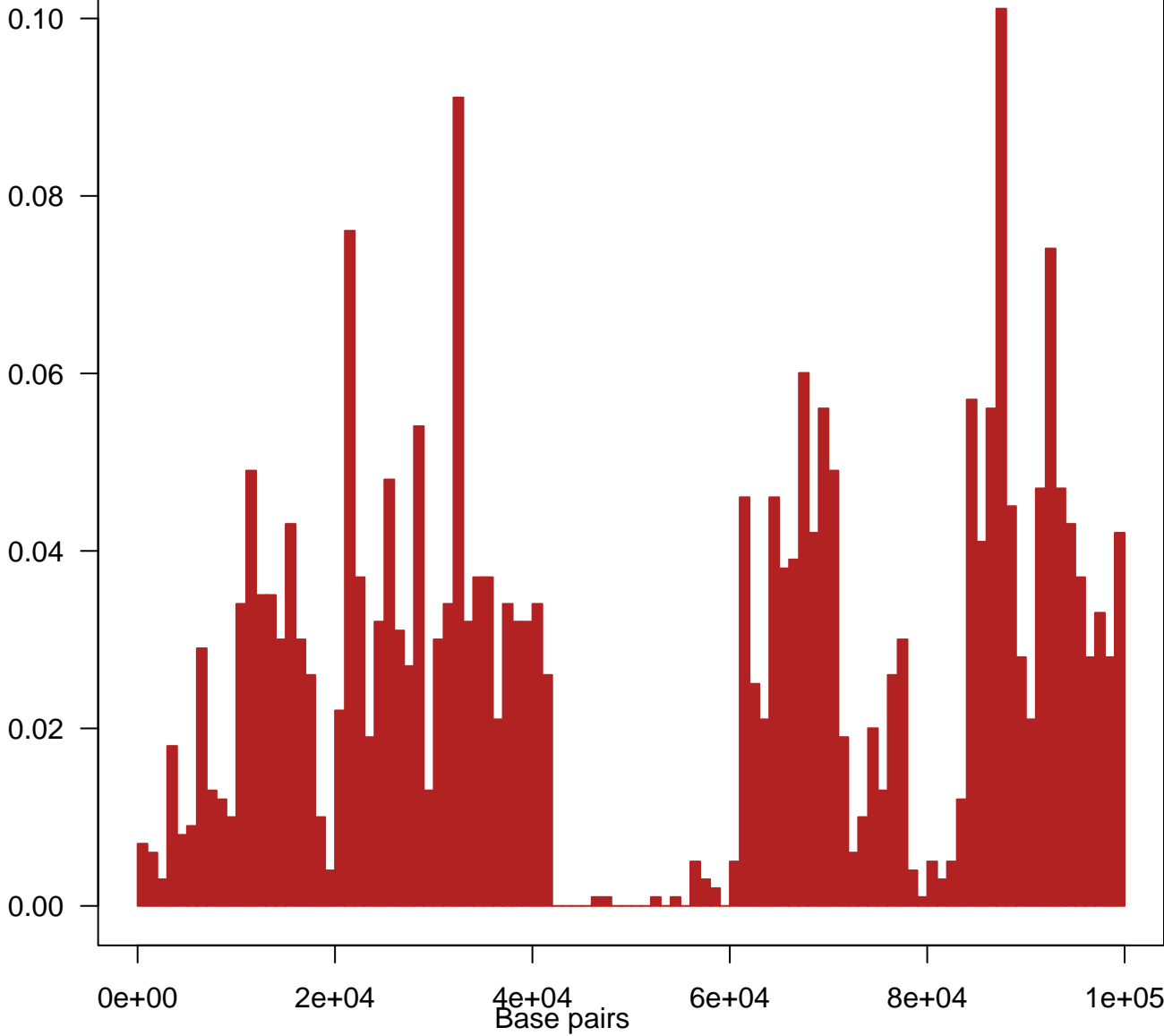


# Supercontig

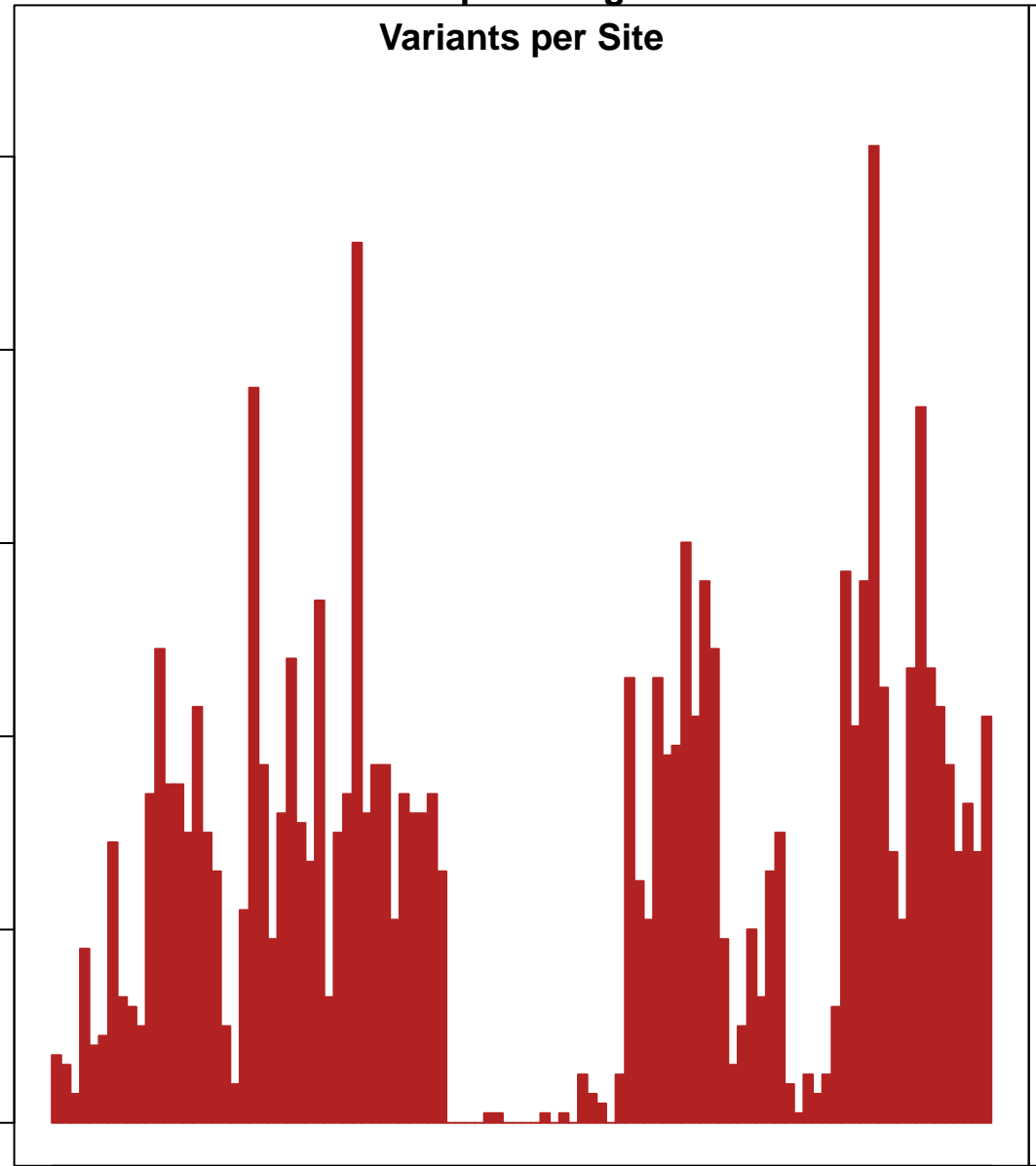
## Variants per Site



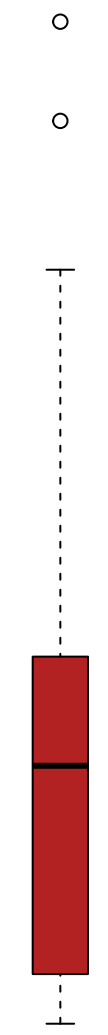
# Supercontig

## Variants per Site

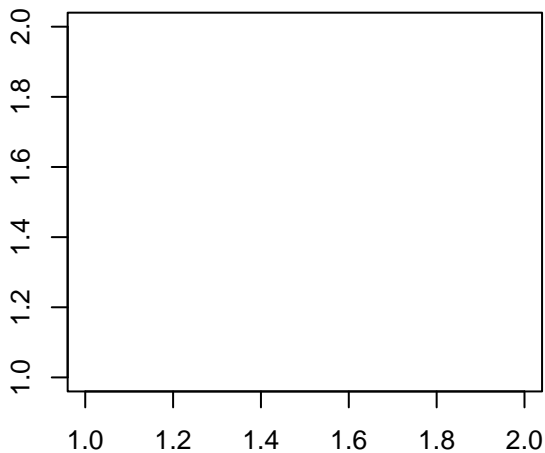
0.10  
0.08  
0.06  
0.04  
0.02  
0.00



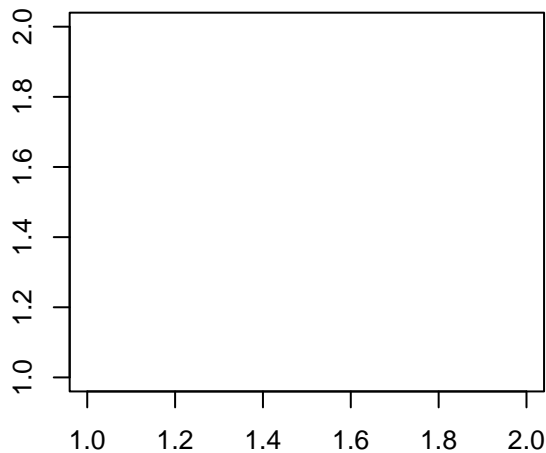
0e+00 2e+04 4e+04 6e+04 8e+04 1e+05  
Base pairs



