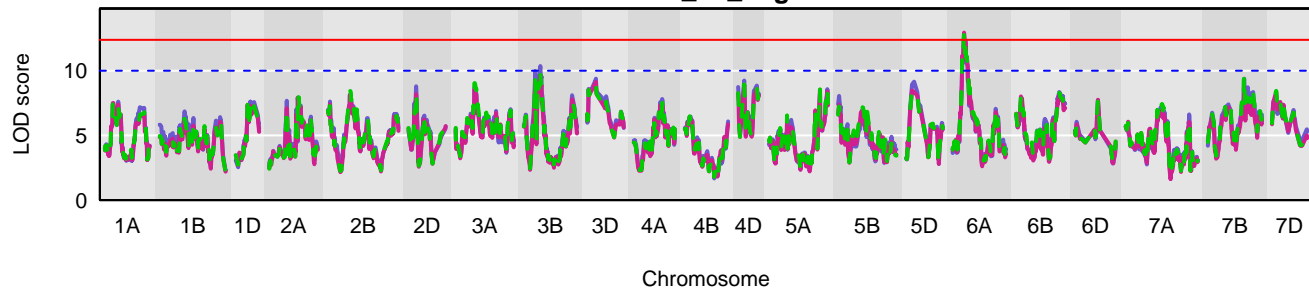
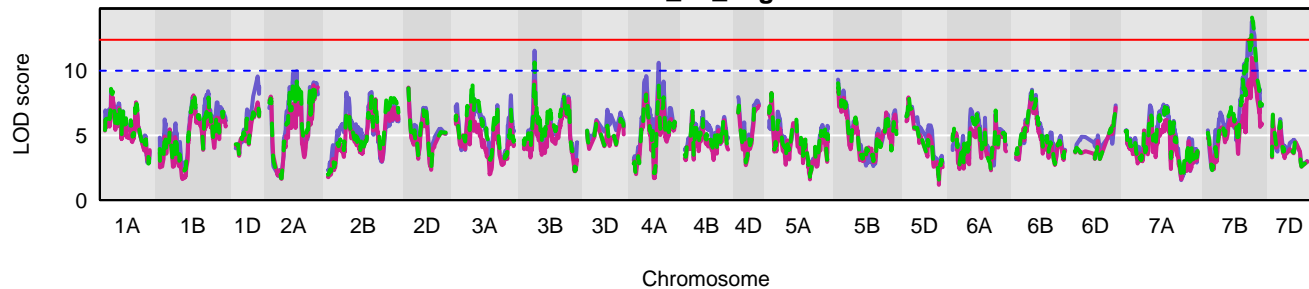


