

**Additional Table A1. Multiple alignment details.** Details of the multiple alignment of the six *Neisseria* genomes generated with M-GCAT. The global multiple alignment was divided into 79 M-GCAT Clusters (or locally co-linear regions) that are devoid of breakpoints such as rearrangements or large segments of lineage specific sequence. **Alignment Coverage** is the average percentage of each genome covered by the Clusters. **Polymorphic sites** are the number of variable sites in the alignment, and **Mono-morphic sites** represent the number of columns with conserved residues. **Conserved positions** indicates the total amount of columns with conserved residues in the multiple alignment, and **Conserved Blocks** designates the number of blocks of conserved positions occurring in at least four of the six genome sequences (as specified by Gblocks).

<b>Alignment Length</b>	<b>2,224,085</b>
<b>Polymorphic sites</b>	<b>192,618</b>
<b>Mono-morphic sites</b>	<b>1,394,876</b>
<b>Sites with &gt;0 Gaps</b>	<b>636,591</b>
<b>Conserved Blocks</b>	<b>5,711</b>
<b>Conserved Positions</b>	<b>1,571,424</b>
<b>Alignment Coverage</b>	<b>82.5%</b>
<b>Clusters/Co-linear Regions</b>	<b>79</b>
<b>Sites per Cluster</b>	<b>28,153</b>