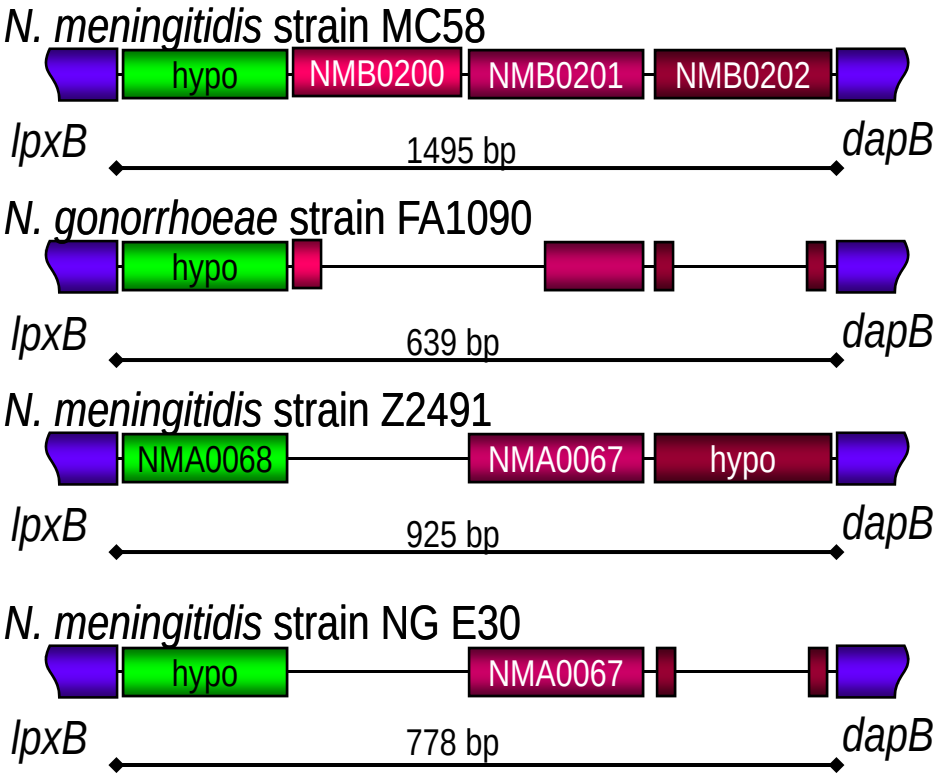
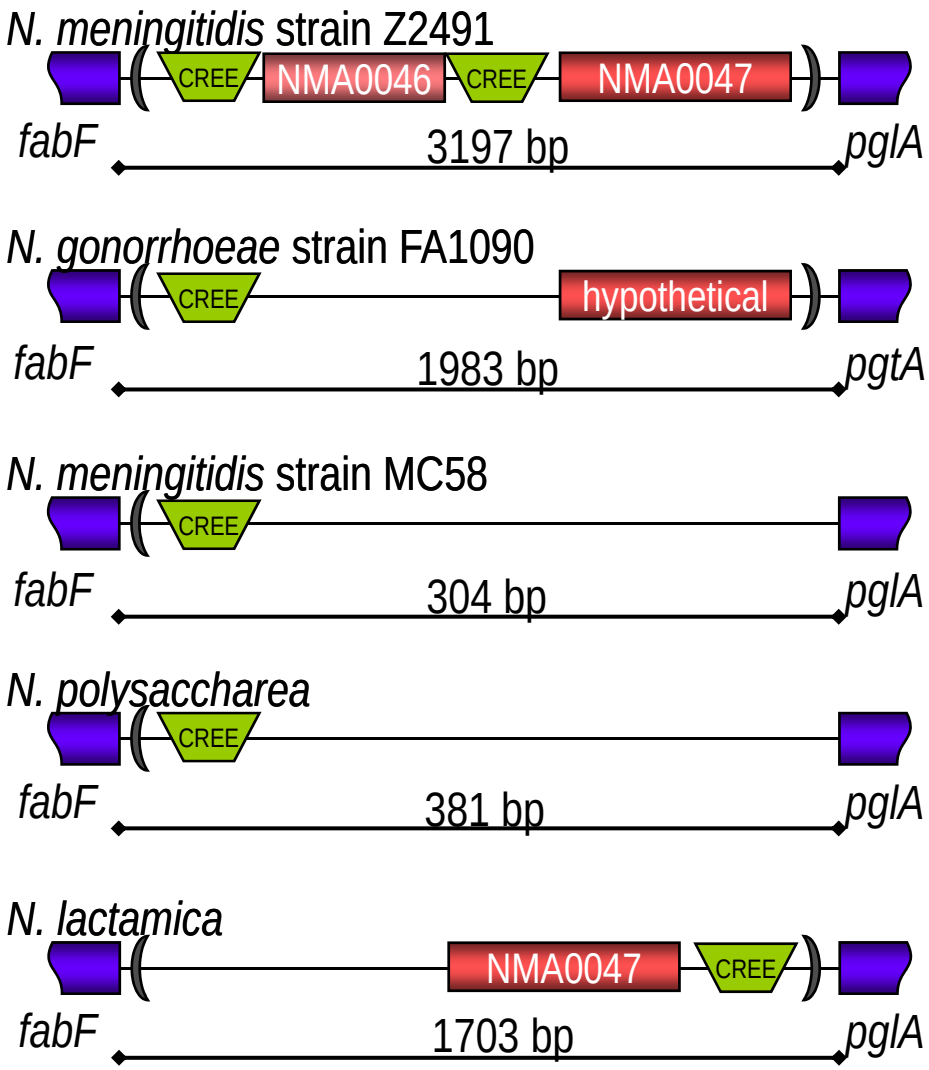
Supplementary Figures

