NCGG Alzheimer's disease GWAS summary statistics (2020)

General Information:

# Number of analyzed samples: 3,962 Alzheimer's disease (AD) cases and 4,074 controls of Japanese individuals (2,974 AD cases and 3,096 controls from the National Center for Geriatrics and Gerontology (NCGG biobank), 978 AD cases and 988 controls from Niigata University)

# Age and gender: The average age 74.6 years, the female ratio 0.60.

#Genotyping platform: Affymetrix Japonica Array (NCGG subjects), Affymetix GeneChip 6.0 microarrays (Niigata subjects).

#Genotype imputation: IMPUTE2 with 3.5K Japanese reference panel developed by Tohoku Medical Megabank Organization (ToMMo) for NCGG subjects and IMPUTE2 with 1000 Genomes Project reference panel (1000 Genomes Phase 3) for Niigata subjects. We used imputed variants with an INFO score ≥ 0.4 in the association analysis.

#Sample QCs: (1) sex inconsistencies (--check-sex), (2) inbreeding coefficient (--het 0.1), (3) genotype missingness (--missing 0.05), (4) kinship coefficient (--genome 0.2) and (5) exclusion of outliers from the clusters of East Asian populations in principal component analysis that was conducted together with 1000 Genomes Phase 3 data.

#Marker (SNPs and Indels) QCs: (1) genotyping efficiency or call rate (--geno 0.95), (2) minor allele frequency (--freq 0.001), (3) Hardy-Weinberg equilibrium (--hwe 0.001).

#Marker number: 4,852,957 genetic markers.

#Phenotype: The common autosomal variants that passed those QC criteria were assessed using logistic regression model with adjustment for sex and age using PLINK software (--logistic).

Uploaded file name:

NCGG\_AD\_GWAS\_2020-2

Column:

|  |  |  |
| --- | --- | --- |
| **Number of column** | **column** | **Description** |
| 1 | CHR | chromosome |
| 2 | SNP | marker name |
| 3 | BP | position (hg19) |
| 4 | A1 | minor allele for whole data |
| 5 | A2 | major allele for whole data |
| 6 | NMISS | Number of non-missing individuals included in analysis |
| 7 | NMISS\_A | Number of non-missing individuals included in analysis for cases |
| 8 | NMISS\_U | Number of non-missing individuals included in analysis for controls |
| 9 | MAF\_A | minor allele frequency for cases |
| 10 | MAF\_U | minor allele frequency for controls |
| 11 | OR | odds ratio |
| 12 | SE | standard error for odds ratio |
| 13 | L95 | Lower bound on confidence interval for odds ratio |
| 14 | U95 | Upper bound on confidence interval for odds ratio |
| 15 | STAT | Coefficient t-statistic |
| 16 | P | p-value for logistic regression model |
| 17 | Info\_NCGG | Imputation info score for NCGG data |
| 18 | Info\_Niigata | Imputation info score for Niigata data |

URLs

[National Bioscience Database Center Human Database](https://humandbs.biosciencedbc.jp/en/)

[National Center for Geriatrics and Gerontology](https://www.ncgg.go.jp/english/)

[NCGG biobank](https://www.ncgg.go.jp/mgc/index.html)

[Brain Research Institute, Niigata University](https://www.bri.niigata-u.ac.jp/index.html)

Reference:

If you use these date, please cite the following paper:

Shigemizu D et al.: Ethnic and trans-ethnic genome-wide association studies identify new loci influencing Alzheimer’s disease risk in Japanese.