

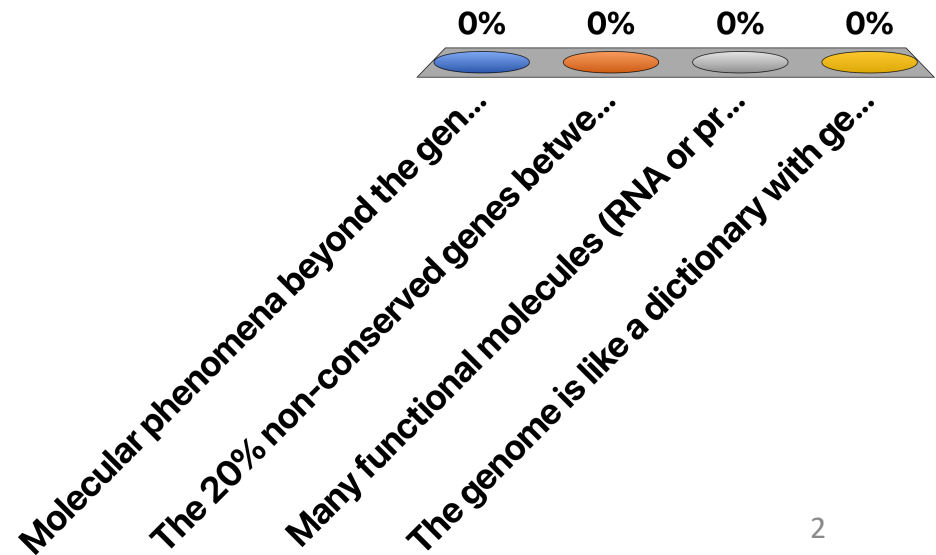
Interactive questions

Lecture 3: The regulatory genome

With correct answers highlighted in green

Why are we so phenotypically different?

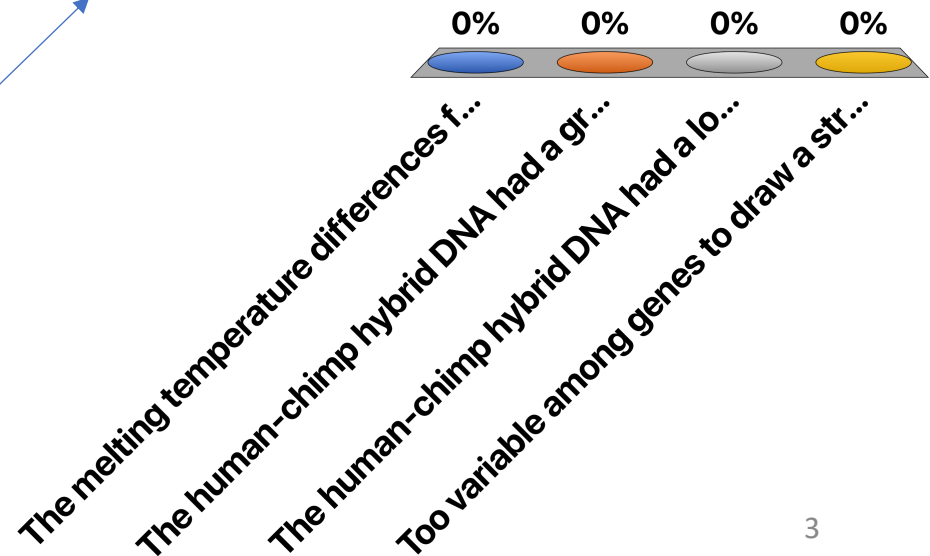
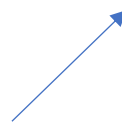
- A. Molecular phenomena beyond the genome (i.e. epigenetics or nurture (e.g. environment)) are key determinants of phenotypic diversity
- B. The 20% non-conserved genes between mouse and human are the main determinants of diversity
- C. Many functional molecules (RNA or protein) that determine diversity remain to be identified and characterized, which may explain diversity
- D. The genome is like a dictionary with genes being words, but each organism makes different sentences with the same words, resulting in diversity



What did King and Wilson see?

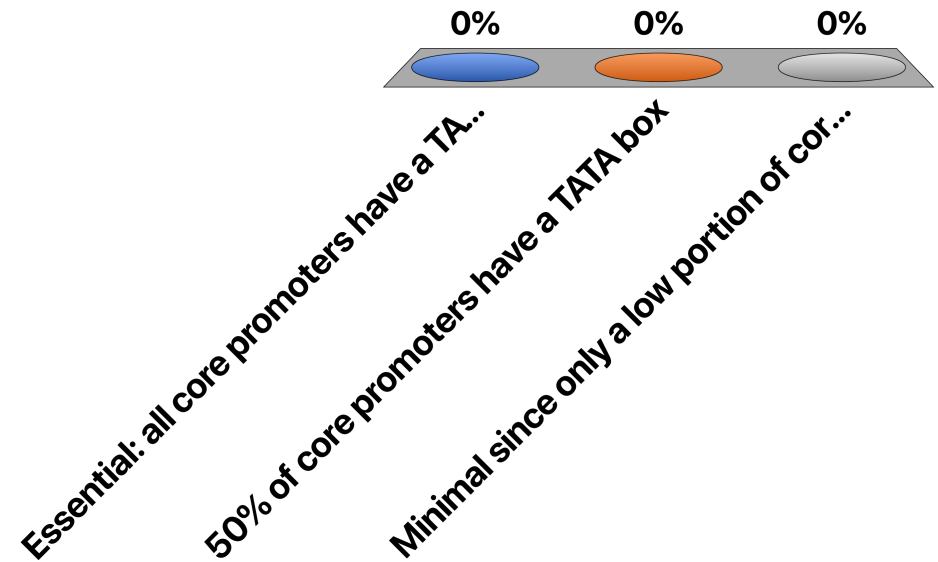
- A. The melting temperature differences for all three DNA “types” is **negligible**
- B. The human-chimp hybrid DNA had a **greater** melting temperature than that of only human or chimp
- C. The human-chimp hybrid DNA had a **lower** melting temperature than that of only human or chimp
- D. Too **variable** among genes to draw a strong conclusion

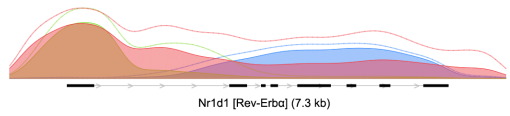
While lower, the difference was still much smaller than expected.



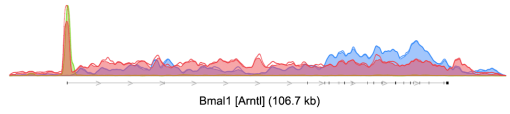
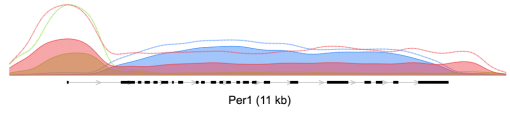
What is the distribution of the well-known TATA box among gene promoters?

- A. Essential: all core promoters have a TATA box
- B. 50% of core promoters have a TATA box
- C. Minimal since only a low portion of core promoters feature such a box



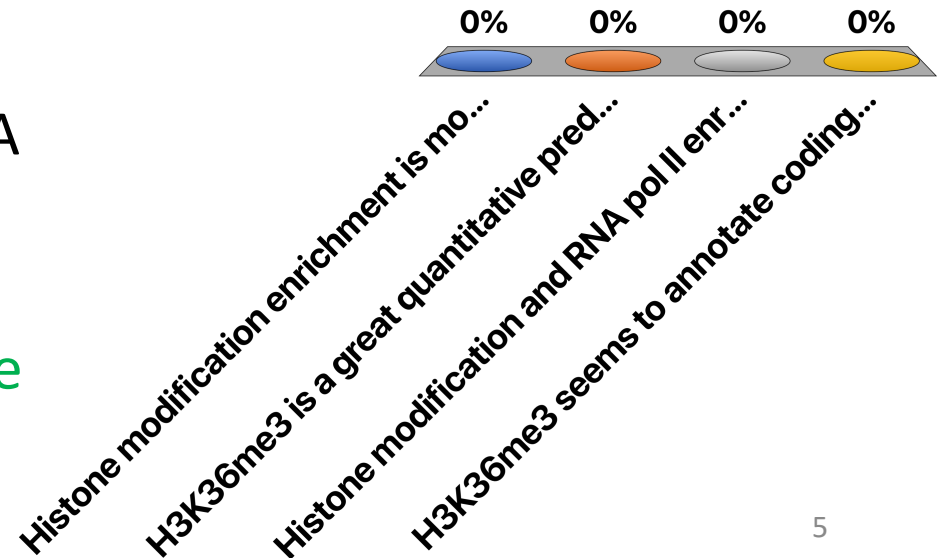


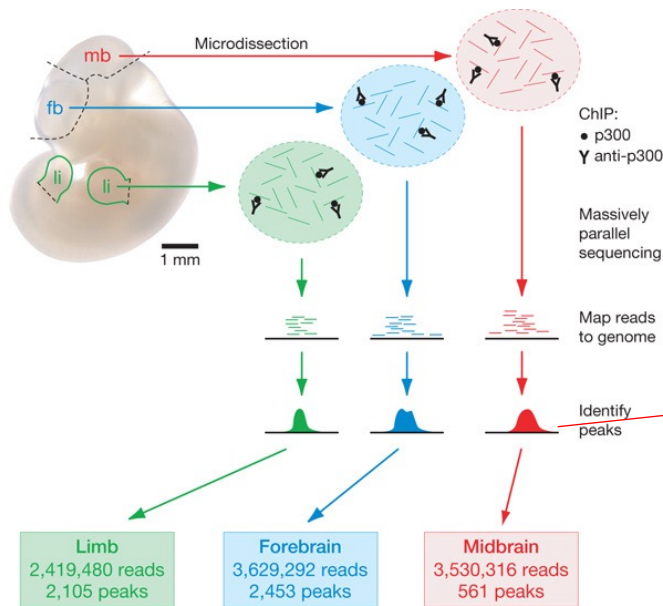
What can you conclude from these data?



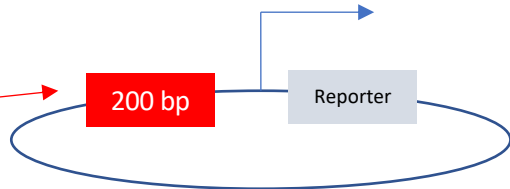
L3Q7

- A. Histone modification enrichment is more dynamic than RNA pol II DNA occupancy
- B. H3K36me3 is a great quantitative predictor of RNA pol II activity
- C. Histone modification and RNA pol II enrichments are completely synchronized
- D. H3K36me3 seems to annotate coding regions, whereas H3K4me3 promoters





