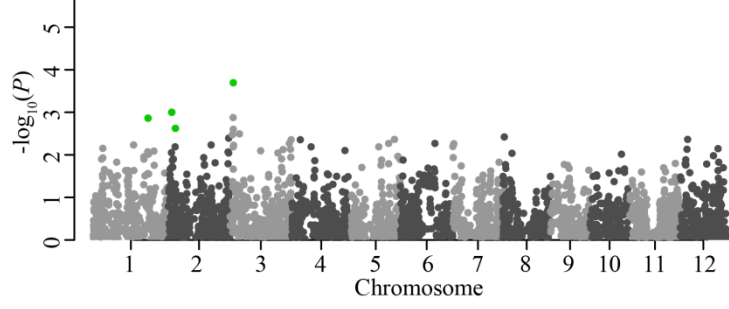
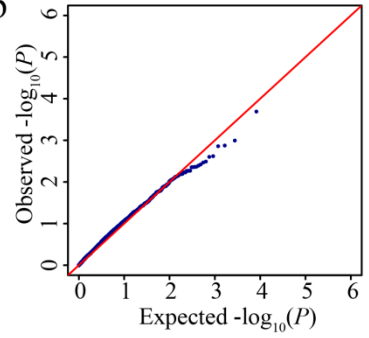


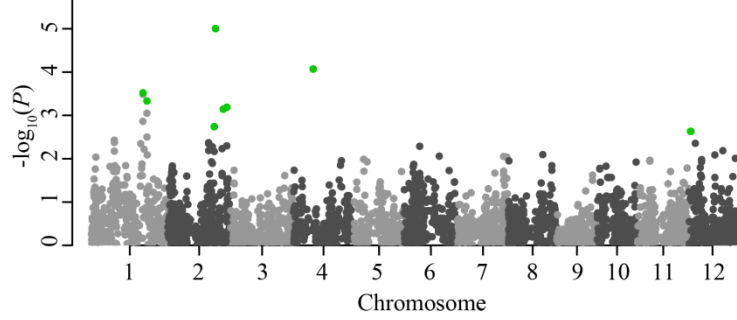
a TN-LS



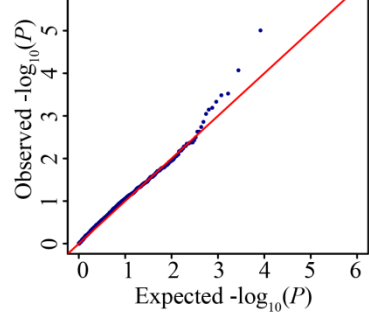
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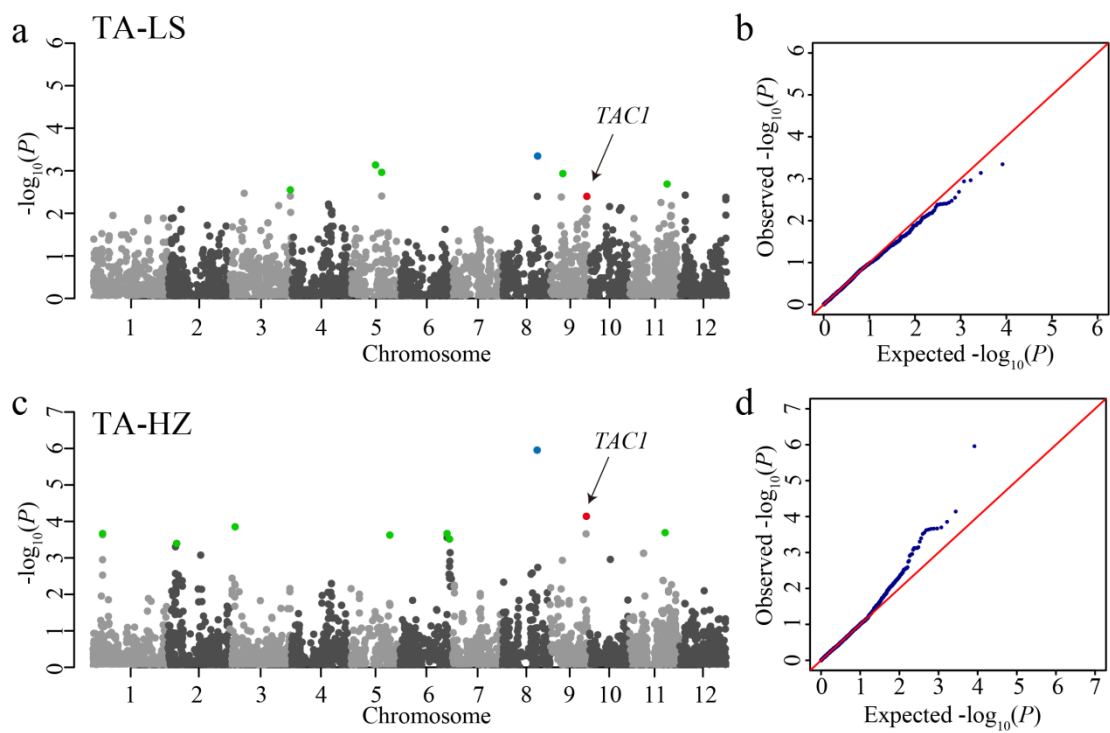
c TN-HZ



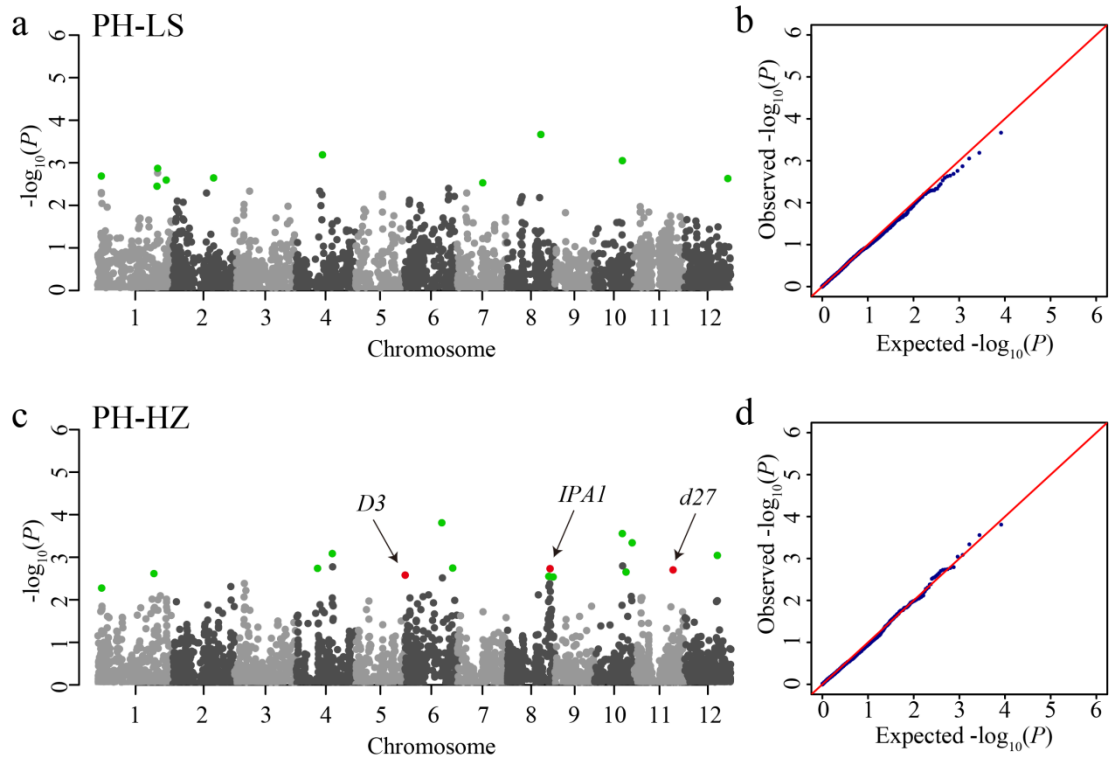
