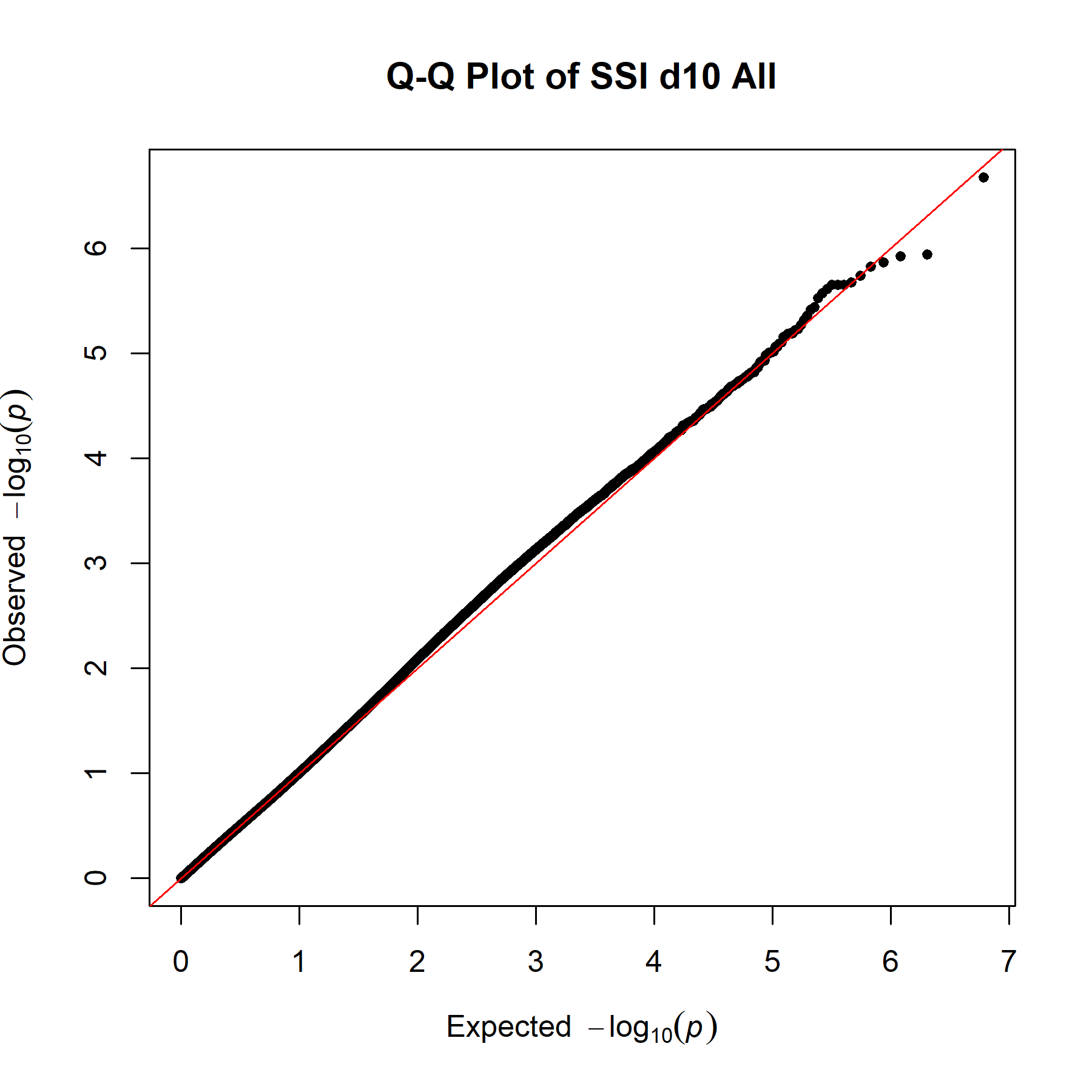
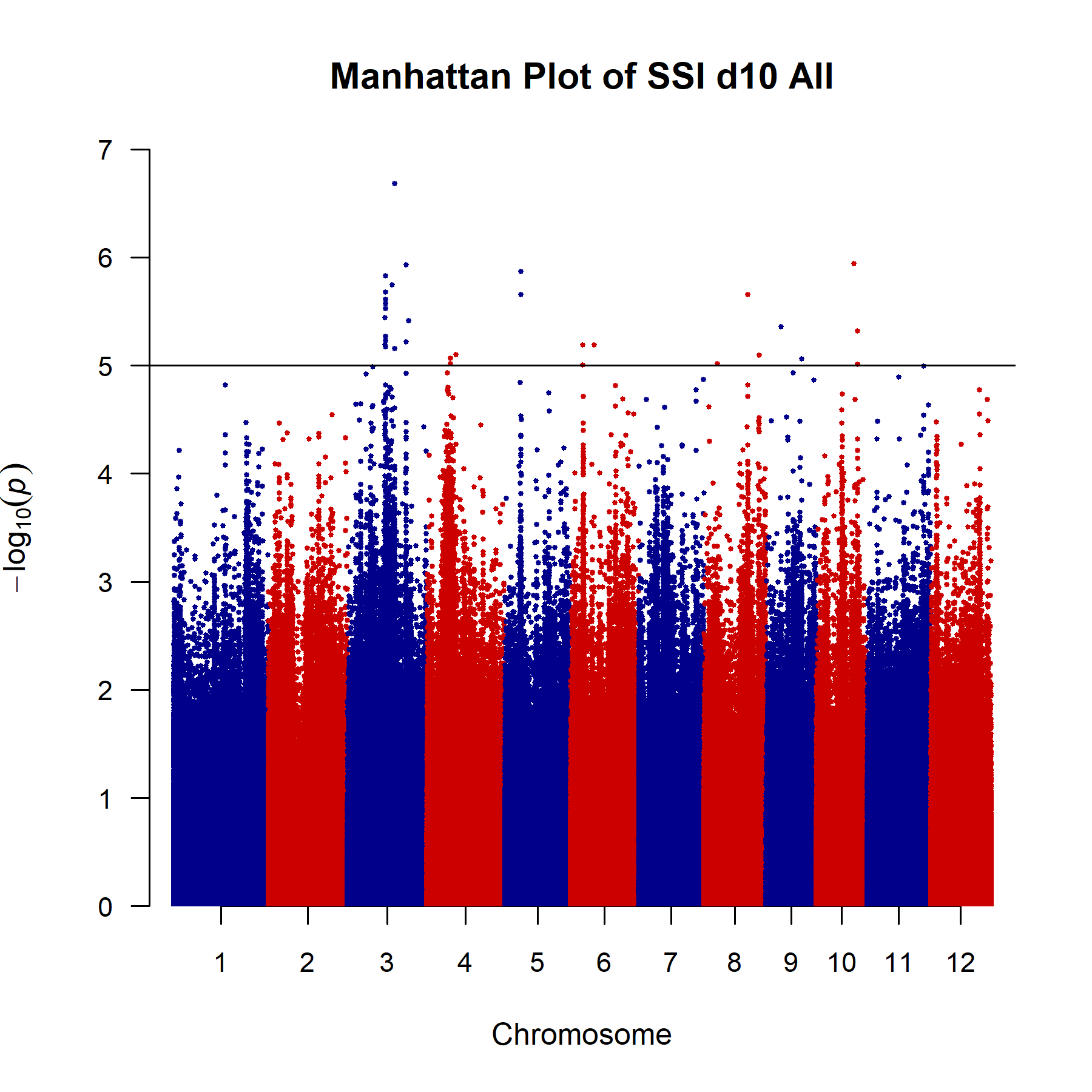
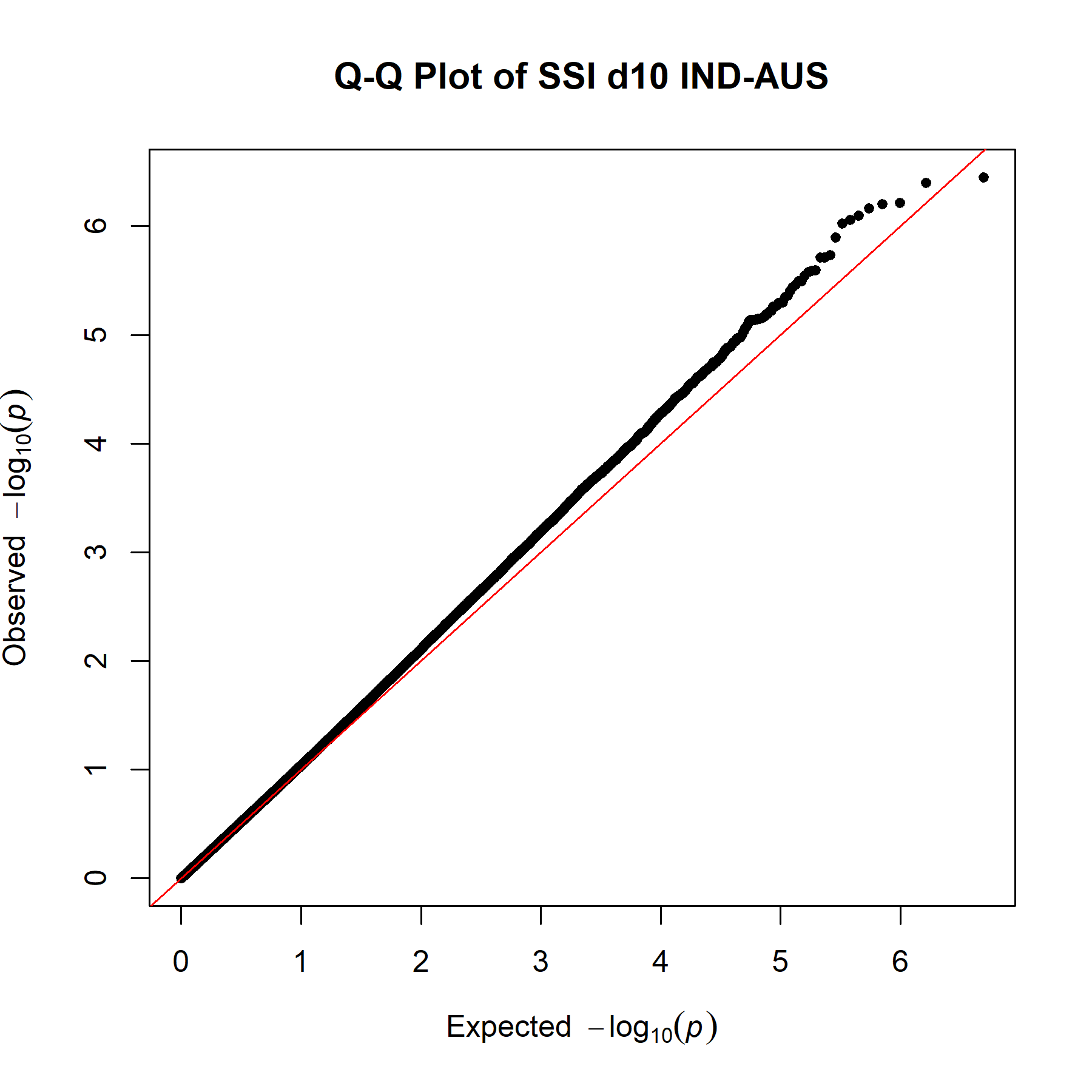
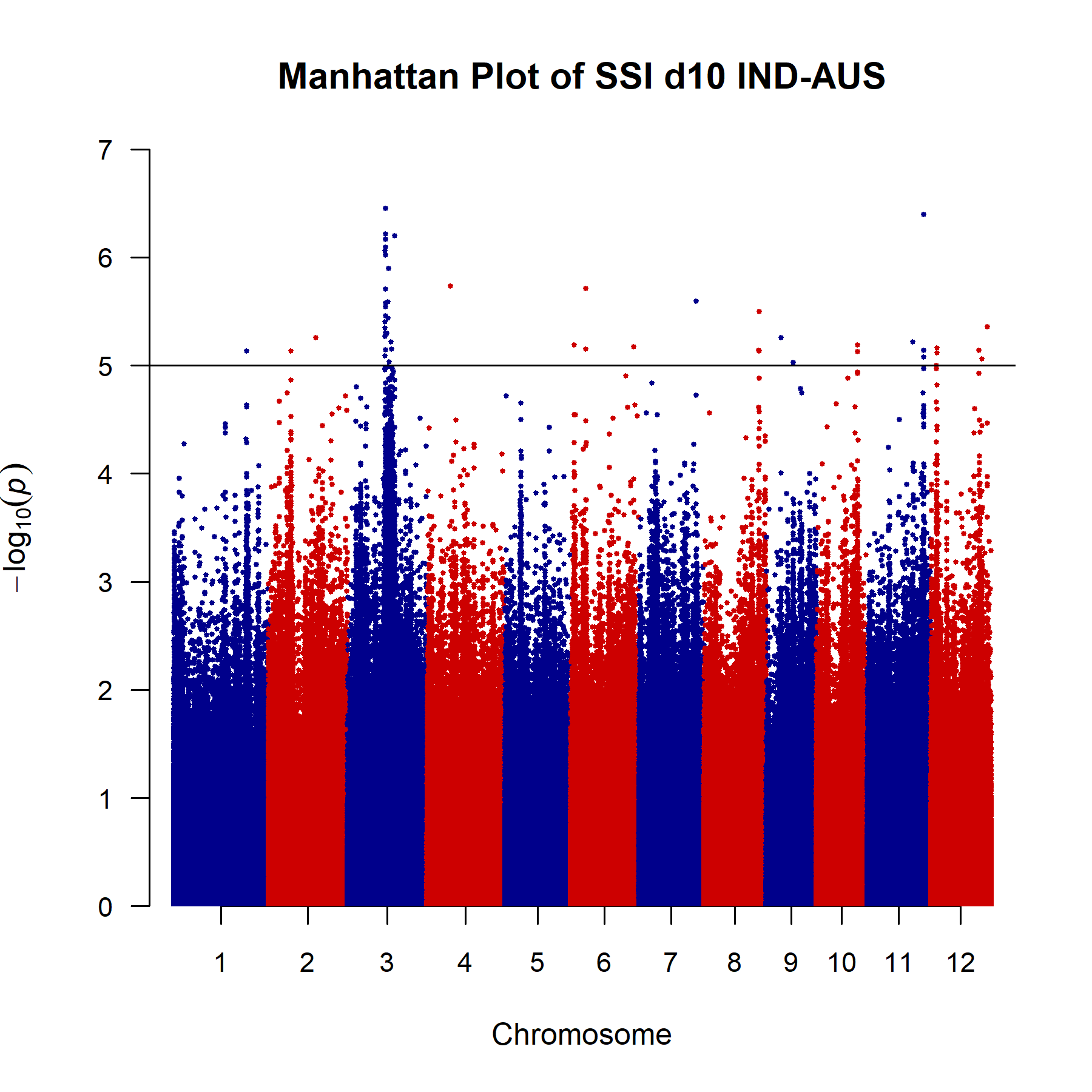
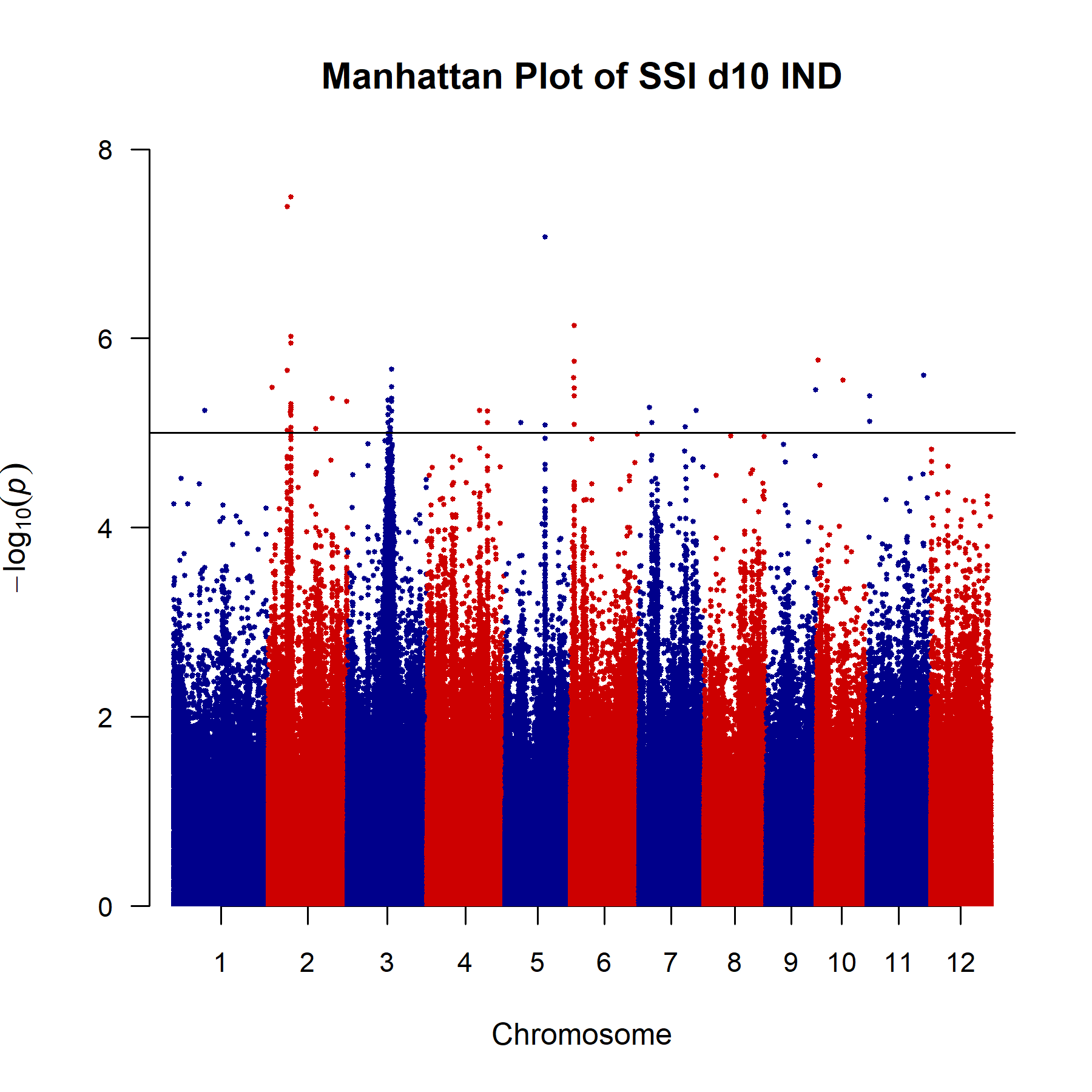
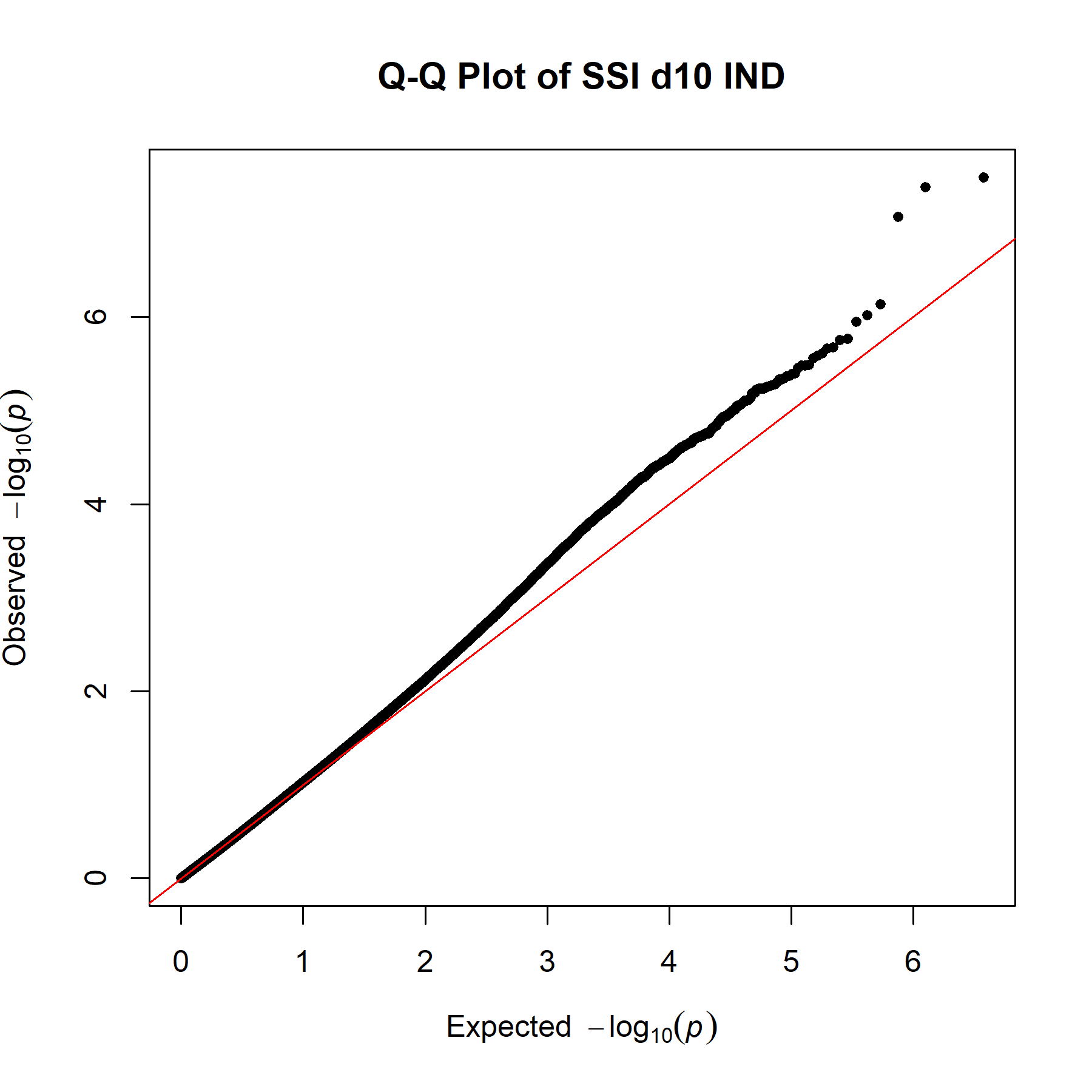
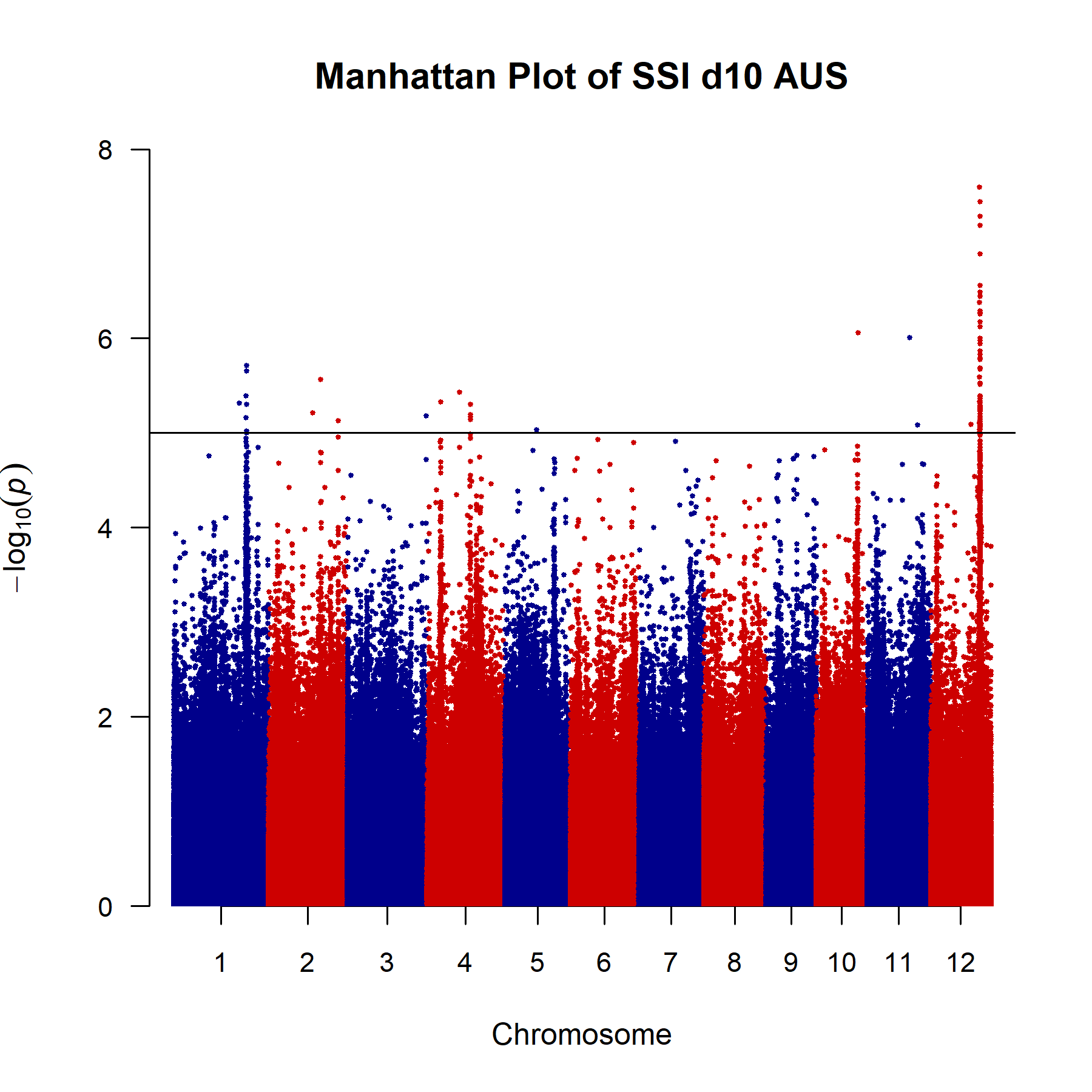
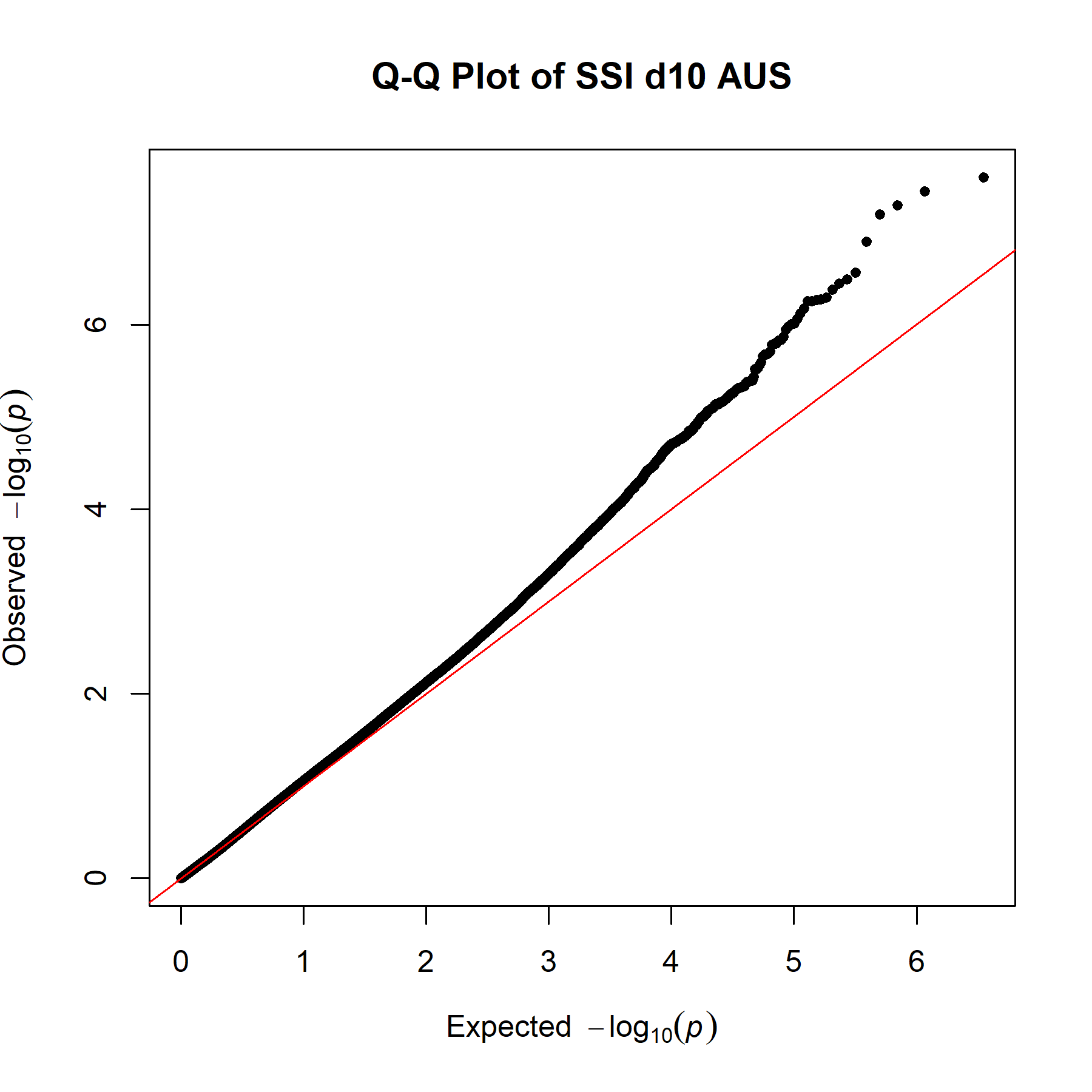
**Supplemental Figure S1. Manhattan and quantile-quantile (Q-Q) plots for the entire GWA analysis conducted in this study.**

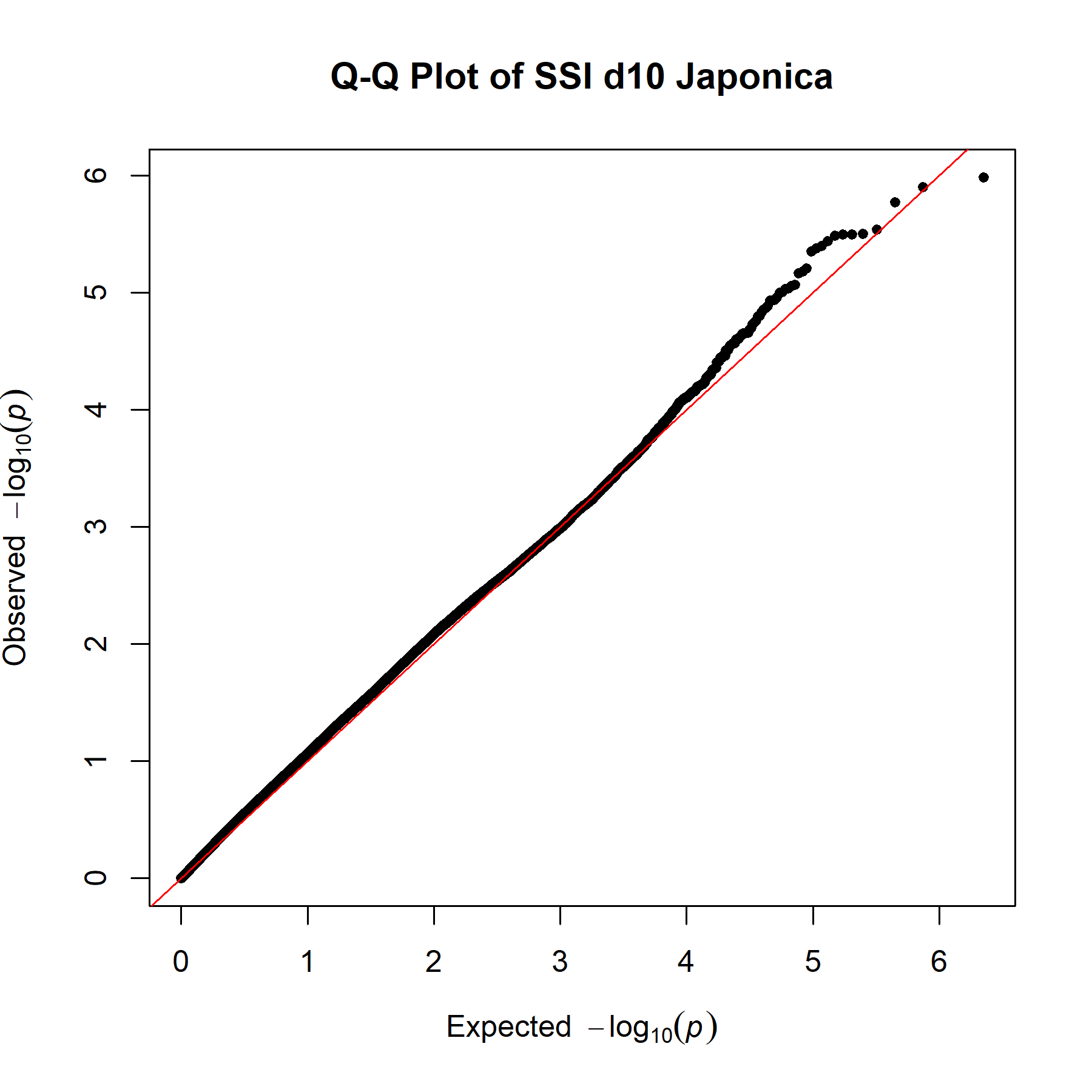
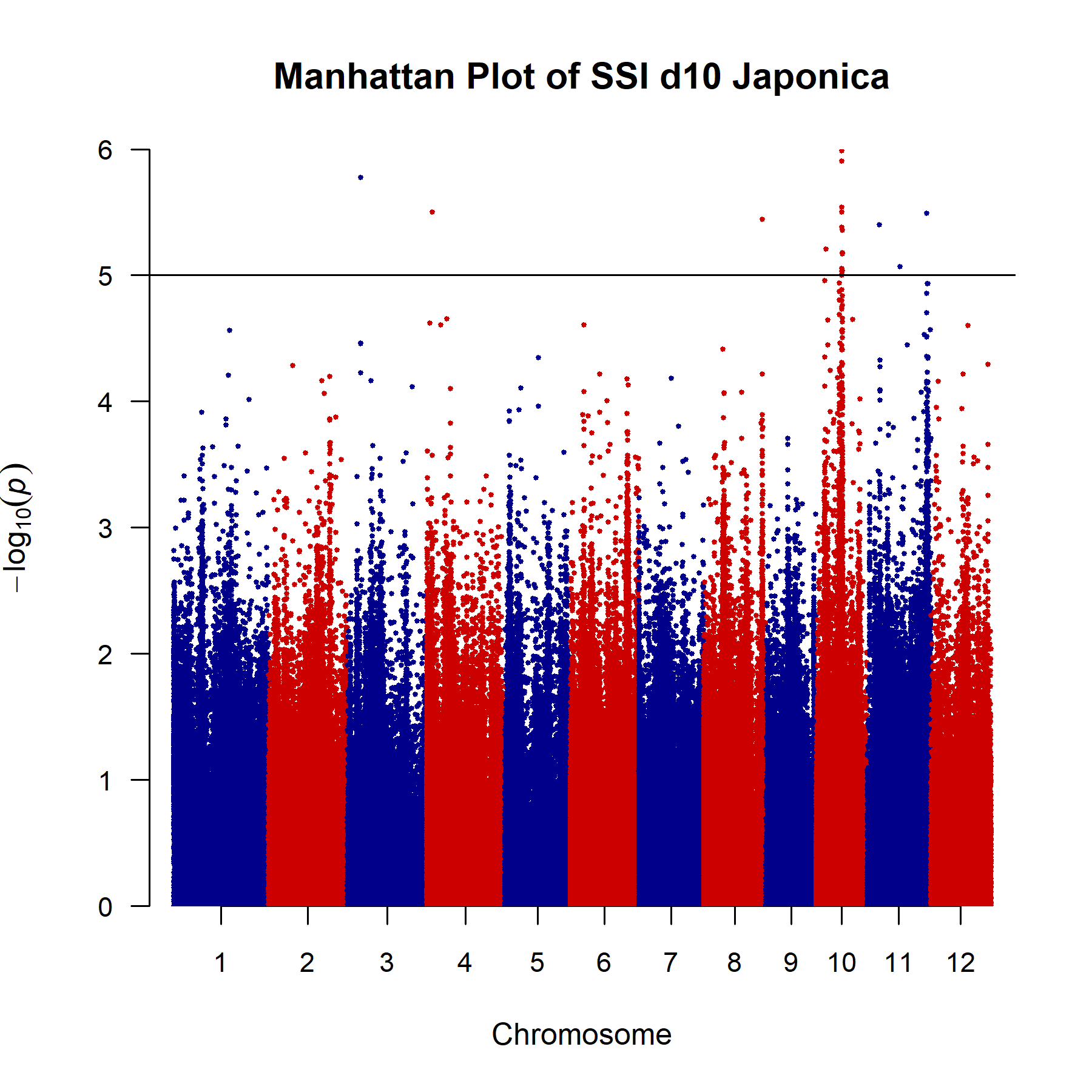
(A). Genome wide analysis of salt stress injury 10 days after the initiation of salt stress. Manhattan and quantile-quantile plots are shown for the 6 panels derived from the USDA rice mini core; (All) all 118 accessions used in the study, (IND\_ AUS) is the Indica subspecies composed of the indica and aus subpopulations, (IND) is the indica subpopulation, (AUS) is aus, (JAP) is the Japonica subspecies composed of the temperate and tropical japonica subpopulations and (TRJ) is tropical japonica. The fifth rice subpopulation, Aromatic, was not present in the study. In the Manhattan plots the X axis shows the SNPs position across the 12 rice chromosomes and the Y axis is the –log10 (p) value for each SNP. The horizontal black line at –log10(p) = 5 is the significance threshold for SNPs. In the quantile-quantile plots the X axis is the expected SNP distribution and the Y axis displays the –log10(p) observed SNP distribution.

