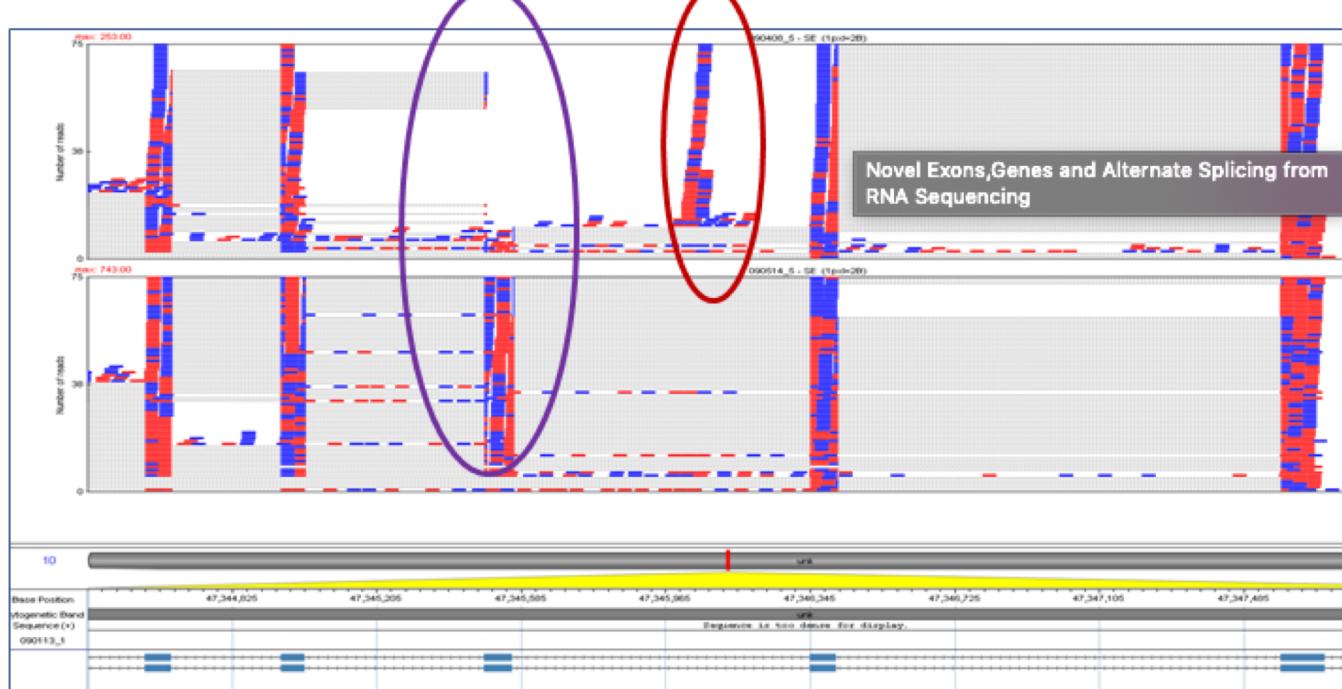


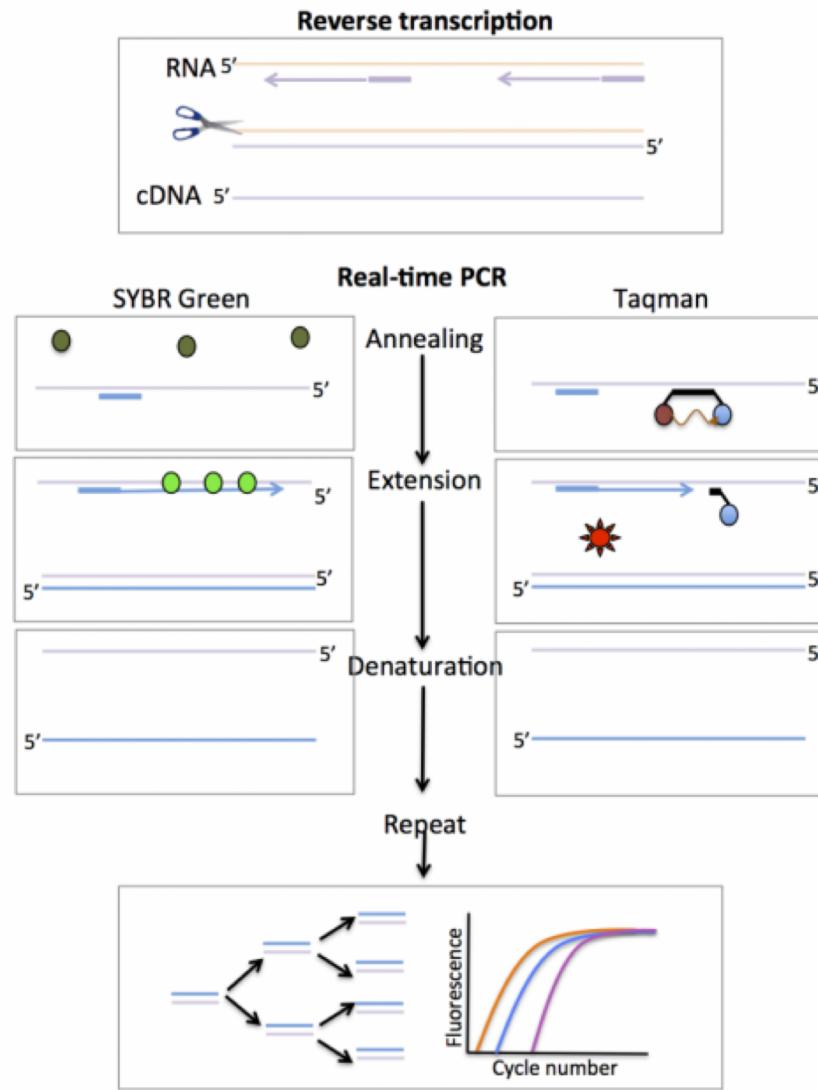
RNA dizileme

RNA dizileme ne işe yarar?

