

Table S1: Complete reference genomes used in this study

Strain	Accession	Reference
FA1090	NC_002946	unpublished
MS11	CP003909	unpublished
NCCP11945	NC_011035	Chung et al. J Bacteriol. 190:6035
FA19	CP012026	Abrams et al. Genome Announc 3:e01052-15
WHO_F	LT591897	Unemo et al. J Antimicrob Chemother. 71: 3096
WHO_G	LT591898	Unemo et al. J Antimicrob Chemother. 71: 3096
WHO_K	LT591908	Unemo et al. J Antimicrob Chemother. 71: 3096
WHO_L	LT591901	Unemo et al. J Antimicrob Chemother. 71: 3096
WHO_M	LT591904	Unemo et al. J Antimicrob Chemother. 71: 3096
WHO_N	LT591910	Unemo et al. J Antimicrob Chemother. 71: 3096
WHO_O	LT592146	Unemo et al. J Antimicrob Chemother. 71: 3096
WHO_P	LT592157	Unemo et al. J Antimicrob Chemother. 71: 3096
WHO_U	LT592159	Unemo et al. J Antimicrob Chemother. 71: 3096
WHO_V	LT592150	Unemo et al. J Antimicrob Chemother. 71: 3096
WHO_W	LT592163	Unemo et al. J Antimicrob Chemother. 71: 3096
WHO_X	LT592155	Unemo et al. J Antimicrob Chemother. 71: 3096
WHO_Y	LT592161	Unemo et al. J Antimicrob Chemother. 71: 3096
WHO_Z	LT592153	Unemo et al. J Antimicrob Chemother. 71: 3096

Table S2: Sequenced *Neisseria gonorrhoeae* isolates

Source	Phylogenetic analysis (Dataset 1)	SNP analysis* (Dataset 2)
China	435	435
USA	192	186
UK	1867	0
WHO	14	14
Other	4	0
Total	2512	635

*include isolates with the information of susceptibility to ceftriaxone.

Table S3: Characteristics of all sequenced isolates in this study

Sample	Province	Ceftriaxone	Spectinomycin	Ciprofloxine	TRNG	PPNG	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	MLST	penA pattern	porB allele	tbpB allele	NG_MAST	Lineage
NG001	ZJ	0.125	16	8	1	0	109	39	67	78	148	153	65	7356	X III	6073	4	10328	L2.6
NG002	ZJ	0.032	16	8	1	0	126	39	67	111	148	153	65	7365	II	581	33	1866	L2.3
NG003	ZJ	0.016	16	8	1	0	126	39	67	158	148	153	65	1904	2.002 (partial)	6061	33	10315	L2.3
NG004	ZJ	0.032	16	8	0	0	109	39	67	158	148	668	65	12969	X VIII	6067	477	10321	L2.1
NG005	ZJ	0.032	16	8	1	0	59	39	67	158	148	153	65	7827	X IX	6068	4	10322	L2.6
NG006	ZJ	0.016	16	8	0	1	109	39	67	111	148	153	133	7367	X IX	6069	1036	10323	L2.1
NG007	ZJ	0.016	8	4	1	1	109	39	67	78	148	153	65	7356	X III	4	752	4539	L2.6
NG008	ZJ	0.016	16	4	0	1	59	39	67	158	148	153	65	7827	X IX	1448	4	4846	L2.6
NG009	ZJ	0.016	16	8	1	1	109	39	67	111	148	153	133	7367	II	1135	1093	5161	L2.9
NG010	ZJ	0.016	16	4	1	0	435	39	67	111	148	153	65	12515	II	581	479	10407	L2.3
NG011	ZJ	0.008	16	4	0	1	59	39	67	158	148	153	65	7827	X IX	1448	4	4846	L2.6
NG012	ZJ	0.032	16	8	0	1	109	39	67	111	148	153	65	1579	X III	6071	110	10325	L2.1
NG013	ZJ	0.032	16	8	1	1	126	39	67	111	148	153	65	7365	X XI	3531	110	10408	L2.2
NG014	ZJ	0.5	16	8	0	0	109	39	67	111	148	153	65	1579	X X X IV	6076	110	10332	L2.1
NG015	ZJ	0.032	16	4	0	0	59	39	67	158	148	153	65	7827	X III	6077	4	10333	L2.4
NG016	ZJ	0.125	16	8	0	1	59	39	67	78	147	154	65	11231	X VIII	6059	33	10313	L2.2
NG017	ZJ	0.125	16	8	1	0	126	39	67	78	148	153	65	1600	X III	543	33	809	L2.2
NG018	ZJ	0.125	16	8	1	1	126	39	67	78	148	153	65	1600	X VIII	6063	186	10317	L2.5
NG019	ZJ	0.125	32	8	1	0	59	39	67	78	147	154	65	11231	X VIII	6064	4	10318	L2.2
NG020	ZJ	0.125	16	8	0	0	59	39	67	158	148	153	65	7827	X III	6073	4	10328	L2.4
NG021	ZJ	0.125	16	8	0	1	126	39	67	111	148	153	65	7365	X III	1053	21	3435	L2.5
NG022	ZJ	0.032	8	8	1	0	126	39	67	78	148	153	65	1600	X XI	6065	737	10319	L2.2
NG023	SH	0.06	8	32	0	0	109	39	67	111	148	153	133	7367	X VIII	580	1070	10384	L2.9
NG024	SH	0.06	16	8	1	0	126	39	67	78	148	153	65	1600	X III	206	75	2135	L2.2
NG025	SH	0.125	16	8	1	0	126	39	67	78	148	153	65	1600	X III	1496	1827	10269	L2.2
NG026	SH	0.125	32	16	0	1	109	39	67	111	148	153	133	7367	X III	6026	1036	10270	L2.1
NG027	SH	0.06	8	8	0	1	109	39	67	158	148	153	65	9304	X VIII	2035	526	3356	L2.1
NG028	SH	0.125	32	16	1	1	59	39	67	158	148	153	65	7827	X III	1053	4	2318	L2.4
NG029	SH	0.06	32	8	1	1	59	39	67	111	148	153	65	1583	X III	90	1829	10272	L2.2
NG030	SH	0.06	16	16	1	0	126	39	67	78	148	153	65	1600	X XI	1275	737	10343	L2.2
NG031	SH	0.125	32	16	0	1	59	39	67	78	147	154	65	11231	X VIII	1053	4	2318	L2.2
NG032	SH	0.06	16	16	0	1	59	39	67	111	147	154	65	12970	X VIII	543	1830	10273	L2.2
NG033	SH	0.06	8	8	0	0	435	39	67	158	148	153	65	12971	X III	246	4	10386	L2.4
NG034	SH	0.125	16	8	0	1	109	39	67	111	148	153	65	1579	X X VIII	908	110	1407	L2.1
NG035	SH	0.06	16	16	0	0	59	39	67	158	148	153	65	7827	X III	6037	4	10285	L2.4
NG036	SH	0.06	16	16	0	0	109	39	67	111	147	153	65	6960	X VIII	182	1473	7856	L2.1
NG037	SH	0.06	16	4	0	0	109	39	67	78	148	153	65	7356	X III	1053	4	2318	L2.6
NG038	SH	0.125	16	16	0	1	109	39	67	78	147	154	65	12972	X III	2922	156	4831	L2.2
NG039	SH	0.06	16	8	0	0	59	39	67	158	148	153	65	7827	X III	6028	1831	10275	L2.4
NG040	SH	0.03	32	32	0	0	59	39	67	78	148	153	65	7363	XII/ X X X VI	2978	1058	5061	L2.6
NG041	SH	0.03	16	16	1	0	126	39	67	78	148	153	65	1600	X XI	1275	737	10343	L2.2
NG042	SH	0.016	16	8	1	0	126	39	67	111	148	153	65	7365	II	6027	33	10274	L2.3
NG043	GX	0.125	8	8	0	0	109	39	67	78	148	153	65	7356	X III	4	752	4539	L2.6
NG044	GX	0.125	32	16	1	1	59	112	67	157	148	153	65	11191	X III	581	33	1866	L2.7
NG045	GX	0.125	16	8	1	1	126	39	67	111	148	153	65	7365	II	251	483	1927	L2.3
NG046	GX	0.125	16	16	0	0	109	39	67	78	148	153	65	7356	X III	4	752	4539	L2.6
NG047	GX	0.008	32	2	0	1	59	112	67	157	148	153	65	11191	X III	251	483	1927	L2.7
NG048	GX	0.008	16	16	0	1	59	39	67	78	146	154	65	12973	II	908	953	8426	L2.6

