

# Ancient Origins of the Global Variation in Economic Preferences<sup>\*</sup>

Anke Becker

Benjamin Enke

Armin Falk

September 4, 2016

## Abstract

Using novel globally representative preference data, this paper shows that the structure and timing of the migratory movements of our very early ancestors have left a footprint in the contemporary cross-country distributions of risk, time, and social preferences. Across a wide range of regression specifications, differences in preferences between populations are significantly increasing in the length of time elapsed since the respective groups shared common ancestors, as proxied by genetic, linguistic, and predicted migratory distance data. The results are strongest for risk aversion and the prosocial traits altruism, positive reciprocity, and trust; similar, but weaker, findings hold for patience and negative reciprocity. These patterns point to the very long-run roots of the global variation in preferences and associated economic behaviors.

*JEL classification:* D01, D03

*Keywords:* Risk preferences, time preferences, social preferences, temporal distance, Out of Africa hypothesis

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<sup>\*</sup>An earlier version of this paper circulated as “The Ancient Origins of Cross-Country Heterogeneity in Risk Preferences”. We thank Quamrul Ashraf, Oded Galor, and Ömer Özak, for generous data sharing. Armin Falk acknowledges financial support from the European Research Council through ERC # 209214. Becker: University of Bonn, Department of Economics, anke.becker@uni-bonn.de; Enke: Harvard University, Department of Economics, enke@fas.harvard.edu; Falk: University of Bonn, Department of Economics and Behavior and Inequality Research Institute (briq), armin.falk@uni-bonn.de.

# 1 Introduction

Preferences over risk, the timing of rewards, and social interactions form the building blocks of a large class of models in both micro- and macroeconomics. Empiricists have shown that these preferences vary substantially within populations and – in line with economic models – predict a plethora of individual-level economic decisions ranging from stock and labor market behavior over savings and schooling choices to volunteering, donating, and cooperation. By introducing the Global Preference Survey (GPS), [Falk et al. \(2015a\)](#) show that there is a large variation in preferences not just between individuals, but also across entire countries. What explains this cross-country variation in preferences? Our key contribution is to show that the structure of mankind’s ancient migration out of Africa and around the globe has had a persistent impact on the between-country distribution of preferences as of today. These findings add to the emerging literature on endogenous preferences ([Bowles, 1998](#); [Fehr and Hoff, 2011](#)) in highlighting very deep population-level historical events as a key driver in shaping preferences, and hence also contribute to understanding the ultimate sources of cross-country economic heterogeneity.

According to the widely accepted “Out of Africa hypothesis”, starting around 50,000-60,000 years ago, early mankind migrated out of East Africa and continued to explore and populate our planet through a series of successive migratory steps. Each of these steps consisted of some sub-population breaking apart from the previous colony and moving on to found new settlements. This pattern implies that some contemporary population pairs have spent a longer time of human history apart from each other than others. As a result, the time elapsed since two groups shared common ancestors differs across today’s population pairs. The key idea underlying our analysis is that these differential time frames of separation might have affected the cross-country distribution of preferences over risk, time, and social interactions. First, populations that have spent a long time apart from each other were exposed to different historical experiences and environments, which could affect risk, time, and social preferences ([Voors et al., 2012](#); [Callen et al., 2014](#); [Rao, 2015](#); [Kosse et al., 2015](#); [Lowes et al., 2015](#)). Second, due to random genetic drift or selection pressures, long periods of separation lead to different population-level genetic endowments, which might in turn shape attitudes.<sup>1</sup> We use a formal model to show that both of these channels imply the prediction that – on average – populations that have been separated for a longer time in the course of human history, should also exhibit larger (absolute) differences in preferences.

To investigate this hypothesis, we use data on economic preferences across countries

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<sup>1</sup>[Cesarini et al. \(2008, 2009, 2012\)](#) use a series of twin studies to provide evidence for a genetic effect on risk, time, and social preferences.

in combination with proxies for long-run human migration patterns and the resulting temporal distances. Our data on preferences stem from the Global Preference Survey (GPS), which includes survey measures of risk, time, and social preferences (see [Falk et al., 2015a](#), for details). The sample of 80,000 people from 76 countries is constructed to provide representative population samples within each country and geographical representativeness in terms of countries covered. The survey items were selected and tested through a rigorous ex ante experimental validation procedure involving real monetary stakes. The elicitation followed a standardized protocol that was implemented through the professional infrastructure of the Gallup World Poll. These data allow the computation of nationally representative levels of risk aversion, patience, altruism, positive reciprocity, negative reciprocity, as well as trust, and hence allow the calculation of the absolute difference of a given trait within a country pair.

We combine these data with three classes of proxies for the temporal patterns of ancient population fissions, i.e., proxies for the length of time since two populations shared common ancestors. (i) First, we employ the  $F_{ST}$  and Nei genetic distances between populations ([Spolaore and Wacziarg, 2009, 2016](#)). As population geneticists have long noted, whenever two populations split apart from each other in order to found separate settlements, their genetic distance increases over time due to random genetic drift. Thus, the genetic distance between two populations is a measure of *temporal distance* since separation. (ii) Second, we use measures of *predicted* migratory distance between contemporary populations. These measures were constructed by [Ashraf and Galor \(2013b\)](#) and [Özak \(2010\)](#), respectively. The predicted migratory distance variable of [Ashraf and Galor \(2013b\)](#) exploits information on the geographic patterns of early migratory movements and constitutes a proxy for the predicted length of separation of two populations. The human-mobility-index measure of [Özak \(2010\)](#), on the other hand, explicitly computes the walking time between two countries' capitals, taking into account topographic, climatic, and terrain conditions, as well as human biological abilities. (iii) Finally, we make use of the observation that linguistic trees closely follow the structure of separation of human populations and employ a measure of linguistic distance between two populations as explanatory variable. We collapse these various measures into a summary statistic of temporal distance between populations. The origins of the vast majority of the variation in this temporal distance measure are temporally very distant, i.e., thousands of years old.

Our empirical analysis of the relationship between preferences and ancient migration patterns starts with documenting that the absolute difference in preferences between two countries is significantly increasing in the respective populations' temporal distance. These results are strongest for risk aversion as well as the prosocial traits al-

truism, positive reciprocity, and trust; similar, but weaker, findings hold for patience and negative reciprocity.

In a second step, we investigate to what extent the relationships between preferences and temporal distance are driven by contemporary environmental conditions, i.e., omitted variables. We establish that the effect of temporal distance on differences in risk and social preferences is robust to an extensive set of covariates, including controls for differences in the countries' demographic composition, their geographic position, prevailing climatic and agricultural conditions, institutions, and economic development. In all of the corresponding regressions, the point estimate is very stable, which suggests that unobserved heterogeneity is unlikely to drive our results (Altonji et al., 2005). In contrast, the relationships between patience and negative reciprocity on the one hand and temporal distance on the other hand disappear once covariates are accounted for.

We then investigate the robustness of our results by employing all genetic, migratory, and linguistic distance variables separately as explanatory variables. The results closely mirror those established with our composite temporal distance variable: essentially all explanatory variables are significantly positively related to differences in risk aversion and prosociality. In regressions with differences in patience or negative reciprocity as dependent variable, the patterns are again slightly weaker, i.e., the point estimates are always positive, but usually small and often not statistically significant. In sum, our findings on the relationship between temporal distance and preferences do not hinge on any particular proxy for temporal distance. We further provide evidence that multiple testing issues (that may arise because we analyze six different preferences and also employ multiple explanatory variables) do not drive our findings; if anything, accounting for multiple testing concerns by, e.g., collapsing all preference differences into one measure, or adjusting  $p$ -values using the false discovery rate (FDR) procedure (Anderson, 2012; Cantoni et al., forthcoming) only strengthens the results.

In a final step, we provide suggestive evidence that the relationship between preferences and temporal distance reflects the accumulation of preference changes over thousands of years subsequently to the original population breakups, rather than characteristics of the breakup process itself, such as selective migration. To this end, we leave the realm of bilateral regressions, and instead consider the *level* of a given preference. If it was true that our bilateral results were purely driven by monotonic selective migration (whose effects on preferences persist until today), then today's average preferences should evolve monotonically along humans' migratory route out of East Africa. In other words, preferences should be correlated with genetic diversity, i.e., migratory distance from Ethiopia (Ashraf and Galor, 2013b). We find that none of our preference measures exhibits a robust monotonic relationship with genetic diversity. Instead, risk

aversion, patience, and the prosocial traits are all non-linearly related to genetic diversity, although these relationships vanish with the inclusion of continent fixed effects. These results suggest that the relationship between temporal distance and preference differences is not driven by features of the breakup process that persisted until today, but rather by the accumulation of idiosyncratic shocks over thousands of years.

A number of recent contributions argue that the (cultural) diversity caused by long-run migration can have aggregate economic effects. [Spolaore and Wacziarg \(2009, 2011, 2016\)](#) find a strong relationship between genetic distance and income differences across countries and posit that lower cultural distance facilitates the diffusion of knowledge.<sup>2</sup> [Ashraf and Galor \(2013b\)](#) and [Ashraf et al. \(2014\)](#) establish a hump-shaped relationship between national income and genetic diversity and argue that the non-monotonicity reflects the trade-off between more innovation and lower cooperation that is associated with higher cultural diversity.<sup>3</sup> Our paper dovetails with these contributions as it shows that the genetic variables which proxy for migratory flows indeed capture variation in economically important traits.

This paper also forms part of an active recent literature on the historical, biological, and cultural origins of beliefs and preferences. [Chen \(2013\)](#) and [Galor and Özak \(2014\)](#) show that future-orientation is affected by a structural feature of languages and historical agricultural productivity, respectively. [Tabellini \(2008\)](#) and an earlier version of [Guiso et al. \(2009\)](#) relate interpersonal trust to linguistic features and the genetic distance between two populations. [Nunn and Wantchekon \(2011\)](#), [Voigtländer and Voth \(2012\)](#) and [Alesina et al. \(2013\)](#) establish the deep roots of trust, beliefs over the appropriate role of women in society, and anti-semitism, respectively. [Desmet et al. \(2011\)](#) and [Spolaore and Wacziarg \(2015\)](#) show that genetic and linguistic distance correlates with differences in opinions and attitudes as expressed in the World Values Survey. However, this paper is the first contribution to study the origins of cross-country variation in risk, time, and social preferences.

The remainder of this paper proceeds as follows. In Section 2, we develop our hypothesis on the relationship between the structure of migratory movements and preferences, while Section 3 presents the data. Section 4 discusses our result on the connection between preference differences and length of separation. Section 5 studies the relationship between the level of preferences and genetic diversity, and Section 6 concludes.

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<sup>2</sup>[Gorodnichenko and Roland \(2010\)](#), [Spolaore and Wacziarg \(2014\)](#), and [Giuliano and Spilimbergo \(2014\)](#) analyze the relationships between genetic distance and individualism, conflict, and trade.

<sup>3</sup>Also see [Arbatli et al. \(2013\)](#) and [Ashraf and Galor \(2013a\)](#).

## 2 Preferences and the Great Human Expansion

According to the widely accepted “Out of Africa” theory of the origins and the dispersal of early humans, the single cradle of mankind lies in East or South Africa and can be dated back to roughly 100,000 years ago (see, e.g., [Henn et al. \(2012\)](#) for an overview). Starting from East Africa, a small sample of hunters and gatherers exited the African continent around 50,000-60,000 years ago and thereby started what is now also referred to as the “great human expansion”. This expansion continued throughout Europe, Asia, Oceania, and the Americas, so that mankind eventually came to settle on all continents. A noteworthy feature of this very long-run process is that it occurred through a large number of discrete steps, each of which consisted of a sub-sample of the original population breaking apart and leaving the previous location to move on and found new settlements elsewhere. The main hypothesis underlying this paper is that the pattern of successive breakups and the resulting distribution of temporal distances across populations affected the distribution of economic preferences we observe around the globe today.

In particular, the series of migratory steps implied a frequent breakup of formerly united populations. After splitting apart, these sub-populations often settled geographically distant from each other, i.e., lived in separation. There are at least two channels through which the length of separation of two groups might have had an impact on between-group differences in preferences.<sup>4</sup>

First, if two populations have spent a long time apart from each other, they were subject to different historical experiences. Recent work highlights that economic preferences are malleable by idiosyncratic experiences or, more generally, by the composition of people’s environment (see, e.g., [Callen et al. \(2014\)](#) on risk preferences, [Rao \(2015\)](#) and [Kosse et al. \(2015\)](#) on prosocial attitudes, or [Voors et al. \(2012\)](#) on negative reciprocity). Thus, the differential historical experiences which have accumulated over thousands of years of separation might have given rise to different preferences as of today.

Second, whenever two populations spend time apart from each other, they develop different population-level genetic pools due to random genetic drift or location-specific selection pressures. Given that attitudes like risk aversion, trust, and altruism are transmitted across generations and that part of this transmission is genetic in nature ([Cesarini et al., 2009](#); [Dohmen et al., 2012](#)), the different genetic endowments induced by long periods of separation could also generate differences in preferences.

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<sup>4</sup>It is conceivable that differences in preferences are correlated with temporal distance proxies because of the structure of the population breakups *as such*, rather than the temporal distances that were caused by the population breakups. Section 5 provides a discussion of this issue.

We now formally illustrate how both of these channels (historical experiences and genetic pools) yield the prediction that longer separation implies larger absolute differences in preferences. Our corresponding model will assume that each population's preference pool gets hit by a shock in each period; an important assumption is then how these shocks are distributed across populations and time. Evidently, making intuitively appealing assumptions such as “populations that have been separated for a shorter time and hence likely live close geographically are subject to more similar shocks”, would trivially yield the prediction that temporal distance predicts preference differences. However, as we discuss in detail below, we derive our prediction in its arguably starkest form by showing that preference differences should depend on temporal difference *even* if the shocks are independently distributed across time and space, i.e., random.

Formally, suppose that there is a set of  $N$  contemporary populations. In period  $t = 0, 1, \dots, T$ , each population  $i$  has a scalar-representable preference endowment  $x_i^t$ . In period  $t = 0$ , all contemporary populations were part of one “parental” population and we normalize the preference endowment to  $x^0 = 0$ . Over time, populations successively broke apart from each other. For each time  $t = 0, 1, \dots$  let  $\mathcal{P}_t$  be a partition of  $\{1, \dots, N\}$ , that is,  $\mathcal{P}_t$  is a collection of disjoint nonempty sets whose union is  $\{1, \dots, N\}$ . The elements of  $\mathcal{P}_t$  represent the different populations at time  $t$ . For each  $t \geq 0$  and  $i \in \{1, \dots, N\}$  let  $P_t(i)$  be the unique  $A \in \mathcal{P}_t$  that contains  $i$ .

In each period, a given population's preference endowment is subject to a random shock, which could result from experiences or changes in the genetic pool, or both. That is, as long as two populations are not separated, they get hit by the same shock, but once they split up, they are subject to separate, and potentially different, shocks. For each  $t \geq 1$  and each  $A \in \mathcal{P}_t$  let  $\epsilon_A^t$  be such a random shock. Even though this is technically redundant, we will assume that the shocks have mean zero to ease interpretation. Let

$$x_i^t = \sum_{\tau=1}^t \epsilon_{P_\tau(i)}^\tau.$$

That is, a population's preference endowment in period  $t$  is given by the sum of the accumulated shocks. The object of interest in the empirical analysis is the expression

$$E \left[ \left| x_i^T - x_j^T \right| \right]$$

for  $i, j \in \{1, \dots, N\}$ . We will show that under arguably very mild assumptions this absolute difference in preferences between populations  $i$  and  $j$  is increasing in the number of periods in which the populations were separated. Fix  $T \geq 1$ . For populations  $i, j \in \{1, \dots, N\}$  let  $s_{ij} = |\{t \in \{1, \dots, T\} : P_t(i) \neq P_t(j)\}|$ . Thus,  $s_{ij}$  is the number of periods up to time  $T$  where  $i$  and  $j$  were separated.

