Figures

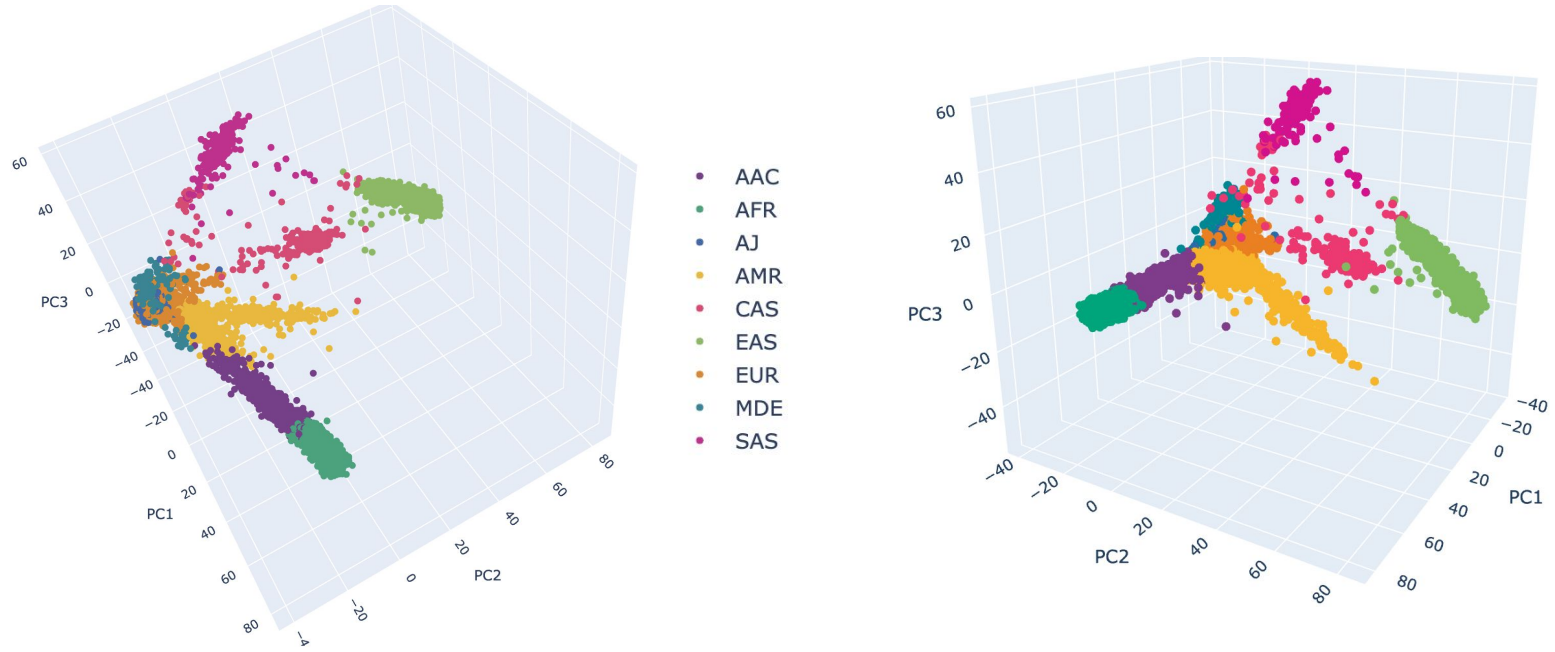


Figure 1. Ancestry prediction clustering for samples genotyped on the NeuroBooster array

3 dimensional principal components analysis to group individuals based on their genetic makeup. A total of 2,793 samples from the Global Parkinson's Genetics Program were included, including 2,373 Parkinson's disease cases and 420 Gaucher disease cases. Each point represents a sample and the colors depict the ancestral background as shown in the color legend: EUR = orange, EAS = lemon green, AMR = yellow, AJ = lapis blue, AFR = teal blue, AAC = purple, SAS = magenta, CAS = dark pink, MDE = cerulean blue. EUR (Europe), EAS(East Asian), AMR (Latino/Admixed American), AJ (Ashkenazi Jewish), AAC (African-Admixed), AFR (African), SAS (South-Asian), CAS (Central-Asian), MDE (Middle East).

