

## Bioinformatics FISH546 Flowchart of Steps

Download data

unzip

fastQC

bowtie2 alignment

index reference

align samples

SNP calling mpileup

sort samples

mpileup

bcftools file conversion

convert bcf to vcf

bedtools intersect

download annotated genome

bedtools intersect, output as .txt

IGV visualization

vcf, annotated genome, and bam against reference