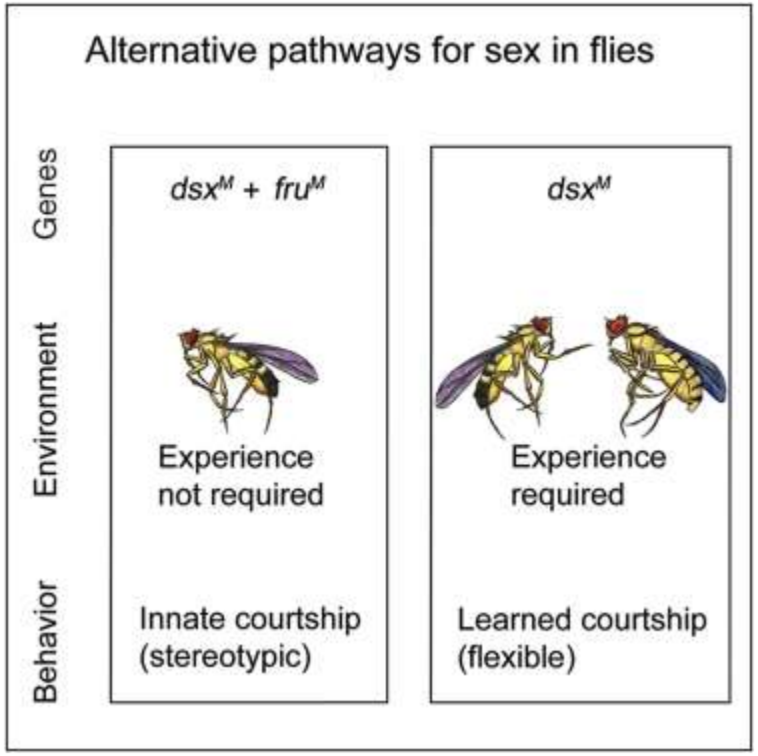
# FlyBase: a Database of Drosophila Genes and Genomes

赵环、陈洁、马铭泽

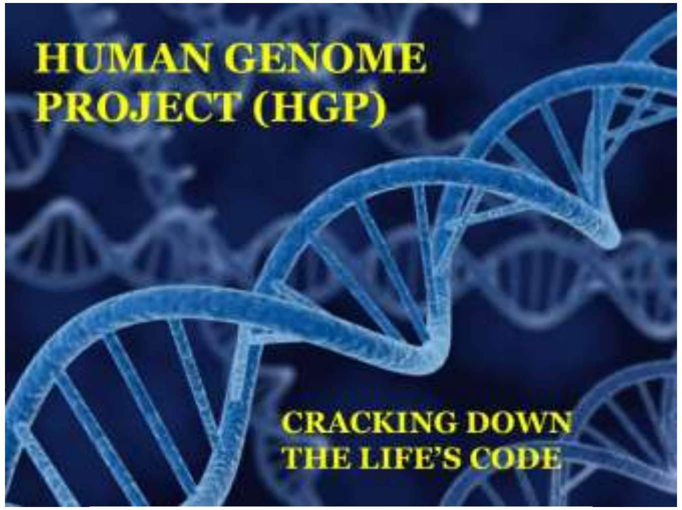
20210527

# Innate Behaviors are Closely Controlled by Genes

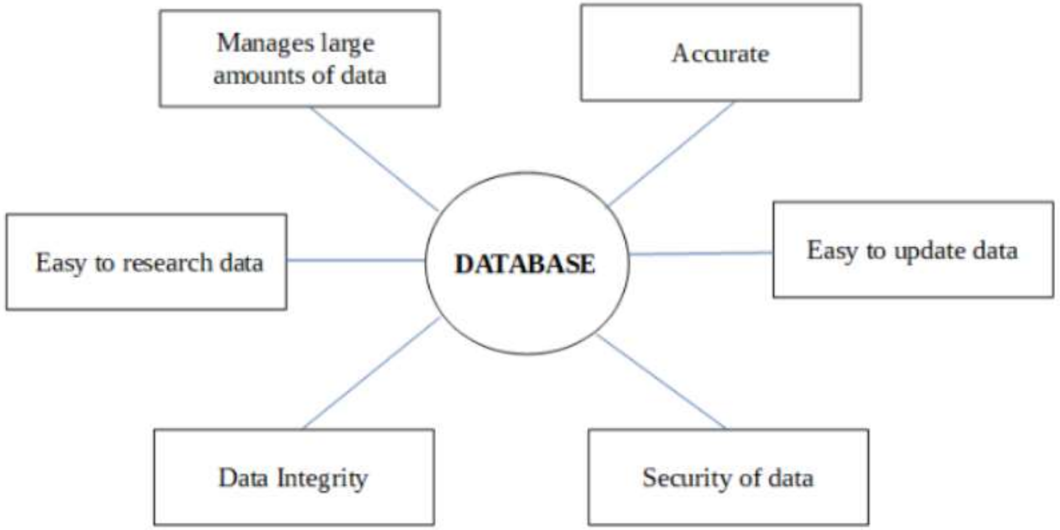


*Pan Y , Baker B ., Cell, 2014.*

# Why we need databases?



mod ENCODE



Manages large amounts of data

Accurate

Easy to research data

**DATABASE**

Easy to update data

Data Integrity

Security of data

FlyBase

neuPRINT+

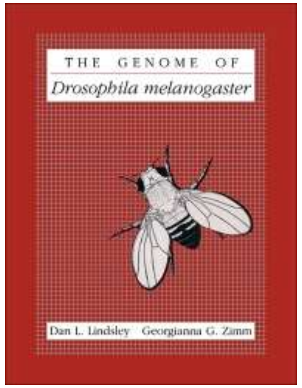
exploring inter and intra cellular interactions

**BABAM User Guide**

The Browsable Atlas of Behavior-Anatomy Maps (BABAM) is a Graphical User Interface for exploring hypotheses of correlations between neural activity in regions of the brain and behavior for *Drosophila melanogaster*. These correlation hypotheses are the result of our thermogenetic neural activation screen of 2,205 lines from the Janelia GAL4 collection. More information on this data can be found here.

# FlyBase

whole-genome studies



THE GENOME OF
*Drosophila melanogaster*
Dan L. Lindsley Georgianna G. Zimm

DNA microarray

**FlyBase**

*In 1992*

ALLIANCE of GENOME RESOURCES
UniProt
NCBI
Ensembl

other databases

RNA-Seq

# Species Information

**1992**

12 species

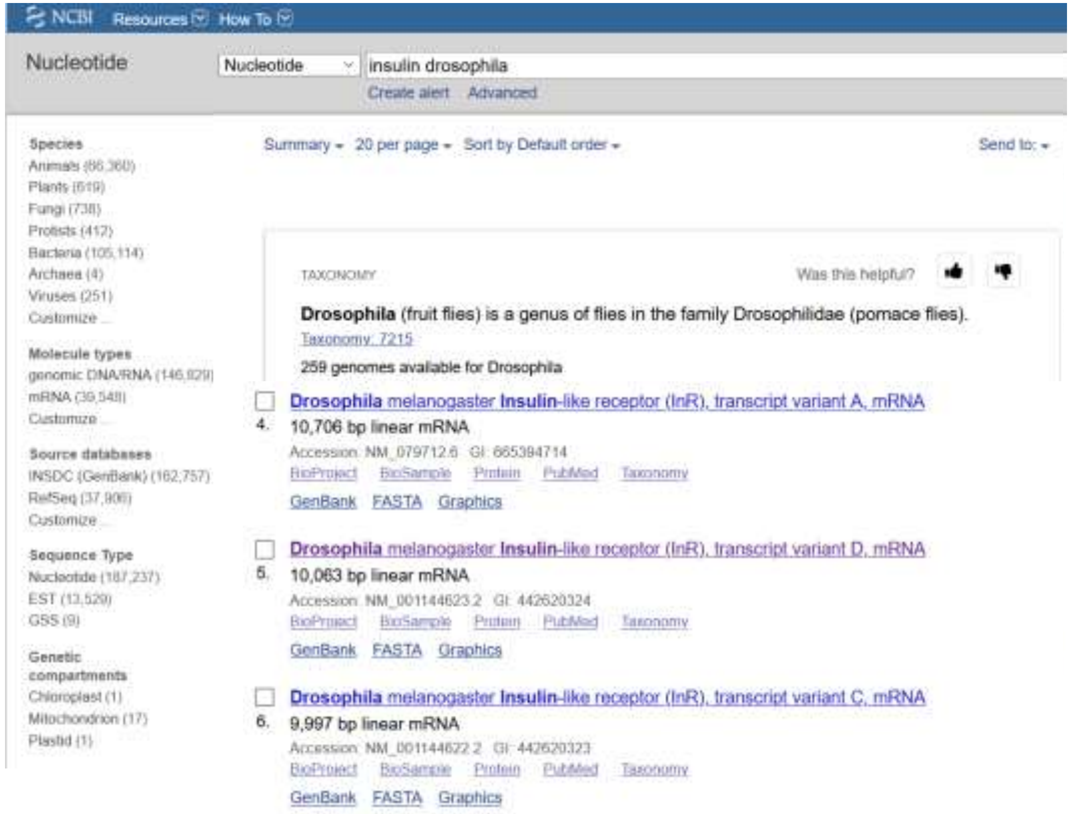
***D. melanogaster***
***D. simulans***
***D. ananassae***
***D. pseudoobscura***
***D. virilis***
*D. erecta*
*D. yakuba*
*D. persimilis*
*D. willistoni*
*D. sechellia*
*D. mojavensis*
*D. grimshwi*

**2018**

5 species

***D. melanogaster***
***D. simulans***
***D. ananassae***
***D. pseudoobscura***
***D. virilis***

# NCBI vs. FlyBase



insulin drosophila

Species
Animals (86,360)
Plants (619)
Fungi (738)
Protists (417)
Bacteria (105,114)
Archaea (4)
Viruses (251)
Customize ...

Molecule types
genomic DNA/RNA (146,829)
mRNA (39,548)
Customize ...

Source databases
INSDC (GenBank) (162,757)
RefSeq (37,906)
Customize ...

Sequence Type
Nucleotide (187,237)
EST (13,529)
GSS (9)

Genetic compartments
Chloroplast (1)
Mitochondrion (17)
Plastid (1)

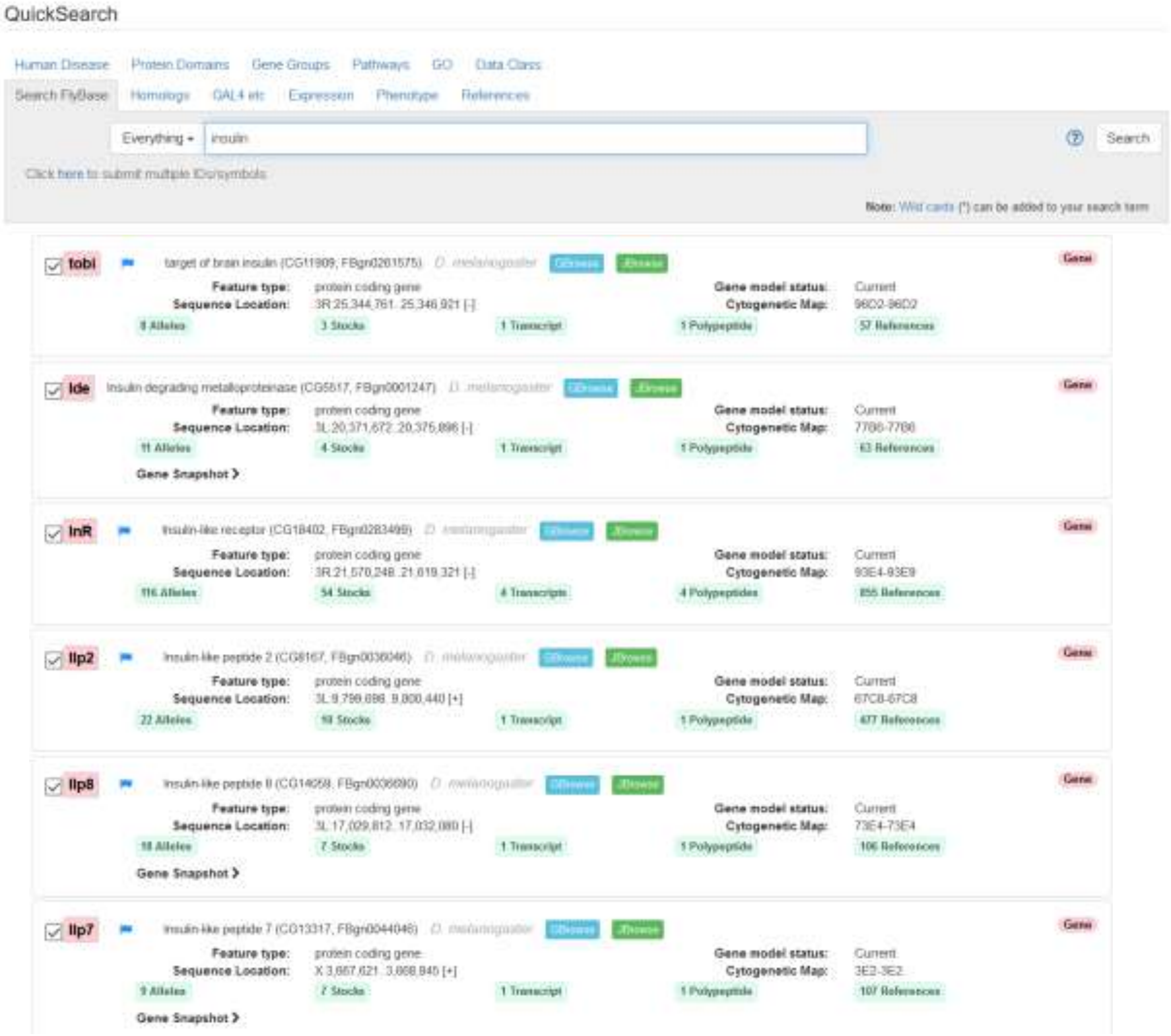
TAXONOMY

**Drosophila** (fruit flies) is a genus of flies in the family Drosophilidae (pomace flies).
Taxonomy: 7215
259 genomes available for Drosophila

☐ 4. **Drosophila** melanogaster **Insulin**-like receptor (InR), transcript variant A, mRNA
10,706 bp linear mRNA
Accession: NM_079712.6 GI: 665394714
BioProject BioSample Protein PubMed Taxonomy
GenBank FASTA Graphics

☐ 5. **Drosophila** melanogaster **Insulin**-like receptor (InR), transcript variant D, mRNA
10,063 bp linear mRNA
Accession: NM_001144623.2 GI: 442620324
BioProject BioSample Protein PubMed Taxonomy
GenBank FASTA Graphics

☐ 6. **Drosophila** melanogaster **Insulin**-like receptor (InR), transcript variant C, mRNA
9,997 bp linear mRNA
Accession: NM_001144622.2 GI: 442620323
BioProject BioSample Protein PubMed Taxonomy
GenBank FASTA Graphics



insulin

Click here to submit multiple IDs/symbols

Note: Wild cards (*) can be added to your search term

☑ **tobi** target of brain insulin (CG11909, FBgn0261575) *D. melanogaster*
Feature type: protein coding gene
Sequence Location: 3R:25,344,761..25,346,921 [-]
Gene model status: Current
Cytogenetic Map: 96D2-96D2
8 Alleles · 3 Stocks · 1 Transcript · 1 Polypeptide · 57 References

☑ **Ide** Insulin degrading metalloproteinase (CG5517, FBgn0001247) *D. melanogaster*
Feature type: protein coding gene
Sequence Location: 3L:20,371,672..20,375,896 [-]
Gene model status: Current
Cytogenetic Map: 77B6-77B6
11 Alleles · 4 Stocks · 1 Transcript · 1 Polypeptide · 63 References
Gene Snapshot ❯

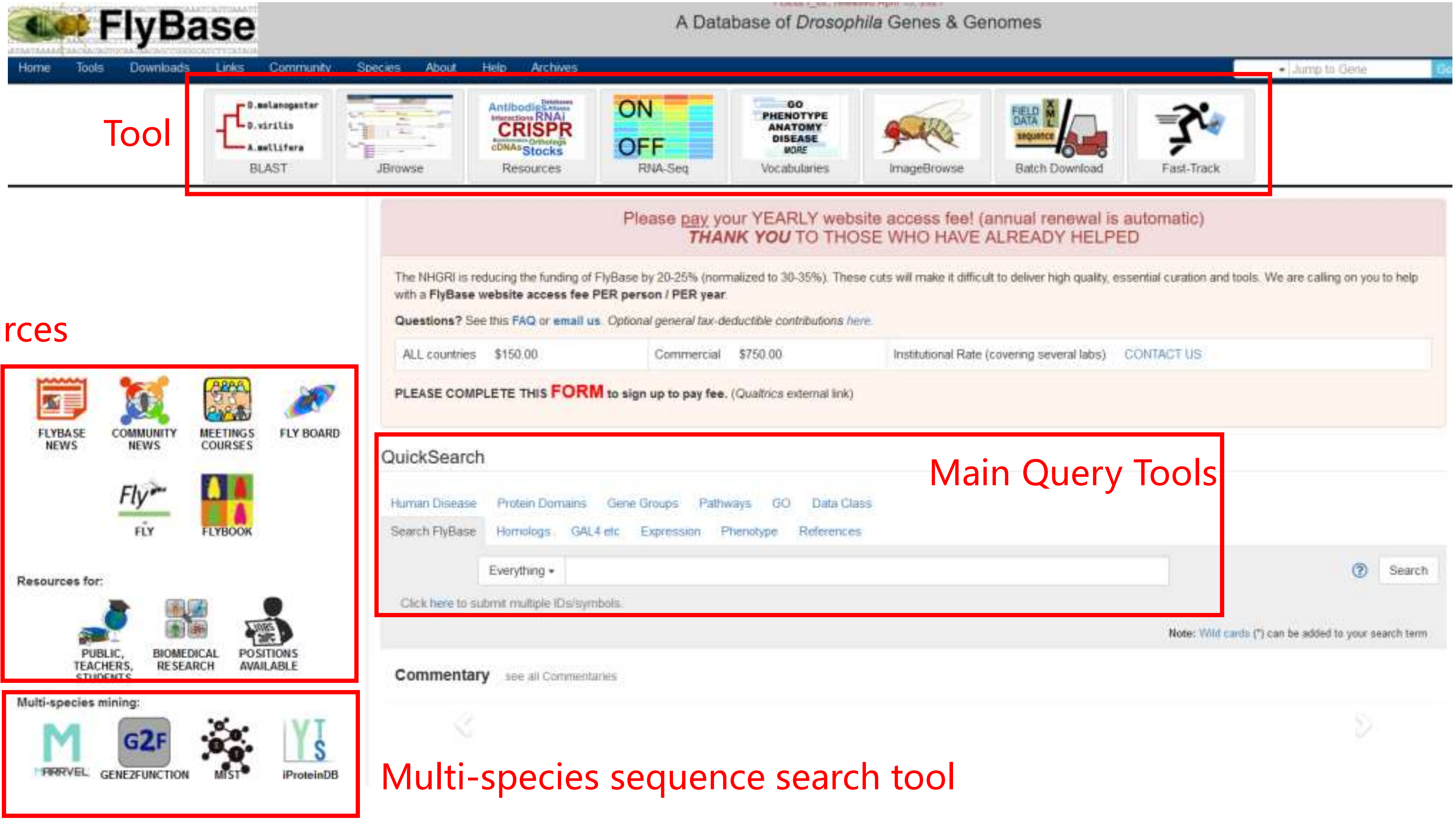
☑ **InR** Insulin-like receptor (CG18402, FBgn0283499) *D. melanogaster*
Feature type: protein coding gene
Sequence Location: 3R:21,570,248..21,619,321 [-]
Gene model status: Current
Cytogenetic Map: 93E4-93E9
116 Alleles · 54 Stocks · 4 Transcripts · 4 Polypeptides · 855 References

☑ **Ilp2** Insulin-like peptide 2 (CG8167, FBgn0036046) *D. melanogaster*
Feature type: protein coding gene
Sequence Location: 3L:9,798,698..9,800,440 [+]
Gene model status: Current
Cytogenetic Map: 67C8-67C8
22 Alleles · 18 Stocks · 1 Transcript · 1 Polypeptide · 477 References

☑ **Ilp8** Insulin-like peptide 8 (CG14059, FBgn0036690) *D. melanogaster*
Feature type: protein coding gene
Sequence Location: 3L:17,029,812..17,032,080 [-]
Gene model status: Current
Cytogenetic Map: 73E4-73E4
18 Alleles · 7 Stocks · 1 Transcript · 1 Polypeptide · 106 References
Gene Snapshot ❯

☑ **Ilp7** Insulin-like peptide 7 (CG13317, FBgn0044046) *D. melanogaster*
Feature type: protein coding gene
Sequence Location: X:3,867,621..3,868,845 [+]
Gene model status: Current
Cytogenetic Map: 3E2-3E2
9 Alleles · 7 Stocks · 1 Transcript · 1 Polypeptide · 107 References
Gene Snapshot ❯

# FlyBase Home Page



Please pay your YEARLY website access fee! (annual renewal is automatic)
***THANK YOU*** TO THOSE WHO HAVE ALREADY HELPED

The NHGRI is reducing the funding of FlyBase by 20-25% (normalized to 30-35%). These cuts will make it difficult to deliver high quality, essential curation and tools. We are calling on you to help with a **FlyBase website access fee PER person / PER year**.

**Questions?** See this FAQ or email us. *Optional general tax-deductible contributions here.*

| | | | | | |
|---|---|---|---|---|---|
| ALL countries | $150.00 | Commercial | $750.00 | Institutional Rate (covering several labs) | CONTACT US |

**PLEASE COMPLETE THIS FORM to sign up to pay fee.** (*Qualtrics* external link)

**Note:** Wild cards (*) can be added to your search term

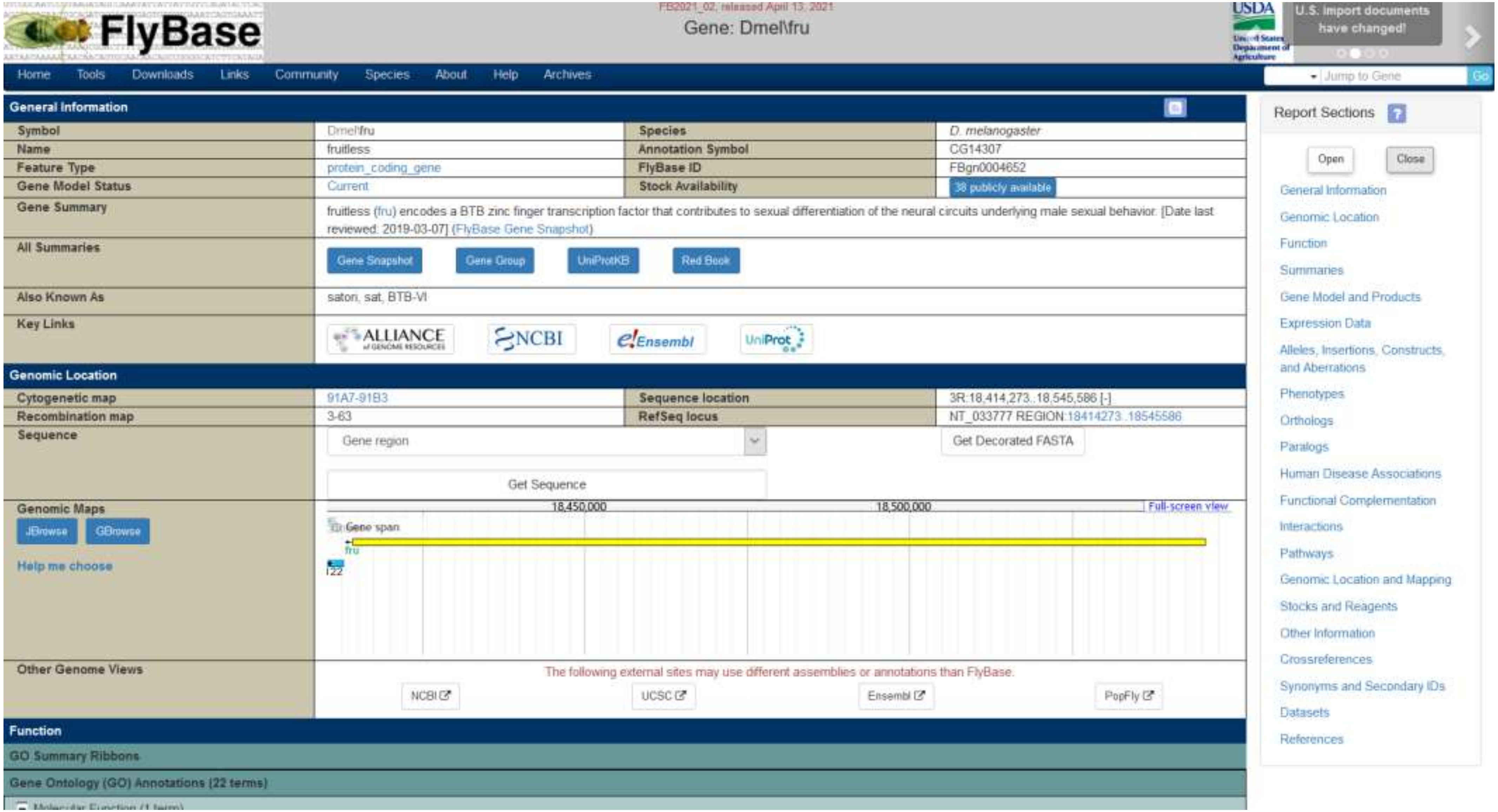
Tool

Resources

Main Query Tools

Multi-species sequence search tool

# Report page



FB2021_02, released April 13, 2021

Gene: Dmel\fru

**General Information**

| | | | |
|---|---|---|---|
| **Symbol** | Dmel\fru | **Species** | *D. melanogaster* |
| **Name** | fruitless | **Annotation Symbol** | CG14307 |
| **Feature Type** | protein_coding_gene | **FlyBase ID** | FBgn0004652 |
| **Gene Model Status** | Current | **Stock Availability** | 38 publicly available |
| **Gene Summary** | fruitless (fru) encodes a BTB zinc finger transcription factor that contributes to sexual differentiation of the neural circuits underlying male sexual behavior. [Date last reviewed: 2019-03-07] (FlyBase Gene Snapshot) | | |
| **All Summaries** | Gene Snapshot<br>Gene Group<br>UniProtKB<br>Red Book | | |
| **Also Known As** | satori, sat, BTB-VI | | |
| **Key Links** | ALLIANCE<br>NCBI<br>Ensembl<br>UniProt | | |

**Genomic Location**

| | | | |
|---|---|---|---|
| **Cytogenetic map** | 91A7-91B3 | **Sequence location** | 3R:18,414,273..18,545,586 [-] |
| **Recombination map** | 3-63 | **RefSeq locus** | NT_033777 REGION:18414273..18545586 |
| **Sequence** | Gene region | | |
| **Genomic Maps** | | | |
| **Other Genome Views** | The following external sites may use different assemblies or annotations than FlyBase. | | |

**Function**

GO Summary Ribbons

Gene Ontology (GO) Annotations (22 terms)

Molecular Function (1 term)

Overview and Main Query Tools.

——赵环

Genomic Search Tools and Browsers.

——陈洁

RNA-seq Tool and Other Tools.

——马铭泽

# Overview of Flybase and the main query tools

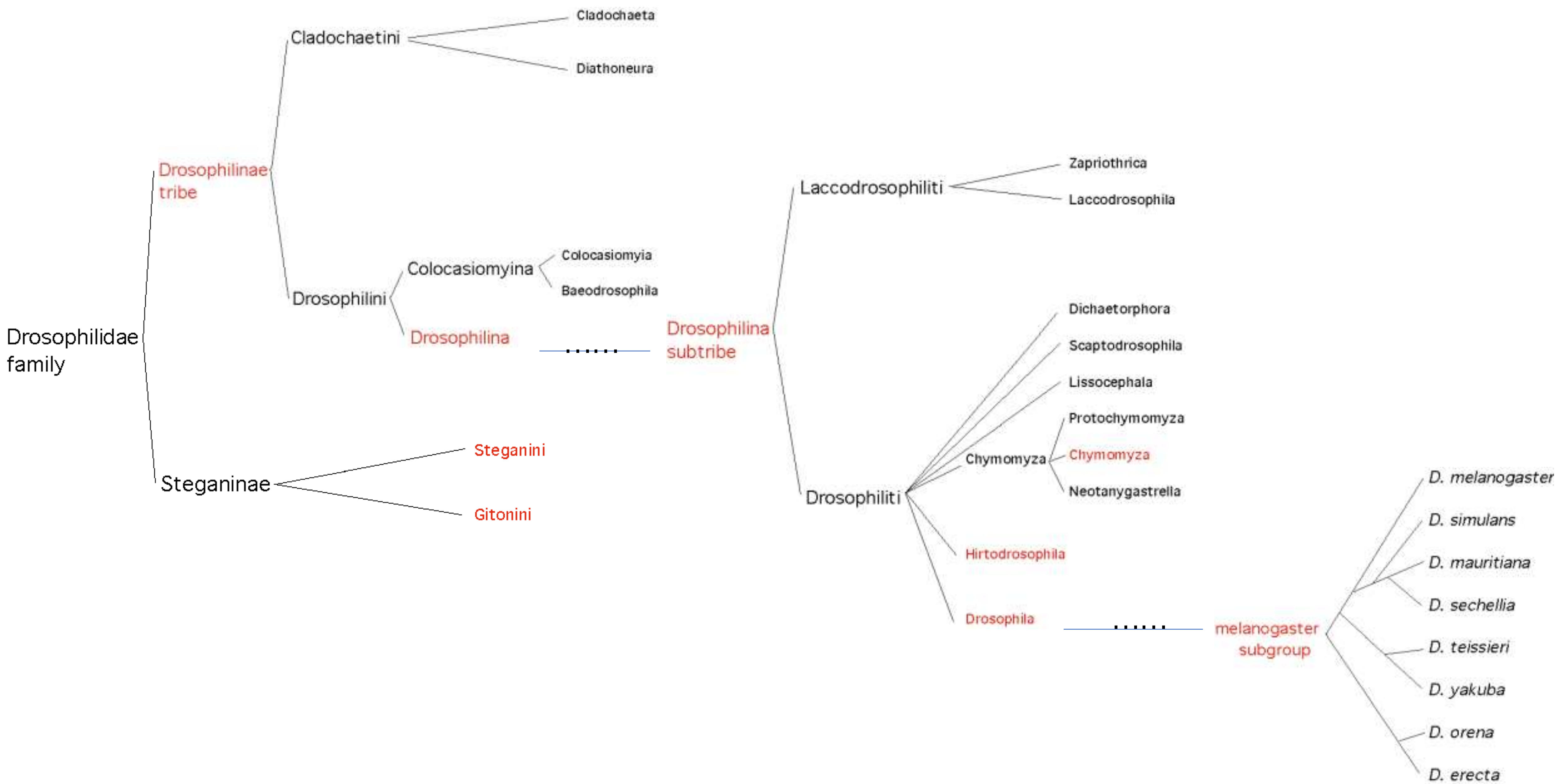
赵环

2021-05-27

# outline

- Species
- Cytologically mapped features
- Expression data
- Vocabularies (Termlink)
- Mutant phenotype data
- Main query tools
- References and stocks

# Species phylogeny



Cladochaetini

Cladochaeta

Diathoneura

Drosophilinae tribe

Colocasiomyina

Colocasiomyia

Baeodrosophila

Drosophilini

Drosophilina

Drosophilidae family

Steganini

Steganinae

Gitonini

Drosophilina subtribe

Laccodrosophiliti

Zapriothrica

Laccodrosophila

Dichaetorphora

Scaptodrosophila

Lissocephala

Protochymomyza

Chymomyza

Chymomyza

Neotanygastrella

Drosophiliti

Hirtodrosophila

Drosophila

melanogaster subgroup

D. melanogaster

D. simulans

D. mauritiana

D. sechellia

D. teissieri

D. yakuba

D. orena

D. erecta

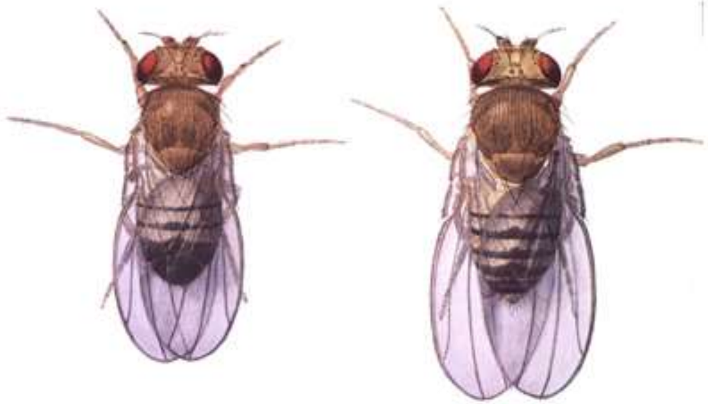
# Appearance and distributions

**Most of the relationships on this page were obtained from:**

**Jeffs, P.S., E. C. Holmes, and M Ashburner. 1994. The molecular evolution of the alcohol dehydrogenase and alcohol dehydrogenase-related genes in the *Drosophila melanogaster* species group. Mol. Biol. Evol. 11(2):287-304.**

**Most of the figures on this page where obtained from:**

**Lemeunier, F., J.R. David, L. Tsacas, and M. Ashburner. "The *melanogaster* species group." The Genetics and Biology of Drosophila. Ed. M. Ashburner, H.L. Carson, and J.N. Thompson, Jr. New York: New York Academic Press, 1986. 147-256.**

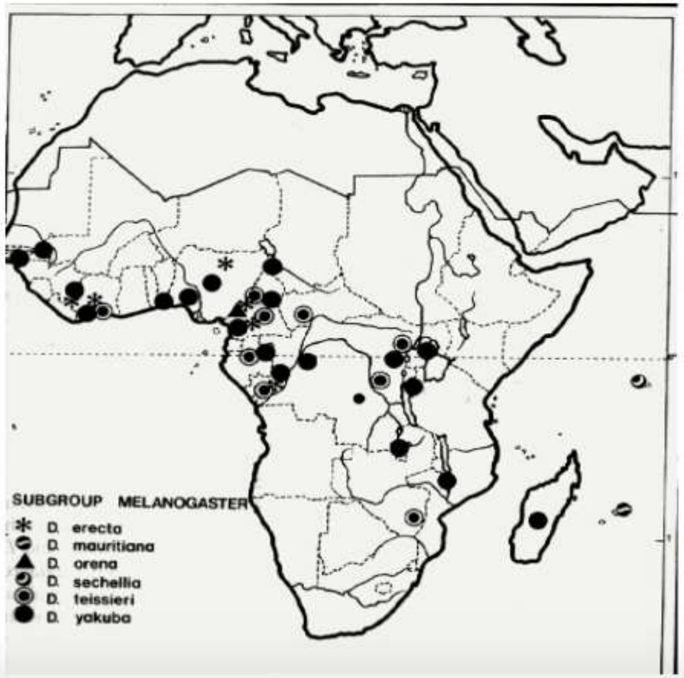


*D. melanogaster* male and female

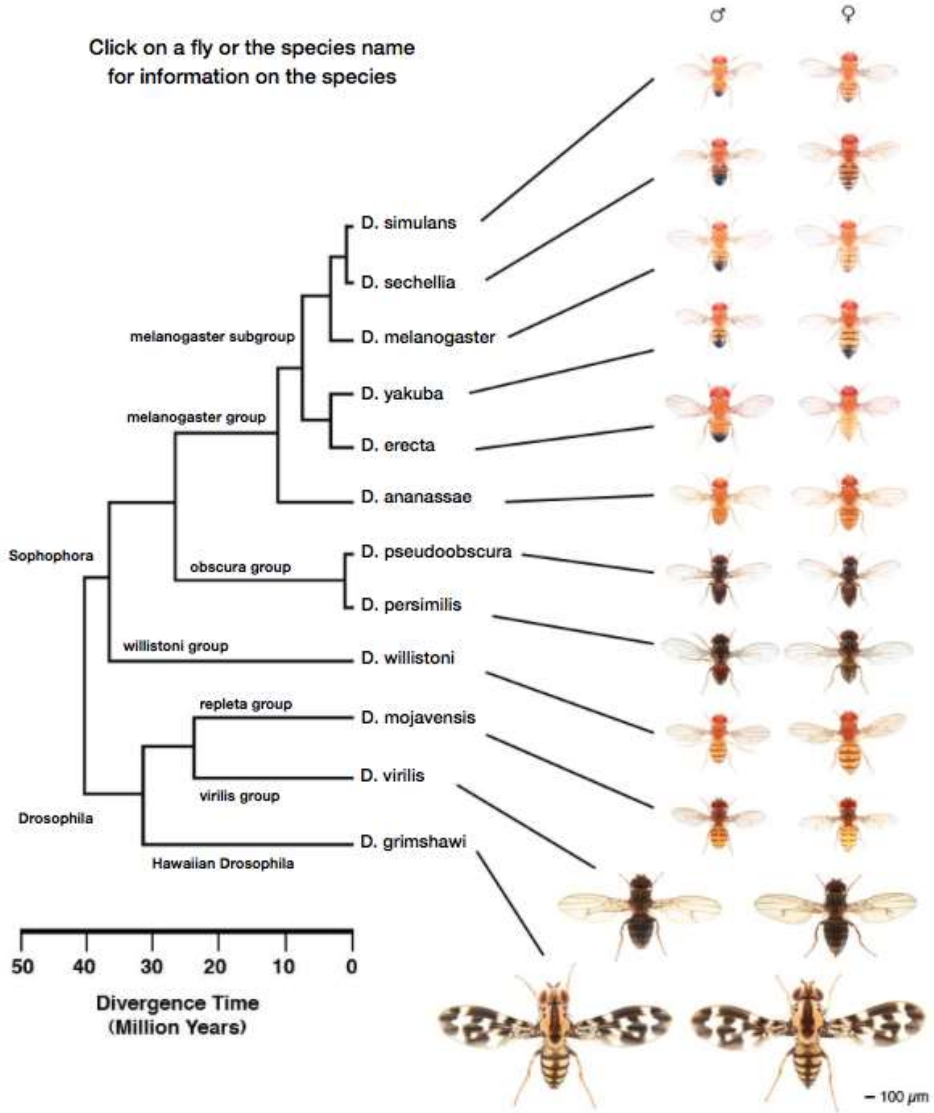
*D. simulans* (small fly on right)

