

Merging SSNS GWAS data with 1000 Genomes

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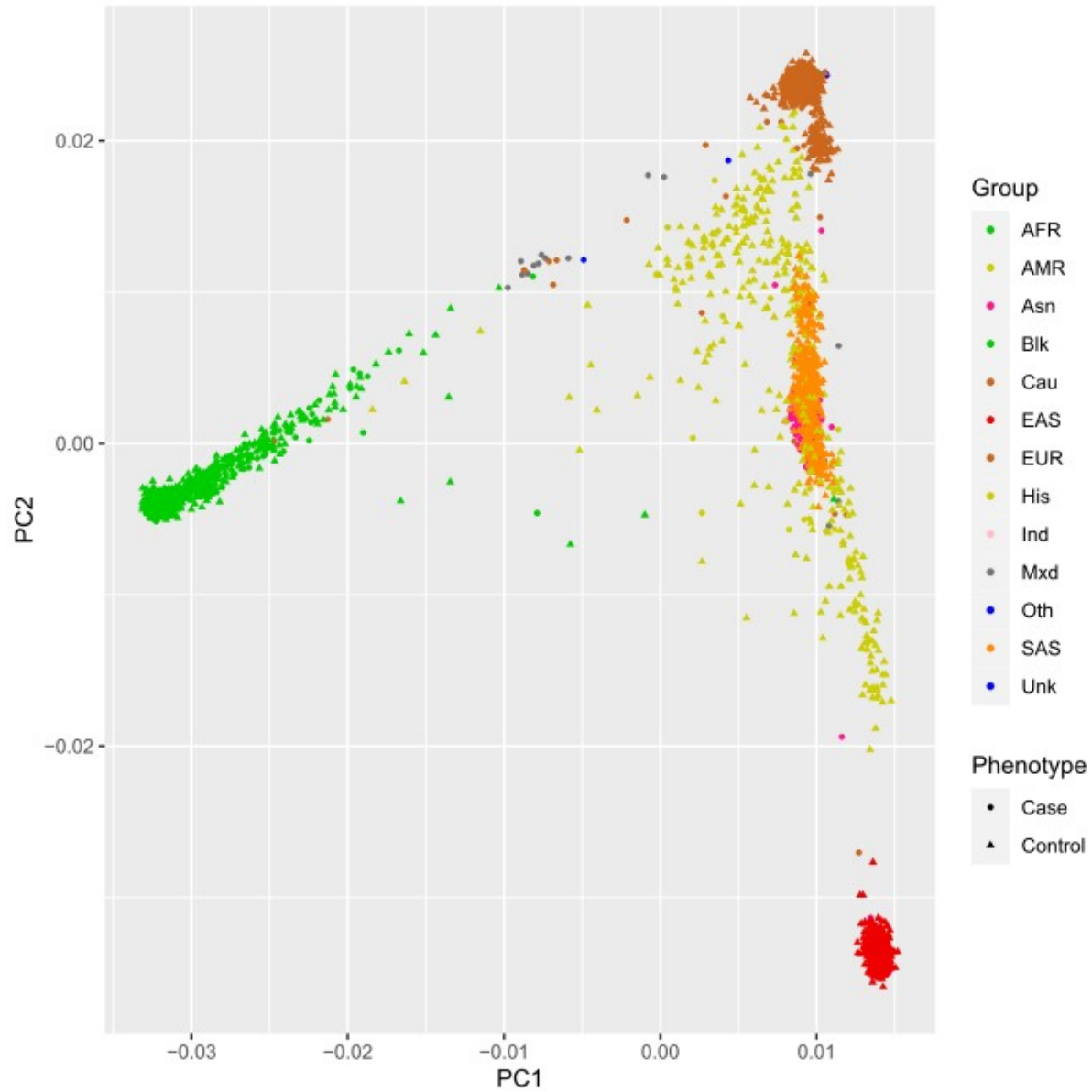
Department of Biostatistics and Bioinformatics

