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UNIVERSITAS MASARYKIANA BRUNENSIS

## Modern methods for genome analysis (PřF:Bi7420)

# Lecture 4 : Structural variants

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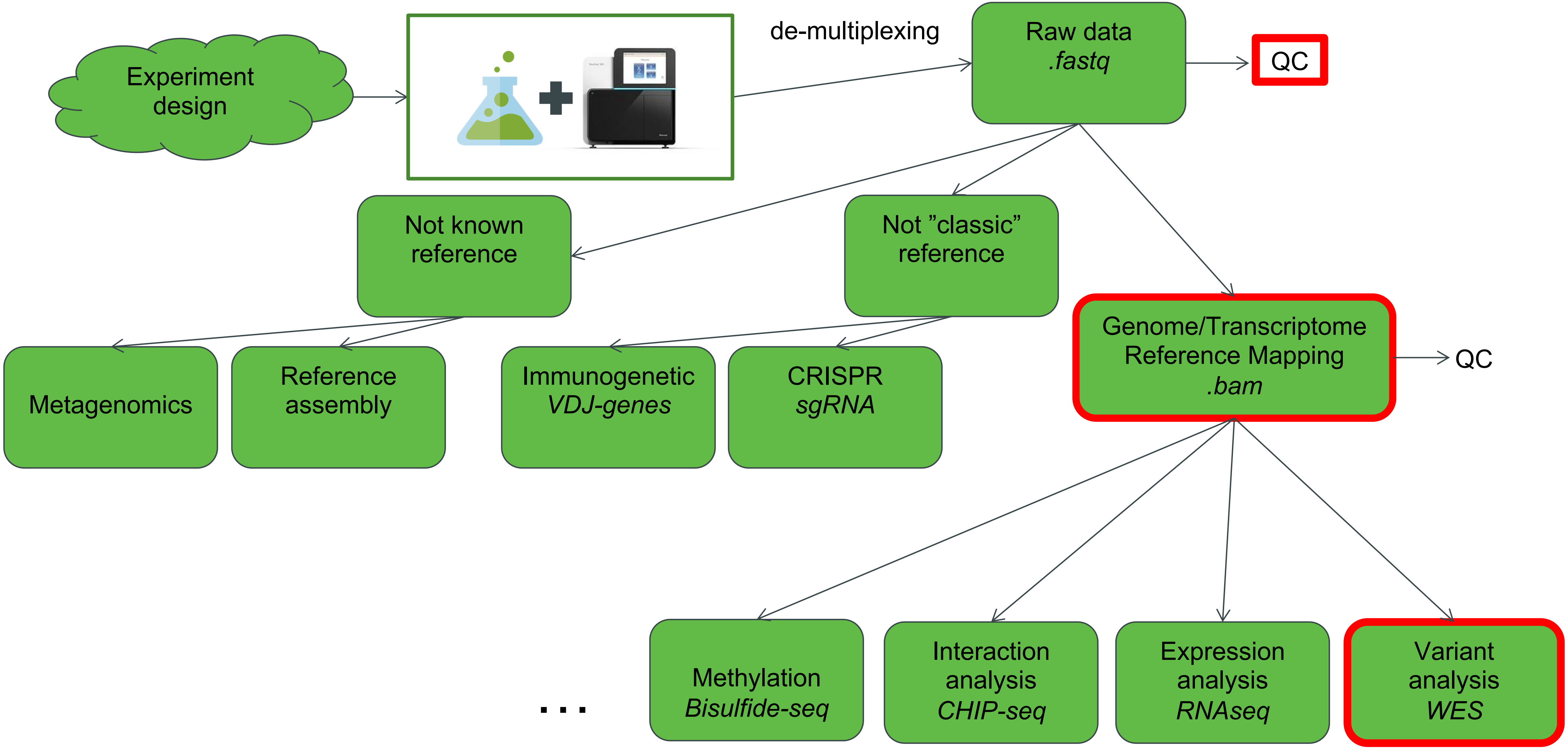
# NGS data analysis



Experiment design

de-multiplexing

Raw data *.fastq*

QC

Not known reference

Not ”classic” reference

Genome/Transcriptome Reference Mapping *.bam*

QC

Metagenomics

Reference assembly

Immunogenetic *VDJ-genes*

CRISPR *sgRNA*

...

