Input file: Raw fastq/fq reads

1. Quality assessment report: FastQC (fastqc.pbs)
2. Removing Adapters/low quality reads: Trimmometric
3. Mapping filtered, high-quality reads to the human genome: STAR/Bowtie2/BWA (we use STAR). Mapping output: .bam file (STAR-align\_human.gencode.pbs)
4. Sort the bam file: SAMTOOLS
   1. Counting reads mapped per gene: HTSeq
      1. Remove the bottom rows that are not read count/gene
   2. Perform residual and DEG analysis: normalize abundance (getGeneFilteredGeneExpMatrix.R), normalize ( voom), lmfit (residual analysis, differential expression)
5. Sort the bam file: SAMTOOLS
6. Get exome mapping rate: RNAseqC
   * 1. Of all the files consider \*Matrix.tsv)
     2. Concatenate the matrix to the right side of covariate table
7. Draw Variance partition plot to observe the contribution of each covariate from the table in total variance: TargetALS.RNA.VPA.R