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Genetic distance, cultural differences, and the formation of regional trade agreements^{*}

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Abstract: Genetic distance between countries' populations has been shown to proxy cross-country differences in cultures and preferences. In a panel of 176 countries from 1970 to 2014, we find that higher genetic distance between two countries decreases their probability of having a trade agreement, even when controlling for geographic distance and other controls. The impact of cultural differences proxied by genetic distance is persistent over time and economically significant: while increasing the geographic distance distance between two countries by 1% decreases the probability of a regional trade agreement by 1.6%, increasing their genetic distance by 1% decreases the probability by 0.9%.

JEL Classification Codes: F13; F14; F15; Z10

Keywords: trade agreements, trade policy, genetic distance, cultural differences

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1 Introduction

Negotiations of trade agreements are time-consuming and do not always reach an agreement. Understanding the determinants of successfully concluded agreements can help to identify drivers and potential pitfalls for future trade agreements. The formation of trade agreements may be difficult due to a lack of trust and communication difficulties arising from ethnic or cultural differences between potential members.¹ Differences in cultural norms and expectations about the behavior of the other party can lead to misunderstandings and negatively affect negotiations.² Individuals from different cultural backgrounds differ in their level of trust, differ in how they act when confronting social dilemma such as, e.g., prisoner's dilemma or contributing to public goods, and have differing degrees of willingness to punish others when they free-ride.³ Establishing trust, escaping the prisoner's dilemma of strategic trade policy and how to deal with free riders are well-known key problems of international trade negotiations.⁴ More specifically, negotiation and bargaining styles differ across countries, and cultural

 $^{^{1}}$ Knack and Keefer (1997) find that countries which are ethnically more homogeneous have higher levels of trust.

 $^{^{2}}$ Zou et al. (2009) show that individuals' behavior depends on what they perceive to be the consensus or "common sense" view within their culture; for similar arguments see also Roth et al. (1991). Henrich (2000) and Henrich et al. (2001) show that behavior in the ultimatum game depends on the culture of the experiment subjects.

³Buchan et al. (2002) find that Japanese experiment subjects have a lower level of trust than their American counterparts. Gächter et al. (2010) and Herrmann et al. (2008) find significant differences in the willingness to punish non-cooperative players in experiments in different cultural backgrounds. These are not isolated findings: cross-cultural differences in behavior in trust games are corroborated in a metaanalysis by Johnson and Mislin (2011).

⁴ Brander (1986) is probably the first one to characterize trade negotiations as an attempt to escape the prisoner's dilemma of unilateral strategic trade policy.

differences are more pronounced in bargaining settings.⁵ Trade negotiations are particularly affected by cultural differences as they involve infrequent, high stakes interactions between often changing high-level politicians or bureaucrats where establishing trust and a common understanding may be difficult. Cultural differences may also reflect different preferences for policy outcomes in the countries' populations, making it harder for negotiators to reach a consensus and hence successfully conclude a trade agreement.

These cultural differences and associated costs are difficult to measure, particularly at a bilateral level between a large set of countries. We propose to use Spolaore and Wacziarg's (2009) genetic distance, a measure of how genetically related populations are in terms of their last common ancestor, as a readily available proxy for communication and negotiation costs arising from differences in culture and norms as a determinant of trade agreements. Anthropologic studies have shown that genetic distance can help to identify common cultural groups, in addition to geographic distance and shared language, two measures of cultural difference routinely used in the trade literature.⁶ Similarly, Desmet et al. (2011) and find that genetic distance correlates well with measures of cultural distances based on survey responses

⁵Roth et al. (1991) find that while subjects in different countries exhibit similar behavior in experimental markets, individual bargaining behavior varies considerably across countries. Gelfand et al. (2015) find that strategies which lead to successful negotiations in the United States are detrimental in Egypt. For a literature survey on cultural differences and negotiations, see Gelfand et al. (2012).

⁶ For example, cross-cultural differences such as norms around kinship correlate with human genetic diversity, see Jones (2003). For a general introduction to the relationship between human genetic and cultural diversity, see Stone and Lurquin (2007).

We use a sample of 176 countries and 45 years and a battery of control variables to examine the role of genetic distance in establishing RTAs across countries. Our results show that genetic distance has a significant negative and economically meaningful influence on the probability of forming an RTA, even after controlling for geographic distance, linguistic distance, religious distance, and other control variables used in the literature. Contrary to other measures of cultural differences, genetic distance is a readily available proxy variable for a large set of country pairs, so it can easily be included within the set of standard regressors used to model RTAs.

It goes without saying that our results should not and cannot be construed as to imply that countries should not engage in trade negotiations with countries which have a larger genetic distance, nor do we argue for a biological determinism of trade policy. Instead, insofar as genetic distance proxies cultural differences, our results highlight the potential usefulness of heightened awareness of possible misunderstandings which may arise during trade negotiations due to cultural differences.

We contribute to the literature which has documented the effect of cultural differences proxied by genetic distance on economic outcomes. The seminal contribution is Spolaore and Wacziarg (2009) who show that genetic distance between countries can explain cross-country differences in income per capita. They focus on a population's cultural distance to the population which represents the current technological frontier, which they proxy by the US. The larger these cultural differences, proxied by genetic distance, the more difficult the diffusion and adaptation of the frontier technology. In our paper, we focus on genetic distance between any two countries, not to the US, as trade negotiations typically only occur between potential member states of a trade agreement, and do not typically involve the US.

Our interpretation of genetic distance as a proxy for unobserved barriers to economic integration such as cultural heterogeneity is in line with a broader literature which links ethnic diversity measured by genetic distance and cultural heterogeneity.⁷ Desmet et al. (2011) and document that genetic distance allows to improve predictions of similarity of individuals' survey responses in comparison when only using geographic and linguistic information. They find that genetic distance predicts the dissolution of deeper agreements such as the endogenous formation of nation states from culturally diverse regions. We find that genetic distance affects economic integration which falls short of creating a joint nation state. RTAs can create aggregate welfare gains when signatory parties act cooperatively. To establish an RTA and reap its welfare gains, signatories must overcome differences in norms and preferences as well as coordinate differences in socio-economic policies.

Guiso et al. (2009) also use genetic distance as a proxy for cultural difference. They show that respondents in the Eurobarometer survey trust individuals less who have a higher genetic distance. This lower trust at the individual level is correlated with lower trade and portfolio investment between countries with larger genetic distance. Bove and

⁷Ahlerup and Olsson (2012) provide a recent overview of this literature; see also Ashraf and Galor (2013).

Gokmen (2018) replicate Spolaore and Wacziarg (2009) and show that the impact of genetic distance on income differences between countries is stable over time. We find that genetic distance has a stable and significant impact on RTA formation over more than four decades. Davies and Guillin (2014) use genetic distance as a proxy for communication barriers and find that US outbound services FDI is correlated between countries with low genetic distance. Leblang (2010) does not find a significant effect of genetic distance on bilateral FDI and portfolio investment in a single cross-section of countries.⁸ Finally, Chaudhry and Ikram (2015) find that long-run GDP growth is correlated between countries with lower genetic distance.

Our paper also contributes to the literature on the determinants of RTAs, see, e.g., Magee (2003), Baier and Bergstrand (2004), Chen and Joshi (2010), and Egger et al. (2011).⁹ None of these papers studies the impact of genetic distance.¹⁰

We also, for the first time, point out the importance of considering the correlation in the error structure for correct inference when estimating regressions which seek to identify the determinants of RTAs. By construction, unobserved country-specific factors which

⁸ FDI data are often missing for many country pairs, restricting Leblang's (2010) analysis to 28 FDIreceiving countries. Our sample comprises more countries and over 40 years.

⁹ All the cited papers use probit models in their analysis. Besides probit models, a plethora of methods have been used to analyse the determinants of RTAs: Egger and Larch (2008) use spatial econometric probit models and Márquez-Ramos et al. (2011) use ordered probit models to explain the drivers of different levels of trade integration between countries. Kohl and Brouwer (2014) use a clustering algorithm to identify "natural" trade integration blocs and estimate the impact of determinants of these blocs using a probit model.

¹⁰ The single exception is Martin et al. (2012) who use genetic distance in one specification for a crosssectional regression for the year 2000. Using panel data, we can analyse the impact of genetic distance while controlling for time-varying country-specific unobserved drivers of trade policy.

determine whether countries sign an RTA are correlated across country pairs. We propose using two-way clustered standard errors by Cameron et al. (2011) as an easy solution to this problem. The literature on RTA determinants has neglected this correlation so far and hence overstates the precision of estimated coefficients.¹¹

The remainder of the paper is organized as follows: Section 2 describes our data. Section 3 describes our empirical strategy and main results. Section 4 discusses several robustness checks. Section 5 concludes.

2 Data

RTA and genetic distance

Our dependent variable is RTA_{ijt} , a binary variable which takes the value 1 if there is a customs union or free trade agreement between two countries, and 0 otherwise.¹² We use a panel from 1970 to 2014, purely driven by data restrictions.¹³

We use the genetic distance measure between populations of countries introduced by Spolaore and Wacziarg (2009).¹⁴ Genetic distance measures rely on the fact that during

¹¹ Baier and Bergstrand (2004) discuss correlation of errors across countries within an RTA (e.g., across EU member countries) but do not consider the more general case of correlation of a given country's trade policy across all its potential partner countries which we consider. The potential correlation within an RTA of Baier and Bergstrand (2004) is modelled on the value of the dependent variable, potentially introducing endogeneity bias in the calculation of the standard errors. Our approach avoids this.

¹² We use Mario Larch's Regional Trade Agreements Database from Egger and Larch (2008):

http://www.ewf.uni-bayreuth.de/en/research/RTA-data/index.html

¹³ Variables including GDP and polity factors are not available for many countries before 1970.

