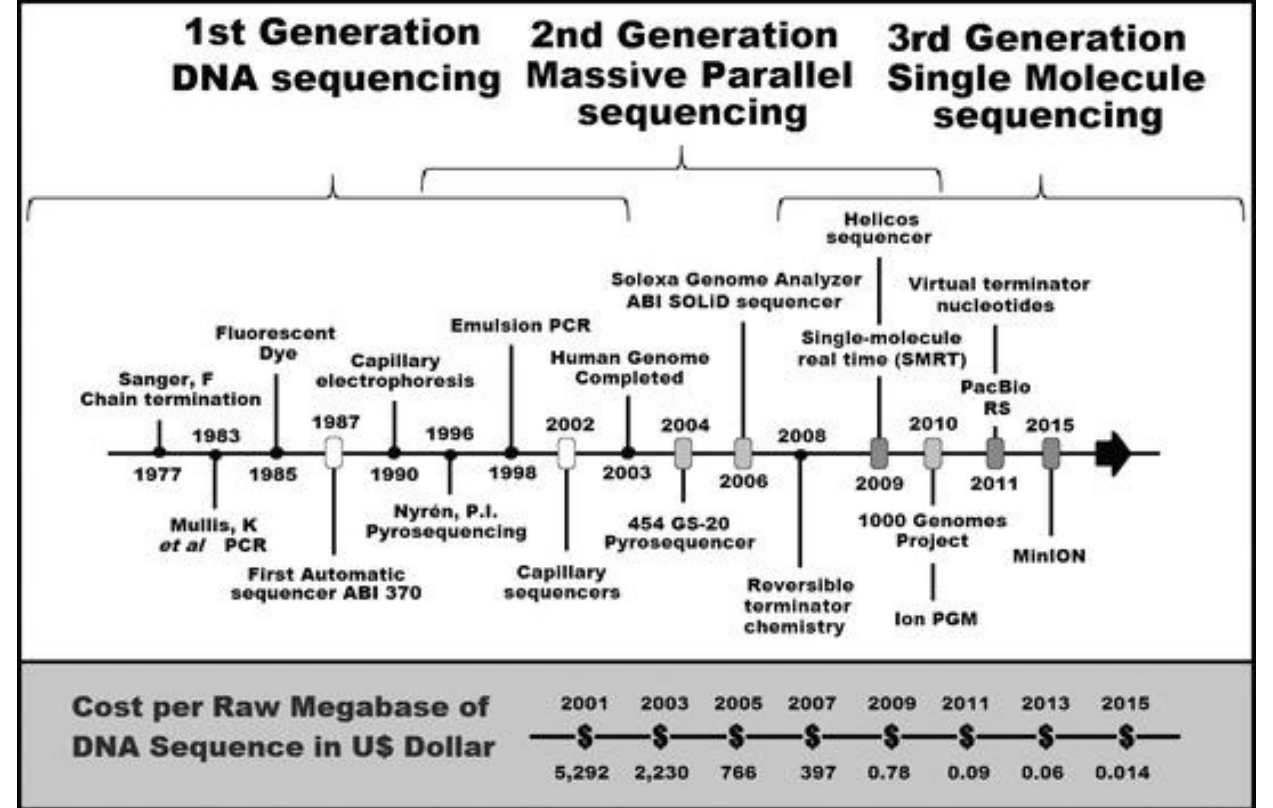


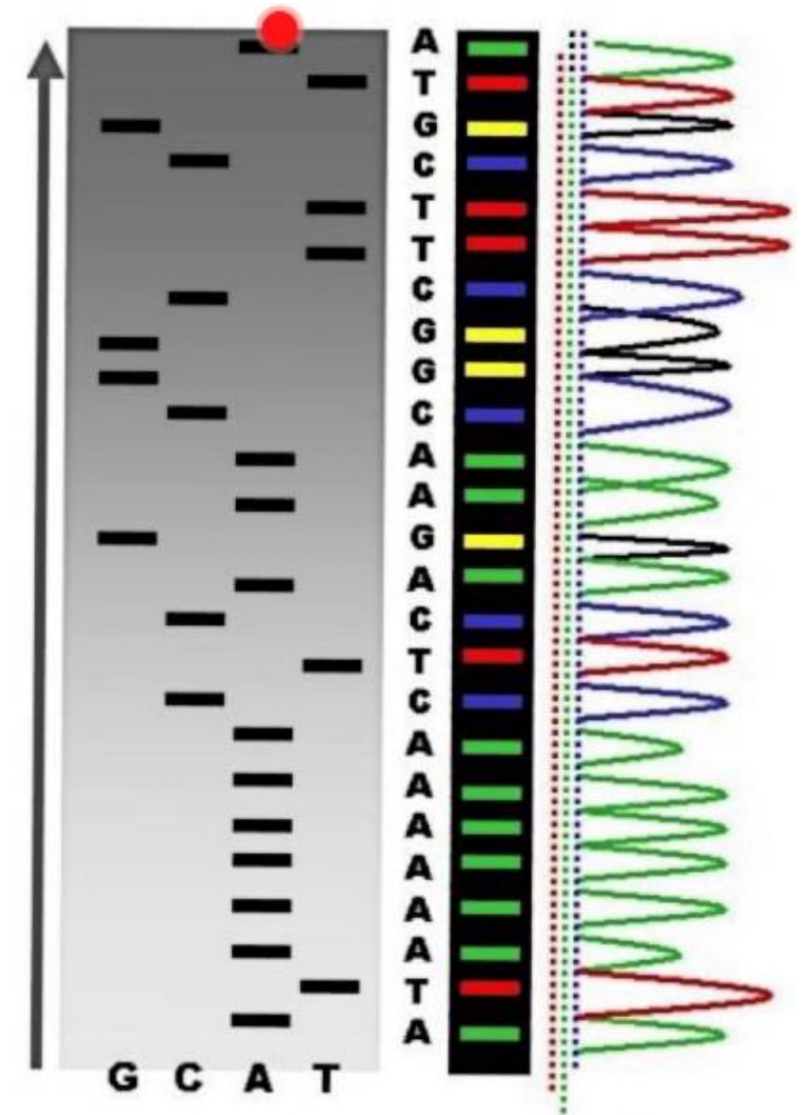
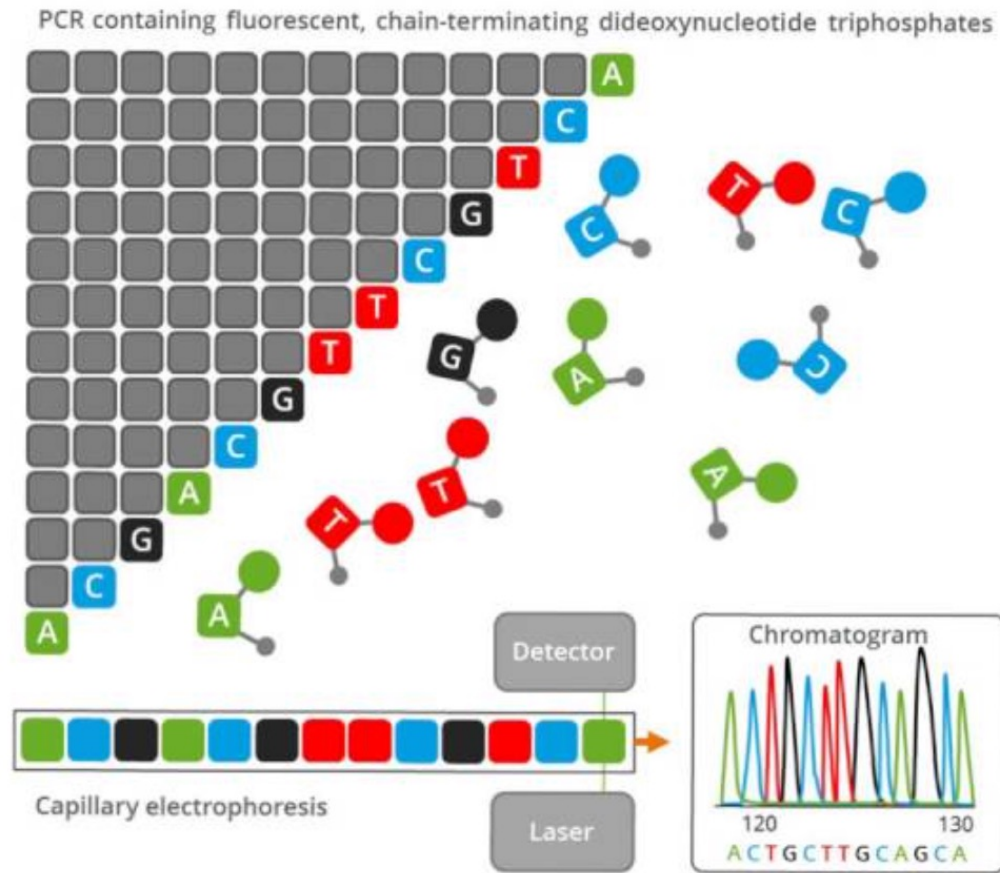
# Dizileme Teknolojileri

