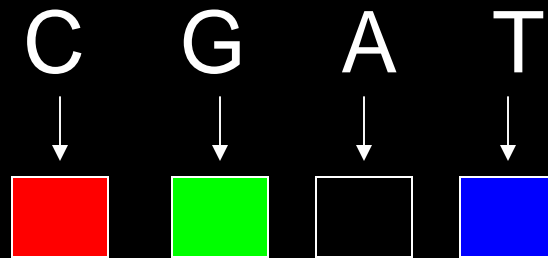
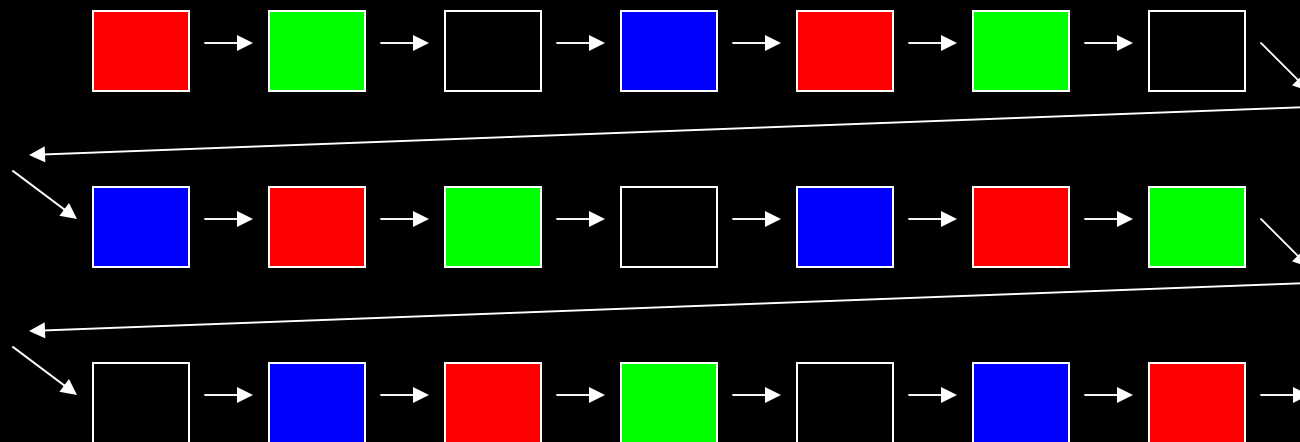


