

**Supplementary Table 1: Genes, genome locations, primers, length of products**

PID	name		position in <i>Pto</i> DC3000 genome	forward primer	reverse primer	length of analyzed sequence
28867247	DNA gyrase subunit B	gyrB	4147..6564	TGCVTTCGTTGARTACCTGA	ACGGAAGAAGAAGGTSAGCA	701
na	Magnesium chelatase pseudogene	Mg_Ch	81732..82382	ACYTGCTCCAGATCCGCC	GCTGGAGGTTYTRCGTGAGCC	310
28867765	RNA polymerase sigma factor	rpoD	588846..590696	GAAGGCATCCGTGAAGTGAT <sup>1</sup>	GCCACGGTTGGTGTACTTCT	645
28868169	hypothetical protein	PSPTO0949	1026472..1028727	AYTGACCCGCSATYGTGCGAG	AATGCGCTGAAACGCGCAG	674
28868179	glucose-6-phosphate isomerase	pgi	1040763..1042427	GCGTACTACCGYAMYCCB TC	CCACATMGGRAARATRTTYT	569
28868192	iron-sulfur cluster-binding protein	PSPTO0972	1057534..1057866	AGCGAYRCCCAGATBCCC	YGCCRTGMGGGAARTTGAC	620
28868479	valyl-tRNA synthetase	valS	1389375..1392221	CCAGATACCAGTCGCAACTG	TGGACCTTCTCCACGCTC	588
28868497	glyceraldehyde-3-phosphate dehydro	gap-1	1415258..1416259	CGTATCGCAATCAACGGTTT	GACTCTCCGTATCGCAATCA	600
28868573	glutathione S-transferase	gstA	1502901..1503527	GCGACCCGAAAASCAAYC	RTAYTCVCCGCCCTGCTC	506
28868577	hopAA1-1 effector plus up-stream re	hopAA1-1	1504948..1505427	ACTCCYTTGCTGGKTTGGAA	KGTCGARCTTYTCCGCCTTG	677
28868585	type III effector avrE1 <sub>PtoDC3000</sub>	avrE1	1514116..1519503	TTGTCGTTYTTCTGGGTCAR	CMGAYATGGGCTTTACCGAT	636
28868589	type III helper protein HrpA1	hrpA1	1524281..1524622	GCCTGGARCTSGAYRTSCCAC	CAGAVGCRCCRAARTTGTCRCC	753
28868612	RNA polymerase sigma factor HrpL	hrpL	1542838..1543392	GATCCGYAATCACTTCCG	TCCTGATAATTGCCRTCCA	205
28869396	citrate synthase	gltA	2414332..2415621	WYTRACCGGYACMGTBGGY	TGGGCTGATSGGYTTRATYT	507
28869961	amino acid ABC transporter	PSPTO2775	3094410..3095261	GGMGCRGACGGMAAGTTG	CGGAAAACCGATTGCMGG	589
28870907	aconitate hydratase	acnB	4239241..4241841	TGATGTTTGATGCCTTCCAC	TAAAACCTTGTTGCTTTCG	650
28870953	arsenical pump membrane protein	arsB	4300065..4301345	TCAGYACGATRCCGACCTTG	ACATCGTKTCGGCGGAYTAC	1094
28871024	lipid A biosynthesis lauroyl acyltransf	htrB	4383469..4384401	ATACTGTTCCGGGCATTCTG	CTTCTACAGGCATCGCCTTC	526
28871138	potassium uptake protein	kup	4503214..4505109	CTGATCTTCTGGTCGCTGATC	TTCCAGGTGGTCATGAGGA	1943 <sup>1</sup>
28871137	hypothetical protein	PSPTO3992	4505431..4506519	AYACCACCATCATCATTTGC	CCGTACAGMAAMGGYACGAC	1943 <sup>1</sup>
28871145	type III effector avrPto1 <sub>PtoDC3000</sub>	avrPto1	4514766..4515260	GTCATKGCAGTGTTATRCRAGA	GYTGCAGGCTCCKAAAAACTG	various <sup>2</sup>
28871162	hypothetical protein	PSPTO4019	4530408..4531739	AAGGTTACGAAGTCGTTGCG	CTCGCGCCAGTCTTGAT	720
28871164	S4 domain protein	PSPTO4021	4532376..4533086	GAGCTGGTCGGTTGCTCC	GGCGTGTTTCTGATAAGTCG	1837
28871598	pmbA protein	pmbA	5024076..5025422	GCTTGCGRCCGGAATAVG	GCGCTGATGGCCAAAGAG	778

1 F primer starts within Kup and PCR product encompasses intergenic region

2 primers are located in the genes up- and downstream of the *avrPto1* gene. The length of the product is different in different strains.