Duke University

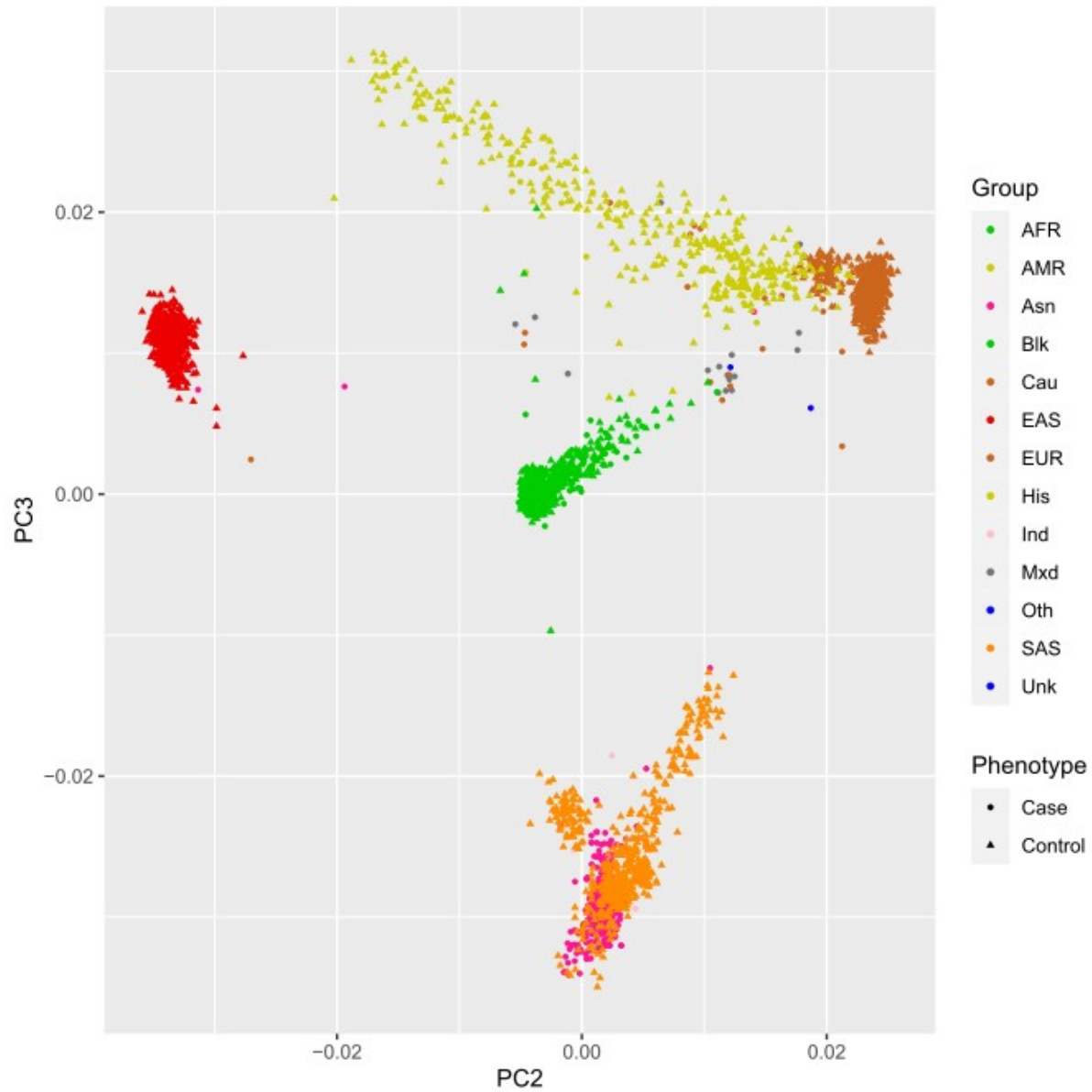
Merge 1000 Genome with GWAS

	SNP's removed	Remaining
common SNPS		1404856
non standard allele	769	1404087
missingness (variant)	8824	1395263
missingness (sample)	12	
Hardy-Weinberg $P < 10^{-4}$	61108	1334155
transversions	145853	1188302
combined without flip	129250	1059052
Hardy-Weinberg $P < 10^{-4}$	227130	831922

