

The figure displays six Manhattan plots, each representing a different trait. The x-axis for all plots is genomic position, ranging from 66,000 to 68,000. The y-axis represents $-\log_{10}(p\text{-value})$. Each plot includes a black line representing the data, a yellow line representing a baseline or threshold, and vertical green lines indicating specific genomic regions. Red circles highlight significant associations.

- pigment_HAIR**: The y-axis ranges from 0.0 to 10.0. Significant associations are visible at approximately 66,000, 66,500, 67,000, 67,500, and 68,000.
- pigment_HAIR_blonde**: The y-axis ranges from 0 to 8. Significant associations are visible at approximately 66,000, 66,500, 67,000, 67,500, and 68,000.
- pigment_HAIR_darkbrown**: The y-axis ranges from 0.0 to 10.0. Significant associations are visible at approximately 66,000, 66,500, 67,000, 67,500, and 68,000.
- pigment_SUNBURN**: The y-axis ranges from 0.0 to 10.0. Significant associations are visible at approximately 66,000, 66,500, 67,000, 67,500, and 68,000.
- pigment_SKIN**: The y-axis ranges from 0 to 4. Significant associations are visible at approximately 66,000, 66,500, 67,000, 67,500, and 68,000.
- blood_HIGH_LIGHT_SCATTER_RETICULOCYTE_COUNT**: The y-axis ranges from 0 to 15. Significant associations are visible at approximately 66,000, 66,500, 67,000, 67,500, and 68,000.
- blood_PLATELET_COUNT**: The y-axis ranges from 0 to 6. Significant associations are visible at approximately 66,000, 66,500, 67,000, 67,500, and 68,000.

A grey line at the bottom of the figure represents the recombination rate across the genomic region.