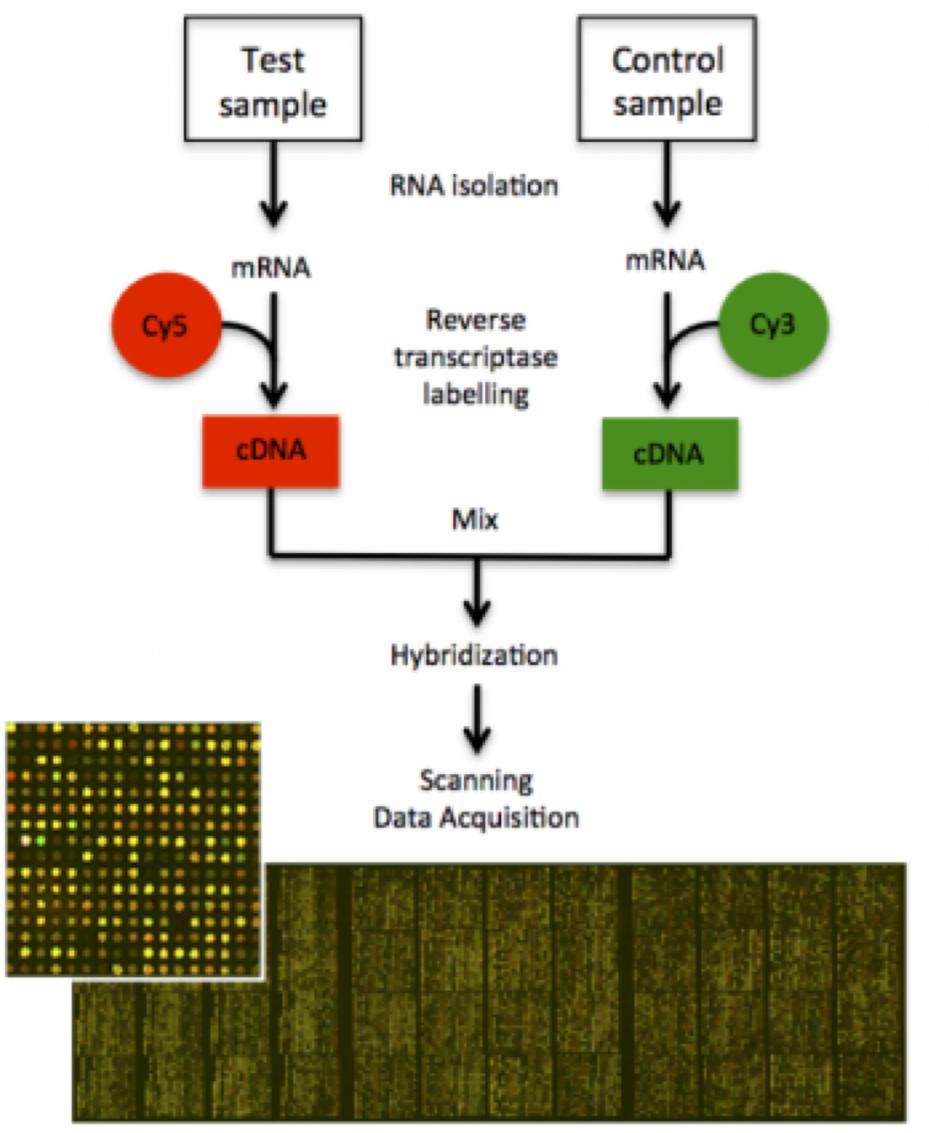
- RNA'nın paralel ve eş zamanlı olarak dizilenmesiyle transkripte olan tüm genler ve izoformları,
- genlerin 5' ve 3' uçlarının belirlenmesi,
- tek nükleotid değişimleri, insersiyon, delesyon, füzyon genler, genlerin ifadesi

