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# Cyclin G, Developmental Stability and Transcriptional Control

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**Delphine Dardalhon-Cuménal<sup>1</sup>**, Camille A. Dupont<sup>1</sup>, Valérie Ribeiro<sup>1</sup>, Neel B. Randsholt<sup>1</sup> and Frédérique Peronnet<sup>1</sup>

**Collaborations** : Juliette Pouch<sup>2</sup>, Stéphane Le Crom<sup>2</sup> and Vincent Debat<sup>3</sup>.

<sup>1</sup>UMR7622 – Laboratoire de Biologie du Développement – Institut de Biologie Paris Seine, CNRS-UPMC, Paris

<sup>2</sup>Genomic Paris Centre, IBENS - Institut de Biologie Paris Seine, CNRS-UPMC, Paris

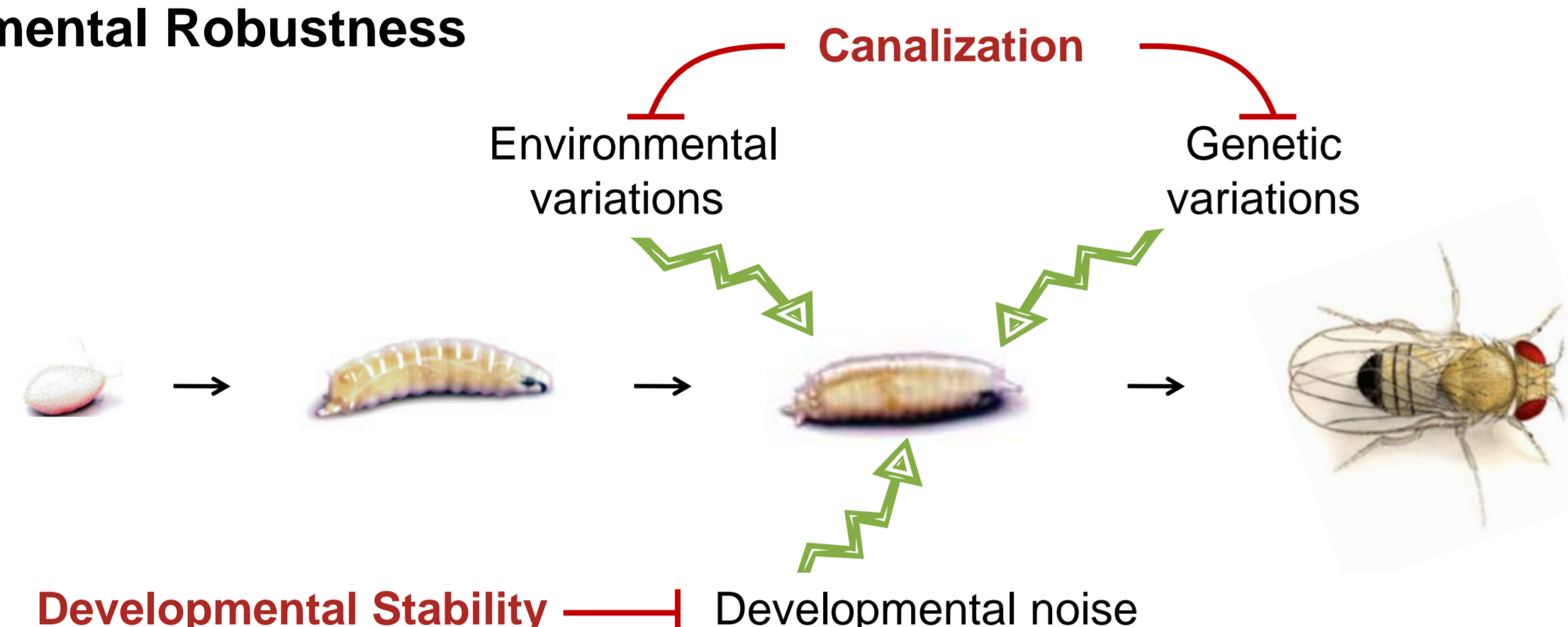
<sup>3</sup>OSEB, Museum National d'Histoire Naturelle, Paris

A central challenge in developmental and evolutionary biology is to understand how organisms cope with developmental noise, the stochastic variations of developmental processes. Nevertheless, **developmental stability**, the buffering of developmental noise, remains poorly understood. In bilaterians, developmental noise is estimated by **Fluctuating Asymmetry (FA)**, the random deviation from perfect symmetry within an isogenic population bred in a standardized environment. We recently reported that an individual gene, *Cyclin G* (*CycG*), encoding a cyclin involved in the regulation of transcription and in the cell cycle, plays a central role in developmental stability in *Drosophila* (Debat et al., 2011; Debat and Peronnet, 2013). Indeed, overexpression of *CycG* induces an unprecedented increase in developmental noise. Using *CycG* overexpression as a tool, we aim at highlighting gene networks underlying developmental stability.

Here, we investigate the role of *CycG* in transcription. Our data show that Cyclin G interacts with Polycomb and Trithorax factors as well as with components of the spliceosome. Furthermore, several mutations of both Polycomb/Trithorax members and components of the spliceosome increase *CycG*-induced developmental noise. Exploring the transcriptional targets of Cyclin G by RNA-seq, we have isolated a sub-network of 87 deregulated genes, mostly repressed by *CycG* overexpression, that is enriched in GO terms related to transcriptional activity. Such a sub-network might be involved in the control of developmental noise.