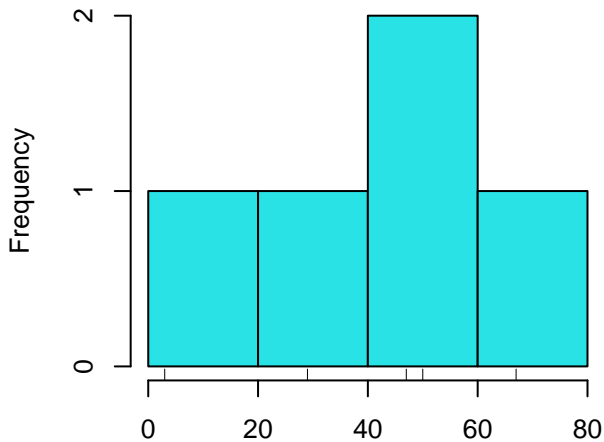
**No depths found**



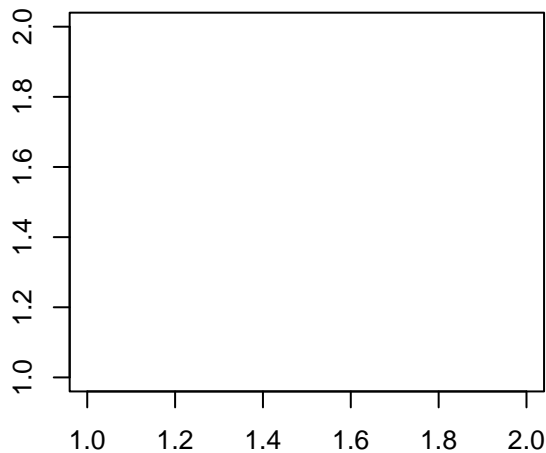
**No mapping qualities found**



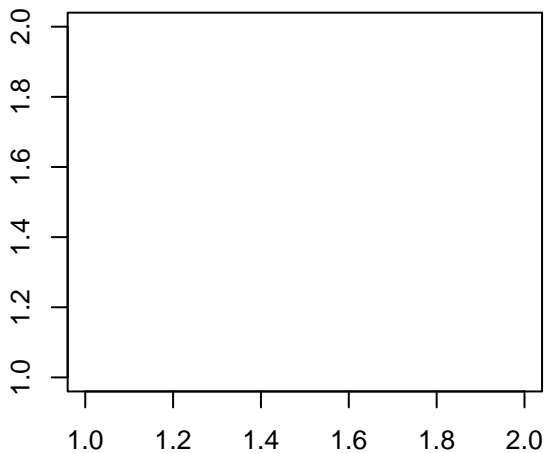
**Quality (QUAL)**



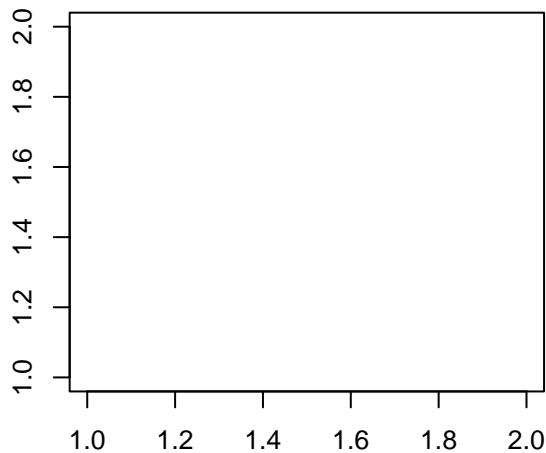
**No SNP densities found**



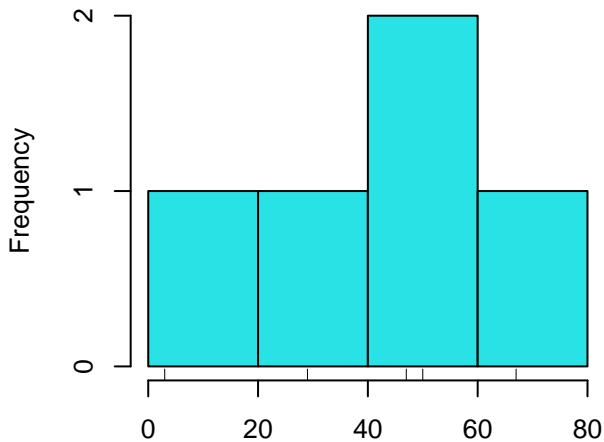
**No depths found**



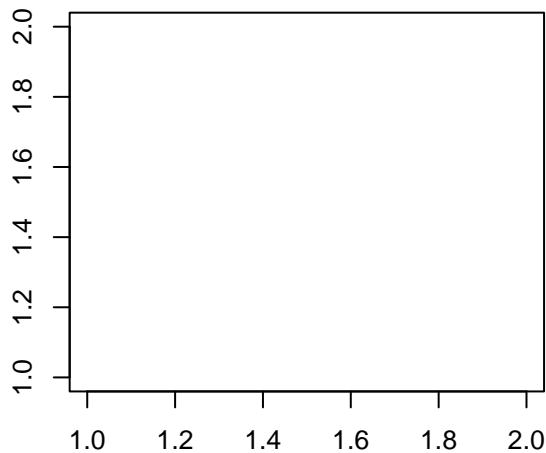
