GLOSSARY OF TERMS

Anonymous DNA: a length of DNA of unknown gene content.

Chromosome bands: alternating light- or dark-staining sections along a chromosome that are visible by light microscopy after staining procedures are used.

Chromosome walk: a method of aligning pieces of DNA by consecutive hybridizations in which probes corresponding to one end of a cloned piece of DNA are used to identify the next clone in line.

Contig: a set of overlapping pieces of DNA that span an uninterrupted stretch of the genome.

Cosmid: a piece of DNA (35 to 45 kb) cloned into a vector that usually consists of *cos* sequences required for packaging the DNA into a bacteriophage, an origin of replication, and a drug resistance marker.

Genetic linkage map: a map that shows the relative position of loci on the basis of frequency of recombination events. Units are in centimorgans (cM) where, over small distances, 1 cM is equivalent to a 1% chance of recombination.

Physical map: a map in which the distances between landmarks such as clones, restriction endonuclease sites, or specific loci are expressed in kilobases.

Polymerase chain reaction (PCR): a technique that involves repeated cycles of DNA denaturation, renaturation with short lengths of DNA (primers) separated by up to 4 kb, and polymerase-mediated replication. This results in an exponential increase in the number of copies of the sequence between the primers.

Polymorphic marker: a locus at which there is normal sequence variation within the population that is inherited and occurs with a frequency of >1%.

Polytene chromosome: a giant chromosome consisting of many identical, slightly condensed strands of chromatin held together in parallel and in register.

GENO

The wall chart this year is divi
genome mapping for many of
shows a summary of pro

REC

Chromosome	1	2	3	4
Number of genes				
Estimated	4150	3950	3200	3050
Mapped	236	131	72	84
Disease-related	43	18	16	22
Number of polymorphic markers				
Total	158	99	333	148
PCR-based	13	15	12	14
Kilobases of sequence	450	558	104	181

This table is a depiction of the current progress on th
1991. There are an estimated 3,000 megabases (Mb
containing an estimated 50,000 to 100,000 genes. S
1990 [*Science* 250, 262a (1990)], 359 new mapped g
added to the map.

The estimated number of genes is based on the estimated to
distributed proportionally according to the relative size of eac
237 (1990)]. The number of genes mapped is the number of g
The number of disease-related genes is based on locus entries
Inheritance in Man (Johns Hopkins Univ. Press, Baltimore, M
genes and anonymous DNA segments. They are useful in ge
specific regions within a chromosome. The number of polym

SCIENCE

GENOME M

The wall chart this year is divided in two parts. At the top is presented an update of progress genome mapping for many of the model systems that have been essential in understanding ge shows a summary of progress in mapping and sequencing the fruit fly, an organism that

RECENT ADVANCES IN HUMA

e	1	2	3	4	5	6	7	8	9	10	11	12	13	
s														
d	4150	3950	3200	3050	2900	2750	2700	2250	2200	2200	2200	2050	1800	1
d	236	131	72	84	82	115	128	59	63	75	142	117	28	
d	43	18	16	22	15	14	16	15	17	11	33	17	6	
f s														
l	158	99	333	148	202	165	196	88	50	91	265	69	58	
d	13	15	12	14	13	12	12	11	9	4	20	10	4	
e	450	558	104	181	142	471	381	167	177	158	655	416	82	

ction of the current progress on the mapping of the human genome as of 28 July, an estimated 3,000 megabases (Mb) of DNA sequence in the human genome, mated 50,000 to 100,000 genes. Since the publication of The Human Genome Map , 262a (1990)], 359 new mapped genes and 673 new polymorphic markers have been

genes is based on the estimated total number of genes in the human genome, ccording to the relative size of each chromosome [J. C. Stephens *et al.*, *Science* 250, f genes mapped is the number of genes that have been localized to the chromosome. ted genes is based on locus entries that are referenced in V. McKusick, *Mendelian* Hopkins Univ. Press, Baltimore, MD ed. 9, 1990). Polymorphic markers include A segments. They are useful in genetic linkage studies for the localization of genes to romosome. The number of polymerase chain reaction (PCR)-based polymorphic

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There ar the numbe completene physically chromosom In addition amount of table, beca in sequenc status of th

SCIENCE

E MAPS 199

esented an update of progress in the human genome. There have also been major advances i
essential in understanding gene function. As a first example, the bottom section of the chart
the fruit fly, an organism that is a classic model for studies in genetics and development.

ES IN HUMAN GENE MAPPING

10	11	12	13	14	15	16	17	18	19	20	21	22	X
2200	2200	2050	1800	1750	1650	1400	1350	1250	1150	1050	900	950	235
75	142	117	28	65	59	71	121	22	104	42	39	71	20
11	33	17	6	12	12	12	18	4	20	11	4	18	9
91	265	69	58	54	55	130	192	35	73	57	71	124	25
4	20	10	4	8	5	8	20	2	12	31	10	4	2
158	655	416	82	260	102	309	623	94	266	124	51	141	44

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to known loci are based on analysis of information obtained from GenBank, Los Alam

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status of the human genome map will be presented in the Perspective (P. Pearso

1991

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he bottom section of the chart
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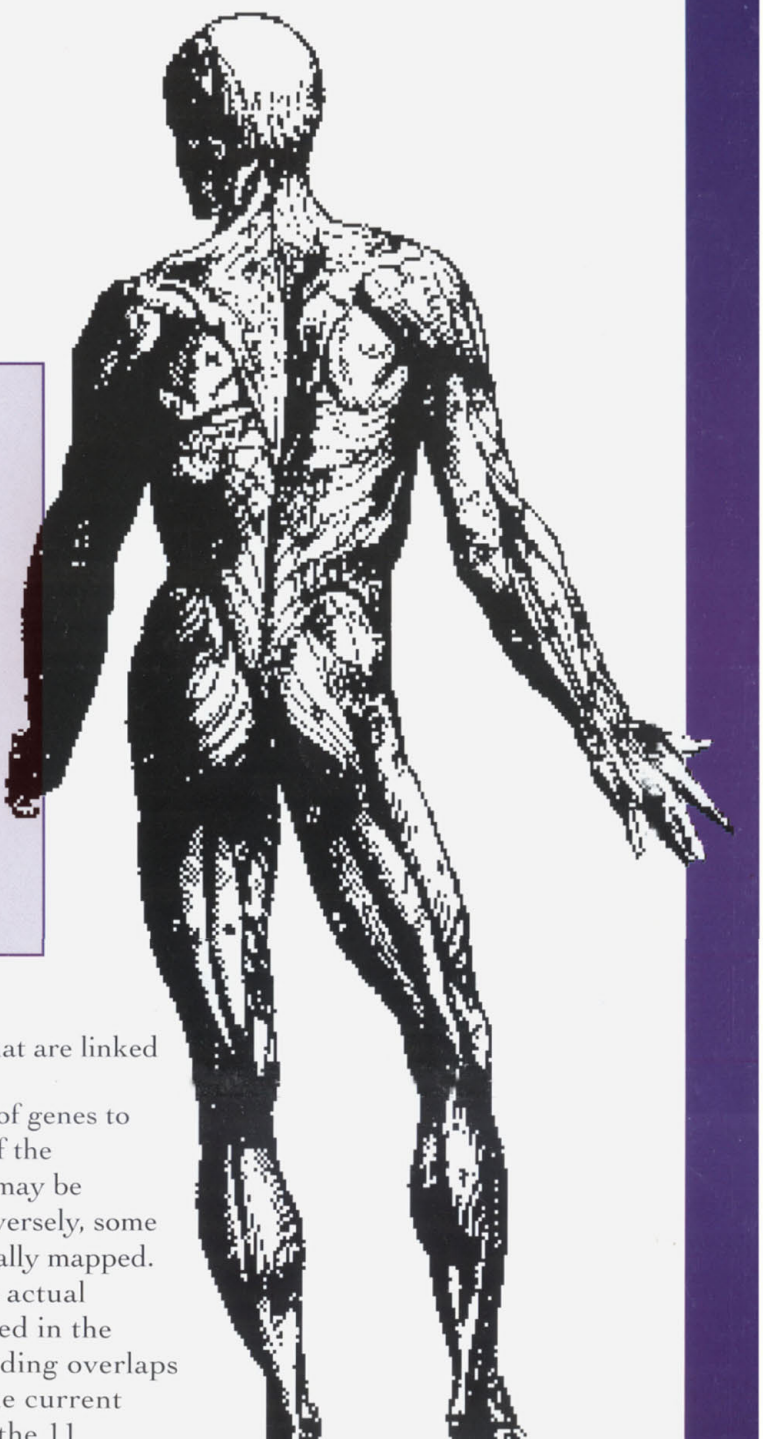
PING

