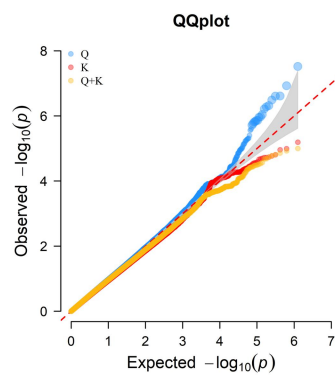
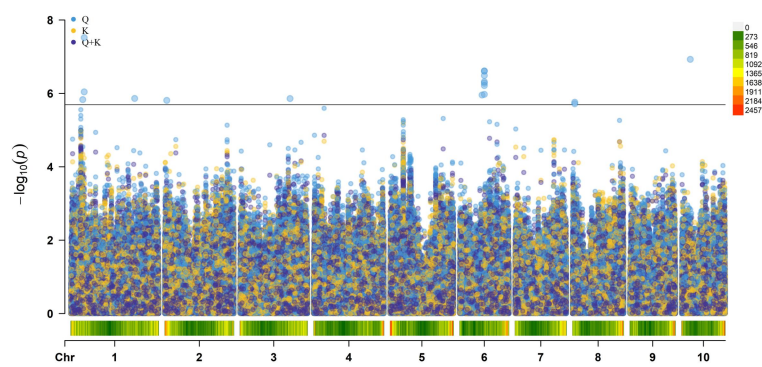
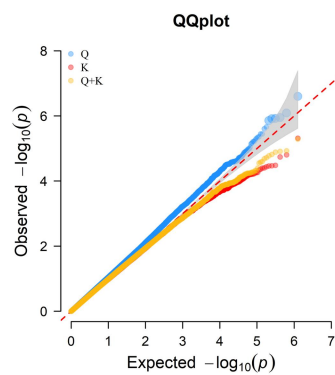
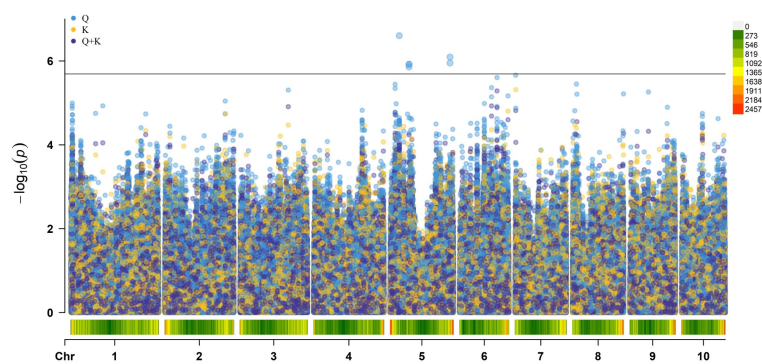
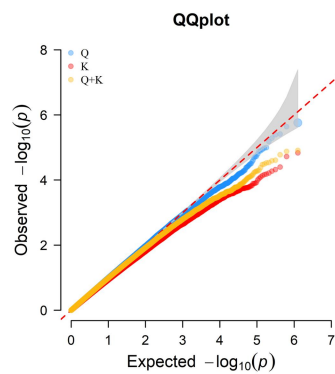
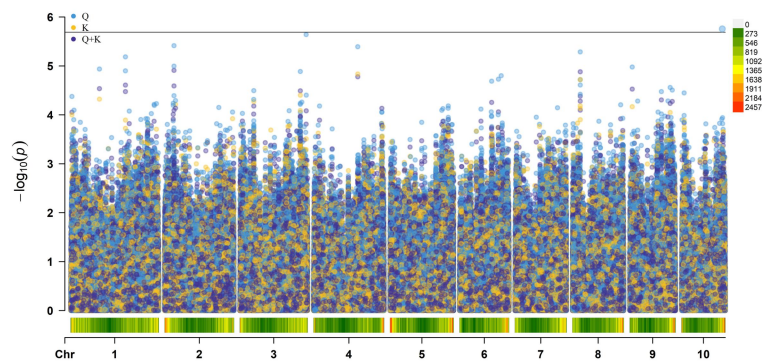
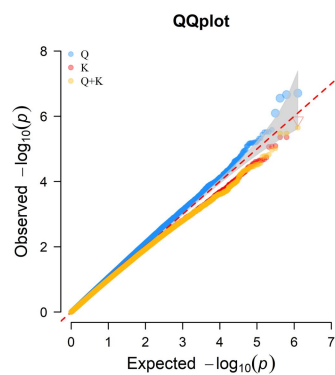
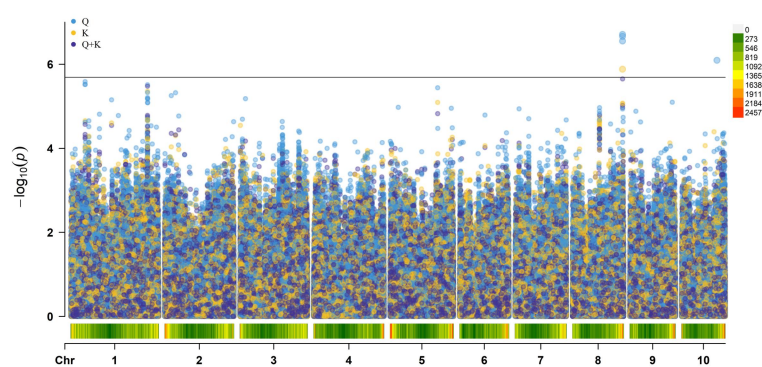
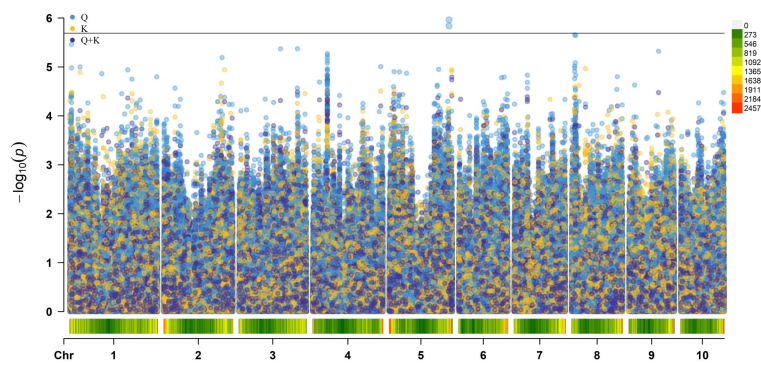
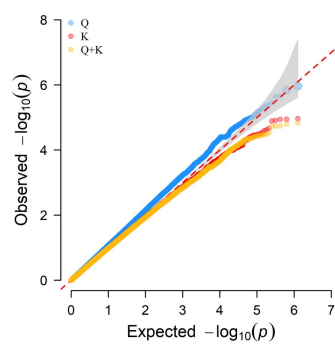
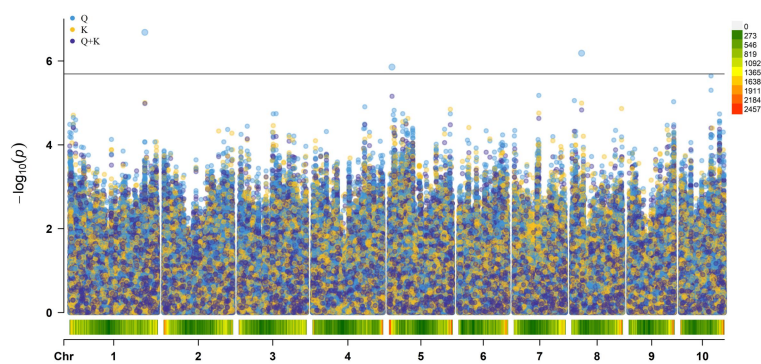
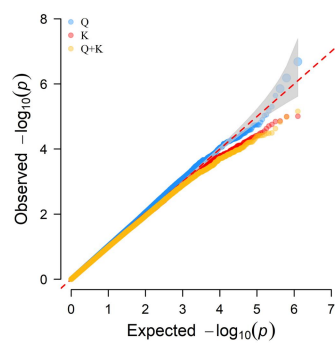
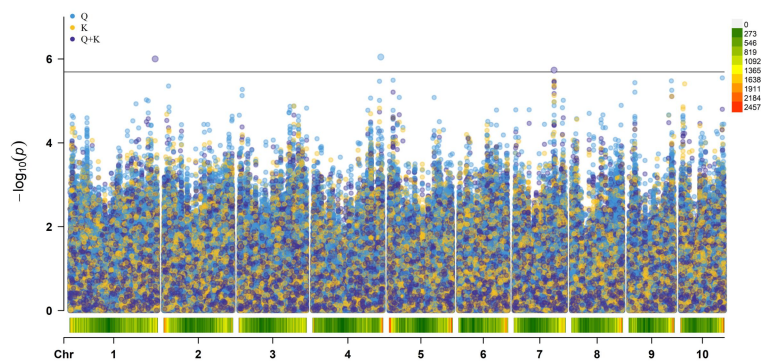
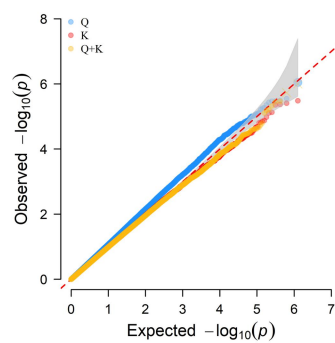
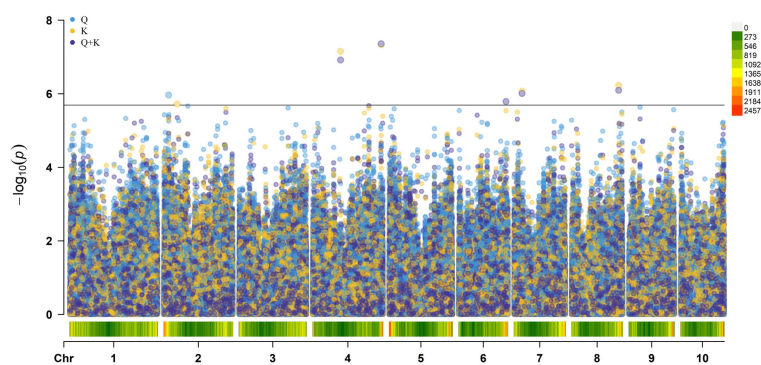
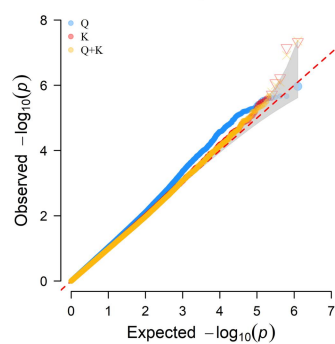
