Thank you for your interest in The International Genomics of Alzheimer's Project (IGAP) Alzheimer’s disease GWAS of Kunkle et al. , *Nat Genet*, 2019. IGAP is releasing the summary results data from this analysis in order to enable other researchers to examine particular variants or loci for their evidence of association. We welcome your request with the proviso that these summary data should not be used for research into the genetics of intelligence, education, social outcomes such as income, or potentially sensitive behavioral traits such as alcohol or drug addictions. The files include p-values and direction of effect at over 11 million directly genotyped or imputed single nucleotide polymorphisms (SNPs). Due to the possibility of identification of individuals from these summary results, allele frequency data are accessible through the NIAGADS application process.

**Data file description**

Two dataset are provided. The first one corresponds to the meta-analysis results obtained in stage 1 including genotyped and imputed data (11,480,632 variants, phase 1 integrated release 3, March 2012) of 21,982 Alzheimer’s disease cases and 41,944 cognitively normal controls. The second one corresponds to the meta-analysis results of the 11,632 variants that were genotyped on the I-select chip and tested for association in an independent set of 8,362 Alzheimer's disease cases and 10,483 controls with the combined stage1/stage2 P-values. 11,540 of the I-select chip variants were available for meta-analysis with the stage 1 dataset. The Stage 3A (n = 11,666) and Stage 3B (n = 30,511) (for variants in regions not well captured on the I-select chip) results are available in the manuscript. The final sample was 35,274 clinical and autopsy-documented Alzheimer’s disease cases and 59,163 controls.

Each file consists of the following information for each SNP and its association to Alzheimer's disease based on meta-analysis in the publication mentioned below. Although the individual datasets examined excluded any SNPs with call rates <95%, IGAP meta-analysis only analyzed SNPs either genotyped or successfully imputed in at least 30% of the AD cases and 30 % of the control samples across all datasets. Please see the Supplementary methods for further details on quality control steps performed.

**Chromosome:** Chromosome of the SNP (Build 37, Assembly Hg19)

**Position:** Position of the SNP (Build 37, Assembly Hg19)

**MarkerName:** SNP rsID or chromosome:position:I/D if rsID not available. I/D indicates indel or deletion respectively.

**Effect\_allele:** Reference allele (coded allele)

**Non\_Effect\_allele:** Non reference allele (non coded allele)

**Beta:** Overall estimated effect size for the effect allele

**SE:** Overall standard error for effect size estimate

**Pvalue:** Meta-analysis Pvalue using regression coefficients (beta and standard error)

**Use of IGAP data for publications**

If IGAP data are used in publications, IGAP should be cited in acknowledgments, Materials and Methods, and References sections of the manuscript as follows:

**Acknowledgments**

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**Material and methods**

International Genomics of Alzheimer's Project (IGAP) is a large three-stage study based upon genome-wide association studies (GWAS) on individuals of European ancestry. In stage 1, IGAP used genotyped and imputed data on 11,480,632 single nucleotide polymorphisms (SNPs) to meta-analyse GWAS datasets consisting of 21,982 Alzheimer’s disease cases and 41,944 cognitively normal controls from four consortia: The Alzheimer Disease Genetics Consortium (ADGC); The European Alzheimer's disease Initiative (EADI); The Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium (CHARGE); and The Genetic and Environmental Risk in AD Consortium Genetic and Environmental Risk in AD/Defining Genetic, Polygenic and Environmental Risk for Alzheimer’s Disease Consortium (GERAD/PERADES). In stage 2, 11,632 SNPs were genotyped and tested for association in an independent set of 8,362 Alzheimer's disease cases and 10,483 controls. Meta-analysis of variants selected for analysis in stage 3A (n = 11,666) or stage 3B (n = 30,511) samples brought the final sample to 35,274 clinical and autopsy-documented Alzheimer’s disease cases and 59,163 controls.

**Reference**

Your manuscript should cite the following reference:

Kunkle et al. Genetic meta-analysis of diagnosed Alzheimer’s disease identifies new risk loci and implicates Aβ, Tau, immunity and lipid processing. *Nature Genetics*, 2019. doi: 10.1038/s41588-019-0358-2 Pubmed: