

Interact (and bigInteract) tracks in the UCSC browser

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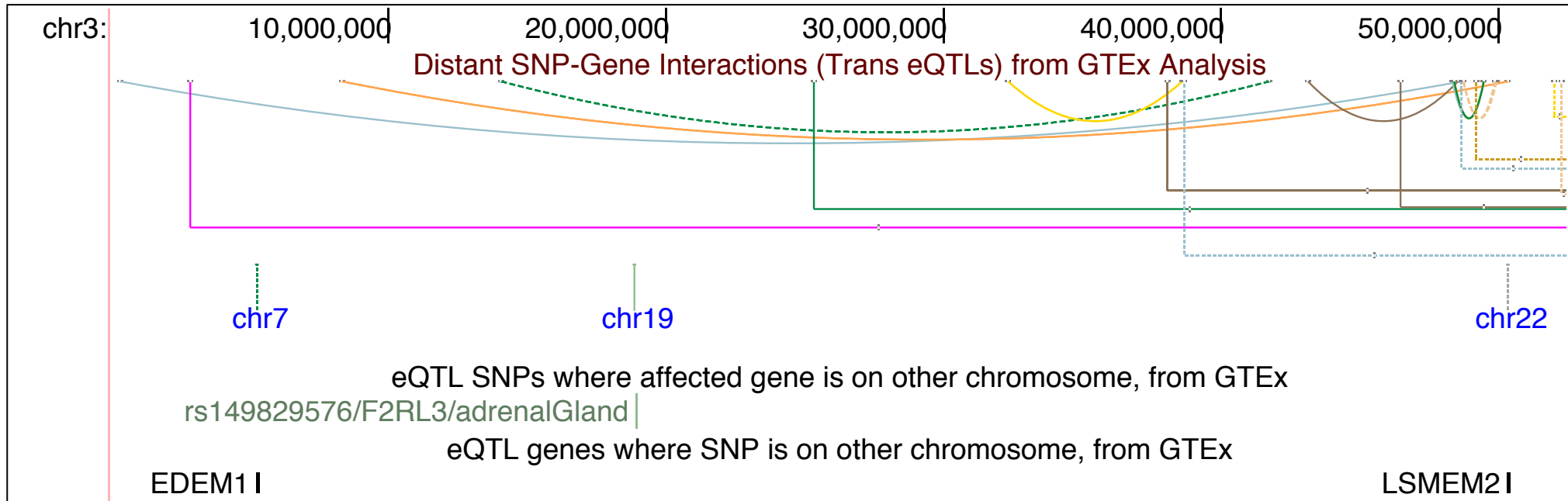
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Motivation

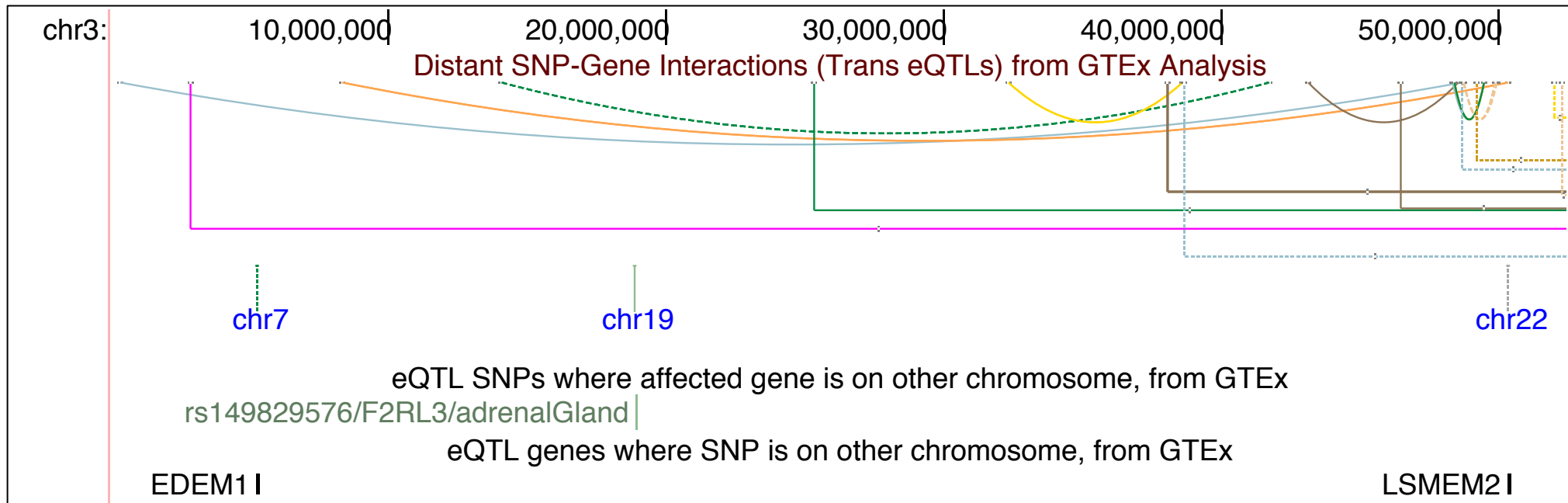
- Show long-range pairwise interactions/relationships
- Support cross-chromosome as well as same chromosome interactions
- Handle multiple data types:
 - Regulatory elements (e.g. SNP/gene)
 - Chromatin interactions (e.g. chiaPet)
 - Genomic rearrangements

Example: GTEx trans-eQTLs



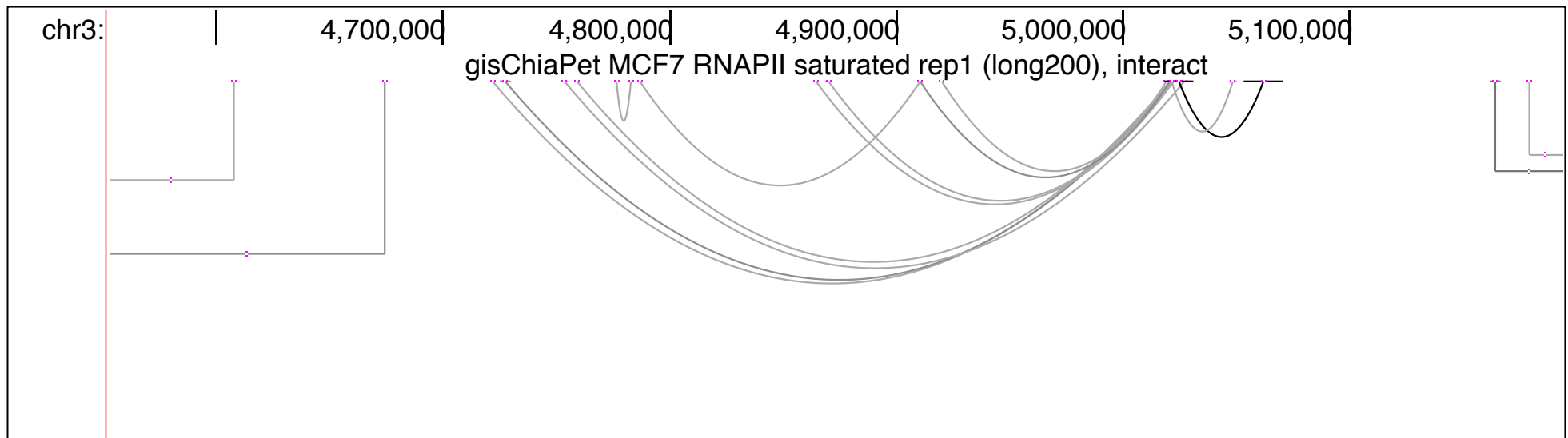
50 Mbp region of chromosome 3 where GTEx analysis identifies 15 significant long-distance eQTLs spanning the region, one variant affecting expression of a gene on another chromosome (F2RL3 on chromosome 19) and two genes (EDEM1 and LSMEM2) affected by variants on other chromosomes. Interactions are colored to indicate tissue.

Interact track features



- Curved connectors represent interactions with both endpoints on-screen. Curve type is configurable (bezier, ellipse)
- Dashed lines represent reverse direction
- Mouseover and click-through on endpoints and 'peaks' (with glyph)
- Vertical in lower band represents off-chromosome interaction. Labeled if space permits
- User-colored or grayscale coloring

Example: chiaPET chromatin interactions



16 ChiaPet chromatin interactions identified in a 640 Kbp region of chromosome 3 in the MCF7 cell line (courtesy Genome Institute of Singapore). Interactions are displayed in gray-scale, with stronger interactions shown darker.

Interact track example

Interaction name: inter1

Interaction region: [chr6:99,790,008-99,798,261](#) 8,254 bp

Score: 233

Value: 4.000

Experiment: brain

Lower region: rs1 [chr6:99,790,008-99,793,559](#) 3,552 bp

Upper region: gene1 [chr6:99,794,573-99,798,261](#) + 3,689 bp

Distance between midpoints: 4,633 bp

Details page

[Go to User Track track co](#)

Data last updated: 2018

User Track Track Settings

Interact track example [\(▲All Custom Tracks\)](#)

Display mode:

Minimum score:

Track height: pixels (range: 20 to 300, default: 200)

Draw mode: curve ellipse rectangle

[View table schema](#)

Data last updated: 2018-05-01

Configuration page



Implementation

- Based on longTabix track type
 - Extended drawing modes (curves, dashed)
 - New schema to support more display and data mining features, and more standard BED layout. (vs. WashU+Ensembl schema used in longTabix).
 - Additional enhancements: e.g. cross-chrom item layout, endpoint and peak mouseovers
- Implemented for native tracks, custom tracks, and hubs

Schema

% cat interact.as

table interact

"Interaction between two regions"

```
(
  string chrom;      "Chromosome (or contig, scaffold, etc.). For interchromosomal, use 2 records"
  uint chromStart;  "Start position in chromosome of lower region.
                    For interchromosomal, set to chromStart of this region"
  uint chromEnd;    "End position in chromosome of upper region.
                    For interchromosomal, set to chromEnd of this region"
  string name;      "Name of item, for display. Usually 'name1/name2' or empty"
  uint score;       "Score from 0-1000."
  double value;     "Strength of interaction or other data value. Typically basis for score"
  string exp;       "Experiment name (metadata for filtering). Use . if not applicable"
  uint color;       "Item color, as itemRgb in bed9. Typically based on strength or filter"

  string sourceChrom; "Chromosome of source region (directional) or lower region.
                    For non-directional interchromosomal, chrom of this region."
  uint sourceStart;  "Start position in chromosome of source/lower/this region"
  uint sourceEnd;    "End position in chromosome of source/lower/this region"
  string sourceName; "Identifier of source/lower/this region. Can be used as link to related table"
  string sourceStrand; "Orientation of source/lower/this region: + or -. Use . if not applicable"

  string targetChrom; "Chromosome of target region (directional) or upper region.
                    For non-directional interchromosomal, chrom of other region"
  uint targetStart;  "Start position in chromosome of target/upper/this region"
  uint targetEnd;    "End position in chromosome of target/upper/this region"
  string targetName; "Identifier of target/upper/this region. Can be used as link to related table"
  string targetStrand; "Orientation of target/upper/this region: + or -. Use . if not applicable"
)
```

NOTE: BigInteract users are strongly encouraged to rename and describe fields to fit their data

Create your own interact track

Custom Track file with 4 interactions:

```
track type=interact visibility=full
# Interact
# chrom start end name score value exp color Source Target
# chrom start end name strand chrom start end name strand
chr6 99790007 99798261 inter1 233 4.0 brain 255,0,0 chr6 99790007 99793559 rs1 . chr6 99794572 99798261 gene1 +
chr6 99797231 99875440 inter2 175 3.2 blood 0,255,0 chr6 99797231 99801068 rs2 . chr6 99873105 99875440 gene2 +
chr6 99834530 99843149 inter3 175 3.1 liver 0,0,255 chr6 99834530 99837680 rs3 . chr6 99839323 99843149 gene3 -
chr6 99848067 99857519 inter4 175 3.5 kidney 0 chr6 99848067 99852034 rs4 . chr6 99855098 99857519 gene4 +
```

