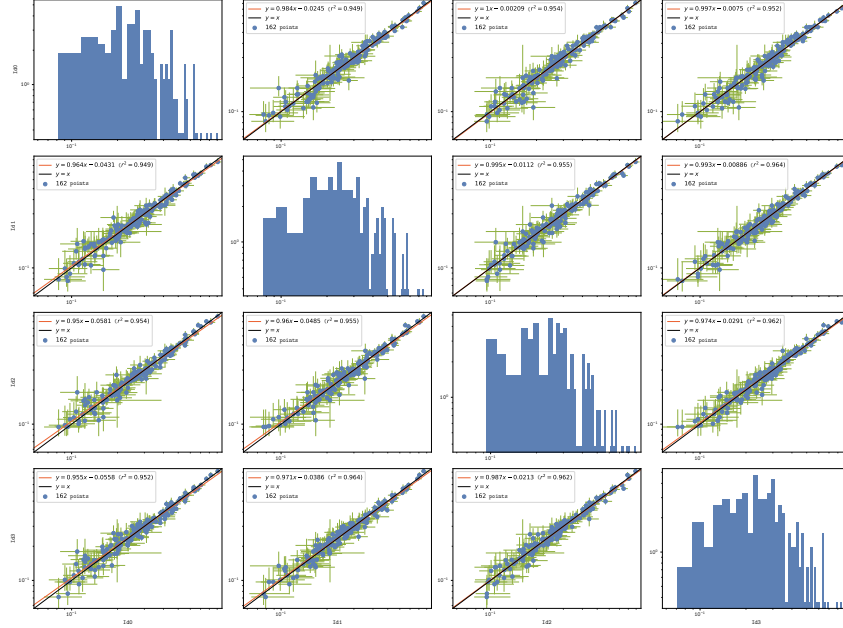


Each experiment consist of randomly choosing 18 CDS and run the analysis on the concatenate. The purpose of having 4 independent experiment is to assess for the replicability of our method and the results.

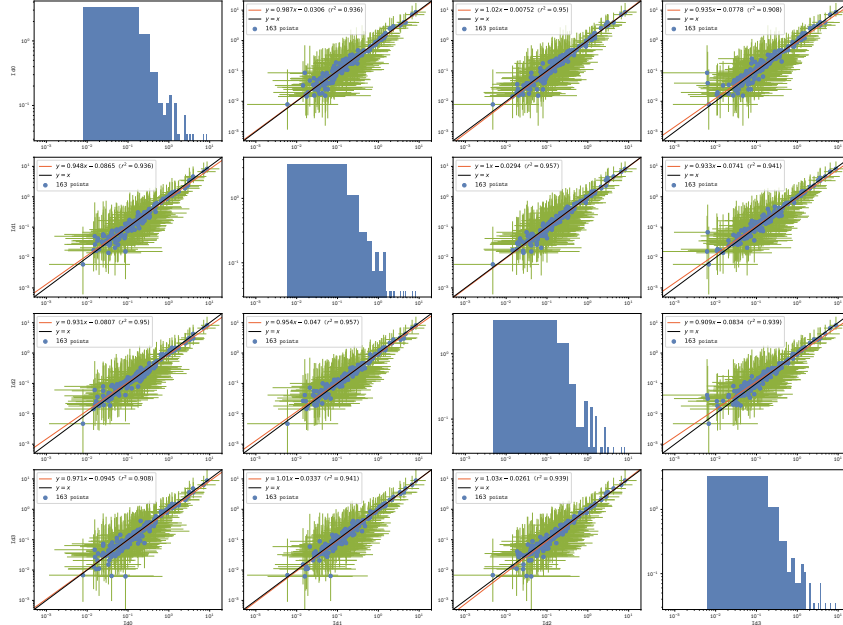
Overall the results are replicable, the mean value of the correlation coefficient between population size and genome size is negative (between 0.069 and  $-0.14$ ), meaning population with high  $N_e$  tend to have lower genome size. However, the correlation is not statistically significant. The analysis using dN/dS ( $\omega$ ) instead of  $N_e$  also don't detect any statistically significant correlation between  $\omega$  and genome size.

## 1 Replicability between the 4 experiments

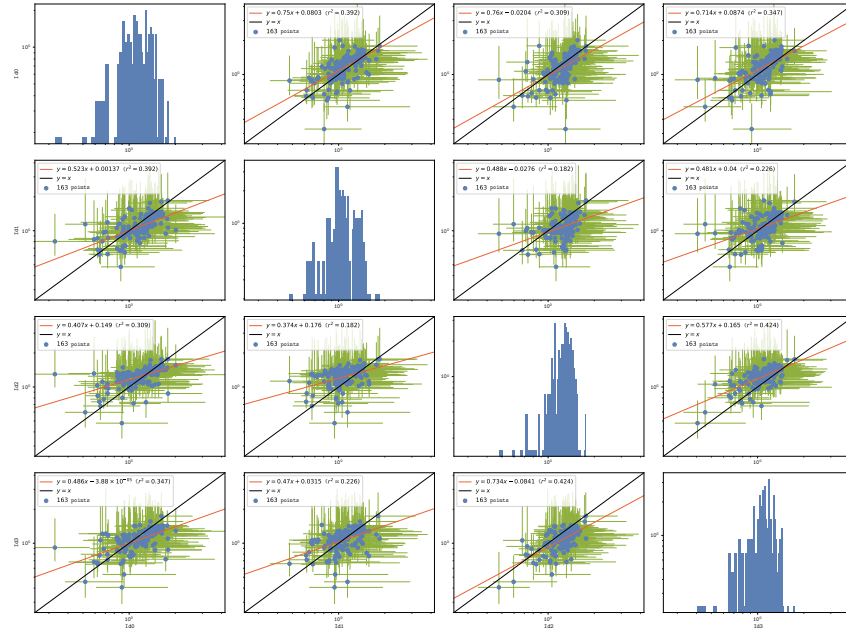
### 1.1 Inferred log of branch length.



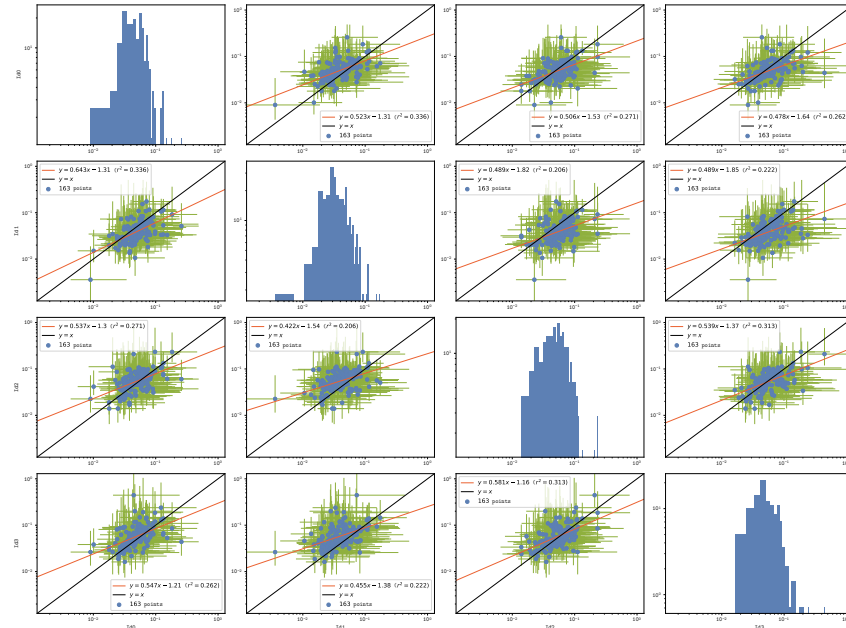
### 1.2 Inferred log of mutation rate per unit of time.



### 1.3 Inferred log of effective population size ( $N_e$ )



### 1.4 Inferred log of dN/dS ( $\omega$ ).



## 2 Experiment 1

Asterisks indicate strength of support (\* $pp > 0.95$ , \*\* $pp > 0.975$ )

