

# Supporting Information for “An article template”

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## Supplemental methods

Generation times needed to explain long-lasting differences between populations

Allele ages from GEVA

Allele ages from Relate

Allele ages from tsdate

## 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.

# 1 Tables and figures

Dataset	A→C	A→G	A→T	C→A	C→G	C→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 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→A and C→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→A and C→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→C	A→G	A→T	C→A	C→G	C→T
AFR ( <b>GEVA</b> )	0.103	0.354	0.094	0.127	0.098	0.224
EAS	0.111	0.341	0.103	0.131	0.094	0.220
EUR	0.102	0.355	0.093	0.125	0.102	0.222
SAS	0.095	0.355	0.090	0.123	0.099	0.238
AFR ( <b>Relate</b> )	0.099	0.356	0.084	0.116	0.110	0.236
EAS	0.095	0.359	0.089	0.115	0.097	0.245
EUR	0.100	0.368	0.085	0.110	0.102	0.235
SAS	0.104	0.344	0.090	0.108	0.107	0.246
AFR ( <b>tsdate</b> )	0.092	0.354	0.087	0.116	0.110	0.241
EAS	0.098	0.356	0.097	0.112	0.103	0.233
EUR	0.091	0.363	0.089	0.117	0.102	0.238
SAS	0.091	0.359	0.088	0.114	0.107	0.241

Table S2: **Mutation profiles from the past 100 generations in continental population groups.**

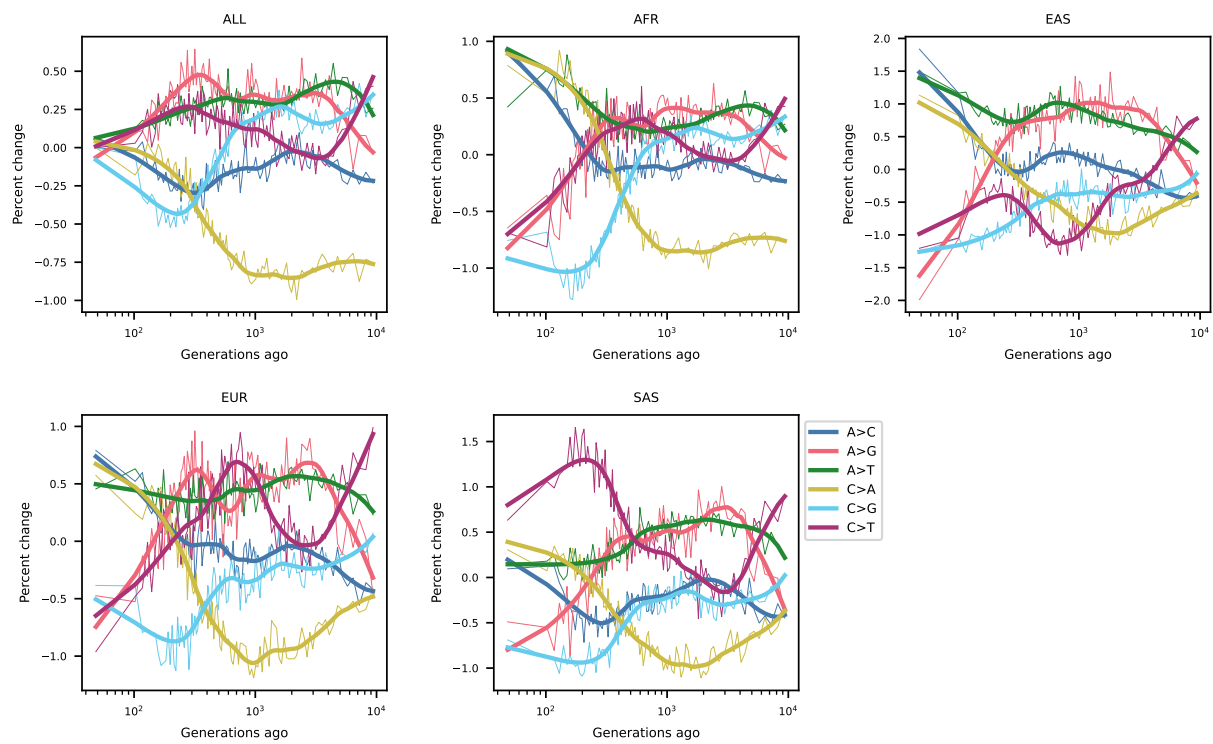


Figure S1: GEVA-inferred mutation spectrum history.

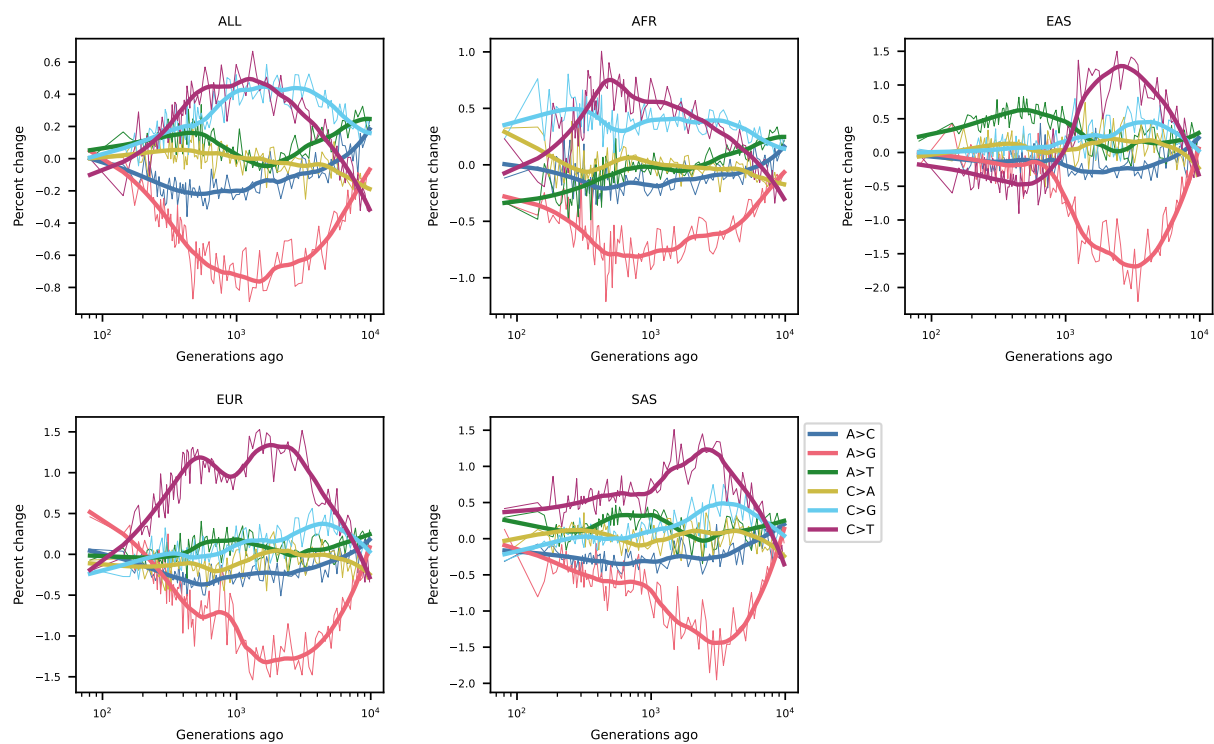


Figure S2: Relate-inferred mutation spectrum history.

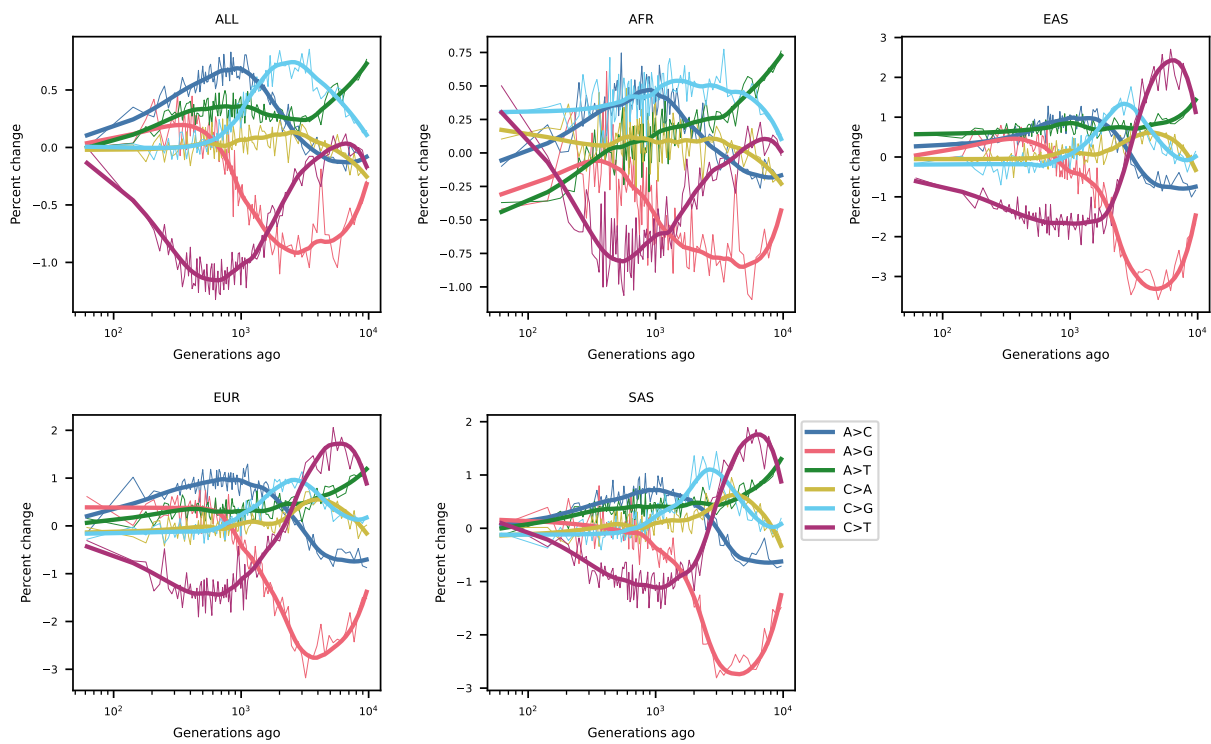


Figure S3: tssdate-inferred mutation spectrum history.

