Studio	СT	$m \circ dA \circ 11 \circ 1 \circ d$	Demosta ACCC ^b	ON/OEE^{b}	$m \circ dD \circ 11 \circ 1 \circ d$	D ensets CCC $\land \land \overset{b,c}{}$	
MC58 a	31	modA 11 ^h	20	ON/OFF	mod B18	16	ON/OFF
72401 ª	32	modA12	20	OFF	modP2	8	OFF
153	-	modA12	3	ON	ND	0	OPT
E6124	5	modA12	22	OFE	ND		
14/76	32	modA11	18	OFF	modB18	ND	
14/1455	5	modA12	18	ON	modB?	11	OFF
E4608	5	modA12	2	OFE	modD2	11	OFF
2006	17	ModA12	2	OFF	MDaB2	15	ULL
3900 NG DB24	32	modA11 ^h	20	OFF	modBl	10	OFF
P7 160	22	modA11 ^h	23	OFF	modPls	10	OFF
500	11	modA12	23	OFF	ND	10	OFF
D7 10	0	modA11	9 AGTC	ULL	ND		
DZ 10	0	modA11	8 AUIC	- OEE	ND modP2	5	OEE
DZ190	41	modA12	3	OFF	modD2	7	OFF
207.0	40	modA12	27	OFF	modD2		ON
1000	49	modAIS	21	OFF	MOAB2	9 ICCAA	UN
1000	20	modA12	3	OFF	ND		
8080	32	modA15	27	OFF	ND		
AK50	41	modA12	10	OFF	ND		
860060	24	modA12	3	OFF	ND		
B6116///	10	modA12	24	OFF	ND	17.0004.4	OFF
M40/94	41	modA12	10	ON	modB2	T/ GCCAA	OFF
M-101/93	41	modA12	13	ON	modB2	6 GCCAA/CCCAA	ON
312 901	8	modA12	10	ON	ND		
890326	28	modA12	/	ON	ND		<u></u>
88/03415	46	modA12	16	ON	modB2	9	ON
G2136	8	modA12	19	ON	ND		OFF
SB25	8	modA12	15	OFF	modB2	8	OFF
2059001	4	modA12	3	OFF	ND	10	0.77
A22	22	modA12	3	OFF	modB2	13	OFF
E26	39	modA12	11	OFF	ND		
N45/96	41	modA11	32	OFF	ND		
E32	29	modA12	24	OFF	ND		
204/92	31	modA11	27	OFF	ND		
94/155	23	modA12	10	ON	ND		
50/94	33	modA12	16	ON	ND		
400	66	modA12	15	OFF	modB2	6 GCCAA	ON
931905	45	modA12	23	OFF	ND		
91/40	40	modA12	22	ON	ND		
AK22	41	modA12	10	ON	modB2	16 GCCAA	OFF
L93/4286	42	modA12	15	OFF	ND		
7891	8	modA12	3	OFF	modB2	10	OFF
D8	11	modA12	3	OFF	modB2	8	OFF
C751	5	modA12	3	OFF	ND		

