

bcftools

How to use:

Available versions of bcftools and modules:

Version	Module
1.15.1	bioinfo/bcftools

Example script how to run a bcftools job on the cluster:

bcftools.sge

```
#!/bin/bash
#$      -N bcftools
#$      -cwd
#$      -q a16.q

module load bioinfo/bcftools/1.15.1

bcftools roh -G30 --AF-dflt 0.4 file.vcf
```



If using `--threads` or `-t`, instead of `-q a16.q` use `-pe *mpisingle 2`

Starting a job

```
qsub bcftools.sge
```