Exploring ChIA-PET cis-and-trans interactions in IGV WebApp

December 24, 2021

Chee-Hong WONG
Wei Lab

Getting started..

- Watch youtube video
  - IGV Web | Introduction to the IGV Web App
  - https://www.youtube.com/watch?v=sFeK-25K5PE

- Custom GT Installation: http://ctgenometech02.jax.org/igv-webapp/

  - Example: Exploring HF-3177 per YanFen's paper

DISCLAIMER:

We intend to contribute these customizations to IGV.

Reference to IGV does not mean endorsement / acceptance of these customization(s) by the IGV team.

Cancer Cell Supports open access

ARTICLE | VOLUME 39, ISSUE 5, P694-707.E7, MAY 10, 2021

Oncogenic extrachromosomal DNA functions as mobile enhancers to globally amplify chromosomal transcription

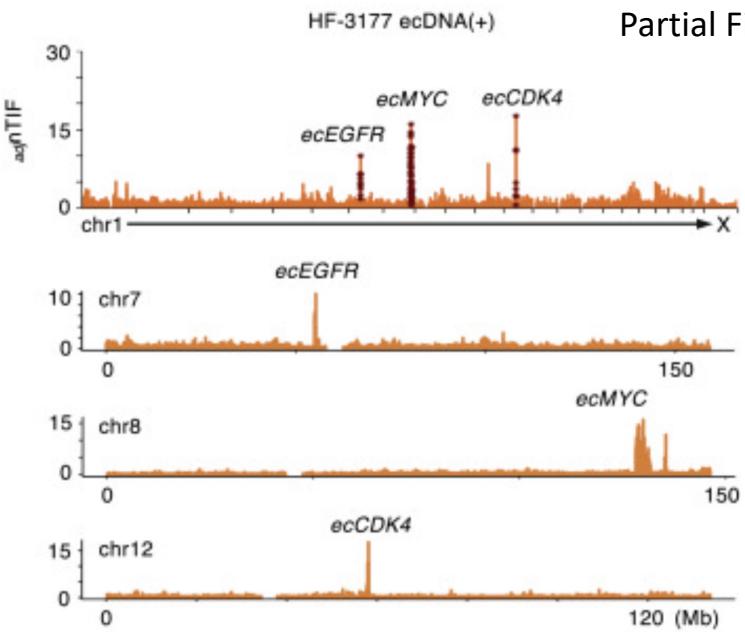
Yanfen Zhu [3] • Amit D. Gujar [3] • Chee-Hong Wong [3] • ... Yijun Ruan • Roel G.W. Verhaak • Chia-Lin Wei [4] • Show all authors • Show footnotes

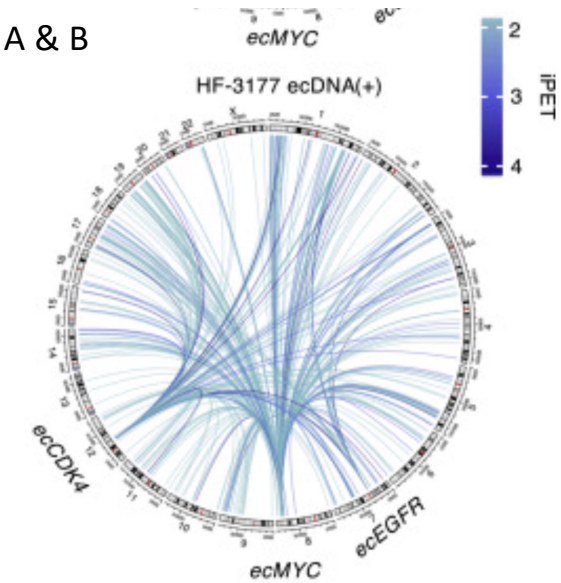
Published: April 08, 2021 • DOI: https://doi.org/10.1016/j.ccell.2021.03.006 • Check for updates

Data downloaded from
https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM3553630

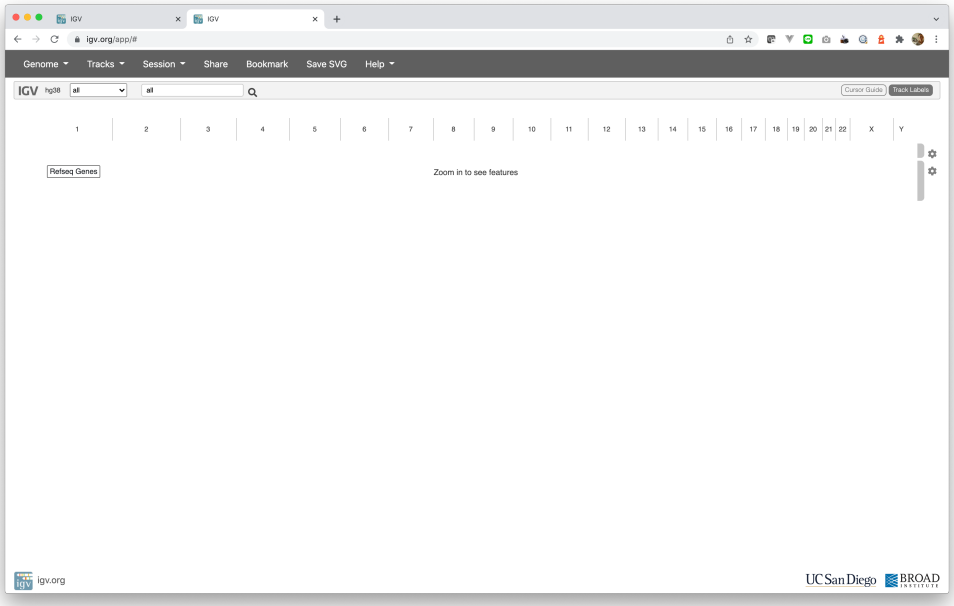
```
# cis-interactions
gzip -dc GSM3553630_HF-3177_chiapet.cis.chiasig.sigf.interactions.txt.gz \
| grep -v '#' \
| awk -v FS="\t" -v OFS="\t" '{print $1,$2,$3,$4,$5,$6,"R"NR,$8;}' \
| gzip -c - > GSM3553630_HF-3177_chiapet.cis.chiasig.sigf.itx.bedpe.gz

# trans-interactions
gzip -dc GSM3553630_HF-3177_chiapet.trans.chiasig.interactions.txt.gz \
| awk -v FS="\t" -v OFS="\t" '{if ($7>=2) {print $1,$2,$3,$4,$5,$6,"R"NR,$7;}}' \
| gzip -c - > GSM3553630_HF-3177_chiapet.trans.chiasig.itx.ge2.bedpe.gz
```

