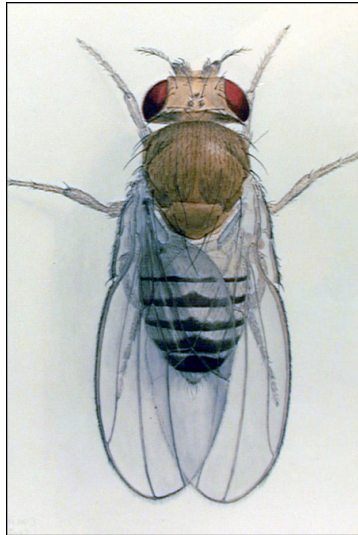


# Comprehensive Identification of Worm and Fly Transcription Factor Binding Sites

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Fly Transgenic Production and RNAi  
Sue Celniker



1. Summary of BAC DNA Preparation
2. Summary of Transgenics Production
3. Transgenic Plan
  1. RNAi Production and Plan
  2. ChIP-peaks in oenocyte genes

The Transcription Factor Group Call  
May 12, 2016

## Injection Status as of 5/12/2016

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Stabs sent	385 (301 < 35kb and 84 > 60kb)
Transformed BACs	256
Small BACs	229
Large BACs	27 (23 by BDGP, 4 by Genetivision)

33 new lines since last call:	31 small BACs
	2 large BACs

TOTAL TFs in list	<u>708</u>
Completed prior effort	106
Completed this grant	256
TFs still to do	346

## New Small BACs into AttP40 on 2nd chromosome (31)

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<i>bigmax</i>	<i>trem</i>	<i>CG8301</i>
<i>D</i>	<i>CG1233</i>	<i>CG9797</i>
<i>DII</i>	<i>CG2199</i>	<i>CG13296</i>
<i>ERR</i>	<i>CG2678</i>	<i>CG13894</i>
<i>E(spl)m5</i>	<i>CG5180</i>	<i>CG14711</i>
<i>Fer2</i>	<i>CG6791</i>	<i>CG14962</i>
<i>Fer3</i>	<i>CG7271</i>	<i>CG15514</i>
<i>MBD-R2</i>	<i>CG7691</i>	<i>CG17802</i>
<i>pfk</i>	<i>CG8216</i>	<i>CG18764</i>
<i>phol</i>	<i>CG8281</i>	<i>CG31365</i>
<i>sqz</i>		

## New Large BACs into AttP40 on 2nd chromosome (2)

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*lab*  
*C15*

## Lines shipped to Chicago

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<u>Year 0</u>	<u>Year 1</u>	<u>Year 2</u>	<u>Year 3</u>	<u>Year 4</u>
	Q1 2013    0	Q1 2014    10	Q1 2015    20	Q1 2016    34
	Q2 2013    15	Q2 2014    16	Q2 2015    26	Q2 2016    est 35
	Q3 2013    21	Q3 2014    12	Q3 2015    34	Q3 2016
Q4 2012    3	Q4 2013    0	Q4 2014    10	Q4 2015    16	Q4 2016
 TOTALS:    3	 36	 48	 96	 140

## Lines shipped to Chicago

---

<u>Year 0</u>	<u>Year 1</u>	<u>Year 2</u>	<u>Year 3</u>	<u>Year 4</u>
	Q1 2013    0	Q1 2014    10	Q1 2015    20	Q1 2016    34
	Q2 2013    15	Q2 2014    16	Q2 2015    26	Q2 2016    36
	Q3 2013    21	Q3 2014    12	Q3 2015    34	Q3 2016    35
Q4 2012    3	Q4 2013    0	Q4 2014    10	Q4 2015    16	Q4 2016    35
 TOTALS:    3	 36	 48	 96	 140

At 35 per quarter, achieve 400 lines shipped around July 1, 2017.

## Lines shipped to Chicago

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<u>Year 0</u>	<u>Year 1</u>	<u>Year 2</u>	<u>Year 3</u>	<u>Year 4</u>
	Q1 2013    0	Q1 2014    10	Q1 2015    20	Q1 2016    34
	Q2 2013    15	Q2 2014    16	Q2 2015    26	Q2 2016    36
	Q3 2013    21	Q3 2014    12	Q3 2015    34	Q3 2016    35
Q4 2012    3	Q4 2013    0	Q4 2014    10	Q4 2015    16	Q4 2016    35
 TOTALS:    3	 36	 48	 96	 140

We can make about 140 more lines by July 21, 2017.

