

Comprehensive Genome and Transcriptome Structural Analysis of a Breast Cancer Cell Line using PacBio Long Read Sequencing

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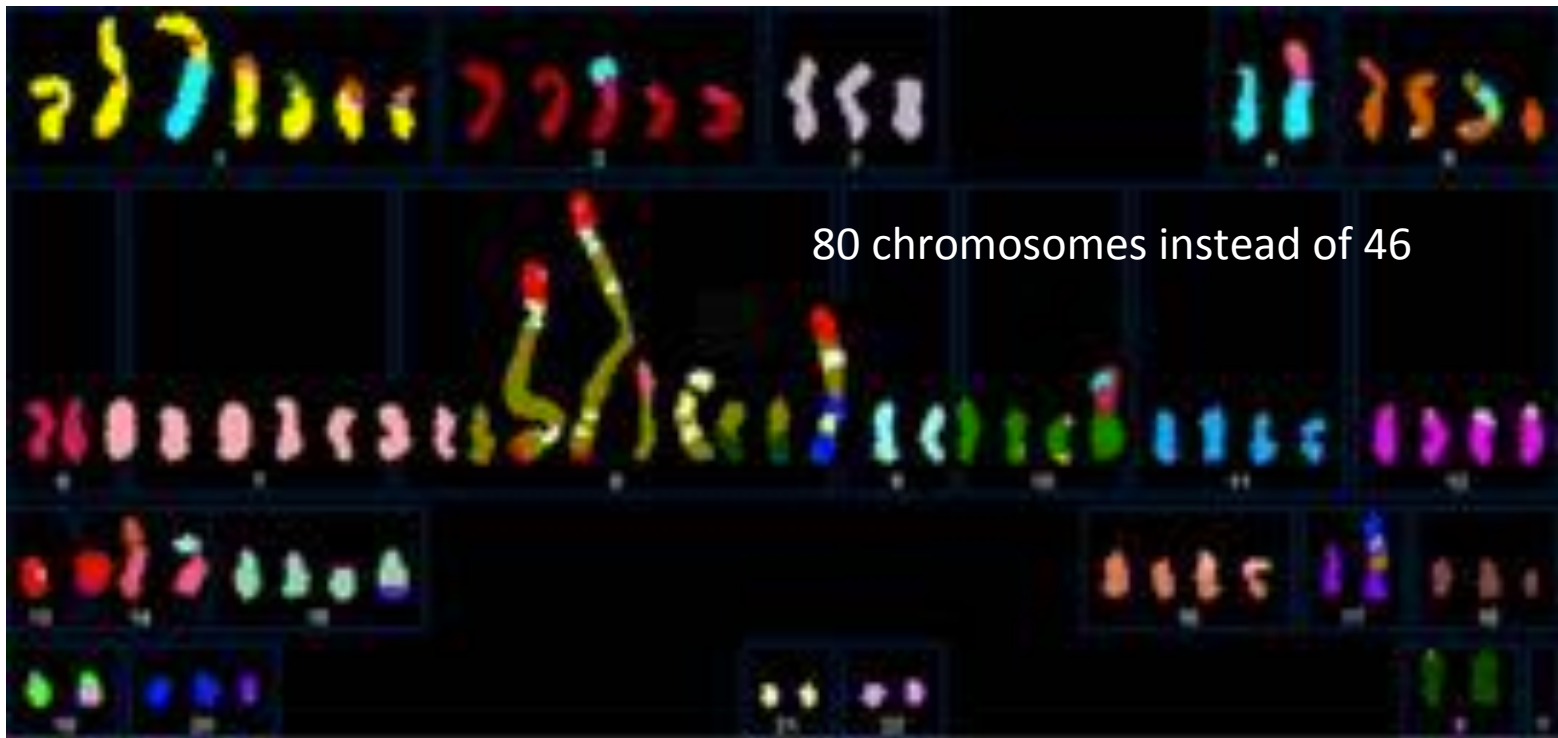
Pacific Biosciences

