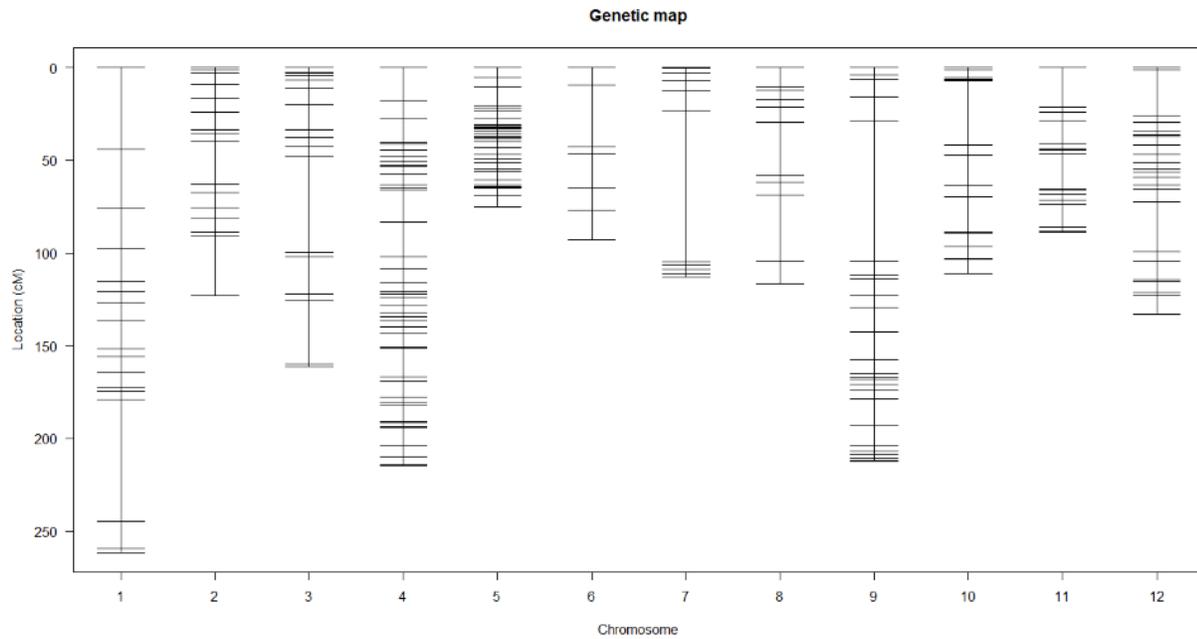


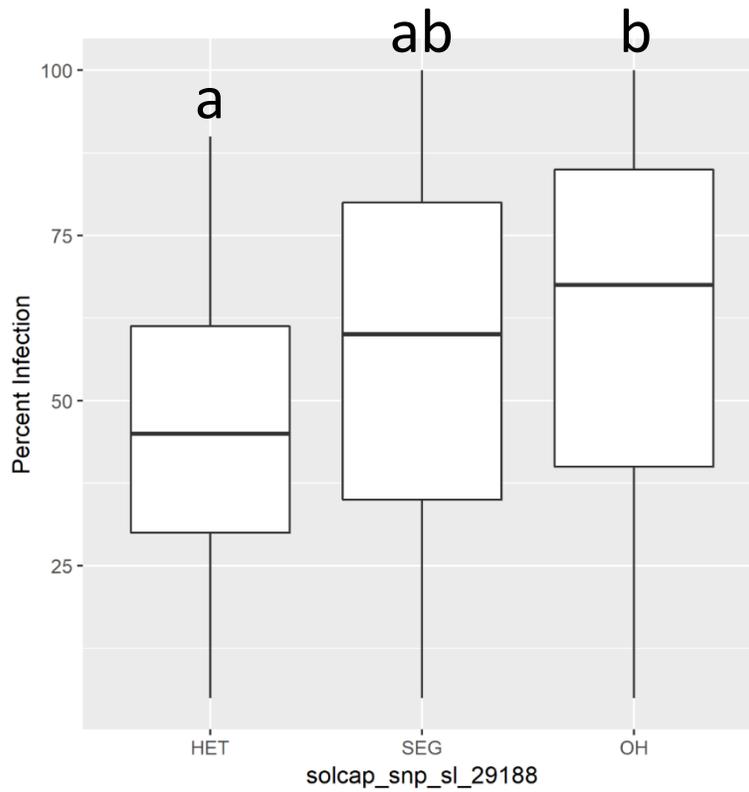
**Supplement to Chapter 2 from the dissertation:**