19	20	21	22	X	Y
150	1050	900	950	2350	1000
104	42	39	71	202	16
20	11	4	18	93	1
73	57	71	124	255	25
12	31	10	4	24	0
266	124	51	141	441	19



r molecular studies. Kilobases of sequence that are linked
obtained from GenBank, Los Alamos, NM.
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renaturation with short lengths of DNA (primers) separated by up to 4 kb, and polymerase-mediated replication. This results in an exponential increase in the number of copies of the sequence between the primers.

Polymorphic marker: a locus at which there is normal sequence variation within the population that is inherited and occurs with a frequency of >1%.

Polytene chromosome: a giant chromosome consisting of many identical, slightly condensed strands of chromatin held together in parallel and in register.

Yeast artificial chromosome (YAC): a cloning vector in which sections of yeast chromosomes needed for initiation of DNA synthesis and stability are used to replicate large (>100 kb) pieces of DNA.

This table is a depiction of the current progress on th
1991. There are an estimated 3,000 megabases (MB
containing an estimated 50,000 to 100,000 genes. S
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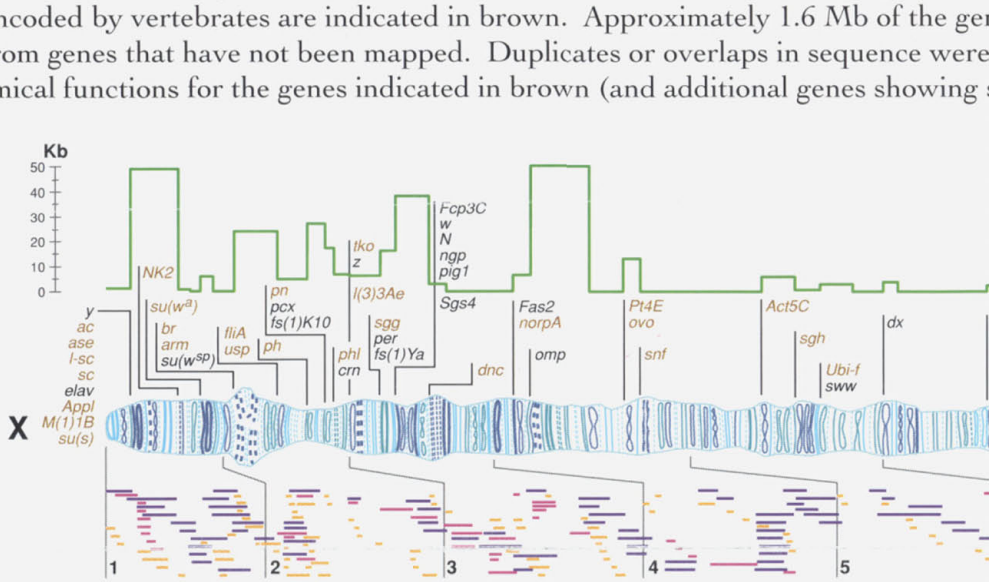
specific regions within a chromosome. The number of polym
markers is the subset of polymorphic markers that can be det

This figure relates the locations of sequence information, sequenced genes, c
on the polytene chromosomes of the fruit fly, *Drosophila melanogaster*. The
from C. B. Bridges [*J. Hered.* **26**, 60 (1935); by permission]; numbers 1 to
divisions. The Y chromosome and other heterochromatic blocks, which do
haploid genome consists of approximately 165 Mb of DNA of which 110 Mb are includ
Estimates of total gene number range from 5,000 (based on the number of lethal mutati
the number of transcription units).

Genes that have been sequenced as of 31 May, 1991 and a graph of kilobases (kb) se
(updated from M. Ashburner, *Drosophila Genetic Maps*, Drosophila Information Servic
vol. 69] are shown directly above their chromosome subdivisions. *Drosophila* genes tha
genes encoded by vertebrates are indicated in brown. Approximately 1.6 Mb of the ge
40 kb from genes that have not been mapped. Duplicates or overlaps in sequence were
Biochemical functions for the genes indicated in brown (and additional genes showing



— **200 kb** – For sizes of YACs, cosmids, and chromosome walks

■ – Kb sequenced per chromosome subdivision

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DROSOPHILA MELAN

e information, sequenced genes, chromosome bands, and DNA clones
fly, *Drosophila melanogaster*. The chromosomes pictured were taken
5); by permission]; numbers 1 to 102 represent standard chromosome
heterochromatic blocks, which do not polytenize, are not shown. The
DNA of which 110 Mb are included in the polytene chromosomes.
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1 and a graph of kilobases (kb) sequenced per chromosome subdivision
ps, Drosophila Information Service, W. Gelbart, Ed. (Harvard, 1991),
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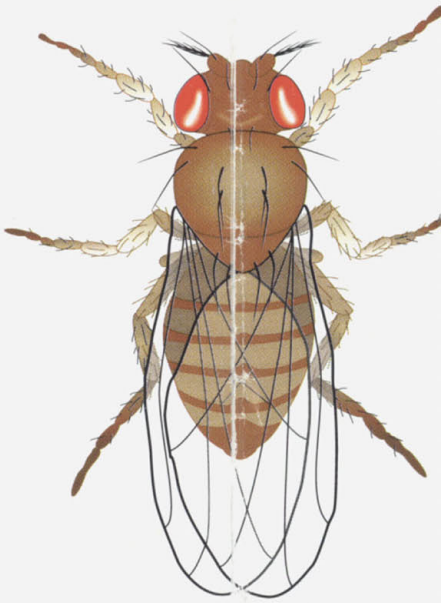
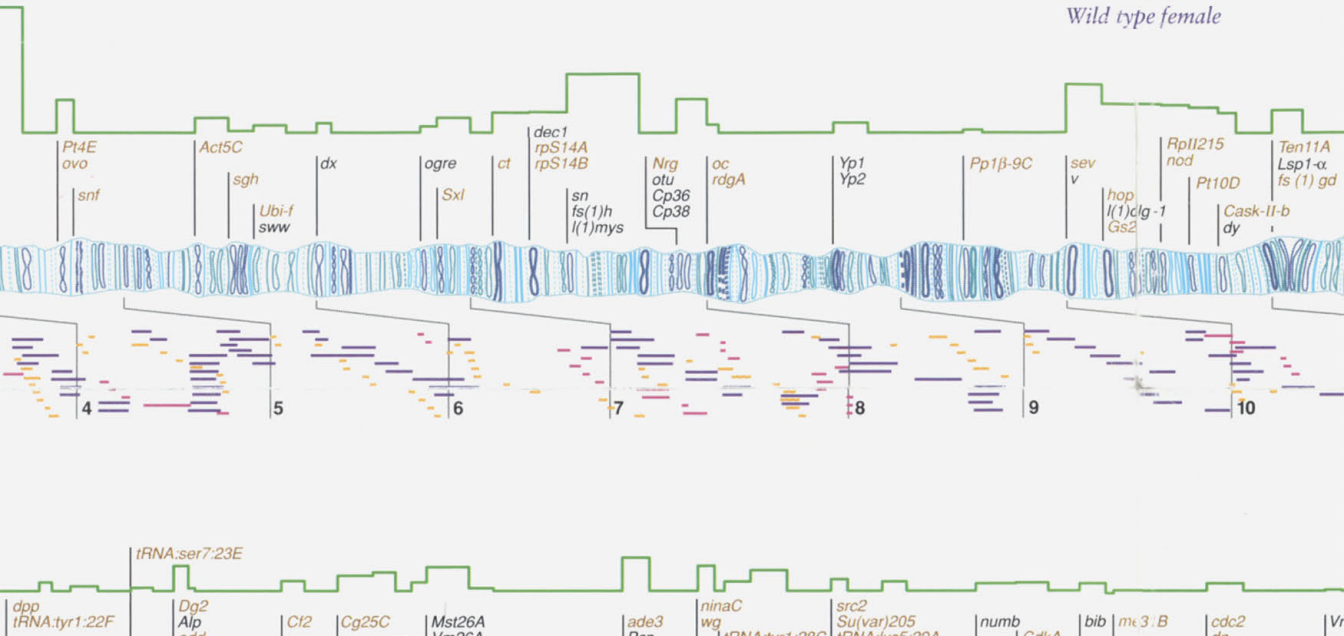
Approximately 1.6 Mb of the genome have been sequenced, including
cates or overlaps in sequence were not counted more than once.
vn (and additional genes showing such similarities that have not been