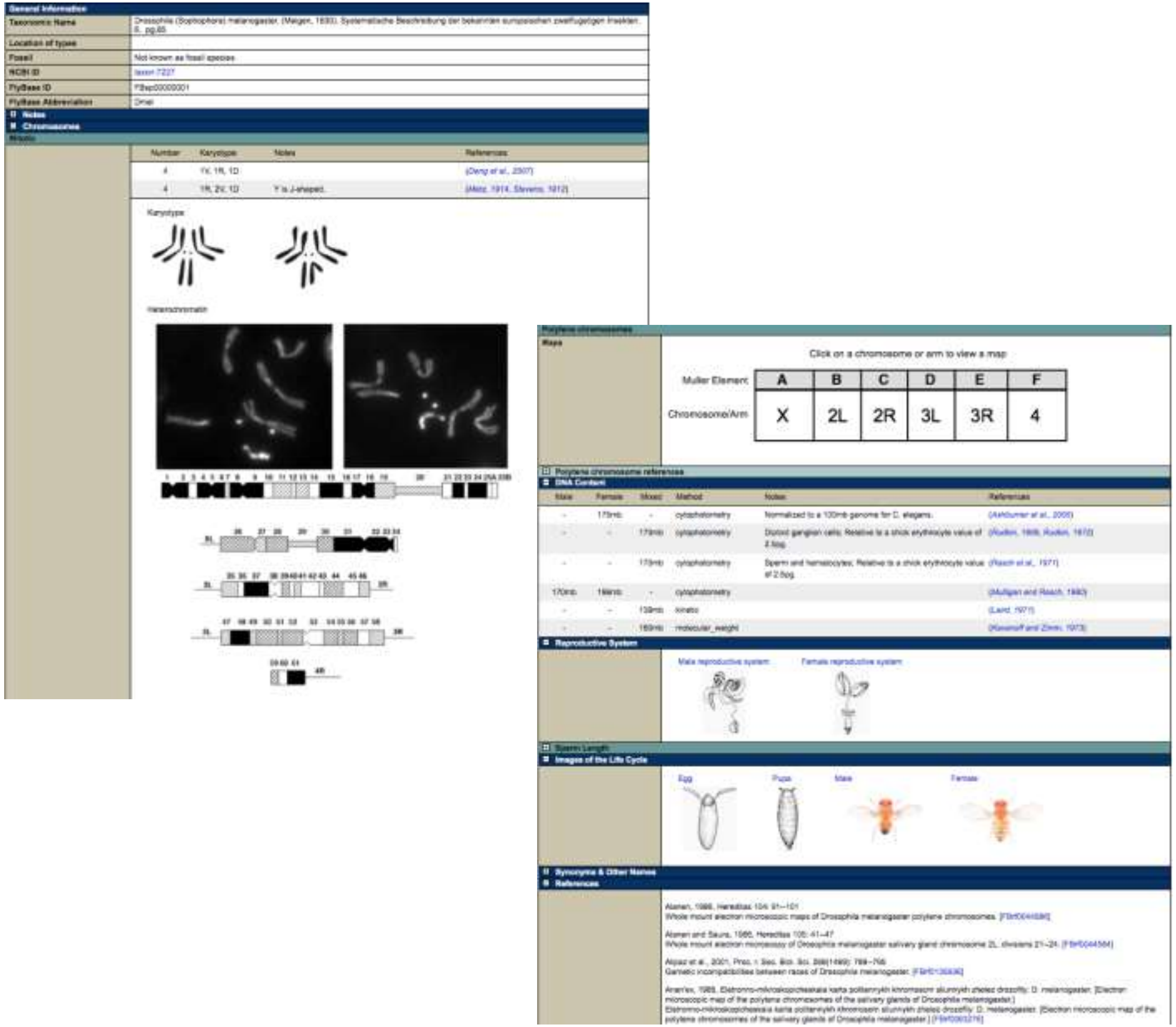
*D. orena, D. erecta, and D. yakuba* male genetal phallus

Distribution of the melanogaster subgroup



# Sequenced species





**General Information**

| | |
|---|---|
| Taxonomic Name | Drosophila (Sophophora) melanogaster, (Meigen, 1830). Systematische Beschreibung der bekannten europäischen zweiflügeligen Insekten. 6., pg.85 |
| Location of types | |
| Fossil | Not known as fossil species |
| NCBI ID | taxon:7227 |
| FlyBase ID | FBsp00000001 |
| FlyBase Abbreviation | Dmel |

Notes

Chromosomes

| Number | Karyotype | Notes | References |
|---|---|---|---|
| 4 | 1X, 1R, 1D | | (Deng et al., 2007) |
| 4 | 1R, 2V, 1D | Y is J-shaped. | (Metz, 1914, Stevens, 1912) |

Karyotype

Heterochromatin

Polytene chromosomes

Maps

Click on a chromosome or arm to view a map

| Muller Element | A | B | C | D | E | F |
|---|---|---|---|---|---|---|
| Chromosome/Arm | X | 2L | 2R | 3L | 3R | 4 |

Polytene chromosome references

DNA Content

Reproductive System

Male reproductive system

Female reproductive system

Sperm Length

Images of the Life Cycle

Egg

Pupa

Male

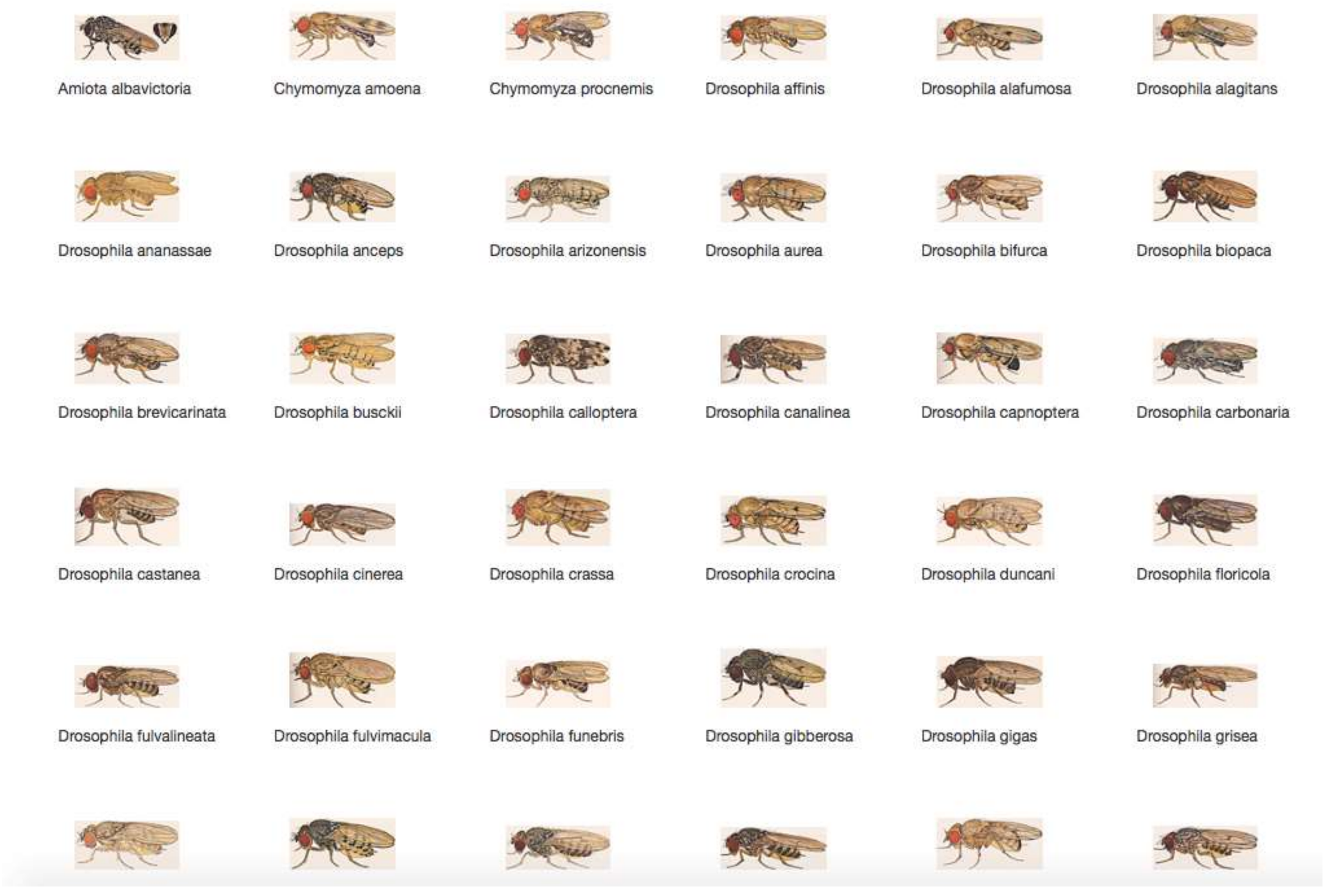
Female

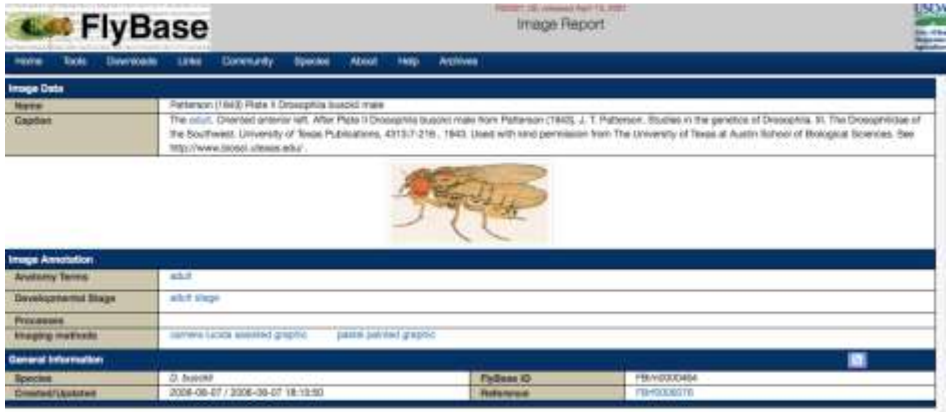
Synonyms & Other Names

References

The images were kindly provided by Nicolas Gompel

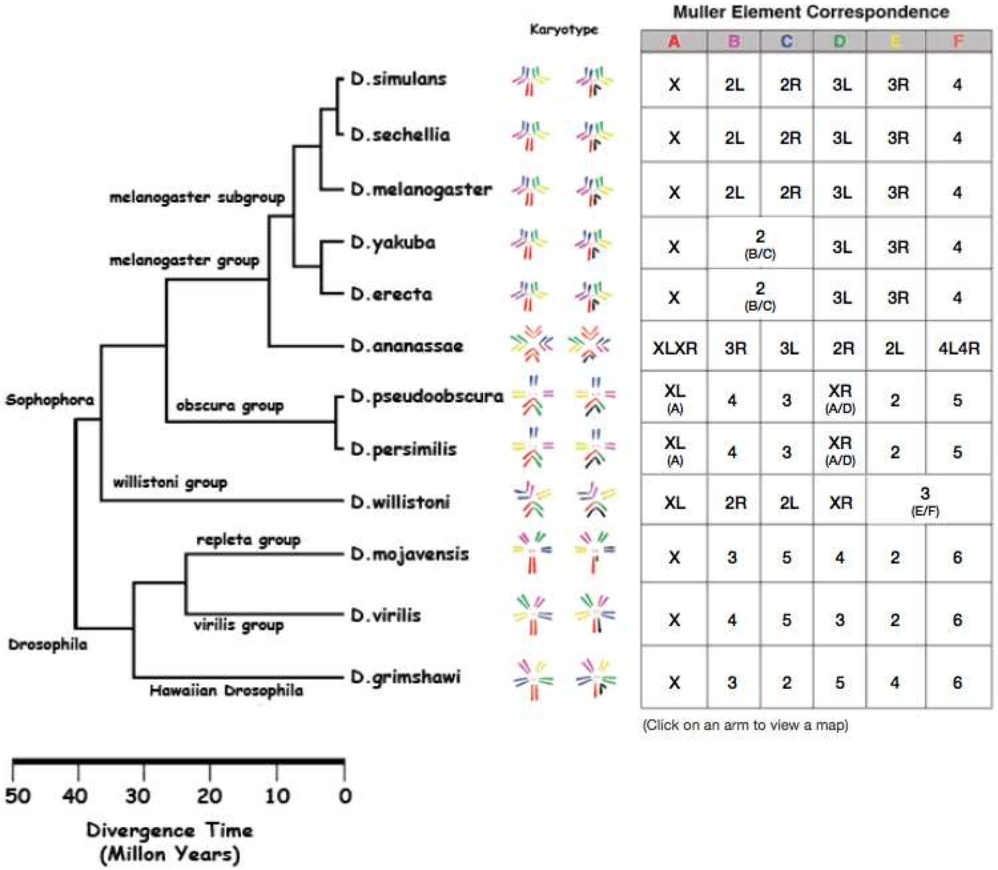
# Color illustrations





在这108株果蝇中，其中82个是在墨西哥发现的，43个是美国和墨西哥共有的，26个是在美国收集的，39个是在墨西哥收集的。

# Cytologically Mapped Features

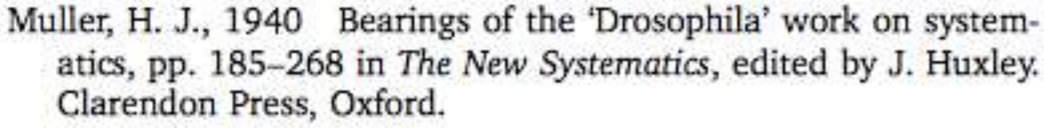


Muller Element Correspondence

| | A | B | C | D | E | F |
|---|---|---|---|---|---|---|
| D.simulans | X | 2L | 2R | 3L | 3R | 4 |
| D.sechellia | X | 2L | 2R | 3L | 3R | 4 |
| D.melanogaster | X | 2L | 2R | 3L | 3R | 4 |
| D.yakuba | X | 2<br>(B/C) | | 3L | 3R | 4 |
| D.erecta | X | 2<br>(B/C) | | 3L | 3R | 4 |
| D.ananassae | XLXR | 3R | 3L | 2R | 2L | 4L4R |
| D.pseudoobscura | XL<br>(A) | 4 | 3 | XR<br>(A/D) | 2 | 5 |
| D.persimilis | XL<br>(A) | 4 | 3 | XR<br>(A/D) | 2 | 5 |
| D.willistoni | XL | 2R | 2L | XR | 3<br>(E/F) | |
| D.mojavensis | X | 3 | 5 | 4 | 2 | 6 |
| D.virilis | X | 4 | 5 | 3 | 2 | 6 |
| D.grimshawi | X | 3 | 2 | 5 | 4 | 6 |

(Click on an arm to view a map)

Hermann J.Muller（1946年诺贝尔奖）

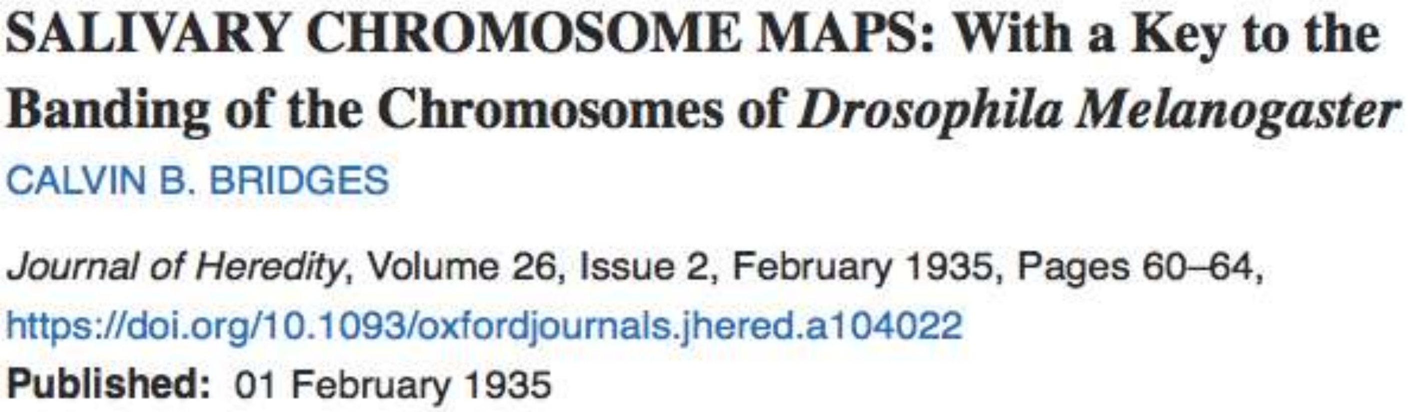


Muller, H. J., 1940 Bearings of the 'Drosophila' work on systematics, pp. 185–268 in *The New Systematics*, edited by J. Huxley. Clarendon Press, Oxford.

Muller element designation

# Chromosome map builder

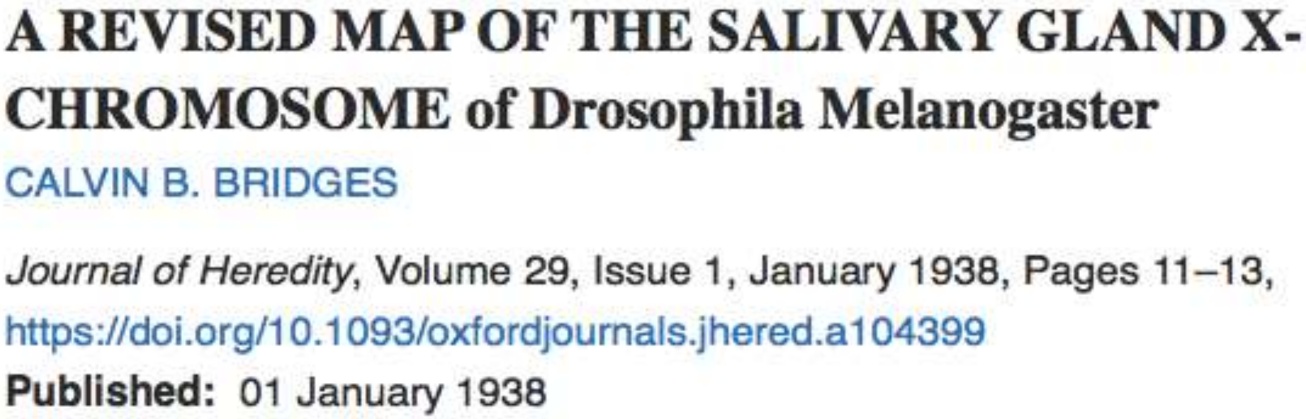
Calvin Blackman Bridges



**SALIVARY CHROMOSOME MAPS: With a Key to the Banding of the Chromosomes of *Drosophila Melanogaster***

CALVIN B. BRIDGES

*Journal of Heredity*, Volume 26, Issue 2, February 1935, Pages 60–64, https://doi.org/10.1093/oxfordjournals.jhered.a104022
**Published:** 01 February 1935

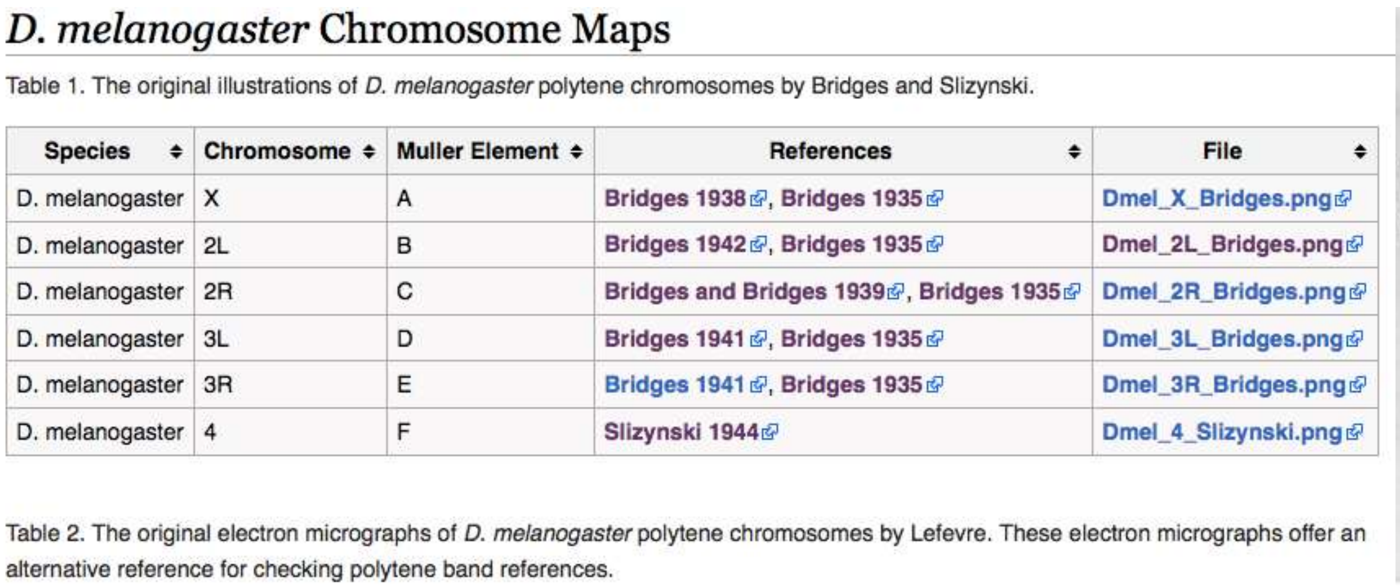


**A REVISED MAP OF THE SALIVARY GLAND X-CHROMOSOME of Drosophila Melanogaster**

CALVIN B. BRIDGES

*Journal of Heredity*, Volume 29, Issue 1, January 1938, Pages 11–13, https://doi.org/10.1093/oxfordjournals.jhered.a104399
**Published:** 01 January 1938

# Chromosome maps

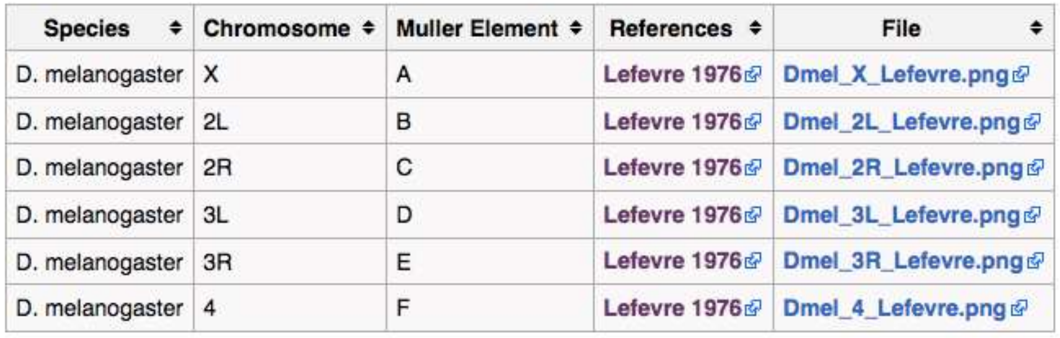


## *D. melanogaster* Chromosome Maps

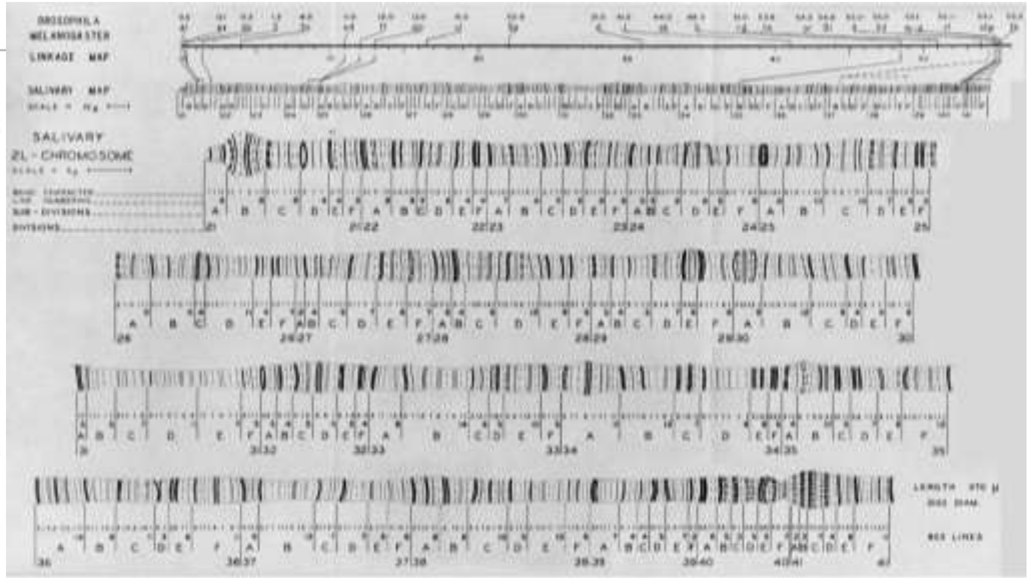
Table 1. The original illustrations of *D. melanogaster* polytene chromosomes by Bridges and Slizynski.

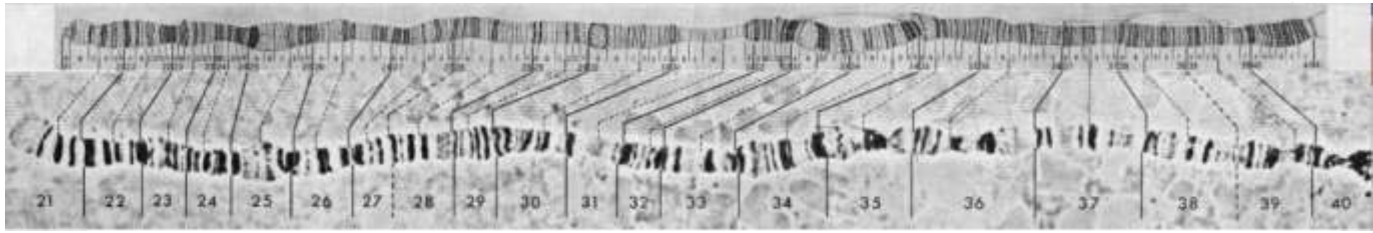
| Species ⬍ | Chromosome ⬍ | Muller Element ⬍ | References ⬍ | File ⬍ |
|---|---|---|---|---|
| D. melanogaster | X | A | Bridges 1938, Bridges 1935 | Dmel_X_Bridges.png |
| D. melanogaster | 2L | B | Bridges 1942, Bridges 1935 | Dmel_2L_Bridges.png |
| D. melanogaster | 2R | C | Bridges and Bridges 1939, Bridges 1935 | Dmel_2R_Bridges.png |
| D. melanogaster | 3L | D | Bridges 1941, Bridges 1935 | Dmel_3L_Bridges.png |
| D. melanogaster | 3R | E | Bridges 1941, Bridges 1935 | Dmel_3R_Bridges.png |
| D. melanogaster | 4 | F | Slizynski 1944 | Dmel_4_Slizynski.png |

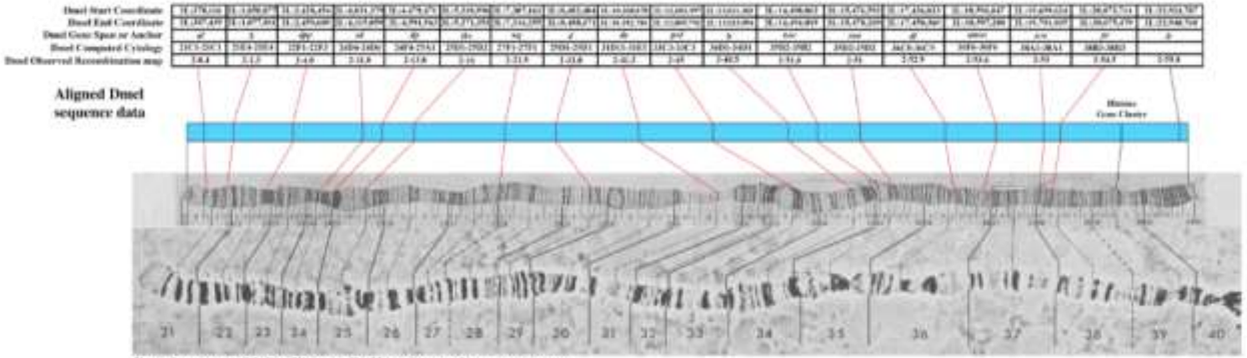
Table 2. The original electron micrographs of *D. melanogaster* polytene chromosomes by Lefevre. These electron micrographs offer an alternative reference for checking polytene band references.



| Species ⬍ | Chromosome ⬍ | Muller Element ⬍ | References ⬍ | File ⬍ |
|---|---|---|---|---|
| D. melanogaster | X | A | Lefevre 1976 | Dmel_X_Lefevre.png |
| D. melanogaster | 2L | B | Lefevre 1976 | Dmel_2L_Lefevre.png |
| D. melanogaster | 2R | C | Lefevre 1976 | Dmel_2R_Lefevre.png |
| D. melanogaster | 3L | D | Lefevre 1976 | Dmel_3L_Lefevre.png |
| D. melanogaster | 3R | E | Lefevre 1976 | Dmel_3R_Lefevre.png |
| D. melanogaster | 4 | F | Lefevre 1976 | Dmel_4_Lefevre.png |

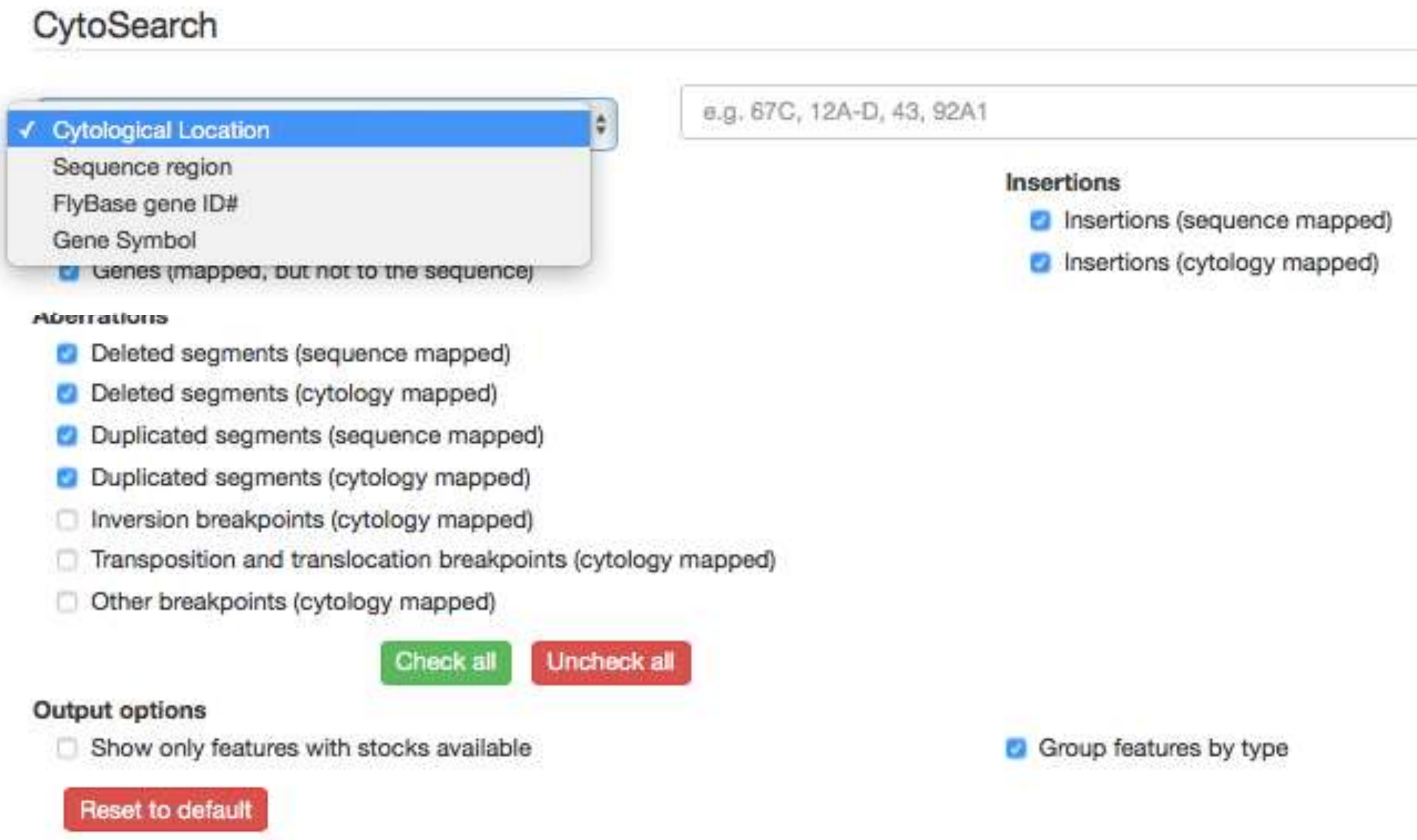






D. melanogaster Muller Element B (2L) polytene chromosome map

# CytoSearch results



☑ Genes (mapped, but not to the sequence)

**Aberrations**

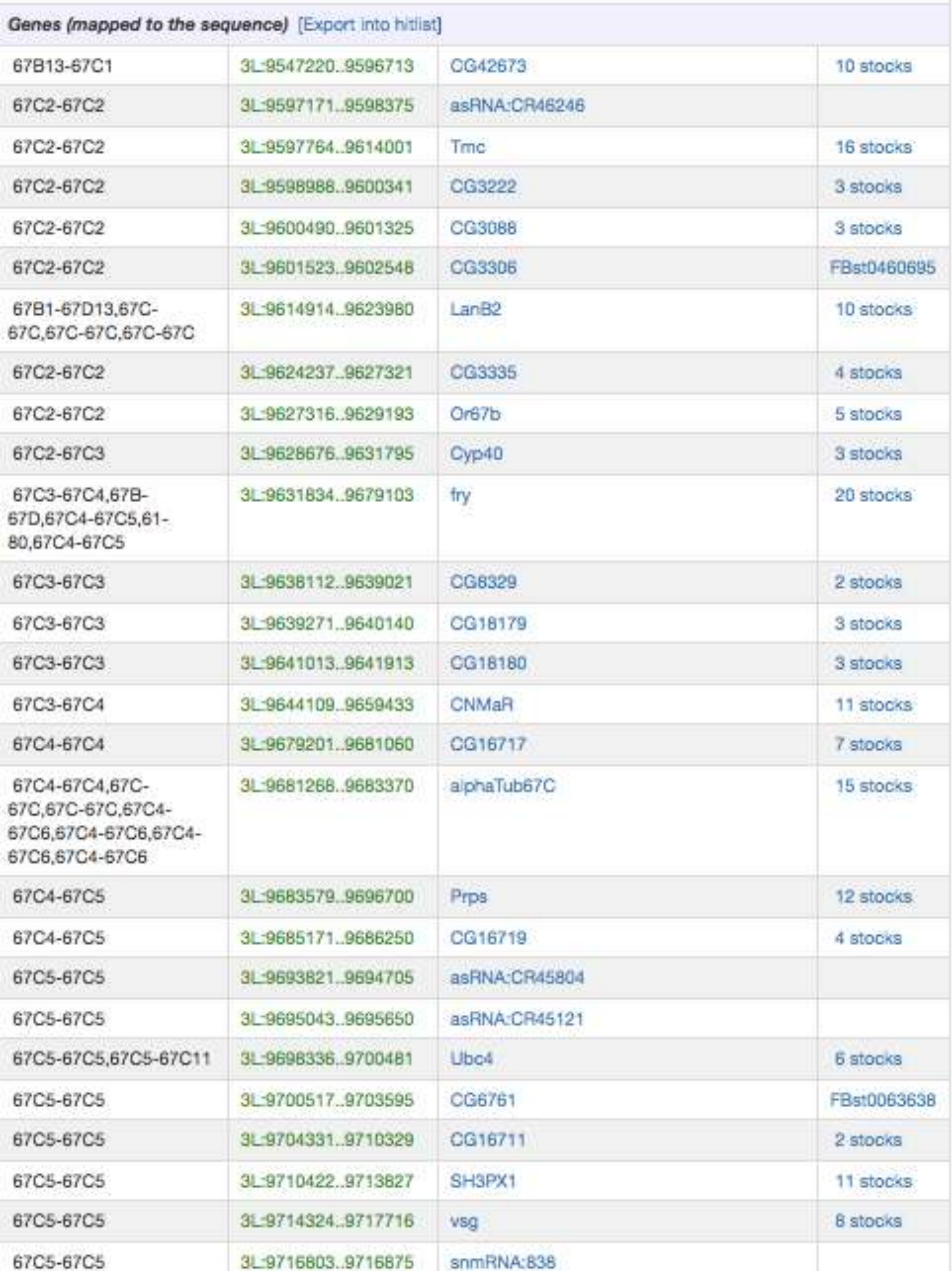
☑ Deleted segments (sequence mapped)
☑ Deleted segments (cytology mapped)
☑ Duplicated segments (sequence mapped)
☑ Duplicated segments (cytology mapped)
☐ Inversion breakpoints (cytology mapped)
☐ Transposition and translocation breakpoints (cytology mapped)
☐ Other breakpoints (cytology mapped)

**Insertions**

☑ Insertions (sequence mapped)
☑ Insertions (cytology mapped)

**Output options**

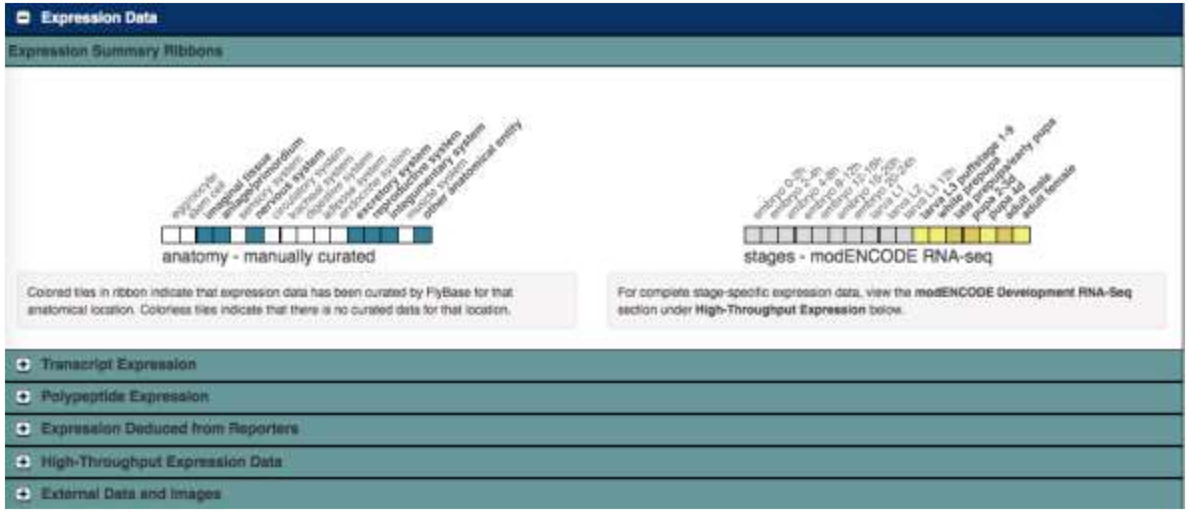
☐ Show only features with stocks available
☑ Group features by type



***Genes (mapped to the sequence)*** [Export into hitlist]

| | | | |
|---|---|---|---|
| 67B13-67C1 | 3L:9547220..9596713 | CG42673 | 10 stocks |
| 67C2-67C2 | 3L:9597171..9598375 | asRNA:CR46246 | |
| 67C2-67C2 | 3L:9597764..9614001 | Tmc | 16 stocks |
| 67C2-67C2 | 3L:9598988..9600341 | CG3222 | 3 stocks |
| 67C2-67C2 | 3L:9600490..9601325 | CG3088 | 3 stocks |
| 67C2-67C2 | 3L:9601523..9602548 | CG3306 | FBst0460695 |
| 67B1-67D13,67C-67C,67C-67C,67C-67C | 3L:9614914..9623980 | LanB2 | 10 stocks |
| 67C2-67C2 | 3L:9624237..9627321 | CG3335 | 4 stocks |
| 67C2-67C2 | 3L:9627316..9629193 | Or67b | 5 stocks |
| 67C2-67C3 | 3L:9628676..9631795 | Cyp40 | 3 stocks |
| 67C3-67C4,67B-67D,67C4-67C5,61-80,67C4-67C5 | 3L:9631834..9679103 | fry | 20 stocks |
| 67C3-67C3 | 3L:9638112..9639021 | CG8329 | 2 stocks |
| 67C3-67C3 | 3L:9639271..9640140 | CG18179 | 3 stocks |
| 67C3-67C3 | 3L:9641013..9641913 | CG18180 | 3 stocks |
| 67C3-67C4 | 3L:9644109..9659433 | CNMaR | 11 stocks |
| 67C4-67C4 | 3L:9679201..9681060 | CG16717 | 7 stocks |
| 67C4-67C4,67C-67C,67C-67C,67C4-67C6,67C4-67C6,67C4-67C6,67C4-67C6 | 3L:9681268..9683370 | alphaTub67C | 15 stocks |
| 67C4-67C5 | 3L:9683579..9696700 | Prps | 12 stocks |
| 67C4-67C5 | 3L:9685171..9686250 | CG16719 | 4 stocks |
| 67C5-67C5 | 3L:9693821..9694705 | asRNA:CR45804 | |
| 67C5-67C5 | 3L:9695043..9695650 | asRNA:CR45121 | |
| 67C5-67C5,67C5-67C11 | 3L:9698336..9700481 | Ubc4 | 6 stocks |
| 67C5-67C5 | 3L:9700517..9703595 | CG6761 | FBst0063638 |
| 67C5-67C5 | 3L:9704331..9710329 | CG16711 | 2 stocks |
| 67C5-67C5 | 3L:9710422..9713827 | SH3PX1 | 11 stocks |
| 67C5-67C5 | 3L:9714324..9717716 | vsg | 8 stocks |
| 67C5-67C5 | 3L:9716803..9716875 | snmRNA:838 | |

# Expression Data: Search *dsx* as an example



**Expression Data**

Expression Summary Ribbons

Colored tiles in ribbon indicate that expression data has been curated by FlyBase for that anatomical location. Colorless tiles indicate that there is no curated data for that location.

