
| NEIS0081 | Hypothetical protein | 228 | 33.77 | | | |
| NEIS0083 | Membrane protein | 189 | 22.87 | | | |
| NEIS0084 | Membrane protein | 138 | 26.81 | | | |
| NEIS0085 | Secretion protein | 1266 | 37.44 | | | |
| NEIS0086 | Processing peptidase | 2088 | 34.24 | | | |
| NEIS0089 | Hypothetical protein | 147 | 34.69 | | | |
| NEIS0169 | Abi-like family protein/CAAX protease | 723 | 35.41 | | | |
| NEIS0193 | Hypothetical protein | 390 | 28.72 | 4 | Hypothetical | |
| NEIS0231 | SMI1 / KNR4 family protein | 540 | 45.93 | | | |
| NEIS0232 | Hypothetical protein | 216 | 30.56 | | | |
| NEIS0233 | Hypothetical protein | 360 | 27.5 | | | |
| NEIS0249 | NmFic | 576 | 46.01 | 8A (NmFic) | Cell wall synthesis | |

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|----------|---|------|-------|--------------|--------------------------|---|
| NEIS0250 | Hypothetical protein | 342 | 39.77 | | | |
| NEIS0267 | Membrane protein | 297 | 22.22 | 10 | Hypothetical | |
| NEIS0295 | DNA methylase | 2589 | 38.32 | 11 | Restriction Modification | (Claus et al., 2005) |
| NEIS0298 | Hypothetical protein | 372 | 33.33 | | | |
| NEIS0380 | PgII | 1875 | 53.61 | 14 (PgII) | Membrane | (Warren et al., 2004) |
| NEIS2376 | Maf immunity protein | 336 | 33.64 | 23A (CDI) | Toxin | Proximal core gene is NEIS0222 Structure of locus is similar to MGI-3 (Jamet et al., 2015) |
| NEIS0678 | Vsr | 447 | 45.86 | 25A (Vsr) | Restriction Modification | |
| NEIS0680 | type II restriction enzyme NmeDIP | 1056 | 42.99 | | | |
| NEIS0447 | Hemagglutinin | 375 | 34.13 | 21A/BTspA/B) | Toxin | Proximal core gene is NEIS0441 (Arenas et al., 2013) |
| NEIS0449 | Hemagglutinin | 264 | 31.82 | | | |
| NEIS0451 | Hemagglutinin | 384 | 25.52 | | | |
| NEIS0453 | Hemagglutinin | 489 | 32.23 | | | |
| NEIS0454 | Hemagglutinin | 273 | 32.33 | | | |
| NEIS0589 | Maf immunity protein | 288 | 26.69 | 23B | | |
| NEIS0771 | cytosine-specific DNA methyltransferase | 1236 | 33.58 | 26 | Restriction Modification | |
| NEIS0772 | type II restriction endonuclease | 1119 | 31.59 | | | |
| NEIS0840 | Phage related protein | 918 | 52.94 | 29 | Phage | |
| NEIS0855 | Hypothetical protein | 387 | 48.32 | | | |
| NEIS0879 | Plasmid toxin PemK | 348 | 51.72 | | | |
| NEIS0880 | Transcriptional regulator | 237 | 55.69 | | | |
| NEIS0881 | Death on curing protein | 492 | 41.06 | | Toxin | |
| NEIS0887 | HlyD family secretion protein | 1263 | 36.9 | 30 | Other | |
| NEIS0888 | ABC transporter | 2097 | 40.3 | | | |

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|----------|--------------------------------------|------|-------|---------------|-------|--------------------------|
| NEIS0892 | Hypothetical protein | 117 | 27.35 | | | |
| NEIS0893 | ParB | 204 | 35.29 | | | |
| NEIS0989 | Phage integrase | 264 | 54.35 | 32A (P2-like) | Phage | |
| NEIS0992 | Phage integrase | 639 | 62.33 | | | |
| NEIS0993 | Phage protein | 876 | 54.41 | | | |
| NEIS0995 | DNA phage binding protein | 297 | 53.69 | | | |
| NEIS0996 | Phage associated protein | 156 | 51.92 | | | |
| NEIS0997 | Phage repressor | 378 | 41.27 | | | |
| NEIS0998 | Hypothetical protein (Phage related) | 246 | 41.46 | | | |
| NEIS0999 | Hypothetical protein (Phage related) | 93 | 44.09 | | | |
| NEIS1000 | Hypothetical protein (Phage related) | 912 | 37.94 | | | |
| NEIS1001 | Hypothetical protein (Phage related) | 483 | 32.51 | | | |
| NEIS1002 | Hypothetical protein (Phage related) | 504 | 56.75 | | | |
| NEIS1005 | Hypothetical protein (Phage related) | 411 | 50.36 | | | |
