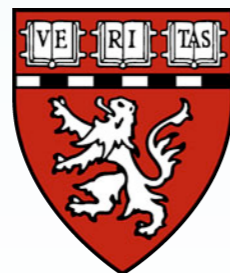


Supporting Subtype Characterization through Integrative Visualization of Cancer Genomics Data Sets

Alexander Lex / *Graz University of Technology*

Peter J Park / *Harvard Medical School*

Nils Gehlenborg / *Harvard Medical School & Broad Institute*



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Austrian Research Promotion Agency / *inGeneious project (385567)*



Gene expression patterns of breast carcinomas distinguish tumor subclasses with **clinical implications**

Theresa Sorlie, Charles M. Perou, et al.

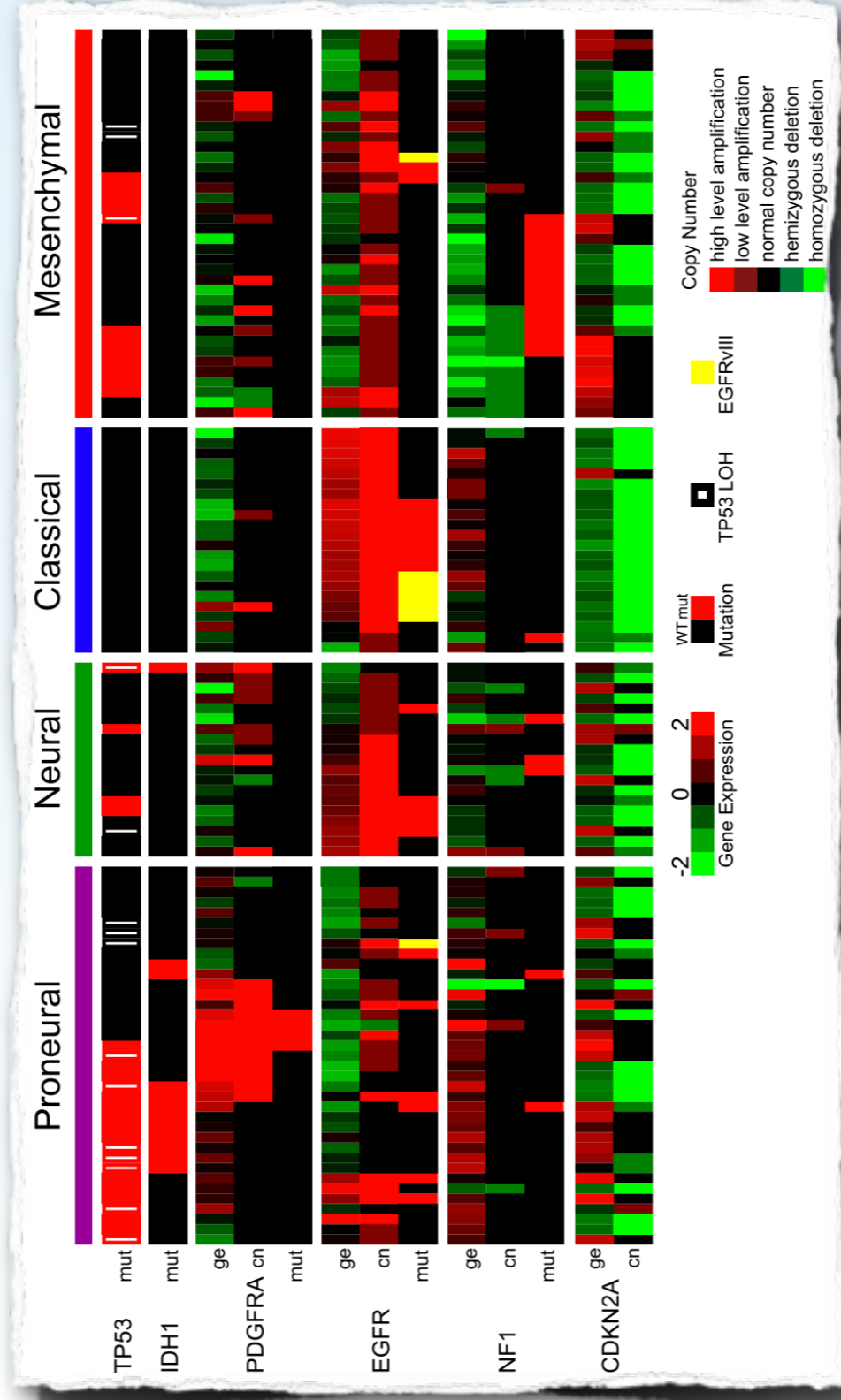
Molecular subclasses of high-grade glioma **predict prognosis**, delineate a pattern of disease progression, and resemble stages in neurogenesis

Gene expression profiling identifies **clinically relevant** subtypes of prostate cancer

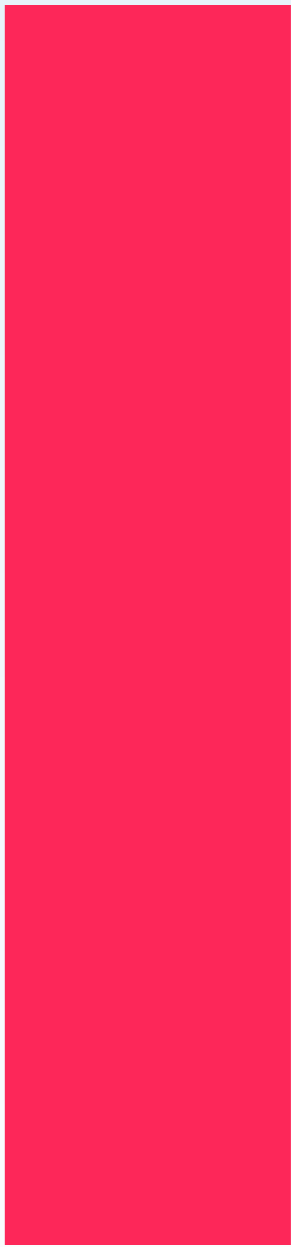
Integrated Genomic Analysis Identifies Clinically Relevant Subtypes of Glioblastoma Characterized by Abnormalities in *PDGFRA*, *IDH1*, *EGFR*, and *NF1*

Roel G.W. Verhaak,^{1,2,17} Katherine A. Hoadley,^{3,4,17} Elizabeth Purdom,⁷ Victoria Wang,⁸ Yuan Qi,^{4,5} Matthew D. Wilkerson,^{4,5} C. Ryan Miller,^{4,6} Li Ding,⁹ Todd Golub,^{1,10} Jill P. Mesirov,¹ Gabriele Alexe,¹ Michael Lawrence,^{1,2} Michael O'Kelly,^{1,2} Pablo Tamayo,¹ Barbara A. Weir,^{1,2} Stacey Gabriel,¹ Wendy Winckler,^{1,2} Supriya Gupta,¹ Lakshmi Jakkula,¹¹ Heidi S. Feiler,¹¹ J. Graeme Hodgson,¹² C. David James,¹² Jann N. Sarkaria,¹³ Cameron Brennan,¹⁴ Ari Kahn,¹⁵ Paul T. Spellman,¹¹ Richard K. Wilson,⁹ Terence P. Speed,^{7,16} Joe W. Gray,¹¹ Matthew Meyerson,^{1,2} Gad Getz,¹ Charles M. Perou,^{3,4,8} D. Neil Hayes,^{4,5,*} and The Cancer Genome Atlas Research Network

← Patients



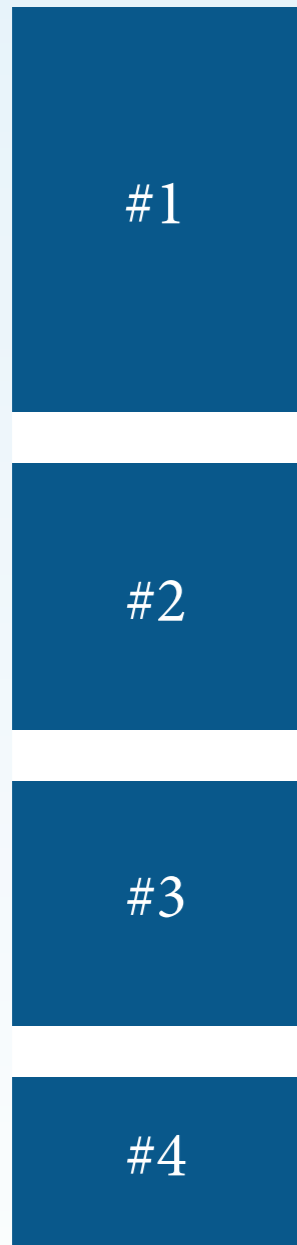
Patients



Groupings



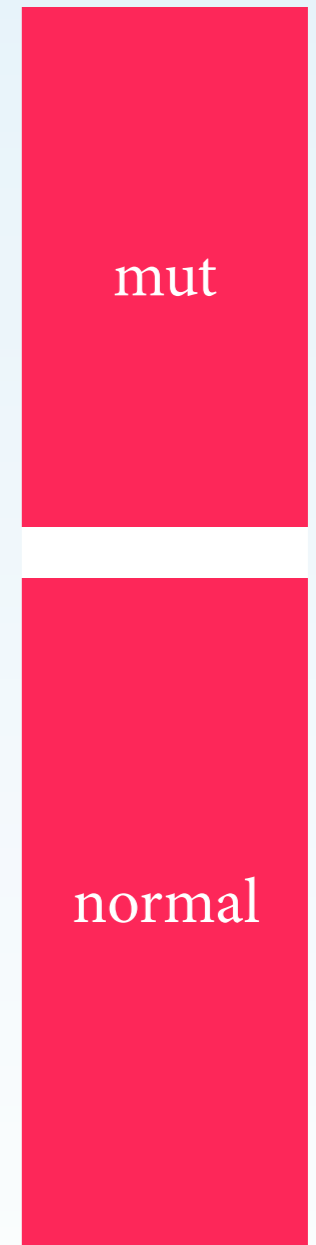
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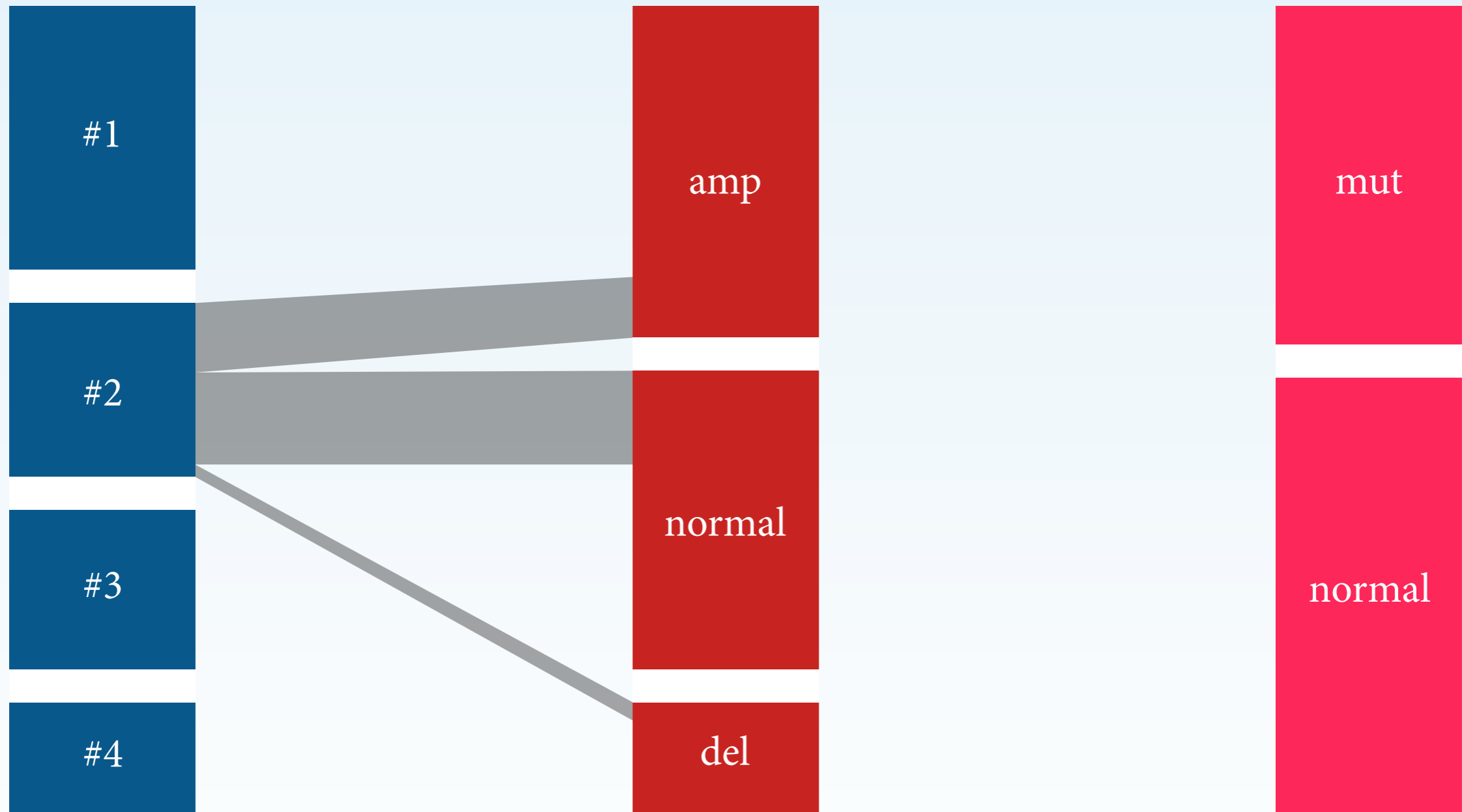
Mutation