DNAexus



SK-BR-3

Most commonly used Her2-amplified breast cancer cell line



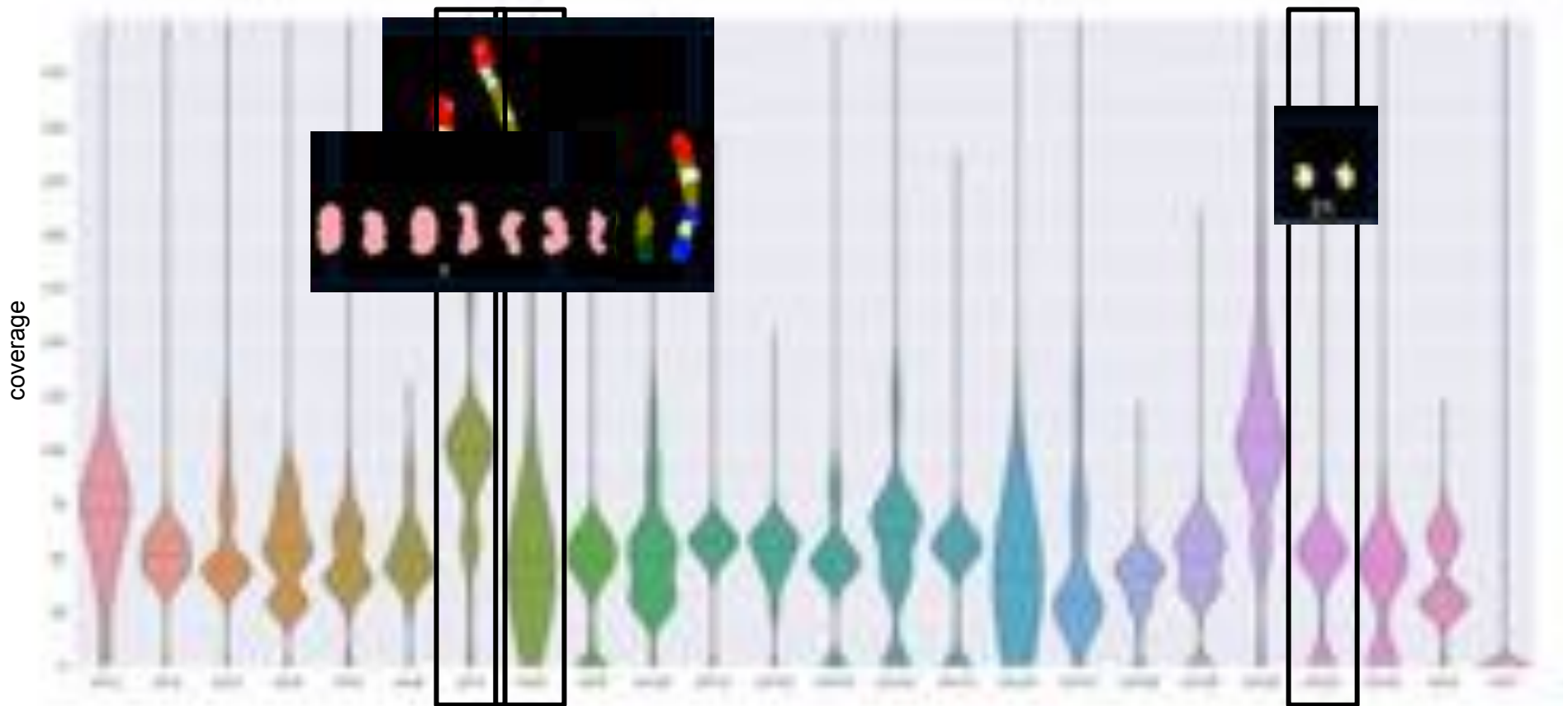
Often used for pre-clinical research on Her2-targeting therapeutics such as Herceptin (Trastuzumab) and resistance to these therapies.

(Davidson et al, 2000)

PacBio long-read DNA sequencing

mean read length: 9 kb
max read length: 71 kb

72X coverage

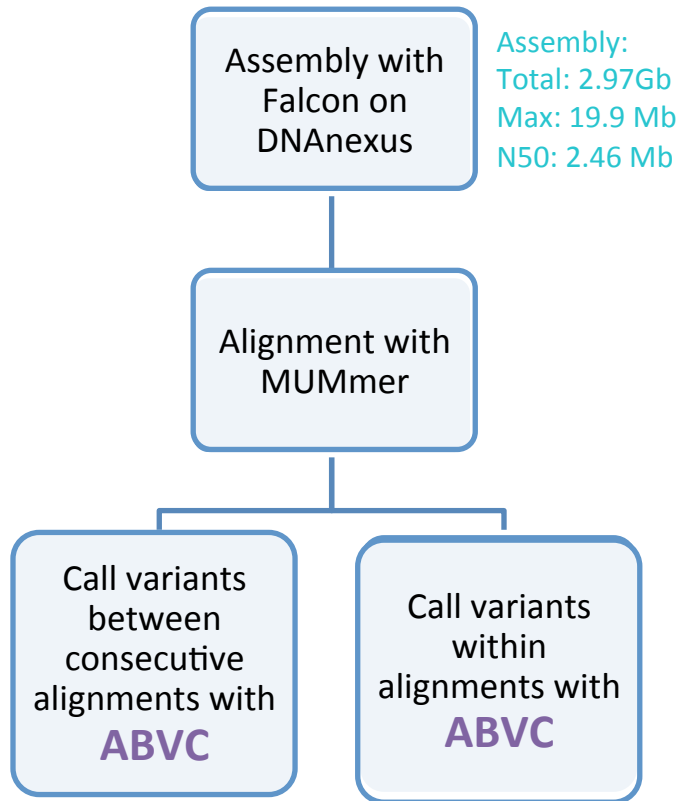


Genome-wide coverage averages around 54X

Coverage per chromosome varies greatly as expected from previous karyotyping results

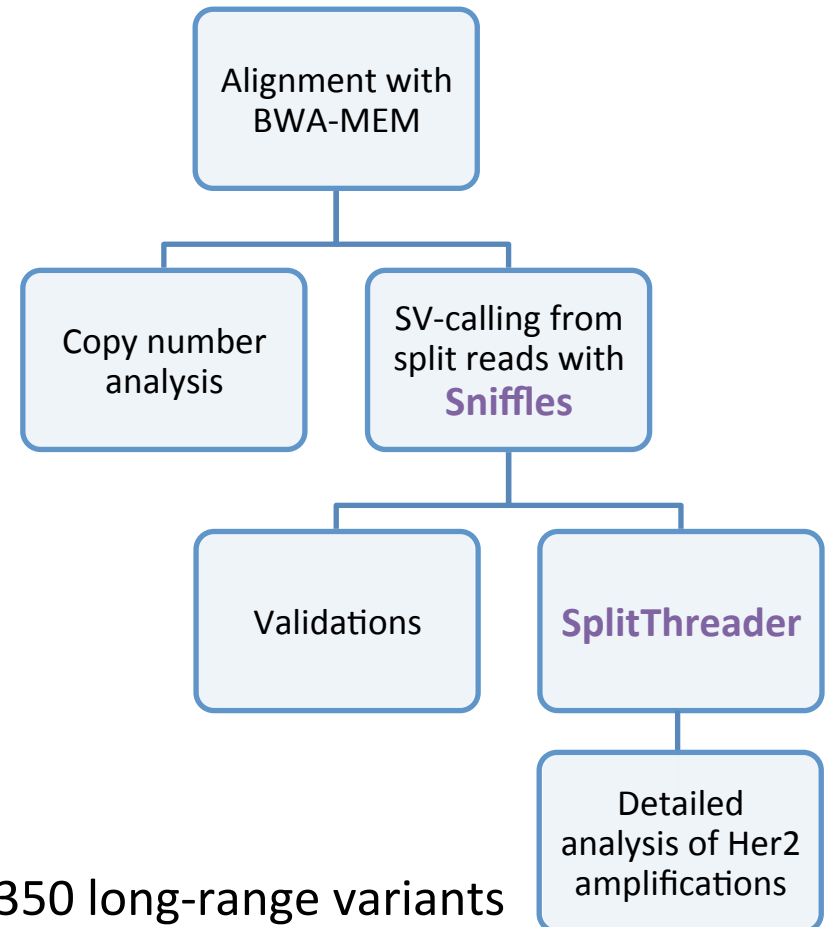
Structural variant detection

Assembly-based



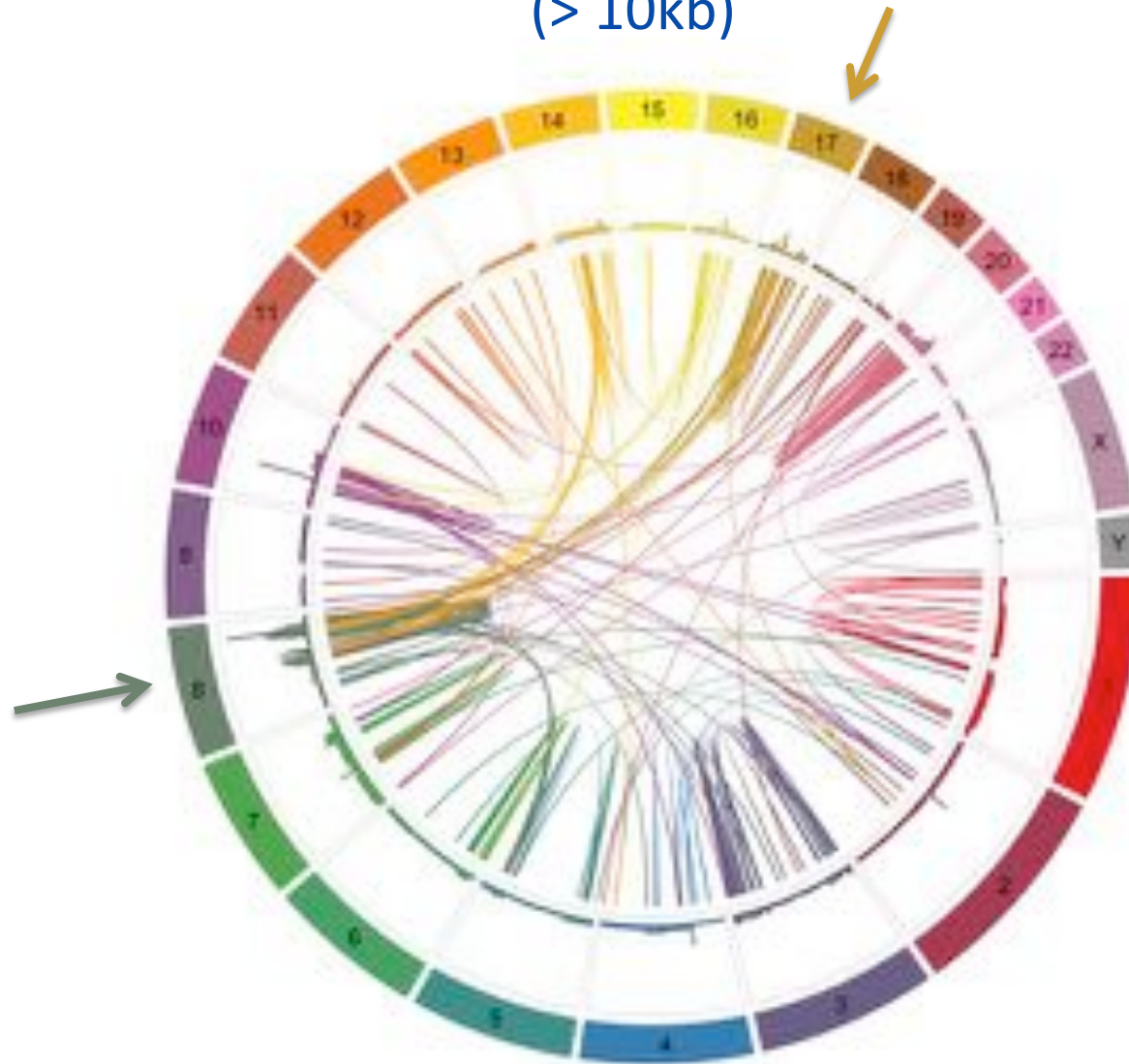
~ 11,000 local variants
50 bp < size < 10 kbp

