

Meningococcal Genetic Variation Mechanisms

Strain	Z2491	MC58	FAM18
Serogroup	A	B	C
MLST sequence type	ST-4	ST-74	ST-11
MLST clonal complex	ST-4 complex/subgroup IV	ST-32 complex/ET-5 complex	ST-11 complex/ET-37 complex
Genome size (bp)	2184406	2272351	2194961
G + C content (%)	51.81	51.53	51.62
Number of CDS	1,999	2,024	1,976
Number of CDS that degenerate	51	5	33
Coding percentage	79.9	81.5	81.4
rRNA operons	4	4	4
tRNAs	58	59	59

Note that the CDS counts for Z2491 and MC58 reflect the annotation edited during the three-way comparison.

MLST, multilocus sequence typing

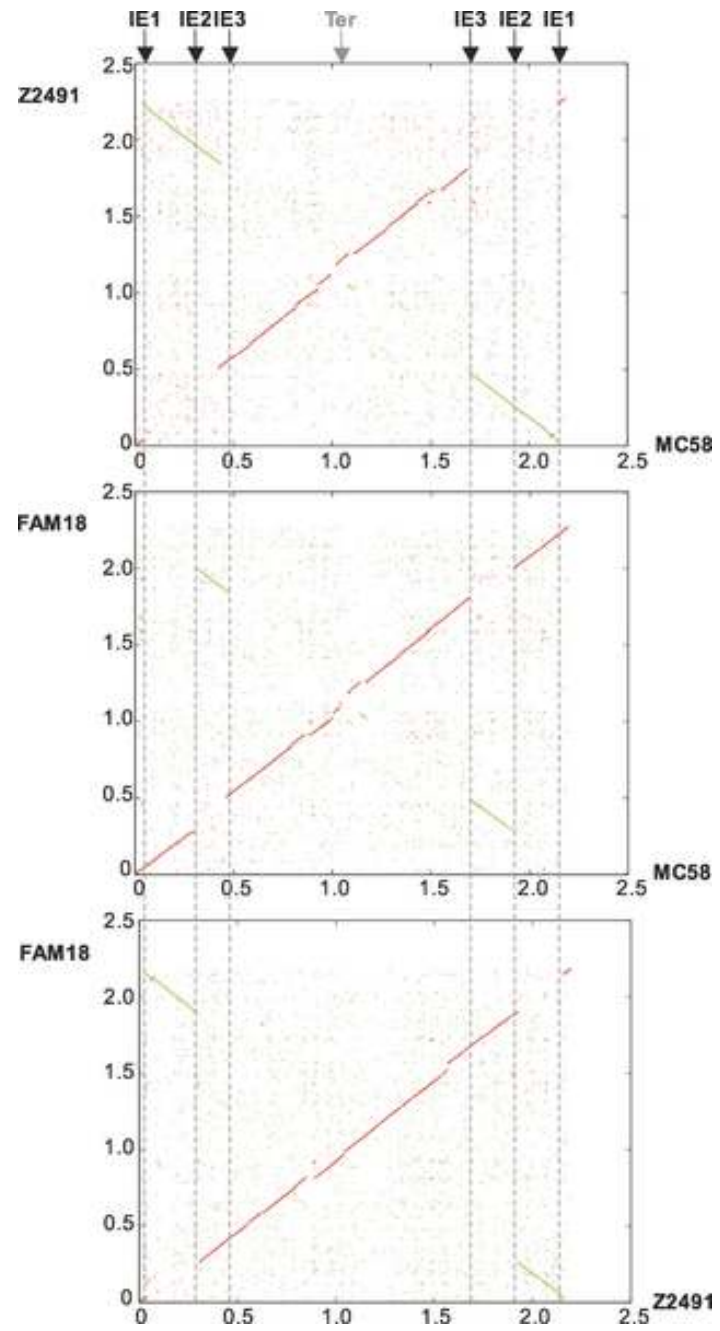
doi:10.1371/journal.pgen.0030023.t001

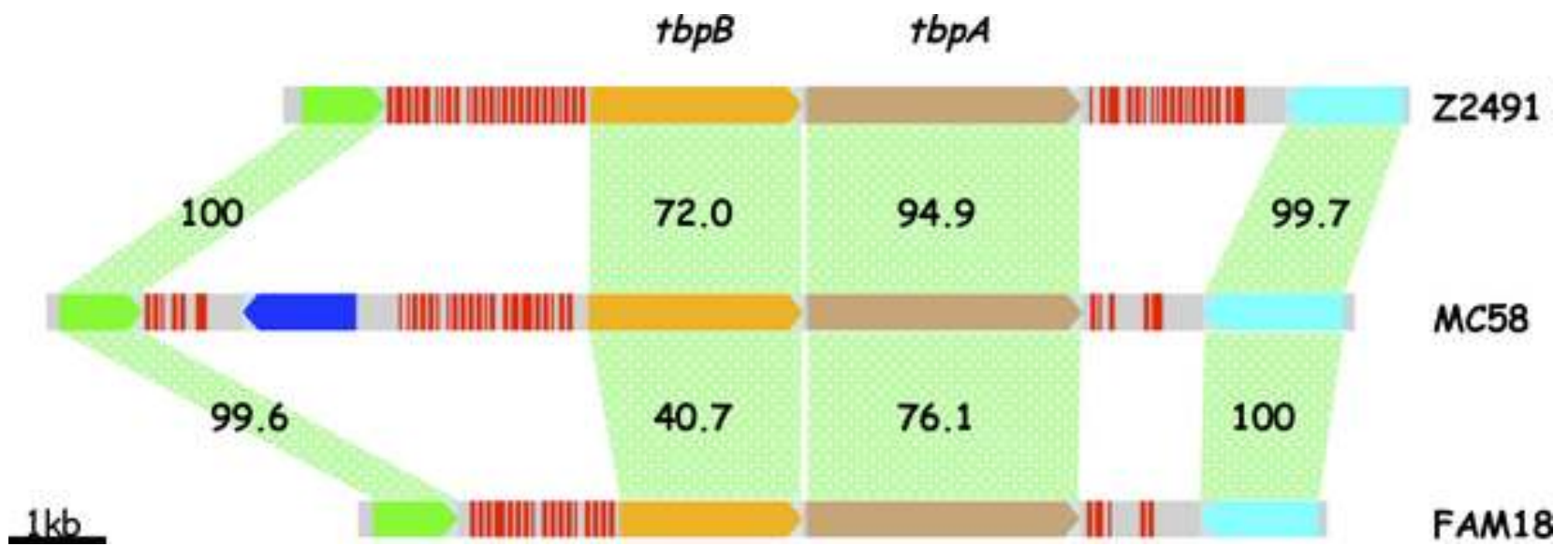
Repeat type^a	FAM18	Z2491	MC58
DUS	1,888	1,892	1,935
RS	611	681	617
dRS3	718	772	756
CREE (full)	168	173	161
CREE (internal deletion)	78	84	82
CREE (partial)	28	29	19
ATR	13	19	13
REP 2	22	26	24
REP 3	8	13	9
REP 4	18	20	18
REP 5	10	9	10

^aSee text for further details.

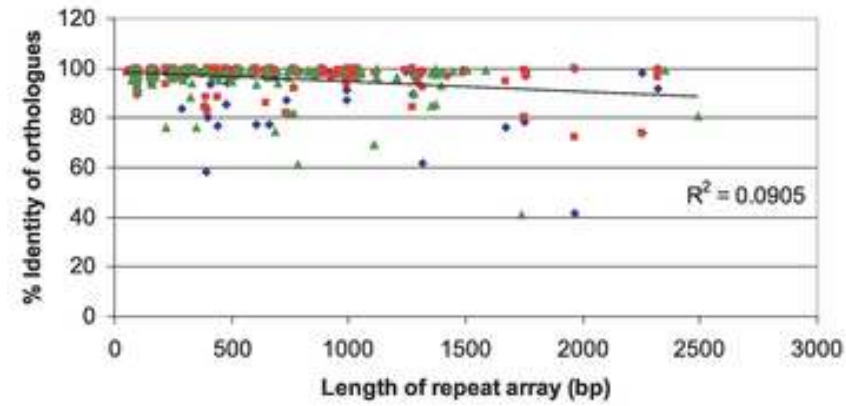
ATR, A + T-rich repeat; dRS3, bp-inverted repeats (ATTCCN>NNNNNNNGGGAAT); DUS, DNA uptake sequence; RS, repeat sequence element flanked by dRS3 repeats; REP, other repeat families