To derive our main prediction, we will assume that the preference shocks are independently and identically distributed across time and populations. As noted above, this assumption *only* serves to derive the prediction in its starkest (and arguably non-trivial) form. As we discuss below, other assumptions would often trivially generate the prediction that longer separation induces larger preference differences.

**Proposition 1.** *Suppose the shocks  $\epsilon_{A^t}^t$ ,  $A \in \mathcal{P}_t$ ,  $t = 1, \dots, T$ , are i.i.d. nondegenerate integrable random variables. Let  $i, j, k, l \in \{1, \dots, N\}$ . Then*

$$s_{ij} > s_{kl} \quad \Leftrightarrow \quad E \left[ \left| x_i^T - x_j^T \right| \right] > E \left[ \left| x_k^T - x_l^T \right| \right].$$

The proof is in Appendix B.<sup>5</sup> The proposition says that if two populations are separated for a longer time period, their absolute difference in preferences will be larger, in expectation. Intuitively, this holds true because a longer time spent apart implies a larger number of idiosyncratic shocks, which – in expectation – generate larger *absolute* differences. To see the most basic intuition, suppose that populations  $i$  and  $j$  are still one population in  $T$ , i.e., they got hit by the same sequence of shocks, so that their absolute difference in preferences is zero. Suppose further that populations  $i$  and  $k$  were separated for one period, implying that their absolute difference in preferences is given by  $|x_i^T - x_k^T| = |\epsilon_i - \epsilon_k|$ . However, in expectation, this expression is strictly greater than zero (see the Appendix for a corresponding lemma). The proposition shows that this intuition holds for arbitrary population breakups and time spans.

**Hypothesis.** *The absolute difference in preferences between two countries increases in the length of separation of the respective populations in the course of human history.*

Note that the assumptions in Proposition 1 are sufficient, but not necessary, to generate the prediction that longer separation implies larger expected absolute differences. In particular, the proposition assumes that the shocks be independently and identically distributed across time and space. Several remarks are in order.

**Remark 1.** *It is conceivable that the preference shocks are drawn from different distributions along the migratory path, say because the further populations migrate the larger the average preference shock. However, if preferences evolved monotonically along the migratory path, then temporal distance trivially ought to be predictive of preference differences, which is why we refrain from making such strong assumptions. In addition, there is no biological principle according to which the evolution of a scalar-representable trait must*

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<sup>5</sup>We are deeply indebted to Lorens Imhof for proposing the proof to us.



follow a monotonic path. While there are reasons to believe that traits like risk aversion, time preference, or altruism are subject to local selection pressures, these selection pressures might operate in different directions along the migratory path as groups of humans and their descendants pass through many different environments.

**Remark 2.** *The assumption that preference shocks are independent of each other across space is likely to be unrealistic: for example, if population  $i$  gets hit by a natural disaster, then the probability of getting hit by the same disaster is naturally higher for those populations with low temporal distance to  $i$  because they are likely to live relatively close. However, again, making natural assumptions on the dependence of the shocks across populations would trivially imply the prediction that populations with low temporal distance have more similar preference profiles.*

**Remark 3.** *Notice that Proposition 1 makes no assumptions on the partitions  $\mathcal{P}_t$ . If one assumes that for  $t = 1, \dots, T-1$ ,  $\mathcal{P}_{t+1}$  is a refinement of  $\mathcal{P}_t$ , then the assumption that all the shocks  $\epsilon_A^t$  are identically distributed can be weakened to the assumption that for each fixed  $t$ , all the  $\epsilon_A^t$ ,  $A \in \mathcal{P}_t$ , are identically distributed, but their common distribution may vary with  $t$ .*

## 3 Data

### 3.1 Risk, Time, and Social Preferences Across Countries

The data on risk, time, and social preferences are part of the Global Preference Survey (GPS), which constitutes a unique dataset on economic preferences from representative population samples around the globe. In a wide range of countries around the world, the Gallup World Poll regularly surveys representative population samples about social and economic issues. In 76 countries, we included as part of the regular 2012 questionnaire a set of survey items which were explicitly designed to measure a respondent's preferences (see [Falk et al., 2015a](#), for a detailed description of the dataset).

Four noteworthy features characterize these data. First, the preference measures have been elicited in a comparable way using a standardized protocol across countries. Second, contrary to small- or medium-scale experimental work, we use preference measures that have been elicited from representative population samples in each country. This allows for inference on between-country differences in preferences, in contrast to existing cross-country comparisons of convenience (student) samples. The median sample size was 1,000 participants per country; in total, we collected preference measures for more than 80,000 participants worldwide. Respondents were selected through

probability sampling and interviewed face-to-face or via telephone by professional interviewers. Third, the dataset also reflects geographical representativeness. The sample of 76 countries is not restricted to Western industrialized nations, but covers all continents and various development levels. Specifically, our sample includes 15 countries from the Americas, 24 from Europe, 22 from Asia and Pacific, as well as 14 nations in Africa, 11 of which are Sub-Saharan. The set of countries contained in the data covers about 90% of both the world population and global income. Fourth, the preference measures are based on experimentally validated survey items for eliciting preferences. In order to ensure behavioral relevance, the underlying survey items were designed, tested, and selected through an explicit ex-ante experimental validation procedure (Falk et al., 2015b). In this validation step, out of a large set of preference-related survey questions, those items were selected which jointly performed best in explaining observed behavior in standard financially incentivized experimental tasks to elicit preference parameters. In order to make these items cross-culturally applicable, (i) all items were translated back and forth by professionals, (ii) monetary values used in the survey were adjusted along the median household income for each country, and (iii) pretests were conducted in 21 countries of various cultural heritage to ensure comparability. The preference measures are derived as follows (see Appendix A and Falk et al. (2015a) for details):<sup>6</sup>

**Risk Taking.** The set of survey items includes two measures of the underlying risk preference – one qualitative subjective self-assessment and one quantitative measure. The subjective self-assessment directly asks for an individual’s willingness to take risks: *“Generally speaking, are you a person who is willing to take risks, or are you not willing to do so? Please indicate your answer on a scale from 0 to 10, where a 0 means “not willing to take risks at all” and a 10 means “very willing to take risks”. You can also use the values in between to indicate where you fall on the scale.”*

The quantitative measure is derived from a series of five interdependent hypothetical binary lottery choices, a format commonly referred to as the “staircase procedure”. In each of the five questions, participants had to decide between a 50-50 lottery to win € $x$  or nothing (which was the same in each question) and varying safe payments  $y$ . The questions were interdependent in the sense that the choice of a lottery resulted in an increase of the safe amount being offered in the next question, and conversely. For instance, in Germany, the fixed upside of the lottery  $x$  was €300, and in the first question, the fixed payment was €160. In case the respondent chose the lottery (the safe payment), the safe payment increased (decreased) to €240 (80) in the second question. In essence, by adjusting the fixed payment according to previous choices, the questions

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<sup>6</sup>The description of the survey items closely follows the one in Falk et al. (2015a).

“zoom in” around the respondent’s certainty equivalent and make efficient use of limited and costly survey time. This procedure yields one of 32 ordered outcomes. The subjective self-assessment and the outcome of the quantitative lottery staircase were then aggregated into a single index which describes an individual’s degree of risk taking.

**Patience.** The measure of patience is also derived from the combination of responses to two survey measures, one with a quantitative and one with a qualitative format. The quantitative survey measure consists of a series of five hypothetical binary choices between immediate and delayed financial rewards. In each of the five questions, participants had to decide between receiving a payment today or larger payments in 12 months. Conceptually similar to the elicitation of risk preferences, the questions were interdependent in the sense that the delayed payment was increased or decreased depending on previous choices. The qualitative measure of patience is given by the respondent’s self-assessment regarding their willingness to wait on an 11-point Likert scale, asking “how willing are you to give up something that is beneficial for you today in order to benefit more from that in the future?”.

**Prosociality: Altruism, Positive Reciprocity, and Trust.** The GPS includes six survey items which map into three prosocial traits: altruism, positive reciprocity, and trust. While these behavioral traits are conceptually distinct, they share in common that they are commonly associated with “positive” social interactions.

Altruism was measured through a combination of one qualitative and one quantitative item, both of which are related to donation. The qualitative question asked people how willing they would be to give to good causes without expecting anything in return on an 11-point scale. The quantitative scenario depicted a situation in which the respondent unexpectedly received € 1,000 and asked them to state how much of this amount they would donate.

People’s propensity to act in a positively reciprocal way was also measured using one qualitative item and one question with a quantitative component. First, respondents were asked to provide a self-assessment about how willing they are to return a favor on an 11-point Likert scale. Second, participants were presented a choice scenario in which they were asked to imagine that they got lost in an unfamiliar area and that a stranger – when asked for directions – offered to take them to their destination. Participants were then asked which out of six presents (worth between € 5 and € 30 in € 5 intervals) they would give to the stranger as a “thank you”.

Finally, to measure trust, people were asked whether they assume that other people only have the best intentions (Likert scale, 0-10).

**Negative Reciprocity.** Negative reciprocity was elicited through three self-assessments. First, people were asked how willing they are to take revenge if they are treated very unjustly, even if doing so comes at a cost (0-10). The second and third item probed respondents about their willingness to punish someone for unfair behavior, either towards *themselves* or towards a *third person*.

**Discussion.** As discussed in Falk et al. (2015a), the preference measures are constructed by linearly combining responses to the survey items using weights that are derived from the experimental validation procedure (Falk et al., 2015b). All preference measures are then standardized to have mean zero and standard deviation of one. Falk et al. (2015a) show that all preferences exhibit a large amount of variation across countries. For example, calculating t-tests of all possible pairwise country comparisons reveals that about 80% of all country differences are statistically significant at the 1% level, for each preference. We investigate the origins of this heterogeneity through a bilateral regression approach in which absolute differences in preferences serve as dependent variable. Thus, we compute the absolute difference in a given trait and standardize these variables again. Furthermore, for each country pair, we calculate an overall summary statistic of preference differences by summing up these absolute differences across preference dimensions. This summary statistic can be understood as a measure of overall (multidimensional) preference dissimilarity, and hence as a proxy for cultural differences in contexts involving economic preference parameters.

### 3.2 Proxies for Ancient Migration Patterns

We use three separate but conceptually linked classes of variables to proxy for the length of time since two populations split apart: (i) Genetic distance, (ii) predicted migratory distance, and (iii) linguistic distance.

**Genetic Distance.** First, whenever populations break apart, they stop interbreeding, thereby preventing a mixture of the respective genetic pools. However, since every genetic pool is subject to random drift (“noise”) or local selection pressures, geographical separation implies that over time the genetic distance between sub-populations gradually becomes (on average) larger. Thus, the genealogical relatedness between two populations reflects the length of time elapsed since these populations shared common ancestors. In fact, akin to a molecular clock, population geneticists have made use of this observation by constructing mathematical models to compute the timing of separation between groups. This makes clear that, at its very core, genetic distance constitutes not only a measure of genealogical relatedness, but also of *temporal distance*.

Technically, genetic distance constitutes an index of expected heterozygosity, which can be thought of as the probability that two randomly matched individuals will be genetically different from each other in terms of a pre-defined spectrum of genes. Indices of heterozygosity are derived using data on allelic frequencies, where an allele is a particular variant taken by a gene. Intuitively, the relative frequency of alleles at a given locus can be compared across populations and the deviation in frequencies can then be averaged over loci. This is the approach pursued in the work of the population geneticists [Cavalli-Sforza et al. \(1994\)](#). The main dataset assembled by these researchers consists of data on 128 different alleles for 42 world populations. By aggregating differences in these allelic frequencies, the authors compute the  $F_{ST}$  genetic distance, which provides a comprehensive measure of genetic relatedness between any pair of 42 world populations. Using the same dataset, [Cavalli-Sforza et al. \(1994\)](#) also compute the so-called Nei distance for all population pairs, which has slightly different theoretical properties than  $F_{ST}$ . Since genetic distances are available only at the population rather than at the country level, [Spolaore and Wacziarg \(2009\)](#) matched the 42 populations in [Cavalli-Sforza et al. \(1994\)](#) to countries.<sup>7</sup> Thus, the genetic distance measures we use measure the expected genetic distance between two randomly drawn individuals, one from each country, according to the contemporary composition of the population. The key advantage of the genetic distance data relative to predicted measures of length of separation (see below) is that the measurement and imputation apply to *contemporary* populations. Thus, for example, the effects of smaller-scale migratory movements after the human exodus from Africa on the temporal distance between populations are by construction incorporated in these measures.

Recently, [Spolaore and Wacziarg \(2016\)](#) introduced a new dataset of cross-country  $F_{ST}$  genetic distances that is based on the work by [Pemberton et al. \(2013\)](#). While the data from [Cavalli-Sforza et al. \(1994\)](#) are based on classic genetic markers, this new dataset is based on microsatellite variation, covering 645 microsatellite loci and 267 populations, thus providing a more comprehensive and detailed coverage of world populations. [Spolaore and Wacziarg \(2016\)](#) again matched these population-level  $F_{ST}$  distances to countries using ethnic composition data from [Fearon \(2003\)](#). In sum, this more recent genetic distance measure has the same conceptual basis, but is based on different biological information and samples.

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<sup>7</sup>To this end, the authors used ethnic composition data from [Fearon \(2003\)](#): the data by [Cavalli-Sforza et al. \(1994\)](#) contain information on the groups that were sampled to obtain genetic distance estimates, and these groups can be matched one-to-one to the ethnic groups that populate countries. Thus, the data from one group in [Cavalli-Sforza et al. \(1994\)](#) can be assigned to sub-populations in potentially multiple countries, so that, in principle, even the relatively small number of 42 populations is sufficient to compute genetic distances between more than 100 countries.

**Predicted Migratory Distance.** Rather than physically *measure* the genetic composition of populations to investigate their kinship, one can also derive *predicted* migration measures (Ashraf and Galor, 2013b; Özak, 2010). Key idea behind using these variables is that populations that have lived far apart from each other (in terms of migratory, not necessarily geographic, distance), have usually spent a large portion of human history apart from each other. Notably, these data are independent of those on observed genetic distance and thus allow for an important out-of-sample robustness check.

First, the derivation of the predicted migratory distance variable of Ashraf and Galor (2013b) follows the methodology proposed in Ramachandran et al. (2005) by making use of today’s knowledge of the migration patterns of our ancestors. Specifically, Ashraf and Galor (2013b) obtain an estimate of bilateral migratory distance by computing the shortest path between two countries’ capitals. Given that until recently humans are not believed to have crossed large bodies of water, these hypothetical population movements are restricted to landmass as much as possible by requiring migrations to occur along five obligatory waypoints, one for each continent. By construction, these migratory distance estimates only pertain to the *native* populations of a given pair of countries. Thus, in contrast to the genetic distance measures, these distance estimates need to be adjusted to the extent that the contemporary populations in a country pair differ from the native ones. While this objective is difficult to achieve for geographically scattered waves of temporally very distant events, adjustment for post-Columbian migration flows can be implemented using the “World Migration Matrix” of Putterman and Weil (2010), which describes the share of the year 2000 population in every country that has descended from people in different source countries as of the year 1500. To derive values of predicted migratory distance pertaining to the *contemporary* populations, we combine the dataset of Ashraf and Galor (2013b) with this migration matrix. Thus, the contemporary predicted migratory distance between two countries equals the weighted migratory distance between the contemporary populations.<sup>8</sup> This ancestry-adjusted predicted migratory distance between two countries can be thought of as the expected migratory distance between the ancestors of two randomly drawn individuals, one from each country. Further note that migratory distance and observed genetic distance tend to be highly correlated (Ramachandran et al., 2005). Ashraf and Galor (2013b) exploit this fact by linearly transforming migratory distance into a measure

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<sup>8</sup>Formally, suppose there are  $N$  countries, each of which has one native population. Let  $s_{1,i}$  be the share of the population in country 1 which is native to country  $i$  and denote by  $d_{i,j}$  the migratory distance between the native populations of countries  $i$  and  $j$ . Then, the (weighted) predicted ancestry-adjusted migratory distance between countries 1 and 2 as of today is given by

$$\text{Predicted migratory distance}_{1,2} = \sum_{i=1}^N \sum_{j=1}^N (s_{1,i} \times s_{2,j} \times d_{i,j})$$

of predicted  $F_{ST}$  genetic distance. Our measure of predicted migratory distance might hence as well be interpreted as predicted genetic distance.