Some Regions of Degeneration

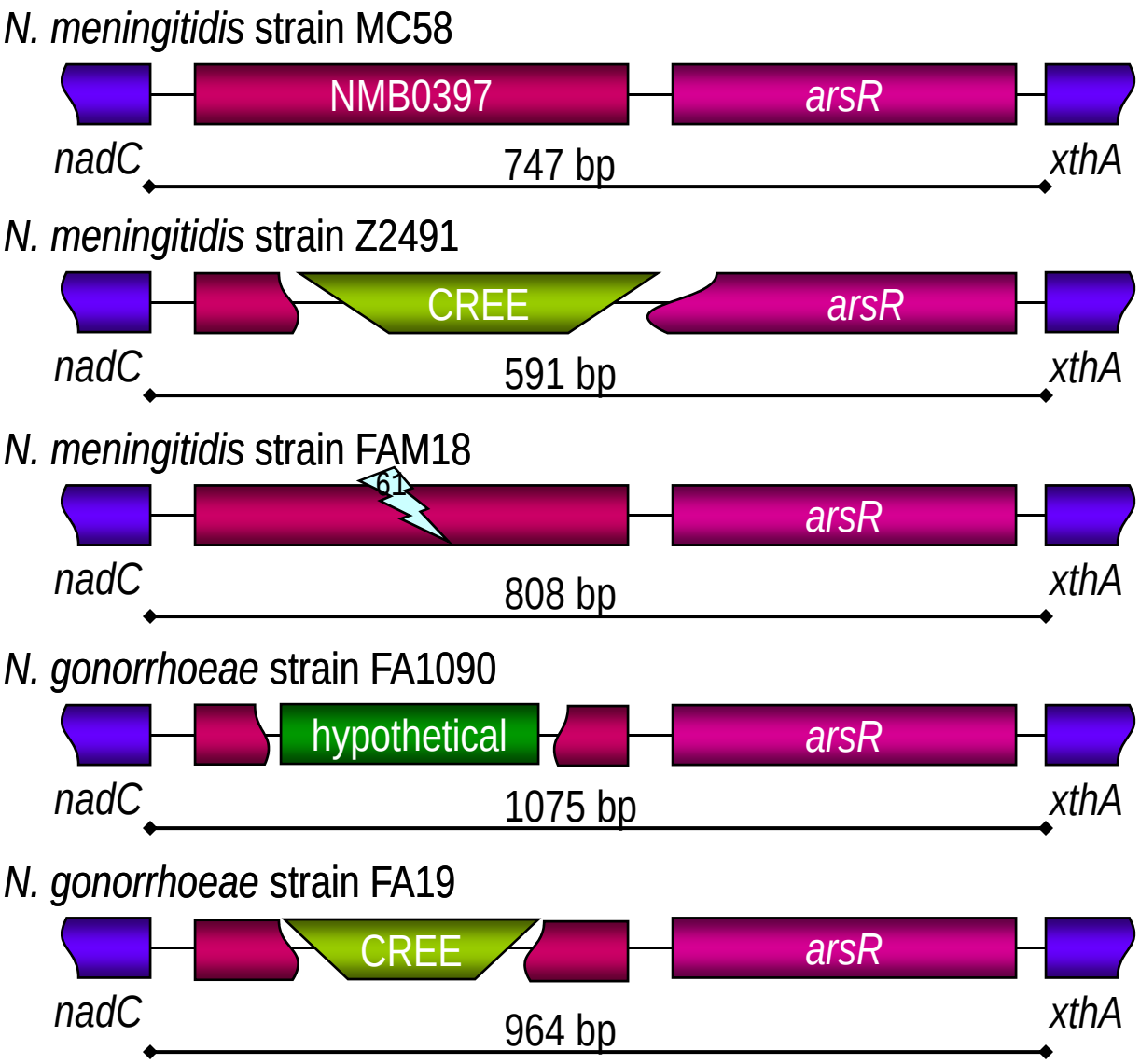
Further analysis of the neisserial genome sequences and the PCR and sequence data generated here indicated that some regions of the neisserial genomes are sites of degeneration or sequence divergence, rather than MMEs. Initially, such regions may appear to be MMEs based on genome sequence annotations, however closer examination reveals that this is not the case. For example, the region between *lpxB* and *dapB* would appear to contain different regions within different genes between the strains investigated. The differences, however, can all be attributed to degeneration of the hypothetical genes NMB0200, NMB0201, and NMB0202. While all three genes are complete in *N. meningitidis* strain MC58, close examination of the *N. gonorrhoeae* strain FA1090 genome sequence data revealed fragments of each of these genes. *N. meningitidis* strain Z2491 lacks NMB0200 completely, yet has copies of NMB0201 and NMB0202. Sequencing of *N. meningitidis* strain NG E30 revealed that NMB0200 is completely gone, as in strain Z2491, and the central portion of NMB0202 is also gone, as in strain FA1090.



