```
touch$HOME/data/status.org.txt
echo -e "PIPELINE_REPLICATE\t01\t02\t03\t04\t05\t06\t07\t08\t09\t10" >
$HOME/data/status.org.txt
for item in $(seq 1 25); do
simphyReplicateID=$item
pipelinesName="ssp"
replicatesNumDigits=5
replicateID="$(printf "%0${replicatesNumDigits}g" $simphyReplicateID)"
ngsphyReplicatePath="$HOME/data/NGSphy_${pipelinesName}.${replicateID}"
replicates=(01 02 03 04 05 06 07 08 09 10)
numInds=()
val=0
for rep in ${replicates[]}; do # echo $ngsphyReplicatePath/PE150DFLT/$rep if [[ -d
$ngsphyReplicatePath/PE150DFLT/$rep ]]; then val=$(ls -l
$ngsphyReplicatePath/PE150DFLT/$rep| grep R1 | wc -l) else val=0 fi numInds+="\t$val" done
echo -e "${pipelinesName}.${replicateID}${numInds[]}" >> $HOME/data/status.org.txt
done

<<RCOMMANDS
inds=read.table("numinds.rep.txt", header=T)
status=read.table("status.org.txt",header=T)
repALL=inds[,1]
inds=inds[,2:11]
status=status[,2:11]
rownames(inds)=repALL
rownames(status)=repALL
inds-status
apply(inds-status, 1,sum)
ssp.00001 ssp.00002 ssp.00003 ssp.00004 ssp.00005 ssp.00006 ssp.00007 ssp.00008
0 -54 0 0 24 81 25 17
ssp.00009 ssp.00010 ssp.00011 ssp.00012 ssp.00013 ssp.00014 ssp.00015 ssp.00016
22 192 137 51 88 43 0 42
ssp.00017 ssp.00018 ssp.00019 ssp.00020 ssp.00021 ssp.00022 ssp.00023 ssp.00024
74 38 59 183 50 43 145 0
ssp.00025
54

RCOMMANDS

################################################################################
####
```

Generate file with number of ST replicates per SIMPHY replicate

```
################################################################################
####
echo -e
"SIMPHY_REPLICATE\tSTs_REPLICATES\tREPLICATES_ID(NUM_LOCI)"$HOME/src/vc-
benchmark-cesga/info/num.replicates.txt
for item in $(seq 1 25); do
simphyReplicateID=$item
pipelinesName="ssp"
replicatesNumDigits=5
replicateID="$(printf "%0${replicatesNumDigits}g" $simphyReplicateID)"
numReplicates=$(cat "$HOME/src/vc-benchmark-
cesga/files/${pipelinesName}.${replicateID}.indelible.folders.txt" | wc -l)
replicates=($(ls $HOME/data/NGSphy_${pipelinesName}.${replicateID}/reads))
locPerReplicate=()
for item in ${replicates[]}; do locPerReplicate+=" $(ls
$HOME/data/${pipelinesName}.${replicateID}/$item/TRUE.fasta | wc -l)"
done
totalNum=${#replicates[]} locPerReplicate=($locPerReplicate) let totalNum=totalNum-1 values=()
for index in $(seq 0 $totalNum);do values+=("${replicates[index]}(${locPerReplicate[index]})")
done echo -e "${pipelinesName}.${replicateID}\t$numReplicates\t${values[]}" >> $HOME/src/vc-
benchmark-cesga/info/num.replicates.txt
done

################################################################################
####
```

Generate file with INFORMATION about NGS progress of the replicates

```
################################################################################
####

for item in $(seq 1 25); do
simphyReplicateID=$item
pipelinesName="ssp"
```

```
replicatesNumDigits=5
replicateID="$(printf "%0${replicatesNumDigits}g" $simphyReplicateID)"
ls $HOME/data/NGSphy_${pipelinesName}.${replicateID}/reads
value=$(cat "$HOME/src/vc-benchmark-
cesga/files/${pipelinesName}.${replicateID}.indelible.folders.txt" | wc -l)
echo -e "${pipelinesName}.${replicateID}\t $value"
done
```