 **S1 Fig. Maximum likelihood phylogeny of *TRI1* gene sequences from the 60 isolates of *F. graminearum* used for genome sequencing***.* The phylogeny was inferred using the Kimura 2-parameter model of nucleotide substitution [135] with a Gamma parameter to account for rate heterogeneity. Bootstrap values (%, based on 100 replications) ≥ 50 are indicated on branches. The tree was rooted at midpoint and drawn to scale, with branch lengths measured in the number of substitutions per site.