¹⁴ The remaining paragraph is a succinct summary of Spolaore and Wacziarg (2009). We use the updated genetic distance data from Spolaore and Wacziarg (2018): https://sites.tufts.edu/enricospolaore/category/personal-webpage/

human evolution, random variations in the form of genes (so-called alleles) occur over time. Geneticists use the difference in the frequency of alleles to measure genetic distance between populations. It is important to stress that these measures only focus on random drift variation in genes, i.e., neutral variations which do not give any discernible advantage for evolutionary selection. Geneticists can use these variations to calculate the proximate time elapsed since two populations became separated and hence the number of genealogical steps one must take to reach the last common ancestor population. Spolaore and Wacziarg (2009) use F_{ST} , a measure of genetic distance, for 42 ethnic groups by Cavalli-Sforza et al. (1994). ${\cal F}_{ST}$ is a normalized difference in allele frequencies in two populations: the larger F_{ST} , the more different the distribution of alleles, and hence the more generations one has to go back in time to reach the last common ancestor, and hence the larger the genetic distance. As countries typically are populated by multiple ethnic groups, Spolaore and Wacziarg (2009) combine the genetic distances with country-level ethnic data from Alesina et al. (2003) to measure the genetic distances between countries, weighted by the ethnic composition of countries' populations. When country i consists of K ethnic groups and country j consists of M ethnic groups, genetic distance between i and j is calculated as:

$$Genetic \ Distance_{ij} = \sum_{k=1}^{K} \sum_{l=1}^{L} (s_{ik} \times s_{jl} \times d_{kl}), \tag{1}$$

where s_{ik} is the share of ethnic group k in country i, s_{jl} is the share of ethnic group l in country j and d_{kl} is the F_{ST} genetic distance between ethnic groups k and l. It can be interpreted as the expected genetic distance between two individuals picked at random from countries i and j and therefore is a measure of the average genetic distance between two countries.

Control variables

Standard gravity-type regressors have been shown to be important drivers of RTA formation. Time-invariant variables such as geographic distance between countries, territorial contiguity and colonizer-colony relationship are collected from Centre d'Études Prospectives et d'Informations Internationales (CEPII), see Mayer and Zignago (2011). Population and GDP data are from the World Development Indicators from the World Bank. Following Egger et al. (2011), we use the absolute difference in GDP per capita to proxy endowment differences such as the difference in the capital labor ratio which is highly correlated with GDP per capita. This measure controls for Heckscher-Ohlin-type arguments which may influence the formation of trade agreements between countries with different endowments.

Spolaore and Wacziarg (2016)b show that genetic distance is correlated with measures of linguistic and religious distance between countries. One reason for this may be that genetic distance captures differences in language and religion due to differences in the composition of countries' populations which are not captured by simple country-pair dummy variables like common language typically used in empirical international trade. For their linguistic distance measure, Spolaore and Wacziarg (2016)b use classifications of languages into language trees which count the number of common nodes in such a language tree. For example, both French and Italian are part of the Indo-European -Italic – Romance - Italo-Western branch of languages, i.e., they share four common nodes. Similar to genetic distance, these linguistic distances can be weighted with the respective population share of a language in a given country. Similar measures can be constructed between religions. For example, Christianity, Islam, and Judaism can be classified as "Near-Eastern Monotheistic Religions". Again, these religious distance measures can then be weighted according to the share of a religion within a given country.¹⁵ To control for the effects of linguistic and religious similarity, we therefore also control for both linguistic and religious distance.¹⁶

Differences in countries' political systems have been shown to be important drivers of the timing of RTA formation, see Bergstrand et al. (2016). We therefore include the difference in the political freedom between countries i and j at time t (*Dif Polity_{ijt}*) using the political freedom index by Marshall et al. (2016). We also use their indices to include measures of the difference in political regimes (democracy and autocracy scores, *Dif Democracy_{ijt}* and *Dif Auto_{ijt}*, respectively), the difference in party competition in

¹⁵ For further details on the calculation of these measures, see Appendix A.2. Spolaore and Wacziarg (2016)b also show that genetic distance is correlated with a cultural difference measure based on question-specific distances from the World Valued Survey (WVS) for 98 questions. Contrary to genetic distance which is available for 180 countries, this measure is only available for 74 countries (70 in our sample). Also, as we interpret genetic distance as a proxy for cultural differences, we do not use this cultural difference measure to avoid multicollinearity issues.

¹⁶ In unreported regressions, we used the standard common language dummy instead of religious and linguistic distance. Results remain unchanged.

parliament (*Dif Parcomp*_{ijt}), the difference in regulation of political participation (DIF $Parreg_{ijt}$) and in the political competition in government (*Dif Polcomp*_{ijt}).¹⁷

Giuliano et al. (2014) argue that in addition to geographic distance, geographic features such as terrain ruggedness which determined transportation costs in the distant past have also led to separations of populations and hence to genetic distance. At the same time, the probability of forming a trade agreement might still be lower due to high transportation costs. Our country fixed effects control for the overall ruggedness of a country's terrain but do not control for the bilateral transportation cost caused by ruggedness. We therefore interact the origin and destination countries' ruggedness to proxy for these historic transportation costs. We use the ruggedness measure by Nunn and Puga (2012).

3 Empirical specification and results

We follow Chen and Joshi (2010) and estimate a linear probability model of RTA formation. Linear probability models are preferable to limited dependent variable models as they are easy to interpret and do not suffer from downward biased coefficient estimates in the presence of uncorrelated unobserved heterogeneity.¹⁸ They also allow us

 $^{^{\}rm 17}\,{\rm We}$ describe the construction of the variables used in

Table A5. Variable Definitions in the Appendix.

¹⁸Logit and probit model coefficients are biased if there are omitted variables determining RTA formation, even if these are uncorrelated with the regressors, see Mood (2010). Linear probability models do not suffer from this problem. They also allow us to include more than 15000 dummies (30800 country pairs in 45 years), circumventing the large computational burden of non-linear probit models with a high number

to control for time-varying unobserved variables for each origin and destination country by including country-specific dummy variables. Given the dyadic nature of the data set, we expect correlation in the error term between all observations involving country i or j as a country's general attitude towards trade policy and RTAs and other countryspecific unobserved factors may drive the overall willingness of a country to sign RTAs with all bilateral partners. This is corroborated by the large degree of correlation for a given exporter i and a given importer j of trade flows, see, e.g., Spolaore and Wacziarg (2009) and Egger and Tarlea (2015). We therefore use two-way clustered standard errors using the method from Cameron et al. (2011).¹⁹ We estimate the following model:

$$RTA_{ijt} = \beta_1 \ln(Genetic \ Distance)_{ij} + \beta_2 \ln(Geographic \ Distance)_{ij} + \mathbf{x}'_{ijt}\boldsymbol{\beta} + \mu_{it} + \eta_{jt} + \varepsilon_{ijt}$$

$$(2)$$

where RTA_{ijt} is a binary variable indicating if there is a regional trade agreement between country *i* and country *j* in year *t*. $\ln(Genetic Distance)_{ij}$ and $\ln(Geographic Distance)_{ij}$ are the logarithm of genetic and geographic distance, respectively. \mathbf{x}_{ijt} includes bilateral control variables which may be correlated with genetic distance. μ_{jt} and η_{jt} represent country-year fixed effects that control for

of dummies. We use the Stata command reghdfe by Guimarães and Portugal (2010) which allows efficient estimation of linear regression models with high-dimensional fixed effects. However, our main results are robust to using a Probit model, see Table A1 in the appendix.

¹⁹ Two-way clustering also controls for the fact that $\varepsilon_{ijt} = \varepsilon_{jit}$, $\forall i, j$, in our application, as $RTA_{ijt} = RTA_{jit}$, $\forall i, j$, see Section A.1 in the Appendix. Also note that two-way clustering is strictly more general than one-way clustering at the country-pair level. Using the latter would lead to too small standard errors in the presence of two-way clustering, see Cameron et al. (2011).

unobserved country-level determinants of RTAs which may vary over time, effectively controlling for overall changes in countries' trade policy as well as country-specific business cycle effects which may trigger RTA negotiations.²⁰ The country-year fixed effects also control for the interdependence of trade policy decisions as a country's willingness to sign an RTA with another country depends on the number of RTAs it has already signed with other countries. Baier et al. (2014) measure this interdependence of trade policy using so-called "multilateral FTA terms" which measure the number of RTAs country *i* has signed with another country $k \neq j$ at time *t*. We capture these terms by the μ_{it} and η_{jt} fixed effects.²¹ We start our sample in 1970 to avoid our fixed effects to perfectly predict the variation of RTA_{ijt} .²²

Table 1 Inserts Here

Table 1 reports the estimates of Equation (2). In column (1), we include (log) genetic distance as well as country-year fixed effects, but no controls. Genetic distance has a significant negative impact on RTA formation. As genetic distance is highly correlated with standard regressors used in the literature (bilateral geographic distance, colonial relationship, and contiguity), we explore whether this result holds up. In column (2), we

 $[\]varepsilon_{ij} = \varepsilon_{ji}, \forall i, j$ also implies that $\mu_{it} = \eta_{it}, \forall i$ and hence only one set of country-specific dummy variables are needed, not the origin and destination-specific dummies as used, e.g., in trade gravity models. ²¹ Baier et al. (2014) approximate these multilateral resistance terms by GDP-weighted averages of bilateral distances with trade partners. These terms also control for a country's remoteness, i.e., for its average trade costs across all its trade partners, similar to the approximation proposed by Baier and Bergstrand (2009) in a trade gravity context. Our fixed effects control for these terms, circumventing the need to construct proxy indices.