## I - Developmental Stability and Fluctuating Asymmetry

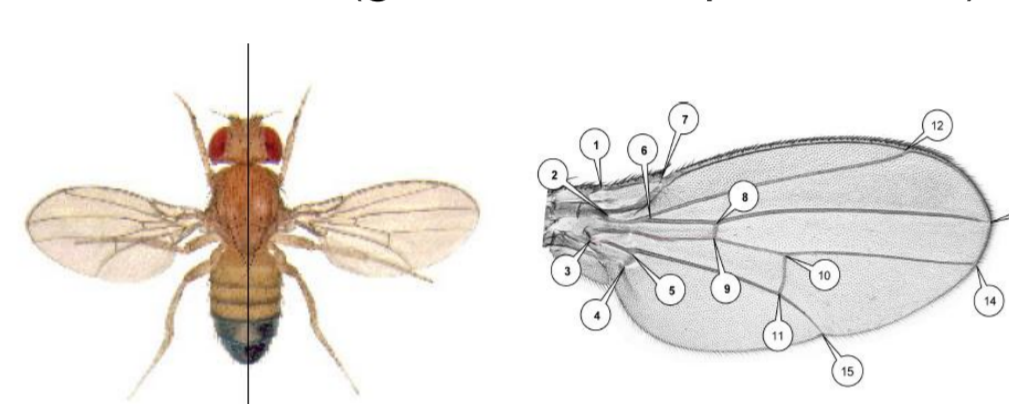
### Developmental Robustness



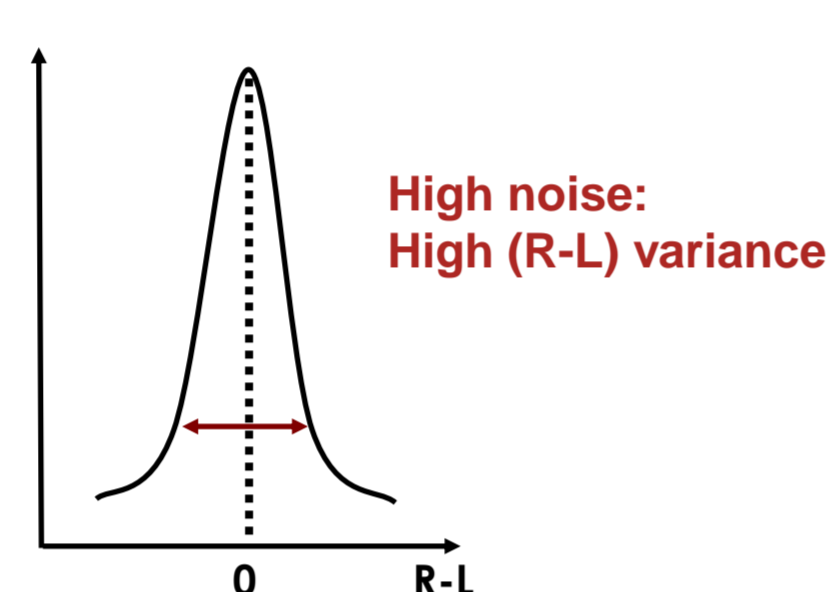
In bilaterians, developmental noise is assessed by **Fluctuating Asymmetry (FA)** in a population of isogenic flies raised in a standardized environment.

Measure of the centroid size of right (R) and left (L) wings using a set of 15 landmarks (geometric morphometrics)

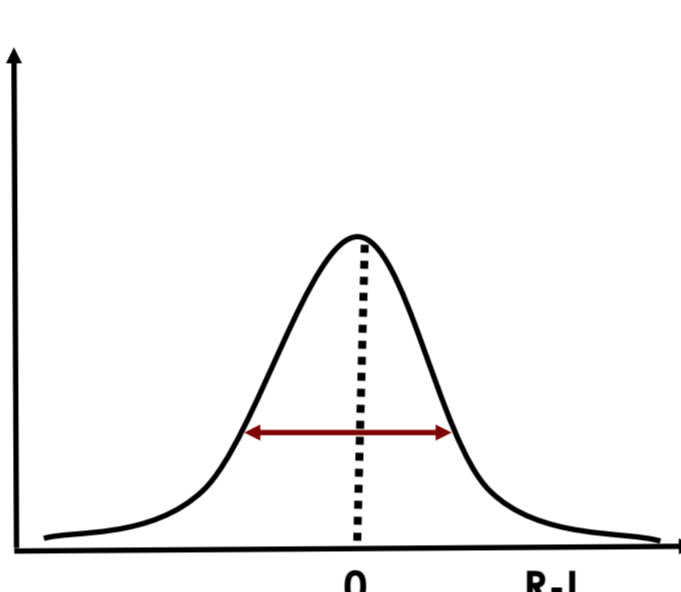
Distribution of (R-L) within a population