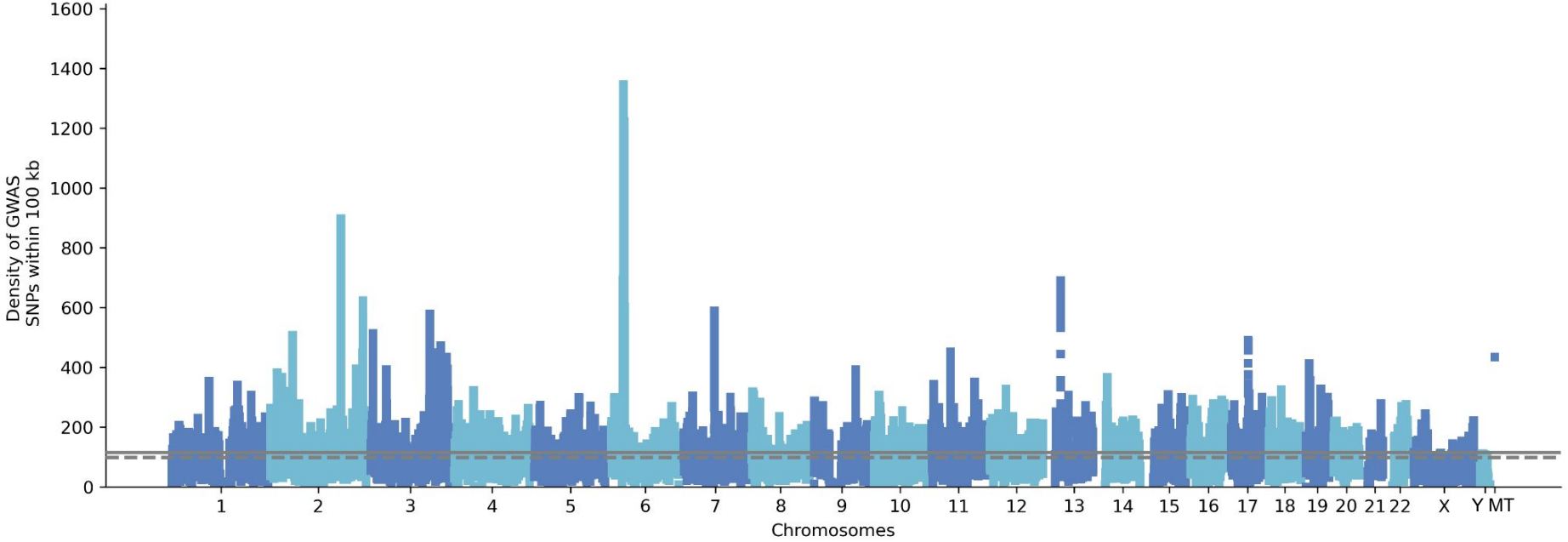


Figure 2. Brisbane plot showing the genomic density of SNPs on GP2 raw genotyped data generated on the NeuroBooster array

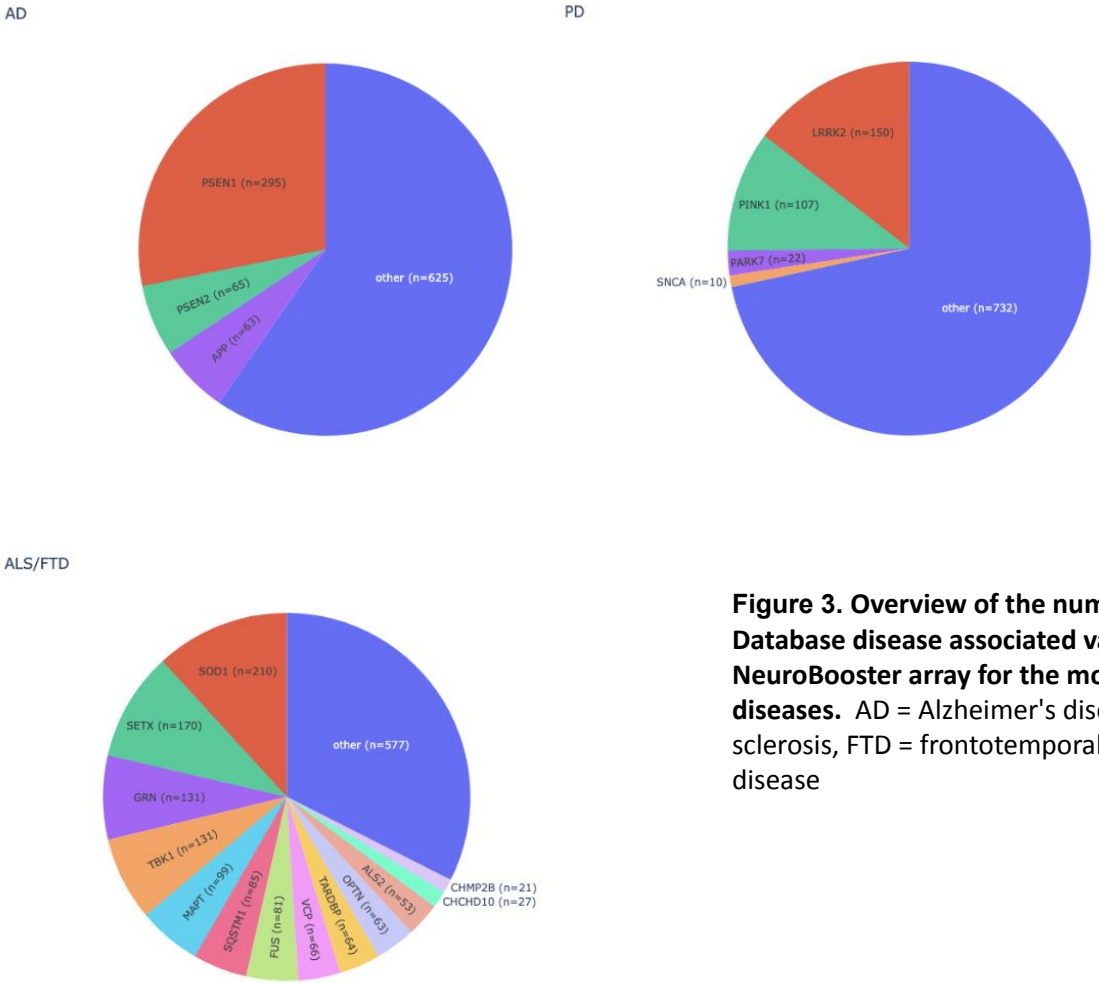


Figure 3. Overview of the number of Human Gene Mutation Database disease associated variants that are present on the NeuroBooster array for the most prevalent neurodegenerative diseases. AD = Alzheimer's disease, ALS = amyotrophic lateral sclerosis, FTD = frontotemporal dementia, and PD = Parkinson's disease

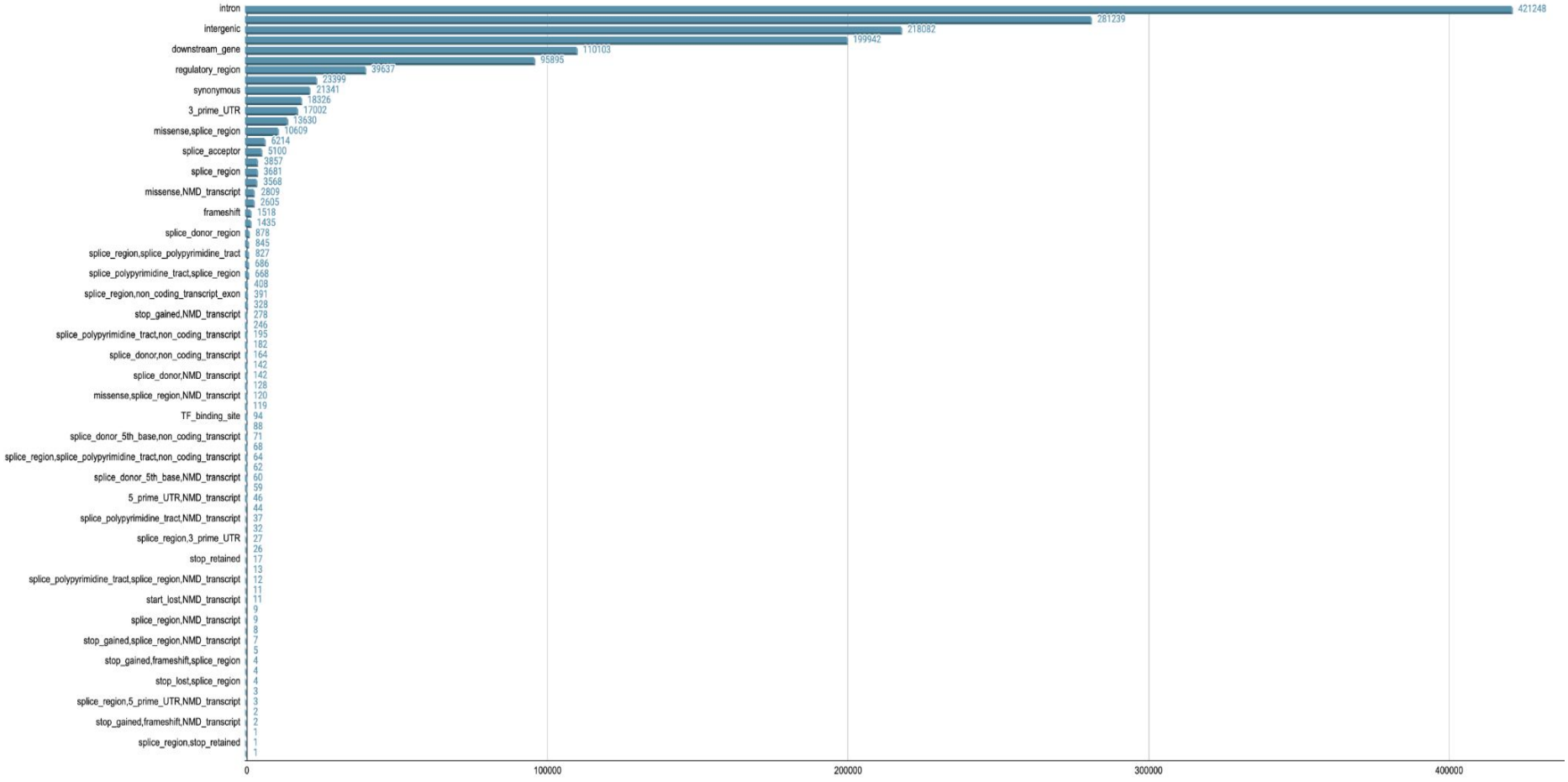


Figure 4A. Overview of NeuroBooster