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IMAGE

Genome-wide association reveals dopamine-related genetic effects on caudate volume

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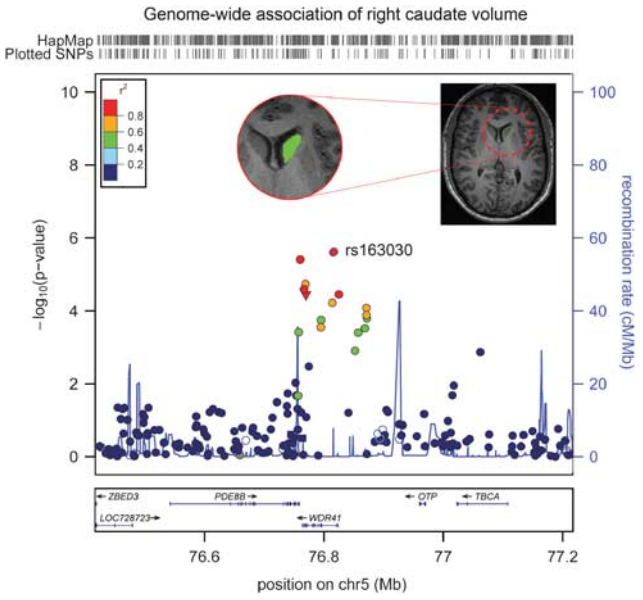

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Genome-wide search was used to identify common genetic variants associated with caudate nucleus volume. Two large independent samples comprising young and elderly populations were used to replicate any associations. Here a detailed view of the most associated locus is shown. Markers are represented as circles (single-nucleotide polymorphisms (SNPs) with no known function) or downward-pointing triangles (coding non-synonymous mutations). Markers are placed at their position on chromosome 5 (x axis) and graphed based on the $-\log_{10}$ (P-values) of their association with the phenotype (y axis). The level of linkage disequilibrium to the most associated SNP (rs163030) is represented in color using the CEU panel from HapMap Phase II. The location of genes is shown below the plots, and two genes *WDR41* and *PDE8B* implicated in the locus are involved with dopamine development and signaling. For more information on this topic, please refer to the article by Stein *et al.* on pages 927–937.

[9]Data used in the preparation of this article were obtained from the Alzheimer's Disease Neuroimaging Initiative (ADNI) database (http://www.loni.ucla.edu/ADNI). As such, the investigators within the ADNI contributed to the design and implementation of ADNI and/or provided data but did not participate in analysis or writing of this report. A complete listing of ADNI investigators is available at http://www.loni.ucla.edu/ADNI/Collaboration/ADNI_Manuscript_Citations.pdf.