# Skittle Genome Visualizer

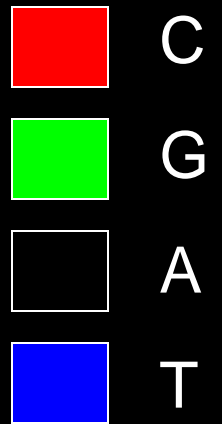
Symbol → Color



Text Wrap Sequence

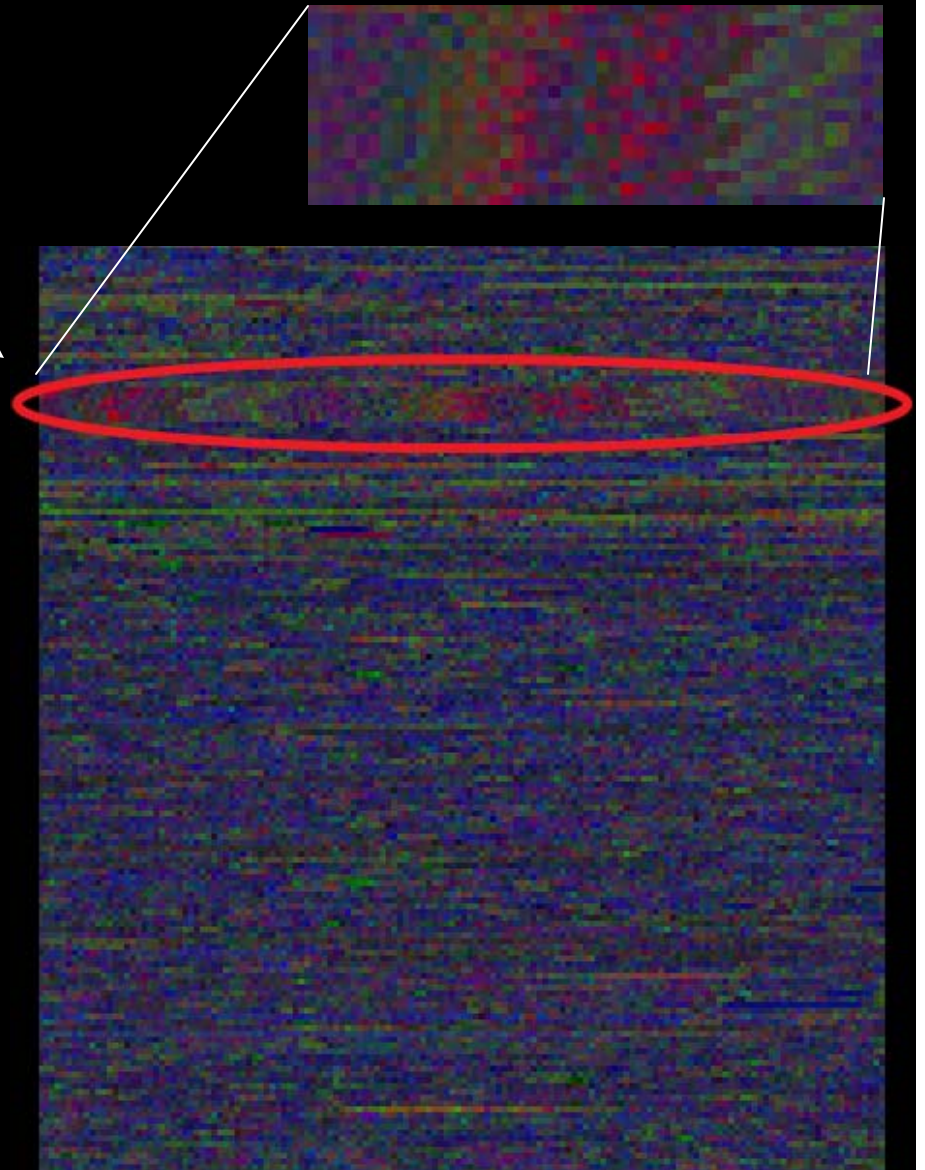
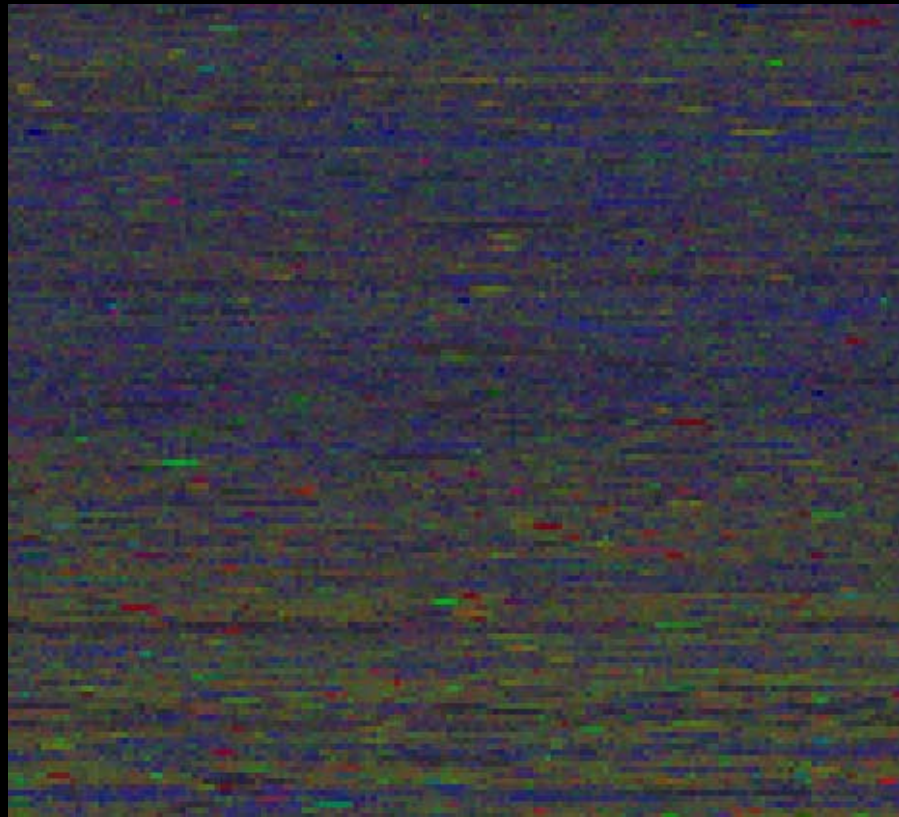