Second, as an additional independent measure of migratory distance, we use the so-called “human mobility index”-based (HMI) migratory distance developed by [Özak \(2010\)](#). This measure is more sophisticated than the raw migratory distance using the five intermediate waypoints in that it measures the walking time along the optimal route between any two locations, taking into account the effects of temperature, relative humidity, and ruggedness, as well as human biological capabilities. Given that the procedure assumes travel by foot (as is appropriate if interest lies in migratory movements thousands of years ago), the data do not include islands, but assume that the Old World and the New World are connected through the Bering Strait, over which humans are believed to have entered the Americas. The original data contain the travel time between two countries’ capitals, which we again adjust for post-Columbian migration flows using the ancestry-adjustment methodology outlined above. Thus, this variable measures the expected travel time between the ancestors of two randomly drawn individuals, one from each country.

**Linguistic Distance.** Population geneticists and linguists have long noted the close correspondence between genetic distance and linguistic “trees”, intuitively because population break-ups do not only produce diverging gene pools, but also differential languages. Hence, we employ the degree to which two countries’ languages differ from each other as an additional proxy for the timing of separation. The construction of linguistic distances follows the methodology proposed by [Fearon \(2003\)](#). The Ethnologue project classifies all languages of the world into language families, sub-families, sub-sub-families etc., which gives rise to a language tree. In such a tree, the degree of relatedness between different languages can be quantified as the number of common nodes two languages share.<sup>9</sup> As in the case of predicted migratory distances, for each country pair, we calculate the weighted linguistic distance according to the population shares speaking a particular language in the respective countries today.

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<sup>9</sup>If two languages belong to different language families, the number of common nodes is 0. In contrast, if two languages are identical, the number of common nodes is 15. Following [Fearon \(2003\)](#), who argues that the marginal increase in the degree of linguistic relatedness is decreasing in the number of common nodes, we transformed these data according to

$$\text{Linguistic distance} = 1 - \sqrt{\frac{\# \text{ Common nodes}}{15}}$$

to produce distance estimates between languages in the interval  $[0, 1]$ . We restricted the Ethnologue data to languages which make up at least 5% of the population in a given country.

**Construction of Composite Measure of Temporal Distance.** In sum, we have access to six separate proxies for temporal distance.<sup>10</sup> Given that these measures follow different methods of construction and are likely to be plagued by measurement error, we exploit the complementarity of the different data sources by constructing a composite index of temporal distance. This index is computed as unweighted average of the standardized values (z-scores) of the two  $F_{ST}$  genetic distance measures (based on Cavalli-Sforza et al. (1994) and Pemberton et al. (2013), respectively), Nei genetic distance, predicted migratory distance, and linguistic distance. We do not include the HMI migratory distance variable in the composite measure because it results in a loss of almost 600 observations.

Our procedure of constructing the composite measure implies that genetic data receive a higher weight in the construction of the composite index than linguistic and predicted migratory distance data. This appears appropriate in that there are strong ex ante reasons to believe that genetic distance is a higher-quality proxy for temporal distance than linguistic or predicted migratory data. For example, notice that the migratory distance measures are by construction coarse in nature. In addition, migratory distance can only be adjusted for the post-1500 mass migratory movements that are captured in the “World Migration Matrix”, but not for the smaller and more diverse migration waves that have taken place throughout modern history. Likewise, it is well-known that genetic distance appears to be a higher-quality measure of separation patterns than linguistic distance (Cavalli-Sforza, 1997). First, while languages generally maintain a certain structure over long periods of time, in some cases they change or evolve very quickly, for example when the colonial powers brought Indo-European languages into Africa, or when Arabic was brought to Egypt during the Muslim conquest. In addition, any quantitative measure of linguistic distance suffers from the fact that language trees are rather coarse in nature.

In sum, predicted migratory and linguistic distance are more likely to be plagued by measurement error, hence justifying a higher weight on genetic data. Nevertheless, to demonstrate robustness, Appendix D.2 reports analyses in which the composite measure is constructed as unweighted average of  $F_{ST}$  genetic distance, predicted migratory distance, and linguistic distance, so that all data types receive equal weight. In what follows, we present the main results using the composite temporal distance variable. We then report robustness checks in which we employ each temporal distance proxy (including HMI migratory distance) separately. Our sample covers 72 countries.<sup>11</sup>

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<sup>10</sup>Appendix C reports raw correlations among these proxies.

<sup>11</sup>The GPS dataset includes 76 countries. However, one or more of the temporal distance proxies are missing for Bosnia and Herzegovina, Serbia, Suriname, and Tanzania.



## 4 Preferences and Temporal Distance

### 4.1 Baseline Results

This section develops our main result on the relationship between differences in preferences between countries and the temporal distance between the respective populations. Since temporal distance is an inherently bilateral variable, this analysis will necessitate the use of a *dyadic* regression framework, which takes each possible pair of countries as unit of observation. Accordingly, we match each of the 72 countries with every other country into a total of 2,556 country pairs and, for each trait, compute the absolute difference in (average) preferences between the two countries.<sup>12</sup> We then relate our temporal distance measure to this absolute difference in preferences between the respective populations. Our regression equation is hence given by:

$$|\text{pref}_i - \text{pref}_j| = \alpha + \beta \times \text{temporal distance}_{i,j} + \gamma_i \times d_i + \gamma_j \times d_j + \epsilon_{i,j}$$

where  $\text{pref}_i$  and  $\text{pref}_j$  represent some average preference in countries  $i$  and  $j$ , respectively,  $d_i$  and  $d_j$  country fixed effects, and  $\epsilon_{i,j}$  a country pair specific disturbance term.

As is standard practice in dyadic analyses such as in gravity regressions of bilateral trade, every specification to be presented below will include country fixed effects  $d_i$  and  $d_j$ , i.e., a fixed effect for each of the two countries that appears in a country pair observation to take out any unobservables that are country-specific.<sup>13</sup> To illustrate, with country fixed effects, the regressions do not relate, say, the raw difference in preferences between Sweden and Mexico to the respective raw temporal distance. Rather, the regression relates the difference in preferences between Sweden and Mexico *relative* to Sweden's and Mexico's average differences in preferences in all country pairs to their temporal distance, again relative to all other temporal distances involving these two countries. For instance, if Mexico had very large differences in preferences to all countries, then the fixed effects would ensure that these uniform large differences are treated as a Mexico-specific effect, rather than attribute them to the bilateral relationships between Mexico and other countries. Thus, country-specific factors are netted out of the analysis and the regression equation estimates the bilateral effect of interest.<sup>14</sup>

Furthermore, regarding the noise term, because our empirical approach implies that

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<sup>12</sup>Since the analysis is not directional, each country pair is only used once, i.e., when country  $i$  is matched with country  $j$ ,  $j$  cannot be matched with  $i$ , so that the bilateral dataset contains no redundant information.

<sup>13</sup>See also the working paper version of [Spolaore and Wacziarg \(2009\)](#).

<sup>14</sup>The empirical results suggest that such country fixed effects indeed go a long way in addressing omitted variable concerns. For instance, in the analyses to be presented below, for patience and negative reciprocity we sometimes observe statistically significant *negative* coefficients on temporal distance if country fixed effects are not included, which we find very hard to interpret. These results entirely disappear with country fixed effects.

each country will appear multiple times as part of the (in)dependent variable, we need to allow for clustering of the error terms at the country-level. We hence employ the two-way clustering strategy of [Cameron et al. \(2011\)](#), i.e., we cluster at the level of the first and of the second country of a given pair. This procedure allows for arbitrary correlations of the error terms within a group, i.e., within the group of country pairs which share the same first country or which share the same second country, respectively, see Appendix II of [Spolaore and Wacziarg \(2009\)](#).

Table 1 provides the results of OLS regressions of absolute differences in preferences on temporal distance as well as  $F_{ST}$  genetic distance as theoretically most appealing proxy for temporal distance. Throughout the paper, all regression coefficients (except for those of binary variables) are expressed in terms of standardized betas, i.e., both the dependent and the independent variables are normalized into z-scores and the dependent variable is then multiplied with 100, so that the coefficient can be interpreted as the percent change of a standard deviation in the dependent variable in response to a one standard deviation increase in the independent variable.

Columns (1) and (2) show that the summary statistic of preference differences (which consists of the sum of the absolute differences across preference dimensions) is strongly and significantly related to temporal distance. The associated t-statistic equals 5.7 and the point estimate suggests that a one standard deviation increase in temporal distance is associated with an increase of roughly 25 percent of a standard deviation in differences in preferences.

Columns (3) and (4) provide evidence that temporal distance is a significant predictor of differences in average risk attitudes. In columns (5) through (10), we show that very similar results obtain for all of the prosocial traits, i.e., altruism, positive reciprocity, and trust. Given that these three traits are also positively correlated at the country-level, we keep the subsequent analysis concise by collapsing the three measures into a simple unweighted average that we refer to as “prosociality” and report robustness checks using each prosocial trait separately in the Appendix.<sup>15</sup>

Finally, columns (11)-(12) and (13)-(14) present analogous analyses using differences in patience and negative reciprocity as dependent variables. Across specifications, the point estimates are positive, but rather small in magnitude. These coefficients are statistically significant when we use the composite temporal distance measure, but not with  $F_{ST}$  genetic distance. As we discuss below, this pattern shows that differences in patience and negative reciprocity are better predicted by the non-genetic temporal distance proxies, perhaps suggesting that the different proxy variables capture slightly dif-

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<sup>15</sup>The country-level correlations between the three measures range between 0.27 and 0.71, see [Falk et al. \(2015a\)](#). To derive the prosociality index, we computed a simple unweighted average of altruism, positive reciprocity, and trust at the individual level and collapsed this measure at the country-level.

Table 1: Preferences and temporal distance

	<i>Dependent variable: Absolute difference in...</i>																					
	All preferences	Risk taking	Altruism	Pos. reciprocity	Trust	Patience	Neg. reciprocity	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)	(13)	(14)	
Temporal distance	0.23*** (0.04)	0.15** (0.07)	0.027* (0.01)	0.11** (0.05)	0.20*** (0.05)	0.089* (0.05)	0.035** (0.02)															
Fst genetic distance (Cavalli-Sforza)	0.23*** (0.04)	0.16** (0.08)	0.039** (0.02)	0.13*** (0.05)	0.22*** (0.06)	0.038 (0.03)	0.018 (0.02)															
Observations	2556	2556	2556	2556	2556	2556	2556	2556	2556	2556	2556	2556	2556	2556	2556	2556	2556	2556	2556	2556	2556	2556
R <sup>2</sup>	0.470	0.469	0.630	0.631	0.555	0.555	0.509	0.511	0.438	0.442	0.504	0.501	0.467	0.467	0.467	0.467	0.467	0.467	0.467	0.467	0.467	0.467

Notes. OLS estimates, twoway-clustered standard errors in parentheses. All regressions are conditional on country fixed effects. The temporal distance variable is the composite measure constructed from the two  $F_{ST}$  genetic distance measures, Nei genetic distance, predicted migratory distance, and linguistic distance. \*  $p < 0.10$ , \*\*  $p < 0.05$ , \*\*\*  $p < 0.01$ .

ferent cultural or biological processes. In sum, differences in all preferences are increasing in the length of separation of the respective populations, albeit to heterogeneous degrees.

## 4.2 Conditional Regressions

The argument made in this paper is that the relationship between temporal distance on the one hand and preferences on the other hand reflects the impact of ancient migration patterns and the resulting distribution of temporal distances across populations, rather than contemporary differences in idiosyncratic country characteristics.

We hence proceed by investigating the robustness of the relationship between temporal distance and preferences through conditional regressions. Since our dependent variables consist of absolute differences, all of our control variables will also be bilateral variables that reflect cross-country differences. In essence, in what follows, our augmented regression specification will be:

$$|pref_i - pref_j| = \alpha + \beta \times \text{temporal distance}_{i,j} + \gamma_i \times d_i + \gamma_j \times d_j + \eta \times g_{i,j} + \epsilon_{i,j}$$

where  $g_{ij}$  is a vector of bilateral measures between countries  $i$  and  $j$  (such as their geodesic distance or the absolute difference in per capita income). Details on the definitions and sources of all control variables can be found in Appendix F.

We start our analysis by considering the summary statistic of preference differences. To check that our coefficient of interest does not spuriously pick up the effect of demographic differences or differential population characteristics, column (2) of Table 2 adds to the baseline specification the absolute differences in proportion of females, religious fractionalization, and the fraction of the population who are of European descent. This joint set of covariates reduces the point estimate of temporal distance by only about 5%, and the coefficient remains statistically significant.

A potential concern with our baseline specification is that it ignores differences in development and institutions across countries, in particular given that temporal distance has been shown to correlate with differences in national income ([Spolaore and Wacziarg, 2009](#)). Column (3) of Table 2 therefore introduces absolute differences in (log) GDP per capita, democracy, and a common legal origin dummy. The inclusion of this vector of controls reduces the temporal distance coefficient by 15%, but it remains well in the magnitude of the previous estimations and is statistically highly significant.

Human migration patterns (and hence temporal distance proxies) are correlated with geographic and climatic variables. To ensure that effects stemming from variations in geography or climate are not attributed to temporal distance, we now condition on an exhaustive set of corresponding control variables. Column (4) introduces four dis-

Table 2: Preferences and temporal distance: Robustness

	<i>Dependent variable:</i> Absolute difference in all preferences				
	(1)	(2)	(3)	(4)	(5)
Temporal distance	0.23*** (0.04)	0.22*** (0.04)	0.19*** (0.04)	0.18*** (0.05)	0.18*** (0.05)
$\Delta$ Proportion female		0.053 (0.03)	0.072* (0.04)	0.070* (0.04)	0.065 (0.04)
$\Delta$ Religious fractionalization		0.011 (0.02)	0.011 (0.02)	0.0093 (0.02)	0.0093 (0.02)
$\Delta$ % Of European descent		0.011 (0.02)	-0.048* (0.03)	-0.056** (0.03)	-0.054* (0.03)
$\Delta$ Democracy index			0.015 (0.04)	0.017 (0.04)	0.014 (0.04)
$\Delta$ Log [GDP p/c PPP]			0.16*** (0.05)	0.16*** (0.05)	0.16*** (0.05)
Log [Geodesic distance]				0.064 (0.04)	0.061 (0.05)
1 for contiguity				0.031 (0.11)	0.040 (0.11)
$\Delta$ Distance to equator				0.0050 (0.04)	0.010 (0.04)
$\Delta$ Longitude				-0.085* (0.05)	-0.080* (0.05)
$\Delta$ Land suitability for agriculture					0.034 (0.02)
$\Delta$ Mean elevation					-0.0038 (0.04)
$\Delta$ SD Elevation					-0.0041 (0.03)
$\Delta$ Ave precipitation					-0.0038 (0.04)
$\Delta$ Ave temperature					-0.0060 (0.04)
$\Delta$ Log [Area]					0.0076 (0.04)
Colonial relationship dummies	No	No	Yes	Yes	Yes
Observations	2556	2556	2485	2485	2485
$R^2$	0.470	0.472	0.489	0.491	0.491

*Notes.* OLS estimates, twoway-clustered standard errors in parentheses. All regressions are conditional on country fixed effects. The temporal distance variable is the composite measure constructed from the two  $F_{ST}$  genetic distance measures, Nei genetic distance, predicted migratory distance, and linguistic distance. \*  $p < 0.10$ , \*\*  $p < 0.05$ , \*\*\*  $p < 0.01$ .

tance metrics as additional controls into this regression. Our first geographical control variable consists of the geodesic distance (measuring the shortest distance between any two points on earth) between the most populated cities of the countries in a given pair. Relatedly, we introduce a dummy equal to one if two countries are contiguous. Finally, we also condition on the “distance” between two countries along the two major geographical axes, i.e., the difference in the distance to the equator and the longitudinal (east-west) distance. Again, the introduction of these variables has virtually no effect on the coefficient of temporal distance.

