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

www.ensembl.org

Select rabbit

Genome assembly: OryCun2.0 (GCA_000003625.1)

ⓘ More information and statistics

⤓ Download DNA sequence (FASTA)

⧉ Display your data in Ensembl

Other assemblies

📄 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_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

Check the manual of bwa and samtools and explore other commands. Enjoy. ☕ For any question: