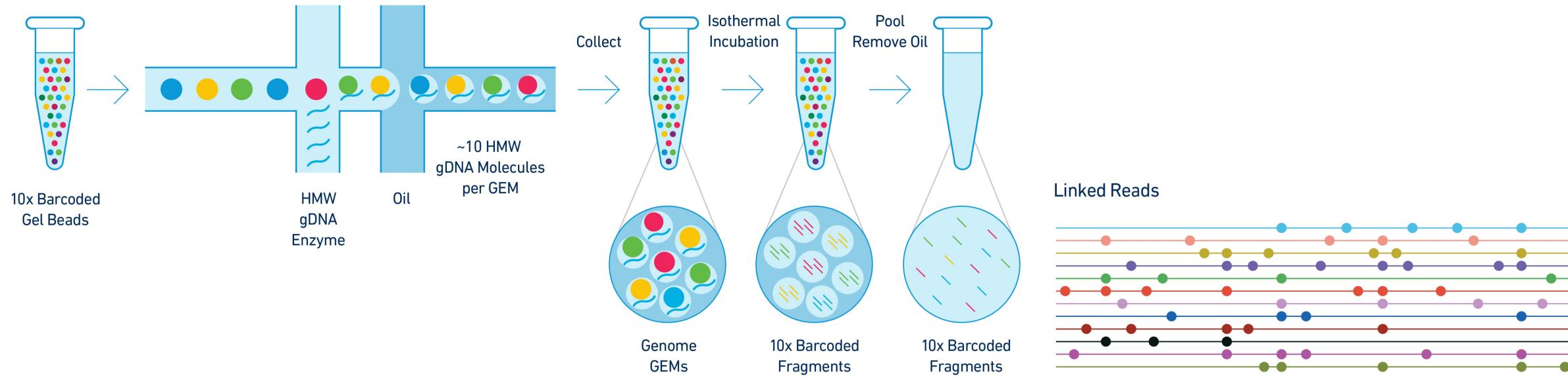


Webinar Outline

- Overview of Loupe
- Visualizing simple events
- Deriving complex events

Linked Read Datatype



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Support > Genome & Exome > Software

SEARCH CONTACT SUPPORT

SOFTWARE > VISUALIZATION

What is Loupe?

System Requirements
Downloads
Installation
Getting Started
Summary View
Run Alerts
Haplotype Browser
Structural Variants
Linked-Reads
Phase Blocks
Application Examples
WGS vs WES
NA12878 Deletion
Phasing BRCA1/BRCA2
NPM1-ALK Gene Fusion

What is Loupe?

Loupe is a genome browser designed to visualize the Linked-Read data produced by the 10x Chromium Platform. Loupe is named for a [jeweler's loupe](#), which is used to inspect gems.

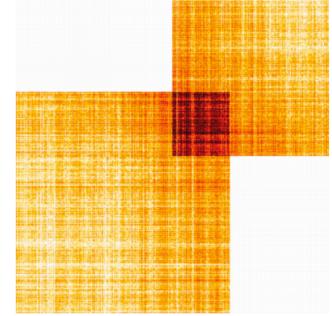
If your question is not answered here, please email us at: support@10xgenomics.com

10x Chromium	Sequencer	10x Long Ranger	10x Loupe
~1 ng DNA	Barcoding & Library Construction	Sequence genome	Pipelines

Loupe is a desktop application for Windows, Mac, and Linux. It loads the `.loupe` files produced by the Long Ranger pipeline. Its features include:

Application Note

10X GENOMICS®



CHROMIUM™
Structural Variant Analysis
with Linked-Reads

[10xGenomics.com/products/#genome](https://10xgenomics.com/products/#genome)

<https://www.10xgenomics.com/application-notes/>

<https://support.10xgenomics.com/genome-exome/software/visualization/latest/what-is-loupe>

Loupe Visualization Views:

Loupe · Sample 31036 · Whole Genome · VV2.0 Strip8-58 FL

SUMMARY HAPLOTYPES STRUCTURAL VARIANTS LINKED-READS Search by gene name or locus

Performance statistics

Barcode overlap evidence

Phasing data

Linked-Read visualization

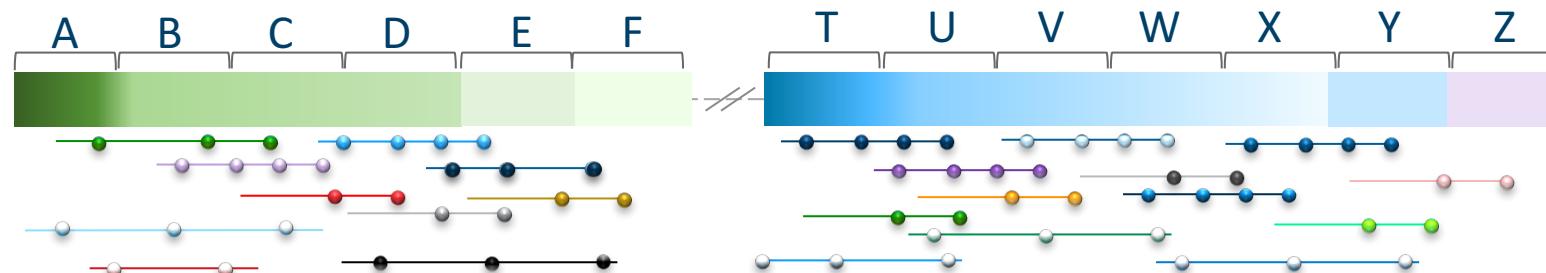
The image shows a screenshot of the Loupe visualization interface. At the top, there's a header bar with the 10X Genomics logo, the sample name "Loupe · Sample 31036 · Whole Genome · VV2.0 Strip8-58 FL", and a search bar. Below the header are tabs for "SUMMARY", "HAPLOTYPES", "STRUCTURAL VARIANTS", and "LINKED-READS". Four blue callout boxes with white text are overlaid on the interface: "Performance statistics" (top left), "Barcode overlap evidence" (top right), "Phasing data" (bottom left), and "Linked-Read visualization" (bottom right). Blue lines connect each callout box to its corresponding element in the Loupe interface.

