

The figure displays four vertically stacked Manhattan plots, each representing the association of genetic variants with a specific trait. The x-axis for all plots is genomic position, ranging from 84,500 to 86,500. The y-axis represents the negative logarithm of the p-value ($-\log_{10}(p\text{-value})$).

- Top Plot:** Trait is `body_HEIGHTz`. The y-axis ranges from 0 to 30. Significant associations are marked with red circles and vertical green lines.
- Second Plot:** Trait is `impedance_BASAL_METABOLIC_RATEz`. The y-axis ranges from 0 to 15. Significant associations are marked with red circles and vertical green lines.
- Third Plot:** Trait is `blood_RBC_DISTRIB_WIDTH`. The y-axis ranges from 0 to 15. Significant associations are marked with red circles and vertical green lines.
- Bottom Plot:** Trait is `blood_HIGH_LIGHT_SCATTER_RETICULOCYTE_COUNT`. The y-axis ranges from 0 to 5. Significant associations are marked with red circles and vertical green lines.

In all plots, black dots represent individual genetic variants, and the orange line represents the recombination rate. Vertical green lines indicate the positions of the lead variants for each trait.