*Anderson, T (2020) Genetics and breeding of early blight and bacterial spot resistant tomatoes. Cornell University, Ithaca NY*

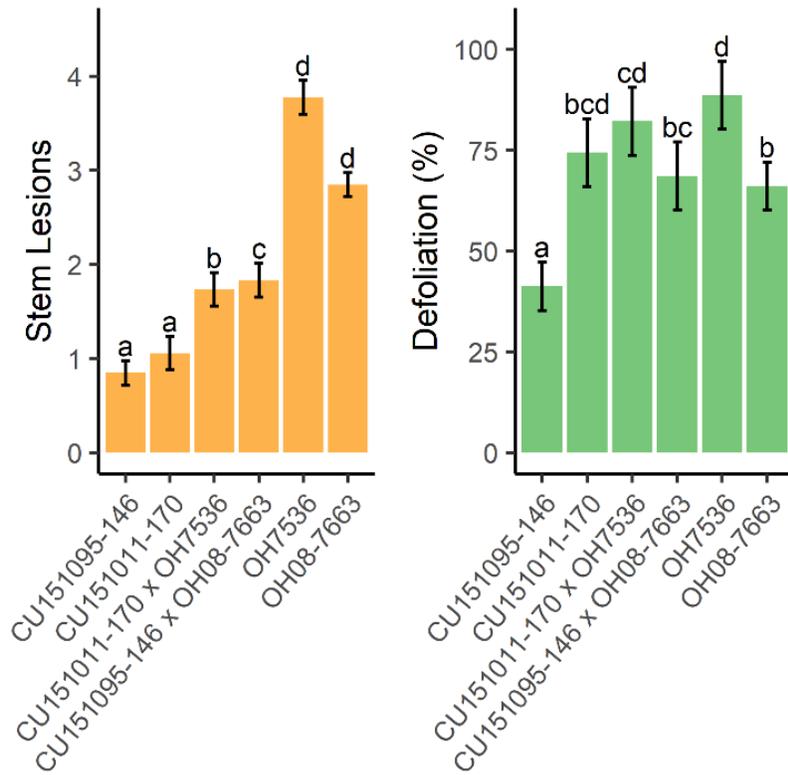
**Fig. S1** Genetic map created for the F<sub>2</sub> mapping population in R/qtI showing the distribution of 274 conservatively filtered molecular markers across the SL3.0 tomato genome



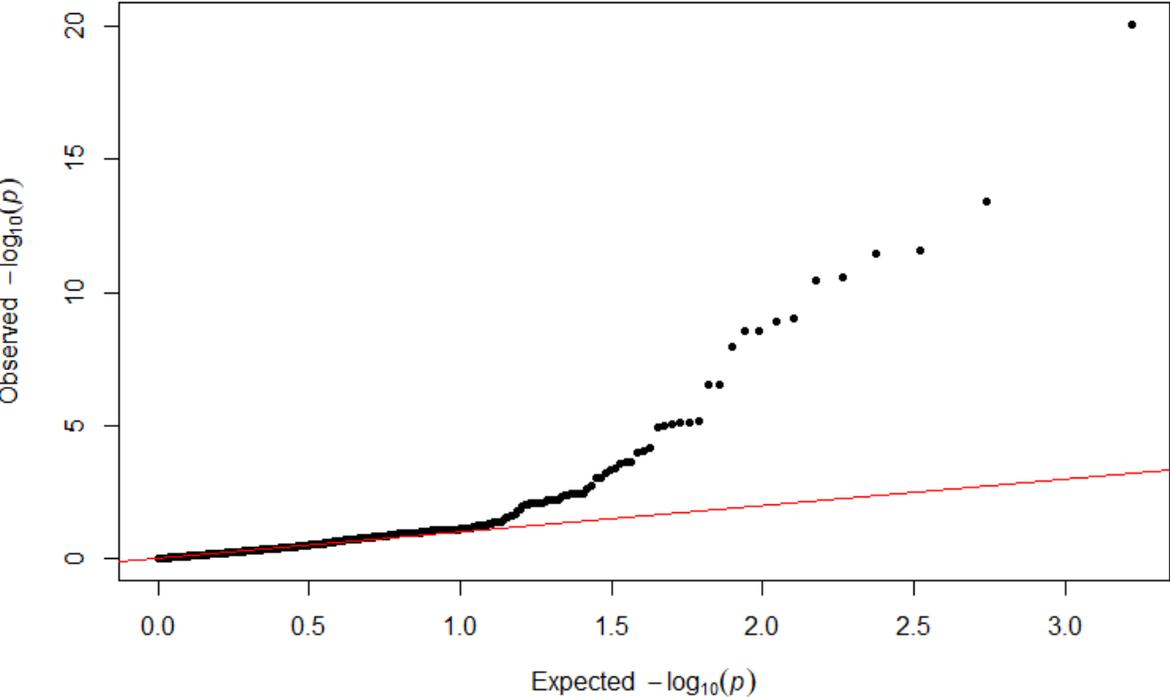
**Fig. S2** The chromosome 9 QTL `solcap_snp_sl_29188` had a statistically significant impact on the percentage of the stems affected by early blight lesions in the second indoor disease screen. Alleles were either homozygous for the OSU processing tomato alleles (OH), heterozygous for the OH and CU151011-170 alleles (HET) or segregating 1:1 for the presence/absence of the CU151011-170 alleles (SEG). The boxplots show that tomatoes heterozygous for the CU151011-170 alleles were more resistant to stem lesions than those segregating at the locus or fixed for the processing tomato alleles. Tukey-adjusted letter groups ( $\alpha=.05$ ) are shown at top



