

# Supporting Information for “An article template”

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## 1 Supplemental methods

### References

JÓNSSON, H., P. SULEM, B. KEHR, S. KRISTMUNSDOTTIR, 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  $\approx 150$  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	A $\rightarrow$ C	A $\rightarrow$ G	A $\rightarrow$ T	C $\rightarrow$ A	C $\rightarrow$ G	C $\rightarrow$ T
<b>GEVA</b>	0.0946	0.3600	0.0886	0.1201	0.1057	0.2310
<b>tsdate</b>	0.0931	0.3579	0.0899	0.1146	0.1061	0.2384
<b>tsdate</b> (w/singletons)	0.0989	0.3598	0.0908	0.1168	0.1062	0.2275
<b>Relate</b>	0.0991	0.3610	0.0863	0.1124	0.1038	0.2374
<b>Relate</b> (w/singletons)	0.1002	0.3590	0.0921	0.1164	0.1060	0.2263
Trios (phased)	0.0953	0.3649	0.0890	0.0960	0.1216	0.2332
Trios (all mutations)	0.0962	0.3638	0.0923	0.0951	0.1202	0.2324

Table S2: Some ? populations.

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

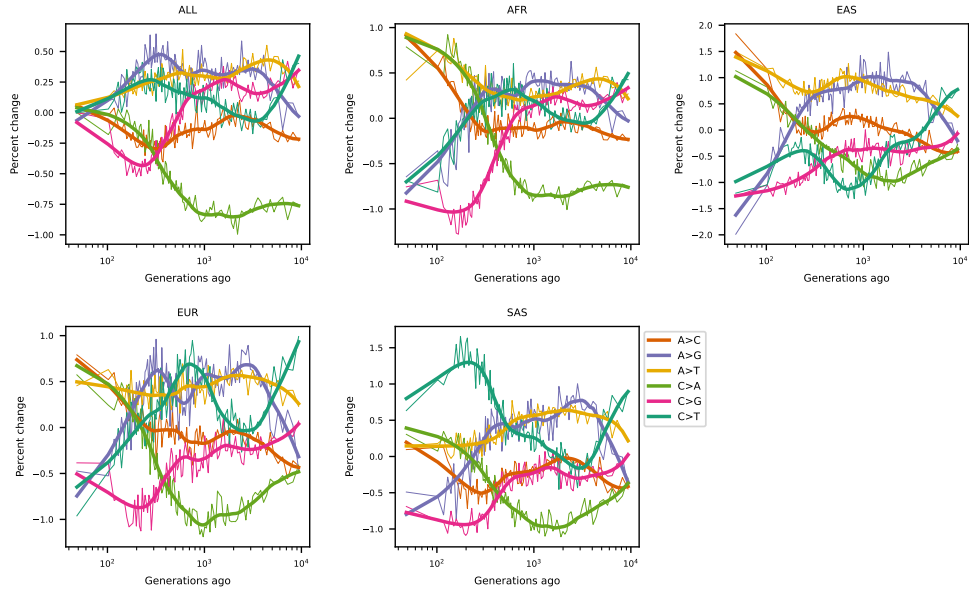


Figure S1: GEVA-inferred mutation spectrum history.

