Supplementary Material

Supplementary Table 1. Most frequent (in more than five isolates) factor H binding protein (fHbp) peptide identities in the panel of 3912 strains, by Meningococcal Antigen Typing System (MATS) coverage.

fHbp peptide	Number of isolates covered	Number of isolates not covered	Prop.test p-value[a]	Prop.test significance[a]	Proportion of covered
1	483	6	9.0E-103	**	99%
2	6	0	4.1E-02	*	100%
4	437	8	1.6E-91	**	98%
10	6	2	2.9E-01		75%
12	6	1	1.3E-01		86%
13	109	142	4.3E-02	*	43%
14	271	36	1.1E-40	**	88%
15	242	51	1.3E-28	**	83%
16	2	89	2.0E-19	**	2%
19	4	356	2.1E-76	**	1%
21	2	65	3.6E-14	**	3%
22	1	8	4.6E-02	*	11%
23	2	9	7.0E-02		18%
24	1	71	4.2E-16	**	1%
25	2	38	3.1E-08	**	5%
29	0	21	1.3E-05	**	0%
30	0	17	1.0E-04	**	0%
31	0	75	1.3E-17	**	0%
37	56	4	4.6E-11	**	93%
45	4	112	2.9E-23	**	3%
47	0	72	5.9E-17	**	0%
62	5	1	2.2E-01		83%
89	6	0	4.1E-02	*	100%
90	6	0	4.1E-02	*	100%
106	1	11	9.4E-03	*	8%
108	6	1	1.3E-01		86%
109	0	9	7.7E-03	*	0%
110	29	1	8.2E-07	**	97%
119	0	8	1.3E-02	*	0%
144	19	0	3.6E-05	**	100%
160	0	7	2.3E-02	*	0%
174	0	6	4.1E-02	*	0%
213	0	6	4.1E-02	*	0%
215	7	1	7.7E-02		88%
224	27	7	1.1E-03	*	79%
232	6	0	4.1E-02	*	100%
245	7	0	2.3E-02	*	100%
249	6	0	4.1E-02	*	100%
252	6	0	4.1E-02	*	100%
260	2	6	2.9E-01		25%
321	3	5	7.2E-01		38%
510	19	1	1.4E-04	**	95%

[a] Chi-squared statistical test for proportions performed with the prop.test() function, by testing the 50% proportion as null hypothesis.

Peptide numbers correspond to identification numbers in PubMLST *Neisseria* sequence typing database.

*p<0.05; **p<0.001.

Supplementary Table 2. Most frequent (in more than five isolates) Neisserial Heparin-Binding Antigen (NHBA) peptide identities in the panel of 3912 strains, by Meningococcal Antigen Typing System (MATS) coverage.

NHBA peptide	Number of isolates covered	Number of isolates not covered	Prop.test p-value[a]	Prop.test significance[a]	Proportion of covered
1	24	1	1.1E-05	**	96%
2	656	30	7.5E-126	**	96%
3	234	122	4.0E-09	**	66%
5	113	20	1.5E-15	**	85%
6	3	76	5.5E-16	**	4%
10	48	13	1.3E-05	**	79%
12	7	1	7.7E-02		88%
13	0	6	4.1E-02	*	0%
17	50	202	1.9E-21	**	20%
18	7	199	2.1E-40	**	3%
19	0	10	4.4E-03	*	0%
20	140	76	1.8E-05	**	65%
21	267	115	1.1E-14	**	70%
24	32	60	4.9E-03	*	35%
25	0	16	1.8E-04	**	0%
26	1	6	1.3E-01		14%
29	35	48	1.9E-01		42%
30	0	17	1.0E-04	**	0%
31	0	20	2.2E-05	**	0%
43	13	44	7.1E-05	**	23%
44	5	2	4.5E-01		71%
47	5	31	3.1E-05	**	14%
58	0	7	2.3E-02	*	0%
63	1	7	7.7E-02		13%
112	4	26	1.3E-04	**	13%
113	10	0	4.4E-03	*	100%
114	0	18	6.2E-05	**	0%
115	3	10	9.6E-02		23%
116	5	2	4.5E-01		71%
118	28	42	1.2E-01		40%
120	1	55	1.4E-12	**	2%
122	0	14	5.1E-04	**	0%
130	8	3	2.3E-01		73%
160	1	20	8.6E-05	**	5%
187	0	8	1.3E-02	*	0%
188	1	5	2.2E-01		17%
197	2	8	1.1E-01		20%
243	7	0	2.3E-02	*	100%
253	0	6	4.1E-02	*	0%
607	5	1	2.2E-01		83%

[a] Chi-squared statistical test for proportions performed with the prop.test() function, by testing the 50% proportion as null hypothesis.

Peptide numbers correspond to identification numbers in PubMLST *Neisseria* sequence typing database.

*p<0.05; **p<0.001.

Supplementary Table 3. Predicted strain coverage of 4CMenB by gMATS and MATS in national panels among gMATS predictable strains and the deviation between gMATS and MATS estimates.