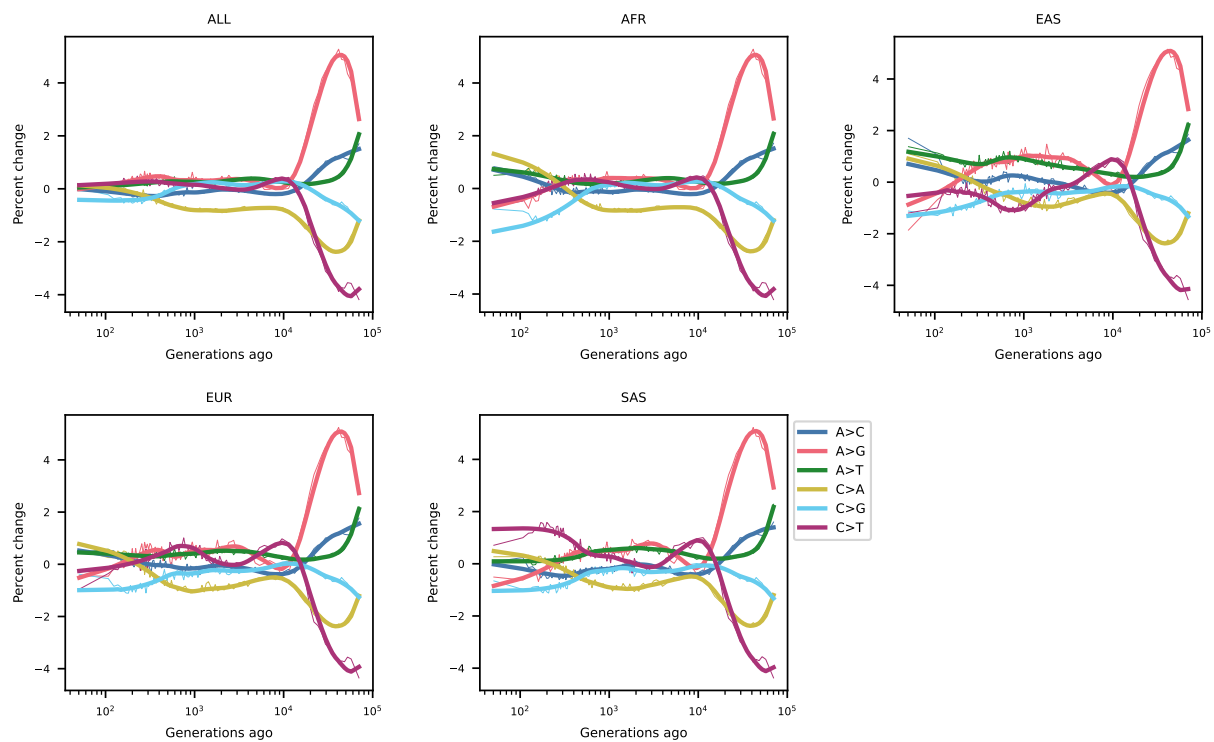


Figure S4: GEVA-inferred mutation spectrum history, extending to 80,000 generations.