array content by variant category

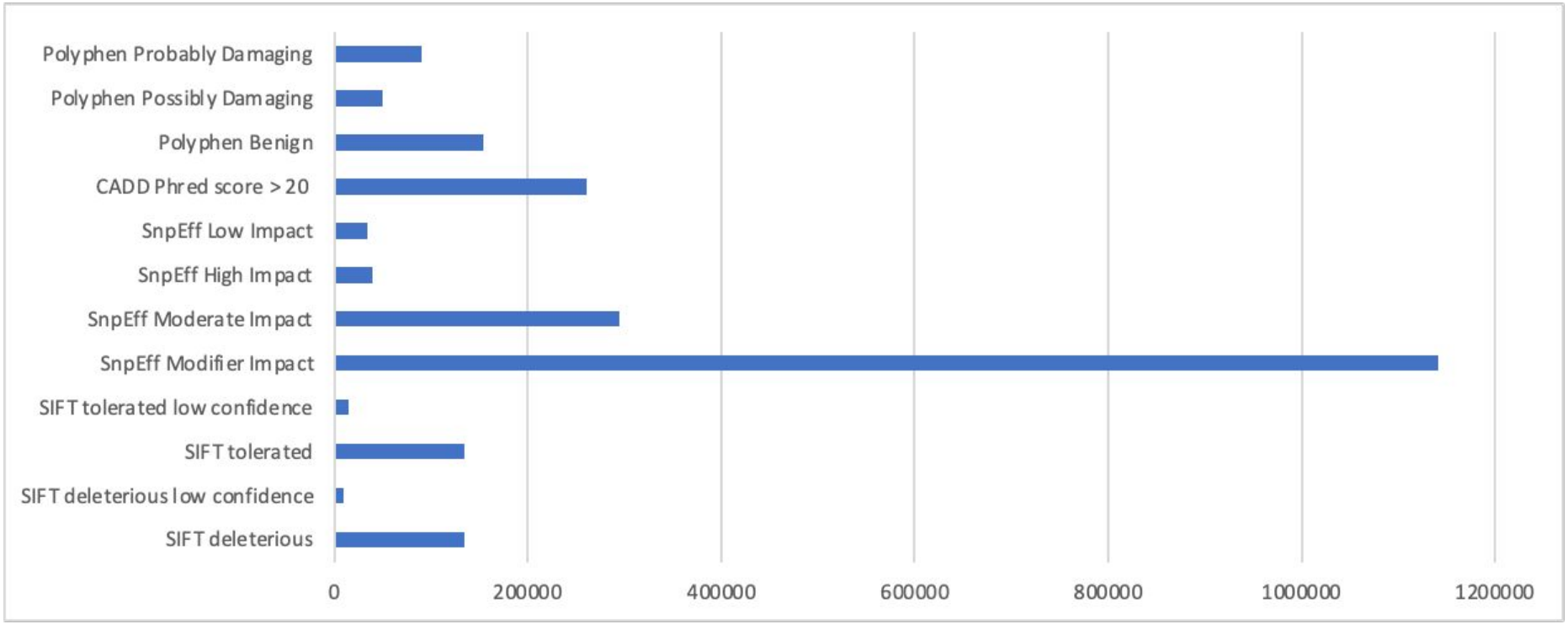
