

Genome-wide association analysis identified newly natural variation of photosynthesis-related traits in a large maize panel

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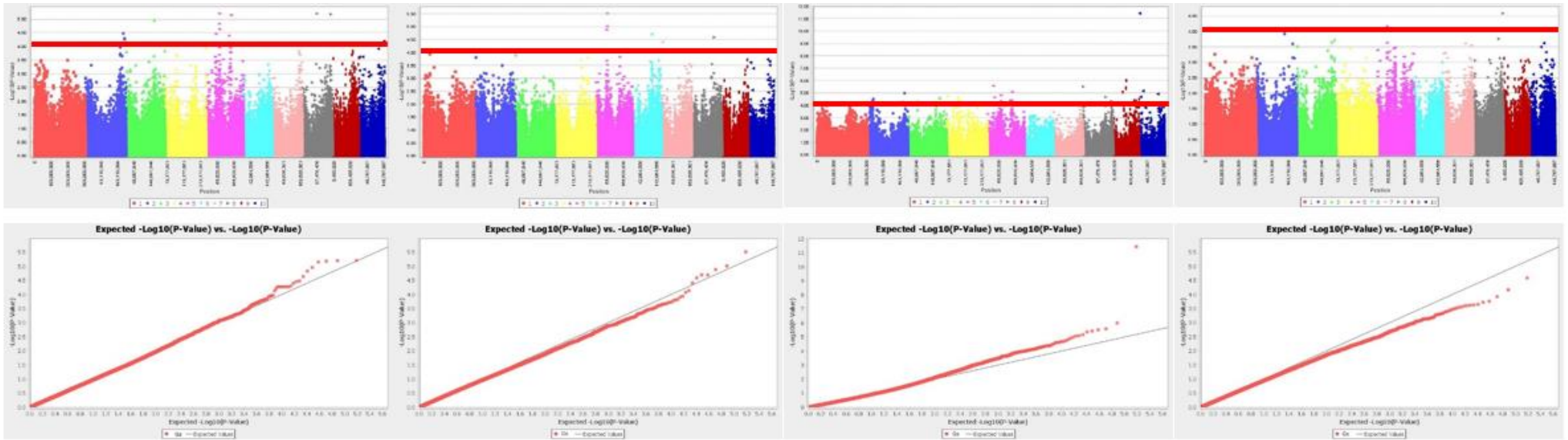
Combined analyses