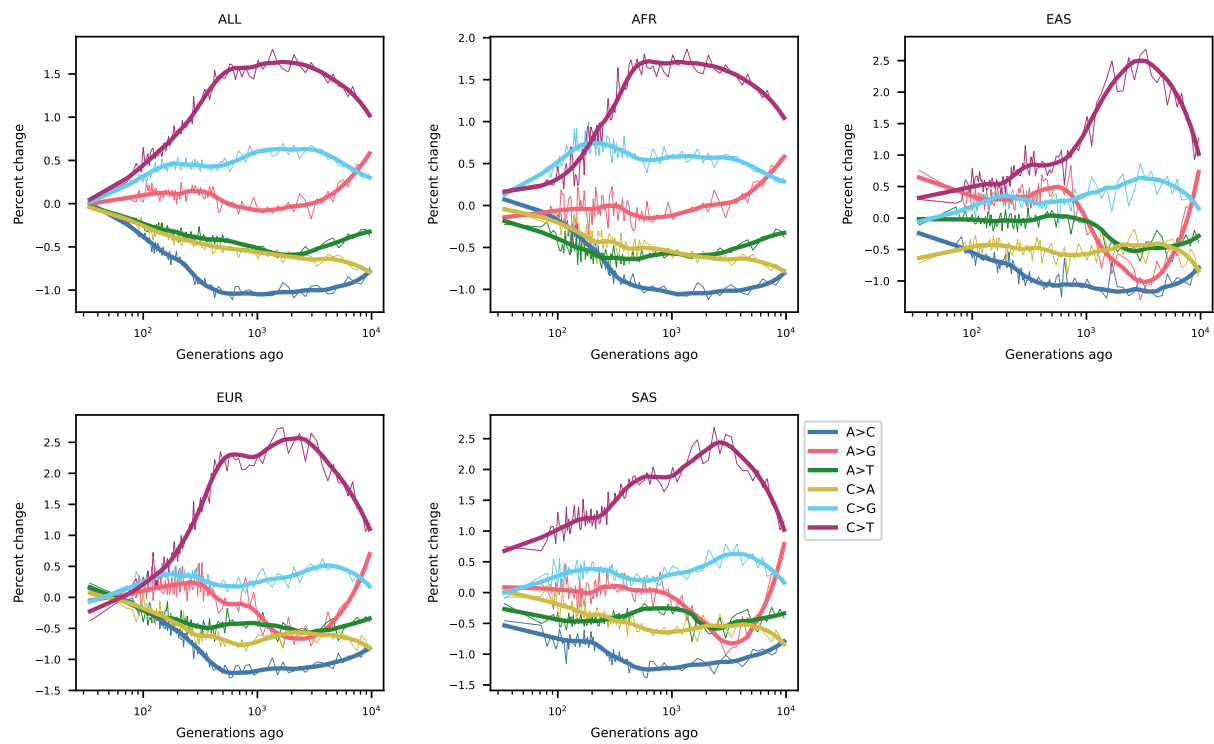


Figure S5: Relate-inferred mutation spectrum history, including singletons.

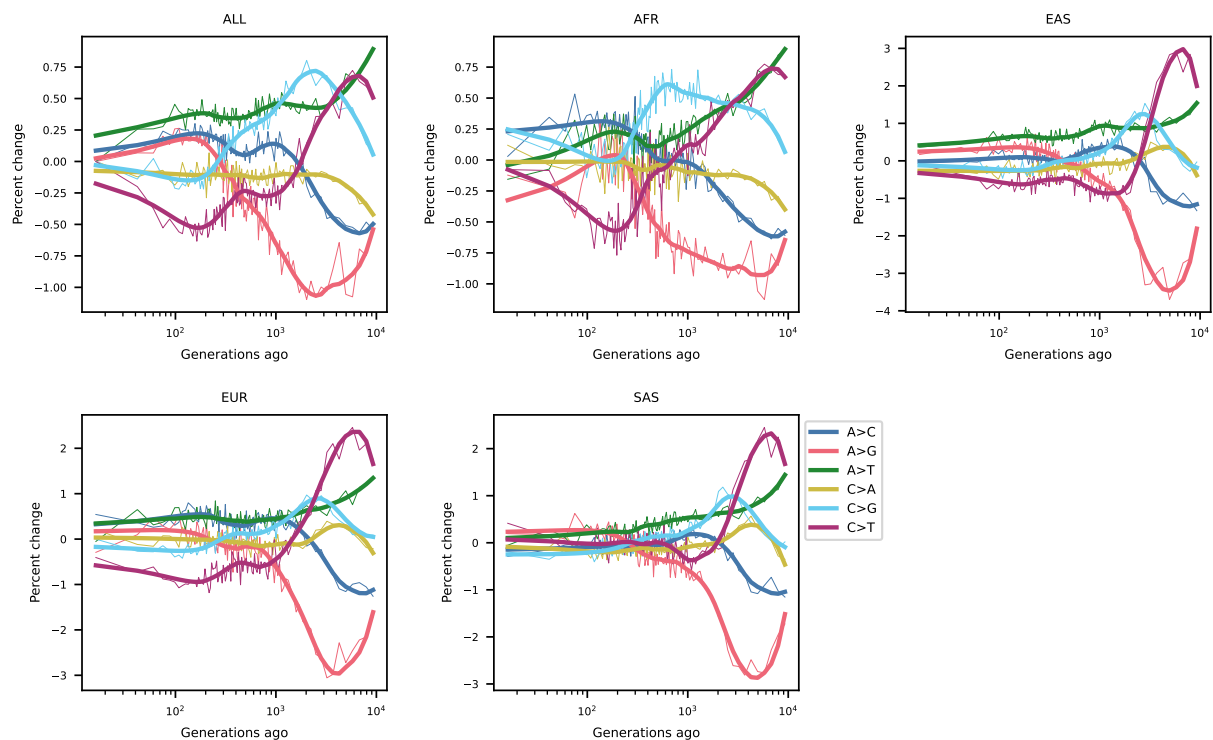


Figure S6: tsdate-inferred mutation spectrum history, including singletons.

