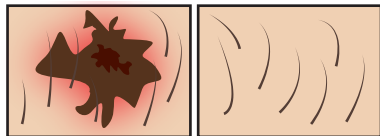


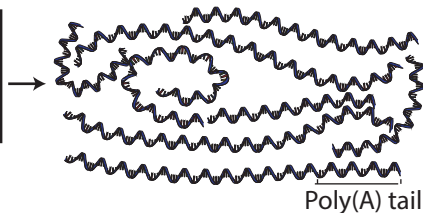
## Samples of interest



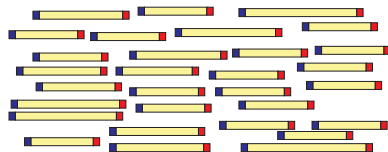
Condition 1  
(e.g. tumor)

Condition 2  
(e.g. normal)

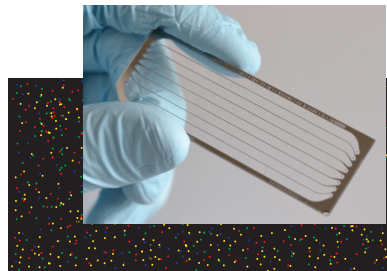
## Isolate RNAs



## Generate cDNA, Fragment, size select, add linkers

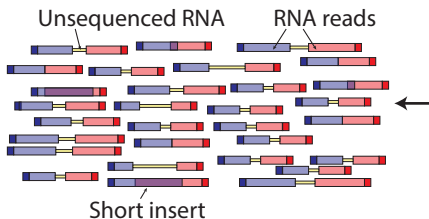
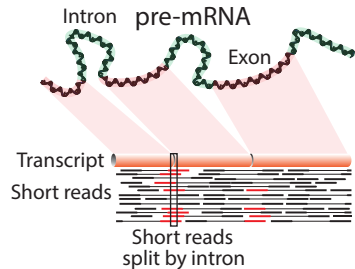


## Sequence ends



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

## Map to genome, transcriptome, and predicted exon junctions



## Downstream analysis