

UCSC Genome Browser Track Decorators

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Overview

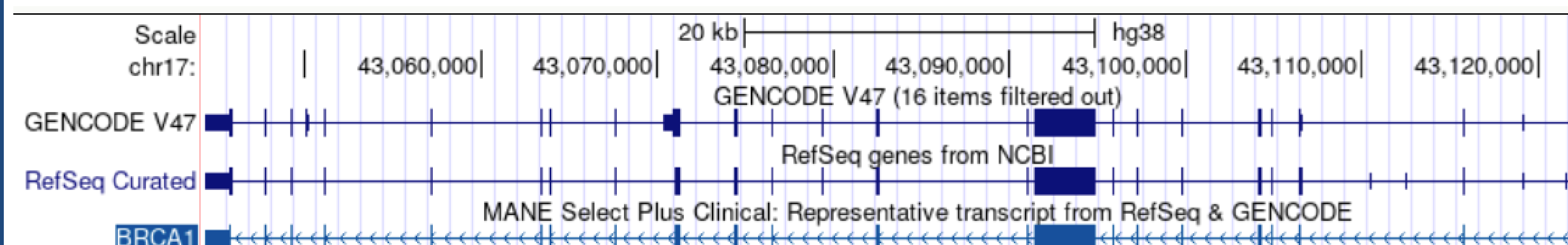
The UCSC Genome Browser is a popular web-based tool used to view and analyze genomic data from over 5,000 different organisms. In the browser, genome annotations—called "features"—are usually shown as colored rectangles (representing "exons") connected by thin lines (representing "introns").

Many types of annotations have a second layer of information: transcripts contain protein domains, transposons include other repeats, and Chip-Seq peaks have summits. Previously, this meant users had to create another annotation track to show features on the annotations.

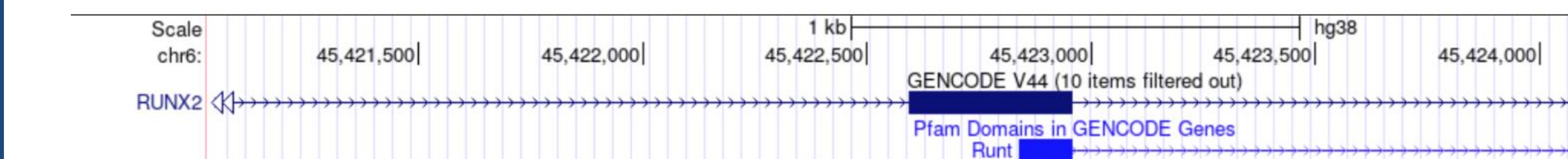
To solve this, we introduced track decorators. They add extra visual information directly onto features using colored shapes and symbols. Track decorators offer two display styles: blocks, for highlighting ranges with bars, and glyphs, for drawing symbols on single-nucleotide positions.

Annotating the genome

The genome browser's primary way to annotate the genome is colored rectangles ("exons" for gene tracks) linked by thin lines ("introns"). We usually call these annotations "features".

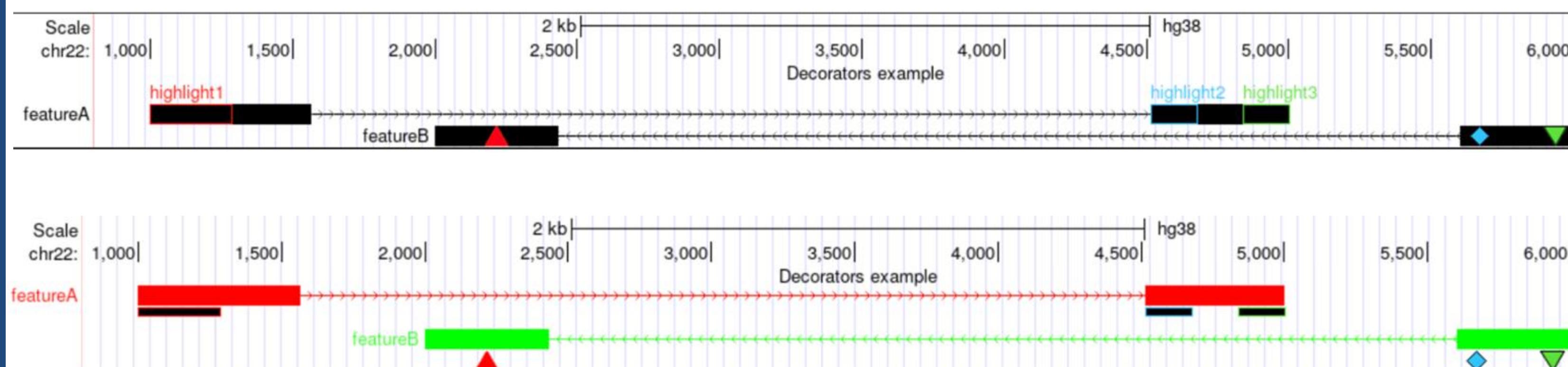


Each rectangle of a feature has the same color and individual parts cannot be highlighted. If you wanted to highlight parts of the features, traditionally this required a second track.