| NEIS2552 | Putative phage associated protein | 213 | 57.28 | | | |
| NEIS1042 | Hypothetical protein | 180 | 46.67 | 33A (IHT-E) | Phage | (Masignani et al., 2001) |
| NEIS1044 | Transcriptional regulator | 900 | 38.89 | | | |
| NEIS1045 | Transcriptional regulator | 252 | 38.49 | | | |
| NEIS1046 | Phage transposase | 1980 | 54.34 | | | |
| NEIS1048 | Phage transposase | 915 | 50.82 | | | |
| NEIS1049 | Hypothetical protein (Phage related) | 291 | 48.45 | | | |
| NEIS1050 | Hypothetical protein (Phage related) | 126 | 44.44 | | | |
| NEIS1051 | Hypothetical protein (Phage related) | 174 | 52.87 | | | |

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|-----------------|---|------|-------|-----------------|--------------------------|---|
| NEIS1052 | Hypothetical protein (Phage related) | 168 | 52.38 | | | |
| NEIS1053 | Hypothetical protein (Phage related) | 228 | 35.53 | | | |
| NEIS1054 (gam) | host-nuclease inhibitor protein | 519 | 52.22 | | | |
| NEIS1057 | Phage tail protein | 561 | 61.68 | | | |
| NEIS1058 | Tail protein | 1974 | 58.21 | | | |
| NEIS1059 | Hypothetical protein (Phage related) | 606 | 59.24 | | | |
| NEIS1060 | DNA helicase | 297 | 50.92 | | | |
| NEIS1083 | Hypothetical protein | 354 | 36.72 | 35 | Hypothetical | |
| NEIS1158 | Type I restriction enzyme | 327 | 41.28 | 38 | Restriction Modification | |
| NEIS1193 | Type III restriction-modification system endonuclease protein | 2940 | 48.37 | 39 (ModB) | Restriction Modification | (Srikhanta et al., 2009) |
| NEIS1194 | Type III restriction/modification system methyltransferase | 1975 | 45.11 | | | |
| NEIS1357 | Addiction module protein | 1128 | 50.62 | 41 | Toxin | |
| NEIS1424 | hypothetical protein | 330 | 47.58 | 42 | Hypothetical | |
| NEIS1803 | hypothetical protein | 336 | 38.69 | 52 | Hypothetical | |
| NEIS1886 | Helicase | 660 | 39.39 | 54 | Metabolism | |
| NEIS1946 (HpuA) | haemoglobin-haptoglobin utilisation protein (HpuA) | 1026 | 52.53 | 56 (HpuA/B) | Iron acquistion | (Lewis et al., 1997) |
| NEIS1947 (HpuB) | haemoglobin-haptoglobin utilisation protein (HpuB) | 2433 | 55.03 | | | |
| NEIS2011 (LgtG) | LgtG | 1059 | 56.37 | 59 (LgtG) | Membrane | (Banerjee et al., 1998), (Kahler et al., 2005) |
| NEIS2012 (Lpt6) | Lpt6 | 1653 | 53.96 | 60 (Lpt6) | Membrane | (Wright et al., 2004, Kahler et al., 2005) |
| NEIS2091 | MafB protein | 348 | 35.92 | 62 (MafI-MGI-3) | Toxin | (Jamet et al., 2015) |
| NEIS2092 | Maf immunity protein | 324 | 24.07 | | | |
| NEIS2093 | hypothetical protein | 345 | 28.12 | | | |
| NEIS1584 | Death on curing protein | 387 | 42.64 | 45 | Toxin | |

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|-----------------|---|------|-------|--------|---------|---------------------------------------|
| NEIS1585 | Prevent host death protein | 246 | 39.36 | | | |
| NEIS0364 | Hypothetical protein | 549 | 30.6 | HI 1 | Phage | |
| NEIS0365 | Hypothetical protein | 564 | 30.32 | | | |
| NEIS1861 | Replication initiation factor | 1209 | 40.45 | HI 2 | Phage | |
| NEIS1866 | TspB protein | 1506 | 48.14 | | | |
| NEIS1862 | Hypothetical protein | 312 | 41.03 | | | |
| NEIS1863 | Hypothetical protein | 201 | 36.32 | | | |
| NEIS1864 | Hypothetical protein | 231 | 44.59 | | | |
| NEIS1865 | Hypothetical protein | 303 | 42.9 | | | |
| NEIS1867 | Hypothetical protein | 285 | 44.91 | | | |
| NEIS1868 | Hypothetical protein | 1188 | 44.7 | | | |
| NEIS2451 | Hypothetical protein | 222 | 34.68 | HI 3 | Phage | Proximal core gene is NEIS1719 |