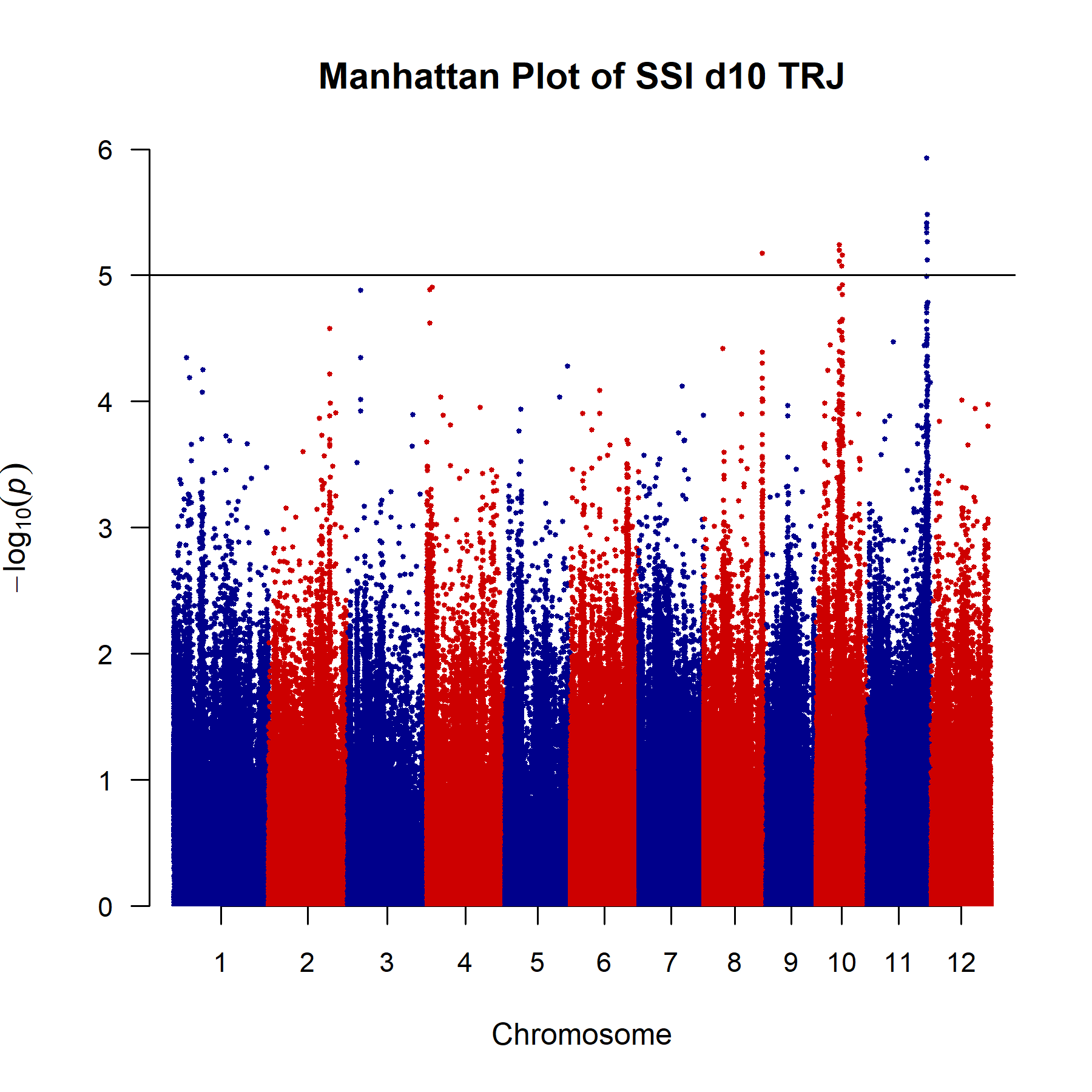
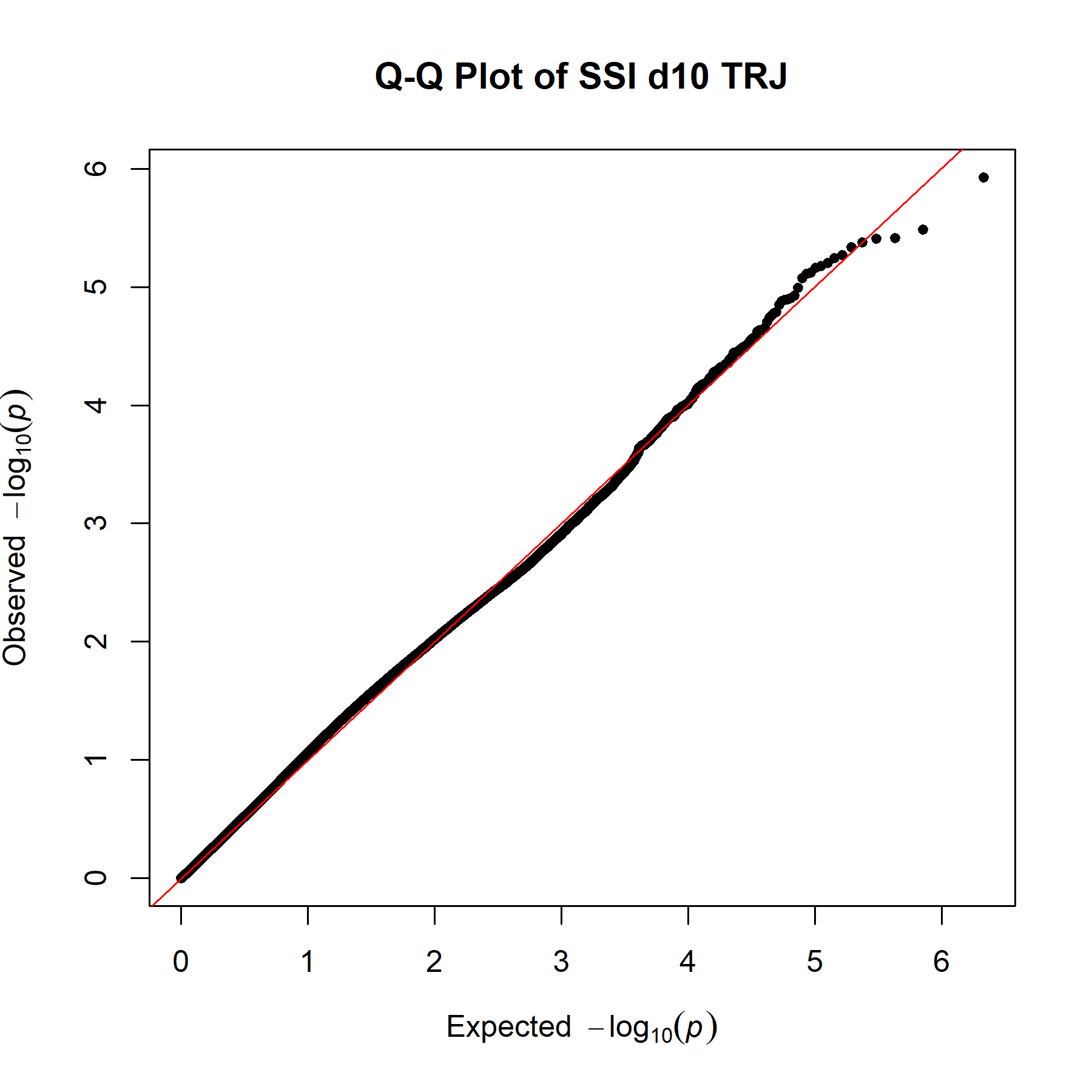




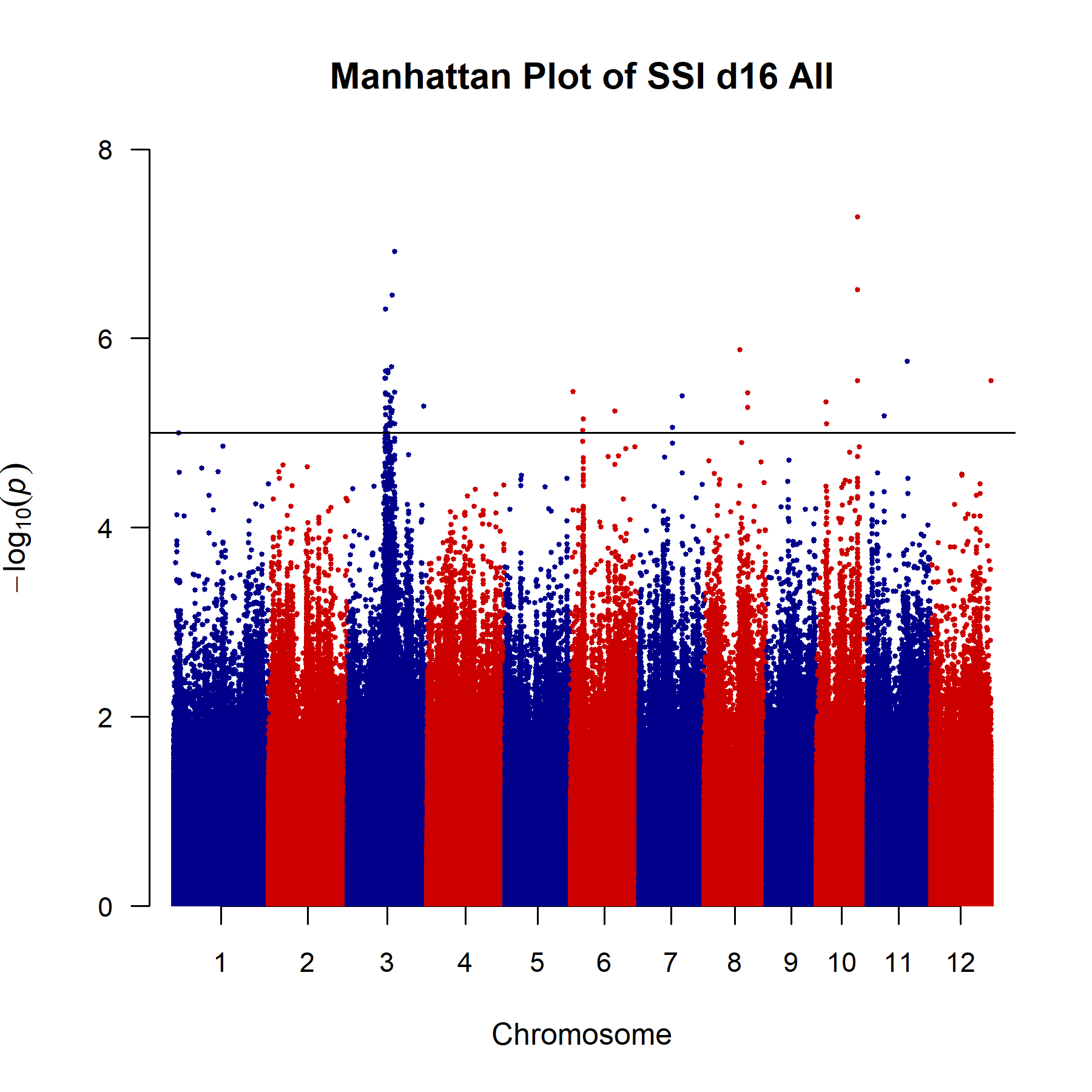
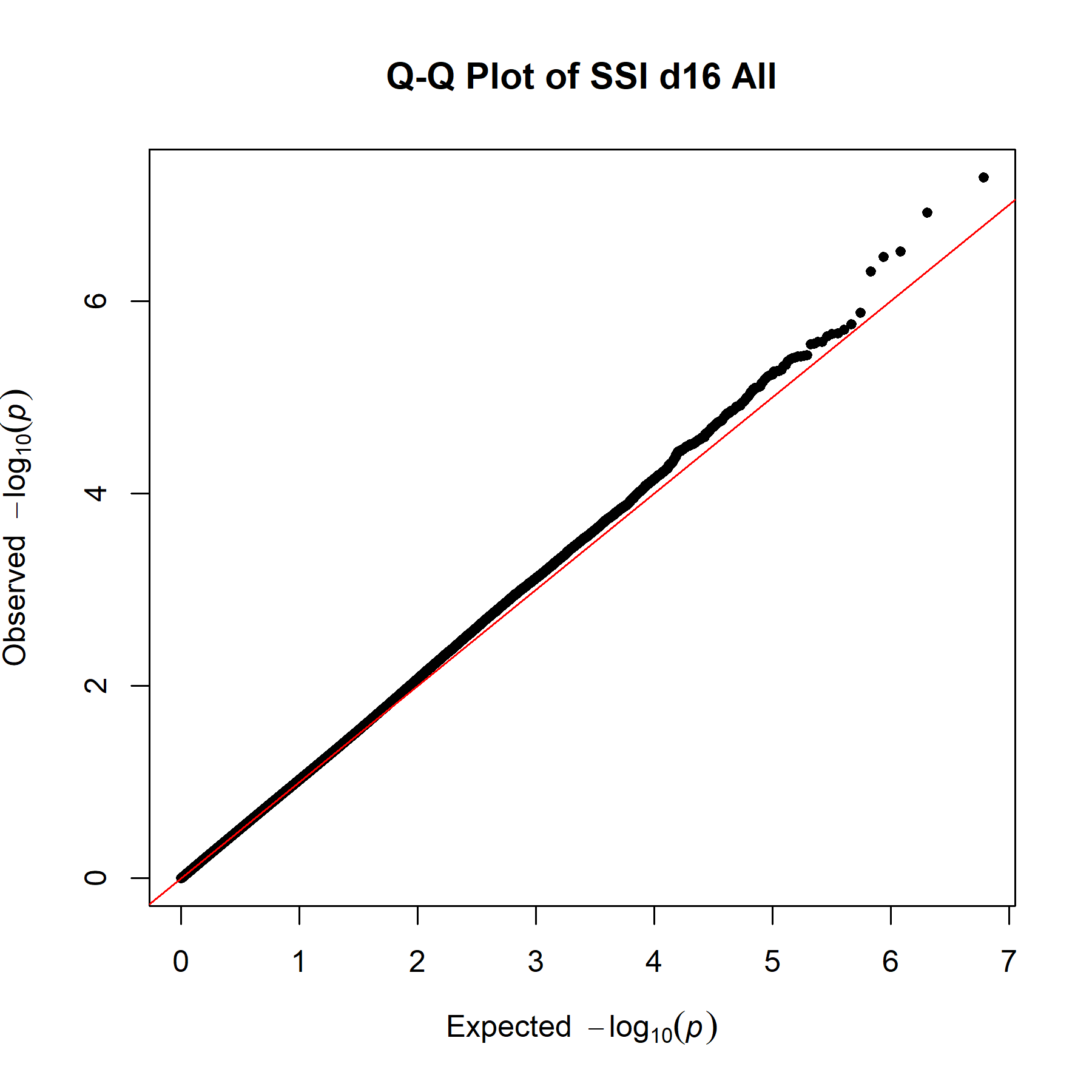
 

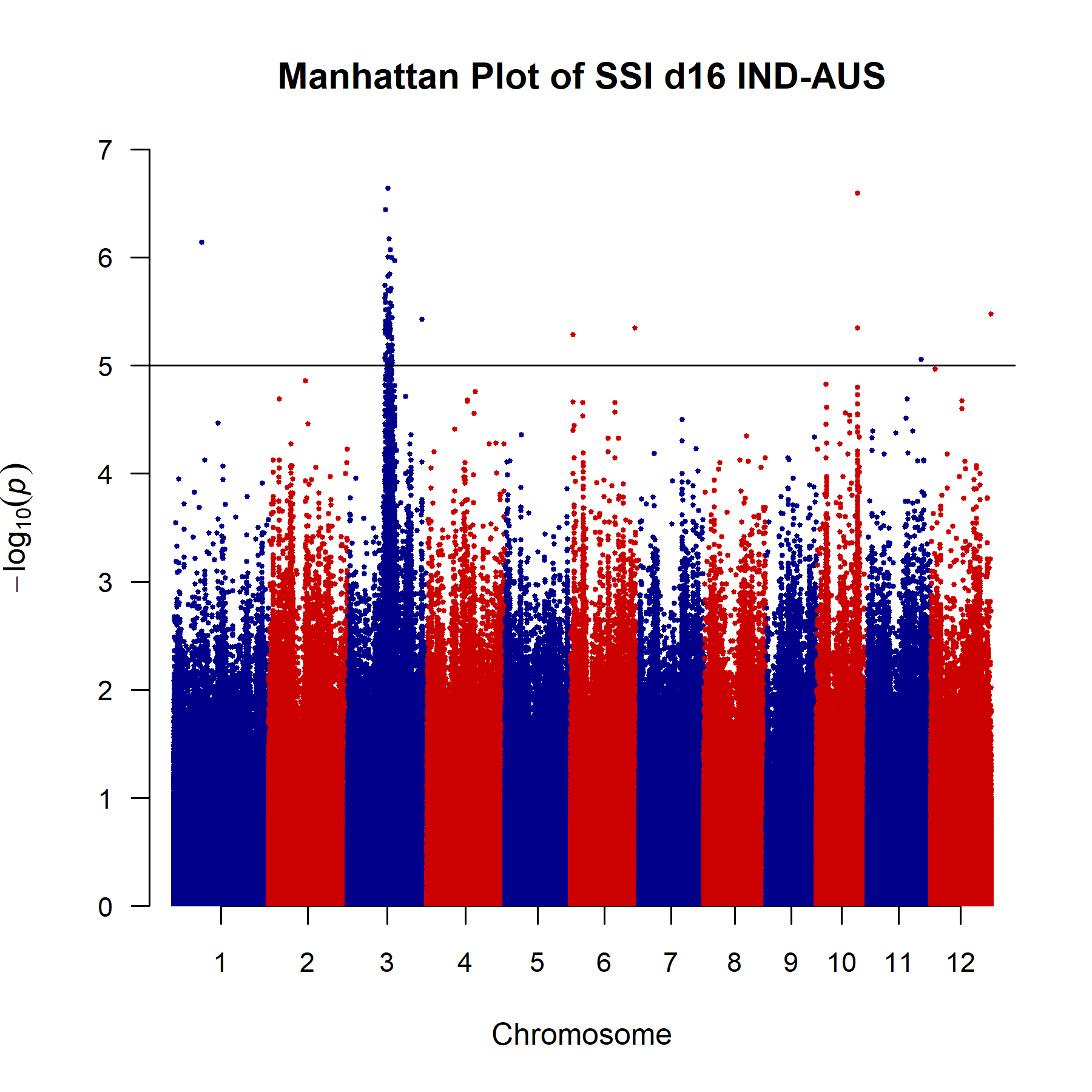
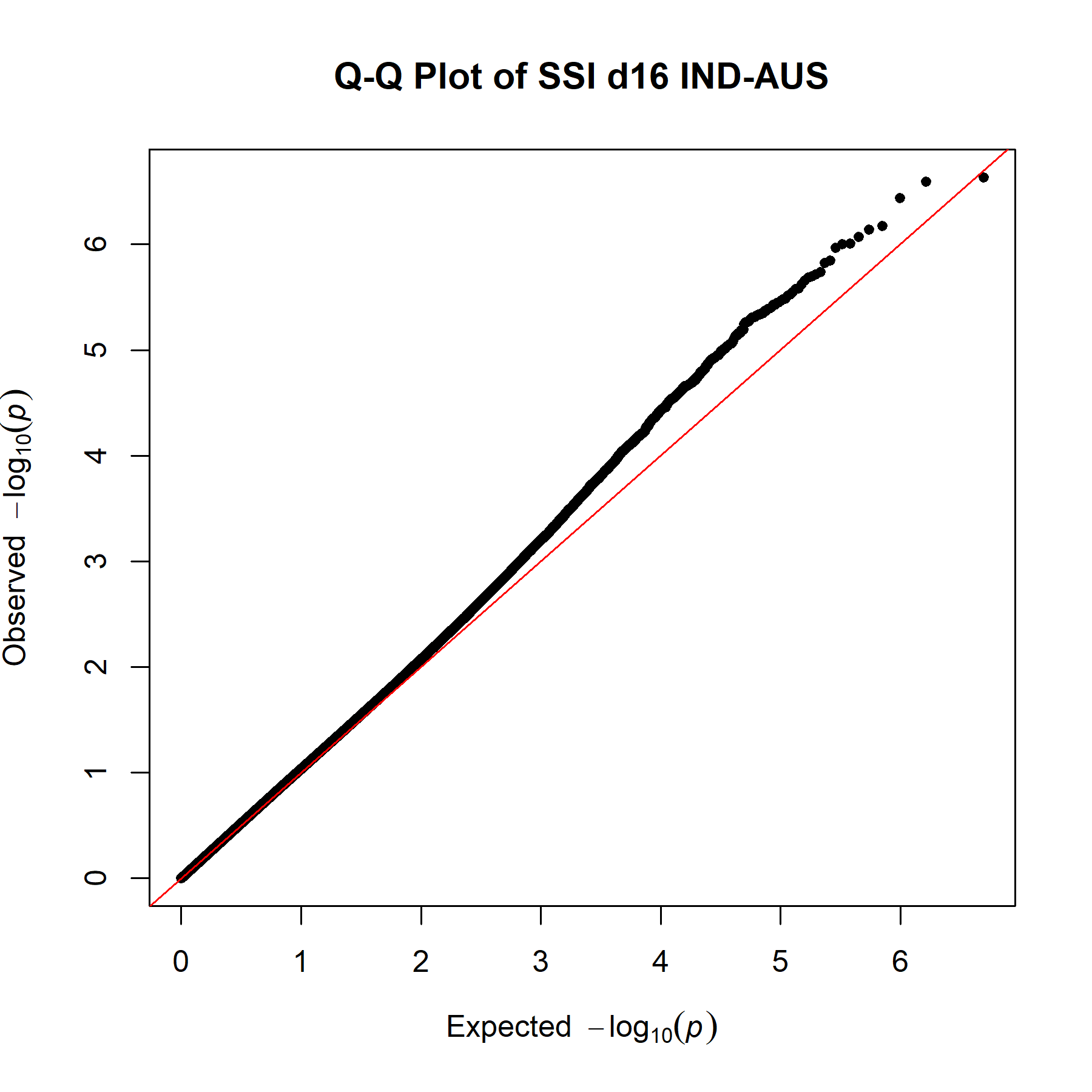
 

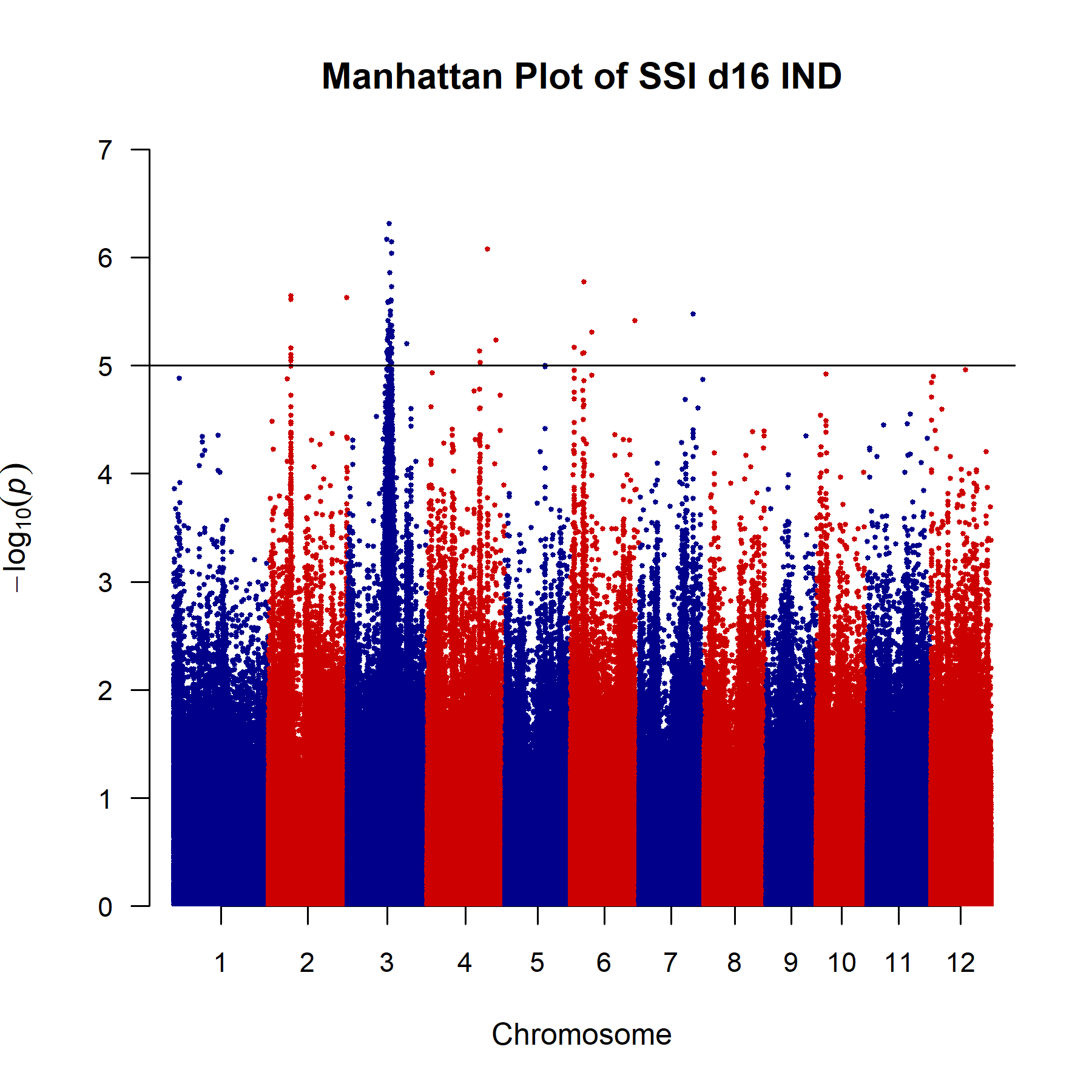
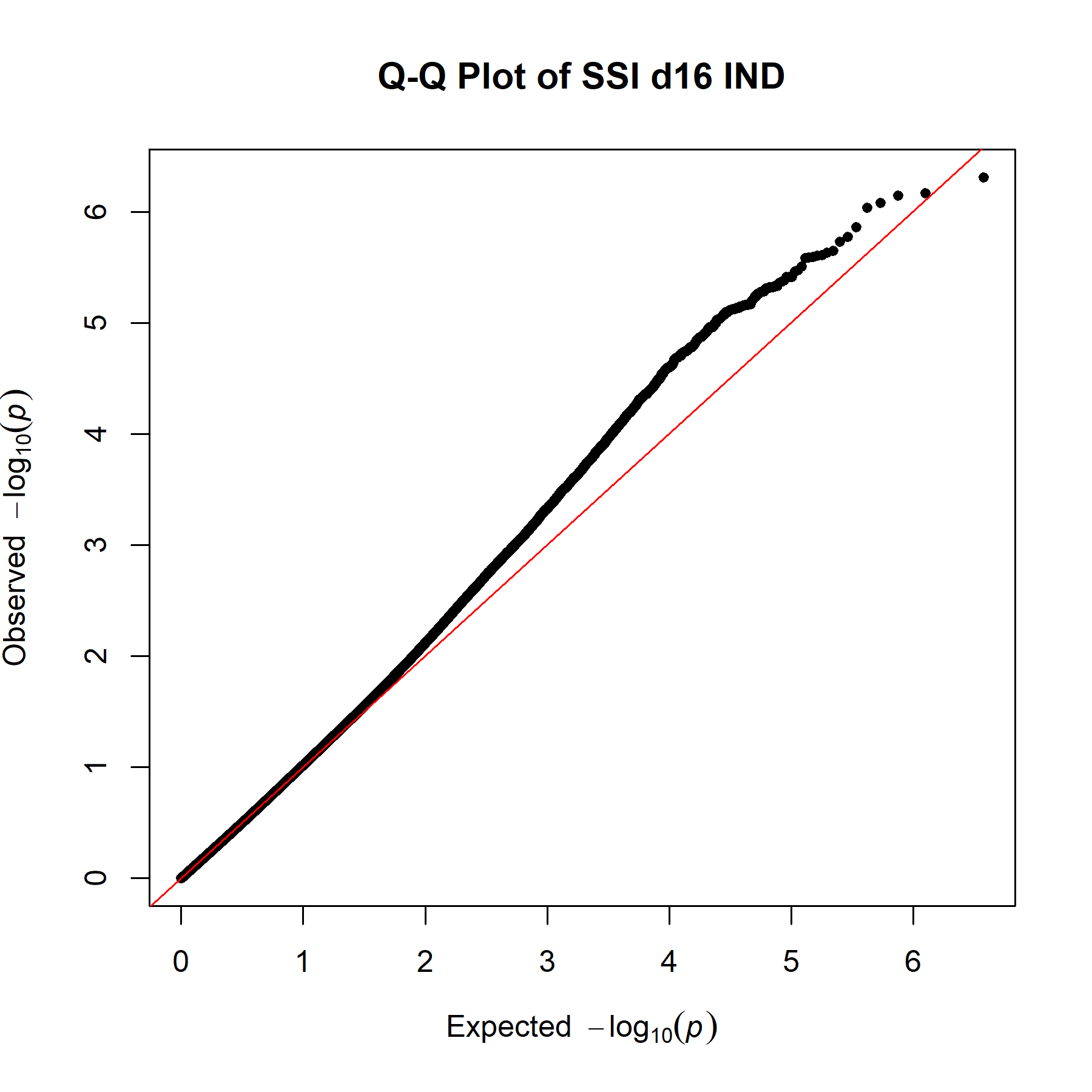


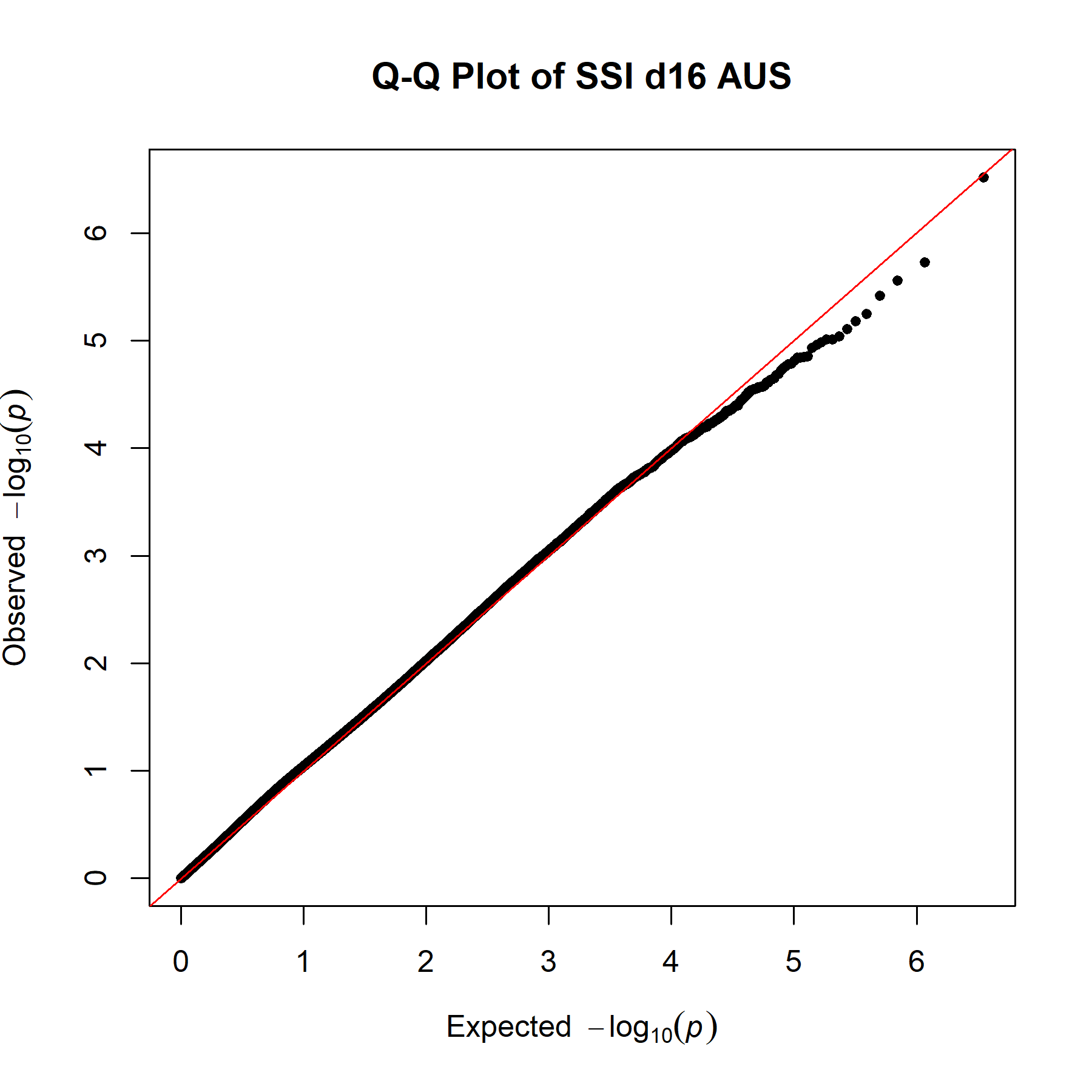
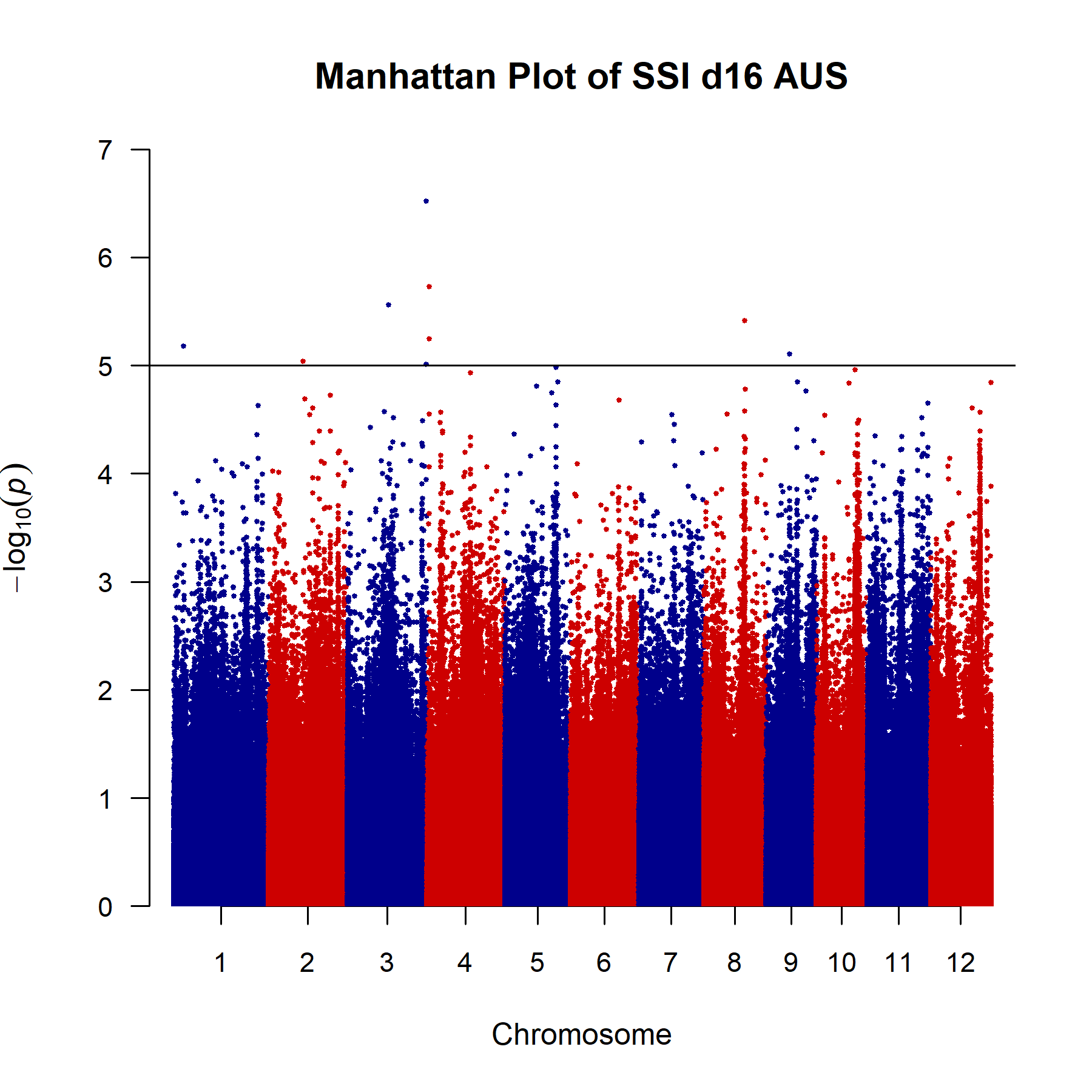
 

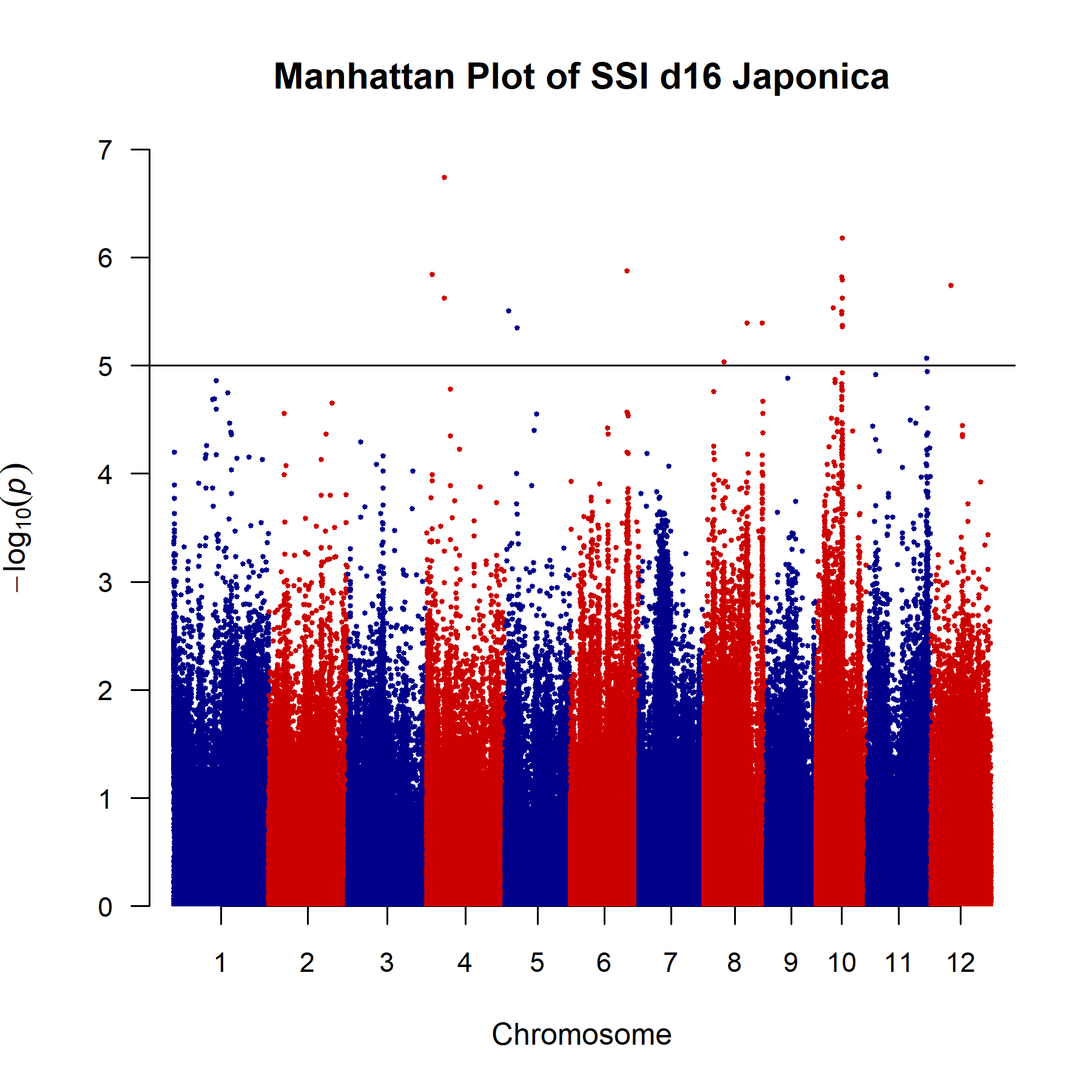
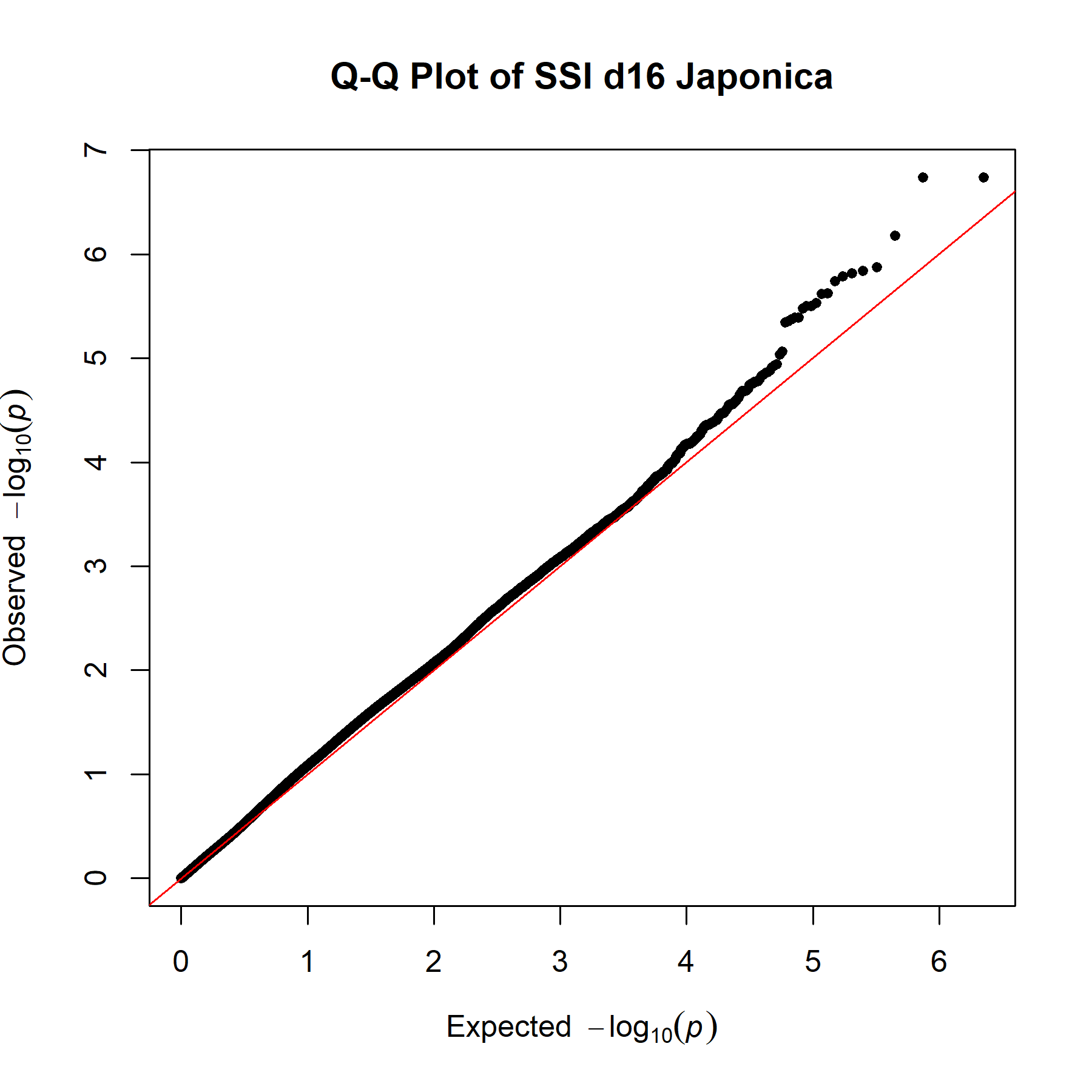
(B). Genome wide analysis of salt stress injury 16 days after the initiation of salt stress. Fig. 1. Manhattan and quantile-quantile plots are shown for the 6 panels derived from the USDA rice mini core; (All) all 118 accessions used in the study, (IND\_ AUS) is the Indica subspecies composed of the indica and aus subpopulations, (IND) is the indica subpopulation, (AUS) is aus, (JAP) is the Japonica subspecies composed of the temperate and tropical japonica subpopulations and (TRJ) is tropical japonica. The fifth rice subpopulation, Aromatic, was not present in the study. In the Manhattan plots the X axis shows the SNPs position across the 12 rice chromosomes and the Y axis is the –log10 (p) value for each snp. The horizontal black line at –log10(p) = 5 is the significance threshold for SNPs. In the quantile-quantile plots the X axis is the expected SNP distribution and the Y axis displays the –log10(p) observed SNP distribution.

