Kin-based institutions and economic development*

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August 25, 2022

Abstract

Though many theories have been advanced to account for global differences in economic prosperity, little attention has been paid to the oldest and most fundamental of human institutions: kin-based institutions—the set of social norms governing descent, marriage, clan membership, post-marital residence and family organization. Here, focusing on an anthropologically well established dimension of kinship, we establish a robust and economically significant negative association between the tightness and breadth of kin-based institutions—their kinship intensity—and economic development. To measure kinship intensity and economic development, we deploy both quantified ethnographic observations on kinship and genotypic measures (which proxy endogamous marriage patterns) with data on satellite nighttime luminosity and regional GDP. Our results are robust to controlling for a suite of geographic and cultural variables and hold across countries, within countries at both the regional and ethnolinguistic levels, and within countries in a spatial regression discontinuity analysis. Considering potential mechanisms, we discuss evidence consistent with kinship intensity indirectly impacting economic development via its effects on the division of labor, cultural psychology, institutions, and innovation.

Keywords: kin-based institutions, cousin marriage, inbreeding coefficient, cultural evolution, economic development

JEL classifications: D01, J12, J16, N30, Z12, Z13

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*We thank James Fenske, Oded Galor, David Levine, Stelios Michalopoulos and Nathan Nunn for helpful comments and suggestions. We thank seminar and conference participants at George Mason University, the ASREC Conference, the NBER Economics of Culture and Institutions Meeting, the Brown Conference on the Roots of Comparative Development, the University of Essex, the University of Waterloo, and Bowdoin College. For research assistance, we are grateful to Gareth Markel and Stephen Tino. We are grateful to David Reich for sharing the Human Origins (HO) data with us; to Nick Patterson and Swapan Mallick for answering our questions about the HO data; and to Jim Wilson and David Clark for sharing the ROHgen2 software pipeline and answering our questions. Research reported in this publication was supported by the John Templeton Foundation under Award Number 62161.

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1 Introduction

Understanding the origins of global and regional differences in economic prosperity is among the oldest endeavors in economics, tracing back through Adam Smith (2005[1776]) to the likes of Machiavelli (1991[1531]) and Ibn Kaldun (2015[1377]). In recent decades, the availability of new data sources and improved approaches to causal identification have shed fresh light on the topic. Researchers have argued for the role of a suite of important factors, including climate and geography (Diamond, 1997; Hibbs and Olsson, 2004; Dell et al., 2012), disease (Sarma et al., 2019), political institutions (Acemoglu et al., 2002; Rodrik et al., 2004), colonialism (Dell, 2010), human capital (Glaeser et al., 2004), the slave trade (Nunn, 2008), and culture (Landes, 2000; Tabellini, 2010; Alesina et al., 2013). The emerging picture is one of a complex causal network in which aspects of climate, geography, ecology and endemic disease (e.g., malaria) operate, at least partly, through their impact on technologies (e.g., agriculture, writing, and the plow), social norms, preferences (e.g., impersonal fairness), supernatural beliefs (Barro and McCleary, 2003; Becker and Woessmann, 2009) and aspects of psychology like individualism (Gorodnichenko and Roland, 2016), patience (Dohmen et al., 2015) and trust (Spolaore and Wacziarg, 2013; Henrich, 2020).

Though perhaps the oldest and most fundamental of human institutions, kin-based institutions have to date received little attention as a potential contributor to global differences in economic prosperity. Kin-based institutions are formed by clusters of social norms that have evolved culturally in ways that variously extend, suppress or re-enforce blood and affinal ties, forging large kin groups or networks. By anchoring themselves in aspects of human nature, including our instincts to help close relatives, form pair-bonds and avoid inbreeding (e.g., with siblings), they form potent and enduring institutions. Kinship norms regulate marriage, descent, clan membership, inheritance, post-marital residence, the corporate ownership of resources, obligations to kinfolk (e.g., related to protection, honor and care), and much more (Murdock, 1949). In many societies, kinship norms operate over generations to continuously weave together the threads of each person's most important social ties (Greif and Tabellini, 2010; Henrich, 2020). While kin-based institutions vary along several important dimensions, anthropologists have long highlighted the importance of *kinship intensity* (Walker et al., 2013): the degree to which individuals are enmeshed in broad and tight kin networks that demand their loyalty and prescribe much of their behavior (Enke, 2019; Schulz et al., 2019). Societies dominated by small, monogamous nuclear families tend to have low levels of kinship intensity while polygynous societies dominated by endogenous patrilineal clans tend to have high levels of kinship intensity. Kinship practices like cousin marriage (Bittles and Black, 2010; Leutenegger et al., 2011), customary inheritance (Bahrami-Rad, 2020; Bau, 2021), post-marital residence (Lowes, 2018; Bau, 2021) and polygamy (Fenske, 2015; Tertilt, 2006) remain important throughout the world.

A growing body of research suggests that kinship intensity has wide-ranging effects on incentives, constraints, social networks, and psychology. For instance, intensive kinship has been linked to lower levels of impersonal trust, individualism, public goods provision and democratic governance as well as to higher levels of corruption, nepotism and conformity (Greif and Tabellini, 2010; Alesina and Giuliano, 2011, 2015; Edlund, 2018; Schulz et al., 2019; Akbari et al., 2019; Enke, 2019; Henrich, 2020; Moscona et al., 2020; Bergeron, 2020; Schulz, 2022). These patterns, in turn, have been argued to influence economic growth or innovation (Mauro, 1995; Algan and Cahuc, 2013; Gorodnichenko and Roland, 2016; Acemoglu et al., 2019).

In this paper, we empirically establish a tight and robust negative reduced-form association between kinship intensity—proxied using both ethnographic and genetic data—and economic prosperity—assessed using satellite nighttime luminosity and regional GDP. To enrich this key result, we also explore potential channels through which kinship intensity might impact economic prosperity.

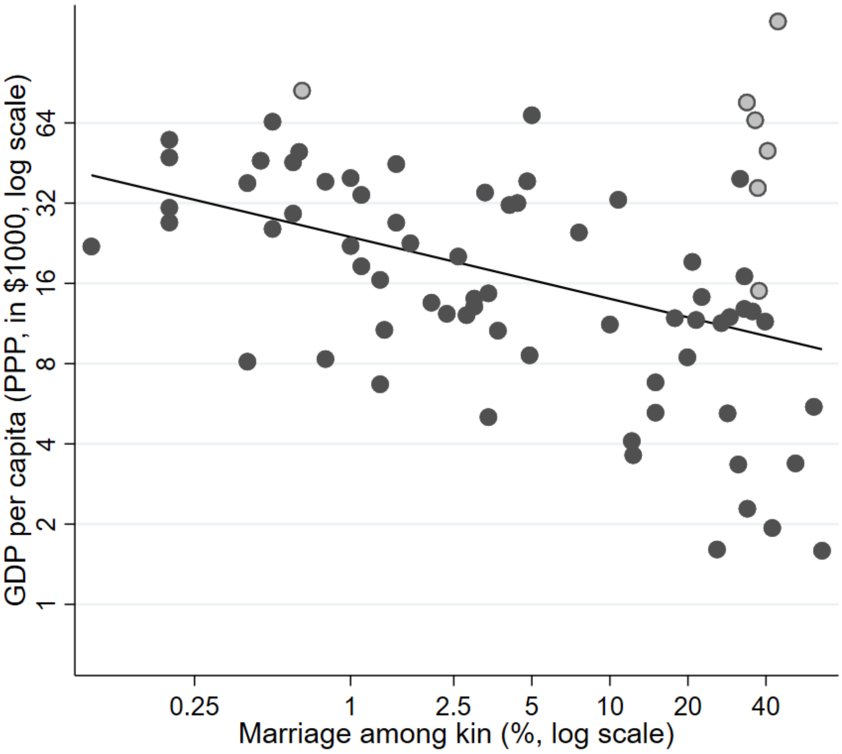

Figure 1: GDP per capita in 2018 vs. prevalence of marriage among kin (second cousins or closer) across countries. The light gray dots denote oil-rich countries with oil output above 250 barrels per day per capita in 2000. The GDP data comes from the Maddison project (Bolt and van Zanden, 2020) and the prevalence of marriage among kin is computed based on Bittles and Black (2010).

Motivating our investigation, Figure 1 shows the cross-country relationship between national GDP per capita in 2018 (in constant PPP 2011 dollars) and a simple proxy for kinship intensity, the prevalence of marriages among kin (second cousins and closer) (Spearman's $\hat{\rho} = -0.37$, $p = 0.001$, $n = 74$).

Below, we present an array of more detailed analyses that interrogate the relationship between kinship intensity and economic prosperity. To measure economic prosperity at fine scales, we rely primarily on the logarithm of pixel-level satellite nighttime luminosity (Michalopoulos and Papaioannou, 2013; Donaldson and Storeygard, 2016), but hold constant the logarithm of population density. Because the coefficient on log population density is usually close to unity in our regressions, we interpret the the coefficient on kinship intensity as a measure of the association with nighttime luminosity *per capita*. As a alternative measure of economic prosperity, we also use regional GDP per capita (Gennaioli et al., 2014).

To measure kinship intensity, we deploy an existing approach from our previous work (Schulz et al., 2019) that combines data from the Ethnographic Atlas (EA)—a compilation of anthropological observations that aim to capture life prior to industrialization and European colonization based on the coding of ethnographies from over 1,200 societies—

and global language phylogenies for over 5,000 ethnolinguistic groups (Kirby et al., 2016; Giuliano and Nunn, 2018; Schulz et al., 2019; Enke, 2019; Bahrami-Rad et al., 2021). Our Kinship Intensity Index (KII) aggregates measures of societies' intensive kinship practices across five dimensions that capture preferences or norms related to cousin marriage, polygamy, co-residence of extended families, lineage organization, and community organization.[1] In our prior work, which did not examine the association with economic development, we had developed the KII on purely theoretical grounds, rooted in anthropological research and the available data.

As an alternative measure of kinship intensity, we use genetic data from the Human Origins (HO) dataset (Reich Lab, 2020) to estimate the average inbreeding coefficient for a diverse swath of populations. The HO dataset contains genetic data from nearly 10,000 modern-day individuals from across the world. The inbreeding coefficient is a fundamental variable in the field of population genetics that measures the relatedness of one's parents; we estimate it using genetic data with an estimator, F_{ROH}, that captures the share of one's genome that occurs in runs of homozygosity (ROHs)—long genomic segments where the paternally and maternally inherited DNA is identical. As we explain below, though measured with genetic data, the inbreeding coefficient and F_{ROH} capture *cultural practices* and are not genetically determined. As far as we know, both the HO dataset and our genetic-data-based estimator of the inbreeding coefficient, F_{ROH}, are novel in the economics literature.

We show that populations' average F_{ROH}, which we denote $\overline{F_{ROH}}$, robustly correlates with cousin marriage practices across populations (consistent with previous work in genetics—e.g., Pemberton and Rosenberg 2014; Sahoo et al. 2021) as well as with the KII and most of its other component measures. These relationships not only confirm the ground truth of our KII, but also imply that it captures enduring and important cultural practices—important enough to be detectable in contemporary genetic data. Proxying kinship intensity with $\overline{F_{ROH}}$ also complements the KII because it captures actual behavior—matings—and thus avoids any reliance on qualitative ethnographic observation, self-reports and coding judgments.

Across an array of analyses, we establish a statistically significant and economically important negative association between kinship intensity and economic prosperity. We begin by estimating cross-sectional regressions to document the association between the KII and nighttime luminosity across geographic pixels and ethnicities, and then panel data regressions to document the association between the KII and regional GDP per capita across subnational regions. To test for the robustness of these associations, we present an extensive battery of regressions that include country fixed effects and control for a broad range of geographic, cultural and ecological variables. We also show that these associations are robust to alternative ways of matching the various datasets we analyze. And we show that most of the five KII sub-indicators are negatively associated with nighttime luminosity, and that none is positively associated, thus giving us confidence in the theoretical soundness of our approach of using the KII to study the link between kinship intensity and economic prosperity.

To address concerns that unobservable omitted factors that vary smoothly across space may drive our results, we then conduct a spatial regression discontinuity (RD) analysis at the boundaries between pairs of neighboring ethnicities from the same countries. We use the KII to predict nighttime luminosity at the geographic pixel level and adjust for the same suite of control variables as in our earlier cross-sectional regressions. We verify

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[1] Enke (2019) follows a similar approach to construct his index of "kinship tightness."

the robustness of our RD specification to controlling for each geographic pixel's distance to the ethnic boundary in flexible ways, by allowing for a different coefficient on the distance-to-the-boundary term for each ethnicity in each ethnicity pair or by interacting latitude and longitude with each ethnicity pair. We further confirm the robustness of our RD specification in a sample that includes pairs of neighboring ethnicities from different countries and by using pixels within different ranges of distance to the ethnic boundary. This latter analysis accounts for spillover effects of both light and economic activity as well as for gradual changes in the fraction of the population that belongs to each neighboring ethnicity at the ethnic boundary. Lastly, we estimate placebo spatial RD regressions, replacing nighttime luminosity as the dependent variable with each of a series of geographic controls. Here, using these placebo variables, we find no association with the KII.

Across our analyses, the association between the KII and economic prosperity is robust and the estimated coefficient on the KII remains remarkably stable, implying that a one-standard deviation increase in the KII is associated with a $\sim 30-50\%$ decrease in per capita economic output across the globe and a $\sim 7-12\%$ decrease within countries; this holds for both of our measures of economic output (nighttime luminosity and regional GDP per capita).

Next, in a series of OLS regressions that parallel those we ran earlier with the KII, we examine the association between $\overline{F_{ROH}}$ estimated using genetic data from HO and nighttime luminosity across geographic pixels. Again, we document a robust and economically significant association. Our estimates imply that nighttime luminosity is $\sim 30\%$ lower for a hypothetical ethnicity in which everyone is the offspring of second cousins vs. an ethnicity in the same country in which everyone is the offspring of unrelated parents (the difference in $\overline{F_{ROH}}$ between two such ethnicities is slightly smaller than the standard deviation of $\overline{F_{ROH}}$ across ethnicities).

Finally, we consider the causal pathways that may account for the link between kinship intensity and economic prosperity. First, since we have previously argued that historical exposure to the Western Church decreased kinship intensity in European ancestry populations (Schulz et al., 2019; Henrich, 2020), we verify that our main results—from across the array of analyses we report—generally hold when we control for historical exposure to Christianity as well as when we drop all observations from Europe and European-descent societies.

Second, we examine whether reverse causality from economic development to kinship intensity could account for our results, but conclude that this is unlikely to be the case. Among other reasons for this, the KII is based on observations that aim to capture life prior to industrialization, while our measures of economic prosperity are from recent years. Further, the results of our spatial RD analysis undermine alternative explanations that involve factors that vary smoothly across space (such as most geographic variables and distance to trade routes or power centers); thus, for example, for past economic prosperity to have caused both lower kinship intensity and current-day economic prosperity, that past economic prosperity would have had to stem from factors that vary discontinuously at or around the boundaries that separate ethnic groups in the same countries. Importantly, we also show that our main results are robust to controlling for a proxy for past levels of economic prosperity (settlement complexity, from the EA), and that the KII remains a strong predictor of modern-day GDP per capita across countries even when controlling for past GDP per capita (from 1950). Finally, we show that the pixel-level association between the KII and nighttime luminosity holds in the sub-sample of pixels with very low population density, thus undermining explanations revolving around urbanization as a mediating factor.

Third, gesturing to future work, we examine mechanisms that may account for a causal effect of kinship intensity on economic development. We integrate findings from the existing literature with a small battery of new analyses that together support the view that lower kinship intensity is causally associated with a suite of variables that plausibly contribute to economic prosperity. These variables include (1) the division of labor and comparative advantage, (2) an array of cultural-psychological traits, including trust, impersonal cooperation, individualism, conformity, in-group loyalty and nepotism, (3) institutional quality and (4) innovation. We also examine whether inbreeding depression (ID)—whereby the offspring of inbred individuals have lower health, intelligence, and fitness—could mediate the impact of kinship intensity on prosperity, but conclude that it is unlikely to play an important role.

1.1 Related literature

This paper builds on, and contributes to, a number of interrelated lines of research within economics. To begin, our demonstration of a robust negative link between kinship intensity and economic prosperity contributes to addressing questions from economic history surrounding the origins of the industrial revolution in Europe and the "rise of the West" more generally (Clark, 2007; Mokyr, 2016). Economists (Greif, 2006a; Greif and Tabellini, 2017), following both historians and anthropologists (Goody, 1983; Mitterauer, 2010), have argued that the transformation of European kinship into what has been dubbed the "European Marriage Pattern" (Hajnal, 1982) was central to the emergence of the pluralist, impersonal political and economic institutions that underpinned the European expansion after 1500 and eventually the industrial revolution (Greif, 2006b; Tabellini, 2010; Henrich, 2020).

Second, our results also inform a closely related literature that identifies important clusters of institutions and cultural practices that have deep roots in history and are important contributors to economic growth (Nunn, 2012; Spolaore and Wacziarg, 2013; Alesina and Giuliano, 2015). Unlike the commonly used measures of formal institutions such as constraints on the executive, kin-based institutions are generally vertically culturally transmitted at the group-level and strikingly persistent across time: analyses from economics, genetics and anthropology using diverse measures of kin-based institutions demonstrate that these cultural traits are among the most persistent (Guglielmino et al., 1995; Alesina and Giuliano, 2014; Skoglund et al., 2016; Bahrami-Rad et al., 2021). Such stability may contribute to explaining the long-term persistence of economic prosperity (Comin et al., 2010; Edlund, 2018) as well as the lasting influence of both early European settlements (Easterly and Levine, 2016) and Christian missions (Bai and Kung, 2015; Calvi and Mantovanelli, 2016).

Finally, our analyses contribute to the growing literature that links kin or family ties to economic growth, political institutions, rates of intergroup violence, and economically-relevant aspects of psychology. Pioneering this effort, Alesina and Giuliano (2010) have shown that weaker nuclear family ties, based on attitudes from the World Values Survey, are associated with fewer family businesses and greater economic prosperity at the country-level (Alesina et al., 2015). More recently, focusing on economic growth within the U.S. over the last two centuries, Ghosh et al. (2021) take advantage of the checkered imposition of laws prohibiting cousin marriage at the state-level to demonstrate how declines in rates of cousin marriage precipitated by these legal changes fostered greater economic prosperity. [2]

Existing research has also linked kin and family measures to economically relevant political institutions. Alesina et al. (2013) show that looser ties within the nuclear families are associated more democratically-oriented political attitudes. Complementing this work, Schulz (2022) argues that the reduction in cousin marriage rates and kinship intensity driven by the spread of the Western Church opened the door to the historical formation of representative, pluralistic political institutions. Similarly, Akbari et al. (2019) show that higher rates of cousin marriage are associated with more corruption across countries and European regions.[3]

Testing venerable ideas from anthropology on the origins of honor cultures (Sahlins, 1961), Moscona et al. (2017) show that segmentary lineage organizations in Africa are associated with more intergroup violence.

Some authors have also linked kin ties to economically-relevant aspects of psychology. Focusing on African populations, Moscona et al. (2020) shows that populations with segmentary lineage organization are less trusting of strangers compare to other similar communities. In the Democratic Republic of Congo, using the historical locations of Christian missions, Bergeron (2020) shows that city dwellers whose home villages were closer to historical missions revealed greater moral universalism and reported social networks with more people outside their families and ethnolinguistic groups. Using a broad range of data from around the world, Enke (2019), Schulz et al. (2019) and Henrich (2020) layout a battery of robust correlations between kinship intensity and diverse measures of impersonal trust, moral universalism, conformity, analytic thinking, individualism and cooperation with strangers.

1.2 Paper structure

Our approach rolls out as follows: we begin, in Section 2, by introducing kin-based institutions, discussing how we measure kinship intensity using both the Kinship Intensity Index (KII) and the inbreeding coefficient ($\overline{F_{ROH}}$), and then illustrating how kinship influences life on the ground using ethnographic cases. Next, in Section 3, we describe our primary data, emphasizing our measures of economic performance and population density along with our battery of control variables. In Section 4, our analyses proceed by first linking the KII to nighttime luminosity across either pixels or ethnicities, then linking the KII to regional GDP per capita, and finally linking the KII to luminosity again, but now across contiguous ethnicities in a spatial RD analysis. In Section 5, to complement our analyses with the KII, we first show how $\overline{F_{ROH}}$ relates to the KII and its sub-components and then repeat our analysis linking kinship intensity to nighttime

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[2] Other authors who have suggested an important role for kinship in economic development include Platteau (2000), Fafchamps (2011), Hoff and Sen (2011), and Edlund (2018).

[3] Research has also linked aspect of kinship to gender inequality and educational investment. In Indonesia and Ghana, Bau (2021) shows that traditional norms about post-marital residence—patrilocality or matrilocality—interact with the arrival of pension systems to influence the education of either males or females. Similarly, focusing on the impact of different kin-based institutions in the Democratic Republic of Congo, Lowes 2018 shows experimentally that matrilineal wives are less cooperative with their spouses than patrilineal wives—as had long been suggested by anthropologists—but experience less domestic violence and have healthier and better educated children. Looking both historically within Europe and cross-nationally today, de Moor and van Zanden (2010), Carmichael and Rijpma (2017), and van Zanden et al. (2019) investigate the effect of family systems on women's agency and labor market participation.

luminosity, now swapping in $\overline{F_{ROH}}$ to replace the KII. In Section 6, we discuss plausible causal pathways, including possible confounding by Christianity or European ancestry, reverse causality from economic development to kinship intensity, and mechanisms that may account for a causal impact of kinship intensity on economic prosperity. Section 7 consolidates our findings and emphasizes caution in considering any policy implications.

2 Kin-based institutions

Representing perhaps the oldest and most fundamental of human institutions, kin-based institutions are packages of social norms that govern marriage and regulate family relationships. Well back into our evolutionary past, these institutions have played a central role in organizing economic production, distribution, consumption, political decision-making and social insurance (Murdock, 1949; Parkin, 1997). Kinship norms variously prescribe and prohibit particular inheritance customs (e.g., matrilineal descent of identity or land), polygamy (e.g., men may take as many wives as they can afford), cousin marriage, arranged marriage, clan membership, corporate ownership of land, household organizations (e.g., extended households), and post-marital residence (e.g., patrilocality, where the bride resides with the husband's family). The durability of kin-based institutions, along with their universality, likely arises from their anchoring in several well-established aspects of human nature (Henrich, 2016), including our inclinations for kin-based altruism, incest avoidance, and pair-bonding (Henrich, 2020).

Kin-based institutions vary considerably across societies, having evolved culturally in response to diverse ecologies, novel technologies, religious beliefs, and state policies (Daynes, 2001; Holden and Mace, 2003; Dalton and Leung, 2014; Fenske, 2015; Schulz et al., 2019; Henrich, 2020; Bau and Fernández, 2021; Bahrami-Rad et al., 2021; Tène, 2021; Schulz, 2022). Today, for example, roughly 1.1 billion people in Africa, the Middle East, and parts of Asia reside in regions in which between 20 to 60 percent of marriages are between second cousins or closer kin (Romeo and Bittles, 2014), and cousin marriage rates are stable or increasing in some populations, including in Pakistan (Hussain and Bittles, 1998), Iran (Abbasi-shavazi et al., 2008), Oman (Islam, 2012) and Yemen (Jurdi and Saxena, 2003). Similarly, many populations still trace descent primarily through either the male line or the female line (Lowes, 2018; Moscona et al., 2020; Tène, 2021). This contrasts with Western societies, where social structure is characterized by a strong emphasis on the monogamous nuclear family, kin marriages are virtually absent, and descent is traced bilaterally through both the mother's and the father's sides (Goody, 1983; Greif, 2006a; Mitterauer, 2010). Interestingly, despite the parallels with genetic inheritance, anthropological data suggest that fewer than half of societies trace descent bilaterally (Henrich, 2020).

In considering how kinship shapes people's lives, minds and societies, anthropologists have characterized cross-societal variation in kin-based institutions according to their kinship intensity (Walker et al., 2013; Walker and Hill, 2014; Schulz et al., 2019; Henrich, 2020) (Enke (2019) calls this "kinship tightness"). Intensive kinship norms foster tight, dense and overlapping relationships, which often create essentialized "corporate groups" such as clans or lineages that are relationally isolated from other such groups. Cousin marriage, for example, weaves families together into dense kin-based networks, which provide preferred and privileged partners for economic exchanges, mutual aid, insurance and political alliances. Cousins, of course, are already kinfolk, but cousin marriage reenforces and tightens these bonds with additional ties and, perhaps more importantly, helps guarantee that these relationships endure into later generations. Similarly, norms that promote co-residence, where children grow up in extended families or clans live in the same dwelling, strengthen the cohesion, interdependence and loyalty within such groups. Norms that establish unilineal descent, prescribe post-marital residence, favor arranged marriage, and encourage polgynyous arrangements all also intensify kinship by building networks of dense, overlapping and enduring kin ties.

By contrast, extensive kinship systems, such as those found among mobile hunter-gathers, are characterized by marriage to non-kin (incest taboos often prohibit cousin marriage), bilateral descent, limited polygyny and flexible residential norms. Marrying and residing with non-kin creates large and more diverse kin networks, as does bilateral descent, where people trace relatedness through both their mothers and fathers. Such norms create large, interconnected, and non-exclusive kin networks in which everyone except siblings has a unique combination of relatives.

From an economic perspective, kin-based institutions dramatically shape people's social networks, relationships, loyalties, obligations, responsibilities, incentives, constraints and, as we have argued elsewhere, their motivations and ways of thinking, feeling and reasoning (Schulz et al., 2019; Henrich, 2020). In many societies, kinship networks play important roles in informal exchanges, public goods provisioning, information sharing and insurance against adverse shocks such as injuries or illnesses (Cox and Fafchamps, 2007). As we examine in Section 6, kinship intensity may influence economic specialization and the division of labor, cultural-psychological traits such as impersonal trust and individualism, political institutions, and innovation. Given the profound ways in which kinship intensity shapes people's lives and decisions, it is worth considering whether it can be robustly linked to economic growth.

Efforts to understand why populations vary in their kin-based institutions are just beginning. The most important determinant of a population's current kin-based institutions are the kin-based institutions of its forebears—cultural persistence (Guglielmino et al., 1995; Jordan et al., 2009; Alesina and Giuliano, 2014; Bahrami-Rad et al., 2021)—but several ecological, economic, epidemiological, legal and religious factors have been shown to shape kinship. First, the spread of sedentary farming, with the consequent need to invest in and defend territory, likely fostered an intensification of kinship (Ember and Ember, 1971; Jones, 2011; Henrich, 2020). Focusing on China, Noblit (2021) has recently shown that both a county's suitability for paddy rice agriculture and its susceptibility to rainfall shocks (associated with typhoons) favored the gradual diffusion of lineage organizations over centuries after the year 1000 CE. Similarly, focusing on matrilineal inheritance in Africa, Tene (2021) points to a role for ecological factors that favor hoe agriculture (done by women) and those that inhibit large-animal pastoralism (done by men). Consistent with this, Holden and Mace (2003) argue that the spread of cattle across Africa led to the decline of matrilineal descent.

Diseases, laws and religious taboos have also shaped kinship. Considering disease, Enke (2019) links kinship intensity to the ecological potential for malaria and tsetse flies (which cause sleeping sickness and kill livestock). Focusing on the impact of laws in India, Bahrami-Rad (2021) shows that policies prohibiting unilineal inheritance (effectively allowing women to inherit equally) fostered more arranged marriages to cousins and reduced gender equality. Similarly, scholars have argued that Islam's prescriptions regarding inheritance by daughters (they get half of what sons get) fostered more marriages of daughters to their fathers' brothers' sons (patrilateral parallel cousin marriage)—a type of cousin marriage rarely observed outside of Islamic societies (Korotayev, 2015). Finally, a number of economists, historians and anthropologists have argued that the branch of Christianity that evolved into the Roman Catholic Church has dramatically transformed kinship around the world with its prohibitions and prescriptions regarding polygyny, cousin marriage, bilateral inheritance and other practices related to marriage and the family (Goody, 1983; Korotayev, 2003; Greif, 2006a; Mitterauer, 2010; Henrich, 2020). Schulz and colleagues (2019; 2022) link historical exposure to the Church to the rate of cousin marriage across European regions and to kinship intensity across countries. Focusing on Africa, Fenske (2015) and Bergeron (2020) show that distance from historical Christian missions predicts greater polygyny and stronger kin ties, respectively.

2.1 Measuring kinship intensity

Our analyses rely on two main measures of kinship intensity. The first measure, which we use in most of our analyses, is the Kinship Intensity Index (KII) from Schulz et. al. (2019). The KII is an omnibus measure of the overall strength of kin-based institutions constructed using anthropological data and available for nearly 1,000 societies in the Ethnographic Atlas (EA) (as curated and expanded in D-Place (Kirby et al., 2016)). To complement this ethnographic measure and verify the robustness of our main results to using a more contemporaneous measure of kinship intensity that captures actual behavior (rather than relying on ethnographic reports), we deploy genetic data from the Human Origins (HO) dataset (Reich Lab, 2020) to compute the average inbreeding coefficient for a few hundred populations.

The Kinship Intensity Index (KII)

The Kinship Intensity Index (KII), which we developed in previous work (Schulz et al., 2019), is calculated using quantified anthropological observations from over 1,200 societies from the EA and, for a version of our analyses, is extended to populations around the world using language phylogenies. With the average observation occurring around 1900 CE, the EA is based on ethnographies written by anthropologists aiming to reconstruct people's lifeways prior to European colonization, global market integration and industrialization.[4] The KII is thus a "deep" historical measure that aims to capture enduring norms and practices before modernization.

In Schulz et al. (2019), which did not examine the link with economic prosperity, we developed the KII based on purely theoretical grounds—aiming to operationalize the anthropologists' concept of kinship intensity. We used the same approach to calculate the KII as Schulz et al. (2019), but used data from the latest versions of the EA (Kirby et al., 2016), Ethnologue (Gordon, 2005; Lewis, 2009) and Glottolog (Hammarström et al., 2016).

The KII aggregates five sub-indicators that capture key dimensions of kin-based organization:

1. *Cousin marriage preference* captures the intensity of the norms about marrying cousins. Preference for cousin marriage inhibits the formation of extensive ties among previously unconnected families or clans, encourages the creation of additional links among already related families and households, and increases the genetic relatedness of family members.

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[4] 8 of the 1,291 societies in the EA were coded based on pre-1500 CE historical observations; we excluded them from our analyses.

2. *Polygynous marriage norms* permit men to marry multiple wives. This results in larger and more extended households and introduces social and economic interdependence among co-wives and half-siblings. At a societal level, polygynous marriage norms result in fewer fathers, larger reproductive skew, and greater genetic relatedness.

3. *Co-residence of extended families* captures the degree to which several generations of a family, each with their own spouses and children, co-reside. Such residential norms create stronger emotional bonds and greater economic interdependence among the co-residing individuals. This contrasts with the neolocal nuclear family, where only the two spouses with their children live together, separate from other relatives.

4. *Lineage organization* captures the social norms governing descent and identity. In societies with unilineal descent, people reckon descent and social identity primarily or entirely through either their mother's or father's side. The exclusive membership on one side determines social identity and increases cohesion and interdependence within the lineage. This contrasts with bilateral descent where membership is non-exclusive and everyone except siblings has a unique combination of relatives, resulting in more diverse and diffuse kin networks and lower kinship intensity.

5. *Community organization* captures whether extended family and clan members reside within the same localized area of a settlement (e.g., a neighborhood), and whether there is community-level endogamy (e.g., people can only marry co-villagers). Localization decreases the interaction with outsiders while endogamous marriages mean that communities form denser clusters (since no outsiders from different villages join the community through marriage), thereby increasing kinship intensity and inbreeding.

As we further describe in Section 3.3, we matched the EA data (including the KII sub-indicators) to languages from the Ethnologue (Gordon, 2005; Lewis, 2009)—a comprehensive map of the world's languages—and these languages are in turn associated with "country-ethnicities" and geographic pixels.[5] To compute the KII for each Ethnologue language, we first standardized the five sub-indicators using their means and standard deviations across the EA societies; then, we take the average of the language's five matched sub-indicators and standardize it using its mean and standard deviation computed across the EA societies. The resulting KII is defined for the Ethnologue's languages but is standardized based on the EA societies.[6]

Figure 2 shows the distribution of the KII across country-ethnicities around the world, and Appendix A.1 provides further details on the construction of the five sub-indicators and of the KII. As can be seen in Table B.1.1, the five sub-indicators turn out to be

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[5] We used two alternative matching methods: the direct matching method and the language-tree matching method. When using the language-tree matching method, we imputed missing observations for the cousin-marriage preference and co-residence-of-extended-families sub-indicators—see Appendix A.1 and Schulz et al. (2019) for details.

