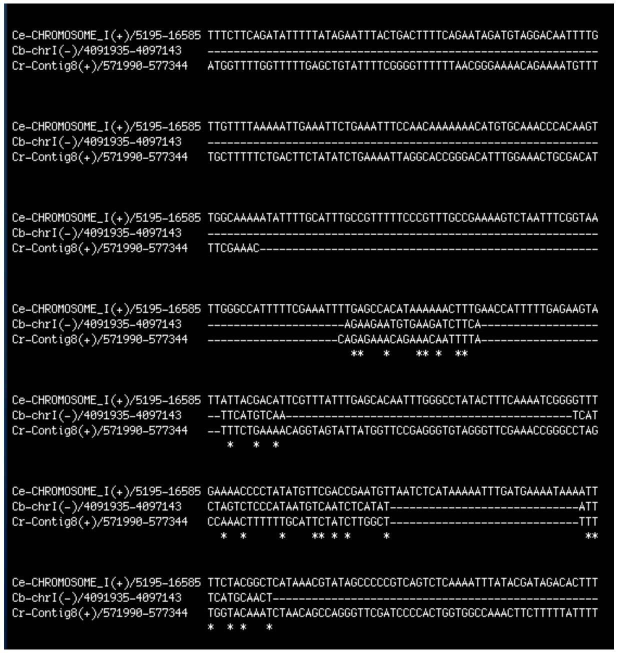
GBrowse_syn

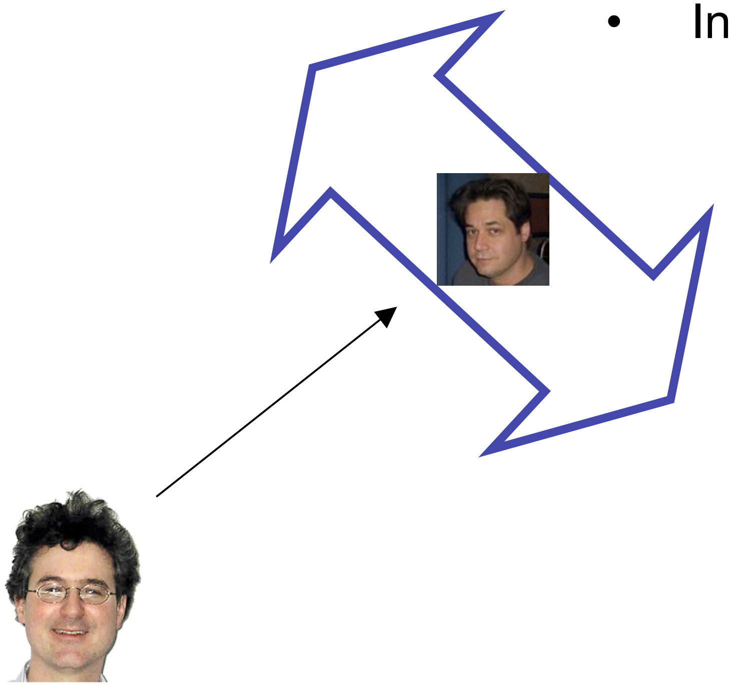
Sheldon McKay, CSHL

Goals

- More than two species
- Nucleotide-level resolution (gapped alignments)
- High-level resolution (synteny)
- Intuitive graphical rendering



```
Ce-CHROMOSOME_I(+)/5195-16585 TTTCTTCAGATATTTTTATAGAATTTACTGACTTTTCAGAATAGATGTAGGACAATTTTG
Cb-chrI(-)/4091935-4097143    ------------------------------------------------------------
Cr-Contig8(+)/571990-577344   ATGGTTTTGGTTTTTGAGCTGTATTTTCGGGGTTTTTTAACGGGAAAACAGAAAATGTTT


Ce-CHROMOSOME_I(+)/5195-16585 TTGTTTTAAAAATTGAAATTCTGAAATTTCCAACAAAAAAACATGTGCAAACCCACAAGT
Cb-chrI(-)/4091935-4097143    ------------------------------------------------------------
Cr-Contig8(+)/571990-577344   TGCTTTTTCTGACTTCTATATCTGAAAATTAGGCACCGGGACATTTGGAAACTGCGACAT


Ce-CHROMOSOME_I(+)/5195-16585 TGGCAAAAATATTTTGCATTTGCCGTTTTTCCCGTTTGCCGAAAAGTCTAATTTCGGTAA
Cb-chrI(-)/4091935-4097143    ------------------------------------------------------------
Cr-Contig8(+)/571990-577344   TTCGAAAC----------------------------------------------------


Ce-CHROMOSOME_I(+)/5195-16585 TTGGGCCATTTTTCGAAATTTTGAGCCACATAAAAAACTTTGAACCATTTTTGAGAAGTA
Cb-chrI(-)/4091935-4097143    ---------------------AGAAGAATGTGAAGATCTTCA------------------
Cr-Contig8(+)/571990-577344   --------------------CAGAGAAACAGAAACAATTTTA------------------
                                                    **   *    ** *  **


Ce-CHROMOSOME_I(+)/5195-16585 TTATTACGACATTCGTTTATTTGAGCACAATTTGGGCCTATACTTTCAAAATCGGGGTTT
Cb-chrI(-)/4091935-4097143    --TTCATGTCAA--------------------------------------------TCAT
Cr-Contig8(+)/571990-577344   --TTTCTGAAAACAGGTAGTATTATGGTTCCGAGGGTGTAGGGTTCGAAACCGGGCCTAG
                                 *   *  *


Ce-CHROMOSOME_I(+)/5195-16585 GAAAACCCCTATATGTTCGACCGAATGTTAATCTCATAAAAATTTGATGAAAATAAAATT
Cb-chrI(-)/4091935-4097143    CTAGTCTCCCATAATGTCAATCTCATAT-----------------------------ATT
Cr-Contig8(+)/571990-577344   CCAAACTTTTTTGCATTCTATCTTGGCT-----------------------------TTT
                                *  *     *    ** * *     *                              **


Ce-CHROMOSOME_I(+)/5195-16585 TTCTACGGCTCATAAACGTATAGCCCCCGTCAGTCTCAAAATTTATACGATAGACACTTT
Cb-chrI(-)/4091935-4097143    TCATGCAACT--------------------------------------------------
Cr-Contig8(+)/571990-577344   TGGTACAAATCTAACAGCCAGGGTTCGATCCCCACTGGTGGCCAAACTTCTTTTTATTTT
                              *  * *   *
```



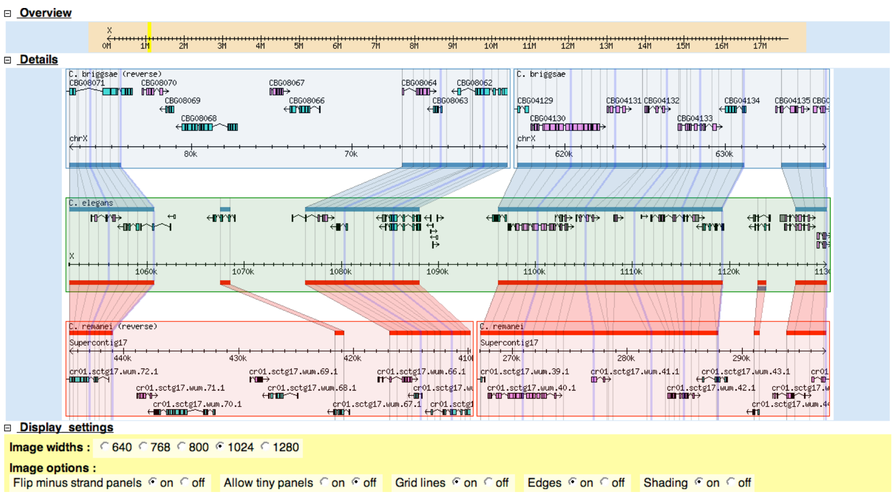
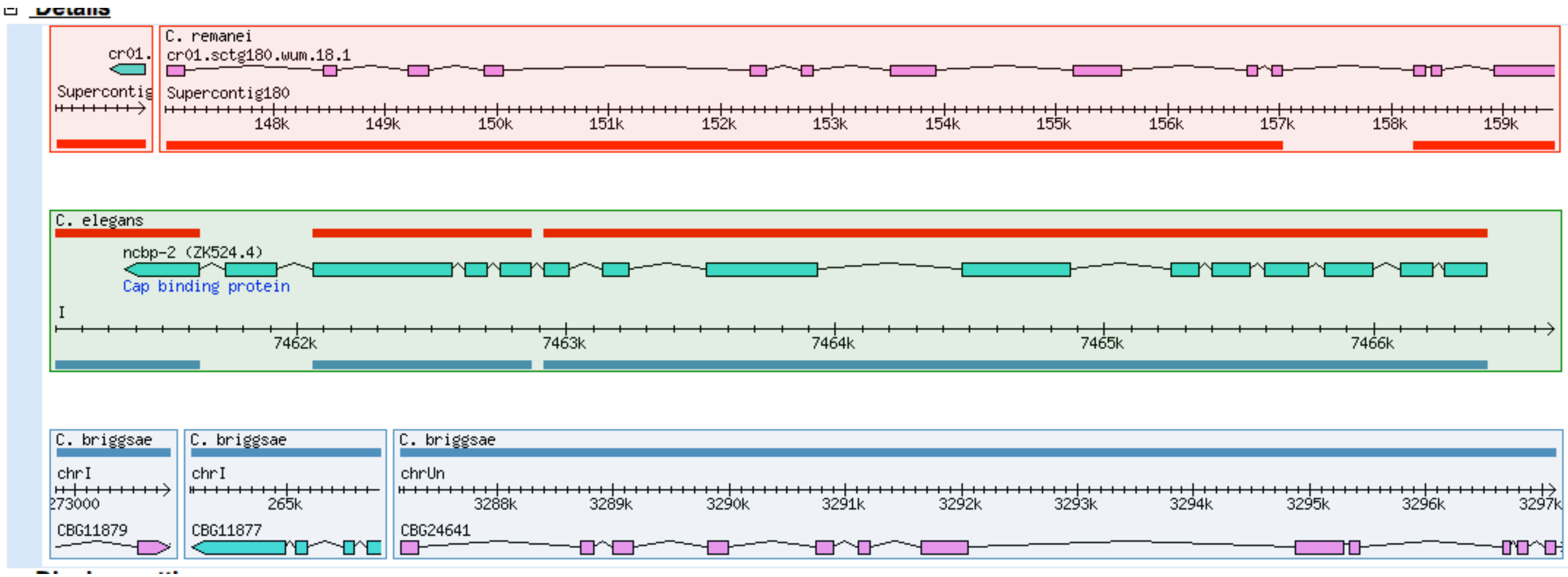


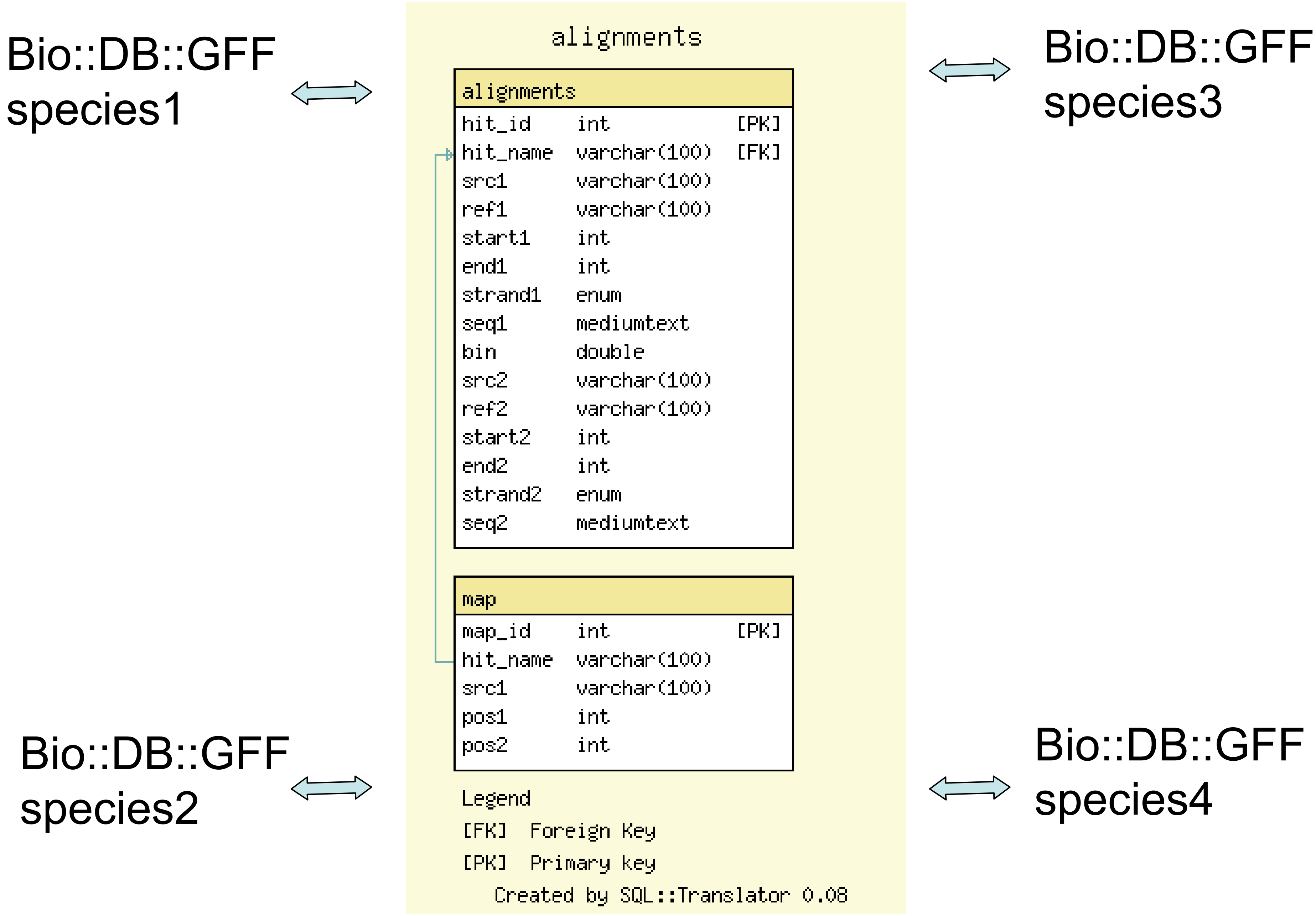
Image widths : ○ 640 ○ 768 ○ 800 ● 1024 ○ 1280

Image options :

Flip minus strand panels ● on ○ off
Allow tiny panels ○ on ● off
Grid lines ● on ○ off
Edges ● on ○ off
Shading ● on ○ off

How to get the most information about the alignments?





Bio::DB::GFF
species1

Bio::DB::GFF
species2

Bio::DB::GFF
species3

Bio::DB::GFF
species4

alignments

alignments

hit_id	int	[PK]
hit_name	varchar(100)	[FK]
src1	varchar(100)	
ref1	varchar(100)	
start1	int	
end1	int	
strand1	enum	
seq1	mediumtext	
bin	double	
src2	varchar(100)	
ref2	varchar(100)	
start2	int	
end2	int	
strand2	enum	
seq2	mediumtext	

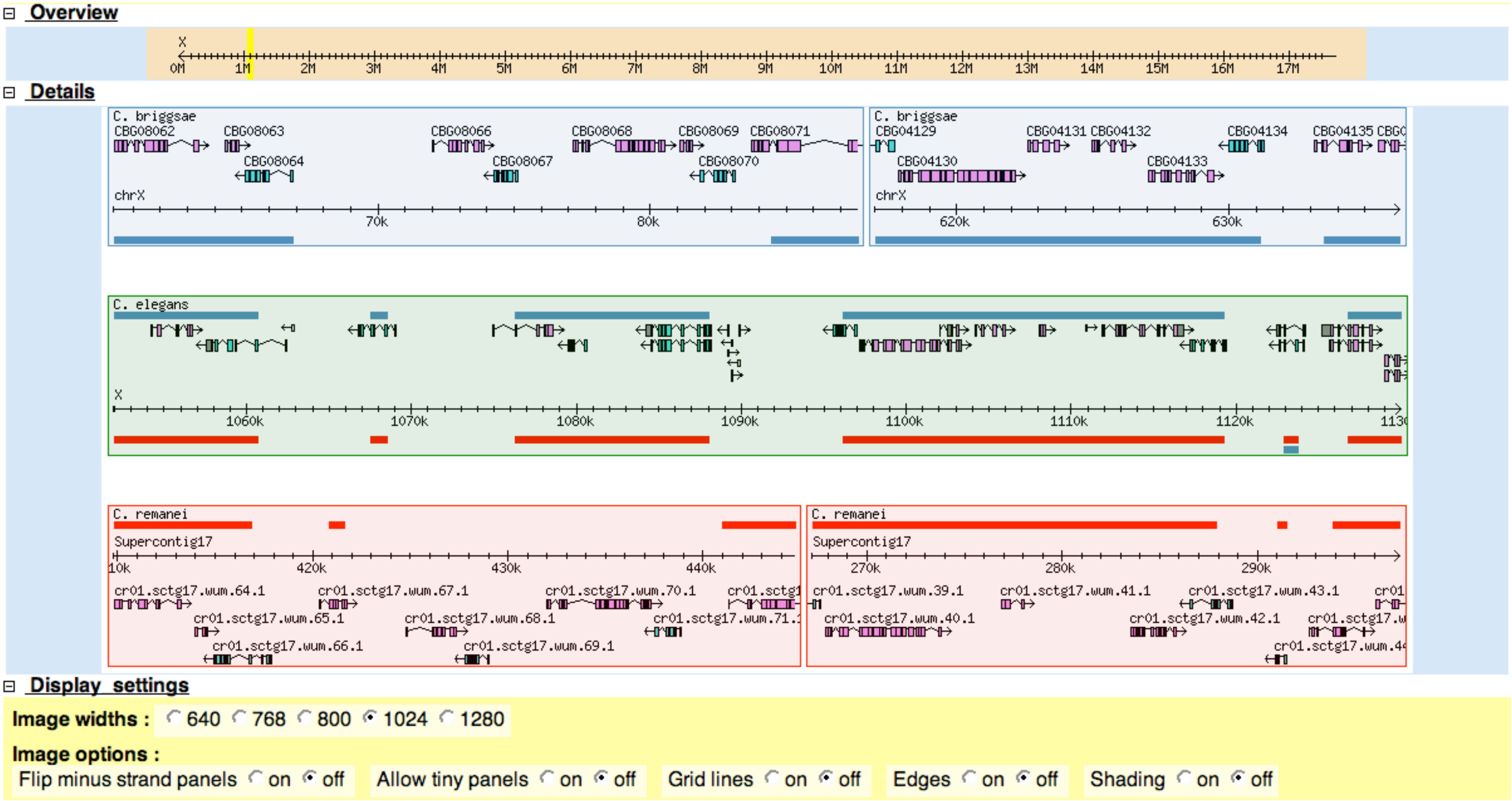
map

map_id	int	[PK]
hit_name	varchar(100)	
src1	varchar(100)	
pos1	int	
pos2	int	

Legend
[FK] Foreign Key
[PK] Primary key

Created by SQL::Translator 0.08

Gbrowse_syn: quick tour



⊟ **Overview**

⊟ **Details**

⊟ **Display settings**

Image widths : ○ 640 ○ 768 ○ 800 ● 1024 ○ 1280

Image options :

Flip minus strand panels ○ on ● off

Allow tiny panels ○ on ● off

Grid lines ○ on ● off

Edges ○ on ● off

Shading ○ on ● off

Gbrowse_syn: quick tour (shaded alignments)

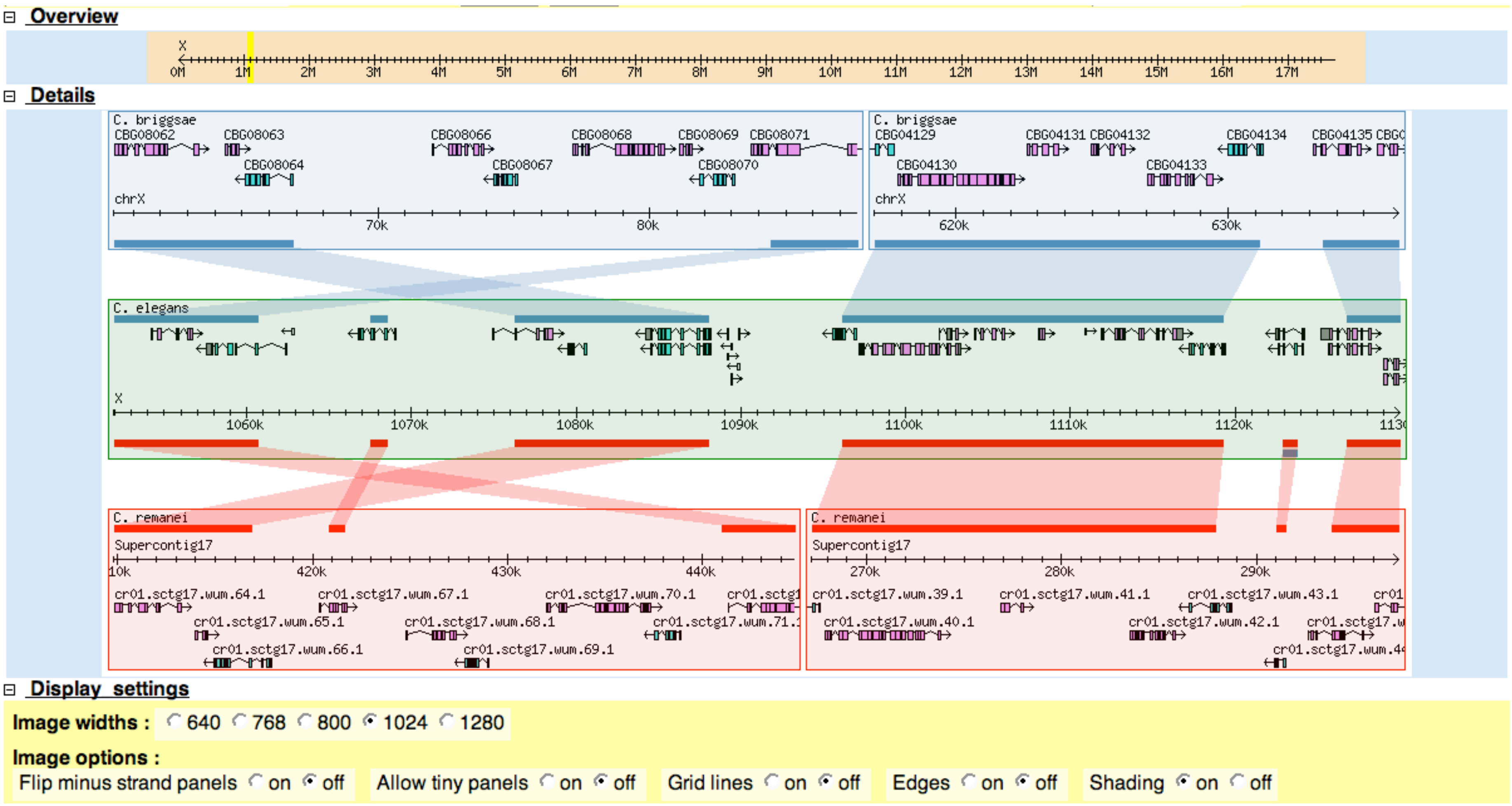
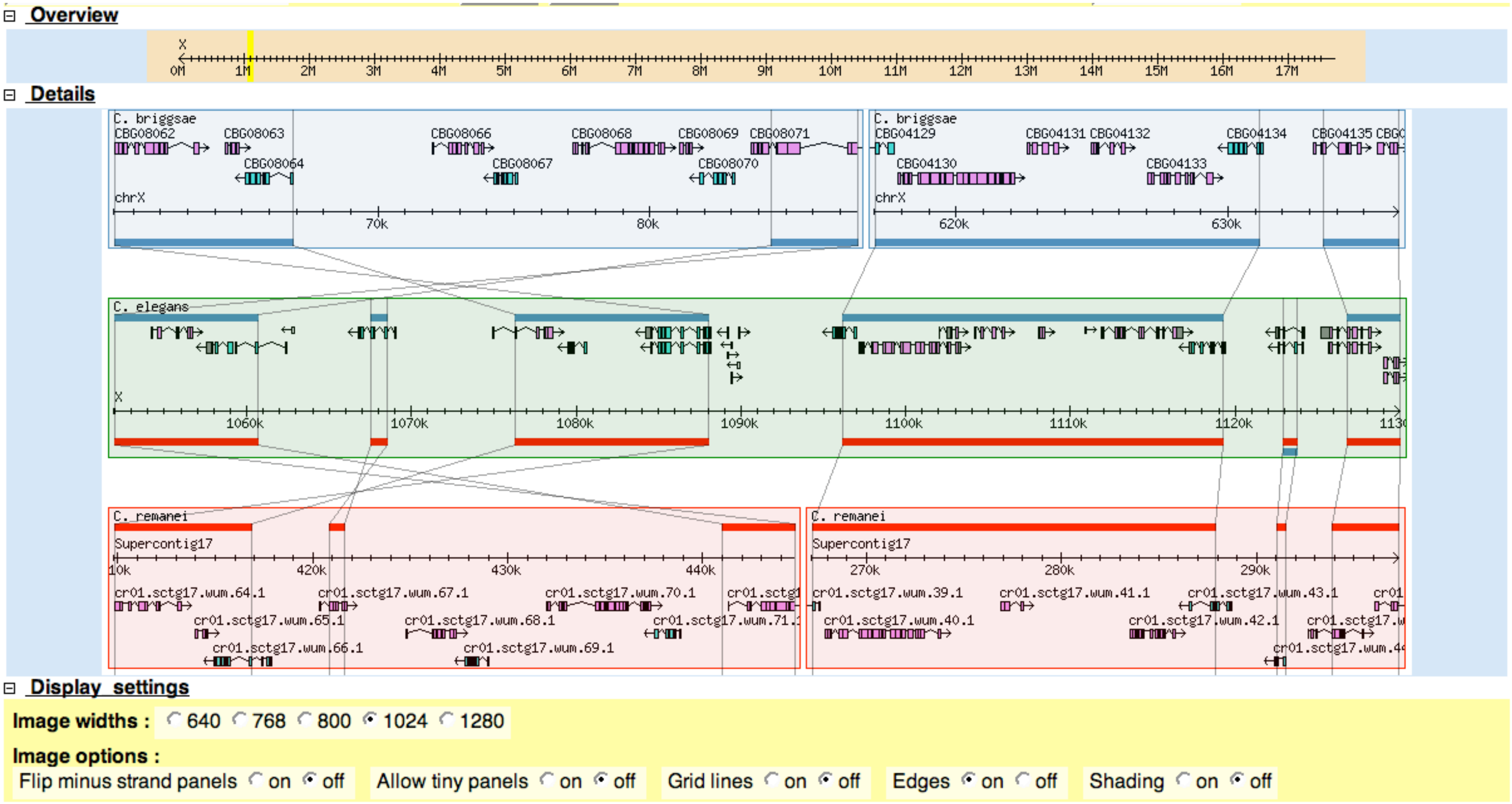


