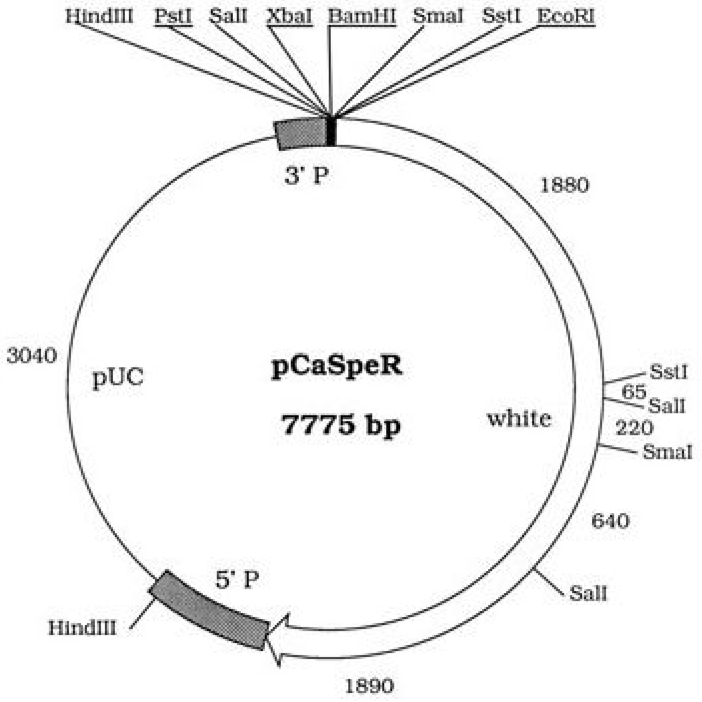
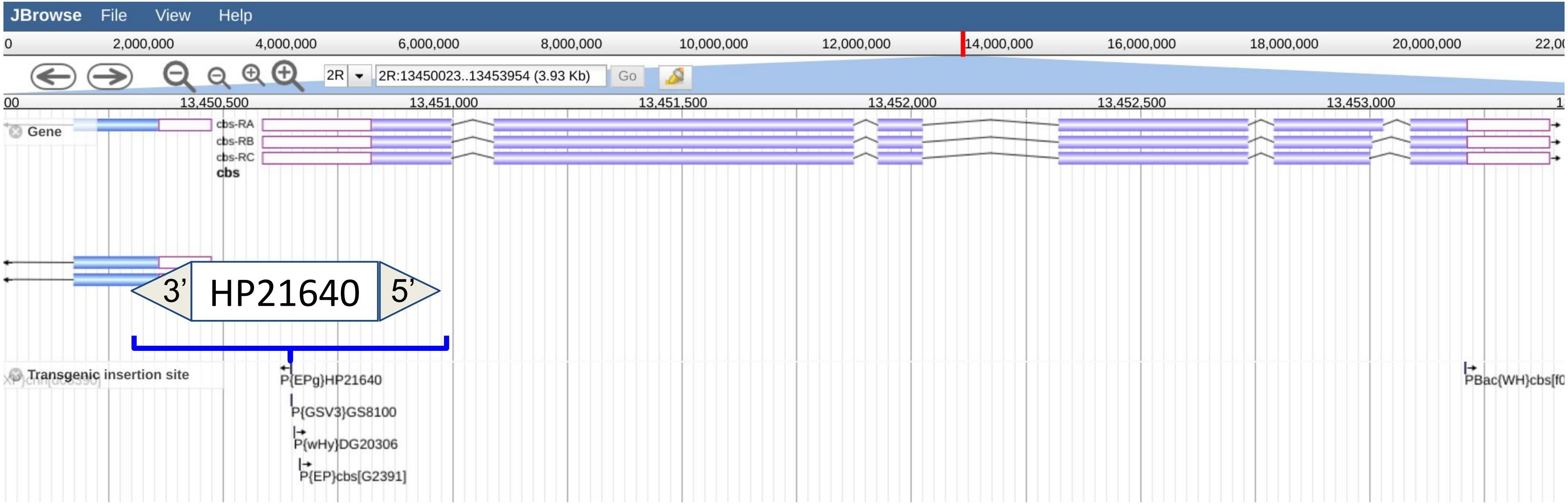
The orientation of a transposon insertion is reported with respect to the transposon's inherent asymmetry, like the P-element's distinct 5' and 3' ends.