Partial Fig 2 A & B

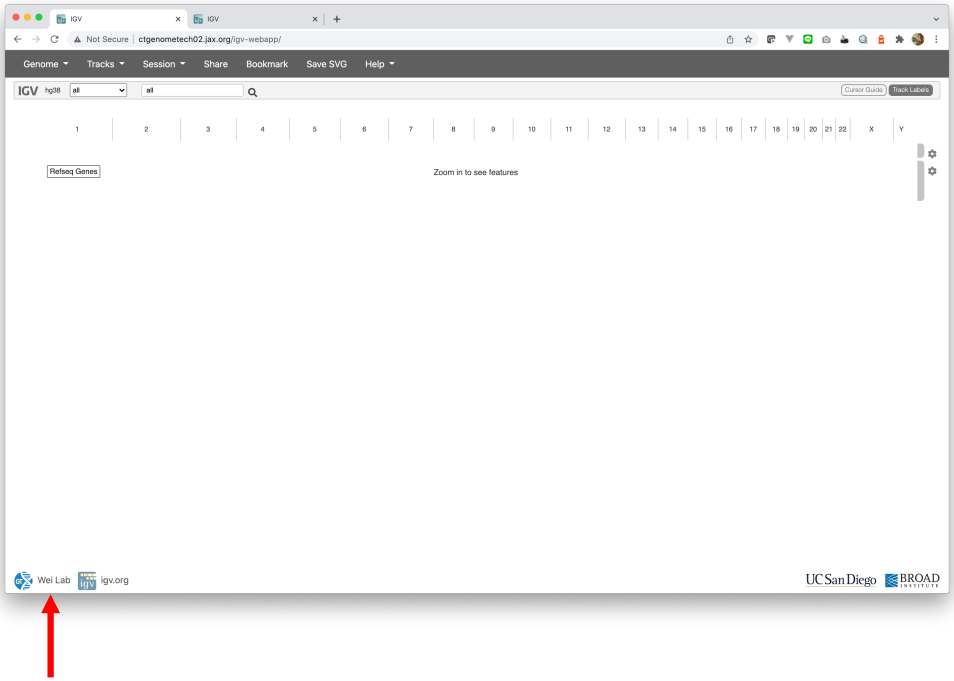


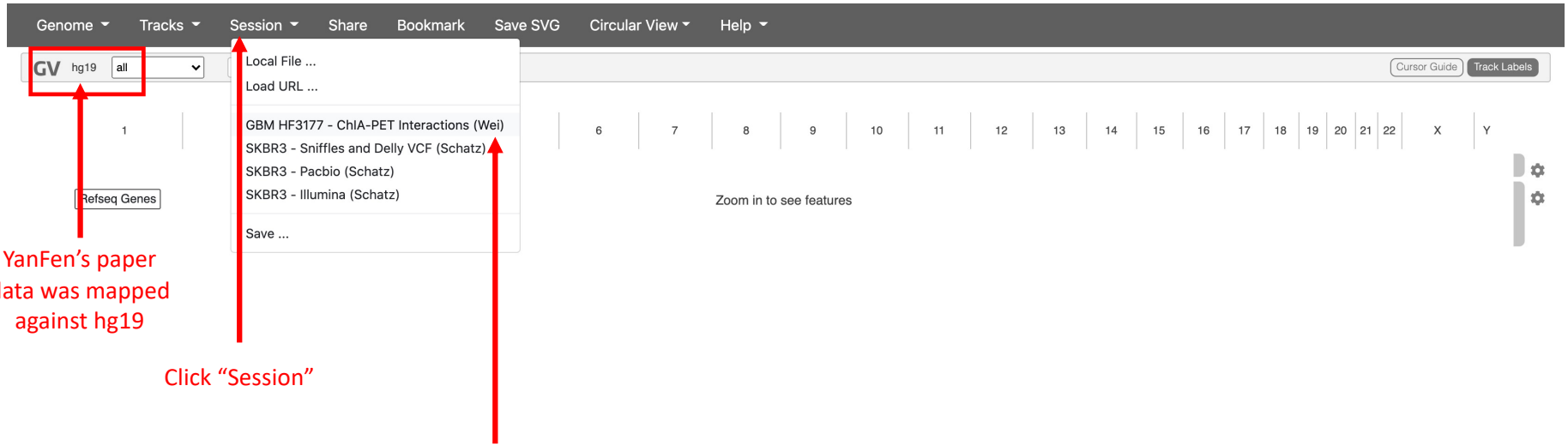


https://igv.org/app/#



http://ctgenometech02.jax.org/igv-webapp/



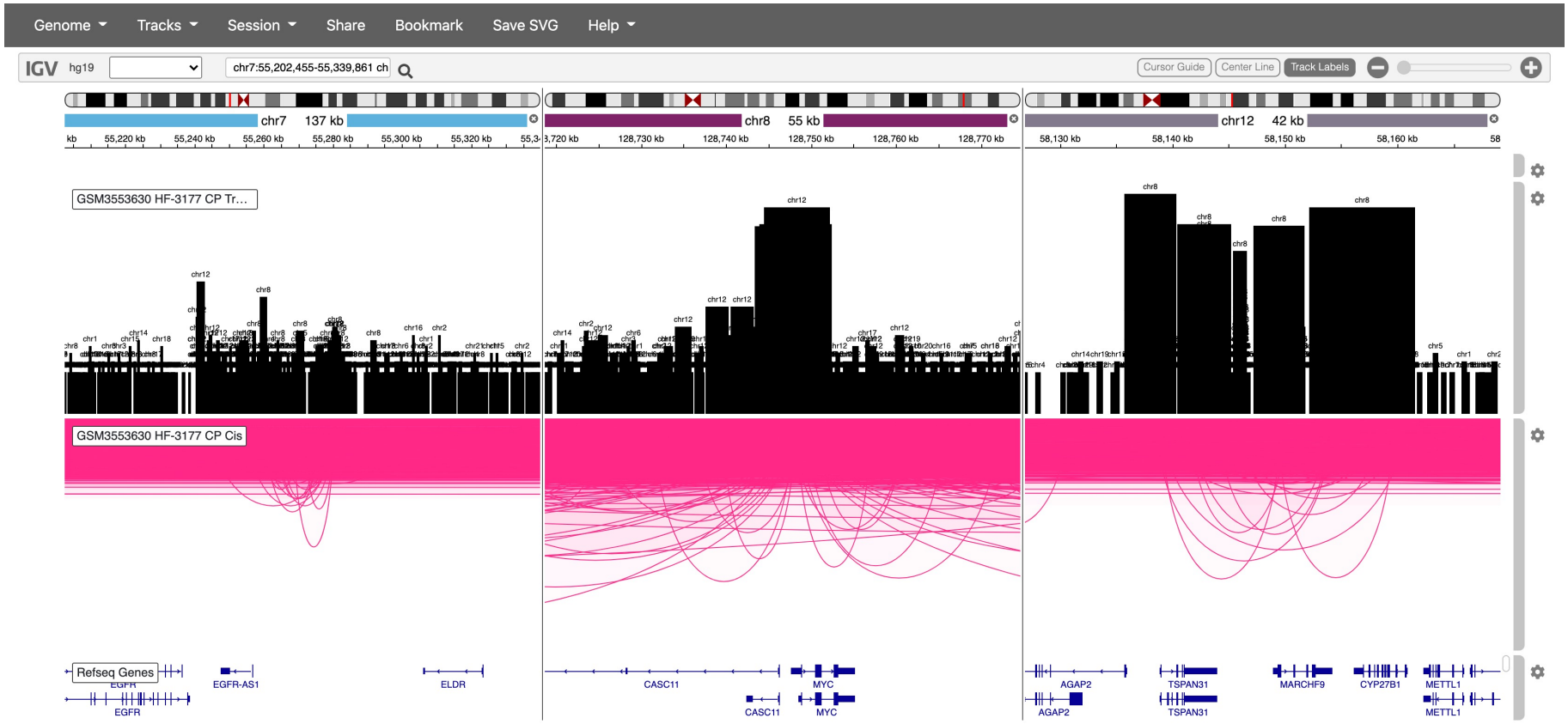


YanFen's paper data was mapped against hg19

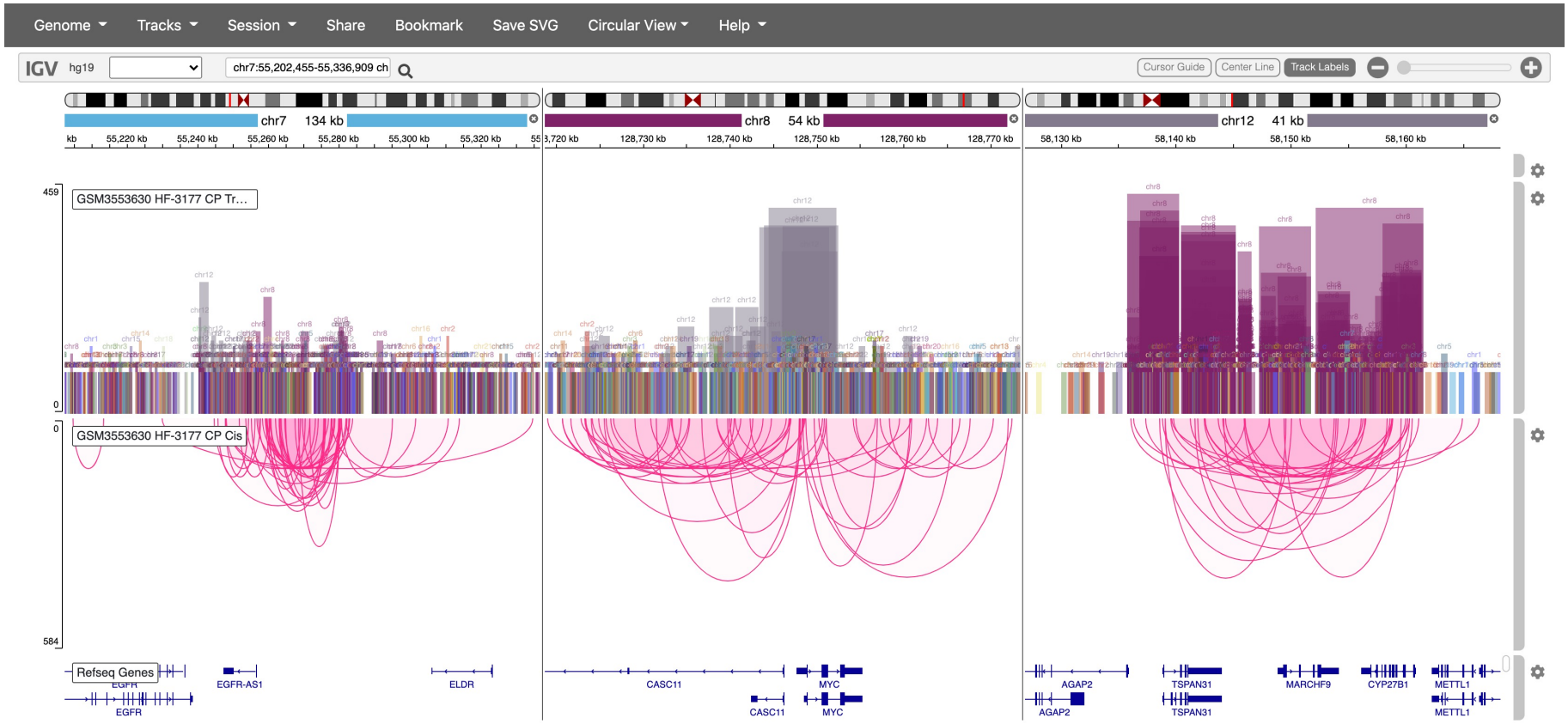
Click "Session"

Click to load the canned example session from Wei's lab.
(GM HF3177 session contains reference to the data published in PMID:33836152, data accession #GSM3553630).

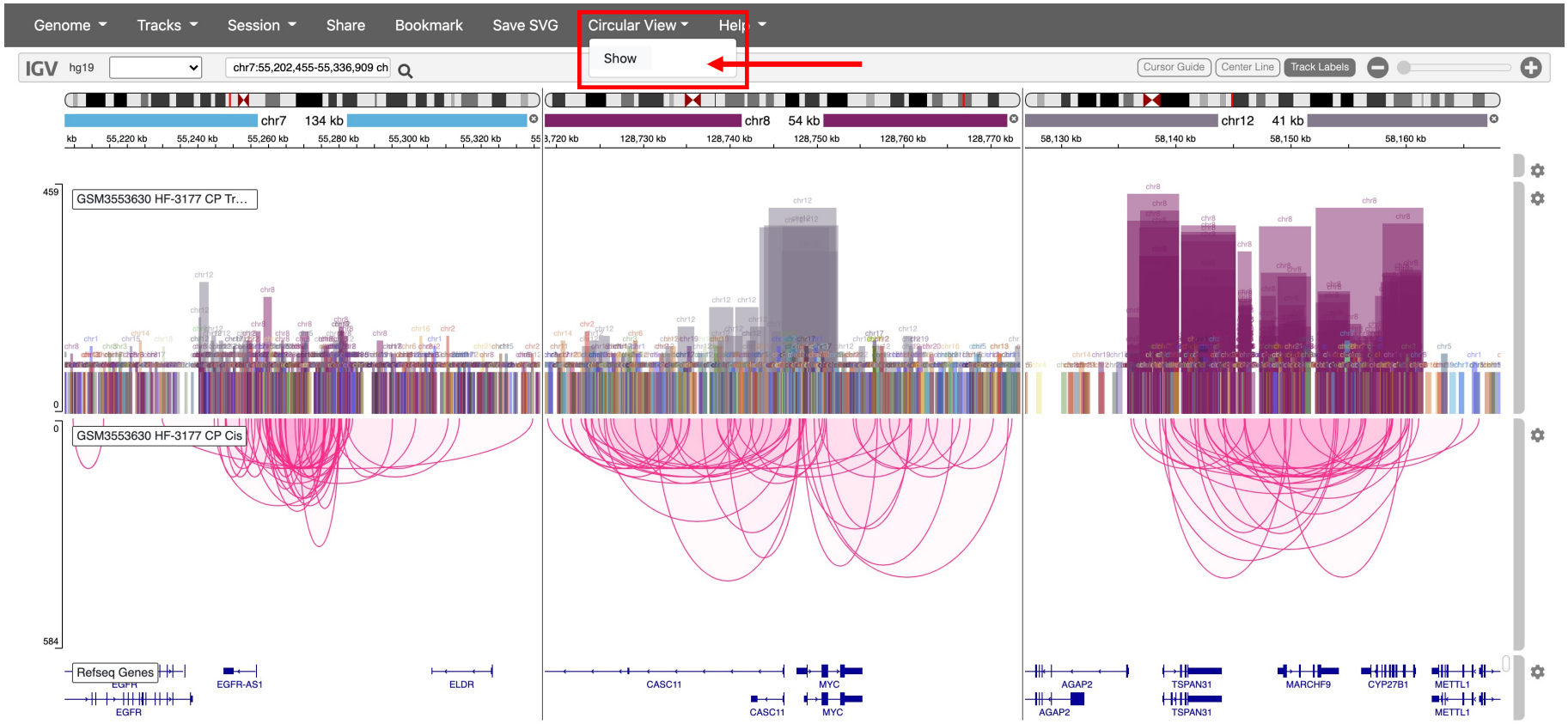
The next three canned SKBR3 sessions are what IGV team has shared.



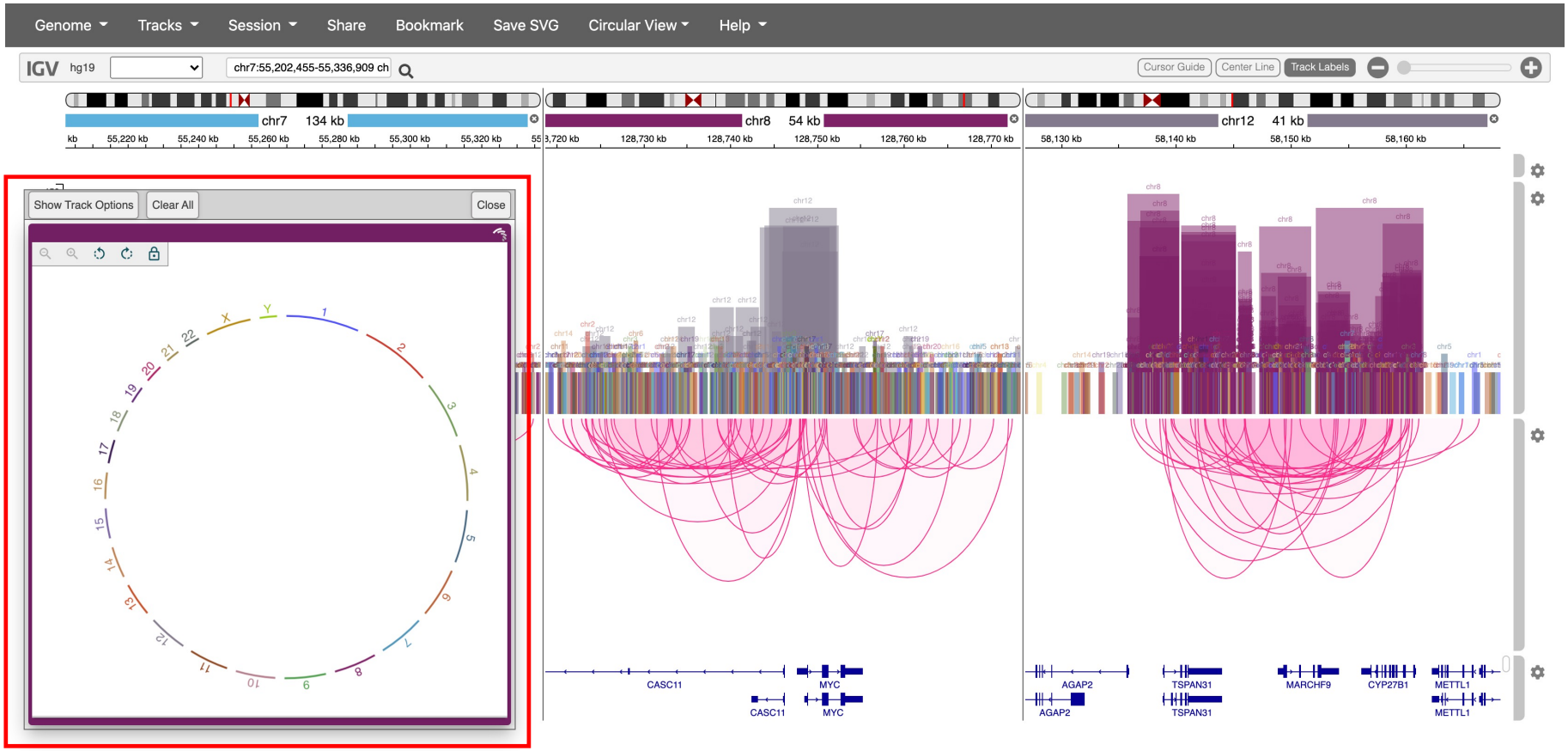
If you see this display instead, you are not using the IGV-WebApp with Wei Lab customizations.