**No mapping qualities found**



**Quality (QUAL)**

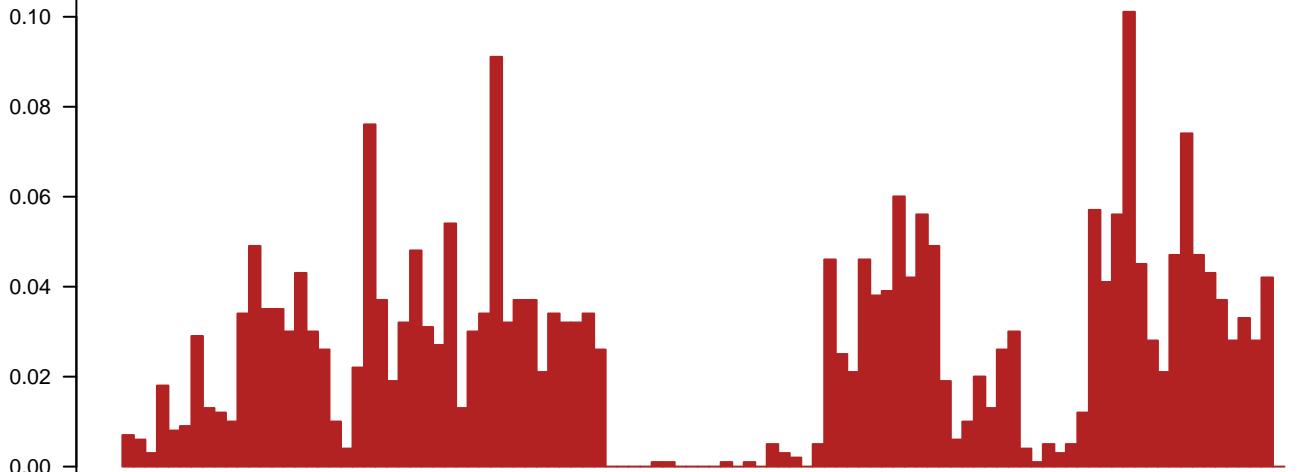


**No SNP densities found**



### Supercontig

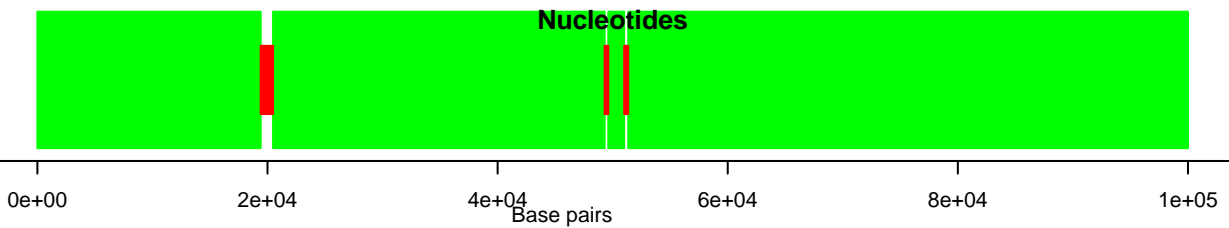
#### Variants per Site



#### Nucleotide Content

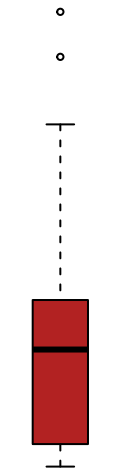
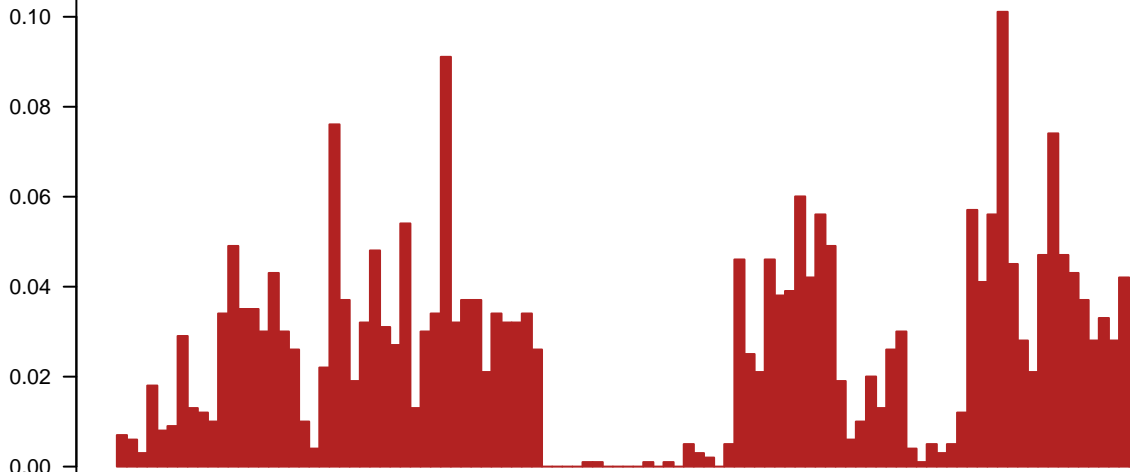