doi:10.1371/journal.pgen.0030023.t003

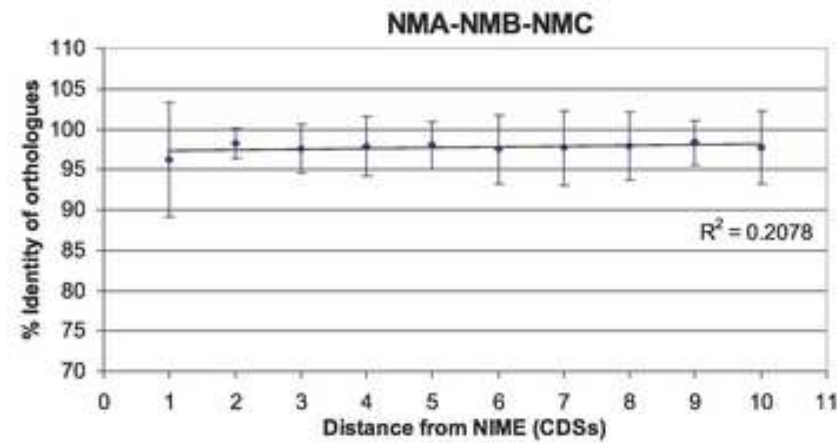




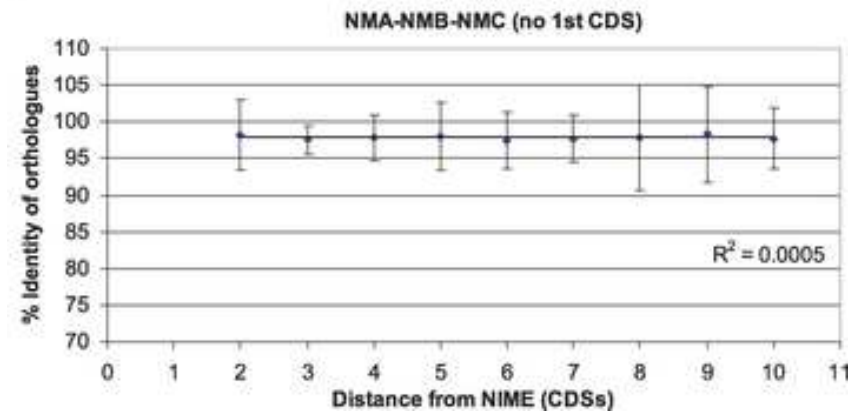
A



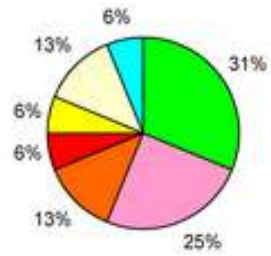
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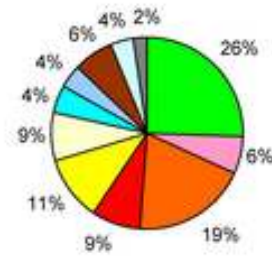
C



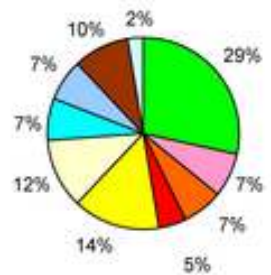
Gene Functional Classification - Repeat array length: 1-500b



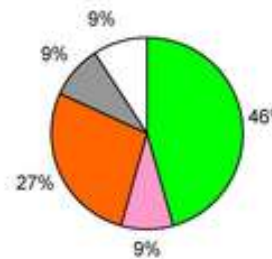
Gene Functional Classification - Repeat array length: 501-1000b



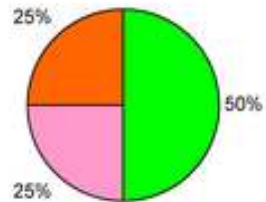
Gene Functional Classification - Repeat array length: 1001-1500b