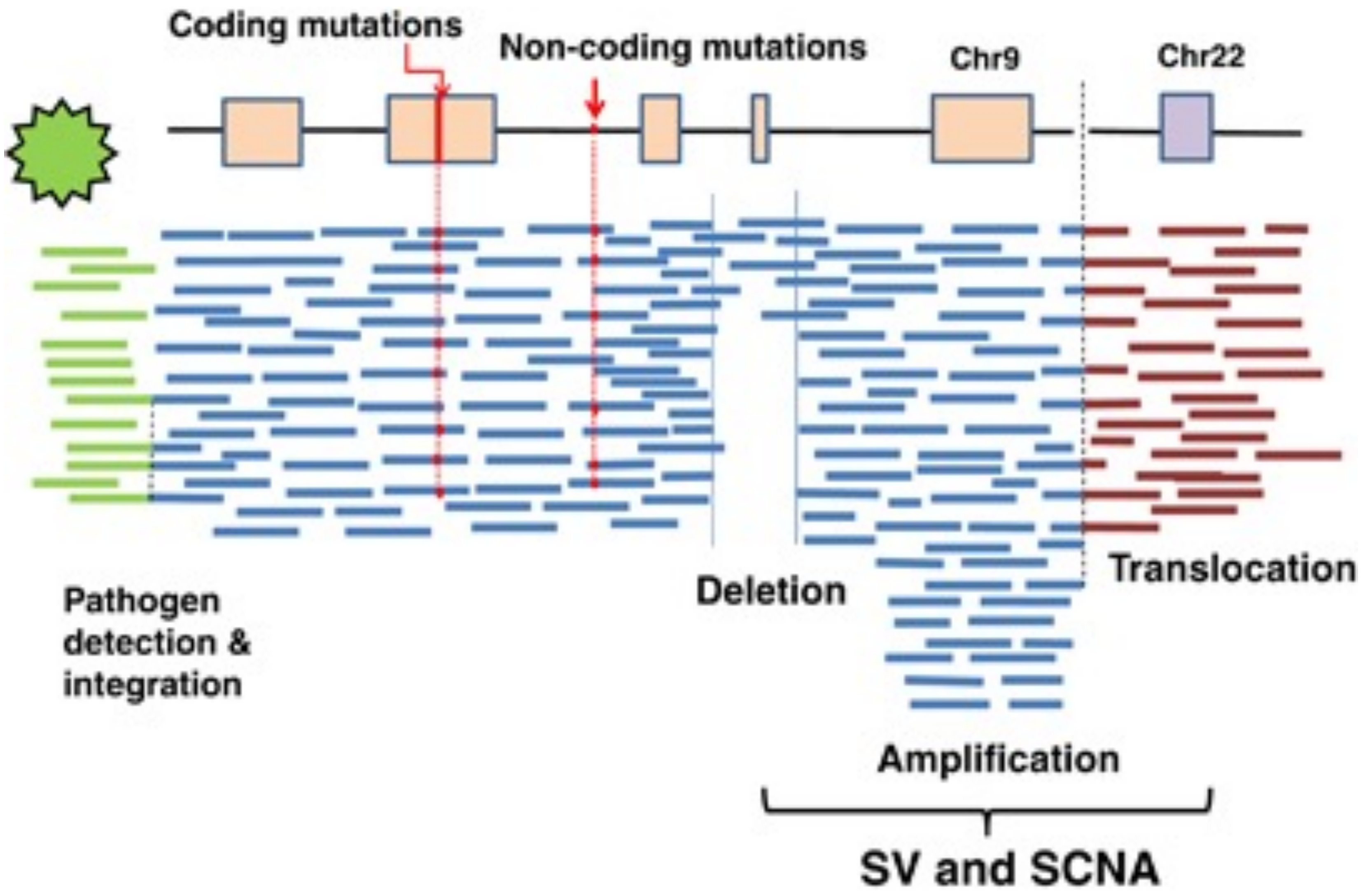
Methylation *Bisulfide-seq*

Interaction analysis *CHIP-seq*

Expression analysis *RNAseq*

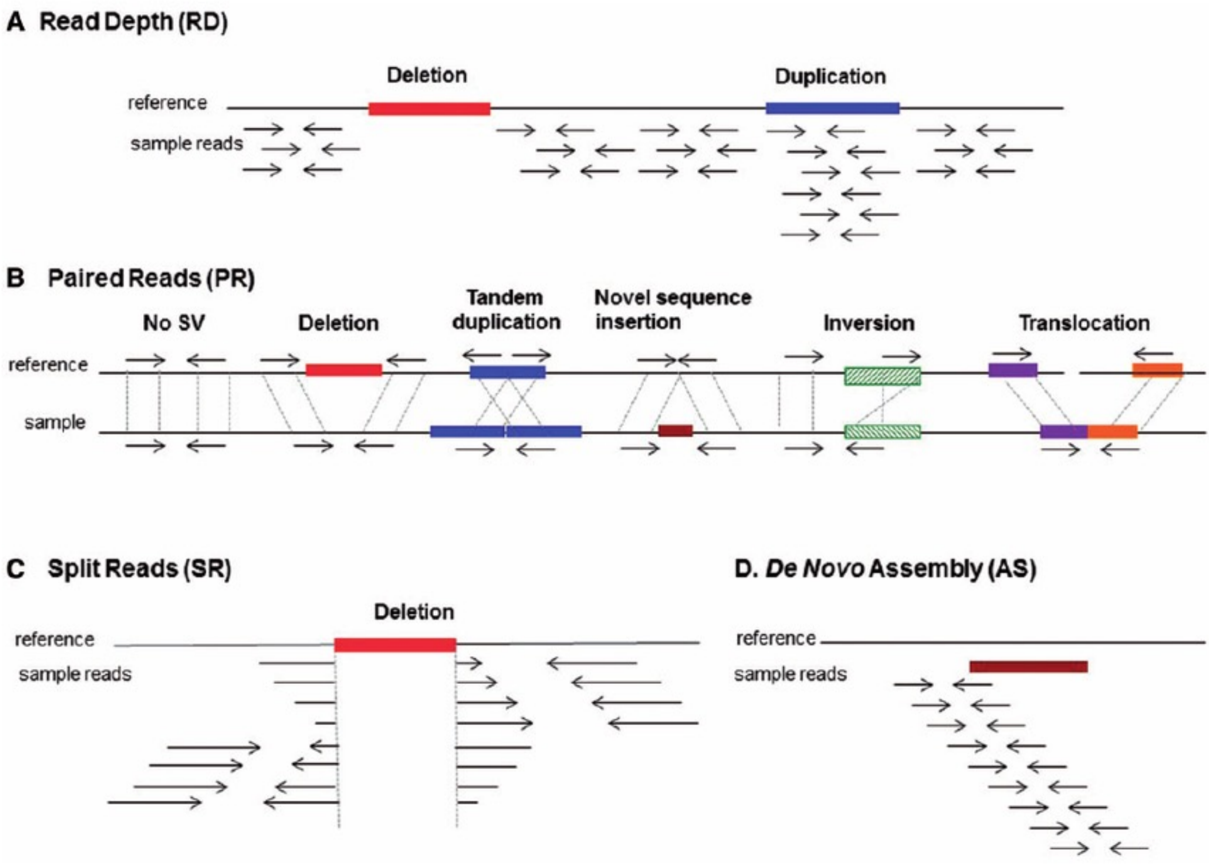
Variant analysis *WES*

# Structural variants calling



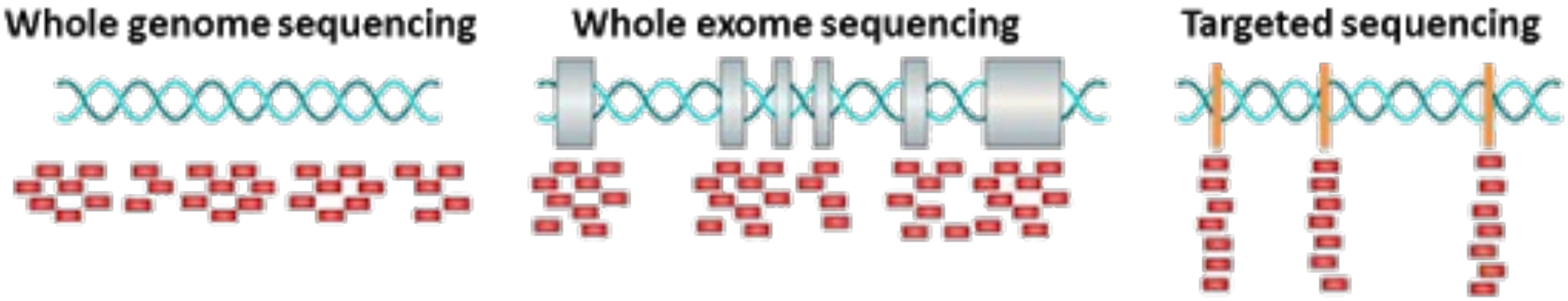
# Structural variants calling

- Copy number variants (CNV)
  - Copy number analysis (CNA)
- Structural variants (SV)
  - Discordant reads analysis
  - Mainly from WGS
- Fusion genes analysis
  - From RNA-seq
  - SV in genes
  - Medical application



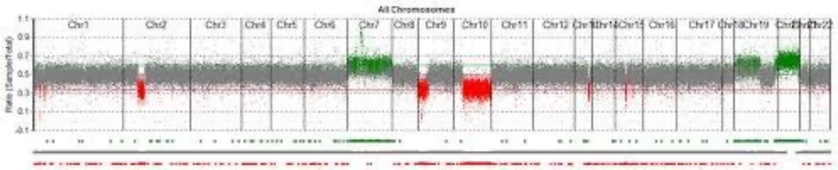
# Copy number variants

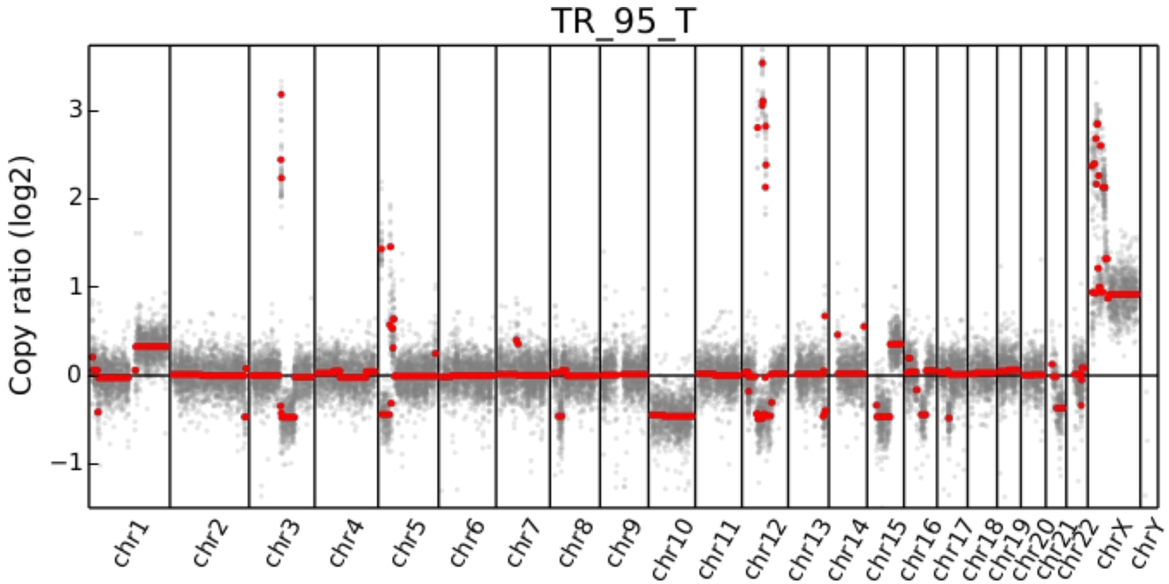
- Not-PCR amplified (WGS)
- PCR amplified (WES,targeted)