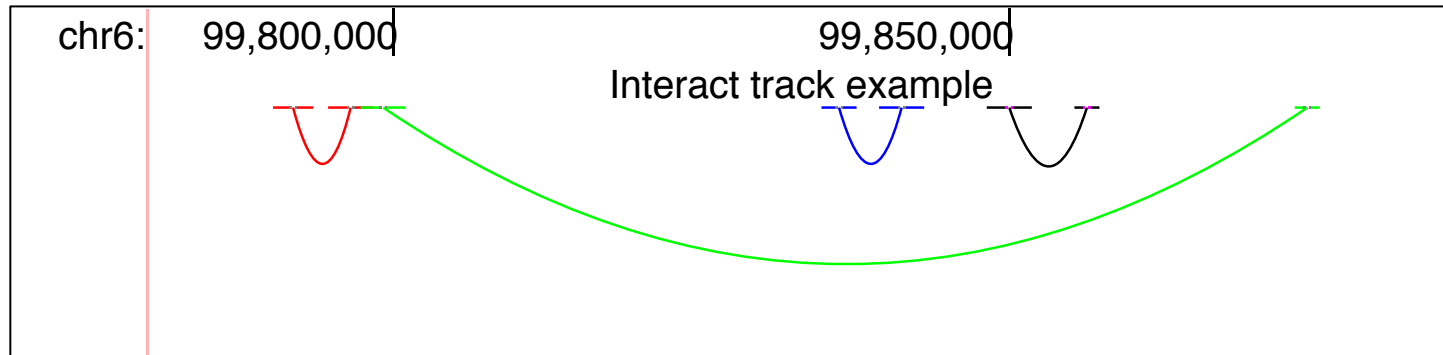
First data row:

```
chr6 # chrom
99790007 # start
99798261 # end
inter1 # name
233 # score
4.0 # value
brain # exp
255,0,0 # color
chr6 # sourceChrom
99790007 # sourceStart
99793559 # sourceEnd
rs1 # sourceName
. # sourceStrand
chr6 # targetChrom
99794572 # targetStart
99798261 # targetEnd
gene1 # targetName
+ # targetStrand
```

Track line:

```
track type=interact visibility=full
description="Interact track example"
```

Browser image:



Format as bigInteract track, for a *track hub*

```
bedToBigBed -tab -type=bed5+13 -as=interact.as
myData.inter.bed chrom.sizes myData.inter.bigBed
```



Track settings

bigInteract - Pairwise interaction display"

`type bigInteract`

`bigDataUrl <url/relativePath>`

`interactDirectional <true/false>`

Additional settings defined in other sections are also available for displaying bigInteract tracks.

[maxHeightPixels](#) [scoreMin](#) [spectrum](#),

Example of an interact/bigInteract track

```
track snpGeneInteractions
type bigInteract
interactDirectional true
maxHeightPixels 300:150:20
bigDataUrl http://...
```

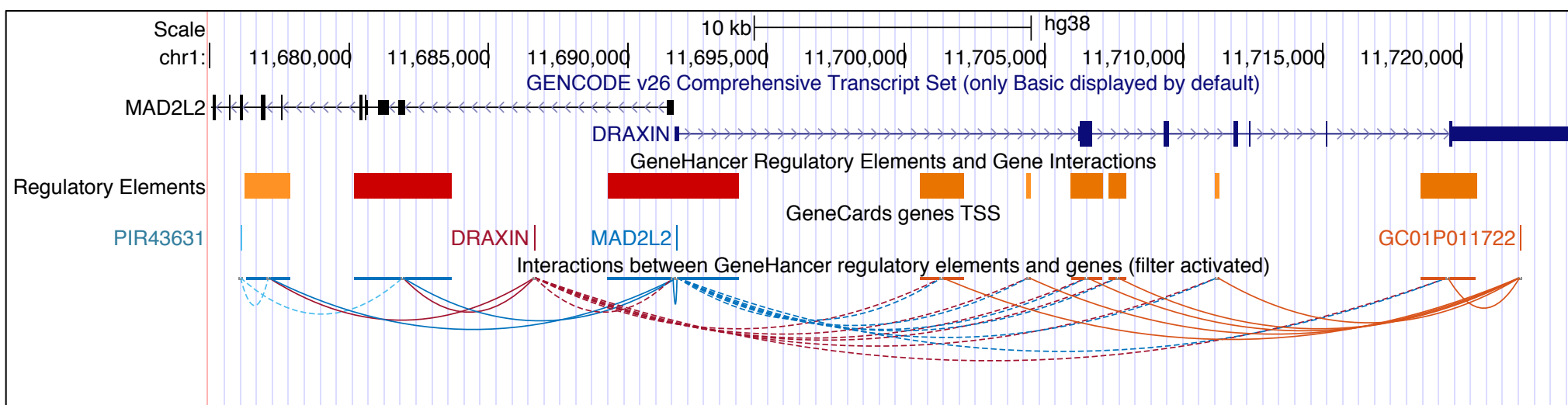
Enhancements in progress

- Display
 - Offset source/target
 - Directionality arrow (when zoomed in on few interactions)
- Configuration
 - Limit to interactions with endpoint(s) in window
 - New bigBed filters

