

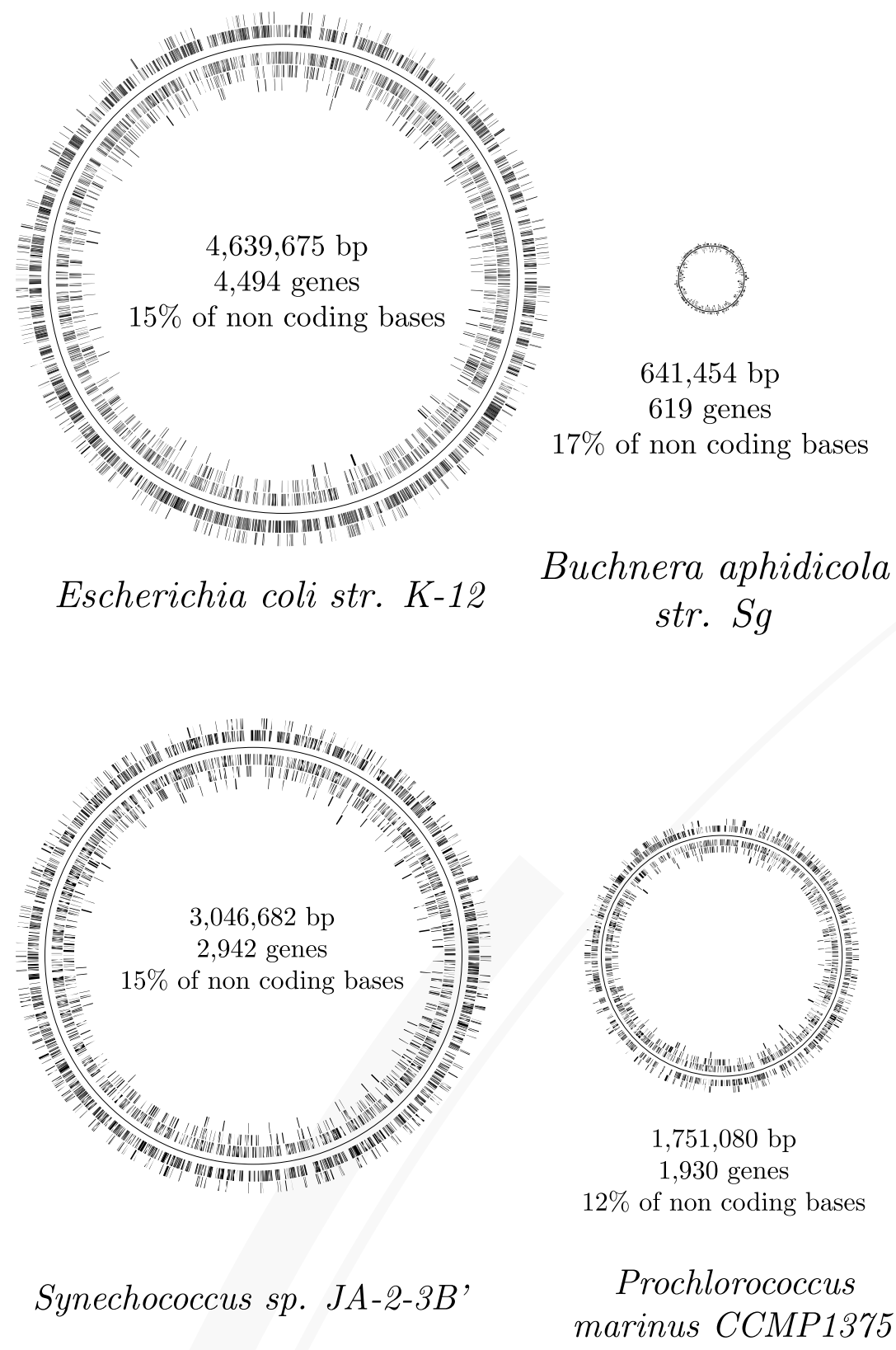
# Simulating evolutionary scenarios to test whether they can induce reductive evolution

