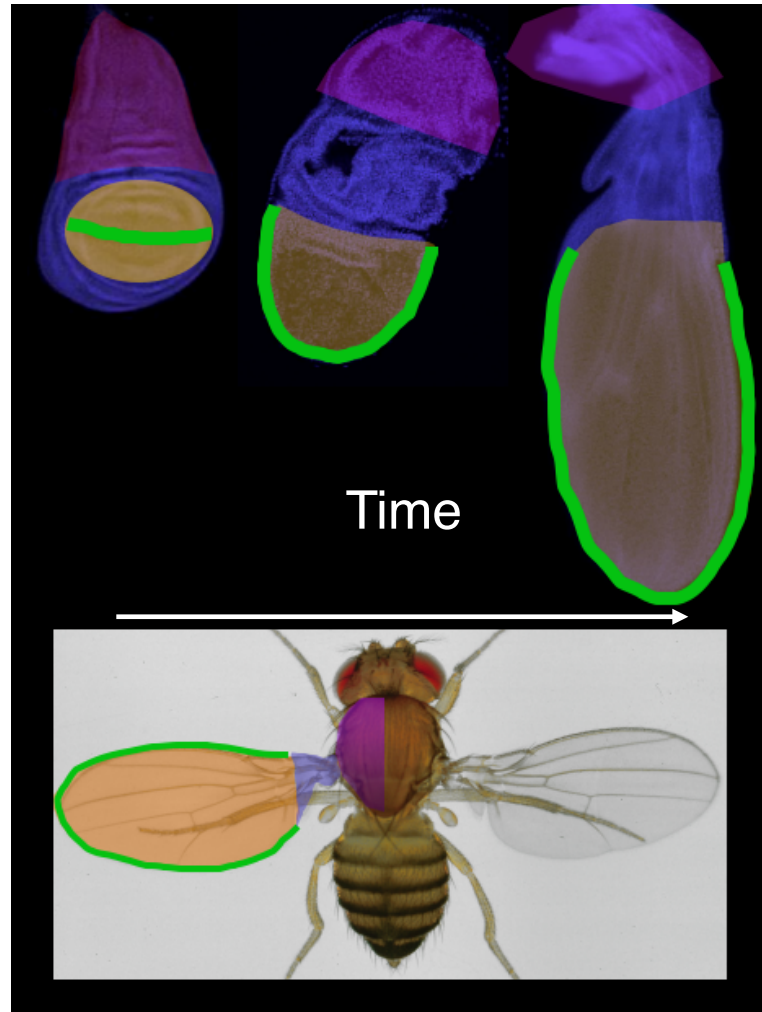


Temporal regulation of the cell cycle in the *Drosophila* wing during metamorphosis

Buttitta Lab, University of Michigan



Distinct states of cell cycle exit:



Yiqin Ma



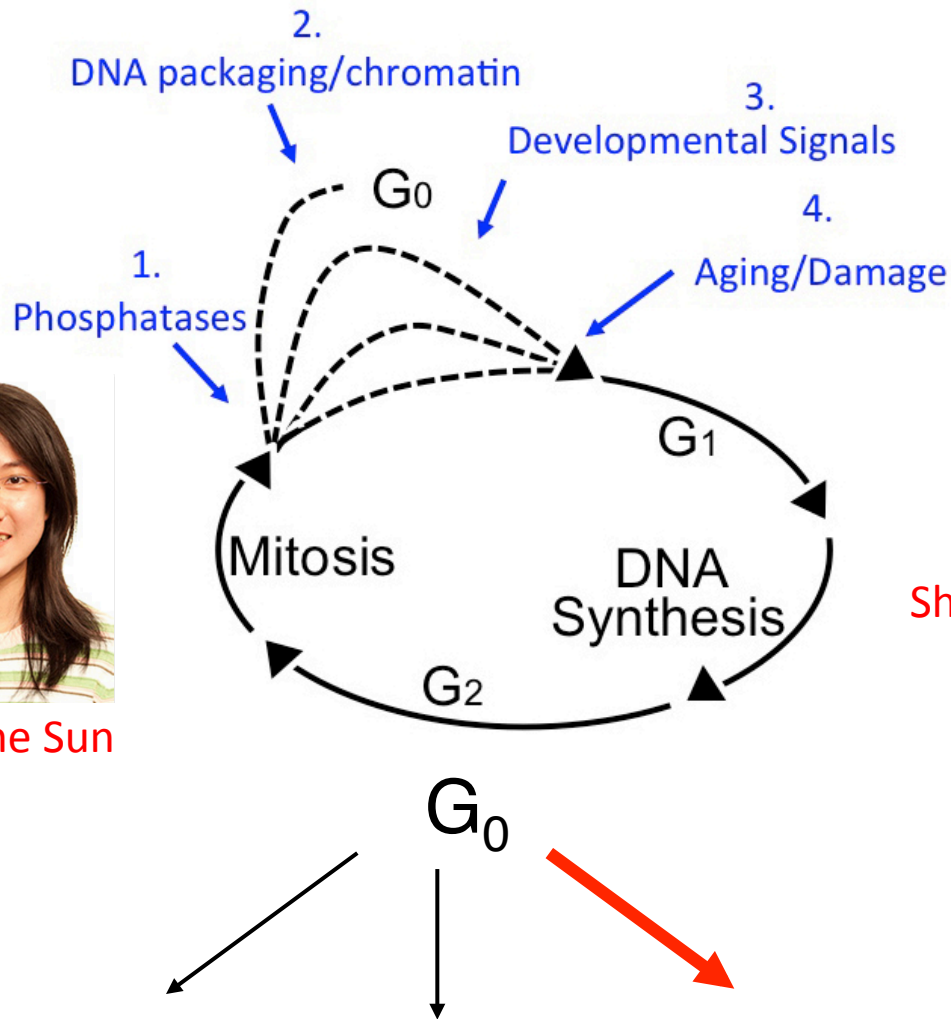
Rosaline Sun



Kerry Flegel



Shyama Nandakumar

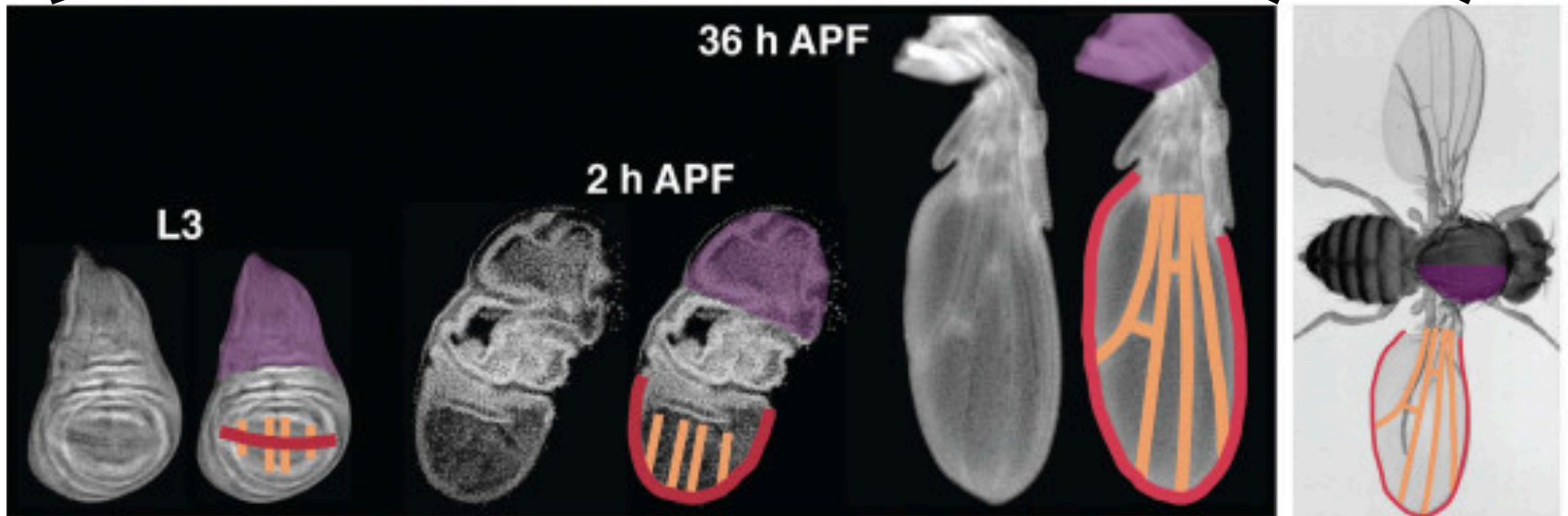
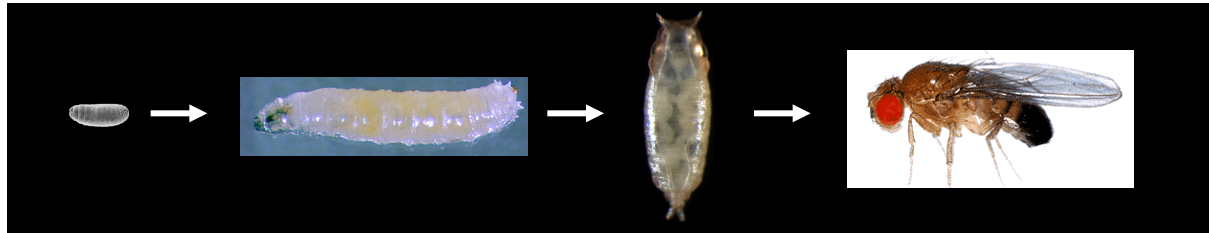


