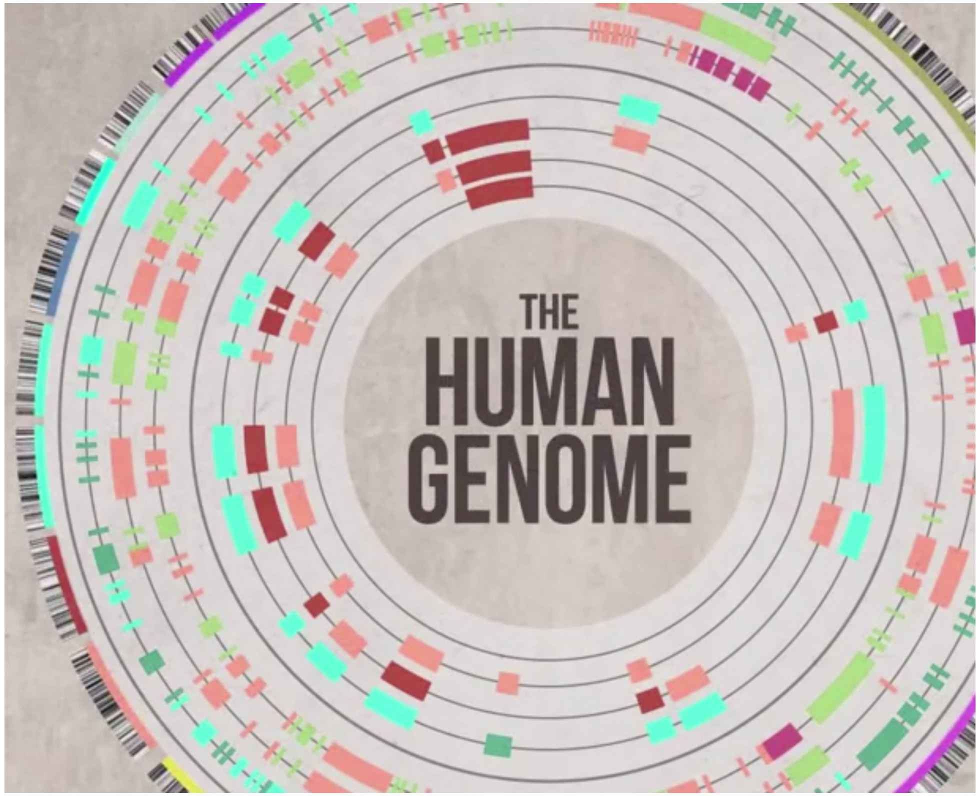
Genome sequencing story

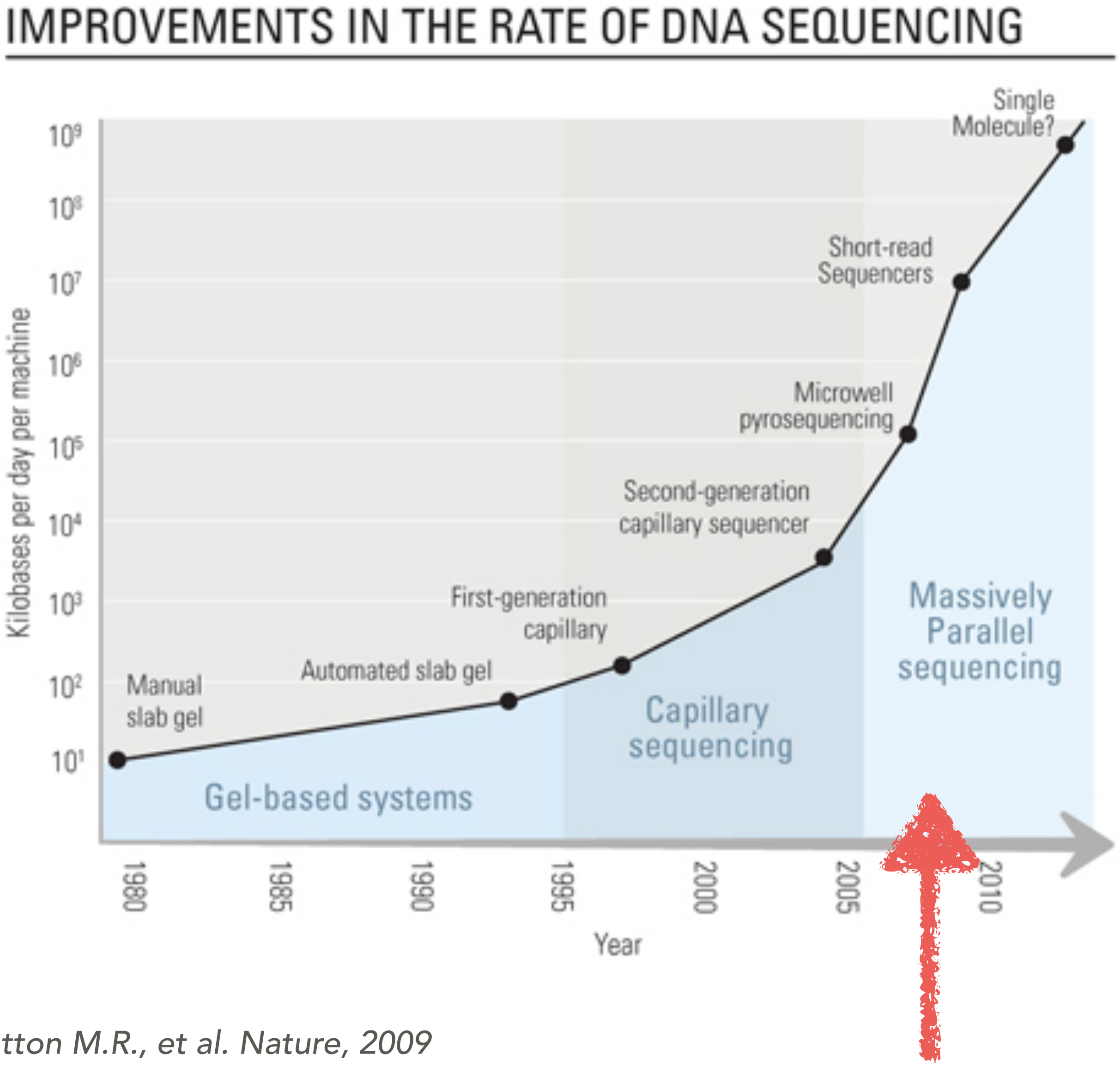
The sequencing of Human Reference genome provided a roadmap that is the foundation for modern biomedical research.



