Figure S4: Comparison of the true weight $w(x) = (1-x)^n - (1-x)^N$ used in the infinite-genome expression (2) for the number of missed variants (thick solid line) to the jackknife approximate weights (with jackknife order indicated by the number of dashes). From top to bottom, we consider extrapolations from 100 to 200, 100 to 400, and 100 to 1000 chromosome. For twofold extrapolation, the third-order weight is a good approximation to the exact weight and the jackknife will be accurate independent of the underlying allele frequency distribution $\Phi(f)$, whereas for 10-fold extrapolation, the accuracy of the results will depend much more on the cancellation of errors, in the integral of Eq. (2), making results sensitive to model assumptions.