Gene Functional Classification - Repeat array length: 1501-2000b

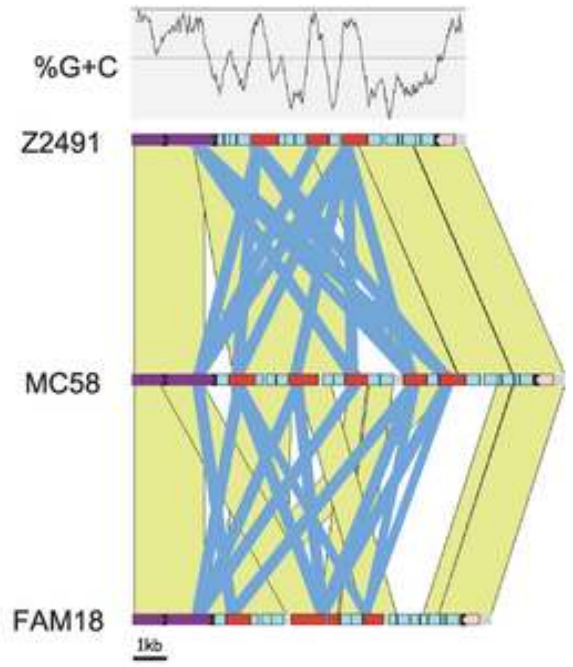


Gene Functional Classification - Repeat array length: >2000b

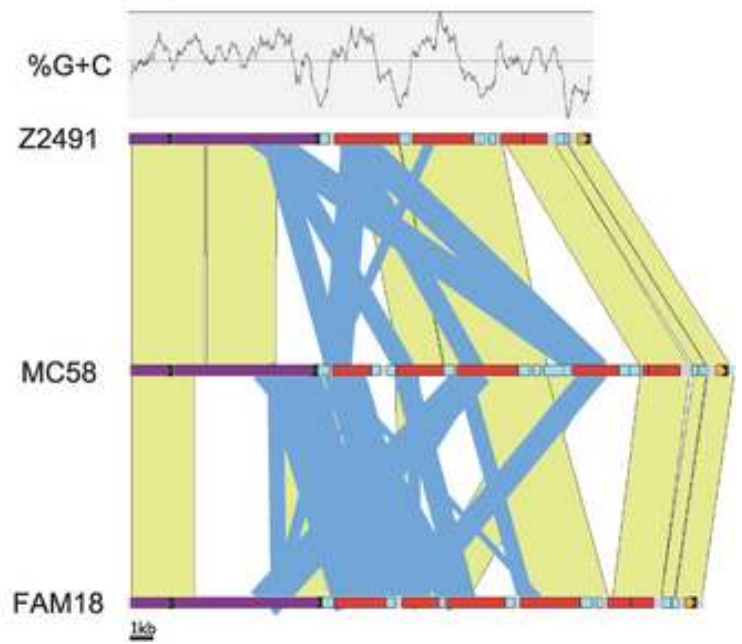


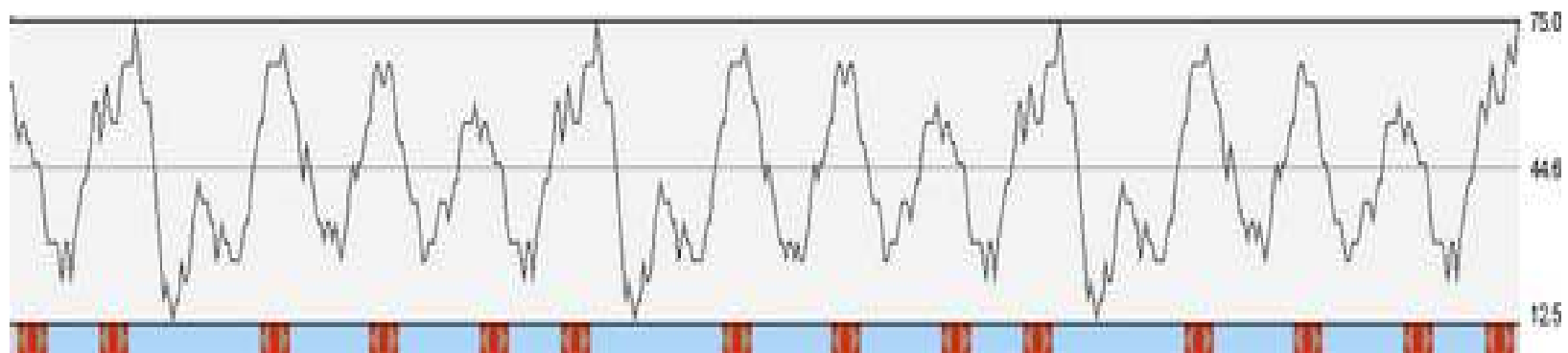
- Regulators
- Unknown
- Central/intermediary/misc metabolism
- Degradation of small molecules
- Degradation of large molecules
- Phage/IS elements
- Surface (IM, OM, secreted, surface structures[LPS etc])
- Information transfer (transcription/translation + DNA/RNA modification)
- Pseudogenes and partial genes (remnants)
- Energy metabolism (glycolysis, electron transport etc.)
- Conserved hypothetical
- Pathogenicity/Adaptation/Chaperones
- Stable RNA

