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Cyclin G deregulation, a tool to decipher gene network(s) controlling developmental stability

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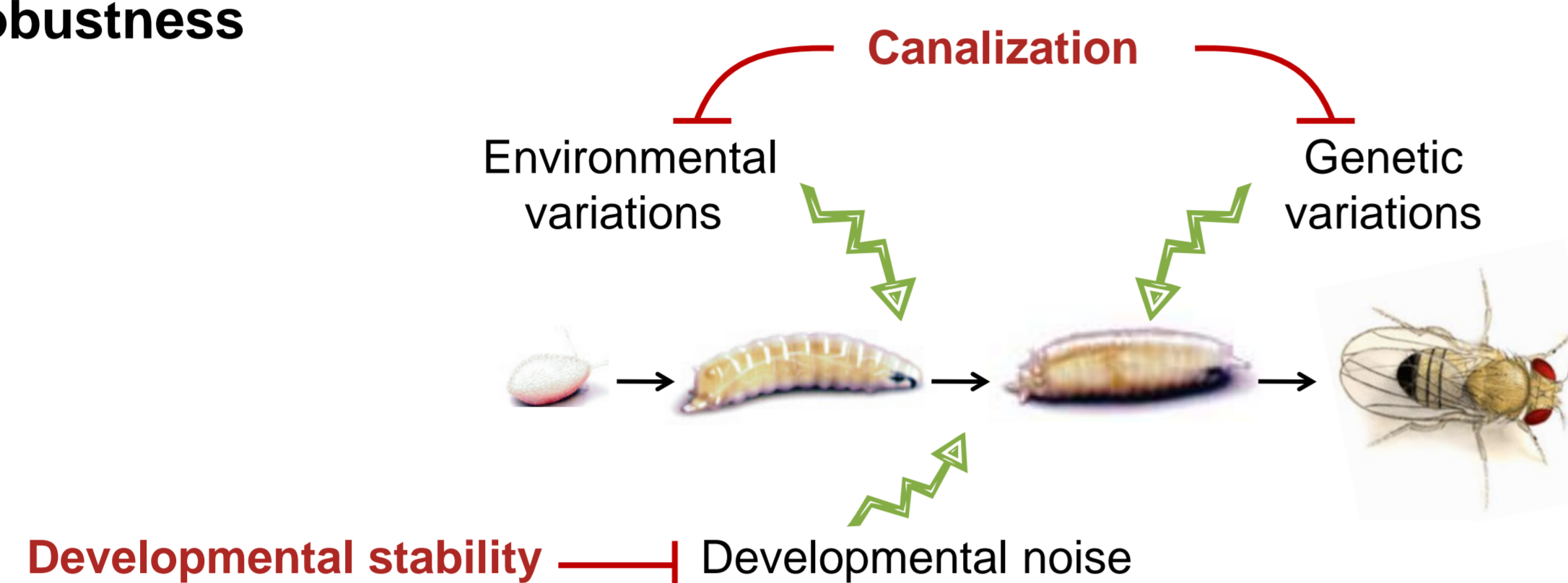
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A central challenge in developmental and evolutionary biology is to understand **developmental stability**, the process that buffers developmental noise. In bilaterians, developmental stability is estimated by **Fluctuating Asymmetry (FA)**, the random deviation from perfect symmetry within an isogenic population bred in a standardized environment.