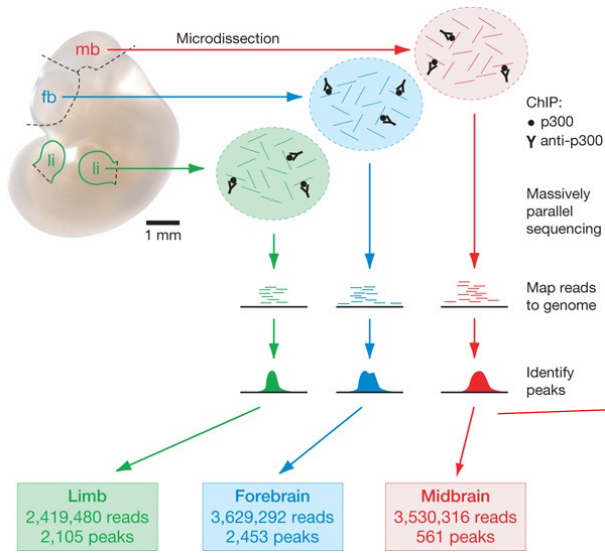
What will happen (in most cases) if we take for example the sequence underneath **the red peak**, link it to a reporter gene (e.g. lacZ or GFP) and integrate it randomly in the mouse genome?



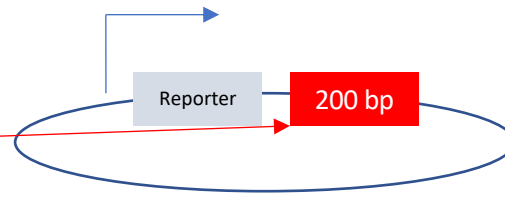
- A. No expression (no signal in the embryo)
- B. Partial expression (only part of the expected expression pattern is observed)
- C. Accurate expression pattern (expression pattern based on p300 binding is reproduced)
- D. Non-specific expression pattern (random)

Although biology is never black and white of course.



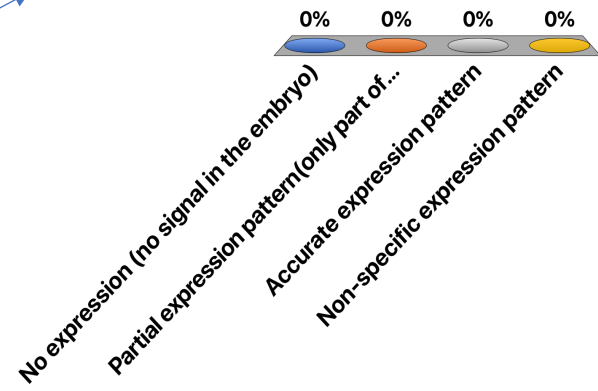


What will happen (in most cases) if we now take this same enhancer and put it downstream of the reporter gene?



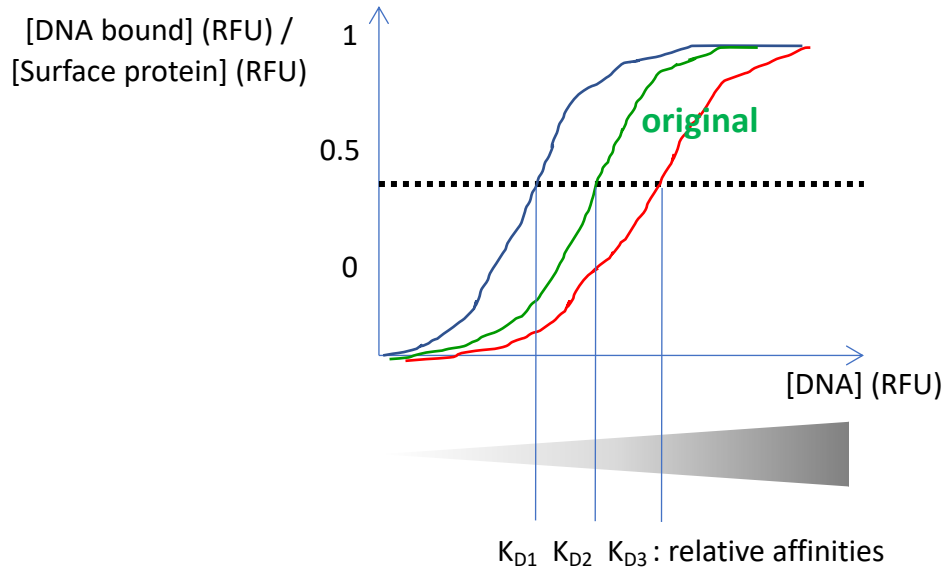
- A. No expression (no signal in the embryo)
- B. Partial expression pattern (only part of the expected expression pattern is observed)
- C. Accurate expression pattern
- D. Non-specific expression pattern