The technology that sequences the human genome was based on capillary electrophoresis of individual fluorescently labelled Sanger sequencing reaction.

500-600 bases from 96 reactions in 10 hours
24-hour reactions = 115 Kbp

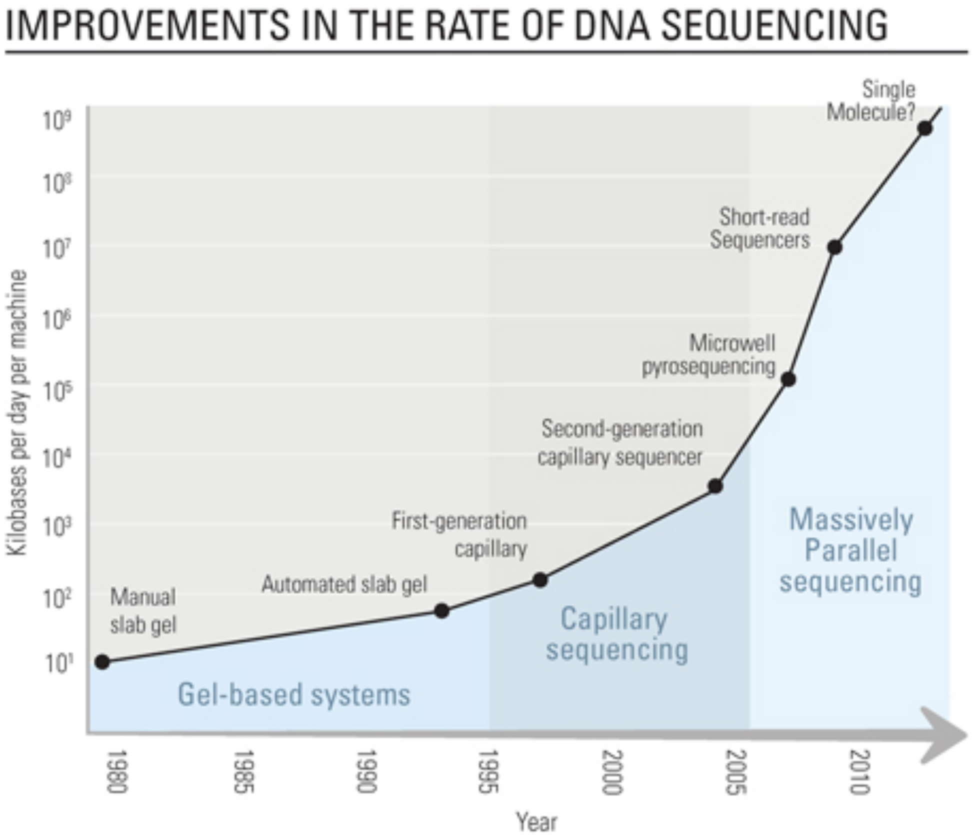
Moving forward in the genomic era, the Next generation DNA sequencing technology is enable a revolutionary advances