NG049	GX	0.016	16	16	0	0	126	39	67	78	148	153	65	1600	X III	6021	137	10260	L2.6
NG050	GX	0.008	32	4	0	1	126	39	67	111	148	153	65	7365	X III	90	1077	5096	L2.2
NG051	GX	0.004	16	4	0	0	59	39	67	158	148	153	65	7827	X III	6023	21	10263	L2.4
NG052	GX	0.03	32	16	1	1	435	39	67	111	148	153	65	12515	X XI	328	913	10381	L2.3
NG053	GX	0.03	32	16	0	0	59	39	67	111	148	154	65	8109	X XI	242	1825	10266	
NG054	GX	0.03	16	16	1	0	126	39	67	111	149	71	65	6714	X XI	206	156	421	L2.5
NG055	GX	0.008	8	16	1	1	126	39	67	78	149	71	65	1927	X XI	3099	156	7154	L2.5
NG056	GX	0.03	16	16	1	0	59	39	67	158	148	154	65	12974	XII/X X X VI	4700	580	10382	L2.4
NG057	GX	0.03	16	16	0	1	126	39	67	78	149	71	65	1927	II	5924	156	10342	L2.5
NG058	GX	0.06	16	8	0	1	59	39	67	158	148	153	65	7827	X III	1053	4	2318	L2.4
NG059	GX	0.06	8	2	0	0	109	39	67	78	149	153	65	8157	X XII	6020	278	10247	L2.6
NG060	GX	0.25	8	16	0	0	59	39	67	78	148	153	65	7363	X/X X X V	917	10	1424	L2.8
NG061	GX	0.06	16	4	0	0	59	39	67	78	148	153	65	7363	44.001	581	563	10380	L2.6
NG062	TJ	0.125	16	32	0	0	59	39	67	78	148	153	65	7363	X/X X X V	917	10	1424	L2.8
NG063	TJ	0.016	16	4	0	1	59	112	67	157	148	153	65	11191	X III	251	1833	10290	L2.7
NG064	TJ	0.032	16	16	0	0	59	39	67	158	148	153	65	7827	X III	1132	1834	10291	L2.4
NG065	TJ	0.008	16	4	0	0	59	112	67	157	148	153	65	11191	X III	251	1833	10290	L2.7
NG066	TJ	0.032	16	16	0	0	59	39	67	111	148	153	65	1583	X VIII	6042	328	10292	L2.1
NG067	TJ	0.032	16	8	1	0	109	39	67	158	148	153	65	9304	X VIII	581	33	1866	L2.1
NG068	TJ	0.016	16	8	0	0	126	39	67	111	148	153	65	7365	II	2035	1835	10294	L2.3
NG069	TJ	0.016	16	8	1	1	126	39	67	111	148	153	65	7365	X III	6044	75	10295	L2.3
NG070	TJ	0.016	16	8	1	1	126	39	67	111	148	153	65	7365	X III	489	75	10344	L2.3
NG071	TJ	0.016	8	2	0	0	126	39	67	78	148	153	133	8126	X III	1053	75	10346	L2.6
NG072	TJ	0.032	16	8	0	0	59	39	67	78	148	153	65	7363	44.001	130	1836	10296	L2.6
NG073	TJ	0.008	16	8	1	1	126	39	67	111	148	153	133	1580	II	6045	186	10297	L2.3
NG074	TJ	0.032	8	8	0	0	59	39	67	158	148	153	65	7827	X III	1132	4	2083	L2.4
NG075	TJ	0.016	16	2	0	1	59	39	67	78	147	154	65	11231	II	833	33	1410	L2.2
NG076	TJ	0.032	16	8	0	0	59	39	67	78	148	153	65	7363	44.001	130	1837	10298	L2.6
NG078	TJ	0.125	16	16	0	0	109	39	67	78	148	153	65	7356	X VIII	2103	4	10392	L2.6
NG079	TJ	0.125	16	16	0	0	109	39	67	111	147	153	65	6960	X VIII	182	1473	7856	L2.1
NG080	CQ	0.125	32	4	1	0	59	39	67	158	148	153	65	7827	X IX	1448	1931	11109	L2.6
NG081	CQ	0.015	8	8	0	1	59	39	67	158	148	153	65	7827	X III	83%-1032	99%-4	1931	L2.4
NG082	CQ	0.125	32	8	0	0	59	39	67	78	148	153	65	7363	X/X X X V	6479	21	11114	L2.6
NG083	CQ	0.06	16	16	1	1	126	39	67	111	146	153	65	9902	V	6480	858	11115	L2.1
NG084	CQ	0.06	16	16	1	0	59	39	67	158	148	153	65	7827	X III	1053	4	2318	L2.4
NG085	CQ	0.03	16	4	1	0	59	39	67	158	148	153	65	7827	X III	6481	21	11117	L2.6
NG086	CQ	0.25	32	16	1	0	126	39	67	111	146	153	65	9902	V	6480	858	11115	L2.1
NG087	CQ	0.125	32	16	0	0	109	39	67	111	148	153	133	7367	II	3029	1036	5062	L2.1
NG088	CQ	0.03	8	16	0	0	59	39	67	111	148	153	65	1583	X VIII	6482	137	11118	L2.1
NG089	CQ	0.06	16	16	0	1	126	39	67	111	148	153	65	7365	X III	5228	21	11119	L2.5
NG090	CQ	0.125	16	16	0	0	59	39	67	158	148	153	65	7827	X IX	1448	4	4846	L2.6
NG091	CQ	0.03	16	8	0	0	59	39	67	78	148	153	65	7363	X/X X X V	6479	21	11114	L2.6
NG092	CQ	0.03	16	16	1	1	59	39	67	158	148	153	65	7827	X III	1132	4	2083	L2.4
NG093	CQ	0.125	16	16	1	1	59	39	67	158	148	153	65	7827	X III	1053	4	2318	L2.4
NG094	CQ	0.004	4	0.015	0	0	59	39	67	158	148	153	65	7827	X III	6481	21	11117	L2.6
NG095	CQ	0.06	16	4	0	1	126	39	67	111	148	153	65	7365	XII/X X X VI	1135	75	2780	L2.2
NG096	CQ	0.03	16	4	0	0	126	39	67	111	148	153	65	7365	XII/X X X VI	1135	75	2780	L2.2
NG097	CQ	0.06	32	4	1	0	109	39	67	158	148	153	65	9304	X VIII	90	477	4022	L2.1
NG098	CQ	0.015	16	4	1	0	59	39	67	158	148	153	65	7827	X IX	1448	4	4846	L2.6
NG099	CQ	0.004	16	8	1	0	59	39	67	158	148	153	65	7827	X III	95%-1067	4	2083	L2.4

NG100	CQ	0.06	16	8	1	1	126	39	67	78	148	153	65	1600	X III	1132	186	2422	L2.2
NG101	XJ	0.016	8	2	0	0	59	39	67	158	148	153	65	7827	X IX	6563	4	11270	L2.6
NG102	XJ	0.03	4	16	0	0	109	39	67	111	146	153	65	8151	X VII	6564	367	11271	L2.5
NG103	XJ	0.008	4	2	0	0	59	39	67	158	148	153	65	7827	X IX	1448	33	11237	L2.6
NG104	XJ	0.03	8	2	0	0	59	39	67	158	148	153	65	7827	X IX	1448	4	4846	L2.6
NG105	XJ	0.016	4	2	0	0	59	39	67	158	148	153	65	7827	X IX	1448	1955	11272	L2.6
NG106	XJ	0.008	4	4	0	0	59	39	67	158	148	153	65	7827	X IX	1448	33	11237	L2.6
NG107	XJ	0.06	8	8	0	0	59	39	67	158	148	153	65	7827	X III	6565	4	11273	L2.4
NG108	XJ	0.016	4	4	0	1	59	112	67	157	148	153	65	11191	X III	6566	483	11274	L2.7
NG109	XJ	0.125	8	8	0	0	59	39	67	158	148	153	65	7827	X III	6561	4	11265	L2.4
NG110	XJ	0.008	4	2	0	1	59	112	67	157	148	153	65	11191	X III	90%-1019	483	1927	L2.7
NG111	XJ	0.03	8	8	0	1	59	39	67	158	148	153	65	7827	X III	83%-477	4	2083	L2.4
NG112	XJ	0.016	4	8	0	1	126	39	67	78	149	71	65	1927	X XI	206	156	421	L2.5
NG113	XJ	0.03	8	2	0	0	59	39	67	158	148	153	65	7827	X IX	3534	4	5916	L2.6
NG114	XJ	0.016	4	4	0	1	109	39	67	111	148	153	133	7367	II	251	1036	11246	L2.1
NG115	XJ	0.125	8	8	1	1	109	39	67	157	148	153	133	12975	VII	1135	1093	5161	L2.9
NG116	XJ	0.03	8	8	0	0	59	39	67	158	148	153	65	7827	X III	6562	4	11266	L2.4
NG117	XJ	0.008	4	4	1	0	59	39	67	78	149	71	65	1890	X XI	609	137	11267	L2.5
NG118	XJ	0.03	4	16	0	0	59	39	67	158	148	71	65	1588	X IX	3318	4	11268	L2.6
NG119	XJ	0.03	8	4	0	0	59	39	67	158	148	153	65	7827	X IX	1448	137	11269	L2.6
NG120	LN	0.06	64	16	0	0	59	39	67	158	149	153	65	8118	X III	866	186	10352	L2.4
NG121	LN	0.06	64	16	1	0	109	39	67	158	149	153	65	12976	X VIII	2035	526	3356	L2.1
NG122	LN	0.125	64	16	0	0	126	39	67	111	148	153	133	1580	X XI	6571	156	11280	L2.1
NG123	LN	0.03	64	8	0	0	109	39	67	111	148	153	133	7367	IX	5924	4	10091	L2.1
NG124	LN	0.06	32	16	1	1	126	39	67	111	146	153	65	9902	V	809	186	2051	L2.1
NG125	LN	0.03	32	8	0	1	109	39	67	111	148	153	133	7367	IX	2978	1336	11181	L2.1
NG126	LN	0.015	64	16	0	1	126	39	67	78	148	153	65	1600	X III	1132	752	11284	L2.2
NG127	LN	0.06	64	16	0	0	59	39	67	158	148	153	65	7827	X III	1132	4	2083	L2.4
NG128	LN	0.03	64	16	0	1	109	39	67	111	148	153	133	7367	IX	2978	1336	11181	L2.1
NG129	LN	0.06	64	8	1	1	126	39	67	158	148	153	65	1904	II	2869	1958	11286	L2.3
NG130	LN	0.06	64	16	0	0	59	39	67	78	147	154	65	11231	X III	609	33	4745	L2.2
NG131	LN	0.03	64	8	1	1	126	39	67	111	148	153	65	7365	II	1115	1960	NA	L2.3
NG132	LN	0.008	64	16	0	0	59	39	67	158	148	153	65	7827	X IX	1448	33	11237	L2.6
NG133	LN	0.125	32	16	1	0	59	39	67	158	149	153	65	8118	X III	866	186	10352	L2.4
NG134	LN	0.06	64	8	1	1	126	39	67	78	148	153	65	1600	XI	365	33	NA	L2.2
NG135	LN	0.06	64	4	0	0	109	39	67	158	148	153	65	9304	X VIII	2035	526	3356	L2.1
NG136	LN	0.06	32	16	1	1	126	39	67	158	148	153	133	7828	IX	1053	33	1614	L2.6
NG137	LN	0.06	64	16	0	0	126	39	67	78	148	153	65	1600	IX	6578	119	11290	L2.6
NG138	LN	0.06	64	4	0	1	126	39	67	111	148	153	133	1580	X XI	1140	156	NA	L2.1
NG139	LN	0.125	64	16	1	0	59	39	67	78	147	154	65	11231	X VIII	543	4	1790	L2.2
NG140	LN	0.015	64	8	0	1	109	39	67	78	148	153	65	7356	XII/ X X X VI	6660	1962	NA	L2.6
NG141	LN	0.03	16	16	0	0	126	39	67	78	148	153	65	1600	IX	6578	119	11290	L2.6
NG142	LN	0.03	64	16	0	0	59	39	67	78	148	153	65	7363	XII/ X X X VI	2978	1336	11181	L2.6
NG143	LN	0.06	32	2	0	1	59	39	67	111	148	153	65	1583	X VIII	580	328	5699	L2.1
NG144	LN	0.03	64	16	0	0	126	39	67	111	148	153	65	7365	86.001 (partial)	6066	137	11294	L2.1
NG145	LN	0.06	64	16	1	0	126	39	67	111	148	153	65	7365	II	5990	1960	11295	L2.3
NG146	GD_SZ	0.125	16	16	1	1	59	39	67	111	148	153	65	1583	X VIII	5873	1780	9960	L2.1
NG147	GD_SZ	0.125	16	16	0	0	126	39	67	78	148	153	65	1600	X III	2261	186	3741	L2.6
NG148	GD_SZ	0.125	16	≥32	1	1	59	39	67	78	148	153	65	7363	XII/ X X X VI	2978	1058	5061	L2.6
NG149	GD_SZ	0.125	32	4	1	0	109	39	67	111	149	154	65	12977	88.001(partial)	1053	1018	13421	L2.5

NG150	GD_SZ	0.125	32	≥32	0	1	126	39	67	111	148	153	65	7365	X III	1449	33	13582	L2.3
NG151	GD_SZ	0.008	32	16	0	0	126	39	67	158	148	153	65	1904	X III	1132	428	13677	L2.4
NG152	GD_SZ	0.008	16	16	0	0	126	39	67	78	148	153	65	1600	X III	1132	33	1766	L2.2
NG153	GD_SZ	0.008	16	16	1	0	126	39	67	111	148	153	65	7365	X III	3971	21	13681	L2.5
NG154	GD_SZ	0.004	16	8	1	1	126	39	67	111	148	153	65	7365	X III	581	33	1866	L2.3
NG155	GD_SZ	0.008	32	8	0	0	126	39	67	111	148	153	133	1580	X XI	4686	156	7794	L2.1
NG156	GD_SZ	0.004	64	4	1	1	109	39	67	158	148	153	65	9304	X III	7866	4	13629	L2.4
NG157	GD_SZ	0.004	16	4	1	1	59	39	67	78	147	154	65	11231	X III	130	33	1743	L2.2
NG158	GD_SZ	0.008	32	16	0	1	126	39	67	158	148	153	65	1904	X III	1132	428	13677	L2.4
NG159	GD_SZ	≤0.002	32	4	1	1	59	39	67	111	148	71	65	1921	X VIII	147	328	13661	L2.6
NG160	GD_SZ	0.004	64	8	0	1	59	39	67	111	148	153	65	1583	X III	6544	4	11224	
NG161	GD_SZ	0.125	32	>16	0	0	59	39	67	111	148	153	65	1583	X VIII	5873	1780	9960	L2.1
NG162	GD_SZ	0.032	32	>16	0	0	59	39	67	78	148	153	65	7363	X/X X X V	3215	10	5308	L2.8
NG163	GD_SZ	0.25	64	16	0	0	126	39	67	78	148	153	65	1600	X III	7879	33	13663	L2.2
NG165	JS	0.015	8	8	1	0	126	39	67	158	148	153	65	1904	XII/X X X VI	5166	33	8724	L2.3
NG166	JS	0.015	16	16	0	0	126	39	67	158	148	153	133	7828	IX	1053	33	1614	L2.6
NG167	JS	0.015	16	16	0	0	59	39	67	78	148	153	65	7363	XII/X X X VI	2978	1058	5061	L2.6
NG168	JS	0.03	16	4	0	1	109	39	67	78	148	153	65	7356	X VIII	90	33	568	L2.1
NG169	HN	0.125	16	8	0	0	126	39	67	111	148	153	65	7365	86.001 (partial)	581	33	1866	L2.3
NG170	HN	0.03	16	8	1	0	126	39	67	111	148	153	65	7365	X XI	3531	186	5913	L2.3
NG171	HN	0.125	16	1	0	0	109	39	67	78	148	153	65	7356	X III	90	156	1742	L2.6
NG172	HN	0.03	16	32	0	1	59	39	67	158	148	153	65	7827	X III	4639	4	11170	L2.4
NG173	HN	0.125	16	4	0	0	59	39	67	158	148	153	65	7827	X III	6515	1943	11172	L2.4
NG174	HN	0.03	16	8	1	1	126	39	67	111	148	153	65	7365	X XII	6516	186	11173	L2.3
NG175	HN	0.125	16	8	0	0	59	39	67	158	148	153	65	7827	X III	6517	4	11174	L2.4
NG176	HN	0.03	16	8	0	0	126	39	67	111	149	71	65	6714	X XI	206	156	421	L2.5
NG177	HN	0.125	16	8	0	0	59	39	67	158	148	153	65	7827	X III	1053	287	11175	L2.4
NG178	HN	0.125	16	4	0	0	126	39	67	158	148	153	65	1904	X III	158	443	3340	L2.4
NG179	HN	0.032	16	16	0	0	59	39	67	78	148	153	65	7363	X/X X X V	3215	10	5308	L2.8
NG180	HN	0.25	16	2	0	0	59	39	67	158	148	153	65	7827	X III	5692	4	9652	L2.6
NG181	HN	0.125	16	8	0	1	59	39	67	158	148	153	65	7827	X III	1053	4	2318	L2.4
NG182	HN	0.125	16	4	0	0	59	39	67	158	148	153	65	7827	X III	1053	4	2318	L2.4
NG183	HN	0.125	16	8	0	0	109	39	67	111	148	153	133	7367	II	3723	1036	6312	L2.1
NG184	HN	0.125	16	2	0	1	59	39	67	158	148	153	65	7827	X III	3534	4	5916	L2.6
NG185	HN	0.03	16	0.25	1	0	126	39	67	111	148	154	65	9899	X XI	246	1817	11183	L2.6
NG186	HN	0.125	16	16	0	0	126	39	67	111	148	153	133	1580	X XI	6521	156	11184	L2.1
NG187	HN	0.016	8	2	1	1	126	39	67	111	148	153	65	7365	X XI	6522	33	11185	L2.3
NG188	HN	0.016	8	2	1	1	109	39	67	111	148	153	133	7367	II	1123	1036	11187	L2.1
NG189	HN	0.03	8	0.125	1	0	126	39	67	78	148	153	65	1600	II	1042	737	3282	L2.2
NG190	HN	0.03	16	8	1	0	126	39	67	111	148	153	65	7365	X XI	3531	473	11189	L2.3
NG191	HN	0.06	16	16	0	0	126	39	67	111	148	153	133	1580	X XI	1508	156	11180	L2.1
NG192	HN	0.125	16	2	1	0	126	39	67	111	148	153	65	7365	X XI	6526	186	11192	L2.3
NG193	HN	0.015	8	8	0	0	59	39	67	78	148	153	65	7363	NA	6527	1946	11193	L2.3
NG194	HN	0.125	16	8	0	0	109	39	67	158	148	153	65	9304	X VIII	6528	477	11194	L2.1
NG195	HN	0.125	16	2	0	1	59	39	67	158	148	153	65	7827	X III	1053	4	2318	L2.4
NG196	HN	0.25	16	16	0	1	59	39	67	158	148	153	65	7827	X III	1053	4	2318	L2.4
NG197	HN	0.125	16	8	0	0	126	39	67	158	148	153	65	1904	X III	6538	4	11216	L2.4
NG198	SC	0.125	16	16	0	1	59	39	67	78	147	154	65	11231	X VIII	543	107	4676	L2.2
NG199	SC	0.125	8	16	0	1	59	39	67	78	147	154	65	11231	X VIII	6059	4	11248	L2.2
NG200	SC	0.125	8	16	0	1	126	39	67	111	148	153	65	7365	X III	184	21	11255	L2.5

NG201	SC	0.25	64	16	0	1	59	39	67	78	148	153	65	7363	X/X X X V	917	10	1424	L2.8
NG202	SC	0.008	16	8	1	0	109	39	67	111	148	153	133	7367	II	6549	4	11234	L2.1
NG203	SC	0.008	16	16	0	1	109	39	67	111	148	153	133	7367	II	1135	1093	5161	L2.9
NG204	SC	0.008	16	16	1	1	109	39	67	111	148	153	133	7367	II	1135	1093	5161	L2.9
NG205	SC	0.015	16	16	1	0	109	39	67	111	148	153	133	7367	II	3029	1036	5062	L2.1
NG206	SC	0.015	32	4	0	1	59	112	67	157	148	153	65	11191	X III	251	156	10354	L2.7
NG207	SC	0.015	16	8	1	1	59	39	67	158	148	71	65	1588	X IX	217	33	2366	L2.6
NG208	SC	0.015	8	8	1	1	126	39	67	111	148	153	65	7365	X III	6554	21	11251	L2.5
NG209	SC	0.015	16	4	1	0	59	112	67	157	148	153	65	11191	X III	251	1921	11227	L2.7
NG210	SC	0.015	16	16	1	1	109	39	67	111	148	153	133	7367	II	1135	446	1768	L2.9
NG211	SC	0.015	32	0.125	0	1	126	39	67	157	148	153	65	1903	II	90	18	621	L2.9
NG212	SC	0.03	16	16	1	1	109	39	67	111	148	153	65	1579	II	3029	1036	5062	L2.1
NG213	SC	0.03	16	16	1	0	109	39	67	111	148	153	133	7367	II	3029	4	4991	L2.1
NG214	SC	0.03	8	16	0	0	109	39	67	111	148	153	133	7367	II	6232	1036	10650	L2.1
NG215	SC	0.25	16	≥16	1	0	126	39	67	111	148	153	65	7365	X III	6545	4	11226	L2.5
NG216	SC	0.25	16	≥16	0	1	59	39	67	111	148	153	133	1963	V	731	75	11236	L2.1
NG217	SC	0.25	32	≥16	1	1	435	39	67	111	148	153	65	12515	X III	2022	186	11241	L2.3
NG218	SC	0.25	32	≥16	1	1	109	39	67	111	147	153	65	6960	X XI	130	1951	11243	L2.6
NG219	SC	0.25	32	≥16	1	0	59	39	67	78	148	154	65	1597	X VIII	1132	4	2083	L2.2
NG220	SC	0.25	32	≥16	1	1	126	39	67	111	148	153	65	7365	II	581	137	8784	L2.3
NG221	SC	0.25	16	≥16	1	0	59	39	67	78	147	153	65	11648	X VIII	543	1952	11245	L2.2
NG222	SC	0.25	32	≥16	1	1	126	39	67	111	148	153	65	7365	X III	1053	21	3435	L2.5
NG223	ZJ	0.016	16	8	0	0	59	39	67	158	148	153	65	7827	X III	1132	526	10403	L2.4
NG224	ZJ	0.032	16	8	0	0	59	39	67	158	148	153	65	7827	X III	3971	470	10404	L2.4
NG225	ZJ	0.032	16	2	0	0	109	39	67	158	148	668	65	12969	X VIII	90	1312	10348	L2.1
NG226	ZJ	0.032	16	8	1	0	59	39	67	78	148	153	65	7363	XII/X X X VI	1135	446	1768	L2.6
NG227	ZJ	0.008	16	4	0	1	126	39	67	78	149	71	65	1927	X XI	1448	1036	10400	L2.5
NG228	ZJ	0.032	16	8	1	0	109	39	67	158	148	668	65	12969	X VIII	1879	33	3102	L2.1
NG229	ZJ	0.016	16	8	1	1	126	39	67	111	148	153	65	7365	X III	6058	1841	10312	L2.5
NG230	ZJ	0.016	16	8	1	1	126	39	67	78	148	153	65	1600	X III	1132	1843	10326	L2.2
NG231	ZJ	0.016	32	8	1	0	126	39	67	78	148	153	65	1600	X III	315	33	566	L2.2
NG232	ZJ	0.0625	16	8	0	1	59	39	67	78	149	153	65	10634	X III	1053	1583	8720	L2.5
NG233	ZJ	0.0625	32	8	0	0	126	39	67	111	148	153	65	7365	X XI	4	4	225	L2.1
NG234	ZJ	0.0625	16	8	0	1	59	39	67	158	148	153	65	7827	X III	3760	33	10401	L2.6
NG235	ZJ	0.0625	16	8	0	0	109	39	67	111	148	153	133	7367	X III	6062	1058	10316	L2.9
NG236	ZJ	0.0625	16	4	0	1	126	39	67	78	148	153	65	1600	X III	6567	156	11275	L2.2
NG237	ZJ	0.0625	16	8	0	0	126	39	67	111	146	153	65	9902	5.002 (partial)	6066	107	10320	L2.1
NG238	ZJ	0.0625	16	8	0	1	109	39	67	158	148	153	65	9304	X VIII	1053	4	2318	L2.1
NG239	ZJ	0.0625	16	8	1	1	59	39	67	78	148	153	65	7363	44.001	206	33	270	L2.6
NG240	ZJ	0.0625	16	8	1	1	59	39	67	157	189	153	65	8112	X IV	206	33	270	L2.7
NG241	ZJ	0.0625	16	8	1	1	126	485	67	111	148	153	65	12978	X III	543	156	1996	L2.5
NG242	ZJ	0.0625	16	4	1	0	126	39	67	78	148	153	65	1600	X III	3578	107	10405	L2.6
NG243	ZJ	0.0625	16	8	1	1	109	39	67	111	148	153	133	7367	II	1448	446	10349	L2.1
NG244	ZJ	0.0625	16	8	1	0	126	39	67	111	148	153	65	7365	X XI	1135	446	1768	L2.3
NG245	ZJ	0.0625	16	8	1	1	435	39	67	111	148	153	65	12515	X III	206	33	270	L2.3
NG246	ZJ	0.0625	16	8	0	1	126	39	67	78	148	153	65	1600	X III	6075	75	10331	L2.2
NG247	ZJ	0.0625	16	8	0	0	126	39	67	111	148	153	133	1580	X XI	2035	526	3356	L2.1
NG248	SH	0.016	16	8	0	0	109	39	67	111	148	153	65	1579	44.001	1489	563	2400	L2.1
NG249	SH	0.004	4	4	1	1	126	39	67	78	148	153	65	1600	X III	6029	60	10276	L2.2
NG250	SH	0.03	2	8	0	0	109	39	67	111	148	153	65	1579	X III	708	21	8812	L2.6

NG251	SH	0.016	8	32	0	0	126	39	67	111	148	153	65	7365	X VIII	6030	137	10277	L2.3
NG252	SH	0.004	8	4	0	0	126	39	67	158	148	153	65	1904	X III	1284	1036	10387	L2.3
NG253	SH	0.016	16	8	1	1	126	39	67	111	148	153	65	7365	X XI	3531	1826	10268	L2.3
NG254	SH	0.03	16	1	1	0	59	39	67	158	148	153	65	7827	X III	6031	186	10278	L2.4
NG255	SH	0.016	8	1	1	0	59	39	67	158	148	153	65	7827	X III	6032	4	10279	L2.4
NG256	SH	0.004	2	8	0	1	109	39	67	158	148	153	65	9304	X VIII	2328	156	10388	L2.1
NG258	SH	0.03	8	8	1	0	126	39	67	111	146	154	65	12979	II	1132	857	5304	L2.6
NG259	SH	0.03	4	8	1	0	126	39	67	78	148	153	65	1600	X III	1053	4	2318	L2.6
NG260	SH	0.016	16	2	1	1	126	39	67	78	148	153	65	1600	X III	1448	1832	10280	L2.6
NG261	SH	0.016	8	8	0	1	126	39	67	78	148	153	65	1600	44.001	1879	33	3102	L2.6
NG262	SH	0.016	16	8	1	1	126	39	67	78	149	71	65	1927	II	905	186	10389	L2.5
NG263	SH	0.016	16	8	0	0	126	39	67	111	148	153	133	1580	X XI	1132	4	2083	L2.1
NG264	SH	0.008	8	8	0	0	59	39	67	78	147	154	65	11231	X VIII	6033	137	10281	L2.2
NG265	SH	0.008	4	1	0	1	109	39	67	78	148	153	65	7356	X III	2035	526	3356	L2.6
NG266	GX	0.03	16	4	1	1	126	39	67	111	148	153	65	7365	X XI	1135	1822	10248	L2.3
NG267	GX	0.008	16	0.125	1	0	126	39	67	111	148	154	65	9899	X XI	182	21	247	L2.6
NG268	GX	0.03	8	16	0	0	59	39	67	78	148	153	65	7363	X VIII	6021	137	10260	
NG269	GX	0.06	32	8	1	0	109	39	67	158	148	153	65	9304	X VIII	2261	1823	10262	L2.1
NG270	GX	0.06	32	16	0	0	126	39	67	78	149	153	65	1590	VII	6024	563	10265	L2.5
NG271	GX	0.06	32	4	1	0	126	39	67	111	148	153	65	7365	X III	5924	156	10342	L2.5
NG272	GX	0.06	32	16	0	0	126	39	67	111	148	153	65	7365	X III	6025	156	10267	L2.5
NG273	GX	0.008	8	16	0	1	109	39	67	111	148	153	133	7367	X III	206	865	4823	L2.1
NG274	GX	0.03	8	4	0	0	109	39	67	111	148	153	133	7367	X III	206	156	421	L2.9
NG275	GX	0.008	8	4	1	0	109	39	67	111	147	153	65	6960	X XI	251	483	1927	L2.1
NG276	GX	0.5	32	16	1	1	126	39	67	158	148	153	65	1904	II	206	1817	11129	L2.3
NG277	GX	0.008	8	2	0	0	126	39	67	158	148	153	65	1904	II	1132	156	2271	L2.3
NG278	GX	0.03	8	8	0	0	109	39	67	111	148	153	133	7367	X III	2035	215	11133	L2.1
NG279	GX	0.03	16	16	0	0	126	39	67	158	148	153	65	1904	II	915	21	1422	L2.3
NG280	TJ	0.0625	16	32	0	0	126	39	67	78	146	153	65	1601	V	6040	75	10288	L2.1
NG281	TJ	0.25	16	32	0	0	59	39	67	78	148	153	65	7363	X/X X X V	917	10	1424	L2.8
NG282	TJ	0.0625	8	4	1	1	59	39	67	157	148	153	65	1599	X III	6041	479	10289	L2.3
NG283	TJ	0.0625	16	4	1	0	59	39	67	111	148	153	65	1583	X III	1715	547	10345	L2.2
NG284	TJ	0.0625	16	8	0	0	59	39	67	78	148	153	65	7363	X III	1053	4	2318	L2.4
NG285	TJ	0.0625	8	4	0	0	59	39	67	111	148	153	65	1583	X III	1715	547	10345	L2.2
NG286	TJ	0.0625	8	16	0	0	109	39	67	78	148	71	65	1603	X XI	6046	1838	10299	L2.5
NG287	TJ	0.0625	16	32	0	0	59	39	67	111	148	153	65	1583	X VIII	6049	328	10302	L2.1
NG288	TJ	0.0625	8	4	1	0	59	39	67	111	148	153	65	1583	X III	1715	547	10345	L2.2
NG289	CQ	0.06	16	16	0	1	126	39	67	111	148	153	65	7365	X III	6475	21	11110	L2.5
NG290	CQ	0.06	16	16	0	1	126	39	67	78	148	153	65	1600	IX	6476	1932	11111	L2.6
NG291	CQ	0.06	32	16	1	1	126	39	67	111	148	153	65	7365	II	6477	186	11112	L2.3
NG292	CQ	0.06	16	16	0	0	109	39	67	111	148	153	133	7367	II	3029	1036	5062	L2.1
NG293	CQ	0.06	16	16	1	1	126	39	67	158	148	153	65	1904	X III	6478	4	11113	L2.4
NG294	CQ	0.06	32	4	0	0	59	39	67	158	148	153	65	7827	19.001 (partial)	1448	4	4846	L2.6
NG295	CQ	0.06	32	8	0	1	126	39	67	111	148	153	65	7365	XII/X X X VI	1135	1933	11116	L2.2
NG296	GD	0.25	16	4	1	0	126	39	67	111	149	153	65	1928	X VIII	1226	137	10339	L2.3
NG297	GD	0.25	16	4	1	1	126	39	67	78	148	153	65	1600	X III	1733	156	2841	L2.2
NG298	GD	0.25	16	16	1	0	109	39	67	111	148	153	133	7367	II	6015	1817	10241	L2.9
NG299	GD	0.25	8	32	0	1	126	39	67	111	148	153	65	7365	X III	6016	1818	10242	L2.5
NG300	GD	0.25	16	32	0	0	109	39	67	111	148	153	133	7367	II	2978	1058	5061	L2.9
NG301	GD	0.25	16	32	0	1	126	39	67	111	148	153	65	7365	X III	6016	1818	10242	L2.5

