

# Investigation of baker's yeast production robustness

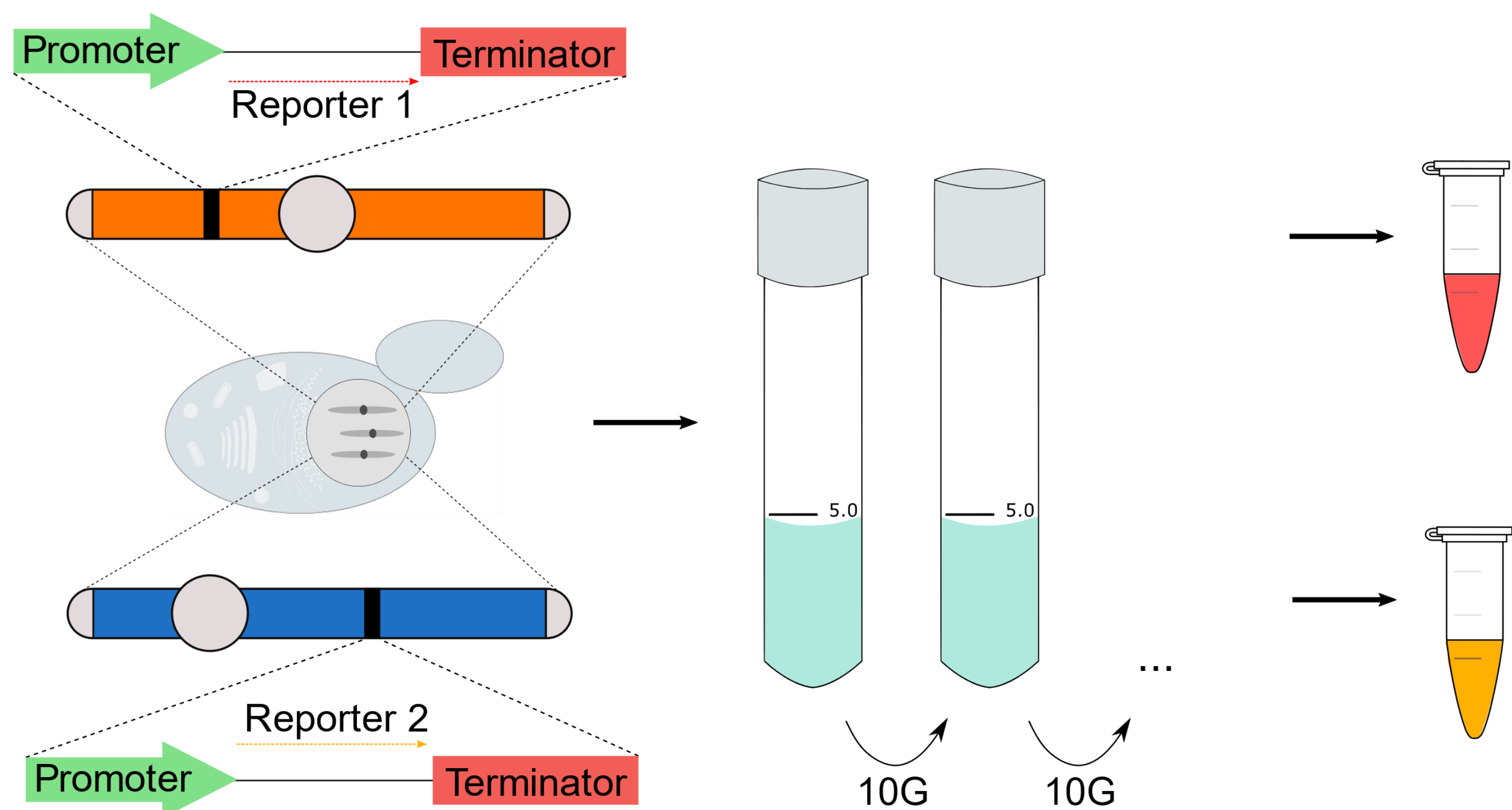
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## Introduction

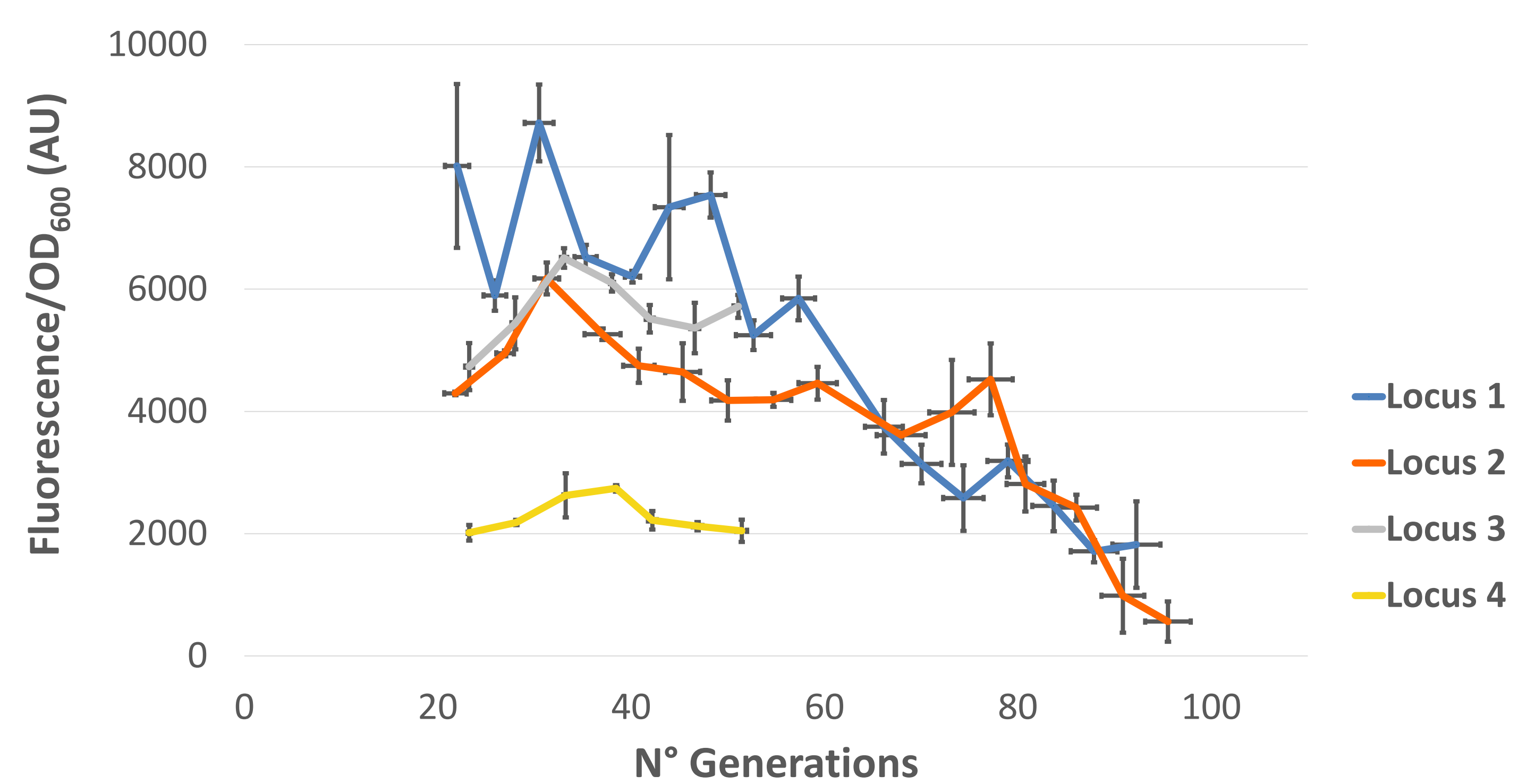
*Saccharomyces cerevisiae* has historically grown to a major microbial production host for the synthesis of specialty compounds applicable in pharmaceuticals, food, feed, biofuels and more. Industrial processes require cultivation of this yeast for many generations before the actual production phase begins (**seed train**). During this seed train yeast cells multiply, specialize and potentially evolve, introducing **population heterogeneity**. This heterogeneity is maximal at the start of the production phase, which means the economic viability can be jeopardized. Seed train heterogeneity is at this point poorly studied. To alleviate this issue, we started studying the impact of loci of genomic integration on seed train heterogeneity and identifying **stable genomic loci**.

