

# Wellbeing: A Dynamic Interplay Between Genes and Environment

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## Background

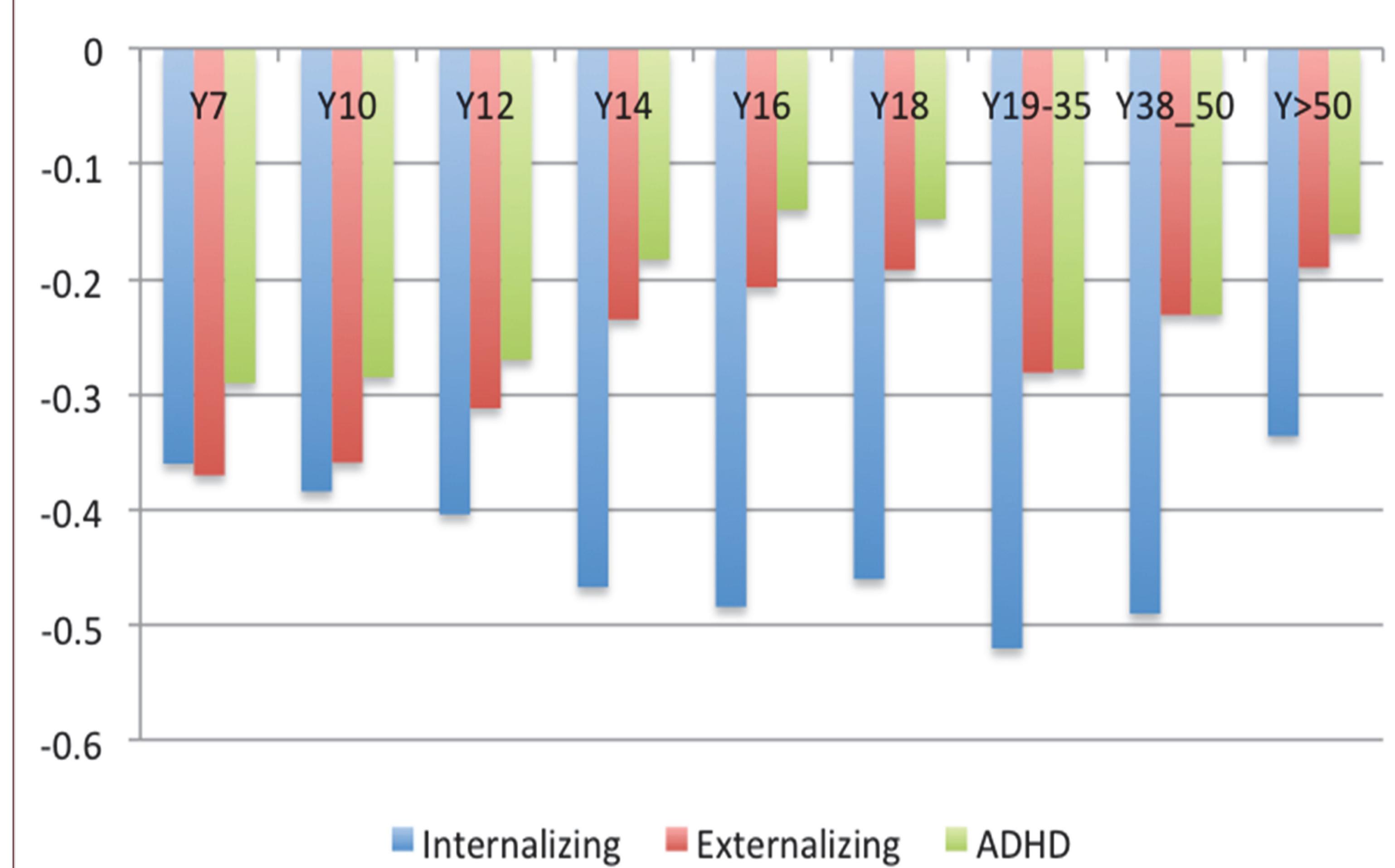
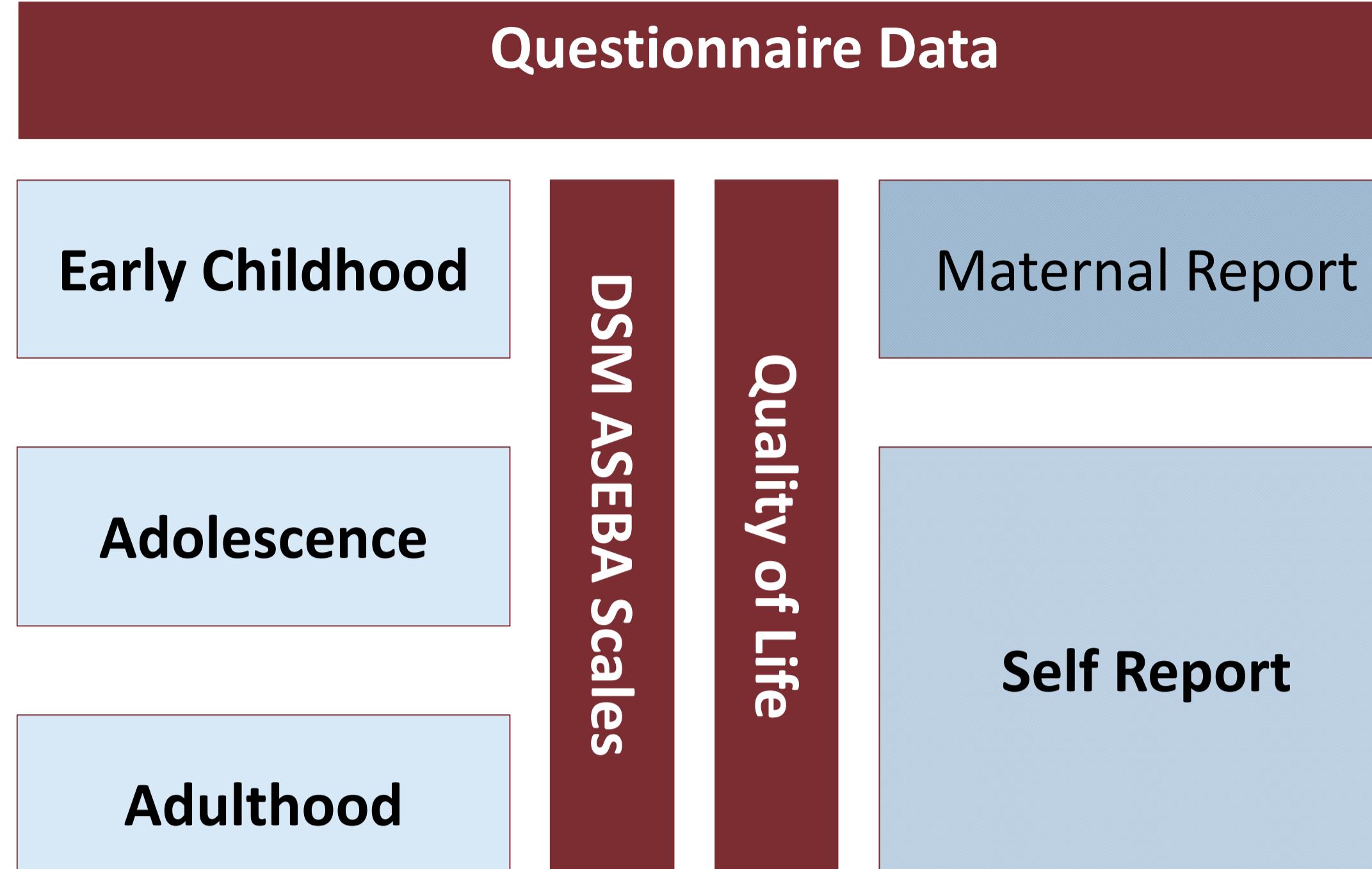
In recent years, wellbeing has become a topic of research across several scientific disciplines. Wellbeing (WB) is associated with physical health, mental health, and resilience. It predicts longevity among healthy populations and the observed positive effect is of similar magnitude as the **negative effect of smoking**.