Image widths : ○ 640 ○ 768 ○ 800 ● 1024 ○ 1280

Image options :

Flip minus strand panels ○ on ● off
Allow tiny panels ○ on ● off
Grid lines ○ on ● off
Edges ○ on ● off
Shading ● on ○ off

Gbrowse_syn: quick tour (outlines)



⊟ Overview

⊟ Details

⊟ Display settings

Image widths : ○ 640 ○ 768 ○ 800 ● 1024 ○ 1280

Image options :

Flip minus strand panels ○ on ● off

Allow tiny panels ○ on ● off

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Edges ● on ○ off

Shading ○ on ● off

Gbrowse_syn: quick tour (strand correction)

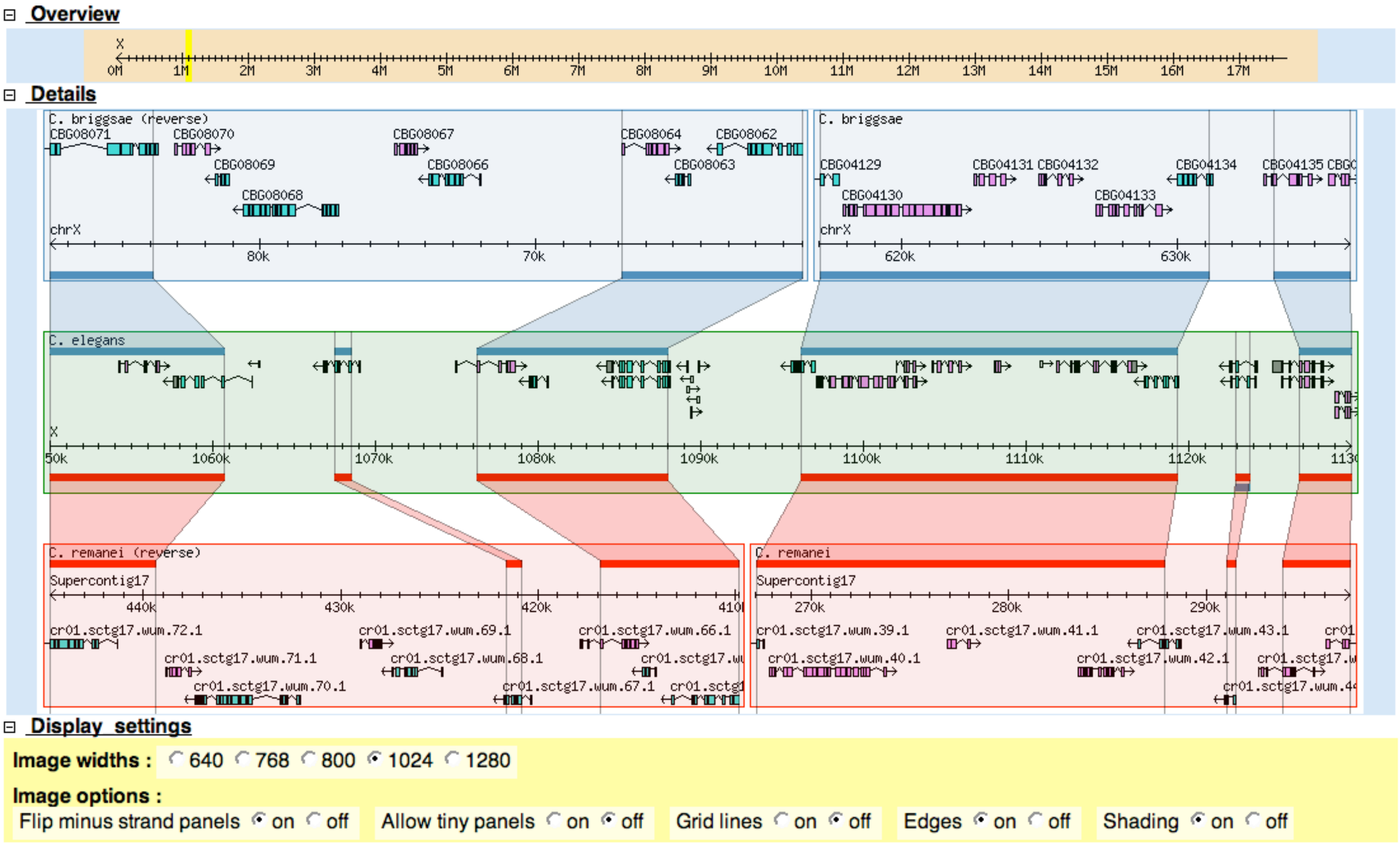


Image widths : ○ 640 ○ 768 ○ 800 ● 1024 ○ 1280

Image options :

