

Table S1: Identity between *stx_{2a}*-phage regulatory gene and encoded protein sequences from JH2010 and JH2016. Regulatory genes and predicted proteins were identified based on location within the phage genome and synteny to lambda phage, as well as NCBI annotation. Percent nucleotide and amino acid identity were calculated using Clustal Omega.

Regulatory Gene/Protein	% Nucleotide Identity	% Amino Acid Identity
<i>N/N</i>	38.3	15.3
<i>cI/CI</i>	41.1	16.9
<i>cro/Cro</i>	39.7	23.4
<i>cII/CII</i>	88.6	86.7