#### Nucleotides

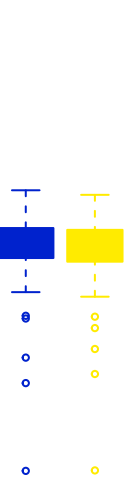


# Supercontig

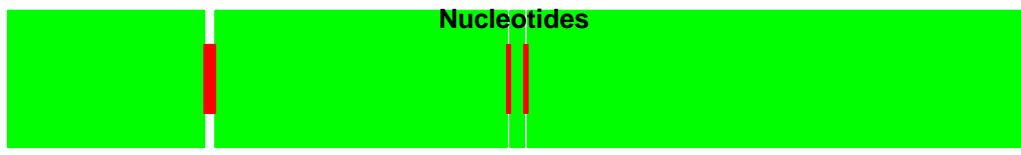
## Variants per Site



## Nucleotide Content



## Nucleotides



0e+00

2e+04

4e+04

Base pairs

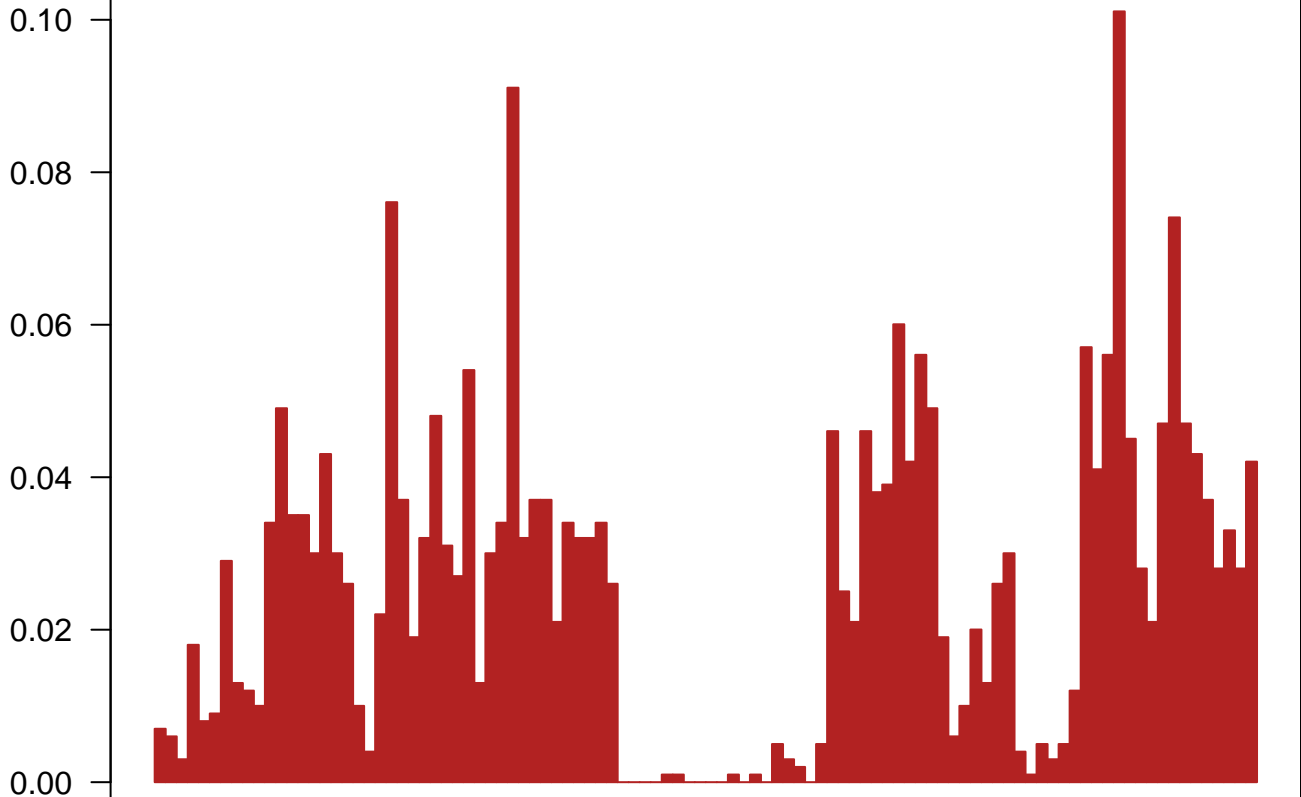
6e+04

8e+04

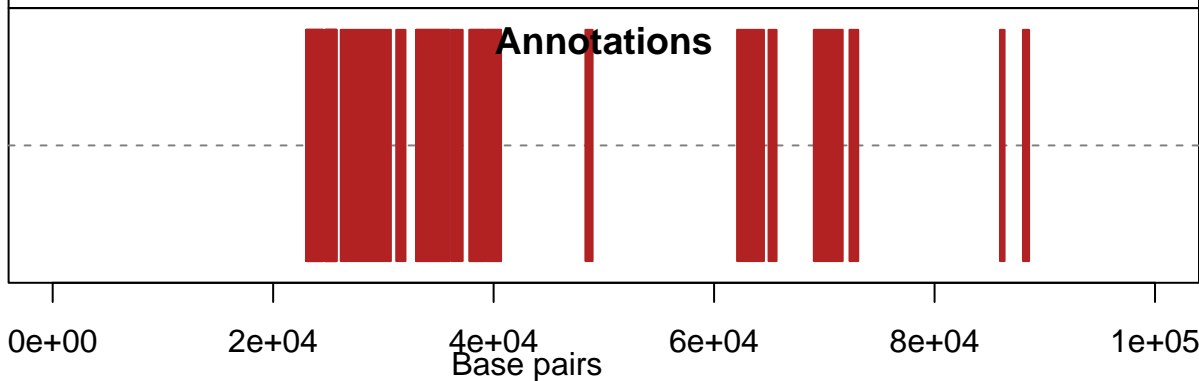
1e+05

# Supercontig

## Variants per Site

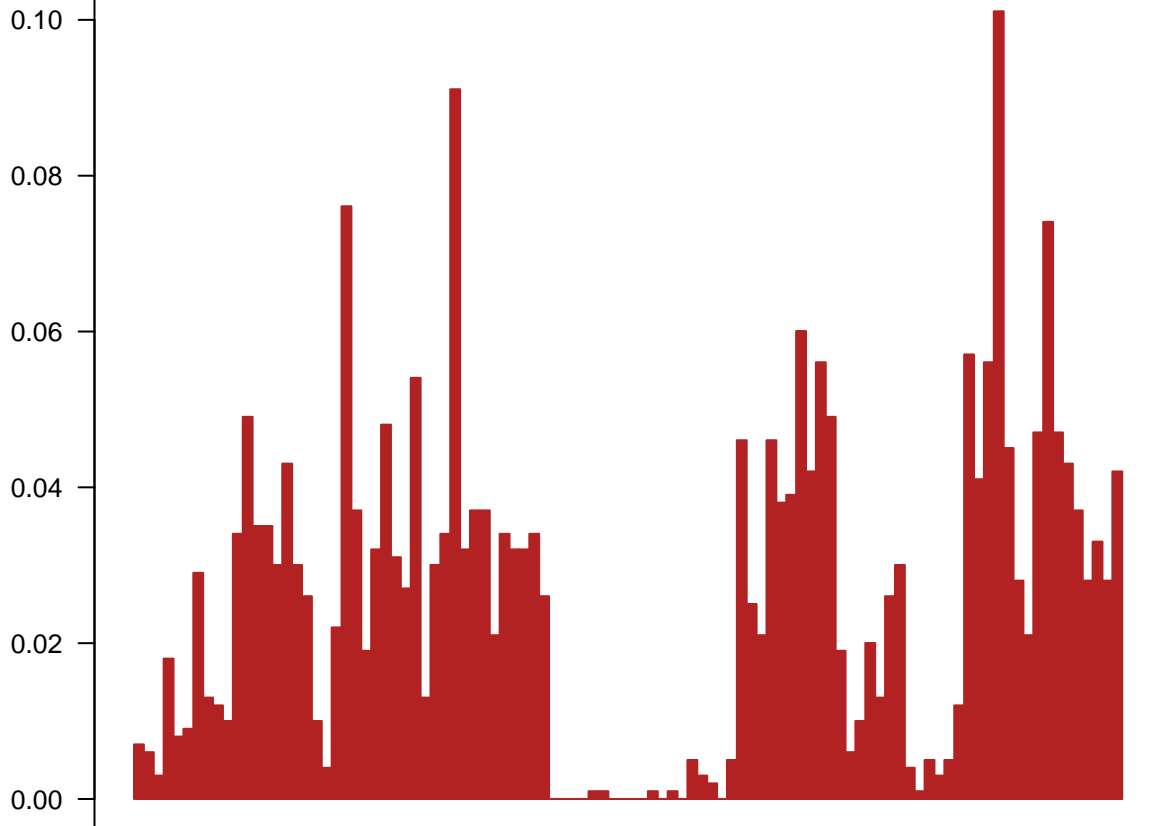