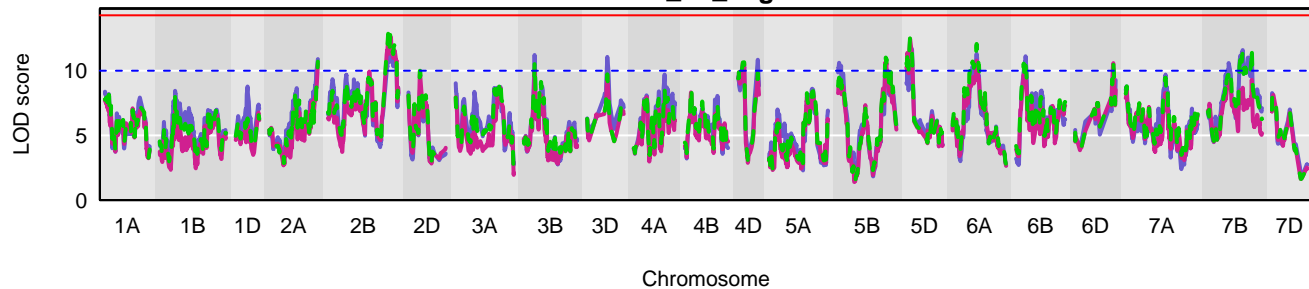
2016_T1_flag



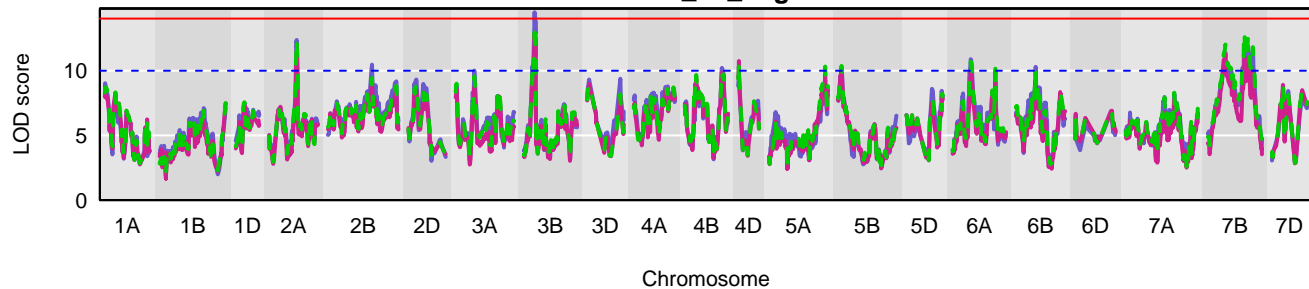
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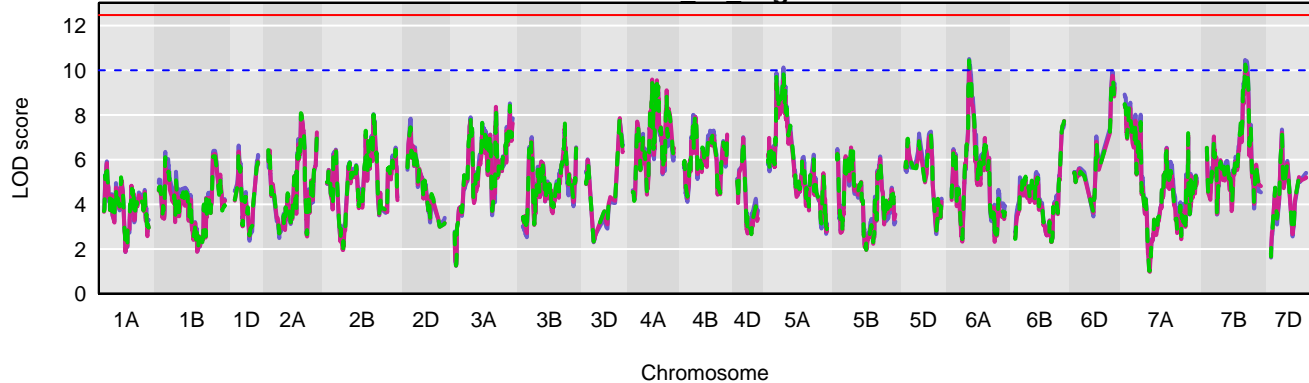
2016_T1_flag-2



