



Figure S2. Chromosome distribution of 445 candidate resistance gene analogs (RGA) and 87 non-RGAs (labeled with ‘*’) co-located with 269 quantitative trait nucleotides (QTNs) within 200 Kb genome regions of the QTNs. R^2 represents the proportion of phenotypic variation explained by a QTN or a SNP on a candidate gene. The brackets show candidate gene clusters that contain at least three genes.