²² The number of observations is only 40 in 1960 when including all variables. It increases to 1274 in 1970.

only include (log) geographic distance, and, as expected, we find a significant negative effect of geographic distance on RTA formation, of a similar magnitude of the effect we found for genetic distance. The size of the coefficient is also in the same ballpark as results, e.g., by Bergstrand et al. (2016). In column (3), we include both distance measures simultaneously. Both genetic and geographic distance have a significant and negative impact on RTA formation: if genetic distance between two countries increases by one percent, the probability of an RTA between them decreases by 0.06 percentage points²³, whereas the same increase in geographic distance decreases the probability of an RTA by 0.10 percentage points. This effect of genetic distance is economically meaningful given that the mean of RTA_{ijt} across all years is 0.0657. Then, the probability of an RTA decreases by (0.06/100)/0.0657 = 0.009, i.e., about one percent. We can compare this to the effect of geographic distance: if geographic distance increases by one percent, the probability of an RTA decreases by (0.104/100)/0.0657 = 1.6%. Hence, genetic distance has a dampening effect on RTA formation of about half the magnitude of the commonly accepted effect of geographic distance. The effect of genetic distance remains stable when including the measures of linguistic and religious distance in column (4) which are correlated with genetic distance. Bergstrand et al. (2016) stress the importance of political factors for RTA formation. In column (5), we follow their strategy and include several measures for the difference in the political systems of the

²³ If genetic distance increases by one percent, the probability for an RTA increases by $\beta_1/100$ units, i.e., $\frac{\beta_1}{100} \times 100 = \beta_1 = -0.06$ percentage points.

two countries. The coefficient of genetic distance remains basically unchanged. Finally, in column (6), we follow Baier and Bergstrand (2004), Egger et al. (2011) and Baier et al. (2014) and include a measure for market size, the sum of both countries' GDP, $SUM \ GDP_{ijt}$, as well as proxies for differences in endowments, the difference in the levels of GDP and GDP per capita, $DIF \ GDP_{ijt}$ and $DIF \ GDP \ Per \ Capita_{ijt}$. These proxy for motives for RTAs along the arguments for trade in monopolistic competition and Heckscher-Ohlin-type models, respectively. Our estimated coefficient of genetic distance remains nearly unchanged.

Summing up, genetic distance reduces the probability of RTA formation in a large panel of countries, even when controlling for a wide variety of variables typically used in the literature. It therefore seems to be a simple and readily available catch-all proxy for coordination costs arising from cultural differences which have a negative impact on RTA formation.

Geographic distance has been shown to have a stable negative impact on trade flows over time, see Disdier and Head (2008).²⁴ As trade flows and RTA formation are driven by common factors, it seems natural to explore whether genetic and geographic distance have a constant effect on RTA formation over time or whether there are trends in their

²⁴ The persistent negative effect of distance on bilateral trade flows has been referred to as the distance puzzle. It has spurred a large literature which tries to explain this fact, e.g., Lin and Sim (2012), Yotov (2012), and Larch et al. (2016). None of these papers investigates the impact of genetic distance over time on bilateral trade flows.

effects. To do so, we estimate a series of cross-sectional regressions for every year t in our sample using the following specification:

$$RTA_{ij} = \beta_1 \ln(Genetic \ Distance)_{ij} + \beta_2 \ln(Geographic \ Distance)_{ij} + \mathbf{x}'_{ij}\boldsymbol{\beta} + \mu_i + \ \eta_j + \varepsilon_{ij}$$
(3)

Table 2 Inserts Here

 μ_i and η_j are country fixed effects for the paired countries. Table 2 presents the regression results for selected years. Results are similar to our panel regressions: genetic distance negatively affects RTA formation in all columns except for the regression using data from 1970 in column (1). For the remaining years the effect remains constant. Geographic distance has a negative effect on RTA formation which increases for the years 2005, 2010, and 2014. The influence of both religious and linguistic distance, conditional on genetic distance and geographic distance is mostly not significant, in line with our panel results. Colonial status loses its significance over time, in line with the deterioration in trade between former colonies over time as documented by Head et al. (2010). This effect seems to spill over into RTA formation as well. The measures for the differences in political systems have a significant impact on RTA formation, but not consistently over time. Similarly, the measures for market size and endowments, as predicted by theories of economic drivers of RTA formation such as Baier and

Bergstrand (2004), do not consistently explain RTA formation, except for the difference in GDP per capita.²⁵

In Table 2, the number of observations increases over time which may drive results. We therefore re-estimate Table 2 using only the observations in 1970 throughout the whole sample period. We present these results in Table A2 in the Appendix. Results remain similar. Importantly, genetic distance continues to exert a negative impact on RTA formation.

In addition to the years presented in Table 2, we estimate Equation (3) for all years in our sample beginning in 1970. We plot the estimated coefficients for each year for both (log) genetic and (log) geographic distance in Figure 1.

Figure 1 Inserts Here

Both geographic and genetic distance have a persistent and negative impact on RTA formation, except for 1970, probably due to the relatively small number of RTAs in 1970, see Figure 2. Interestingly, until 1990, we cannot reject the null hypothesis that the impact of genetic distance on RTA formation is as large as the impact of geographic distance, the measure of distance typically used in the literature. With the end of the Cold War, the negative impact of geographic distance becomes stronger. Genetic

²⁵ We also estimate a probit model equivalent to the linear probability model from Equation (3). We report results in Table 3. in the Appendix. Estimates are qualitatively similar. Note that the difference in sample size compared to Table 2 stems from the fact that many observations must be dropped to avoid a perfect predictor problem for the probit estimator. The number of observations increases over time which may drive results. We therefore re-estimate Table 2 using only the observations in 1970 throughout the whole sample period. We present these results in Table A2 in the Appendix. Results remain similar. Importantly, genetic distance continues to exert a negative impact on RTA formation.

distance also matters more, but to a lesser extent. Overall, cultural differences and communication or negotiation costs proxied by genetic distance seem to act as a significant and economically important barrier to RTA formation.

4 Robustness Checks

In the following, we probe our results for robustness across a battery of specifications, subsamples, and different potential omitted variables. We present results of these robustness checks for our panel regressions in Table 3. For convenience, column (1) reproduces column (6) of Table 1, our most stringent specification so far. We have used the logarithm of genetic distance to mimic the specification typically used in the literature for geographic distance. In our data, 30 country pairs have a genetic distance of 0 and hence these observations are excluded from the sample when taking the log of genetic distance.²⁶ We therefore include the level of genetic distance in column (2) to include these observations. We again find a significant and negative impact of genetic distance on RTA formation.

Differences in legal origin of countries reduce the amount of trade between countries, see, e.g., Felbermayr and Toubal (2010). Trade agreements may therefore be particularly

²⁶ There are 15400 distinct country pairs (176 countries) in our sample and 30 pairs are with zero genetic distance. Among those, 6 are between European countries: Belgium, Iceland, Ireland, and the Netherlands, i.e., $4 \times 3/2$ distinct pairs). Observations with zero genetic distance account for 0.2% of all observations in the panel for the world sample and 18% of all observations in the Europe 22 sample we use in columns (5) and (6).

important for countries with different legal origins to overcome these additional trade costs, increasing the likelihood of an RTA. At the same time, trade negotiations may be particularly difficult between countries with different legal systems.²⁷ Baier and Bergstrand (2004) do not find evidence that common legal origin matters for RTA formation, but it could be that our genetic distance measure picks up this variation and leads us to attribute the effect of difference in legal systems to genetic distance. We therefore use the La Porta et al. (1998) measure of legal origin and define a binary variable *Common Legal Origin_{ij}* which is 1 if countries *i* and *j* share the same legal origin, and 0 otherwise. A drawback of this measure is that it is only available for 49 countries, reducing our sample considerably. Genetic distance, both in logs and levels, still has a significant negative effect on RTA formation, see columns (3) and (4).

Giuliano et al. (2014) argue that geographic features which determined transportation costs in the distant past have also led to separations of populations and hence to genetic distance. Indeed, geographic distance highly correlates with genetic distance.²⁸ In their analysis of 22 European countries, they find that genetic distance does not exert a significant effect on trade flows once one controls for geographic distance. Genetic

²⁷ During the stalled negotiations for a potential trade agreement between the European Union and the United States, a commonly repeated argument was that differences in legal philosophies in consumer protection law (precautionary principle in the EU versus risk assessment and cost-benefit principles in the US) made an agreement difficult to reach, see Bergkamp and Kogan (2013).

 $^{^{28}}$ The correlation between genetic distance and geographic distance in levels across all years is 0.542 in our sample. In logarithms, their correlation is 0.600.

distance is lower within Europe than in our worldwide sample of 176 countries.²⁹ In column (5), we use the same 22 countries as Giuliano et al. (2014). Our results are consistent with their results for trade flows: genetic distance does not affect RTA formation within Europe. This is also confirmed when controlling for common legal origin, see column (6). Hence our results indicate that genetic distance is important for RTA formation between countries with higher genetic distance.

Our sample from 1970 to 2014 includes the end of the Cold War and the collapse of the Soviet Union (USSR). These events have significantly changed the geopolitical environment in which trade agreement negotiations take place: Gowa and Mansfield (1993) argue that this shift from a bipolar to a multipolar world affects the formation (and dissolution) of trade agreements. This shift is also clearly visible in the number of RTAs in place which has picked up after the dissolution of the USSR in 1991, see Figure 2. Relatedly, the countries which emerged from the former USSR increase our sample and results may be driven by these new countries. We therefore rerun our regressions after excluding all former Soviet Union countries.³⁰ Accordingly, Figure A1 in the Appendix redraws Figure 1. Still, genetic distance remains significant throughout the sample period, with the exception from 1970 to 1972. For most of the sample period, we cannot reject the null hypothesis that genetic distance has a similar impact as geographic

²⁹ The average genetic distance between the countries in Giuliano et al. (2014)'s sample is 0.00502 (sd. 0.00421), whereas in our full sample it is 0.03692 (sd. 0.01854). See Table A8 in the Appendix.
³⁰ The list of excluded countries is presented in Table A9 in the Appendix.

distance on RTA formation, strengthening our baseline results. Only for the last ten years of our sample, geographic distance has a larger effect than genetic distance, but genetic distance remains exerting a significant negative impact on RTA formation. Table A3 presents the cross-sectional estimates underlying Figure A1, i.e., re-estimates Table 2 on a smaller sample by excluding former USSR countries. Results remain similar.