mRNA

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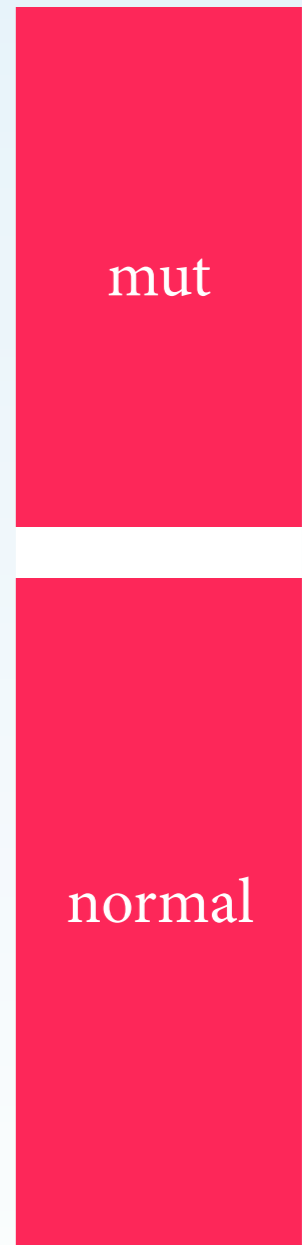
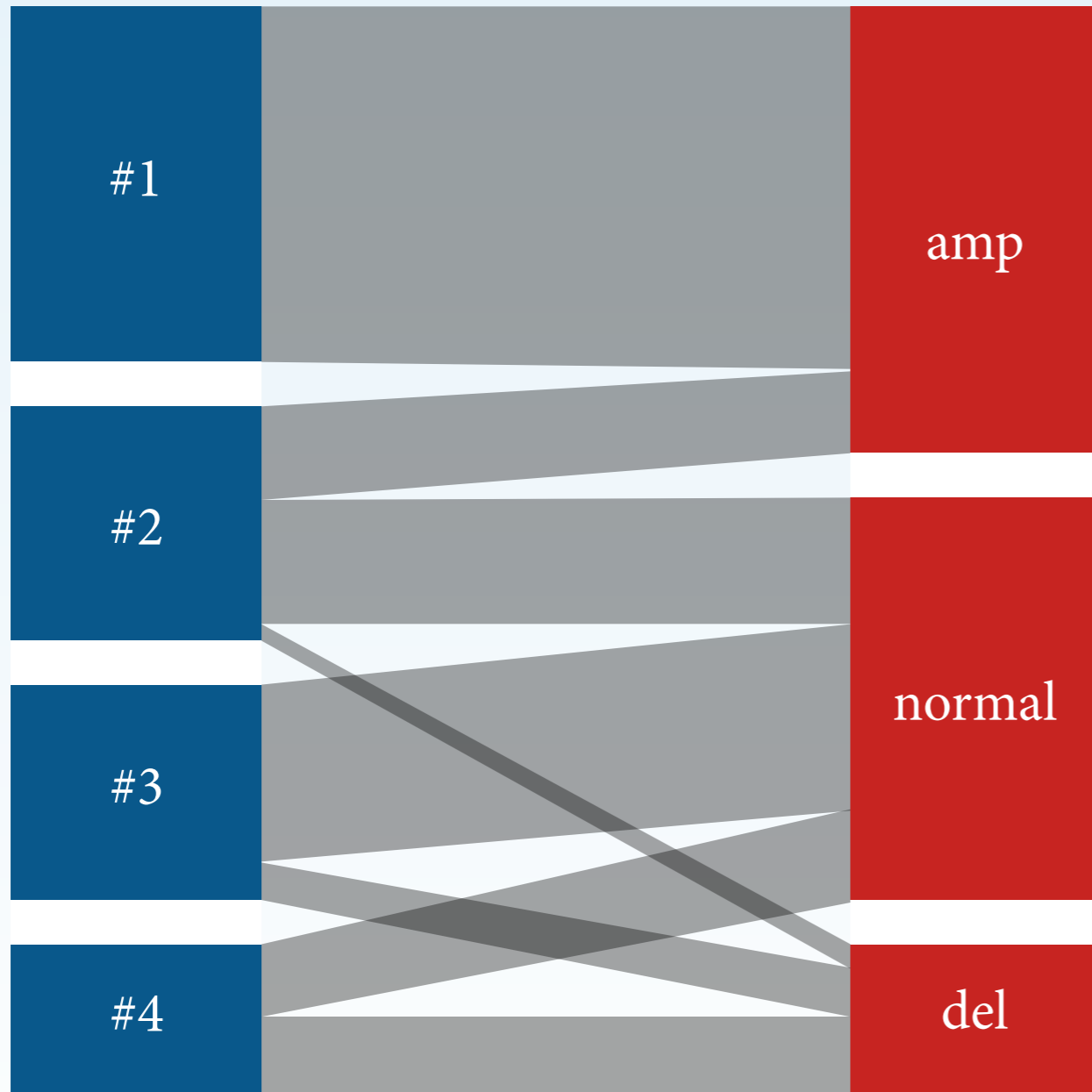
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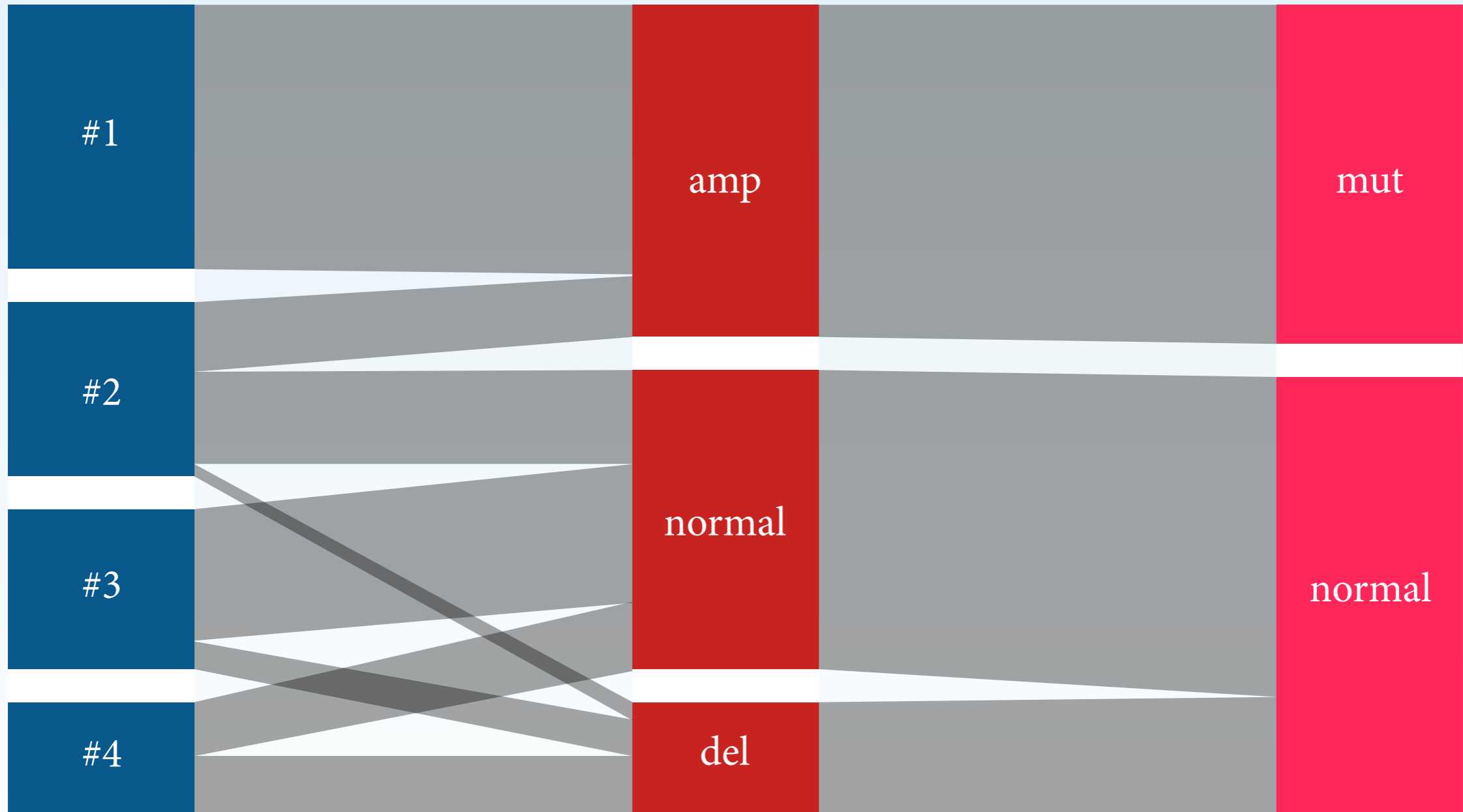
Mutation



mRNA

Copy Number

Mutation



VisBricks: Multifform Visualization of Large, Inhomogeneous Data

Alexander Lex, Hans-Jörg Schulz, Marc Streit, Christian Partl, and Dieter Schmalstieg

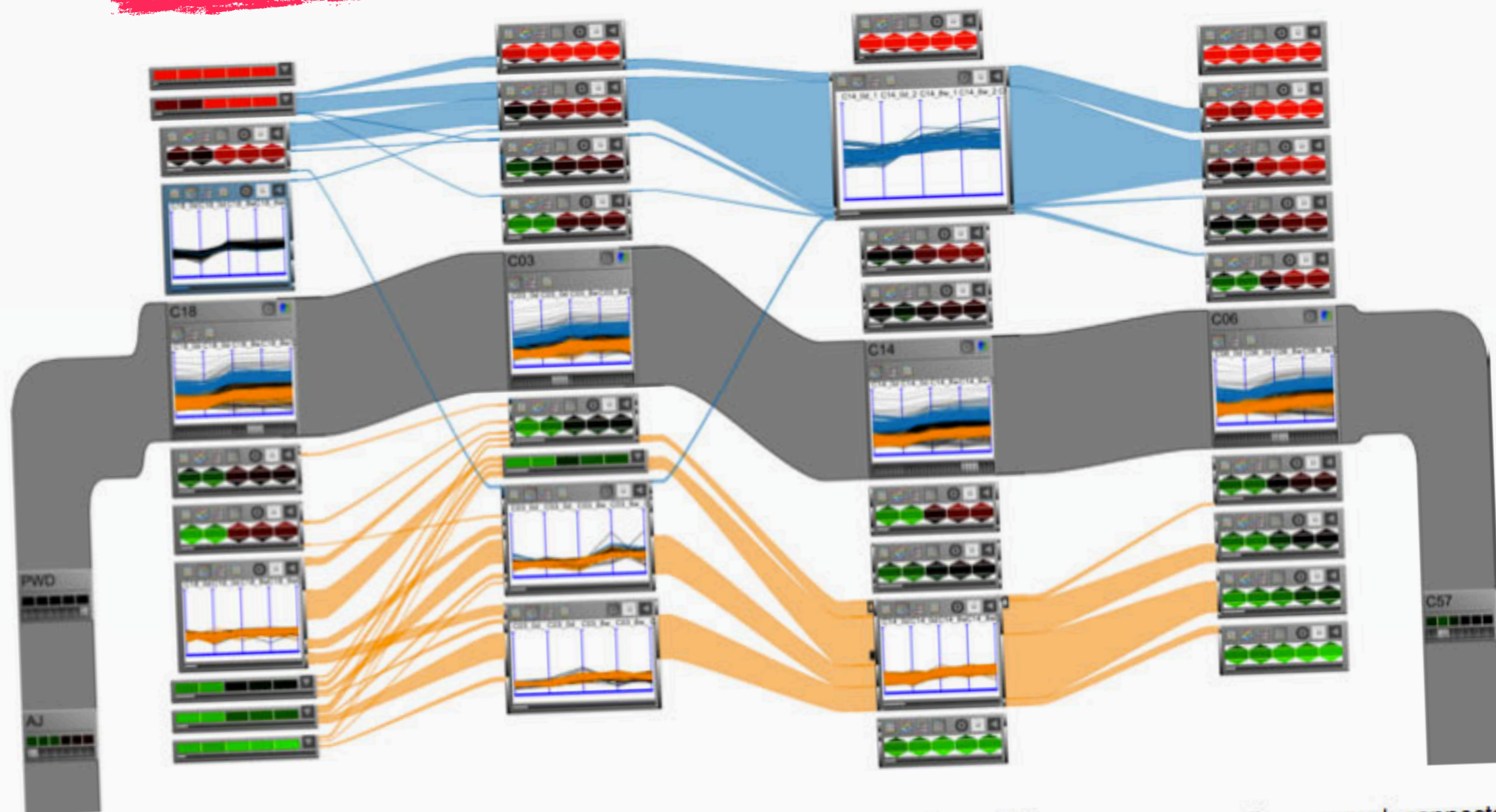


Fig. 1. *VisBricks* in action: Four different groups of dimensions with different numbers of clusters per group. The gray arch connects the overviews of the groups. The arches show how the data is distributed over the clusters in that group, thus summarizing the specifics of a dimension group. The clusters themselves are shown in stacked *VisBricks* above and below the arch depending on whether their average data values are higher or lower than the overall average for the group. Colored ribbons indicate how data items are distributed across clusters of multiple dimension groups.



