The Genetic Architecture of Economic and Political Preferences

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Daniel J. Benjamin[1]*, David Cesarini[2], Matthijs J.H.M. van der Loos[3], Christopher T. Dawes[4], Philipp D. Koellinger[3], Patrik K.E Magnusson[5], Christopher Chabris[6], Dalton Conley[7], David Laibson[8] and Magnus Johannesson[9]

[1]*Department of Economics, Cornell University, 480 Uris Hall, Ithaca, N.Y. 14853, USA.*

[2]*Center for Experimental Social Science, Department of Economics, New York University, 19 W. 4th Street, New York, NY 10012, USA.*

[3] *Department of Applied Economics, Erasmus Universiteit Rotterdam, Post Box 1738, 3000 DR Rotterdam, Netherlands.*

[4] *Department of Politics, New York University, 19 W. 4th Street, New York, NY 10012, USA.*

[5] *Department of Medical Epidemiology and Biostatistics, Karolinska Institutet, Box 281, SE-171 77 Stockholm, Sweden.*

[6] *Department of Psychology, Union College, 807 Union Street, Schenectady, NY 12308, USA.*

[7] *Department of Sociology, New York University, Department of Sociology, New York University, 295 Lafayette Street, 4th floor, New York, NY 10012, USA.*

[8] *Department of Economics, Harvard University, Littauer Center, 1805 Cambridge Street, Cambridge, MA 02138, USA.*

[9] *Department of Economics, Stockholm School of Economics, Box 6501, SE-113 83 Stockholm, Sweden.*

Abstract: Preferences are fundamental constructs in all models of economic and political behavior and important precursors to many lifetime outcomes. Twin studies suggest that preferences are heritable, but twin-based heritability estimates remain controversial. Here, with a new sample of comprehensively-genotyped subjects with data on political and economic preferences, as well as income and educational attainment, we use genome-wide data to estimate the proportion of variation in these traits explained by common SNPs. The overall pattern of results is consistent with findings for other complex traits: (1) the estimated fraction of phenotypic variation that can ultimately be explained by dense SNP arrays is approximately half the heritability as estimated using twin and family studies; and (2) GWAS and prediction analyses reveal that many common SNPs with large explanatory power for these traits are unlikely to exist. These findings have implications for evaluating the extent to which the potential benefits of molecular genetic data in the social sciences will be borne out in the near future. The results are also useful for evaluating existing published associations in candidate gene studies of economic and political phenotypes. We propose some constructive responses to the inferential challenges posed by the small explanatory power of individual SNPs.

Introduction

Preferences are fundamental constructs in most theories of economic and political behaviour. Risk aversion, patience, fair-mindedness, and trust are considered particularly fundamental preferences within economics because they explain a wide range of behaviours, and political ideology plays a similar role within political science. For example, measures of risk preferences predict diverse risky behaviours, such as smoking, drinking, and holding stocks rather than bonds (Barsky et al., 1997; Dohmen et al., 2011). Experimentally-elicited patience predicts body mass index, smoking behaviour, and frequency of exercise (Chabris et al., 2008), as well as credit card borrowing (Meier and Sprenger, 2010). Political preferences similarly predict a wide range of political behaviours, including voting (Jost, 2006) and giving monetary campaign contributions (Morton and Cameron, 1992), as well as campaign activities like volunteering, attending rallies, and displaying yard signs (Claassen, 2007).

Behaviour genetic studies, beginning with the seminal work of Martin et al. (1986), have suggested that some of the variation in political and economic preferences can be statistically accounted for by genetic differences (Alford et al., 2005; Cesarini et al., 2009; Hatemi et al., 2007, 2011; Zhong et al., 2009; Zyphur et al., 2009). However, these conclusions continue to be contested (e.g., Charney, 2008). Critics point out that the twin-based estimates of "heritability"—which compare the correlation of an outcome across monozygotic (MZ) twin pairs with that correlation across dizygotic (DZ) twin pairs—rely on strong assumptions which render it difficult to draw any definite conclusions. For example, one criticism sometimes levelled against twin studies is that the similarity of MZ twins may be inflated due to failure of the equal-environment assumption (Stenberg, 2011), a bias which could cause heritability estimates to be positive even if the true value were zero.

Other researchers, along with various funding agencies, have embraced the twin-based heritability estimates as fuelling their enthusiasm regarding the transformative promise of molecular genetic data for social science research. By indicating that there is *some* variance in social science phenotypes explainable by genes, the heritability estimates imply that predictive genetic markers exist and could, in principle, be identified. If specific genetic markers can be identified that are associated with a preference, then it might be possible to predict a given individual's preference without access to any phenotypic data (a feat that cannot be accomplished just using heritability estimates). Identifying such predictive markers

may shed light on the biological pathways underlying preferences and ultimately help us better understand how genes affect outcomes (Jencks, 1980). Even more exciting for many social scientists, if a set of genetic markers is sufficiently predictive, then these markers could be used in social science research as covariates, as instrumental variables* (Davey Smith and Ebrahim, 2003; Ding et al., 2006), or as factors for identifying at-risk populations who might benefit from policy interventions.

Even if social-science traits are heritable, the extent to which these promises of molecular genetic data will be fulfilled for a given trait hinges crucially on its "molecular genetic architecture," i.e., the joint distribution of effect sizes and allele frequencies of the causal genetic markers (Benjamin, 2010; Beauchamp et al., 2011). The molecular genetic architecture determines the difficulty with which the genetic variants associated with a trait can be identified and what sample sizes will be required. It also determines the out-of-sample aggregate predictability that can be derived from a set of SNPs considered jointly.

In this paper, we use a new sample of comprehensively-genotyped subjects from the Swedish Twin Registry who were recently administered, as part of a survey called SALTY, a rich set of questions measuring economic and political preferences. We study four fundamental economic preferences—risk aversion, patience, trust and fair-mindedness—and five dimensions of political preferences, derived from a factor analysis of a comprehensive battery of attitudinal items. The five attitudinal dimensions are immigration/crime, economic policy, environmentalism, feminism, and foreign policy.

We also study educational attainment and income because much is known about their heritability not only from twin studies (Taubman, 1976), but unlike the preference measures, also from behaviour-genetic estimates that use other pedigree relationships (Björklund, Jäntti and Solon, 2005; Cesarini, 2010). Educational attainment and income are available for a larger sample of genotyped individuals because they are obtained from administrative records. For comparability with previous work and with our other estimates, we report twin-based estimates of heritability from this new sample, but our main focus is on using the whole-genome data to (1) provide new evidence regarding heritability as estimated directly from the genetic data, and (2) learn about the genetic architecture of these traits.

First, we employ a recently-developed method (Visscher et al., 2010; Yang et al., 2010) that uses the whole-genome data to estimate a lower bound of the heritability of these traits. The

technique—which we will call Genomic-Relatedness-Matrix Restricted Maximum Likelihood (GREML)—has been applied to both height (Yang et al., 2010) and intelligence (Davies et al., 2011) but never before to economic and political phenotypes. Since these lower-bound estimates of heritability do not rest on the same assumptions used in twin studies, they provide an additional source of evidence regarding heritability. The method is instead based on a different key assumption: among individuals who are unrelated—i.e., distantly related, since all humans are related to some extent—environmental factors are uncorrelated with differences in the degree of genetic relatedness. Crucially, genetic relatedness is directly estimated from the single nucleotide polymorphism (SNP) data, unlike in behaviour-genetic studies, where *expected* relatedness is inferred from the family pedigree. Some of the concern about behaviour-genetic studies is that expected relatedness could be correlated with environmental factors that are not endogenous to genotype. Since there is more random variation in the realized degree of genome sharing relative to the expected degree as the expected relatedness declines (Visscher, 2009), environmental confounding is less likely to drive estimates that are based on realized relatedness among individuals whose expected relatedness is negligible.

Under the key assumption of no environmental confounding, an estimate of heritability can be obtained by examining how the correlation in phenotype between pairs of individuals relates to the realized genetic distance between those individuals. The resulting estimate is a lower bound for heritability for two reasons: (1) because the method assumes that genetic effects are additive, it attributes any epistatic or dominance effects to the environment; and (2) the estimated relationship between phenotype and genetic relatedness is attenuated because relatedness is measured imperfectly; the common SNPs typed on the genotyping chip capture much but not all of the variation in genetic variation across individuals (Yang et al., 2010). †

Second, we use the whole-genome data to explore the molecular genetic architecture of the phenotypes. Specifically, we estimate heritability using relatedness measured separately by chromosome to test how evenly distributed the genetic effects are across the genome. We supplement these results with a standard genome-wide association studies (GWAS) for each trait, in which individual SNPs are tested for association with the outcome of interest. Finally, we also perform a risk prediction exercise in which we randomly split the dataset into a discovery and a validation sample. We use a pruned set of SNPs from the discovery sample

to build a predictor and then examine to what extent the predictor is correlated with the outcome in the validation sample. Similar approaches have been applied in the study of schizophrenia (Purcell, 2009), height (Lango Allan et al., 2010) and intelligence (Davies et al., 2011), but none of these methods have been applied to economic or political preferences.

Results

We began by computing the sibling correlations for all eleven variables and the retest reliabilities for the nine preference measures. ‡ Table 1 reports the results. In total, the sample of SALTY respondents is comprised of 1,143 complete MZ pairs (464 of them male); 1,237 complete, same-sex DZ pairs (502 of them female); 1,114 complete, opposite-sex DZ pairs; and 4,394 singletons. A total of 491 respondents answered the survey twice, allowing us to estimate retest reliabilities for the preference measures. The sibling correlations for the SALTY questions on discounting (Cesarini et al., 2011), political preferences (Oskarsson et al., 2010), and risk aversion (Beauchamp et al., 2011) have previously been analysed and are reproduced here to facilitate comparison with the remaining results. The income and educational attainment variables we used have also been previously studied in partially overlapping samples (Björklund, Jäntti and Solon, 2005; Cesarini, 2010). We report the correlations in educational attainment and the natural logarithm of earnings averaged over the 1985 and 1990 censuses. The implied heritabilities of the economic preferences are typically in the vicinity of 30% and the estimates for political preferences are typically around 40%. The final column of the table shows the estimated reliability of each of the preferences phenotypes. These reliabilities are estimated from a subset of respondents who were administered the survey twice.

We estimated, for each trait, the proportion of phenotypic variation accounted for by all SNPs, following the method of Yang et al. (2010). These lower-bound heritability estimates for the nine traits are reported in Table 2. For economic preferences, only one of the four variables, trust, is borderline significant ($p = 0.047$), with the point estimate suggesting that the common SNPs explain over twenty percent of phenotypic variation. The remaining effects are lower, in one case zero, and not statistically distinguishable from zero. For political preferences, three out of the five derived attitudinal dimensions have non-zero point estimates. These estimates are 0.203 ($p = 0.079$) for immigration/crime, 0.344 ($p = 0.012$) for economic policy, and 0.353($p = 0.001$) for foreign policy attitudes. Evidently the estimates

are noisier for phenotypes with lower retest reliabilities. Keeping in mind that these are noisy and are lower bounds, the estimates taken as a whole are consistent with low to moderate heritabilities for these traits. The cumulative effect of the SNPs is much more precisely estimated for educational attainment, because this phenotype is available for all the genotyped individuals in the sample, not just the survey respondents. For this phenotype, the larger sample decreases the standard error of the estimates substantially, while the point estimate of 0.191 ($p = 0.001$) is only somewhat higher than the average point estimate for the other phenotypes. These analyses are all based on mixed-sex samples, controlling for sex, age, and the first ten principal components of the genotypic data. For our last variable, log earnings, we restrict the sample to males only and report additional specifications for women and the pooled samples in the Supplementary Online Appendix. § Our point estimate for log earnings in males is 0.061 ($p = 0.313$). In the Supplementary Online Materials, we show that when we pool men and women, the point estimate is 0.084 ($p = 0.085$).

