

- effect of consanguinity on between-individual-identity-by-descent sharing. *Genetics* 212:305–316.
- Severson, A. L., S. Carmi, and N. A. Rosenberg. 2021. Variance and limiting distribution of coalescence times in a diploid model of a consanguineous population. *Theor. Popul. Biol.* 139:50–65.
- Sharma, S. K., M. A. Kalam, S. Ghosh et al. 2021. Prevalence and determinants of consanguineous marriage and its types in India: Evidence from the National Family Health Survey, 2015–2016. *J. Biosoc. Sci.* 53:566–576.
- Sheridan, E., J. Wright, N. Small et al. 2013. Risk factors for congenital anomaly in a multiethnic birth cohort: An analysis of the Born in Bradford study. *Lancet* 382:1,350–1,359.
- Stone, L. 1977. *Family, Sex and Marriage in England 1500–1800*. New York: Harper and Row.
- Szpiech, Z. A., J. Xu, T. J. Pemberton et al. 2013. Long runs of homozygosity are enriched for deleterious variation. *Am. J. Hum. Genet.* 93:90–102.
- Wall, J. D., J. F. Sathirapongsasuti, R. Gupta et al. 2020. South Asian patient population genetics reveal strong founder effects and high rates of homozygosity—New resources for precision medicine. Preprint, <https://www.biorxiv.org/content/10.1101/2020.10.02.323238v1>.

### Supplementary Table S1. Quasi-Poisson Regression Fitted for Long (>10 cM) Runs of Homozygosity (NROH10; cM) for Populations (Unweighted)

Predictor Variable	Estimate	Std. Error	t-Value	Pr(> t )
Intercept	3.99	2.52	1.58	1.14e-01
NROH2	0.07	0.01	7.12	5.51e-12
NROH1	-0.06	0.02	-2.67	8.00e-03
Heterozygosity	-11.76	6.71	-1.75	8.06e-02
Consanguinity score = 1	0.29	0.20	1.46	1.45e-01
Consanguinity score = 2	0.78	0.14	5.63	3.47e-08

Abbreviations: NROH1, number of runs of homozygosity longer than 1 cM but shorter than 2 cM; NROH2, number of runs of homozygosity longer than 2 cM but shorter than 5 cM. Consanguinity scores of 1 and 2 represent populations that permit and prefer cousin unions, respectively. Ten genetic PCs (calculated for the full sample) were also included in the model, but their beta coefficients are not shown. Poisson dispersion parameter = 1.57,  $p$ -value =  $1.13 \times 10^{-11}$ .

### Supplementary Table S2. Poisson Regression Fitted for Long (>10 cM) Runs of Homozygosity (NROH10; cM) for Populations (Weighted)

Predictor Variable	Estimate	Std. Error	z-Value	Pr(> z )
Intercept	0.31	2.42	0.13	8.97e-01
NROH2	0.08	0.01	6.79	1.14e-11
NROH1	-0.04	0.02	-1.84	6.53e-02
Heterozygosity	-2.30	6.39	-0.36	7.20e-01
Consanguinity score = 1	0.27	0.15	1.79	7.41e-02
Consanguinity score = 2	0.76	0.12	6.44	1.22e-10

Abbreviations: NROH1, number of runs of homozygosity longer than 1 cM but shorter than 2 cM; NROH2, number of runs of homozygosity longer than 2 cM but shorter than 5 cM. Consanguinity scores of 1 and 2 represent populations that permit and prefer cousin unions, respectively. Ten genetic PCs (calculated for the full sample) were also included in the model, but their beta coefficients are not shown. Poisson dispersion parameter = 1.06,  $p$ -value = 0.201.

**Supplementary Table S3. Quasi-Poisson Regression Fitted for Long (>10 cM) Runs of Homozygosity (NROH10; cM) in South Asian Individuals**

Predictor Variable	Estimate	Std. Error	t-Value	Pr(> t )
Intercept	7.9779	3.3975	2.35	0.0190
NROH1	-0.0655	0.0157	-4.16	0.0000
NROH2	0.0744	0.0079	9.44	0.0000
Heterozygosity	-23.4837	9.0324	-2.60	0.0094
Consanguinity score = 1	0.4268	0.2129	2.00	0.0452
Consanguinity score = 2	1.1840	0.1695	6.98	0.0000

Abbreviations: NROH1, number of runs of homozygosity longer than 1 cM but shorter than 2 cM; NROH2, number of runs of homozygosity longer than 2 cM but shorter than 5 cM. Consanguinity scores of 1 and 2 represent populations that permit and prefer cousin unions, respectively. Ten genetic PCs (calculated in South Asians only) were also included in the model, but their beta coefficients are not shown. Poisson dispersion parameter = 5.17, p-value = 0.

