Supplemental Fig. S1. Genetic linkage map of 150 doubled haploid lines derived from UH007×UH006 based on 123 simple sequence repeat markers. Marker positions are given on the left of the chromosomes in cM. Marker names, given on the right, which are followed by (+) and (-) indicate segregation distortion ($P < 0.05$) toward UH006 and UH007, respectively. Hatched segments of the chromosome indicate loose linkage between chromosomal regions (LOD = 0.15 to 0.30). Vertical bars indicate the support intervals of QTL from the analyses for Gibberella ear rot (GER) resistance, low deoxynivalenol (DON) and zearalenone (ZEA) contaminations.