Low noise:  
Low (R-L) variance

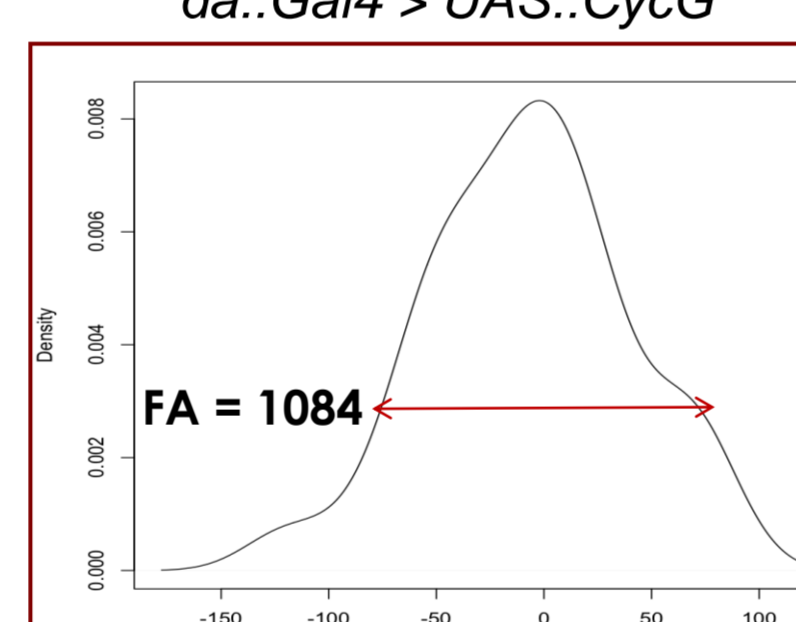
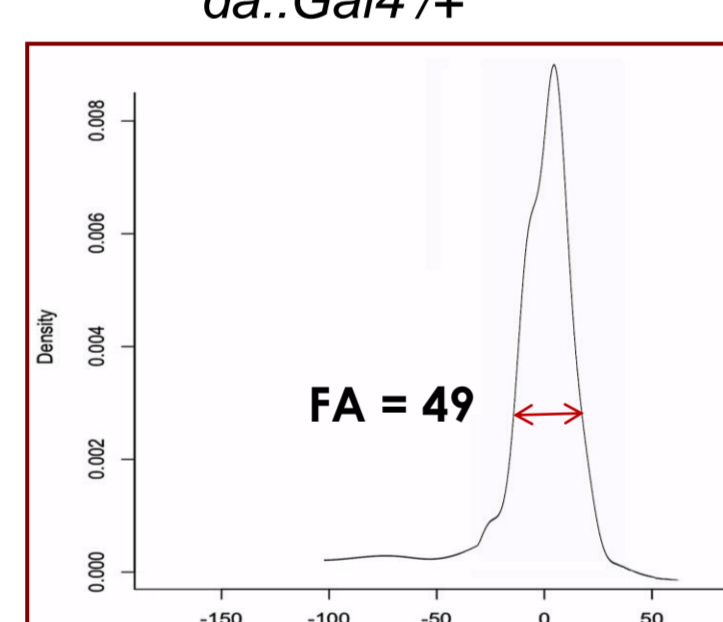
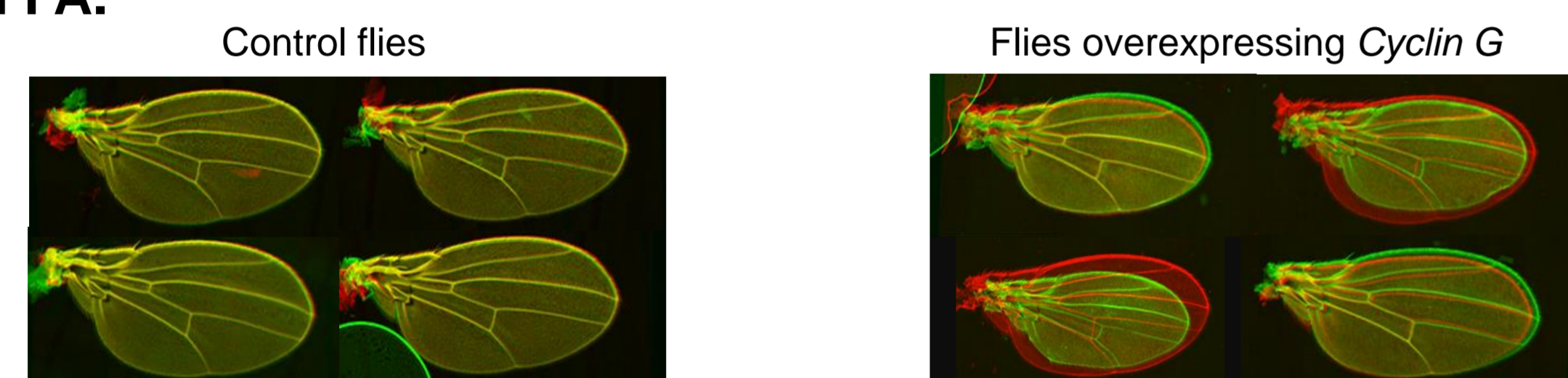


High noise:  
High (R-L) variance



## II - Cyclin G overexpression increases developmental noise

Overexpression of *CycG* in isogenic flies raised in a standardized environment induces high FA.



