

**Table S2: inverted DUS repeats in *Neisseriaceae***

bacterium	fuzznuc <sup>1</sup> search pattern	counts	counts (2 mut <sup>1</sup> )
<i>Eikenella corrodens</i> ATCC 23834	GCTACCTGAA-N(1,19)-TTCAGGTAGC	431	529
<i>Kingella denitrificans</i> ATCC 33394	GCAGCCTGCA-N(1,19)-TGCAGGCTGC	401	554
<i>Kingella oralis</i> ATCC 51147	GCAGCCTGAA-N(1,19)-TTCAGGCTGC	550	686
<i>Neisseria wadsworthii</i> 9715	CCTGTCTGAA-N(1,19)-TTCAGACAGG	582	683
<i>Neisseria elongata</i> subsp. <i>glycolytica</i> ATCC 29315	GCCGTCTGAA-N(1,19)-TTCAGACGGC	487	598
<i>Neisseria mucosa</i> ATCC 25996	GTCGTCTGAA-N(1,19)-TTCAGACGAC	674	776
<i>Neisseria flavescens</i> SK114	GCCGTCTGAA-N(1,19)-TTCAGACGGC	556	675
<i>Neisseria meningitidis</i> MC58	GCCGTCTGAA-N(1,19)-TTCAGACGGC	380	555

<sup>1</sup> = part of the EMBOSS package [1]

<sup>2</sup> = two mutations in the search pattern allowed

**Reference:**

1. Rice P, Longden I, Bleasby A (2000) EMBOSS: the European Molecular Biology Open Software Suite. Trends Genet 16: 276-277.