For complete stage-specific expression data, view the **modENCODE Development RNA-Seq** section under **High-Throughput Expression** below.

Transcript Expression

Polypeptide Expression

Expression Deduced from Reporters

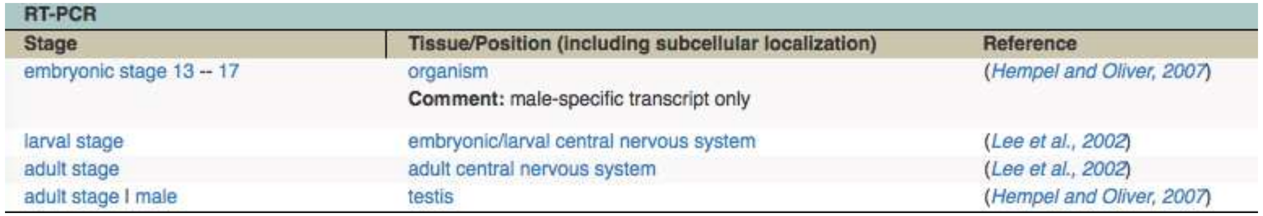
High-Throughput Expression Data

External Data and Images

**Transcript Expression**

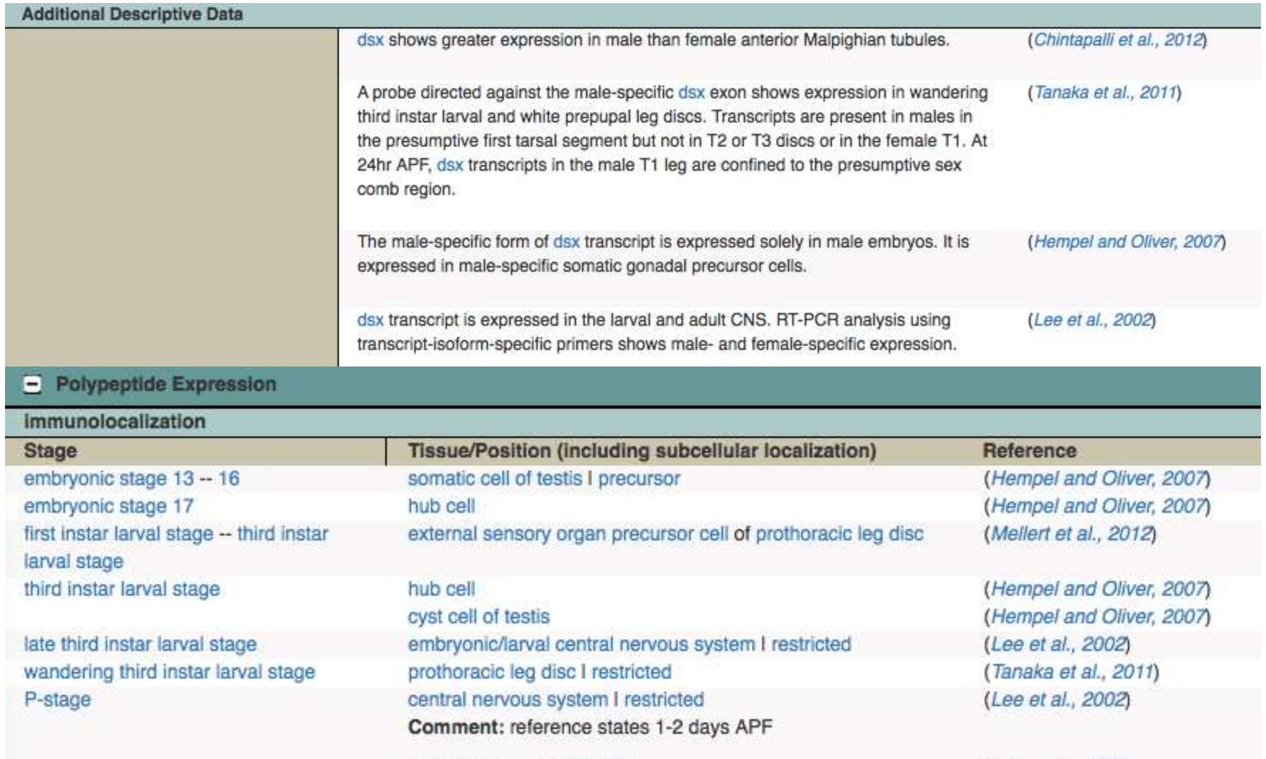
**Immunolocalization**

| Stage | Tissue/Position (including subcellular localization) | Reference |
|---|---|---|
| wandering third instar larval stage | prothoracic leg disc \| restricted | (*Tanaka et al., 2011*) |
| prepupal stage P1 -- P4 | prothoracic leg disc \| restricted | (*Tanaka et al., 2011*) |
| pupal stage P6 | prothoracic leg disc \| restricted<br>**Comment:** male | (*Tanaka et al., 2011*) |
|  | sex comb<br>**Comment:** male | (*Tanaka et al., 2011*) |



**RT-PCR**

| Stage | Tissue/Position (including subcellular localization) | Reference |
|---|---|---|
| embryonic stage 13 -- 17 | organism<br>**Comment:** male-specific transcript only | (*Hempel and Oliver, 2007*) |
| larval stage | embryonic/larval central nervous system | (*Lee et al., 2002*) |
| adult stage | adult central nervous system | (*Lee et al., 2002*) |
| adult stage \| male | testis | (*Hempel and Oliver, 2007*) |



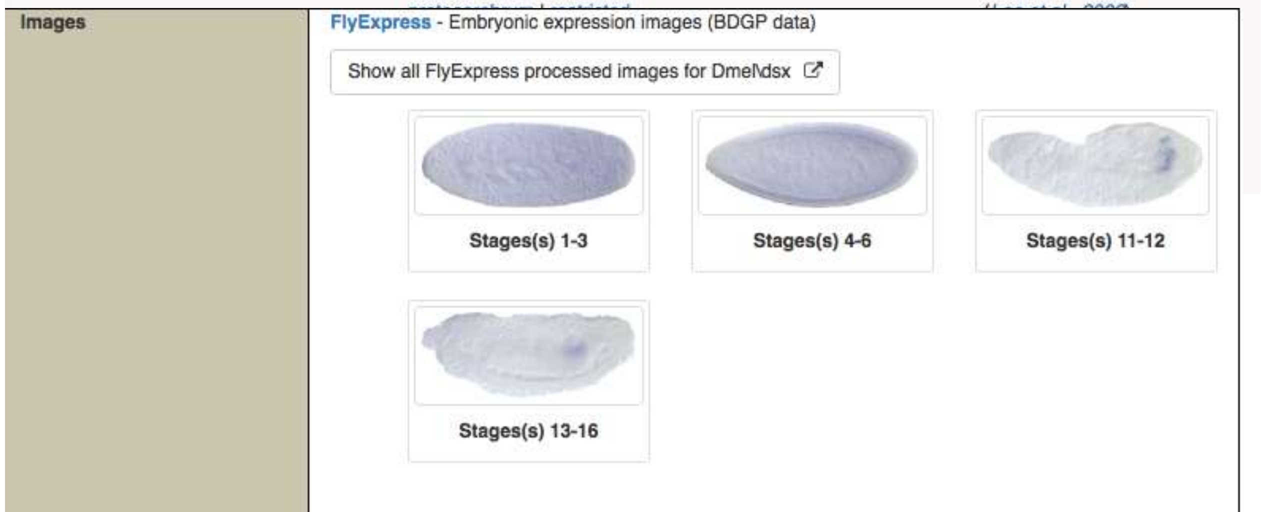
**Additional Descriptive Data**

| | |
|---|---|
| dsx shows greater expression in male than female anterior Malpighian tubules. | (*Chintapalli et al., 2012*) |
| A probe directed against the male-specific dsx exon shows expression in wandering third instar larval and white prepupal leg discs. Transcripts are present in males in the presumptive first tarsal segment but not in T2 or T3 discs or in the female T1. At 24hr APF, dsx transcripts in the male T1 leg are confined to the presumptive sex comb region. | (*Tanaka et al., 2011*) |
| The male-specific form of dsx transcript is expressed solely in male embryos. It is expressed in male-specific somatic gonadal precursor cells. | (*Hempel and Oliver, 2007*) |
| dsx transcript is expressed in the larval and adult CNS. RT-PCR analysis using transcript-isoform-specific primers shows male- and female-specific expression. | (*Lee et al., 2002*) |

**Polypeptide Expression**

**Immunolocalization**

| Stage | Tissue/Position (including subcellular localization) | Reference |
|---|---|---|
| embryonic stage 13 -- 16 | somatic cell of testis \| precursor | (*Hempel and Oliver, 2007*) |
| embryonic stage 17 | hub cell | (*Hempel and Oliver, 2007*) |
| first instar larval stage -- third instar larval stage | external sensory organ precursor cell of prothoracic leg disc | (*Mellert et al., 2012*) |
| third instar larval stage | hub cell<br>cyst cell of testis | (*Hempel and Oliver, 2007*)<br>(*Hempel and Oliver, 2007*) |
| late third instar larval stage | embryonic/larval central nervous system \| restricted | (*Lee et al., 2002*) |
| wandering third instar larval stage | prothoracic leg disc \| restricted | (*Tanaka et al., 2011*) |
| P-stage | central nervous system \| restricted<br>**Comment:** reference states 1-2 days APF | (*Lee et al., 2002*) |



**Images**

**FlyExpress** - Embryonic expression images (BDGP data)

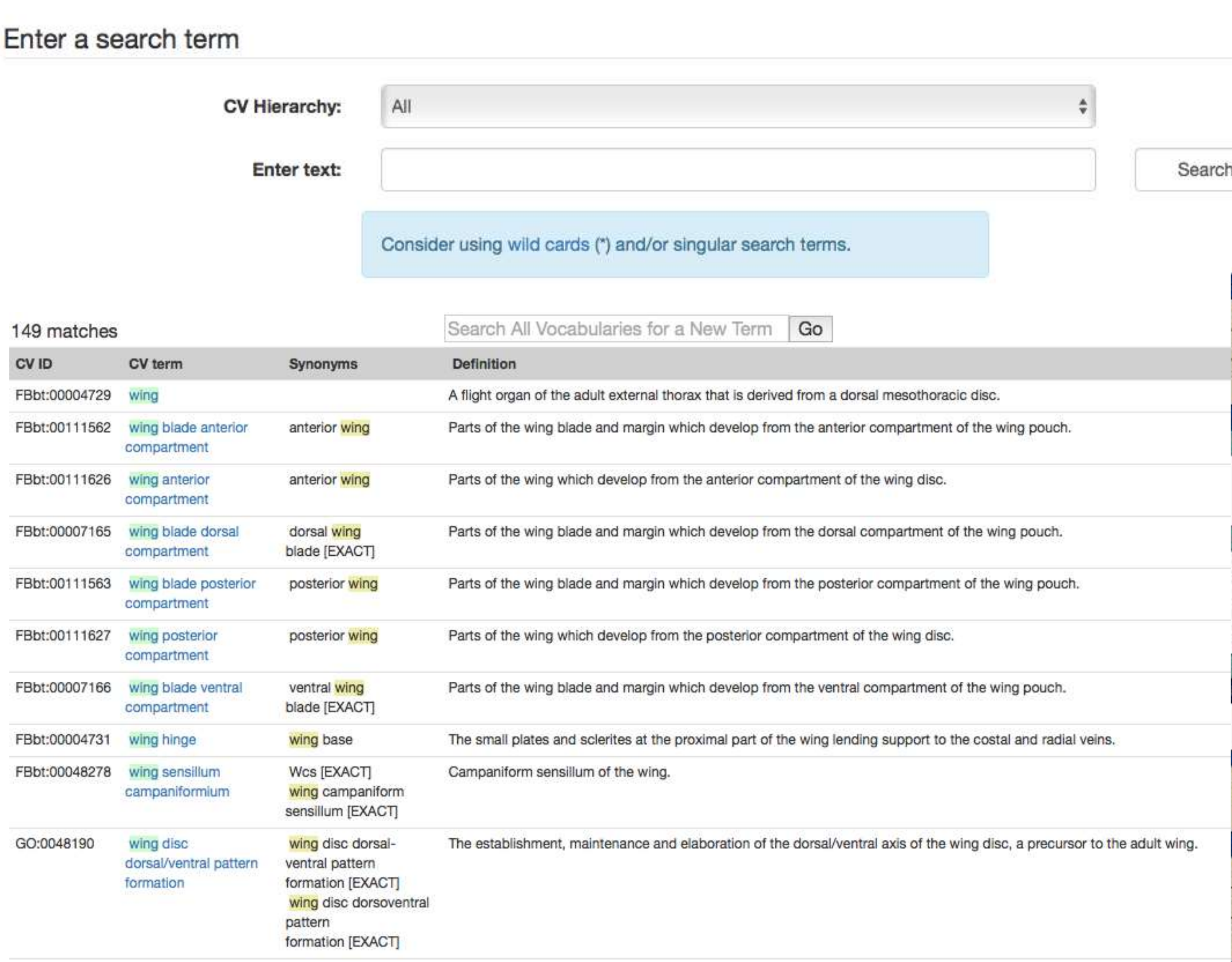
Show all FlyExpress processed images for Dmel\dsx

# Vocabularies

The controlled vocabularies currently used by FlyBase are:

- Gene Ontology (GO).
- Fly Anatomy (FBbt).
- Fly Development (FBdv).
- Sequence Ontology (SO).
- FlyBase controlled vocabulary (FBcv).
- FlyBase stock ontology (FBsv).
- Biological Imaging Methods Ontology (FBbi, image ontology).
- Disease Ontology (DO).
- Molecular Interactions Ontology (MI).

# Mutant phenotype data



CV Hierarchy: All

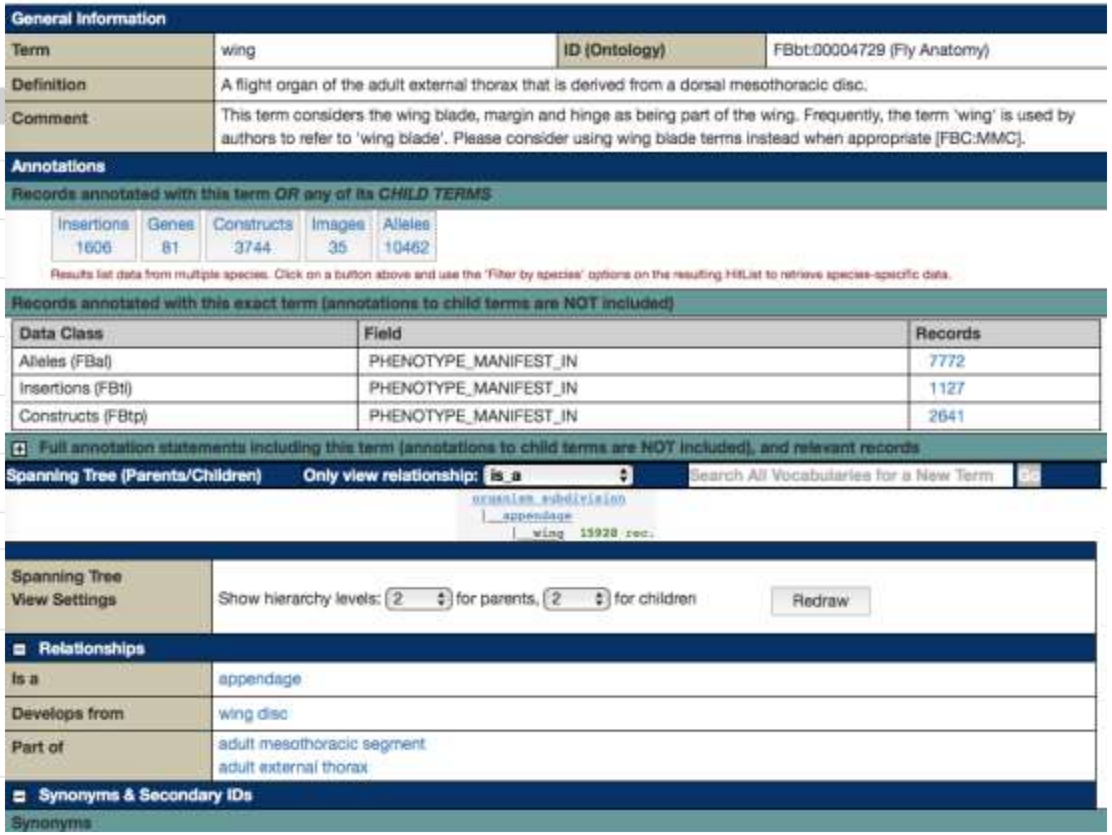
Enter text:

Consider using wild cards (*) and/or singular search terms.

149 matches

Search All Vocabularies for a New Term

| CV ID | CV term | Synonyms | Definition |
|---|---|---|---|
| FBbt:00004729 | wing | | A flight organ of the adult external thorax that is derived from a dorsal mesothoracic disc. |
| FBbt:00111562 | wing blade anterior compartment | anterior wing | Parts of the wing blade and margin which develop from the anterior compartment of the wing pouch. |
| FBbt:00111626 | wing anterior compartment | anterior wing | Parts of the wing which develop from the anterior compartment of the wing disc. |
| FBbt:00007165 | wing blade dorsal compartment | dorsal wing blade [EXACT] | Parts of the wing blade and margin which develop from the dorsal compartment of the wing pouch. |
| FBbt:00111563 | wing blade posterior compartment | posterior wing | Parts of the wing blade and margin which develop from the posterior compartment of the wing pouch. |
| FBbt:00111627 | wing posterior compartment | posterior wing | Parts of the wing which develop from the posterior compartment of the wing disc. |
| FBbt:00007166 | wing blade ventral compartment | ventral wing blade [EXACT] | Parts of the wing blade and margin which develop from the ventral compartment of the wing pouch. |
| FBbt:00004731 | wing hinge | wing base | The small plates and sclerites at the proximal part of the wing lending support to the costal and radial veins. |
| FBbt:00048278 | wing sensillum campaniformium | Wcs [EXACT]<br>wing campaniform sensillum [EXACT] | Campaniform sensillum of the wing. |
| GO:0048190 | wing disc dorsal/ventral pattern formation | wing disc dorsal-ventral pattern formation [EXACT]<br>wing disc dorsoventral pattern formation [EXACT] | The establishment, maintenance and elaboration of the dorsal/ventral axis of the wing disc, a precursor to the adult wing. |



| | | | |
|---|---|---|---|
| Term | wing | ID (Ontology) | FBbt:00004729 (Fly Anatomy) |
| Definition | A flight organ of the adult external thorax that is derived from a dorsal mesothoracic disc. | | |
| Comment | This term considers the wing blade, margin and hinge as being part of the wing. Frequently, the term 'wing' is used by authors to refer to 'wing blade'. Please consider using wing blade terms instead when appropriate [FBC:MMC]. | | |

| Insertions | Genes | Constructs | Images | Alleles |
|---|---|---|---|---|
| 1606 | 81 | 3744 | 35 | 10462 |

Results list data from multiple species. Click on a button above and use the 'Filter by species' options on the resulting HitList to retrieve species-specific data.

Records annotated with this exact term (annotations to child terms are NOT included)

| Data Class | Field | Records |
|---|---|---|
| Alleles (FBal) | PHENOTYPE_MANIFEST_IN | 7772 |
| Insertions (FBti) | PHENOTYPE_MANIFEST_IN | 1127 |
| Constructs (FBtp) | PHENOTYPE_MANIFEST_IN | 2641 |

Full annotation statements including this term (annotations to child terms are NOT included), and relevant records

Spanning Tree (Parents/Children) Only view relationship: is_a

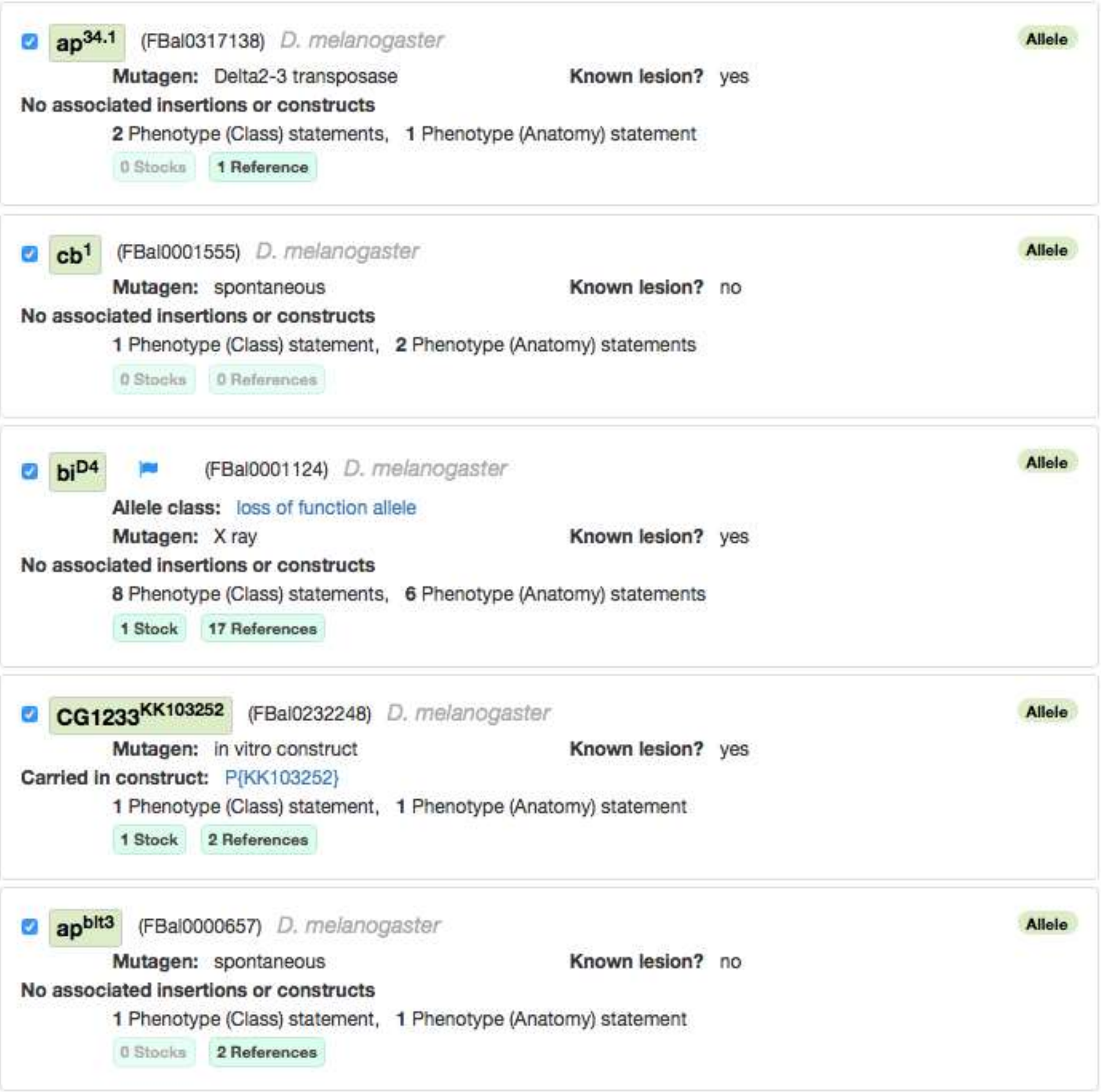
Search All Vocabularies for a New Term

```
organism subdivision
 |__appendage
    |__wing  13928 rec.
```

Spanning Tree View Settings: Show hierarchy levels: 2 for parents, 2 for children

| | |
|---|---|
| Is a | appendage |
| Develops from | wing disc |
| Part of | adult mesothoracic segment<br>adult external thorax |

# Alleles and phenotype



☑ **$ap^{34.1}$** (FBal0317138) *D. melanogaster* **Allele**

**Mutagen:** Delta2-3 transposase **Known lesion?** yes

**No associated insertions or constructs**

**2** Phenotype (Class) statements, **1** Phenotype (Anatomy) statement

0 Stocks | **1 Reference**

☑ **$cb^{1}$** (FBal0001555) *D. melanogaster* **Allele**

**Mutagen:** spontaneous **Known lesion?** no

**No associated insertions or constructs**

**1** Phenotype (Class) statement, **2** Phenotype (Anatomy) statements

0 Stocks | 0 References

☑ **$bi^{D4}$** (FBal0001124) *D. melanogaster* **Allele**

**Allele class:** loss of function allele

**Mutagen:** X ray **Known lesion?** yes

**No associated insertions or constructs**

**8** Phenotype (Class) statements, **6** Phenotype (Anatomy) statements

**1 Stock** | **17 References**

☑ **$CG1233^{KK103252}$** (FBal0232248) *D. melanogaster* **Allele**

**Mutagen:** in vitro construct **Known lesion?** yes

**Carried in construct:** P{KK103252}

**1** Phenotype (Class) statement, **1** Phenotype (Anatomy) statement

**1 Stock** | **2 References**

☑ **$ap^{blt3}$** (FBal0000657) *D. melanogaster* **Allele**

**Mutagen:** spontaneous **Known lesion?** no

**No associated insertions or constructs**

**1** Phenotype (Class) statement, **1** Phenotype (Anatomy) statement

0 Stocks | **2 References**

**Phenotypic Data**

**Phenotypic Class**

| | |
|---|---|
| lethal \| recessive | (*Lepage et al., 1995*, *Strutt et al., 1995*) |
| visible | (*Strutt et al., 1995*) |

**Phenotype Manifest In**

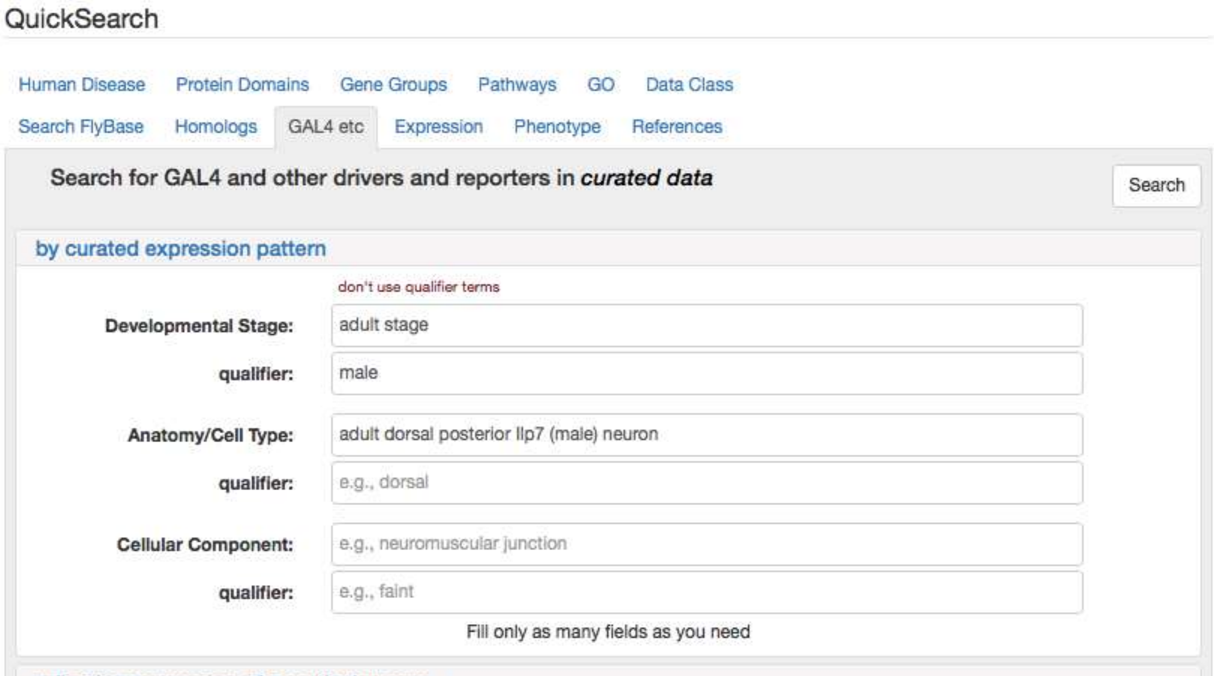
| | |
|---|---|
| eye | (*Strutt et al., 1995*) |
| eye-antennal disc | (*Wiersdorff et al., 1996*) |
| leg anterior compartment | (*Lepage et al., 1995*) |
| wing blade anterior compartment | (*Lepage et al., 1995*) |

**Detailed Description**

| Statement | Reference |
|---|---|
| Double mutant clones of $Mad^{1-2}$ with $Pka\text{-}C1^{k08918}$ located in posterior locations show a phenotype similar to Mad single mutant clones, except that they are more frequently associated with overgrowth. Double mutant clones in more anterior positions show a novel phenotype, and are always associated with overgrowth with no ectopic furrow or photoreceptor differentiation. These clones give rise to head cuticle in adult flies. | (*Wiersdorff et al., 1996*) |
| Homozygous mutant clones that cross the dorsal ventral compartment boundary cause bifurcations. Clones present at the anterior posterior wing boundary or on the dorsal or ventral surface of the posterior wing compartment have no phenotype. Clones present in the anterior compartment of the male foreleg cause bifurcation. | (*Lepage et al., 1995*) |
| Homozygous mutant clones in the compound eye demonstrate non-autonomous eye roughening. Bulging of the eye surface is commonly seen in anterior positioned clones, clones in the posterior region are often smooth. | (*Strutt et al., 1995*) |

# Quick search

- Gal4



QuickSearch

Search for GAL4 and other drivers and reporters in *curated data*

**by curated expression pattern**

don't use qualifier terms

**Developmental Stage:** adult stage

**qualifier:** male

**Anatomy/Cell Type:** adult dorsal posterior Ilp7 (male) neuron

**qualifier:** e.g., dorsal

**Cellular Component:** e.g., neuromuscular junction

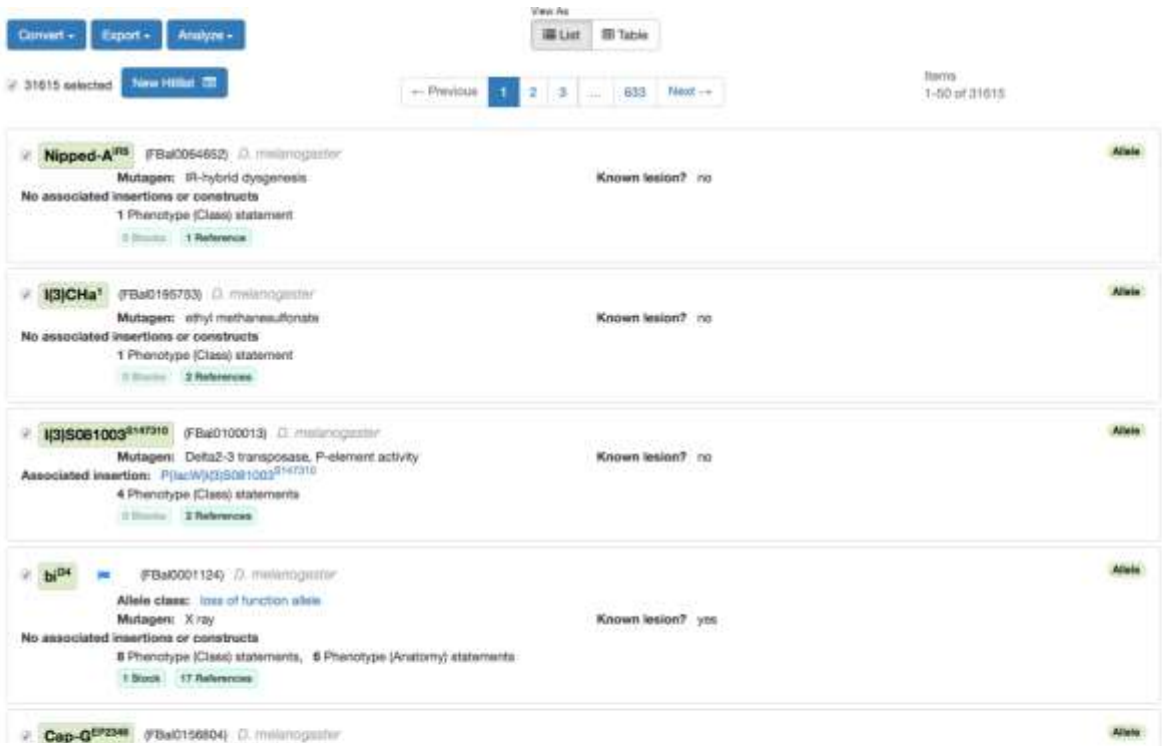
**qualifier:** e.g., faint

Fill only as many fields as you need

**reflecting expression of a particular gene**

**Frequently Used GAL4 Drivers** table

- Phenotype(lethal)



31615 selected

Items 1-50 of 31615

**Nipped-A$^{IR5}$** (FBal0054652) *D. melanogaster*
**Mutagen:** IR-hybrid dysgenesis
**Known lesion?** no
**No associated insertions or constructs**
1 Phenotype (Class) statement
0 Stocks 1 Reference

**l(3)CHa$^{1}$** (FBal0195783) *D. melanogaster*
**Mutagen:** ethyl methanesulfonate
**Known lesion?** no
**No associated insertions or constructs**
1 Phenotype (Class) statement
0 Stocks 2 References

**l(3)S081003$^{S147310}$** (FBal0100013) *D. melanogaster*
**Mutagen:** Delta2-3 transposase, P-element activity
**Known lesion?** no
**Associated insertion:** P{lacW}l(3)S081003$^{S147310}$
4 Phenotype (Class) statements
0 Stocks 2 References

**bi$^{D4}$** (FBal0001124) *D. melanogaster*
**Allele class:** loss of function allele
**Mutagen:** X ray
**Known lesion?** yes
**No associated insertions or constructs**
8 Phenotype (Class) statements, 6 Phenotype (Anatomy) statements
1 Stock 17 References

**Cap-G$^{EP2348}$** (FBal0156804) *D. melanogaster*

- Reference

QuickSearch

Search by ☑ Author ☐ Year ☐ Title/Abstract ☑ Journal ☐ Pub type ☐ ID ☐ Any field

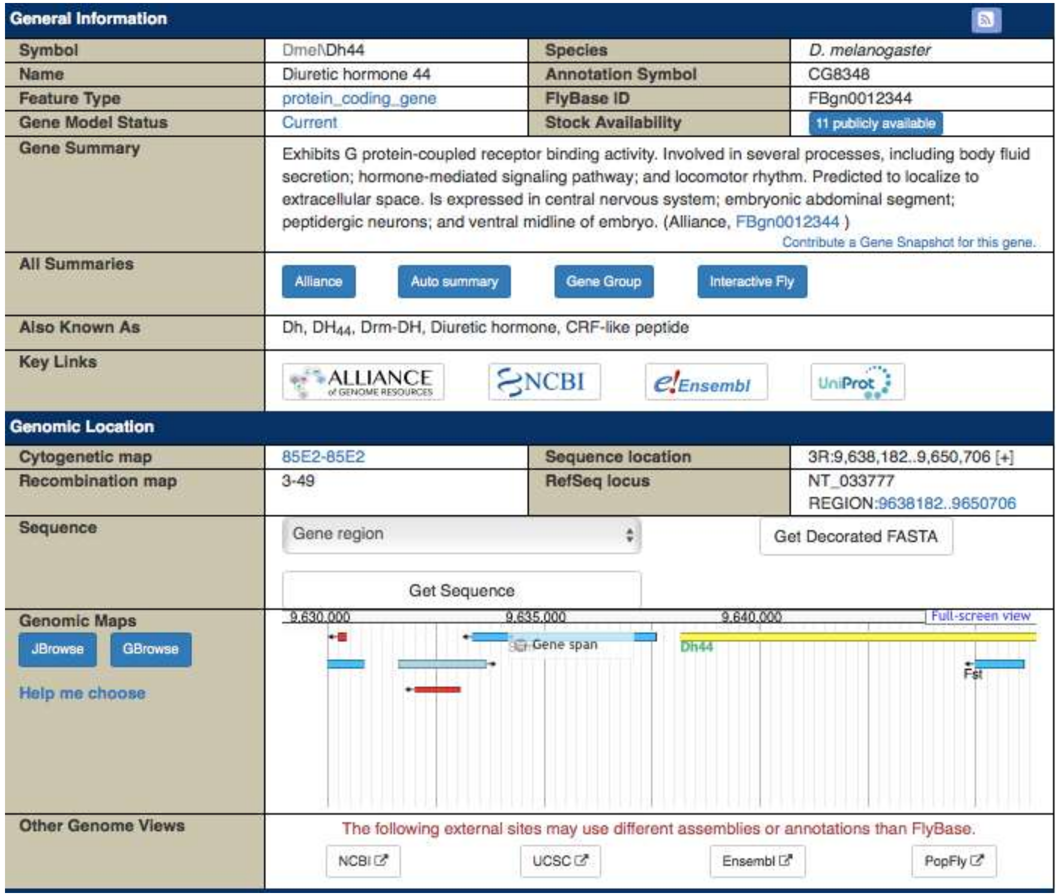
**Author** e.g. 'Smith NOT Johnson'