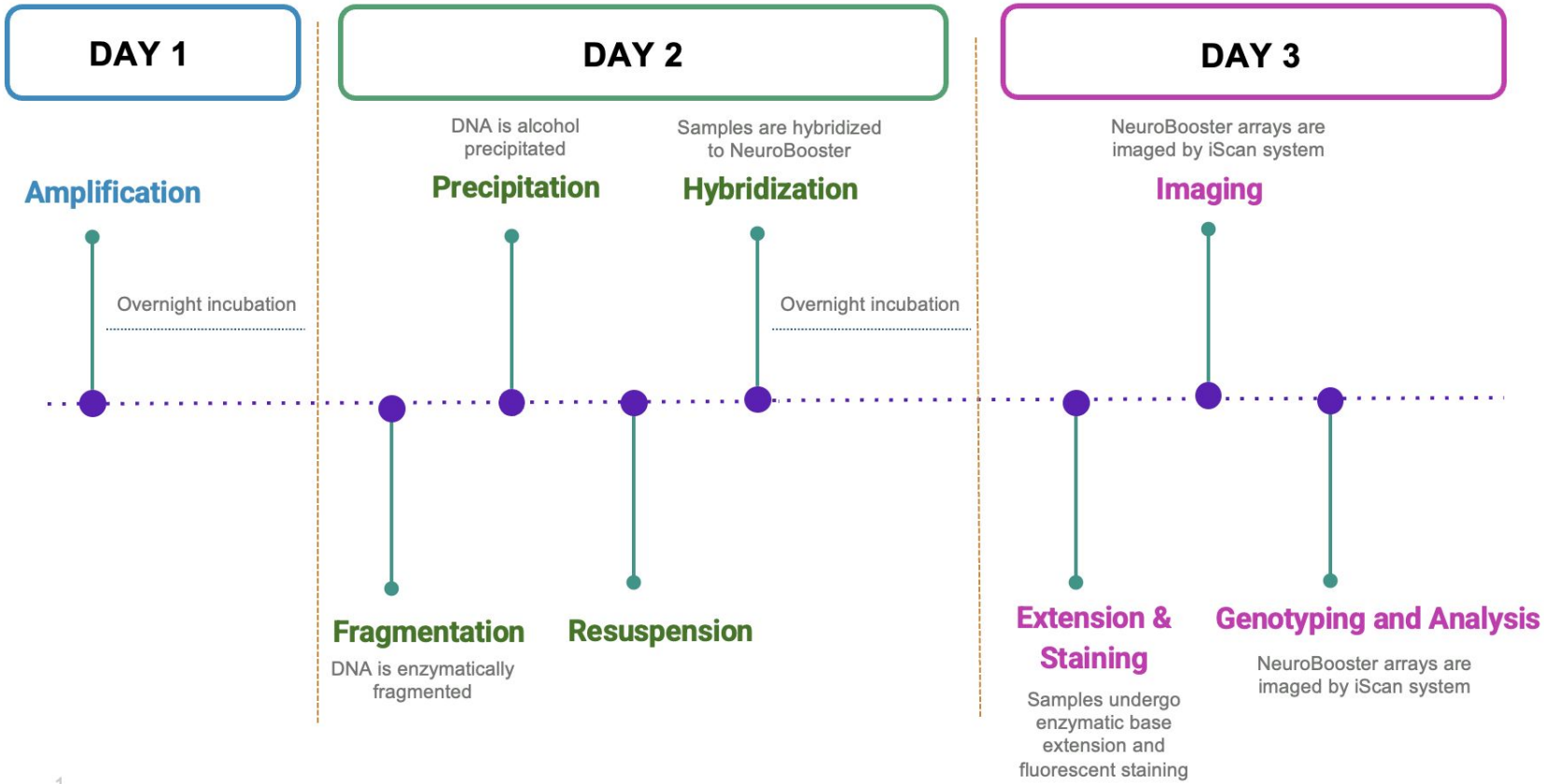
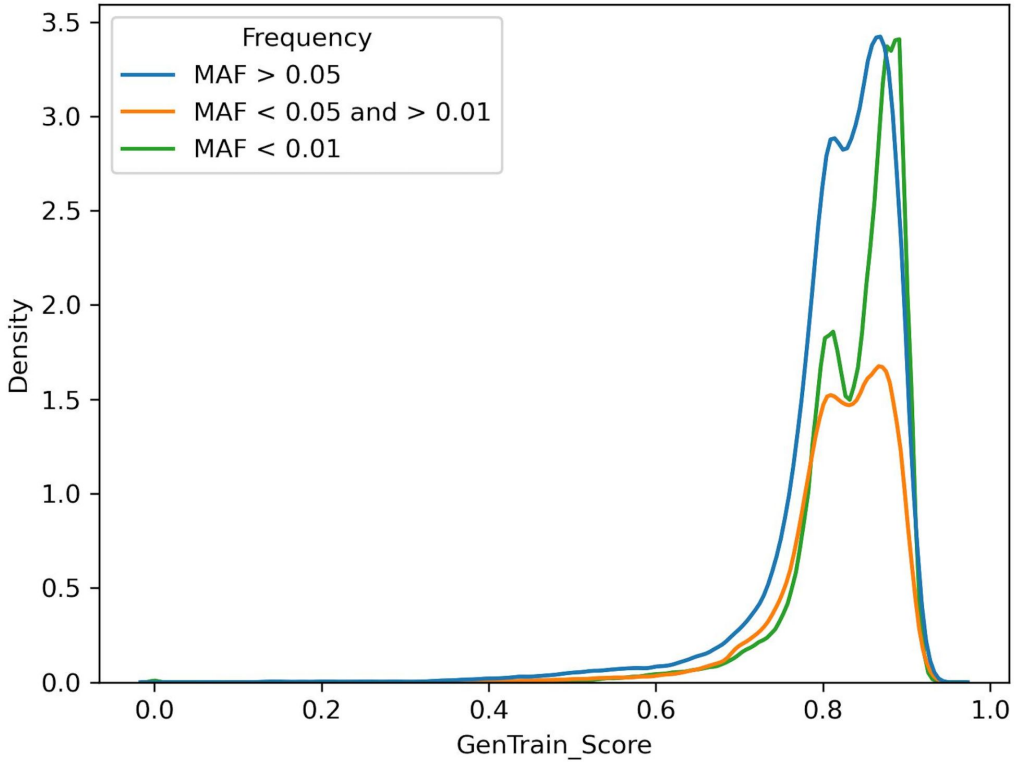


