Comparing the effect of mutations in two different versions of the *eve* stripe 2 enhancer

Francheska López Rivera

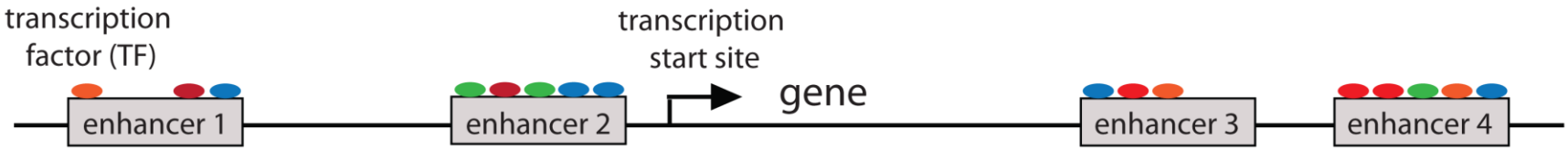
Group meeting

February 25, 2015

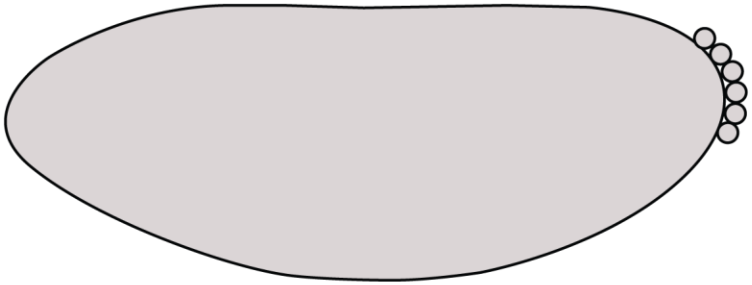
Goals for this meeting

- Introduction and previous results
- Results after merging data from different stains
- Discussion about how to communicate the story

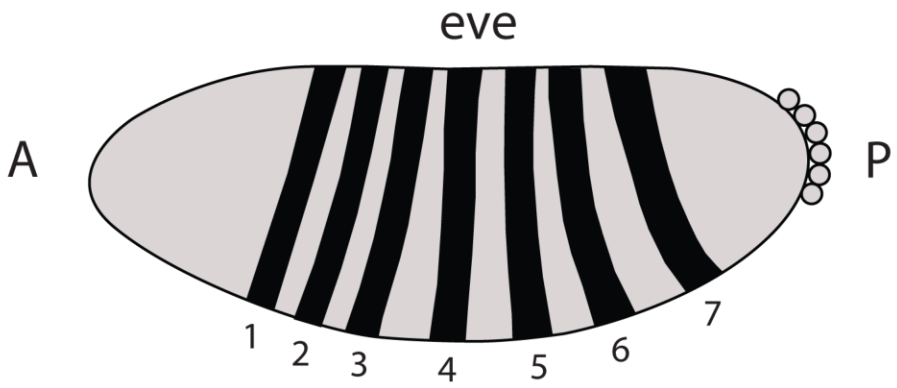
Enhancers control gene expression in animals.



We use the *Drosophila melanogaster* embryo as our system.



We focused on the *even-skipped* (*eve*) stripe 2 enhancer in *Drosophila melanogaster* embryos.



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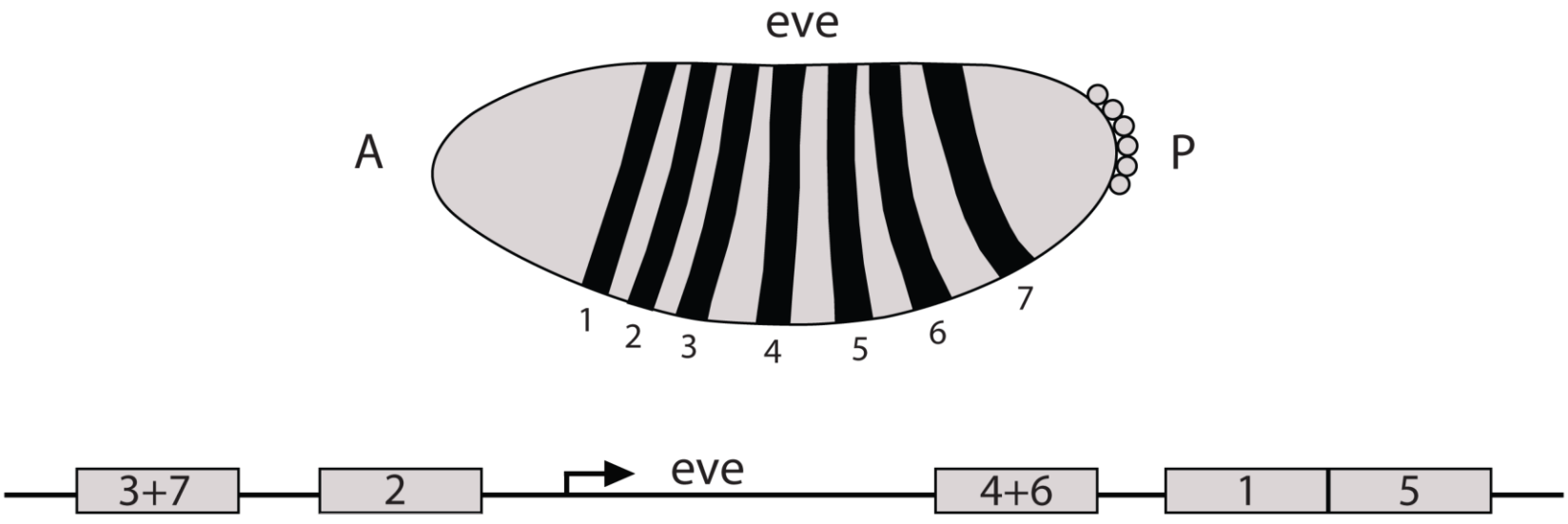

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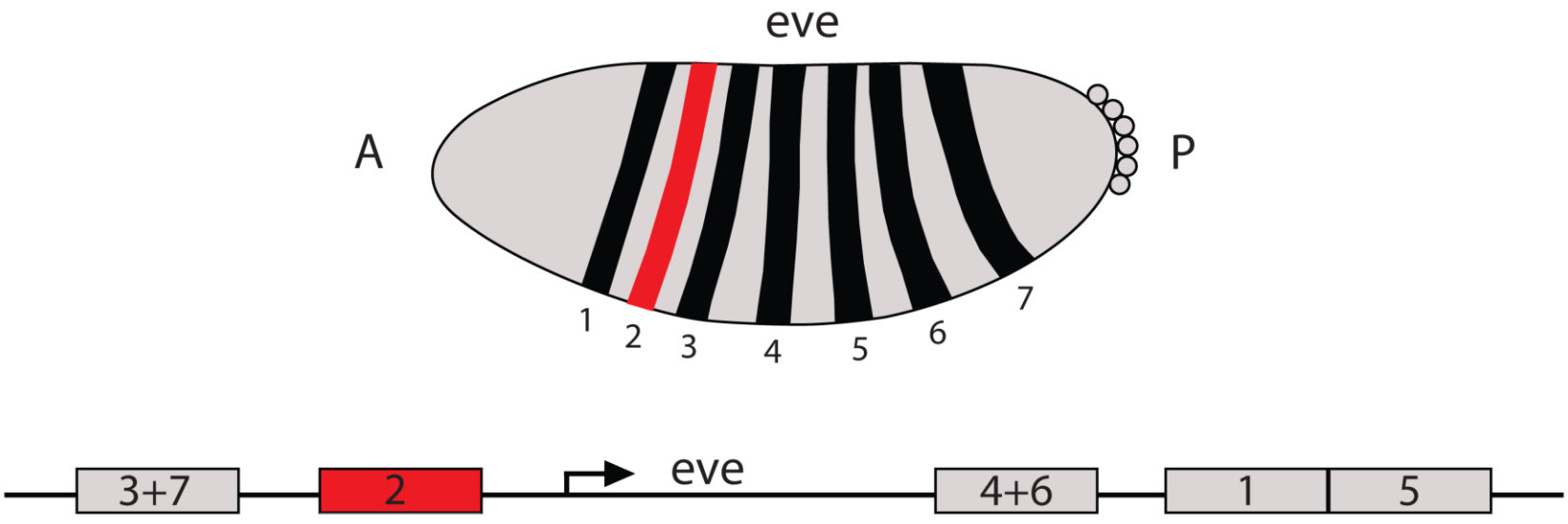

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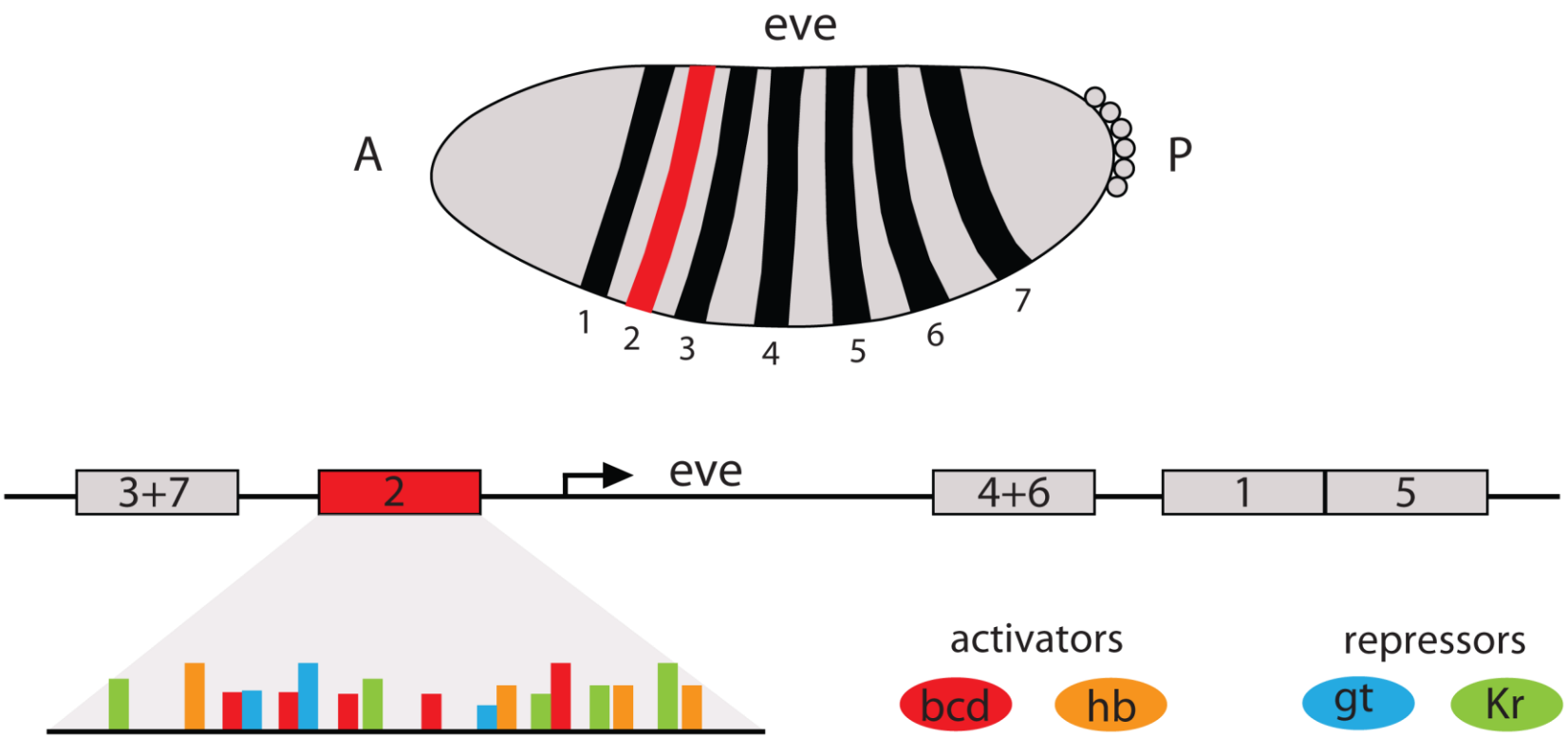
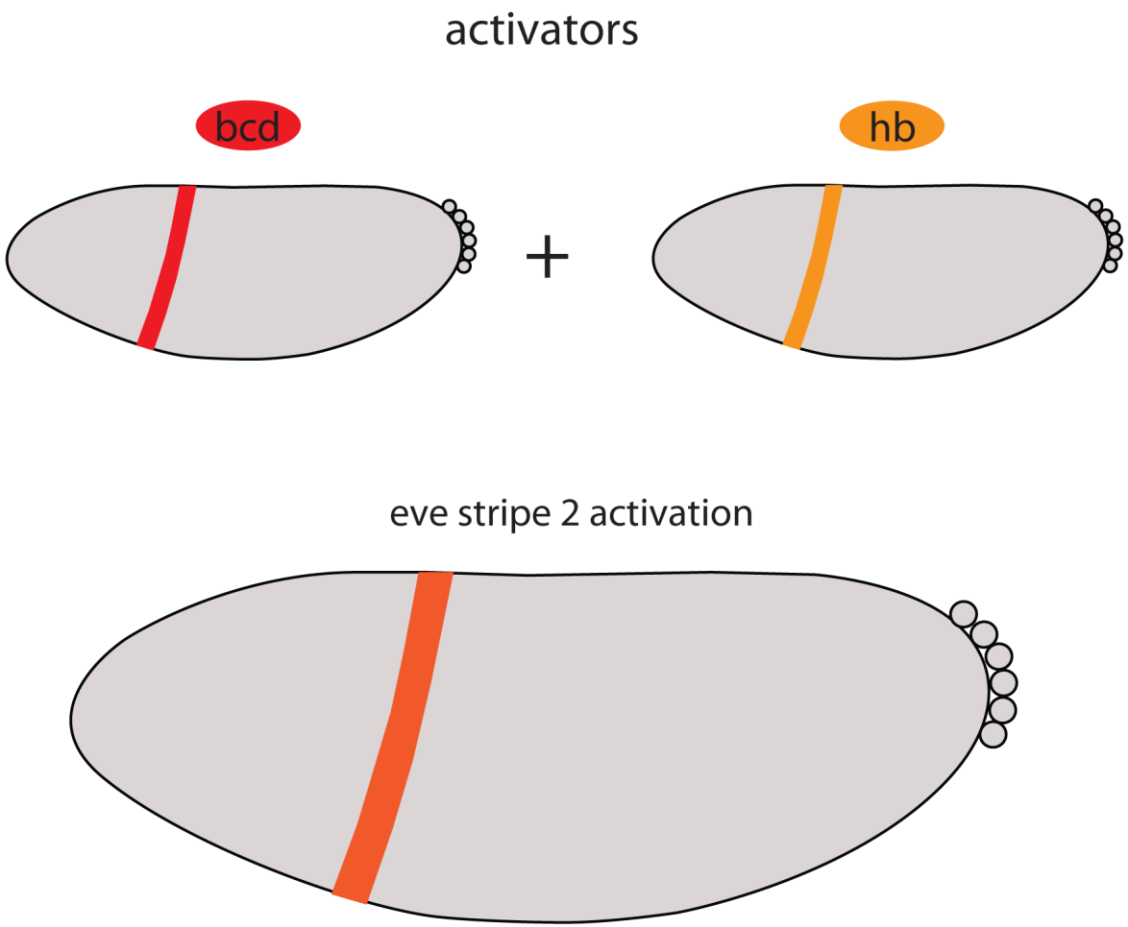


The position of *eve* stripe 2 is determined by four transcription factors.