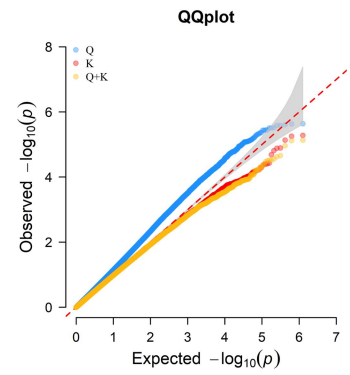
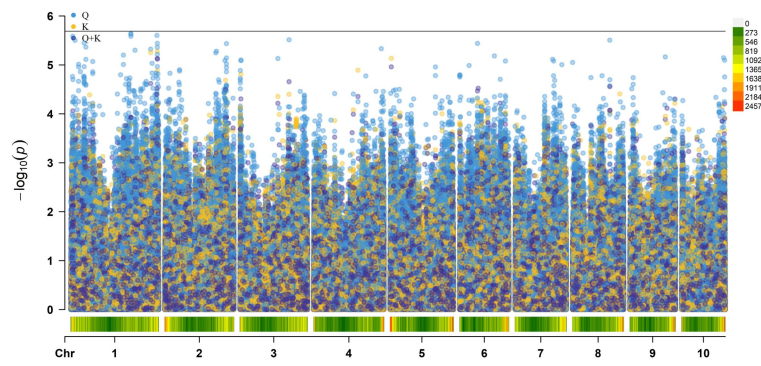
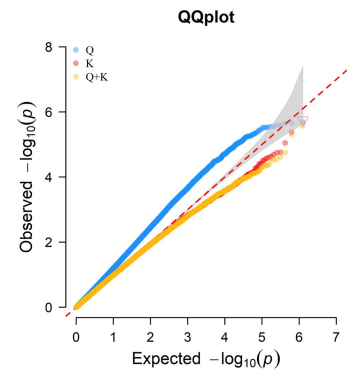
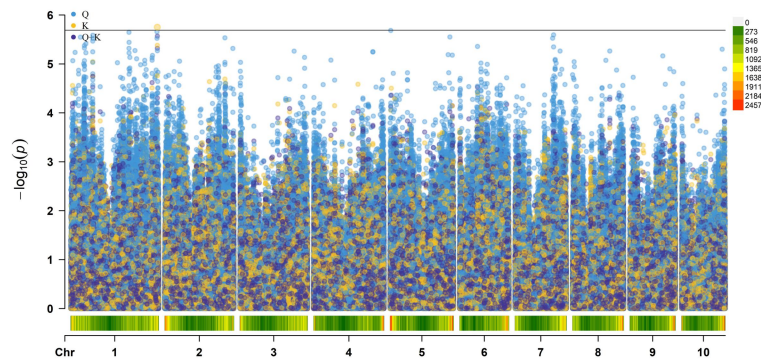
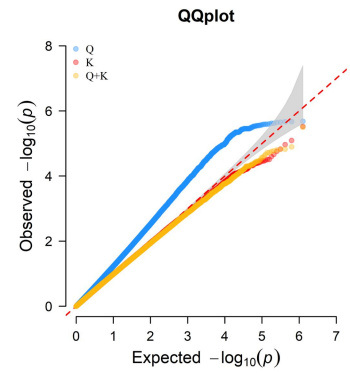
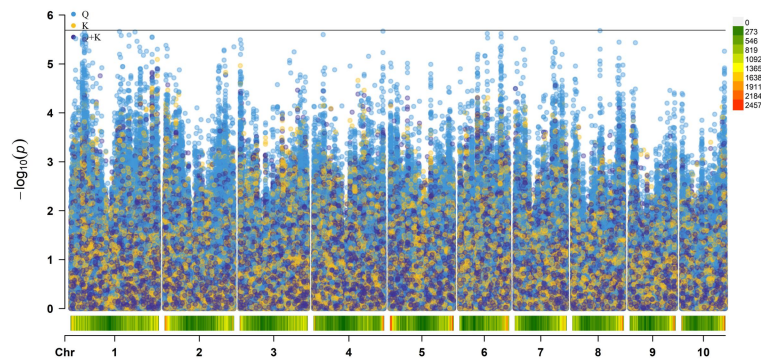
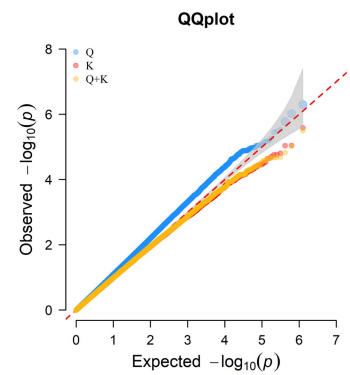
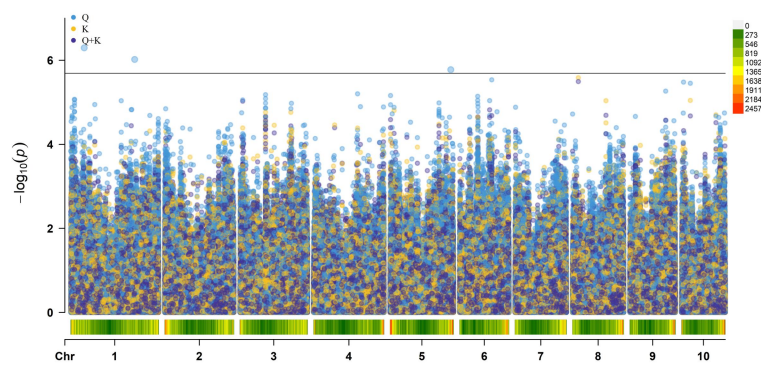
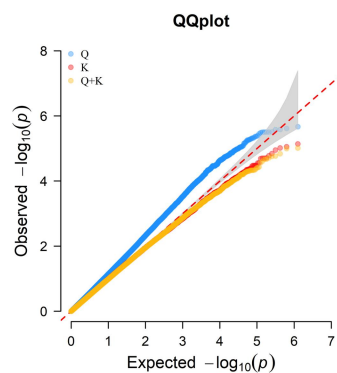
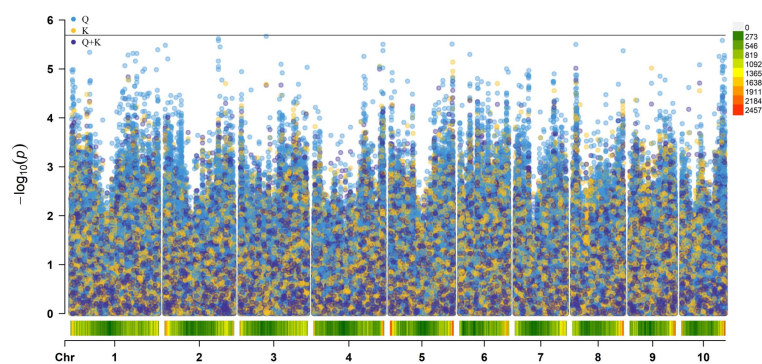


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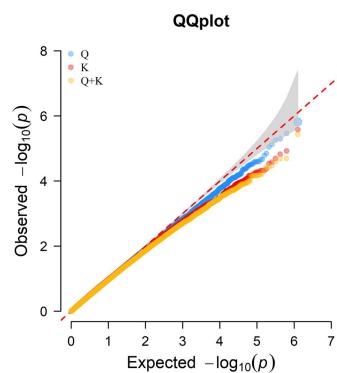
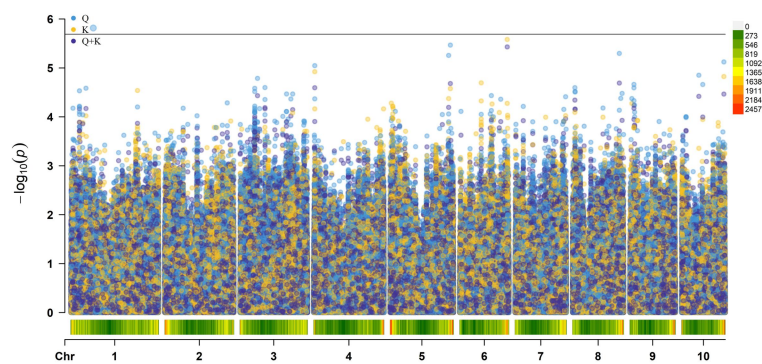
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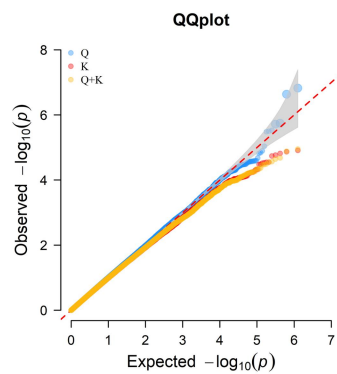
