a) Database isolates

Sample	Lineage confidently detected	Matched k-mers	Serotype		Antibiogram CRO		Antibiogram ERY		Antibiogram PEN		Antibiogram SXT		Antibiogram TET		MLST match	CC match
			Actual	Best match	Actual	Best match	Actual	Best match	Actual	Best match	Actual	Best match	Actual	Best match		
SP01	yes	16%	11D	11D	S	S	S	S	S	S	S	S	S[1]	S[1]	Yes	Yes
SP02	yes	9.6%	19A	19A	R	R	R	R	R	R	R	R	R[2]	R[2]	Yes	Yes

b) Non-database isolates

Sample	Lineage confidently detected	Matched k-mers	Serotype		Antibiogram CRO		Antibiogram ERY		Antibiogram PEN		Antibiogram SXT		Antibiogram TET		MLST match	CC match
			Actual	Best match	Actual	Best match	Actual	Best match	Actual	Best match	Actual	Best match	Actual	Best match		
SP03	yes	3.1%	23F	23F	R	R	R	S[3]	R	R	R	R	S	S	OoD	Yes
SP04	yes	12%	19A	19A	R	R	R	R	R	R	R	R	R	R[4]	OoD	Yes
SP05	no	1.8%	19F	19F	R	R	R	R!	R	R	R	R!	R	R!	OoD	Yes
SP06	yes	8.3%	23F	23F	R	R	R	S[3]	R	R	R	R	S	S	OoD	Yes

c) Metagenomes

Sample	Lineage confidently detected	SP	Matched k-mers	Antibiogram ERY		Antibiogram PEN		Antibiogram TET	
				Actual	Best match	Actual	Best match	Actual	Best match
SP07	no	2.3%	0.2%	NA	S	S	S	R	S[5]
SP08	no	2.5%	0.9%	S	S	S	S!	S	S[6]
SP09	no	4.0%	1.2%	NA	S	S	S	S	S[7]
SP10	yes	21%	5.2%	R	R	R	R	R	R[8]
SP11	yes	70%	14%	R	R	R	R	R	R[8]
SP12	yes	86%	17%	S	S	S	S	R	S[5]

Legend

Correct prediction
Incorrect prediction
Cannot be evaluated

S — Susceptible
R — Non-susceptible
! — Low confidence call
NA — Not available
OoD — Out-of-database
(…) — ID of a retested sample
SP — Fraction of S. pneumoniae reads