# WGS copy number variants

- Running window
- Normalization to the absolute coverage
- Low-coverage WGS CNV
  - Over large regions
  - Good for somatic low tumor purity
  - Minimal variant size vs. coverage trade-off





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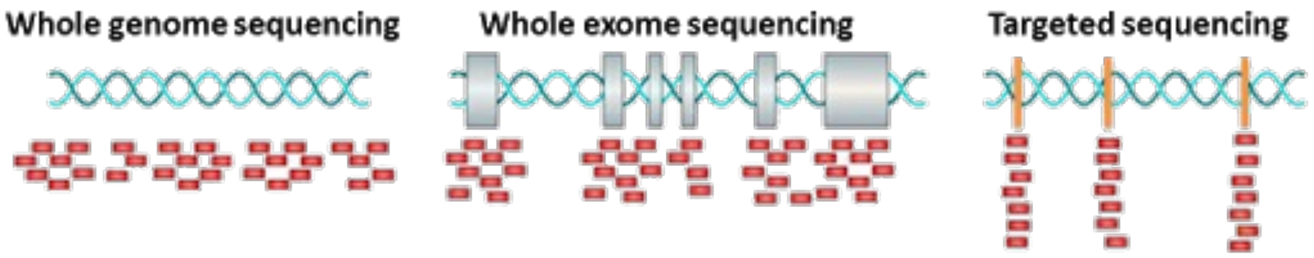
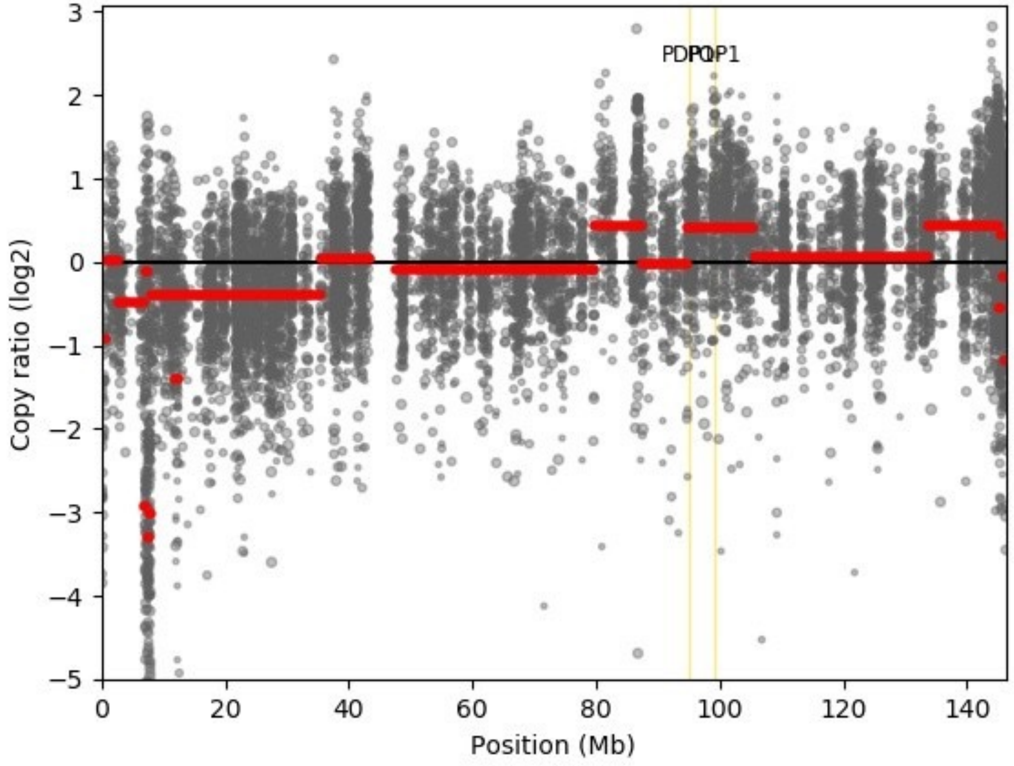
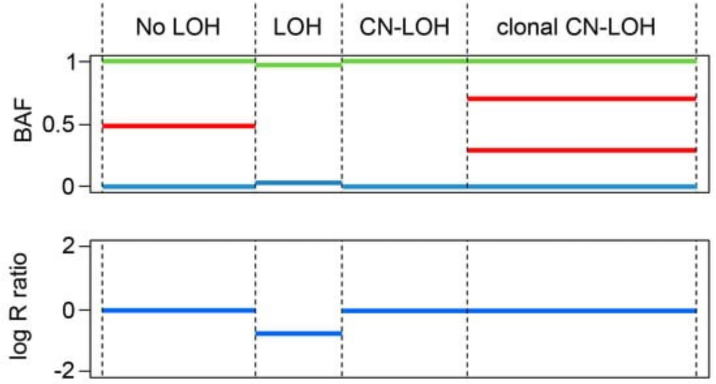
# PCR amplified CNV



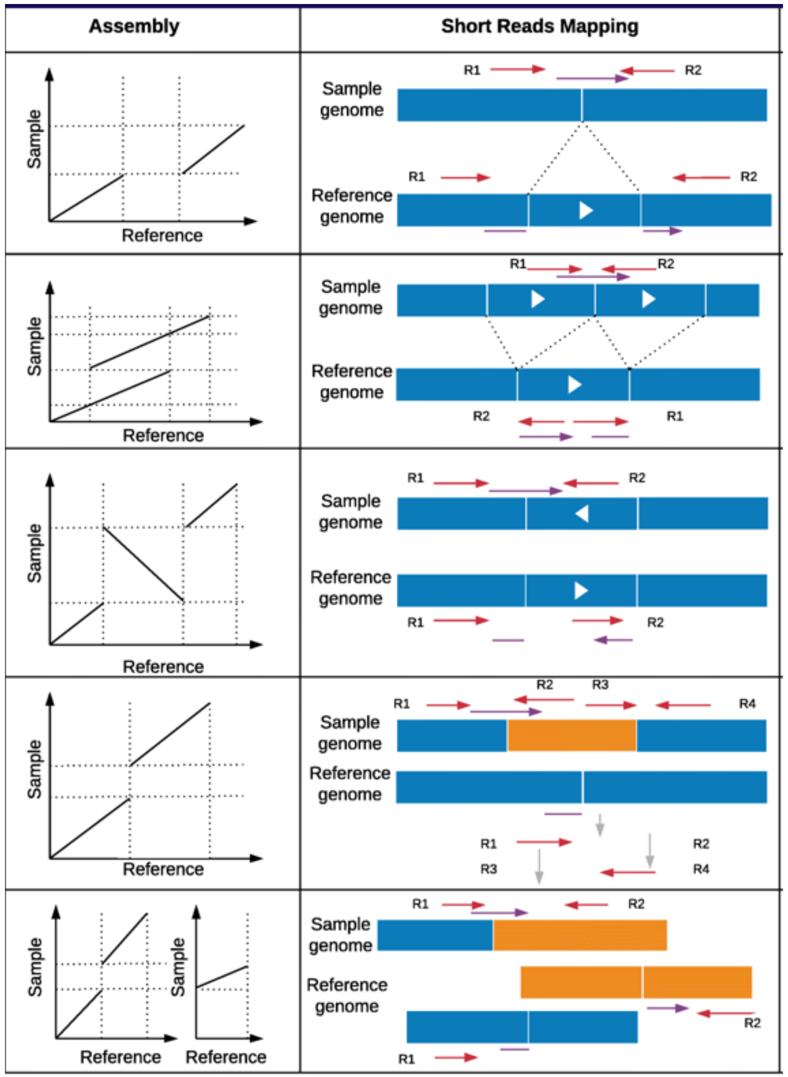
- Individual analysis problematic
- Panel of (normal) samples
- BAF frequency
  - Help CNA
  - Can call “loss of heterozygosity” LOH