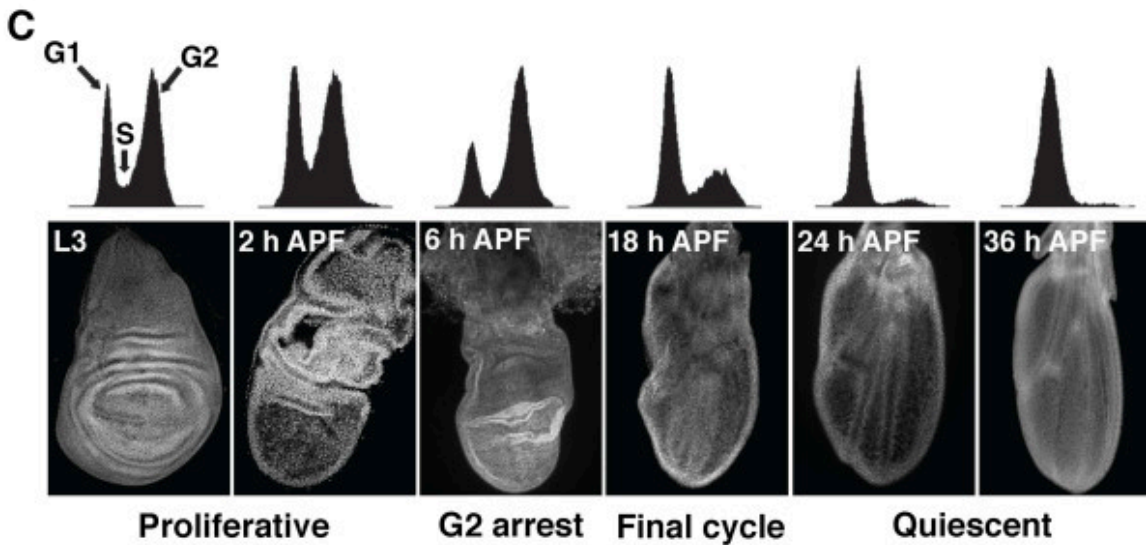
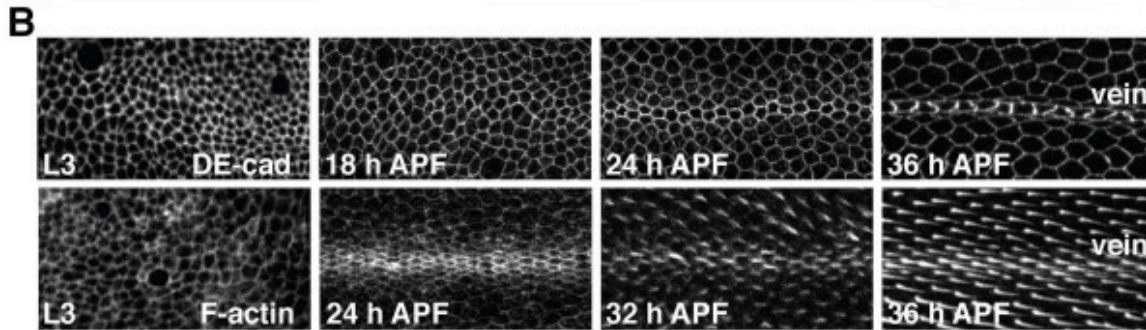
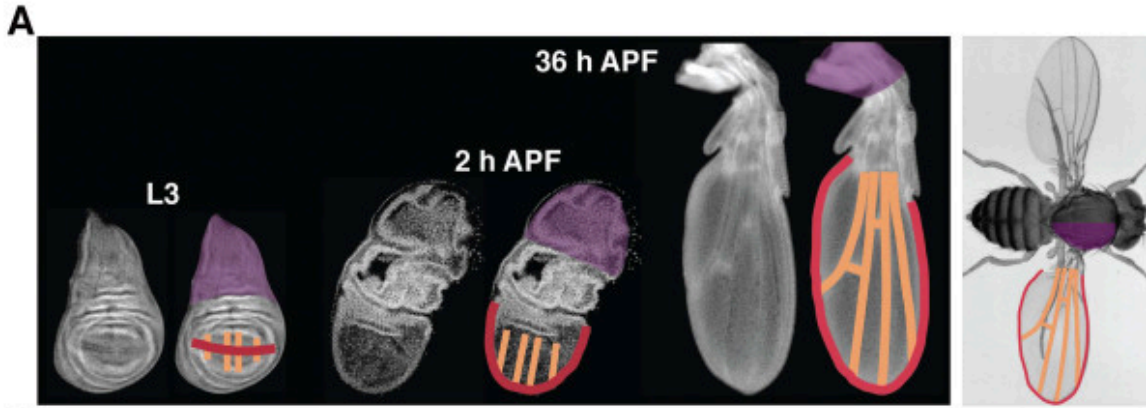
Reversible Quiescence

Senescence

Terminal differentiation

Drosophila metamorphosis – remarkably cool, and complicated





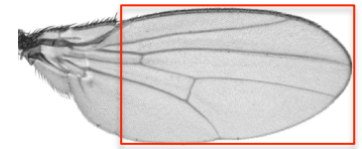
Cell shape/identity

Hair differentiation

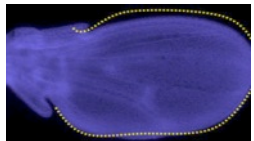
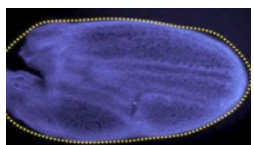
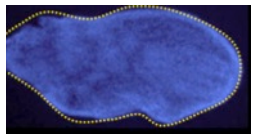
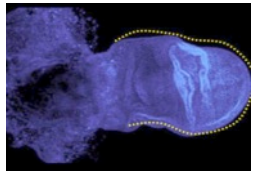
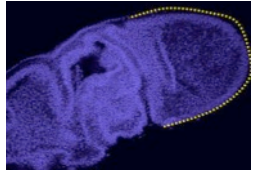
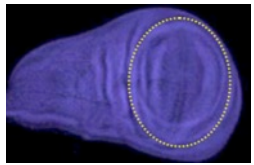
Cell cycle changes

Morphological changes

The transition to G0 in the fly wing



DNA



0h APF
(After Pupa-
rium
Formation)

2h APF

6h APF

18h APF

24h APF

36h APF

Adult

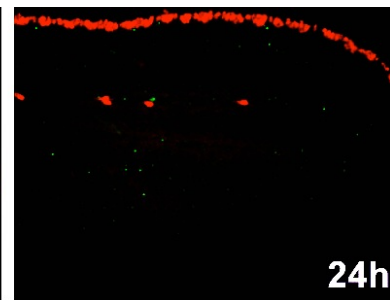
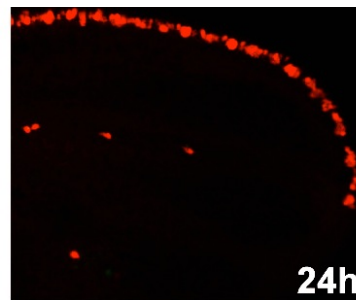
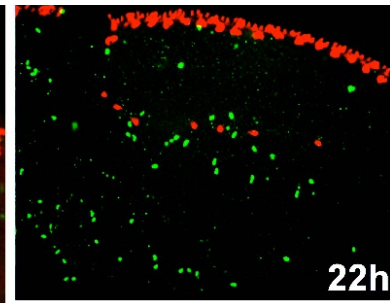
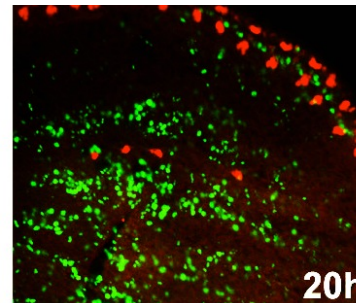
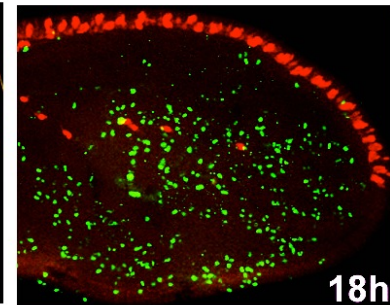
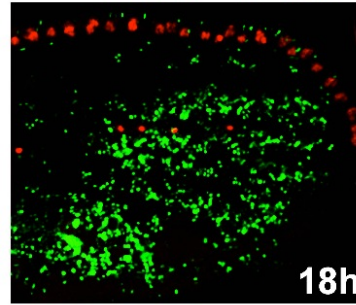
Proliferation