NG302	GD	0.125	16	16	0	0	59	39	67	78	148	153	65	7363	X/X X X V	5979	10	10199	L2.8
NG303	GD	0.125	8	4	0	1	59	39	67	78	147	154	65	11231	X III	1448	4	4846	L2.2
NG304	GD	0.125	8	32	0	0	59	39	67	111	148	153	65	1583	X VIII	5987	1780	10207	L2.1
NG305	GD	0.125	32	8	0	0	59	39	67	158	148	153	65	7827	X III	4197	110	9176	L2.6
NG306	GD	0.032	4	8	0	0	59	39	67	78	148	153	65	7363	X/X X X V	6003	1815	10228	L2.8
NG307	GD	0.002	16	2	0	1	109	39	67	158	148	668	65	12969	X VIII	6006	367	10231	L2.1
NG308	GD	0.004	16	16	0	0	435	39	67	78	148	153	65	12980	V	90	33	568	L2.6
NG309	GD	0.004	16	2	0	0	59	39	67	78	149	154	65	11956	II	6011	953	10237	L2.6
NG310	GD	0.004	16	4	1	0	59	39	67	78	148	153	65	7363	X III	6013	566	10239	L2.5
NG311	GD	0.004	16	16	0	1	126	39	67	111	146	153	65	9902	3.001 (partial)	609	186	1056	L2.1
NG312	GD	0.004	16	2	1	0	59	39	67	111	148	153	65	1583	II	90	137	1691	
NG313	GD	0.004	8	2	0	1	109	39	67	111	148	153	65	1579	V	4	1812	10212	L2.1
NG314	GD	0.016	8	0.25	1	0	109	39	67	111	149	153	65	11115	X III	4179	21	10350	L2.5
NG315	GD	0.0312	16	4	1	0	126	39	67	111	148	153	65	7365	II	581	33	1866	L2.3
NG316	GD	0.25	16	32	0	0	126	39	67	111	146	153	65	9902	X VII	182	870	10378	L2.1
NG317	GD	0.125	16	16	0	0	109	39	67	111	148	153	65	1579	V	489	110	10367	L2.1
NG318	GD	0.125	16	16	1	0	59	39	67	78	148	153	65	7363	XII/X X X VI	1226	137	10339	L2.6
NG319	GD	0.125	8	4	0	0	59	39	67	111	148	153	65	1583	X VIII	6012	470	10238	L2.1
NG320	GD	0.125	8	16	0	1	109	39	67	111	148	153	65	1579	V	6018	110	10244	L2.1
NG321	GD	0.125	16	8	0	1	59	39	67	158	148	153	65	7827	X/X X X V	6001	21	10225	L2.6
NG322	GD	0.125	8	16	0	1	109	39	67	111	148	153	133	7367	II	3029	1036	5062	L2.1
NG323	GD	0.125	16	16	1	0	126	39	67	78	148	153	65	1600	V	1053	913	5114	L2.1
NG324	GD	0.125	16	8	0	0	59	39	67	158	148	153	65	7827	X III	1132	4	2083	L2.4
NG325	GD	0.032	16	16	1	0	126	39	67	111	148	153	65	7365	50.001 (patial)	1971	33	3242	L2.3
NG326	GD	0.125	8	8	0	0	109	39	67	78	148	153	65	7356	X III	4	752	4539	L2.6
NG327	GD	0.125	16	16	0	0	59	39	67	78	148	153	65	7363	X/X X X V	3215	10	5308	L2.8
NG328	TJ	0.0625	8	4	0	0	59	39	67	111	148	153	65	1583	X III	1715	547	10345	L2.2
NG329	TJ	0.008	8	8	0	0	59	39	67	78	148	153	65	7363	XII/X X X VI	2978	1058	5061	L2.6
NG330	TJ	0.016	16	8	0	1	109	39	67	78	148	153	65	7356	XII/X X X VI	1273	571	2438	L2.6
NG331	TJ	0.008	16	4	1	0	126	39	67	111	148	153	133	1580	II	4	186	1731	L2.3
NG332	TJ	0.008	16	16	0	1	59	39	67	158	148	153	65	7827	X III	1053	33	1614	L2.4
NG333	TJ	0.008	16	8	0	0	126	39	67	111	149	71	65	6714	X XI	206	156	421	L2.5
NG334	TJ	0.016	16	8	0	0	109	39	67	111	148	153	65	1579	V	4	4	225	L2.1
NG335	TJ	0.0625	16	8	0	0	109	39	67	78	148	153	65	7356	X III	4	752	4539	L2.6
NG336	SH	0.004	4	16	0	0	126	39	67	111	146	153	65	9902	V	1226	738	10390	L2.1
NG337	SH	0.03	16	32	1	1	126	39	67	111	148	153	65	7365	X VIII	1226	137	10339	L2.3
NG338	SH	0.06	16	4	0	0	109	39	67	111	148	153	65	1579	X/X X X V	4431	110	7393	L2.1
NG339	SH	0.016	8	1	0	1	59	112	67	158	148	153	65	11976	19.001 (partial)	1448	4	4846	L2.6
NG340	SH	0.06	16	8	0	0	59	39	67	158	148	153	65	7827	X III	1053	4	2318	L2.4
NG341	SH	0.016	8	16	0	0	59	39	67	111	148	153	65	1583	X VIII	206	470	2268	L2.1
NG342	SH	0.004	8	8	1	0	126	39	67	158	148	153	65	1904	II	581	33	1866	L2.3
NG343	SH	0.016	8	8	0	1	126	39	67	111	148	153	65	7365	X III	90	21	436	L2.5
NG344	JS	0.03	16	8	1	1	126	39	67	111	148	153	65	7365	II	5167	75	8725	L2.3
NG345	JS	0.03	16	8	1	1	126	39	67	111	148	153	65	7365	II	5167	75	8725	L2.3
NG347	JS	0.03	16	16	0	1	126	39	67	111	146	153	65	9902	V	5168	858	8726	L2.1
NG348	JS	0.03	16	16	0	0	109	39	67	78	148	153	65	7356	XII/X X X VI	1053	137	8727	L2.6
NG349	JS	0.015	16	16	1	1	109	39	67	111	148	153	133	7367	II	1135	446	1768	L2.9
NG350	JS	0.03	16	16	0	1	126	39	67	111	146	153	65	9902	V	5168	858	8726	L2.1
NG351	JS	0.03	16	16	0	0	126	39	67	111	146	153	65	9902	V	1445	738	3284	L2.1
NG352	JS	0.03	16	8	0	0	59	39	67	158	148	153	65	7827	X III	5169	33	8729	L2.4