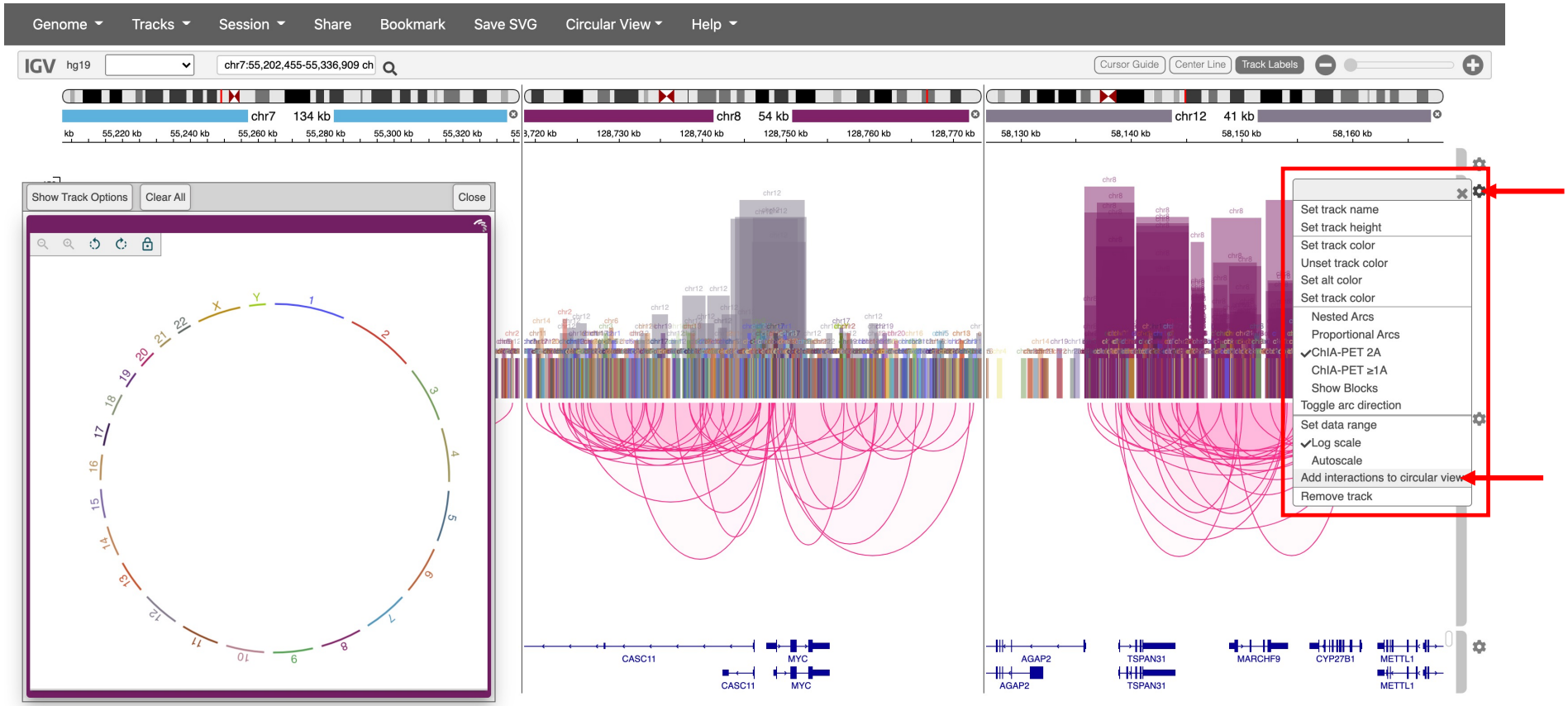
Canned session “GBM HF3177 - ChIA-PET Interactions (Wei)” loaded successfully after a few moment.



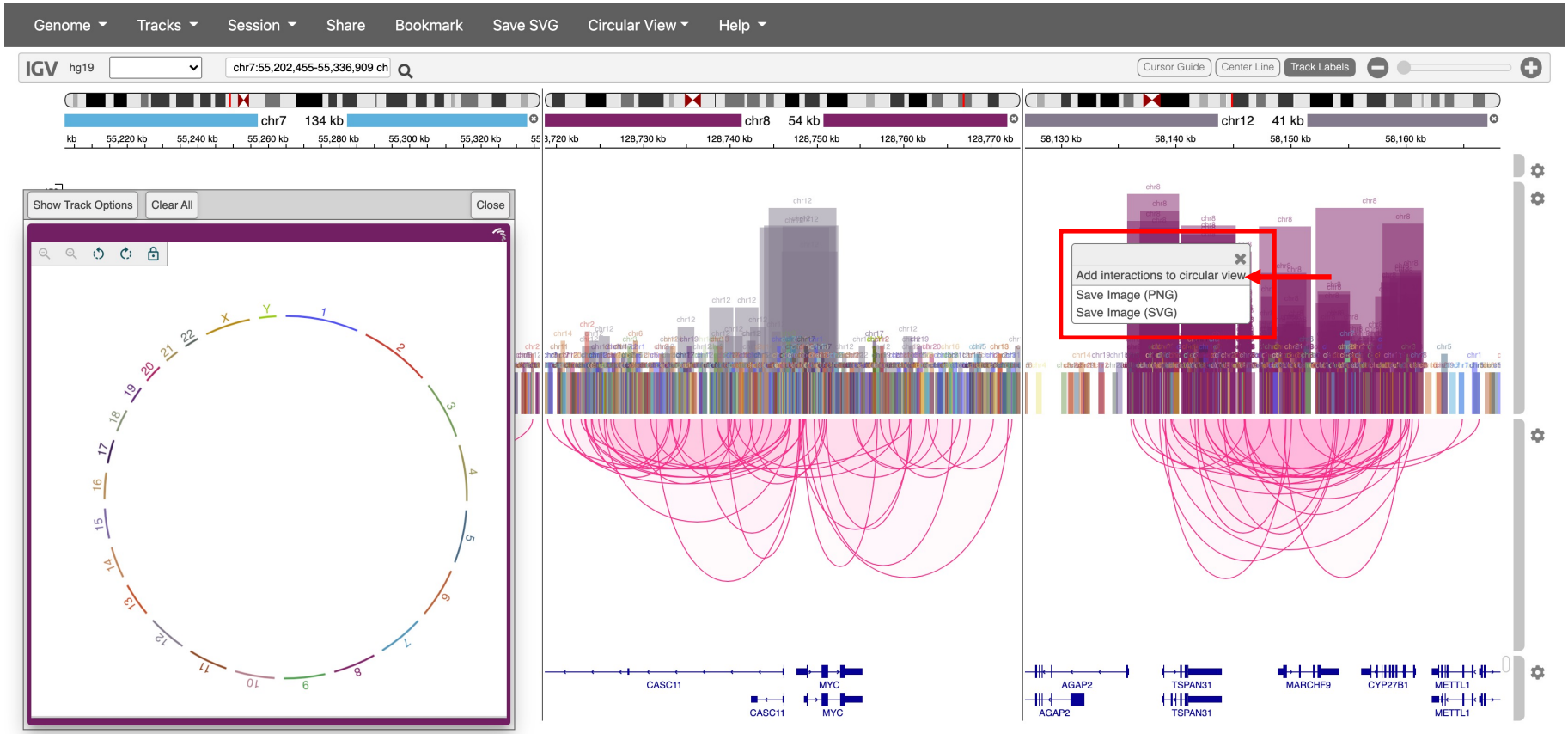
Circular View floating panel is accessed via top menu “Circular View”, “Show”.



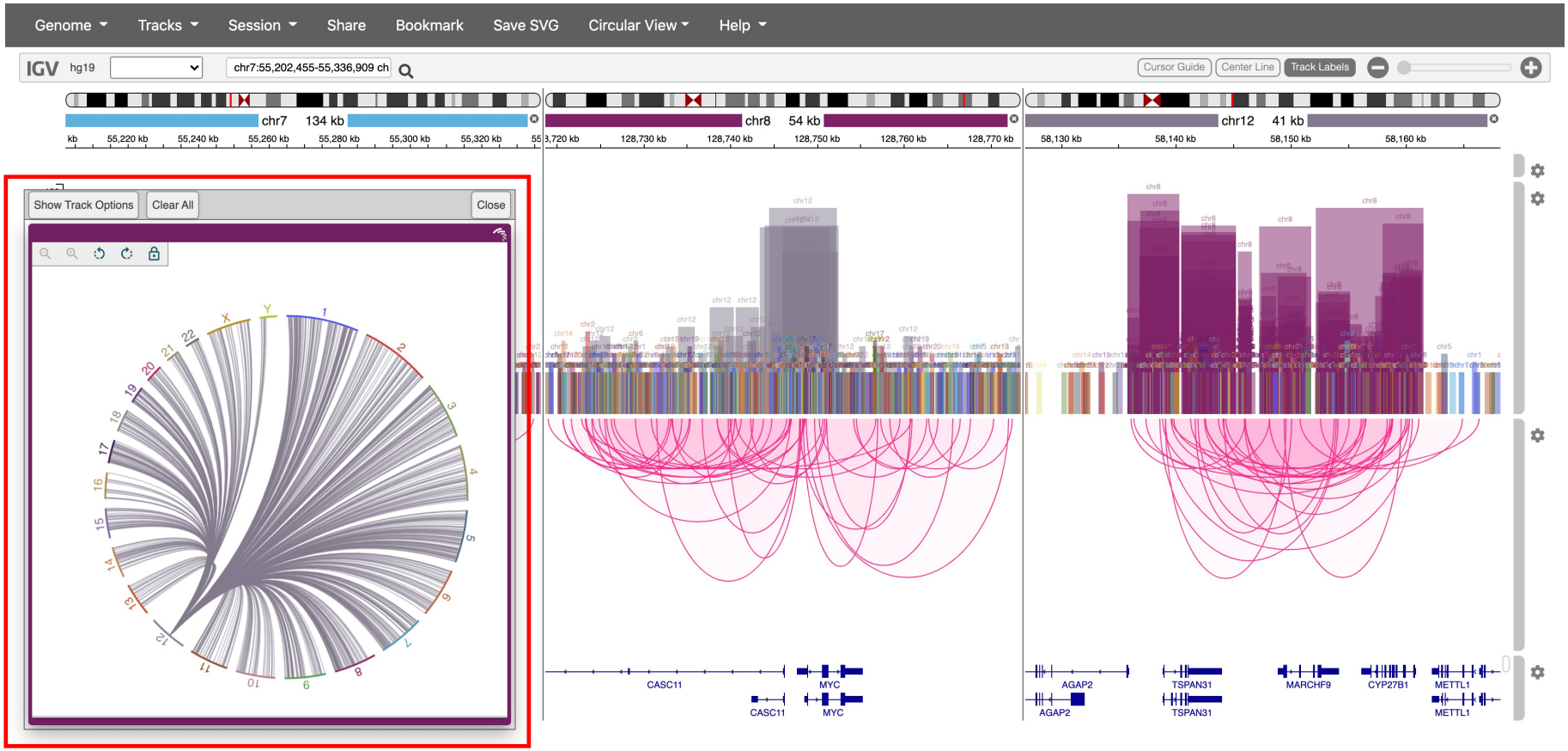
Circular View floating panel starts with only the genome backbone and interactions of interest can be “collected” for illustration.