Wild type female



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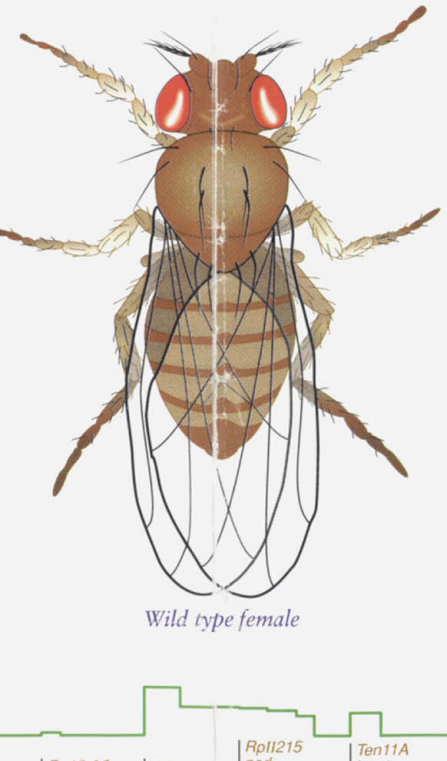
HILA MELANOGASTER



Wild type female

mapped) are shown in the table below the chart. Numbers in parenthes
category.

Below each chromosome, the approximate locations and sizes of clon
chromosome walks larger than 40 kb (magenta) are pictured in proport
horizontal scale bar at the left. Grey lines indicate the locations of the D
used to relate those locations back to the chromosome bands. The size
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Louis, C. Savakis, and M. Ashburner (current as of 1 July, 1991); and
Lee, and J. Johnsen (current as of 31 May, 1991). DNA localization is
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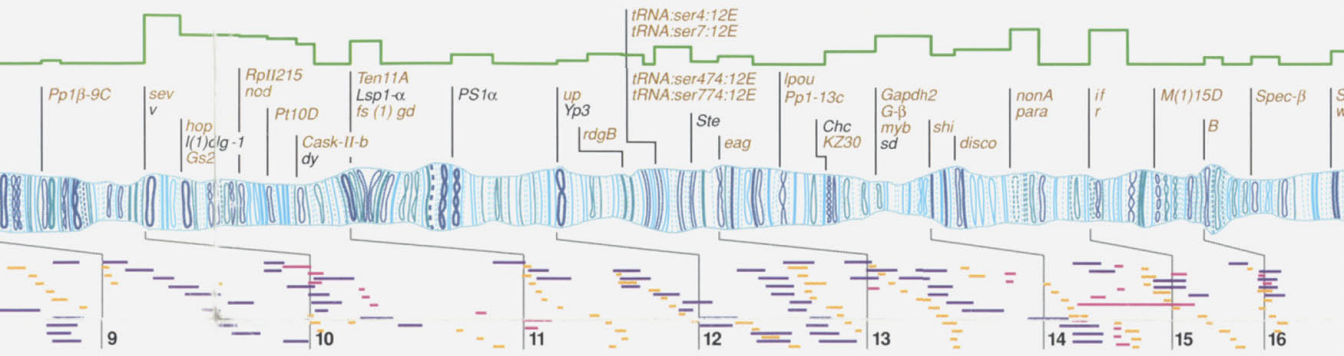

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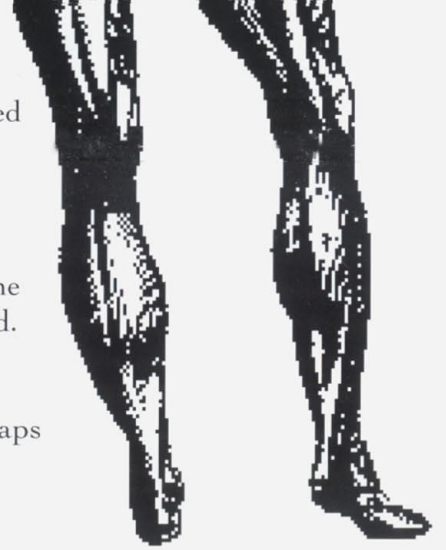

v the chart. Numbers in parentheses indicate the presence of more than one gene in that

oximate locations and sizes of cloned DNA in YACs (blue), cosmids (orange), or
(magenta) are pictured in proportion to their lengths. Cloned DNA sizes are relative to the
ines indicate the locations of the DNAs relative to chromosome divisions and should be
the chromosome bands. The size of each chromosome division in kilobases has been
Maps in Drosophila (CRC Press, Boca Raton, FL, 1988)]. Data on YACs were supplied by
f 15 June, 1991); on cosmids by D. Glover, R. Saunders, F. Kafatos, I. Sidén-Kiamos, C.
(current as of 1 July, 1991); and on chromosome walks were compiled by J. Merriam, G.
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in situ hybridization. The lengths of cosmid contigs were estimated from the number of
cosmids, and chromosome walks are available from the authors upon request; further
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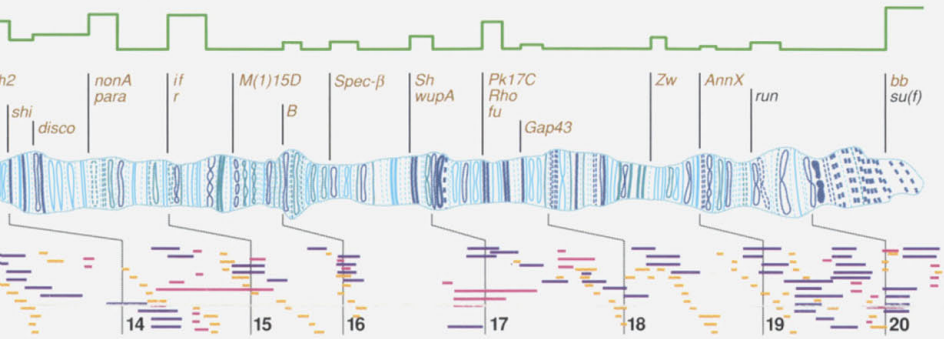
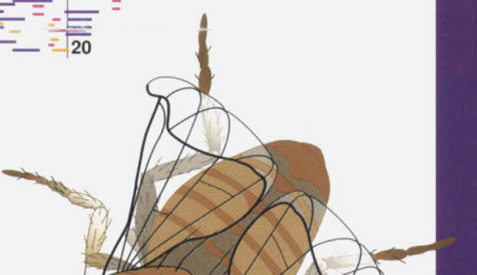




