

CLEAR: Composition of Likelihoods for Evolve And Resequencing Experiments

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Abstract

The advent of next generation sequencing technologies has made whole-genome and whole-population sampling possible, even for eukaryotic organisms. With this development, experimental evolution studies can be designed to observe molecular evolution “in-action” by Evolving-and-Resequencing (E&R) populations. Among other applications, E&R studies can be used to locate the genes and variants responsible for genetic adaptation. To analyze E&R datasets, majority of the existing literature on time-series data analysis, is mainly devoted to the settings with large population sizes, allele frequency as input data and wide time spans, these assumptions does not hold in many E&R studies.

In this article, we propose a method, Composition of Likelihoods for Evolve-And-Resequencing experiments (CLEAR), to identify selection in short-term (as well as long-term), E&R of *small* sexual populations. CLEAR takes whole-genome sequence of pool of individuals (pool-seq) as input, and properly addresses heterogeneous ascertainment bias, due to uneven coverages. CLEAR also provides unbiased estimates of model parameters, including selection strength and over-dominance, and population size, while being computationally efficient. Extensive simulations show that CLEAR achieves higher power in detecting and localizing selection over a wide range of parameters. Moreover, we show CLEAR statistic is robust to variation of coverage. We applied CLEAR statistic to previously published datasets, including, data from a study of *D. melanogaster* adaptation to alternating temperatures and study of outcrossing Yeast populations. Result XXXX

1 Introduction

Natural selection is a key force in evolution, and a mechanism by which populations can adapt to external ‘selection’ constraints. Examples of adaptation abound in the natural world [27], including for example, classic examples like lactose tolerance in Northern Europeans [12], human adaptation to high altitudes [72, 89], but also drug resistance in pests [19], HIV [30], cancer [35, 90], malarial parasite [5, 56], and other antibiotic resistance [73]. In these examples, understanding the genetic basis of adaptation can provide actionable information, underscoring the importance of the problem.

Experimental evolution refers to the study of the evolutionary processes of a model organism in a controlled [9, 14, 37, 47, 48, 59, 60] or natural [7, 11, 20, 21, 52, 65, 88] environment. Recent advances in whole genome sequencing have enabled us to sequence populations at a reasonable cost even for large genomes. Perhaps more important for experimental evolution studies, we can now evolve and resequence (E&R) multiple replicates of a population to obtain *longitudinal time-series data*, in order to investigate the dynamics of evolution at molecular level. Although constraints

such as small sizes, limited timescales, and oversimplified laboratory environments may limit the interpretation of E&R results, these studies are increasingly being used to test a wide range of hypotheses [44] and have been shown to be more predictive than static data analysis [16, 22, 69]. In particular, longitudinal E&R data is being used to estimate model parameters including population size [43, 62, 78, 83, 84, 86], strength of selection [15, 39, 40, 51, 54, 74, 78], allele age [51] recombination rate [78], mutation rate [8, 78], quantitative trait loci [6] and for tests of neutrality hypotheses [11, 17, 29, 78].

While objectives, designs and organisms of E&R studies can be entirely different [8, 70], here we restrict our attention to the adaptive evolution of multi-cellular sexual organisms. For simplicity, we assume fixed population size, and for the most part, positive single locus selection (only one favored mutation). This regime has been considered earlier, typically with *D. melanogaster* as the model organism of choice, to identify adaptive genes in longevity and aging [17, 66] (600 generations), courtship song [81] (100 generations), hypoxia tolerance [91] (200 generations), adaptation to new laboratory environments [32, 59] (59 generations), egg size [42] (40 generations), C virus resistance [53] (20 generations), and dark-fly [41] (49 generations).

The task of identifying genetic adaptation can be addressed at different levels of specificity. At the coarsest level, identification could simply refer to deciding whether some genomic region (or a gene) is under selection or not. In the following, we refer to this task as *detection*. In contrast, the task of *site-identification* corresponds to the process of finding the favored mutation/allele at nucleotide level. Finally, *estimation of model parameters*, such as strength of selection and overdominance at the site, can provide a comprehensive description of the selection process.

In an effort for analyzing E&R selection experiments many authors chose to adopt existing tests that originally used for static data, for scanning dynamic data with two time-points. For instance, Zhu *et al.* [91] used the ratio of the estimated population size of case and control populations to compute test statistic for each genomic region. Burke *et al.* [17] applied Fisher exact test to the last observation of data on case and control populations. Orozco-terWengel *et al.* [59] used the Cochran-Mantel-Haenszel (CMH) test [2] to detect SNPs whose read counts change consistently across all replicates of two time-point data. Turner *et al.* [81] proposed the diffStat statistic to test whether the change in allele frequencies of two populations deviate from the distribution of change in allele frequencies of two drifting populations. Bergland *et al.* [11] applied F_{st} to populations throughout time to signify their differentiation from ancestral (two time-point data) as well as geographically different populations. Jha *et al.* [42] computed test statistic of generalized linear-mixed model directly from read counts.

Early *direct* methods for analyzing time-series data devoted to estimate population size in neutral populations [4, 10, 13, 83, 86], using statistical (HMM) and population genetics (Coalescent) models. The first effort to properly address the problem of parameter estimation in time series selection data was done by Bollback *et al.* [15]. They provided a diffusion approximation to the continuous Wright Fisher Markov process and estimated s numerically for large population sizes. Malaspina *et al.* [51] extended Bollback *et al.*'s method to estimate allele age in ancient-DNA (aDNA). Steinrücken and Song [74] proposed a general diploid selection model which takes into account of dominance of the favored allele and approximates likelihood analytically. Mathieson and McVean [54] adopted HMMs to structured populations and estimated parameters using an Expectation Maximization (EM) procedure, on discretized allele frequency. Feder *et al.* [29] modeled increments in allele frequency with a Brownian motion process, proposed the Frequency Increment Test (FIT). More recently, Topa *et al.* [80] proposed a Gaussian Process (GP) for modeling single-locus time-series pool-seq data. Terhorst *et al.* [78] extended GP to compute joint likelihood of multiple loci under null and alternative hypotheses. Recently, Schraiber *et al.* [71] proposed a Bayesian framework to estimate parameters using Monte Carlo Markov chain sampling.

While existing methods have been successfully applied to their corresponding application, they make several key assumptions which does not hold in many of E&R studies. First, they assume that the underlying population size is large, if not infinity, (See Table 3 in [50] for illustration). As a result, they provide continuous state models for dynamics of allele frequencies. In addition, most these methods, originally designed to process wide time spans, i.e. aDNA studies. Also, they assume input data is allele frequency or at least is *sampled* allele frequency, where ascertainment bias is uniform along genome.

This manuscript, explicitly posits a “small-population-size” assumption on Williamson *et al.* [86] and Bollback *et al.*’s model [15], and as a consequence, the resulting model become a discrete state (frequency) model. We show that for small population sizes discrete models can compute likelihood exactly, which make a difference in the statistical performance, especially in short term experiments. Additionally, we add another level of sampling-noise to the traditional HMM, which models heterogeneous ascertainment bias due to uneven coverages among variants. We show for a wide range of parameters that CLEAR provides higher power for detecting selection, is robust to ascertainment bias due to coverage heterogeneity, estimates model parameters consistently, and localizes favored allele more accurately compared to the state-of-the-art methods, while being computationally efficient.

2 Materials and Methods

To identify the genes and variants that are responding to the selection pressure, we consider the following statistical procedure:

- (i) **Estimating population size.** The procedure starts by finding the maximum likelihood estimate of population size, \hat{N} , over the whole genome.
- (ii) **Estimating selection parameters.** Given \hat{N} , maximizing the likelihood of the time series data w.r.t. selection and overdominance parameters s, h , for each polymorphism.
- (iii) **Computing likelihood statistics.** For each variant, it calculates the log-odds ratio of the likelihood of selection model to the likelihood of neutral evolution/drift model. Likelihood ratios in a genomic region are combined to compute the CLEAR statistic.
- (iv) **Hypothesis testing.** The null distribution of the CLEAR (or likelihood ratio) statistics are computed on a set of whole-genome (single locus, respectively) drift simulations with population size of \hat{N} , and variant starting frequency and coverage of the experimental data. Given the null distribution of statistics, p -values and corresponding False Discovery Rate (FDR) are calculated. The overlapping genes with the regions (or variants) that satisfy FDR criterion, will be reported for functional analysis or imported to the Gene Set Enrichment Analysis (GSEA).

In the subsequent of this section, we outline different steps of the statistical procedure.

2.1 Estimating Population Size

Estimating population sizes from temporal neutral evolution data has been previously studied [4, 15, 43, 78, 86]. Existing methods are well designed for when the allele frequencies are computed from a finite sample, that is the ascertainment bias is uniform over the genome. However, in the case of pool-seq data in addition to uniform ascertainment bias, each variant is sampled at different rate, due to finite sequencing coverage. In addition, bulk of existing models [15, 29, 78, 80] are designed

for large populations, and model frequency as a continuous quantity. However, we show that smooth approximations is inadequate for small populations, low starting frequencies and sparse sampling (in time) that are typical in experimental evolution (see Results, Fig 3A-C, and Fig 2). To this end, we model Wright-Fisher Markov process for generating pool-seq data (S1 Fig) via a *discrete* HMM, Fig 1-B. In order to find an estimate of population size, we first need to find likelihood of the population size given neutral pool-seq data.

Likelihood for Neutral Model. Consider a neutrally evolving diploid population with fixed size of N individuals where ν_t denotes allele frequency of the derived allele at generation t . Experimental evolution for R replicates is conducted so that at generations $\mathcal{T} = \{\tau_i : 0 \leq \tau_0 < \tau_1, \dots < \tau_T\}$, n individuals are chosen for sequencing.

At the highest level, the consecutive allele frequencies of the population in a fixed-size Wright-Fisher model evolves by Binomial sampling

$$\nu_0 \sim \pi, \quad 2N\nu_t | \nu_{t-1} \sim \text{Binomial}(2N, \nu_{t-1}) \quad (1)$$

where π is the global (marginal) distribution of allele frequencies in the base population. In general, π depends on demographic history of the founder lines. Here we simply assume π is the site frequency spectrum of fixed sized neutral population S2 Fig.

To compute distributions after τ transitions, it is enough to specify the $2N \times 2N$ transition matrix $P^{(\tau)}$, where $P^{(\tau)}[i, j]$ denotes probability of change in allele frequency from $i/2N$ to $j/2N$ in τ generations:

$$P^{(1)}[i, j] = \Pr\left(\nu_{t+1} = \frac{j}{2N} \mid \nu_t = \frac{i}{2N}\right) = \binom{2N}{j} \nu_t^j (1 - \nu_t)^{2N-j}, \quad (2)$$

$$P^{(\tau)} = P^{(\tau-1)} P^{(1)} \quad (3)$$

As at each generation n out of N individuals are randomly selected for sequencing. The sampled allele frequencies, $\{y_t\}_{t \in \mathcal{T}}$, are also Binomially distributed

$$2ny_t \sim \text{Binomial}(2n, \nu_t) \quad (4)$$

We introduce the $2N \times 2n$ sampling matrix Y , where $Y[i, j]$ stores the probability that the sample allele frequency is $i/2n$ given that the true allele frequency is $j/2N$.

We denote the pool-seq data for that variant as $\{x_t = \langle c_t, d_t \rangle\}_{t \in \mathcal{T}}$ where d_t, c_t represent the read depth, and the read count of the derived allele, respectively, at time τ_t . Let $\{\lambda_t\}_{t \in \mathcal{T}}$ be the sequencing coverage at different generations, then, the observed data are sampled according to

$$d_t \sim \text{Poisson}(\lambda_t), \quad c_t \sim \text{Binomial}(d_t, y_t) \quad (5)$$

where the emission probabilities for a observed tuple $x_t = \langle d_t, c_t \rangle$ is

$$\mathbf{e}_i(x_t) = \binom{d_t}{c_t} \left(\frac{i}{2n}\right)^{c_t} \left(1 - \frac{i}{2n}\right)^{d_t - c_t}. \quad (6)$$

For $1 \leq t \leq T$, let $\alpha_{t,i}$ denote the probability of emitting x_1, x_2, \dots, x_t and reaching state i at τ_t . Then, $\alpha_{t,i}$ can be computed using the forward-procedure [23]:

$$\begin{aligned} \alpha_{t,i} &= \left(\sum_{1 \leq j \leq 2N} \alpha_{t-1,j} P^{(\delta_t)}[j, i] \right) Y \mathbf{e}_i(x_t) \\ \alpha_t &= \text{Diag}(\alpha_{t-1}) P^{(\delta_t)} Y \mathbf{e}(x_t) \end{aligned} \quad (7)$$

where $\delta_t = \tau_t - \tau_{t-1}$. The joint likelihood of the observed data from R independent observations is given by

$$\Pr(\{\mathbf{x}^{(r)}\}|N, n) = \mathcal{L}(N|\{\mathbf{x}^{(r)}\}, n) = \prod_{r=1}^R \mathcal{L}(N|\mathbf{x}^{(r)}, n) = \prod_{r=1}^R \sum_i \alpha_{T,i}^{(r)} \quad (8)$$

where $\mathbf{x} = \{x_t\}_{t \in \mathcal{T}}$. The graphical model and the generative process for which data is being generated is depicted in Fig 1-B and S1 Fig, respectively.

Finally, the last step is to find the \hat{N} in which maximizes the likelihood of the all the M variants in whole genome:

$$\hat{N} = \arg \max_N \prod_i^M \mathcal{L}(N|\{\mathbf{x}_i^{(r)}\}) \quad (9)$$

2.2 Estimating Selection Parameters

Likelihood for Selection Model. Assume that the site is evolving under selection constraints $s \in \mathbb{R}$, $h \in \mathbb{R}_+$, where s and h denote selection strength and overdominance parameters, respectively. By definition, the relative fitness values of genotypes 0|0, 0|1 and 1|1 are given by $w_{00} = 1$, $w_{01} = 1 + hs$ and $w_{11} = 1 + s$. Recall that ν_t denotes the frequency of the site at time $\tau_t \in \mathcal{T}$. Then, ν_{t+} , the frequency at time $\tau_t + 1$ (one generation ahead), can be estimated using:

$$\begin{aligned} \hat{\nu}_{t+} &= \mathbb{E}[\nu_{t+}|s, h, \nu_t] = \frac{w_{11}\nu_t^2 + w_{01}\nu_t(1 - \nu_t)}{w_{11}\nu_t^2 + 2w_{01}\nu_t(1 - \nu_t) + w_{00}(1 - \nu_t)^2} \\ &= \nu_t + \frac{s(h + (1 - 2h)\nu_t)\nu_t(1 - \nu_t)}{1 + s\nu_t(2h + (1 - 2h)\nu_t)}. \end{aligned} \quad (10)$$

The machinery for computing likelihood of the selection parameters is identical to that of population size, except for transition matrices. Hence, here we only describe the definition transition matrix $Q_{s,h}$ of the selection model. Let $Q_{s,h}^{(\tau)}[i, j]$ denote the probability of transition from $i/2N$ to $j/2N$ in τ generations, then (See [25], Pg. 24, Eqn. 1.58-1.59):

$$Q_{s,h}^{(1)}[i, j] = \Pr\left(\nu_{t+} = \frac{j}{2N} \middle| \nu_t = \frac{i}{2N}; s, h, N\right) = \binom{2N}{j} \hat{\nu}_{t+}^j (1 - \hat{\nu}_{t+})^{2N-j} \quad (11)$$

$$Q_{s,h}^{(\tau)} = Q_{s,h}^{(\tau-1)} Q_{s,h}^{(1)} \quad (12)$$

The maximum likelihood estimates are given by

$$\hat{s}, \hat{h} = \arg \max_{s, h} \prod_i^M \mathcal{L}(s, h|\{\mathbf{x}_i^{(r)}, \hat{N}\}) \quad (13)$$

The parameters in Eqs. 9, 13 are optimized using grid search. By broadcasting and vectorizing the grid search operations across all variants, the genome scan on millions of polymorphisms can be done in significantly smaller time than iterating a numerical optimization routine for each variant (see Results and Fig 4).

2.3 Empirical Likelihood Ratio Statistics

The likelihood ratio statistic for testing directional selection, to be computed for each variant, is given by

$$H = -2 \log \left(\frac{\mathcal{L}(\hat{s}, 0.5|\{\mathbf{x}^{(r)}, \hat{N}\})}{\mathcal{L}(0, 0.5|\{\mathbf{x}^{(r)}, \hat{N}\})} \right) \quad (14)$$

Similarly we can define test statistic for testing if selection is over-dominant

$$D = -2 \log \left(\frac{\mathcal{L}(\hat{s}, \hat{h} | \{\mathbf{x}^{(r)}\}, \hat{N})}{\mathcal{L}(\bar{s}, 0.5 | \{\mathbf{x}^{(r)}\}, \hat{N})} \right), \text{ where } \bar{s} = \arg \max_s \prod_i^M \mathcal{L}(s, 0.5 | \{\mathbf{x}_i^{(r)}\}, \hat{N}). \quad (15)$$

While extending the single-locus WF model to a multiple linked-loci can improve the power of the model [78], it is computationally and statistically expensive to compute exact likelihood. haplotype resolved data, which pool-seq does not provide. Instead, similar to Nielse *et al* [58], we calculate Composite Likelihood Ratio score for a genomic region.

$$\mathcal{H} = \frac{1}{|L|} \sum_{\ell \in L} H_{\ell}. \quad (16)$$

where L to be a collection of segregating sites and H_{ℓ} is the likelihood ratio score based for each variant ℓ in L . The optimal value of the hyper-parameter L depends upon a number of factors, including, initial frequency of the favored allele, recombination rates, initial linkage of the favored allele to its surrounding variation, population size, coverage, and time since the onset of selection (duration of the experiment). However, we provide a heuristic choose size of L for an experiment.

In general, as selection acts locally in the genome, size of L have a direct effect on the power. For instance, when L is chosen to be a large region (e.g. chromosome), power will be degraded since distribution of null and alternative \mathcal{H} statistics converge together. Hence, we choose L to be the largest, such that it provides enough discoveries that satisfies experiment's FDR.

2.4 Hypothesis Testing

Single-Locus. Under neutrality, Wilkss theorem [85] states that $H \sim \mathcal{X}_1^2$, asymptotically, and p -values can be computed directly. However, Feder *et al.* [29] showed that when the number of independent samples (replicates) is small, \mathcal{X}^2 is a crude approximation to the true null distribution and underestimates FDR. They suggested to compute p -values based on the empirical distribution of statistic on simulations with \hat{N} . Here, take the same approach and conduct single locus drift simulations starting from initial frequencies of the experimental data. Then we sample read counts of the derived allele given coverage and allele frequency, see S1 Fig for step-by-step procedure. Test statistic is then computed for simulated drifting pool-seq data and p -value of an experimental samples is computed as fraction of null statistics that have a higher or equal value than testing statistic. Finally, we use Storey and Tibshirani's method [76], to control for False Discovery Rate in multiple testing.

