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Öffnen ▾ + From_SortedTSO500BAMss_to_PDFs_Custom_Controls_hg19_1MB_Modell.sh Speichern ×
ADATA /media/rmej..._für_das_Gespräch

# README:
# Check if you want to use that reference genome.
Path_2_myscript=/home/isilon/HumGenTempData/TS500_offtarget/Code
my_WIGs_dir=/home/isilon/HumGenTempData/for_Raul_TS0500/Data_for_ichor/250516_TS0500_Onco # <- Input to change
path hmm=/usr/bin # (doesn't matter)
reference_genome=/home/isilon/HumGenTempData/TS500_offtarget/Data/Common_Data_4_Projects/Reference_Genome/UCSC/hg19/
hg19.fa
path_to_ichor=/home/isilon/users/o_mejiaped/Code_bk/ichorCNA_Installation_Repo_Running/ichorCNA # your own installation
>

bash $Path_2_myscript/From_SortedBam_2_PDFs_CustomPoN-TS0500-10samples_1Mb_hg19_shared-folder.sh -idir $my_WIGs_dir -phmm
$path hmm -gref $reference_genome -pichor $path_to_ichor &> $my_WIGs_dir/Logfile.log
>

# example:
#bash ./ichor_From_Markdups_to_PDFs_hg19.sh -idir $my_AvBAs_dir -phmm $path hmm -gref $reference_genome -pichor
$path_to_ichor &> my_AvBAs_dir/Logfile.log
```

/home/isilon/HumGenTempData/TS500\_offtarget/Code/From\_SortedBam\_2\_PDFs\_CustomPoN-TS0500-
10samples\_1Mb\_hg19\_shared-folder.sh

Datei Bearbeiten Reiter Hilfe

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echo "STEP5: running ichorCNA"
if ! ls | grep "Results_ichorCNA_${1}"; then

mkdir ./Results_ichorCNA_${1} # Raúl added create the directory to save results
Rscript $4/scripts/runIchorCNA.R \
--WIG ${1}.wig \
--gcWig $4/inst/extdata/gc_hg19_1000kb.wig \
--mapWig $4/inst/extdata/map_hg19_1000kb.wig \
--ploidy "c(2,3,4)" \
--normal "c(0.35,0.4,0.45,0.5,0.55,0.6,0.65,0.7,0.75,0.8,0.85,0.9,0.95)" \
--maxCN 7 \
--id ${1} \
--estimateNormal TRUE \
--estimatePloidy TRUE \
--includeHOMD FALSE \
--chrs "c(1:22,\"X\")" \
--chrTrain "c(1:18)" \
--centromere $4/inst/extdata/GRCh37.p13_centromere_UCSC-gapTable.txt \
--normalPanel /home/isilon/HumGenTempData/TS500_offtarget/Data/CustomPoN_10TS0500_1MB_Hg19/PoN_of_10controls_fromTS0_1000kb.txt_median.rds \
--chrTrain "c(1:18)" \
--txnE 0.999 \
--txnStrength 100000 \
--scStates "c(1,3)" \
--estimateScPrevalence TRUE \
--maxFracGenomeSubclone 0.5 \
--maxFracCNASubclone 0.7 \
--minSegmentBins 50 \
--altFracThreshold 0.7 \
--lambdaScaleHyperParam 3 \
--outDir ./Results_ichorCNA_${1}

else
    echo "STEP5: Already done"
:

```

/home/isilon/HumGenTempData/for\_Raul\_TSO500/Data\_for\_ichor/