

Supplemental Material

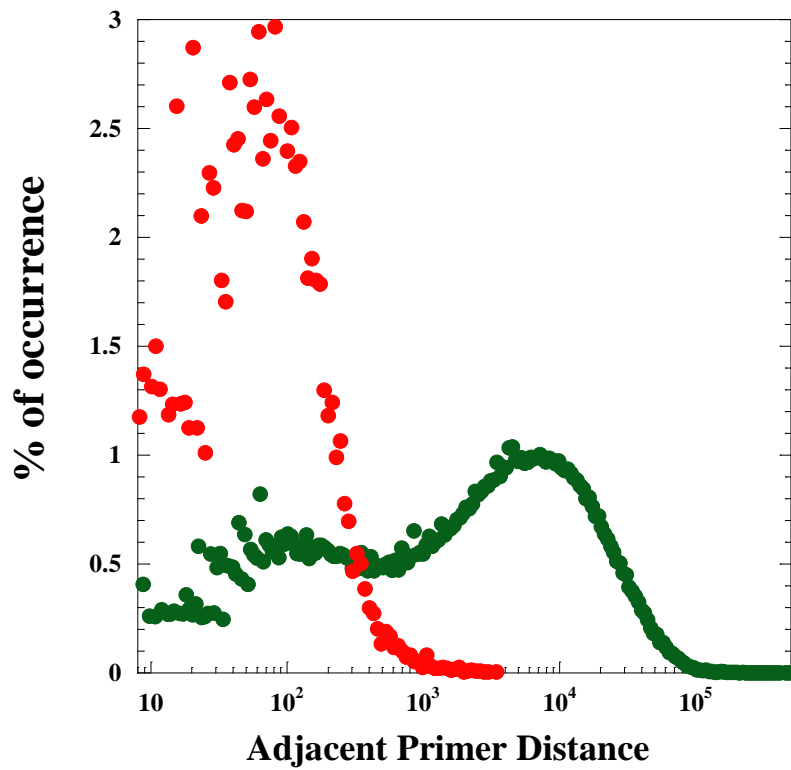


Figure S1. Distribution of distances between adjacent heptamers bound to Nm (red) or human (green) DNA. Shorter inter-primer distances indicate higher density of binding to the DNA.

