

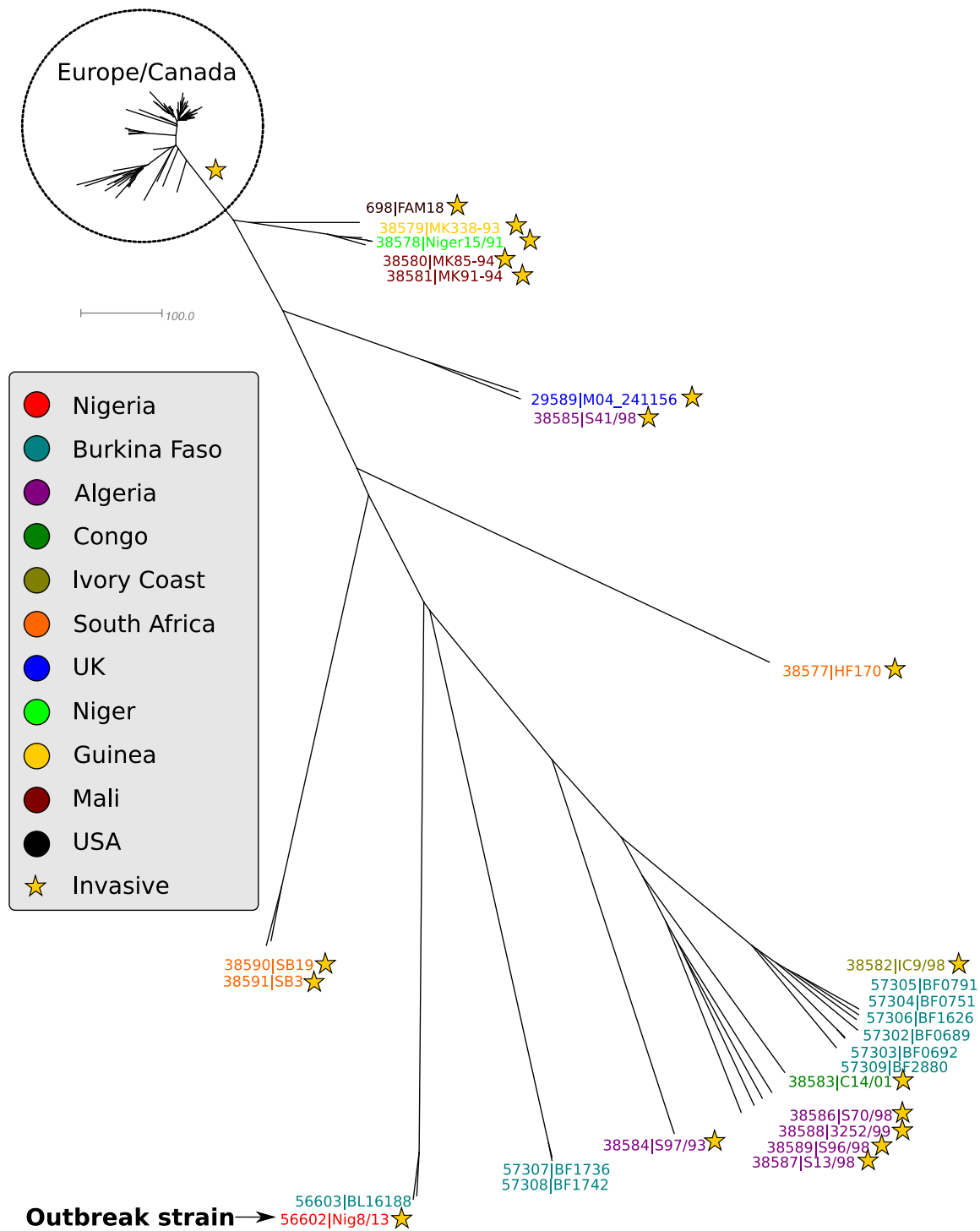
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2464_15	2015	Niger	Niamey	diseased	C	21-15,16	10217	102	206.5	ERS2071210	39218
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MM_B_4593	2017	Nigeria	Sokoto	diseased	C	21-15,16	10217	94	98.0	ERS2071239	56544
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SK307	2017	Nigeria	Sokoto	diseased	C	21-15,16	10217	125	129.3	ERS2071313	56568
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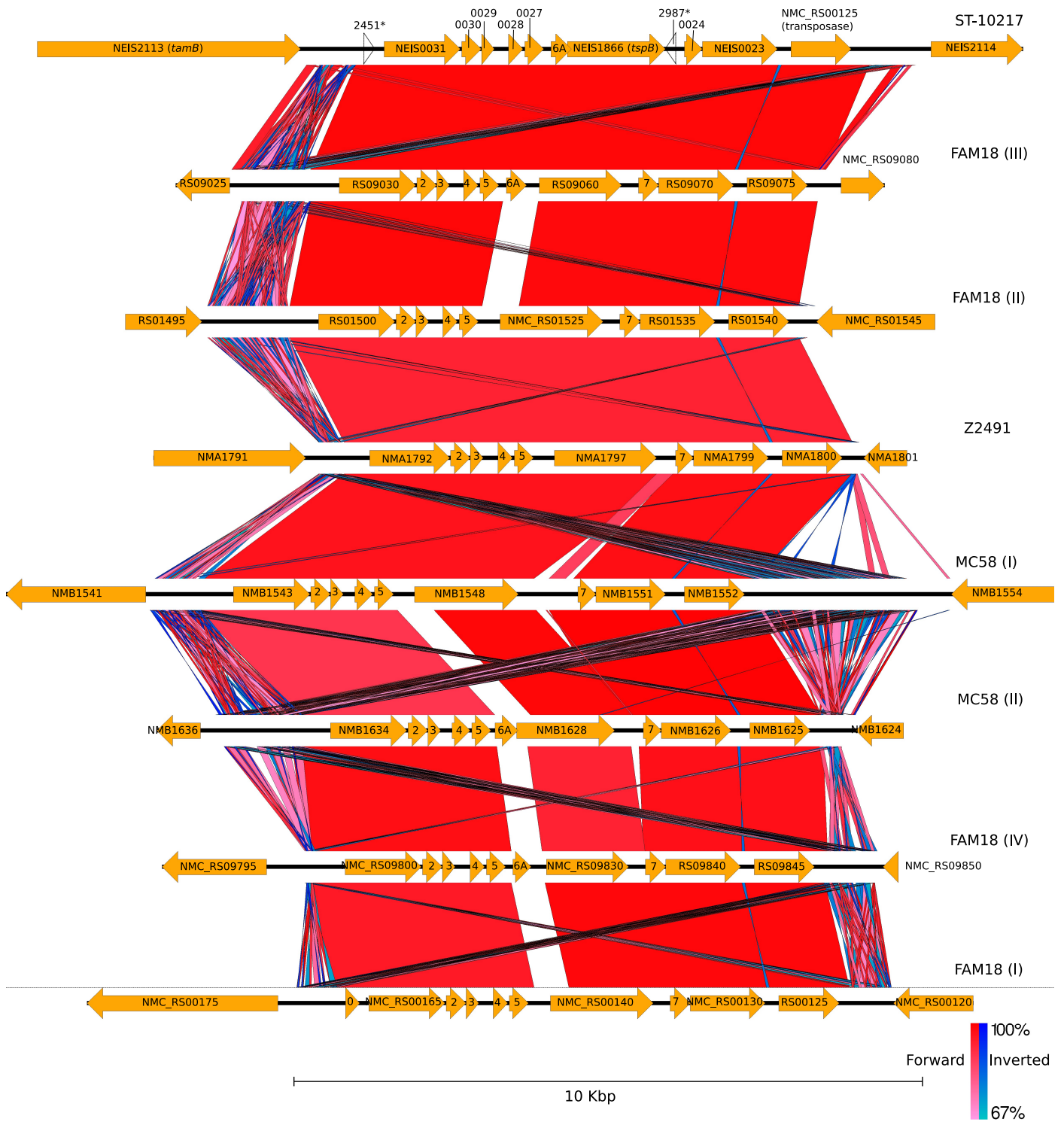
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SK327	2017	Nigeria	Sokoto	diseased	C	21-15,16	10217	96	105.6	ERS2071317	56572
SK336	2017	Nigeria	Sokoto	diseased	C	21-15,16	10217	96	93.0	ERS2071318	56573
SK352	2017	Nigeria	Sokoto	diseased	C	21-15,16	10217	87	141.1	ERS2071319	56574
SK356	2017	Nigeria	Sokoto	diseased	C	21-15,16	10217	86	97.3	ERS2071320	56575
SK150	2017	Nigeria	Sokoto	diseased	C	21-15,16	10217	104	134.4	ERS2071294	56577