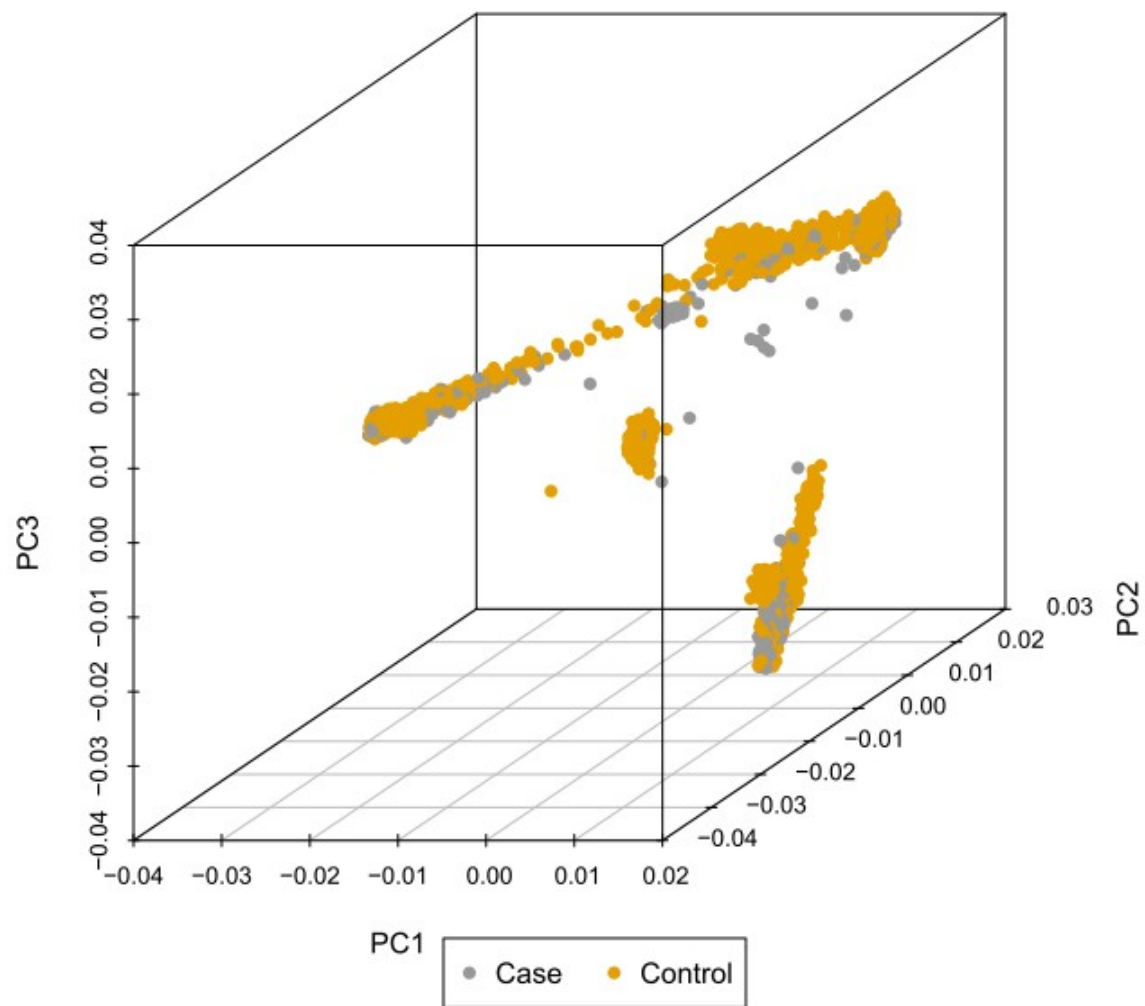
PCA analysis



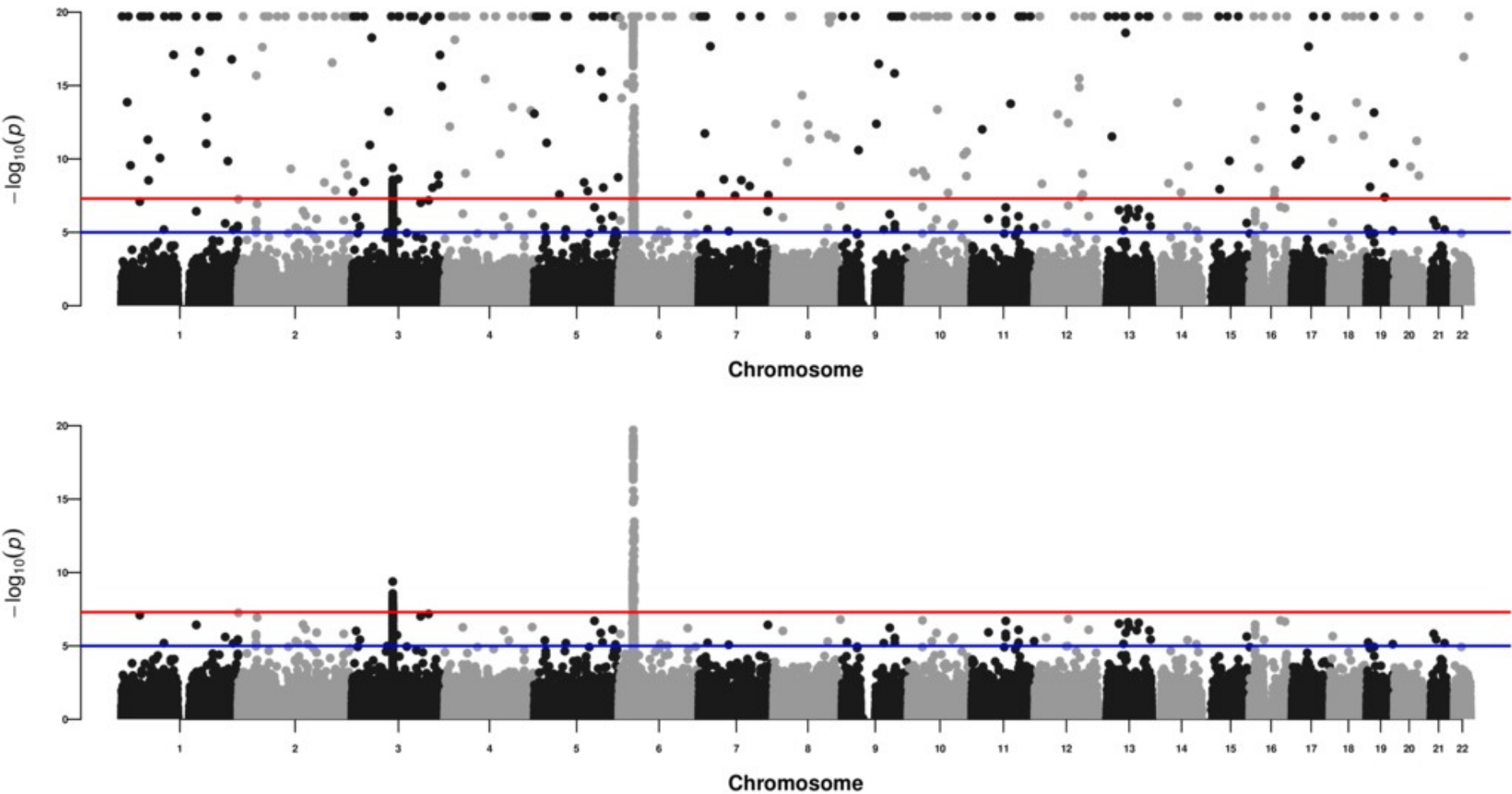
PCA analysis



PCA analysis

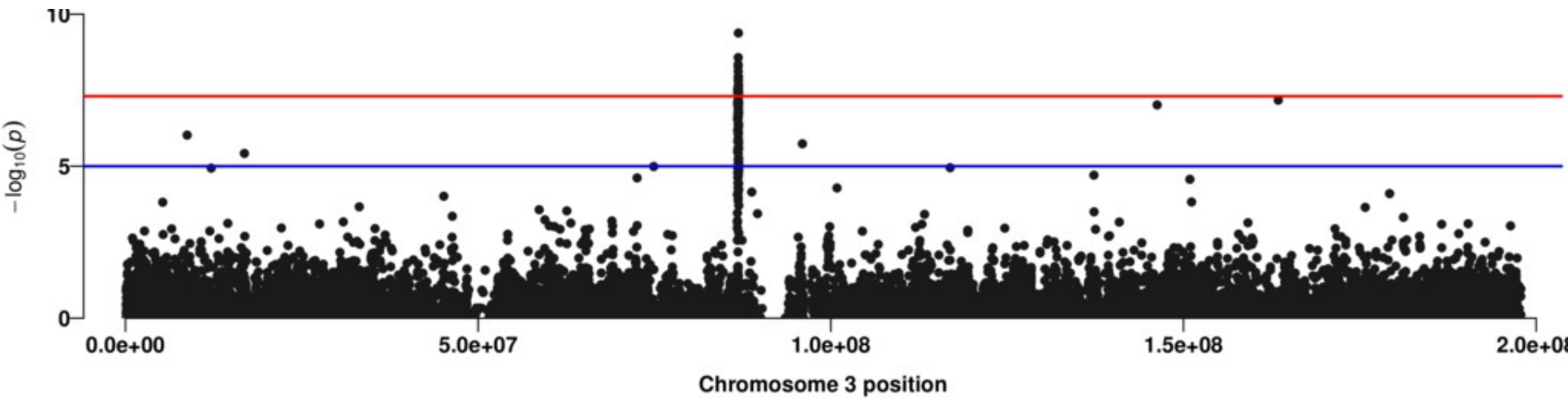