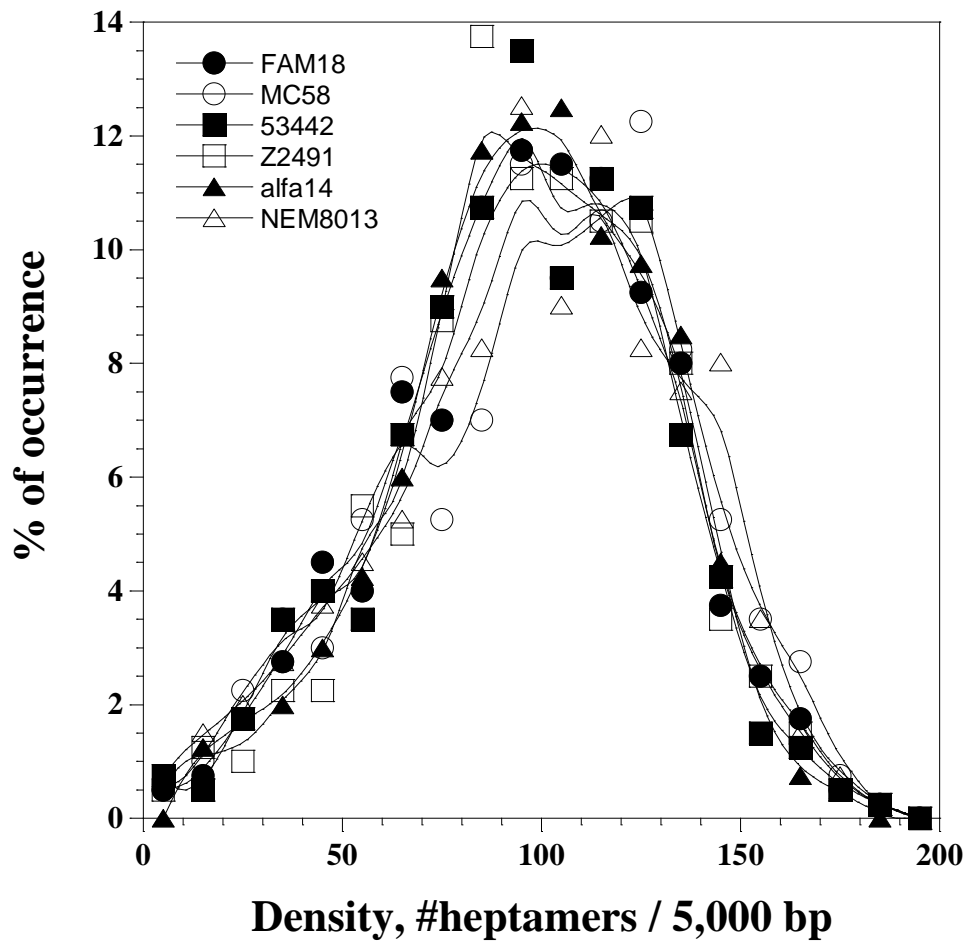


Figure S2. Density distribution of 25 selected heptamers on multiple complete Nm genomes.

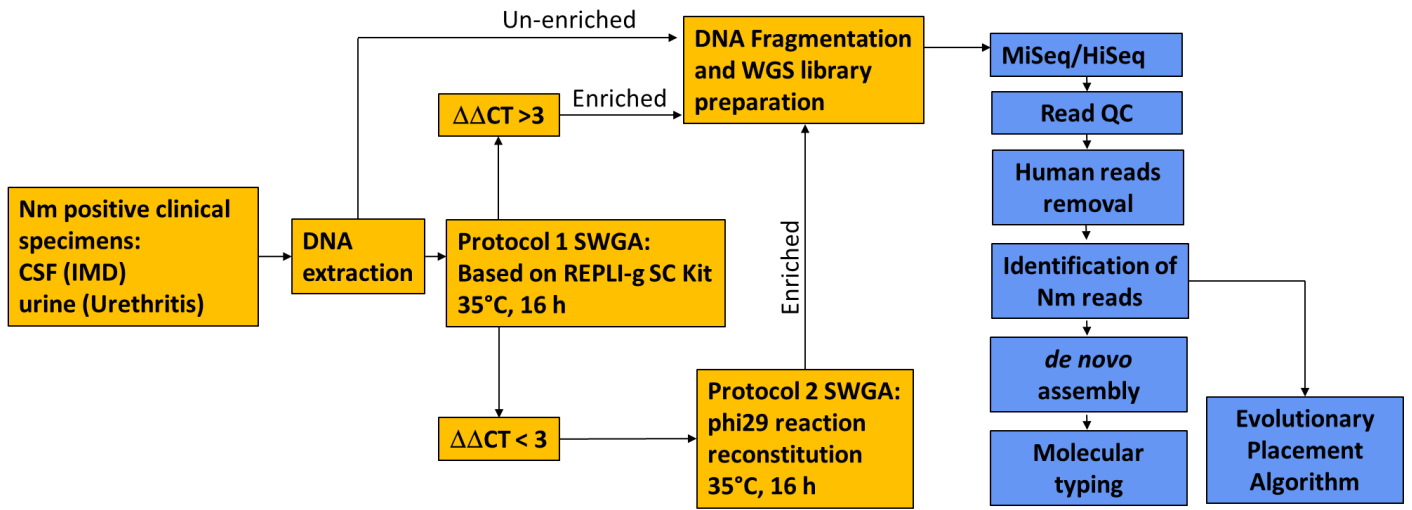


Figure S3. Scheme of the workflow used in the study. Orange boxes - bench work; Blue boxes – data analysis

Table S1: Primers used for selective whole genome amplification.

Heptamer sequence	No. of Nm DNA binding sites	No. of Human DNA binding sites	Nm DNA binding bias score
TTCGGCG	1,500	7,863	256
CGCCGAT	1,127	6,306	240
GTCGGCG	1,326	12,429	143
CGGCGAA	1,219	11,702	140
TCGGCGG	1,615	17,251	125
AACGGCG	1,200	13,852	116
CGGCGGT	1,460	17,293	113
CGACGGC	1,141	13,689	112
AACGCCG	1,182	14,483	109
ACGGCGG	1,597	20,873	103
GACGGCG	1,553	21,078	99
CGGCGCG	1,931	29,762	87
CGTCGCC	1,073	17,350	83
CGTGCCG	1,106	17,898	83
GCGGCGA	1,182	19,363	82
TCCGCCG	1,248	20,634	81
GACGGCA	2,973	50,481	79
TGCGCCG	1,226	21,125	78
GCGGCAA	2,077	36,333	77
TGCCGCG	1,033	18,548	75
TGCGCGG	1,087	19,724	74
ACGGCAT	2,542	49,591	69
GCCGCCG	3,283	69,500	63
TGCGGCG	1,130	24,057	63
TTGCCGA	1,907	41,873	61
Total	38,718	593,058	

