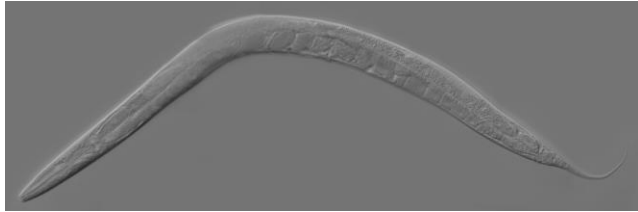


HTS

Muriel Ritsch

anne.muriel.christin.ritsch@uni-jena.de

Modellorganismen



Caenorhabditis elegans



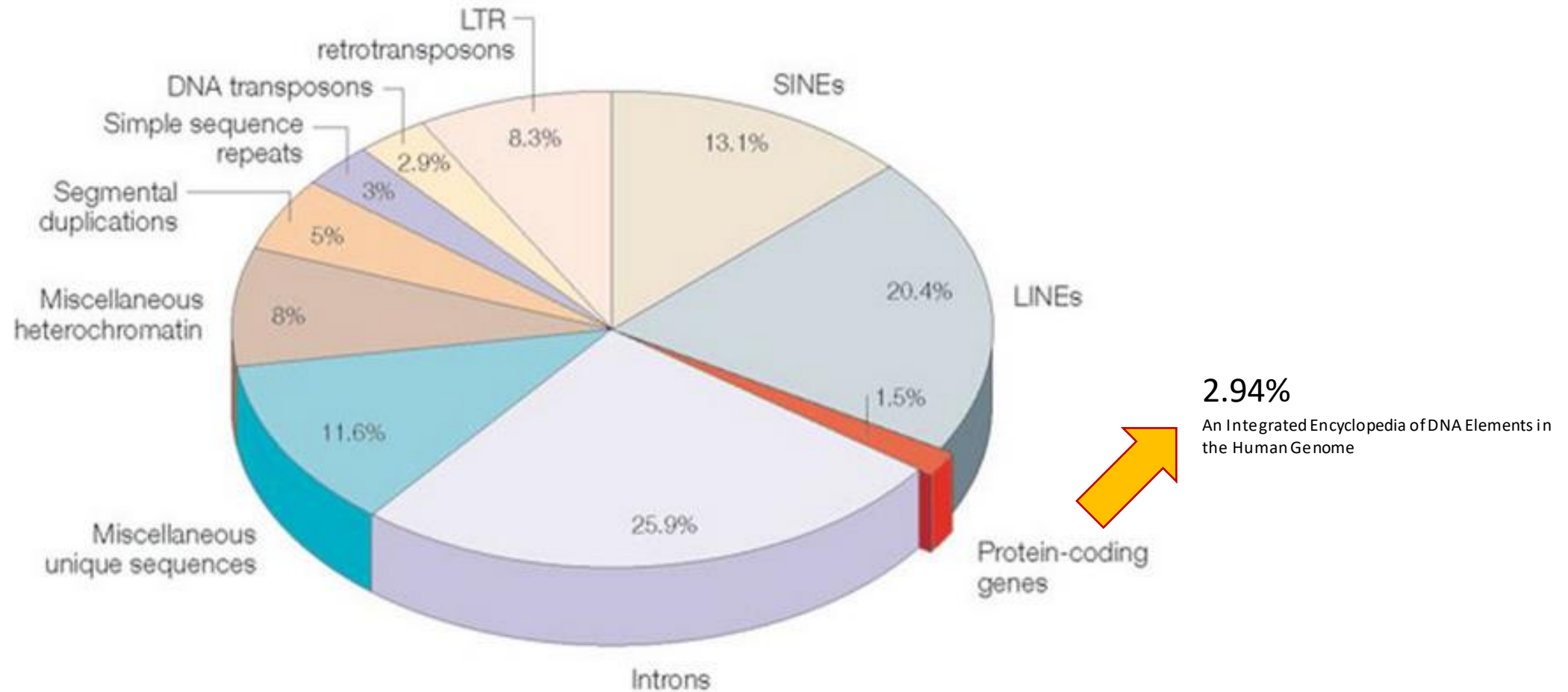
Drosophila



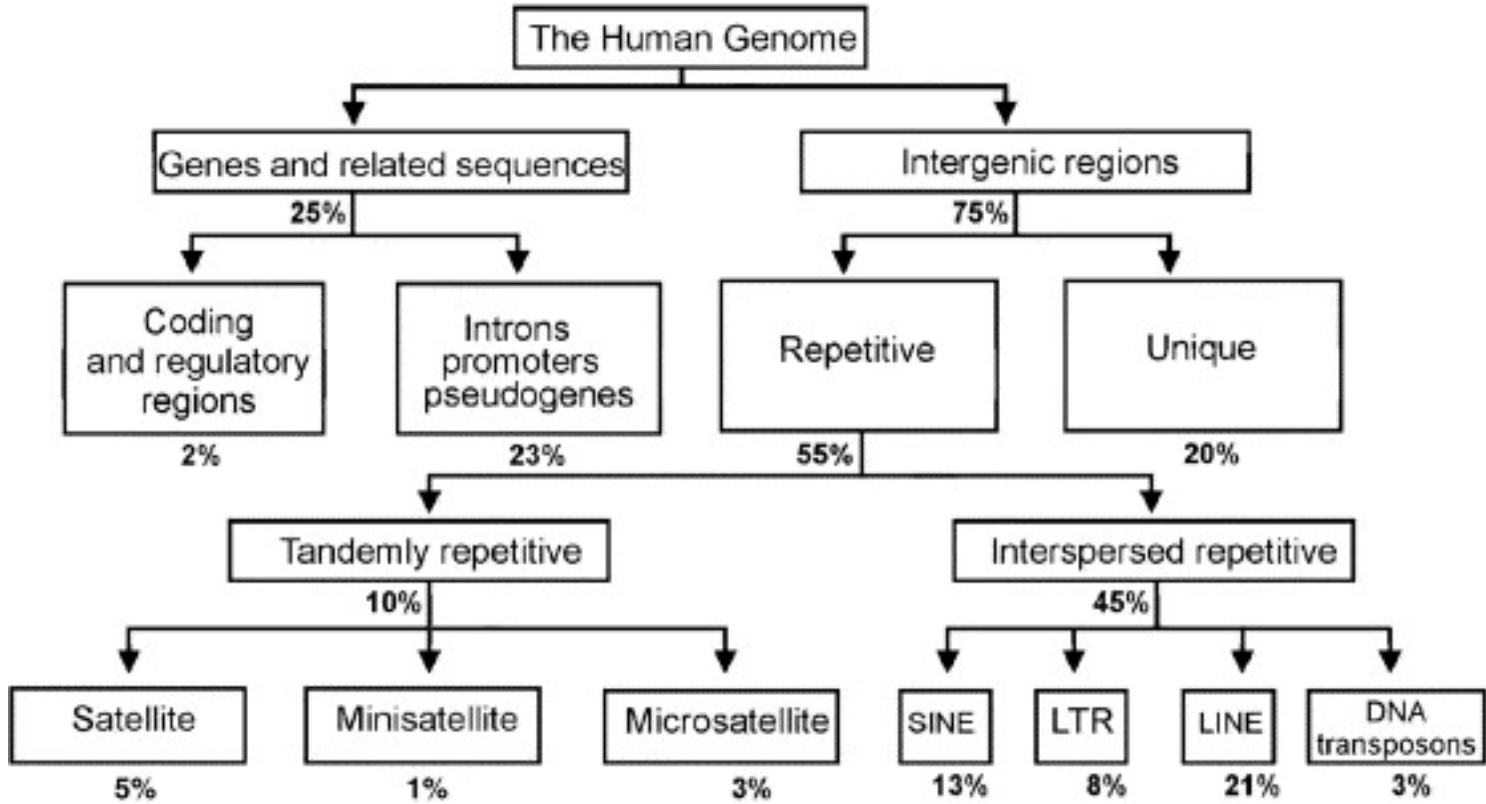
Danio rerio

Initial sequencing and analysis of the human genome

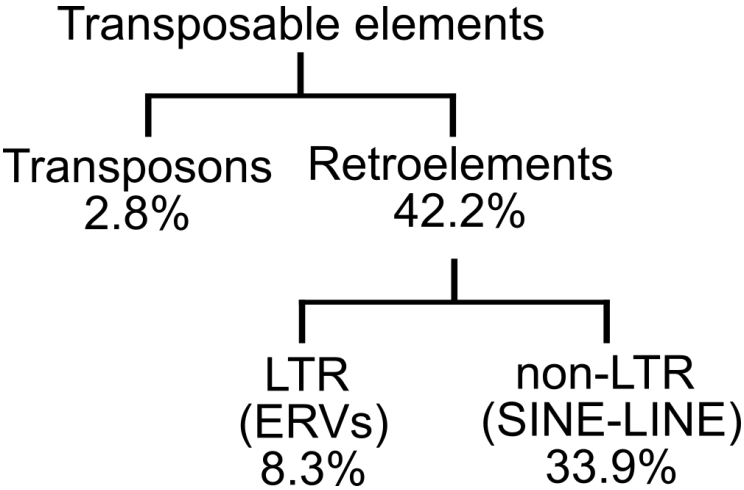
International Human Genome Sequencing Consortium



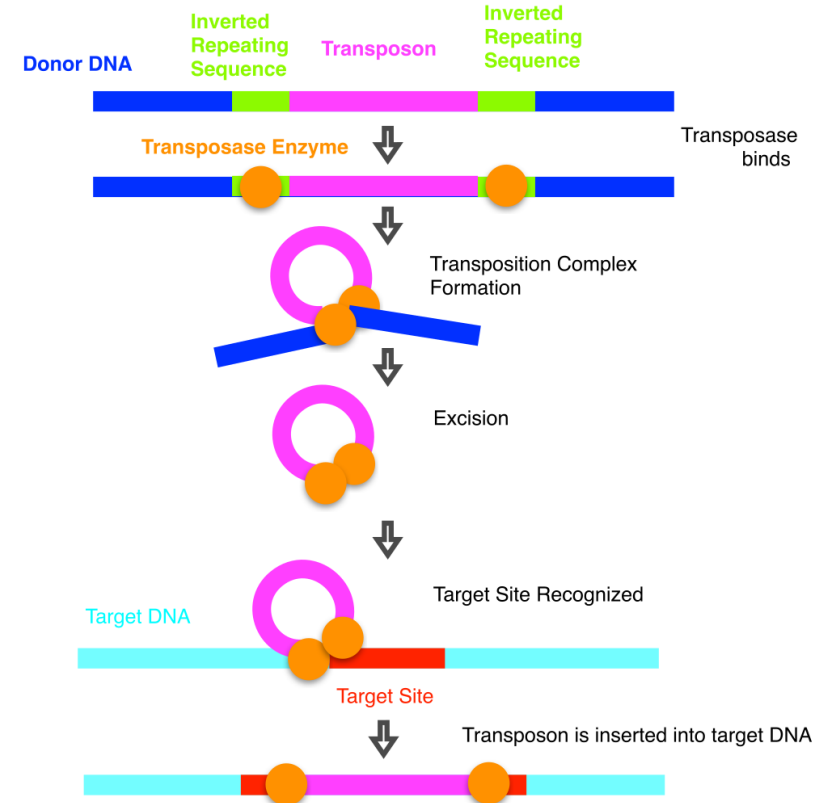
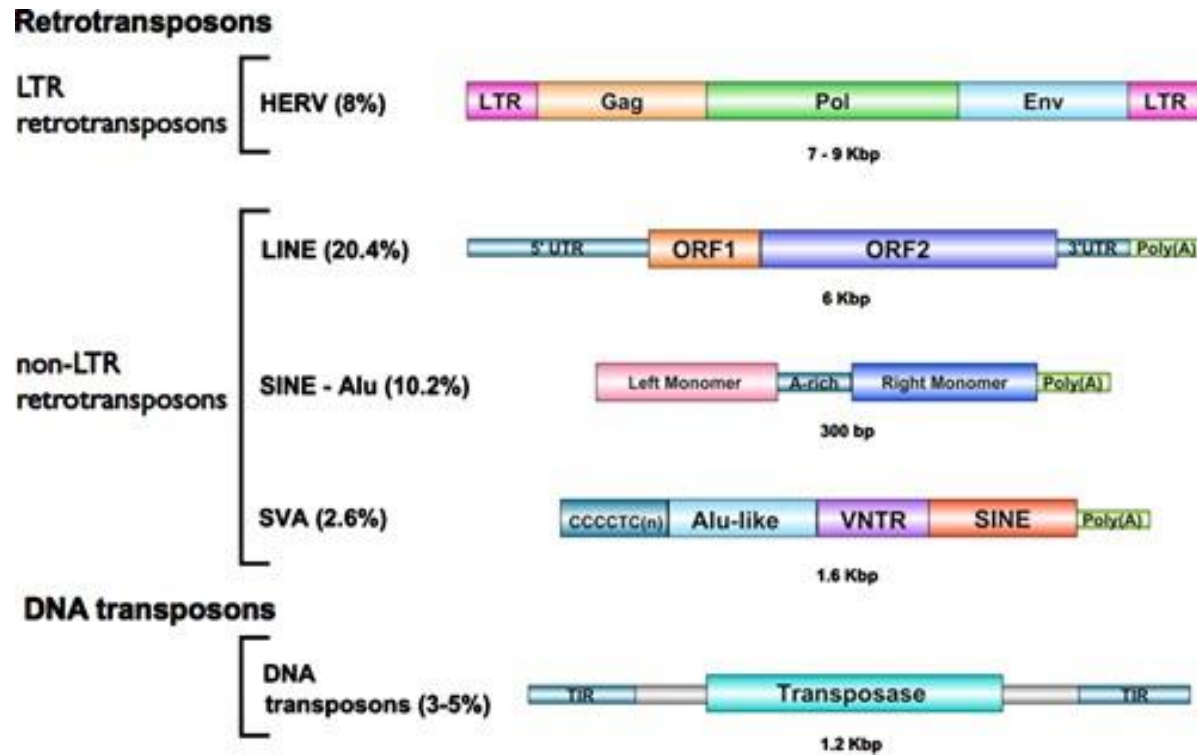
Repetitive sequences that shape the human transcriptome