## Methods



- ✓ Reporter gene at a reference chromosomal location as **benchmark**
- ✓ Second **reporter** gene at one or more chromosomal locations
- ✓ Fluorescence over time in a sequential batch cultivation

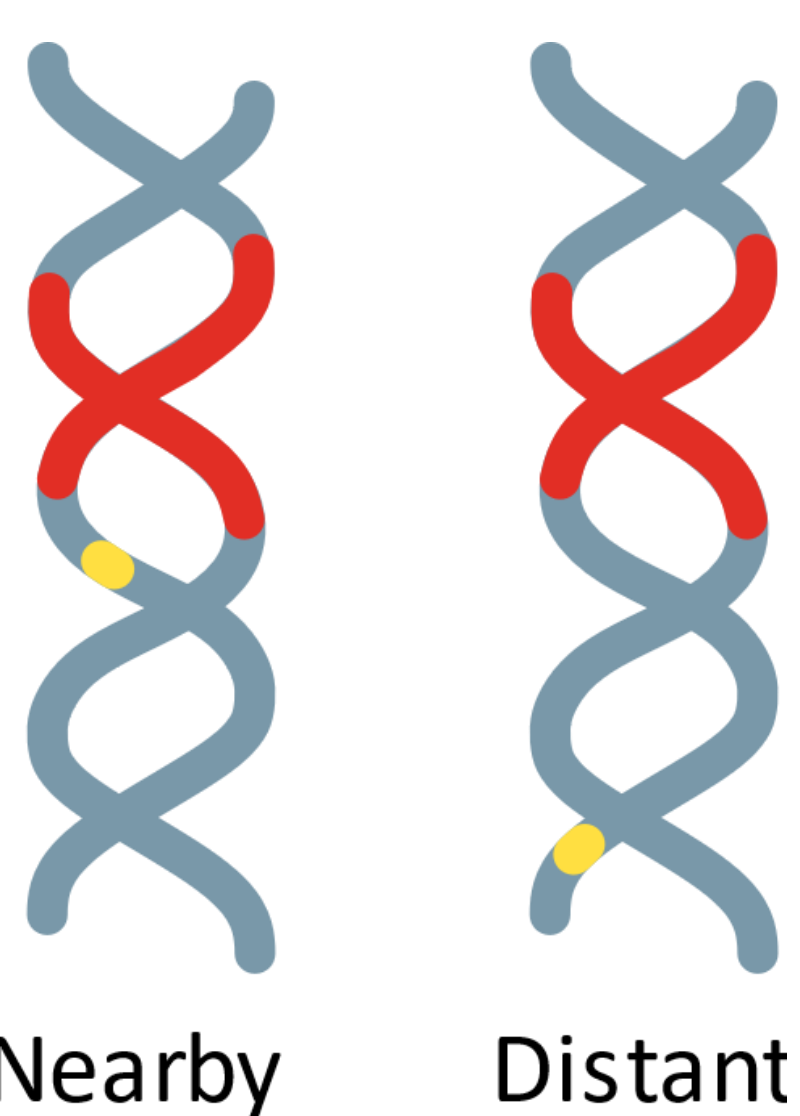
## Preliminary results



- 🔍 Locus-dependent **expression level**
- 🔍 Locus-dependent **robustness**

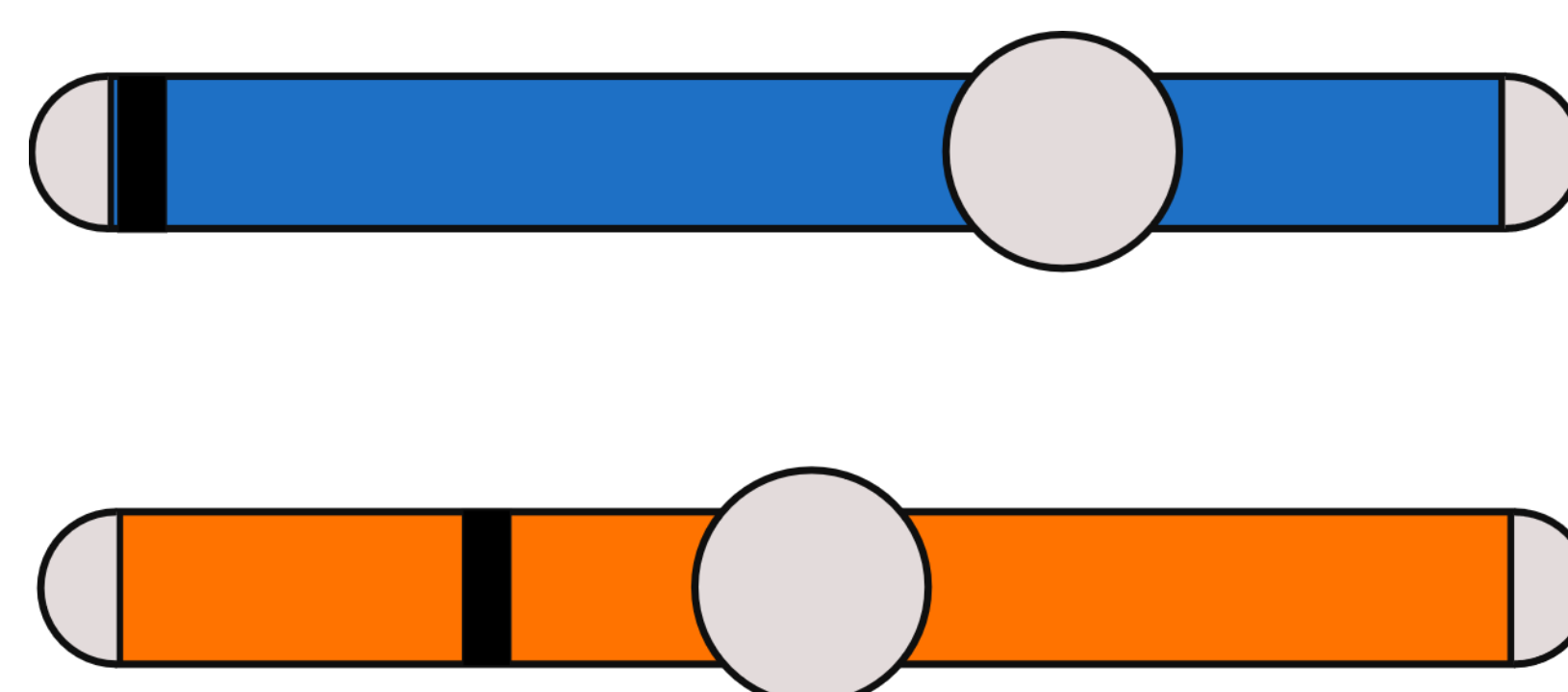
