Supporting Information for "An article template"

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1 Supplemental methods

References

JÓNSSON, H., P. SULEM, B. KEHR, S. KRISTMUNDSDOTTIR, F. ZINK, et al., 2017 Parental influence on human germline de novo mutations in 1,548 trios from Iceland. Nature **549**: 519–522.

2 Tables and figures

Table S1: Mutation profiles from the past 100 generations, compared to Iceland trios. The most recent time bin for each method included the past ≈ 150 generations. When singletons were included (when using data from tsdate and Relate), the spectra of estimated recent standing variation were unchanged. Note that GEVA does not report ages for singletons. While the three methods provide similar spectra from recent mutations, the spectrum from the Iceland pedigrees differs, in particular for the C \rightarrow A and C \rightarrow G classes. These differences are up to 2% of the proportion among all mutations, which corresponds to an under- or over-count of up to $\sim 20\%$ of C \rightarrow A and C \rightarrow G mutations, respectively. This difference remains whether the spectrum is estimated from only mutations that were phased in Jónsson et al. (2017) or from all mutations (phased and unphased).

Dataset	$\mid A \rightarrow C$	$A{ ightarrow}G$	$A{ ightarrow}T$	$C{\rightarrow}A$	$C{\rightarrow}G$	$C{\rightarrow}T$
GEVA	0.0946	0.3600	0.0886	0.1201	0.1057	0.2310
tsdate	0.0931	0.3579	0.0899	0.1146	0.1061	0.2384
$ exttt{tsdate} (w/singletons)$	0.0989	0.3598	0.0908	0.1168	0.1062	0.2275
Relate	0.0991	0.3610	0.0863	0.1124	0.1038	0.2374
Relate $(w/singletons)$	0.1002	0.3590	0.0921	0.1164	0.1060	0.2263
Trios (phased) Trios (all mutations)	$\begin{vmatrix} 0.0953 \\ 0.0962 \end{vmatrix}$	$0.3649 \\ 0.3638$	$0.0890 \\ 0.0923$	$0.0960 \\ 0.0951$	$0.1216 \\ 0.1202$	0.2332 0.2324

Table S2: Some ? populations.

Code	Description	Region
ESN GWD LWK MSL YRI	Esan in Nigeria Gambian in Western Divisions in the Gambia Luhya in Webuye, Kenya Mende in Sierra Leone Yoruba in Ibadan, Nigeria	Africa Africa Africa Africa Africa
CEU GBR FIN IBS TSI	Utah Residents (CEPH) with Northern and Western European Ancestry British in England and Scotland Finnish in Finland Iberian Population in Spain Toscani in Italia	Europe Europe Europe Europe
CDX CHB CHS JPT KHV	Chinese Dai in Xishuangbanna, China Han Chinese in Beijing, China Southern Han Chinese Japanese in Tokyo, Japan Kinh in Ho Chi Minh City, Vietnam	East Asia East Asia East Asia East Asia

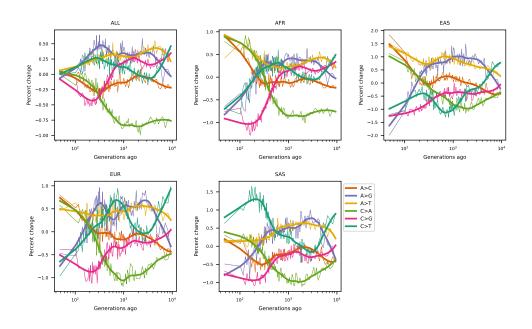


Figure S1: GEVA-inferred mutation spectrum history.

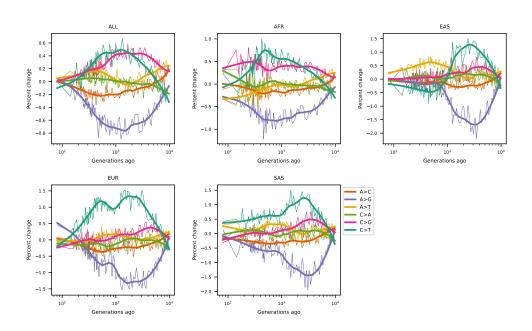


Figure S2: Relate-inferred mutation spectrum history.

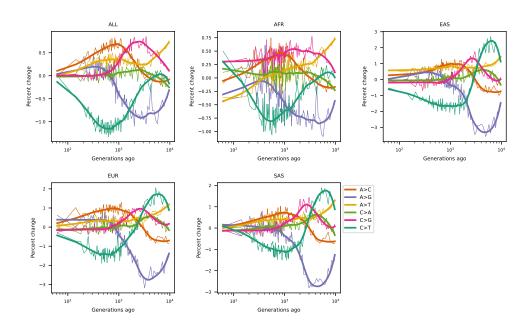


Figure S3: tsdate-inferred mutation spectrum history.

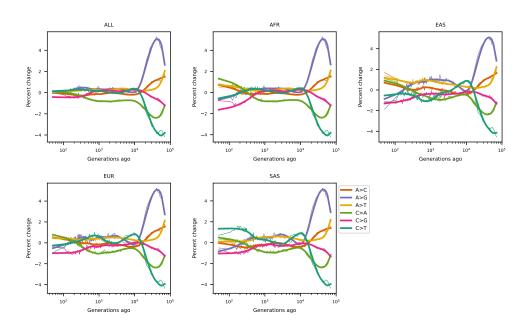


Figure S4: GEVA-inferred mutation spectrum history, extending to 80,000 generations.

