

Transcriptional atlas of *Drosophila melanogaster* imaginal discs

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Outline

Introduction

- Our model

- Overview of RNA-seq samples

Eye, leg and wing

- DEG across tissues and time

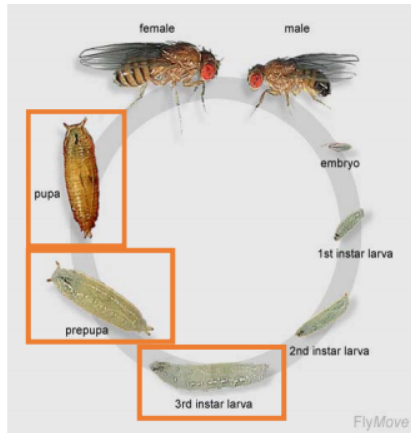
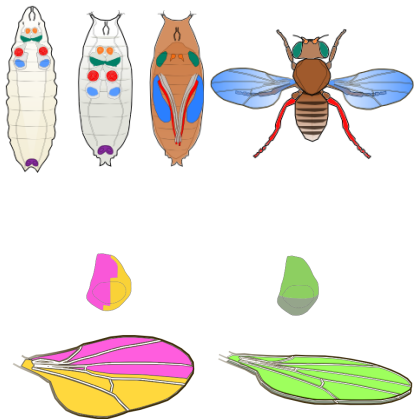
- Isoform Usage

Wing compartments

- DEG across wing compartments

Conclusion and perspectives

Our model



Outline

Introduction

Our model

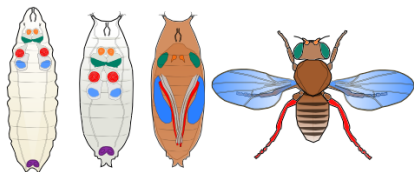
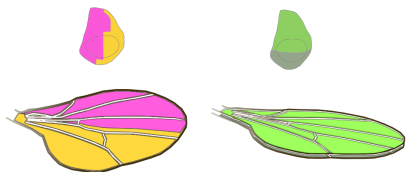
Overview of RNA-seq samples

Eye, leg and wing

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Overview of processed RNA-seq samples



anterior	2	2	2
posterior	2	2	2
dorsal	2	2	2
ventral	2	2	2
wing	2	2	2
eye	2	2	2
antenna	2	2	-
female_genitalia	2	2	-
male_genitalia	2	2	-
leg	2	2	2

tissue

- antenna
- eye
- genitalia
- leg
- wing

L3 white pupa late pupa

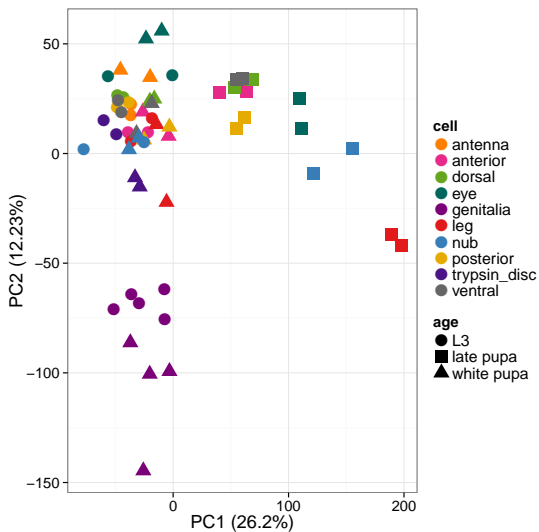
RNA-seq pipeline

- ▶ Assembly: dm6
- ▶ Annotation: FlyBase r6.05
 - ▶ 17,158 genes
 - ▶ 34,152 transcripts
 - ▶ 186,431 exons