We have 75 small BACs in-house awaiting transformation. If we do 20 more large BACs, that leaves room for another 45 small BACs.

How to prioritize large BACs?

# Small BACs ready to go into AttP40 on 2nd chromosome

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<i>D1</i>	<i>CG6813</i>
<i>fd64A</i>	<i>CG6854</i>
<i>pzg</i>	<i>CG6905</i>
<i>Spps</i>	<i>CG7046</i>
<i>Sry-Beta</i>	<i>CG7056</i>
<i>tap</i>	<i>CG9705</i>
<i>Trl-RA, RF</i>	<i>CG10267</i>
<i>zen</i>	<i>CG10669</i>
<i>zen2</i>	<i>CG14655</i>
<i>CG4328</i>	<i>CG15696</i>
<i>CG4936</i>	<i>CG17186</i>
<i>CG6254</i>	<i>CG18599</i>

## Small BACs ready to go into KV33 on 3rd chromosome

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<i>Br140</i>	<i>schlank</i>	<i>CG8290</i>
<i>CoRest</i>	<i>Ssrp</i>	<i>CG8944 (2<sup>nd</sup> isoform)</i>
<i>Dek</i>	<i>Su(var)2-HP2</i>	<i>CG9437</i>
<i>dmrt11E</i>	<i>Su(var)2-10 (4 isoforms)</i>	<i>CG10209</i>
<i>Dp</i>	<i>wek</i>	<i>CG10431</i>
<i>E2f2</i>	<i>zf30C</i>	<i>CG11906</i>
<i>ewg</i>	<i>CG1529</i>	<i>CG12219</i>
<i>fd59A</i>	<i>CG1603</i>	<i>CG12299</i>
<i>fd102c</i>	<i>CG1621</i>	<i>CG12391</i>
<i>gsb-n</i>	<i>CG2202</i>	<i>CG12659</i>
<i>Hand</i>	<i>CG2875</i>	<i>CG12769</i>
<i>Hmr</i>	<i>CG2889</i>	<i>CG13204</i>
<i>Lhr</i>	<i>CG3407</i>	<i>CG13424</i>
<i>MESR4</i>	<i>CG4707</i>	<i>CG17385</i>
<i>PHDP</i>	<i>CG7101</i>	<i>CG32778</i>
<i>Oli</i>	<i>CG7745</i>	<i>CG34367</i>