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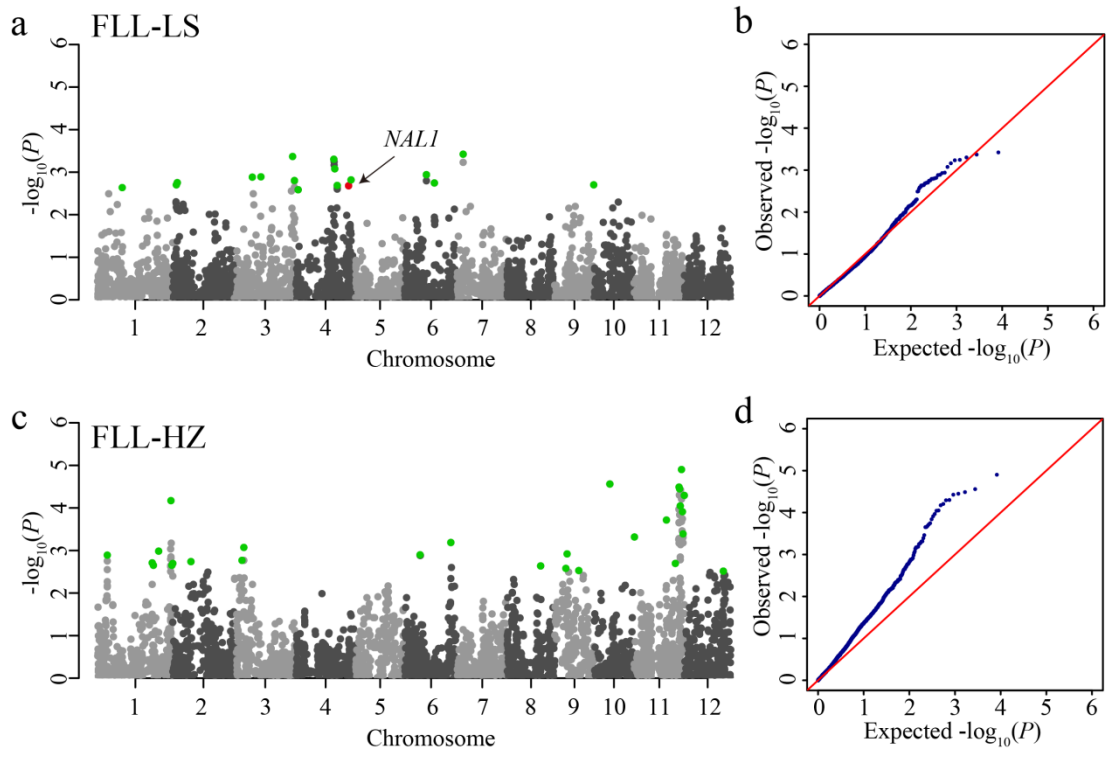
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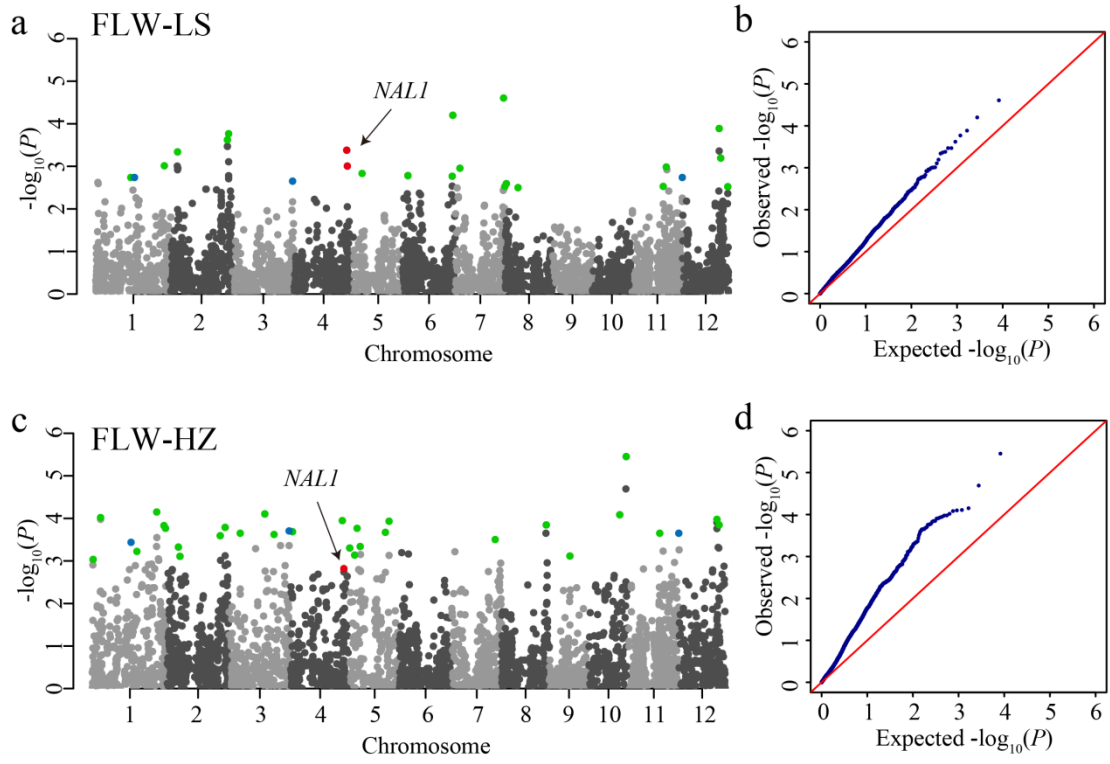
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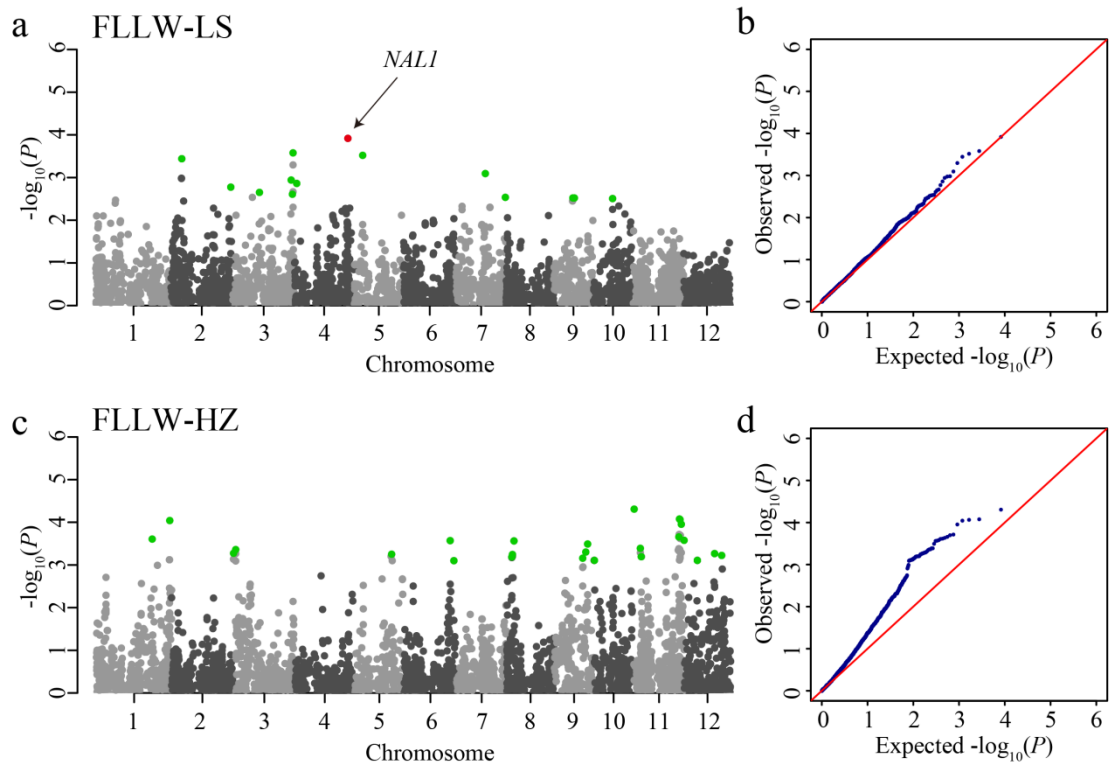
