

Supplementary Material

GWAS

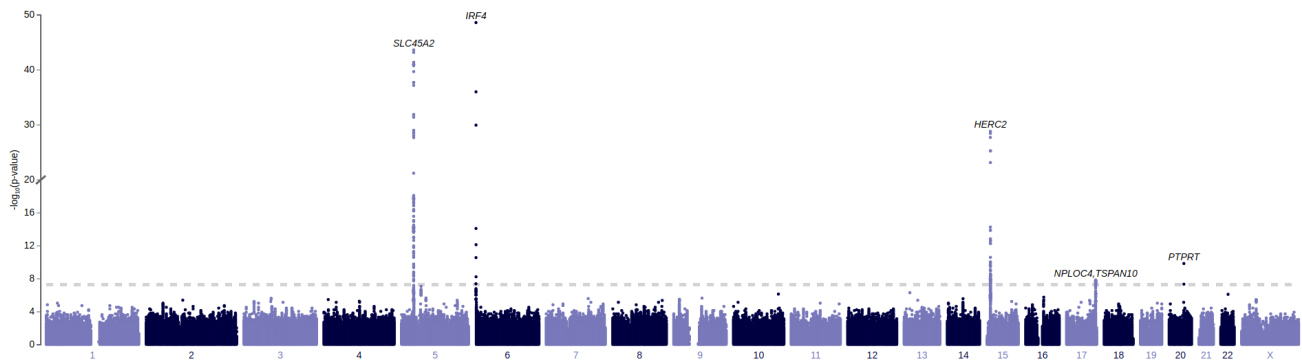


Figure 9: Black hair's Manhattan plot. Each point represents an associated variant. The x axis corresponds to the chromosomes and the y axis represents the $-\log_{10}(\text{p-value})$. The horizontal dashed line indicates the threshold for genome-wide significance at $5e-8$.

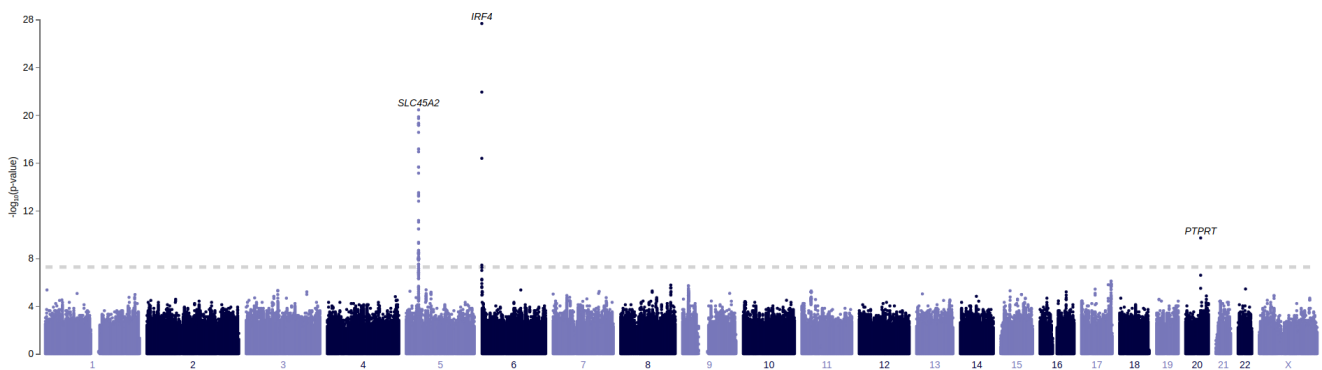


Figure 10: Brown hair's Manhattan plot. Each point represents an associated variant. The x axis corresponds to the chromosomes and the y axis represents the $-\log_{10}(\text{p-value})$. The horizontal dashed line indicates the threshold for genome-wide significance at $5e-8$.

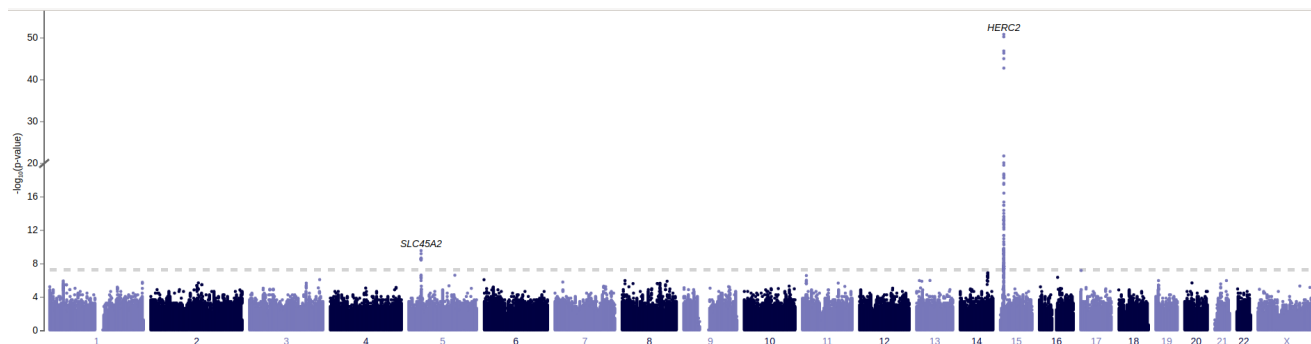


Figure 11: Blond hair's Manhattan plot. Each point represents an associated variant. The x axis corresponds to the chromosomes and the y axis represents the $-\log_{10}(p\text{-value})$. The horizontal dashed line indicates the threshold for genome-wide significance at $5e-8$.

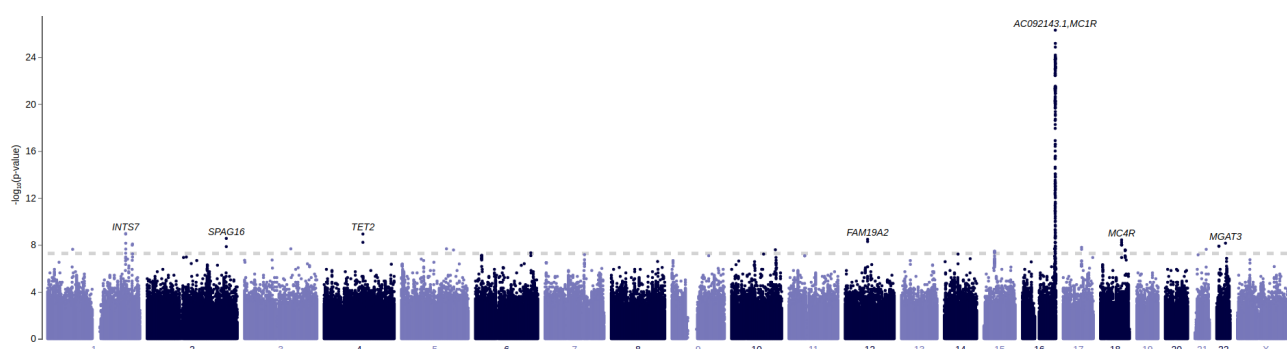


Figure 12: Red hair's Manhattan plot. Each point represents an associated variant. The x axis corresponds to the chromosomes and the y axis represents the $-\log_{10}(p\text{-value})$. The horizontal dashed line indicates the threshold for genome-wide significance at $5e-8$.

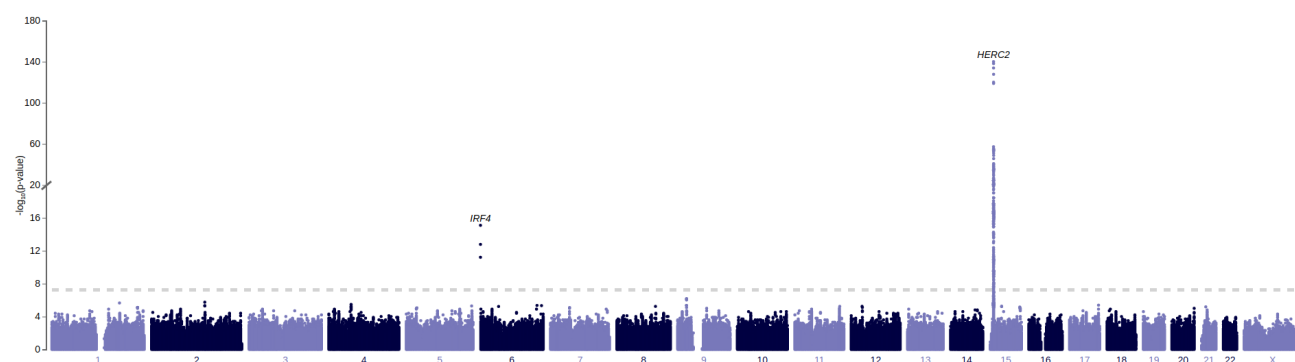


Figure 13: Brown eyes' Manhattan plot. Each point represents an associated variant. The x axis corresponds to the chromosomes and the y axis represents the $-\log_{10}(p\text{-value})$. The horizontal dashed line indicates the threshold for genome-wide significance at $5e-8$.

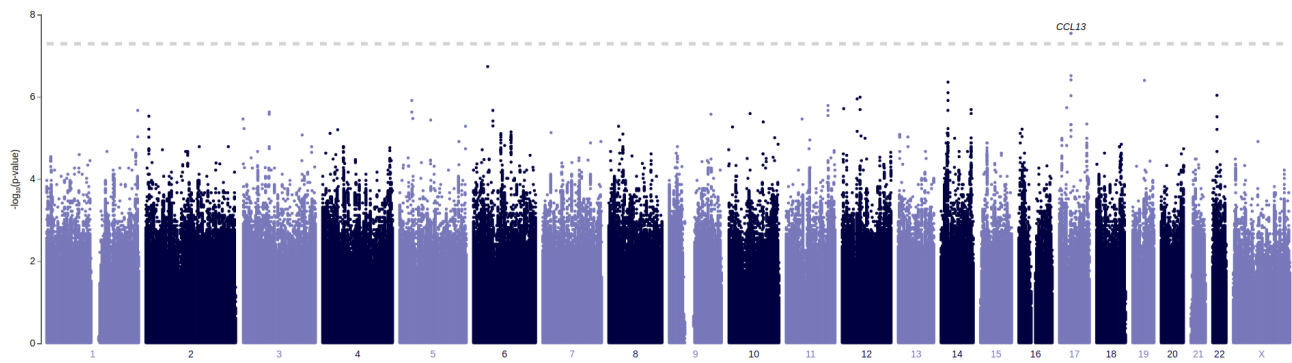


Figure 14: Light brown eyes' Manhattan plot. Each point represents an associated variant. The x axis corresponds to the chromosomes and the y axis represents the $-\log_{10}(p\text{-value})$. The horizontal dashed line indicates the threshold for genome-wide significance at $5e-8$.

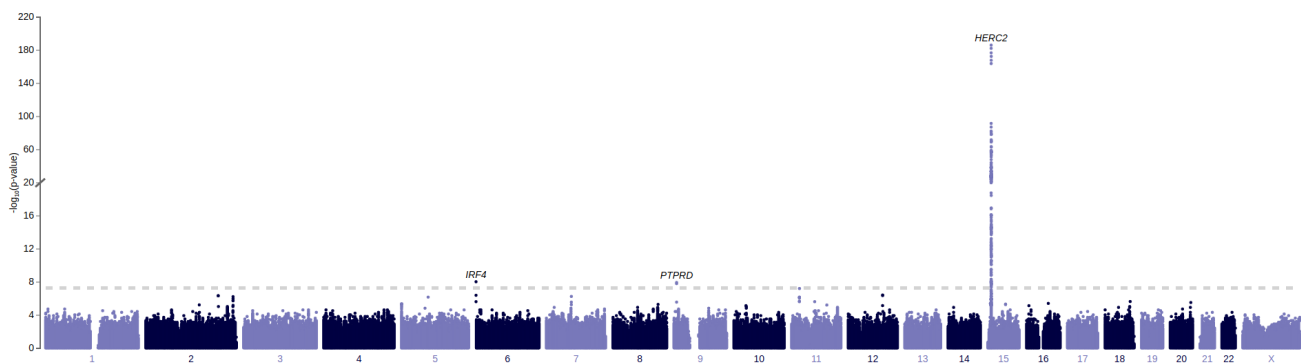


Figure 15: Blue/green eyes' Manhattan plot. Each point represents an associated variant. The x axis corresponds to the chromosomes and the y axis represents the $-\log_{10}(p\text{-value})$. The horizontal dashed line indicates the threshold for genome-wide significance at $5e-8$.

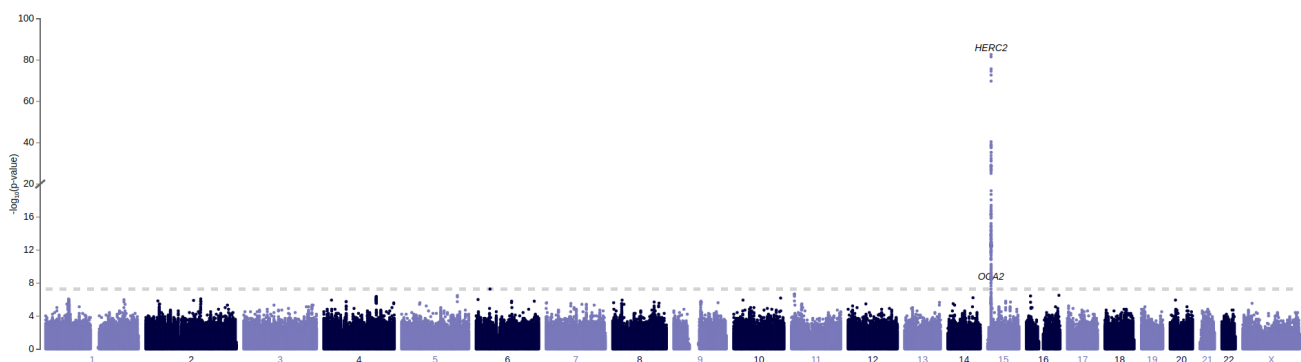


Figure 16: Light blue/green eyes' Manhattan plot. Each point represents an associated variant. The x axis corresponds to the chromosomes and the y axis represents the $-\log_{10}(p\text{-value})$. The horizontal dashed line indicates the threshold for genome-wide significance at $5e-8$.

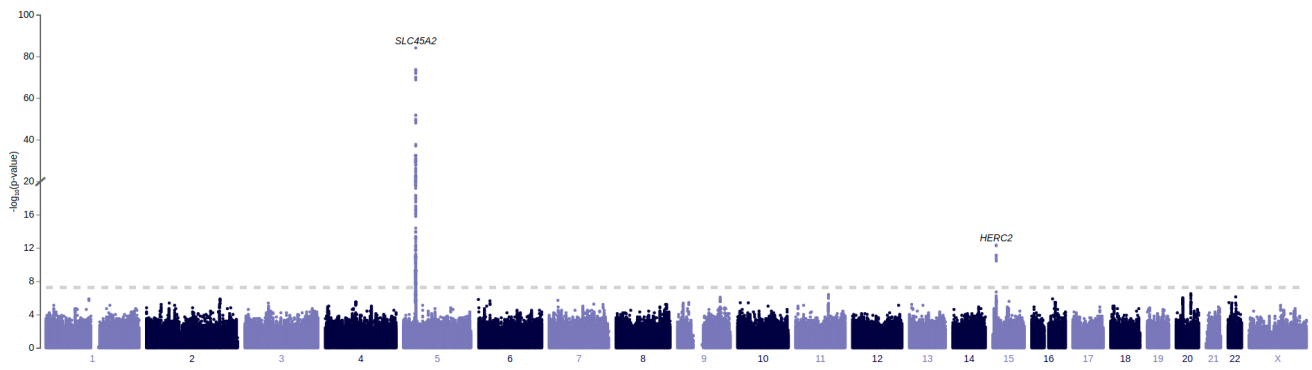


Figure 17: Brown skin's Manhattan plot. Each point represents an associated variant. The x axis corresponds to the chromosomes and the y axis represents the $-\log_{10}(\text{p-value})$. The horizontal dashed line indicates the threshold for genome-wide significance at $5e-8$.

