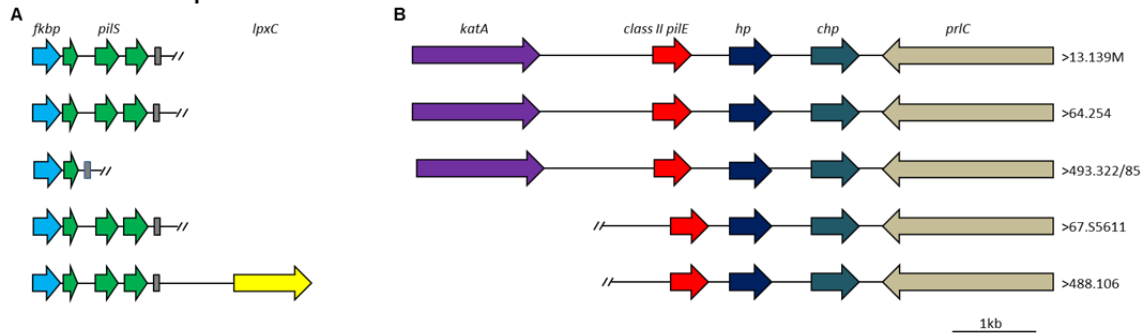
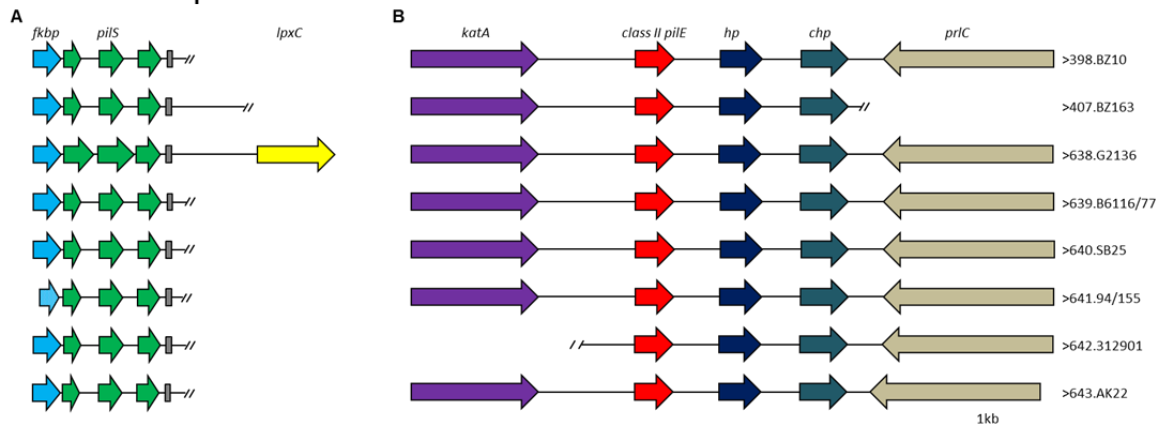


Additional file 6. Schematic diagrams of class II *pilS* (A) and (B) *pilE* genome regions from meningococcal isolates in the pubMLST database.