A history of military conflicts can motivate countries to deepen trade integration between them, an argument particularly applied to the European integration process, see Martin et al. (2012). Also, military conflicts lead to lower levels of trust between countries, negatively affecting trade, see Guiso et al. (2009). At the same time, countries with lower genetic distance have a higher likelihood to engage in wars as they share similar preferences and compete for similar rival goods, see Spolaore and Wacziarg (2016)a, leading to a potential omitted variable bias. We measure the experience of conflict and war related events by a series of variables³¹: the total duration of previous wars between two countries, measured in days, $(WAR \ Duration_{ij})$ ³² the recentness of the latest war between the two countries, $(WAR \ Recentness_{ijt})$, measured by a dummy variable which is 1 when the two countries have experienced wars in the last 20 years 0 otherwise, the frequency between 1870 and 1945 and of wars $(WAR \ Freq \ (pre \ 1945)_{ij})$, the existence of a military alliance between the two countries

 $^{^{31}}$ We describe the construction of the variables used in Table A5 in the Appendix.

 $^{^{32}}$ Data are from Kreutz (2010).

 $(Military Alliance Relationship_{ij})^{33}$, and the bilateral correlation in UN votes $(UN \ Vote \ Correlation_{ij})^{34}$ as a measure of implicit political alliance. We present results of these regressions in Table A4. Note that due to data availability, these regressions are run on smaller samples than our baseline results. Geopolitical motives are drivers behind RTA formation, as both military alliance and UN vote correlation have significant and positive effects for most years. Interestingly, a common history of war between countries does not have a stable impact. Importantly, higher genetic distance remains to have a significant and negative impact on RTA formation. It appears as an economically important driver of the formation of regional trade agreements of similar magnitude as the commonly used geographic distance. It therefore should be included as a simple proxy variable for difficult to observe cultural differences and communication costs in studies of RTA formation.

5 Conclusion

Negotiations of trade agreements are often time-consuming and do not always reach an agreement. Understanding the determinants of successfully concluded regional trade agreements can help to identify drivers and potential pitfalls for future trade agreements. This paper examines the role of genetic distance between the populations

³³ Data of military conflicts and military alliance are taken from the Correlates of War project <u>http://www.correlatesofwar.org/</u>, see Gibler (2009) and Maoz et al. (2018).

 $^{^{34}\,\}mathrm{Data}$ are from Voeten et al. (2009).

of countries on RTA formation. Genetic distance measures how genetically related to populations are in terms of their last common ancestor. It is a readily available proxy for communication costs arising from differences in culture and preferences. Trade negotiations are particularly affected by these costs as they involve infrequent, high stakes interactions between often changing high-level politicians or bureaucrats from different cultural backgrounds where establishing trust and a common understanding may be difficult. We find that country pairs with larger genetic distances between their populations have a lower probability of signing an RTA. This effect is stable over time, has increased in its importance since the end of the Cold War and is distinct from the impact of geographic distance on RTA formation. It is robust to controlling for other determinants of RTA formation typically used in the literature and holds across different subsamples. Our results are consistent with a larger literature which documents the impact of cultural differences proxied by genetic distance on economic outcomes. Our results should not be interpreted as evidence for genetic determinism of trade policy. Instead, our results document the usefulness of genetic distance as a readily available proxy for difficult to measure bilateral communication and negotiation costs due to cultural differences across countries. Trade policy makers who want to engage in trade negotiations should be aware of these differences to avoid the premature failure of negotiations of a mutually beneficial trade agreement.

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Figure 1. Coefficients of $\ln(Genetic \ Distance)_{ij}$ and $\ln(Geographic \ Distance)_{ij}$ (1970-2014)

Notes: Coefficients from cross-sectional OLS regressions based on Equation (3). Red and blue lines are the coefficients of genetic and geographic distance, respectively. The grey areas are the 95% critical interval for coefficients (1.96 times the standard error of the estimated regression coefficient).



Figure 2. Total Number of Country Pairs with RTAs, 1950-2014

Note: Graph depicts the total number of country pairs which are covered by an RTA (free trade agreement and/or customs union). Number of countries is N = 176, hence the total number of country pairs is $N \times (N-1) = 30800$.

	(1)	(2)	(3)	(4)	(5)	(6)
$Ln(Genetic \ Distance)_{ii}$	-0.115***		-0.060***	-0.063***	-0.066***	-0.063***
$Distance)_{ij}$	(0.008)		(0.008)	(0.010)	(0.010)	(0.010)
$Ln(Geographic \ Distance)_{ii}$		-0.137***	-0.104***	-0.105***	-0.116***	-0.137***
$En(Geographic Distance)_{ij}$		(0.009)	(0.008)	(0.012)	(0.014)	(0.016)
$Ln(Religious \ Distance)_{ii}$				-0.017	0.017	0.025
$En(neugious Distance)_{ij}$				(0.021)	(0.021)	(0.024)
$Ln(Linguistic \ Distance)_{ii}$				0.003	0.008	0.02
$Ln(Linguistic Distance)_{ij}$				(0.011)	(0.011)	(0.014)
Colonial Polation shin					-0.014	-0.006
Colonial $Relationship_{ij}$					(0.031)	(0.030)
Q+:					0.097^{***}	0.095***
$Contiguous_{ij}$					(0.029)	(0.030)
					-0.003	-0.005
$DIF \ Democracy_{ijt}$					(0.003)	(0.003)
					0.010**	0.008*
$DIF \ Auto_{ijt}$					(0.005)	(0.005)
					-0.008**	-0.005
$DIF \ Polity_{ijt}$					(0.004)	(0.004)
					-0.002	0.001
$DIF \ Parreg_{ijt}$					(0.004)	(0.004)
					-0.016**	-0.014**
$DIF \ Parcomp_{ijt}$					(0.007)	(0.007)
					0.011***	0.010***
$DIF \ Polcomp_{ijt}$						
					(0.003)	(0.003)
$Ruggedness_i imes Ruggedness_j$						-0.001
-						(0.002)
$DIF \ GDP_{ijt}$						-0.001
						(0.003)
$SUM \ GDP_{ijt}$						-0.013
						(0.010) -0.013***
DIF GDP Per Capita _{ijt}						
$Country imes Year \ Fixed \ Effect.$	s Yes	Yes	Yes	Yes	Yes	(0.004) Yes
$\frac{Country \times Tear Fixed Effect}{N}$	$\frac{s}{1383300}$	1336320	1336320	467550	367318	310692
$adj. R^2$	0.303	0.337	0.356	0.348	0.364	0.393

Table 1. OLS Panel Regression Coefficient Estimates (1970-2014)

Notes: Two-way cluster-robust standard errors clustered at the origin and destination country in parenthesis. * p < 0.1, ** p < 0.05, *** p < 0.01. Regressions are based on Equation (2).

	(1)	(2)	(3)	(4)	(5)	(6)	(7)
	1970	1975	1985	1990	2005	2010	2014
$Ln(Genetic \ Distance)_{ij}$	0.009	-0.065***	-0.045***	-0.037**	-0.083***	-0.075***	-0.067***
× • • • •	(0.009)	(0.018)	(0.017)	(0.017)	(0.016)	(0.017)	(0.019)
$Ln(Geographic \ Distance)_{ij}$	-0.072***	-0.110***	-0.087***	-0.088***	-0.182***	-0.199***	-0.171***
	(0.016)	(0.021)	(0.019)	(0.019)	(0.021)	(0.021)	(0.025)
$Ln(Religious \ Distance)_{ij}$	0.04	-0.006	0.002	0.012	0.058^{*}	0.027	-0.096*
ij	(0.036)	(0.034)	(0.036)	(0.034)	(0.032)	(0.039)	(0.055)
$Ln(Linguistic \ Distance)_{ij}$	0.000	0.035^{***}	0.036^{***}	-0.007	0.004	0.011	0.021
(1)	(0.011)	(0.013)	(0.013)	(0.026)	(0.023)	(0.013)	(0.020)
$Colonial \ Relationship_{ij}$	-0.003**	0.006	0.004	0.004	-0.005**	-0.004**	-0.005**
	(0.001)	(0.004)	(0.003)	(0.003)	(0.002)	(0.002)	(0.002)
$Contiguous_{ij}$	0.156	-0.069**	-0.049***	-0.075***	0.019	0.036	0.058
Sontrguous _{ij}	(0.101)	(0.030)	(0.013)	(0.015)	(0.043)	(0.044)	(0.055)
DIF Democracy _{ijt}	0.063	0.083^{*}	0.022	0.066	0.117^{**}	0.126^{***}	0.117^{**}
$Diff Democracy_{ijt}$	(0.045)	(0.044)	(0.037)	(0.043)	(0.045)	(0.045)	(0.047)
$DIF \ Auto_{ijt}$	-0.002	0.002	0.013**	-0.007	-0.004	-0.009	-0.017**
	(0.003)	(0.005)	(0.006)	(0.005)	(0.006)	(0.006)	(0.008)
$DIF Polity_{ijt}$	0.000	0.005	0.017^{**}	0.012^{*}	0.005	-0.004	-0.003
$g_{11} = 10 m g_{ijt}$	(0.004)	(0.006)	(0.007)	(0.006)	(0.006)	(0.008)	(0.008)
$DIF \ Parreg_{ijt}$	0.004	-0.006	-0.018***	-0.005	-0.003	-0.001	0.004
g_{ijt}	(0.003)	(0.005)	(0.006)	(0.005)	(0.005)	(0.005)	(0.007)
IF Danaomn	-0.012**	-0.002	-0.006	-0.007	0.012*	0.011	0.017^{*}
$DIF \ Parcomp_{ijt}$	(0.006)	(0.007)	(0.005)	(0.005)	(0.007)	(0.007)	(0.009)
	0.025**	-0.001	-0.043***	-0.009	-0.018*	-0.004	0.007
$DIF \ Polcomp_{ijt}$	(0.010)	(0.014)	(0.015)	(0.012)	(0.011)	(0.010)	(0.012)
	-0.010**	0.001	0.019***	0.011**	0.005	0.007	-0.004
$Ruggedness_i imes Ruggedness_j$	(0.005)	(0.006)	(0.006)	(0.005)	(0.005)	(0.005)	(0.006)
<i>ח</i> ת <i>ח</i> ת <i>ח</i> ת	-0.006	0.000	-0.002	0.001	-0.003	-0.002	0.000
$DIF \ GDP_{ijt}$	(0.005)	(0.005)	(0.004)	(0.004)	(0.005)	(0.004)	(0.005)
SUM CDP	0.031**	-0.006	-0.014	-0.016	-0.026	-0.01	-0.008
$SUM \ GDP_{ijt}$	(0.014)	(0.014)	(0.012)	(0.012)	(0.016)	(0.013)	(0.015)
NIE CDP Dom Comita	-0.008*	-0.011**	-0.012***	-0.018***	-0.017***	-0.014**	-0.009
$DIF \ GDP \ Per \ Capita_{ijt}$	(0.004)	(0.004)	(0.004)	(0.005)	(0.006)	(0.006)	(0.007)
$Country imes Year \ Fixed \ Effects$	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Ν	3883	4337	5636	6179	8863	8997	8735
$adj. R^2$	0.227	0.383	0.365	0.362	0.441	0.409	0.431