Manhattan plots, before and after “neighbor” filtering

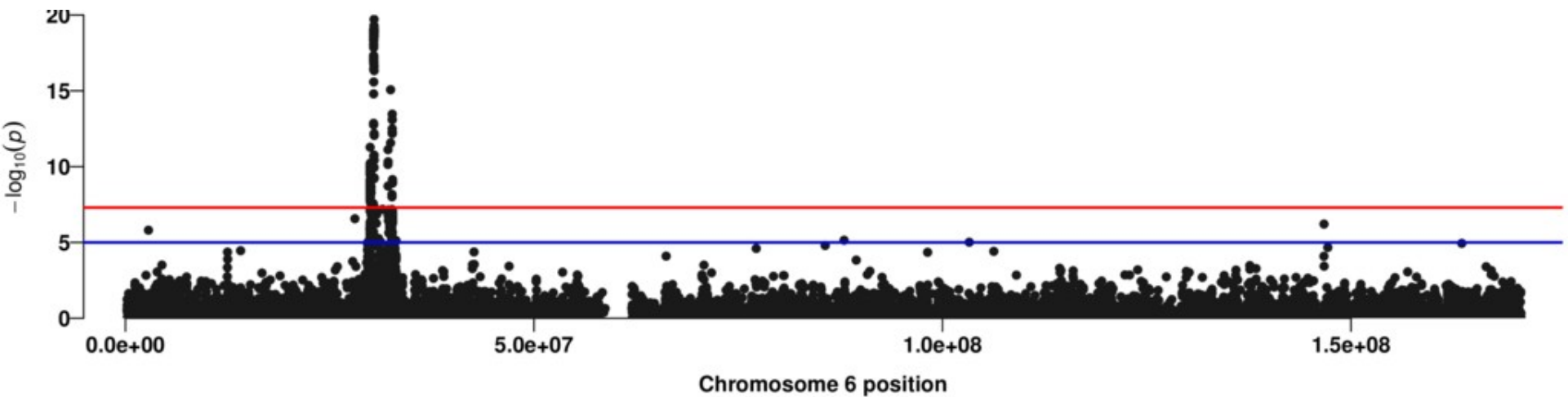


Clean version (bottom) removed loci with $p < 5e-8$ and no direct neighbors with $p < 1e-5$. Full version (top) capped p-values to minimum p-value in clean version ($\sim 1e-20$).