Visualizing a Simple Event

Deletion

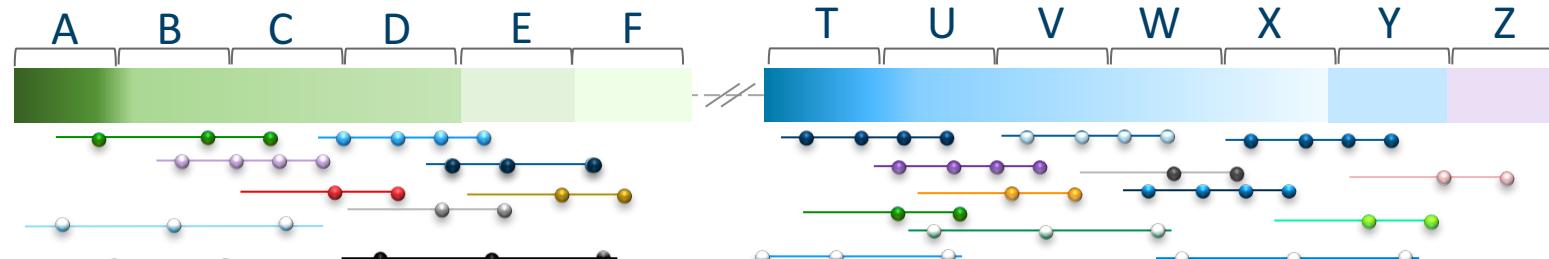
Deletions: Linked Reads

SAMPLE
WITHOUT SV

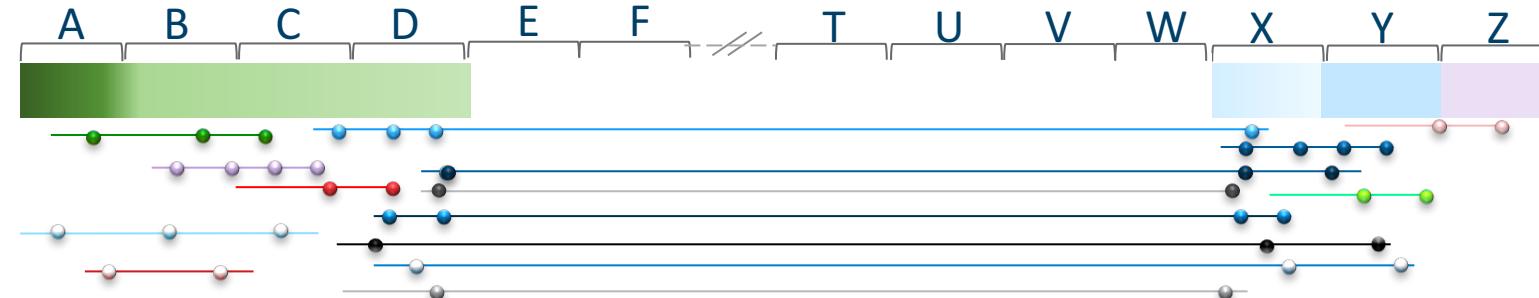


Deletions: Linked Reads

SAMPLE
WITHOUT SV



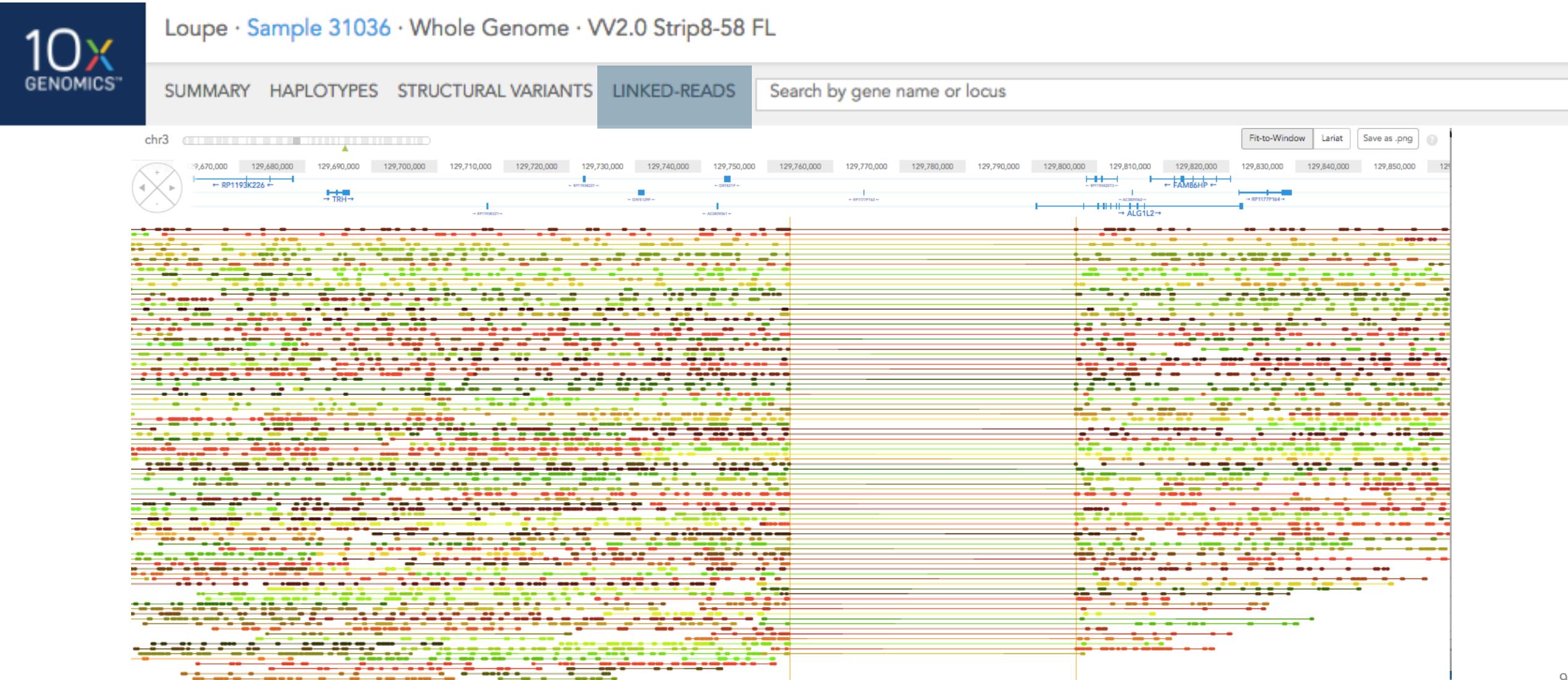
SAMPLE
WITH SV



Deletions: Linked Reads

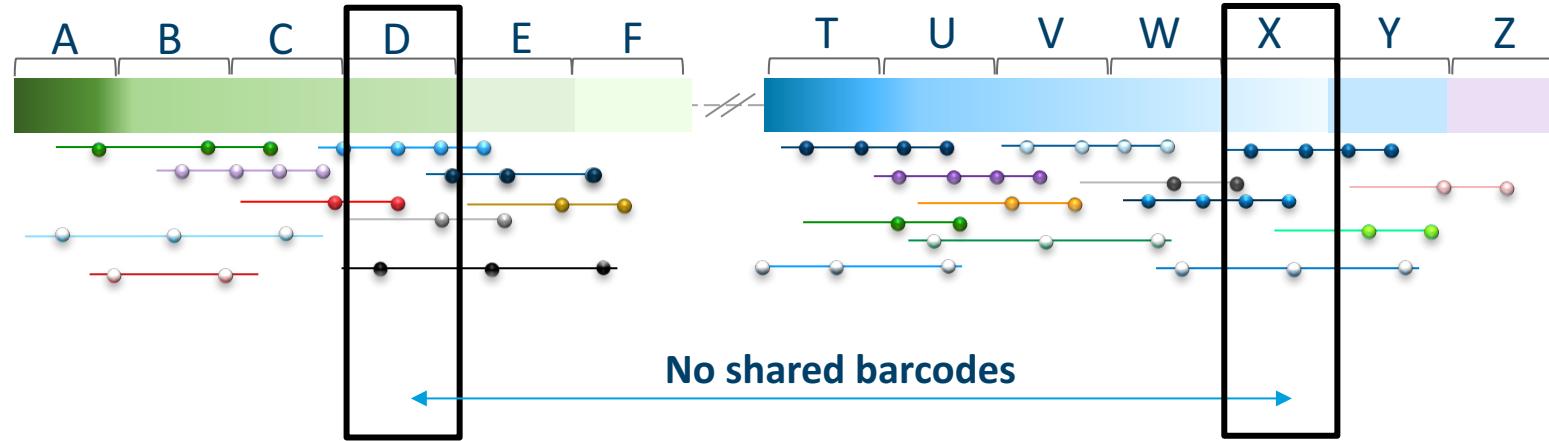


Deletions: Linked Reads



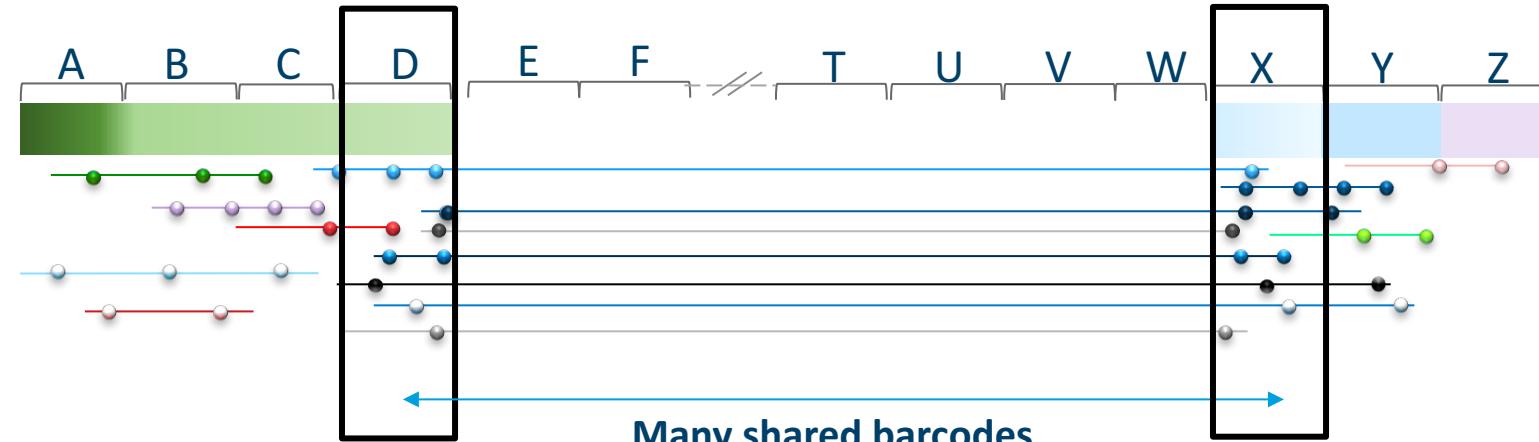
Deletions: Barcode Overlap

SAMPLE
WITHOUT SV



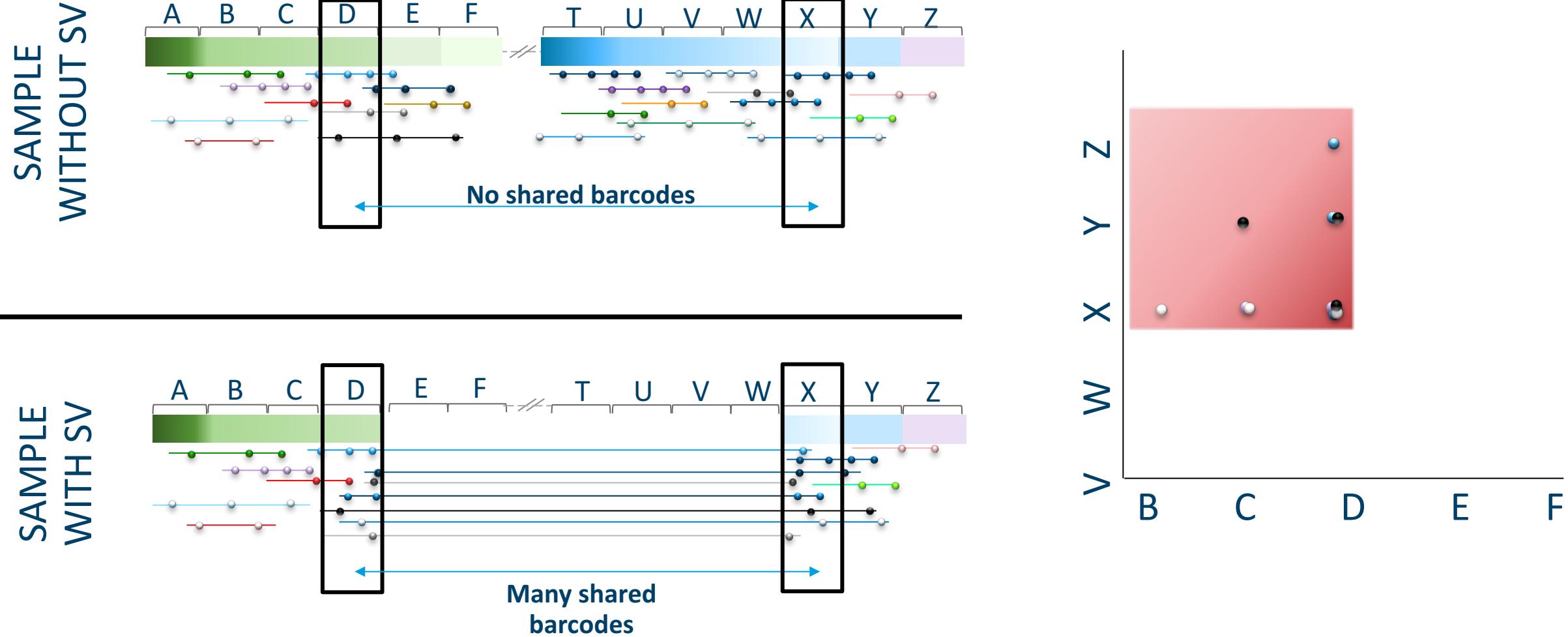
No shared barcodes

SAMPLE
WITH SV

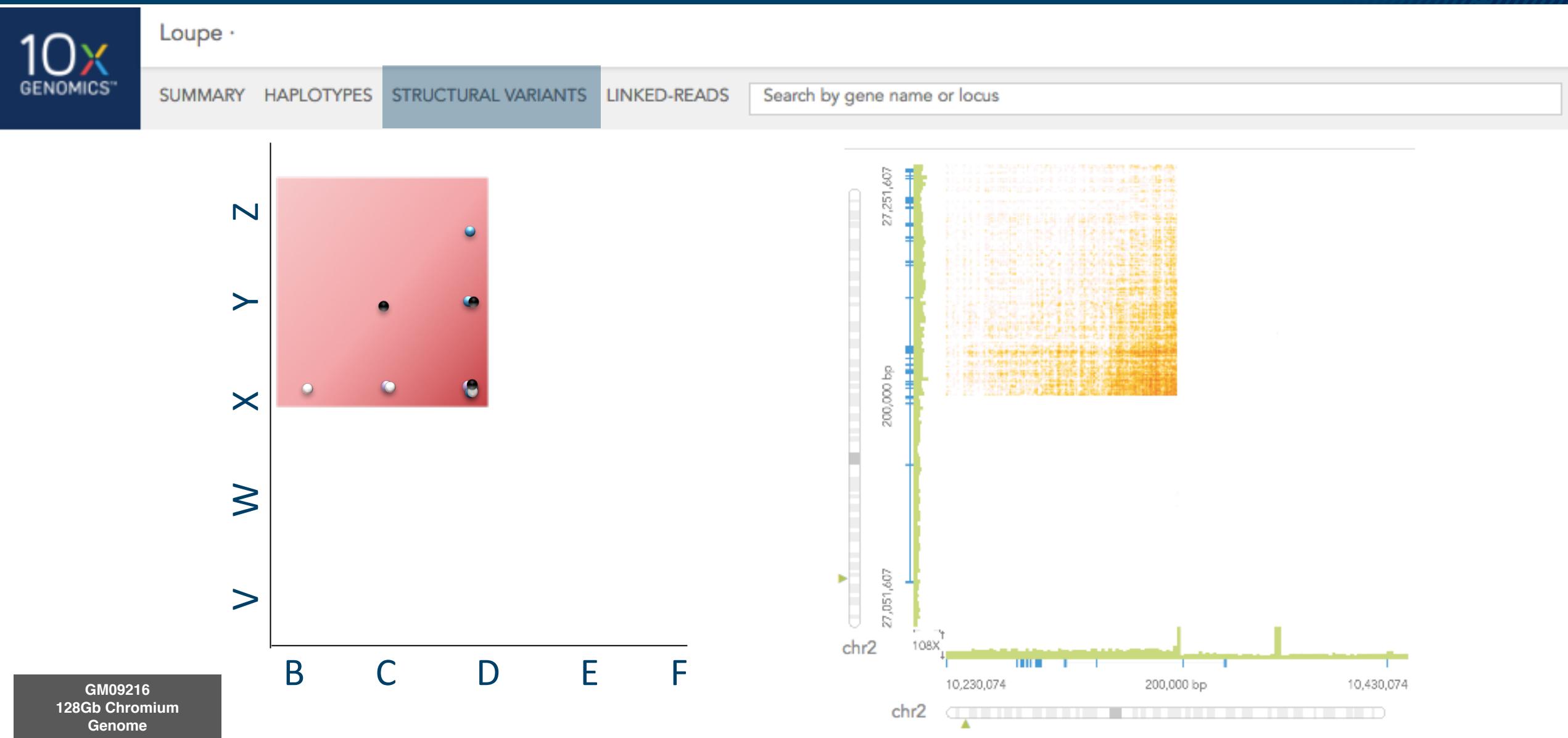


Many shared barcodes

Deletions: Barcode Overlap



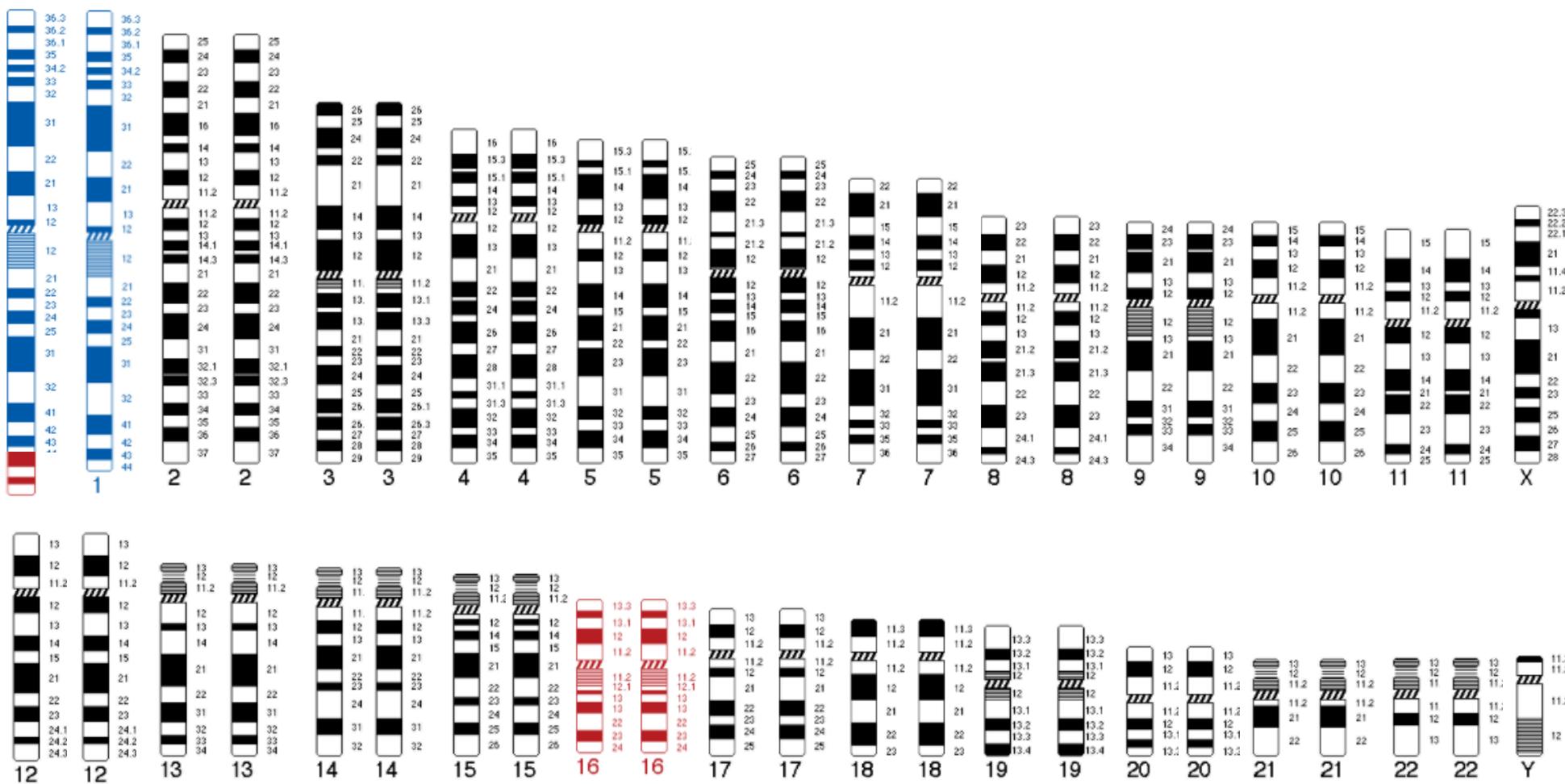
