NeuroBooster Array: Update

NeuroBooster Array: Overview

- NeuroBooster = GDA (1.9M variants) + NDD related content (95K variants)
 - NDD related content can be also combined with MEG or GSA.
- GDA includes genetic markers gathered from individuals of diverse ethnic groups
 - African Americans, Hispanics, Pacific Islanders, East Asians, admixed ancestry



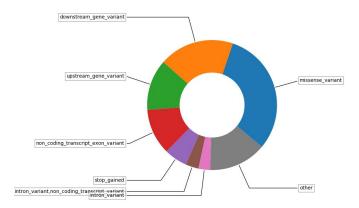
Figure 1: Infinium Global Diversity Array-8 v1.0 BeadChip—Built on the trusted 8-sample Infinium platform.

NeuroBooster Array: Aims

- Generally improve imputation quality across populations of diverse continental ancestries to facilitate risk loci discovery.
- Improve imputation of known GWAS loci for NDDs across populations of diverse ethnicity to facilitate trans-ethnic studies.
- Identify coding and low frequency variants of interest to researchers on the NDD field.

NeuroBooster Array: Design

- STEP 1: Selection of tagging NDD related coding & low frequency variants
 - Systematic review on the Human Genome Mutation Database
 - Genomics England disease-specific expert panels in concert with Gnomad
 - IPDGC and CARD collaborators



NeuroBooster Array: Design

- STEP 2: Identification of the best multi-population tag SNPs
 - AMR <-- MXL, CLM, PEL, PUR (Latino ancestry populations)
 - EAS <-- JPT, CDX, CHB, CHS, KHV, CHD (East Asian populations)
 - EUR <-- TSI, IBS, GBR, CEU (European populations, note the FIN are excluded as outliers in PCA)
 - SAS <-- PJL, ITU, STU, GIH, BEB (South Asian populations)
 - AFR <-- GWD, MSL, ESN, GWJ, YRI, LWK, GWF, GWW (African populations)
 - AAC <-- ASW, ACB (African American and Caribbean populations)
 - ** LD comparisons and allele frequency calculation

NeuroBooster Array: Design

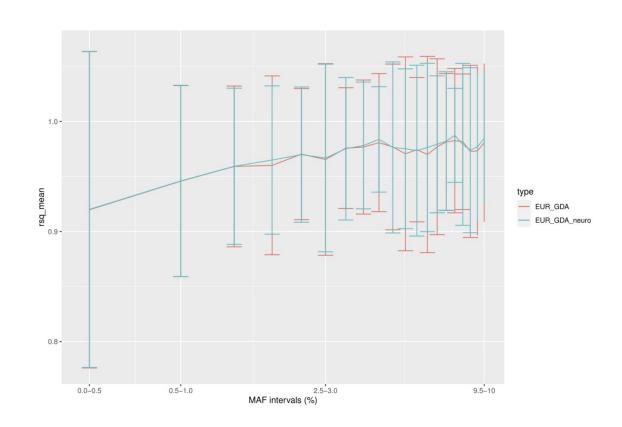
• STEP 3: Dense selection of tag SNPs within NDD GWAS regions.

199 NDD related loci

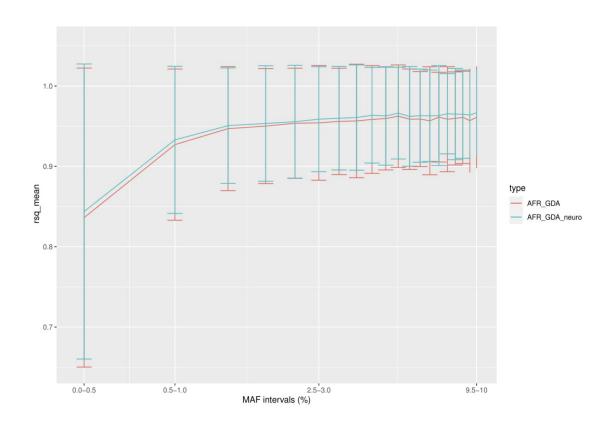
- AD: Jansen et al, 2019, Kunkle et al, 2019
- PD: Nalls et al, 2019 and PD progression Iwaki et al, 2019
- ALS: Nicolas et al, 2019
- O DLB: Guerreiro et al, 2018, PSP: Hoglinger et al, 2011, FTD: Ferrari et al, 2014
 - ** 1809 PRS SNPs nominated by PRSice
- STEP 4: Imputation boosters for diverse populations.

- WGS data from six 1000 Genomes populations
 - O AAC (157), AFR (504), AMR (347), EAS (504), EUR (404), SAS (489)
- Extract only GDA content -> Imputation
- Extract GDA + Neuro content -> Imputation
- Imputation versus various panels
 - HRC, CAAPA, GAsP, TopMed
- Imputation performance for the 199 NDD related loci
 - GDA content *versus* GDA + Neuro content

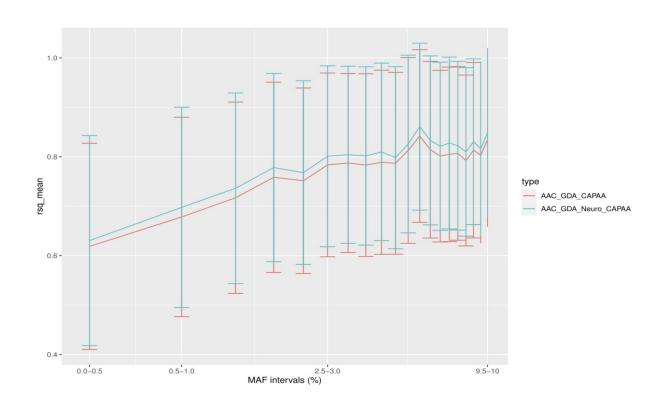
EUR population (HRC panel)



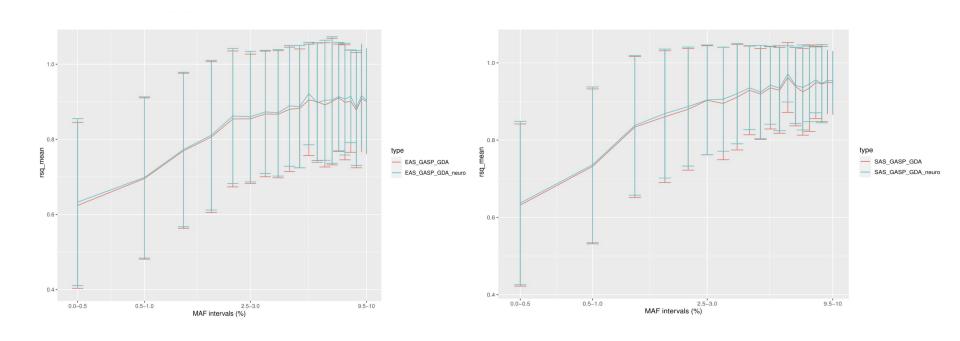
AFR population (CAAPA panel)



AAC population (CAAPA panel)



SAS & EAS populations (GAsP panel)



AMR populations (HRC panel *versus* GAsP panel *versus* CAAPA panel)