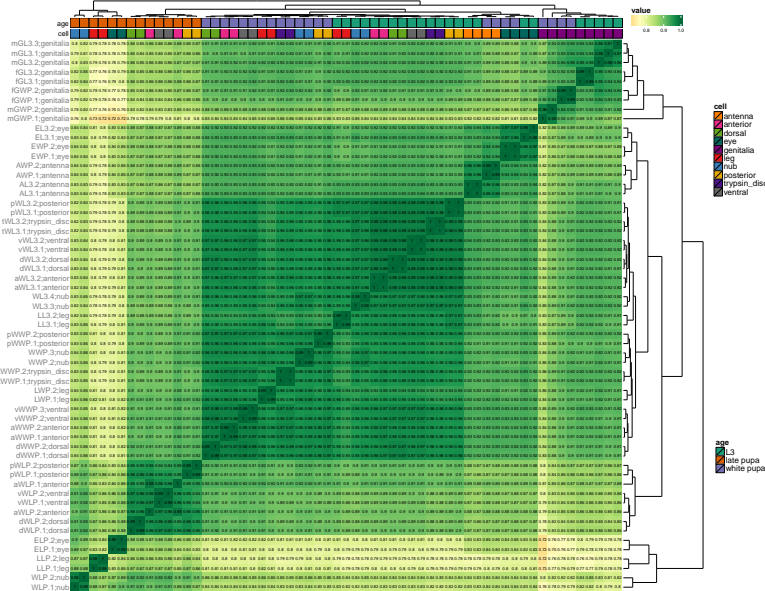
 - ▶ 13,920 mRNA
 - ▶ 2,470 ncRNA
 - ▶ 308 pseudogene
 - ▶ 147 rRNA
 - ▶ 313 tRNA
- ▶ TruSeq from Illumina
- ▶ 75bp
- ▶ stranded
- ▶ paired-end
- ▶ polyA

- ▶ Grape pipeline - STAR+RSEM
<https://github.com/guigolab/grape-nf>

Principal Component Analysis



Clustering by gene expression (Spearman)