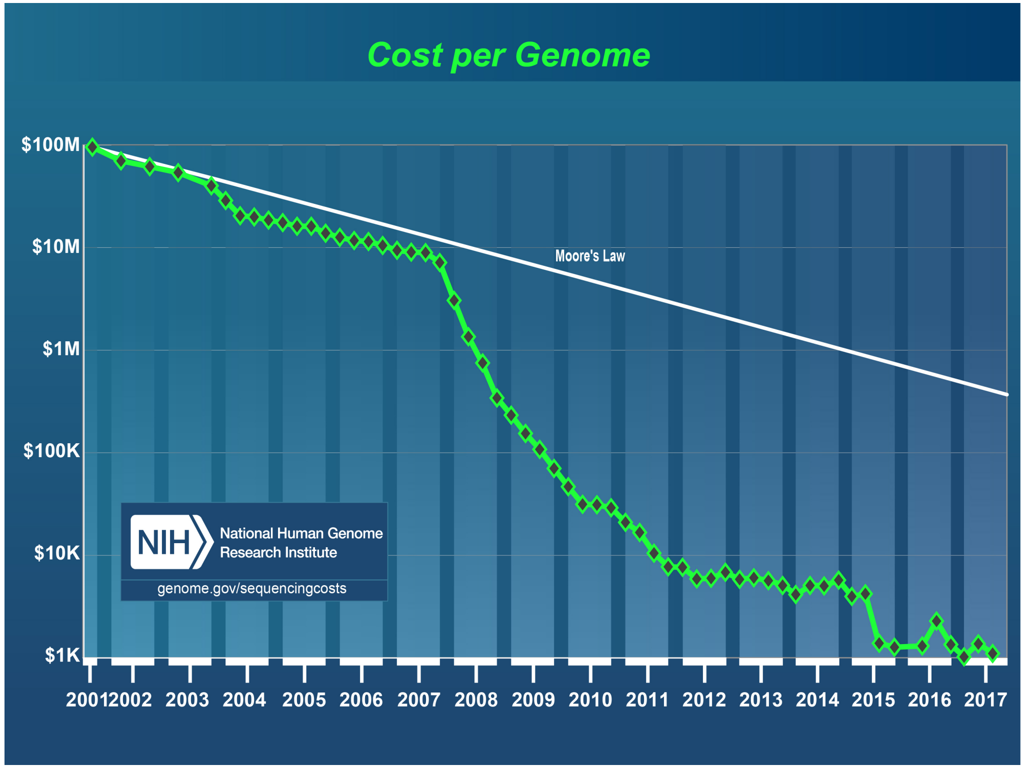
Stratton M.R., et al. Nature, 2009

The alliance between biology/clinic and computer science

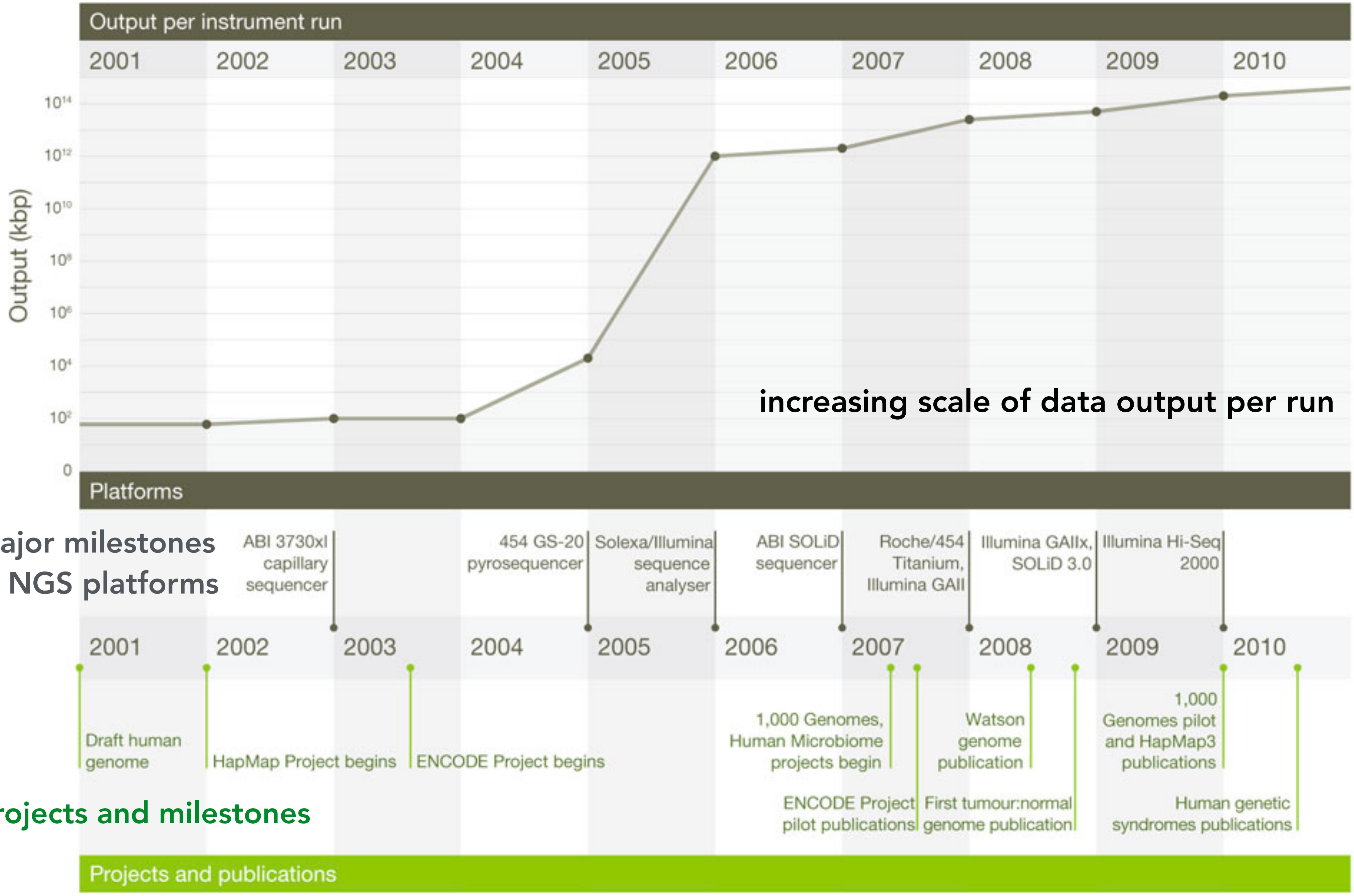
Bioinformatics: The term computational biology is defined as the development and application of theoretical data-analytical methods, mathematical modeling and computational simulation techniques in the context of the study of biological systems.