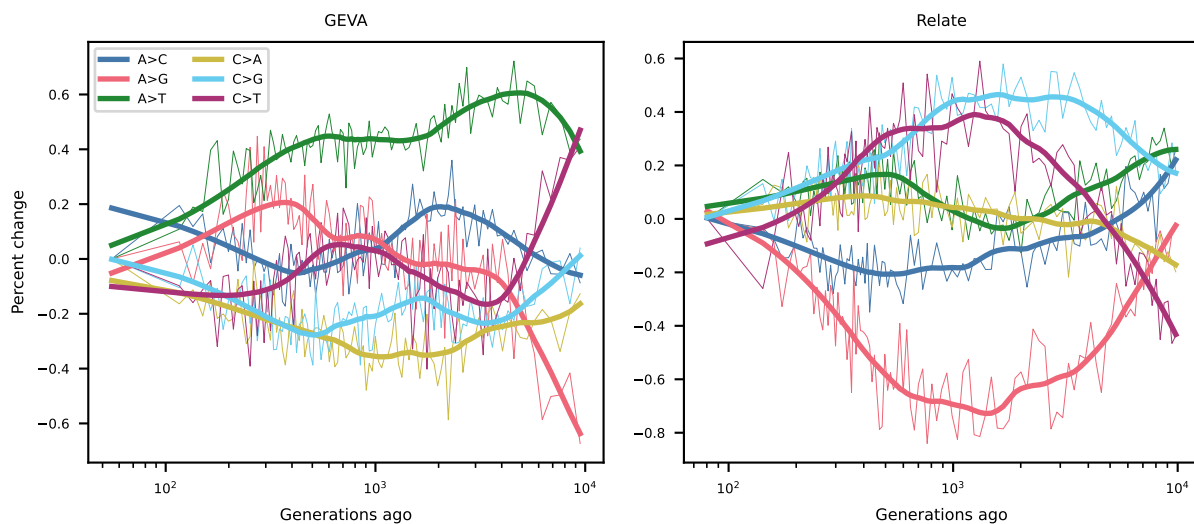


Figure S7: Mutation spectrum histories from mutations that were dated by both GEVA and Relate.



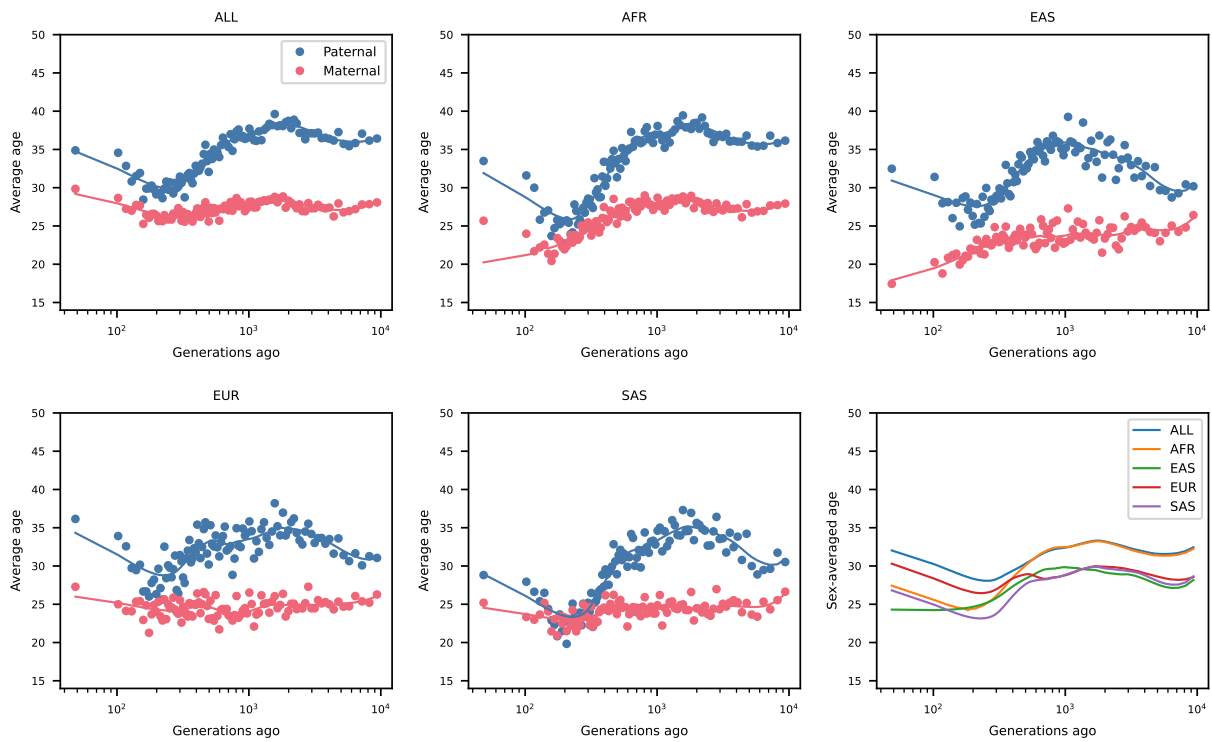


Figure S8: GEVA-inferred generation time histories.