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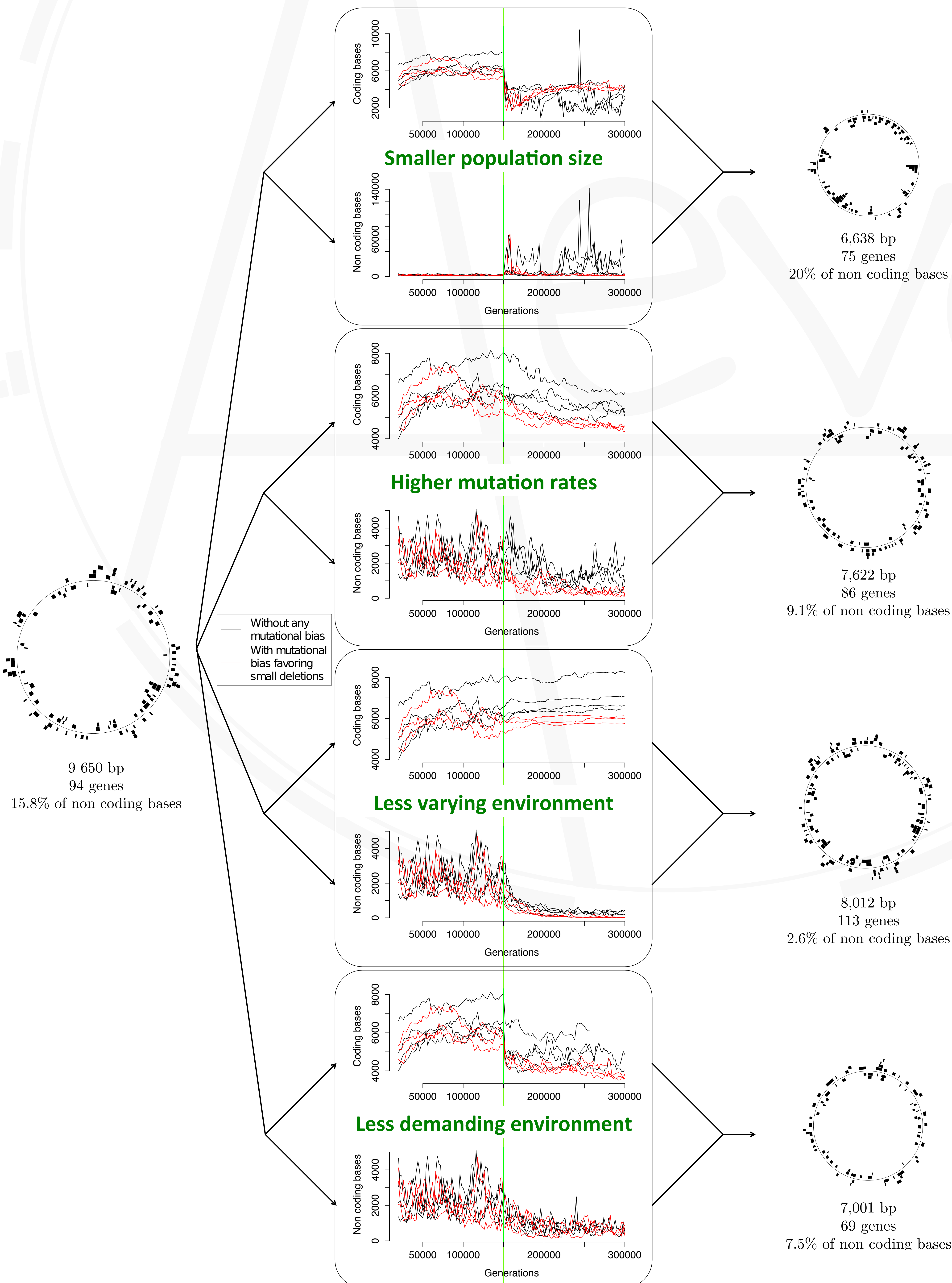


Some bacterial lineages have undergone significant genome shrinkage over the last millions of years, a process called **reductive evolution**. For example, the genome of *Buchnera aphidicola* is only one-seventh the size of the genome of its close relative *E. coli* (Moran and Mira, 2001)

This reductive evolution was initially thought to be a signature of intracellular lifestyle. Thus, explanatory mechanisms related to lifestyle were proposed, like a smaller effective population size, a lower exposure to horizontal transfer, or the uselessness of some genes.

However, reduced genomes were also found in some free-living cyanobacteria with large population sizes like *Prochlorococcus marinus* (Rocap et al., 2003) or *Pelagibacter ubique* (Giovannoni et al., 2005).

