

SUPPLEMENTARY TABLE 2. Number of single nucleotide polymorphism differences between clinical isolates from two patients and hospital environmental isolates* of IMP-producing *Pseudomonas aeruginosa* , compared with a representative genome — Idaho, 2021–2022.**

		Clinical isolates		Environmental isolates			Reference ****
		Patient 1	Patient 2	Sink counter	Sink p-trap	Sink drain ***	
Clinical isolates	Patient 1	-	14	41	28	22	47,561
	Patient 2	14	-	24	21	16	47,511
Environmental isolates	Sink counter	41	24	-	47	31	47,486
	Sink p-trap	28	21	47	-	28	47,481
	Sink drain	22	16	31	28	-	47,464
	Reference	47,561	47,511	47,486	47,481	47,464	-

* Clinical isolates from patient 1 and patient 2 are from sputum specimens collected while patients were being treated in intensive care unit (ICU) room X of hospital A. Environmental isolates are from one sink in ICU room X.

** active-on-imipenem (IMP) metallo-beta-lactamase-producing *Pseudomonas aeruginosa*

*** Of the environmental isolates, the sink drain isolate was most similar to both clinical isolates, differing by 22 and 16 SNPs.

**** Reference genome for *Pseudomonas aeruginosa* is build GCF_000006765.1_ASM676v1 from National Center for Biotechnology Information (https://www.ncbi.nlm.nih.gov/assembly/GCF_000006765.1/).