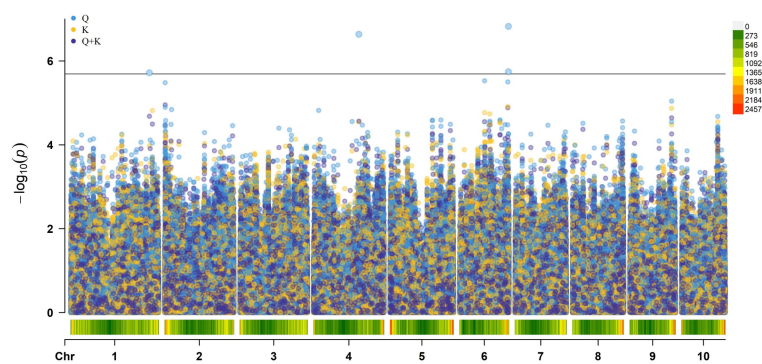
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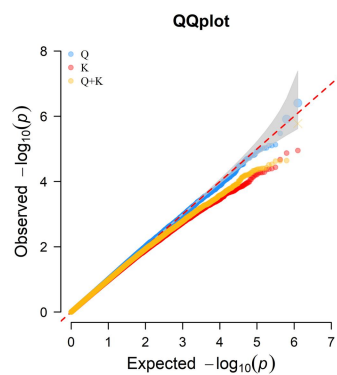
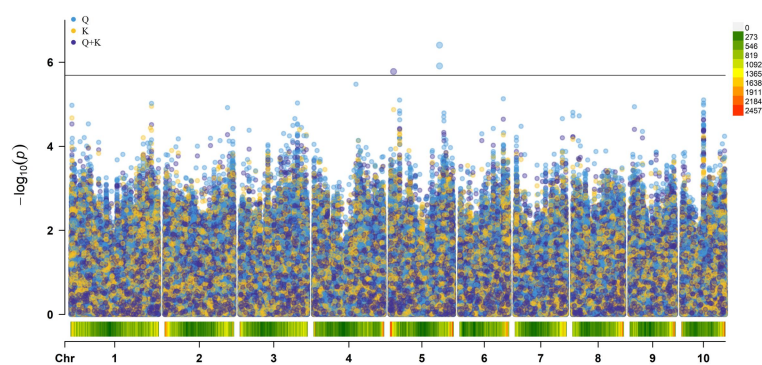
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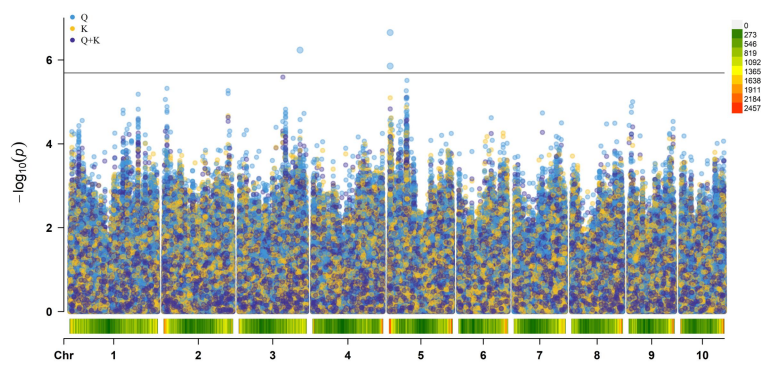
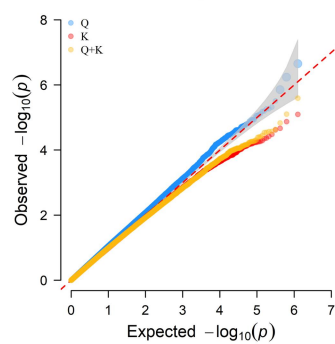
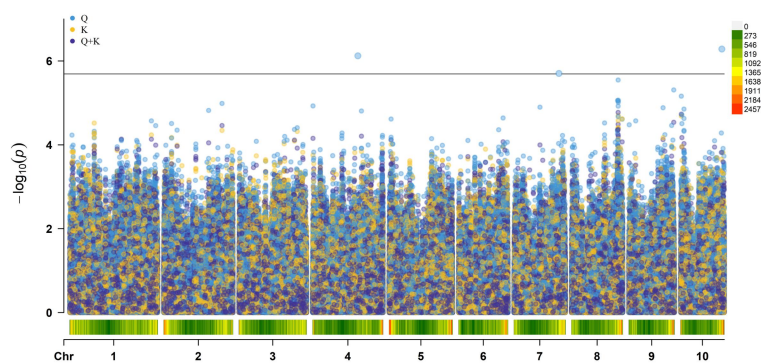
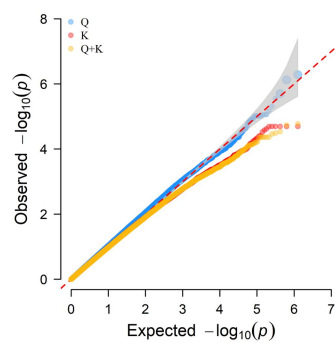
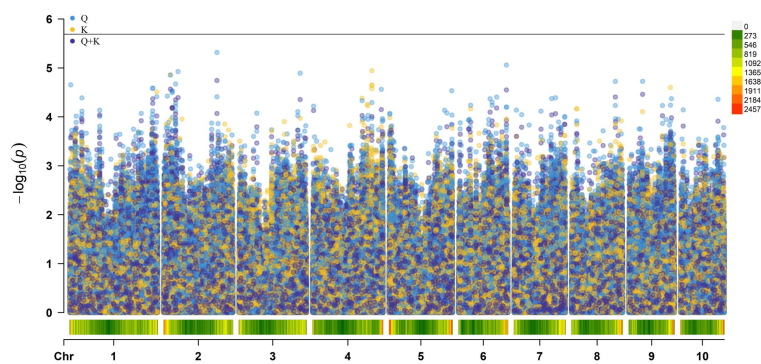
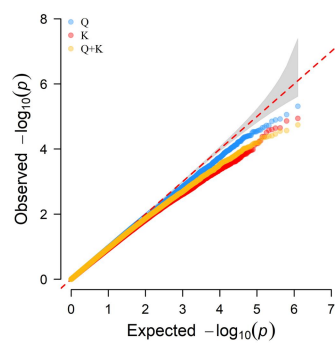
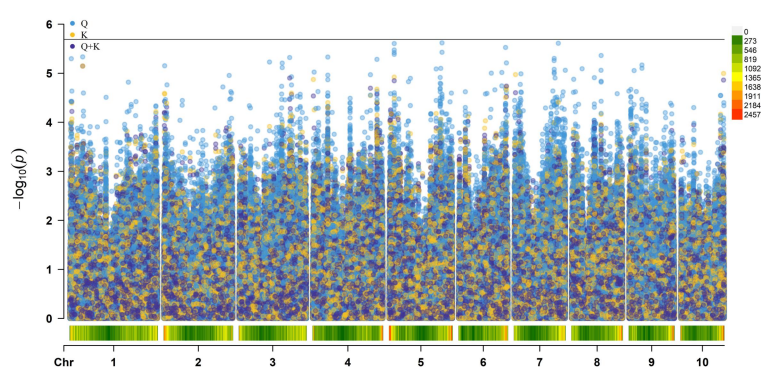
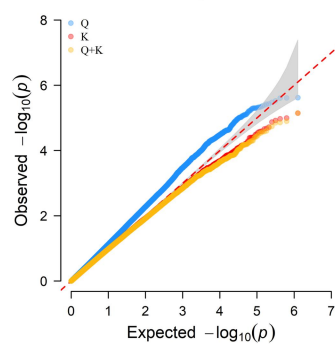


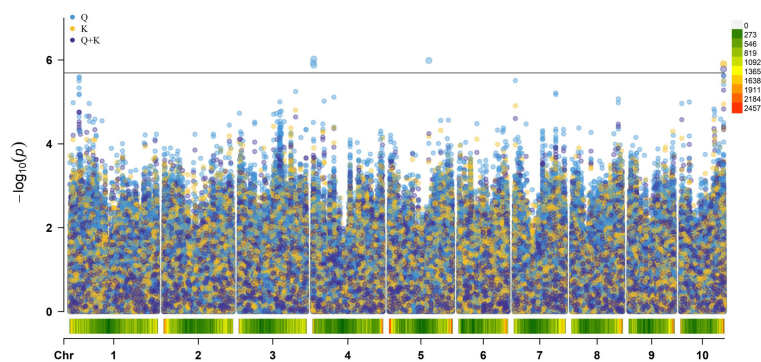