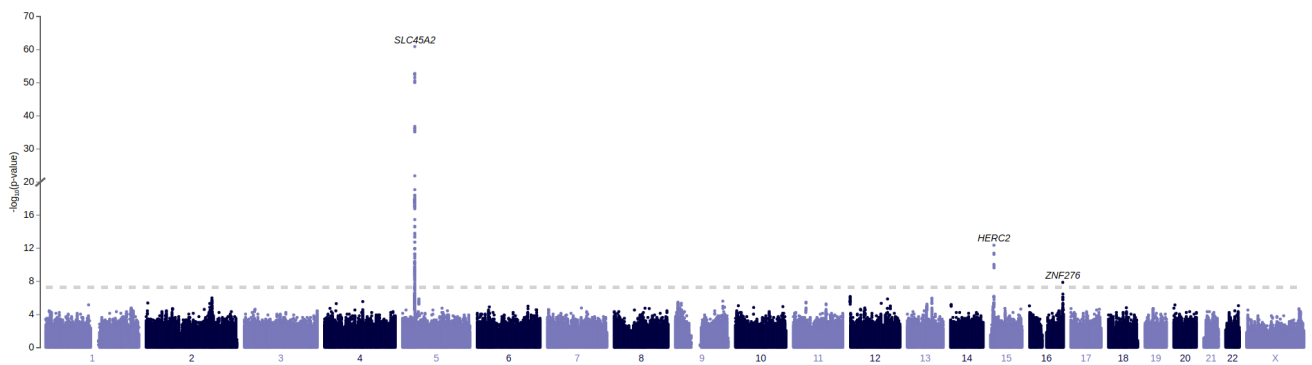


Figure 18: White skin's Manhattan plot. Each point represents an associated variant. The x axis corresponds to the chromosomes and the y axis represents the $-\log_{10}(\text{p-value})$. The horizontal dashed line indicates the threshold for genome-wide significance at $5e-8$.

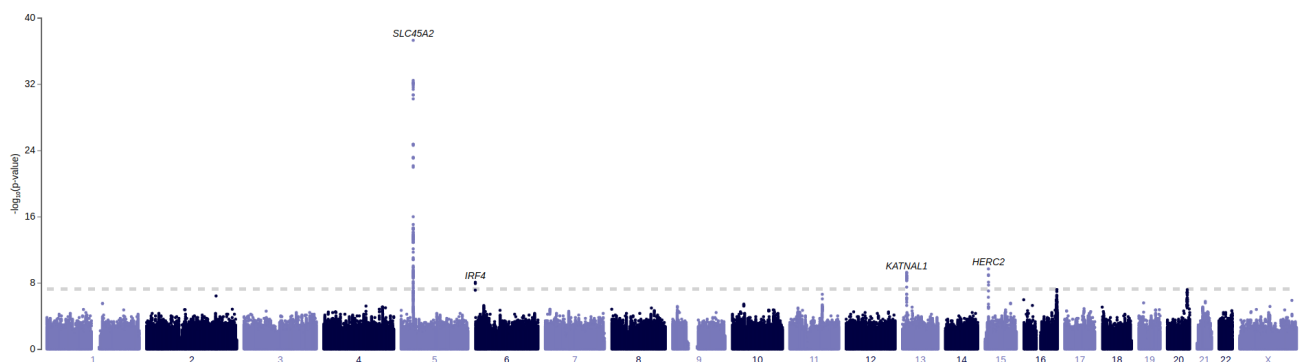


Figure 19: Skin sensitivity's Manhattan plot. Each point represents an associated variant. The x axis corresponds to the chromosomes and the y axis represents the $-\log_{10}(\text{p-value})$. The horizontal dashed line indicates the threshold for genome-wide significance at $5e-8$.

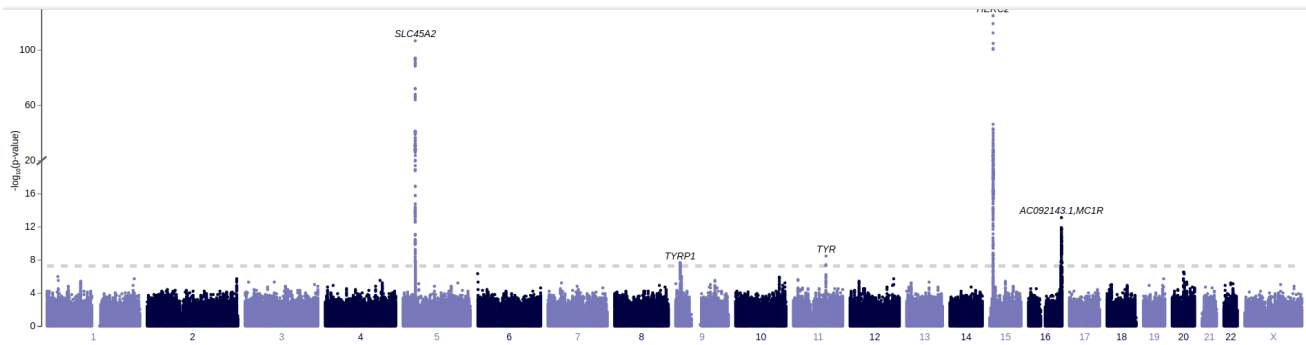


Figure 20: Phototype's Manhattan plot. Each point represents an associated variant. The x axis corresponds to the chromosomes and the y axis represents the $-\log_{10}(\text{p-value})$. The horizontal dashed line indicates the threshold for genome-wide significance at $5e-8$.

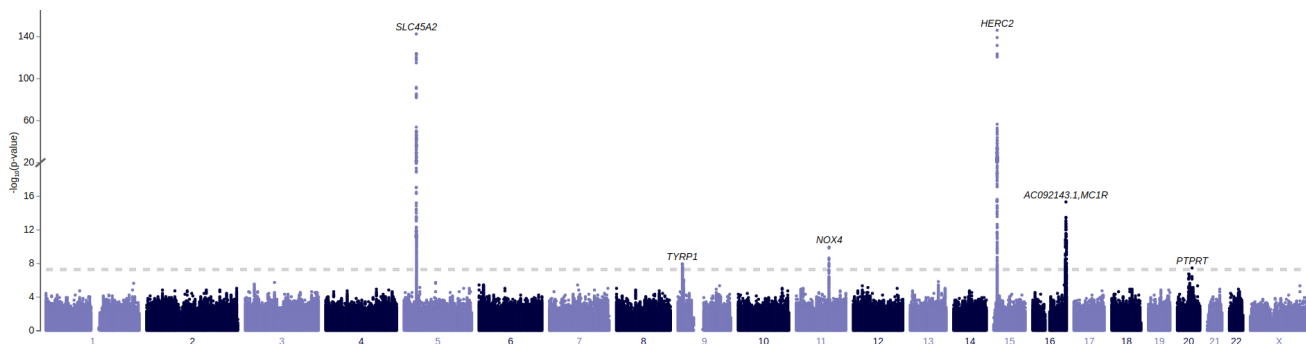


Figure 21: Phototype score's Manhattan plot. Each point represents an associated variant. The x axis corresponds to the chromosomes and the y axis represents the $-\log_{10}(\text{p-value})$. The horizontal dashed line indicates the threshold for genome-wide significance at $5e-8$.

Fine mapping

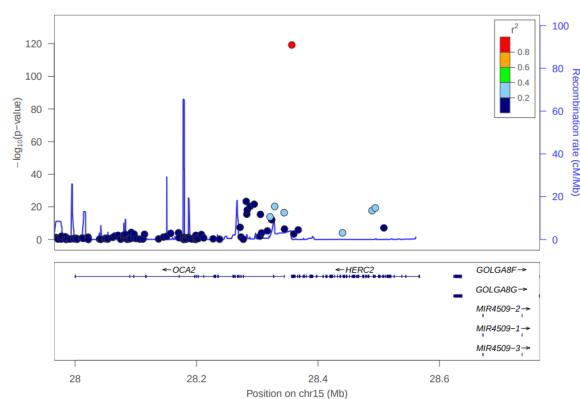


Figure 22: LocusZoom plot for the skin phototype phenotype. We plotted chromosome 15, the chromosome with the most significant variants in this trait.

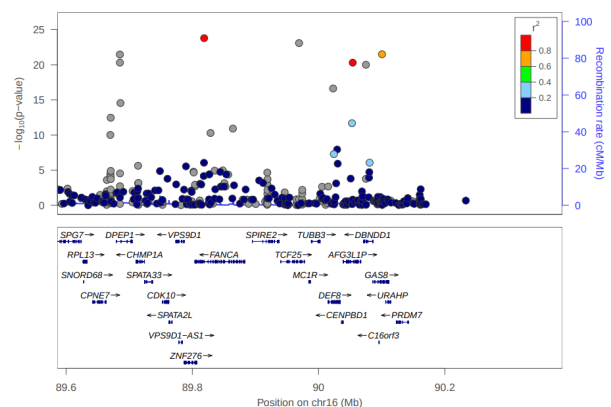


Figure 23: LocusZoom plot for the red hair phenotype. We plotted chromosome 16, the chromosome with the most significant variants in this trait.

Joint analysis of GWAS

You can find here the plots from the phenotypes that gave a different GWAS result when performing the analysis jointly with other traits.

First analysis:

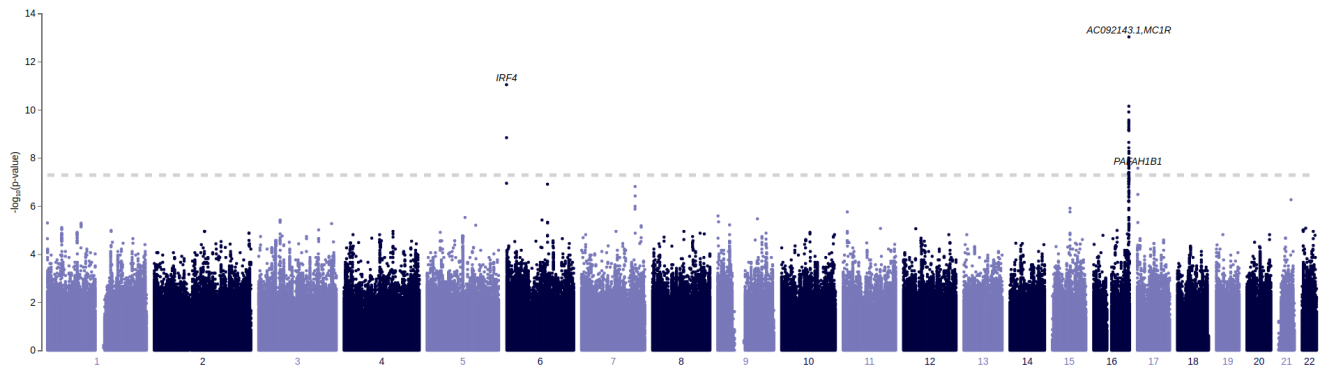


Figure 24: Brown hair's Manhattan plot. Each point represents an associated variant. The x axis corresponds to the chromosomes and the y axis represents the $-\log_{10}(\text{p-value})$. The horizontal dashed line indicates the threshold for genome-wide significance at $5e-8$.

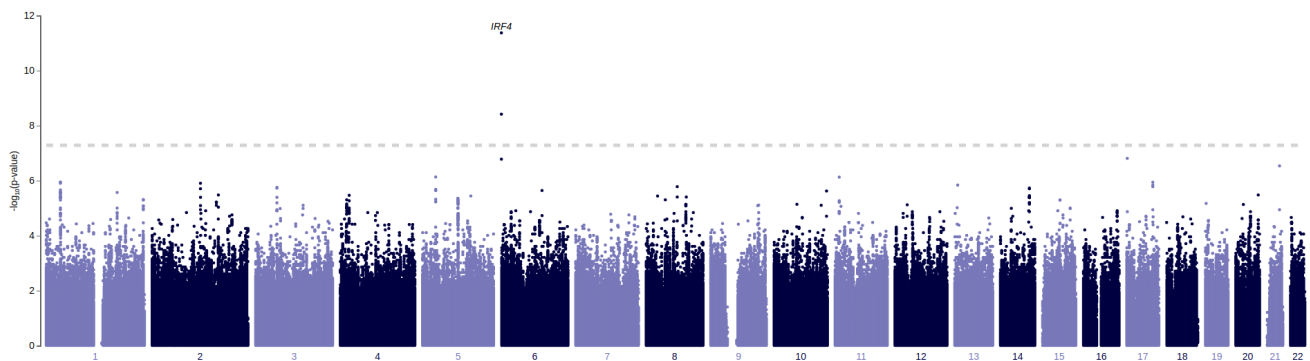


Figure 25: Blond hair's Manhattan plot. Each point represents an associated variant. The x axis corresponds to the chromosomes and the y axis represents the $-\log_{10}(\text{p-value})$. The horizontal dashed line indicates the threshold for genome-wide significance at $5e-8$.

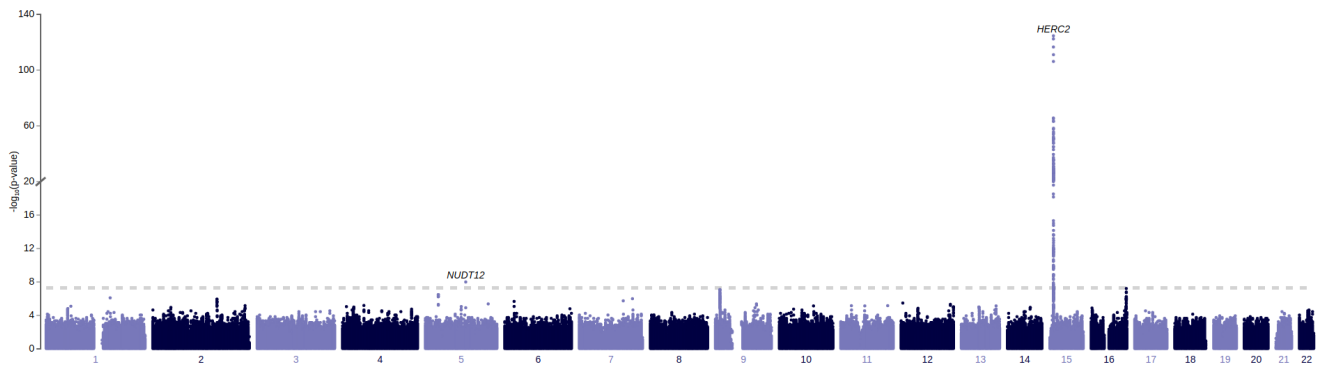


Figure 26: Black eyes' Manhattan plot. Each point represents an associated variant. The x axis corresponds to the chromosomes and the y axis represents the $-\log_{10}(\text{p-value})$. The horizontal dashed line indicates the threshold for genome-wide significance at $5e-8$.

