A Grammar of Graphics for Genomics

The *ggbio* Package

Michael Lawrence

Genentech

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Outline

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Data on the Genome

- Comes in two flavors:
  - Annotations (genes, TF binding sites, ...)
  - Experimental measurements (sequence reads)
- Both types are tied to genomic coordinates, providing a common axis that permits cross-dataset comparison and inference
- Typically stored as a table, with the range as a fundamental variable type, plus metadata

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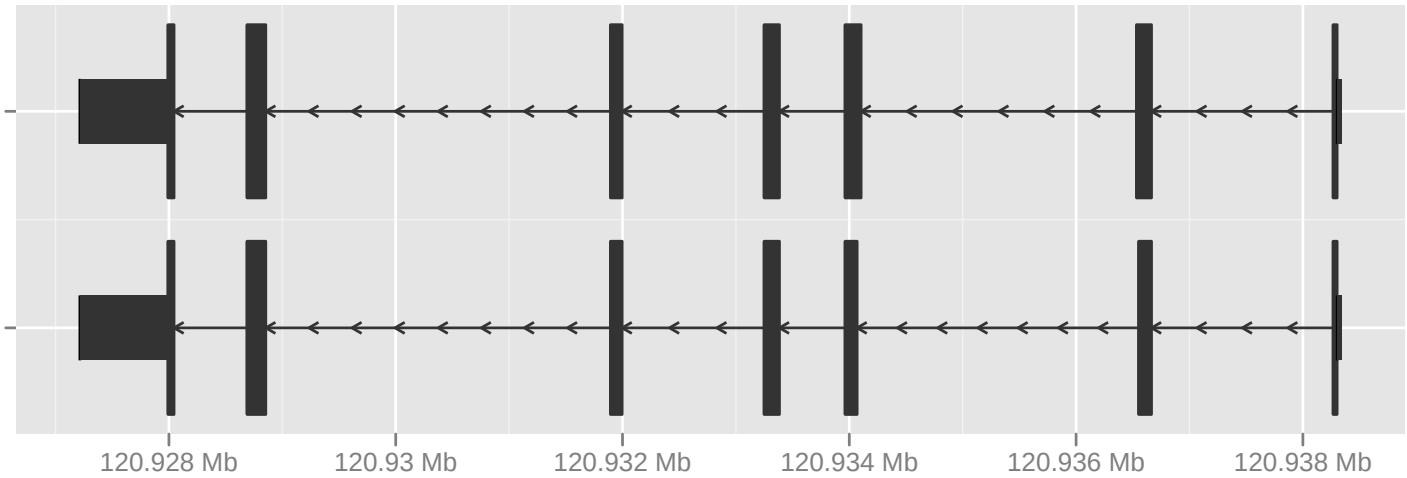

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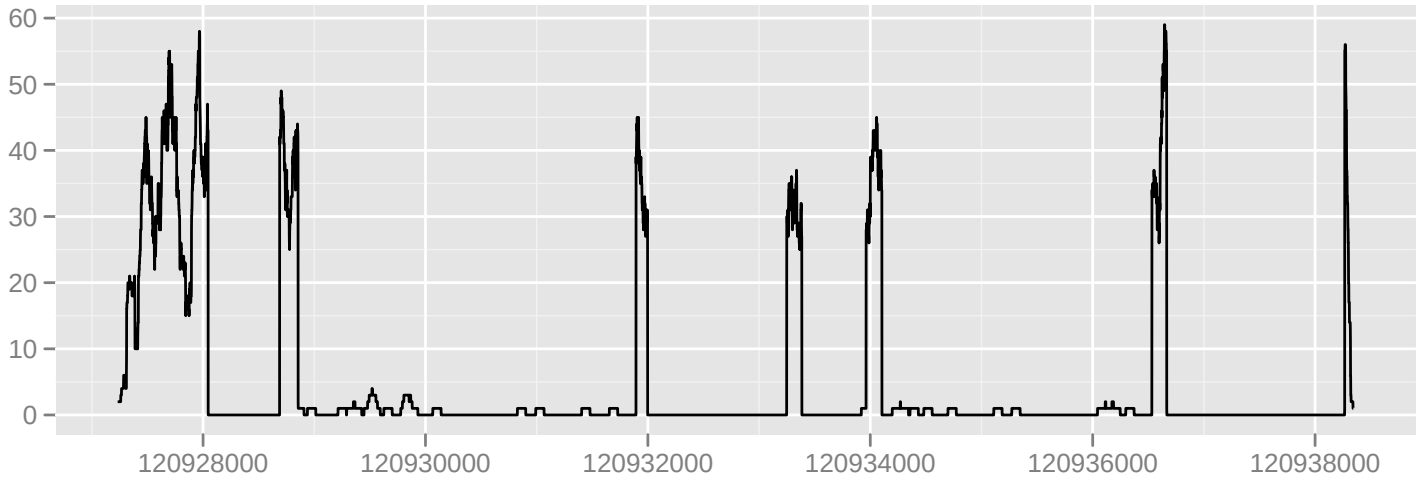

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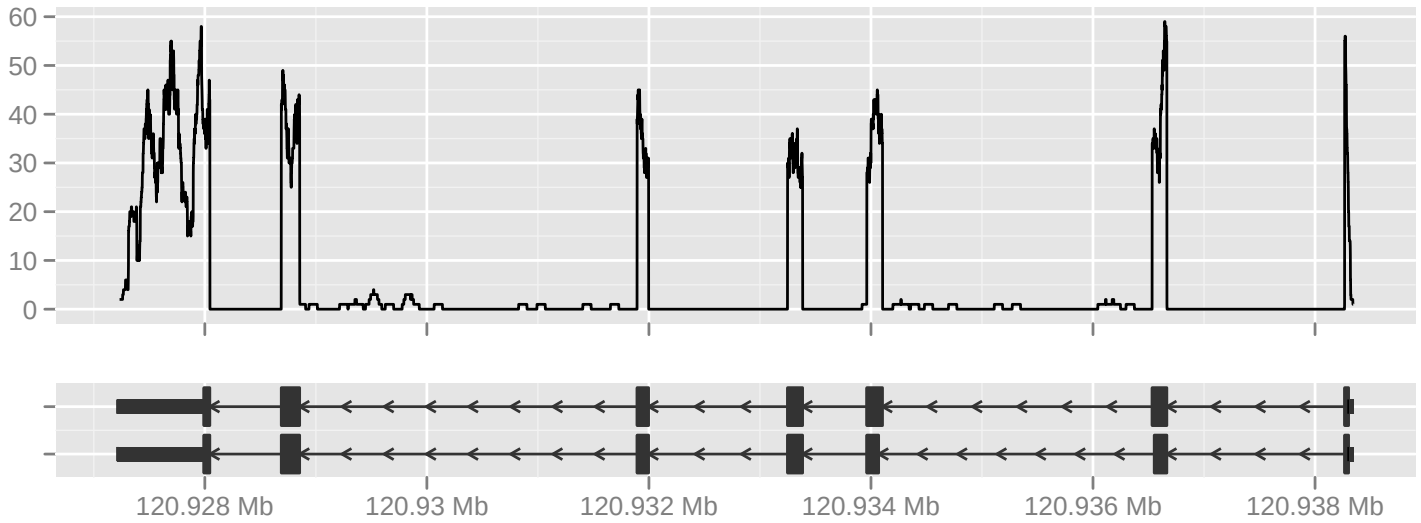

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seqnames	start	end	strand	exon_id	tx_id
10	120927215	120928045	-	129230	14886,14887
10	120928689	120928854	-	129229	14886,14887
10	120931894	120931997	-	129228	14886,14887
10	120933249	120933384	-	129227	14886,14887
10	120933963	120934069	-	129226	14886
10	120933963	120934104	-	119757	14887
10	120936533	120936665	-	119756	14887
10	120936552	120936665	-	129225	14886
10	120938267	120938345	-	129224	14886,14887

Challenges

Big data, wide spaces

- Need summaries that are efficiently computed, communicate more with less and expose the most interesting aspects of the data
- Need different ways of viewing the data, depending on the density and scale, from whole genome to single basepair

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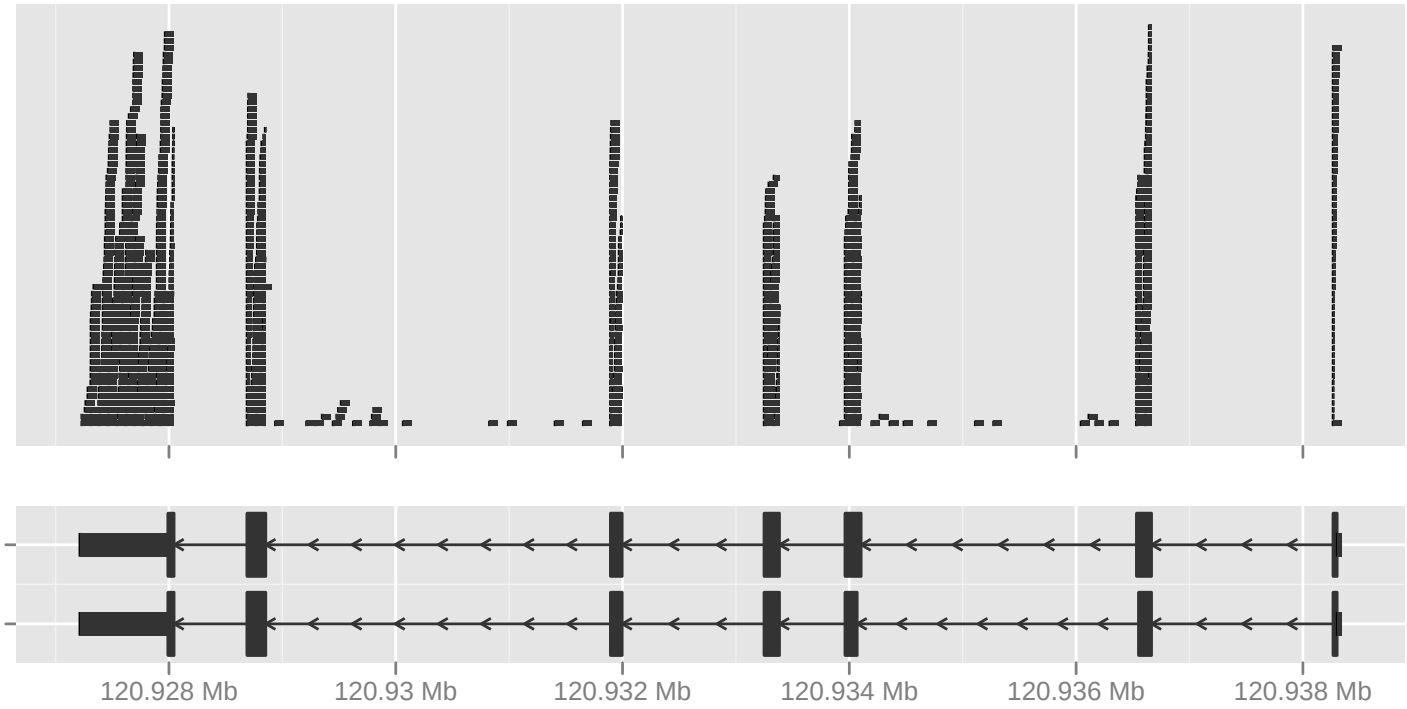

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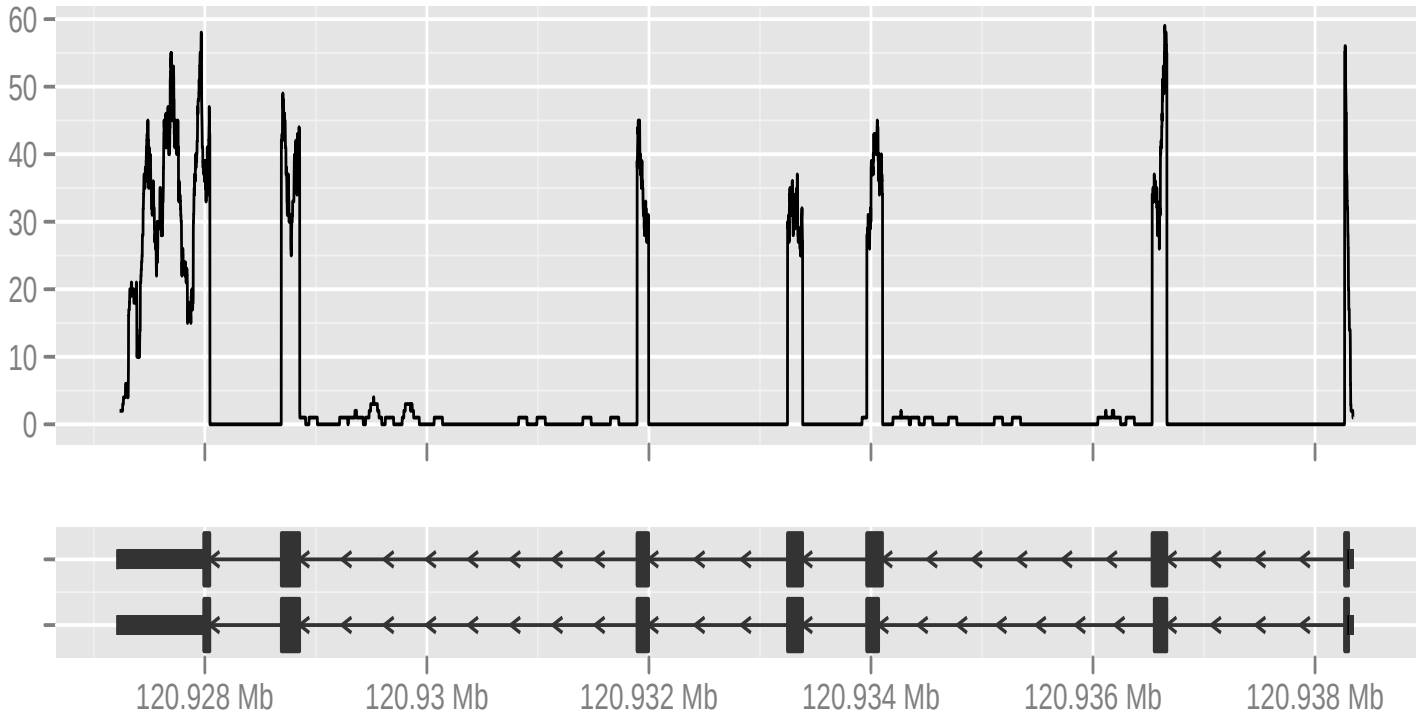

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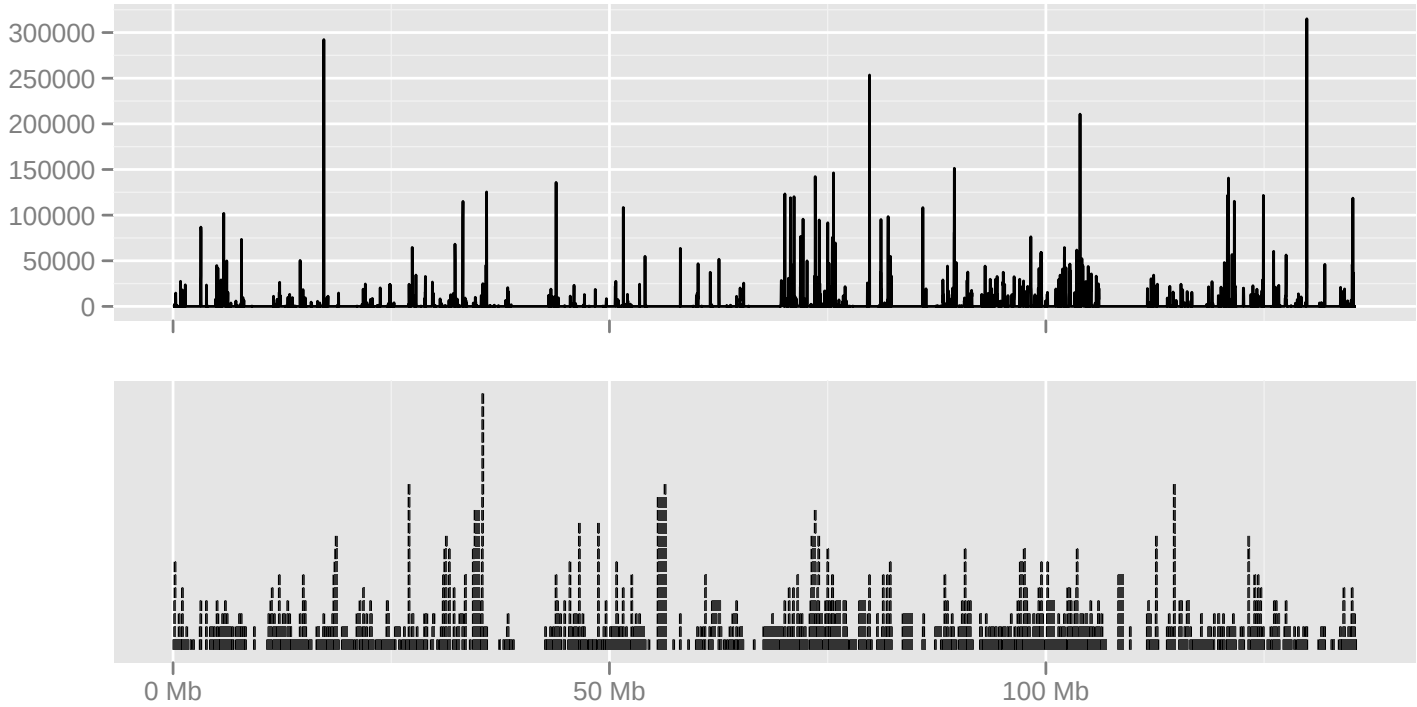