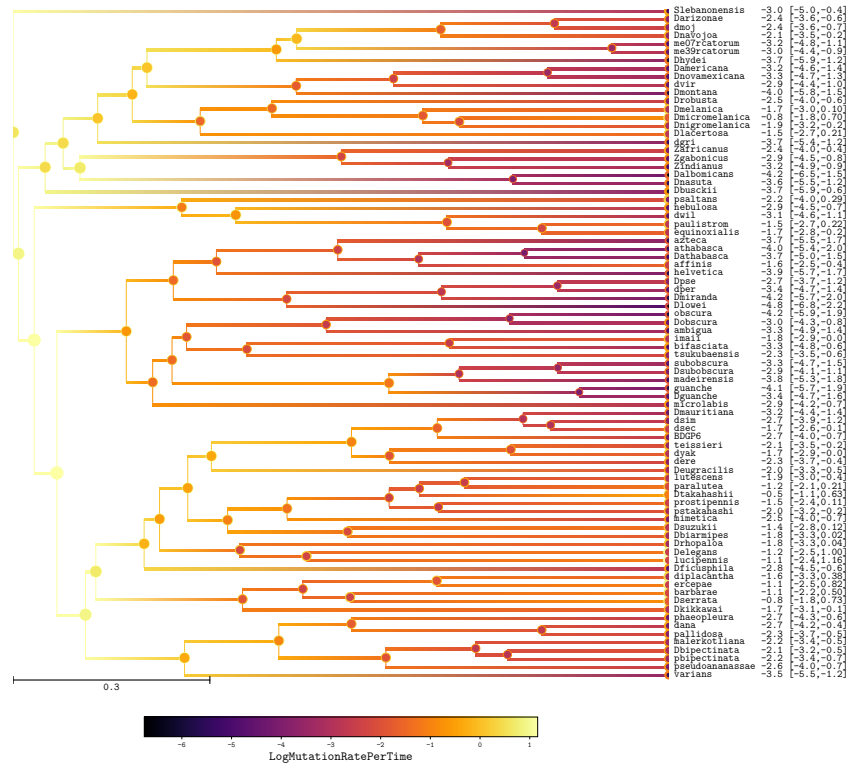
### 2.1 Correlation coefficient between $N_e$ and genome size.

	$N_e$	$\mu$	LogGenomeSize
$N_e$	...	0.28**	-0.13
$\mu$	0.28**	...	0.2
LogGenomeSize	-0.13	0.2	...

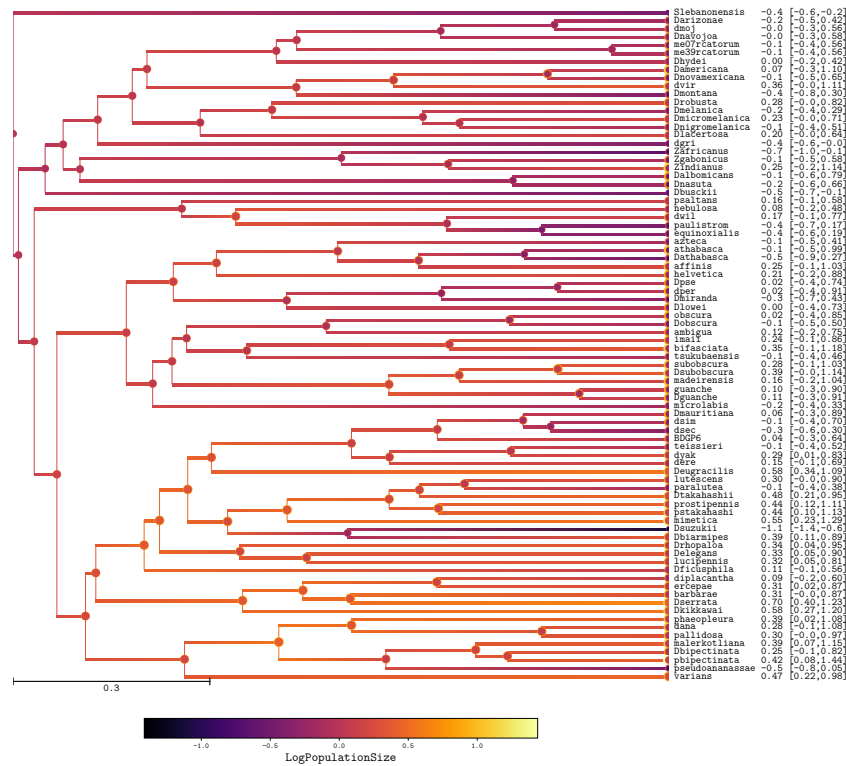
## 2.2 Correlation coefficient between $\omega$ and genome size.

	$\omega$	$\mu$	LogGenomeSize
$\omega$	...	0.23*	0.19
$\mu$	0.23*	...	0.26
LogGenomeSize	0.19	0.26	...

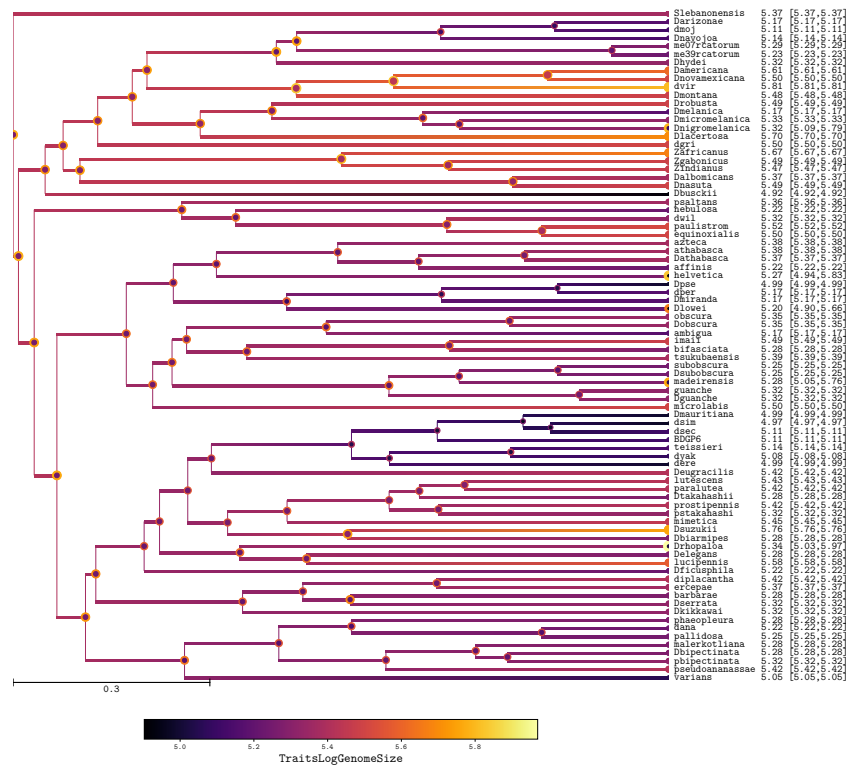
### 2.3 Inferred log of mutation rate per unit of time.



## 2.4 Inferred log of effective population size ( $N_e$ )



## 2.5 Inferred log of genome size.



### 3 Experiment 2

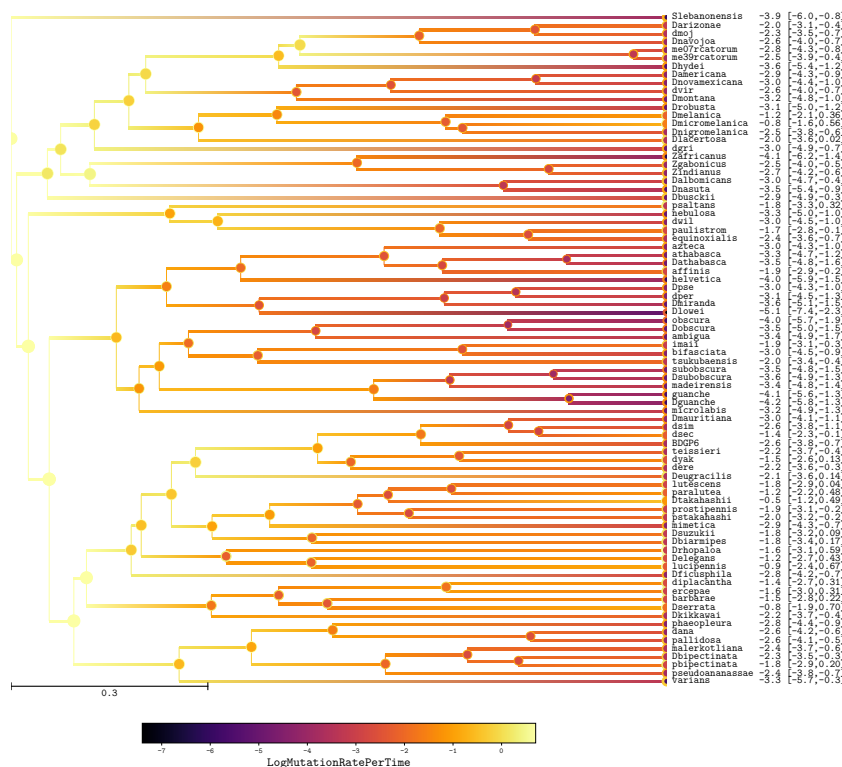
### 3.1 Correlation coefficient between $N_e$ and genome size.

	$N_e$	$\mu$	LogGenomeSize
$N_e$	...	0.097	-0.069
$\mu$	0.097	...	0.059
LogGenomeSize	-0.069	0.059	...

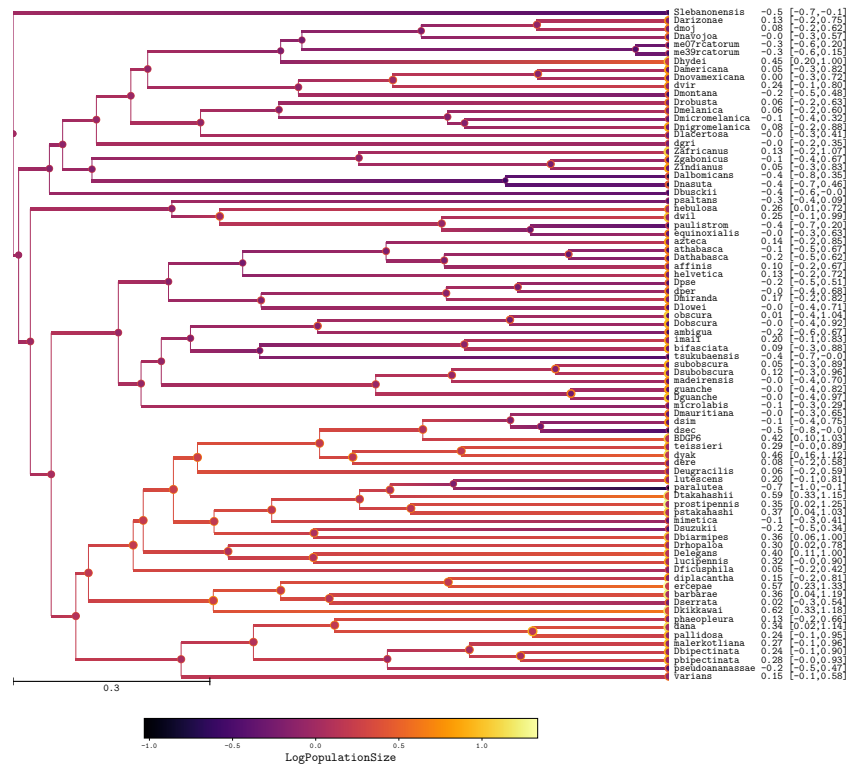
### 3.2 Correlation coefficient between $\omega$ and genome size.

	$\omega$	$\mu$	LogGenomeSize
$\omega$	...	0.33**	0.21
$\mu$	0.33**	...	0.061
LogGenomeSize	0.21	0.061	...

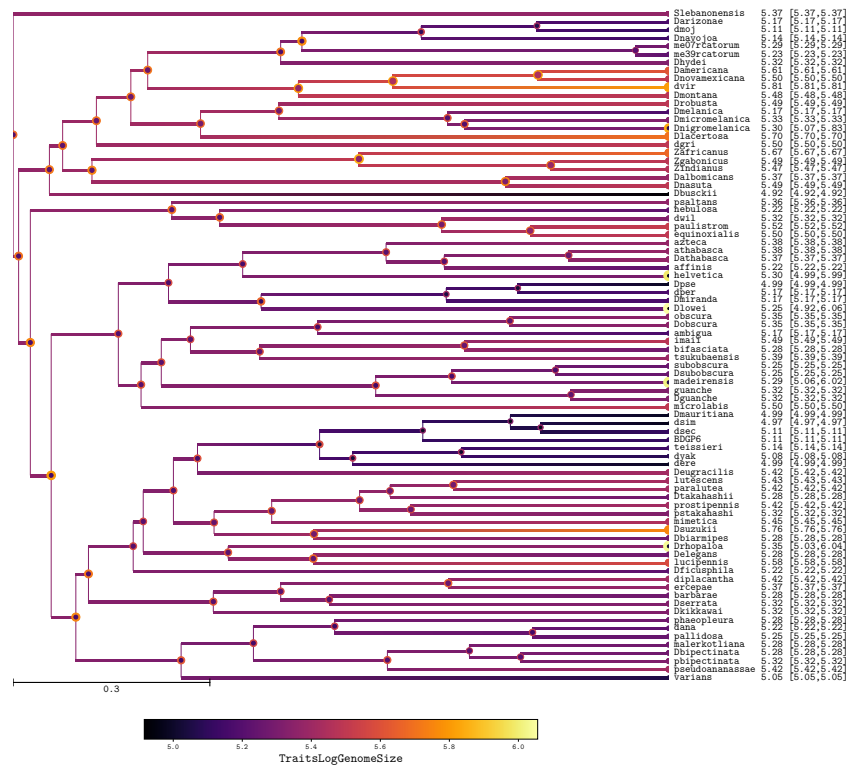
### 3.3 Inferred log of mutation rate per unit of time.