**Supplementary Table ST1** – Isolates used in this study.



**Supplementary Figure SF1:** cgMLST-based tree of the outbreak and carrier strains, as well as other African NmC and isolates found to have relatively similar capsule through allele-based comparison. Colors are according to country of isolation, and a star is used to indicate invasiveness. (For the Europe/Canada cluster, every strain is invasive and individual country information has not been added.) Nig8/13 represents

the entire outbreak (ST-10217) in this figure. BL16188 and the outbreak strain are very closely related compared to all other hitherto publicly available sequences.



**Supplementary Figure SF2:** Comparison of the MDAΦ prophage in Nig8/13 (representing ST-10217) to those found in Z2491, MC58 and FAM18, using the Bille *et al.* (2005) terminology. For Nig8/13, the annotations have been made using NEIS numbers from pubmlst. Genes that were called by pubmlst but not by an independent gene caller (Prokka) have been left transparent. (NEIS2451 corresponds to ORF10 of MDAΦ and is likely a transcribed gene. NEIS2987 has not been previously described and is in the opposite

direction and might be an incidental finding. NMC\_RS00125 does not have a corresponding NEIS number and was only called by Prokka. However, this gene clearly corresponds to the previously described ORF9.) For Z2491, MC58 and FAM18, short ORFs have only been annotated with a single number, corresponding to the ORF number in MDAΦ's nomenclature. Red color corresponds to sequence homology in the forward direction, and blue to sequence homology in the reverse direction.