## Annotations

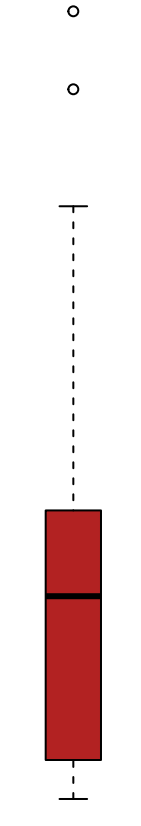
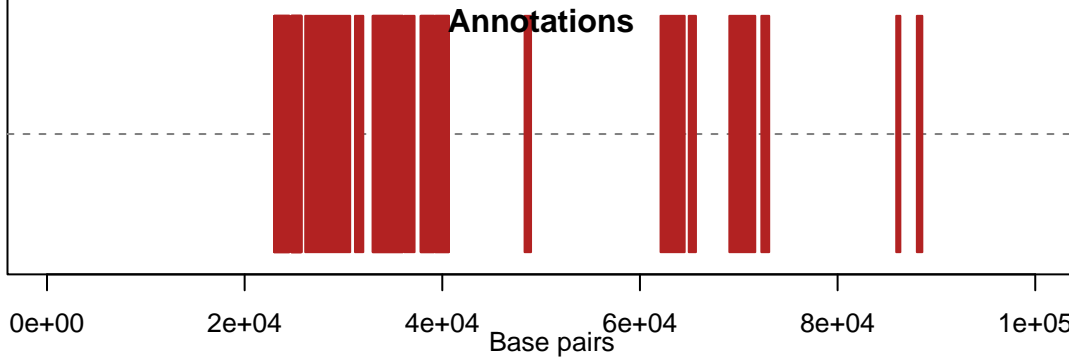


# Supercontig

## Variants per Site



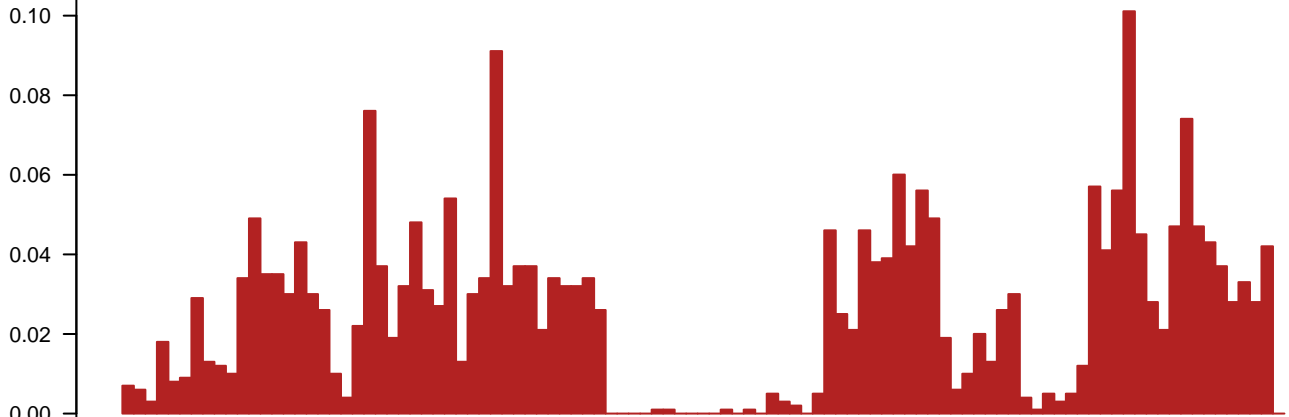
## Annotations





# Supercontig

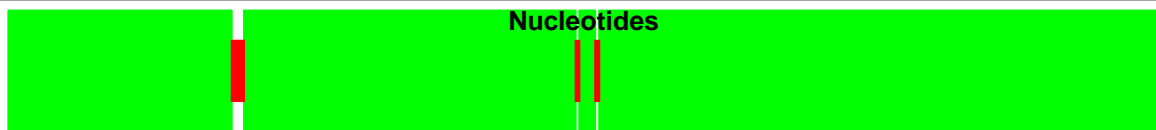
## Variants per Site



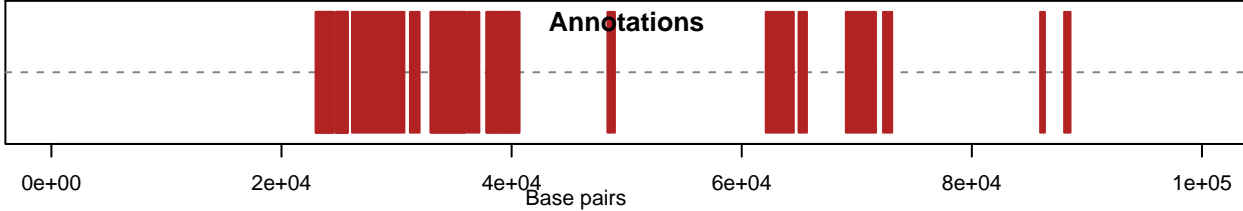
## Nucleotide Content



## Nucleotides

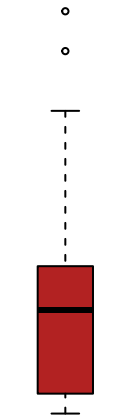
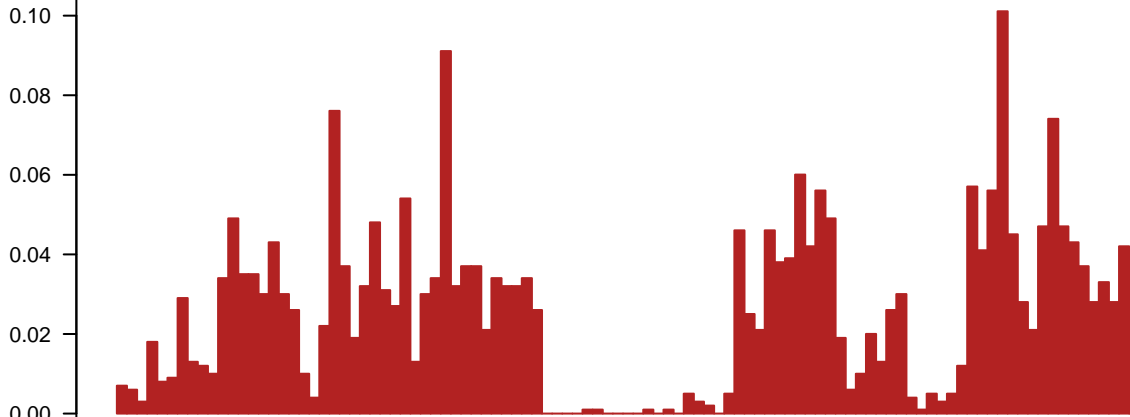