# Large BACs ready to go into AttP40 on 2nd chromosome

---

*Abd-A (2 isoforms)*

*bap*

*Blimp1*

*croc*

*cwo*

*dan*

*dmrt99B*

*Doc2*

*E(spl)mdelta*

*exex*

*ftz*

*gl*

*Jarid 2*

*kni*

*mirr*

*mod(mdg) 5 isoforms*

*nerfin-1*

*nerfin-2*

*Poxm*

*ro*

*scrt*

*Sox100B*

*vvl*

*CG11560*

*CG12605*

*CG12768*

*CG16779*

*CG17806*

*CG31224*

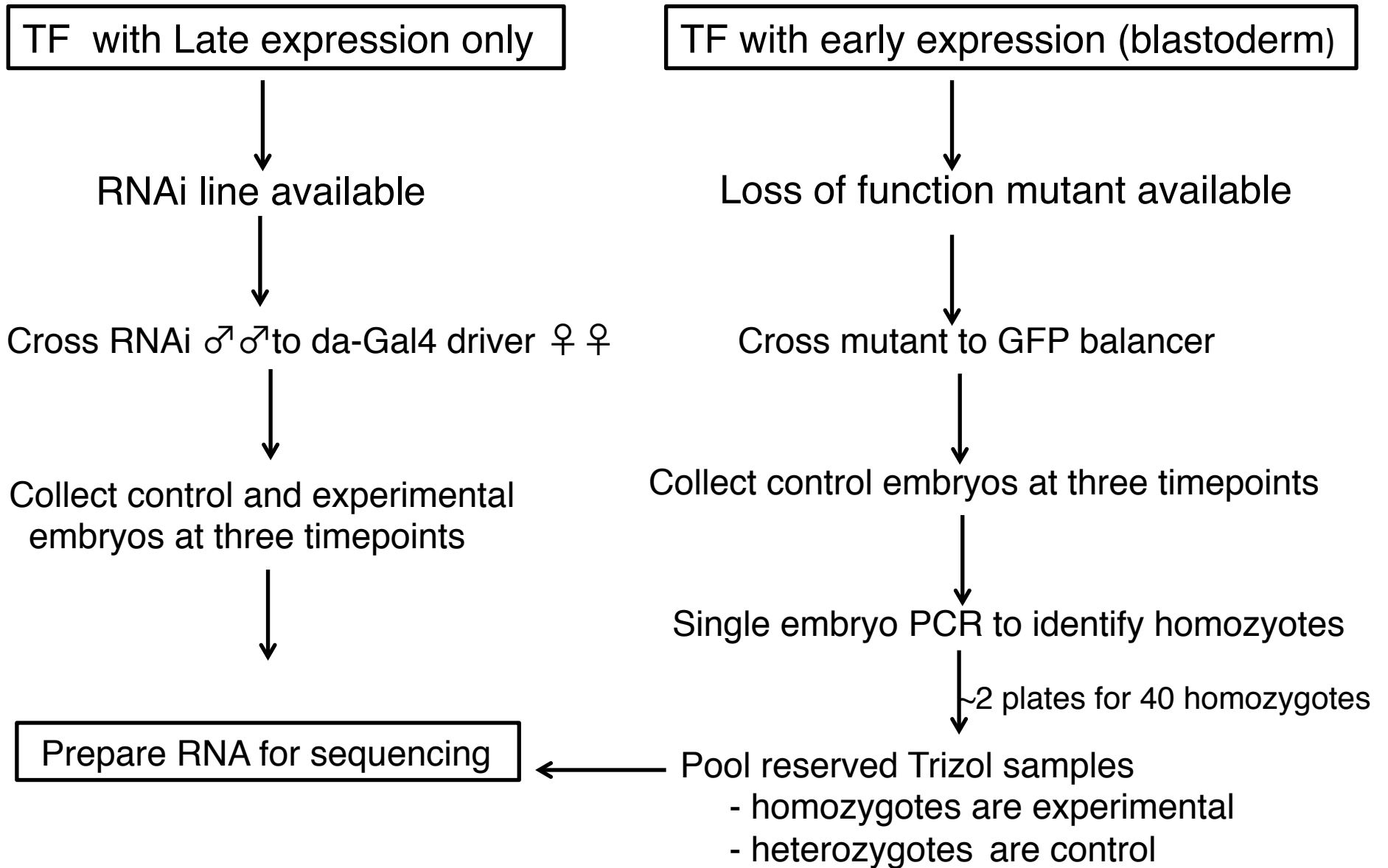
# Large BACs ready to go into KV33 on 3rd chromosome

---

<i>*ATbp</i>	<i>ac</i>	<i>RunxA</i>
<i>*B-H2</i>	<i>Bsg25A</i>	<i>Set2</i>
<i>*Bap170</i>	<i>gem</i>	<i>slp1</i>
<i>*Dref</i>	<i>Gsc</i>	<i>so</i>
<i>*Optix</i>	<i>H15</i>	<i>sob</i>
<i>*peb</i>	<i>Oaz</i>	<i>wor</i>
<i>*salm</i>	<i>Poxn</i>	<i>CG5953</i>
<i>*CG11085</i>	<i>Pph13</i>	<i>CG10348</i>
	<i>rib</i>	<i>CG17612</i>

