

精子单细胞全基因组测序

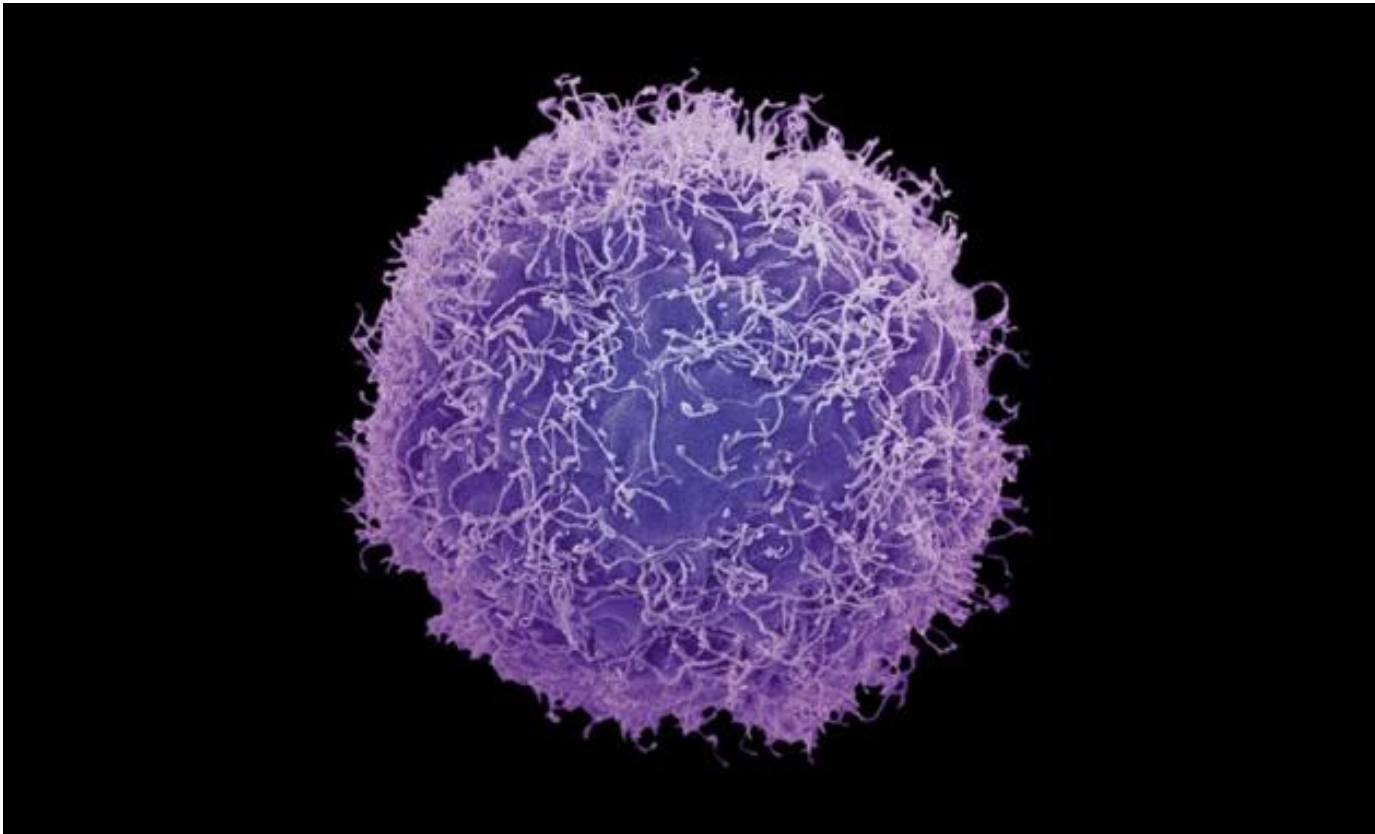
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Outline

1. Introduction to single cell sequencing
2. Whole genome amplification technologies
3. The 100 single sperm sequencing project

Introduction to single cell sequencing



Everyone of us developed from a single cell – the zygote.

Why we need single cell sequencing?