# Structural variants calling

- RP = Read pair
  - Pair-end sequencing
- SR = Split reads



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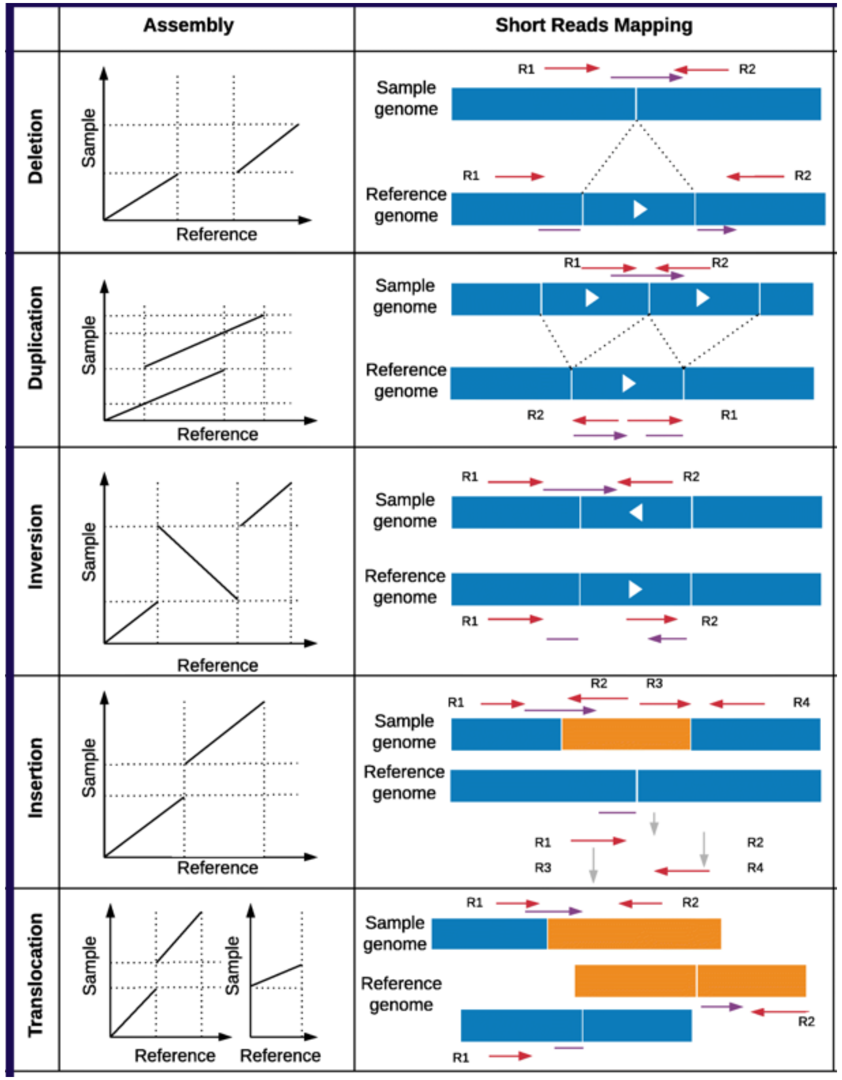
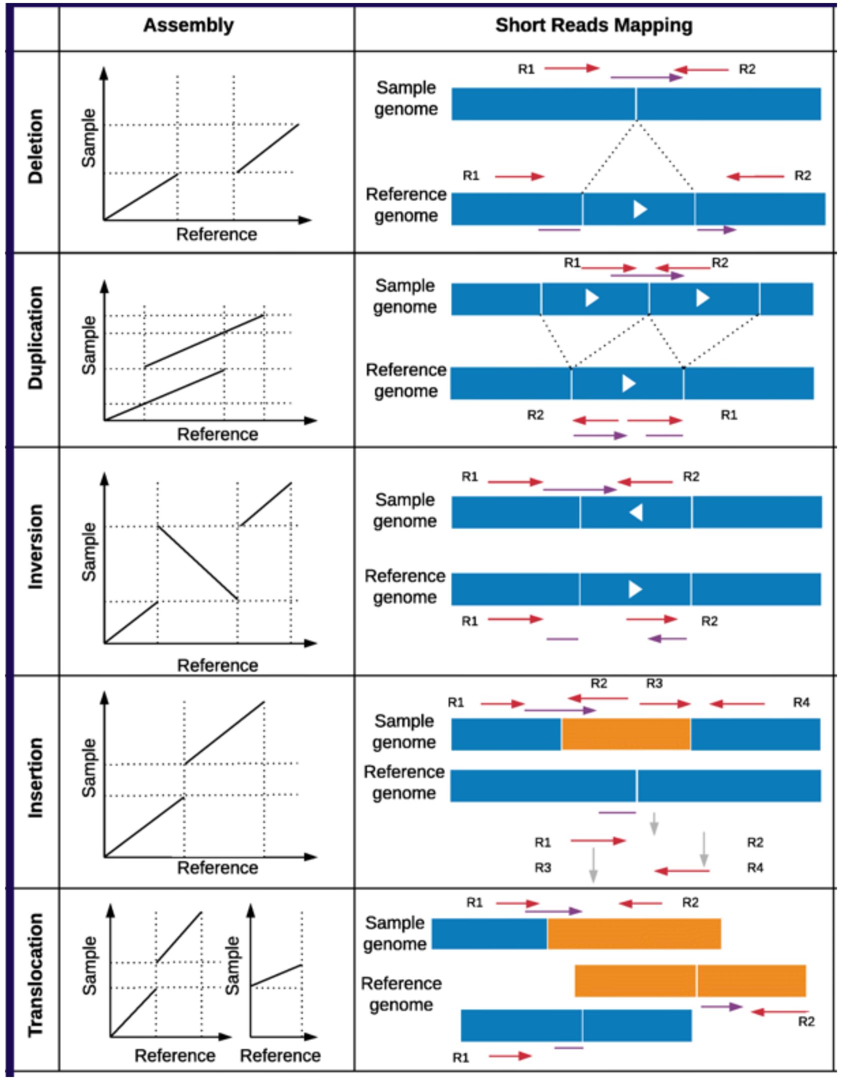
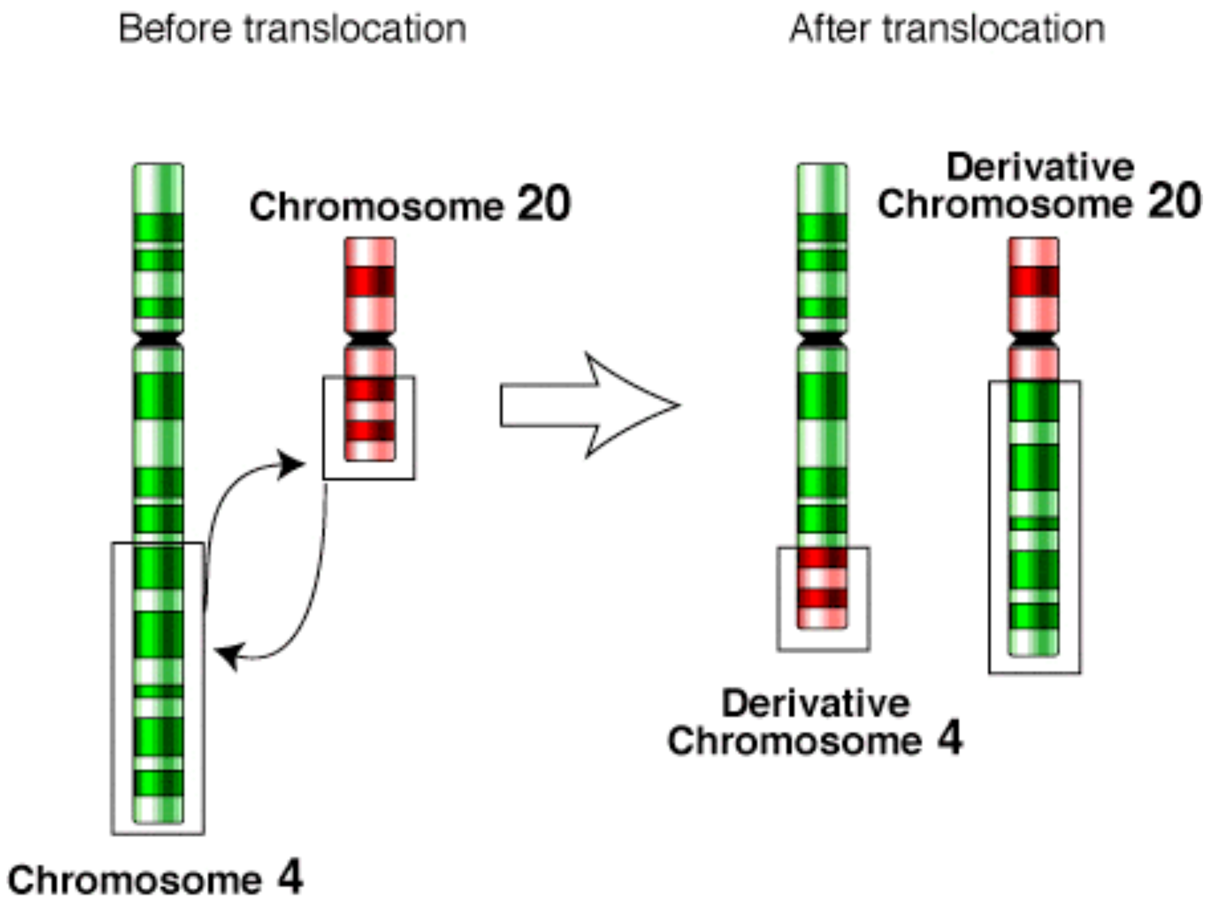