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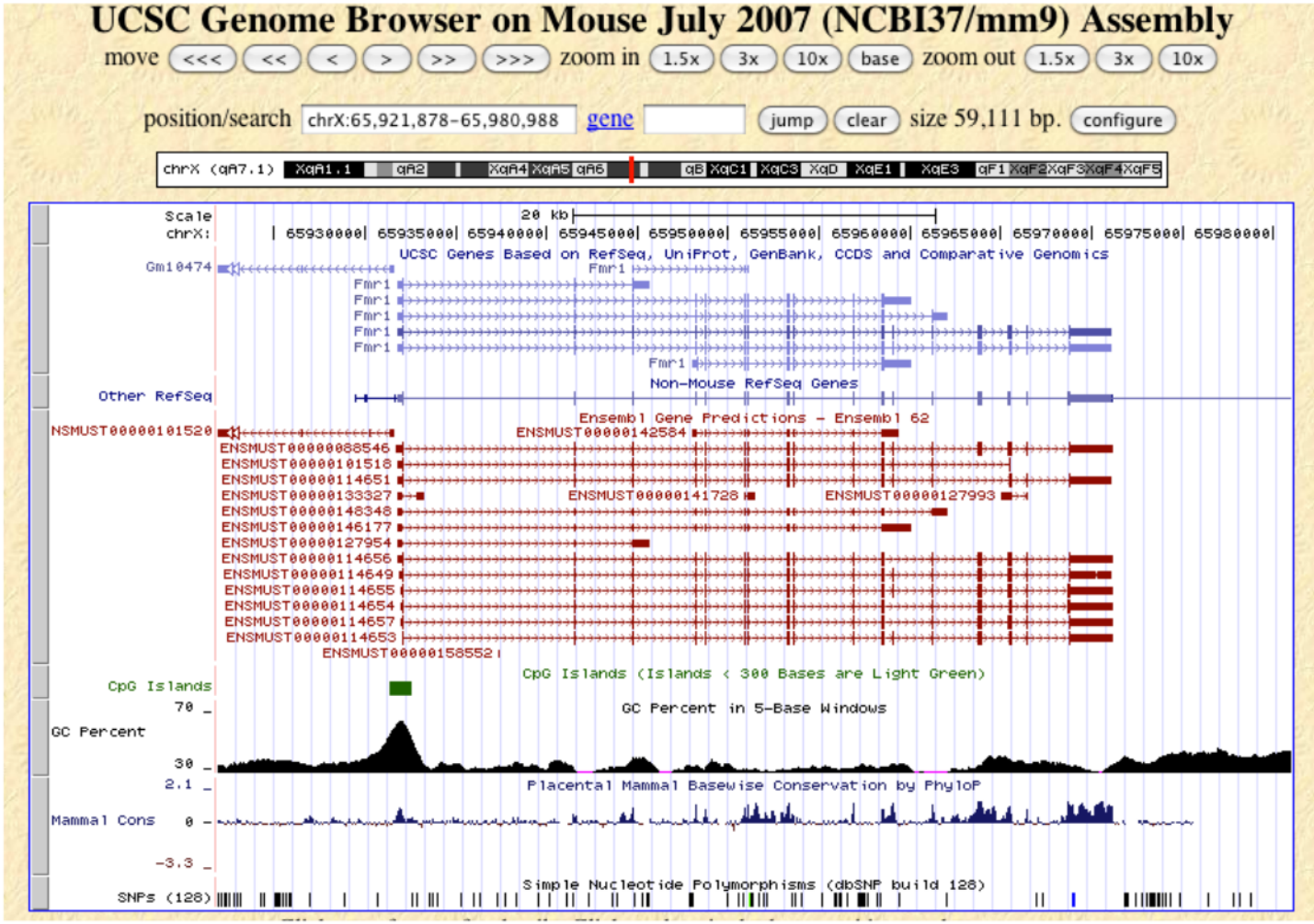

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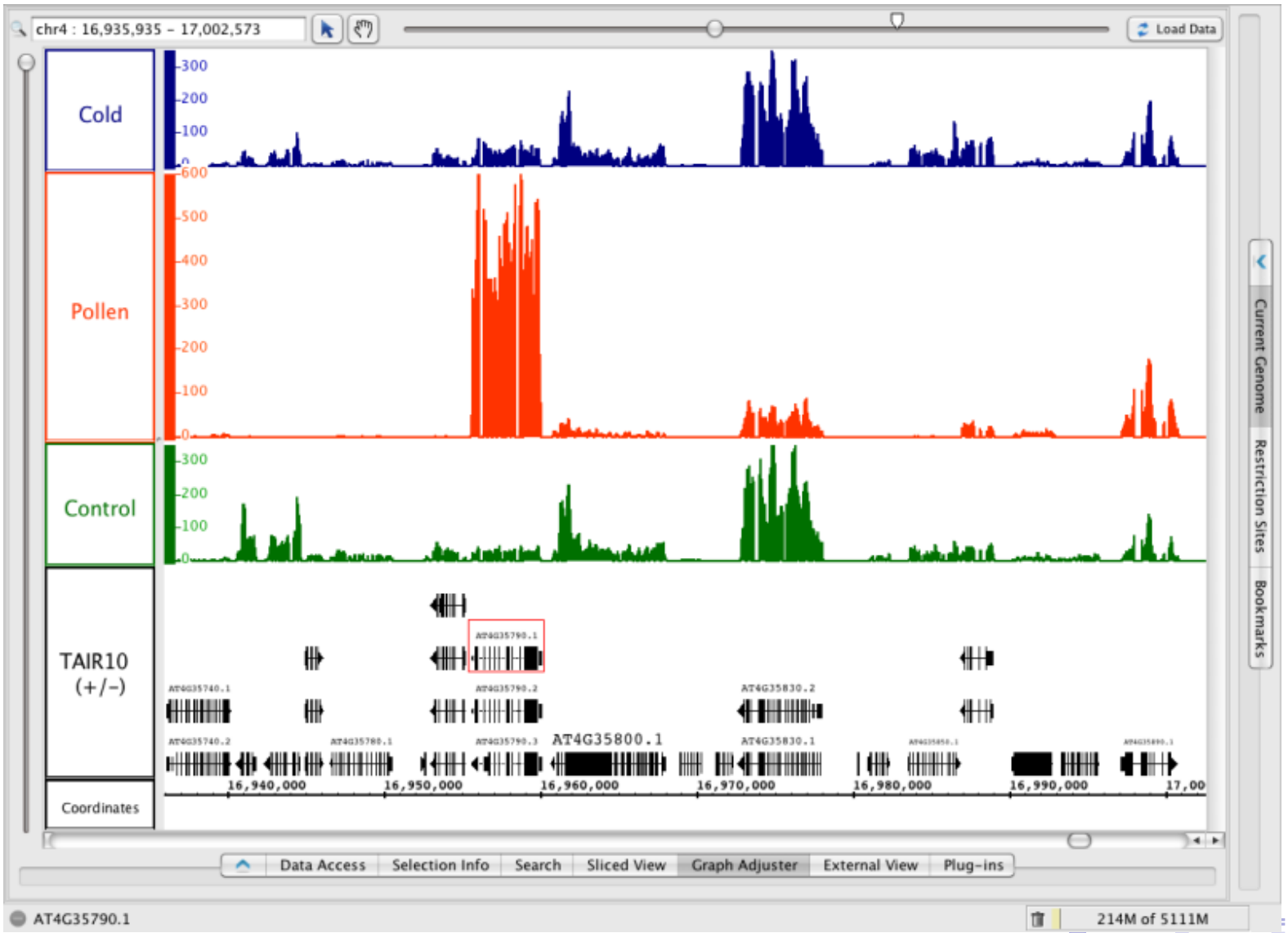

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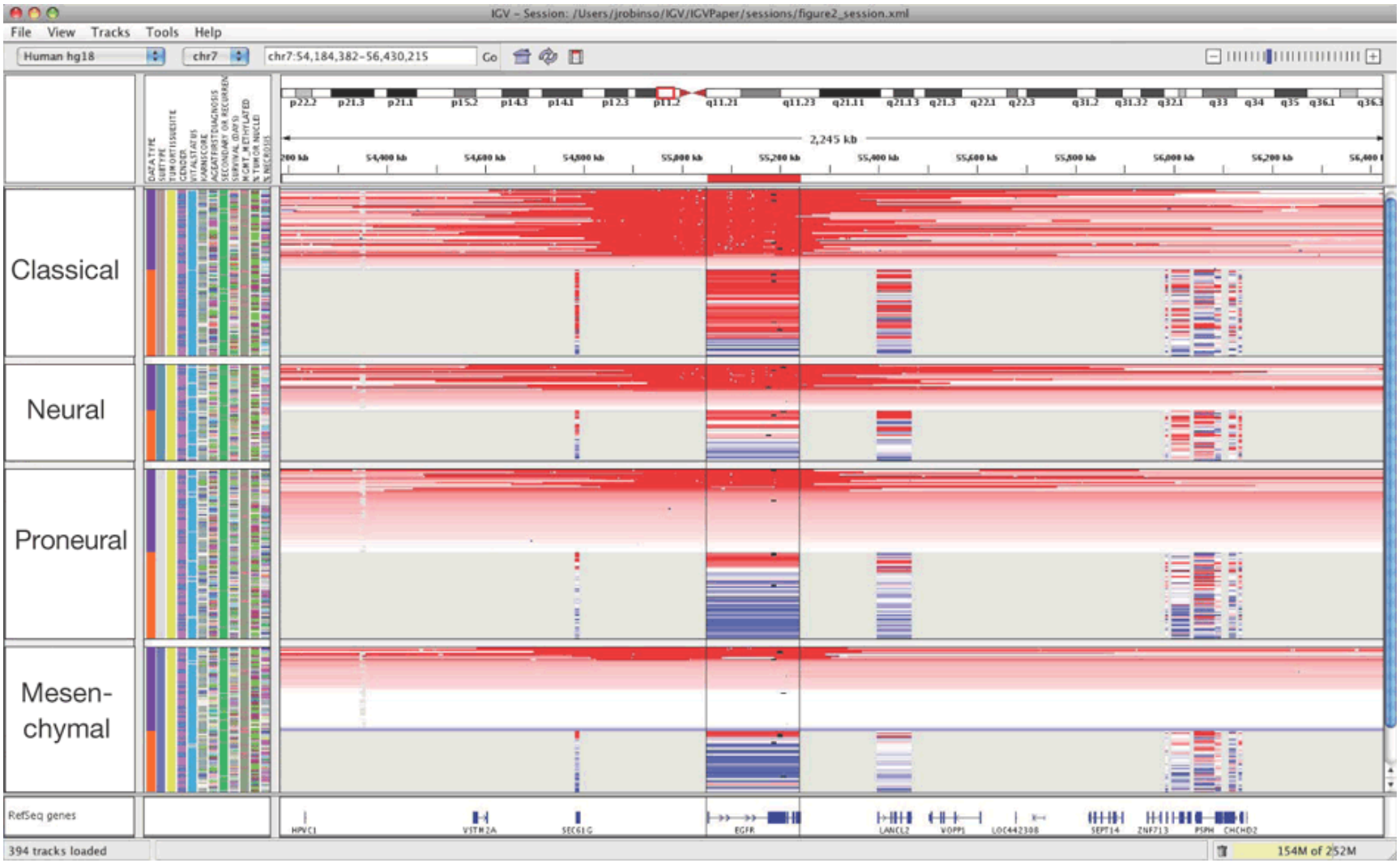

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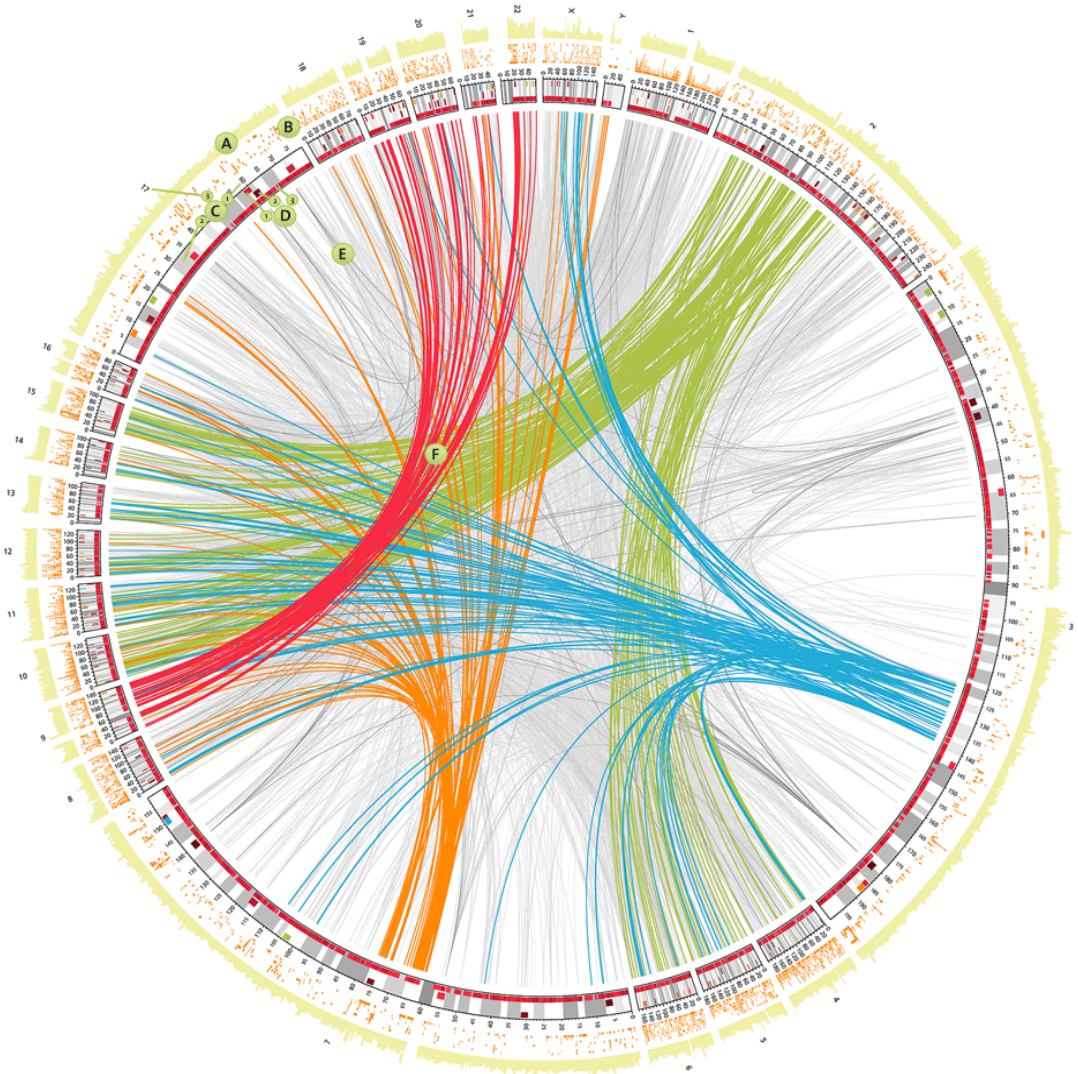