Friendly viruses: the special relationship between endogenous retroviruses and their host



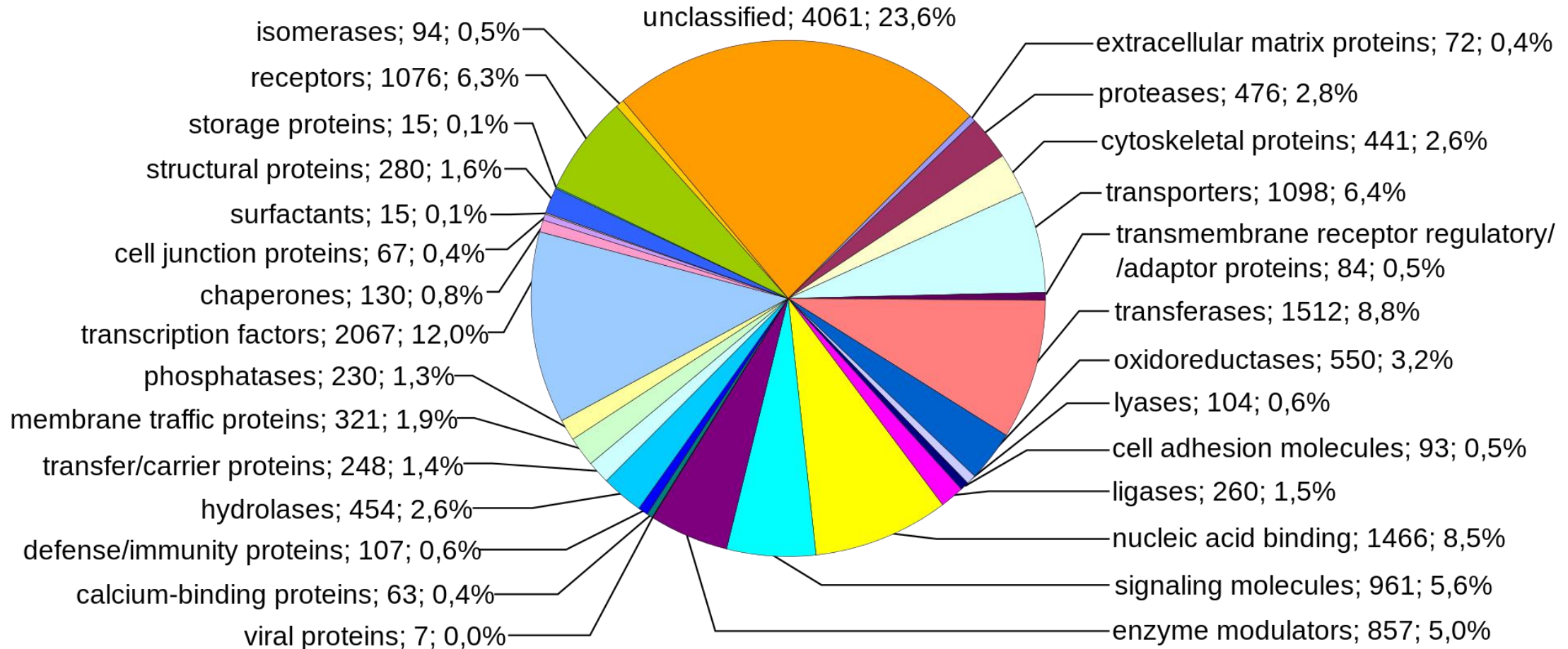
Transposons



https://www.researchgate.net/figure/Transposable-element-classification-and-molecular-structure-LTR-transposons-or-human_fig2_260446945

https://en.wikipedia.org/wiki/DNA_transposon

2.94%



Sequenziertechnologien

1. Generation

- Sanger Sequencing: <https://www.youtube.com/watch?v=KTstRrDTmWI>
- Maxam-Gilbert Sequencing: <https://www.youtube.com/watch?v=B5Dj8PL4E0>

NGS (short-read NGS)

- Illumina Sequencing: <https://www.youtube.com/watch?v=fCd6B5HRaZ8>
- Roche 454 Sequencing: <https://www.youtube.com/watch?v=KzdWZ5ryBIA>
- SOLiD sequencing: <https://www.youtube.com/watch?v=nlvyF8bFDwM>

NGS (long-read NGS)

- Pacbio: https://www.youtube.com/watch?v=_ID8JyAbwEo
- Nanopore Sequencing: <https://www.youtube.com/watch?v=RcP85JHLmnl>
<https://www.youtube.com/watch?v=CGWZvHli3i0>

THE EVOLUTION OF SEQUENCING

First Generation

Sanger Sequencing
Maxam and Gilbert
Sanger Chain-termination

- Infer nucleotide identity using dNTPs then visualize with electrophoresis
- 500-1000 bp fragments
- Relatively slow and expensive

Second Generation Next Generation Sequencing

454, Solexa, Ion Torrent, Illumina

- High throughput from the parallelization of sequencing reactions
- High accuracy
- ~50-500 bp fragments
- Faster and more affordable