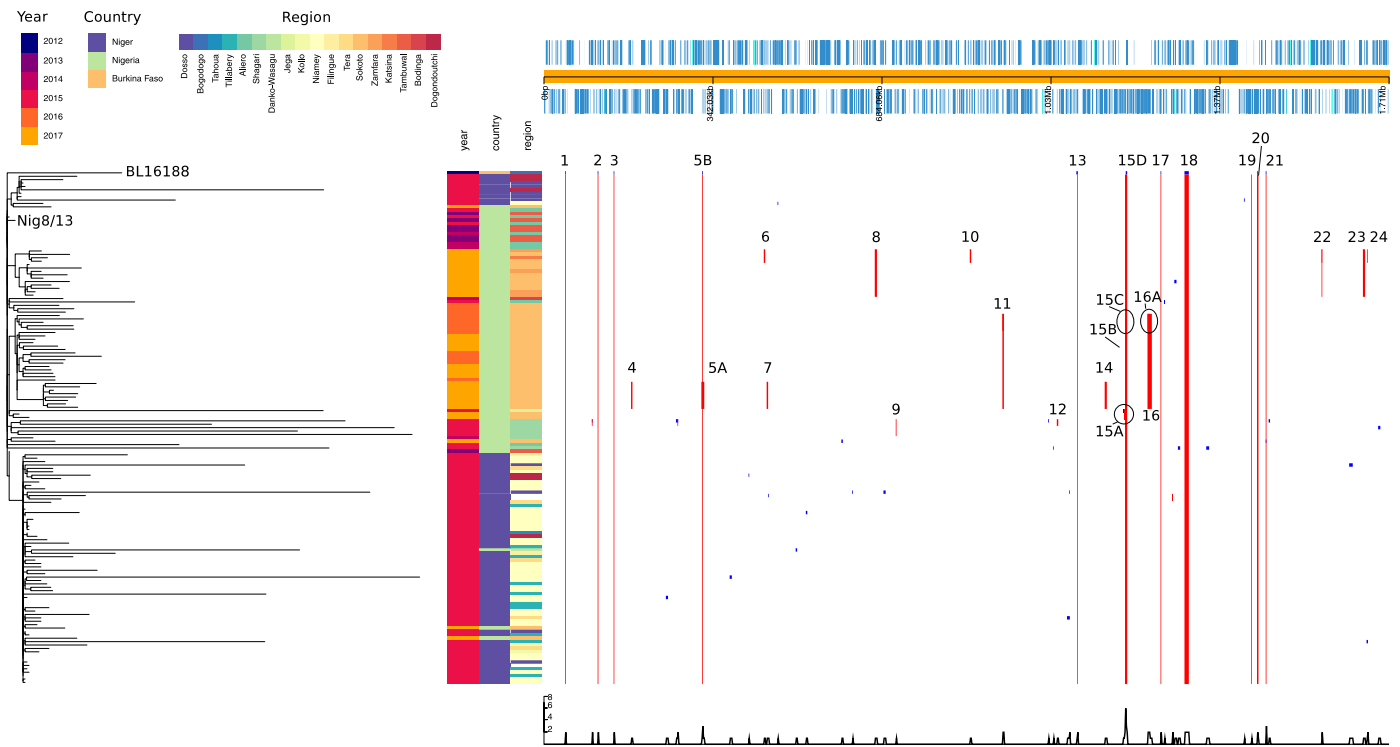


Isolate	Type	Upstream	ORF10	ORF1	ORF2	ORF3	ORF4	ORF5	ORF6A	ORF6	ORF7	ORF8	ORF9	Downstream
Nig8/13	I	NEIS2113	NEIS2451**	NEIS0031	NEIS0030	NEIS0029	NEIS0028	NEIS0027	NMC_RS09055*	NEIS1866	NEIS0024	NEIS0023	NMC_RS00125*	NEIS2114
Z2491	I	NMA1791		NMA1792	NMA1793	NMA1794	NMA1795	NMA1796		NMA1797	NMA1798	NMA1799	NMA1800	NMA1801
MC58	I	NMB1541		NMB1543	NMB1544	NMB1545	NMB1546	NMB1547		NMB1548	NMB1550	NMB1551	NMB1552	NMB1554
MC58	II	NMB1636		NMB1634	NMB1633	NMB1632	NMB1631	NMB1630	NMB1629	NMB1628	NMB1627	NMB1626	NMB1625	NMB1624
FAM18	I	RS00175	RS00170	RS00165	RS00160	RS00155	RS00150	RS00145		RS00140	RS00135	RS00130	RS00125	RS00120
FAM18	II	RS01495		RS01500	RS01505	RS01510	RS01515	RS01520		RS01525	RS01530	RS01535	RS01540	RS01545
FAM18	III	RS09025		RS09030	RS09035	RS09040	RS09045	RS09050	RS09055	RS09060	RS09065	RS09070	RS09075	RS09080
FAM18	IV	RS09795		RS09800	RS09805	RS09810	RS09815	RS09820	RS09825	RS09830	RS09835	RS09840	RS09845	RS09850