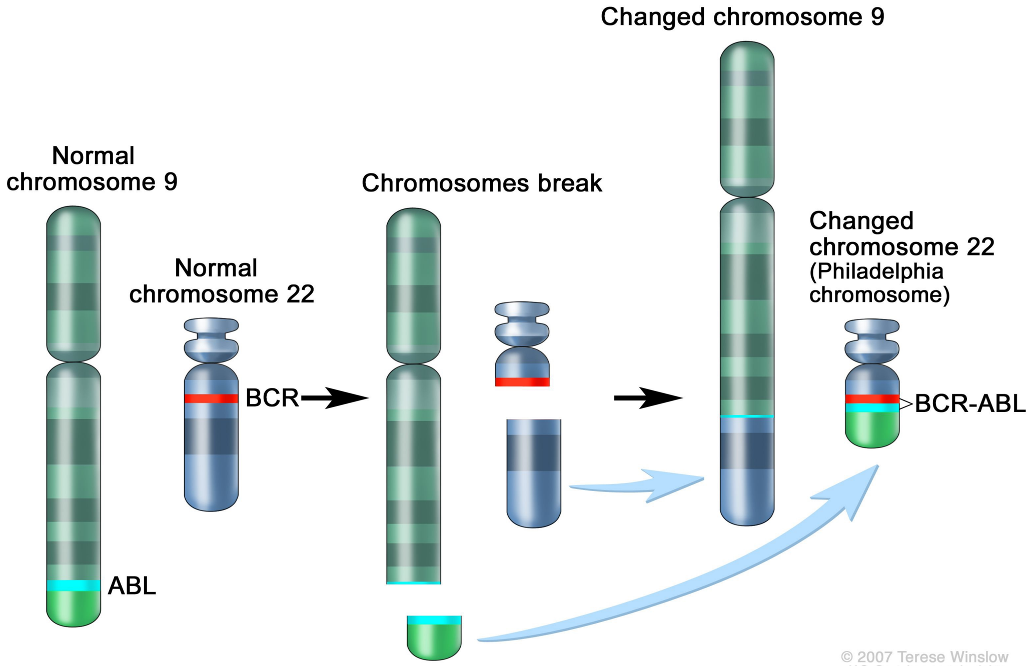
# Structural variants calling

- RP = Read pair
  - Pair-end sequencing
- SR = Split reads
- Tools:
  - Delly, Manta, GRIDSS



# Fusion genes





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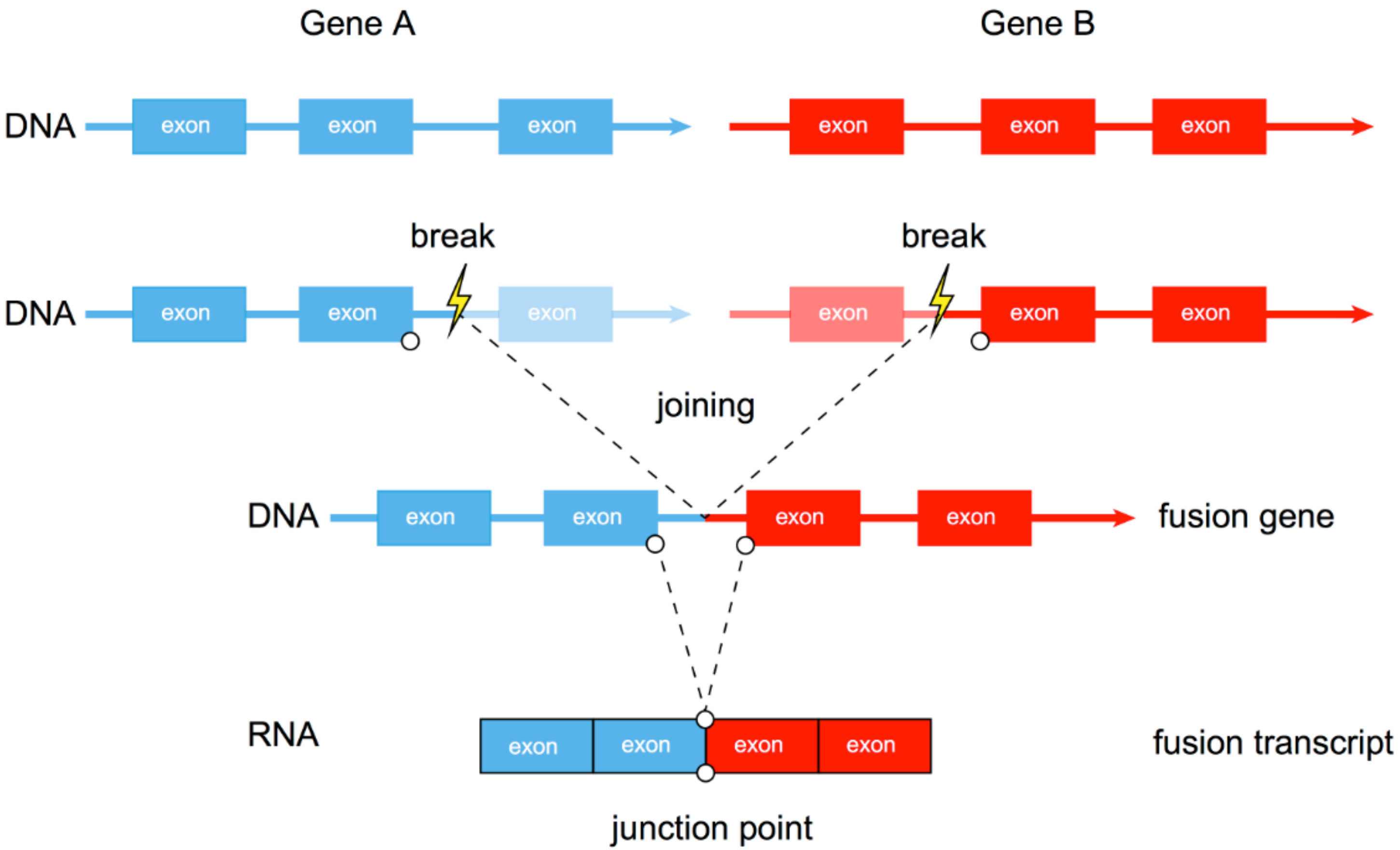