We also conduct the analysis separately by chromosome, as in Davies et al. (2011). Between unrelated individuals, realized relatedness is random and independent across chromosomes, and the expected relatedness measured from any chromosome is zero. If, rather than being concentrated in a particular location, the genetic variation that predicts a trait were uniformly distributed across the genome, then greater realized relatedness from any given chromosome will predict greater phenotypic similarly, and this association will be stronger from longer chromosomes. The bottom row of Table 2 shows the estimated correlation between chromosomal length, measured in centimorgans, and the fraction of variance explained by the estimates of realized relatedness estimated using only data from one chromosome. The correlation is positive for 8 out of 11 phenotypes. Davies et al. (2011) report an analogous positive correlation for cognitive ability and interpret it as evidence that the trait is highly polygenic.

Next, we examine whether we can identify individual SNPs that predict economic and political preferences. For none of the eleven traits did we identify any SNPs that pass the conventional genome-wide significance threshold of $p < 5 \times 10^{-8}$ (McCarthy et al., 2008). The standard diagnostic for population stratification (i.e., ethnic confounding) in GWAS is inflated test statistics in the QQ-plot (e.g., Pearson and Manolio, 2008); there is no evidence of inflated test statistics across the traits, with estimated lambdas in the range 0.987 (economic policy attitudes) to 1.023 (educational attainment), suggesting that our controls for

population structure worked well. The lowest p-value we observe is also for the economic policy attitude variable, with one SNP attaining a p-value of 8.7×10^{-8}. In the supplementary materials, we provide details on the full set of SNPs with p-values below 5×10^{-6}, but we are sceptical that any of these associations will be replicable, given the relatively high p-values.

Finally, we examine the aggregate, out-of-sample predictive power of the SNPs. Following Purcell et al. (2009), we first estimate the regression coefficient for each SNP in a discovery set. From this set of coefficients, we form a prediction equation based on a pruned set of 107,360 markers that includes only SNPs that are approximately in linkage equilibrium (to avoid double counting SNPs that are correlated with other SNPs). In a validation sample, we evaluate the correlation between individuals' predicted phenotype and their observed phenotype. We do not find any significant out-of-sample predictability for any of the traits, and for most phenotypes, the explanatory power of the predictor is well below $R^2 = 0.1\%$. These results are reported in Table 4.

Discussion

The data reported here reveal a number of descriptive facts about the heritability and genetic architecture of political and economic preferences. First, we report sibling correlations for several traits, some of which have never before been studied in large samples, and we confirm that there is a robust separation of the MZ and DZ correlations. We obtain heritability estimates that are consistent with typical estimates previously been reported for both political attitudes (Alford et al., 2005; Hatemi et al., 2007) and economic preferences (Cesarini et al., 2009, 2010, 2011; Zhong et al., 2009), as well as educational attainment (Miller, Mulvey and Martin, 2001). Our estimates for income are actually a little higher than what has previously been reported in Swedish data (Björklund, Jäntti, and Solon, 2005). Overall, these results are consistent with the hypothesis that there exists a moderate correlation between genotype and the eleven phenotypes. A plausible conjecture is that the lower heritabilities of the economic preferences relative to the political preferences result from attenuation bias due to greater measurement error, as evidenced by their lower reliabilities.

Second, our molecular-genetic-based estimates of heritability partially corroborate the twin-based estimates and suggest that molecular genetic data *could* be predictive of preferences.

When we estimate the cumulative effect of genotyped SNPs using the method of Yang et al. (2010), we find that the estimated heritabilities are lower than the twin-based estimates, but the overall pattern of results suggests that heritabilities are generally positive. Previous papers on height (Yang et al., 2010) and intelligence (Davies et al., 2011) have found that the SNP-based heritability estimates are about half the size of the twin-study estimates. These papers have interpreted the gap as indicating that genotyped SNPs tag approximately half the genetic variation in those traits. The gap may also reflect an upward bias in twin-based estimates of narrow heritability estimates due to environmental confounding or non-additive variation, both of which will cause an upward bias in the estimated additive genetic proportion of variance. Consistent with the interpretation that some of the gap is due to bias, behaviour-genetic heritability estimates for income and education based on non-twin siblings, for example adoptees and full siblings, are somewhat lower than those based on twins (Björklund, Jänti and Solon, 2005, Cesarini, 2010).

Do economic and political preferences parallel height and intelligence in having SNP-based heritabilities that are about half the size as the twin-study estimates? If so, it would suggest that economic and political preferences have a similar genetic architecture, a similar degree of bias in twin-based estimates, or both. Since the economic and political preference measures have twin-based heritabilities around 0.30 (Beauchamp et al., 2011; Benjamin et al,. 2011; Cesarini et al., 2009) and 0.40 (see Table 1), respectively, the hypotheses would be GREML point estimates of around 0.15 and 0.20. Our evidence, considered in its entirety, is not inconsistent with these hypotheses, but the point estimates are quite noisy. An alternative approach is to examine the number of statistically significant associations. For economic preferences, if the SNP-based heritability parameter in the population is 0.15, and if sample estimates have a standard error of 0.15 (as suggested by Table 2), then our power to statistically reject the null hypothesis of zero heritability in a one-sided test at the five percent level is about 26%. For political attitudes, if we assume a SNP-based heritability parameter in the population of 0.20, and we assume a standard error of 0.15 (again as suggested by Table 2), then the corresponding statistical power is about 38%. If the traits are independently distributed, this calculation implies that for the nine preference variables, we should expect to observe 2.9 significant associations at the five percent level. In fact, we observe three significant associations at the five percent level and one more at the eight percent level. The results, therefore, are close to what one would expect under the hypothesis that the SNP-based heritability estimates are about half the magnitude of the twin-based estimates.¶

Third, our analysis of individual SNPs does not reveal any associations that are significant at the conventional threshold of genome-wide significance required in genetic association studies. This is unsurprising in light of the accumulating evidence that the effects of common variants on complex outcomes are small (Visscher, 2008), especially in the context of social science traits (Beauchamp et al., 2011; Benjamin et al., 2011). Figure 1 displays power calculations, given the SALTY sample size, for detecting true associations across a range of effect sizes as measured by the R^2. For the preference measures, the study was well-powered to detect individual markers which explain at least 1.5% of trait variation at a nominal significance level of 8×10^{-8}—yet no single SNP in our sample attains this level of significance in our sample. Moreover, 1.5% is an upper bound to the effect sizes we can rule out because: (1) since 8×10^{-8} is the smallest of many millions of p-values we estimated, it almost surely capitalizes on chance to some extent and overstates the strongest genetic association in our data (the well-known "winner's curse" in statistical inference; Garner, 2007); and (2) for many of the variables, the lowest observed p-value was considerably higher than 8×10^{-8}. To illustrate our statistical power another way, if across the nine traits there are a total of twenty independently-distributed SNPs each with R^2 of 0.75%, our study was extremely well-powered to detect at least one of them—and yet we found none. We conclude that is unlikely that many markers with such effect sizes exist. Hence our failure to detect associations at these levels of significance indicates that true associations between common SNPs and economic and political phenotypes are likely to have very small effect sizes. ‖

Fourth, the results from our prediction exercise show that in a sample of approximately 4,000 individuals, a standard polygenic risk score has negligible out-of-sample predictability. This does not in any way contradict the results from the GREML analysis. GREML uses the measured SNPs to estimate realized relatedness between individuals, and given the large number of SNPs in a dense SNP array, realized relatedness can be estimated relatively precisely. In contrast, estimating a prediction equation that can predict well out of sample requires precise estimates of the effects of individual SNPs. In the limit of an infinite sample, it would be possible to perfectly estimate the effects of individual SNPs and thereby construct a polygenic risk score whose predictive power reaches the theoretical upper bound that is estimated by GREML. The smaller the discovery sample used to estimate the prediction equation, the noisier are the estimates of the individual SNP effects, and hence the lower will

be the out-of-sample predictive power of the polygenic risk score that is constructed based on these estimates. Evidently a discovery sample of 4,000 individuals is far too small to obtain even mildly useful predictive power for standard measures of economic or political preferences.

These findings fit in nicely with an emerging consensus in medical genetics, according to which common SNPs that explain a substantial share of the variation in complex traits are unlikely to exist. If anything, the problem is likely to be even more acute in the social sciences, since the phenotypes are usually several degrees removed from genes in the chain of causation (Benjamin et al., 2007, 2011; Beauchamp et al., 2011). Our results suggest that much of the "missing heritability" (Manolio et al,. 2009)—the gulf between the explanatory power of genetic variants identified to date and the heritability as estimated in behaviour-genetic studies—for social science traits reflects the fact that these traits have a complicated genetic architecture with thousands of SNPs exerting small effects. If the genetic architecture of social science traits involves many genetic variants with small effects, then large samples will be needed to detect those variants.**

These conclusions have a number of implications for research at the intersection of genetics and social science. There has recently been an explosion of reported associations in samples of several hundred individuals (for reviews of work to date, see Ebstein et al., 2010, and Beauchamp et al., 2011). These samples are very small by the standards of medical genetics, often based on samples in the hundreds or less. Such studies are only adequately powered if the R^2 is considerably larger than the upper bounds established by the GWAS findings reported here. Our findings, based on a sample an order of magnitude larger, suggest that adequate power actually requires a sample size that is yet an order of magnitude larger even than ours. Statistically significant associations obtained in a small sample should be approached with caution for two reasons: (1) since most existing published studies are dramatically underpowered, the probability that an association study will detect a true signal is vanishingly small; hence if a significant association is observed, Bayesian calculations indicate that the posterior odds of a true association are low (Benjamin, 2010; Beauchamp et al., 2011); and (2) publication bias—the tendency for findings, as opposed to non-findings, to be selectively reported by researchers and selectively published by journals—are magnified in genetic association work because the typical dataset has many behavioral measures and many genetic markers (Hewitt, 2011).

Our conclusions regarding the molecular genetic architecture of economic and political preferences also have implications for whether, how, and how soon molecular genetic information can contribute to, and potentially transform, research in social science. One possibility is that genetic associations may shed light on biological pathways of precursors to important behaviors and outcomes, such as preferences. More speculatively, such insights may also help inspire the development of new theoretical constructs which are more closely aligned with the underlying biology than the existing concepts such as "risk preference" or "time preference" that we study here (Benjamin et al., 2007). Contributions such as these require the identification of specific genetic variants that correlate robustly with behavior. As discussed above, the results reported here suggest the need to construct samples which are several orders of magnitude larger than those presently employed in this sort of research.