# Nucleotide Bias



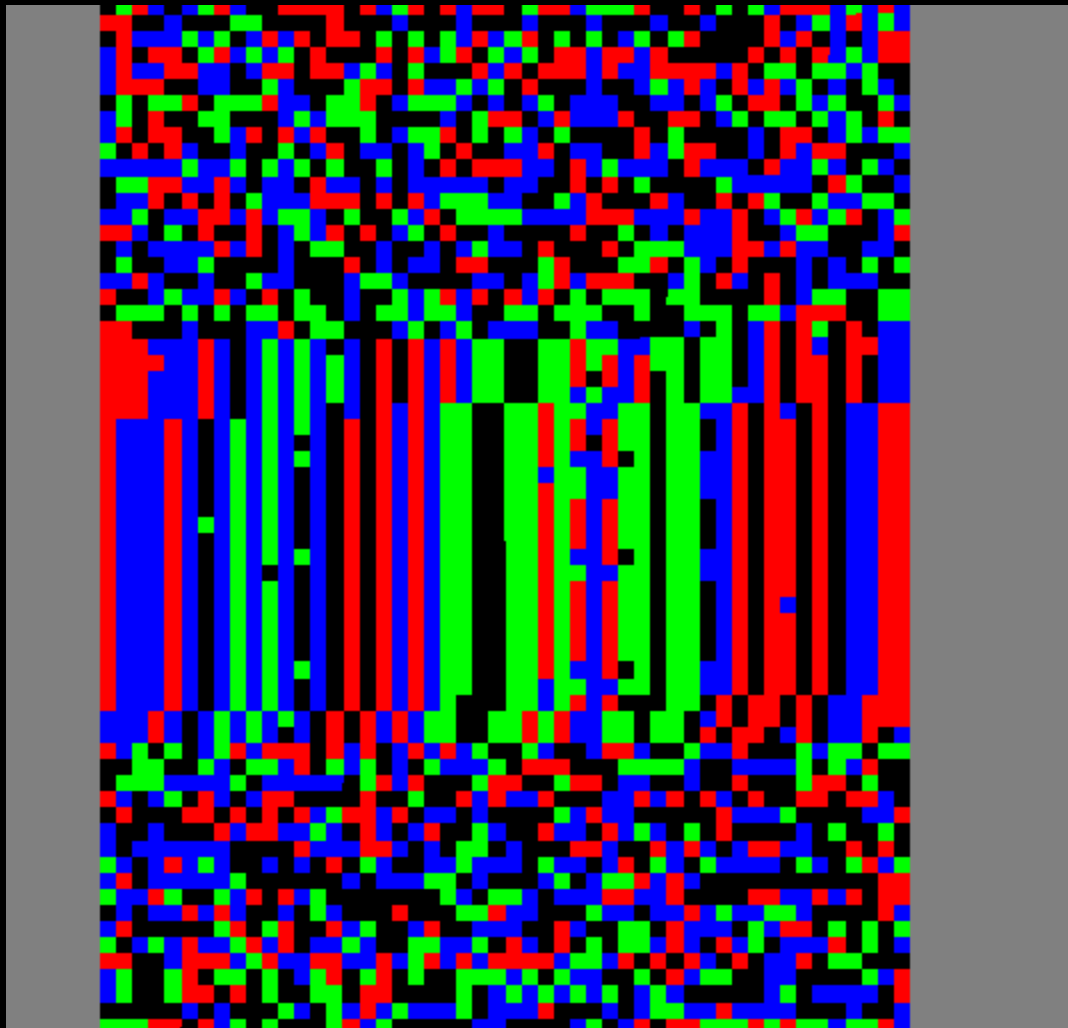
# Chromosome Overview

- “Zoom out” using color averaging
- Whole chromosome navigation
- Identify segmental duplications



# Periodicity → Tandem Repeats

When the display width is a multiple of the periodicity, tandem repeats appear as vertical bar patterns.

