

NGS

- De novo Assembly with Spades
- Call Variants with SAMtools
- ChIP-Seq Coverage
- ChIP-seq Analysis with Cistrome Tools
- Extract Consensus from Assembly
- Extract Coverage from Assembly
- Extract Transcript Sequences
- Quality Control by FastQC
- Raw ChIP-Seq Data Processing
- Raw DNA-Seq Data Processing
- Raw RNA-Seq Data Processing
- RNA-seq Analysis with Tuxedo Tools
- Get Unmapped Reads
- Variation Annotation with SnpEff