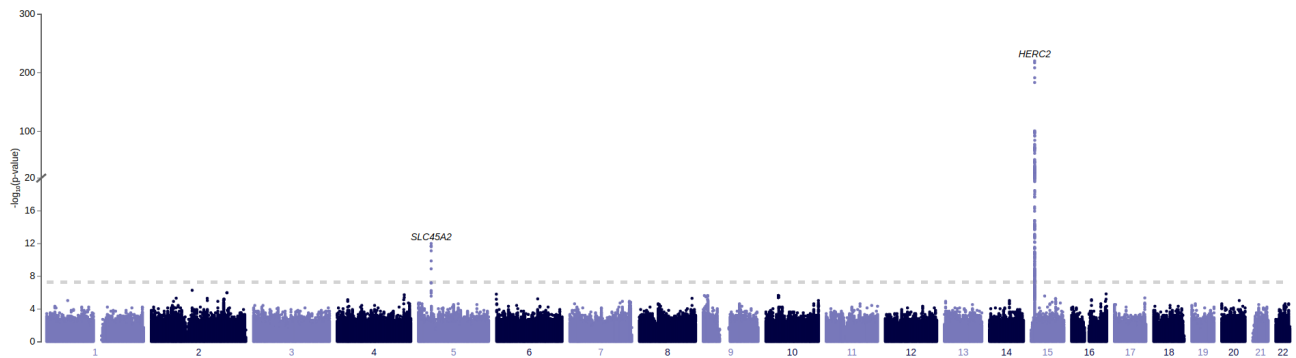


Figure 27: Brown eyes' Manhattan plot. Each point represents an associated variant. The x axis corresponds to the chromosomes and the y axis represents the $-\log_{10}(\text{p-value})$. The horizontal dashed line indicates the threshold for genome-wide significance at $5e-8$.

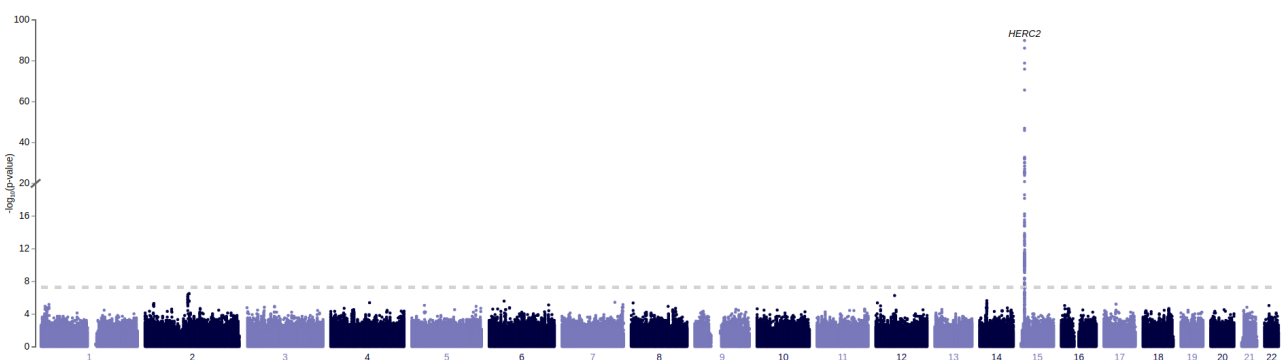


Figure 28: Light brown eyes' Manhattan plot. Each point represents an associated variant. The x axis corresponds to the chromosomes and the y axis represents the $-\log_{10}(\text{p-value})$. The horizontal dashed line indicates the threshold for genome-wide significance at $5e-8$.

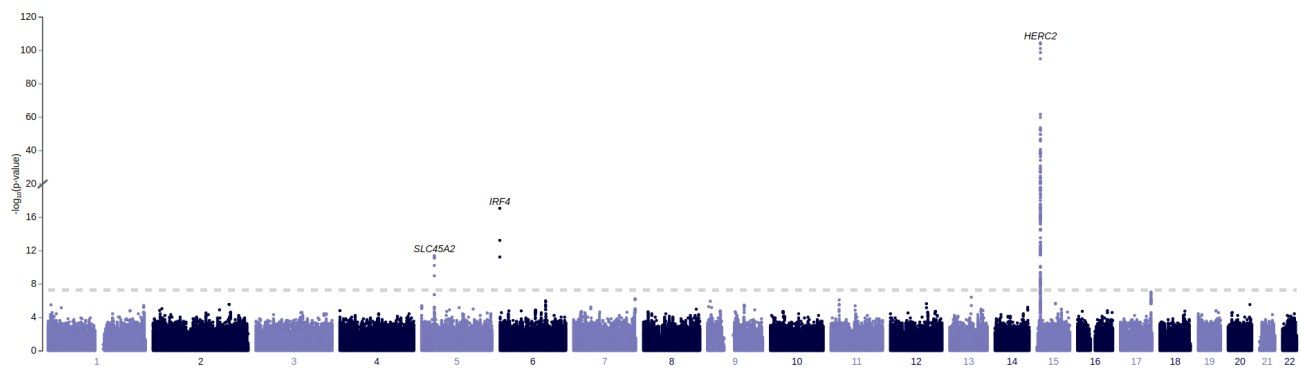


Figure 29: Blue/green eyes. Each point represents an associated variant. The x axis corresponds to the chromosomes and the y axis represents the $-\log_{10}(\text{p-value})$. The horizontal dashed line indicates the threshold for genome-wide significance at $5e-8$.

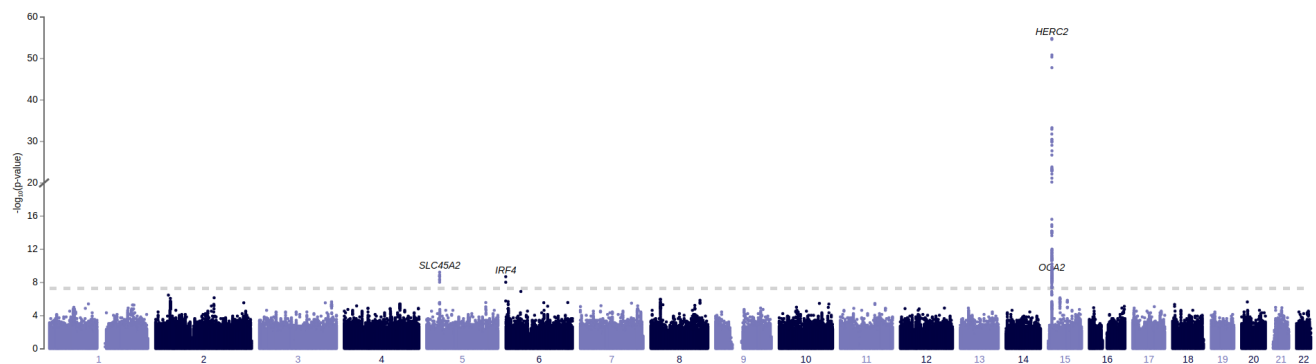


Figure 30: Light blue/green eyes' Manhattan plot. Each point represents an associated variant. The x axis corresponds to the chromosomes and the y axis represents the $-\log_{10}(\text{p-value})$. The horizontal dashed line indicates the threshold for genome-wide significance at $5e-8$.