time

Differentiation

S-phase

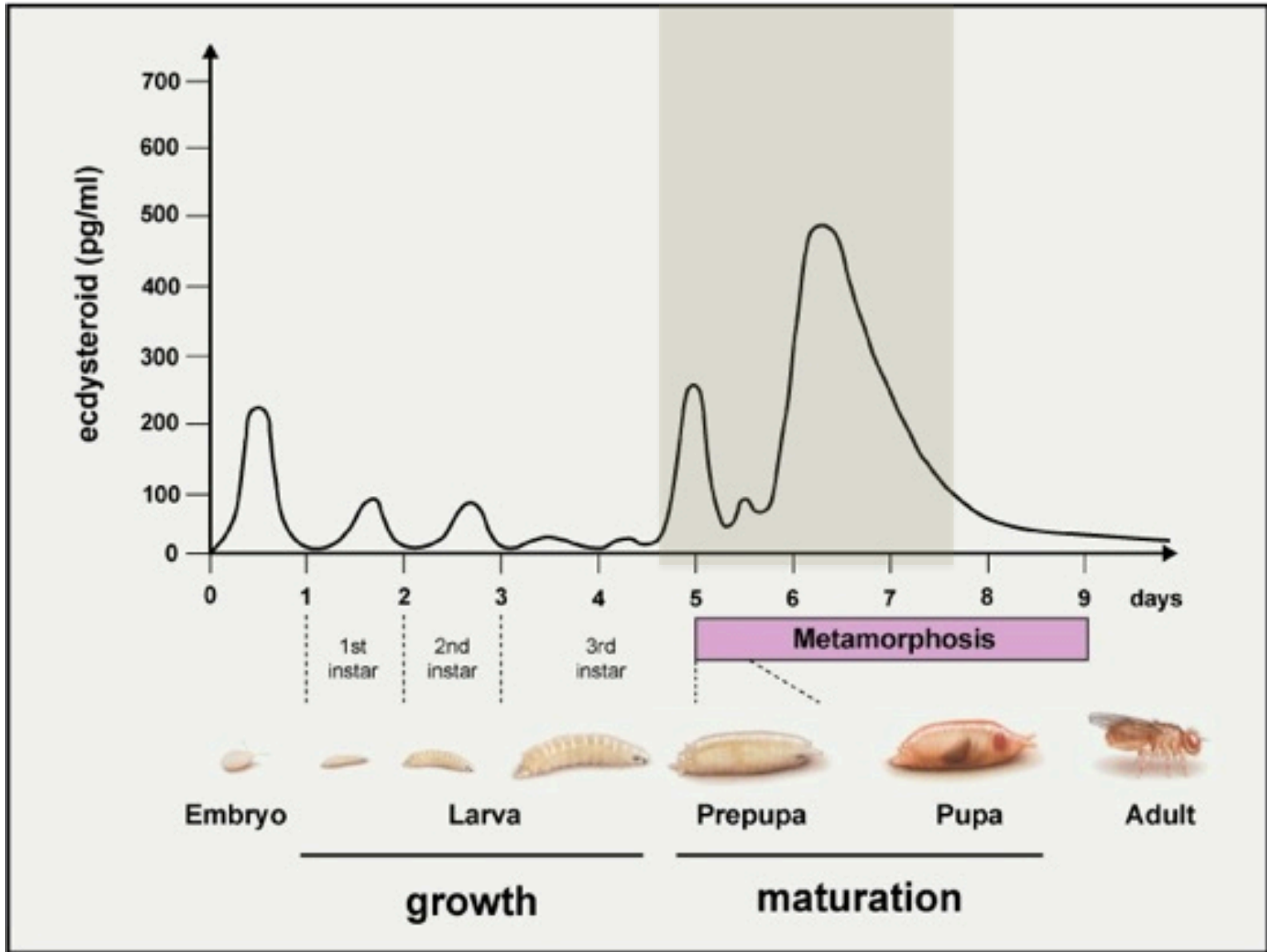
Mitosis



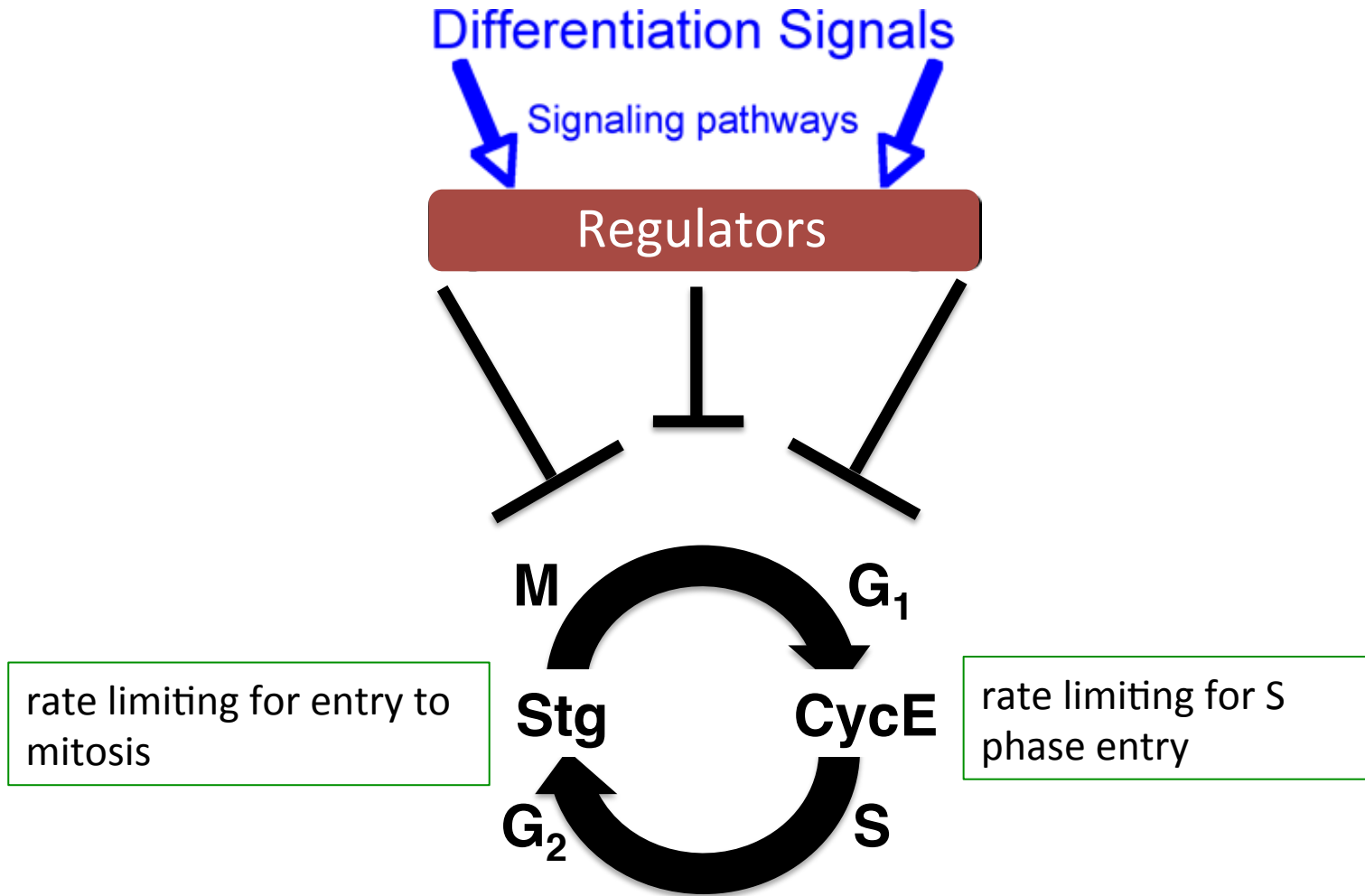
S-phase / neurons

mitoses / neurons

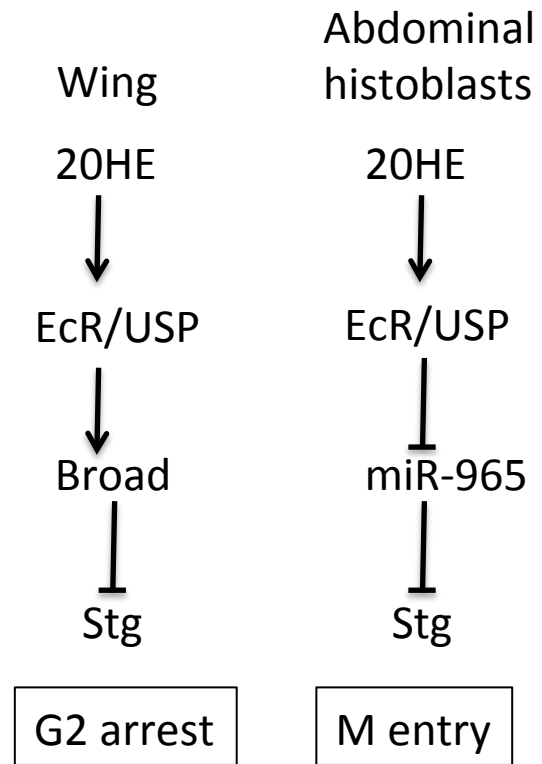
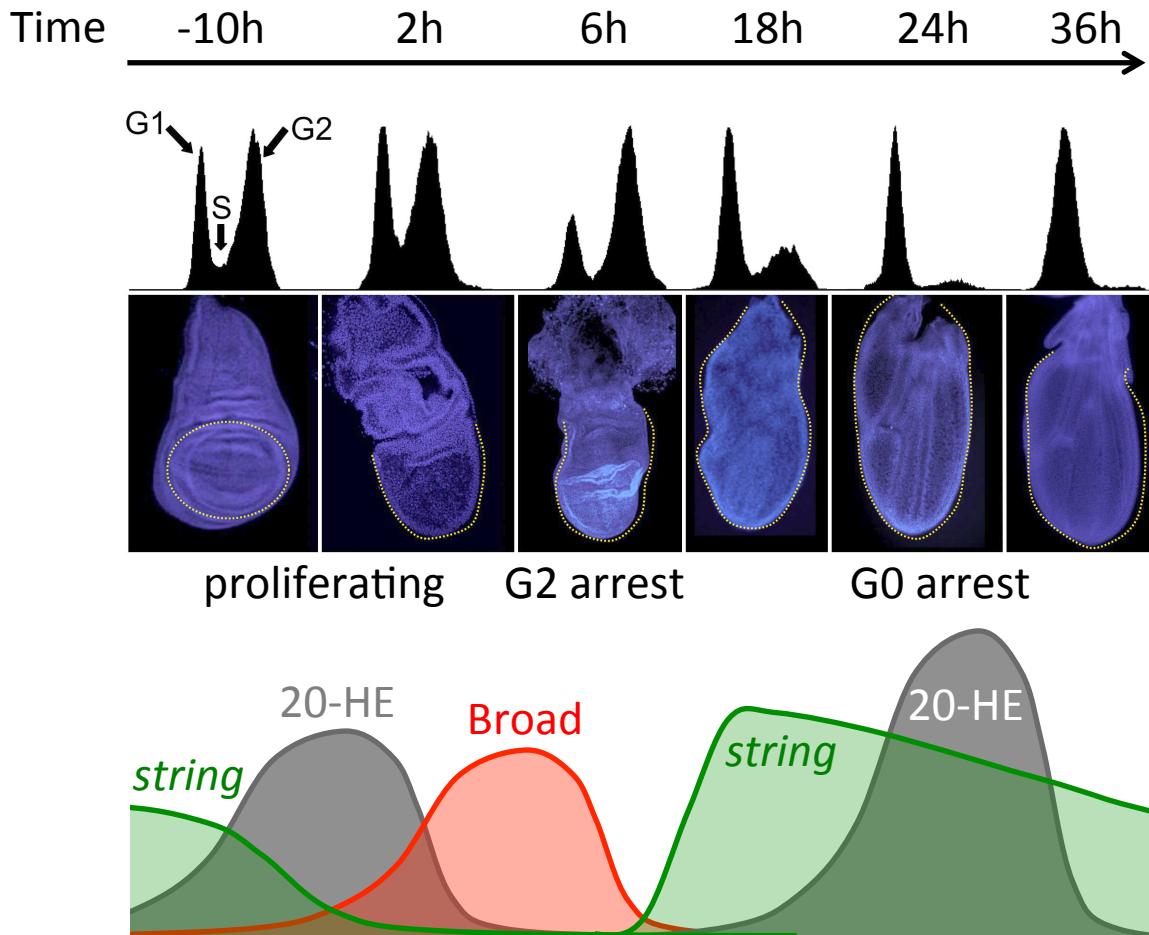
Temporal events are regulated by the hormone Ecdysone