[6] We standardized the sub-indicators and the KII based on their means and standard deviations across the EA societies, rather than across the Ethnologue languages, because the different matching methods we use led to different sets of languages being matched to the EA, and some of these languages correspond to very small groups; standardizing based on the EA societies allows us to consistently interpret the coefficients we estimate across our analyses.

positively correlated across the EA societies with nonmissing data, with the first principal component accounting for 35 percent of the variation.[7]

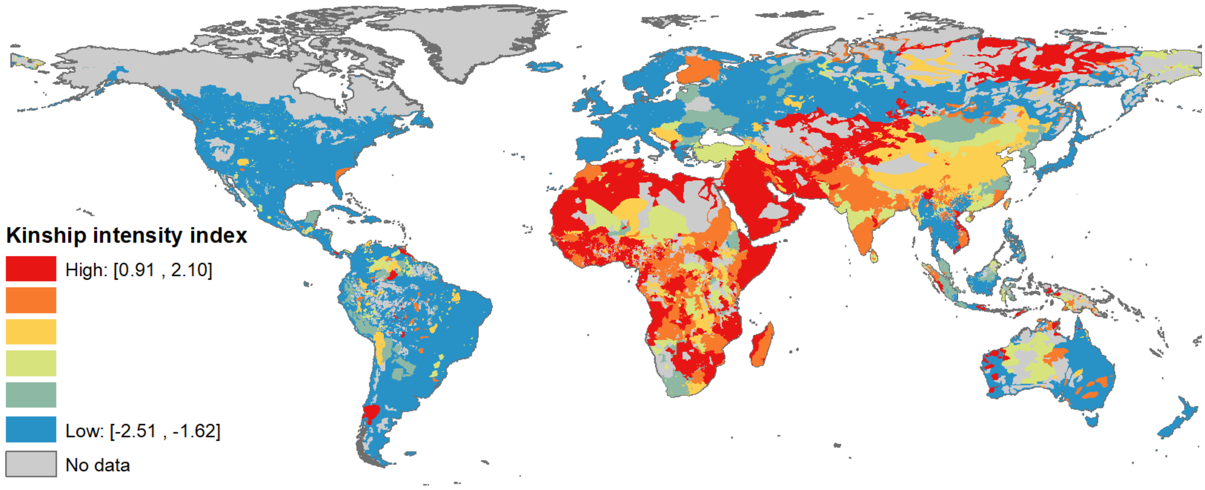

Figure 2: Distribution of the KII around the world for the 2,352 country-ethnicities matched with the language-tree matching method (described below).

The inbreeding coefficient (F)

Our second measure of kinship intensity, the inbreeding coefficient (denoted F), is a key variable in the field of population genetics that can be estimated using genetic data. F is an individual-level measure of the relatedness of one's parents, and so a society's average F should in principle correlate with its kinship intensity and in particular with its rate of endogamous marriage. Our estimator of F, which we denote F_{ROH}, uses an individual's genetic data to compute the fraction of their genome that is in runs of homozygosity (ROHs)—i.e., where the DNA inherited from the mother and father is identical. As we describe in more detail in Section 5, we estimated F_{ROH} for contemporary individuals in the Human Origins (HO) dataset (Reich Lab, 2020)—a dataset of genotyped individuals from populations around the world—and then computed $\overline{F_{ROH}}$, the mean F_{ROH} across the HO individuals matched to each Ethnologue language with at least eight matched HO individuals.

Because the KII ultimately derives from ethnographic observations, often made over the course of a year or so of field research, one might worry that it represents merely ideal behavior (vs. the ground truth of how people live their lives), or a snapshot in time of an otherwise unstable or rapidly changing pattern of kinship (Leach, 1964). Further, because it is based on observations from before industrialization and European colonization, one may be concerned that the KII does not reflect current practices. Using $\overline{F_{ROH}}$ measured among contemporary individuals as our alternative measure of kinship intensity allows us to verify that the KII captures stable cultural practices that have (at least partly) endured to this day. As we report below (in Table 6), F_{ROH} is positively associated with the KII and particularly strongly associated with the cousin-marriage-preference sub-indicator. Consistent with this, Pemberton and Rosenberg (2014) and Sahoo et al. (2021) also report positive associations between F and cousin marriage preferences or practices.

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[7] This is consistent with a model in which different societies' environments influence their optimal levels of kinship intensity, which can be achieved by adopting different kinship practices to varying degrees. That is, some kinship norms can substitute for others.

We emphasize that, although we estimate it using genetic data, F is not genetically determined. Rather, F provides us with a proxy that should track marriage practices—cultural traits that contribute to kinship intensity. To the extent it captures deep-rooted cultural practices, however, F should be rather stable through time.

2.2 Kinship intensity on the ground

To illustrate how kinship intensity shapes individual decision-making and societies, let's take a closer look at three populations with high, medium and low kinship intensity based on both their KII and F values.

2.2.1 The Marri Baluch ($KII = 2.10$; $\overline{F_{ROH}} = 0.062$)

Exemplifying a society with intensive kinship, the Marri Baluch are agro-pastoralists in Pakistan who live enmeshed in a hierarchy of patrilineages in a mountainous region lying about midway between Islamabad and Karachi. As described in Pehrson (1977)—on whom we mainly rely for this short ethnography—the nomadic Marri Baluch have traditionally relied primarily on herding sheep and goats, though some households (particularly elites) maintain mud houses in villages and engage in cereal farming, growing mostly wheat. The ownership of both land and animals is communal, though animals can be individually owned, and both forms of wealth are transferred corporately by the inheritance of a Marri identity from one's father. All pasture land is held in common (among Marris) but agricultural land is reapportioned every decade or so among large patrilineal groups according to the number of Marri men in each. Interestingly, although paternal kinship is the central factor in economic, political and social life, getting "counted" for land apportionment depends also on not having a low-caste or enslaved mother.

Marriages powerfully bind these patrilineages together, especially the small sub-lineages formed by fathers, sons and brothers—termed *wari*. To forge these ties, marriages are typically arranged for adolescent girls, who are "sold" by their fathers for a brideprice (e.g., 80 sheep) to other men. There are strong biases toward marriages within the same *wari*, a pattern reflected in the lower brideprices associated with such marriages. In one survey, 30 percent of marriages were between patrilateral parallel cousins—i.e., the children of two brothers—and another third were among other patrilateral relatives. In total, 72 percent of marriages were among kin and no marriages occurred outside of the Marri Baluch ethnic group. However, compared to many societies with intensive kinship, incest taboos are not particularly constraining on spousal choice: beyond primary female relatives (i.e., sisters, daughters, and mothers), men are only tabooed from having sex with the wives of their fathers, father's brothers, brothers, sons and brothers' sons.[8] Polygynous marriage is permitted up to four wives following Islamic law, though the relative equality among most men means this is largely limited to political elites (whose positions often depend on paternal succession). Curiously, inherited political offices among the Marri have no customary power to tax except for the purposes of paying brideprices for wives—thus, taxation facilitates polygyny, allowing elite men to weave larger kin networks through marriage. In one study, only 5 percent of Marri households were polygynous at any one time. Upon marriage, new wives move to live with their husband's family: post-marital

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[8] Note that we describe this from the male point of view here because males among the Marri Baluch are the primary decision-makers in this domain.

residence is strongly patrilocal. Women are essentially owned and controlled by either their fathers or husbands.

Economically, labor is primarily organized along kinship lines, with a division of labor by age and sex, and decision-making authority depends on the relationships involved such that fathers dictate to sons, husbands to wives, and elder brothers to younger siblings. The ability of households to protect their domesticated animals and women from theft and kidnapping depends on the honor and reputation (for revenge) of the *wari* and larger patrilineage. The honor and shame of men in the same patrileage is intertwined, so a son who acts cowardly stains the honor of his father and brothers (and other more distant paternal relatives to a diminishing degree).

This package of social norms creates substantial economic, social and political interdependence among relatives, especially among close patrilineal men, but also creates zero-sum competitions for farmland, pasture and mates. Several customs help bind together the *wari* that forms the core of economic life. For example, the extended incest taboos, by applying to precisely the women with whom a man might live in a nomadic camp, reduce sexual competition and mitigate concerns that men have about their wives engaging in adulterous affairs (which are rampant). Similarly, the preference for endogenous unions within the patrilineage effectively tightens the bonds within the *wari*, though it also forgoes an opportunity to forge marital alliances with other patrilineages or beyond. The combination of incest taboos and patrilineal endogamous marriage further reduces sexual competition within the *wari* and residential camps because it creates a situation in which, spouses aside, all co-resident adults fall under a sex taboo. Such a situation is particularly important in the nomadic herding context where men often leave their households for weeks at a time for herding, trading, raiding and wage labor.

These kin-based institutions create a tight circle of trust and sense of obligation that declines rapidly outside the *wari* and residential camp. Close matrilineal and affinal ties are recognized, and do matter, but they carry none of the sense of closeness or "duty" found in patrilineal relationships. The divisions created by kinship norms are reflected in frequent contrasts between *jind* ("one's own": *wari*), *azziz* (capturing "kinfolk," including in-laws), and *seyyal*, referring to strangers of equal status (e.g., the Pashtun or even unrelated Marri). To get a sense of how people think about these different categories, consider the following comment from a Marri about affines (from Pehrson (1977)):

> When you become affinally related to someone, then it is God's command not to do badness or rottenness to them. If they are strangers (*seyyal*), then there is no duty, it does not matter if you steal or fight. But when they become affines, then there is law... There are really no definite duties. But if you are going to do meritorious acts to someone, then you should do it to your affines.

Distrust of strangers pervades many economic interactions among the Marri Baluch. For example, managing farming and herding in small camps inevitably creates labor shortages. To hire a shepherd, a man first goes to his poorer patrilineal relatives, next to the matrilineal relatives, and finally to his affines. If he exhausts these labor sources, he reluctantly turns to strangers, but anticipates problems. As one man explained Pehrson (1977): "I usually give a shepherd three chances—on theft, lying, etc, and then send him away. For adultery, however, he goes immediately." Of 35 shepherds in 5 camps, only 3 were unrelated to the owners.

When conducting trading, Marri men rely on a network of *bradirs* as they move among camps, villages and towns. *Bradirs* represent an institutionalized friendship of sorts and act as primary trading partners, hosts and sources of information. Crucially, *bradirs* are inherited from father to son. Men report not trading in places where they lack *bradirs*—so trade hinges on a network of enduring personal relationships (Pehrson, 1977).

2.2.2 The Kurukh ($KII = -0.18$; $F = 0.016$)

Moving to a society with intermediate levels of kinship intensity, the Kurukh or Oraon communities (Roy, 1915) of the Nagpur Plateau (northeastern India) have kin-based institutions that are similar to the Marri Baluch's in important ways, but that have over time been weakened or replaced by non-kin-based institutions. Like the Marri Baluch, the Kurukh are patrilineal and patrilocal (brides move to live with their husbands), marriages are arranged, and men maintain patriarchal authority over their wives and children. Traditionally, the Kurukh were organized in patri-clans, but since moving from nomadic pastoralism into settled agriculture, which led to sustained contact with Hindu communities, Kurukh clans began to operate primarily as exogamous marriage units, considering it incestuous to marry someone from the same clan. Notably, such clan exogamy is the opposite of the tight clan endogamy preferred by the Marri Baluch. In addition to clan exogamy, the Kurukh also taboo sex or marriage among couples known to be related within three generations—so, anyone who shares a great grandparent is forbidden (thus, second cousins are taboo, but third cousins are not). However, ethnographic data suggest that families possess rather short genealogical memories so some second-cousin marriages do occur. Both polygynous marriage and communal property were probably important among the herding and hunting ancestors of the Kurukh, but monogamous marriage and privately owned land became universal when they adopted agricultural lifestyles.

Kurukh also possess institutions and public rituals for establishing formal, life-long, friendships. As with the Marri Baluch marrying out of their *wari*, new wives arrive from other communities and move into their husband's villages. Usually, these young women do not know anyone in their new home since wives arrive from many villages. However, unlike the Marri Baluch, the Kurukh have rituals that nurture a set of kin-like relationships among women. For example, approximately every three years, the word goes out from the female elders that every woman must select a *sahia*, or special village friend, from among the other married women in the village. Women may renew a prior *sahia* or add to their social network. At a communal ceremony, the ritual friends publicly greet each other and begin a series of ritualized and reciprocal exchanges of gifts, food, conversation and fellowship, including a visit to the goddess Devi. Their sacred friendship establishes life-long bonds that link not just the two wives, but also their entire (often unrelated) families.

The Kurukh often share their villages with other ethnic groups, including Hindus. Economically, the Kurukh depend on village norms that govern their interactions with other ethnic groups, who engage in a variety of occupations that support the Kurukh's farming efforts. Disagreements among households are adjudicated and policies set by a pluralistic council of elders, which includes members from across the village. There is also a higher council, with representatives from many villages, that addresses inter-village issues. These councils appear to be a retrofit version of the supra-clan institution that once organized the Kurukh's ancestors, modified to draw representatives from either diverse ethnic groups or different communities (instead of different clans).

Kin-based institutions play important roles for both the Marri Baluch and the Kurukh, but among the Marri Baluch kinship norms weave political, social and economic interdependence around a tightly bound patrilineage. Distinctively, though the Kurukh have clans and authoritarian fathers, their incest taboos compel marriages to socially distant Kurukh families, and other non-kin-based social norms govern economic and political interactions with both Kurukh and non-Kurukh villagers. Obviously, neither our KII or $\overline{F_{ROH}}$ measures directly tap all of these complexities—such as the ritualized friendships among Kurukh wives—but when non-kin-based institutions exist to support interaction, they often replace or supplant elements or reproductive events that are captured by our measures. Kinship norms that encourage, for example, economic interdependence or physical security among kinfolk tend to foster kin-based community organizations, alliances fashioned by cousin marriage, or extended families in co-residence. When other non-kin-based institutions take up these functions, these kin-based practices generally deteriorate.

2.2.3 The English ($KII = -2.14$; $F = 0.007$)

The Marri Baluch's and the Kurukh's more intensive kin-based institutions contrast with those found in European and European-descent societies, such as the English, who are characterized by love-based marriages (but often with taboos on cousins) that form small, monogamous nuclear families in which new couples reside neither with the bride's or the groom's families but establish a new residence. Descent is not a source of identity and is traced roughly equally through both mothers and fathers. With such tiny, ephemeral families, individuals must necessarily build their own network of friends and partners and seek out voluntary groups for economic production, religious devotion, and political activity. While debate about precisely when European kinship transformed into this peculiar pattern, ample evidence indicates that this occurred by the end of the Middle Ages and well before the Glorious, Scientific or Industrial Revolutions (Macfarlane, 1978; Mitterauer, 2010). A growing number of anthropologists and economists, building on work by historians, argue that by the High Middle Ages, the emergence of low intensity kinship fostered the proliferation of charter towns, guilds, universities and monastic orders as well as the expansion of impersonal trade and commerce (Greif, 2006a,b; Greif and Tabellini, 2010; Henrich, 2020; Schulz, 2022).

3 Data

This section describes the data used in our main analyses (aside from our kinship intensity data), including our measures of economic performance and our control variables. Here, we outline how we matched data from various sources. Appendix A.1 describes in detail all the variables and data sources, and Tables B.2.1, B.3.1, B.4.1, B.5.1, B.6.1, B.7.4, and B.7.5 provide summary statistics for all the variables.

3.1 Measuring economic performance

In most of our analyses, we rely on nighttime luminosity data from satellites to measure economic prosperity at the micro-level (pixels). Because we are interested in *per capita* levels of economic development, in most specifications we control for log population density. Specifically, we regress the logarithm of nighttime luminosity on the KII (or $\overline{F_{ROH}}$)

and log population density (and other controls). When the coefficient on log population density is unity, this is equivalent to regressing log nighttime luminosity *per capita* on the KII (and other controls). In fact, in nearly all the regressions we report below with luminosity as the dependent variable, the estimated coefficient on log population density is close to unity. We further discuss this below in Section 4.1. To verify the validity of our results with the luminosity data, in some analyses we use regional GDP per capita as an alternative measure of economic performance.

3.1.1 Satellite nighttime luminosity data

As our primary measure of economic development, we followed a now common practice in using satellite nighttime luminosity data, also referred to as light density data, to capture economic development around the globe (Donaldson and Storeygard, 2016; Michalopoulos and Papaioannou, 2018; Henderson et al., 2018). Ample evidence, including our own analyses using regional GDP per capita, indicate that luminosity is a good proxy for economic prosperity (Chen and Nordhaus, 2011). Importantly, for our purposes, nighttime luminosity data is available at fine scales, which allows us to aggregate and match it to the geographic areas peopled by the ethnolinguistic groups for which our kinship intensity measures are available.

Following Henderson et al. (2018), we use the 2010 Global Radiance Calibrated Nighttime Lights data.[9] The raw luminosity data is presented as a grid of pixels with dimensions of 30 arc-seconds ($\frac{1}{120}$ of a degree) by 30 arc-seconds, or approximately one square kilometer at the Equator.[10] We aggregate the original pixels—henceforth labeled as "subpixels"—to larger pixels of size 0.125 ($\frac{1}{8}$) degrees x 0.125 degrees ($\sim$ 191 square kilometers at the Equator) by taking the mean of nighttime luminosity across the 225 original subpixels. This aggregation mitigates the problem of overglow into a pixel due to light emanated from nearby pixels and also mitigates concerns about spatial correlation at finer scales.

Next, we apply several filters to prepare the luminosity data for our analyses. First, we drop all pixels that do not cover land within the borders of a country, and thus all pixels in large bodies of water. Some of the remaining pixels after that step are partially covered by water or permanent ice. Luminosity is recorded as zero for subpixels that fall on water or permanent ice, so we normalize the pixels' mean luminosity by dividing it by the fraction of their component subpixels that are covered by land.[11] This gives us a sample of 926,864 pixels around the globe.

Second, and relatedly, night lights may appear brighter than they are over water or ice-covered areas. We largely avoid this blurring issue by dropping the pixels for which more than 25 percent of the area is covered by water or permanent ice ($\sim$ 2.5% of the remaining pixels at this stage). We also drop pixels through which a coastline passes

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[9] These data are available online at `https://ngdc.noaa.gov/eog/dmsp.html`. Other, uncalibrated versions of the data use a strong amplification to detect low levels of light, which can saturate measurement in the most brightly lit pixels such as those in large cities, leading to top coding of those pixels. The radiance-calibrated data we use combines a high-amplification regime for low-light pixels and a low-amplification regime for more brightly lit pixels, thus removing all top coding (Henderson et al., 2018).

[10] There are 3,600 arc-seconds in a degree. Pixel size varies with latitude: the higher the latitude, the smaller the pixel. This will not be an issue in our analyses since the luminosity data measure the *density* of light (i.e., the light emitted from a pixel divided by the pixel's area).

[11] This is similar to the approach used by Henderson et al. (2018).

(∼ 3.5% of the remaining pixels).

Third, around 70% of the remaining pixels emit too little light and are coded as zero. Following Henderson et al. (2018), we consider this a censoring problem since the lowest nonzero values are considered noise and generally recoded to zero in the initial data processing by the data's curators. Assuming that all pixels emit some positive amount of light, we assign the lowest nonzero value (0.013) from across all the pixels to the pixels that are coded as zero. Since we will take the logarithm of nighttime luminosity, this step allows us to include these recoded pixels in our analyses.

Fourth, we drop pixels with zero population density (∼ 9.7% of the remaining pixels) and pixels where one or more of the geographic control variables (which we include in our main specifications) are missing (∼ 0.5%).

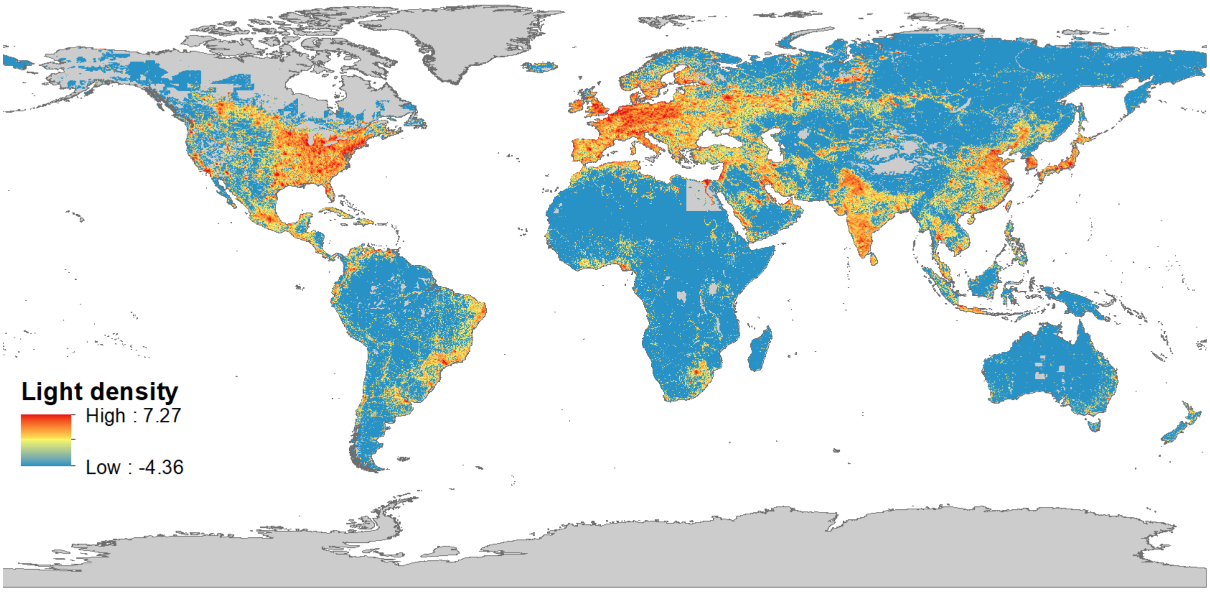

Figure 3: Distribution of log nighttime luminosity across the world. Unpopulated regions are in gray. In some areas or countries, such as Egypt, population data is available at a fine scale and unpopulated areas (like deserts) are coded as such; in other areas, population data is more heavily smoothed.

Applying these filters leaves 783,525 pixels in our sample. Figure 3 displays the variation in log nighttime luminosity across these pixels around the world. Appendix Figure B.1.1 shows histograms of nighttime luminosity, but without the pixels that were recoded with the lowest nonzero value (0.013). As can be seen, the log transformation reduces skewness. Therefore, and following the literature (Michalopoulos and Papaioannou, 2018), in the rest of the paper we will use the natural logarithm of nighttime luminosity.

3.1.2 Population data

We use fine-grained population density data for the year 2010 from the Gridded Population of the World (GPW), adjusted to the 2015 Revision of the United Nation's World Population Prospects (Center for International Earth Science Information Network (CIESIN) at Columbia University, 2016). The GPW assumes uniform population density within statistical units. Therefore, population estimates are more heavily smoothed in countries with lower statistical capacity and in more sparsely populated regions. The GPW population density data is reported at a 30 arc-second resolution. We aggregate the data to 0.125-degree pixels by taking the mean across component subpixels, and then take the natural logarithm of population density for each pixel.

Although population density is itself often used as a proxy for economic development, our primary analyses focus on the relationship between kinship intensity and nighttime luminosity while holding population density constant. As illustrated in Appendix Figure B.1.2, log population density has a convex relationship with log nighttime luminosity. The relationship is flat when population density is lower than 1 person per square kilometer (i.e., when log population density is less than 0), but increasing and approximately linear at higher levels of population density. To avoid large variations in log population density driven by minor differences in population density across low density pixels, we recoded to 1 the population density of all pixels whose original population density was less than 1 person per square kilometer.[12]

3.1.3 Regional GDP per capita data

To verify that our analyses of the association between kinship intensity and nighttime luminosity are robust to using a more direct measure of economic development, we also analyze data from Gennaioli et al. (2014) on regional per capita GDP (in Section 4.2). The data include GDP per capita in constant 2005 PPP dollars for 1,528 regions in 83 countries between 1950 and 2010. We drop regions that are too small (consisting of less than five pixels) and end up with a sample of 1,452 regions. Appendix Figure B.3.1 shows the variation in per capita GDP across these regions.

3.1.4 Nighttime luminosity, population density, and regional GDP per capita

We conducted a simple exercise, following Henderson et al. (2018), to verify that global variation in nighttime luminosity reflects not just variation in population density, but also differences in income per capita. We aggregated our luminosity and population data to the level of subnational regions and, using Gennaioli et al.'s regional GDP per capita data for the year 2010 (the latest year available), regressed log nighttime luminosity on log population density and then log regional GDP per capita. Without country fixed effects, the R^2's from regressing log luminosity on log population density, then on GDP per capita alone, and finally on both, are 0.530, 0.338 and 0.839, respectively. When the data are demeaned by country, the corresponding R^2's are 0.819, 0.112, 0.856. These results highlight that much of the variation in nighttime luminosity across world regions is predicted by both population density and GDP per capita; within countries, much of the variation in luminosity is predicted by variation in population density, though some residual variation is also predicted by GDP per capita.

3.2 Control variables

Throughout our analyses, we estimate specifications with controls for geographic, ecological and cultural variables that capture potentially relevant factors based on prior research. Our baseline set of geographic controls includes temperature, precipitation, agricultural suitability, absolute latitude, elevation, ruggedness, distance to coast, and

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[12] For comparison, Mongolia is the least densely populated country in the world, with 2.1 people per square km.

distance to the nearest river or lake. These variables are important for agriculture and trade and are associated with worldwide and within-country variation in economic development and nighttime luminosity (Henderson et al., 2018). The raw data for these variables comes from various sources and are reported at different scales ranging from 1/120- to 1/2-degree pixels (see Table A.1 for details). For the variables that are defined at smaller scales than 0.125 degrees, we convert the data to 0.125-degree pixels by taking the mean across component subpixels. For variables that are defined at larger scales, all 0.125-degree pixels that fall inside a larger pixel receive the same value.

We also verify the robustness of our results to controlling for a pixel-level measure of ecological suitability for malaria (Kiszewski et al., 2004). The prevalence of malaria positively correlates with kinship intensity ($\hat{\rho} = 0.406$, $p < 0.001$, $n = 713$ country-ethnicities), and may foster the cultural evolution of higher levels of kinship intensity (Enke, 2019).

Additionally, we verify the robustness of our results to controlling for subsistence activities and a political hierarchy variable. To control for subsistence activities, we include a set of variables from the EA that measure the fraction of each society's economy that depends on gathering, hunting, fishing, animal husbandry, and agriculture (see Appendix A.1 for details). The EA includes five variables—one for each mode of subsistence—and we adjusted these so that they sum to 1 for each society and omitted the variable for gathering from the regressions. As discussed above, a population's mode of subsistence likely influences its KII. For instance, anthropologists have long argued that mobile hunter-gatherers culturally evolved extensive kinship as a form of social insurance against environmental shocks with low spatial autocorrelation (Yellen and Harpending, 1972; Kramer and Greaves, 2011). "Political hierarchy", also commonly referred to as "jurisdictional hierarchy", is a variable from the EA that counts the jurisdictional levels beyond the local community for each society (Michalopoulos and Papaioannou, 2013). This variable correlates negatively with the KII ($\hat{\rho} = -0.190$, $p < 0.001$, $n = 678$ EA societies) and has previously been linked to nighttime luminosity, so it could confound our results.

3.3 Matching data

To integrate the various datasets we draw on, we first matched ethnographic variables from the EA (including the KII) and genetic variables from the HO dataset (including the inbreeding coefficient) to languages from the 17th edition of the Ethnologue (Gordon, 2005; Lewis, 2009). To match the EA variables, we followed the method developed by Giuliano and Nunn (2018) and matched the language spoken by each EA society to the languages in the Ethnologue (each EA society is associated with a single language). The Ethnologue maps the geographic boundaries within which each contemporary language is spoken. We refer to the ethnolinguistic group that speaks a given language within a given country as a "country-ethnicity" and to the area where the country-ethnicity lives as its "country-homeland", but sometimes only use the terms "ethnicity" and "homeland" for simplicity. Thus, in our terminology, a language that is spoken in multiple countries is associated with multiple country-ethnicities. The homelands of separate country-ethnicities often overlap, but we exclude overlapping areas from our analyses.

We employed two different matching methods. With the direct matching method, we matched the language spoken by each EA society to the exact same Ethnologue language and dropped unmatched languages. In the language-tree matching method, we followed

Giuliano and Nunn (2018) and Bahrami-Rad et al. (2021) and, for each EA variable, we matched each Ethnologue language to the linguistically closest EA society that speaks a language within the same language family and with nonmissing data for the variable. If no such society exists, the variable was coded as missing for that language. We report the analyses using the direct matching method in the main text and those using the language-tree matching method in the Appendix.

For the analyses using the inbreeding coefficient (F), we matched each population from the Human Origins (HO) dataset to a single Ethnologue language (and to the single or multiple country-ethnicities associated with that language). This is similar to the direct-matching method described above for the EA data, but details of the two procedures differ because the HO data typically does not indicate the language spoken by each population. Appendix C.2 provides more details.

Next, we used a shapefile provided by the World Language Mapping System (World GeoDatasets)[13] to match the country-ethnicities associated with the Ethnologue languages to pixels. We dropped pixels that were matched to more than one country-ethnicity, fell on the boundaries of a country-homeland, or matched to a country-ethnicity with a very small country-homeland comprising less than five pixels. Tables B.2.1 and B.6.1 show summary statistics for the resulting samples of pixels.

Finally, to match pixel-level data to subnational regions (in Section 4.2) or countries (in Section 6.3), we computed the population-weighted mean of each ethnographic variable as well as the simple mean of each geographic control across the pixels in each region or country. We then dropped regions or countries for which the pixels with nonmissing KII data accounted for less than 75% of the population. For the analyses at the country-ethnicity level, each country-ethnicity was assigned its matched EA variables and we took the simple mean of each geographic control across the pixels in its country-homeland.

Appendix A.2 provides additional details on the matching process.

4 Kinship intensity and economic development

We now examine the association between our primary measure of kinship intensity, the KII, and economic development. To begin, in Section 4.1, we estimate a battery of OLS regressions of nighttime luminosity on the KII and controls. Next, in Section 4.2, we perform a parallel set of analyses by replacing our luminosity measure with a measure of regional GDP per capita. Finally, in Section 4.3, we conduct a spatial regression discontinuity (RD) analysis of the association between luminosity and the KII.

4.1 Kinship intensity and nighttime luminosity

We begin by examining the relationship between nighttime luminosity and the KII, focusing on the sample that includes the country-ethnicities matched using the direct matching method. Figure 4 shows a negative relationship across country-ethnicities between the KII and the logarithm of nighttime luminosity after partialling out log population density ($\hat{\rho} = -0.350$, $p < 0.001$, $n = 713$).

To more thoroughly examine the association between luminosity and the KII, we adopt the following baseline specification, using geographic pixels as the unit of observation:

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[13] The shapefile is available at `worldgeodatasets.com/language`.

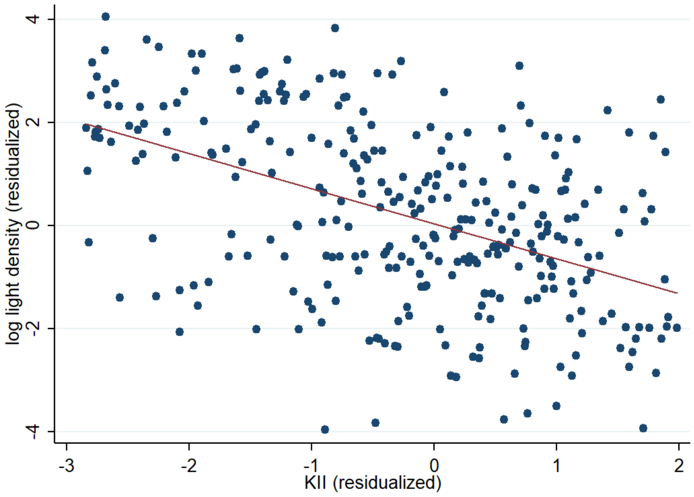

Figure 4: Log nighttime luminosity vs. the KII, both residualized on log population density, across country-ethnicities.

$$L_{i,e,c} = \alpha + \beta KII_e + \delta \log(P_{i,e,c}) + \gamma X_{i,e,c} + \lambda_c + \theta V_{(i),e} + \epsilon_{i,c}, \tag{1}$$

where $L_{i,e,c}$ is the natural logarithm of the nighttime luminosity of pixel i in country-ethnicity e's homeland in country c. KII_e is the KII of country-ethnicity e, which takes the same value for all the pixels in e's homeland; $P_{i,e,c}$ is the pixel's population density; $X_{i,e,c}$ is the vector of geographic variables that includes temperature, precipitation, agricultural suitability, absolute latitude, elevation, ruggedness, distance from the coast, and the distance to the nearest river or lake; λ_c denotes continent or country fixed effects; and, $V_{(i),e}$ includes additional controls (defined at the pixel or country-ethnicity level, in some specifications).

As mentioned earlier, we control for log population density in most specifications because we are interested in *per capita* levels of economic development. If we subtract $\log(P_{i,e,c})$ from both sides of equation (1) and let $\delta = 1$, the left-hand-side becomes the logarithm of luminosity per capita. We estimate δ as a free parameter to allow the luminosity-population density elasticity to differ from unity (Michalopoulos and Papaioannou, 2018).[14] As it happens, our estimates of δ are close to unity in nearly all our regressions with luminosity as the dependent variable (including those in other sections reporting other types of analyses), and so we can interpret the β coefficient on the KII in equation (1) as capturing the association between the KII and the logarithm of luminosity *per capita*.

In most specifications, we account for spatial correlation in the data by clustering standard errors at the country level. We also verify the robustness of our results to clustering at the level of the language families (based on the Ethnologue) and at both the country and language family level using two-way clustering (Cameron and Miller, 2015). [15] When computationally feasible (i.e., for analyses for which the unit of observation

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[14] Even if the true luminosity-population density elasticity were unity, the population density data is noisy, so the elasticity of luminosity with *measured* population density may be lower than unity.

[15] This approach is conservative. Language families often encompass a wide range of regionally dispersed ethnicities (e.g., Indo-European languages have historically been spoken from Europe to the North of India), and together with country clusters they capture spatial autocorrelation and non-independence due to shared history and culture.

is larger than a geographic pixel), we also compute Conley standard errors; following Colella et al. (2019), we estimate these for various distance cutoffs and report the largest standard error across these cutoffs (we use cutoffs ranging from 500 km to 10,000 km, with increments of 500 km).