— 200 kb – For sizes of YACs, cosmids, and chromosome walks

■ – Kb sequenced per chromosome subdivision

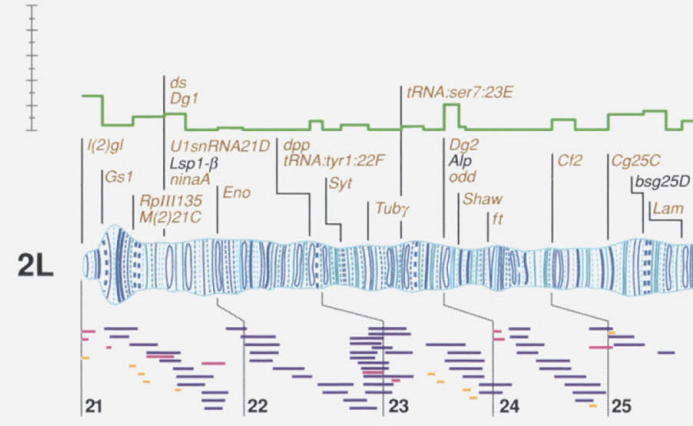
■ – Genes similar in *Drosophila* and vertebrates

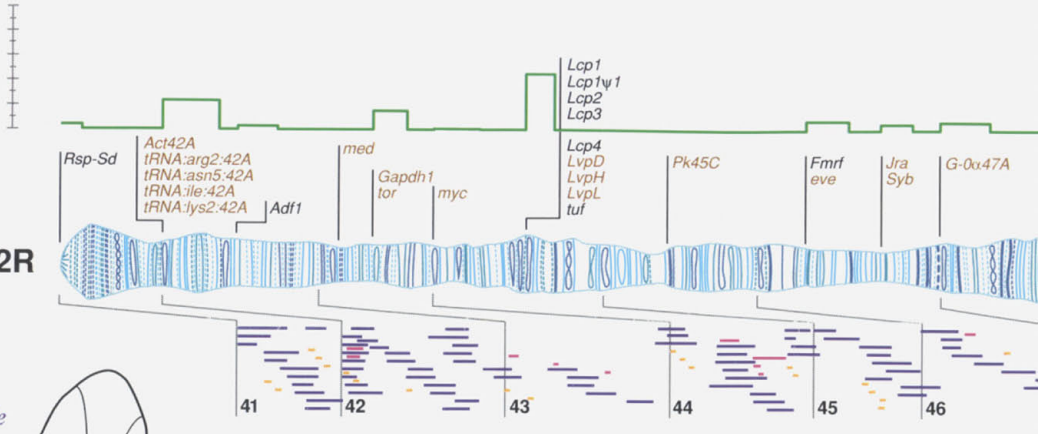
■ – YACs

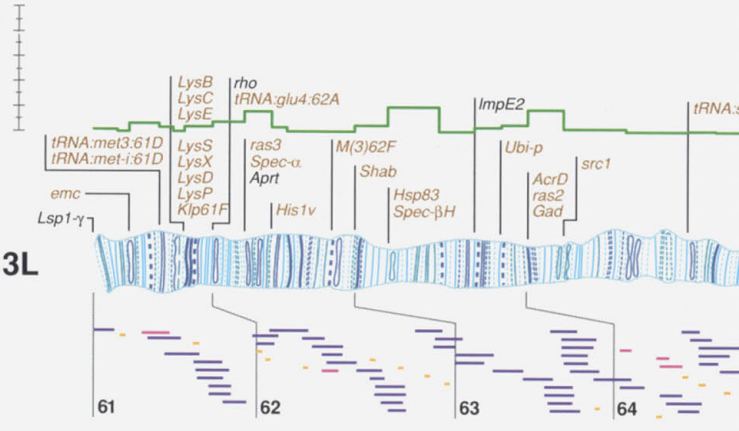
■ – Chromosome walks

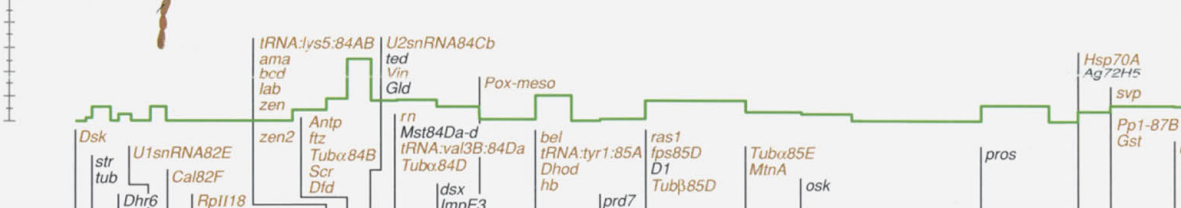
■ – Cosmids

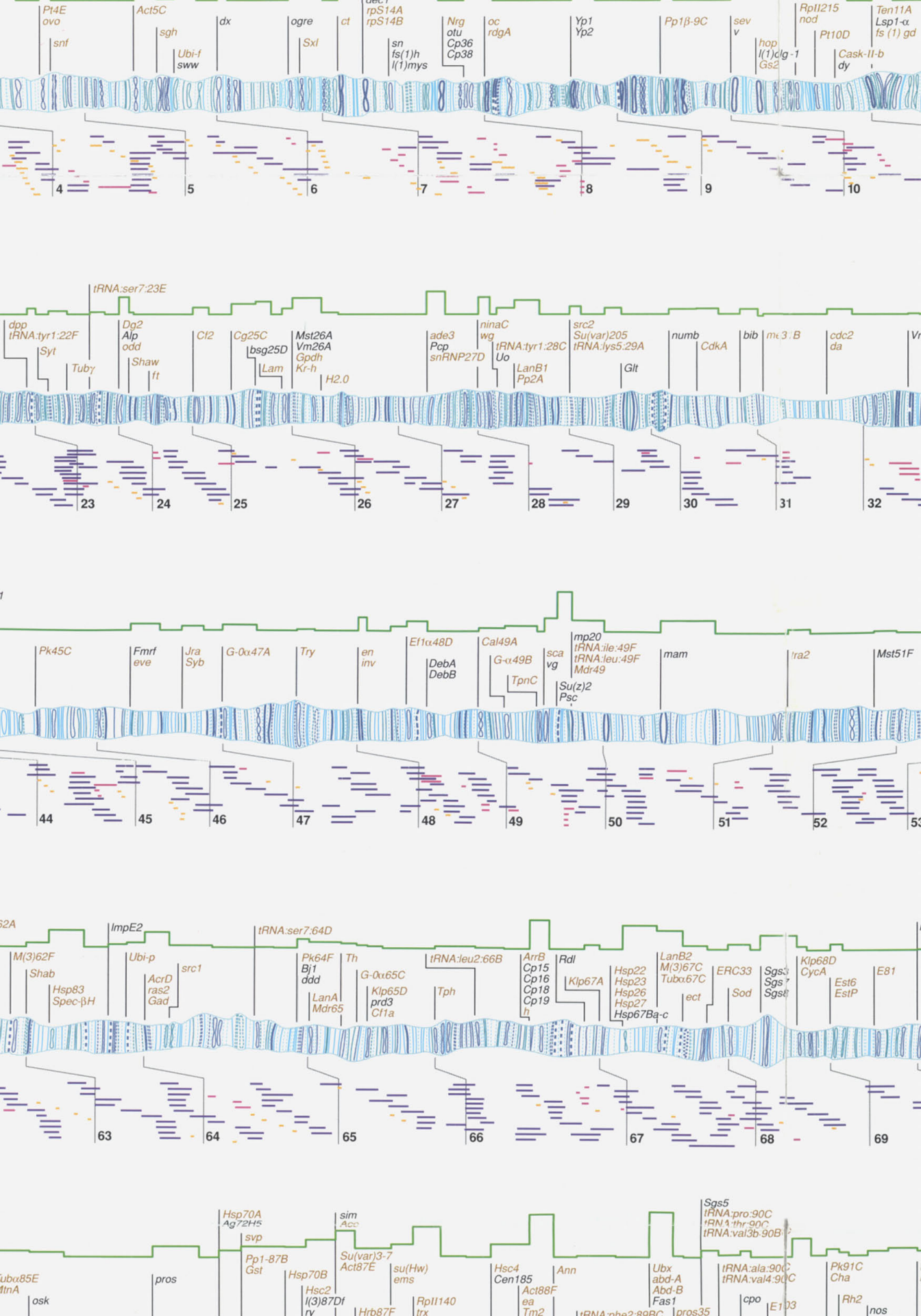
Sepia-eyed male







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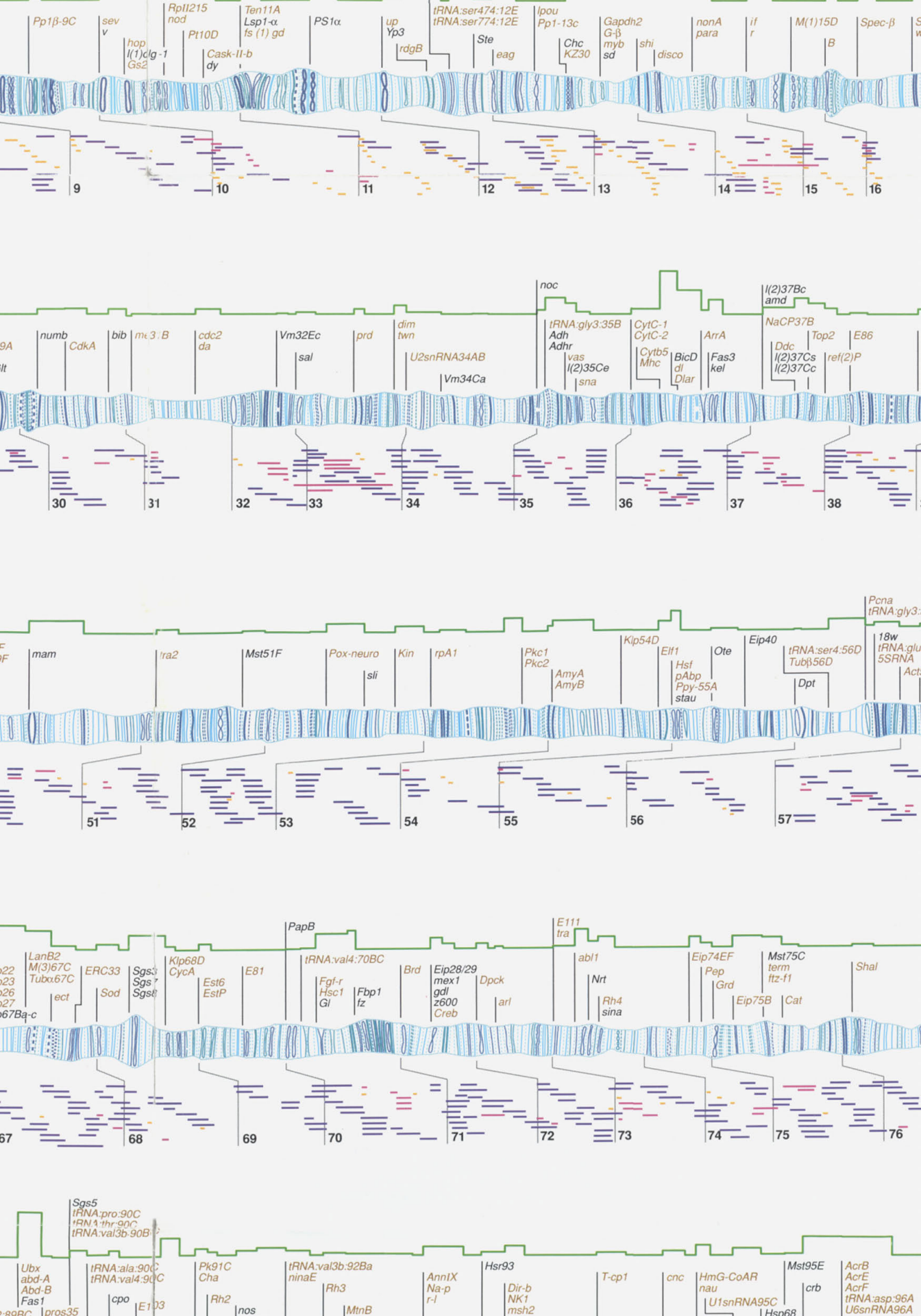