Alignment-based

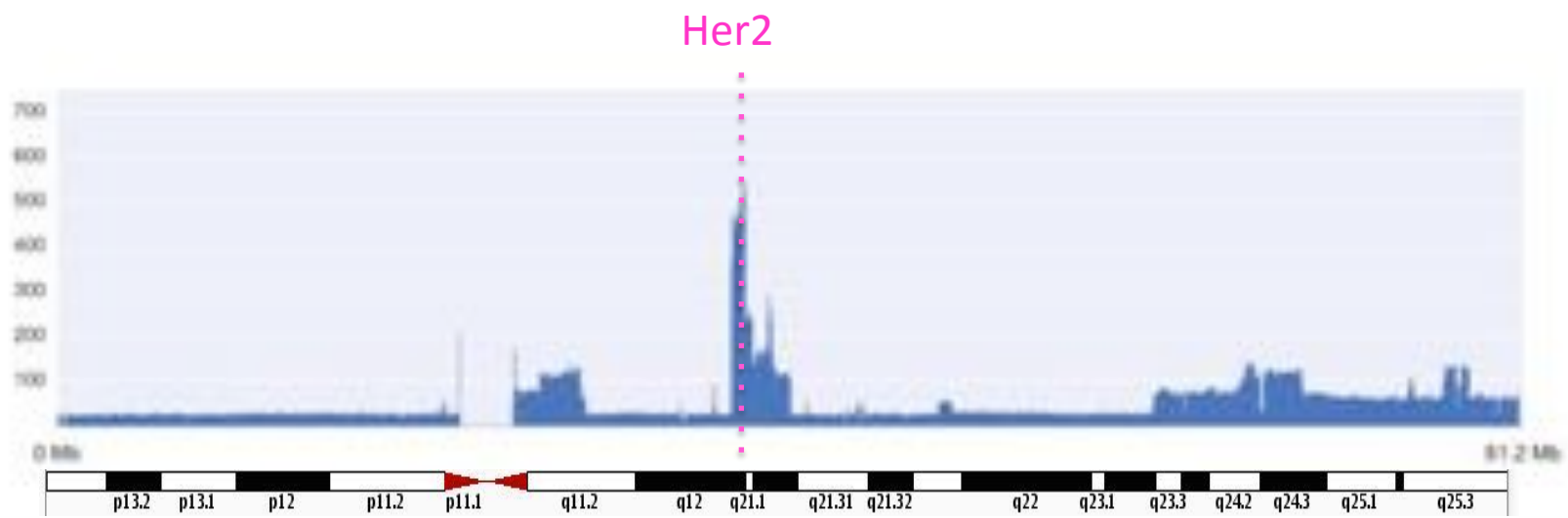


350 long-range variants
(>10kb distance)

Long-range structural variants found by Sniffles (> 10kb)

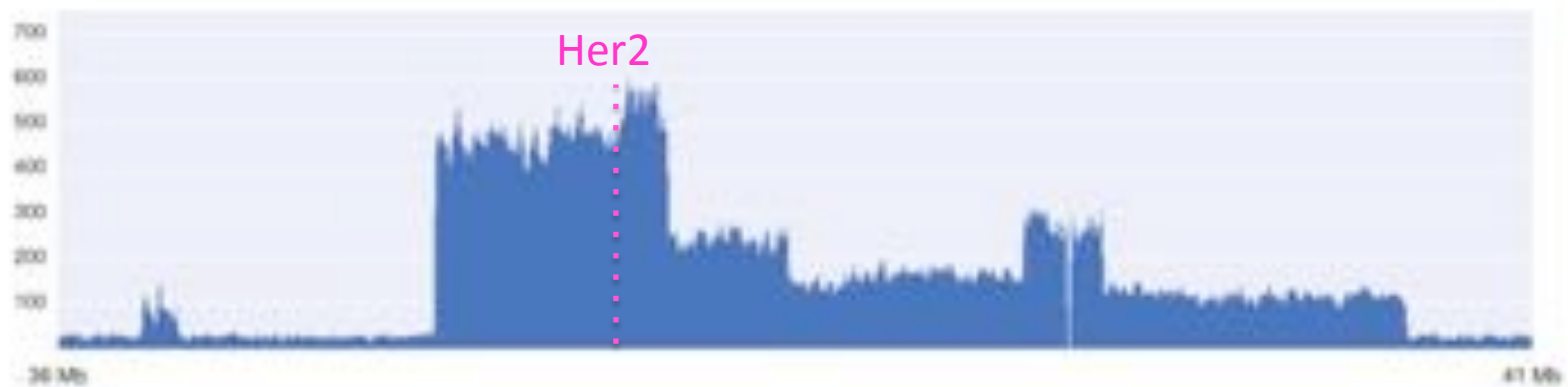
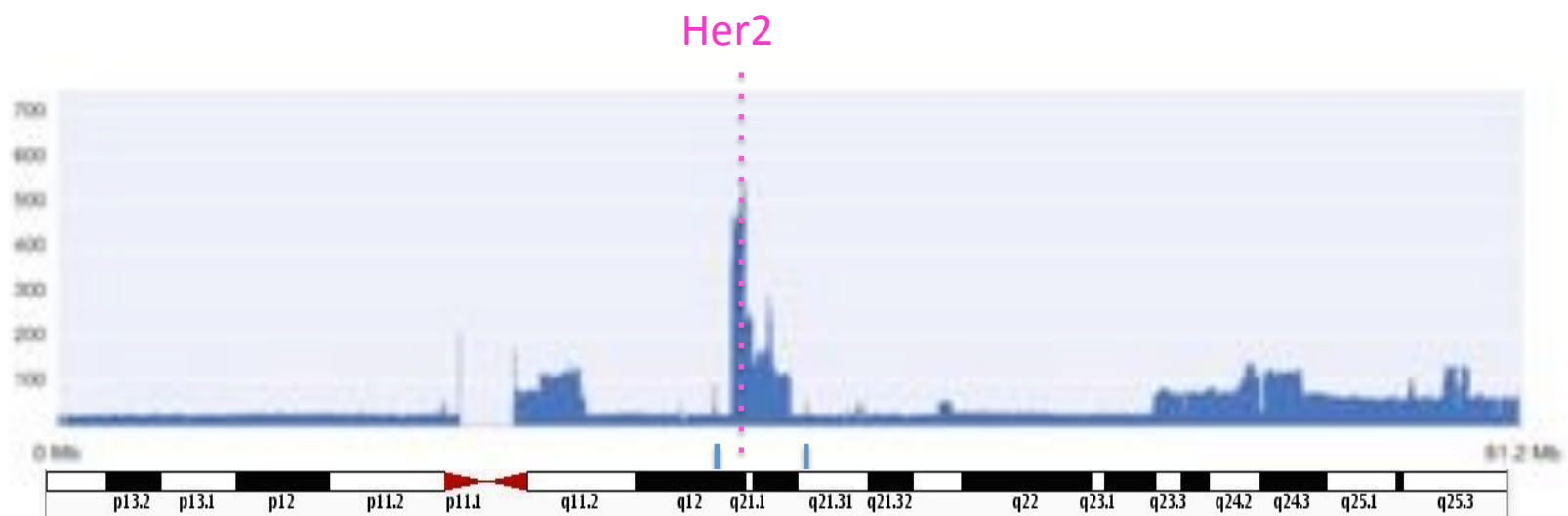