**Journal** e.g. 'Dev. Biol.'

**or search fly preprints at** Europe PMC

**Note:** Wild cards (*) can be added to your search term

# Jump to gene/Search Flybase



**General Information**

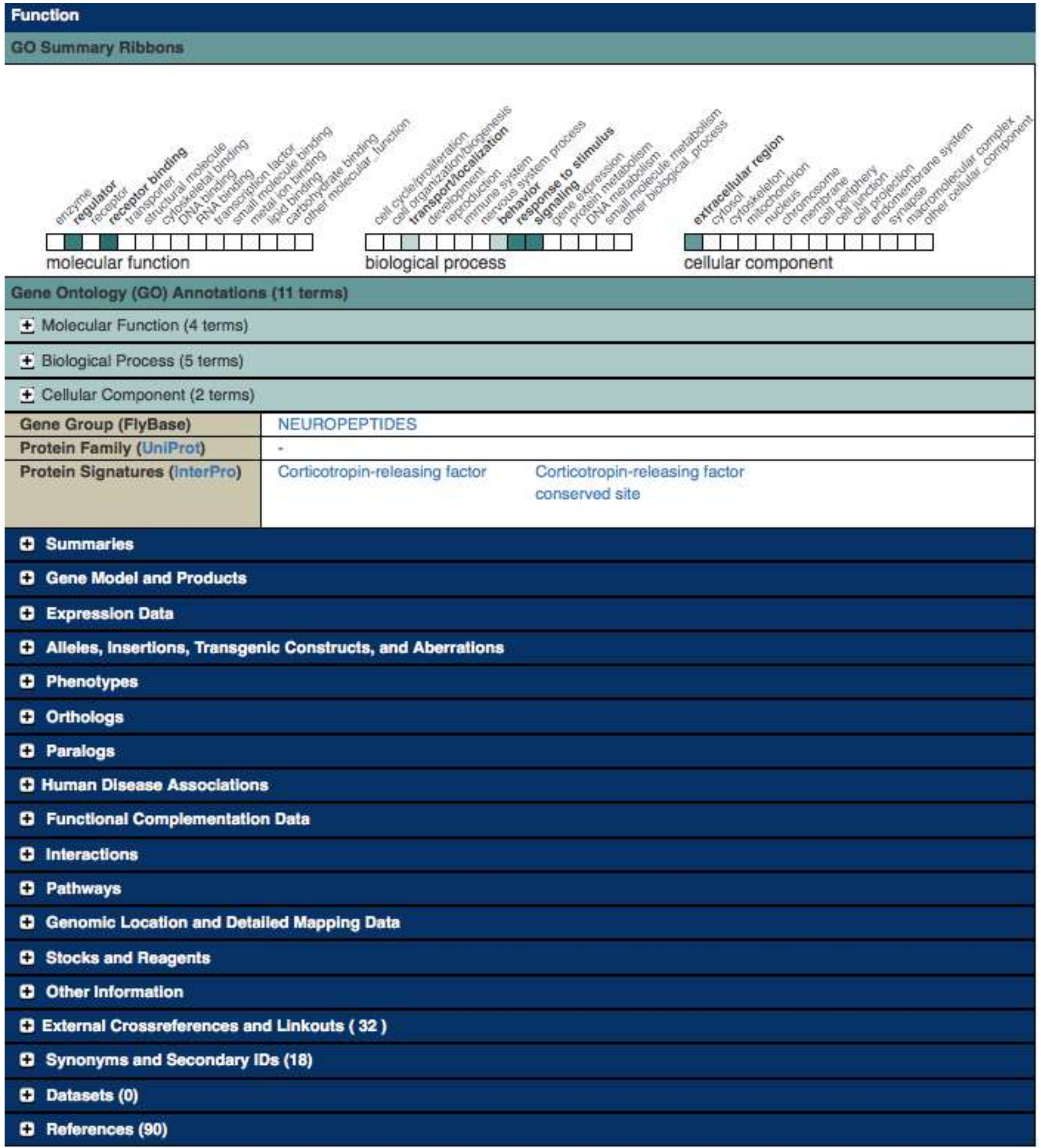
| | | | |
|---|---|---|---|
| **Symbol** | Dmel\Dh44 | **Species** | *D. melanogaster* |
| **Name** | Diuretic hormone 44 | **Annotation Symbol** | CG8348 |
| **Feature Type** | protein_coding_gene | **FlyBase ID** | FBgn0012344 |
| **Gene Model Status** | Current | **Stock Availability** | 11 publicly available |

| | |
|---|---|
| **Gene Summary** | Exhibits G protein-coupled receptor binding activity. Involved in several processes, including body fluid secretion; hormone-mediated signaling pathway; and locomotor rhythm. Predicted to localize to extracellular space. Is expressed in central nervous system; embryonic abdominal segment; peptidergic neurons; and ventral midline of embryo. (Alliance, FBgn0012344 )<br>Contribute a Gene Snapshot for this gene. |
| **All Summaries** | Alliance<br>Auto summary<br>Gene Group<br>Interactive Fly |
| **Also Known As** | Dh, DH$_{44}$, Drm-DH, Diuretic hormone, CRF-like peptide |
| **Key Links** | ALLIANCE of GENOME RESOURCES<br>NCBI<br>Ensembl<br>UniProt |

**Genomic Location**

| | | | |
|---|---|---|---|
| **Cytogenetic map** | 85E2-85E2 | **Sequence location** | 3R:9,638,182..9,650,706 [+] |
| **Recombination map** | 3-49 | **RefSeq locus** | NT_033777<br>REGION:9638182..9650706 |

| | |
|---|---|
| **Sequence** | Gene region<br>Get Decorated FASTA<br>Get Sequence |
| **Genomic Maps** | JBrowse<br>GBrowse<br>Help me choose |
| **Other Genome Views** | The following external sites may use different assemblies or annotations than FlyBase.<br>NCBI<br>UCSC<br>Ensembl<br>PopFly |



**Function**

**GO Summary Ribbons**

**Gene Ontology (GO) Annotations (11 terms)**

- Molecular Function (4 terms)
- Biological Process (5 terms)
- Cellular Component (2 terms)

| | | |
|---|---|---|
| **Gene Group (FlyBase)** | NEUROPEPTIDES | |
| **Protein Family (UniProt)** | - | |
| **Protein Signatures (InterPro)** | Corticotropin-releasing factor | Corticotropin-releasing factor conserved site |

- **Summaries**
- **Gene Model and Products**
- **Expression Data**
- **Alleles, Insertions, Transgenic Constructs, and Aberrations**
- **Phenotypes**
- **Orthologs**
- **Paralogs**
- **Human Disease Associations**
- **Functional Complementation Data**
- **Interactions**
- **Pathways**
- **Genomic Location and Detailed Mapping Data**
- **Stocks and Reagents**
- **Other Information**
- **External Crossreferences and Linkouts ( 32 )**
- **Synonyms and Secondary IDs (18)**
- **Datasets (0)**
- **References (90)**

# Thank you！

# Genomic Search Tools and Browsers

Chen jie

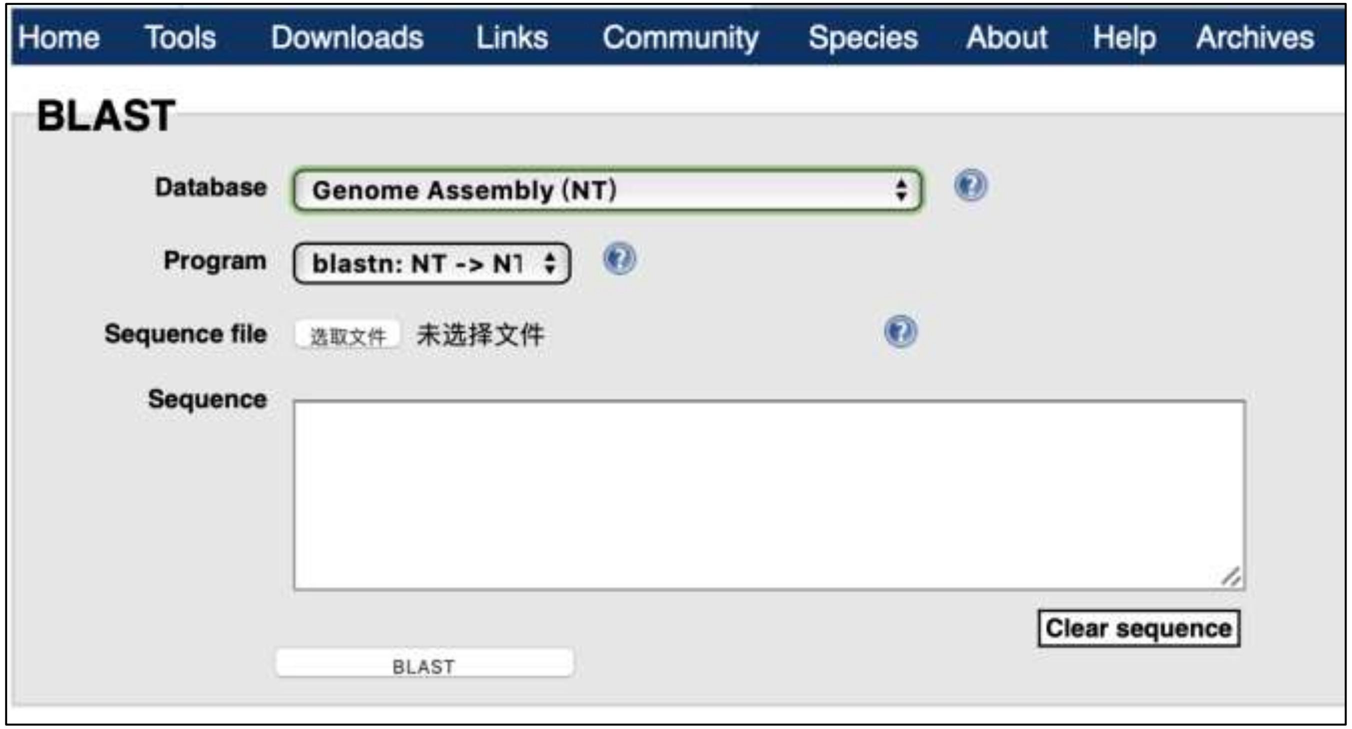
Genomic Search Tools and Browsers

- BLAST
- Gbrowse and JBrowse
- Chromosome Maps
- CytoSearch
- Coordinate Converter
- Feature Mapper
- Sequence Downloader

# BLAST

BLAST : Basic Local Alignment Search Tool

provides a method for rapid searching of nucleotide and protein databases



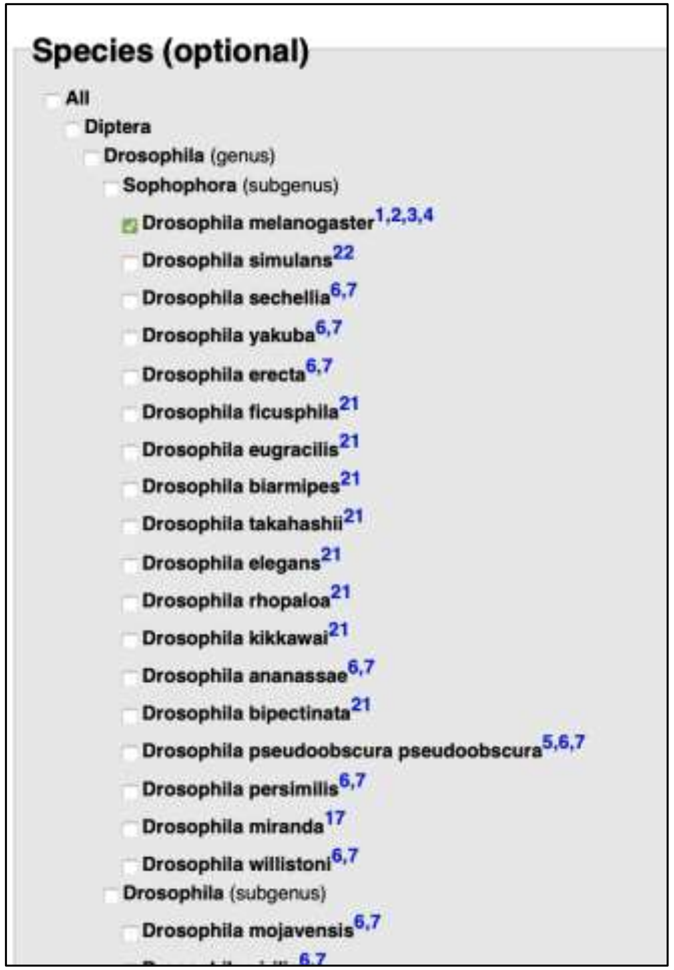
**BLAST**

Database: Genome Assembly (NT)

Program: blastn: NT -> NT

Sequence file: 选取文件 未选择文件

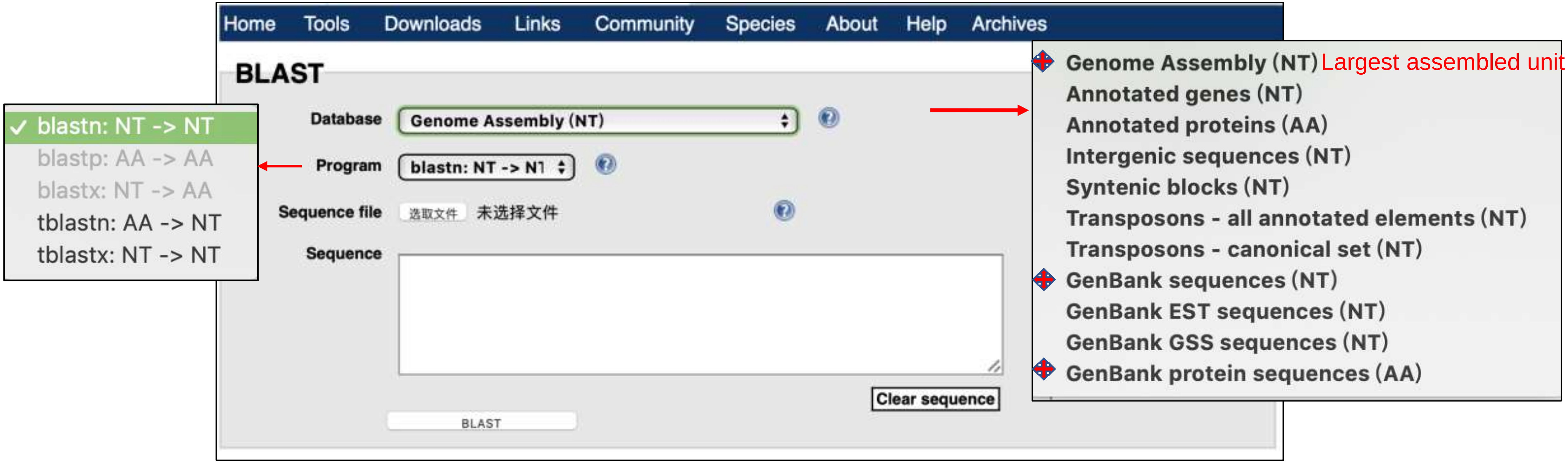
Sequence



**Species (optional)**

- ☐ All
  - ☐ Diptera
    - ☐ Drosophila (genus)
      - ☐ Sophophora (subgenus)
        - ☑ Drosophila melanogaster$^{1,2,3,4}$
        - ☐ Drosophila simulans$^{22}$
        - ☐ Drosophila sechellia$^{6,7}$
        - ☐ Drosophila yakuba$^{6,7}$
        - ☐ Drosophila erecta$^{6,7}$
        - ☐ Drosophila ficusphila$^{21}$
        - ☐ Drosophila eugracilis$^{21}$
        - ☐ Drosophila biarmipes$^{21}$
        - ☐ Drosophila takahashii$^{21}$
        - ☐ Drosophila elegans$^{21}$
        - ☐ Drosophila rhopaloa$^{21}$
        - ☐ Drosophila kikkawai$^{21}$
        - ☐ Drosophila ananassae$^{6,7}$
        - ☐ Drosophila bipectinata$^{21}$
        - ☐ Drosophila pseudoobscura pseudoobscura$^{5,6,7}$
        - ☐ Drosophila persimilis$^{6,7}$
        - ☐ Drosophila miranda$^{17}$
        - ☐ Drosophila willistoni$^{6,7}$
      - ☐ Drosophila (subgenus)
        - ☐ Drosophila mojavensis$^{6,7}$

# BLAST



Database: Genome Assembly (NT)

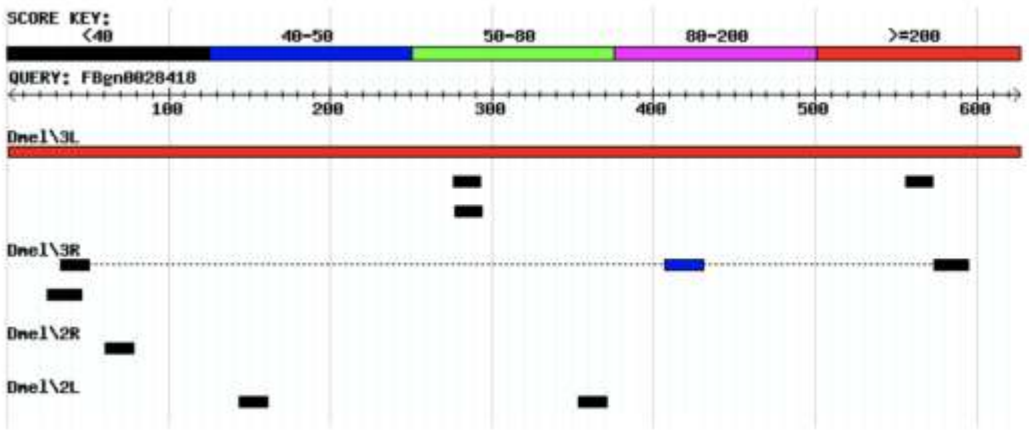
Program: blastn: NT -> NT

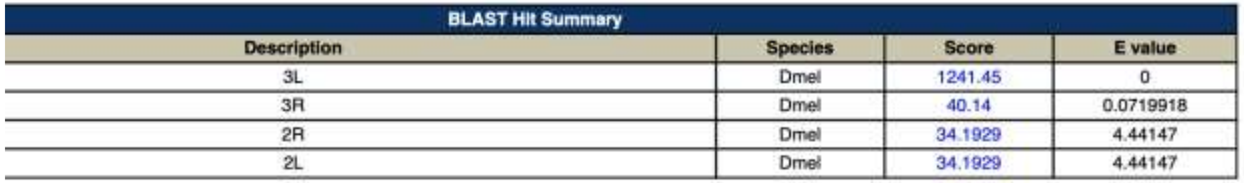
Sequence file: 选取文件 未选择文件

Largest assembled unit

# BLAST

## Genome assembly

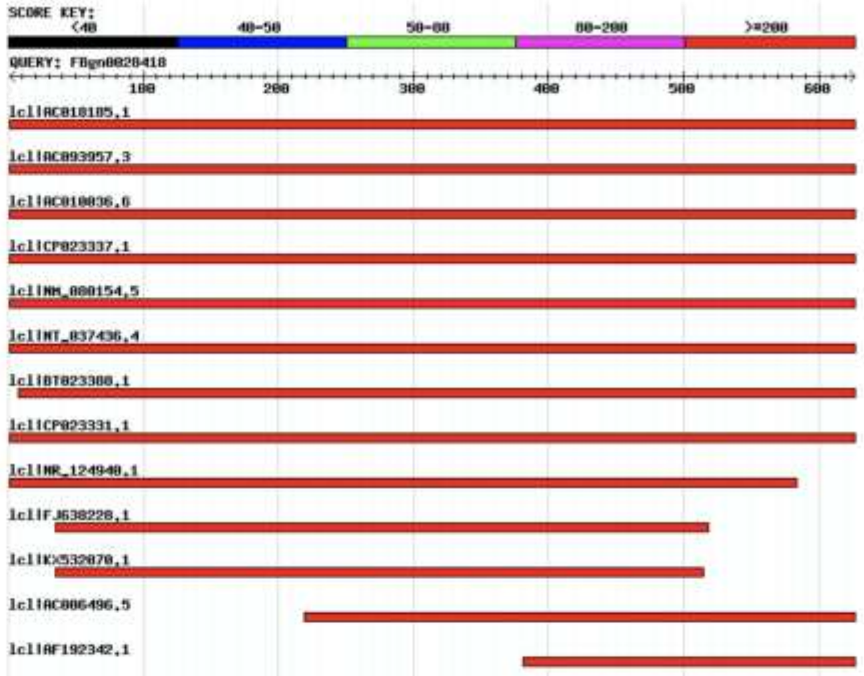


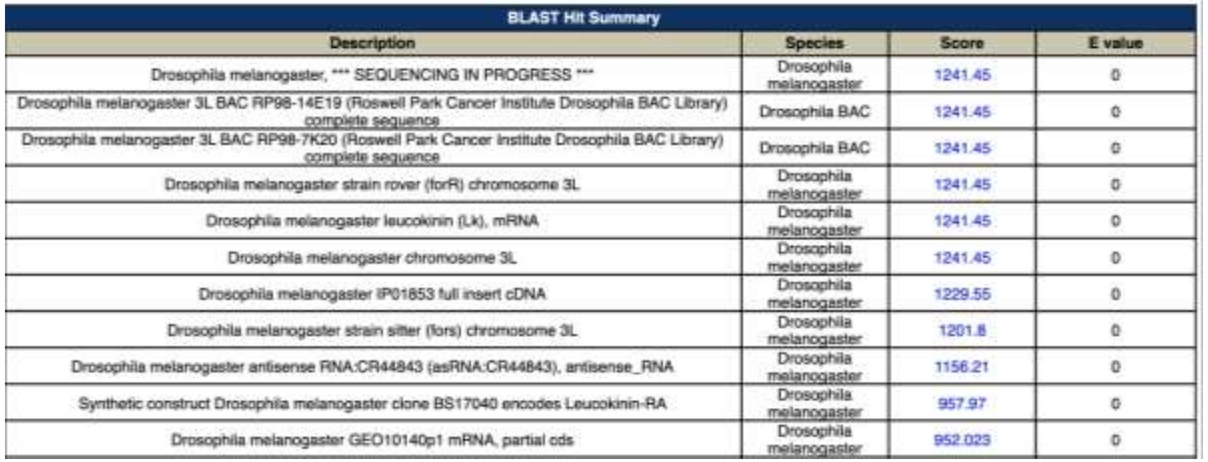


BLAST Hit Summary

| Description | Species | Score | E value |
|---|---|---|---|
| 3L | Dmel | 1241.45 | 0 |
| 3R | Dmel | 40.14 | 0.0719918 |
| 2R | Dmel | 34.1929 | 4.44147 |
| 2L | Dmel | 34.1929 | 4.44147 |

## GenBank





BLAST Hit Summary

| Description | Species | Score | E value |
|---|---|---|---|
| Drosophila melanogaster, *** SEQUENCING IN PROGRESS *** | Drosophila melanogaster | 1241.45 | 0 |
| Drosophila melanogaster 3L BAC RP98-14E19 (Roswell Park Cancer Institute Drosophila BAC Library) complete sequence | Drosophila BAC | 1241.45 | 0 |
| Drosophila melanogaster 3L BAC RP98-7K20 (Roswell Park Cancer Institute Drosophila BAC Library) complete sequence | Drosophila BAC | 1241.45 | 0 |
| Drosophila melanogaster strain rover (forR) chromosome 3L | Drosophila melanogaster | 1241.45 | 0 |
| Drosophila melanogaster leucokinin (Lk), mRNA | Drosophila melanogaster | 1241.45 | 0 |
| Drosophila melanogaster chromosome 3L | Drosophila melanogaster | 1241.45 | 0 |
| Drosophila melanogaster IP01853 full insert cDNA | Drosophila melanogaster | 1229.55 | 0 |
| Drosophila melanogaster strain sitter (fors) chromosome 3L | Drosophila melanogaster | 1201.8 | 0 |
| Drosophila melanogaster antisense RNA:CR44843 (asRNA:CR44843), antisense_RNA | Drosophila melanogaster | 1156.21 | 0 |
| Synthetic construct Drosophila melanogaster clone BS17040 encodes Leucokinin-RA | Drosophila melanogaster | 957.97 | 0 |
| Drosophila melanogaster GEO10140p1 mRNA, partial cds | Drosophila melanogaster | 952.023 | 0 |

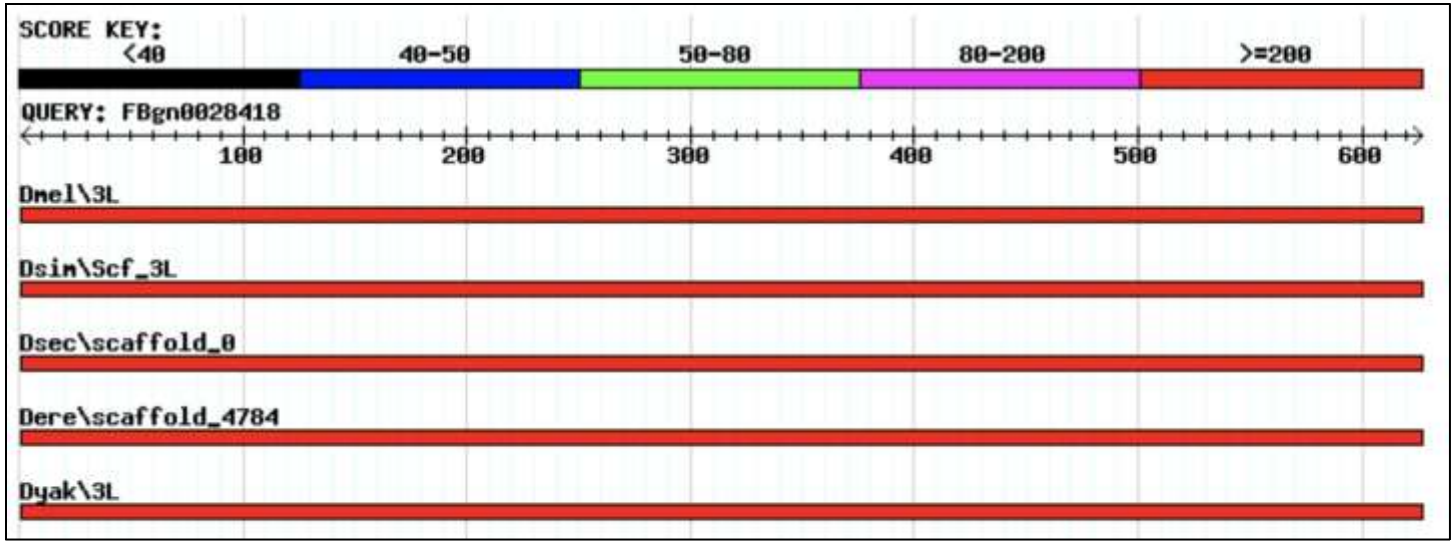
# BLAST

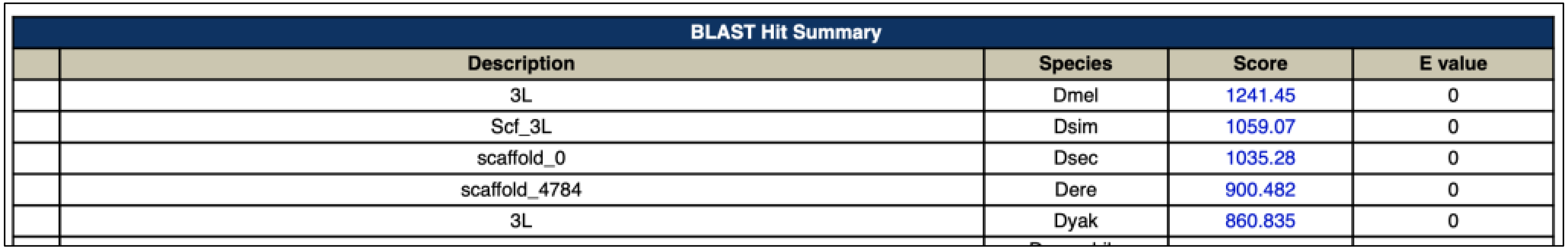
**Species (optional)**

- **All**
  - **Diptera** 双翅目
    - **Drosophila** (genus)
      - **Sophophora** (subgenus)
        - **Drosophila melanogaster**[1,2,3,4]
        - **Drosophila simulans**[22]
        - **Drosophila sechellia**[6,7]
        - **Drosophila yakuba**[6,7]
        - **Drosophila erecta**[6,7]
        - **Drosophila ficusphila**[21]
        - **Drosophila eugracilis**[21]
        - **Drosophila biarmipes**[21]
        - **Drosophila takahashii**[21]
        - **Drosophila elegans**[21]
        - **Drosophila rhopaloa**[21]
        - **Drosophila kikkawai**[21]
        - **Drosophila ananassae**[6,7]
        - **Drosophila bipectinata**[21]
        - **Drosophila pseudoobscura pseudoobscura**[5,6,7]
        - **Drosophila persimilis**[6,7]
        - **Drosophila miranda**[17]
        - **Drosophila willistoni**[6,7]
      - **Drosophila** (subgenus)
        - **Drosophila mojavensis**[6,7]
        - **Drosophila virilis**[6,7]
        - **Drosophila albomicans**[18]
        - **Drosophila grimshawi**[6,7]
    - **Musca domestica (House fly)**[19]
    - **Glossina morsitans morsitans (Tsetse fly)**[20]
    - **Culex quinquefasciatus (Southern house mosquito)**[6,7]
    - **Aedes aegypti (Yellow fever mosquito)**[13]
    - **Anopheles darlingi (American malaria mosquito)**[16]
    - **Anopheles gambiae (Malaria mosquito)**[11,12]
    - **Mayetiola destructor (Hessian fly)**[16]
  - **Lepidoptera** 鳞翅目
    - **Bombyx mori (silkworm)**[9,10]
    - **Danaus plexippus (Monarch butterfly)**[16]
  - **Coleoptera** 鞘翅目
    - **Tribolium castaneum (Red flour beetle)**[14]
  - **Hymenoptera** 膜翅目
    - **Nasonia giraulti (Parasitic wasp)**[16]
    - **Nasonia longicornis (Parasitic wasp)**[16]
    - **Nasonia vitripennis (Parasitic wasp)**[16]
    - **Apis mellifera (Western honey bee)**[8]
    - **Apis florea (Dwarf honey bee)**[16]
    - **Bombus impatiens (Common eastern bumblebee)**[16]
    - **Bombus terrestris (Buff-tailed bumblebee)**[16]
    - **Megachile rotundata (Alfalfa leafcutter bee)**[16]
    - **Acromyrmex echinatior (Panamanian leafcutter ant)**[16]
    - **Atta cephalotes (Leafcutter ant)**[16]
    - **Camponotus floridanus (Florida carpenter ant)**[16]
    - **Harpegnathos saltator (Jerdon's jumping ant)**[16]
    - **Linepithema humile (Argentine ant)**[16]
    - **Pogonomyrmex barbatus (Red harvester ant)**[16]
    - **Solenopsis invicta (Red fire ant)**[16]
  - **Hemiptera** 半翅目
    - **Acyrthosiphon pisum (Pea aphid)**[16]
    - **Rhodnius prolixus (Kissing bug)**[16]
  - **Phthiraptera** 虱目
    - **Pediculus humanus corporis (Human body louse)**[16]
  - **Ixodida** 真蜱目
    - **Ixodes scapularis (Deer tick)**[16]
    - **Rhipicephalus microplus (Southern cattle tick)**[16]

49 different arthropod genomes

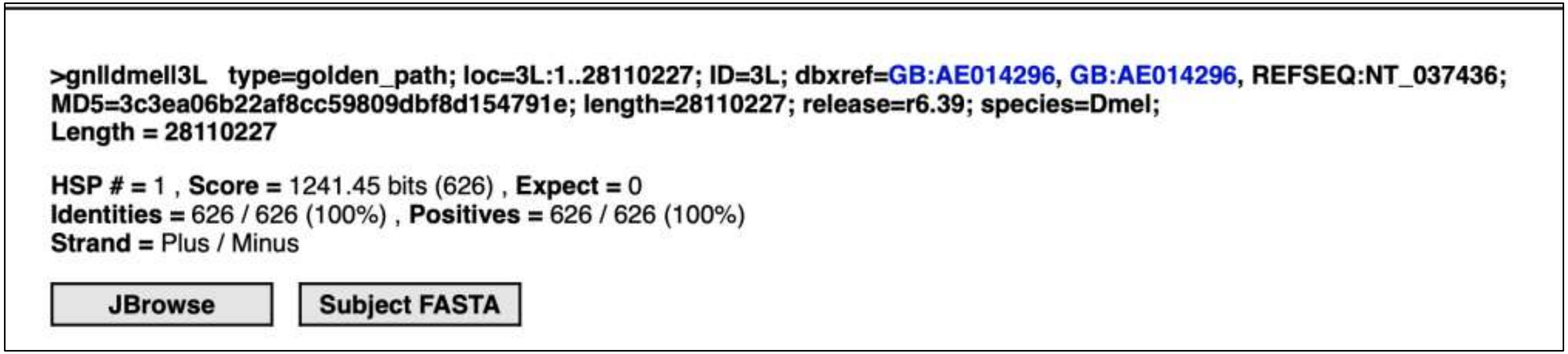
# BLAST





BLAST Hit Summary

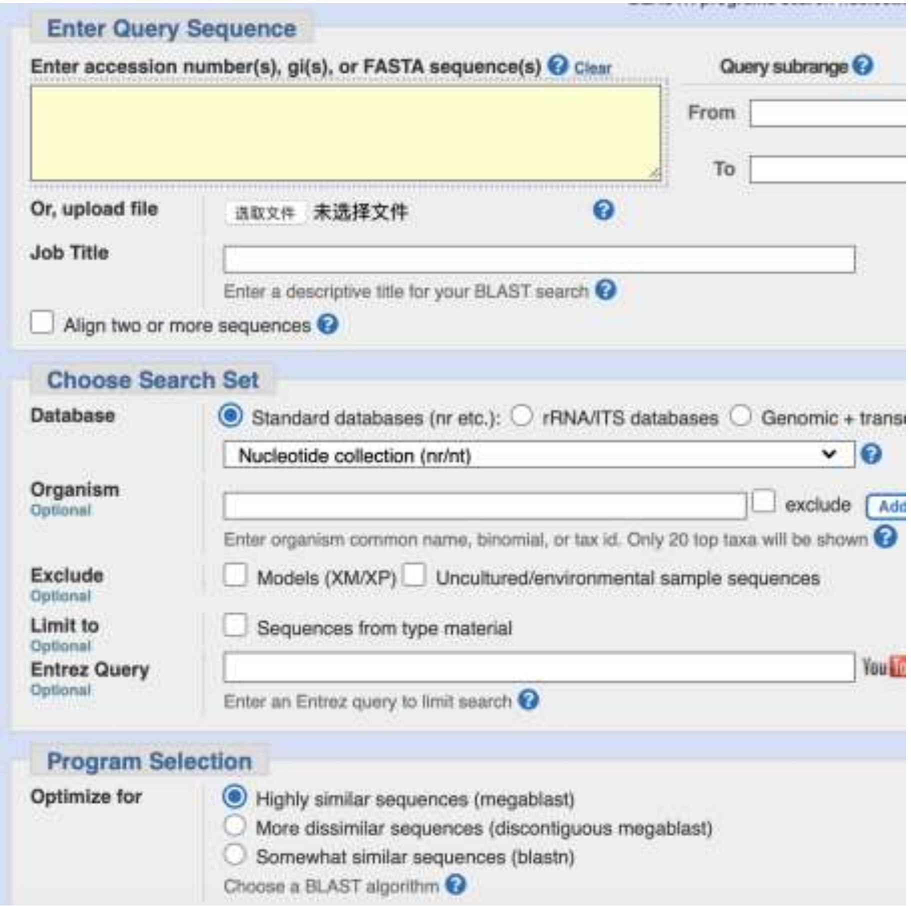
| | Description | Species | Score | E value |
|---|---|---|---|---|
| | 3L | Dmel | 1241.45 | 0 |
| | Scf_3L | Dsim | 1059.07 | 0 |
| | scaffold_0 | Dsec | 1035.28 | 0 |
| | scaffold_4784 | Dere | 900.482 | 0 |
| | 3L | Dyak | 860.835 | 0 |



**>gnl|dmel|3L type=golden_path; loc=3L:1..28110227; ID=3L; dbxref=GB:AE014296, GB:AE014296, REFSEQ:NT_037436; MD5=3c3ea06b22af8cc59809dbf8d154791e; length=28110227; release=r6.39; species=Dmel;**
**Length = 28110227**

**HSP # =** 1 , **Score =** 1241.45 bits (626) , **Expect =** 0
**Identities =** 626 / 626 (100%) , **Positives =** 626 / 626 (100%)
**Strand =** Plus / Minus

# NCBI Blast



**Enter Query Sequence**

Enter accession number(s), gi(s), or FASTA sequence(s) Clear

Query subrange: From ☐ To ☐

Or, upload file: 选取文件 未选择文件

Job Title: Enter a descriptive title for your BLAST search

☐ Align two or more sequences

**Choose Search Set**

Database: ● Standard databases (nr etc.): ○ rRNA/ITS databases ○ Genomic + trans

Nucleotide collection (nr/nt)

Organism (Optional): ☐ exclude

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown

Exclude (Optional): ☐ Models (XM/XP) ☐ Uncultured/environmental sample sequences

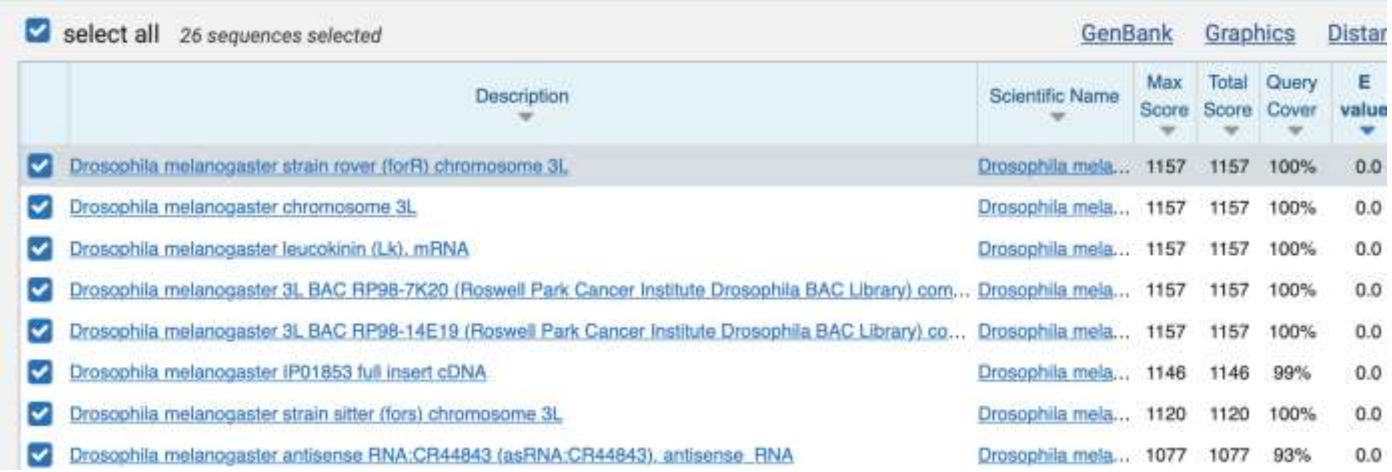
Limit to (Optional): ☐ Sequences from type material

