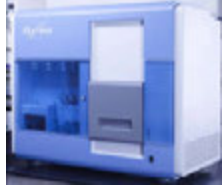


**36 bp cDNA  
libraries  
prepared**



**FastQC**

**Bowtie**

Bowtie SAM files  
sorted and  
duplicates  
stripped

**HTseq**

**EdgeR**

**InnateDB**

**GOseq**