Table 1: The KII and nighttime luminosity: cross-section

	Log nighttime luminosity									
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)
KII	-0.340**	-0.512***	-0.420***	-0.136***	-0.110***	-0.066	-0.085**	-0.101***	-0.110***	-0.110***
	(0.138)	(0.143)	(0.129)	(0.046)	(0.024)	(0.045)	(0.041)	(0.025)	(0.024)	(0.024)
Log population density		0.985***	0.992***	1.084***	1.067***	1.066***	1.066***	1.063***	1.067***	1.067***
		(0.064)	(0.051)	(0.071)	(0.061)	(0.063)	(0.063)	(0.061)	(0.104)	(0.106)
Subsistence variables						yes				
Political hierarchy							yes			
Malaria index								yes		
Geographic controls			yes	yes	yes	yes	yes	yes	yes	yes
Continent FE				yes						
Country FE					yes	yes	yes	yes	yes	yes
Observations	377,656	377,656	377,656	377,656	377,656	377,656	373,070	377,656	377,656	377,656
R-squared	0.032	0.488	0.537	0.582	0.660	0.660	0.661	0.660	0.660	0.660
Number of clusters	138	138	138	138	138	138	138	138	62	62 & 138

Notes: Each observation is a pixel in the homeland of a country-ethnicity matched with the direct matching method. The geographic controls include temperature, precipitation, agricultural suitability, absolute latitude, elevation, ruggedness, distance to coast, and distance to the nearest river or lake. The subsistence variables measure the fraction of an ethnicity's subsistence economy that depends on hunting, fishing, animal husbandry, and agriculture (with gathering as the omitted category). Standard errors in parentheses are clustered at the country level in all regressions, except in column 9, where they are clustered at the language-family level, and in column 10, where they are clustered two-way at both the country and language-family levels. *** $p < 0.01$, ** $p < 0.05$, * $p < 0.1$

Table 1 summarizes the results of specifications that include various subsets of the covariates in equation (1). Column 1 reports a simple regression of log luminosity on the KII only and column 2 report the same regression with log population density added as a control. Adding log population density to the simple regression, which permits us to interpret KII's estimated coefficient, $\hat{\beta}$, in per capita terms, increases the estimate to -0.512, indicating that a one-standard deviation increase in the KII is associated with a $\sim 40\% \ (= (1 - e^{-0.512}) \cdot 100\%)$ decrease in luminosity per capita. In all columns, the estimated coefficient on log population density is close to unity. In column 3, where we add the geographic controls, β decreases in magnitude to -0.42. Adding continent and country fixed effects, in columns 4 and 5, reduces the magnitude of the estimates to -0.136 and -0.110, but also decreases the standard errors, so the estimates of β remain significant. This latter estimate, with country fixed effects, implies that a one-standard-deviation increase in the KII is associated with a $\sim 10.4\%$ decrease in luminosity within countries.

In columns 6 to 8, we control for potentially endogenous correlates of the KII that may confound its association with luminosity. In columns 6 and 7, respectively, we control for each ethnicity's subsistence economic activities and degree of political hierarchy; and in column 8, we control for the pixel-level malaria index. Finally, in column 9, we cluster standard errors at the language-family level, and in column 10, we use two-way clustering at both the country and language-family levels. Our results are robust to these alternative specifications.[16]

To confirm that these results do not hinge on our use of the direct matching method, we re-run the above analyses using the expanded sample based on matches from the language-tree matching method. Table B.2.2 shows similar, if slightly smaller (in magnitude) estimates for β.

We also examined the robustness of these results to analyzing the data at the country-ethnicity level instead of at the pixel level, using both the direct (Table B.2.3 Panel A) and language-tree matching methods (Table B.2.3 Panel B). In addition to specifications that parallel those in Table 1, we report Conley standard errors (in column 11); following Colella et al. (2019), we report these for the cutoff that maximizes the standard error (1,500 km, here). With the direct-matching method, the estimates of β are similar but somewhat larger in magnitude and are robust across the specifications, including with Conley standard errors. With the language-tree matching method, the results are only significant without continent or country fixed effects.

To examine whether the associations between luminosity and the KII are driven by a subset of the five KII sub-indicators, we estimated the specification in columns 3 (with the geographic controls) and 5 (with country fixed effects as well) of Table 1 again, but separately replacing the KII with each of the five sub-indicators in turn. Panel A of Table B.2.4 shows the results obtained with the direct matching method. The associations between luminosity and the sub-indicators are all negative (except for cousin marriage preference in column 2, which is nearly 0), and most are significant at the 5% level. The results with the language-tree matching method (in Panel B) are similar. Thus, most of our five sub-indicators are associated with less nighttime luminosity, and none is associated with greater prosperity. This gives us confidence in the theoretical soundness of our KII construct and in the appropriateness of aggregating the five sub-indicators into the KII to study its association with economic development.

4.2 Kinship intensity and regional GDP per capita

Now, using a more direct, but less fine-grained measure of economic development, log regional GDP per capita (mapped in Figure B.3.1), we verify the predicted association between kinship intensity and economic development. To remain consistent with the above analyses of nighttime luminosity, we estimate similar specifications, except that we now include year, year-continent, or year-country fixed effects in the models (because of the panel nature of the data), and do not include population density (since the dependent variable is already in per capita terms). As above, we cluster standard errors at the country level. We use the same set of control variables, constructed from the same data sources, and estimate one additional specification that also controls for a dummy equal to 1 if the national capital is located in the region as well as for each region's cumulative oil, gas, and liquid natural gas production from the time production began to 2000.

Table 2 reports the results based on the direct matching method. In column 1, where we only control for year fixed effects, the estimated coefficient on the KII is -0.445, implying that a one-standard-deviation increase in the KII is associated with a $\sim 36\%$ decrease in GDP per capita. Adding the geographical controls (in column 2) and year-continent (in column 3) or year-country (in column 4) fixed effects reduces the magnitude

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[16] The KII's estimated coefficient loses significance in column 6, but the analogous result is significant in the sample obtained with the language-tree matching method (Table B.2.2) and our results are generally robust to controlling for the subsistence variables in our other analyses.

Table 2: The KII and regional GDP per capita: panel data

	Log regional GDP per capita								
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)
KII	-0.445***	-0.459***	-0.455***	-0.085**	-0.168***	-0.129***	-0.081**	-0.081**	-0.085**
	(0.105)	(0.092)	(0.094)	(0.034)	(0.039)	(0.046)	(0.034)	(0.038)	(0.040)
Subsistence variables					yes				
Political hierarchy						yes			
Malaria index							yes		
Oil and Gas production								yes	
Capital is in Region								yes	
Geographic controls		yes	yes	yes	yes	yes	yes	yes	yes
Year FE	yes	yes							
Year × Continent FE			yes						
Year × Country FE				yes	yes	yes	yes	yes	yes
Observations	5,514	5,514	5,514	5,514	5,514	5,514	5,514	5,514	5,514
R-squared	0.313	0.511	0.610	0.889	0.890	0.889	0.890	0.902	0.112
Number of clusters	61	61	61	61	61	61	61	61	

Notes: Each observation is a region-year in the analysis sample obtained with the direct matching method. The geographic controls include temperature, precipitation, agricultural suitability, absolute latitude, elevation, ruggedness, distance to coast, and distance to the nearest river or lake. The subsistence variables measure the population-weighted fraction of a region's ethnicities' subsistence economies that depend on hunting, fishing, animal husbandry, and agriculture (with gathering as the omitted category). Standard errors in parentheses are clustered at the country level in all regressions, except in column 9 where Conley standard errors (with a distance cut-off of 3,500 km) are reported. *** $p < 0.01$, ** $p < 0.05$, * $p < 0.1$

of the estimated coefficient on the KII, but also increases precision; as a result, the coefficients remain significant at the 1% or 5% level. The estimated coefficient in column 4, with country-year fixed effects, is -0.085, implying that a one-standard-deviation increase in the KII is associated with a $\sim 8\%$ decline in GDP per capita within countries. These estimates are strikingly similar to those in Table 1, which imply that a one-standard deviation increase in the KII is associated with a $\sim 40\%$ decrease in luminosity per capita, and a $\sim 10\%$ decrease within countries.

Columns 5 to 7 parallel the specifications in Table 1 with additional controls for the subsistence variables, political hierarchy, and the malaria index. In column 8, we control for cumulative oil and gas production and for the dummy indicating whether the national capital is located in the region. In column 9, we follow Colella et al. (2019) and report the Conley standard error at the distance cutoff at which it is the largest (3,500 km). Table B.3.2 shows the results in the expanded sample obtained using the language-tree matching method. The results remain robust across all of these alternative specifications.

4.3 Spatial regression discontinuity analysis

Our estimates of the association between the KII and economic development are generally robust to the inclusion of a rich set of control variables, including geographic, ecological and cultural variables as well as country fixed effects. Despite this, it is possible that unobservable factors may confound our results. To address these concerns, we conducted a spatial regression discontinuity (RD) analysis following Michalopoulos and Papaioannou (2013) and Moscona et al. (2020). We compared the luminosity of pixels that are geographically close to one another but belong to the homelands of neighboring country-ethnicities that vary in their kinship intensity. This estimation strategy helps account for unobservable factors that vary smoothly across space, such as distance to the central government and power centers, distance to trade routes, infrastructure, and geographic characteristics like suitability for certain subsistence practices that co-determine kinship intensity and economic prosperity.

For our baseline RD analysis, we restrict the sample to pixels that belong to pairs of contiguous country-ethnicities and whose centroids are within 200 km of the ethnic boundary between two country-ethnicities. To address concerns that country-level unobservables such as national institutions may bias the estimates, we further restrict the sample to pairs of ethnicities located in the same country. Below, we report results based on the sample obtained with the direct matching method (Section 3.3), but we verified that they are robust to using the language-tree matching method (Table B.4.2).

Figure 5 illustrates this setup for a pair of contiguous country-ethnicities in Zimbabwe: the Ndebele and the Venda. All pixels within 200 km of the boundary are included, with the exception of pixels that fall directly onto an ethnic boundary or a country border (since those pixels cannot readily be attributed to only one ethnicity or country). The Venda, whose KII is 1.95, have higher kinship intensity than the Ndebele, whose KII is −0.16.

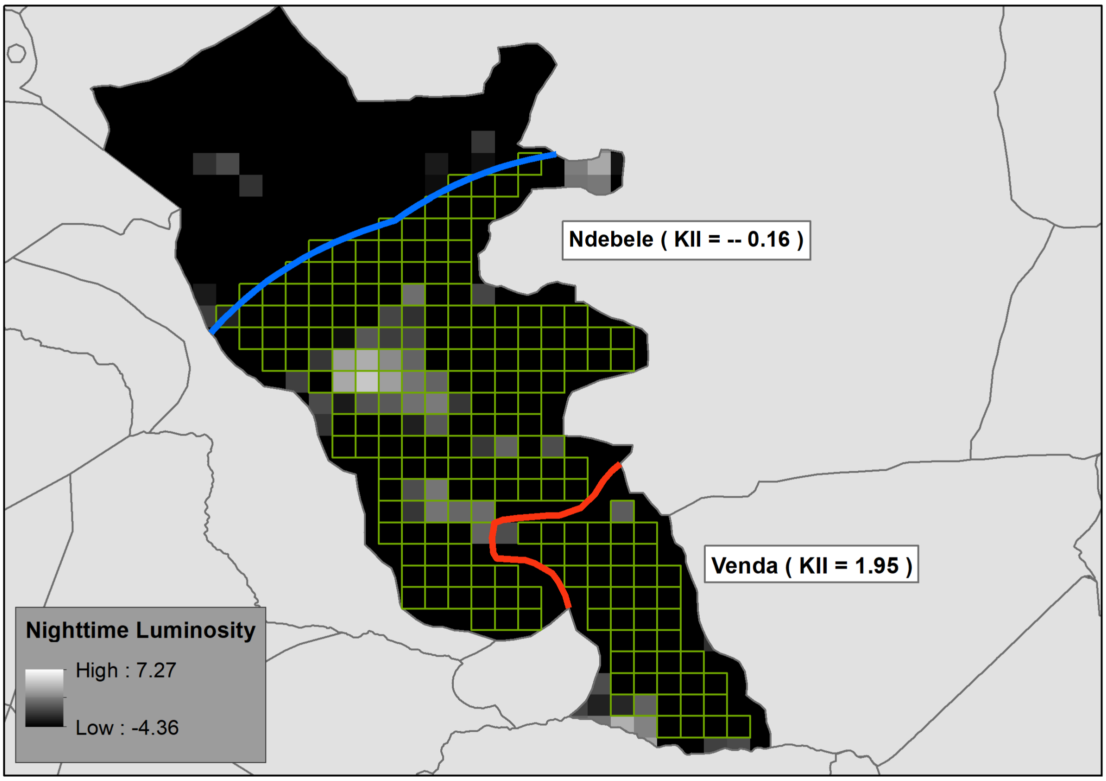

Figure 5: The map shows the nighttime luminosity of the pixels (marked by green squares) for a pair of contiguous country-ethnicities in Zimbabwe: the Ndebele (to the North) and the Venda (to the South). The red line is the ethnic boundary that separates the two ethnicities, and the blue line is located 200 km away from it. We drop pixels whose centroid is not located within 200 km of the ethnic boundary as well as pixels that are crossed by an ethnic boundary or by national borders.

We begin by graphically examining the relationship between luminosity and the distance to the boundary separating the ethnicities in the pairs, for the set of pixels used in our baseline analysis. Figure 6 shows a binned scatterplot of log luminosity residualized on log population density (on the y-axis) vs. distance to the ethnic boundary (on the x-axis). Distance to the boundary is negative for pixels in the homeland of the country-ethnicity that has the lower KII in a pair, and positive for the country-ethnicity with the higher KII. The figure reveals a discontinuity at the boundary. While luminosity is rather uniformly distributed to the left and to the right of the boundary, it sharply drops at the ethnic boundary as we move from groups with lower KII values to those with higher values.

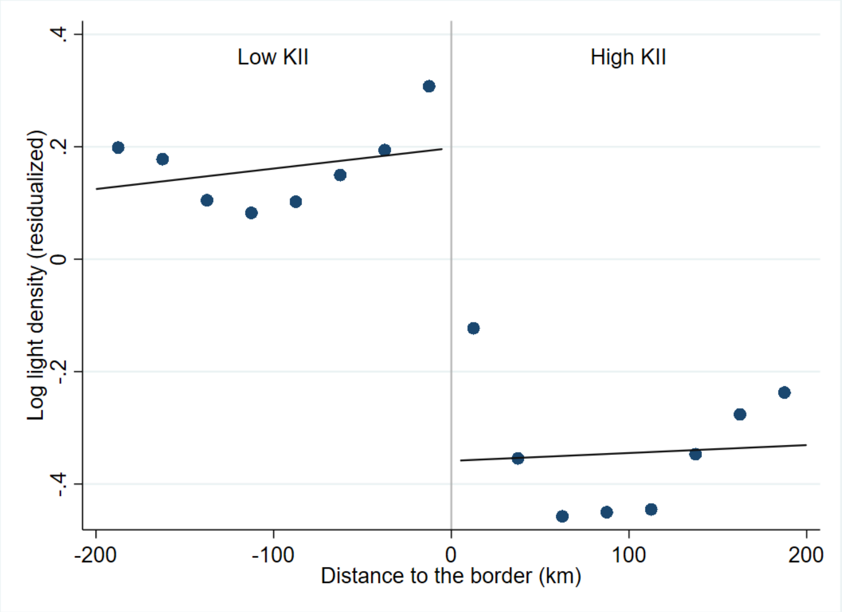

Figure 6: Binned scatterplot of the relationship between distance to the boundary and luminosity, across pixels located in the homelands of pairs of adjacent country-ethnicities in the same country. The y-axis shows log luminosity residualized on log population density. The x-axis shows the distance to the boundary in kilometers, with negative distances for pixels associated with the country-ethnicity with the lower KII in a pair, and positive distances for the country-ethnicity with the higher KII. We created 16 bins based on the pixels' distances to the boundary (each bin spans 25km). The average KII across the pixels that belong to ethnicities with the relatively low KII is -1.54; for ethnicities with relatively high KII values, $KII = 0.09$.

Next, to implement our formal spatial RD analysis, we adopt the following specification:

$$L_{i,e(e'),c} = \beta KII_e + \delta \log(P_{i,e,c}) + \gamma X_{i,e,c} + \theta V_{(i),e} + \lambda_{ee',c} + f(D_{i,e(e'),c}) + \epsilon_{i,e(e'),c}. \qquad (2)$$

The dependent variable $L_{i,e(e'),c}$ is the natural logarithm of the nighttime luminosity of pixel i in the homeland of country-ethnicity e that is adjacent to the homeland of country-ethnicity e', with both e and e' in the same country c.[17] We include ethnicity-pair fixed effects ($\lambda_{ee',c}$), which account for all (unobserved) factors unique to each ethnicity-pair. Following Gelman and Imbens (2019) and Moscona et al. (2020), we also include a local linear polynomial based on the geodesic distance of each pixel's centroid from the boundary between the two adjacent ethnicities, $f(D_{i,e(e'),c})$, with different coefficients on the distance term for the relatively high and the relatively low KII ethnicities in the pairs. As in equation (1), KII_e is the KII for country-ethnicity e, $P_{i,e,c}$ is the pixel's population density, $X_{i,e,c}$ is the vector of geographic controls, and $V_{(i),e}$ denotes the additional controls used in some specifications.

Table 3 reports the results for this baseline specification. In column 1, the simple regression of nighttime luminosity on the KII but without log population density delivers

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[17] Note that a pixel can enter the regression multiple times as separate observations if it falls in the homeland of a country-ethnicity that is in multiple pairs.

an estimate of $\hat{\beta} = -0.081$. Adding log population density reduces the magnitude of the estimate to $\hat{\beta} = -0.060$ (column 2) but also more than halves the standard error.[18] Further holding constant our battery of geographic variables (column 3) yields $\hat{\beta} = -0.072$. Since all the ethnicity pairs in this analysis are in the same country, these results imply that a one-standard deviation increase in the KII is associated with a $\sim 7\%$ decrease in luminosity within countries.

Table 3: The KII and nighttime luminosity: spatial RD analysis

	Log nighttime luminosity							
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
KII	-0.081	-0.060***	-0.072***	-0.085**	-0.078**	-0.071***	-0.072***	-0.072***
	(0.050)	(0.019)	(0.017)	(0.039)	(0.038)	(0.017)	(0.018)	(0.018)
Log population density		1.088***	1.059***	1.056***	1.061***	1.056***	1.059***	1.059***
		(0.084)	(0.077)	(0.079)	(0.076)	(0.077)	(0.112)	(0.115)
Subsistence variables				yes				
Political hierarchy					yes			
Malaria index						yes		
Log population density		yes	yes	yes	yes	yes	yes	yes
Geographic controls			yes	yes	yes	yes	yes	yes
Distance-to-the-boundary polynomial	yes	yes	yes	yes	yes	yes	yes	yes
Ethnicity pair FE	yes	yes	yes	yes	yes	yes	yes	yes
Observations	290,669	290,669	290,669	290,669	289,740	290,669	290,669	290,669
R-squared	0.375	0.600	0.613	0.613	0.614	0.614	0.613	0.613
Number of clusters	70	70	70	70	70	70	58	58 & 70

Notes: Each observation is a pixel that belongs to a country-ethnicity in a pair of contiguous ethnicities in the same country, and that falls within 200 km of the boundary between the two ethnicities. The geographic controls include temperature, precipitation, agricultural suitability, absolute latitude, elevation, ruggedness, distance to coast, and distance to the nearest river or lake. "Distance-to-the-boundary polynomial" is the geodesic distance of each pixel's centroid from the boundary between the two adjacent ethnicities; we allow the coefficient on the distance term to differ between the relatively high and the relatively low KII ethnicities in the pairs. The subsistence variables measure the fraction of an ethnicity's subsistence economy that depends on hunting, fishing, animal husbandry, and agriculture (with gathering as the omitted category). Standard errors in parentheses are clustered at the country level (in columns 1-6), language family level (in column 7), and two-way clustered at both the country and language-family levels (in column 8). *** $p < 0.01$, ** $p < 0.05$, * $p < 0.1$

In columns 4–6, $\hat{\beta}$ remains fairly stable when we add controls for the subsistence variables, political hierarchy, and the malaria index. Similarly, in columns 7 and 8, in which we cluster at the language-family level or use two-way clustering at both the country and language-family levels, $\hat{\beta}$ remains stable and the standard error does not appreciably increase.

Table 4 shows the results of several additional robustness checks. In columns 1 and 2, we exclude ethnicity-pairs for which the difference in KII is less than 0.1 or 1 standard deviations, respectively. In column 3, to address concerns that some pixels that are part of a large number of ethnicity-pairs receive too much weight in the regressions, we drop pixels that are part of more than 20 different ethnicity pairs. In column 4, we include pairs of neighboring ethnicities that are located in different countries and include country fixed effects. Finally, in columns 5 and 6, we use alternative approaches to control for the pixels' distances to the ethnic boundaries. Column 5 interacts the distance-to-the-boundary polynomial with ethnicity-pair fixed effects, and so includes a different

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[18] The large standard error in column 1 may reflect that pixel-level nighttime luminosity is a noisy measure of economic development when it is not residualized on population density. For example, many pixels in low-KII but economically prosperous Canada have low luminosity because they are virtually uninhabited.

coefficient on the distance term for each country-ethnicity in each of the 572 ethnicity pairs. This is a demanding specification, but it allows us to control for distance patterns specific to each country-ethnicity in each pair. In column 6, rather than controlling for the distance to the boundary, we interact the longitude and latitude of each pixel with ethnicity-pair fixed effects; this specification controls more directly for features that vary in two-dimensional space in the homelands of each ethnicity pair. The results are robust to these alternative specifications.

Table 4: Spatial RD analysis: additional robustness checks

	Log nighttime luminosity					
	(1) KII diff. ≥ 0.1	(2) KII diff. ≥ 1	(3) Only in $\leq$20 pairs	(4) Cross-country sample	(5)	(6)
KII	-0.069***	-0.037*	-0.072***	-0.070***	-0.057**	-0.051***
	(0.018)	(0.022)	(0.017)	(0.017)	(0.024)	(0.012)
Log population density	yes	yes	yes	yes	yes	yes
Ethnicity pair FE	yes	yes	yes	yes	yes	yes
Log population density	yes	yes	yes	yes	yes	yes
Geographic controls yes	yes	yes	yes	yes	yes	yes
Country FE				yes		
Distance-to-the-boundary polynomial	yes	yes	yes	yes		
Dist. to the boundary poly. X ethnicity pair					yes	
Latitude & longitude X ethnicity pair						yes
Observations	277,946	164,191	287,624	370,771	290,669	290,669
R-squared	0.609	0.578	0.614	0.637	0.633	0.646
Number of clusters	70	46	70	104	70	70

Notes: Each observation is a pixel that belongs to a country-ethnicity in a pair of contiguous ethnicities in the same country (except in column 4), and within 200 km of the boundary between the two ethnicities. The geographic controls include temperature, precipitation, agricultural suitability, absolute latitude, elevation, ruggedness, distance to coast, and distance to the nearest river or lake. In columns 1–4, "Distance-to-the-boundary polynomial" is the geodesic distance of each pixel's centroid from the boundary between the two adjacent ethnicities; we allow the coefficient on the distance term to differ between the relatively high and the relatively low KII ethnicities in the pairs. In columns 1 and 2, we drop ethnicity pairs whose KII difference is less than 0.1 and 1 standard deviations, respectively. In column 3, we drop pixels that appear in more than 20 ethnicity pairs. In column 4, we also include in the analysis ethnicity pairs with ethnicities in different countries, and include country fixed effects in the regression. Column 5 interacts the distance-to-the-boundary polynomial with ethnicity pair fixed effects, and column 6 interacts instead each pixel's latitude and longitude with ethnicity-pair fixed effects. Standard errors in parentheses are clustered at the country level. *** $p < 0.01$, ** $p < 0.05$, * $p < 0.1$

For several reasons, our analysis so far may underestimate the true magnitude of β. First, our estimates may capture the spillover effects of light across ethnic boundaries—i.e., some pixels may appear brighter than they actually are due to overglow from bright nearby pixels in the neighboring ethnicity's homeland. Second, there may be spillovers in economic activity across the boundaries. And third, the fraction of the population belonging to each ethnicity may not change discontinuously at the ethnic boundary, for instance due to intermarriage, trade, or the presence of multi-ethnic urban agglomerations.

To address these concerns, Table 5 presents specifications using subsets of pixels that fall within different distance ranges to the ethnic boundary. In columns 1 to 3, we still start at the boundary, but reduce the maximal distance to the boundary from 200 km (our baseline specification, also reported in column 2 of Table 3) to 150 km and then 100 km. In columns 4–6 and 7–9, to mitigate potential bias due to light and economic spillovers and the smooth variation in population composition across boundaries, we drop pixels that are within 25 km and 50 km of the boundary, respectively.

The estimates are remarkably robust to using these alternative subsets of pixels. Con-

Table 5: Spatial RD analysis with pixels at various distances from the ethnic boundaries

	Log nighttime luminosity								
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)
Distance to border (in km)	0-200	0-150	0-100	25-200	25-150	25-100	50-200	50-150	50-100
KII	-0.072***	-0.065***	-0.046*	-0.096***	-0.093***	-0.079**	-0.118***	-0.121***	-0.115**
	(0.017)	(0.021)	(0.028)	(0.022)	(0.025)	(0.034)	(0.028)	(0.030)	(0.045)
Log population density	yes	yes	yes	yes	yes	yes	yes	yes	yes
Geographic controls	yes	yes	yes	yes	yes	yes	yes	yes	yes
Distance-to-the-boundary polynomial	yes	yes	yes	yes	yes	yes	yes	yes	yes
Ethnicity pair FE	yes	yes	yes	yes	yes	yes	yes	yes	yes
Observations	290,669	219,874	146,438	268,628	197,833	124,397	227,620	156,825	83,389
R-squared	0.613	0.619	0.623	0.615	0.621	0.626	0.616	0.624	0.630
Number of clusters	70	70	70	70	70	70	70	70	70

Notes: Each observation is a pixel that belongs to a country-ethnicity in a pair of contiguous ethnicities in the same country. The various specifications are identical, but the analysis samples include pixels located at different ranges of distances from the boundary separating the two ethnicities in a pair. The geographic controls include temperature, precipitation, agricultural suitability, absolute latitude, elevation, ruggedness, distance to coast, and distance to the nearest river or lake. "Distance-to-the-boundary polynomial" is the geodesic distance of each pixel's centroid from the boundary between the two adjacent ethnicities; we allow the coefficient on the distance term to differ between the relatively high and the relatively low KII ethnicities in the pairs. Standard errors in parentheses are clustered at the country level. *** $p < 0.01$, ** $p < 0.05$, * $p < 0.1$

sistent with our intuition that light and economic spillovers and the smooth variation in population composition at the boundary may bias our estimates downward, the estimates for $\hat{\beta}$ become larger in magnitude as we drop pixels that are within 25 and then 50 km of the ethnic boundary. When the pixels within 50 km of the boundary are dropped, our estimates imply that a one-standard-deviation increase in the KII is associated with a decrease of $\sim 11\%$ $(= (1 - e^{-0.12}) \cdot 100\%)$ in luminosity.

Since all the ethnicity pairs in our baseline RD analysis sample are in the same country, we can compare our RD estimates to those of the earlier OLS regressions with country fixed effects. With log luminosity and log regional GDP per capita as the dependent variables, the earlier corresponding estimates, reported in column 5 of Table 1 and column 4 of Table 2, were -0.110 and -0.085, similar to our spatial RD estimates when pixels within 25 or 50 km from the ethnic boundaries are dropped. This reveals a noteworthy consistency across the results of the three main empirical approaches presented thus far.

Our spatial RD analysis helps account for potential bias from unobservables that vary smoothly across ethnic boundaries. While it is not possible to test whether there are unobservables that vary discontinuously at the boundary, we can conduct a "placebo" RD analysis and examine whether observable variables show any signs of discontinuities at the boundaries. To do so, we estimated equation (2) again in our baseline analysis sample of pixels, but dropped the geographic controls and swapped each of our geographic controls in turn for log luminosity as the dependent variable. The results, reported in Table B.4.3, show that the estimated coefficients on the KII are not significant at the 5% level for any of the geographic controls. Overall, we find no evidence that discontinuities in observable geographic characteristics are present at ethnic boundaries.

While establishing a causal effect from kinship intensity to economic development is difficult in the absence of random assignment, the results of our spatial RD analysis make many alternative explanations unlikely. In particular, any valid alternative explanations are likely to involve factors that tend to vary discontinuously, rather than smoothly, at or around ethnic boundaries within countries.

5 The inbreeding coefficient, kinship intensity, and economic development

Our primary measure of kinship intensity, the KII, is ultimately based on the coding of qualitative anthropological observations, which may capture only what people say about their practices (as opposed to their actual behavior) and may be influenced by the perceptions, expectations or idiosyncratic experiences of particular ethnographers. To address such shortcomings, we take advantage of the fact that some kinship customs leave footprints in the genomes of practicing populations. Specifically, we used genetic data from the Human Origins dataset (Reich Lab, 2020) to calculate inbreeding coefficients. The inbreeding coefficient, denoted F, is a core variable in population genetics that measures the relatedness of ones' parents. The Human Origins Dataset (HO) contains genetic data on 9,460 present-day individuals and 3,723 ancient individuals [19] from populations around the world, compiled from previously published genetics studies (including Pickrell et al., 2012; Lazaridis et al., 2014, 2016; Nakatsuka et al., 2017; Lipson et al., 2018; and Jeong et al., 2019). We matched the present-day HO individuals to Ethnologue languages and used the associated country-ethnicities' average inbreeding coefficients estimates as our alternative measure of kinship intensity.

We begin this section by briefly describing the inbreeding coefficient and laying out the methodology we use to estimate it, and then define several additional control variables we compute using the HO data (Appendix C provides further details). We then examine the inbreeding coefficient's (F's) associations with the KII, the KII sub-indicators, and economic development.

5.1 The inbreeding coefficient and other genetic variables

To understand inbreeding and its measurement, recall that for each of our 23 pairs of chromosomes, we inherit one chromosome from our mother and the other from our father. Inbreeding occurs when two related individuals produce offspring. Related individuals share identical stretches of DNA from one or more recent common ancestors, and thus inbreeding increases the probability that at a given location on a chromosome, their offspring inherits such identical DNA segments on the maternal and paternal copies of the chromosome (Ceballos et al., 2018). First cousins, for instance, share both a grandmother and a grandfather, so some DNA segments they inherit from their shared grandparents will likely be identical across their two genomes. As a result, if two first cousins produce a child, that child will have locations in their genome where they will have inherited identical stretches of DNA from their related parents, which originate from their shared grandmother or grandfather. The maternal and paternal variants at such genomic location are said to be homozygous (since they are identical) and identical-by-descent (IBD) since they can also be traced back to a common ancestor.

A common measure of the intensity of inbreeding is the *inbreeding coefficient*, denoted F. F measures the probability that the maternal and paternal variants at a location in the genome are IBD. An individual's F coefficient is typically equal to the coefficient of kinship, or one-half the coefficient of relationship, between their two parents (Falconer and Mackay, 1996; Cavalli-Sforza and Bodmer, 1999). The latter is a measure of the relatedness between the two parents; for example, the F coefficient of the offspring of

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[19] The ancient individuals lived between $\sim 88,000$ BCE and ~ 1900 CE; we did not analyze their data.

two second-degree cousins is 0.015625 ($= \frac{1}{2} \cdot \frac{1}{64}$), whereas it is 0.0625 ($= \frac{1}{2} \cdot \frac{1}{8}$) for the offspring of first-degree cousins and 0.25 ($= \frac{1}{2} \cdot \frac{1}{2}$) for the offspring of two siblings. Thus, F measures the degree to which an individuals' two parents are related, and a population's average F should in principle correlate positively with its rate of endogamy and with its KII.

Until recently, pedigree data was required to compute F, but various methods have been developed in recent years to estimate F using an individual's molecular genetic data. Our main measure of F, denoted F_{ROH}, is the fraction of an individual's autosomal genome that contains runs of homozygosity (ROHs) of at least 1.5 Mb in length. The autosomal genome comprises the 22 pairs of chromosomes other than the sex chromosomes (X and Y), and ROHs are continuous segments of homozygous variants. Because the length of the autosomal genome is estimated at 3,000 Mb[20] (Clark et al., 2019), an individual's F_{ROH} can be calculated as

$$F_{ROH} = \sum_i \frac{l_i}{3,000}, \tag{3}$$

where the sum is over the individual's ROHs that are at least 1.5 Mb in length and l_i is the length of ROH i in Mb.

Longer ROHs (e.g., ROHs of at least 1.5 Mb in length) typically result from inbreeding (Ceballos et al., 2018) and have been shown to correlate positively with both pedigree-based estimates of inbreeding (McQuillan et al., 2008; Pemberton and Rosenberg, 2014; Kang et al., 2017) and population-level cousin marriage preferences (Sahoo et al., 2021). Below in Section 5.2, we too find that F_{ROH} (or, equivalently, longer ROHs) correlates positively with cousin marriage preferences; we also find that F_{ROH} correlates positively with the KII.

We estimated F_{ROH} for 4,756 present-day individuals in the Human Origins (HO) data set whose genetic data were collected using the Affymetrix Human Origin genotyping array and who passed a number of quality control filters. As we describe in more detail in Appendix C, we used the ROHgen2 software pipeline developed by the ROHgen consortium (Clark et al., 2019)[21] to estimate F_{ROH}, and conducted diagnostic checks to verify the reliability of our F_{ROH} estimates. We then matched the HO individuals to 551 Ethologue languages using a procedure that resembles the direct matching method we used to match the EA data (see Section 3.3). We computed the average F_{ROH}, which we denote $\overline{F_{ROH}}$, across the HO individuals matched to each language. We dropped languages with fewer than eight individuals, leaving 416 country-ethnicities associated with the remaining languages in the sample. For our main analysis with $\overline{F_{ROH}}$—of its relationship with luminosity at the pixel level—we further dropped pixels that did not pass the filters described in Sections 3.1 and 3.3, thus leaving 281,177 pixels that fall in the country-homelands of 245 country-ethnicities.

We note that while F is the fraction of the genome that is IBD, F_{ROH} is the fraction that is in ROHs longer than 1.5 Mb. Because some ROHs that are shorter than 1.5 Mb are IBD and some longer ROHs are not IBD, F_{ROH} is merely as estimate of F. ROHs can arise in individuals for a variety of reasons unrelated to marital practices and kinship systems. Using only ROHs that are at least 1.5 Mb long to compute F_{ROH} helps

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[20] A megabase (Mb) is a unit of physical distance in the genome

[21] The ROHgen consortium is a large consortium of research groups that seeks to estimate the effect of inbreeding on various traits (Joshi et al., 2015; Clark et al., 2019).

mitigate, but does not eliminate, concerns that F_{ROH} may capture influences other than consanguineous marriage practices and intensive kinship.

To address such concerns, we also used the HO genetic data to compute the following "genetic controls" that may correlate with $\overline{F_{ROH}}$ but are unrelated to kinship intensity and consanguineous marriage practices, and included them in our empirical analyses as controls:

- *Expected heterozygosity* and *migratory distance from East Africa*: Expected heterozygosity is a measure of genetic diversity in a population and is defined as the probability that two randomly selected individuals from a population have different genetic variants at a randomly selected location on one chromosome in the genome. Expected heterozygosity has been shown to correlate negatively across populations with mean F estimated with genetics data (Pemberton and Rosenberg, 2014) and to correlate nonlinearly with economic development (Ashraf and Galor, 2013). Expected heterozygosity is highly negatively correlated with migratory distance from East Africa, consistent with a migration model that predicts increased genetic drift and decreased heterozygosity with longer distance from Africa (Ramachandran et al., 2005). We include expected heterozygosity and its square as well as migratory distance from East Africa and its square among our genetic controls.

- *The top 20 principal components of the genotypic data*: We computed the top 20 principal components (PCs) of the genotypic data for each individual and took the average value of each PC in each ethnicity. It has been shown that the top PCs are good proxies for individuals' geographic origins and that including them as controls in regressions helps mitigate bias related to population stratification (Price et al., 2006; Novembre et al., 2008). Population stratification refers to systematic differences in genetic variants' frequencies that correlate with cultural or environmental differences (Hamer, 2000).

- *Mean regional pairwise* F_{ST}: Both F and F_{ROH} tend to be inflated in populations that are genetically isolated (due to geographical or cultural distance or taboos prohibiting mating with individuals from other populations—see Pemberton and Rosenberg (2014)). In such populations, reduced mate choice can lead to increased cryptic inbreeding, in which two parents may have a recent common ancestor by chance and not due to a deliberate cultural practice of mating with relatives. Following Pemberton and Rosenberg (2014), we estimate the degree of genetic isolation of a population using the average pairwise genetic distance "F_{ST}" between that population and other populations in the same geographic world region with sufficient sample sizes.

Appendix C provides additional details on these genetic controls and Table B.5.1 shows summary statistics for $\overline{F_{ROH}}$ and these genetic controls (except the PCs, whose scale is arbitrary). Across 416 Ethnologue country-ethnicities, $\overline{F_{ROH}}$ ranges from 0.003 to 0.146, with a mean of 0.020 and a standard deviation of 0.018. To put these figures in perspectives, two populations in which everyone were the offspring of second-cousin and uncle-niece unions would have mean F of 0.015625 and 0.125, respectively, close to the mean and maximum $\overline{F_{ROH}}$ in our sample. We estimated the mean $\overline{F_{ROH}}$'s of the English, Kurukh, and Marri Baluch (each described in Section 2.2) to be 0.0065, 0.0157, and 0.0617, respectively.

5.2 The inbreeding coefficient and kinship intensity

As mentioned above, ROHs and F_{ROH} have been shown to correlate with inbreeding and both consanguineous marriage preferences and practices (McQuillan et al., 2008; Pemberton and Rosenberg, 2014; Kang et al., 2017; Ceballos et al., 2018; Sahoo et al., 2021). Aside from explicit norms favoring consanguineous marriage, inbreeding can theoretically be influenced by other kinship norms that encourage endogamy and polygamy. Consequently, the sub-indicators within the KII that capture community organization and polygamy should be positively associated with $\overline{F_{ROH}}$. Norms favoring endogamy mean that people marry and mate within a relatively small population or constrained social network, thus increasing the likelihood of consanguineous unions (without explicit prescriptions). The role of polygyny can be more difficult to understand. Polygyny, all else being equal, increases inbreeding in a population by decreasing the total number of fathers who provide genes each generation—meaning more people share the same fathers, grandfathers and great grandfathers, and are thus effectively paternal cousins.[22]

To further validate our estimates of $\overline{F_{ROH}}$ as a proxy for kinship intensity, we examined its association with the cousin-marriage-preference KII sub-indicator, with the KII itself, as well as with the four other KII sub-indicators. Across the 398 country-ethnicities with non-missing data, the correlation between $\overline{F_{ROH}}$ and the cousin-marriage-preference sub-indicator is 0.28; after partialling out the effects of the genetic controls from $\overline{F_{ROH}}$, the correlation increases to 0.32. Unsurprisingly, given that the cousin-marriage-preference sub-indicator is one of the five components of the KII and that some other dimensions of the KII can impact consanguinity, $\overline{F_{ROH}}$ also correlates with the KII ($\hat{r} = 0.26$), though the correlation is lower if $\overline{F_{ROH}}$ is first residualized on the genetic controls ($\hat{r} = 0.14$).

Table 6: The inbreeding coefficient and kinship intensity

	Cousin marriage preference				KII			
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
$\overline{F_{ROH}}$	18.491***	45.744***	44.566***	37.557***	11.641***	13.185***	13.319***	14.549***
	(5.346)	(5.653)	(5.772)	(8.379)	(3.067)	(2.714)	(2.761)	(4.033)
Genetic controls		yes	yes	yes		yes	yes	yes
Continent FE			yes				yes	
Country FE				yes				yes
Observations	398	397	397	397	396	395	395	395
R-squared	0.077	0.433	0.453	0.683	0.066	0.717	0.720	0.843
$\Delta R^2(\overline{F_{ROH}})$	0.0775	0.0951	0.115	0.0419	0.0665	0.0171	0.0200	0.0136
Number of clusters	127	127	127	127	127	127	127	127

Notes: Each observation is a country-ethnicity. The genetic controls include expected heterozygosity and its square, migratory distance from East Africa and its square, the top 20 PCs, and mean regional pairwise F_{ST}. $\Delta R^2(\overline{F_{ROH}})$ is the incremental R^2 of $\overline{F_{ROH}}$, defined as the difference in R^2 between the regression on $\overline{F_{ROH}}$ and all the controls and the regression on all the controls only. Standard errors in parentheses are clustered at the country level. *** $p < 0.01$, ** $p < 0.05$, * $p < 0.1$

Table 6 shows the results of regressions of the cousin-marriage-preference sub-indicator and of the KII on $\overline{F_{ROH}}$. In all specifications, the coefficient on $\overline{F_{ROH}}$ is highly statistically

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[22] To see this, consider a world in which every child in the focal generation derives from a unique mating pair (no full siblings). Under extreme polygyny, everyone in the focal generation has the same father but different mothers—everyone is a half sibling, so $F = 0.125$. At the other extreme, with monogamous mating, everyone has both a different mother and a different father (and this goes on for many generations). Here, F will be zero.

significant and large in magnitude. For instance, in the regressions in columns 2 and 6 with the genetic controls, the coefficient estimates of 45.744 and 13.185 imply that the cousin-marriage preferences and KII of an ethnicity in which everyone is the offspring of second cousins ($\overline{F_{ROH}} = \frac{1}{64} = 0.0156$, assuming no influences other than inbreeding), are $\sim$ 0.7 and $\sim$ 0.2 standard deviations higher than those of an ethnicity in which everyone is the offspring of unrelated parents ($\overline{F_{ROH}} = 0$; by comparison, recall that the standard deviation of $\overline{F_{ROH}}$ across country-ethnicities is 0.018). Further, $\overline{F_{ROH}}$ accounts for a nontrivial share of the variation in cousin marriage preferences: its incremental R^2, defined as the difference in R^2 between the regression on $\overline{F_{ROH}}$ and the controls and the same regression but on the controls only, is 0.095. As shown in Table B.5.2, these results are robust to alternative specifications.

Table B.5.3 shows the results of regressions of the four other KII sub-indicators on $\overline{F_{ROH}}$. As expected, the polygamy, community organization, and lineage organization sub-indicators are positively associated with $\overline{F_{ROH}}$. Interestingly, the co-residence sub-indicator is negatively associated with $\overline{F_{ROH}}$. We speculate that this may arise from the fact that co-residence with a larger number of relatives, such as various cousins, will induce our species' innate mechanisms for avoiding incest (cued by early life proximity) and thereby reduce the probability of a genetically close union.

5.3 The inbreeding coefficient and nighttime luminosity

Table 7 reports the results of regressions of nighttime luminosity on $\overline{F_{ROH}}$ across pixels. The analysis mirrors that of the association between luminosity and the KII in Section 4.1, but with $\overline{F_{ROH}}$ substituted for the KII as the focal explanatory variable and with the genetic controls also included in most specifications.

Table 7: The inbreeding coefficient and nighttime luminosity: cross-section

	Log nighttime luminosity										
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)
$\overline{F_{ROH}}$	-47.748	-41.297**	-27.265**	-25.841**	-27.094**	-21.026***	-18.235**	-15.943**	-20.923***	-21.026***	-21.026***
	(32.014)	(18.654)	(11.294)	(11.267)	(12.315)	(7.633)	(8.357)	(6.766)	(7.460)	(5.584)	(7.995)
Subsistence variables							yes				
Political hierarchy								yes			
Malaria index									yes		
Log population density		yes	yes	yes	yes	yes	yes	yes	yes	yes	yes
Genetic controls			yes	yes	yes	yes	yes	yes	yes	yes	yes
Geographic controls				yes	yes	yes	yes	yes	yes	yes	yes
Continent FE					yes						
Country FE						yes	yes	yes	yes	yes	yes
Observations	281,177	281,177	281,177	281,177	281,177	281,177	281,177	281,100	281,177	281,177	281,177
R-squared	0.021	0.503	0.633	0.652	0.652	0.674	0.674	0.674	0.674	0.674	0.674
Number of clusters	98	98	98	98	98	98	98	98	98	30	30 & 98

Notes: Each observation is a pixel. The genetic controls include expected heterozygosity and its square, migratory distance from East Africa and its square, the top 20 PCs, and mean regional pairwise F_{ST}. The geographic controls include temperature, precipitation, agricultural suitability, absolute latitude, elevation, ruggedness, distance to coast, and distance to the nearest river or lake. The subsistence variables measure the fraction of an ethnicity's subsistence economy that depends on hunting, fishing, animal husbandry, and agriculture (with gathering as the omitted category). Standard errors in parentheses are clustered at the country level in all regressions, except in column 10, where they are clustered at the language-family level, and in column 11, where they are clustered two-way at both the country and language-family levels. *** $p < 0.01$, ** $p < 0.05$, * $p < 0.1$

Consistent with our estimates of a negative relationship between luminosity and the KII, the association between luminosity and $\overline{F_{ROH}}$ is consistently negative and significant at the 5% level in all specifications, except in column 1 where we do not control for population density (and where the standard error is consequently large—see footnote 18). When population density along with both the genetic and geographic controls as well as country fixed effects are included (in column 6), the coefficient estimate of −21.026 implies that luminosity is $\sim 28\%$ lower $(= (1 - e^{(-21.026 \cdot \frac{1}{64})}) \cdot 100\%)$ for an ethnicity in which everyone is the offspring of second cousins compared to an ethnicity in which everyone is the offspring of unrelated parents. These results are robust to controlling for the subsistence variables, political hierarchy, and the malaria index (columns 7–9); as well as to clustering standard errors at the language-family level and two-way at both the country and language-family levels (columns 10–11).

Table B.6.2 reports additional regressions to further assess the robustness of the results. Column 1 shows that our results hold when the genetic controls are dropped from our baseline specification with country fixed effects (the one in column 6 of Table 7). As mentioned above, for our baseline analyses, we dropped country-ethnicities to which fewer than 8 HO individuals could be matched, so columns 2–4 explore the sensitivity of the results to using alternative cutoffs of 5, 10, and 15 individuals. The association between luminosity and $\overline{F_{ROH}}$ is robust to using a cutoff of 5 individuals; however, with larger cutoffs of 10 and 15 individuals, the estimated coefficient on $\overline{F_{ROH}}$ shrinks slightly in magnitude (but remains negative) while the standard error increases and the association loses statistical significance.

6 Causal pathways

Having now empirically established a robust and economically relevant negative association between kinship intensity and economic development, we turn our attention to the potential causal pathways that may account for this association.

We begin, in Section 6.1, by verifying that the association between kinship intensity and economic development is robust to accounting for two potentially important confounders: Christianity and European ancestry. Next, in Section 6.2, we discuss the role of reverse causality—i.e., the potential causal impact of economic development on kinship intensity. We conclude that, while economic development likely does erode kin-based institutions, it is unlikely to account for much of the association between kinship intensity and economic development that we document.

In light of all our analyses, we cautiously interpret our findings as suggesting that greater kinship intensity causally suppresses economic growth. To begin to dissect this, Section 6.3 discusses mechanisms that may account for such a negative causal effect. To pursue this, we briefly review the relevant literature and supplement that review with our own exploratory analyses. We consider the potential roles of (1) the division of labor and comparative advantage; (2) cultural psychology, including the role of impersonal trust, impersonal cooperation, impartiality, individualism, and conformity; (3) institutions; (4) innovation; and (5) inbreeding depression. We find supportive evidence for a role for the first four channels, but argue that inbreeding depression is unlikely to play an important role.

6.1 The Church, European ancestry, kinship intensity, and economic development

Could the influence of Christianity and European ancestry confound our findings regarding the impact of kin-based institutions? In Schulz et al. (2019), Henrich (2020) and Schulz (2022), we argue that the Western Church—the branch of Christianity that evolved into the Roman Catholic Church—had a profound impact on European kin-based institutions during the Middle Ages through its "Marriage and Family Program," which involved a set of policies that forbade cousin marriage and promoted neolocal residence and weak family ties. Relatedly, Christian missions often explicitly preached against polygyny, cousin marriage, arranged marriages and other elements of intensive kinship (Fenske, 2015; Bergeron, 2020) while actively working to spread Christian supernatural beliefs. The Western Church, or Christianity more generally, may also have directly impacted economic prosperity by encouraging schooling and literacy, as has been argued for Protestantism (Becker and Woessmann, 2009). Empirically, both Christianity and historical exposure to the Western Church are negatively correlated with kinship intensity (Schulz et al., 2019) and positively correlated with economic development. It is thus possible that the association we have documented between kinship intensity and economic development is in fact driven by an omitted variable related to Christianity.

Similarly, European populations are characterized by the lowest levels of kinship intensity. Empirical work has also found that greater levels European ancestry is associated with more economic prosperity (Easterly and Levine, 2016); this may arise from the correlation of such ancestry with a variety of institutional and cultural differences, including not only low kinship intensity, but also pluralistic political institutions and long exposure to the Western Church.

To explore the impact of these variables, we reran all our baseline analyses (1) excluding observations (pixels, ethnicities, or subnational regions) located in Europe, the Americas, Australia and New Zealand, and (2) controlling for deep Christianization, a variable that indicates if an EA society has been Christianized for at least 500 years (Korotayev, 2003). Table B.7.1 summarizes the estimations. Panels D.1 and D.2 show the results for our spatial RD analysis, which helps deal with unobservable confounding factors that vary smoothly across space and thus comes closest to causal identification. In Panel D.1, which shows results for the analysis sample that includes all pixels within 200 km of the boundary between two contiguous ethnicities, the estimates of $\hat{\beta}$ are similar to those in our main RD analysis (Table 3), though less precisely estimated. In Panel D.2, pixels within 50 km of the boundary are dropped (as there may be spillovers in lights and economic activity and population composition may not change precipitously at the boundary). The resulting estimates of $\hat{\beta}$ are larger in magnitude than the earlier corresponding estimates (in column 7 of Table 5) and remain statistically significant, even though the standard errors are larger. In Panels B and C, in regressions of nighttime luminosity at the country-ethnicity level and of regional GDP per capita, the KII remains a mostly robust predictor of economic prosperity. The results also hold when we replace the KII with $\overline{F_{ROH}}$ (in Panel E). For completeness, Panel A provides our pixel-level analysis of luminosity on the KII, though inference here is in question because the KII and the deep Christianization variable are highly multicollinear (correlated at ~ -0.9 with both matching methods).[23]

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[23] The KII and the deep Christianization variable are similarly highly multicollinear in our spatial RD analysis in Panel D, which helps accounts for the inflated standard errors in that analysis (versus in our

We conclude that Christianity and European ancestry cannot fully account for the kinship intensity-economic development association, though adjusting for these factors weakens the association and decreases the precision of our estimates. Consistent with our theoretical approach (Schulz et al., 2019; Henrich, 2020; Schulz, 2022), we interpret these results as reflecting the Western Church's negative impact on European kinship intensity during the Middle Ages, which in turn fueled economic development in Europe and its cultural descendants.

6.2 Reverse causation: from economic development to kinship intensity

The negative association between kinship intensity and economic development could in principle be the result of greater economic development having fostered weaker kin-based institutions. As economies grow, rising urbanization and migration as well as increasing interactions and exchanges with non-kin may make it difficult to maintain the tight bonds and fulfill the obligations that characterize intensive kinship networks (Bittles and Black, 2010; Shenk et al., 2016). For example, the Kurukh, whom we encountered earlier, were traditionally organized in endogamous patri-clans, but became more exogamous when they transitioned from pastoralism to settled agriculture and experienced sustained contact with Hindu communities. Further, rising wealth and education may directly erode preferences for maintaining kin-related traditions (Khlat, 1988; Bittles and Black, 2010; Bittles et al., 1991). Consistent with this, Akyol and Mocan (2020) find that a Turkish reform that increased compulsory schooling by three years increased women's preferences for personal autonomy and decreased their tendency to marry cousins or blood relatives. Finally, economic development may also allow governments to establish social safety nets that replace some of the functions of kin-based institutions, which may alter incentives to maintain some kin-based practices. For instance, Bau (2021) finds that new pension policies in Ghana and Indonesia reduced the practice of matrilocality and patrilocality.

Of course, these effects are not robust across all contexts: Shenk et al. (2016) suggests that rates of cousin marriage in Matlab, Bangladesh, are likely holding steady or even increasing despite rising market integration, urbanization and educational levels. An increasing acceptance of "love marriage" has meant that more women are choosing to marry their cousins, and declining family size has left fewer women with brothers, which favors cousin marriage in this context. As noted earlier, similar temporal trends with stable or increasing cousin marriage rates appear in Pakistan, Iran, Oman and Yemen (Jurdi and Saxena, 2003; Abbasi-shavazi et al., 2008; Hussain and Bittles, 1998; Islam, 2012).

Nevertheless, though economic development likely reduces kinship intensity at least in some contexts, it is unlikely that our findings are driven primarily by such reverse causality. First, the data used to construct the KII derive from ethnographic observations that capture, or aimed to capture, the customary practices of traditional populations prior to European colonization and industrialization (with an average observation date of 1900); our two measures of economic prosperity, by contrast, are from 2010 (nighttime luminosity) and from 1950 to 2010 (regional GDP per capita).

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baseline spatial RD analysis in Table 3). The level of multicollinearity is lower in the other specifications in Table B.7.1 (in Panels B and C), with the correlation between the KII and the deep Christianization variable not exceeding ~ 0.6 in magnitude across those specifications.

Second, while it is possible that past economic prosperity impacted both kinship intensity and contemporary prosperity, our spatial RD analysis undermines any alternative explanations involving factors that would vary smoothly across ethnic boundaries. This means that geographic variables such as soil quality—which could influence past economic conditions—or remoteness (e.g., from the national capital, government agencies, infrastructure, and trading routes) are unlikely to drive our results. Thus, for past prosperity to confound our results, that past prosperity would have had to stem from factors other than these—from factors that are discontinuous at the traditional borders between ethnic groups within countries.

Third, we verify the robustness of our results to controlling for earlier levels of economic development. We do not have a direct measure of past economic prosperity for any of our analyses at the pixel, country-ethnicity, and region level.[24] Instead, we rerun all our baseline analyses with an additional control for settlement complexity, a variable from the EA that is frequently used as a proxy for past levels of economic development (Giuliano and Nunn, 2018). As can be seen in Panels A to E of Table B.7.2, the results remain robust and most estimated coefficients on the KII do not change appreciably. We also verify that the association between the KII and economic prosperity also holds at the country level when controlling for a direct measure of past economic prosperity. Using national GDP data (in constant PPP 2011 dollars) from the Maddison Project (Bolt and van Zanden, 2020), we estimate cross-country regressions of GDP per capita in 2018 on the KII and the geographic controls while also controlling for GDP per capita in 1950. Panel F of Table B.7.2 reveals a statistically and economically significant association: across countries, a one-standard-deviation increase in the KII is associated with a larger than 20% decrease in GDP per capita in 2018 when holding 1950 GDP per capita constant.

Finally, we examined whether urbanization, which typically accompanies economic growth and may plausibly impact kinship intensity, might drive our results. We reran the baseline regressions in columns 3 and 5 of Table 1, but using only pixels with population density (1) less than or equal to 1, (2) between 1 and 10, and (3) higher than 10 (high population density typically reflects urbanization or modernization). Table B.7.3 shows that our results hold across each sub-sample of pixels except when comparing only the most densely populated (urbanized) pixels within countries (in column 6). Crucially, our results hold when we only use pixels with the lowest population densities (≤ 1), indicating that urbanization is unlikely to account for the association we have documented between kinship intensity and economic development.

6.3 Potential Mechanisms: from kinship intensity to economic development

We have shown that the association between kinship intensity and economic development is unlikely to be driven primarily by reverse causality or omitted factors such as Christianity or European ancestry. Now, we consider four mechanisms that likely contribute to the impact of kinship intensity on economic development, as well as a fifth one (inbreeding depression) which we argue is unlikely to play an important role.

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[24] For the region-level analysis, we have regional GDP-per-capita data from the 1950s and 1960s only for a subset of the regions, so controlling for that leads to most observations being dropped and to reduced statistical power.

6.3.1 The division of labor and comparative advantage

At the heart of economics lie the concepts of the division of labor and comparative advantage, which can raise productivity and increase prosperity (Smith, 1776). We postulate that high kinship intensity makes it difficult for a society to fully exploit opportunities created by specialization and trade. Harnessing that potential requires individuals to openly and earnestly engage in exchanges and transactions with strangers. However, intensive kinship norms obligate or encourage individuals to seek occupational, training, and exchange opportunities through their kin networks. Norms demand loyalty to kinfolk: one must hire, teach or help culturally-defined kin over non-kin. Individuals may engage with others they've never met before but these individuals should be socially connected to members of their broader kin network. For example, the high kinship intensity Marri Baluch reported not trading in towns where they lacked life-long and often inherited "trading friends" (*bradirs*) and being reluctant to hire herders who were non-relatives. Overall, they tend to organize labor and production primarily along kinship lines.

As we discuss below, intensive kinship is also associated with low levels of trust towards strangers, which directly inhibits trading. The same norms can inhibit occupational specialization because one's customers would be largely circumscribed to one's kinfolk, who may be too few to make this profitable. And, one's business can be dramatically affected by the actions of one's relative: a cousin who get into a scrap with the member of another clan could terminate all the customers from that clan (corporate responsibility and guilt are common under intensive kinship (Curtin et al., 2020)).

To explore the link between kinship intensity and specialization, we use data from the EA to construct an index of labor specialization across 10 different tasks: metal working, weaving, leather working, pottery, boat building, house building, hunting, fishing, animal husbandry, and agriculture. Task specialization can take one of three values: no or only age specialization (0), craft specialization (1), or industrial specialization (2). The specialization index for a society is obtained by taking the average across all tasks with nonmissing data and then standardizing the resulting average.[25]

To explore the link between kinship intensity and trade, we analyzed measures of market participation and of intercommunity trade in food from the Standard Cross-Cultural Sample (SCCS; (Kirby et al., 2016)). Market participation is a binary variable that takes the value of 1 if a society's production is more oriented toward exchange than toward consumption. The degree of intercommunity trade in food can take one of four values: no trade or food imports absent (0), less than 10 percent (1), less than 50 percent (2), or more than 50 percent (3).

Table 8 reports results of OLS regressions of these three variables on the KII and control variables. Consistent with our expectations, columns 1-3 show a negative association between the KII and the specialization index: a one-standard-deviation increase in the KII is associated with a ~ 0.15 standard-deviation decrease in the specialization index. This association is at least marginally significant ($p < 0.10$) while holding constant the geographic controls (in all three columns) and the subsistence variables (in columns 2 & 3) as well as with country fixed effects (in column 3).[26] To address concerns about

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[25] In our regression analysis, we include all societies that have data for at least 8 tasks. Tasks with missing data or that are coded as absent for a society do not enter into a society's average. In our regressions, we included 10 dummy variables indicating whether each task has missing data and 10 indicating whether it is coded as absent.

[26] We report a regression with country fixed effects for consistency with our main analyses above, even though both the KII and the specialization index capture ancestral characteristics measured at a time

Table 8: The KII, specialization, and market integration

	(1) Specialization index	(2) Specialization index	(3) Specialization index	(4) Market participation	(5) Intercommunity trade in food
KII	-0.148*	-0.156**	-0.108*	-0.092***	-0.009
	(0.076)	(0.072)	(0.056)	(0.025)	(0.056)
Geographic controls	yes	yes	yes	yes	yes
Subsistence dummies		yes	yes	yes	yes
Country FEs			yes		
Observations	553	553	545	91	162
R-squared	0.573	0.602	0.783	0.282	0.248
Number of clusters	112	112	112	48	73

Notes: Each observation is a society from the EA (columns 1-3) or from the SCCS (columns 4-5). The geographic controls include temperature, precipitation, agricultural suitability, absolute latitude, elevation, ruggedness, distance to coast, and distance to the nearest river or lake. The subsistence variables measure the fraction of a society's subsistence economy that depends on hunting, fishing, animal husbandry, and agriculture (with gathering as the omitted category). In columns 1 to 3, we include dummy variables indicating whether data is missing for a task and whether a task was coded as absent for each society. Standard errors in parentheses are clustered at the language-family level. *** $p < 0.01$, ** $p < 0.05$, * $p < 0.1$

the non-independence of error terms due to shared cultural histories, we conservatively cluster standard errors at the language-family level. Clustering instead at the country level decreases the standard errors such that all coefficients for the specialization index become significant at the 1% level.

Focusing on trade, columns 4 and 5 regress market participation (using a linear probability model) and intercommunity trade in food on the KII, geographic controls, and subsistence dummies.[27] We find the expected negative relationship between kinship intensity and market participation (in column 4), but find no relationship between kinship intensity and intercommunity trade in food (in column 5). That null result may reflect that among intensive kinship societies intercommunity trade in food may occur among established exchange partners with enduring personal relationships, and thus may be an inappropriate measure for the overall degree of market exchange.

Moving from the level of ancestral populations to modern countries, column 1 of Table 9 shows the results of a cross-country regression of openness to trade—defined as the sum of imports and exports as a share of a country's GDP—on the KII and the geographic controls.[28]) As expected, countries with higher levels of kinship intensity trade less, though the association is not precisely estimated.

6.3.2 Cultural psychology

Several recent studies have linked measures of either kinship intensity ("tightness") or family ties with less trust toward out-group members (Alesina and Giuliano, 2015; Enke,

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when many contemporary countries did not exist.

[27] We do not include country fixed effects because the SCCS was designed with the aim of sampling independent societies from around the world, and many of these are the only SCCS society in their country (Murdock, 1969; Kirby et al., 2016).

[28] For all the regressions in Table 9, the sample derived from the language-tree matching method was used in order to maximize sample size and ensure that most of a country's languages are used to compute its KII and other EA variables.

2019; Schulz et al., 2019). Trust, in turn, has been shown to contribute to economic growth (e.g., Algan and Cahuc (2013)). As Arrow (1972) noted, “Virtually every commercial transaction has within itself an element of trust... It can be plausibly argued that much of the economic backwardness in the world can be explained by the lack of mutual confidence.” Bloom et al. (2013) observe, in a sample of large Indian textile firms, that all top managers were members of the owning families, apparently due to distrust of non-family members; this constrained well managed firms’ ability to expand and dominate the market and helped poorly managed firms to survive.

Table 9: The KII and trade, cultural psychology, institutional quality, and innovation

	(1) Openness to trade	(2) Out-in-group trust	(3) Blood donations	(4) Expropriation Risk	(5) Institutional quality	(6) CPI	(7) Articles per m.	(8) Patents per m.
KII	-0.040*	-0.234**	-2.399***	-0.424***	-0.116***	-32.508***	-94.045***	-14.847
	(0.022)	(0.106)	(0.895)	(0.105)	(0.036)	(9.389)	(28.716)	(12.554)
	[0.043]	[0.052]	[1.070]	[0.139]	[0.046]	[12.870]	[39.500]	[13.358]
Geographic controls	yes	yes	yes	yes	yes	yes	yes	yes
Observations	151	71	142	86	79	154	159	75
R-squared	0.261	0.443	0.560	0.634	0.272	0.506	0.559	0.177

Notes: Each observation is a country in the sample obtained with the language-tree matching method. The eight outcome variables are defined in Appendix A.1. The geographic controls include temperature, precipitation, agricultural suitability, absolute latitude, elevation, ruggedness, distance to coast, and distance to the nearest river or lake. “CPI” stands for “Corruption Perceptions Index”. Robust standard errors are reported in parentheses and Conley standard errors in square brackets; following Colella et al. (2019), in each column we report the Conley standard error for the distance cutoff that maximizes it (we use cutoffs ranging from 500 km to 10,000 km, with increments of 500 km). *** $p < 0.01$, ** $p < 0.05$, * $p < 0.1$

Column 2 of Table 9 shows the results of a cross-country regression of out-in-group trust—defined as the difference between the level of trust towards outsiders (people of another religion or nationality, or strangers) and trust towards in-group members (family relatives, neighbors, and other acquaintances)—on the KII and our geographic controls. As expected, greater kinship intensity is associated with lower levels of out-in-group trust.

We also regressed the frequency of anonymous blood donations per capita on the KII (and geographic controls). Anonymous blood donations is a measure of impersonal cooperation, which is plausibly important for the functioning of impersonal institutions and economic growth. Consistent with our prior work—which included both similar cross-country regressions and within-country analyses in Italy (Schulz et al., 2019)—we find that kinship intensity is associated with fewer blood donations across countries.

Impersonal trust and cooperation are only two aspects of psychology that have been linked to kin-based institutions. In Schulz et al. (2019), we document that lower levels of kinship intensity are associated with cultural-psychological bundles that also include higher levels of impartiality, individualism, and independence, but lower levels of conformity, obedience, in-group loyalty, and nepotism. Enke (2019) and Henrich (2020) also document similar associations. By thus altering people’s psychology, kinship intensity is a likely contributor to the efficient functioning of formal economic and political institutions which, in turn, contribute to economic development (discussed more below). Further, as Gorodnichenko and Roland (2016) argue, more individualism and less conformity and obedience may foster economic growth in part through their impact on innovation: individualistic cultures create incentives for innovation by awarding greater social status to personal accomplishments such as making important discoveries. Similarly, populations with looser social norms and higher tolerance for deviance also tend to exhibit more creativity (e.g., Jackson et al. (2019)).

6.3.3 Institutions

There is a sizeable literature linking economic prosperity to well-functioning formal political and economic institutions (Coase, 1960; North et al., 2009; Acemoglu and Robinson, 2012). But what accounts for the fact that similar or even identical formal institutions operate very differently in different populations? Part of the answer may be psychology and social norms and obligations. For example, the strong loyalty demanded by kin in intensive kinship societies can undermine large-scale formal institutions (Greif, 2006a,b; Henrich, 2020): without high levels of trust in strangers and impartiality, corruption and nepotism will erode such institutions at their foundations.

Existing work has already shown that across the world, among countries, regions, and ethnicities, kinship intensity is associated with more autocratic rule and less participation in the political process (Schulz, 2022). Similarly, Akbari et al. (2019) and Akbari et al. (2020) find that cousin marriage is associated with more corruption. We add to this body of evidence by separately regressing expropriation risk, institutional quality[29] and the Corruption Perceptions Index (CPI) on the KII (and the geographic controls) at the country level (see Appendix A.1 for details on these outcome variables). The results, in columns 4-6 of Table 9 imply that higher kinship intensity is associated with higher expropriation risk, lower institutional quality, and greater perceptions of corruption.

6.3.4 Innovation

To test more directly for a link between kinship intensity and innovation, we regressed two measures of innovation on the KII (and the geographic controls): the number of scientific and technical journal articles per capita and the number of patents per capita (Appendix A.1 provides details on these variables). As expected, columns 7-8 of Table 9 reveal that kinship intensity is negatively associated with these two measures of innovation across countries, though the coefficient for patents per capita is imprecisely estimated. Plausibly compounding this negative link between kinship intensity and innovation, de la Croix et al. (2018) argue that new ideas and best-practice techniques diffuse more slowly in societies where economic relationships are organized primarily along kinship lines.

6.3.5 Inbreeding depression (ID)

Inbreeding depression (ID) is the reduction in biological fitness and related traits (such as health, cognitive ability and height) observed in the offspring of related individuals.[30] Higher levels of ID are to be expected in intensive-kinship societies, since these societies tend to have more marriages among relatives. Indeed, our second main measure of kinship intensity is the inbreeding coefficient, which is a direct measure of inbreeding intensity.

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[29] This variable, from Gennaioli et al. (2013), is constructed using data from the World Bank Enterprise Surveys and Doing Business report; it captures institutional features conducive for business.

[30] In economics, Ottinger and Voigtländer (2021) demonstrate, using genealogy data of royal lineages, that the inbreeding coefficient is a strong predictor of past European monarchs' intellectual abilities, which ultimately had a sizeable effect on state performance during their rule.

To assess the potential impact of ID on economic development, we compared our estimate of the association between the inbreeding coefficient and economic development across country-ethnicities to estimates from previous research of the effect of ID on educational attainment. To our knowledge, the largest study to date of the effects of ID is Clark et al. (2019). Clark et al. (2019) estimated the effects of ID by regressing various individual-level outcomes on F_{ROH}. Their main estimates imply that the educational attainment of the offspring of second cousins is ~ 0.11 years lower (and their cognitive performance ~ 0.7 IQ points lower) than that of the offspring of unrelated individuals.[31] This implies that the direct effect of ID would reduce the average educational attainment of an ethnicity in which everyone were the offspring of second cousins by ~ 0.11 years.

We do not have comparable educational attainment data at the level of the Ethnologue country-ethnicities, so to benchmark that figure, we used data from Gennaioli et al. (2014): across 1,190 subnational regions with nonmissing data for the year 2000, the mean average educational attainment is 8.19 years and the standard deviation is 2.69 years. Thus, the direct effects of ID in the offspring of second cousins represents only $\sim \frac{1}{25}$ of the standard deviation in average educational attainment across subnational regions.

By contrast, our estimate of -25.841 in column 4 of Table 7 implies that log luminosity for an ethnicity in which everyone is the offspring of second cousins is 0.40 units lower, conditional on log population density (and the other control variables). This represents nearly one fourth of the standard deviation of log luminosity residualized on log population density (1.76) across the 245 Ethnologue country-ethnicities in the analysis sample for that regression, and nearly half of the standard deviation of log luminosity residualized on log population density (0.89) across 1,209 subnational regions with nonmissing data for the year 2000 in the Gennaioli et al. (2014) data.[32]

This exercise is necessarily imperfect due to the lack of data allowing for a direct comparison of the effect of ID to our estimates, but it illustrates that ID is unlikely to have sufficiently large effects to account for much of the association we document between kinship intensity and economic development.

Overall, a cluster of findings in the extant literature, along with our own exploratory analyses, suggest that kinship intensity may impact economic development indirectly, via its effects on the division of labor and comparative advantage, cultural psychology, institutions, and innovation, but not principally via ID. Future work should focus on nailing down these pathways.

7 Conclusion

Over much of our species' history, kin-based institutions provided the primary means by which communities organized production, distribution, collective decision-making (politics) and social life. Even today, these institutions are among the first that individuals

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[31] As mentioned earlier, the inbreeding coefficient of the offspring of second cousins (0.015625) is a little smaller than the standard deviation of $\overline{F_{ROH}}$ across country-ethnicities (0.018).

[32] We also regressed regional average educational attainment in the year 2000 on the KII (and the geographic controls) across the 1,141 regions with nonmissing data for that regression. The result imply that a one-standard deviation increase in the KII is associated with a 0.65-year decrease in regional average educational attainment, which is also considerably larger than the direct effect of ID in the offspring of second cousins.

encounter upon entering the world and the most important social structure they must learn to navigate while growing up. Consequently, broader political and economic institutions are populated by individuals who have first been shaped by kinship and who may have developed strong bonds and intense loyalties as well as particular ways of thinking, feeling and reasoning during their early lives. Here, we have asked whether one anthropologically well-established dimension of kin-based institutions—kinship intensity—might inhibit economic development.

Empirically, our efforts reveal a robust and economically significant negative association between kinship intensity and economic prosperity. Our primary analyses used a pixel-level measure of economic prosperity based on satellite nighttime luminosity and a measure of kinship intensity based on ethnographic data captured at the country-ethnicity level prior to industrialization (the KII). In a battery of regressions, we compared pixels within the same countries and controlled for a wide range of geographic, epidemiological, and cultural variables. We conducted a spatial RD analysis at the boundaries between neighboring pairs of country-ethnicities, to mitigate concerns that unobservable confounders that tend to vary smoothly at the borders (such as geographic factors) may drive our results. We also replicated our main analyses with an alternative dependent variable—regional GDP per capita—and an alternative explanatory variable—an ethnicity's average inbreeding coefficient, proxied by $\overline{F_{ROH}}$ based on contemporary genetic data. Lastly, we conducted most of these analyses both in a sample where ethnographic variables were merged to pixels using direct language matches and in a sample where the matches were based on language phylogenies. Throughout, the estimated association between kinship intensity and economic prosperity remained robust, sizeable, and relatively stable in magnitude.

Turning to the possible causal pathways, we showed that neither reverse causality nor confounders related to Christianity or European ancestry are likely to fully account for the association. Further, we discussed existing evidence and presented novel results consistent with kinship intensity reducing prosperity via its effects on (1) the division of labor and trade, (2) cultural psychological variables such as trust, individualism, and impartiality, (3) the quality of formal institutions and (4) innovation.

In the absence of a natural experiment that quasi-randomly assigns kin-based institutions across societies, establishing an indisputable causal link between kinship intensity and economic development remains elusive. Nevertheless, taken together, the evidence we present strongly suggests that kinship intensity inhibits economic development, at least in the modern world (in earlier eras, kinship intensity may have had different effects).

In light of their probable relationship to modern economic growth, we caution against concluding that intensive kin-based institutions are less desirable and that policy should seek to dismantle them: in many places, intensive kin-based institutions play a critical role in providing a safety net and maintaining social order (Fox, 1967; Cox and Fafchamps, 2007). Similarly, dense and strong family networks likely nurture happiness and foster life satisfaction (Alesina and Giuliano, 2012). Thus, in addition to more precisely elucidating the mechanisms through which kin-based institutions impact economic prosperity, future research should seek ways to mitigate their inhibitory effects on prosperity without undermining their many benefits.

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Kin-based institutions and economic development

ONLINE APPENDIX

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August 25, 2022

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A Data Appendix

A.1 Variables construction

Pixel-level variables:

Variable name	**Description**
Satellite nighttime luminosity	Nighttime luminosity or light density (light emitted from a pixel divided by pixel area) measured by satellites in the year 2010-2011. The Global Radiance Calibrated Nighttime Lights data is presented at the resolution of 30 arc-seconds. We aggregate the data to 0.125 × 0.125 degree pixels by taking the mean across the 225 constituent subpixels from the raw data, and then divide it by fraction of subpixels covered by land. Source: Elvidge et al. (1999).
Population density	Population density (number of persons per square kilometer) in the year 2010. The Gridded Population of the World (GPWv4) collected population data at the most detailed spatial resolution available from the 2010 round of Population and Housing Censuses (occurred between 2005 and 2014). The input data are extrapolated to generate population estimates for different years and is adjusted to match the 2015 Revision of UN WPP Country Totals. GPWv4 is gridded with an output resolution of 30 arc-seconds. We aggregate the data to 0.125 × 0.125 degree pixels by taking the mean of the 225 constituent subpixels from the raw data. Source: Center for International Earth Science Information Network (CIESIN) at Columbia University (2016).
Land and water area	Surface areas of land and water in square kilometers per pixel. The Land Area raster provides estimates of the land area within each pixel, excluding permanent ice and water. The Water Area raster provides estimates of the water area (permanent ice and water) within each pixel. The sum of the land and water areas of a pixel equals the total surface area of the pixel. The data files were produced at 30 arc-second resolution. We aggregate the data to 0.125 × 0.125 degree pixels by taking the sum of the 225 constituent subpixels from the raw data. Source: Center for International Earth Science Information Network (CIESIN) at Columbia University (2016).
Temperature/Precipitation	Mean monthly temperature/precipitation over the period 1901-2017. The gridded Climatic Research Unit (CRU) Time-series (TS) version 4.02 data includes monthly variations in climate over the period January 1901 – December 2017, based on monthly data calculated by National Meteorological Services and other external agents. The data is provided for 0.5 × 0.5 degree pixels. Therefore, the 16 constituent 0.125 × 0.125 degree pixels of each 0.5 × 0.5 degree pixel from the raw data are assigned the same value. Source: University of East Anglia Climatic Research Unit; University of East Anglia Climatic Research Unit et al. (2017): CRU TS4.02.

Elevation	Mean elevation in 100 meters. The data is provided at 30-arc-second resolution by the Global 30 Arc-Second Elevation data set. We aggregate the data to 0.125 × 0.125 degree pixels by taking the mean of the 225 constituent subpixels from the raw data. Source: U.S. Geological Survey, Global Digital Elevation Model (GTOPO30) (`https://www.usgs.gov/centers/eros/science/`).
Ruggedness	Mean terrain ruggedness. As a measure of the local variance in elevation, terrain ruggedness at an individual pixel is defined as the square root of the sum of the squared differences in elevation between the central pixel and the eight adjacent pixels. The data is provided at the resolution of 30 arc-seconds. We aggregate the data to 0.125-degree pixels by taking the mean of the 225 constituent subpixels from the raw data. Source: Nunn and Puga (2012).
Suitability for agriculture	The fraction of each pixel that is suitable for agriculture. It is based on the temperature and soil conditions of each pixel and is constructed based on the global map (0.5 × 0.5 degree pixels) obtained from Suitability for Agriculture. Therefore, the 16 constituent 0.125-degree pixels of each 0.5 × 0.5 degree pixel from the raw data are assigned the same value. Source: Ramankutty et al. (2002), Atlas of the Biosphere.
Distance to the nearest coast	Distances in kilometers from the 0.125-degree-pixel centroids to the nearest coast. Source: Natural Earth, Coastline.
Distance to the nearest river or lake	Distances in kilometers from the 0.125-degree-pixel centroids to the nearest river or lake centerline. Source: Natural Earth, River and Lake Centerline.
Malaria index	An index representing the contribution of the regionally dominant biological characteristics of vector mosquitoes to malaria transmission. The data is constructed based on the world map of 0.5 × 0.5 degree pixels. Therefore, the 16 constituent 0.125-degree pixels of each 0.5 × 0.5 degree pixel from the raw data are assigned the same value. Source: (Kiszewski et al., 2004).

Ethnicity-level variables: **Variable name**	**Description**
Cousin marriage preference	Following Schulz et al. (2019), the variable is based on Ethnographic Atlas (EA) entry EA026 and is standardized using its mean and standard deviation across the EA societies. The variable takes the value 0 if cousin marriage is not preferred, 1 if second- (but not first-) cousin marriage is preferred, 2 if cross-cousin marriage is preferred, and 3 if parallel-cousin marriage is preferred. For the analysis with the language-tree matches (but not for that with the direct matches), we imputed missing observations. To do so, we first predicted cousin marriage preference based on the cousin terms in entry EA027, which classifies cousin terms into eight categories (Crow, Descriptive, Eskimo, Hawaiian, Iroquois, Omaha, Sudanese, and Mixed). To predict cousin marriage preference, we first analyzed the sample of ethnicities with data on both cousin marriage preference and cousin terms. For each cousin term category, we calculated the mean of the cousin marriage sub-indicator and used the resulting mean values to predict the expected cousin marriage preference sub-indicator for ethnicities where only data on cousin terms is available. See Schulz et al. (2019) for additional details. Source: Ethnographic Atlas Murdock (1967); Kirby et al. (2016).
Polygamy	Following Schulz et al. (2019), the variable is based on EA entry EA009 and is standardized using its mean and standard deviation across the EA societies. The variable takes value 0 for monogamy, value 1 for occasional or limited polygyny, and value 2 for common polygyny and polyandary. Source: Ethnographic Atlas (Murdock, 1967; Kirby et al., 2016).
Co-residence of extended families	Following Schulz et al. (2019), the variable is based on EA entries EA008 and EA012 and is standardized using its mean and standard deviation across the EA societies. We created a variable for domestic organization based on EA008 that takes value 0 for nuclear and polygamous families, 1 for minimal extended or stem families, 2 for small extended families and 3 for large extended families. We also created a second variable, marital residence, based on EA012 that takes the value 0 for neolocality (spouses move to a new location), 1 for ambilocality (individuals can choose which side of the family they relocate to), and 2 for the remaining cases (e.g., patrilocality or matrilocality). We take the average of the two variables (domestic organization and marital residence) to create the sub-indicator for the co-residency of extended families. As for the cousin-marriage-preference sub-indicator, for the analysis with the language-tree matches (but not for that with the direct matches), we imputed missing observations. For the societies with data on only one of the two variables (domestic organization or marital residence), the sub-indicator is based on the non-missing variable only and is obtained using a procedure analogous to the one used to predict cousin marriage from the cousin-term variable. Source: Ethnographic Atlas (Murdock, 1967; Kirby et al., 2016).

Lineage organization	Following Schulz et al. (2019), the variable is created based on EA entry EA043 and is standardized using its mean and standard deviation across the EA societies. The variable takes value 0 for bilateral descent and 1 otherwise (i.e., patrilineal, matrilineal, duolateral, quasi-lineage, and ambilineal descent). Source: Ethnographic Atlas (Murdock, 1967; Kirby et al., 2016).
Community organization	Following Schulz et al. (2019), the variable is based on EA entry EA015 and is standardized using its mean and standard deviation across the EA societies. The variable takes value 1 if localized clans are present and/or if community endogamy exists, and takes value 0 if both are absent (i.e., agamous communities without localized clans and exogamous communities without clan structure). Source: Ethnographic Atlas (Murdock, 1967; Kirby et al., 2016).
Kinship Intensity Index (KII)	Following Schulz et al. (2019), the KII is constructed by taking the average of the five (standardized) KII sub-indicators (cousin marriage preference, polygamy, co-residence of extended families, lineage organization, community organization) and then standardized using its mean and standard deviation across the EA societies.
Subsistence variables (gathering, hunting, fishing, animal husbandry, and agriculture)	The five variables are based on EA entries EA001-EA005 of the Ethnographic Atlas (EA). The five variables measure the fraction of a population's economic subsistence that depends on gathering, hunting, fishing, animal husbandry, and agriculture, respectively. Each entry takes the values 0 to 9 respectively for 0–5%, 6–15%, 16–25%, 26–35%, 36–45%, 46–55%, 56–65%, 66–75%, 76–85%, 86–100% dependence on the activity. We normalized the variables separately for each population so that they sum to 1 for each population. Source: Ethnographic Atlas (Murdock, 1967; Kirby et al., 2016).
Settlement complexity	The variable is based on EA entry EA030. The variable classifies "settlement patterns" in the following categories: 1- nomadic; 2- seminomadic; 3- semisedentary; 4- impermanent; 5- dispersed homesteads; 6- hamlets; 7- village/town; 8- complex permanent. Source: Ethnographic Atlas (Murdock, 1967; Kirby et al., 2016).
Political hierarchy	The variable is based on EA entry EA033. The variable captures the number of jurisdictional levels beyond the local community, with the following possible values: 1- acephalous (e.g., autonomous bands and villages); 2- one level (e.g., petty chiefdoms); 3- two levels (e.g., larger chiefdoms); 4- three levels (e.g., states); 5- four levels (e.g., large states). Source: Ethnographic Atlas (Murdock, 1967; Kirby et al., 2016).

Migratory distance from Addis Ababa	The raw data from the Human Mobility Index provides the potential minimum travel time on land and is measured in months of travel from Addis Ababa to the centroid of 1 km × 1 km pixels. Whenever two pieces of land are disconnected by waters, we connect them manually in the closest linear distance using values from adjacent pixels. We calculated the potential minimum travel time from Addis Ababa to the centroid pixel of each Ethnologue country-ethnicity. Centroid pixels of country-ethnicities are defined using polygons provided by World Language Mapping System (WLMS Version 19) for all languages of the world catalogued by the 17th edition of the Ethnologue (Lewis, 2009). Source: Özak (2018), Human Mobility Index (HMI).
Average inbreeding coefficient ($\overline{F_{ROH}}$)	The average inbreeding coefficient was computed across the Human Origins (HO) individuals matched to each Ethnologue language (and the associated country-ethnicities). Individual inbreeding coefficients were computed using the ROHgen2 software pipeline developed by the ROHgen consortium (Clark et al., 2019). Source: computed using the HO data (Reich Lab, 2020) for this paper; see Appendix C for details.
Mean regional pairwise F_{ST}	Mean regional pairwise F_{ST} was first computed for each Human Origins (HO) population with at least five individuals as the average of the pairwise F_{ST} between that population and all other populations in the same region with at least eight individuals in the (QCed) data. Then, each HO individual was assigned their HO population's mean regional pairwise F_{ST} estimate, and the mean regional pairwise F_{ST} was computed for each Ethnologue language (and the associated country-ethnicities) by taking the average across its matched individuals. Source: computed using the HO data for this paper; see Appendix C for details.
Expected heterozygosity	For each Human Origins (HO) population j with at least five individuals, expected heterozygosity was computed for each SNP i using Nei and Roychoudhury's formula (Nei and Roychoudhury, 1974); the HO population j's expected heterozygosity was then estimated by summing up the estimated heterozygosities across all SNPs. Then, each HO individual was assigned their HO population's expected heterozygosity estimate, and each Ethnologue language's expected heterozygosity was computed by taking the average across its matched individuals. Source: computed using the HO data (Reich Lab, 2020) for this paper; see Appendix C for details.
Top 20 PCs	The top 20 principal components (PCs) of the genotypic data (i.e., of the $N \times N$ matrix with the entry in row i and column j equal to the correlation between individuals i and j's SNP data) were computed for each Human Origins (HO) individual. For each Ethnologue language (and its associated country-ethnicities), the mean of each PC was then computed across the language's matched individuals. Source: computed using the HO data (Reich Lab, 2020) for this paper; see Appendix C for details.

Specialization index	The Ethnographic Atlas (EA) contains data on labor specialization across 10 different tasks: metal working, weaving, leather working, pottery, boat building, house building, hunting, fishing, animal husbandry, and agriculture. For each task and society, the EA codes which of the following categories best describes the task: (1) the task is absent or unimportant in the particular society; (2) there is junior age specialization—i.e., the activity is largely performed by boys and/or girls before the age of puberty; (3) there is senior age specialization—i.e., the activity is largely performed by men and/or women beyond the prime of life; (4) the task is normally performed by many or most adult men, women, or both; (5) there is craft specialization—i.e., the activity is largely performed by a small minority of adult males or females who possess specialized skills (occupational castes are treated as instances of craft specialization); (6) there is industrial specialization—i.e., the activity is largely removed from the domain of a division of labor by sex, age, or craft specialization and is performed in an industrialized manner mainly by techniques of production. We assigned each task one of three values: the first four EA categories (the task is absent or unimportant, only age specialization, or no specialization) are assigned the value 0; craft specialization is assigned the value 1; and industrial specialization is assigned the value 2. In addition, for each society, we then took the average across all tasks that were not coded as absent or had no missing entries and standardized the resulting average (note that in our regression analysis we control for dummies indicating both missing observations and whether the task is absent in a society). Source: Ethnographic Atlas (Murdock, 1967; Kirby et al., 2016).
Market participation	This variable is from the Standard Cross Cultural Sample (SCCS) and was obtained from D-PACE (Kirby et al., 2016). It is a binary variable that takes the value of 0 if production for consumption is more important and the value of 1 if production for consumption and production for market exchange are of equal importance.
Intercommunity food trade	This indicator is based on the variable "Intercommunity trade as a food source" of the SCCS and was obtained from D-PACE (Kirby et al., 2016). We coded the variable such that it takes the values 0 for the categories "no trade" or "no food imports", 1 for the category "less than 10 percent of food", 2 for "less than 50 percent of food", and 3 for "more than 50 percent of food".

Region-level variables:

Variable name	**Description**
Regional GDP per capita	Gross domestic product per capita in the region in constant 2005 PPP dollars. Source: Gennaioli et al. (2014).
Capital is in region	Dummy equal to 1 if the region contains a national capital, 0 otherwise. Source: Gennaioli et al. (2014).
Educational attainment (EA)	The average years of schooling from primary school onward for the population aged 15 years or older. Source: Gennaioli et al. (2014).
Oil and gas production	Cumulative oil, gas and liquid natural gas production from the time production began to 2000. Source: Gennaioli et al. (2014).

Country-level variables:

Variable name	**Description**
GDP	GDP per capita in constant PPP 2011 dollars from the Maddison Project. For methodological details, see Bolt and van Zanden (2020). Source: Maddison Project Database 2020.
Openness	Following Gennaioli et al. (2014), we calculated the sum of exports and imports as a share of GDP. Source: Penn World Tables.
Articles per million	Following Ashraf and Galor (2013a), we use number of scientific and technical journal articles and population from the World Bank to generate the variables. The variable is calculated as the average from 2000 to 2018. Source: The World Bank.
Patents per million	The sum of patents granted by the European Patent Office, the Japanese Patent Office, and the U.S. Patent and Trademark Office to residents of each country. The variable is produced by the Economist Intelligence Unit (2007; 2009). Source: Gorodnichenko and Roland (2016).
Expropriation risk	Risk of "outright confiscation and forced nationalization" of property. This variable ranges from 0 to 10 where higher values indicate a lower probability of expropriation and is calculated as the average from 1982 through 1997. The variable is from the International Country Risk Guide and was obtained from Gennaioli et al. (2013). Source: Gennaioli et al. (2013).
Institutional quality	The variable is generated based on data from the World Bank Enterprise Surveys and Doing Business report. It is a latent variable of: (1) (minus) Informal payments; (2) (minus) Ln(tax days); (3) (minus) Ln(days without electricity); (4) (minus) Security costs; (5) (minus) Access to land, (6) (minus) Access to finance; (7) Government predictability; and (8) (minus) Doing Business percentile rank. Higher values indicate better institutions. Source: Gennaioli et al. (2013).
CPI	The Corruption Perceptions Index (CPI) measures "perceived levels of public sector corruption, as determined by expert assessments and opinion surveys." The CPI ranges from 0 to 100, where lower values indicate higher corruption. Source: Transparency International.

Blood donations	Voluntary blood donations per 1,000 inhabitants. The variable is taken from the WHO report on Global Status on Blood Safety and Availability 2016. The report contains data for the years 2011, 2012, and 2013. Following Schulz et al. (2019), we use the averages across these years. When data for a year is missing for a country, the indicator is based on the non-missing years. In about a third of the countries, not all blood centers are covered. In these cases, we did the following: The WHO report states the estimated percentage of blood donations covered; we calculated the total amount of blood donated based on those estimates. In the non-fully covered countries, the coverage is still reasonably high: for 60% of those countries, the report is based on data that covers at least 75% of the estimated blood donations. The WHO report gives further information on the types of donations: (i) voluntary non-remunerated donations, (ii) family/replacement donations, (iii) paid donations, or (iv) other. Our main variable of interest is voluntary non-remunerated donations per 1,000 inhabitants. To calculate per capita values, we divided the number of voluntary non-remunerated donations by the World Bank's population estimates (in 1000s) for the year 2012. Source: WHO (2016).
Out-in-group trust	This measure is based on the World Values Survey's (WVS) trust questions that are specific about which group of people can be trusted or not (Haerpfer and et al., 2020) . These questions can be classified into outgroup and ingroup trust. The questions are posed in the following way (and answers are on a four-point scale): "I'd like to ask you how much you trust people from various groups. Could you tell me for each whether you trust people from this group completely, somewhat, not very much or not at all?" The various groups are (i) the respondent's family, (ii) the respondent's neighbors, (iii) people the respondent knows personally, (iv) people s/he meets for the first time, (v) people of another religion, and (vi) people of another nationality. While the three former questions all relate to people the respondent is relatively familiar with, the latter three questions refer to more unfamiliar people. Following Schulz et al. (2019), the Out-in-group trust measure is constructed by taking the difference between the average of the last three questions (which plausibly capture outgroup trust) and the average of the first three questions (which plausibly capture in-group trust). We then take country means and standardize the variable. Source: Schulz et al. (2019).

A.2 Matching data

This Appendix section complements Section 3.3 and provides more detail on the procedures we used to match the various datasets we analyzed. At a high level, we matched ethnographic variables from the EA and genetic variables from the HO dataset to languages from the Ethnologue; then, we matched Ethnologue languages to geographic pixels; finally, for the analyses at the country-ethnicity, region, and country levels, we collapsed the resulting pixel-level data to country-ethnicities, regions, or countries.

Matching ethnographic and genetic variables to the Ethnologue languages

As we describe in the main text, to match the KII and other EA-derived variables to the pixel-level data, we first matched each EA society to contemporary languages from the 17th edition of the Ethnologue (Gordon, 2005; Lewis, 2009). We employed two different matching methods. The direct-matching method does one-to-one matches. With that method, the 911 EA societies with non-missing KII data are matched to 911 Ethnologue languages corresponding to 1,254 country-ethnicities (as some of the languages are spoken in multiple countries).

The language-tree matching method does many-to-one matches. For each EA variable, the vast majority of the 5,756 Ethnologue languages[1] are matched to one of the EA societies with no missing data for the variable.[2] Specifically, for each variable, each Ethnologue language is matched to the linguistically closest EA society that speaks a language within the same language family and with nonmissing data for the variable; when no such society exists for a language and variable, the variable is coded as missing for the language.

After matching the Ethnologue languages to geographic pixels and applying quality-control filters, as described below and in Section 3.1, we are left with 713 country-ethnicities with the direct matching method and 2,352 country-ethnicities with the language-tree matching method.

For the analyses using the inbreeding coefficients (F), we matched each population from the Human Origins (HO) dataset to a single Ethnologue language (and to the single or multiple country-ethnicities associated with that language). Appendix C.2 provides more details.

Matching to pixels

We used a shapefile provided by the World Language Mapping System (World GeoDatasets)[3] to match pixels to Ethnologue country-ethnicities. Of the 783,525 pixels that remain after applying the filters described in Section 3.1, 133,614 ($\sim$ 17%) could not be matched to any ethnicity (either because the pixel is unpopulated according to the Ethnologue or because Ethnologue data is missing).

For the pixel-level analyses, we applied three additional filters. We dropped (1) 52,782 pixels ($\sim$ 8%) that were matched to more than one country-ethnicity, as well as a further 104,965 ($\sim$ 18%) pixels that (2) fell on the boundaries of a country-homeland or (3) were matched to a country-ethnicity with a very small country-homeland comprising less than five pixels.

With the language-tree matching method, we dropped a further 3,606 pixels due to missing data for a KII indicator, thus leaving 488,558 pixels located in the country-homelands of 2,352 country-ethnicities around the world (which account for $\sim$ 52% of the world population). The

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[1] As mentioned in the main text, some languages are spoken in multiple countries and we refer to the (ethnolinguistic) group that speaks a given language within a given country as a "country-ethnicity". There are 5,756 languages and 7,651 country-ethnicities in the Ethnologue.

[2] Following Schulz et al. (2019) and as described in Appendix A.1, before this matching step with the language-tree matching method, we imputed missing observations for the cousin-marriage preference and co-residence-of-extended-families sub-indicators. We did not impute these variables with the direct-matching method and we did not impute any other EA variables that way.

[3] The shapefile is available at `worldgeodatasets.com/language`.

direct matching method left 377,656 pixels with nonmissing KII data located in the country-homelands of 713 country-ethnicities (which account for ∼ 38% of the world population). And matching the HO data to pixels leaves 281,177 pixels located in the homelands of 245 country-ethnicities.

Matching to subnational regions and countries

To match pixel-level data to subnational regions or countries, we collapsed the pixel data—along with the ethnographic variables already matched to that data using either matching method—to the regions or countries. We did not apply here the three additional filters described just above for the pixel-level analyses, nor did we apply the filters listed in Section 3.1 to the pixel data prior to collapsing it, since these filters are only needed for the nighttime luminosity data and these data were not used for our main region- and country-level analyses. Specifically, to collapse the data for each ethnographic variable, we computed the population-weighted mean of the variable across the regions' or countries' pixels. For pixels matched to more than one Ethnologue language, we took the simple average of the EA variable across each pixel's matched languages. For variables defined at the pixel level, such as the geographic controls, we proceeded analogously, except that we took the simple (instead of the population-weighted) mean of each variable across each region's or county's pixels.

Finally, we dropped regions or countries for which the pixels with nonmissing KII data account for less than 75% of the population. With the language-tree matching method, this left 1452 regions in 83 countries for the region-level analyses with the Gennaioli et al. (2014) data; with the direct matching method, this left 873 regions in 61 countries.

Matching to country-ethnicities

For the analyses at the country-ethnicity level, each country-ethnicity was assigned its matched EA variables. The filters described above and in Section 3.1 for the pixel-level analyses were applied. We took the simple mean of each geographic control across the pixels in each country-homeland, and we computed nighttime luminosity (i.e., light density) for each country-homeland by dividing the total luminosity by the total area calculated across the country-homeland's pixels.

B Additional graphs and tables

B.1 Additional graphs and tables for Section 3 (Data)

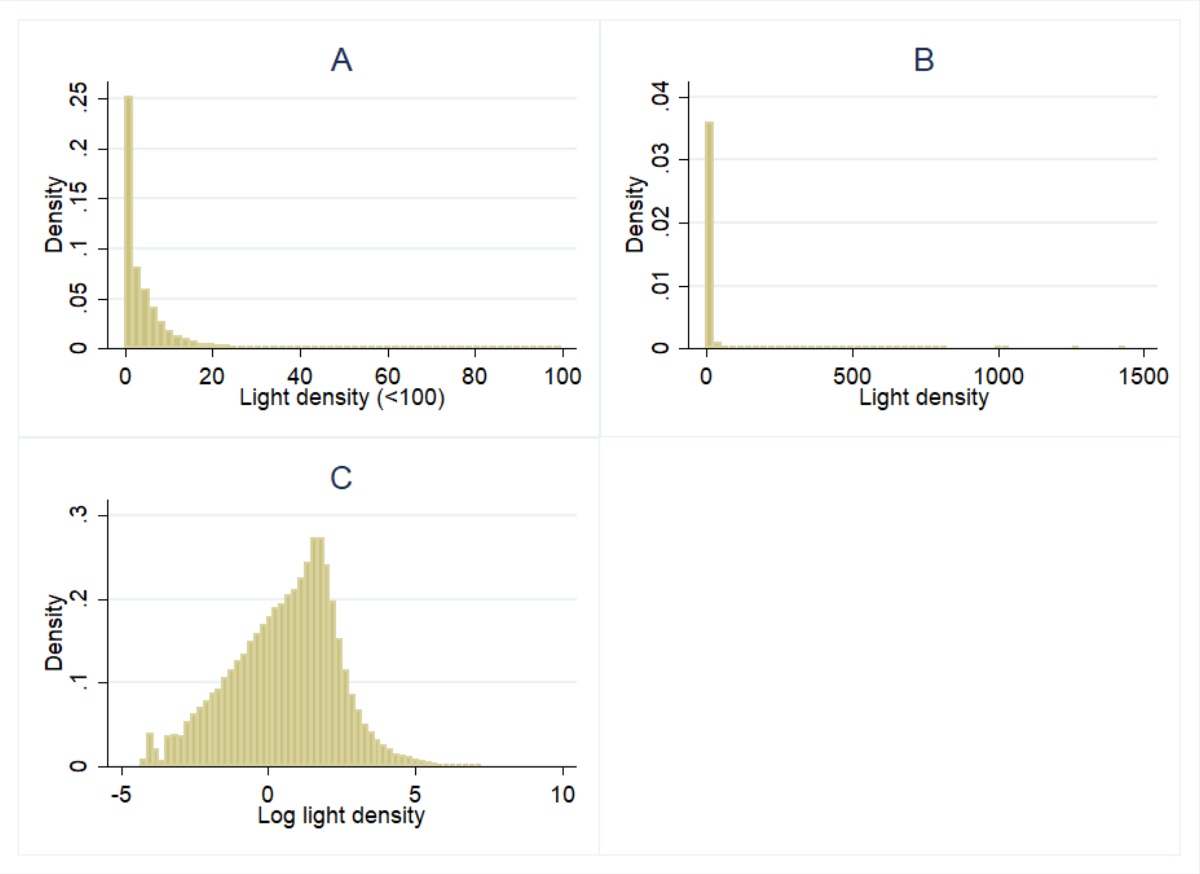

Figure B.1.1: Histograms of light and log nighttime luminosity for the 255,813 pixels in our sample with luminosity exceeding the lowest nonzero value (i.e., 0.013). Panel A shows a histogram for the subset of these pixels with luminosity less than 100; Panel B shows the same histogram but for all these pixels; and Panel C shows a histogram of log luminosity, also for all these pixels.