### 3.4 Inferred log of effective population size ( $N_e$ )



### 3.5 Inferred log of genome size.



## 4 Experiment 3

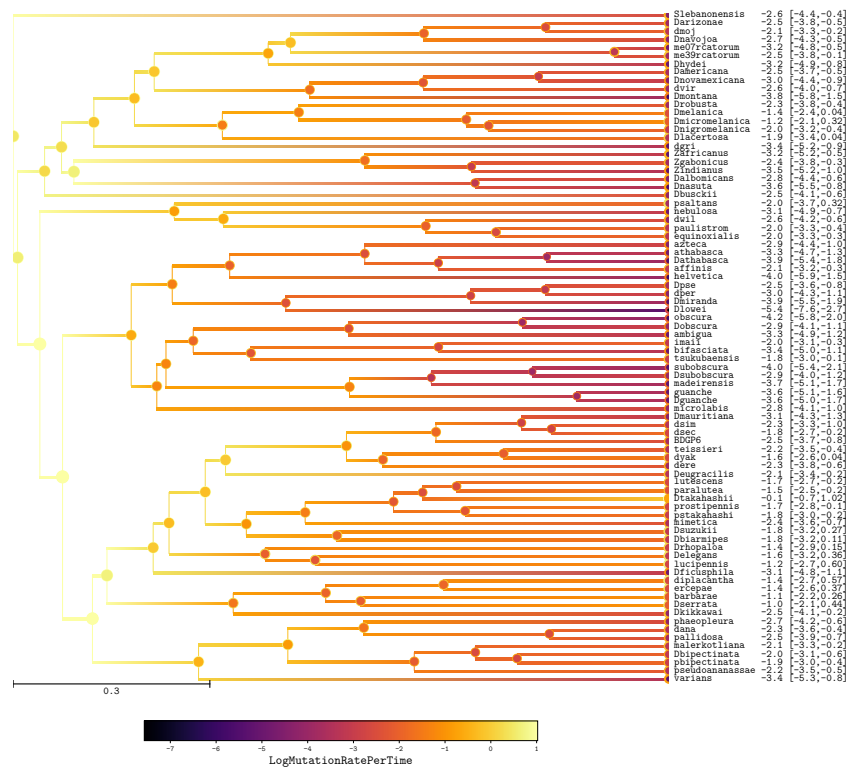
#### 4.1 Correlation coefficient between $N_e$ and genome size.

	$N_e$	$\mu$	LogGenomeSize
$N_e$	...	0.3**	-0.11
$\mu$	0.3**	...	0.064
LogGenomeSize	-0.11	0.064	...

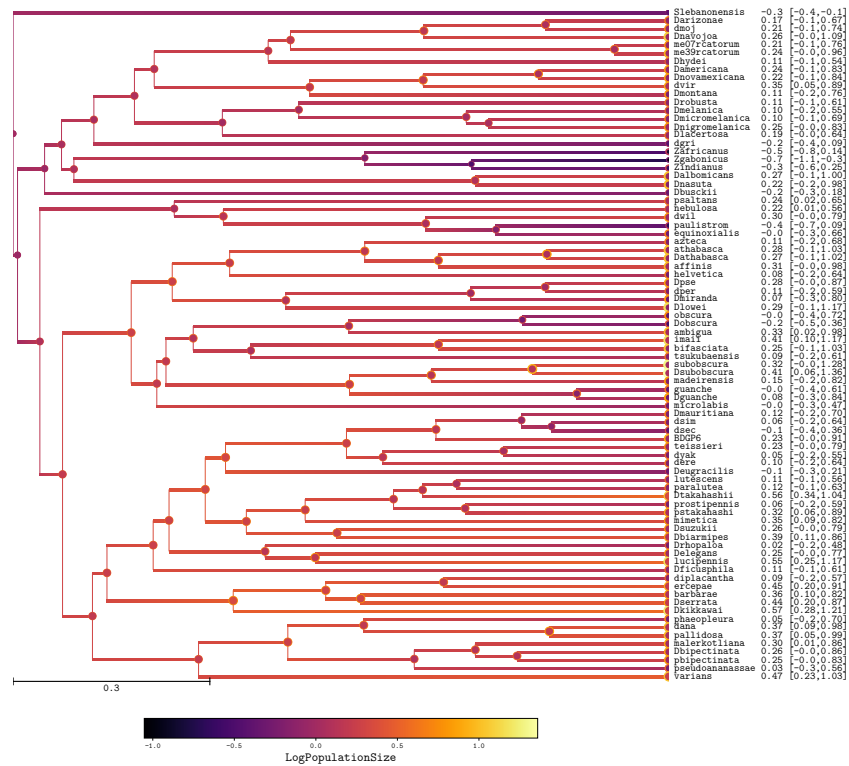
## 4.2 Correlation coefficient between $\omega$ and genome size.

