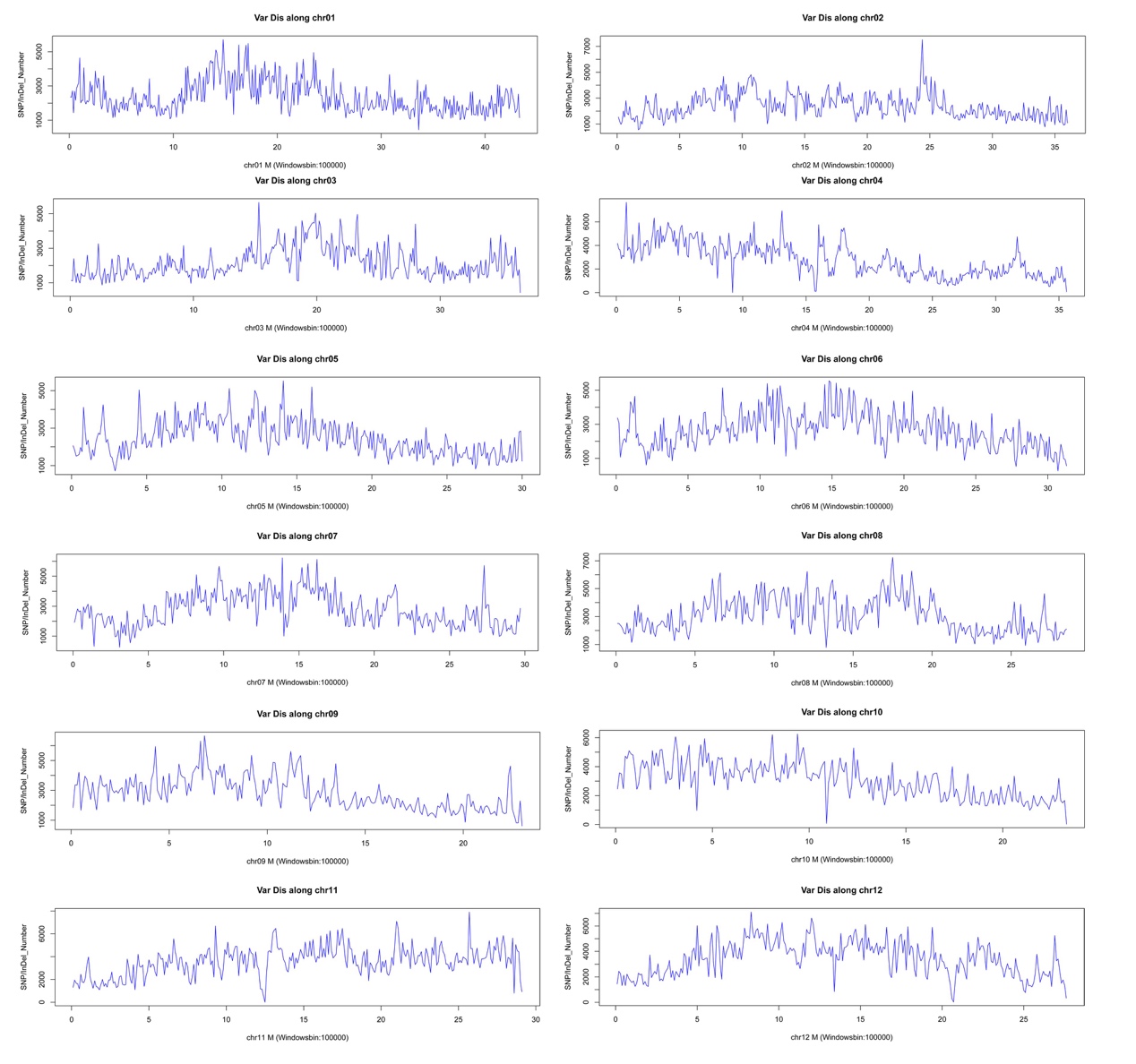
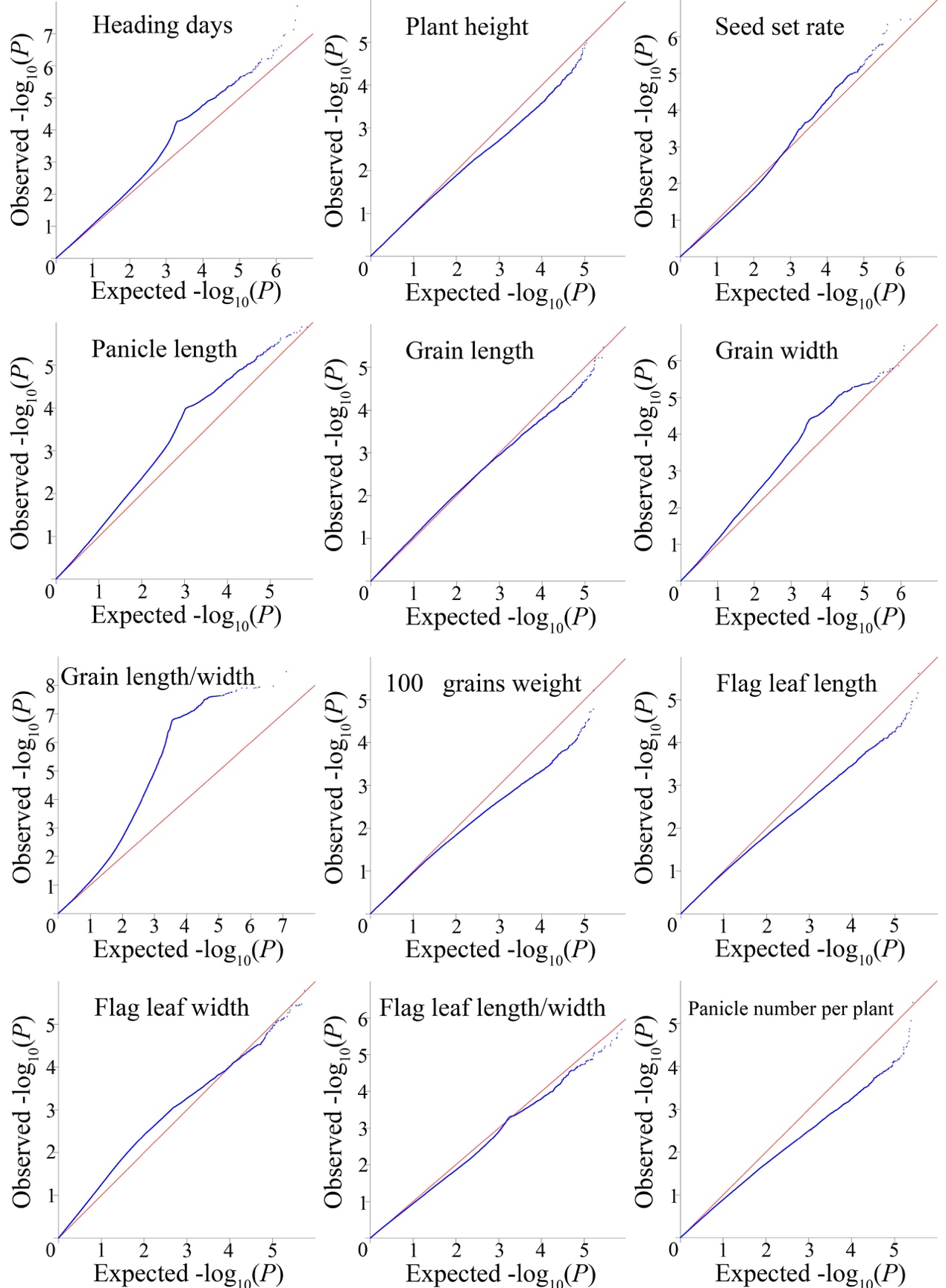
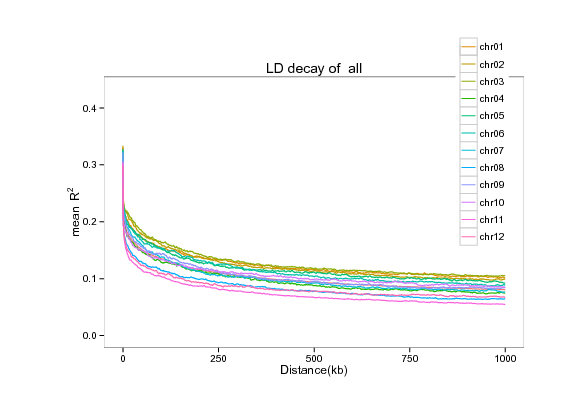
**Fig. S1** SNP distribution along position in each chromosome.

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**Fig. S2** Genome-wide average LD decay estimated in Ting’s core collection on 12 chromosomes.

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**Fig. S3** Distribution of pairwise relative 1 kinship values based on 3.8 million SNPs in Ting’s core collection. The height of blue bar represents the percentage of varieties in different range of kinships.

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**Fig. S4** Plots of observed versus expected *P*-values using EMMAX for 12 agronomic traits. Red symbol represents expected *P*-values, and Blue symbol represents observed *P*-values.