How that inherent transposon asymmetry relates to other features of a construct, like FRT or Gal4 binding sites, depends on how a given construct is made.

This information can be tracked down in FlyBase. Here’s how...



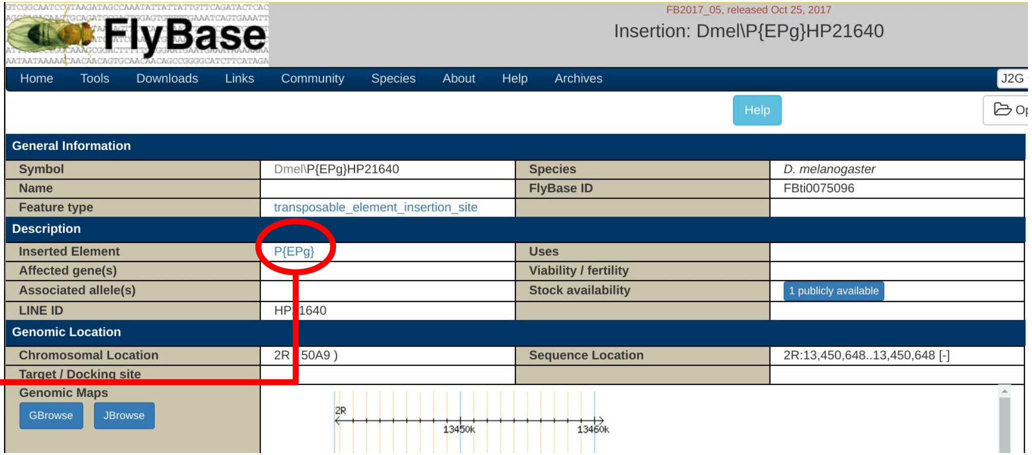
I want to drive ectopic *cbs* expression:



There are 2 EP/EP-like insertions near the *cbs* 5'end. The arrow indicates the orientation of the transposon (5' > 3'). The P{EPg}HP21640 insertion (highlighted) has a "minus" orientation; the P{EP}cbs[G2391] has a "plus" orientation.

Next step - click on an insertion glyph to get information about the related construct.

Clicking on the glyph for HP21640 takes you to the transposon insertion report. From there, look for the "Inserted element" section, and click to get to a report about the construct itself.



FB2017_05, released Oct 25, 2017

Insertion: Dmel\P{EPg}HP21640

General Information

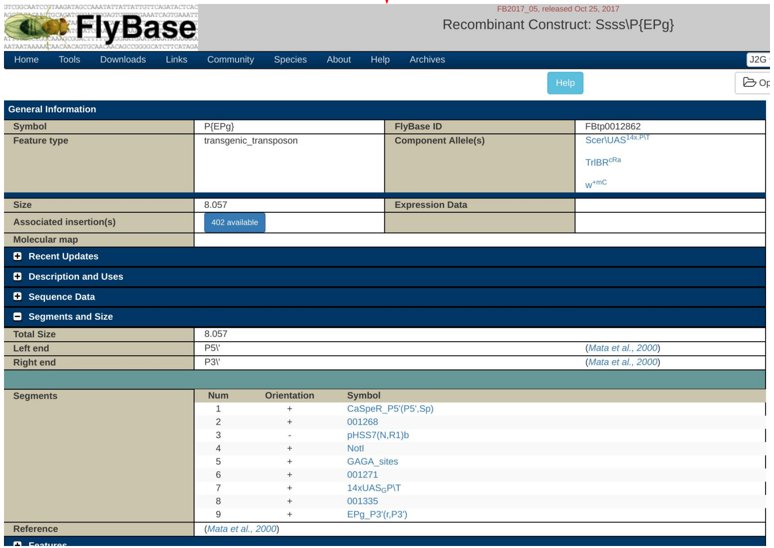
Symbol	Dmel\P{EPg}HP21640	**Species**	*D. melanogaster*
Name		**FlyBase ID**	FBti0075096
Feature type	transposable_element_insertion_site		