Stratton M.R., et al. Nature, 2009



Genome sequencing story



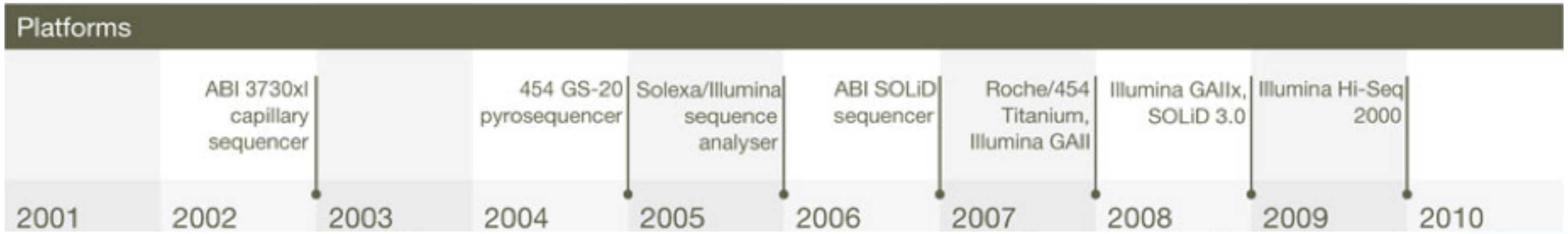
increasing scale of data output per run

major milestones in NGS platforms

projects and milestones

Mardis E.R., Nature 2012

NGS platforms



illumina

Roche

life technologies

PACIFIC BIOSCIENCES

Helicos BioSciences Corporation

ion torrent

Oxford NANOPORE Technologies

Each NGS instrument is distinctly different on its specifics

Shared attributes

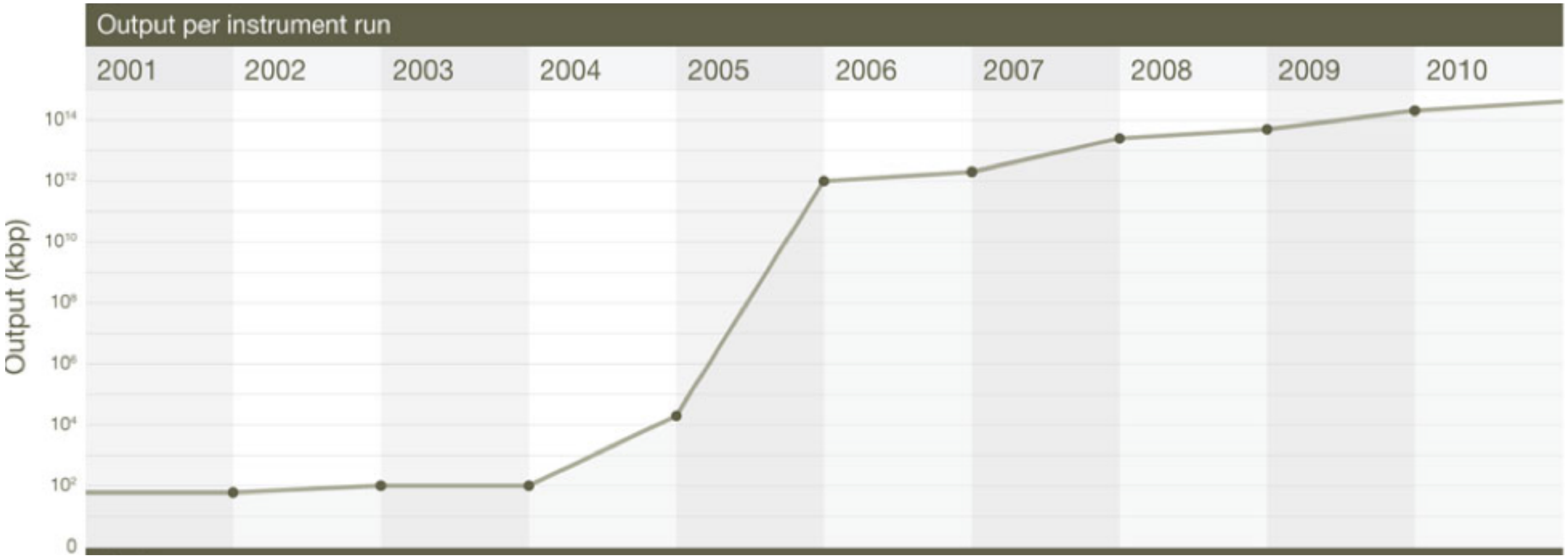
Library preparation step platform-specific adapters are ligated to the fragment to be sequenced