Second analysis:

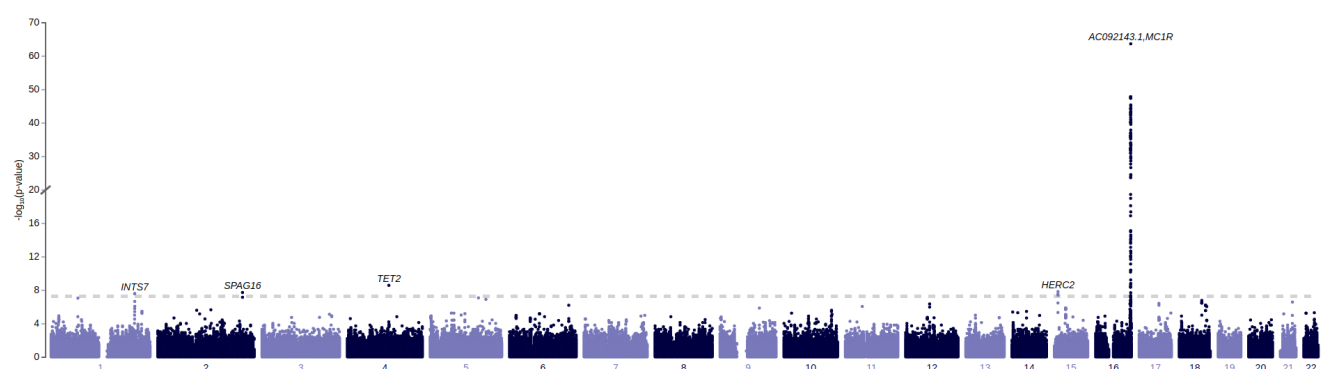


Figure 31: Black hair's Manhattan plot. Each point represents an associated variant. The x axis corresponds to the chromosomes and the y axis represents the $-\log_{10}(\text{p-value})$. The horizontal dashed line indicates the threshold for genome-wide significance at $5e-8$.

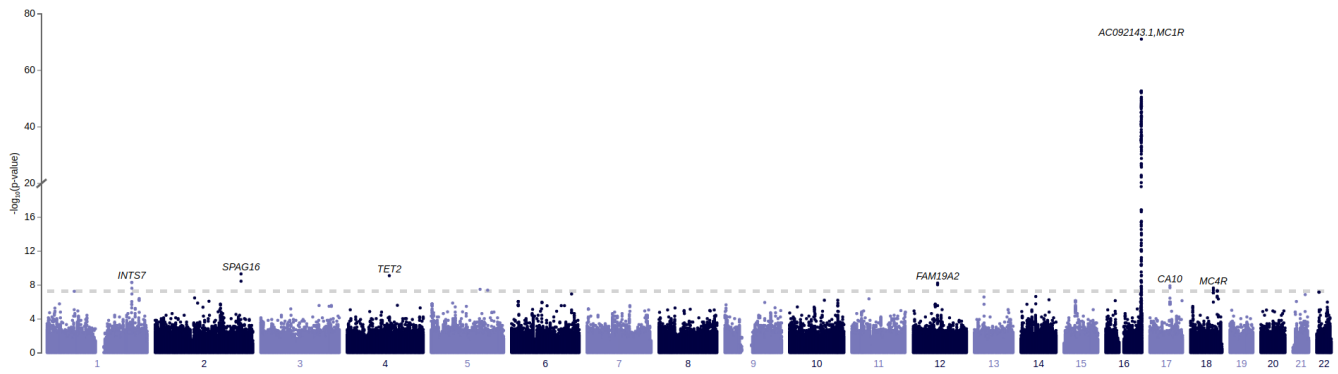


Figure 32: Brown hair's Manhattan plot. Each point represents an associated variant. The x axis corresponds to the chromosomes and the y axis represents the $-\log_{10}(p\text{-value})$. The horizontal dashed line indicates the threshold for genome-wide significance at $5e-8$.

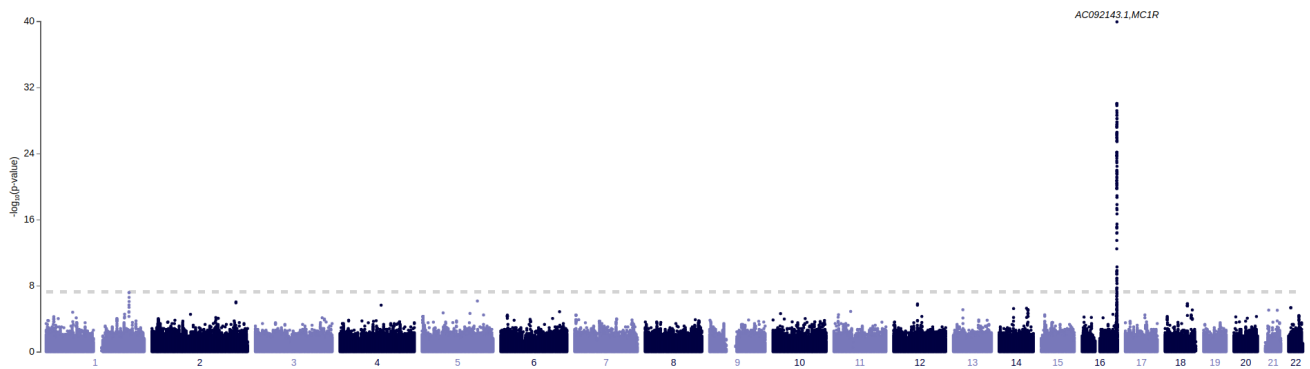


Figure 33: Blond hair's Manhattan plot. Each point represents an associated variant. The x axis corresponds to the chromosomes and the y axis represents the $-\log_{10}(p\text{-value})$. The horizontal dashed line indicates the threshold for genome-wide significance at $5e-8$.

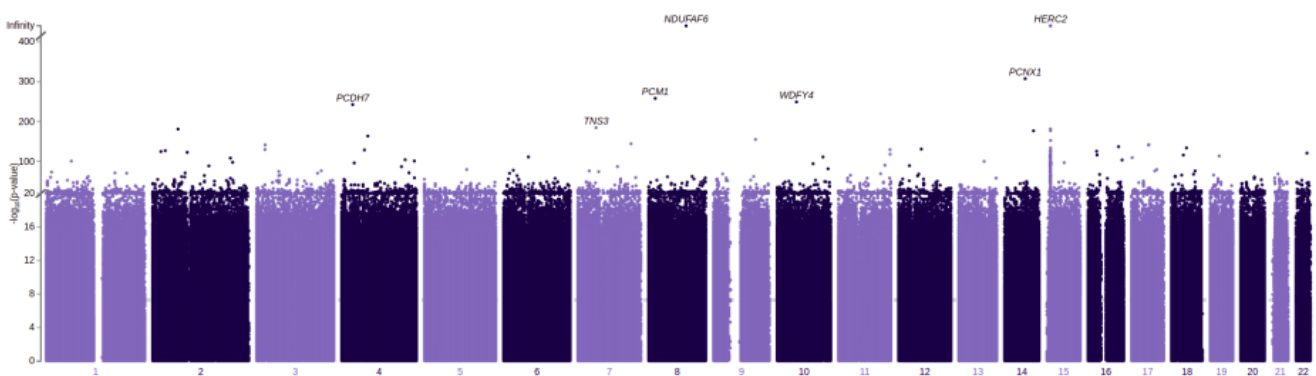


Figure 34: Brown eyes' Manhattan plot. Each point represents an associated variant. The x axis corresponds to the chromosomes and the y axis represents the $-\log_{10}(p\text{-value})$. The horizontal dashed line indicates the threshold for genome-wide significance at $5e-8$.