Figure 4B. Overview of NeuroBooster array content by pathogenicity predictors

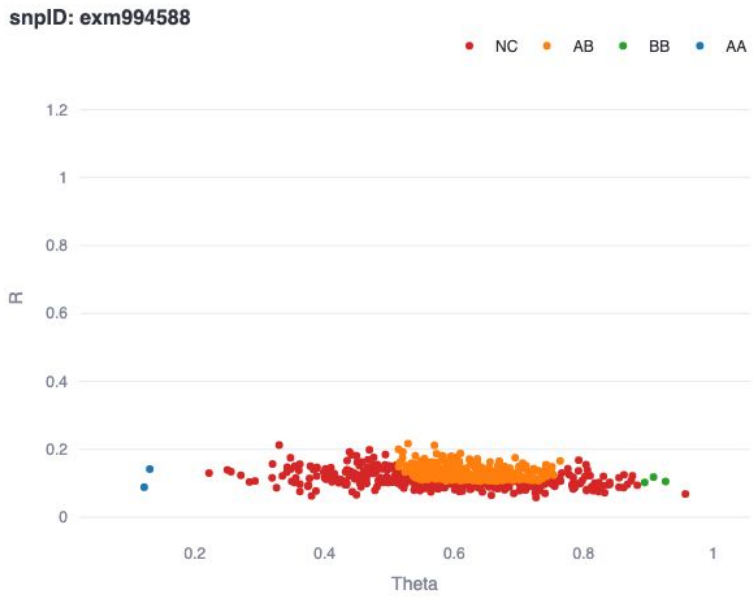


Supplementary Figure 1. Overview of NeuroBooster Array genotyping protocol

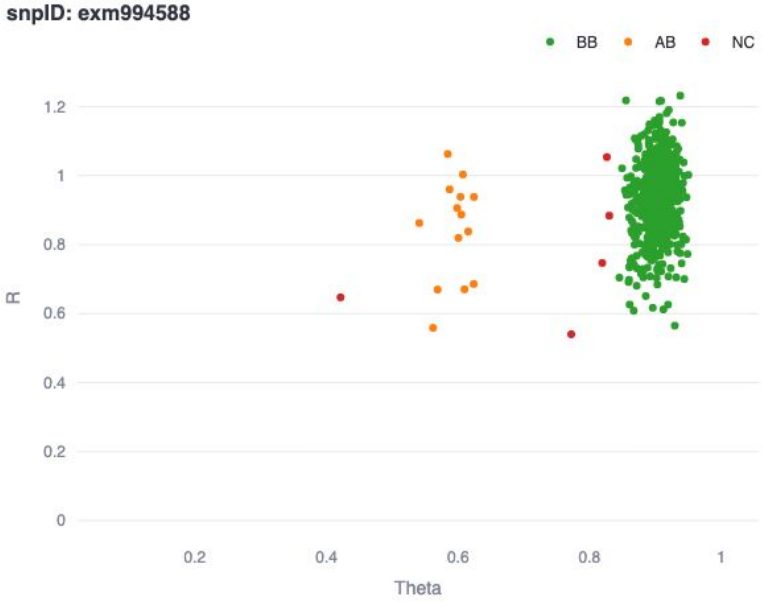


Supplementary Figure 2. GenTrain scores of the NeuroBooster divided by minor allele frequency. NeuroBooster variants were divided in three group by minor allele frequency (MAF): larger than 5%, between 5-1% and lower than 1%.

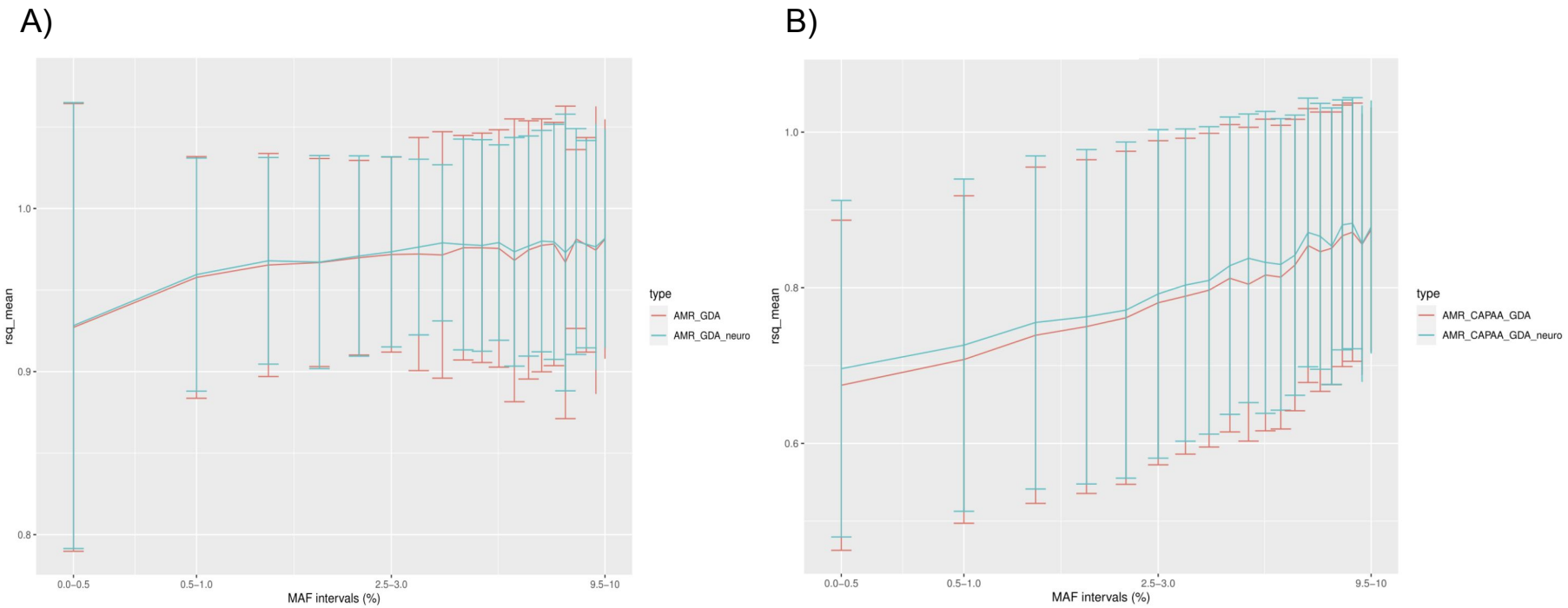
A)



B)

