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| --- | --- | --- | --- |
| **Step** | **Package** | **Version** | **Default command** |
| Preprocess | trim\_galore | 06.05.2015Cutadapt v0.4.0 | trim\_galore --gzip --no\_report\_file --length %d --output\_dir <outdir> --quality 10 \--stringency 3 --paired <R1.fq> <R2.fq> |
| fastq\_illumina\_filter | 0.1 | fastq\_illumina\_filter -N |
| Khmer | 2.0 | normalize-by-median.py -M %s –paired --output - -  |
|  | Trinity | 2.2.0 | insilico\_read\_normalization.pl --seqType fq --JM %dG --CPU %d --output tmp\_norm \--max\_cov 50 --pairs\_together --PARALLEL\_STATS --left <R1.fq> --right <R2.fq> |
| DBG assembly | Trinity | 2.2.0 | Trinity --no\_cleanup --seqType fq --max\_memory %dG --bflyHeapSpaceMax 4G --CPU %d \--output <outdir> --no\_normalize\_reads --run\_as\_paired --single %s/Sequences |
| Velvet | 1.2.07 | velveth <outdir> 27 -shortPaired -fastq - -noHashvelveth <outdir> <kmer> -strand\_specific -reuse\_Sequencesvelvetg <outdir> -read\_trkg yes -min\_contig\_lgth 100 -cov\_cutoff 4 |
| Oases | 0.2.06 | oases <outdir> -cov\_cutoff 4 |
| DBG cleaning | seqclean | x86\_64\_20110222 | seqclean <input.fa> -o <output.fa>cdbyank -l <input.cidx> |
| NCBI tools | 6.1 (Dec 2012) | vecscreen -i <input.fa> -d <database.fa> -f 3 |
| Inclusion removing | cd-hit | 4.6 (Feb 10 2015) | cd-hit-est -i <input.fa> -o <outdir> -M 0 -d 0 -c 0.98cd-hit -i <input.fa> -o <outdir> -M 0 -d 0 -c 0.90 -g 1 |
| OLC assembly | tgicl | 2.1 | tgicl -F <input.fa> -l 60 -p 96 -s 100000 |
| Cleaning | TransDecoder | 2.0.1 | TransDecoder.LongOrfs -t <input.fa>TransDecoder.Predict -t <input.fa> |
| bedtools | 2.22.1 | bedtools merge -c 4 -o distinct -i - |
| EMBOSS | 6.4.0.0 | getorf -auto -filter |
| Editing by reads alignment | bwa | 0.7.12-r1039 | bwa [aln|sampe|samse] |
| STAR | 2.4.0i | STAR --genomeDir <dir> --readFilesIn <R1.fq> <R2.fq> --alignIntronMin 10 \--alignIntronMax 25000 --outFilterMultimapNmax 10000 |
| samtools | 1.1 | samtools [mpileup|sort|index|flagstat|view|merge|faidx] |
| Filtering by reads alignment | express | 1.5.1 | express --no-update-check --no-bias-correct --logtostderr --output-dir <outdir> \<reference.fa> <input.bam> |
| Scoring | TransRate | 1.0.1-linux-x86\_64 | transrate --assembly=<input.fa> --left=<R1.fq> --right=<R2.fq> --threads=%d \--output=<outdir> |
| Reference alignment | Exonerate | 2.2.0 | exonerate --percent 50 --showalignment no --showvulgar no <queries.fa> <targets.fa> |
| Blat | BlatSuite v34 | blat <targets.fa> <queries.fa> -noHead <output.psl> |