CALEUDO

mRNA

Data

Gene-level *TCGA* Glioblastoma Multiforme (July 2011)

mRNA

mRNA

mRNA

Analyses

GenePattern Consensus NMF Clustering & *GISTIC 2*

mRNA

mRNA

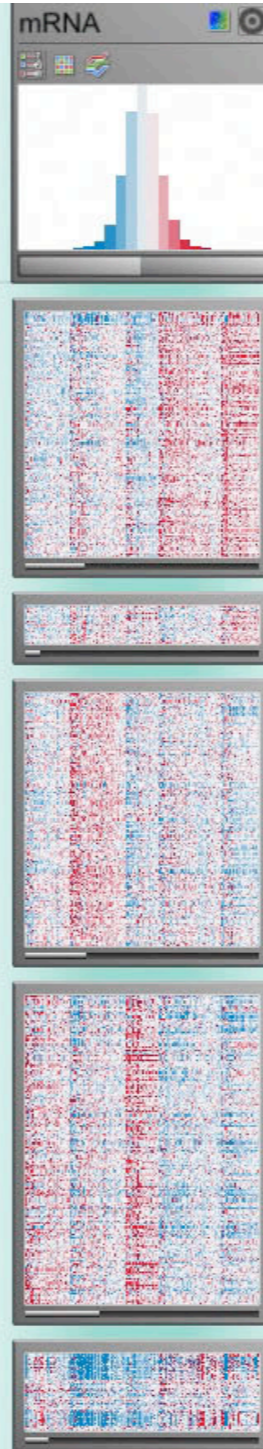
mRNA

mRNA

mRNA

mRNA

mRNA



mRNA

mRNA

mRNA



mRNA



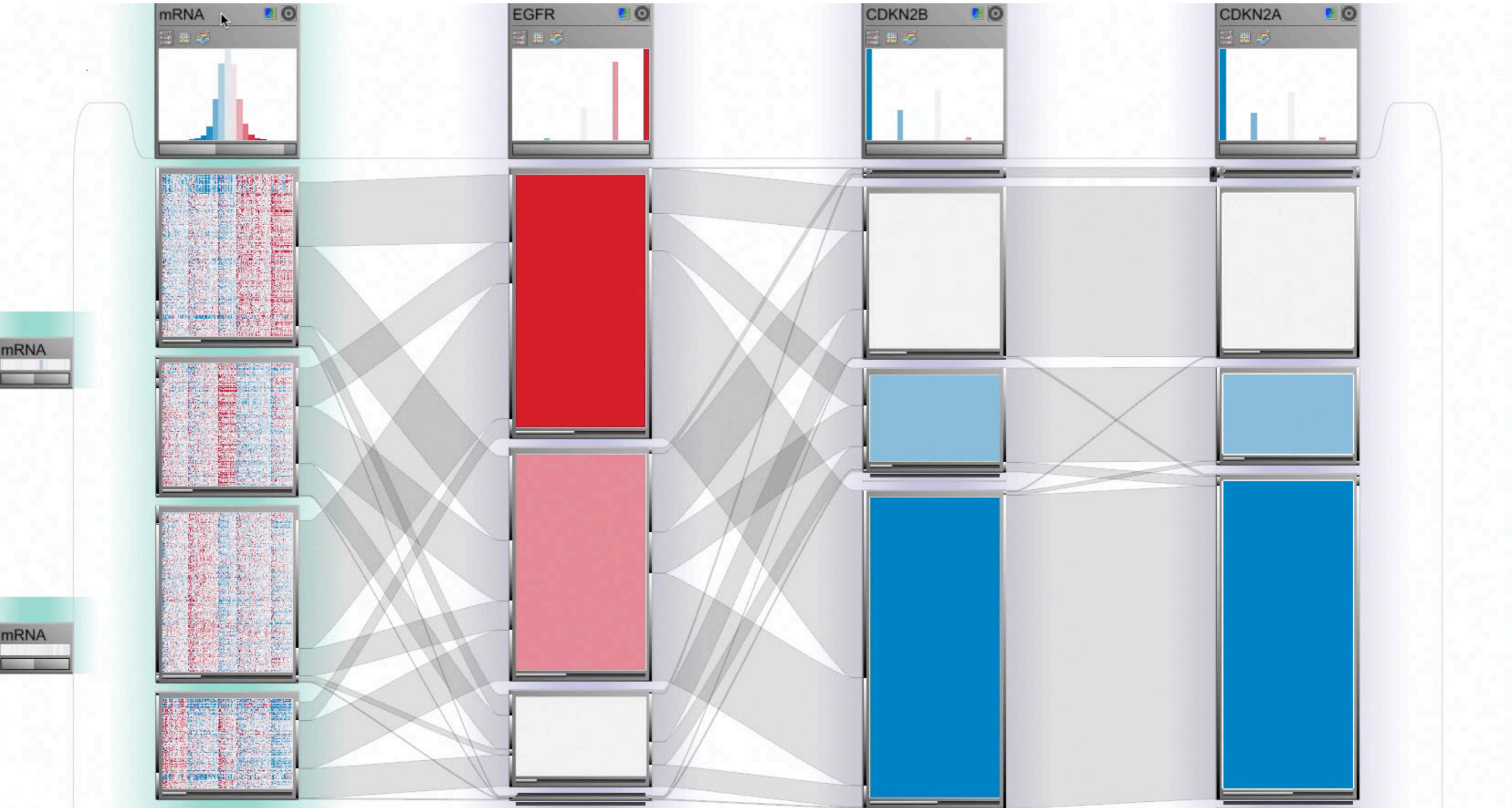
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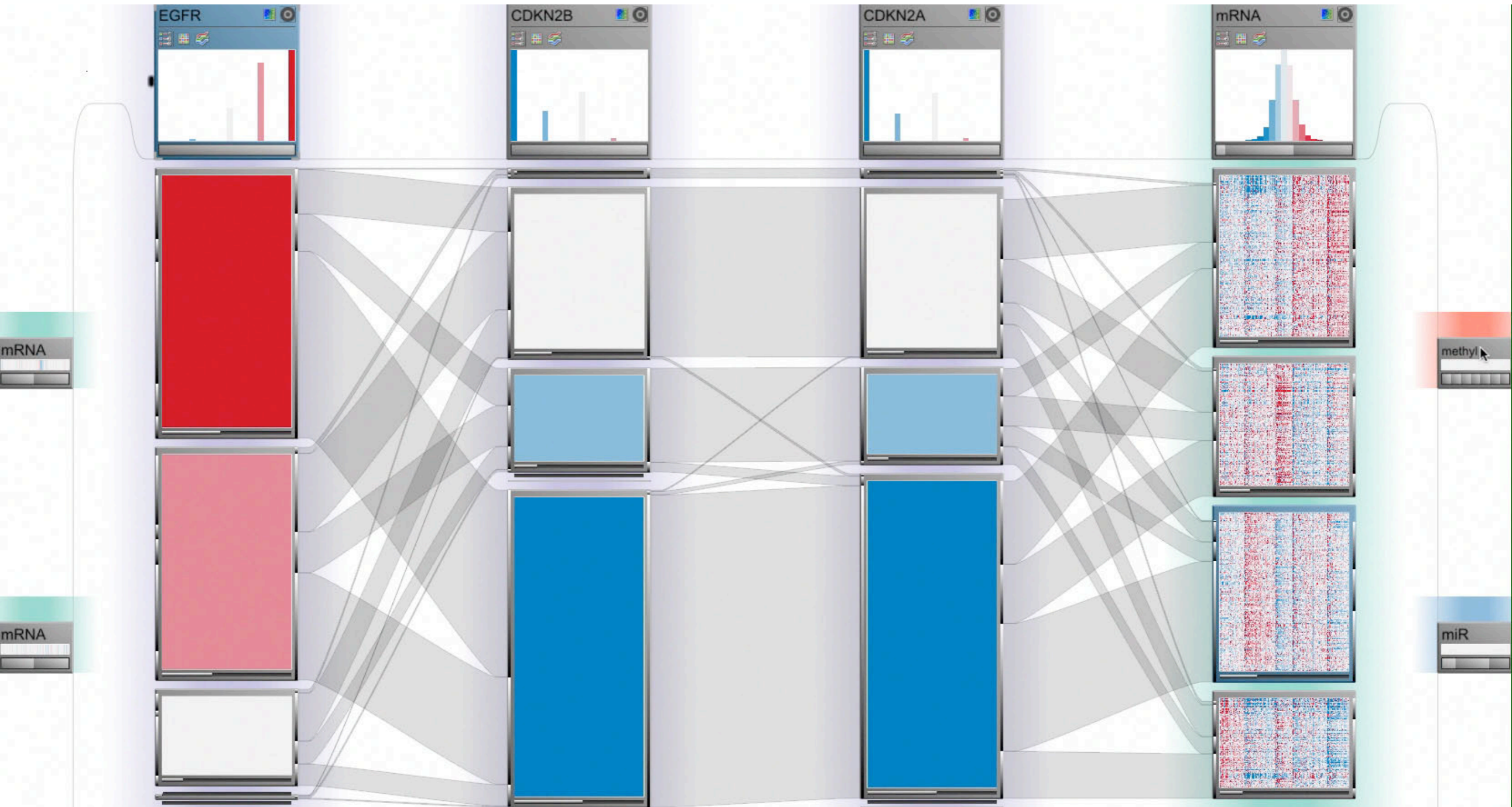
mRNA + Copy Number