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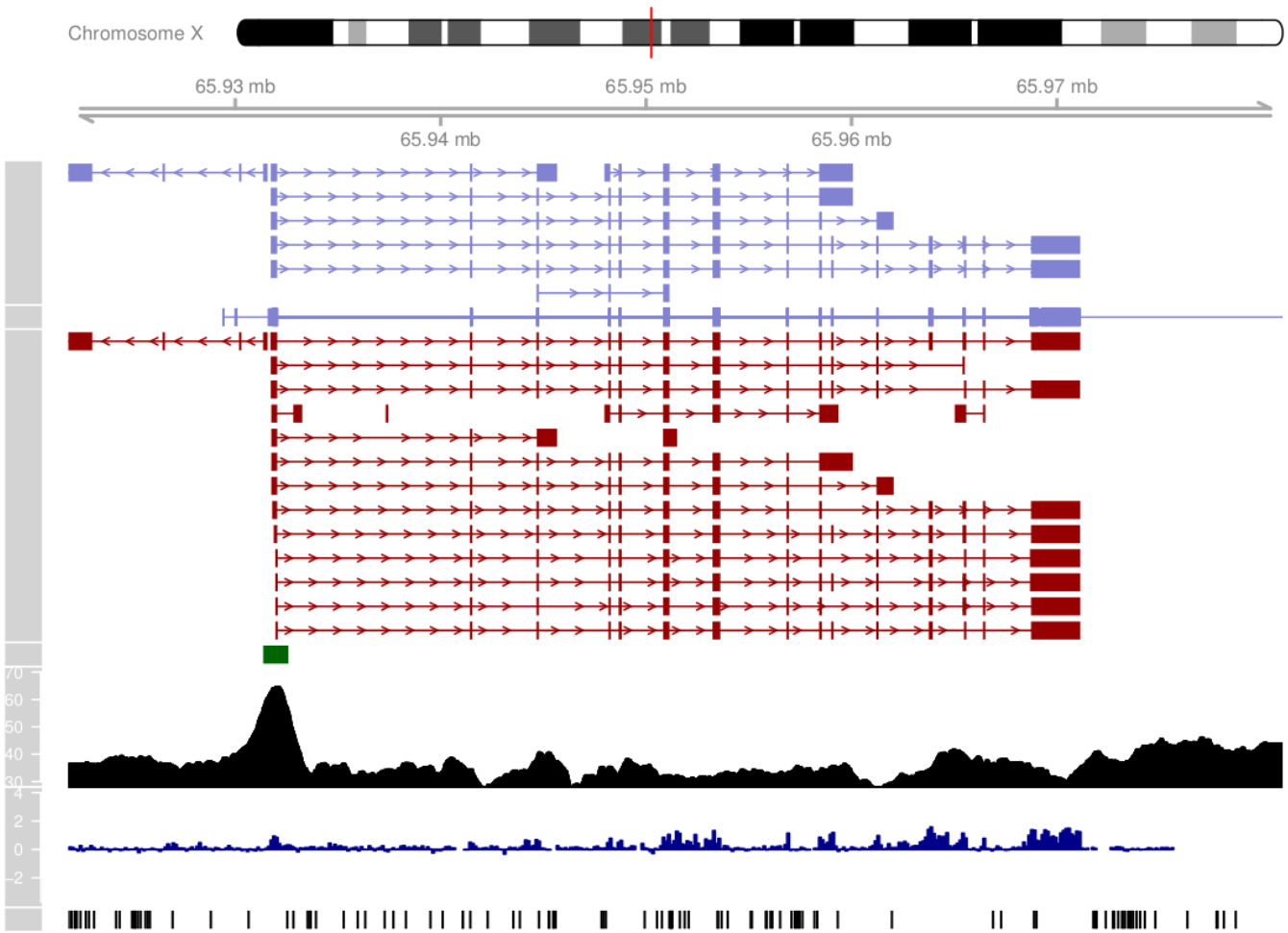

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Limitations

- Limited to one type of view (linear or circular)
- Not tightly integrated with an analysis environment through standard, abstract data structures (except GViz)
- No low-level toolkit for prototyping new types of graphics

Grammars of Graphics

- A grammar of graphics is a language for expressing plots
- Graphics are constructed through the combination of various types of primitives; like legos for graphics
- The most prominent grammar was introduced by Wilkinson's book *The Grammar of Graphics*
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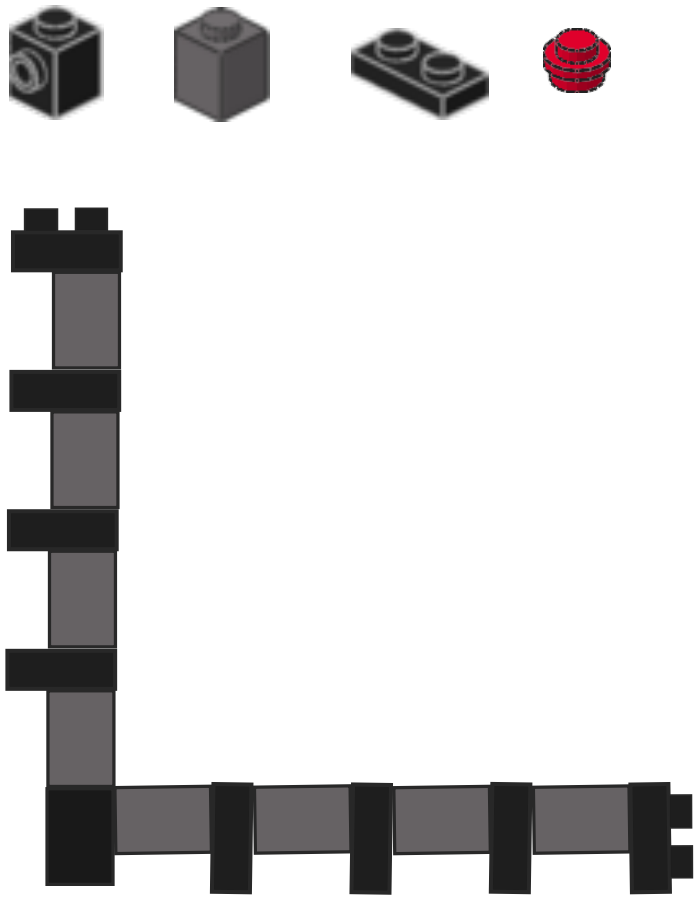

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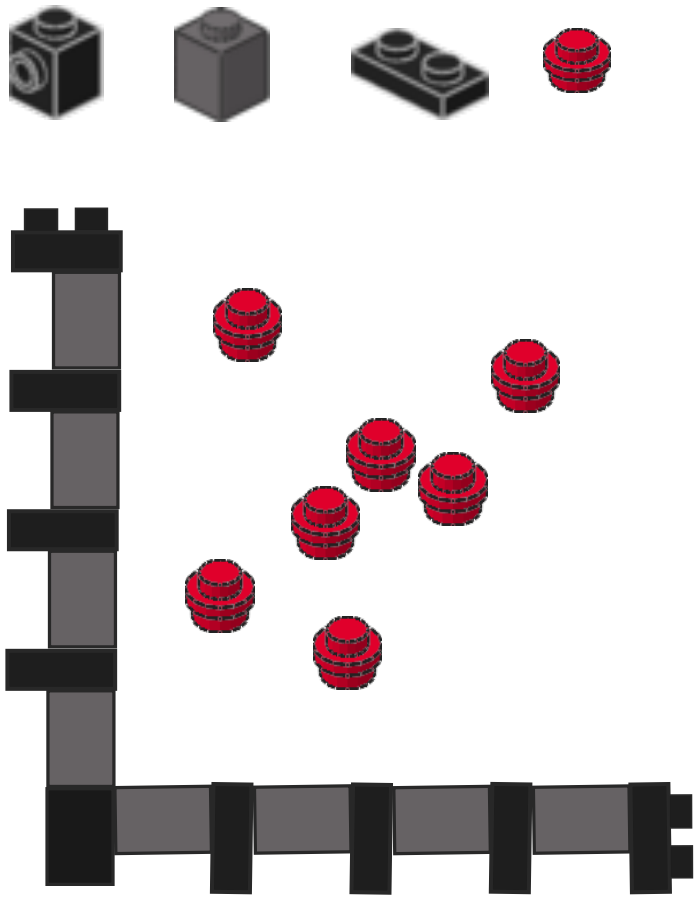

The *ggbio* Package

- An R/Bioconductor package that extends the Wilkinson/Wickham grammar for applications in genomics
- Integrated with Bioconductor
  - Operates on standard, abstract genomic data structures
  - Leverages efficient range-based algorithms
- Programming interface has two levels of abstraction:

  `autoplot` Maps Bioconductor data structures to plots

  `grammar` Mix and match to create custom plots

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Basic Plots

Gene Structures | Read Alignments | Sequence | Multiple

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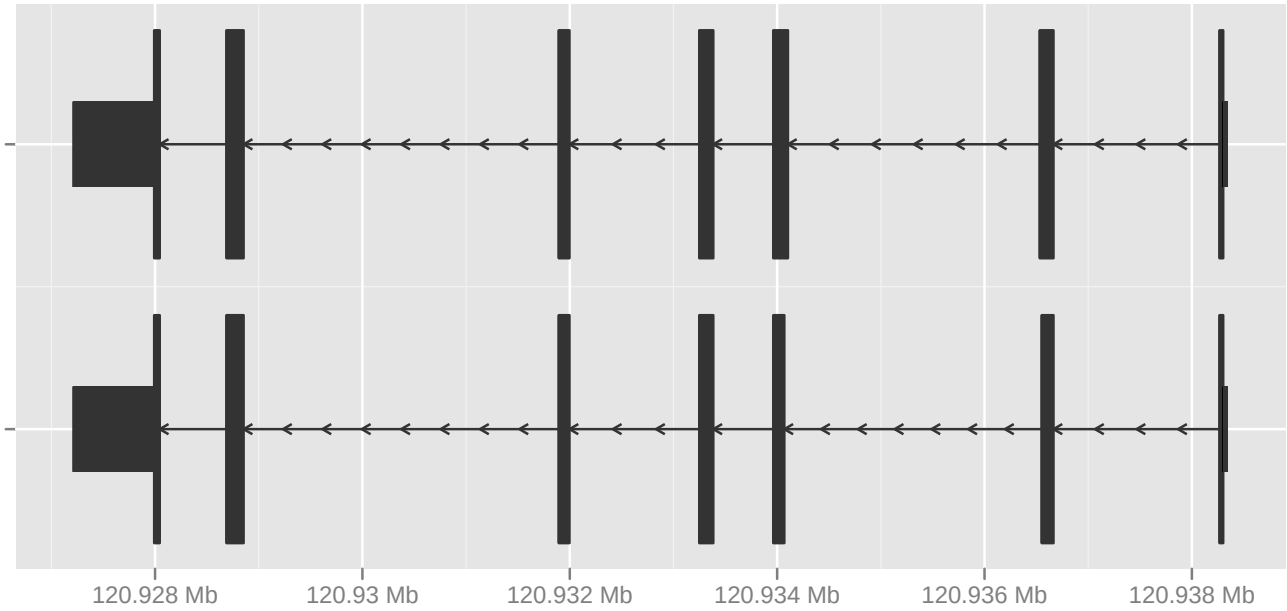

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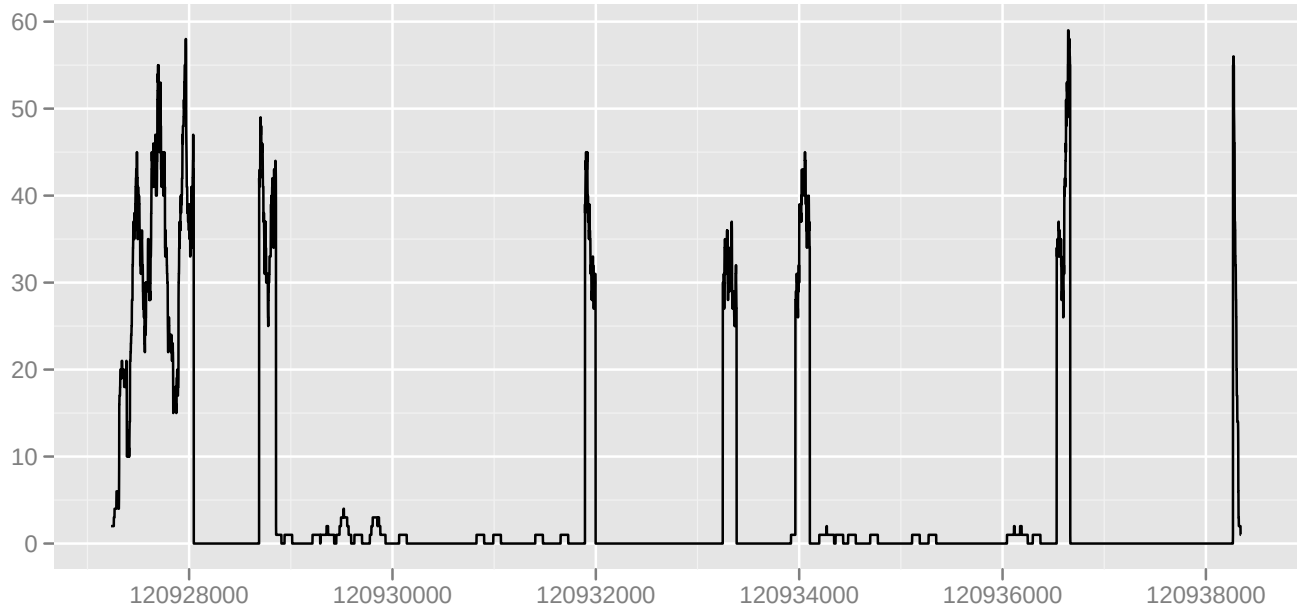

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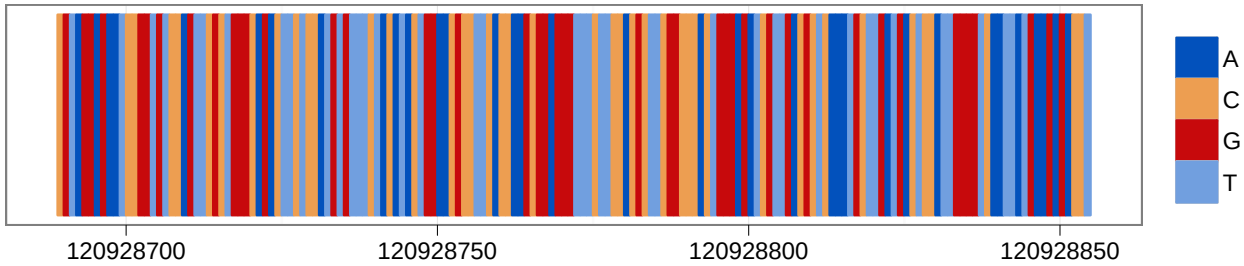

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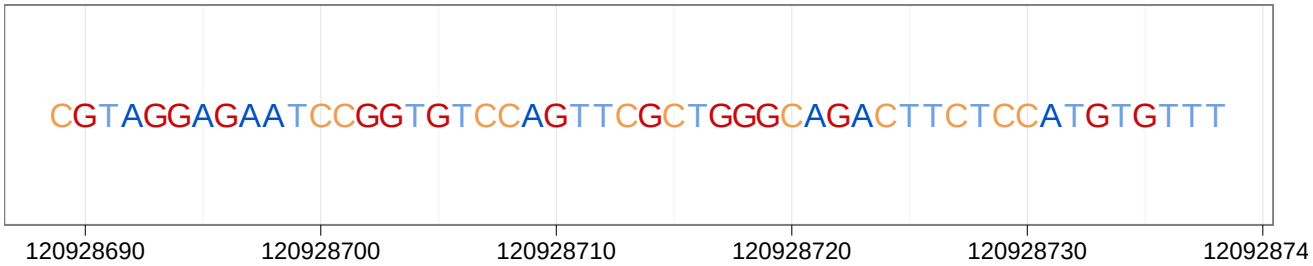

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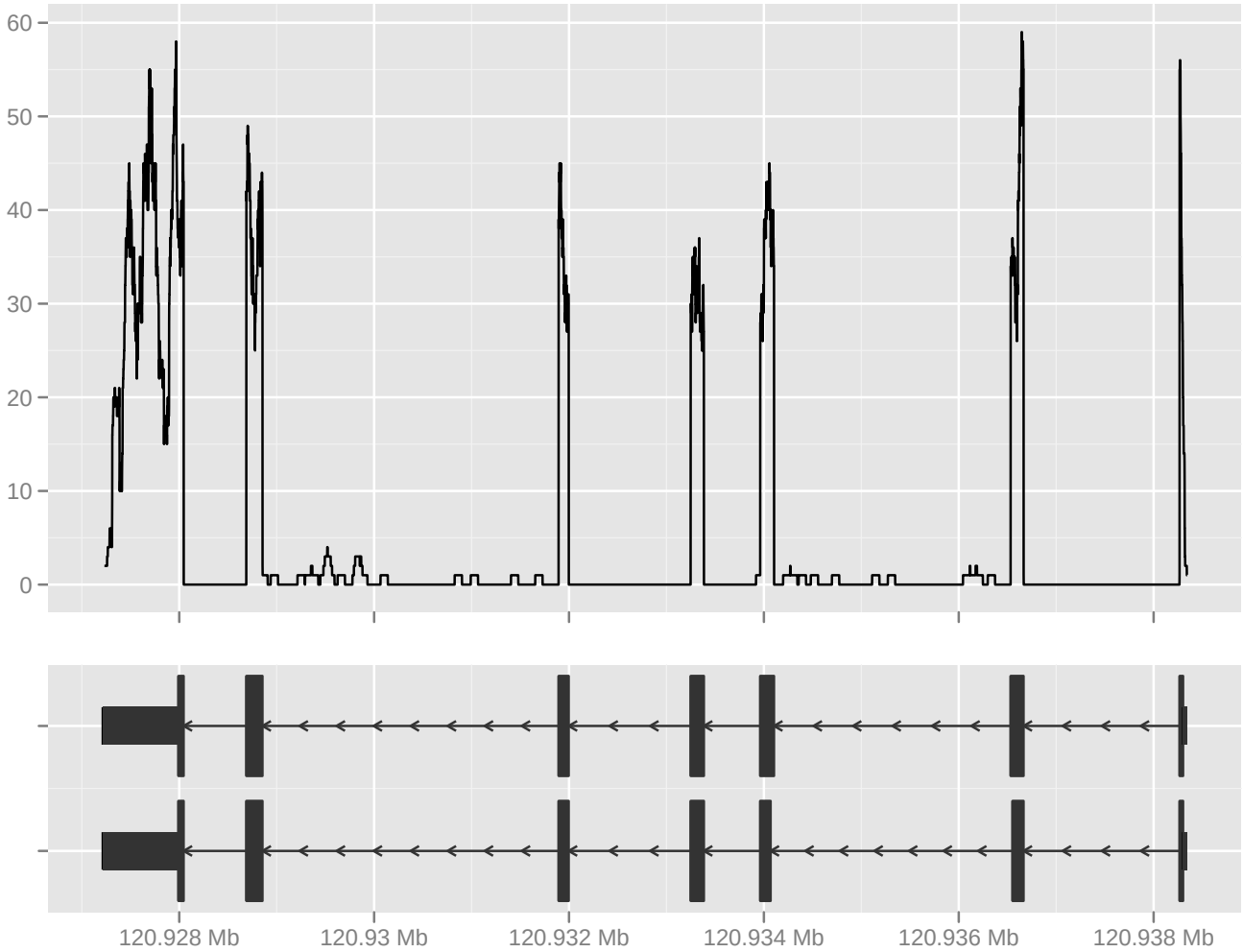