Deletions: Barcode Overlap



Deriving a Complex Event

GM06226: 46,XY,der(1)t(1;16)(q44;p12)

GM06226: 46,XY,der(1)t(1;16)(q44;p12)



Structural Variant Call:

1q44

827 1 247,302,436 ZNF124
16 21,887,894 NPIPBP4

16p12

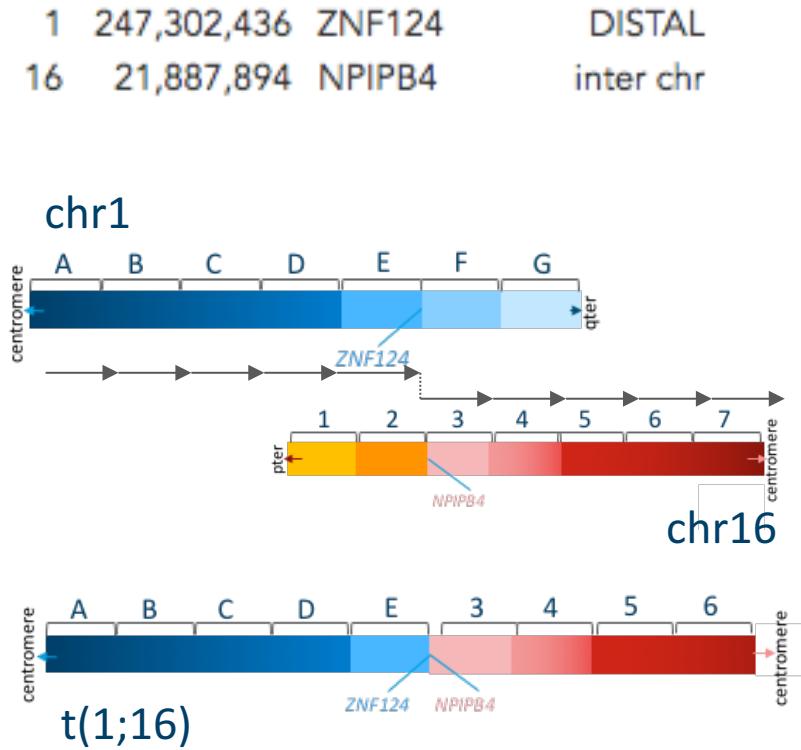
DISTAL
inter chr

	qual	chr	position	genes	distance
CALLS					
1326	12	9,553,636	RP11599J...	DISTAL	
	12	31,407,917	RP11627K...		21.9 Mb
827	1	247,302,436	ZNF124	DISTAL	
	16	21,887,894	NPIPBP4	inter chr	
513	11	76,903,842	MYO7A_CH...	DISTAL	
	19	14,706,843	CLEC17A	inter chr	
377	20	56,549,874		DISTAL	
	22	20,150,116		inter chr	
313	12	17,922,964		INV	
	12	18,011,964			89.0 kb
262	8	140,510,389	-	INV	
	8	140,612,960	KCNK9		103 kb
186	1	152,555,542		DEL	
	1	152,587,728			32.2 kb
180	10	22,889,014	PIP4K2A	DISTAL	
	19	21,907,105	ZNF100_C...	inter chr	
178	6	168,052,097		DUP	
	6	168,087,742			35.6 kb
170	6	67,008,730		DEL	
	6	67,048,901			40.2 kb
156	22	20,150,689	-	DISTAL	
	9	134,839,653	MED27	inter chr	
152	1	72,766,324		DEL	
	1	72,811,861	RPL31P12		45.5 kb
151	2	52,749,663		DEL	
	2	52,785,248	-		35.6 kb
145	16	20,094,747		DUP	
	16	20,175,129	-		80.4 kb
110	2	34,695,829	AC073218...	DEL	
	2	34,736,589	AC073218...		40.8 kb
107	7	54,296,192		INV	
	7	54,386,192	-		90.0 kb
105	22	45,476,135	-	DISTAL	
	4	186,748,592	SORBS2	inter chr	
CANDIDATES					