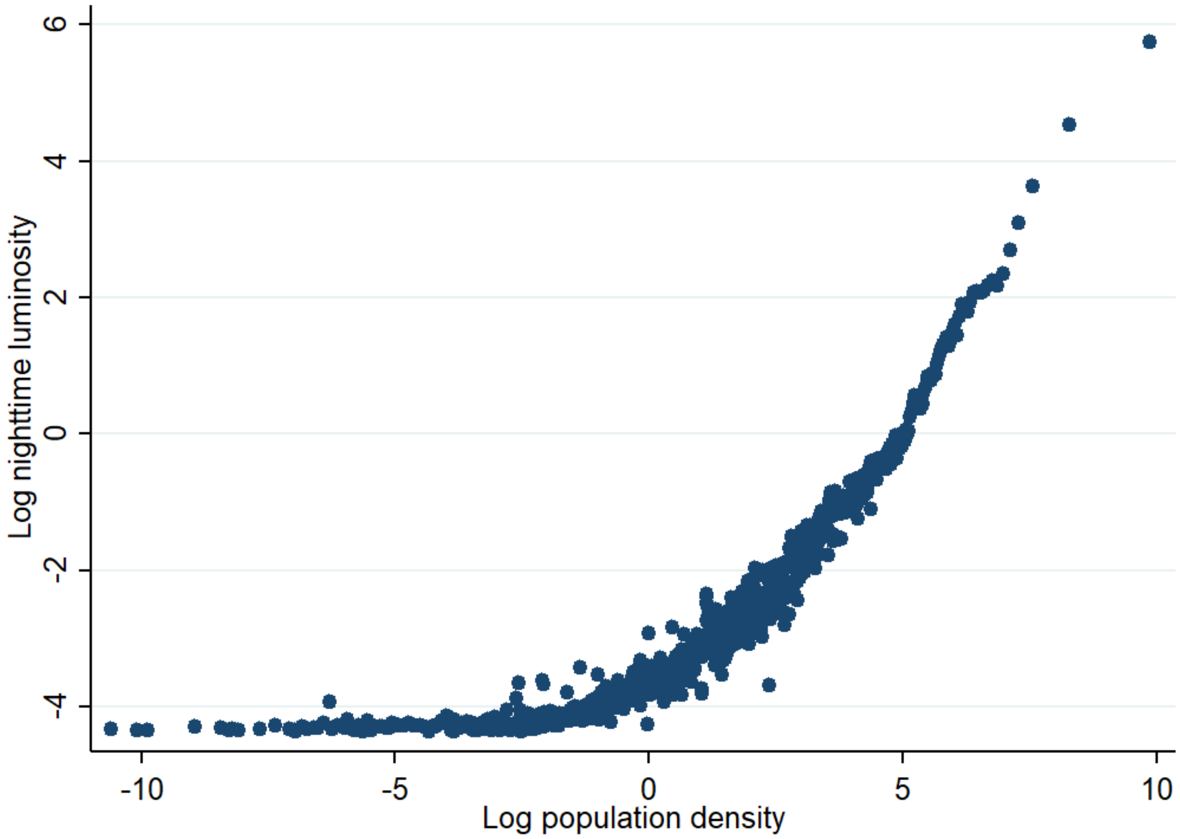

Figure B.1.2: Binned scatterplot (with one bin for every 1,000 observations) of the relationship between log nighttime luminosity and log population density across the 783,525 pixels in our sample. In the analyses reported in the paper, unlike for this figure, we recoded to 1 the population density of pixels whose original population density was less than 1 person per square kilometer.

	KII	Cousin marriage preference	Polygyny	Co-residence of extended families	Lineage organization	Community organization
KII	1					
Cousin marriage preference	0.4727***	1				
Polygyny	0.5511***	0.0261	1			
Co-residence of extended family	0.5553***	0.0737**	0.2041***	1		
Lineage organization	0.7206***	0.2135***	0.2779***	0.2408***	1	
Community organization	0.5935***	0.0375	0.1323***	0.1536***	0.4375***	1

Table B.1.1: Pearson correlation between the KII and its five sub-indicators across the 911 EA societies with non-missing KII data. *** $p < 0.01$, ** $p < 0.05$, * $p < 0.1$

B.2 Additional graphs and tables for Section 4.1 (Kinship intensity and nighttime luminosity

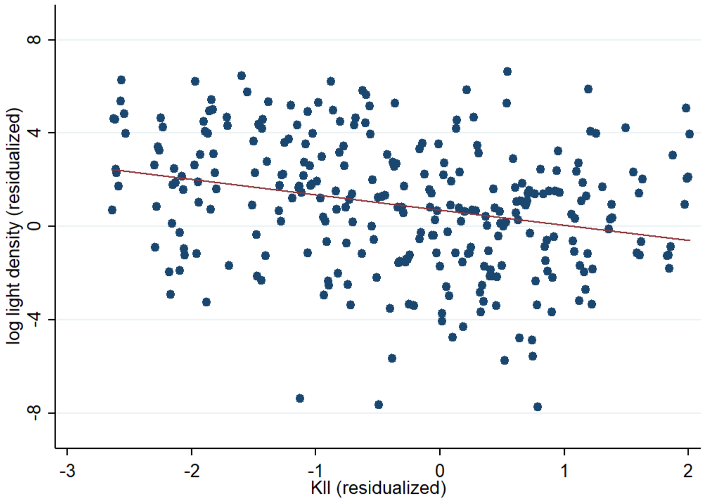

Figure B.2.1: Log nighttime luminosity vs. the KII across country-ethnicities, for the sample of country-ethnicities matched with the language-tree matching method. Both variables have been residualized on log population density.

Table B.2.1: The KII and nighttime luminosity: summary statistics

Panel A.

377,656 pixels (in the homelands of 713 ethnicities)

	mean	sd	min	max
Log nighttime luminosity	-2.381	2.672	-4.360	7.142
Kinship intensity index	-1.121	1.389	-2.510	2.104
Log population density	1.659	1.847	0.000	10.215
Monthly temperature (degree Celsius)	1.489	21.231	-54.400	33.800
Precipitation (cm)	5.593	8.348	0.000	76.650
Agricultural suitability	0.298	0.322	0.000	0.999
Absolute latitude	36.167	18.426	0.063	74.813
Elevation (km)	0.611	0.706	-0.089	6.121
Ruggedness (km)	0.085	0.124	0.000	1.317
Distance to coast (1000 km)	0.595	0.497	0.003	2.464
Distance to nearest river/lake (1000 km)	0.122	0.182	0.000	1.376
Hunting	0.463	0.859	0.000	9.000
Fishing	0.816	0.907	0.000	7.500
Animal husbandry	3.486	1.986	0.000	9.000
Agriculture	4.962	2.279	0.000	9.000
Political hierarchy	3.611	1.215	1.000	5.000
Malaria index	1.643	4.590	0.000	38.081
Settlement complexity	5.775	2.288	1.000	8.000
Deep Christianization	0.577	0.492	0.000	1.000

Panel B.

488,558 pixels (in the homelands of 2,352 ethnicities)

	mean	sd	min	max
Log nighttime luminosity	-2.418	2.674	-4.360	7.142
Kinship intensity index	-0.819	1.456	-2.510	2.104
Log population density	1.773	1.877	0.000	10.215
Monthly temperature (degree Celsius)	3.256	20.383	-54.400	33.800
Precipitation (cm)	5.479	8.148	0.000	76.650
Agricultural suitability	0.277	0.313	0.000	0.999
Absolute latitude	34.759	18.566	0.063	74.813
Elevation (km)	0.660	0.804	-0.137	6.184
Ruggedness (km)	0.092	0.135	0.000	1.518
Distance to coast (1000 km)	0.576	0.493	0.003	2.464
Distance to nearest river/lake (1000 km)	0.146	0.232	0.000	1.537
Hunting	0.561	0.963	0.000	9.000
Fishing	0.811	0.966	0.000	8.000
Animal husbandry	3.401	2.080	0.000	9.000
Agriculture	4.887	2.339	0.000	9.000
Political hierarchy	3.493	1.273	1.000	5.000
Malaria index	1.925	5.096	0.000	38.081
Settlement complexity	5.580	2.354	1.000	8.000
Deep Christianization	0.484	0.498	0.000	1.000

Notes: The table shows summary statistics for the main variables used in the analysis of the relationship between the KII and nighttime luminosity, for the pixels in the analysis samples obtained with the direct (Panel A) and language-tree (Panel B) matching methods.

Table B.2.2: The KII and nighttime luminosity with the language-tree matching method: cross section

	Log nighttime luminosity									
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)
KII	-0.373***	-0.500***	-0.391***	-0.120***	-0.096***	-0.063**	-0.068**	-0.088***	-0.096***	-0.096***
	(0.123)	(0.123)	(0.114)	(0.037)	(0.020)	(0.031)	(0.029)	(0.019)	(0.017)	(0.021)
Log population density		0.930***	0.964***	1.035***	1.012***	1.012***	1.010***	1.008***	1.012***	1.012***
		(0.056)	(0.042)	(0.070)	(0.062)	(0.063)	(0.063)	(0.062)	(0.112)	(0.115)
Subsistence variables						yes				
Political hierarchy							yes			
Malaria index								yes		
Geographic controls			yes	yes	yes	yes	yes	yes	yes	yes
Continent FE				yes						
Country FE					yes	yes	yes	yes	yes	yes
Observations	488,558	488,558	488,558	488,558	488,558	488,558	486,936	488,558	488,558	488,558
R-squared	0.041	0.462	0.530	0.570	0.653	0.653	0.654	0.654	0.653	0.653
Number of clusters	162	162	162	162	162	162	162	162	74	74 & 162

Notes: Each observation is a pixel in the country-homeland of a country-ethnicity matched with the language-tree matching method. The geographic controls include temperature, precipitation, agricultural suitability, absolute latitude, elevation, ruggedness, distance to coast, and distance to nearest river or lake. The subsistence variables measure the fraction of an ethnicity's subsistence economy that depends on hunting, fishing, animal husbandry, and agriculture (with gathering as the omitted category). Standard errors in parentheses are clustered at the country level in all regressions, except in column 8, where they are clustered at the language-family level, and in column 9, where they are clustered two-way at both the country and language-family levels. *** $p < 0.01$, ** $p < 0.05$, * $p < 0.1$

Table B.2.3: The KII and nighttime luminosity at the country-ethnicity level: cross section

Panel A.	Log nighttime luminosity										
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)
KII	-0.607***	-0.671***	-0.375***	-0.097*	-0.142***	-0.150***	-0.115**	-0.130**	-0.142***	-0.142***	-0.142**
	(0.113)	(0.098)	(0.061)	(0.053)	(0.053)	(0.052)	(0.058)	(0.050)	(0.045)	(0.048)	(0.058)
Log population density		yes	yes	yes	yes	yes	yes	yes	yes	yes	yes
Subsistence variables						yes					
Political hierarchy							yes				
Malaria index								yes			
Geographic controls			yes	yes	yes	yes	yes	yes	yes	yes	yes
Continent FE				yes							
Country FE					yes	yes	yes	yes	yes	yes	yes
Observations	659	659	659	659	659	659	655	659	659	659	659
R-squared	0.077	0.348	0.646	0.715	0.831	0.833	0.833	0.832	0.831	0.831	0.543
Number of clusters	135	135	135	135	135	135	135	135	60	60 & 135	

Panel B.	Log nighttime luminosity										
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)
KII	-0.457***	-0.442***	-0.286***	-0.029	0.006	0.001	0.017	0.010	0.006	0.006	0.006
	(0.121)	(0.125)	(0.076)	(0.053)	(0.040)	(0.041)	(0.044)	(0.038)	(0.047)	(0.042)	(0.053)
Log population density		yes	yes	yes	yes	yes	yes	yes	yes	yes	yes
Subsistence variables						yes					
Political hierarchy							yes				
Malaria index								yes			
Geographic controls			yes	yes	yes	yes	yes	yes	yes	yes	
Continent FE				yes							
Country FE					yes	yes	yes	yes	yes	yes	
Observations	2,143	2,143	2,143	2,143	2,143	2,143	2,137	2,143	2,143	2,143	2,143
R-squared	0.045	0.281	0.538	0.609	0.737	0.738	0.738	0.737	0.737	0.737	0.440
Number of clusters	161	161	161	161	161	161	161	161	72	72 & 161	

Notes: Each observation is a country-ethnicity matched with the direct (Panel A) and language-tree (Panel B) matching methods. The geographic controls include temperature, precipitation, agricultural suitability, absolute latitude, elevation, ruggedness, distance to coast, and distance to nearest river or lake. The subsistence variables measure the fraction of a country-ethnicity's subsistence economy that depends on hunting, fishing, animal husbandry, and agriculture (with gathering as the omitted category). Standard errors in parentheses are clustered at the country level in columns 1-8, at the language-family level in column 9, and two-way at both the country and language-family levels in column 10; Conley standard errors (with a distance cut-off of 1,500 km) are reported in column 11. *** $p < 0.01$, ** $p < 0.05$, * $p < 0.1$

Table B.2.4: KII sub-indicators and nighttime luminosity: cross section

Panel A.	Log nighttime luminosity									
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)
Cousin marriage preference	-0.057	0.037								
	(0.094)	(0.066)								
Coresidence of extended families			-0.409***	-0.121***						
			(0.140)	(0.027)						
Polygamy					-0.485***	-0.057				
					(0.135)	(0.044)				
Community organization							-0.138	-0.168***		
							(0.110)	(0.040)		
Lineage organization									-0.655***	-0.133***
									(0.188)	(0.033)
Log population density	yes	yes	yes	yes	yes	yes	yes	yes	yes	yes
Geographic controls	yes	yes	yes	yes	yes	yes	yes	yes	yes	yes
Country FE	no	yes	no	yes	no	yes	no	yes	no	yes
Observations	386,160	386,160	390,720	390,720	390,350	390,350	381,151	381,151	390,542	390,542
R-squared	0.496	0.652	0.527	0.652	0.525	0.652	0.502	0.659	0.539	0.652
Number of clusters	140	140	141	141	141	141	138	138	141	141

Panel B.	Log nighttime luminosity									
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)
Cousin marriage preference	-0.085	0.003								
	(0.084)	(0.044)								
Coresidence of extended families			-0.343***	-0.092***						
			(0.125)	(0.019)						
Polygamy					-0.464***	-0.063*				
					(0.120)	(0.033)				
Community organization							-0.120	-0.122***		
							(0.079)	(0.038)		
Lineage organization									-0.597***	-0.101***
									(0.162)	(0.024)
Log population density	yes	yes	yes	yes	yes	yes	yes	yes	yes	yes
Geographic controls	yes	yes	yes	yes	yes	yes	yes	yes	yes	yes
Country FE	no	yes	no	yes	no	yes	no	yes	no	yes
Observations	488,717	488,717	489,114	489,114	489,106	489,106	488,793	488,793	489,114	489,114
R-squared	0.500	0.652	0.526	0.653	0.530	0.653	0.501	0.653	0.541	0.653
Number of clusters	162	162	162	162	162	162	162	162	162	162

Notes: Each observation is a pixel in the country-homeland of a country-ethnicity matched with the direct (Panel A) and language-tree (Panel B) matching methods. The geographic controls include temperature, precipitation, agricultural suitability, absolute latitude, elevation, ruggedness, distance to coast, and distance to nearest river or lake. The subsistence variables measure the fraction of an ethnicity's subsistence economy that depends on hunting, fishing, animal husbandry, and agriculture (with gathering as the omitted category). Standard errors in parentheses are clustered at the country level in all regressions. *** $p < 0.01$, ** $p < 0.05$, * $p < 0.1$

B.3 Additional graphs and tables for Section 4.2 (Kinship intensity and regional GDP per capita)

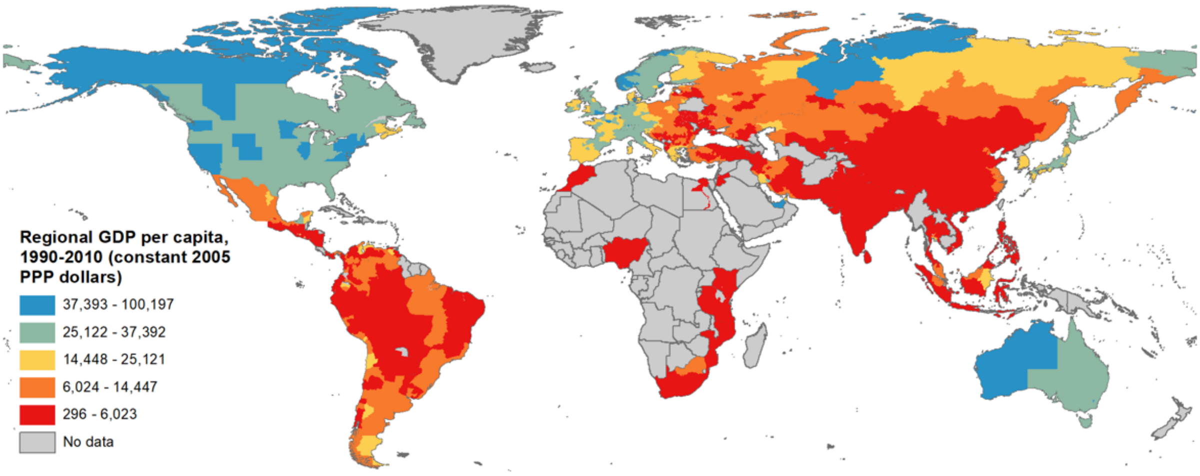

Figure B.3.1: GDP per capita (in constant 2005 PPP dollars) for 1,452 regions around the world. For this map, we take the average GDP per capita for each region for the period from 1990 to 2010 (since all regions in the dataset have at least one nonmissing observation during that period). Our regression analyses use panel data from 1950 to 2010.

Table B.3.1: The KII and regional GDP per capita: summary statistics

Panel A.

5,514 region-years (in 873 distinct subnational regions in 61 countries)

	mean	sd	min	max
Log GDP per capita	8.876	1.019	5.545	11.340
Kinship intensity index	-1.603	1.046	-2.576	1.714
Oil and Gas production	0.001	0.006	0.000	0.122
Capital is in Region	0.050	0.218	0.000	1.000
Monthly temperature (degree Celsius)	5.806	13.636	-42.781	28.272
Precipitation (cm)	5.875	5.922	0.000	53.476
Agricultural suitability	0.536	0.280	0.001	0.998
Absolute latitude	34.762	15.296	0.583	66.671
Elevation (km)	0.555	0.596	-0.008	3.308
Ruggedness (km)	0.125	0.110	0.000	0.818
Distance to coast (1000 km)	0.258	0.342	0.003	2.225
Distance to nearest river/lake (1000 km)	0.080	0.087	0.005	0.580
Hunting	0.138	0.315	0.000	3.198
Fishing	0.667	0.787	0.000	3.105
Animal husbandry	2.717	1.234	0.000	8.000
Agriculture	6.359	1.518	0.975	9.000
Political hierarchy	3.964	0.912	1.000	5.000
Malaria index	0.905	2.297	0.000	23.446
Settlement complexity	6.847	1.093	1.838	8.000
Deep Christianization	0.624	0.481	0.000	1.000

Panel B.

9,019 region-years (in 1,452 distinct subnational regions in 83 countries)

	mean	sd	min	max
Log GDP per capita	8.798	1.149	5.242	12.020
Kinship intensity index	-1.335	1.099	-2.510	2.045
Oil and Gas production	0.001	0.006	0.000	0.122
Capital is in Region	0.044	0.206	0.000	1.000
Monthly temperature (degree Celsius)	6.431	13.487	-42.781	30.749
Precipitation (cm)	5.998	6.193	0.000	53.476
Agricultural suitability	0.501	0.279	0.000	0.998
Absolute latitude	33.543	16.362	0.228	70.117
Elevation (km)	0.606	0.680	-0.008	4.801
Ruggedness (km)	0.142	0.129	0.000	0.818
Distance to coast (1000 km)	0.253	0.331	0.002	2.225
Distance to nearest river/lake (1000 km)	0.080	0.097	0.003	0.896
Hunting	0.220	0.469	0.000	5.272
Fishing	0.749	0.736	0.000	5.144
Animal husbandry	2.624	1.289	0.000	9.000
Agriculture	6.276	1.485	0.000	9.000
Political hierarchy	3.860	0.975	1.000	5.000
Malaria index	1.122	2.811	0.000	28.724
Settlement complexity	6.724	1.189	1.000	8.000
Deep Christianization	0.572	0.493	0.000	1.000

Notes: Summary statistics for the main variables used in the analysis of the relationship between the KII and regional GDP per capita, for the region-years in the analysis samples obtained with the direct (Panel A) and language-tree (Panel B) matching methods.

Table B.3.2: The KII and regional GDP per capita with the language-tree matching method: panel data

	Log regional GDP per capita								
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)
KII	-0.493***	-0.456***	-0.334***	-0.090**	-0.121***	-0.088**	-0.094**	-0.084**	-0.090**
	(0.099)	(0.074)	(0.068)	(0.039)	(0.042)	(0.041)	(0.039)	(0.036)	(0.035)
Subsistence variables					yes				
Political hierarchy						yes			
Malaria index							yes		
Oil and Gas production								yes	
Capital is in Region								yes	
Geographic controls		yes	yes	yes	yes	yes	yes	yes	yes
Year FE	yes	yes							
Year × Continent FE			yes						
Year × Country FE				yes	yes	yes	yes	yes	yes
Observations	9,019	9,019	9,019	9,019	9,019	9,019	9,019	9,014	9,019
R-squared	0.329	0.597	0.673	0.896	0.897	0.896	0.898	0.906	0.084
Number of clusters	83	83	83	83	83	83	83	83	

Notes: Each observation is a region-year in the analysis sample obtained with the language-tree matching method. The geographic controls include temperature, precipitation, agricultural suitability, absolute latitude, elevation, ruggedness, distance to coast, and distance to nearest river or lake. The subsistence variables measure the population-weighted fraction of a region's ethnicities' subsistence economies that depend on hunting, fishing, animal husbandry, and agriculture (with gathering as the omitted category). Standard errors in parentheses are clustered at the country level in all regressions, except in column 9 where Conley standard errors (with a distance cut-off of 6,500 km) are reported. *** $p < 0.01$, ** $p < 0.05$, * $p < 0.1$

B.4 Additional graphs and tables for Section 4.3 (Spatial regression discontinuity (RD) analysis)

Table B.4.1: Spatial RD analysis: summary statistics

Panel A. 290,669 pixels (in the homelands of 572 pairs of neighboring ethnicities)

	mean	sd	min	max
Log nighttime luminosity	-2.694	2.483	-4.360	7.142
KII	-1.014	1.414	-2.576	2.087
Log population density	1.642	1.834	0.000	10.215
Agricultural suitability	0.273	0.303	0.000	0.999
Absolute latitude	34.401	20.017	0.063	73.938
Monthly temperature (degree Celsius)	0.880	21.652	-52.900	32.800
Precipitation (cm)	6.362	9.321	0.000	76.650
Elevation (km)	0.732	0.707	-0.089	5.543
Ruggedness (km)	0.093	0.125	0.000	1.317
Distance to coast (1000 km)	0.677	0.513	0.003	2.464
Distance to nearest river/lake (1000 km)	0.082	0.107	0.000	1.090
Hunting	0.562	0.922	0.000	9.000
Fishing	0.875	0.935	0.000	7.500
Animal husbandry	3.225	1.964	0.000	9.000
Agriculture	5.052	2.185	0.000	9.000
Political hierarchy	3.506	1.295	1.000	5.000
Malaria index	2.592	5.808	0.000	36.849
Settlement complexity	5.896	2.124	1.000	8.000
Deep Christianization	0.524	0.499	0.000	1.000

Panel B. 750,996 pixels (in the homelands of 2,716 pairs of neighboring ethnicities)

	mean	sd	min	max
Log nighttime luminosity	-2.758	2.441	-4.360	7.142
KII	-0.703	1.442	-2.510	2.104
Log population density	2.042	1.929	0.000	10.215
Agricultural suitability	0.278	0.298	0.000	0.999
Absolute latitude	28.306	19.251	0.063	73.938
Monthly temperature (degree Celsius)	7.583	19.852	-52.900	33.800
Precipitation (cm)	7.051	9.688	0.000	76.650
Elevation (km)	0.779	0.828	-0.137	6.184
Ruggedness (km)	0.103	0.147	0.000	1.518
Distance to coast (1000 km)	0.637	0.506	0.003	2.464
Distance to nearest river/lake (1000 km)	0.104	0.167	0.000	1.499
Hunting	0.584	0.944	0.000	9.000
Fishing	0.820	0.989	0.000	8.000
Animal husbandry	3.062	1.903	0.000	9.000
Agriculture	5.231	2.152	0.000	9.000
Political hierarchy	3.473	1.311	1.000	5.000
Malaria index	3.540	6.729	0.000	38.081
Settlement complexity	5.987	2.019	1.000	8.000
Deep Christianization	0.418	0.493	0.000	1.000

Notes: Summary statistics for the main variables used in the spatial RD analysis, for the pixels in the analysis samples obtained with the direct (Panel A) and language-tree (Panel B) matching methods.

Table B.4.2: The KII and nighttime luminosity: spatial RD analysis with the language-tree matching method

	Log nighttime luminosity							
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
KII	-0.084**	-0.045**	-0.054***	-0.047**	-0.036	-0.054***	-0.054***	-0.054***
	(0.038)	(0.018)	(0.018)	(0.020)	(0.022)	(0.017)	(0.018)	(0.020)
Subsistence variables				yes				
Political hierarchy					yes			
Malaria index						yes		
Log population density		yes	yes	yes	yes	yes	yes	yes
Geographic controls			yes	yes	yes	yes	yes	yes
Distance-to-the-boundary polynomial	yes	yes	yes	yes	yes	yes	yes	yes
Ethnicity pair FE	yes	yes	yes	yes	yes	yes	yes	yes
Observations	750,996	750,996	750,996	750,996	748,603	750,996	750,996	750,996
R-squared	0.432	0.614	0.623	0.623	0.624	0.623	0.623	0.623
Number of clusters	104	104	104	104	104	104	69	69 & 104

Notes: Each observation is a pixel that belongs to a country-ethnicity matched with the language-tree matching method, in a pair of contiguous country-ethnicities in the same country, and within 200 km of the boundary between the two ethnicities. The geographic controls include temperature, precipitation, agricultural suitability, absolute latitude, elevation, ruggedness, distance to coast, and distance to nearest river or lake. "Distance-to-the-boundary polynomial" is the geodesic distance of each pixel's centroid from the boundary between the two adjacent ethnicities; we allow the coefficient on the distance term to differ between the relatively high and the relatively low KII ethnicities in the pairs. The subsistence variables measure the fraction of an ethnicity's subsistence economy that depends on hunting, fishing, animal husbandry, and agriculture (with gathering as the omitted category). Standard errors in parentheses are clustered at the country level (in columns 1-6), language family level (in column 7), and two-way clustered at both the country and language-family levels (in column 8). *** $p < 0.01$, ** $p < 0.05$, * $p < 0.1$

Table B.4.3: Spatial RD analysis for the geographic controls

	(1) Temperature	(2) Precipitation	(3) Agricultural suitability	(4) Elevation	(5) Ruggedness	(6) Distance to coast	(7) Distance to river/lake	(8) Malaria index
KII	-0.377	0.064	0.005	-0.006	-0.005	-0.020*	0.003	-0.061
	(0.297)	(0.093)	(0.007)	(0.026)	(0.005)	(0.011)	(0.003)	(0.095)
Distance-to-the-boundary polynomial	yes	yes	yes	yes	yes	yes	yes	yes
Ethnicity pair FE	yes	yes	yes	yes	yes	yes	yes	yes
Observations	290,669	290,669	290,669	290,669	290,669	290,669	290,669	290,669
R-squared	0.981	0.907	0.638	0.664	0.370	0.809	0.714	0.883
Number of clusters	70	70	70	70	70	70	70	70

Notes: Each observation is a pixel that belongs to a country-ethnicity matched with the direct matching method, in a pair of contiguous country-ethnicities in the same country, and within 200 km of the boundary between the two ethnicities. "Distance-to-the-boundary polynomial" is the geodesic distance of each pixel's centroid from the boundary between the two adjacent ethnicities; we allow the coefficient on the distance term to differ between the relatively high and the relatively low KII ethnicities in the pairs. Standard errors in parentheses are clustered at the country level. *** $p < 0.01$, ** $p < 0.05$, * $p < 0.1$

B.5 Additional graphs and tables for Section 5.2 (The inbreeding coefficient and kinship intensity)

Table B.5.1: The inbreeding coefficient and kinship intensity: summary statistics

	No. ethnicities	mean	sd	min	max
HO sample size	416	29.0	42.7	8	203
KII	396	-0.242	0.782	-1.511	1.210
Cousin marriage preference	398	0.101	1.148	-0.546	2.808
Co-residence	410	-0.252	1.278	-2.542	1.408
Polygamy	410	-0.637	1.066	-1.801	0.937
Community organization	407	-0.053	0.968	-1.072	0.931
Lineage organization	410	-0.278	1.087	-1.595	0.626
$\overline{F_{ROH}}$	416	0.020	0.018	0.003	0.146
Expected heterozygosity	415	17,410	1,084	12,156	18,630
Migratory distance (months)	416	2.798	1.805	0.229	8.412
Mean regional pairwise F_{ST}	415	0.024	0.017	0.001	0.117

Notes: Summary statistics for the main variables used in the analysis of the relationship between kinship intensity and the inbreeding coefficient, for the Ethnologue country-ethnicities in the analysis sample. "HO sample size" denotes the number of individuals in the HO dataset used to compute $\overline{F_{ROH}}$, expected heterozygosity, mean regional pairwise F_{ST}, and the top 20 PCs; summary statistics are not shown for the top 20 PCs because they have been normalized and thus have zero mean and unit variance.

Table B.5.2: The inbreeding coefficient and kinship intensity: robustness checks

	Cousin marriage preference				KII			
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
$\overline{F_{ROH}}$	43.636***	38.142***	52.054***	43.308***	10.783***	9.411***	15.391***	13.591***
	(6.228)	(4.828)	(5.307)	(6.101)	(2.923)	(2.474)	(2.712)	(3.505)
Genetic controls	yes	yes	yes	yes	yes	yes	yes	yes
Geographic controls	yes				yes			
Min. HO sample per ethnicity	8	5	10	15	8	5	10	15
Observations	364	488	324	210	362	486	322	208
R-squared	0.496	0.414	0.495	0.621	0.751	0.641	0.753	0.799
$\Delta R^2(\overline{F_{ROH}})$	0.0765	0.0922	0.113	0.0706	0.0103	0.0137	0.0210	0.0159
Number of clusters	117	137	123	92	117	137	123	92

Notes: Each observation is a country-ethnicity from the Ethnologue. The genetic controls include expected heterozygosity and its square, migratory distance from East Africa and its square, the top 20 PCs, and mean regional pairwise F_{ST}. The geographic controls include temperature, precipitation, agricultural suitability, absolute latitude, elevation, ruggedness, distance to coast, and distance to nearest river or lake. "Min. HO sample per ethnicity" denotes the minimum number of matched HO individuals for an Ethnologue language (and its associated country-ethnicities) to be included in the regression (the baseline used for all the specifications in Table 6 is 8). $\Delta R^2(\overline{F_{ROH}})$ is the incremental R^2 of $\overline{F_{ROH}}$, defined as the difference in R^2 between the regression on $\overline{F_{ROH}}$ and the controls and the regression on the controls only. Standard errors in parentheses are clustered at the country-level. *** $p < 0.01$, ** $p < 0.05$, * $p < 0.1$

Table B.5.3: The inbreeding coefficient and kinship intensity: other KII sub-indicators

VARIABLES	Co-residence (1)	 (2)	Polygamy (3)	 (4)	Community organization (5)	 (6)	Lineage organization (7)	 (8)
$\overline{F_{ROH}}$	-14.666***	-13.799*	9.753*	15.722**	11.025**	16.013***	6.650*	9.818*
	(5.012)	(7.326)	(5.326)	(7.474)	(4.489)	(6.012)	(3.920)	(5.394)
Genetic controls	yes	yes	yes	yes	yes	yes	yes	yes
Country FE		yes		yes		yes		yes
Observations	409	409	409	409	406	406	409	409
R-squared	0.498	0.717	0.608	0.704	0.244	0.511	0.706	0.841
Number of clusters	127	127	127	127	127	127	127	127
$\Delta R^2(\overline{F_{ROH}})$	0.008	0.005	0.005	0.009	0.008	0.011	0.002	0.003

Notes: Each observation is a country-ethnicity from the Ethnologue. The genetic controls include expected heterozygosity and its square, migratory distance from East Africa and its square, the top 20 PCs, and mean regional pairwise F_{ST}. $\Delta R^2(\overline{F_{ROH}})$ is the incremental R^2 of $\overline{F_{ROH}}$, defined as the difference in R^2 between the regression on $\overline{F_{ROH}}$ and the controls and the regression on the controls only. Standard errors in parentheses are clustered at the country-level. *** $p < 0.01$, ** $p < 0.05$, * $p < 0.1$

B.6 Additional graphs and tables for Section 5.3 (The inbreeding coefficient and nighttime luminosity)

Table B.6.1: The inbreeding coefficient and nighttime luminosity: summary statistics

281,177 pixels (in the homelands of 245 ethnicities)				
	mean	sd	min	max
Log nighttime luminosity	-1.919	2.833	-4.360	7.142
$\overline{F_{ROH}}$	0.012	0.009	0.003	0.146
Mean regional pairwise F_{ST}	0.017	0.016	0.001	0.095
Expected heterozygosity	17,799	469	12,156	18,630
Log population density	1.758	1.913	0.000	10.152
Migratory distance (months)	3.441	1.917	0.229	8.412
Monthly temperature (degree Celsius)	-4.748	20.080	-54.400	33.800
Precipitation (cm)	3.660	5.115	0.000	61.930
Agricultural suitability	0.327	0.334	0.000	0.999
Absolute latitude	43.322	16.042	0.063	74.813
Elevation (km)	0.569	0.660	-0.137	5.547
Ruggedness (km)	0.095	0.134	0.000	1.459
Distance to coast (1000 km)	0.574	0.523	0.003	2.464
Distance to nearest river/lake (1000 km)	0.096	0.142	0.000	1.353
Hunting	0.340	0.861	0.000	8.000
Fishing	0.905	0.985	0.000	7.500
Animal husbandry	3.195	1.540	0.000	9.000
Agriculture	5.313	2.182	0.000	9.000
Political hierarchy	3.728	1.122	1.000	5.000
Malaria index	0.434	2.084	0.000	32.635
Settlement complexity	6.295	1.991	1.000	8.000
Deep Christianization	0.683	0.463	0.000	1.000

Notes: Summary statistics for the main variables used in the analysis of the relationship between the inbreeding coefficient and nighttime luminosity, for the pixels in the analysis sample.

