

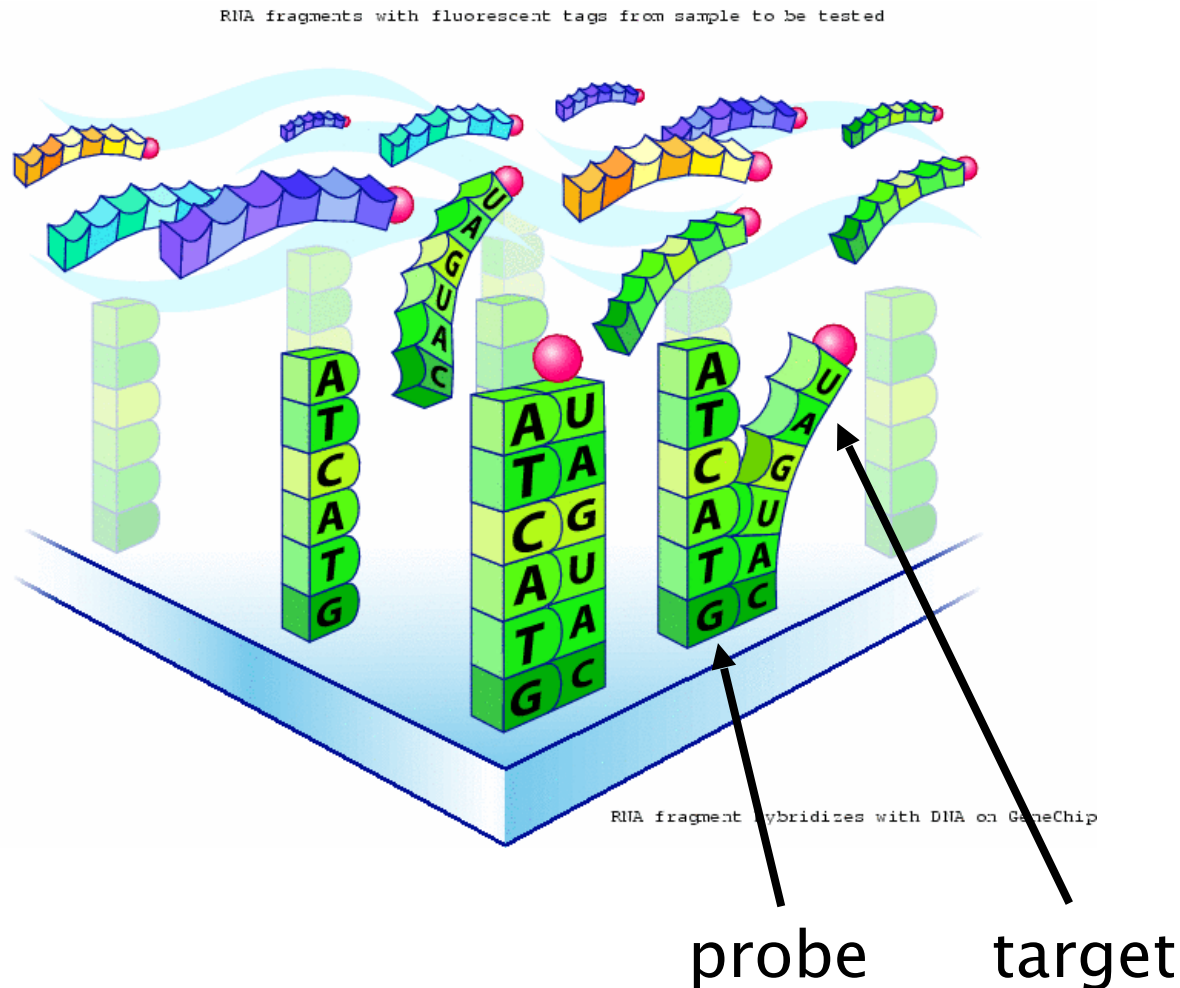


Quick intro to genomic technologies:

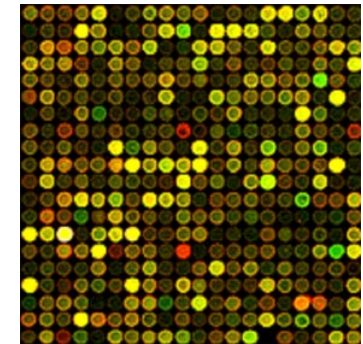
- **microarrays, sequencing**
- **DNA methylation (450k array, RRBS)**
- **gene expression (RNA sequencing)**