Table S2. Primers and probes used for 7 gene markers used in the study

Marker	Position in Nm Genome ^a	Primer Name	Sequence ^b	Final nM
<i>sdhA</i>	925,196	Forward	AAGTAATTTGGGGGTAAGTATGGG	300
		Reverse	CGGATTTGGATAATTGGAGGGC	300
		Probe	TTGTCGGCGGTGGTGGTGCAGGTTT	100
NEIS2381 ^c	743,614	Forward	CCGCTTCCAAATTCTGCAT	300
		Reverse	TTCCACTCCTCGACAATCCT	300
		Probe	CCGCCGCCGCTT"TCGTCTTTTTTACTT	100
NEIS0417	436,233	Forward	GGCGGAATAAACACACAATGAG	300
		Reverse	GAGCAAAGCGACCGCAAA	300
		Probe	AGCTGAAAAAAGCGAACCCACGGACGGGAAA	100
NEIS2065	2,119,668	Forward	CGCGGGGTTTCCATGTCAA	300
		Reverse	CGCTGGCTGGTGCTGAATAA	300
		Probe	AGTGCGCGTT"TTGGGCTTCTTCTCGT	100
NEIS1699	1,733,621	Forward	CCCATACTGTTCTCCCCGT	300
		Reverse	ATTTTACCGTTGCCCCCAT	300
		Probe	CGCGCTTTTGCG"TTTCGCTGTCCGTT	100
<i>sodC</i>	1,325,109	Forward	GCACACTTAGGTGATTTACCTGCAT	300
		Reverse	CCACCCGTGTGGATCATAATAGA	600
		Probe	CATGATGGCACAGCAACAAATCCTGTTT	100
RNase P gene ^d (<i>rnp</i>)		Forward	CCAAGTGTGAGGGCTGAAAAG	400
		Reverse	TGTTGTGGCTGATGAACTATAAAAAGG	400
		Probe	CCCCAGTCTCTGTCAGCACTCCCTTC	100

^a Position of 5' end of forward primer binding site on the FAM18 Nm reference genome

^b All probes contain FAM on 5' and BHQ1 on 3' except those containing BHQ1 on internal thymines designated as "T". In the latter cases probes contain SpC6 on 3'.

^c 'NEIS' markers are defined according to PubMLST Neisseria database.

^d *Homo sapiens* ribonuclease P/MRP subunit p30 (RPP30), transcript variant 2, mRNA; NCBI Reference Sequence: NM_006413.4

Table S3. Expanded data on analysis of unenriched and SWGA-enriched specimens by rt-PCR and sequencing