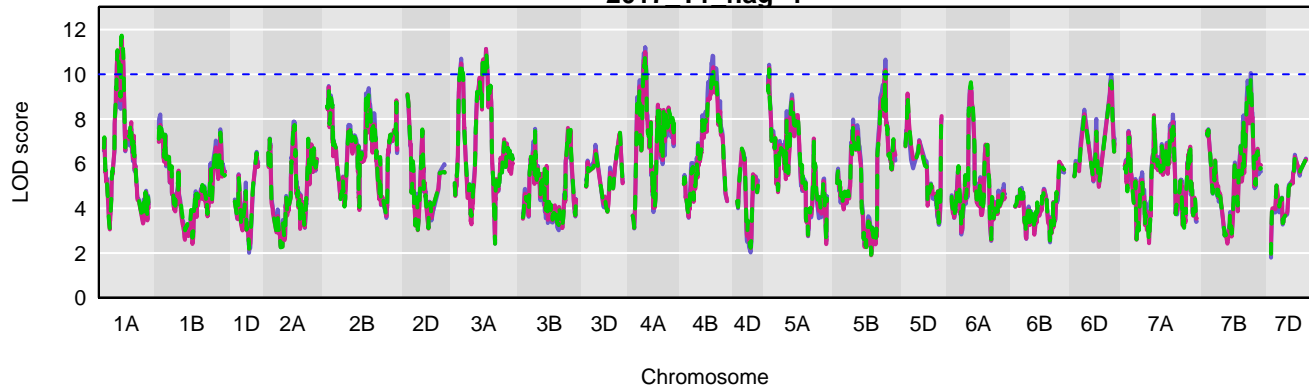
2016_T2_flag



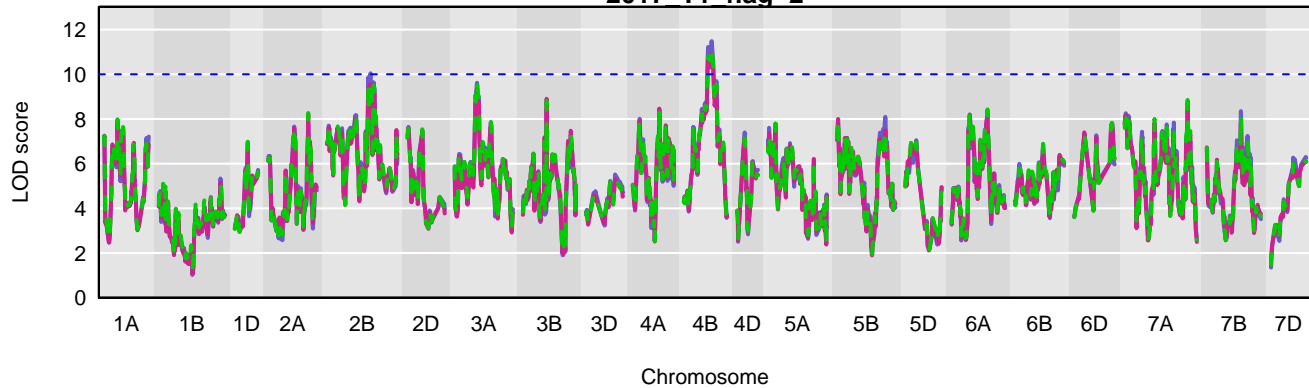
2017 T1 flag



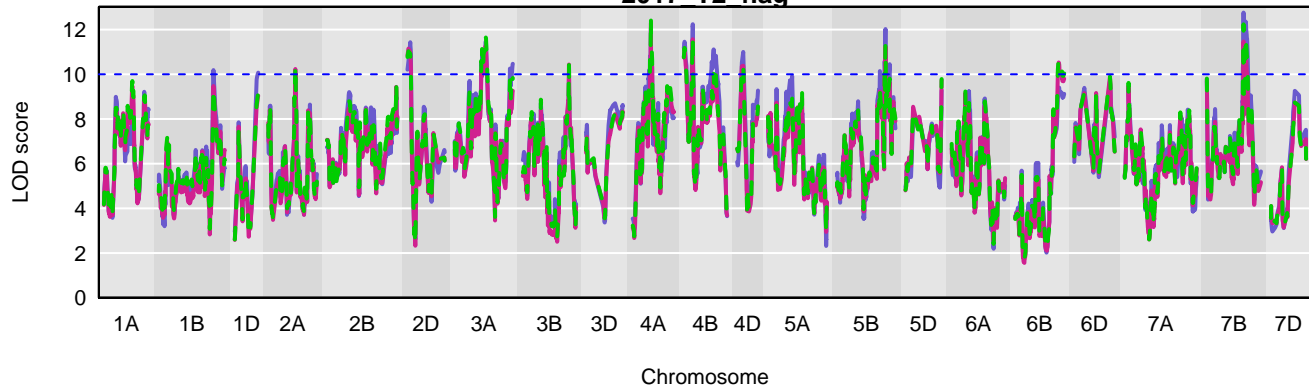