| NEIS2452 | Hypothetical protein | 312 | 41 | | | |
| NEIS2453 | Hypothetical protein | 201 | 36.3 | | | |
| NEIS2459 | Hypothetical protein | 201 | 36 | HI 4 | Phage | Proximal core gene is NEIS1469 (LbpB) |
| NEIS2460 | Hypothetical protein | 312 | 41.03 | | | |
| NEIS2461 | Hypothetical protein | 222 | 34.68 | | | |
| NEIS2836 | Plasmid maintenance system killer protein | 279 | 48.02 | HI 5 | Toxin | Proximal core gene is NEIS1059 |
| NEIS2837 (ybaQ) | Transcriptional regulator | 312 | 48.07 | | | |
| NEIS0049 | ctrG | 957 | 33.33 | Cps GI | capsule | (Harrison et al., 2013) |
| NEIS0050 | cssE | 1383 | 28.78 | | | |
| NEIS0051 | csc | 1479 | 31.51 | | | |
| NEIS0052 | cssC | 1050 | 40.95 | | | |
| NEIS0053 | cssB | 687 | 40.17 | | | |
| NEIS0054 | cssA | 1134 | 38.1 | | | |

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|----------|--|------|-------|-------------------------|--------------|--------------------------------|
| NEIS0055 | ctrA | 1176 | 46.68 | | | |
| NEIS0056 | ctrB | 1164 | 46.99 | | | |
| NEIS0057 | ctrC | 798 | 42.73 | | | |
| NEIS0058 | ctrD | 651 | 46.54 | | | |
| NEIS0066 | ctrE | 2115 | 51.77 | | | |
| NEIS0067 | ctrF | 1260 | 48.73 | | | |
| NEIS0068 | Hypothetical protein | 1407 | 57.5 | | | |
| NEIS0209 | Hypothetical protein | 501 | 49.3 | | Hypothetical | |
| NEIS0223 | Maf immunity protein | 336 | 27.5 | MafI-MGI-2 | Toxin | (Jamet et al., 2015) |
| NEIS0393 | Hypothetical protein | 402 | 31.09 | | Hypothetical | |
| NEIS0445 | Hypothetical protein | 510 | 25.49 | | Hypothetical | |
| NEIS0955 | Hypothetical protein | 288 | 29.86 | | Hypothetical | |
| NEIS1012 | Hypothetical protein | 546 | 36.08 | | Hypothetical | |
| NEIS1268 | Hypothetical protein | 288 | 35.76 | | Hypothetical | |
| NEIS1715 | TspB protein | 1620 | 47.04 | TspB | Other | (Arenas et al., 2013) |
| NEIS1969 | Neisseria adhesin A | 1197 | 48.2 | NadA | Other | (Capecci et al., 2005) |
| NEIS2064 | ATP-binding protein | 1050 | 39.33 | | Other | Proximal core gene is NEIS1625 |
| NEIS2380 | Hypothetical protein | 240 | 45.83 | | Hypothetical | Proximal core gene is NEIS0684 |
| NEIS2404 | Hypothetical protein | 174 | 56.32 | | Hypothetical | Proximal core gene is NEIS1002 |
| NEIS2406 | Bacteriophage transposase (Mu phage) | 1986 | 52.92 | | Phage | Proximal core gene is NEIS1045 |
| NEIS2463 | Antitoxin Phd_YefM, type II toxin-antitoxin system | 249 | 39.57 | Type II toxin-antitoxin | Toxin | Proximal core gene is NEIS1584 |
| NEIS2536 | Hypothetical protein | 210 | 55.23 | | Hypothetical | Proximal core gene is NEIS1060 |
| NEIS2537 | Baseplate J-like protein (P2 bacteriophage) | 612 | 59.8 | | Phage | Proximal core gene is NEIS1054 |

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|----------|------------------------|------|-------|--|--------------------------|--|
| NEIS2551 | Hypothetical protein | 282 | 52.48 | | Hypothetical | Proximal core gene is NEIS0986 |
| NEIS2583 | Hypothetical protein | 240 | 52.5 | | Hypothetical | Proximal core gene is NEIS1547 (GpxA) |
| NEIS2778 | Maf B related protein | 1239 | 45.27 | | Toxin | (Jamet et al., 2015) |
| NEIS2789 | Hypothetical protein | 426 | 49.29 | | Hypothetical | Proximal core gene is NEIS0269 |
| NEIS2854 | Methyltransferase D12 | 345 | | | Restriction Modification | Located in the cps locus (Clemence et al., 2019) |
| NEIS2910 | Modification methylase | 1002 | 39.83 | | Restriction Modification | Located in the cps locus (Clemence et al., 2019) |

REFERENCES for Supplementary TABLE 4.