\*=Predicted, not called by  
pubmlst

\*\*=Not predicted but called by pubmlst

**Supplementary Table ST2** – Comparison of open reading frames in the MDAΦ phage with those in the corresponding regions of Z2491, MC58 and FAM18. The type is annotated as in Bille *et al.*, 2005. For FAM18, the prefix “NMC\_” has been removed from all annotations.



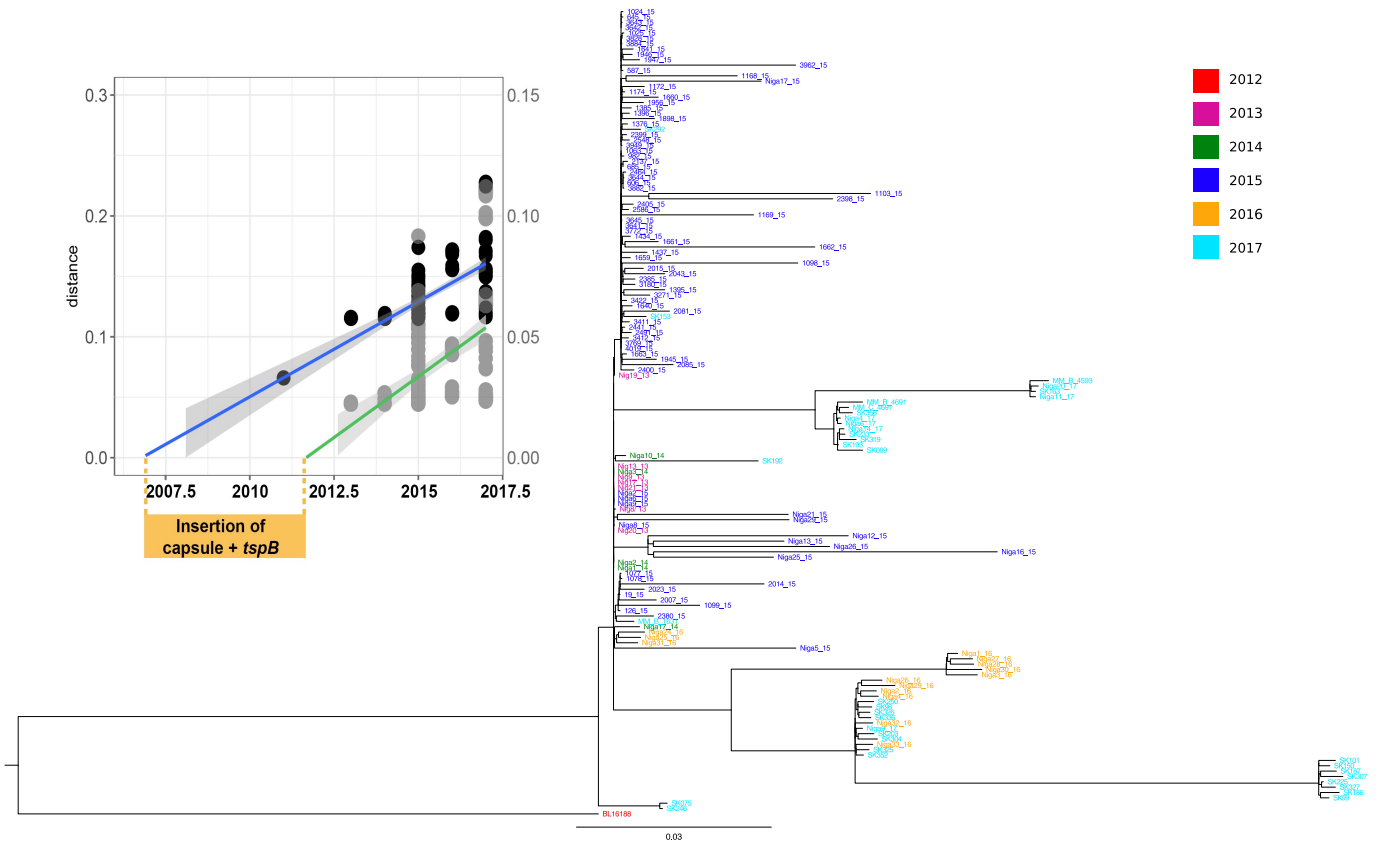
**Supplementary Figure SF3:** Phandango plot showing recombination events within ST-10217 and between BL16188 and ST-10217. The numbering of recombination events corresponds to Supplementary Table ST3, where all affected genes are described. The tall red blocks (1, 2, 3, 5B, 13, 15D, 17, 18, 19, 20, 21) are recombination events that have happened on the branch between the carrier (BL16188) and the outbreak. The horizontal axis corresponds to an alignment of the core *N. meningitidis* genome. The tree used in this figure is the recombination-filtered tree from Gubbins.