	$\omega$	$\mu$	LogGenomeSize
$\omega$	...	0.14	0.23
$\mu$	0.14	...	0.11
LogGenomeSize	0.23	0.11	...

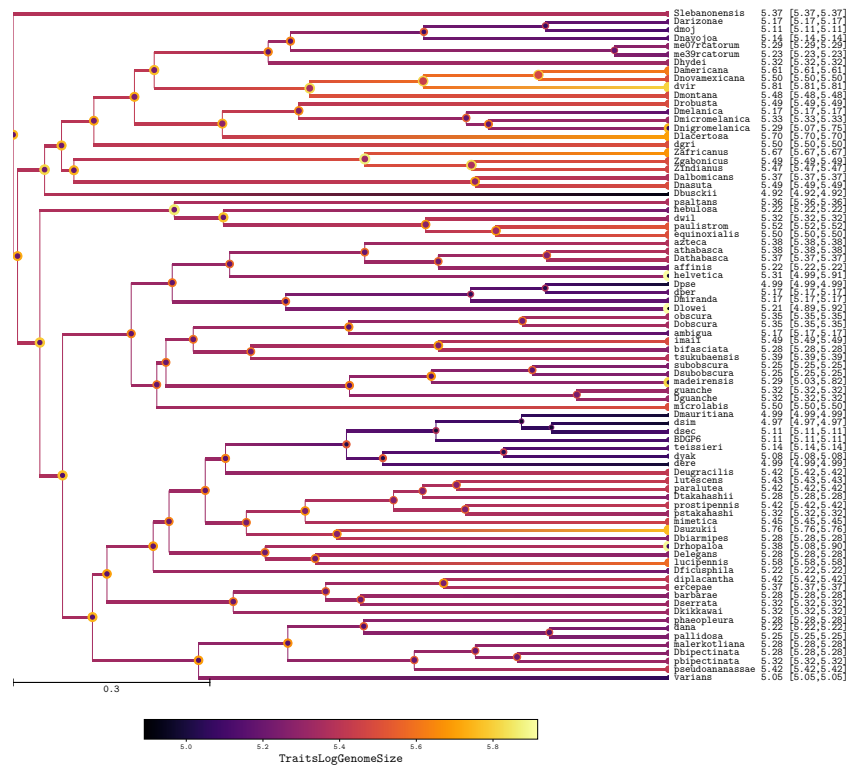
### 4.3 Inferred log of mutation rate per unit of time.