2017 T1 flag-1



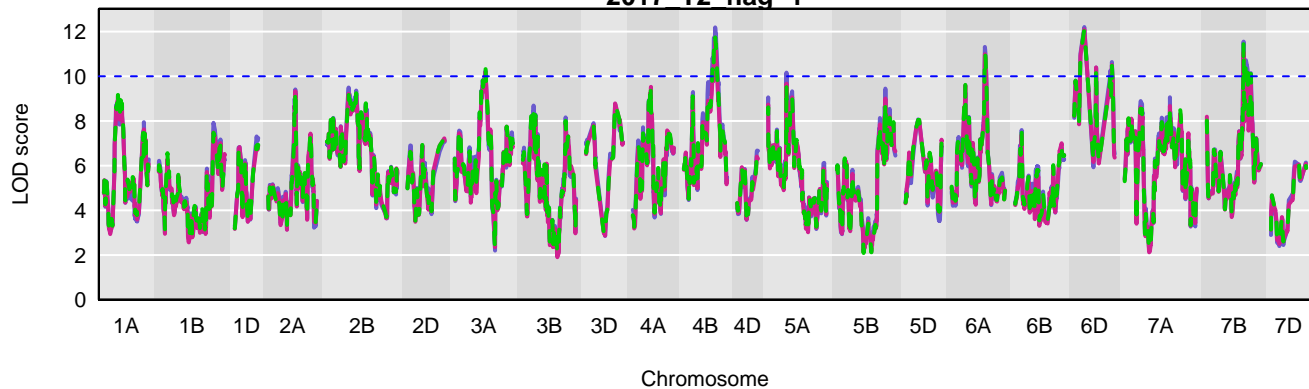
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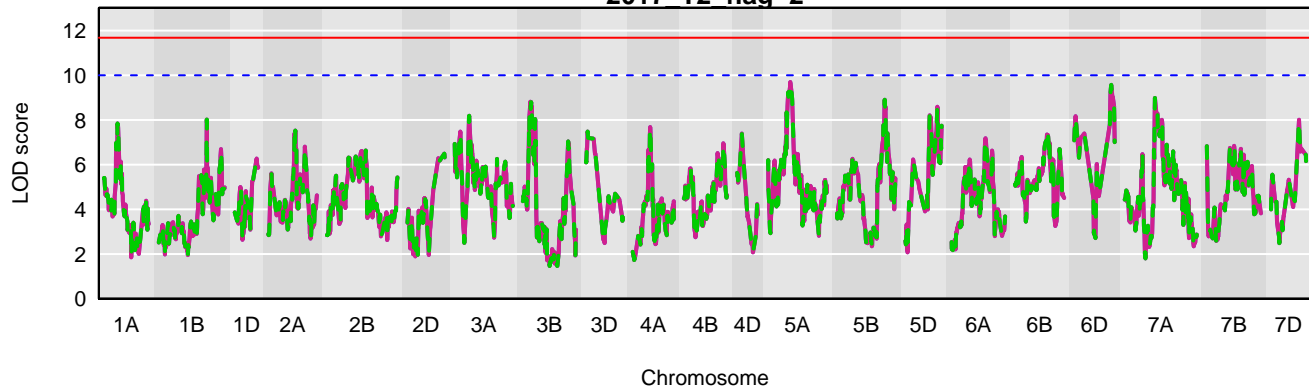
2017 T2 flag