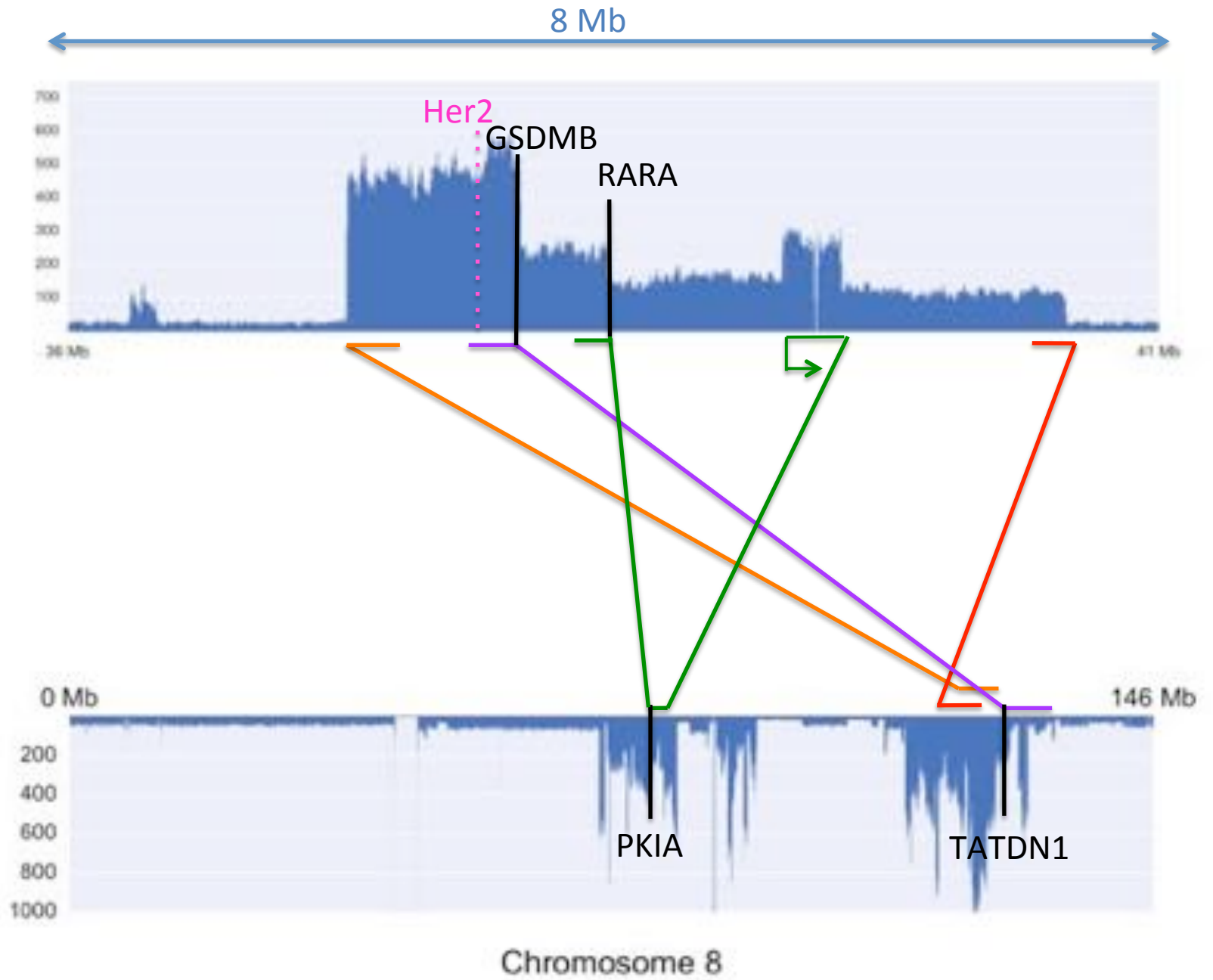
Threshold: 10 split reads broken within a 200 bp interval on both sides of the translocation