How is ecdysone signaling connected to the cell cycle?



How is ecdysone signaling connected to the cell cycle?

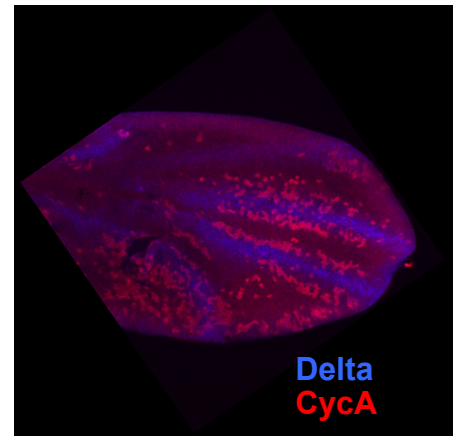
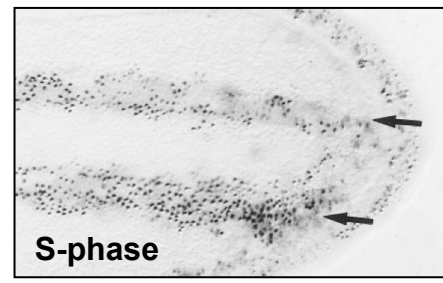


Verma & Cohen

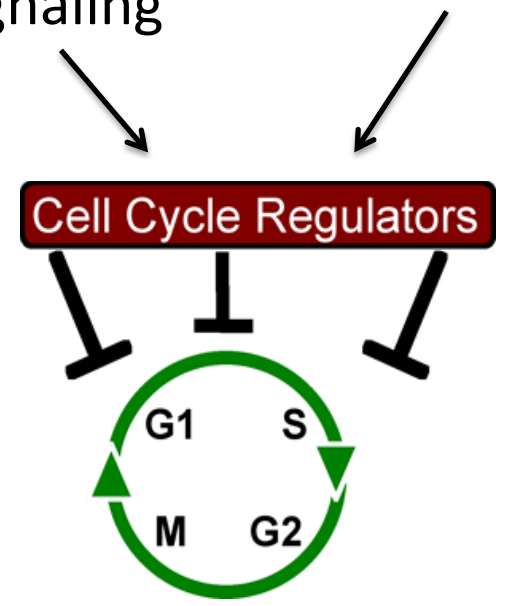
Y. Guo, K. Flegel

0h 6h 18h 24h

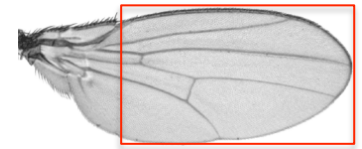
pMad
dpERK
Notch



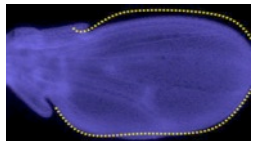
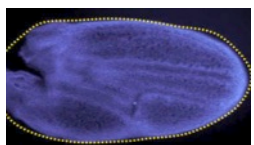
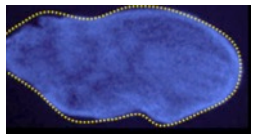
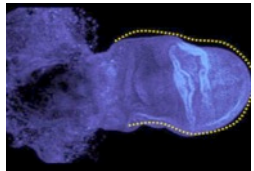
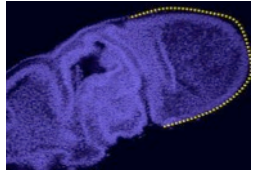
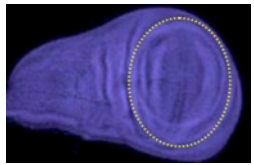
temporal patterning
Hormone signaling Vein/intervein



The transition to G0 in the fly wing



DNA



0h APF
(After Pupa-
rium
Formation)

2h APF

6h APF

18h APF

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36h APF

Adult

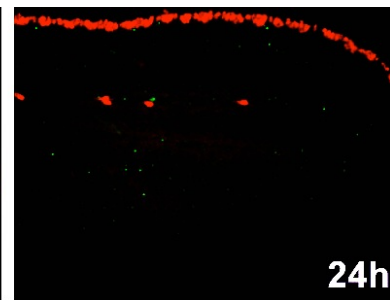
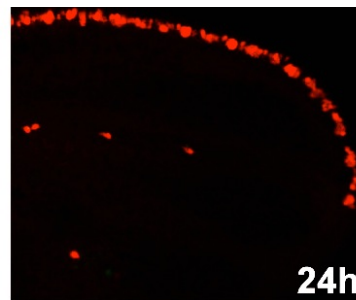
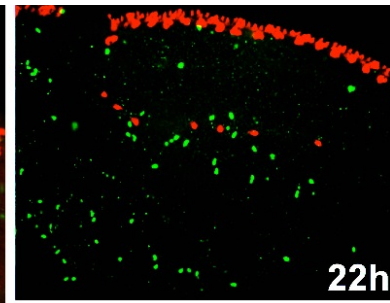
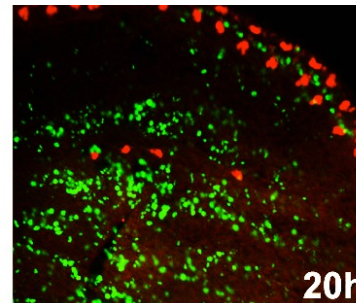
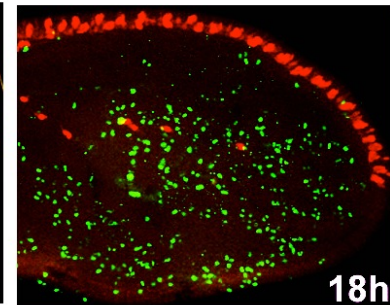
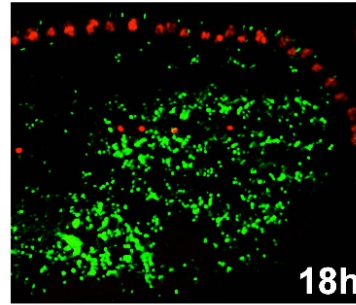
Proliferation