An enhancer functions as well upstream or downstream of its TSS

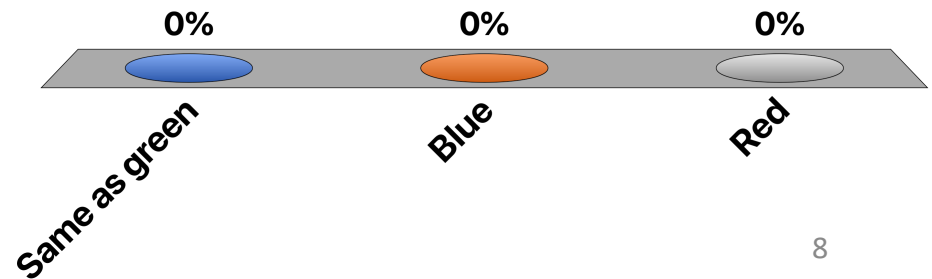


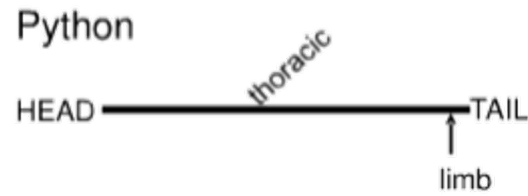
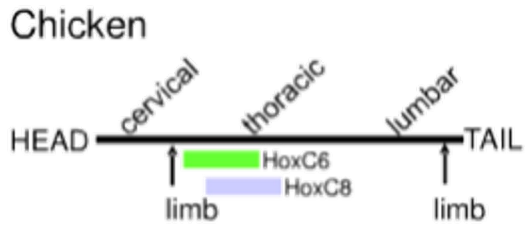


We change the G at position 4 from a G to a T, how will the dissociation curve look like as compared to the original motif (green curve)?