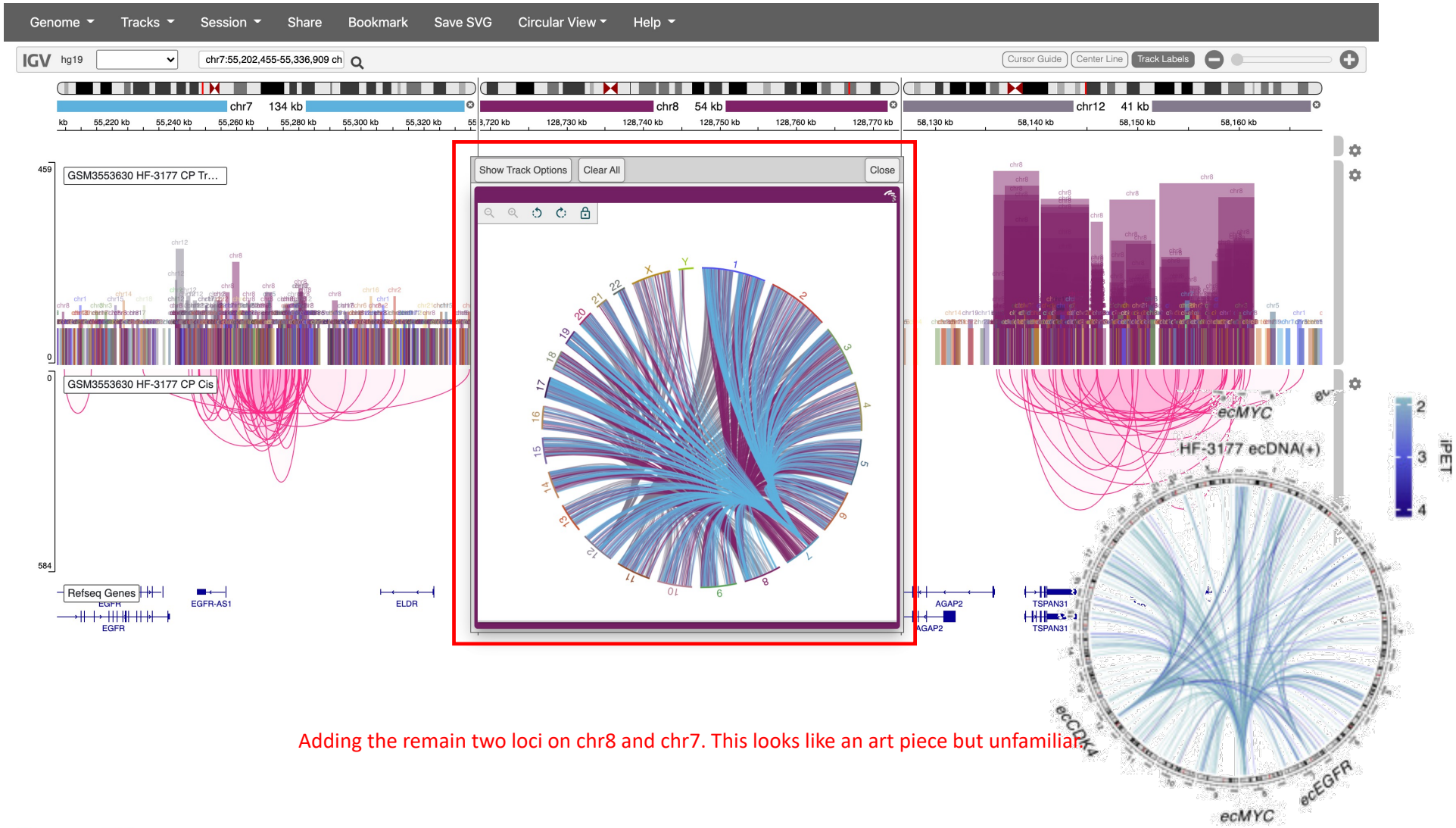
Gear icon for track will add all interactions in the track. Will be overwhelming without any focus.



Right click in the track area will allow adding interactions in your current view / locus. E.g. chr12 locus of 41kb in this example.



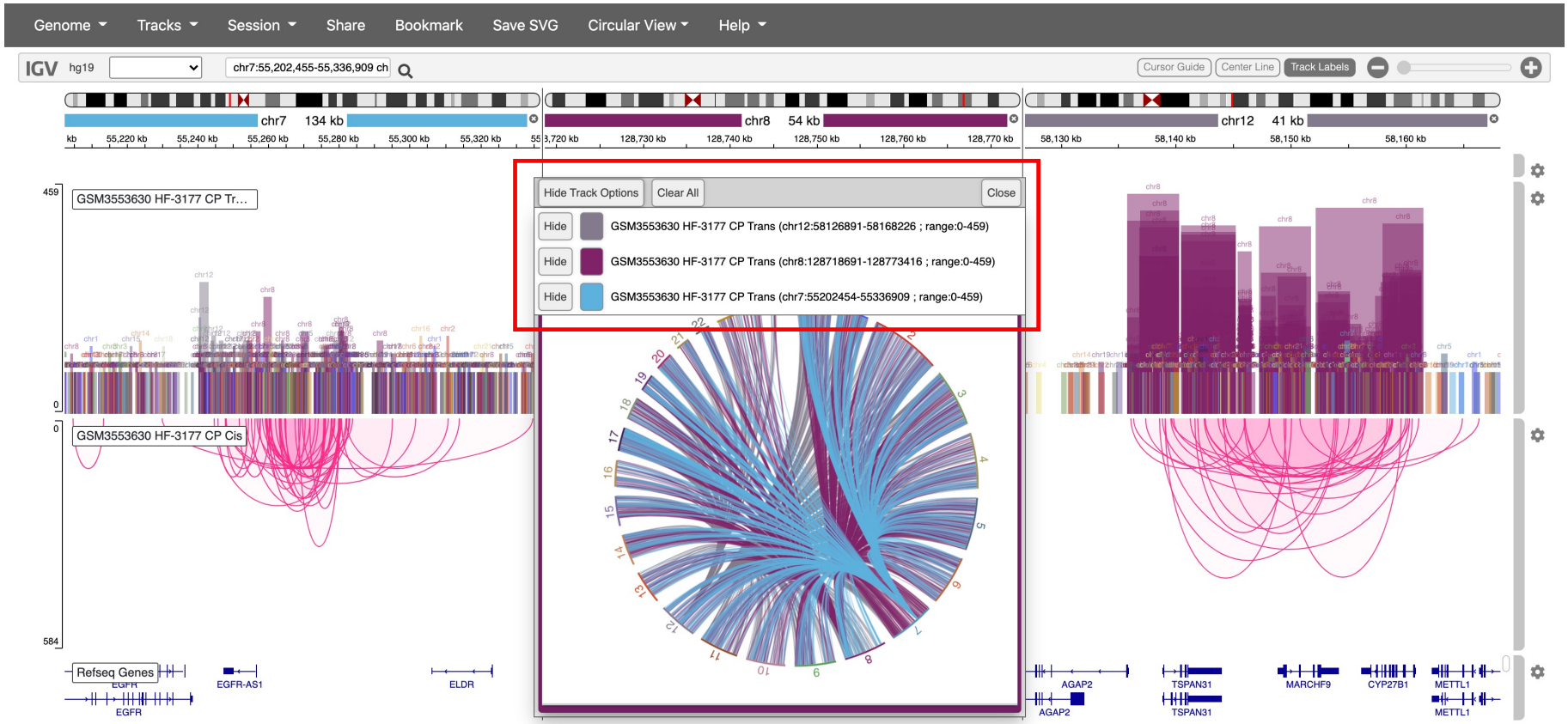
The circular view reflects that this 41kb region has genome wide interactions!



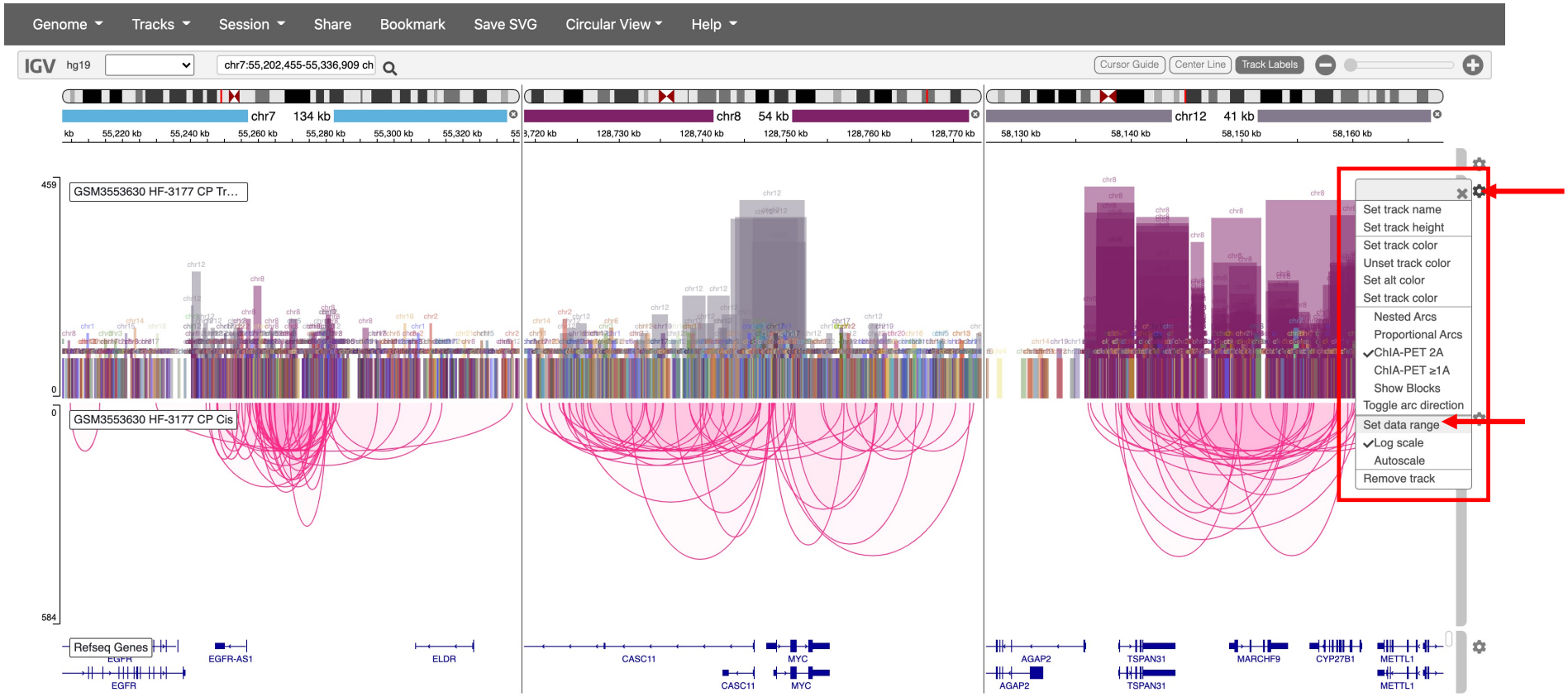
Adding the remain two loci on chr8 and chr7. This looks like an art piece but unfamiliar.