Given that geographic distance as such does not seem to drive our result, we now control for more specific information about differences in the micro-geographic and climatic conditions between the countries in a pair. To this end, we make use of information on the agricultural productivity of land, different features of the terrain, and climatic factors. As column (4) shows, the inclusion of corresponding controls has no effect on the temporal distance point estimate. In sum, columns (4) and (5) suggest that the precise migration patterns of our ancestors, rather than simple shortest-distance calculations between contemporary populations, need to be taken into account to understand the cross-country variation in risk aversion.

Tables 3 and 4 repeat the conditional regressions from Table 2 for risk aversion, prosociality, patience, and negative reciprocity, respectively. Each column follows the same logic as the corresponding column in Table 2. As Table 3 shows, the relationship between risk preferences and prosociality on the one hand and temporal distance on the other hand is robust to this large and comprehensive vector of covariates.<sup>16</sup> At the same time, as illustrated in Table 4, the effects on patience and negative reciprocity vanish once covariates are accounted for. Thus, consistent with the fact that the point estimates for these dependent variables were rather small to begin with, it appears as if temporal distance has a larger effect on risk preferences and prosocial traits than on patience and negative reciprocity.

In sum, conditioning on a large set of variables, the relationships between temporal distance and differences in risk preferences and prosociality are highly significant. Furthermore, in both cases, the corresponding point estimate is very robust, suggesting that – in order for omitted variable bias to explain our results – unobservables would have to bias our results by much more than the very large and comprehensive set of covariates in our regressions (Altonji et al., 2005; Bellows and Miguel, 2009).<sup>17</sup>

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<sup>16</sup>Appendix D.1 reports analyses for each of the three prosocial traits separately.

<sup>17</sup>A potential concern is that temporal distance might simply pick up regional effects. Thus, we construct an extensive set of 28 continental dummies each equal to one if the two countries are from two given continents. When we include this vector of fixed effects, we cannot condition on country fixed effects any longer because the resulting set of fixed effects would be too extensive to leave meaningful variation to identify our coefficient of interest off. Appendix D.3 presents the results, which are very

Table 3: Preferences and temporal distance: Robustness (1/2)

	Dependent variable: Absolute difference in...									
	Risk taking					Prosociality				
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)
Temporal distance	0.15** (0.07)	0.14** (0.07)	0.15** (0.07)	0.16** (0.07)	0.16** (0.07)	0.17*** (0.04)	0.20*** (0.05)	0.19*** (0.05)	0.23*** (0.05)	0.23*** (0.05)
Population controls	No	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes
Economic and institutional controls	No	No	Yes	Yes	Yes	No	No	Yes	Yes	Yes
Colonial relationship dummies	No	No	Yes	Yes	Yes	No	No	Yes	Yes	Yes
Distance controls	No	No	No	Yes	Yes	No	No	No	Yes	Yes
Geographic controls	No	No	No	No	Yes	No	No	No	No	Yes
Observations	2556	2556	2485	2485	2485	2556	2556	2485	2485	2485
R <sup>2</sup>	0.630	0.631	0.632	0.635	0.637	0.480	0.482	0.491	0.493	0.493

Notes. OLS estimates, twoway-clustered standard errors in parentheses. All regressions are conditional on country fixed effects. See Table 2 for a complete list of the control variables. The temporal distance variable is the composite measure constructed from the two  $F_{ST}$  genetic distance measures, Nei genetic distance, predicted migratory distance, and linguistic distance. \*  $p < 0.10$ , \*\*  $p < 0.05$ , \*\*\*  $p < 0.01$ .

Table 4: Preferences and temporal distance: Robustness (2/2)

	Dependent variable: Absolute difference in...									
	Patience					Neg. reciprocity				
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)
Temporal distance	0.089* (0.05)	0.011 (0.03)	-0.034 (0.03)	-0.064* (0.04)	-0.055 (0.04)	0.035*** (0.02)	0.047*** (0.02)	0.035* (0.02)	-0.0072 (0.02)	-0.011 (0.02)
Population controls	No	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes
Economic and institutional controls	No	No	Yes	Yes	Yes	No	No	Yes	Yes	Yes
Colonial relationship dummies	No	No	Yes	Yes	Yes	No	No	Yes	Yes	Yes
Distance controls	No	No	No	Yes	Yes	No	No	No	Yes	Yes
Geographic controls	No	No	No	No	Yes	No	No	No	No	Yes
Observations	2556	2556	2485	2485	2485	2556	2556	2485	2485	2485
R <sup>2</sup>	0.504	0.515	0.579	0.584	0.586	0.467	0.469	0.482	0.485	0.486

Notes. OLS estimates, two-way-clustered standard errors in parentheses. All regressions are conditional on country fixed effects. See Table 2 for a complete list of the control variables. The temporal distance variable is the composite measure constructed from the two  $F_{ST}$  genetic distance measures, Nei genetic distance, predicted migratory distance, and linguistic distance. \*  $p < 0.10$ , \*\*  $p < 0.05$ , \*\*\*  $p < 0.01$ .



In many of the countries furthest from East Africa, the majority of the population is not indigenous. Our analysis addressed this aspect by employing observed genetic and linguistic distance as well as ancestry-adjusted migratory distance as inputs into the explanatory variable, which by construction pertain to contemporary populations. Still, to rule out that the mass migration post-1500 and its effect on temporal distances drives our results, Appendix D.4 presents the results of an additional robustness check in which we restrict the sample to countries in the Old World, i.e., we exclude Australia, the Americas, and the Caribbean. Reassuringly, the results are very similar to the baseline results. Finally, Appendix D.5 presents an extensive set of robustness checks in which we restrict the sample by excluding observations from the left or right tail of the distributions of temporal distance and preferences. These analyses show that the relationships between differences in risk taking and prosociality on the one hand and temporal distance on the other hand is not driven by outliers.

### 4.3 Separate Temporal Distance Proxies

So far, our analysis has made use of the composite temporal distance and  $F_{ST}$  genetic distance measures as proxies for temporal distance. We now extend our analysis by employing Nei genetic distance,  $F_{ST}$  genetic distance based on [Pemberton et al. \(2013\)](#), predicted migratory distance, predicted HMI migratory distance, and linguistic distance as explanatory variables. Columns (1) through (5) of Table 5 describe the relationship between differences in preferences and temporal distance. Columns (6) through (10) and columns (11) through (15) analyze the effect of temporal distance on differences in risk preferences and prosociality, respectively. Across specifications, the respective temporal distance proxies have a positive coefficient that is almost always statistically significant, hence showing that our results do not hinge on employing the composite temporal distance measure or [Cavalli-Sforza et al.'s \(1994\)](#)  $F_{ST}$  measure.<sup>18</sup>

Table 6 performs an analogous analysis for patience and negative reciprocity. Consistent with the results reported above, the point estimates of the temporal distance proxies are always positive, but often not statistically significant. At the same time, the stronger results for linguistic distance perhaps suggest that different preferences might be subject to different biological or cultural processes and that these different processes are partly captured by the different temporal distance proxy variables.

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similar to those using country fixed effects.

<sup>18</sup>Unreported regressions show that when we use non-ancestry adjusted migratory distance measures in the regressions (as opposed to the ancestry adjusted variables used throughout this paper), the results are weaker, again suggesting that the precise migration patterns of our ancestors need to be taken into account to understand the cross-country variation in preferences.

Table 5: Robustness: Separate temporal distance proxies (1/2)

	<i>Dependent variable: Absolute difference in...</i>														
	All preferences					Risk taking					Prosociality				
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)	(13)	(14)	(15)
Nei genetic distance	0.22*** (0.04)					0.14** (0.07)					0.22*** (0.05)				
Fst genetic distance (Pemberton et al.)		0.23*** (0.05)					0.18** (0.09)					0.16*** (0.05)			
Migratory distance			0.21*** (0.06)					0.13 (0.08)					0.13** (0.06)		
HMI migratory distance														0.12** (0.06)	
Linguistic distance															0.067** (0.03)
Observations	2556	2556	2556	2016	2556	2556	2556	2556	2016	2556	2556	2556	2556	2016	2556
R <sup>2</sup>	0.468	0.465	0.457	0.488	0.462	0.629	0.632	0.624	0.637	0.624	0.488	0.476	0.472	0.522	0.470

Notes. OLS estimates, twoway-clustered standard errors in parentheses. All regressions are conditional on country fixed effects. \*  $p < 0.10$ , \*\*  $p < 0.05$ , \*\*\*  $p < 0.01$ .

Table 6: Robustness: Separate temporal distance proxies (2/2)

	<i>Dependent variable: Absolute difference in...</i>									
	Patience					Neg. reciprocity				
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)
Nei genetic distance	0.041 (0.04)					0.017 (0.02)				
Fst genetic distance (Pemberton et al.)		0.082* (0.05)					0.018 (0.01)			
Migratory distance			0.12* (0.07)					0.040** (0.02)		
HMI migratory distance				0.051 (0.04)					0.042 (0.03)	
Linguistic distance					0.11* (0.06)					0.053*** (0.02)
Observations	2556	2556	2556	2016	2556	2556	2556	2556	2016	2556
$R^2$	0.501	0.503	0.505	0.527	0.508	0.467	0.467	0.467	0.462	0.468

Notes. OLS estimates, twoway-clustered standard errors in parentheses. All regressions are conditional on country fixed effects. \*  $p < 0.10$ , \*\*  $p < 0.05$ , \*\*\*  $p < 0.01$ .

## 4.4 Multiple Testing

Strictly speaking, our empirical analysis is subject to multiple testing concerns because we evaluate the hypothesis “temporal distance affects preference differences” through estimations that feature six dependent and six independent variables, i.e., 36 different specifications. At the same time, such concerns are arguably greatly reduced by our procedure of collapsing all dependent and all independent variables into a summary statistic each. In doing so, we have only one regression specification to evaluate, and here overall preference differences are strongly related to temporal distance (see columns (1) and (2) of Table 1). We further address concerns about multiple testing in Appendix D.6 by presenting  $p$ -values which are adjusted using the false discovery rate (FDR) procedure (Anderson, 2012; Cantoni et al., forthcoming). Again, these results support the picture developed in the main text. For example, when we adjust the  $p$ -values in Table 1 (i.e., the baseline results using the composite temporal distance measure) across dependent variables, the adjusted  $p$ -values are even smaller than the unadjusted ones and temporal distance is uniformly significantly linked to preference differences. At the same time, as Appendix D.6 shows, the results are again weaker for patience and negative reciprocity than for risk taking and the prosocial variables.

## 5 Preferences and the Length of the Migratory Path

The previous section established that larger genetic distance is associated with larger differences in preferences. However, the economics literature that makes use of concepts from population genetics considers not only interpopulation genetic distance, but also intrapopulation genetic diversity (Ashraf and Galor, 2013b). Whenever a subpopulation split apart from its parental colony, those humans breaking new ground took with them only a fraction of the genetic diversity of the previous genetic pool, intuitively because they were usually small, and hence non-representative, samples. In consequence, through the sequence of successive fissions, the total diversity of the gene pool significantly decreases along human migratory routes out of East Africa. Ashraf and Galor (2013b) make use of this observation by constructing a predicted measure of genetic diversity, which is a linear transformation of migratory distance from East Africa (Ethiopia).

In light of the previous findings, the question emerges whether the *level* of a given preference is related to genetic diversity, i.e., migratory distance from Ethiopia. Indeed, analyzing the relationship between the level of preferences and migratory distance from the cradle of mankind might shed light on the mechanisms that drive the patterns reported in Section 4. The argument underlying this paper is that the relation-

ship between temporal distance and preference differences reflects the accumulation of population-specific preference changes (through historical experiences and / or genetic drift) over thousands of years. However, it is also conceivable that this relationship is not driven by what happened *after* the population breakups, but rather by the structure of the breakups itself. In particular, it may be that the characteristics of the new founder populations systematically differed from those of the parental colonies, as would be the case if, e.g., only the least risk averse types split away. In such a scenario, preferences would evolve *monotonically* along the migratory path out of East Africa, hence mechanically producing the correlation between temporal distance and preference differences.<sup>19</sup> If true, this would still leave the main insight of the paper – that the structure and timing of population breakups in the very distant past have left a footprint in the contemporary global distribution of preferences – intact. At the same time, the interpretation of this relationship would change slightly. Because we only observe preferences today, we cannot evaluate whether such systematic population breakups actually took place. However, what is relevant for our purposes is to investigate whether the results of such systematic breakups are still visible in the data today and hence potentially drive our result on the relationship between temporal distance and contemporary differences in preferences.

We relate the level of the preference pool in a given country to the ancestry-adjusted length of the migratory path of the respective population from Ethiopia (i.e., genetic diversity) from [Ashraf and Galor \(2013b\)](#) using the following specification:

$$\text{pref}_i = \alpha + \beta_1 \times \text{genetic diversity}_i + \beta_2 \times \text{genetic diversity sq}_i + \gamma \times x_i + \epsilon_i$$

where  $\text{pref}_i$  is the average trait in country  $i$ ,  $x_i$  is a vector of covariates, and  $\epsilon_i$  a disturbance term. Note that this regression does *not* constitute a special case of the bilateral migratory distance regressions discussed above, because here the dependent variable is the *level* of a given preference, rather than the absolute difference to East Africa, i.e., Ethiopia. Thus, the regressions estimated above do not imply any prediction on the sign or significance of  $\beta_1$  and  $\beta_2$ .<sup>20</sup>

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<sup>19</sup>Slightly more subtly, it is also possible that the correlation between temporal distance and preference differences is driven by a monotonic evolution of the *dispersion* of the preference pool along the migratory path out of Africa, akin to the serial founder effect in population genetics: if the dispersion of the preference pool decreased monotonically along the migratory path, then differences in preferences between later founder populations would mechanically be smaller than those between earlier ones because the respective parental preference pool has lower variation to begin with. However, as shown in Appendix E.2, the relationship between preference dispersion and genetic diversity is very weak.

<sup>20</sup>A special case of the general bilateral regression framework estimated in Section 4 would be

$$|\text{pref}_i - \text{pref}_{\text{Ethiopia}}| = \alpha + \beta \times \text{genetic diversity}_i + \gamma \times |x_i - x_{\text{Ethiopia}}| + \epsilon_i$$

Since Ethiopia is not included in the Global Preference Survey, we cannot estimate this equation.

Table 7: Average preferences and genetic diversity

	Risk taking		Dependent variable: Average ...						Neg. reciprocity			
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)
Genetic diversity	2.08*	-74.1**	52.9	-1.27	153.0***	76.4	-0.14	127.1**	73.5	1.47	31.5	-78.4*
	(1.15)	(33.86)	(60.18)	(1.68)	(56.60)	(64.27)	(1.08)	(57.46)	(56.00)	(1.03)	(35.86)	(42.51)
Genetic diversity sq.		53.9**	-39.0		-109.3***	-54.8		-90.1**	-55.3		-21.3	57.5*
		(24.37)	(43.64)		(40.07)	(46.57)		(40.44)	(40.55)		(25.40)	(31.03)
Continent FE	No	No	Yes	No	No	Yes	No	No	Yes	No	No	Yes
Observations	74	74	74	74	74	74	74	74	74	74	74	74
R <sup>2</sup>	0.038	0.074	0.309	0.009	0.107	0.279	0.000	0.067	0.317	0.023	0.029	0.191

Notes. OLS estimates, robust standard errors in parentheses. \*  $p < 0.10$ , \*\*  $p < 0.05$ , \*\*\*  $p < 0.01$ .