Another interesting potential contribution to economics and political science would be the use of genetic markers as instrumental variables in (non-genetic) empirical work. In order for the gene-as-instrument to be convincing, not only must the marker be robustly associated with the "endogenous regressor," but *all* of the behaviors associated with that marker must be understood. Otherwise, if the marker has pleiotropic effects, then the exclusion-restriction assumption may be violated, making the marker invalid as an instrumental variable. It will take a long time to accumulate the evidence required to demonstrate with reasonable confidence that a given genetic marker mostly operates through a particular causal pathway.

A different potential use of molecular genetic data to social science would be as control variables for genetic heterogeneity in (non-genetic) empirical work, in order to reduce the variance of the error term and shrink the standard errors of coefficient estimates. For such an application to have any practical utility, the markers that are selected as controls need to explain a non-negligible share of the variation. Similarly, use of genetic data to target interventions requires that the aggregate predictive power of a set of genetic variants for the trait be sufficiently large. As we have shown here, given presently-attainable sample sizes, this does not appear to be feasible for economic and political traits.†† It is likely that extremely large—perhaps impossibly large—samples will be required. If so, some of the most exciting possible uses of molecular genetic data in the social sciences lie many years in the future.

In summary, our molecular-genetic-based estimates of heritability partially corroborate the twin-based estimates and suggest that molecular genetic data *could* be predictive of preferences. Our other results, however, suggest that excitement about the utility of molecular genetic data in social science research likely needs to be tempered by an appreciation that much of that the heritable variation is likely explained by a large number of markers, each with a small effect in terms of variance explained. As a consequence, for economic and political preferences, much larger samples than currently used will be required to robustly identify individual SNP associations or sizeable predictive power from many SNPs considered jointly.

Rather than being destructive to the enterprise of incorporating genetic data into social science, an understanding the molecular genetic architecture of economic and political preferences can help guide research in more productive directions. Indeed, there are several constructive and complementary responses one might imagine to the inferential challenges posed by the genetic architecture documented here. One is to undertake efforts to actually obtain very large samples that contain both genetic and social science data. A second response is to carefully evaluate the psychometric properties of social science phenotypes to minimize attenuation bias due to error in measurement and thereby maximize power for any given sample size. In our view, the larger GREML estimates for the political preference measures relative to the less reliable economic measures phenotypes illustrates these potential gains. A third suggestion is to focus on traits that are more biologically proximate, where it is more likely that any associations have non-trivial effect sizes and biologically plausible interpretations.

Materials and Methods

Between December 2010 and May 2011, 10,946 Swedish Twins were genotyped by the SNP&SEQ Technology Platform, Uppsala, using the Illumina HumanOmniExpress BeadChip genotyping platform. A total of 79,893 SNPs were omitted because their minor allele frequency was lower than 0.01; 3,071 markers were excluded because they failed a test of Hardy Weinberg equilibrium at $p < 10^{-7}$; and 3,922 SNPs were dropped because of a missingness greater than 3%. IMPUTE Version 2 (Howie et al., 2009) was used to impute all

autosomal SNPs on HapMap, using the publicly-available phased haplotypes from HapMap2 (release 22, build 36, CEU population) as a reference panel.

As part of the quality control, one of the authors (van der Loos) conducted a careful analysis designed to detect pedigree errors. We estimated the proportion of genome-wide allele sharing among all pairs of individuals in the dataset by calculating mean identity-by-descent across a set of 547 randomly selected markers, selected to have a minor allele frequency of at least 0.20. Inspection revealed a small number of pairs ($n = 38$) with misclassified zygosity; we corrected this misclassification. We also detected a small number of inconsistencies which were corrected. All molecular genetic analyses reported in the paper are based on the dataset with respondents who are cryptically related removed from the sample.

The principal components of the genotypic data were computed using EIGENSTRAT (Price et al., 2006). We used the program *smartpca* of the EIGENSTRAT software to calculate the principal components of the genotypic data from a subsample of 6,813 unrelated individuals and to project the other individuals in the sample onto those principal components, thus obtaining the loadings of each individual on each of the top 10 principal components. We dropped individuals whose score is at least six standard deviations from the mean on one of the top ten principal components.

We computed the GREML estimates using the publicly-available GCTA software (Yang et al., 2011). Before computing the matrix of genetic relatedness for the SALTY sample, we dropped one twin per pair, always the twin with a larger number of missing phenotypes. If the same number of observations were available for both twins, we selected one randomly. After restricting the genotypic data to the selected individuals, we performed additional quality control: we dropped 6 SNPs because they failed a test of Hardy-Weinberg equilibrium at $p < 1{\times}10^{-6}$; excluded 629 SNPs with a minor allele frequency lower than 0.01; and removed 2 SNPs because of a missingness greater than 5%. 4 individuals were dropped because more than 1% of their genotypic data were missing. The pairwise genetic relationships were then estimated from 628,599 autosomal SNPs. We used the same matrix of genetic relatedness for all the SALTY phenotypes. The matrix of genetic relatedness for the larger, administrative-record-based sample was estimated in a similar way: before computing the matrix, we randomly dropped one twin per pair and performed additional quality control of the genotypic data. A total of 48 SNP were dropped because they failed a test of Hardy-

Weinberg equilibrium at $p < 1 \times 10^{-6}$; 249 SNPs with a minor allele frequency lower than 0.01 were excluded; and 13 individuals were omitted because more than 1% of their genotypic data were missing. The matrix of genetic relatedness was then estimated from 628,922 autosomal SNPs. We used the same matrix for both educational attainment and income. In all our GREML analyses, we control for the first ten principal components, sex and year of birth.

Our individual-SNP analyses are based on the imputed data. In all our GWAS analyses, we control for the first ten principal components of the genotypic data, sex and age. The standard errors are adjusted for the non-independence of the residuals within twins using the *fastAssoc* function in the software Merlin Offline. The software assumes a behavior genetic AE model for the distribution of the error terms within family. SNPs with an imputation quality (*info* measure from IMPUTE) smaller than 0.4 or a minor allele frequency smaller than 0.01 were dropped. Genomic control (Devlin and Roeder, 1999) was used to adjust the test statistics for inflation due to any remaining population stratification.

For our prediction exercise we use the non-imputed data with the same filters as the pre-imputation quality controls previously described. We randomly split the sample into a 80% training sample and a 20% validation sample, randomizing at the level of the family to ensure non-independence across samples. We ran linkage-disequilibrium-based pruning of the validation sample using the software PLINK. Following Purcell et al. (2009), we used a linkage disequilibrium threshold of 0.2 with a 200-SNP window that slides by 25 SNP. The process started with 643,826 markers and left us with 107,360 markers which are approximately in linkage equilibrium. For each phenotype in turn, we then constructed the polygenic risk score for each individual in the validation sample. The polygenic risk score is defined as the sum of the estimated regression coefficients (from a regression of the phenotype on each SNP within the training sample) multiplied by the number of reference alleles. If a genotype in the score is missing for a particular individual, then the expected value is imputed based on the sample allele frequency. Finally, within the validation sample, we regressed the phenotype on the polygenic risk score, controlling for the number of non-missing SNPs.

Footnotes

* For critical perspectives, see Conley (2009) and Cawley et al. (2011).

† Another approach is to estimate the genetic variance from within-family variation in genetic relatedness (see Visscher et al., 2006). The estimates derived from such an analysis are unbiased estimates of heritability rather than lower bounds because the identical-by-descent probabilities for all variants, including the rare ones not tagged by the genotyped SNPs or microsatellites, can be inferred if one has sibling data.

‡ Additional details on variable construction and materials and methods are available in the Online Supplementary Materials.

§ Labor economists usually study earnings because it is taken to be a proxy for productivity. This assumption is most reasonable in prime aged males, whose attachment to the labor market tends to be strong and who typically work full time, making variation in hours worked less of a confound for measuring productivity. For a discussion of the difficulties with analyzing female labor supply and earnings, see Heckman and Killingsworth (1986).

¶The fact that we observe some GREML point estimates of zero is not surprising. Since the estimator is constrained to produce a non-negative estimate, the bound at zero will often be attained when the true population parameter is low and estimated imprecisely.

‖ While the survey measures we use here are common in economics (e.g., Barsky et al., 1997), it is also common in economics to measure preferences using laboratory tasks that attach financial incentives to performance (Hertwig and Ortmann, 1998). It is sometimes argued that these incentivized laboratory tasks produce measures of preferences that are more reliable and more correlated with real-world behaviour than the survey measures. In fact, however, existing work does not support the hypothesis that such incentivized measures of risk aversion or other preferences are measured more reliably than survey-based measures (Beauchamp et al., 2011; Lönnkvist et al., 2011). Moreover, our conclusion that effects of individual SNPs on risk preferences are very small would hold even with measures of preferences were much more reliable than those we use. For example, suppose we could improve the reliability of one of the measures from 0.58 (the average reliability across our four economic preference measures) to 0.80. Then the upper bound of 1.5% that we calculate would imply an upper bound of 2.07% for this better-measured phenotype.

** While we have emphasized the possibility that the heritability of preferences is composed of many common SNPs of small effect, we also note that the common SNPs (the heritable variation measured on dense SNP arrays) do not tag all the heritable variation in the genome. If the twin-based estimates of heritability are correct, then rare, perhaps non-SNP, causal variants that are not in close linkage disequilibrium with the genotyped markers may explain some of the heritable variation. If such variants exist, they may have large effects. Nonetheless, since such variants will be rare, large samples will also be required for adequate power to detect those markers.

†† Were it the case that economic behaviors, or their precursors in the form of various preferences, traits and skills, could be predicted from molecular genetic information, it would raise a host of ethical questions about if and how such information should be used. In principle, the information may be used to help people make more informed decisions. For example, if dyslexia could be predicted at a relatively early age, such information could in principle be used to help parents make better information about treatment strategies (Benjamin, 2010). Such potential benefits must of course be carefully weighed against the costs. For example, insurance markets may break down due to adverse selection (Benjamin et al., 2007) unless there are restrictions placed on the availability of genetic data.

Acknowledgements

Table 1: Sibling Correlations

	Economic Outcomes		Economic Preferences				Political Preferences				
	Education	Income	Risk	Time	Social	Trust	Imm./ Crime	Econ. Policy	Environ.	Femin.	Foreign Policy
ρ_{MZM}	0.70	0.47	0.41	0.05	0.32	0.37	0.56	0.42	0.26	0.48	0.48
	(.65-.75)	(.31-.61)	(.33-.49)	(-.04-.15)	(.23-.42)	(.29-.45)	(.49 -.62)	(.34-.50)	(.17-.34)	(.40-.57)	(.40-.54)
ρ_{DZM}	0.50	0.22	0.20	0.07	0.24	0.18	0.33	0.34	0.09	0.27	0.16
	(.42-.57)	(.11-.33)	(.12-.28)	(-.04-.20)	(.15-.33)	(.08-.27)	(.25-.42)	(.26-.42)	(.01-0.18)	(.19-.35)	(.07-.24)
ρ_{MZF}	0.74	0.37	0.35	0.16	0.24	0.33	0.60	0.45	0.34	0.41	0.47
	(.70-.78)	(.25-.50)	(.27-.43)	(.07-.25)	(.16-.32)	(.25-.40)	(.55-.65)	(.37-.51)	(.23-.46)	(.34-.48)	(.39-.53)
ρ_{DZF}	0.54	0.22	0.13	0.11	0.10	0.19	0.37	0.22	0.16	0.19	0.21
	(.49-.59)	(.14-.32)	(.05-.21)	(.03-.20)	(.03-.17)	(.11-.26)	(.29-.44)	(.14-.29)	(.09-.24)	(.12-.26)	(.14-.29)
N_{MZM}	561	560	443	491	450	458	448	448	448	448	448
N_{DZM}	614	612	477	655	482	486	487	487	487	487	487
N_{MZF}	544	538	594	700	652	659	630	630	630	630	630
N_{DZF}	845	815	636	1108	681	714	665	665	665	665	665
ρ_{RETEST}	-	-	0.71	0.40	0.57	0.63	0.86	0.84	0.62	0.78	0.72
			(.66-.76)	(.27-.52)	(.49-.65)	(.57-.69)	(.84-.88)	(.84-.88)	(.84-.88)	(.84-.88)	(.84-.88)
N_{RETEST}	-	-	475	483	469	482	471	471	471	471	471

Note: This table gives the sibling and retest Pearson correlations for the eleven phenotypes. The 95% confidence intervals given in parentheses are computed by bootstrapping with 500 draws.