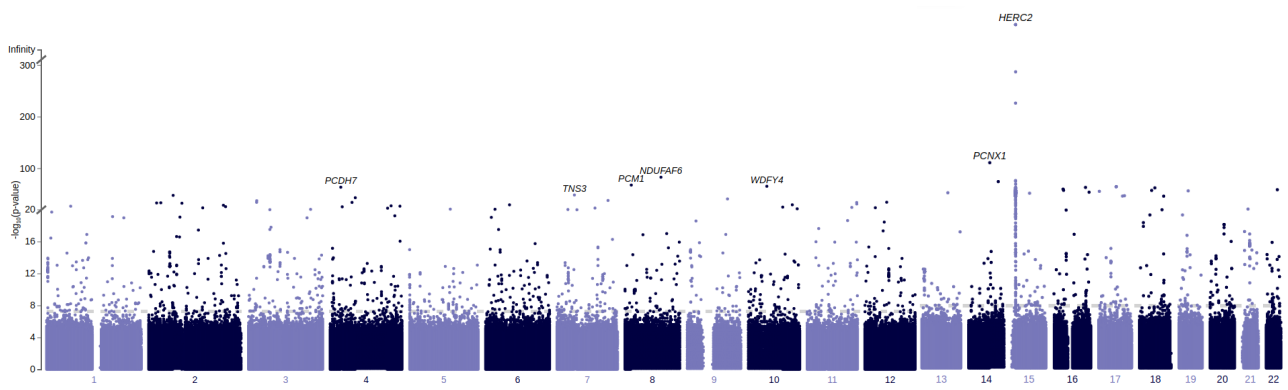


Figure 35: Blue/green eyes' Manhattan plot. Each point represents an associated variant. The x axis corresponds to the chromosomes and the y axis represents the $-\log_{10}(\text{p-value})$. The horizontal dashed line indicates the threshold for genome-wide significance at $5e-8$.

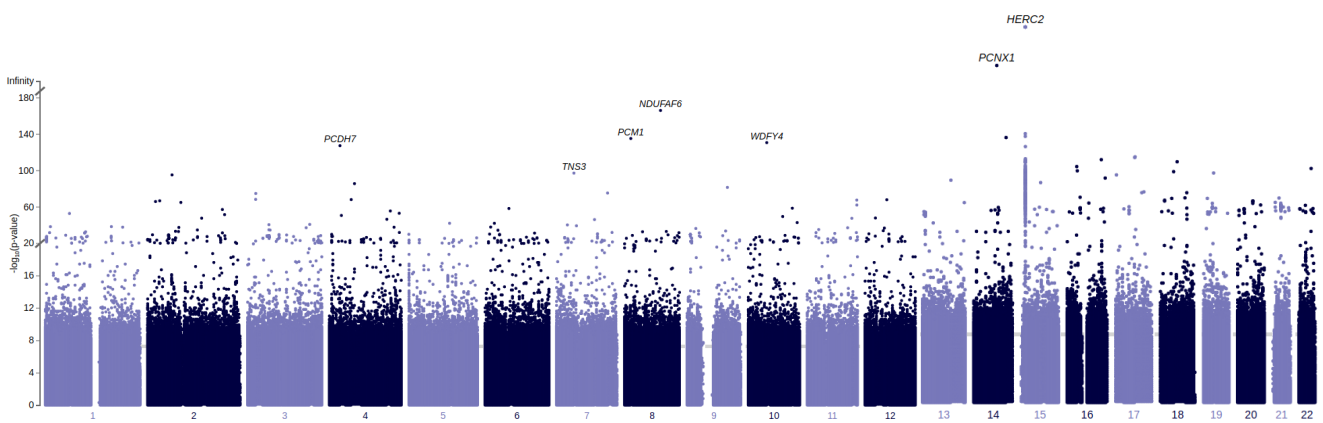


Figure 36: Light blue/green eyes. Each point represents an associated variant. The x axis corresponds to the chromosomes and the y axis represents the $-\log_{10}(\text{p-value})$. The horizontal dashed line indicates the threshold for genome-wide significance at $5e-8$.

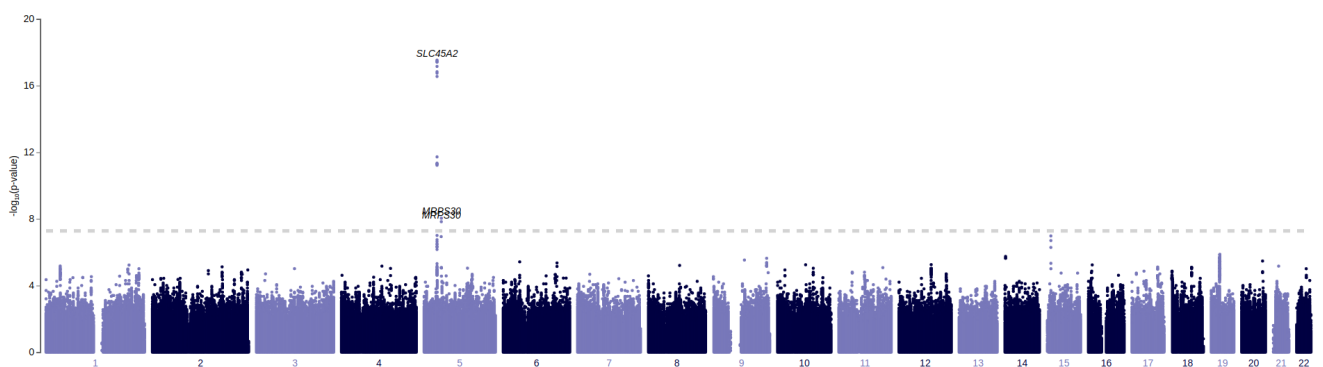


Figure 37: White skin's Manhattan plot. Each point represents an associated variant. The x axis corresponds to the chromosomes and the y axis represents the $-\log_{10}(\text{p-value})$. The horizontal dashed line indicates the threshold for genome-wide significance at $5e-8$.

PheWas

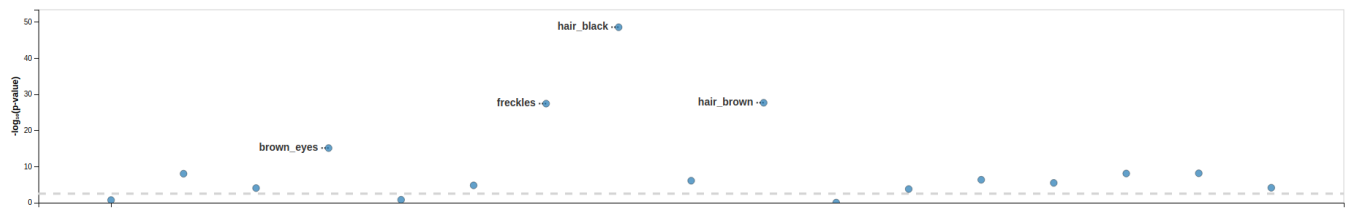


Figure 38: PheWas for *IRF4* (rs12203592) in the population of our study. The x axis corresponds to the phenotypes (in alphabetical order) and the y axis represents the $-\log_{10}(\text{p-value})$.