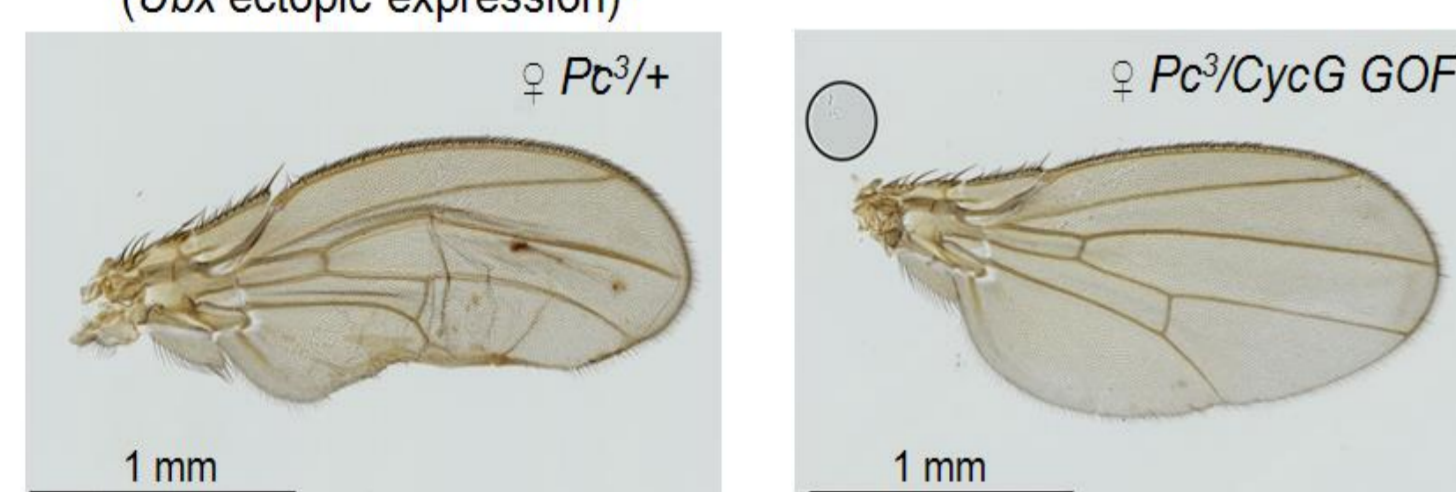
X 22

(Debat et al. 2011; Debat and Peronnet, 2013)

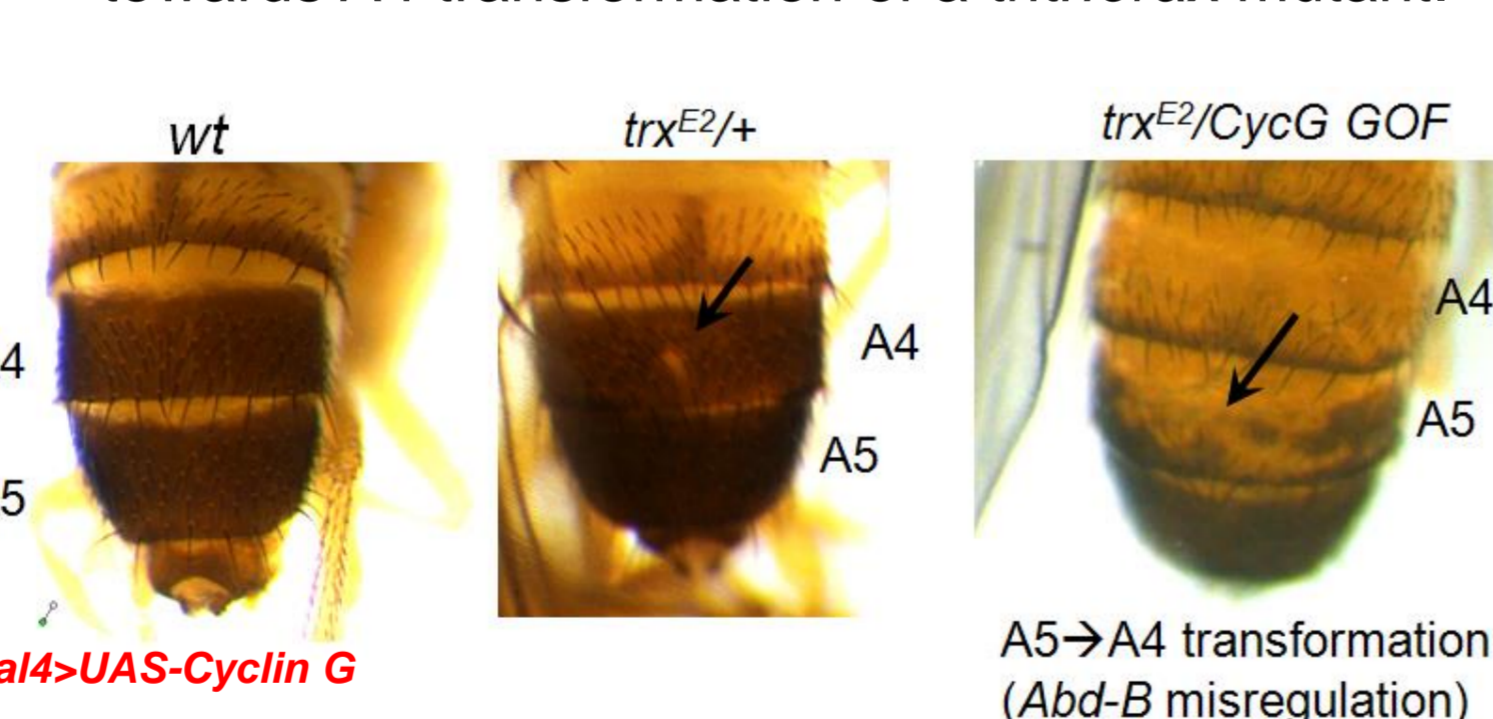
## III - Cyclin G interacts with Polycomb and Trithorax factors