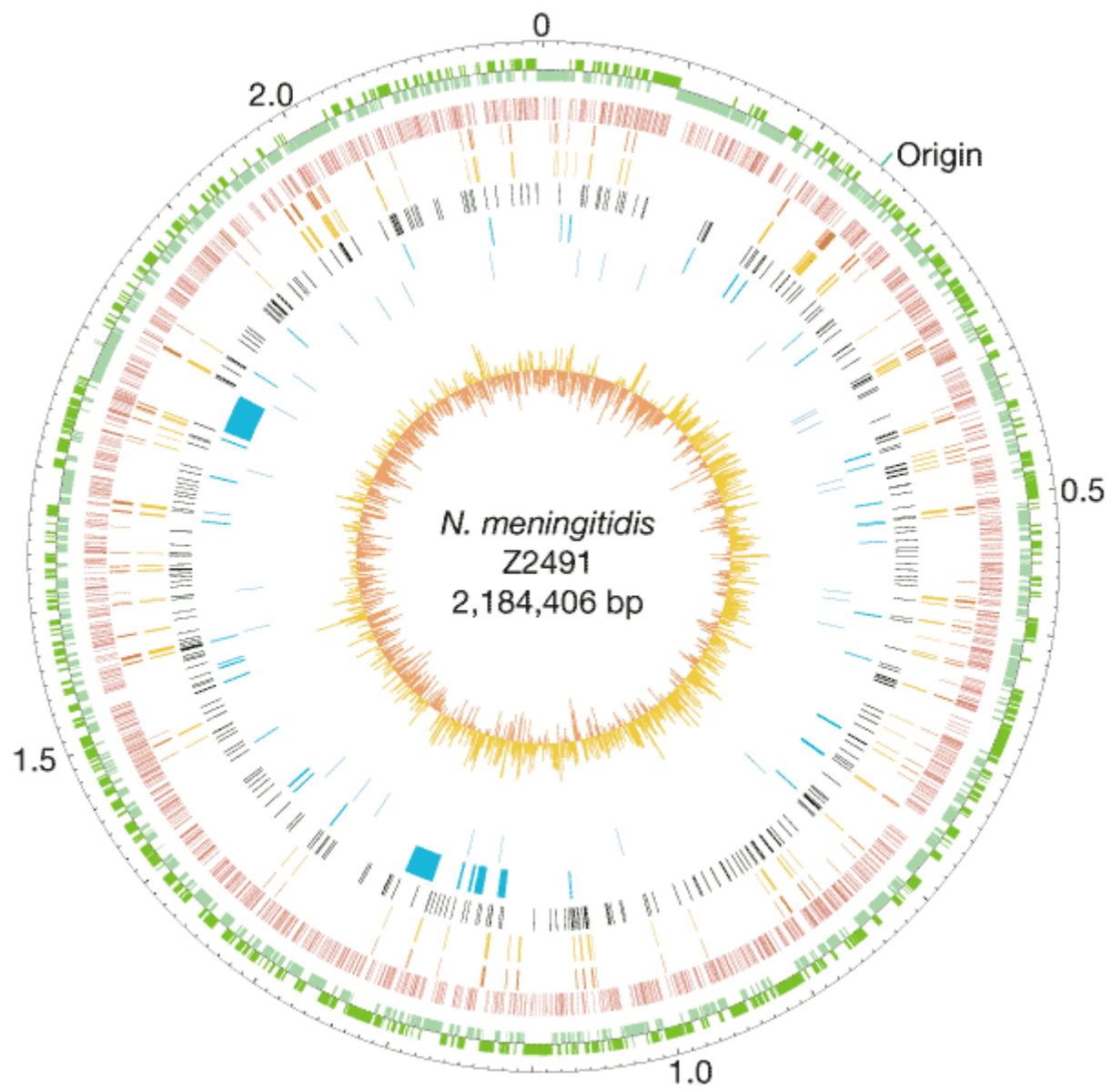
A



B







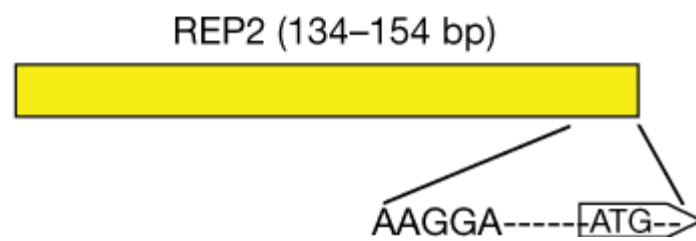
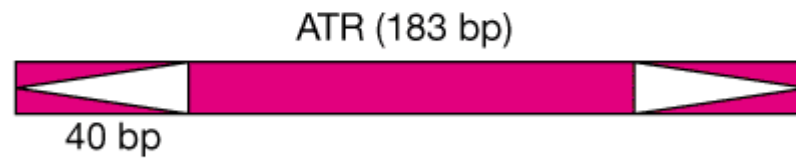
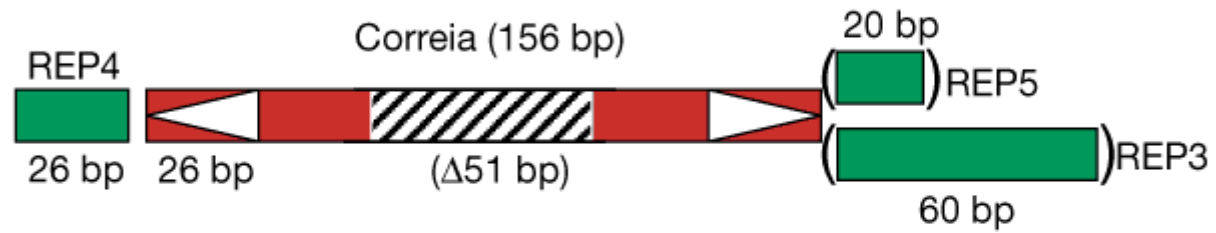
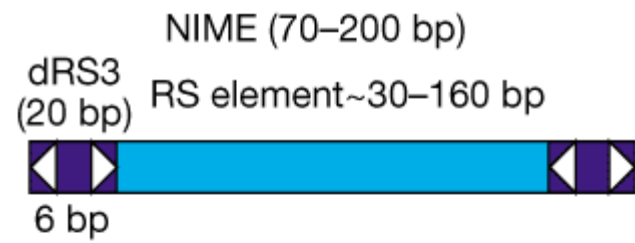


Table 1 Number of repeats by type in *N. meningitidis* Z2491

Type	Size (bp)	Frequency
DNA uptake sequence: gccgtctgaa	10	1,892
RS	24–161	681
dRS3: attcccnnnnnnngggaat	20	772
Correia (full)	150–159	173
Correia (internal deletion)	~104	84
Correia (partial)	37–145	29
ATR	183	19
REP 2	59–154	26
REP 3	60	13
REP 4	26	20
REP 5	20	9
IS1016	256–740	14 (including partial)
IS1106	263–1219	22 (including partial)
IS1655	1,074–1,257	7 (including partial)
Prophage	2,330–38,964	5

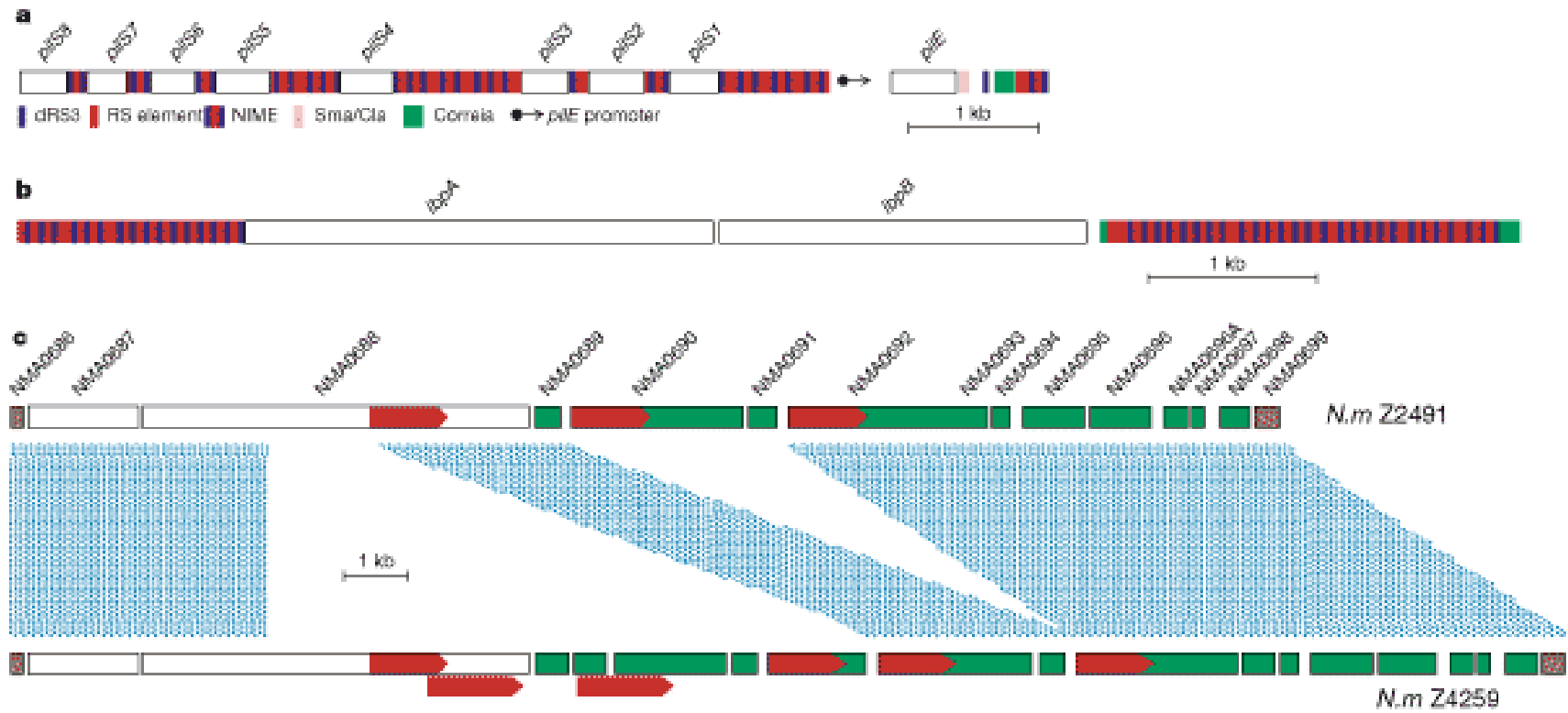
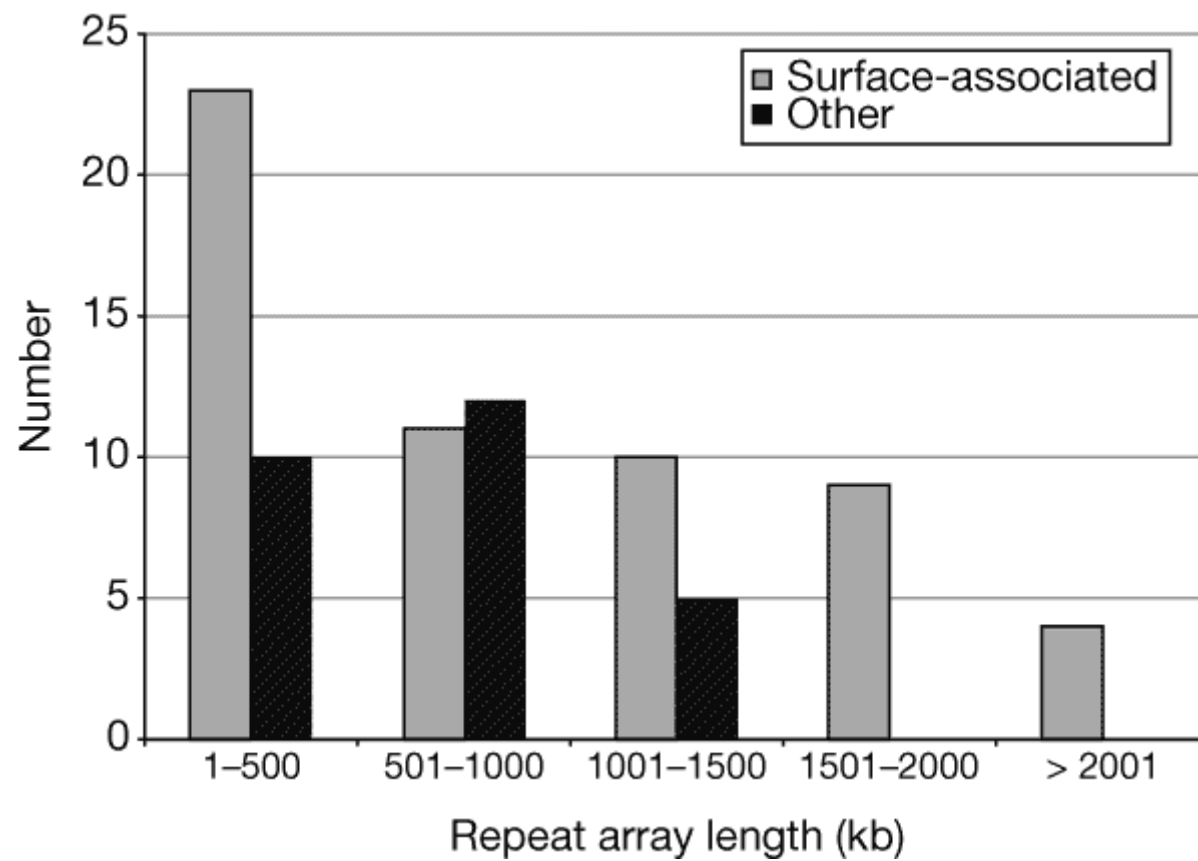


