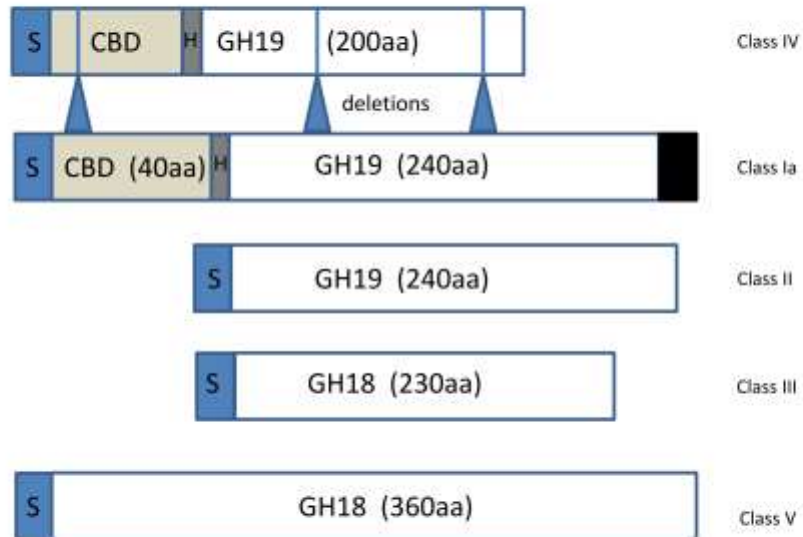**Supporting Information**

S1 Fig. Domains and classes for glycoside hydrolase 18 and 19 (chitinases) from the *Eucalyptus grandis* sequences. S = signal sequence, H = hinge region (proline/threonine-rich in Class IV and glycine-rich in Class I), CBD = chitin binding domain, black box indicates C-terminal vacuolar extension, aa = amino acid residue with approximate sizes. Diagrammatic concept from Collinge, Kragh et al. (1993).
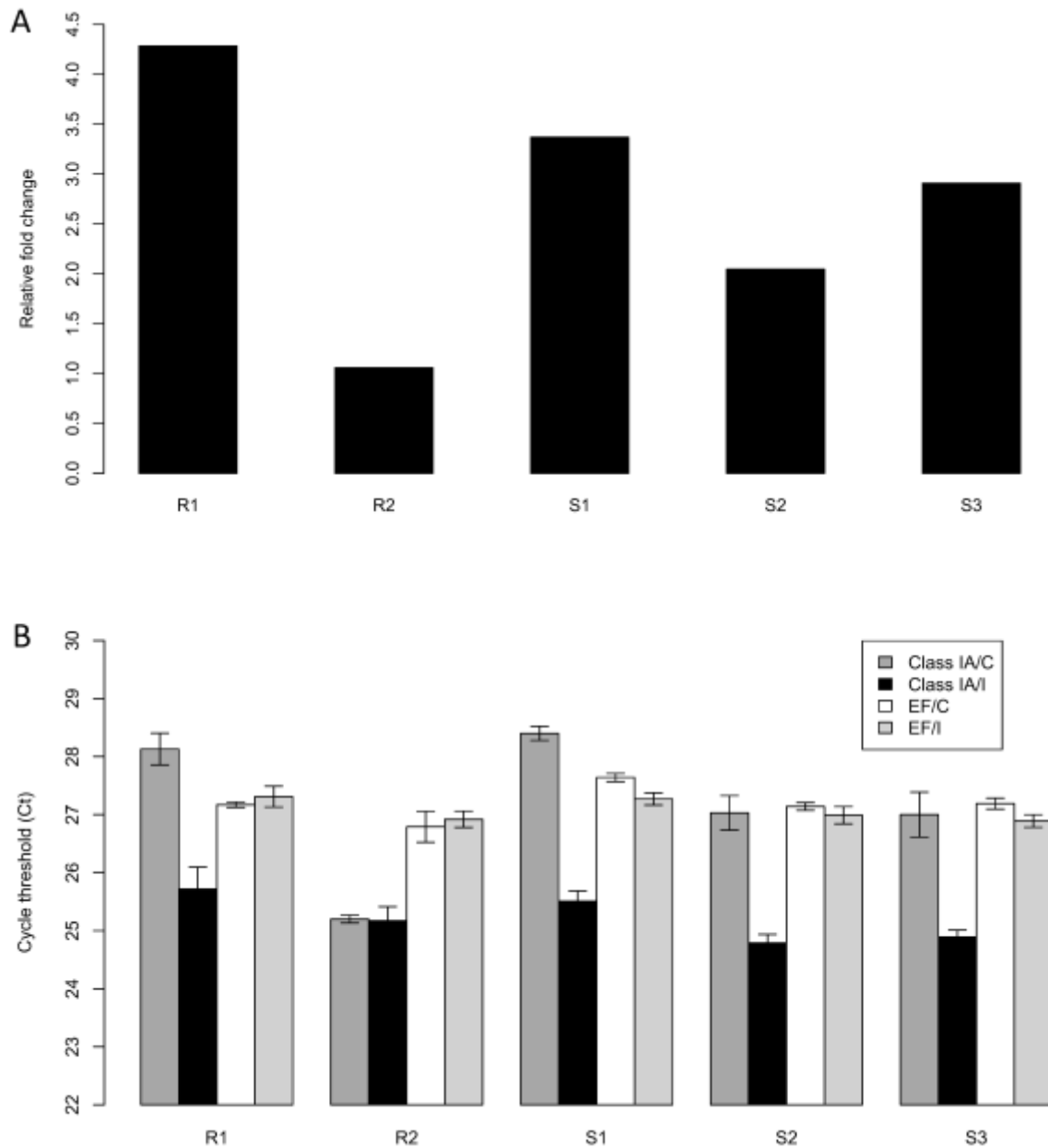
S2 Fig. Quantitative reverse-transcriptase polymerase chain reaction relative expression change (A) of putative *Class 1A chitinase* (Eucgr. I01495) in *Eucalyptus grandis* in response to *Chrysoporthe austroafricana* inoculation (three days post-inoculation). Expression is relative to reference gene *Elongation factor S-II* (B). R = resistant, S = susceptible.
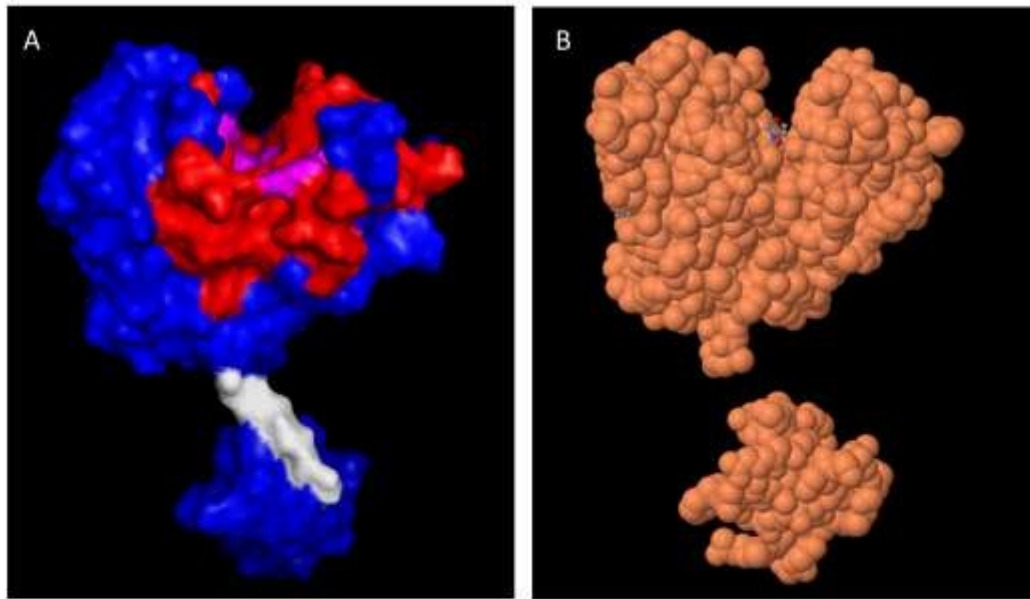
S3 Fig. Predicted tertiary structure for (A) *Eucalyptus grandis* Class IA chitinase peptide with cleaved signal and vacuolar sequences had a C-score of 1.72 (with range being between 5 and 2) and estimated TM-score of 0.96 (structural similarity score between 0 and 1) (Roy et al. 2010). (B) The putative mature protein matched tertiary structure for *Oryza sativa* L. japonica Class IA chitinase crystal structure (Kezuka et al. 2010) with TM score of 0.95 (http://www.rcsb.org/pdb/explore/jmol.do?structureId=2DKV&bionumber=1&opt=3&jmolMod e=HTML5). Blue = GH19 and Chitin binding domains (linked by hinge region), white = hinge region (glycine-rich in *E.grandis* Class I but usually proline/threonine rich), red = catalytic regions as identified by 0.6nm of bound substrate, magenta = essential residues for catalytic activity determined with mutagenesis (Bishop *et al.* 2000).