Description

Inserted Element	P{EPg}	**Uses**	
Affected gene(s)		**Viability / fertility**	
Associated allele(s)		**Stock availability**	1 publicly available
LINE ID	HP 1640		

Genomic Location

Chromosomal Location	2R 50A9)	**Sequence Location**	2R:13,450,648..13,450,648 [-]
Target / Docking site			
Genomic Maps			



FB2017_05, released Oct 25, 2017

Recombinant Construct: Ssss\P{EPg}

General Information

Symbol	P{EPg}	**FlyBase ID**	FBtp0012862
Feature type	transgenic_transposon	**Component Allele(s)**	Scer\UAS$^{14x.P\T}$ TrlBR^{cRa} w^{+mC}
Size	8.057	**Expression Data**	
Associated insertion(s)	402 available		
Molecular map			

Recent Updates

Description and Uses

Sequence Data

Segments and Size

Total Size	8.057	
Left end	P5\'	(*Mata et al., 2000*)
Right end	P3\'	(*Mata et al., 2000*)

Segments

Num	Orientation	Symbol
1	+	CaSpeR_P5'(P5',Sp)
2	+	001268
3	-	pHSS7(N,R1)b
4	+	NotI
5	+	GAGA_sites
6	+	001271
7	+	14xUAS$_G$P\T
8	+	001335
9	+	EPg_P3'(r,P3')

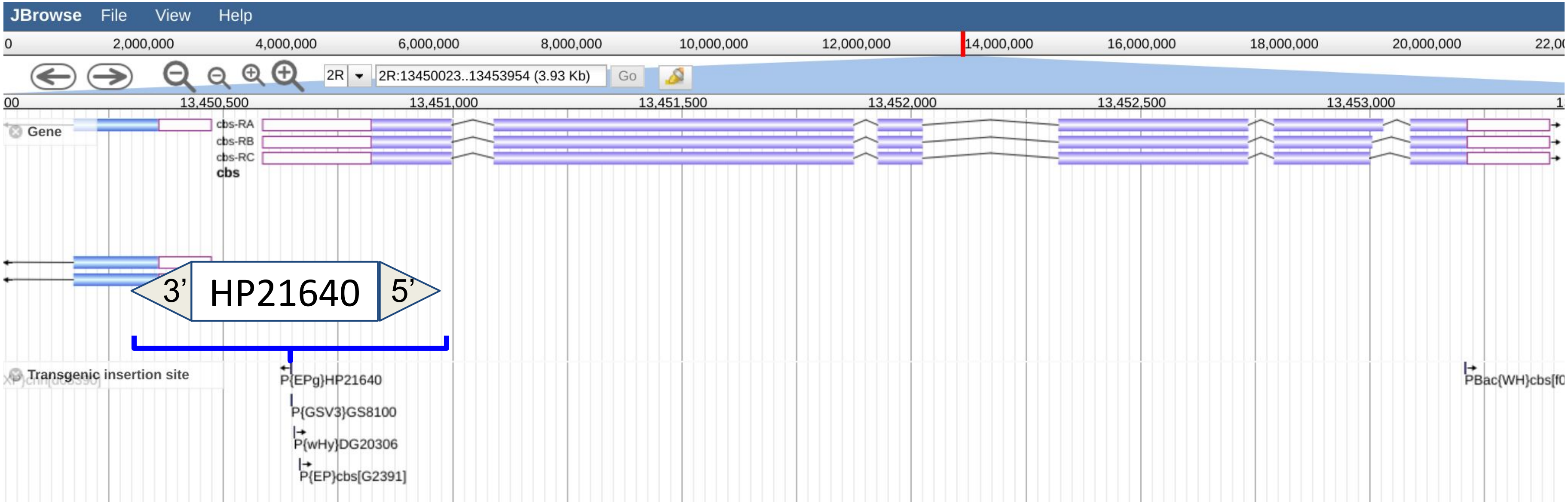
Reference (*Mata et al., 2000*)