#### 4.4 Inferred log of effective population size ( $N_e$ )



#### 4.5 Inferred log of genome size.





## 5 Experiment 4

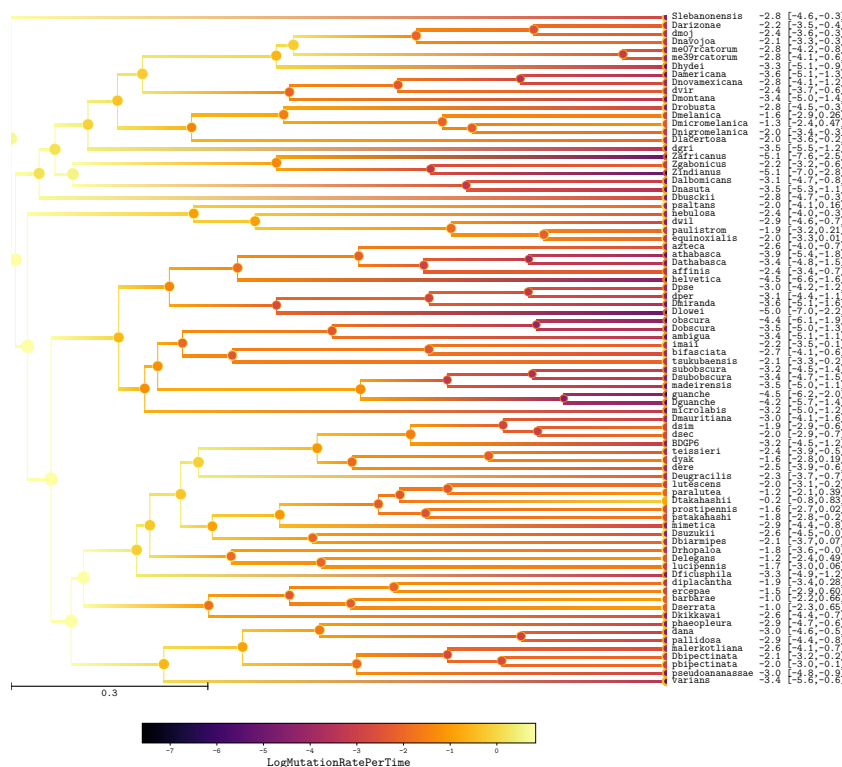
### 5.1 Correlation coefficient between $N_e$ and genome size.

	$N_e$	$\mu$	LogGenomeSize
$N_e$	...	0.29**	-0.14
$\mu$	0.29**	...	-0.13
LogGenomeSize	-0.14	-0.13	...

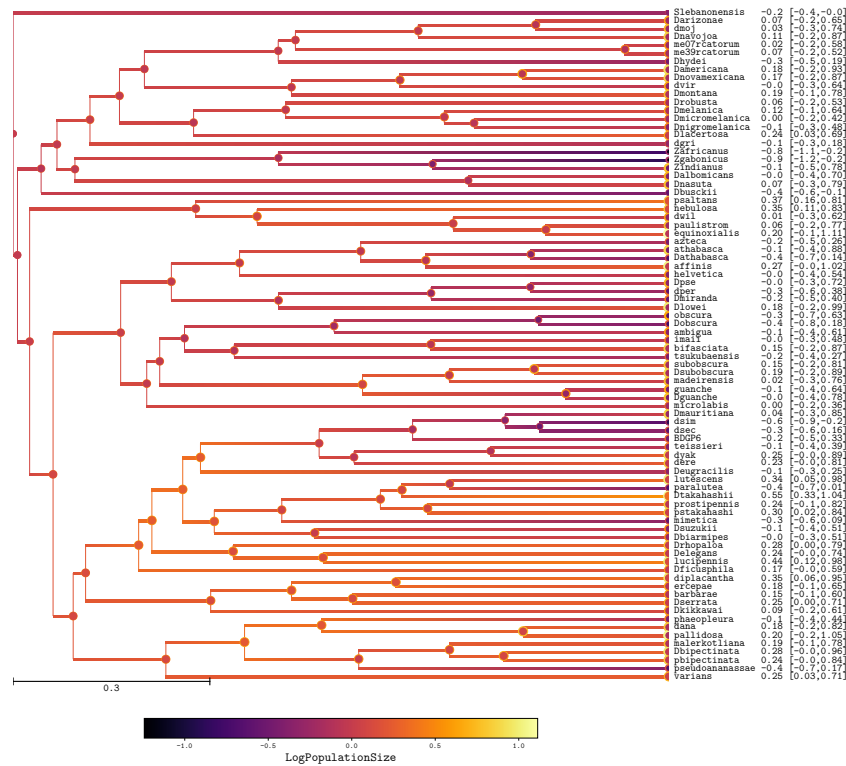
## 5.2 Correlation coefficient between $\omega$ and genome size.

	$\omega$	$\mu$	LogGenomeSize
$\omega$	...	0.042	0.13
$\mu$	0.042	...	-0.089
LogGenomeSize	0.13	-0.089	...

### 5.3 Inferred log of mutation rate per unit of time.



#### 5.4 Inferred log of effective population size ( $N_e$ )



### 5.5 Inferred log of genome size.

