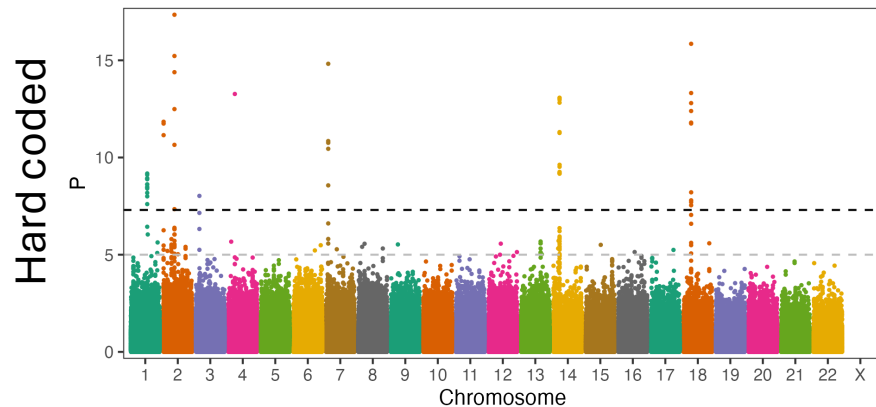


A

## GWAS Manhatten (hard\_coded)

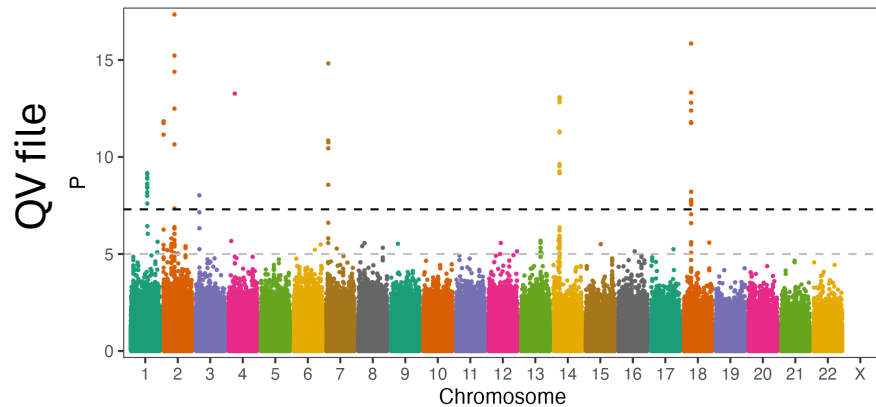
Before main variant filters, 1198 founders and 199 nonfounders present.  
Total genotyping rate is 0.99727.  
1143775 variants and 1397 people pass filters and QC.  
Among remaining phenotypes, 689 are cases and 708 are controls.



B

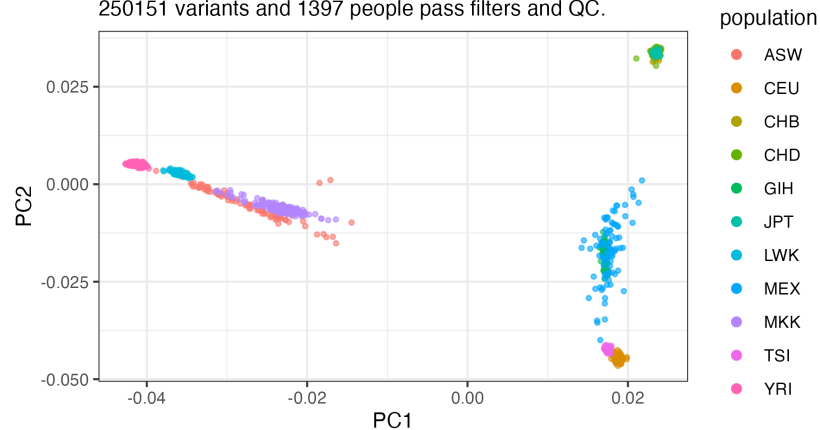
## GWAS Manhatten (qv\_gwas\_common)

Before main variant filters, 1198 founders and 199 nonfounders present.  
Total genotyping rate is 0.99727.  
1143775 variants and 1397 people pass filters and QC.  
Among remaining phenotypes, 689 are cases and 708 are controls.



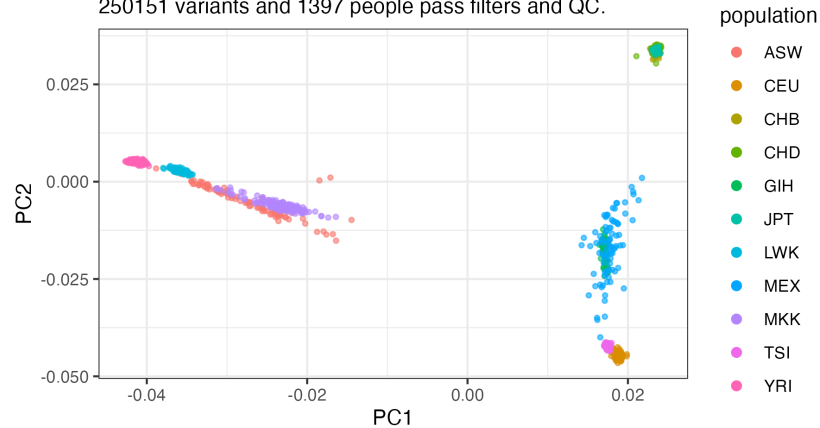
## PCA bi-plot PC1 vs PC2 (hard\_coded)

250151 variants remaining.  
Before main variant filters, 1198 founders and 199 nonfounders present.  
Total genotyping rate is 0.997159.  
250151 variants and 1397 people pass filters and QC.



## PCA bi-plot PC1 vs PC2 (qv\_gwas\_common)

250151 variants remaining.  
Before main variant filters, 1198 founders and 199 nonfounders present.  
Total genotyping rate is 0.997159.  
250151 variants and 1397 people pass filters and QC.



C

## MD5 checksum

step6 gwas.assoc	9165ff40	9165ff40
step5 hwe.bed	a6954e48	a6954e48
step4 maf.bed	74fcce2b	74fcce2b
step3 geno.bed	be4c9b72	be4c9b72
step2 mind.bed	be4c9b72	be4c9b72
step1 autosomal.bed	be4c9b72	be4c9b72
	A_hard_coded	B_qv_yamli
MD5 match <span style="background-color: #2e8b57; color: white; padding: 2px 5px;">TRUE</span>		