Regions. To compute null distribution of \mathcal{H} one should compute \mathcal{H} on a set of neutral genome-wide neutral simulations. Also, as selection is expected to have local effect on the genome, we normalize \mathcal{H} with respect to each chromosome both in simulated and experimental data in computing p -values:

$$\mathcal{H}_i^* = \frac{\mathcal{H}_i - \mu_C}{\sigma_C}, \quad \forall i \in \mathcal{C} \quad (17)$$

where μ_C and σ_C are the chromosome-wise mean and standard deviation. p -values and FDR can be computed in the same regime as single locus. After discovering intervals that satisfy FDR requirement, we further select those variants within selected intervals that their individual score H is significantly using single locus hypothesis testing and then find the intersecting genes accordingly.

2.5 Simulations

We performed extensive simulations using parameters that have been used for *D. melanogaster* experimental evolution [46]. See also Fig 1-A for illustration. To implement real world pool-seq experimental evolution, we conducted simulations as follows:

I. Creating initial founder line haplotypes. Using `msms` [26], we created neutral populations for F founding haplotypes with command `$. /msms <F> 1 -t <2μLNe> -r <2rNeL> <L>`, where $F = 200$ is number of founder lines, $N_e = 10^6$ is effective population size, $r = 2 \times 10^{-8}$ is recombination rate, $\mu = 2 \times 10^{-9}$ is mutation rate and $L = 50K$ is the window size in base pairs which gives $\theta = 2\mu N_e L = 200$ and $\rho = 2N_e r L = 2000$.

II. Creating initial diploid population. To simulate experimental evolution of diploid organisms, initial haplotypes were first cloned to create F diploid homozygotes. Next, each diploid individual was cloned N/F times to yield diploid population of size N .

III. Forward Simulation. We used forward simulations for evolving populations under selection. We also consider selection regimes which the favored allele is chosen from standing variation (not *de novo* mutations). Given initial diploid population, position of the site under selection, selection strength s , number of replicates $R = 3$, recombination rate $r = 2 \times 10^{-8}$ and sampling times $\mathcal{T} = \{0, 10, 20, 30, 40, 50\}$, `simuPop` [61] was used to perform forward simulation and compute allele frequencies for all of the R replicates. For hard sweep (respectively, soft sweep) simulations we randomly chose a site with initial frequency of $\nu_0 = 0.005$ (respectively, $\nu_0 = 0.1$) to be the favored allele.

IV. Sequencing Simulation. Give allele frequency trajectories we sampled depth of each site identically and independently from $\text{Poisson}(\lambda)$, where $\lambda \in \{30, 100, 300\}$ is the coverage for the experiment. Once depth d is drawn for the site with frequency ν , the number of reads c carrying the derived allele are sampled according to $\text{Binomial}(d, \nu)$. For experiments with finite depth the tuple $\langle c, d \rangle$ is the input data for each site.

3 Results

Modeling Allele Frequency Trajectories in Small Populations. We first tested the goodness of fit of the discrete versus continuous models in modeling allele frequency trajectories, under general E&R parameters. For this purpose, we conducted 100K simulations with two time samples $\mathcal{T} = \{0, \tau\}$ where $\tau \in \{1, 10, 100\}$ is the parameter controlling the density of sampling in time. In addition, we repeated simulations for different values of starting frequency $\nu_0 \in \{0.005, 0.1\}$ (i.e., hard and soft sweep) and selection strength $s \in \{0, 0.1\}$ (i.e., neutral and selection). Then, given initial frequency ν_0 , we computed the expected distribution of the frequency of the next sample ν_τ under two models and compared them with empirical distributions calculated from simulated data. Fig 2A-F shows that Brownian motion (continuous model) is inadequate when ν_0 is far from 0.5, or when sampling times are sparse ($\tau > 1$). If the favored allele arises from standing variation in a neutral population, it is unlikely to have frequency close to 0.5, and the starting frequencies are usually much smaller (see S2 Fig). Moreover, in typical *D. melanogaster* experiments for example, sampling is sparse. Often, the experiment is designed so that $10 \leq \tau \leq 100$ [32, 46, 59, 91].

In contrast to the Brownian motion results, discrete Markov chain can provide predictions when the allele is under selection. In addition Fig 2A-M also shows that Markov chain predictions (Eq. 12) are highly consistent with empirical data for a wide range of simulation parameters.

Detection Power. We compared the performance of CLEAR against other methods for detecting selection. For each method we calculated detection power as the percentage of true-positives identified with false-positive rate ≤ 0.05 . For each configuration (specified with values for selection coefficient s , starting allele frequency ν_0 and coverage λ), power of each method is evaluated over 2000 distinct simulations, half of which modeled neutral evolution and the rest modeled positive selection.

We compared the power of CLEAR with Gaussian process (GP) [78], FIT [29], and CMH [2] statistics. FIT and GP convert read counts to allele frequencies prior to computing the test statistic. CLEAR shows the highest power in all cases and the power stays relatively high even for low coverage (Fig 3 and S1 Table). In particular, the difference in performance of CLEAR with other methods is pronounced when starting frequency is low. The advantage of CLEAR stems from the fact that favored allele with low starting frequency might be missed by low coverage sequencing. In this case, incorporating the signal from linked sites becomes increasingly important. We note that methods using only two time points, such as CMH, do relatively well for high selection values and high coverage. However, the use of time-series data can increase detection power in low coverage experiments or when starting frequency is low. Moreover, time-series data provide means for estimating selection parameters s, h (see below). Finally, as CLEAR is robust to change of coverage, our results (Fig 3B,C) suggest that taking many samples with lower coverage is preferable to sparse sampling with higher coverage.

Site-identification. In general, localizing the favored variant, using pool-seq data is a nontrivial task [79]. We used the simple approach of ranking each site in a region detected as being under selection. The variants were ranked according to the likelihood ratio scores (Eqn. 14). For each setting of ν_0 and s , we conducted 1000 simulations and computed the rank of the favored mutation in each simulation. The cumulative distribution of the rank of the favored allele in 1000 simulation for each setting (Fig 5) shows that CLEAR outperforms other statistics.

An interesting observation is revisiting the contrast between site-identification and detection [49, 79]. When selection coefficient is high, detection is easier (Fig 3A-F), but site-identification is harder due to the high LD between hitchhiking sites and the favored allele (Fig 5A-F). Moreover, site-identification is harder in hard sweep scenarios relative to soft sweeps. For example, when coverage $\lambda = 100$ and selection coefficient $s = 0.1$, the detection power is 75% for hard sweep, but 100% for soft sweep (Fig 3B-E). In contrast, the favored site was ranked as the top in 14% of hard sweep cases, compared to and 95% of soft sweep simulations.

Estimating Parameters. CLEAR computes the selection parameters \hat{s} and \hat{h} as a byproduct of the hypothesis testing. We computed bias of selection fitness ($s - \hat{s}$) and overdominance ($h - \hat{h}$) for of CLEAR and GP in each setting. The distribution of the error (bias) for $100\times$ coverage is presented in Fig 6 for different configurations. S4 Fig and S5 Fig provide the distribution of estimation errors for $30\times$, and infinite coverage, respectively. For hard sweep, CLEAR provides estimates of s with lower variance of bias (Fig 6A). In soft sweep, GP and CLEAR both provide unbiased estimates with low variance (Fig 6B). Fig 6C-D shows that CLEAR provides unbiased estimates of h as well.

Running Time. As CLEAR does not compute exact likelihood of a region (i.e., does not explicitly model linkage between sites), the complexity of scanning a genome is linear in number of polymorphisms. Calculating score of each variant requires and $\mathcal{O}(TRN^2)$ computation for \mathcal{H} . However, most of the operations are can be vectorized for all replicates to make the effective running time for each variant. We conducted 1000 simulations and measured running times for computing site statistics H , FIT, CMH and GP with different number of linked-loci. Our analysis reveals (Fig 4) that CLEAR is orders of magnitude faster than GP, and comparable to FIT. While slower than

CMH on the time per variant, the actual running times are comparable after vectorization and broadcasting over variants (see below).

These times can have a practical consequence. For instance, to run GP in the single locus mode on the entire pool-seq data of the *D. melanogaster* genome from a small sample (≈ 1.6 M variant sites), it would take 1444 CPU-hours (≈ 1 CPU-month). In contrast, after vectorizing and broadcasting operations for all variants operations using `numba` package, CLEAR took 75 minutes to perform an scan, including precomputation, while the fastest method, CMH, took 17 minutes.

3.1 Analysis of a *D. melanogaster* Adaptation to Cold and Hot Temperatures

We applied CLEAR to the data from a study of *D. melanogaster* adaptation to alternating temperatures [32, 59], where 3 replicate samples were chosen from a population of *D. melanogaster* for 59 generations under alternating 12-hour cycles of hot (28°C) and cold (18°C) temperatures and sequenced. In this dataset, sequencing coverage is different across replicates and generations (see S2 Fig of [78]) which makes variant depths highly heterogeneous (S3 Fig).

We first filtered out heterochromatic, centromeric and telomeric regions [31], and those variant that have collective coverage of more than 1500 in all 13 populations: three replicates at the base population, two replicates at generation 15, one replicate at generation 23, one replicate at generation 27, three replicates at generation 37 and three replicates at generation 59. After filtering, we ended up with 1,605,714 variants.