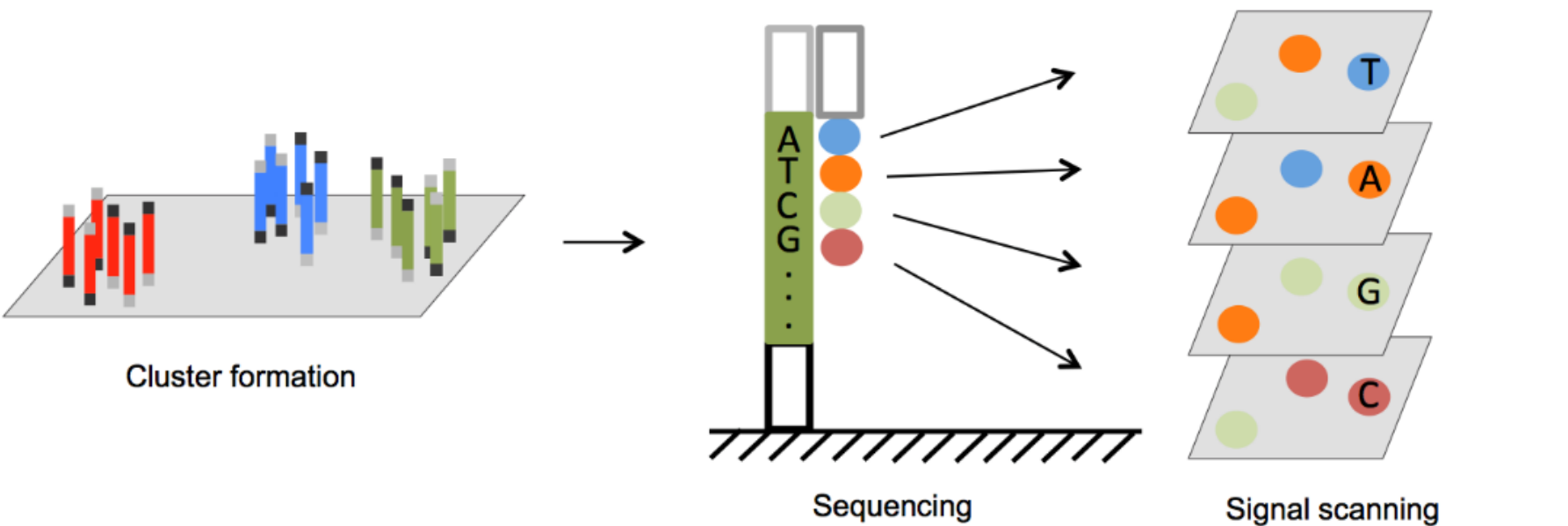
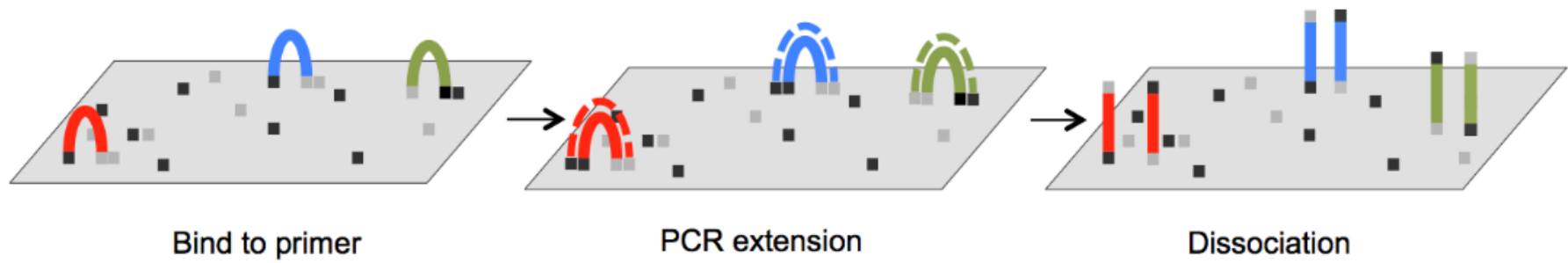
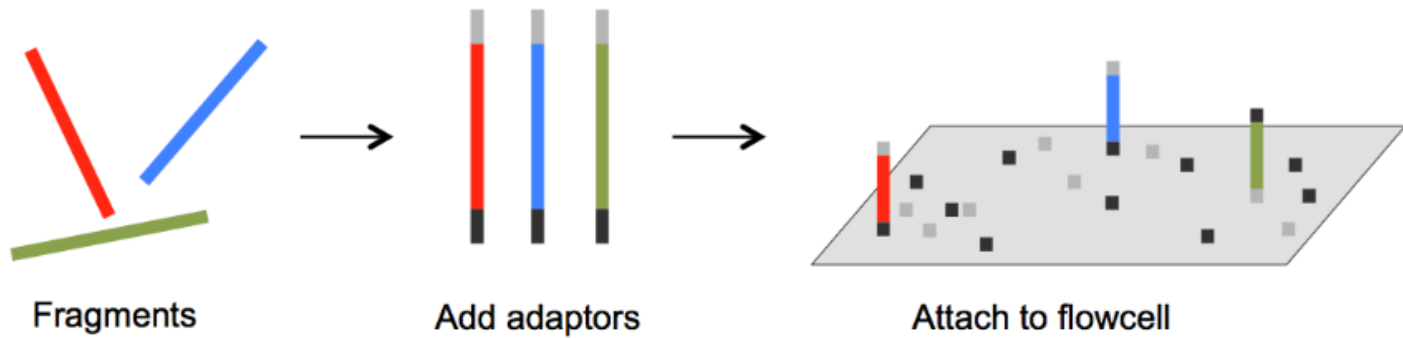
Third Generation