Overview Plots

Grand Linear | Karyogram | Circular

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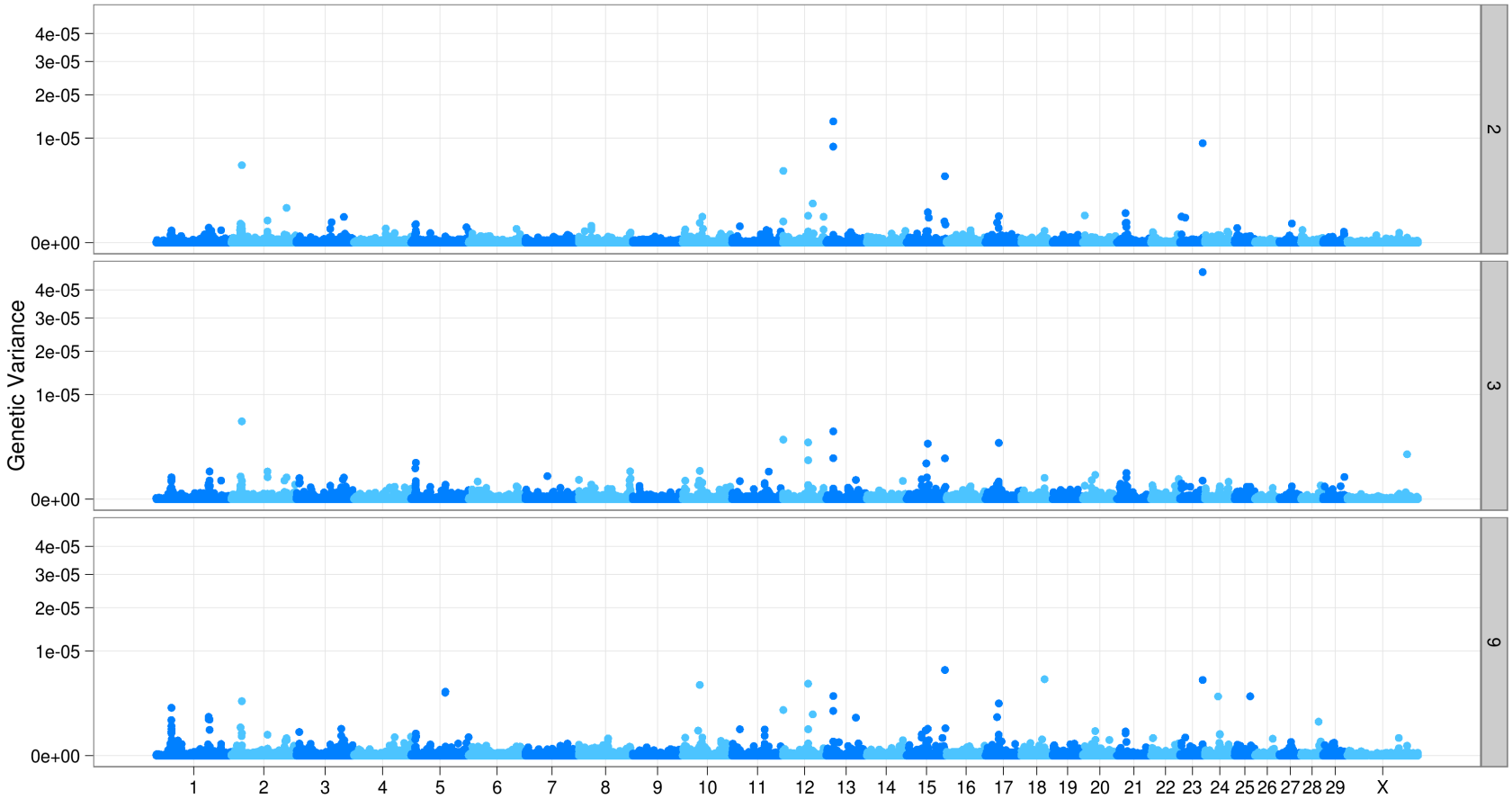

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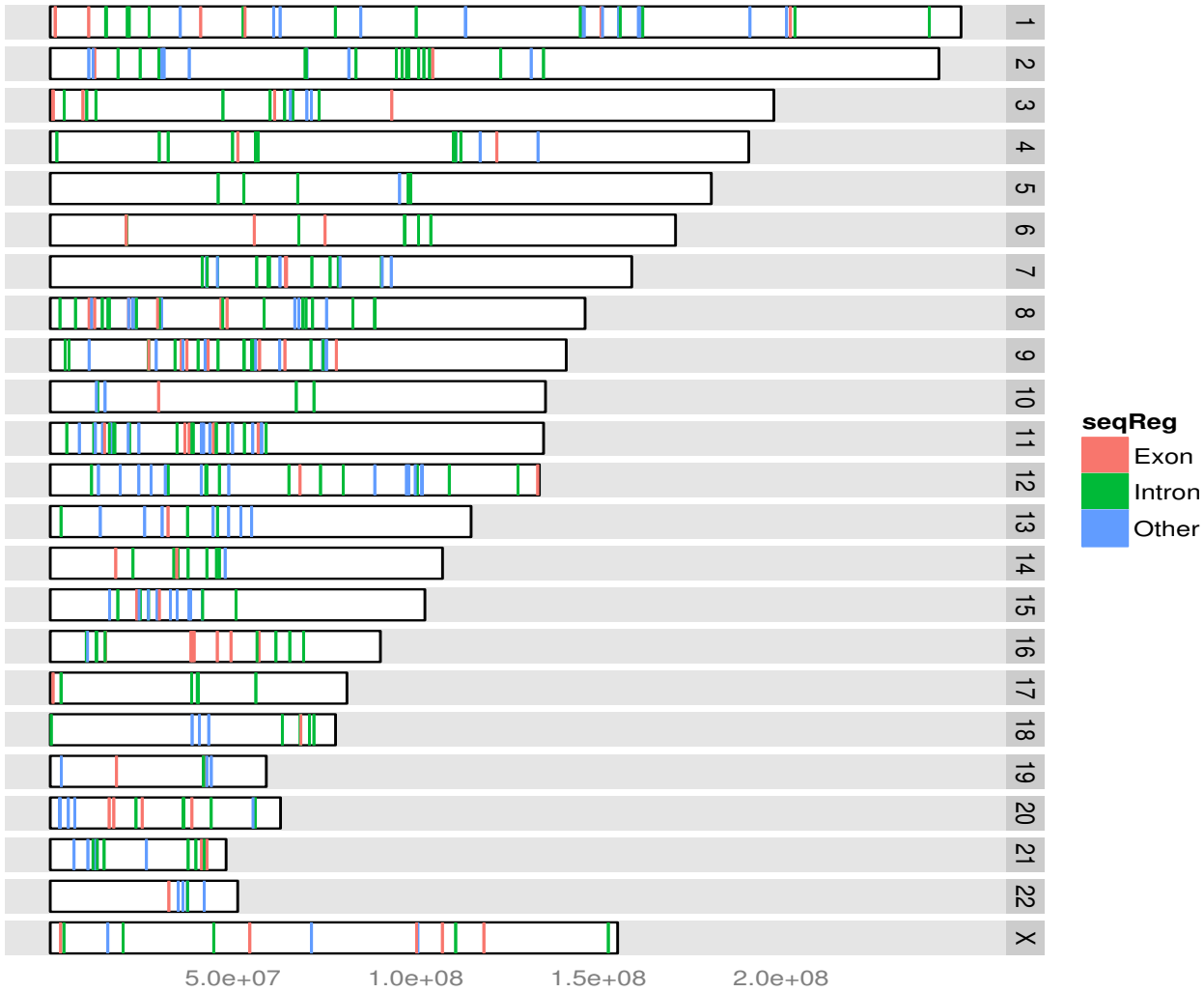

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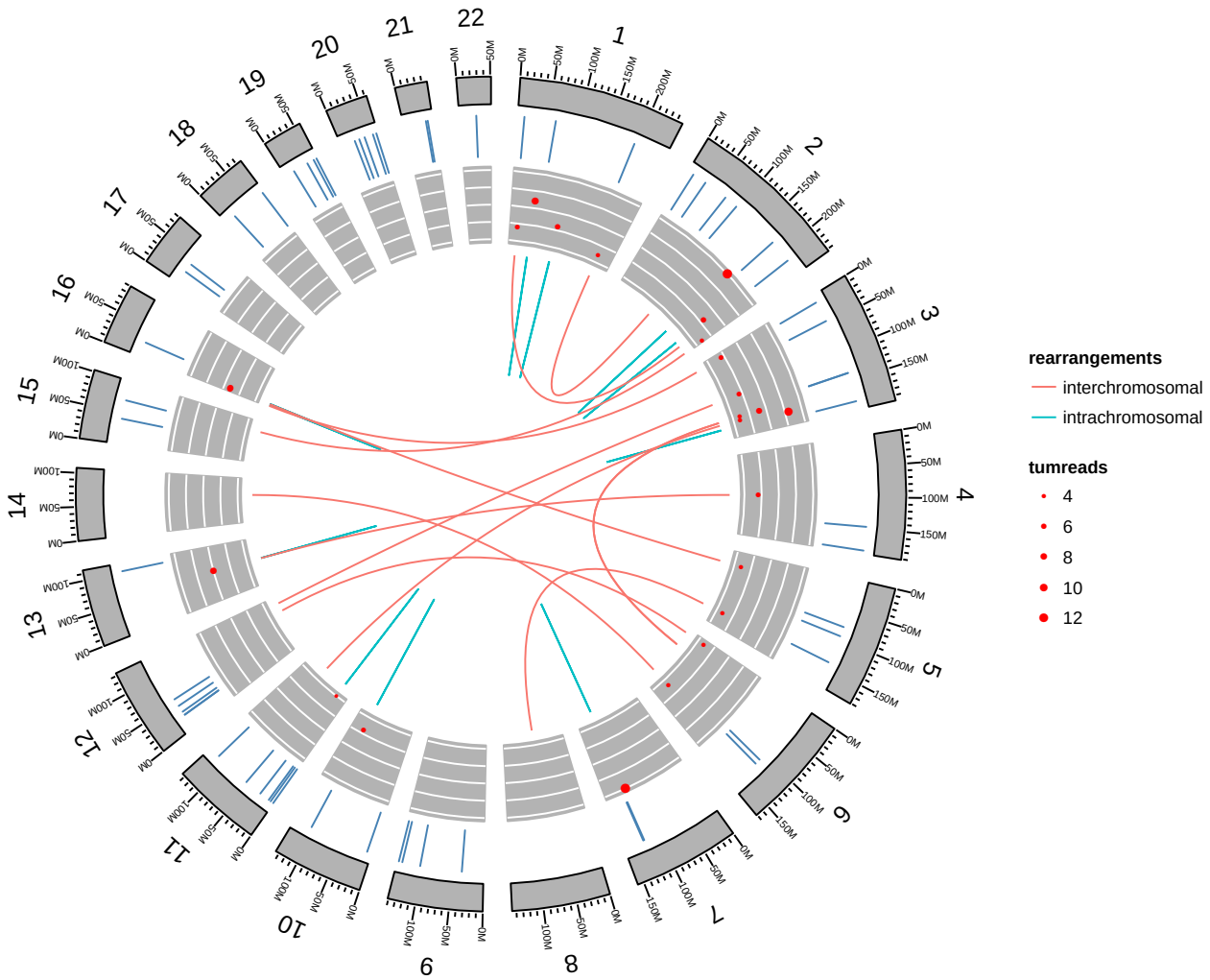

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Mismatch summary + VCF

Edge-linked Intervals

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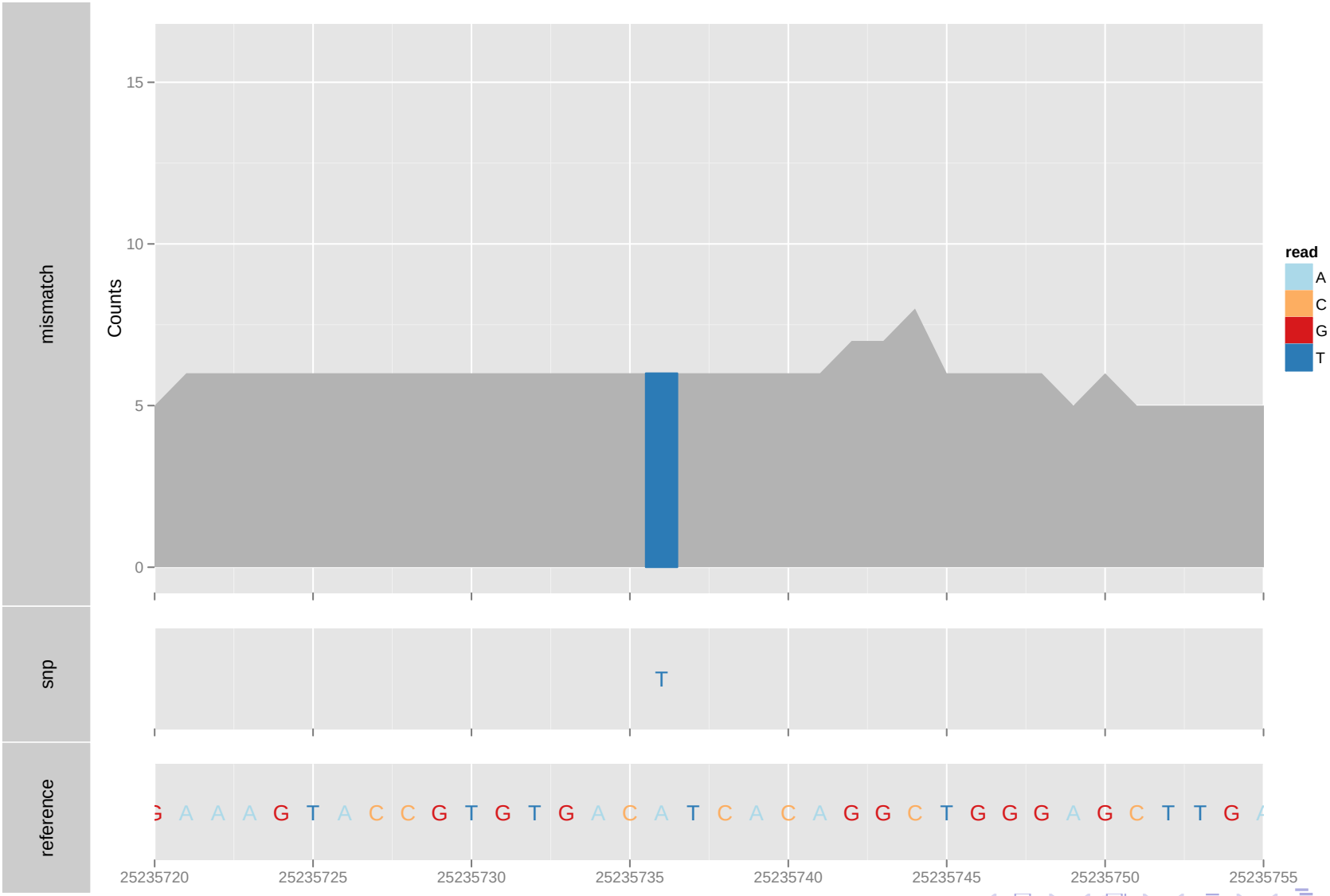