First we estimated population size $\hat{N} = 250$ over the whole genome, Fig 7. The likelihood curves of CLEAR is sharper around the optimum compared to Bollback et. al [15] (see Supplementary Fig. 1 in [59]). Also, chromosomes 3L and 3R appear to have smaller population size Fig 7-D, $\hat{N} = 200, 150$, respectively. Next, we found maximum likelihood estimates of s , and computed the test statistic \mathcal{H}^* with $N = 250$ on sliding windows of size of 500 SNPs and step size of 100 variants over the genome. We computed null distribution of \mathcal{H}^* by creating 100 chromosome simulations using experimental data parameters and length of 20Mbp. After correcting for multiple testing, only 16 intervals Fig 9 satisfy $\text{FDR} \leq 0.05$, which form 5 contiguous interval ?? covering 3740 polymorphic sites. We then selected the 216 significant variants with $\text{FDR} \leq 0.05$ within selected regions using single locus hypothesis testing. To compute p -values of H statistics, we calculated single locus Wright-Fisher simulations for $\hat{N} = 250$, initial frequencies and variant depths of real data (see S1 Fig). We repeated forward simulations 50 times for whole genome, to collect ≈ 90 M pool-seq trajectories with starting frequencies and coverage of real data. Then, p -value of each variant in the real data is calculated as the fraction of null statistics that are greater than or equal of test statistic (see S8 Fig). The selected 216 variants fall within 33 genes S3 Table. We also performed GO enrichment using `Gowinda` [45] and found 4 enriched GO terms including XXXX, XXXX ??.

Finally, we tested if variants showing signal of overdominance, we computed D statistic on simulated and experimental data, and computed p -values accordingly. After correcting for multiple testing, 96 variants discovered with $\text{FDR} \leq 0.01$ Fig 8.

Here is UCSC track for this data.

3.2 Analysis of Outcrossing Yeast Populations

We also applied CLEAR to outcrossing Yeast populations [18], with 12 replicates where samples are taken at generations $\mathcal{T} = \{0, 180, 360, 540\}$. While this experiment is being conducted with larger set of replicates, population size, and number of generations, it appears that a number of replicates undergoing severe demographic events S9 Fig. Hence we chose seven replicates $r \in$

{3, 7, 8, 9, 10, 11, 12} that exhibit consistent genome-wide site-frequency spectrum over the whole experiment [S10 Fig](#).

We estimated population size to be $\hat{N} = 2000$ haplotypes, and computed \hat{s} , \hat{h} and H statistic accordingly. To compute p -values, we created 1M single-locus neutral simulations according to experimental data's initial frequency and coverage. By setting FDR cutoff to 0.05, only 18 and 16 variants show significant signal for directional and overdominant selection, respectively, see [Fig 8](#).

Here is [UCSC track](#) for this data.

4 Discussion

We developed a computational tool, CLEAR, that can detect regions and variants under selection E&R experiments of sexual populations. Using extensive simulations, we show that CLEAR outperforms existing methods in detecting selection, locating the favored allele, and estimating selection parameters. Also, while being computationally efficient, CLEAR provide means for estimating populations size and hypothesis testing.

Many factors such as small population size, finite coverage, linkage disequilibrium, finite sampling for sequencing, duration of the experiment and the small number of replicates can limit the power of tools for analyzing E&R. Here, by a discrete modeling, CLEAR estimates population size, and provides unbiased estimates of s, h . It adjusts for uniform and heterogeneous ascertainment bias of pooled-seq data, and exploits presence of high linkage within a region to compute composite likelihood ratio statistic.

It should be noted that, even though we outlined CLEAR for small populations for small and fixed N , it can be adjusted for such scenarios. For instance, for a *known* changing population sizes, transition probabilities can be readily computed. For large populations, transitions can be computed for a fixed size of frequencies.

The comparison of hard and soft sweep scenarios showed that initial frequency of the favored allele can have a nontrivial effect on the statistical power for identifying selection. Interestingly, while in stronger selections it is easier to detect regions of selection, it is difficult to locate favored allele in those regions.

There are many directions to improve the analyses presented here. In particular, we plan to focus our attention on other organisms with more complex life cycles, experiments with variable population size and longer sampling-time-spans. As evolve and resequencing experiments continue to grow, deeper insights into adaptation will go hand in hand with improved computational analysis.

Software and Data Availability. The source code and running scripts for CLEAR are publicly available at <https://github.com/bafnalab/clear>.

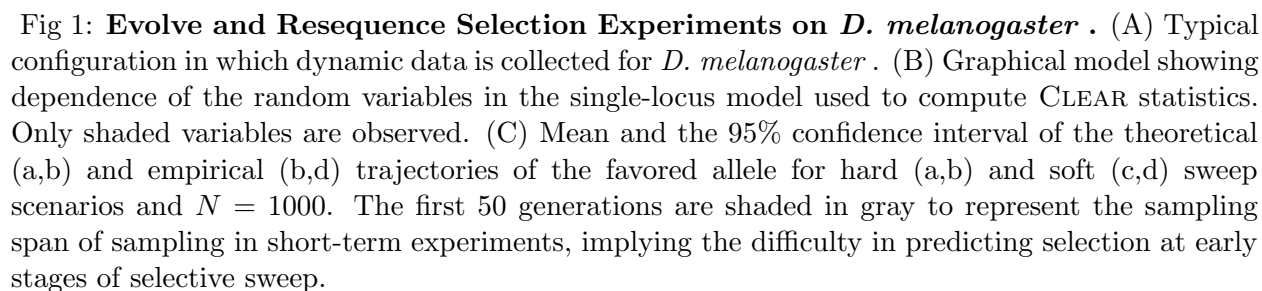
D. melanogaster data originally published [32, 59]. The dataset of the *D. melanogaster* study, until generation 37, is obtained from Dryad digital repository (<http://datadryad.org>) under accession DOI: [10.5061/dryad.60k68](https://doi.org/10.5061/dryad.60k68). Generation 59 of the *D. melanogaster* study is accessed from European Sequence Read Archive (<http://www.ebi.ac.uk/ena/>) under the project accession number: PRJEB6340. The dataset containing experimental evolution of Yeast populations [18] is downloaded from <http://wfitch.bio.uci.edu/~tdlong/PapersRawData/BurkeYeast.gz> (last accessed 01/24/2017). UCSC browser tracks for *D. melanogaster* and Yeast data analysis are found in Suppl. Data 1 and 2, respectively.

Acknowledgments

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Conflict of interest

VB is a co-founder, has an equity interest, and receives income from Digital Proteomics, LLC (DP). The terms of this arrangement have been reviewed and approved by the University of California, San Diego in accordance with its conflict of interest policies. DP was not involved in the research presented here.



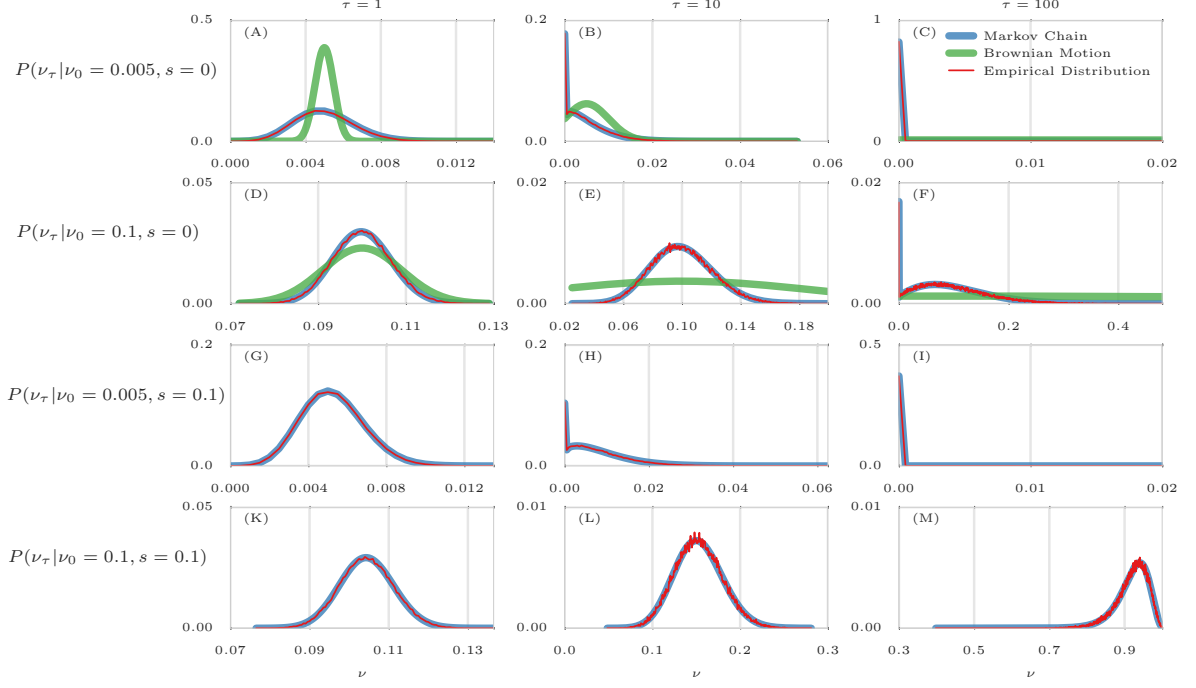


Fig 2: Comparison of empirical distributions of allele frequencies (red) versus predictions from Brownian Motion (green), and Markov chain (blue).

Comparison of empirical and theoretical distributions under neutral evolution (panels A-F) and selection (panels G-M) with different starting frequencies $\nu_0 \in \{0.005, 0.1\}$ and sampling times of $\mathcal{T} = \{0, \tau\}$, where $\tau \in \{1, 10, 100\}$. For each panel, the empirical distribution was computed over 100,000 simulations. Brownian motion (Gaussian approximation) provides poor approximations when initial frequency is far from 0.5 (A) or sampling is sparse (B,C,E,F). In addition, Brownian motion can only provide approximations under neutral evolution. In contrast, Markov chain consistently provide a good approximation in all cases.

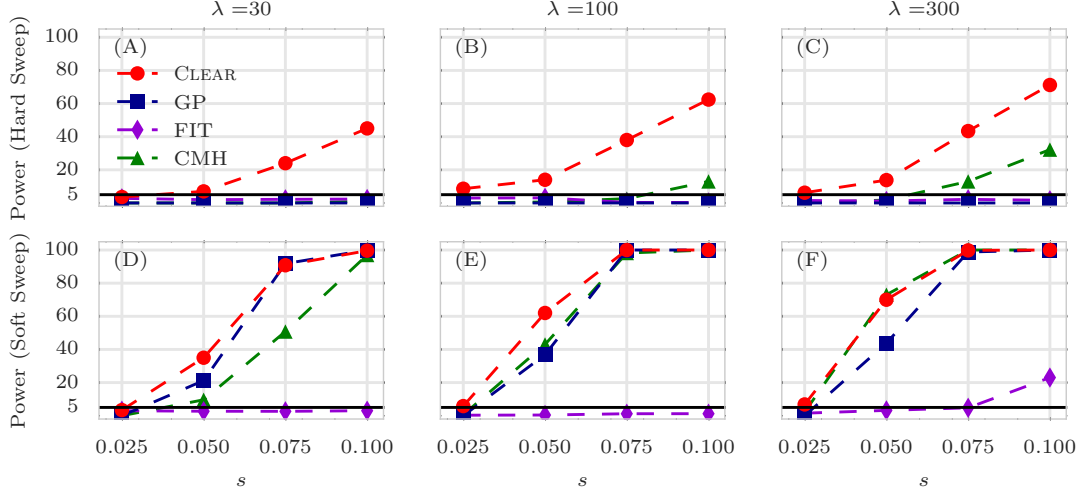


Fig 3: **Power calculations for detection of selection.**

Detection power for $\text{CLEAR}(\mathcal{H})$, Frequency Increment Test (FIT), Gaussian Process (GP), and CMH under hard (A-C) and soft sweep (D-F) scenarios. λ , s denote the mean coverage and selection coefficient, respectively. The y -axis measures power – sensitivity with false positive rate $\text{FPR} \leq 0.05$ – for 2,000 simulations of 50Kbp regions. The horizontal line reflects the power of a random classifier. In all simulations, 3 replicates are evolved and sampled at generations $\mathcal{T} = \{0, 10, 20, 30, 40, 50\}$.

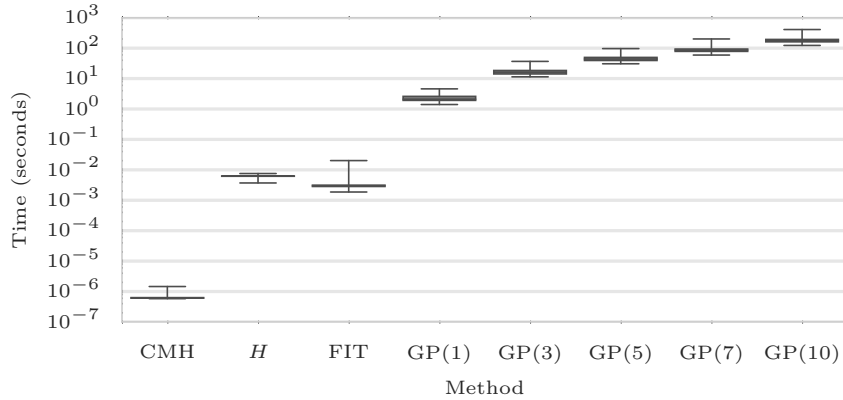


Fig 4: **Running time.**

Box plots of running time per variant (CPU-secs.) of $\text{CLEAR}(\mathcal{H})$, CMH, FIT, and GP with single, 3, 5, 7, and 10 loci over 1000 simulations conducted on a workstation with Intel Core i7 processor. The average running time for each method is shown on the x-axis. In all simulations, 3 replicates are evolved and sampled at generations $\mathcal{T} = \{0, 10, 20, 30, 40, 50\}$.

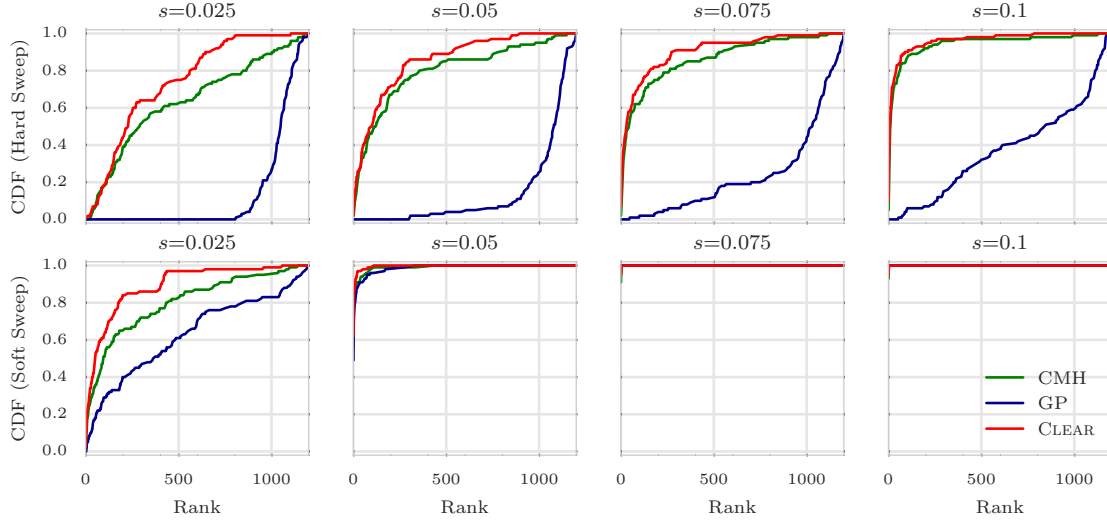


Fig 5: **Ranking performance for $100\times$ coverage.**

Cumulative Distribution Function (CDF) of the distribution of the rank of the favored allele in 1000 simulations for CLEAR (H), Gaussian Process (GP), CMH, and Frequency Increment Test (FIT), for different values of selection coefficient s and initial carrier frequency. Note that the individual variant CLEAR score (H) is used to rank variants. The Area Under Curve (AUC) is computed as an overall quantitative measure to compare the performance of methods for each configuration. In all simulations, 3 replicates are evolved and sampled at generations $\mathcal{T} = \{0, 10, 20, 30, 40, 50\}$.

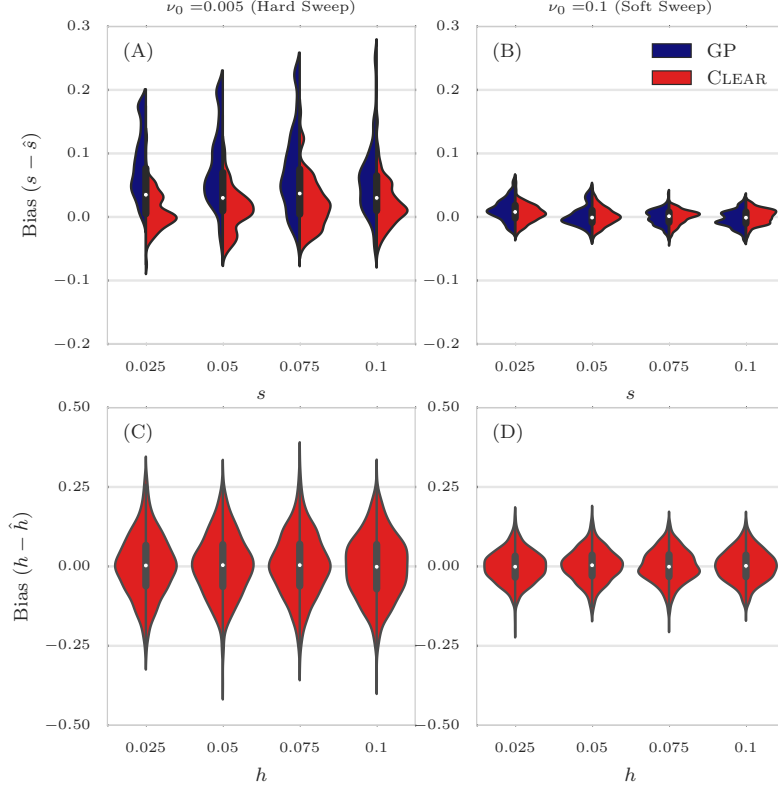


Fig 6: **Distribution of bias for 100 \times coverage.**

The distribution of bias ($s - \hat{s}$) in estimating selection coefficient over 1000 simulations using Gaussian Process (GP) and CLEAR (H) is shown for a range of choices for the selection coefficient s and starting carrier frequency ν_0 , when coverage $\lambda = 100$ (Panels A,B). GP and CLEAR have similar variance in estimates of s for soft sweep, while CLEAR provides lower variance in hard sweep. Also see [S2 Table](#). Panels C,D show the variance in the estimation of h . In all simulations, 3 replicates are evolved and sampled at generations $\mathcal{T} = \{0, 10, 20, 30, 40, 50\}$.

