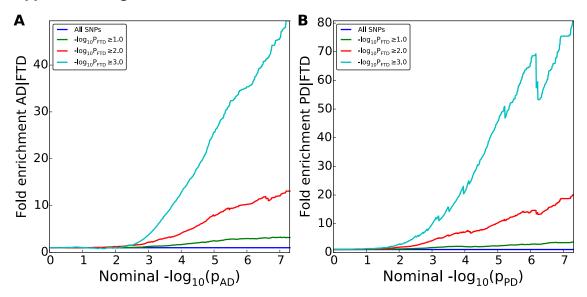
# SUPPLEMENTAL INFORMATION

#### SUPPLEMENTAL FIGURE

**Supplemental Figure 1.** Fold enrichment plots of enrichment versus nominal  $-\log_{10} p$ -values (corrected for inflation) in Alzheimer's disease (AD, panel A) and Parkinson's disease (PD, panel B) below the standard GWAS threshold of  $p < 5x10^{-8}$  as a function of significance of association with frontotemporal dementia (FTD) and at the level of  $-\log_{10}(p) \ge 0$ ,  $-\log_{10}(p) \ge 1$ ,  $-\log_{10}(p) \ge 2$  corresponding to  $p \le 1$ ,  $p \le 0.1$ ,  $p \le 0.01$ , respectively. Blue line indicates all SNPs.

# **Supplemental Figure 1**



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The International Genomics of Alzheimer's Project (IGAP)

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## **IGAP** Cohort

International Genomics of Alzheimer's Project (IGAP) is a large two-stage study based upon genome-wide association studies (GWAS) on individuals of European ancestry. In stage 1, IGAP used genotyped and imputed data on 7,055,881 single nucleotide polymorphisms (SNPs) to meta-analyse four previously-published GWAS datasets consisting of 17,008 Alzheimer's disease cases and 37,154 controls (The European Alzheimer's disease Initiative – EADI the Alzheimer Disease Genetics Consortium – ADGC The Cohorts for Heart and Aging Research in Genomic Epidemiology consortium – CHARGE The Genetic and Environmental Risk in AD consortium – GERAD). In stage 2, 11,632 SNPs were genotyped and tested for association in an independent set of 8,572 Alzheimer's disease cases and 11,312 controls. Finally, a meta-analysis was performed combining results from stages 1 & 2. In this study, we focused on the stage 1 IGAP SNPs.

#### **IGAP** reference

The summary statistics used in this work have been generated in: Jean-Charles Lambert et al. Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease. *Nature Genetics*, 2013, **45** : 1452–1458. doi:10.1038/ng.2802 [PubMed ID: 24162737]

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