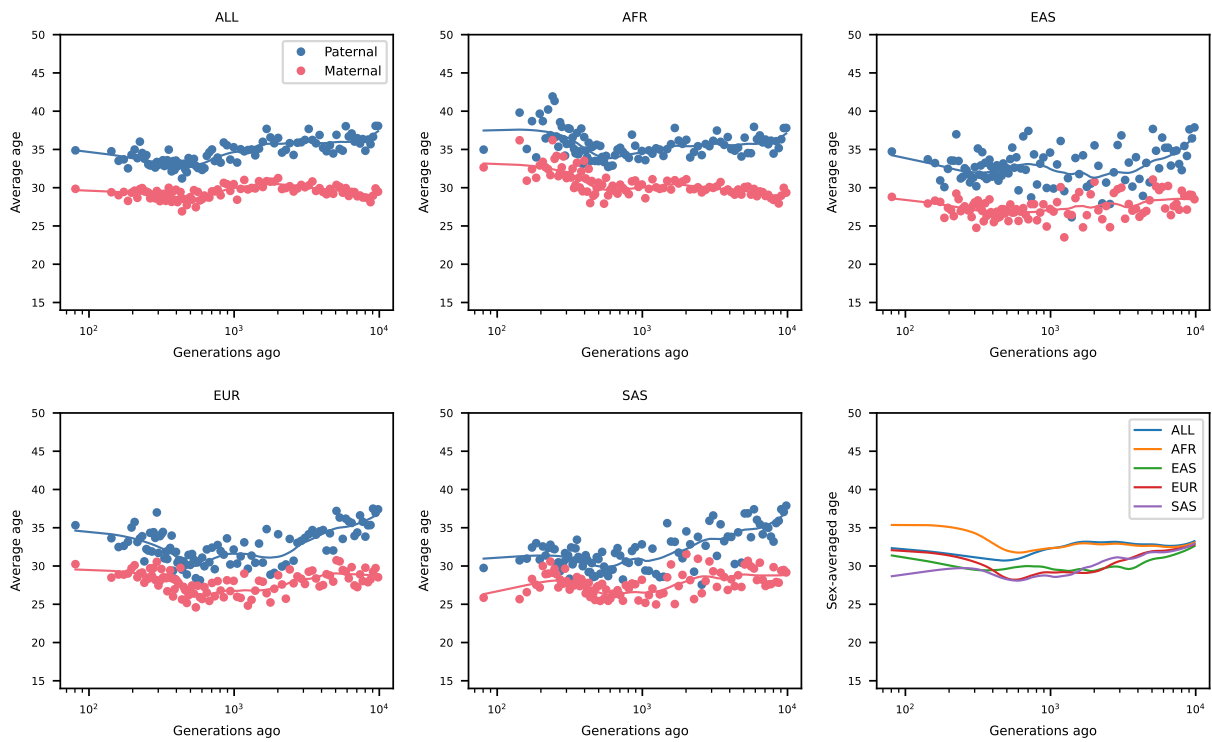


Figure S9: Relate-inferred generation time histories.