- ALLUNANS, J., KRISTIANSEN, K. I., ASSALKHOU, R. & BJORAS, M. 2008. Bacteriocins (meningocins) in Norwegian isolates of *Neisseria meningitidis*: possible role in the course of a meningococcal epidemic. *APMIS*, 116, 333-44.
- ARENAS, J., SCHIPPER, K., VAN ULSEN, P., VAN DER ENDE, A. & TOMMASSEN, J. 2013. Domain exchange at the 3' end of the gene encoding the fratricide meningococcal two-partner secretion protein A. *BMC Genomics*, 14, 622.
- BANERJEE, A., WANG, R., ULJON, S. N., RICE, P. A., GOTTSCHLICH, E. C. & STEIN, D. C. 1998. Identification of the gene (*IgtG*) encoding the lipooligosaccharide beta chain synthesizing glucosyl transferase from *Neisseria gonorrhoeae*. *Proc Natl Acad Sci U S A*, 95, 10872-7.
- BILLE, E., URE, R., GRAY, S. J., KACZMARSKI, E. B., MCCARTHY, N. D., NASSIF, X., MAIDEN, M. C. & TINSLEY, C. R. 2008. Association of a bacteriophage with meningococcal disease in young adults. *PLoS One*, 3, e3885.
- CAPECCHI, B., ADU-BOBIE, J., DI MARCELLO, F., CIUCCHI, L., MASIGNANI, V., TADDEI, A., RAPPOLI, R., PIZZA, M. & ARICO, B. 2005. *Neisseria meningitidis* NadA is a new invasin which promotes bacterial adhesion to and penetration into human epithelial cells. *Mol Microbiol*, 55, 687-98.
- CLAUS, H., MAIDEN, M. C., WILSON, D. J., MCCARTHY, N. D., JOLLEY, K. A., URWIN, R., HESSLER, F., FROSCH, M. & VOGEL, U. 2005. Genetic analysis of meningococci carried by children and young adults. *Journal of Infectious Diseases*, 191, 1263-1271.
- CLEMENCE, M. E. A., HARRISON, O. B. & MAIDEN, M. C. J. 2019. *Neisseria meningitidis* has acquired sequences within the capsule locus by horizontal genetic transfer. *Wellcome Open Res*, 4, 99.

- HARRISON, O. B., CLAUS, H., JIANG, Y., BENNETT, J. S., BRATCHER, H. B., JOLLEY, K. A., CORTON, C., CARE, R., POOLMAN, J. T., ZOLLINGER, W. D., FRASCH, C. E., STEPHENS, D. S., FEAVERS, I., FROSCH, M., PARKHILL, J., VOGEL, U., QUAIL, M. A., BENTLEY, S. D. & MAIDEN, M. C. 2013. Description and nomenclature of *Neisseria meningitidis* capsule locus. *Emerg Infect Dis*, 19, 566-73.
- JAMET, A., JOUSSET, A. B., EUPHRASIE, D., MUKORAKO, P., BOUCHARLAT, A., DUCOUSSO, A., CHARBIT, A. & NASSIF, X. 2015. A new family of secreted toxins in pathogenic *Neisseria* species. *PLoS Pathog*, 11, e1004592.
- KAHLER, C. M., DATTA, A., TZENG, Y. L., CARLSON, R. W. & STEPHENS, D. S. 2005. Inner core assembly and structure of the lipooligosaccharide of *Neisseria meningitidis*: capacity of strain NMB to express all known immunotype epitopes. *Glycobiology*, 15, 409-19.
- LEWIS, L. A., GRAY, E., WANG, Y. P., ROE, B. A. & DYER, D. W. 1997. Molecular characterization of hpuAB, the haemoglobin–haptoglobin-utilization operon of *Neisseria meningitidis*. *Molecular microbiology*, 23, 737-749.
- MASIGNANI, V., GIULIANI, M. M., TETTELIN, H., COMANDUCCI, M., RAPPOLI, R. & SCARLATO, V. 2001. Mu-like prophage in serogroup B *Neisseria meningitidis* coding for surface-exposed antigens. *Infection and immunity*, 69, 2580-2588.