\* Transformant line inserted ectopically

# Two Strategies for fly TF knockdown



Can group samples of same peak expression with parallel control mCherry samples

Need equal number of control and experimental samples

# Fly TFs for single embryo mutant selection

<b>fly TF</b>	<b>worm ortholog</b>	<b>worm sequencing status</b>	<b>fly sequencing status</b>	<b>strategy</b>
ems	ceh-2	low depth data	making RNA	single embryo genotyping
run	rnt-1	high depth data	GFP stock ready	single embryo genotyping
pros	ceh-26	bad deletion strain	GFP stock ready	single embryo genotyping
shn	sma-9	studied previously	crossing mutant to GFP balancer	single embryo genotyping
Antp	mab-5	high depth data	crossing mutant to GFP balancer	single embryo genotyping
pdm2	ceh-18	in progress	crossing mutant to GFP balancer	single embryo genotyping
Lim1	mec-3	low depth data	crossing mutant to GFP balancer	single embryo genotyping
btd	sptf-2	deletion strain order list	crossing mutant to GFP balancer	single embryo genotyping
ftz	no match	N/A	mutant at BDGP	single embryo genotyping
hb	hbl-1	not on worm lists?	mutant at BDGP	single embryo genotyping

Keep these in the pipeline but accelerate RNAi plan for late expressed TFs

## Priority List for next 75-100 Fly TF knockdown targets

- TFs with patterned expression in embryos
  - where expression is only late, and RNAi line available
  - where expression is early, and loss of function mutant is available
- TFs with ChIP data available or tagged line made
- Fly TFs with worm orthologs
- Prioritize TFs expressed in selected organ systems?
- Prioritize uncharacterized TFs?

# Revised plan for RNAi knockdown of TFs with late expression

Group by peak expression for more efficient use of controls and Illumina kits

Fly TF	worm ortholog	worm sequencing status	RNAi line	fly sequencing status	peak expression	estimated RNA ship date	number of samples including controls
twi	hlh-8	no deletion strain	HMS01317	sequenced			
nau	hlh-1	studied previously	HMC02974	sequenced		<b>7/24/15</b>	
E5	ceh-2	low depth data	HMJ21631	sequenced			
						<b>shipped</b>	
sens-2	pag-3	in progress	HMS01394	waiting for new kit		<b>3/24/16</b>	12
Hr51	fax-1	high depth data	HMS01951	setting up RNAi cross	14-16 h	<b>5/24/16</b>	12
scrt	ces-1	low depth data	HMC03996	expanding RNAi line	10-12h	<b>6/14/16</b>	18
Blimp-1	blmp-1	high depth data	HMC04792	expanding new RNAi line	10-12h	6/14/16	
scro	ceh-24	4x backcrossed	HMS00828	expanding RNAi line	12-14 h	<b>6/28/16</b>	24
onecut	ceh-48		HMS01438	RNAi line ordered	12-14 h	6/28/16	
CG9876			HMC03056	RNAi line ordered	12-14 h	6/28/16	
ss	ahr-1		HMS00296	RNAi line ordered	12-14h		
Ets65A	ast-1		HMS02246	on order list	12-14h		
AP-2	aptf-1		HMS02159	RNAi line ordered	10-12h	<b>7/5/16</b>	24
caup			HMS02716	on order list	10-12h		
fd59A	unc-130		HMC03155	on order list	10-12h		
CG33557	hlh-16		HMC03056	RNAi line ordered	6-8h		
dmrt99B	dmd-5		HMC03088	RNAi line ordered	6-8h		
pb			HMC03065	on order list	8-10h		
esn	prkl-1		HMS01360	in order list	14-16h		

Most efficient: Group three TFs (3 x 6 samples) with matching mCherry RNAi control for 24 samples per group. Two groups of 24 will use one Illumina kit.

# mCherry RNAi control experiments

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Control embryos for RNAi experiments:

- Expresses dsRNA for RNAi of mCherry under UAS control
- Activates RNAi system, but against a non-fly gene
- Tried first with *sens-2* RNAi experiments

$\frac{\text{da-Gal4}; \text{da-Gal4}}{\text{da-Gal4}; \text{da Gal4}} \quad \text{♀} \quad \text{♀} \quad \times \quad \frac{\text{UAS-}m\text{Cherry RNAi}}{\text{UAS-}m\text{Cherry RNAi}} \quad \text{♂} \quad \text{♂}$

For *sens-2* experiment:

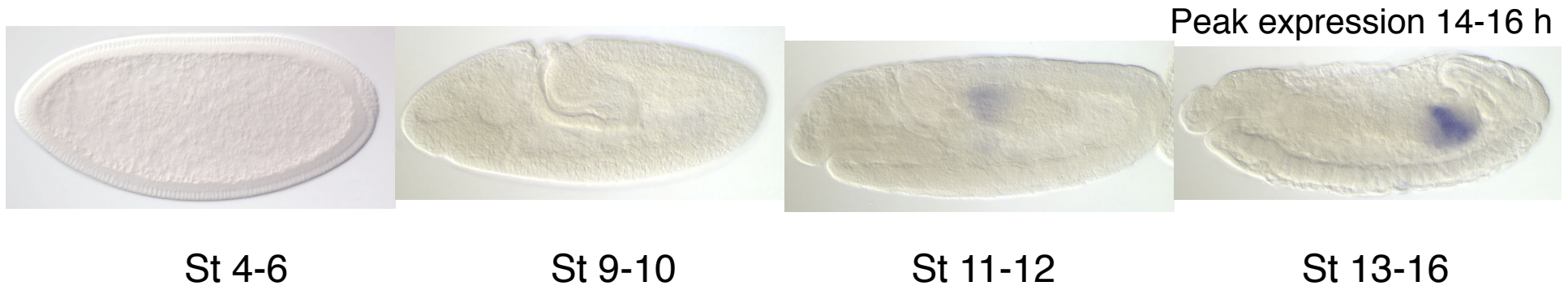
Three timepoints, 0-1.5, 14-16h (peak expression for target TF), 16-18 h

Early and late timepoints always the same, peak time point will vary with target TF

$\text{UAS-}m\text{Cherry RNAi} = y1 \text{ sc}^* v1; P\{\text{VALIUM20-}m\text{Cherry}\}\text{attP2}$

## *sens-2* knockdown by RNAi

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Expressed in subset of the midgut starting at stage 11

da-driven RNAi for RNA-seq:

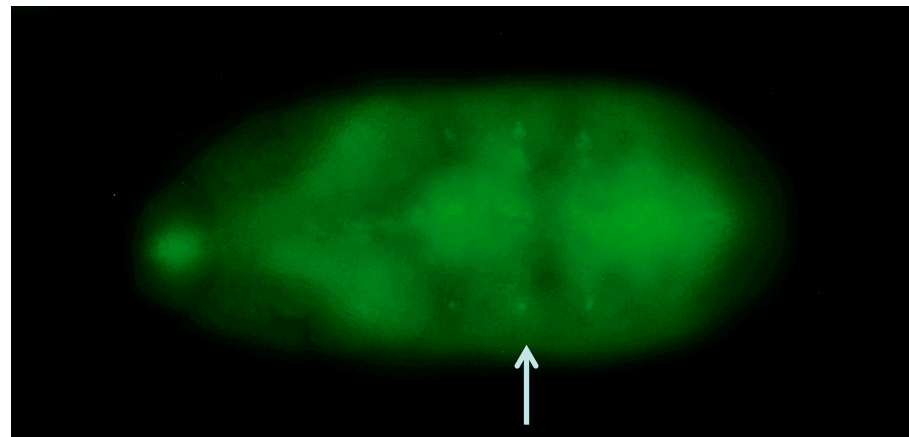
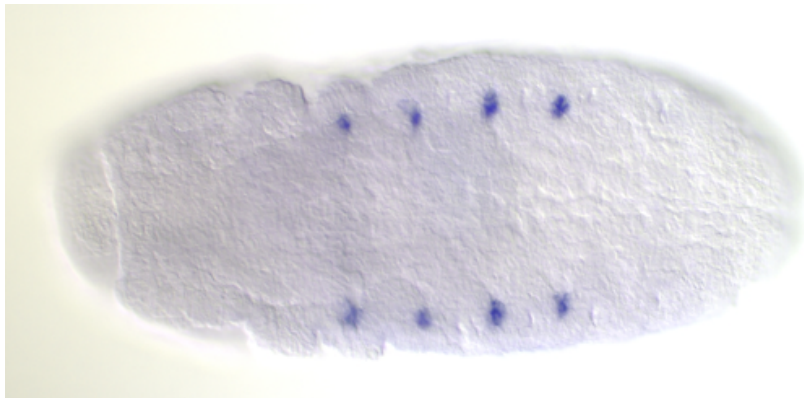
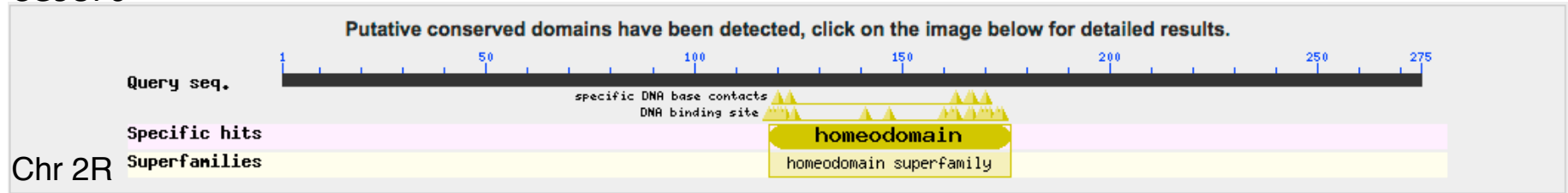
$$\frac{\text{da-Gal4}; \text{da-Gal4}}{\text{da-Gal4}; \text{da Gal4}} \quad \text{♀} \quad \text{♀} \quad \times \quad \frac{\text{UAS-*sens-2* RNAi}}{\text{UAS-*sens-2* RNAi}} \quad \text{♂} \quad \text{♂}$$