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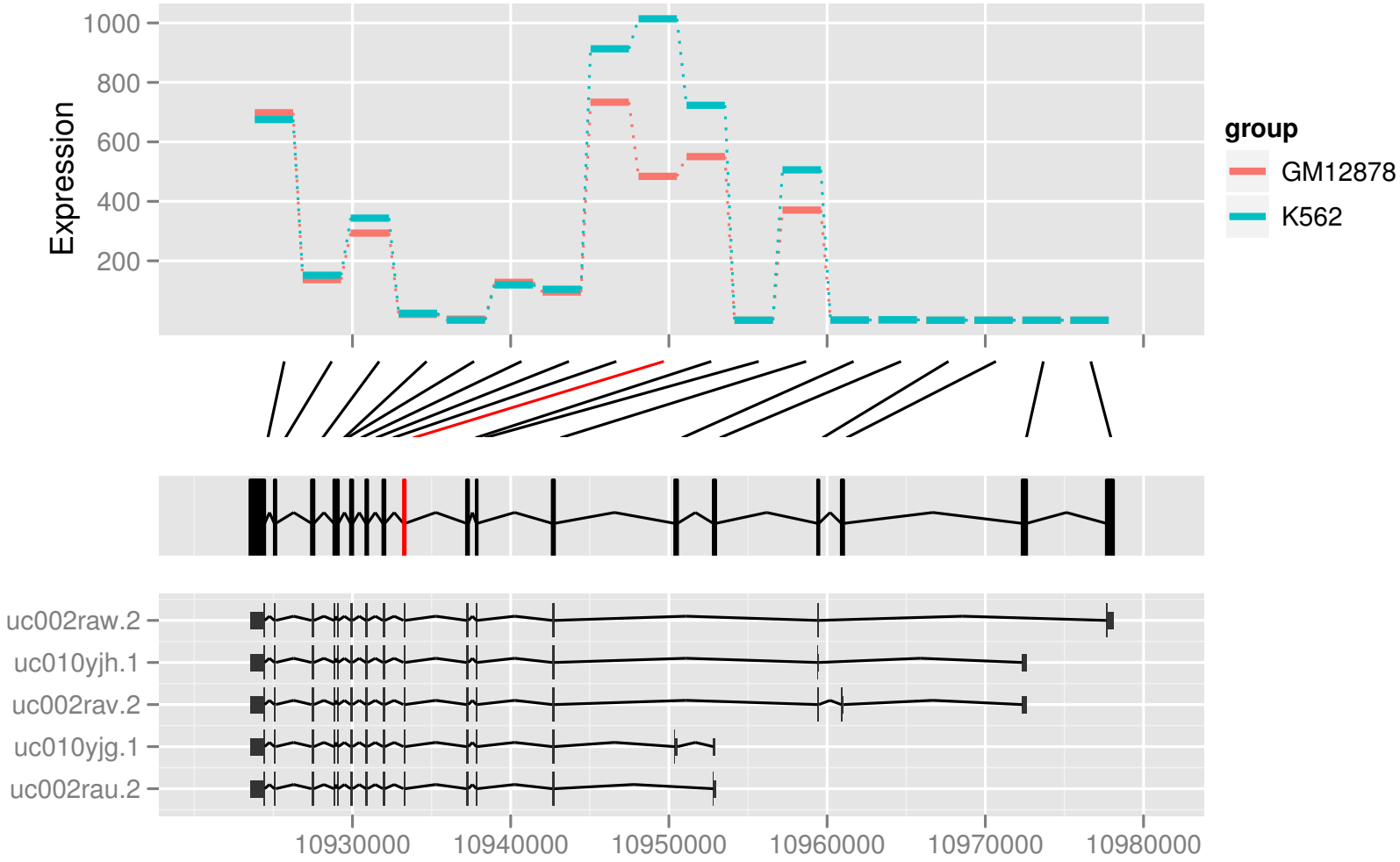

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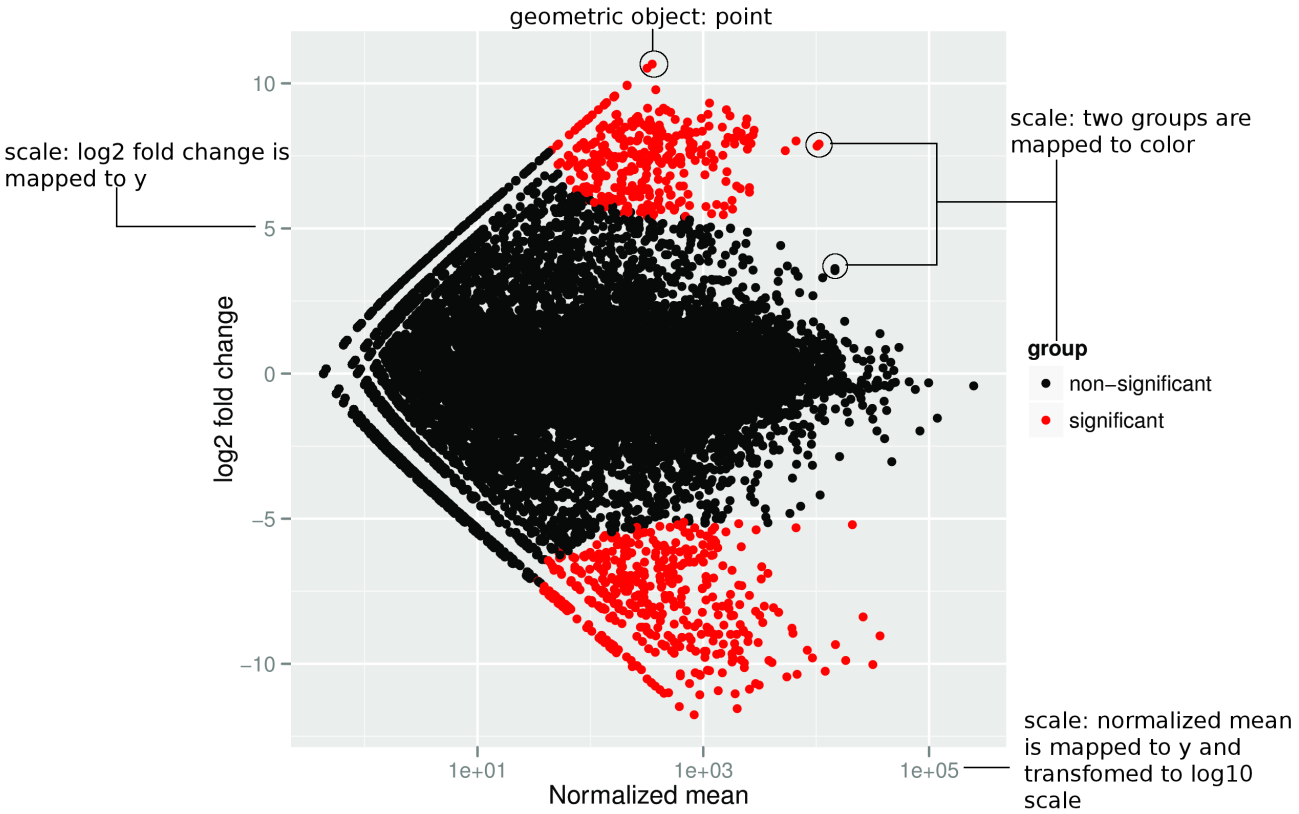
The Wilkinson/Wickham Grammar of Graphics



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Coord Maps from geom space to device space

Facet Small multiples of data subsets (trellis)

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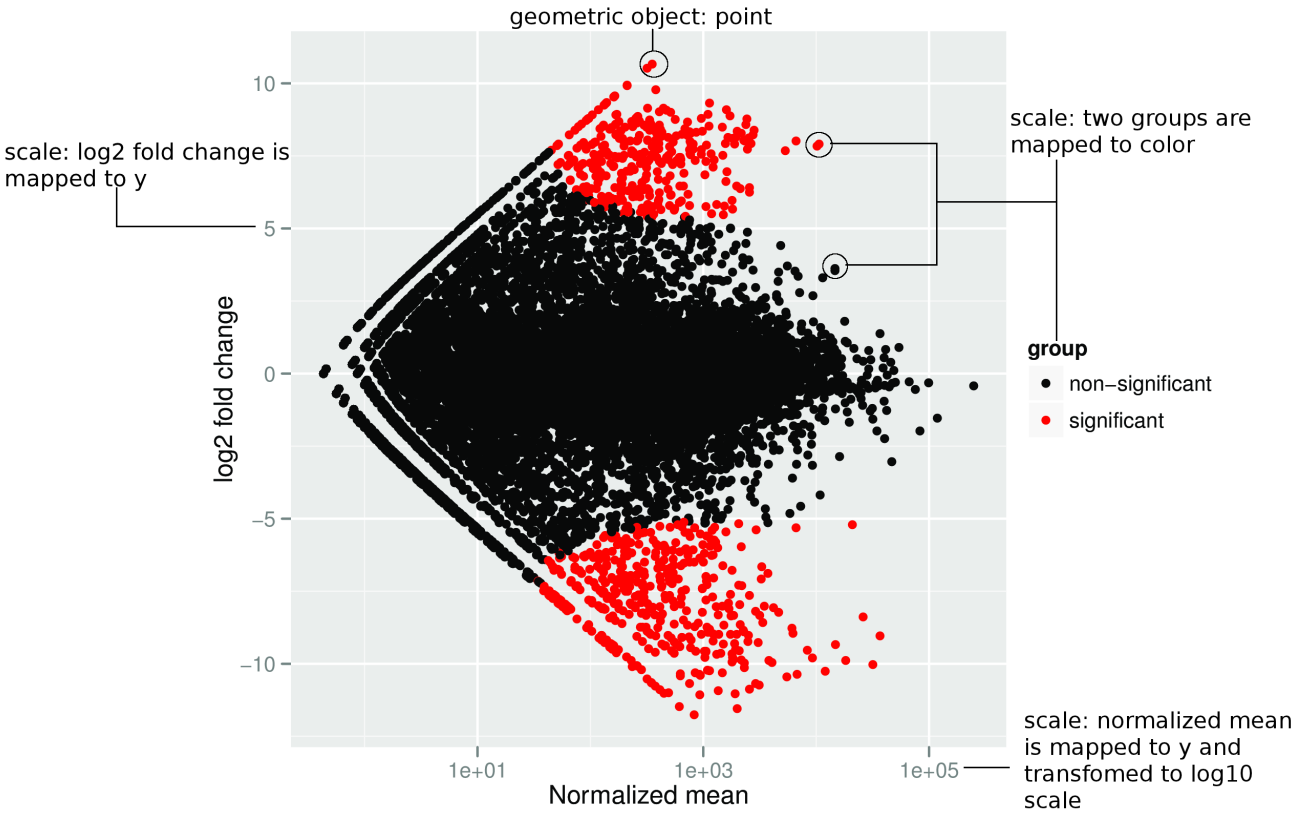

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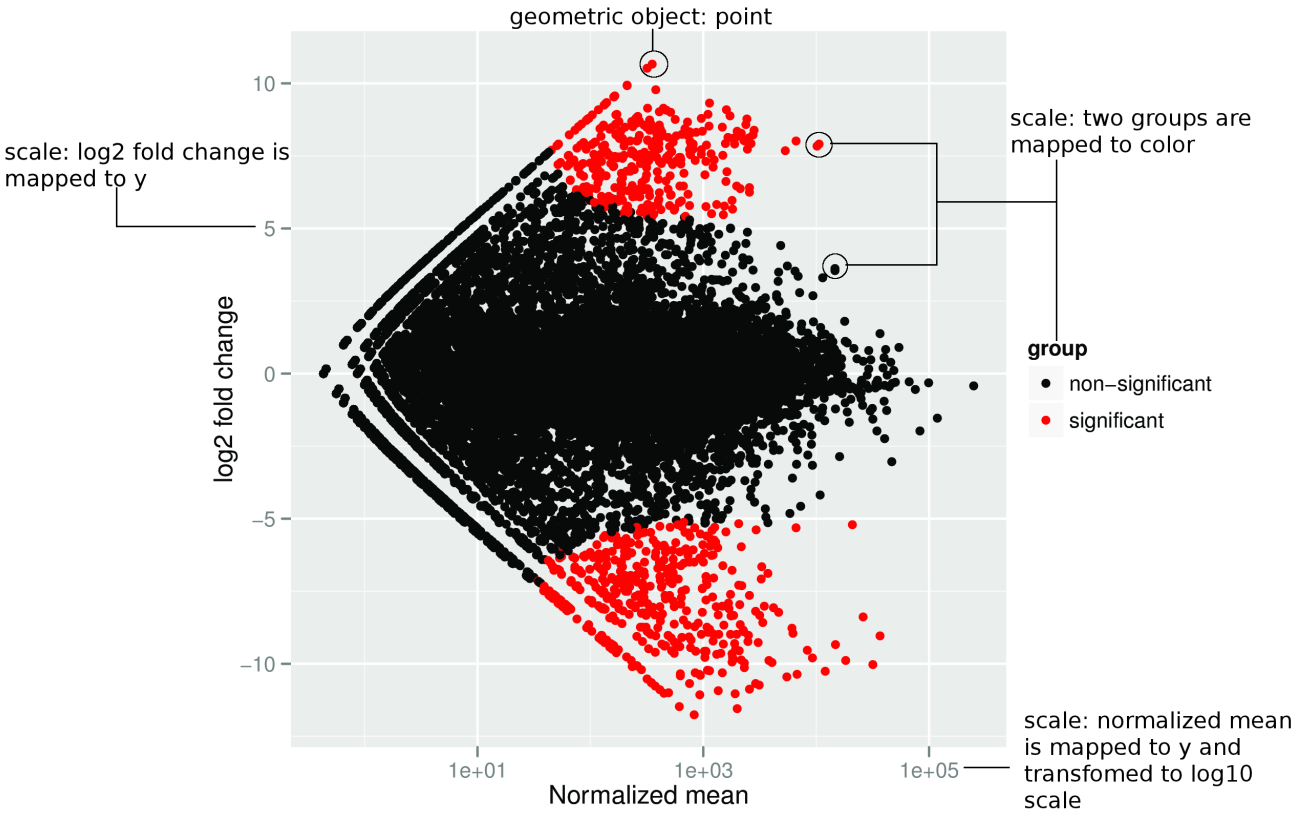

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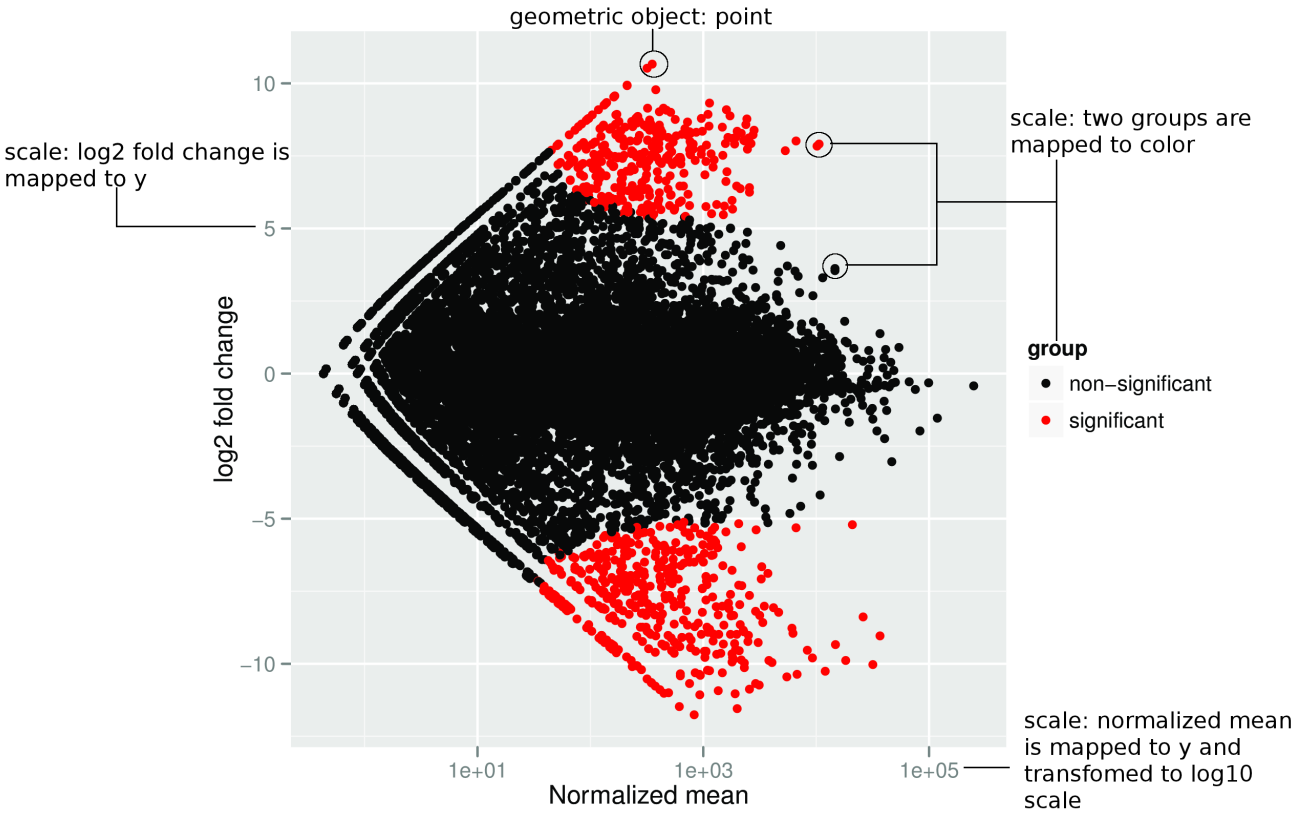