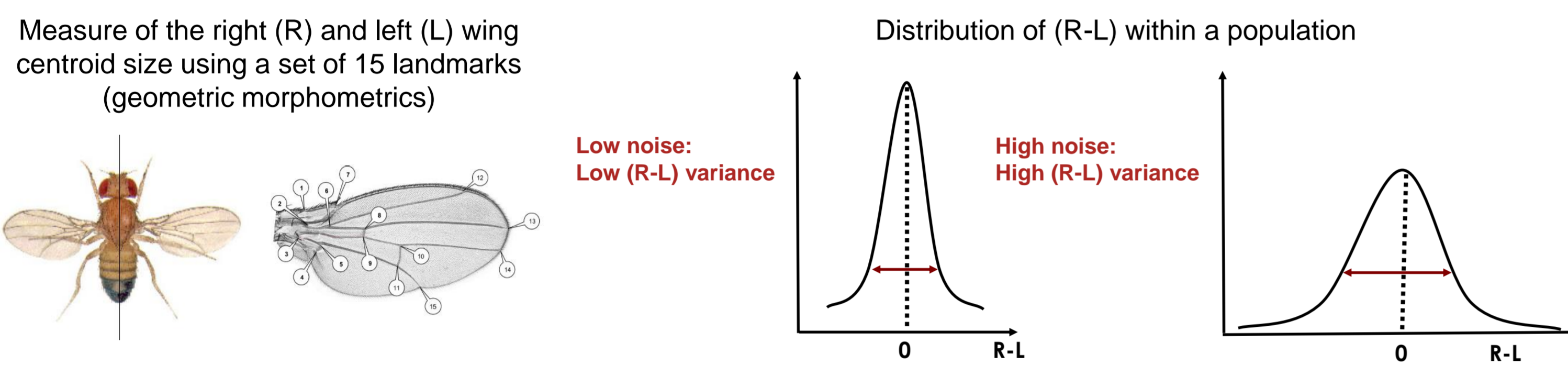
Overexpression of *Cyclin G* (*CycG*), encoding a cyclin involved in the regulation of transcription and in the cell cycle, induces an unprecedented increase in wing FA. This phenotype is associated with loss of correlation between total cell number and mean cell size in adult wings. Moreover, it is linked to the role of Cyclin G in transcriptional regulation. *CycG* deregulation is used as a tool to identify gene networks underlying developmental stability.