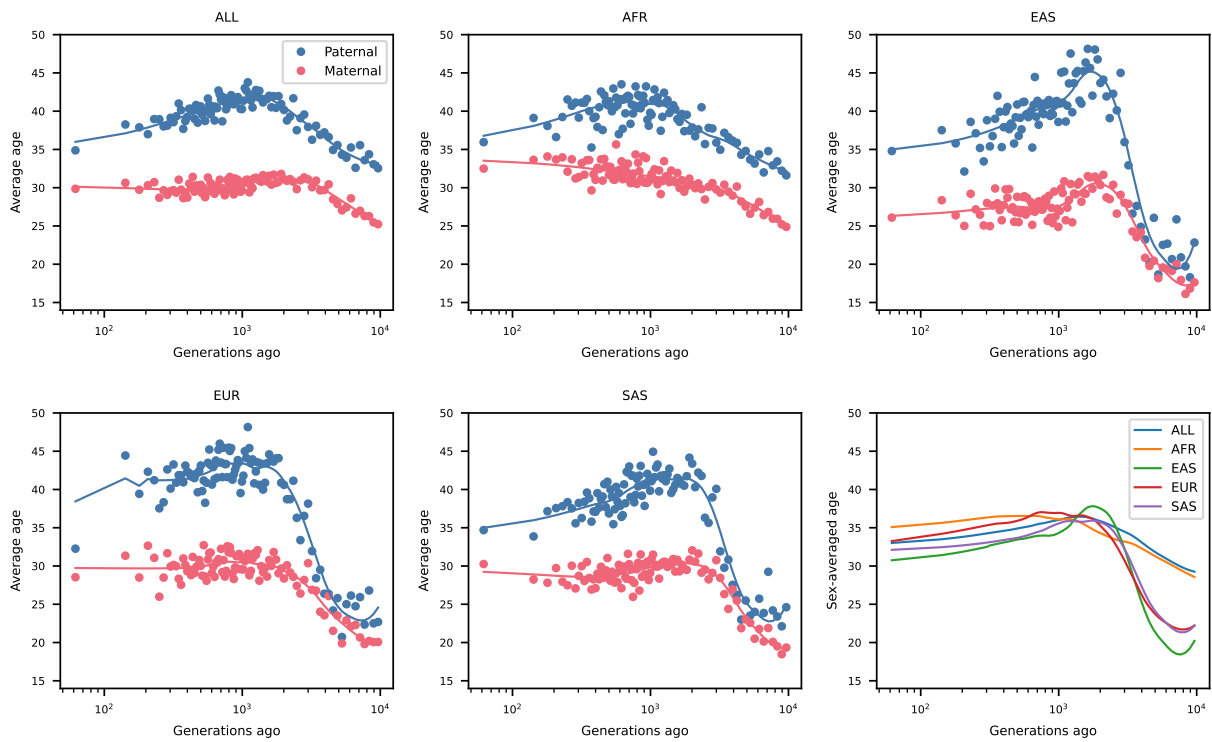


Figure S10: tsdate-inferred generation time histories.

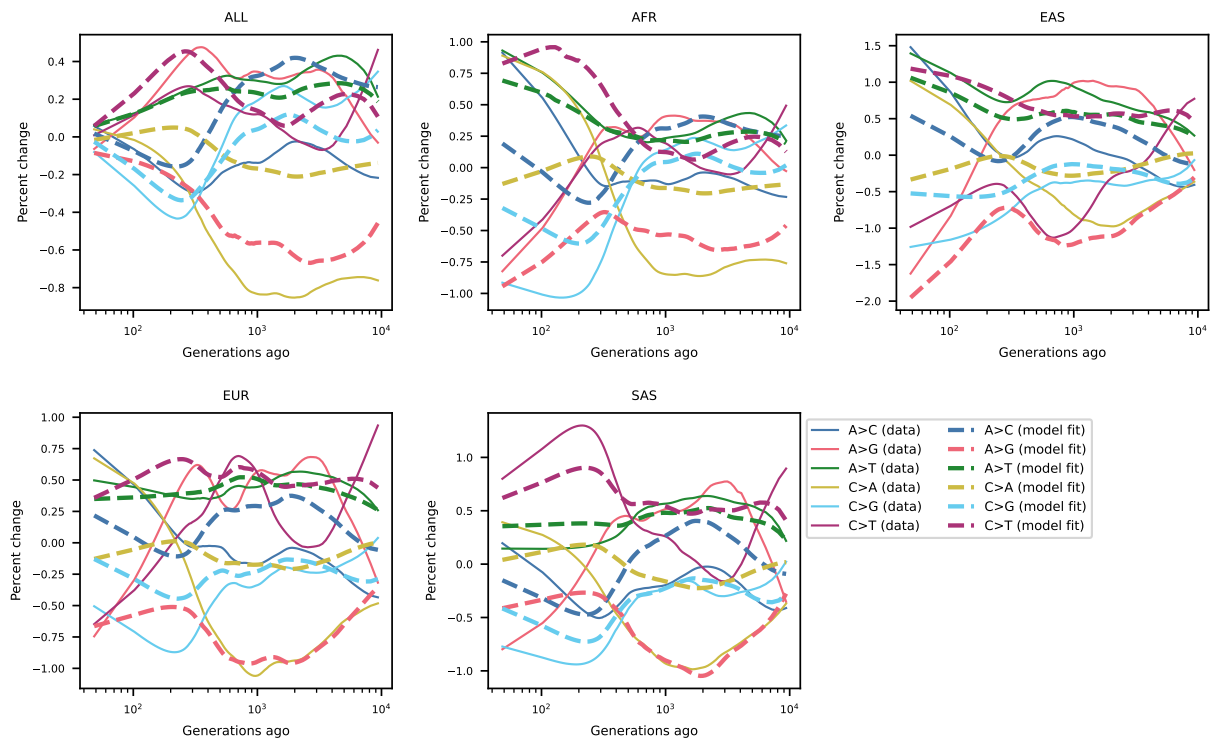


Figure S11: Prediction of mutation spectrum history from GEVA-inferred generation times.

