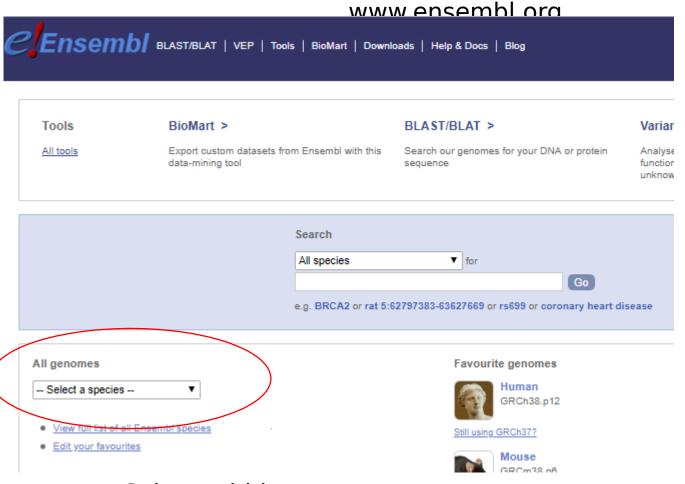
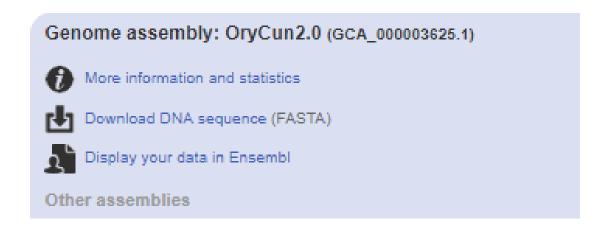
You need:

A fastq file (provided= Rabbit.fastq) + Reference sequence - you can download it from:



Select rabbit



Oryctolagus_cuniculus.OryCun2.0.dna.chromosome.8.fa.gz
Oryctolagus_cuniculus.OryCun2.0.dna.chromosome.9.fa.gz
Oryctolagus_cuniculus.OryCun2.0.dna.chromosome.MT.fa.gz
Oryctolagus_cuniculus.OryCun2.0.dna.chromosome.X.fa.gz
Oryctolagus_cuniculus.OryCun2.0.dna.nonchromosomal.fa.gz
Oryctolagus_cuniculus.OryCun2.0.dna.toplevel.fa.gz
Oryctolagus_cuniculus.OryCun2.0.dna.toplevel.fa.gz
Oryctolagus_cuniculus.OryCun2.0.dna rm.chromosome.1.fa.gz

Choose: Oryctolagus_cuniculus.OryCun2.0.dna.toplevel.fa.gz

In unix, to decompress: gunzip Oryctolagus_cuniculus.OryCun2.0.dna.toplevel.fa.gz

1)Index the reference:

bwa index -a bwtws Reference.fa #It will create several files in you directory with the same name of the Reference

2) align reads (you can choose between different command, we chose mem because it is indicated for NGS)

bwa mem Reference.fa Rabbit.fastq > Rabbit.sam #it creates the alignment file (plain text) that you want to have in binary format

3) Use samtools, as input give the sam files, as output obtain the bam

samtools view -bS Rabbit.sam > Rabbit.bam

sort and index (also the bam file needs to be indexed) - you need to specify the input and the output name of your new sorted output

samtools sort Rabbit.bam Raddit_sorted
#will create a new file named Raddit_sorted.bam

samtools index Rabbit_sorted.bam
#will create Rabbit sorted.bam.bai

4(index the reference file with samtools (needed for IGV) Samtools faidx Reference.fa

At the end you have:

Reference.fa Reference.fa.fai Rabbit_sorted.bam Rabbit_sorted.bam.bai And they are all needed for using IGV

Chack the manual of bwa and camteels and explore other commands. Enjoy * For any question.