### 1) Cyclin G behaves as a Polycomb gene in the regulation of homeotic genes.

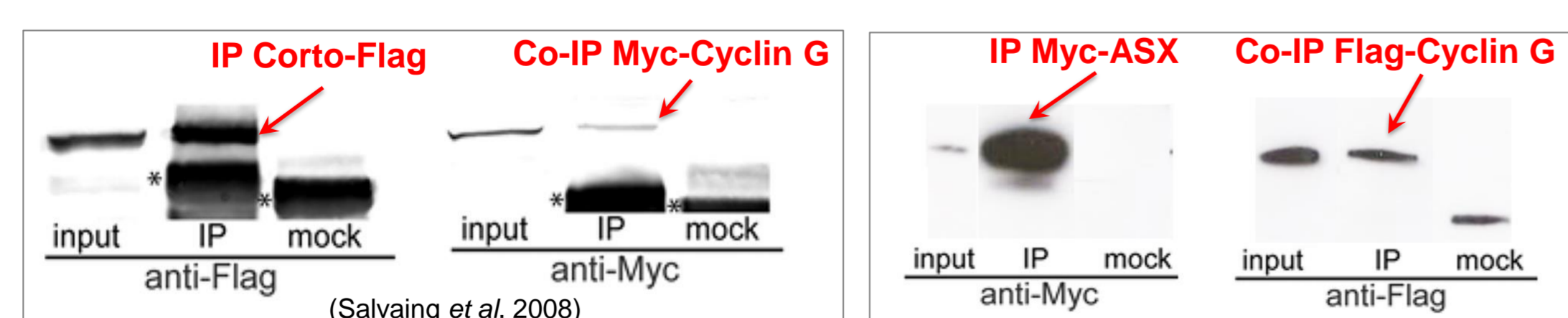
Overexpression of *CycG* suppresses the *Contra-bithorax* phenotype of a *Polycomb* mutant.  
wing → haltere  
(*Ubx* ectopic expression)



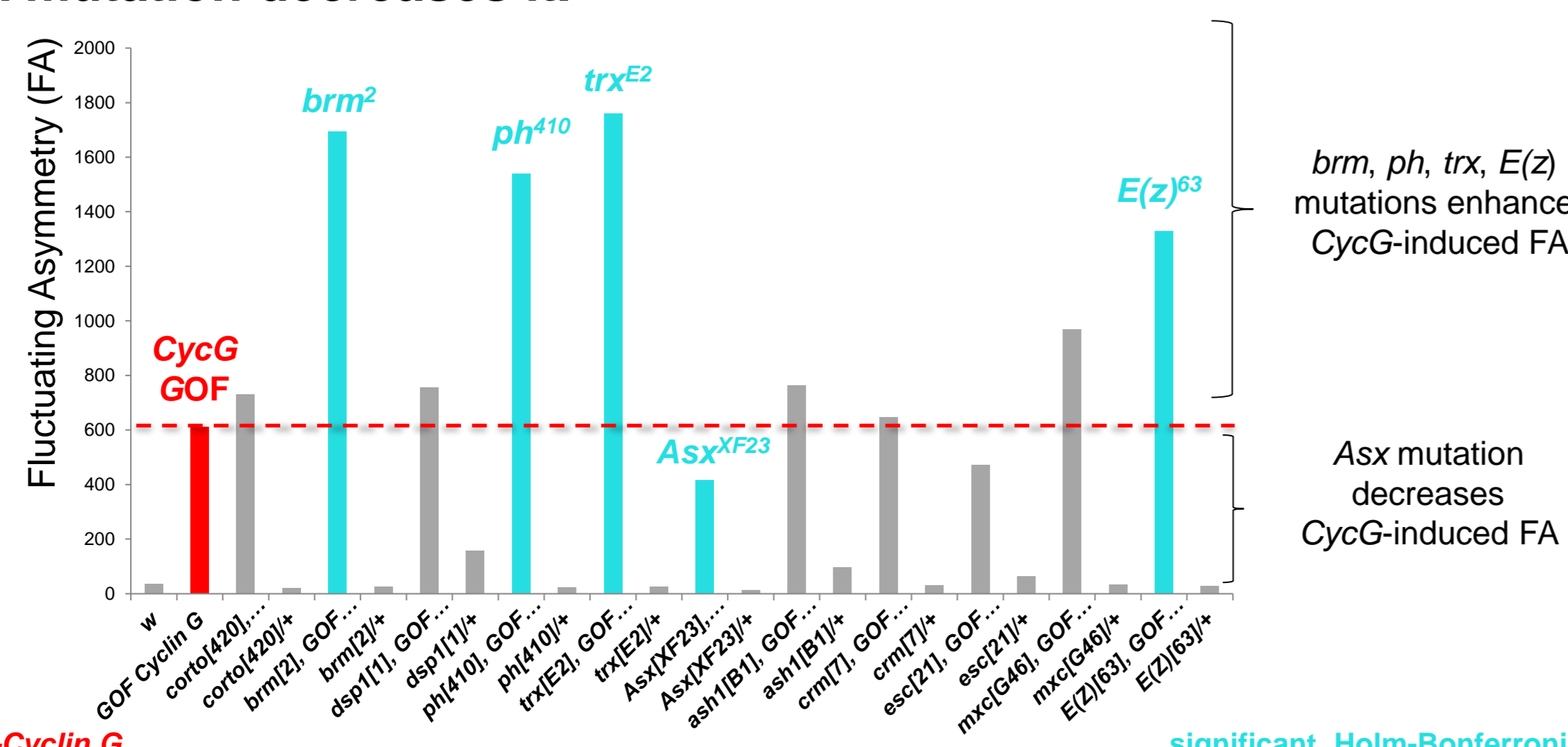
Overexpression of *CycG* enhances the A5 towards A4 transformation of a *trithorax* mutant.