Alternatif splicing

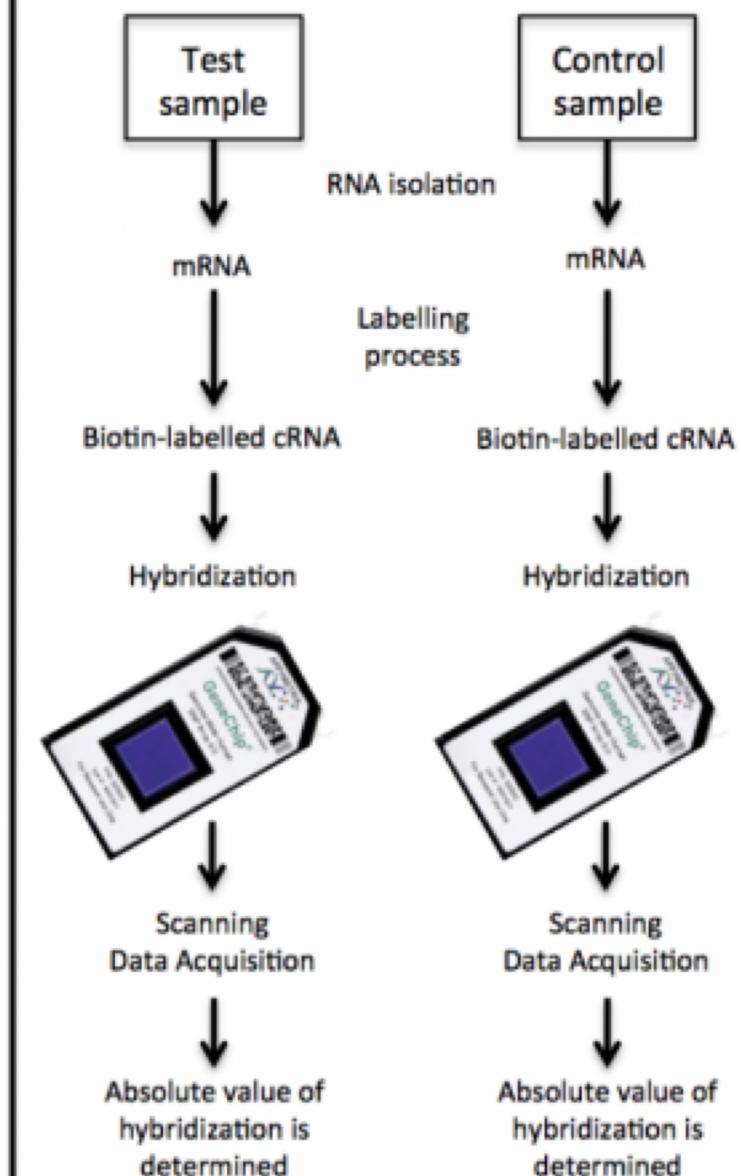




Two color array



One color array



Microarrays

Pros

- Well-established protocols
- Cost-effective technology
- Suitable for small studies

Cons

- Difficult to identify lowly-expressed genes
- Need for probe design sequences
- Can't detect novel transcripts

RNA-Seq

- Can identify lowly expressed genes
- Can use novel transcripts
- Suitable for discovery-based studies

- Large data generated
- Protocols are very new
- High expertise required

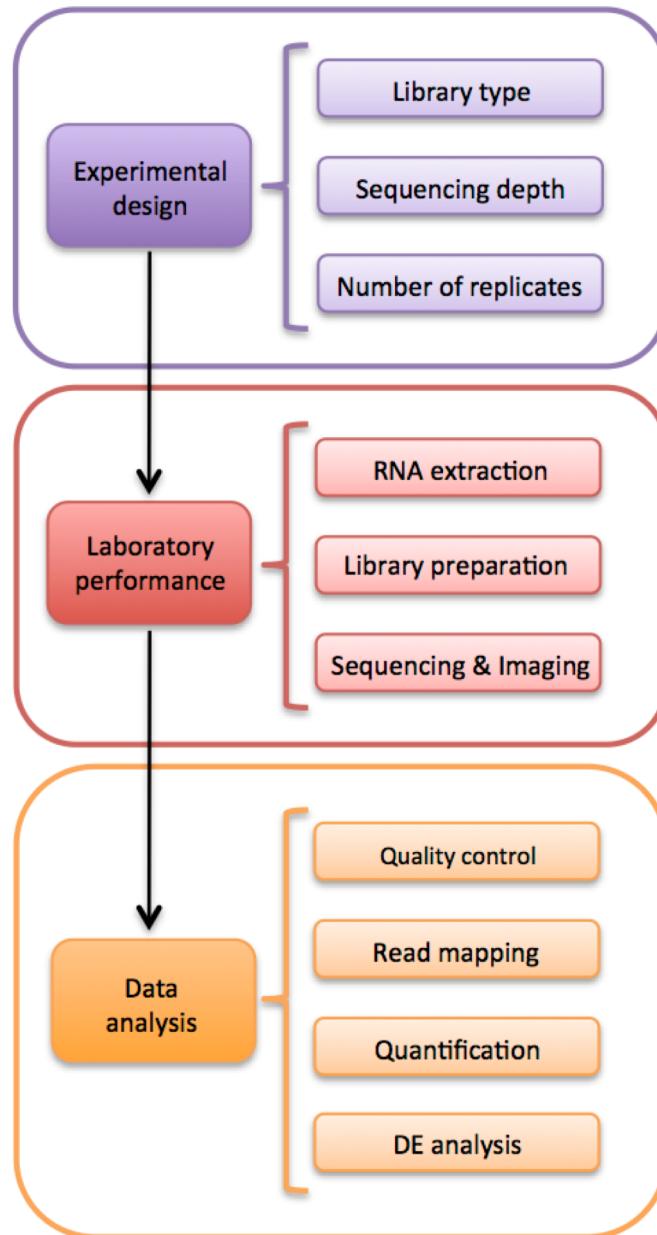
RNA seq avantajlari

- Dusuk ve yada cok yuksek ifade edilen genler
- Teknik olarak veriler arasında varyasyon az ve tekrar edilebilirligi yüksek
- Genomu bilmek gerekli degil
- Tek baz duzeyinde cozunurluk sagliyor
- Cross contaminasyon yok hatta bias hic yok
- GC?