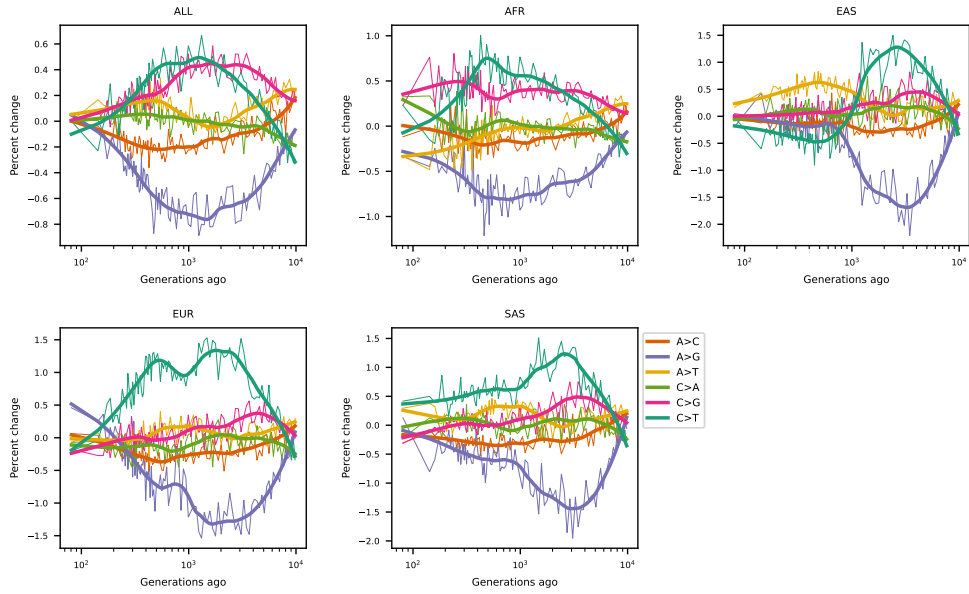


Figure S2: Relate-inferred mutation spectrum history.

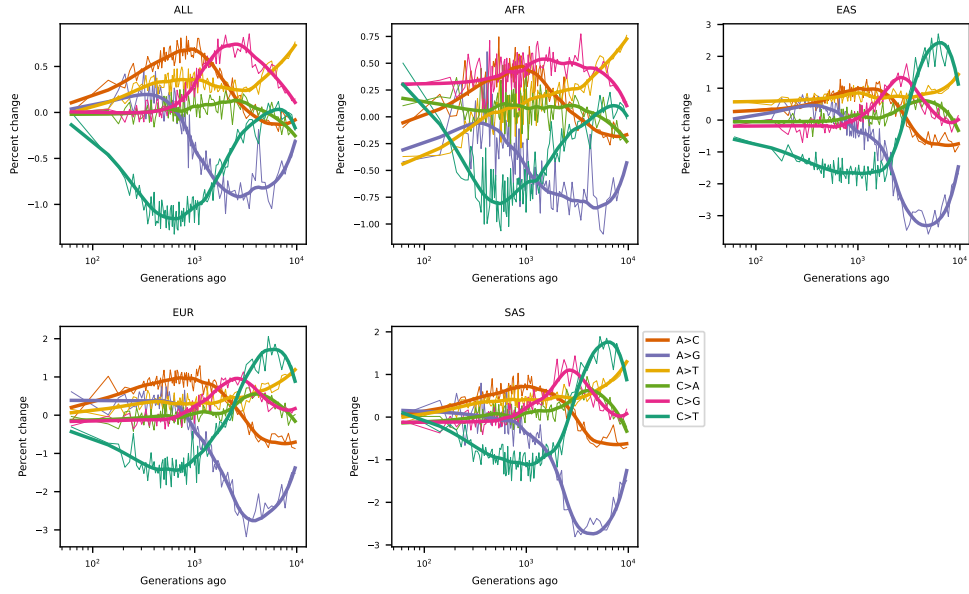


Figure S3: tsdate-inferred mutation spectrum history.