Entrez Query (Optional): Enter an Entrez query to limit search

**Program Selection**

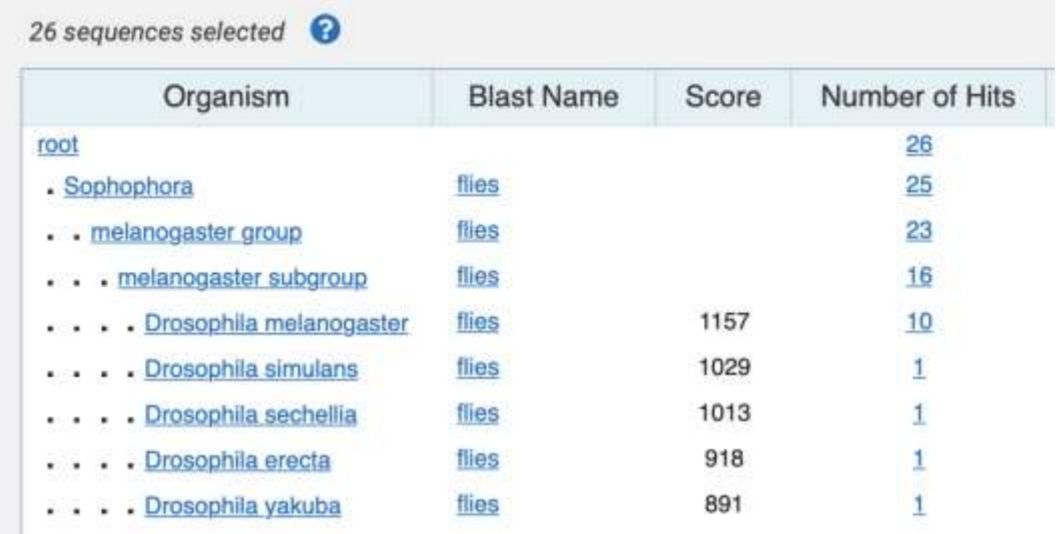
Optimize for:
- ● Highly similar sequences (megablast)
- ○ More dissimilar sequences (discontiguous megablast)
- ○ Somewhat similar sequences (blastn)

Choose a BLAST algorithm



☑ select all *26 sequences selected*

| | Description | Scientific Name | Max Score | Total Score | Query Cover | E value |
|---|---|---|---|---|---|---|
| ☑ | Drosophila melanogaster strain rover (forR) chromosome 3L | Drosophila mela... | 1157 | 1157 | 100% | 0.0 |
| ☑ | Drosophila melanogaster chromosome 3L | Drosophila mela... | 1157 | 1157 | 100% | 0.0 |
| ☑ | Drosophila melanogaster leucokinin (Lk), mRNA | Drosophila mela... | 1157 | 1157 | 100% | 0.0 |
| ☑ | Drosophila melanogaster 3L BAC RP98-7K20 (Roswell Park Cancer Institute Drosophila BAC Library) com... | Drosophila mela... | 1157 | 1157 | 100% | 0.0 |
| ☑ | Drosophila melanogaster 3L BAC RP98-14E19 (Roswell Park Cancer Institute Drosophila BAC Library) co... | Drosophila mela... | 1157 | 1157 | 100% | 0.0 |
| ☑ | Drosophila melanogaster IP01853 full insert cDNA | Drosophila mela... | 1146 | 1146 | 99% | 0.0 |
| ☑ | Drosophila melanogaster strain sitter (fors) chromosome 3L | Drosophila mela... | 1120 | 1120 | 100% | 0.0 |
| ☑ | Drosophila melanogaster antisense RNA:CR44843 (asRNA:CR44843), antisense_RNA | Drosophila mela... | 1077 | 1077 | 93% | 0.0 |

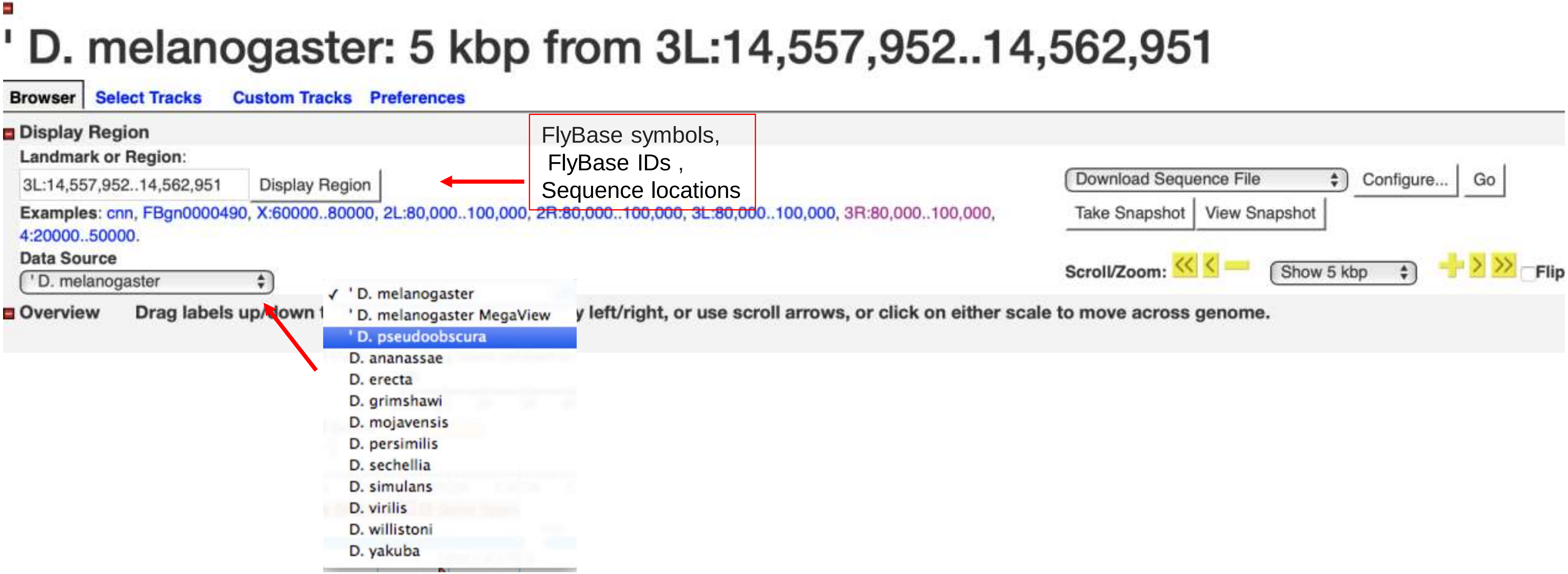


*26 sequences selected*

| Organism | Blast Name | Score | Number of Hits |
|---|---|---|---|
| root | | | 26 |
| . Sophophora | flies | | 25 |
| . . melanogaster group | flies | | 23 |
| . . . melanogaster subgroup | flies | | 16 |
| . . . . Drosophila melanogaster | flies | 1157 | 10 |
| . . . . Drosophila simulans | flies | 1029 | 1 |
| . . . . Drosophila sechellia | flies | 1013 | 1 |
| . . . . Drosophila erecta | flies | 918 | 1 |
| . . . . Drosophila yakuba | flies | 891 | 1 |

# Gbrowse

GBrowse is a GMOD tool that displays features of the genome aligned to the genomic sequence. By default, FlyBase presents a view of D. melanogaster that displays gene models, transcript and polypeptide data, natural transposon insertion sites, cDNAs and many additional tracks.



FlyBase symbols,
FlyBase IDs ,
Sequence locations

' D. melanogaster: 5 kbp from 3L:14,557,952..14,562,951

**Display Region**

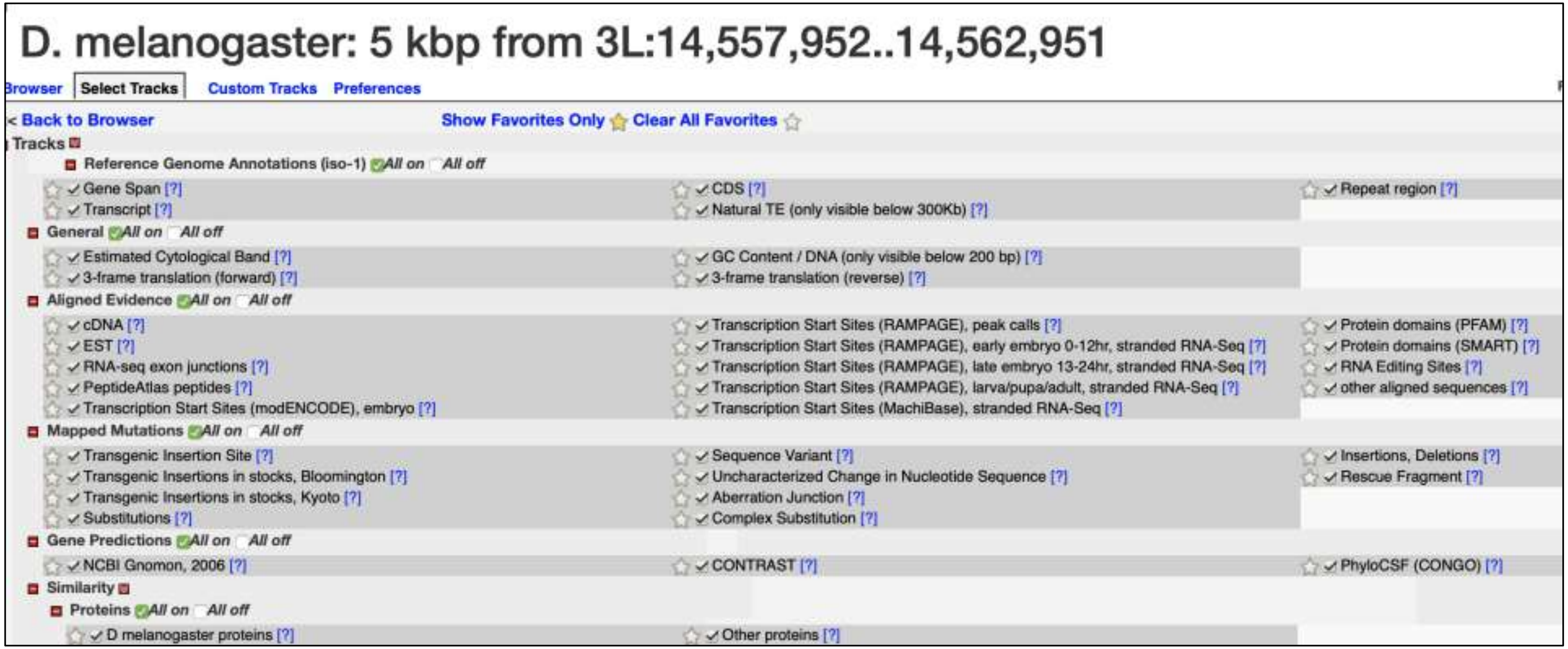
Landmark or Region: 3L:14,557,952..14,562,951

Examples: cnn, FBgn0000490, X:60000..80000, 2L:80,000..100,000, 2R:80,000..100,000, 3L:80,000..100,000, 3R:80,000..100,000, 4:20000..50000.

Data Source: ' D. melanogaster

**Overview** Drag labels up/down t… y left/right, or use scroll arrows, or click on either scale to move across genome.

# Gbrowse



## D. melanogaster: 5 kbp from 3L:14,557,952..14,562,951

Tracks

Reference Genome Annotations (iso-1) ☑ All on ☐ All off

- ☆ ✓ Gene Span [?]
- ☆ ✓ Transcript [?]
- ☆ ✓ CDS [?]
- ☆ ✓ Natural TE (only visible below 300Kb) [?]
- ☆ ✓ Repeat region [?]

General ☑ All on ☐ All off

- ☆ ✓ Estimated Cytological Band [?]
- ☆ ✓ 3-frame translation (forward) [?]
- ☆ ✓ GC Content / DNA (only visible below 200 bp) [?]
- ☆ ✓ 3-frame translation (reverse) [?]

Aligned Evidence ☑ All on ☐ All off

- ☆ ✓ cDNA [?]
- ☆ ✓ EST [?]
- ☆ ✓ RNA-seq exon junctions [?]
- ☆ ✓ PeptideAtlas peptides [?]
- ☆ ✓ Transcription Start Sites (modENCODE), embryo [?]
- ☆ ✓ Transcription Start Sites (RAMPAGE), peak calls [?]
- ☆ ✓ Transcription Start Sites (RAMPAGE), early embryo 0-12hr, stranded RNA-Seq [?]
- ☆ ✓ Transcription Start Sites (RAMPAGE), late embryo 13-24hr, stranded RNA-Seq [?]
- ☆ ✓ Transcription Start Sites (RAMPAGE), larva/pupa/adult, stranded RNA-Seq [?]
- ☆ ✓ Transcription Start Sites (MachiBase), stranded RNA-Seq [?]
- ☆ ✓ Protein domains (PFAM) [?]
- ☆ ✓ Protein domains (SMART) [?]
- ☆ ✓ RNA Editing Sites [?]
- ☆ ✓ other aligned sequences [?]

Mapped Mutations ☑ All on ☐ All off

- ☆ ✓ Transgenic Insertion Site [?]
- ☆ ✓ Transgenic Insertions in stocks, Bloomington [?]
- ☆ ✓ Transgenic Insertions in stocks, Kyoto [?]
- ☆ ✓ Substitutions [?]
- ☆ ✓ Sequence Variant [?]
- ☆ ✓ Uncharacterized Change in Nucleotide Sequence [?]
- ☆ ✓ Aberration Junction [?]
- ☆ ✓ Complex Substitution [?]
- ☆ ✓ Insertions, Deletions [?]
- ☆ ✓ Rescue Fragment [?]

Gene Predictions ☑ All on ☐ All off

- ☆ ✓ NCBI Gnomon, 2006 [?]
- ☆ ✓ CONTRAST [?]
- ☆ ✓ PhyloCSF (CONGO) [?]

Similarity

Proteins ☑ All on ☐ All off

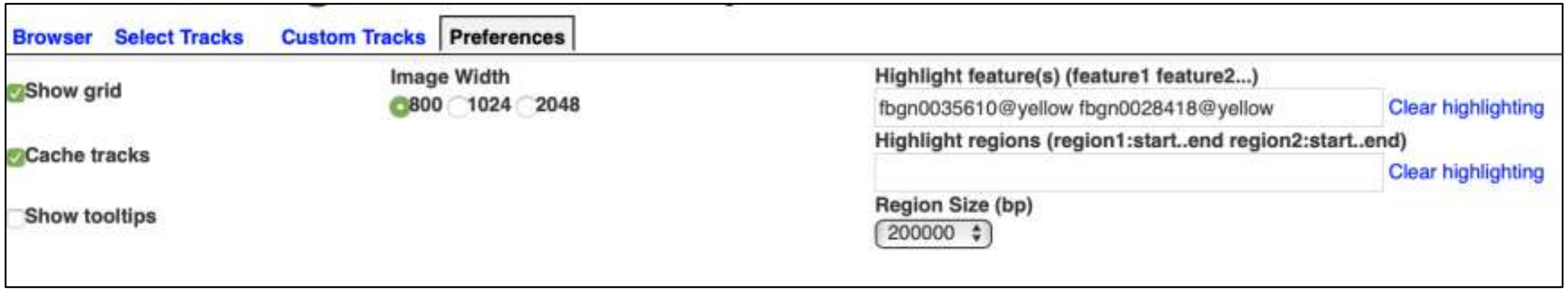
- ☆ ✓ D melanogaster proteins [?]
- ☆ ✓ Other proteins [?]

## Custom Tracks

*[Help with uploading custom tracks]*

There are no tracks yet.

**Add custom tracks :** [From text] [From a URL] [From a file]



☑ Show grid

☑ Cache tracks

☐ Show tooltips

Image Width
● 800 ○ 1024 ○ 2048

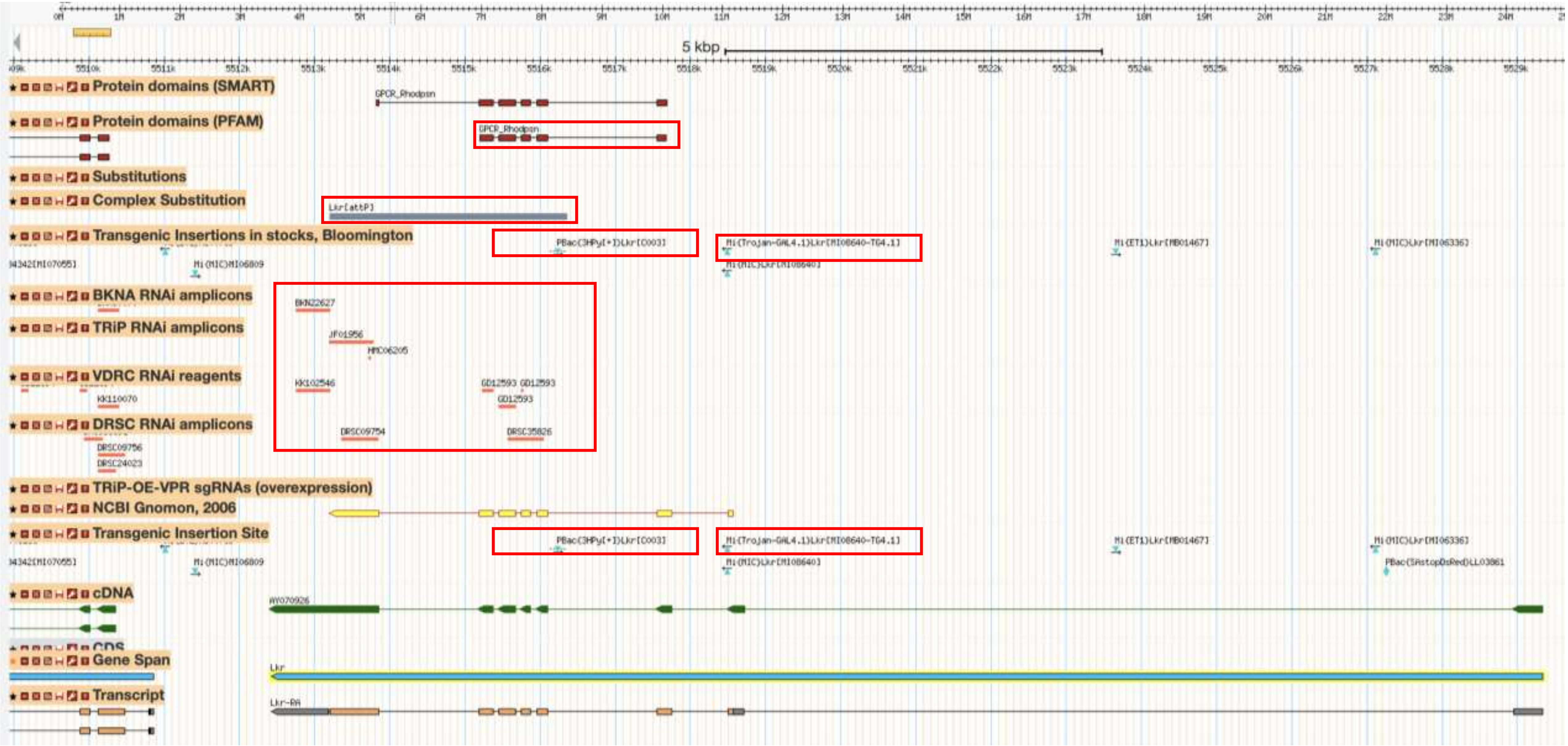
Highlight feature(s) (feature1 feature2...)
fbgn0035610@yellow fbgn0028418@yellow

Highlight regions (region1:start..end region2:start..end)

Region Size (bp)
200000

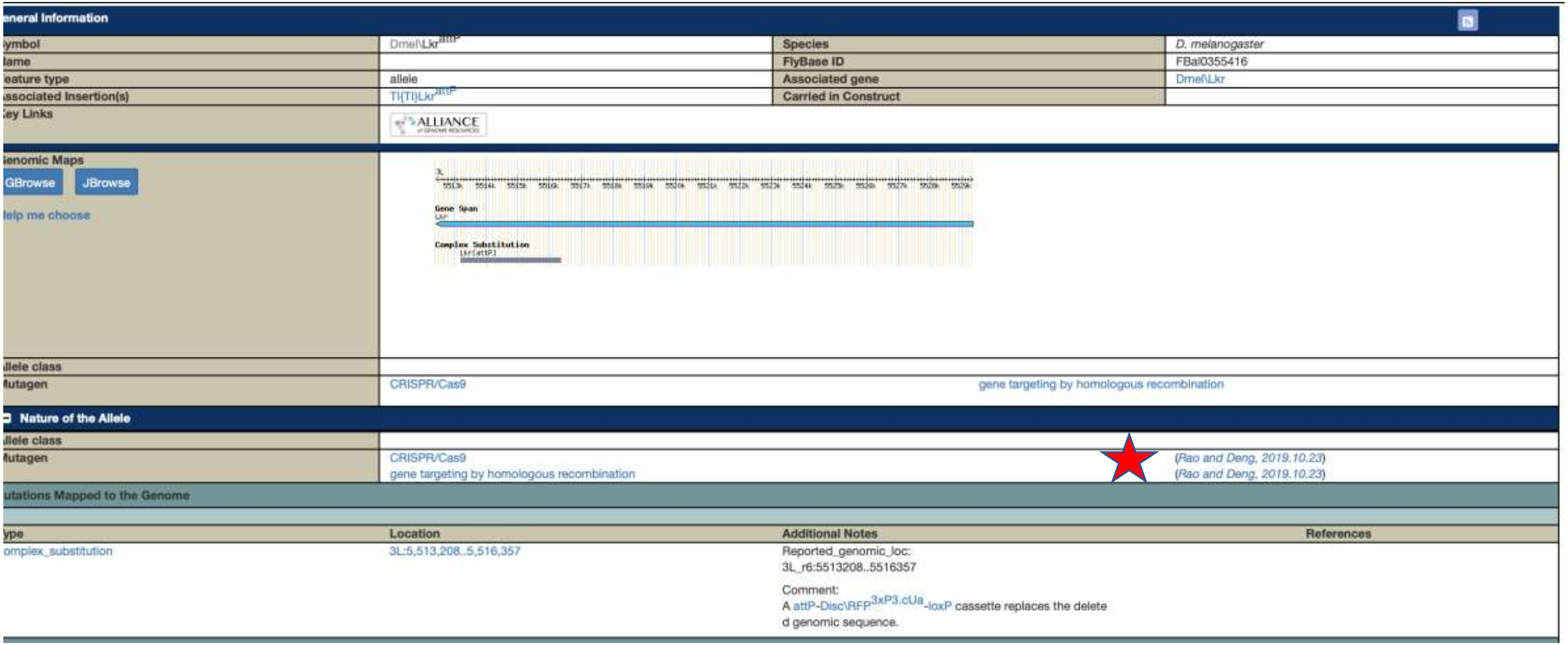
**Example**

# Gbrowse of Lkr



**Example**

# Gbrowse of Lkr



**eneral Information**

| | | | |
|---|---|---|---|
| **ymbol** | Dmel\Lkr$^{attP}$ | **Species** | *D. melanogaster* |
| **lame** | | **FlyBase ID** | FBal0355416 |
| **eature type** | allele | **Associated gene** | Dmel\Lkr |
| **ssociated Insertion(s)** | TI{TI}Lkr$^{attP}$ | **Carried in Construct** | |
| **ey Links** | ALLIANCE | | |
| **enomic Maps**<br>GBrowse JBrowse<br>elp me choose | | | |
| **llele class** | | | |
| **utagen** | CRISPR/Cas9 | gene targeting by homologous recombination | |

**Nature of the Allele**

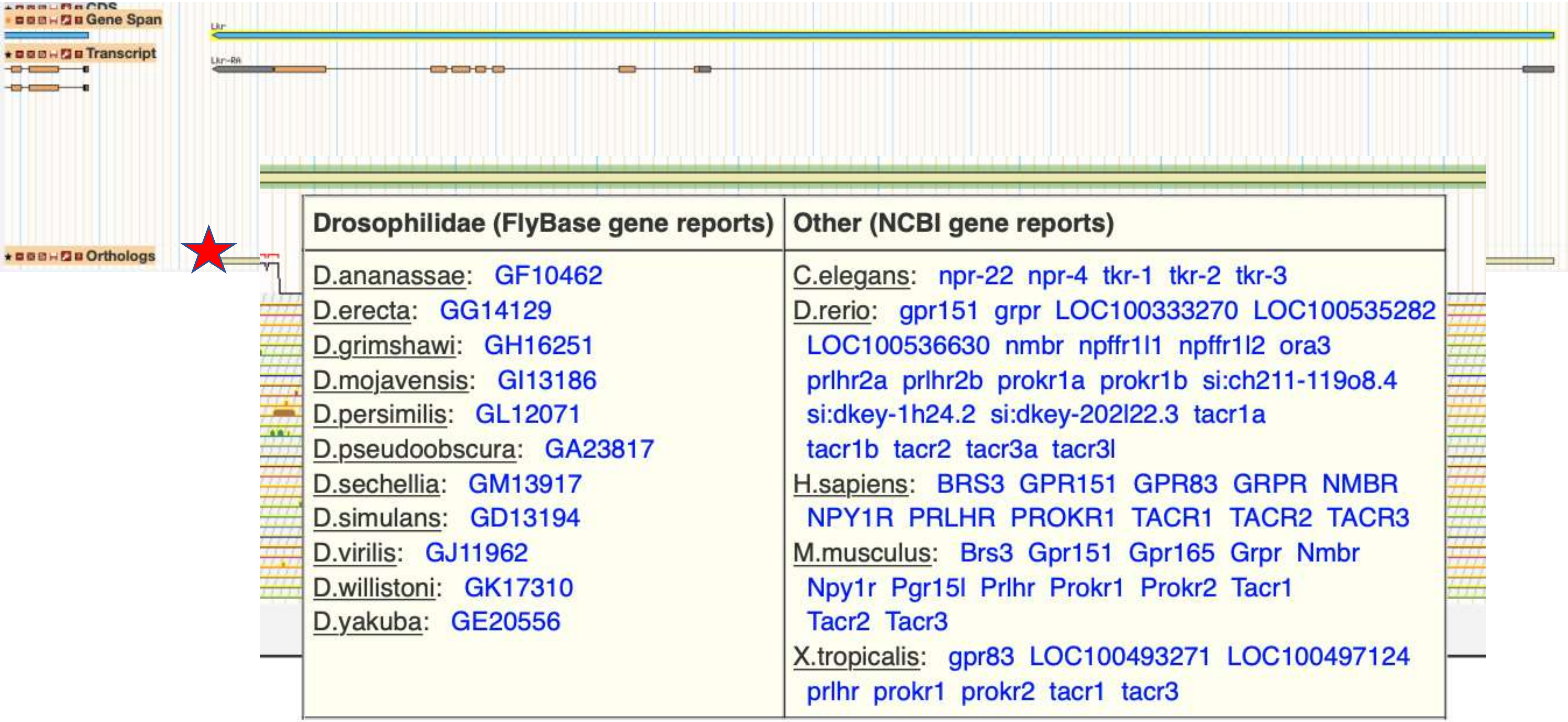
| | | |
|---|---|---|
| **llele class** | | |
| **utagen** | CRISPR/Cas9<br>gene targeting by homologous recombination | (*Rao and Deng, 2019.10.23*)<br>(*Rao and Deng, 2019.10.23*) |

**utations Mapped to the Genome**

| **ype** | **Location** | **Additional Notes** | **References** |
|---|---|---|---|
| omplex_substitution | 3L:5,513,208..5,516,357 | Reported_genomic_loc:<br>3L_r6:5513208..5516357<br>Comment:<br>A attP-Disc\RFP$^{3xP3.cUa}$-loxP cassette replaces the delete d genomic sequence. | |

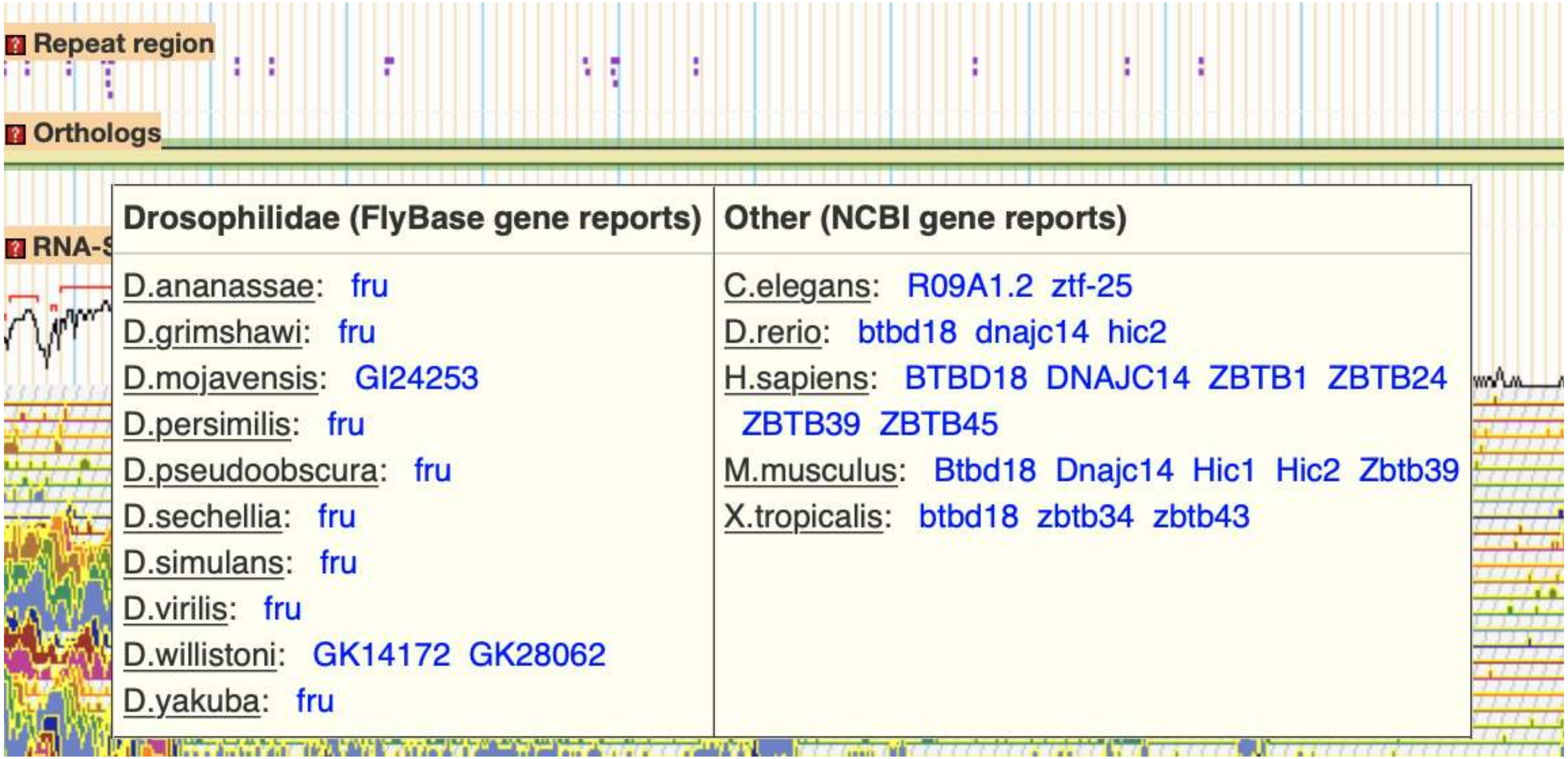
Example

# Finding orthologs using GBrowse



| Drosophilidae (FlyBase gene reports) | Other (NCBI gene reports) |
|---|---|
| D.ananassae: GF10462<br>D.erecta: GG14129<br>D.grimshawi: GH16251<br>D.mojavensis: GI13186<br>D.persimilis: GL12071<br>D.pseudoobscura: GA23817<br>D.sechellia: GM13917<br>D.simulans: GD13194<br>D.virilis: GJ11962<br>D.willistoni: GK17310<br>D.yakuba: GE20556 | C.elegans: npr-22 npr-4 tkr-1 tkr-2 tkr-3<br>D.rerio: gpr151 grpr LOC100333270 LOC100535282 LOC100536630 nmbr npffr1l1 npffr1l2 ora3 prlhr2a prlhr2b prokr1a prokr1b si:ch211-119o8.4 si:dkey-1h24.2 si:dkey-202l22.3 tacr1a tacr1b tacr2 tacr3a tacr3l<br>H.sapiens: BRS3 GPR151 GPR83 GRPR NMBR NPY1R PRLHR PROKR1 TACR1 TACR2 TACR3<br>M.musculus: Brs3 Gpr151 Gpr165 Grpr Nmbr Npy1r Pgr15l Prlhr Prokr1 Prokr2 Tacr1 Tacr2 Tacr3<br>X.tropicalis: gpr83 LOC100493271 LOC100497124 prlhr prokr1 prokr2 tacr1 tacr3 |

# Gbrowse



**Drosophilidae (FlyBase gene reports)**

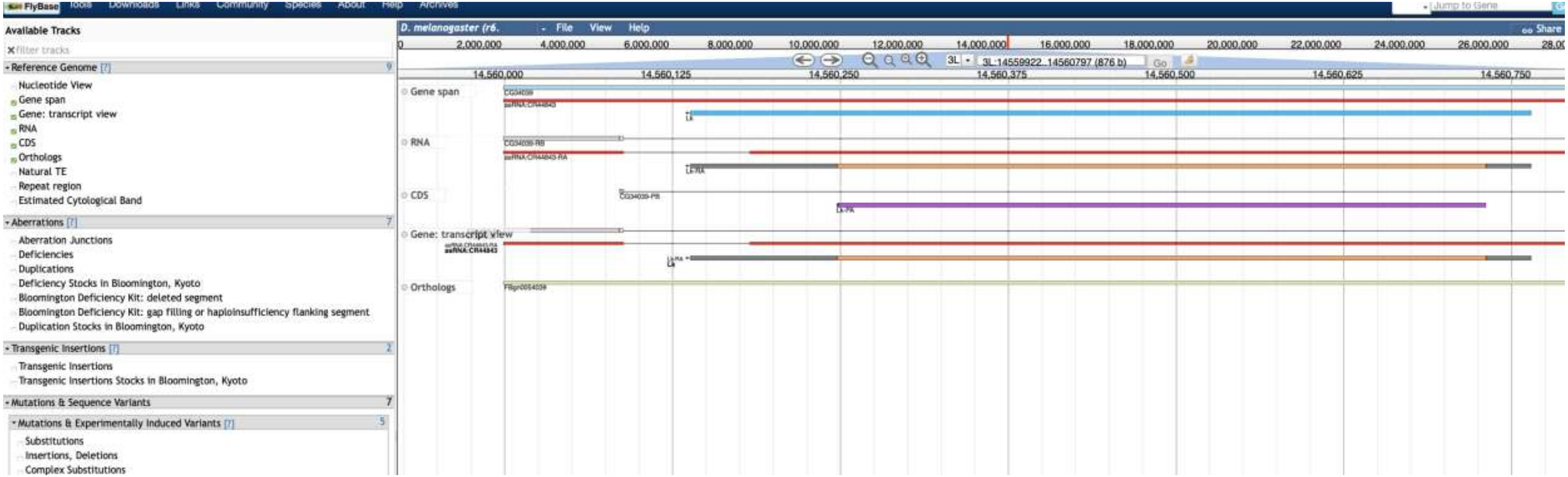
D.ananassae: fru
D.grimshawi: fru
D.mojavensis: GI24253
D.persimilis: fru
D.pseudoobscura: fru
D.sechellia: fru
D.simulans: fru
D.virilis: fru
D.willistoni: GK14172 GK28062
D.yakuba: fru

**Other (NCBI gene reports)**

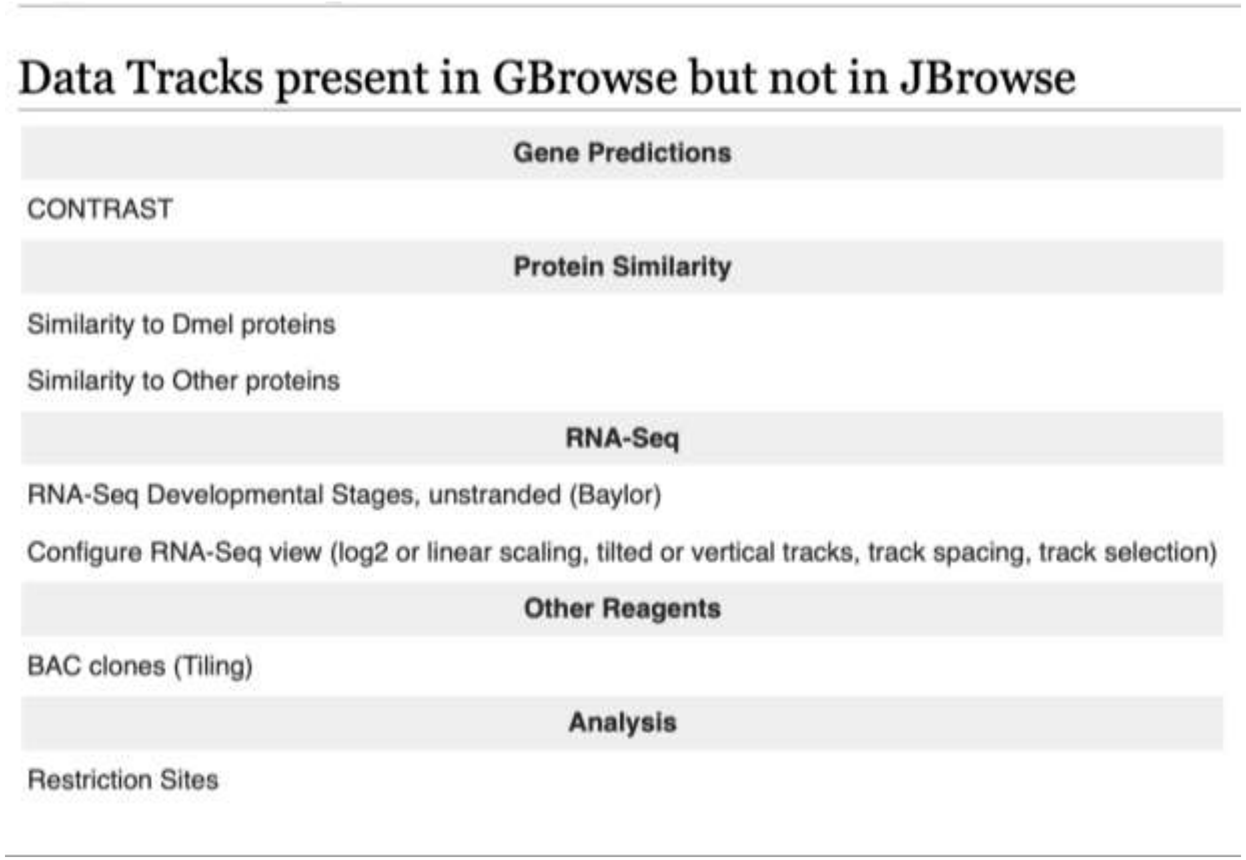
C.elegans: R09A1.2 ztf-25
D.rerio: btbd18 dnajc14 hic2
H.sapiens: BTBD18 DNAJC14 ZBTB1 ZBTB24 ZBTB39 ZBTB45
M.musculus: Btbd18 Dnajc14 Hic1 Hic2 Zbtb39
X.tropicalis: btbd18 zbtb34 zbtb43

# JBrowse

JBrowse was developed by the Generic Model Organism Database (GMOD) consortium to be the eventual successor to GBrowse



# FlyBase:Complete list of GBrowse/JBrowse Track Differences



## Data Tracks present in GBrowse but not in JBrowse

**Gene Predictions**

CONTRAST

**Protein Similarity**

Similarity to Dmel proteins

Similarity to Other proteins

**RNA-Seq**

RNA-Seq Developmental Stages, unstranded (Baylor)