**Supplementary Table S4. Quasi-Poisson Regression Fitted for Long (>10 cM) Runs of Homozygosity (NROH10; cM) in South Asian Populations (Unweighted)**

Predictor Variable	Estimate	Std. Error	t-Value	Pr(> t )
Intercept	21.18	6.37	3.33	1.08e-03
NROH2	0.17	0.03	6.82	1.70e-10
NROH1	-0.24	0.04	-5.48	1.60e-07
Heterozygosity	-57.14	17.01	-3.36	9.74e-04
Consanguinity score = 1	0.15	0.34	0.45	6.55e-01
Consanguinity score = 2	0.93	0.24	3.87	1.56e-04

Abbreviations: NROH1, number of runs of homozygosity longer than 1 cM but shorter than 2 cM; NROH2, number of runs of homozygosity longer than 2 cM but shorter than 5 cM. Consanguinity scores of 1 and 2 represent populations that permit and prefer cousin unions, respectively. Ten genetic PCs (calculated in South Asians only) were also included in the model, but their beta coefficients are not shown. Poisson dispersion parameter = 1.6, p-value =  $1.53 \times 10^{-6}$ .

**Supplementary Table S5. Poisson Regression Fitted for Long (>10 cM) Runs of Homozygosity (NROH10; cM) in South Asian Populations (Weighted)**

Predictor Variable	Estimate	Std. Error	z-Value	Pr(> z )
Intercept	19.1731	6.4089	2.99	0.0028
NROH2	0.1212	0.0278	4.36	0.0000
NROH1	-0.1396	0.0459	-3.04	0.0024
Heterozygosity	-52.5470	16.9158	-3.11	0.0019
Consanguinity score = 1	0.3571	0.2635	1.36	0.1754
Consanguinity score = 2	0.9184	0.1921	4.78	0.0000

Abbreviations: NROH1, number of runs of homozygosity longer than 1 cM but shorter than 2 cM; NROH2, number of runs of homozygosity longer than 2 cM but shorter than 5 cM. Consanguinity scores of 1 and 2 represent populations that permit and prefer cousin unions, respectively. Ten genetic PCs (calculated in South Asians only) were also included in the model, but their beta coefficients are not shown. Poisson dispersion parameter = 1.12, p-value = 0.131.

**Supplementary Table S6. Linear Regression Fitted for Total Length of Regions of Homozygosity Longer Than 10 cM (LROH10; cM) for Individuals**

Predictor Variable	Estimate	Std. Error	t-Value	Pr(> t )
Intercept	23.54	36.63	0.64	5.21e-01
LROH1	-1.41	0.18	-7.84	5.98e-15
LROH2	1.26	0.06	21.46	1.58e-96
Heterozygosity	-176.49	87.25	-2.02	4.32e-02
Consanguinity score = 1	0.33	2.72	0.12	9.05e-01
Consanguinity score = 2	21.23	2.18	9.75	3.23e-22
Central Asia and Siberia	49.40	15.61	3.17	1.56e-03
East Asia	46.13	16.19	2.85	4.41e-03
Middle East and North Africa	52.30	16.55	3.16	1.59e-03
Oceania	58.92	47.88	1.23	2.19e-01
South Asia	56.21	16.27	3.46	5.55e-04
Sub-Saharan Africa	83.28	23.21	3.59	3.38e-04
Western Eurasia	38.07	15.87	2.40	1.65e-02

Abbreviations: LROH1, total length of runs of homozygosity longer than 1 cM but shorter than 2 cM; LROH2, total length of runs of homozygosity longer than 2 cM but shorter than 5 cM. Consanguinity scores of 1 and 2 represent populations that permit and prefer cousin unions, respectively. Ten genetic PCs (calculated for the full sample) were also included in the model but their beta coefficients are not shown.

**Supplementary Table S7. Linear Regression Fitted for Total Length of Regions of Homozygosity Longer Than 10 cM (LROH10; cM) for Populations (Unweighted)**

Predictor Variable	Estimate	Std. Error	t-Value	Pr(> t )
Intercept	5.92	2.86	2.07	3.90e-02
LROH2	0.05	0.01	7.66	1.60e-13
LROH1	-0.06	0.02	-3.07	2.33e-03
Heterozygosity	-11.24	7.56	-1.49	1.38e-01
Consanguinity score = 1	0.01	0.22	0.06	9.50e-01
Consanguinity score = 2	0.83	0.15	5.62	3.78e-08

Abbreviations: LROH1, total length of runs of homozygosity longer than 1 cM but shorter than 2 cM; LROH2, total length of runs of homozygosity longer than 2 cM but shorter than 5 cM. Consanguinity scores of 1 and 2 represent populations that permit and prefer cousin unions, respectively. Ten genetic PCs (calculated for the full sample) were also included in the model but their beta coefficients are not shown.