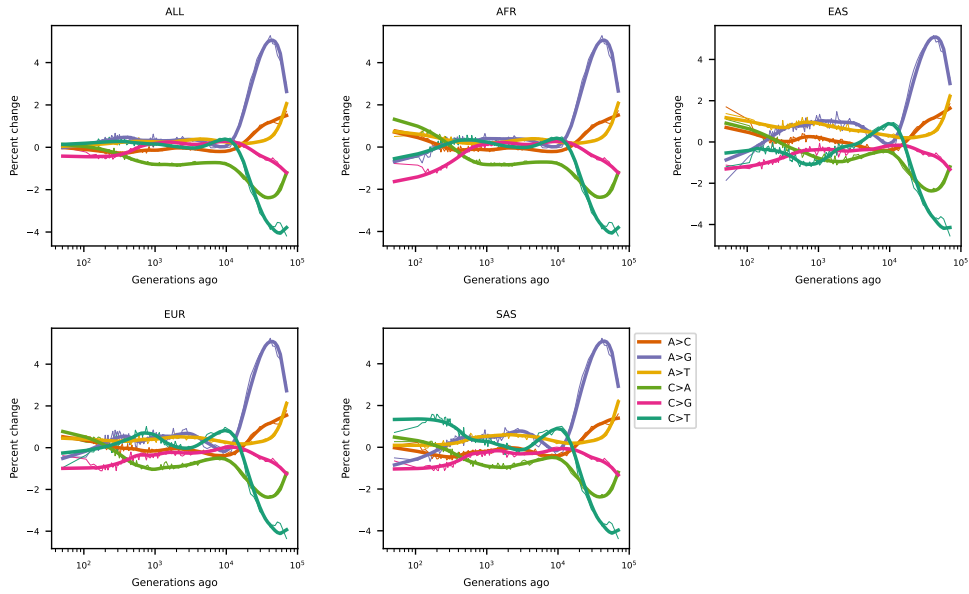


Figure S4: GEVA-inferred mutation spectrum history, extending to 80,000 generations.

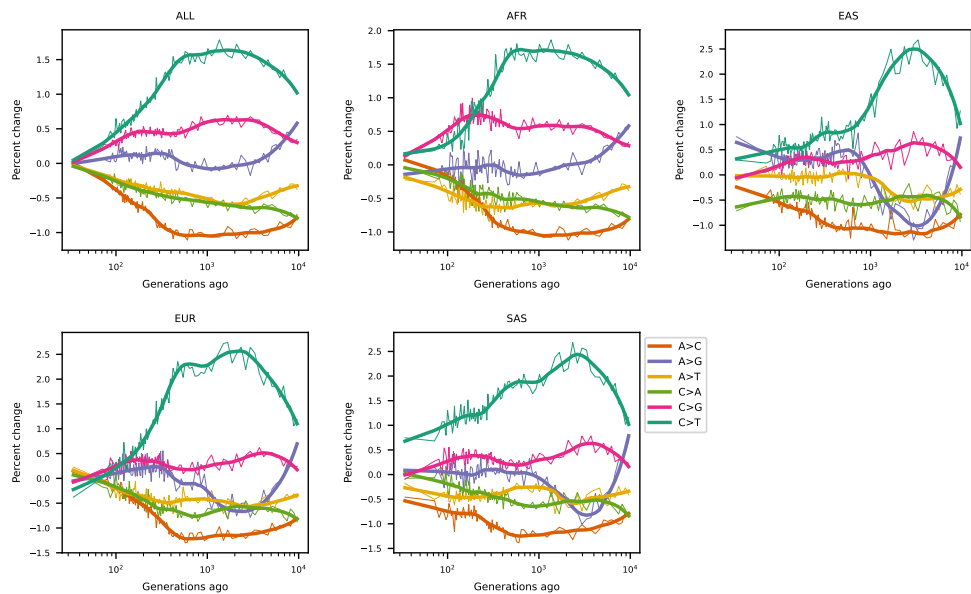


Figure S5: Relate-inferred mutation spectrum history, including singletons.