- A. Same as green
- B. Blue
- C. Red

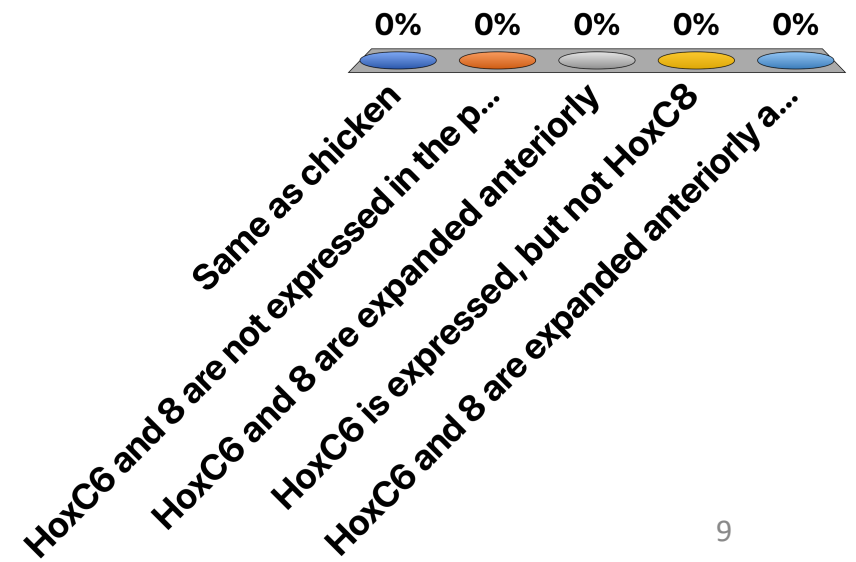


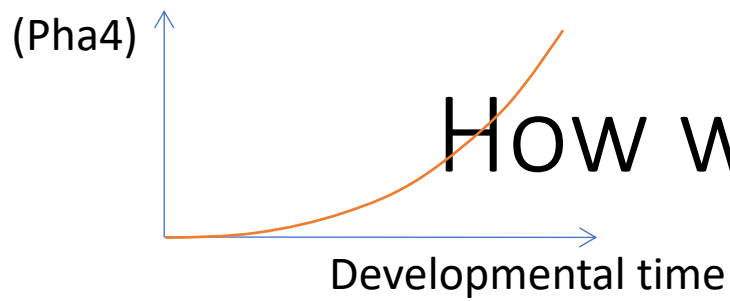


How may the expression pattern of HoxC 6 and 8 look like in the python embryo?



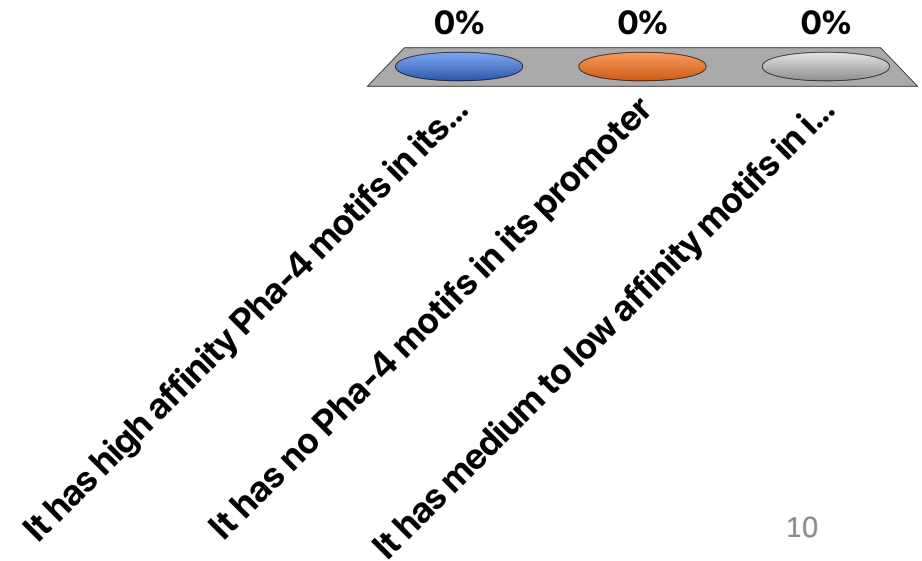
- A. Same as chicken
- B. HoxC6 and 8 are not expressed in the python
- C. HoxC6 and 8 are expanded anteriorly
- D. HoxC6 is expressed, but not HoxC8
- E. HoxC6 and 8 are expanded anteriorly and posteriorly