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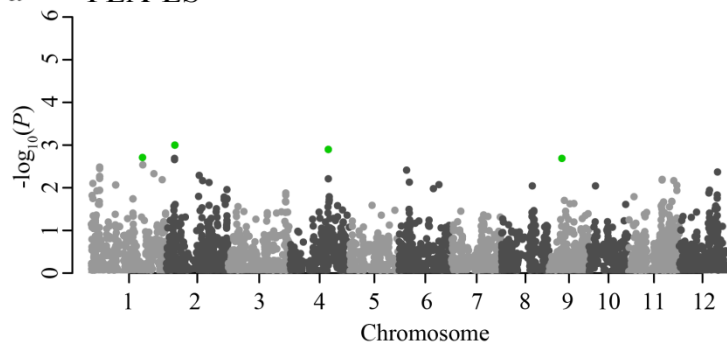


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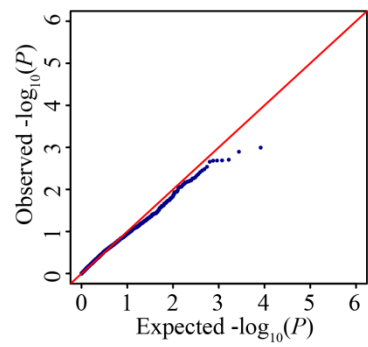


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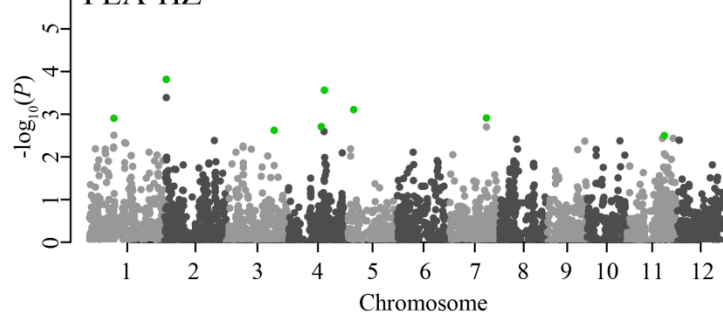
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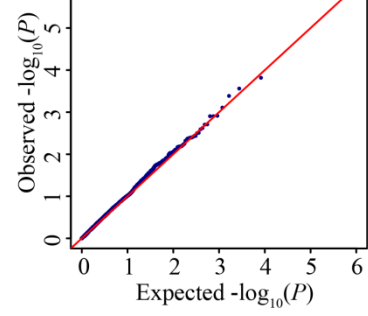