First native interact track (in progress): Genehancer

[GeneHancer: genome-wide integration of enhancers and target genes in GeneCards](#)

Contributors: Simon Fishelivich and Marilyn Safran, Genecards group, Weizmann Institute



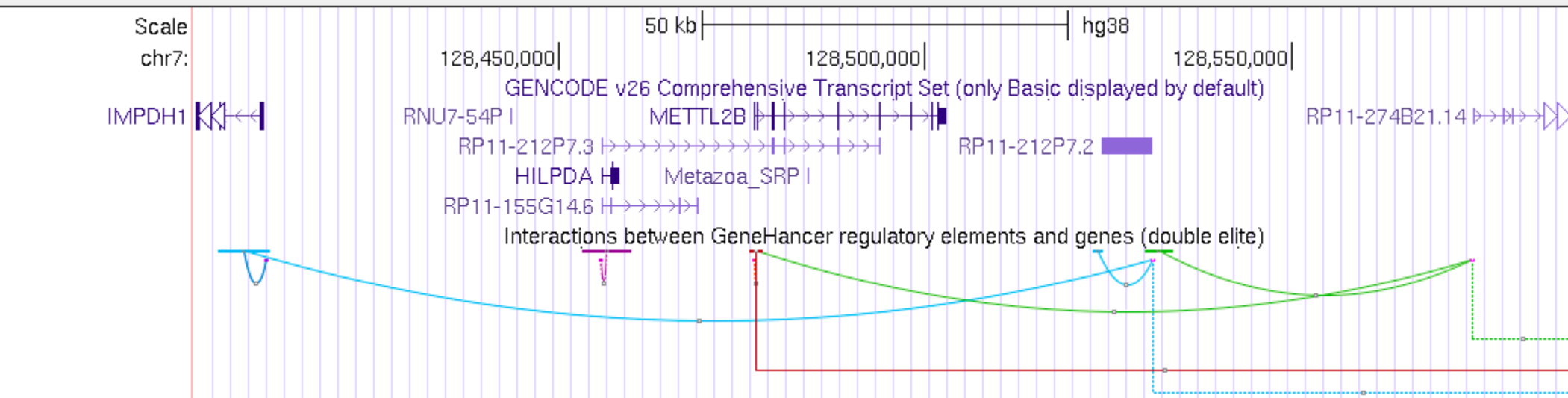
Test hub session:

https://hgwdev-kate.gi.ucsc.edu/cgi-bin/hgTracks?hgS_doOtherUser=submit&hgS_otherUserName=kate&hgS_otherUserSessionName=Genehancer

Test hub trackDb:

<https://hgwdev.gi.ucsc.edu/~kate/hubs/geneHancer/hg38/trackDb.txt>

Interact track: Offset source/target display



Source (enhancers) are shown immediately below track title, and targets (gene TSS) are shown on a horizontal some pixels lower in the image.

Proposed trackDb setting extension:

`interactDirectional offset<on|Source|Target>`

GeneHancer Regulatory Elements and Gene Interactions

Maximum display mode: [Reset to defaults](#)Select view ([help](#)):[GeneHancer](#) Gene TSS [Interaction](#)

Interaction Configuration

Minimum score: Show interactions: all at least one end both ends in windowTrack height: pixels (range: 50 to 200, default: 100)Draw mode: curve ellipse rectangle

Select subtracks by set and view:

	<input type="checkbox"/> + <input type="checkbox"/> - All	Double	
	View	Set	Elite All
			<input type="checkbox"/> + <input type="checkbox"/> - <input type="checkbox"/> + <input type="checkbox"/> -
GeneHancer	<input type="checkbox"/> + <input type="checkbox"/> -	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
Gene TSS	<input type="checkbox"/> + <input type="checkbox"/> -	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
Interaction	<input type="checkbox"/> + <input type="checkbox"/> -	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

