Supplementary table 1: Primer sequences used for amplification of FetA, fHbp, PorA and PorB

Primers		Sequence (5' - 3')[1]	Product length (bp)	Reference
fetA_Fw	Forward	CGGCGCAAGCGTATTCGG	1189	(1)
fetA_Rv	Reverse	CGCGCCCAATTCGTAACCGTG		
fHbp_Fw	Forward	GTCCGAACGGTAAATTATYGTG	895	(2)
fHbp_Rv	Reverse	CTATTCTGVGTATGACTAG		
PorA_Fw	Forward	AAACTTACCGCCCTCGTA	1100	(3)
PorA_Rv	Reverse	TTAGAATTTGTGGCGCAAACCGAC		
PorB2_Fw	Forward	GAAGTTTCTCGCGTAAAARAT	966	This study
PorB2_Rv	Reverse	CATGCTGGCAGTTTKTTC		
PorB3_Fw	Forward	GCGTAGAAACTTCCCGCTC	810	This study
PorB3_Rv	Reverse	CAGAAGTGCGTTTGG AGAAGT		

[1]IUPAC Nucleotide Designations: V = A, C or G; Y = C or T; R = A or G; K = G or T; Fw: Forward; Rv: Reverse

Supplementary table 2 : Primer sequences used for MLST

Primers		Sequence (5' - 3')	Product length (bp)	Reference
abcZ-Fw	Forward	TGTTCCGCTTCGACTGCCAAC	433	(2)
abcZ-Rv	Reverse	TCCCCGTCGTAAAAAACAATC		
adk-Fw	Forward	CCAAGCCGTGTAGAATCGTAAACC	465	(2)
adk-Rv	Reverse	TGCCCAATGCGCCCAATAC		
aroE-Fw	Forward	TTTGAAACAGGCGGTTGCGG	490	(2)
aroE-Rv	Reverse	CAGCGGTAATCCAGTGCGAC		
fumC-Fw	Forward	TCCCCGCCGTAAAAGCCCTG	465	(2)
fumC-Rv	Reverse	GCCCGTCAGCAAGCCCAAC		
gdh-Fw	Forward	CTGCCCCCGGGGTTTTCATCT	501	(2)
gdh-Rv	Reverse	TGTTGCGCGTTATTTCAAAGAAGG		
pdhC-Fw	Forward	CCGGCCGTACGACGCTGAAC	480	(2)
pdhC-Rv	Reverse	GATGTCGGAATGGGGCAAACA		
pgm-Fw	Forward	CTTCAAAGCCTACGACATCCG	450	(2)
pgm-Rv	Reverse	CGGATTGCTTTCGATGACGGC		

Fw: Forward; Rv: Reverse

Supplementary table 3: Primer sequences used for amplification and sequencing

Primers		Sequence (5' - 3') [1]	Reference
fetA S12	Forward	TTCAACTTCGACAGCCGCCTT	(1)
fetA S15	Reverse	TTGCAGCGCGTCRTACAGGCG	
fHbpP1	Forward	GTCCGAACGGTAAATTATYGTG	(2)
fHbpP2	Reverse	CTATTCTGVGTATGACTAG	
PorA_Fw	Forward	AAACTTACCGCCCTCGTA	This study
PorA_Rv	Reverse	TTAGAATTTGTGGCGCAAACCGAC	
PorB2_Fw	Forward	GAAGTTTCTCGCGTAAAARAT	This study
PorB2_Rv	Reverse	CATGCTGGCAGTTTKTTC	
PorB3_Fw	Forward	GCGTAGAAACTTCCCGCTC	This study
PorB3_Rv	Reverse	CAGAAGTGCGTTTGGAGAAGT	
abcZ-S1A	Forward	AATCGTTTATGTACCGCAGR	(2)
abcZ-S2	Reverse	GAGAACGAGCCGGGATAGGA	
adk-S1A	Forward	AGGCWGGCACGCCCTTGG	(2)
adk-S2	Reverse	CAATACTTCGGCTTTCACGG	
aroE-S1A	Forward	GCGGTCAAYACGCTGRTK	(2)
aroE-S2	Reverse	ATGATGTTGCCGTACACATA	(2)
fumC-S1	Forward	TCCGGCTTGCCGTTTGTCAG	(2)
fumC-S2	Reverse	TTGTAGGCGGTTTTGGCGAC	(2)
gdh-S3	Forward	CCTTGGCAAAGAAAGCCTGC	(2)
gdh-S4C	Reverse	RCGCACGGATTCATRYGG	(2)
pgm-S1	Forward	CGGCGATGCCGACCGCTTGG	(2)
pgm-S2A	Reverse	GGTGATGATTTCGGTYGCRCC	(2)
pdhC-S1	Forward	TCTACTACATCACCCTGATG	(2)
pdhC-S2	Reverse	ATCGGCTTTGATGCCGTATTT	(2)

[1]IUPAC Nucleotide Designations: V = A, C or G; Y = C or T; R = A or G; K = G or T

Supplementary table 4: Association of *fHbp* genotype with the virulence of *N. meningitidis*

fHbp genotype	All Isolates	From Patients	From Carriers	P value	OR (95%CI)
fHbp Novartis Variant Group				NS	ND
1	2 (1.9)	1 (4)	1 (1.2)		
2	104 (98.1)	24 (96)	80 (98.8)		
fHbp Sub Family				NS	ND
A	1 (0.9)	0	1 (1.2)		
A07	5 (4.7)	1 (4)	4 (4.9)		
A20	8 (7.5)	1 (4)	7 (8.6)		
A22	62 (58.5)	18 (72)	44 (54.3)		
A24	2 (1.9)	0	2 (2.5)		
A32	26 (24.5)	4 (16)	22 (27.2)		
B	2 (1.9)	1 (4)	1 (1.2)		
fHbp Modul Group				NS	ND
III	31 (29.2)	5 (20)	26 (32.1)		
IV	72 (67.9)	19 (76)	53 (65.4)		
ND	3 (2.8)	1 (4)	2 (2.5)		

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3. Taha MK, Alonso JM, Cafferkey M, Caugant DA, Clarke SC, Diggle MA, et al. Interlaboratory comparison of PCR-based identification and genogrouping of Neisseria meningitidis. J Clin Microbiol. 2005;43(1):144-9.