mRNA + Copy Number



mRNA + Copy Number + miR + methylation





Mutation Data

Clinical Data

External Classifications

Multivariate Data

Batch Information

mRNA

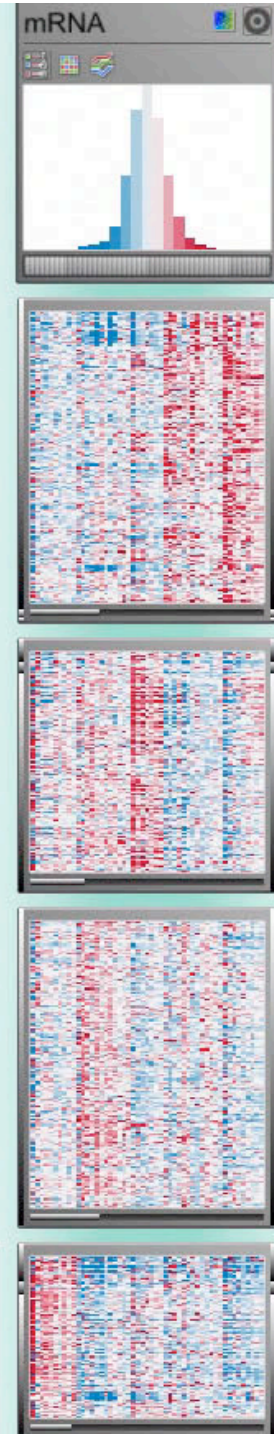
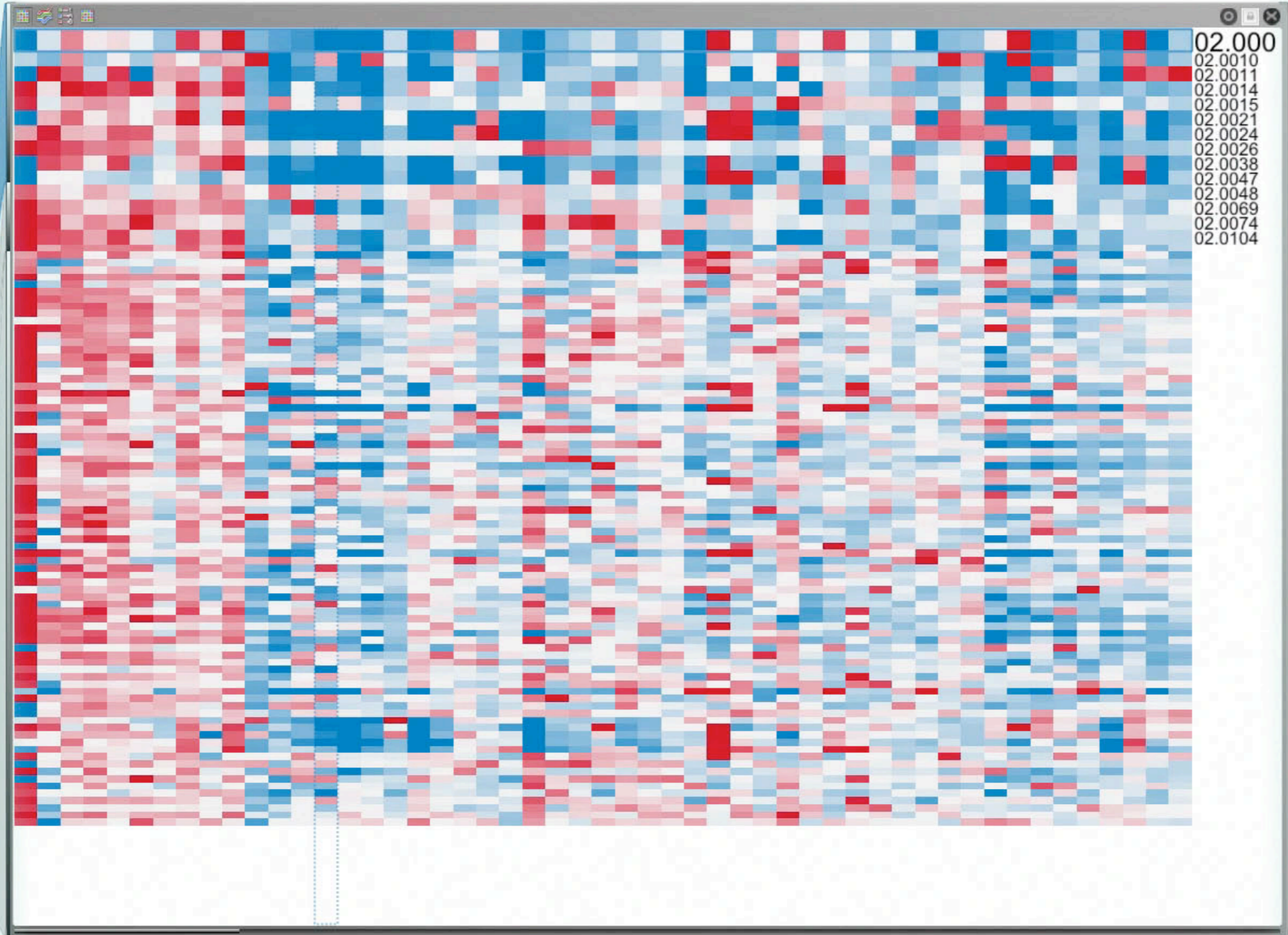
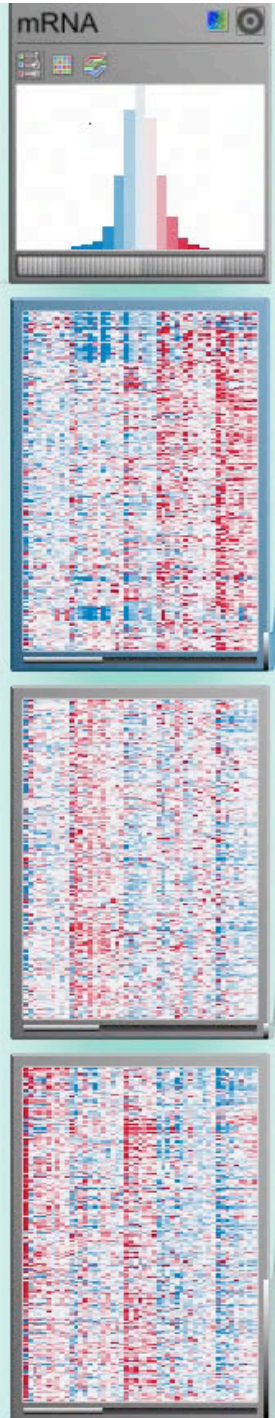
mRNA