time

Differentiation

S-phase

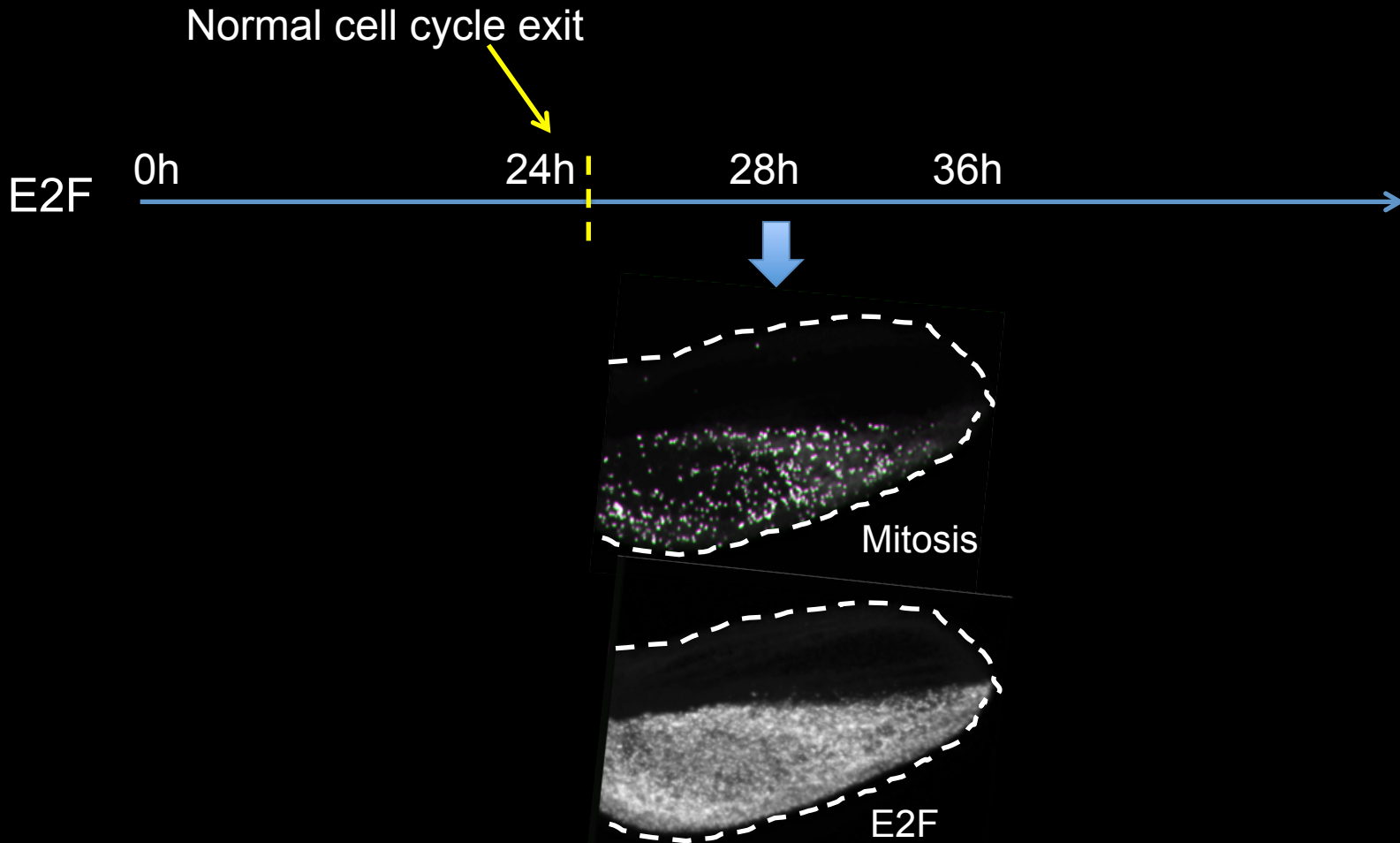
Mitosis



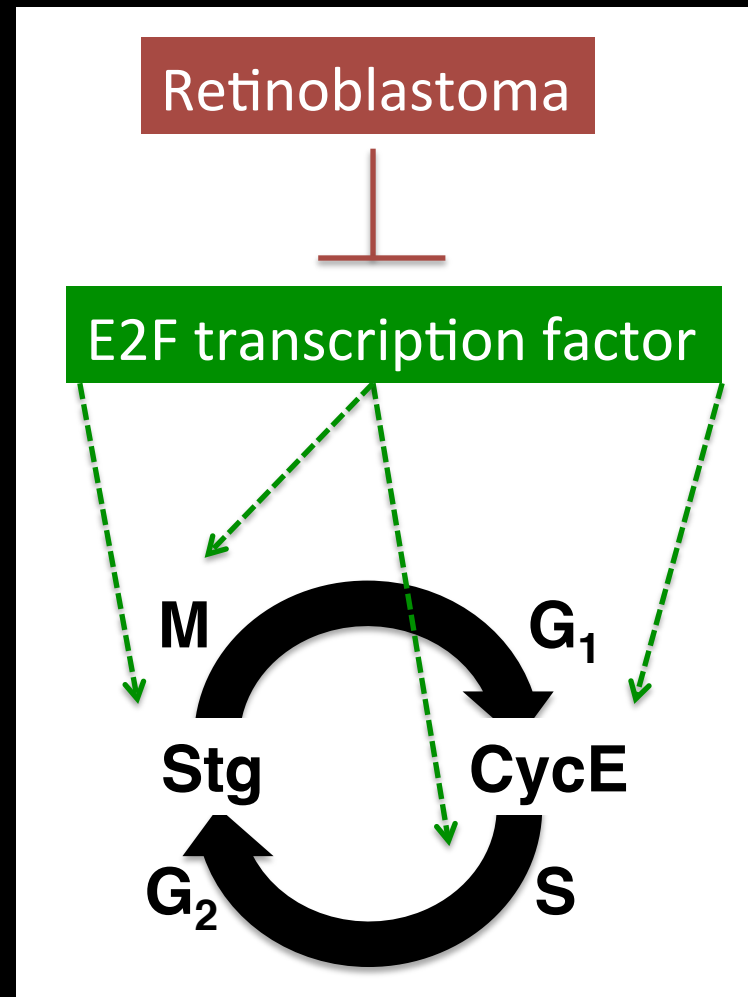
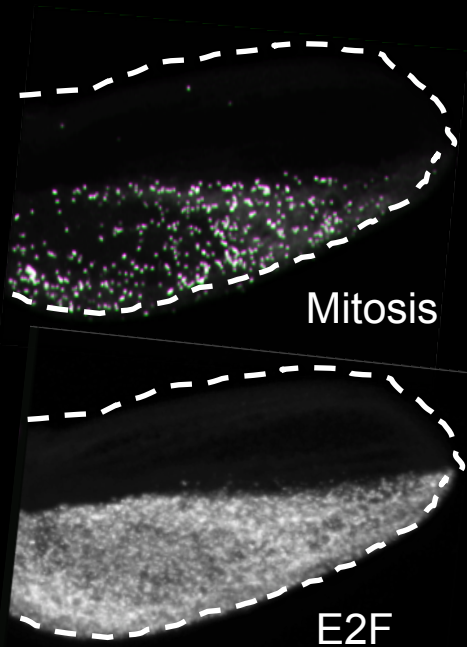
S-phase / neurons

mitoses / neurons

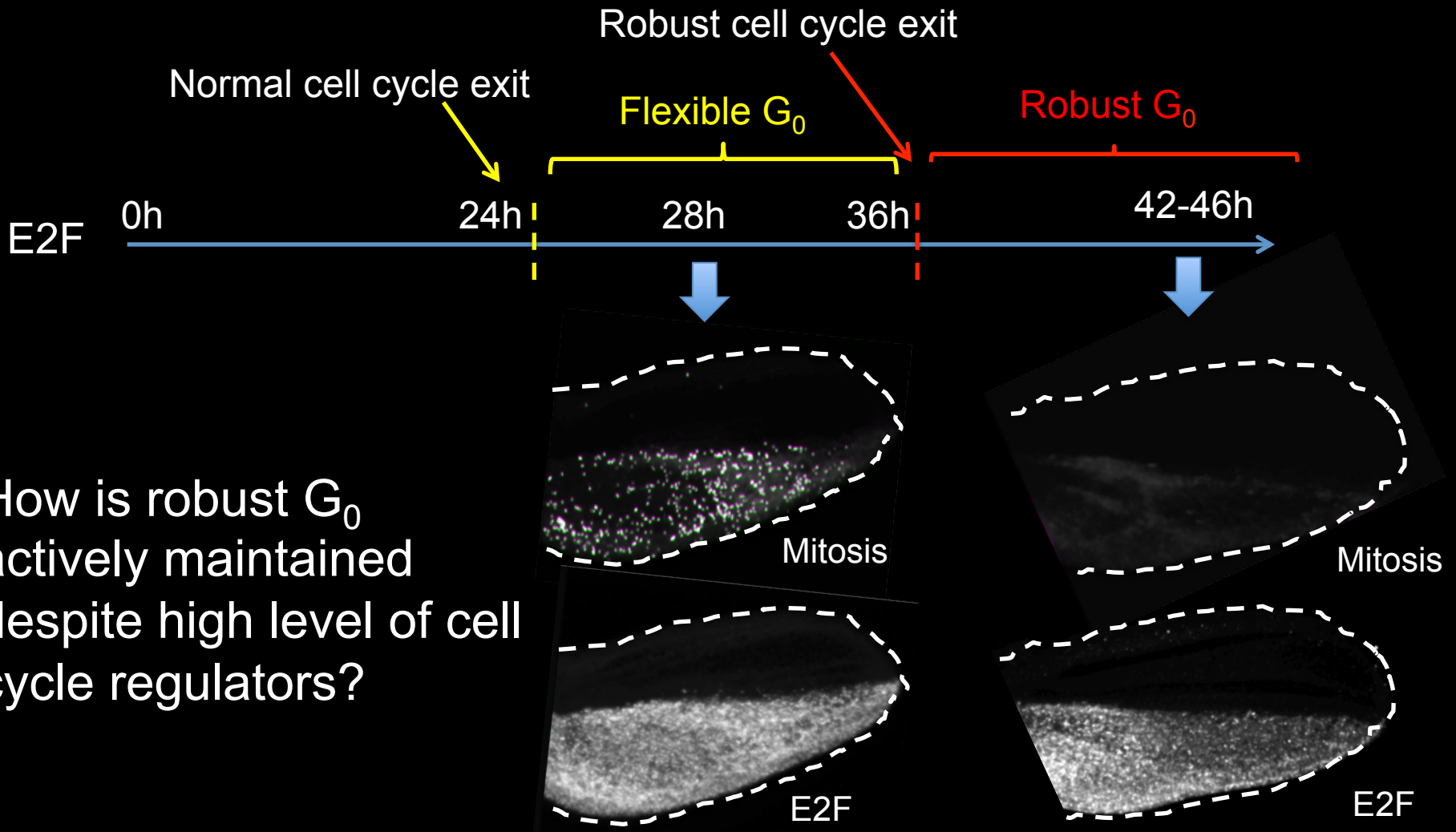
Two stages of G_0 imply multiple levels of cell cycle shut down



How do we manipulate cell cycle exit?