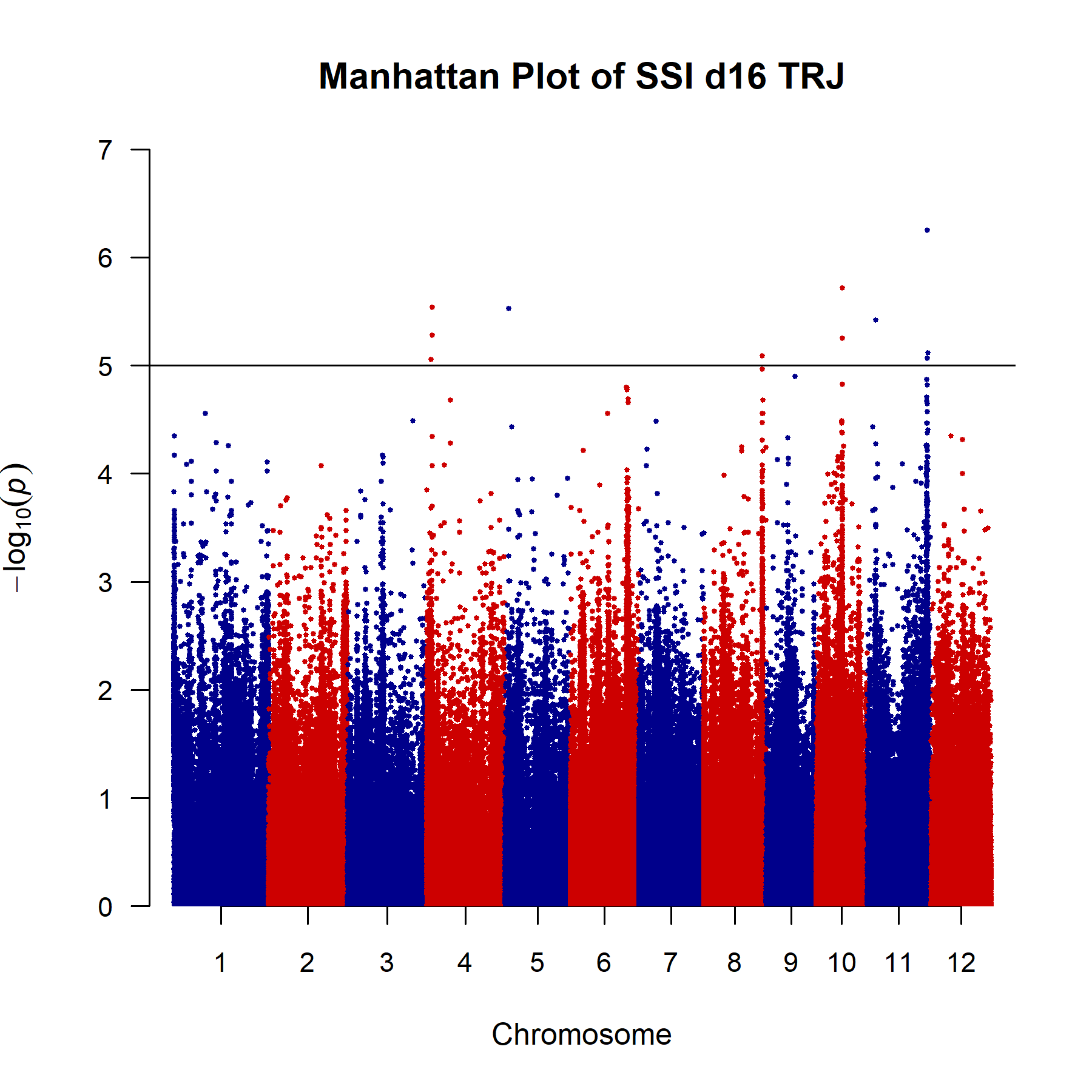
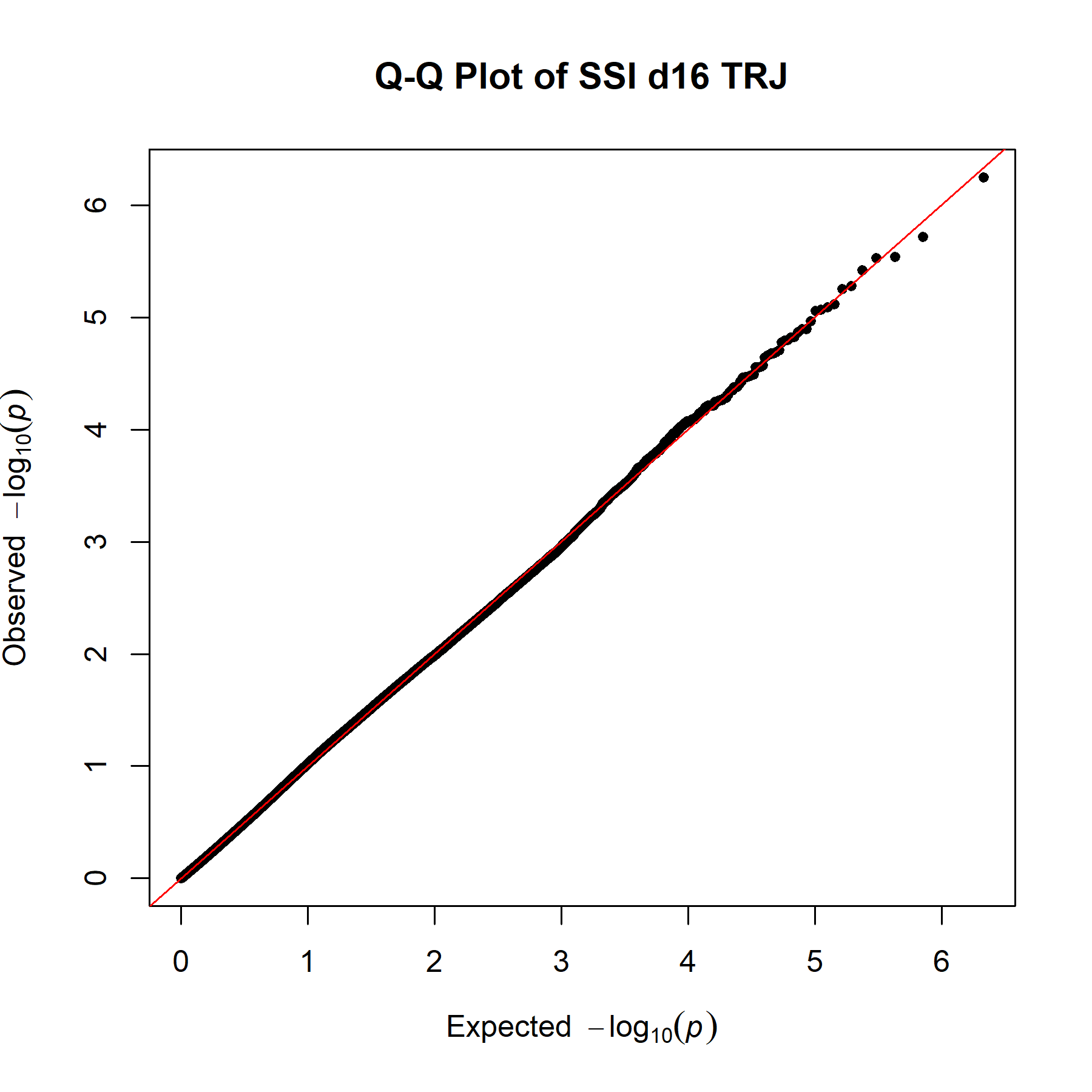
 

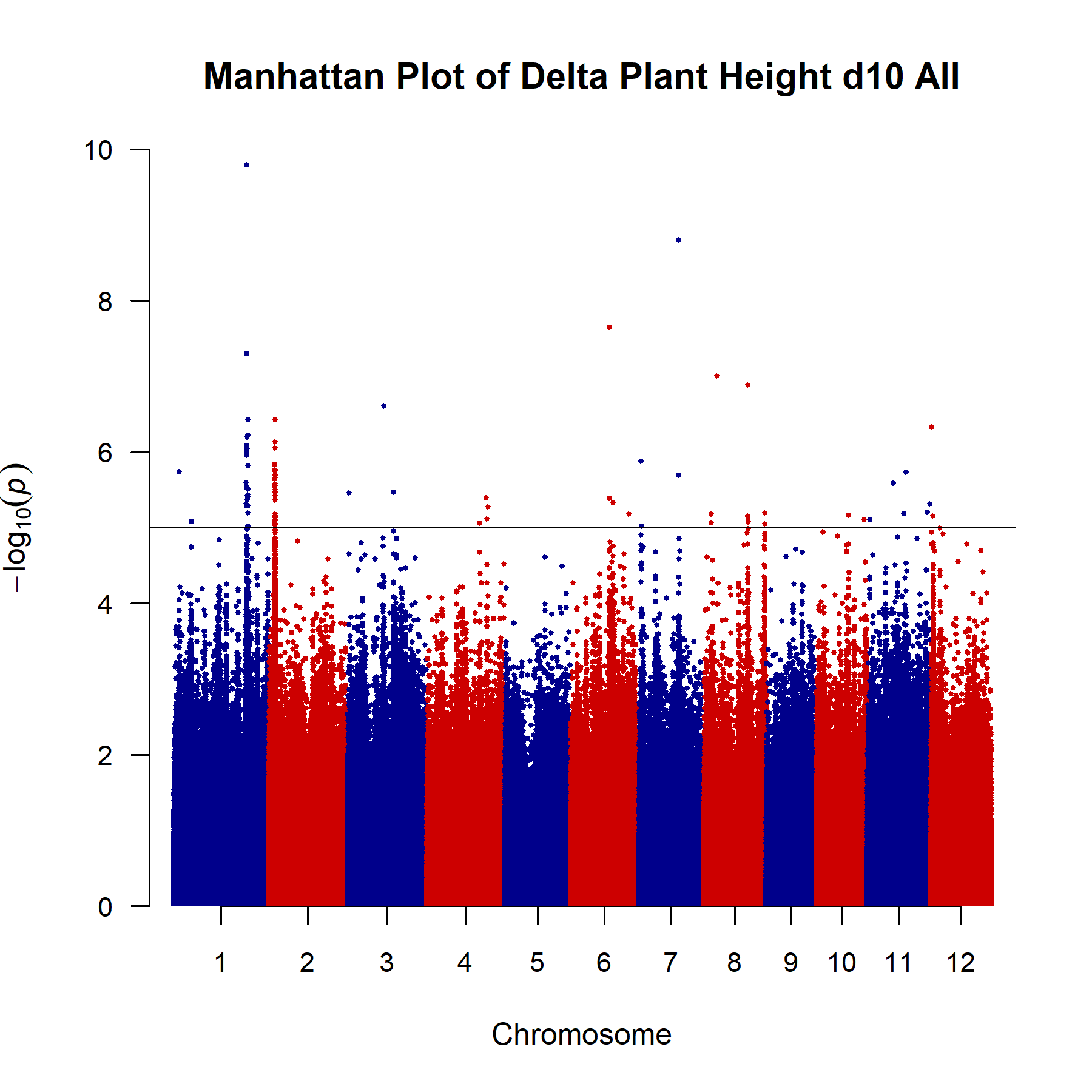
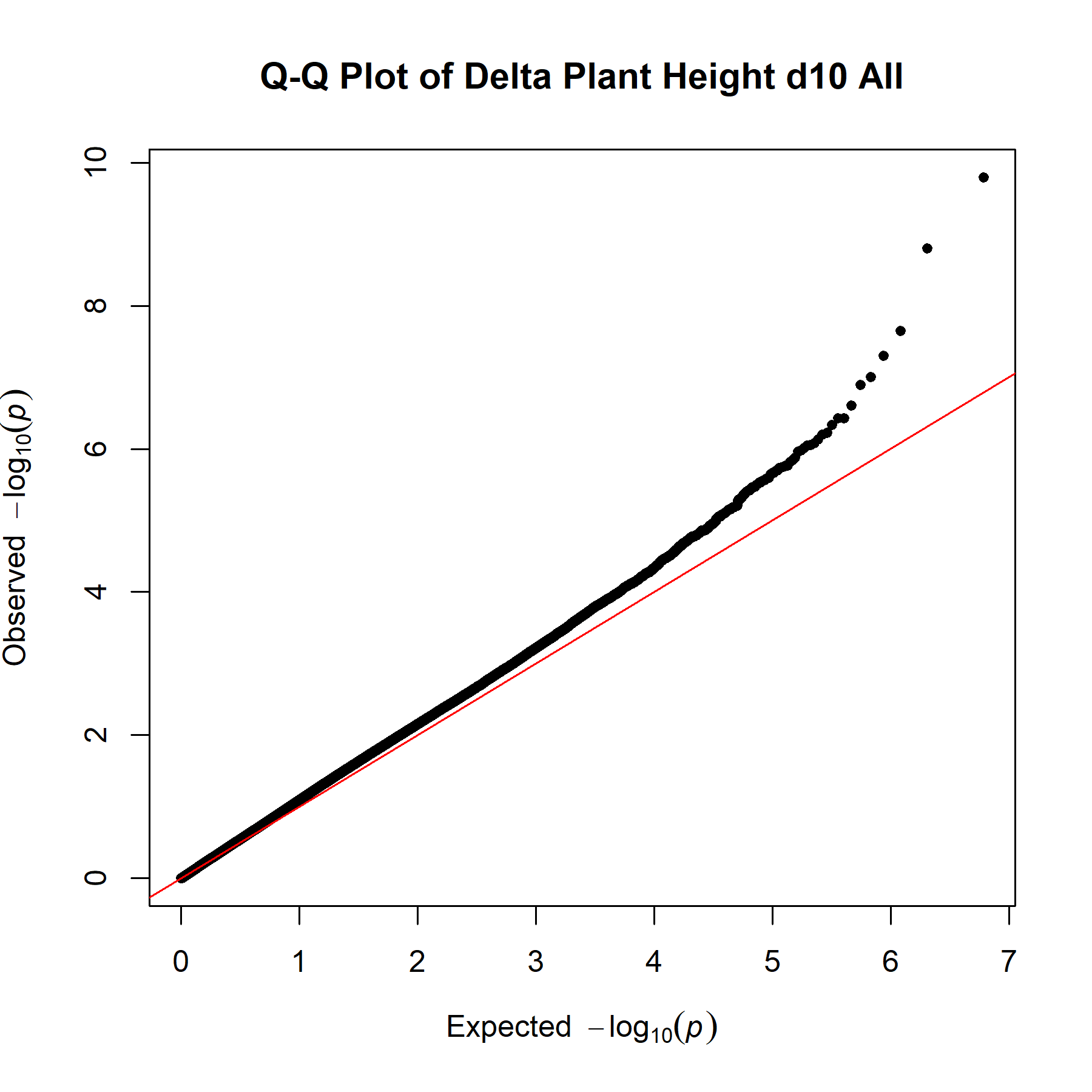
 

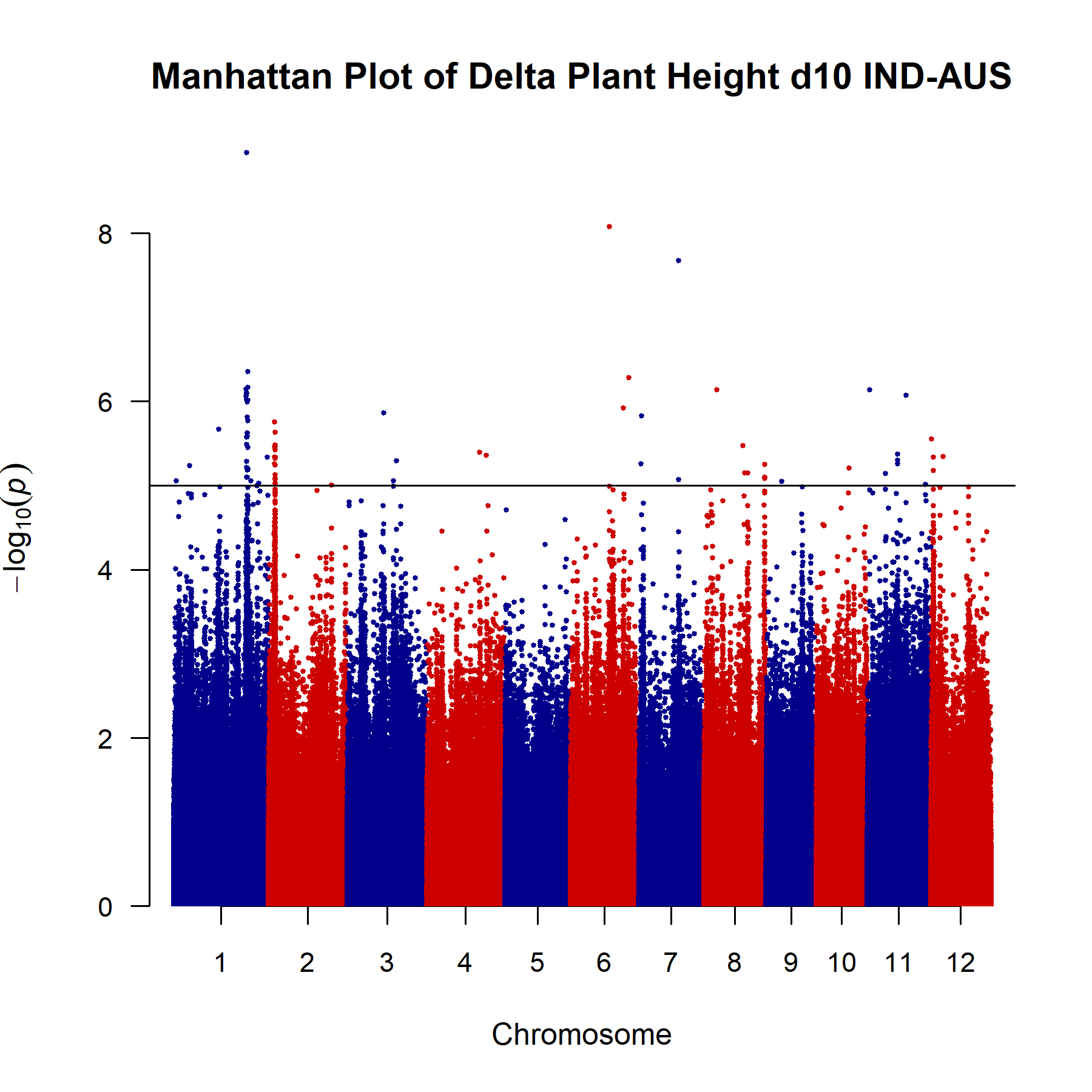
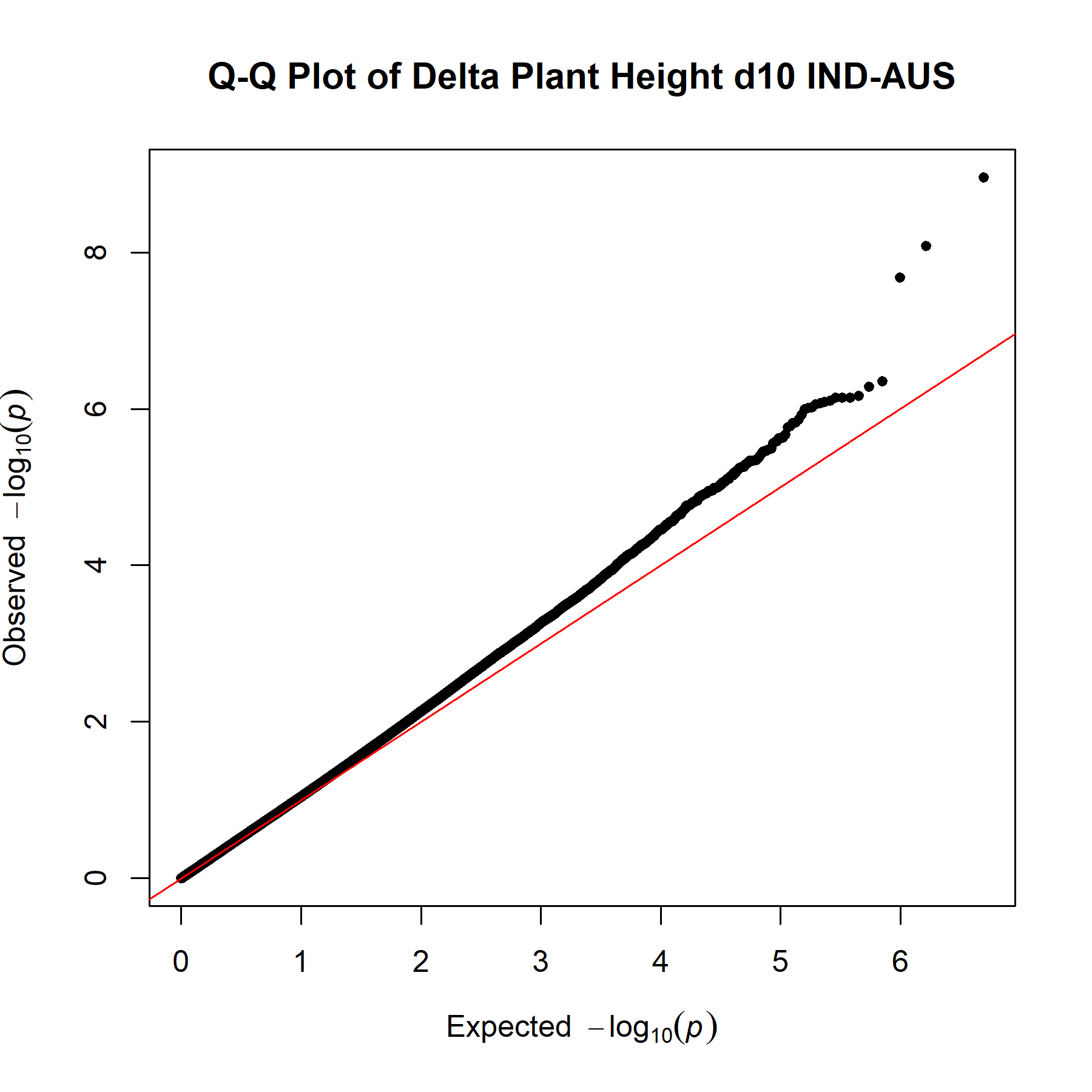


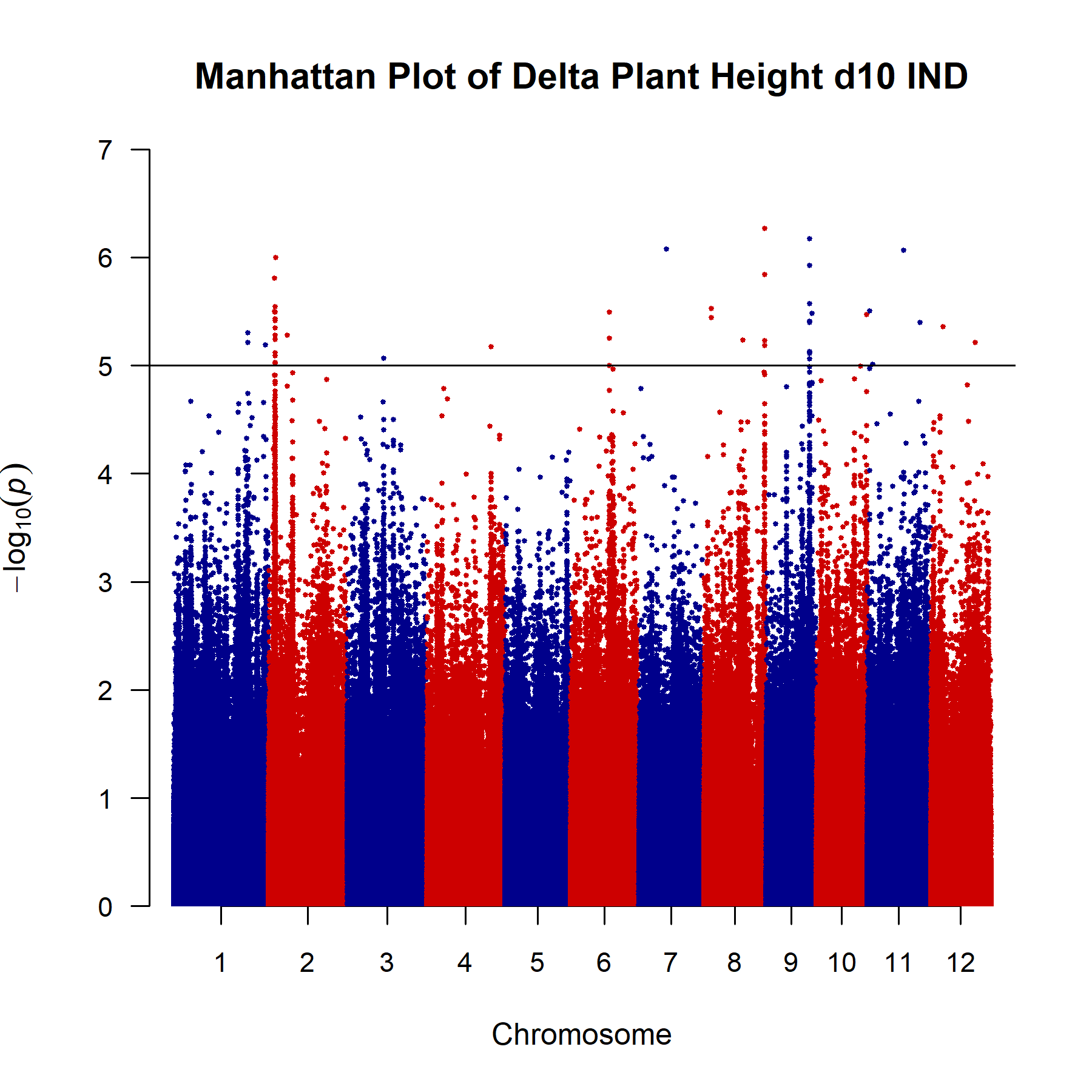
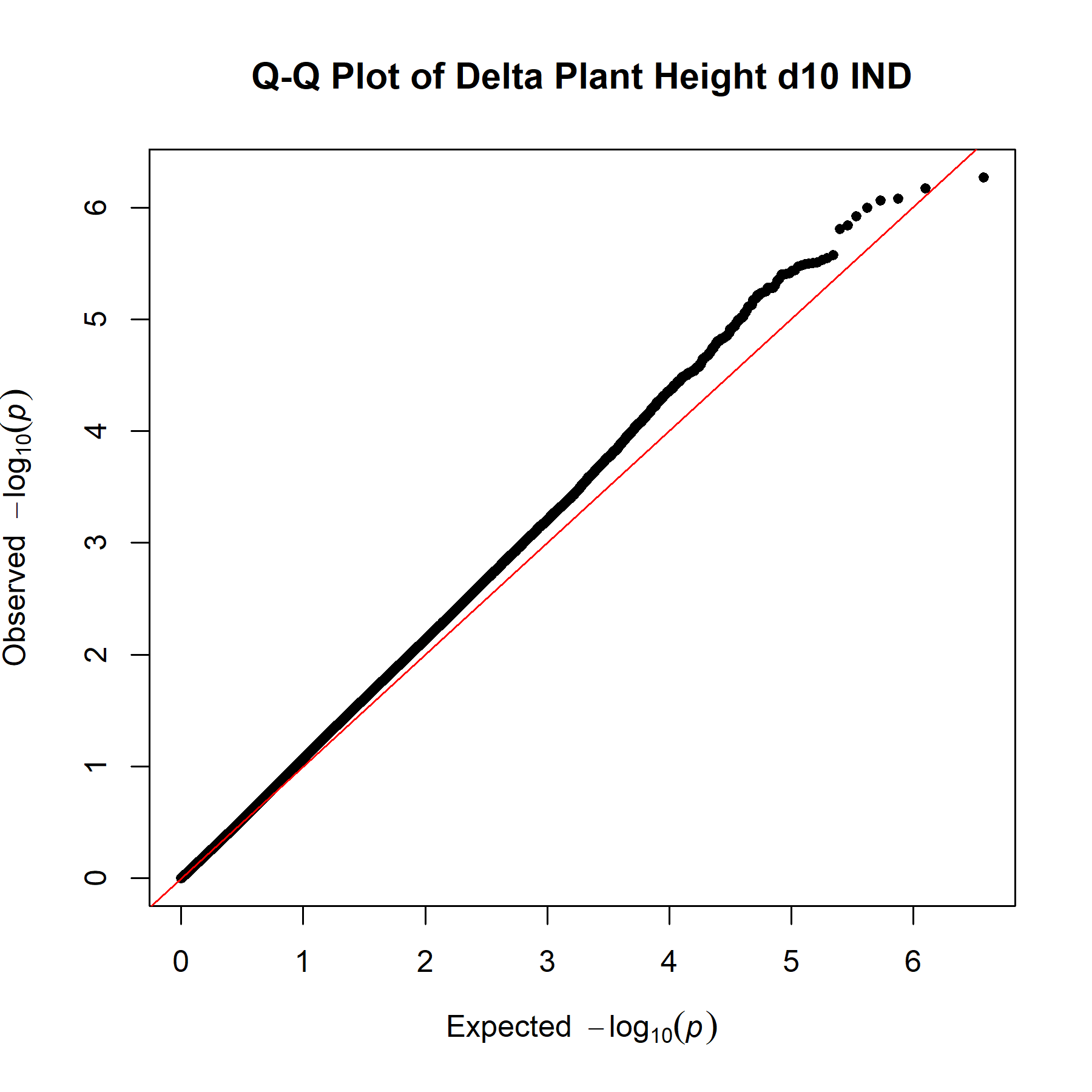
 

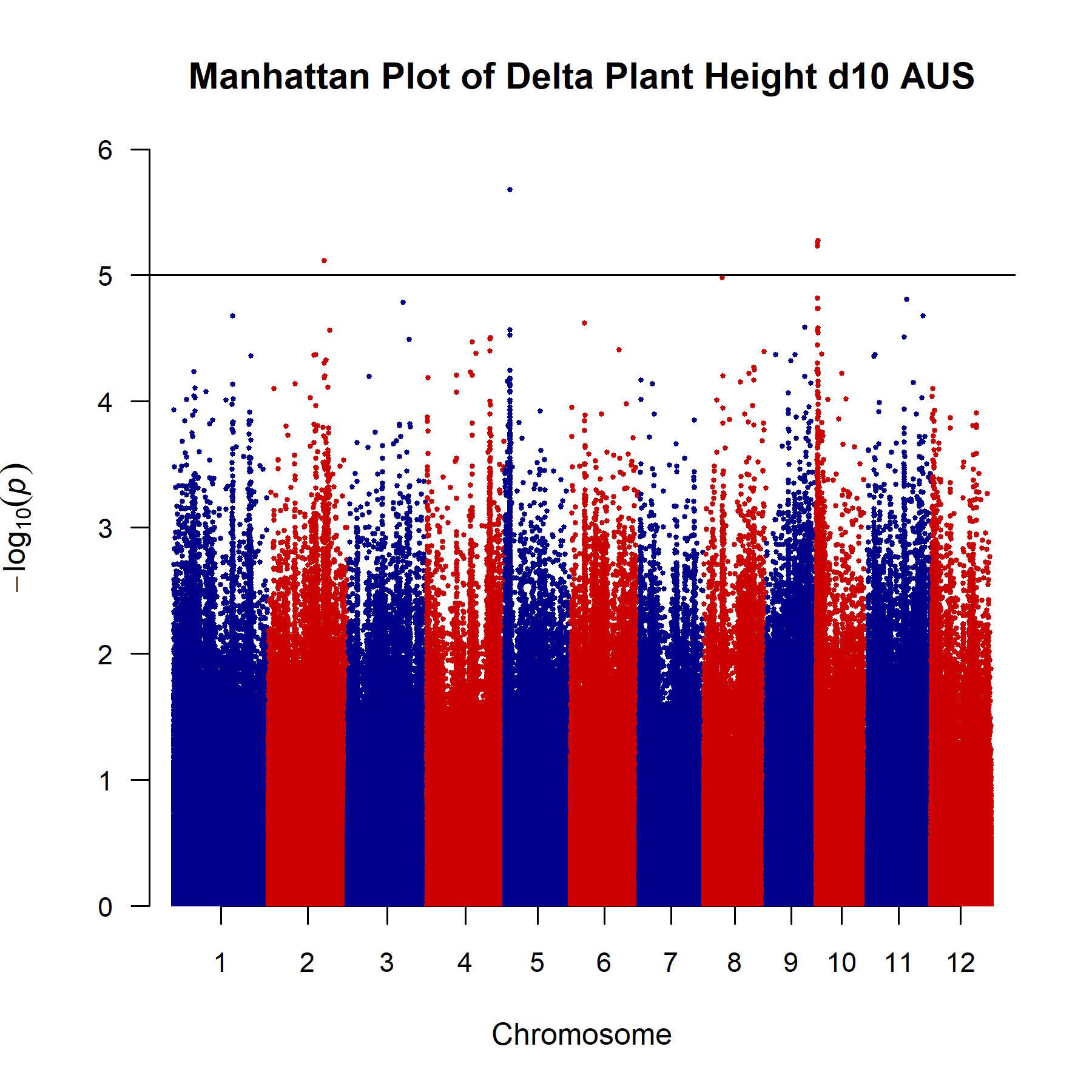
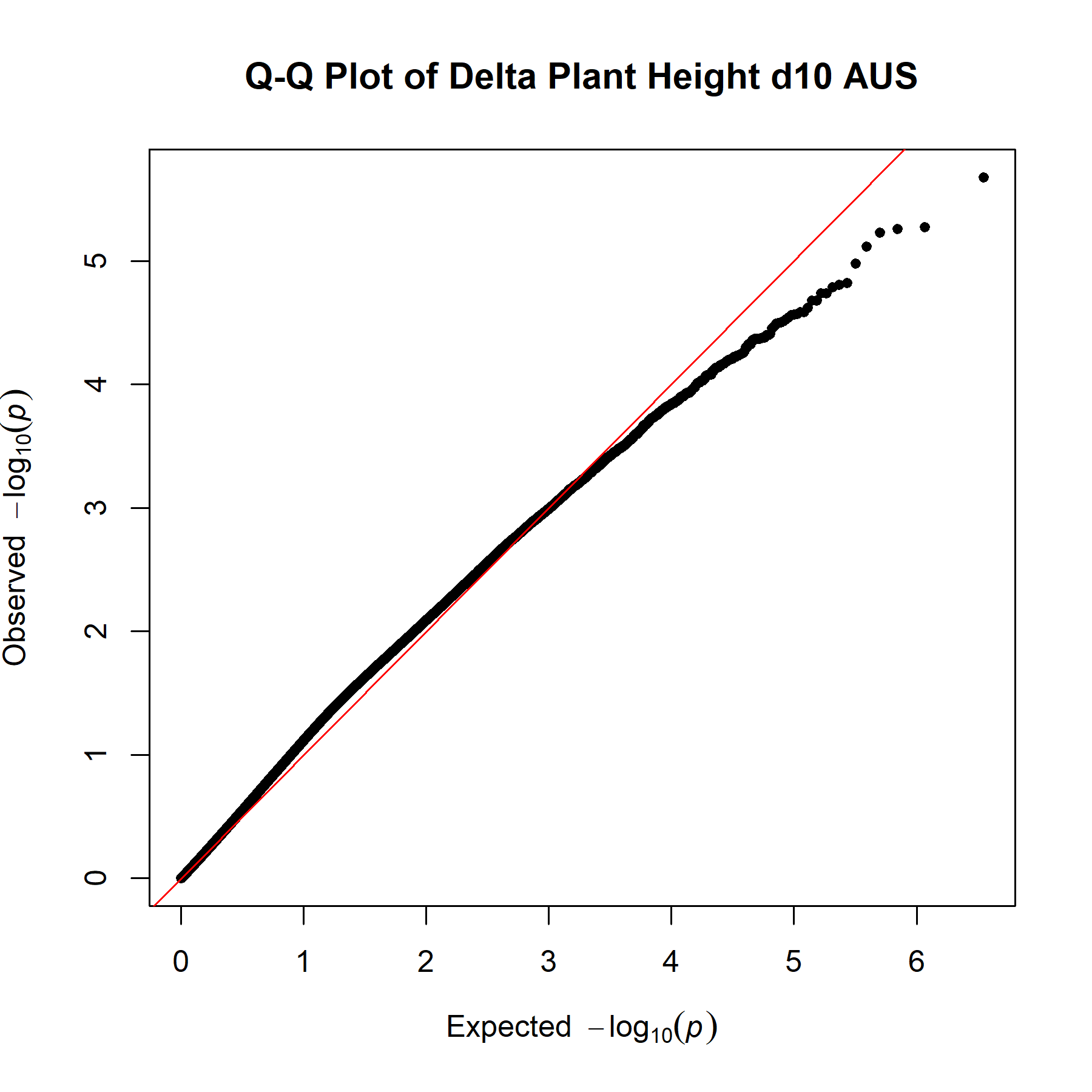
 