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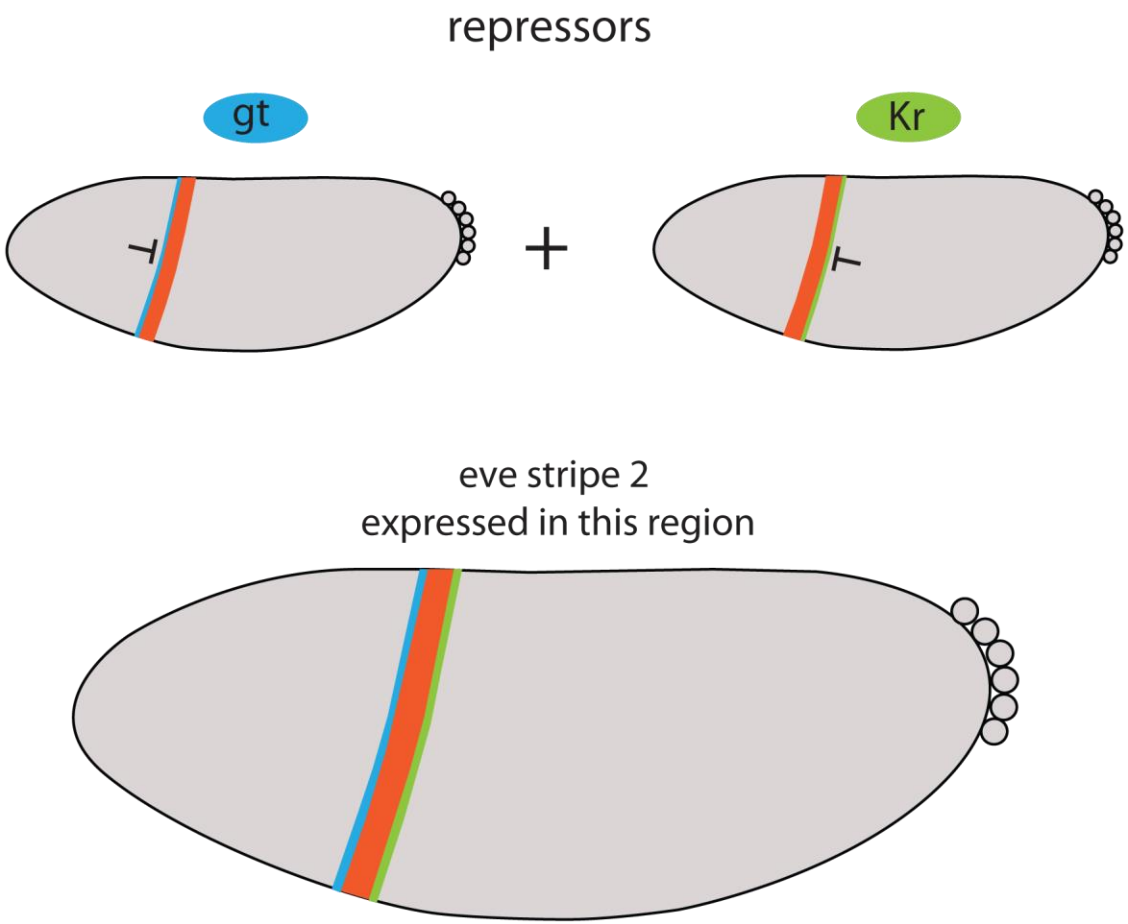
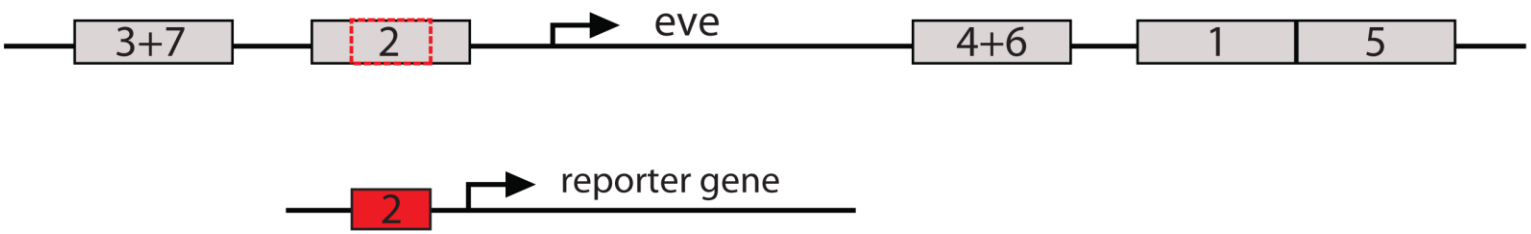
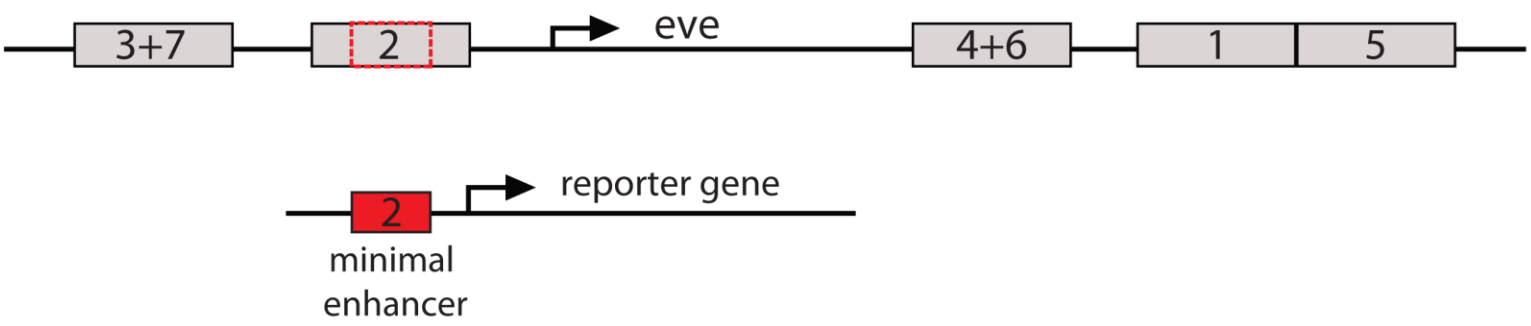


Reporter constructs have been used to study the *eve* stripe 2 enahncer.



Minimal reporter constructs have been used to study the *eve* stripe 2 enhancer.