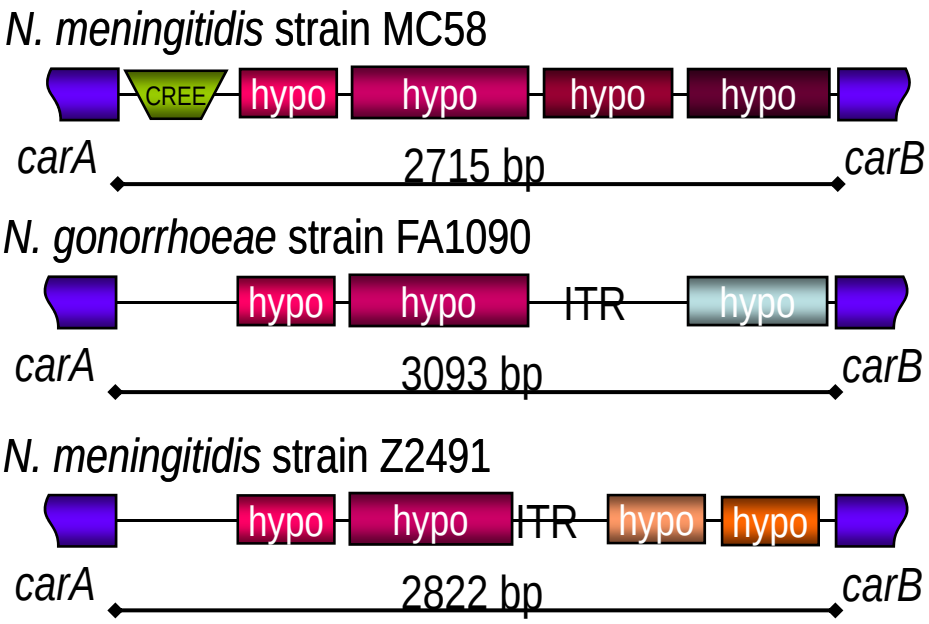
The region between *lpxB* and *dapB*: Analysis and sequencing of this site revealed that this is an area of degeneration containing gene fragments, rather than an MME. The region sequenced from *N. meningitidis* strain NG E30 contains intact versions of 2 of the 4 potential genes in this region (DQ115776).



The region between *fabF* and *pglA*: Analysis and sequencing of this site suggested that the observed strain divergence was due to the presence of the CREE (Correia Repeat Enclosed Elements) and inverted repeat (crescents) sequences. The region sequenced from *N. polysaccharea* is similar to that from *N. meningitidis* strain MC58 (DQ115760) and the region sequenced from *N. lactamica* shares features with *N. meningitidis* strain Z2491 (DQ115759).



The region between *nadC* and *xthA*: Analysis and sequencing of this site revealed that this is an area of degeneration, rather than an MME. Inactivation of NMB0397 has occurred by a variety of mechanisms. The sequence of MME*nadCxthA* from *N. gonorrhoeae* strain FA19 (AY386268) was obtained previously (Snyder, Davies & Saunders, 2004).



The region between *carA* and *carB*: Analysis of this site revealed that this is an area of divergence, rather than an MME. In some strains there is a CREE (Correia Repeat Enclosed Element) and in some there is a variable length intergenic tandem repeat sequence (ITR), which differs in length between strains FA1090 and 28539.