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Eip40
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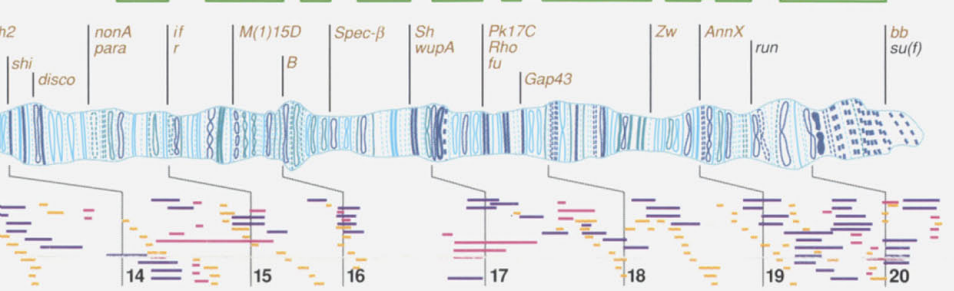
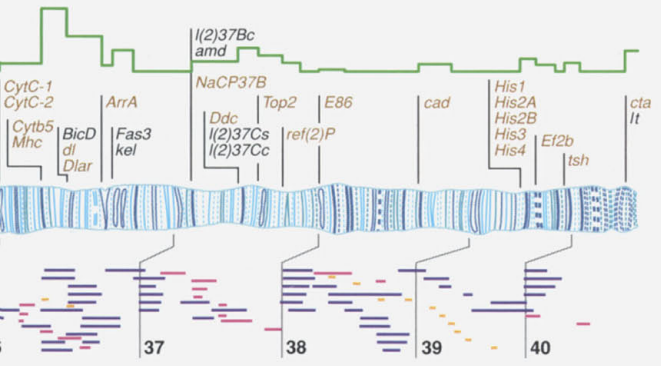
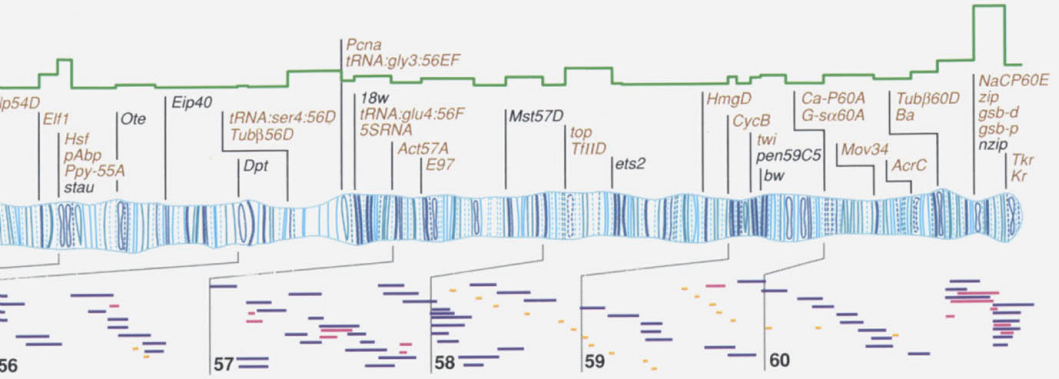
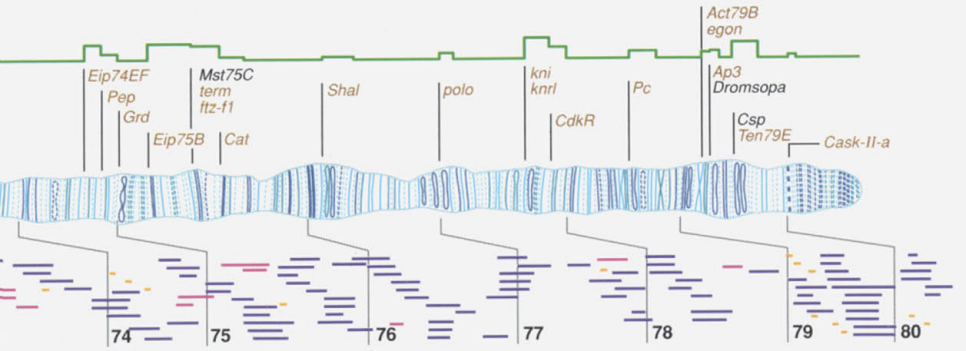
Pk91C
Cha
Rh2
nos
tRNA:val3b:92Ba
ninaE
Rh3
MtnB
AnnIX
Na-p
r-l
Hsr93
Dir-b
NK1
msh2
T-cp1
cnc
HmG-CoAR
nau
U1snRNA95C
Mst95E
crb
Hsp68
AcrB
AcrE
AcrF
tRNA:asp:96A
U6snRNA96A

