Table S1. 5448Δslo covR/S mutants[a].

Name	**Gene mutated**	**Mutation[b]**	**Length of operon[c]**
5448Δ*slo* *covR*1	*CovR*	G substituted for T at nt 341	*CovR* = 228 AA *CovS* = 500 AA
5448Δ*slo* *covS*1	*CovS*	TT insertion at nt 473	*CovR* = 228 AA *CovS* = 159 AA
5448Δ*slo* *covS*2	*CovS*	G substituted for T at nt 199	*CovR* = 228 AA *CovS* = 66 AA
5448Δ*slo* *covS*3	*CovS*	C substituted for T at nt 9	*CovR* = 228 AA *CovS* = 3 AA

[a] The 5448 *covR/S* sequencing details were as previously described (6).

[b] Mutation locations are based upon the nucleotide (nt) position in the *covR* or *covS* gene relative to the gene-specific ATG start codon.

[c] Length of operon is based upon the number of amino acids (AA) from the ATG start codon.