Specimen ID	Protocol	rt-PCR					No. Nm reads (%) ^a		Fold Enrichment ^b	% of genome with ≥ 10 -fold coverage depth	
		Ct _{sodC} unenriched	Ct _{sodC} enriched	Δ Ct _{sodC}	Δ Ct _{rnp}	$\Delta\Delta$ Ct	Unenriched	Enriched		Unenriched	Enriched
Ur-1	1	27.4	15.9	11.5	-1.1	12.6	22,840(0.4)	1,964,728(66.1)	165	1.8	35.5
Ur-2	2	28.8	10.9	17.9	0.9	17.0	4,706(0.1)	4,077,546(90.5)	905	0.03	97.6
Ur-3	1	28.6	13.2	15.5	-0.8	16.3	2,648(0.05)	1,589,045(67.3)	1346	0.01	51.8
Ur-4	2	28.1	16.9	11.1	-5.2	16.3	1,584(0.03)	2,352,295(57.2)	1907	<0.01	48.9
Ur-5	1	25.5	9.9	15.6	0	15.6	14,685(0.4)	1,314,987(77.7)	194	0.6	97.6
Ur-6	2	29.0	18.8	10.2	1.8	8.4	34,454(0.7)	48,235(1.1)	2	7.4	14.1
Ur-7	1	24.5	10.0	14.5	-1.4	15.9	15,547(0.4)	824,190(61.9)	155	0.6	93.3
Ur-8	1	28.3	12.3	16.1	-1.8	17.9	54,350(1.6)	1,137,691(65.9)	41	36.9	40.0
Ur-9	1	18.8	15.5	3.3	-3.3	6.6	710(0.02)	243,875(3.7)	185	<0.01	89.6
Ur-10	1	20.2	14.8	5.4	-3.4	8.8	1,150(0.04)	148,803(6.2)	155	<0.01	76.3
Ur-11	2	30.0	12.8	17.2	10.4	6.8	2,452(0.09)	679,812(21.1)	234	<0.01	90.0
Ur-12	1	30.8	23.3	7.6	-0.2	7.8	2,156(0.04)	81,622(2.2)	55	0.01	3.0
CSF-1	1	22.4	11.9	10.5	3.2	7.3	29,320(1)	734,365(33.3)	33	7.4	93.5
CSF-2	1	18.6	16.7	1.9	1.5	0.4	11,466(0.2)	23,543(0.7)	4	0.4	9.1
CSF-3	1	19.5	17.8	1.7	1.2	0.5	39,292(0.9)	30,744(1)	1	20.7	16.9
CSF-4	1	29.4	16.9	12.5	7	5.5	6,252(0.2)	149,523(4.5)	23	0.04	74.9
CSF-5	1	23.9	12.7	11.2	5.1	6.1	12,633(0.4)	300,389(19.7)	49	0.7	91.8
CSF-6	1	19.4	15.0	4.4	-0.4	4.8	7,337(0.3)	275,393(6.8)	23	0.1	90.8
CSF-7	1	19.8	10.9	9.0	3.8	5.2	87,433(2.7)	1,186,651(61)	23	77.7	97.9
CSF-8	2	19.9	18.1	1.8	2.4	-0.6	26,124(0.9)	1,378,208(27.4)	30	3.6	56.0
CSF-9	1	22.4	13.0	9.4	-0.2	9.6	16,934(0.5)	1,359,812(65.7)	131	1.1	96.0
CSF-10	2	17.3	11.4	5.9	2.8	3.1	68,024(2.4)	496,848(22.6)	9	50.0	85.8
CSF-11	1	24.6	17.0	7.7	1.9	5.8	1,908(0.05)	318,036(15.6)	312	<0.01	83.7
CSF-12	1	21.2	11.0	10.2	-5.6	15.8	11,344(0.3)	1,694,167(86.5)	288	0.3	97.8

^aThe numbers represent Nm read pairs and their percentage (in parentheses) of total read pairs obtained from the specimen.

^bFold enrichment is equal to % of enriched Nm reads/% of unenriched Nm reads.