Table 2. Cross-section OLS Coefficient Estimates for Specific Years

Notes: Two-way cluster-robust standard errors in brackets. * p < 0.1, ** p < 0.05, *** p < 0.01. Regressions are based on Equation (3).

	(1)	(2)	(3)	(4)	(5)	(6)
	All	All	All	All	Europe 22	Europe 22
$Ln(Genetic \ Distance)_{ij}$	-0.063***		-0.044***		-0.006	-0.009
En(Generic Distance) _{ij}	(0.010)		(0.015)		(0.006)	(0.015)
Genetic $Distance_{ij}$		-1.832***		-1.574^{*}		
Genetic Distance _{ij}		(0.484)		(0.920)		
Common Legal Origin _{ii}			0.046^{**}	0.043^{**}		0.080***
$Common \ Degut \ Origin_{ij}$			(0.019)	(0.020)		(0.019)
$Ln(Religious \ Distance)_{ij}$	0.025	0.027	0.185^{***}	0.183***	-0.062	-0.061
$Ln(neuglous Distance)_{ij}$	(0.024)	(0.025)	(0.045)	(0.048)	(0.036)	(0.052)
$Ln(Linguistic \ Distance)_{ij}$	0.02	0.025^{*}	0.008	0.010	0.119	0.328
$En(Einguistic Distance)_{ij}$	(0.014)	(0.014)	(0.011)	(0.011)	(0.171)	(0.232)
$Ln(Geographic \ Distance)_{ii}$	-0.137***	-0.150***	0.000	-0.262***	0.003	0.027
$En(Geographic Distance)_{ij}$	(0.016)	(0.016)	(0.000)	(0.020)	(0.018)	(0.017)
$Ruggedness_i imes Ruggedness_i$	-0.001	-0.001	-0.021	-0.019	-0.007	-0.01
$maggeaness_i \land maggeaness_j$	(0.002)	(0.002)	(0.013)	(0.012)	(0.007)	(0.012)
Colonial Polationshin	-0.006	-0.014	-0.05	-0.080***	0.027	0.012
Colonial $Relationship_{ij}$	(0.030)	(0.033)	(0.030)	(0.029)	(0.027)	(0.088)
$Contiguous_{ij}$	0.095^{***}	0.101^{***}	-0.133*	-0.142*	0.027	0.005
$_{j}$	(0.030)	(0.031)	(0.076)	(0.072)	(0.018)	(0.027)
$DIF \ Democracy_{ijt}$	-0.005	-0.004	-0.006	-0.003	-0.043	-0.036
DIF $Democracy_{ijt}$	(0.003)	(0.004)	(0.009)	(0.009)	(0.033)	(0.045)
$DIF \ Auto_{ijt}$	0.008^{*}	0.011**	0.004	0.008	-0.019*	-0.018
DIF Auto _{ijt}	(0.005)	(0.005)	(0.011)	(0.011)	(0.011)	(0.011)
DIE Dolita	-0.005	-0.007*	-0.004	-0.008	0.033***	0.030***
$DIF \ Polity_{ijt}$	(0.004)	(0.004)	(0.008)	(0.008)	(0.008)	(0.008)
DIF Dannag	0.001	0.000	-0.002	-0.005	-0.043***	-0.028
$DIF \ Parreg_{ijt}$	(0.004)	(0.004)	(0.012)	(0.012)	(0.006)	(0.086)
$DIF \ Parcomp_{ijt}$	-0.014**	-0.017**	-0.005	-0.011	0.120***	0.084
$DII' I ar comp_{ijt}$	(0.007)	(0.007)	(0.018)	(0.018)	(0.035)	(0.122)
DIF Palaama	0.010***	0.011***	0.010**	0.012***	-0.012	0.000
$DIF \ Polcomp_{ijt}$	(0.003)	(0.003)	(0.004)	(0.004)	(0.032)	(0.000)
	-0.001	-0.001	0.001	-0.001	0.005	0.008
$DIF \ GDP_{ijt}$	(0.003)	(0.003)	(0.005)	(0.006)	(0.009)	(0.018)
SUM CDP	-0.013	-0.016	0.038	0.044	-0.050*	-0.076
$SUM \ GDP_{ijt}$	(0.010)	(0.011)	(0.028)	(0.029)	(0.028)	(0.064)
DIE CDD Dom Consister	-0.013***	-0.015***	-0.006	-0.009	-0.002	-0.011
$DIF \; GDP \; Per \; Capita_{ijt}$	(0.004)	(0.004)	(0.010)	(0.010)	(0.005)	(0.008)
$Country imes Year \ Fixed \ Effects$	Yes	Yes	Yes	Yes	Yes	Yes
N	310692	311463	41300	41480	4688	3285
$adj. R^2$	0.393	0.389	0.582	0.581	0.816	0.549

Table 3. OLS Panel Regression Coefficient Estimates (1970-2014): Robustness Checks

Notes: Two-way cluster-robust standard errors in brackets. * p < 0.1, ** p < 0.05, *** p < 0.01. Regressions are based on Equation (3).

Appendix

A.1 On Clustering Standard Errors

In our regression in both Equation (2) and (3), we use the two-way clustering proposed by Cameron, Gelbach and Miller (2011), treating the origin country i and the destination country j as two groups.

In the following, we show that two-way clustering also accounts for the fact that $\varepsilon_{ij} = \varepsilon_{ji}, \forall i, j$, i.e., that the residuals for a given country pair is identical for the two occurrences of a country pair within a data set. How do we know that the residuals are identical?

Note that $RTA_{ijt} = RTA_{jit}$, $\forall i, j$, i.e., the regional trade agreement dummy does not have a direction (this is different to, e.g., trade flows: exports from China to Germany are different from exports from Germany to China). Similarly, $X_{ij} = X_{ji}$, $\forall i, j$, i.e., our regressors also do not have a direction. It can be shown that this immediately implies that $\eta_i = \mu_j$, $\forall i, j$.³⁵

Having established that $\varepsilon_{ij} = \varepsilon_{ji}, \forall i, j$, we can proceed to establish that two-way clustering accounts for this perfect correlation of the residual for the two observations

³⁵ This is a well-known fact in the gravity literature, see, e.g., Head and Mayer (2014), p. 140: In a bilateral gravity equation of symmetric bilateral trade flows regressed on symmetric trade cost measures, it can be shown that estimated importer and exporter dummies are identical. The proof applies in our setting as we can interpret our dependent variable as a trade flow. This is not model dependent but is simply a fact of the properties of OLS. This in turn implies that $\varepsilon_{ij} = \varepsilon_{ji}, \forall i, j$, i.e., there is a (perfect) correlation between the error terms. We therefore cluster our standard errors to account for clustering within the country pair.

of the country pair. The variance-covariance estimator by Cameron, Gelbach and Miller (2011) assumes that

$$E(\varepsilon_{ijgh}\varepsilon_{lmg'h'}|\mathbf{x}_{ijgh},\mathbf{x}_{lmg'h'})=0, \text{unless } g=g' \text{ or } h=h',$$

where ij and lm refer to two country pairs (i.e., observations in the data set) and where we now indicate explicitly the two groups (i.e., clusters), in our application the first and the second country in a country pair, by g and h. If g = g' or h = h', i.e., within an origin or destination country, the estimator by Cameron, Gelbach and Miller (2011) allows for arbitrary correlation between the errors, including perfect correlation, i.e., $\varepsilon_{ij} = \varepsilon_{ji}$. We have shown above that $\varepsilon_{ij} = \varepsilon_{ji} \forall i, j$. This implies $E(\varepsilon_{ijgh}\varepsilon_{jig'h'}|\mathbf{x}_{ijgh},\mathbf{x}_{jig'h'}) = E(\varepsilon_{ijgh}\varepsilon_{ijgh}|\mathbf{x}_{ijgh},\mathbf{x}_{ijgh})$, and hence the estimator allows for arbitrary correlation between ε_{ijgh} and $\varepsilon_{jig'h'}$, including our case of perfect correlation.

It is helpful to illustrate with an example. Imagine we have a data set of RTAs between three countries A, B, and C. Hence, we have the following observations in our data set: AB, AC, BA, BC, CA, and CB. We have three groups indicated by g, which are the three groups where each country is the first country in the country pair, and three groups indicated by h, which are the three groups where each country is the second country in the country pair. Label the groups in the following way: g = 1 consists of country pairs AB and AC, g = 2 consists of BA and BC, and g = 3 of CA and CB. Similarly, label h = 1 the country pairs BA and CA, h = 2 consists of AB and CB, and h = 3 of AC and BC. Then, $E(\varepsilon_{AB12}\varepsilon_{BA21}|\mathbf{x}_{AB12},\mathbf{x}_{BA21}) = E(\varepsilon_{AB12}\varepsilon_{AB12}|\mathbf{x}_{AB12},\mathbf{x}_{AB12})$, and hence two-way clustering between origin and destination countries using the estimator of Cameron, Gelbach and Miller (2011) allows for the perfect correlation between ε_{AB12} and ε_{BA21} .