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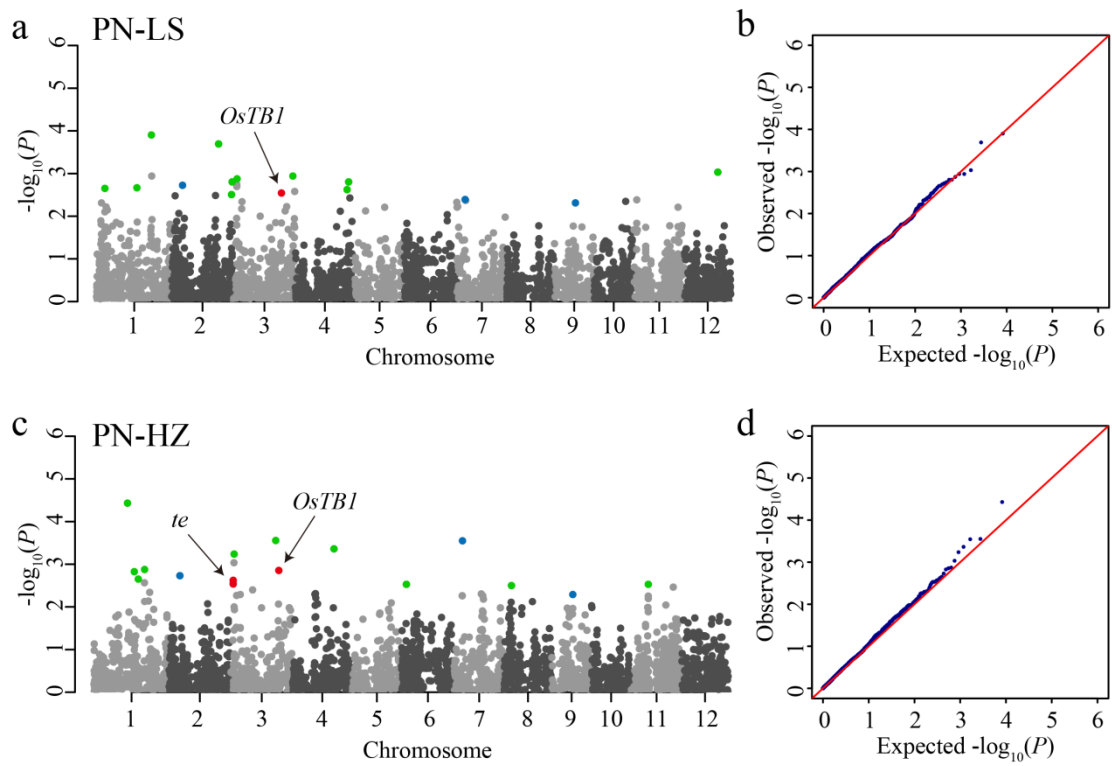
c FLA-HZ



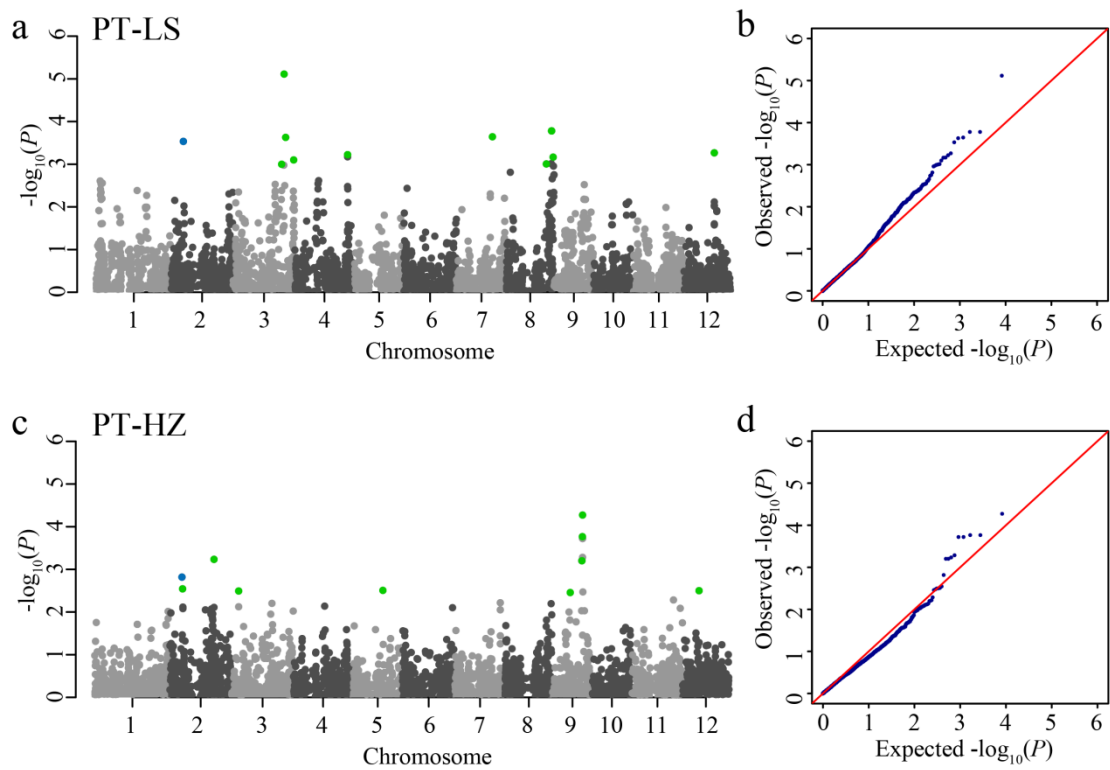
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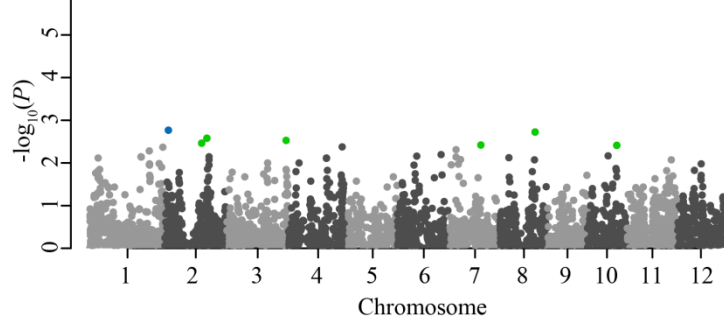


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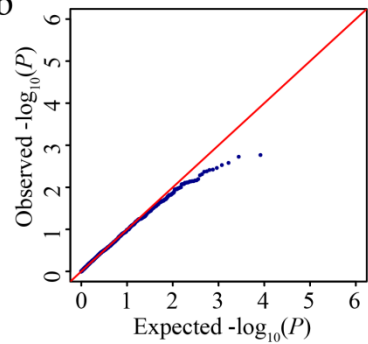