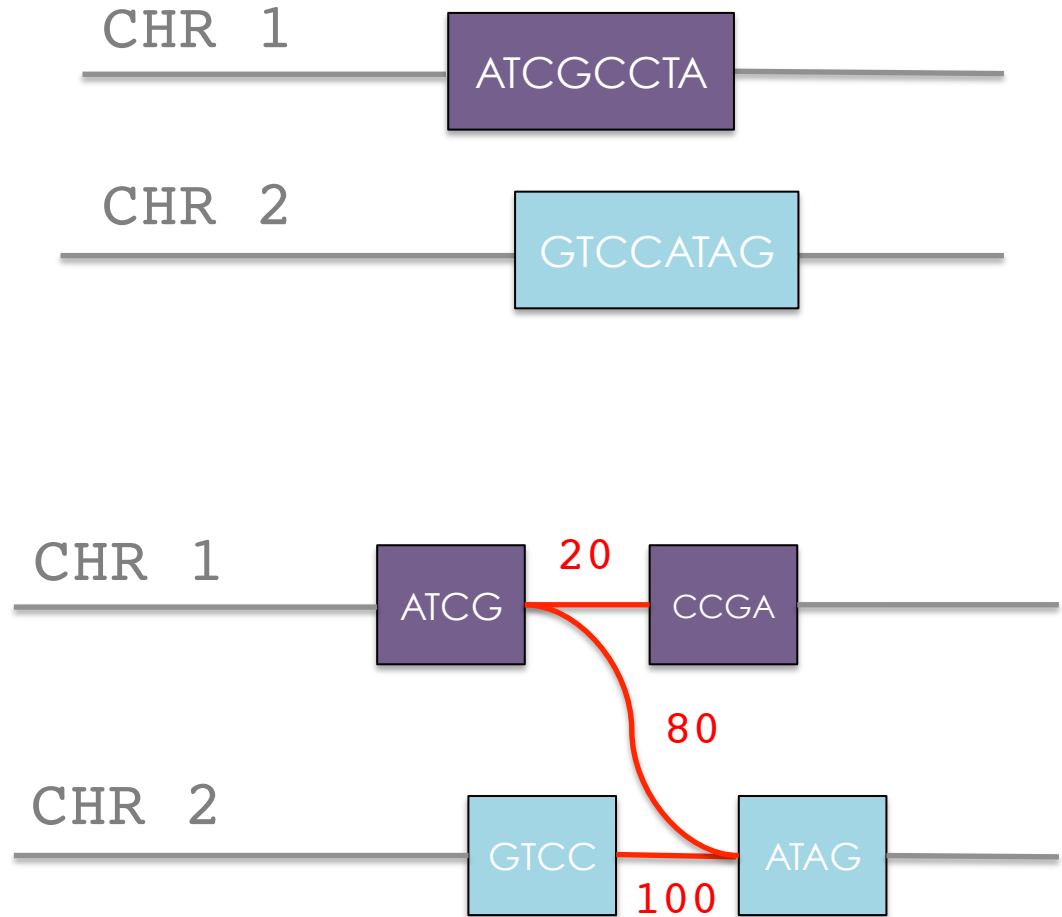
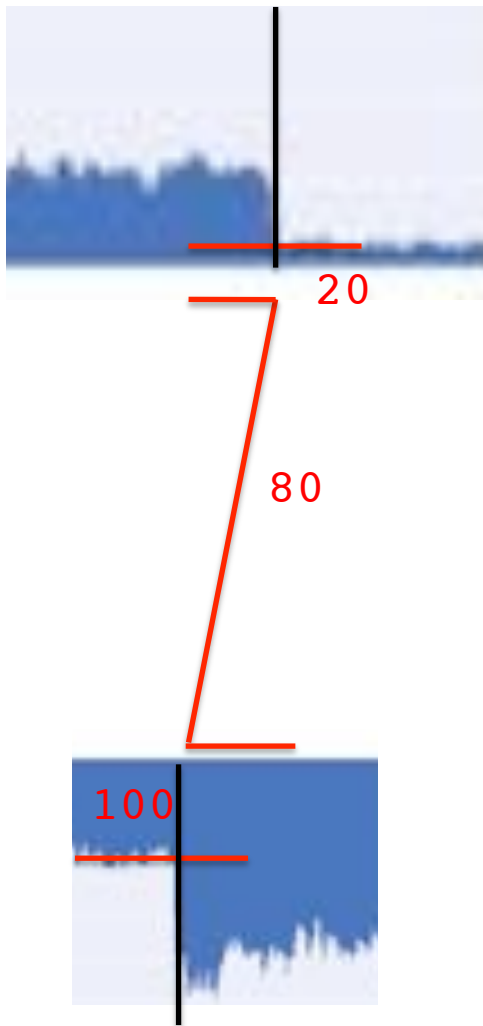
← Chr 17: 83 Mb →