**Supplementary Table S8. Linear Regression Fitted for Total Length of Regions of Homozygosity Longer Than 10 cM (LROH10; cM) for Populations (Weighted)**

Predictor Variable	Estimate	Std. Error	t-Value	Pr(> t )
Intercept	147.52	73.36	2.01	4.50e-02
LROH2	1.63	0.17	9.44	3.97e-19
LROH1	-2.56	0.58	-4.44	1.20e-05
Heterozygosity	-357.34	193.03	-1.85	6.49e-02
Consanguinity score = 1	-0.72	4.49	-0.16	8.73e-01
Consanguinity score = 2	20.14	3.47	5.80	1.43e-08

Abbreviations: LROH1, total length of runs of homozygosity longer than 1 cM but shorter than 2 cM; LROH2, total length of runs of homozygosity longer than 2 cM but shorter than 5 cM. Consanguinity scores of 1 and 2 represent populations that permit and prefer cousin unions, respectively. Ten genetic PCs (calculated for the full sample) were also included in the model but their beta coefficients are not shown

**Supplementary Table S9. Linear Regression Model Fitted for Total Length of Regions of Homozygosity Longer Than 10 cM (LROH10; cM) in South Asian Individuals**

Predictor Variable	Estimate	Std. Error	t-Value	Pr(> t )
Intercept	158.33	69.05	2.29	2.20e-02
LROH1	-1.70	0.34	-5.05	5.04e-07
LROH2	1.13	0.12	9.74	1.02e-21
Heterozygosity	-404.67	183.02	-2.21	2.72e-02
Consanguinity score = 1	0.32	5.10	0.06	9.50e-01
Consanguinity score = 2	25.09	3.69	6.79	1.66e-11

Abbreviations: LROH1, total length of runs of homozygosity longer than 1 cM but shorter than 2 cM; LROH2, total length of runs of homozygosity longer than 2 cM but shorter than 5 cM. Consanguinity scores of 1 and 2 represent populations that permit and prefer cousin unions, respectively. Ten genetic PCs (calculated in South Asians only) were also included in the model but their beta coefficients are not shown.

**Supplementary Table S10. Linear Regression Model Fitted for Total Length of Long Runs of Homozygosity Longer Than 10 cM (LROH10; cM) in South Asian Populations (Unweighted)**

Predictor Variable	Estimate	Std. Error	t-Value	Pr(> t )
Intercept	707.06	219.89	3.22	1.57e-03
LROH2	2.23	0.35	6.45	1.18e-09
LROH1	-6.95	1.20	-5.79	3.52e-08
Heterozygosity	-1808.79	581.42	-3.11	2.20e-03
Consanguinity score =1	-3.40	9.48	-0.36	7.20e-01
Consanguinity score =2	20.75	6.54	3.17	1.80e-03

Abbreviations: LROH1, total length of runs of homozygosity longer than 1 cM but shorter than 2 cM; LROH2, total length of runs of homozygosity longer than 2 cM but shorter than 5 cM. Consanguinity scores of 1 and 2 represent populations that permit and prefer cousin unions, respectively. Ten genetic PCs (calculated in South Asians only) were also included in the model but their beta coefficients are not shown.

**Supplementary Table S11. Linear Regression Model Fitted for Total Length of Long Runs of Homozygosity Longer Than 10 cM (LROH10; cM) for South Asia Populations (Weighted)**

Predictor Variable	Estimate	Std. Error	z-Value	Pr(> z )
Intercept	19.17	6.41	2.99	2.78e-03
LROH2	0.12	0.03	4.36	1.28e-05
LROH1	-0.14	0.05	-3.04	2.38e-03
Heterozygosity	-52.55	16.92	-3.11	1.89e-03
Consanguinity score = 1	0.36	0.26	1.36	1.75e-01
Consanguinity score = 2	0.92	0.19	4.78	1.74e-06

Abbreviations: LROH1, total length of runs of homozygosity longer than 1 cM but shorter than 2 cM; LROH2, total length of runs of homozygosity longer than 2 cM but shorter than 5 cM. Consanguinity scores of 1 and 2 represent populations that permit and prefer cousin unions, respectively. Ten genetic PCs (calculated in South Asians only) were also included in the model but their beta coefficients are not shown.

**Supplementary Table S12. Wilcoxon Signed-Rank Test Results for Differences between Pairs of Populations Preferring and Prohibiting Consanguinity (Outliers Removed)**

Variable	Wilcoxon Signed-Rank Sum	P-Value
NROH10	1469.50	4.78e-03
NROH5	1402.50	3.51e-01
NROH2	1486.00	4.58e-01
NROH1	1177.00	3.42e-01
Heterozygosity	1408.00	7.54e-01

Abbreviations: NROH10, number of runs of homozygosity longer than 10 cM; NROH5, number of runs of homozygosity longer than 5 cM but shorter than 10 cM; NROH2, number of runs of homozygosity longer than 2 cM but shorter than 5 cM; NROH1, number of runs of homozygosity longer than 1 cM but shorter than 2 cM.

**SUPPLEMENTARY DATA FILE S1.** Population-level data used to generate most of the results and figures in this study. The columns contain information such as latitude, longitude, and numbers of runs of homozygosity for each population (rows). The last column indicates the paired population used for the paired analysis. Go to the following link to download the file: [https://digitalcommons.wayne.edu/cgi/viewcontent.cgi?filename=0&article=1194&context=humbiol\\_preprints&type=additional](https://digitalcommons.wayne.edu/cgi/viewcontent.cgi?filename=0&article=1194&context=humbiol_preprints&type=additional)