At Pontevedra in 2017

At Pontevedra in 2018

At Pontevedra in 2019

Stomatal conductance



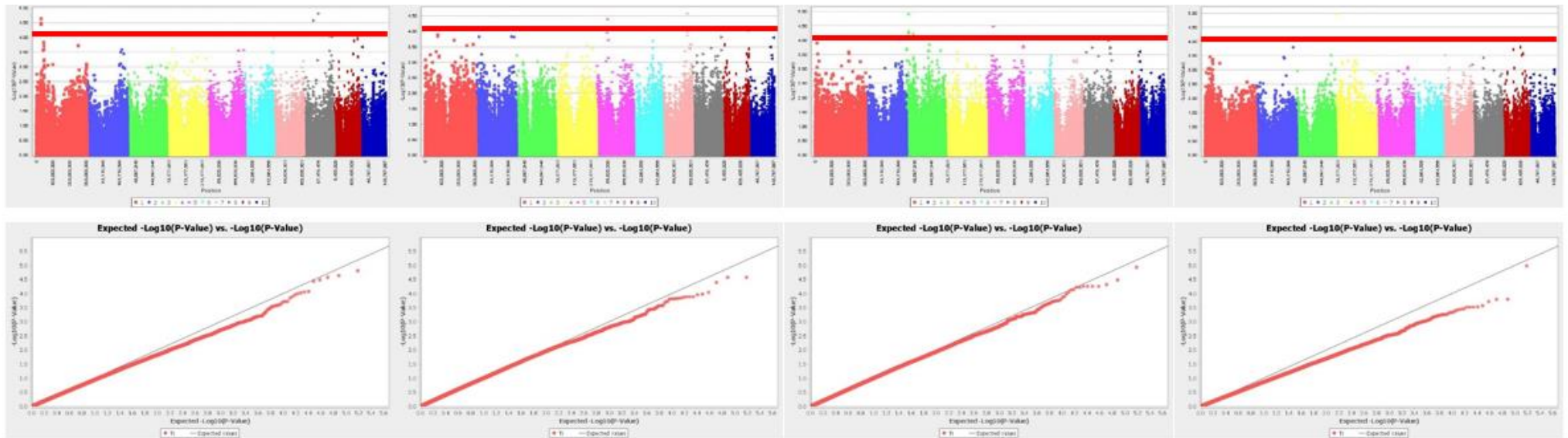
Combined analyses

At Pontevedra in 2017

At Pontevedra in 2018

At Pontevedra in 2019

Transpiration rate



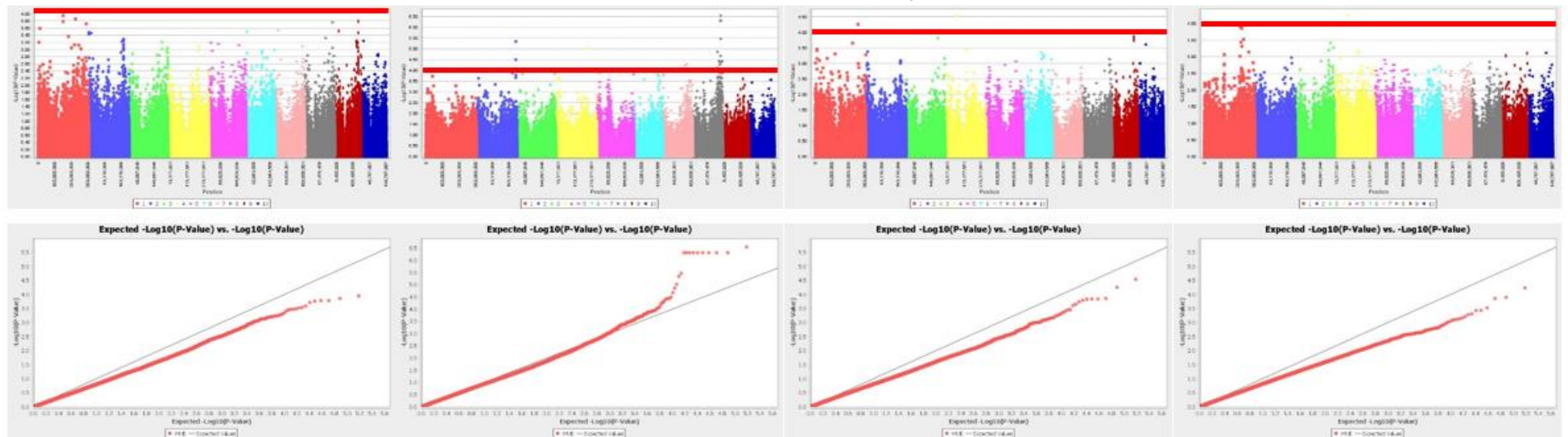
Combined analyses

At Pontevedra in 2017

At Pontevedra in 2018

At Pontevedra in 2019

Intrinsic Water Use Efficiency



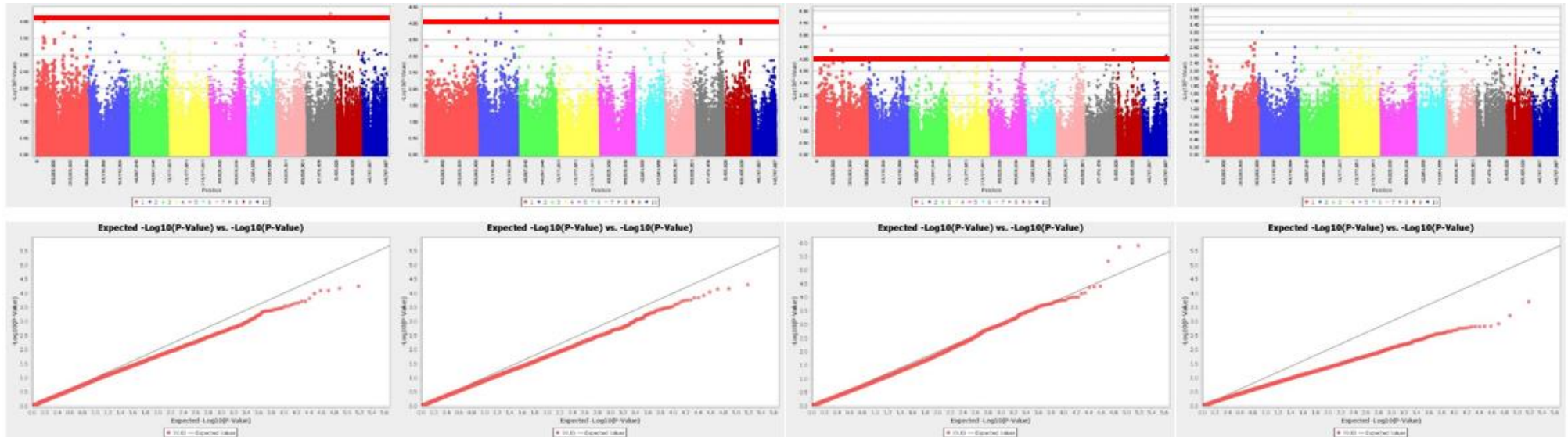
Combined analyses

At Pontevedra in 2017

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Instantaneous Water Use Efficiency