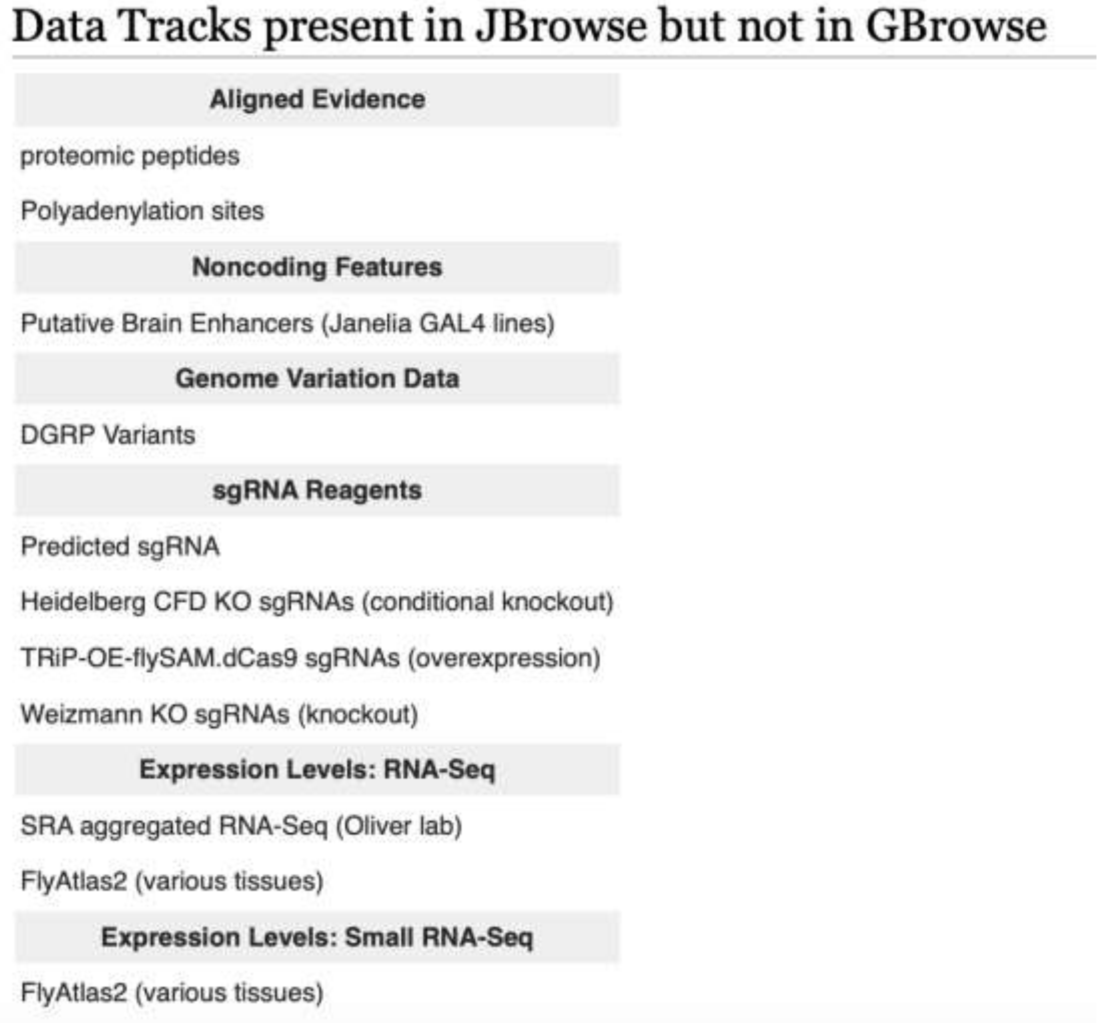
Configure RNA-Seq view (log2 or linear scaling, tilted or vertical tracks, track spacing, track selection)

**Other Reagents**

BAC clones (Tiling)

**Analysis**

Restriction Sites



## Data Tracks present in JBrowse but not in GBrowse

**Aligned Evidence**

proteomic peptides

Polyadenylation sites

**Noncoding Features**

Putative Brain Enhancers (Janelia GAL4 lines)

**Genome Variation Data**

DGRP Variants

**sgRNA Reagents**

Predicted sgRNA

Heidelberg CFD KO sgRNAs (conditional knockout)

TRiP-OE-flySAM.dCas9 sgRNAs (overexpression)

Weizmann KO sgRNAs (knockout)

**Expression Levels: RNA-Seq**

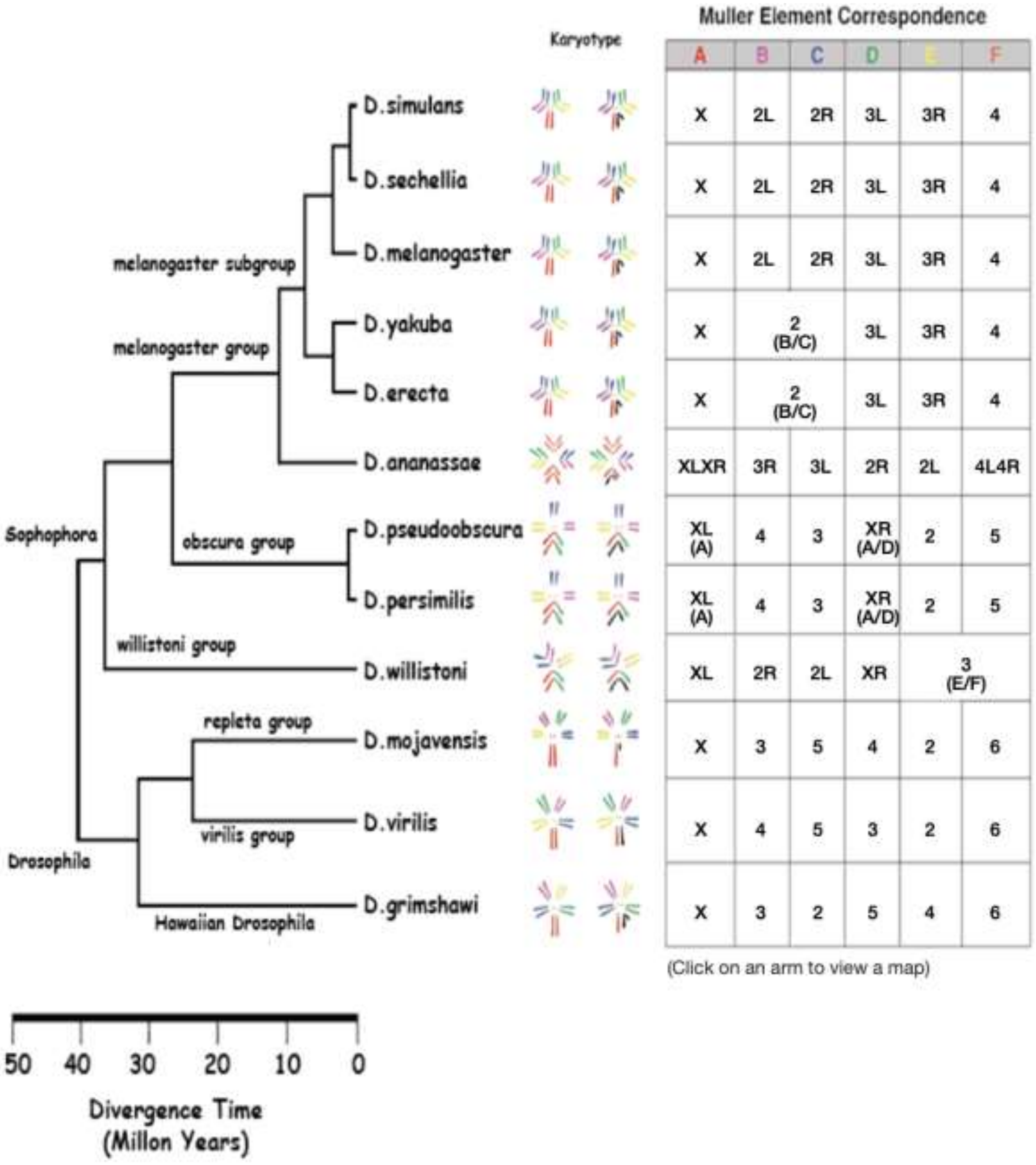
SRA aggregated RNA-Seq (Oliver lab)

FlyAtlas2 (various tissues)

**Expression Levels: Small RNA-Seq**

FlyAtlas2 (various tissues)

# Chromosome Maps

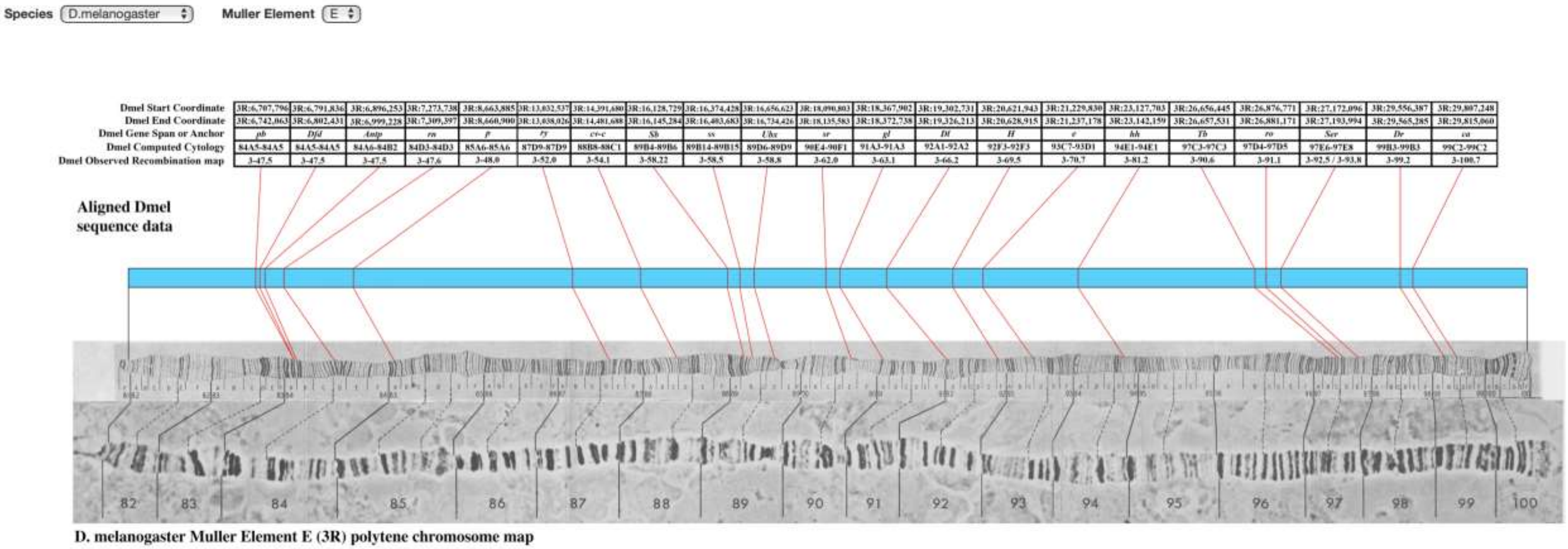


Muller Element Correspondence

| | A | B | C | D | E | F |
|---|---|---|---|---|---|---|
| D.simulans | X | 2L | 2R | 3L | 3R | 4 |
| D.sechellia | X | 2L | 2R | 3L | 3R | 4 |
| D.melanogaster | X | 2L | 2R | 3L | 3R | 4 |
| D.yakuba | X | 2<br>(B/C) | | 3L | 3R | 4 |
| D.erecta | X | 2<br>(B/C) | | 3L | 3R | 4 |
| D.ananassae | XLXR | 3R | 3L | 2R | 2L | 4L4R |
| D.pseudoobscura | XL<br>(A) | 4 | 3 | XR<br>(A/D) | 2 | 5 |
| D.persimilis | XL<br>(A) | 4 | 3 | XR<br>(A/D) | 2 | 5 |
| D.willistoni | XL | 2R | 2L | XR | 3<br>(E/F) | |
| D.mojavensis | X | 3 | 5 | 4 | 2 | 6 |
| D.virilis | X | 4 | 5 | 3 | 2 | 6 |
| D.grimshawi | X | 3 | 2 | 5 | 4 | 6 |

(Click on an arm to view a map)

# Chromosome Maps



**Species** D.melanogaster **Muller Element** E

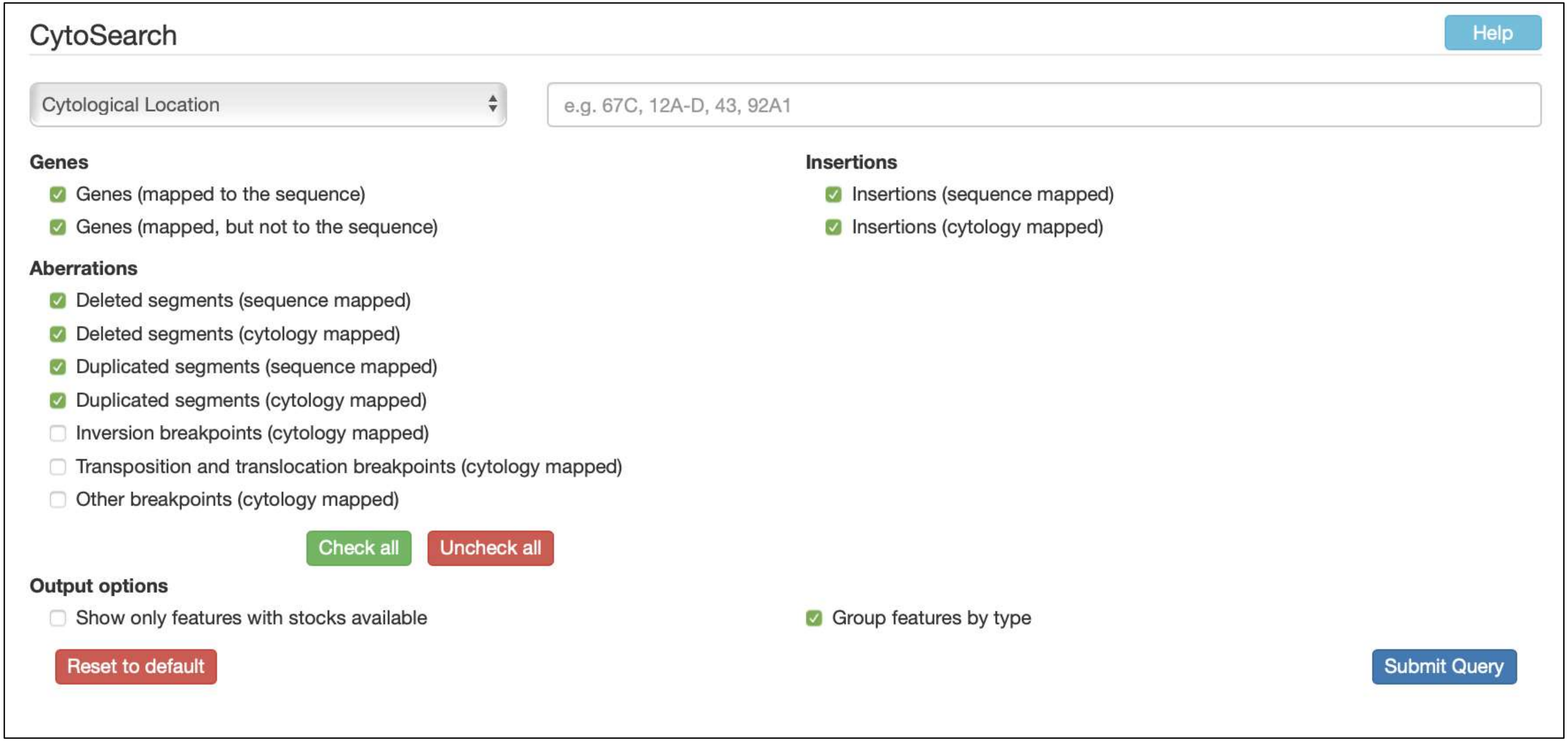
| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **Dmel Start Coordinate** | 3R:6,707,796 | 3R:6,791,836 | 3R:6,896,253 | 3R:7,273,738 | 3R:8,663,885 | 3R:13,032,537 | 3R:14,391,680 | 3R:16,128,729 | 3R:16,374,428 | 3R:16,656,623 | 3R:18,090,803 |
| **Dmel End Coordinate** | 3R:6,742,063 | 3R:6,802,431 | 3R:6,999,228 | 3R:7,309,397 | 3R:8,660,900 | 3R:13,038,026 | 3R:14,481,688 | 3R:16,145,284 | 3R:16,403,683 | 3R:16,734,426 | 3R:18,135,583 |
| **Dmel Gene Span or Anchor** | *pb* | *Dfd* | *Antp* | *rn* | *p* | *ry* | *cv-c* | *Sb* | *ss* | *Ubx* | *sr* |
| **Dmel Computed Cytology** | 84A5-84A5 | 84A5-84A5 | 84A6-84B2 | 84D3-84D3 | 85A6-85A6 | 87D9-87D9 | 88B8-88C1 | 89B4-89B6 | 89B14-89B15 | 89D6-89D9 | 90E4-90F1 |
| **Dmel Observed Recombination map** | 3-47.5 | 3-47.5 | 3-47.5 | 3-47.6 | 3-48.0 | 3-52.0 | 3-54.1 | 3-58.22 | 3-58.5 | 3-58.8 | 3-62.0 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| **Dmel Start Coordinate** | 3R:18,367,902 | 3R:19,302,731 | 3R:20,621,943 | 3R:21,229,830 | 3R:23,127,703 | 3R:26,656,445 | 3R:26,876,771 | 3R:27,172,096 | 3R:29,556,387 | 3R:29,807,248 |
| **Dmel End Coordinate** | 3R:18,372,738 | 3R:19,326,213 | 3R:20,628,915 | 3R:21,237,178 | 3R:23,142,159 | 3R:26,657,531 | 3R:26,881,171 | 3R:27,193,994 | 3R:29,565,285 | 3R:29,815,060 |
| **Dmel Gene Span or Anchor** | *gl* | *Dl* | *H* | *e* | *hh* | *Tb* | *ro* | *Ser* | *Dr* | *ca* |
| **Dmel Computed Cytology** | 91A3-91A3 | 92A1-92A2 | 92F3-92F3 | 93C7-93D1 | 94E1-94E1 | 97C3-97C3 | 97D4-97D5 | 97E6-97E8 | 99B3-99B3 | 99C2-99C2 |
| **Dmel Observed Recombination map** | 3-63.1 | 3-66.2 | 3-69.5 | 3-70.7 | 3-81.2 | 3-90.6 | 3-91.1 | 3-92.5 / 3-93.8 | 3-99.2 | 3-100.7 |

D. melanogaster Muller Element E (3R) polytene chromosome map

# CytoSearch

CytoSearch: Search for genetic objects mapped via cytology-based data



CytoSearch

Cytological Location

e.g. 67C, 12A-D, 43, 92A1

**Genes**

- ☑ Genes (mapped to the sequence)
- ☑ Genes (mapped, but not to the sequence)

**Insertions**

- ☑ Insertions (sequence mapped)
- ☑ Insertions (cytology mapped)

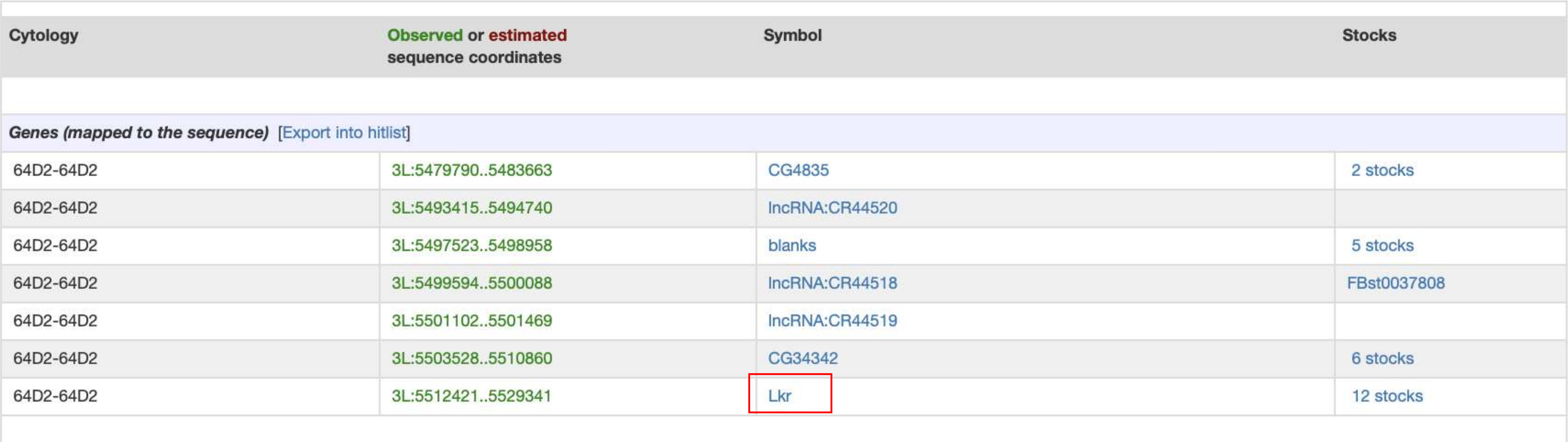
**Aberrations**

- ☑ Deleted segments (sequence mapped)
- ☑ Deleted segments (cytology mapped)
- ☑ Duplicated segments (sequence mapped)
- ☑ Duplicated segments (cytology mapped)
- ☐ Inversion breakpoints (cytology mapped)
- ☐ Transposition and translocation breakpoints (cytology mapped)
- ☐ Other breakpoints (cytology mapped)

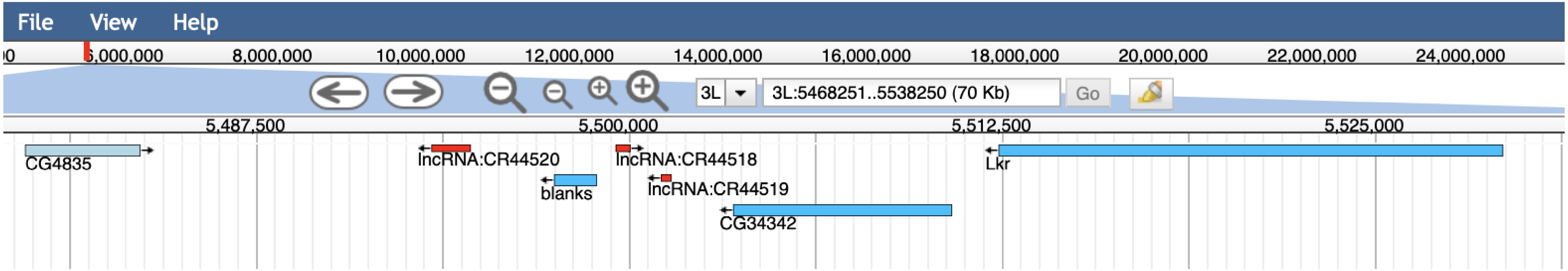
**Output options**

- ☐ Show only features with stocks available
- ☑ Group features by type

# CytoSearch



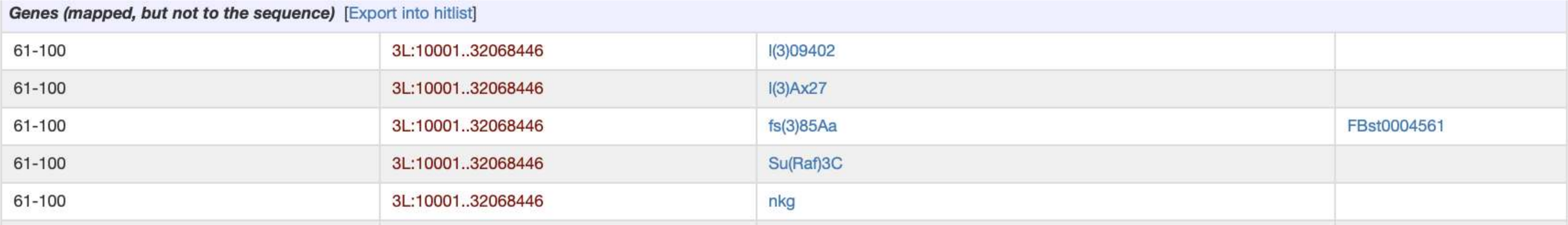
| Cytology | Observed or estimated sequence coordinates | Symbol | Stocks |
|---|---|---|---|
| ***Genes (mapped to the sequence)*** [Export into hitlist] | | | |
| 64D2-64D2 | 3L:5479790..5483663 | CG4835 | 2 stocks |
| 64D2-64D2 | 3L:5493415..5494740 | lncRNA:CR44520 | |
| 64D2-64D2 | 3L:5497523..5498958 | blanks | 5 stocks |
| 64D2-64D2 | 3L:5499594..5500088 | lncRNA:CR44518 | FBst0037808 |
| 64D2-64D2 | 3L:5501102..5501469 | lncRNA:CR44519 | |
| 64D2-64D2 | 3L:5503528..5510860 | CG34342 | 6 stocks |
| 64D2-64D2 | 3L:5512421..5529341 | Lkr | 12 stocks |



3L

3L:5468251..5538250 (70 Kb)

# CytoSearch



***Genes (mapped, but not to the sequence)*** [Export into hitlist]

| | | | |
|---|---|---|---|
| 61-100 | 3L:10001..32068446 | l(3)09402 | |
| 61-100 | 3L:10001..32068446 | l(3)Ax27 | |
| 61-100 | 3L:10001..32068446 | fs(3)85Aa | FBst0004561 |
| 61-100 | 3L:10001..32068446 | Su(Raf)3C | |
| 61-100 | 3L:10001..32068446 | nkg | |

***Insertions (sequence mapped)*** [Export into hitlist]

| | | | |
|---|---|---|---|
| 64D2 | 3L:5466031..5466031 | P{GSV2}GS51531 | FBst0324621 |
| 64D2 | 3L:5516233..5516373 | PBac{3HPy[+]}Lkr[C003] | FBst0016250 |
| 64D2 | 3L:5518497..5518497 | Mi{MIC}Lkr[MI08640] | FBst0051094 |
| 64D2_r6 | 3L:5518497..5518497 | Mi{Trojan-GAL4.1}Lkr[MI08640-TG4.1] | FBst0076198 |
| 64D2 | 3L:5523657..5523657 | Mi{ET1}Lkr[MB01467] | FBst0023316 |

***Insertions (cytology mapped)*** [Export into hitlist]

| | | | |
|---|---|---|---|
| 64D2-64D2 | 3L:5463495..5530550 | TI{2A-GAL4}Lkr[2A-GAL4] | FBst0084648 |
| 64D2-64D2 | 3L:5463495..5530550 | TI{2A-lexA::GAD}Lkr[2A-lexA] | FBst0084400 |
| 64D2-64D2 | 3L:5463495..5530550 | TI{GAL4::VP16}Lkr[KO.GAL4] | |
| 64D2-64D2 | 3L:5463495..5530550 | TI{TI}Lkr[attP] | FBst0084518 |
| 64D2-64D2 | 3L:5463495..5530550 | TI{GAL4::VP16}Lkr[GAL4::VP16] | |

# Coordinate Converter

*Drosophila* Sequence Coordinates Converter

**Enter *Drosophila* Coordinates:** 3L:5,510,421..5,531,341

**or Upload File of Coordinates:**

**Species:** *D. melanogaster*

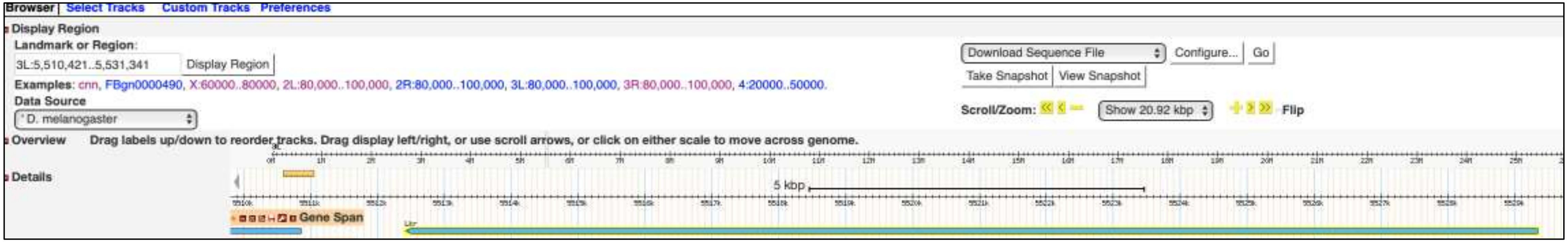
**Send results to:** Browser

**Input Assembly:** 5 / 2

**Output Assembly:** 6 (current) / 3 (current)

R6 → R5 backwards *D. mel* convertor tool is available here

Standalone R5 → R6 *D. mel* ID convertor script can be downloaded here



**Display Region**

Landmark or Region: 3L:5,510,421..5,531,341

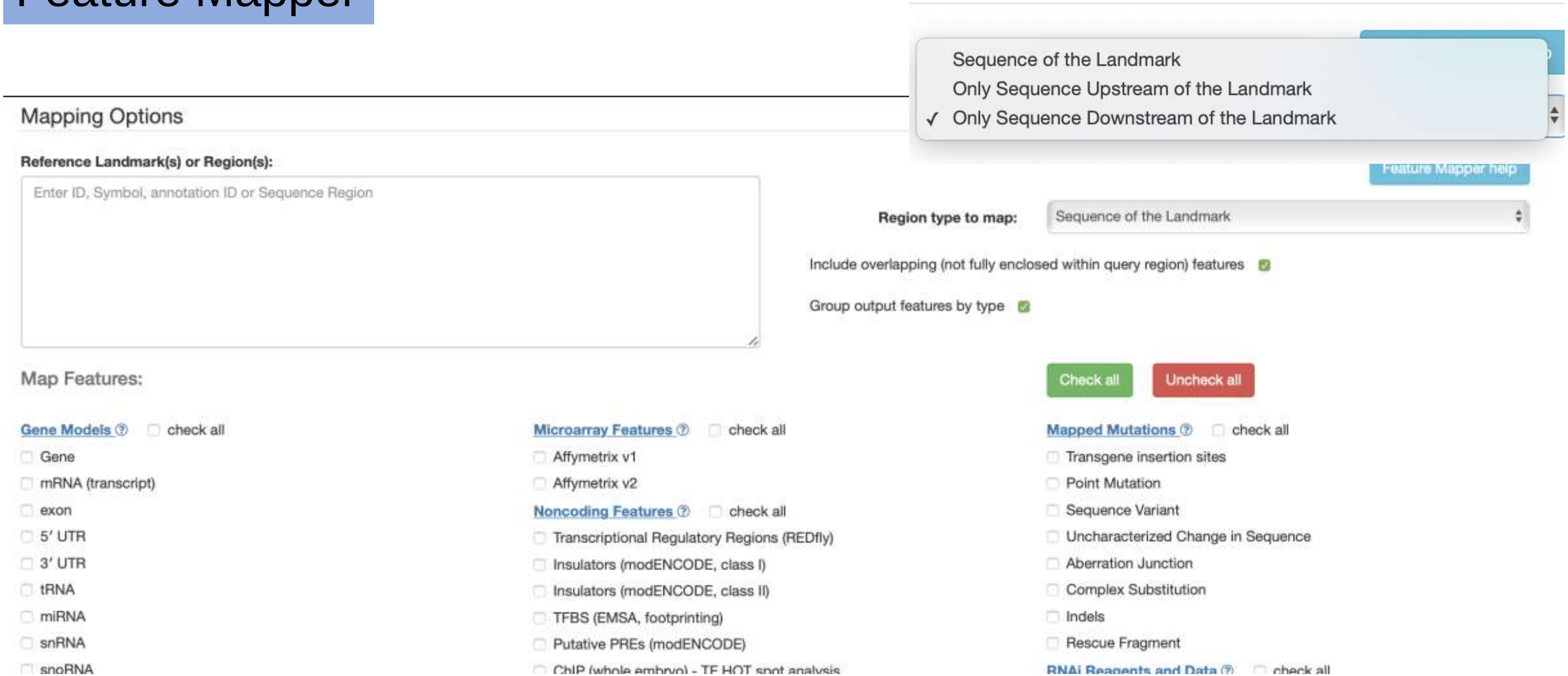
Examples: cnn, FBgn0000490, X:60000..80000, 2L:80,000..100,000, 2R:80,000..100,000, 3L:80,000..100,000, 3R:80,000..100,000, 4:20000..50000.

Data Source: D. melanogaster

Scroll/Zoom: Show 20.92 kbp

Overview: Drag labels up/down to reorder tracks. Drag display left/right, or use scroll arrows, or click on either scale to move across genome.

# Feature Mapper



Sequence of the Landmark
Only Sequence Upstream of the Landmark
✓ Only Sequence Downstream of the Landmark

## Mapping Options

**Reference Landmark(s) or Region(s):**

Enter ID, Symbol, annotation ID or Sequence Region

**Region type to map:** Sequence of the Landmark

Include overlapping (not fully enclosed within query region) features ☑

Group output features by type ☑

Map Features:

Gene Models ⓘ ☐ check all
☐ Gene
☐ mRNA (transcript)
☐ exon
☐ 5′ UTR
☐ 3′ UTR
☐ tRNA
☐ miRNA
☐ snRNA
☐ snoRNA

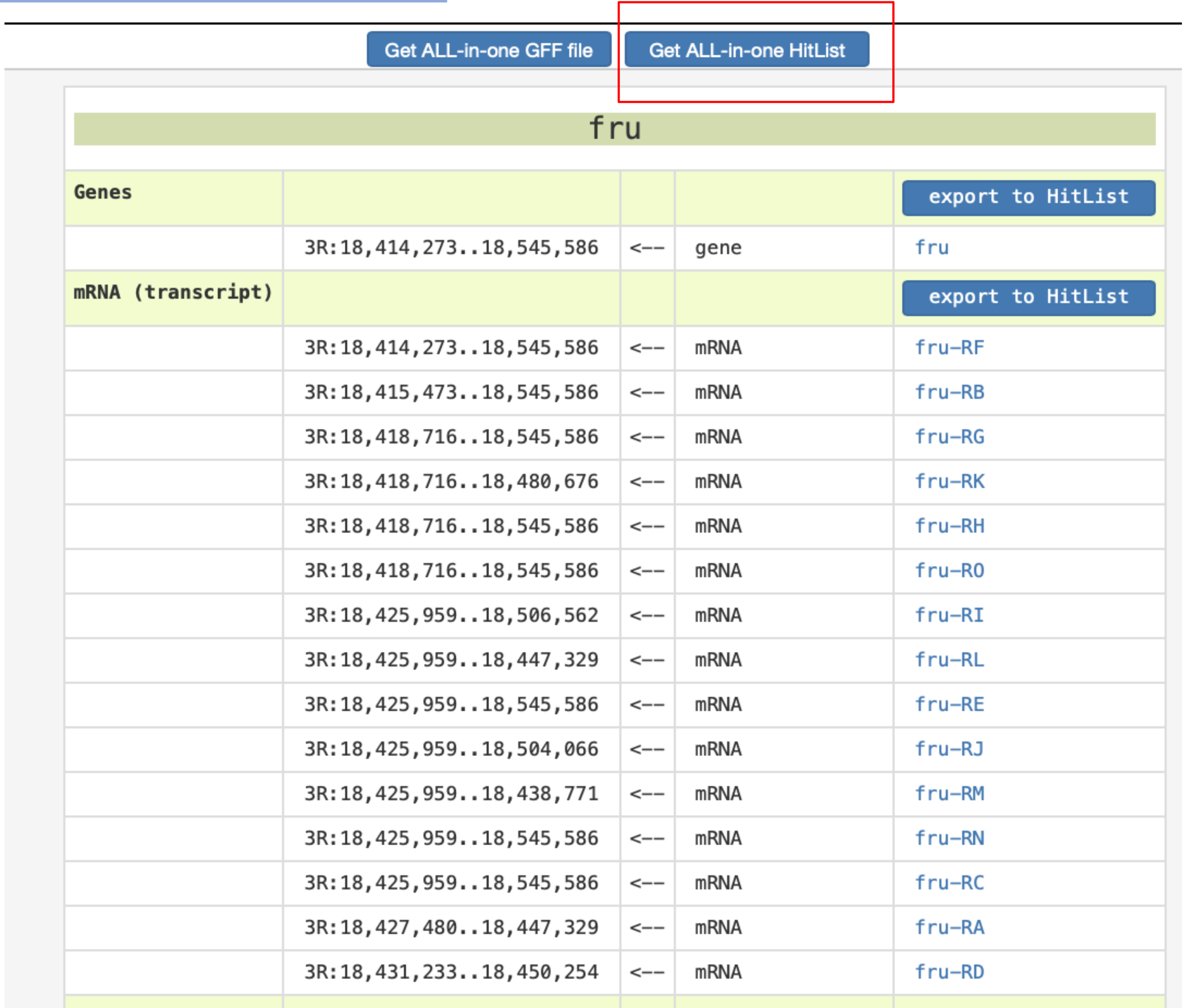
Microarray Features ⓘ ☐ check all
☐ Affymetrix v1
☐ Affymetrix v2

Noncoding Features ⓘ ☐ check all
☐ Transcriptional Regulatory Regions (REDfly)
☐ Insulators (modENCODE, class I)
☐ Insulators (modENCODE, class II)
☐ TFBS (EMSA, footprinting)
☐ Putative PREs (modENCODE)
☐ ChIP (whole embryo) - TF HOT spot analysis

Mapped Mutations ⓘ ☐ check all
☐ Transgene insertion sites
☐ Point Mutation
☐ Sequence Variant
☐ Uncharacterized Change in Sequence
☐ Aberration Junction
☐ Complex Substitution
☐ Indels
☐ Rescue Fragment

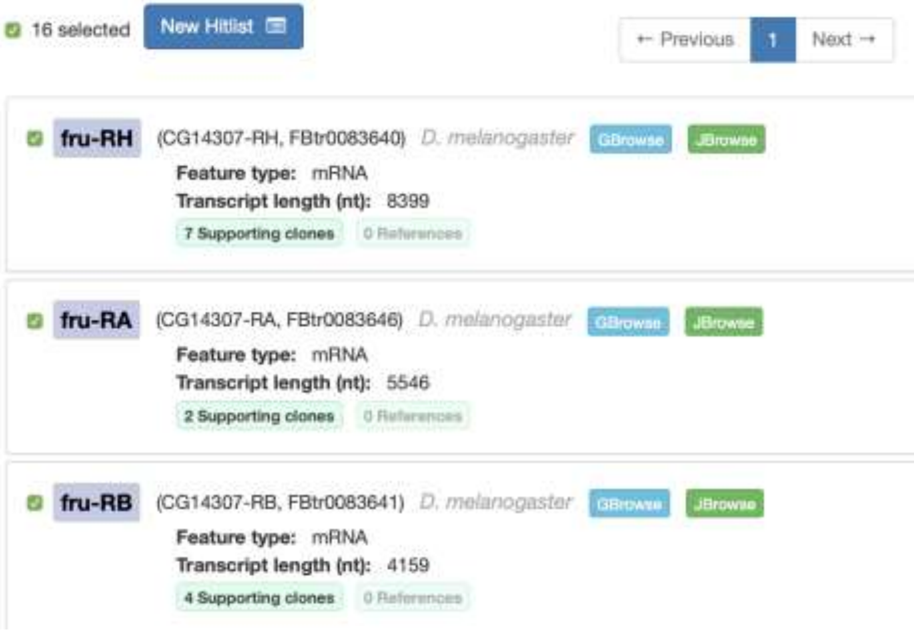
RNAi Reagents and Data ⓘ ☐ check all

# Feature Mapper



fru

| | | | | |
|---|---|---|---|---|
| **Genes** | | | | export to HitList |
| | 3R:18,414,273..18,545,586 | <-- | gene | fru |
| **mRNA (transcript)** | | | | export to HitList |
| | 3R:18,414,273..18,545,586 | <-- | mRNA | fru-RF |
| | 3R:18,415,473..18,545,586 | <-- | mRNA | fru-RB |
| | 3R:18,418,716..18,545,586 | <-- | mRNA | fru-RG |
| | 3R:18,418,716..18,480,676 | <-- | mRNA | fru-RK |
| | 3R:18,418,716..18,545,586 | <-- | mRNA | fru-RH |
| | 3R:18,418,716..18,545,586 | <-- | mRNA | fru-RO |
| | 3R:18,425,959..18,506,562 | <-- | mRNA | fru-RI |
| | 3R:18,425,959..18,447,329 | <-- | mRNA | fru-RL |
| | 3R:18,425,959..18,545,586 | <-- | mRNA | fru-RE |
| | 3R:18,425,959..18,504,066 | <-- | mRNA | fru-RJ |
| | 3R:18,425,959..18,438,771 | <-- | mRNA | fru-RM |
| | 3R:18,425,959..18,545,586 | <-- | mRNA | fru-RN |
| | 3R:18,425,959..18,545,586 | <-- | mRNA | fru-RC |
| | 3R:18,427,480..18,447,329 | <-- | mRNA | fru-RA |
| | 3R:18,431,233..18,450,254 | <-- | mRNA | fru-RD |