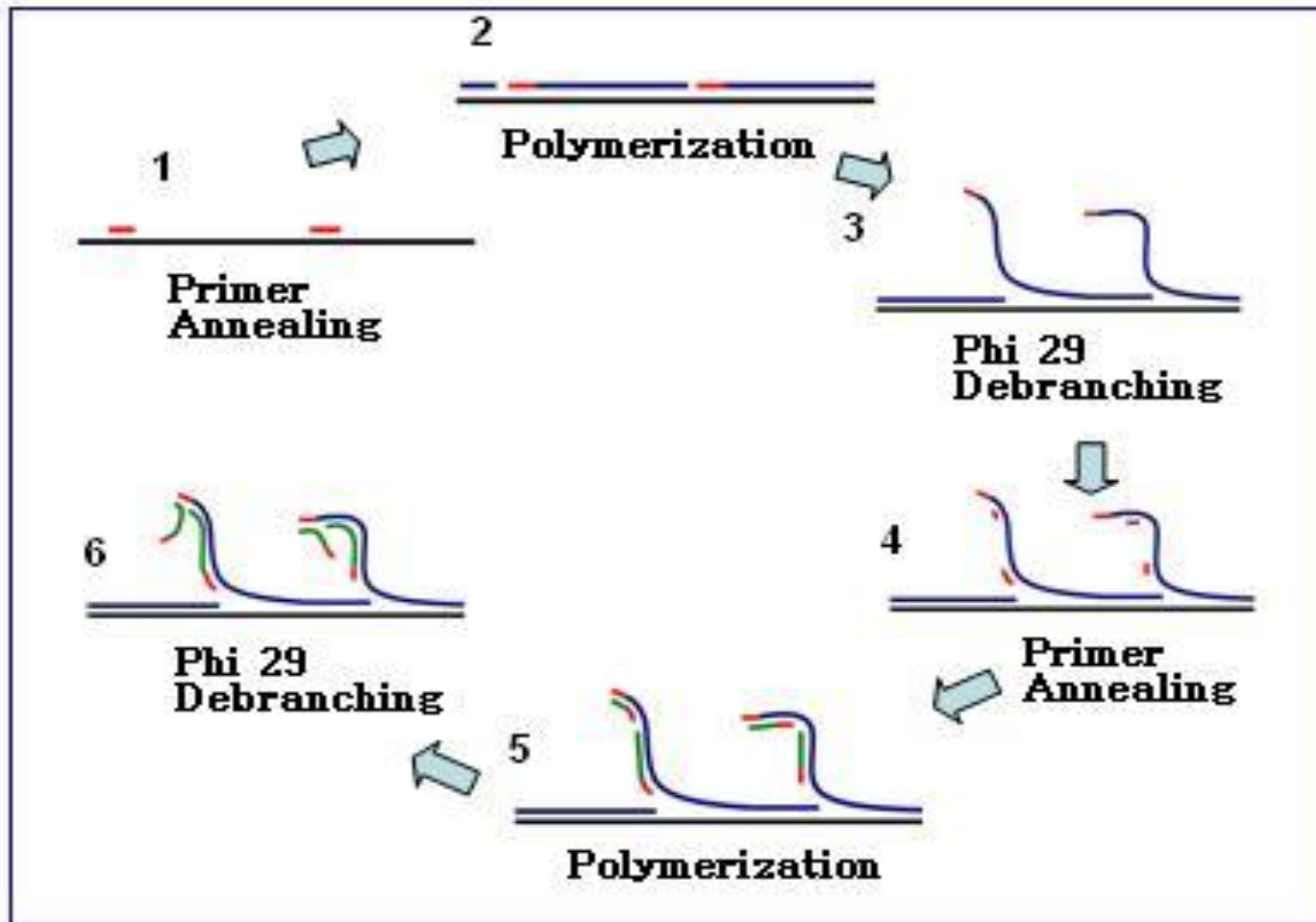
Cells in our body are different in:

- genome
- transcriptome
- epigenome

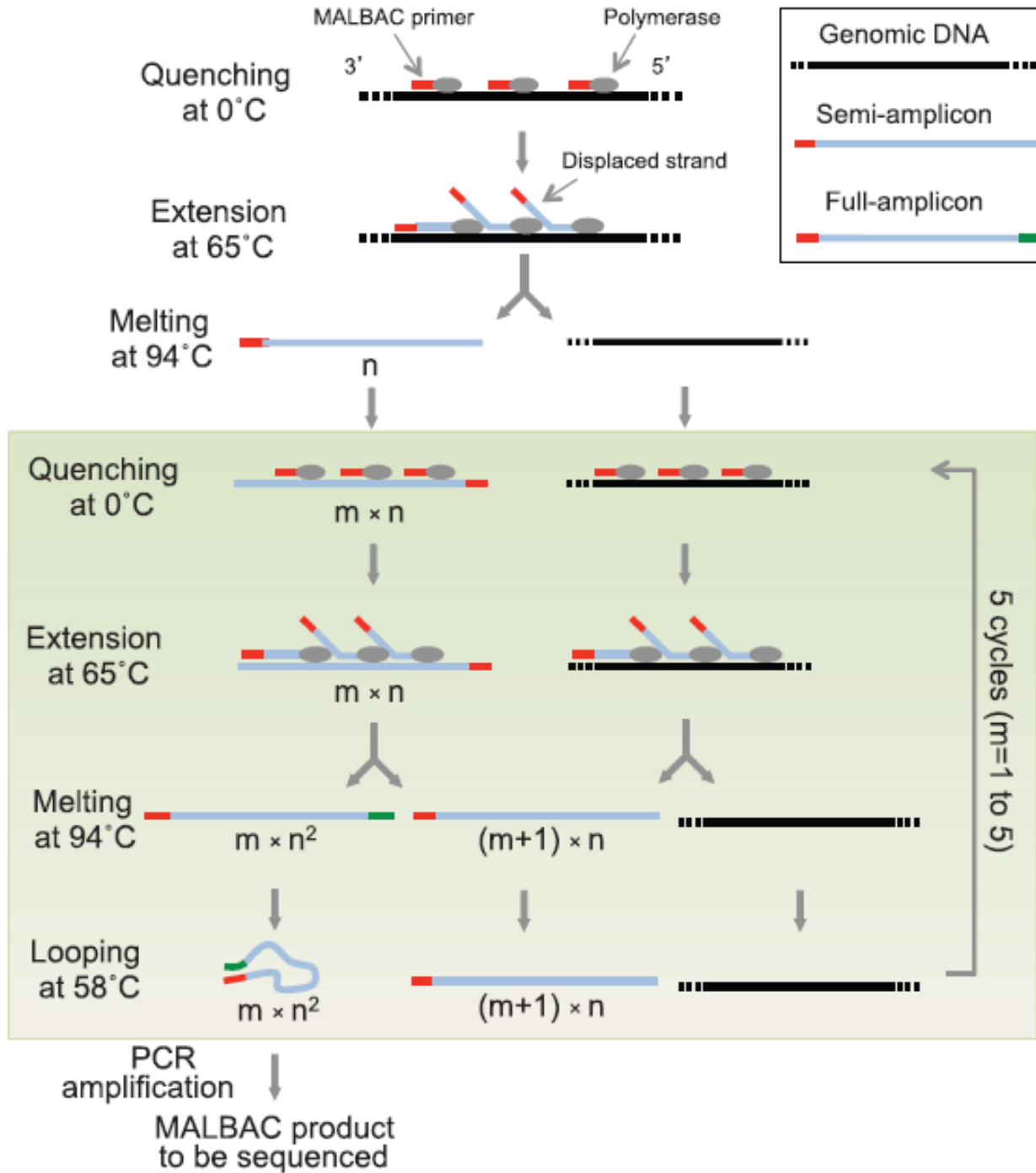
Ways to achieve single cell sequencing

- Separate single cells
Microscopy, Flow Cytometry.
- DNA amplification
MDA, MALBAC, etc.
- High-throughput sequencing
HiSeq, Solid, Ion Torrent, etc.