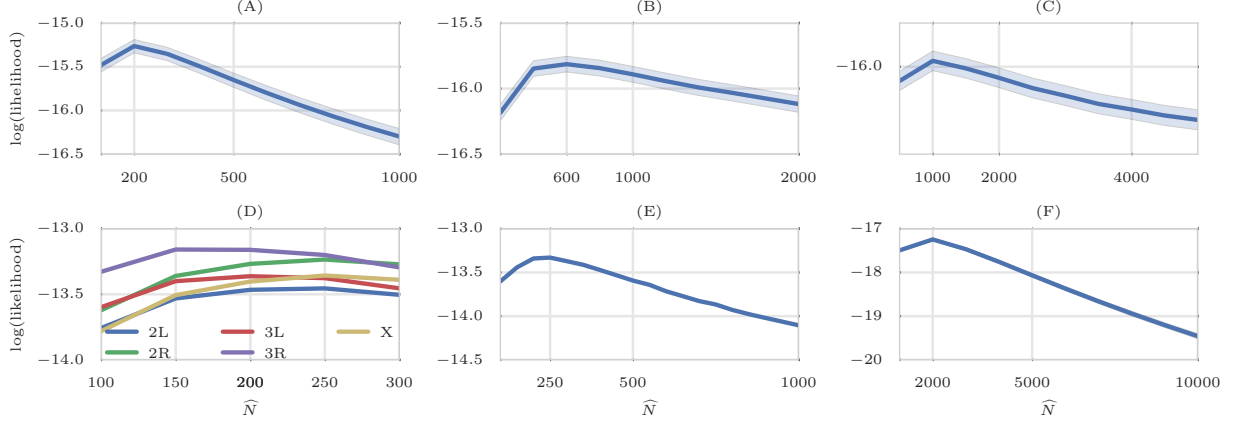


Fig 7: **Estimating N on simulated and real data.** Average and 95% confidence interval if likelihood of simulated data with $N = 200$ (A), $N = 600$ (B), and $N = 1000$ individuals, over 100 simulations, shows that estimator is unbiased. Chromosome-wise (D) and genome-wide (E) estimation of population size for data from a study of *D. melanogaster* adaptation to alternating temperatures. Chromosome 3R fits population size of 150, while genome-wide population size is 250. (F) Despite large census population size ($10^6 - 10^7$ [18]), Yeast dataset exhibits much smaller ($\hat{N} = 2000$) populations size.

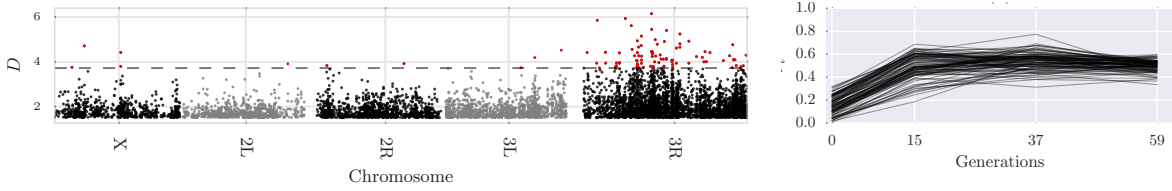


Fig 8: **Single locus analysis of the data from a study of *D. melanogaster* adaptation to alternating temperatures.**

Manhattan plot of scan for testing directional selection (A) and overdominant selection (C). Significant variants with $FDR \leq 0.001$ and $FDR \leq 0.01$ are denoted in red, and their trajectories are depicted in panels (B) and (D).

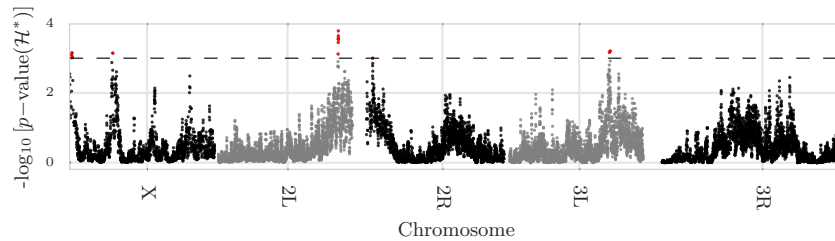


Fig 9: **Scan of composite statistic on data from a study of *D. melanogaster* adaptation to alternating temperatures.** Manhattan plot of scan for \mathcal{H}^* statistic over the genome. The dashed line represents cutoff for genome-wide $FDR \leq 0.05$, selecting 16 regions.

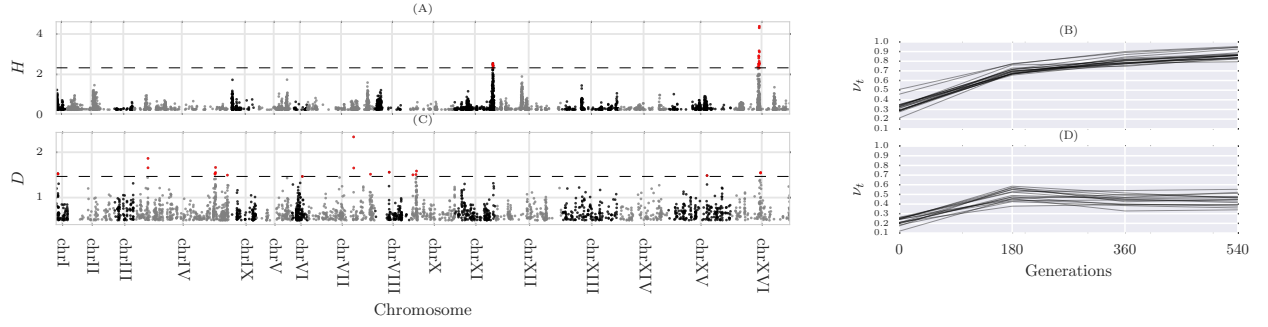


Fig 10: **Single locus analysis of the data from a study of *D. melanogaster* adaptation to alternating temperatures.**

Manhattan plot of scan for testing directional selection (A) and overdominant selection (C). dashed The dashed line represents cutoff for genome-wide $FDR \leq 0.05$. Trajectories of the selected variants are depicted in panels (B) and (D).

Generative Process 1: The Generative Process for Dynamic Pool-seq Data.

Input: $N, n, R, \{\lambda_{\tau_0}, \dots, \lambda_{\tau_T}\}, \mathcal{T} = \{\tau_0, \dots, \tau_T\}$

Output: Time-series pool-seq data for R replicates of a single locus $\{\mathbf{c}^{(r)}\}$ and $\{\mathbf{d}^{(r)}\}$.

for $r \leftarrow 1$ **to** R **do**

for $t \leftarrow \tau_0$ **to** τ_T **do**

$2N\nu_t \sim \text{Binomial}(2N, \nu_{t-1});$

if $t \in \mathcal{T}$ **then**

$d_t^{(r)} \sim \text{Poisson}(\lambda_{\tau_i});$

$2ny_t \sim \text{Binomial}(2n, \nu_t);$

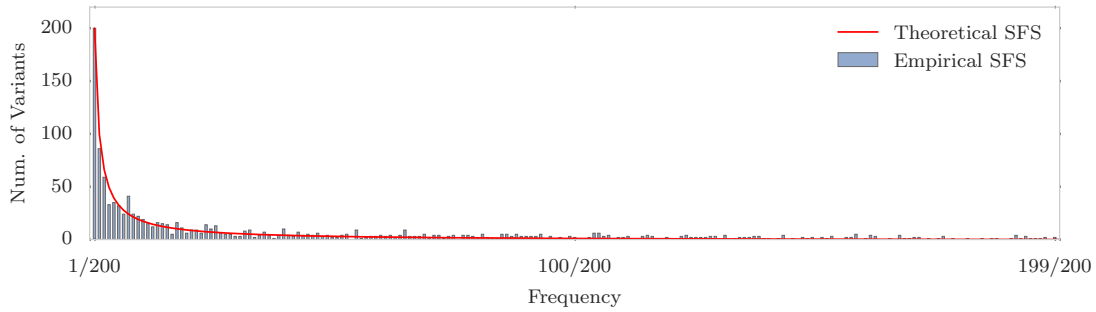
$c_t^{(r)} \sim \text{Binomial}(d_t^{(r)}, y_t);$

end

end

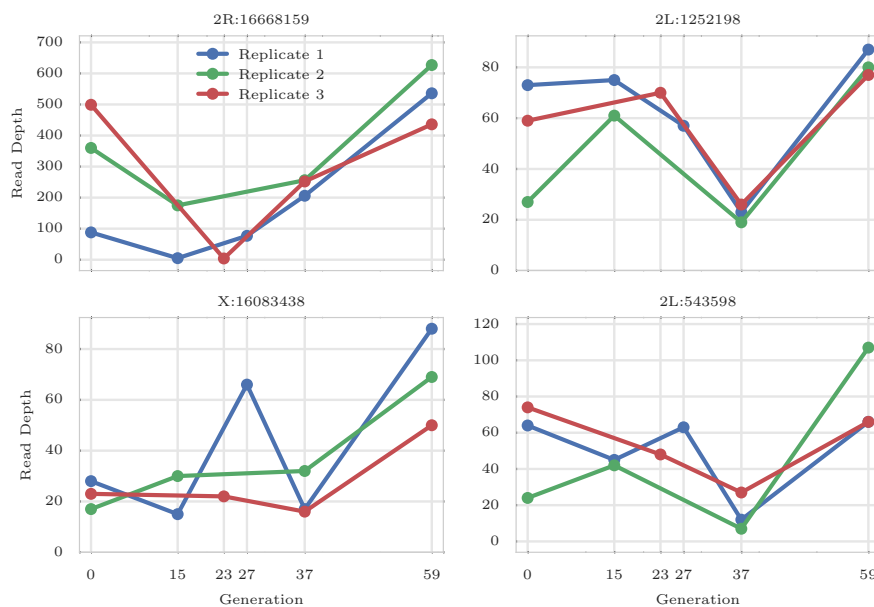
end

S1 Fig: The Generative Process for Dynamic Pool-seq Data.