A.2 On the Calculation of Linguistic and Religious Distance

Spolaore and Wacziarg (2016)b use data from Fearon (2003) on linguistic trees to calculate the distance between languages in a similar way they calculate genetic distances. To continue the example from the main text, French is categorized as "Indo-European - Italic - Romance - Italo-Western - Western - Gallo-Iberian - Gallo-Romance -Gallo-Rhaetian - Oil – Francais". Similarly, Italian is classified as "Indo-European - Italic – Romance - Italo-Western - Italo-Dalmatian". Therefore, the number of common nodes between Italian and French is 4: Indo-European, Italic, Romance, Italo-Western. As with genetic distance, we use their weighted distance measure, i.e., the expected or weighted number of common nodes:

$$CN_{kl}^w = \sum_{i=1}^I \sum_{j=1}^J \bigl(s_{ik} \times s_{jl} \times c_{ij} \bigr)$$

where s_{ik} is the share of ethnic group k in country i, s_{jl} is the share of ethnic group lin country j and c_{kl} is the number of common nodes between languages of ethnic groups k and l. CN^{W} ranges from 0 to 15. We also follow the transformation of Spolaore and Wacziarg (2016)b and Fearon (2003) to adjust the value of CN_{kl}^{w} to 0 and 1 as

$$TLD_{kl}^w = \sqrt{\frac{15 - CN_{kl}^w}{15}},$$

where TLD_{kl}^{w} refers to tree-based linguistic distance.

The calculation of religious distance by Spolaore and Wacziarg (2016) b also uses a treebased method. The trees are consisting of broad classified religious groups. Then these broad group religious are further divided into finer classifications. The number of common nodes measure the similarity of the two religions, analogous to the calculation of linguistic distance.

Compared to using dummies like common official language or common religion, both the linguistic and religious distance measures provide more accurate information about the corresponding differences between two countries as they take into account the composition of the population.

A.3 Additional Figures and Tables

	(1)	(2)	(3)	(4)	(5)	(6)	(7)
	1970	1975	1985	1990	2005	2010	2014
In (Constic Distance)	0.173	-0.688***	-0.770**	-0.645*	-0.367***	-0.358***	-0.441***
$Ln(Genetic \ Distance)_{ij}$	(0.126)	(0.226)	(0.355)	(0.362)	(0.073)	(0.058)	(0.063)
Lu(Communitie Distance)	-1.473***	-3.057***	-2.552***	-3.003***	-1.783***	-1.363***	-1.137***
$Ln(Geographic \ Distance)_{ij}$	(0.174)	(0.322)	(0.310)	(0.320)	(0.093)	(0.062)	(0.062)
In (Paliniana Distance)	-0.424	0.312	0.860^{*}	1.234***	0.221	-0.447***	-0.854***
$Ln(Religious \ Distance)_{ij}$	(0.319)	(0.484)	(0.459)	(0.382)	(0.159)	(0.130)	(0.118)
In (Lin quistic Distance)	-1.411***	-1.704***	-4.116***	-1.612**	-0.121	-0.147	0.173
$Ln(Linguistic \ Distance)_{ij}$	(0.296)	(0.408)	(1.058)	(0.651)	(0.106)	(0.142)	(0.107)
Colonial Polationship	0.865***	-0.442	-0.780*	-0.602*	0.702^{***}	0.469^{**}	0.497^{***}
$Colonial \ Relationship_{ij}$	(0.315)	(0.441)	(0.403)	(0.363)	(0.261)	(0.194)	(0.191)
Contiguous	0.067	0.304	-1.546**	-1.222*	-0.351	0.239	0.437^{*}
$Contiguous_{ij}$	(0.394)	(0.857)	(0.762)	(0.633)	(0.247)	(0.218)	(0.230)
$DIF \ Democracy_{ijt}$	0.817**	0.375**	-0.141	-0.573***	-0.107***	-0.083***	-0.112***
DIF Democracy _{ijt}	(0.391)	(0.147)	(0.546)	(0.199)	(0.031)	(0.031)	(0.035)
DIE Asita	0.807**	0.409^{***}	-0.207	-0.144	0.008	-0.069***	-0.005
$DIF \ Auto_{ijt}$	(0.397)	(0.123)	(0.410)	(0.125)	(0.029)	(0.025)	(0.025)
DIE Dolito	-0.657*	-0.438***	-0.041	0.047	0.004	0.026	0.033
$DIF Polity_{ijt}$	(0.391)	(0.110)	(0.501)	(0.136)	(0.023)	(0.024)	(0.027)
$DIF \ Parreg_{ijt}$	0.275	1.050^{***}	1.242***	0.499^{***}	0.227^{***}	0.101^{***}	0.123***
$DII' I urreg_{ijt}$	(0.221)	(0.358)	(0.256)	(0.163)	(0.037)	(0.031)	(0.029)
$DIF \ Parcomp_{ijt}$	1.570^{***}	0.22	-2.470***	-0.423	-0.186**	0.055	0.041
$DII' I ar comp_{ijt}$	(0.309)	(0.323)	(0.487)	(0.471)	(0.084)	(0.080)	(0.084)
$DIF \ Polcomp_{ijt}$	-0.860***	-0.301	1.008***	0.614^{***}	0.054	0.005	-0.047
$DIP T bicomp_{ijt}$	(0.145)	(0.204)	(0.191)	(0.159)	(0.040)	(0.037)	(0.039)
$Ruggedness_i \times Ruggedness_i$	-0.175**	-0.442***	-0.141	-0.037	-0.068**	-0.021	-0.022
$nuggeaness_i \times nuggeaness_j$	(0.081)	(0.130)	(0.113)	(0.128)	(0.027)	(0.018)	(0.019)
$DIF \ GDP_{ijt}$	-0.198	-0.058	0.056	0.199	0.035	-0.009	-0.008
DIF GDI _{ijt}	(0.160)	(0.127)	(0.177)	(0.133)	(0.044)	(0.034)	(0.033)
$SUM \ GDP_{ijt}$	1.425^{***}	-0.488*	-0.612*	-0.863***	-0.584***	-0.149*	-0.074
SOM GDI _{ijt}	(0.353)	(0.290)	(0.354)	(0.279)	(0.114)	(0.077)	(0.076)
$DIF \ GDP \ Per \ Capita_{iit}$	-0.256***	-0.378**	-0.253*	-0.314**	-0.138***	-0.082***	-0.035
Dir GDI ICI Capita _{ijt}	(0.086)	(0.159)	(0.143)	(0.136)	(0.028)	(0.023)	(0.024)
Country Fixed Effects	Yes	Yes	Yes	Yes	Yes	Yes	Yes
N	1028	1172	1003	1347	6949	8018	7796
$Pseudo R^2$	0.5776	0.8143	0.8256	0.8305	0.6462	0.5461	0.5448

Table A1. Cross-section Probit Coefficient Estimates for Specific Years

Notes: Robust standard errors in brackets. * p < 0.1, ** p < 0.05, *** p < 0.01.