Amplification library fragments are amplified on a solid surface

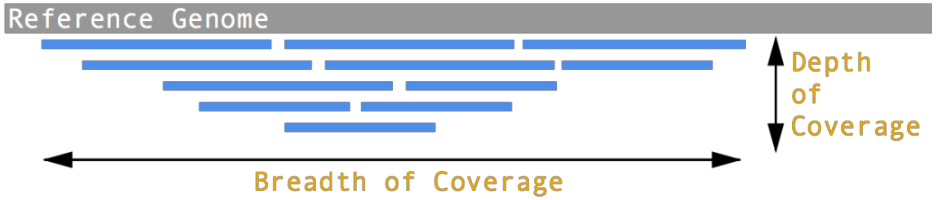
Sequencing reactions series of repeating steps that are performed to detect automatically the nucleotides

Data available it is possible obtain the sequencing information from both the ends of the fragments

NGS main features

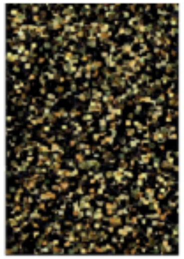


Coverage

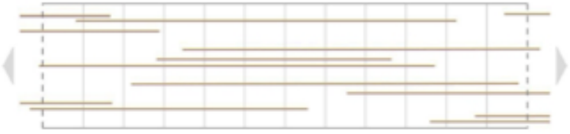


Reads

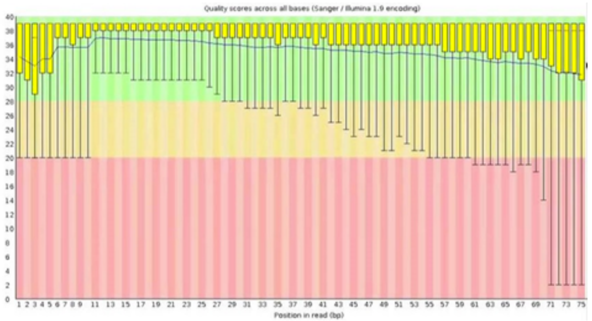
Short reads



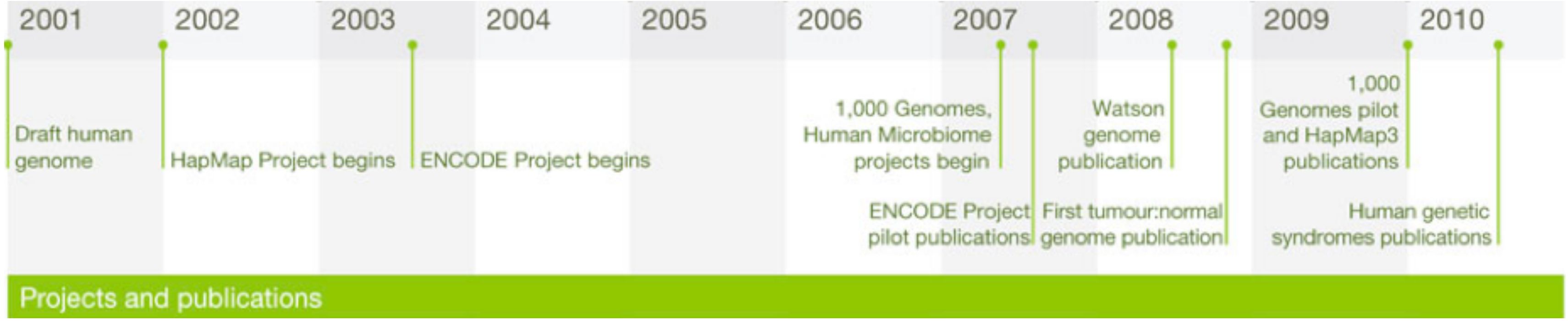
Long reads



Base calling accuracy



NGS projects



International HapMap Project

International project for SNP discovery to map the haplotype diversity in the human genome.

Identification of common SNP variation in multiple human populations.