Block	All ST-10217	Coord start	Coord stop	NEIS no.	Pubmlst annotation
1	X	43 948	44 504	NEIS0372	hypothetical protein
2	X	109 960	110 518	NEIS0433	ATP-dependent DNA helicase <i>RecG</i>
3	X	141 525	143 376	NEIS0484	hypothetical protein
				NEIS0486	alcohol dehydrogenase ( <i>adhA</i> )
4		176 337	179 224	NEIS0521	ABC transporter ATP-binding protein
				NEIS0523	electron transfer flavoprotein-ubiquinone oxidoreductase
				NEIS0694	putative DNA repair protein
				NEIS0695	hypothetical protein
5A		319 497	324 686	NEIS0696	hypothetical protein
				NEIS0697	ubiquinone/menaquinone biosynthesis methyltransferase
				NEIS0698	hypothetical protein
5B	X	320 135	321 968	NEIS0694	putative DNA repair protein
				NEIS0695	hypothetical protein
6		444 926	448 680	NEIS0897	<i>icd</i> - isocitrate dehydrogenase (NADP+)
				NEIS0899	<i>Ist</i> (alpha-2,3-sialyltransferase)
				NEIS0900	putative C-type cytochrome
				NEIS0901	putative oxidoreductase
				NEIS0907	dihydrodipicolinate synthase
7		451 181	453 942	NEIS0908	transmembrane transport protein
				NEIS0909	RNA methylase
				NEIS1166	hypothetical protein
8		670 548	673 840	NEIS1168	ferredoxin--NADP reductase
				NEIS1170	putative P-type cation-transporting ATPase
9		712548	714621	NEIS1210	site-specific recombinase
				NEIS1212	murein hydrolase
				NEIS1365	transcription elongation factor <i>GreA</i>
10		862 315	865 354	NEIS1366	3-phosphoshikimate 1-carboxyvinyltransferase
				NEIS1367	putative lipoprotein
				NEIS1368	phospholipase D-family protein
				NEIS1429	aspartate kinase
11		928 127	932 002	NEIS1430	ribonuclease PH
				NEIS1431	hypothetical protein
				NEIS1432	hypothetical protein
				NEIS1433	hypothetical protein
				NEIS1435	nicotinate phosphoribosyltransferase
12		1 038 062	1 041 948	NEIS2458	Tellurite resistance protein <i>TehB</i>
				NEIS1544	ribonuclease H
				NEIS1545	hypothetical protein