Table S4. Full molecular typing results for assembled specimen sequence data

Spec ^a	Genome assembly size (kb)	No. cgMLST loci identified (% of the total)	cgMLST Accuracy ^b %	Typing Accuracy	PorA VR1	PorA VR2	FetA	PorB	FHbp	NhbA	NadA	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	MLST
<u>Ur-1</u>	1,100	209(13)	NA	NA	-	10-8	F3-6	-	-	-	-	-	-	N	-	-	-	-	-
<u>Ur-6</u>	1,495	410(25.5)	79.7	6/7	5-1	10-8	F3-6	-	-	-	2	2	-	-	-	8	N ^e	-	-
<u>Ur-8</u>	1,926	1,262(78.6)	93.8	12/13	5-1	10-8	F3-6	2-2	896	20	-	2	3	4	3	N*	4	6	New ST*; CC11
<u>Ur-1</u>	866	584(36.4)	NA	NA	-	-	F3-6	-	-	20	-	2	-	-	-	8	-	-	-
<u>Ur-2</u>	2,092	1,561(97.3)	99.2	14/14	5-1	10-1	F3-6	2-2	896	20	2	2	3	4	3	8	4	6	ST-11; CC11
<u>Ur-3</u>	1,249	842(52.5)	90.3	5/5	-	-	F3-6	-	-	-	-	2	-	4	-	-	4	6	-
<u>Ur-4</u>	1,115	776(48.3)	92.1	5/5	-	-	F3-6	-	-	-	2	-	3	4	3	-	-	-	-
<u>Ur-5</u>	2,095	1,562(97.3)	99.6	14/14	5-1	10-1	F3-6	2-2	896	20	2	2	3	4	3	8	4	6	ST-11; CC11
<u>Ur-6</u>	769	365(22.7)	86.5	4/5	5-1	10-8	-	-	-	20	-	-	-	4	927*	-	-	-	-
<u>Ur-7</u>	2,043	1,519(94.6)	98.5	13/13	-	10-8	F3-6	2-2	896	20	2	2	3	4	3	8	4	6	ST-11; CC11
<u>Ur-8</u>	994	634(39.5)	90.8	5/6	-	-	F3-6	-	896	-	2	-	-	-	-	N*	4	6	-
<u>Ur-9</u>	2,044	1,535(95.6)	97.7	13/13	5-1	10-8	F3-6	-	896	20	2	2	3	4	3	8	4	6	ST-11; CC11
<u>Ur-10</u>	2,015	1,482(92.3)	95.7	14/14	5-1	10-8	F3-6	2-2	896	20	2	2	3	4	3	8	4	6	ST-11; CC11
<u>Ur-11</u>	1,980	1,474(91.8)	98.2	14/14	5-1	10-8	F3-6	2-2	896	20	2	2	3	4	3	8	4	6	ST-11; CC11
<u>CSF-1</u>	1,848	874(54.5)	NA	NA	5	2	F1-1	2-2	613	- ^c	6	672	3	-	-	8	-	-	-
<u>CSF-3</u>	1,988	1,235(76.9)	NA	NA	5	2	N ^d	2-2	613	-	6	-	3	-	-	8	-	6	-
<u>CSF-5</u>	1,257	343(21.4)	NA	NA	21-15	16	-	-	-	-	-	-	-	-	-	-	-	-	-
<u>CSF-7</u>	2,080	1,527(95.1)	NA	NA	21-15	16	F1-7	3-463	27	-	-	12	11	4	643	187	2	120	ST-12446; CC10217
<u>CSF-8</u>	1,476	452(28.2)	NA	NA	5	2	F1-1	-	-	-	-	2	3	4	-	8	4	6	-
<u>CSF-10</u>	2,024	1,413(88)	NA	NA	5-1	10-1	F1-31	2-231	74	359	-	10	3	15	7	5	41	31	ST-181; CC181
<u>CSF-1</u>	2,058	1,554(96.8)	NA	NA	5	2	F1-1	2-2	613	96	6	2	3	4	3	8	4	6	ST-11; CC11
<u>CSF-2</u>	1,641	828(51.6)	NA	NA	-	2	-	-	-	96	6	2	-	4	-	8	4	6	-
<u>CSF-3</u>	1,664	894(55.7)	NA	NA	5	2	F1-1	2-61	-	96	N	2	3	4	3	8	4	6	ST-11; CC11
<u>CSF-4</u>	1,882	1,377(85.8)	NA	NA	5-1	10-1	-	-	74	359	-	10	3	15	7	5	41	31	ST-181; CC181
<u>CSF-5</u>	2,010	1,517(94.5)	NA	NA	21-15	16	F1-7	3-463	27	-	-	12	11	4	643	187	2	120	ST-12446; CC10217
<u>CSF-6</u>	2,040	1,518(94.6)	NA	NA	21-15	16	F1-7	3-463	27	798	-	12	5	4	643	187	2	120	ST-10217; CC10217
<u>CSF-7</u>	2,036	1,553(96.8)	NA	NA	21-15	16	F1-7	3-463	27	798	-	12	11	4	643	187	2	120	ST-12446; CC10217
<u>CSF-8</u>	1,696	164(10.2)	NA	NA	-	2	-	N	-	-	-	2	-	-	N	-	4	-	-
<u>CSF-9</u>	2,064	1,512(94.2)	NA	NA	5-1	10-1	F1-31	2-231	74	359	-	10	3	15	7	5	41	31	ST-181; CC181
<u>CSF-10</u>	2,032	1,369(85.3)	NA	NA	5-1	10-1	F1-31	-	74	N	-	10	3	15	7	5	N	31	New ST; CC181
<u>CSF-11</u>	1,901	1,391(86.7)	NA	NA	5	2	F1-1	2-2	613	96	6	2	3	4	3	8	4	6	ST-11; CC11
<u>CSF-12</u>	2,092	1,570(97.8)	NA	NA	5	2	F1-1	2-2	613	96	6	2	3	4	3	8	4	6	ST-11; CC11

- a. Spec – Specimen ID; Underlined - enriched specimens; non - underlined-non-enriched specimens. No assembly was produced for 15 unenriched and 1 enriched specimen.
- b. Percentage of identified cgMLST loci or individual typing loci that are identical to those from the matching isolate. Available only for urine specimens
- c. Dash indicates that an allele could not be identified in the assembled specimen sequence data
- d. “N” indicates a new allele, not listed in PubMLST allele list
- e. Asterisk indicates that a different allele was identified in the matching isolate

Table S5. Evolutionary tree distance (substitutions per site) between Nm sequences from urine specimens and isolates obtained from the same urethritis case.