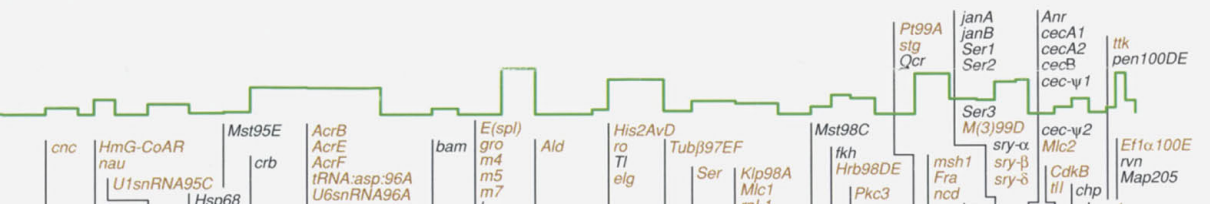


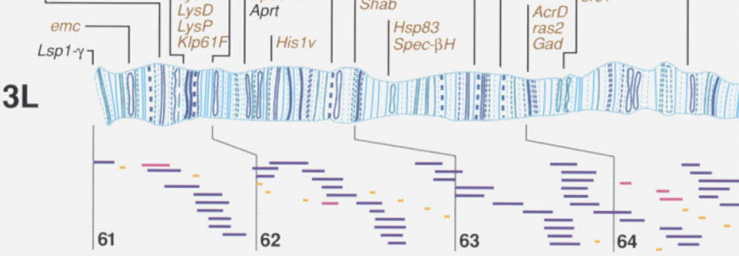


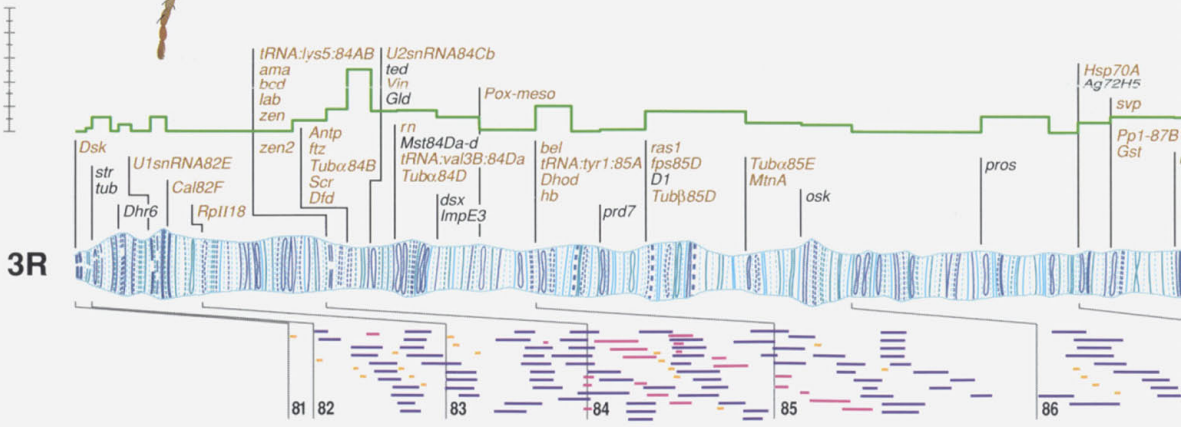
White-eyed female, curly wings

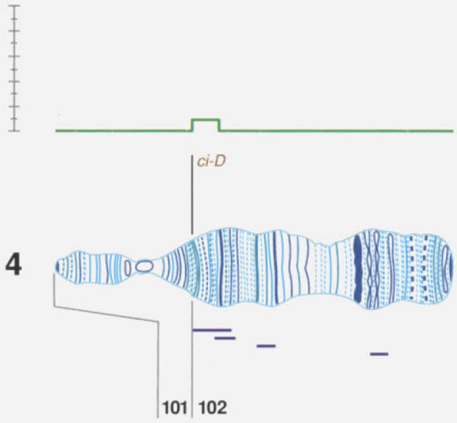










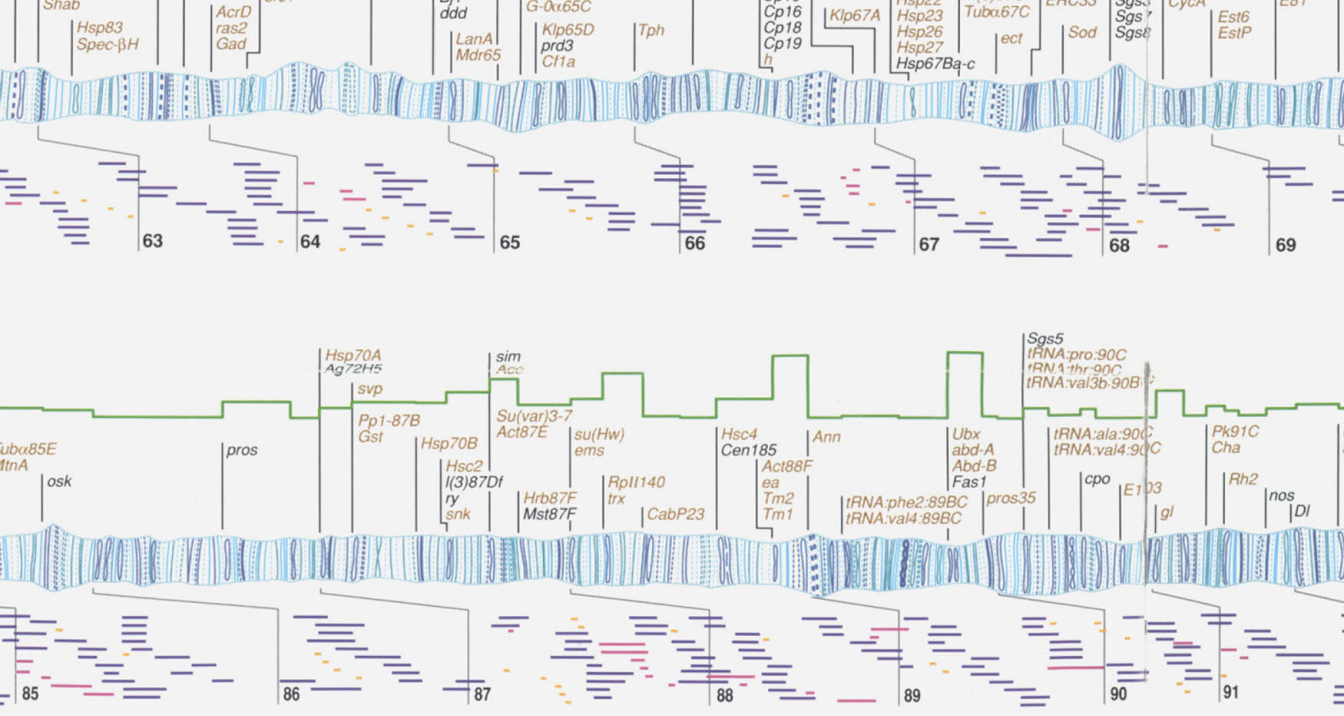


Cell cycle proteins
- Cdc2-like proteins (2)
- Cdc25-like
- Cyclin A
- Cyclin B

Cell and substrate adhesion proteins
- Cadherin (3)
- Collagen (3)
- Immunoglobulin superfamily (2)
- Integrin (3)
- Laminin (3)
- N-CAM-like
- Neural adhesion molecule L1
- Plakoglobin
- Tenascin (2)

Cytoskeleton
- Actin (6)
- α Actinin
- Cytoplasmic myosin
- Cytoplasmic myosin
- Dynamin
- Kinesin (11)
- Lamin
- Myosin heavy chain
- Myosin light chain (2)
- Paramyosin
- α Spectrin

GENOME MAPS 1991 • Barbara R. Jasny: *Science* Coordinator • ***Homo sapiens*** component: Authors: Michael Chipperfield, Bo
Dundee, Scotland; Ian Duncan and Daniel Hartl–Washington University, St. Louis, MO; John Merriam, Geunbae Lee, Joy



GENES SIMILAR IN

cycle proteins