Two stages of G_0 imply multiple levels of cell cycle shut down



How is robust G_0 actively maintained despite high level of cell cycle regulators?

Common “lockdown” models

Key cell cycle genes recruited to periphery/constitutive heterochromatin
VanSteensel Lab

Key cell cycle genes silenced by PRC or HP1 heterochromatin formation

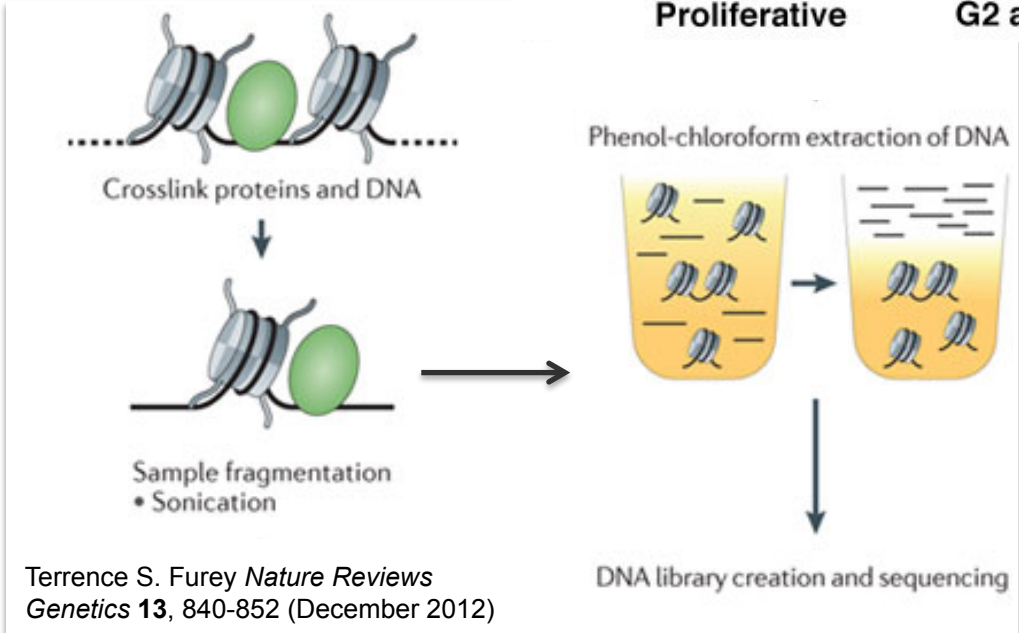
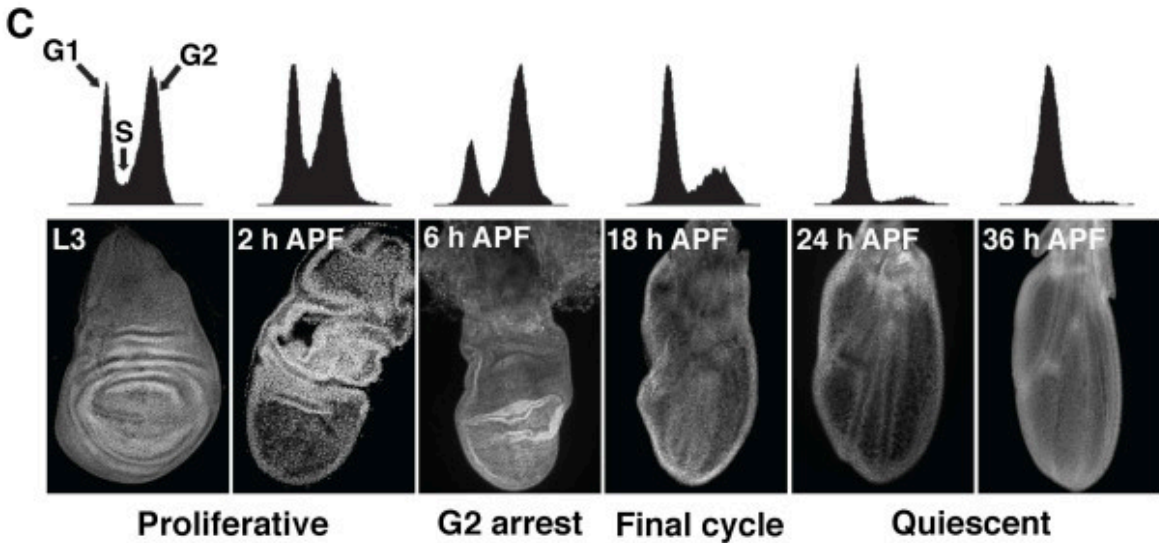
Dynlacht, MacLellan Labs

Origins become inaccessible

Crescenzi Lab

Regulatory element accessibility + RNAseq during metamorphosis

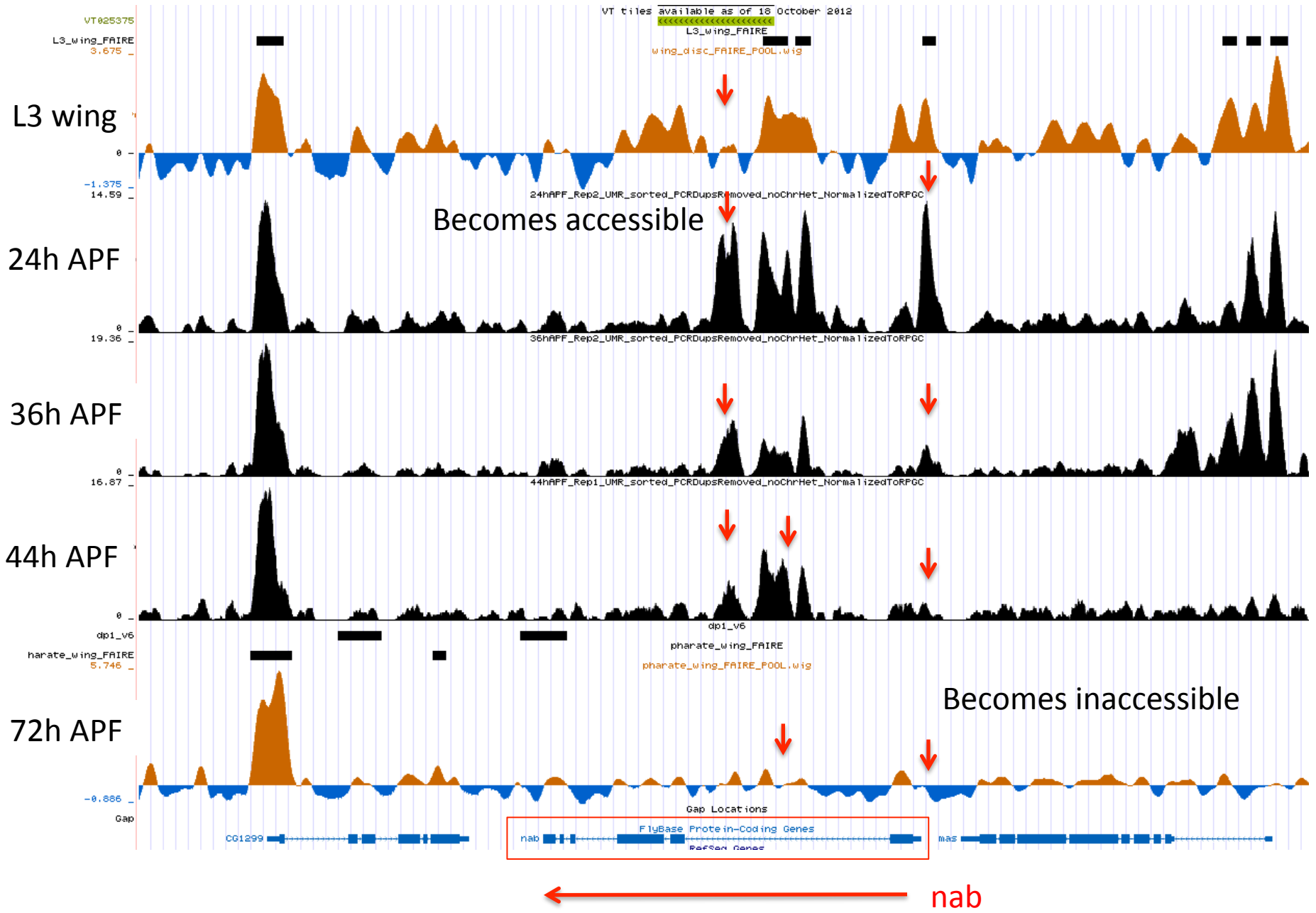
FAIRE-seq (Formaldehyde-Assisted Isolation of Regulatory Elements)



Terrence S. Furey *Nature Reviews Genetics* 13, 840-852 (December 2012)