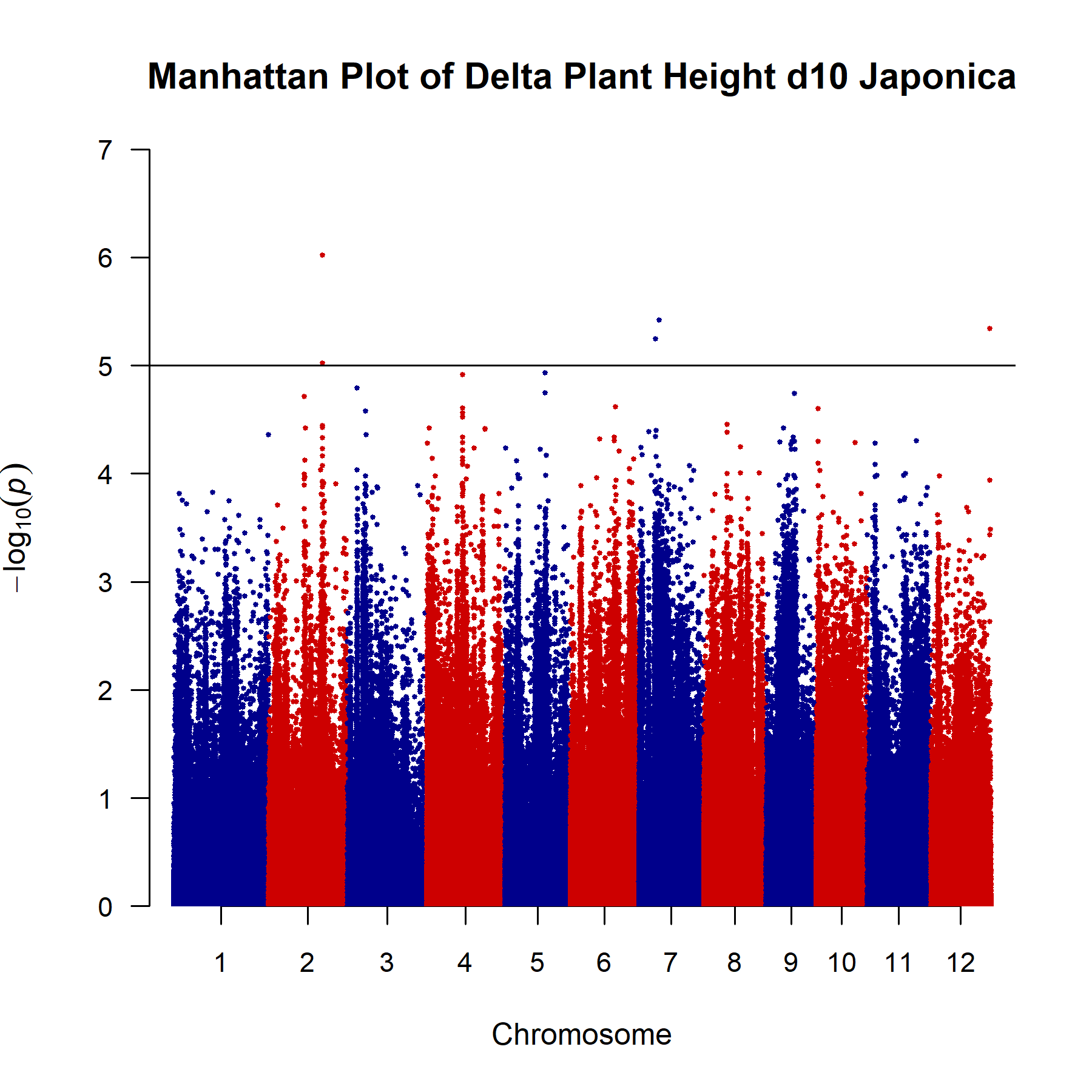
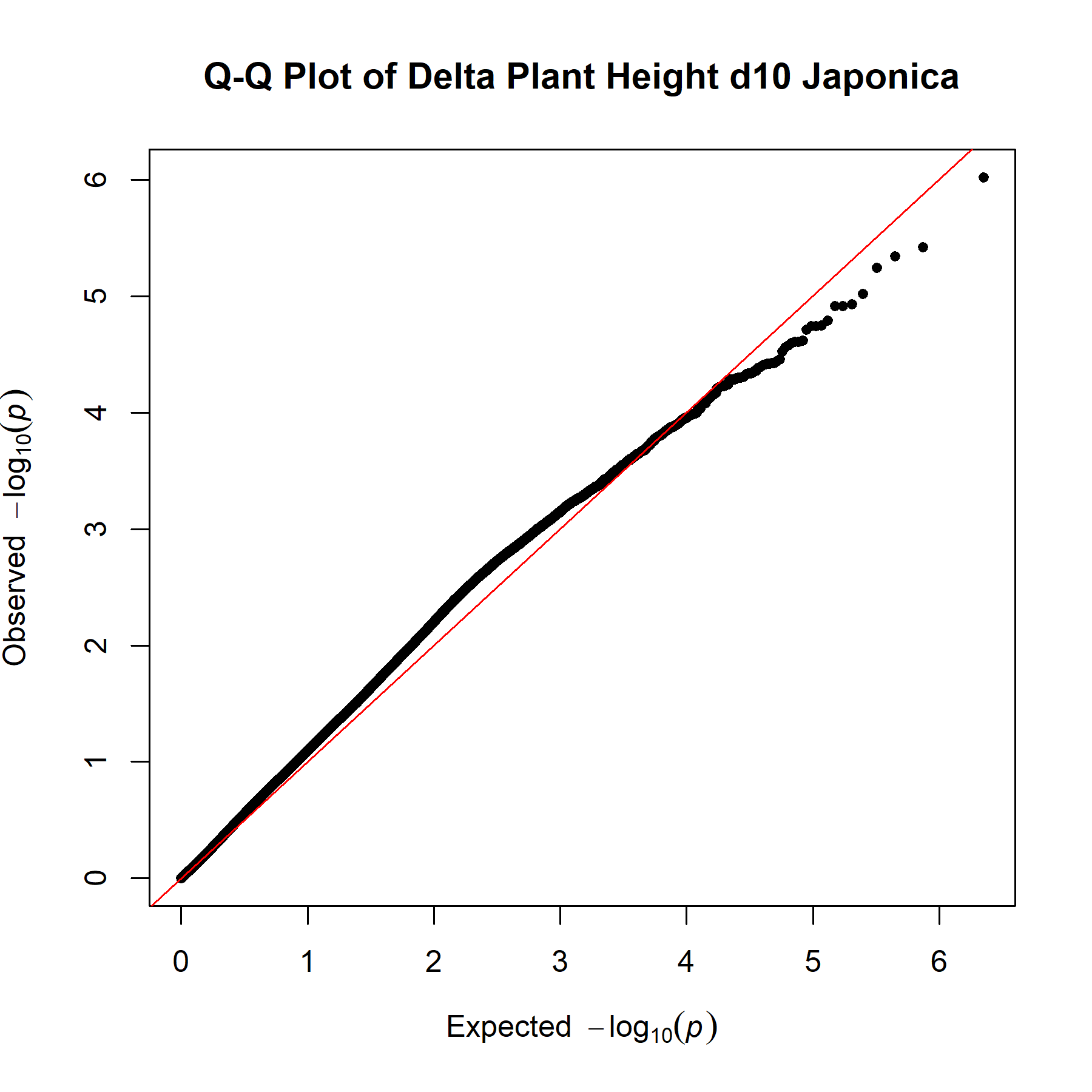
(C). Genome wide analysis of the change in plant height 10 days after the initiation of salt stress. Fig. 1. Manhattan and quantile-quantile plots are shown for the 6 panels derived from the USDA rice mini core; (All) all 118 accessions used in the study, (IND\_ AUS) is the Indica subspecies composed of the indica and aus subpopulations, (IND) is the indica subpopulation, (AUS) is aus, (JAP) is the Japonica subspecies composed of the temperate and tropical japonica subpopulations and (TRJ) is tropical japonica. The fifth rice subpopulation, Aromatic, was not present in the study. In the Manhattan plots the X axis shows the SNPs position across the 12 rice chromosomes and the Y axis is the –log10 (p) value for each snp. The horizontal black line at –log10(p) = 5 is the significance threshold for SNPs. In the quantile-quantile plots the X axis is the expected SNP distribution and the Y axis displays the –log10(p) observed SNP distribution.

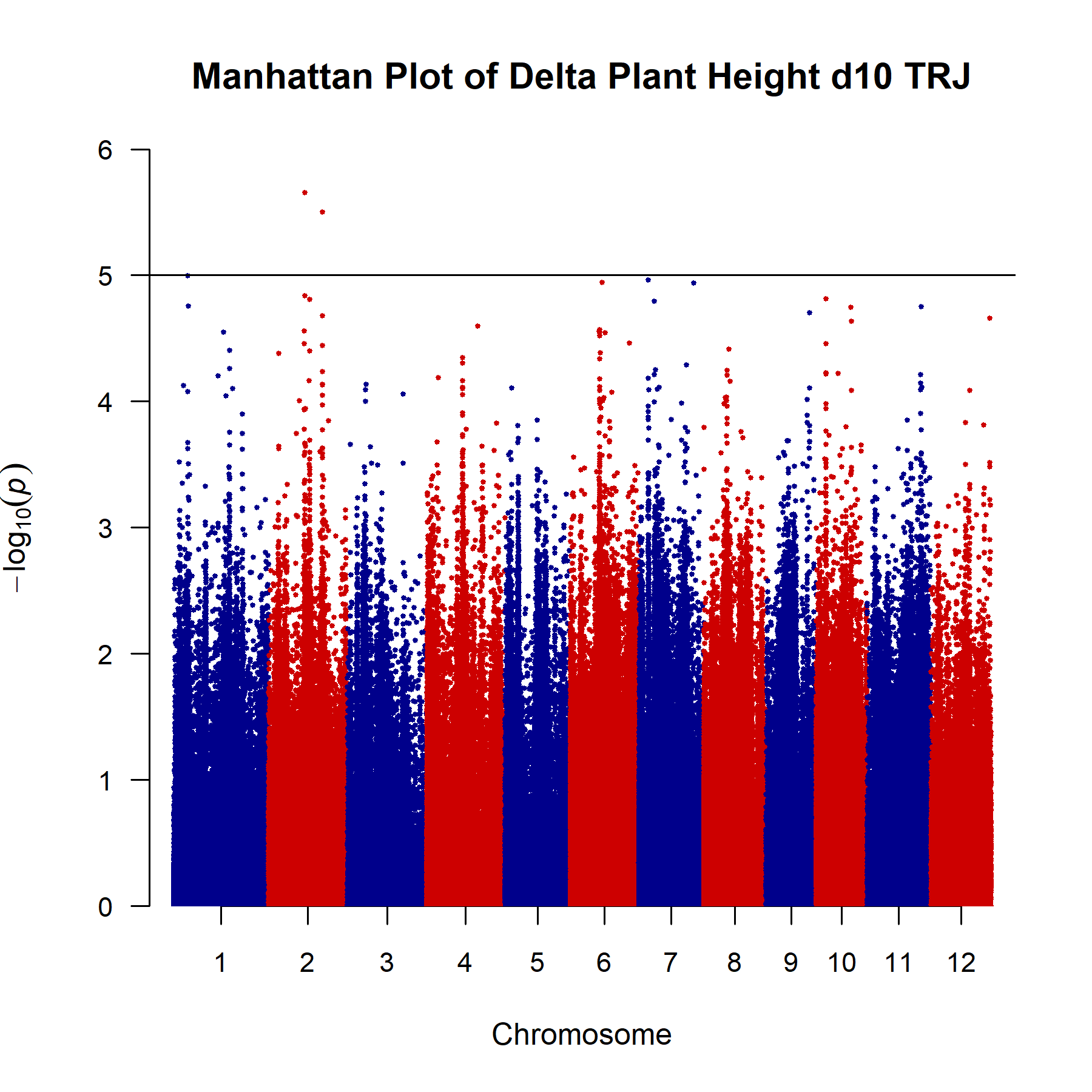
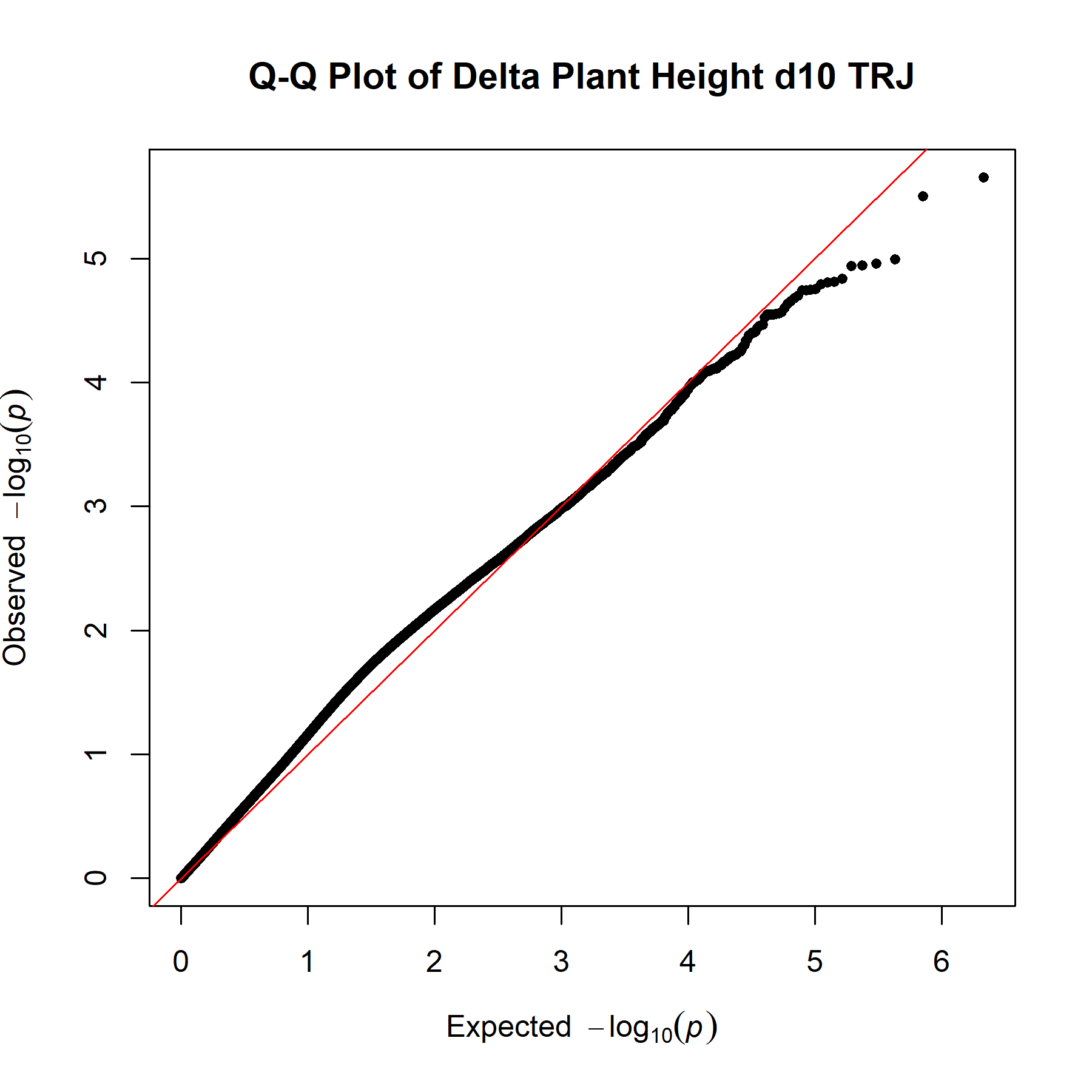
 

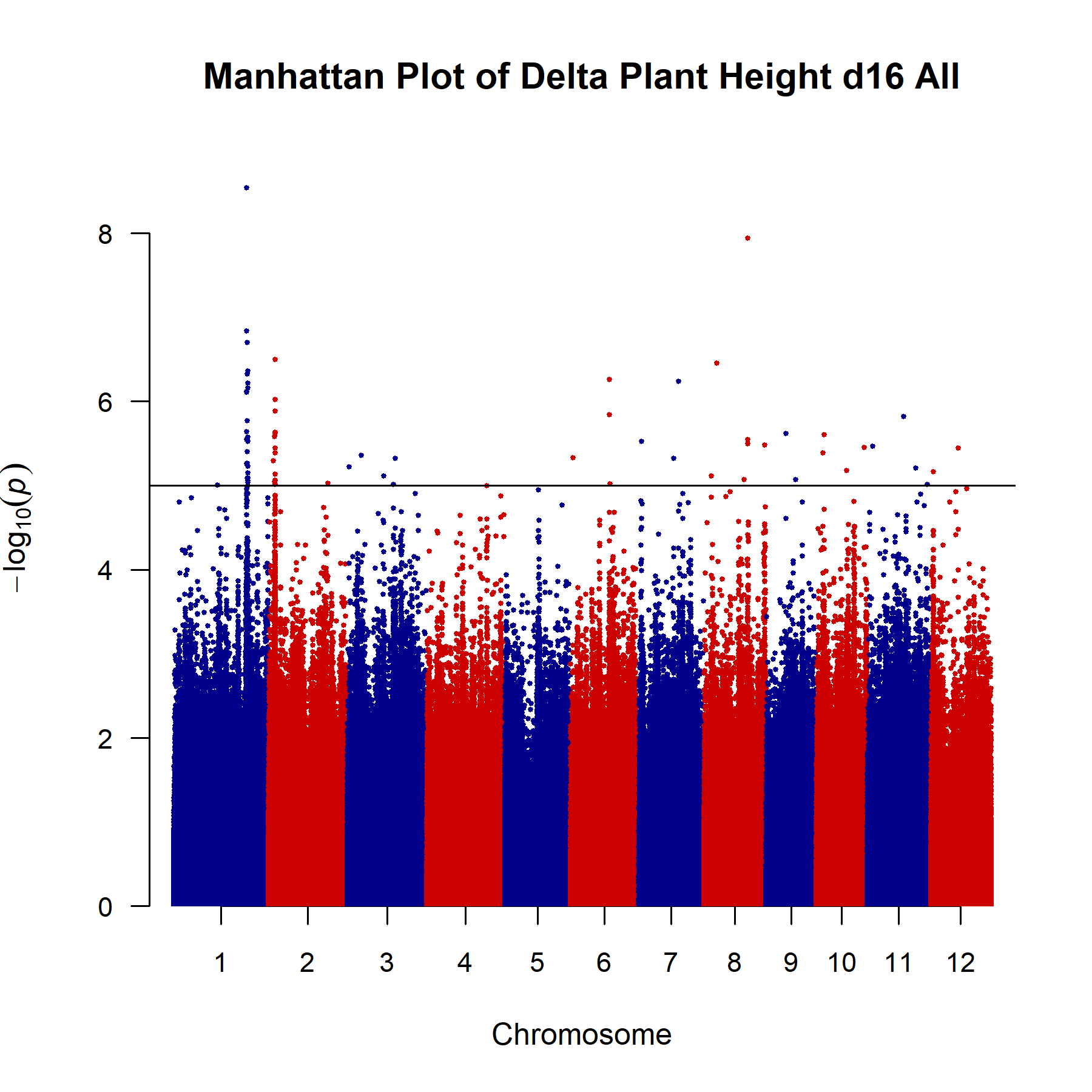
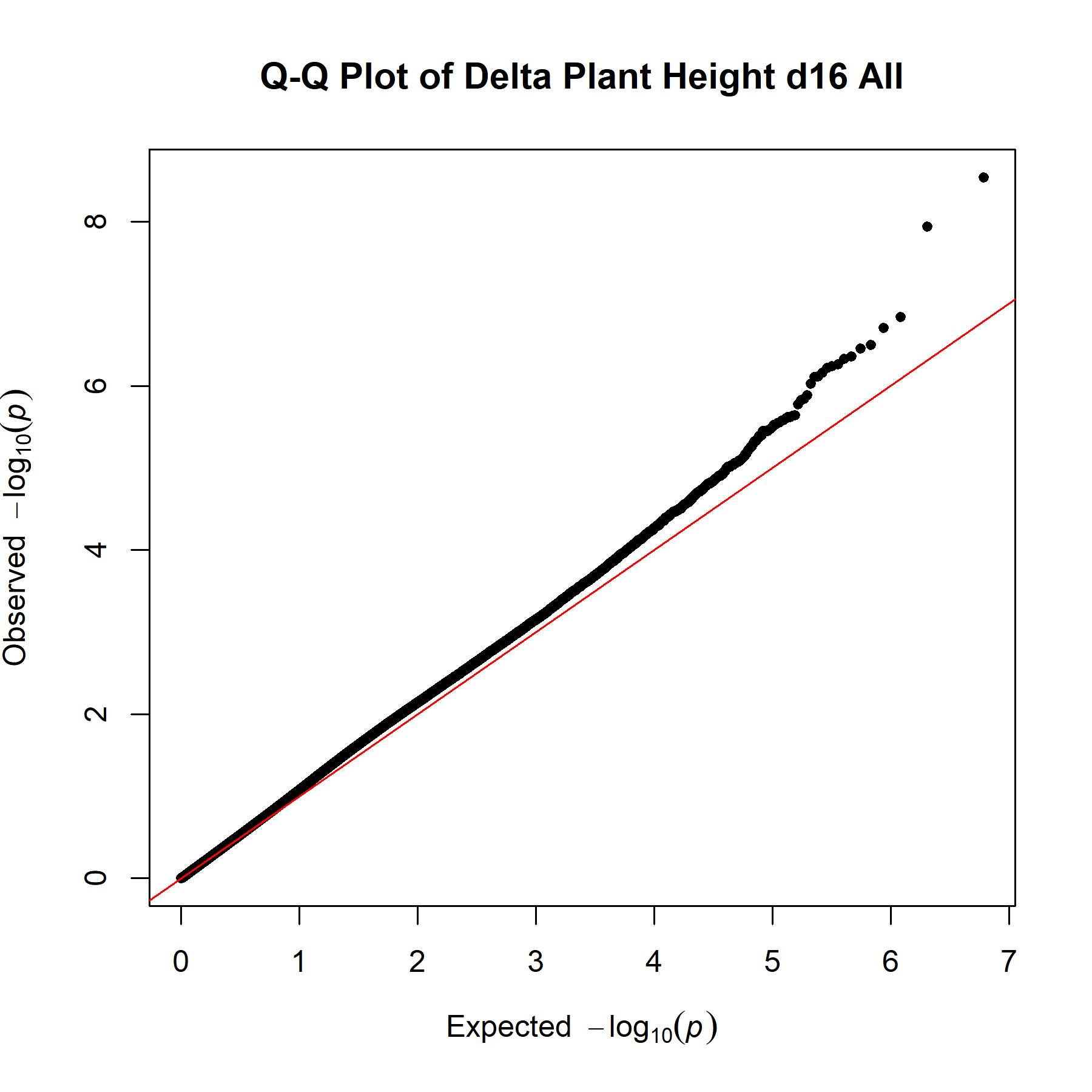
 

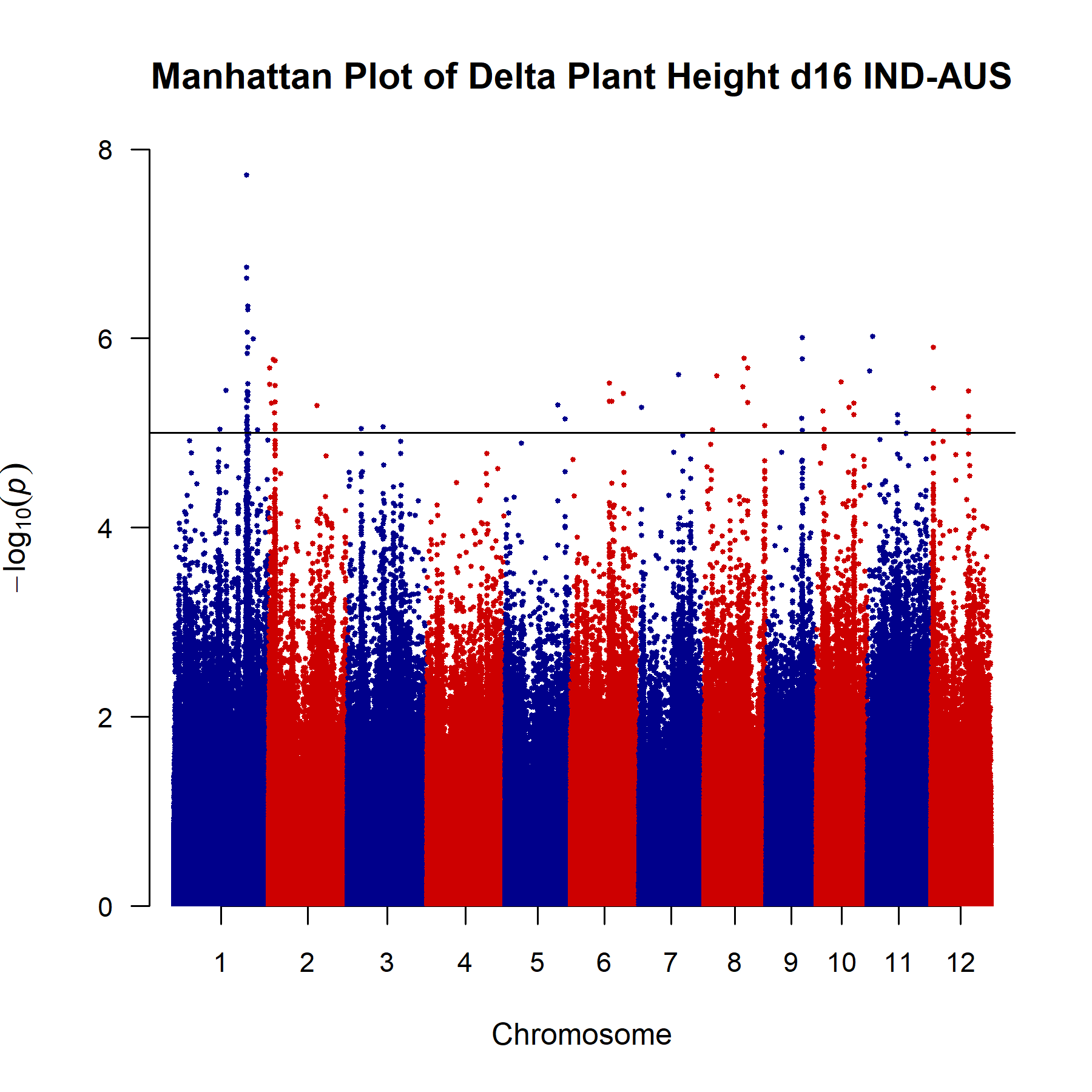
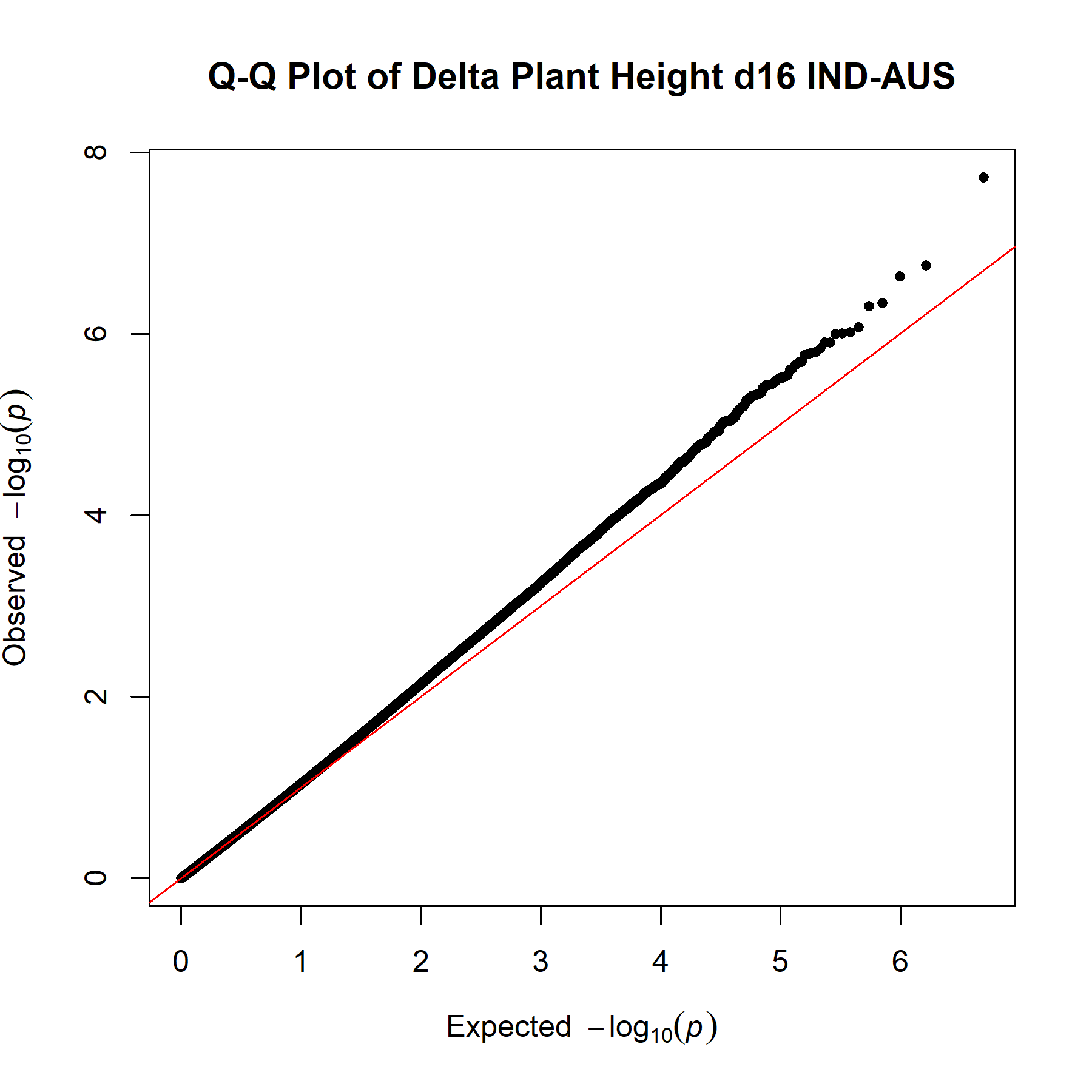
 

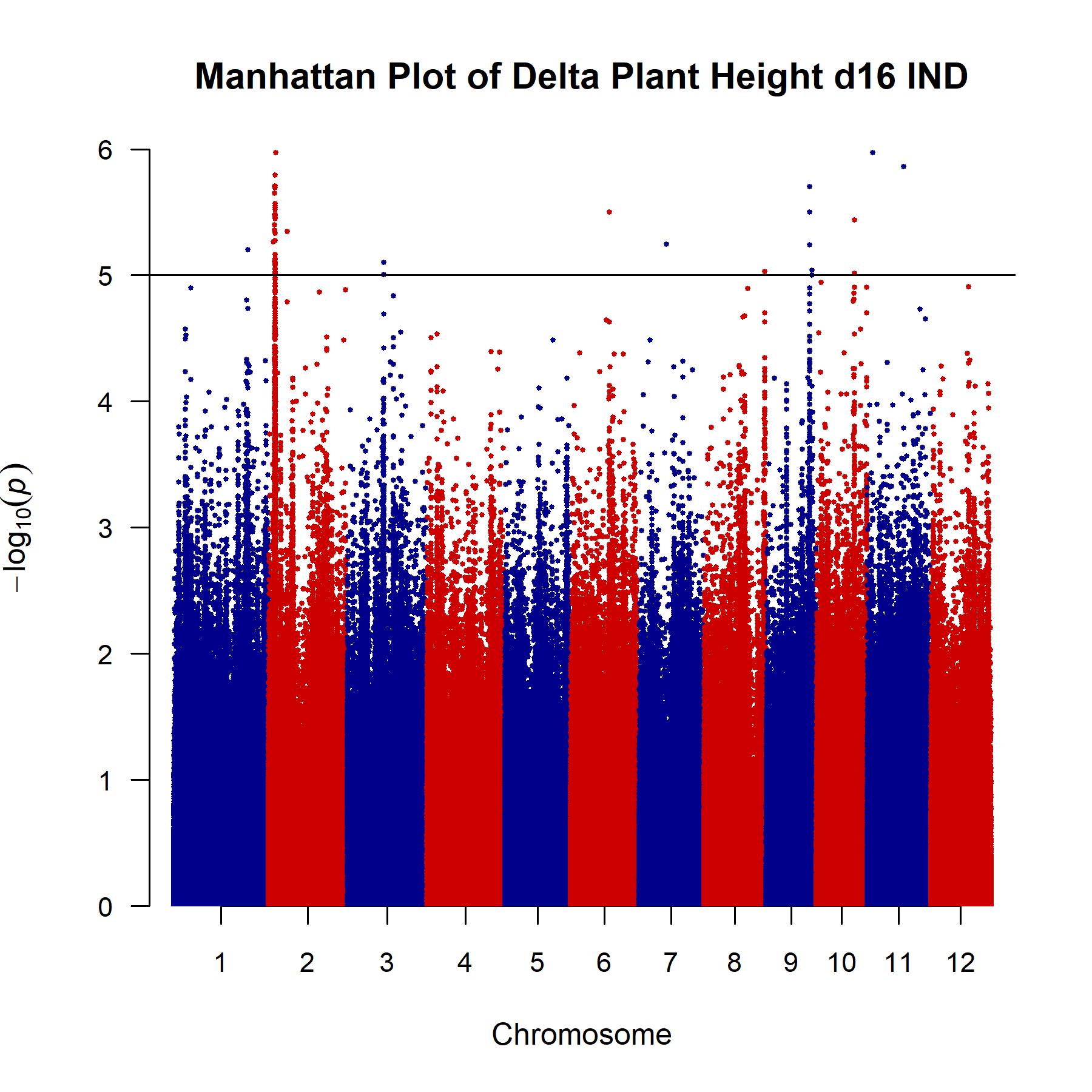
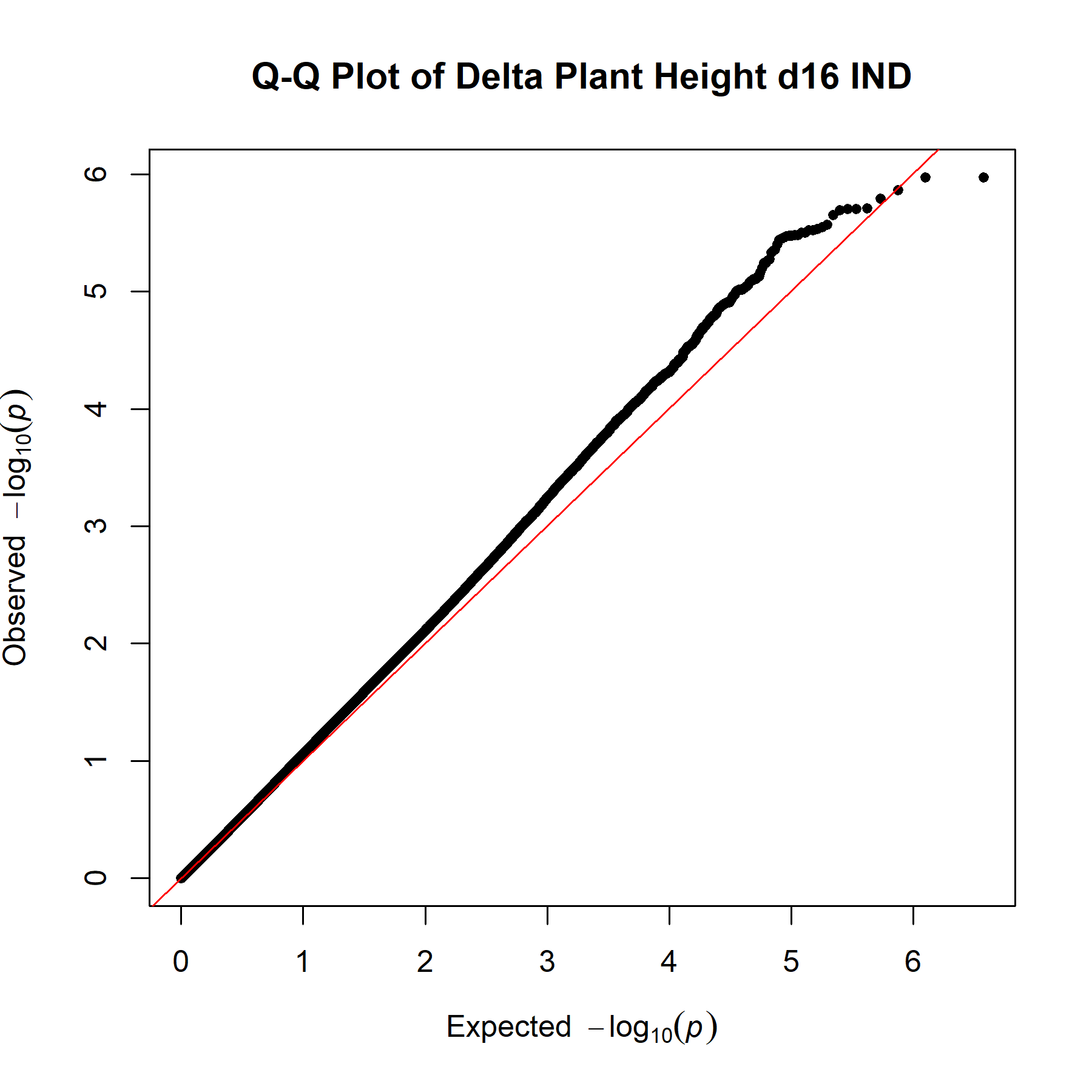
 