Mark D. Robinson, Institute of Molecular Life Sciences

The old technology: DNA microarray



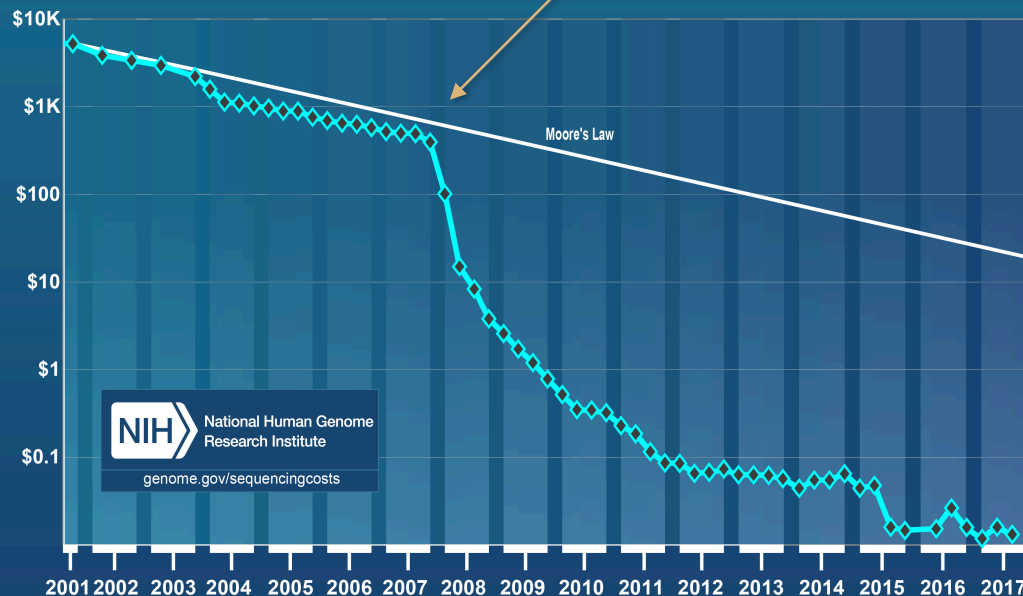
Abundance (of
complementary
DNA species)
measured by
fluorescence
intensity



High-throughput (or “next generation”) sequencing

(Solexa) Illumina

Cost per Raw Megabase of DNA Sequence



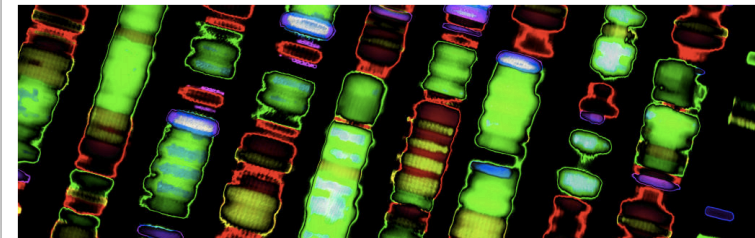
<https://www.statnews.com/2017/01/09/illumina-ushering-in-the-100-genome/>

BUSINESS

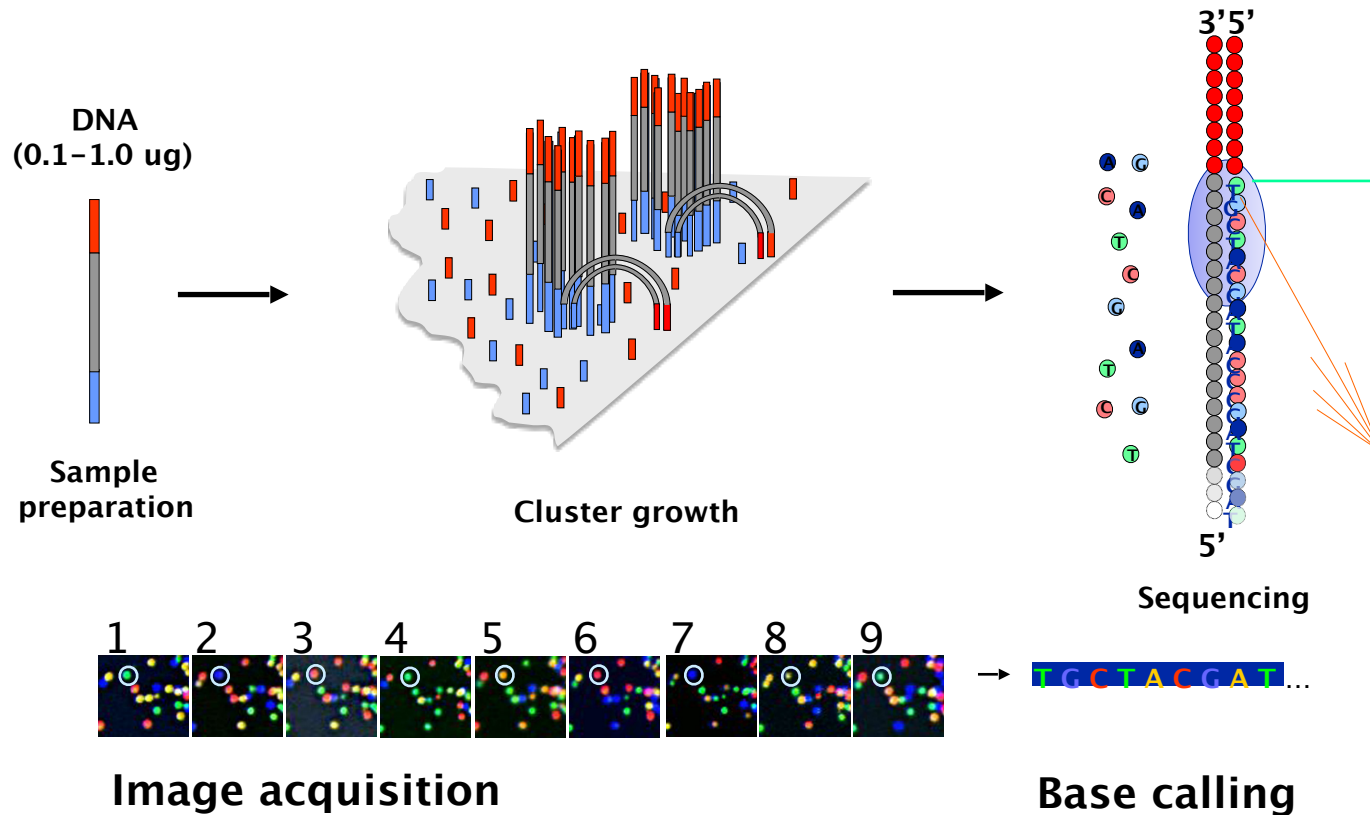
STAT+

Illumina says it can deliver a \$100 genome — soon

By MEGHANA KESHAVAN @megkesh / JANUARY 9, 2017

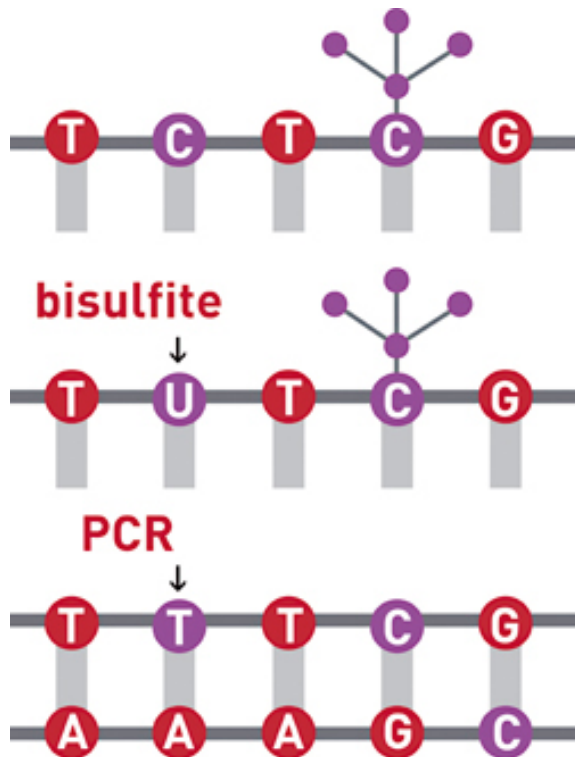


Illumina Sequencing Technology



This slide courtesy of Gary Schroth, Illumina

Bisulphite sequencing

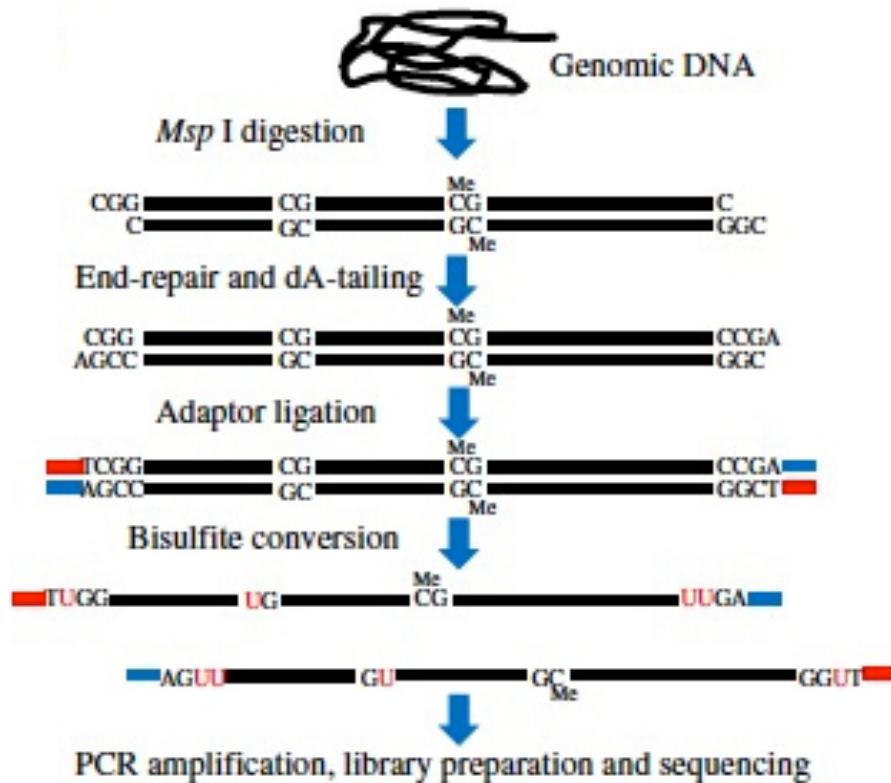


Sodium bisulphite converts methylated **C**ytosine into **U**racil, which can be read as **T**hymine after PCR

In combination with sequencing (Sanger or NGS), can achieve methylation mapping at single base resolution

Can be nicely combined with genotyping arrays (e.g. Illumina HumanMethylation 450k) or with high-throughput sequencing.

DNA Methylation: reduced representation bisulphite sequencing



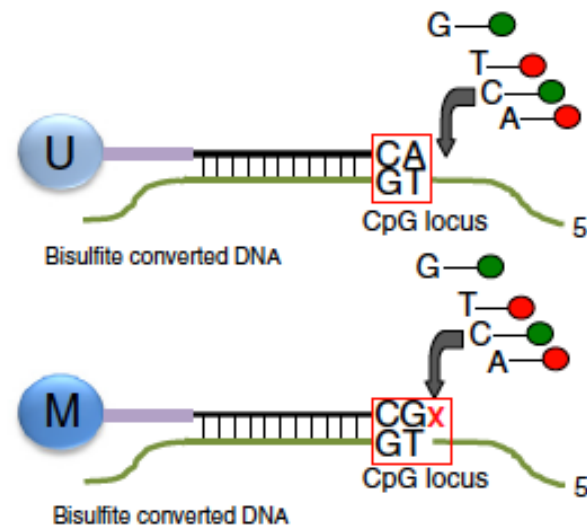
J Genet Genomics, 2014, 41:513-528



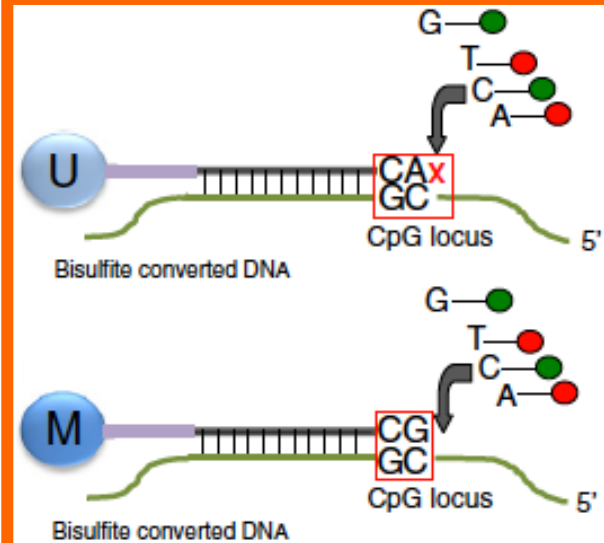
Bisulphite conversion + “genotyping” array (Illumina HumanMethylation450)

Type I
(2 probes)