RNA seq uygulamalari

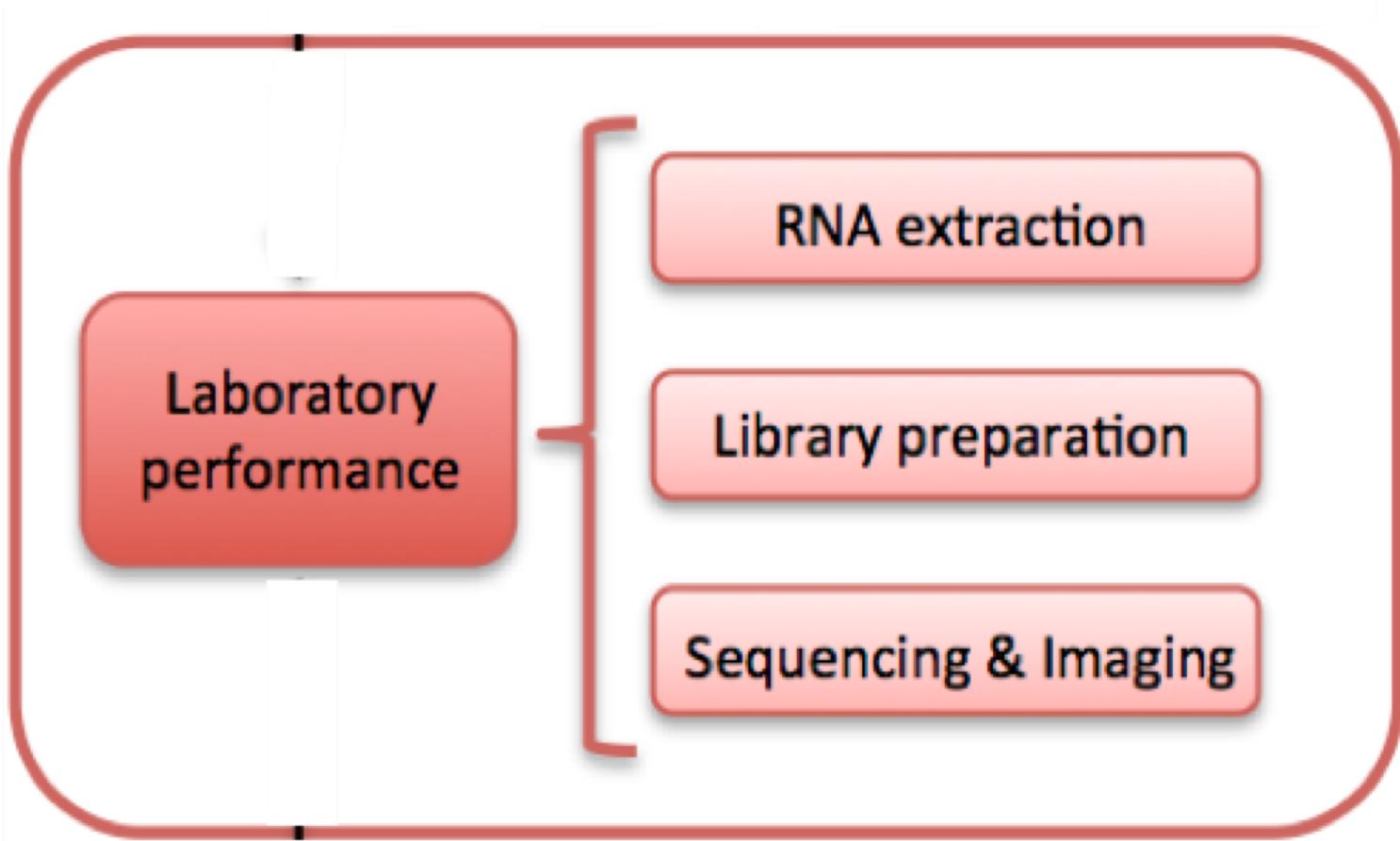
- Ornekler rasinda gen ifadesi profillerinin karsilastirilmasi
- Ozellikle hastaliklarla ilskili olarak Alternatif splays olaylarinin belirlenmesi
- Alel spesifik ifadenin tanimlanması, hastaliklarla iliskili olarak snp tanimlanmsi ve gen fuzyonlarinin anlasilmasi yani hastalikla iliskili varyantlarin belirlenmesi vs
- Ayrıca karmasık biyolojik sureclerin tanimlanması, hucresel heterojenitiy ve cesitlilik ozellikle noroscience ve kok hucre calismalari

Gen ifadesi farkliliklarini belirlemek



Calisma dizayni

- Kutuphane olusturma
- Dizileme derinligi ya da kutuphane buyuklugu
- Kac tekrar