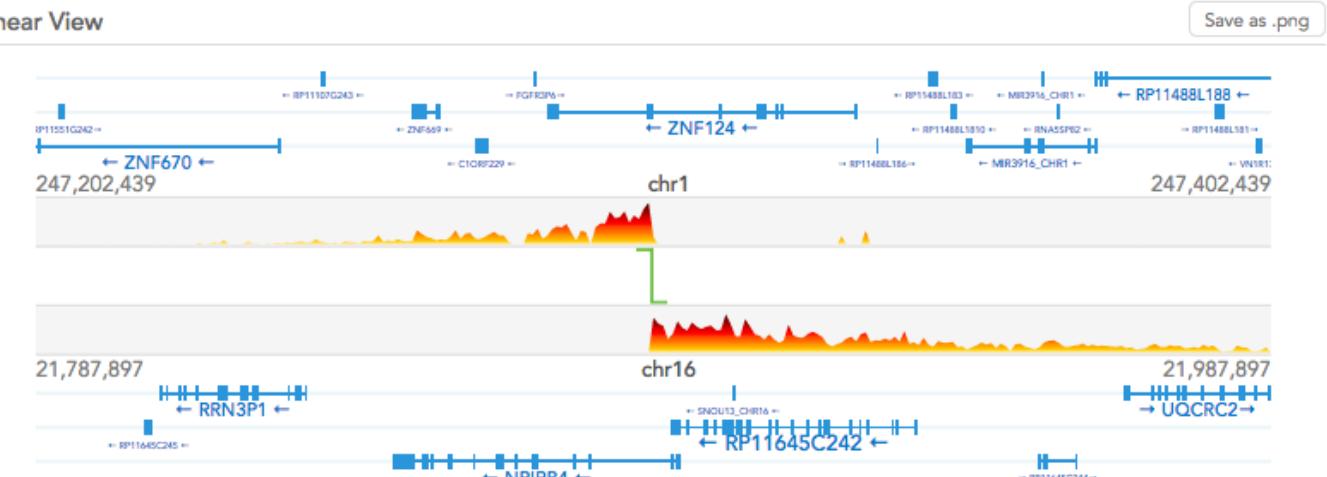


From Call to Structure: Linear View

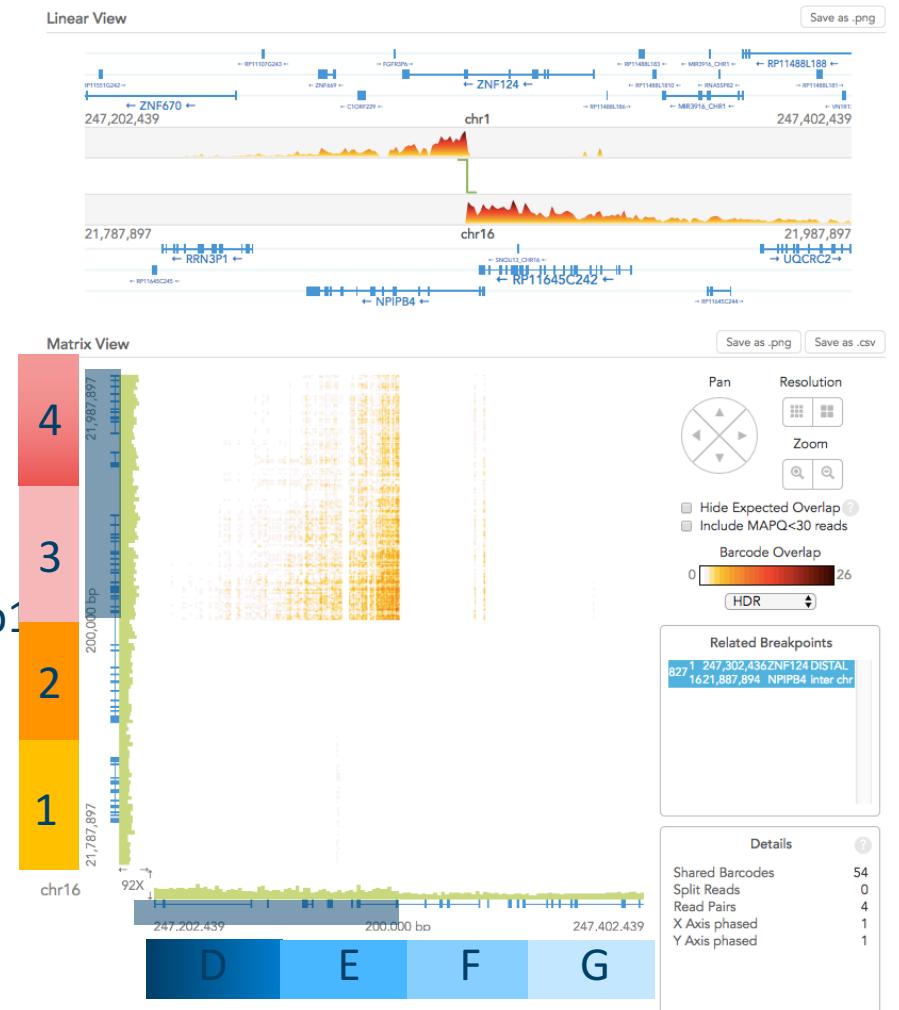
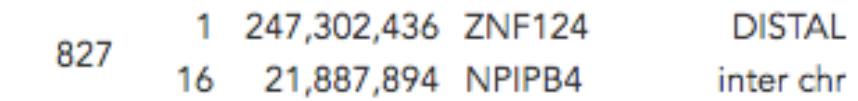
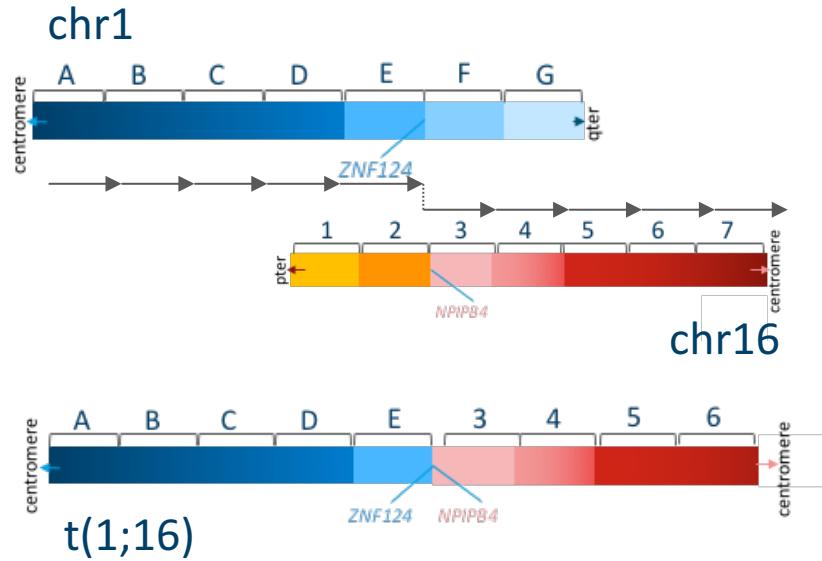
827



