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Supplementary Data

Genetic Determinants of "Cognitive Impairment, No Dementia"

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Supplementary Table 1

Gene	SNP	TaqMan	Primer sequence	Conditions
MetaboChip-related SNP genotyping assays				
FLJ22536	rs16901621	N	5′-TCCTTTCCAGGGTGCAAGTC-3′ 5′-ATCTTCATTCAGCCCCAGAC-3′	58°C annealing
IRX1	rs13186537	N	5′-ATTGAGGATTCATTTGTGGC-3′ 5′-AGCCCCTGTTTTTTACCTGTC-3′	56°C annealing
ME1	rs1145909	N	5′-CCATCCCACATTTATGCAG-3′ 5′-GCTTTTGGCAACCACTTTCTAG-3′	58°C annealing
EHD4	rs1704405	Y	5′-TCAGACTTCACAAAGTGGGAATTTGA-3′ 5′-TTGCCACTGCCCTTTGTCT-3′	NA
Alzheimer-related SNP genotyping assays				
CD2AP	rs9349407	Y	5′-AATGTAGTTAGCTTTAGTGTATGGTGTTTATAAAATCT-3′ 5′-CAGTGAGTGGTGAGCAAATGTG-3′	NA
CD33	rs3865444	Y	5′-GAGTCGCAGCCTCACCTA-3′ 5′-CTCACACGGACCCTATAGAATCCTA-3′	NA

SNPs not listed here were genotyped using pre-designed TaqMan SNP genotyping assays. The manufacturer's suggested assay conditions were used. NA, not applicable.

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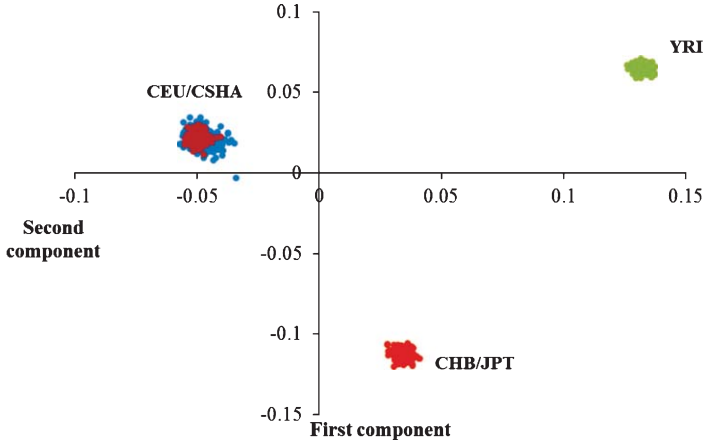
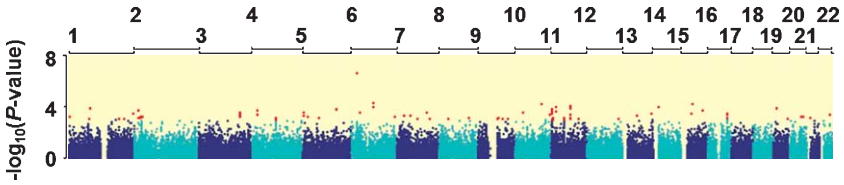
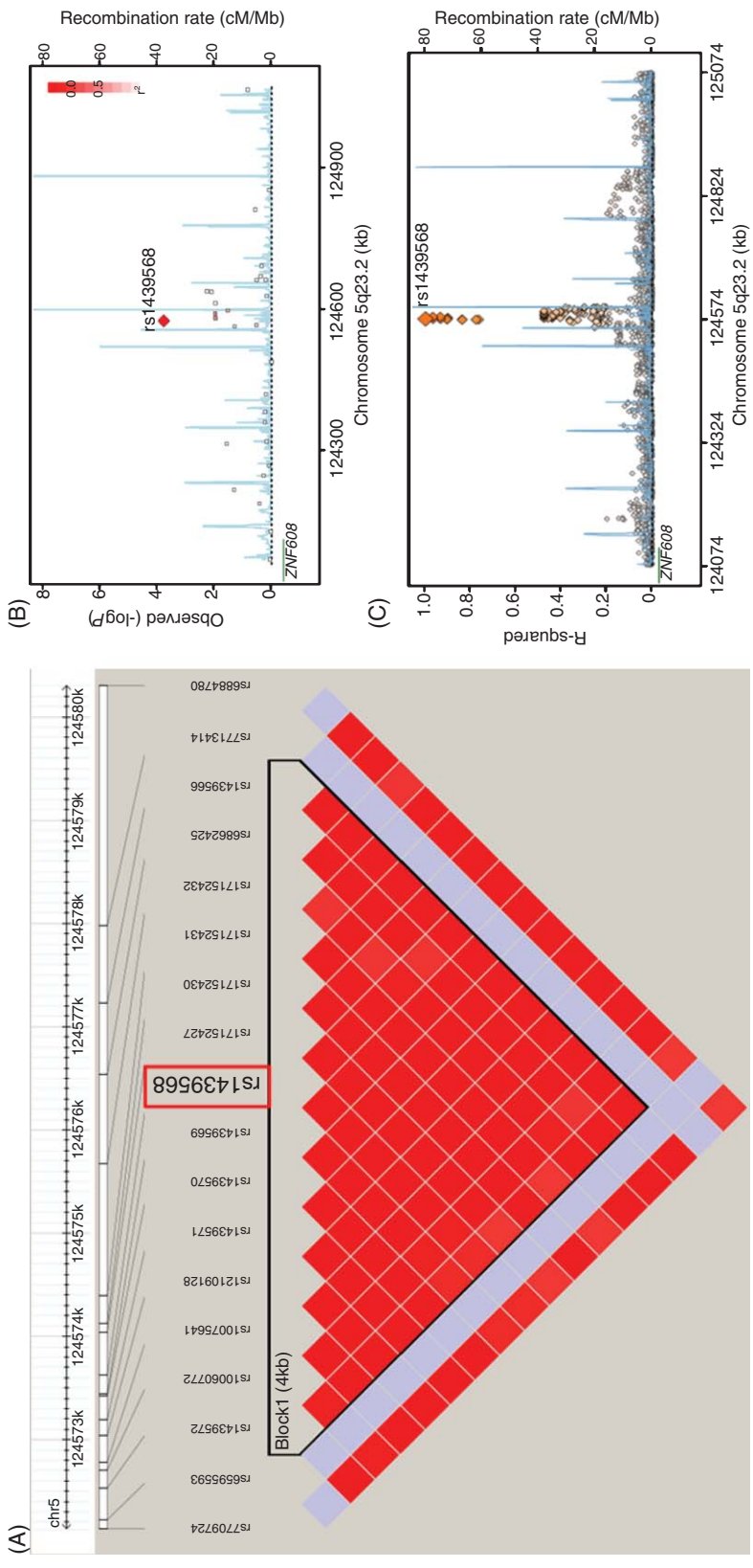


