

```

params{
    MAPQ      = 50

    delDup = true

    CGcorrect = false

    chrs      ="all"

    chrPlotYlim="0 8"

    binPlotYlim="0 3"

    binOverviewSize="400 1000"

    customCoverageLimits="1.5 0.5"

    binSize=300

    covPerBinSigOPT="--minLen 0 --pThresh 0.001 --padjust BY"

    covPerGeSigOPT="--pThresh 0.001 --padjust BH --minLen 0"

    covPerGeRepeatRange = 1000

    freebayesOPT="--read-indel-limit 1 --read-mismatch-limit 3 --read-
snp-limit 3 --min-alternate-fraction 0.05 --min-base-quality 5 --min-
alternate-count 2 --pooled-continuous"

    filterFreebayesOPT="--minFreq 0.1 --maxFreq 1 --minAO 2 --
minAOhomopolymer 20 --contextSpan 5 --homopolymerFreq 0.4 --minMQMR 20 --
minMQM 20 --MADrange 4"

    filterDellyOPT="--minDV 2 --minPercentDVDR 5 --PRECISE no --maxBanSeq
90 --chrEndFilter 100"

    minNormCovForDUP = 0

    maxNormCovForDEL = 100

    binSizeCircos = 25000

    bigWigOPT="--binSize 10 --smoothLength 30"
}
process{
    executor='slurm'
    clusterOptions='-p aTeam --qos fast'
    container='/pasteur/p2p5/gip/giptools'
    errorStrategy='terminate'
    scratch=false
    cache=true
    echo=false
    stageInMode='symlink'
    time='20h'
    cpus=1
    memory='30000'
    withName: prepareGenome {

```

```

        cpus=2
    }
    withName: map {
        cpus=3
    }
    withName: covPerChr {
        memory='30000'
    }
    withName: covPerBin {
        memory='30000'
    }
    withName: mappingStats{
        memory='10000'
    }
    withName: covPerGe {
        memory='30000'
    }
    withName: freebayes {
        memory='40000'
    }
    withName: snpEff {
        memory='30000'
    }
    withName: delly {
        memory='30000'
    }
    withName: bigWigGenomeCov {
        memory='10000'
    }
    withName: report {
        memory='10000'
    }
}
singularity{
    enabled      = true
    autoMounts   = true
    runOptions = '--bind /pasteur'
}

```