

**Table S2.** SNPs observed comparing phage within the PST1-1 cluster

Position on phage genome	Host Strain	SNPs using PA4 as reference	Predicted function	Amino acid change
5453	PA50, PA16	G-A	intergenic	-
9377	PA16	T-G	Predicted operator O <sub>R2</sub>	-
16107	PA42, PA21	A-G	hypothetical	K-R
24363	PA42	G-T	hypothetical	synonymous
25476	PA29	G-A	IS629	P-S
27482	PA32	A-G	intergenic	-
32341	PA5	C-T	portal protein	R-W
43963	PA11	C-T	tail fiber	T-I
58904	PA42	A-C	hypothetical	synonymous