2-like proteins (2)
25-like
n A
n B

and substrate
sion proteins
herin (3)
agen (3)
unoglobulin superfamily (2)
grin (3)
nin (3)
AM-like
al adhesion molecule L1
Plakoglobin
Tenascin (2)

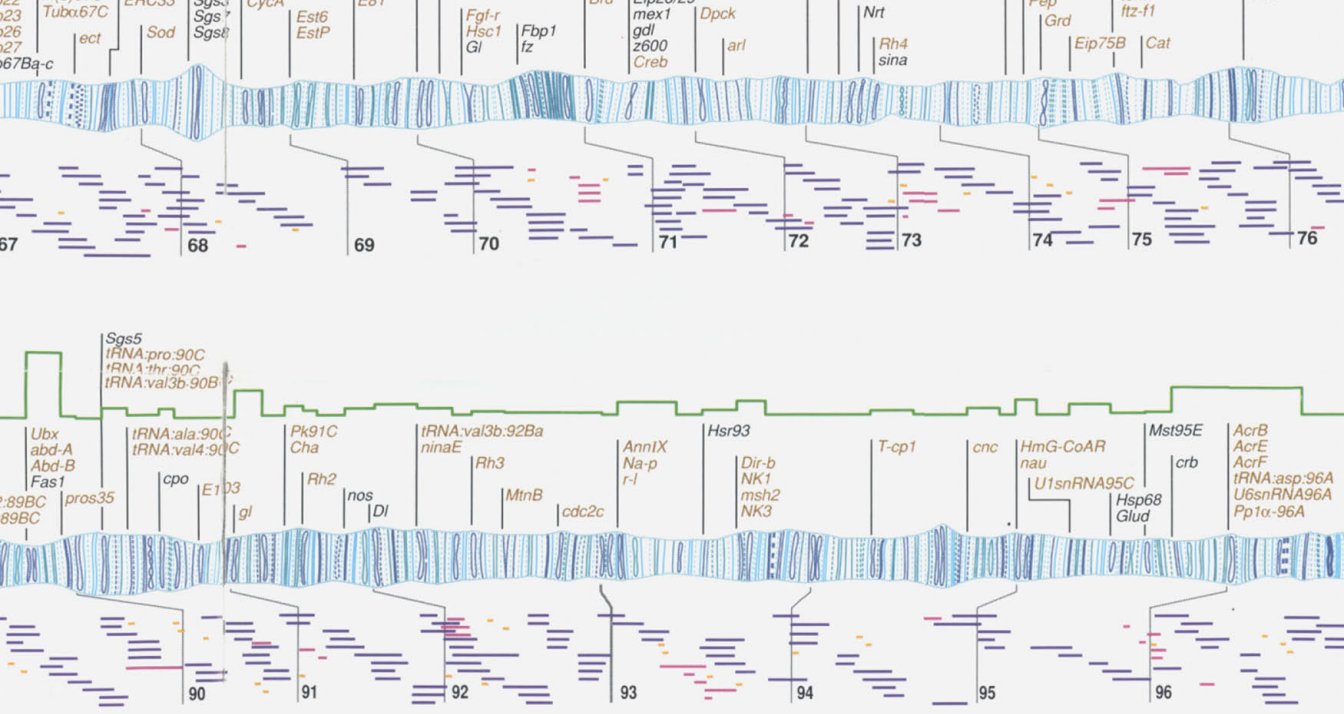
Cytoskeleton
Actin (6)
α Actinin
Cytoplasmic myosin heavy chain
Cytoplasmic myosin light chain
Dynamin
Kinesin (11)
Lamin
Myosin heavy chain
Myosin light chain (2)
Paramyosin
α Spectrin
β Spectrin (2)
Tropomyosin (2)
Troponin (4)
α Tubulin (4)
β Tubulin (4)
γ Tubulin
Vinculin

Growth factors and receptors
EGF receptor
FGF receptor
Insulin receptor (2)
TGF β

Neuronal function
Acetylcholinesterase
Acetylcholine receptor (6)
Ca^{2+}-activated ATPase (3)
Ca^{2+} channel protein
Choline acetyltransferase
Dopa decarboxylase
Glutamic acid decarboxylase
Glycine receptor
Growth-related protein GAP43
K^+ channel proteins (5)
Na^+ channel proteins (3)
Na^+, K^+ ATPase
Serotonin receptor
Synaptobrevin
Synaptotagmin
Tryptophan hydrolase
Tyrosine-3-hydroxylase

