

CORRECTION

Correction: Predicting Carriers of Ongoing Selective Sweeps without Knowledge of the Favored Allele

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In panel B of [Fig 1](#), the two haplotypes on the right have incorrect scores of 17. The correct scores of these haplotypes are 18. Please view the correct [Fig 1](#) here.



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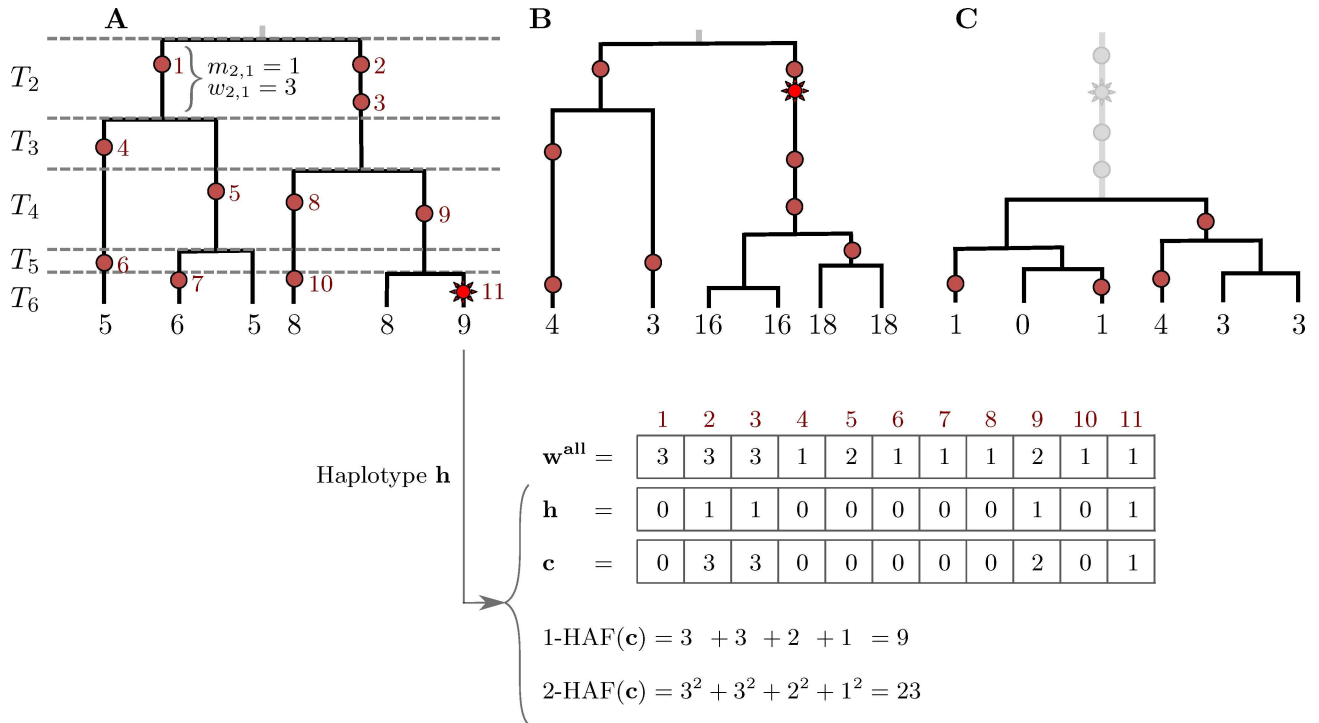


Fig 1. The HAF score. Genealogies of three samples ($n = 6$) progressing through a selective sweep, from left to right. Neutral mutations are shown as red circles, and are numbered in red; the favored allele is shown as a red star. The 1-HAF score of each haplotype is shown below its corresponding leaf, in black. For the rightmost haplotype in (A), the binary haplotype vector h is shown along with its HAF-vector c , and 1-HAF and 2-HAF scores. Vector w^{all} lists the frequencies of all mutations. (A) The favored allele appears on a single haplotype. At this point in time, both the genealogy and the HAF score distribution are largely neutral. Coalescence times (T_2, \dots, T_6) are shown on the left, where T_k spans the epoch with exactly k lineages. (B) Carriers of the favored allele are distinguished by high HAF scores (in large part due to the long branch of high-frequency hitchhiking variation); non-carriers have low HAF scores. (C) After fixation, there is a sharp loss of diversity causing low HAF scores across the sample.

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Reference

- Ronen R, Tesler G, Akbari A, Zakov S, Rosenberg NA, Bafna V (2015) Predicting Carriers of Ongoing Selective Sweeps without Knowledge of the Favored Allele. *PLoS Genet* 11(9): e1005527. doi:10.1371/journal.pgen.1005527 PMID: 26402243