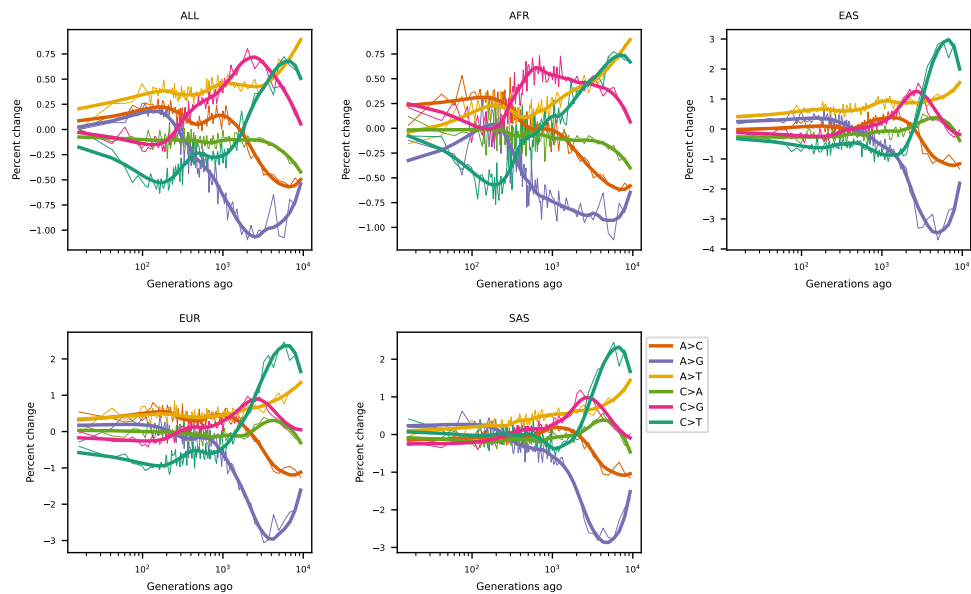


Figure S6: tsdate-inferred mutation spectrum history, including singletons.

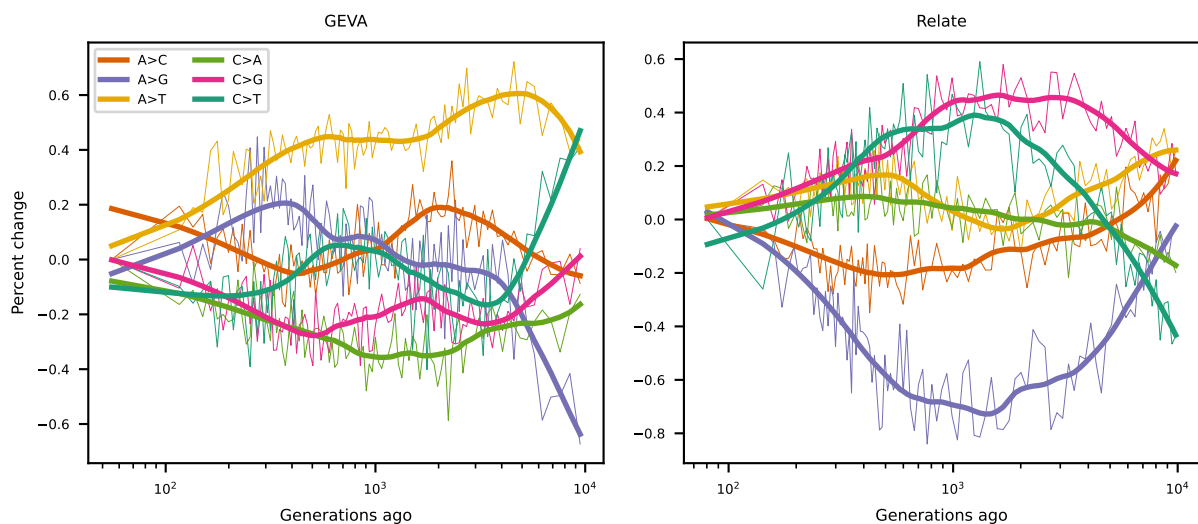


Figure S7: Mutation spectrum histories from mutations that were dated by both GEVA and Relate.