PacBio, Oxford Nanopore

- Sequence native DNA in real time with single-molecule resolution
- Traditionally lower accuracy than NGS
- Tens of kb fragments, on average

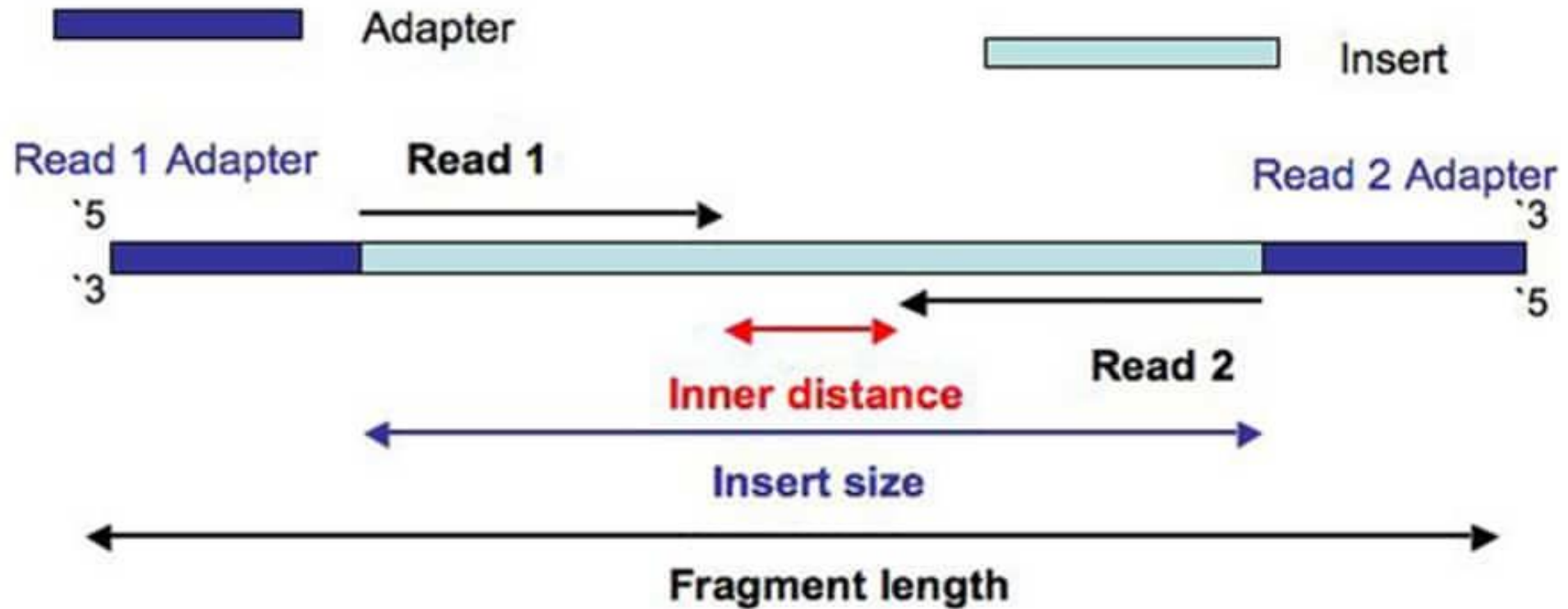
Short-read sequencing

Long-read sequencing



<http://en.biomarker.com.cn/platforms/illumina>

Paired-end reads (PE)

