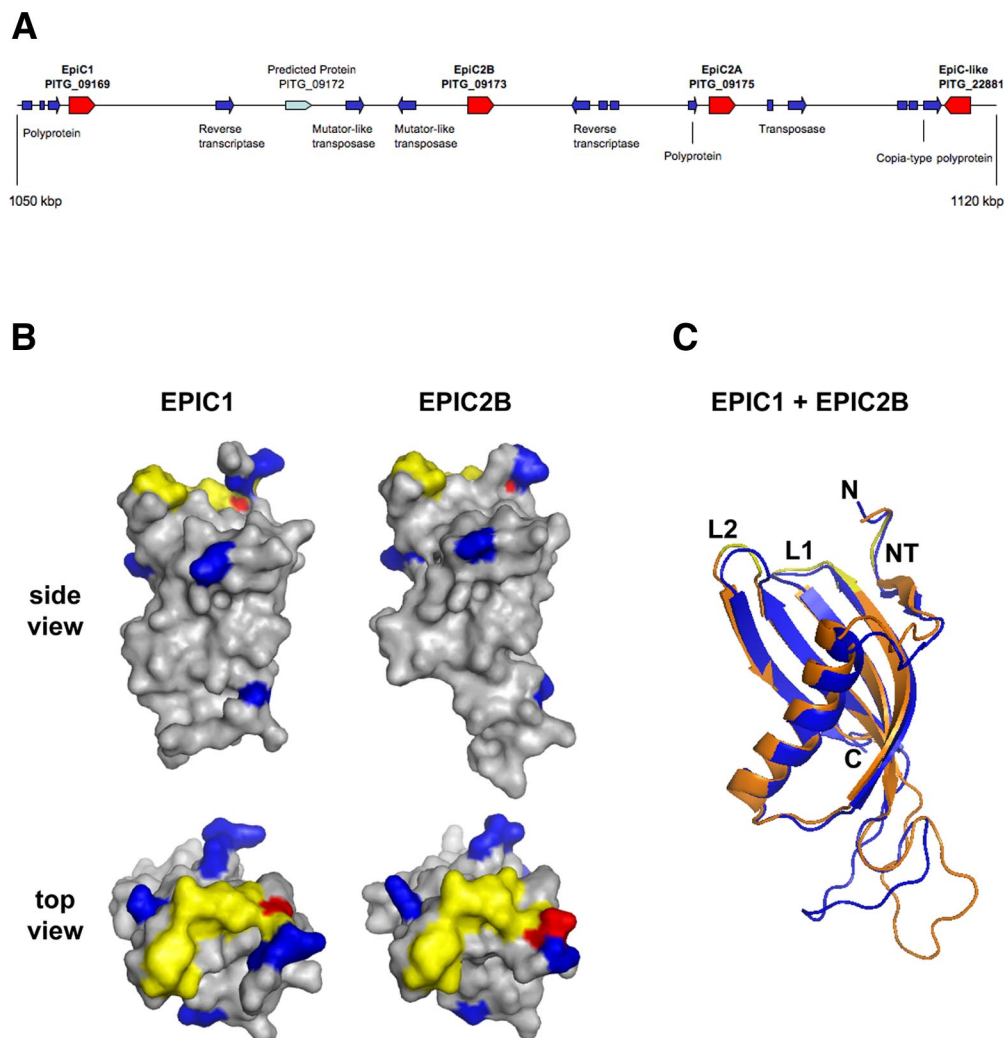


# Supporting Information

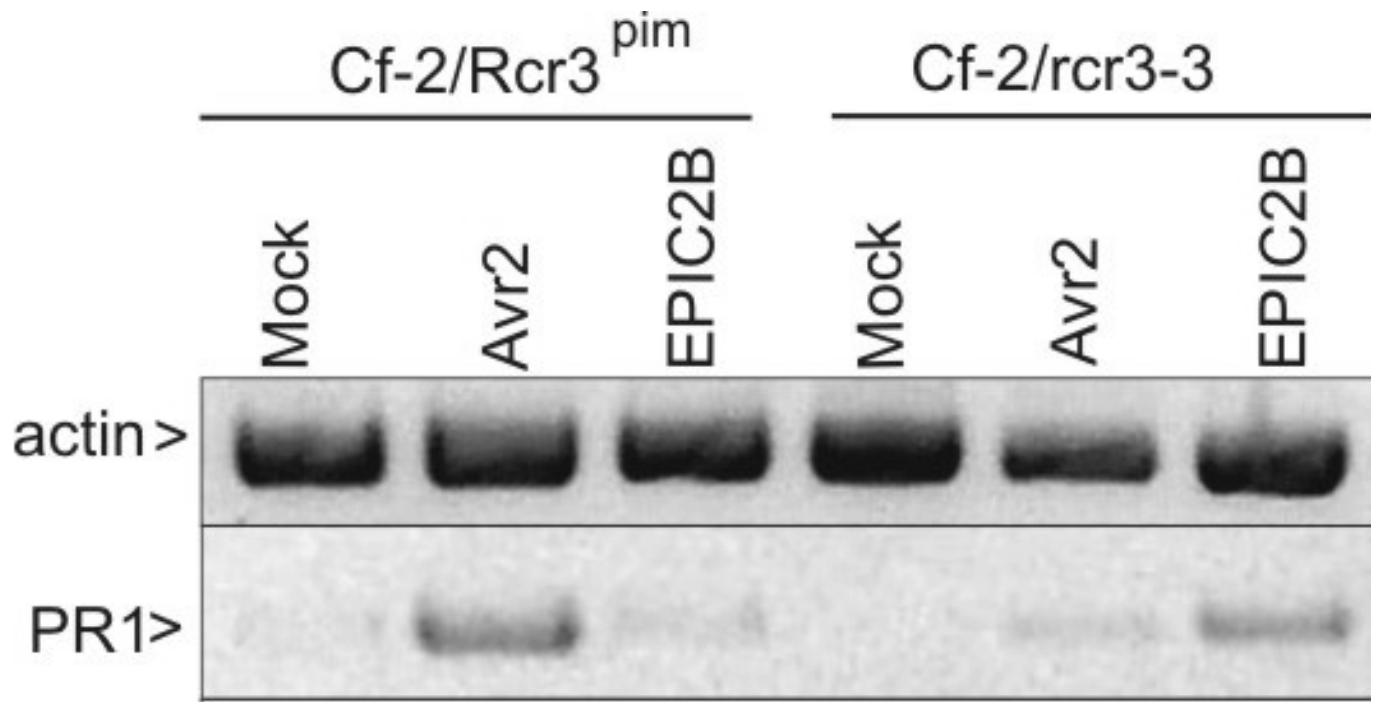
Song *et al.* 10.1073/pnas.0809201106



**Fig. S1.** (A) The *epiC* genes are clustered within a 70-kbp region in supercontig 14 of the genome of *P. infestans* T30–4. Graphic view of the cluster, illustrating the cluster with the four genes *epiC1*, *epiC2B*, *epiC2A*, and *epiC1-like*. Other genes are also marked with their PITG identifiers (Broad Institute annotation Web site). Note how the region is interspersed with remnants of transposable elements (blue arrows). There are two additional cysteine protease inhibitor genes in the genome, *epiC3* and *epiC4*, as described by Tian *et al.* (14). (B) Surface models of EPIC1 and EPIC2B. Structural prediction with Bioinfo metaserver service ([www.bioinfo.pl](http://www.bioinfo.pl)), modeled on ORYZACYSTATIN-I (pdb: 1eqkA) using MODELLER. The conserved binding regions are yellow, polymorphic