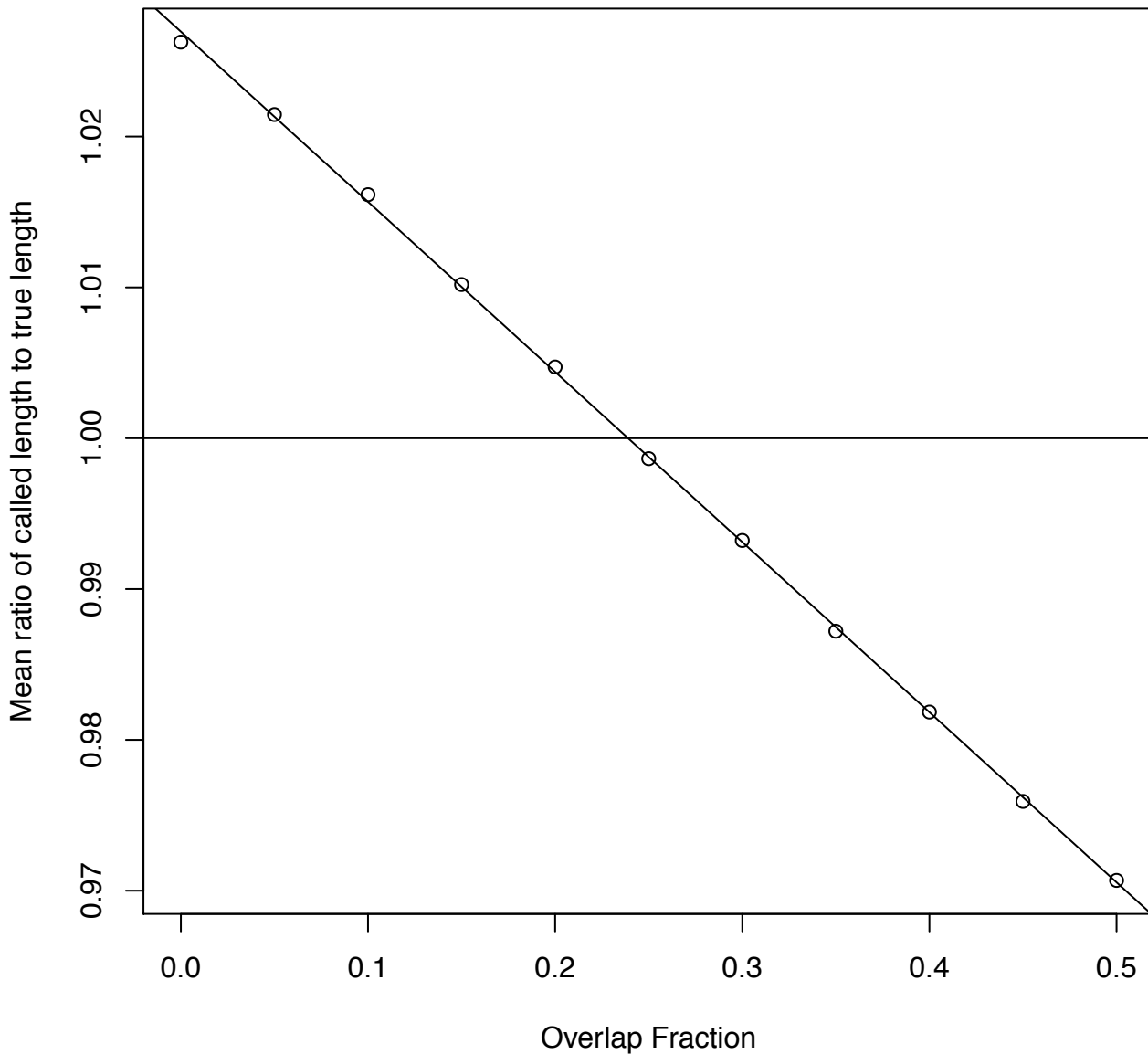
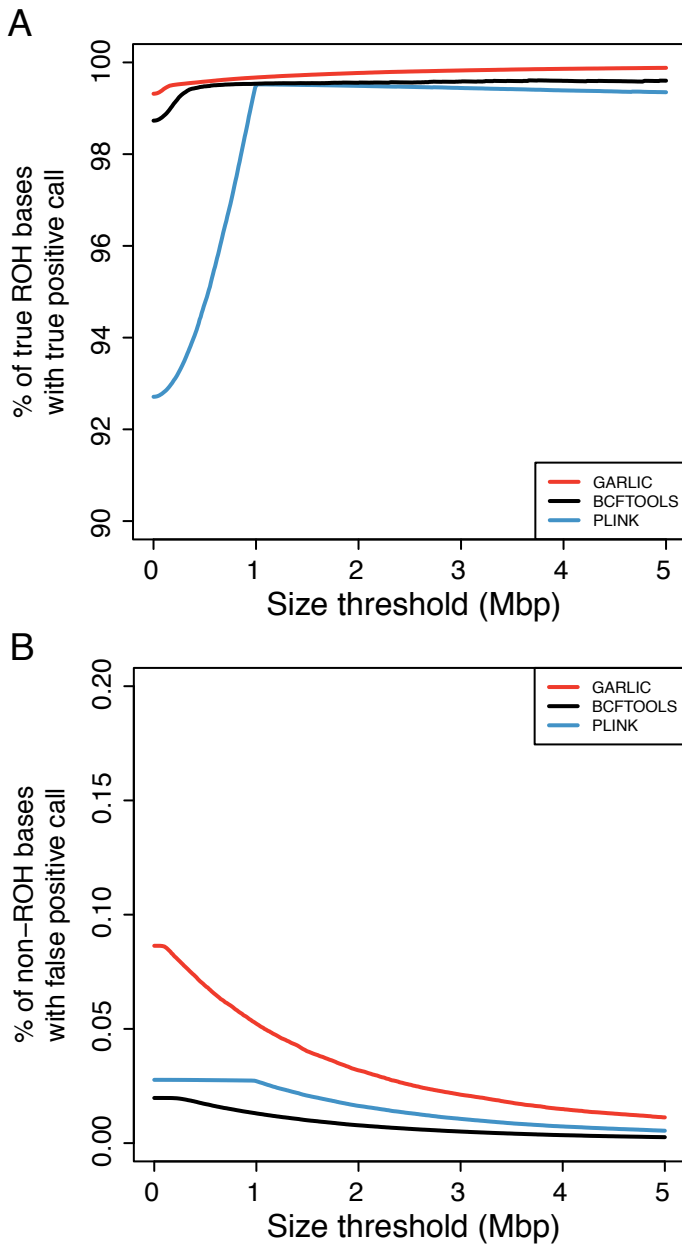


