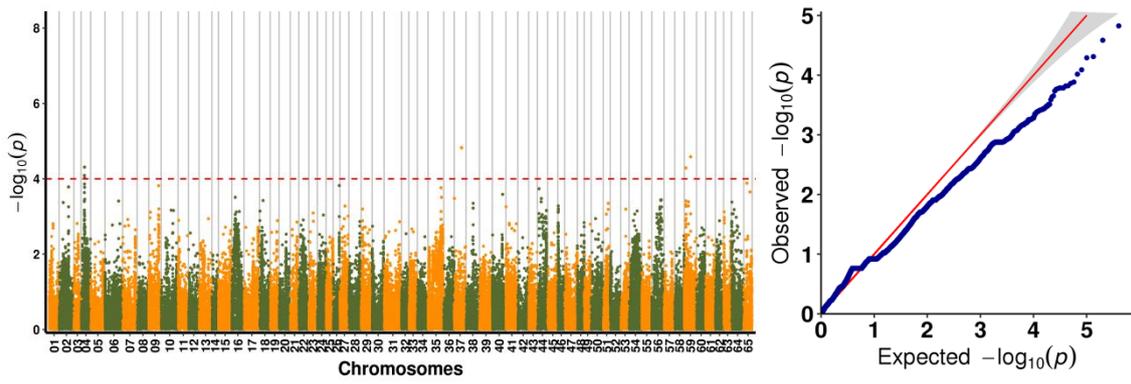
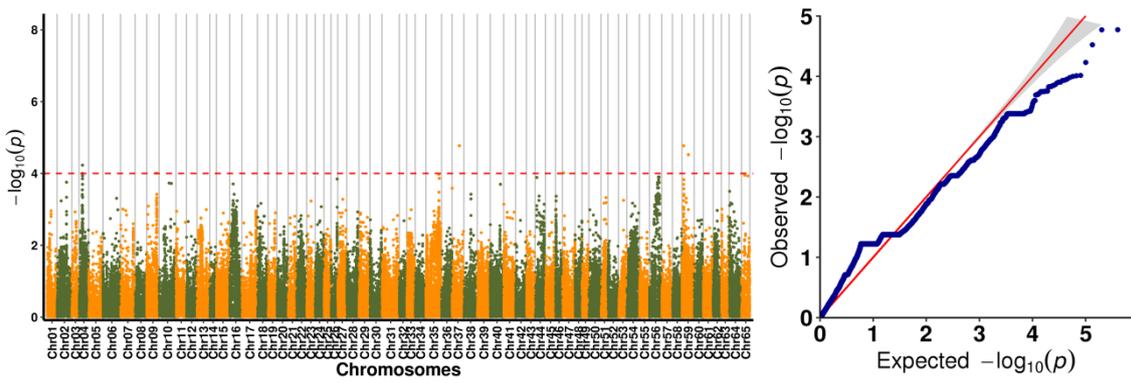


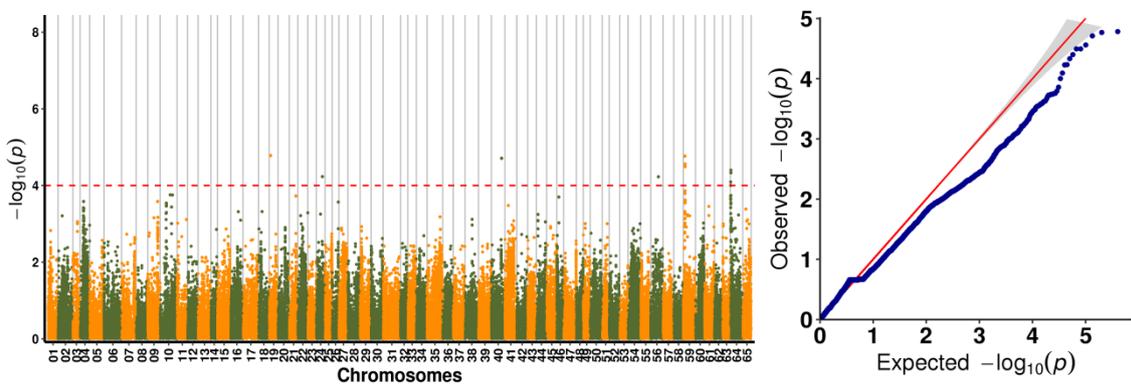
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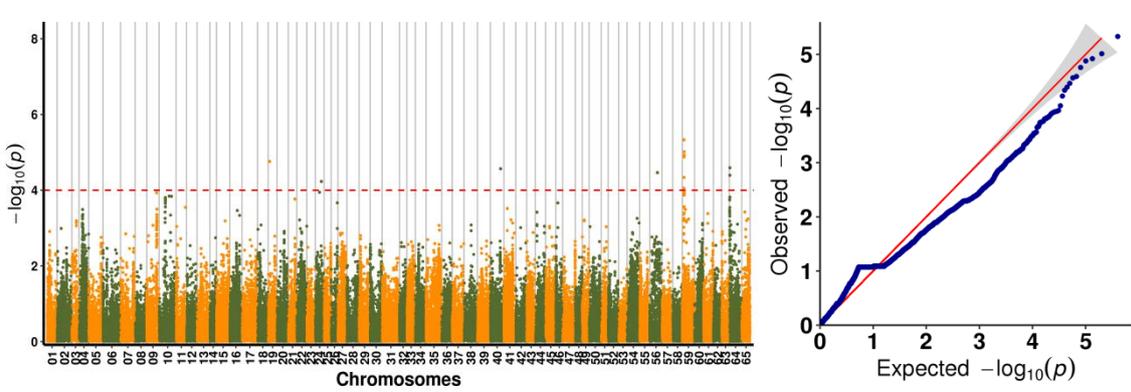
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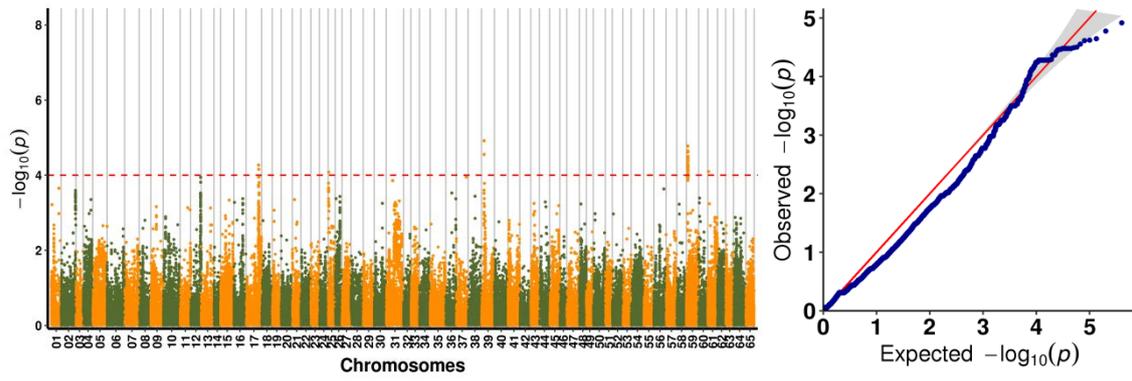
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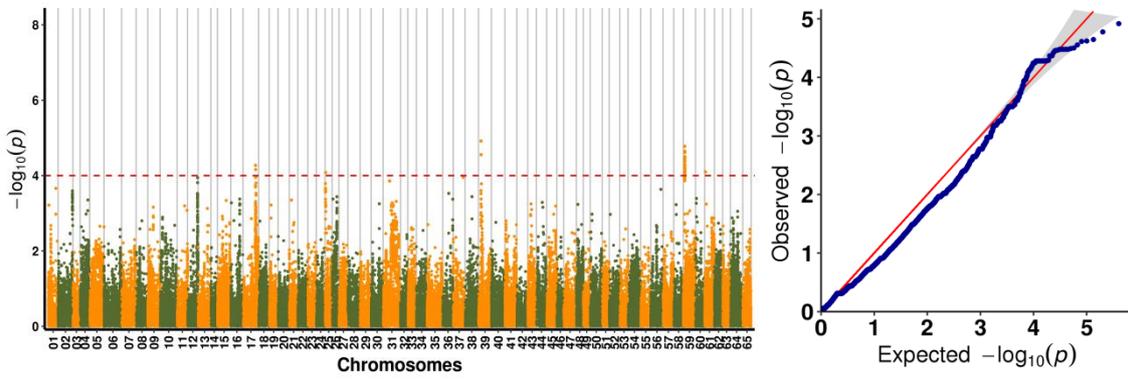
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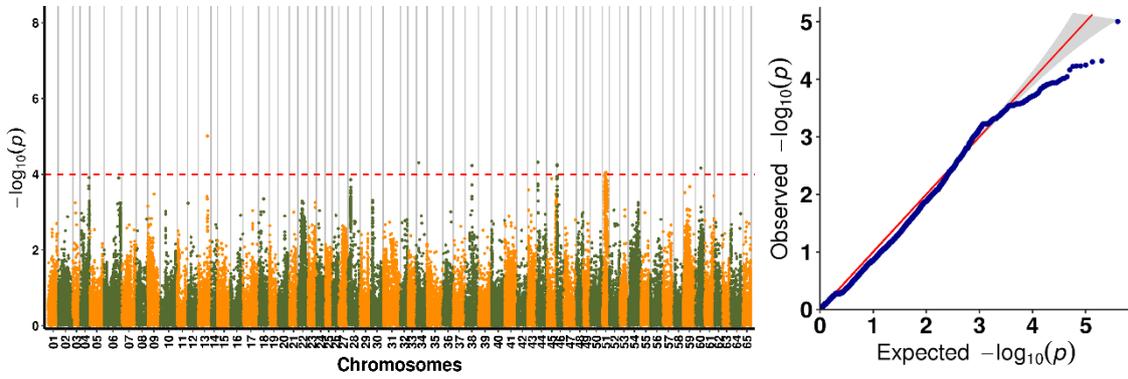