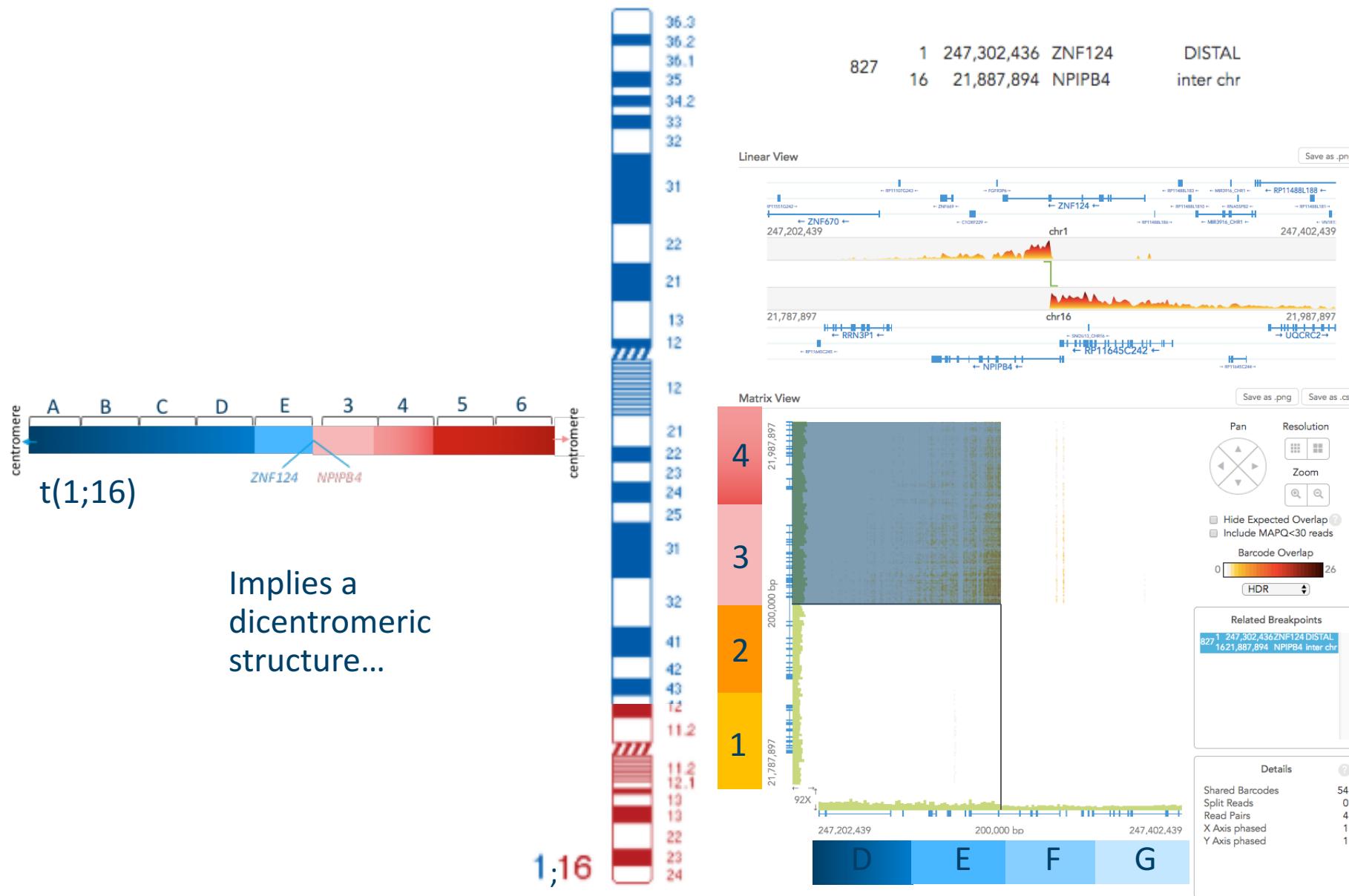
Linear View



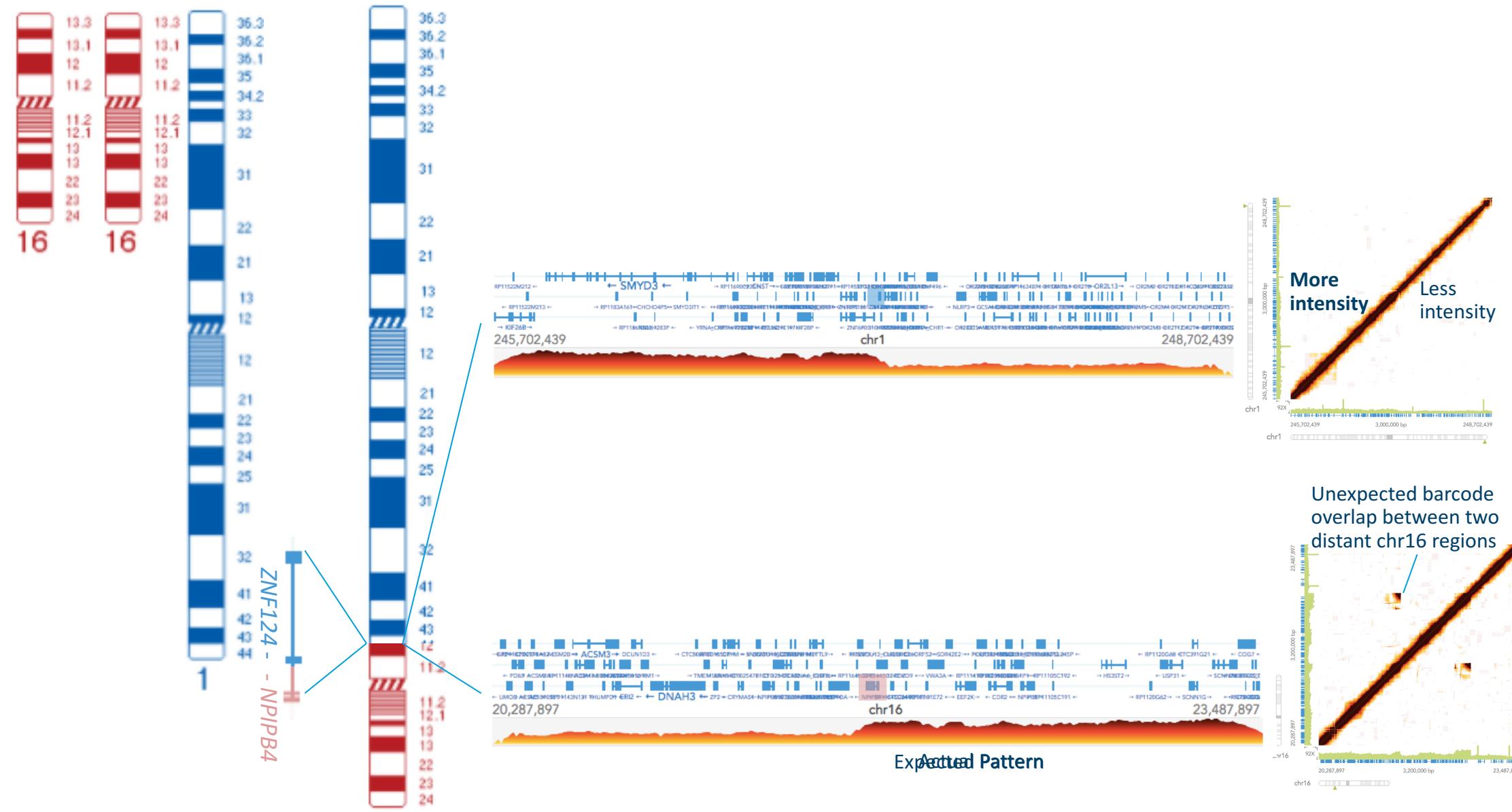
From Call to Structure: Linear View



From Call to Structure: Matrix View

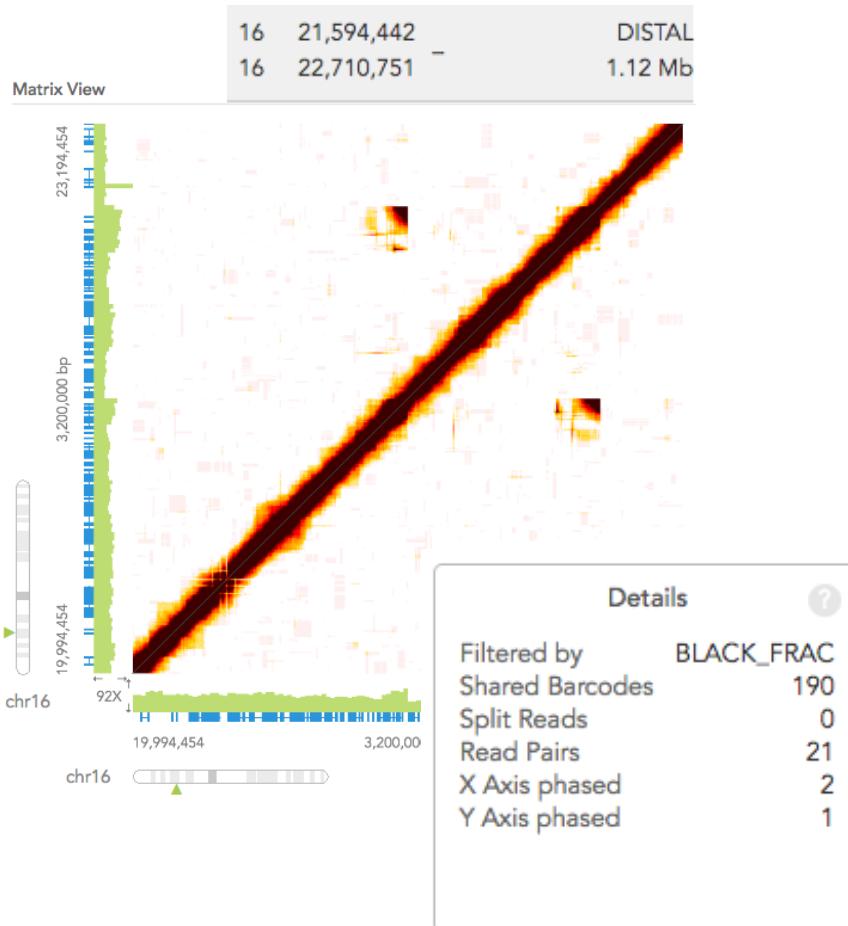


Loupe Self/Self Barcode Overlap Patterns

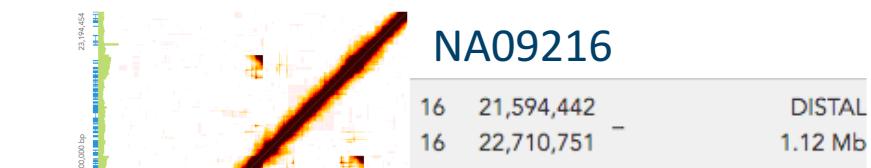


Specificity of Overlap

Test Sample (NA06226)