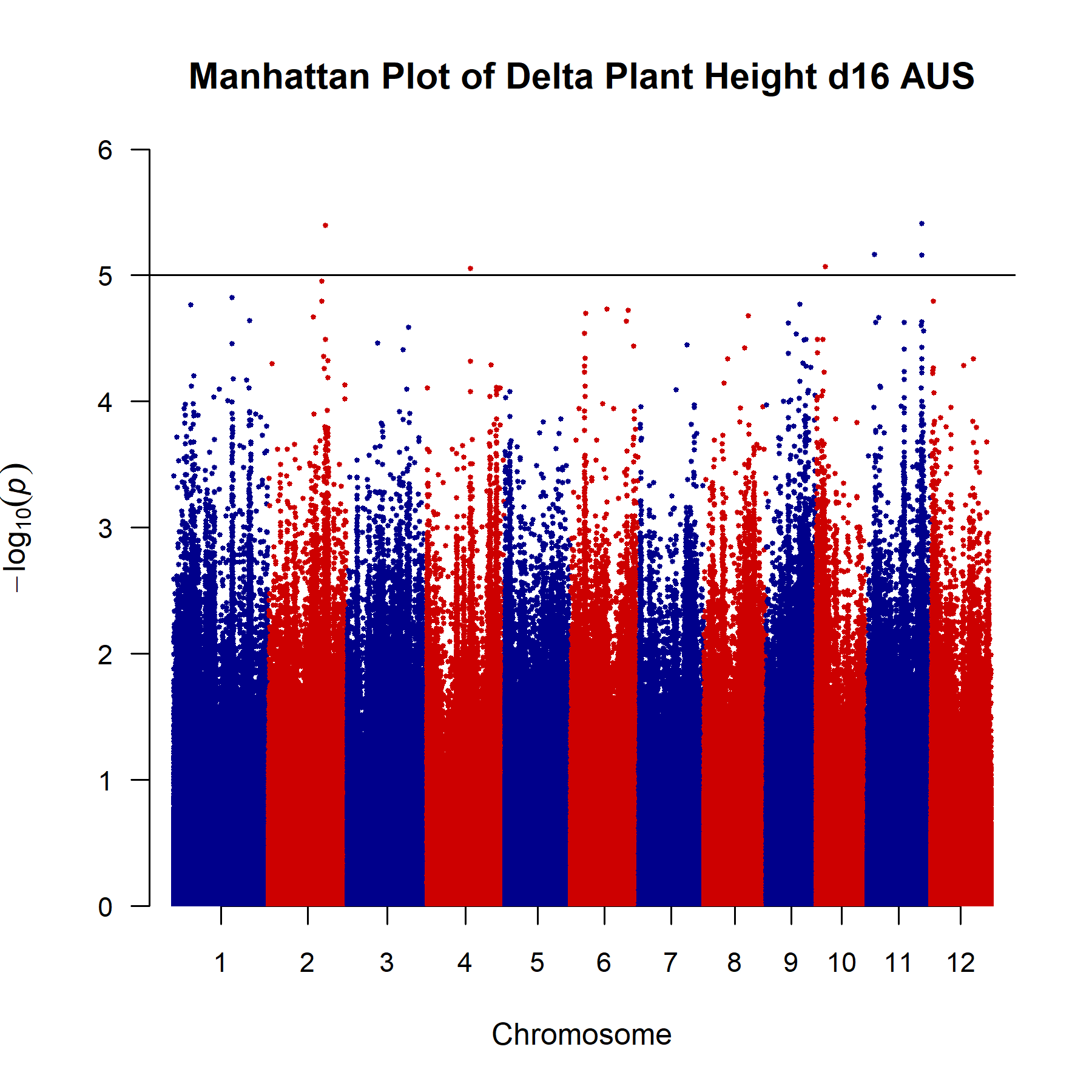
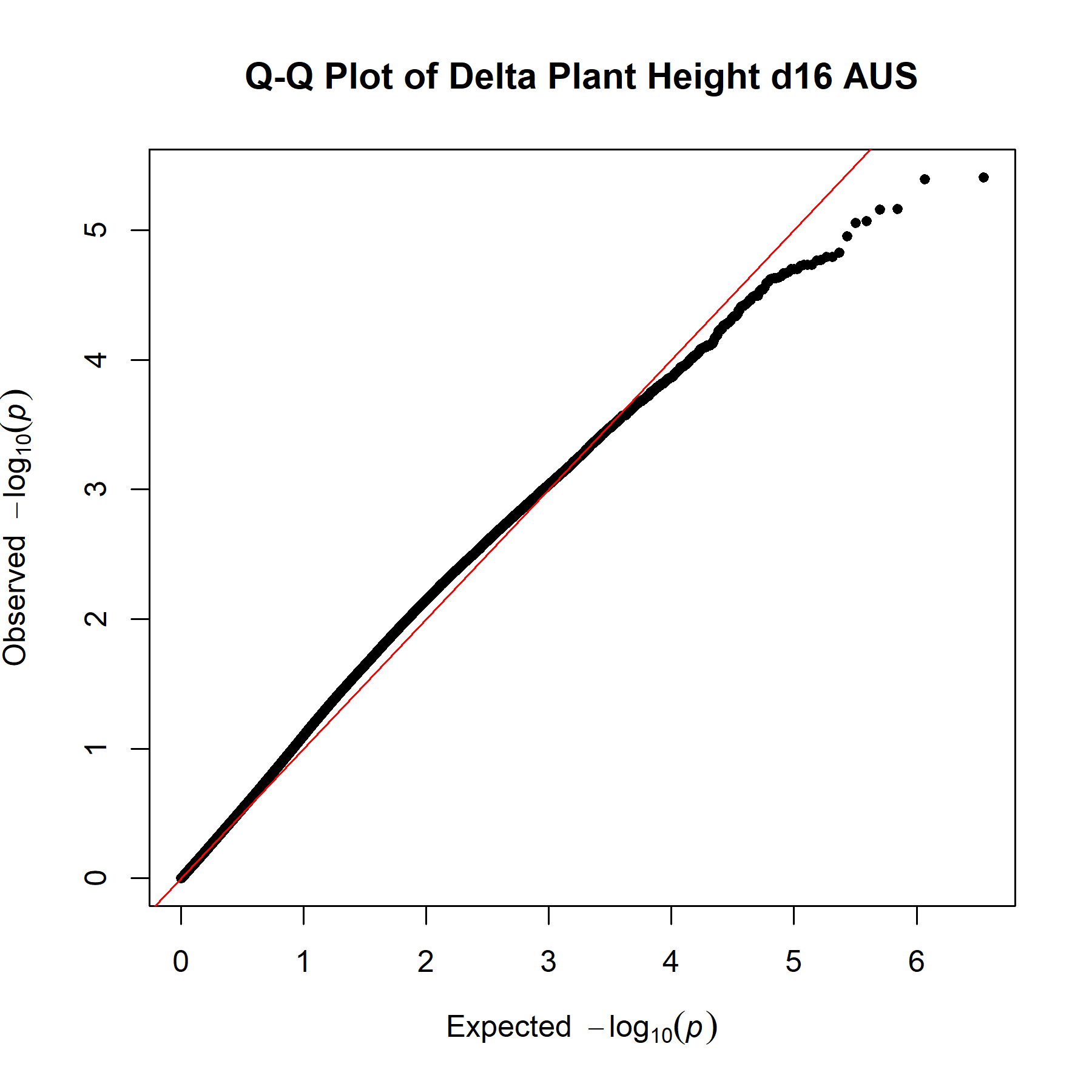
 

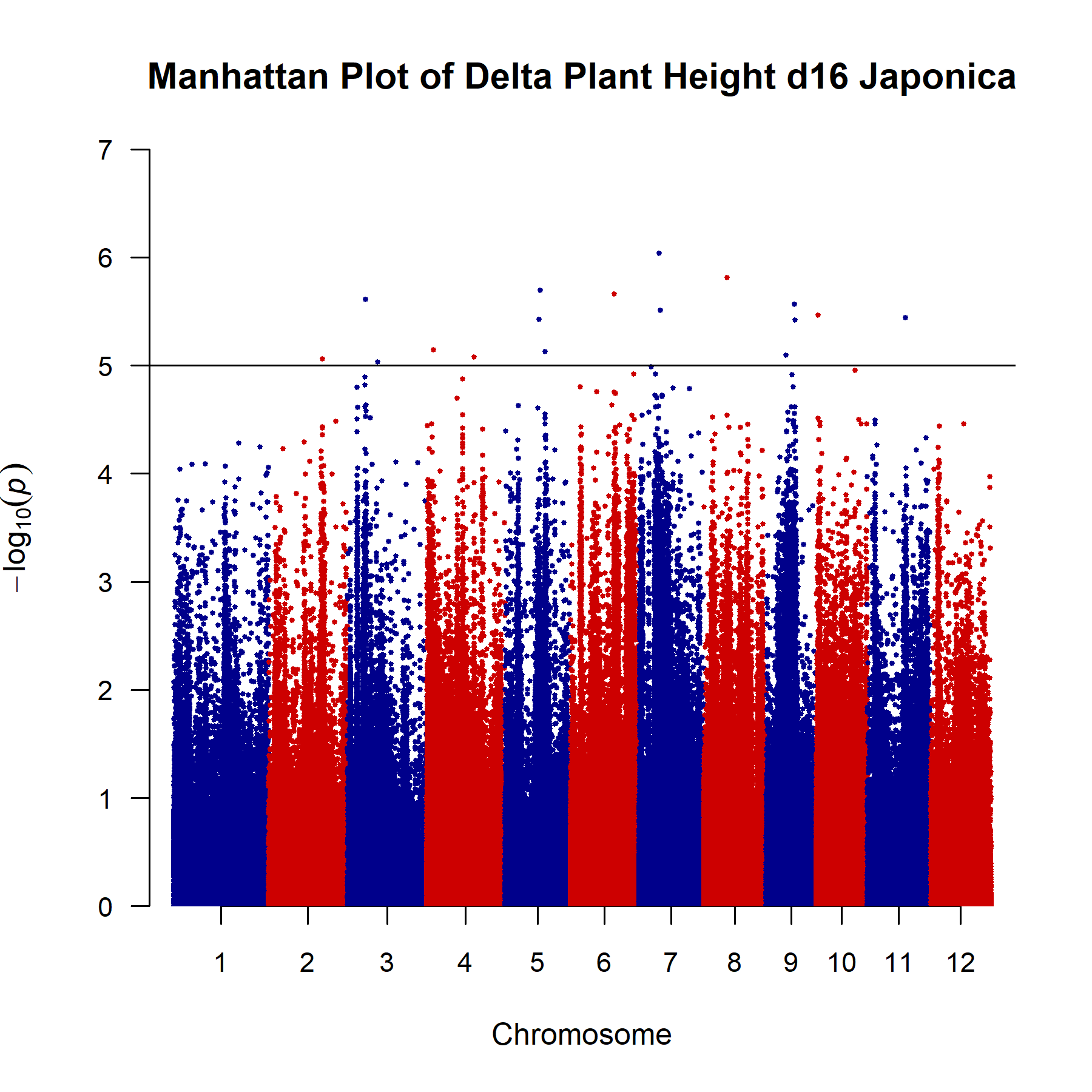
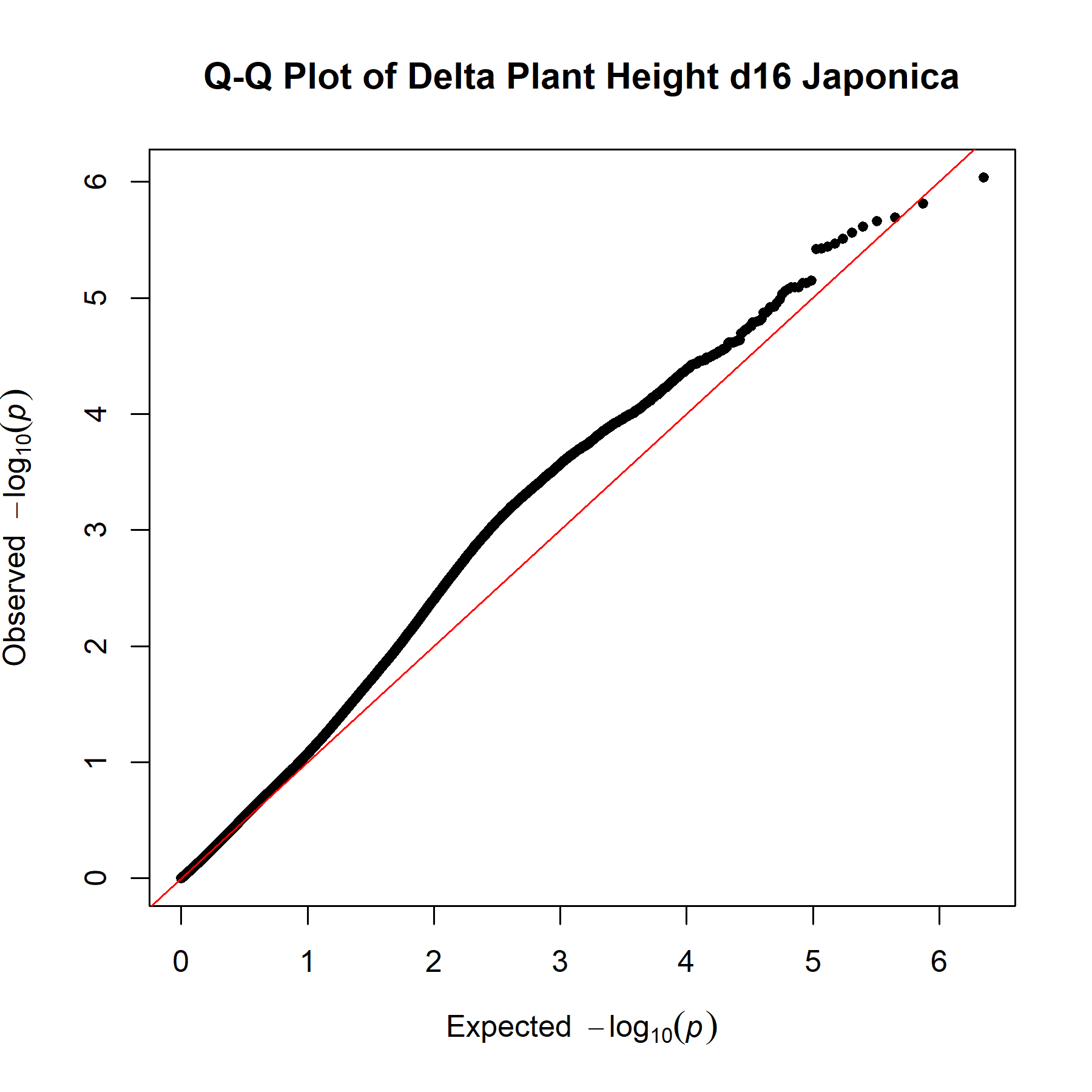
(D). Genome wide analysis of the change in plant height 16 days after the initiation of salt stress. Fig. 1. Manhattan and quantile-quantile plots are shown for the 6 panels derived from the USDA rice mini core; (All) all 118 accessions used in the study, (IND\_ AUS) is the Indica subspecies composed of the indica and aus subpopulations, (IND) is the indica subpopulation, (AUS) is aus, (JAP) is the Japonica subspecies composed of the temperate and tropical japonica subpopulations and (TRJ) is tropical japonica. The fifth rice subpopulation, Aromatic, was not present in the study. In the Manhattan plots the X axis shows the SNPs position across the 12 rice chromosomes and the Y axis is the –log10 (p) value for each snp. The horizontal black line at –log10(p) = 5 is the significance threshold for SNPs. In the quantile-quantile plots the X axis is the expected SNP distribution and the Y axis displays the –log10(p) observed SNP distribution.

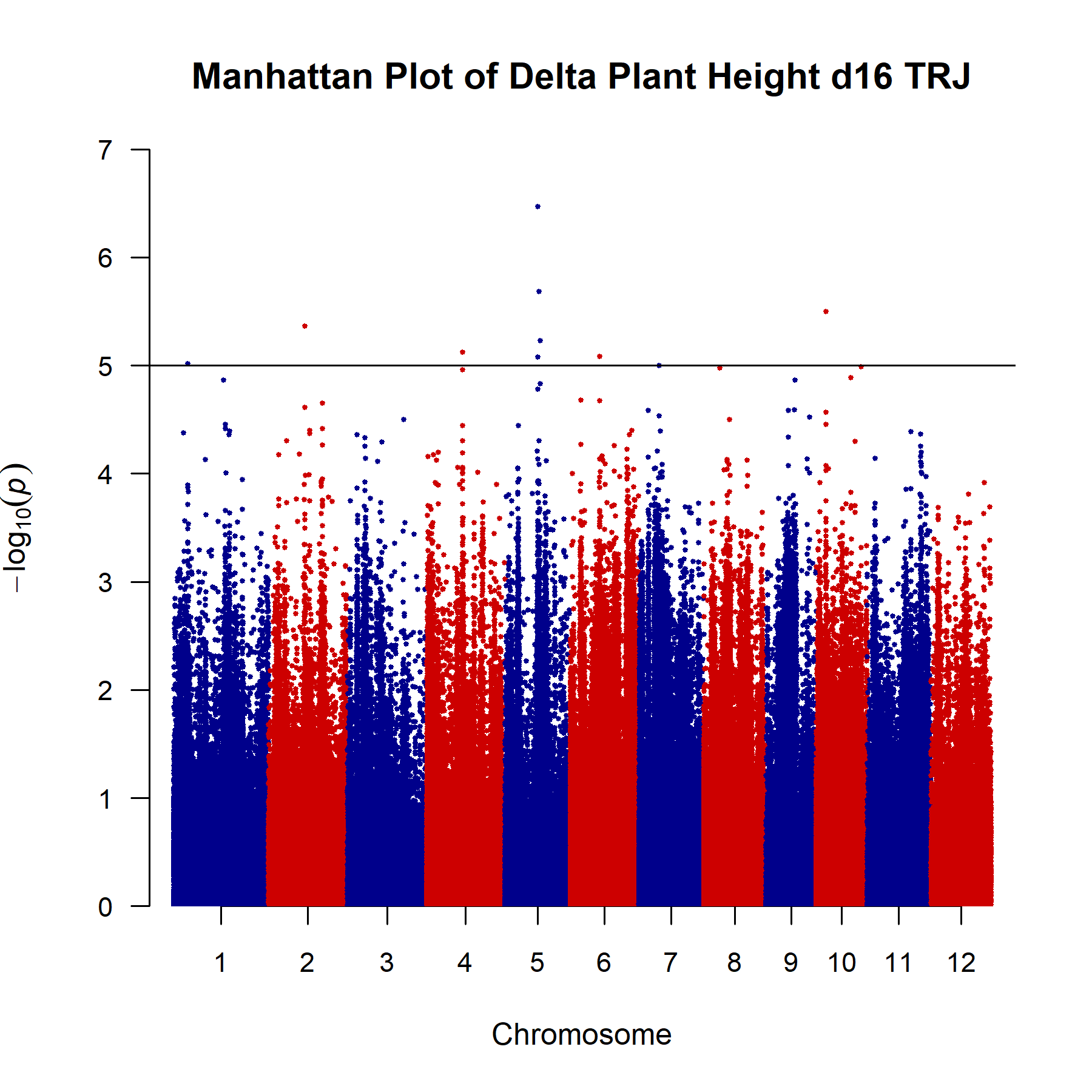
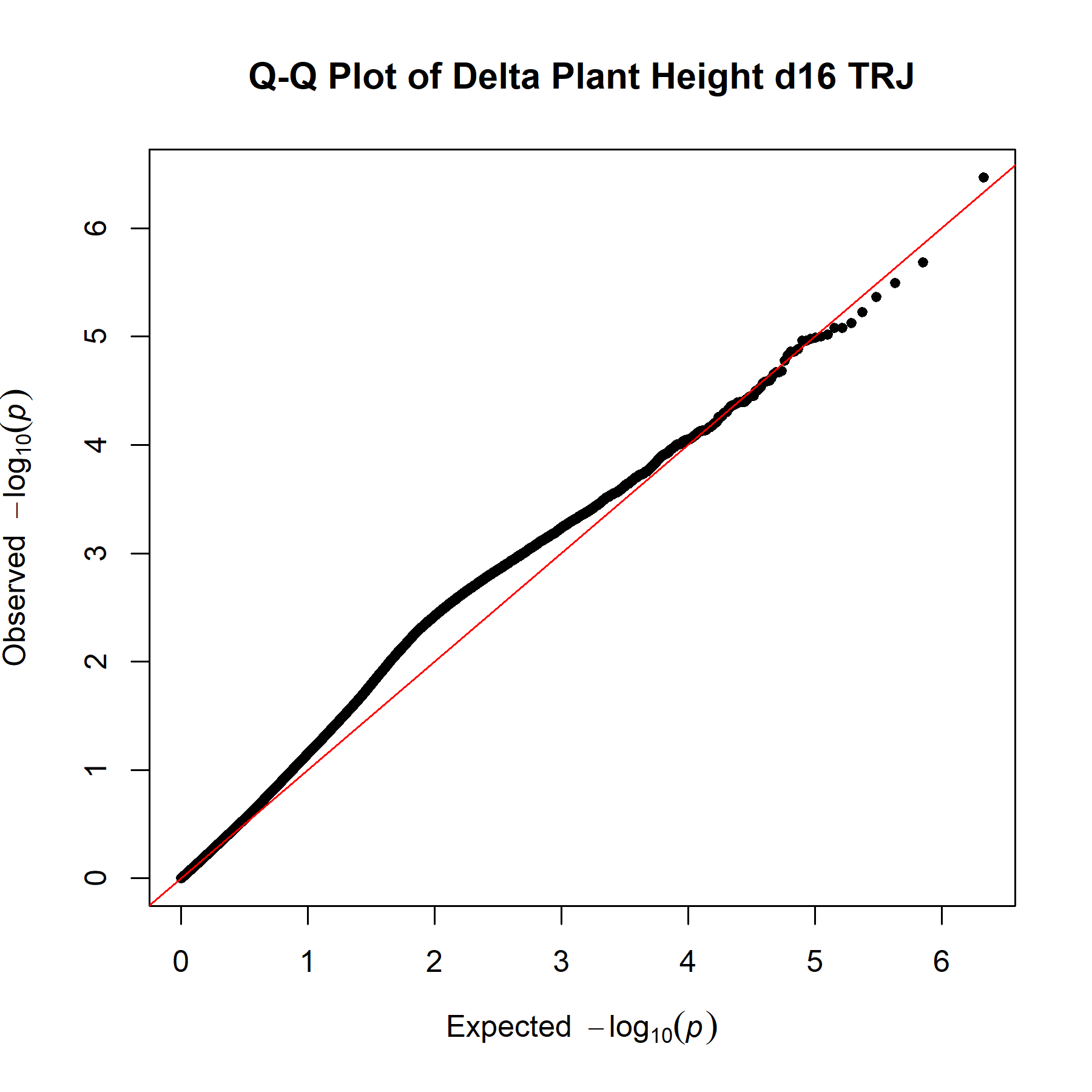
 

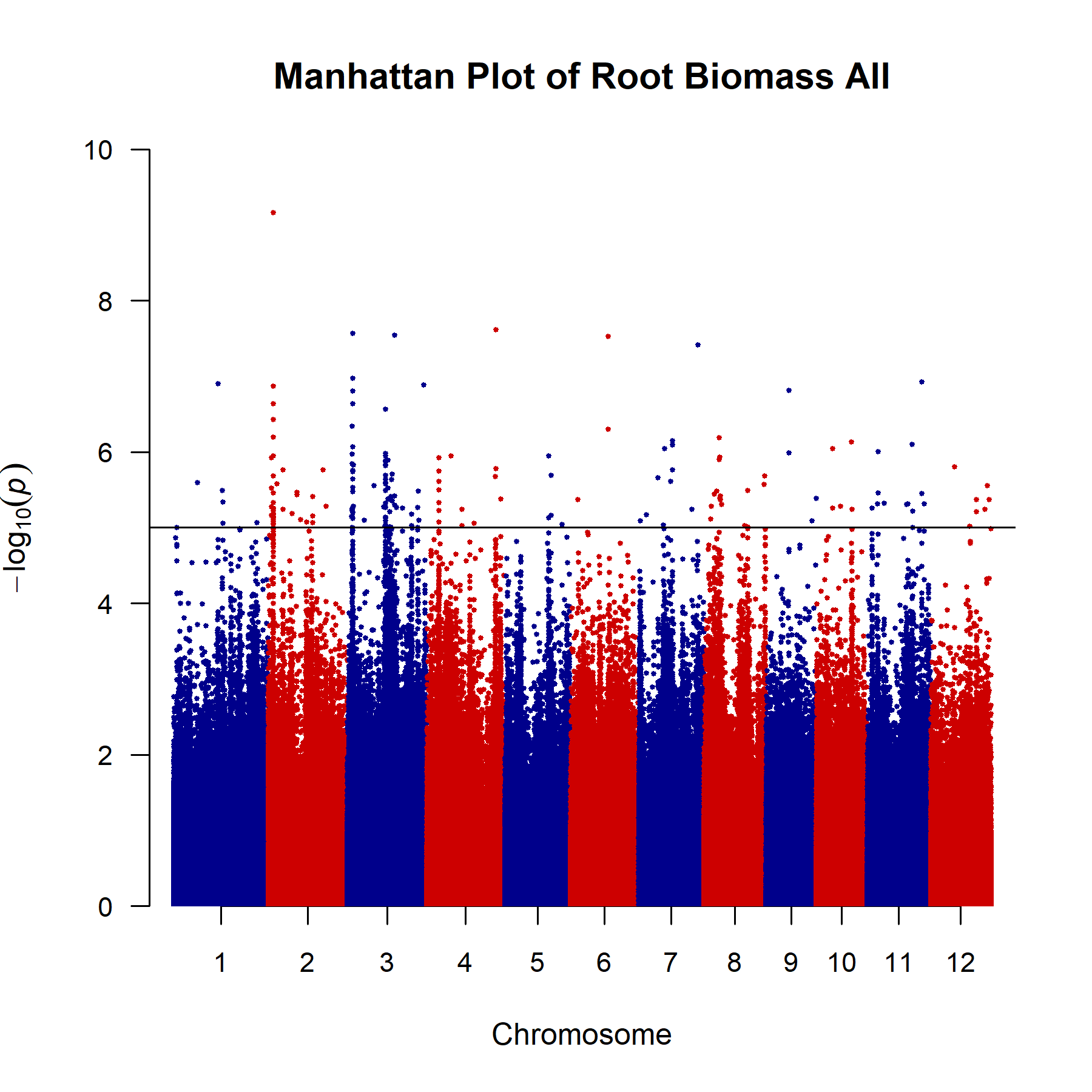
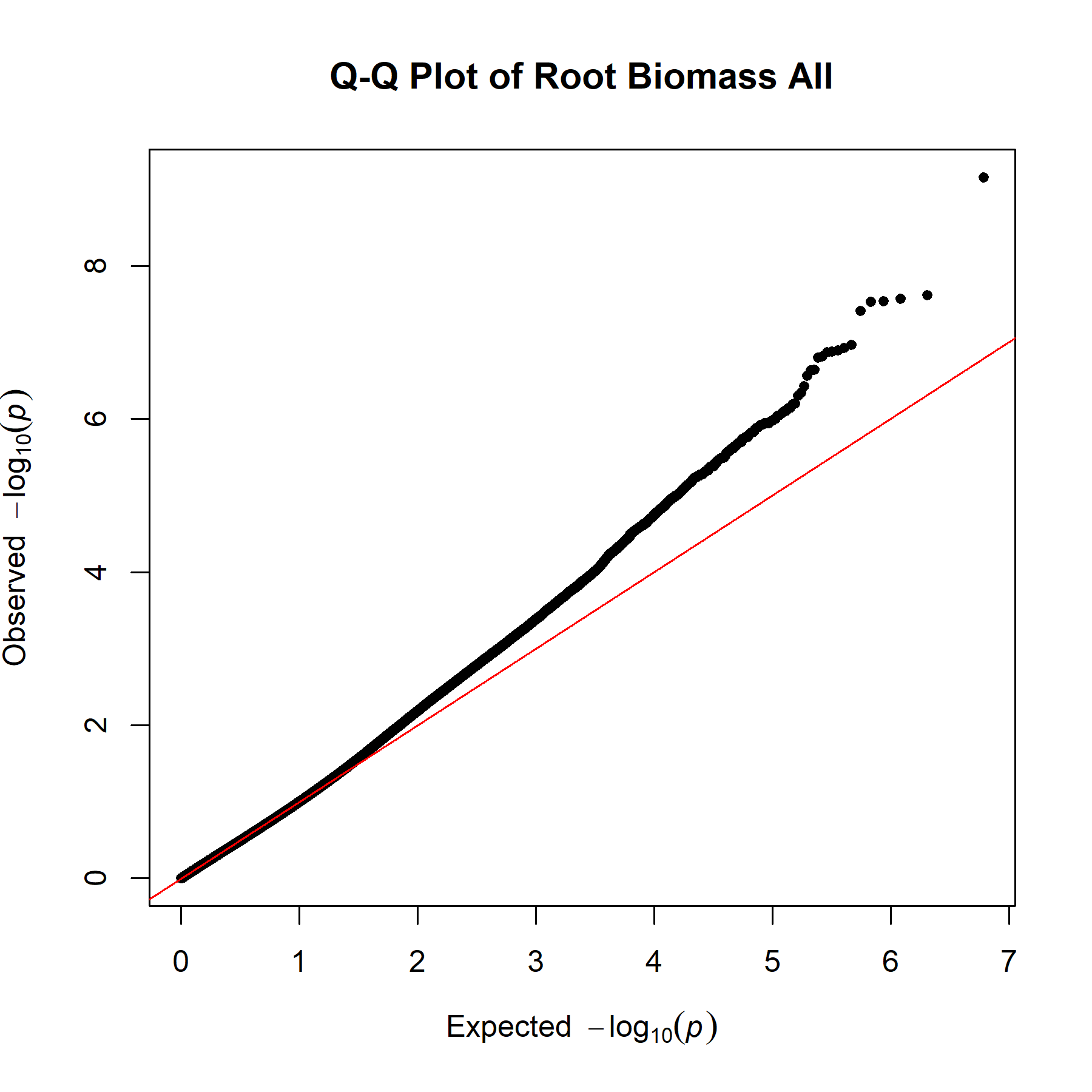
 

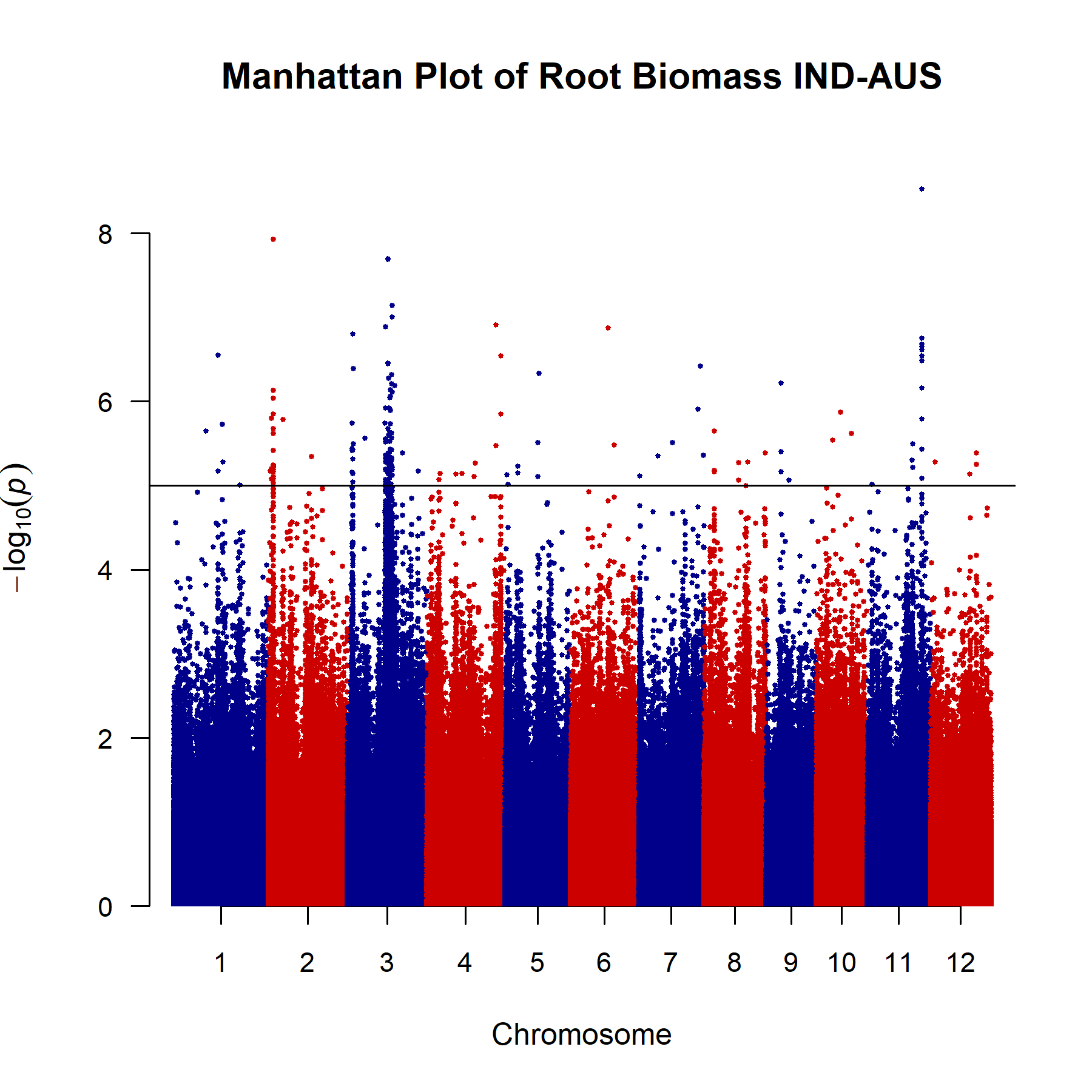
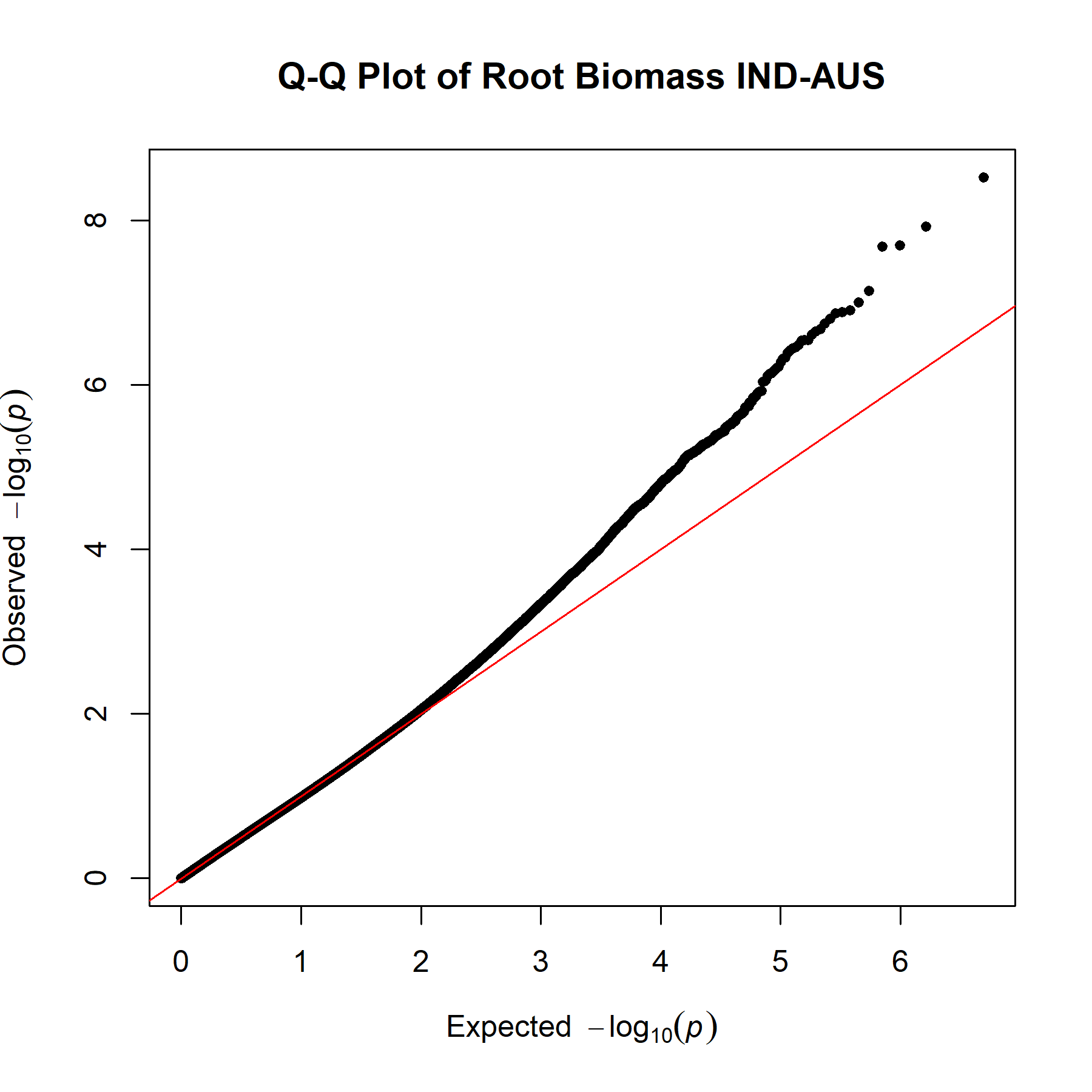
 