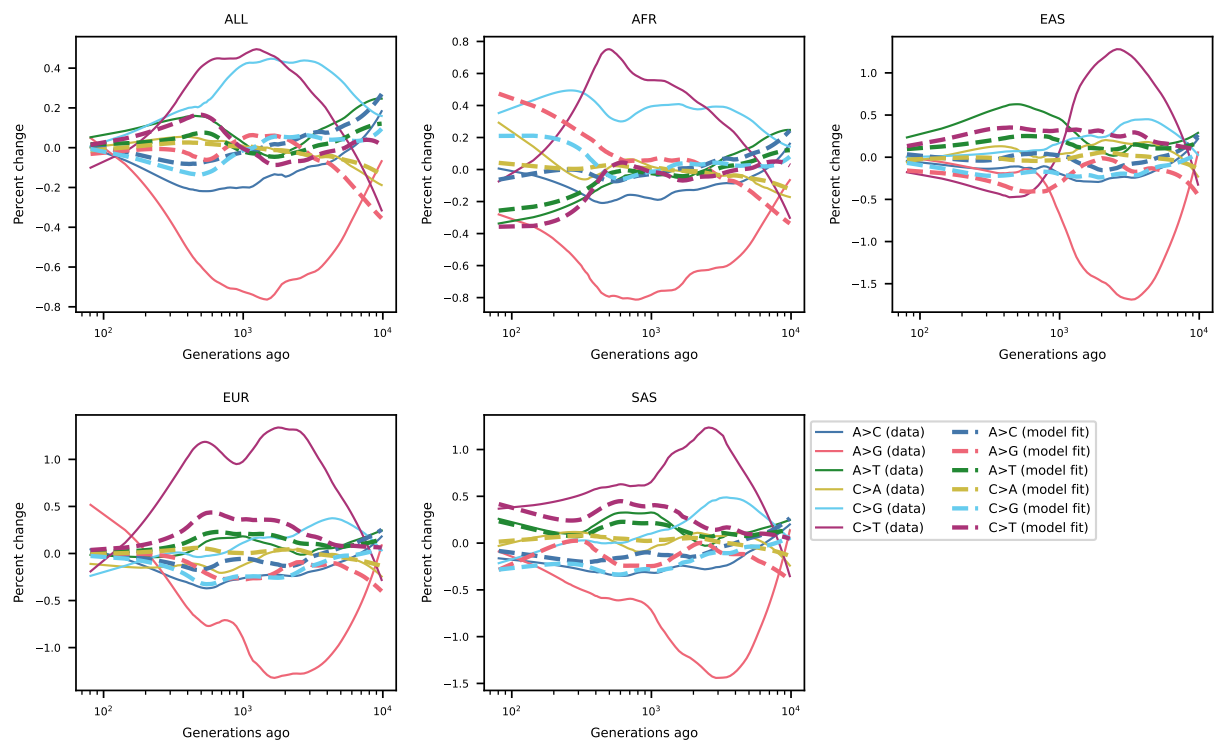


Figure S12: **Prediction of mutation spectrum history from Relate-inferred generation times.**

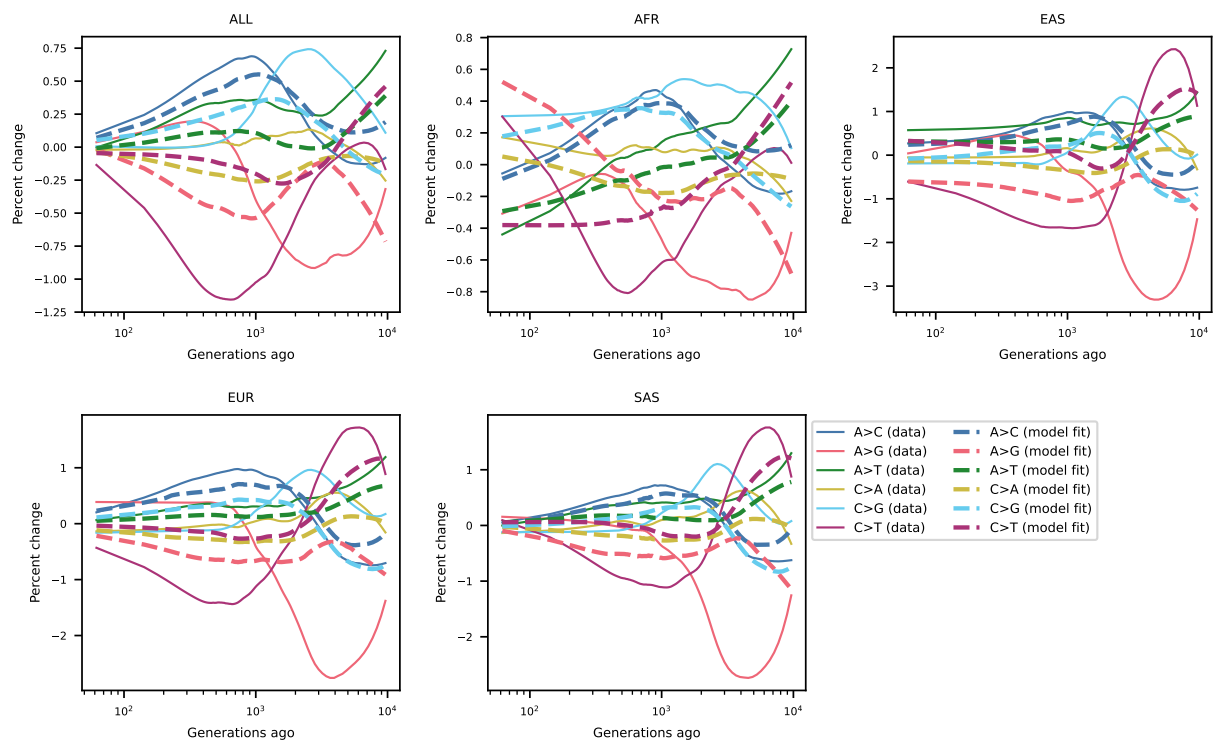


Figure S13: **Prediction of mutation spectrum history from *tsdate*-inferred generation times.**