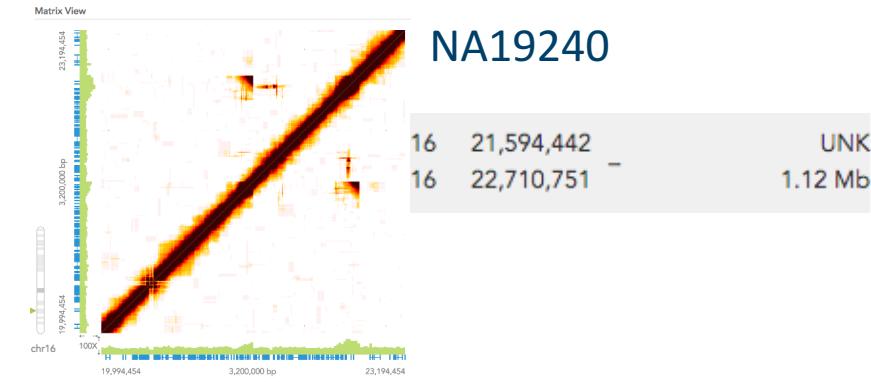
NA09216



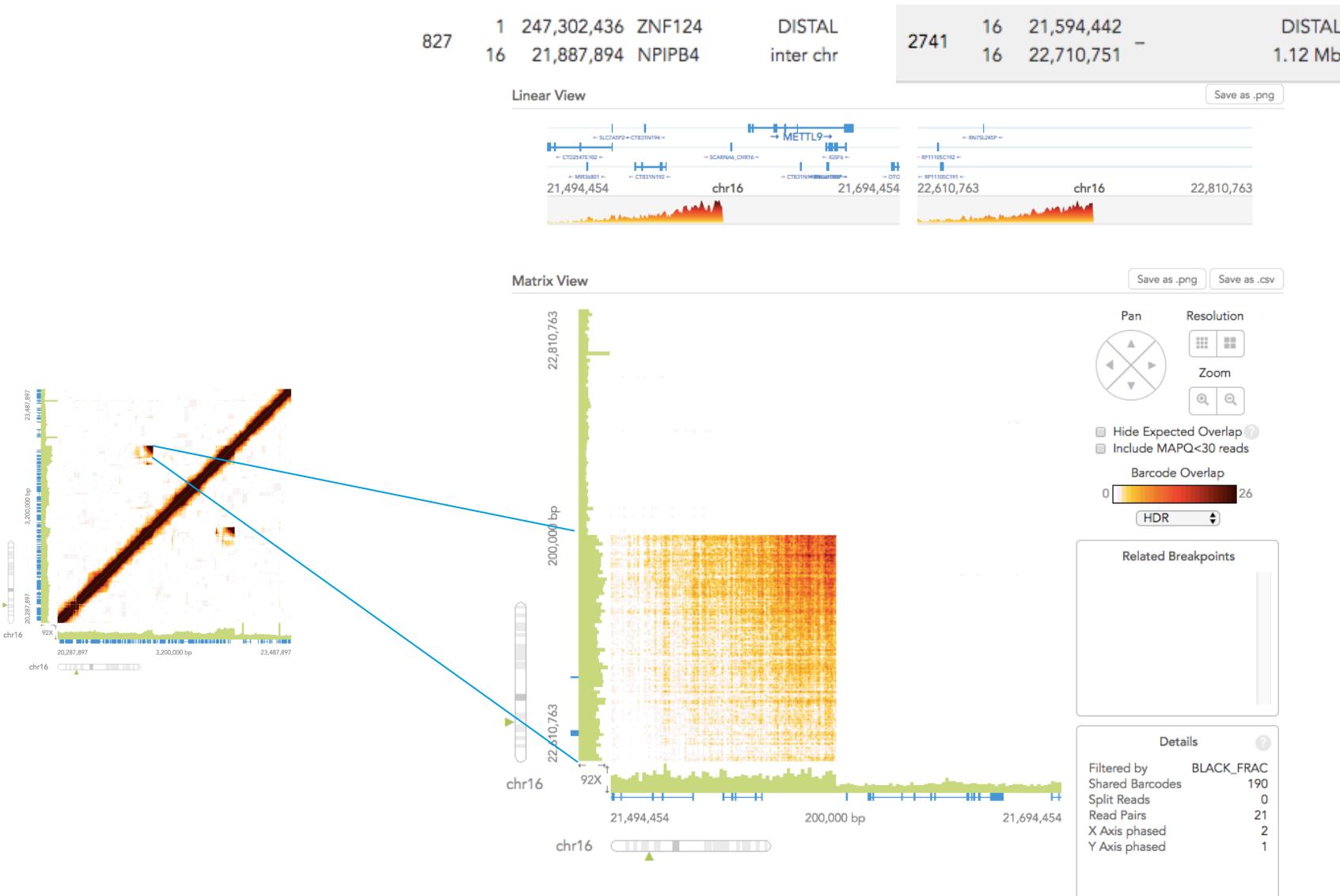
NA12878



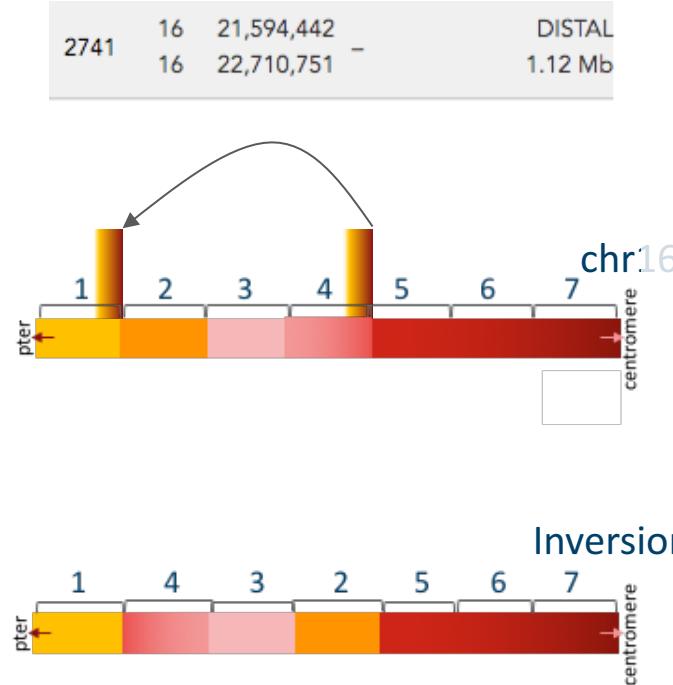
NA19240



What is this signal?



What is this signal?



827

1 247,302,
16 21,887,

Linear View

HG-926

region: HG-926
type: Path Problem
status: Resolved
status_text: none
resolution: GRC Resolved by Experimental Method
resolution_text: The GRCh38 path between components AF001550.1 and AC009021.8 has been replaced with a CHORI-17 pathway, which contains the S2 haplotype and a 1.1Mb inversion.
description: The sequence for this region of the genome represents a mis-assembly or rare variant. New tiling paths are being generated to represent a more common haplotype in this region.
affect_version: GRCh37
fix_version: GRCh39,GRCh38.p10
Location: 21,461,507..22,772,309
Length: 1,310,803

Matrix View

3
2
1

chr16 92

Links & Tools

BLAST Genomic: [NC_000016.9 \(21,461,507..22,772,309\)](#)
FASTA View: [NC_000016.9 \(21,461,507..22,772,309\)](#)
GRC: [HG-926](#)
GenBank View: [NC_000016.9 \(21,461,507..22,772,309\)](#)

DISTAL
1.12 Mb

as .png

63

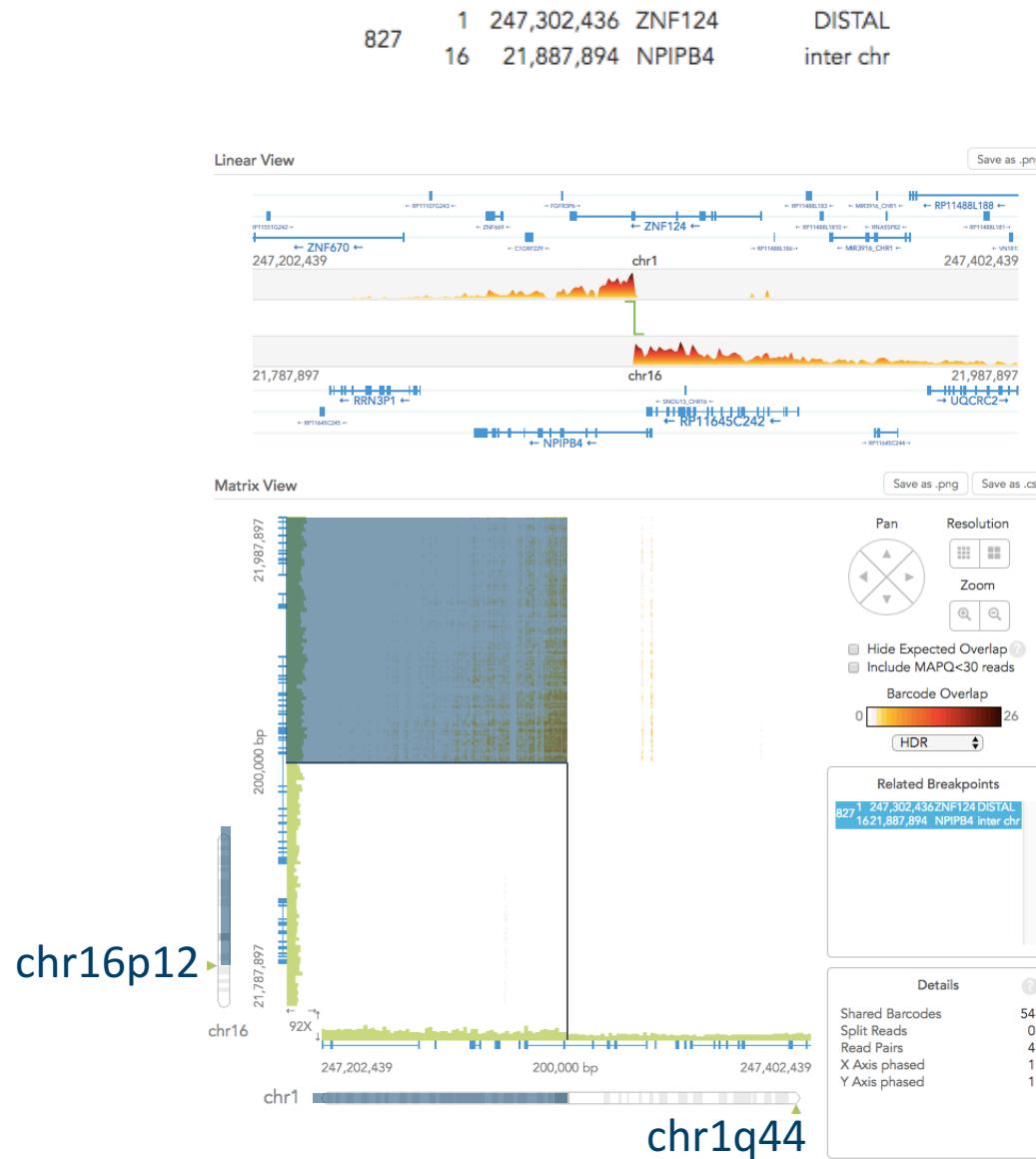
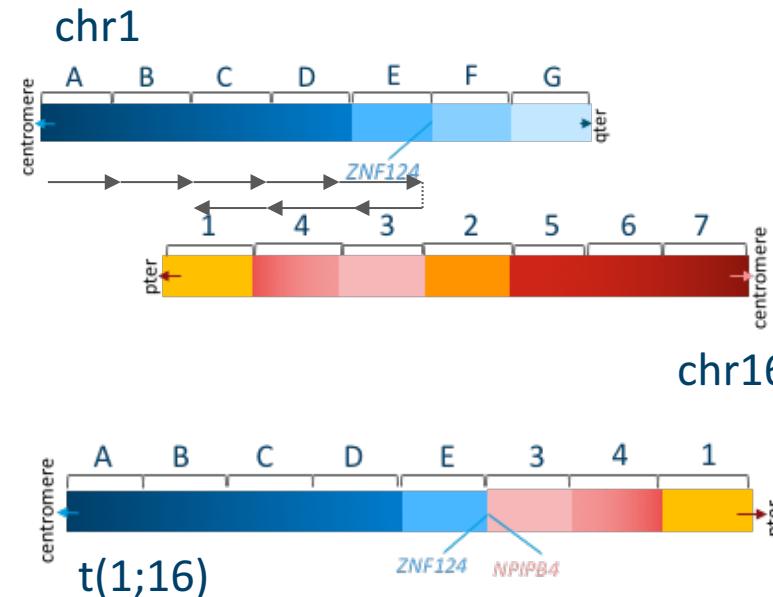
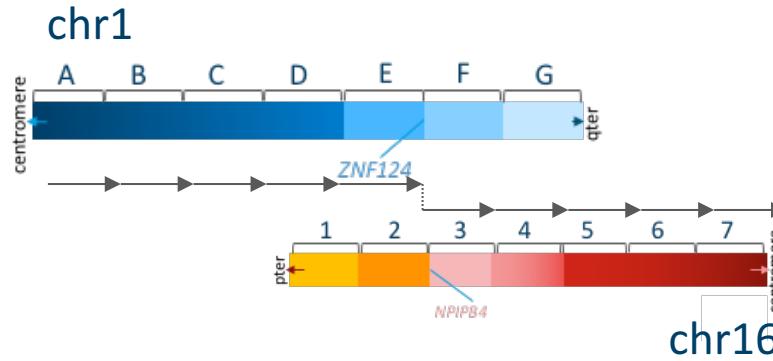
as .csv