$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	$(7) \\ 2014 \\ -0.088^{***} \\ (0.028) \\ -0.085 \\ (0.069) \\ 0.017 \\ (0.018) \\ (0.018)$
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	-0.088*** (0.028) -0.085 (0.069) 0.017
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	(0.028) -0.085 (0.069) 0.017
(0.009) (0.019) (0.018) (0.018) (0.018) (0.018) (0.022)	-0.085 (0.069) 0.017
0.04 -0.012 0.007 0.026 0.074* 0.068	(0.069) 0.017
In(Coographia Distance)	0.017
$Ln(Geographic Distance)_{ij} (0.036) (0.039) (0.042) (0.044) (0.038) (0.042)$	
$Ln(Religious Distance)_{ii} = \begin{pmatrix} 0.000 & 0.039^{***} & 0.045^{***} & 0.001 & -0.002 & 0.007 \\ (0.010) & (0.010) & (0.010) & (0.010) & (0.010) \\ (0.010) & (0.010) & (0.010) & (0.010) & (0.010) \\ (0.010) & (0.010) & (0.010) & (0.010) & (0.010) \\ (0.010) & (0.010) & (0.010) & (0.010) & (0.010) \\ (0.010) & (0.010) & (0.010) & (0.010) & (0.010) \\ (0.010) & (0.010) & (0.010) & (0.010) & (0.010) \\ (0.010) & (0.010) & (0.010) & (0.010) & (0.010) \\ (0.010) & (0.010) & (0.010) & (0.010) & (0.010) \\ (0.010) & (0.010) & (0.010) & (0.010) & (0.010) \\ (0.010) & (0.010) & (0.010) & (0.010) & (0.010) & (0.010) \\ (0.010) & (0.010) & (0.010) & (0.010) & (0.010) & (0.010) & (0.010) & (0.010) \\ (0.010) & ($	(0.018)
(0.011) (0.013) (0.015) (0.029) (0.025) (0.012)	
$Ln(Linguistic Distance)_{ij} \qquad -0.072^{***} -0.117^{***} -0.110^{***} -0.118^{***} -0.188^{***} -0.214^{***}$	-0.181***
$(0.016) \qquad (0.022) \qquad (0.023) \qquad (0.026) \qquad (0.026)$	(0.032)
Colonial Relationship _{ij} $0.156 -0.057^{**} -0.043^{**} -0.069^{***} -0.003 0.027$	0.024
$(0.101) \qquad (0.025) \qquad (0.016) \qquad (0.021) \qquad (0.019) \qquad (0.024)$	(0.058)
Contiguous 0.063 0.084^* 0.033 0.06 0.139^{**} 0.123^{**}	0.139**
Contiguous_{ij} (0.045) (0.045) (0.042) (0.050) (0.056) (0.057)	(0.058)
-0.002 0.000 0.01 -0.014^{**} -0.004 -0.02	0.018
$DIF \ Democracy_{ijt} \qquad (0.003) \qquad (0.006) \qquad (0.008) \qquad (0.006) \qquad (0.006) \qquad (0.008) \qquad (0.008) \qquad (0.002)$	(0.017)
$DIF \ Auto_{ijt} \qquad 0.000 0.002 0.015^* 0.006 -0.001 -0.023 (0.000) (0.$	0.018
$(0.004) \qquad (0.006) \qquad (0.008) \qquad (0.006) \qquad (0.007) \qquad (0.019)$	(0.016)
$DIF \ Polity_{ijt} \qquad 0.004 \ -0.004 \ -0.016^{**} \ 0.001 \ -0.002 \ 0.013 $	-0.023
$(0.003) \qquad (0.005) \qquad (0.007) \qquad (0.005) \qquad (0.006) \qquad (0.017)$	(0.016)
$DIF \ Parreg_{ijt} \qquad \begin{array}{c} -0.012^{**} & -0.001 & -0.004 & -0.003 & 0.019^{*} & 0.007 \\ (0.002) & (0.002) & (0.002) & (0.002) & (0.002) \\ \end{array}$	0.023
$(0.006) \qquad (0.007) \qquad (0.006) \qquad (0.005) \qquad (0.009) \qquad (0.012)$	(0.016)
$DIF \ Parcomp_{ijt} \qquad 0.025^{**} \qquad 0.001 \qquad -0.040^{**} \qquad -0.001 \qquad -0.034^{**} \qquad -0.032^{*} \qquad (0.015) \qquad ($	0.000
$(0.010) \qquad (0.015) \qquad (0.017) \qquad (0.012) \qquad (0.015) \qquad (0.017)$	(0.018)
$DIF \ Polcomp_{iit} \qquad -0.010^{**} \qquad 0.001 \qquad 0.018^{***} \qquad 0.012^{**} \qquad 0.019^{**} \qquad 0.022^{**} $	-0.005
$(0.005) \qquad (0.006) \qquad (0.006) \qquad (0.005) \qquad (0.008) \qquad (0.009)$	(0.010)
$P_{uagedpass} \times P_{uagedpass} = -0.003^{**} = 0.006 = 0.007 = 0.007 = 0.004 = 0.004$	0.004
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	(0.006)
$DIF \ GDP_{iit} \qquad -0.006 -0.002 -0.002 0.000 -0.002 0.002 (0.002) (0.0$	0.006
$(0.005) \qquad (0.006) \qquad (0.005) \qquad (0.009) \qquad (0.009)$	(0.009)
$SUM \ GDP_{iit} \qquad 0.031^{**} -0.002 -0.005 -0.017 -0.002 -0.002 -0.0017 -0.002 -0.002 -0.0017 -0.002 -0.002 -0.0017 -0.002 -0.002 -0.0017 -0.002 -0.002 -0.0017 -0.002 -$	-0.007
$(0.014) \qquad (0.014) \qquad (0.014) \qquad (0.014) \qquad (0.021) \qquad (0.019)$	(0.021)
$DIF \ GDP \ Per \ Capita_{iit} \qquad -0.008^* \qquad -0.011^{**} \qquad -0.015^{***} \qquad -0.020^{***} \qquad -0.011 \qquad -0.006$	-0.001
$(0.004) \qquad (0.005) \qquad (0.005) \qquad (0.007) \qquad (0.007) \qquad (0.008)$	(0.010)
Country Fixed Effects Yes Yes Yes Yes Yes Yes	Yes
N 3883 3883 3883 3883 3795 3883	3800
<i>adj.</i> R^2 0.227 0.388 0.427 0.433 0.471 0.422	0.416

Table A2. Cross-section OLS Coefficient Estimates for Specific Years (Using Country

Pairs with Data Available for 1970)

Note: All columns are controlled with the same sample number in 1970. The drop in the number of observations in 2005 and 2014 is due to some variables not being available for those years. Regressions are based on Equation (3).



Figure A1. Coefficients of $Ln(Genetic \ Distance)_{ij}$ and $Ln(Geographic \ Distance)_{ij}$

(1970-2014) (Exclude Former USSR Countries)

Notes: Coefficients from cross-sectional OLS regressions based on Equation (3) and exclude all the USSR countries. Red and blue lines are the coefficients of genetic and geographic distance, respectively. The grey areas are the 95% critical interval for coefficients (1.96 times the standard error of the estimated regression coefficient).

Table A3. Cross-section OLS Coefficients for Specific Years (Exclude Former USSR

Countries)

(2) 1975	(3)	(4)	(5)		
1975	1095		(0)	(6)	(7)
	1985	1990	2005	2010	2014
-0.065***	-0.045***	-0.036**	-0.098***	-0.093***	-0.084***
(0.018)	(0.017)	(0.017)	(0.015)	(0.016)	(0.020)
-0.110***	-0.087***	-0.089***	-0.172***	-0.190***	-0.173***
(0.021)	(0.019)	(0.019)	(0.022)	(0.022)	(0.027)
-0.006	0.002	0.012	0.072^{**}	0.033	-0.094
(0.034)	(0.036)	(0.034)	(0.032)	(0.037)	(0.057)
0.035^{***}	0.036***	-0.007	-0.005	0.005	0.019
(0.013)	(0.013)	(0.026)	(0.023)	(0.012)	(0.019)
-0.069**	-0.049***	-0.076***	-0.039*	-0.02	-0.001
(0.030)	(0.013)	(0.015)	(0.022)	(0.027)	(0.043)
0.083^{*}	0.022	0.068	0.151***	0.152***	0.132***
(0.044)	(0.037)	(0.044)	(0.048)	(0.048)	(0.050)
0.002	0.013**	-0.007	-0.003	-0.002	-0.01
(0.005)	(0.006)	(0.005)	(0.006)	(0.007)	(0.008)
0.005	0.017**	0.012*	-0.001	-0.008	-0.008
(0.006)	(0.007)	(0.006)	(0.006)	(0.008)	(0.008)
-0.006	-0.018***	-0.005	0.000	-0.002	0.004
(0.005)	(0.006)	(0.005)	(0.005)	(0.006)	(0.007)
-0.002	-0.006	-0.007	0.014**	0.01	0.019*
(0.007)	(0.005)	(0.005)	(0.007)	(0.008)	(0.010)
-0.001	-0.043***	-0.009	-0.012	-0.009	0.003
(0.014)	(0.015)	(0.012)	(0.011)	(0.010)	(0.011)
0.001	0.019***	0.011**	0.002	0.008	-0.003
(0.006)	(0.006)	(0.005)	(0.005)	(0.006)	(0.006)
0.006	0.004	0.004	-0.003	-0.002	-0.003
(0.004)	(0.003)	(0.003)	(0.002)	(0.002)	(0.002)
0.000	-0.002	0.001	0.000	-0.001	0.001
(0.005)	(0.004)	(0.004)	(0.006)	(0.004)	(0.005)
-0.006	-0.014	-0.017	-0.027*	-0.011	-0.01
					(0.016)
· /	· · ·	(/	()	· · · ·	-0.008
					(0.008)
					Yes
					14494
					0.418
	(0.014) -0.011** (0.004) Yes 9290 0.399	-0.011**-0.012***(0.004)(0.004)YesYes9290124100.3990.374	-0.011**-0.012***-0.018***(0.004)(0.004)(0.005)YesYesYes929012410133140.3990.3740.387	-0.011**-0.012***-0.018***-0.012**(0.004)(0.004)(0.005)(0.006)YesYesYesYes92901241013314147360.3990.3740.3870.468	-0.011**-0.012***-0.018***-0.012**-0.010*(0.004)(0.004)(0.005)(0.006)(0.006)YesYesYesYesYes9290124101331414736149800.3990.3740.3870.4680.42

Notes: Two-way cluster-robust standard errors in brackets. * p < 0.1, ** p < 0.05, *** p < 0.01. Regressions are based on Equation (3) and exclude all USSR countries.