Figure S1. GARLIC pipeline schematic.



**Figure S2. Identification of default value for the overlap fraction parameter.**

Here we plot the mean of the ratio of called ROH length to true length for all simulated ROH as a function of the “overlap fraction” parameter, which controls the minimum fraction of high-scoring windows covering a site required to be included in an ROH call. Ratios above 1 indicate a tendency to over-call a region by falsely including non-autozygous regions near the boundaries of a call. Ratios below 1 indicate a tendency to under-call a region by falsely excluding true autozygous regions near the boundaries of a call. We choose a default parameter value of 0.25, as this is closest to 1. This parameter can be changed with the `--overlap-frac` flag.



**Figure S3. Evaluation of GARLIC performance.**

Here we plot the mean across 100 replicates of **(A)** the percentage of true positive base pair calls, **(B)** the percentage of false positive base pair calls as a function of the minimum size threshold. For a given size threshold true ROH are only included in a calculation if they are at least as large as the threshold. As *PLINK* does not report ROH < 1 Mbp, performance suffers substantially up to that point.

**Table S1. Probability model for genotypes under autozygosity and non-autozygosity.**

Observed genotype $G_k$	$\Pr [G_{j,k} X_k = 1]$	$\Pr [G_{j,k} X_k = 0]$
$AA$	$(1 - \varepsilon)p_A + \varepsilon p_A^2$	$p_A^2$
$AB$	$2\varepsilon p_A p_B$	$2p_A p_B$
$BB$	$(1 - \varepsilon)p_B + \varepsilon p_B^2$	$p_B^2$
Missing	1	1

Per-genotype likelihoods are as previously reported by (Broman and Weber, 1999; Wang, et al., 2009).