Table 7 provides an overview of the results. Columns (1), (4), (7), and (10) show that our preference variables are generally not significantly linearly related to genetic diversity. At the same time, as shown in columns (2), (5), and (8), risk taking, patience, and prosociality all exhibit significant non-linear relationships with genetic diversity, i.e., risk aversion, patience, and prosociality are all hump-shaped in genetic diversity.<sup>21</sup> However, all of these significant non-linearities disappear with the inclusion of continent fixed effects (columns (3), (6), and (9)). Moreover, as shown in Appendix E.3, if we use the composite temporal distance to Ethiopia instead of genetic diversity (i.e., predicted migratory distance from Ethiopia) as explanatory variable, then all of the non-linearities disappear even without continent fixed effects. These results show that – at least as of today – preferences do not evolve monotonically along the migratory path out of Africa. This pattern is indicative that the relationship between temporal distance and preference differences is indeed driven by what happened *after* the various population breakups, rather than selective breakup patterns as such.

## 6 Conclusion

A growing body of empirical work highlights the importance of heterogeneity in risk, time, and social preferences for understanding a myriad of economic, social, and health behaviors. This paper takes a first step towards understanding the deep roots of variation in these preferences across entire populations. Our main contribution is to establish that a significant fraction of the substantial between-country heterogeneity in economic preferences has its historical origins in the structure and timing of very distant ancestral migration patterns, which highlights that if we aim to understand the ultimate roots of preference heterogeneity, we might have to consider events very far back in time.

Our results bear an interesting relationship to interdisciplinary work on cultural evolution (e.g., [Boyd and Richerson, 1988](#); [Henrich, 2015](#)). In particular, our findings provide indirect evidence that preferences are indeed subject to evolutionary processes, as is assumed in models of cultural or genetic evolution. In this respect, this paper did not attempt to shed light on the mechanisms through which temporal distance might drive preference differences. A priori, the observed patterns are consistent with differential historical experiences, genetic drift, or combinations thereof (also given recent evidence on gene-environment interaction). An important question for future research is which role socialization practices have played in these long-run processes.

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<sup>21</sup>The linear and squared genetic diversity coefficients are also jointly statistically significant. Note that this hump is not inconsistent with the results presented in Section 4 because here the dependent variable is not the absolute difference to Ethiopia.

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## ONLINE APPENDIX

### A Details on Global Preference Survey

Taken from [Falk et al. \(2015a\)](#).

#### A.1 Overview

The cross-country dataset measuring risk aversion, patience, positive and negative reciprocity, altruism, and trust, was collected through the professional infrastructure of the Gallup World Poll 2012. The data collection process consisted of three steps. First, an experimental validation procedure was conducted to select the survey items. Second, there was a pre-test of the selected survey items in a variety of countries to ensure implementability in a culturally diverse sample. Third, the final data set was collected through the regular professional data collection efforts in the framework of the World Poll 2012.

#### A.2 Experimental Validation

To ensure the behavioral validity of the preference measures, all underlying survey items were selected through an experimental validation procedure (see [Falk et al. \(2015b\)](#) for details). To this end, a sample of 409 German undergraduates completed standard state-of-the-art financially incentivized laboratory experiments designed to measure risk aversion, patience, positive and negative reciprocity, altruism, and trust. The same sample of subjects then completed a large battery of potential survey items. In a final step, for each preference, those survey items were selected which jointly performed best in explaining the behavior under real incentives observed in the choice experiments.

#### A.3 Pre-Test and Adjustment of Survey Items

Prior to including the preference module in the Gallup World Poll 2012, it was tested in the field as part of the World Poll 2012 pre-test, which was conducted at the end of 2011 in 22 countries. The main goal of the pre-test was to receive feedback on each item from various cultural backgrounds in order to assess potential difficulties in understanding and differences in the respondents' interpretation of items. Based on respondents' feedback and suggestions, minor modifications were made to several items before running the survey as part of the World Poll 2012.

The pre-test was run in 10 countries in central Asia (Armenia, Azerbaijan, Belarus, Georgia, Kazakhstan, Kyrgyzstan, Russia, Tajikistan, Turkmenistan, Uzbekistan) 2 countries in South-East Asia (Bangladesh and Cambodia), 5 countries in Southern and Eastern Europe (Croatia, Hungary, Poland, Romania, Turkey), 4 countries in the Middle East and North Africa (Algeria, Jordan, Lebanon, and Saudi-Arabia), and 1 country in Eastern Africa (Kenya). In each country, the sample size was 10 to 15 people. Overall, more than 220 interviews were conducted. In most countries, the sample was mixed in terms of gender, age, educational background, and area of residence (urban / rural).

Participants in the pre-test were asked to state any difficulties in understanding the items and to rephrase the meaning of items in their own words. If they encountered difficulties in understanding or interpreting items, respondents were asked to make suggestions on how to modify the wording of the item in order to attain the desired meaning.

Overall, the understanding of both the qualitative items and the quantitative items was satisfactory. In particular, no interviewer received any complaints regarding difficulties in assessing the quantitative questions or understanding the meaning of the probability used in the hypothetical risky choice items. When asked about rephrasing the qualitative items in their own words, most participants seemed to have understood the items in exactly the way that was intended. Nevertheless, some (sub-groups of) participants suggested adjustments to the wording of some items. This resulted in minor changes to four items, relative to the “original” experimentally validated items:

1. The use of the term “lottery” in hypothetical risky choices was troubling to some Muslim participants. As a consequence, we dropped the term “lottery” and replaced it with “draw”.
2. The term “charity” caused confusion in Eastern Europe and Central Asia, so it was replaced it with “good cause”.
3. Some respondents asked for a clarification of the question asking about one’s willingness to punish unfair behavior. This feedback lead to splitting the question into two separate items, one item asking for one’s willingness to punish unfair behavior towards others, and another asking for one’s willingness to punish unfair behavior towards oneself.
4. When asked about hypothetical choices between monetary amounts today versus larger amounts one year later, some participants, especially in countries with current or relatively recent phases of volatile and high inflation rates, stated that their answer would depend on the rate of inflation, or said that they would always

take the immediate payment due to uncertainty with respect to future inflation. Therefore, we decided to add the following phrase to each question involving hypothetical choices between immediate and future monetary amounts: “Please assume there is no inflation, i.e., future prices are the same as today’s prices.”

## **A.4 Selection of Countries**

The goal when selecting countries was to ensure representative coverage of the global population. Thus, countries from each continent and each region within continents were chosen. Another goal was to maximize variation with respect to observables, such as GDP per capita, language, historical and political characteristics, or geographical location and climatic conditions. Accordingly, the selection process favored non-neighborhood and culturally dissimilar countries. This procedure resulted in the following sample of 76 countries:

*East Asia and Pacific:* Australia, Cambodia, China, Indonesia, Japan, Philippines, South Korea, Thailand, Vietnam

*Europe and Central Asia:* Austria, Bosnia and Herzegovina, Croatia, Czech Republic, Estonia, Finland, France, Georgia, Germany, Greece, Hungary, Italy, Kazakhstan, Lithuania, Moldova, Netherlands, Poland, Portugal, Romania, Russia, Serbia, Spain, Sweden, Switzerland, Turkey, Ukraine, United Kingdom

*Latin America and Caribbean:* Argentina, Bolivia, Brazil, Chile, Colombia, Costa Rica, Guatemala, Haiti, Mexico, Nicaragua, Peru, Suriname, Venezuela

*Middle East and North Africa:* Algeria, Egypt, Iran, Iraq, Israel, Jordan, Morocco, Saudi Arabia, United Arab Emirates

*North America:* United States, Canada

*South Asia:* Afghanistan, Bangladesh, India, Pakistan, Sri Lanka

*Sub-Saharan Africa:* Botswana, Cameroon, Ghana, Kenya, Malawi, Nigeria, Rwanda, South Africa, Tanzania, Uganda, Zimbabwe

## **A.5 Sampling and Survey Implementation**

### **A.5.1 Background**

Since 2005, the international polling company Gallup has conducted an annual World Poll, in which it surveys representative population samples in almost every country around the world on, e.g., economic, social, political, and environmental issues. The collection of our preference data was embedded into the regular World Poll 2012 and hence made use of the pre-existing polling infrastructure of one of the largest profes-

sional polling institutes in the world.<sup>22</sup>

### *Selecting Primary Sampling Units*

In countries in which face-to-face interviews are conducted, the first stage of sampling is the identification of primary sampling units (PSUs), consisting of clusters of households. PSUs are stratified by population size and / or geography and clustering is achieved through one or more stages of sampling. Where population information is available, sample selection is based on probabilities proportional to population size. If population information is not available, Gallup uses simple random sampling.

In countries in which telephone interviews are conducted, Gallup uses a random-digit-dialing method or a nationally representative list of phone numbers. In countries with high mobile phone penetration, Gallup uses a dual sampling frame.

### *Selecting Households and Respondents*

Gallup uses random route procedures to select sampled households. Unless an outright refusal to participate occurs, interviewers make up to three attempts to survey the sampled household. To increase the probability of contact and completion, interviewers make attempts at different times of the day, and when possible, on different days. If the interviewer cannot obtain an interview at the initially sampled household, he or she uses a simple substitution method.

In face-to-face and telephone methodologies, random respondent selection is achieved by using either the latest birthday or Kish grid methods.<sup>23</sup> In a few Middle East and Asian countries, gender-matched interviewing is required, and probability sampling with quotas is implemented during the final stage of selection. Gallup implements quality control procedures to validate the selection of correct samples and that the correct person is randomly selected in each household.

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<sup>22</sup>See <http://www.gallup.com/strategicconsulting/156923/worldwide-research-methodology.aspx>

<sup>23</sup>The latest birthday method means that the person living in the household whose birthday among all persons in the household was the most recent (and who is older than 15) is selected for interviewing. With the Kish grid method, the interviewer selects the participants within a household by using a table of random numbers. The interviewer will determine which random number to use by looking at, e.g., how many households he or she has contacted so far (e.g., household no. 8) and how many people live in the household (e.g., 3 people, aged 17, 34, and 36). For instance, if the corresponding number in the table is 7, he or she will interview the person aged 17.

### *Sampling Weights*

Ex post, data weighting is used to ensure a nationally representative sample for each country and is intended to be used for calculations within a country. These sampling weights are provided by Gallup. First, base sampling weights are constructed to account for geographic oversamples, household size, and other selection probabilities. Second, post-stratification weights are constructed. Population statistics are used to weight the data by gender, age, and, where reliable data are available, education or socioeconomic status.

#### **A.5.2 Translation of Items**

The items of the preference module were translated into the major languages of each target country. The translation process involved three steps. As a first step, a translator suggested an English, Spanish or French version of a German item, depending on the region. A second translator, being proficient in both the target language and in English, French, or Spanish, then translated the item into the target language. Finally, a third translator would review the item in the target language and translate it back into the original language. If differences between the original item and the back-translated item occurred, the process was adjusted and repeated until all translators agreed on a final version.

#### **A.5.3 Adjustment of Monetary Amounts in Quantitative Items**

All items involving hypothetical monetary amounts were adjusted for each country in terms of their real value. Monetary amounts were calculated to represent the same share of a country's median income in local currency as the share of the amount in Euro of the German median income since the validation study had been conducted in Germany. Monetary amounts used in the validation study with the German sample were "round" numbers to facilitate easy calculations (e.g., the expected return of a lottery with equal chances of winning and losing) and to allow for easy comparisons (e.g., 100 Euro today versus 107.50 in 12 months). To proceed in a similar way in all countries, monetary amounts were always rounded to the next "round" number. For example, in the quantitative items involving choices between a lottery and varying safe options, the value of the lottery was adjusted to a round number. The varying safe options were then adjusted proportionally as in the original version. While this necessarily resulted in some (very minor) variations in the real stake size between countries, it minimized cross-country differences in the understanding the quantitative items due to difficulties in assessing the involved monetary amounts.



## A.6 Wording of Survey Items

In the following, “willingness to act” indicates the following introduction: *We now ask for your willingness to act in a certain way in four different areas. Please again indicate your answer on a scale from 0 to 10, where 0 means you are “completely unwilling to do so” and a 10 means you are “very willing to do so”. You can also use any numbers between 0 and 10 to indicate where you fall on the scale, like 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10.*

Similarly, “self-assessments” indicate that the respective statement was preceded by the following introduction: *How well do the following statements describe you as a person? Please indicate your answer on a scale from 0 to 10. A 0 means “does not describe me at all” and a 10 means “describes me perfectly”. You can also use any numbers between 0 and 10 to indicate where you fall on the scale, like 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10.*

### A.6.1 Patience

1. (Sequence of five interdependent quantitative questions:) *Suppose you were given the choice between receiving a payment today or a payment in 12 months. We will now present to you five situations. The payment today is the same in each of these situations. The payment in 12 months is different in every situation. For each of these situations we would like to know which you would choose. Please assume there is no inflation, i.e, future prices are the same as today’s prices. Please consider the following: Would you rather receive 100 Euro today or  $x$  Euro in 12 months?*

The precise sequence of questions was given by the “tree” logic in Figure 1.

2. (Willingness to act:) *How willing are you to give up something that is beneficial for you today in order to benefit more from that in the future?*

### A.6.2 Risk Taking

1. (Similar to self-assessment:) *Please tell me, in general, how willing or unwilling you are to take risks. Please use a scale from 0 to 10, where 0 means “completely unwilling to take risks” and a 10 means you are “very willing to take risks”. You can also use any numbers between 0 and 10 to indicate where you fall on the scale, like 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10.*
2. (Sequence of five interdependent quantitative questions:) *Please imagine the following situation. You can choose between a sure payment of a particular amount of money, or a draw, where you would have an equal chance of getting amount  $x$  or getting nothing. We will present to you five different situations. What would you prefer: a draw with a 50 percent chance of receiving amount  $x$ , and the same 50*