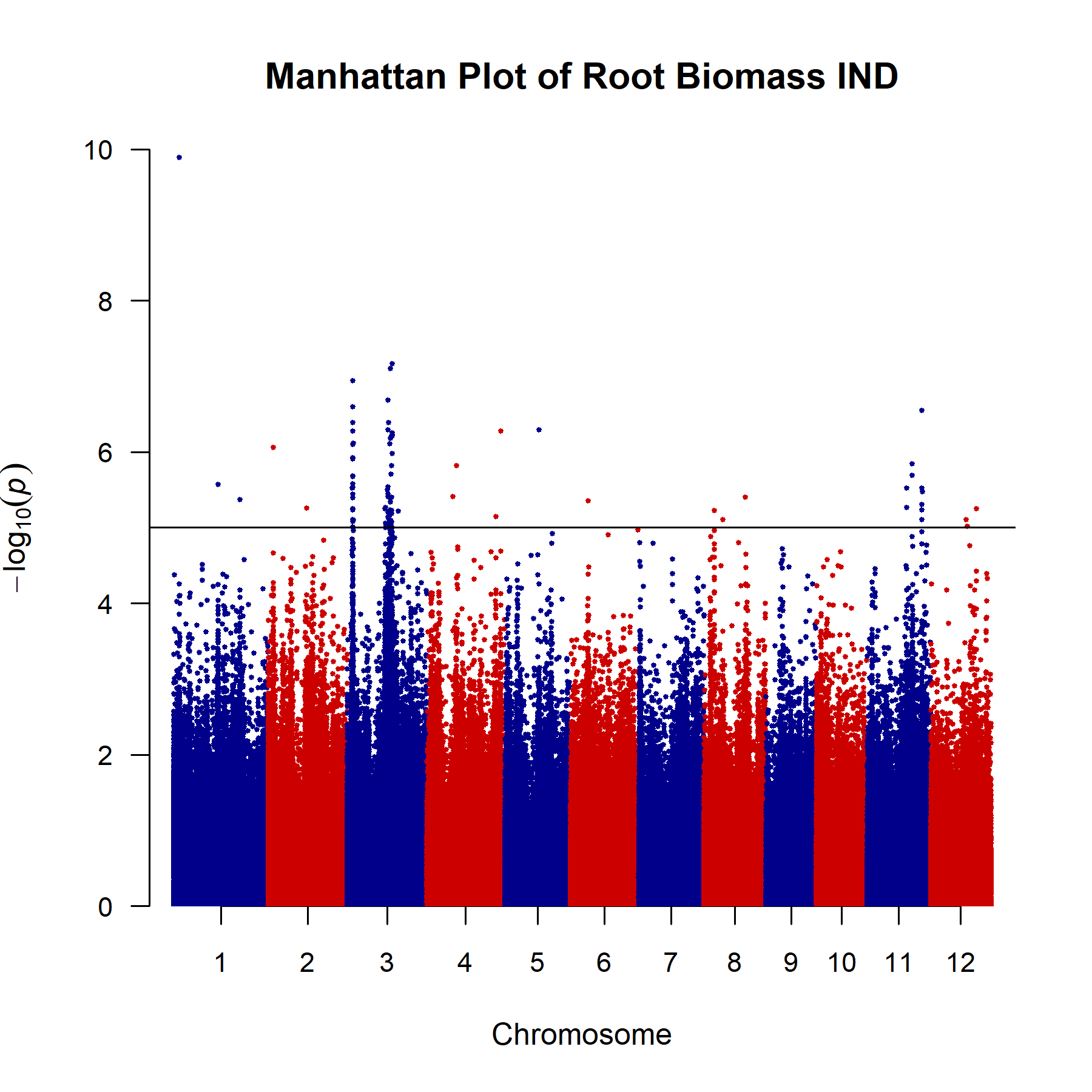
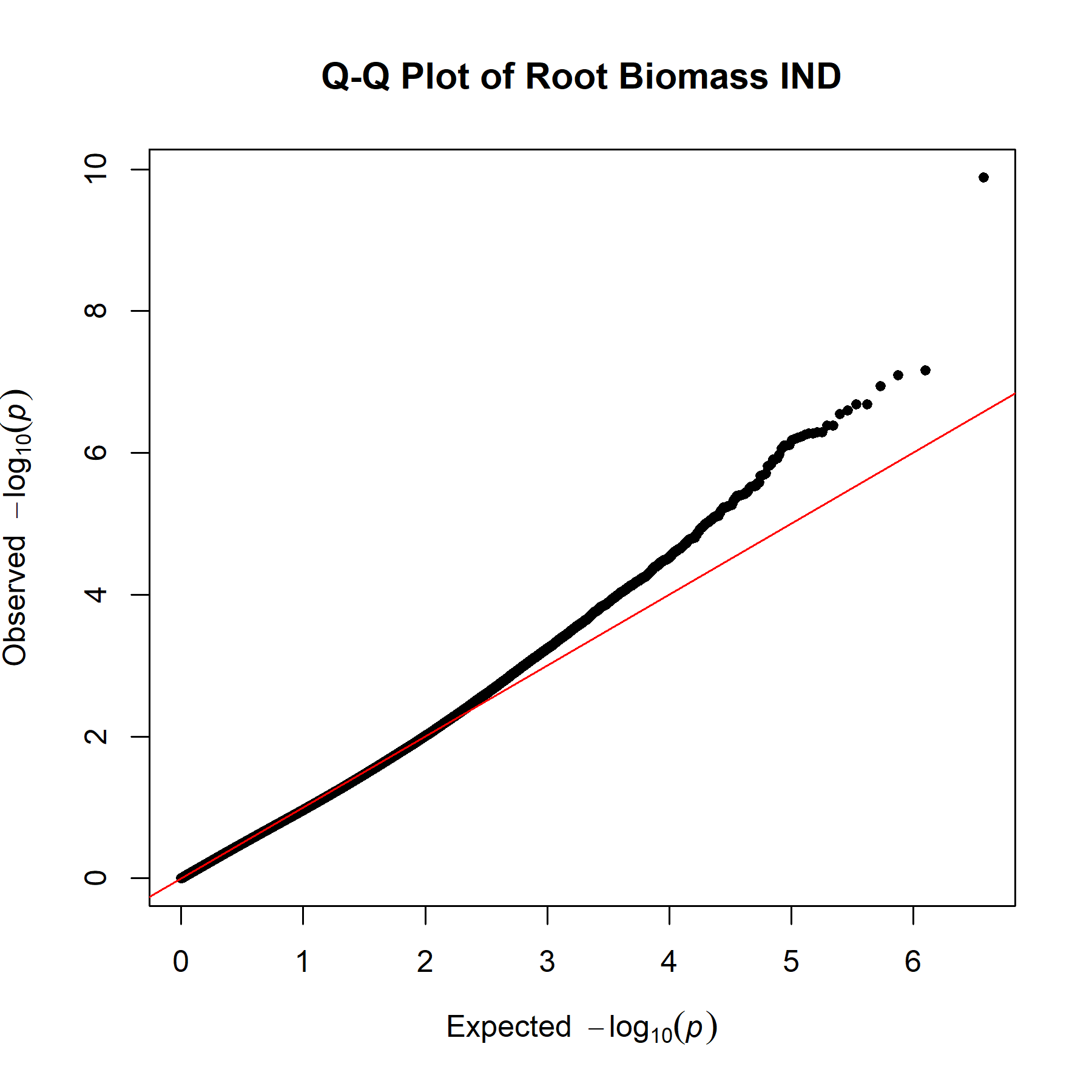
 

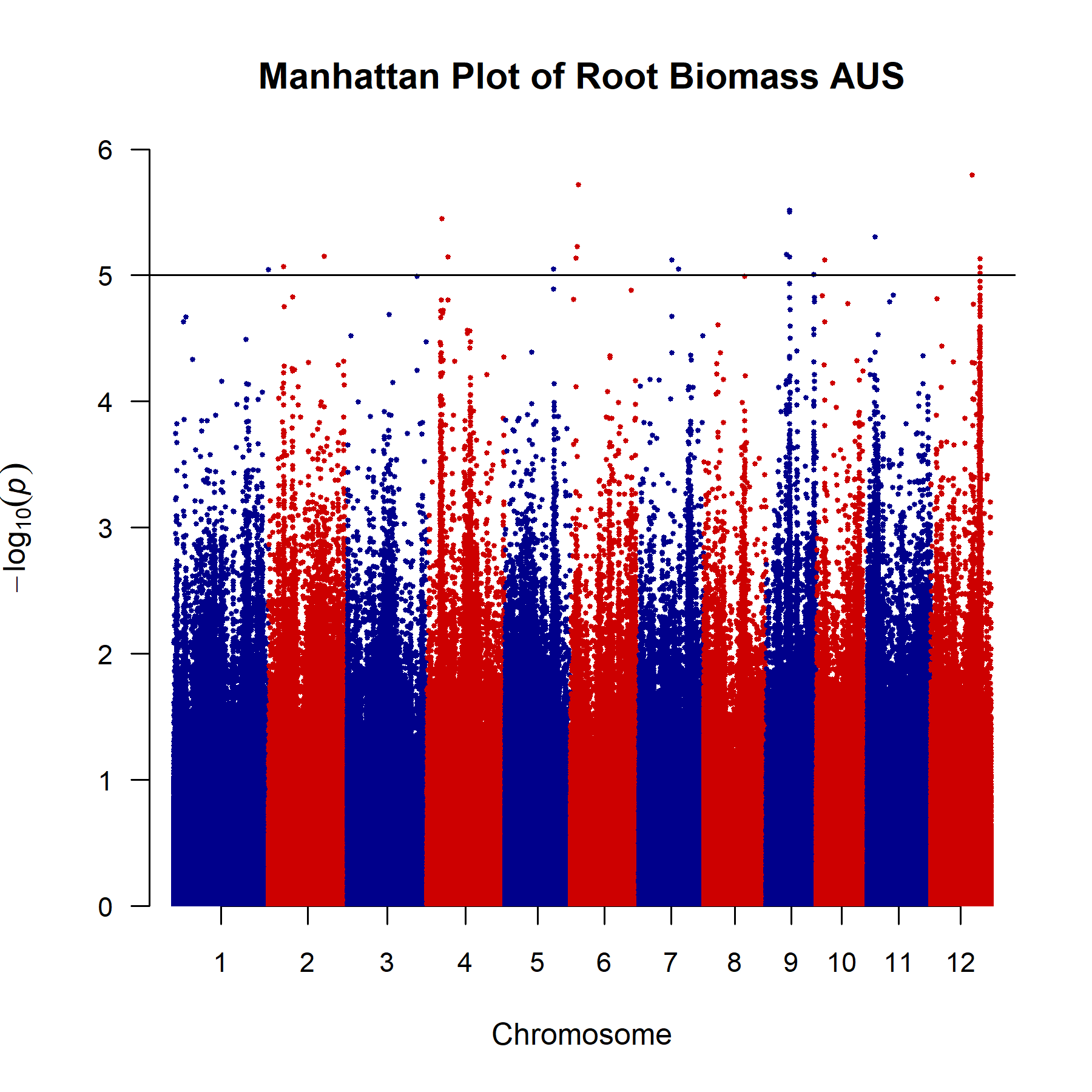
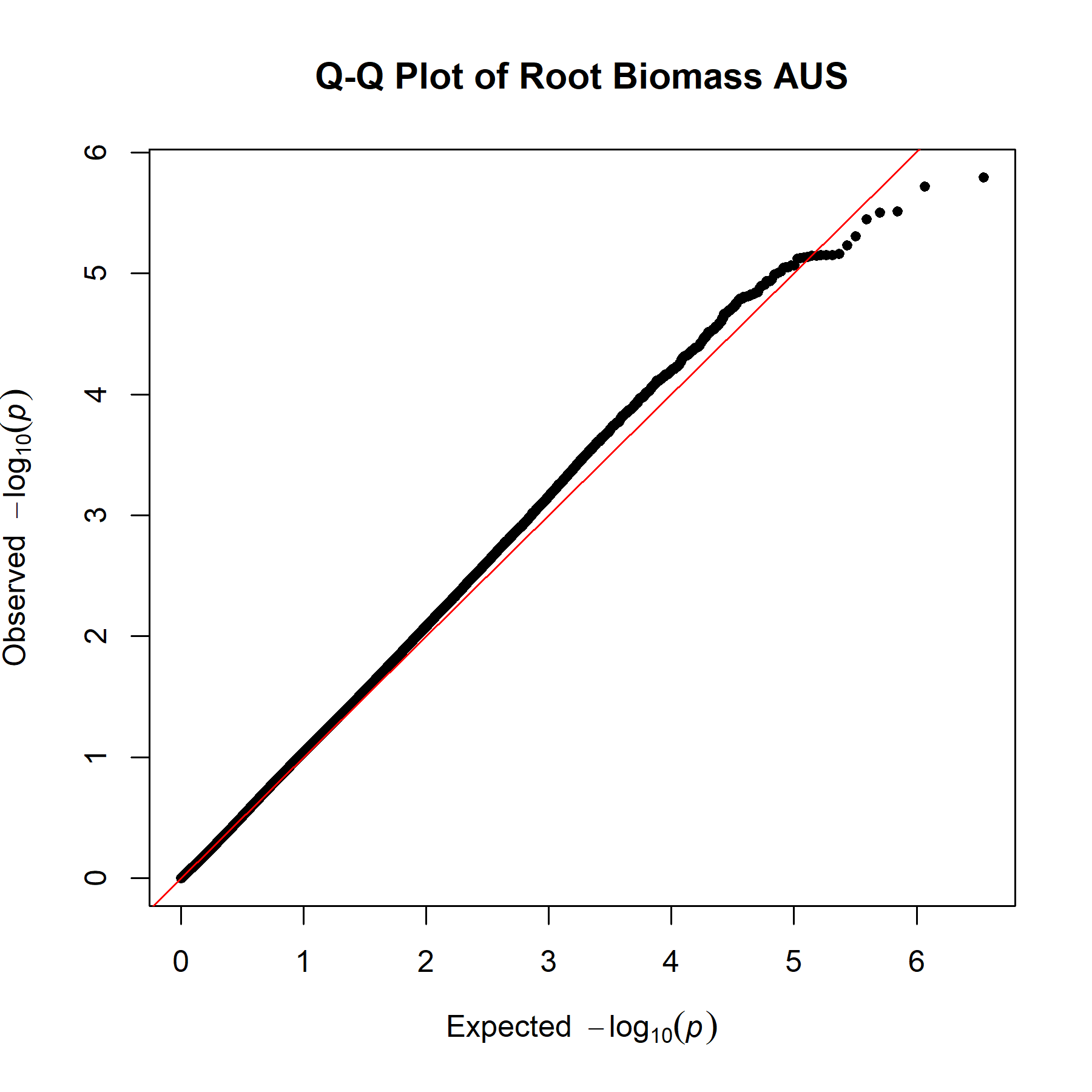
 

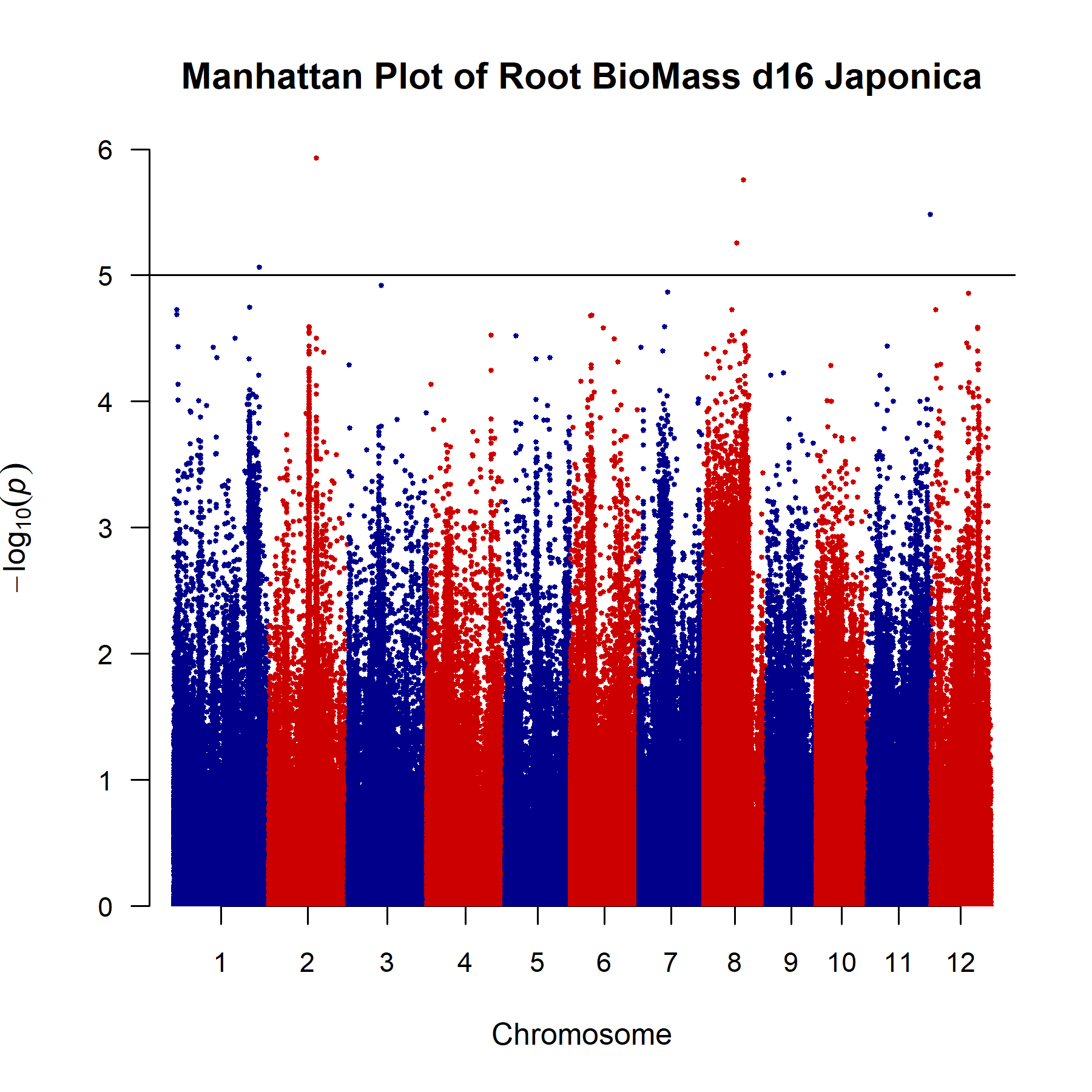
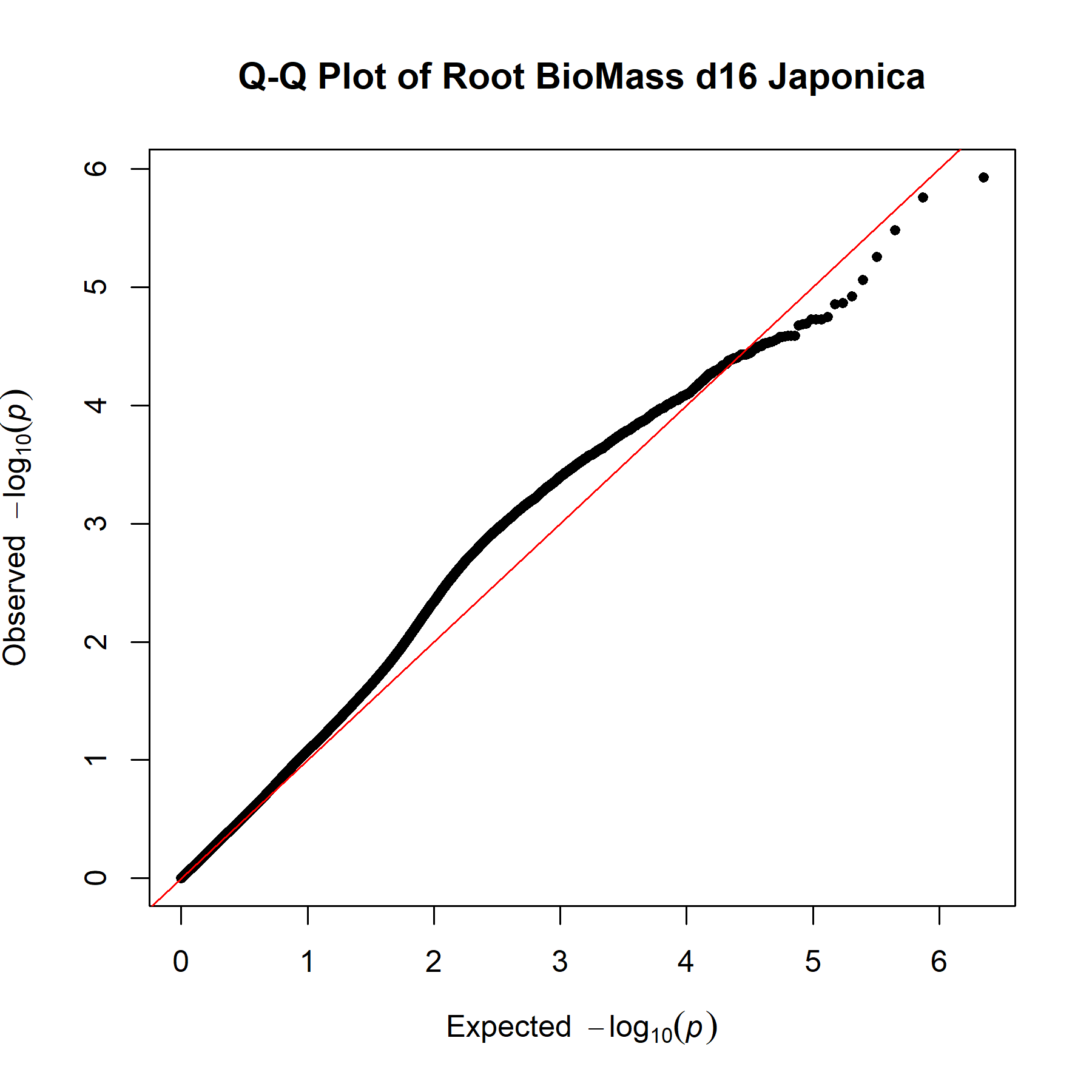
(E). Genome wide analysis of root biomass 16 days after the initiation of salt stress. Fig. 1. Manhattan and quantile-quantile plots are shown for the 6 panels derived from the USDA rice mini core; (All) all 118 accessions used in the study, (IND\_ AUS) is the Indica subspecies composed of the indica and aus subpopulations, (IND) is the indica subpopulation, (AUS) is aus, (JAP) is the Japonica subspecies composed of the temperate and tropical japonica subpopulations and (TRJ) is tropical japonica. The fifth rice subpopulation, Aromatic, was not present in the study. In the Manhattan plots the X axis shows the SNPs position across the 12 rice chromosomes and the Y axis is the –log10 (p) value for each snp. The horizontal black line at –log10(p) = 5 is the significance threshold for SNPs. In the quantile-quantile plots the X axis is the expected SNP distribution and the Y axis displays the –log10(p) observed SNP distribution.

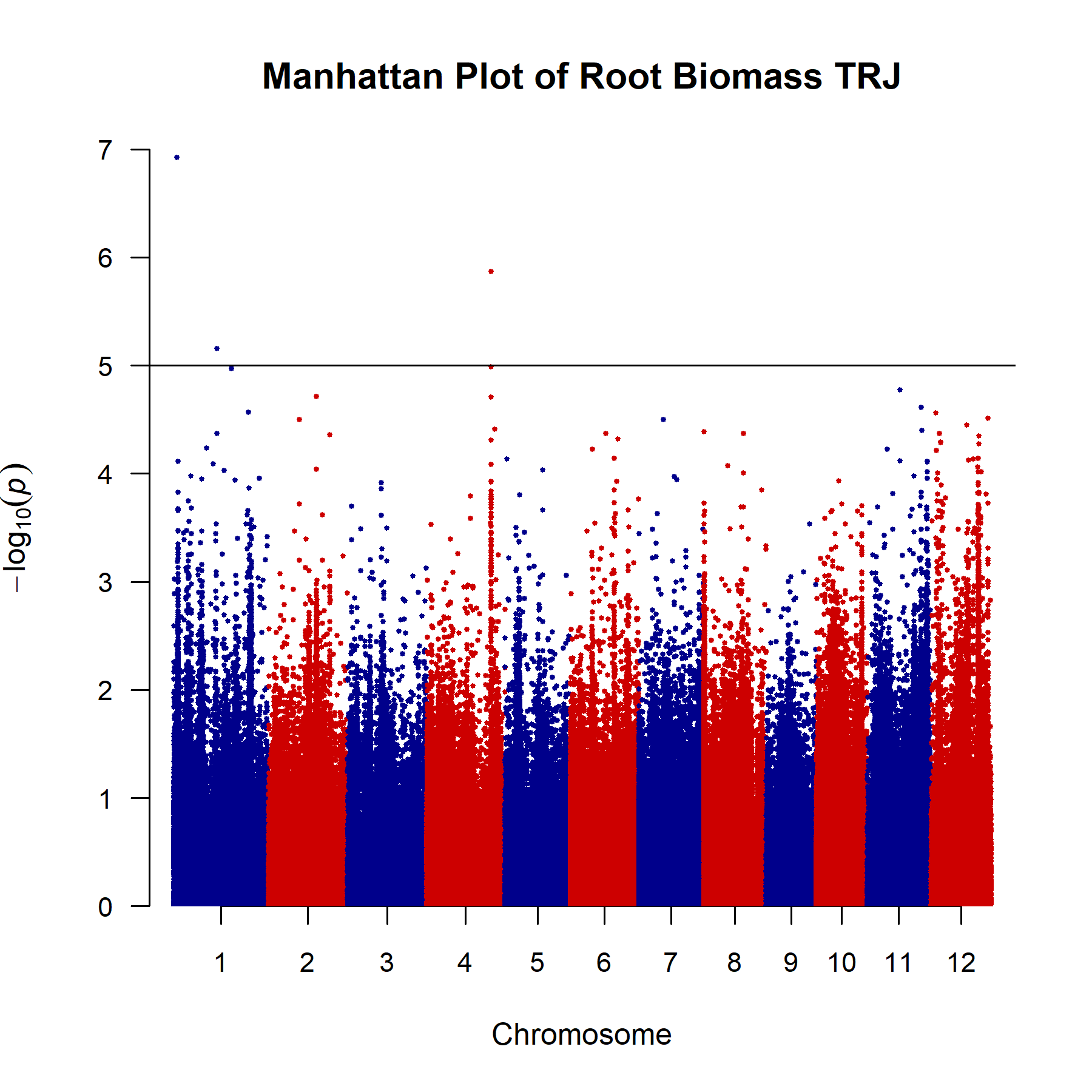
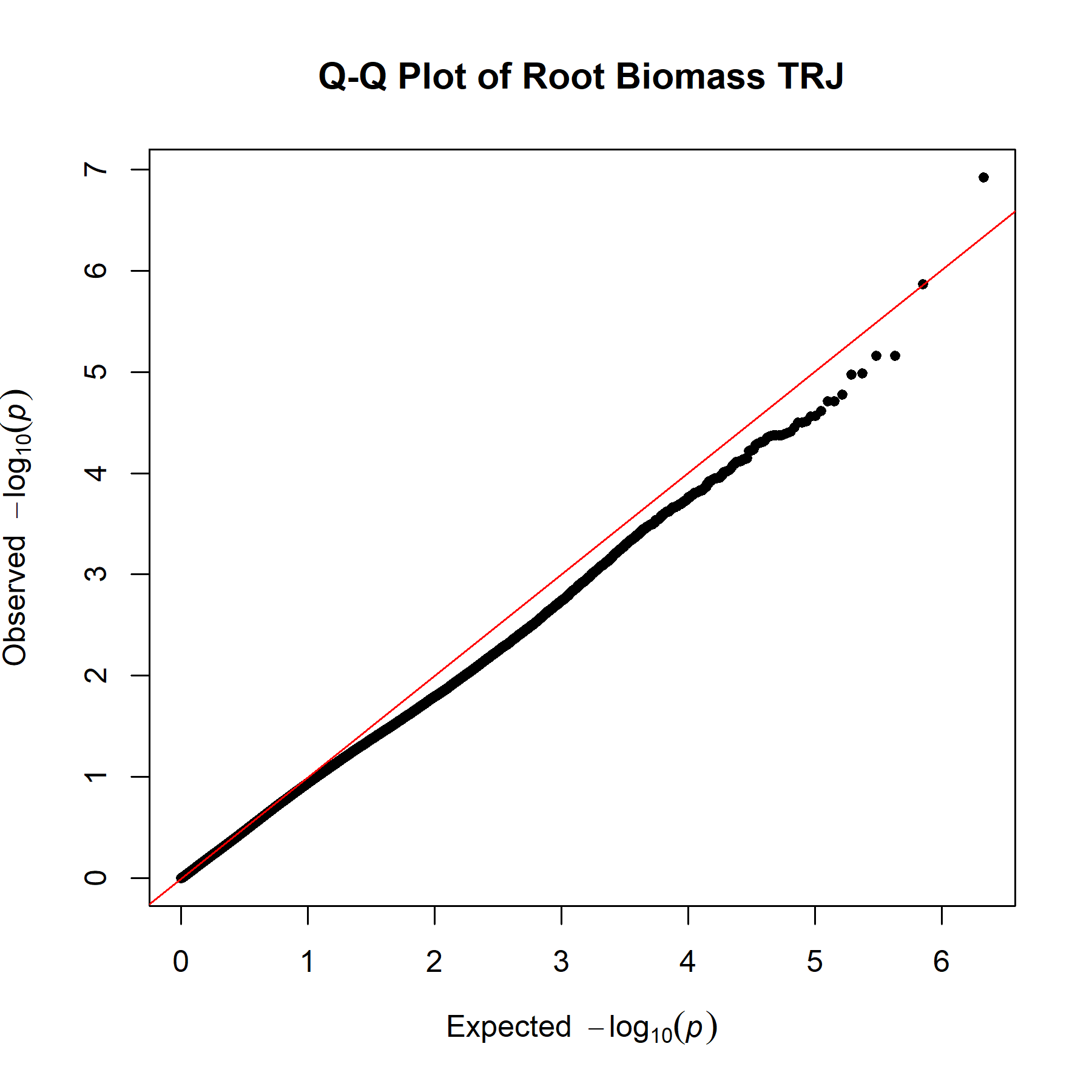
 

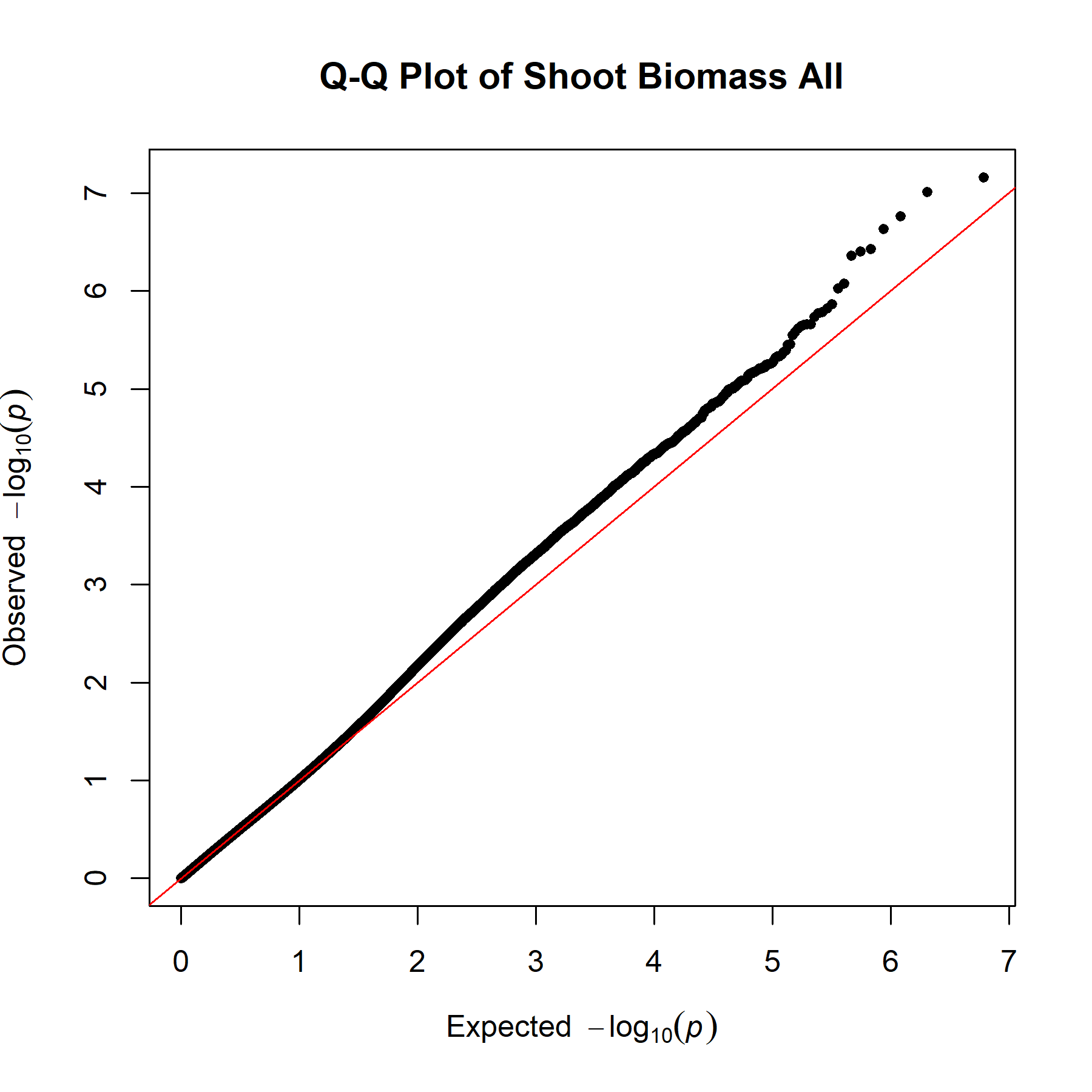
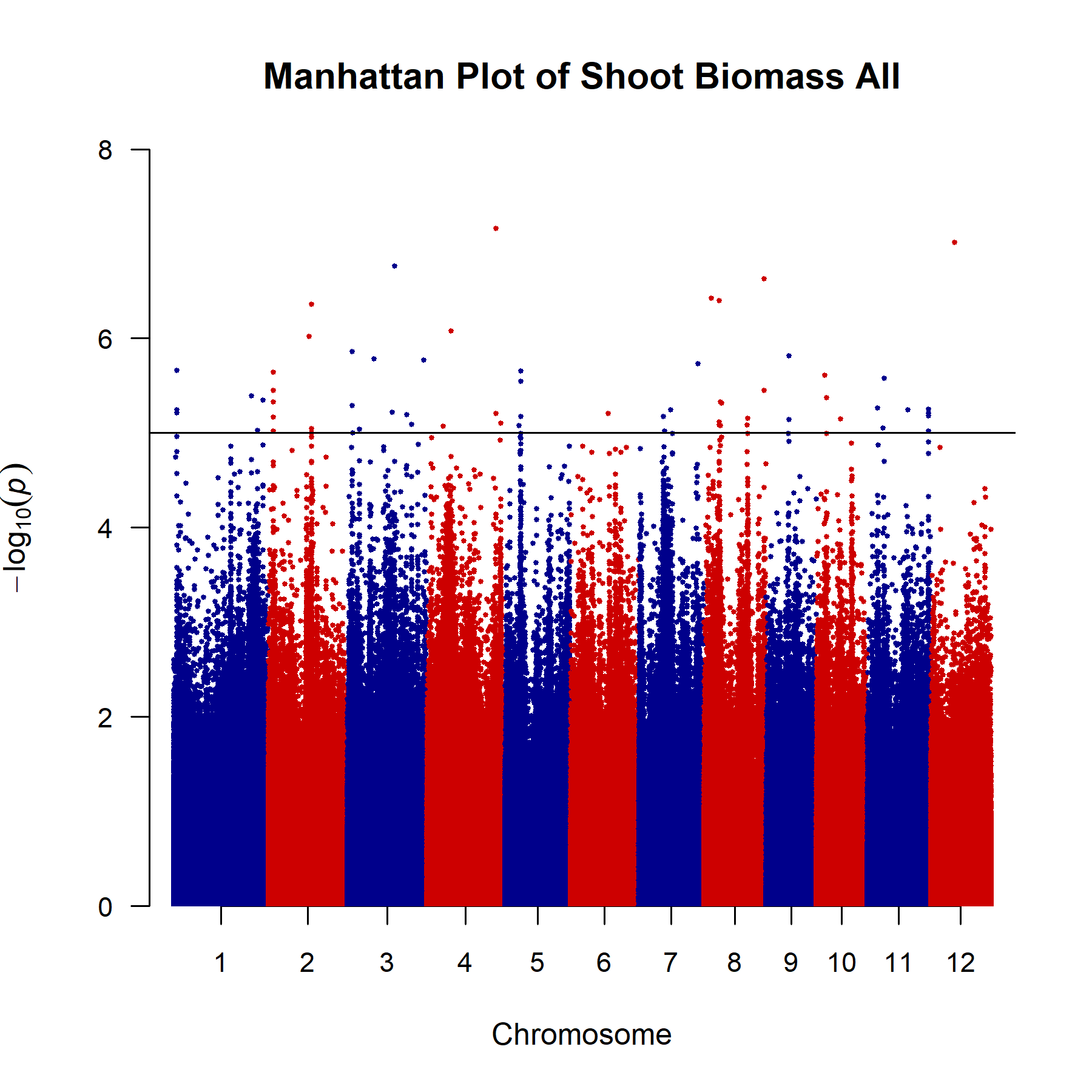
 

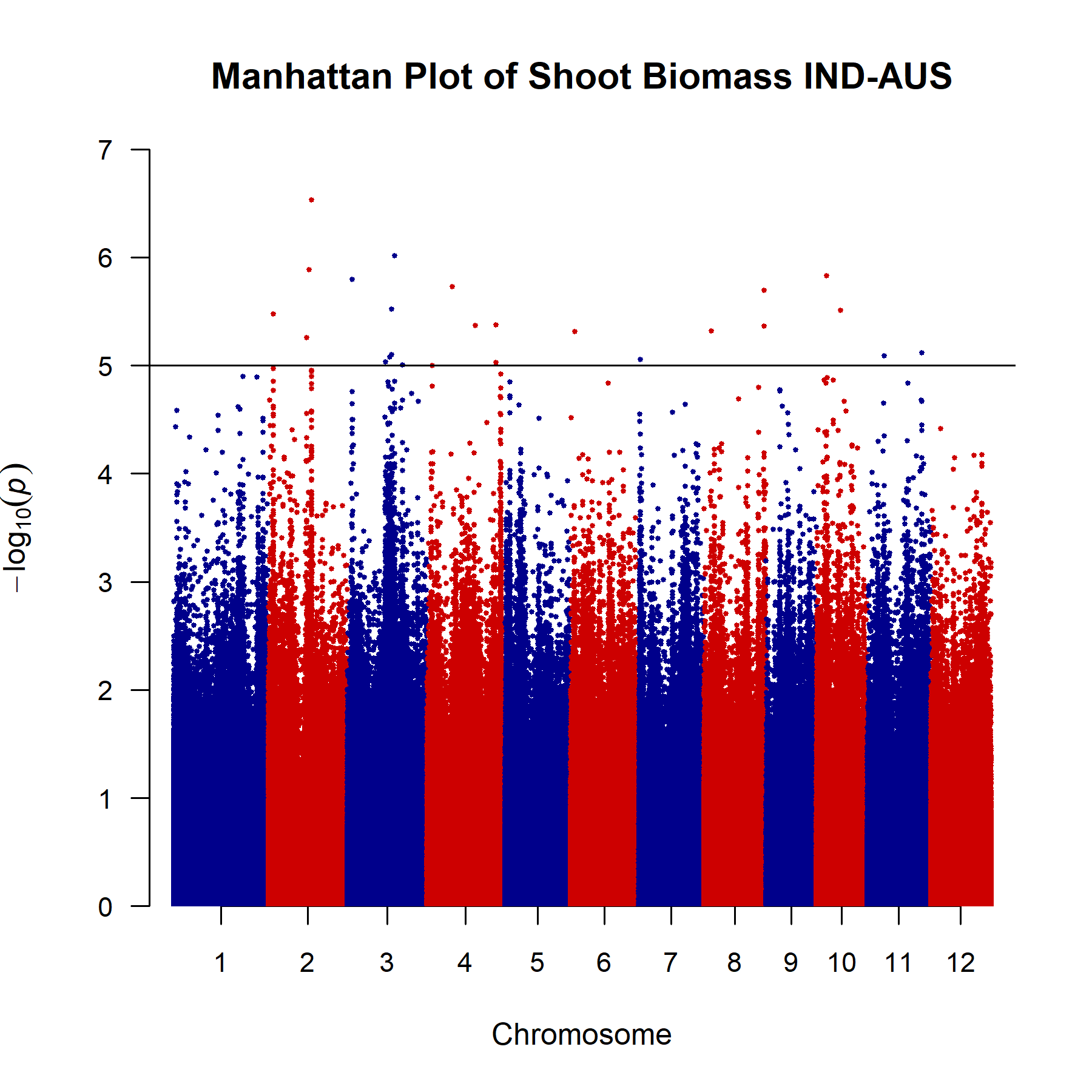
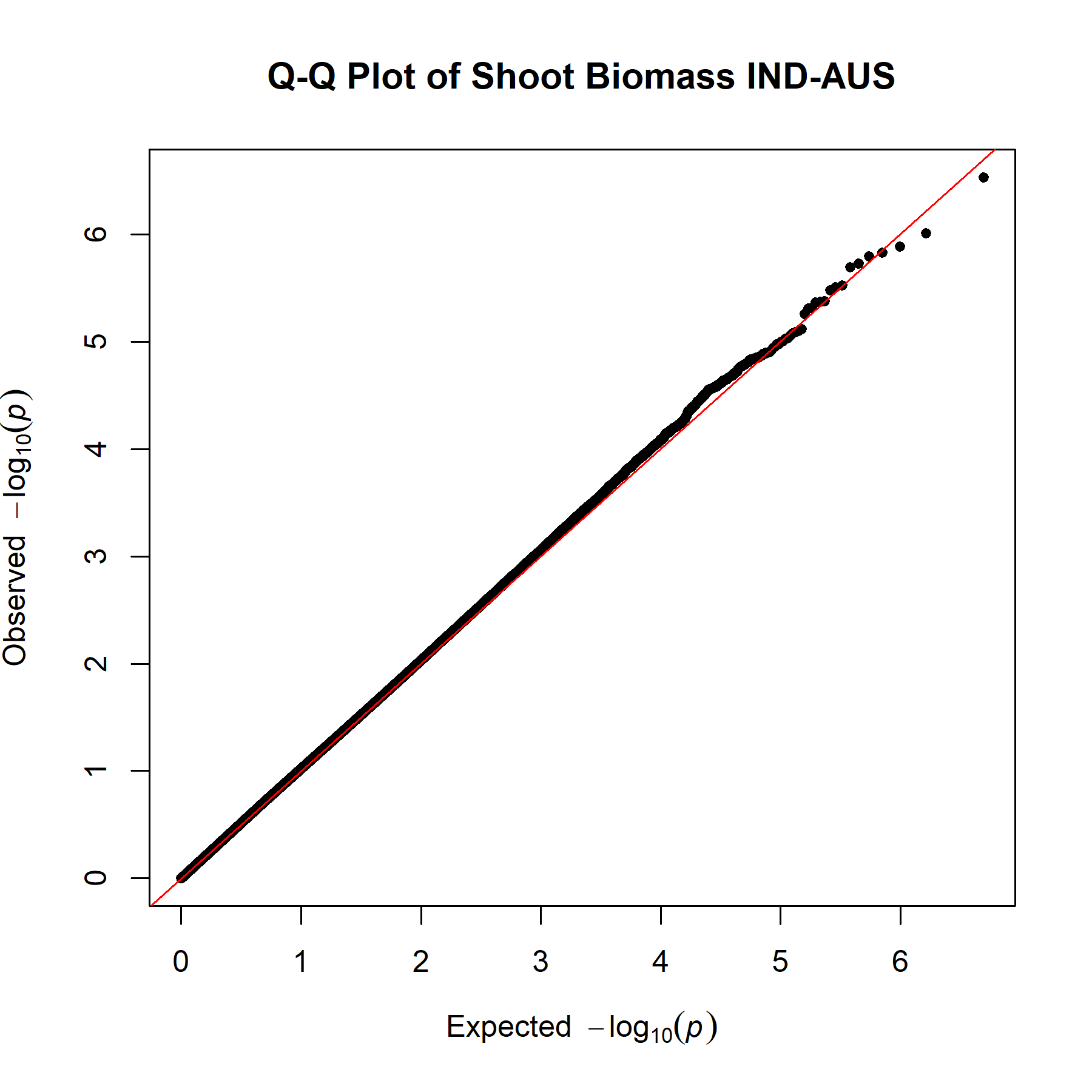
 