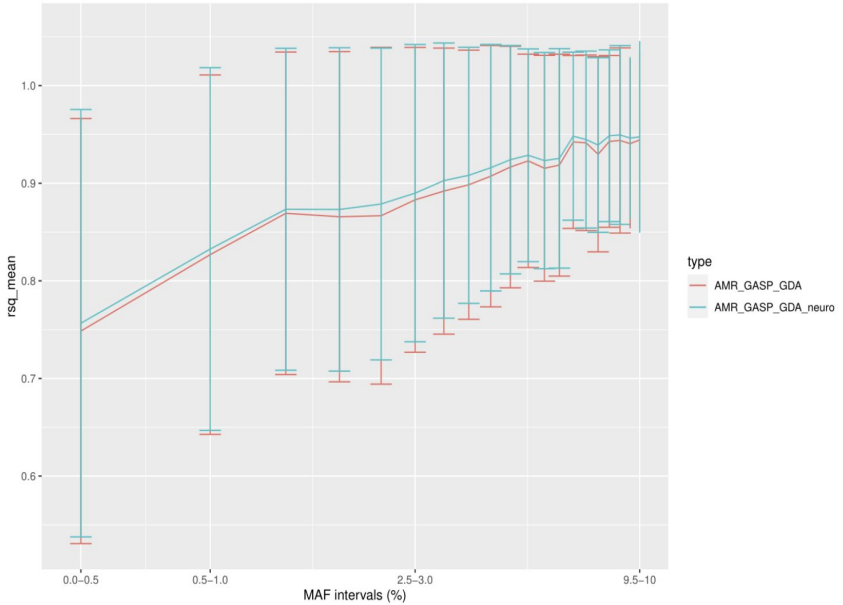


Supplementary Figure 3. Cluster plot comparison of NeuroChip versus NeuroBooster array probes for *LRRK2* p.Thr1410Met.
A) chr12:40309145 probe on NeuroChip array B) chr12:40309145 probe on NeuroBooster array

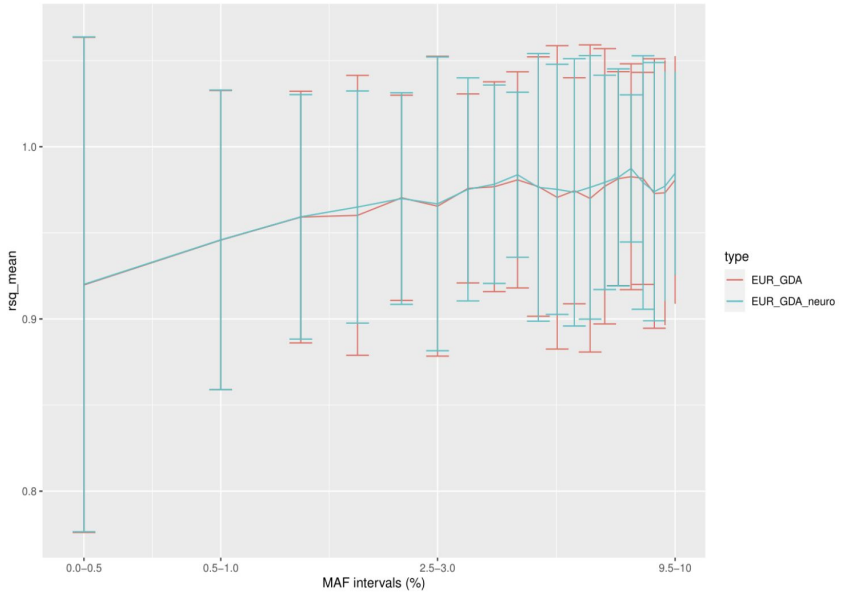


Supplementary Figure 4A-H. Imputation accuracy of tag GWAS hits across diverse populations from 1000 genomes data using diverse imputation panels
A) American admixed imputed versus the Haplotype Reference Consortium panel B) American admixed imputed versus the Consortium on Asthma among African-Ancestry Populations in the Americas (CAAPA) panel C) American admixed imputed versus the Genome Asia Pilot (GAsP) panel D) European imputed versus the Haplotype Reference Consortium panel E) African imputed versus the CAAPA panel F) African admixed imputed versus the CAAPA G) East Asians imputed versus the GAsP panel H) South Asians imputed versus the GAsP panel. Blue denotes Global Diversity Array + custom content imputation and red denotes Global Diversity Array imputation

C)



D)



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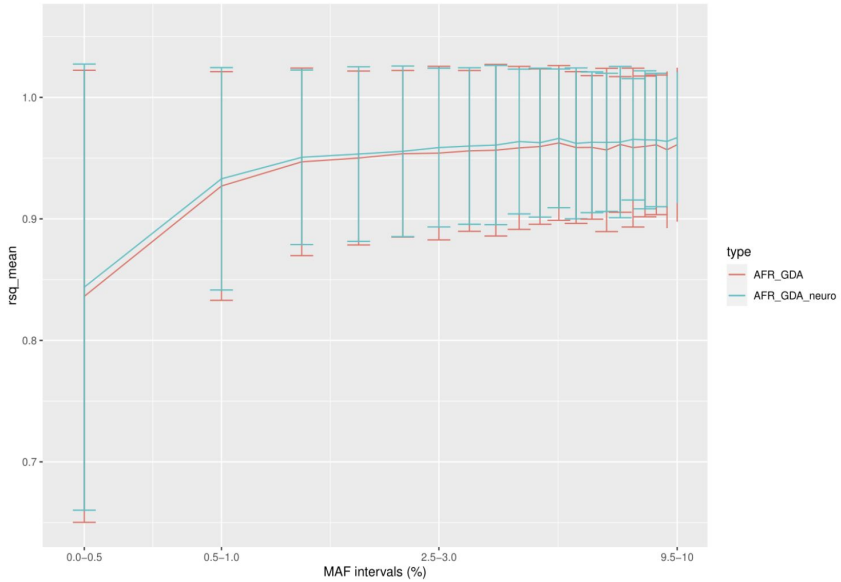
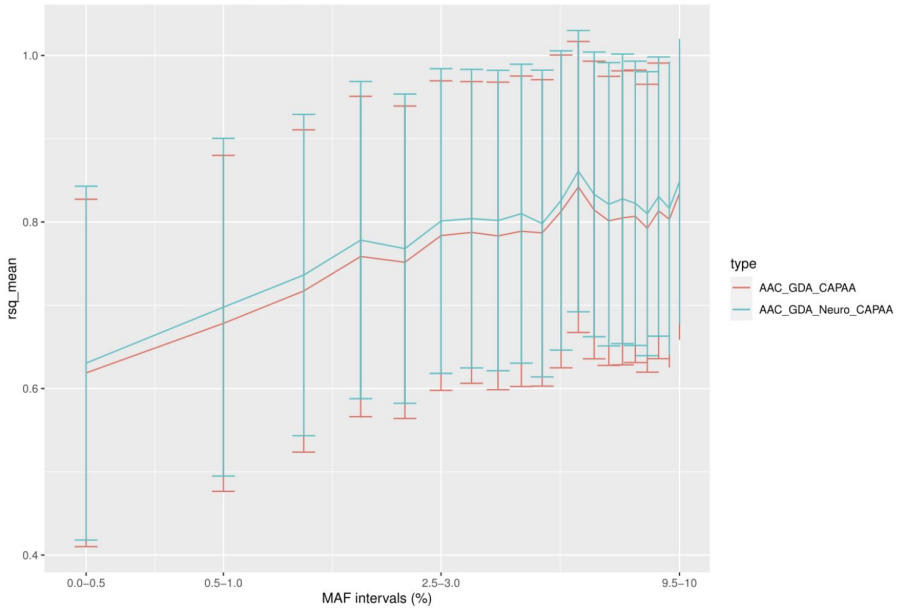