Specimen	Unenriched	Enriched
Ur-1	2.7×10^{-3}	1.8×10^{-4}
Ur-3	- ^a	0
Ur-4	-	2.2×10^{-4}
Ur-5	6.8×10^{-4}	0
Ur-6	2.1×10^{-4}	8.4×10^{-4}
Ur-7	2.9×10^{-3}	2.7×10^{-6}
Ur-8	0	0
Ur-9	-	9.3×10^{-5}
Ur-10	-	0
Ur-11	2.4×10^{-4}	1.1×10^{-5}
Ur-12	-	1.2×10^{-3}

a. Dash indicates insufficient data to perform EPA

Table S6. Molecular typing of Nm in specimens from Togo and Burkina-Faso meningitis outbreak, 2019

Spec ^a	Seq method ^b	Ct sodC	Genome assembly size (kb)	No. cgMLST loci identified	PorA VR1	PorA VR2	FetA	PorB	FHbp	NhbA	NadA	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	MLST
BF_1	Unenr	17	2,136,395	1,559	21-15	16	F1-7	3-463	27	798	- ^d	12	5	4	643	187	2	120	ST-10217; CC10217
BF_2	Unenr	19	2,132,672	1,556	21-15	16	F1-7	3-463	27	798	-	12	5	4	643	187	2	120	ST-10217; CC10217
BF_3	Unenr	17	2,132,682	1,557	21-15	16	F1-7	3-463	27	798	-	12	5	4	643	187	2	120	ST-10217; CC10217
BF_4	Unenr	16	2,064,493	1,560	21-15	16	F1-7	3-463	27	798	-	12	5	4	643	187	2	120	ST-10217; CC10217
BF_5	Unenr	16	2,063,009	1,564	21-15	16	F1-7	3-463	27	798	-	12	5	4	643	187	2	120	ST-10217; CC10217
BF_6	Unenr	19	2,052,439	1,559	21-15	16	F1-7	3-463	27	798	-	12	5	4	643	187	2	120	ST-10217; CC10217
BF_7	Unenr	18	2,064,961	1,556	21-15	16	F1-7	3-463	27	798	-	12	5	4	643	187	2	120	ST-10217; CC10217
BF_8	Unenr	19	2,069,327	1,563	21-15	16	F1-7	3-463	27	798	-	12	5	4	643	187	2	120	ST-10217; CC10217
BF_9	Unenr	16	2,069,218	1,560	21-15	16	F1-7	3-463	27	798	-	12	5	4	643	187	2	120	ST-10217; CC10217
BF_10	Unenr	17	2,093,455	1,553	21-15	16	F1-7	3-463	27	798 ^f	-	12	5	4	643	187	2	120	ST-10217; CC10217
BF_11	SWGA_1	21	2,104,298	1,530	21-15	16	F1-7	3-463	27	798	-	12	5	4	643	187	2	120	ST-10217; CC10217
BF_12	SWGA_1	30	2,059,934	1,509	21-15	16	F1-7	3-463	27	798	-	12	5	4	643	187	2	120	ST-10217; CC10217
BF_13^c	SWGA_1	25	1,351,960	534	21-15	16	F1-7	-	27	-	-	New^e	-	4	-	187	2	120	-
BF_14	SWGA_1	30	2,133,478	1,535	21-15	16	F1-7	3-463	27	798	-	12	5	4	643	187	2	120	ST-10217; CC10217
BF_15	SWGA_1	22	2,064,379	1,520	21-15	16	F1-7	3-463	27	798	-	-	5	4	643	187	2	120	-
BF_16	SWGA_1	33	2,095,986	1,551	21-15	16	F1-7	3-463	27	798	-	12	5	4	643	187	2	120	ST-10217; CC10217
BF_17	SWGA_1	26	2,085,832	1,549	21-15	16	F1-7	3-463	27	798	-	12	5	4	643	187	2	120	ST-10217; CC10217