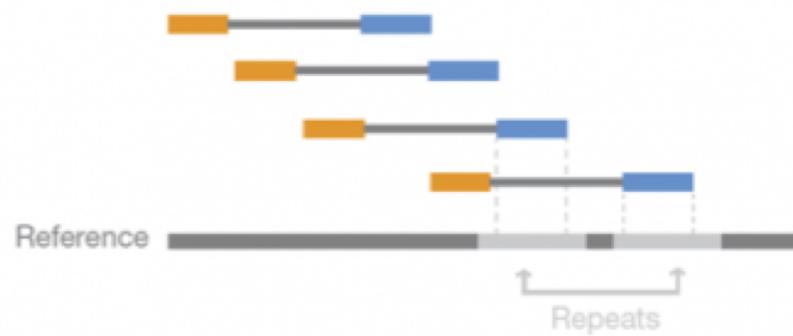


Kutuphane olusturma

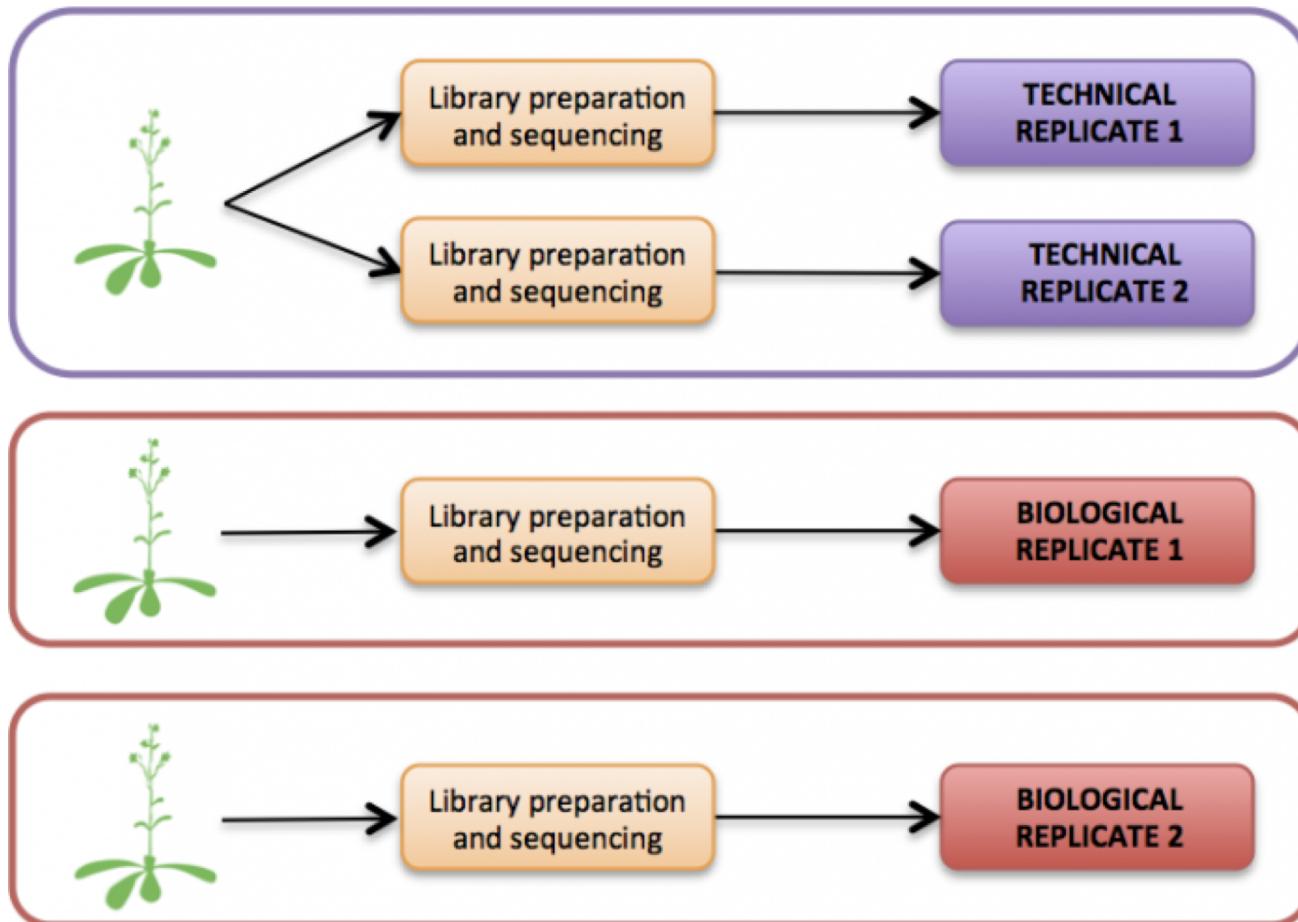
Paired-End Reads