mRNA

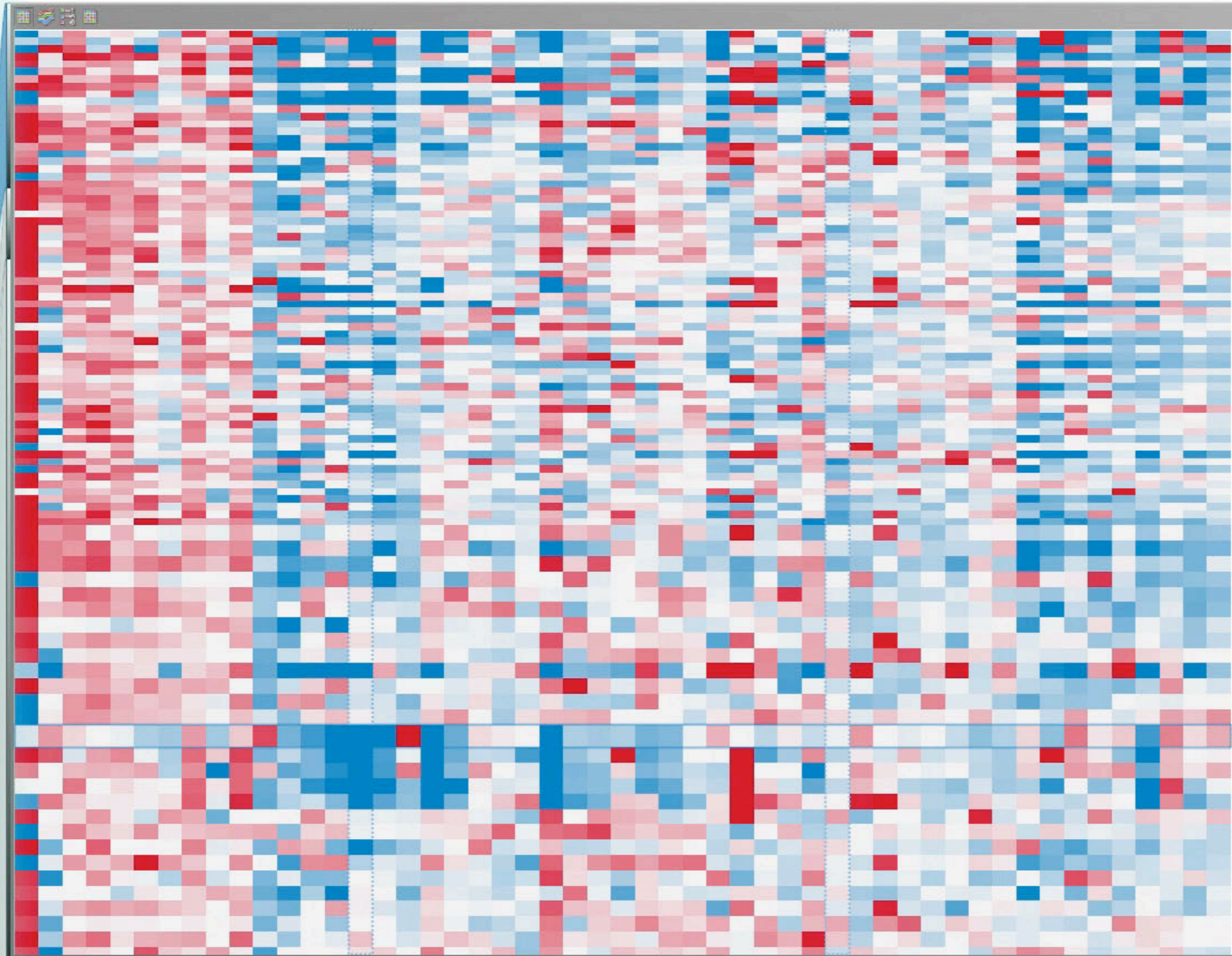
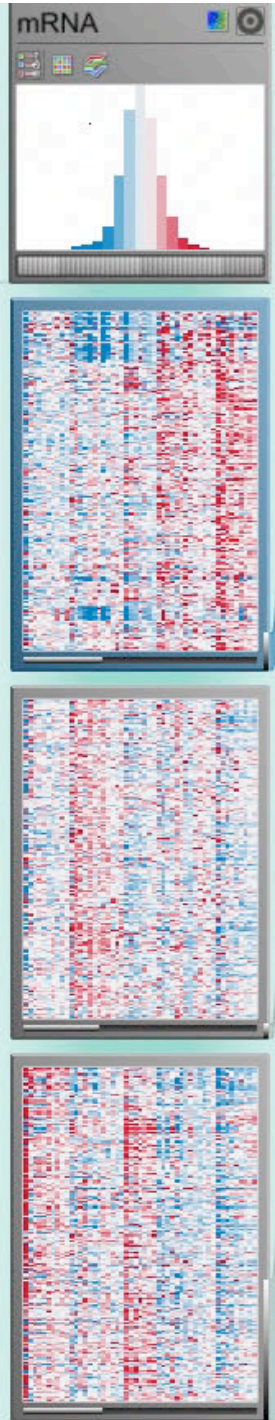
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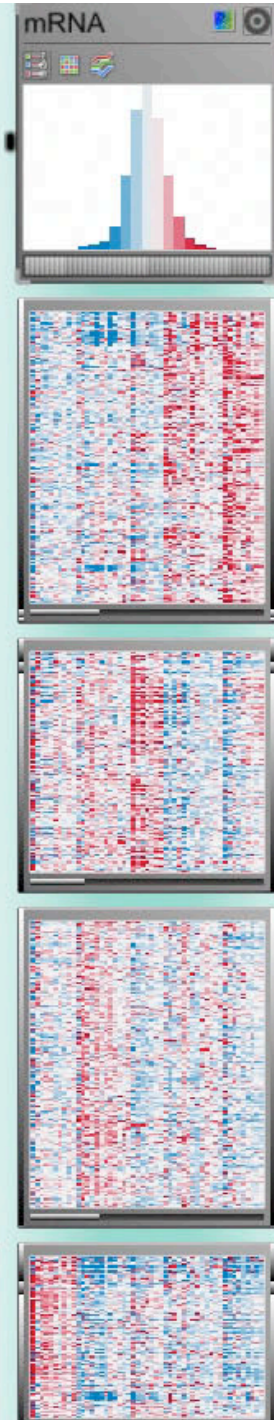
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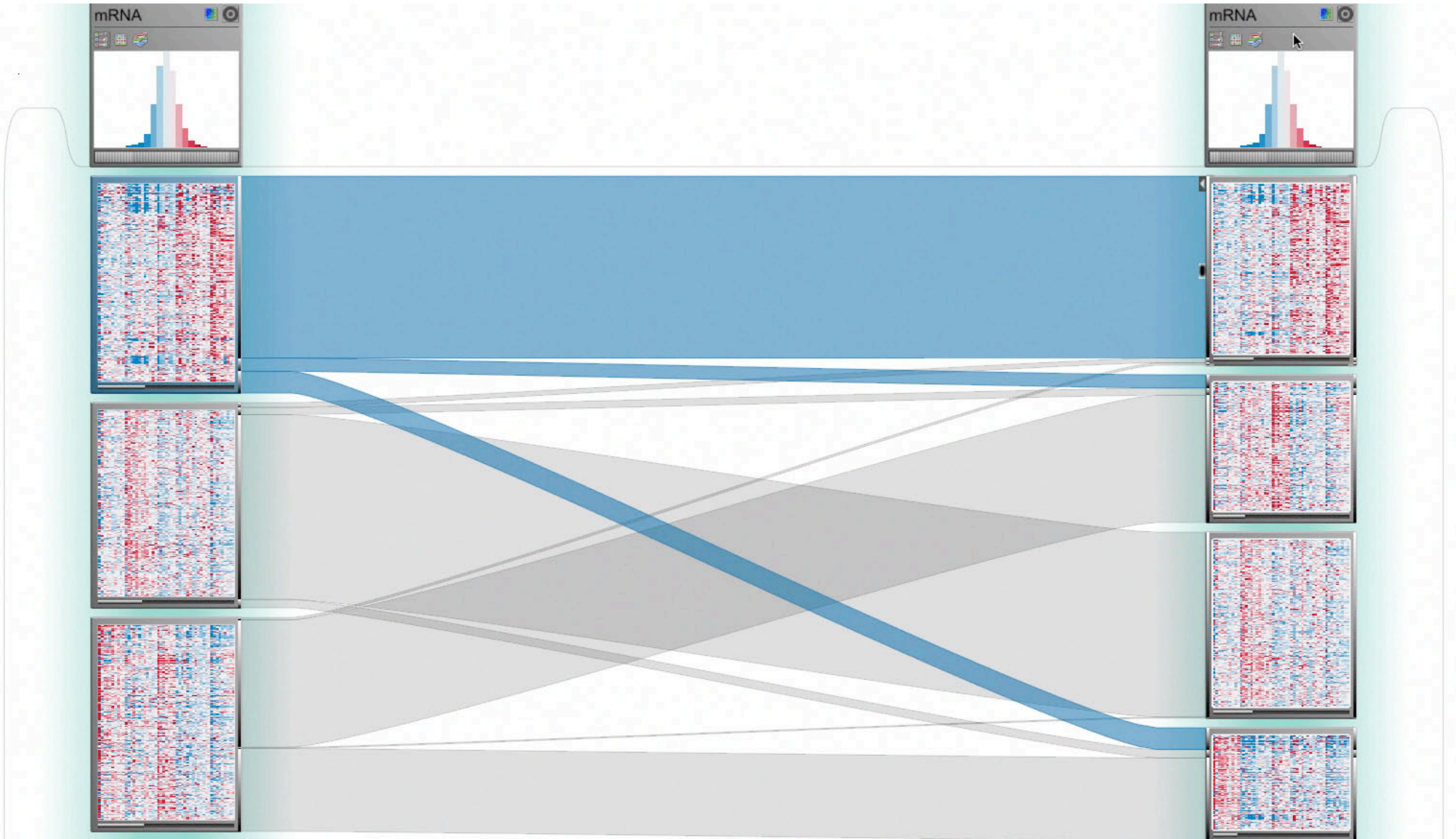
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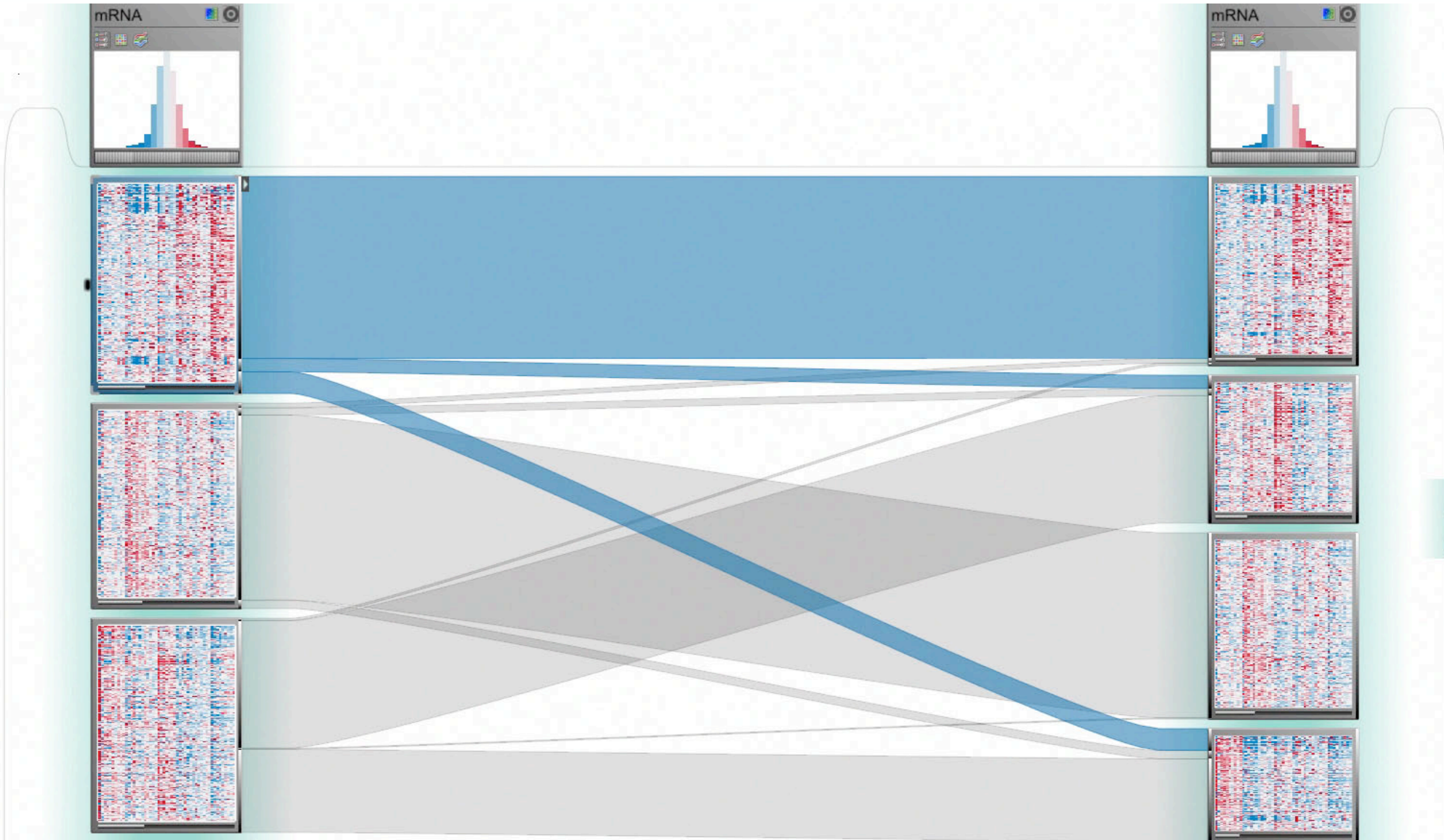
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76.6191