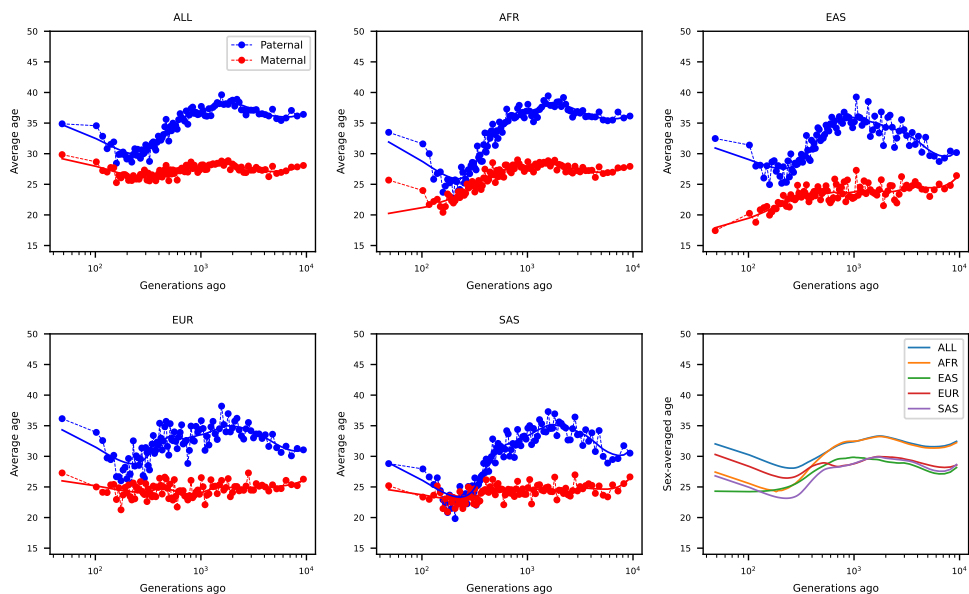


Figure S8: GEVA-inferred generation time histories.

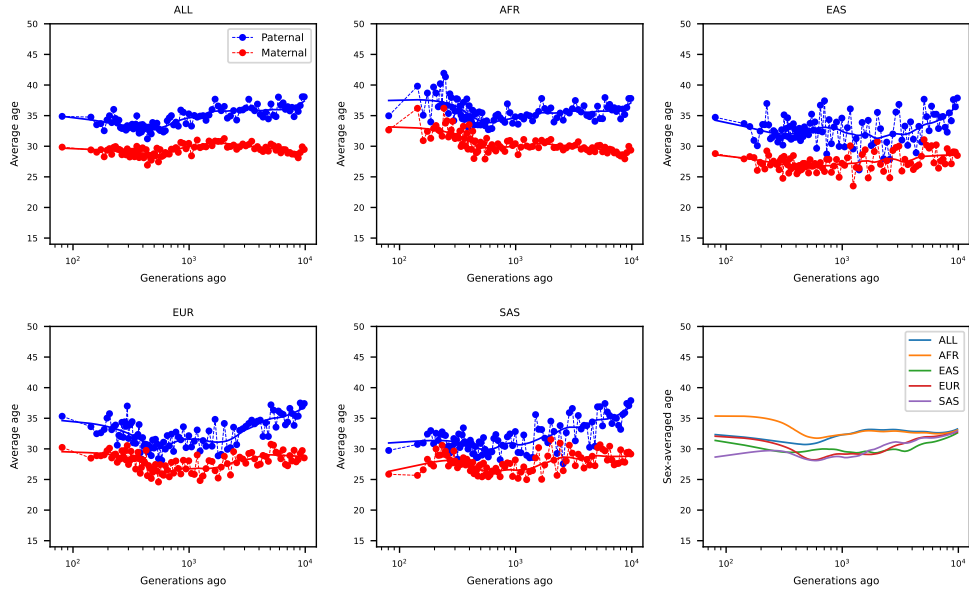


Figure S9: Relate-inferred generation time histories.

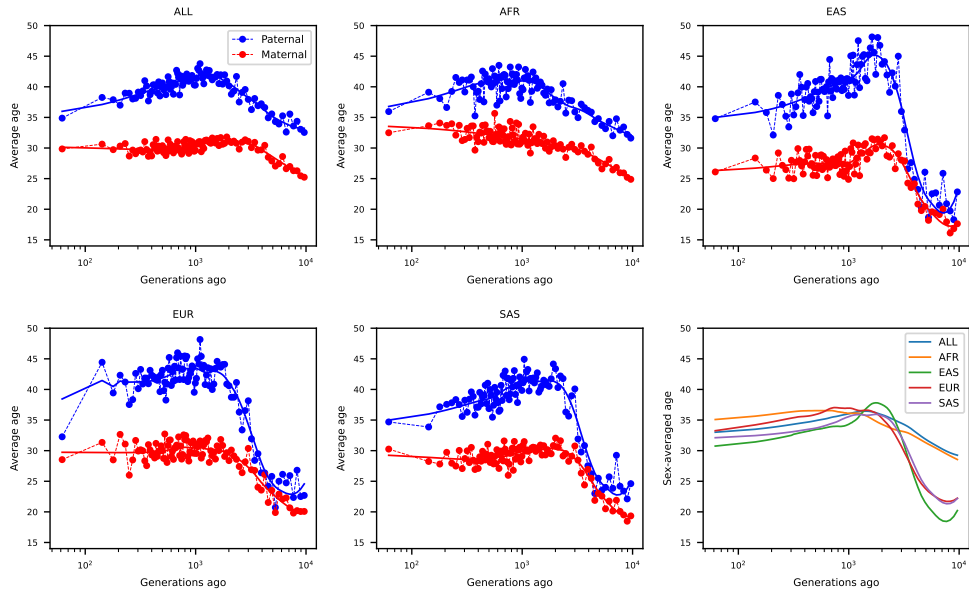


Figure S10: tsdate-inferred generation time histories.



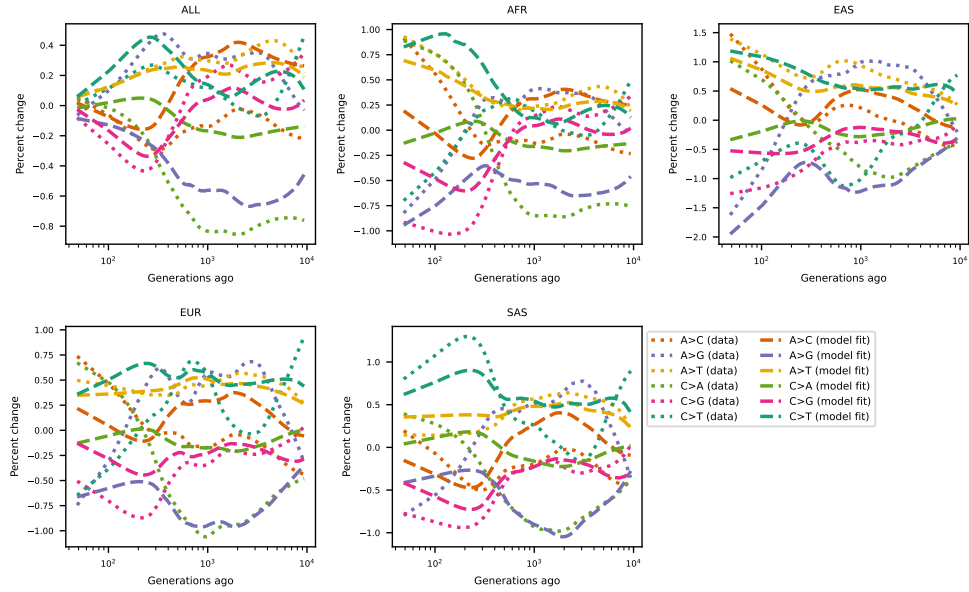


Figure S11: Prediction of mutation spectrum history from GEVA-inferred generation times.