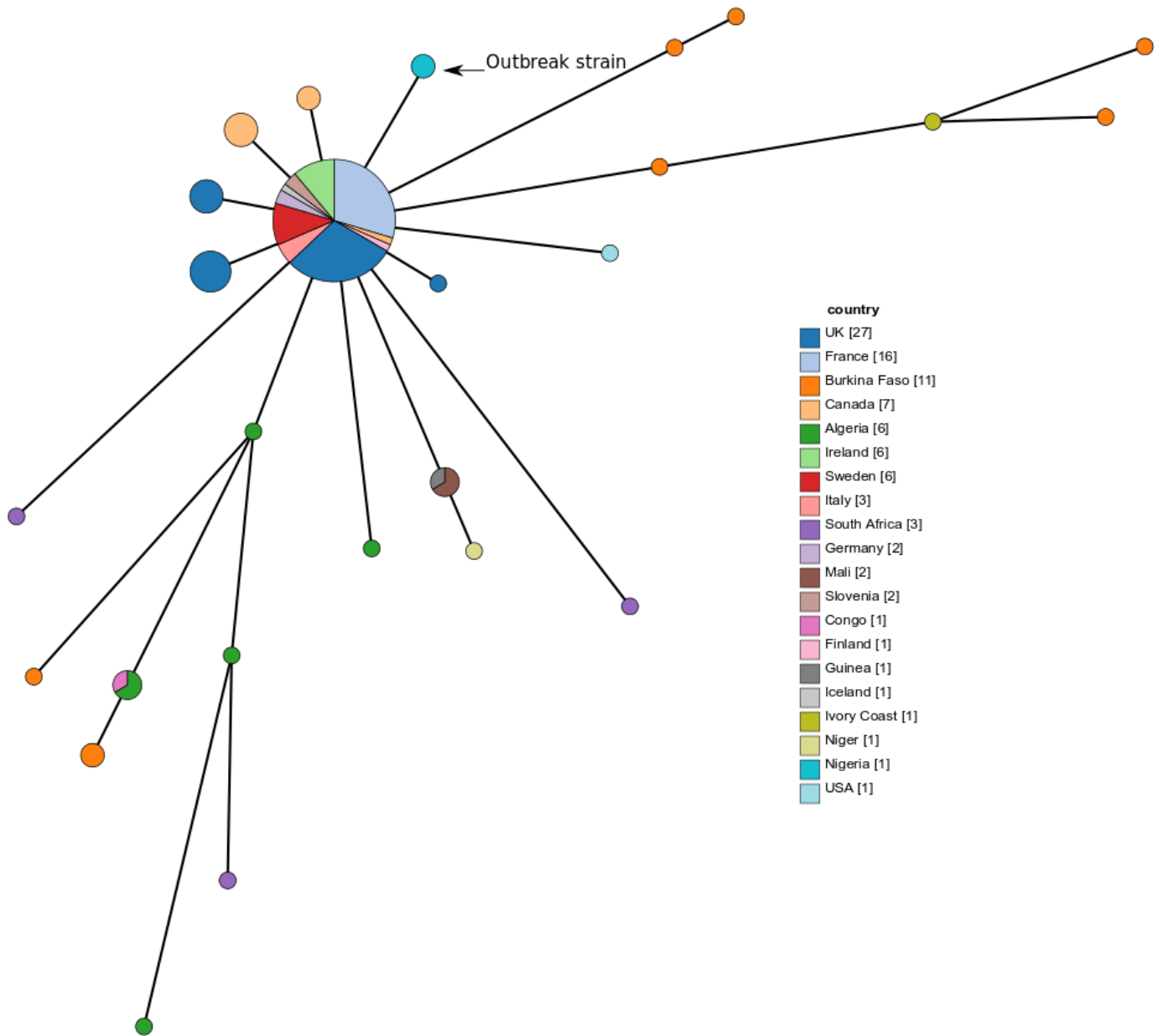
				NEIS1546	hypothetical protein
				<i>hmbR</i>	haemoglobin receptor protein
<b>13</b>	X	1 078 946	1 081 671	NEIS1587	haem utilisation protein ( <i>hemO</i> )
				NEIS1588	putative paraquat-inducible protein A
				NEIS1638	exodeoxyribonuclease V
<b>14</b>		1 135 732	1 139 568	NEIS1639	putative integral membrane protein
				NEIS1640	cytochrome c oxidase subunit III
<b>15A</b>		1 175 591	1 178 486	NEIS1691	transferrin-binding protein 1 ( <i>tbpB</i> )
				NEIS1692	glutamate racemase
<b>15B</b>		1 177 124	1 178 099	NEIS1691	transferrin-binding protein 1 ( <i>tbpB</i> )
				NEIS1692	glutamate racemase
				NEIS1691	transferrin-binding protein 1 ( <i>tbpB</i> )
<b>15C</b>		1 177 124	1 179 806	NEIS1692	glutamate racemase
				NEIS1693	hypothetical protein
				NEIS1694	N-acetylmuramoyl-L-alanine amidase ( <i>amiC</i> )
				NEIS1691	transferrin-binding protein 1 ( <i>tbpB</i> )
				NEIS1692	glutamate racemase
<b>15D</b>	X	1 177 150	1 181 038	NEIS1693	hypothetical protein
				NEIS1694	N-acetylmuramoyl-L-alanine amidase ( <i>amiC</i> )
				NEIS1695	hypothetical protein
				NEIS1750	hypothetical protein
<b>16A</b>		1 222 382	1 226 133	NEIS1751	UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelate ligase
				NEIS1753	penicillin-binding protein 2 ( <i>penA</i> )
				NEIS1750	hypothetical protein
				NEIS1751	UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelate ligase
				NEIS1753	penicillin-binding protein 2 ( <i>penA</i> )
<b>16B</b>		1 222 382	1 230 880	NEIS1754	putative small periplasmic protein
				NEIS1755	S-adenosyl-methyltransferase <i>MraW</i>
				NEIS1756	cell division protein <i>MraZ</i>
				NEIS1757	hypothetical protein
				NEIS1759	undecaprenyl pyrophosphate phosphatase
<b>17</b>	X	1 247 776	1 250 014	NEIS1777	maltose phosphorylase ( <i>mapA</i> )
				NEIS1779	integral membrane transport protein
				NEIS0275	putative outer membrane solvent tolerance protein
				NEIS0274	hypothetical protein
				NEIS0273	thiol:disulphide interchange protein encodes DsbA1; oxidoreductase
<b>18</b>	X	1 297 533	1 305 508	NEIS0272	putative inner membrane protein
				NEIS0271	hypothetical protein
				NEIS0270	indole-3-glycerol-phosphate synthase
				NEIS0269	ATP-dependent DNA helicase