# Dizileme teknolojileri

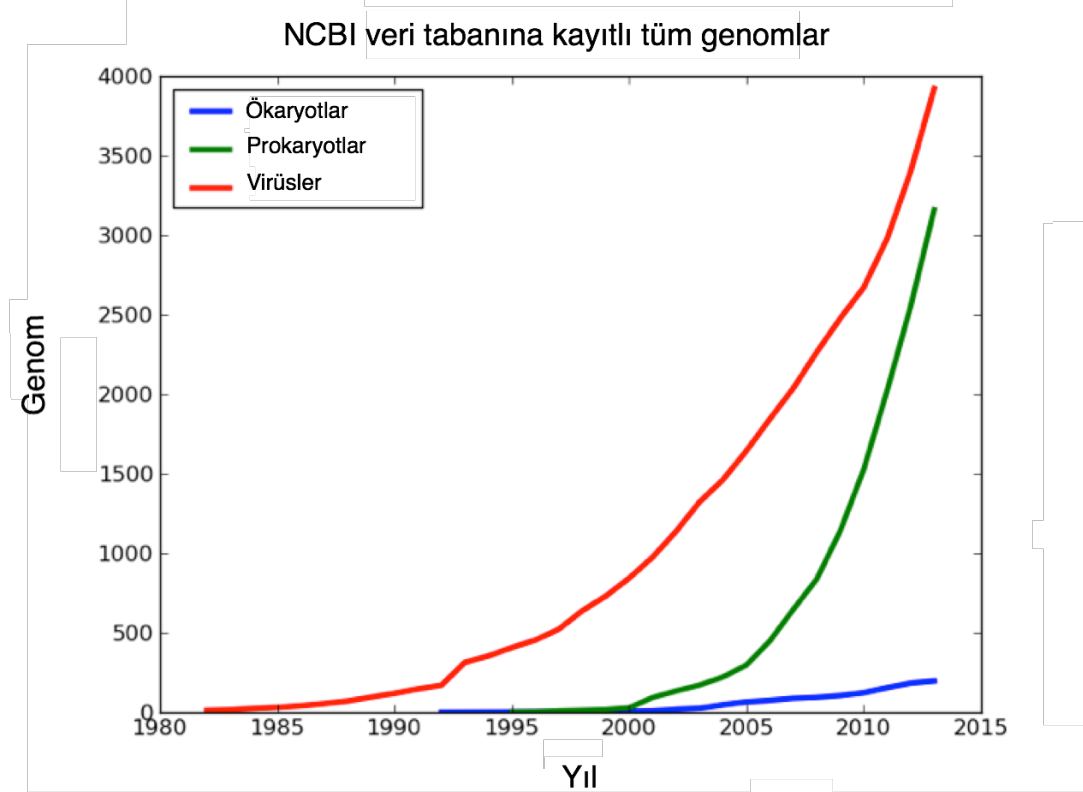
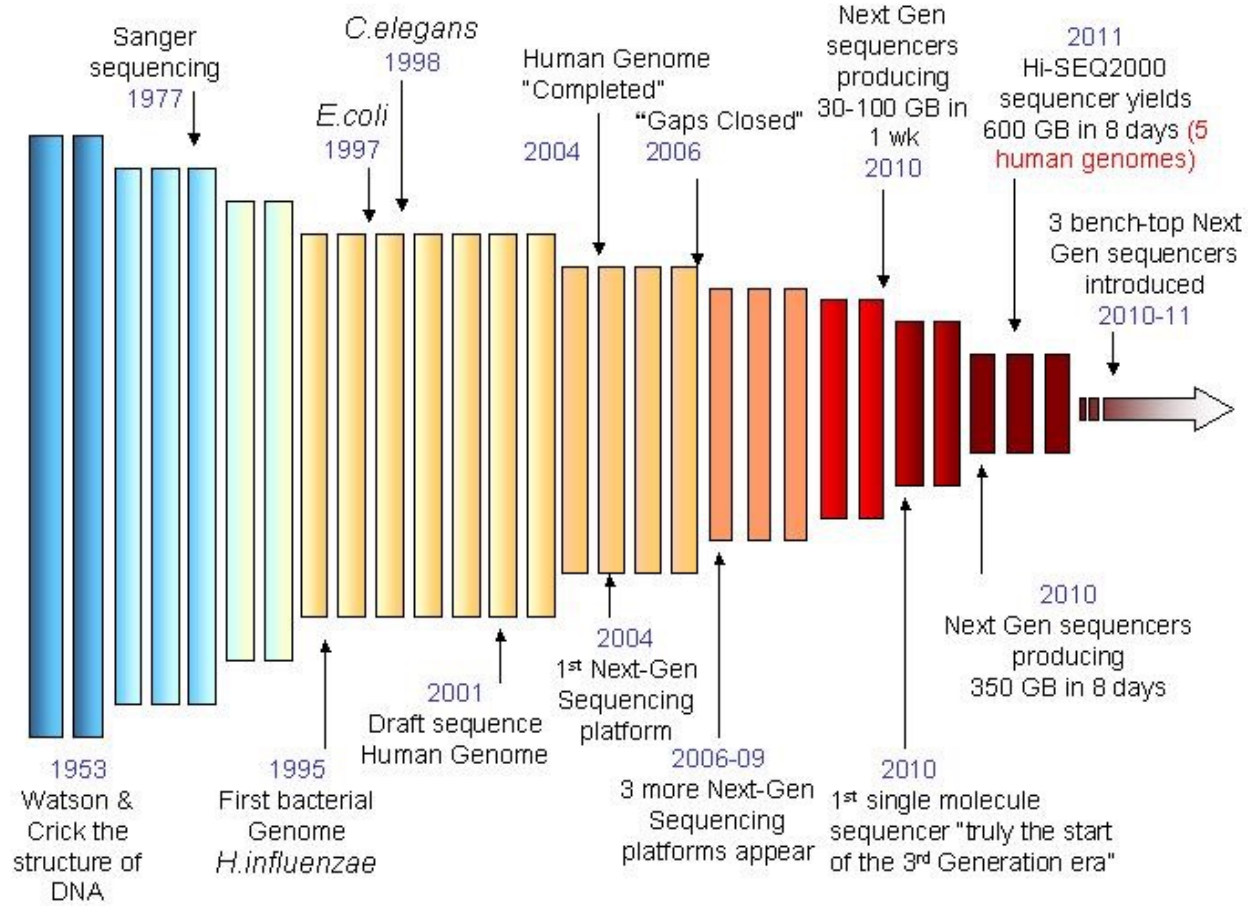
- Sanger dizileme (1977`den beri)
- Yeni nesil dizileme (2005`den beri)
  - \* 454
  - \* Ion Torrent
  - \* Illumina
- 3. nesil dizileme (2012`den beri)
  - \* PacBio ya da SMRT dizileme
  - \* Oxford Nanopore



