

A Manhattan plot showing the results of a genome-wide association study (GWAS). The y-axis represents the negative logarithm of the p-value, $-\log_{10}(p)$, ranging from 0 to 400. The x-axis represents the genes being tested. The plot shows a dense cluster of points at the bottom, indicating many genes with low p-values. A prominent peak is visible in the center, with several genes reaching high $-\log_{10}(p)$ values. The top of the plot shows a cluster of points exceeding 400, with the highest point reaching approximately 450. Several points are highlighted in blue, indicating genes of particular interest.

A Manhattan plot showing the results of a genome-wide association study (GWAS). The y-axis represents the negative logarithm of the p-value, $-\log_{10}(p)$, ranging from 0.0 to 2.5. The x-axis represents the genomic position, with labels at 100,000,000, 200,000,000, 300,000,000, and 400,000,000. The plot displays numerous data points, each representing a genetic variant. Most points are black circles, while a few are blue circles, indicating significant associations. The blue circles are scattered across the plot, with one notable point at approximately 400,000,000 reaching a $-\log_{10}(p)$ value of about 2.2.