MZM: number of male monozygotic pairs; DZM: male dizygotic pairs; MZF: female monozygotic pairs; DZF: female dizygotic pairs.

Table 2: GREML Analyses

	Economic Outcomes		Economic Preferences				Political Preferences				
							Imm./	Econ.			Foreign
	Education	Income	Risk	Time	Social	Trust	Crime	Policy	Environ.	Femin.	Policy
V(g)/V(P)	0.191	0.061	0.137	0.085	0.000	0.242	0.203	0.344	0.000	0.000	0.353
s.e.	0.062	0.123	0.152	0.148	0.150	0.146	0.147	0.150	0.148	0.147	0.149
p-value	0.001	0.313	0.186	0.285	0.500	0.047	0.079	0.012	0.500	0.500	0.001
N	5682	2866	2327	2399	2376	2410	2368	2368	2368	2368	2368
Chrom.	0.240	0.139	0.118	-0.195	-0.111	0.460	0.117	0.496	-0.311	0.247	0.462

Note: This table reports GREML estimates for the eleven variables. We estimated the matrix of genetic relatedness after omitting one twin per pair and then restricted the analyses to individuals whose relatedness did not exceed 0.025 in absolute value. The row Chrom. shows the estimated correlation between chromosomal length (measured in centimorgan) and the proportion of variation explained by relatedness estimated from that chromosome. As explained in the text, the results for income are based exclusively on men.

Table 3: Results of Prediction Analysis

	Economic Outcomes		Economic Preferences				Political Preferences				
							Imm./	Econ			Foreign
	Education	Income	Risk	Time	Social	Trust	Crime	Policy	Environ.	Femin.	Policy
R^2	0.0012	0.0004	0.0004	0.0000	0.0018	0.0001	0.0007	0.0008	0.0002	0.0000	0.0024
N	1875	888	634	657	654	663	653	653	653	653	653
p-value	0.1934	0.5448	0.6268	0.9153	0.2593	0.9153	0.518	0.4871	0.7511	0.9577	0.2339

Note: This table reports the results from the prediction analyses. Following Purcell et al. (2009), we constructed a polygenic risk score for each phenotype by splitting the sample into an 80% discovery sample and a 20% validation sample. The row N gives the number of individuals in the validation sample. The score is defined as the sum of the estimated regression coefficients multiplied by the number of reference alleles. If a genotype in the score is missing for a particular individual, then the expected value is imputed based on the sample allele frequency. Finally, we regressed the dependent variable on the score, controlling for the number of non-missing SNPs. The $R2$ is the incremental $R2$ obtained when adding the score as a regressor. The p-value is obtained from the Wald test of the null hypothesis that the coefficient on the polygenic risk score is zero.

Figure 1: Power Analysis
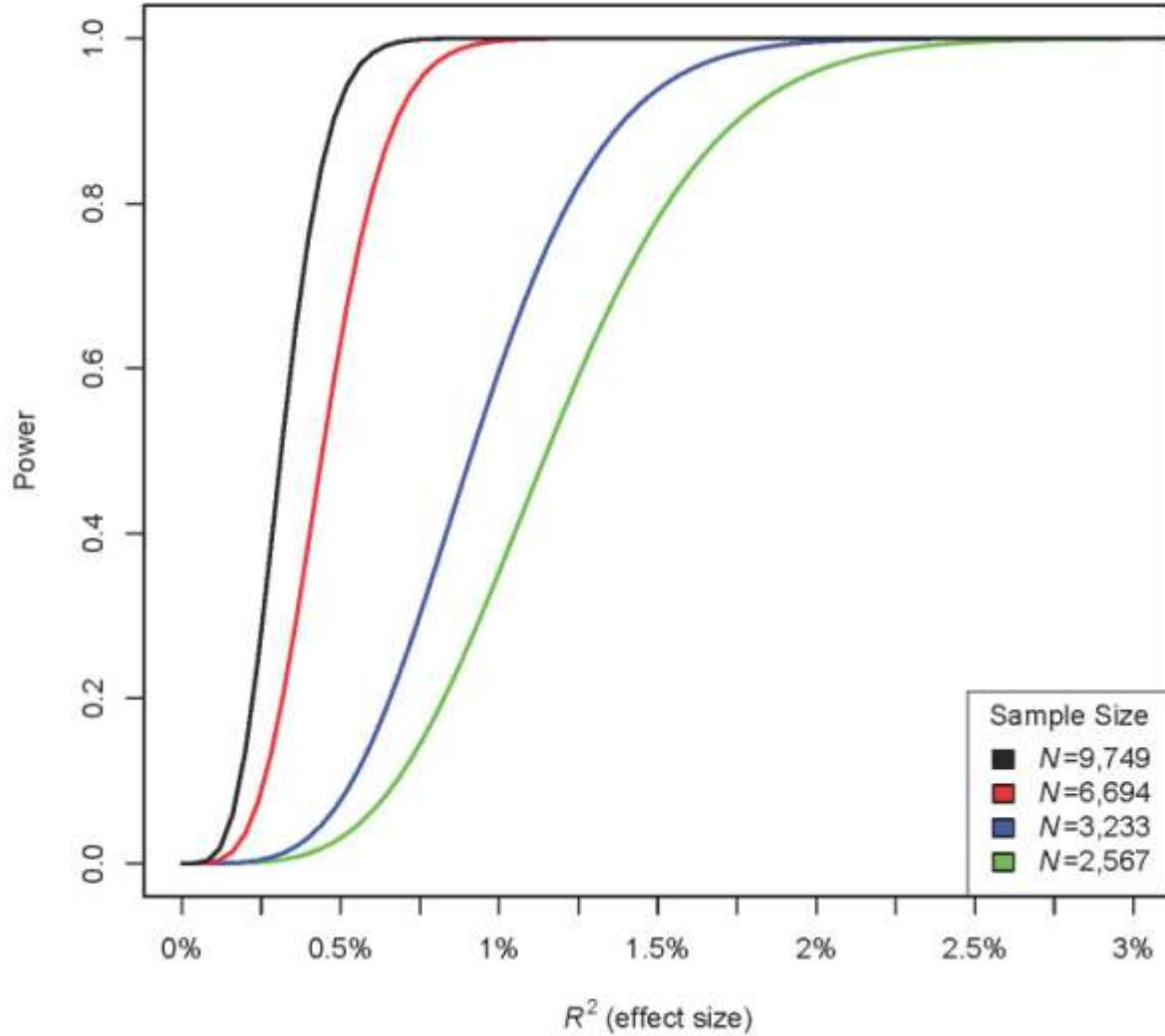
This figure shows how the power to detect a marker at a nominal significance level of 8×10^{-8} as a function of sample size and the fraction of variance (R^2) explained by the marker. This p-value threshold was selected because no single SNP attained this level of nominal significance in any of the analyses. For educational attainment, there were 6,694 independent observations (i.e., from unrelated individuals) and a total of 9,749 observations – the true power therefore lies somewhere in between the two lines shown. For the political preference measures, we had 2,567 independent observations and a total of 3,233 observations. The true power again lies somewhere between the lines shown. Even for the preference variables, where the sample size is smaller, the study was well-powered to detect a marker with an R^2 of 1.5% at a nominal significance level of 8×10^{-8}. The fact that we did not observe any associations at this level of significance suggests that it is unlikely that common variants with effects of that magnitude exist. For several of the traits, the lowest p-values observed were considerably higher than 8×10^{-8}. Hence, the 1.5% estimate of the upper bound is conservative. For educational attainment and income, the study was well-powered to detect markers with an R^2 of 0.6%.

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Online Supplementary Materials:

"The Genetic Architecture of Economic

and Political Preferences"

This document provides additional details about data and additional analyses to accompany the article "The Genetic Architecture of Economic and Political Preferences."

Contents

AI. Variable Construction

AII. Samples

AIII. Additional Analyses

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AV. References

AI.A. Risk Attitudes

We used three survey measures from SALTY to construct an overall index of risk attitudes. The first measure elicits the subjective level of general risk taking of the individual:

"How do you see yourself: Are you <u>generally</u> a person who is fully prepared to take risks or do you try to avoid taking risks? Please tick a box on the scale, where the value 1 means 'unwilling to take risks' and the value 10 means 'fully prepared to take risks.'"

The second measure is the same as the first, except it is specific to financial risks:

"Are you a person who is fully prepared to take <u>financial risks</u> or do you try to avoid taking financial risks? Please tick a box on the scale, where the value 1 means 'unwilling to take risks' and the value 10 means 'fully prepared to take risks.'"

These two measures have been used in the German Socioeconomic Panel (Dohmen et al., forthcoming), except with a 0-10 scale rather than the 1-10 scale used in SALTY.

Our third measure of risk attitudes is adapted from the Health and Retirement Survey questions first described in Barsky et al. (1997). Subjects answer three questions about hypothetical gambles. The first question is phrased:

"Imagine the following hypothetical situation. You are the sole provider for your household, and you have the choice between two equally good jobs:

Job A will with certainty give you SEK 25,000 per month after taxes for the rest of your life.

Job B will give you a 50-50 chance of SEK 50,000 per month after taxes for the rest of your life, and a 50-50 chance of SEK 20,000 per month after taxes for the rest of your life.

Which job do you choose?"

The second and third questions are identical, except that instead of being SEK 20,000, the low-income outcome in job B is SEK 22,000 and SEK 17,000, respectively. For each subject, our third measure of risk-taking is the number of questions out of the three that the subject chose Job B (the risky job), generating a measure with a 0 (never choosing the risky job) to 3 (always choosing the risky job). (Only 2.6% of subjects behave inconsistently in the sense of choosing job B in a question but choosing job A in another question that offers more money for job B; we retain these inconsistent subjects in the sample.)

To combine our three measures of risk taking into an overall index, we calculate the z-score for each of the three measures, and the index is defined as the average z-score.

AI.B. Time Preference

To measure the rate of time preference, we used a sequence of three hypothetical choice questions from SALTY. Subjects were asked to choose between an amount of money today and a larger amount of money in one week. The first of these questions is phrased:

"Imagine that you can choose between receiving a sum of money today, or to wait and receive a larger sum in one week. Which would you choose?