residues are blue, and the G>N polymorphism in the N terminus is red. (C) Superimposition of EPIC1 (blue) and EPIC2B (orange) ribbon models. Arrows and helical stretches represent b-strands and a-helical regions. N-terminal truck (NT), loop1 (L1) and loop2 (L2) depict conserved regions. N, amino terminus; c, carboxy terminus.







**Fig. S4.** Unlike Avr2, EPIC2B does not induce the expression of PR1 in Cf-2/Rcr3<sup>pim</sup> tomato. RT-PCR analysis of pathogenesis-related *PR1* gene in tomato after infiltration with purified rAvr2 and rEPIC2B. Total RNA isolated from infiltrated leaves of Cf-2/Rcr3<sup>pim</sup> and Cf-2/rcr3-3 tomato was used in RT-PCR amplifications. Amplifications of tomato actin were used as constitutive controls to determine the relative expression of the *PR1* gene.

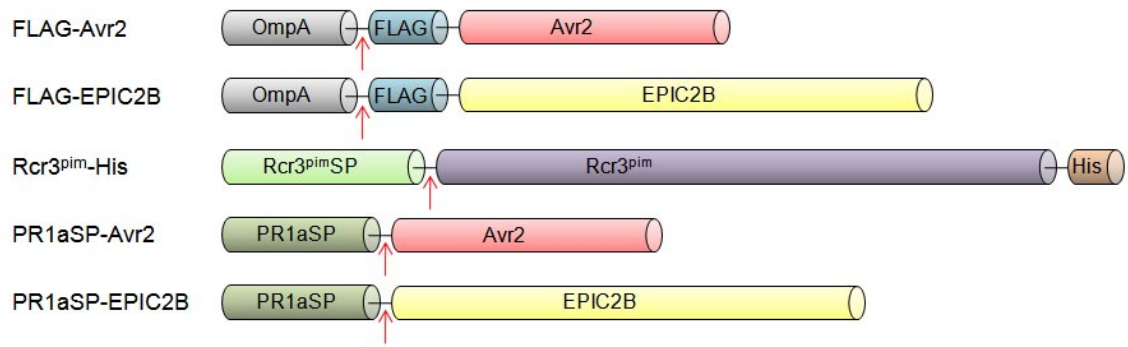


Fig. S5. Graphic view of the recombinant proteins used in this study. Arrow indicates the signal peptide cleavage site.