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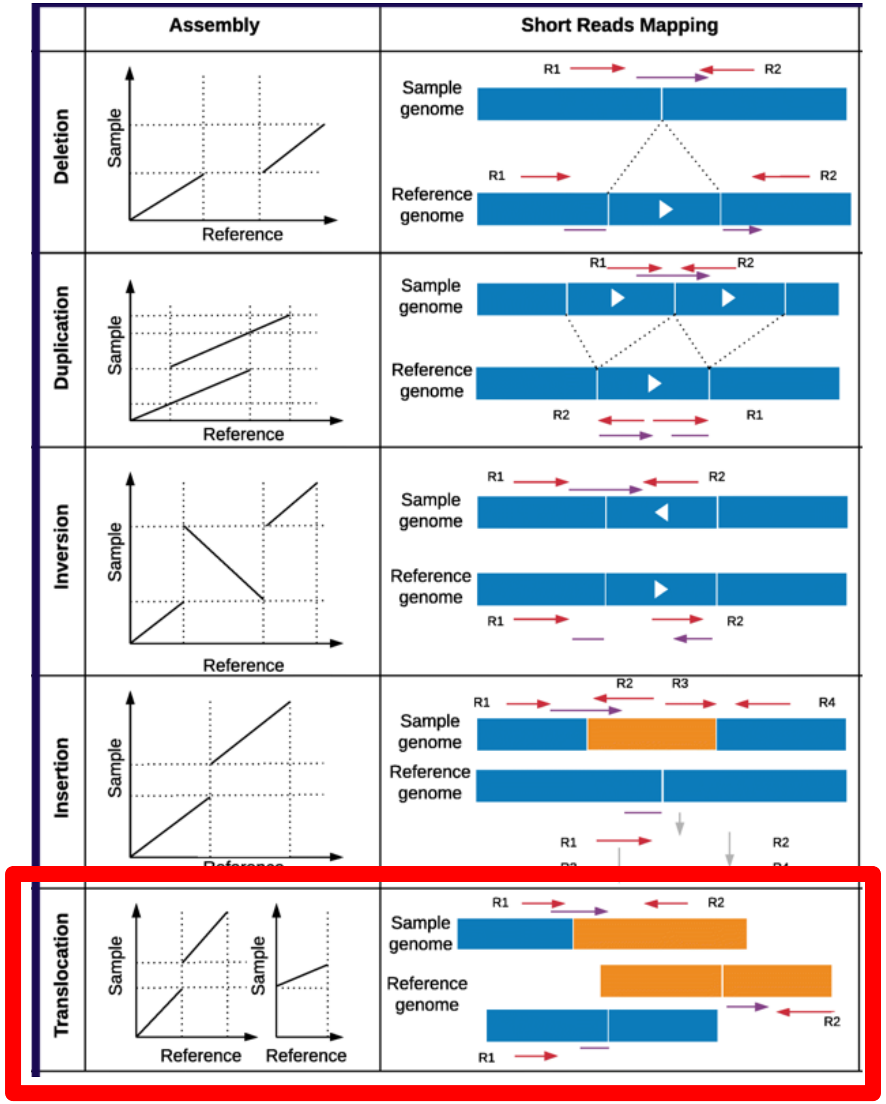

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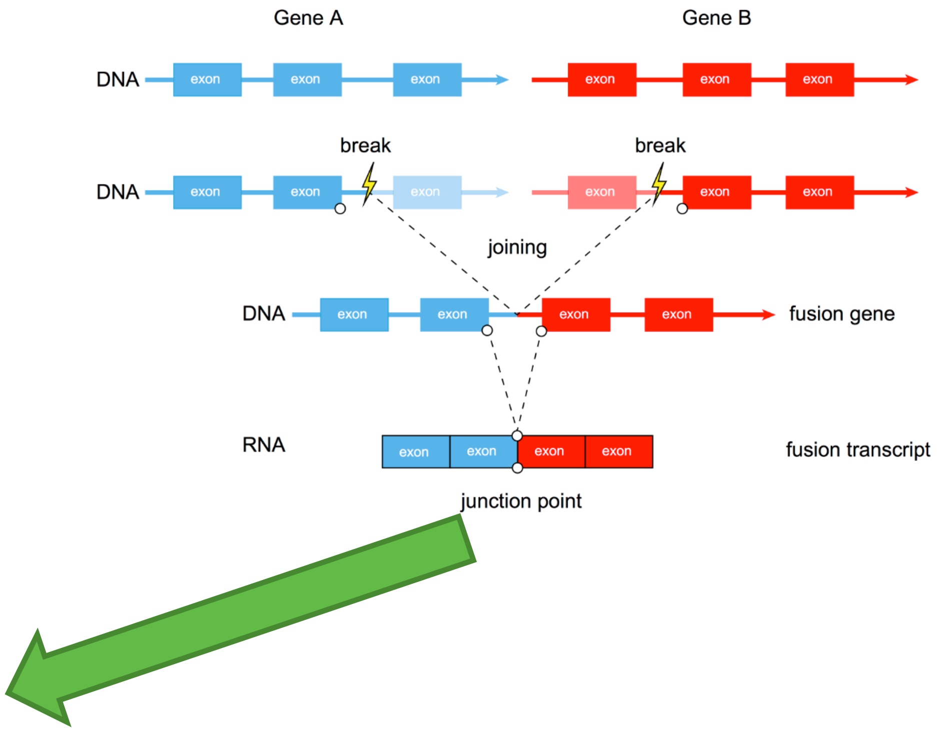
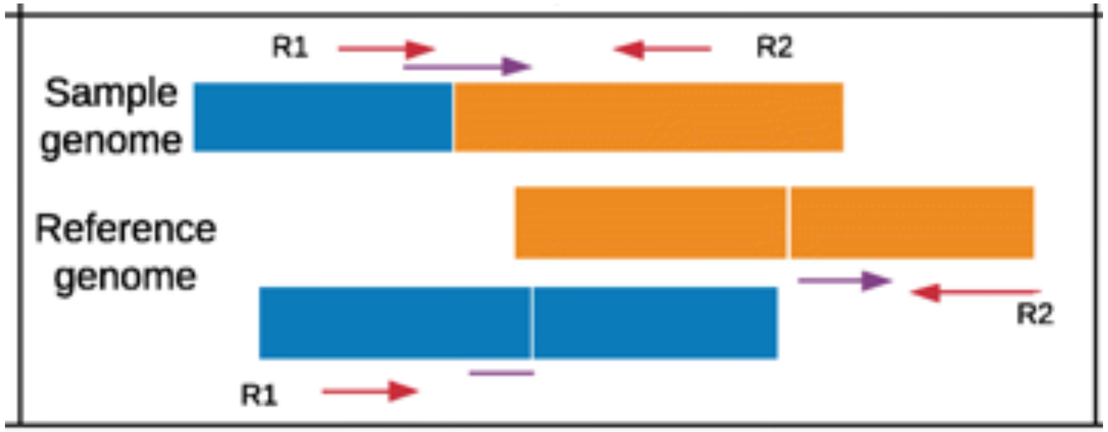
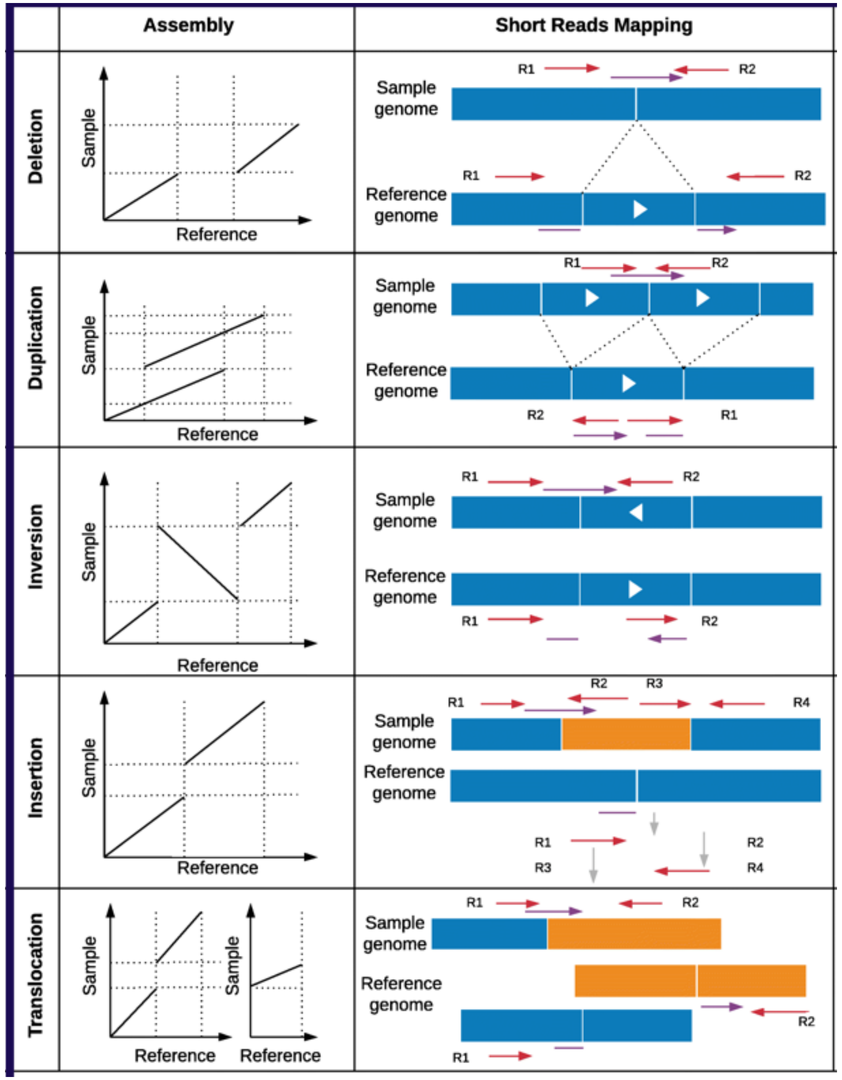
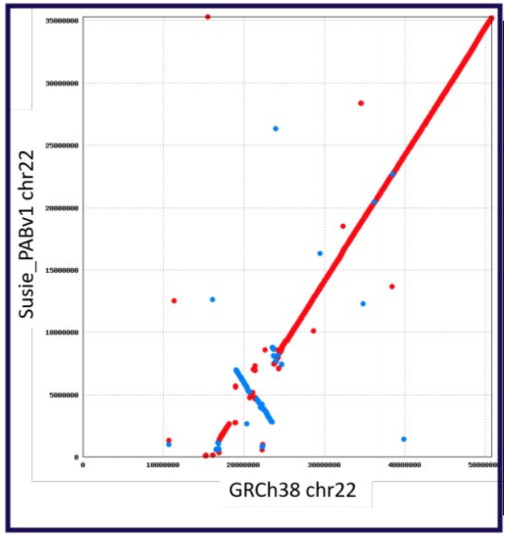