SEK 5,000 today

SEK 6,000 in a week"

The second and third questions are identical, except that instead of being SEK 6,000*,* the delayed outcome is SEK 7,000 and SEK 5,500, respectively. For each subject, we calculate the number of questions out of the three that the subject chose the delayed outcome, generating a variable with a 0 (never choosing the delayed reward) to 3 (always choosing the delayed reward) scale. (Only 1.1% of subjects behave inconsistently in the sense of choosing job B in a question but choosing job A in another question that offers more money for job B; we retain these inconsistent subjects in the sample.) Our measure of patience is the z-score of this variable.

Note that the questions ask about a short time horizon (one week) to get a proxy for short-term time discounting, which appears to be distinct from long-term discounting (e.g., Laibson, 1997) and responsible for many impatient behaviours (DellaVigna, 2009). Similar questions (but with smaller real stakes) are used, for instance, by

Benjamin et al. (2006); see also the survey by Frederick et al. (2001), who discuss this

and other approaches of measuring time preferences.

AI.C. Trust

To measure trust, we use two questions included in SALTY. Both are taken from the National Opinion Research Center's General Social Survey (GSS), except that they SALTY questions use a 10-point scale instead of a binary scale. The first question is a classic measure of trust used widely in political science (Nannestad, 2008) and other social sciences:

"Generally speaking, would you say that most people can be trusted or that you need to be very careful in dealing with people? Please tick on the scale below, where the value 1 means 'need to be very careful' and the value 10 means 'most people can be trusted.'"

We also included a second question from the GSS:

"Do you think that most people would try to take advantage of you if they got the chance, or would they try to be fair? Please tick on the scale below, where the value 0 means 'would take advantage of me' and the value 10 means 'would treat me fairly.'"

For each subject, we calculate the z-score for each response to the two questions, and we use the average z-score as our index of trust. Glaeser et al. (2000) used the above two trust questions (as well as a third question not asked in SALTY) and provide a thorough discussion about different measures of trust.

AI.D. Fairness

To measure attitudes about fairness we used three survey questions in SALTY, which are adapted from Kahneman et al. (1986, their question 1, question 4A, and question 11B):

"A hardware store has been selling snow shovels for SEK 150. The morning after a large snowstorm, the store raises the price to SEK 200. How fair do you think that is?

Completely fair

Acceptable

Unfair

Very unfair"

"A company is making a small profit. However, due to a recession, unemployment is high, and it is easy to hire people. The company therefore decides to decrease wages and salaries by 10% for all its employees. How fair do you think that is?

Completely fair

Acceptable

Unfair

Very unfair"

"A small factory is making kitchen tables. Because of changes in the price of materials, the cost of making each table has decreased by SEK 200. But the factory does not lower its price for the tables. How fair do you think that is?

Completely fair

Acceptable

Unfair

Very unfair"

We coded the responses from 1 (completely fair) to 4 (very unfair) for each question, and we summed the answers from the three questions. We then use the z-score of this variable as our index of fairness attitudes.

AI.E. Political Attitudes

We measure political attitudes using a battery of 34 questions included in SALTY that elicit attitudes towards various policy issues. These items have also been included in other Swedish surveys, such as the Swedish Election studies. On each question the respondents rate their attitude towards a policy on a 5-point scale from (1) "very good proposal" to (5) "very bad proposal." The battery of questions is reproduced below.

Below is a table with proposals some people think should be implemented in Sweden. State what you think about each of these proposals.

	Very good proposal	Fairly good proposal	Neither good or bad proposal	Fairly bad proposal	Very bad proposal
1. Decrease the public sector	☐	☐	☐	☐	☐
2. Decrease defense expenses	☐	☐	☐	☐	☐
3. Decrease welfare benefits	☐	☐	☐	☐	☐

4. Decrease taxes ☐ ☐ ☐ ☐ ☐

5. Keep property taxes ☐ ☐ ☐ ☐ ☐

6. Sell public companies to ☐ ☐ ☐ ☐ ☐
   private buyers

7. Decrease income inequality ☐ ☐ ☐ ☐ ☐
   in society

8. Have more private ☐ ☐ ☐ ☐ ☐
   companies in health care

9. Decrease the influence of ☐ ☐ ☐ ☐ ☐
   financial markets on politics

10 Keep the "maxtaxa" in ☐ ☐ ☐ ☐ ☐
. daycare

11 Have more private schools ☐ ☐ ☐ ☐ ☐

.

12 Introduce grades earlier in ☐ ☐ ☐ ☐ ☐
. school

13 Increase the economic ☐ ☐ ☐ ☐ ☐
. support to rural areas

14.	Introduce 6-hour working day for all employees	☐	☐	☐	☐	☐
15.	Forbid all kinds of pornography	☐	☐	☐	☐	☐
16.	Limit the right to free abortion	☐	☐	☐	☐	☐
17.	Introduce much harder punishments for criminals	☐	☐	☐	☐	☐
18.	Strengthen animal rights	☐	☐	☐	☐	☐
19.	Sweden should in the long run carry through a nuclear phase-out	☐	☐	☐	☐	☐
20.	Stop motoring in the inner city	☐	☐	☐	☐	☐
21.	Invest more to prevent environmental damages	☐	☐	☐	☐	☐
22.	Decrease carbon dioxide emissions	☐	☐	☐	☐	☐

23.	Increase labor immigration to Sweden	☐	☐	☐	☐	☐
24.	Introduce a language test to become a Swedish citizen	☐	☐	☐	☐	☐
25.	Decrease foreign aid	☐	☐	☐	☐	☐
26.	Accept fewer refugees in Sweden	☐	☐	☐	☐	☐
27.	Increase the economic support to immigrants so that they can preserve their own culture	☐	☐	☐	☐	☐
28.	Remit debt to developing countries	☐	☐	☐	☐	☐
29.	Give private companies more freedom	☐	☐	☐	☐	☐
30.	Sveden should leave the EU	☐	☐	☐	☐	☐

31.	Sweden should introduce the EURO	☐	☐	☐	☐	☐
32.	Sweden should become members in NATO	☐	☐	☐	☐	☐
33.	Sweden should work for increased free trade all over the world	☐	☐	☐	☐	☐
34.	Sweden should actively support the US war on terrorism	☐	☐	☐	☐	☐

83.4% of subjects responded to all 34 questions, and 97% responded to at least 29. We dropped the 3% of subjects who answered fewer than 29 questions, and for the subjects we retained, we replaced missing values by the question-specific sample mean. We factor-analyzed the items, retaining five factors, and performed a varimax rotation of the data (Kaiser, 1958). An inspection of the factor loadings shows that the first factor can be interpreted as an "immigration factor," the second as an "economic policy factor," the third as "environmentalism factor," the fourth as an "international affairs," factor and the last as a "feminism and inequality" factor. The table below reports the rotated factor loadings with the highest absolute value of each factor. The factor structure is similar to what has previously been reported for this scale (Oskarsson et al., 2010; Statistics Sweden, 2008).

Table S1: Factor Structure of Political Attitudes Battery.

	Questions With Highest Loading	Interpretation
Factor 1	23,24,25,26,27	Immigration
Factor 2	1,4,6,8,11	Economic Policy
Factor 3	18,19,20,21,22	Environmentalism
Factor 4	19,30,31,32,33	Foreign Policy
Factor 5	7,13,14,15,18	Feminism & Inequality

Note: For each of the factors, this table show the five rotated factor loadings that are highest in absolute value.

AI.F. Educational Attainment

Our measure of educational attainment is obtained from subjects' responses on the 1990 Swedish census. The original census variable is categorical and takes one of seven distinct values. Each category corresponds to a highest educational attainment level, ranging from minimum compulsory schooling to postgraduate education. We assign to each category the population average of the number of years of schooling, as estimated by Isacsson (2004).

AI.G. Income

Our income variable is obtained from the 1985 and 1990 Swedish census data. The variable (arbetsinkomst) is defined as the income from work, including self-employment and sickness and child benefits. To test robustness to alternative ways of measuring income, we create two income measures.

Our first income measure is the average across the two years of the logarithm of income. Our second income measure is defined the same way, but we discard observations below SEK 40,000. This restriction is in order to restrict the sample to individuals who are plausibly working full time (cf., Isacsson, 2004). For both measures, when income data are present in both years, we average income across the two years in order to smooth out some of the transitory fluctuations. We use income from only one year when income from the other year is missing; this occurs for 5.5% of the subjects for the first measure and 11.3% for the second measure. As explained in the manuscript, our main specification uses the first income measure and restricts the sample to males.

AII.A. Sample Definitions

The first sample we use is the *SALTY sample*. SALTY is a survey administered by the Swedish Twin Registry between 2008 and 2010 to twins born between 1943 and 1958. The response rate from contacted individuals was 47.1%, leaving a sample of 11,743 subjects. Of these, 11,418 (97.2%) gave informed consent to have their answers stored and analyzed. In addition, 491 respondents answered the survey twice (out of 800 contacted a second time). Cesarini et al. (2011) contains an analysis of non-response both to the original survey and to the re-test survey. We refer to the *SALTY* re-test respondents as *SALTY Retest*.

The second sample is *TwinGene*, a sample of 10,946 twins born between 1926 and 1958 who have been genotyped using the Illumina HumanOmniExpress BeadChip genotyping platform. The *TwinGene* and *SALTY* samples partly overlap; 4,040 *SALTY* respondents are also in *TwinGene*. We refer to these genotyped *SALTY* twins as *SALTY-Geno.* The *SALTY* respondents who are not in *SALTY-Geno* have not been genotyped.

The economic and political preference data are available from the survey administered to the *SALTY* sample (and administered twice to the *SALTY Retest* sample). These data are *not* available for the *TwinGene* sample, except for those in *SALTY-Geno*. Data on educational attainment and income are available for nearly all members of the *TwinGene*

sample, as these variables are drawn from administrative records (and hence do not require participation in the SALTY

survey).

AII.B. Descriptive Statistics

Table S2: Summary Statistics

	Economic Outcomes		Economic Preferences				Political Preferences				
	Education	Income	Risk	Time	Fairness	Trust	Imm./ Crime	Econ. Policy	Environ.	Femin.	Foreign Policy
SALTY	-	-	0.00	-0.02	-0.00	-0.00	-0.00	0.00	-0.01	-0.02	-0.01
	(-)	(-)	(1.00)	(1.00)	(1.00)	(1.00)	(1.00)	(1.00)	(1.00)	(1.00)	(1.00)
N	-	-	10,788	11,187	11,045	11,237	11,000	11,000	11,000	11,000	11,000
SALTY-Geno	-	-	0.06	0.02	0.01	0.02	0.02	0.02	-0.04	-0.02	-0.00
	(-)	(-)	(0.98)	(0.99)	(0.98)	(0.99)	(1.00)	(0.98)	(0.99)	(0.99)	(0.97)
N	-	-	3,818	3,970	3,922	3,986	3,886	3,886	3,886	3,886	3,886
SALTY-Retest	-	-	-0.00	-0.00	0.00	0.03	-0.10	-0.03	0.06	0.11	0.01
	(-)	(-)	(0.98)	(0.94)	(0.98)	(0.94)	(0.98)	(1.00)	(0.89)	(0.97)	(0.93)
N	-	-	487	486	486	487	480	480	480	480	480
TwinGene	11.05	6.95	-	-	-	-	-	-	-	-	-

	(2.83)	(0.76)	(-)	(-)	(-)	(-)	(-)	(-)	(-)	(-)	(-)
N	10,793	10,669	-	-	-	-	-	-	-	-	-

Note: This table reports sample summary statistics. Standard deviations in parentheses. We report the data for the entire SALTY sample, the subset of the SALTY sample

which has been genotyped, and the entire TwinGene sample. The TwinGene sample only party overlaps with the SALTY sample, which is why the number of genotyped

subjects with information on educational attainment and income is larger. The economic and political variables were standardized to have mean zero and variance one

using all of SALTY as a standardization sample.

