**Whole genome model quality checks**

* MAF > 0.01
* Format: bed, bim, fam
* Variant missingness <= 1
* HWE: 1e-6
* Bi-allelic SNPs only
* Remove regions with extended LD
* Autosomal chromosomes 1-22

**Imputation variables quality checks**

* Format: bgen / sample
* HWE in cases: 1e-10
* HWE in controls: 1e-6

Covariates in both steps: phenotype ~ snp + age + age^2 + sex + age · sex + p1 + … + p10 + genetic\_batch