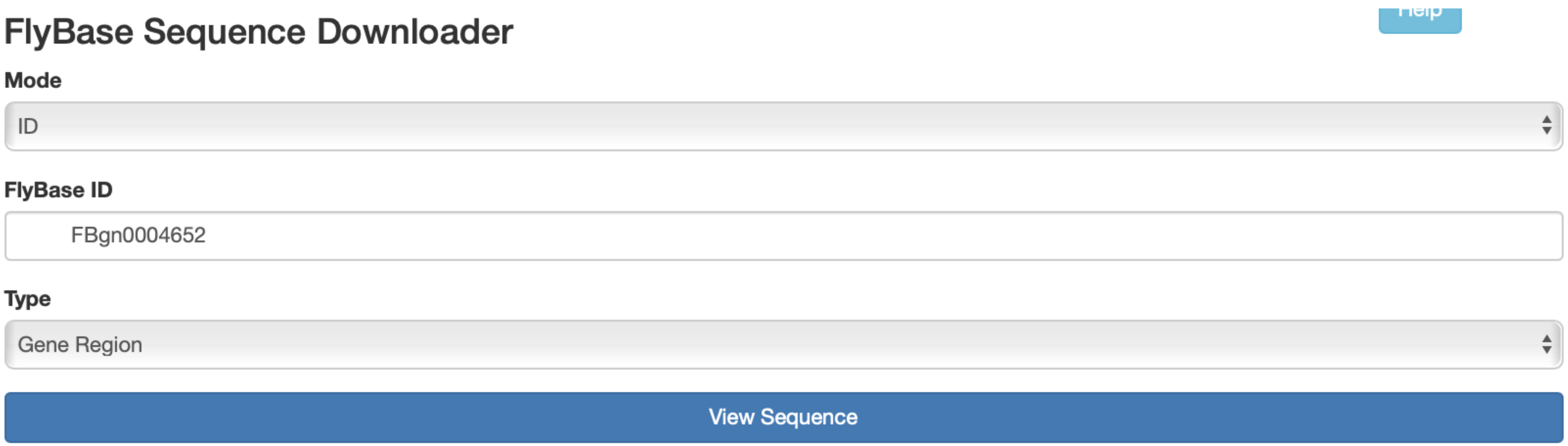
☑ 16 selected

☑ **fru-RH** (CG14307-RH, FBtr0083640) *D. melanogaster*
**Feature type:** mRNA
**Transcript length (nt):** 8399
7 Supporting clones 0 References

☑ **fru-RA** (CG14307-RA, FBtr0083646) *D. melanogaster*
**Feature type:** mRNA
**Transcript length (nt):** 5546
2 Supporting clones 0 References

☑ **fru-RB** (CG14307-RB, FBtr0083641) *D. melanogaster*
**Feature type:** mRNA
**Transcript length (nt):** 4159
4 Supporting clones 0 References

# Sequence Downloader



FlyBase Sequence Downloader

**Mode**

ID

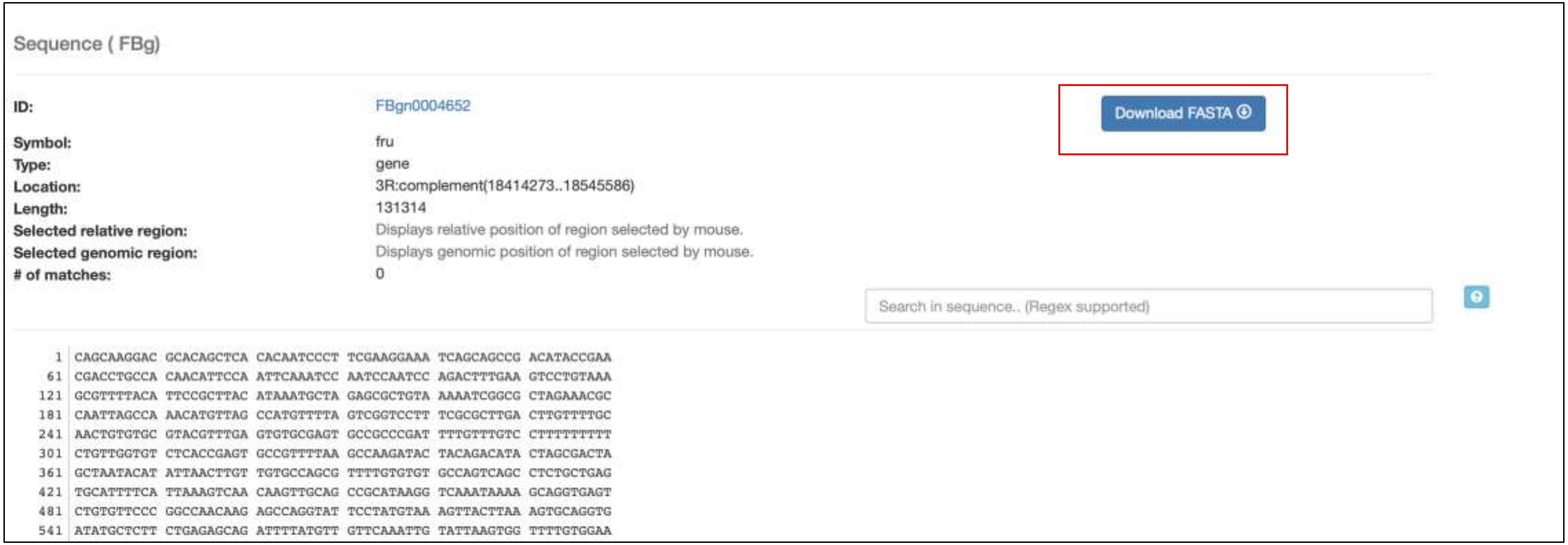
**FlyBase ID**

FBgn0004652

**Type**

Gene Region

# Sequence Downloader



Sequence ( FBg)

**ID:** FBgn0004652

**Symbol:** fru
**Type:** gene
**Location:** 3R:complement(18414273..18545586)
**Length:** 131314
**Selected relative region:** Displays relative position of region selected by mouse.
**Selected genomic region:** Displays genomic position of region selected by mouse.
**# of matches:** 0

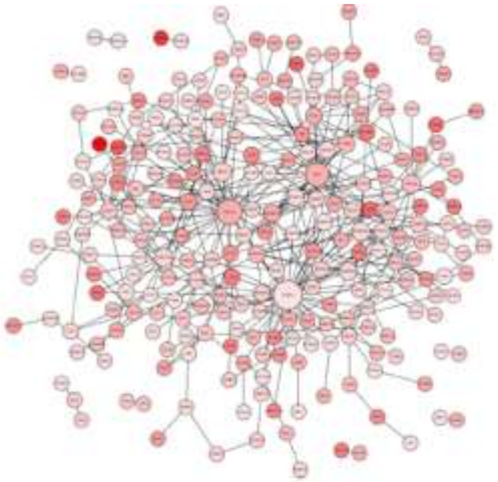
```
  1 CAGCAAGGAC GCACAGCTCA CACAATCCCT TCGAAGGAAA TCAGCAGCCG ACATACCGAA
 61 CGACCTGCCA CAACATTCCA ATTCAAATCC AATCCAATCC AGACTTTGAA GTCCTGTAAA
121 GCGTTTTACA TTCCGCTTAC ATAAATGCTA GAGCGCTGTA AAAATCGGCG CTAGAAACGC
181 CAATTAGCCA AACATGTTAG CCATGTTTTA GTCGGTCCTT TCGCGCTTGA CTTGTTTTGC
241 AACTGTGTGC GTACGTTTGA GTGTGCGAGT GCCGCCCGAT TTTGTTTGTC CTTTTTTTTT
301 CTGTTGGTGT CTCACCGAGT GCCGTTTTAA GCCAAGATAC TACAGACATA CTAGCGACTA
361 GCTAATACAT ATTAACTTGT TGTGCCAGCG TTTTGTGTGT GCCAGTCAGC CTCTGCTGAG
421 TGCATTTTCA TTAAAGTCAA CAAGTTGCAG CCGCATAAGG TCAAATAAAA GCAGGTGAGT
481 CTGTGTTCCC GGCCAACAAG AGCCAGGTAT TCCTATGTAA AGTTACTTAA AGTGCAGGTG
541 ATATGCTCTT CTGAGAGCAG ATTTTATGTT GTTCAAATTG TATTAAGTGG TTTTGTGGAA
```

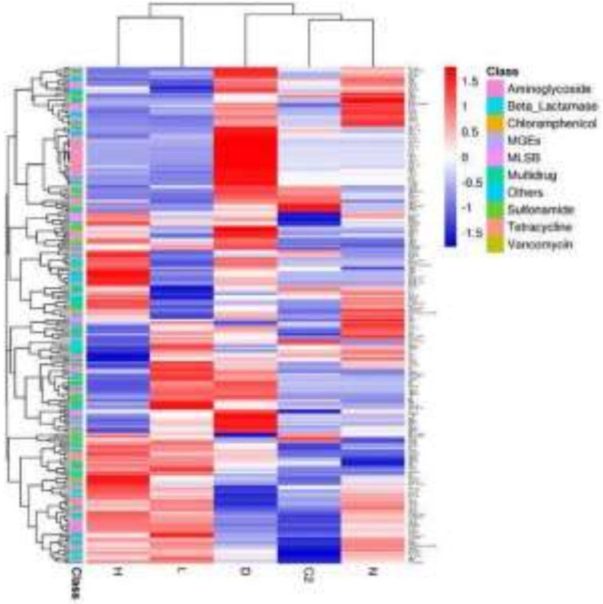
# References

1. Marygold, S.J., M.A. Crosby, and J.L. Goodman, Using FlyBase, a Database of Drosophila Genes and Genomes, in Drosophila. 2016. p. 1-31.
2. McQuilton, P., S.E. St. Pierre, and J. Thurmond, FlyBase 101 - the basics of navigating FlyBase. Nucleic Acids Research, 2011. 40(D1): p. D706-D714.
3. St Pierre, S.E., et al., FlyBase 102--advanced approaches to interrogating FlyBase. Nucleic Acids Res, 2014. 42(Database issue): p. D780-8.
4. Wilson, R.J., et al., FlyBase: integration and improvements to query tools. Nucleic Acids Res, 2008. 36(Database issue): p. D588-93.

# RNA-seq Tool and Other Tools

Ma Mingze



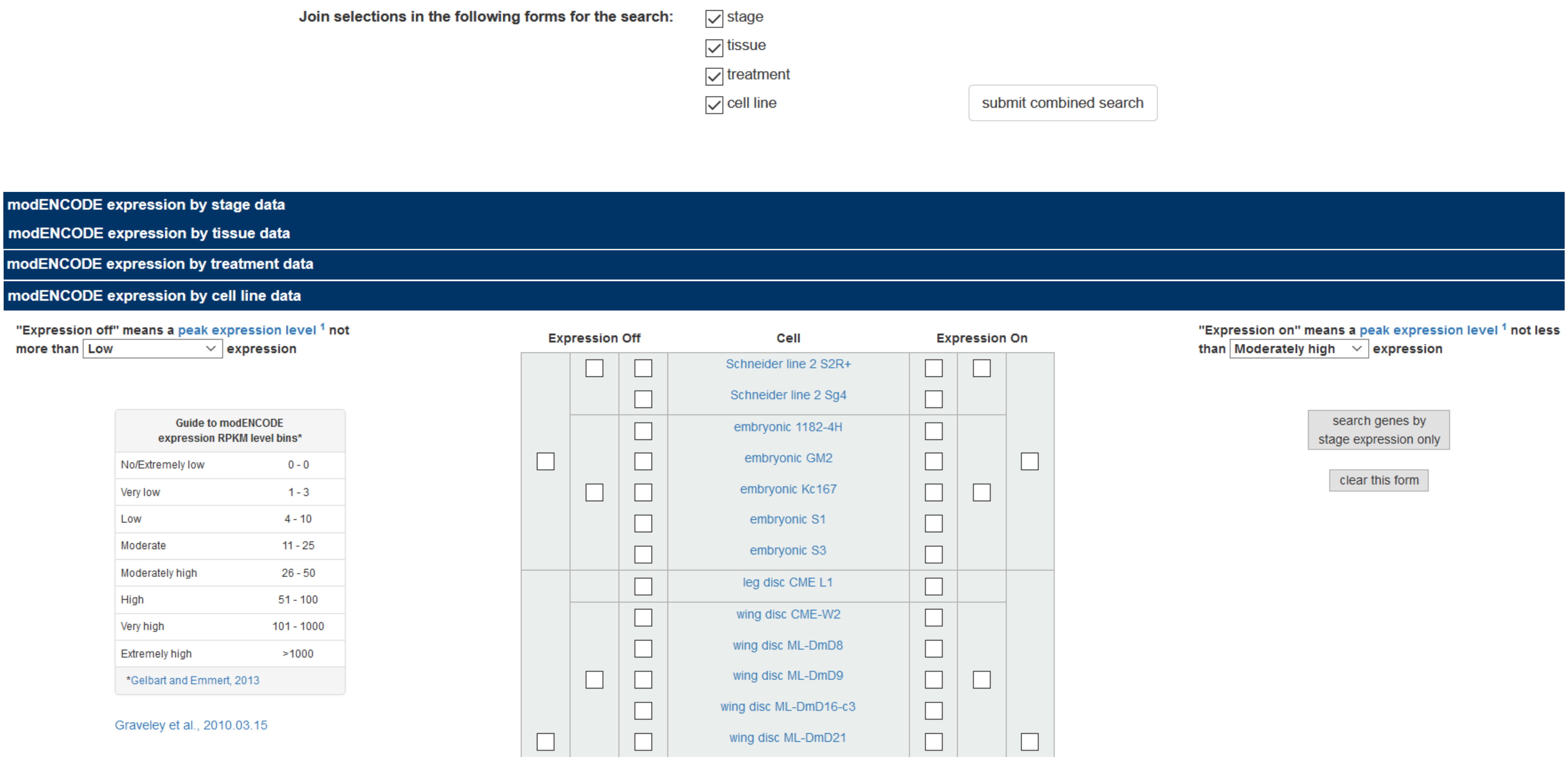


- RNA-seq Tools
- Interactions Browse
- ImageBrowse
- Application——Human Disease Model Reports

# RNA-seq tools

- RNA-Seq Expression Profile Search
- RNA-Seq Expression Similarity Search
- RNA-Seq Levels by Exon or Genomic Region

# RNA-Seq Expression Profile Search



**Join selections in the following forms for the search:**

☑ stage
☑ tissue
☑ treatment
☑ cell line

**modENCODE expression by stage data**

**modENCODE expression by tissue data**

**modENCODE expression by treatment data**

**modENCODE expression by cell line data**

**"Expression off" means a peak expression level [1] not more than** Low **expression**

| Guide to modENCODE expression RPKM level bins* | |
|---|---|
| No/Extremely low | 0 - 0 |
| Very low | 1 - 3 |
| Low | 4 - 10 |
| Moderate | 11 - 25 |
| Moderately high | 26 - 50 |
| High | 51 - 100 |
| Very high | 101 - 1000 |
| Extremely high | >1000 |

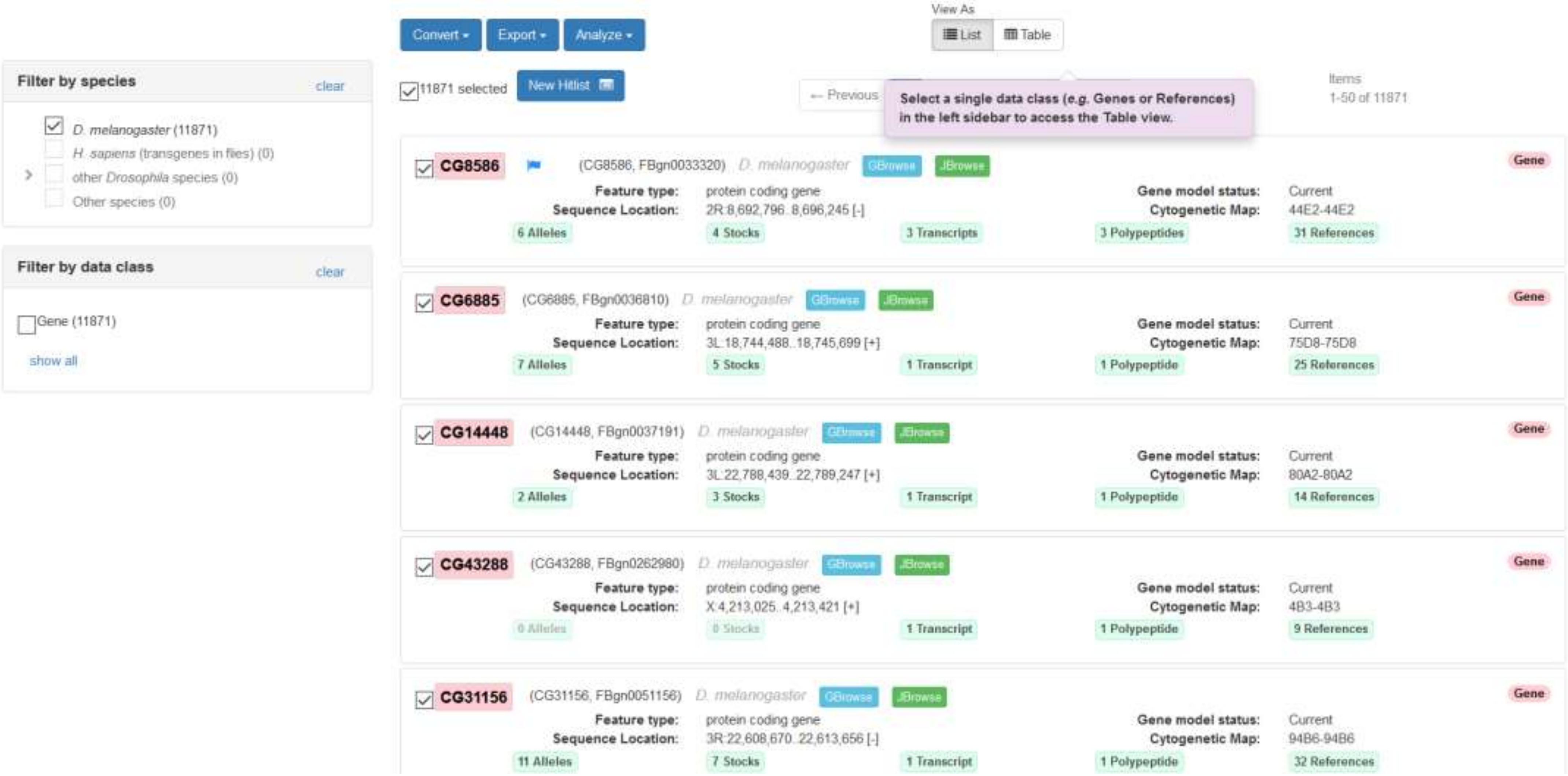
*Gelbart and Emmert, 2013

Graveley et al., 2010.03.15

| Expression Off | | | Cell | Expression On | | |
|---|---|---|---|---|---|---|
| ☐ | ☐ | ☐ | Schneider line 2 S2R+ | ☐ | ☐ | ☐ |
| | | ☐ | Schneider line 2 Sg4 | ☐ | | |
| | ☐ | ☐ | embryonic 1182-4H | ☐ | ☐ | |
| | | ☐ | embryonic GM2 | ☐ | | |
| | | ☐ | embryonic Kc167 | ☐ | | |
| | | ☐ | embryonic S1 | ☐ | | |
| | | ☐ | embryonic S3 | ☐ | | |
| ☐ | | ☐ | leg disc CME L1 | ☐ | | ☐ |
| | ☐ | ☐ | wing disc CME-W2 | ☐ | ☐ | |
| | | ☐ | wing disc ML-DmD8 | ☐ | | |
| | | ☐ | wing disc ML-DmD9 | ☐ | | |
| | | ☐ | wing disc ML-DmD16-c3 | ☐ | | |
| | | ☐ | wing disc ML-DmD21 | ☐ | | |

**"Expression on" means a peak expression level [1] not less than** Moderately high **expression**

# RNA-Seq Expression Profile Search



**Filter by species** clear

☑ *D. melanogaster* (11871)
☐ *H. sapiens* (transgenes in flies) (0)
› ☐ other *Drosophila* species (0)
☐ Other species (0)

**Filter by data class** clear

☐ Gene (11871)
show all

☑ 11871 selected

Select a single data class (e.g. Genes or References) in the left sidebar to access the Table view.

Items
1-50 of 11871

☑ **CG8586** (CG8586, FBgn0033320) *D. melanogaster*
**Feature type:** protein coding gene
**Sequence Location:** 2R:8,692,796..8,696,245 [-]
**Gene model status:** Current
**Cytogenetic Map:** 44E2-44E2
6 Alleles | 4 Stocks | 3 Transcripts | 3 Polypeptides | 31 References

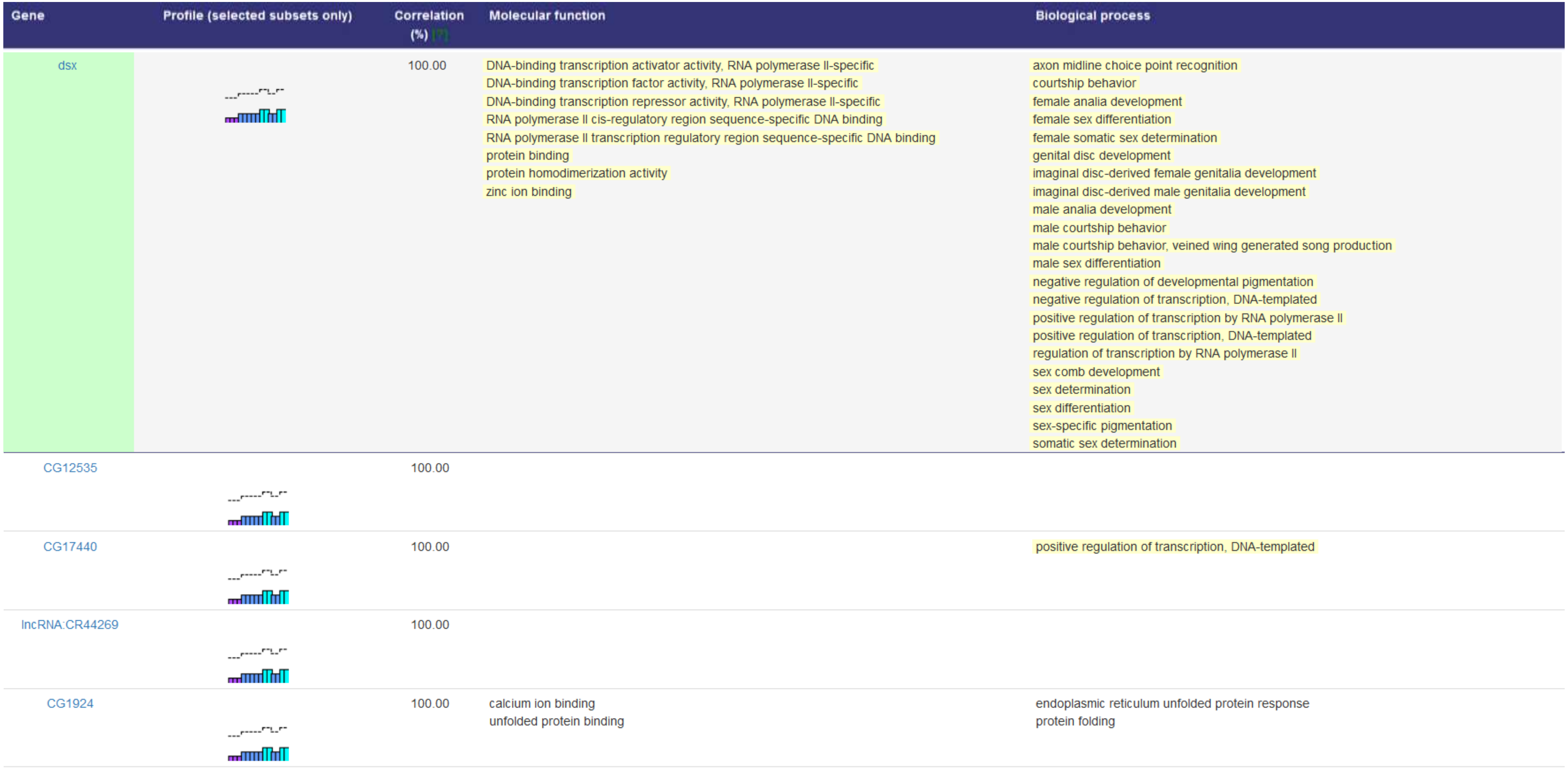
☑ **CG6885** (CG6885, FBgn0036810) *D. melanogaster*
**Feature type:** protein coding gene
**Sequence Location:** 3L:18,744,488..18,745,699 [+]
**Gene model status:** Current
**Cytogenetic Map:** 75D8-75D8
7 Alleles | 5 Stocks | 1 Transcript | 1 Polypeptide | 25 References

☑ **CG14448** (CG14448, FBgn0037191) *D. melanogaster*
**Feature type:** protein coding gene
**Sequence Location:** 3L:22,788,439..22,789,247 [+]
**Gene model status:** Current
**Cytogenetic Map:** 80A2-80A2
2 Alleles | 3 Stocks | 1 Transcript | 1 Polypeptide | 14 References

☑ **CG43288** (CG43288, FBgn0262980) *D. melanogaster*
**Feature type:** protein coding gene
**Sequence Location:** X:4,213,025..4,213,421 [+]
**Gene model status:** Current
**Cytogenetic Map:** 4B3-4B3
0 Alleles | 0 Stocks | 1 Transcript | 1 Polypeptide | 9 References

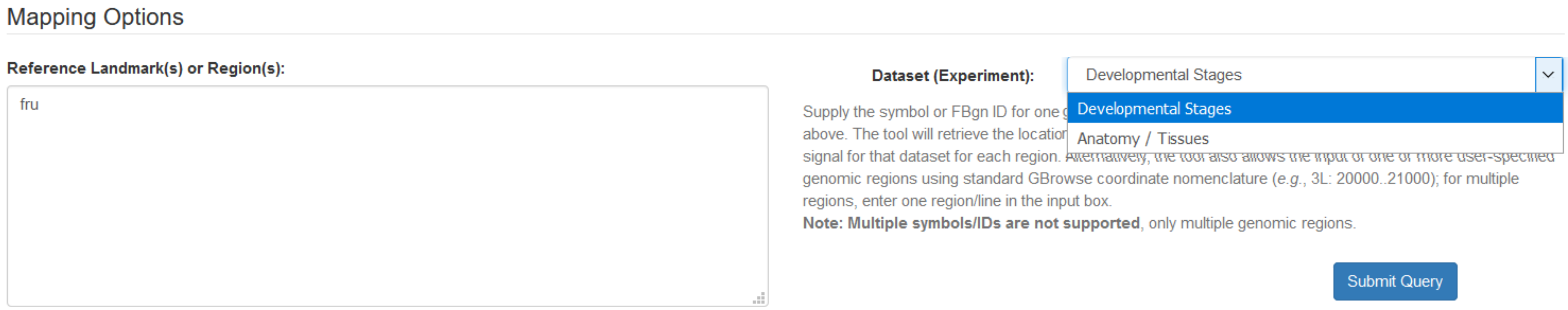
☑ **CG31156** (CG31156, FBgn0051156) *D. melanogaster*
**Feature type:** protein coding gene
**Sequence Location:** 3R:22,608,670..22,613,656 [-]
**Gene model status:** Current
**Cytogenetic Map:** 94B6-94B6
11 Alleles | 7 Stocks | 1 Transcript | 1 Polypeptide | 32 References

# RNA-Seq Expression Similarity Search



| Gene | Profile (selected subsets only) | Correlation (%) [?] | Molecular function | Biological process |
|---|---|---|---|---|
| dsx | | 100.00 | DNA-binding transcription activator activity, RNA polymerase II-specific<br>DNA-binding transcription factor activity, RNA polymerase II-specific<br>DNA-binding transcription repressor activity, RNA polymerase II-specific<br>RNA polymerase II cis-regulatory region sequence-specific DNA binding<br>RNA polymerase II transcription regulatory region sequence-specific DNA binding<br>protein binding<br>protein homodimerization activity<br>zinc ion binding | axon midline choice point recognition<br>courtship behavior<br>female analia development<br>female sex differentiation<br>female somatic sex determination<br>genital disc development<br>imaginal disc-derived female genitalia development<br>imaginal disc-derived male genitalia development<br>male analia development<br>male courtship behavior<br>male courtship behavior, veined wing generated song production<br>male sex differentiation<br>negative regulation of developmental pigmentation<br>negative regulation of transcription, DNA-templated<br>positive regulation of transcription by RNA polymerase II<br>positive regulation of transcription, DNA-templated<br>regulation of transcription by RNA polymerase II<br>sex comb development<br>sex determination<br>sex differentiation<br>sex-specific pigmentation<br>somatic sex determination |
| CG12535 | | 100.00 | | |
| CG17440 | | 100.00 | | positive regulation of transcription, DNA-templated |
| lncRNA:CR44269 | | 100.00 | | |
| CG1924 | | 100.00 | calcium ion binding<br>unfolded protein binding | endoplasmic reticulum unfolded protein response<br>protein folding |

# RNA-Seq Levels by Exon or Genomic Region



## Mapping Options

**Reference Landmark(s) or Region(s):**

fru

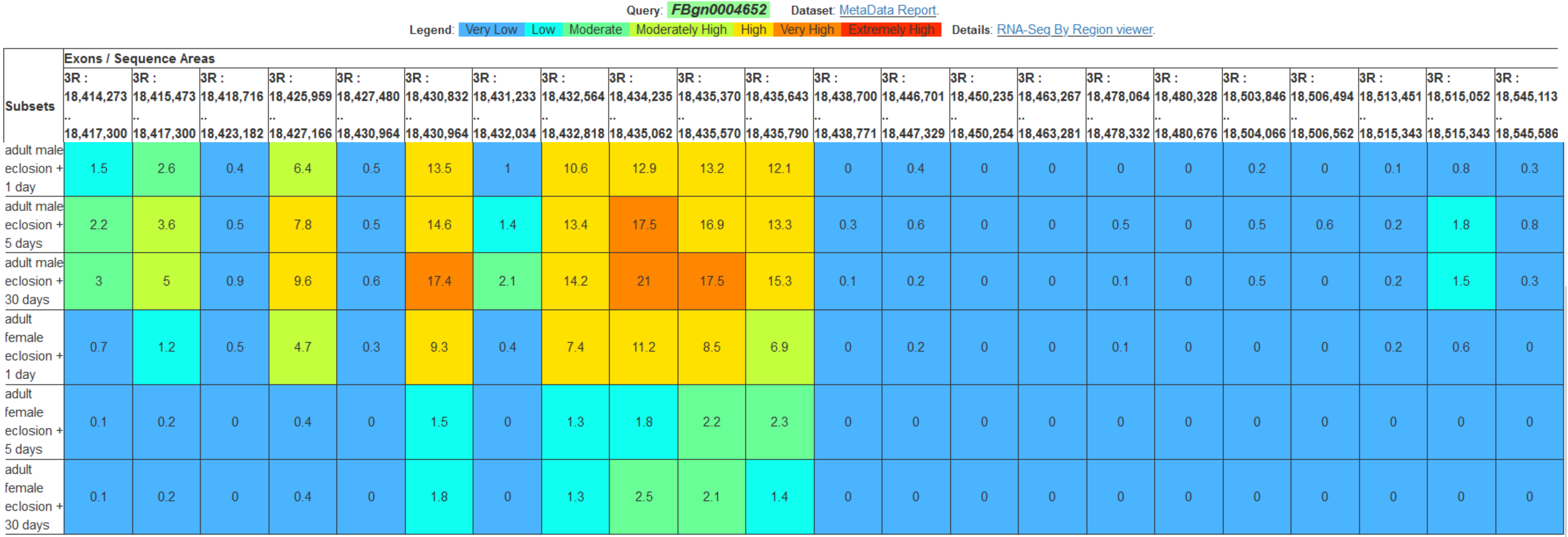
**Dataset (Experiment):** Developmental Stages

Supply the symbol or FBgn ID for one g
above. The tool will retrieve the locatior
signal for that dataset for each region. Alternatively, the tool also allows the input of one or more user-specified genomic regions using standard GBrowse coordinate nomenclature (*e.g.*, 3L: 20000..21000); for multiple regions, enter one region/line in the input box.

**Note: Multiple symbols/IDs are not supported**, only multiple genomic regions.

# RNA-Seq Levels by Exon or Genomic Region

## *fru* expression pattern in developmental stages

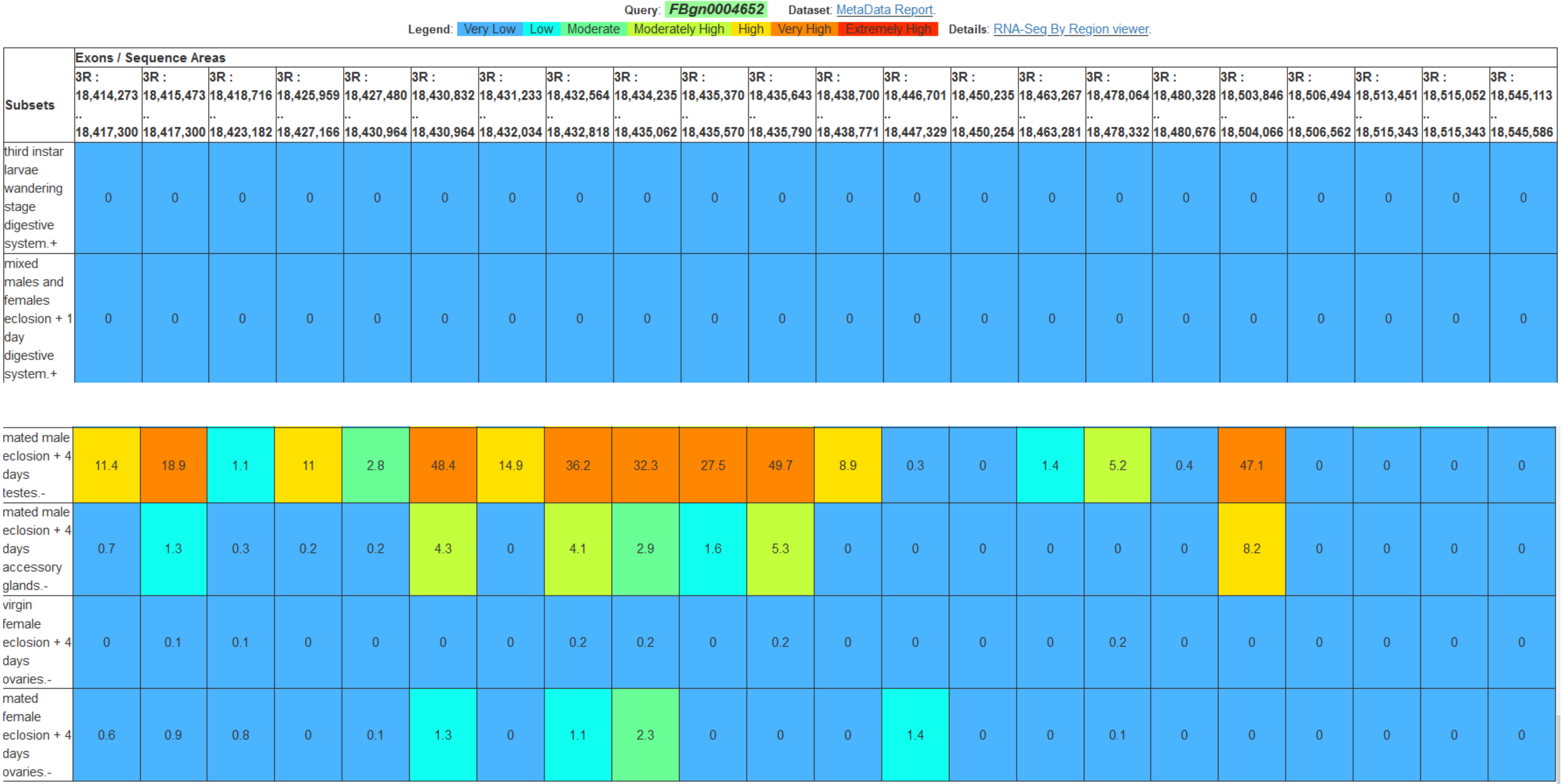


**Query:** ***FBgn0004652*** **Dataset:** MetaData Report.

**Legend:** Very Low Low Moderate Moderately High High Very High Extremely High **Details:** RNA-Seq By Region viewer.

| **Subsets** | **Exons / Sequence Areas** | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **3R : 18,414,273 .. 18,417,300** | **3R : 18,415,473 .. 18,417,300** | **3R : 18,418,716 .. 18,423,182** | **3R : 18,425,959 .. 18,427,166** | **3R : 18,427,480 .. 18,430,964** | **3R : 18,430,832 .. 18,430,964** | **3R : 18,431,233 .. 18,432,034** | **3R : 18,432,564 .. 18,432,818** | **3R : 18,434,235 .. 18,435,062** | **3R : 18,435,370 .. 18,435,570** | **3R : 18,435,643 .. 18,435,790** | **3R : 18,438,700 .. 18,438,771** | **3R : 18,446,701 .. 18,447,329** | **3R : 18,450,235 .. 18,450,254** | **3R : 18,463,267 .. 18,463,281** | **3R : 18,478,064 .. 18,478,332** | **3R : 18,480,328 .. 18,480,676** | **3R : 18,503,846 .. 18,504,066** | **3R : 18,506,494 .. 18,506,562** | **3R : 18,513,451 .. 18,515,343** | **3R : 18,515,052 .. 18,515,343** | **3R : 18,545,113 .. 18,545,586** |
| adult male eclosion + 1 day | 1.5 | 2.6 | 0.4 | 6.4 | 0.5 | 13.5 | 1 | 10.6 | 12.9 | 13.2 | 12.1 | 0 | 0.4 | 0 | 0 | 0 | 0 | 0.2 | 0 | 0.1 | 0.8 | 0.3 |
| adult male eclosion + 5 days | 2.2 | 3.6 | 0.5 | 7.8 | 0.5 | 14.6 | 1.4 | 13.4 | 17.5 | 16.9 | 13.3 | 0.3 | 0.6 | 0 | 0 | 0.5 | 0 | 0.5 | 0.6 | 0.2 | 1.8 | 0.8 |
| adult male eclosion + 30 days | 3 | 5 | 0.9 | 9.6 | 0.6 | 17.4 | 2.1 | 14.2 | 21 | 17.5 | 15.3 | 0.1 | 0.2 | 0 | 0 | 0.1 | 0 | 0.5 | 0 | 0.2 | 1.5 | 0.3 |
| adult female eclosion + 1 day | 0.7 | 1.2 | 0.5 | 4.7 | 0.3 | 9.3 | 0.4 | 7.4 | 11.2 | 8.5 | 6.9 | 0 | 0.2 | 0 | 0 | 0.1 | 0 | 0 | 0 | 0.2 | 0.6 | 0 |
| adult female eclosion + 5 days | 0.1 | 0.2 | 0 | 0.4 | 0 | 1.5 | 0 | 1.3 | 1.8 | 2.2 | 2.3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| adult female eclosion + 30 days | 0.1 | 0.2 | 0 | 0.4 | 0 | 1.8 | 0 | 1.3 | 2.5 | 2.1 | 1.4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