Flip minus strand panels ● on ○ off

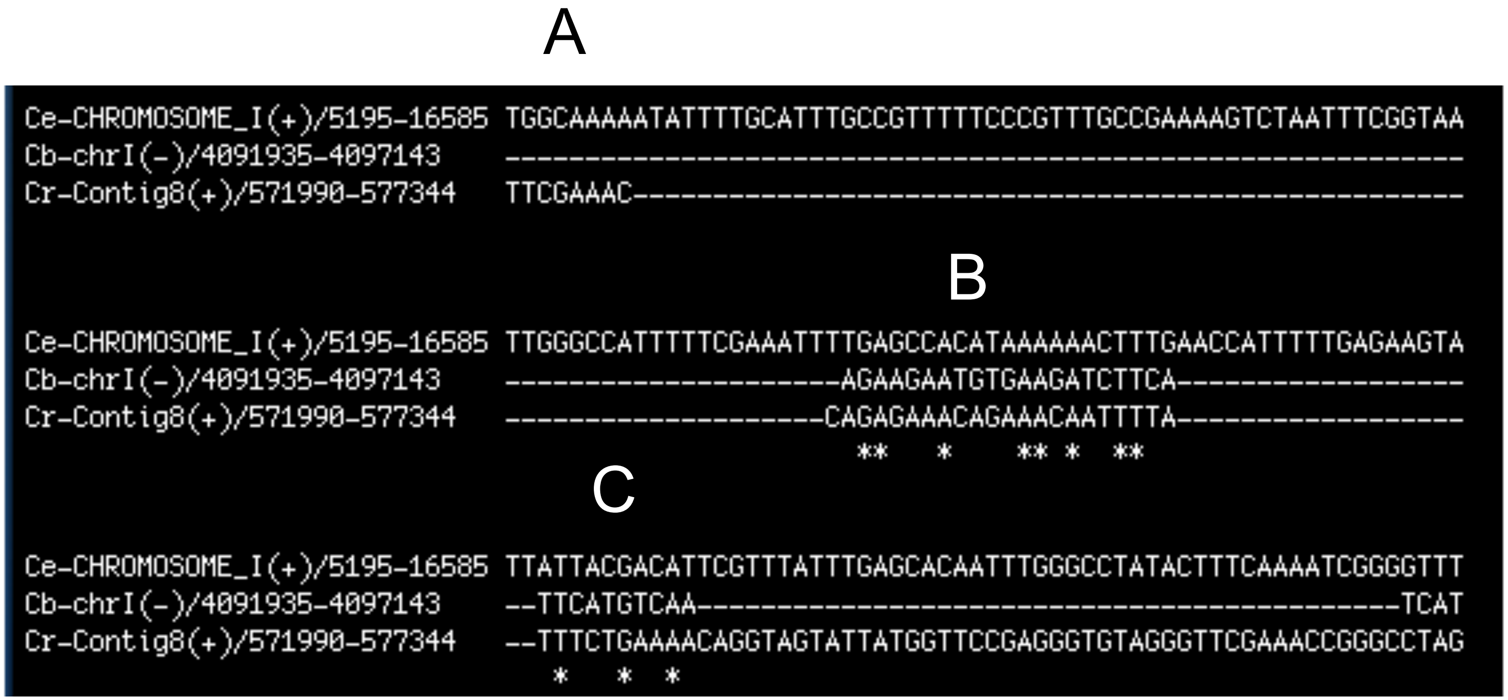
Allow tiny panels ○ on ● off

Grid lines ○ on ● off

Edges ● on ○ off

Shading ● on ○ off

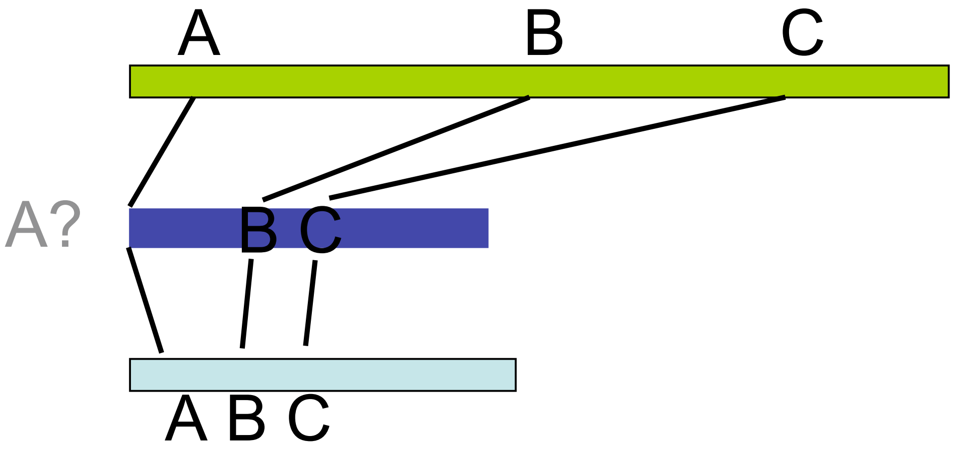
Some performance and display issues…

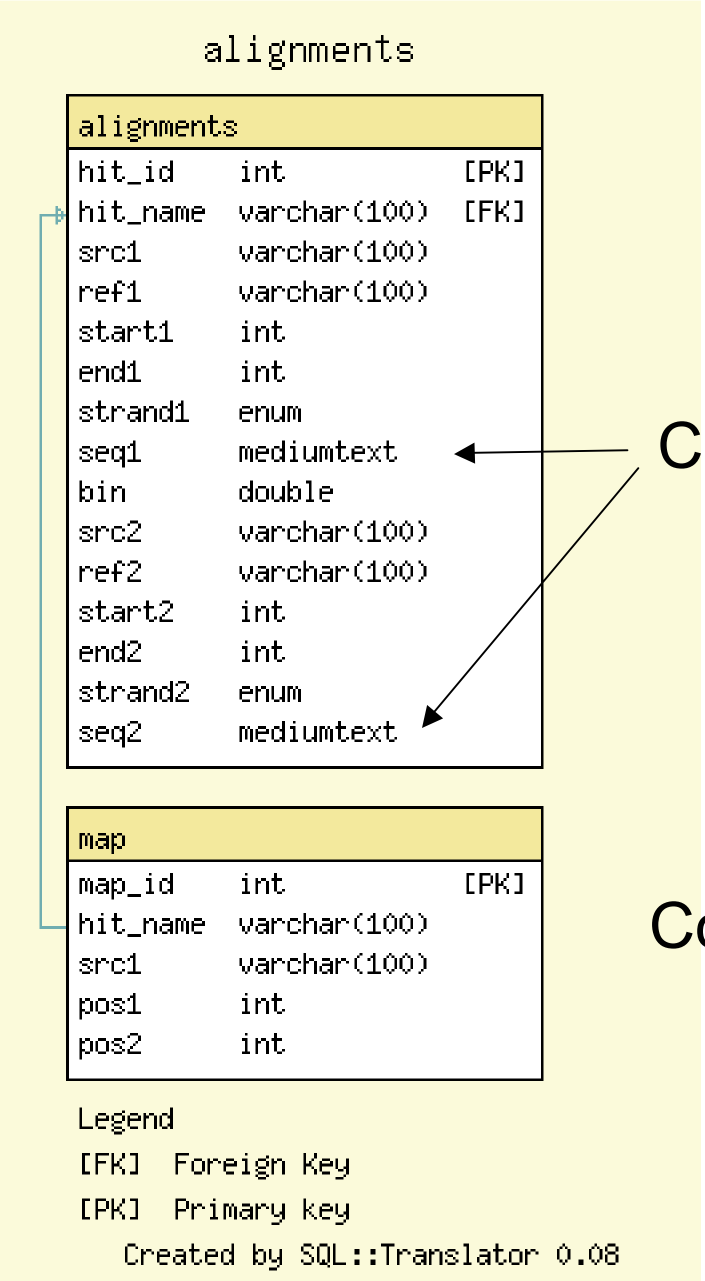


```
Ce-CHROMOSOME_I(+)/5195-16585 TGGCAAAAATATTTTGCATTTGCCGTTTTTCCCGTTTGCCGAAAAGTCTAATTTCGGTAA
Cb-chrI(-)/4091935-4097143    ------------------------------------------------------------
Cr-Contig8(+)/571990-577344   TTCGAAAC----------------------------------------------------

Ce-CHROMOSOME_I(+)/5195-16585 TTGGGCCATTTTTCGAAATTTTGAGCCACATAAAAAACTTTGAACCATTTTTGAGAAGTA
Cb-chrI(-)/4091935-4097143    ---------------------AGAAGAATGTGAAGATCTTCA------------------
Cr-Contig8(+)/571990-577344   --------------------CAGAGAAACAGAAACAATTTTA------------------
                                                    **   *    ** *  **

Ce-CHROMOSOME_I(+)/5195-16585 TTATTACGACATTCGTTTATTTGAGCACAATTTGGGCCTATACTTTCAAAATCGGGGTTT
Cb-chrI(-)/4091935-4097143    --TTCATGTCAA--------------------------------------------TCAT
Cr-Contig8(+)/571990-577344   --TTTCTGAAAACAGGTAGTATTATGGTTCCGAGGGTGTAGGGTTCGAAACCGGGCCTAG
                                 *   *  *
```





alignments

alignments		
hit_id	int	[PK]
hit_name	varchar(100)	[FK]
src1	varchar(100)	
ref1	varchar(100)	
start1	int	
end1	int	
strand1	enum	
seq1	mediumtext	
bin	double	
src2	varchar(100)	
ref2	varchar(100)	
start2	int	
end2	int	
strand2	enum	
seq2	mediumtext	

map		
map_id	int	[PK]
hit_name	varchar(100)	
src1	varchar(100)	
pos1	int	
pos2	int	

Legend

[FK] Foreign Key

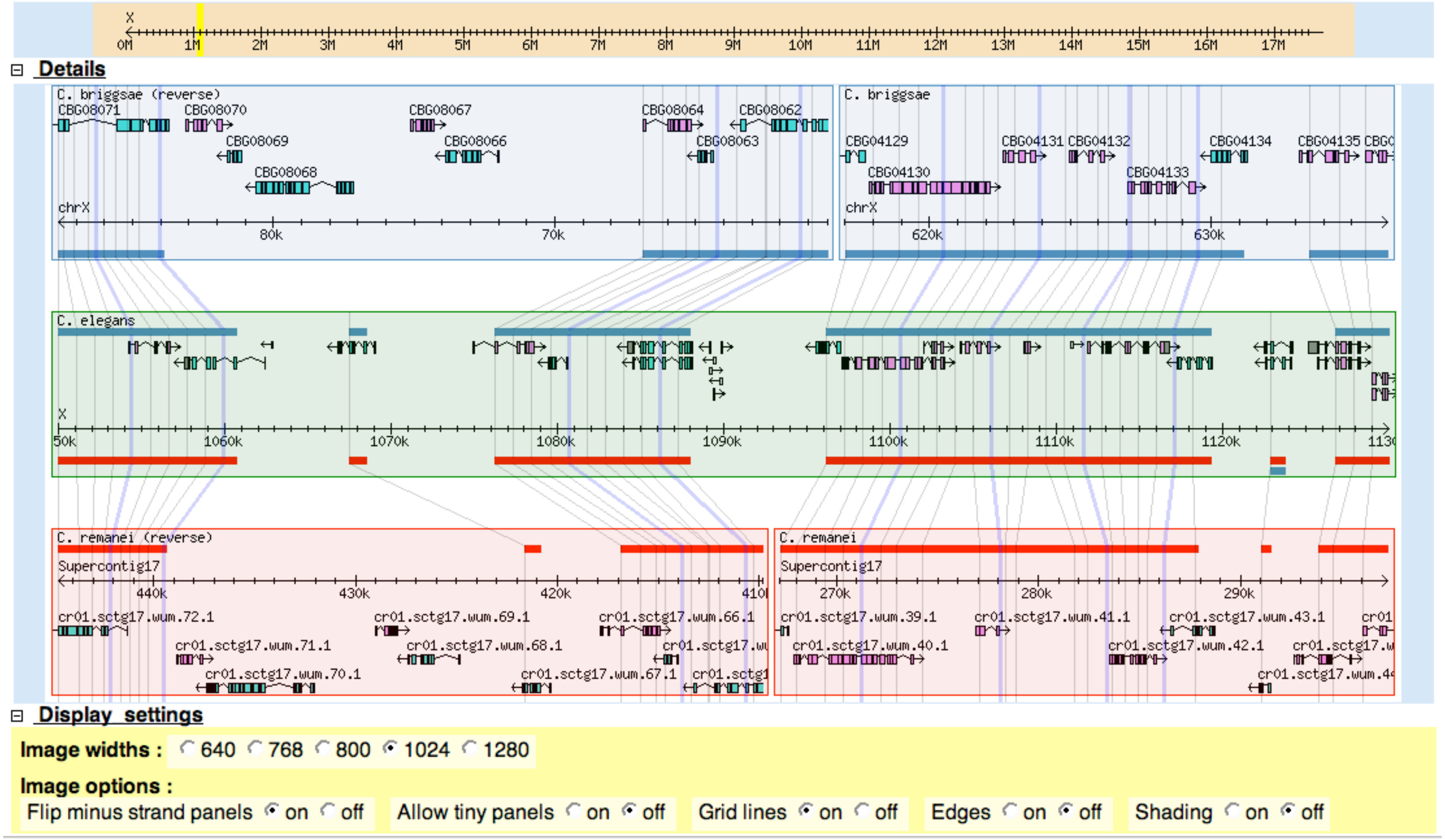
[PK] Primary key

Created by SQL::Translator 0.08

Cigar-string

Coordinate map

Gbrowse_syn: quick tour (grid lines)



⊟ **Details**

⊟ **Display settings**

Image widths : ○ 640 ○ 768 ○ 800 ● 1024 ○ 1280

Image options :

Flip minus strand panels ● on ○ off

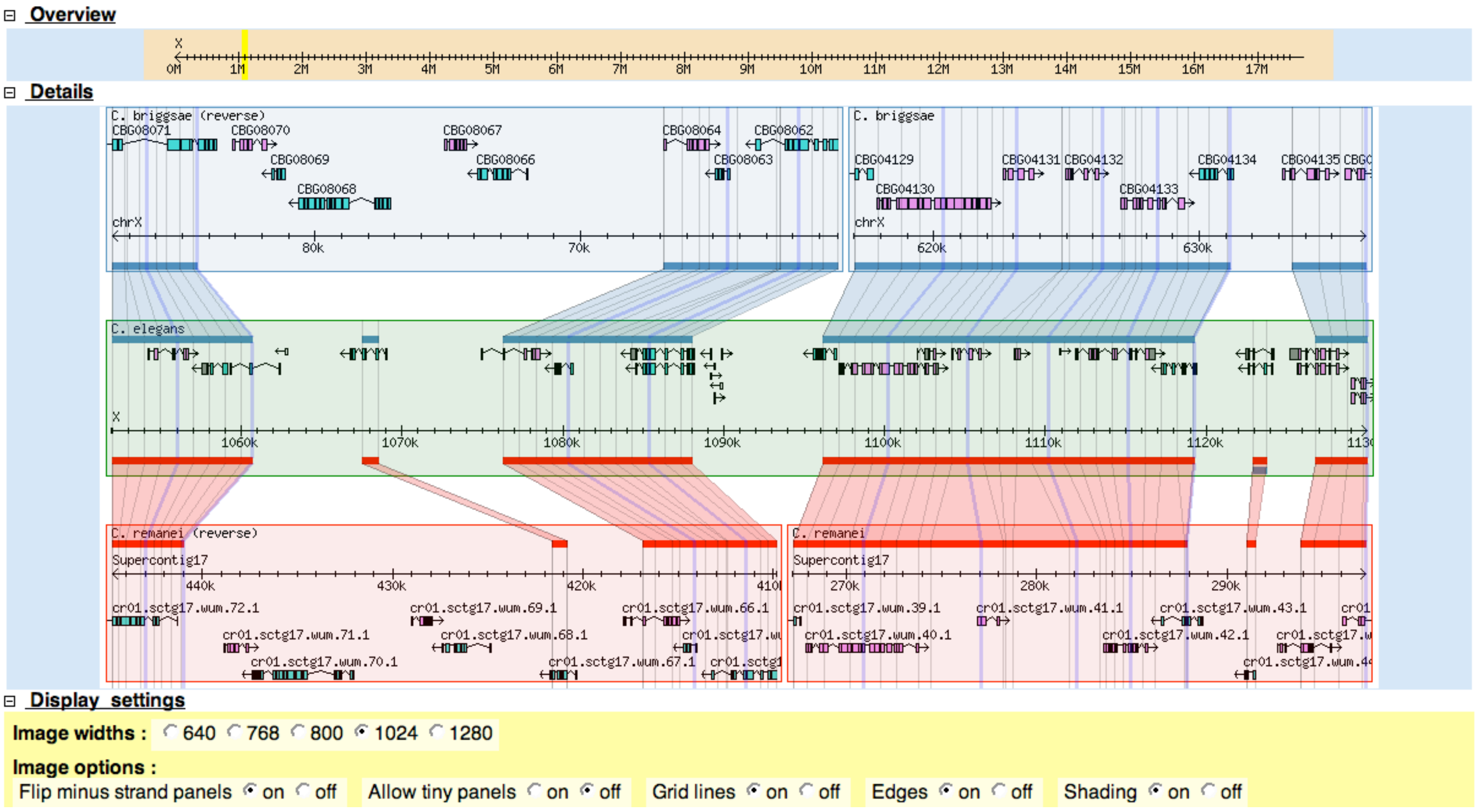
Allow tiny panels ○ on ● off

Grid lines ● on ○ off

Edges ○ on ● off

Shading ○ on ● off

Gbrowse_syn: quick tour (the works)



⊟ **Overview**

⊟ **Details**

⊟ **Display settings**

Image widths : ○ 640 ○ 768 ○ 800 ● 1024 ○ 1280

Image options :