I - Developmental stability and Fluctuating Asymmetry

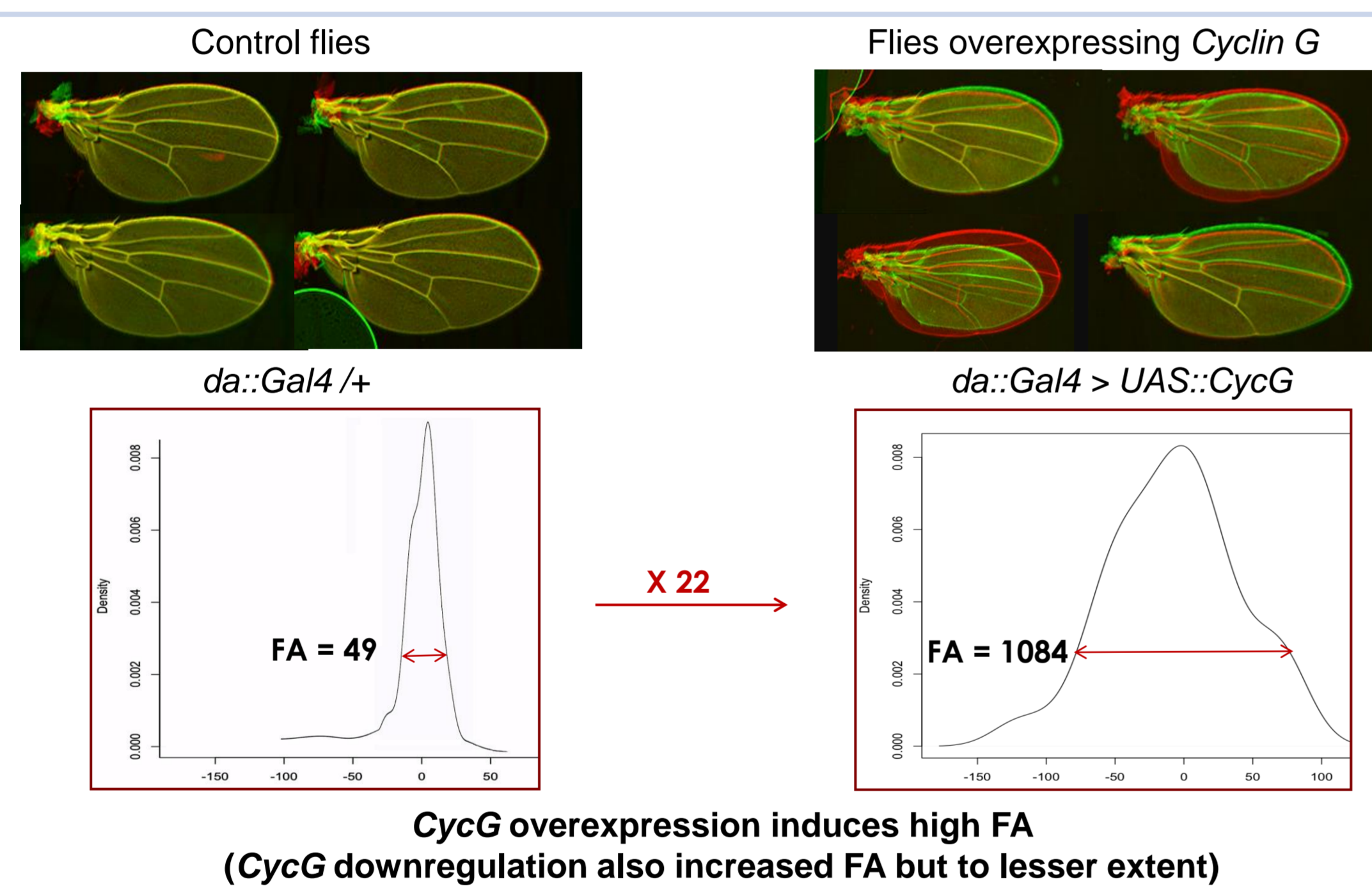
Developmental robustness



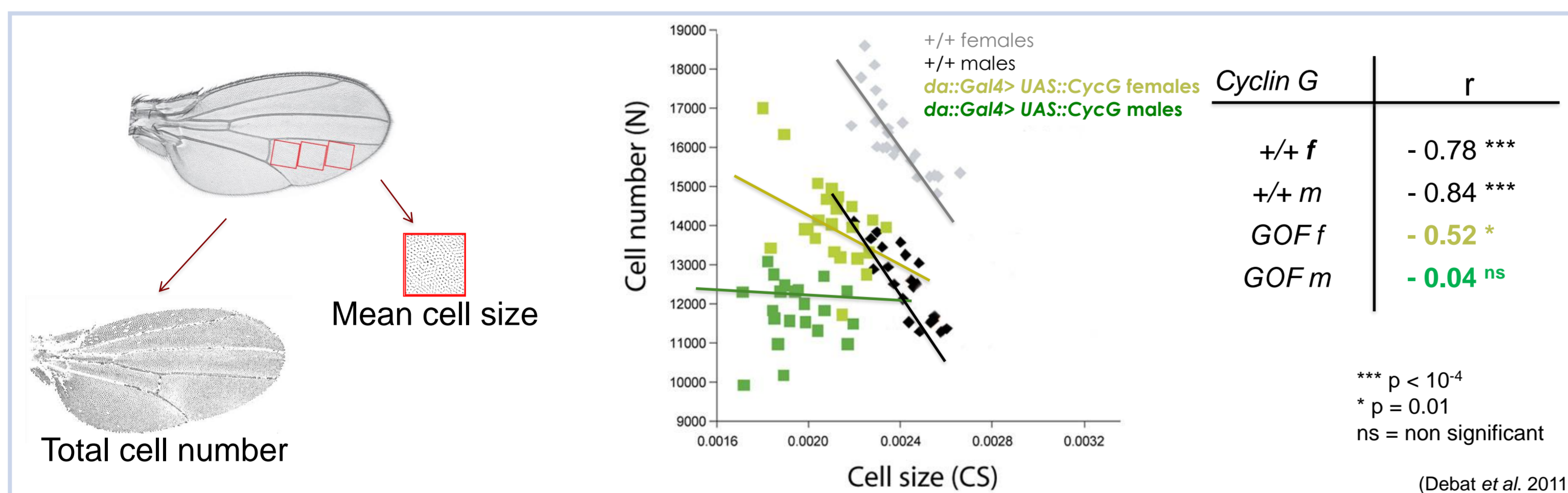
Developmental noise is assessed by Fluctuating Asymmetry (FA) in isogenic lines raised in a standardized environment