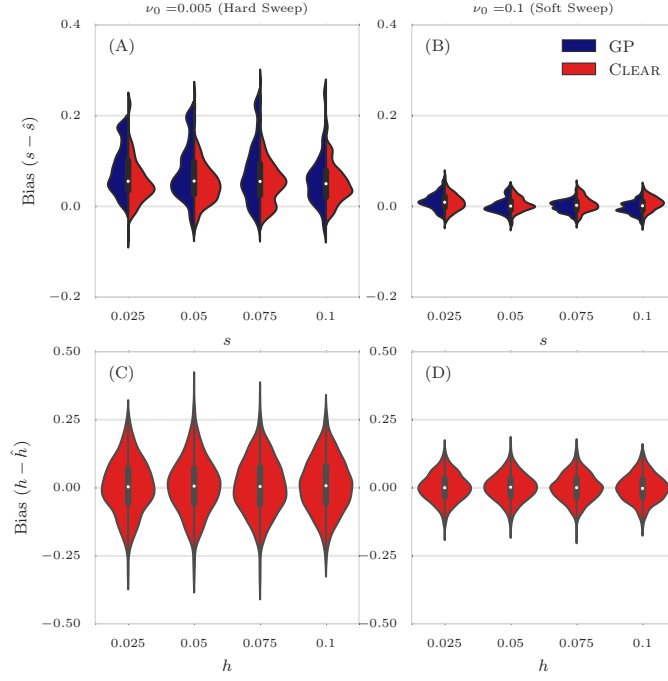
S2 Fig: **Site Frequency Spectrum.**

Theoretical and Empirical SFS in a 50Kbp region for a neutral population of 200 individuals when $N_e = 10^6$ and $\mu = 10^{-9}$. The x -axis corresponds to site frequency, and the y -axis to the number of variants with a specific frequency. In a neutral population, majority of the variations stand in low frequency.



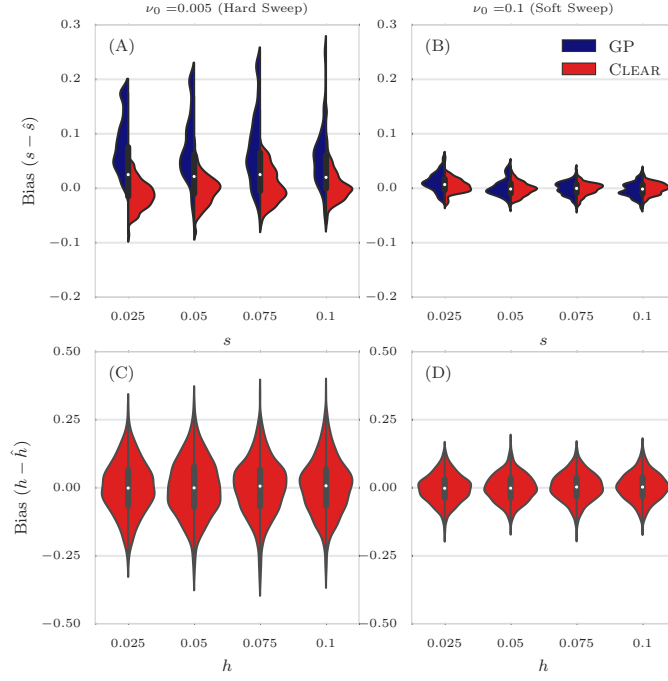
S3 Fig: Coverage heterogeneity in time series data.

Each panel shows the read depth for 3 replicates of the data from a study of *D. melanogaster* adaptation to alternating temperatures data (see section 3.1). Heterogeneity in depth of coverage is seen between replicates, and also at different time points, in all 4 variants. None of these sites pass the the hard filtering with minimum depth of 30.



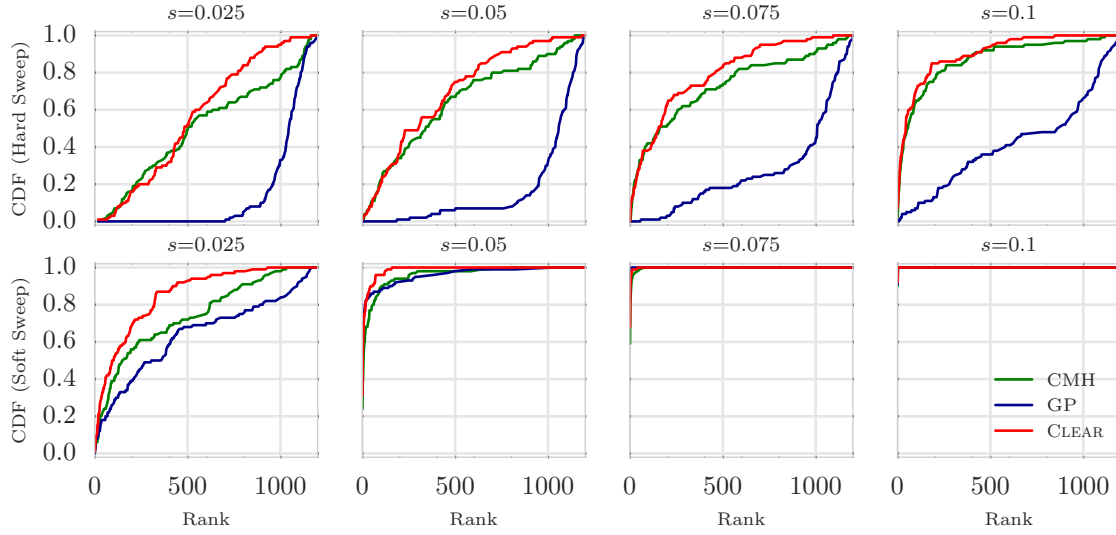
S4 Fig: **Distribution of bias for 30 \times coverage.**

The distribution of bias ($s - \hat{s}$) in estimating selection coefficient over 1000 simulations using Gaussian Process (GP) and CLEAR (H) is shown for a range of choices for the selection coefficient s and starting carrier frequency ν_0 , when coverage $\lambda = 30$ (Panels A,B). GP and CLEAR have similar variance in estimates of s for soft sweep, while CLEAR provides lower variance in hard sweep. Also see S2 Table. Panels C,D show the variance in the estimation of h .



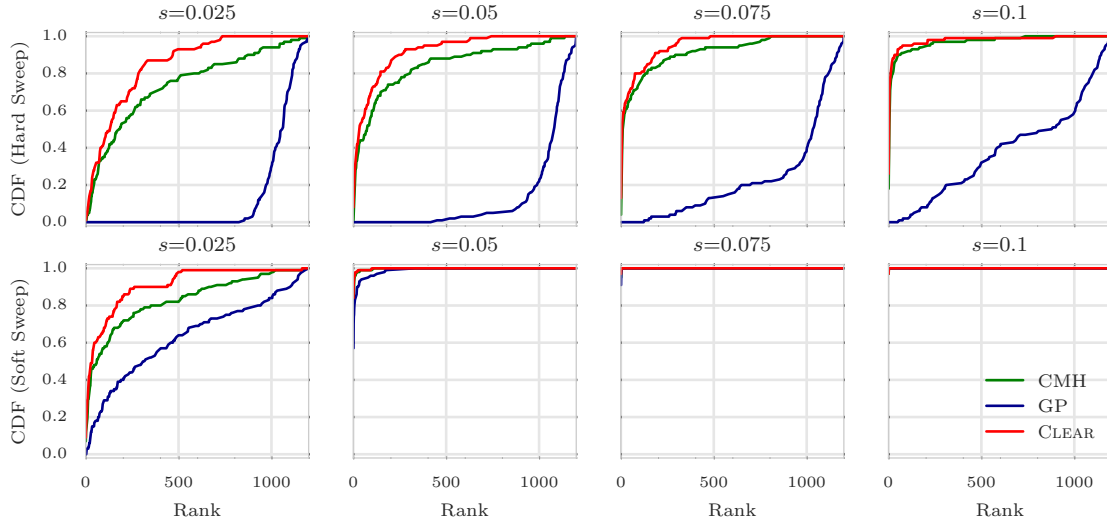
S5 Fig: **Distribution of bias for infinite coverage.**

The distribution of bias ($s - \hat{s}$) in estimating selection coefficient over 1000 simulations using Gaussian Process (GP) and CLEAR (H) is shown for a range of choices for the selection coefficient s and starting carrier frequency ν_0 , when coverage $\lambda = \infty$ (Panels A,B). GP and CLEAR have similar variance in estimates of s for soft sweep, while CLEAR provides lower variance in hard sweep. Also see S2 Table. Panels C,D show the variance in the estimation of h .



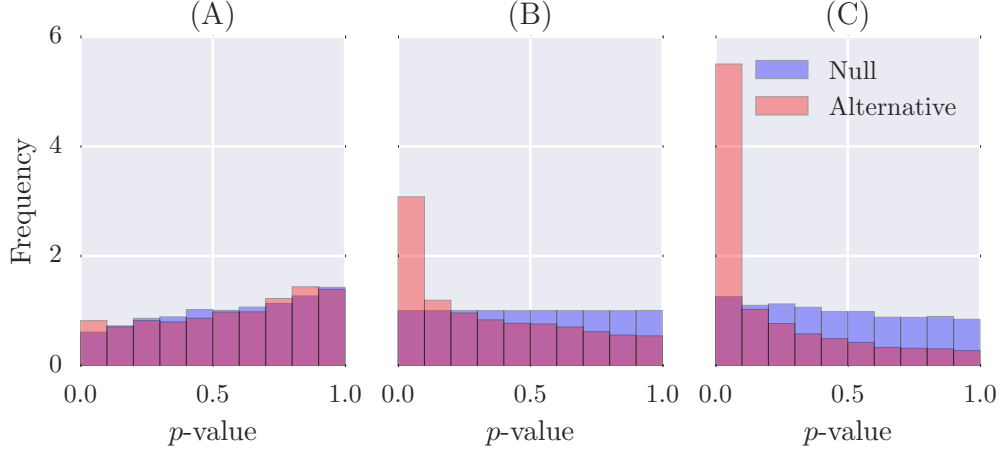
S6 Fig: Ranking performance for $30\times$ coverage.