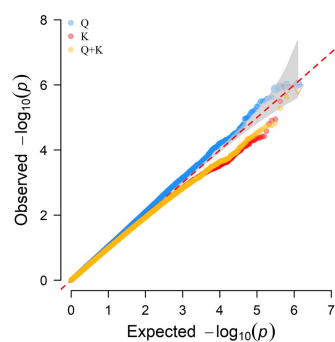
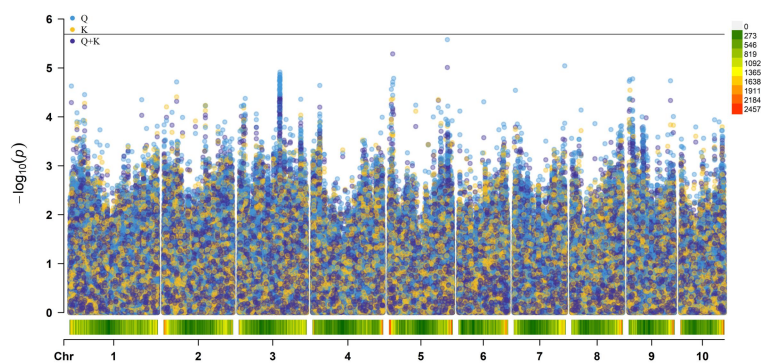
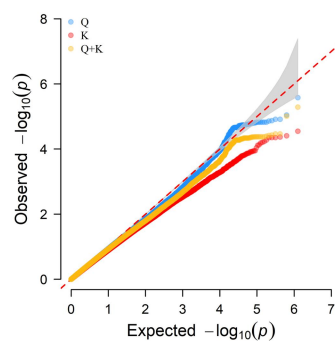
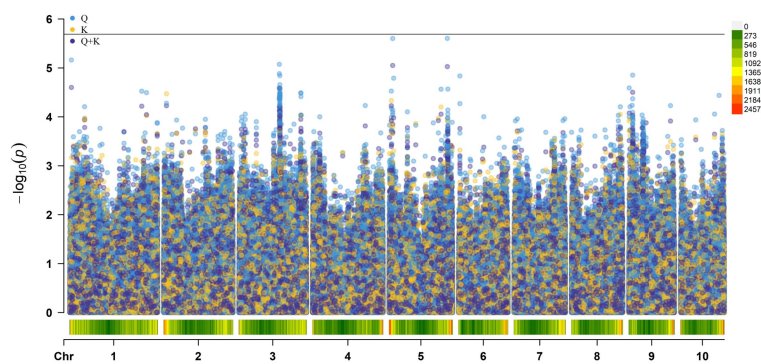
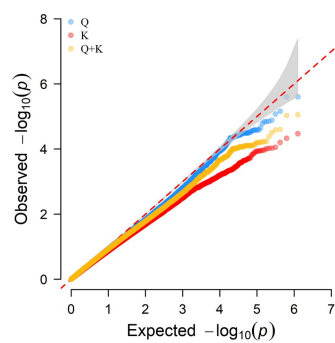
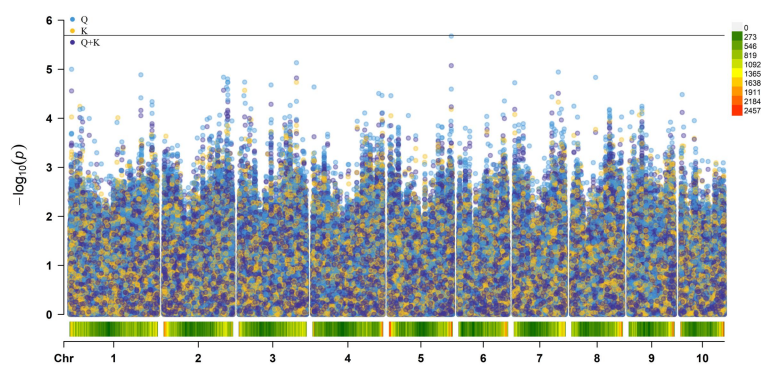
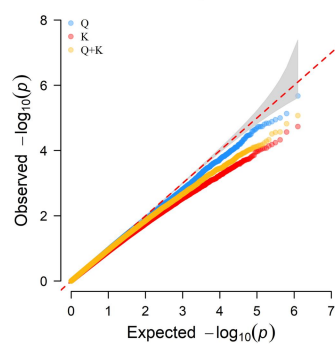
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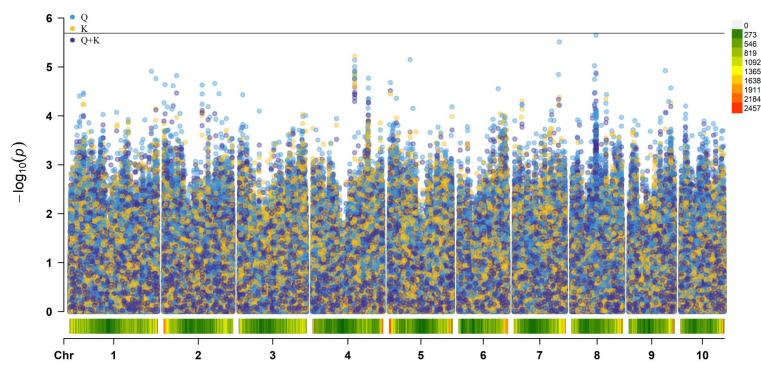
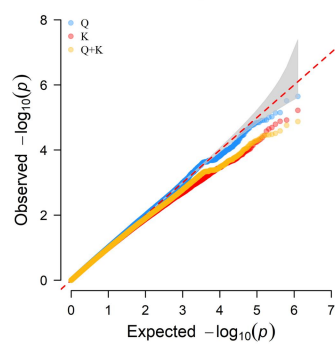
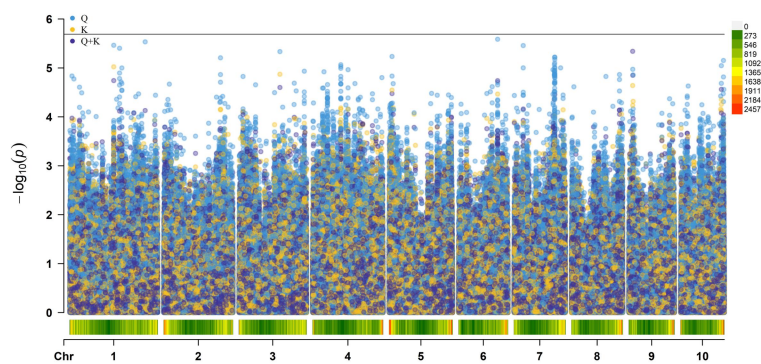
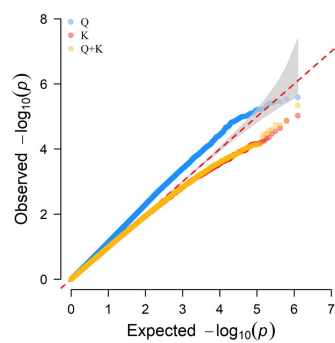
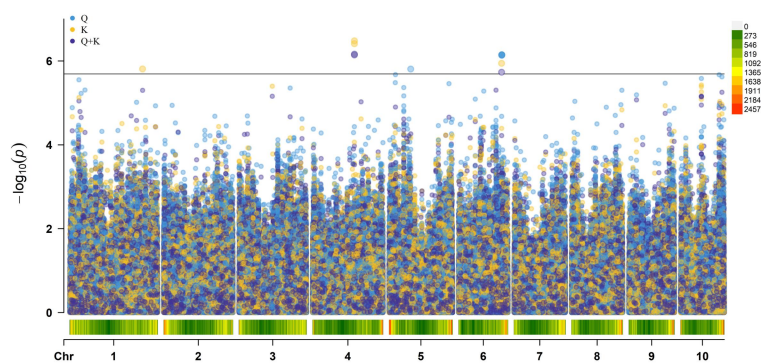
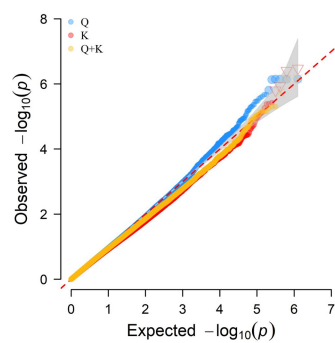
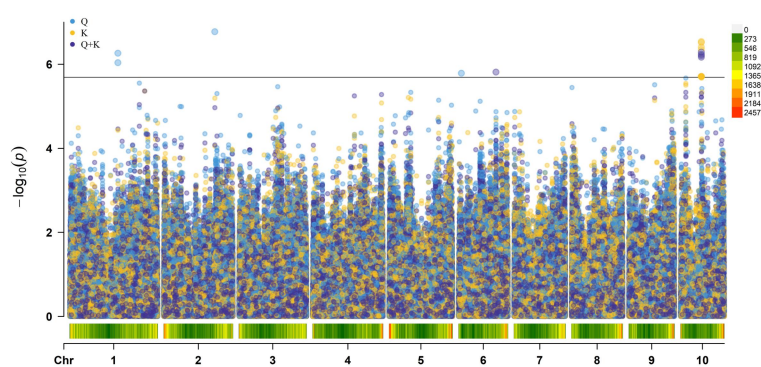
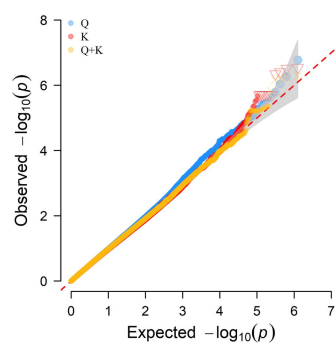