AIII.A. GREML Analyses Without Threshold for Genetic Relatedness

Table S3: GREML Analyses, No Threshold

	Economic Outcomes		Economic Preferences				Political Preferences				
							Imm./	Econ.			Foreign
	Education	Income	Risk	Time	Fairness	Trust	Crime	Policy	Environ.	Femin.	Policy
$V(g)/V(P)$	0.187	0.000	0.157	0.040	0.000	0.258	0.207	0.294	0.000	0.000	0.344
s.e.	0.053	0.108	0.139	0.134	0.136	0.134	0.134	0.139	0.135	0.132	0.138
p-value	<0.001	0.499	0.130	0.385	0.500	0.026	0.058	0.019	0.500	0.497	0.006
N	6,694	3,211	2,519	2,604	2,579	2,613	2,567	2,567	2,567	2,567	2,567
Chrom.	0.392	0.048	0.301	-0.170	-0.044	0.391	0.310	0.523	-0.110	0.186	0.554
p-value	0.071	0.832	0.173	0.449	0.846	0.072	0.160	0.013	0.626	0.407	0.007

Note: This table reports GREML estimates for the eleven variables. We estimated the matrix of genetic relatedness after omitting one twin per pair but did not impose a relatedness threshold before estimating the model. The row Chrom. shows the estimated correlation between chromosomal length (measured in centimorgan) and the proportion of variation explained by relatedness estimated from that chromosome. As explained in the text, the results for income are based exclusively on men. The third row gives the p-value for the test of the null hypothesis that the proportion of variation explained by common SNPs on the autosomes is zero. The sixth row gives the p-value for the test of the hypothesis that,

across the 22 autosomes, the correlation between chromosomal length and the proportion of variation explained by the chromosome is zero.

AIII.B. Additional GREML Analyses for Income

Table S4: GREML Analyses, Additional Income Results

	Men		Women		Pooled	
	Income 1	Income 2	Income 1	Income 2	Income 1	Income 2
$V(g)/V(P)$	0.062	0.018	0.195	0.181	0.085	0.067
s.e.	0.124	0.122	0.113	0.122	0.062	0.064
p-value	0.313	0.439	0.037	0.068	0.084	0.143
N	2,866	2,814	3,045	2,895	5,609	5,432
Chrom.	0.139	0.532	0.060	0.266	0.089	0.245
p-value	0.537	0.011	0.791	0.231	0.694	0.272

Note: This table reports additional GREML estimates for income. We estimated the matrix of genetic

relatedness after omitting one twin per pair and then restricted the analyses to individuals whose

relatedness did not exceed 0.025. Income 1 is the average of the logarithm of income in the censuses of

1985 and 1990. Income 2 is defined analogously but omitting observations below a threshold of SEK

40,000. The row Chrom. shows the estimated correlation between chromosomal length (measured in

centimorgan) and the proportion of variation explained by relatedness estimated from that chromosome.

The third row gives the p-value for the test of the null hypothesis that the proportion of variation explained

by common SNPs on the autosomes is zero. The sixth row gives the p-value for the test of the hypothesis

that, across the 22 autosomes, the correlation between chromosomal length and the proportion of variation

explained by the chromosome is zero.

AIV.A. Individual SNP Analyses

Table S5: Top Hits from GWA of the Eleven Variables

Chr.	SNP	Effect allele	Gene	Function	Beta	SE	p-value	Phenotype
2	rs10204325	T			0.134	0.025	1.18×10^{-7}	Fairness
11	rs11233413	T	*RAB30*	intronic	-0.108	0.021	3.53×10^{-7}	Feminism
3	rs10937540	T			-0.091	0.018	4.28×10^{-7}	Environmentalism
3	rs6775909	T			0.090	0.018	5.51×10^{-7}	Environmentalism
18	rs41418949	T	*NETO1*	intronic	-0.358	0.072	5.86×10^{-7}	Time
3	rs9821642	G			-0.092	0.019	7.13×10^{-7}	Environmentalism
2	rs436000	T			0.125	0.025	8.03×10^{-7}	Fairness
3	rs9820695	G			0.091	0.019	8.54×10^{-7}	Environmentalism
8	rs2299587	T	*PCM1*	intronic	-0.125	0.026	9.27×10^{-7}	Trust
10	rs11203100	T	*IFIT1L*	5' upstream	0.130	0.027	1.03×10^{-6}	Income 2 women
3	rs4856162	G			0.091	0.019	1.03×10^{-6}	Environmentalism
3	rs1397924	T			-0.092	0.019	1.03×10^{-6}	Environmentalism
8	rs10112514	T	*PCM1*	intronic	-0.124	0.025	1.08×10^{-6}	Fairness
10	rs2250149	T			0.114	0.023	1.23×10^{-6}	Feminism
3	rs7628767	G			0.087	0.018	1.24×10^{-6}	Environmentalism
3	rs4493441	G			0.087	0.018	1.26×10^{-6}	Environmentalism
18	rs8083633	T	*DLGAP1*	intronic	0.154	0.032	1.39×10^{-6}	Time
14	rs4902960	G	*RGS6*	intronic	0.193	0.040	1.40×10^{-6}	Environmentalism
6	rs210648	G	*DCBLD1*	intronic	-0.122	0.025	1.59×10^{-6}	Risk
10	rs2250245	G			-0.112	0.023	1.62×10^{-6}	Feminism

6	rs240768	T	*ASCC3*	coding	0.267	0.056	1.77×10^{-6}	Immigration / crime
1	rs574773	T			0.197	0.041	1.78×10^{-6}	Trust
3	rs7612581	T			0.088	0.018	1.89×10^{-6}	Environmentalism
1	rs4384209	G	*PDE4B*	intronic	0.126	0.027	1.98×10^{-6}	Feminism
18	rs1346987	C			0.180	0.038	1.99×10^{-6}	Immigration / crime
3	rs10511217	T			-0.092	0.019	1.99×10^{-6}	Environmentalism
3	rs12485744	T			0.091	0.019	2.14×10^{-6}	Environmentalism
17	rs2291447	T	*ACBD4*	5' upstream	0.114	0.024	2.22×10^{-6}	Risk
4	rs12499086	G			-0.129	0.027	2.26×10^{-6}	Time
4	rs11730243	T			0.129	0.027	2.30×10^{-6}	Time
6	rs6931919	C	*ASCC3*	intronic	-0.263	0.056	2.34×10^{-6}	Immigration / crime
6	rs3213542	T	*ASCC3*	coding	-0.263	0.056	2.39×10^{-6}	Immigration / crime
11	rs4944425	C	*RAB30*	intronic	-0.099	0.021	2.59×10^{-6}	Feminism
11	rs7101446	T	*SLC22A9*	intronic	-0.145	0.031	2.71×10^{-6}	Economic policy
12	rs2120771	G			-0.107	0.023	2.72×10^{-6}	Feminism
22	rs4823246	G			-0.100	0.021	2.82×10^{-6}	Feminism
13	rs7984869	T			0.115	0.025	2.90×10^{-6}	Fairness
14	rs12434047	G			-0.127	0.027	2.94×10^{-6}	Fairness
11	rs17504704	G	*RAB30*	intronic	-0.102	0.022	3.30×10^{-6}	Feminism
3	rs13073838	T			-0.116	0.025	3.30×10^{-6}	Economic policy
18	rs8090196	T			-0.179	0.038	3.35×10^{-6}	Immigration / crime
17	rs2360111	T	*NXN*	intronic	-0.113	0.024	3.43×10^{-6}	Economic policy
4	rs1850744	T			0.305	0.066	3.56×10^{-6}	Risk
18	rs7235528	T			0.167	0.036	3.74×10^{-6}	Immigration / crime
6	rs11969893	G			0.324	0.070	4.06×10^{-6}	Immigration / crime
2	rs3789119	T	*ACOXL*	intronic	-0.136	0.029	4.17×10^{-6}	Immigration / crime
1	rs12125250	C			-0.124	0.027	4.18×10^{-6}	Foreign Policy
3	rs1682825	T			-0.118	0.026	4.28×10^{-6}	Feminism
18	rs12606301	G			0.171	0.037	4.54×10^{-6}	Immigration / crime
12	rs10772939	T			-0.112	0.024	4.56×10^{-6}	Economic policy
21	rs16998084	G			-0.400	0.088	4.82×10^{-6}	Immigration / crime

10	rs4586057	T	*RPP30*	intronic	0.141	0.031	5.08×10^{-6}	Time
12	rs10748180	G	*THAP2*	3' utr	-0.123	0.027	5.14×10^{-6}	Time
17	rs218676	G	*SLC13A5*	intronic	0.149	0.033	5.19×10^{-6}	Time
11	rs470763	G			0.113	0.025	5.24×10^{-6}	Fairness
5	rs1978633	T	*FBXL7*	intronic	-0.090	0.020	5.40×10^{-6}	Feminism
18	rs7231412	T			0.170	0.037	5.67×10^{-6}	Immigration / crime
13	rs7327064	T	*SOHLH2*	intronic	0.140	0.031	5.69×10^{-6}	Foreign Policy
10	rs2904804	T	*AKR1C1*	intronic	0.117	0.026	5.69×10^{-6}	Immigration / crime
3	rs10937544	C			-0.088	0.019	5.74×10^{-6}	Environmentalism
3	rs1488193	G	*CD200R1*	intronic	-0.230	0.051	5.80×10^{-6}	Economic policy
3	rs13325751	T	*CADPS*	intronic	0.132	0.029	6.17×10^{-6}	Environmentalism
14	rs1951681	G	*AKAP6*	intronic	0.194	0.043	6.17×10^{-6}	Environmentalism
6	rs9267663	T	*EHMT2*	5' upstream	-0.290	0.064	6.20×10^{-6}	Environmentalism
2	rs12713280	T			0.123	0.027	6.25×10^{-6}	Risk
5	rs17376026	T			-0.121	0.027	6.28×10^{-6}	Immigration / crime
9	rs2226006	T	*ASTN2*	intronic	-0.111	0.025	6.45×10^{-6}	Fairness
1	rs438895	G			0.384	0.085	6.67×10^{-6}	Education
14	rs10146615	T			-0.138	0.031	6.71×10^{-6}	Immigration / crime
3	rs16854884	C			0.103	0.023	6.74×10^{-6}	Feminism
10	rs1570854	T			0.079	0.018	7.03×10^{-6}	Environmentalism
7	rs1399090	T	*PLXNA4*	intronic	-0.216	0.048	7.06×10^{-6}	Foreign Policy
7	rs2598202	T	*PLXNA4*	intronic	-0.216	0.048	7.06×10^{-6}	Foreign Policy
22	rs117294	C			0.110	0.025	7.08×10^{-6}	Fairness
22	rs138597	G	*LOC388910*	3' downstream	0.123	0.027	7.30×10^{-6}	Time
14	rs3784178	T	*AKAP6*	intronic	-0.192	0.043	7.37×10^{-6}	Environmentalism
1	rs10754644	G			0.090	0.020	7.40×10^{-6}	Feminism
3	rs13068298	T			-0.102	0.023	7.71×10^{-6}	Feminism
5	rs784420	G			-0.120	0.027	7.85×10^{-6}	Trust
6	rs9364813	G			0.265	0.059	8.17×10^{-6}	Immigration / crime
3	rs10511400	T	*LRRC58*	3' utr	0.157	0.035	8.22×10^{-6}	Feminism
12	rs11178918	G			-0.184	0.041	8.32×10^{-6}	Time