- SRIKHANTA, Y. N., DOWIDEIT, S. J., EDWARDS, J. L., FALSETTA, M. L., WU, H. J., HARRISON, O. B., FOX, K. L., SEIB, K. L., MAGUIRE, T. L., WANG, A. H., MAIDEN, M. C., GRIMMOND, S. M., APICELLA, M. A. & JENNINGS, M. P. 2009. Phasevarions mediate random switching of gene expression in pathogenic *Neisseria*. *PLoS Pathog*, 5, e1000400.
- WARREN, M. J., RODDAM, L. F., POWER, P. M., TERRY, T. D. & JENNINGS, M. P. 2004. Analysis of the role of pgII in pilin glycosylation of *Neisseria meningitidis*. *FEMS Immunology & Medical Microbiology*, 41, 43-50.
- WRIGHT, J. C., HOOD, D. W., RANDLE, G. A., MAKEPEACE, K., COX, A. D., LI, J., CHALMERS, R., RICHARDS, J. C. & MOXON, E. R. 2004. lpt6, a gene required for addition of phosphoethanolamine to inner-core lipopolysaccharide of *Neisseria meningitidis* and *Haemophilus influenzae*. *J Bacteriol*, 186, 6970-82.

Supplementary Table 5. Results of the Phaser analysis of the meningococcal genomes.

See methods for the definitions for simple sequence repeats (SSR), INDEL and the calculation of percentage INTACT. Zero percent = gene is present but phased off in all instances. Grey boxes= not present in the genome.

| NEIS code | BLASTp ID | Function | Core/ accessory | SSR/ INDEL | cc53 | cc32 | cc5 | cc213 | cc41/44 | cc22 | cc11 | cc60 | cc461 | cc269 | cc23 | |
|-----------|--|-------------------------|--------------------|---------------|--------|--------|--------|--------|---------|--------|--------|--------|--------|---------|---------|-------|
| NEIS0390 | RNA-binding S4 domain-containing protein | Transcription | Core | INDEL | 12.24% | 12.24% | 12.24% | 92.00% | 74.00% | 12.24% | 12.24% | 82.00% | 96.00% | 12.24% | 98.00% | |
| NEIS0038 | RNA binding protein | Uncharacterised protein | Core | INDEL | 97.96% | 97.96% | 97.96% | 97.96% | 22.00% | 97.96% | 97.96% | 97.96% | 97.96% | 52.00% | 97.96% | |
| NEIS0095 | Hypothetical protein | Uncharacterised protein | Core | SSR | 97.96% | 97.96% | 0.00% | 2.00% | 12.00% | 97.96% | 9.52% | 14.00% | 97.96% | 97.96% | 97.96% | |
| NEIS0180 | Putative inner membrane protein | Uncharacterised protein | Core | SSR | 95.92% | 95.92% | 95.92% | 95.92% | 95.92% | 95.92% | 95.92% | 95.92% | 95.92% | 6.00% | 95.92% | |
| NEIS0308 | Hypothetical protein | Uncharacterised protein | Core | SSR | 91.84% | 91.84% | 14.00% | 4.00% | 91.84% | 91.84% | 91.84% | 91.84% | 91.84% | 4.00% | 80.00% | |
| NEIS0579 | DUF4375- domain containing protein | Uncharacterised protein | Core | INDEL | 95.92% | 95.92% | 95.92% | 95.92% | 4.00% | 0.00% | 0.00% | 2.00% | 2.00% | 8.00% | 0.00% | |
| NEIS0595 | Hypothetical protein | Uncharacterised protein | Core | SSR | 93.88% | 93.88% | 93.88% | 93.88% | 93.88% | 93.88% | 93.88% | 70.00% | 93.88% | 93.88% | 93.88% | |
| NEIS0630 | cryptic protein cnp1 | Uncharacterised protein | Core | SSR | 89.80% | 89.80% | 89.80% | 89.80% | 89.80% | 89.80% | 89.80% | 89.80% | 89.80% | 80.00% | 89.80% | |
| NEIS0779 | Hypothetical protein | Uncharacterised protein | Core | SSR | 6.12% | 6.12% | 98.00% | 98.00% | 92.00% | 98.00% | 6.12% | 44.00% | 90.00% | 98.00% | 88.00% | |
| NEIS1072 | DUF2134 domain containing protein | Uncharacterised protein | Core | INDEL | 97.96% | 97.96% | 0.00% | 97.96% | 97.96% | 93.88% | 97.96% | 97.96% | 97.96% | 97.96% | 97.96% | |