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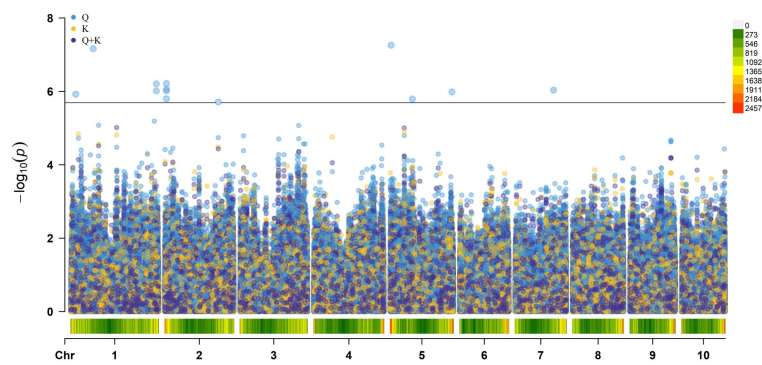


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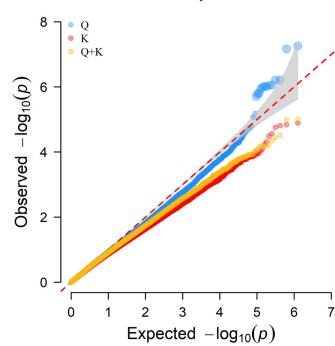
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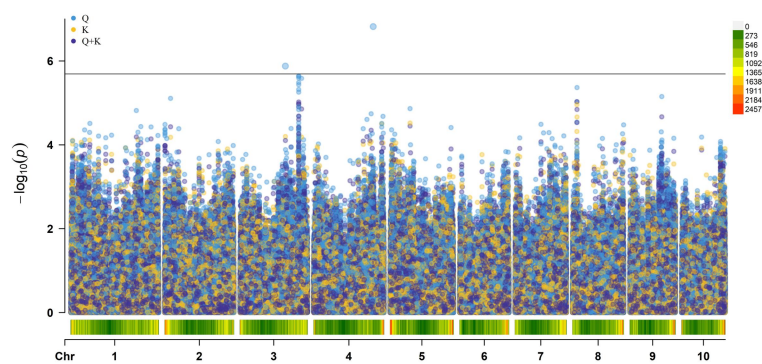
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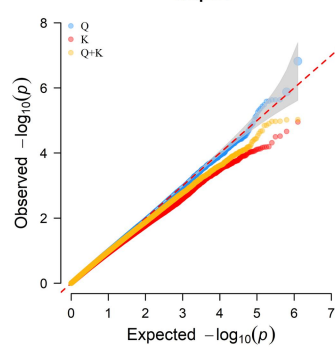
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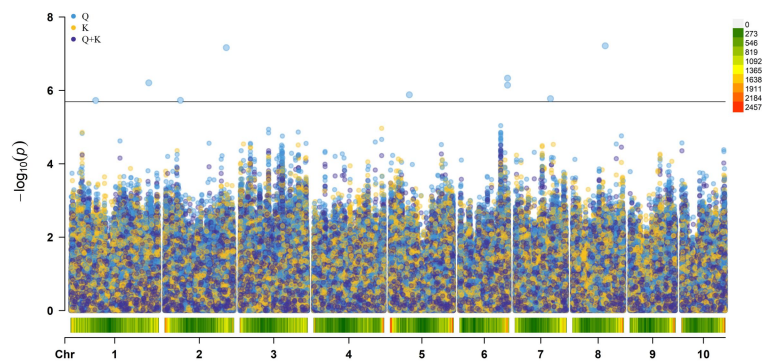
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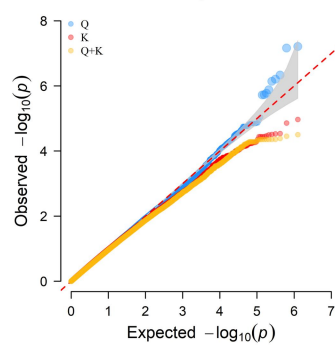
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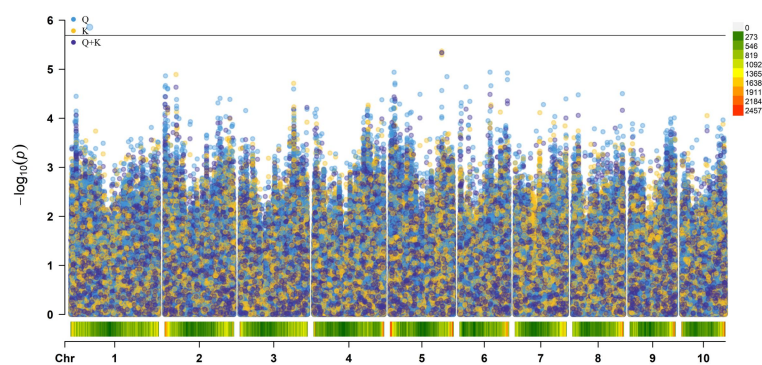