II - CycG misregulation increases developmental noise

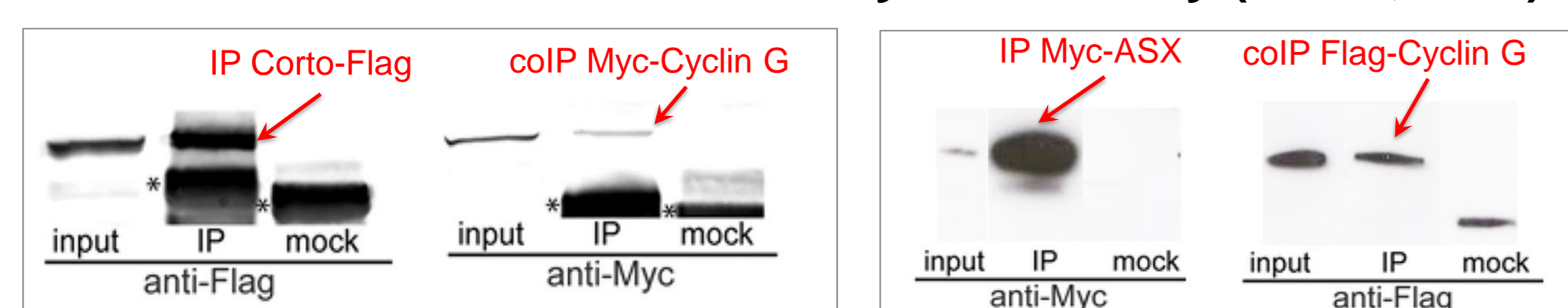


III - In *CycG* deregulated wings, the correlation between cell size and total cell number is lost

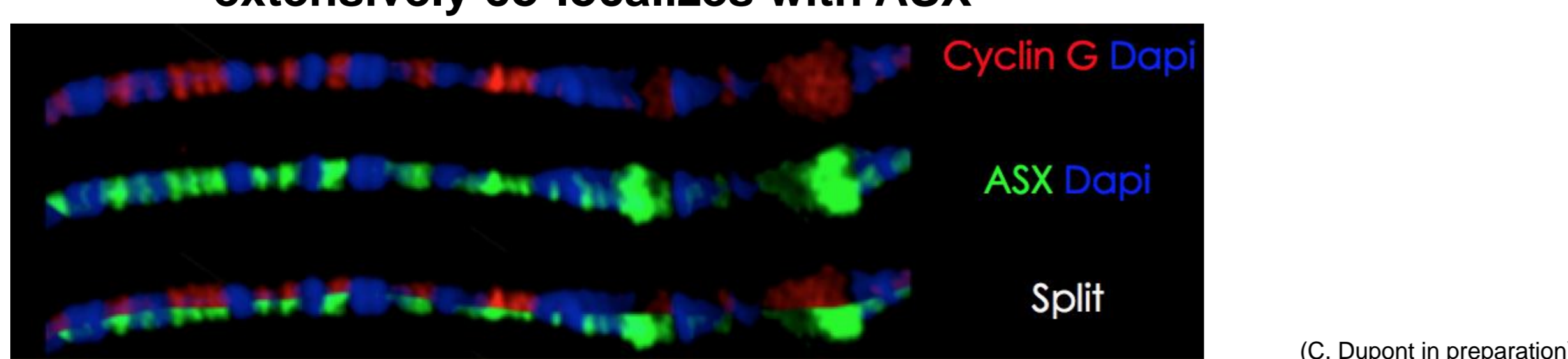


IV - Cyclin G is a transcriptional regulator

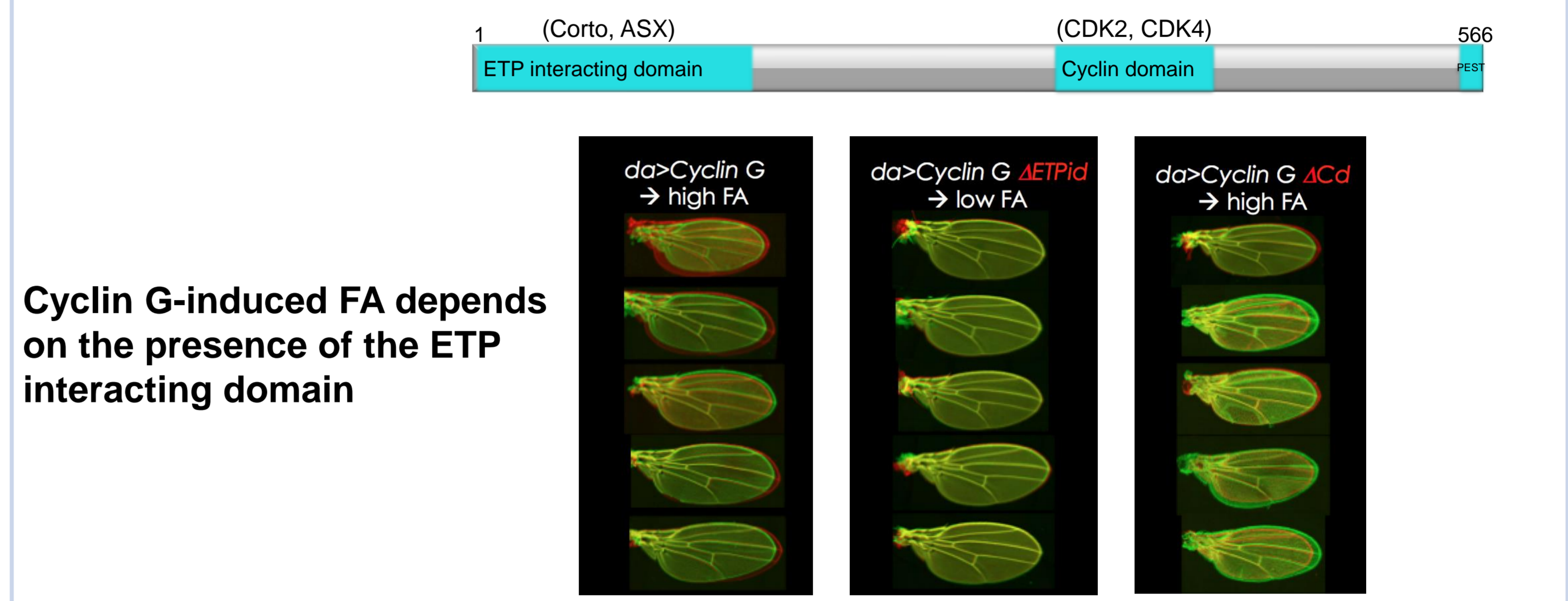
Cyclin G interacts with two chromatin regulators of the Enhancers of Trithorax and Polycomb family (Corto, ASX)