Label	Panel: Country, years	Predictable (%)	MATS coverage (%)	gMATS coverage (%)	gMATS-MATS deviation (%)
1	UK, 2007-08	82.2	78.4	78.2	-0.2
2	UK, 2014-15	74.9	73.9	79.8	5.9
3	UK, 2015-16	70.7	81.3	82.9	1.6
4	Australia, 2007-11	88.1	79.7	85.2	5.5
5	USA, 2000-08	81.7	94.2	93.4	-0.8
6	Canada, 2006-09	84.1	69.7	76.5	6.8
7	Finland, 2010-14	88.3	84.9	90.6	5.7
8	Greece, 2008-10	82.7	93.0	95.3	2.3
9	Ireland, 2009-13	86.7	78.0	87.9	9.9
10	Poland, 2010-11	85.2	89.8	93.4	3.6
11	Germany, 2007-08	86.0	85.9	89.0	3.1
12	France, 2007-08	86.0	85.5	84.3	-1.2
13	France, 2013-14	79.7	79.6	84.7	5.1
14	Italy, 2007-08	70.4	97.4	100.0	2.6
15	Norway, 2007-08	80.5	93.9	93.9	0.0
16	Spain, 2009-10	67.7	70.9	61.1	-9.9

gMATS, genetic Meningococcal Antigen Typing System; MATS, Meningococcal Antigen Typing System.

Supplementary Table 4. Predicted strain coverage of 4CMenB by gMATS and MATS in all national panels and the deviation between gMATS and MATS estimates. The gMATS coverage point estimate was defined as the proportion of covered strains plus half the proportion of unpredictable strains, with ‘covered’ as the 95% lower limit and ‘covered’ plus ‘unpredictable’ as the 95% upper limit of the prediction.

Label	Panel: Country, years	gMATS coverage point estimate (%)	gMATS coverage lower limit estimate (%)	gMATS coverage upper limit estimate (%)	MATS coverage point estimate (%)	MATS coverage 95% lower limit (%)	MATS coverage 95% upper limit (%)	gMATS-MATS deviation (%)
1	UK, 2007-08	73.2	64	82	73.1	57	87	0.1
2	UK, 2014-15	72.3	60	85	66.9	52	81	5.4
3	UK, 2015-16	73.3	59	88	73.0	56	83	0.3
5	USA, 2000-08	85.4	76	95	91.2	72	96	-5.8
8	Greece, 2008-10	87.5	79	96	88.5	64	99	-1.0
14	Italy, 2007-08	85.2	70	100	87.0	70	93	-1.9
15	Norway, 2007-08	85.4	76	95	85.4	76	98	0.0
12	France, 2007-08	79.5	73	87	84.5	69	93	-5.0
10	Poland, 2010-11	87.0	80	94	83.7	79	91	3.3
11	Germany, 2007-08	83.6	77	91	81.5	69	92	2.0
7	Finland, 2010-14	85.8	80	92	78.3	72	88	7.5
4	Australia, 2007-11	81.0	75	87	74.6	61	86	6.3
13	France, 2013-14	77.6	67	88	70.3	60	80	7.3
9	Ireland, 2009-13	82.9	76	90	69.5	65	85	13.3
16	Spain, 2009-10	57.5	41	74	68.7	48	85	-11.2
6	Canada, 2006-09	72.3	64	80	66.2	46	78	6.1
17	Brazil, 2010				80.8	71	95	
18	Czech Republic, 2007-10				74.1	58	87	
19	Portugal, 2011-15				67.9	56	81	
20	Austria, 2008-11				67.8	56	73	

gMATS, genetic Meningococcal Antigen Typing System; MATS, Meningococcal Antigen Typing System.

Supplementary Table 5. Comparison of gMATS and other phenotype/genotype typing methods proposed to estimate 4CMenB (Bexsero, GSK) coverage [1, 2].

		gMATS	**BAST single antigen genotypes**	**Australia phenotype/genotype**
Strain panel	Number of countries	13 (Global)	2 (Europe)	1
	Number of isolates	3481	1052	278
fHbp	Covered	Peptides 1, 2, 4, 14, 15, 37, 89, 90, 110, 144, 224, 232, 245, 249, 252, 510	Peptides 1, 4, 13, 14, 15, 37, 232	All variant 1 peptides except 13
	Not covered	Peptide 213 and all variant 2 and 3 peptides	Not applicable	13 and all variant 2 and 3 peptides
NHBA	Covered	Peptides 1, 2, 3, 5, 10, 20, 21, 113, 243	Peptide 2	Peptides 1, 2
	Not covered	Peptides 6, 13, 17, 18, 19, 24, 25, 30, 31, 43, 47, 58, 112, 114, 120, 122, 160, 187, 253	Not applicable	All other peptides
NadA	Covered	Never	Any peptide	All variant NadA-1 and NadA-2/3 peptides
	Not covered	Always	Not applicable	All other peptides
OMV	Covered	PorA VR2 = 4	PorA VR1 = 7-2, PorA VR2 = 4	PorA VR1 = 7-2, PorA VR2 = 4
	Not covered	PorA VR2 ≠ 4	Not applicable	All other peptides

gMATS, genetic Meningococcal Antigen Typing System; BAST, Bexsero Antigen Sequence Type. fHbp, factor H binding protein; NHBA, Neisserial Heparin-Binding Antigen; NadA, *Neisseria* adhesin A; OMV, outer membrane vesicles; PorA VR1, porin A variant 1; PorA VR2, porin A variant 2.

[1] Brehony C, Rodrigues CMC, Borrow R, et al. Distribution of Bexsero® Antigen Sequence Types (BASTs) in invasive meningococcal disease isolates: Implications for immunisation. Vaccine 2016; 34:4690-7.

[2] Mowlaboccus S, Perkins TT, Smith H, et al. Temporal changes in BEXSERO® antigen sequence type associated with genetic lineages of *Neisseria meningitidis* over a 15-year period in Western Australia. PLoS One 2016;11:e0158315.