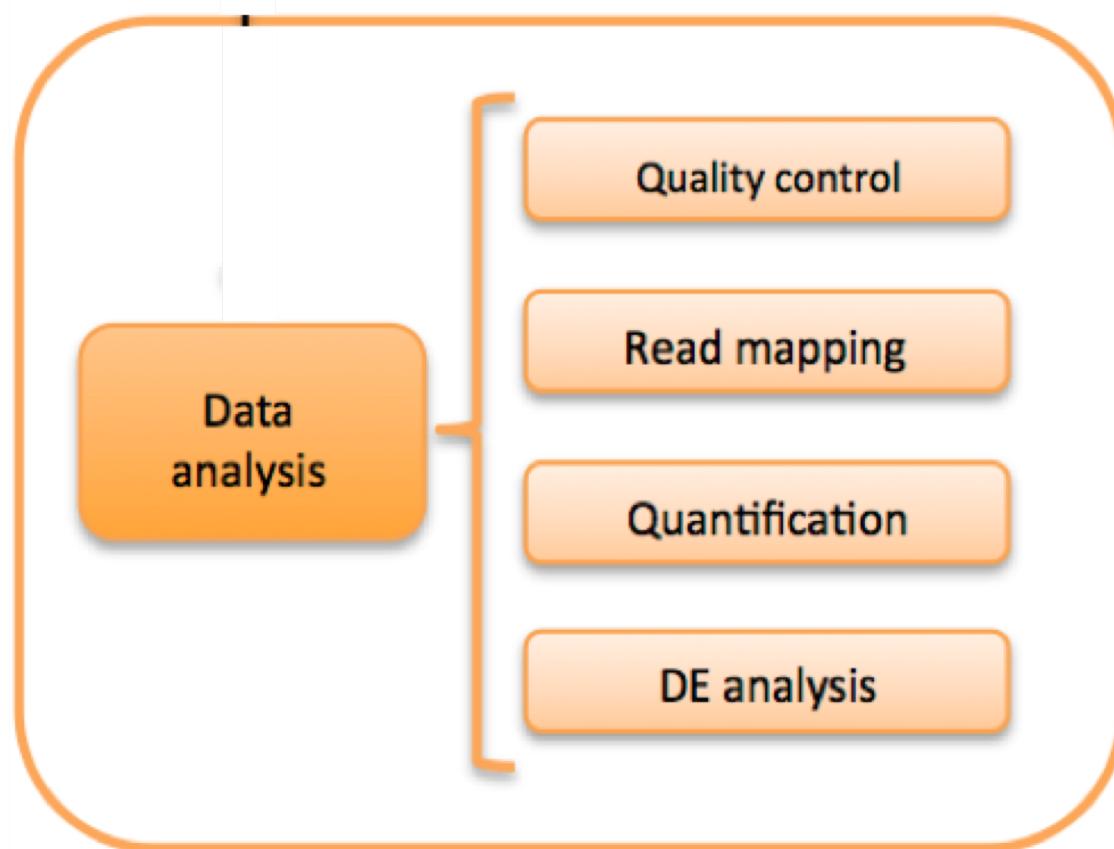
Alignment to the Reference Sequence



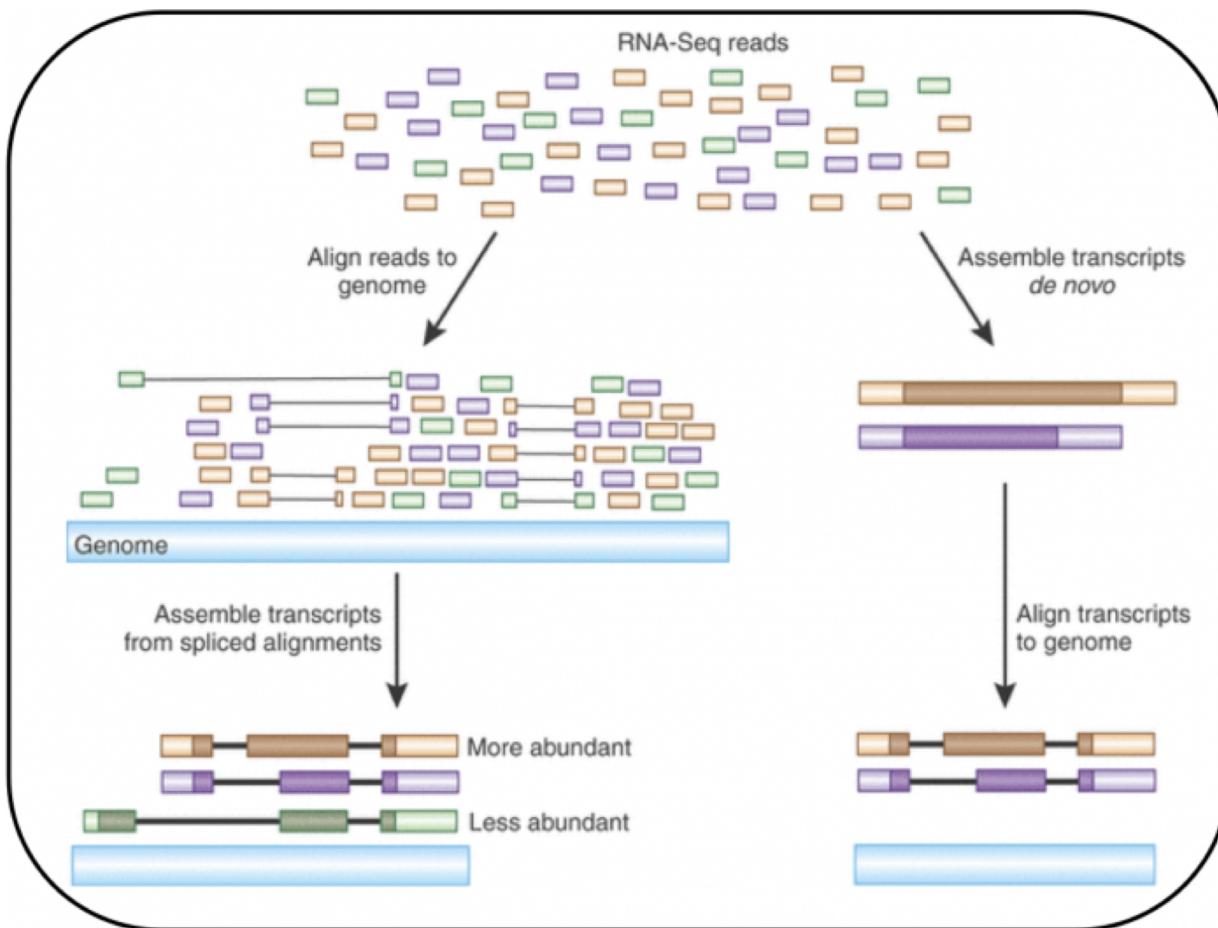