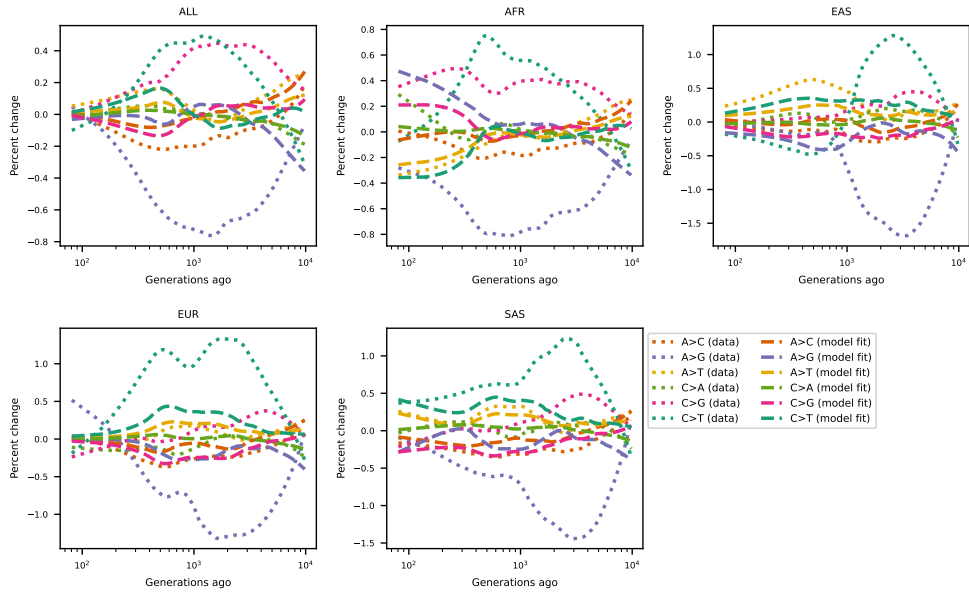


Figure S12: Prediction of mutation spectrum history from Relate-inferred generation times.

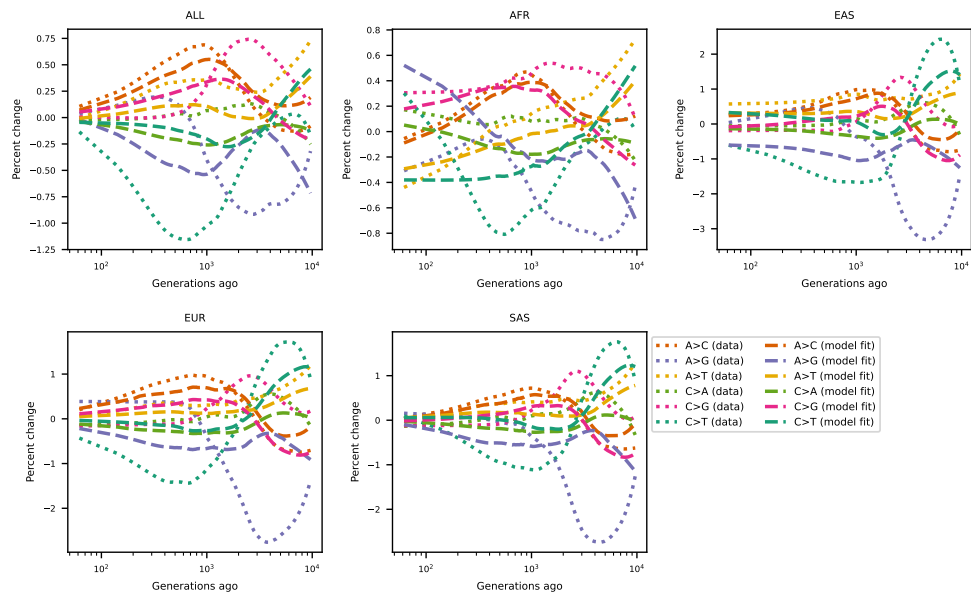


Figure S13: **Prediction of mutation spectrum history from tsdate-inferred generation times.**