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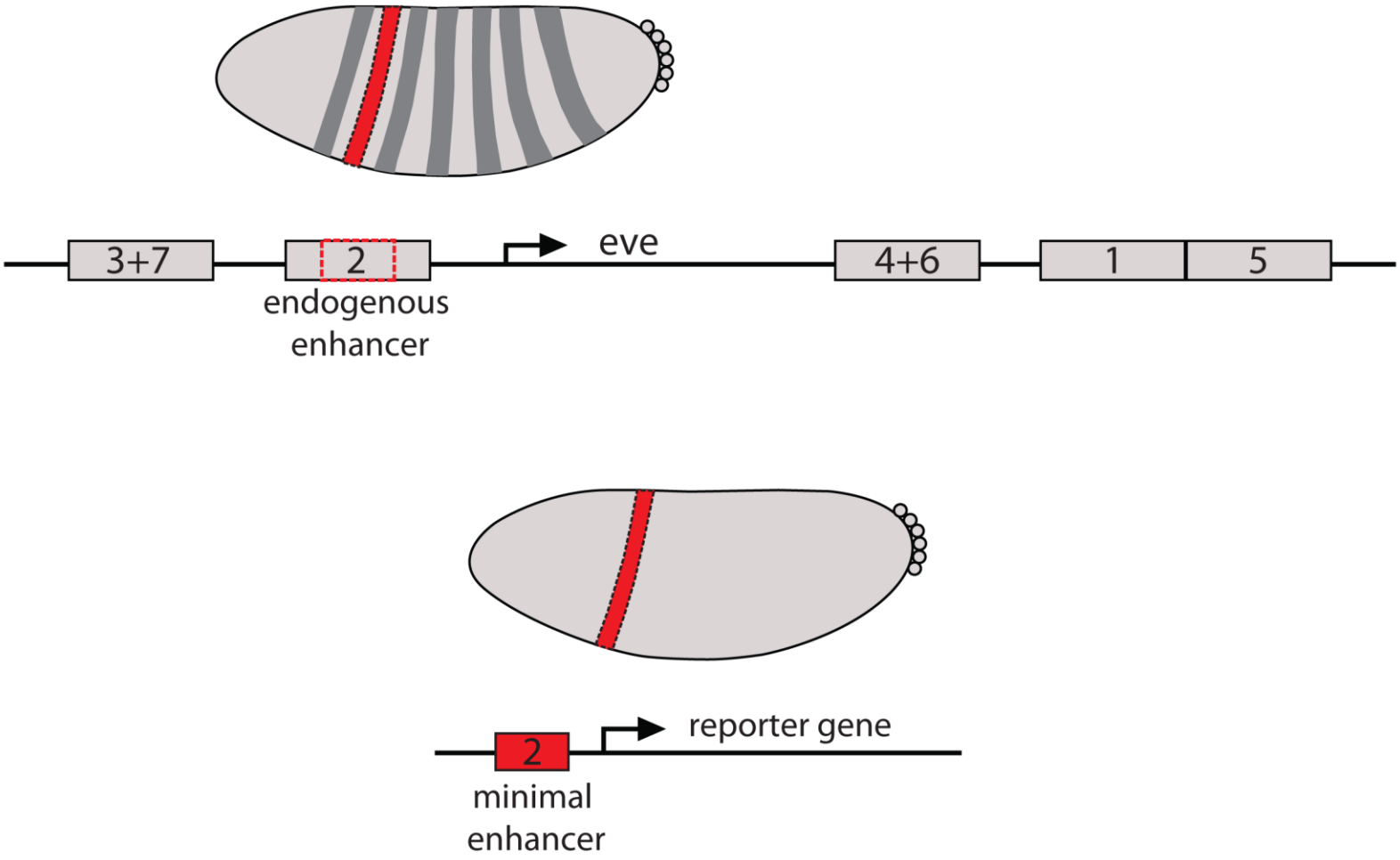
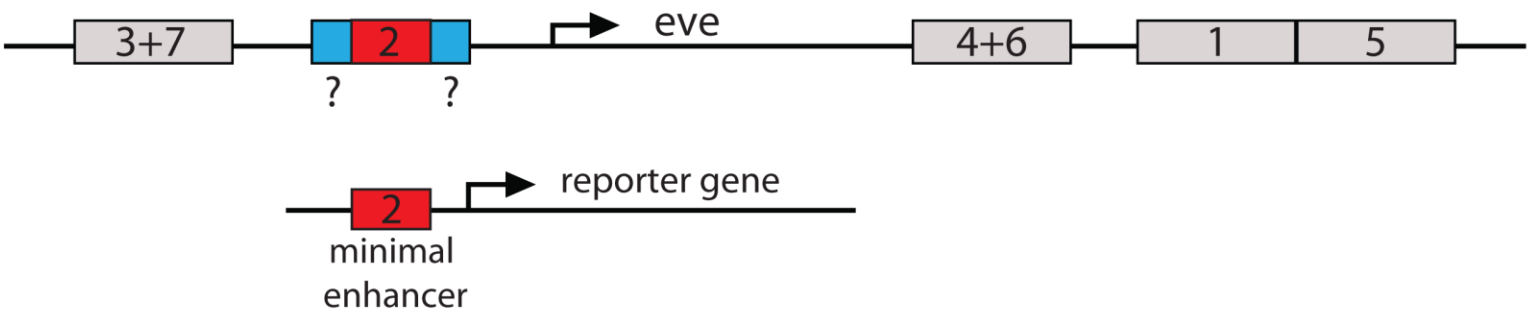


What is the role of sequences flanking the *eve* stripe 2 enhancer?



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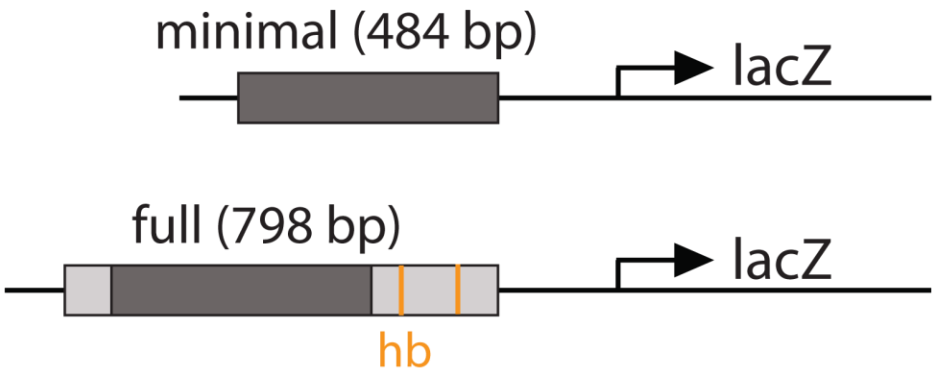
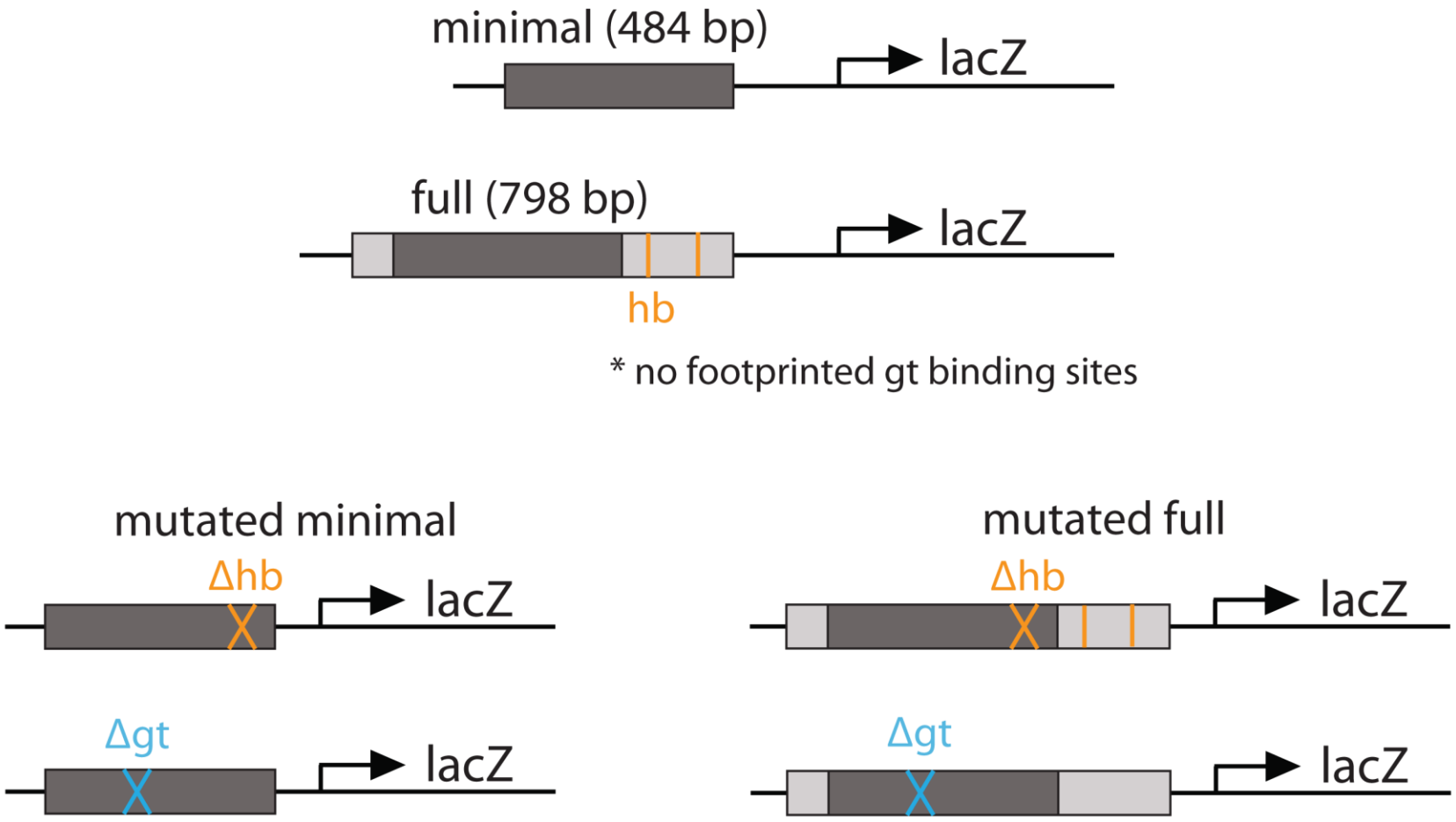


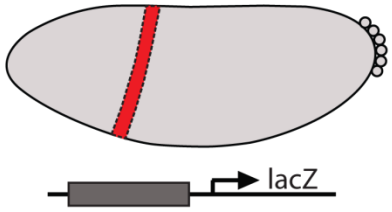
* no footprinted gt binding sites

We mutated *eve* stripe 2 minimal and full enhancers.