Whole genome amplification technologies



MDA
(Multiple
Displace-
ment
Amplifi-
cation)



MALBAC
(multiple
annealing
and
looping-
based
Amplification
cycles)

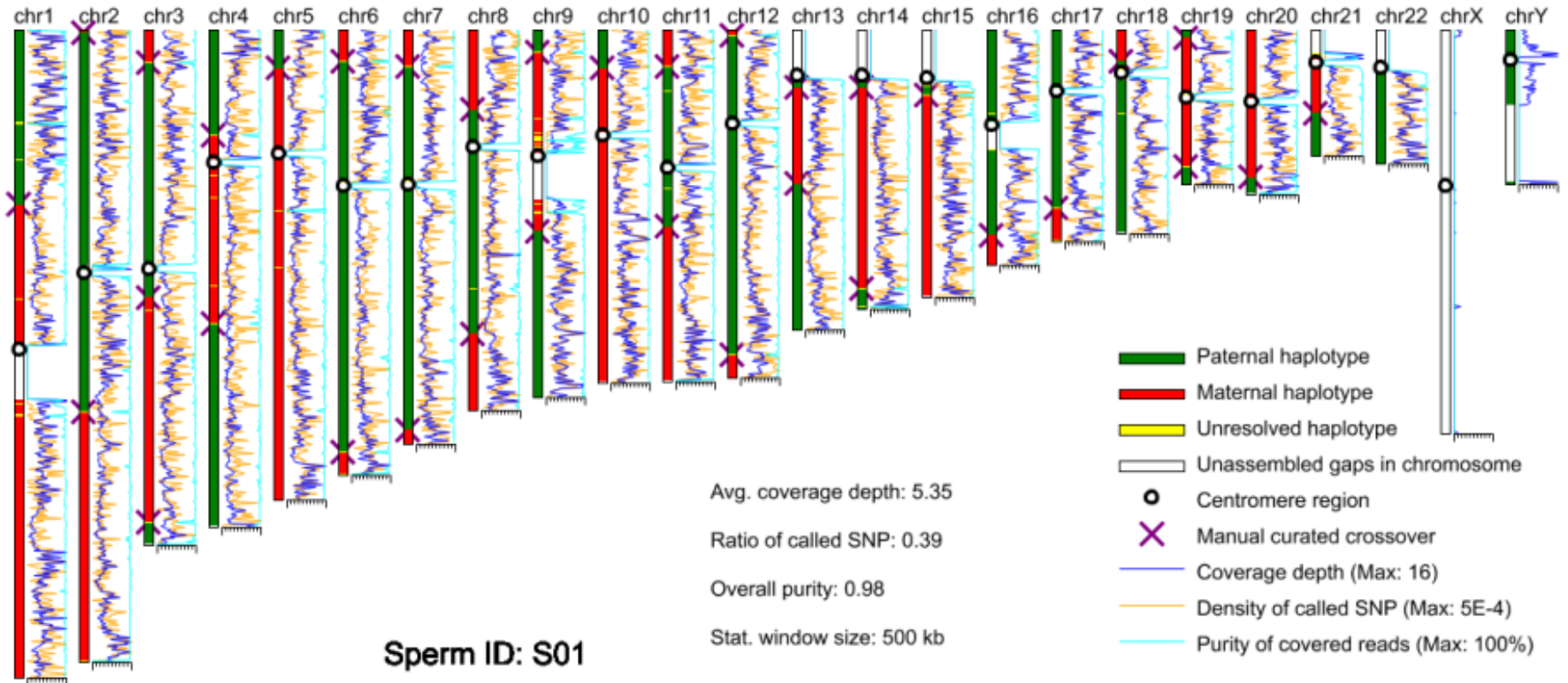
Compare the available amplification technologies

	MALBAC	MDA
Primer类型	随机引物 + common 27-bp	随机引物
Polymerase	Bst large fragment	Phi 29
Error rate	1.00E-05	1.00E-07
反应过程	多轮循环，每轮均需添加聚合酶	常温，一次反应完成
扩增均匀度	接近线性扩增，均匀性较好	指数级扩增，均匀性较差
商品化程度	即将商品化	已经商品化