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DEG across tissues and time

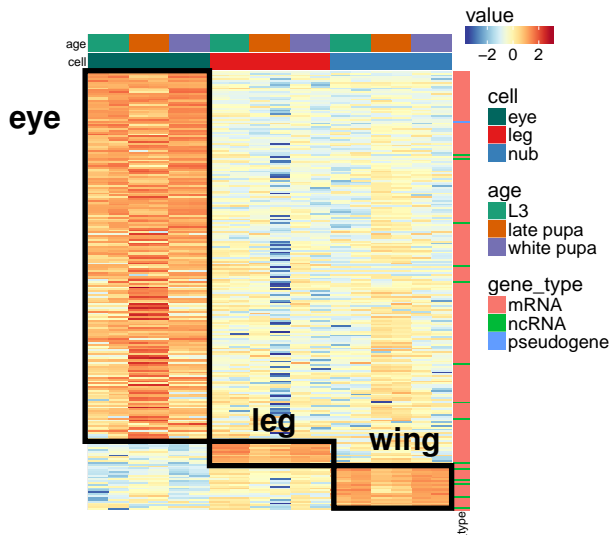
Isoform Usage

Wing compartments

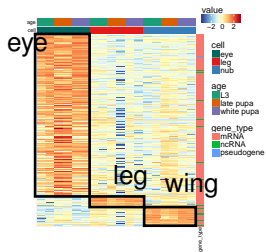
Conclusion and perspectives

DEG across tissues

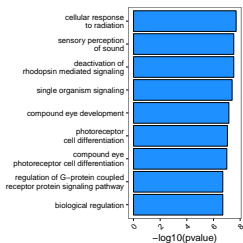
EdgeR - $\log_2FC \geq 2$, FDR ≤ 0.01



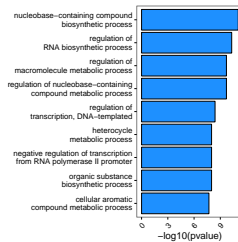
DEG across tissues



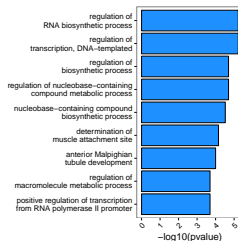
Eye



Leg

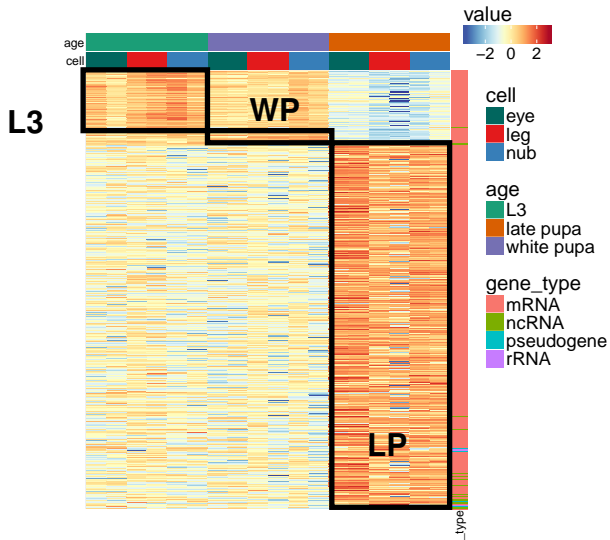


Wing

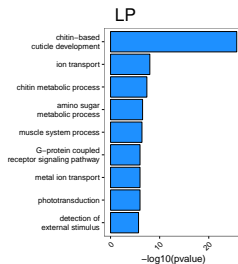
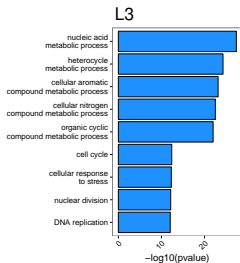
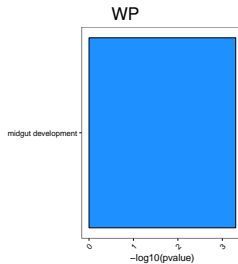
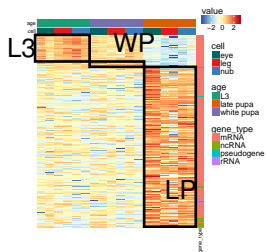


DEG across time

EdgeR - $\log_{2}FC > 2$, $FDR \leq 0.01$



DEG across time



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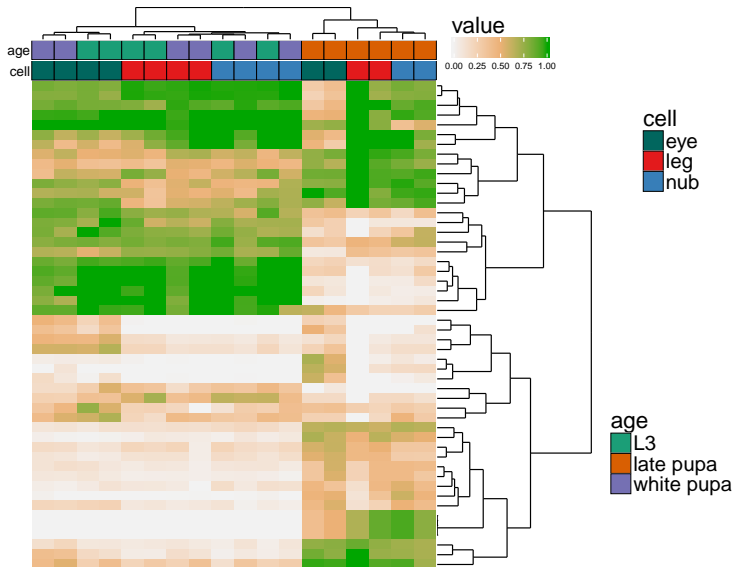
Conclusion and perspectives