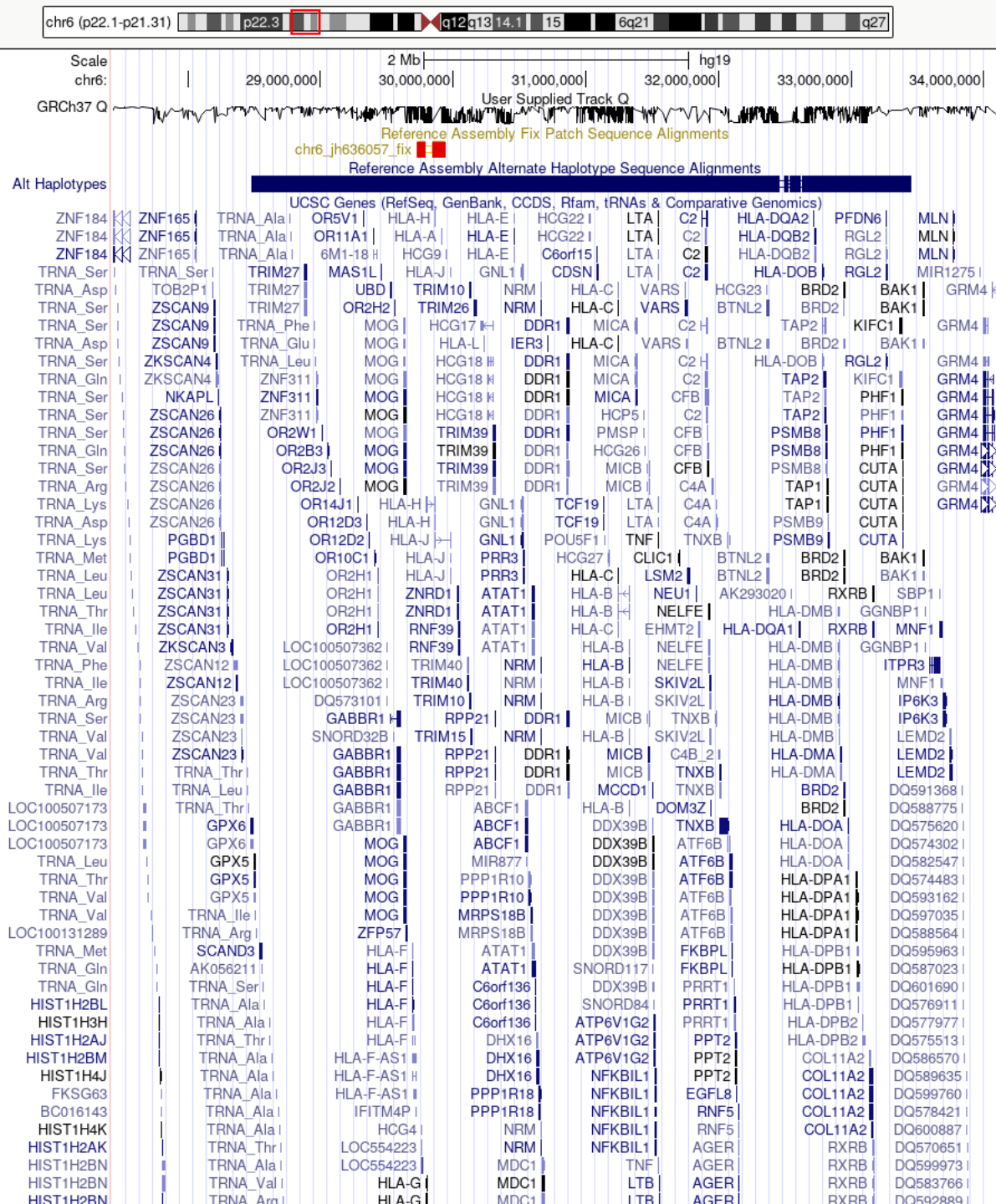
Chr 3 peak: 86,793,259 - 86,917,711



Chr 6 peak: 29,938,571 - 32,681,568



Chr 6 peak: HLA region



Chr 3
peak:
VGLL3?

UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

chr3:86,399,796-87,399,795 1,000,000 bp.

enter position, gene symbol, HGVS or search terms

go

The Genome Browser is up for grant renewal. Survey: Please let us know how you use our site and tools.

chr3 (p12.1-p11.2) 24.3 13 23 24 28 29