What are track decorators

Track decorators allow highlighting parts of features with colors and/or symbols (glyphs/shapes) within a single track. Decorators can be added to **BED 12+**, **bigBed**, **PSL**, and **bigGenePred** tracks. The decorations can either be overlaid onto the feature or shown directly underneath.



Block: Colors exons/introns. Supports labels. Overlay or place decorations adjacent to the original feature.

Glyph: Different types of symbols. Customizable color and transparency. Valid glyph entries include: "Circle", "Square", "Diamond", "Triangle", "InvTriangle", "Octagon", "Star", and "Pentagram".

How to build track decorators

The decorators are stored in a separate bigBed file that includes extra fields to identify the decorated items.

```
BED 12 {
  string chrom;           "Chromosome (or contig, scaffold, etc.)"
  uint  chromStart;       "Start position in chromosome"
  uint  chromEnd;         "End position in chromosome"
  string name;            "Name of item"
  uint  score;            "Score from 0-1000"
  char[1] strand;        "+ or -"
  uint  thickStart;       "Start of where display should be thick (start codon)"
  uint  thickEnd;         "End of where display should be thick (stop codon)"
  uint  color;            "Primary RGB color for the decoration"
  int  blockCount;        "Number of blocks"
  int[blockCount] blockSizes; "Comma separated list of block sizes"
  int[blockCount] chromStarts; "Start positions relative to chromStart"
  string decoratedItem;    "Identity of the decorated item in chr:start-end:item_name format"
  string style;            "Draw style for the decoration (e.g. block, glyph)"
  string fillColor;        "Secondary color to use for filling decoration, blocks, supports RGBA"
  string glyph;           "The glyph to draw in glyph mode; ignored for other styles"
}
```

The **decoratedItem** field (chr:start-end:item_name format) links a decoration to a track item.

Consider the item in the BED entry as a "feature":

```
chr1 1000 2000 feature 0 + 1000 2000 0 2 400,400 0,600
```

Block decoration: To highlight chr1:1200–1800 in red on the item "feature":

```
chr1 1200 1800 highlight 0 + 1200 1800 255,0,0,255 1 600 0 chr1:1000-2000:feature block 255,0,0,128 Ignored
```

highlight: name of the decorator item
255,0,0,255: red outline (RGB + alpha)
chr1:1000-2000:feature: links to the item named "feature" in the BED entry
block: decoration style
255,0,0,128: red fill with transparency
Ignored: not used in block decorations

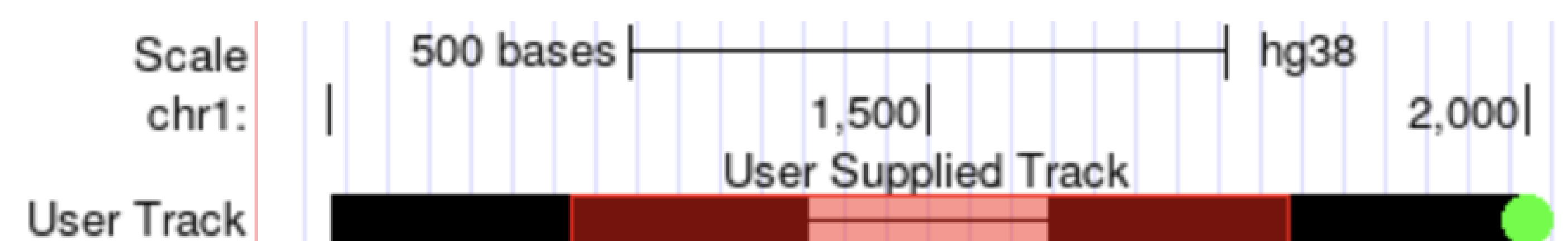
Glyph decoration: To mark the last base with a green circle:

```
chr1 1999 2000 green_circle 0 + 1999 2000 0,255,0,255 1 1 0 chr1:1000-2000:feature glyph 0,255,0,255 Circle
```

green_circle: name of the glyph
0,255,0,255 (9th field): green outline (RGB + alpha)
chr1:1000-2000:feature: links to the item named "feature" in the BED entry
glyph: decoration style
0,255,0,255 (13th field): green fill (RGB + alpha)
Circle: glyph type

Use bedToBigBed to convert the BED entry to bigBed format, then use the bigBed track decorator in the following:

Custom Track	Hub trackDb Settings
track type=bigBed name="Decorators Example"	track testTrack
description="bigBed with decorators" visibility=pack	type bigBed 12
bigDataUrl=https://.../mainEx.bb	bigDataUrl https://.../mainEx.bb
decorator.default.bigDataUrl=https://.../decoratorsEx.bb	decorator.default.bigDataUrl https://.../decoratorsEx.bb



More information



Here is the Track Decorators help page:

<https://genome.ucsc.edu/goldenPath/help/decorator.html>

Here is a session that shows a track decorator set consisting of UniProt annotations on individual GENCODE V45 protein-coding transcripts:

https://genome.ucsc.edu/s/QAtester/GENCODE_V45_UniProt



Contact us for more information, questions, or comments:

<https://genome.ucsc.edu/contacts.html>