

TABLE S1. Sexually transmitted infections detected from study participants with male urethritis syndrome in Johannesburg, South Africa (n=51)

Microorganism	Men who have sex with	Heterosexual	P-value
	men	men	
	(n=32) ^a	(n=19) ^b	
	n (%)	n (%)	
<i>Neisseria gonorrhoeae</i>	29 (91)	13 (68)	p=0.04
<i>Chlamydia trachomatis</i>	7 (22)	4 (21)	-
<i>Mycoplasma genitalium</i>	5 (16)	4 (21)	-
<i>Trichomonas vaginalis</i>	4 (13)	3 (16)	-

Note. P-value is calculated for the proportion of *Neisseria gonorrhoeae* as aetiological agent of urethral discharge between men who have sex with men and heterosexual men.

^a13 men had a mixed infection detected: *Neisseria gonorrhoeae* and *Chlamydia trachomatis* (n=7), *Neisseria gonorrhoeae* and *Mycoplasma genitalium* (n=2), and *Neisseria gonorrhoeae* and *Trichomonas vaginalis* (n=2).

^b8 men had a mixed infection detected: *Neisseria gonorrhoeae* and *Chlamydia trachomatis* (n=2), *Neisseria gonorrhoeae* and *Mycoplasma genitalium* (n=4), and *Neisseria gonorrhoeae* and *Trichomonas vaginalis* (n=3).

TABLE S2. NG-STAR profiles of *Neisseria gonorrhoeae* strains isolated from high-risk men in Johannesburg, South Africa (n=27)

Isolate number	<i>penA</i>	<i>mtrR</i>	<i>porB</i>	<i>ponA</i>	<i>gyrA</i>	<i>parC</i>	23S	NG-STAR
							rRNA	ST
JR-401	19.001	278 ^a	100	100	100	103 ^a	100	1942*
JR-402	19.001	10	14	1	7	26	100	1931*
JR-403	9.001	69	14	1	1	22	22	1940*
JR-404	2.002	18	14	1	1	4	100	1934*
JR-405	19.001	18	3	1	1	4	100	1937*
JR-406	19.001	18	3	1	7	102 ^a	100	1935*
JR-407	9.001	69	19	1	1	22	100	1623
JM-510	9.001	69	19	1	1	22	100	1623
JR-408	19.001	18	100	1	7	15	100	1632
JR-409	9.001	10	23	1	1	55	100	1932*
JR-410	19.001	279 ^a	24	1	7	15	100	1945*
JR-411	1.001	54	14	1	7	26	100	1939*
JR-412	2.002	10	3	100	1	89	100	1929*
JR-413	14.001	277 ^a	41	100	1	4	100	1944*
JR-414	2.002	40	100	100	7	4	100	427
JR-415	2.002	171	13	100	1	90	100	1941*
JM-501	14.001	130	3	100	100	2	100	520
JM-502	2.002	69	100	100	100	2	100	1835
JM-503	2.002	40	3	100	7	4	100	1938*
JM-504	9.001	276 ^a	14	1	1	49	100	1943*
JM-509	9.001	276 ^a	14	1	1	49	100	1943*

JM-505	2.002	280 ^a	14	1	1	4	100	1946*
JM-506	9.001	1	8	1	100	2	100	139
JM-508	9.001	1	8	1	100	2	100	139
JM-507	19.001	10	100	1	7	26	100	1933*
JM-511	19.001	18	100	1	100	89	100	1936*
JM-512	2.002	10	3	100	1	102 ^a	100	1930*

Novel NG-STAR Sequence Types that were identified are indicated with an asterix (*)

^a Novel NG-STAR allele as identified in this study

Tree scale: 0.01 ⇄

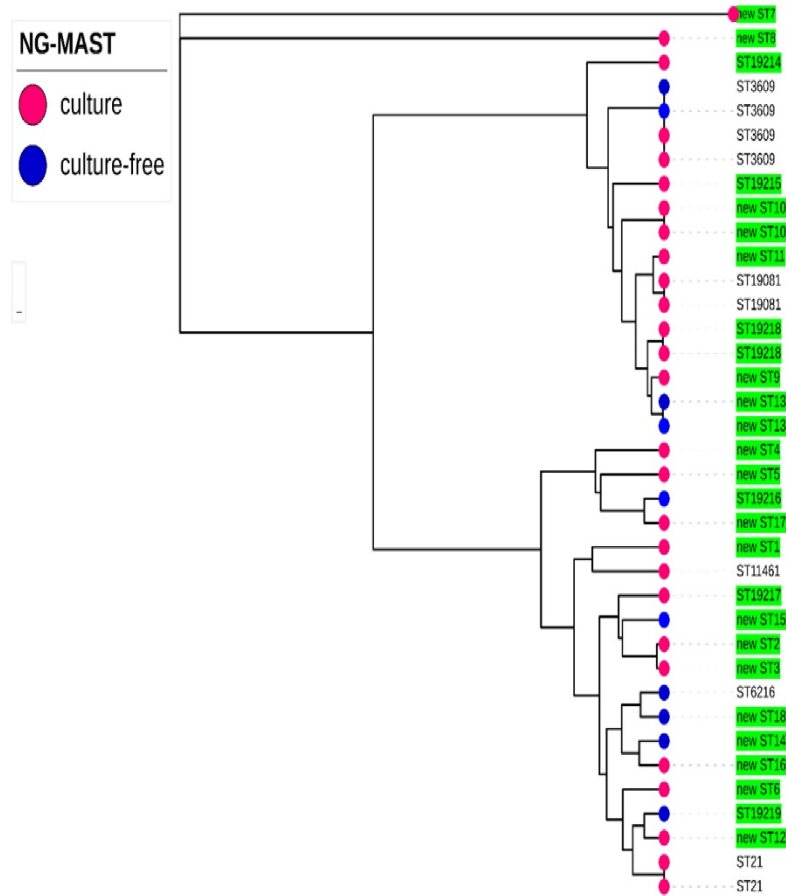


FIGURE S1. Dendrogram constructed by multiple alignment of concatenated *porB* and *tbpB* sequences clustered with unweighted pair group method with arithmetic mean (UPGMA) algorithm. New NG-MAST sequence types identified in this study are highlighted in green.