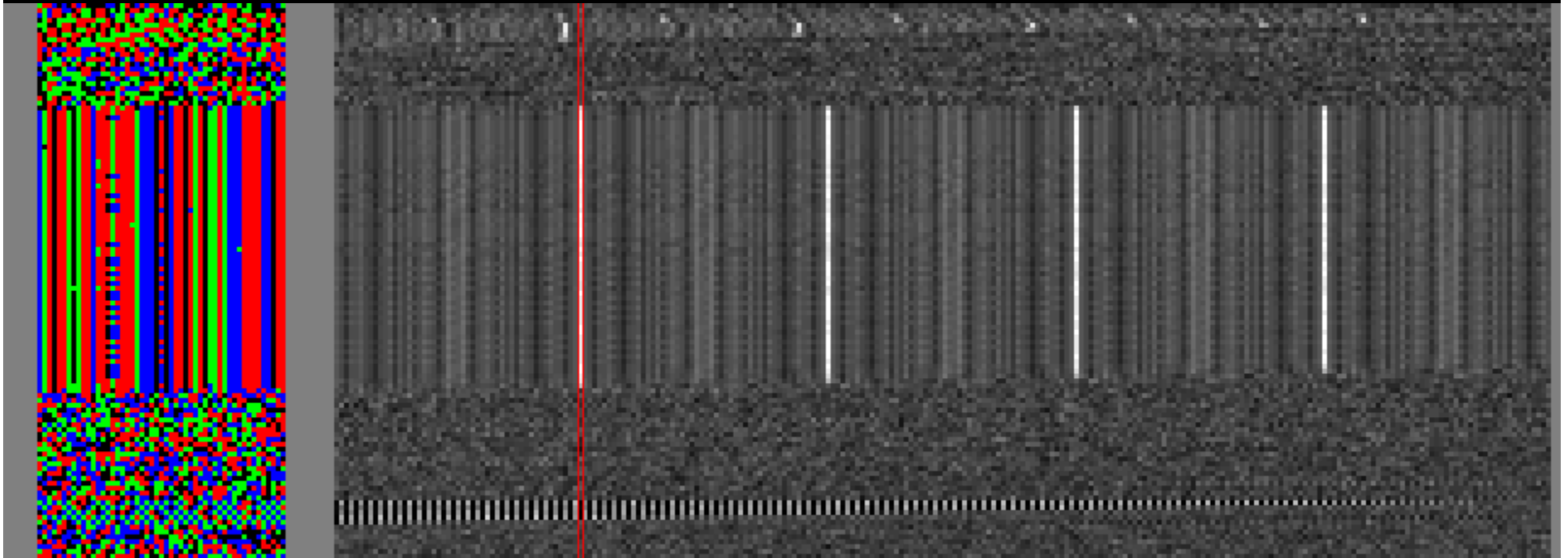


- Point substitutions are seen as deviations from the norm.
- Insertions/deletions appear as right or left shifts in the pattern.
- Tandem repeats (especially short ones) can often be spotted because of a change in nucleotide bias.