List subtracks: only selected/visible all (6 of 6 selected)

		Set ¹	View ²	Track Name ³	
<input checked="" type="checkbox"/>	<input type="text" value="dense"/>	Double Elite	GeneHancer	Enhancers and promoters from GeneHancer (double elite)	schema
<input checked="" type="checkbox"/>	<input type="text" value="pack"/>	Double Elite	Gene TSS	GeneCards genes TSS (double elite)	schema
<input checked="" type="checkbox"/>	<input type="text" value="full"/>	Double Elite	Interaction	Interactions between GeneHancer regulatory elements and genes (double elite)	schema
<input checked="" type="checkbox"/>	<input type="text" value="dense"/>	All	GeneHancer	Enhancers and promoters from GeneHancer	schema
<input checked="" type="checkbox"/>	<input type="text" value="pack"/>	All	Gene TSS	GeneCards genes TSS	schema
<input checked="" type="checkbox"/>	<input type="text" value="full"/>	All	Interaction	Interactions between GeneHancer regulatory elements and genes	schema

6 of 6 selected

Documentation

<http://genome.ucsc.edu/goldenPath/help/interact.html>



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interact and bigInteract Track Format

The interact (and bigInteract) track format displays pairwise interactions as arcs or half-rectangles connecting two genomic regions on the same chromosome. Cross-chromosomal interactions can also be represented in this format; the display shows the region on the currently viewed chromosome, with a vertical bar, labeled with the chromosome of the connected region (space permitting). For directional interactions such as SNP/gene, the interactions in the reverse direction are displayed as a dashed line or curve.

This format is useful for displaying functional element interactions such as SNP/gene interactions, and is also suitable for low-density chromatin interactions, such as ChIA-PET, and other use cases with a limited number of interactions on the genome. It is not suitable for high-density chromatin data such as Hi-C.

The interact format is available as a standalone plain text `bed5+13` format for use with smaller datasets as a custom track, and as a binary indexed format (bigInteract) suitable for track hubs and custom tracks. The bigInteract format provides more track customization features (i.e. schema customization), and is recommended for users who can use command-line tools and have web-accessible data storage. If you do not have web-accessible data storage, please see the [Hosting](#) section of the Track Hub Help documentation. Interact format files are converted to bigInteract files using the program `bedToBigBed`, run with the `-as` option to pull in a special [autoSql](#) (.as) schema file defining the fields of the bigInteract.

Interact format definition

The following autoSql definition illustrates the basic schema supporting interact (and bigInteract) tracks.

```
table interact
"interaction between two regions"
(
  string chrom;           "Chromosome (or contig, scaffold, etc.). For interchromosomal, use 2 records"
  uint chromStart;       "Start position of lower region. For interchromosomal, set to chromStart of this region"
  uint chromEnd;        "End position of upper region. For interchromosomal, set to chromEnd of this region"
  string name;          "Name of item, for display. Usually 'sourceName/targetName/exp' or empty"
  uint score;           "Score (0-1000)"
  double value;         "Strength of interaction or other data value. Typically basis for score"
  string exp;           "Experiment name (metadata for filtering). Use . if not applicable"
  string color;         "Item color. Specified as r,g,b or hexadecimal #RRGGBB or html color name, as in //www.w
  string sourceChrom;    "Chromosome of source region (directional) or lower region. For non-directional interchromo
  uint sourceStart;     "Start position in chromosome of source/lower/this region"
  uint sourceEnd;       "End position in chromosome of source/lower/this region"
  string sourceName;    "Identifier of source/lower/this region"
  string sourceStrand;  "Orientation of source/lower/this region: + or -. Use . if not applicable"
  string targetChrom;   "Chromosome of target region (directional) or upper region. For non-directional interchromo
  uint targetStart;     "Start position in chromosome of target/upper/this region"
  uint targetEnd;       "End position in chromosome of target/upper/this region"
  string targetName;    "Identifier of target/upper/this region"
  string targetStrand;  "Orientation of target/upper/this region: + or -. Use . if not applicable"
)
```