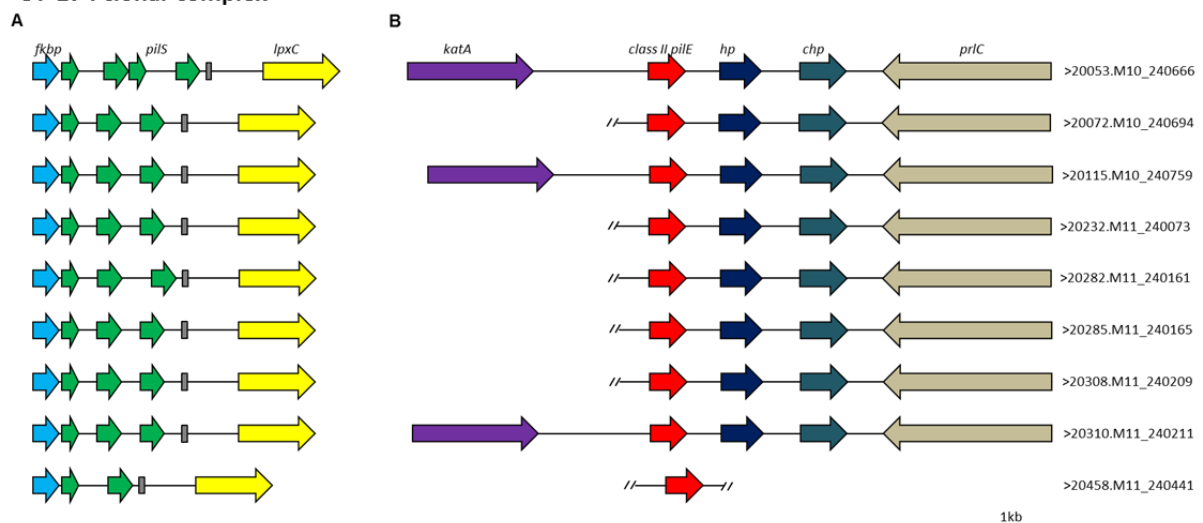
ST-1 clonal complex



ST-8 clonal complex

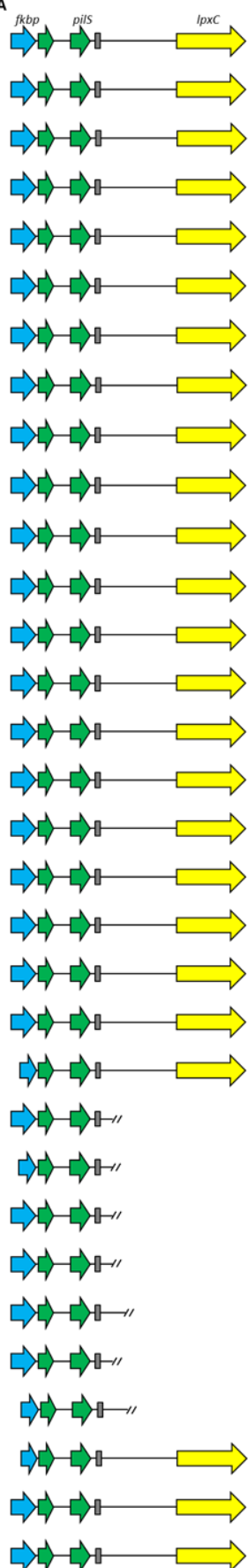


ST-174 clonal complex

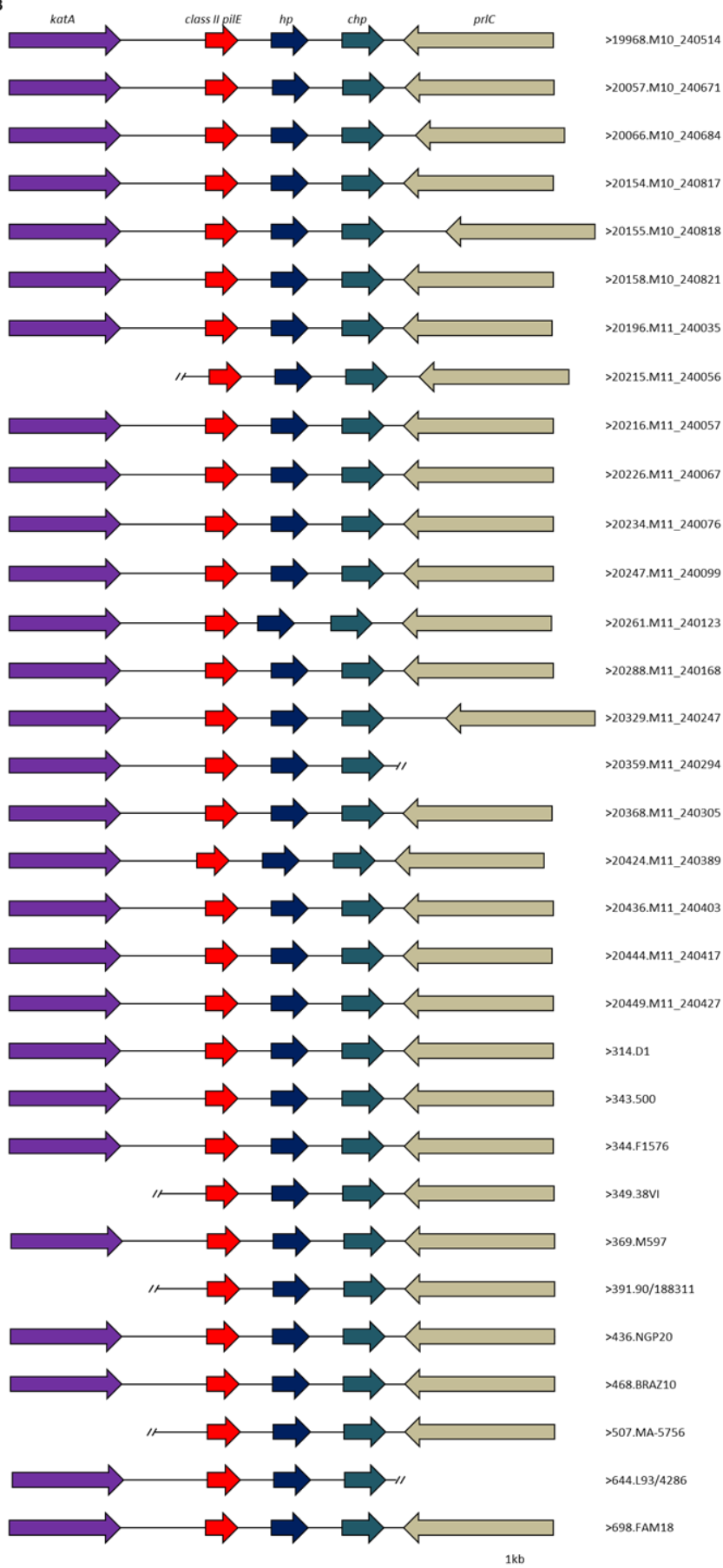


ST-11 clonal complex

A



B



Identification code and name (>ID.name) of each isolate are indicated. Diagonal lines represent the end of the contig. Putative Sma/Cla sequences are shown as hatched boxes.

lpxC: UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase), *fkbp*: peptidyl-prolyl cis-trans isomerase, *pilS* : silent *pilS* cassettes, *pilE*: gene encoding major pilin subunit, *katA*: catalase, *hp*: hypothetical protein, *chp*: conserved hypothetical protein, *prlC*: putative oligopeptidase A. Scale bar represents 1kb.