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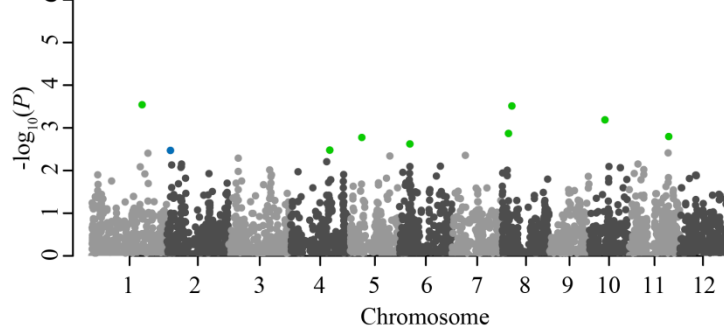
a PL-LS



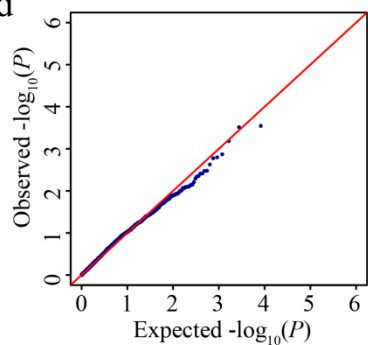
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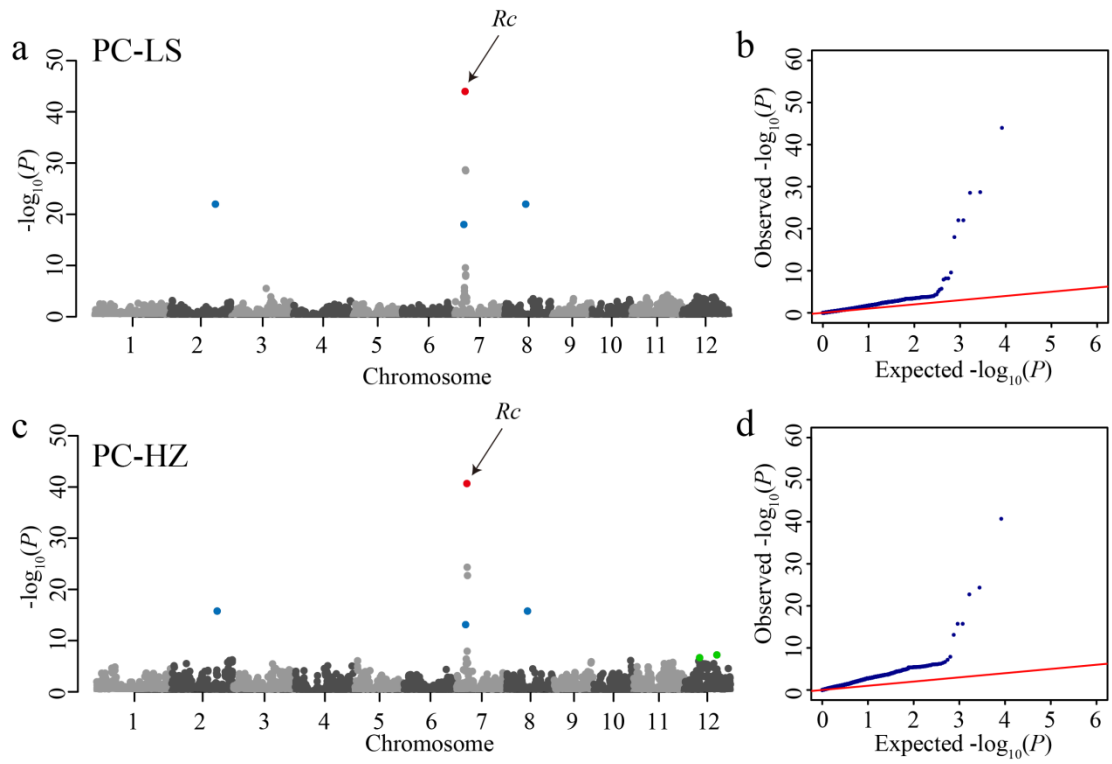
c PL-HZ



d



(Continued)



(Continued)