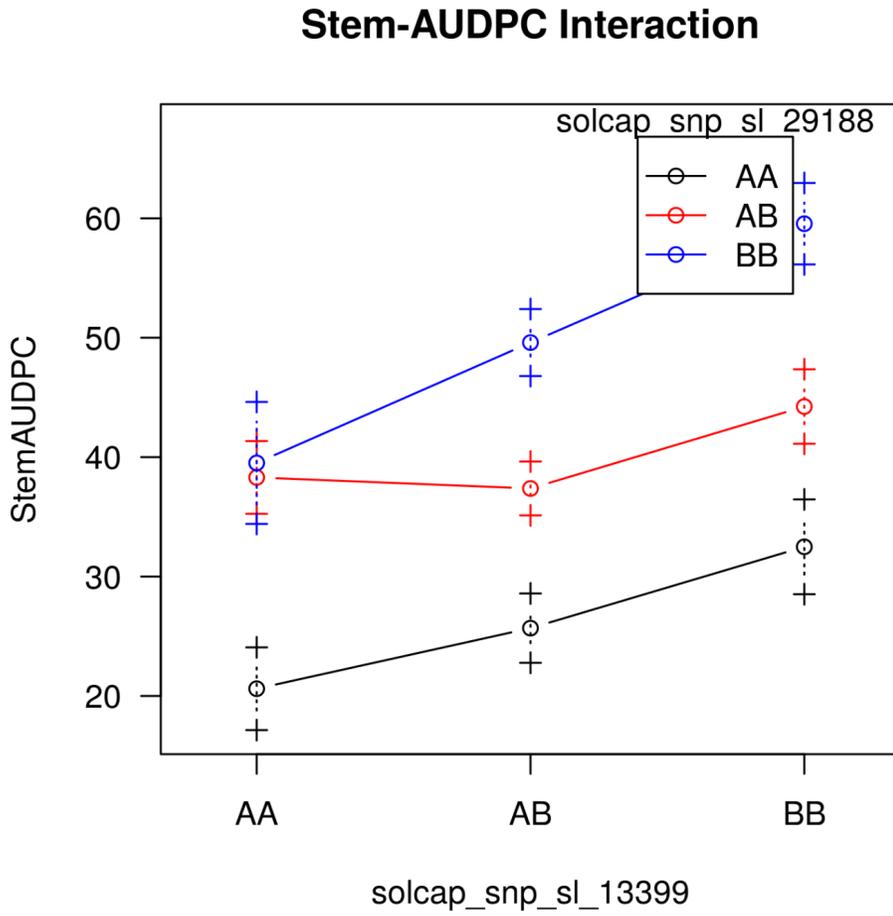
**Fig. S3** Early blight symptoms on tomato breeding lines and  $F_1$  hybrids in a 2017 inoculated field trial. Entries varied in their degree of resistance to early blight stem lesions,  $F_{5,138} = 111.91, p \sim 0$ , and defoliation,  $F_{5,138} = 22.86, p \sim 0$ . Error bars depict 95% confidence intervals, with Tukey-adjusted 95% confidence level letter groups at top