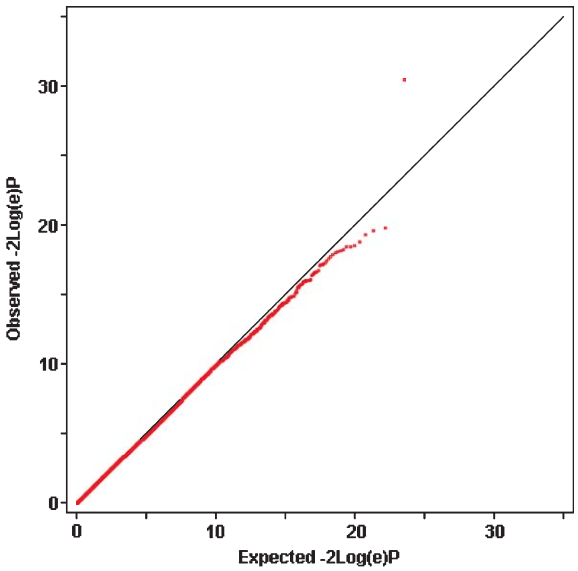
Supplementary Figure 1. Principal components analysis with Canadian Study of Health and Aging (CSHA)- and HapMap-derived populations. The first two principal components were plotted with HapMap populations of known ancestry to confirm the reported ancestry of CSHA participants. CEU (red, $n = 165$), Caucasians; CSHA (blue, $n = 575$), CSHA discovery phase cohort; CHB/JPT (orange, $n = 250$), Chinese/Japanese; YRI (green, $n = 203$), African.



Supplementary Figure 2. Manhattan plot showing results from the MetaboChip genome-wide association study in the discovery phase. Each point represents the *p*-value of a test for association between a genetic variant with CIND status. The significance of association is plotted on the y-axis with increasing significance ranking higher on the y-axis. The genomic position the SNP corresponding to each test for association is plotted on the x-axis. Polymorphisms with *p*-values $<10^{-3}$ are shown in red.



Supplementary Figure 3. Regional genetic variation in the vicinity of rs1439568. A) Haplotype block surrounding rs1439568 based on data from the HapMap CEU population. Red boxes represent a high degree of linkage disequilibrium (LD) between two markers whereas grey boxes suggest weak linkage disequilibrium. The relative position of rs1439568 is outlined in red. B) LD between MetaboChip genotyped SNPs and rs1439568. Discovery phase-calculated *p*-values (left y-axis) for SNP association with CIND determine the height of each point. The degree of LD between a SNP and rs1439568 is proportional to the intensity of red colouration. Blue peaks identify sites of recombination (right y-axis). C) Regional LD between rs1439568 and neighboring SNPs based on the HapMap CEU dataset. Each point represents a SNP and its height on the left y-axis indicates the strength of linkage disequilibrium between a particular SNP and rs1439568. Blue peaks correspond to sites of recombination (right y-axis). Data from panels A) and C) were generated using the hg18 build.



Supplementary Figure 4. Quantile-quantile plot showing expected and observed *p*-values from the MetaboChip discovery phase. The distribution of *p*-values suggests that there was no artificial inflation of test statistics ($\lambda_{GC} = 0.99$).