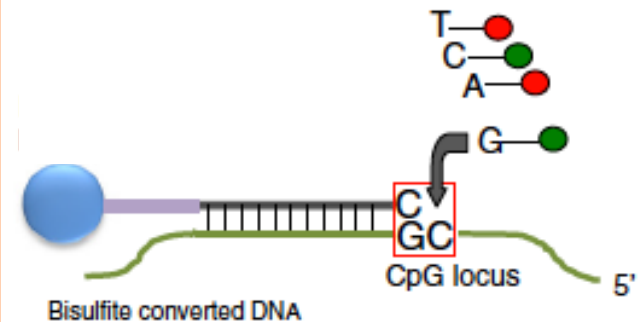
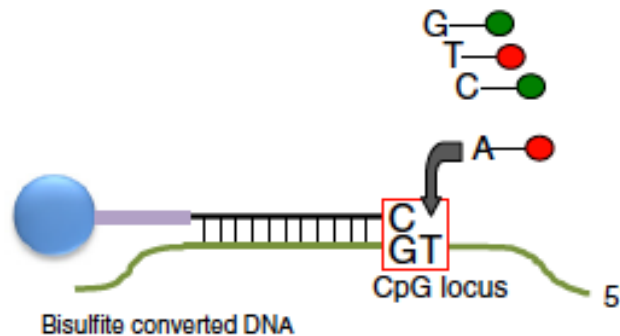
Unmethylated CpG site



Methylated CpG site

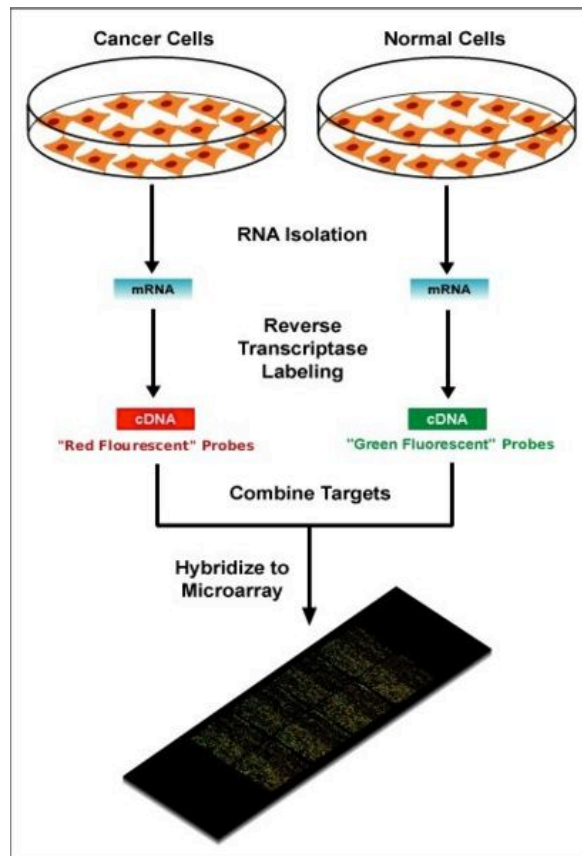


Type II
(1 probe)

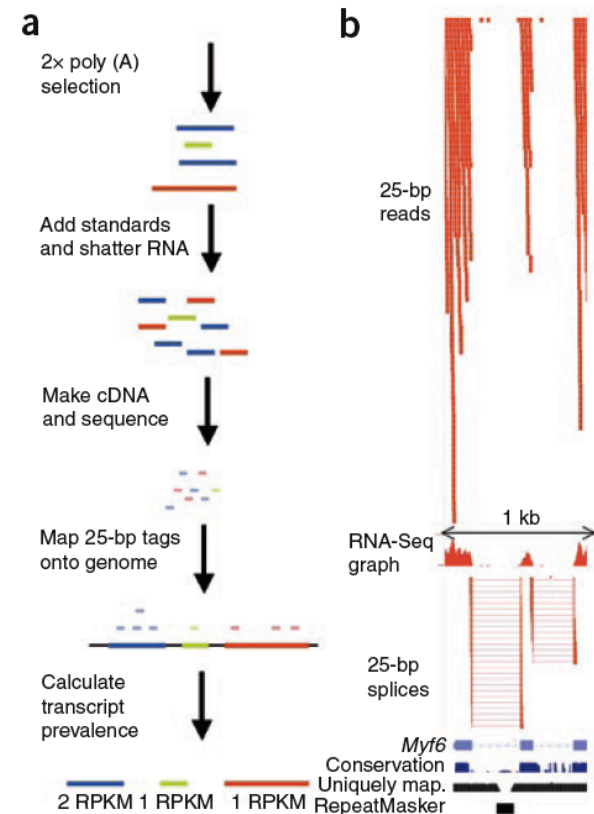


Gene expression

Abundance by Fluorescence Intensity

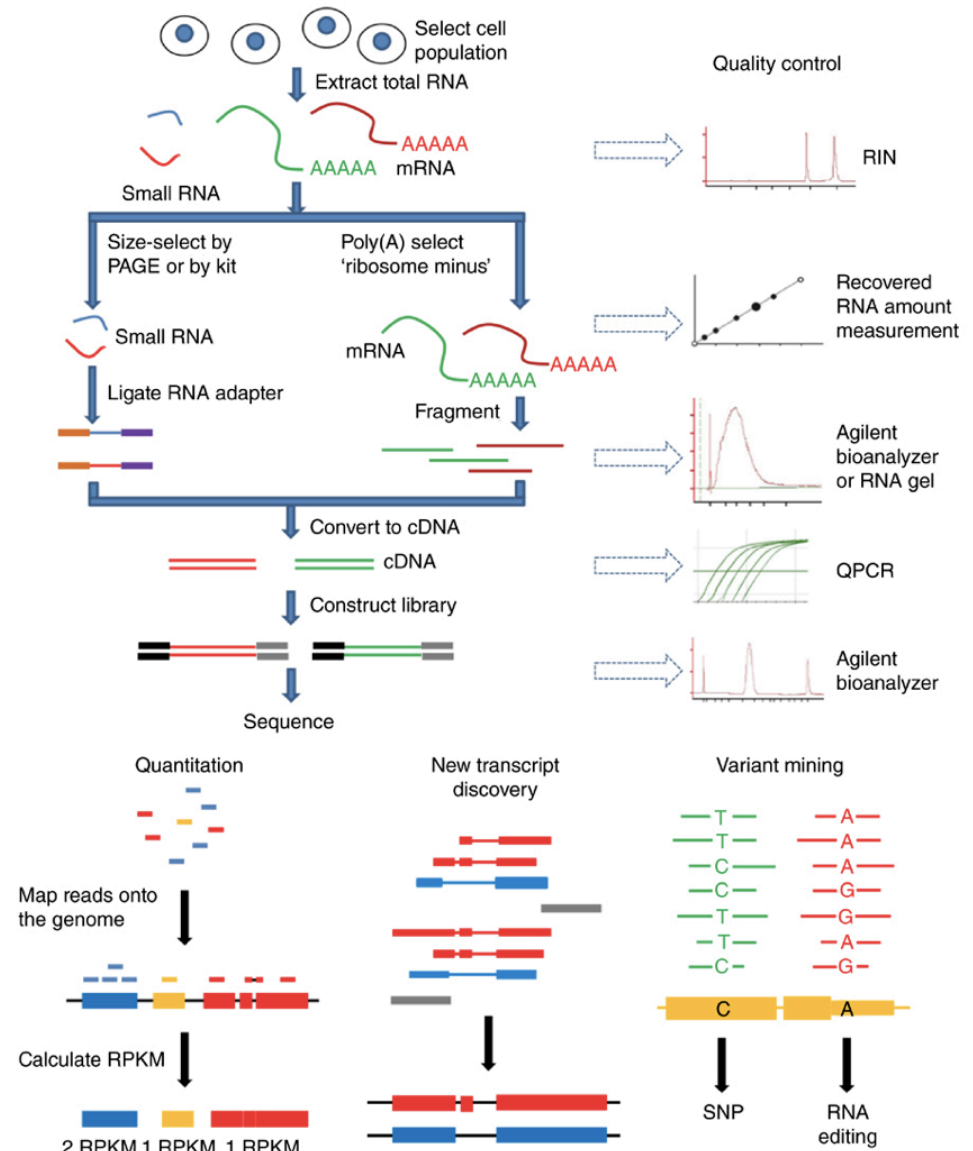


Abundance by Counting



RNA-seq differential expression analyses

1. **Map** the reads to reference sequences
2. **“Count”** reads that map to genes (quantify)
3. Compute DE **Statistics**





Epigenetics definition

Epi - "on top of" or "in addition to"

“Epigenetics”:

- **heritable alterations in gene expression caused by mechanisms other than changes in DNA sequence.**
- the study of the mechanisms of temporal and spatial control of gene activity during the development of complex organisms

Dogma: CpG methylation and transcription (cancer)

