# Supplemental Materials

## Appendix S1 – Yield Trials

For yield trials in 2014, lines were evaluated at Crookston, MN; Morris, MN; and Saint Paul, MN. For 2015 yield trials, lines were evaluated at Crookston and Morris. Lines were grown in an augmented block design (Lin and Poushinsky, 1985). The check varieties were used to adjust for spatial variation across trial plots. Checks included ‘Lacey’ (96 replicates), ‘Quest’ (24 replicates), ‘Stellar-ND’ (20 replicates), and ‘Tradition’ (20 replicates).

For DON concentration trials, each chosen F3:5 line was evaluated at five year-locations in disease nurseries (Massman et al., 2011). Similar to the yield trials, lines were grown in an augmented block design. DON concentration was evaluated at Crookston, MN in 2013, 2014, and 2015. DON concentration was evaluated at Saint Paul, MN in 2013 and 2014. Check varieties for DON trials were ‘Quest’ (123 replicates), ‘ND20448’ (26 replicates), ‘Tradition’ (25 replicates), and ‘Lacey’ (25 replicates).

## Appendix S2 – Linear Interpolation of Genetic and Physical SNP Positions

Among the 384 SNPs on the Veracode assay, two were missing genetic positions and 14 were missing physical positions. To interpolate genetic or physical positions, we use the positions of flanking SNPs. We take half the distance between known positions. In the formulas, D is average distance, G is genetic distance, P is physical distance, and the subscripts k and u refer to known and unknown positions and subscripts 1 and 2 refer to positions up and downstream of the position to be interpolated.

### **Unknown genetic position**

D = (P2 - Pk) / (P2 - P1)

Gu = G2 - D \* (G2 - G1)

if Gu= G2 ; Gu = (G2 - G1)/2

### **Unknown physical position**

D = (G2 - Gk) / (G2 - G1)

Pu = P2 - D \* (P2 - P1)

if Pu = P2; Pu = (P2 - P1)/2