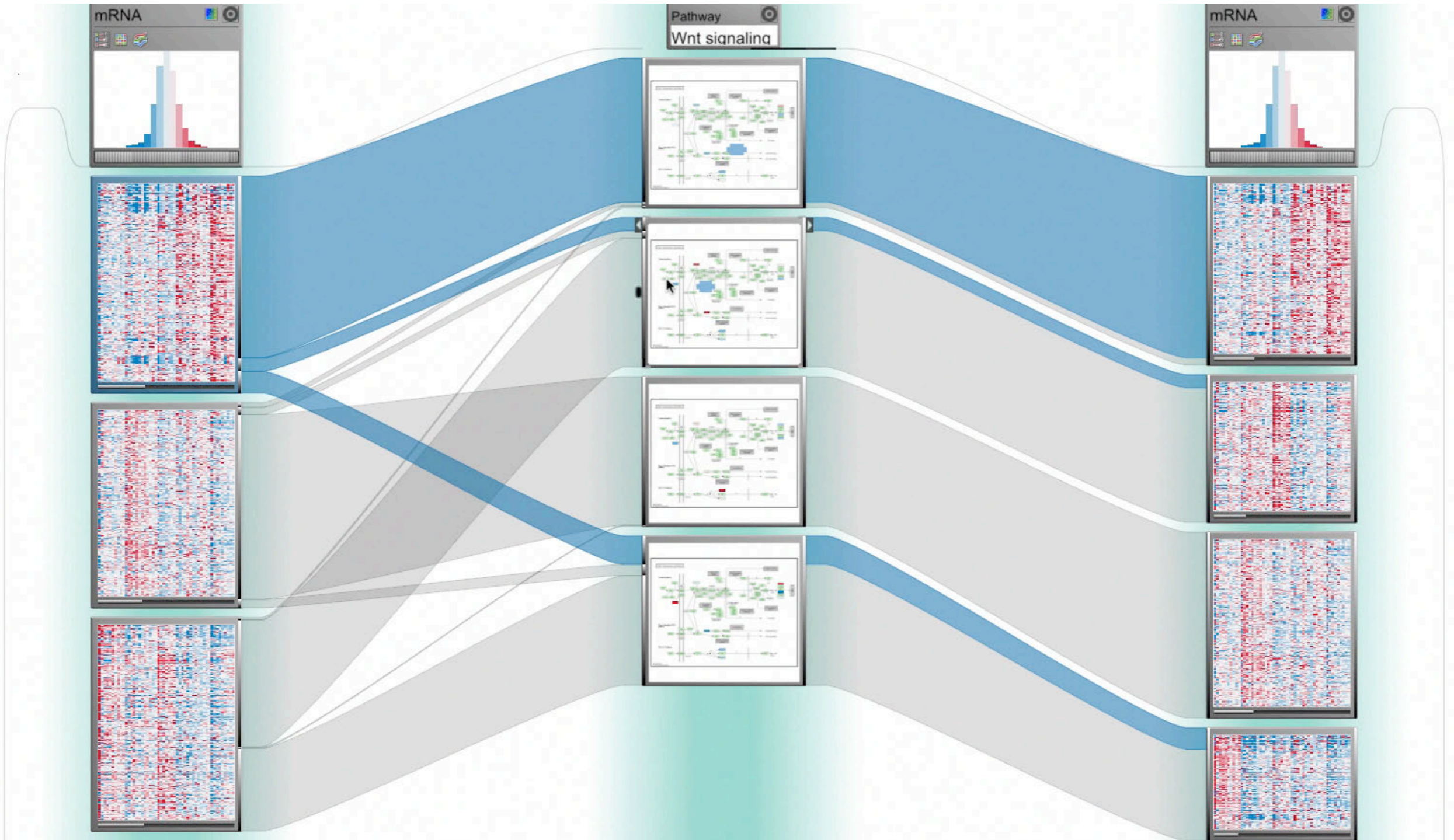
mRNA + pathways



mRNA + pathways

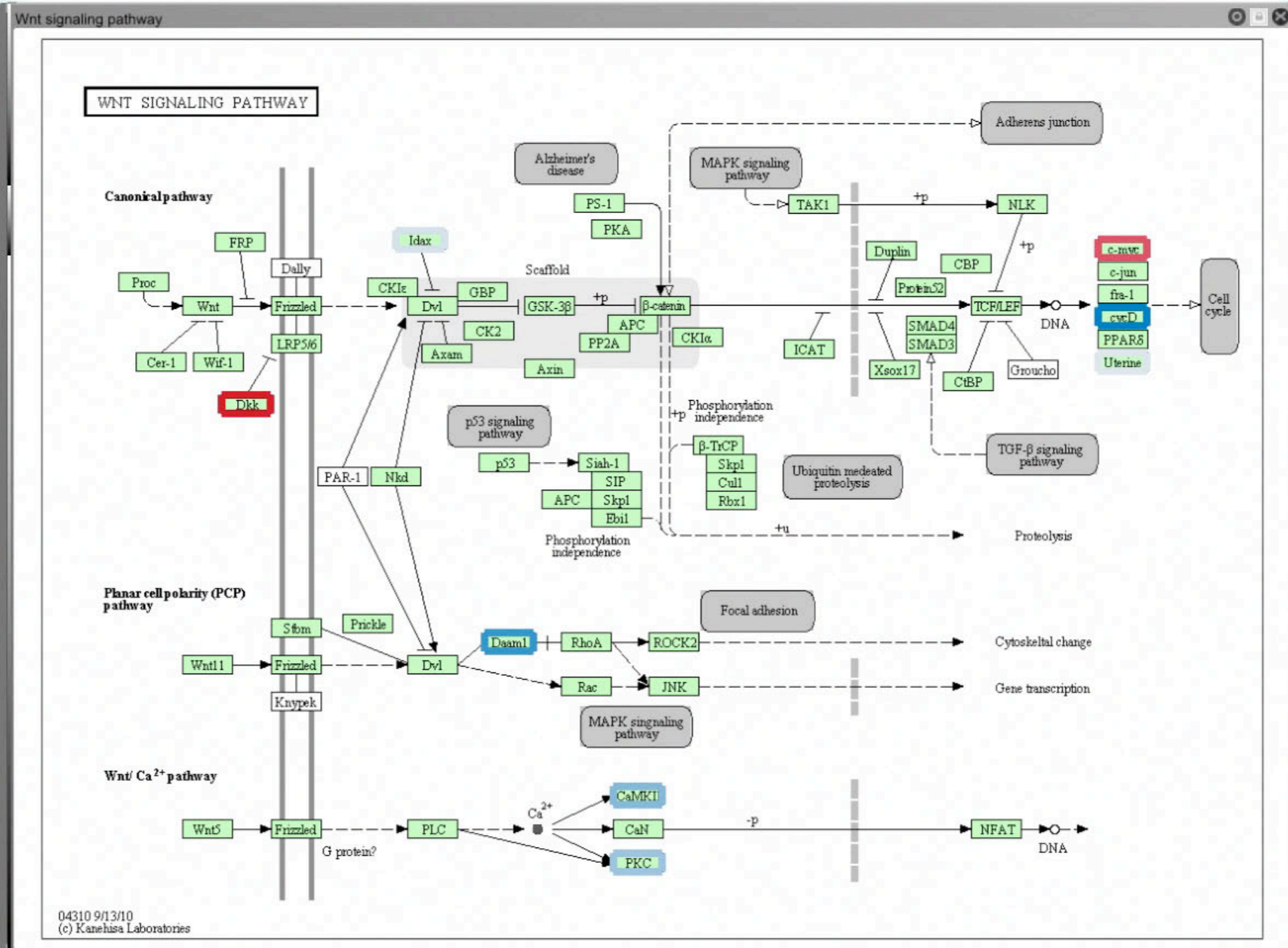
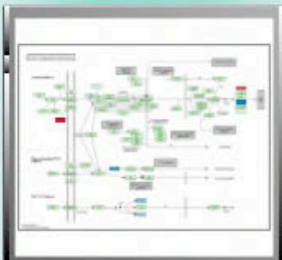
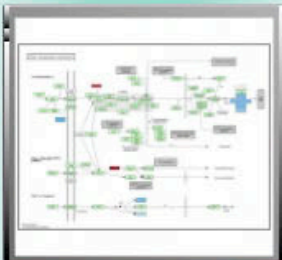


