Supplementary

P <u></u>		AO1 ref
	PABO48	
	PABOG8 AZPAE14722	
	AZPAE14722	
	MAD04_010	
	- CVA01.029	
	CVA03.033	
	CVA02.005	
	- CVA02.023	
	ARA02_017	
	CVA01.006	
	- MAD02.014	
	- GAL06.015	
	AZPAE15010	
	AZPAE14880	AD02.007
	MAD03_033	MADU2.007
	CVA03.025	
	- MUR01.009	
	- CLM02 005	
	CLM02.043	
	- AZPAE14403	
	AZPAE14890	
	- ICA01_031	
	- CAT05.001 - ICA01.030	
	- CA01.030	
	AZPAE14909	
	- BAL01.003	
	BAL04-027	
	- AST01.026	
	AST01.007	
	- BAL04.015	
	- CAT05.005	
	- CAT01_015	
	- CAT06.008 CAT08.034	
	CAT08.034	
	- CAT03.004	
	- CAT09 009	
	- CAT05.019	
	BAL03_002	
	- CAT04.032	
	- CLE02_032	
	MAD06.017	
	CLE02.016	
	- PVA01_007 - CAT02_007	
	CAT02.020	
	CAT02.020	
	CAT09.018	
	CAT06.019	
(i)		
5.0E_4		

Figure S1. Maximum likelihood phylogenetic tree based on the SNPs in the core genomes of ST175 *Pseudomonas aeruginosa* clinical strains. Strains associated with transmission event described in this study are highlighted in red.

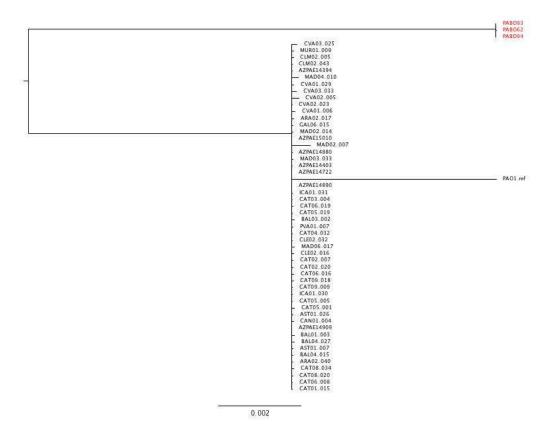


Figure S2. Maximum likelihood phylogenetic tree based on the SNPs in the core genomes of ST235 *Pseudomonas aeruginosa* environmental strains. Strains associated with transmission event described in this study are highlighted in red.