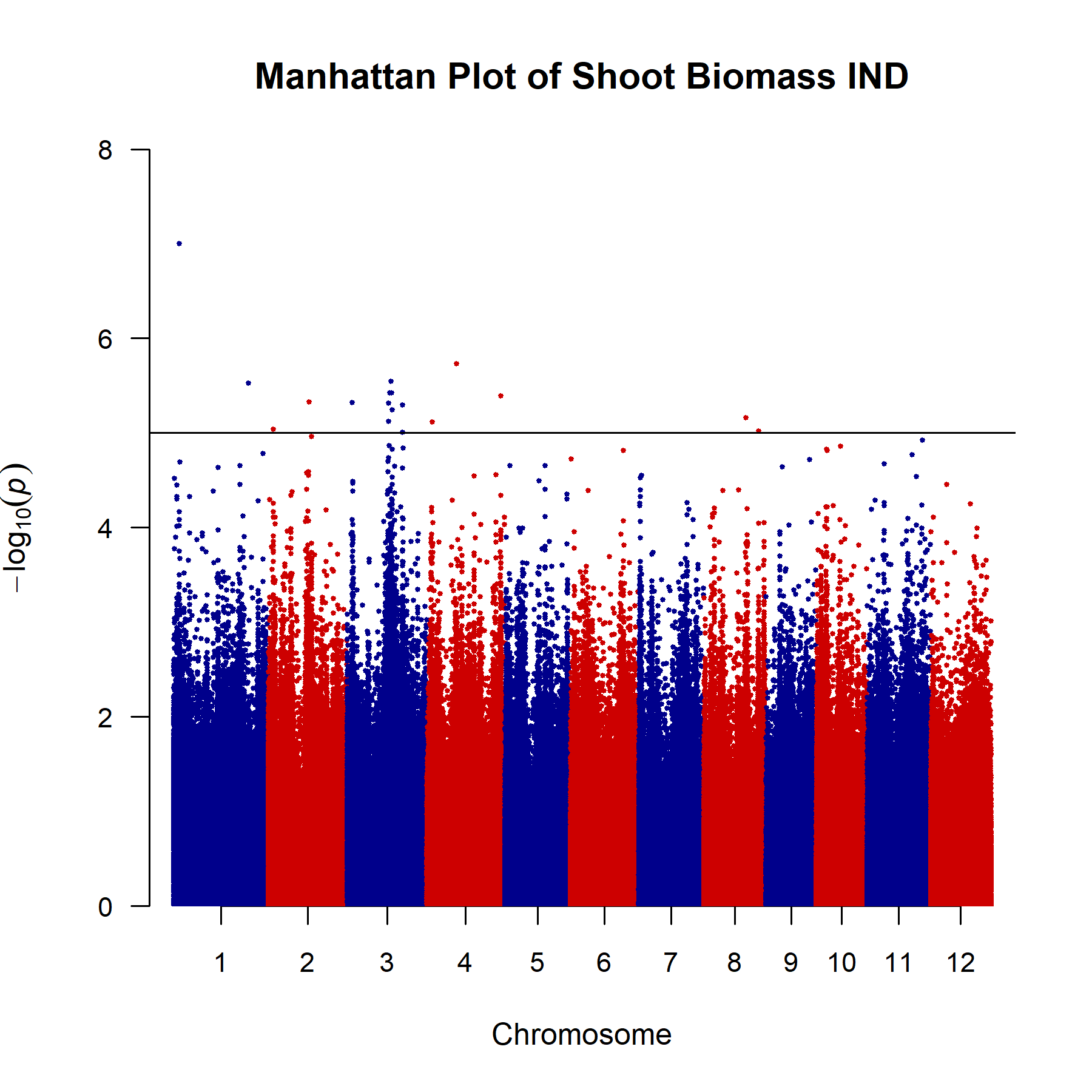
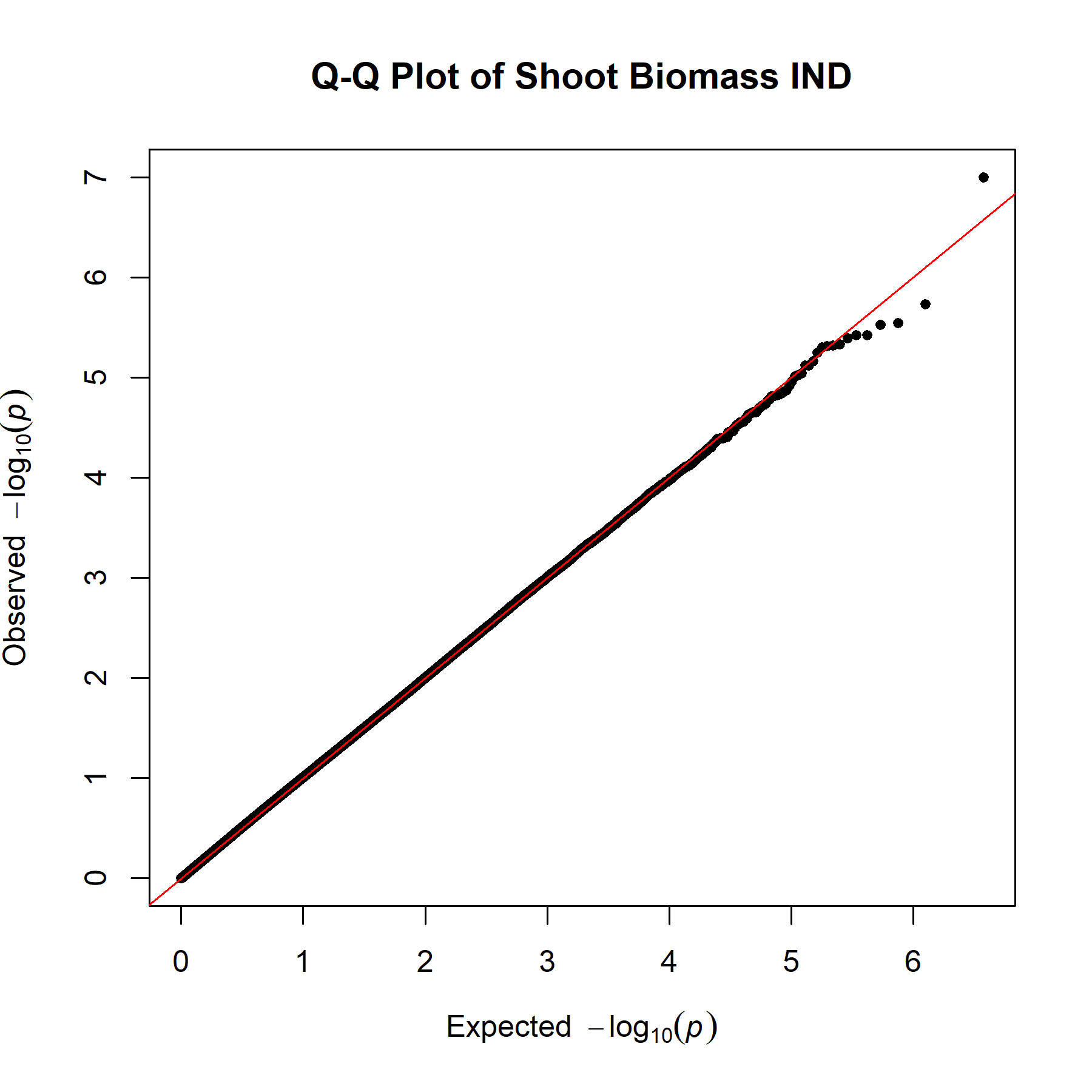
 

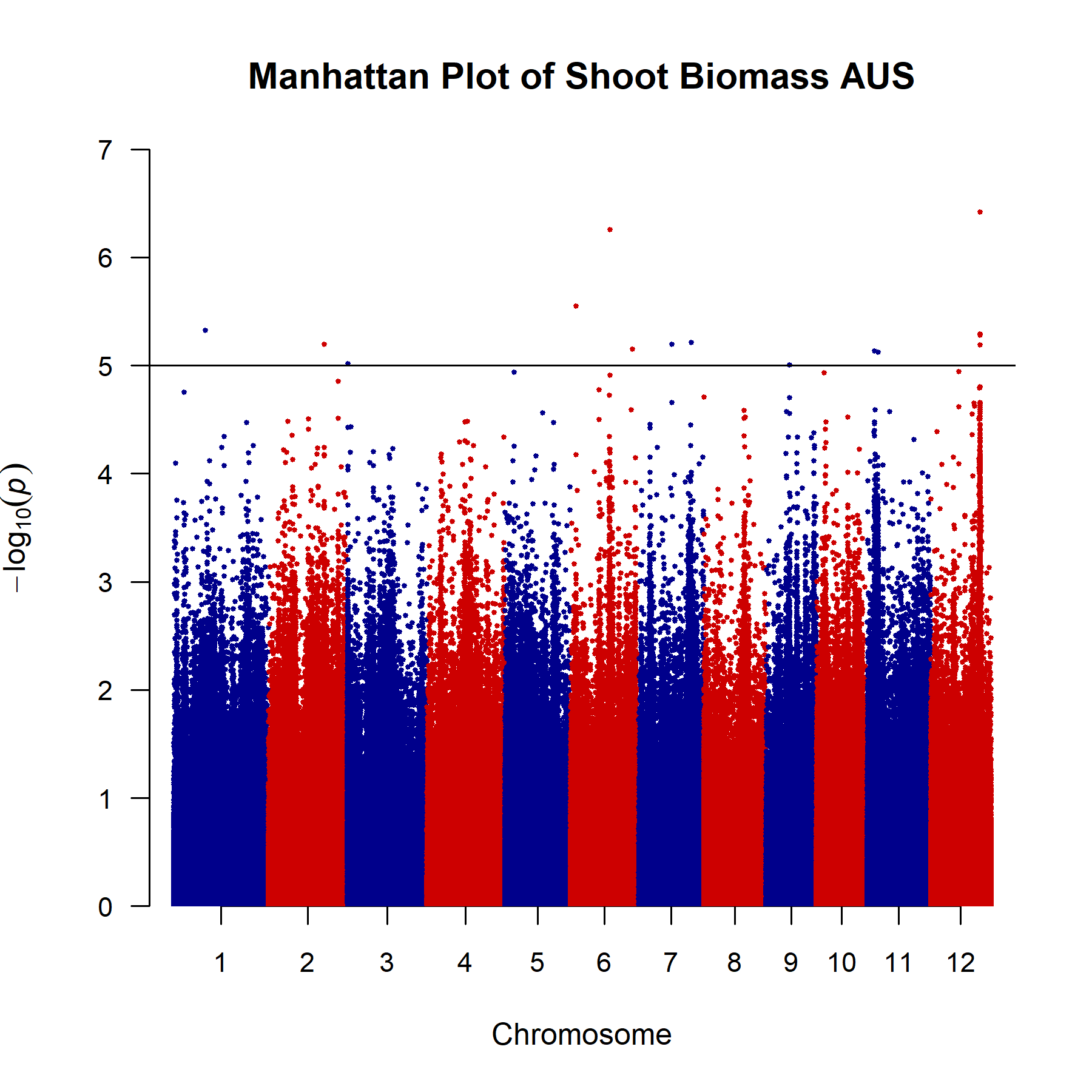
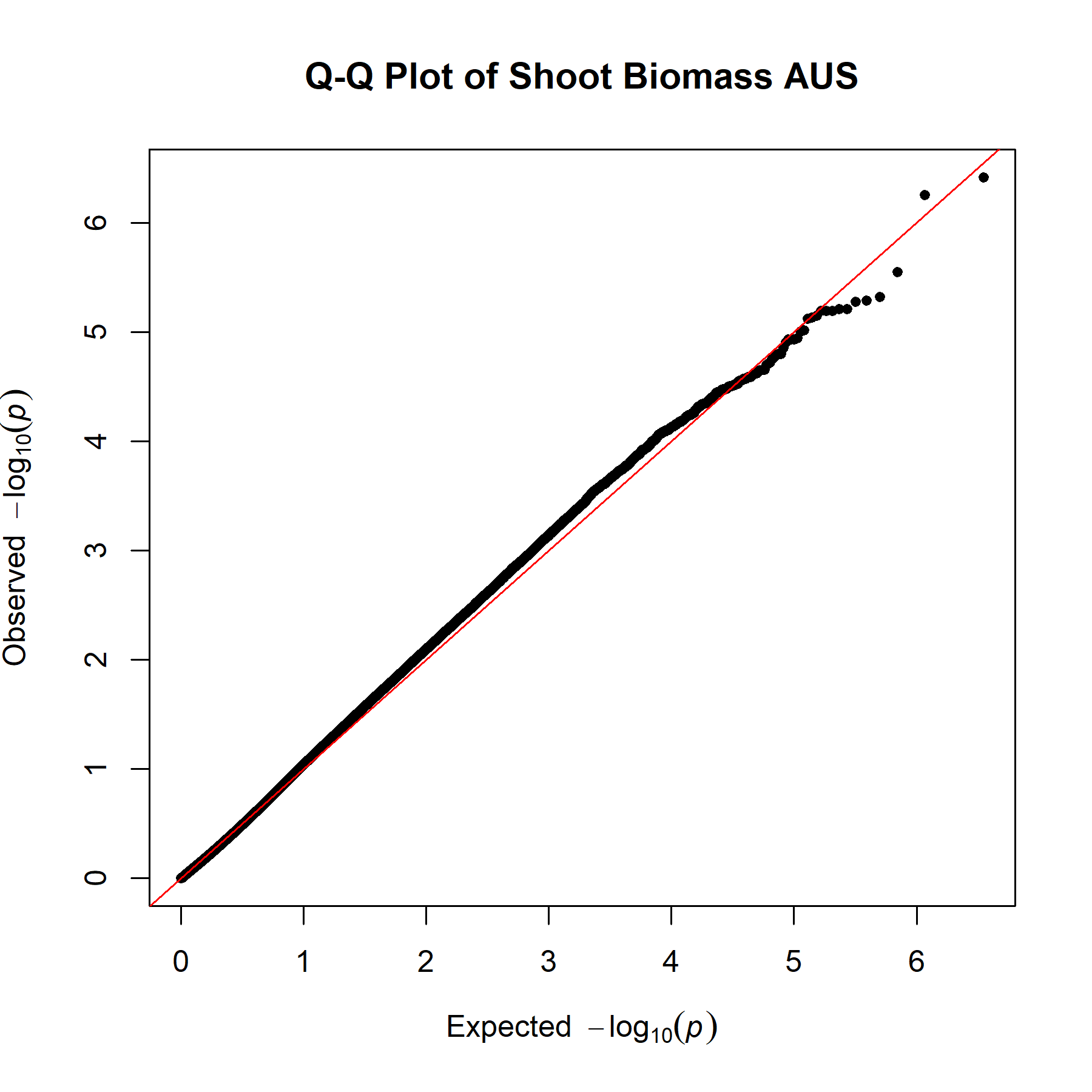
 

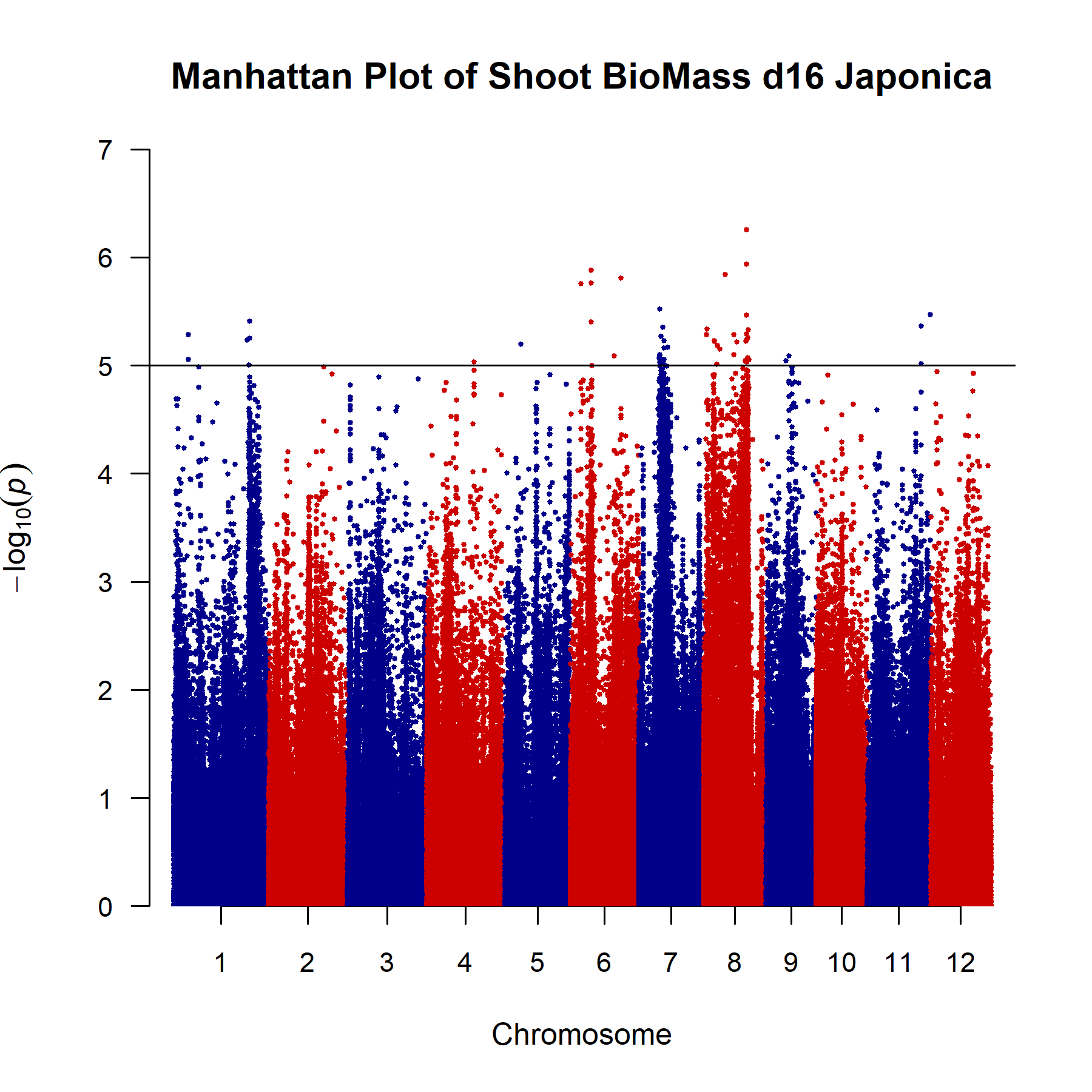
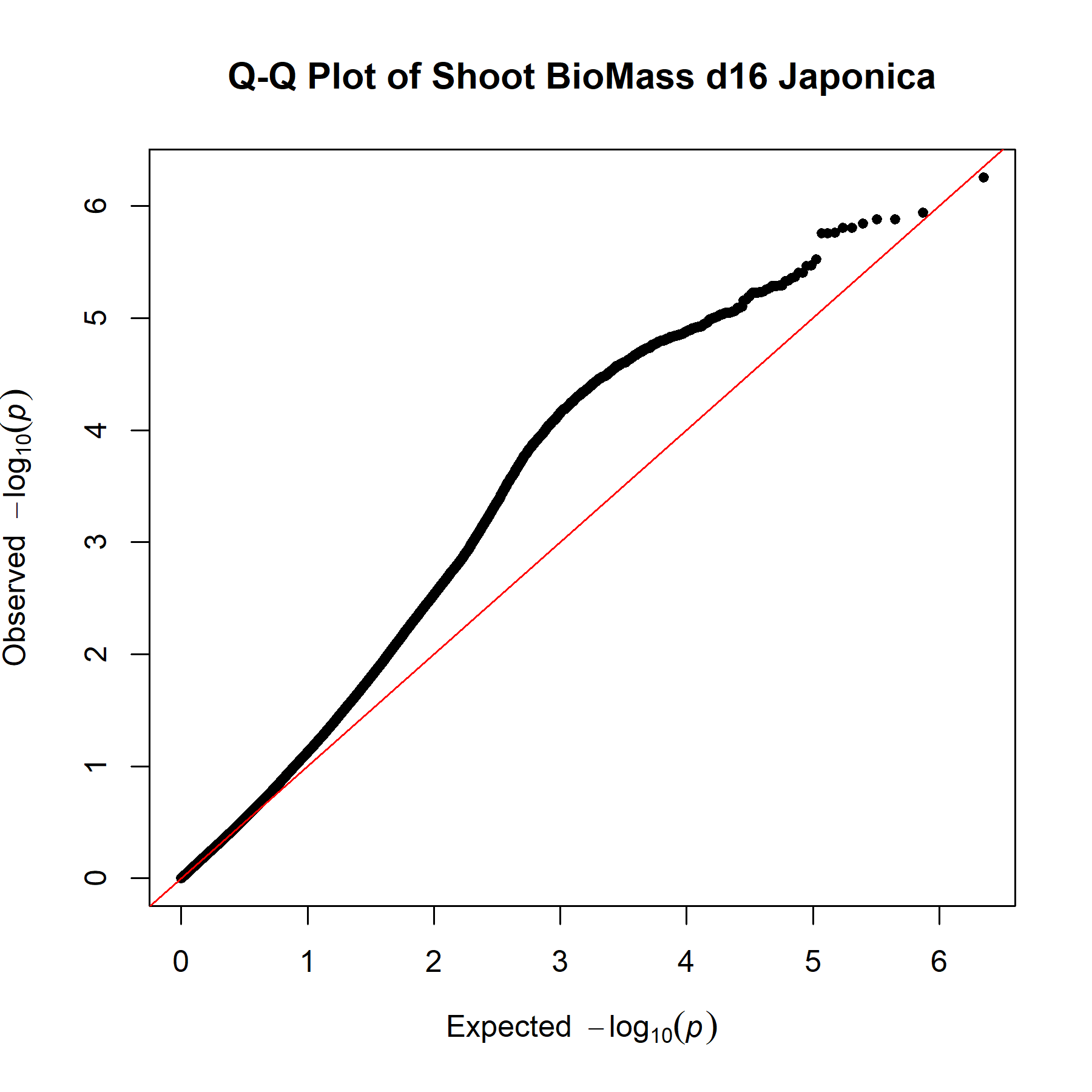
(F). Genome wide analysis of shoot biomass 16 days after the initiation of salt stress. Fig. 1. Manhattan and quantile-quantile plots are shown for the 6 panels derived from the USDA rice mini core; (All) all 118 accessions used in the study, (IND\_ AUS) is the Indica subspecies composed of the indica and aus subpopulations, (IND) is the indica subpopulation, (AUS) is aus, (JAP) is the Japonica subspecies composed of the temperate and tropical japonica subpopulations and (TRJ) is tropical japonica. The fifth rice subpopulation, Aromatic, was not present in the study. In the Manhattan plots the X axis shows the SNPs position across the 12 rice chromosomes and the Y axis is the –log10 (p) value for each snp. The horizontal black line at –log10(p) = 5 is the significance threshold for SNPs. In the quantile-quantile plots the X axis is the expected SNP distribution and the Y axis displays the –log10(p) observed SNP distribution.

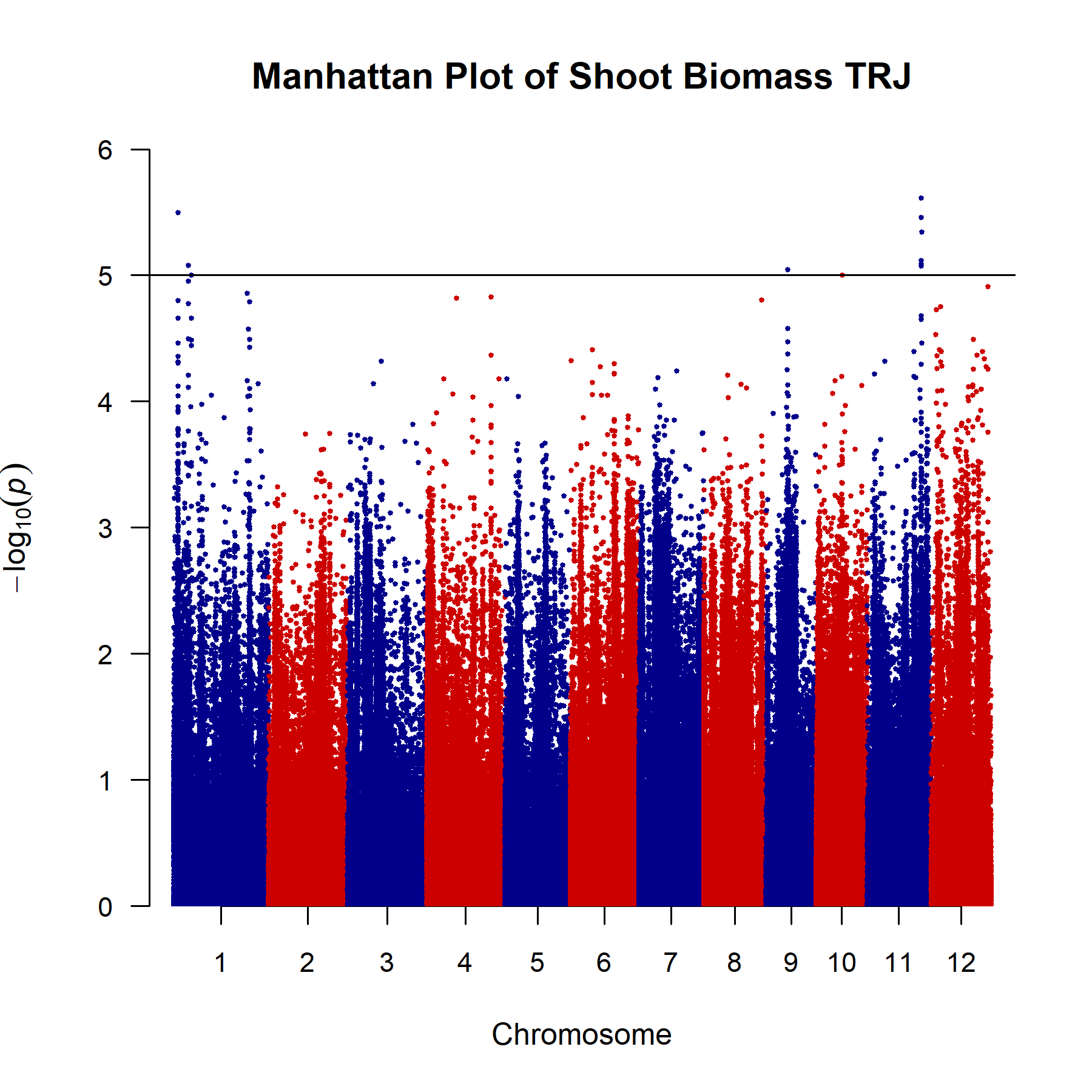
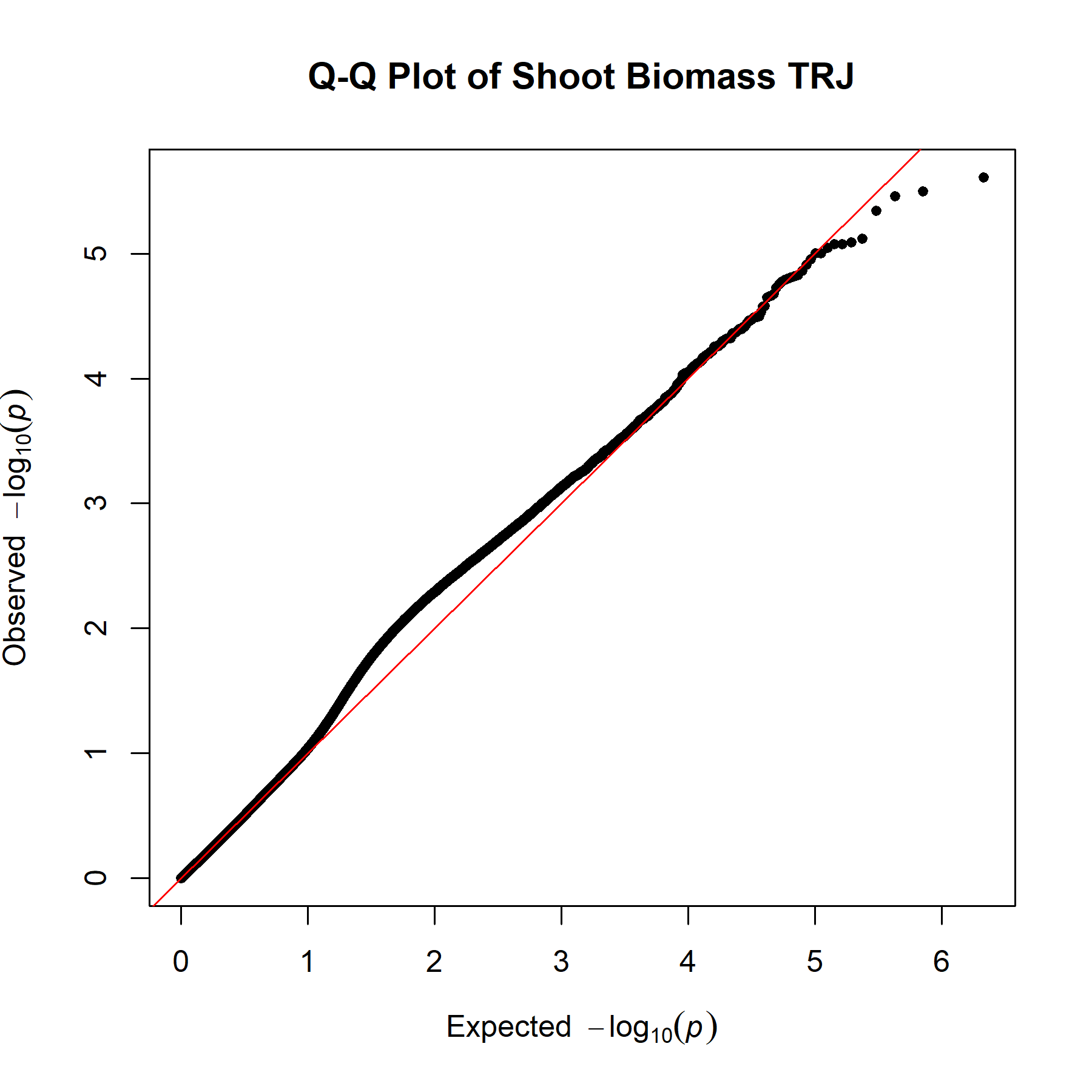


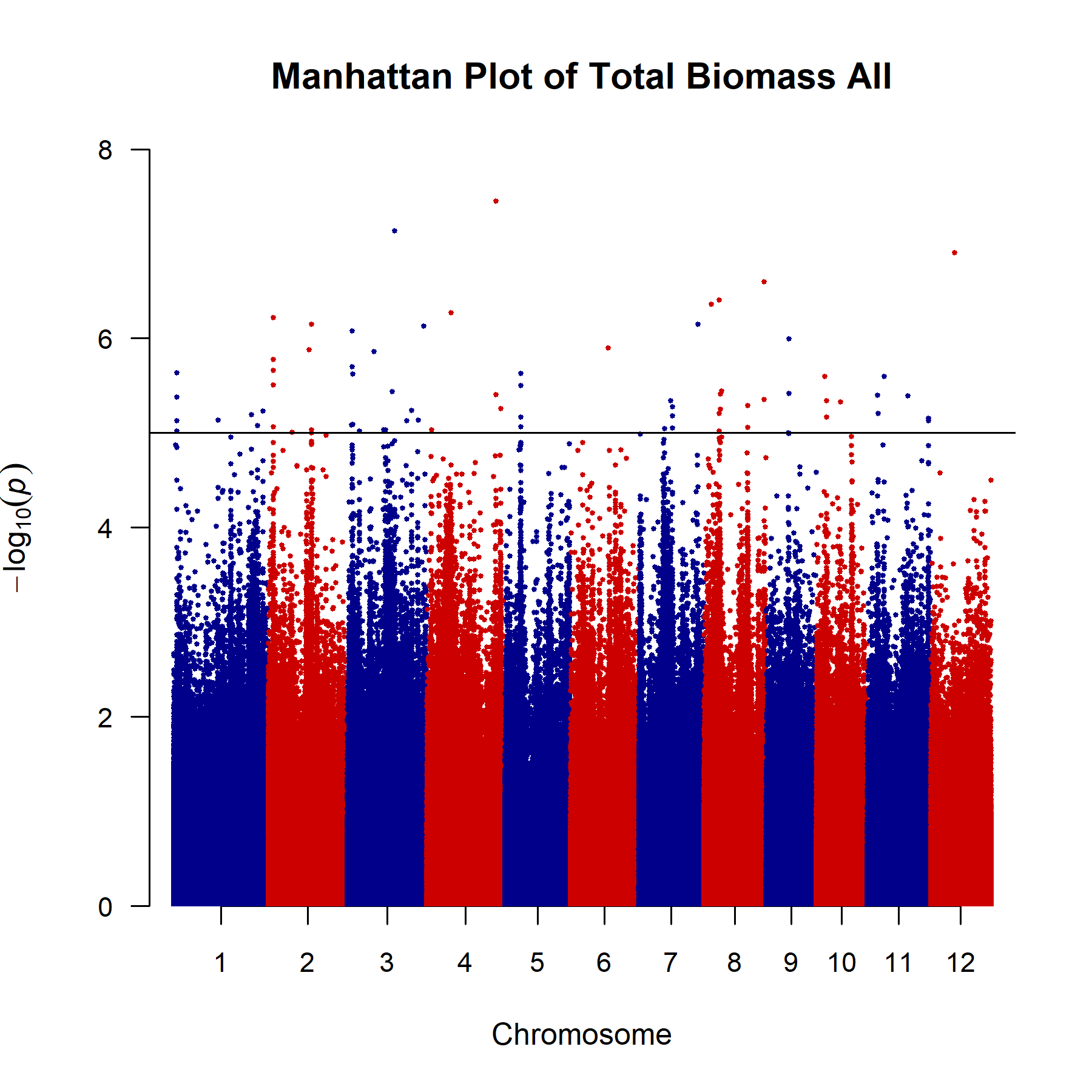
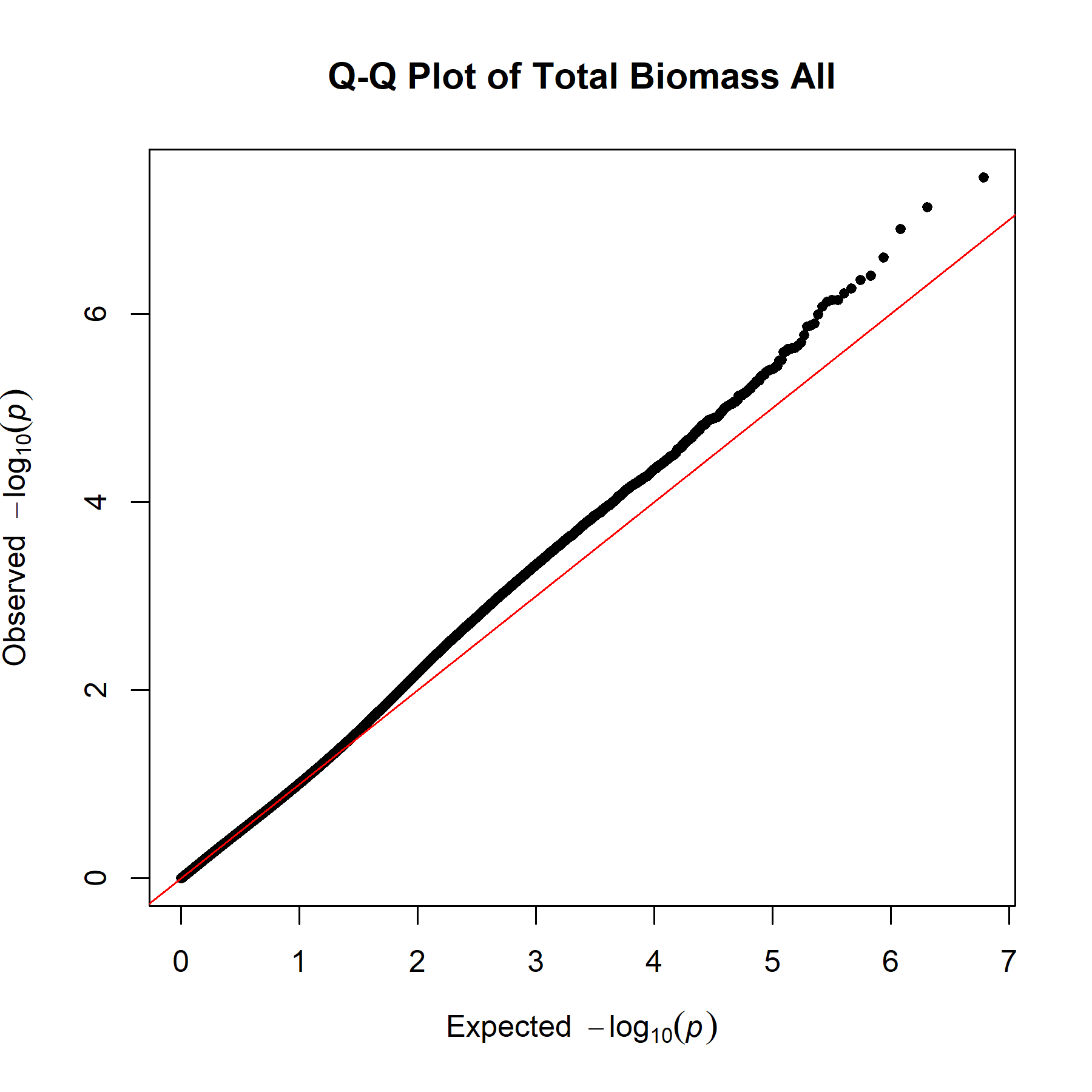
 