## Annotations

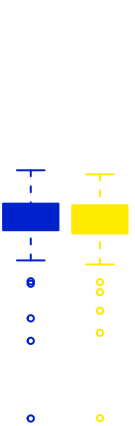


# Supercontig

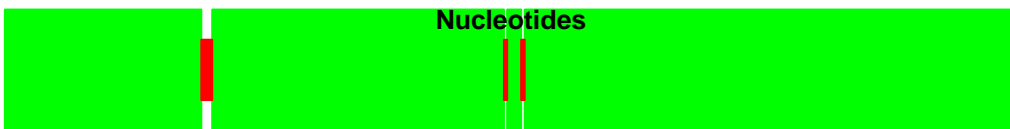
## Variants per Site



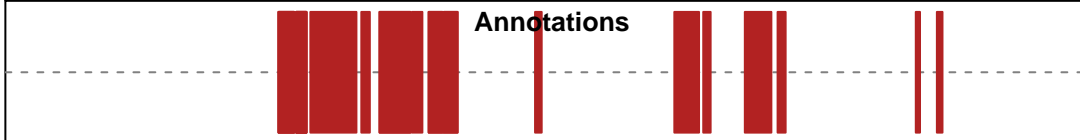
## Nucleotide Content



## Nucleotides



## Annotations



0e+00

2e+04

4e+04

Base pairs