Table B.6.2: The inbreeding coefficient and nighttime luminosity: robustness checks

	Log nighttime luminosity			
	(1)	(2)	(3)	(4)
$\overline{F_{ROH}}$	-15.186***	-19.712***	-15.246	-15.758
	(5.780)	(6.891)	(12.315)	(12.347)
Log population density	yes	yes	yes	yes
Genetic controls		yes	yes	yes
Geographic controls	yes	yes	yes	yes
Country FE	yes	yes	yes	yes
Min. HO sample per ethnicity	8	5	10	15
Observations	281,177	305,467	273,018	178,616
R-squared	0.671	0.668	0.675	0.614
Number of clusters	98	111	92	61

Notes: Each observation is a pixel. The genetic controls include expected heterozygosity and its square, migratory distance from East Africa and its square, the top 20 PCs, and mean regional pairwise F_{ST}. The geographic controls include temperature, precipitation, agricultural suitability, absolute latitude, elevation, ruggedness, distance to coast, and distance to nearest river or lake. "Min. HO sample per ethnicity" denotes the minimum number of matched HO individuals for an Ethnologue language (and its associated country-ethnicities) to be included in the regression (the baseline used for all the specifications in Table 7 is 8). Standard errors in parentheses are clustered at the country level. *** $p < 0.01$, ** $p < 0.05$, * $p < 0.1$

B.7 Additional graphs and tables for Section 6 (Causal pathways)

Table B.7.1: Robustness to excluding European-ancestry countries and to controlling for deep Christianization

	Direct matches				Language-tree matches			
	Subsample, no Europeans		Control for deep Christ.		Subsample, no Europeans		Control for deep Christ.	
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
	Panel A. Regressions of log nighttime luminosity at the pixel level							
KII	-0.097	0.035	0.062	-0.062	-0.141*	-0.016	0.002	-0.059
	(0.101)	(0.079)	(0.137)	(0.065)	(0.085)	(0.065)	(0.088)	(0.052)
Observations	129,168	129,168	377,656	377,656	201,391	201,391	488,558	488,558
R-Squared	0.558	0.642	0.551	0.660	0.515	0.601	0.546	0.653
Number of clusters	85	85	138	138	96	96	162	162
	Panel B. Regressions of log nighttime luminosity at the country-ethnicity level							
KII	-0.209**	-0.175***	-0.392***	-0.098	-0.124*	0.023	-0.271***	0.031
	(0.082)	(0.066)	(0.082)	(0.067)	(0.074)	(0.050)	(0.081)	(0.043)
Observations	482	482	659	659	1,711	1,711	2,143	2,143
R-Squared	0.650	0.802	0.646	0.831	0.543	0.695	0.538	0.737
Number of clusters	85	85	135	135	95	95	161	161
	Panel C. Regressions of log regional GDP per capita at the region level							
KII	-0.508***	-0.054	-0.466***	-0.113**	-0.360***	-0.103	-0.375***	-0.111**
	(0.113)	(0.052)	(0.102)	(0.046)	(0.078)	(0.074)	(0.073)	(0.046)
Year FE	yes		yes		yes		yes	
Country × year FE		yes		yes		yes		yes
Observations	1,786	1,786	5,514	5,514	3,182	3,182	9,019	9,019
R-Squared	0.732	0.890	0.511	0.889	0.645	0.856	0.608	0.896
Number of clusters	23	23	61	61	30	30	83	83
	Panel D.1. Regressions of log nighttime luminosity at the pixel level: spatial RD analysis							
KII	-0.113*		-0.120		-0.083*		-0.068	
	(0.060)		(0.091)		(0.043)		(0.048)	
Dist.-to-the-boundary poly.	yes		yes		yes		yes	
Ethnicity pair FE	yes		yes		yes		yes	
Observations	115,660		290,669		378,764		750,996	
R-Squared	0.659		0.613		0.634		0.623	
Number of clusters	48		70		71		104	
	Panel D.2. Regressions of log nighttime luminosity at the pixel level: spatial RD analysis excluding pixels less than 50 km from the ethnic boundary							
KII	-0.156**		-0.163*		-0.125**		-0.119**	
	(0.067)		(0.093)		(0.056)		(0.051)	
Dist.-to-the-boundary poly.	yes		yes		yes		yes	
Ethnicity pair FE	yes		yes		yes		yes	
Observations	87,421		227,620		293,211		593,989	
R-Squared	0.657		0.616		0.637		0.630	
Number of clusters	48		70		71		104	

(Continues)

Table B.7.1—*Continued*

	Direct matches				Language-tree matches			
	Subsample, no Europeans		Control for deep Christ.		Subsample, no Europeans		Control for deep Christ.	
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
	Panel E. Regressions of log nighttime luminosity at the pixel level with $\overline{F_{ROH}}$							
$\overline{F_{ROH}}$	-29.364**	-35.593***	-26.052**	-20.328***				
	(11.368)	(11.866)	(11.094)	(7.475)				
Genetic controls	yes	yes	yes	yes				
Observations	63,142	63,142	281,177	281,177				
R-Squared	0.621	0.641	0.652	0.674				
Number of clusters	51	51	98	98				
Log population density$^+$	yes	yes	yes	yes	yes	yes	yes	
Deep Christianization			yes	yes			yes	yes
Geographic controls	yes	yes	yes	yes	yes	yes	yes	yes
Country FE$^\#$		yes		yes		yes		yes

Notes: Each observation is a pixel (in Panels A, D, and E), a country-ethnicity (in Panel B), or a region-year (in Panel C). Columns 1-4 and 5-8 show results in the samples obtained using the direct and language-tree matching methods, respectively. Columns 1-2 and 5-6 show results in the subsample that excludes Europe, the Americas, Australia, and New Zealand, for regressions without (columns 1 and 5) and with (columns 2 and 6) country fixed effects. Columns 3-4 and 7-8 show results of regressions (in the full sample) that include controls for deep Christianization without (columns 3 and 7) and with (columns 4 and 8) country fixed effects. In Panel D.1, the analysis sample comprises all pixels within 200 km of the boundary between two contiguous ethnicities in the same country; in Panel D.2, pixels within 50 km of the boundary are dropped. The geographic controls include temperature, precipitation, agricultural suitability, absolute latitude, elevation, ruggedness, distance to coast, and distance to nearest river or lake. Standard errors in parentheses are clustered at the country level in all regressions.
*** $p < 0.01$, ** $p < 0.05$, * $p < 0.1$

$^+$ No control for log population density in Panel C.

$^\#$ Country × year FE (instead of country FE) in Panel C.

Table B.7.2: Robustness to controlling for earlier levels of economic development

	Direct matches		Language-tree matches	
	(1)	(2)	(3)	(4)
	Panel A. Regressions of log nighttime luminosity at the pixel level			
KII	-0.388***	-0.087**	-0.366***	-0.080***
	(0.116)	(0.040)	(0.104)	(0.029)
Settlement complexity	yes	yes	yes	yes
Observations	375,089	375,089	488,025	488,025
R-Squared	0.538	0.660	0.531	0.653
Number of clusters	138	138	162	162
	Panel B. Regressions of log nighttime luminosity at the country-ethnicity level			
KII	-0.375***	-0.125**	-0.289***	0.005
	(0.061)	(0.056)	(0.077)	(.041)
Settlement complexity	yes	yes	yes	yes
Observations	659	638	2,141	2,141
R-Squared	0.646	0.834	0.540	0.737
Number of clusters	135	135	161	161
	Panel C. Regressions of log regional GDP per capita at the region level			
KII	-0.359***	-0.100**	-0.422***	-0.081**
	(0.077)	(0.037)	(0.068)	(0.035)
Settlement complexity	yes	yes	yes	yes
Year FE	yes		yes	
Country × year FE		yes	yes	
Observations	5,514	5,514	9,019	9,019
R-Squared	0.541	0.889	0.601	0.896
Number of clusters	61	61	83	83
	Panel D.1. Regressions of log nighttime luminosity at the pixel level: spatial RD analysis			
KII	-0.061		-0.033	
	(0.041)		(0.022)	
Settlement complexity	yes		yes	
Dist.-to-the-boundary poly.	yes		yes	
Ethnicity pair FE	yes		yes	
Observations	288,031		750,762	
R-Squared	0.614		0.623	
Number of clusters	70		104	
	Panel D.2. Regressions of log nighttime luminosity at the pixel level: spatial RD analysis excluding pixels less than 50 km from the ethnic boundary			
KII	-0.101**		-0.100**	
	(0.040)		(0.039)	
Settlement complexity	yes		yes	
Dist.-to-the-boundary poly.	yes		yes	
Ethnicity pair FE	yes		yes	
Observations	226,050		470,187	
R-Squared	0.616		0.637	
Number of clusters	70		87	

(Continues)

Table B.7.2—*Continued*

	Direct matches		Language-tree matches	
	(1)	(2)	(3)	(4)
	Panel E. Regressions of log nighttime luminosity at the pixel level with $\overline{F_{ROH}}$			
$\overline{F_{ROH}}$	-40.647**	-0.046		
	(20.437)	(15.858)		
Settlement complexity	yes	yes		
Genetic controls	yes	yes		
Observations	253,880	253,880		
R-Squared	0.650	0.670		
Number of clusters	79	79		
	Panel F. Regressions of log national GDP per capita at the country level			
KII	-0.223***		-0.247***	
	(0.066)		(0.056)	
GDP pc 1950	yes		yes	
Observations	118		127	
R-Squared	0.689		0.723	
Log population density^{+}	yes	yes	yes	yes
Geographic controls	yes	yes	yes	yes
Country FE$^{\#}$		yes		yes

Notes: Each observation is a pixel (in Panels A, D, and E), a country-ethnicity (in Panel B), a region-year (in Panel C), or a country (in Panel F). Columns 1-2 and 3-4 show results in the samples obtained using the direct and language-tree matching methods, respectively. Columns 1 and 3 show results for regressions without country fixed effects, and columns 2 and 4 show results for regressions with country fixed effects. In Panel D.1, the analysis sample comprises all pixels within 200 km of the boundary between two contiguous ethnicities in the same country; in Panel D.2, pixels within 50 km of the boundary are dropped. The geographic controls include temperature, precipitation, agricultural suitability, absolute latitude, elevation, ruggedness, distance to coast, and distance to nearest river or lake. Standard errors in parentheses are clustered at the country level in all regressions.
*** $p < 0.01$, ** $p < 0.05$, * $p < 0.1$

$^{+}$ No control for log population density in Panels C and F.

$^{\#}$ Country × year FE (instead of country FE) in Panel C.

Table B.7.3: The KII and nighttime luminosity in subsamples defined by population density: cross section

Panel A.	(1) Pop. Density ≤ 1	(2) Pop. Density ≤ 1	(3) Pop. Density >1 & ≤ 10	(4) Pop. Density >1 & ≤ 10	(5) Pop. Density >10	(6) Pop. Density >10
KII	-0.143***	-0.110***	-0.313**	-0.053**	-0.700***	-0.070
	(0.035)	(0.025)	(0.125)	(0.026)	(0.158)	(0.053)
Log population density			yes	yes	yes	yes
Geographic controls	yes	yes	yes	yes	yes	yes
Country FEs		yes		yes		yes
Observations	138,148	138,148	113,903	113,903	125,605	125,605
R-squared	0.066	0.125	0.200	0.419	0.519	0.696
Number of clusters	59	59	108	108	130	130

Panel B.	(1) Pop. Density ≤ 1	(2) Pop. Density ≤ 1	(3) Pop. Density >1 & ≤ 10	(4) Pop. Density >1 & ≤ 10	(5) Pop. Density >10	(6) Pop. Density >10
KII	-0.108***	-0.069**	-0.273**	-0.067***	-0.641***	-0.074
	(0.036)	(0.032)	(0.121)	(0.018)	(0.144)	(0.054)
Log population density			yes	yes	yes	yes
Geographic controls	yes	yes	yes	yes	yes	yes
Country FEs		yes		yes		yes
Observations	165,715	165,715	147,425	147,425	175,418	175,418
R-squared	0.052	0.118	0.206	0.410	0.543	0.701
Number of clusters	72	72	135	135	159	159

Notes: Each observation is a pixel in the homeland of a country-ethnicity matched with the direct (Panel A) and language-tree (Panel B) matching methods. Regressions were estimated in the subsamples of pixels with population density less than or equal to 1 (columns 1 and 2; recall that we recoded population density to 1 for pixels whose original population density was less than 1), between 1 and 10 (columns 3 and 4), and higher than 10 (columns 5 and 6). The geographic controls include temperature, precipitation, agricultural suitability, absolute latitude, elevation, ruggedness, distance to coast, and distance to nearest river or lake. Standard errors in parentheses are clustered at the country level in all regressions. *** $p < 0.01$, ** $p < 0.05$, * $p < 0.1$

Table B.7.4: The KII, specialization, and market integration: summary statistics

	No. societies	mean	sd	min	max
Specialization	661	-0.116	1.009	-0.687	6.274
Food trade	175	0.903	0.748	0.000	3.000
Market Exchange	93	0.269	0.446	0.000	1.000
KII	911	0.000	1.000	-2.574	2.087

Notes: Summary statistics for the outcome variables used in the analysis of the relationship between the KII and specialization and market integration. For specialization, the summary statistics are reported for those ethnicities that had data on at least 8 (out of 10) tasks.

Table B.7.5: Country-level outcome variables: summary statistics

Panel A.

	No. countries	mean	sd	min	max
Log GDP per capita, 1950	127	7.733	0.993	6.136	10.788
Log GDP per capita, 2008	127	9.160	1.269	6.435	11.943

Panel B.

	No. countries	mean	sd	min	max
Openness to trade	151	0.596	0.438	0.102	2.659
Out-in-group trust	71	-0.056	0.986	-2.425	1.644
Blood donation	142	14.439	15.585	0.000	57.467
Expropriation risk	86	7.456	1.619	4.686	9.986
Institutional quality	79	0.007	0.454	-1.273	0.885
CPI	154	376.974	174.466	82.000	805.000
Articles per m.	159	306.456	516.552	0.215	2,277.362
Patents per m.	75	65.338	171.145	0.001	1,243.818
KII	162	-0.362	1.331	-2.510	2.097

Notes: Summary statistics for variables used in the country-level analysis of the association between the KII and log GDP per capita (Panel A) and for the outcome variables used in the analysis of the relationship between the KII and trade, cultural psychology, institutional quality, and innovation (Panel B). Summary statistics are shown for the sample obtained with the language-tree matching method.

C Computing the inbreeding coefficient and other variables in the Human Origins (HO) dataset

To obtain a contemporaneous, on-the-ground measure of kinship intensity, we analyze genetic data from the Human Origins (HO) dataset from the David Reich Lab (Reich Lab, 2020). HO contains genetic data on thousands of present-day and ancient individuals from populations around the world. We use the genetic data to compute each population's average inbreeding coefficient—which we use in our analyses as a measure of kinship intensity generally and as a proxy for cousin marriage rates in particular—and other control variables for each population.

This Appendix begins by describing the HO dataset (Section C.1) and then the matching procedure we employ to match the HO individuals and populations to Ethnologue languages and the associated country-ethnicities (Section C.2). This Appendix then provides some background on key genetics concepts (Section C.3); summarizes the quality control (QC) filters that were applied to the HO data before the data were analyzed (Section C.4); provides an overview of the variables we computed using the HO data (Section C.5); describes the methods we employed to compute the inbreeding coefficient (Section C.6) and other control variables (Sections C.7, C.8, C.9) using the HO individuals' genetic data; and reports summary statistics for the variables we computed (Section C.10).

C.1 The Human Origins dataset

We obtained a non-public version of the Human Origins (HO) dataset (Reich Lab, 2020) from the David Reich Lab on February 17, 2020. The HO version we obtained contains genetic data on 13,183 individuals, including 9,460 present-day individuals and 3,723 ancient individuals who lived between $\sim 88,000$ BCE and ~ 1900 CE. It is a compiled dataset that includes individuals from many populations around the world and from many published studies (including Pickrell et al. 2012, Lazaridis et al. 2014, Lazaridis et al. 2016, Nakatsuka et al. 2017, Lipson et al. 2018 and Jeong et al. 2019).

We only include in our analyses a subset of 4,756 present-day (i.e., non-ancient) individuals who have been genotyped on the Affymetrix Human Origin array. These individuals were genotyped at a set of 597,573 genetic variants called single nucleotide polymorphisms (SNPs).

C.2 Matching the HO's populations to Ethnologue country-ethnicities

As we further describe below, the subset of the HO we used in our analyses contains 4,756 individuals in 435 populations.[4] For each individual, HO has data on the individual's population, country, latitude, longitude, and in some cases on the individual's city or region. HO also lists the original publication from which each individual's data comes from, and some original publications include the individual's language ISO code. We used this information, as well as various linguistic resources, Wikipedia entries, and an Ethnologue shapefile, to match each HO population to one of the Ethnologue's 5,756 languages (and to one or more of the associated 7,651 country-ethnicities).

As a first step, we conducted a many-to-one match to match each of the 435 HO populations to a single Ethnologue language in the HO population's country, and then dropped Ethnologue languages that contain less than five individuals. This step resulted in 313 distinct

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[4] We use the term "HO population" to describe the group identifier included for each individual in the HO dataset under the heading "Group Label", but the terms "ethnolinguistic group" or "ethnicity" could also apply in many cases.

Ethnologue languages in our data. As a second step, we conducted a many-to-one match to match each of these 313 Ethnologue languages to all country-ethnicities that speak the same Ethnologue language but are located in different countries. This second step resulted in 551 distinct Ethnologue country-ethnicities in our data. The combination of steps 1 and 2 amounts to a many-to-many match from the 435 HO populations to 551 Ethnologue country-ethnicities.

This matching procedure is similar to the direct-matching method employed to match the EA data to Ethnologue languages, but details of the two procedures differ because the HO data typically does not indicate the language spoken by each population.

Some of the variables we computed (the inbreeding coefficient and the top principal components (PCs)) were computed at the individual level and then averaged across the individuals matched to each Ethnologue language. For other variables (the mean regional pairwise genetic distance and expected heterozygosity), the variable was first computed for each HO population and each individual was then assigned their HO population's value for the variable, which was then averaged across the individuals matched to each Ethnologue language.

Though we matched the HO data to 551 Ethnologue country-ethnicities, we note that the analyses with the inbreeding coefficient reported in the main text (in Section 5) only use subsets of these country-ethnicities. The analysis of the relationship between the inbreeding coefficient and cousin marriage preferences and the KII (Tables 6) only uses the Ethnologue country-ethnicities with eight or more HO individuals (and with nonmissing data; there are 416 Ethnologue country-ethnicities with eight or more HO individuals). Our analysis of the relationship between the inbreeding coefficient and nighttime luminosity only uses 245 of these 416 country-ethnicities that could be matched to a pixel that was not dropped from the data because of the filters we applied to the pixels (and which we describe in the main text).

C.3 Genetics background

We provide here a brief overview of some of the core genetic concepts needed to follow the remainder of this Appendix. Other specific concepts are introduced below as needed. For a more detailed overview, see Beauchamp et al. (2011).

Humans have 23 pairs of chromosomes: they inherit 23 copies of each chromosomes from their mother and another 23 from their father. The elementary building blocks of DNA are nucleotide pairs associated with the four bases A, C, T, and G. The human genome thus consists of approximately three billion *pairs of nucleotide pairs* on the 23 pairs of chromosomes, and each nucleotide pair is associated with one of the four bases.[5]

Any two humans share ~ 99.9% of their genomes. At the remaining ~ 0.1%, different genetic variants exist in the populations. Single nucleotide polymorphism (SNPs) are the most prevalent type of genetic variants and our analyses only rely on SNP data. The possible forms at a given SNP's location in the genome are called alleles, and a SNP typically has exactly two possible alleles.[6] A SNP's minor allele frequency (MAF) is the fraction the SNP's alleles in the population that are its rarer allele.

Autosomes are chromosomes other than the sex (X or Y) chromosomes, and our analyses only use SNPs on the 22 pairs of autosomes. Non-autosomal variants are variants on the sex

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[5] To be precise, each nucleotide pair is associated with a *pair* of bases rather than with a single base. However, due to the principle of complementarity, the base A is always paired with the base T, the base C is always paired with the base G, and vice-versa. For that reason, here we ignore these subtleties and refer to only one of the two bases associated with a nucleotide pair.

[6] By definition, a SNP must have at least two alleles (else it would not be a SNP). SNPs with more than two alleles do exist but are rare.

(X or Y) chromosomes and are not used in our analyses.

C.4 Description of baseline quality control (QC) filters applied

As is customary when working with genetic data, we applied a number of quality control (QC) filters to the HO data to ensure that the data we analyzed was of sufficiently high quality. To do so, we used PLINK v2.00a3 (Chang et al., 2015), a software tool that is commonly used to work with genetic data.[7] Our QC procedure is similar to the one employed by Ochoa and Storey (2019).

We applied the following QC filters, in this order:

- Step 1: removed all variants that are not single nucleotide polymorphisms (SNPs), all non-autosomal variants, and all monomorphic SNPs.[8]
- Step 2: removed all ancient individuals and individuals who were not genotyped on the Affymetrix Human Origins array, all individuals flagged by the David Reich Lab as being outliers, all individuals who could not be mapped to a language in the Ethnologue (including all individuals in admixed populations, since the Ethnologue does not contain admixed populations), and all individuals who were not mapped to at least one language in the Ethnologue to which at least four other HO individuals were also mapped (i.e., at this stage we only kept Ethnologue languages (and the associated country-ethnicities) with at least five matched Human Origins individuals). This left 4,771 individuals.
- Step 3: removed variants with missing call rates greater than 0.03 (108,180 SNPs removed).[9]
- Step 4: removed individuals with missing genotype rates greater than 0.03 (15 individuals removed).[10]

Before any QC, there were 13,776 ancient and present-day individuals and 597,573 variants in the HO data. After the baseline QC filters above were applied, the data contained information on 484,944 SNPs and 4,756 present-day individuals (1008 females, 3,679 males, 69 unknown) in 435 HO populations.[11] (As mentioned above, these 435 HO populations were matched to 551 Ethnologue country-ethnicities, but for the analyses with the inbreeding coefficient reported in the main text, we only used subsets of these country-ethnicities.)

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[7] We also used PLINK v1.90b6.17 for some calculations because some PLINK commands had not been incorporated yet into PLINK v2.00a3.

[8] Monomorphic SNPs are SNPs that show no variation across all individuals; the variables corresponding to these SNPs are thus constants and can't be used in our analyses.

[9] The missing call rate for a given SNP is equal to N_{miss}/N, where N_{miss} is the number of individuals missing data for that SNP and N is the total number of individuals in the dataset.

[10] The missing genotype rate for an individual is equal to M_{miss}/M, where M_{miss} is the number of SNPs that are missing calls for that individual, and M is the total number of SNPs in the dataset.

[11] We do not apply minor allele frequency (MAF) filters in our baseline QC (other than removing monomorphic SNPs). The reason why is that, for some calculations, MAF filters are applied after calculating MAF at the language level, but for other calculations, MAF filters are applied after calculating MAF using all individuals in the HO data. These MAF filters are described below. We also do not apply a Heidy-Weinberg Equilibrium (HWE) filter because this needs to be applied separately for each population, and we choose not to do this due to small population sizes.

C.5 Variables computed with the HO genetic data: Overview

Our goal is to infer consanguineous marriage practices from inbreeding coefficients, and therefore factors that affect the inbreeding coefficient but are unrelated to parental relatedness are possible confounders in our analyses. Therefore, in addition to computing the inbreeding coefficient, we compute several quantities that are correlated with it but unrelated to parental relatedness, and we include these quantities in our main regressions as controls. Thus, we use the HO genetic data to compute the following quantities:

- *Mean inbreeding coefficient*: Our main variable of interest is each country-ethnicity's average inbreeding coefficient. The inbreeding coefficient, denoted F, is the probability that two alleles at any given location in an individual's genome are identical by descent (IBD)—i.e., that they were inherited from the same ancestor. F measures the degree to which an individuals' two parents were related and thus one's level of inbreeding. We compute F at the individual level and then take the average at the level of the Ethnologue languages (and associated country-ethnicities). We compute two measures of the inbreeding coefficient. The baseline measure we use in the empirical analyses in the paper is F_{ROH}, defined as the fraction of an individual's genome that is located in runs of homozygosity (ROH) that are longer than 1.5 Mb.[12] ROH are segments of the genome that are identical across the maternally and paternally inherited chromosomes and thus could be IBD, and ROH that are longer than 1.5 Mb in length are more likely to arise from inbreeding (Ceballos et al., 2018). We also compute an alternative measure of the inbreeding coefficient, F_{SNP}, which we use in this Appendix to verify that our F_{ROH} estimates are reasonable.

- *Mean regional pairwise F_{ST}*: Following Pemberton and Rosenberg (2014), we estimate the degree of genetic isolation of a population using the average pairwise F_{ST} (genetic distance) between that population and all other populations in the same world geographic region with a post-baseline-QC sample size of at least 8 individuals.

- *Expected heterozygosity*: Controlling for a population's expected heterozygosity is especially important in our setting, since expected heterozygosity correlates negatively with population mean F (Pemberton and Rosenberg, 2014) and nonlinearly with economic development (Ashraf and Galor, 2013b). Expected heterozygosity decreases with migratory distance from East Africa, consistent with a migration model that predicts increased genetic drift and decreased heterozygosity with increased distance from Africa (Ramachandran et al., 2005). In our empirical analyses with our F_{ROH} estimates, we include expected heterozygosity and its square as well as migratory distance from East Africa and its square.

- *The top 20 PCs of the genotype*: We compute the top 20 principal components (PCs) of the genotypic data[13] for each individual, and take the average value of each PC in each population. It has been shown that the top PCs are good proxies for the individuals' geographic origins and that including these as controls in regressions can help mitigate bias related to population stratification (Price et al., 2006; Novembre et al., 2008).

Below, we discuss these quantities in more detail and describe how we compute them.

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[12] A megabase (Mb) is a unit of physical distance in the genome; the entire genome is $\sim 3,100$ Mb in length.

[13] Specifically, we compute the 20 PCs of the $N \times N$ matrix with the entry in row i and column j equal to the correlation between individuals i and j's SNP data.

C.6 The inbreeding coefficient: background and estimation

Inbreeding occurs when related individuals mate and produce offspring. Related individuals share DNA from common ancestors, and thus inbreeding increases the probability that at a given location on a chromosome, their offspring inherits identical DNA segments from both parents (Ceballos et al., 2018). For instance, first cousins share both a grandmother and a grandfather, and so some DNA segments they inherited from the common grandmother or grandfather will be identical across their two genomes. As a result, if two first cousins mate and produce a child, then that child will have locations in their genome where they will have inherited identical DNA segments from their two cousin parents, coming originally from the same grandmother or grandfather. The two alleles at a such genomic location are said to be homozygous—since the two alleles at the location are identical—and identical-by-descent (IBD; or autozygous)—since they are identical and can be traced back to one common ancestor.

A common measure of one's level of inbreeding is the coefficient of inbreeding, denoted F. F measures the probability that two alleles at a location in the genome are IBD, and is also equal to the fraction of the genome that is IBD for a given individual. The expected value of an individual's F coefficient is equal to the coefficient of kinship, or one-half the coefficient of relationship, between his two parents. The latter is a measure of the relatedness between two individuals (the two parents, here). For example, the expected F coefficient of the offspring of two second-degree cousins is 0.015625, whereas it is 0.0625 for the offspring of first-degree cousins and 0.25 for the offspring of two siblings. Thus, F measures the degree to which an individual's two parents are related.

Until recently, pedigree data was required to compute F, but various methods have recently been developed to estimate F using an individual's molecular genetic data. Recent advances in genetic technology have led to the development of methods to identify continuous segments of homozygous alleles, known as runs of homozygosity (ROH), in individual genomes. Longer ROH are typically observed as a result of inbreeding (Ceballos et al., 2018) and have been shown to correlate well with pedigree-based estimates of inbreeding (McQuillan et al., 2008; Kang et al., 2017; Pemberton and Rosenberg, 2014). As Sahoo et al. (2021) found and as we report in Section 5 of the main text, longer ROH also correlate well with population-level cousin marriage preferences.

However, ROH can arise in individuals for a variety of reasons unrelated to marital practices and kinship systems. For example, ROH and inbreeding coefficients are inflated in genetically isolated populations, since low effective population sizes can increase homozygosity (Pemberton and Rosenberg, 2014). In addition, inbreeding coefficients are highly correlated with expected heterozygosity and migratory distance from Africa (Pemberton and Rosenberg, 2014). In the main empirical analyses in the main text, we control for these and other potential confounding variables.

C.6.1 Estimating F_{ROH}

Our main measure of inbreeding, denoted F_{ROH}, is the fraction of an individual's genome in runs of homozygosity (ROH) of at least 1.5 Mb in length (Clark et al., 2019). This is the baseline measure used by the ROHgen consortium, a large consortium of research groups administering cohorts with genetic data that seeks to estimate the effect of inbreeding on various traits (Joshi, 2015; Clark et al., 2019). We estimate F_{ROH} for all individuals in the (post-baseline-QC) HO dataset using the ROHgen2 software pipeline developed by the ROHgen consortium (Clark et al., 2019).

Shorter ROH are more likely to arise from population structure or lack of genetic diversity whereas longer ROH (e.g., ROH 1.5 Mb in length or longer) tend to arise from inbreeding (Pemberton et al., 2012; Kang et al., 2017; Ceballos et al., 2018; Sahoo et al., 2021). Using ROH that are at least 1.5 Mb long to compute F_{ROH} mitigates, but does not eliminate, concerns that an individual's homozygous alleles have arisen due to factors other than parental relatedness, such as low effective population size or low genetic diversity.

Formally, suppose an individual has n ROH longer than 1.5 Mb across their genome. For each of these ROH $i \in \{1, \dots, n\}$, define l_i as the length (in Mb) of ROH i. F_{ROH} is defined as:

$$F_{ROH} = \sum_i \frac{l_i}{3Gb} \tag{1}$$

where the length of the autosomal genome is estimated at 3 Gb base pairs (i.e., 3,000 Mb Clark et al., 2019).

Let $\overline{F_{ROH}}$ denote the average F_{ROH} across the individuals matched to a population or to an Ethnologue language. We obtained estimates of $\overline{F_{ROH}}$ both for each Ethnologue language and the associated country-ethnicities (for the main analyses in our paper) and for each HO population (for Figures C.6.1 and C.6.2 below in this Appendix).

Before calculating the inbreeding coefficient F_{ROH}, we applied one additional QC filter (in addition to the QC filters described above): following the ROHgen2 guidelines, we filtered out the SNPs with minor allele frequency (MAF) less than 0.05. Filtering out SNPs with low MAF is important because including those SNPs may result in more ROH that are not due to marital practices. Ideally, we would calculate MAF for each population before filtering out low-MAF SNPs. However, due to data limitations and small population sizes for many populations, this was not possible. We thus calculated MAF using all (post-baseline-QC) individuals in the dataset before filtering out SNPs with MAF < 0.05. 369,741 autosomal SNPs were left after this step, and these were used to compute F_{ROH}.[14]

After we applied the MAF filter, we calculated F_{ROH} using the ROHgen2 pipeline (Clark et al., 2019). The ROHgen2 pipeline calculates F_{ROH} using PLINK v2.00a3 (Chang et al., 2015) with the following parameters: –homozyg-window-snp 50; –homozyg-snp 50; –homozyg-kb 1500; –homozyg-gap 1000; –homozyg-density 50; –homozyg-window-missing 5; –homozyg-window-het 1. These parameters have been previously shown to call ROH that mainly correspond to alleles that are identical-by-descent (IBD), mitigating concerns that measured ROH are due to chance arrangements of independent homozygous SNPs (Clark et al., 2019). In addition, these parameters have been previously shown to be robust to genotyping array choice (Joshi, 2015).

Table C.6.1 shows summary statistics for F_{ROH} calculated across the individuals in each geographic region of the world.[15] As can be seen, F_{ROH} tends to be higher in regions that are

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[14] Instead of using all individuals in the dataset to calculate MAF, we could have chosen to calculate MAF separately for each language family in the data. This is what we do for our calculations of F_{SNP} (see below). (The language families are higher-level language groupings from the Ethnologue; each Ethnologue language belongs to a language family. Populations in the same language family tend to be ethnically and thus genetically more similar to each other and thus should exhibit similar allele frequencies.) However, we chose not to use language families to calculate MAF prior to MAF filtering for our preferred estimate of F_{ROH} for the following two reasons. First, the correlation between F_{ROH} computed after MAF filtering using MAF calculated with all individuals and F_{ROH} computed after MAF filtering using MAF calculated separately for each language group is almost unity ($\hat{r} = 0.998$). The two methods of computing F_{ROH} thus yield nearly identical quantities. Second, computing allele frequencies using all individuals allows us to compute F_{ROH} for a few individuals that were not mapped to a language family.