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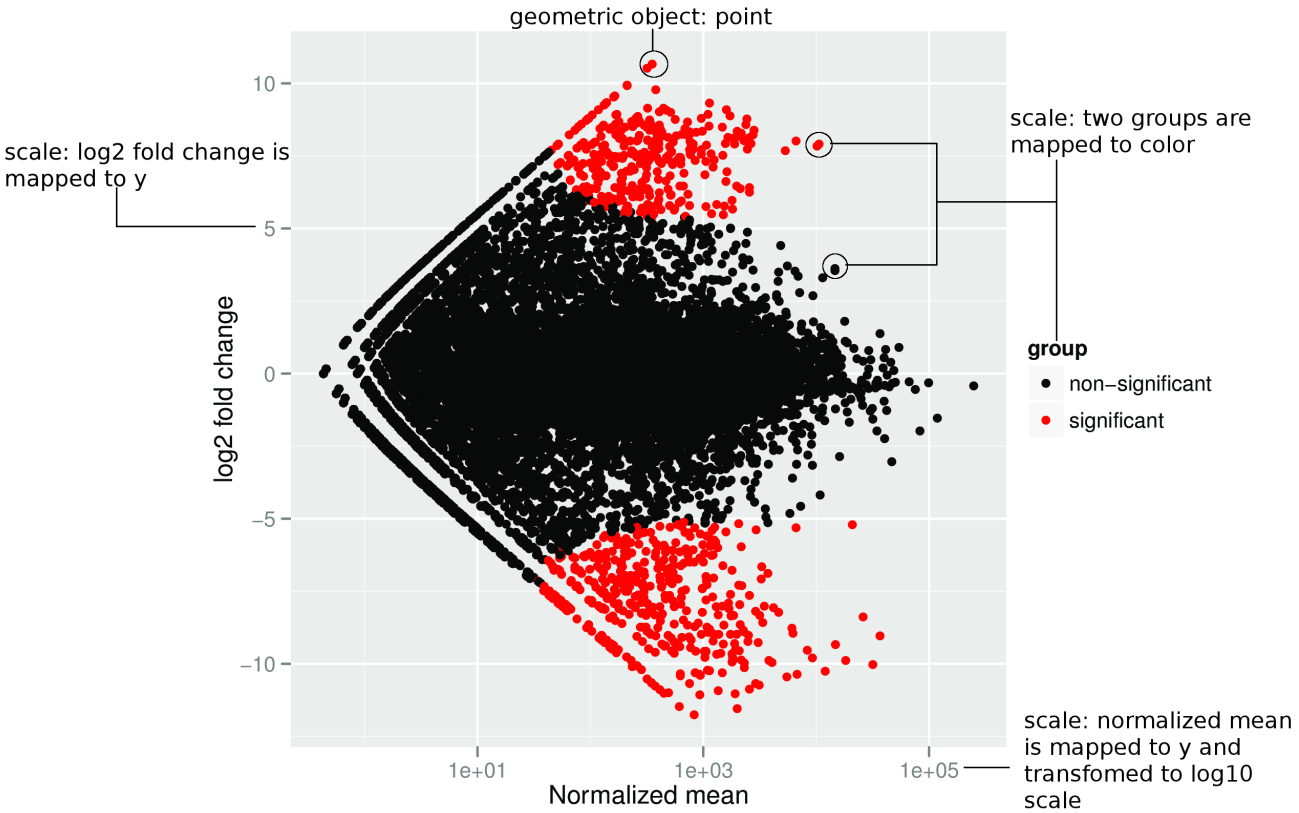

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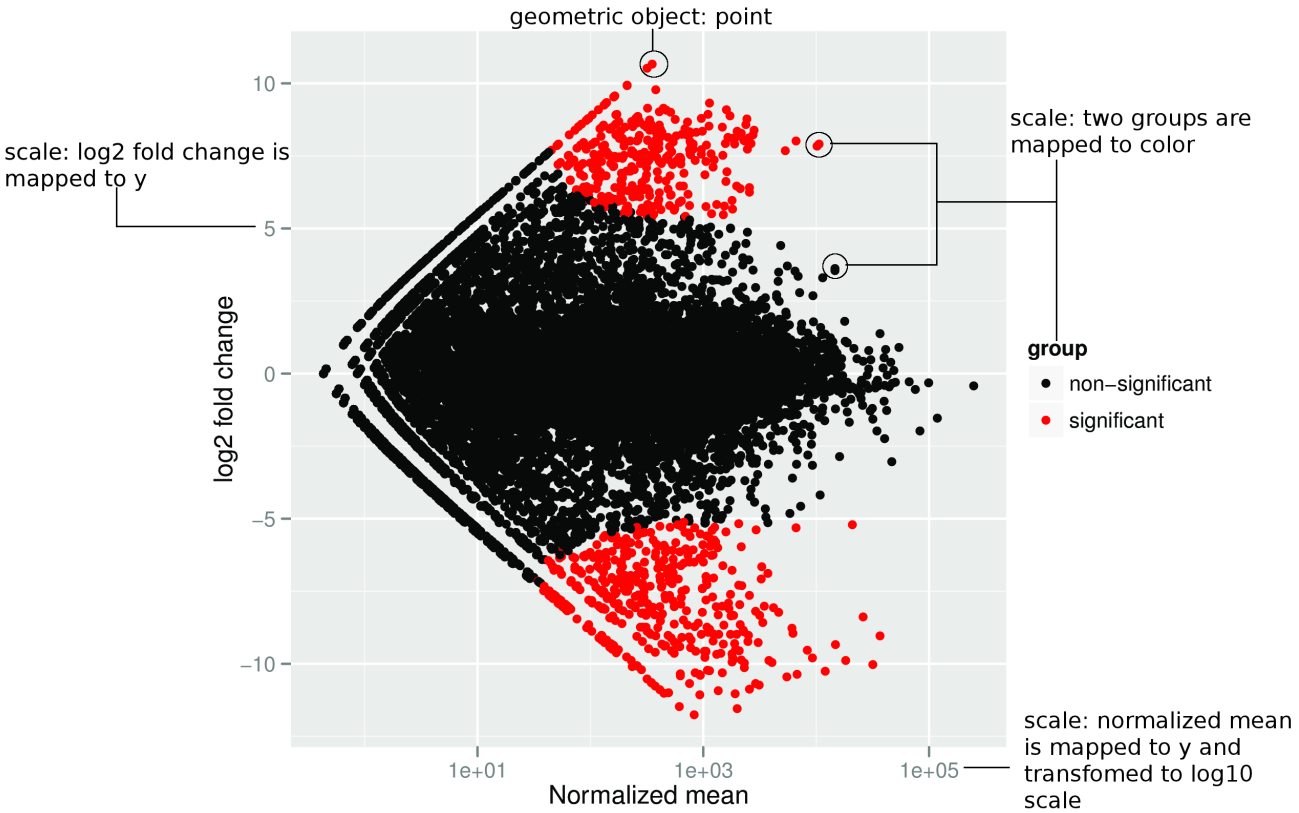

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A Grammar of Graphics for Genomics

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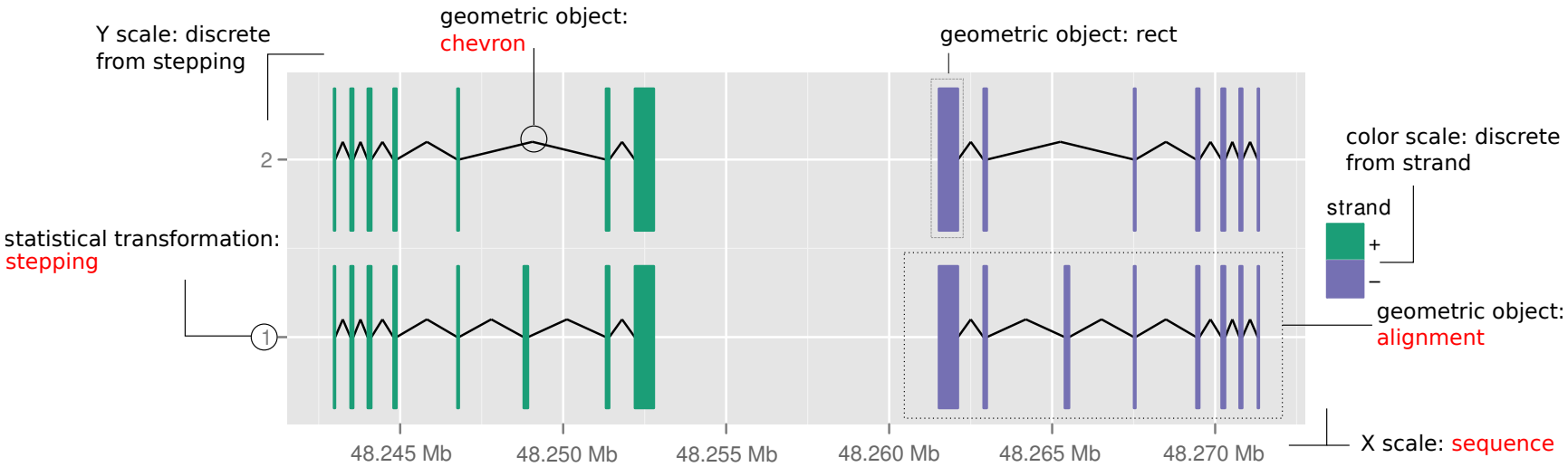

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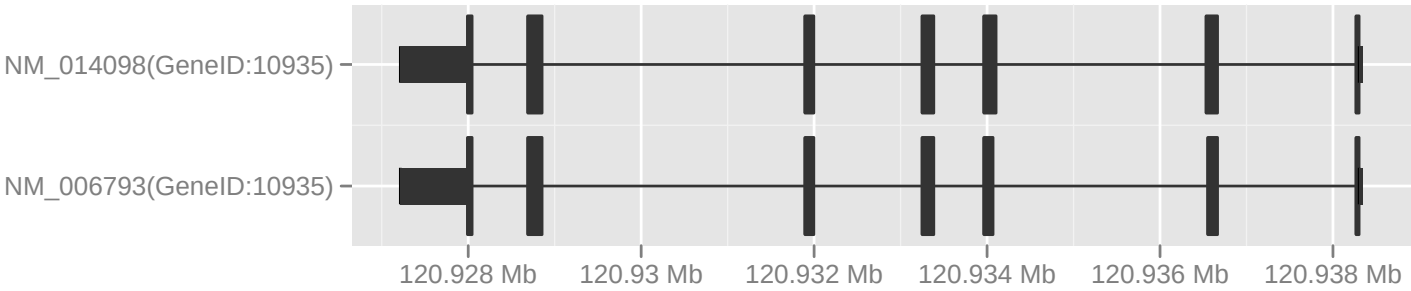

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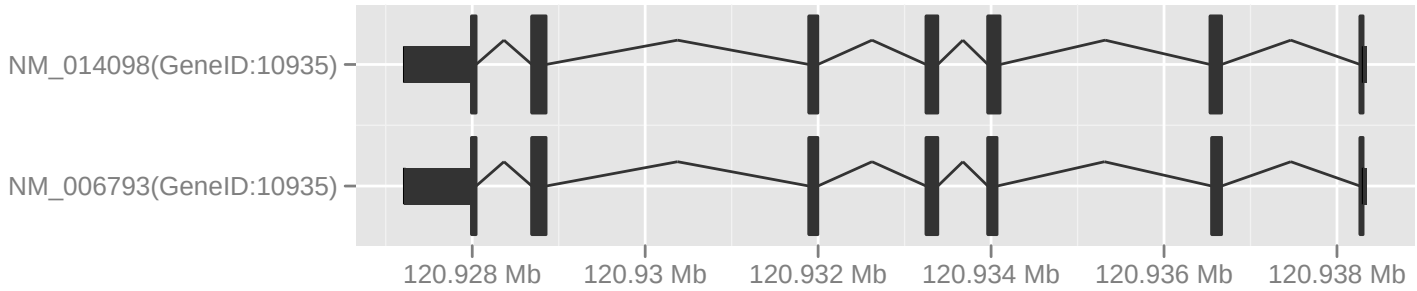

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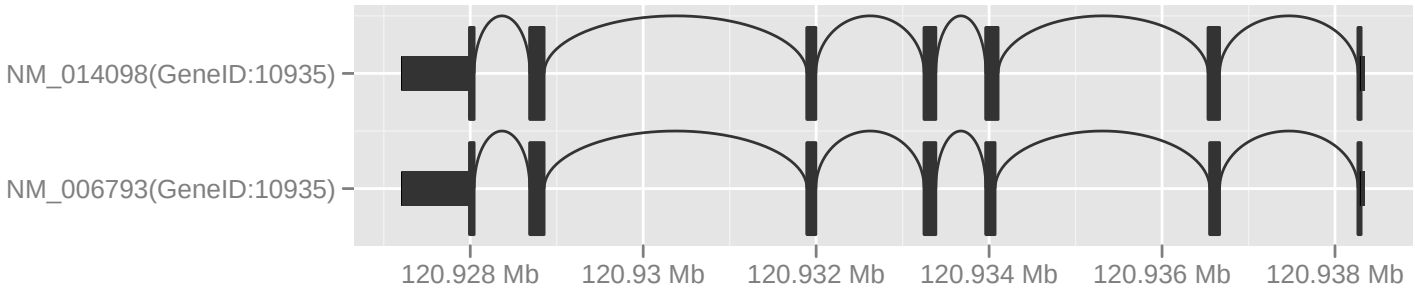

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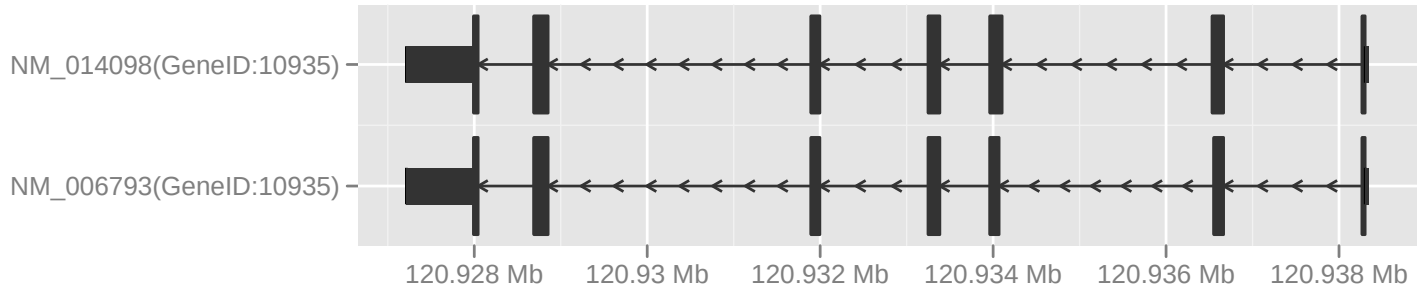

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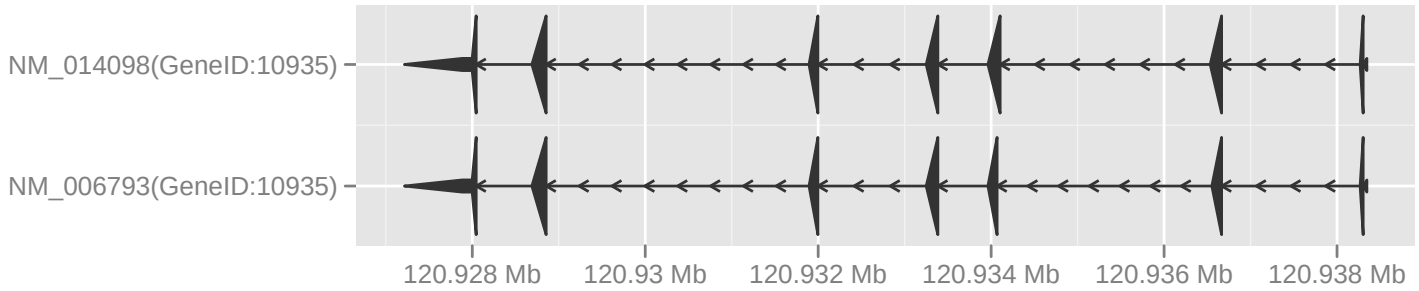