				NEIS0119	50S ribosomal protein L11 ( <i>rplK</i> )
19	X	1 432 459	1 433 843	NEIS0118	transcription antitermination protein ( <i>nusG</i> )
				NEIS0117	<i>secE</i>
				NEIS0116	<i>tuf</i>
20	X	1 443 217	1 446 560	NEIS0106	putative two-component sensor kinase
				NEIS0105	hypothetical protein
				NEIS0104	SUN-family protein
				NEIS0103	methionyl-tRNA formyltransferase
21	X	1 461 464	1 463 242	NEIS0073	outer membrane transport protein
				NEIS2514	hypothetical protein
				NEIS0072	hypothetical protein
22		1 574 985	1 576 160	NEIS0071	putative lipoprotein
				NEIS2044	hypothetical protein
23		1 657 466	1 662 375	NEIS2043	<i>ThiF</i> protein
				NEIS1957	DNA polymerase I
				NEIS1956	S-ribosylhomocysteinase
				NEIS1955	hypothetical protein
				NEIS1954	frataxin-like protein
				NEIS1953	putative lipoprotein
				NEIS1952	diaminopimelate decarboxylase
				NEIS2995	membrane protein
24		1 667 098	1 668 614	NEIS1951	putative sodium-dependent inner membrane transport protein
				NEIS1945	hypothetical protein
				NEIS1944	putative para-aminobenzoate synthase component I

**Supplementary Table ST3** – Recombination blocks identified on the branch between BL16188 and ST-10217 (With “X” in “All ST-10217”) and on internal branches of the ST-10217 phylogeny, with associated loci/products. Block = Recombination block number, corresponding to Supplementary Figure SF3. Coord start/stop = Determined breakpoints of the recombination block in an alignment of all *N. meningitidis* cgMLST v1.0 loci, total length 1 705 235 bp. NEIS no. = Accession number of locus in pubmlst, if available. Pubmlst annotation = Annotation of the locus in pubmlst.



**Supplementary Figure SF4:** Maximum-likelihood tree based on SNPs from a whole-genome alignment of all outbreak isolates, with carrier strain BL16188 set as the outgroup. Colors are according to sample year. This tree is used to infer a root-to-tip time signal, for use in a regression analysis to determine the most probable time of horizontal acquisition of the capsule and the MDA prophage (Left).



**Supplementary Figure SF5:** Allele-based minimum spanning tree of capsule locus only (NEIS0049-NEIS0059), intended to show potential donors of ST-10217s capsule. Colors are according to country of origin. European/Canadian group C capsules appear to be more closely related to ST-10217's capsule than other African NmC.

Isolate name	Year	Country	Host status	Serogroup	PorA type	ST	BIGS id.
BF0689	2009	Burkina Faso	carrier	C	5-2,10-2	206	57302
BF0692	2009	Burkina Faso	carrier	C	5-2,10-2	206	57303
BF0751	2009	Burkina Faso	carrier	C	7,30-8	206	57304
BF0791	2009	Burkina Faso	carrier	C	7,30-11	7929	57305
BF1626	2010	Burkina Faso	carrier	C	7-43,30	206	57306
BF1736	2010	Burkina Faso	carrier	C	5-1,2-2	865	57307
BF1742	2010	Burkina Faso	carrier	C	5-1,2-2	865	57308
BF2880	2012	Burkina Faso	carrier	C	7-2,30-11	206	57309
FAM18	1983	USA	diseased	C	5,2	11	698
HF170	1973	South Africa	diseased	C	5-1,10-4	8245	38577
Niger15/91	1991	Niger	diseased	C	5,2-1	11	38578
MK338/93	1993	Guinea	diseased	C	5,2-1	11	38579
MK85/94	1994	Mali	diseased	C	5,2-1	165	38580
MK91/94	1994	Mali	diseased	C	5,2-1	165	38581
IC9/98	1998	Ivory Coast	diseased	C	7,30-8	206	38582
C14/01	2001	Congo	diseased	C	5-2,10-64	206	38583
S97/93	1993	Algeria	diseased	C	18-1,34	409	38584
S41/98	1998	Algeria	diseased	C	18-1,3	11	38585
S70/98	1998	Algeria	diseased	C	18-23,1	206	38586
S13/98	1998	Algeria	diseased	C	18-3,1	11588	38587
3252/99	1999	Algeria	diseased	C	18-3,1	337	38588
S96/98	1998	Algeria	diseased	C	18-3,1	4711	38589
SB19	1990	South Africa	diseased	C	5-2	8	38590
SB3	1990	South Africa	diseased	C	5-2	8	38591
M12 240255	2012	UK	diseased	C	5-2	11	21458
M12 240716	2012	UK	diseased	C	5-2	11	28084
M04 241156	2004	UK	diseased	C	5-2	11	29589
M07 240686	2007	UK	diseased	C	5-2	7779	29626
M98 253000	1998	UK	other	C	5-2	11	29646
M10 240229	2010	UK	diseased	C	5-2	11	29891
M13 240496	2013	UK	diseased	C	5-2	11	29895
M13 240514	2013	UK	diseased	C	5-2	11	29898
M14 240100	2014	UK	diseased	C	5-2	11	30214
M14 240107	2014	UK	diseased	C	5-2	11	30215
M14 240184	Unknown	Canada	diseased	C	5-2	11	30287
12009-14	2014	Ireland	diseased	B	5-2	11	30694
12038-13	2013	Ireland	diseased	C	5-2	11	30727
M14 240168	2014	UK	diseased	C	5-2	11	35628
M14 240405	2014	UK	diseased	C	5-2	11	35762
M14 240436	2014	UK	diseased	C	5-2	11	35775
12034_2014	2014	Ireland	diseased	C	5-2	11	36156
12035_2014	2014	Ireland	diseased	C	5-2	11	36157
12008_2015	2015	Ireland	diseased	C	5-2	11	36817
12020-2015	2015	Ireland	diseased	C	5-2	11	36828
85Mo	2012	Slovenia	diseased	C	5-2	11	38152
2533	2012	Italy	diseased		5-2	11	38865
LNP28303	2015	France	diseased	C	5-2	11	40239