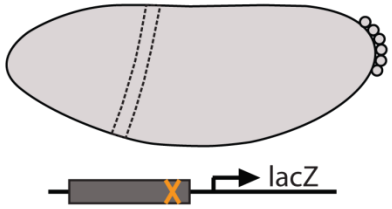


Mutations on important *eve* stripe 2 enhancer binding sites affected *eve* stripe 2 expression.

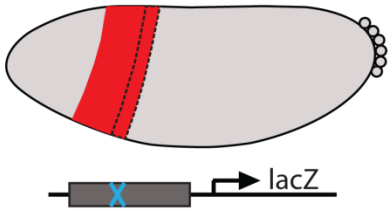
Previous work (Arnosti et. al)
(minimal)



wt

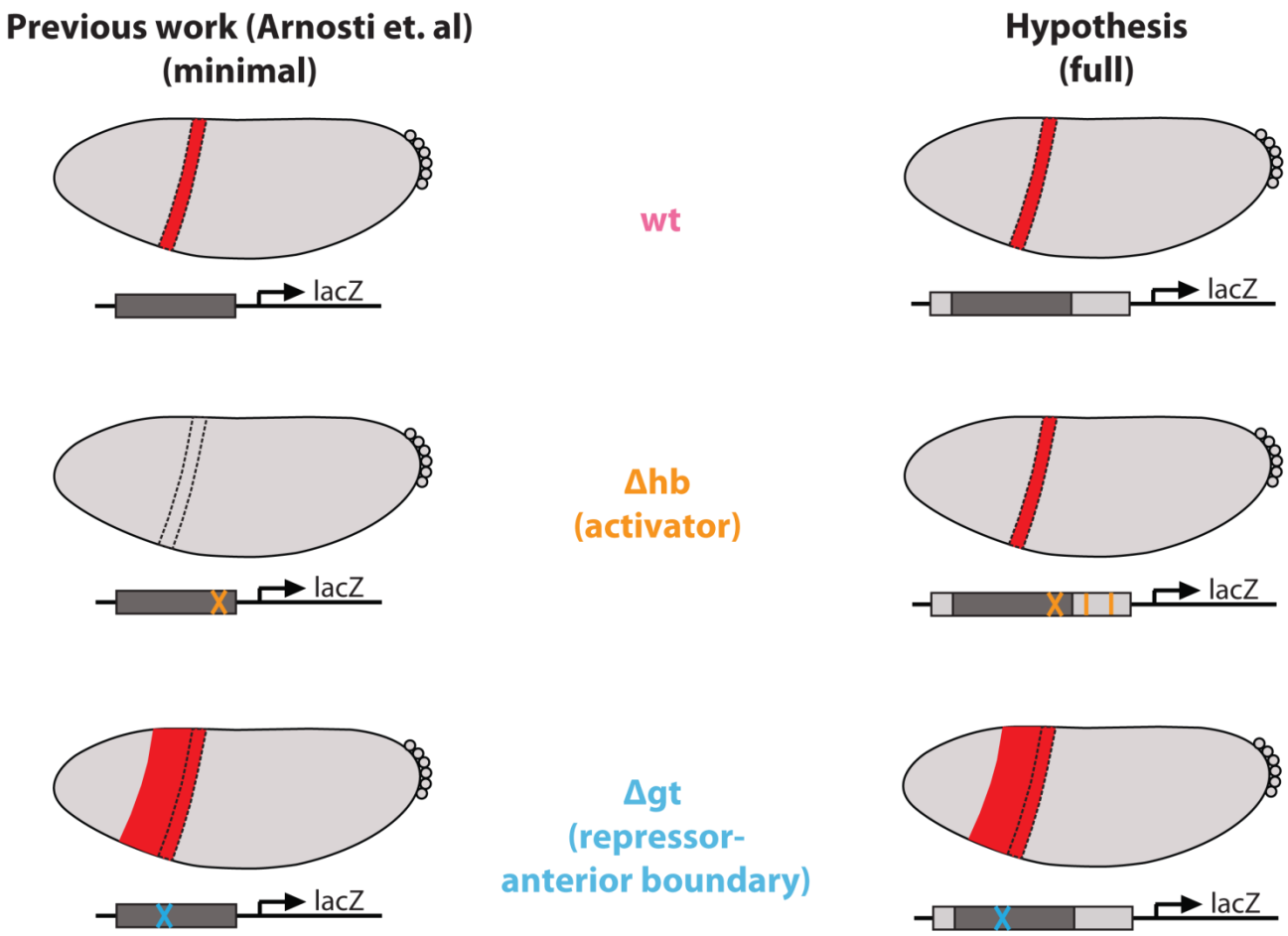


Δhb
(activator)

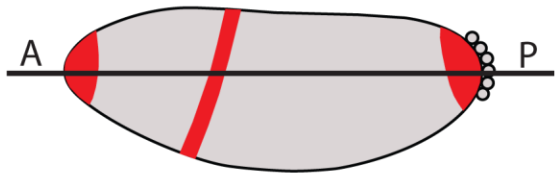


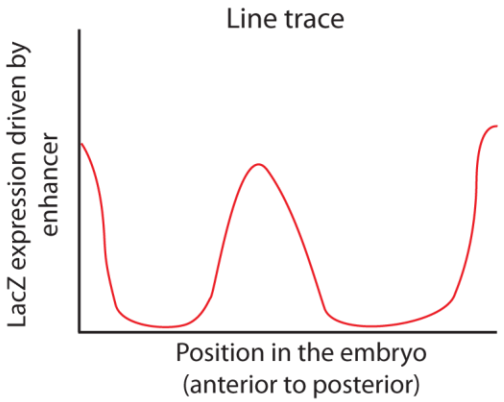
Δgt
(repressor-
anterior boundary)

We expect flanking sequences to compensate for mutations if they contain binding sites.



Data will be presented as line traces.





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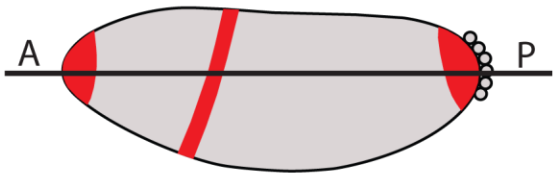

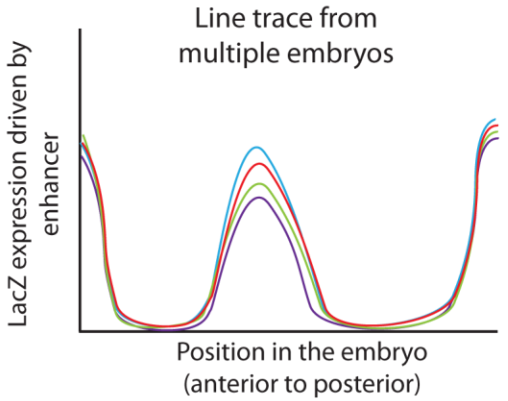

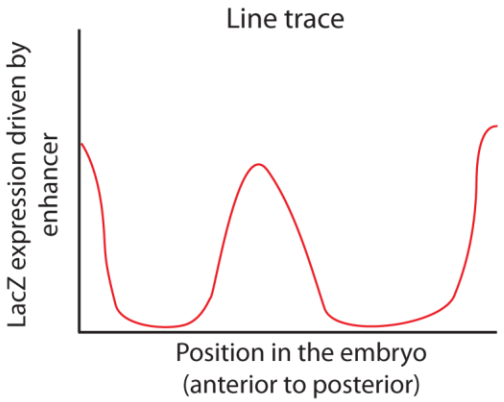

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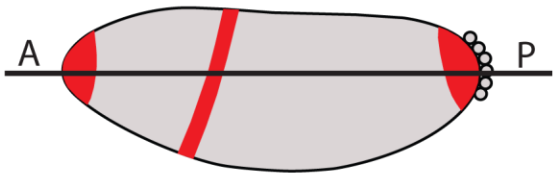
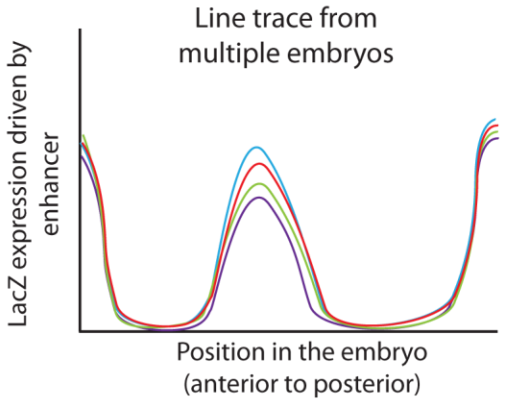
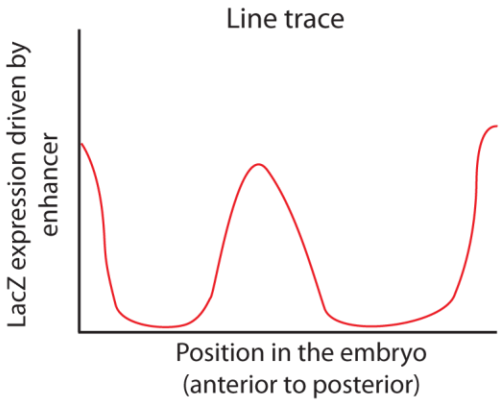
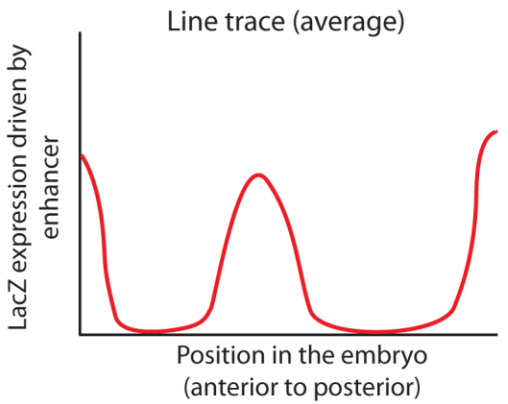
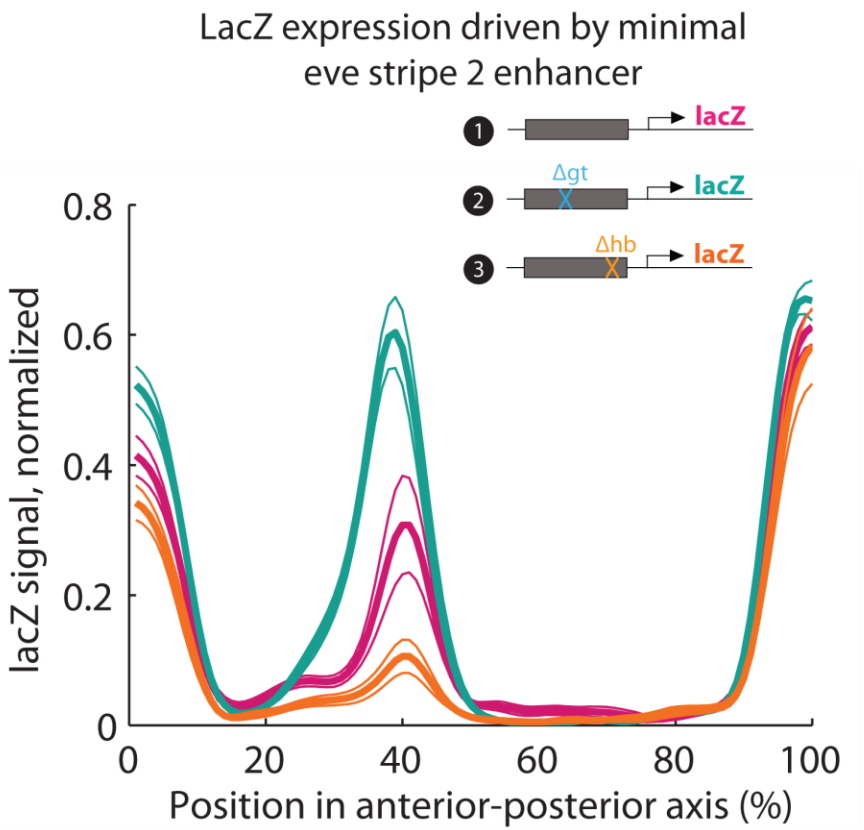




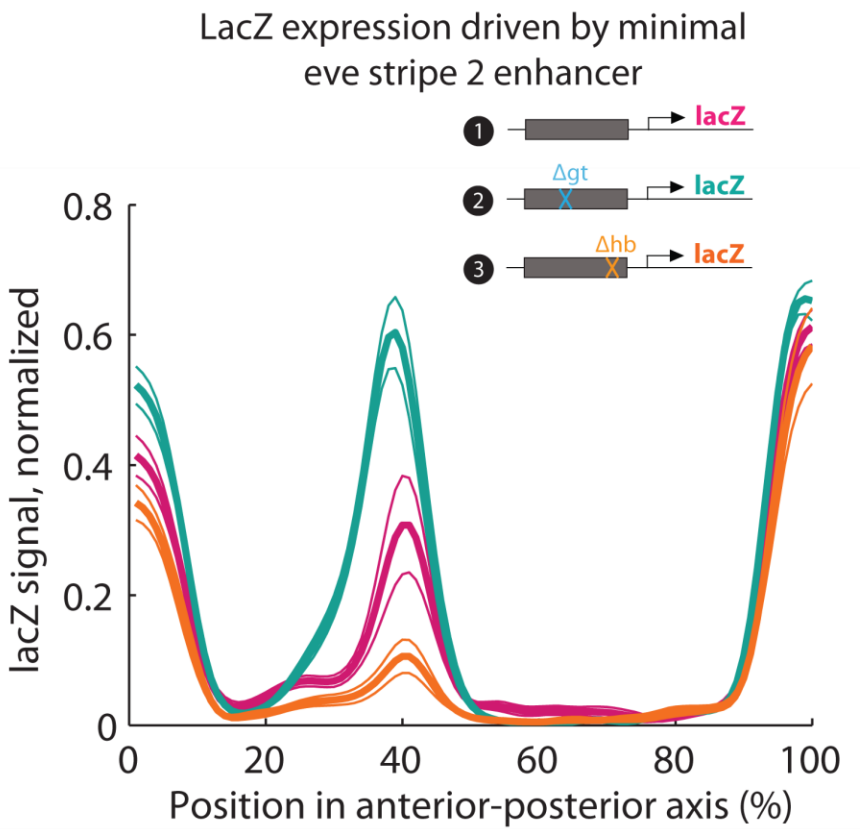


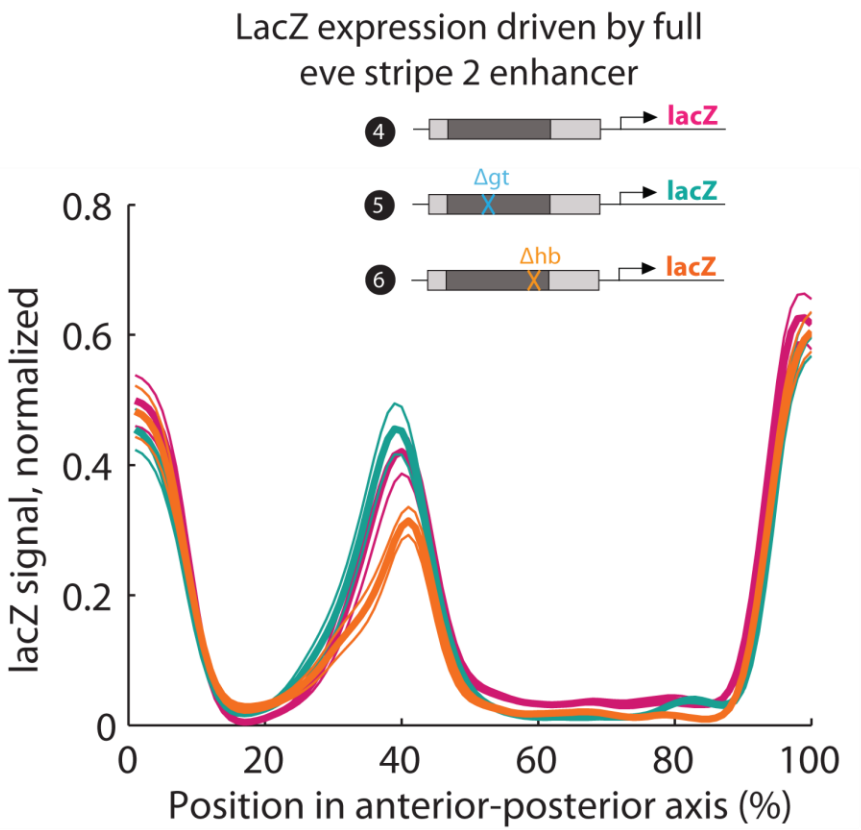


Minimal enhancer levels are consistent with previous observations.