**What mechanisms may be responsible for reductive evolution?**

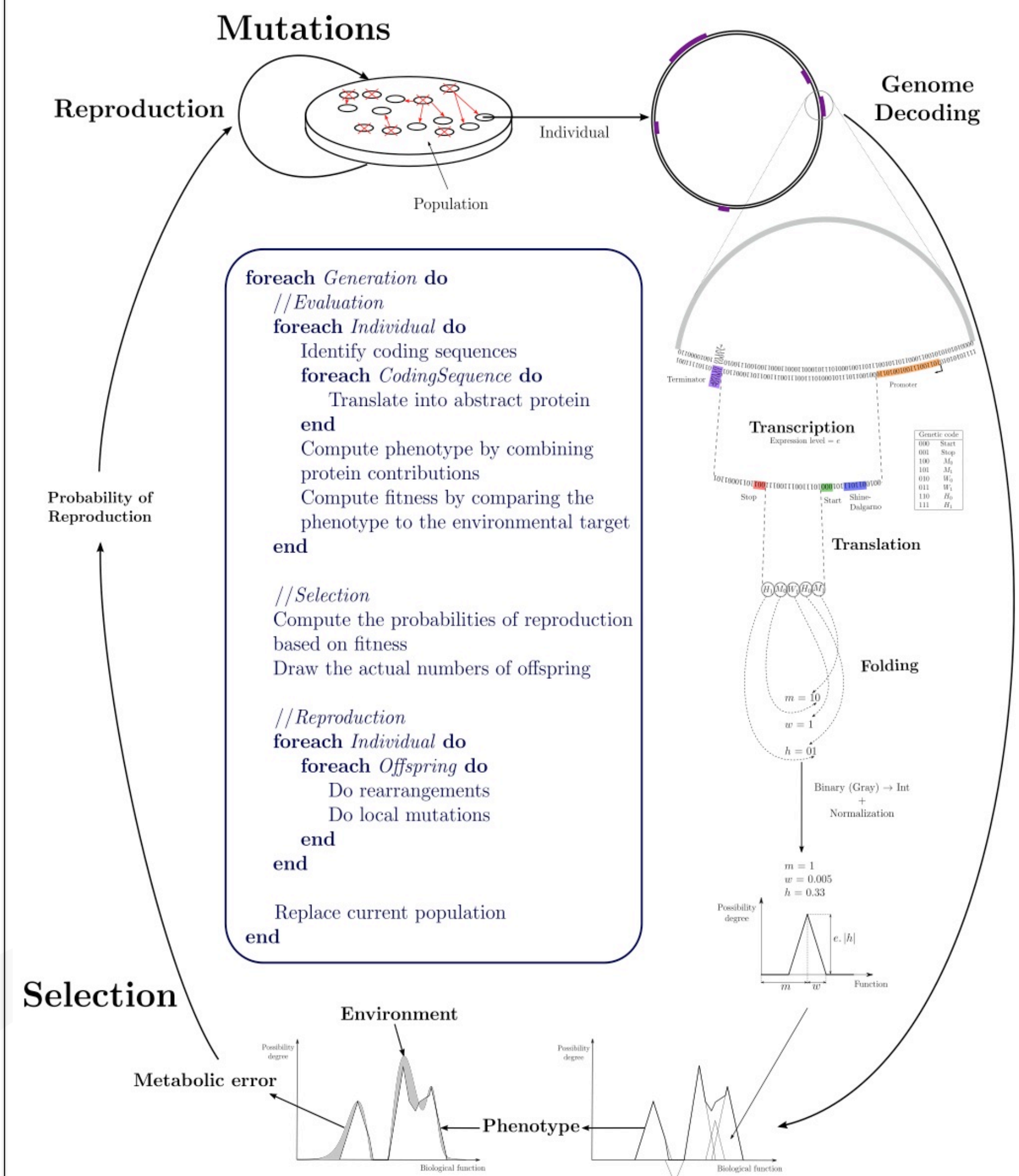


Before change of one parameter

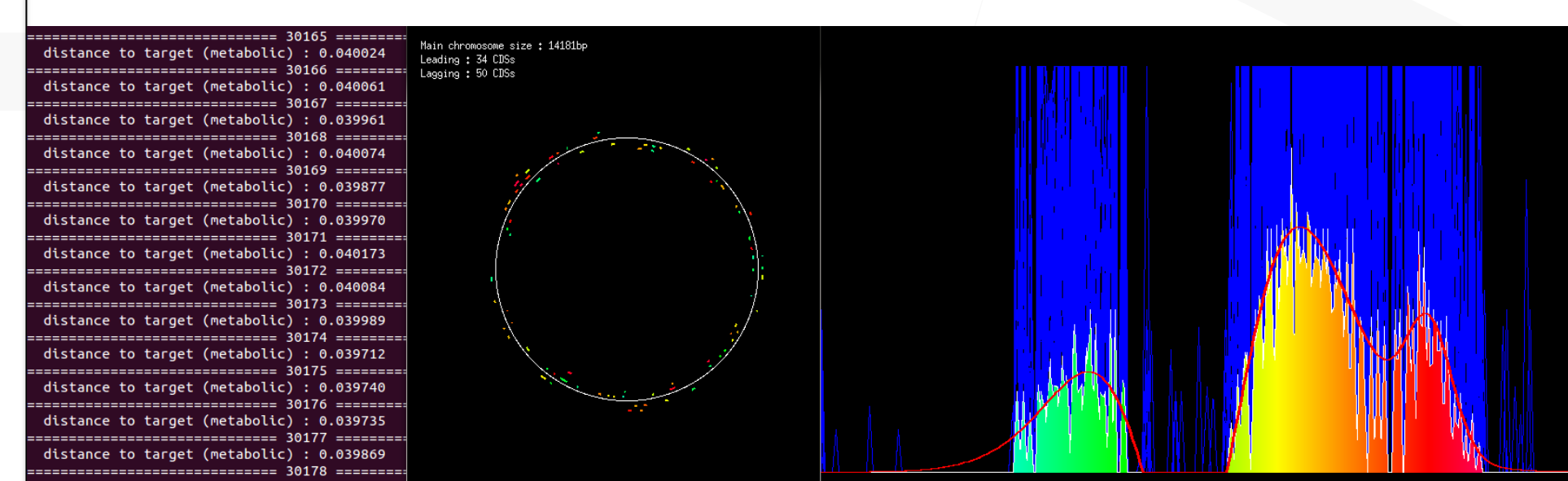
After change of one parameter

## Individual based simulation approach: *Aevol* (Knibbe et al, 2007)

*Aevol* is a digital genetics model: populations of digital organisms are subjected to a process of selection and variation (Hindré et al, 2012).

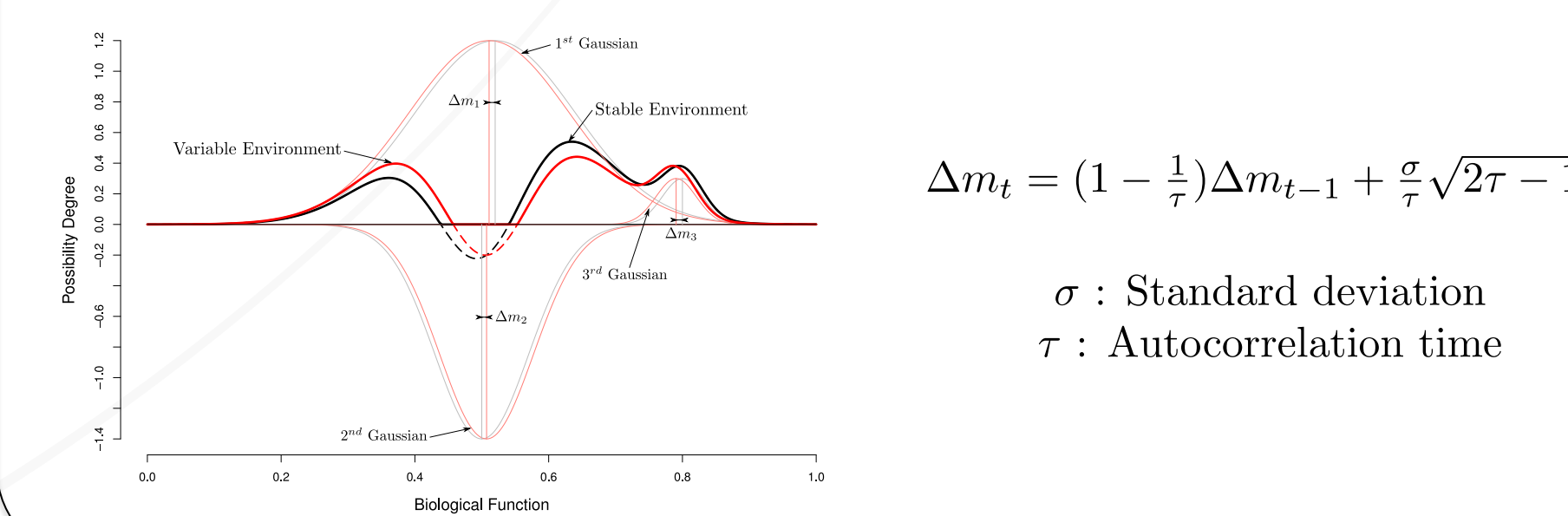


Since *Aevol* integrates a precise and realistic model of the genome, it allows for the study of structural variations of the genome (e.g. number of genes, synteny, proportion of coding sequences)



## Variation of target environment

Gaussian first-order autoregressive process



## Conclusion

- **Smaller population size**
  - Loss of genes
  - Lengthening of intergenic sequences
- **Higher mutation rates & Less demanding environment**
  - Loss of genes
  - Shortening of intergenic sequences
- **Less varying environment**
  - Gain of genes
  - Shortening of intergenic sequences

**Future work**  
Mutation analysis on winning lineages to explain these evolutions

## References

- Giovannoni et al, 2005, *Science*, 309: 1242-1245  
Hindré et al, 2012, *Nat. Rev. Microbiol.*, 10: 352-365  
Knibbe et al, 2007, *Mol. Biol. Evol.*, 24: 2344-2353  
Moran and Mira, 2001, *Genome Biol.*, 2: 1-12  
Rocap et al., 2003, *Nature*, 424: 1042-1047