- all embryos have the same genotype:  $w^*/y1, sc, v1; da\text{-Gal4}/+; daGal4/UAS \text{ sens-2 RNAi}$
- >40% embryonic lethality
- of surviving embryos, 100% die before eclosing



# CG9876 wild type RNA *in situ* compared to GFP tag

CG9876

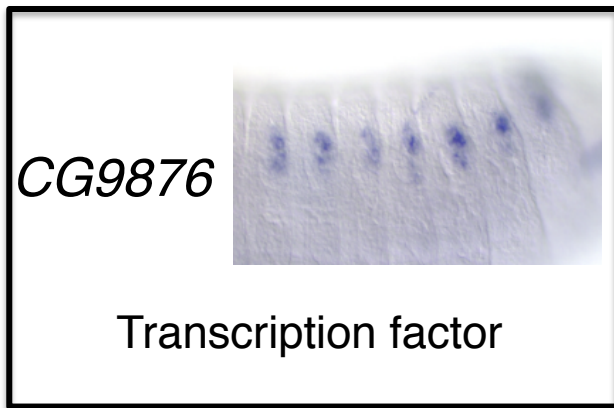


St 11 dorsal

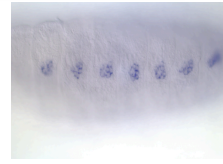
Oenocyte precursors (ectodermal origin)

# Genes with expression restricted to oenocytes

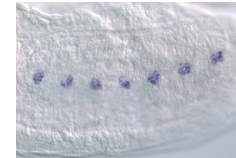
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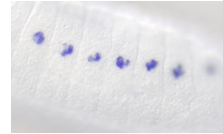
*Cpr*