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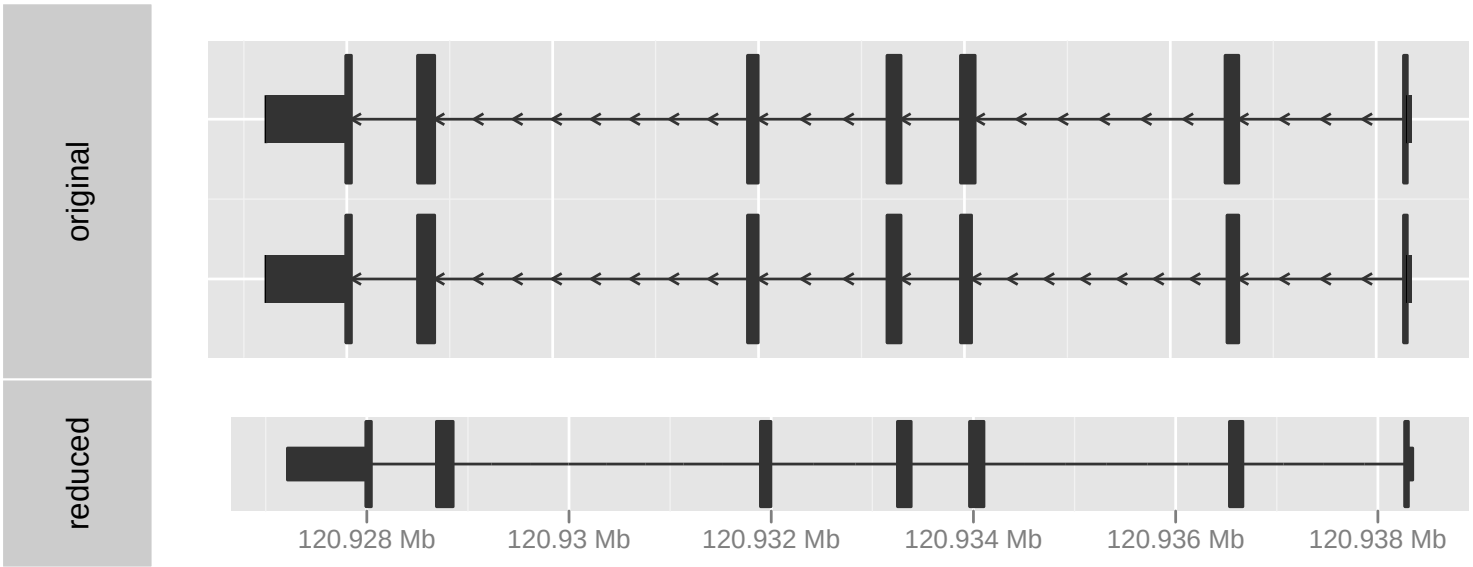

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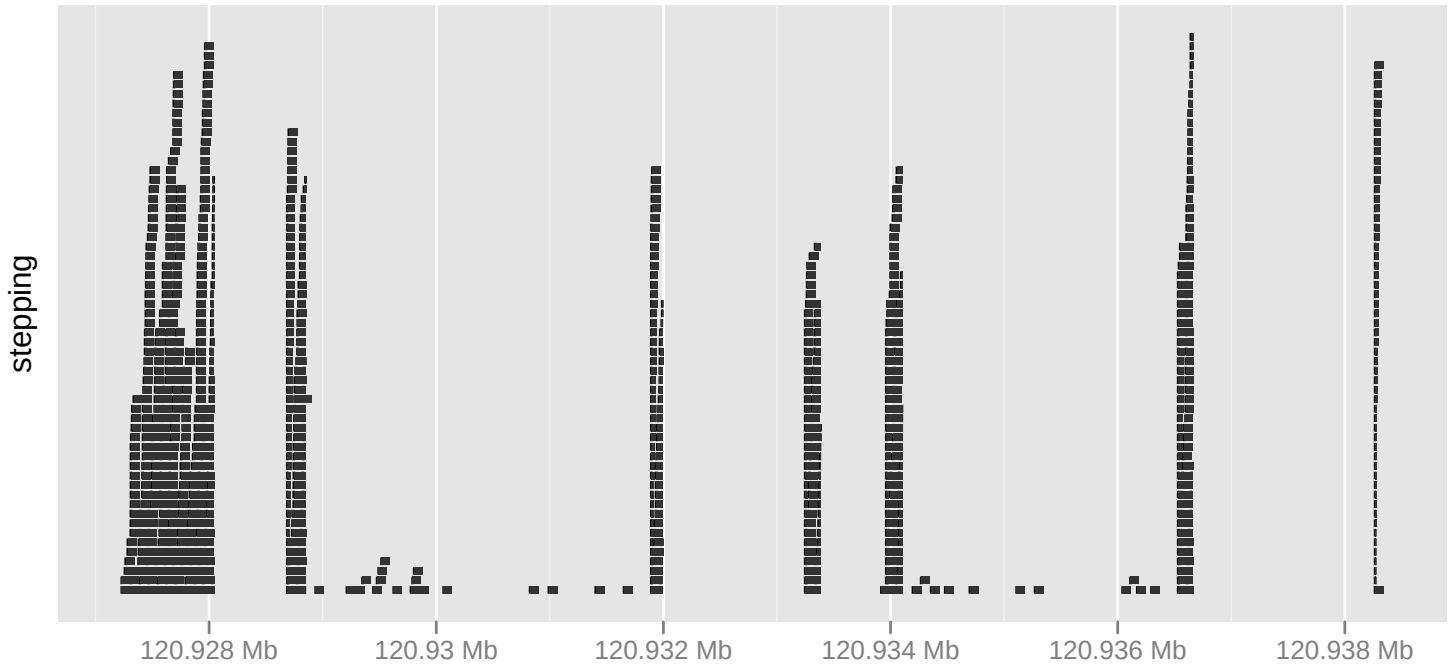

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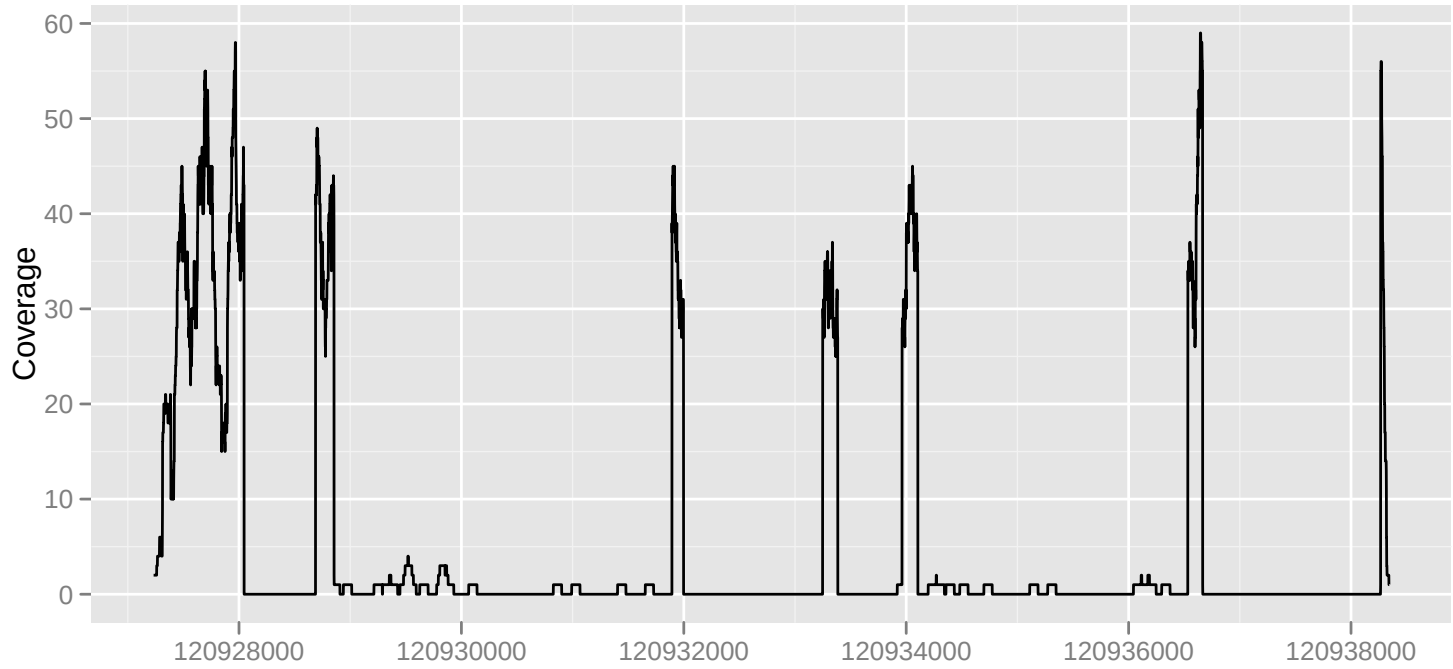

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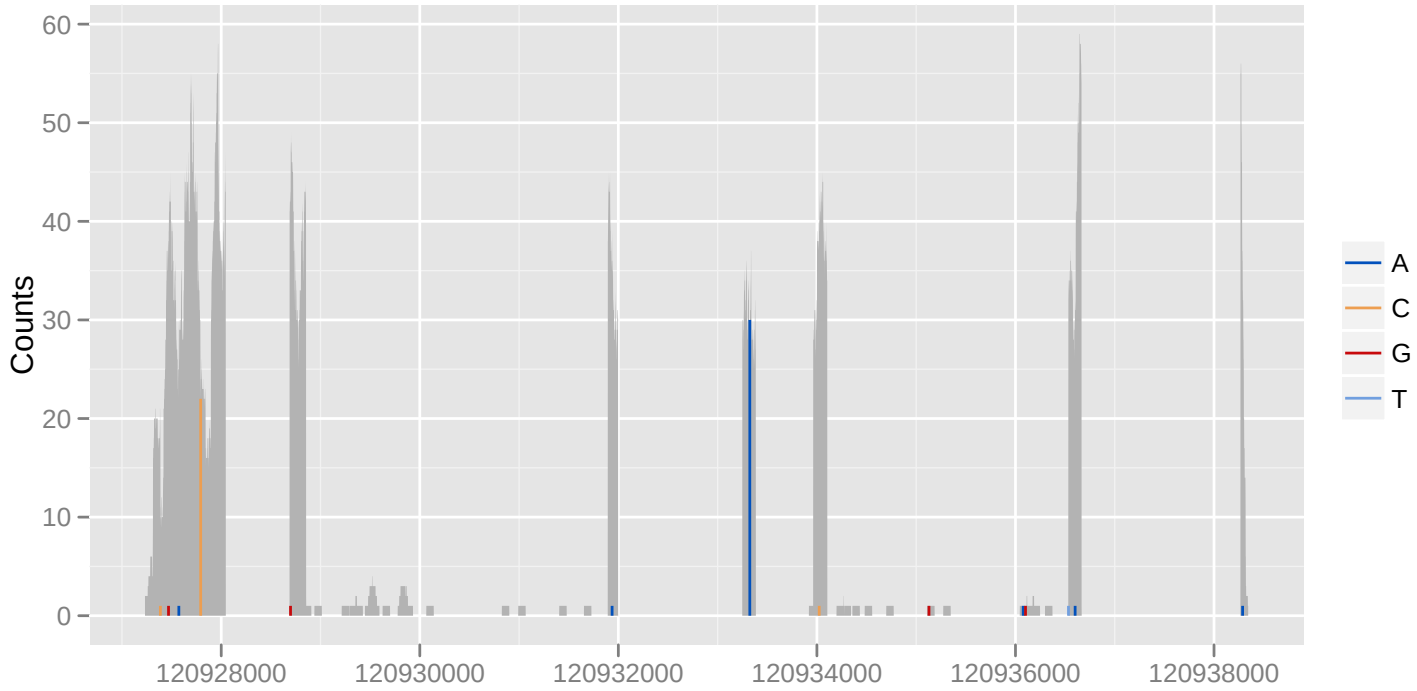

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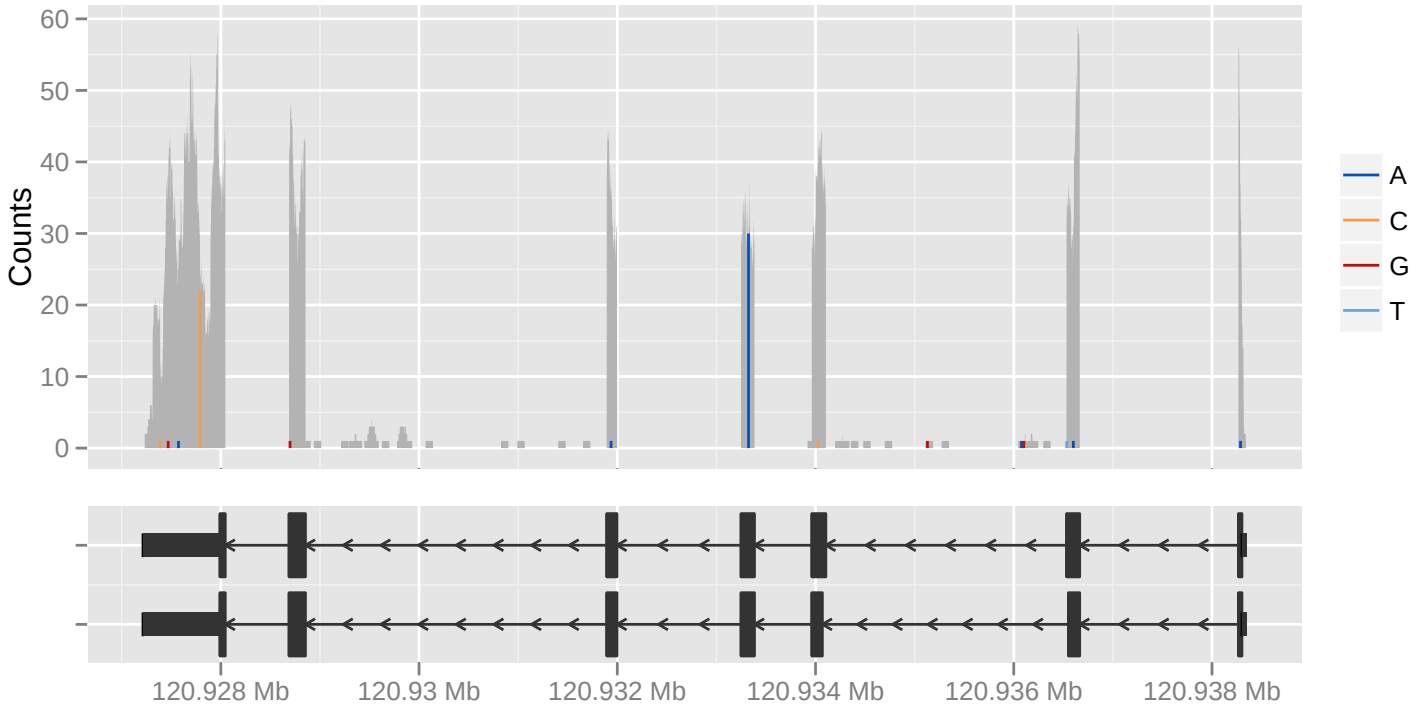

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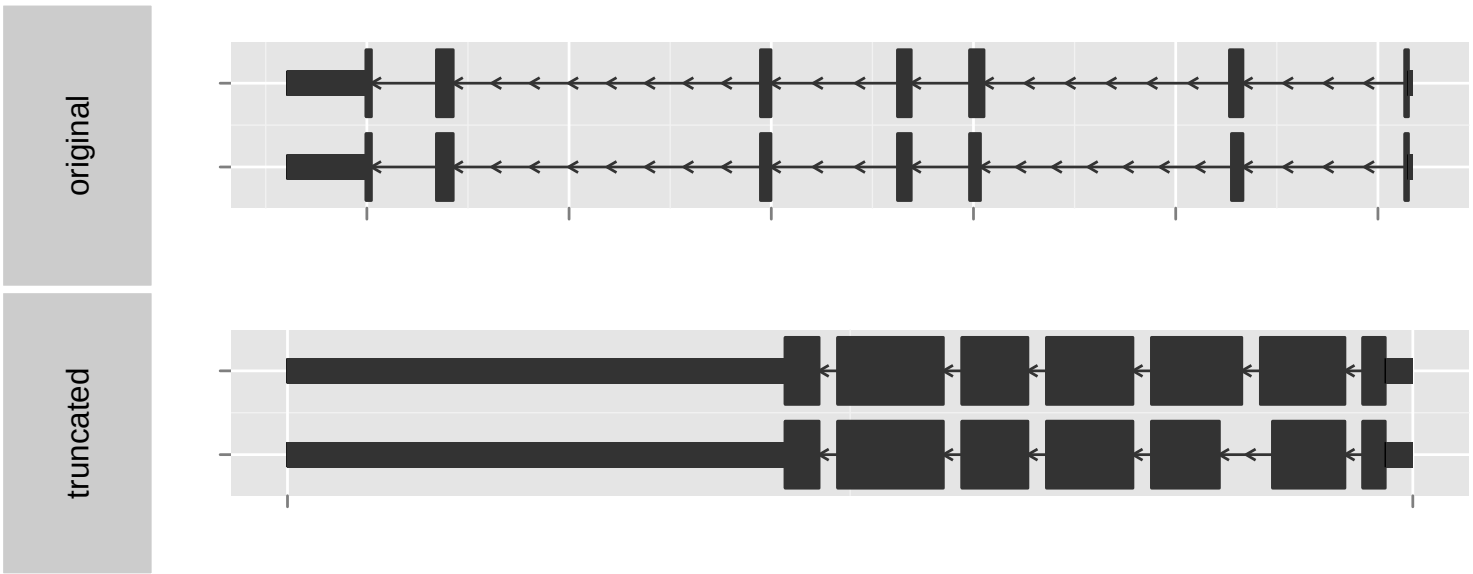

