



Supplementary Figure S11 Mean area under the disease progress curve (AUDPC) effects for three QTL genotypes of the *FaR Pc2* locus under a simple, bi-allelic QTL model for resistance to *Phytophthora cactorum* for QTL validation sets evaluated during the 2013-14 and 2014-15 seasons. Different letters next to each bar within seasons represent statistically significant differences ($P < 0.05$), as determined by the Steele-Dwass non-parametric multiple comparison test. Standard error bars were generated from a GLM analysis to illustrate variation around the means. The number of individuals having each QTL genotype are shown below the genotype designations