NG353	JS	0.06	16	8	1	1	126	39	67	78	148	153	65	1600	X III	1132	33	1766	L2.2
NG354	JS	0.06	16	16	1	0	126	39	67	111	148	153	65	7365	X XI	1422	33	8728	L2.3
NG355	JS	0.06	16	8	1	0	59	39	67	111	148	153	65	1583	X III	5171	1586	8732	L2.2
NG356	JS	0.06	16	16	0	1	126	299	67	78	148	153	133	12981	X XI	3580	156	5990	L2.1
NG357	JS	0.06	16	16	0	0	109	39	67	111	148	153	65	1579	V	1275	4	2016	L2.1
NG358	JS	0.06	8	8	1	0	126	39	67	111	148	153	65	7365	X III	5166	33	8724	L2.3
NG359	JS	0.06	16	8	0	1	59	39	67	158	148	153	65	7827	X III	1053	4	2318	L2.4
NG360	JS	0.06	16	8	0	1	59	39	67	158	148	153	65	7827	X III	1053	4	2318	L2.4
NG361	JS	0.06	16	16	1	0	126	39	67	78	148	153	65	1600	X III	1132	33	1766	L2.2
NG362	JS	0.06	16	16	1	1	59	112	67	157	148	153	65	11191	X III	251	483	1927	L2.7
NG363	JS	0.06	16	16	0	0	109	39	67	111	148	153	65	1579	V	3996	33	6691	L2.1
NG364	ZJ	0.032	16	8	0	0	109	39	67	111	148	153	65	1579	V	5541	110	10402	L2.1
NG365	ZJ	0.016	16	8	0	1	59	112	67	157	148	153	65	11191	X III	760	483	10410	L2.7
NG366	ZJ	0.0625	16	8	0	1	59	39	67	158	148	153	65	7827	X III	1053	4	2318	L2.4
NG367	ZJ	0.0625	16	2	0	1	59	39	67	158	148	153	65	7827	X III	1448	4	4846	L2.6
NG368	ZJ	0.0625	16	8	0	0	109	39	67	158	148	153	65	9304	X VIII	2035	526	3356	L2.1
NG369	ZJ	0.032	16	8	1	0	126	39	67	158	148	153	65	1904	II	505	33	2277	L2.3
NG370	HN	0.125	16	32	0	0	59	39	67	111	148	153	65	1583	X VIII	6524	1780	11190	L2.1
NG371	HN	0.25	16	2	1	0	126	39	67	78	148	153	65	1600	IX	6525	324	11191	L2.5
NG372	HN	0.25	16	2	1	0	59	39	67	158	148	71	65	1588	X VIII	6529	21	11195	L2.6
NG373	HN	0.25	16	2	0	1	59	39	67	78	148	153	133	1587	X XI	6535	33	11203	L2.6
NG374	HN	0.125	16	4	0	0	59	39	67	158	148	153	65	7827	X III	1053	1942	11169	L2.4
NG375	HN	0.125	16	8	0	0	59	39	67	158	148	153	65	7827	X III	1053	287	11175	L2.4
NG376	HN	0.25	16	16	0	0	109	39	67	78	148	153	65	7356	X III	4	752	4539	L2.6
NG377	HN	0.03	16	1	0	0	59	39	67	158	148	153	65	7827	X III	251	4	4367	L2.4
NG378	HN	0.25	8	8	0	0	109	39	67	111	148	153	133	7367	II	3029	1036	5062	L2.1
NG379	HN	0.125	16	8	0	0	59	39	67	158	148	153	65	7827	X III	1053	21	3435	L2.4
NG380	CQ	0.015	32	16	1	1	126	39	67	78	149	71	65	1927	X XII	6490	21	11128	L2.5
NG381	CQ	0.015	16	16	1	1	59	39	67	158	148	71	65	1588	X IX	6486	137	11124	L2.6
NG382	CQ	0.125	16	16	0	1	59	39	67	158	148	71	133	12982	X III	6485	107	11123	L2.1
NG383	CQ	0.06	32	16	1	1	126	39	67	158	148	153	65	1904	X III	6478	1934	11121	L2.4
NG384	CQ	0.06	32	16	0	1	126	39	67	111	148	153	65	7365	X III	5228	21	11119	L2.5
NG385	CQ	0.03	32	4	1	1	126	39	67	111	148	153	65	7365	X VIII	1448	186	2325	L2.3
NG386	CQ	0.015	16	16	1	0	59	39	67	158	148	153	65	7827	X III	1132	4	2083	L2.4
NG387	CQ	0.03	32	16	1	1	126	39	67	158	148	153	65	1904	II	581	33	1866	L2.3
NG388	SC	0.125	32	4	0	0	59	39	67	158	148	153	65	7827	X III	5692	186	11244	L2.6
NG389	SC	0.125	32	≥16	1	0	59	39	67	158	148	153	65	7827	X III	5174	4	11238	L2.4
NG390	SC	0.125	16	16	1	0	59	39	67	78	147	71	65	11961	X VIII	328	1830	11229	L2.2
NG391	SC	0.125	16	≥16	1	0	126	39	67	78	148	153	65	1600	X VIII	1053	186	3289	L2.5
NG392	SC	0.125	32	≥16	1	1	109	39	67	111	148	153	133	7367	II	3029	1036	5062	L2.1
NG393	SC	0.125	32	≥16	1	1	59	39	67	78	148	153	65	7363	X/X X X V	917	10	1424	L2.8
NG394	SC	0.125	32	≥16	1	0	59	39	67	78	148	153	65	7363	X/X X X V	917	10	1424	L2.8
NG395	SC	0.03	16	16	0	0	59	39	67	158	148	153	65	7827	X III	1132	33	1766	L2.4
NG396	SC	0.03	64	0.25	0	0	109	39	67	78	149	71	65	10931	22.001 (partial)	318	74	912	L2.5
NG397	SC	0.016	16	≥16	0	1	109	39	67	111	148	153	133	7367	X XI	5924	4	10091	L2.1
NG398	SC	0.016	0.016	16	0	0	109	39	67	111	148	153	65	1579	II	3029	1036	5062	L2.1
NG399	SC	0.016	16	≥16	1	1	126	39	67	78	148	153	65	1600	X III	1132	33	1766	L2.2
NG400	SC	0.08	32	4	0	1	59	39	67	158	148	153	65	7827	X IX	1448	4	4846	L2.6
NG401	SC	≤0.004	8	8	0	1	126	39	67	111	148	153	65	7365	X XI	4	186	1731	L2.3
NG402	SC	0.06	16	16	1	1	109	39	67	111	148	153	133	7367	X XI	1135	446	1768	L2.9

NG403	TJ	0.032	16	8	0	0	109	39	67	158	148	153	65	9304	X VIII	2035	526	3356	L2.1
NG404	TJ	0.032	16	8	0	0	59	39	67	158	148	153	65	7827	X III	1053	186	3289	L2.4
NG405	TJ	0.008	16	32	0	1	109	39	67	111	148	153	65	1579	V	6054	33	10308	L2.1
NG406	TJ	0.016	16	16	0	0	126	39	67	78	146	153	65	1601	V	6043	75	10293	L2.1
NG407	TJ	0.016	8	8	0	0	126	39	67	111	147	153	65	11196	X III	6048	156	10301	L2.5
NG408	TJ	0.016	16	16	0	0	126	39	67	78	146	153	65	1601	V	609	75	10394	L2.1
NG409	SH	0.03	16	8	0	0	109	39	67	111	148	153	65	1579	V	1912	186	10385	L2.1
NG410	SH	0.004	8	8	1	1	126	39	67	111	146	153	65	9902	V	6036	858	10284	L2.1
NG411	SH	0.016	4	4	1	1	126	39	67	78	149	71	65	1927	X XI	6034	156	10282	L2.5
NG413	GD	0.032	16	8	1	1	126	39	67	78	148	153	65	1600	X III	2261	186	3741	L2.6
NG414	GD	0.032	16	16	1	1	126	39	67	111	148	153	65	7365	X XI	1132	33	1766	L2.3
NG415	GD	0.0312	16	4	1	0	126	39	67	111	148	153	65	7365	IX	581	33	1866	L2.3
NG416	GD	0.016	16	16	0	1	109	39	67	111	148	153	133	7367	II	1135	446	1768	L2.9
NG417	GD	0.016	16	8	1	1	126	39	67	111	148	153	65	7365	X XI	4	4	225	L2.3
NG418	GD	0.032	16	4	0	0	109	39	67	111	148	153	65	1579	X III	6002	1360	10226	L2.1
NG419	GD	0.008	16	8	0	1	109	39	67	111	148	153	133	7367	II	3029	1036	5062	L2.1
NG420	HN	0.125	16	8	0	1	59	39	67	158	148	153	65	7827	X III	6530	4	11196	L2.4
NG421	HN	0.125	16	16	0	0	126	39	67	111	148	153	133	1580	X XI	6532	33	11199	L2.1
NG422	HN	0.125	16	16	0	0	126	39	67	111	148	153	133	1580	X XI	6533	33	11200	L2.1
NG423	HN	0.06	16	2	0	0	59	39	67	158	148	153	65	7827	X III	1448	4	4846	L2.6
NG424	HN	0.03	16	4	0	0	126	39	67	158	148	153	65	1904	13.001 (partial)	5924	4	10091	L2.3
NG425	HN	0.03	8	1	1	1	126	39	67	78	148	153	65	1600	X III	1132	33	1766	L2.2
NG426	HN	0.03	8	0.125	1	0	126	39	67	158	148	153	133	7828	IX	1053	33	1614	L2.6
NG427	HN	0.03	16		0	0	109	39	67	78	149	71	65	10931	22.001 (partial)	318	74	912	L2.5
NG428	CQ	0.03	32	16	1	1	109	39	67	111	148	153	133	7367	II	3029	1036	5062	L2.1
NG429	CQ	0.03	16	16	1	1	126	39	67	78	148	153	65	1600	X III	1132	33	1766	L2.2
NG430	GD	0.032	16	16	1	0	126	39	67	111	148	153	65	7365	X III	6000	33	10224	L2.3
NG431	GD	0.016	16	0.5	0	0	126	39	67	111	148	153	65	7365	X XI	1135	33	3285	L2.3
NG432	GD	0.008	16	16	1	1	126	39	67	111	148	154	65	9899	X XI	543	75	1393	L2.6
NG433	JS	0.06	16	8	1	1	59	39	67	111	148	153	65	1583	87.001	866	156	1750	L2.2
NG434	JS	0.06	16	16	0	0	59	39	67	158	148	153	65	7827	X III	1053	4	2318	L2.4
NG435	SH	0.03	4	4	1	0	59	39	67	78	148	153	65	7363	X VIII	2894	1828	10271	L2.5
NG436	SH	0.03	16	16	0	0	109	39	67	111	148	153	65	1579	V	1053	110	3702	L2.1
NG437	SH	0.03	16	8	0	0	109	39	67	78	148	153	65	7356	X VIII	90	33	568	L2.1
NG438	SH	0.03	16	16	1	1	126	39	67	78	148	153	65	1600	X VIII	609	33	4745	L2.5
NG439	SH	0.03	4	16	0	0	109	39	67	111	147	153	65	6960	X VIII	6035	1473	10283	L2.1
NG440	SH	0.03	16	16	0	0	126	39	67	111	146	153	65	9902	X VIII	182	186	2051	L2.1

Table S4: Summary of specific nucleotides and deduced amino acids for lineage 1 (L1) and lineage 2 (L2)

