

Table S8. Homologs Search for the RR AbrB1.

Amino acid sequence comparisons between different RRs. Pairwise alignments were performed in *EMBOSS Needle* (EMBL-EBI), which uses the Needleman-Wunsch algorithm, applying a BLOSUM62 substitution matrix.

Protein	Organism	Identity	Similarity
AbrB1	<i>Streptomyces coelicolor</i>	34 %	55 %
VraR	<i>Staphylococcus aureus</i>		
VanR	<i>Streptomyces coelicolor</i>	31 %	48 %
VanR	<i>Staphylococcus aureus</i>		
AbrB1	<i>Streptomyces coelicolor</i>	35 %	54 %
LiaR	<i>Enterococcus faecium</i>		