tekrar sayisi



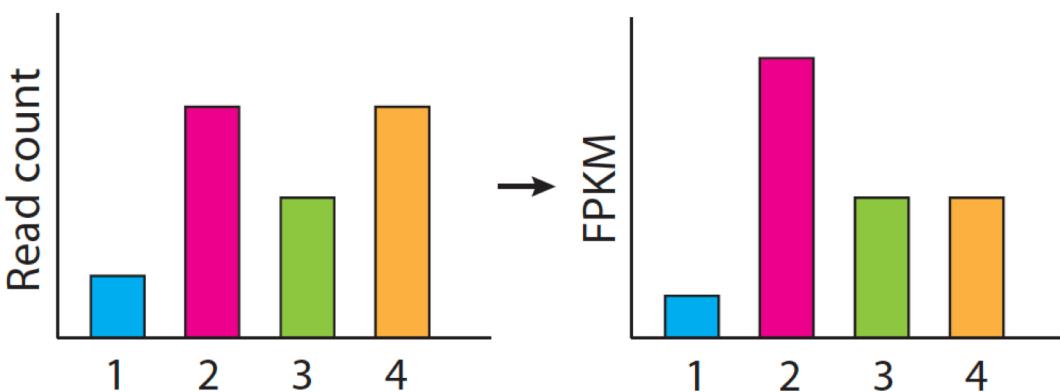
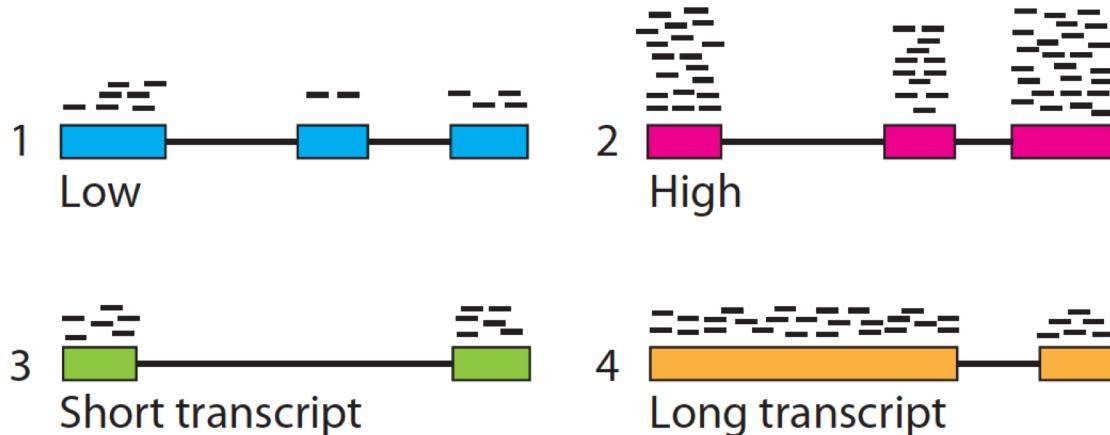
Data analizi