Nucleic acid synthesis a
metabolism
Adenine phosphoribosyl transf
Apurinic endonuclease
Aspartate transcarbamylase
Carbamyl phosphate syntha
DEAD proteins (5)
Dihydroorotase
Dihydroorotate dehydrogena
Excision repair ERCC3
Nucleoside diphosphate kina

s component: Authors: Michael Chipperfield, Bonnie Maidak, Peter Pearson–Genome Data Base, Baltimore, MD; Reviewer: Bertrand R. Jordan–CIML
St. Louis, MO; John Merriam, Geunbae Lee, Joy Johnsen–University of California, Los Angeles, CA; Fotis C. Kafatos, Inga Sidén-Kiamos, Christos Loui



GENES SIMILAR IN *DROSOPHILA* AND VERTEBRATES

- ne receptor (6)
- ated ATPase (3)
- nel protein
- etyltransferase
- rboxylase
- cid decarboxylase
- eptor
- ated protein GAP43
- proteins (5)
- el proteins (3)
- Pase
- eceptor
- vin

- Synaptotagmin
- Tryptophan hydrolase
- Tyrosine-3-hydroxylase

Nucleic acid synthesis and metabolism

- Adenine phosphoribosyl transferase
- Apurinic endonuclease
- Aspartate transcarbamylase
- Carbamyl phosphate synthase
- DEAD proteins (5)
- Dihydroorotase
- Dihydroorotate dehydrogenase
- Excision repair ERCC3
- Nucleoside diphosphate kinase
- PCNA
- Phosphoribosylamine: glycine ligase
- Phosphoribosylformylglycinamide cyclo-ligase
- Phosphoribosylglycinamide formyltransferase
- Poly(A)-binding protein
- Ribonucleoproteins (12)
- RNA polymerase II (3)
- RNA polymerase III (2)
- RNA polymerase elongation factor

Oncogenes

- Abl
- Ets (3)
- Fps
- Gli
- Intl
- Myb
- Myc
- Raf
- Ras (3)
- Rel
- Rhombitin
- Src (2)

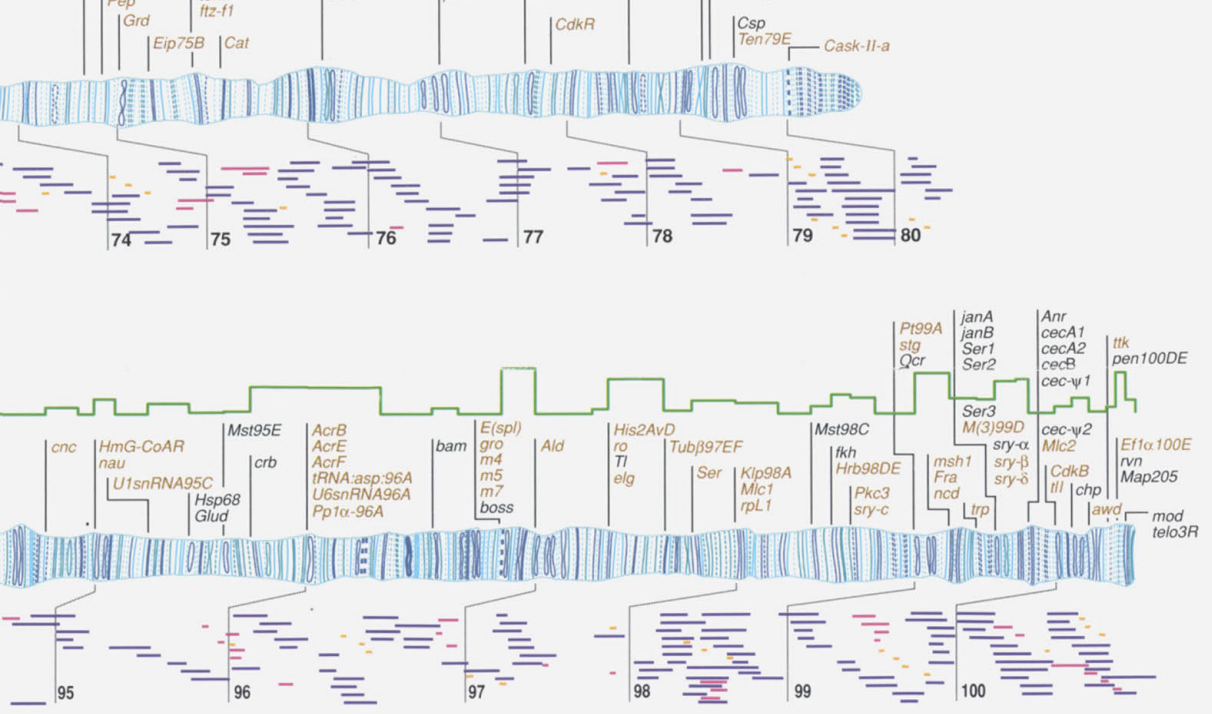
Protein synthesis machinery

- Elongation factors (3)
- Ribosomal proteins (13)

Second messenger systems

- Annexin (3)
- Arrestin (2)
- Calcineurin
- Calmodulin (2)
- Calmodulin inhibitor
- cAMP-dependent kinase (4)
- cAMP phosphodiesterase
- cGMP-dependent kinase (2)
- Cystatin
- Diacylglycerol kinase
- G proteins (9)
- GTPase-activating protein (2)
- GTP-binding protein

ore, MD; Reviewer: Bertrand R. Jordan–CIML CNRS, Marseilles, France • *Drosophila melanogaster* component : Authors: Michael Ashburner–Univers tis C. Kafatos, Inga Sidén-Kiamos, Christos Louis, Charalambos Savakis, Research Center of Crete, Heraklion, Crete, Greece; Reviewer: Gerald M. Rubin ublication of The American Association for the Advancement of Science.



ERTEBRATES

Second messenger systems
- Annexin (3)
- Arrestin (2)
- Calcineurin
- Calmodulin (2)
- Calmodulin inhibitor
- cAMP-dependent kinase (4)
- cAMP phosphodiesterase
- cGMP-dependent kinase (2)
- Cystatin
- Diacylglycerol kinase
- G proteins (9)
- GTPase-activating protein (2)
- GTP-binding protein

s machinery
- (3)
- s (13)

- Opsin (4)
- Peptidyl prolylisomerase (2)
- Phospholipase C
- Serine/threonine kinase (6)
- Serine/threonine phosphatase (6)
- Tyrosine kinase (11)
- Tyrosine phosphatase (5)

Transcription factors
- cAMP response element binding protein (CREB)
- Heat-shock transcription factor
- Helix-loop-helix proteins (16)
- Homeodomain proteins (37)
- Paired-box proteins (5)
- POU domain proteins (4)
- Steroid receptor protein family (10)
- TFIID
- Zn-finger proteins (22)

Other DNA binding proteins
- Chromobox proteins (2)
- High mobility group protein 1
- Histones (7)
- Topoisomerase II

Miscellaneous
- β Amyloid protein precursor–like
- Cholecystokinin
- Clathrin heavy chain
- Cytochromes (3)
- Fibrinogen-like
- Furin-like protease
- Heat-shock proteins (7)
- Lysozyme (7)
- Metallothionein (2)
- Multiple drug resistance (2)
- Proteasome subunits (3)
- Serine protease (9)
- Serine protease inhibitor
- Trypsin
- Ubiquitin (2)
- Other metabolic enzymes (25)

mponent : Authors: Michael Ashburner–University of Cambridge, U.K.; David M. Glover and Robert D. C. Saunders–University of klion, Crete, Greece; Reviewer: Gerald M. Rubin, University of California, Berkley, CA • Graphic Artist: Susan Nowoslawski