Gene (ID [*])	Product	Nucleotides			Amino acids [§]		
		Position	L1	L2	Position	L1	L2
<i>gatC</i> (NGO0663)	aspartyl/glutamyl-tRNA amidotransferase subunit C	65	C	A	22	<u>A</u>	<u>E</u>
		106	G	A	36	<u>A</u>	<u>I</u>
		221	T	C	74	<u>V</u>	<u>A</u>
		237	C	T	79	V	V
		240	A	G	80	A	A
<i>gatA</i> (NGO0662)	aspartyl/glutamyl-tRNA amidotransferase subunit A	6	A	C	2	T	T
		28	A	G	10	<u>S</u>	<u>G</u>
		31	G	A	11	<u>G</u>	<u>S</u>
		32	T	G	11	<u>I</u>	<u>S</u>
		69	A	G	23	L	L
		108	T	C	36	P	P
		171	T	C	57	D	D
		265	A	G	89	<u>I</u>	<u>A</u>
		266	G	C	89	<u>G</u>	<u>A</u>
		279	G	C	93	L	L
		336	C	T	112	G	G
		456	C	A	152	S	S
		513	T	C	171	D	D
		540	G	A	180	A	A
		597	C	T	199	G	G
		717	G	A	239	E	E
		759	T	C	253	L	L
		766	A	G	256	<u>M</u>	<u>V</u>
		835	C	A	279	<u>H</u>	<u>N</u>
		837	T	C	279	N	N
846	C	T	282	D	D		
847	C	T	283	L	L		
849	C	G	283	<u>F</u>	<u>L</u>		
852	C	G	284	L	L		
1089	A	G	363	L	L		
1328	A	G	443	<u>D</u>	<u>G</u>		
1338	A	G	446	L	L		
1342	A	G	448	<u>I</u>	<u>V</u>		
1357	A	G	453	<u>I</u>	<u>V</u>		
1416	T	C	472	N	N		

<i>gatB</i>	aspartyl/glutamyl-tRNA	6	C	T	2	T	T
(NGO0660)	amidotransferase subunit B	15	C	T	5	T	T
		72	C	T	24	G	G
		79	G	A	27	<u>A</u>	<u>I</u>
		91	T	G	31	<u>S</u>	<u>A</u>
		123	G	A	41	E	E
		159	G	C	53	R	R
		186	G	A	62	L	L
		195	C	T	65	A	A
		198	A	G	66	L	L
		204	G	A	68	A	A
		213	T	C	71	N	N
		215	A	G	72	<u>Q</u>	<u>R</u>
		261	C	G	87	P	P
		279	T	C	93	S	S
		288	C	T	96	D	D
		291	A	G	97	L	L
		324	A	G	108	V	V
		332	A	G	111	<u>D</u>	<u>G</u>
		360	T	C	120	R	R
		387	G	A	129	K	K
		396	T	C	132	H	H
		399	A	G	133	E	E
		420	T	C	140	G	G
		471	T	C	157	P	P
		537	A	G	179	L	L
		570	A	G	190	S	S
		577	G	A	193	<u>V</u>	<u>I</u>
		597	G	T	199	V	V
		609	T	C	203	G	G
		614	A	C	205	<u>E</u>	<u>A</u>
		615	A	G	205	A	A
		618	T	A	206	<u>D</u>	<u>E</u>
		636	G	A	212	E	E

* IDs are refer to the reference genome of *N. gonorrhoeae* FA1090 (GenBank accession: NC_002946);

§ Different amino acids between L1 and L2 are underlined.

Table S5: Summary of L2 sublineage specific nucleotides*

Sub-lineage	Gene/Intergenic ID	Genomic location	Reference nucleotide	Specific nucleotide	Mutation type
L2.1	NGO0963-NGO0968	939,972	G	A	noncoding
	NGO1308	1,266,350	C	T	synonymous
	NGO1308	1,266,530	C	T	synonymous
L2.2	NGO1954-NGO1955	1,926,844	A	G [§]	noncoding
	NGO2020	1,990,506	C	T	nonsynonymous
L2.3	NGO0089	97,793	C	T	synonymous
	NGO0187	188,878	G	A	nonsynonymous
	NGO0435	428,633	G	A	nonsynonymous
	NGO1205	1,151,437	C	A	synonymous
L2.4	NGO0110	122,722	C	T	nonsynonymous
	NGO0186-NGO0187	187,520	A	G	noncoding
	NGO0335	330,758	C	T	synonymous
	NGO0781	775,415	C	T	nonsynonymous
	NGO0921	902,281	C	T	synonymous
	NGO_t18-NGO1024	986,226	C	G	noncoding
	NGO1562	1,535,448	G	A	nonsynonymous
	NGO1851-NGO1852	1,823,648	G	A	noncoding
L2.5	NGO0553	529,583	C	T	synonymous
	NGO0553	530,635	C	T	nonsynonymous
L2.6	NGO0186	186,796	A	G	nonsynonymous
	NGO0328-NGO0329	325,581	A	G	noncoding
	NGO1152-NGO1154	1,093,479	A	G	noncoding
	NGO2023-NGO2024	1,994,932	G	A	noncoding
	NGO2026	1,996,783	A	G	nonsynonymous
L2.7	NGO0789	781,842	G	G	-
	NGO1835	1,804,390	C	C	-
L2.8	NGO0318-NGO_t07	317,522	C	T	noncoding
	NGO0988	959,831	G	A	nonsynonymous
L2.9	NGO0754-NGO0755	752,122	C	G	noncoding
	NGO0754-NGO0755	752,128	G	A	noncoding
	NGO1150	1,090,354	G	C	nonsynonymous

* All IDs and genomic locations are refer to the reference genome of *N. gonorrhoeae* FA1090 (GenBank accession: NC_002946); [§] Shared with L2.3.

Table S6: Summary of statistical analysis of MICs.

	Number (MIC)	p value (t test)
ST1600		
L2.2	23(0.064±0.067mg/L)	0.408
L2.6	10(0.045±0.034mg/L)	
ST7363		
L2.6	13(0.054±0.043mg/L)	0.007
L2.8	11(0.134±0.085mg/L)	
ST7365		
L2.3	36(0.046±0.049mg/L)	0.004
L2.5	15(0.107±0.096mg/L)	
ST7367		
L2.1	23(0.057±0.061mg/L)	0.728
L2.9	12(0.066±0.089mg/L)	
ST7827		
L2.4	48(0.071±0.052mg/L)	0.453
L2.6	26(0.061±0.059mg/L)	

Table S7: Results of ceftriaxone genetic resistance determinants

Resistant determinants	Cfx-DS isolates (n=207)	Cfx-S isolates (n=418)
PBP2		
A501T	21	39
A501V	59	158
G542S	28	57
P551S	41	85
P551L	2	17
PORB		
G120K	94	221
G120D	5	35
A121D	71	171
MTRR		
G45D	41	122

Table S8: Characteristics of ceftriaxone-resistant isolates

Identification	Geographic site	Ceftriaxone MIC	penA type by NG-STAR	mosaic penA	pen A			porB			MLST ST	NG-MAST ST	NG-STAR ST	Lineage
					A501	G542	P551	G120	A121	G45				
NG014	Zhejiang	0.5	34	Yes	WT	WT	WT	G120K	A121N	WT	1579	10332	627	L2.1
NG060	Guangxi	0.25	10	Yes	WT	WT	WT	G120K	A121D	G45D	7363	1424	4	L2.8
NG086	Chongqing	0.25	5	No	WT	G542S	WT	G120K	A121D	WT	9902	11115	225	L2.1
NG163	Guangdong	0.25	43	No	A501V	WT	WT	G120D	WT	WT	1600	13663	929	L2.2
NG180	Hainan	0.25	13	No	A501V	WT	P551S	WT	WT	WT	7827	9652	1100	L2.6
NG196	Hainan	0.25	13	No	A501V	WT	P551S	G120K	A121D	G45D	7827	2318	1101	L2.4
NG201	Sichuan	0.25	10	Yes	WT	WT	WT	G120K	A121D	G45D	7363	1424	4	L2.8
NG215	Sichuan	0.25	12	No	A501V	WT	P551S	G120K	A121N	WT	7365	11226	1106	L2.5
NG216	Sichuan	0.25	4	No	WT	G542S	WT	G120K	A121G	WT	1963	11236	1107	L2.1
NG217	Sichuan	0.25	43	No	A501V	WT	WT	G120K	A121D	WT	12515	11241	114	L2.3
NG218	Sichuan	0.25	21	No	A501V	WT	WT	G120K	A121D	WT	6960	11243	1118	L2.6
NG219	Sichuan	0.25	18	No	WT	WT	WT	G120D	WT	G45D	1597	2083	1102	L2.2
NG220	Sichuan	0.25	2	No	WT	WT	WT	G120K	A121D	G45D	7365	8784	73	L2.3
NG221	Sichuan	0.25	18	No	A501V	G542S	WT	G120K	A121G	WT	11648	11245	346	L2.2
NG222	Sichuan	0.25	12	No	A501V	WT	P551S	G120K	A121D	WT	7365	3435	1103	L2.5
NG276	Guangxi	0.5	2	No	WT	WT	WT	G120K	A121D	G45D	1904	11129	73	L2.3
NG281	Tianjin	0.25	10	Yes	WT	WT	WT	G120K	A121D	G45D	7363	1424	4	L2.8
NG296	Guangdong	0.25	18	No	A501T	G542S	WT	G120K	A121G	G45D	1928	10339	1104	L2.3
NG297	Guangdong	0.25	43	No	WT	WT	WT	G120K	A121D	WT	1600	2841	513	L2.2
NG298	Guangdong	0.25	2	No	WT	WT	WT	G120K	A121N	WT	7367	10241	1105	L2.9
NG299	Guangdong	0.25	12	No	A501V	WT	P551S	G120K	A121N	WT	7365	10242	1106	L2.5
NG300	Guangdong	0.25	2	No	WT	WT	P551S	G120K	A121N	WT	7367	5061	1108	L2.9
NG301	Guangdong	0.25	12	No	A501V	WT	WT	G120K	A121D	WT	7365	10242	1106	L2.5
NG316	Guangdong	0.25	17	No	A501V	G542S	P551L	G120K	A121D	WT	9902	10378	1109	L2.1
NG371	Hainan	0.25	18	No	WT	WT	P551L	G120K	A121D	WT	1600	11191	1110	L2.5
NG372	Hainan	0.25	18	No	A501T	G542S	WT	G120K	A121D	WT	1588	11195	1111	L2.6
NG373	Hainan	0.25	21	No	A501V	WT	WT	G120K	WT	WT	1587	11203	1112	L2.6
NG376	Hainan	0.25	18	No	A501V	WT	P551S	G120K	A121D	G45D	7356	4539	495	L2.6
NG378	Hainan	0.25	2	No	WT	WT	WT	G120K	A121D	WT	7367	5062	470	L2.1