| NEIS1147 | ATP binding protein | Uncharacterised protein | Core | INDEL | 95.92% | 95.92% | 95.92% | 95.92% | 95.92% | 95.92% | 95.92% | 20.00% | 95.92% | 95.92% | 95.92% | |
| NEIS1660 | Hypothetical protein | Uncharacterised protein | Core | SSR | 0.00% | 0.00% | 0.00% | 0.00% | 92.00% | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% |
| NEIS1804 | Hypothetical protein | Uncharacterised protein | Core | INDEL | 95.92% | 95.92% | 95.92% | 18.00% | 95.92% | 95.92% | 95.92% | 95.92% | 95.92% | 95.92% | 95.92% | |
| NEIS1819 | Hypothetical protein | Uncharacterised protein | Core | SSR | 97.96% | 97.96% | 6.00% | 97.96% | 97.96% | 93.88% | 97.96% | 97.96% | 97.96% | 97.96% | 97.96% | |
| NEIS3059 | Hypothetical protein | Uncharacterised protein | Core | INDEL | 97.96% | 97.96% | 0.00% | 97.96% | 97.96% | 97.96% | 97.96% | 97.96% | 97.96% | 97.96% | 97.96% | |
| NEIS3160 | Hypothetical protein | Uncharacterised protein | Core | SSR | 95.92% | 95.92% | 0.00% | 95.92% | 4.00% | 95.92% | 95.92% | 95.92% | 95.92% | 95.92% | 95.92% | |
| NEIS1088 | Capsule synthesis protein cap A | Capsule | Accessory | SSR | 97.96% | 97.96% | 97.96% | 0.00% | | 97.96% | 97.96% | 0.00% | 0.00% | 32.00% | 0.00% | |
| NEIS0209 | Transposase | Insertion element | Accessory | INDEL | 0.00% | 0.00% | 96.00% | 0.00% | 0.00% | 0.00% | 96.83% | 0.00% | 0.00% | 0.00% | 0.00% | |
| NEIS1536 | Transposase | Insertion element | Accessory | SSR | 0.00% | | | 98.00% | 86.00% | | | 26.00% | | | | |
| NEIS0493 | NnrS family protein | Metabolism | Accessory | SSR | 2.04% | 60.00% | 96.00% | 96.00% | 0.00% | 96.00% | 90.48% | 92.00% | | 36.00% | 100.00% | |
| NEIS1507 | MdlB domoan. ABC transmembrane transporter responsible for multidrug transport | Metabolism | Accessory | INDEL | 2.04% | 2.04% | 98.00% | 96.00% | 78.00% | 82.00% | 95.24% | 96.00% | | 100.00% | | |
| NEIS1623 | apbE family protein (involved in thiamine synthesis) | Metabolism | Accessory | SSR | 0.00% | 0.00% | 96.00% | 92.00% | 90.00% | 96.00% | 0.00% | 0.00% | | 98.00% | 0.00% | |
| NEIS0962 | Chloride channel protein | Metabolism | Accessory | INDEL | 97.96% | 97.96% | 0.00% | 97.96% | | 97.96% | 97.96% | 97.96% | | | 97.96% | |
| NEIS1265 | Sel1 repeat protein (Cytochrome C oxidase) | Metabolism | Accessory | SSR | 93.88% | 93.88% | 93.88% | | 93.88% | | 0.00% | 93.88% | 93.88% | 93.88% | 93.88% | |

| NEIS code | BLASTp ID | Function | Core/ accessory | SSR/ INDEL | cc53 | cc32 | cc5 | cc213 | cc41/44 | cc22 | cc11 | cc60 | cc461 | cc269 | cc23 |
|---------------------|--|--------------------------|--------------------|---------------|--------|--------|--------|--------|---------|--------|--------|--------|---------|--------|--------|
| NEIS1300 | Hemerythrin domain-containing protein | Metabolism | Accessory | SSR | 95.92% | 95.92% | 95.92% | 95.92% | 95.92% | 95.92% | 95.92% | | | 60.00% | 95.92% |
| NEIS1526 | Sensor histidine kinase | Metabolism | Accessory | INDEL | 97.96% | 97.96% | 97.96% | 97.96% | 16.00% | 97.96% | 97.96% | | 97.96% | 97.96% | 97.96% |
| NEIS1887 | TonB dependant receptor | Metabolism | Accessory | SSR | 89.80% | 89.80% | 2.00% | | | 89.80% | 89.80% | 56.00% | 89.80% | | 62.00% |
| NEIS1929 | Acyltransferase | Metabolism | Accessory | INDEL | 0.00% | 0.00% | 98.00% | 0.00% | 0.00% | | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% |
