

I changed the final output file name from “results.vcf” to “FinalResults.vcf” as shown in red below. We would expect a final file to be outputted from the snakemake pipeline called “FinalResults.vcf” with no other changes.

```
# Rules
rule all:
    input:
        "o3_variants/FinalResults.vcf"

....

rule freebayes:
    input:
        bams=expand("o2_aligned/{sample}_dedup.bam", sample=SAMPLES),
        ref=REF
    output:
        vcf="o3_variants/FinalResults.vcf"
    params:
        bams = " ".join(expand("o2_aligned/{sample}_dedup.bam", sample=SAMPLES))
    shell:
        "freebayes -f {input.ref} {params.bams} > {output.vcf}"
```