blastn –db nt –query nt.fsa –out results.out

blastn -db LAI\_Q23\_DB -query S8\_merged.fastq -out blastS8.txt

blastn -db pt\_ref\_DB -query S8\_merged.fasta -out blastS8.txt -outfmt 6 -max\_target\_seqs 1

cat file1.fasta file2.fasta > combined.fasta

cat K03455.fasta Q23.fa > K03455\_and\_Q23.fasta

makeblastdb -in pt\_ref\_sequences.fasta -dbtype nucl -parse\_seqids -out pt\_ref\_DB

pandaseq -f C9\_S33\_L001\_R1\_001.fastq.gz -r C9\_S33\_L001\_R2\_001.fastq.gz -W

~/ACH2.fastq.bz2 -F

##(The -F allows it to be written in fastq)###

##Aligning the ACH2Sequence Data to the LAV1 Genome

mpankau@rhino1:~$ bowtie2-build LAV1.fasta LAV1

mpankau@rhino3:~$ bowtie2 -I/--minins-500 -x ~/LAV1 -q ~/ACH2.FASTQ

8\_S8\_L001\_R1\_001.fastq.gz

8\_S8\_L001\_R2\_001.fastq.gz

pandaseq -f 8\_S8\_L001\_R1\_001.fastq.gz -r 8\_S8\_L001\_R2\_001.fastq.gz -w S8\_merged.fasta