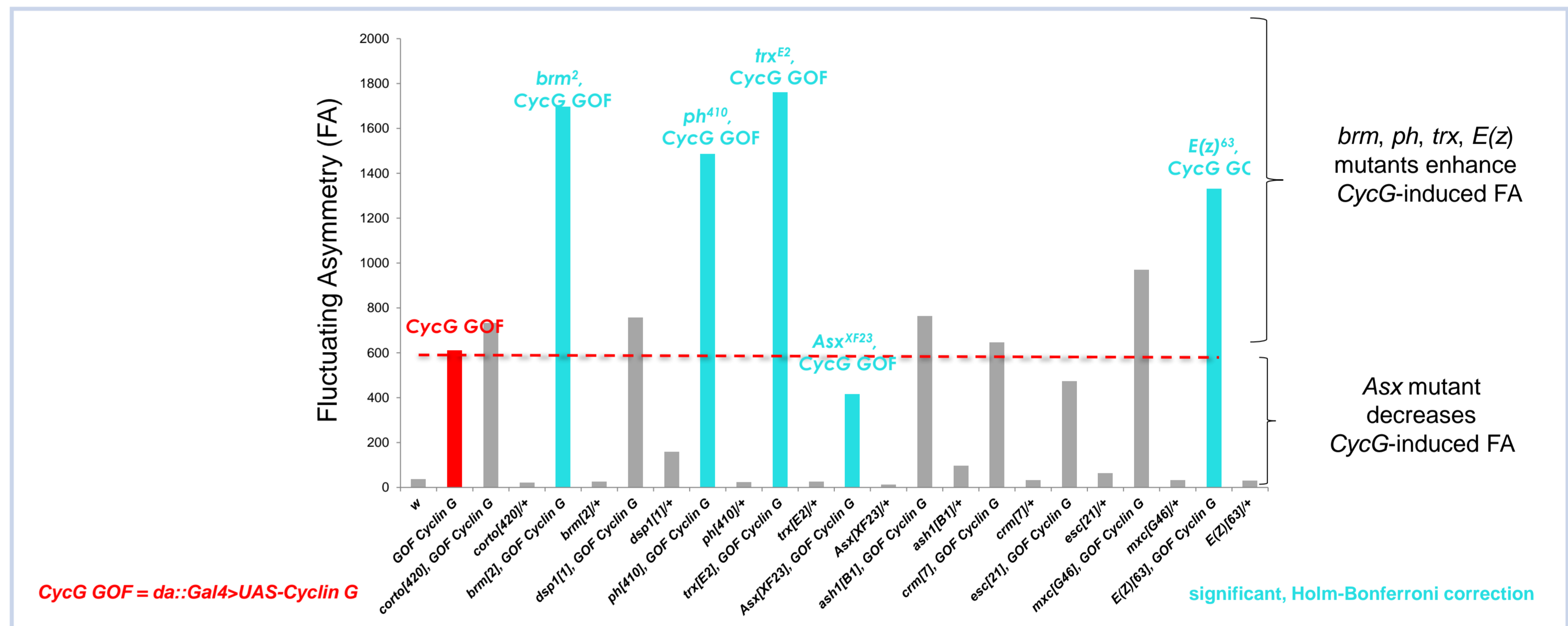
Cyclin G binds polytene chromosomes where it extensively co-localizes with ASX