Wei Lab igv.org

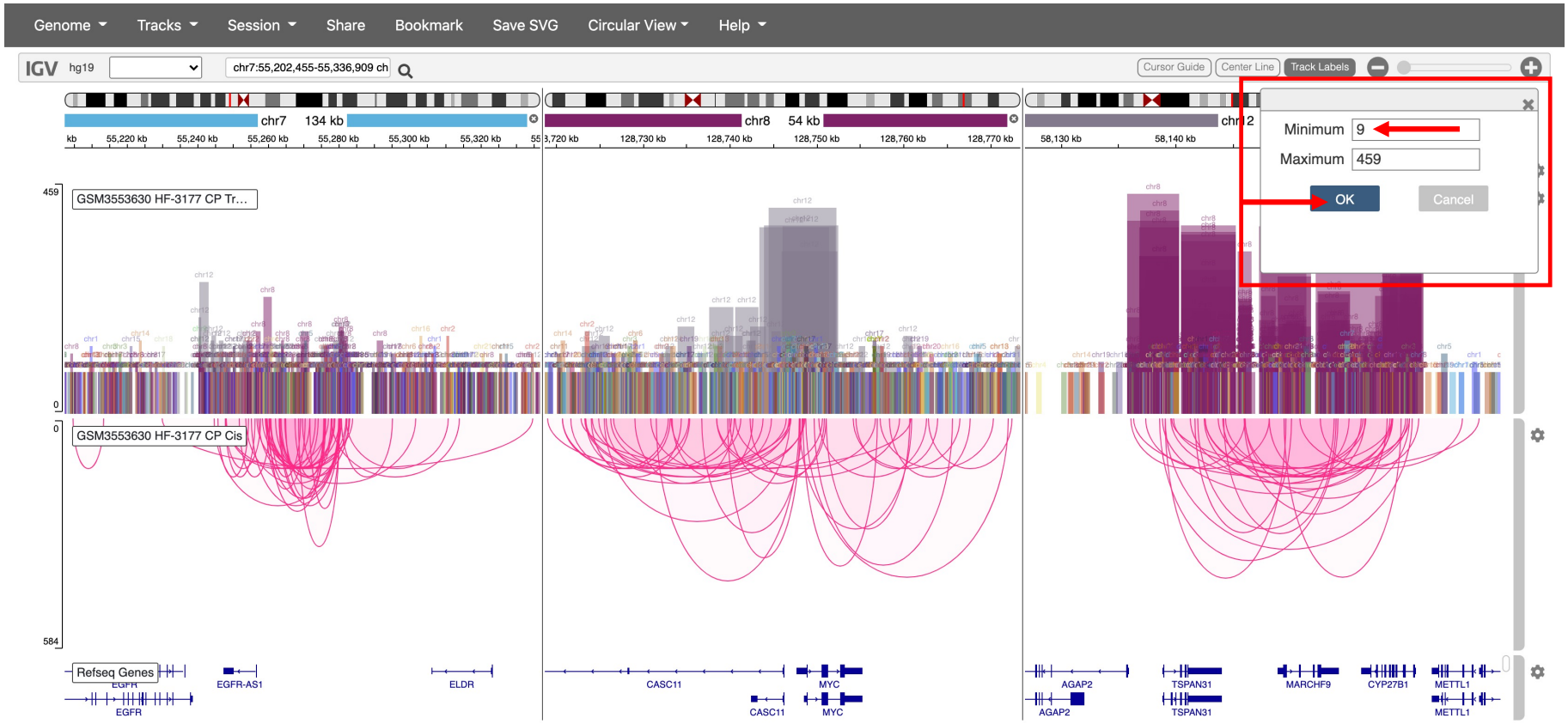
UC San Diego BROAD INSTITUTE



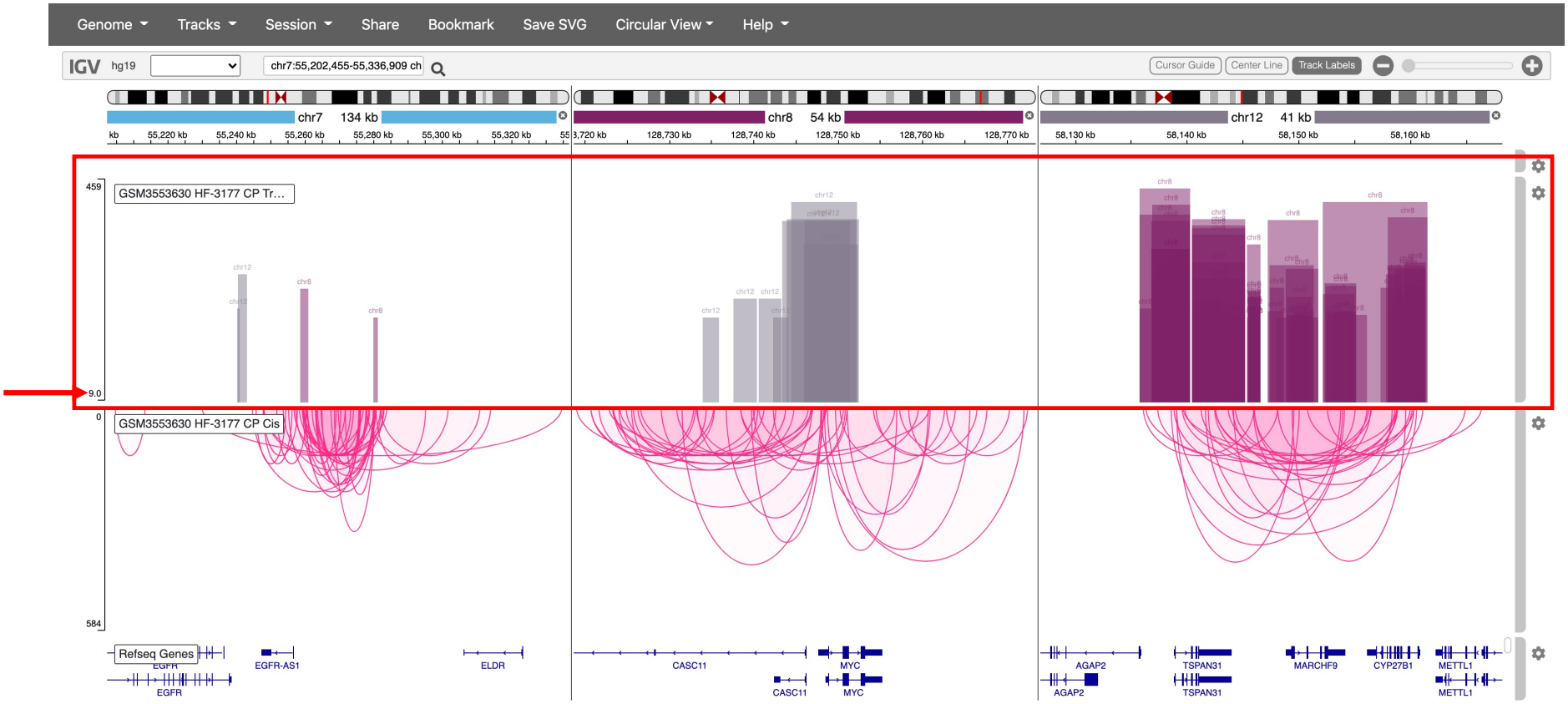
The circular view shows the tracks of interactions and allow both color and visibility controls.



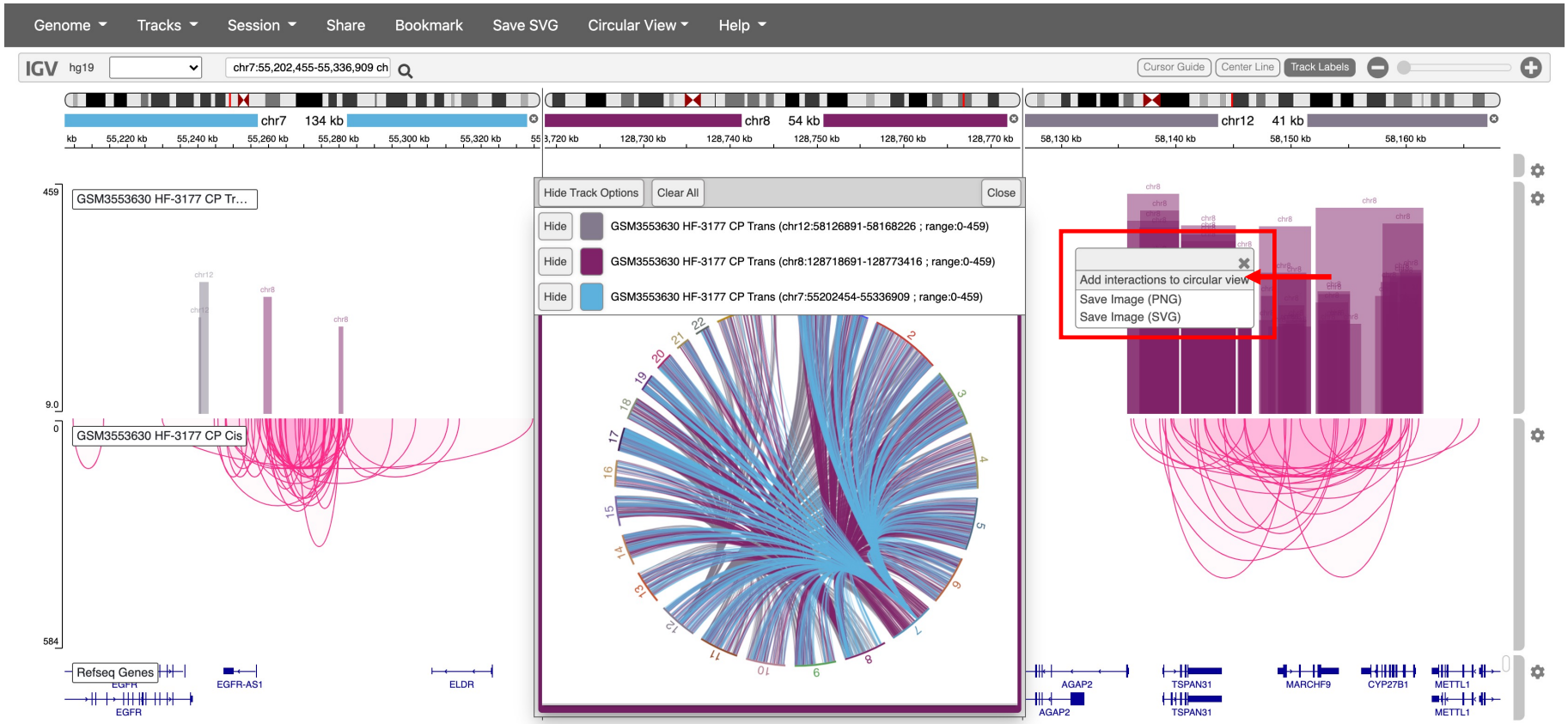
Let’s change the art piece into information via the data range.



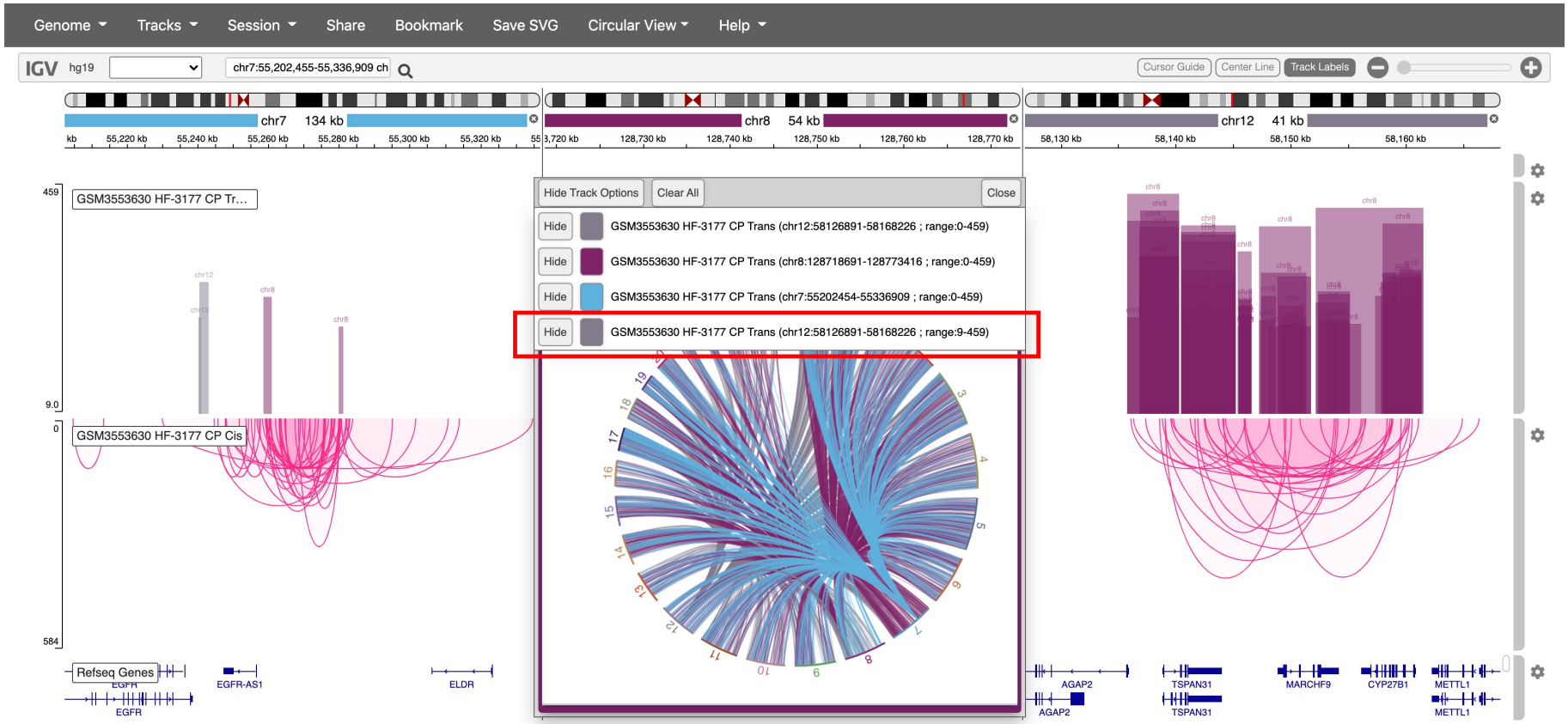
To focus on only the dominant signals, let's set the minimum threshold to be 9.



