

Figure 1 displays five Manhattan plots showing the results of a genome-wide association study (GWAS) for various traits. The x-axis for all plots represents the genomic position (in Mb), ranging from 27,500 to 30,000. The y-axis represents the negative logarithm of the p-value ( $-\log_{10}(p\text{-value})$ ).

The traits analyzed are:

- blood\_MEAN\_SPHERED\_CELL\_VOL**: The y-axis ranges from 0 to 30. A significant association is observed around 29,500 Mb.
- blood\_HIGH\_LIGHT\_SCATTER\_RETICULOCYTE\_COUNT**: The y-axis ranges from 0 to 9. A significant association is observed around 29,500 Mb.
- pigment\_HAIR**: The y-axis ranges from 0 to 5. A significant association is observed around 29,500 Mb.
- body\_BMIz**: The y-axis ranges from 0 to 4. A significant association is observed around 29,500 Mb.
- bmd\_HEEL\_TSCOREz**: The y-axis ranges from 0 to 8. A significant association is observed around 29,500 Mb.

Each plot shows a dense cloud of black points representing SNPs. A yellow line indicates the recombination rate. Vertical green lines are present at regular intervals across all plots.

