1. Quality assessment

fastqc filename.fastq

1. Filtering and trimming sequences:

prinseq-lite-0.20.4/prinseq-lite.pl -fastq RV75\_Alex\_R1\_001.fastq -fastq2 RV75\_Alex\_R2\_001.fastq -trim\_left 30 -custom\_params "CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT";"AC 25" -trim\_right 60 -min\_qual\_score 28 -min\_qual\_mean 30 -min\_len 50 -derep 1 -out\_format 3

1. Assembly of filtered and trimmed sequences:

spades.py --phred-offset 33 --only-assembler -1 /Users/castrolab03/Documents/ranas\_cvaldivia/bt\_results/RV\_all\_R1\_001\_prinseq\_good\_C4Ij.fastq -2 /Users/castrolab03/Documents/ranas\_cvaldivia/bt\_results/RV\_all\_R2\_001\_prinseq\_good\_t7fe.fastq -o /Users/castrolab03/Documents/ranas\_cvaldivia/assemblies

1. Blast of obtained contig against custom database containing Ranavirus genomes:

blastn -query final\_contigs.fasta -db ranavirus -outfmt "6 qseqid qlen sseqid slen qstart qend sstart send qseq sseq lenght nident pident evalue" -out blast\_rv\_genomes\_trimmed\_contig\_k127