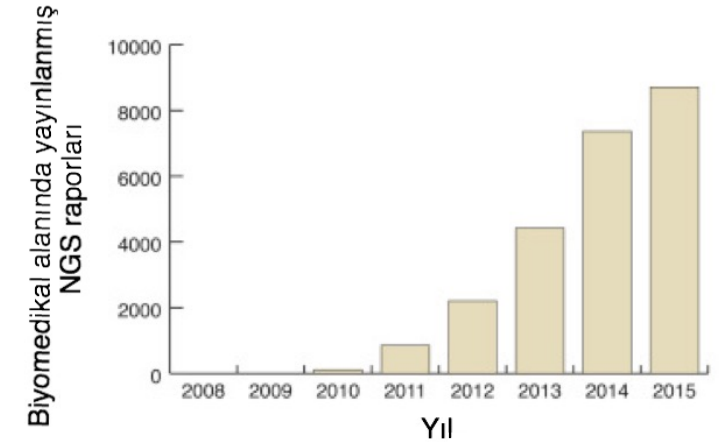
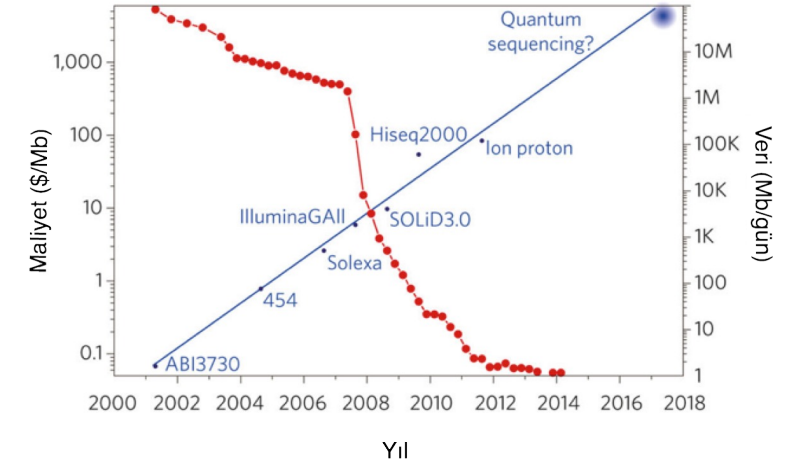
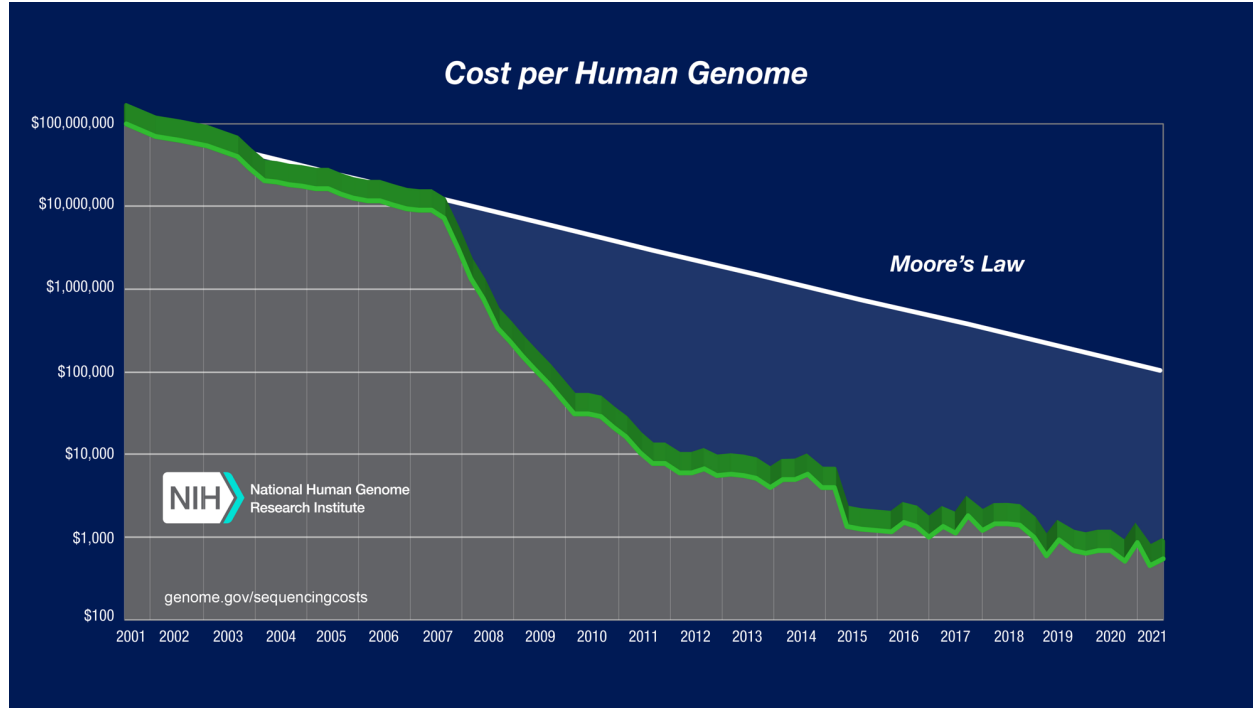
# Sanger Sequencing



# Genomik Devrim



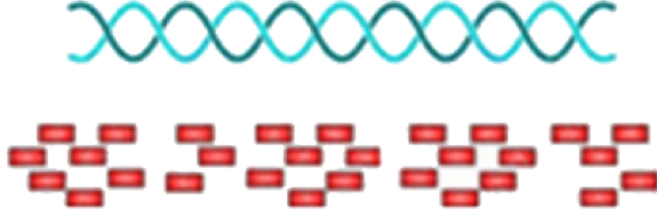
# Genomik Devrim



# Sanger vs NGS

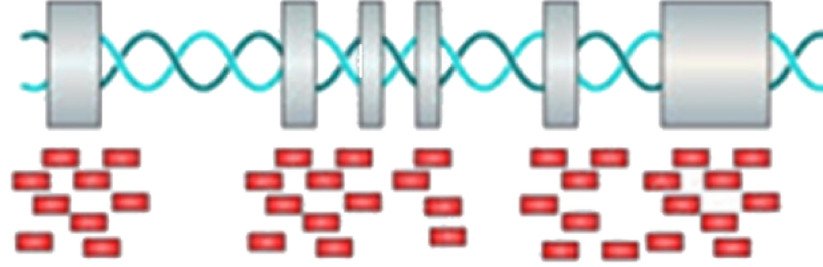
	Sanger	NGS
Örnek	PCR ürünü ya da klonlar	DNA kütüphaneleri
İşlem basamakları	Az sayıda, reax. sonrası temizleme	Çok ve karmaşık
Örnek sayısı	96 ya da 384	1- 16 +
Veri	1 örnek = 1 okuma	1 örnek = binlerce hatta milyonlarca okuma