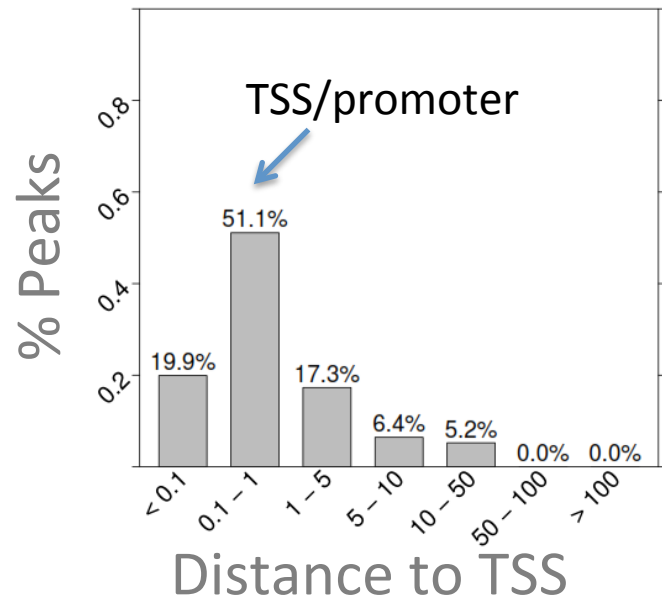
Dan McKay
UNC Chapel Hill

Chromatin accessibility changes at the nab locus during larval->pupal stages



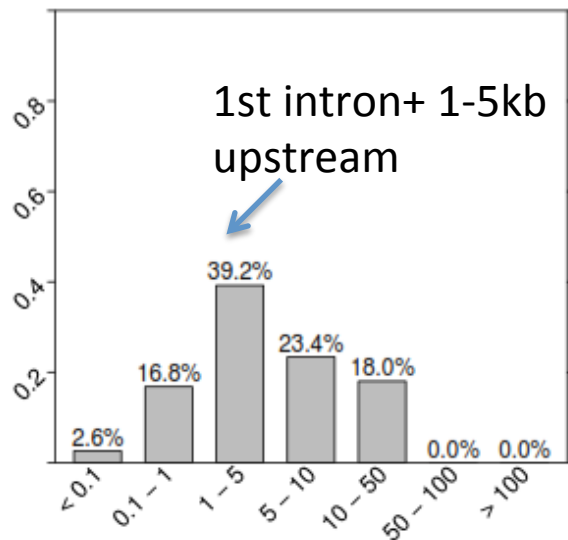
UNCHANGED

Distribution of Distance from Peaks to Nearest TSS



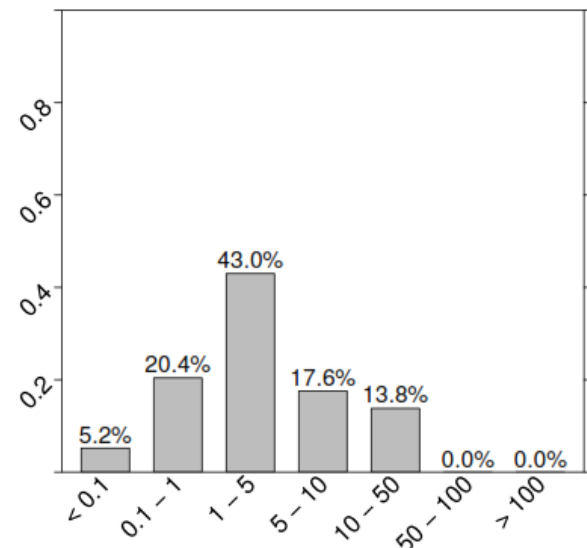
DYNAMIC AT 24H

Distribution of Distance from Peaks to Nearest TSS



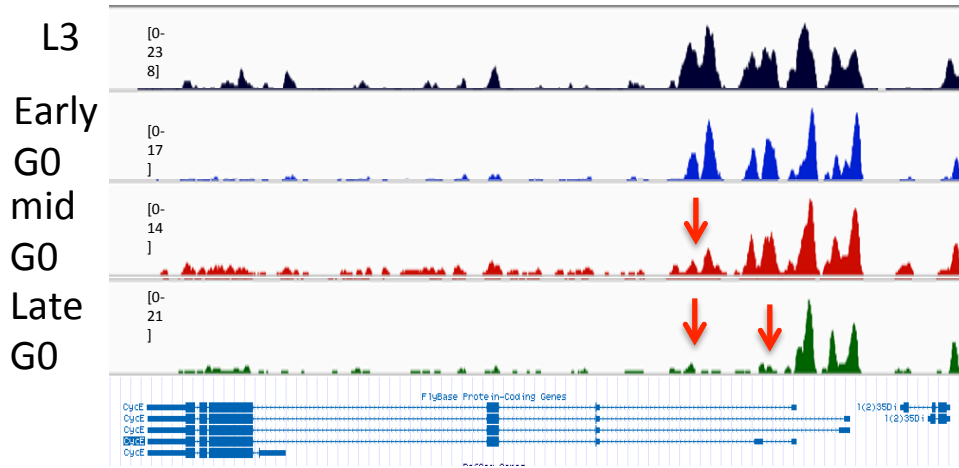
DYNAMIC AT 44H

Distribution of Distance from Peaks to Nearest TSS

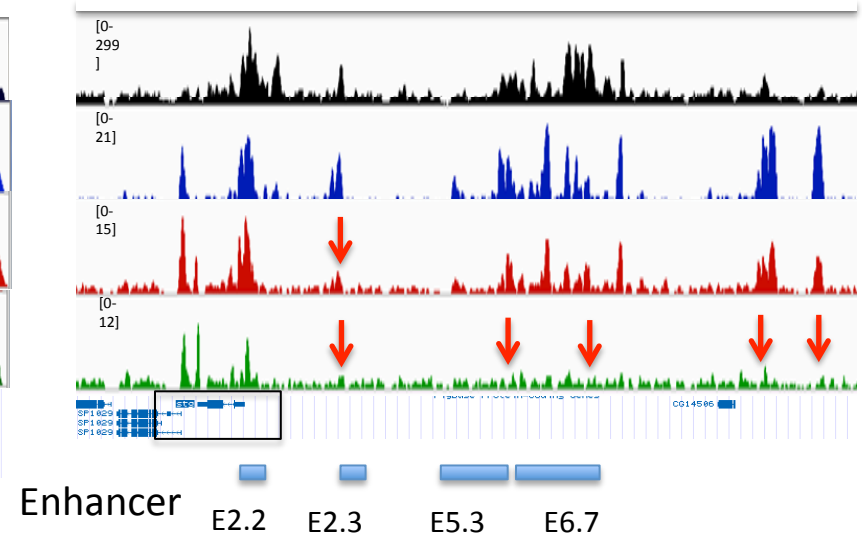


Chromatin accessibility changes at cell cycle genes after cell cycle exit

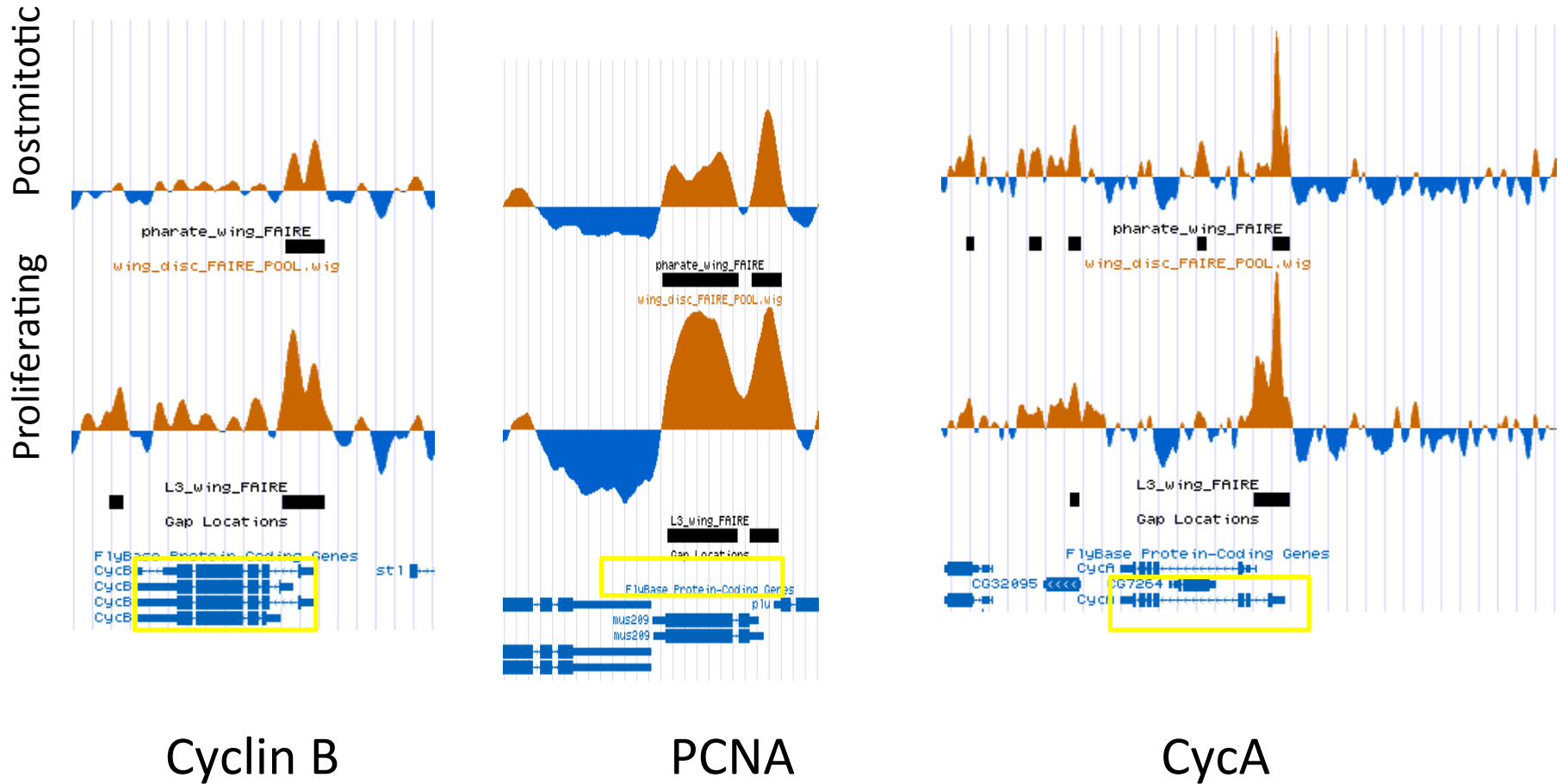
CycE gene locus



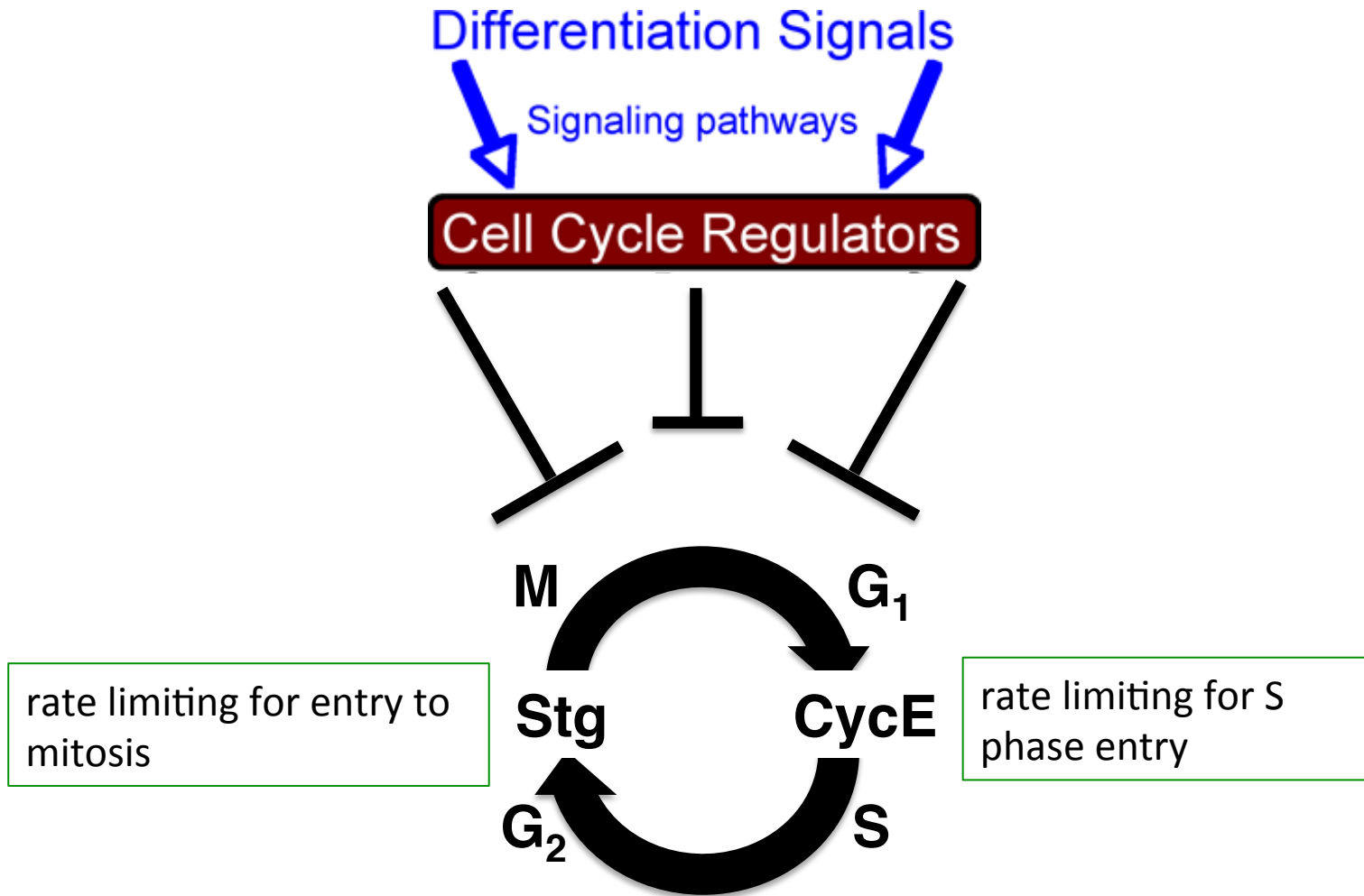
Stg gene locus



...but few chromatin accessibility changes at most other cell cycle genes

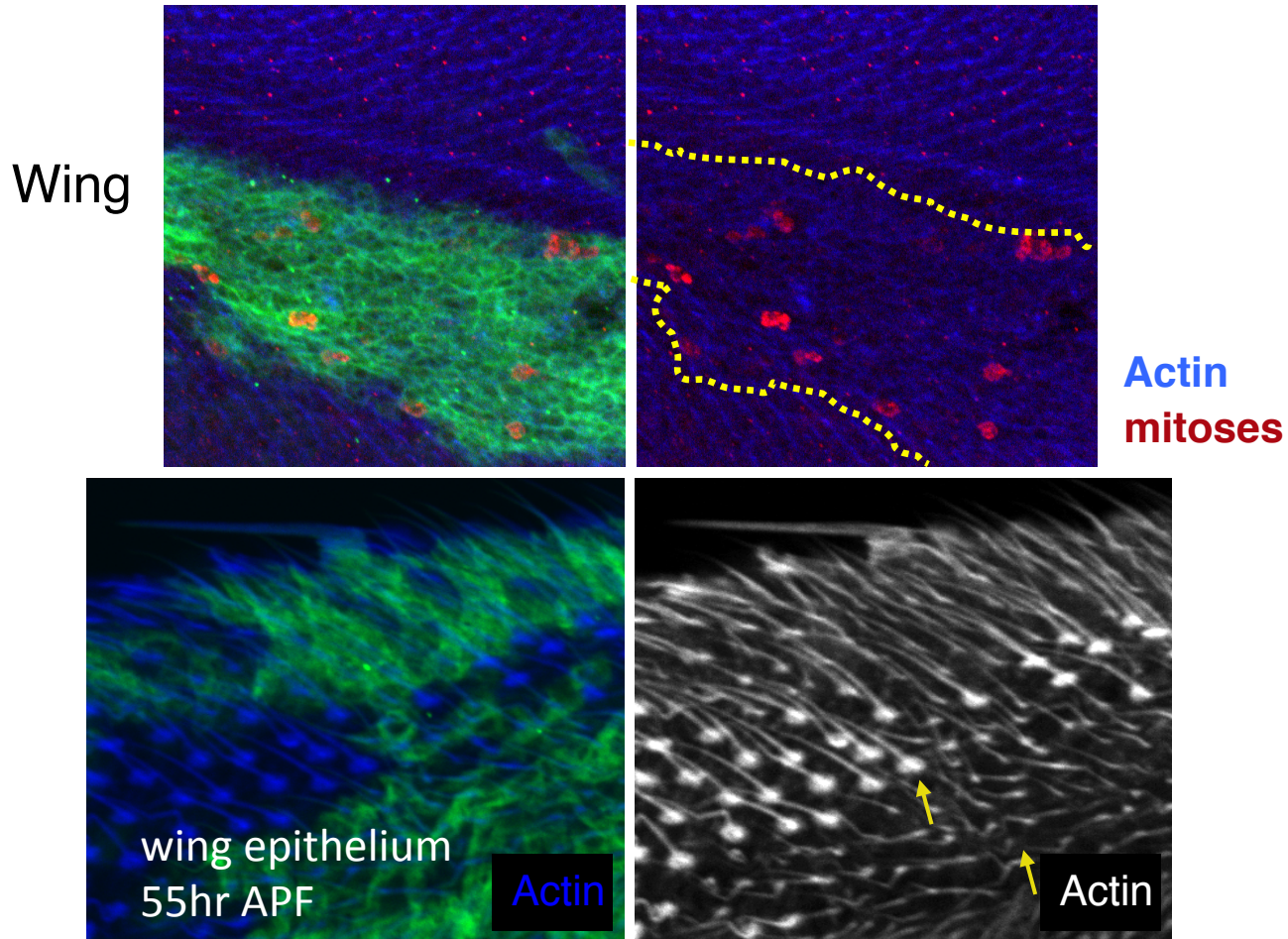


Chromatin accessibility changes at the few “Generals”, not the many “Soldiers”



Adding exogenous CycE+Stg to E2F bypasses G₀

Bypassing G₀ in the fly wing using E2F+CycE+Stg > 44 hr APF



What drives the changes in accessibility at cell cycle genes in G₀?

Many questions remain:

- What happens to accessibility when we bypass G0? (cause or consequence?)
- How does Mi-2 impact chromatin accessibility at cell cycle genes?
- Does preventing changes in accessibility lead to a more flexible G0 state?
- Can we reverse an established G0 state and re-open the inaccessible spots?

Acknowledgements

Buttitta Lab

Kerry Flegel

Rosaline Sun

Yiqin Ma

Olga Grushko

Shyama Nandakumar

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Bloomington Stock Center

Bob Duronio

Collaborators:

Dan McKay (FAIRE-seq)

Funding:

American Cancer Society

NIH NIA

U. Michigan BSSP Award