However, although increased interest:

- environmental and social influences have been studied mostly in isolation of possible genetic background of an individual.
- Genetic studies so far have ignored the dynamic interplay with the environment.

## Project 1: Association Wellbeing and Psychopathology

### Questionnaire Data



## Project 2: Meta-Analysis Genome Wide Association Wellbeing

### Discovery Stage 42 cohorts: $N \sim 150.000$

**Phenotypic def:**  
Broad array of wellbeing measures to maximize sample size

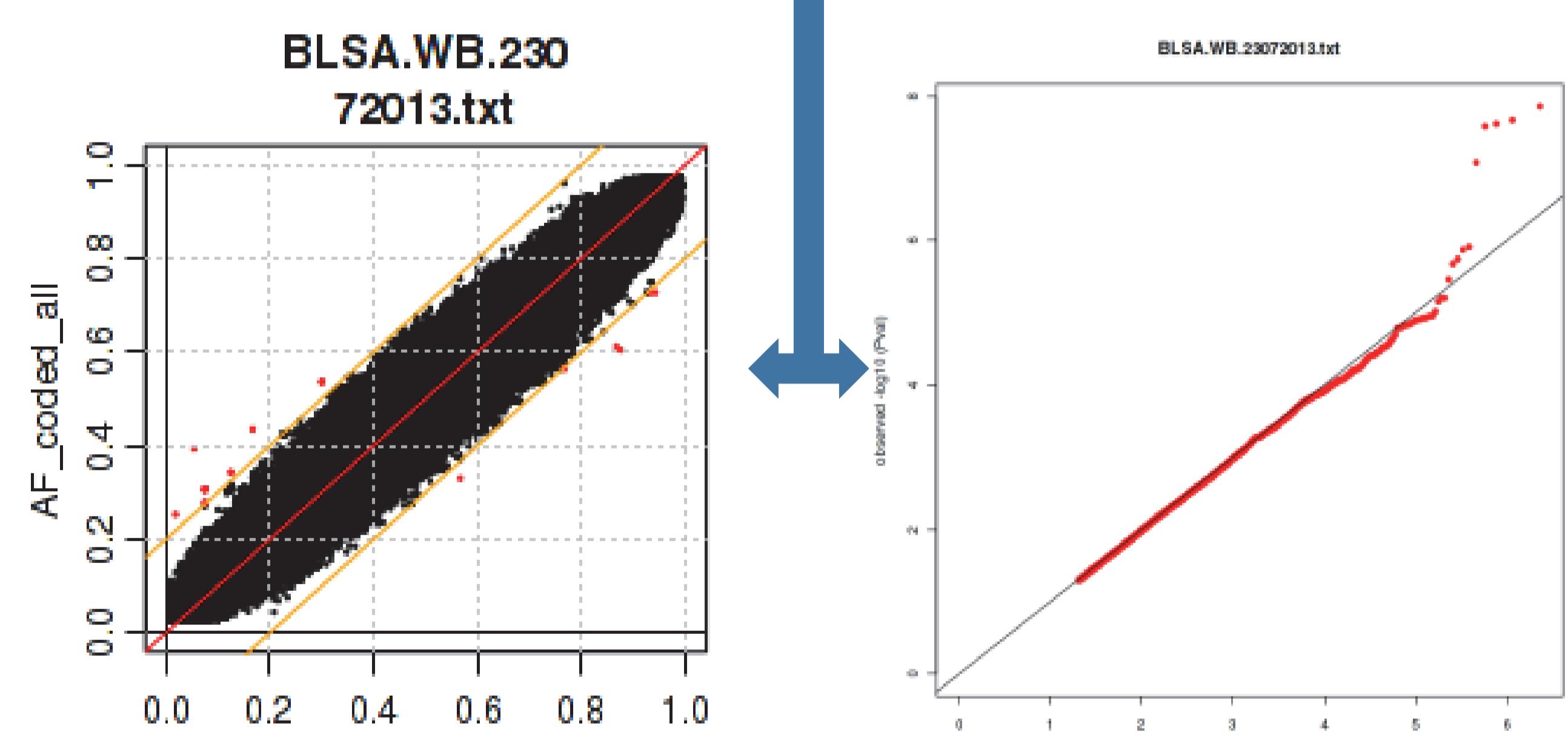
**Pre imputation:**  
-MAF<1%  
-Call rate<95%  
-failure HWE at  $p < 10^{-6}$

**Imputation**  
-HapMap2  
-CEU individuals  
-minority 1000G

### Meta-Analysis

### Quality Control 'EasyQC'

**Association tests**  
-22 autosomals  
-GC correction during meta-analysis



**Visualisation of quality control:** [A] allele frequency plot by creating a scatterplot of each input file versus a reference: [B] QQ plot for detecting outliers, such as stratification