## Tüm Genom Dizileme (WGS)



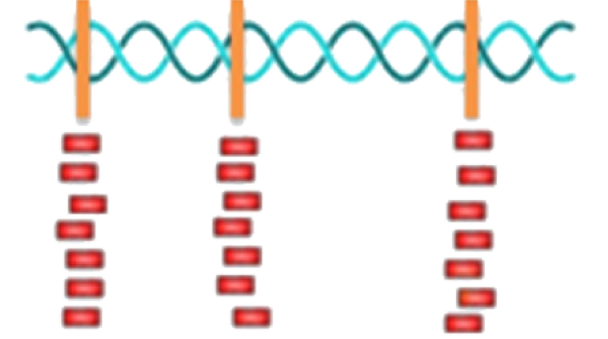
- Dizilenen bölge: tüm genom
- Derinlik > 30X
- Her tür variant tanımlanabilir (SNP, indel, SV vd)

## Tüm Ekzom Dizileme (WES)



- Dizilenen bölge: tüm ekzom
- Derinlik > 50 X ~ 100 X
- Kodlayıcı bölgedeki her tür varyantı tanımlayabilir (SNP, indel, SV vd)
- Maliyeti düşük

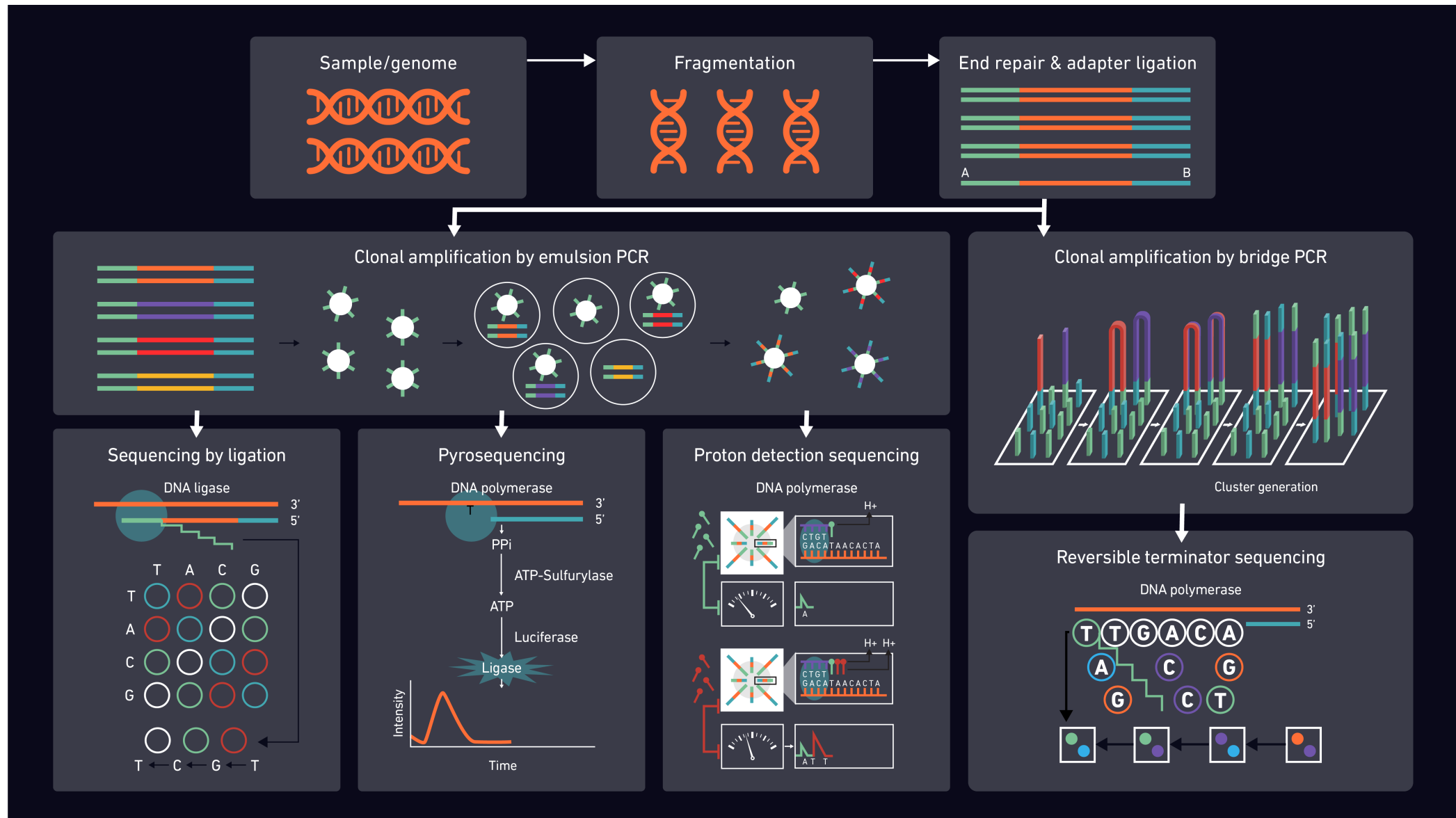
## Hedeflenmiş Dizileme



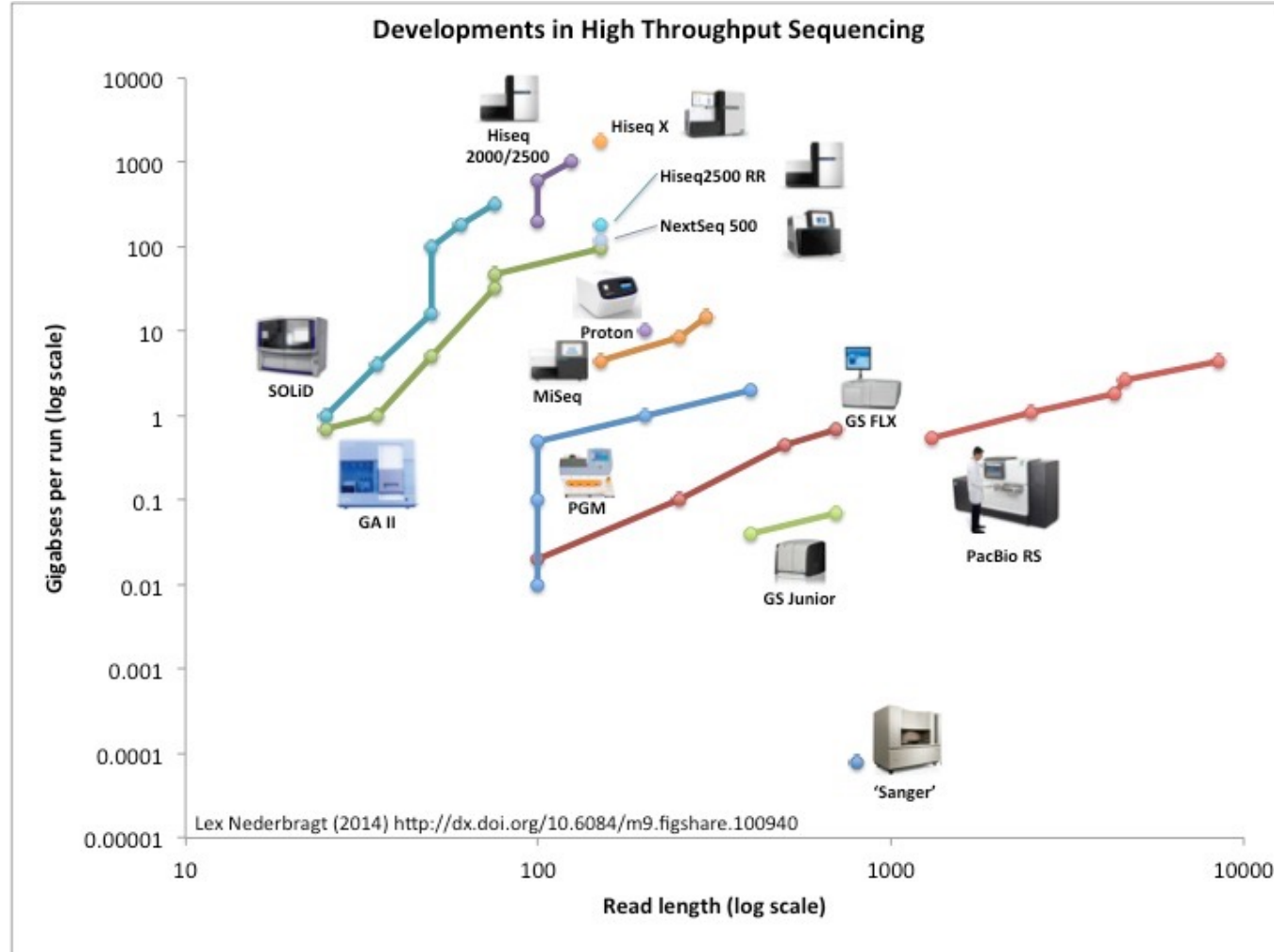
- Dizilenen bölge: özgül bölgeler
- Derinlik > 500X
- İlgilenilen bölgedeki her tür varyantı tanımlayabilir (SNP, indel, SV vd)
- Maliyeti daha da düşük

