

RESEARCH

srnaMapper: an optimal mapping tool for sRNA-Seq reads — Additional file

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Information about the tools

Tool versions:

- bowtie: 1.3.0
- bowtie2: 2.4.1
- bwa: 0.7.17
- HISAT2: 2.2.1
- segemehl: 0.3.4
- STAR: 2.7.9a
- yara: 0.9.11

Tool commands used:

- srnamapper: `srnaMapper -t <THREADS> -r <READS> -g <GENOME> -o <SAM> -n 1000 -f 100 -e <MISMATCHES>`
- bowtie1.beststrata.ml: `bowtie --best --strata -k 1 -m 1 -S -p <THREADS> -x <GENOME> <READS> <SAM>`
- bowtie2.vsl: `bowtie2 --very-sensitive-local -p <THREADS> -x <GENOME> -U <READS> -S <SAM>`
- bowtie2.vs: `bowtie2 --very-sensitive -p <THREADS> -x <GENOME> -U <READS> -S <SAM>`
- bwa.ng: `bwa aln -o 0 -t <THREADS> -f tmp.sai -n <MISMATCHES> <GENOME> <READS> && bwa samse -f <SAM> <GENOME>.fa tmp.sai <READS>`
- bowtie1.mult.beststrata: `bowtie -k 100 --best --strata -S -p <THREADS> -x <GENOME> <READS> <SAM>`
- hisat: `hisat2 --very-sensitive --no-spliced-alignment -x <GENOME> -U <READS> -S <SAM> -p <THREADS>`
- segemehl: `segemehl.x -t <THREADS> -d <GENOME> -i <GENOME>.idx -q <READS> -o <SAM>`
- star: `STAR --outSAMattributes NH HI AS nM NM MD jM jI XS MC --outFilterMismatchNmax <MISMATCHES> --outFilterScoreMinOverLread 0 --outFilterMatchNminOverLread 0 --alignIntronMax 1 --genomeDir <GENOME> --readFilesIn <READS> --runThreadN <THREADS> --outFileNamePrefix <SAM>`
- yara.df: `yara_mapper --version-check FALSE -o <SAM>`