How many duplicated SNPs are there (Section 1f)?

There are a total of 2 duplicated SNPs

How many non-ambiguous SNPs were there (Section 1g)?

There are 499,617 non-ambiguous SNPs

How many SNPs and samples were filtered out of the data (Section 2c)?

14 samples were removed due to a high rate of genotype missingness

5,353 SNP were removed due to missing genotype data

944 SNPs were removed due to being out of Hardy-Weinberg Equilibrium

5,061 SNPs were removed due to low minor allele frequency

How many samples were excluded due to high or low heterozygosity rate (Section 2c)?

2 samples were excluded

How many samples were excluded due to mismatched sex information (Section 2f)?

4 samples were excluded

How many related samples were excluded (Section 2g)?

No samples were excluded

Which P-value threshold generates the “best-fit” PRS (Section 3f)?

0.3

How much phenotypic variance does the “best-fit” PRS explain (Section 3f)?

0.1612372