| NEIS2107 | long-chain-fatty-acid--CoA ligase | Metabolism | Accessory | SSR | 97.96% | 97.96% | | | 6.00% | 97.96% | 97.96% | | | 97.96% | |
| NEIS2779 (aniA) | Nitrite reductase | Metabolism | Accessory | SSR | 93.88% | 93.88% | 93.88% | 93.88% | 93.88% | | 31.75% | | 10.00% | 18.00% | 6.00% |
| NEIS2846 (pglN2) | Glycosyltransferase | Outer Membrane protein | Accessory | INDEL | 2.04% | 2.04% | | 2.04% | 56.00% | 82.00% | | 88.00% | 2.04% | | 98.00% |
| NEIS1668 (tspB) | TspB | Outer Membrane protein | Accessory | SSR | 95.92% | | 95.92% | 95.92% | | | | 95.92% | 26.00% | | |
| NEIS1859 (autA) | autotransporter outer membrane beta-barrel domain-containing protein | Outer Membrane protein | Accessory | SSR | 91.84% | 91.84% | 91.84% | 91.84% | 6.00% | 91.84% | 91.84% | | 91.84% | 91.84% | 91.84% |
| NEIS2573 | Repetetive large surface protein | Outer Membrane protein | Accessory | SSR | 0.00% | | 96.00% | | | | | | 100.00% | | |
| pilS | pilin | Outer Membrane protein | Accessory | INDEL | 79.59% | 36.00% | | | | | 0.00% | | | | |
| NEIS1180 | DNA cytosine methyltransferase | Restriction modification | Accessory | SSR | 0.00% | | | | 90.00% | | | 30.00% | | | 82.00% |
| NEIS2391 | Type I restriction endonuclease subunit R | Restriction modification | Accessory | SSR | 97.96% | 97.96% | 0.00% | | 97.96% | 97.96% | | 97.96% | 97.96% | 97.96% | 97.96% |
| NEIS2566 (cas9) | cas9 endonuclease | Restriction modification | Accessory | SSR | 95.92% | | | 2.00% | | | | | | | 95.92% |
| NEIS0456 | Hemagglutinin/hemolysin like protein | Toxin | Accessory | INDEL | 95.92% | 95.92% | 95.92% | 95.92% | | 95.92% | 95.92% | 14.00% | 95.92% | | |
| NEIS1404 | DUF560 domain-containing protein | Uncharacterised protein | Accessory | INDEL | 97.96% | 97.96% | 97.96% | | 16.00% | 97.96% | 97.96% | 97.96% | 10.00% | 52.00% | 97.96% |
| NEIS2531 | Hypothetical protein | Uncharacterised protein | Accessory | SSR | 97.96% | 97.96% | 0.00% | | 97.96% | 97.96% | 0.00% | 97.96% | 0.00% | 0.00% | 0.00% |
| NEIS0112 | ATP binding protrin | Uncharacterised protein | Accessory | INDEL | 0.00% | 0.00% | 94.00% | 98.00% | 0.00% | 98.00% | 0.00% | 0.00% | | 96.00% | 98.00% |
| NEIS0368 | Hypothetical protein | Uncharacterised protein | Accessory | SSR | 2.04% | | 2.04% | 42.00% | 2.04% | 2.04% | 2.04% | 86.00% | 88.00% | 2.04% | 88.00% |
| NEIS0458 | Hypothetical protein | Uncharacterised protein | Accessory | SSR | 91.84% | 91.84% | 91.84% | 4.00% | 12.00% | 91.84% | 91.84% | 91.84% | 91.84% | | 91.84% |
| NEIS0594 | Hypothetical protein | Uncharacterised protein | Accessory | SSR | 91.84% | | 91.84% | 91.84% | | | | 68.00% | 91.84% | | |
| NEIS0604 | Supressor of fused domain protein (SUFU) | Uncharacterised protein | Accessory | SSR | 85.71% | | | 85.71% | 85.71% | 85.71% | 85.71% | | 85.71% | 56.00% | |

| NEIS code | BLASTp ID | Function | Core/ accessory | SSR/ INDEL | cc53 | cc32 | cc5 | cc213 | cc41/44 | cc22 | cc11 | cc60 | cc461 | cc269 | cc23 |
|-------------------------|--|-------------------------|--------------------|---------------|--------|---------|--------|--------|---------|--------|--------|--------|--------|---------|---------|
| NEIS0607 | Hypothetical protein | Uncharacterised protein | Accessory | SSR | 93.88% | 93.88% | 93.88% | 93.88% | 93.88% | 93.88% | 93.88% | 0.00% | 93.88% | | |
