We are all unique, even if we share certain characteristics with our family members and those around us. The individual differences that can be observed in the population are caused by a combination of genetic and environmental factors. In this PhD program, I endeavor to add to our understanding of the way genetic factors explain individual differences in human complex traits (mainly focus on pigmentation traits like hair color and eye color, and hematological traits: novel biomarkers for blood cell ratios) by applying a variety of methodological tools to different sets of personal characteristics, which in genetics are commonly referred to as ‘phenotypes’. Making use of phenotype and DNA data collected in twins and family members registered with the Netherlands Twin Register, I applied different methods to answer the questions about the etiology of individual differences, which vary from heritability study, Genome-wide association study (GWAS), Genome-wide Complex Trait Analysis (GCTA), Epigenome-wide association study (EWAS), Expression quantitative trait loci studies (eQTLs).

One interesting finding of my studies was that there is a large genetic correlation between hair color and eye color, which means that (some of the) genes that influence hair color also influence eye color. An important finding from my GWAS studies for pigmentation traits and hematological traits was that I verified several previously known color genes. But I also identified one novel locus related to platelet to lymphocyte ratio in blood: the HBS1L-MYB region on chromosome 6, which also affected platelet count and associated with other hematological parameters (such as hemoglobin level and red blood cell count) and blood related diseases (such as myeloproliferative neoplasms, beta-thalassemia and iron deficiency anemia) in previous studies. My studies also provided new insight into the biological pathways that determine blood cell ratios: many of the genetic variants (SNPs) associated with blood cell ratios influence the expression levels of genes involved in immune system pathways, and many other important pathways involved in hematopoietic cell functions. I also found that blood cell ratios are connected to methylation levels of thousands of genes.

The combination of genetic approaches I have used in my thesis provide will lead to a better understanding of the processes and genetic architecture of human complex traits.