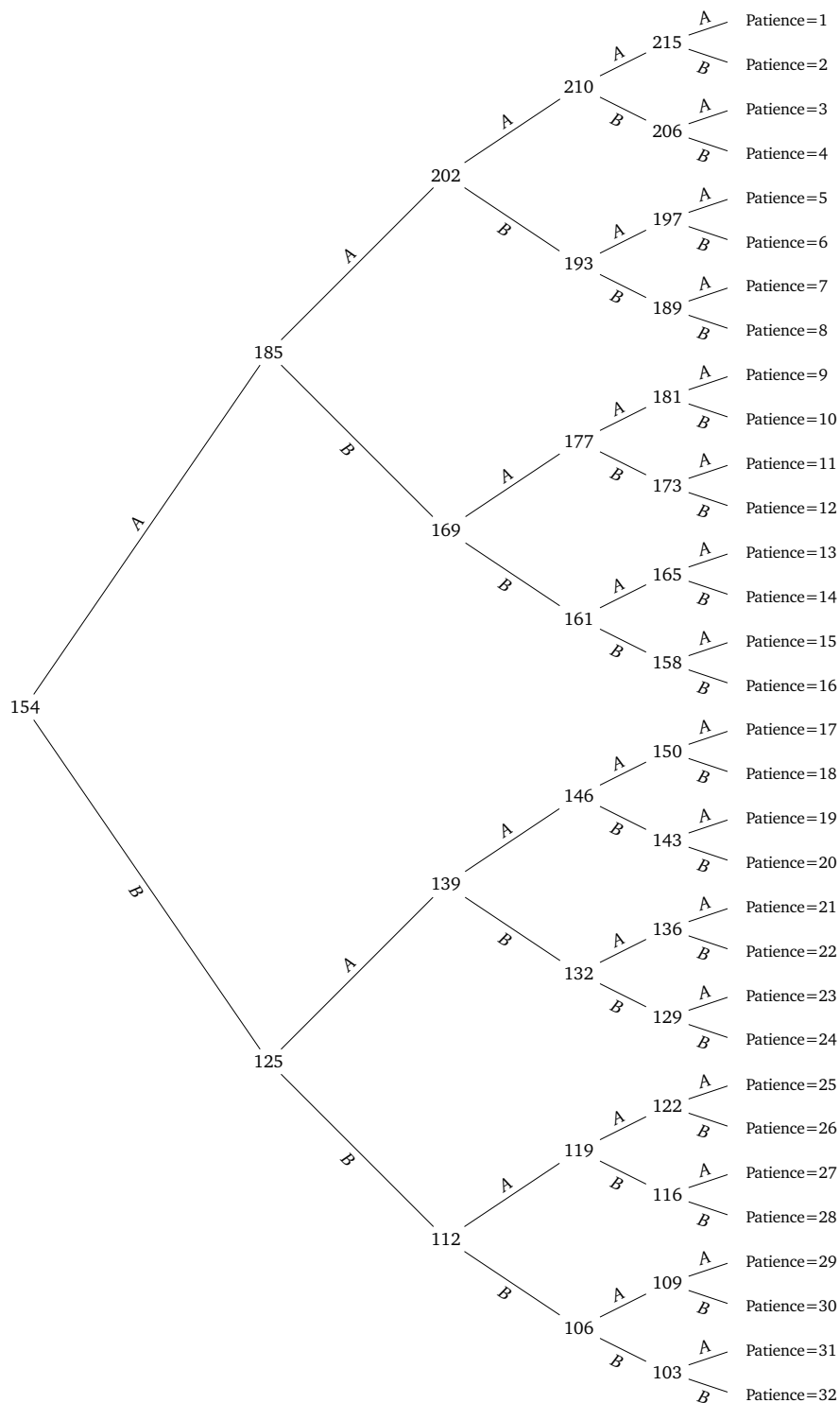


Figure 1: Tree for the staircase time task (numbers = payment in 12 months, A = choice of “100 euros today”, B = choice of “x euros in 12 months”. The staircase procedure worked as follows. First, each respondent was asked whether they would prefer to receive 100 euros today or 154 euros in 12 months from now (leftmost decision node). In case the respondent opted for the payment today (“A”), in the second question the payment in 12 months was adjusted upwards to 185 euros. If, on the other hand, the respondent chose the payment in 12 months, the corresponding payment was adjusted down to 125 euros. Working further through the tree follows the same logic.

percent chance of receiving nothing, or the amount of  $y$  as a sure payment? The precise sequence of questions was given by the “tree” logic in Figure 2.

### **A.6.3 Positive Reciprocity**

1. (Self-assessment:) *When someone does me a favor I am willing to return it.*
2. (Hypothetical situation:) *Please think about what you would do in the following situation. You are in an area you are not familiar with, and you realize you lost your way. You ask a stranger for directions. The stranger offers to take you to your destination. Helping you costs the stranger about 20 Euro in total. However, the stranger says he or she does not want any money from you. You have six presents with you. The cheapest present costs 5 Euro, the most expensive one costs 30 Euro. Do you give one of the presents to the stranger as a “thank-you”-gift? If so, which present do you give to the stranger? No present / The present worth 5 / 10 / 15 / 20 / 25 / 30 Euro.*

### **A.6.4 Negative Reciprocity**

1. (Self-assessment:) *If I am treated very unjustly, I will take revenge at the first occasion, even if there is a cost to do so.*
2. (Willingness to act:) *How willing are you to punish someone who treats you unfairly, even if there may be costs for you?*
3. (Willingness to act:) *How willing are you to punish someone who treats others unfairly, even if there may be costs for you?*

### **A.6.5 Altruism**

1. (Hypothetical situation:) *Imagine the following situation: Today you unexpectedly received 1,000 Euro. How much of this amount would you donate to a good cause? (Values between 0 and 1000 are allowed.)*
2. (Willingness to act:) *How willing are you to give to good causes without expecting anything in return?*

### **A.6.6 Trust**

(Self-assessment:) *I assume that people have only the best intentions.*

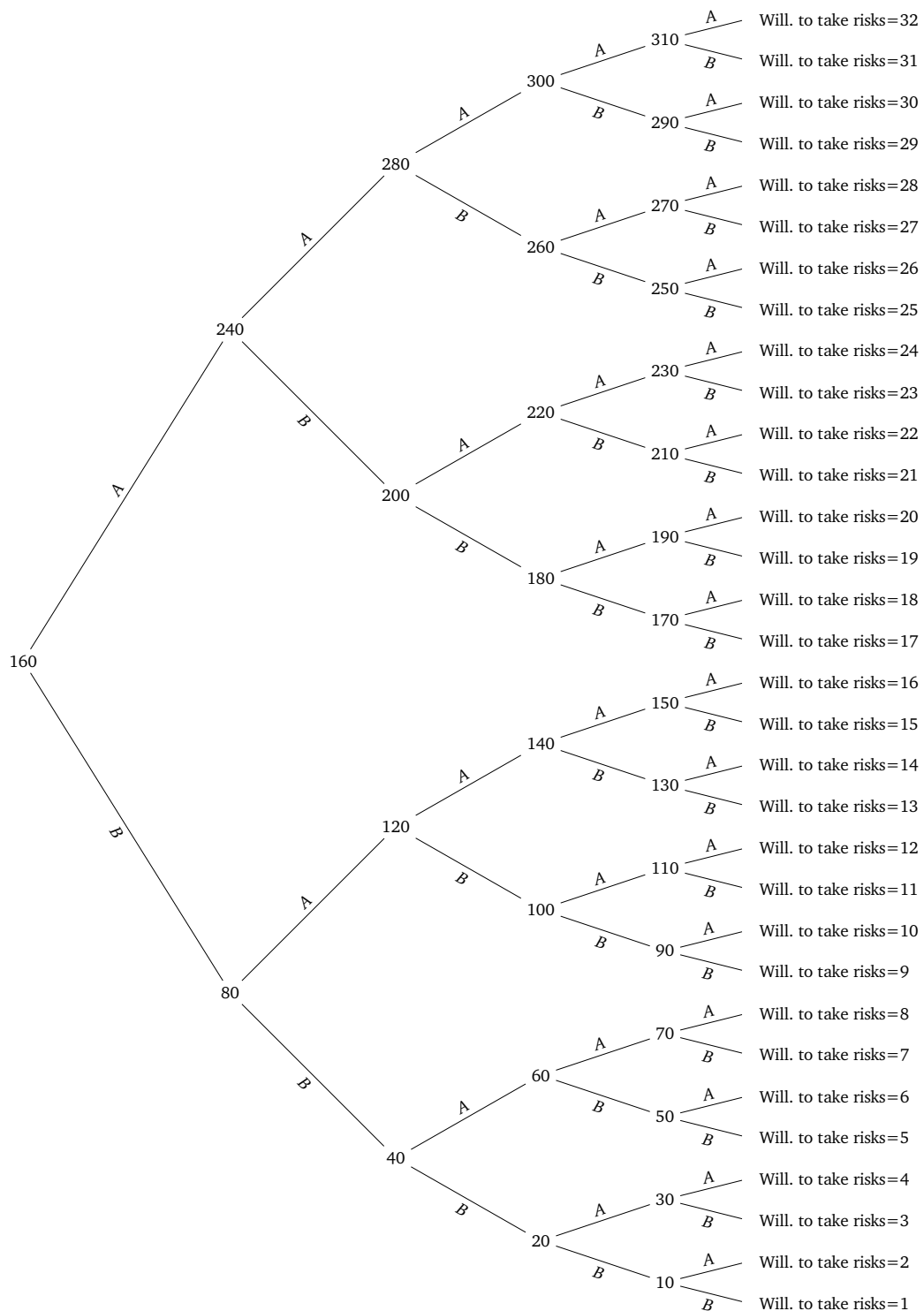


Figure 2: Tree for the staircase risk task (numbers = sure payment, A = choice of sure payment, B = choice of lottery). The staircase procedure worked as follows. First, each respondent was asked whether they would prefer to receive 160 euros for sure or whether they preferred a 50:50 chance of receiving 300 euros or nothing. In case the respondent opted for the safe choice (“B”), the safe amount of money being offered in the second question decreased to 80 euros. If, on the other hand, the respondent opted for the gamble (“A”), the safe amount was increased to 240 euros. Working further through the tree follows the same logic.

## A.7 Computation of Preference Measures

### A.7.1 Cleaning and Imputation of Missings

In order to efficiently use all available information in our data, missing survey items were imputed based on the following procedure:

- If one (or more) survey items for a given preference were missing, then the missing items were predicted using the responses to the available items. The procedure was as follows:
  - Suppose the preference was measured using two items, call them  $a$  and  $b$ . For those observations with missing information on  $a$ , the procedure was to predict its value based on the answer to  $b$  and its relationship to  $a$ , which was estimated by regressing  $b$  on  $a$  for the sub-sample of subjects who had nonmissing information on both,  $a$  and  $b$  (on the world sample).
  - For the unfolding-brackets time and risk items, the imputation procedure was similar, but made additional use of the informational content of the responses of participants who started but did not finish the sequence of the five questions. Again suppose that the preference is measured using two items and suppose that  $a$  (the staircase measure) is missing. If the respondent did not even start the staircase procedure, then imputation was done using the methodology described above. On the other hand, if the respondent answered between one and four of the staircase questions,  $a$  was predicted using a different procedure. Suppose the respondent answered four items such that his final staircase outcome would have to be either  $x$  or  $y$ . A probit was run of the “ $x$  vs.  $y$ ” decision on  $b$ , and the corresponding coefficients were used to predict the decision for all missings (note that this constitutes a predicted probability). The expected staircase outcome was then obtained by applying the predicted probabilities to the respective staircase endpoints, i.e., in this case  $x$  and  $y$ . If the respondent answered three (or less) questions, the same procedure was applied, the only difference being that in this case the obtained predicted probabilities were applied to the expected values of the staircase outcome conditional on reaching the respective node. Put differently, the procedure outlined above was applied recursively by working backwards through the “tree” logic of the staircase procedure, resulting in an expected value for the outcome node.
  - If all survey items for a given preference were missing, then no imputation took place.

- Across the 12 survey items, between 0% and 8% of all responses had to be imputed.

### A.7.2 Computation of Preference Indices at the Individual Level

For each of the traits (risk preferences, time preferences, positive reciprocity, negative reciprocity, altruism, and trust), an individual-level index was computed that aggregated responses across different survey items. Each of these indices was computed by (i) computing the z-scores of each survey item at the individual level and (ii) weighing these z-scores using the weights resulting from the experimental validation procedure of [Falk et al. \(2015b\)](#). Formally, these weights are given by the coefficients of an OLS regression of observed behavior in the experimental validation study on responses to the respective survey items, such that the weights sum to one. In practice, for almost all preferences, the coefficients assign roughly equal weight to all corresponding survey items. The weights are given by:

- Patience:

$$\text{Patience} = 0.7115185 \times \text{Staircase time} + 0.2884815 \times \text{Will. to give up sth. today}$$

- Risk taking:

$$\text{Risk taking} = 0.4729985 \times \text{Staircase risk} + 0.5270015 \times \text{Will. to take risks}$$

- Positive reciprocity:

$$\text{Pos. reciprocity} = 0.4847038 \times \text{Will. to return favor} + 0.5152962 \times \text{Size of gift}$$

- Negative reciprocity:

$$\begin{aligned} \text{Neg. reciprocity} &= 0.5261938/2 \times \text{Will. to punish if oneself treated unfairly} \\ &+ 0.5261938/2 \times \text{Will. to punish if other treated unfairly} \\ &+ 0.3738062 \times \text{Will. to take revenge} \end{aligned}$$

As explained above, in the course of the pre-test, the negative reciprocity survey item asking people for their willingness to punish others was split up into two questions, one asking for the willingness to punish if oneself was treated unfairly and one asking for the willingness to punish if someone was treated unfairly. In order to apply the weighting procedure from the validation procedure to these

items, the weight of the original item was divided by two and these modified weights were assigned to the new questions.

- Altruism:

Altruism =  $0.5350048 \times$  Will. to give to good causes +  $0.4649952 \times$  Hypoth. donation

- Trust: The survey included only one corresponding item.

### **A.7.3 Computation of Country Averages**

In order to compute country-level averages, individual-level data were weighted with the sampling weights provided by Gallup, see above. These sampling weights ensure that our measures correctly represent the population at the country level.

## B Proofs

Proof of Proposition 1. We have

$$x_i^T - x_j^T = \sum_{t=1}^T \epsilon_{P_t(i)}^t - \sum_{t=1}^T \epsilon_{P_t(j)}^t = \sum_{\substack{t=1, \dots, T, \\ P_t(i) \neq P_t(j)}} (\epsilon_{P_t(i)}^t - \epsilon_{P_t(j)}^t),$$

which is a sum of  $s_{ij}$  differences of shocks. Let  $u_1, \dots, u_T, v_1, \dots, v_T$  be i.i.d. random variables having the same distribution as the  $\epsilon_A^t$ . Then  $x_i^T - x_j^T$  has the same distribution as  $\sum_{n=1}^{s_{ij}} (u_n - v_n)$ . A similar argument shows that  $x_k^T - x_l^T$  has the same distribution as  $\sum_{n=1}^{s_{kl}} (u_n - v_n)$ . In particular,

$$E \left[ |x_i^T - x_j^T| \right] = E \left[ \left| \sum_{n=1}^{s_{ij}} (u_n - v_n) \right| \right]$$

and

$$E \left[ |x_k^T - x_l^T| \right] = E \left[ \left| \sum_{n=1}^{s_{kl}} (u_n - v_n) \right| \right].$$

The claimed equivalence will follow if we can show that

$$E \left[ \left| \sum_{n=1}^m (u_n - v_n) \right| \right] < E \left[ \left| \sum_{n=1}^{m+1} (u_n - v_n) \right| \right], \quad m = 0, \dots, T-1. \quad (1)$$

We will apply Lemma 1 below. Fix  $m \in \{0, \dots, T-1\}$  and let  $y = \sum_{n=1}^m (u_n - v_n)$  and  $z = u_{m+1} - v_{m+1}$ . Then  $y$  and  $z$  are independent integrable random variables. Moreover,  $E[z] = E[u_{m+1}] - E[v_{m+1}] = 0$  and since the shocks are nondegenerate,

$$\begin{aligned} P(z \neq 0) &\geq P(u_{m+1} > E[u_{m+1}], v_{m+1} < E[v_{m+1}]) \\ &= P(u_{m+1} > E[u_{m+1}])P(v_{m+1} < E[v_{m+1}]) > 0. \end{aligned}$$

Finally, for every  $c > 0$ , there exists  $\xi \in \mathbb{R}$  such that  $P(|\sum_{n=1}^m u_n - \xi| < \frac{c}{2}) > 0$ . Hence,

$$\begin{aligned} P(|y| < c) &\geq P\left(\left|\sum_{n=1}^m u_n - \xi\right| < \frac{c}{2}, \left|\sum_{n=1}^m v_n - \xi\right| < \frac{c}{2}\right) \\ &= P\left(\left|\sum_{n=1}^m u_n - \xi\right| < \frac{c}{2}\right)^2 > 0, \end{aligned}$$

which shows that the support of the distribution of  $y$  contains the point 0. Inequality (1) now follows from Lemma 1.  $\square$



**Lemma 1.** Let  $y$  and  $z$  be independent integrable random variables. Suppose that 0 is in the support of the distribution of  $y$ ,  $E[z] = 0$  and  $P(z \neq 0) > 0$ . Then  $E[|y + z|] > E[|y|]$ .

