Table S10: Root mean squared error (RMSE) and mean absolute error (MAE) values when predicting selection coefficient (s), initial frequency (f), and time of selection (T_{sel}) for CEU populations when trained and tested with simulations sampling $n = 20$, 50, or 200 haploid genomes. The values show RMSE and MAE measured between standardized log-scaled predicted and actual parameters.

Number of haploids (n)	RMSE(s)	RMSE(f)	RMSE(T_{sel})	MAE(s)	MAE(f)	MAE(T_{sel})
20	1.00	1.04	0.74	0.82	0.89	0.63
50	0.93	1.01	0.69	0.80	0.83	0.55
200	0.89	0.94	0.67	0.71	0.80	0.54