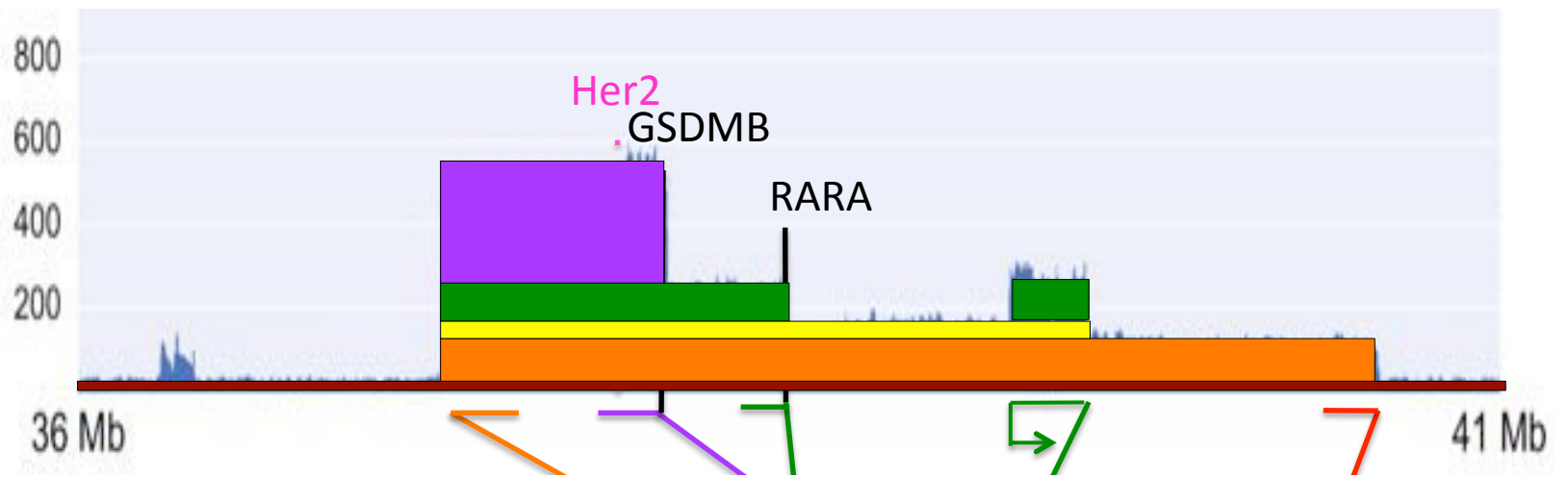
← 8 Mb →





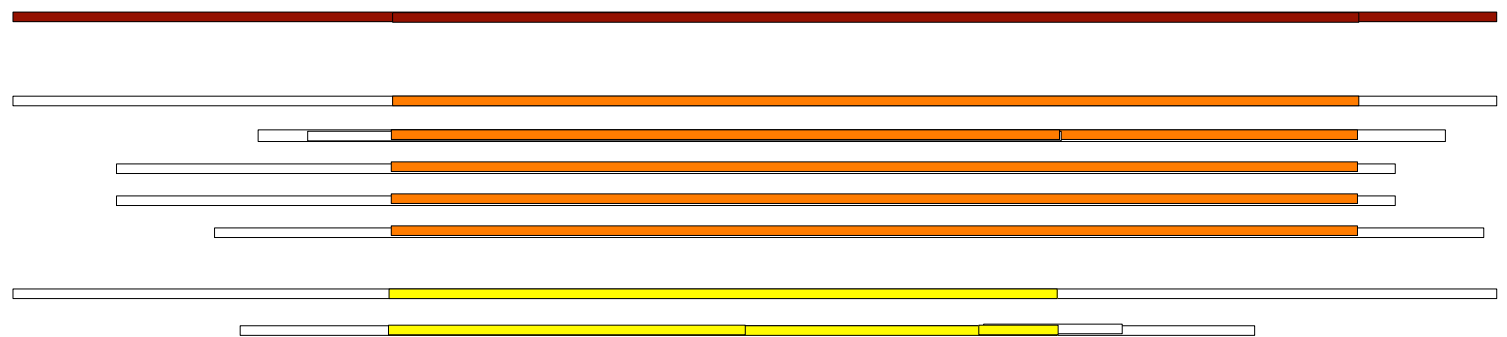
SplitThreader: Graphical threading to retrace complex history of rearrangements in cancer genomes