V - The effect of Cyclin G on developmental noise is related to its role in transcription

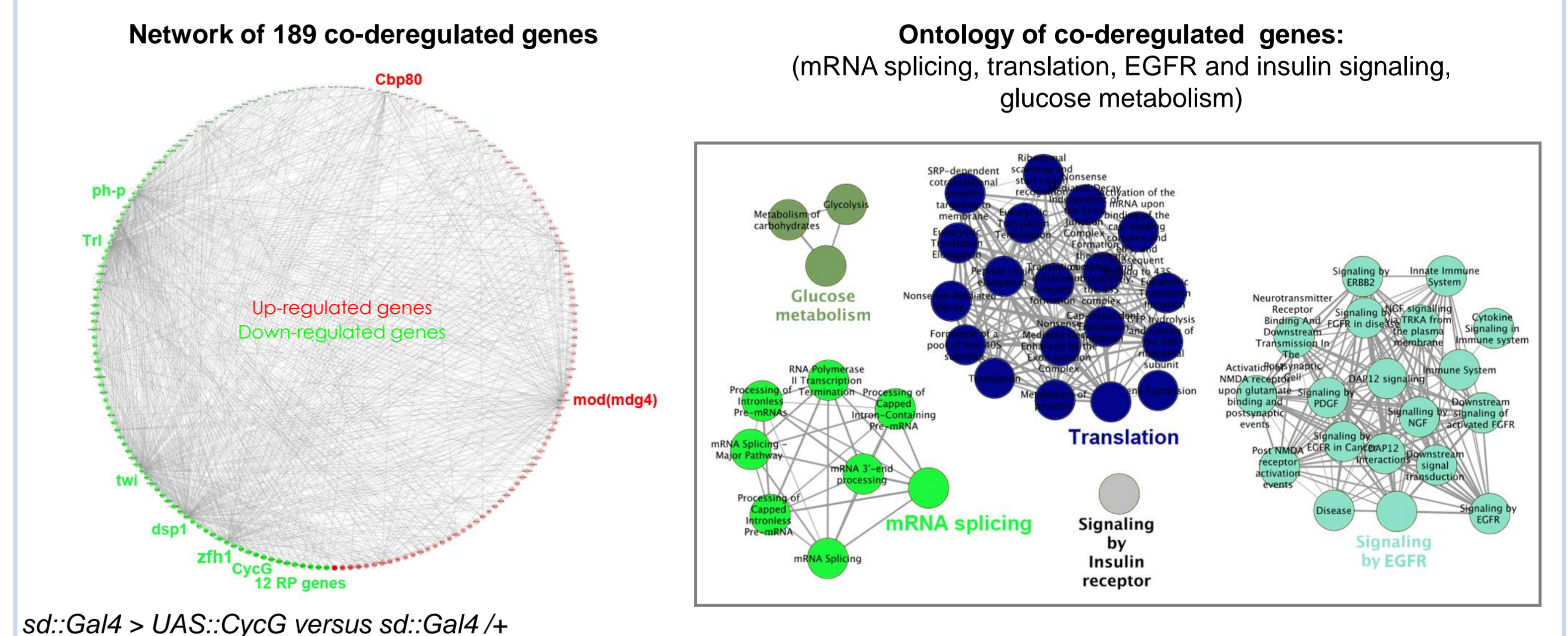


VI - Several Polycomb-group (PcG) or Trithorax-group (trxG) gene mutants modify *CycG*-induced developmental stability



VII - Identification of Cyclin G transcriptional targets

RNA-seq of wing imaginal discs overexpressing *CycG* reveals a sub-network of 189 deregulated genes potentially involved in developmental stability



Ongoing projects and Future investigations

- ✓ Determine **genome-wide binding sites** of Cyclin G (Chip-Seq), to identify direct transcriptional targets by correlation with RNA-seq
- ✓ Continue **the candidate gene approach** to find modifiers of *CycG*-induced FA (gene encoding direct interactors, genes involved in epigenetic memory, in growth pathways)
- ✓ Build gene network(s) that control developmental stability based on modifiers of *CycG*-induced FA

References

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