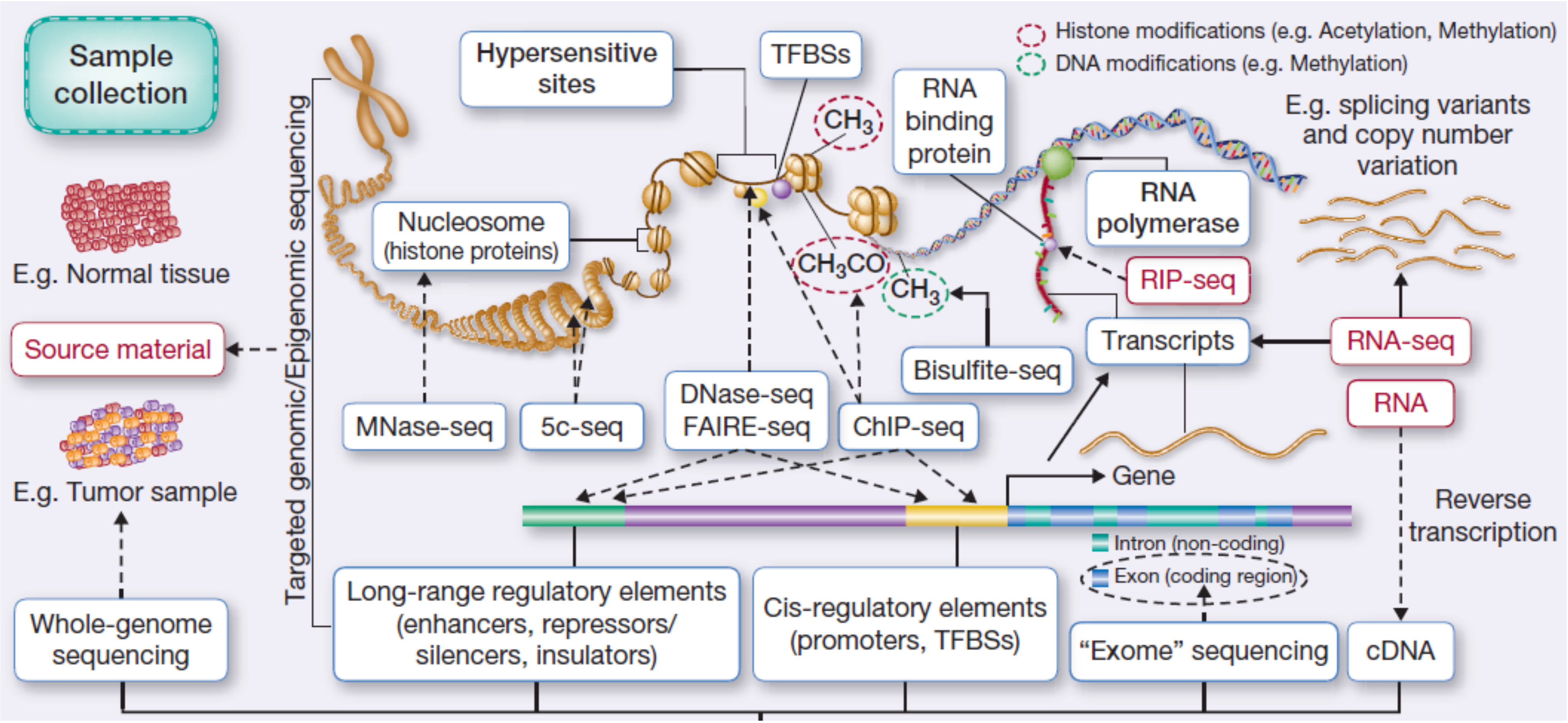
Genome-wide characterisation for placement of regulatory DNA-binding proteins on genomic DNA, genome wide methylation and histone modification.