### 2) Cyclin G directly interacts with two chromatin regulators of the Enhancers of Trithorax and Polycomb family (Corto, ASX).



### 3) Several mutations of Polycomb and Trithorax genes increase *CycG*-induced FA whereas an *Asx* mutation decreases it.



*brm*, *ph*, *trx*, *E(z)* mutations enhance *CycG*-induced FA

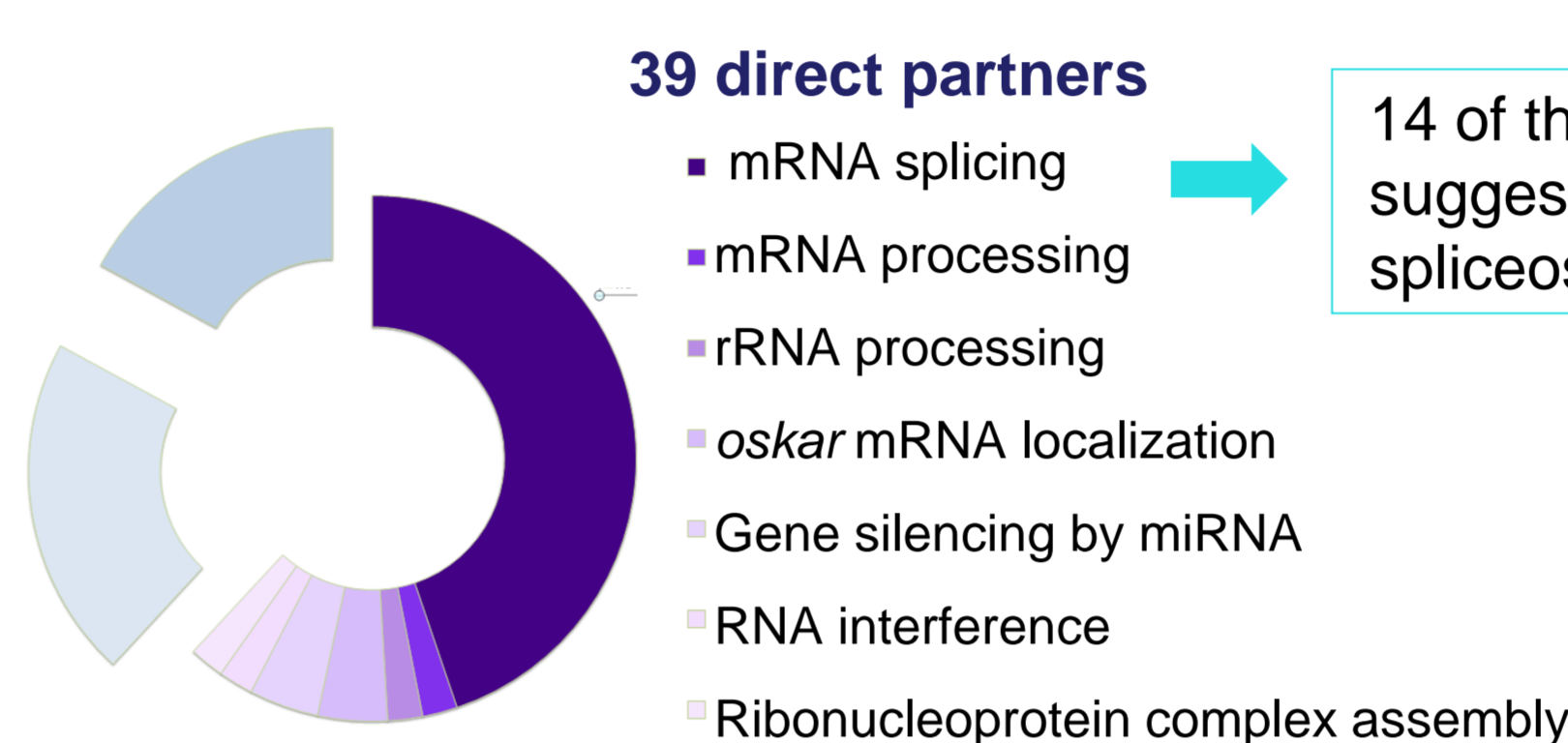
*Asx* mutation decreases *CycG*-induced FA