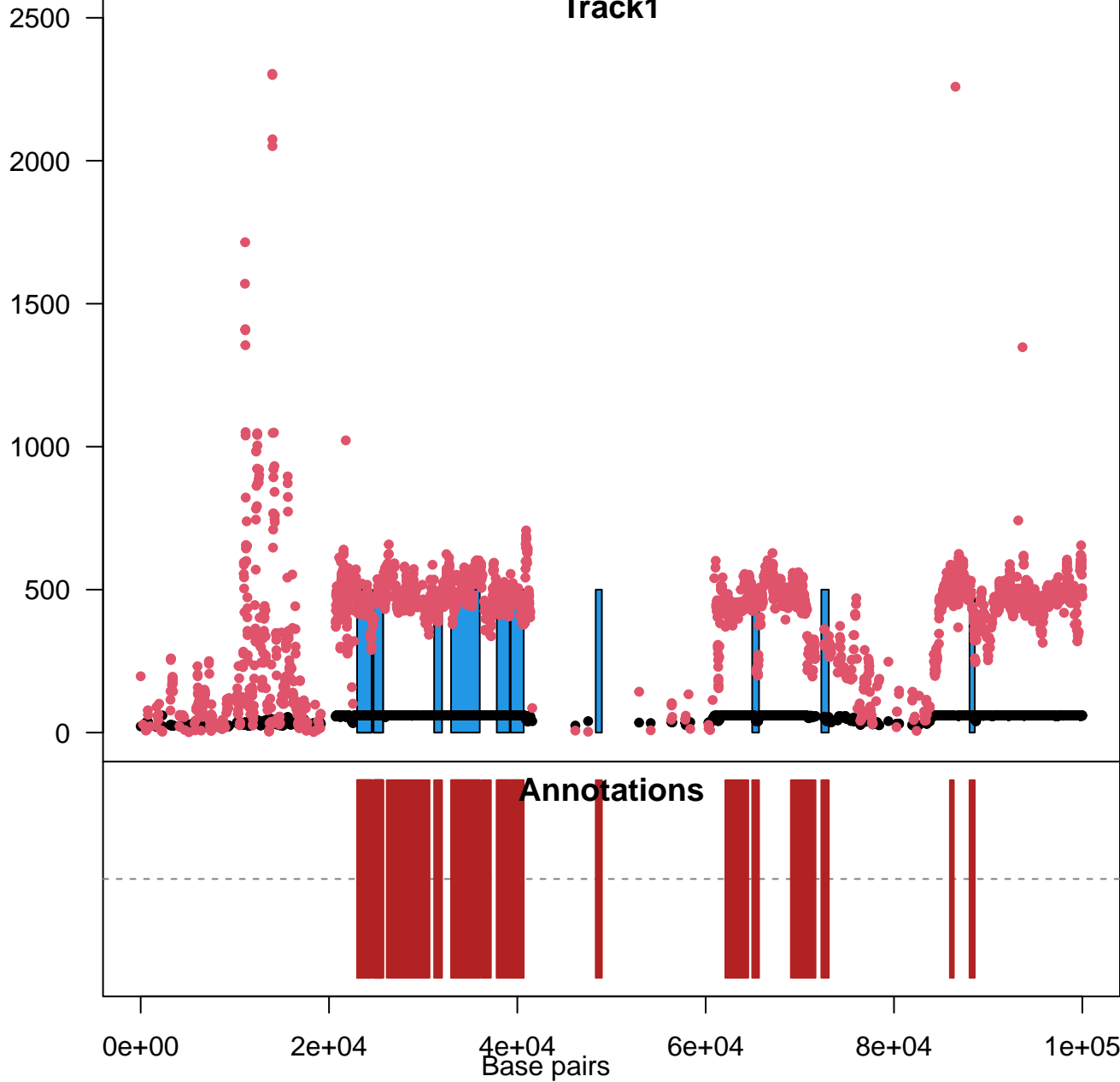
6e+04

8e+04

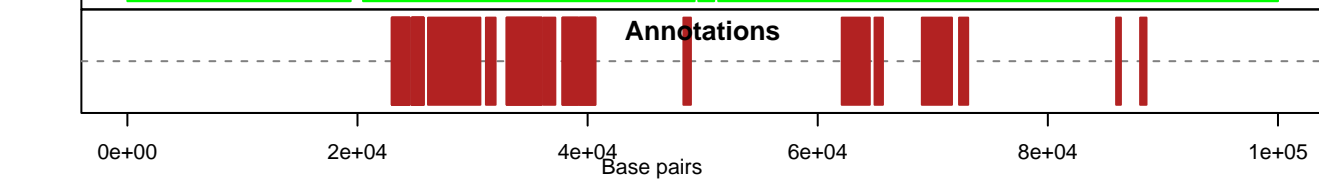
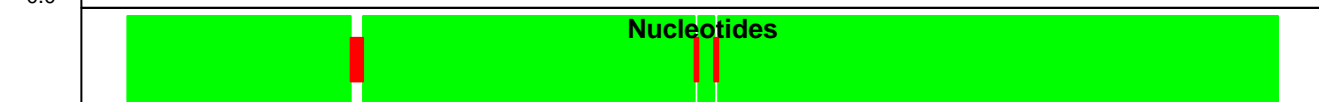
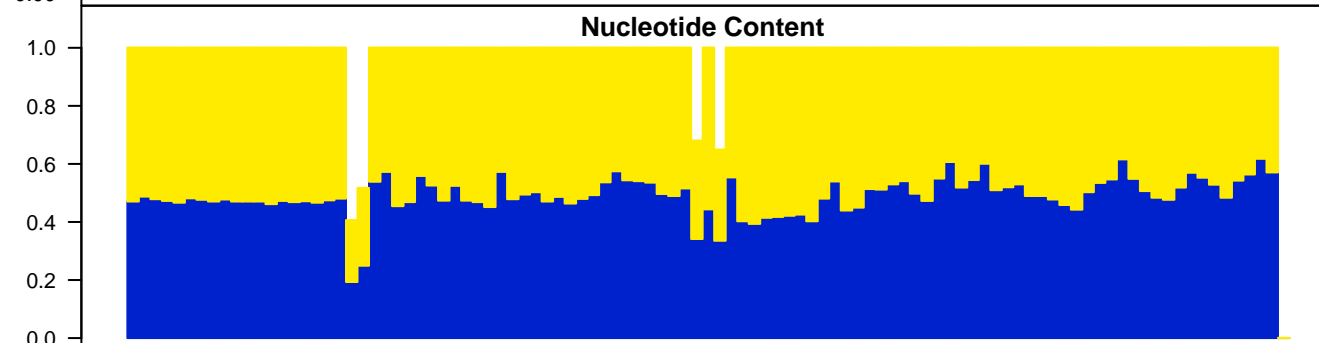
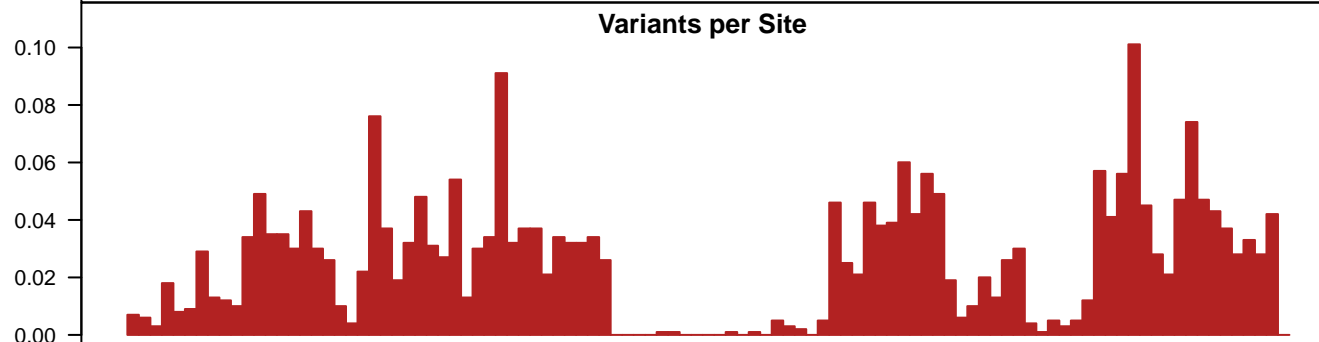
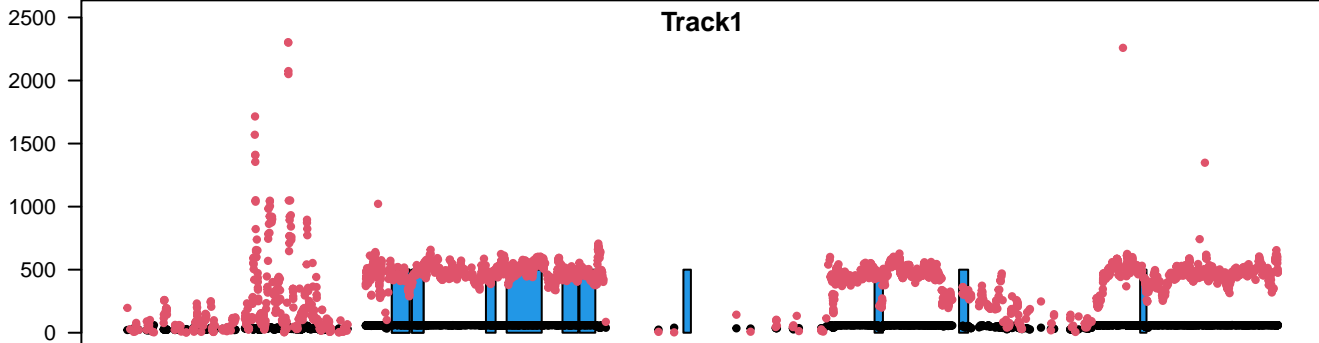
1e+05