2	rs12619788	G			0.112	0.025	8.33×10^{-6}	Immigration / crime
3	rs16831033	T	*LRRC58*	3' downstream	-0.157	0.035	8.88×10^{-6}	Feminism
1	rs9728717	T	*EDG7*	intronic	0.140	0.031	8.95×10^{-6}	Time
9	rs4838320	T			0.197	0.044	9.03×10^{-6}	Immigration / crime
17	rs7209847	G	*RICH2*	intronic	-0.273	0.062	9.39×10^{-6}	Risk
10	rs4282910	G	*RPP30*	5' upstream	0.148	0.033	9.45×10^{-6}	Time
6	rs228146	C	*BMP5*	intronic	0.109	0.025	9.95×10^{-6}	Time

Note: This table reports the full set of SNPs with $p<10^{-5}$ in the GWA analyses for political and economic preferences. Education and income results are not reported because these data are part of ongoing consortium meta-analyses, but none of the p-values for either trait are lower than 10^{-7}. For 5' upstream and 3' downstream, the SNP is located within 2 kb from the UTR start or end.

AIV.B. Q-Q Plots for the Political Phenotypes
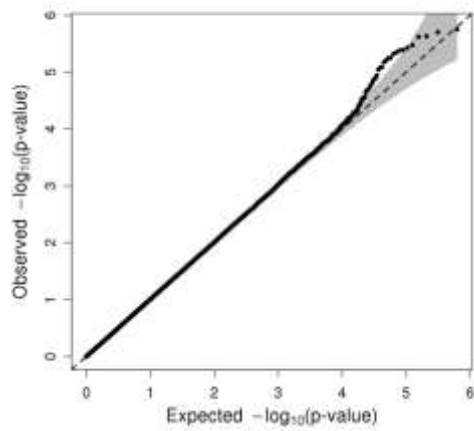
Immigration   Economic policy   Environmentalism
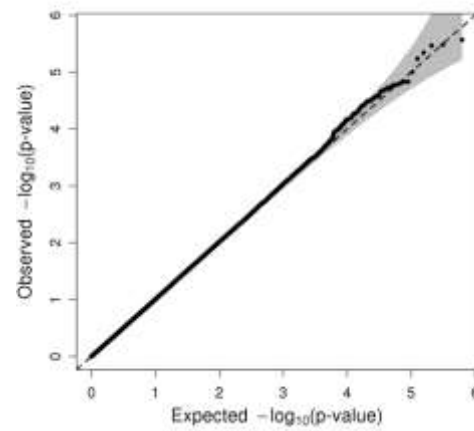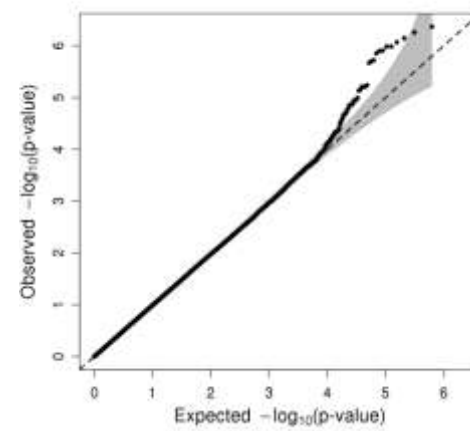
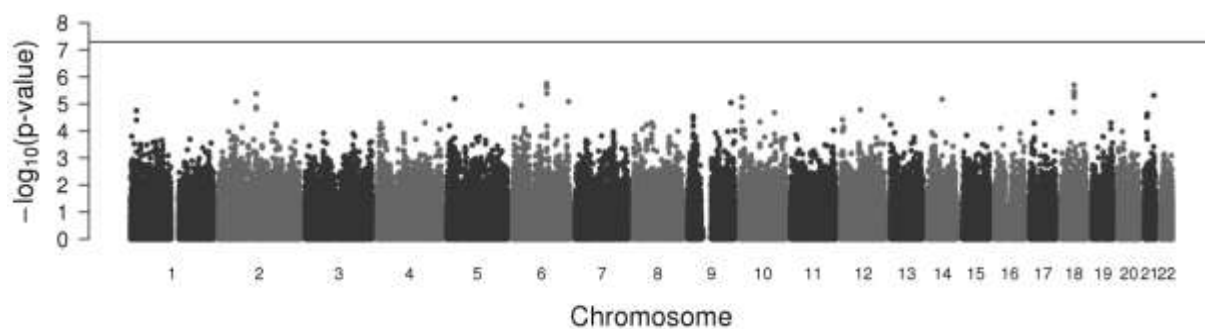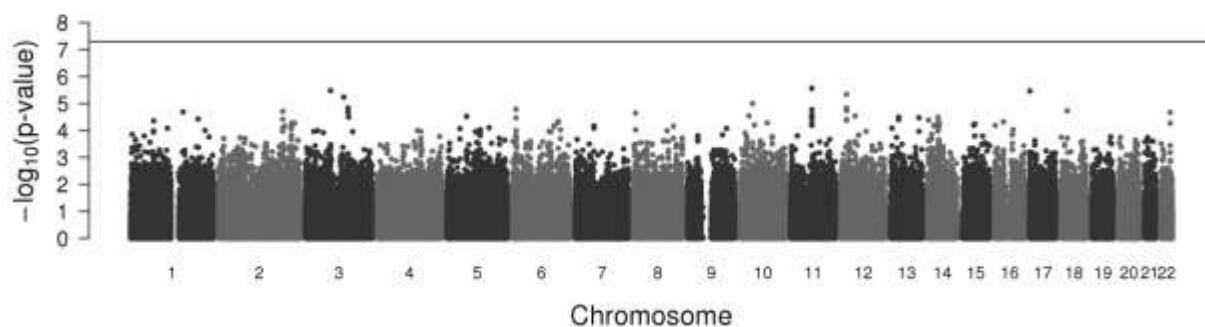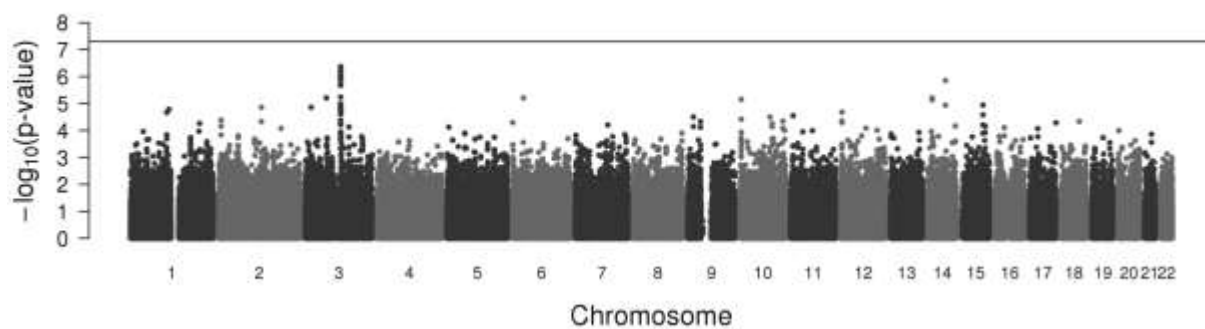Foreign policy   Feminism
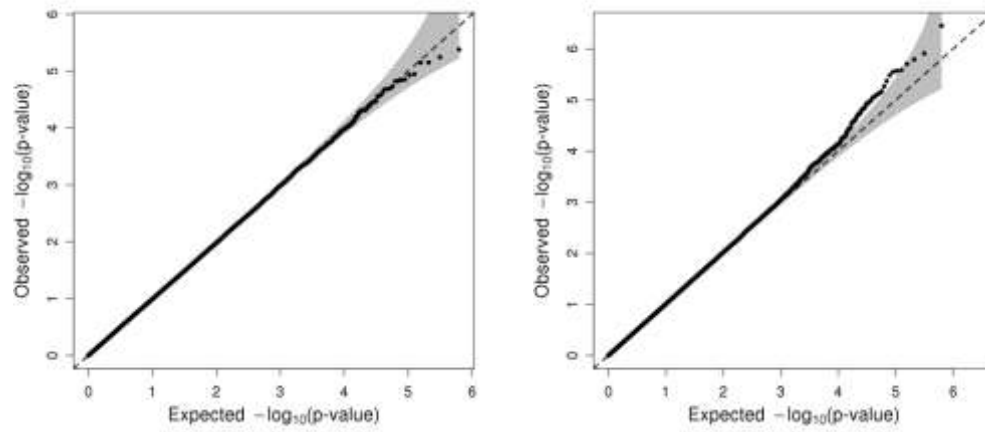
Note: These figures are quantile–quantile plots of the association analysis *p*-values from the GWA of the five political phenotypes. Genomic control was not applied.
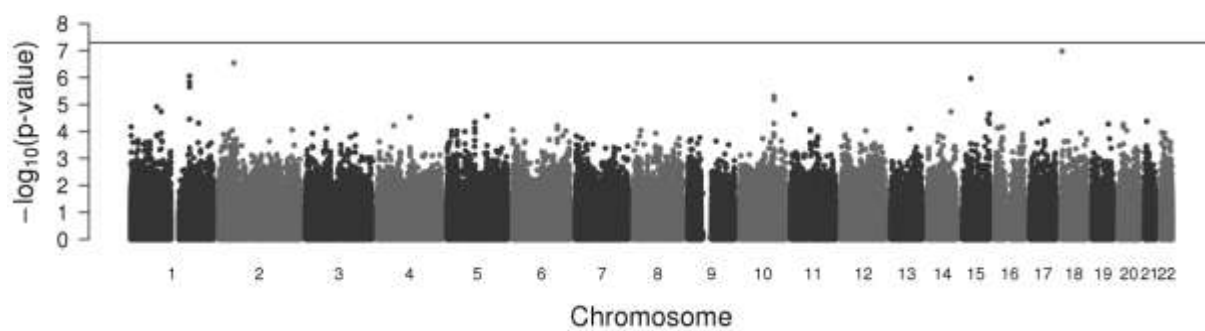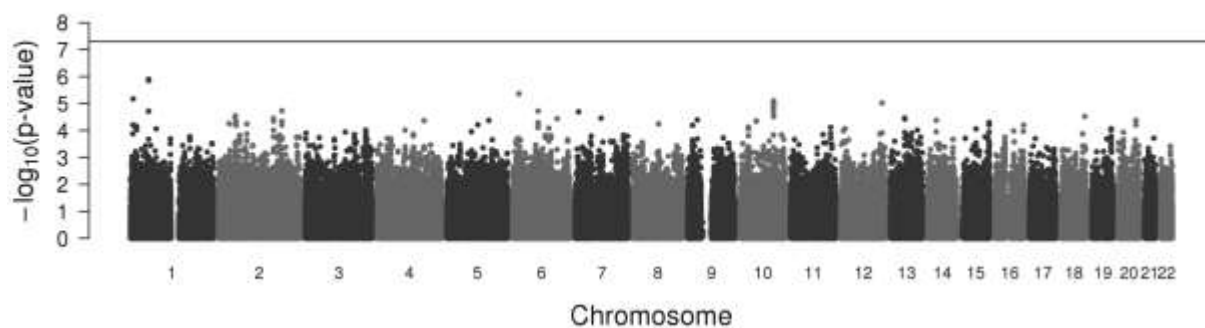
AIV.C. Q-Q Plots for the Economic Phenotypes

