

Table S1. Allelic profiles of loci associated with antimicrobial resistance (NEIS loci) and AMR phenotype (P).

	Beta-lactams					Fluoroquinolones				Macrolides				Plasmids		Efflux pump	
	NEIS0408 (<i>pilQ</i>)	NEIS0414 (<i>ponA</i>)	NEIS1753 (<i>penA</i>)	NEIS2020 (<i>porB</i>)	P	NEIS1320 (<i>gyrA</i>)	NEIS1525 (<i>parC</i>)	NEIS1600 (<i>parE</i>)	P	16S rRNA	23S rRNA	NEIS0149 (<i>rpsE</i>)	P	NEIS2210 (<i>tetM</i>)	NEIS2357 (<i>blaTEM</i>)	NEIS1635 (<i>mtrR</i>)	<i>pro</i> NEIS1635 (<i>mtrR</i> promoter)
NM8250	71	130	5	27	S	9	10	25	S	*	*	1	S	0	0	37	9
NM8307	277	296	371	1182	R	287	309	206	S	1542	522	1	S	0	0	7	5
NM8468	455	2	373	1183	I	302	311	338	S	*	*	1	S	0	0	247	5
NM8525	70	62	62	199	S	202	19	54	S	*	54	45	S	0	0	10	7
NM8558 ^a	456	28	375	1184	R	303	704	339	S	1543	523	1	S	0	0	15	6
NM8572	4	11	354	42	R	249	31	7	S	*	524	1	S	0	0	OFF	5
NM8583	455	2	373	1183	R	302	311	338	S	*	*	1	S	0	0	247	5
NM8602 ^a	33	28	33	149	S	35	313	56	S	1384	525	1	S	0	0	251	5
NM8633	116	1	377 ^b	1	S	1	1	1	S	*	1	1	S	0	0	2	5
NM8652	359	7	380	265	R	255	275	288	S	*	526	1	S	0	0	211	5
NM8674 ^a	241	28	112	1185	I	32	30	60	S	1412	112	1	S	0	0	7	5
NM8726	455	2	373	1183	I	302	311	338	S	*	*	1	S	0	0	247	5
NM8736 ^a	16	16	5	45	S	32	8	25	S	1341	1	0	S	0	0	273	5
NM9062	87	2	5	260	S	9	135	25	S	1407	424	1	S	0	0	107	5
NM9071	347	1	41	38	I	31	26	280	S	1324	528	1	S	0	0	274	5
NM9124 ^a	277	61	382	477	R	7	314	341	S	1544	*	1	S	0	0	275	5
NM9565	16	129	112	42	R	248	17	25	S	1310	20	1	S	0	0	9	5
NM9658 ^a	359	7	380	1186	R	255	275	288	S	1	*	1	S	0	0	211	5
NM9853	457	2	5	1187	S	9	135	25	S	1310	20	1	S	0	0	9	5
NM9905	347	1	41	38	S	31	26	280	S	1324	528	1	S	0	0	7	5
NM9954	16	1	3	1	S	1	1	1	S	*	1	1	S	0	0	8	5
NM10052	99	68	88	198	S	10	29	54	S	1379	191	45	S	0	0	59	5
NM10053	99	68	88	198	I	10	29	54	S	1379	191	45	S	0	0	59	5
NM10313	109	45	8	67	S	107	70	79	S	1332	529	1	S	0	0	7	5
NM10364 ^a	458	78	319	126	R	255	275	288	S	*	526	1	S	0	0	211	5
NM10421 ^a	4	64	38	477	S	304	47	58	S	1386	197	1	S	0	0	35	5
NM10492	109	297	385	1188	R	305	309	348	S	1545	530	1	S	0	0	57	10
NM10762	109	45	8	262	S	107	70	79	S	1332	268	1	S	0	0	7	5
NM10763 ^a	277	298	382	1189	R	7	314	341	S	1544	*	1	S	0	0	275	5
NM10833	459	45	352	234	R	9	17	25	S	*	20	1	S	0	0	8	5
NM10853	3	6	109	27	S	20	13	19	S	1546	531	1	S	0	0	41	5

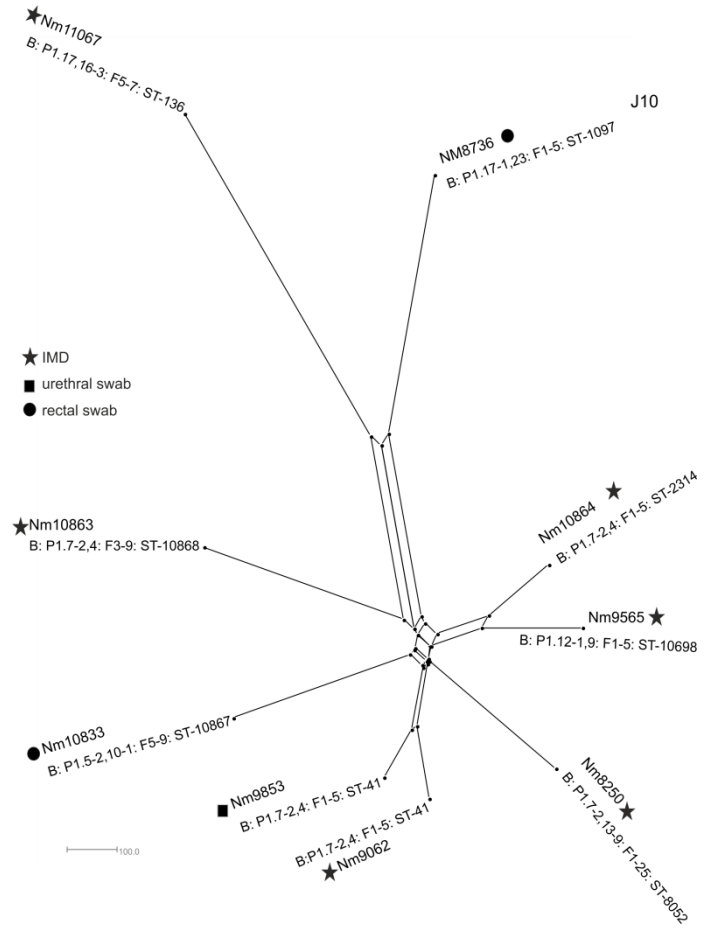
NM10863	7	2	386	45	S	9	84	25		1547	20	1	S	0	0	276	5
NM10864	16	129	112	42	I	9	17	25	S	1310	20	1	S	0	0	9	5
NM10989	4	64	388	43	I	79	47	58	S	1548	197	1	S	0	0	8	5
NM11067	460	19	5	1063	S	32	8	36	S	1344	20	1	S	0	0	9	5

a: dual *N. meningitidis*/*N. gonorrhoeae* infections; b: *penA* allele more commonly found in *N. gonorrhoeae*; * incomplete locus; OFF premature stop codon in locus putatively resulting in loss of function; bold alleles denote the presence of known mutations associated with conferring resistance as described previously [1].

P denotes phenotypic AMR deduced from MIC values with S: susceptible (MIC \leq 0.06), I: intermediate (MIC 0.007 – 0.24), R: resistant (MIC \geq 0.25).

Figure S1. Further genomic analyses of cc41/44 and cc4821 *N. meningitidis* isolates

A.



B.

