

A Genome-Wide Association Study of Voter Turnout
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Fowler, Baker & Dawes (2008) found that more than half of the variation in voter turnout could be attributed to genetic factors. This prompts two important questions: 1) which specific genes are associated with voter turnout; and 2) what is the causal pathway linking these genes to voting behavior? Genome-wide association studies (GWAS) offer the best approach to answer the first question because they investigate hundreds of thousands of variants across the entire human genome and are not constrained by prior hypotheses (Pearson & Manolio 2008). In terms of exploring second question, several recent papers have demonstrated an empirical connection between turnout and personality traits (Gerber et al. 2010, Mondak et al. 2010, Gerber et al. 2009, Gerber et al. 2008 Mondak and Halperin 2008, Denny and Doyle 2008) as well as cognitive ability (Deary et al. 2008, Denny and Doyle 2008).

This paper presents the results of the first genome-wide association study of validated and self-reported voter turnout, testing nearly 600,000 single nucleotide polymorphisms (SNPs) based on a sample of 3700 subjects. For each of the SNPs found to be significantly associated with turnout after correcting for multiple testing, a formal test is performed to determine whether personality traits or cognitive ability mediate the association.