

1 **Supplemental data**

2 **Table S1. Comparison of clinical data for sources of BLNAS, Low/High-BLNAR, BLPAR, and BLPACR isolates.**

Genotype	Group	Number of isolates	Sex		Age (years)			Specimens									
			M	F	≤15	16–64	≥65	Sputum	Pharyngeal mucus	Nasal mucus	Nasal discharge	Otorrhea	Oral cavity	Tonsil	BALF	Other	
BLNAS	-	35	25	10	3	14	18	18	6	4	3	1		1		2	
BLNAR	II	5	2	3		2	3	4			1						
	III	47	31	16	11	18	18	23	7	5	3	2		2	2	3	
	III-like	9	7	2	2	3	4	6	2			1					
	IV*	1		1		1		1									
BLPAR	-	5	5				5	2	1							2	
BLPACRII	III	2		2		1	1	1									1

3 *, SMHi90. BALF, bronchoalveolar lavage fluid

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6 **Figure S1. Comparison of amino acid substitution of PBP3 and nucleotide**
7 **sequence of *ftsI* in *H. influenzae* SMHi90 and representative isolates within group**
8 **III and III-like.**

9 (A) Amino acid changes (Asp350 to Asn611) and (B) nucleotide changes (nucleotide
10 position from 1549 to 1833) of *ftsI* of SMHi90 compared with Rd, group III (SMHi2),
11 and group III-like (SMHi107). SMHi2 and SMHi107 belong to the most common
12 PBP3 amino acid substitution type in group III and group III-like, respectively. ^a and ^b
13 correspond to amino acids at positions 517 and 526, respectively. The nucleotide
14 sequence of *ftsI* of SMHi90 was registered in DNA Data Bank of Japan (DDBJ) as
15 accession number LC379877.

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17 **Figure S2. Phylogenetic tree of *ftsI* sequence of *H. influenzae* isolates.**

18 Neighbor-Joining dendrogram of the BLNAS (n=11), Low-BLNAR (n=5),
19 High-BLNAR (n=57), BLPAR (n=5), and BLPACR isolates (n=2) investigated in this
20 study.

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FIG S2