# Long reads

- Short reads
  - 1kb
- Long reads
  - 100 – 1000kb
- Hot topic





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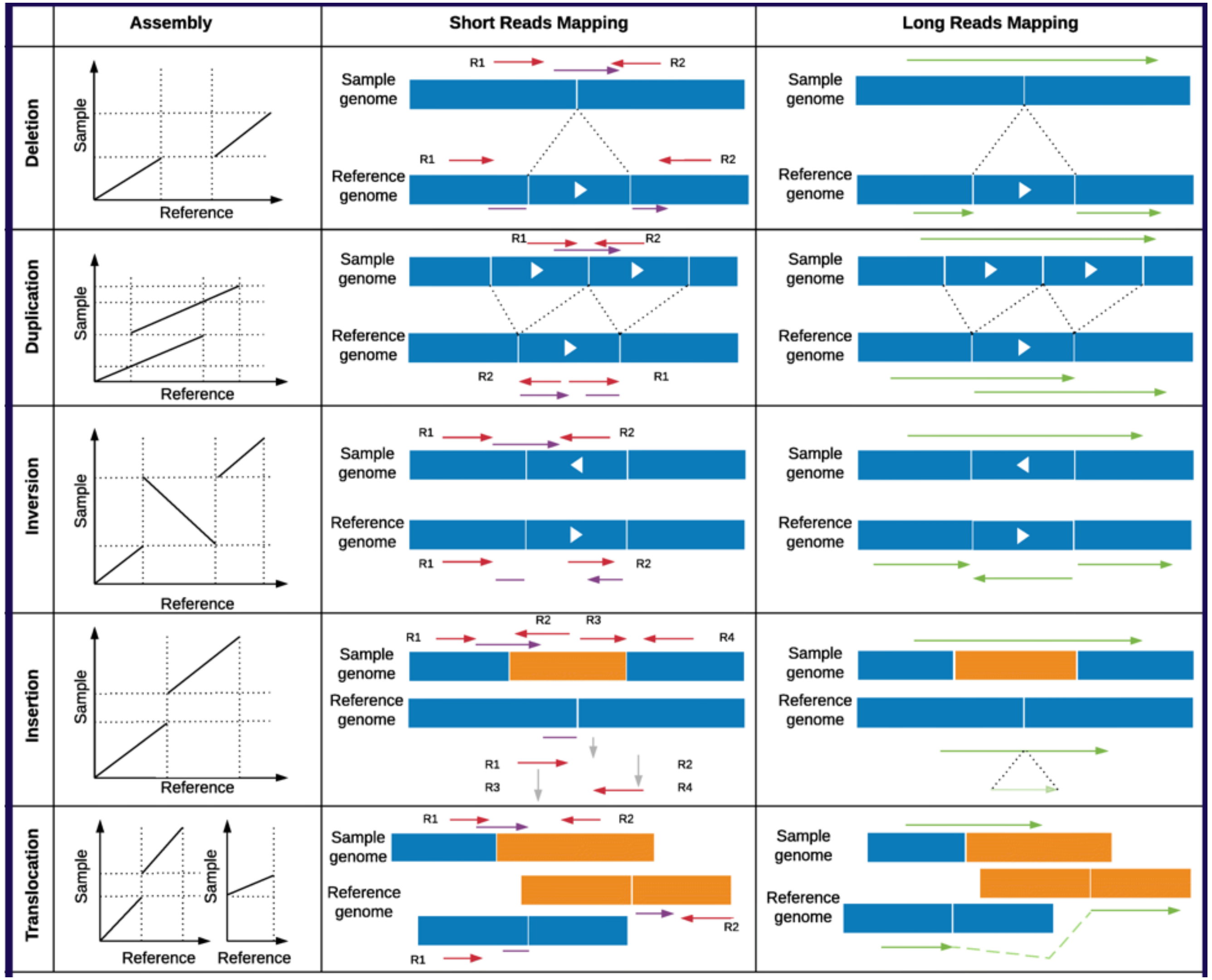