ENCODE

1000 Genomes
A Deep Catalog of Human Genetic Variation

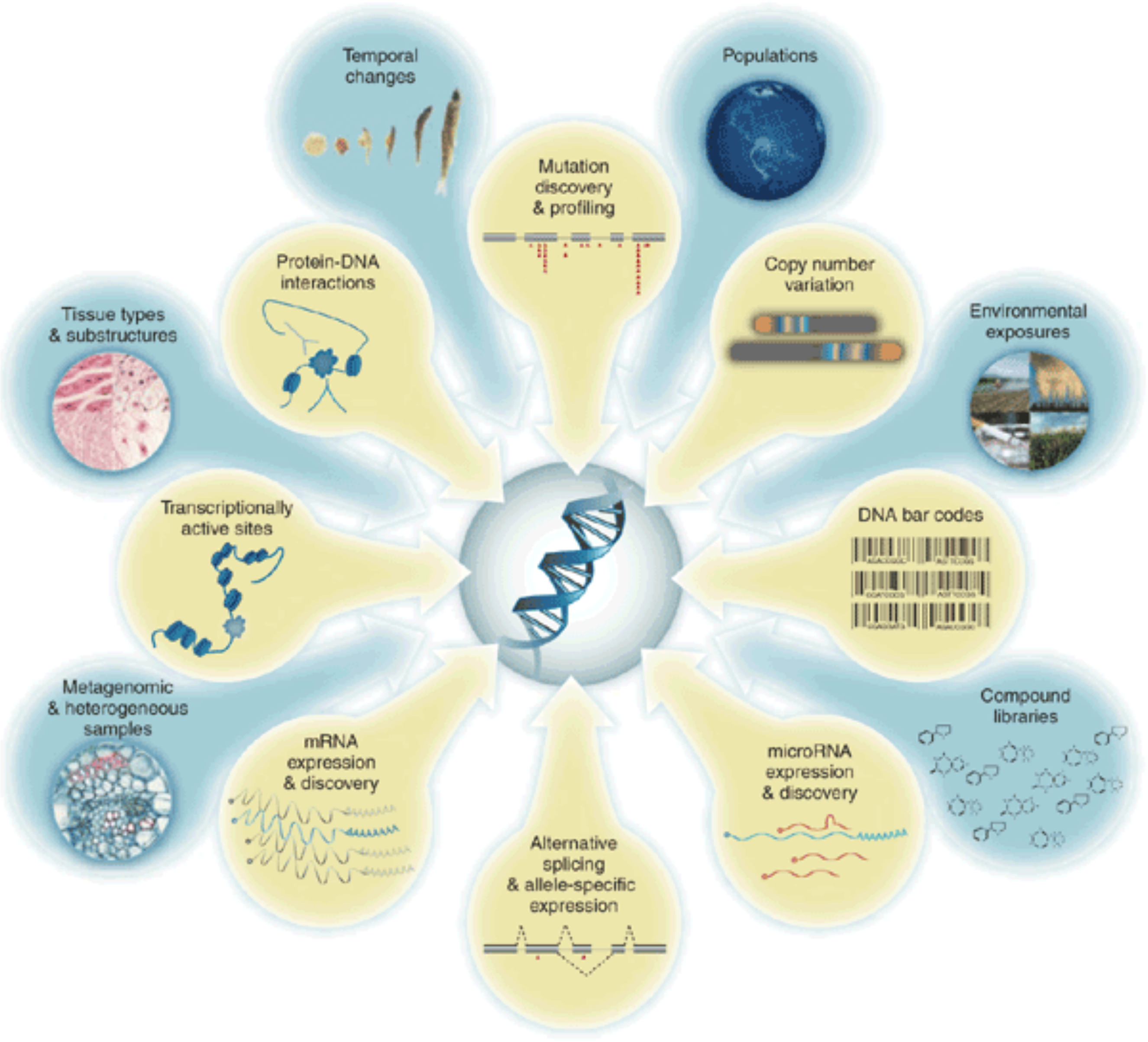
UK
10K

Knowledge and sample sources

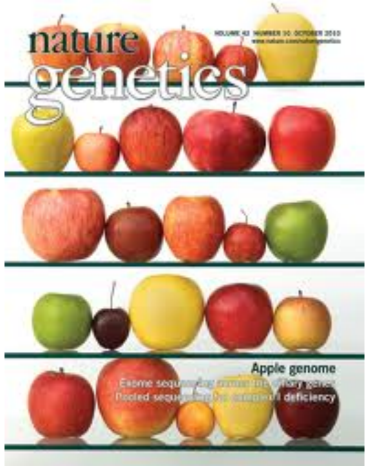


Ritchie MD. et al.,Nat Rev Genet. 2015

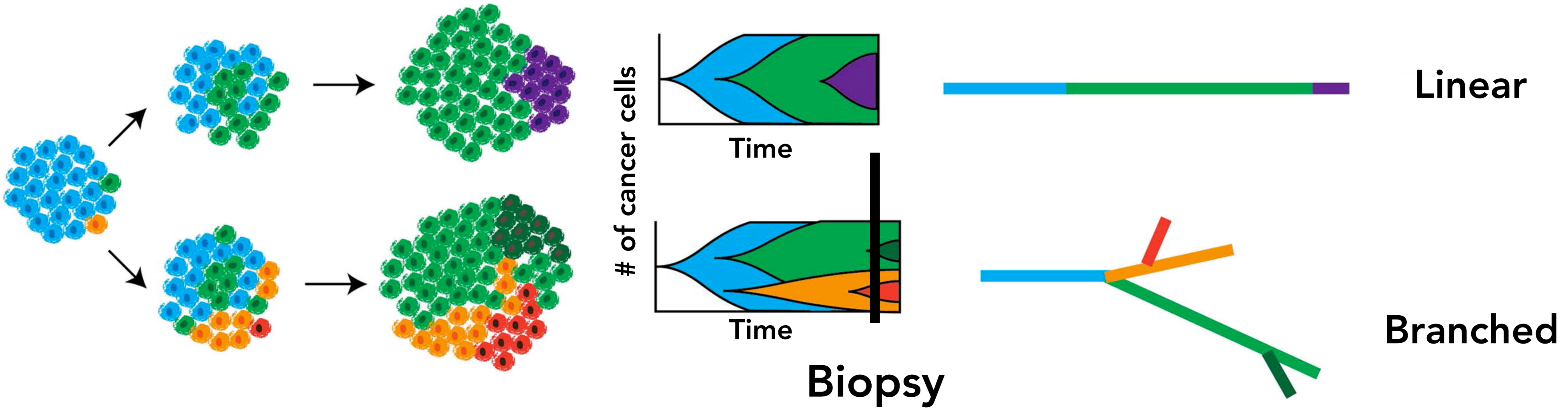
Knowledge and sample sources



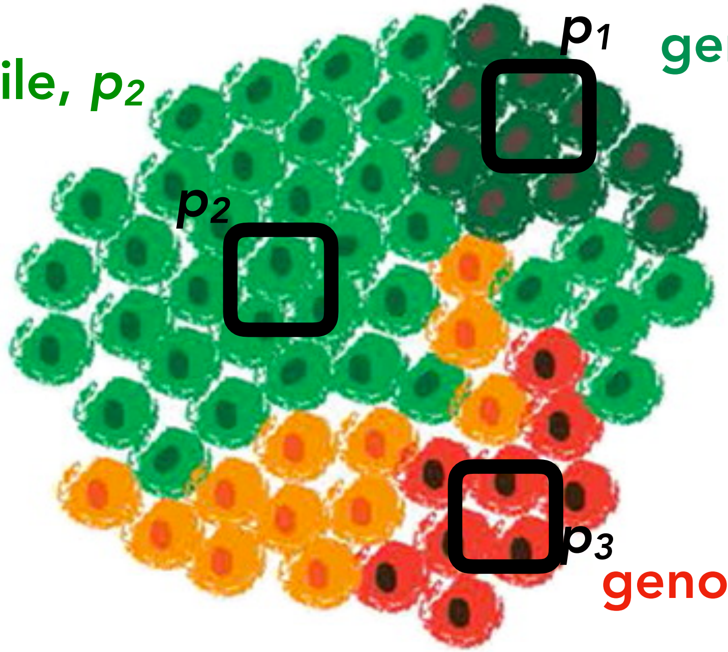
Kahvejian A., et al. Nature Biotech 2008



Cancer Evolution



Burrell, Molecular Oncology, 2014



genomic alterations profile, p_2

genomic alterations profile, p_1

Gerlinger, The New England Journal of medicine, 2012

genomic alterations profile, p_3

Clinical biomarkers discovery

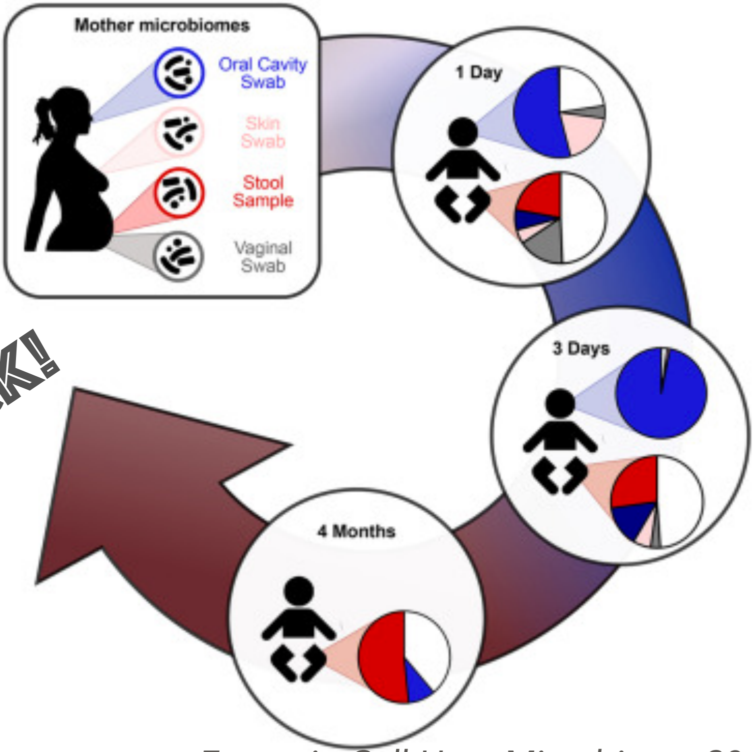
10x more microbial than human cells

1M times as many microbes inside each of us than humans on earth

100x more microbial than human genes

Many evidence suggest an active role of the intestinal bacteria populations (gut microbiome) in the different stages of CRC disease

Mother-to-Infant Microbial Transmission from Different Body Sites Shapes the Developing Infant Gut Microbiome



MOMS ROCK!

Ferretti , Cell Host Microbiome 2018

Who is there?
What are they doing?

Key-points to consider

Biological question
Sample types and treatments
Proper sampling: sample harvesting, isolation techniques
Biological replication, controls
Read-type, read-length, coverage
Data analysis
Validation