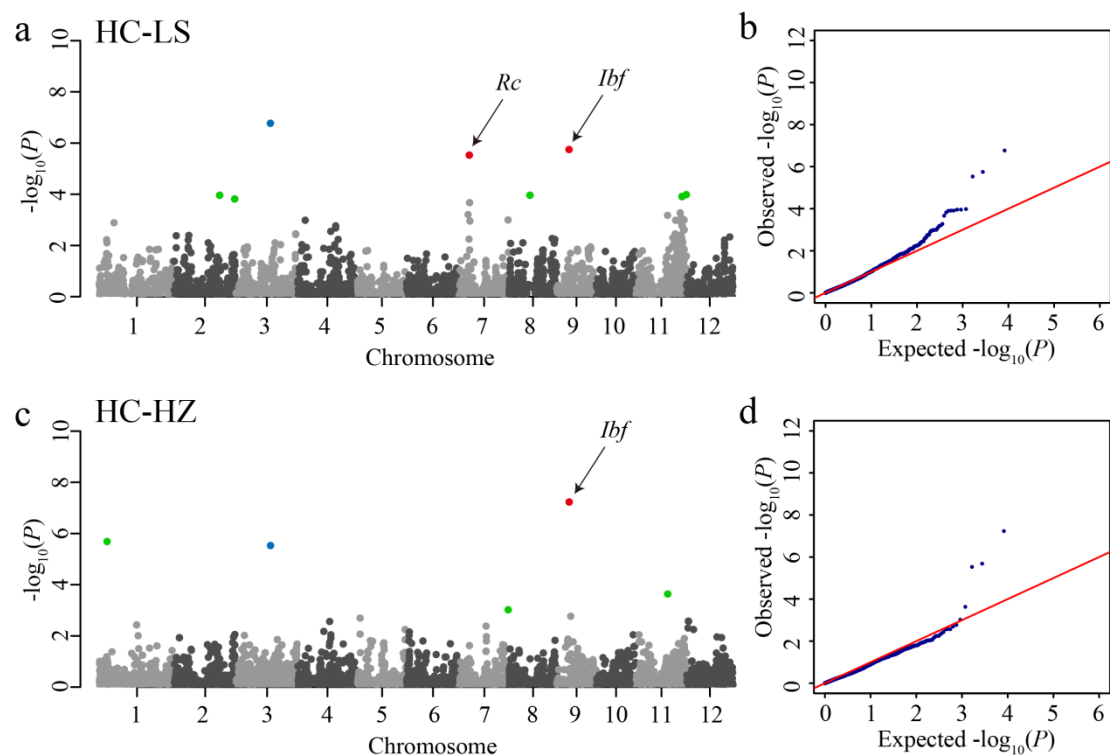


Figure S4. Manhattan and Quantile-Quantile plots of GWAS for all 12 traits in two environments. (a) and (c): Manhattan plot, showing P -values along the genome, calculated by mixed linear model (MLM, Q+K as covariate). (b) and (d): Q-Q plot, showing the expected null distribution of P -values (expected P -values), assuming no association, represented as a red line and distribution of P -values (Observed P -values) using MLM model represented as blue dots. Green dots indicate new significant candidate loci. Blue dots represent new significant loci detected in two environments. Red dots represent known loci. TN, Tiller number; TA, Tiller angle; PH, Plant height; FLL, Flag leaf length; FLW, Flag leaf width; FLLW, The ratio of flag leaf length and flag leaf width; FLA, Flag leaf angle; PN, Panicle number; PT, Panicle type; PL, Panicle length; PC, Pericarp color; HC, Hull color; LS, Lingshui; HZ, Hangzhou.