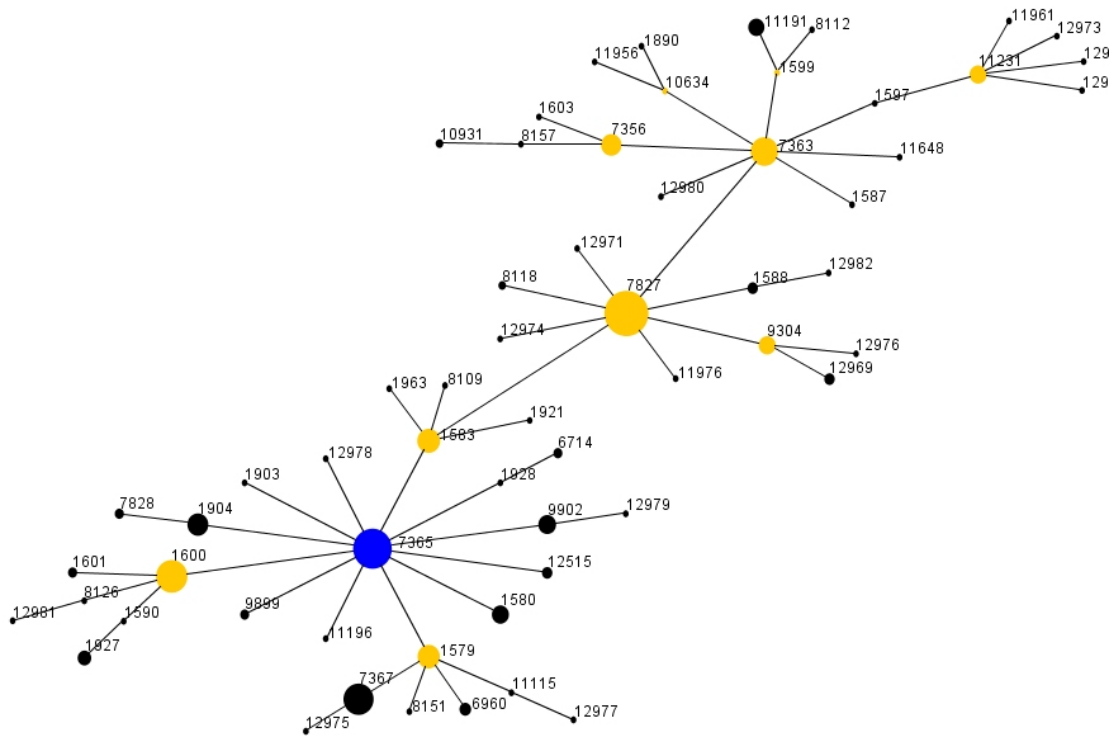


Figure S1: eBURST analysis of 60 STs obtained from isolates collected in this study

eBURST analysis showing the ST relationship of 437 *N. gonorrhoeae* isolates sequenced in this study. The predicted founding genotype was coloured in blue, while subgroup founders were coloured in yellow. STs with single locus variance were linked with a solid line. Frequency of each ST was proportional to the size of circle.

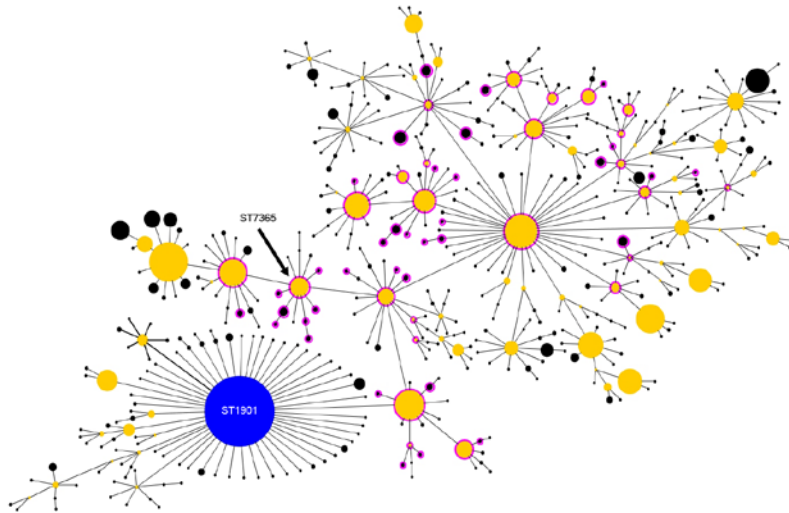


Figure S2: eBURST analysis of 566 identified STs

Group 1 of eBURST analysis of 4287 *N. gonorrhoeae* isolates in PubMLST database. The predicted founding genotype was coloured in blue, while subgroup founders were coloured in yellow. Pink 'halos' denoted STs which were found in this study. STs with single locus variance were linked with a solid line. Frequency of each ST was proportional to the size of circle. ST labels were hidden for clarity.

Tree scale: 0.1

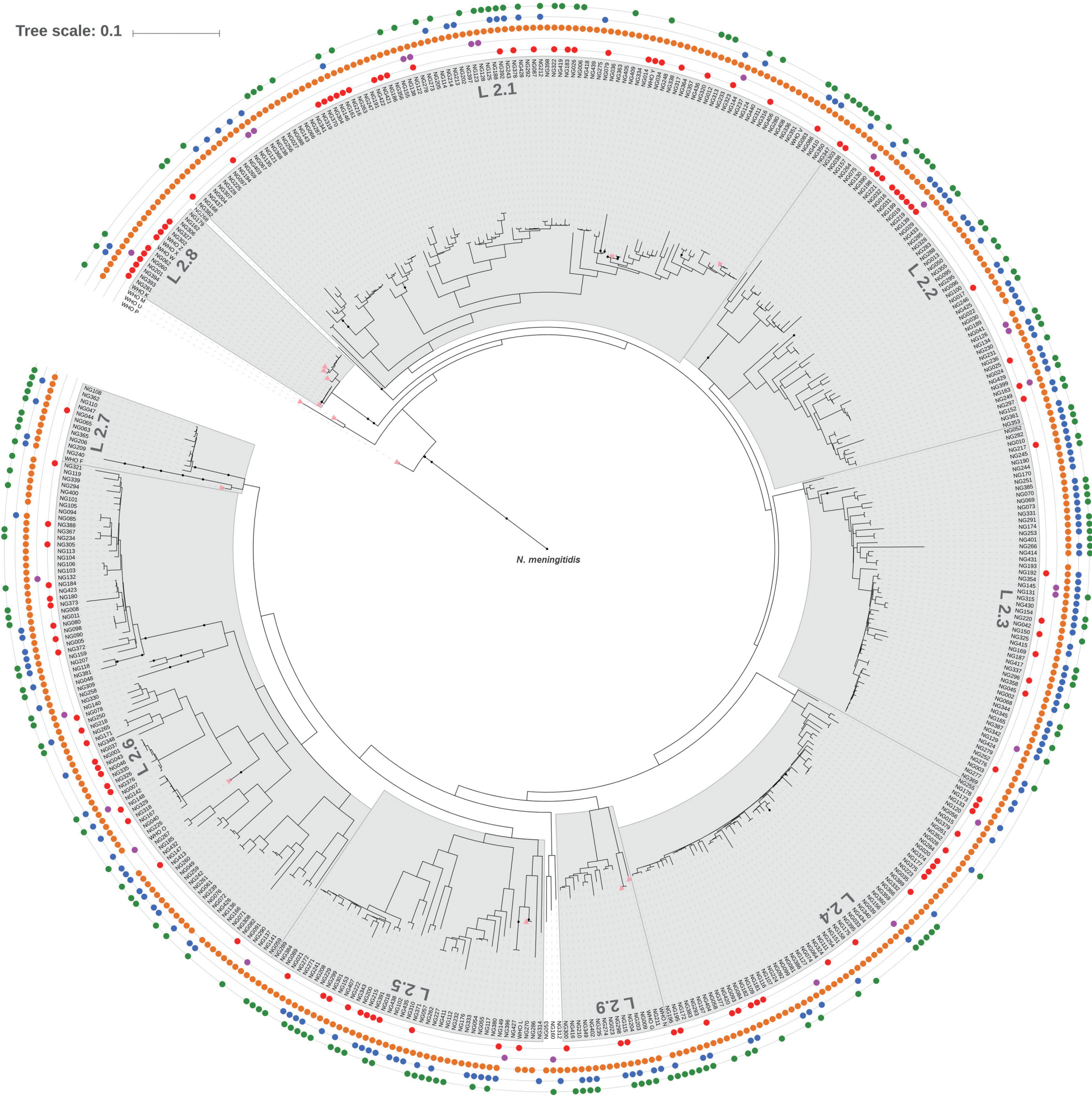


Figure S3

Figure S3: The phylogenetic structure and antibiotics susceptibility details of 435

China *N. gonorrhoeae* strains.

The maximum-likelihood tree was derived from Figure 1 with the same sub-lineages demarcation. The 14 newly sequenced representative strains from WHO are highlighted with pink triangles at the nodes. The antibiotics resistant details of each strain are indicated by external colored dots (from inner to outer): ceftriaxone (red), spectinomycin (purple), ciprofloxacin (orange), tetracycline (blue) and penicillin (green). The scale is in the units of mutations per site.