# Frequency Map

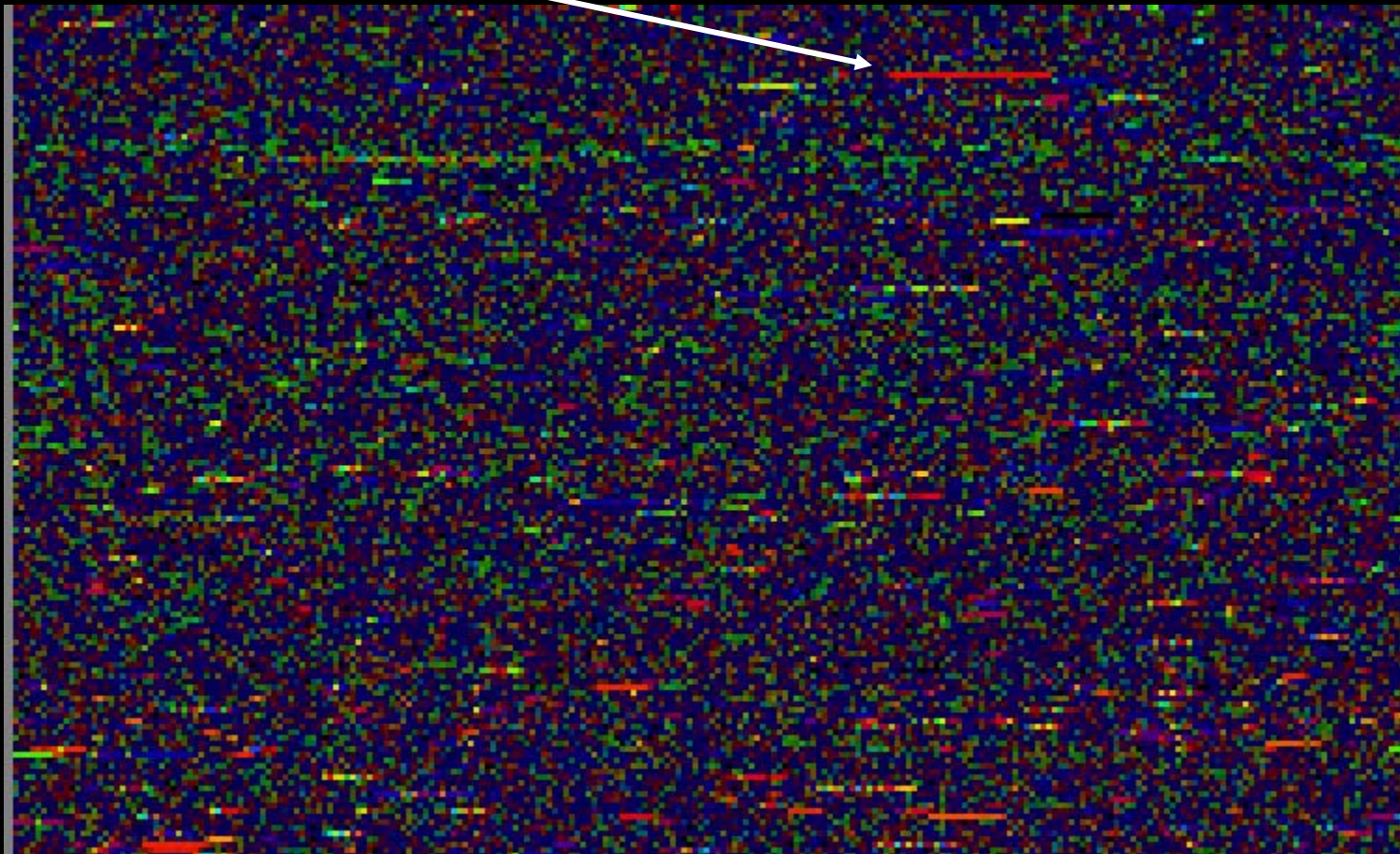
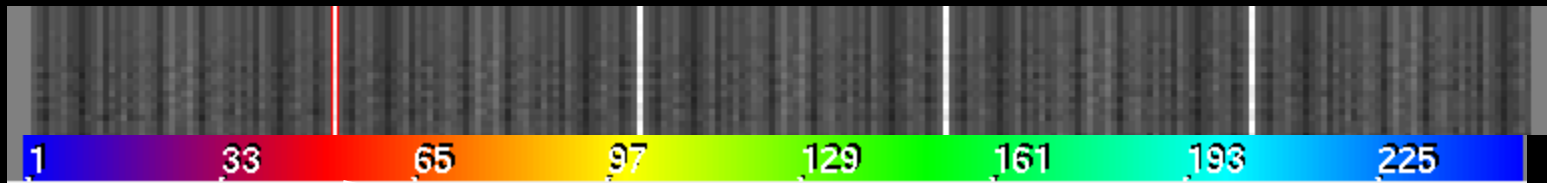
Purpose: Detect tandem repeats without the need to scroll side to side.

- 1 Frequency Map Row = 1 Nucleotide Display Row
- X-axis = comparison offset distance between 1 – 250bp
- Counts the number of matching nucleotides at each comparison offset
- High scores = white. Random (25%) = grey. Zero Similarity = black.



# Repeat Landscape

Color by mapping the 1-250bp offsets to a spectrum.



Scale=  
1 pixel:  
100 bp  
  
4Mbp:  
1 screen