Togo_1	Unenr	17	2,121,115	1,552	21-15	-	F1-7	3-463	111	798	-	12	5	4	7	187	2	120	ST-9367; CC10217
Togo_2	SWGA_1	20	2,508,337	1,222	21-15	-	F1-7	3-463	111	798	-	12	5	4	7	187	-	120	-
Togo_3	SWGA_1	33	1,081,654	442	-	-	-	-	-	-	-	-	-	-	7	-	-	120	-
Togo_4	SWGA_1	25	2,084,690	1,517	21-15	-	F1-7	3-463	111	798	-	12	5	4	7	187	2	120	ST-9367; CC10217
Togo_5	SWGA_1	32	1,077,209	410	-	-	-	-	-	-	-	-	-	-	-	187	-	120	-
Togo_6	SWGA_1	30	1,923,570	1,375	21-15	-	F1-7	-	111	-	-	12	5	4	7	187	2	120	ST-9367; CC10217
Togo_7	SWGA_1	22	2,114,107	1,539	21-15	-	F1-7	3-463	111	798	-	12	5	4	7	187	2	120	ST-9367; CC10217
Togo_8	SWGA_1	26	2,153,980	1,236	21-15	-	F1-7	3-463	111	798	-	12	5	4	7	187	2	120	ST-9367; CC10217
Togo_9	SWGA_1	25	2,114,641	1,533	21-15	-	F1-7	3-463	111	798	-	12	5	4	7	187	2	120	ST-9367; CC10217
Togo_10	SWGA_2	26	2,210,580	1,263	21-15	-	F1-7	-	-	-	-	12	5	4	New	187	2	120	New
Togo_11	SWGA_1	22	1,679,000	952	21-15	-	F1-7	-	111	798	-	-	-	4	7	-	2	120	-
Togo_12	SWGA_1	23	2,116,610	1,540	21-15	-	F1-7	3-463	111	798	-	12	5	4	7	187	2	120	ST-9367; CC10217
Togo_13	SWGA_1	28	2,003,579	1,413	21-15	-	F1-7	3-463	111	-	-	12	-	4	7	187	2	120	-
Togo_14	SWGA_1	27	2,014,369	1,424	-	-	F1-7	3-463	111	798	-	12	-	4	7	187	2	-	-
Togo_15	SWGA_1	21	2,107,985	1,544	21-15	-	F1-7	3-463	111	798	-	12	5	4	7	187	2	120	ST-9367; CC10217
Togo_16	SWGA_2	26	842,874	159	-	-	F1-7	-	-	-	-	-	-	-	-	-	-	-	-
Togo_17	SWGA_1	23	2,365,275	1,377	5-1	10-1	F1-7	2-231	111	New	-	10	3	New	7	117	41	8	New
Togo_18	SWGA_1	22	1,828,557	1,224	21-15	-	F1-7	-	111	-	-	12	New	4	7	187	2	120	New
Togo_19	SWGA_1	20	2,061,090	1,557	21-15	-	F1-7	3-463	111	798	-	12	5	4	7	187	2	120	ST-9367; CC10217

^aSpec – Specimen name: BF – Burkina-Faso specimens; Togo – Togo specimens

^bSeq method – Sequencing method: SWGA_1 – protocol 1; SWGA_2 – protocol 2

^cRed symbols – Specimens which did not pass accuracy cutoff of 1,400 cgMLST identified

^dNot enough information to identify locus or MLST

^eNew locus or MLST

^fNhba marker for this specimen was determined from the corresponding SWGA enriched back up of the specimen

Table S7. Serogroup data of Nm in specimens from Togo and Burkina-Faso meningitis outbreak, 2019

