

The figure displays eight vertically stacked Manhattan plots, each representing the association of genetic variants with a specific trait across a genomic region from 17,000 to 19,000. The y-axis for each plot represents the $-\log_{10}(p\text{-value})$, and the x-axis represents the genomic position. Green vertical lines indicate recombination rates, and red circles highlight specific variants of interest.

- bp_SYSTOLICadjMEDz**: The y-axis ranges from 0 to 10. A significant peak is observed around position 19,000.
- disease_CARDIOVASCULAR**: The y-axis ranges from 0 to 6. A significant peak is observed around position 19,000.
- blood_PLATELET_COUNT**: The y-axis ranges from 0 to 10. A significant peak is observed around position 18,500.
- body_BMIz**: The y-axis ranges from 0 to 4. A significant peak is observed around position 18,500.
- blood_HIGH_LIGHT_SCATTER_RETICULOCYTE_COUNT**: The y-axis ranges from 0 to 6. A significant peak is observed around position 18,500.
- disease_HI_CHOL_SELF_REP**: The y-axis ranges from 0 to 4. A significant peak is observed around position 19,000.
- bp_DIASTOLICadjMEDz**: The y-axis ranges from 0 to 8. A significant peak is observed around position 18,500.
- blood_MEAN_SPHERED_CELL_VOL**: The y-axis ranges from 0 to 8. A significant peak is observed around position 18,500.