# Supercontig

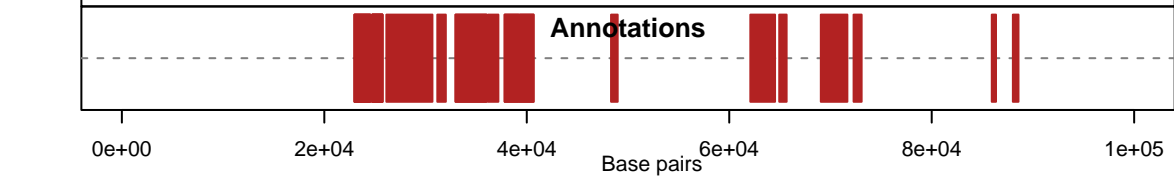
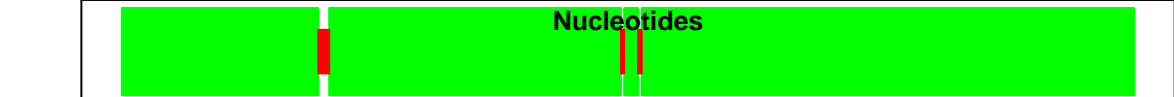
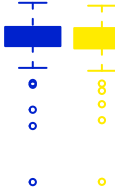
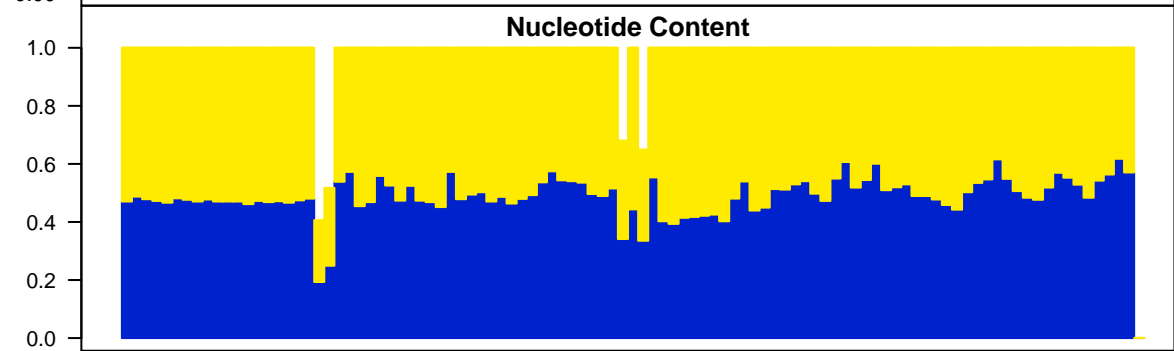
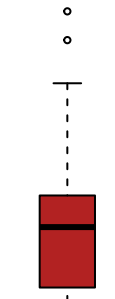
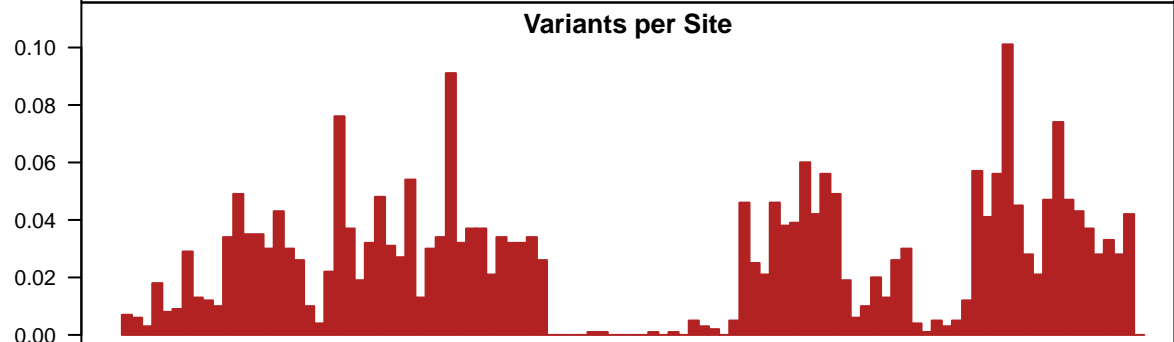
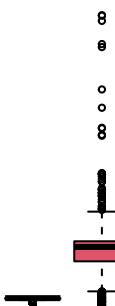
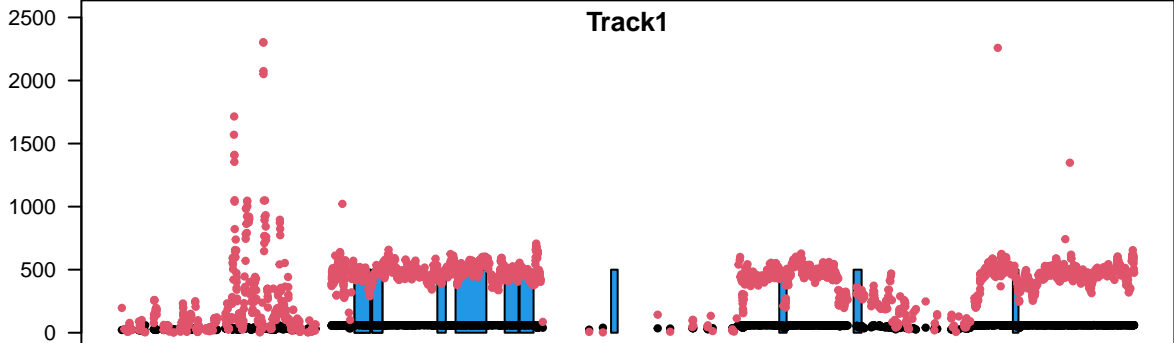
## Track1



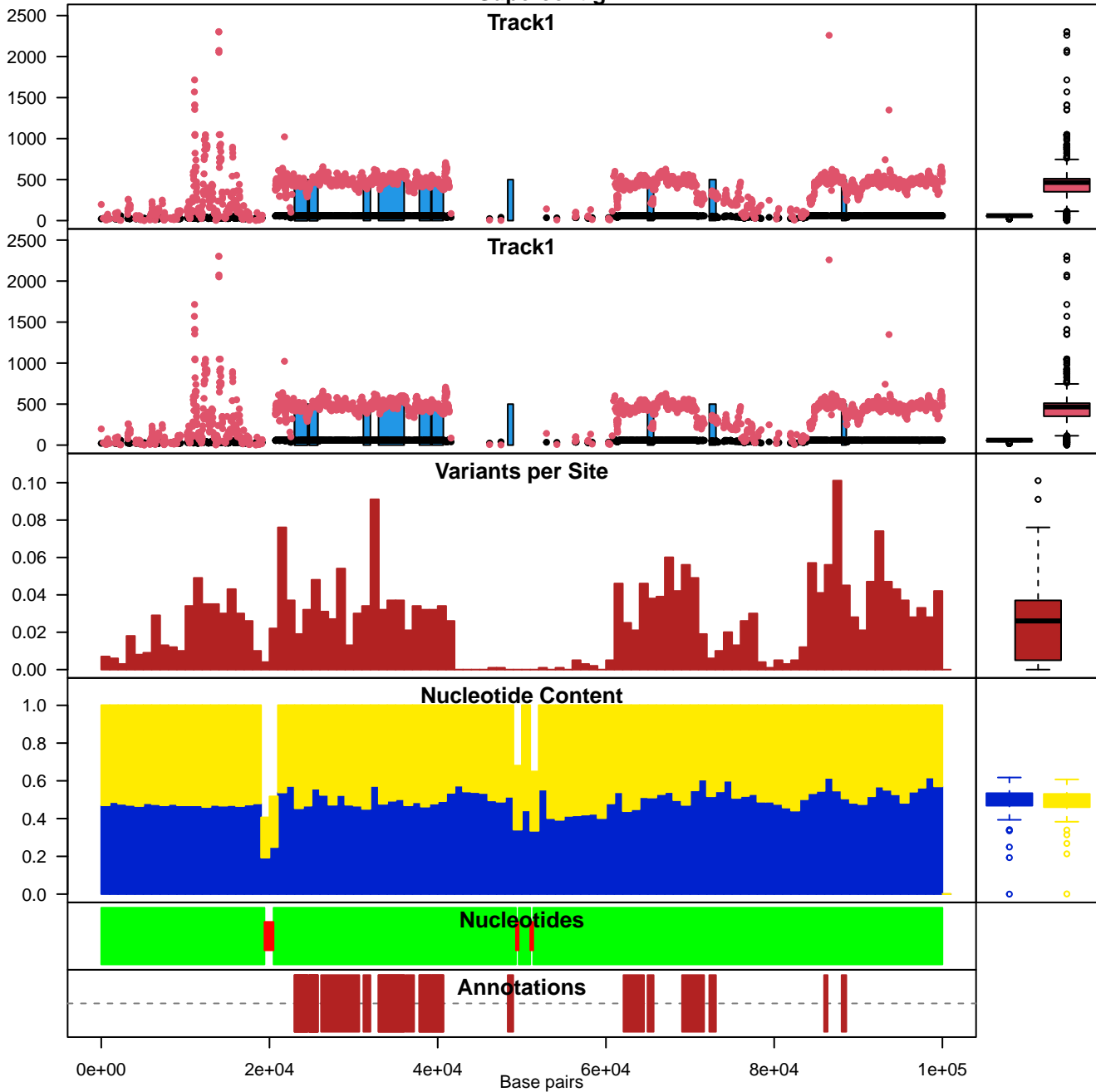
# Supercontig



# Supercontig



# Supercontig



# Supercontig