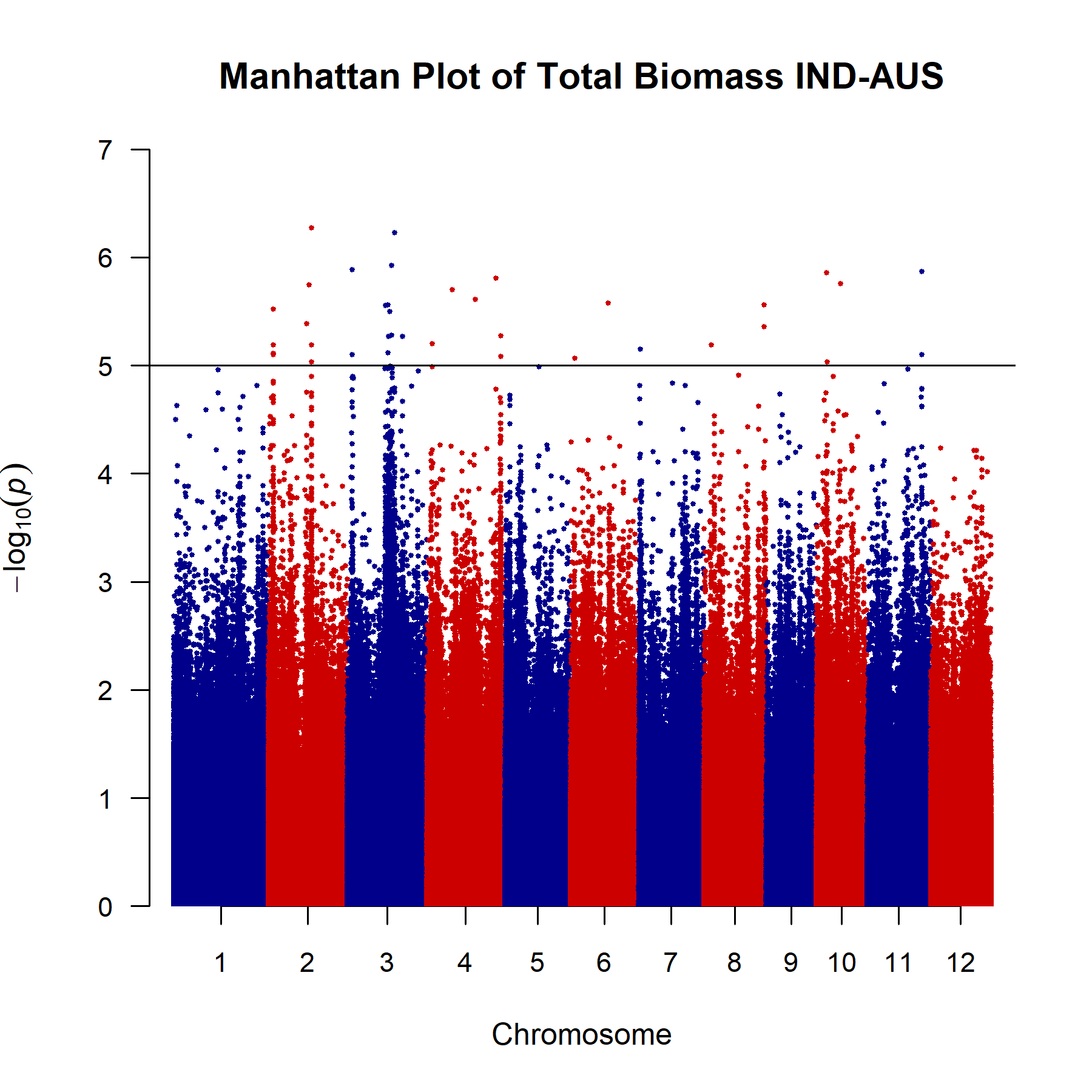
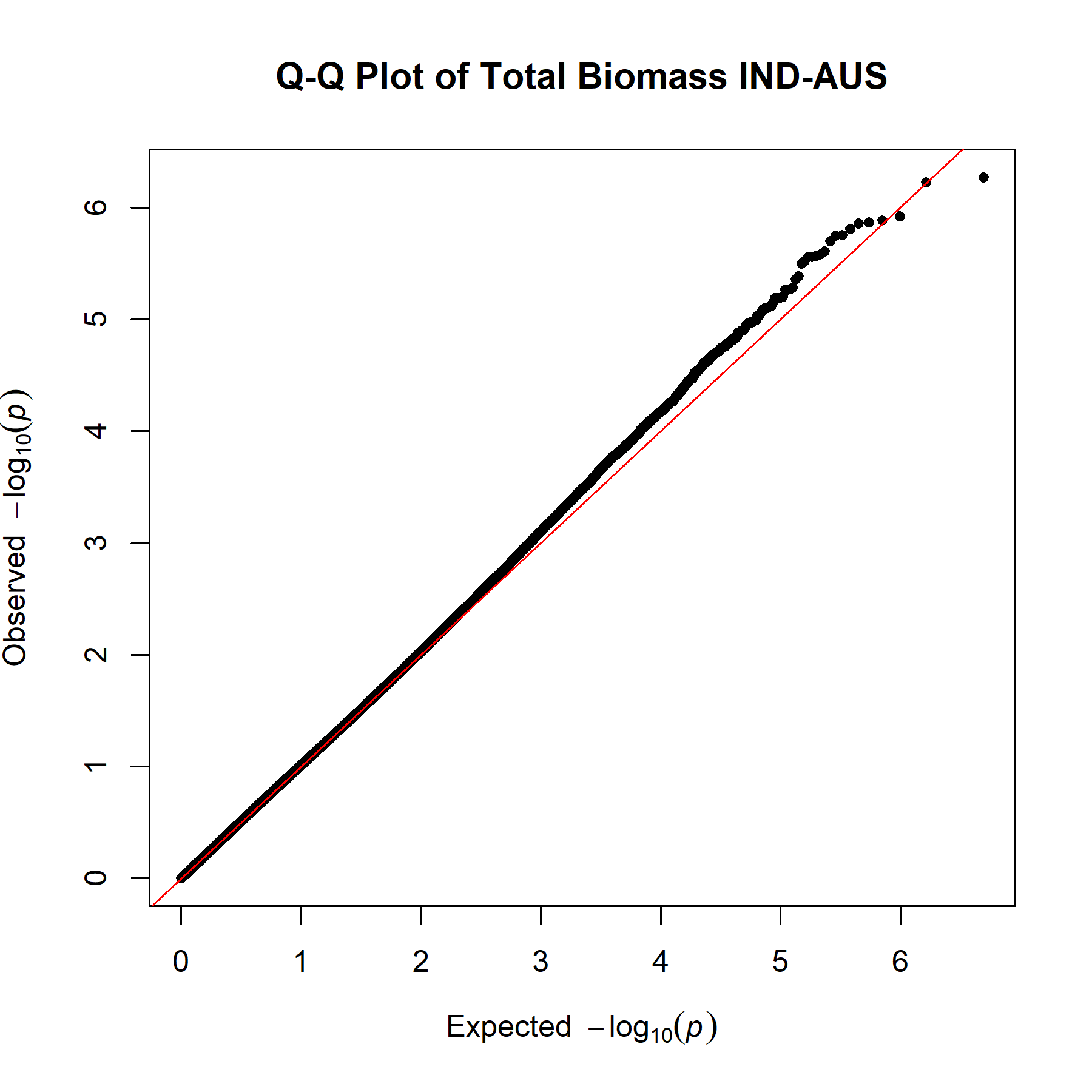
 

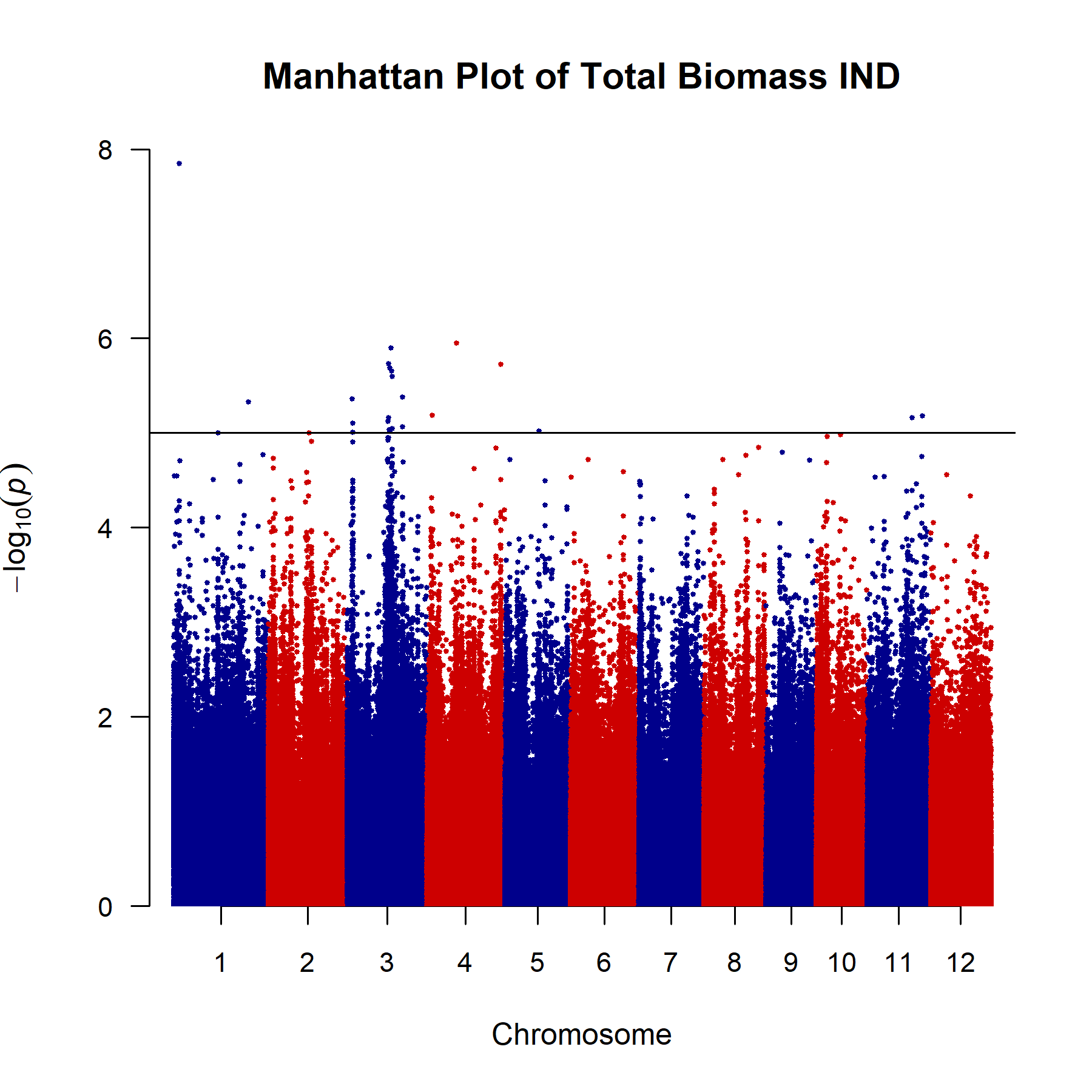
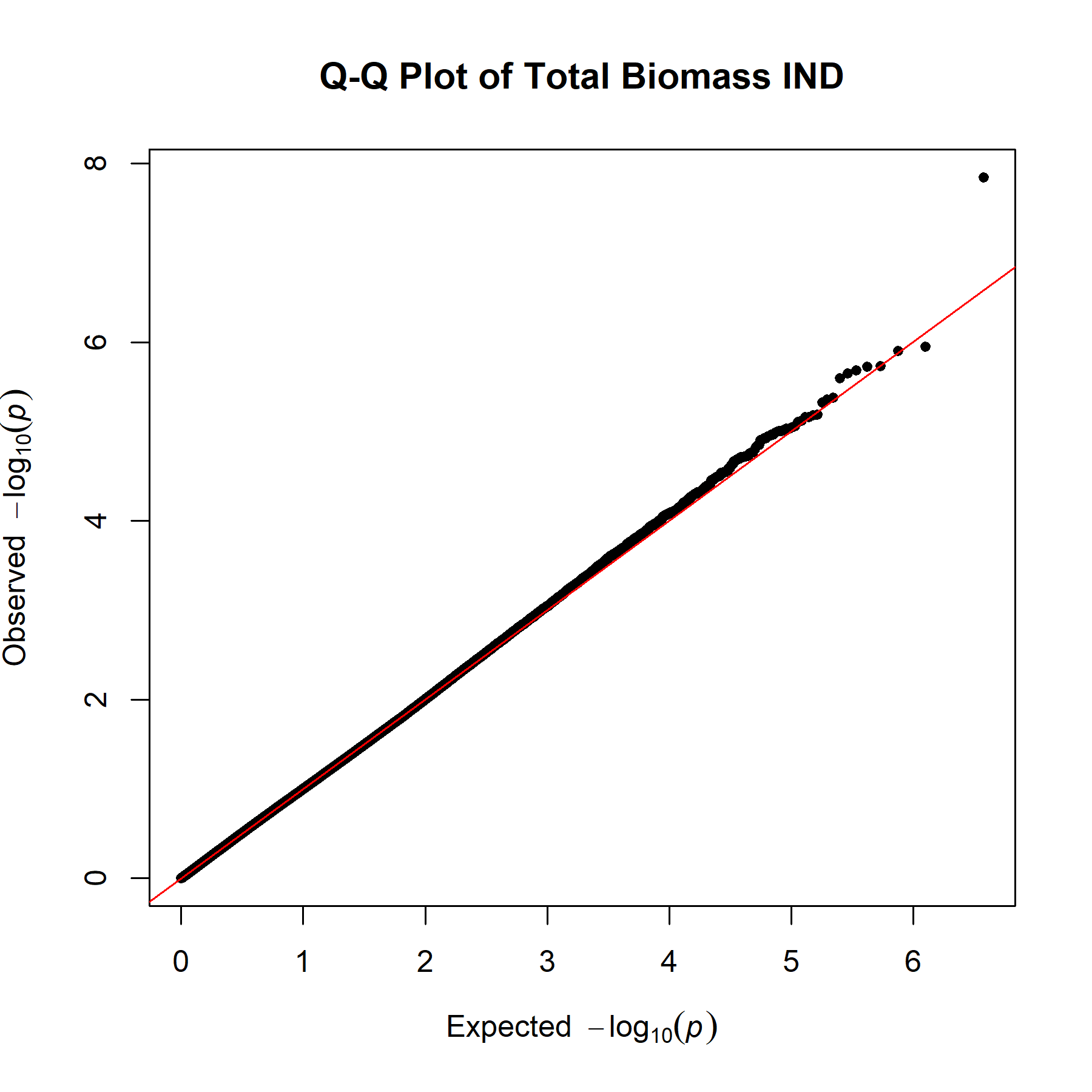
 

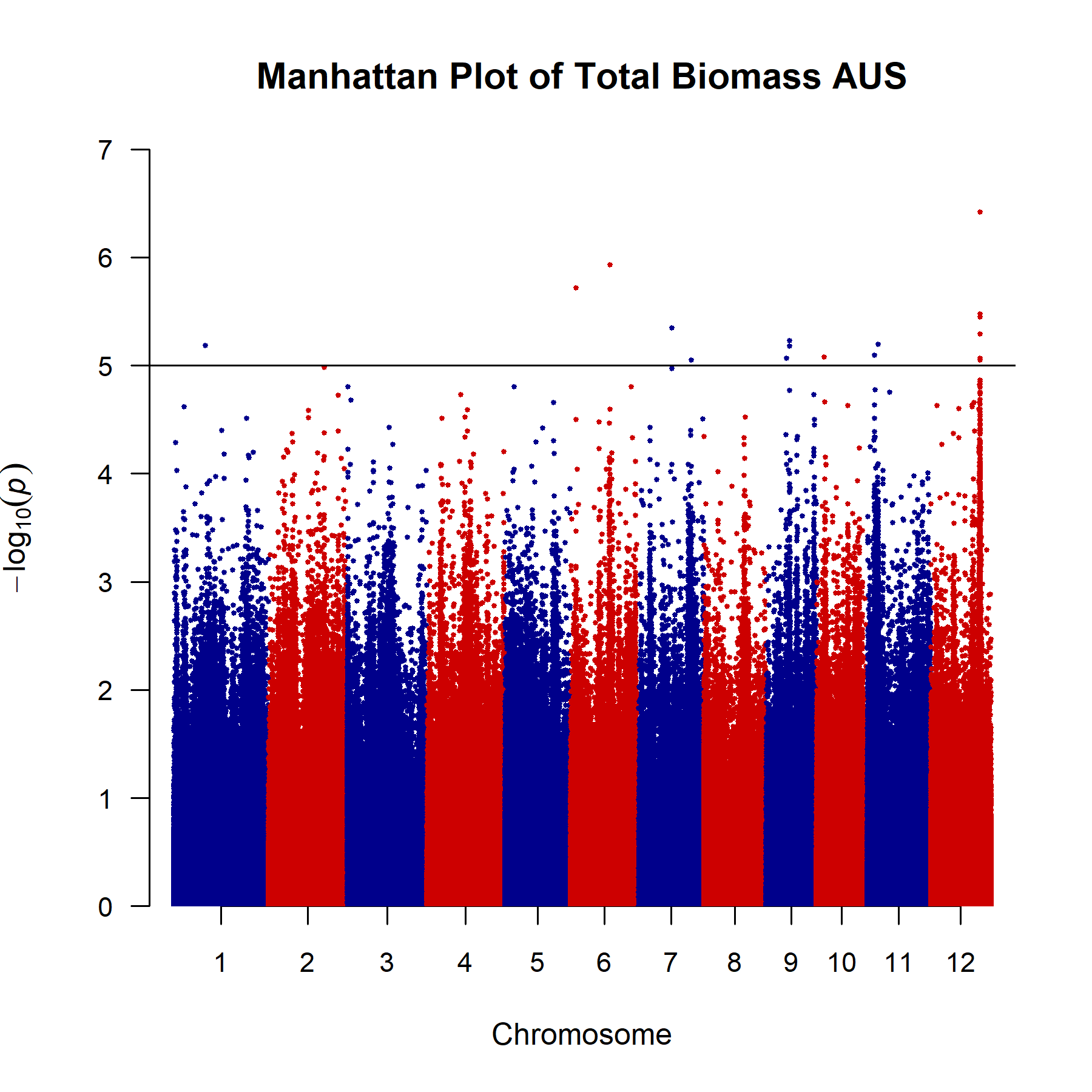
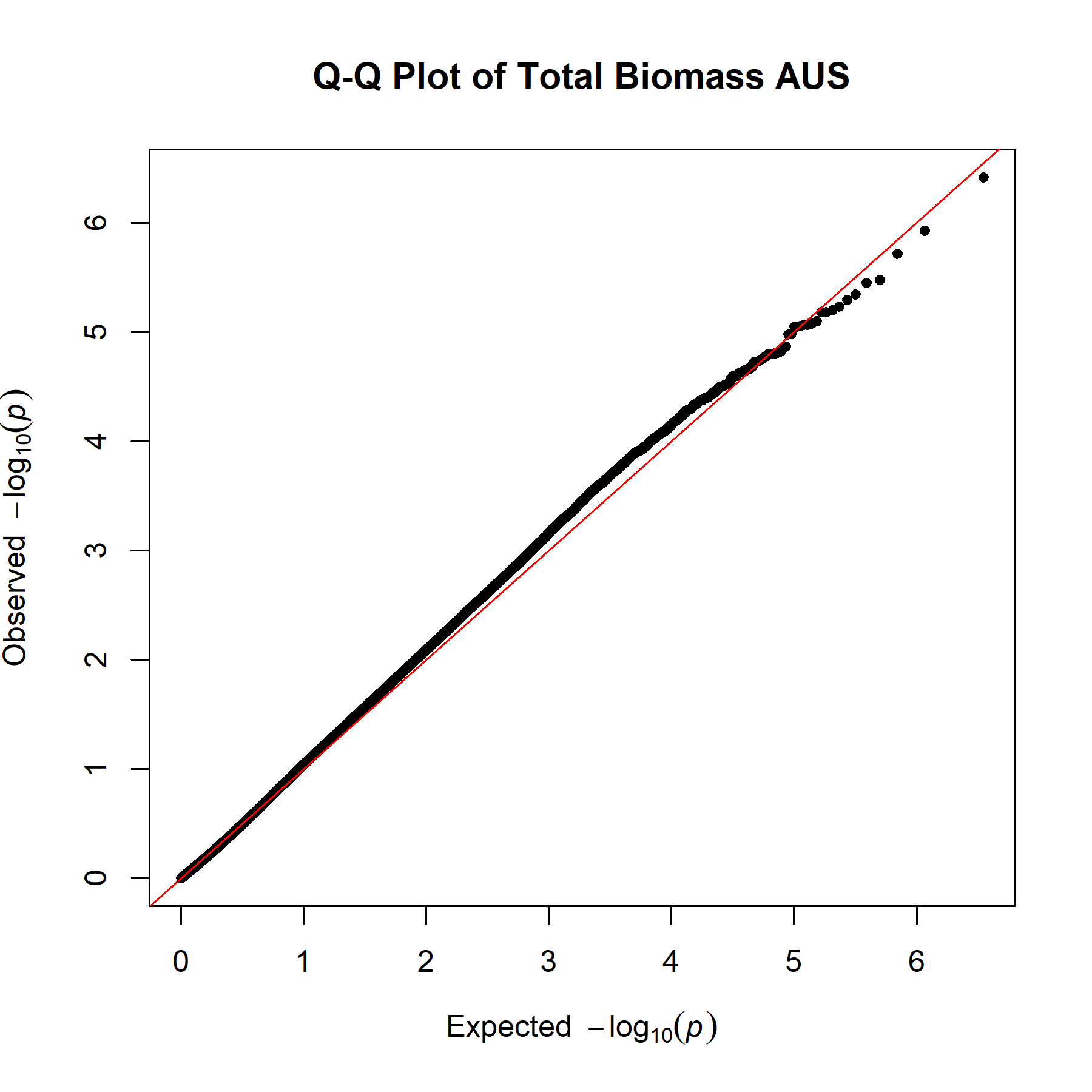
 

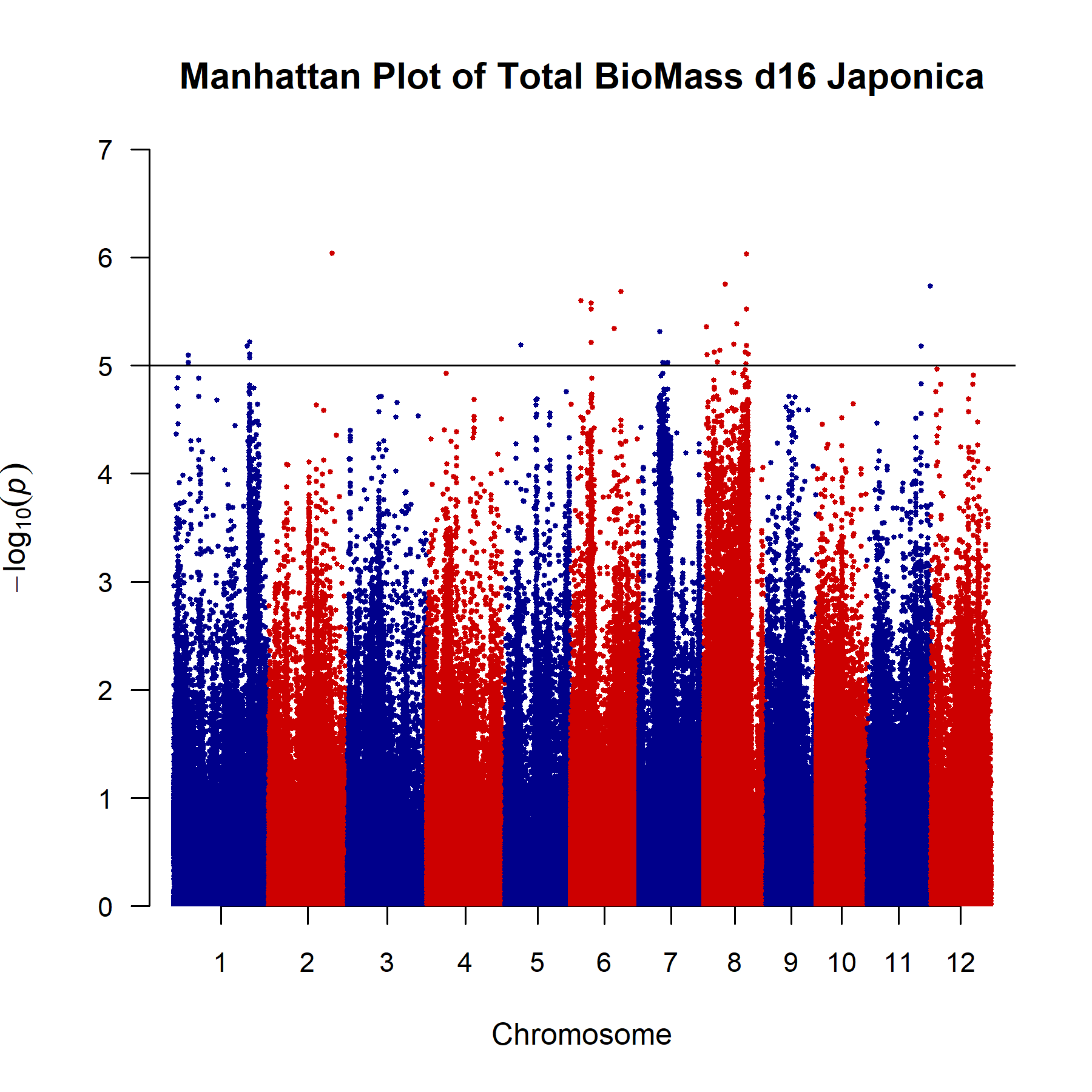
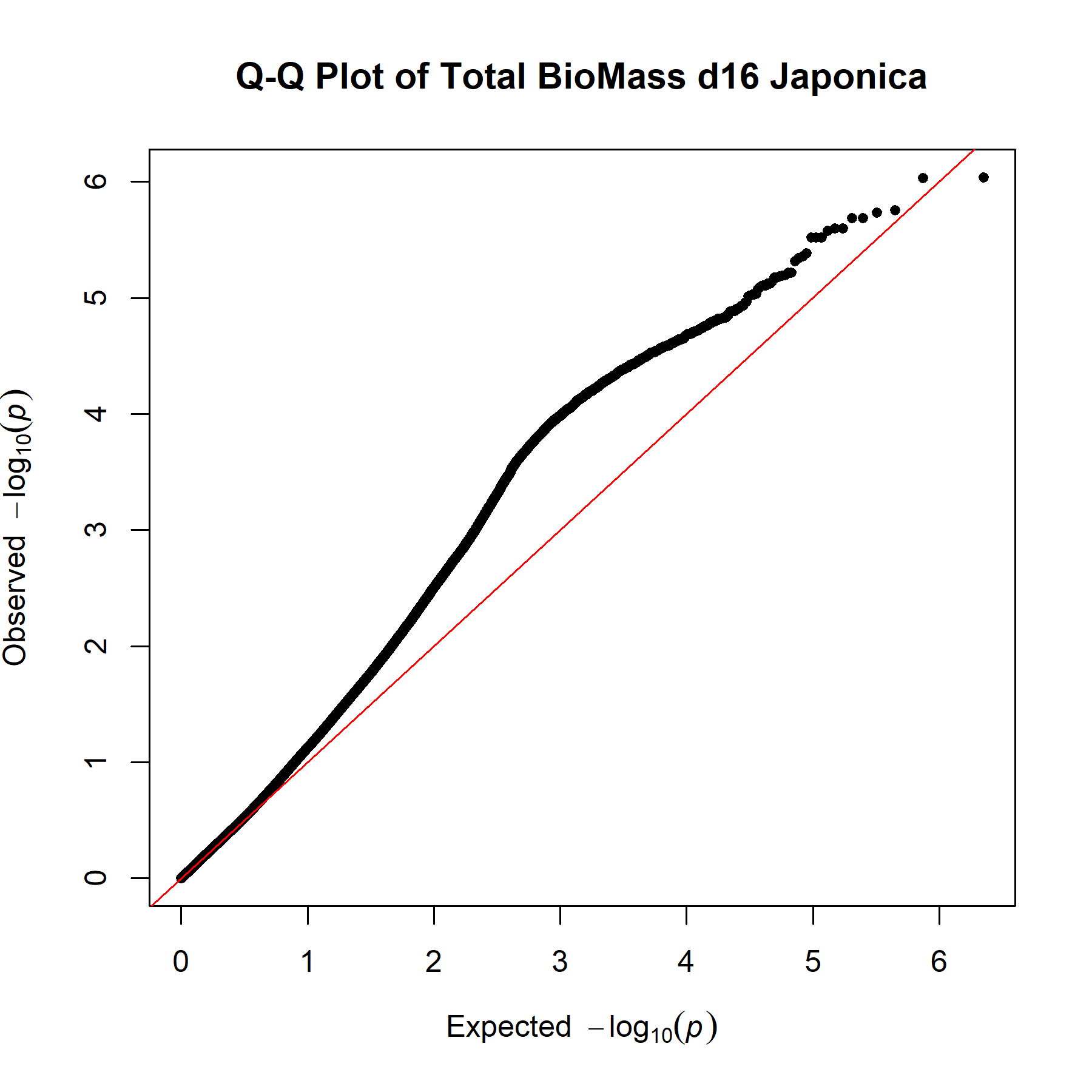
(G). Genome wide analysis of total (shoot and root) biomass 16 days after the initiation of salt stress. Fig. 1. Manhattan and quantile-quantile plots are shown for the 6 panels derived from the USDA rice mini core; (All) all 118 accessions used in the study, (IND\_ AUS) is the Indica subspecies composed of the indica and aus subpopulations, (IND) is the indica subpopulation, (AUS) is aus, (JAP) is the Japonica subspecies composed of the temperate and tropical japonica subpopulations and (TRJ) is tropical japonica. The fifth rice subpopulation, Aromatic, was not present in the study. In the Manhattan plots the X axis shows the SNPs position across the 12 rice chromosomes and the Y axis is the –log10 (p) value for each snp. The horizontal black line at –log10(p) = 5 is the significance threshold for SNPs. In the quantile-quantile plots the X axis is the expected SNP distribution and the Y axis displays the –log10(p) observed SNP distribution.

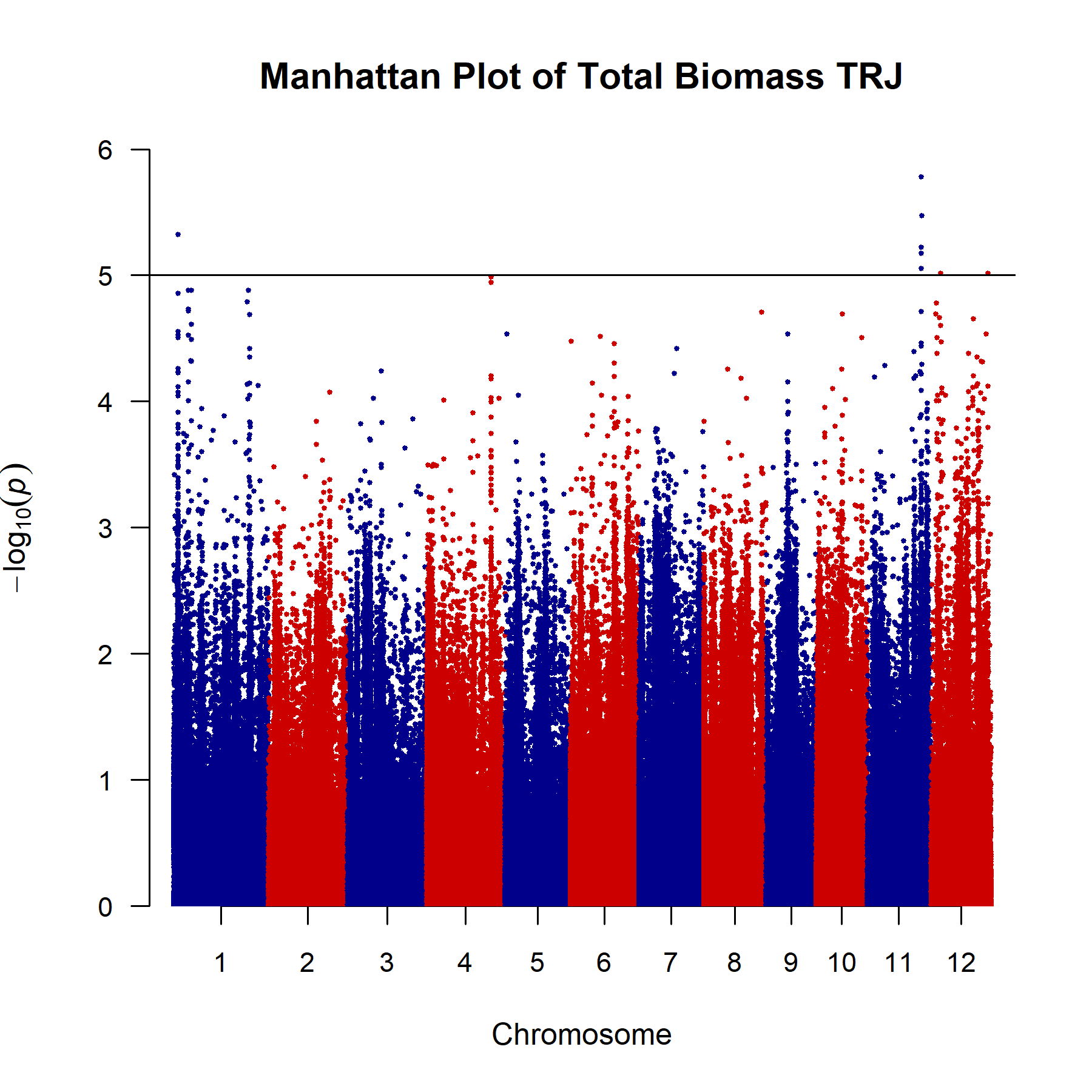
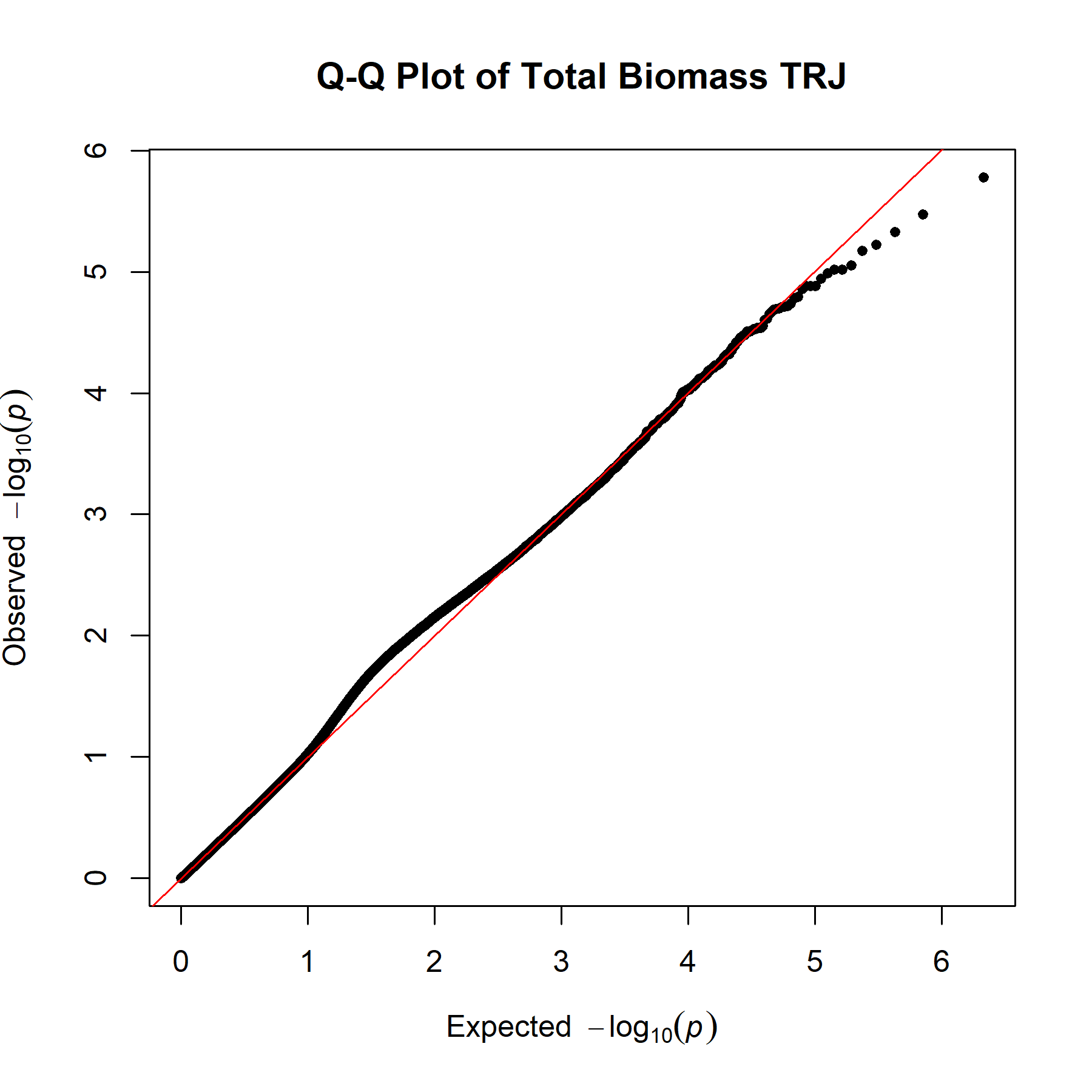
 

(H). Genome wide analysis of the change in green leaf number 14 days after the initiation of salt stress. Fig. 1. Manhattan and quantile-quantile plots are shown for the 6 panels derived from the USDA rice mini core; (All) all 118 accessions used in the study, (IND\_ AUS) is the Indica subspecies composed of the indica and aus subpopulations, (IND) is the indica subpopulation, (AUS) is aus, (JAP) is the Japonica subspecies composed of the temperate and tropical japonica subpopulations and (TRJ) is tropical japonica. The fifth rice subpopulation, Aromatic, was not present in the study. In the Manhattan plots the X axis shows the SNPs position across the 12 rice chromosomes and the Y axis is the –log10 (p) value for each snp. The horizontal black line at –log10(p) = 5 is the significance threshold for SNPs. In the quantile-quantile plots the X axis is the expected SNP distribution and the Y axis displays the –log10(p) observed SNP distribution.