| NEIS0838 | Hypothetical protein | Uncharacterised protein | Accessory | INDEL | 0.00% | 0.00% | | | 96.00% | | 96.83% | | | 92.00% | |
| NEIS1014 | Hypothetical protein | Uncharacterised protein | Accessory | INDEL | 97.96% | | 97.96% | 97.96% | 97.96% | 10.00% | 97.96% | 97.96% | 97.96% | | 97.96% |
| NEIS1161 | Autotransporter | Uncharacterised protein | Accessory | SSR | 93.88% | 78.00% | 93.88% | 2.00% | 68.00% | 93.88% | 58.73% | 93.88% | 93.88% | | 93.88% |
| NEIS1334 | Alcohol dehydrogenase | Uncharacterised protein | Accessory | SSR | 2.04% | 58.00% | 2.04% | | 2.04% | 98.00% | 2.04% | | 98.00% | | |
| NEIS1458 (YbhB/YbcL) | YbhB/YbcL family Raf kinase inhibitor-like protein | Uncharacterised protein | Accessory | INDEL | 95.92% | 95.92% | 95.92% | 0.00% | 95.92% | | 95.92% | | 95.92% | 48.00% | 95.92% |
| NEIS1793 | Supressor of fused domain protein (SUFU) | Uncharacterised protein | Accessory | SSR | 0.00% | 0.00% | 72.00% | 98.00% | 90.00% | 98.00% | 96.83% | 82.00% | 42.00% | 52.00% | 38.00% |
| NEIS1801 | Hypothetical protein | Uncharacterised protein | Accessory | SSR | 10.20% | | 10.20% | | 90.00% | | 95.24% | | | 98.00% | 96.00% |
| NEIS1875 | Hypothetical protein | Uncharacterised protein | Accessory | SSR | 93.88% | 0.00% | | | 93.88% | 93.88% | 93.88% | 93.88% | | 54.00% | |
| NEIS2097 | Hypothetical protein | Uncharacterised protein | Accessory | SSR | 95.92% | | | 95.92% | | 95.92% | 95.92% | 95.92% | 2.00% | 95.92% | 95.92% |
| NEIS2367 | Hypothetical protein | Uncharacterised protein | Accessory | SSR | 95.92% | | | | | | 95.92% | 95.92% | | | 95.92% |
| NEIS2381 | DUF333 domain containing protein | Uncharacterised protein | Accessory | SSR | 97.96% | 97.96% | 97.96% | 97.96% | 97.96% | 26.00% | 97.96% | 97.96% | 97.96% | | 0.00% |
| NEIS2383 | Hypothetical protein | Uncharacterised protein | Accessory | SSR | 0.00% | 95.00% | 0.00% | | 90.00% | | | | | 98.00% | |
| NEIS2387 | Hypothetical protein | Uncharacterised protein | Accessory | INDEL | 0.00% | 94.00% | 84.00% | | 0.00% | 98.00% | | 92.00% | | 100.00% | 100.00% |
| NEIS2405 | Hypothetical protein | Uncharacterised protein | Accessory | INDEL | 0.00% | 100.00% | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% | | 0.00% |
| NEIS2520 | Hypothetical protein | Uncharacterised protein | Accessory | INDEL | 89.80% | | | | | | | | | 44.00% | 18.00% |
| NEIS2743 (cnl) | | Uncharacterised protein | Accessory | SSR | 93.88% | | | | | | 65.08% | | | 64.00% | 0.00% |
| NEIS3025 | Hypothetical protein | Uncharacterised protein | Accessory | INDEL | 0.00% | | | | 84.00% | | | | | | |
| NEIS3053 | Hypothetical protein | Uncharacterised protein | Accessory | INDEL | 93.88% | | 0.00% | | 56.00% | | 0.00% | | | | |
| NEIS3060 | Hypothetical protein | Uncharacterised protein | Accessory | SSR | 0.00% | 100.00% | | 0.00% | 0.00% | | 0.00% | 0.00% | 0.00% | 98.00% | |
| NEIS3091 | Hypothetical protein | Uncharacterised protein | Accessory | SSR | 95.92% | 95.92% | 95.92% | 95.92% | 95.92% | | 95.92% | 95.92% | 38.00% | 48.00% | 95.92% |
| NEIS3112 | Hypothetical protein | Uncharacterised protein | Accessory | INDEL | 0.00% | | | | 80.00% | | 41.27% | 84.00% | 96.00% | | |
| NEIS3119 | Hypothetical protein | Uncharacterised protein | Accessory | SSR | 95.92% | | | | 10.00% | | | 95.92% | | | |