*CycG* GOF = *da::Gal4>UAS-Cyclin G*

significant, Holm-Bonferroni correction

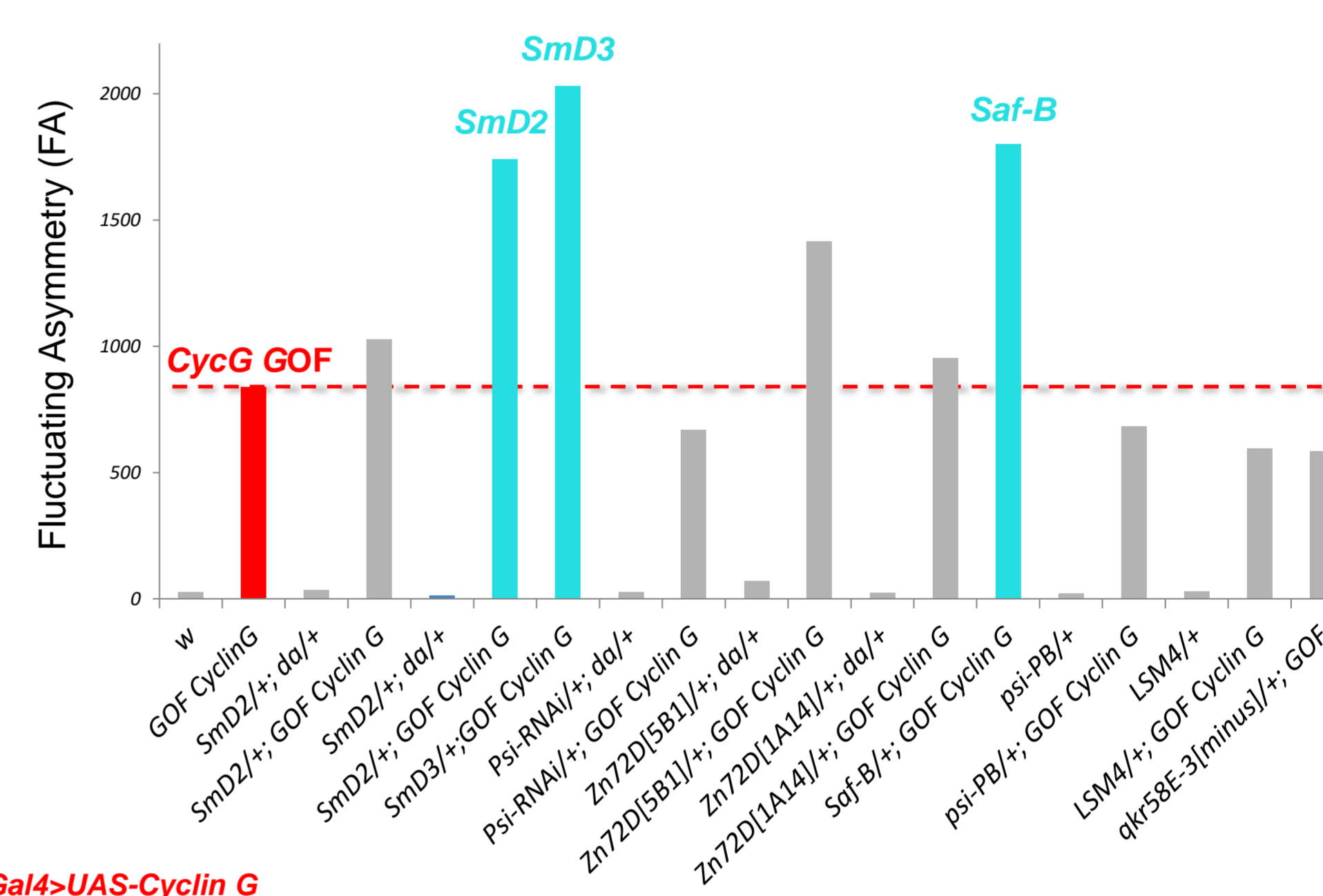
## IV - Cyclin G interacts with components of the spliceosome

### 1) Direct partners of Cyclin G identified by pull-down and mass spectrometry (*Drosophila* Protein Interaction Map; *interfly.med.harvard.edu*)



14 of these partners are involved in mRNA splicing, suggesting that Cyclin G might interact with the spliceosome.

