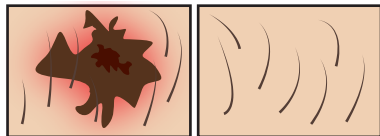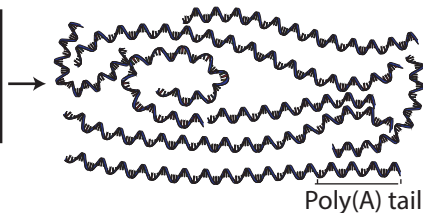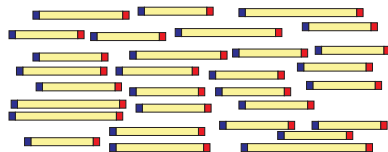Samples of interest

Condition 1 (e.g. tumor)
Condition 2 (e.g. normal)
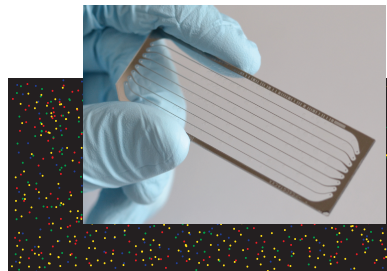
Isolate RNAs

Poly(A) tail

Generate cDNA, fragment, size select, add linkers
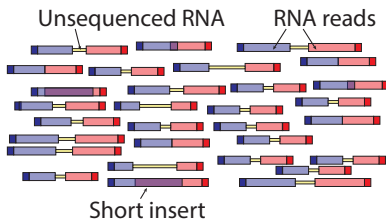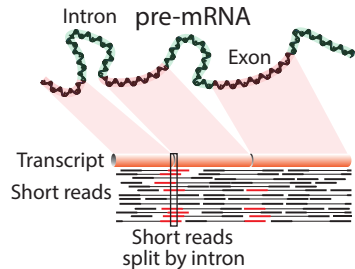
Sequence ends

100s of millions of paired reads
10s of billions bases of sequence

Map to genome, transcriptome, and predicted exon junctions

Intron   pre-mRNA
Exon

Unsequenced RNA   RNA reads

Short insert

Transcript
Short reads

Short reads split by intron

Downstream analysis