Spec ^a	Seq method ^b	Ct sodC	Capsular genes identified	Capsule Locus Integrity Status	Backbone type	Final Interpretation
BF_1	Unenr	17	csc,cssA,cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	All essential capsule genes intact and present	C	C
BF_2	Unenr	19	csc,cssA,cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	All essential capsule genes intact and present	C	C
BF_3	Unenr	17	csc,cssA,cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	All essential capsule genes intact and present	C	C
BF_4	Unenr	16	csc,cssA,cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	All essential capsule genes intact and present	C	C
BF_5	Unenr	16	csc,cssA,cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	All essential capsule genes intact and present	C	C
BF_6	Unenr	19	csc,cssA,cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	All essential capsule genes intact and present	C	C
BF_7	Unenr	18	csc,cssA,cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	All essential capsule genes intact and present	C	C
BF_8	Unenr	19	csc,cssA,cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	All essential capsule genes intact and present	C	C
BF_9	Unenr	16	csc,cssA,cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	All essential capsule genes intact and present	C	C
BF_10	Unenr	17	csc,cssA,cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	All essential capsule genes intact and present	C	C
BF_11	SWGA_1	21	csc,cssA,cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	csc and cssA fragmented; cssB disrupted by Insertion	C	Inconclusive
BF_12	SWGA_1	30	ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	ctrA fragmented	Unclear	NG
BF_13 ^c	SWGA_1	25	csc,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	csc, ctrA, ctrB, ctrC, ctrD, ctrE, ctrF and tex - fragmented; cssA, cssB and cssC - missing	C	NG
BF_14	SWGA_1	30	cssB,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	ctrA fragmented	Unclear	NG
BF_15	SWGA_1	22	cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	Capsule genes present shared across multiple Serogroups	Unclear	NG
BF_16	SWGA_1	33	csc,cssA,cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	csc fragmented	C	Inconclusive
BF_17	SWGA_1	26	csc,cssA,cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	csc, ctrA and ctrB - fragmented	C	Inconclusive
Togo_1	Unenr	17	csc,cssA,cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	All essential capsule genes intact and present	C	C
Togo_2	SWGA_1	19	cssA,cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	cssA, cssB, cssC, ctrE and tex - fragmented	Unclear	NG
Togo_3	SWGA_1	33	ctrC,ctrD,ctrF,tex	ctrC and ctrD - fragmented	Unclear	NG
Togo_4	SWGA_1	25	cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	cssB, cssC and ctrA - fragmented	Unclear	NG
Togo_5	SWGA_1	32	cssC,ctrA,ctrB,ctrC,ctrD,ctrF,tex	cssC, ctrA, ctrB, ctrC, ctrD, ctrF and tex - fragmented	Unclear	NG
Togo_6	SWGA_1	30	cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	cssB and cssC - fragmented; ctrA disrupted by insertion	Unclear	NG
Togo_7	SWGA_1	22	csc,cssA,cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	csc - fragmented	C	Inconclusive
Togo_8	SWGA_1	26	csc,cssA,cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	csc, cssA, cssA, cssB, cssC and tex - fragmented	C	Inconclusive
Togo_9	SWGA_1	25	csc,cssA,cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	csc - fragmented	C	Inconclusive
Togo_10	SWGA_2	26	csc,cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	csc, cssB, cssC, cssC, ctrB, ctrC, ctrE and tex - fragmented; cssA - missing	C	NG
Togo_11	SWGA_1	22	cssB,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	cssB, ctrA, ctrB,ctrC and tex - fragmented	Unclear	NG
Togo_12	SWGA_1	23	csc,cssA,cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	All essential capsule genes intact and present	C	C
Togo_13	SWGA_1	28	csc,cssA,cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	csc - fragmented	C	Inconclusive
Togo_14	SWGA_1	27	cssA,cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	cssA, ctrA - fragmented	Unclear	NG
Togo_15	SWGA_1	21	csc,cssA,cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	All essential capsule genes intact and present	C	C
Togo_16	SWGA_2	26	ctrE,tex	ctrE and tex - fragmented	Unclear	NG
Togo_17	SWGA_1	23	cssA,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	cssA and cssC - fragmented	Unclear	NG
Togo_18	SWGA_1	22	csc,cssA,cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	csc, cssA, cssB, cssC, ctrA, ctrB and ctrD - fragmented	C	Inconclusive
Togo_19	SWGA_1	20	csc,cssA,cssB,cssC,ctrA,ctrB,ctrC,ctrD,ctrE,ctrF,tex	All essential capsule genes intact and present	C	C

^aSpec - Specimen name: BF – Burkina-Faso specimens; Togo – Togo specimens

^bSeq method - Sequencing method: SWGA_1 – protocol 1; SWGA_2 – protocol 2

^cRed symbols - Specimens which did not pass accuracy cutoff of 1,400 cgMLST identified

Green highlighting - specimens having all essential capsule genes intact and present

Yellow highlighting – specimens having all essential capsule genes present but not intact