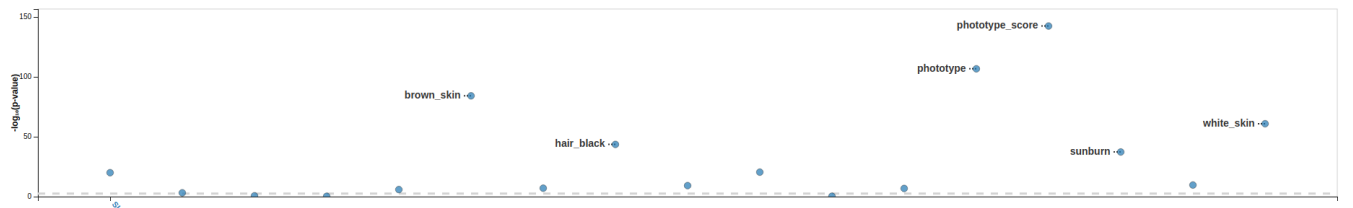


Figure 39: PheWas of *SLC45A2* (rs16891982) in the population of our study. The x axis corresponds to the phenotypes (in alphabetical order) and the y axis represents the $-\log_{10}(\text{p-value})$.

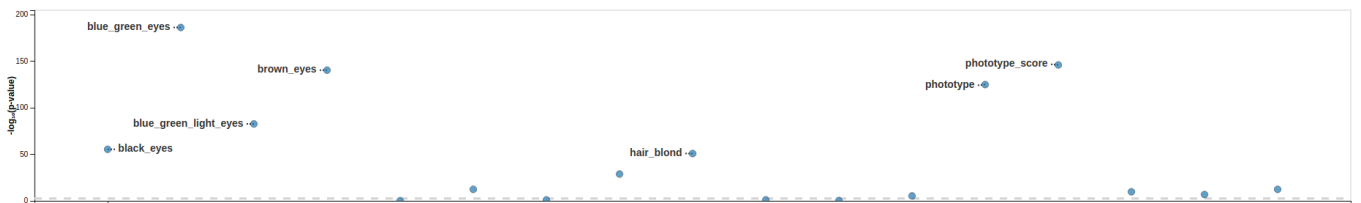


Figure 40: PheWas of *HERC2/OCA2* (rs12913832) in the population of our study. The x axis corresponds to the phenotypes (in alphabetical order) and the y axis represents the $-\log_{10}(\text{p-value})$.

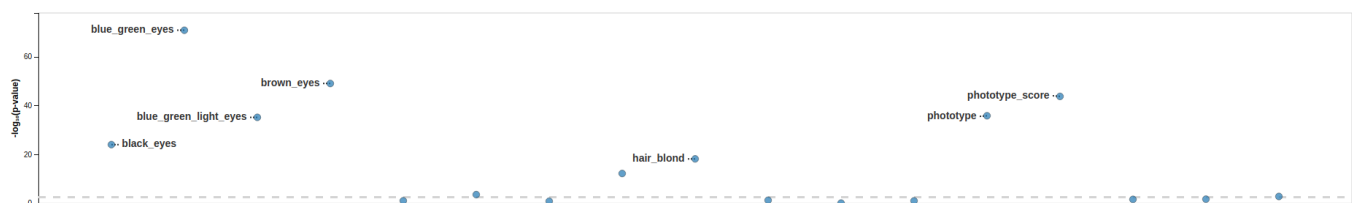


Figure 41: PheWas of *GOLGA8F* (rs148267299) in the population of our study. The x axis corresponds to the phenotypes (in alphabetical order) and the y axis represents the $-\log_{10}(\text{p-value})$.



Figure 42: PheWas of *ADAMTS12* (rs889324) in the population of our study. The x axis corresponds to the phenotypes (in alphabetical order) and the y axis represents the $-\log_{10}(p\text{-value})$.

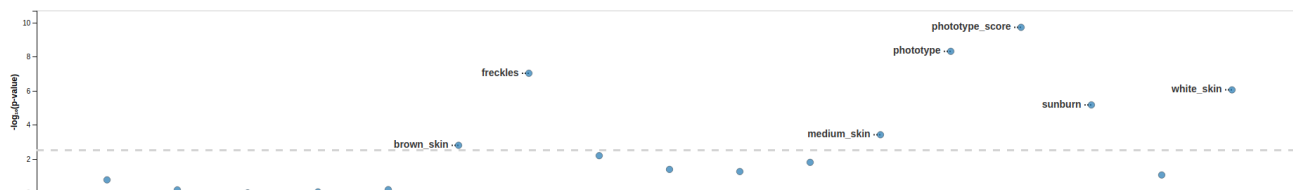


Figure 43: PheWas of *TUBB3* (rs150909008) in the population of our study. The x axis corresponds to the phenotypes (in alphabetical order) and the y axis represents the $-\log_{10}(p\text{-value})$.

Heritability

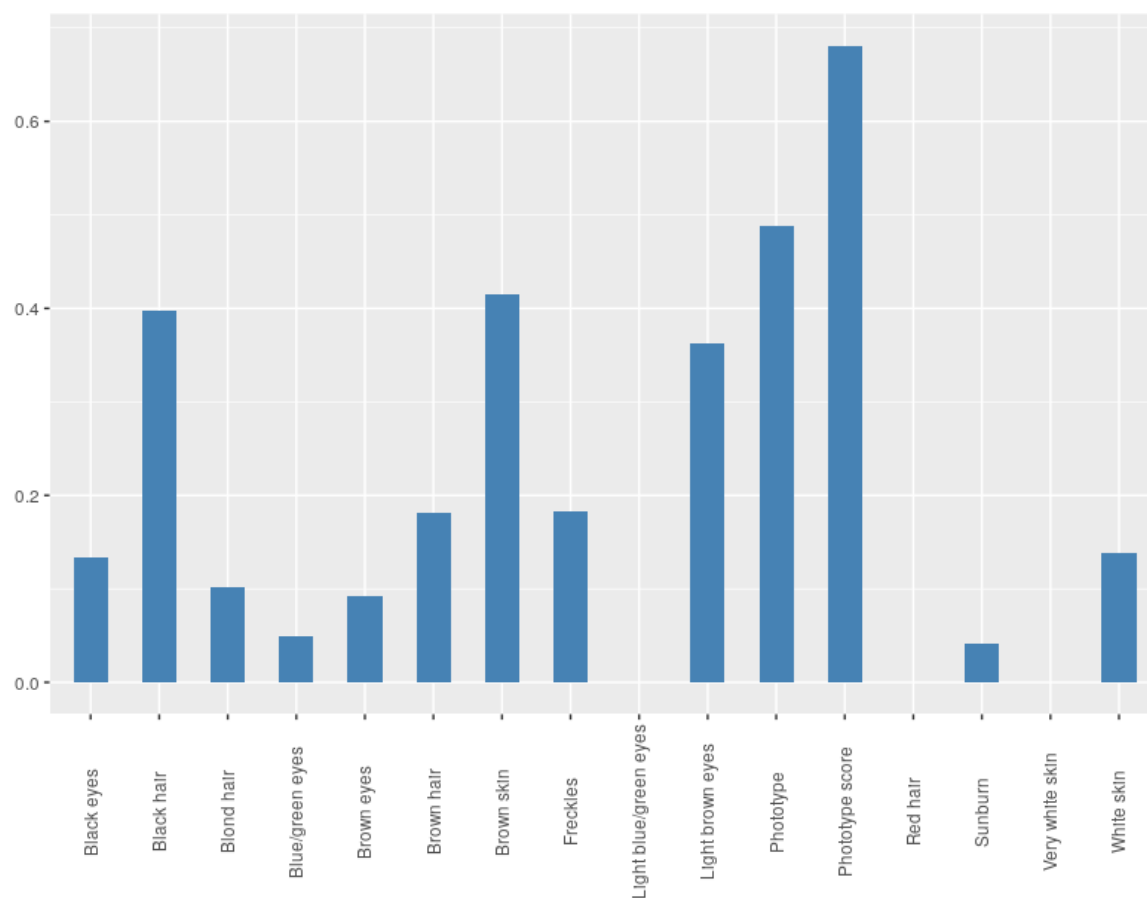


Figure 44: Heritability barplot. The x axis corresponds to the traits and the y axis represents the h^2 .