<b><i>Cihaz</i></b>	<b><i>Nesil</i></b>	<b><i>Yöntem</i></b>	<b><i>Dizi Parça Uzunluğu</i></b>	<b><i>Hata Oranı(%)</i></b>	<b><i>Cihaz Fiyatı(\$)</i></b>	<b><i>Dizileme Maliyeti(\$/Mb)</i></b>
AB 3730xl	1	Sanger	1000	0.1	376.000	1.500
454 FLX	2	Sentez	700	1	500.000	7
Illumina HiSeq2000	2	Sentez	100	0.1	690.000	0.04
SOLiD 5500	2	Ligasyon	75	0.1	595.000	0.07
Pacific Biosciences	3	Sentez	1500	15	695.000	11
Ion Torrent	3	Sentez	200	1	50.000	0.95





## Önemli noktalar: Okuma uzunluğu



## Önemli noktalar: Okuma sayısı

Numbers of Single Reads by Instrument Manufacturer

Platform	Instrument	Unit	Reads / Unit	Reference
Illumina	HiSeq X Ten	Lane	375,000,000	1
Illumina	HiSeq 3000/4000	Lane	312,500,000	1
Illumina	HiSeq NextSeq 500 High-Output	Run	400,000,000	2
Illumina	HiSeq NextSeq 500 Mid-Output	Run	130,000,000	2
Illumina	HiSeq High-Output v4	Lane	250,000,000	3
Illumina	HiSeq High-Output v3	Lane	186,048,000	3
Illumina	HiSeq Rapid Run	Lane	150,696,000	3
Illumina	HiScanSQ	Lane	93,024,000	3
Illumina	GAllx	Lane	42,075,000	3
Illumina	MiSeq v3	Lane	25,000,000	4
Illumina	MiSeq v2	Lane	16,000,000	3
Illumina	MiSeq	Lane	5,000,000	3
Illumina	MiSeq v2 Micro	Lane	4,000,000	5
Illumina	MiSeq v2 Nano	Lane	1,000,000	5

## Önemli noktalar: Kapsama (coverage)



Genom uzunluğu:  $L$

Parçacık sayısı:  $n$

Ortalama parçacık uzunluğu:  $l$

Kapsama / dizileme derinliği (coverage / sequencing depth):  
Genomdaki her baza denk gelen **ortalama** parçacık sayısı

Kapsama  $K = n l / L$

**30X kapsama = baz başına ortalama 30 parçacık**

**Lander-Waterman modeli:**

Tekbiçim dağılım (uniform distribution) varsayımı ile,  $K=10$  ise her 1 milyon nükleotidde 1 boş bölge kalır

Önemli noktalar: Kapsama (coverage)

Estimate of Coverage Requirements by Application Type

Application Type	Coverage
DNA-Seq (Re-Sequencing)	30 - 80X
DNA-Seq (De novo assembly)	100X
SNP Analysis / Rearrangement Detection	10 - 30X
Exome	100 - 200X
ChIP-Seq	10 - 40X

# Farklı uygulamalar için kapsama ve okuma önerileri

Category	Detection or Application	Recommended Coverage (x) or Reads (millions)	References
Whole genome sequencing	Homozygous SNVs	15x	Bentley et al., 2008
	Heterozygous SNVs	33x	Bentley et al., 2008
	INDELs	60x	Feng et al., 2014
	Genotype calls	35x	Ajay et al., 2011
	CNV	1-8x	Xie et al., 2009; Medvedev et al., 2010
Whole exome sequencing	Homozygous SNVs	100x (3x local depth)	Clark et al., 2011; Meynert et al., 2013
	Heterozygous SNVs	100x (13x local depth)	Clark et al., 2011; Meynert et al., 2013
	INDELs	not recommended	Feng et al., 2014
Transcriptome Sequencing	Differential expression profiling	10-25M	Liu Y. et al., 2014; ENCODE 2011 RNA-Seq
	Alternative splicing	50-100M	Liu Y. et al., 2013; ENCODE 2011 RNA-Seq
	Allele specific expression	50-100M	Liu Y. et al., 2013; ENCODE 2011 RNA-Seq
	De novo assembly	>100M	Liu Y. et al., 2013; ENCODE 2011 RNA-Seq