mRNA + pathways



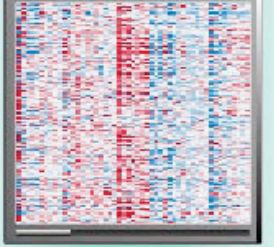
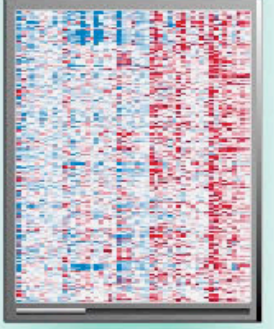
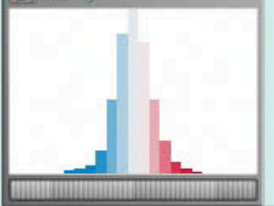
mRNA + pathways

Pathway
Wnt signaling



04310 9/13/10
(c) Kanehisa Laboratories

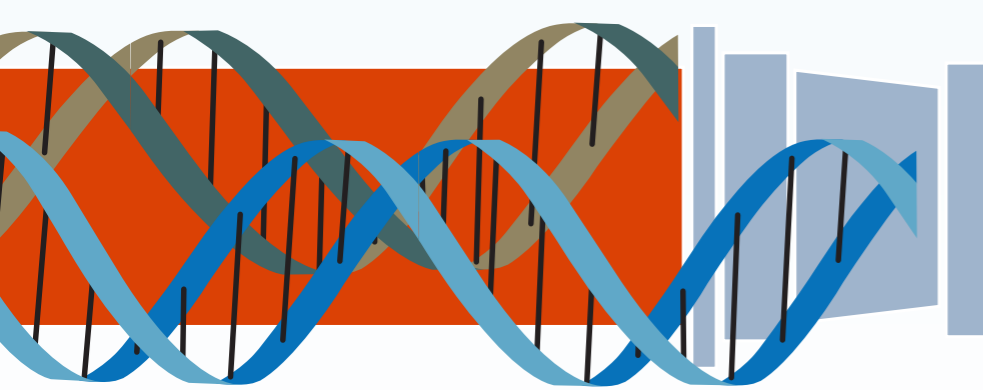
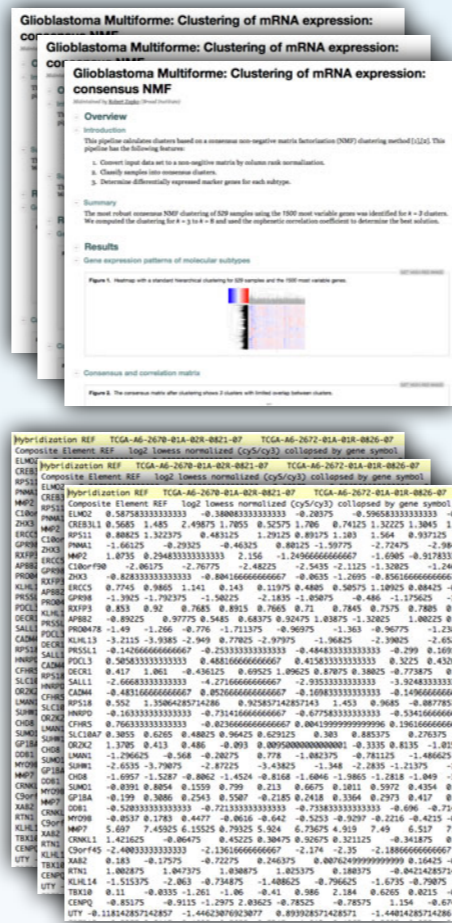
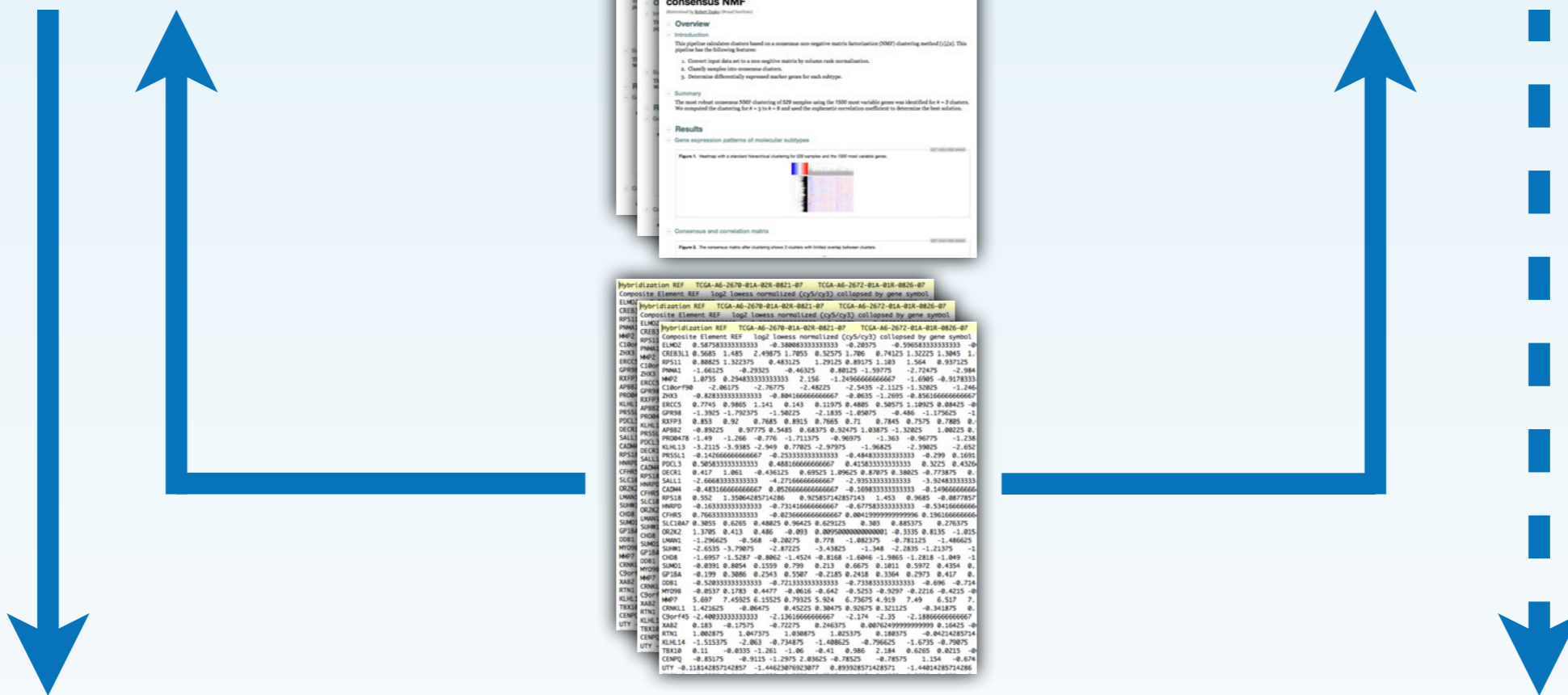
mRNA



mRNA + pathways







FIREHOSE

Broad GDAC



<http://j.mp/caleydo>

Thank you!

nils@hms.harvard.edu

<http://gdac.broadinstitute.org> | *Firehose Analysis Pipeline*

<http://www.caleydo.org> | *Caleydo Visualization Framework*