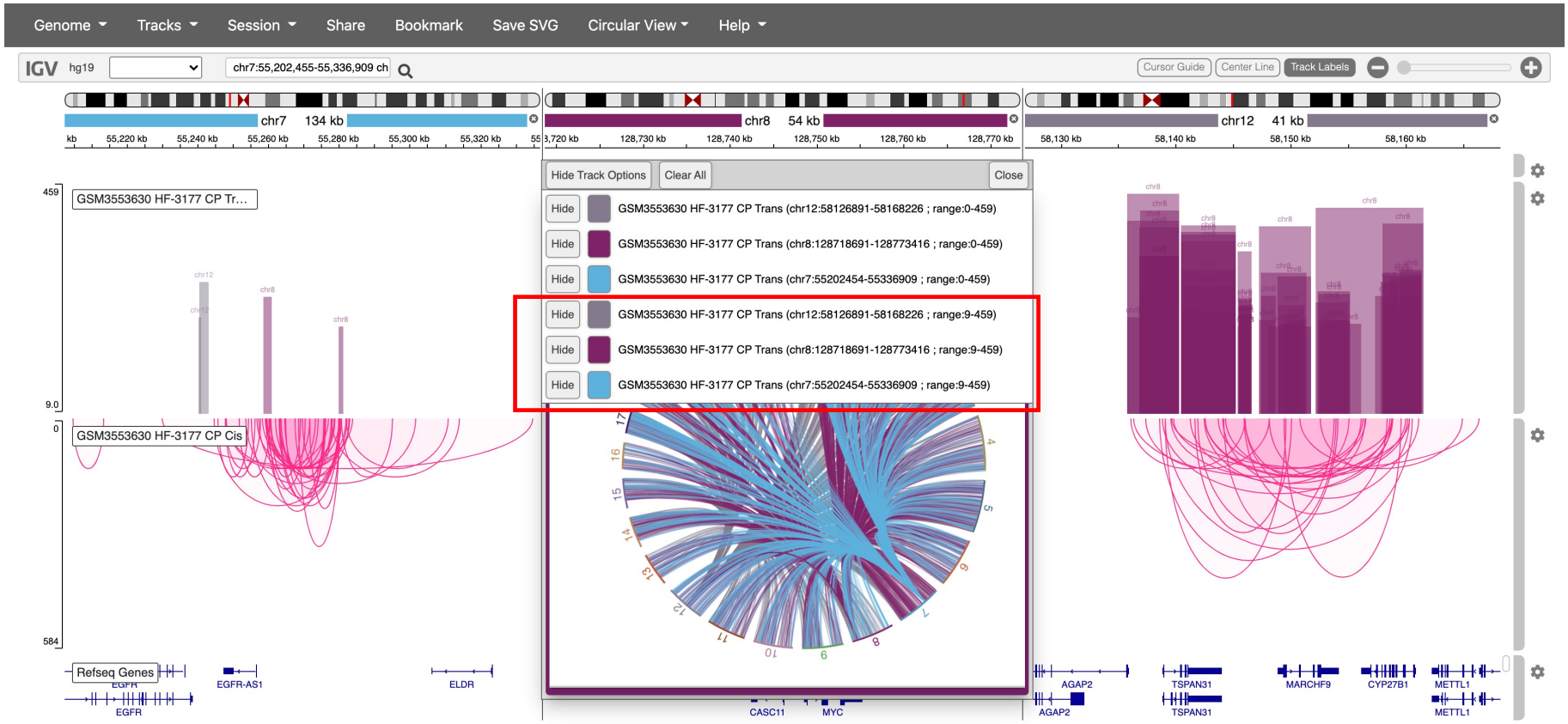
The (trans-)interactions track shows a much cleaner picture now.



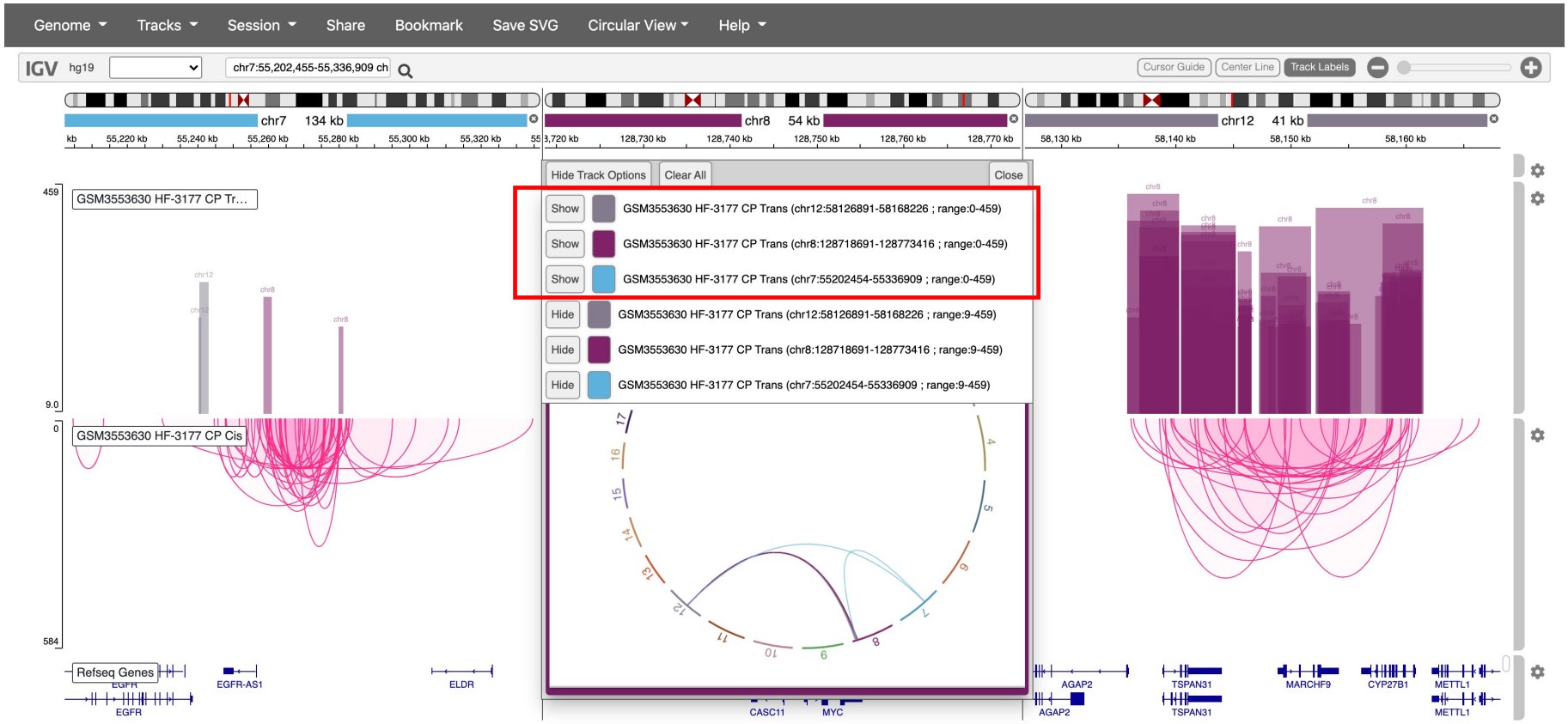
Let's add these new filtered set of interactions to circular view.



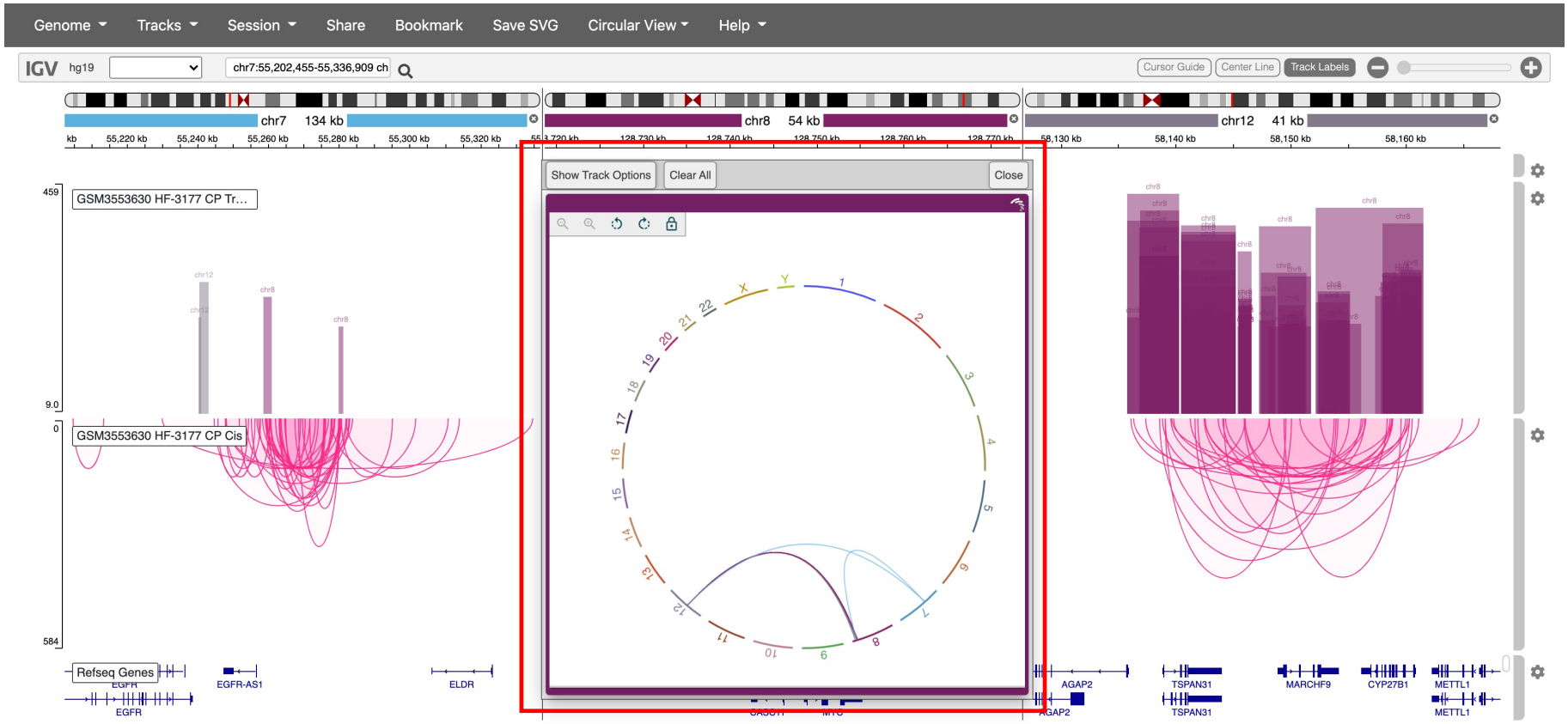
We can't tell the difference visually! Don't worry. Let's finish up with the remaining two loci.



