

Figure S3: Reductions in FHB disease levels in (A) 2017 field season and (B) 2018 field season in UMN_C3 population with two or three QTL models. To obtain these estimates, genets containing QTL with the highest R^2 values observed in each environment were identified with the exception of *Ti_Qfhb.umn-Chr4.1*. This QTL was the second largest in FHB17 and was used since both FHB16 and FHB17 shared the largest QTL, *Ti_Qfhb.umn-Chr4.1*, in both environments. Text accompanied by red bars show the percentage reduction in disease when QTL are combined. Error bars represent the standard deviation of disease distribution.