Flip minus strand panels ● on ○ off

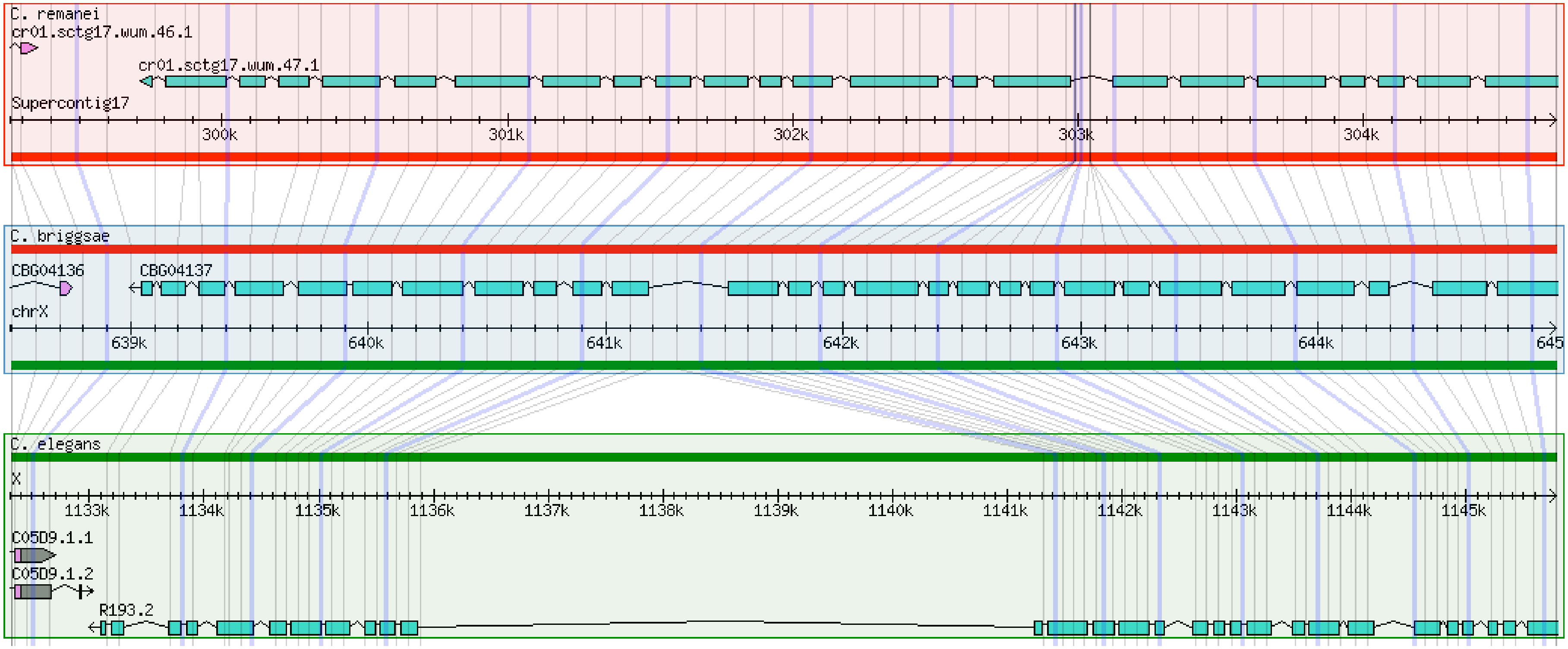
Allow tiny panels ○ on ● off

Grid lines ● on ○ off

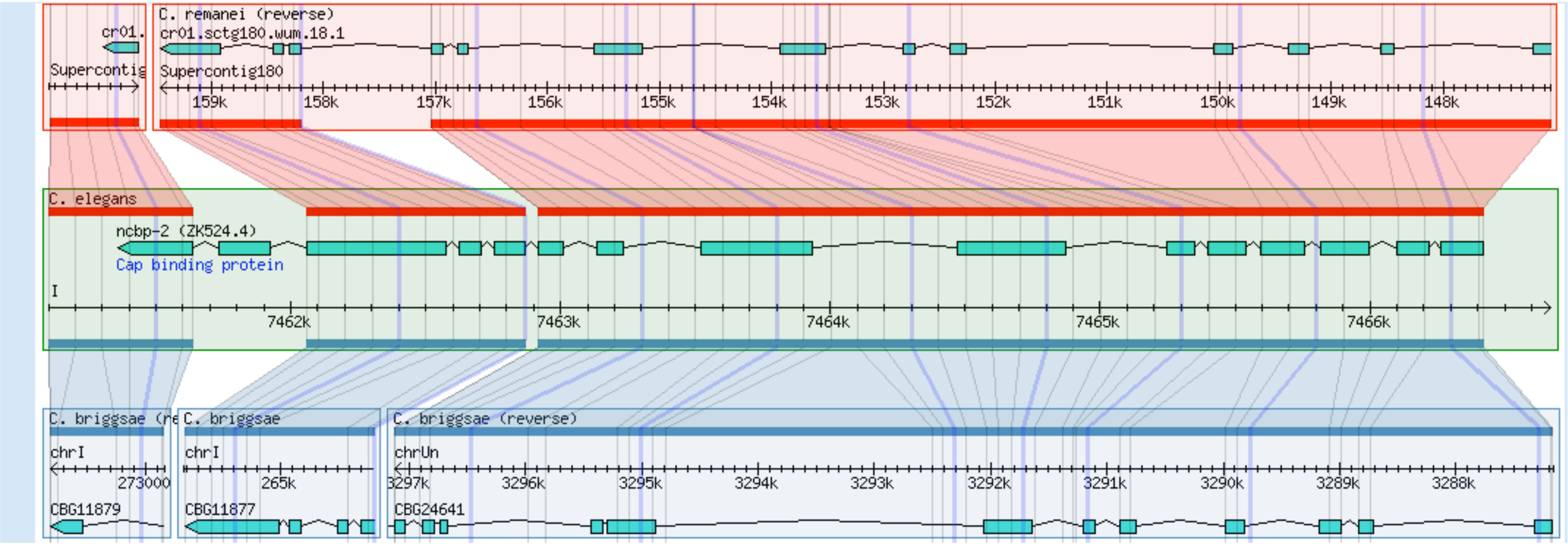
Edges ● on ○ off

Shading ● on ○ off

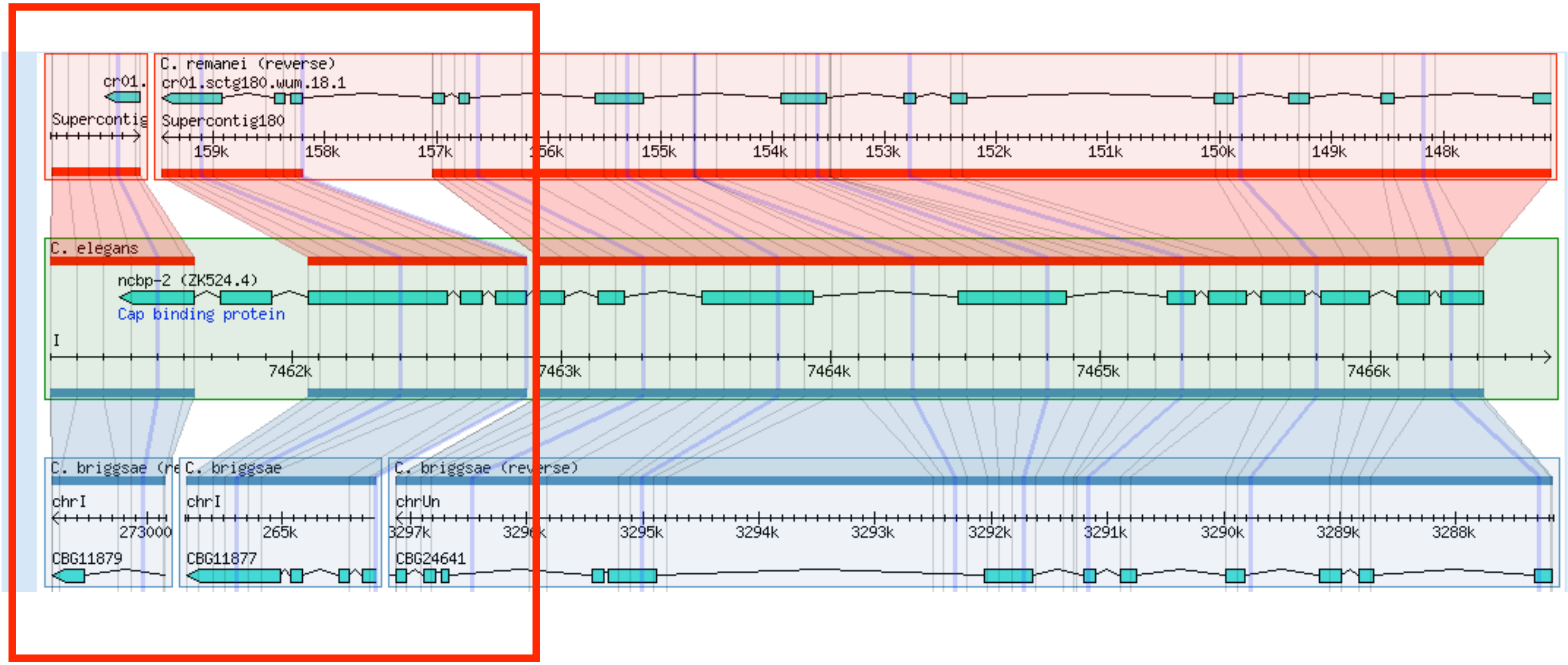
Gene structure changes



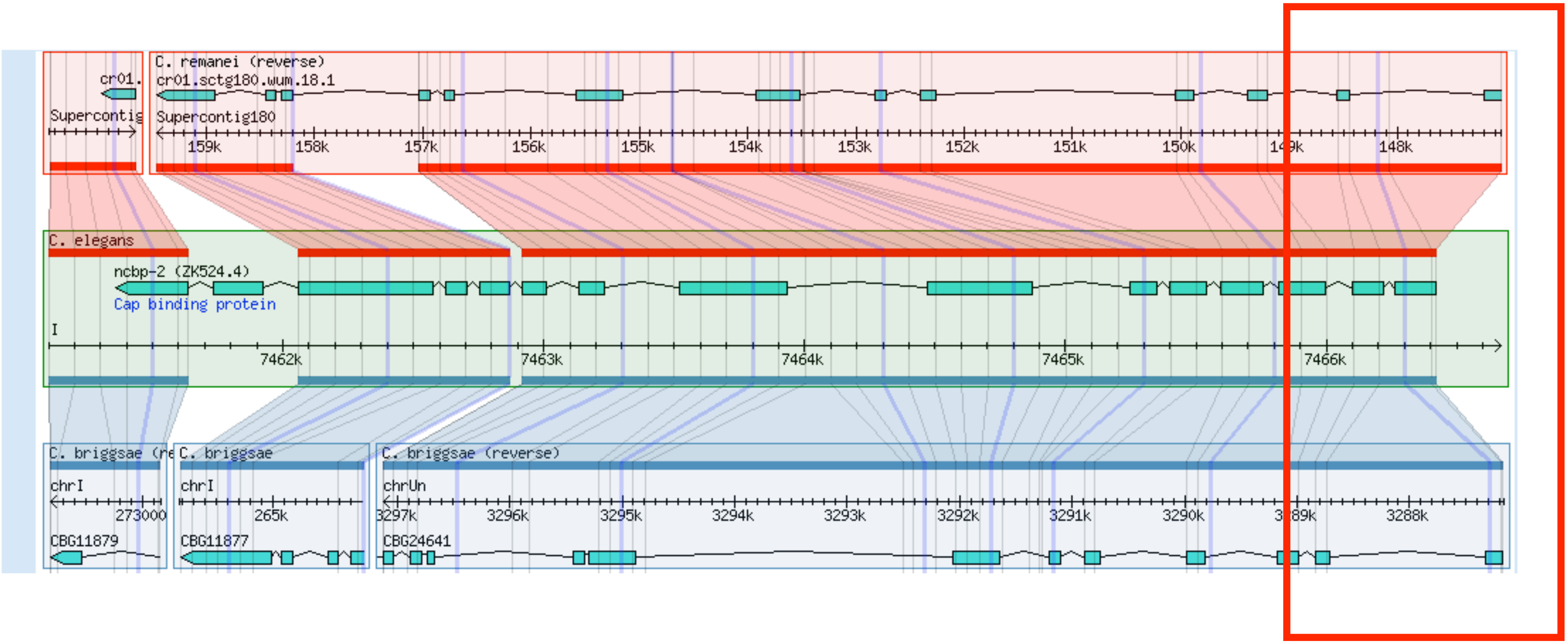
C. elegans ZK524.4 gene



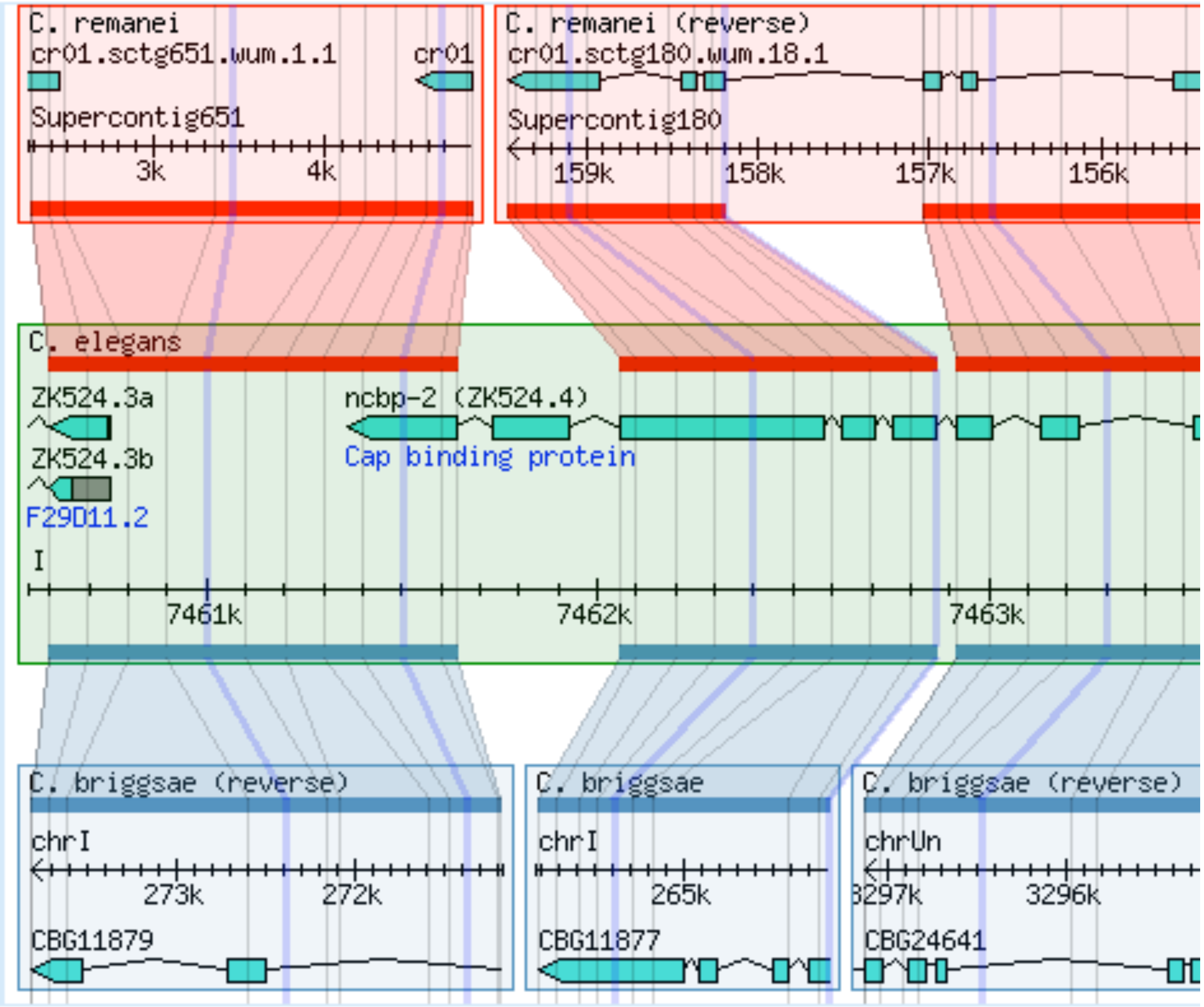
C. elegans ZK524.4 gene



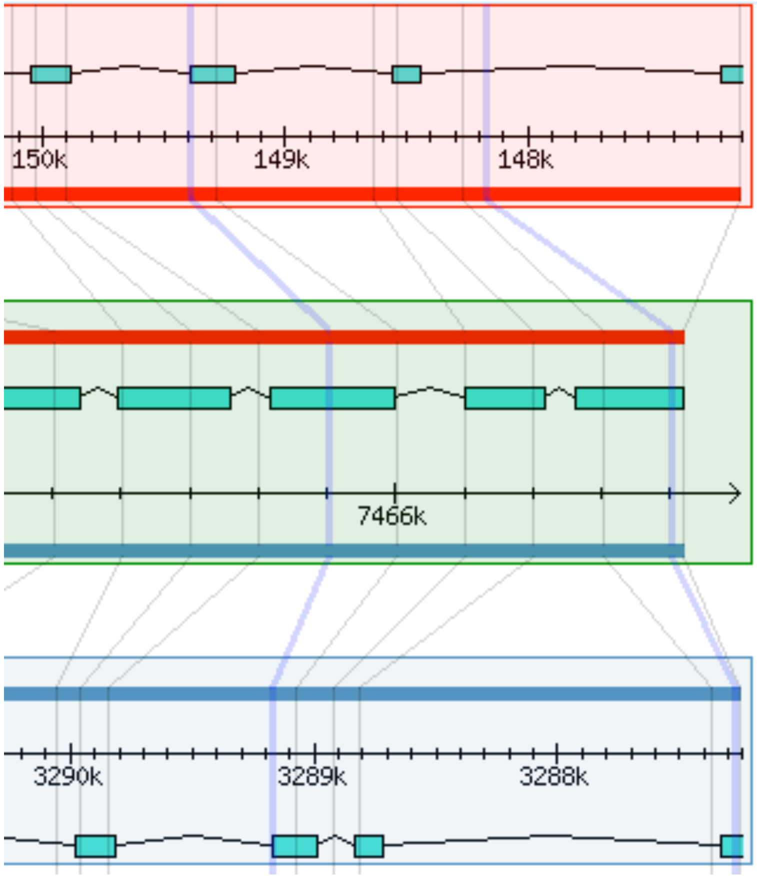
C. elegans ZK524.4 gene



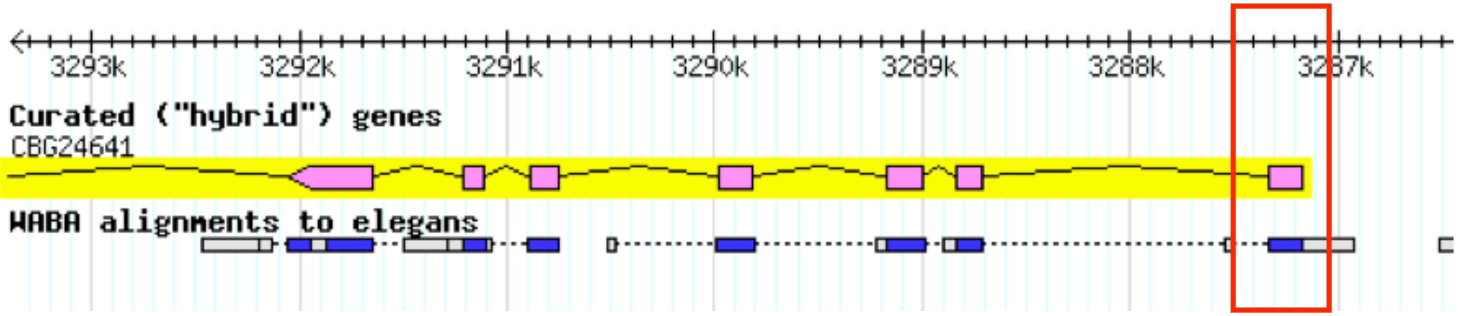
3’ end


C. remanei