The sperm project

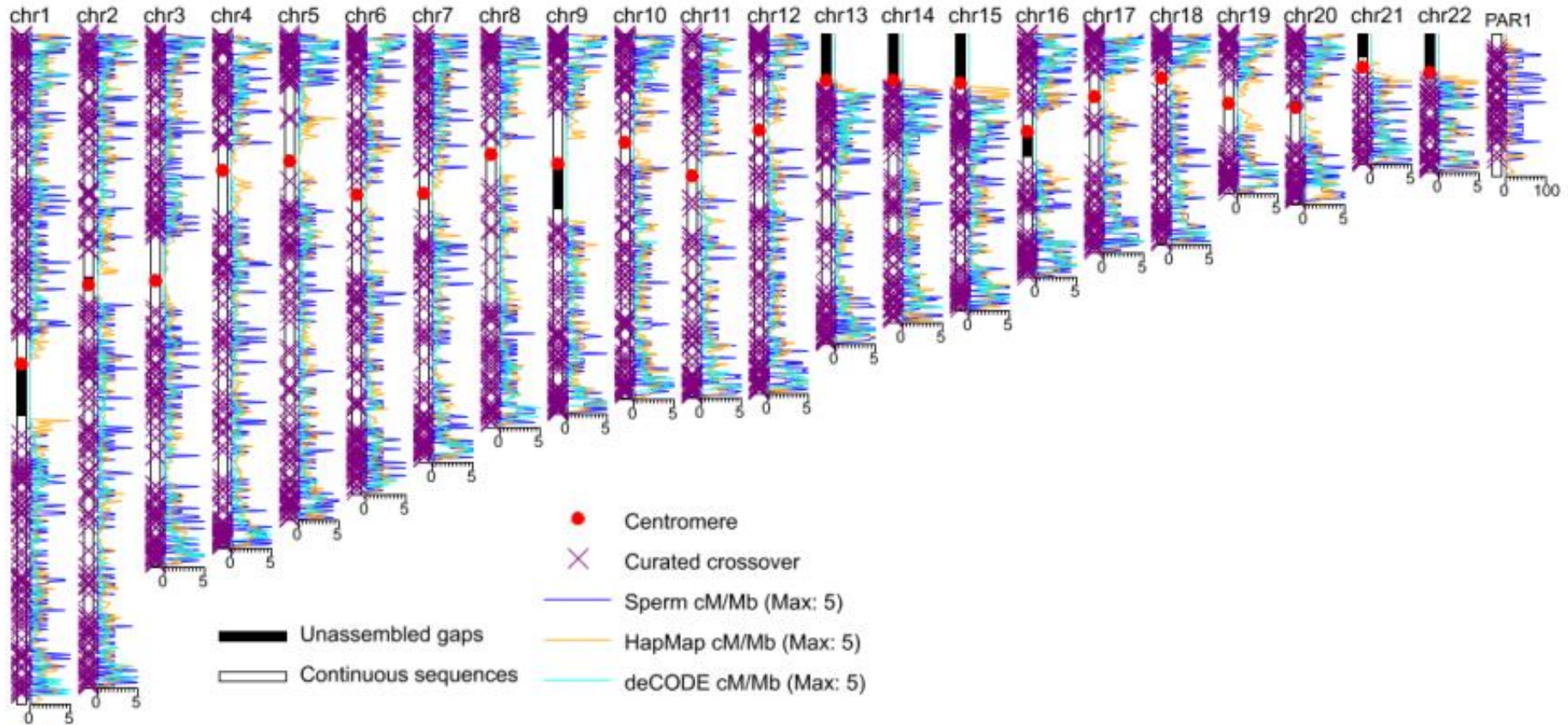
- We sequenced 100 sperms, one at $\sim 1X$ coverage
- Phasing the parental haplotypes with sperm linkage information.
- Construct the first individual genetic map, in contrast with traditional population genetic map.
- Also find $\sim 5\%$ sperms missing or duplicate one or more chromosomes.

Recombination pattern of a sperm



In average, there are 26 recombination events in each sperm.

Recombination rate along each chromosome



The large scale distribution pattern of individual genetic map is consistent with the population derived genetic maps.

Thanks!