Haritalama



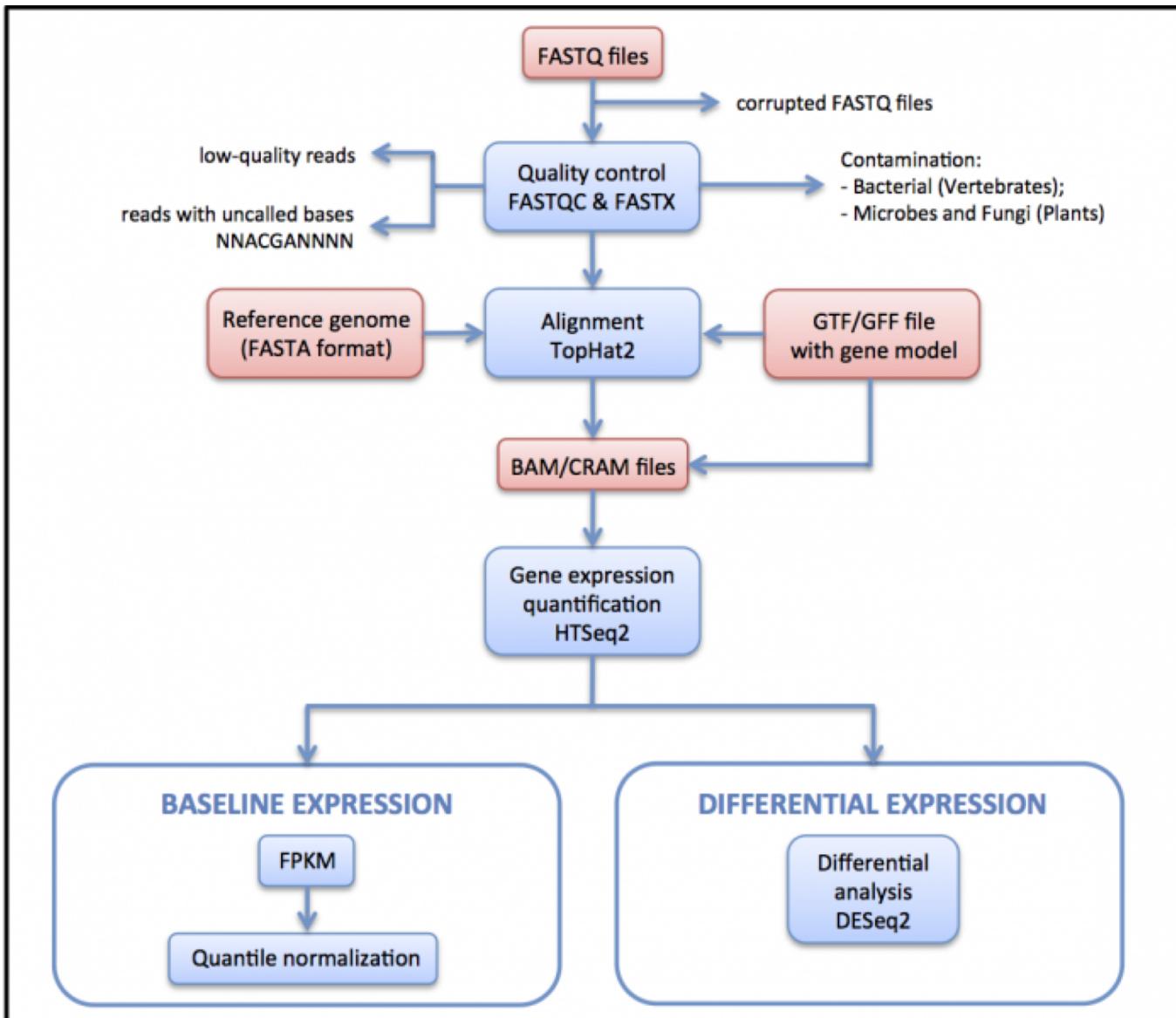
FPKM



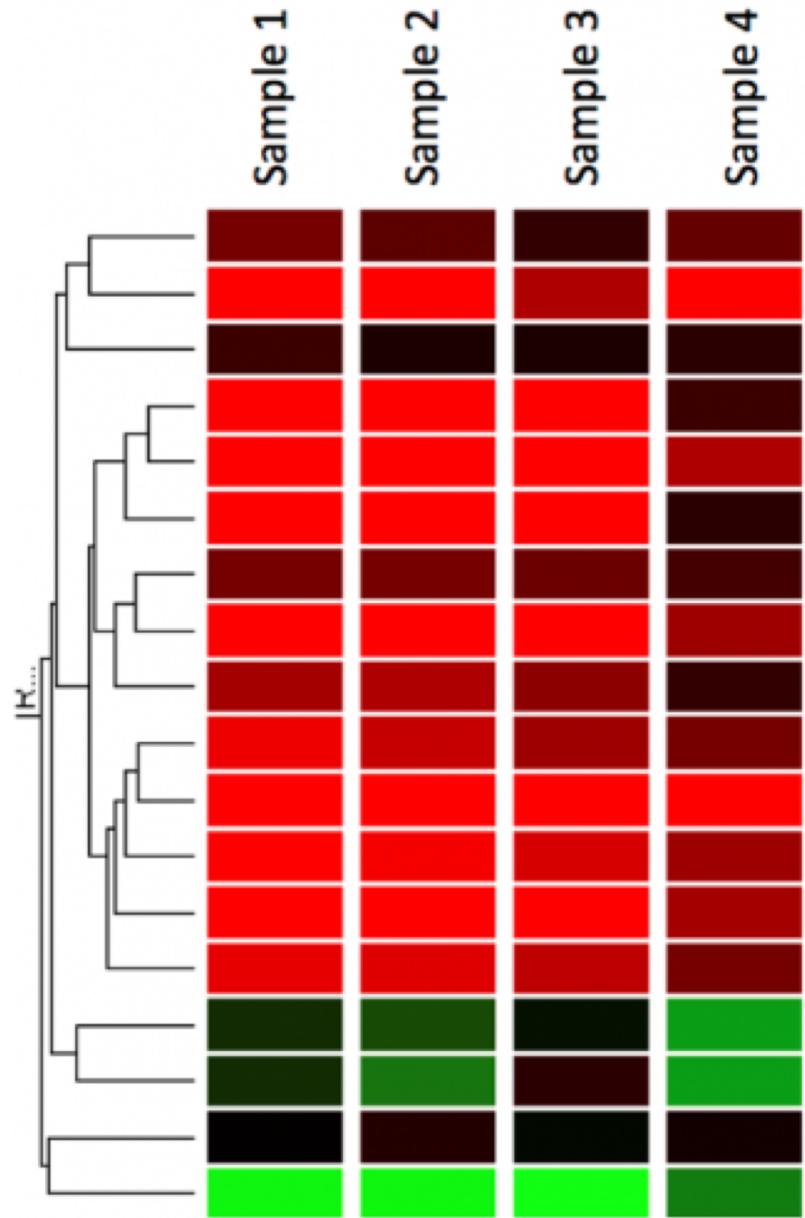
FPKM: Fragments per Kilobase of Exon per Million Fragments Mapped
(Atanmış her milyon fragman için kilobaz ekson başına düşen fragman sayısı)

$$FPKM = \frac{10^9 C}{NL}$$

N: atanmış toplam fragman sayısı
L: atanmış transkriptin uzunluğu
C: atanmış fragmanın uzunluğu



Verilerin yoorumlanması: heat map ve kumeleme



Title: Interferon type I signaling pathway

Availability: CC BY 2.0

Organism: Homo sapiens