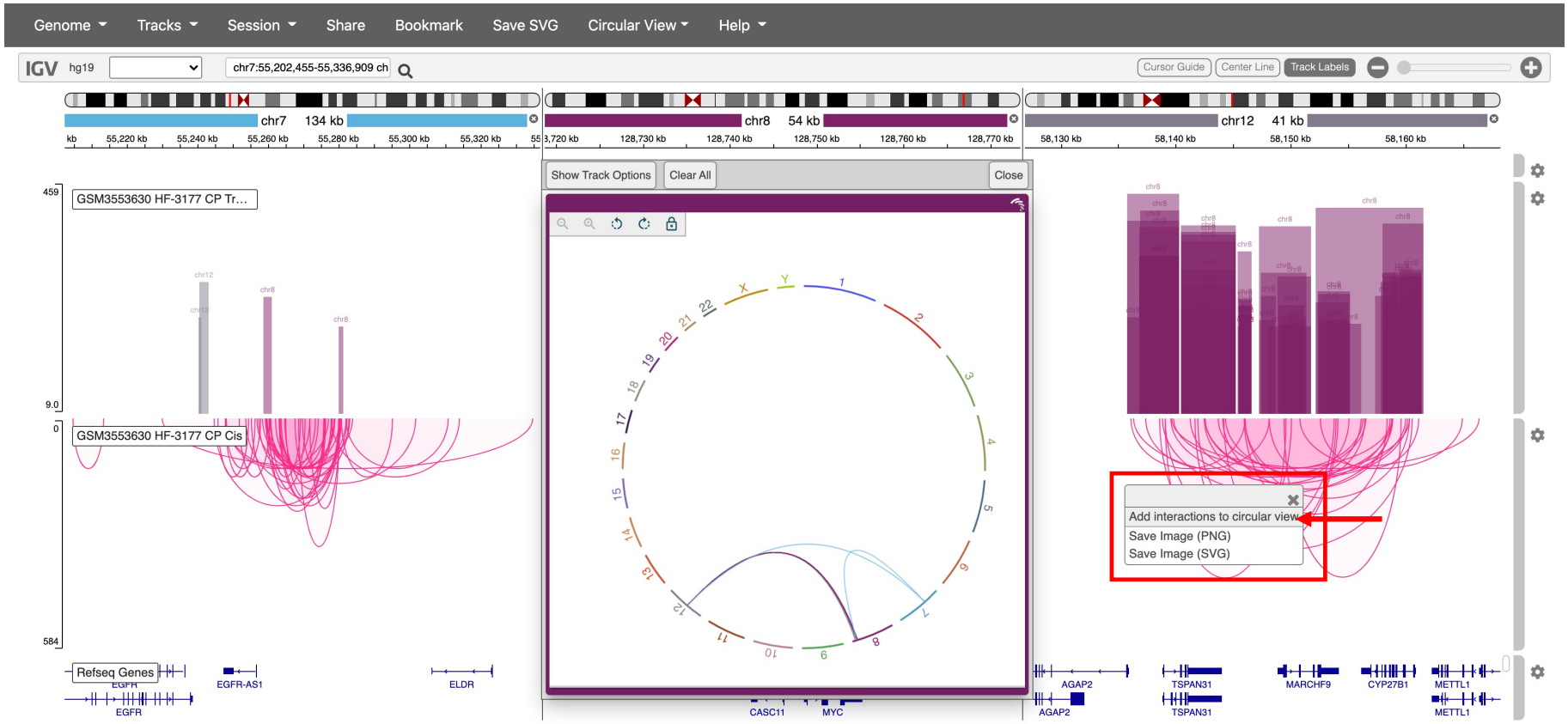
All three loci's interactions have been added. NOT helping!



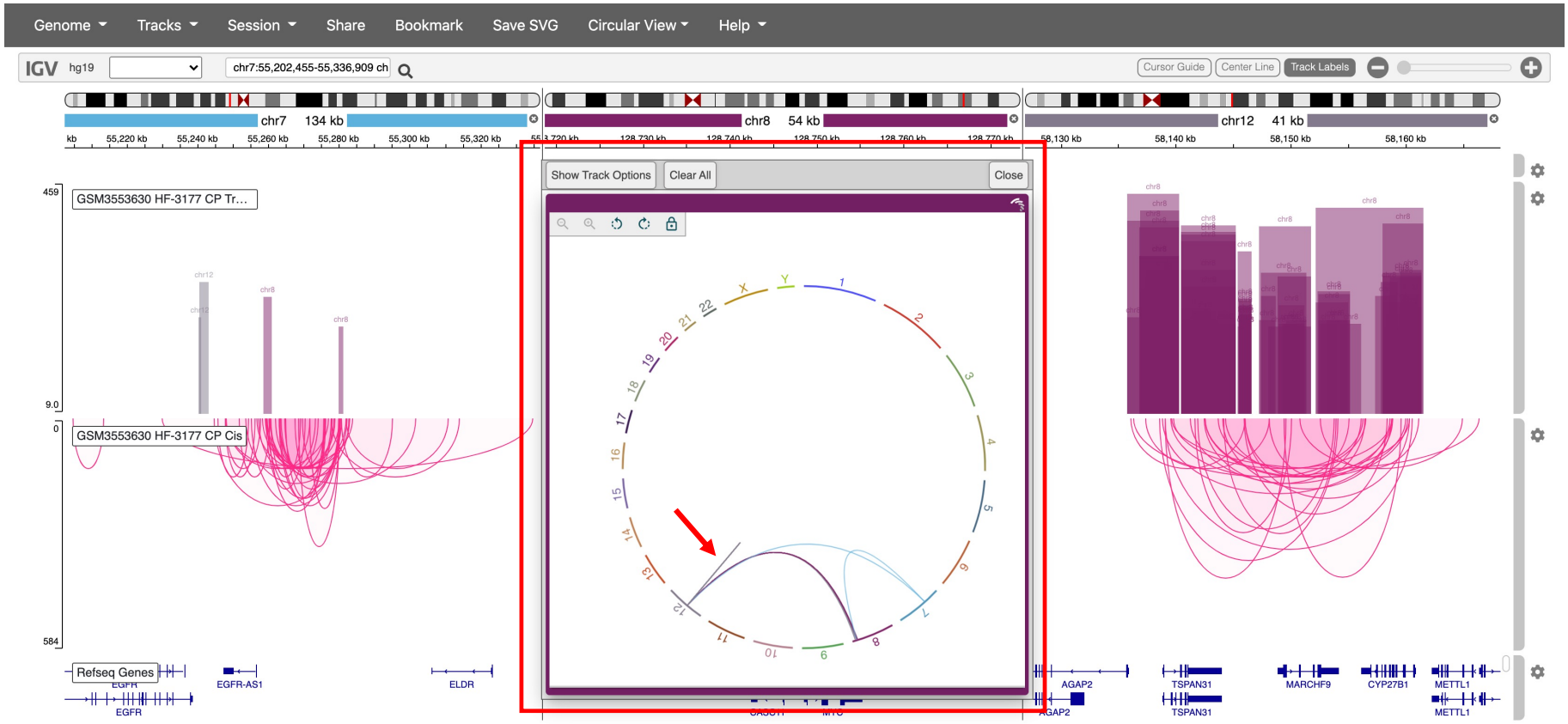
Click on the hide buttons (on the left) of the first three tracks (range: 0-459). Now, it is no longer a mess.



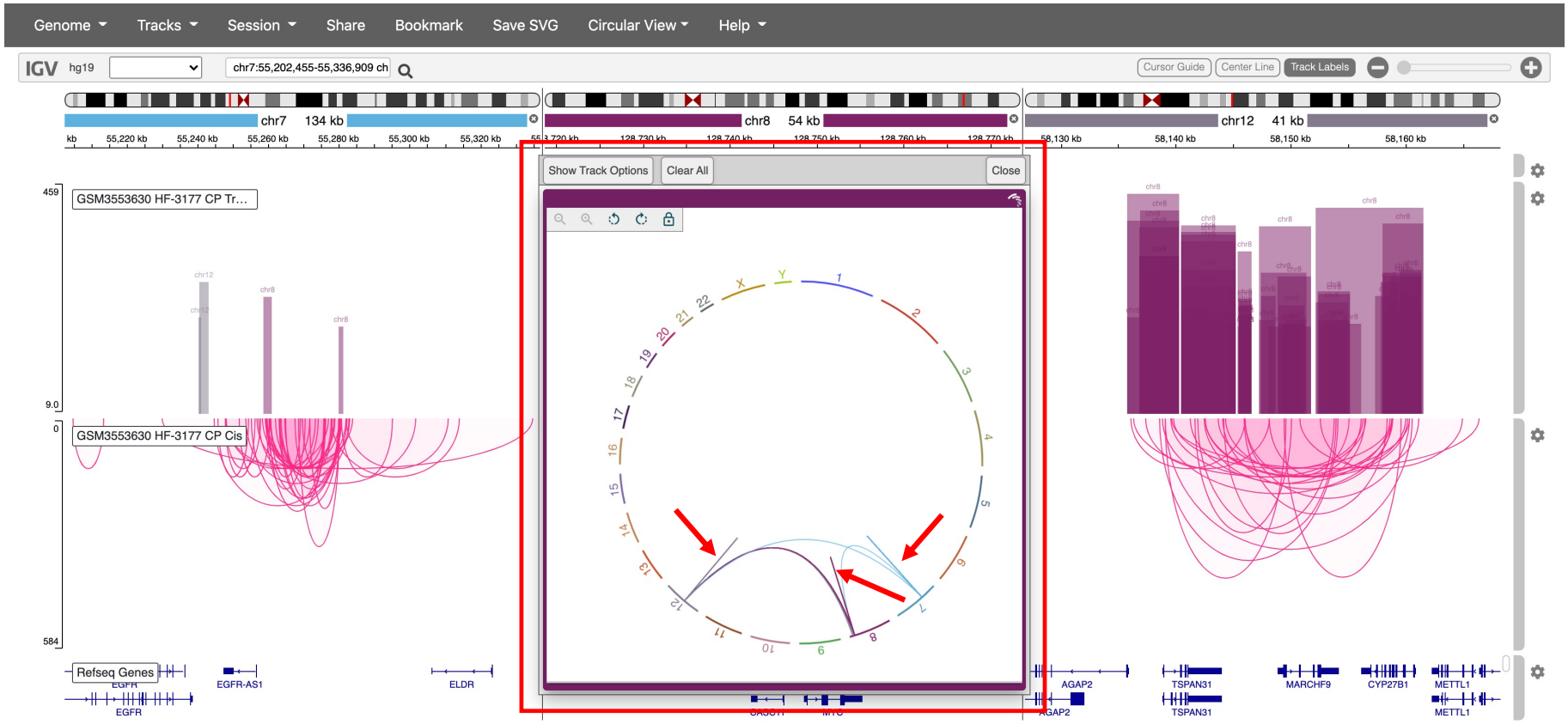
Click on the Hide Track Options button (on the top-left) . The dominants interactions signal involved these three loci.