26

FRAC
190
0
21
2
1

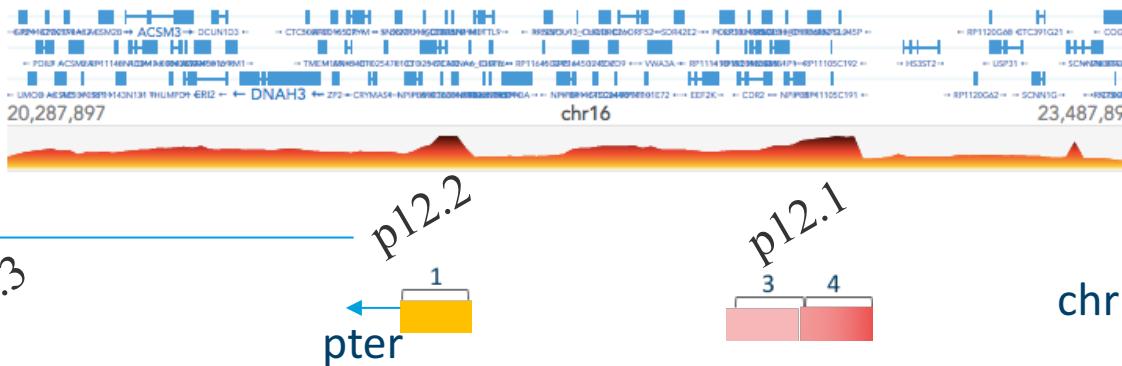
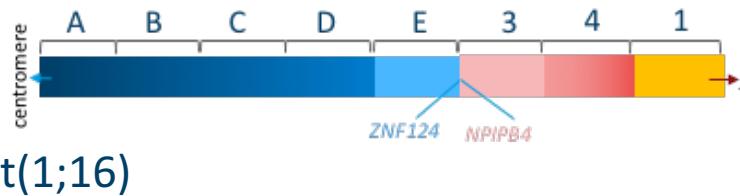
Y Axis phased

From Call to Structure: Linear View

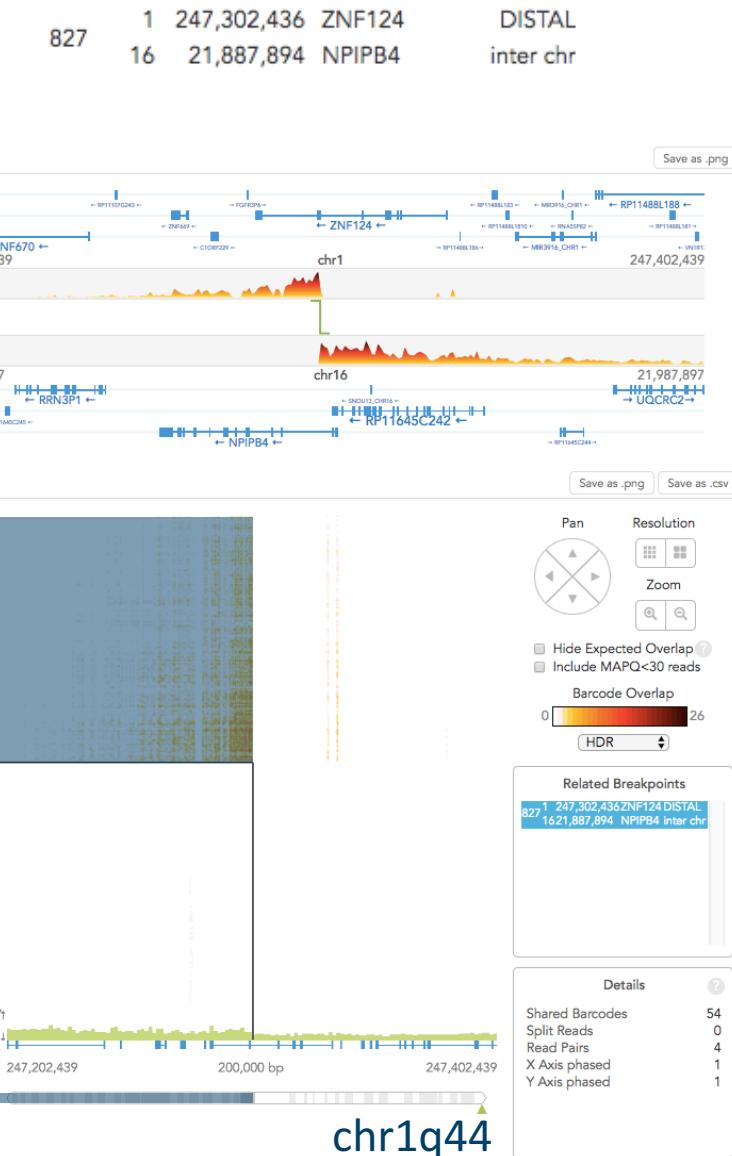
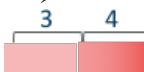


From Call to Structure: Linear View

46,XY,der(1)t(1;16)(q44;p12)mat.arr
 1q44(245373155-247190999)x1,
 16p13.3p12.2(25815-21297471)x3,
 16p12.1(21853546-22612021)x3



chr16p12



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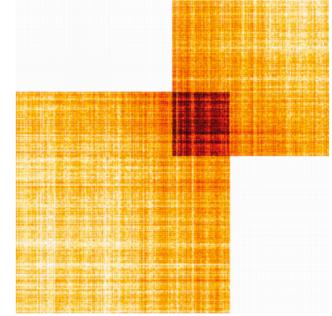
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<https://support.10xgenomics.com/genome-exome/software/visualization/latest/what-is-loupe>