### 2) Several mutations of genes encoding components of the spliceosome increase *CycG*-induced FA.



*CycG* GOF = *da::Gal4>UAS-Cyclin G*

F test;  $p < 0.05$

## V - Cyclin G has many transcriptional targets

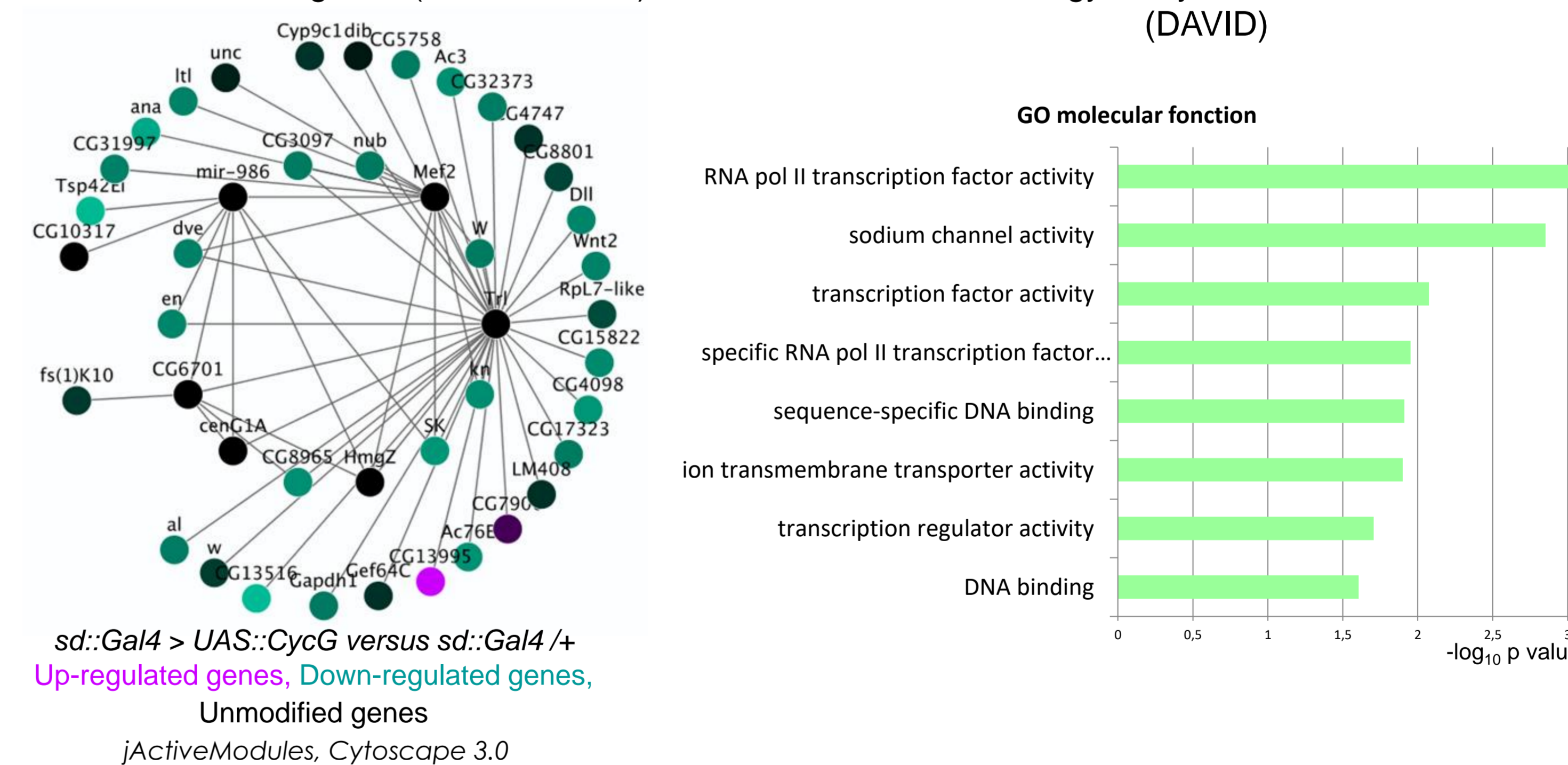
### 1) Cyclin G co-localizes at many sites with RNA Pol II, and with the active marks H3K4me3 and H3K36me3 on polytene chromosomes.



### 2) However, RNA-seq analysis of wing imaginal discs overexpressing *CycG* suggests that Cyclin G represses transcription of many genes; GO analysis of these genes shows an enrichment in terms related to transcriptional regulation.

Sub-network of 87 genes (Active module)

Gene ontology analysis of this sub-network (DAVID)



*sd::Gal4 > UAS::CycG* versus *sd::Gal4 +/-*  
Up-regulated genes, Down-regulated genes, Unmodified genes  
*jActiveModules*, *Cytoscape* 3.0

## Ongoing projects

- ✓ Determine genome-wide binding sites of Cyclin G (Chip-Seq), to identify its direct transcriptional targets by correlation with RNA-seq.
- ✓ Analyze alternative transcripts in *CycG* overexpressing flies.
- ✓ Test the role of genes belonging to the identified sub-network in developmental stability.

## References

Debat, V., Bloyer, S., Faradji, F., Gidaszewski, N., Navarro, N., Orozco-Terwengel, P., Ribeiro, V., Schlotterer, C., Deutsch, J.S., and Peronnet, F. (2011). Developmental Stability: A Major Role for Cyclin G in *Drosophila melanogaster*. *PLoS Genet* 7, e1002314.

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Salvaing, J., Nagel, A.C., Mouchel-Vielh, E., Bloyer, S., Maier, D., Preiss, A., and Peronnet, F. (2008). The Enhancer of Trithorax and Polycomb Corto interacts with Cyclin G in *Drosophila*. *PLoS One* 3, e1658.