F)



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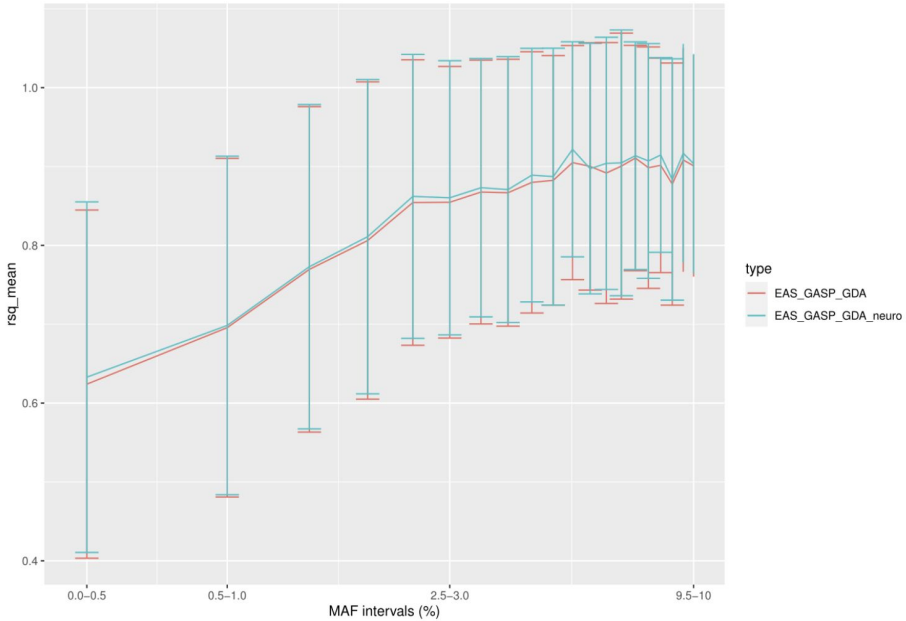
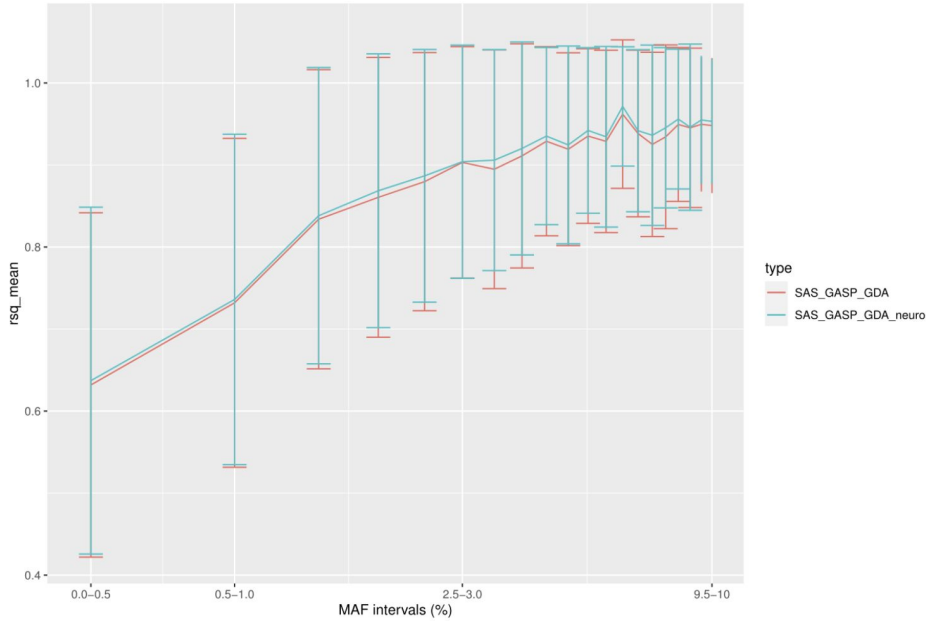
G)



H)



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