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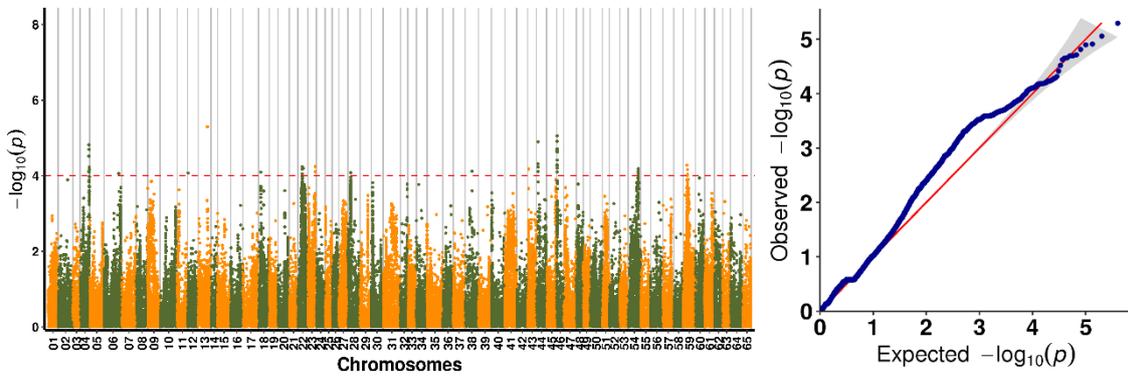
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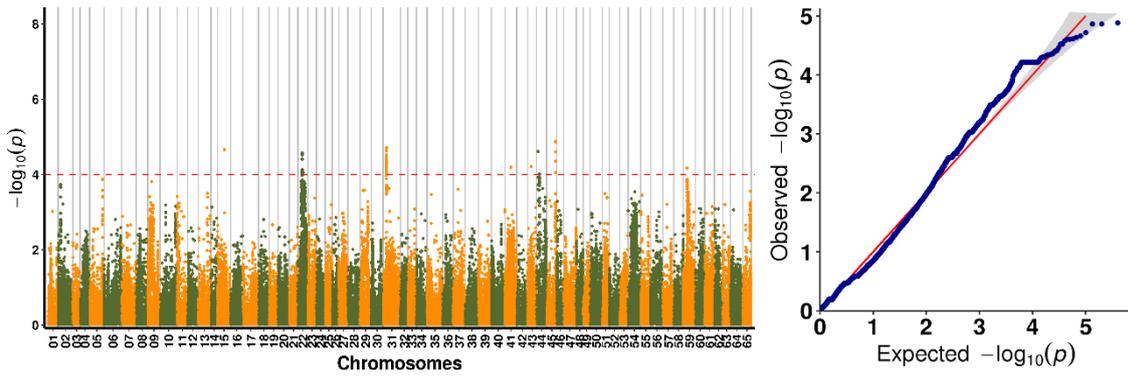
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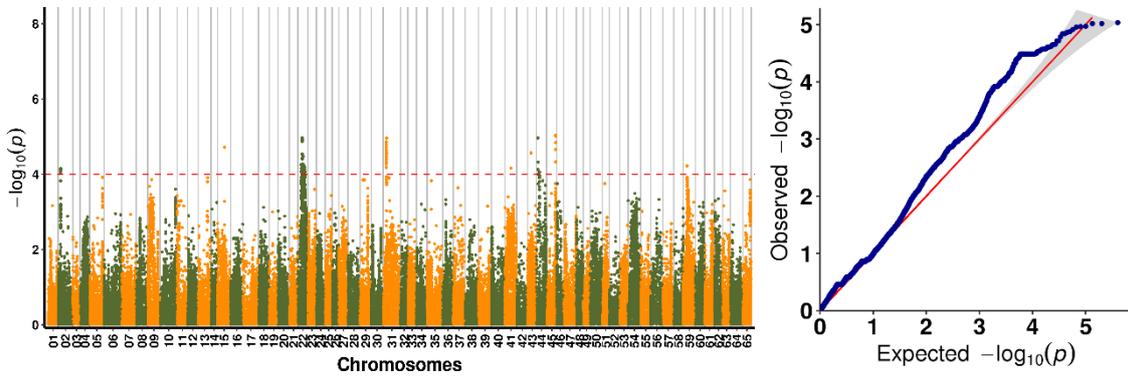
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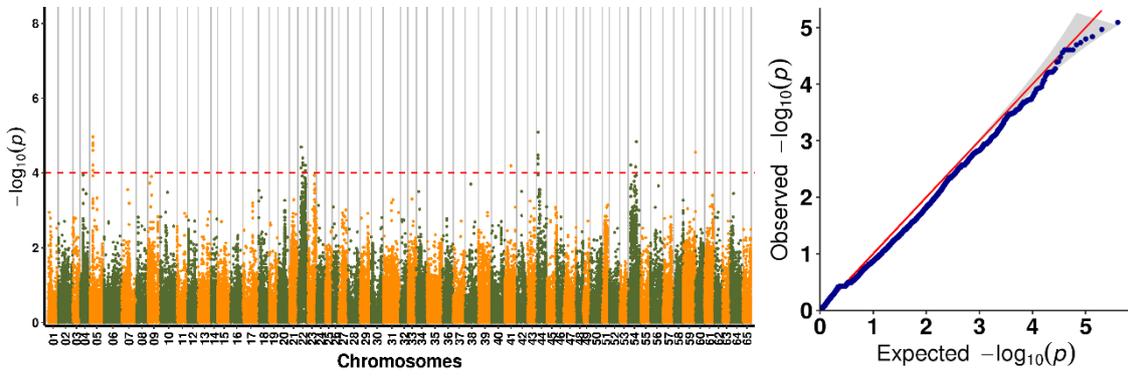
i



j



k



l

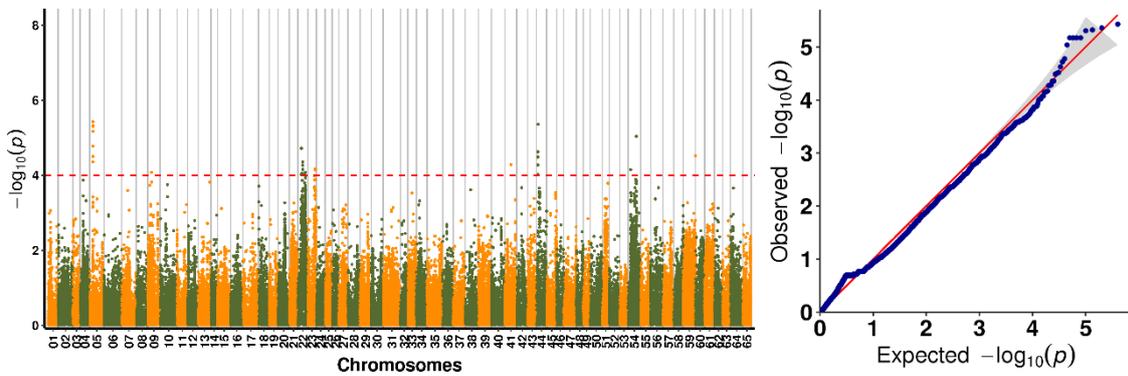


Figure S1. Manhattan plots and quantile-quantile (Q-Q) plots of GWAS for GP in okra. The threshold line of $-\log_{10}(P) > 4$ (red dashed line) was selected as significant association between SNPs and targeted traits. a: association mapping of GP-CK-3 d based on the EMMAX software; b: association mapping of GP-CK-3 d based on the GEMMA software; c: association mapping of GP-T1-3 d based on the EMMAX software; d: association mapping of GP-T1-3 d based on the GEMMA software; e: association mapping of GP-T2-3 d based on the EMMAX software; f: association mapping of GP-T2-3 d based on the GEMMA software; g: association mapping of GP-CK-7 d based on the EMMAX software; h: association mapping of GP-CK-7 d based on the GEMMA software; i: association mapping of GP-T1-7 d based on the EMMAX software; j: association mapping of GP-T1-7 d based on the GEMMA software; k: association mapping of GP-T2-7 d based on the EMMAX software; l: association mapping of GP-T2-7 d based on the GEMMA software.