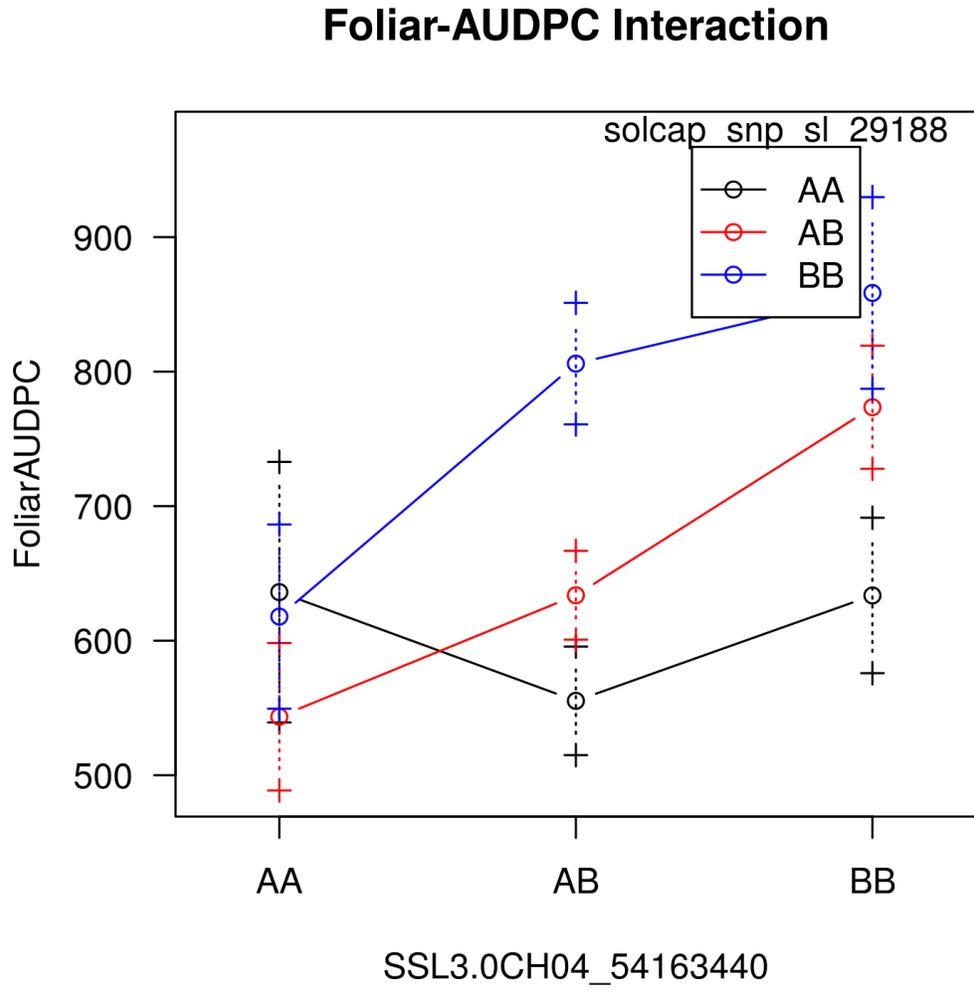
**Fig. S4** Quantile-quantile plot for the results of the GEMMA bivariate mixed-effect regression model



**Fig. S5** QTL interaction plot for stem-AUDPC between the *EB-1.1* marker *solcap\_snp\_sl\_13398* and the *EB-9* marker *solcap\_snp\_sl\_29188*



**Fig. S6** QTL interaction plot for foliar-AUDPC between the *EB-4* marker SL3.0CH04\_54163440 and the *EB-9* marker solcap\_snp\_sl\_29188



**Fig. S7** Interaction plots showing the effects of three QTL x QTL interactions for defoliation among the genotypically-selected  $F_{2:3}$  families. Additivity is assumed because selection was done for homozygosity at QTL genotypes. The foliar-resistant allele is derived from the Cornell tomato background (CU) for the genotypes *solcap\_snp\_sl\_34568* (*EB-1.2*) and *solcap\_snp\_sl\_29188* (*EB-9*). The resistant allele at the SNP SL3.0CH05\_649366933 (*EB-5*) is derived from the Ohio processing tomato background (OH). If the  $F_2$  family's parent was heterozygous at a marker near a QTL (HET), then the  $F_{2:3}$  progeny would have segregated for resistance