# *fru* expression pattern in tissues/anatomy



**Query**: ***FBgn0004652*** **Dataset**: MetaData Report.

**Legend**: Very Low Low Moderate Moderately High High Very High Extremely High **Details**: RNA-Seq By Region viewer.

| **Subsets** | **Exons / Sequence Areas** | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **3R : 18,414,273 .. 18,417,300** | **3R : 18,415,473 .. 18,417,300** | **3R : 18,418,716 .. 18,423,182** | **3R : 18,425,959 .. 18,427,166** | **3R : 18,427,480 .. 18,430,964** | **3R : 18,430,832 .. 18,430,964** | **3R : 18,431,233 .. 18,432,034** | **3R : 18,432,564 .. 18,432,818** | **3R : 18,434,235 .. 18,435,062** | **3R : 18,435,370 .. 18,435,570** | **3R : 18,435,643 .. 18,435,790** | **3R : 18,438,700 .. 18,438,771** | **3R : 18,446,701 .. 18,447,329** | **3R : 18,450,235 .. 18,450,254** | **3R : 18,463,267 .. 18,463,281** | **3R : 18,478,064 .. 18,478,332** | **3R : 18,480,328 .. 18,480,676** | **3R : 18,503,846 .. 18,504,066** | **3R : 18,506,494 .. 18,506,562** | **3R : 18,513,451 .. 18,515,343** | **3R : 18,515,052 .. 18,515,343** | **3R : 18,545,113 .. 18,545,586** |
| third instar larvae wandering stage digestive system.+ | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| mixed males and females eclosion + 1 day digestive system.+ | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| mated male eclosion + 4 days testes.- | 11.4 | 18.9 | 1.1 | 11 | 2.8 | 48.4 | 14.9 | 36.2 | 32.3 | 27.5 | 49.7 | 8.9 | 0.3 | 0 | 1.4 | 5.2 | 0.4 | 47.1 | 0 | 0 | 0 | 0 |
| mated male eclosion + 4 days accessory glands.- | 0.7 | 1.3 | 0.3 | 0.2 | 0.2 | 4.3 | 0 | 4.1 | 2.9 | 1.6 | 5.3 | 0 | 0 | 0 | 0 | 0 | 0 | 8.2 | 0 | 0 | 0 | 0 |
| virgin female eclosion + 4 days ovaries.- | 0 | 0.1 | 0.1 | 0 | 0 | 0 | 0 | 0.2 | 0.2 | 0 | 0.2 | 0 | 0 | 0 | 0 | 0.2 | 0 | 0 | 0 | 0 | 0 | 0 |
| mated female eclosion + 4 days ovaries.- | 0.6 | 0.9 | 0.8 | 0 | 0.1 | 1.3 | 0 | 1.1 | 2.3 | 0 | 0 | 0 | 1.4 | 0 | 0 | 0.1 | 0 | 0 | 0 | 0 | 0 | 0 |

# Interactions Browse

Gene/Allele Symbol or FBid: fru

Interaction Type: Enhancement + Suppression

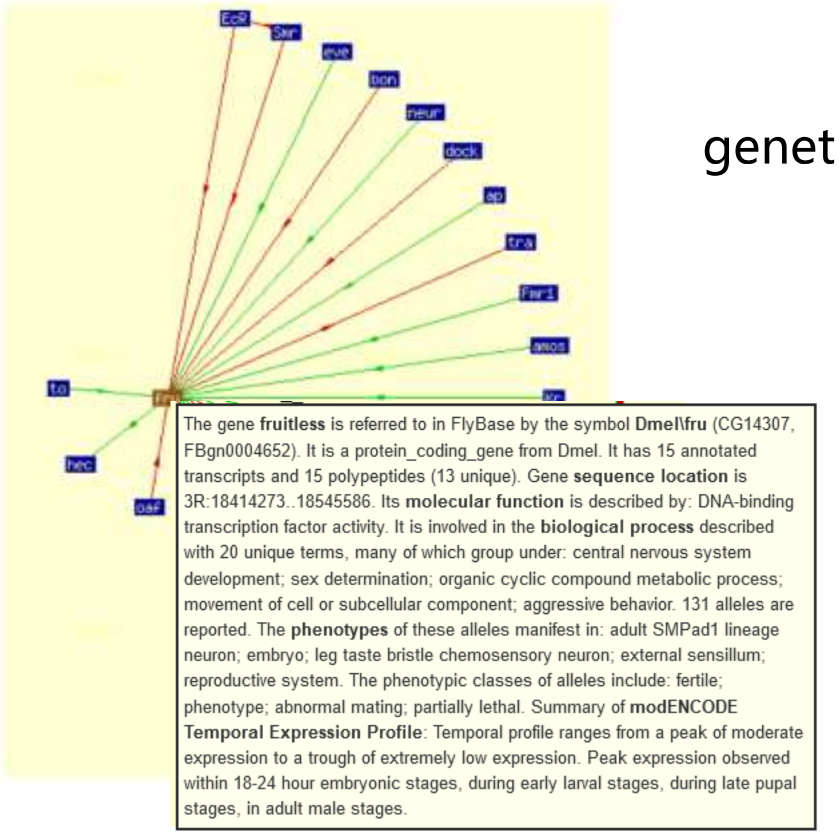
Tree Depth: Auto

Include

☐ Foreign Genes ☐ Fusion Genes

At 0° rotation

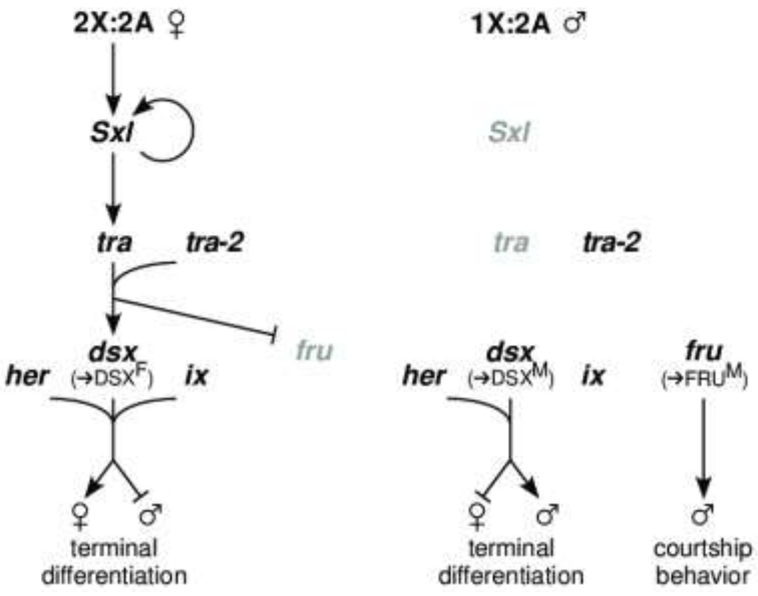
Showing: interactions 1 away



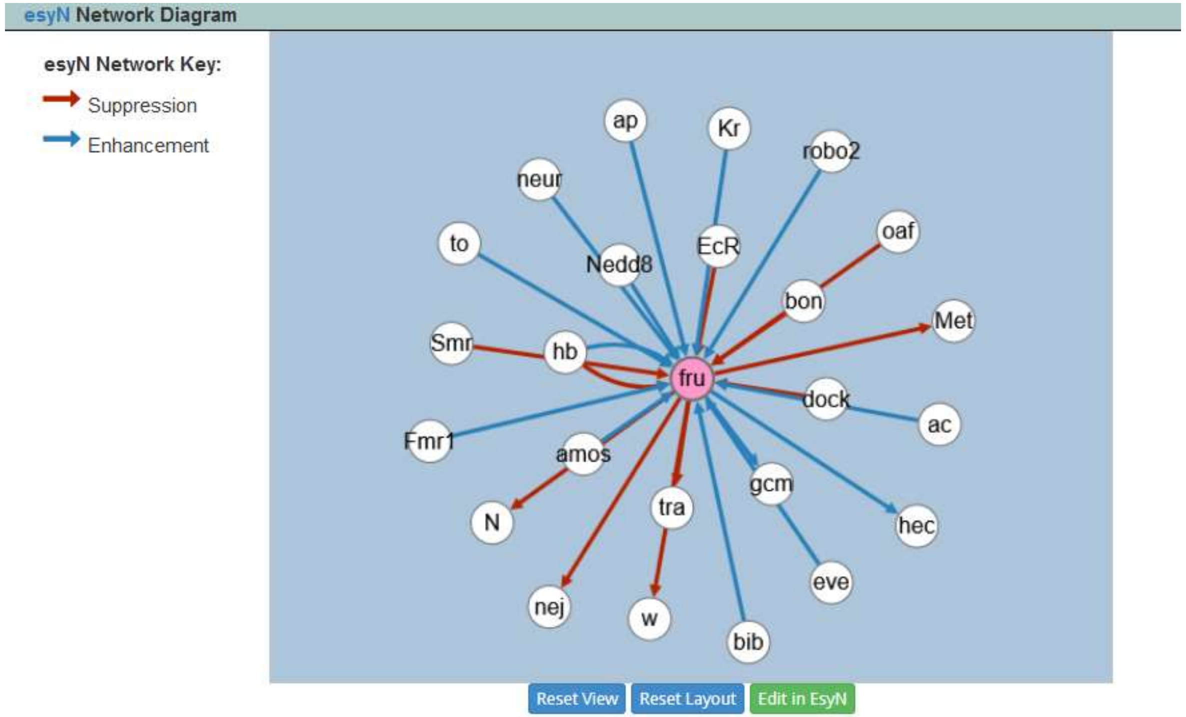
The gene **fruitless** is referred to in FlyBase by the symbol **Dmel\fru** (CG14307, FBgn0004652). It is a protein_coding_gene from Dmel. It has 15 annotated transcripts and 15 polypeptides (13 unique). Gene **sequence location** is 3R:18414273..18545586. Its **molecular function** is described by: DNA-binding transcription factor activity. It is involved in the **biological process** described with 20 unique terms, many of which group under: central nervous system development; sex determination; organic cyclic compound metabolic process; movement of cell or subcellular component; aggressive behavior. 131 alleles are reported. The **phenotypes** of these alleles manifest in: adult SMPad1 lineage neuron; embryo; leg taste bristle chemosensory neuron; external sensillum; reproductive system. The phenotypic classes of alleles include: fertile; phenotype; abnormal mating; partially lethal. Summary of **modENCODE Temporal Expression Profile**: Temporal profile ranges from a peak of moderate expression to a trough of extremely low expression. Peak expression observed within 18-24 hour embryonic stages, during early larval stages, during late pupal stages, in adult male stages.

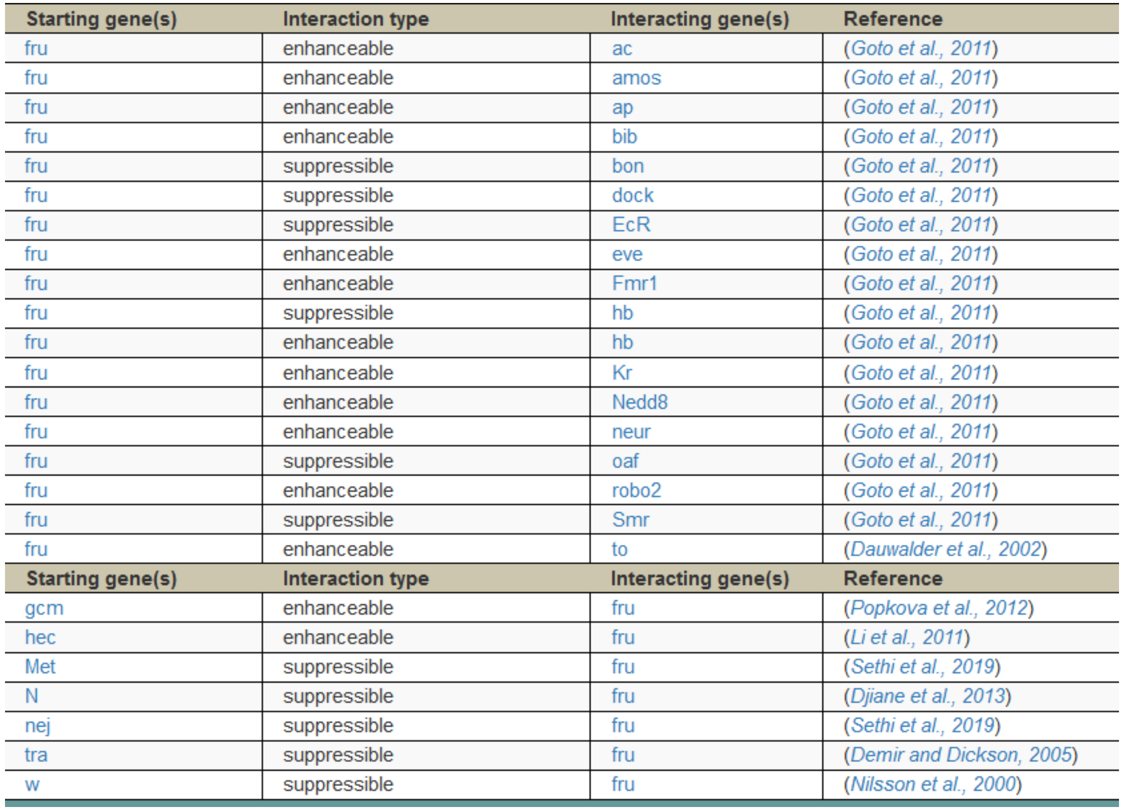
genetic interaction

Location
Function
Expression



# Interactions Browse vs. Genetic Interactions Report

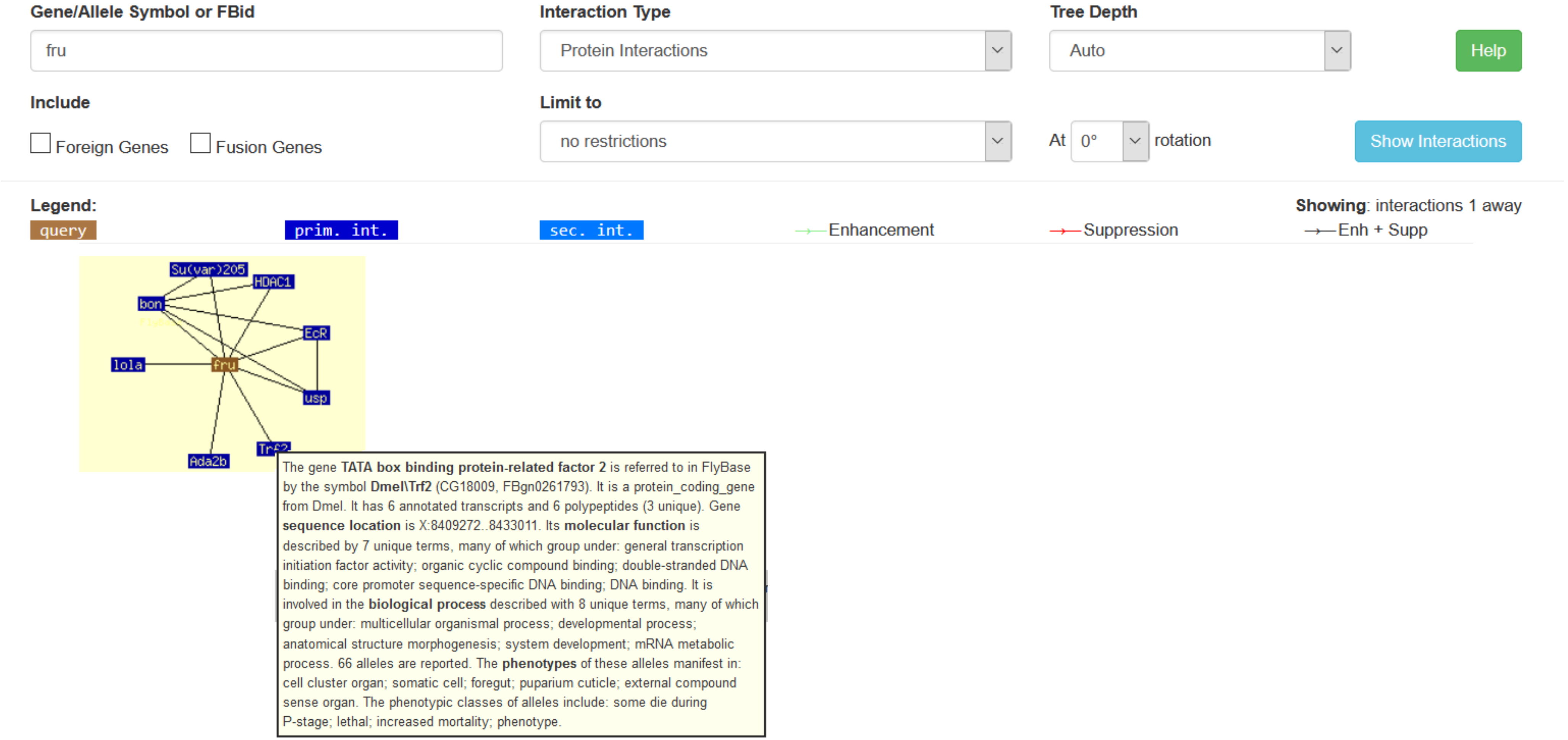




| Starting gene(s) | Interaction type | Interacting gene(s) | Reference |
|---|---|---|---|
| fru | enhanceable | ac | (*Goto et al., 2011*) |
| fru | enhanceable | amos | (*Goto et al., 2011*) |
| fru | enhanceable | ap | (*Goto et al., 2011*) |
| fru | enhanceable | bib | (*Goto et al., 2011*) |
| fru | suppressible | bon | (*Goto et al., 2011*) |
| fru | suppressible | dock | (*Goto et al., 2011*) |
| fru | suppressible | EcR | (*Goto et al., 2011*) |
| fru | enhanceable | eve | (*Goto et al., 2011*) |
| fru | enhanceable | Fmr1 | (*Goto et al., 2011*) |
| fru | suppressible | hb | (*Goto et al., 2011*) |
| fru | enhanceable | hb | (*Goto et al., 2011*) |
| fru | enhanceable | Kr | (*Goto et al., 2011*) |
| fru | enhanceable | Nedd8 | (*Goto et al., 2011*) |
| fru | enhanceable | neur | (*Goto et al., 2011*) |
| fru | suppressible | oaf | (*Goto et al., 2011*) |
| fru | enhanceable | robo2 | (*Goto et al., 2011*) |
| fru | suppressible | Smr | (*Goto et al., 2011*) |
| fru | enhanceable | to | (*Dauwalder et al., 2002*) |
| **Starting gene(s)** | **Interaction type** | **Interacting gene(s)** | **Reference** |
| gcm | enhanceable | fru | (*Popkova et al., 2012*) |
| hec | enhanceable | fru | (*Li et al., 2011*) |
| Met | suppressible | fru | (*Sethi et al., 2019*) |
| N | suppressible | fru | (*Djiane et al., 2013*) |
| nej | suppressible | fru | (*Sethi et al., 2019*) |
| tra | suppressible | fru | (*Demir and Dickson, 2005*) |
| w | suppressible | fru | (*Nilsson et al., 2000*) |

# Interactions Browse

## physical interaction



**Gene/Allele Symbol or FBid** fru

**Interaction Type** Protein Interactions

**Tree Depth** Auto

**Include**

☐ Foreign Genes ☐ Fusion Genes

**Limit to** no restrictions

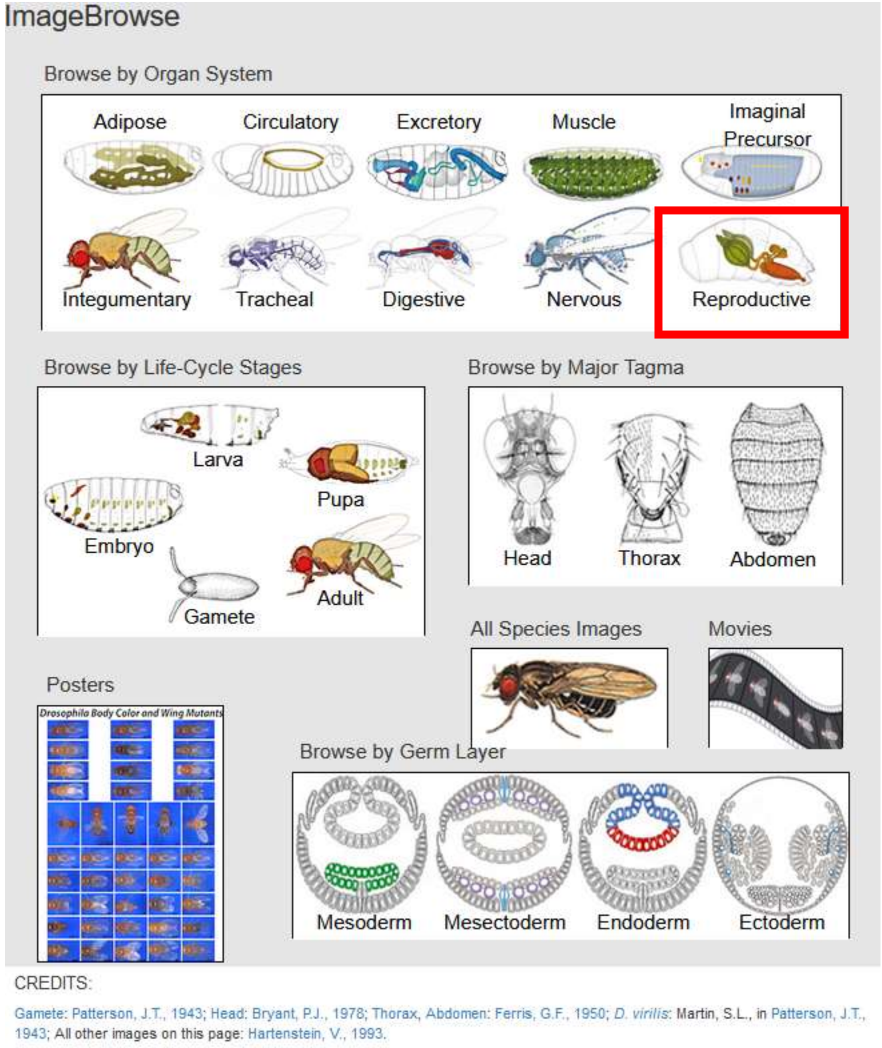
At 0° rotation

**Legend:**

**Showing**: interactions 1 away

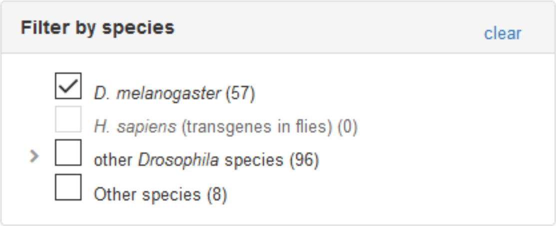
The gene **TATA box binding protein-related factor 2** is referred to in FlyBase by the symbol **Dmel\Trf2** (CG18009, FBgn0261793). It is a protein_coding_gene from Dmel. It has 6 annotated transcripts and 6 polypeptides (3 unique). Gene **sequence location** is X:8409272..8433011. Its **molecular function** is described by 7 unique terms, many of which group under: general transcription initiation factor activity; organic cyclic compound binding; double-stranded DNA binding; core promoter sequence-specific DNA binding; DNA binding. It is involved in the **biological process** described with 8 unique terms, many of which group under: multicellular organismal process; developmental process; anatomical structure morphogenesis; system development; mRNA metabolic process. 66 alleles are reported. The **phenotypes** of these alleles manifest in: cell cluster organ; somatic cell; foregut; puparium cuticle; external compound sense organ. The phenotypic classes of alleles include: some die during P-stage; lethal; increased mortality; phenotype.

# ImageBrowse

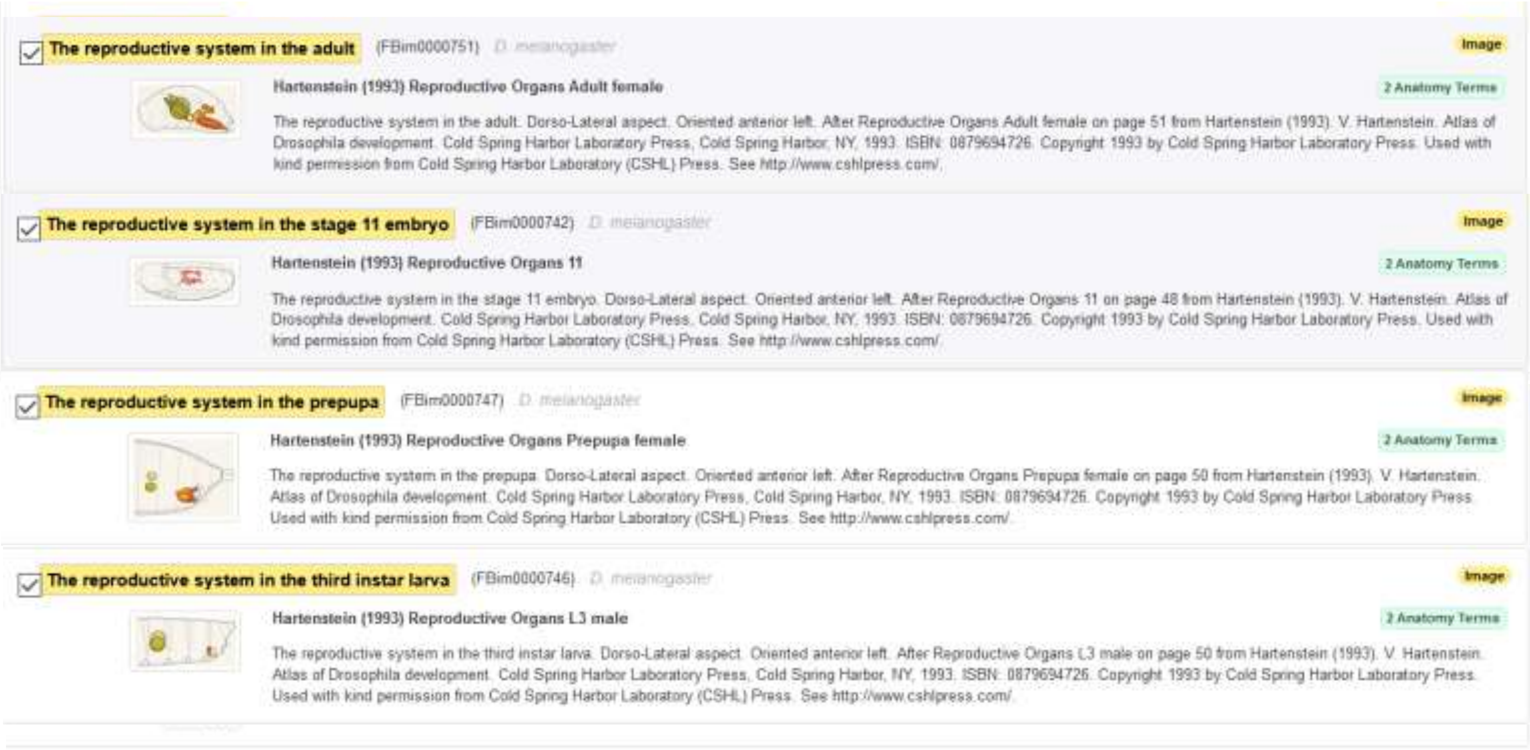


CREDITS:

Gamete: Patterson, J.T., 1943; Head: Bryant, P.J., 1978; Thorax, Abdomen: Ferris, G.F., 1950; *D. virilis*: Martin, S.L., in Patterson, J.T., 1943; All other images on this page: Hartenstein, V., 1993.



☑ *D. melanogaster* (57)
☐ *H. sapiens* (transgenes in flies) (0)
☐ other *Drosophila* species (96)
☐ Other species (8)



☑ **The reproductive system in the adult** (FBim0000751) *D. melanogaster* Image

**Hartenstein (1993) Reproductive Organs Adult female** 2 Anatomy Terms

The reproductive system in the adult. Dorso-Lateral aspect. Oriented anterior left. After Reproductive Organs Adult female on page 51 from Hartenstein (1993). V. Hartenstein. Atlas of Drosophila development. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1993. ISBN: 0879694726. Copyright 1993 by Cold Spring Harbor Laboratory Press. Used with kind permission from Cold Spring Harbor Laboratory (CSHL) Press. See http://www.cshlpress.com/.

☑ **The reproductive system in the stage 11 embryo** (FBim0000742) *D. melanogaster* Image

**Hartenstein (1993) Reproductive Organs 11** 2 Anatomy Terms

The reproductive system in the stage 11 embryo. Dorso-Lateral aspect. Oriented anterior left. After Reproductive Organs 11 on page 48 from Hartenstein (1993). V. Hartenstein. Atlas of Drosophila development. Cold Spring Harbor Laboratory Press. Cold Spring Harbor, NY, 1993. ISBN: 0879694726. Copyright 1993 by Cold Spring Harbor Laboratory Press. Used with kind permission from Cold Spring Harbor Laboratory (CSHL) Press. See http://www.cshlpress.com/.

☑ **The reproductive system in the prepupa** (FBim0000747) *D. melanogaster* Image

**Hartenstein (1993) Reproductive Organs Prepupa female** 2 Anatomy Terms

The reproductive system in the prepupa. Dorso-Lateral aspect. Oriented anterior left. After Reproductive Organs Prepupa female on page 50 from Hartenstein (1993). V. Hartenstein. Atlas of Drosophila development. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1993. ISBN: 0879694726. Copyright 1993 by Cold Spring Harbor Laboratory Press. Used with kind permission from Cold Spring Harbor Laboratory (CSHL) Press. See http://www.cshlpress.com/.

☑ **The reproductive system in the third instar larva** (FBim0000746) *D. melanogaster* Image

**Hartenstein (1993) Reproductive Organs L3 male** 2 Anatomy Terms

The reproductive system in the third instar larva. Dorso-Lateral aspect. Oriented anterior left. After Reproductive Organs L3 male on page 50 from Hartenstein (1993). V. Hartenstein. Atlas of Drosophila development. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1993. ISBN: 0879694726. Copyright 1993 by Cold Spring Harbor Laboratory Press. Used with kind permission from Cold Spring Harbor Laboratory (CSHL) Press. See http://www.cshlpress.com/.

# Application——Human Disease Model Reports

**Volume 9, Issue 3**

March 2016

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SPECIAL ARTICLE | 01 MARCH 2016

**FlyBase portals to human disease research using *Drosophila* models**

Gillian H. Millburn, Madeline A. Crosby, L. Sian Gramates, Susan Tweedie, the FlyBase Consortium

+ Author and article information

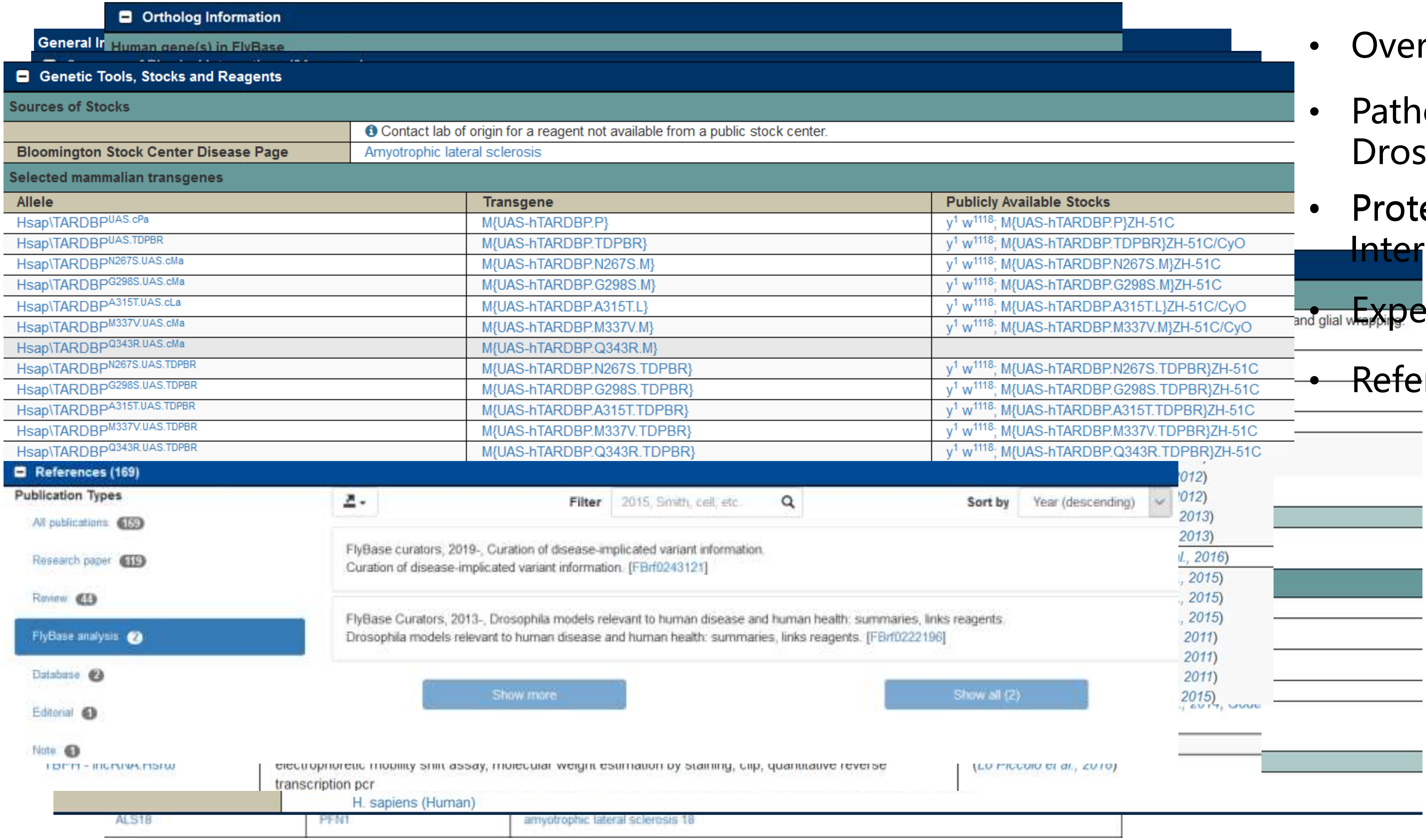
*Dis Model Mech* (2016) 9 (3): 245–252.

https://doi.org/10.1242/dmm.023317

**Related content**

A related article has been published: Exploring human disease using the Rat Genome Database

# What can we know about Amyotrophic Lateral Sclerosis 10?



**Genetic Tools, Stocks and Reagents**

**Sources of Stocks**

ⓘ Contact lab of origin for a reagent not available from a public stock center.

| | |
|---|---|
| **Bloomington Stock Center Disease Page** | Amyotrophic lateral sclerosis |

**Selected mammalian transgenes**

| Allele | Transgene | Publicly Available Stocks |
|---|---|---|
| Hsap\TARDBP$^{UAS.cPa}$ | M{UAS-hTARDBP.P} | y$^{1}$ w$^{1118}$; M{UAS-hTARDBP.P}ZH-51C |
| Hsap\TARDBP$^{UAS.TDPBR}$ | M{UAS-hTARDBP.TDPBR} | y$^{1}$ w$^{1118}$; M{UAS-hTARDBP.TDPBR}ZH-51C/CyO |
| Hsap\TARDBP$^{N267S.UAS.cMa}$ | M{UAS-hTARDBP.N267S.M} | y$^{1}$ w$^{1118}$; M{UAS-hTARDBP.N267S.M}ZH-51C |
| Hsap\TARDBP$^{G298S.UAS.cMa}$ | M{UAS-hTARDBP.G298S.M} | y$^{1}$ w$^{1118}$; M{UAS-hTARDBP.G298S.M}ZH-51C |
| Hsap\TARDBP$^{A315T.UAS.cLa}$ | M{UAS-hTARDBP.A315T.L} | y$^{1}$ w$^{1118}$; M{UAS-hTARDBP.A315T.L}ZH-51C/CyO |
| Hsap\TARDBP$^{M337V.UAS.cMa}$ | M{UAS-hTARDBP.M337V.M} | y$^{1}$ w$^{1118}$; M{UAS-hTARDBP.M337V.M}ZH-51C/CyO |
| Hsap\TARDBP$^{Q343R.UAS.cMa}$ | M{UAS-hTARDBP.Q343R.M} | |
| Hsap\TARDBP$^{N267S.UAS.TDPBR}$ | M{UAS-hTARDBP.N267S.TDPBR} | y$^{1}$ w$^{1118}$; M{UAS-hTARDBP.N267S.TDPBR}ZH-51C |
| Hsap\TARDBP$^{G298S.UAS.TDPBR}$ | M{UAS-hTARDBP.G298S.TDPBR} | y$^{1}$ w$^{1118}$; M{UAS-hTARDBP.G298S.TDPBR}ZH-51C |
| Hsap\TARDBP$^{A315T.UAS.TDPBR}$ | M{UAS-hTARDBP.A315T.TDPBR} | y$^{1}$ w$^{1118}$; M{UAS-hTARDBP.A315T.TDPBR}ZH-51C |
| Hsap\TARDBP$^{M337V.UAS.TDPBR}$ | M{UAS-hTARDBP.M337V.TDPBR} | y$^{1}$ w$^{1118}$; M{UAS-hTARDBP.M337V.TDPBR}ZH-51C |
| Hsap\TARDBP$^{Q343R.UAS.TDPBR}$ | M{UAS-hTARDBP.Q343R.TDPBR} | y$^{1}$ w$^{1118}$; M{UAS-hTARDBP.Q343R.TDPBR}ZH-51C |

**References (169)**

**Publication Types**

- All publications 169
- Research paper 119
- Review 44
- FlyBase analysis 2
- Database 2
- Editorial 1
- Note 1

**Filter** 2015, Smith, cell, etc. **Sort by** Year (descending)

FlyBase curators, 2019-, Curation of disease-implicated variant information.
Curation of disease-implicated variant information. [FBrf0243121]

FlyBase Curators, 2013-, Drosophila models relevant to human disease and human health: summaries, links reagents.
Drosophila models relevant to human disease and human health: summaries, links reagents. [FBrf0222196]

Show more Show all (2)

- Overview & Symptoms
- Pathogenic genes & Drosophila models
- Protein function & Interactions
- Experiments
- References

# Summary

- Flybase contains a variety of Drosophila genome sequence information, and provides many analysis and query tools for users to use.
- flybase homepage provides links to other resource libraries to help users get more information.
- Interaction with users needs to be improved.
- Some links are outdated and not updated in time.

# References

Marygold S J , Crosby M A , Goodman J L , et al. Using FlyBase, a Database of Drosophila Genes and Genomes[J]. Methods in Molecular Biology, 2016.

Larkin A , Marygold S J , Antonazzo G , et al. FlyBase: updates to the Drosophila melanogaster knowledge base[J]. Nucleic Acids Research, 2020.

Gillian H , Millburn, Madeline A , et al. FlyBase portals to human disease research using Drosophila models.[J]. Disease models & mechanisms, 2016.

Thanks for your attention!