Statistics of events in annotation FlyBase r6.05

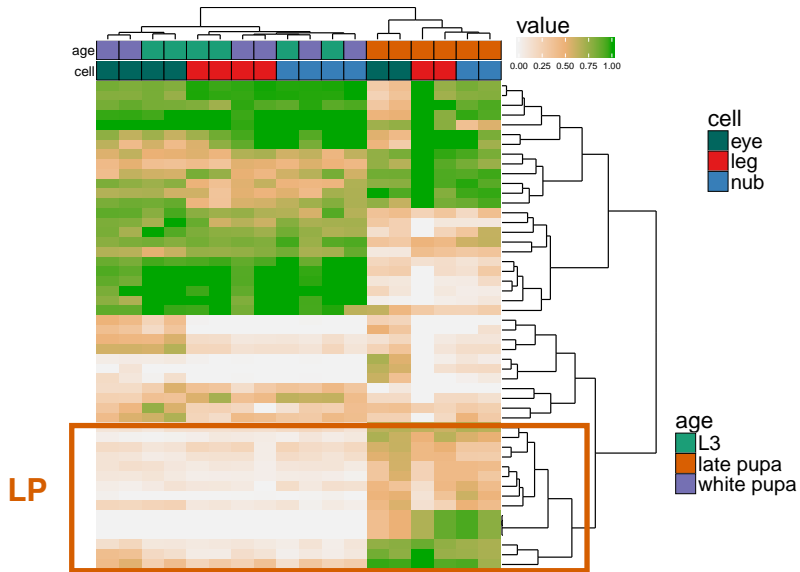
AStalavista: Alternative Splicing transcriptional landscape visualization tool
<http://genome.crg.es/astalavista/>

event	number
single cassette exon	2535
retained intron	1653
alternative donor	2598
alternative acceptor	2506
mutually exclusive	2180
multiple exon skipping	522
alternative first	3982
alternative last	607

