##### GWAS Results

##### Run1\_PCA\_1\_2

None of the SNPs were significant when correcting for PCA 1 and PCA 2. Below you can find the qq-plot for the data after correcting for both of the PCAs.

Genomic inflation est. lambda (based on median chisq) = 1.01828.A screenshot of a cell phone

Description automatically generated

Here is the qq-plot for the data before correcting for PCA 1 & 2

Genomic inflation est. lambda (based on median chisq) = 7.20633.

A close up of a map

Description automatically generated

PCA 1 & 2 were chosen based on the elbow point of the scree plot below.

The PLINK command used to generate these Eigenvalues was:

plink --bfile run1\_p2\_s6--pca --out run1\_pca

The R scripts used to generate all the graphs below were retrieved from:

<https://github.com/MareesAT/GWA_tutorial/blob/master/1_QC_GWAS.zip>

A screenshot of a cell phone

Description automatically generated

Population Stratification was present as illustrated by the two graphs below:

Ethnicity Graph

A screenshot of a cell phone

Description automatically generated

Control Vs Affected Graph

A screenshot of a cell phone

Description automatically generated

In order to get a logistic analyses utilizing only PC1 and PC2, a file containing only PC1 and PC2 was created: “run1\_pca\_first\_two.eigenvec”. This file allows us to only look at PC1 & PC2 instead of PC 1-20 in the original file.

The PLINK command used was as follows:

plink --bfile run1\_p2\_s6 --logistic --covar run1\_pca\_first\_two.eigenvec --assoc --adjust --out run1\_logistic\_pca\_1\_2

The association test taking into account PC1 and PC2 did not yield any statistically significant results.