Table 3 Tandem repeat sequences indicating potential phase variable genes.

Tandem repeat	Gene(s) affected	Status	Function
(G)14	NMA0048 (<i>pglA</i>)	On	glycosyltransferase involved in pilin glycosylation
(GC)6	NMA0072 (<i>pdxA</i>)	On	pyridoxal phosphate biosynthetic protein
(G)9	NMA0132A	On	unknown
(G)11	NMA0293 (<i>pilC2</i>)	Off	pilus-associated protein
(G)9	Upstream of NMA0402 (<i>truA</i>)	?	tRNA pseudouridine synthase; promoter?
(G)12	NMA0406	Off	probable acetyltransferase
(GC)6	NMA0419	On	conserved hypothetical
(C)10	NMA0475 (<i>hpuA</i>)	On	haemoglobin-haptoglobin-utilization protein
(G)10	NMA0478	On	possible outer membrane peptidase
(C)13	NMA0609 (<i>pilC1</i>)	On	pilus-associated protein
(G)10	NMA0619	On	possible lipopolysaccharide modification acyltransferase
(G)16	NMA0641	Off	possible glycosyl transferase
(AAACAAC)26	NMA0832	On	possible glycosyl transferase; translates to 9x NNKQQT repeats
(G)8	NMA1040	Off	type I restriction-modification system specificity protein
(G)11	1142347..1142357 (non-coding)	-	in DNA repeat array



Artemis & ACT visualization ...