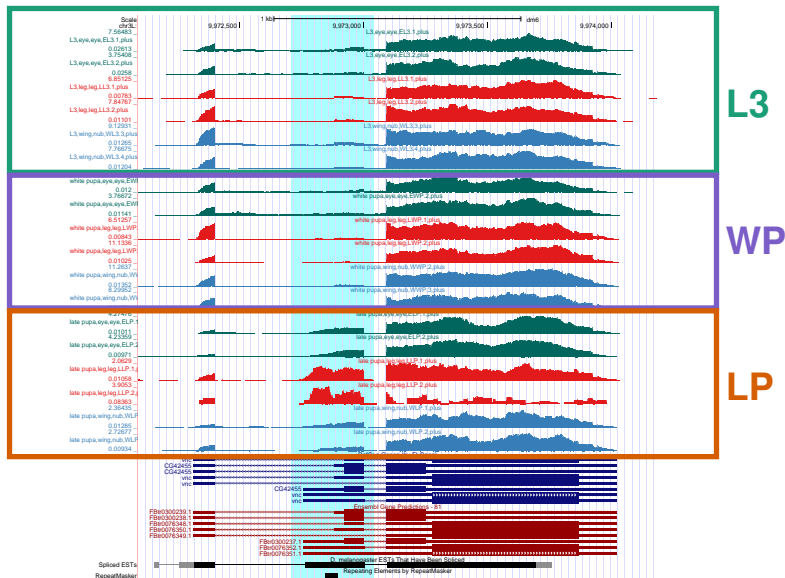
Single exon skipping



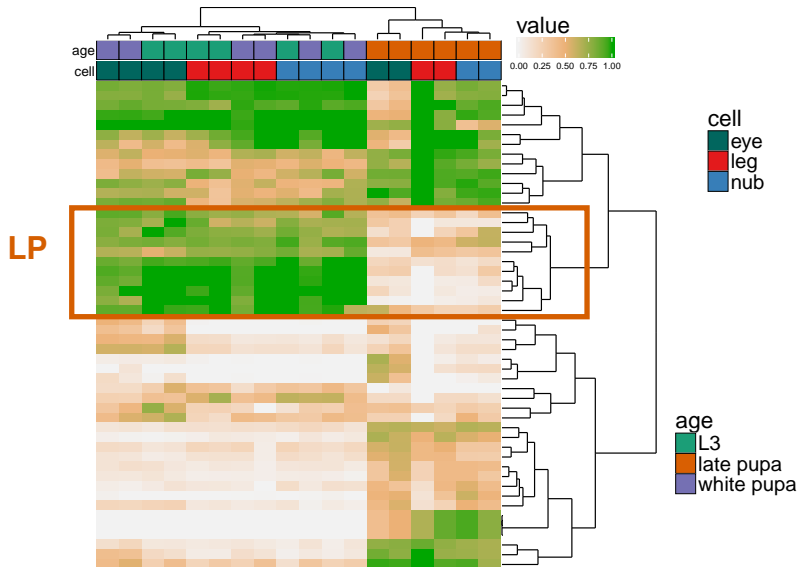
Single exon skipping



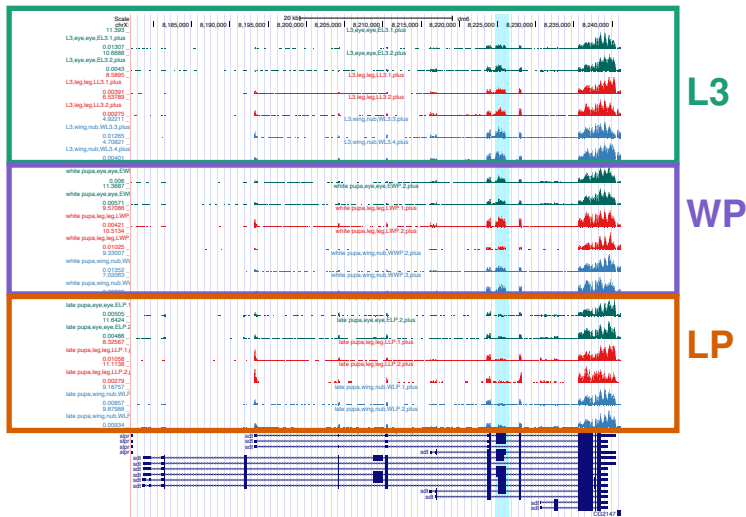
vnc: histone acetyltransferase involved in neurogenesis