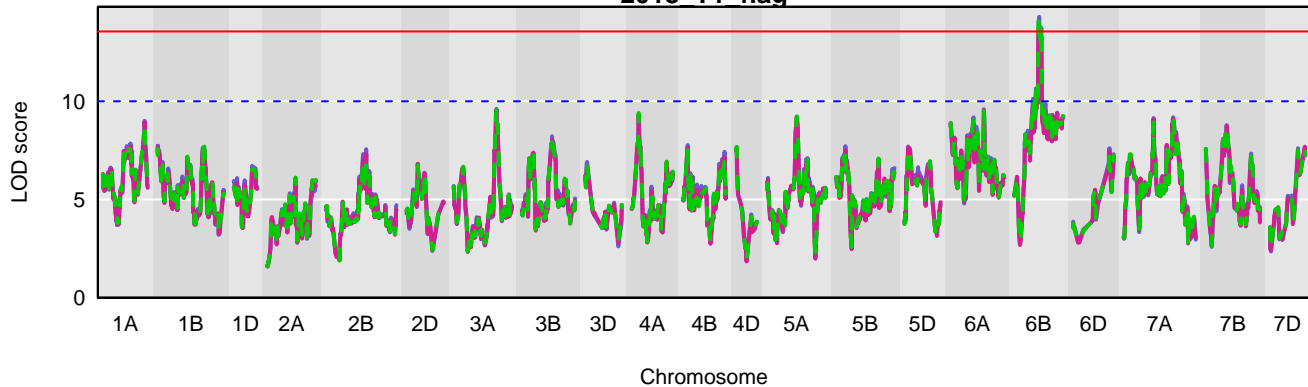
2017 T2 flag-1



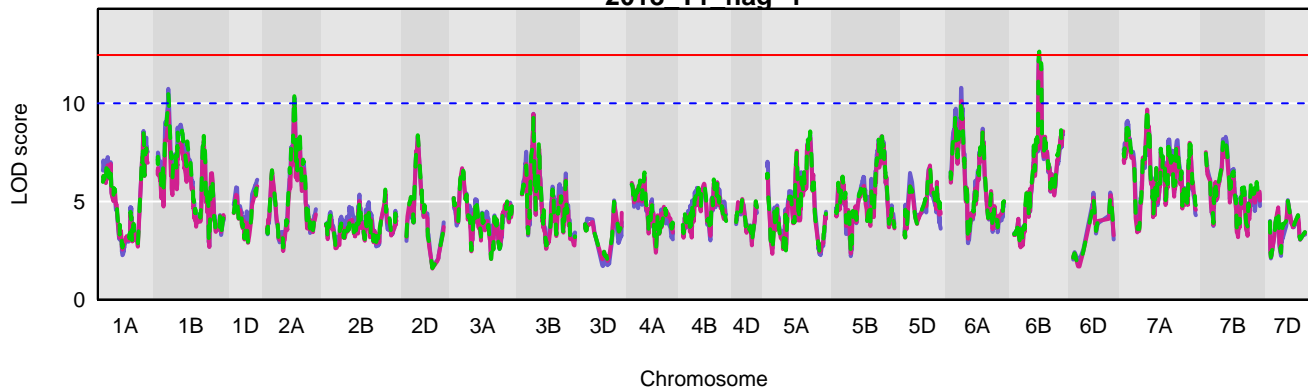
2017 T2 flag-2



2018 T1 flag



2018 T1 flag-1



2018 T1 flag-2

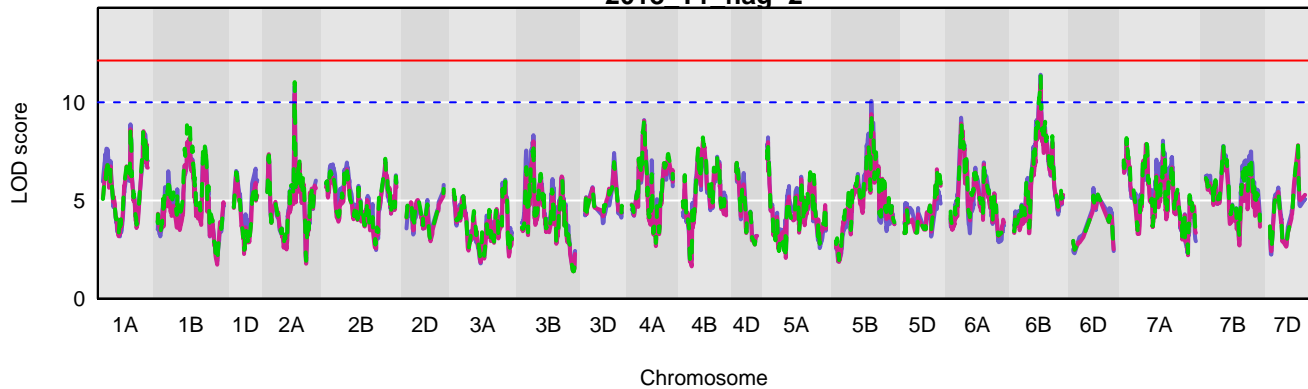


Figure S3. LOD scores from QTL mapping for septoria tritici blotch (STB) resistance in the NIAB Elite MAGIC population, displayed for each dataset. Each of the individual dataset contains the LOD scores of the genome scan using the Haley-Knott regression (blue line), linear mixed model (LMM; violet line), and leave one chromosome out (LOCO; green line) model. The “red” line indicates 5% level of genome-wide significance threshold based on permutation test, while “blue dotted line” represents arbitrary threshold for all the datasets (LOD = 10.0), determining weak QTL.