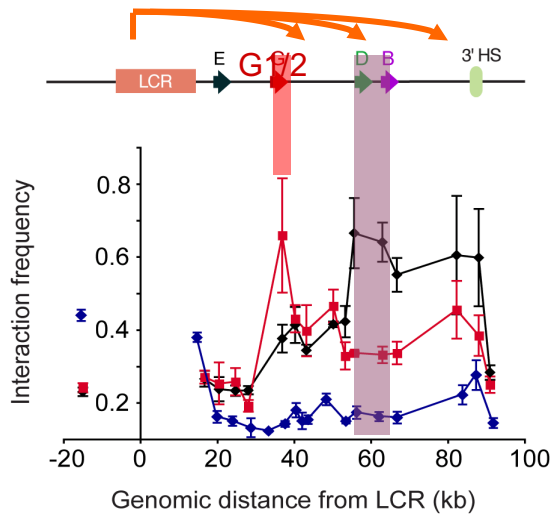




How will Pha-4 itself be regulated

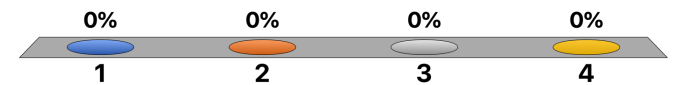
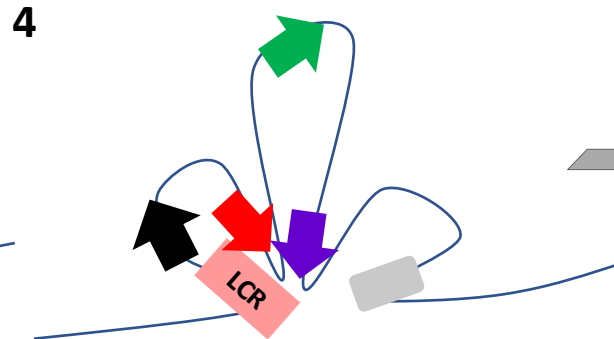
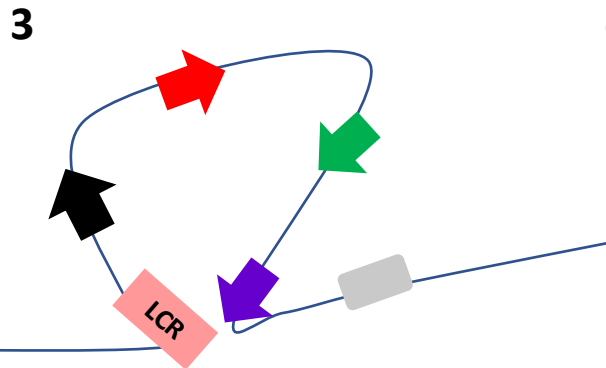
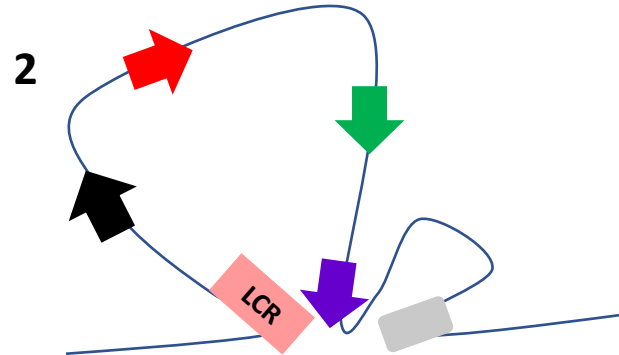
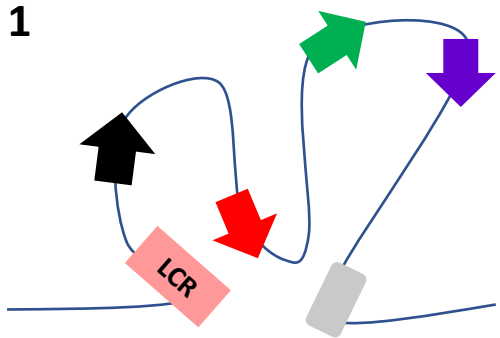
- A. It has high affinity Pha-4 motifs in its promoter
- B. It has no Pha-4 motifs in its promoter
- C. It has medium to low affinity motifs in its promoter



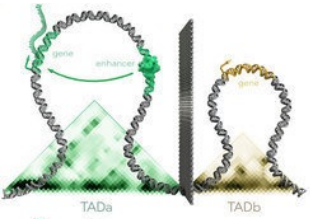


Which topology best approximates the data for B-globin on?

- A. 1
- B. 2
- C. 3
- D. 4



Our current understanding of the hierarchical organization of chromatin structure



The consequence of tearing down the wall....

- A. The genome unfolds and becomes linear
- B. No consequence b/c of architectural robustness
- C. Regions become silenced and gene expression will also be repressed
- D. Enhancers “jump over the fence” and activate genes that are normally not their target genes

