Supplemental Figure S1. Genome-wide association scan of Ethiopian and Eritrean barley landraces germplasm for markers associated with resistance to *Pyrenophora teres* f. *teres* isolate 30107003 using complete set of markers. Vertical axis represents $-\log_{10}(p)$ values of the marker-trait association after correction for multiple testing and the horizontal axis represents the relative chromosomal position of the markers across the genome. Marker 11_10405 at 171.16 cM of chromosome 5H had the highest $-\log_{10}(p)$ value.
**Supplemental Figure S2.** Genome-wide association scan of Ethiopian and Eritrean barley landrace germplasm for markers associated with resistance to *Pyrenophora teres* f. *teres* isolate 30107003 using mapped markers only. Vertical axis represents $-\log_{10}(p)$ values of the marker-trait association after correction for multiple testing and the horizontal axis represents the relative chromosomal position of the markers across the genome. Marker 11_10405 at 171.16 cM of chromosome 5H had the highest $-\log_{10}(p)$ value.
Supplemental Figure S3. Genome-wide association scan of Ethiopian and Eritrean barley landrace germplasm for markers associated with resistance to *Pyrenophora teres f. teres* isolate 30107003 using markers with unique map positions only. Vertical axis represents $-\log_{10}(p)$ values of the marker-trait association after correction for multiple testing and the horizontal axis represents the relative chromosomal position of the markers across the genome. Marker 11_10405 at 171.16 cM of chromosome 5H had the highest $-\log_{10}(p)$ value.
Supplemental Figure S4. Genome-wide association scan of Ethiopian and Eritrean barley landrace germplasm for markers associated with resistance to Pyrenophora teres f. teres isolate 30107004 using complete set of markers. Vertical axis represents -log_{10}(p) values of the marker-trait association after correction for multiple testing and the horizontal axis represents the relative chromosomal position of the markers across the genome. Marker 11_10405 at 171.16 cM of chromosome 5H had the highest -log_{10}(p) value.
Supplemental Figure S5. Genome-wide association scan of Ethiopian and Eritrean barley landrace germplasm for markers associated with resistance to *Pyrenophora teres* f. *teres* isolate 30107004 using mapped markers only. Vertical axis represents $-\log_{10}(p)$ values of the marker-trait association after correction for multiple testing and the horizontal axis represents the relative chromosomal position of the markers across the genome. Marker 11_10405 at 171.16 cM of chromosome 5H had the highest $-\log_{10}(p)$ value.
Supplemental Figure S6. Genome-wide association scan of Ethiopian and Eritrean barley landrace germplasm for markers associated with resistance to *Pyrenophora teres* f. *teres* isolate 30107004 using markers with unique map positions. Vertical axis represents -log_{10}(p) values of the marker-trait association after correction for multiple testing and the horizontal axis represents the relative chromosomal position of the markers across the genome. Marker 11_10405 at 171.16 cM of chromosome 5H had the highest -log_{10}(p) value.
Supplemental Figure S7. Genome-wide association scan of Ethiopian and Eritrean barley landrace germplasm for markers associated with resistance to *Pyrenophora teres* f. *teres* isolate 30112002 using the complete set of SNP markers. Vertical axis represents the -log_{10}(p) values of the marker-trait association after correction for multiple testing and the horizontal axis represents the relative chromosomal position of the markers across the genome. Marker SCRI_RS_221843 at 62.91 cM of chromosome 2H had the highest -log_{10}(p) value.
Supplemental Figure S8. Genome-wide association scan of Ethiopian and Eritrean barley landrace germplasm for markers associated with resistance to *Pyrenophora teres f. teres* isolate 30112002 using mapped markers only. Vertical axis represents \(-\log_{10}(p)\) values of the marker-trait association after correction for multiple testing and the horizontal axis represents the relative chromosomal position of the markers across the genome. Marker SCRI_RS_221843 at 62.91 cM of chromosome 2H had the highest \(-\log_{10}(p)\) value.
Supplemental Figure S9. Genome-wide association scan of Ethiopian and Eritrean barley landrace germplasm for markers associated with resistance to *Pyrenophora teres* f. *teres* isolate 30112002 using markers with unique map positions only. Vertical axis represents \(-\log_{10}(p)\) values of the marker-trait association after correction for multiple testing and the horizontal axis represents the relative chromosomal position of the markers across the genome. Marker SCRI_RS_199178 at 45.2 cM of chromosome 1H had the highest \(-\log_{10}(p)\) value.