LNP28344	2015	France	diseased	C	5-2	11	40274
LNP28383	2016	France	diseased	C	5-2	11	40408
LNP28270	2015	France	diseased	C	5-2		40472
LNP28276	2015	France	diseased	C	5-2	11	40475
LNP28289	2015	France	diseased	C	5-2	11	40482
M15 240872	2015	UK	diseased	C	5-2	11	41468
LNP28411	2016	France	diseased	C	5-2	11	41578
LNP28422	2016	France	diseased	C	5-2	11	41587
149M	2015	Slovenia	diseased	C	5-2	11	41717
LNP28426	2016	France	diseased	C	5-2	11	41793
LNP28448	2016	France	diseased	C	5-2	11	41801
LNP28451	2016	France	diseased	C	5-2	11	41804
LNP28456	2016	France	diseased	C	5-2	11	41809
LNP28470	2016	France	diseased	C	5-2	11	41821
16-88	2016	Sweden	diseased	C	5-2	11	41965
LNP28481	2016	France	diseased	C	5-2	11	42047
1459000190	2014	Sweden	diseased	C	5-2	11	42366
1459000254	2014	Sweden	diseased	C	5-2	11	42374
15-29	2015	Sweden	diseased	C	5-2	11	42414
15-81	2015	Sweden	diseased	C	5-2	11	42437
M16 240142	2016	UK	diseased	C	5-2	11	42577
LNP28568	2016	France	diseased	C	5-2	11	42879
LNP28570	2016	France	diseased	C	5-2	11	42881
16-8702245	2016	UK	diseased	C	5-2	11	44693
M16 240383	2016	UK	diseased	C	5-2	11	44770
704070003	2007	Iceland	diseased	C	5-2		44880
DE8555	2002	Germany			5-2	11	46977
WUE2121	1997	Germany			5-2	11	47012
M16 240564	2016	UK	diseased	C	5-2	11	47298
Nmiss2821	2016	Italy		C	5-2	11	49274
16-482	2016	Sweden	diseased	C	5-2	11	50862
14.8703928	2014	UK	diseased	C	5-2	11	51613
14.8705635	2014	UK		C	5-2	11	52835
16.8710714	2016	UK		C	5-2	11	52888
2636	2016	Italy		C	5-2	11	52959
M16 240752	2016	UK	diseased	C	5-2	11	53088
M16 240760	2016	UK	diseased	C	5-2	11	53095
M16 240775	2016	UK	diseased	C	5-2	11	53105
M17 240066	2017	UK	diseased	C	5-2	11	53262
M17 240136	2017	UK	diseased	C	5-2	11	53303
M17 240153	2017	UK	diseased	C	5-2	11	53317
114728	2017	Finland		C	5-2	11	53426
NMLC249	2006	Canada		C	5-2	11	53786
NMLC113	2009	Canada		C	5-2	11	53788
NMLC203	2009	Canada		C	5-2	11	53789
NMLC066	2013	Canada		C	5-2	11	53796
NMLC102	2014	Canada		C	5-2	11	53797
NMLC107	2014	Canada		C	5-2	11	53798
12010-16	2016	Ireland		C	5-2	11	55530

12020-16	2016	Ireland		C	5-2	11	55537
12027-16	2016	Ireland		C	5-2	11	55542
12030-16	2016	Ireland		C	5-2	11	55543
12046-16	2016	Ireland		C	5-2	11	55554
12048-16	2016	Ireland		B	5-2	11	55555
12001-17	2017	Ireland		C	5-2	11	55566
12002-17	2017	Ireland		C	5-2	11	55567
12016-17	2017	Ireland		C	5-2	11	55577
12017-17	2017	Ireland		C	5-2	11	55578
12026-17	2017	Ireland		C	5-2	11	55585

**Supplementary Table ST4** – Other related isolates (mostly serogroup C) available from pubmlst and used for comparison in Supplementary Figure 1.