Features

The “Segments & Size” section of the construct report describes what’s in the EP element, relative to the P5’ and P3’ ends.
e.g., The GAGA and UAS sites are nested just inside of the P3’.

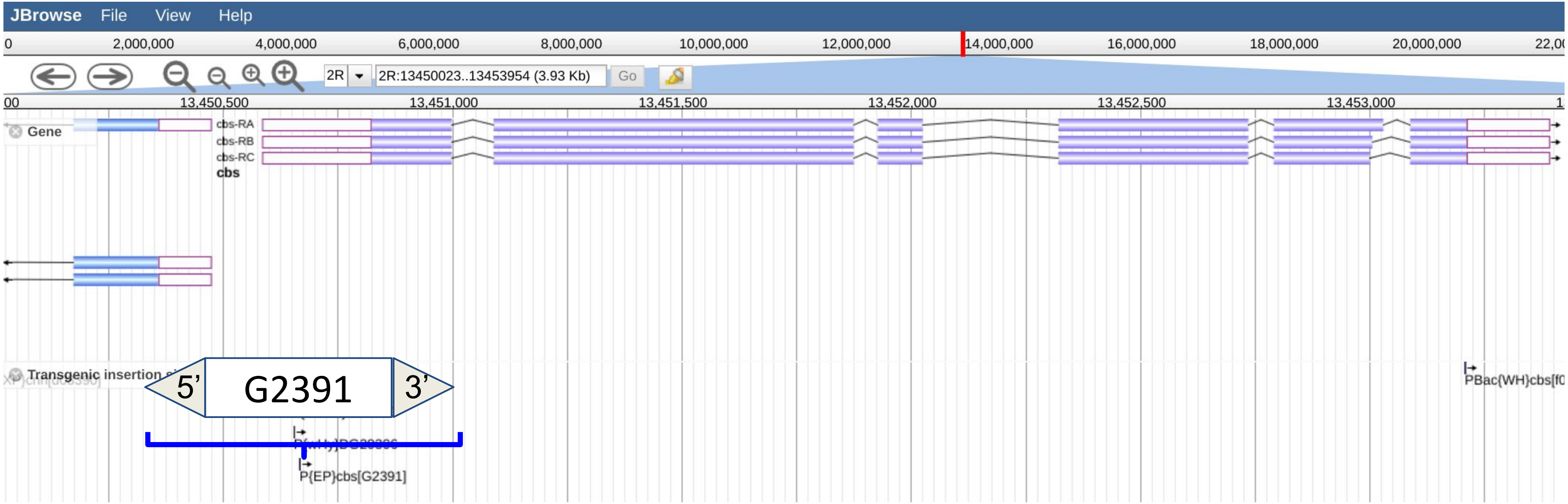
See references listed for more info.

P{EPg}HP21640:



From the info about the “EPg” construct, I would infer that transcription of this HP21640
insertion proceeds through the P3’ ends, away from the “cbs” gene. Not what I want.

P{EP}G2391:



2R:13450023..13453954 (3.93 Kb)

There's another nearby EP element, P{EP}G2391, in which the 5'>3' direction of the transposon is oriented along the "plus" strand. Info about the “EP” construct indicates that the GAGA and UAS sites are nested just within P3’ end. I would infer that transcription proceeds through the P3’ end, along the "plus" genomic strand.

This is the insertion that I want.