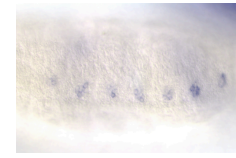
CG9459



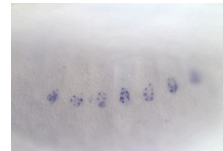
*Cyp4g1*



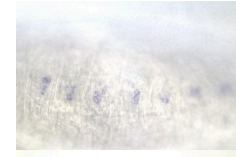
CG12428



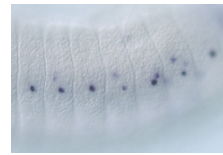
*desat1*



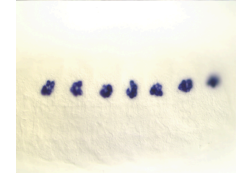
CG14615



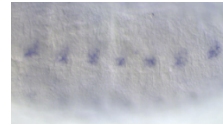
*e*



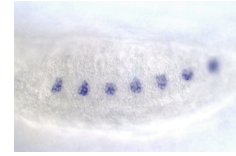
CG17562



*Hsp83*



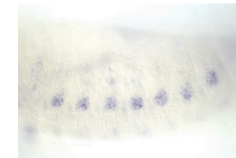
CG18031



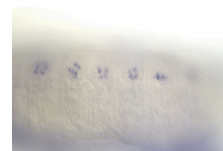
*LpR1*



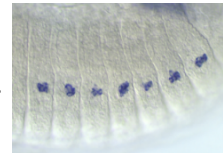
CG18410



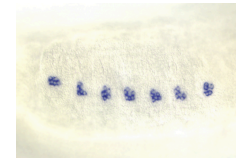
*LpR2*



CG6921

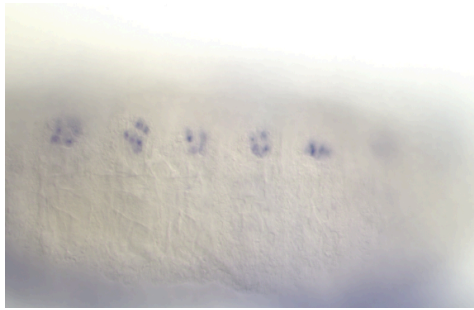


CG18609

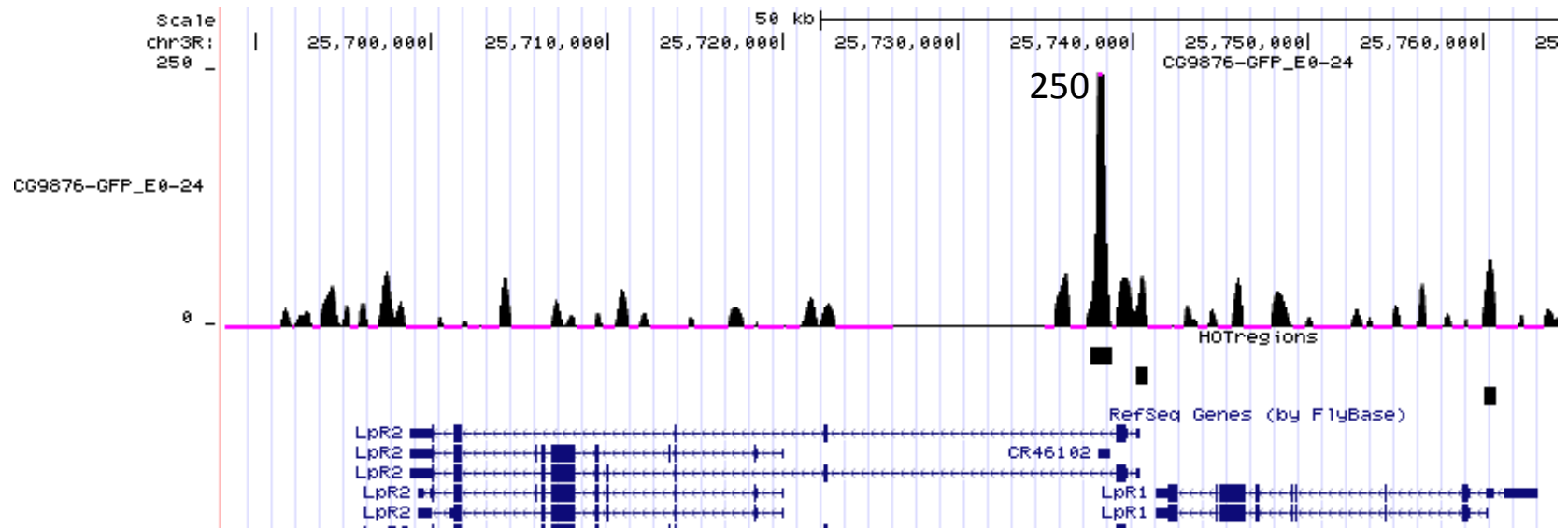


# ChIP peaks for oenocyte Transcription Factor CG9876

LpR2



LpR1



LpR2

LpR1

# ChIP peaks for oenocyte Transcription Factor CG9876

*ebony*