[15] The geographic regions we use are from the United Nations' "M49 standard" (*Standard Country or Area Codes for Statistical Use*).

far from East Africa (such as the Americas and Melanesia), and lower in regions that are close to Africa (such as Northern and Sub-Saharan Africa). The reason for this is that, as mentioned above, F decreases with expected heterozygosity, which in turn decreases with migratory distance from East Africa (Ramachandran et al., 2005; Pemberton and Rosenberg, 2014). In the paper, the empirical analyses with our F_{ROH} estimates include controls for both migratory distance from East Africa (and its square) and expected heterozygosity (and its square).

Table C.6.1: Summary statistics for F_{ROH} in each geographic region of the world

Region	**Mean**	**SD**	**Minimum**	**Maximum**	**IQR***
Latin America and the Caribbean	0.0598	0.0442	0.0080	0.2579	0.0537
Melanesia	0.0363	0.0264	0.0072	0.1815	0.0222
Northern America	0.0345	0.0214	0.0044	0.0953	0.0286
Southern Asia	0.0263	0.0318	0.0005	0.1911	0.0240
South−eastern Asia	0.0247	0.0242	0.0032	0.1172	0.0305
Western Asia	0.0239	0.0243	0.0011	0.1318	0.0259
Eastern Europe	0.0198	0.0198	0.0018	0.3090	0.0187
Northern Africa	0.0178	0.0200	0.0011	0.1079	0.0205
Central Asia	0.0175	0.0265	0.002	0.1511	0.0071
Eastern Asia	0.0151	0.014	0.0019	0.0845	0.0090
Sub-Saharan Africa	0.0142	0.0179	0.0000	0.1441	0.0143
Northern Europe	0.0106	0.0087	0.0017	0.0664	0.0049
Western Europe	0.0100	0.0076	0.0023	0.0494	0.006
Southern Europe	0.0099	0.0079	0.0012	0.0554	0.0057

Notes: The table shows summary statistics for our estimates of F_{ROH} for each geographic region of the world. *Interquartile range.

C.6.2 Estimating F_{SNP}

As a check to ensure that our calculation of F_{ROH} yielded reasonable estimates, we also computed estimates for another measure of inbreeding, F_{SNP}, and then compared the two sets of estimates. F_{SNP} calculates excessive homozygosity in an individual, where the excess is relative to the level of homozygosity one would expect in a population of randomly mating individuals. F_{SNP} can be strongly biased as an estimator of inbreeding due to factors other than inbreeding, such as population structure and small population size (Clark et al., 2019), and we thus do not use F_{SNP} as the main estimator of inbreeding in our analyses. However, following Clark et al. (2019), we calculate F_{SNP} and compare our F_{SNP} and F_{ROH} estimates.

Thus, for each individual in our data we calculate F_{SNP}, defined as

$$F_{SNP} = \frac{O(HOM) - E(HOM)}{M - E(HOM)}, \tag{2}$$

where $O(HOM)$ is the observed number of homozygous SNPs and $E(HOM)$ is the expected number of homozygous SNPs in the individual's autosomal genome, and M is the number of non-missing genotyped SNPs on the individual's autosomes (Clark et al., 2019). The expected number of homozygous SNPs is given by $E(HOM) = \sum_i \left[(p_i)^2 + (1 - p_i)^2\right]$, where p_i is the MAF of SNP i,[16] and is equal to $M\left(1 - \hat{H}\right)$, where $\left(1 - \hat{H}\right)$ is expected homozygosity and $\hat{H}$ is expected heterozygosity (defined below).

We define $\overline{F_{SNP}}$ to be the average F_{SNP} across individuals in a population (this quantity is often denoted as F_{IS}). Populations in which consanguineous marriages are the main drivers of ROH have $\overline{F_{SNP}} \approx \overline{F_{ROH}}$ (Clark et al., 2019).

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[16] This follows from the fact that, if mating is random (i.e., under Hardy-Weinberg equilibrium), the event in which an individual has two copies of the rarer allele or two copies of the more commom allele—i.e., is homozygous—at SNP i has probability $(p_i)^2 + (1 - p_i)^2$ of occurring.

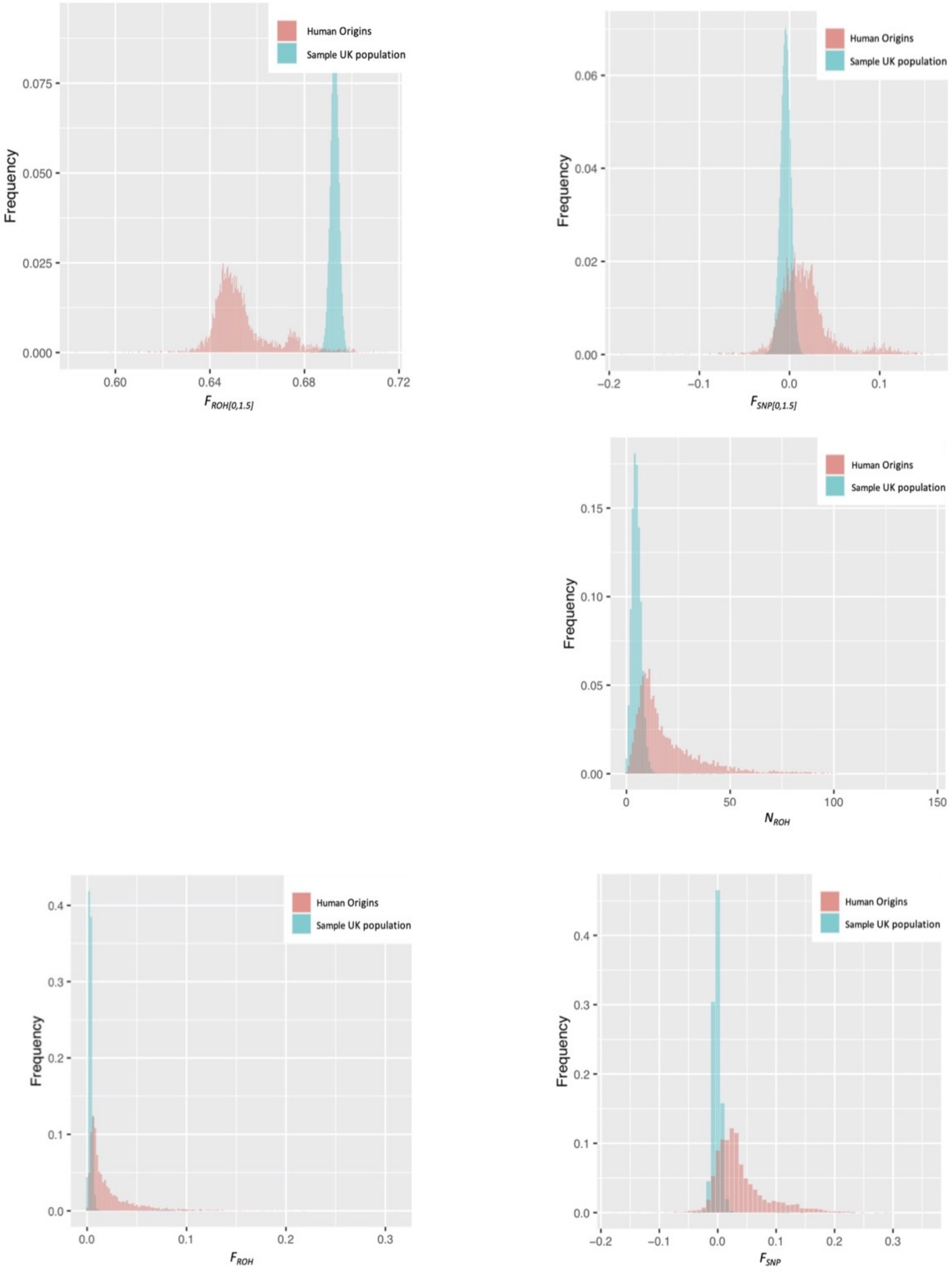

Figure C.6.1: Distributions of $F_{ROH[0,1.5]}$, $F_{SNP[0,1.5]}$, N_{ROH}, F_{ROH}, and F_{SNP} in our HO data and in a sample UK population. This figure is produced by the ROHgen2 pipeline. Note that F_{ROH} and F_{SNP} here are calculated using allele-frequency filters applied separately for each language language family (by contrast, as described in the main text, for our main estimates of F_{ROH}, allele-frequency filters were applied to the full post-QC dataset). F_{ROH}, as described above, is the fraction of the autosomal genome in ROH longer than 1.5 Mb; $F_{ROH[0,1.5]}$ denotes the fraction of the autosomal genome that is homozygous and outside ROH longer than 1.5 Mb. F_{SNP}, as described above, is calculated using all SNPs in the autosomal genome; $F_{SNP[0,1.5]}$ denotes F_{SNP} calculated in the autosomal genome outside ROH longer than 1.5 Mb; N_{ROH} denotes the count of ROH longer than 1.5 Mb.

We used a slightly different set of SNPs to calculate F_{SNP} compared to F_{ROH}. Prior to filtering out SNPs with MAF < 0.05, for F_{ROH} we calculated allele frequencies using all individuals in the data. In contrast, for F_{SNP} we calculated allele frequencies separately for each language family before filtering out SNPs with MAF < 0.05.

Though F_{SNP} is calculated for each individual, the formula uses expected homozygosity as an input. Ideally, we would have calculated expected homozygosity separately for each population in the data. However, due to the small sample sizes for many populations in HO, calculating expected homozygosity separately for each population leads to noisy estimates of F_{SNP}. We thus calculated expected homozygosity for each language family, because populations in the same language family tend to be ethnically and thus genetically more similar to each other and thus should exhibit similar expected homozygosities. We merged language families with fewer than 40 individuals together to eliminate small language families.

We calculated F_{SNP} using the ROHgen2 pipeline (Clark et al., 2019). The ROHgen2 pipeline calculates F_{SNP} using PLINK's "–het" command. Although the ROHgen2 pipeline does not include the "small-sample" flag with the "—het" command, we included the "small-sample" flag for our calculations.

C.6.3 Diagnostic plots and quality checks

In Figure C.6.1, we display several histograms that are produced by the ROHgen2 pipeline, using individual-level estimates of F_{ROH} and F_{SNP}. The figure compares the distribution of F_{ROH} and F_{SNP} to the distribution of these variables in a sample population from the UK. As can be seen, the distributions of F_{ROH} and F_{SNP} in the sample UK population (in light blue) lie in the left tail of the distributions in HO (in pink). (While the set of SNPs we used to compute F_{ROH} in our main analyses is different than the one we used to compute F_{SNP}, for Figure C.6.1, for comparability, for each language family we used the exact same set of SNPs to compute F_{ROH} as the one we used to compute F_{SNP}.)

Figure C.6.2 plots HO-population-level estimates of $\overline{F_{ROH}}$ on the y-axis and of $\overline{F_{SNP}}$ on the x-axis. [17] As Panel A shows, populations in language groups with large sample sizes have a strong tendency to lie close to the 45-degree line in the figure. For populations with data points near the 45-degree line, $\overline{F_{SNP}} \approx \overline{F_{ROH}}$, which signifies that consanguinity is a main driver of excessive homozygosity for these populations (Clark et al., 2019). However, populations in language groups with small samples sizes tend to lie to the left of the 45-degree line; the reason for that is that small sample sizes lead to a more sizeable downward bias in F_{SNP}, which skews data points to the left in the figure.[18] Populations to the right of the 45-degree line tend to be characterized by admixture, since admixture biases F_{SNP} upwards (Clark et al., 2019).

In Panel B, we label several populations that are to the right of the 45-degree line. Three populations in Botswana— "Taa_East:Botswana" (label 400), "Taa_North:Botswana" (label 401), and "Taa_West:Botswana" (label 402)—are located noticeably to the right of the 45-degree line. These three populations are pooled in the "Niger-Congo" language family, and sufficient divergence from other populations in this group may explain the inflation of F_{SNP} relative to F_{ROH} in these populations. A similar explanation likely explains why the populations "Baining_Malasait:Papua New Guinea" (label 37) and "Baining_Marabu:Papua New Guina"

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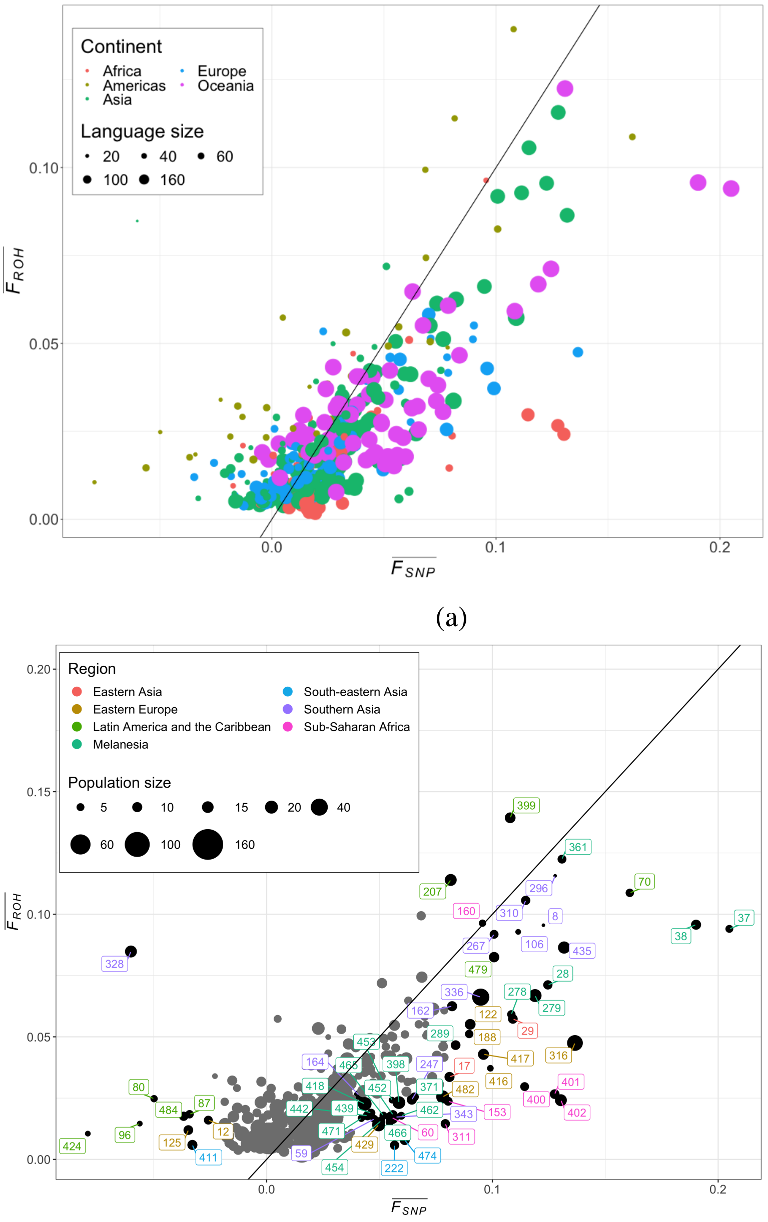
[17] We note that the empirical analyses in the main paper use estimates of $\overline{F_{ROH}}$ for the Ethnologue languages (and associated country-ethnicities) rather than for HO populations.

[18] The reason for the downward bias is that in small samples, MAF ($\hat{p}_i$) is estimated with less precision, which by Jensen's inequality leads to a upward bias in estimates of $(p_i)^2 + (1 - p_i)^2$ and thus upward bias in estimates of $E(HOM)$ and downwards bias in estimates of F_{SNP}.



(a)

(b)

Figure C.6.2: Mean F_{ROH} vs. mean F_{SNP} across populations. The solid black line in both panels is the 45-degree line. In Panel A, each circle is a population and the size of the circle corresponds to the number of individuals in each language family (after merging several smaller language families with less than 40 individuals). In Panel B, the size of each circle corresponds to the number of individuals in each population. Several outliers are labeled in Panel B: populations in the lower right quadrant are labeled if ($\overline{F_{ROH}} \leq 0.0265$ and $\overline{F_{SNP}} \geq 0.04$) or ($\overline{F_{ROH}} > 0.0265$ and $\overline{F_{SNP}} \geq 0.08$). The list of populations corresponding to the numbers labeling the circles in Panel B is shown in Table C.6.2.

Table C.6.2: Labeled populations in Panel B of Figure C.6.2

Label	HO population	Mean F_{ROH}	Mean F_{SNP}	Sample size	Continent
8	Agamudayar:India	0.0955	0.1226	1	Asia
12	Aleut:Russia	0.0160	−0.0258	7	Europe
17	Ami:Taiwan	0.0336	0.0810	10	Asia
28	Ata:Papua New Guinea	0.0712	0.1246	8	Oceania
29	Atayal:Taiwan	0.0573	0.1091	9	Asia
37	Baining_Malasait:Papua New Guinea	0.0940	0.2050	5	Oceania
38	Baining_Marabu:Papua New Guinea	0.0957	0.1902	10	Oceania
59	Bhunjiya:India	0.0165	0.0477	5	Asia
60	Biaka:Central African Republic	0.0170	0.0555	20	Africa
70	Cabecar:Costa Rica	0.1087	0.1609	6	Americas
80	Chilote:Chile	0.0248	−0.0498	4	Americas
87	Chulucanas:Peru	0.0184	−0.0341	6	Americas
96	Cusco2:Peru	0.0146	−0.0562	2	Americas
106	Dhokkali:India	0.0928	0.1114	2	Asia
122	Eskimo_Naukan:Russia	0.0551	0.0902	12	Europe
125	Even:Russia	0.0120	−0.0347	9	Europe
153	Gui:Botswana	0.0237	0.0804	7	Africa
160	Hadza1:Tanzania	0.0964	0.0956	4	Africa
162	Hakki_Pikki:India	0.0625	0.0822	10	Asia
164	Hallaki:India	0.0263	0.0408	9	Asia
188	Itelmen:Russia	0.0512	0.0897	6	Europe
207	Karitiana:Brazil	0.1140	0.0816	16	Americas
222	Kinh:Vietnam	0.0058	0.0567	8	Asia
247	Kusunda:Nepal	0.0244	0.0643	10	Asia
267	Malaikuarvar:India	0.0918	0.1008	7	Asia
278	Mamusi_Paleabu:Papua New Guinea	0.0592	0.1084	6	Oceania
279	Mamusi:Papua New Guinea	0.0668	0.1189	20	Oceania
289	Mengen:Papua New Guinea	0.0466	0.0837	9	Oceania
296	Mudaliar:India	0.1157	0.1278	1	Asia
310	Narikuruvar:India	0.1056	0.1147	8	Asia
311	Naro:Botswana	0.0145	0.0792	8	Africa
316	Nganasan:Russia	0.0475	0.1366	33	Europe
328	Onge:India	0.0848	−0.0601	16	Asia
336	Palliyar:India	0.0662	0.0948	41	Asia
343	Parhaiya:India	0.0173	0.0571	5	Asia
361	Rennell_and_Bellona:Solomon Islands	0.1225	0.1308	7	Oceania
371	Santa_Cruz:Solomon Islands	0.0255	0.0655	7	Oceania
398	Sulka:Papua New Guinea	0.0232	0.0586	19	Oceania
399	Surui:Brazil	0.1394	0.1079	12	Americas
400	Taa_East:Botswana	0.0297	0.1143	7	Africa
401	Taa_North:Botswana	0.0266	0.1276	9	Africa
402	Taa_West:Botswana	0.0241	0.1303	16	Africa
411	Thai:Thailand	0.0059	−0.0329	10	Asia
416	Todzin:Russia	0.0372	0.0991	3	Europe
417	Tofalar:Russia	0.0429	0.0961	13	Europe
418	Tolai:Papua New Guinea	0.0226	0.0435	23	Oceania
424	Tumbes:Peru	0.0105	−0.0792	2	Americas
429	Tuvinian:Russia	0.0141	0.0496	20	Europe
435	Ulladan:India	0.0864	0.1318	17	Asia
439	Vanuatu_Ambrym:Vanuatu	0.0190	0.0463	6	Oceania
442	Vanuatu_Efate_Mele:Vanuatu	0.0178	0.0447	8	Oceania
452	Vanuatu_Malekula:Vanuatu	0.0182	0.0560	8	Oceania
453	Vanuatu_Nguna:Vanuatu	0.0242	0.0556	3	Oceania
454	Vanuatu_Paama:Vanuatu	0.0157	0.0506	7	Oceania
462	Vanuatu_Santo_Mbauk:Vanuatu	0.0178	0.0597	5	Oceania
465	Vanuatu_Santo_Port_Olry:Vanuatu	0.0179	0.0518	5	Oceania
466	Vanuatu_Santo_Rango:Vanuatu	0.0151	0.0545	5	Oceania
471	Vanuatu_Tongoa:Vanuatu	0.0168	0.0420	4	Oceania
474	Vietnamese:Vietnam	0.0079	0.0612	10	Asia
479	Xavante:Brazil	0.0825	0.1008	11	Americas
482	Yakut:Russia	0.0255	0.0780	20	Europe
484	Yaquis:Peru	0.0176	−0.0367	8	Americas

Notes: The table lists the populations corresponding to the numbers labeling the circles in Panel B of Figure C.6.2.

(label 38) from the "Austronesian (Melanesia)" language family are far to the right of the 45-

degree line.

(We also note that, in principle, populations that appear in the North-West quadrant of the figure, with high $\overline{F_{ROH}}$ and low $\overline{F_{SNP}}$, would tend to be genetically isolated (Clark et al., 2019). However, there is no population whose language family has a large sample size that is far to the left of the 45-degree line the figure.)

This comparison exercise between our estimates of F_{ROH} and F_{SNP} suggests that our estimates of F_{ROH} at least partly capture average levels of inbreeding across populations. This is consistent with the results of Sahoo et al. (2021) and with the analyses we report in Section 5.2 of the main text.

C.7 Mean regional pairwise F_{ST}: background and estimation

Genetic isolation occurs when a population has little genetic mixing with other populations. In humans, this can occur due to geographical or cultural distance or taboos prohibiting mating with individuals from other populations. Genetic isolation is associated with reduced mate choice and thus with increased cryptic inbreeding, in which two parents may have a recent common ancestor in common by chance (and not due to a deliberate cultural practice of mating relatives) (Pemberton and Rosenberg, 2014).

F_{ST} is commonly used to quantify genetic distance, or genetic divergence between populations. Two populations with a low genetic distance will have similar distributions of alleles, and two genetically distant populations will have more dissimilar distributions of alleles (Pemberton and Rosenberg, 2014).

Following Pemberton and Rosenberg (2014), we proxy for genetic isolation for a given population by first calculating the mean of the population's pairwise F_{ST} with other populations in the same geographic region of the world.[19] Pemberton and Rosenberg (2014) show that mean regional pairwise F_{ST} correlates positively with ROH.

Our estimator of F_{ST} is the Weir and Cockerham (1984) estimator. We only calculated pairwise F_{ST} for two HO populations in a region if both populations have at least five individuals. After excluding HO populations with less than five individuals, we obtained 371 populations that are mapped to 545 Ethnologue country-ethnicities.[20] For each of these 371 populations, we then calculated the mean regional pairwise F_{ST} as the average pairwise F_{ST} across all other populations in the same region that have at least eight individuals (Thus, while we computed the mean regional pairwise F_{ST} for all HO populations with at least five individuals, we only used other populations in the same region with at least eight individuals to compute each population's mean regional pairwise F_{ST}).

After calculating the mean regional pairwise F_{ST} for each of the 371 HO populations, we assigned each HO individual their HO population's mean regional pairwise F_{ST} estimate, and then obtained estimates of the mean regional pairwise F_{ST} for each of the 545 Ethnologue country-ethnicities by taking the average across the ethnicity's individuals. (As mentioned

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[19] The world geographic regions we use are again those from the United Nations' "M49 standard" (*Standard Country or Area Codes for Statistical Use*). We merged Polynesia and Melanesia for this analysis because the Polynesia region only had 6 individuals.

[20] Note that we have only 371 HO populations here, while the main sample we obtained after applying our baseline QC filters as described in Section C.4) comprised 435 HO populations matched to 313 Ethnologue languages with at least 5 HO individuals and 551 associated country-ethnicities. These numbers differ because in Section C.4), we dropped individuals who belong to Ethnologue *languages* with fewer than 5 individuals, whereas here when calculating F_{ST} we apply an additional filter and drop individuals who belong to *HO populations* with fewer than 5 individuals.

above, for the analyses reported in the main text, we only used subsets of these country-ethnicities.)

To compute pairwise F_{ST} for any two populations, we took the set of SNPs and individuals that passed our baseline QC filters and removed all SNPs with MAF < 0.05. That step removed 115,203 SNPs, resulting in 369,741 remaining SNPs in the data. We then used PLINK to LD prune the remaining SNPs. We used PLINK's "–indep-pairwise" command to LD prune the SNPs, with a window-size of 1E6 kb, a step-size of 50 kb, and a r^2 threshold of 0.1. This left a total of 50,739 quasi-independent SNPs for the F_{ST} calculations. (As mentioned below, we used that same set of SNPs to compute the top 20 Principal Components (PCs) in the HO data.) We calculated pairwise F_{ST} using PLINK's "–fst" and then used the reported weighted global mean as our estimate of pairwise F_{ST}.

C.8 Expected heterozygosity: background and estimation

Another correlate of F_{ROH} is expected heterozygosity (Pemberton and Rosenberg, 2014). Expected heterozygosity is a measure of genetic diversity in a population; it is defined as the probability that two randomly selected individuals from a population have different alleles at a randomly selected location on one chromosome in the genome. Equivalently, if people in the parents' generation mate at random (i.e., under Hardy-Weinberg equilibrium), expected heterozygosity is the probability that at a randomly selected location in one's genome, the two alleles are identical across both chromosomes.

ROH and F_{ROH} are negatively correlated with expected heterozygosity across populations (Pemberton and Rosenberg, 2014). This is because, if there are relatively more homozygotes in the population, individuals will tend to exhibit more ROH, even in the absence of consanguineous cultural practices. Consider the following simple hypothetical example, where there is no genetic variation in the population and all individuals are therefore fully homozygous. If we attempt to infer autozygosity by counting ROH in a sample of individuals from the population, we will incorrectly conclude that the population is fully inbred.

Expected heterozygosity has been shown to be highly correlated with migratory distance from Africa (Ramachandran et al., 2005). This relationship is consistent with a model in which, as human beings migrated outside the "cradle of humankind" in East Africa and spread across the globe, the individuals who migrated to new colonies only carried with them a subset of the genetic diversity of the parent colony (Ramachandran et al., 2005). This is known as the "serial founder effect."

Expected heterozygosity has also been found to be (non-linearly) associated with economic development (Ashraf and Galor, 2013b), though some have questioned the robustness of these results (Rosenberg and Kang, 2015). Thus, it is important to control for expected heterozygosity and its square in order to confidently use F_{ROH} as a proxy for consanguineous unions, especially in our analyses of the relationship between F_{ROH} and economic development.[21]

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[21] Ascertainment bias in genotyping microarrays (Patterson et al., 2012) may also bias our estimates of $\overline{F_{ROH}}$. Only a subset of SNPs are genotyped in microarrays, and SNPs with a higher MAF in a reference population are typically favored. For instance, if the reference population is European, then the inclusion of SNPs with high MAF among Europeans on the genotyping array may lead to an upward bias in estimates of expected heterozygosity and downward bias in estimates of ROH and F among Europeans vs. among other populations. (By definition, MAF are in the interval [0, 0.5], so higher MAF are closer to 0.5.) The Affymetrix Human Origins array used for the dataset we analyze, HO, has been specifically designed to mitigate ascertainment bias (Patterson et al., 2012), but ascertainment bias may nonetheless still be a concern. Controlling for expected heterozygosity (and its square) in our analyses further mitigates this concern.

As we did to estimate mean regional pairwise F_{ST}, we only computed expected heterozygosity for HO populations that have at least five individuals. After excluding populations with less than five individuals, we obtained 371 populations that are mapped to 545 Ethnologue country-ethnicities. After calculating expected heterozygosity (as described below) for each of the 371 HO populations, we assigned each HO individual their HO population's expected heterozygosity estimate, and then obtained estimates of the expected heterozygosity for each of the 545 Ethnologue country-ethnicities by taking the average across the ethnicity's individuals. (As mentioned above, for the analyses with $\overline{F_{ROH}}$ reported in the main text, we only used subsets of these country-ethnicities.)

We calculated expected heterozygosity for each SNP i and each HO population j using Nei and Roychoudhury's formula for expected heterozygosity (Nei and Roychoudhury, 1974)[22]:

$$\hat{h}_{ij} = \frac{n_{ij}}{n_{ij} - 1}\left(1 - (p_{ij})^2 + \left(1 - p_{ij}\right)^2\right) \tag{3}$$

where p_{ij} is the minor allele frequency (MAF) of SNP i in population j and n_{ij} is the number of alleles in the data for SNP i in population j.[23] We calculated expected heterozygosity for population j by summing up the $\hat{h}_{ij}$ across all SNPs:

$$\hat{H}_j = \sum_i \hat{h}_{ij}. \tag{4}$$

Before calculating expected heterozygosity for each population, we took the SNPs that passed our baseline QC filters and removed all SNPs with MAF < 0.05 and missing call rates > 0.01. Note that we calculated MAF here using all individuals in the HO data that passed our baseline QC. We applied a more stringent missing call rate threshold of 0.01 (compared to 0.03, which is the threshold in our baseline QC) to reduce the number of SNPs that have very few individuals in a population with non-missing genotypes for those SNPs.

After applying those QC filters, we used PLINK to LD prune the remaining SNPs (i.e., to obtain a subset of SNPs that are no more than weakly correlated with one another in the genome). We used PLINK's "–indep-pairwise" to LD prune the SNPs, with a window-size of 1E6 kb, a step-size of 50 kb, and a r^2 threshold of 0.1. After LD pruning, we obtained 50,383 quasi-independent SNPs.

We then removed all SNPs that had at least one population with strictly less than four non-missing alleles for that SNP. This resulted in an additional four SNPs being removed. Therefore, we had 50,379 SNPs for our expected heterozygosity calculations.[24]

To obtain the quantities necessary to calculate expected heterozygosity, we used PLINK's "–freq" command, which reports the minor allele frequencies and number of non-missing alleles for each SNP.[25] We then used those calculated quantities to compute each population's expected heterozygosity.

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[22] Nei and Roychoudhury's method (1974) yields unbiased estimates of expected heterozygosity only in samples with no inbred or related individuals (DeGiorgio and Rosenberg, 2009). Here, our F_{ROH} estimates clearly suggest inbreeding is present in some populations and some individuals are likely related, so our estimates of $\hat{H}_j$ are not unbiased. We expect this to generate no more than a small bias in the empirical analyses we report in the paper.

[23] Thus, if there are N_j individuals in population j in the dataset and if there are no missing observations for SNP i, $n_{ij} = 2N_j$.

[24] Note that we also calculated expected heterozygosity after removing all SNPs that had at least one population with strictly less than eight non-missing alleles (instead of less than four non-missing alleles). This removed another 892 SNPs. The estimated correlation between the estimates of expected heterozygosity obtained using these two different sets of SNPs is unity.

[25] Note that, unlike for the estimation of expected homozygosity (which is equal to one minus expected heterozygosity) when computing F_{SNP}, which we computed at the language level using PLINK's "–het" command

C.9 The top 20 Principal Components (PCs): background and estimation

In order to control for population structure, we also calculated the top 20 principal components (PCs) of the genotypic data for each individual. For each Ethnologue language, we then obtained the mean of each PC by taking the average across the language's individuals.

The top PCs have been shown to correlate strongly with ancestry (Novembre et al., 2008; Price et al., 2006). Controlling for the top PCs is standard in analyses with individual-level genetic data and can mitigate bias due to population stratification.[26] Population stratification could pose a threat to our empirical analyses since allele frequencies affect homozygosity and thus F_{ROH}.

To compute the top 20 PCs, we used PLINK's "–pca" command with the same set of 50,739 SNPs that we used to compute pairwise F_{ST} between populations (see Section C.8).

C.10 Summary statistics

Tables B.5.1 and B.6.1 report the mean, standard deviation, minimum, and maximum for the main variables we computed with the genetic data—the inbreeding coefficient ($\overline{F_{ROH}}$), mean regional pairwise F_{ST}, and expected heterozygosity—as well as other variables used in our analyses. These summary statistics were computed across the 416 Ethnologue country-ethnicities with eight or more HO individuals (or across the subset of country-ethnicities with nonmissing data; Table B.5.1) as well as a across the 281,177 pixels in the homelands of these country-ethnicities (Table B.6.1). These tables do not report summary statistics for the top 20 PCs, which are all normalized to have a mean of zero and unit variance.

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with the "small-sample" flag, here we used Nei & Roychoudhury's formula to compute population-level expected heterozygosity. The main reason for the difference is that PLINK's "–het" command computes expected heterozygosity at the individual level using each individual's nonmissing SNPs, and here we wanted to use the same set of SNPs to compute expected heterozygosity for all populations.

[26] Population stratification refers to systematic differences in allele frequencies that correlate across populations with cultural or environmental differences that causally impact variables of interest (Hamer, 2000).

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