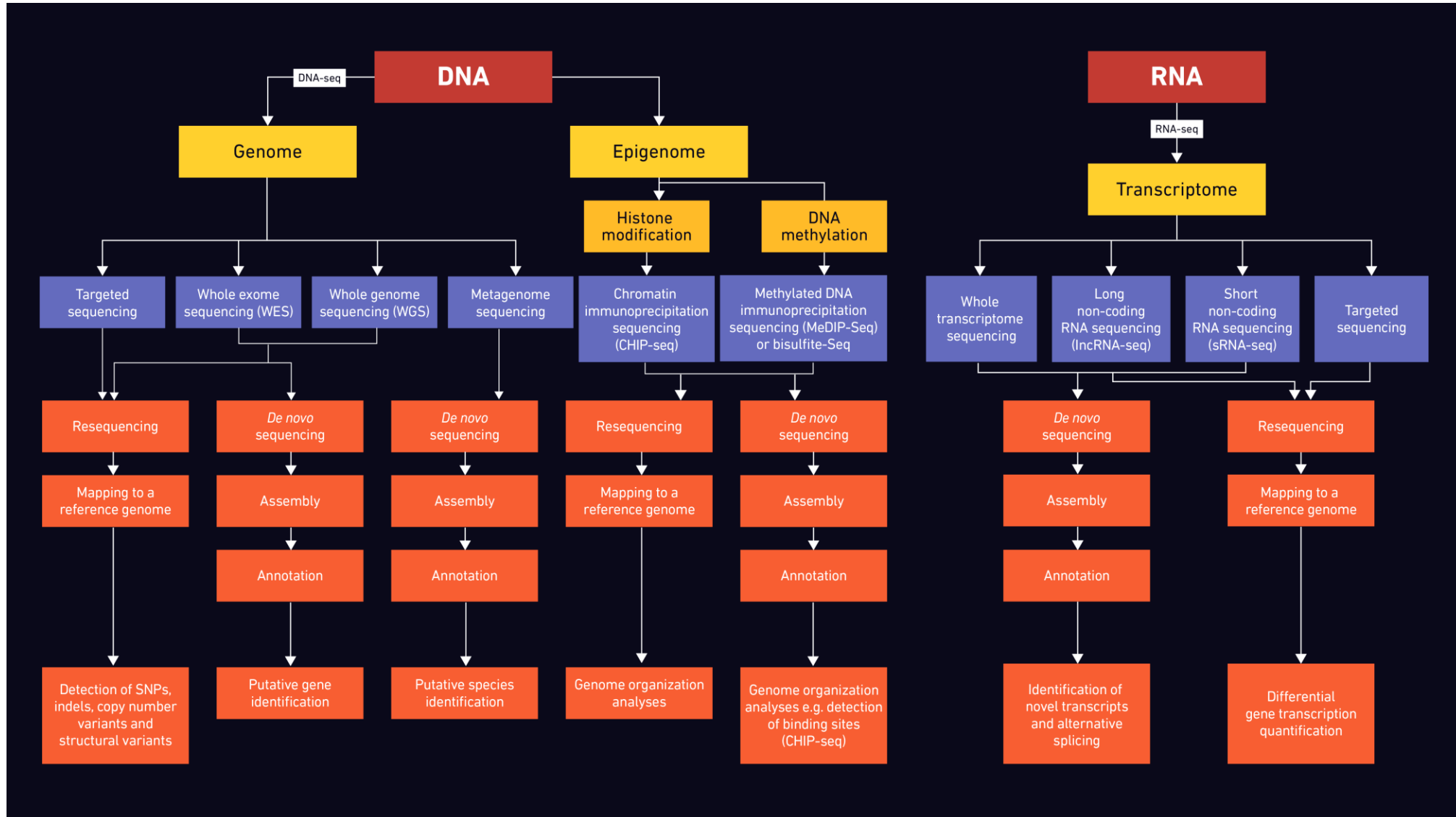


Coverage

```
Read 1: CGGATTACGTGGACCATG (read length of 18)
Read 2:   ATTACGTGGACCATGAATTGCTGACA
Read 3:           ACCATGAATTGCTGACATTTCGTCA
Read 4:           TGAATTGCTGACATTTCGTCAT

Depth:  1 1 1 2 2 2 2 2 2 2 3 3 3 3 4 4 3 3 3 3 3 3 3 3 2 2 2 2 2 2 1
```

possible sequencing strategies



Illumina website

- <https://www.illumina.com/products/by-type/sequencing-kits/cluster-gen-sequencing-reagents/miseq-reagent-kit-v3.html>
- <https://www.illumina.com/products/by-type/sequencing-kits/cluster-gen-sequencing-reagents/novaseq-reagent-kits.html>