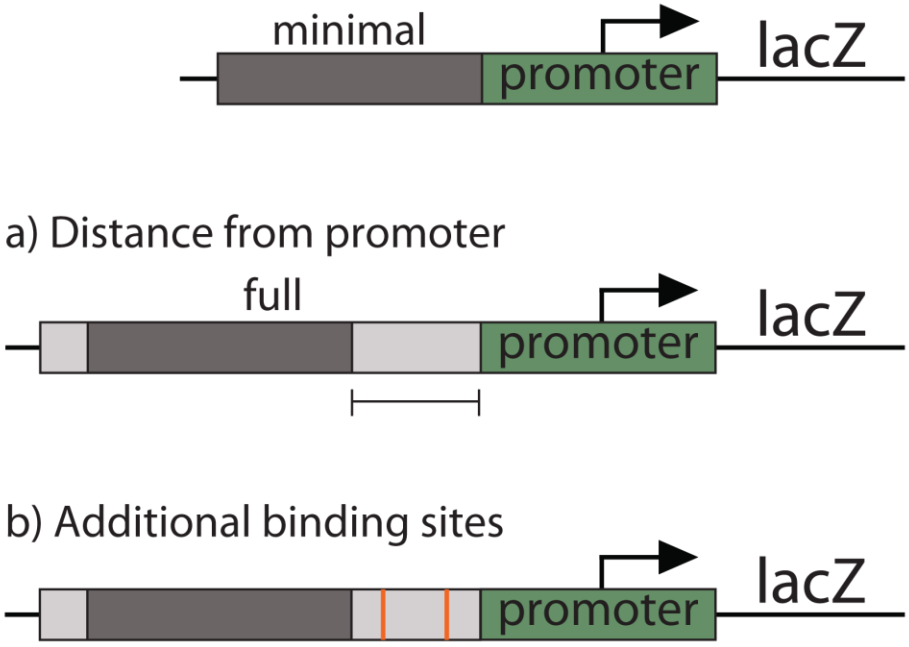


Flanking sequences compensate for mutations even in the absence of footprinted binding sites.



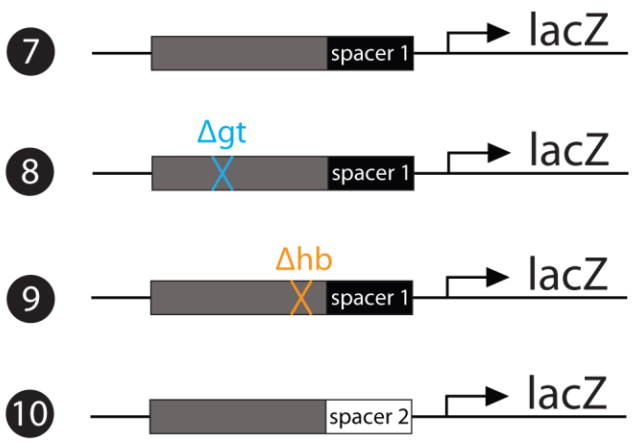


We want to identify the sequence features responsible for compensation.

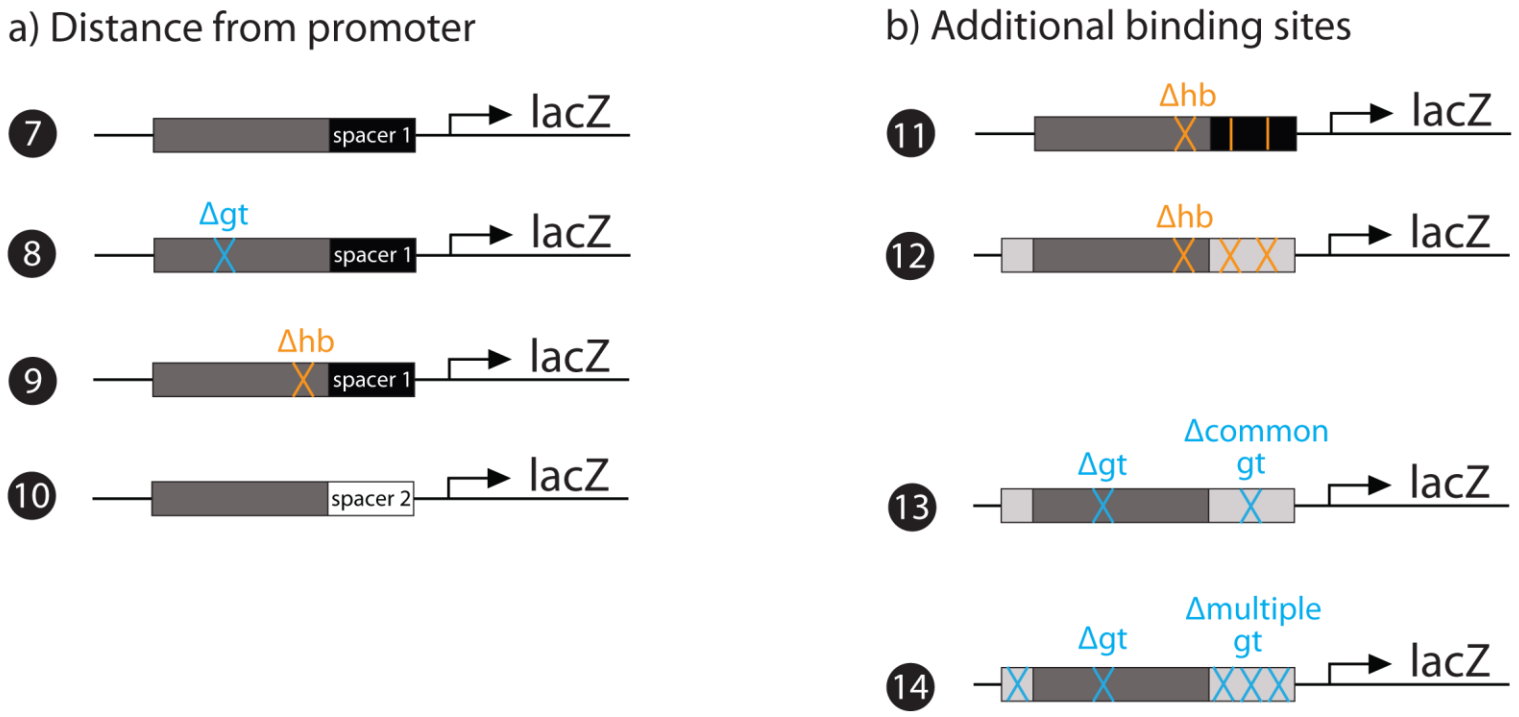


We designed constructs to test for distance from the promoter.