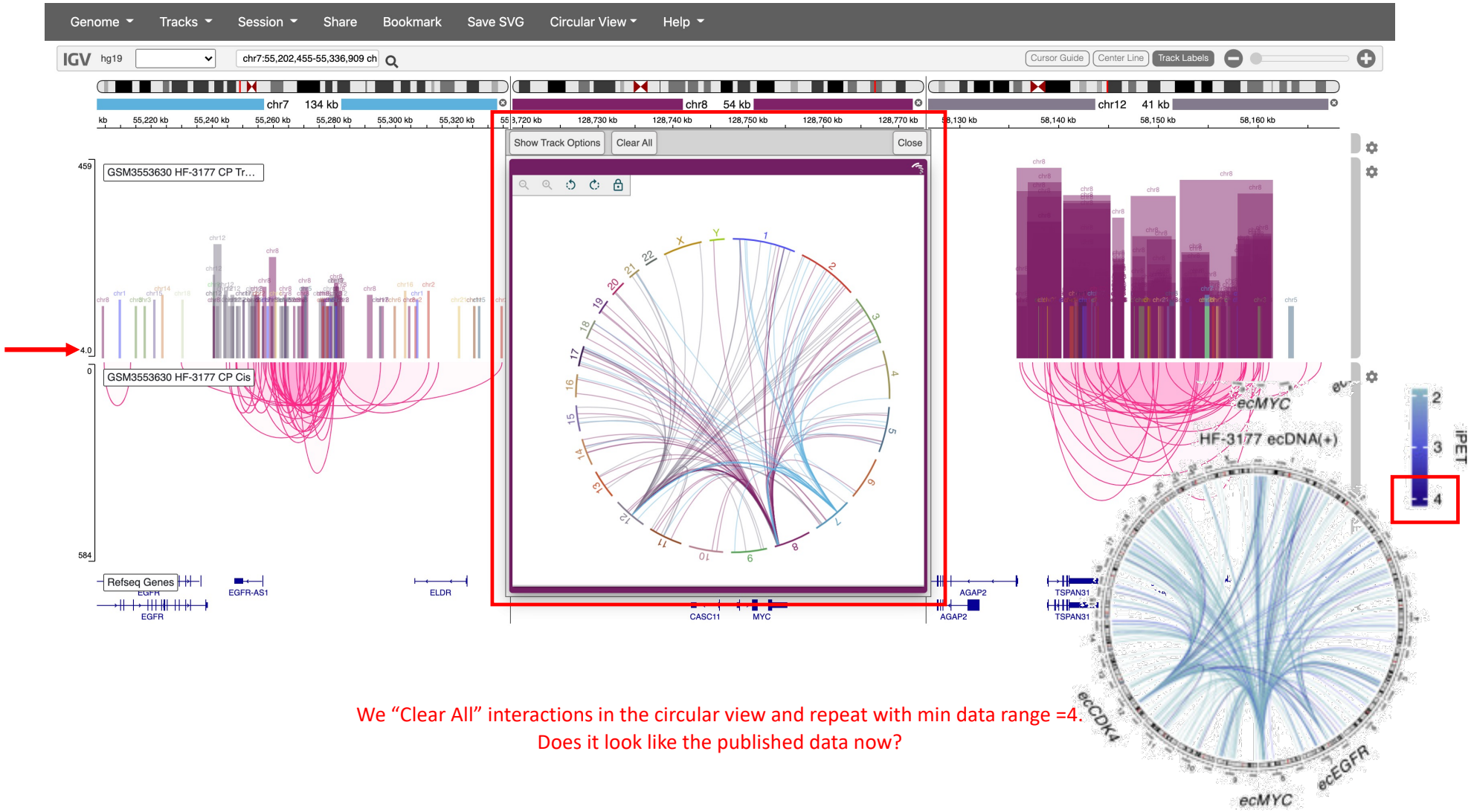
You may also add the cis-interactions to the circular view.



The cis-interactions from chr12 locus have been added to the circular view.



The cis-interactions from all three loci have been added to the circular view.



We “Clear All” interactions in the circular view and repeat with min data range =4.
Does it look like the published data now?

I don’t have loci of interest or magical session(s)…
where do I start?

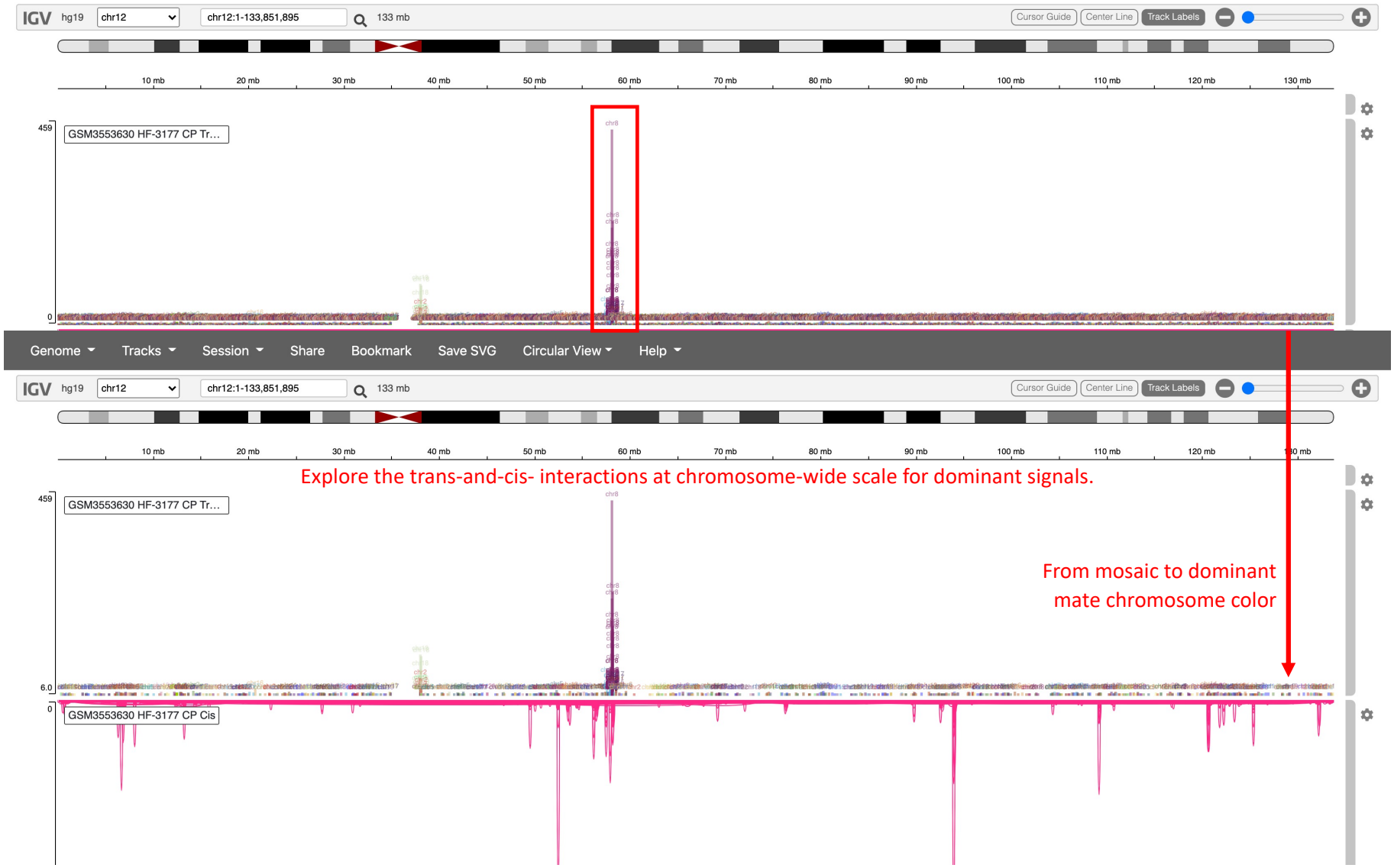
One approach

Discovery / Exploration

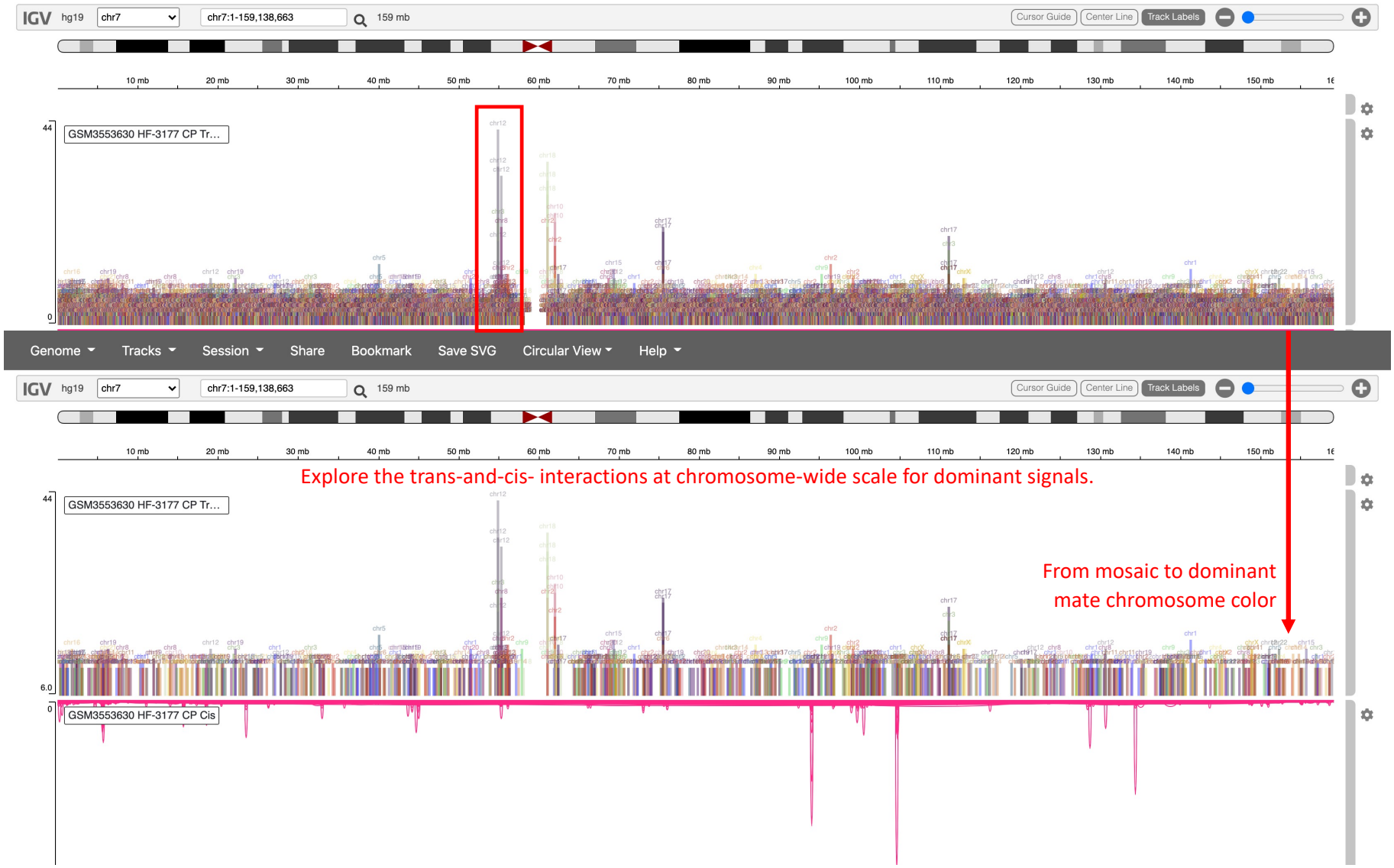
1. Explore the trans-and-cis- interactions at chromosome-wide scale for dominant signals
2. Zoom in on locus of interest
3. Add interactions to circular view
4. Click on the chord in the circular view to have IGV WebApp display the multi-loci view covering both ends of the chord
5. Repeat step 2-4 to build up the dominant interactions

Other tips

- Record the genome coordinates of the region of interest as you explore. (*Bookmark* is a good option.)
- Use the “Show” / “Hide” button to explore the combination of interactions from multiple loci
- Multiple regions can be displayed in the same browser by entering them into the locus search box and separate them with space… examples
  - EGFR MYC CDK4
  - chr7:55,202,455-55,336,909 chr8:128,718,692-128,773,416 chr12:58,126,892-58,168,226
  - *mixture of genes and genome coordiantes*


IGV
hg19
chr12
chr12:1-133,851,895
133 mb
Cursor Guide
Center Line
Track Labels
10 mb
20 mb
30 mb
40 mb
50 mb
60 mb
70 mb
80 mb
90 mb
100 mb
110 mb
120 mb
130 mb
459
0
GSM3553630 HF-3177 CP Tr...
Genome
Tracks
Session
Share
Bookmark
Save SVG
Circular View
Help
Explore the trans-and-cis- interactions at chromosome-wide scale for dominant signals.
From mosaic to dominant mate chromosome color
6.0
GSM3553630 HF-3177 CP Cis

IGV
hg19
chr8
chr8:1-146,364,022
146 mb
Cursor Guide
Center Line
Track Labels
10 mb
20 mb
30 mb
40 mb
50 mb
60 mb
70 mb
80 mb
90 mb
100 mb
110 mb
120 mb
130 mb
140 mb
459
GSM3553630 HF-3177 CP Tr...
0
Genome
Tracks
Session
Share
Bookmark
Save SVG
Circular View
Help
Explore the trans-and-cis- interactions at chromosome-wide scale for dominant signals.
From mosaic to dominant
mate chromosome color
6.0
GSM3553630 HF-3177 CP Cis


IGV
hg19
chr7
chr7:1-159,138,663
159 mb
Cursor Guide
Center Line
Track Labels
GSM3553630 HF-3177 CP Tr...
Genome
Tracks
Session
Share
Bookmark
Save SVG
Circular View
Help
Explore the trans-and-cis- interactions at chromosome-wide scale for dominant signals.
From mosaic to dominant mate chromosome color
GSM3553630 HF-3177 CP Cis