Chr 17

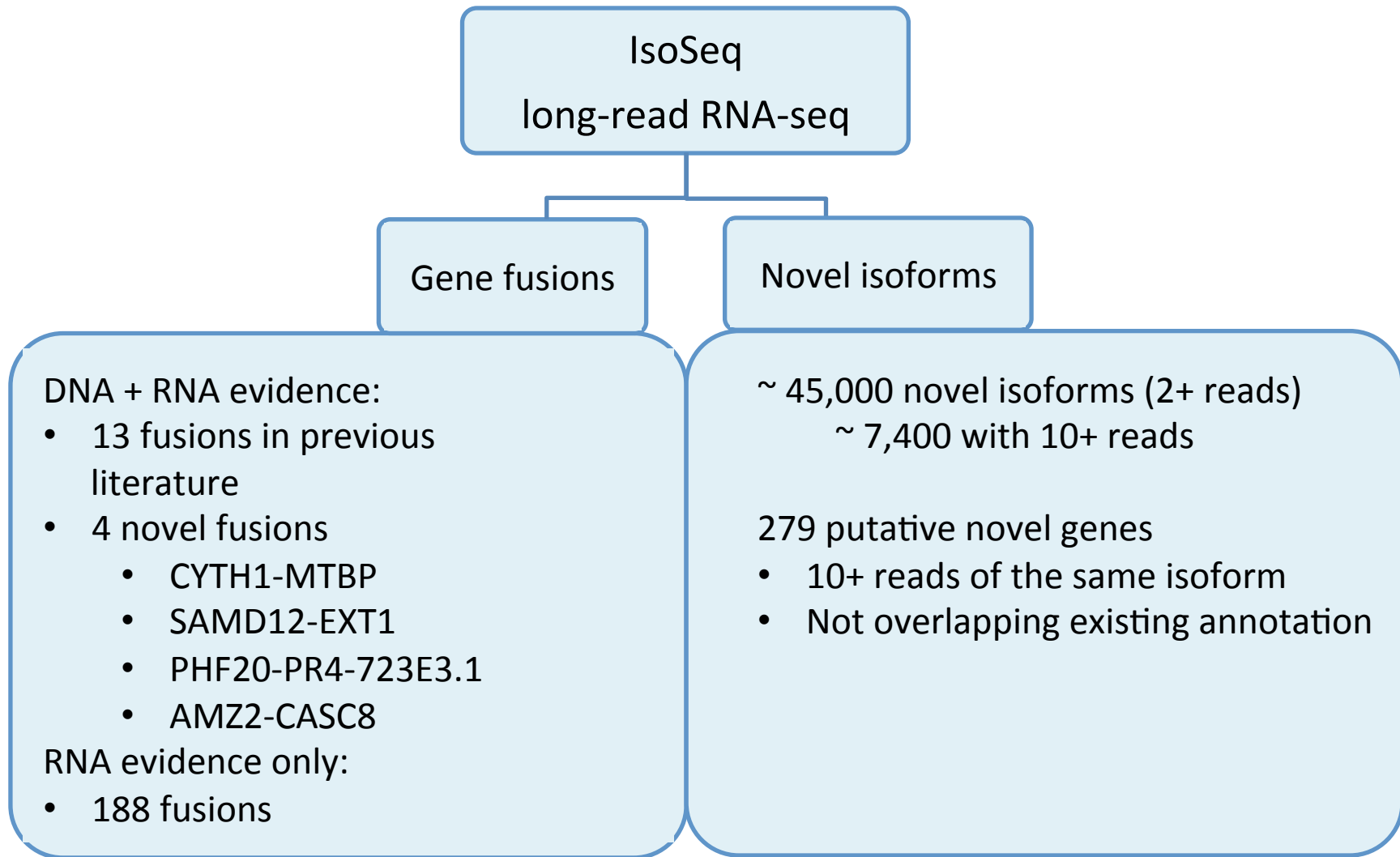
Chr 8



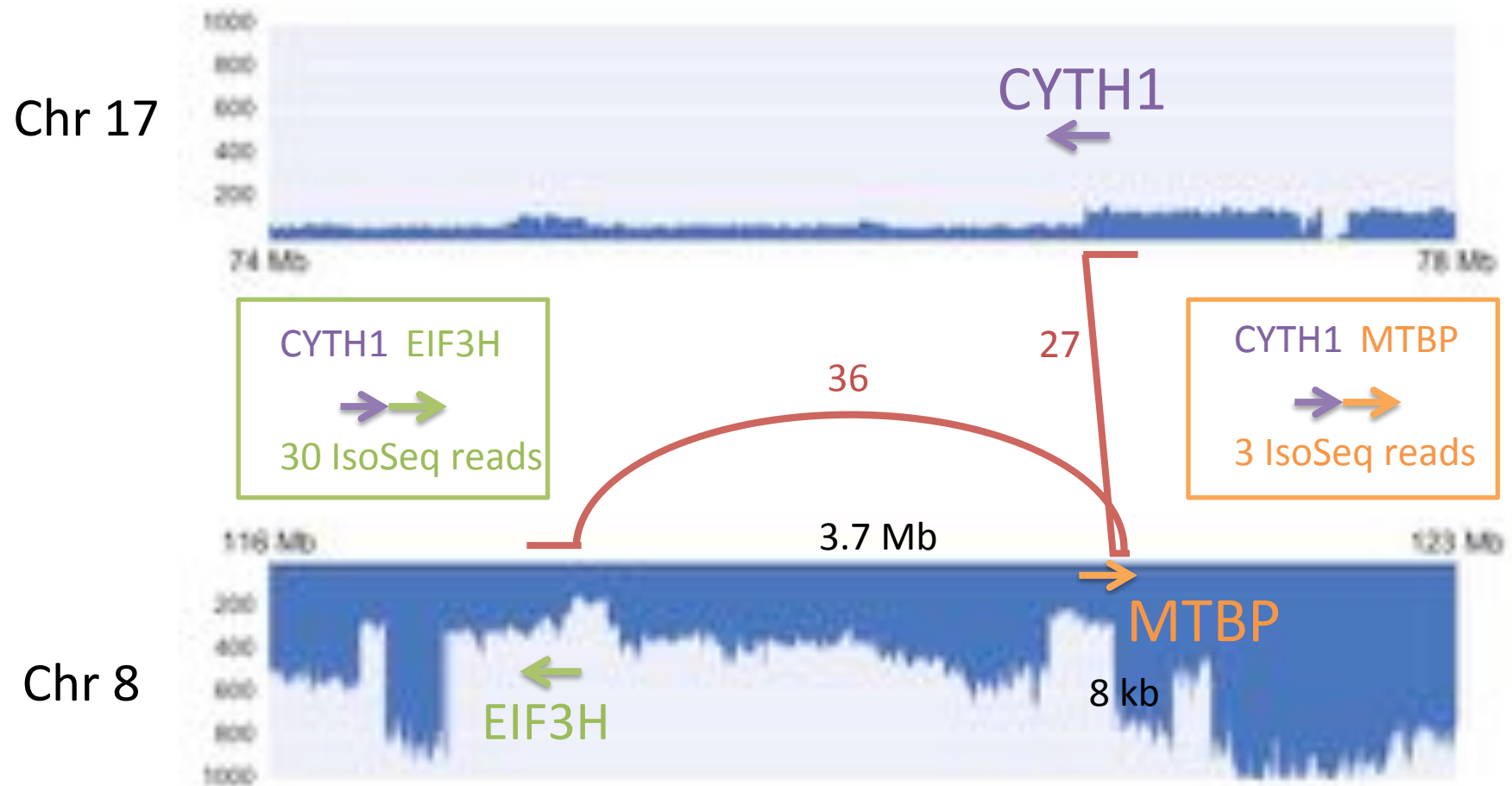
1. Healthy chromosome 17
2. Translocation into chromosome 8
3. Translocation within chromosome 8
4. Complex variant and inverted duplication within chromosome 8
5. Translocation within chromosome 8



Transcriptome analysis with IsoSeq



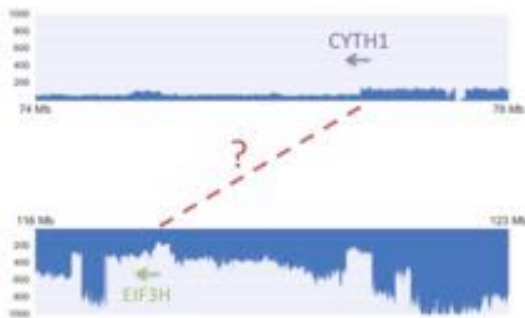
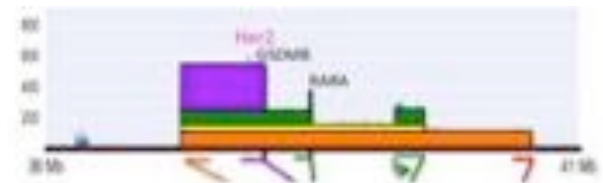
CYTH1-EIF3H gene fusion



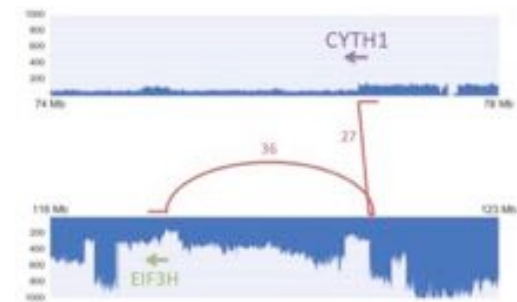
The genome informs the transcriptome



Explain amplifications



Trace gene fusions



Data and additional results: <http://schatzlab.cshl.edu/data/skbr3/>

Acknowledgments



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Our software in development: Sniffles by Fritz, ABVC and SplitThreader by Maria