

A scatter plot showing the association of SNPs on chromosome 1. The y-axis is labeled  $-\log_{10}(p)$  and ranges from 0 to 200. The x-axis represents the genomic position. A dense cluster of points is visible at the bottom, with a few points reaching higher  $-\log_{10}(p)$  values. A single blue point is highlighted at the top, representing the lead SNP. A bracket on the x-axis indicates a region of significant association.

Figure 1 is a log-linear plot showing the probability of a hypothesis  $H$  being the true hypothesis as a function of the number of samples  $n$ . The x-axis represents  $n$  on a logarithmic scale, ranging from  $1e-12$  to  $1e-06$ . The y-axis represents the probability (Prob) on a linear scale, ranging from 0.000 to 0.004. A vertical dashed line is drawn at  $n = 1e-07$ .

The plot displays five hypotheses, labeled  $H_0$  through  $H_4$ , as indicated by the legend:

- $H_0$ : White circle
- $H_1$ : Dark blue circle
- $H_2$ : Teal circle
- $H_3$ : Green circle
- $H_4$ : Yellow circle

The data points for each hypothesis are connected by lines.  $H_2$  and  $H_4$  maintain a high probability (around 0.0045) across the entire range of  $n$ .  $H_0$ ,  $H_1$ , and  $H_3$  maintain a low probability (around 0.000) across the entire range of  $n$ . A sharp increase in probability for  $H_4$  is observed for  $n > 1e-07$ , reaching approximately 0.0045 at  $n = 1e-06$ .