Proof. Since  $y$  and  $z$  are independent,  $E[z|y] = E[z] = 0$ , and so

$$E[|y + z||y] \geq |E[y + z|y]| = |E[y|y]| = |y|. \quad (2)$$

Using the inequality  $|y + z| \geq |z| - |y|$  and again the independence of  $y$  and  $z$ , we obtain

$$E[|y + z||y] \geq E[|z||y] - E[|y||y] = E[|z|] - |y|.$$

Hence, on the event  $\{2|y| < E[|z|]\}$ ,

$$E[|y + z||y] > |y|.$$

The assumption that  $P(z \neq 0) > 0$  implies that  $E[|z|] > 0$ , and since 0 is contained in the support of the distribution of  $y$ ,  $P(2|y| < E[|z|]) > 0$ . That is, inequality (2) holds almost everywhere and the inequality is strict on a set of positive probability. Taking expectations we get  $E[|y + z|] > E[|y|]$ .  $\square$

## C Raw Correlations Among Temporal Distance Proxies

Table 8: Raw correlations among temporal distance proxies

	Fst dist.	Nei dist.	Fst dist. (new)	Migratory dist.	HMI dist.	Linguistic dist.
Fst dist.	1					
Nei dist.	0.945***	1				
Fst dist. (new)	0.840***	0.832***	1			
Migratory dist.	0.519***	0.514***	0.775***	1		
HMI dist.	0.620***	0.633***	0.820***	0.923***	1	
Linguistic dist.	0.443***	0.393***	0.353***	0.0888***	0.193***	1

Pearson raw correlations. Fst dist. (new) refers to the Fst genetic distance measure based on [Spolaore and Wacziarg \(2016\)](#). \*  $p < 0.10$ , \*\*  $p < 0.05$ , \*\*\*  $p < 0.01$ .

## D Additional Bilateral Regressions

### D.1 Prosociality Variables Separately

Table 9: Prosociality and temporal distance: Robustness

	<i>Dependent variable: Absolute difference in...</i>														
	Altruism					Positive reciprocity					Trust				
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)	(13)	(14)	(15)
Temporal distance	0.027*	0.025	0.025	0.016	0.012	0.11**	0.11**	0.11**	0.15**	0.15**	0.20***	0.23***	0.21***	0.23***	0.22***
	(0.01)	(0.02)	(0.02)	(0.03)	(0.03)	(0.05)	(0.05)	(0.05)	(0.06)	(0.06)	(0.05)	(0.06)	(0.06)	(0.06)	(0.06)
Population controls	No	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes
Economic and institutional controls	No	No	Yes	Yes	Yes	No	No	Yes	Yes	Yes	No	No	Yes	Yes	Yes
Colonial relationship dummies	No	No	Yes	Yes	Yes	No	No	Yes	Yes	Yes	No	No	Yes	Yes	Yes
Distance controls	No	No	No	Yes	Yes	No	No	No	Yes	Yes	No	No	No	Yes	Yes
Geographic controls	No	No	No	No	Yes	No	No	No	No	Yes	No	No	No	No	Yes
Observations	2556	2556	2485	2485	2485	2556	2556	2485	2485	2485	2556	2556	2485	2485	2485
$R^2$	0.555	0.555	0.556	0.557	0.558	0.509	0.509	0.511	0.513	0.514	0.438	0.441	0.456	0.457	0.459

Notes. OLS estimates, twoway-clustered standard errors in parentheses. All regressions are conditional on country fixed effects. The temporal distance variable is the composite measure constructed from the two  $F_{S,T}$  genetic distance measures, Nei genetic distance, predicted migratory distance, and linguistic distance. \*  $p < 0.10$ , \*\*  $p < 0.05$ , \*\*\*  $p < 0.01$ .

## **D.2 Alternative Computation of Temporal Distance Proxy**

In the main text, temporal distance was proxied by (the z-score of) the unweighted average of Fst genetic distance, Nei genetic distance, predicted migratory distance, and linguistic distance. This section reports a robustness check in which temporal distance is computed as unweighted average of Fst genetic distance, predicted migratory distance, and linguistic distance. For each preference dimension, Table 10 reports two specifications, one without controls (except for country fixed effects), and one with the full vector of controls employed in the main text. The results closely mirror those reported above.

Table 10: Preferences and temporal distance: Alternative computation of temporal distance

	Dependent variable: Absolute difference in...									
	All prefs.		Risk taking	Prosociality		Patience		Neg. reciprocity		
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)
Temporal distance	0.23*** (0.04)	0.18*** (0.05)	0.15** (0.07)	0.16** (0.07)	0.17*** (0.04)	0.23*** (0.05)	0.089* (0.05)	-0.055 (0.04)	0.035** (0.02)	-0.011 (0.02)
Population controls	No	Yes	No	Yes	No	Yes	No	Yes	No	Yes
Economic and institutional controls	No	Yes	No	Yes	No	Yes	No	Yes	No	Yes
Colonial relationship dummies	No	Yes	No	Yes	No	Yes	No	Yes	No	Yes
Distance controls	No	Yes	No	Yes	No	Yes	No	Yes	No	Yes
Geographic controls	No	Yes	No	Yes	No	Yes	No	Yes	No	Yes
Observations	2556	2485	2556	2485	2556	2485	2556	2485	2556	2485
R <sup>2</sup>	0.470	0.491	0.630	0.637	0.480	0.493	0.504	0.586	0.467	0.486

Notes. OLS estimates, twoway-clustered standard errors in parentheses. All regressions are conditional on country fixed effects. The temporal distance variable is the composite measure constructed from  $F_{ST}$  genetic distance measures, predicted migratory distance, and linguistic distance. \*  $p < 0.10$ , \*\*  $p < 0.05$ , \*\*\*  $p < 0.01$ .

### D.3 Continent Fixed Effects

Table 11: Preferences and temporal distance: Bilateral continent fixed effects

	<i>Dependent variable: Absolute difference in...</i>				
	All prefs.	Risk taking	Prosociality	Patience	Neg. reciprocity
	(1)	(2)	(3)	(4)	(5)
Temporal distance	0.13* (0.07)	0.19*** (0.07)	0.18** (0.09)	-0.21*** (0.05)	-0.060 (0.08)
Population controls	Yes	Yes	Yes	Yes	Yes
Economic and institutional controls	Yes	Yes	Yes	Yes	Yes
Colonial relationship dummies	Yes	Yes	Yes	Yes	Yes
Distance controls	Yes	Yes	Yes	Yes	Yes
Geographic controls	Yes	Yes	Yes	Yes	Yes
Continent FE	Yes	Yes	Yes	Yes	Yes
Observations	2485	2485	2485	2485	2485
$R^2$	0.165	0.312	0.108	0.345	0.117

*Notes.* OLS estimates, twoway-clustered standard errors in parentheses. The regressions do not include country fixed effects, but bilateral continent fixed effects. These 28 continental dummies are constructed from seven “continents”, following the World Bank terminology: Sub-Saharan Africa, North Africa and Middle East, Europe and Central Asia, East Asia and Pacific, South Asia, Northern America, South America and Caribbean. These dummies are each equal to one if the two countries are from two given continents. For example, one of the dummies is equal to one if one country is from South Asia and one from Northern America, and one dummy is equal to one if both countries are from Europe and Central Asia. The temporal distance variable is the composite measure constructed from the two  $F_{ST}$  genetic distance measures, Nei genetic distance, predicted migratory distance, and linguistic distance. \*  $p < 0.10$ , \*\*  $p < 0.05$ , \*\*\*  $p < 0.01$ .

### D.4 Old World Sample

Table 12: Robustness: Restricted sample (Old World)

	<i>Dependent variable: Abs. difference in...</i>				
	All prefs.	Risk taking	Prosociality	Patience	Neg. reciprocity
	(1)	(2)	(3)	(4)	(5)
Temporal distance	0.26*** (0.05)	0.20** (0.09)	0.17*** (0.05)	0.061 (0.05)	0.066* (0.04)
Observations	1596	1596	1596	1596	1596
$R^2$	0.448	0.616	0.438	0.509	0.429

*Notes.* OLS estimates, twoway-clustered standard errors in parentheses. The sample is restricted to countries in the Old World, i.e., we exclude Australia, the Americas, and the Caribbean. All regressions are conditional on country fixed effects. The temporal distance variable is the composite measure constructed from the two  $F_{ST}$  genetic distance measures, Nei genetic distance, predicted migratory distance, and linguistic distance. \*  $p < 0.10$ , \*\*  $p < 0.05$ , \*\*\*  $p < 0.01$ .

## D.5 Excluding Tail Observations

Tables 13 through 17 present the results of regressions in which we restrict the sample of observations by excluding observations from the left or right tail of the distributions of temporal distance or the respective preference differences. Specifically, the regressions either utilize observations below the 90th percentile or above the 10th percentile of the distribution of a given variable.

Note that the location of any given country pair in the distribution of all bilateral variables may depend on whether country fixed effects are taken into account. For instance, if country *A* had very large temporal distances to all but one countries, and an average distance to country *B*, then restricting the sample by temporal distance would never exclude the *A* – *B* observation. However, with country fixed effects, this may change, because (heuristically speaking) the fixed effects for country *A* take out the relatively large average temporal distance for country *A*, implying that the *A* – *B* pair has a very small temporal distance in terms of residuals. Thus, after accounting for country fixed effects, this observation might get excluded based on the above sample restriction criteria. Thus, we apply our robustness exercises to both types of distributions, i.e., to the distributions of raw variables and the distributions of residuals, see the tablenotes for further details.

Table 13: Preferences and temporal distance: Excluding small and large values

		<i>Dependent variable: Absolute difference in all preferences</i>							
$\Delta$ Prefs. > 10th pct		$\Delta$ Prefs. < 90th pct		Temporal dist. > 10th pct		Temporal dist. < 90th pct			
Raw	Residual	Raw	Residual	Raw	Residual	Raw	Residual	Raw	Residual
(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(7)	(8)
Temporal distance	0.16*** (0.03)	0.11*** (0.02)	0.23*** (0.04)	0.22*** (0.04)	0.15*** (0.04)	0.12** (0.05)	0.25*** (0.04)	0.25*** (0.04)	0.25*** (0.04)
Observations	2300	2300	2300	2300	2300	2300	2300	2300	2300

*Notes.* OLS estimates, twoway-clustered standard errors in parentheses. All regressions are conditional on country fixed effects. In all columns, the sample is restricted to observations above or below a certain threshold, where the threshold is either computed with or without country fixed effects. For instance, in columns (1), the sample includes all observations whose absolute difference in risk taking is above the 90th percentile of the distribution of (raw) absolute differences in risk taking. In column (2), the sample includes all observations whose absolute difference in risk taking is above the 90th percentile of the distribution of residual absolute differences in risk taking after taking out country fixed effects. That is, we first regress absolute differences in risk taking on a vector of country fixed effects, compute the residual, and then restrict the sample based on the residuals. Likewise, in column (7), we restrict the sample to observations below the 90th percentile of the distribution of (raw) temporal distances, while column (8) applies the 90th percentile to the distribution of temporal distances after accounting for country fixed effects, i.e., after regressing temporal distance on country fixed effects and computing residuals. All regressions include country fixed effects: the “raw” regressions are standard fixed effects regressions; the “residual” regressions are estimated by (i) partialing country fixed effects out of differences in risk taking and temporal distance (on the full sample), (ii) restricting the sample, (iii) regressing residuals on each other. The temporal distance variable is the composite measure constructed from the two  $F_{57}$  genetic distance measures, Nei genetic distance, predicted migratory distance, and linguistic distance. \*  $p < 0.10$ , \*\*  $p < 0.05$ , \*\*\*  $p < 0.01$ .

Table 14: Risk preferences and temporal distance: Excluding small and large values

	<i>Dependent variable: Absolute difference in risk taking</i>							
	$\Delta$ Risk > 10th pct		$\Delta$ Risk < 90th pct		Temporal dist. > 10th pct		Temporal dist. < 90th pct	
	Raw	Residual	Raw	Residual	Raw	Residual	Raw	Residual
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
Temporal distance	0.15** (0.07)	0.045 (0.03)	0.16** (0.08)	0.17** (0.07)	0.14** (0.07)	0.14** (0.06)	0.14** (0.07)	0.14* (0.07)
Observations	2300	2300	2300	2300	2300	2300	2300	2300

*Notes.* OLS estimates, twoway-clustered standard errors in parentheses. All regressions are conditional on country fixed effects. In all columns, the sample is restricted to observations above or below a certain threshold, where the threshold is either computed with or without country fixed effects. For instance, in columns (1), the sample includes all observations whose absolute difference in risk taking is above the 90th percentile of the distribution of (raw) absolute differences in risk taking. In column (2), the sample includes all observations whose absolute difference in risk taking is above the 90th percentile of the distribution of residual absolute differences in risk taking after taking out country fixed effects. That is, we first regress absolute differences in risk taking on a vector of country fixed effects, compute the residual, and then restrict the sample based on the residuals. Likewise, in column (7), we restrict the sample to observations below the 90th percentile of the distribution of (raw) temporal distances, while column (8) applies the 90th percentile to the distribution of temporal distances after accounting for country fixed effects, i.e., after regressing temporal distance on country fixed effects and computing residuals. All regressions include country fixed effects: the “raw” regressions are standard fixed effects regressions; the “residual” regressions are estimated by (i) partialling country fixed effects out of differences in risk taking and temporal distance (on the full sample), (ii) restricting the sample, (iii) regressing residuals on each other. The temporal distance variable is the composite measure constructed from the two  $F_{ST}$  genetic distance measures, Nei genetic distance, predicted migratory distance, and linguistic distance. \*  $p < 0.10$ , \*\*  $p < 0.05$ , \*\*\*  $p < 0.01$ .



Table 15: Prosociality and temporal distance: Excluding small and large values

		<i>Dependent variable: Absolute difference in prosociality</i>							
$\Delta$ Social > 10th pct		$\Delta$ Social < 90th pct		Temporal dist. > 10th pct		Temporal dist. < 90th pct			
Raw	Residual	Raw	Residual	Raw	Residual	Raw	Residual	Raw	Residual
(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(7)	(8)
Temporal distance	0.15*** (0.04)	0.12*** (0.03)	0.16*** (0.04)	0.14*** (0.04)	0.16*** (0.06)	0.15* (0.09)	0.17*** (0.04)	0.16*** (0.04)	0.16*** (0.04)
Observations	2300	2300	2300	2300	2300	2300	2300	2300	2300

*Notes.* OLS estimates, twoway-clustered standard errors in parentheses. All regressions are conditional on country fixed effects. In all columns, the sample is restricted to observations above or below a certain threshold, where the threshold is either computed with or without country fixed effects. For instance, in columns (1), the sample includes all observations whose absolute difference in prosociality is above the 90th percentile of the distribution of (raw) absolute differences in prosociality. In column (2), the sample includes all observations whose absolute difference in prosociality is above the 90th percentile of the distribution of residual absolute differences in prosociality after taking out country fixed effects. That is, we first regress absolute differences in prosociality on a vector of country fixed effects, compute the residual, and then restrict the sample based on the residuals. Likewise, in column (7), we restrict the sample to observations below the 90th percentile of the distribution of (raw) temporal distances, while column (8) applies the 90th percentile to the distribution of temporal distances after accounting for country fixed effects, i.e., after regressing temporal distance on country fixed effects and computing residuals. All regressions include country fixed effects: the “raw” regressions are standard fixed effects regressions; the “residual” regressions are estimated by (i) partialling country fixed effects out of differences in prosociality and temporal distance (on the full sample), (ii) restricting the sample, (iii) regressing residuals on each other. The temporal distance variable is the composite measure constructed from the two  $F_{ST}$  genetic distance measures, Nei genetic distance, predicted migratory distance, and linguistic distance. \*  $p < 0.10$ , \*\*  $p < 0.05$ , \*\*\*  $p < 0.01$ .

