Strain	eBurst Group	β-l	PBP3 Group	Genotype
10	S		III	gBLNAR
36	S		others	gBLNAR
38	S		III	gBLNAR
44	S		III	gBLNAR
53	S		III	gBLNAR
84	S		III	gBLNAR
100	S		III	gBLNAR
162	S		III	gBLNAR
109	S		III	gBLNAR
79	S		III	gBLNAR
83	S		III	gBLNAR
138	S		III + II c	gBLNAR
149	S		III + II b	gBLNAR
27	4		III	gBLNAR
31	4		III	gBLNAR
106	4		II b	gBLNAR
41	S		III	gBLNAR
78	S		III	gBLNAR
4	3	TEM-1	others	gBLPACR
58	3	TEM-1	III	gBLPACR
93	3	TEM-1	III	gBLPACR
146	3		III	gBLNAR
29	3		III like	gBLNAR
96	S	TEM-1	III	gBLPACR
43	S		III like	gBLNAR
45	S		III	gBLNAR
42	S	TEM-1	III	gBLPACR
23	S		III	gBLNAR
141	S		III	gBLNAR
71	S		III	gBLNAR
148	S		others	gBLNAR
120	S		III	gBLNAR
25	1		III	gBLNAR
128	1		III	gBLNAR
156	1		III	gBLNAR
9	S		III	gBLNAR
35	2		III	gBLNAR
144	2		III	gBLNAR
47	S		III	gBLNAR
131	S		III	gBLNAR
68	S	TEM-1	NC	gBLPAR
46	S	TEM-1	III	gBLPACR
111	S	TEM-1	III	gBLPACR
28	S		III	gBLNAR
34	S		III	gBLNAR
137	S		III	gBLNAR
139	S		III	gBLNAR
5	S	TEM-1	III	gBLPACR
157	S	TEM-1	III	gBLPACR
54	S		III	gBLNAR
48	S		III	gBLNAR
19	S		III	gBLNAR
114	S		III	gBLNAR
21	S		III	gBLNAR
32	S		III	gBLNAR
40	S		III	gBLNAR
62	S		III	gBLNAR
118	S		III	gBLNAR
147	S		III	gBLNAR
6	S	TEM-1	III	gBLPACR
45	S	ROB-1	III	gBLPACR
90	S	TEM-1	NC	gBLPAR
102	S		II a	gBLNAR
140	S		III	gBLNAR
136	S		III	gBLNAR
3	S		III	gBLNAR

0.1

SDC 2

Neighbor-joining phylogenetic tree derived from allelic profile data obtained by multilocus sequence typing (MLST) of 66 *Haemophilus influenzae* isolates with minimum inhibitory concentrations (MICs) of ampicillin ≥ 4 mg/L: β-lactamase-nonproducing ampicillin resistant (BLNAR) (n = 53), β-lactamase-producing ampicillin-resistant (BLPAR) (n = 7), and β-lactamase-producing amoxicillin/clavulanic acid-resistant (BLPACR) (n = 6). STs were only included in a group (Groups 1-4) if they shared alleles at a minimum of six of the seven loci (single-locus variants). On the right, the strain, eBURST group, β-lactamase production, the group based on amino acid substitutions in penicillin-binding protein 3 (PBP3), and the genotype are reported. MLST shows 39 different sequence types, while analysis with eBURST v3 revealed 4 groups and 31 singletons.