## Project 3: Polygenic prediction for NEO-PI personalities and wellbeing

**Aim:** Do NEO-PI polygenic scores (de Moor 2012), predict variance in measures of wellbeing?

### IncludeSNPs

-MAF > 0.05  
 $R^2 > 0.8$

### LD Pruning

-pairwise  $r^2 < 0.25$   
-hwe 0.000001  
-make binary files from unrel. SNPs

### Calculate PRS

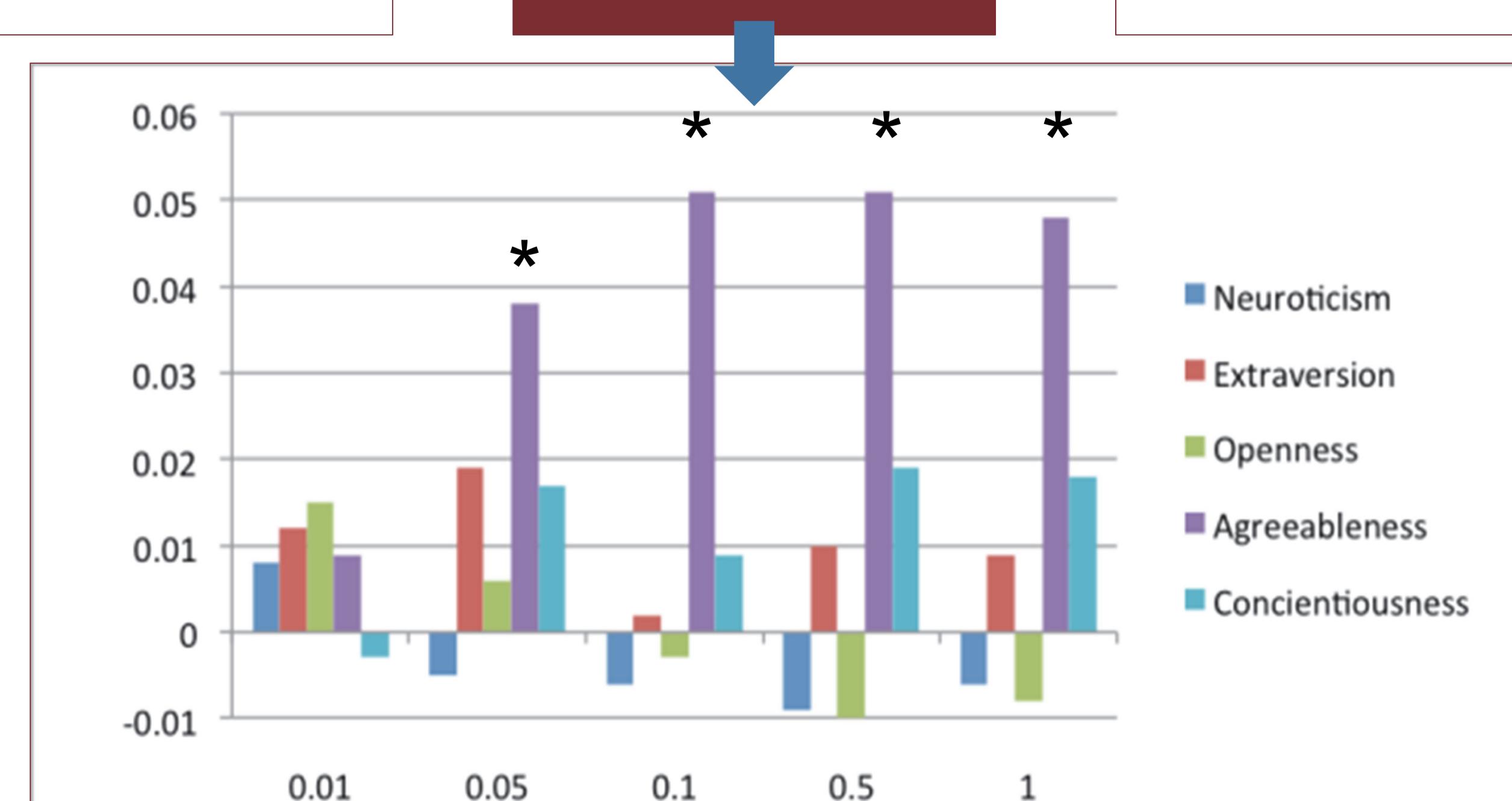
-Pruned data  
-Beta NEO-PI  
-Pvalues NEO-PI  
-Sig. thresholds

### Meta-Analysis

### Regr. Analysis

-Generalized estimation equation

### Merge output files with phenotypic data



Preliminary results: Polygenic scores NEO-PI personality on NTR WB data

## Future Plans

- Identify molecular mechanisms underlying the prospective health advantages underlying wellbeing using different gene-expression profiles.
- Search for differentially methylated regions based on phenotypic discordance or variance in exposure of promising environmental phenotypes (e.g. loneliness).