Figure S1. cgMLST trees differentiate unrelated reference genomes of same ST (in red) from outbreak isolates.
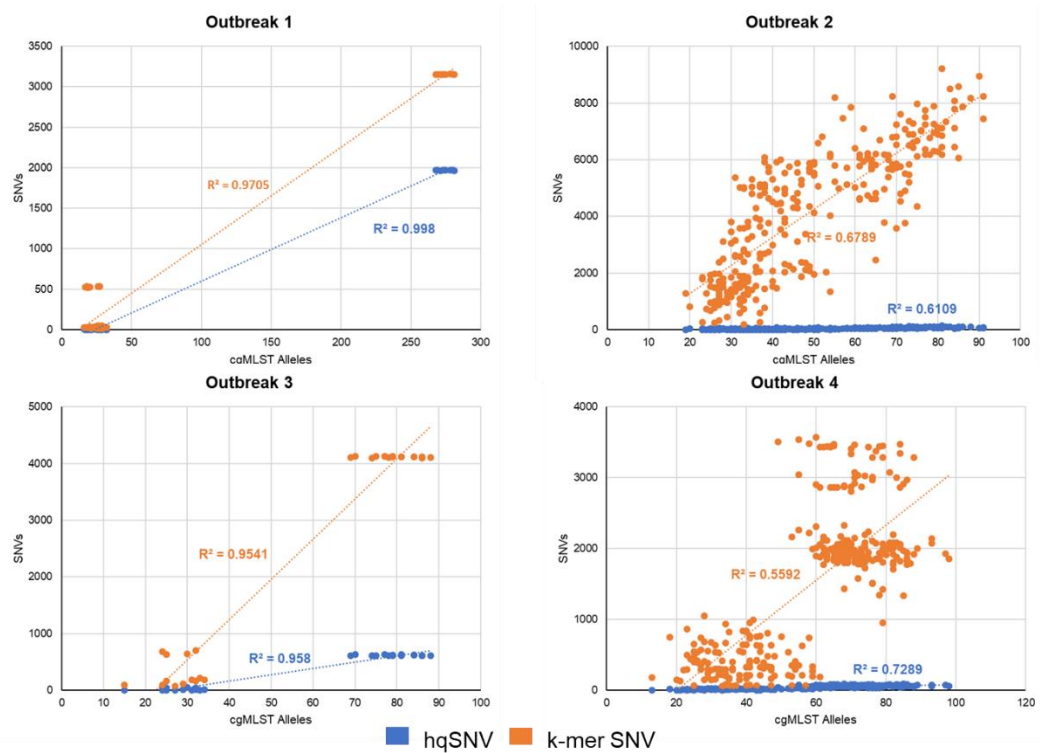
Figure S2. Pairwise comparison of cgMLST allele differences (x-axis) to SNVs (y-axis) for all four outbreaks show correlations for both hqSNV (SNVPhyl) and k-mer SNV (kSNP) pipelines.

Table S1. *P. aeruginosa* cgMLST Allele Counts Found in *P. aeruginosa* Group Reference Genomes

Genome	Species	*P. aeruginosa* cgMLST Alleles Present
GCA_000412695.1_ASM41269v1	*P. resinovorans*	152
GCF_000510765.1_ASM51076v1	*P .oleovorans*	51
GCF_900103845.1_IMG-taxon_2663762768	*P .jinjuensis*	413
GCA_000016565.1_ASM1656v1	*P .mendocina*	87
NZ_AP014862.1	*P .caeni*	0
GCA_900100535.1_IMG-taxon_2663762794	*P .flavescens*	30
GCA_002204635.1_ASM220463v1	*P .nitroreducens*	296
NZ_CP014784.1	*P. alcaligenes*	99
GCA_900105355.1_IMG-taxon_2687453785	*P .anguilliseptica*	9
GCA_900112645.1_IMG-taxon_2663762767	*P .straminea*	36
GCA_001654435.1_ASM165443v1	*P .citronellois*	463
NZ_AP014862.1	*P .furukawaii*	139

Table S2. Comparison of cgMLST Trees Generated by Neighbor Joining (NJ) or Unweighted Pair Group Method with Arithmetic mean (UPGMA) Methods to hqSNV Trees

Outbreak	cgMLST Tree Type	Similarity Score	Average SNV Tree Similarity to 10,000 Random Trees	cgMLST Tree More Similar Than Average	P value
1	NJ	11.40	12.16	Yes	0.30
1	UPGMA	10.44	12.15	Yes	0.12
2	NJ	42.38	44.08	Yes	0.32
2	UPGMA	100.28	44.04	No	N/A
3	NJ	8.54	8.39	No	N/A
3	UPGMA	5.48	8.40	Yes	1.5×10^{-2}*
4	NJ	68.12	59.81	No	N/A
4	UPGMA	35.47	59.75	Yes	1.4×10^{-14}*

* P value < 0.05

Table S3. Description of Outbreaks and Comparison of cgMLST to PFGE Trees

Outbreak	Number of Isolates	MLST ST (# of isolates)	P-value of Tree Similarity
1	12	164 (10), 27 (1), 810 (1)	0.026*
2	12	233 (12)	0.017*
3	9	309 (7), 1158 (1), 2775 (1)	3.6×10^{-5}*

* P value < 0.05

Table S4. Recombined Alleles in Outbreaks

Outbreak	Total Unique Alleles	Recombination Alleles (%)
1	4815	57 (1.2)
2	4928	115 (2.3)
3	4601	35 (0.76)
4	5001	191 (3.8)

Supplemental Spreadsheet Descriptions

Spreadsheet S1. Complete *P. aeruginosa* genomes used to build cgMLST scheme.

Spreadsheet S2. Descriptions of 4400 genes making up cgMLST scheme. The counts of unique, missing, and multiple copy alleles as well as the Z-scores are from the 2049 *P. aeruginosa* genomes from RefSeq included in the study.

Spreadsheet S3. Descriptions of 2049 *P. aeruginosa* genomes from RefSeq used in study.