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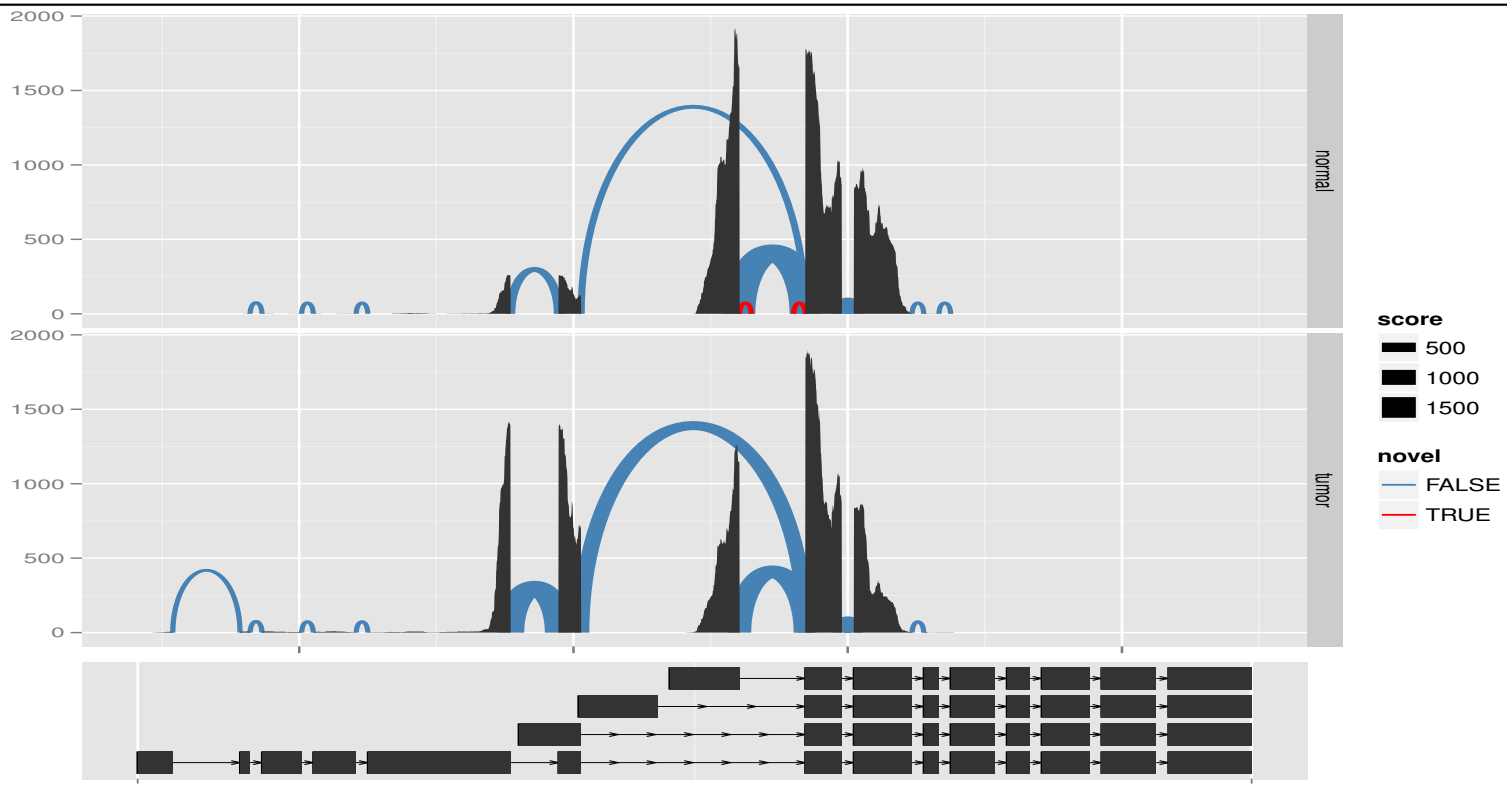

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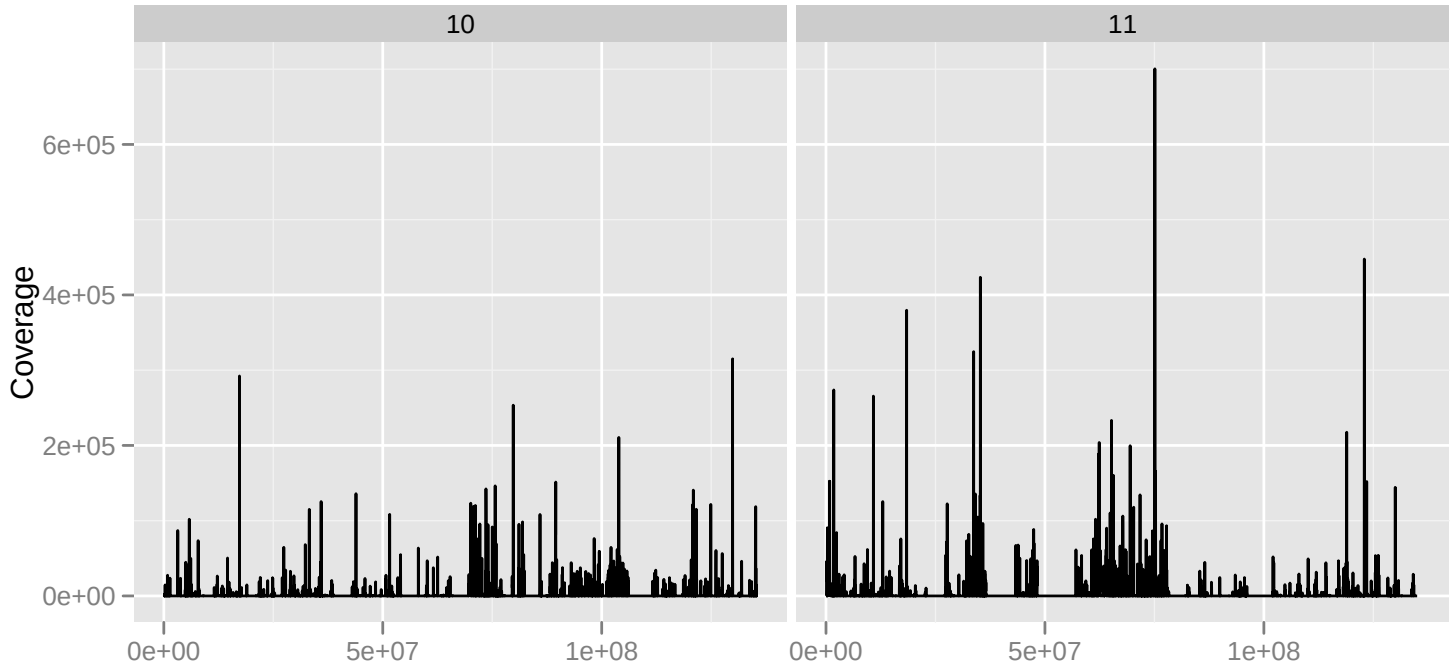

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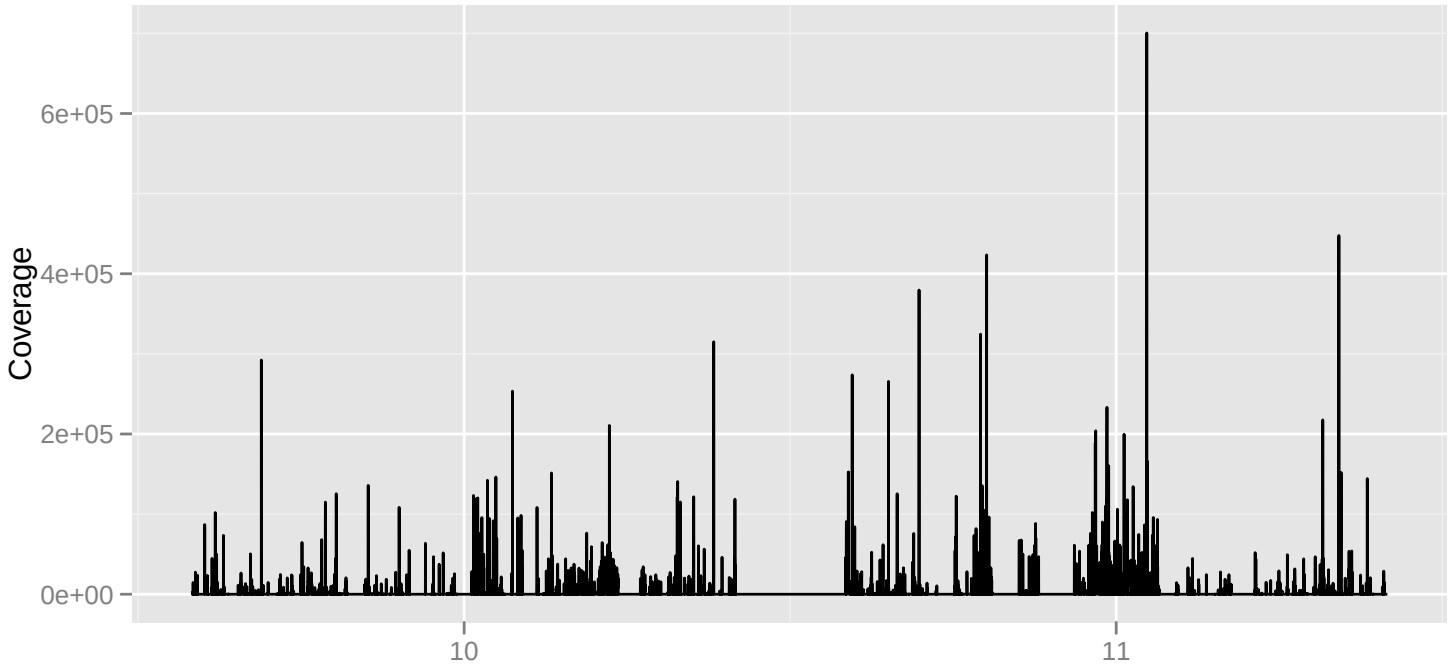

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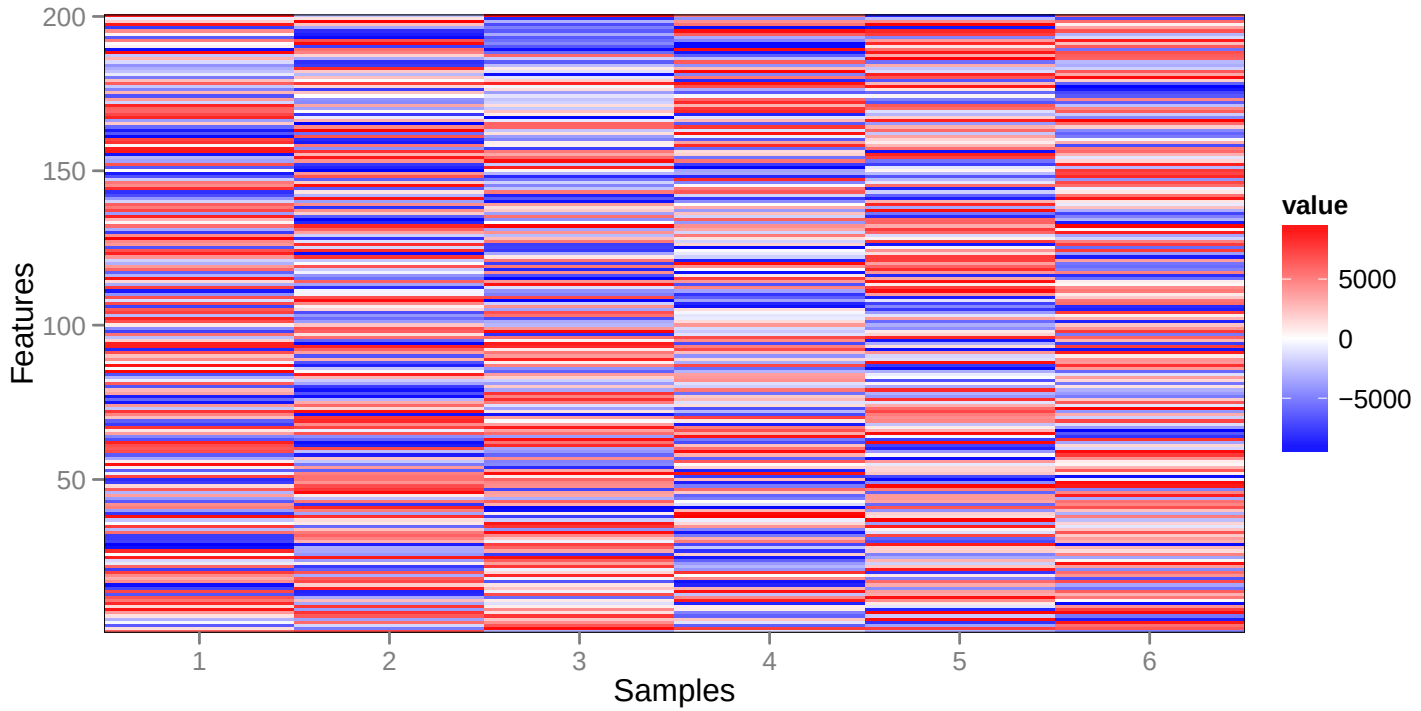

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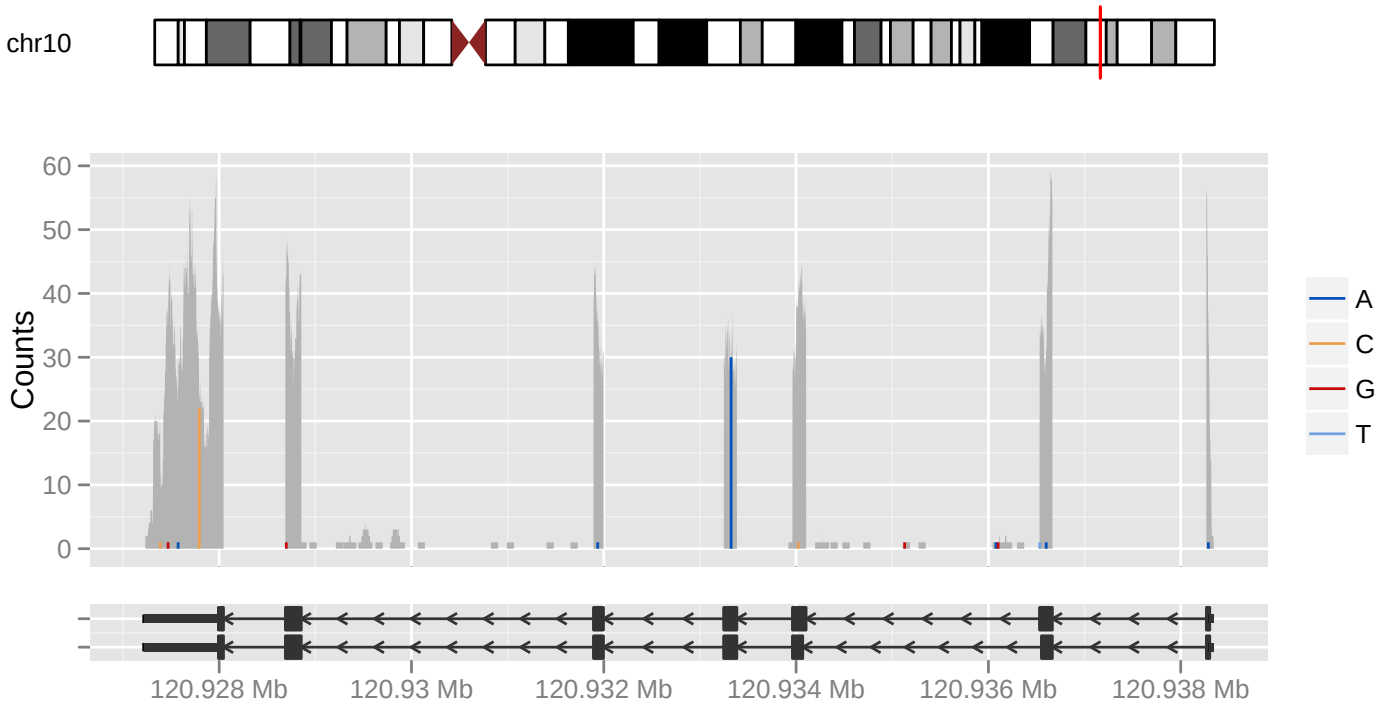

Summary

- The *ggbio* package is a toolkit for plotting genomic data and annotations
- Available as part of the Bioconductor project
- Easy to use and flexible enough to handle the diverse use cases encountered in genomics
- Useful plots are automatically generated from Bioconductor data structures using reasonable defaults
- New types of plots can be constructed from grammar primitives specially designed for genomics

Acknowledgements

Tengfei Yin
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Robert Gentleman