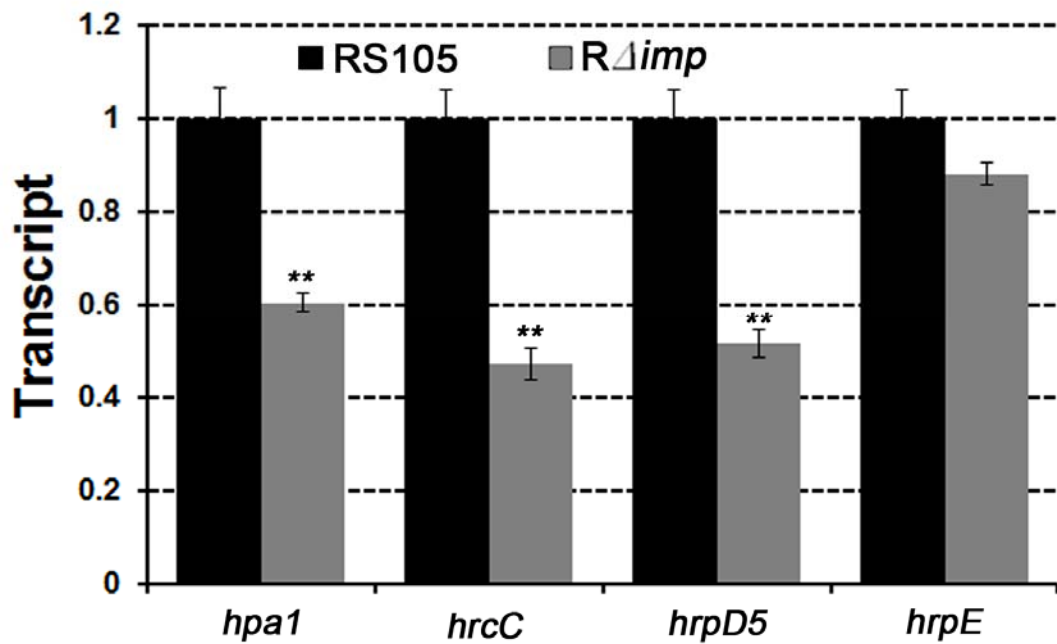


**Appendix A** Functional map and molecular analysis of the *imp* mutation in *X. oryzae* pv. *oryzicola* RS105. The physical location and orientation of *Xoc\_3248*, encoding *Imp*, and adjacent ORFs are shown using the genome sequence of *Xoc* BLS256 strain as a reference (<http://cmr.jcvi.org/cgi-bin/CMR/GenomePage.cgi?org=Xoc>). Arrows indicate the orientation of ORFs, and horizontal lines indicate intergenic sequences. A triangle arrow presents a Tn5 insertion in *Xoc\_3248* resulting in a mutant Mxoc0031. A functional map of the region containing the 966-bp *imp* deletion is shown. Deletion of *imp* was confirmed by PCR with the primer pair upF/downR and by Southern hybridization. RS105, wild-type strain; *RΔimp*, *imp* deletion mutant; M, DL2000 DNA marker (TaKaRa).



**Appendix B** The expression of *hpa1*, *hrcC*, *hrpD5* and *hrpE* in *X. oryzae* pv. *oryzicola* measured by real-time quantitative RT-PCR (qRT-PCR). The bacterial cells of the wild-type strain RS105 and the *imp* mutant R $\Delta$ *imp* were collected from bacterial infiltrated regions of rice leaves (12 h post infiltration) for RNA extraction. Data represent the mean  $\pm$  SD of triplicate measurements from a representative experiment. Similar results were obtained in two other independent experiments. Columns marked with an asterisk mean a significant difference at  $P=0.01$  (student's *t*-test).