

Additional Table A3- Under-representation of DUS in strain specific insertions. We detected a total of 519 strain specific insertions of length >100nt in the M-GCAT alignment. We searched for DUS inside of these insertions and found significantly less DUS than expected (χ^2 , $p < 0.00024$). **# of insertions** indicates the # of insertions >100nt specific only to one strain that were found. **Avg. length** is the mean length of all the insertions specific to a given strain, and **# DUS is** the total number of DUS found inside of all of the strain specific insertions in each genome.

	# of strain specific insertions	Avg. length	# DUS
<i>N. men.</i> Z2491	43	434	1
<i>N. men.</i> MC58	40	365	2
<i>N. men.</i> FAM18	63	429	3
<i>N. men.</i> 8013	47	396	4
<i>N. gonorrhoeae</i>	102	370	12
<i>N. lactamica</i>	224	621	94