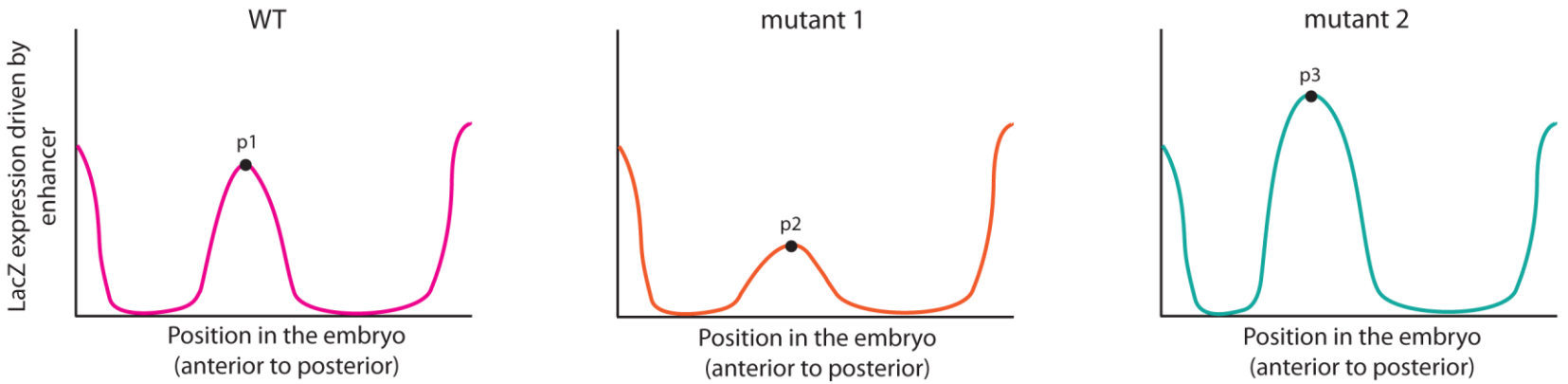
a) Distance from promoter



We designed constructs to test for additional hb or gt binding sites.



Data will be presented as ratios of the peak mean value of two constructs.



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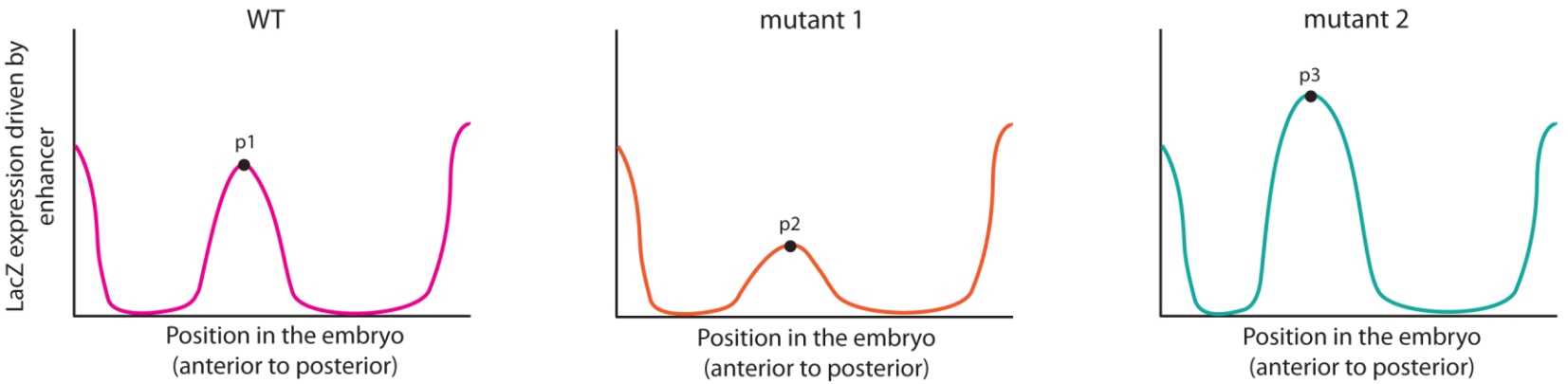

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1		p1	p2	p3
2	Stain 1	0.21	0.11	0.41
3	Stain 2	0.25	0.1	0.45
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5				

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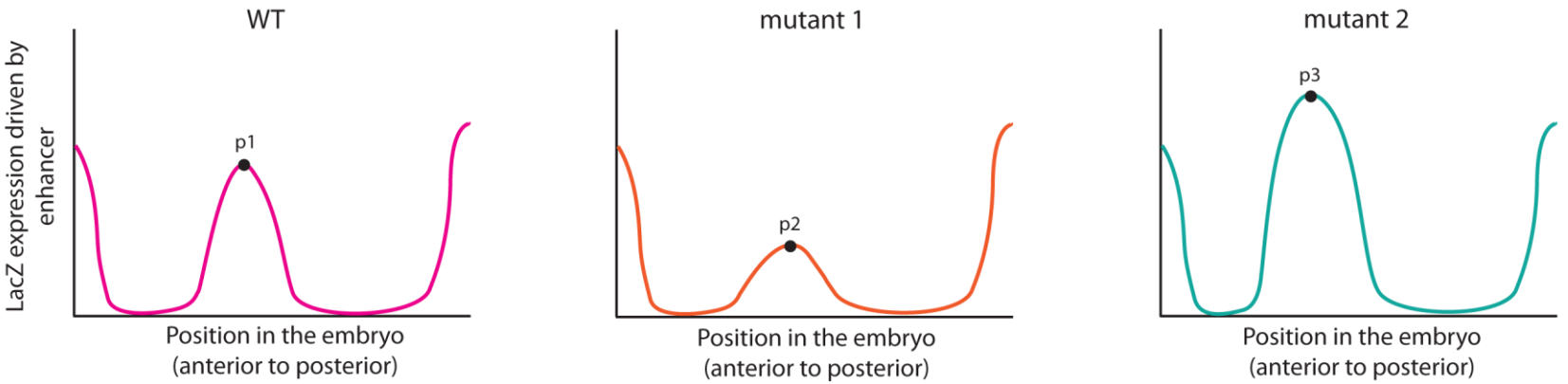

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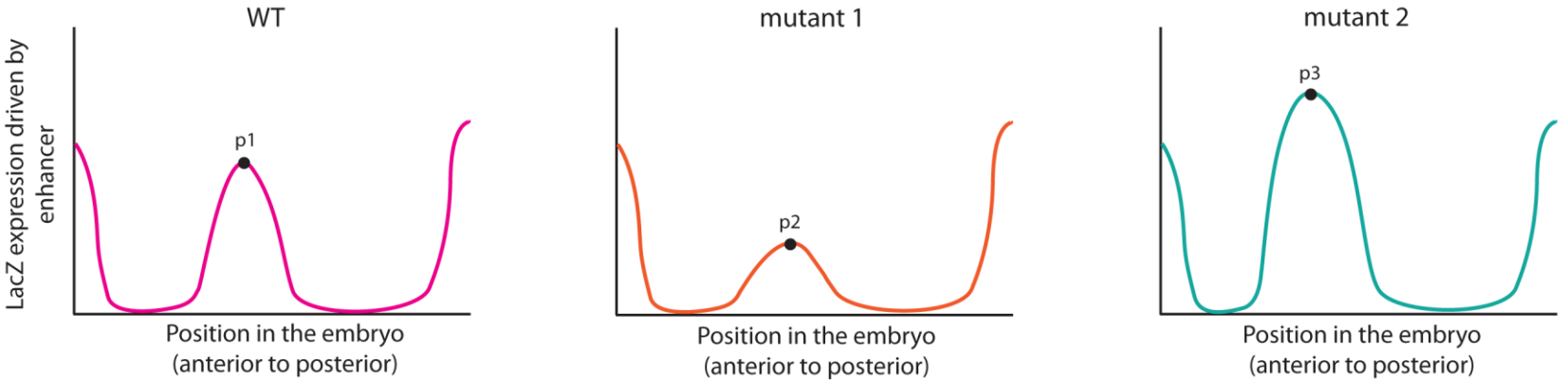

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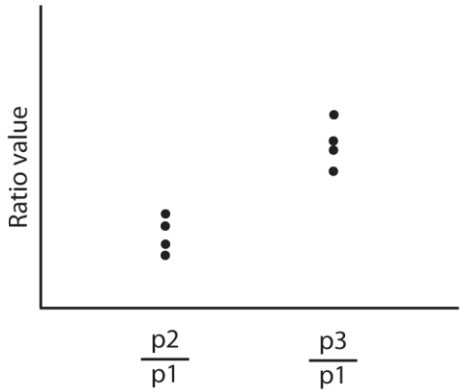

Data discussion

Thank you!