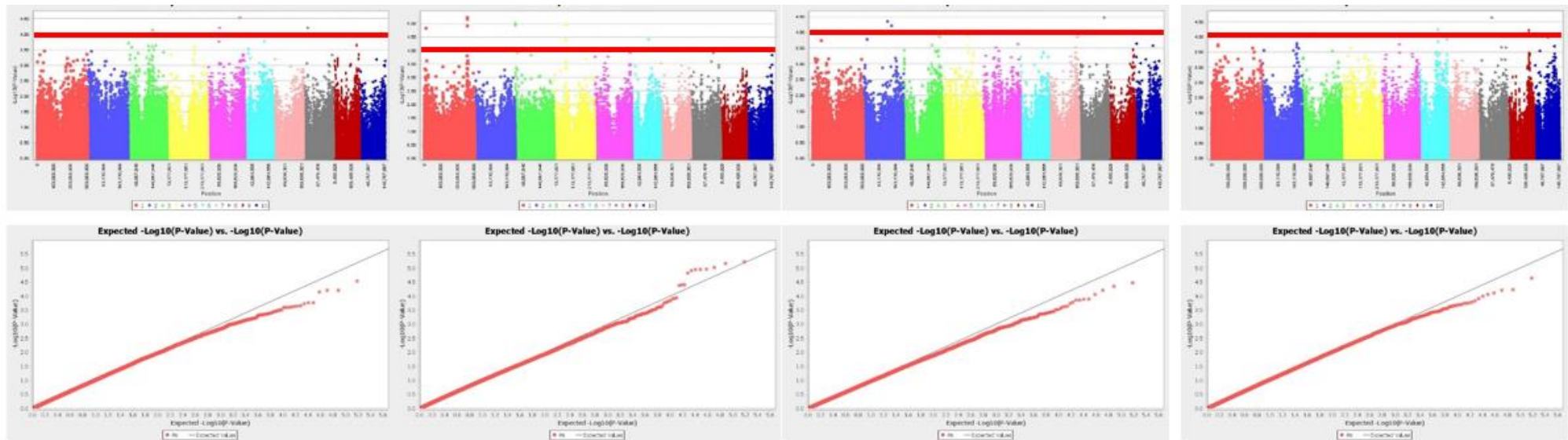
Combined analyses

At Pontevedra in 2017

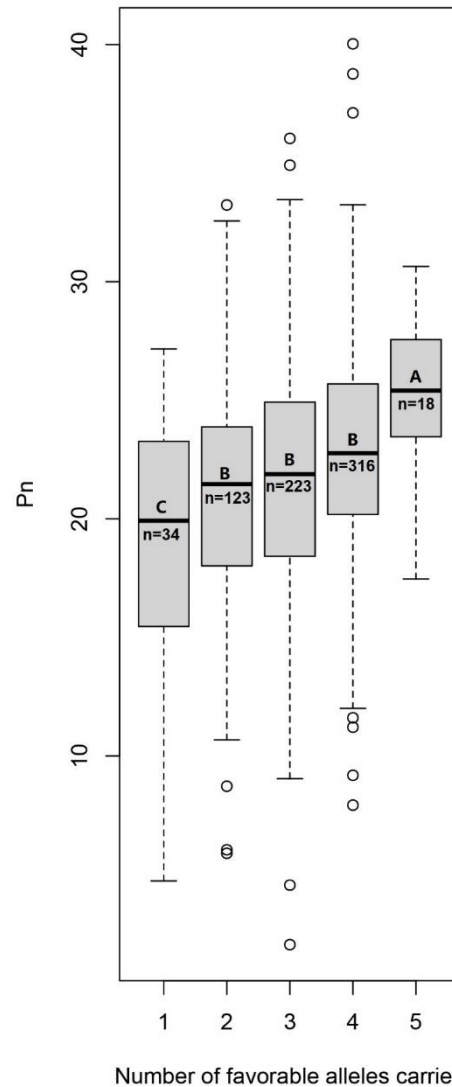
At Pontevedra in 2018

At Pontevedra in 2019

Leaf net photosynthesis



Supplementary Fig. S1 Manhattan plot and Quantile-quantile plot from a mixed linear model for photosynthesis-related traits in a large maize association population via single environment analysis. SNPs with p values \geq the threshold of 1×10^{-4} were considered significantly associated with the trait. The different colors in the Manhattan plot represent the 10 different chromosomes of maize.



Supplementary Fig. S2 Comparison of Leaf net photosynthesis (AN) among groups with the different number of favorable alleles carried in a large maize panel. The x-axis indicates groups 1, 2, 3, 4, and 5 with inbreds carrying 1, 2, 3, 4, and 5 favorable alleles in a large maize panel, respectively. The different upper letters above the mean lines denote significant differences at the probability of $p = 0.05$. The number of inbreds contained in the groups is presented below the mean lines. A total of 18 inbred lines, including EP32, GE129, NC250, Pa392, Oh43E, J47, Mo46, MS24, MS78, MS1, CH9, P39M96, A681, H29w, AusTRCF306303, AusTRCF305819, A665, and ND301, carried five favorable alleles for increasing Pn.