## Experimental design

### Essential regions



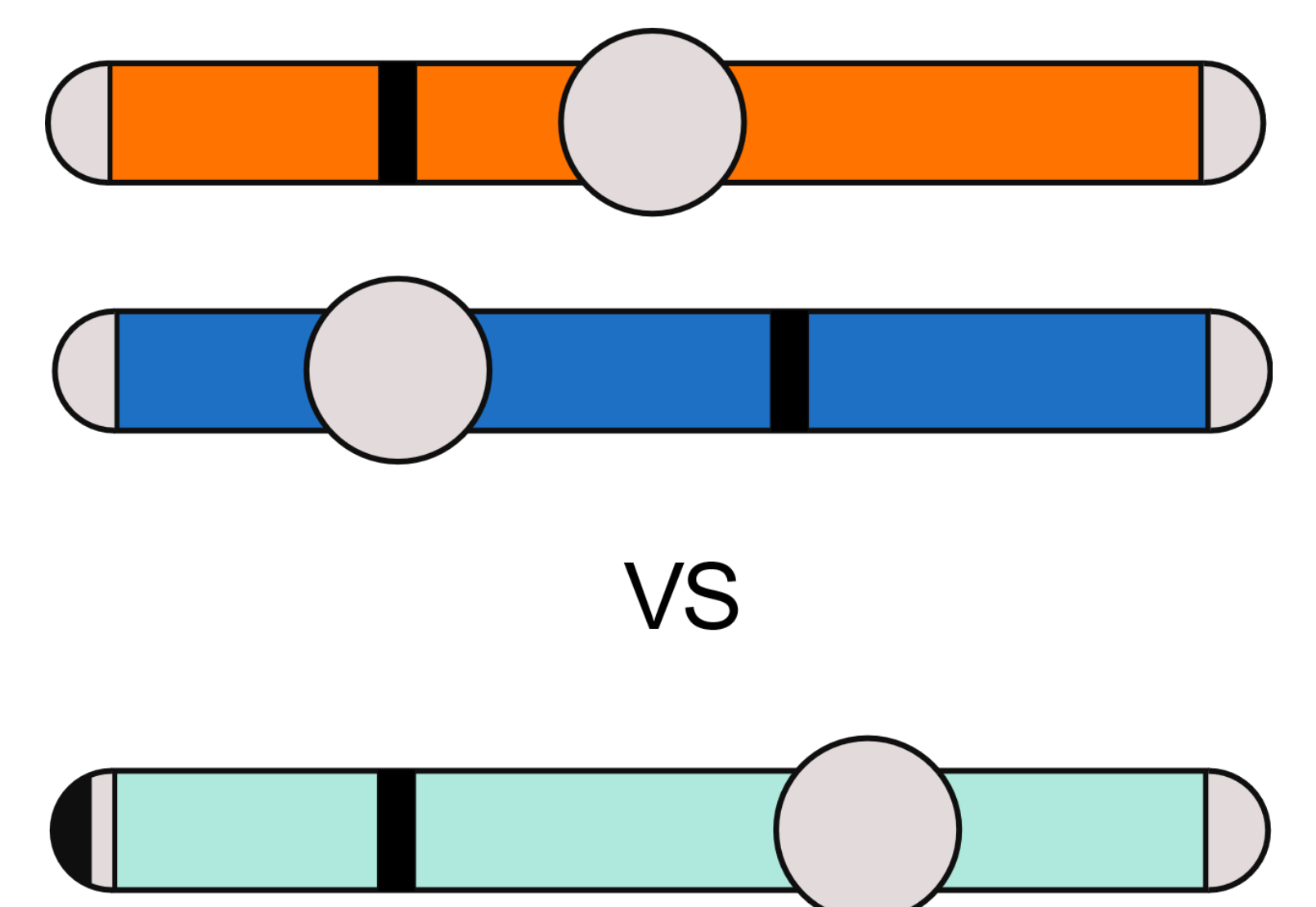
- 📋 Influence of proximity to essential regions e.g. housekeeping genes

### Regulated regions



- 📋 Influence of proximity to regulated or silenced regions e.g. telomeres

### Copy number



- 📋 Influence of gene copy number
- 📋 Interchromosomal VS intrachromosomal

## Conclusions

- ✓ Robustness issues over multiple generations jeopardize production
- ✓ Genomic loci influence both stability and expression level
- ✓ Experimental design-based study to solve seed train heterogeneity

## Collaboration?

Feel free to contact us for any information regarding this research or for collaborations!

Or check out our website: [www.inbio.be](http://www.inbio.be)



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