Table A4. Cross-section OLS Coefficients for Specific Years (with War-related

)				
	(1)	(2)	(3)	(4)	(5)	(6)	(7)
	1970	1975	1985	1990	2005	2010	2014
$Ln(Genetic \ Distance)_{ii}$	0.008	-0.069***	-0.046***	-0.043***	-0.069***	-0.068***	-0.059***
	(0.008)	(0.018)	(0.016)	(0.016)	(0.017)	(0.018)	(0.020)
$Ln(Geographic \ Distance)_{ij}$	-0.061***	-0.111***	-0.053***	-0.054***	-0.157***	-0.179^{***}	-0.167^{***}
	(0.015)	(0.022)	(0.018)	(0.018)	(0.023)	(0.023)	(0.025)
$Ln(Religious \ Distance)_{ii}$	0.063^{*}	0.008	0.042	0.039	0.065^{**}	0.032	-0.098*
$En(neuglous Distance)_{ij}$	(0.034)	(0.037)	(0.031)	(0.028)	(0.031)	(0.039)	(0.055)
$Ln(Linguistic \ Distance)_{ij}$	0.008	0.035^{***}	0.054^{***}	0.005	0.006	0.014	0.015
$En(Einguistic Distance)_{ij}$	(0.010)	(0.013)	(0.019)	(0.030)	(0.025)	(0.015)	(0.020)
Colonial Relationship _{ij}	0.157	-0.068*	-0.038	-0.065**	0.028	0.044	0.061
$Colonial Melationship_{ij}$	(0.098)	(0.037)	(0.029)	(0.026)	(0.045)	(0.045)	(0.056)
<i>Continue</i>	0.064	0.092*	0.038	0.073	0.136^{***}	0.139***	0.135^{***}
$Contiguous_{ij}$	(0.047)	(0.046)	(0.041)	(0.045)	(0.043)	(0.043)	(0.047)
	-0.004	0.000	0.004	-0.009**	-0.004	-0.008	-0.016*
$DIF \ Democracy_{ij}$	(0.004)	(0.005)	(0.005)	(0.004)	(0.005)	(0.006)	(0.008)
	-0.002	0.003	0.009	0.004	-0.001	-0.007	-0.005
$DIF \ Auto_{ij}$	(0.004)	(0.006)	(0.006)	(0.005)	(0.005)	(0.008)	(0.009)
	0.007*	-0.004	-0.009*	0.000	0.002	0.001	0.006
$DIF Polity_{ij}$	(0.004)	(0.004)	(0.005)	(0.004)	(0.002)	(0.001)	(0.007)
	-0.015**	-0.003	0.002	-0.001	(0.004) 0.013^*	· · · · ·	(0.007) 0.017^*
$DIF \ Parreg_{ij}$						0.011	
-0	(0.006)	(0.007)	(0.006)	(0.004)	(0.007)	(0.007)	(0.009)
$DIF \ Parcomp_{ij}$	0.037***	0.004	-0.032**	-0.005	-0.01	-0.001	0.009
	(0.012)	(0.017)	(0.014)	(0.009)	(0.010)	(0.010)	(0.012)
$DIF \ Polcomp_{ij}$	-0.015**	0.001	0.017***	0.011***	0.002	0.005	-0.006
	(0.006)	(0.009)	(0.005)	(0.004)	(0.004)	(0.005)	(0.006)
$Ruggedness_i \times Ruggedness_i$	-0.002*	0.006	0.003	0.003	-0.004**	-0.004**	-0.005**
	(0.001)	(0.004)	(0.002)	(0.002)	(0.002)	(0.002)	(0.002)
$DIF \ GDP_{ii}$	-0.005	-0.001	-0.002	-0.002	-0.005	-0.004	0.000
	(0.005)	(0.006)	(0.004)	(0.005)	(0.005)	(0.004)	(0.005)
SUM GDP _{ii}	0.033^{**}	-0.001	0.000	0.003	-0.02	-0.006	-0.008
Solid GD1 ij	(0.016)	(0.014)	(0.013)	(0.013)	(0.016)	(0.013)	(0.014)
DIF GDP Per Capita _{ii}	-0.006	-0.008**	-0.005	-0.009**	-0.011*	-0.011*	-0.006
DIF GDF Fer Capita _{ij}	(0.004)	(0.004)	(0.003)	(0.004)	(0.006)	(0.006)	(0.007)
	0.004**	-0.002***	-0.000***	-0.000***	0.000	0.000	0.000
$WAR \ Duration_{ij}$	(0.002)	(0.000)	(0.000)	(0.000)	(0.000)	(0.000)	(0.000)
	0.000	0.000	0.000	0.000	0.000	0.000	0.000
$WAR \ Recentness_{ijt}$	(0.000)	(0.000)	(0.000)	(0.000)	(0.000)	(0.000)	(0.000)
	0.087**	0.006	0.243***	0.201**	0.102*	0.093	0.000
Millitary Alliance $Relationship_{ijt}$	(0.035)	(0.044)	(0.074)	(0.077)	(0.059)	(0.061)	(0.000)
	0.644	0.413	0.433	0.734	-0.431	-0.47	-0.766
WAR Freq $(pre \ 1945)_{ij}$	(0.431)	(0.568)	(0.453) (0.551)	(0.754)	(0.496)	(0.535)	(0.478)
	,		. ,	0.232***	· · · ·	. ,	. ,
$UN Vote Correlation_{ij}$	0.049	0.119**	0.155^{**}		0.217***	0.113	0.099
	(0.033)	(0.058)	(0.075)	(0.076)	(0.075)	(0.070)	(0.074)
Country Fixed Effects	Yes	Yes	Yes	Yes	Yes	Yes	Yes
N Dia Dia	7298	8720	12190	12858	20252	20544	19974
$adj. R^2$	0.275	0.412	0.44	0.439	0.466	0.417	0.432

Variables)

Notes: Two-way cluster-robust standard errors in brackets. * p < 0.1, ** p < 0.05, *** p < 0.01. Regressions are based on Equation (3).

Table A5. Variable Definitions

$DIF \ Democracy_{ijt}$	$= \mathrm{abs}(Democracy_{it} - Democracy_{jt})$
$DIF \ Auto_{ijt}$	$= \mathrm{abs}(Autocracy_{it} - Autocracy_{jt})$
$DIF \ Polity_{ijt}$	$= \operatorname{abs}(Polity_{it} - Polity_{jt})$
$DIF \ Parreg_{ijt}$	$= abs(Regulation \ of \ Participation_{it} - Regulation \ of \ Participation_{jt})$
$DIF \ Parcomp_{ijt}$	$= \text{abs}(Party\ Competition_{it} - Party\ Competition_{jt})$
$DIF \ Polcomp_{ijt}$	$= abs(Political\ Competition\ Concept_{it} - Political\ Competition\ Concept_{jt})$
$DIF \ GDP \ Per \ Captia_{ijt}$	$= \ln(\text{abs}(GDP \ Per \ Capita_{it} - GDP \ Per \ Capita_{jt}))$
$DIF \ GDP_{ijt}$	$= \ln(\mathrm{abs}(GDP_{it} - GDP_{jt}))$
$SUM \ GDP_{ijt}$	$= \ln(GDP_{it} + GDP_{jt})$
$Common \ Legal \ Origin_{ij}$	$= \begin{cases} 1 & country \ i, j \ share \ the \ same \ legal \ origin \\ 0 & otherwise. \end{cases}$
$WAR \ Duration_{ij}$	$= War_End_Date_{ij} - War_Start_Date_{ij}$
$WAR \ Recentness_{ijt}$	$= \begin{cases} 1 & country \ i, j \ have \ war \ within \ 20 \ years. \\ 0 & otherwise. \end{cases}$
WAR Freq $(pre \ 1945)_{ij}$	$= Years \ of \ Bilateral \ War_{1870-1945} / \ (1945-1870)$

Table A6. List of Countries

AFG	AGO	ALB	ARE	ARG	ARM	ATG	AUS	AUT	AZE	BDI	BEL
BEN	BFA	BGD	BGR	BHR	BHS	BLR	BLZ	BOL	BRA	BRB	BRN
BTN	BUR	BWA	CAF	CAN	CHE	CHL	CHN	CIV	CMR	COD	COL
COM	CPV	CRI	CUB	CYP	CZE	DEU	DJI	DMA	DNK	DOM	DZA
ECU	EGY	ERI	ESP	EST	ETH	FIN	FJI	FRA	GAB	GBR	GEO
GHA	GIN	GMB	GNB	GNQ	GRC	GRD	GTM	GUY	HKG	HND	HRV
HTI	HUN	IDN	IND	IRL	IRN	IRQ	ISL	ISR	ITA	JAM	JOR
JPN	KAZ	KEN	KGZ	KHM	KIR	KNA	KOR	KWT	LAO	LBN	LBR
LBY	LCA	LKA	LSO	LTU	LUX	LVA	MAR	MDA	MDG	MEX	MKD
MLI	MLT	MNG	MOZ	MRT	MUS	MWI	MYS	NAM	NER	NGA	NIC
NLD	NOR	NPL	NZL	OMN	PAK	PAN	PER	PHL	PNG	POL	PRK
\mathbf{PRT}	PRY	QAT	ROU	RUS	RWA	SAU	SDN	SEN	SGP	SLB	SLE
SLV	SMR	SOM	SUR	SVK	SVN	SWE	SWZ	SYC	SYR	TCD	THA
TJK	TKM	TON	TTO	TUN	TUR	UGA	UKR	URY	USA	UZB	VCT
VEN	VNM	VUT	WSM	ZAF	ZAR	ZMB	ZWE				

Notes: Table shows the ISO codes of the 176 countries included in our sample.

Table A7. 1	List of	Countries	in	European	Sample (Europe 22	2)

Austria	Belgium	Czech Republic	Denmark	Finland	France
Germany	Greece	Hungary	Iceland	Ireland	Italy
Macedonia	Netherlands	Norway	Poland	Portugal	Russia
Spain	Sweden	Switzerland	United Kingdom		

Notes: The sample of 22 European countries is consistent with the sample in the paper of Giuliano, Spilimbergo and Tonon (2014). There are 231 $(22 \times 21/2)$ distinct country pairs. Belgium, Iceland, Ireland and Netherlands are with zero genetic distance in our sample $(4 \times 3/2)$ distinct pairs).

Variable	Mean	Std. Dev.	Min.	Max.
$(Genetic \ Distance)_{ij}$ (Europe 22)	0.0050186	0.0042103	0.00000	0.011633
$\ln(Genetic \ Distance)_{ij}$ (Europe 22)	-6.02764	1.564076	-10.7199	-4.45392
$(Genetic \ Distance)_{ij}$ (Total 176 countries)	0.0369244	0.0185448	0.00000	0.094963
$\ln(Genetic \ Distance)_{ij}$ (Total 176 countries)	-3.507772	0.8197276	-10.7199	-2.35427

Notes: The sample of Europe 22 countries is consistent with the sample in the paper of Giuliano, Spilimbergo and Tonon (2014). There are 4 countries with zeroes genetic distance in Europe 22 in our sample.

Table A9. List of Countries of Former USSR Countries

ALB	ARM	AZE	BIH	BLR	BYS	CSK	CZE	DDR	DEU	EST	GEO
HRV	HUN	KAZ	KGZ	LTU	LVA	MDA	MKD	MNE	POL	RUS	SCG
SRB	SVN	TJK	TKM	UKR	UZB	YUG					

Notes: List of ISO codes of 31 countries in the former USSR countries sample. There are 465 $(31 \times 30/2)$ distinct country pairs.