Cumulative Distribution Function (CDF) of the distribution of the rank of the favored allele in 1000 simulations for CLEAR (H score), Gaussian Process (GP), and Cochran Mantel Haenszel (CMH), for different values of selection coefficient s and initial carrier frequency.

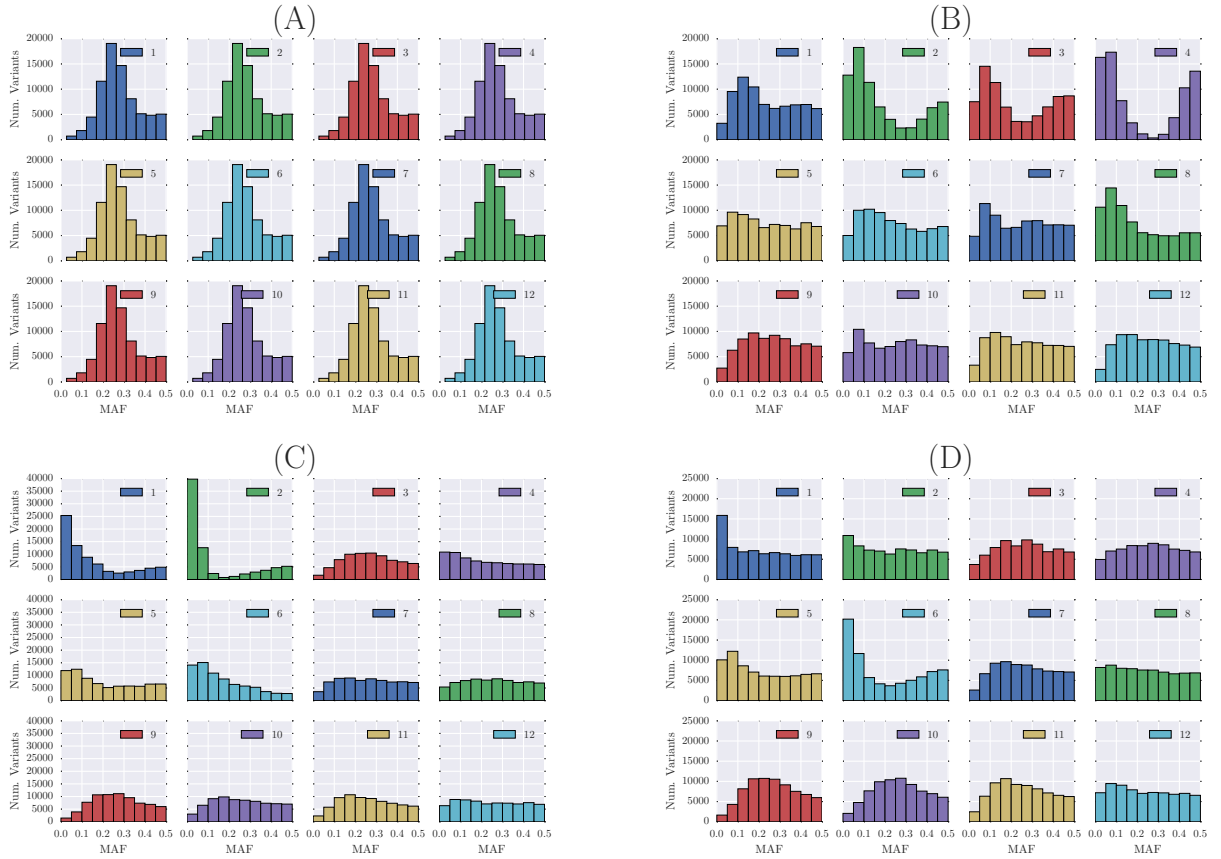


S7 Fig: Ranking performance for $300\times$ coverage.

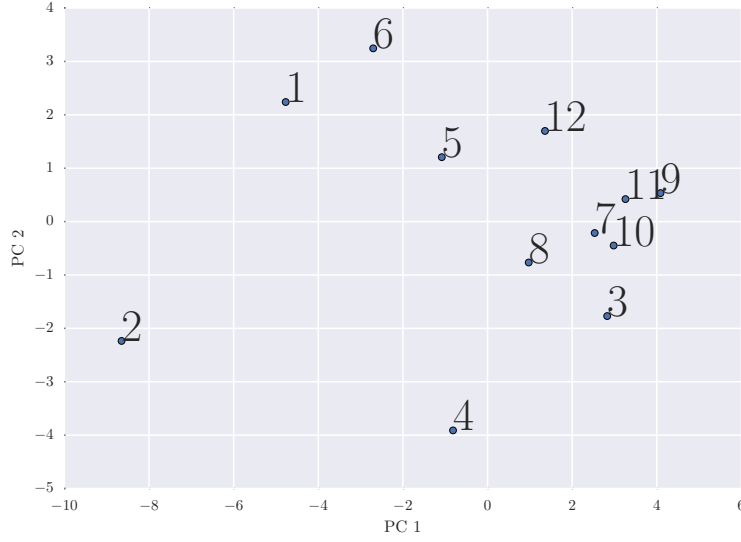
Cumulative Distribution Function (CDF) of the distribution of the rank of the favored allele in 1000 simulations for CLEAR (H score), Gaussian Process (GP), and Cochran Mantel Haenszel (CMH), for different values of selection coefficient s and initial carrier frequency.



S8 Fig: Distribution of p -values. Distribution of p -values of CLEAR in null simulations and experimental data when $N = 250$. Panel (A),(C) shows the effect of under estimations ($\hat{N} = 100$) and over-estimation ($\hat{N} = 500$) of population size in computing p -values, and panel (B) shows the distribution of p -values when unbiased estimate is used to create simulations. .



S9 Fig: Site frequency spectrum of the Yeast dataset. Whole-genome site frequency spectrum of the Yeast dataset at generations 0 (A), 180 (B), 360 (C) and 540 (D). Some replicates, e.g. replicate 2, undergoing severe demographic events.



S10 Fig: **Population similarity.** Principle component analysis of the 12 replicates throughout the experiment, showing that some populations exhibiting distinct frequency spectra.

S1 Table: **Average of power for detecting selection.**

Hard Sweep			Soft Sweep		
λ	Method	Avg Power	λ	Method	Avg Power
300	CLEAR	34	300	CLEAR	69
300	CMH	12	300	CMH	69
300	FIT	2	300	GP	61
300	GP	0	300	FIT	8
100	CLEAR	31	100	CLEAR	67
100	CMH	4	100	CMH	60
100	FIT	2	100	GP	59
100	GP	0	100	FIT	1
30	CLEAR	20	30	CLEAR	57
30	FIT	2	30	GP	53
30	CMH	0	30	CMH	39
30	GP	0	30	FIT	3

Average power is computed for 8000 simulations with $s \in \{0.025, 0.05, 0.075, 0.1\}$. Frequency Increment Test (FIT), Gaussian Process (GP), CLEAR (\mathcal{H} statistic) and Cochran Mantel Haenszel (CMH) are compared for different initial carrier frequency ν_0 . For all sequencing coverages, CLEAR outperform other methods. When coverage is not high ($\lambda \in \{30, 100\}$) and initial frequency is low (hard sweep), CLEAR significantly perform better than others.

S2 Table: **Mean and standard deviation of the distribution of bias ($s - \hat{s}$) of 8000 simulations with coverage $\lambda = 100\times$ and $s \in \{0.025, 0.05, 0.075, 0.1\}$.**

Method	ν_0	Mean	STD
GP	0.005	0.073	0.061
CLEAR	0.005	0.016	0.035
GP	0.1	0.002	0.016
CLEAR	0.1	0.002	0.013

S3 Table: **Overlapping genes with the 216 candidate variants.**

index	FBgn	CHROM	start	end	name
1	FBgn0051810	2L	16849018	16852368	CG31810
2	FBgn0051809	2L	16853620	16858714	CG31809
3	FBgn0264440	2L	16861497	16862431	CR43858
4	FBgn0051781	2L	16869346	16878300	CR31781
5	FBgn0052832	2L	16878326	16879290	CG32832
6	FBgn0032618	2L	16879517	16886319	CG31743
7	FBgn0085342	2L	16879517	16886319	CG34313
8	FBgn0040985	2L	16887109	16887966	CG6115
9	FBgn0261671	2L	16888490	16917052	tweek
10	FBgn0026150	2L	16908229	16910418	ApepP
11	FBgn0262355	2L	16944723	16945374	CR43053
12	FBgn0053179	2L	16973091	16993984	beat-IIIb
13	FBgn0040674	2R	2725579	2726560	CG9445
14	FBgn0033109	2R	2749506	2760223	coro
15	FBgn0033110	2R	2760501	2763324	CG9447
16	FBgn0033113	2R	2768500	2770912	Spn42Dc
17	FBgn0028988	2R	2770785	2772378	Spn42Dd
18	FBgn0033115	2R	2773057	2775767	Spn42De
19	FBgn0050158	2R	2779265	2810118	CG30158
20	FBgn0001085	3L	14267443	14361739	fz
21	FBgn0036421	3L	14362025	14362807	CG13481
22	FBgn0262580	3L	14375013	14376399	CG43120
23	FBgn0036422	3L	14393869	14395825	CG3868
24	FBgn0003459	3L	14396030	14403039	stwl
25	FBgn0087007	3L	14405928	14529376	bbg
26	FBgn0023531	X	1567143	1586801	CG32809
27	FBgn0023130	X	1587648	1589922	a6
28	FBgn0025378	X	1602839	1604215	CG3795
29	FBgn0025391	X	1629978	1648098	Scgdelta
30	FBgn0026086	X	1667758	1682098	Adar
31	FBgn0029939	X	7031756	7135965	CG9650
32	FBgn0029941	X	7175122	7299830	CG1677
33	FBgn0029944	X	7218247	7222839	Dok

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