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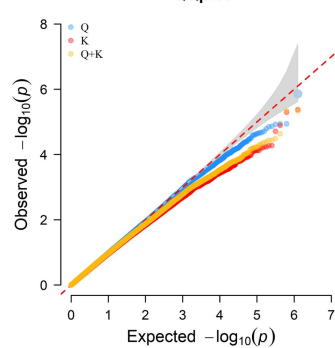
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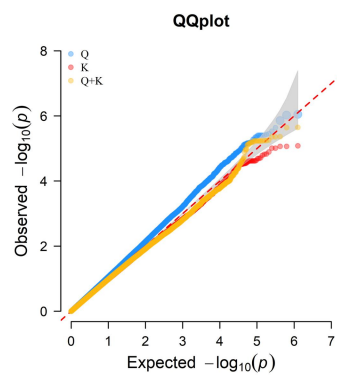
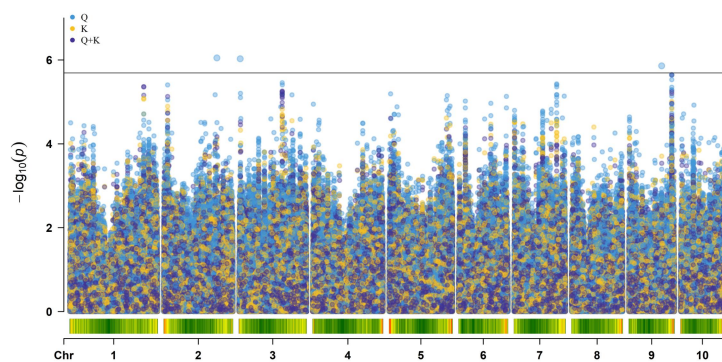
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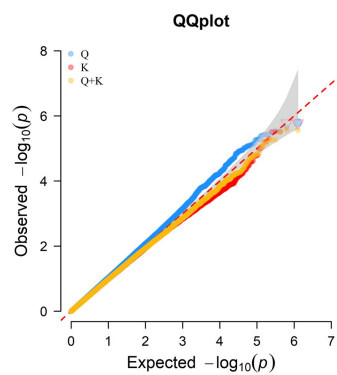
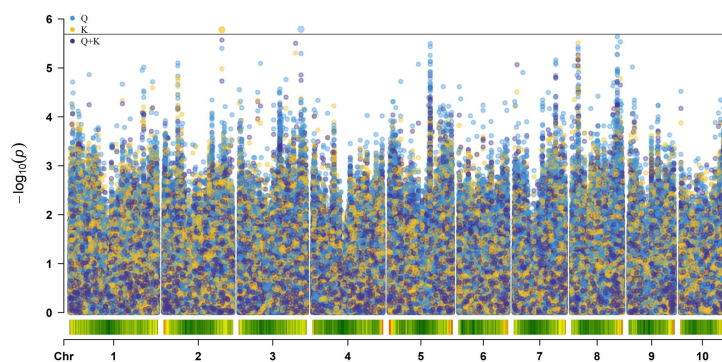
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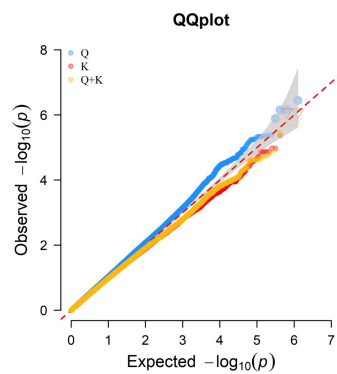
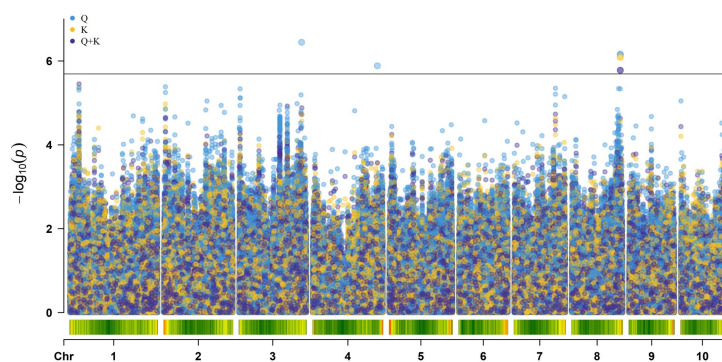
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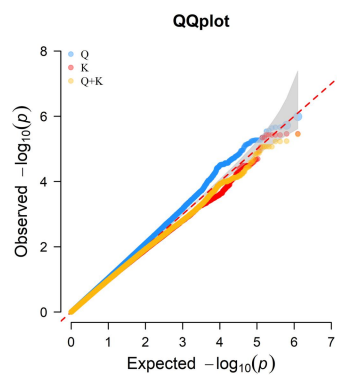
