



Supplementary Figure S8 Posterior evidence of a QTL conferring resistance to crown rot caused by *Phytophthora cactorum* on LG 7D. The X-axis represents genetic locations in centiMorgans, and the Y-axis represents (A) traces of QTLs and (B) posterior intensities based on an additive genetic model executed by FlexQTL™ software. These figures are representative of FlexQTL™ outputs obtained from three independent runs. The black and white colored matrix (C) represents pair-wise linkage disequilibrium (r^2) among SNP markers on LG 7D for unselected seedlings (discovery populations). The r^2 values range from 0 (white) to 1 (black). The triangular boxes represent haploblocks along LG 7D calculated using the four-gamete method in Haploview software.