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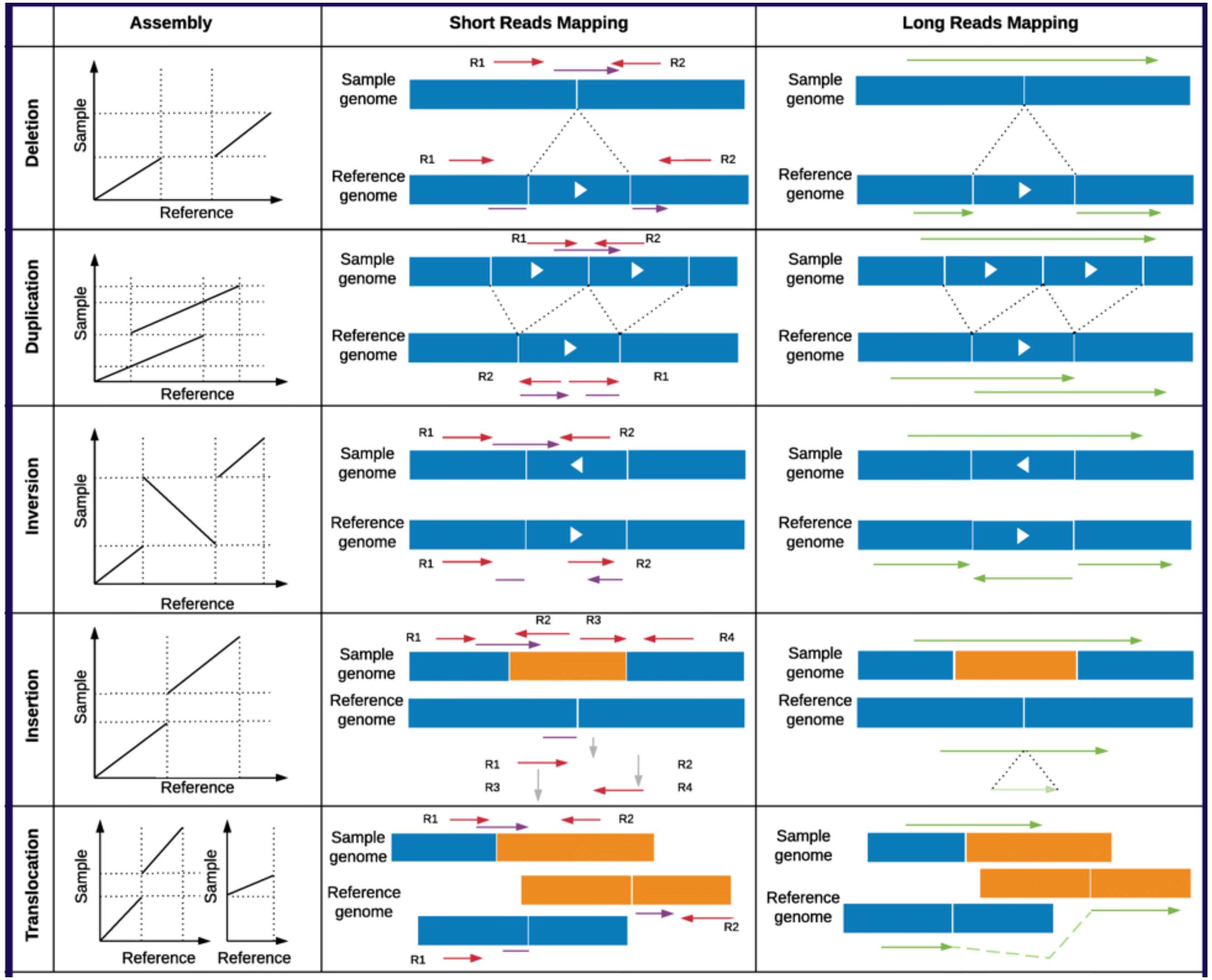
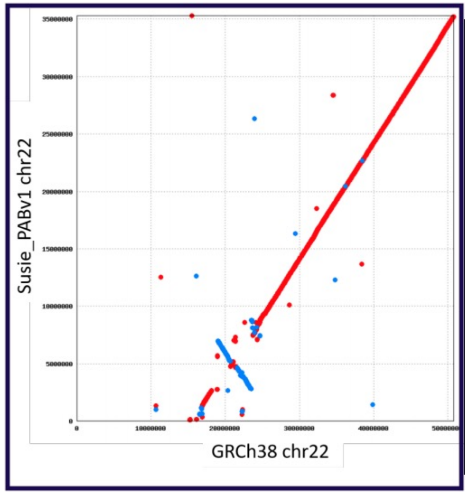
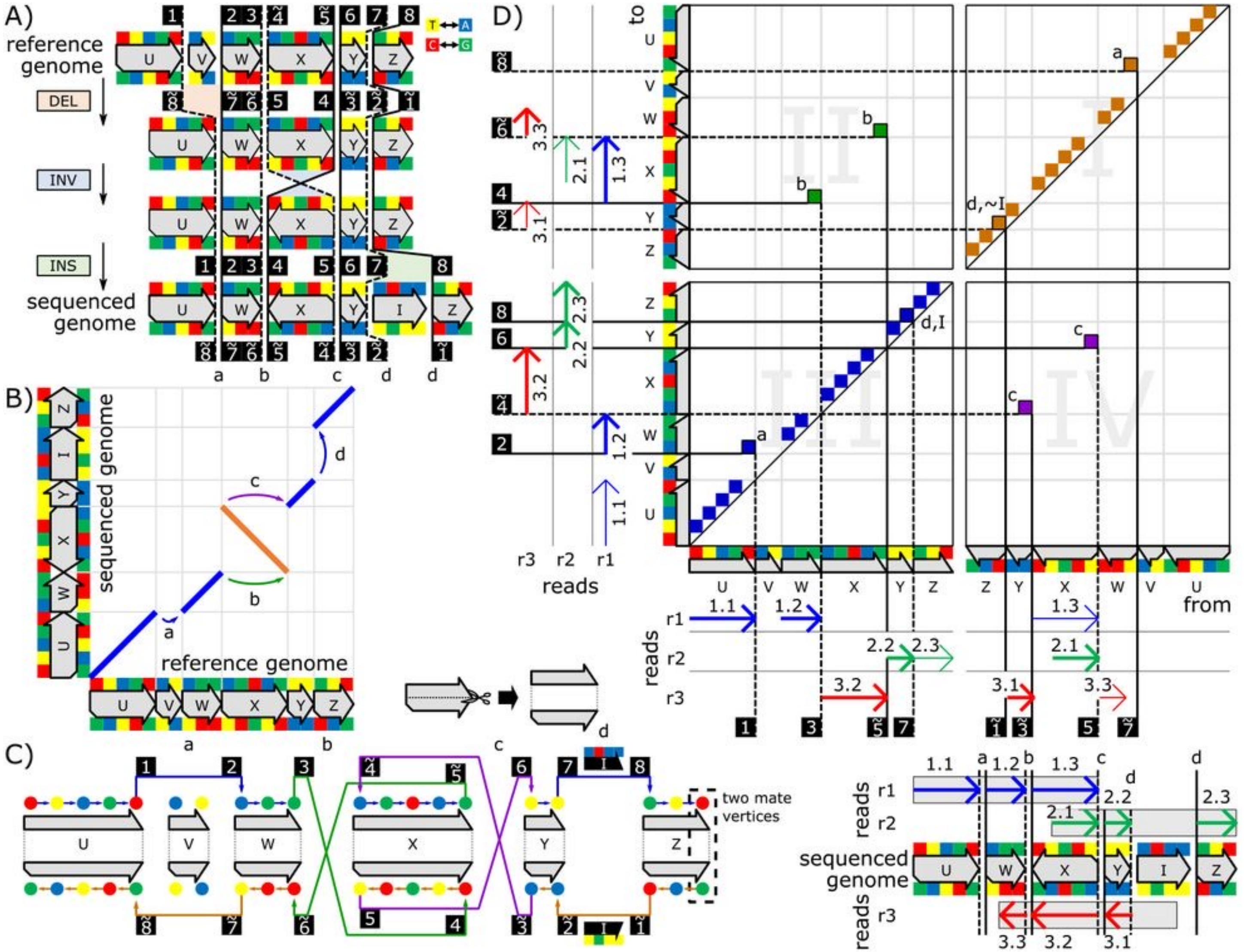




# Complex variants



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Thank you for your attention!

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