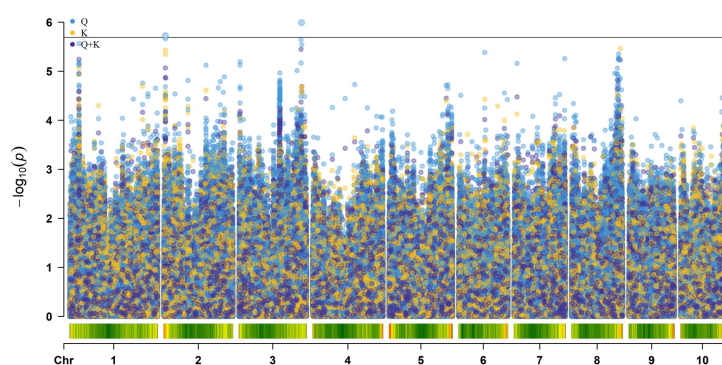
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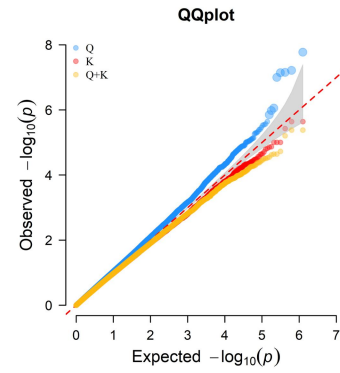
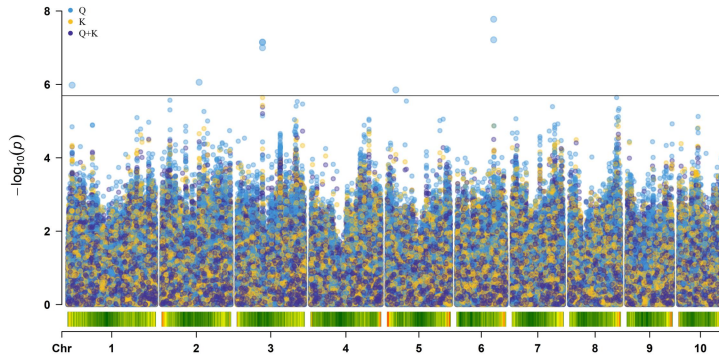
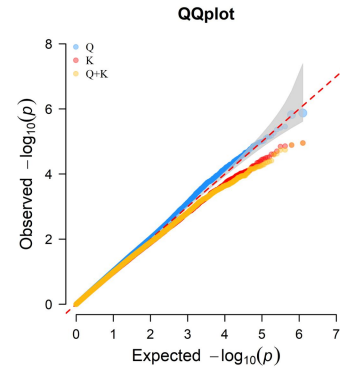
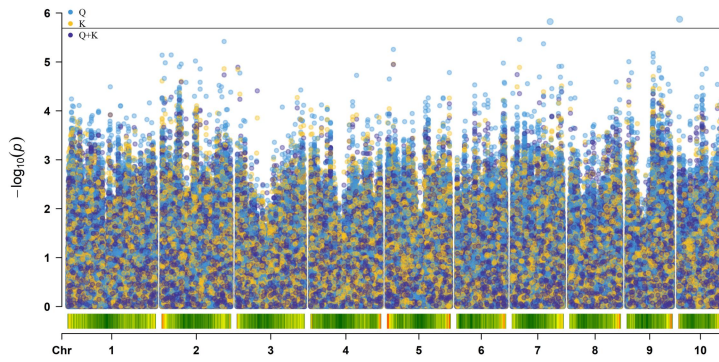
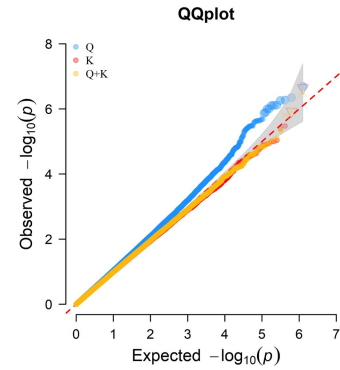
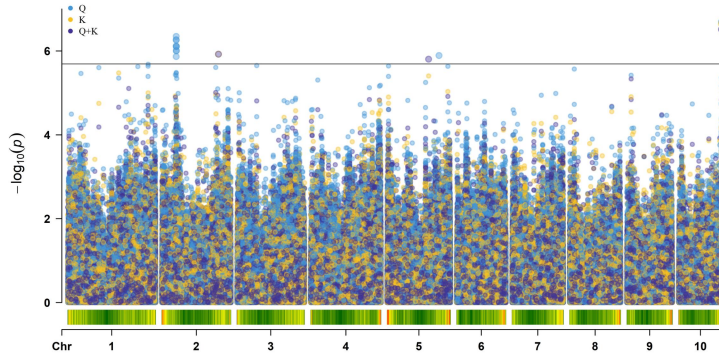
ak**al****am**

Figure S2. Manhattan and quantile-quantile (QQ) plots for all 13 traits under normal (N), salt (S), and salt/normal (S/N) conditions. Each panel presents the Manhattan plot (left) and QQ plot (right) for a given trait under a specific condition. For Manhattan plots, the x-axis indicates chromosomal position, and the y-axis shows $-\log_{10}(P)$. The black horizontal line indicates the genome-wide significance threshold ($P = 2.04 \times 10^{-6}$). For QQ plots, the x-axis represents expected $-\log_{10}(P)$, and the y-axis represents observed $-\log_{10}(P)$; the red diagonal line indicates the null expectation under no association. Panels are organized as: (a–m) N condition: AFW/FW, AFW, DW/FW, DW, FW, PH, RAD, RL, RPA, RSA, RV, UFW/FW, and UFW; (n–z) S condition (same order); (aa–am) S/N condition (same order). Trait abbreviations are defined in Table S2. Detailed GWAS results are provided in Table S3.