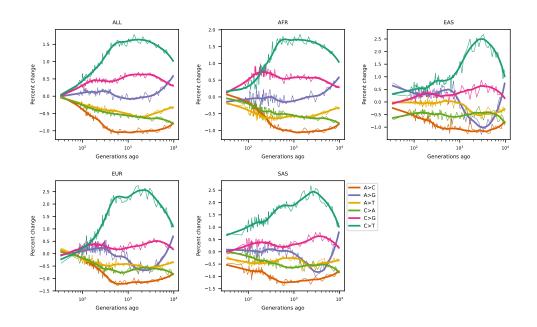


Figure S5: Relate-inferred mutation spectrum history, including singletons.

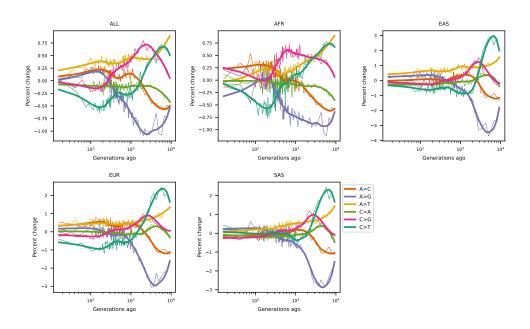


Figure S6: tsdate-inferred mutation spectrum history, including singletons.

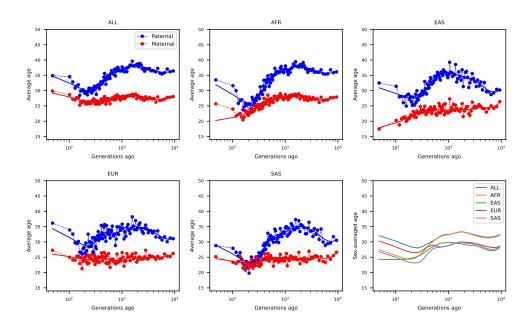


Figure S7: GEVA-inferred generation time histories.

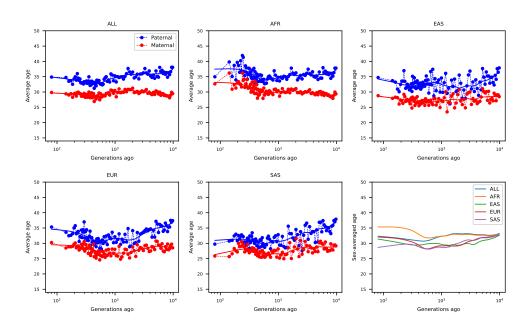


Figure S8: Relate-inferred generation time histories.

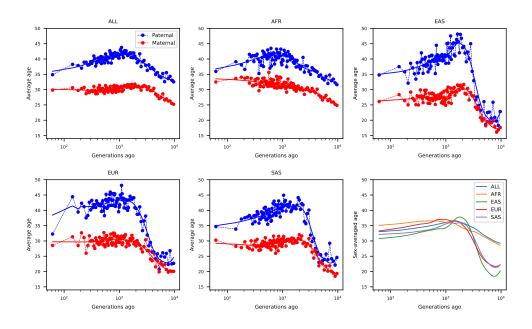


Figure S9: tsdate-inferred generation time histories.

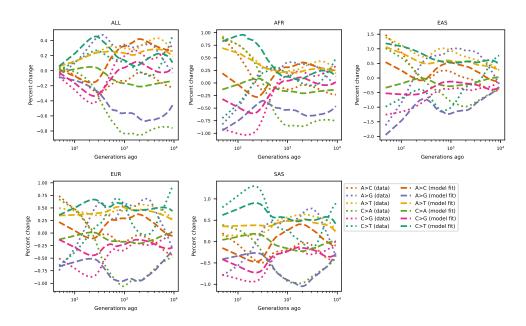


Figure S10: Prediction of mutation spectrum history from GEVA-inferred generation times.

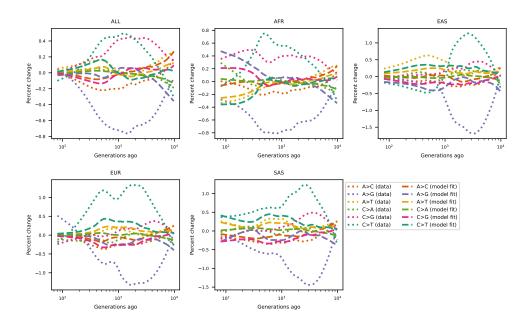


Figure S11: Prediction of mutation spectrum history from Relate-inferred generation times.

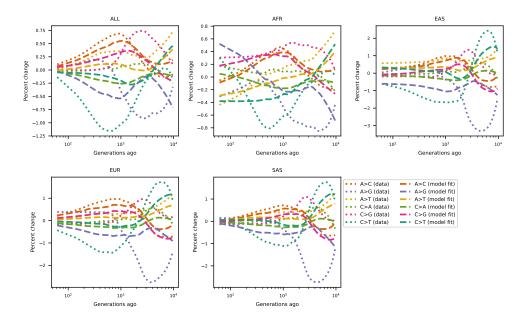


Figure S12: Prediction of mutation spectrum history from tsdate-inferred generation times.