

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 5000. The x-axis represents the genomic position in megabases (Mb), ranging from 0 to 250. A single SNP is highlighted in blue, located at approximately 100 Mb on the x-axis and 5000 on the y-axis. This SNP is the most significant in the study. Other SNPs are shown as open circles, with a dense cluster of points at the bottom of the plot (p-values near 0) and a few other points reaching up to approximately 4000 on the y-axis.

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 3. The x-axis represents the genomic position. The plot displays a dense collection of points, with most being white circles. Several points are highlighted in blue, indicating specific variants of interest. The highest point is a white circle reaching above 3.5, indicating a highly significant association.

p12