cr01.sctg651.wum.1.1
cr01
Supercontig651
3k
4k
C. remanei (reverse)
cr01.sctg180.wum.18.1
Supercontig180
159k
158k
157k
156k
C. elegans
ZK524.3a
ZK524.3b
F29D11.2
ncbp-2 (ZK524.4)
Cap binding protein
I
7461k
7462k
7463k
C. briggsae (reverse)
chrI
273k
272k
CBG11879
C. briggsae
chrI
265k
CBG11877
C. briggsae (reverse)
chrUn
3297k
3296k
CBG24641

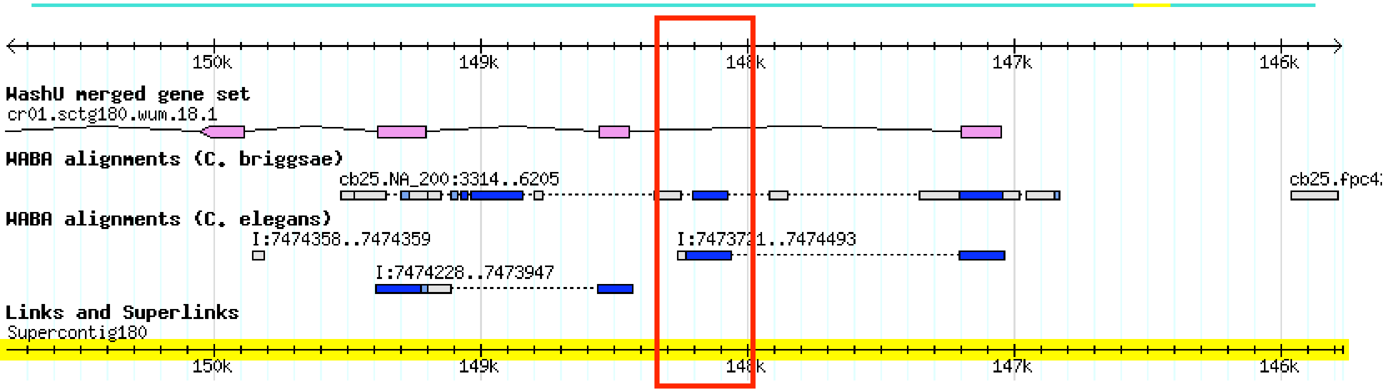
5’ end



C. briggsae



C. remanei



Chaining alignments

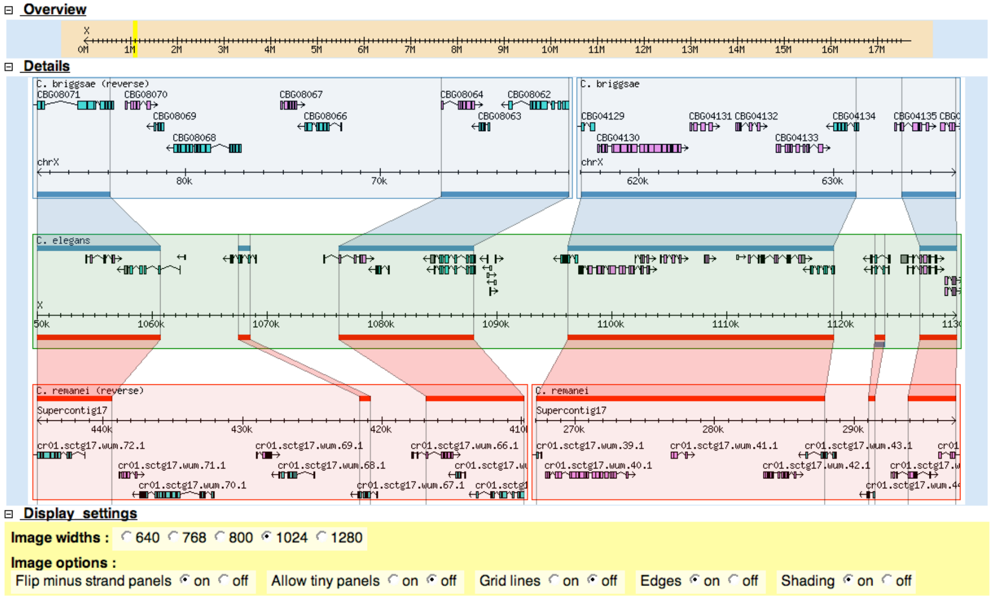
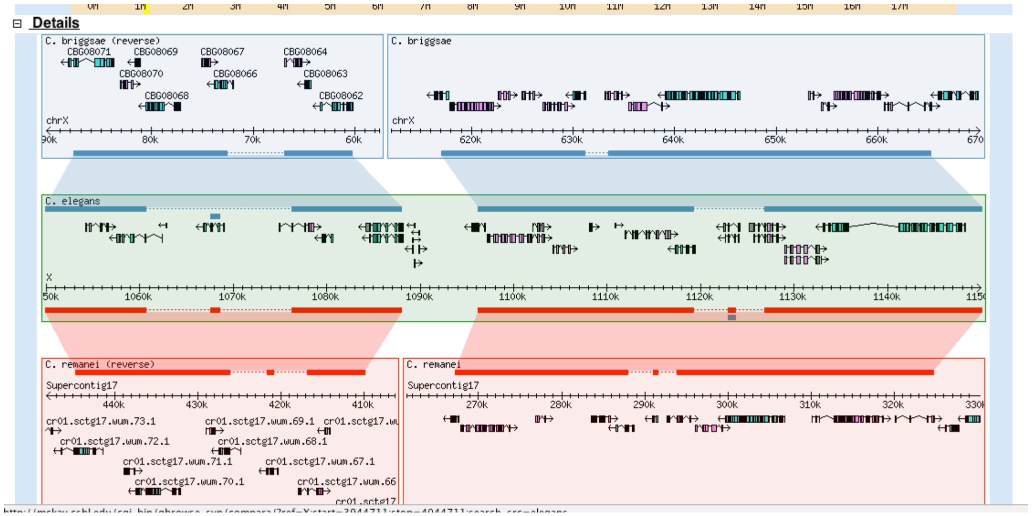


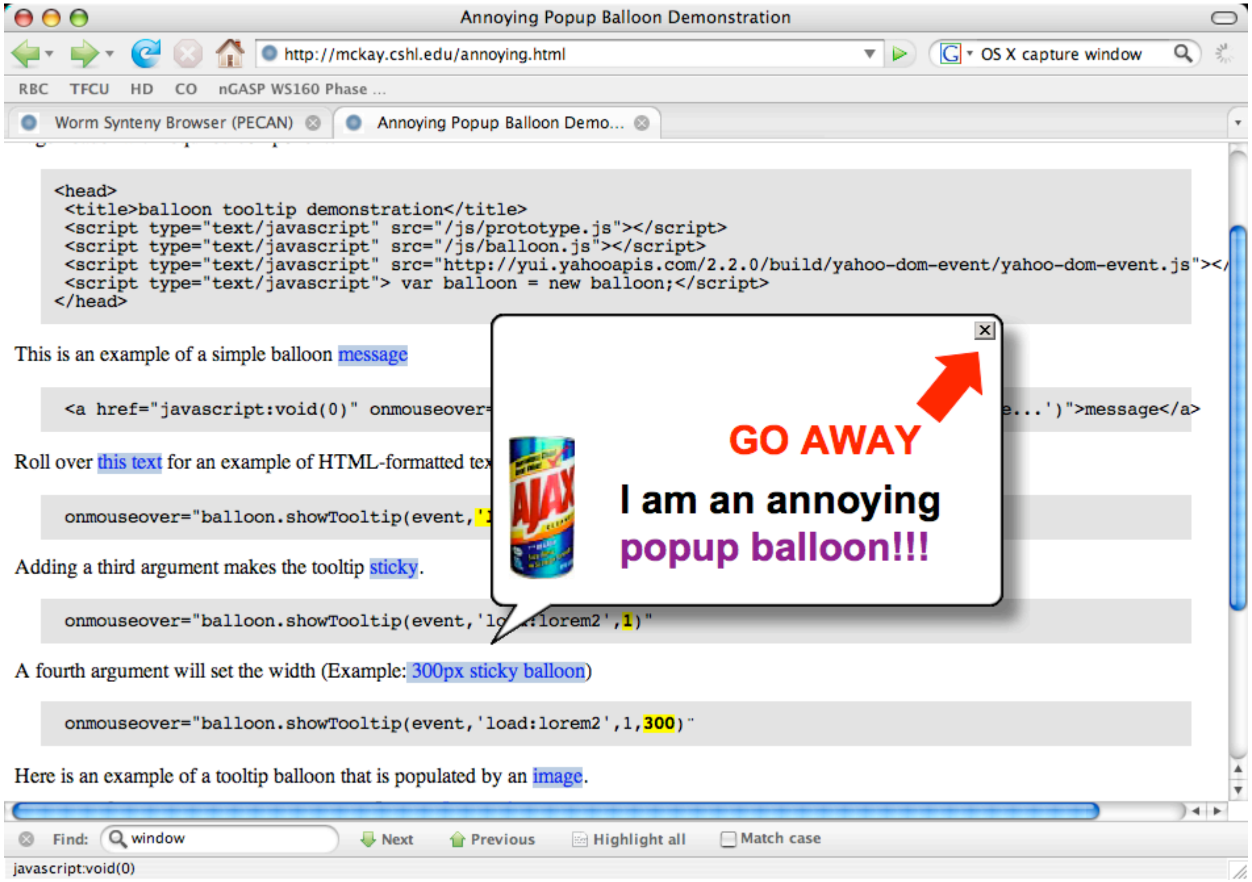
Image widths : ○ 640 ○ 768 ○ 800 ● 1024 ○ 1280

Image options :

Flip minus strand panels ● on ○ off | Allow tiny panels ○ on ● off | Grid lines ○ on ● off | Edges ● on ○ off | Shading ● on ○ off



Other stuff



```
<head>
 <title>balloon tooltip demonstration</title>
 <script type="text/javascript" src="/js/prototype.js"></script>
 <script type="text/javascript" src="/js/balloon.js"></script>
 <script type="text/javascript" src="http://yui.yahooapis.com/2.2.0/build/yahoo-dom-event/yahoo-dom-event.js"></
 <script type="text/javascript"> var balloon = new balloon;</script>
</head>
```

This is an example of a simple balloon message

```
<a href="javascript:void(0)" onmouseover=
e...')">message</a>
```

Roll over this text for an example of HTML-formatted te

```
onmouseover="balloon.showTooltip(event,'
```

Adding a third argument makes the tooltip sticky.

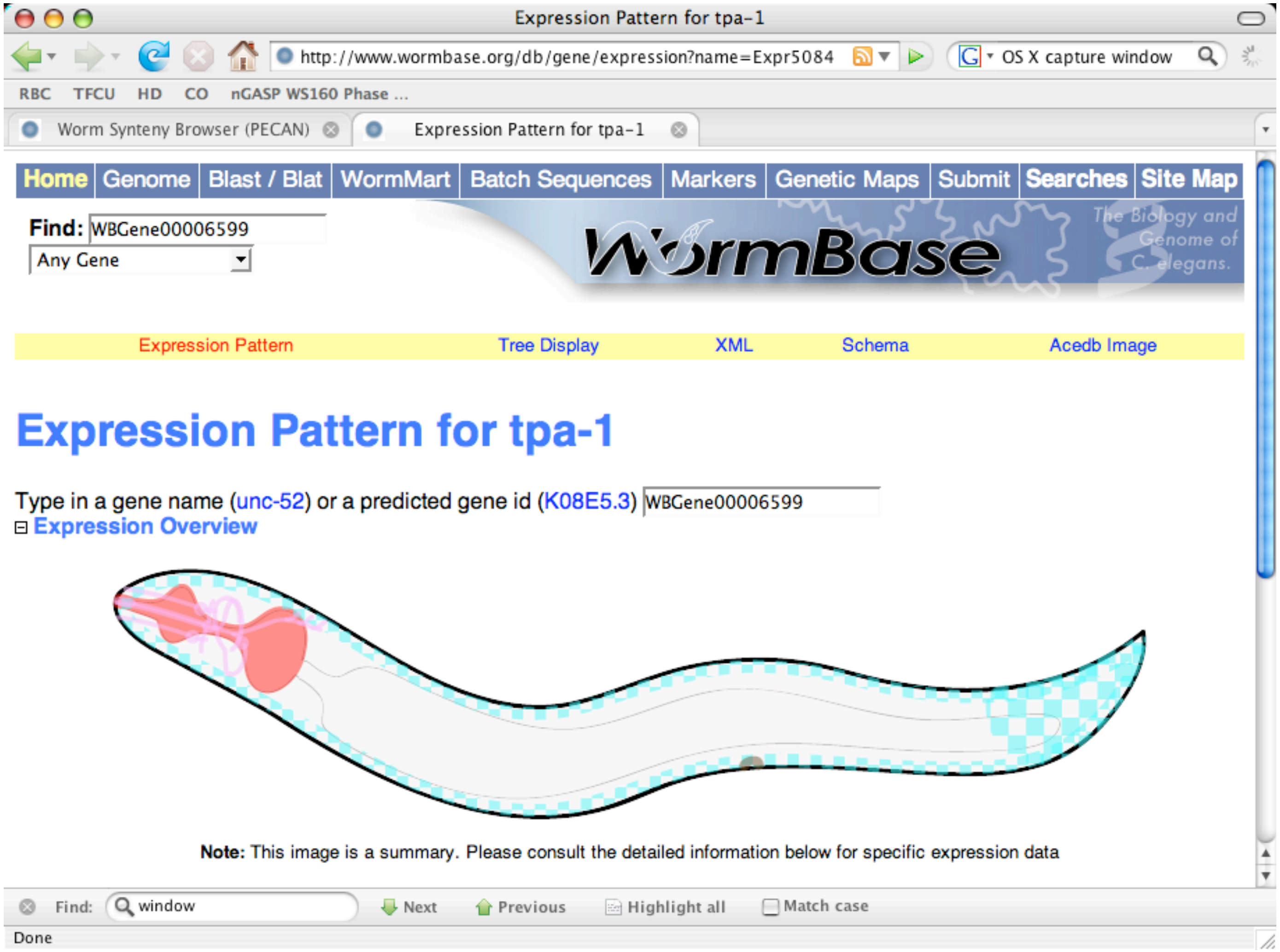
```
onmouseover="balloon.showTooltip(event,'lo
:lorem2',1)"
```

A fourth argument will set the width (Example: 300px sticky balloon)

```
onmouseover="balloon.showTooltip(event,'load:lorem2',1,300)"
```

Here is an example of a tooltip balloon that is populated by an image.

Graphical rendering of Anatomy Ontology



Find: WBGene00006599

Any Gene

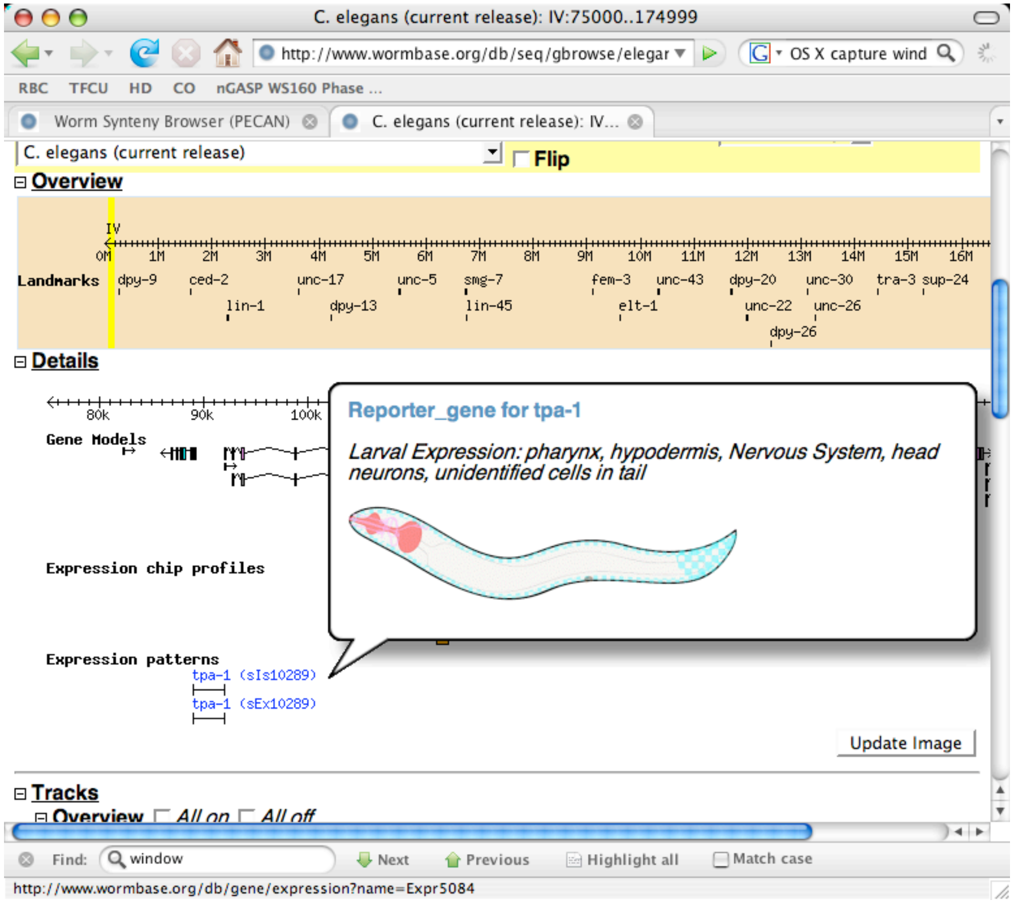
Expression Pattern for tpa-1

Type in a gene name (unc-52) or a predicted gene id (K08E5.3) WBGene00006599

⊟ Expression Overview

Note: This image is a summary. Please consult the detailed information below for specific expression data

Find: window



C. elegans (current release): IV:75000..174999

http://www.wormbase.org/db/seq/gbrowse/elegar

Worm Synteny Browser (PECAN)

C. elegans (current release): IV...

C. elegans (current release)

☐ Flip

Overview

Details

Reporter_gene for tpa-1

Larval Expression: pharynx, hypodermis, Nervous System, head neurons, unidentified cells in tail

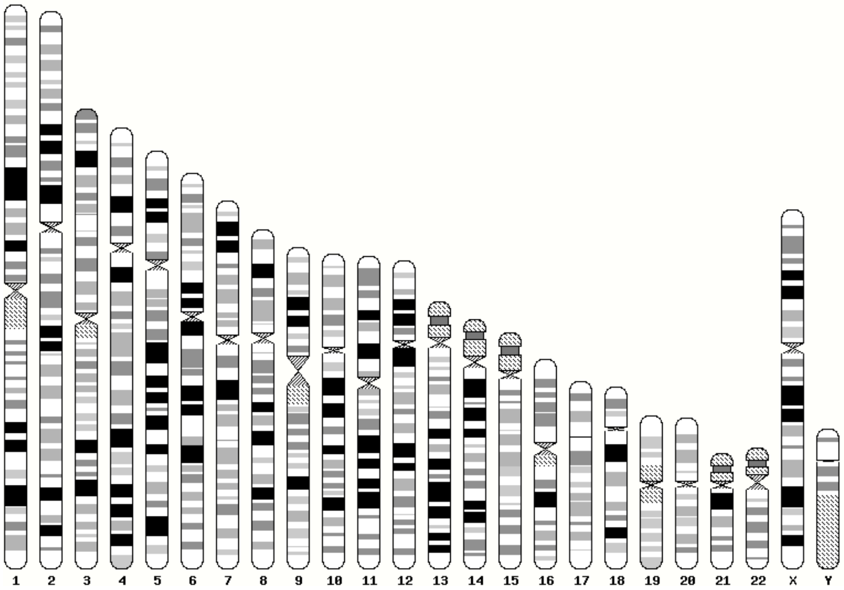
Tracks

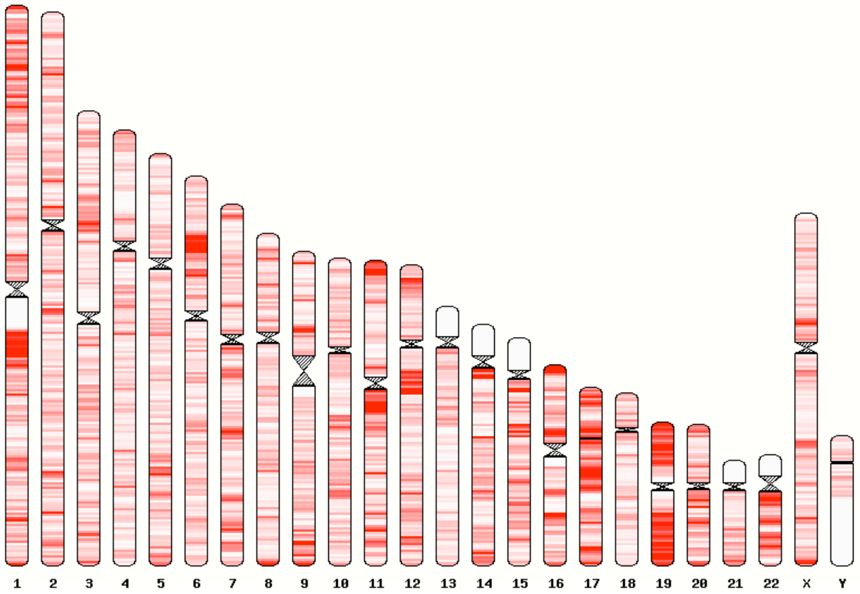
Overview ☐ All on ☐ All off

Find: window

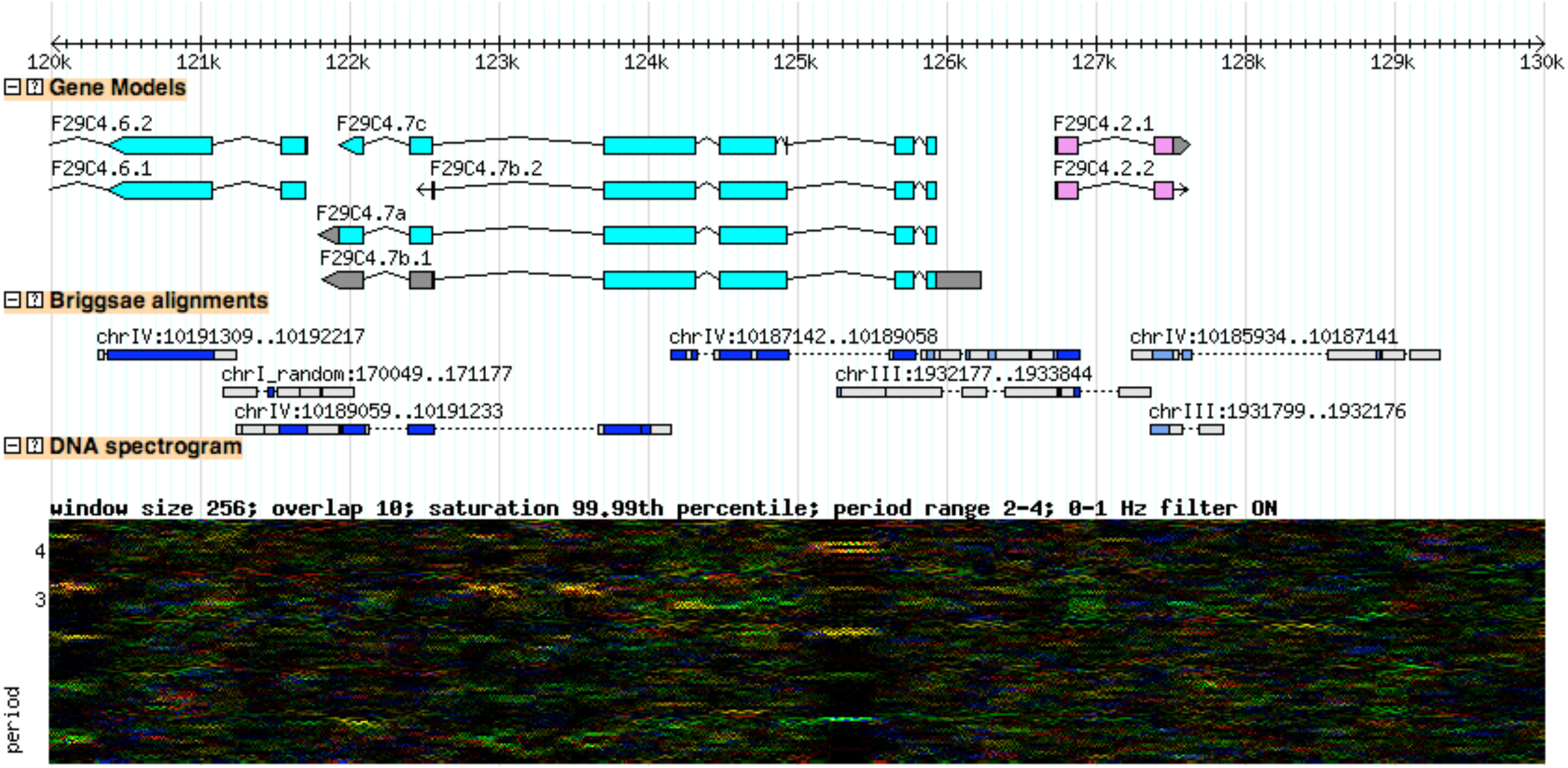
http://www.wormbase.org/db/gene/expression?name=Expr5084

GBrowse_karyotype



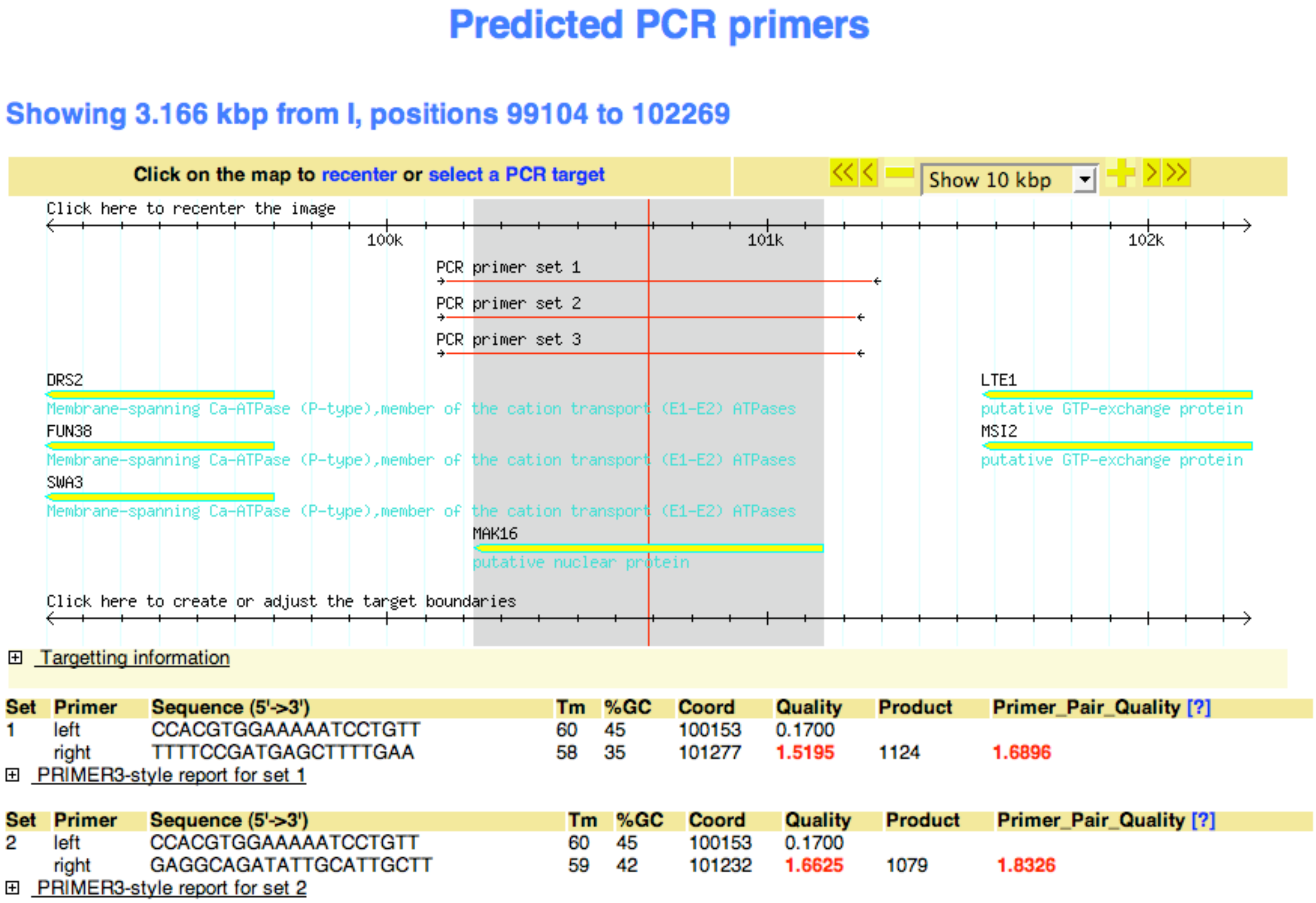


GBrowse DNA Spectrogram plugin



window size 256; overlap 10; saturation 99.99th percentile; period range 2-4; 0-1 Hz filter ON

GBrowse DNA Spectrogram plugin



Predicted PCR primers

Showing 3.166 kbp from I, positions 99104 to 102269

Set	Primer	Sequence (5'->3')	Tm	%GC	Coord	Quality	Product	Primer_Pair_Quality [?]
1	left	CCACGTGGAAAAATCCTGTT	60	45	100153	0.1700		
	right	TTTTCCGATGAGCTTTTGAA	58	35	101277	1.5195	1124	1.6896

⊞ PRIMER3-style report for set 1

Set	Primer	Sequence (5'->3')	Tm	%GC	Coord	Quality	Product	Primer_Pair_Quality [?]
2	left	CCACGTGGAAAAATCCTGTT	60	45	100153	0.1700		
	right	GAGGCAGATATTGCATTGCTT	59	42	101232	1.6625	1079	1.8326

⊞ PRIMER3-style report for set 2

Acknowledgements

Lincoln Stein

CSH

Todd Harris

CSH

Peter Van Buren

CSH

Michael Han

Wellcome Trust Sanger Institute