Income 1 men   Education   Fairness
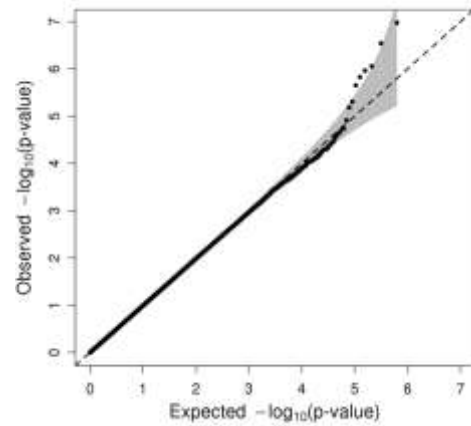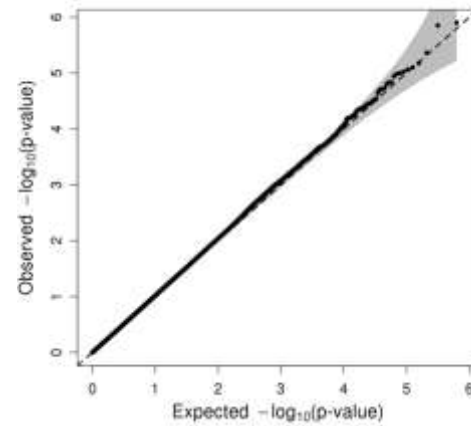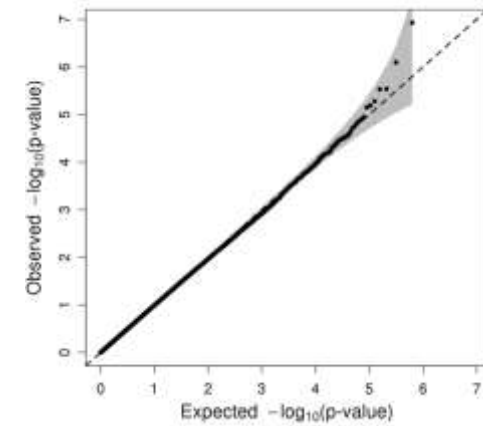
Patience   Trust   Risk

Note: These figures are quantile–quantile plots of the association analysis *p*-values from the GWA of the economic phenotypes. Genomic control was not applied.

AIV.C. Manhattan Plots for the Political Phenotypes

Immigration

Economic policy

Environmentalism

Foreign policy
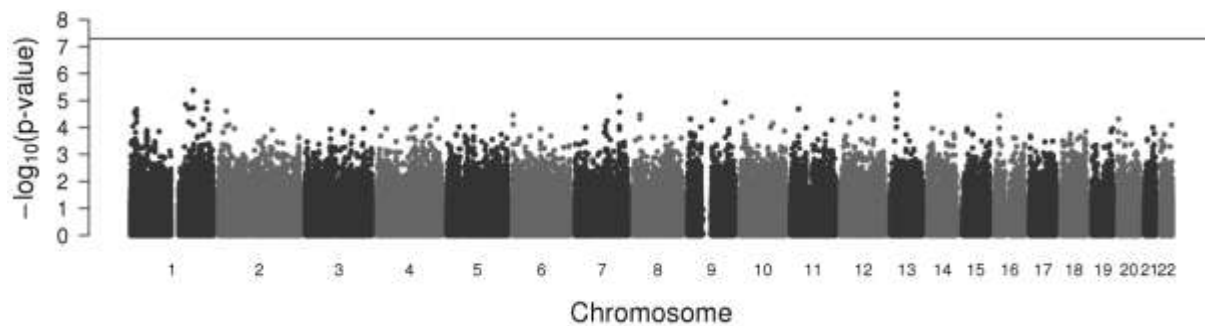
Feminism
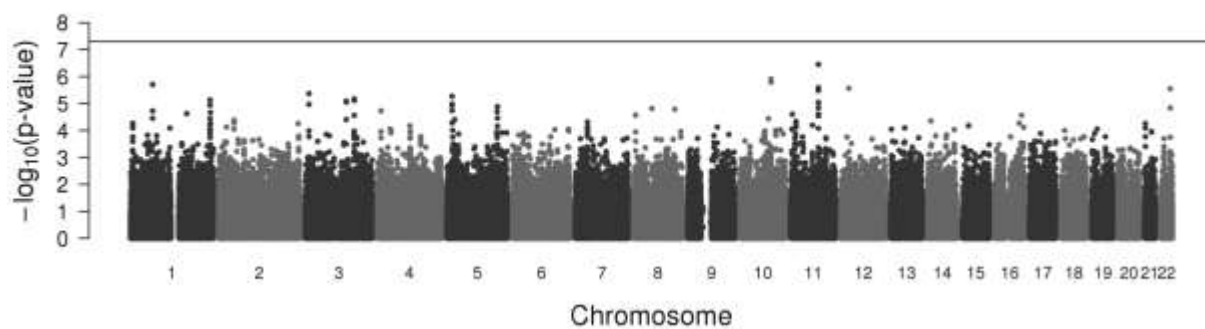
Note: Manhattan plots for the political phenotypes.

AIV.D. Manhattan Plots for the Economic Phenotypes
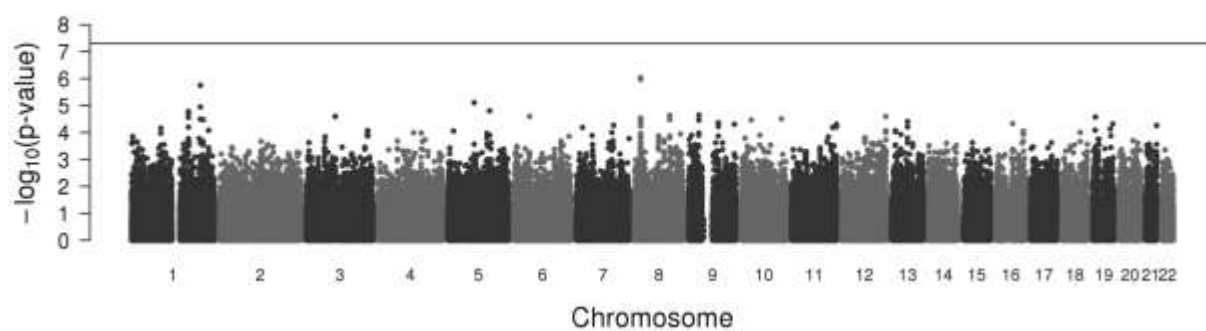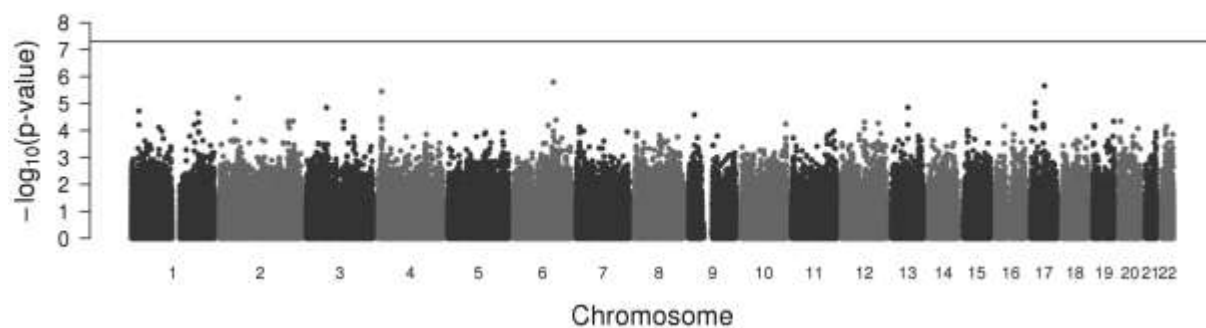
Income 1 Men

Education

Fairness
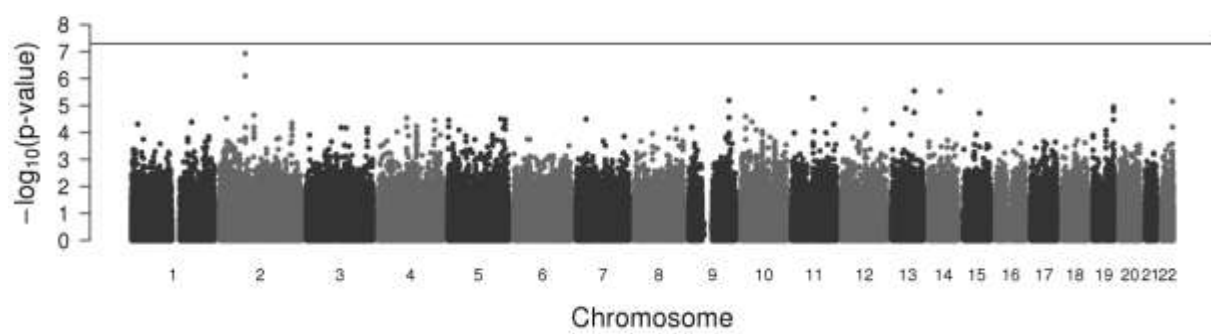
Patience
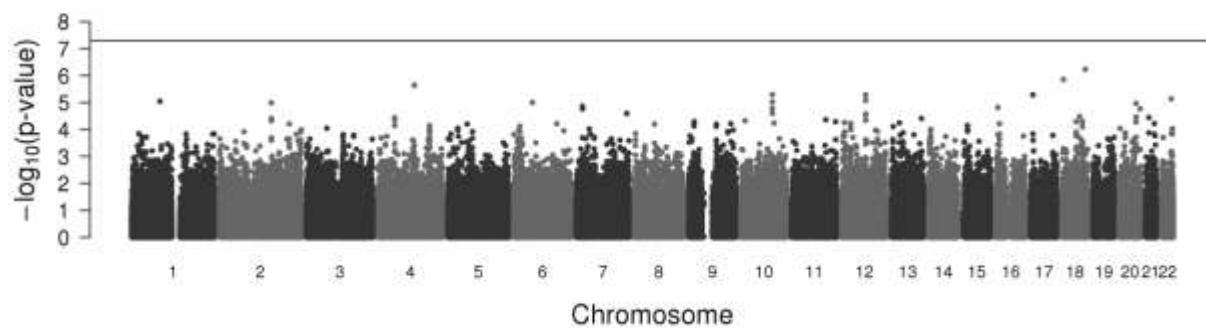
Trust

Risk

Note: Manhattan plots for the economic phenotypes.

AV. References

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