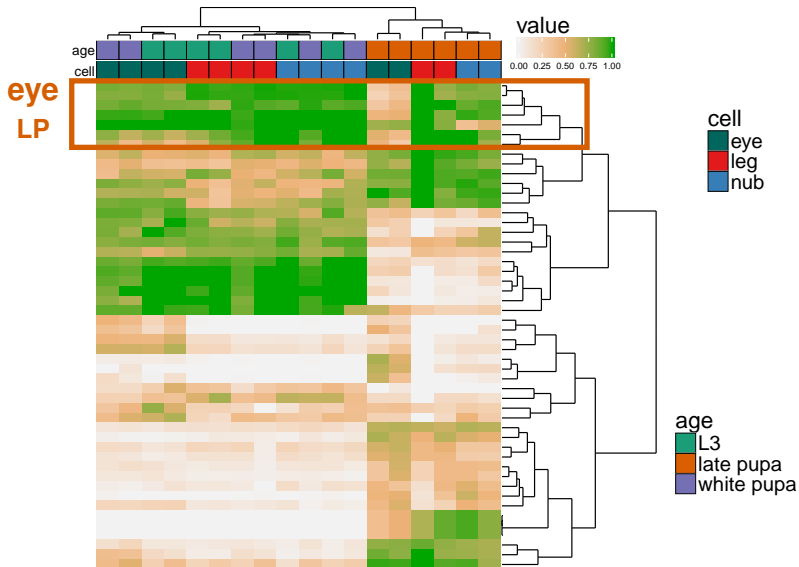
Single exon skipping



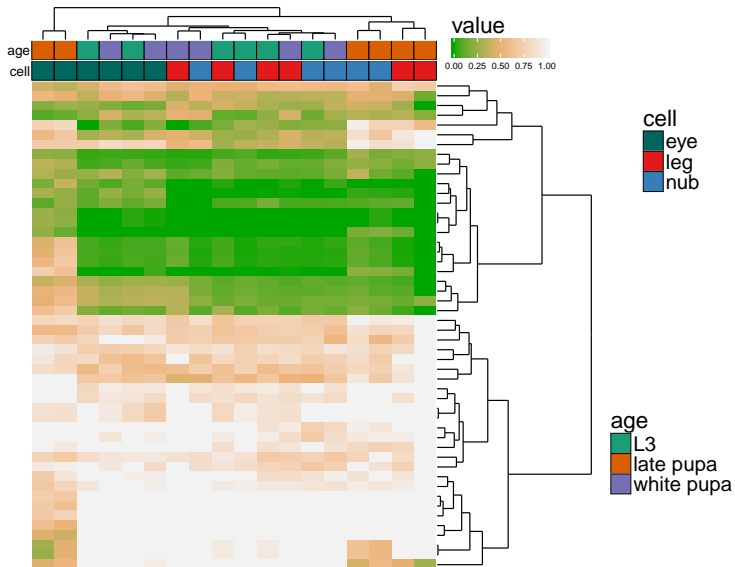
sdt: neural development



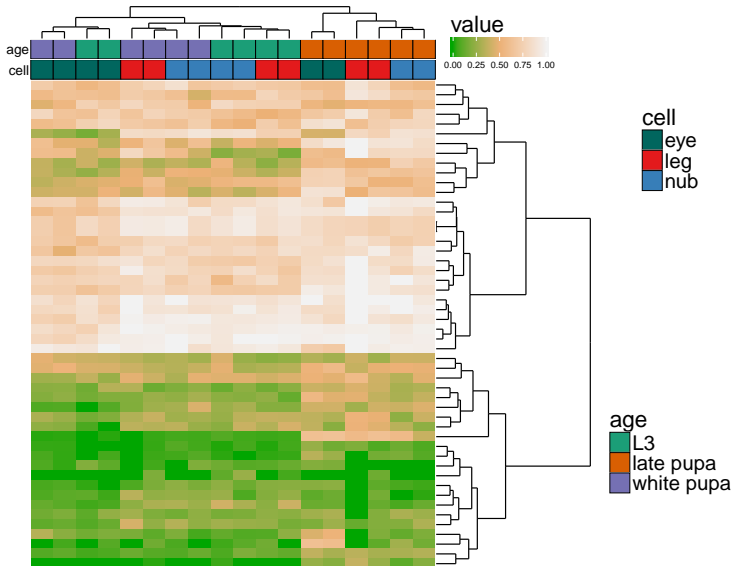
Single exon skipping



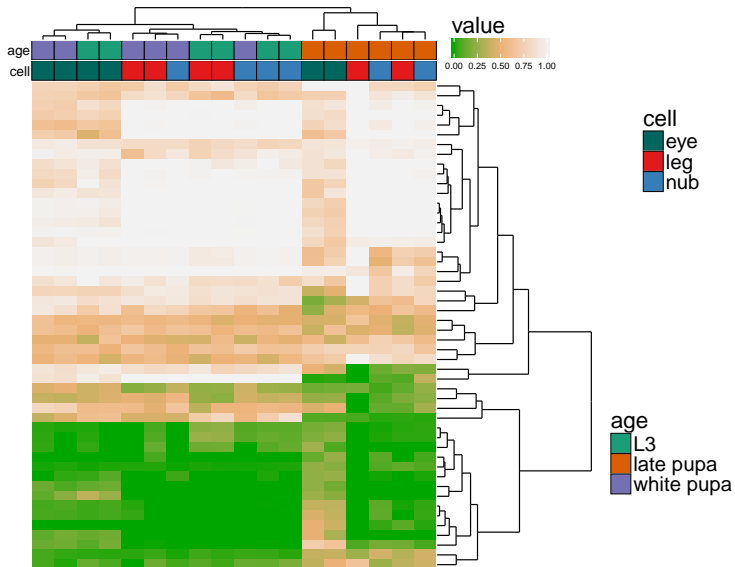
Multiple exon skipping



Retained intron



Mutually exclusive exon



syp (neurogenesis and splicing)



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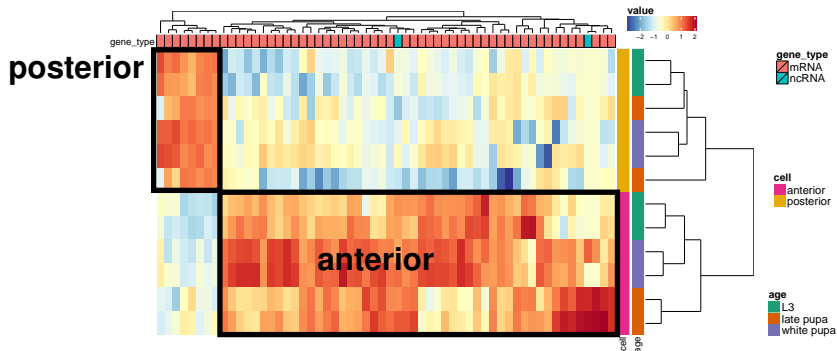
Wing compartments

DEG across wing compartments

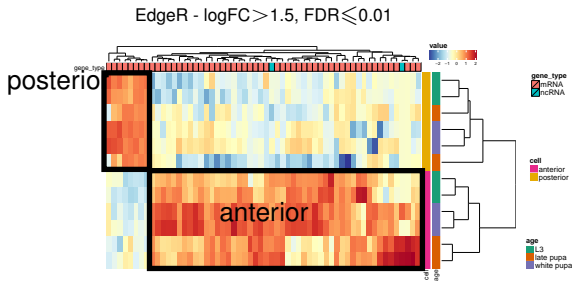
Conclusion and perspectives

DEG across wing compartments - Anterior vs Posterior

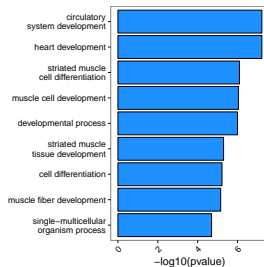
EdgeR - $\log_{2}FC > 2$, $FDR \leq 0.01$



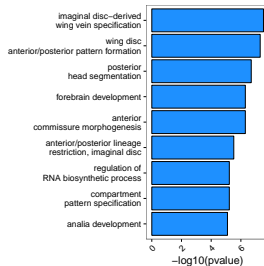
DEG across wing compartments - Anterior vs Posterior



Anterior



Posterior



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Conclusion and perspectives

- ▶ We identified sets of tissue and compartment-specific genes as well as time-specific genes, including genes not yet functionally characterized.
- ▶ GO analysis of tissue and compartment-specific genes reveals an enrichment for development and pattern formation-related terms while time-specific genes are enriched in cell cycle in L3 and WP.
- ▶ There are fewer differences in splicing when compared to gene expression.
- ▶ The differences in isoform usage are mainly found in late pupa stage, suggesting that splicing may play a role during differentiation.
- ▶ Experimentally validate candidate genes by RNAi and CRISPR

Acknowledgements



- ▶ Rory Johnson
- ▶ Sebastian Ullrich
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- ▶ Alessandra Breschi
- ▶ Silvia Perez Lluch
- ▶ Marina Ruiz Romero
- ▶ Amaya Abad
- ▶ Emilio Palumbo
- ▶ Roderic Guigo





obrigado

Dank U

Merci

mahalo

Köszi

chnacuóo

Grazie

Thank
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Takk

Gracias

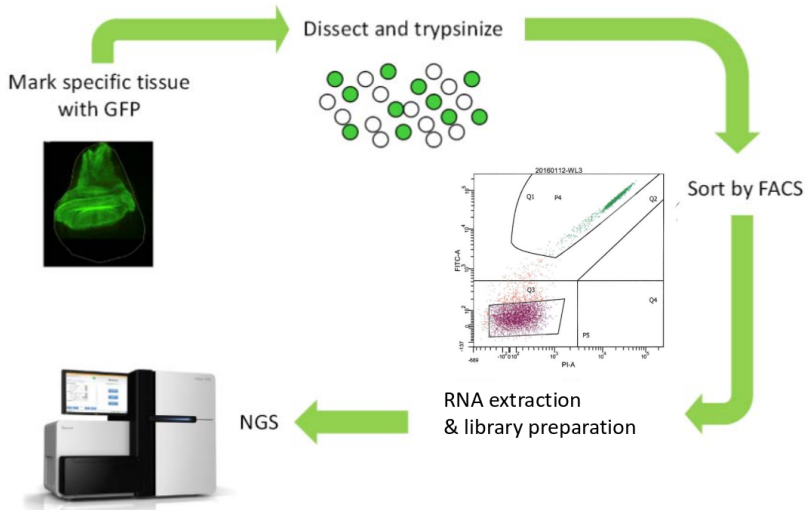
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Experimental Workflow



Experimental Workflow

UAS-GAL4 Binary system