Table 16: Patience and temporal distance: Excluding small and large values

		<i>Dependent variable: Absolute difference in patience</i>							
$\Delta$ Risk > 10th pct		$\Delta$ Risk < 90th pct		Temporal dist. > 10th pct		Temporal dist. < 90th pct			
Raw	Residual	Raw	Residual	Raw	Residual	Raw	Residual	Raw	Residual
(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(7)	(8)
Temporal distance	0.087* (0.05)	0.029* (0.02)	0.066 (0.05)	0.064 (0.05)	0.026 (0.03)	0.000016 (0.06)	0.11* (0.06)	0.11* (0.06)	0.11* (0.06)
Observations	2300	2300	2300	2300	2300	2300	2300	2300	2300

*Notes.* OLS estimates, twoway-clustered standard errors in parentheses. All regressions are conditional on country fixed effects. In all columns, the sample is restricted to observations above or below a certain threshold, where the threshold is either computed with or without country fixed effects. For instance, in columns (1), the sample includes all observations whose absolute difference in patience is above the 90th percentile of the distribution of (raw) absolute differences in patience. In column (2), the sample includes all observations whose absolute difference in patience is above the 90th percentile of the distribution of residual absolute differences in patience after taking out country fixed effects. That is, we first regress absolute differences in patience on a vector of country fixed effects, compute the residual, and then restrict the sample based on the residuals. Likewise, in column (7), we restrict the sample to observations below the 90th percentile of the distribution of (raw) temporal distances, while column (8) applies the 90th percentile to the distribution of temporal distances after accounting for country fixed effects, i.e., after regressing temporal distance on country fixed effects and computing residuals. All regressions include country fixed effects: the “raw” regressions are standard fixed effects regressions; the “residual” regressions are estimated by (i) partialling country fixed effects out of differences in patience and temporal distance (on the full sample), (ii) restricting the sample, (iii) regressing residuals on each other. The temporal distance variable is the composite measure constructed from the two  $F_{ST}$  genetic distance measures, Nei genetic distance, predicted migratory distance, and linguistic distance. \*  $p < 0.10$ , \*\*  $p < 0.05$ , \*\*\*  $p < 0.01$ .

Table 17: Negative reciprocity and temporal distance: Excluding small and large values

		<i>Dependent variable: Absolute difference in neg. reciprocity</i>							
$\Delta$ negrecip > 10th pct		$\Delta$ negrecip < 90th pct		Temporal dist. > 10th pct		Temporal dist. < 90th pct			
Raw	Residual	Raw	Residual	Raw	Residual	Raw	Residual	Raw	Residual
(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(7)	(8)
Temporal distance	0.042** (0.02)	0.031* (0.02)	0.033** (0.01)	0.034** (0.01)	-0.0096 (0.02)	0.0034 (0.05)	0.052** (0.02)	0.046** (0.02)	0.046** (0.02)
Observations	2300	2300	2300	2300	2300	2300	2300	2300	2300

*Notes.* OLS estimates, twoway-clustered standard errors in parentheses. All regressions are conditional on country fixed effects. In all columns, the sample is restricted to observations above or below a certain threshold, where the threshold is either computed with or without country fixed effects. For instance, in columns (1), the sample includes all observations whose absolute difference in negative reciprocity is above the 90th percentile of the distribution of (raw) absolute differences in negative reciprocity. In column (2), the sample includes all observations whose absolute difference in negative reciprocity is above the 90th percentile of the distribution of residual absolute differences in negative reciprocity after taking out country fixed effects. That is, we first regress absolute differences in negative reciprocity on a vector of country fixed effects, compute the residual, and then restrict the sample based on the residuals. Likewise, in column (7), we restrict the sample to observations below the 90th percentile of the distribution of (raw) temporal distances, while column (8) applies the 90th percentile to the distribution of temporal distances after accounting for country fixed effects, i.e., after regressing temporal distance on country fixed effects and computing residuals. All regressions include country fixed effects: the “raw” regressions are standard fixed effects regressions; the “residual” regressions are estimated by (i) partialling country fixed effects out of differences in negative reciprocity and temporal distance (on the full sample), (ii) restricting the sample, (iii) regressing residuals on each other. The temporal distance variable is the composite measure constructed from the two  $F_{ST}$  genetic distance measures, Nei genetic distance, predicted migratory distance, and linguistic distance. \*  $p < 0.10$ , \*\*  $p < 0.05$ , \*\*\*  $p < 0.01$ .

## D.6 Adjusting $p$ -Values Using the FDR Procedure

This section reports  $p$ -values that are adjusted for multiple testing using the FDR procedure (see [Anderson, 2012](#); [Cantoni et al., forthcoming](#), for details). We start by adjusting the  $p$ -values in Table 1 which presents the baseline results. Here, to assess the null hypothesis “temporal distance does not affect preference differences”, we group the regressions across dependent variables, for each temporal distance proxy. For example, we show  $p$ -values that are adjusted for the fact that in using our composite temporal distance summary statistic we employ six different dependent variables (columns (3), (5), (7), (9), (11), and (13)). Table 18 then presents adjusted  $p$ -values for the same regressions as in Table 1. Note that adjusted  $p$ -values can be smaller than unadjusted ones, in particular if the set of regressions in a given category includes many rejections of the null. Indeed, the results show that the adjusted  $p$ -values are consistently smaller than the unadjusted ones, providing evidence that our results are not driven by multiple testing issues.

To delve deeper into this issue, Tables 19 and 20 present adjusted  $p$ -values for the regressions in Tables 5 and 6, respectively, i.e., regressions in which we employ all temporal distance proxies separately. To this end, we group regressions by dependent variable and then adjust  $p$ -values within that group across explanatory variables (in other words, in such an adjustment procedure, the null hypothesis is no longer “temporal distance has no effect on preference differences”, but rather “temporal distance has no effect on risk preferences”, for example). Thus, while the results presented above referred to multiple testing issues because we employ multiple dependent variables, the procedure reported here takes into account the multiplicity of explanatory variables. Again, the results support the picture derived in the main text: the relationship between the temporal distance proxies and risk taking or prosociality is robust, while the relationships between temporal distance and patience or negative reciprocity are often not statistically significant.

Table 18: Adjusted  $p$ -values for the regressions in Table 1

	<i>Dependent variable: Absolute difference in...</i>													
	Risk taking	Altruism	Pos. reciprocity	Trust	Patience	Neg. reciprocity								
Column in Table 1	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)	(13)	(14)		
Unadjusted p-value	0.036	0.034	0.074	0.017	0.018	0.008	0.001	0.001	0.092	0.236	0.022	0.455		
Adjusted p-value	0.045	0.036	0.047	0.025	0.038	0.021	0.002	0.001	0.049	0.105	0.038	0.179		

Table 19: Adjusted  $p$ -values for the regressions in Table 5

	<i>Dependent variable: Absolute difference in...</i>														
	All preferences														
	Risk taking										Prosociality				
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)	(13)	(14)	(15)
Unadjusted p-value	0.001	0.001	0.001	0.001	0.001	0.038	0.031	0.128	0.026	0.081	0.001	0.002	0.026	0.036	0.030
Adjusted p-value	0.001	0.001	0.001	0.001	0.001	0.068	0.068	0.068	0.068	0.068	0.001	0.006	0.023	0.023	0.023

Table 20: Adjusted  $p$ -values for the regressions in Table 6

	<i>Dependent variable: Absolute difference in...</i>									
	Patience					Neg. reciprocity				
Column in Table 6	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)
Unadjusted p-value	0.238	0.097	0.056	0.256	0.056	0.449	0.214	0.028	0.108	0.010
Adjusted p-value	0.182	0.164	0.164	0.182	0.164	0.220	0.191	0.060	0.121	0.052

## E Additional Diversity Regressions

### E.1 Prosocial Traits Separately

Table 21: Preferences and genetic diversity: Prosocial traits separately

	<i>Dependent variable: Average ...</i>								
	Altruism			Positive reciprocity			Trust		
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)
Genetic diversity	-1.14 (1.31)	98.3** (42.84)	91.2 (57.65)	-1.15 (1.50)	107.2** (52.75)	25.8 (65.35)	-0.36 (1.23)	116.5*** (42.37)	43.6 (40.67)
Genetic diversity sqr.		-70.4** (30.46)	-65.9 (41.69)		-76.7** (37.31)	-18.7 (47.64)		-82.8*** (30.29)	-30.5 (29.54)
Continent FE	No	No	Yes	No	No	Yes	No	No	Yes
Observations	74	74	74	74	74	74	74	74	74
R <sup>2</sup>	0.009	0.056	0.181	0.009	0.067	0.174	0.001	0.101	0.383

Notes. OLS estimates, robust standard errors in parentheses. \*  $p < 0.10$ , \*\*  $p < 0.05$ , \*\*\*  $p < 0.01$ .

## E.2 Diversity and the Dispersion of the Preference Pool

Table 22: Preference variability and genetic diversity

	<i>Dependent variable: Standard deviation in ...</i>											
	Risk taking			Prosociality			Patience			Neg. reciprocity		
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)
Genetic diversity	0.67*	-8.30	8.98	-0.56	-24.9	-8.04	-1.09*	39.2	-1.65	-0.44	-9.65	23.2
	(0.37)	(11.08)	(14.20)	(0.47)	(16.80)	(19.22)	(0.57)	(23.57)	(23.85)	(0.33)	(11.45)	(16.68)
Genetic diversity sq:		6.36	-6.63		17.2	5.00		-28.6*	-0.25		6.53	-17.1
		(7.88)	(10.29)		(11.86)	(13.73)		(16.83)	(17.47)		(8.25)	(12.22)
Continent FE	No	No	Yes	No	No	Yes	No	No	Yes	No	No	Yes
Observations	74	74	74	74	74	74	74	74	74	74	74	74
R <sup>2</sup>	0.044	0.050	0.102	0.030	0.071	0.177	0.038	0.075	0.258	0.014	0.019	0.140

Notes. OLS estimates, robust standard errors in parentheses. \*  $p < 0.10$ , \*\*  $p < 0.05$ , \*\*\*  $p < 0.01$ .

Table 23: Preference variability and genetic diversity: Prosocial traits separately

	<i>Dependent variable: SD in ...</i>								
	Altruism			Positive reciprocity			Trust		
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)
Genetic diversity	-0.92** (0.43)	-11.6 (15.33)	-2.89 (17.54)	-0.30 (0.61)	-40.3* (23.91)	-10.9 (25.57)	0.019 (0.37)	-17.4 (13.97)	19.2 (12.74)
Genetic diversity sqr.		7.56 (10.95)	1.53 (12.60)		28.3* (16.80)	7.56 (18.20)		12.4 (9.97)	-13.9 (9.24)
Continent FE	No	No	Yes	No	No	Yes	No	No	Yes
Observations	74	74	74	74	74	74	74	74	74
R <sup>2</sup>	0.055	0.061	0.194	0.006	0.073	0.245	0.000	0.020	0.276

Notes. OLS estimates, robust standard errors in parentheses. \*  $p < 0.10$ , \*\*  $p < 0.05$ , \*\*\*  $p < 0.01$ .



### E.3 Diversity and Average Preferences: Robustness

While the main text analyzed the relationship between the level of a given preference and the genetic diversity of [Ashraf and Galor \(2013b\)](#), Table 24 presents regressions which utilize the composite temporal distance measure. Specifically, each column relates the level of a given preference to the temporal distance to Ethiopia (and its square). The results show that the non-linear relationships reported in the main text disappear entirely, even without continent fixed effects.

## F Definitions and Data Sources of Main Variables

### F.1 Explanatory Variables

**Fst and Nei genetic distance.** Genetic distance between contemporary populations, taken from [Spolaore and Wacziarg \(2009\)](#) and [Spolaore and Wacziarg \(2016\)](#), respectively.

**Linguistic distance.** Weighted linguistic distance between contemporary populations. Derived from the Ethnologue project data, taking into account all languages which are spoken by at least 5% of the population in a given country.

**Predicted migratory distance.** Predicted migratory distance between two countries' capitals, along a land-restricted way through five intermediate waypoints (one on each continent). Taken from [Ashraf and Galor \(2013b\)](#).

**HMI migratory distance.** Walking time between two countries' capitals in years, taking into account topographic, climatic, and terrain conditions, as well as human biological abilities. Data from [Özak \(2010\)](#).

### F.2 Covariates

**Proportion female.** Computed from the sociodemographic background data in the GPS.

**Religious fractionalization.** Index due to [Alesina et al. \(2003\)](#) capturing the probability that two randomly selected individuals from the same country will be from different religious / linguistic groups.

Table 24: Preferences and temporal distance to Ethiopia

	<i>Dependent variable: Average ...</i>											
	Risk taking			Prosociality			Patience			Neg. reciprocity		
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)
Temporal distance to Ethiopia	-0.091** (0.04)	0.025 (0.05)	0.13 (0.08)	0.019 (0.05)	-0.040 (0.09)	0.099 (0.13)	0.033 (0.03)	0.062 (0.07)	0.28** (0.11)	-0.032 (0.04)	-0.064 (0.06)	-0.0041 (0.10)
Fst genetic dist. to Ethiopia sq.		-0.19** (0.08)	-0.16** (0.08)		0.100 (0.12)	-0.092 (0.12)		-0.049 (0.11)	-0.32** (0.16)		0.053 (0.07)	-0.10 (0.08)
Continent FE	No	No	Yes	No	No	Yes	No	No	Yes	No	No	Yes
Observations	72	72	72	72	72	72	72	72	72	72	72	72
R <sup>2</sup>	0.089	0.155	0.301	0.003	0.014	0.251	0.008	0.010	0.367	0.013	0.019	0.189

Notes. OLS estimates, robust standard errors in parentheses. \*  $p < 0.10$ , \*\*  $p < 0.05$ , \*\*\*  $p < 0.01$ .

**Percentage of European descent.** Constructed from the “World Migration Matrix” of [Putterman and Weil \(2010\)](#).

**Contemporary national GDP per capita.** Average annual GDP per capita over the period 2001 – 2010, in 2005US\$. Source: World Bank Development Indicators.

**Democracy index.** Index that quantifies the extent of institutionalized democracy, as reported in the Polity IV dataset. Average from 2001 to 2010.

**Colonial relationship dummies.** Taken from the CEPII Geodist database at [http://www.cepii.fr/CEPII/en/bdd\\_modele/presentation.asp?id=6](http://www.cepii.fr/CEPII/en/bdd_modele/presentation.asp?id=6).

**Geodesic distance, contiguity, longitude, latitude, area** Taken from CEPII GeoDist database. The longitudinal distance between two countries is computed as

Longitudinal distance =  $\min\{|longitude_i - longitude_j|, 360 - |longitude_i - longitude_j|\}$

**Suitability for agriculture.** Index of the suitability of land for agriculture based on ecological indicators of climate suitability for cultivation, such as growing degree days and the ratio of actual to potential evapotranspiration, as well as ecological indicators of soil suitability for cultivation, such as soil carbon density and soil pH, taken from [Michalopoulos \(2012\)](#).

**Mean and standard deviation of elevation.** Mean elevation in km above sea, taken from [Ashraf and Galor \(2013b\)](#). Data originally based on geospatial elevation data reported by the G-ECON project ([Nordhaus, 2006](#)).

**Precipitation.** Average monthly precipitation of a country in mm per month, 1961-1990, taken from [Ashraf and Galor \(2013b\)](#). Data originally based on geospatial average monthly precipitation data for this period reported by the G-ECON project ([Nordhaus, 2006](#)).

**Temperature.** Average monthly temperature of a country in degree Celsius, 1961-1990, taken from [Ashraf and Galor \(2013b\)](#). Data originally based on geospatial average monthly temperature data for this period reported by the G-ECON project ([Nordhaus, 2006](#)).