Table S1. Mod alleles and repeat numbers for N. meningitidis isolate strains

26	12	modA12	3	OFF	ND		
S5611	4	modA12	3	OFF	ND		
154	4	modA12	3	OFF	modB2	9	ON
20	4	modA12	3	OFF	modB2	9	ON
CN100	1	modA12	3	OFF	modB2	3	ON
371	6	modA12	3	OFF	ND		
DK 353	1	modA11	16	ON	modB1	10	OFF
NG 6/88	21	modA11	29	OFF	ND		
EG 328	1	modA12	29	OFF	ND		
NG G40	37	modA11	16	ON	modB1	9 GCCAA	
BZ 147	13	modA12	7	ON	modB1	4	OFF
528	18	modA12	9	OFF	ND		
EG 011	25	modA11	11	OFF	ND		
79126	48	modA12	3	OFF	ND		
NG 080	18	modA11 ^h	24	OFF	modB1 ^g	ND	
243	36	modA12	3	OFF	ND		
MA-5756	3	modA12	11	OFF	ND		
M597	32	modA12	19	ON	ND		
BRAZ10	4	modA12	3	OFF	modB2	7	OFF
92001	11	modA12	10	ON	modB2	8	
6748	11	modA12	2	OFF	modB2	3	
D1	11	modA12	19	ON	ND		
90/18311	7	modA12	11	OFF	ND		
BZ 163	1	modA12	22	ON	modB2	ND	
NG H41	11	modA12	12	OFF	modB2	16	OFF
NG F26	11	modA11	17	OFF	modB1	9	ON
NG E28	9	modA18 ^f	18	OFF	ND		
80049	27	modA12	24	OFF	modB2	7	OFF
NG H36	14	modA12	23	OFF	modB1	ND	
139M	26	modA12	3	OFF	modB2	4	OFF
H1964	5	modA12	3	OFF	ND		
SWZ107	47	modA11	11	OFF	modB1	11	OFF
EG 327	1	modA12	12	OFF	modB1	38 GCCAA	OFF
NG H15	5	modA12	26	OFF	modB2	8	OFF
79128	35	modA12	3	OFF	ND		
BZ 232	19	ModA4 ^e	15	OFF	modB1	6 GCCAA	ON
DK 24	43	modA12	11	OFF	ND		
A4/M1027	3	modA12	3	OFF	ND		
NG E30	38	modA12	20	OFF	modB1	7 GCCAA	OFF
690	16	modA12	4	ON	ND		
S4355	4	modA12	3	OFF	modB2	10	OFF
38VI	44	modA12	3	OFF	ND		
106	4	modA12	3	OFF	modB2	3	OFF
196/87	5	modA11	24	OFF	ND		
322/85	11	modA12	3	OFF	ND		
255	1	modA12	3	OFF	ND		

254	32	modA12	3	OFF	modB2	8	OFF
S3131	2	modA12	3	OFF	ND		
NG E31	4	modA12	3	OFF	ND		
NG 4/88	1	modA12	24	OFF	modB2	6	ON
IAL2229	4	modA12	3	OFF	ND		
NG H38	15	modA11	11	OFF	modB2	17 GCCAA	OFF
EG 329	30	modA11 ^h	26	OFF	modB1 ^g	ND	
NG144/82	5	modA11 ^h	18	OFF	modB1 ^g	ND	
BZ 83	36	modA11 ^h	18	OFF	modB1	4	OFF
1014	32	modA12	3	OFF	ND		
120M	32	modA12	3	OFF	ND		
393	34	modA12	3	OFF	ND		
BZ 133	4	modA12	3	OFF	modB1	3	OFF
10	1	modA12	3	OFF	ND		
11-004	1	modA12	3	OFF	ND		
F1576	1	modA12	3	OFF	ND		
129E	4	modA12	3	OFF	ND		
NG 3/88	12	modA12	14	OFF	modB1 ^g	4	OFF

^aGenome strains

^b Number and expression state of repeats within the *ModA11* or *ModB1* gene; in-frame (ON) or out-of-frame (OFF)

^c Repeats can be either CCCAA, GCCAA or TCCAA

^d A strain was defined as having the *modA11* allele if the DNA recognition region was $\ge 95\%$ identical at the nucleotide level to *modA11* gene of *N. meningitidis* strain MC58 (NMB1375; see Figure 1). A strain was defined as having the *modB2* allele if the DNA recognition region was $\ge 95\%$ identical at the nucleotide level to *modB2* gene of *N. meningitidis* strain Z2491 (NMA1467; see Figure 1)

^e Strain defined as having *modA4* or *modA15* allele as defined in Fox *et al.* 2007 [17]

^f Strain has a new allele henceforth defined as modA18 in this paper. Shares similarity to *H. influenzae* strain 2019

^g modB1 strains that contain a premature stop codon

^h Frame shift mutation in *res* at nucleotide 2093

ND: not determined

Refer to Figure 1 and to the text.