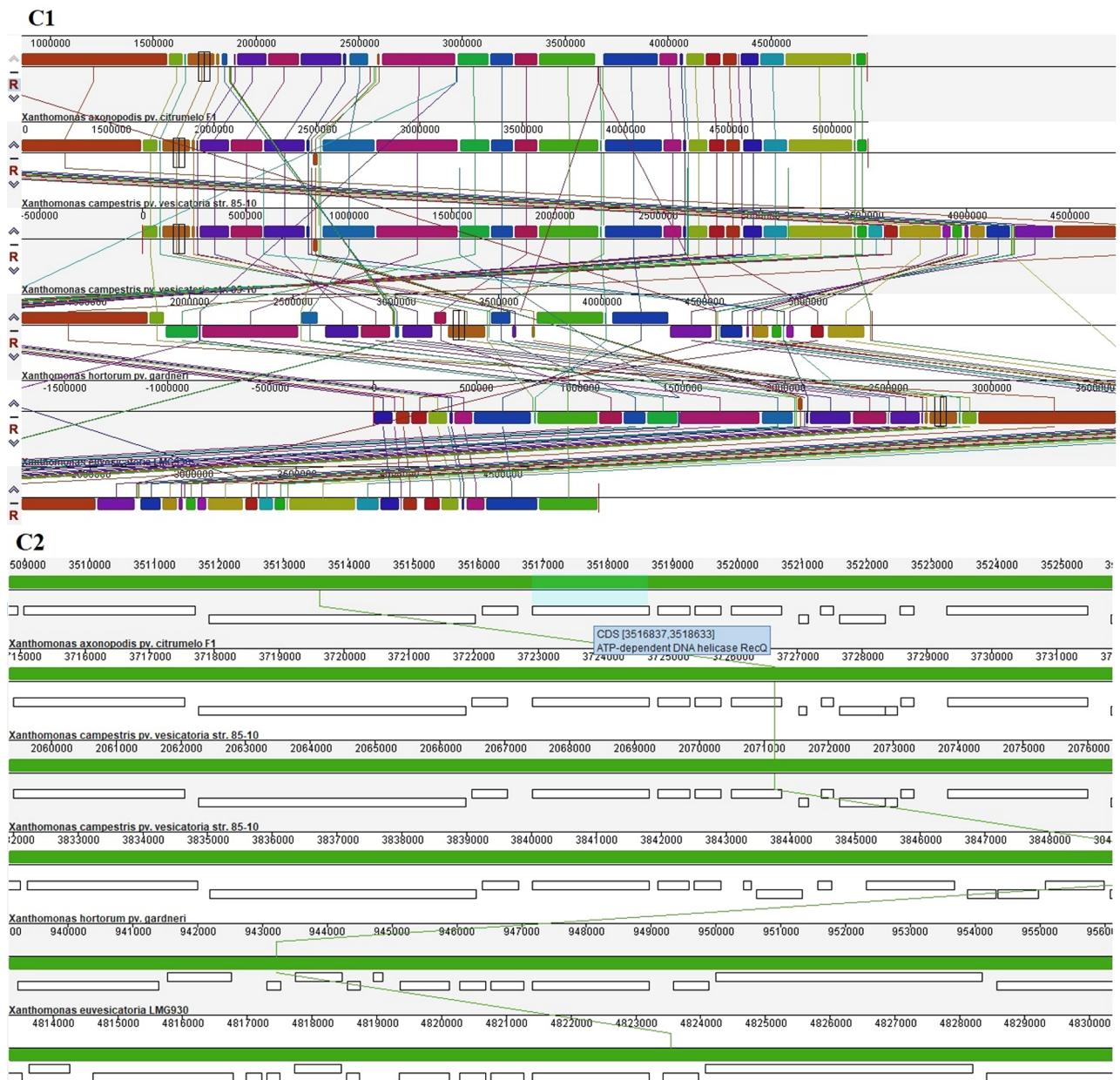


44	<i>Xanthomonas vesicatoria</i>	Xv1	-	-	-
45	<i>Xanthomonas vesicatoria</i>	Xv2	-	-	-
46	<i>Xanthomonas gardneri</i>	Xg1	-	-	-
47	<i>Xanthomonas gardneri</i>	Xg2	-	-	-
48	<i>Xanthomonas perforans</i>	Xp1	-	+	-
49	<i>Xanthomonas perforans</i>	Xp2	+	-	+
50	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i>	YH	-	-	-
51	<i>Pseudomonas syringae</i> pv. <i>syringae</i>	Pss1	-	-	-
52	<i>Pseudomonas syringae</i> pv. <i>syringae</i>	Pss2	-	-	-



Supplementary Fig. 1. Alignment of whole genomes of *Xanthomonas euvesicatoria*, *X. perforans*, *X. vesicatoria*, *X. gardneri*, *X. axonopodis* pv. *citrumelo*, and *X. campestris* pv. *vesicatoria* for selection and location of target specific gene RecQ through progressive mauve alignment.