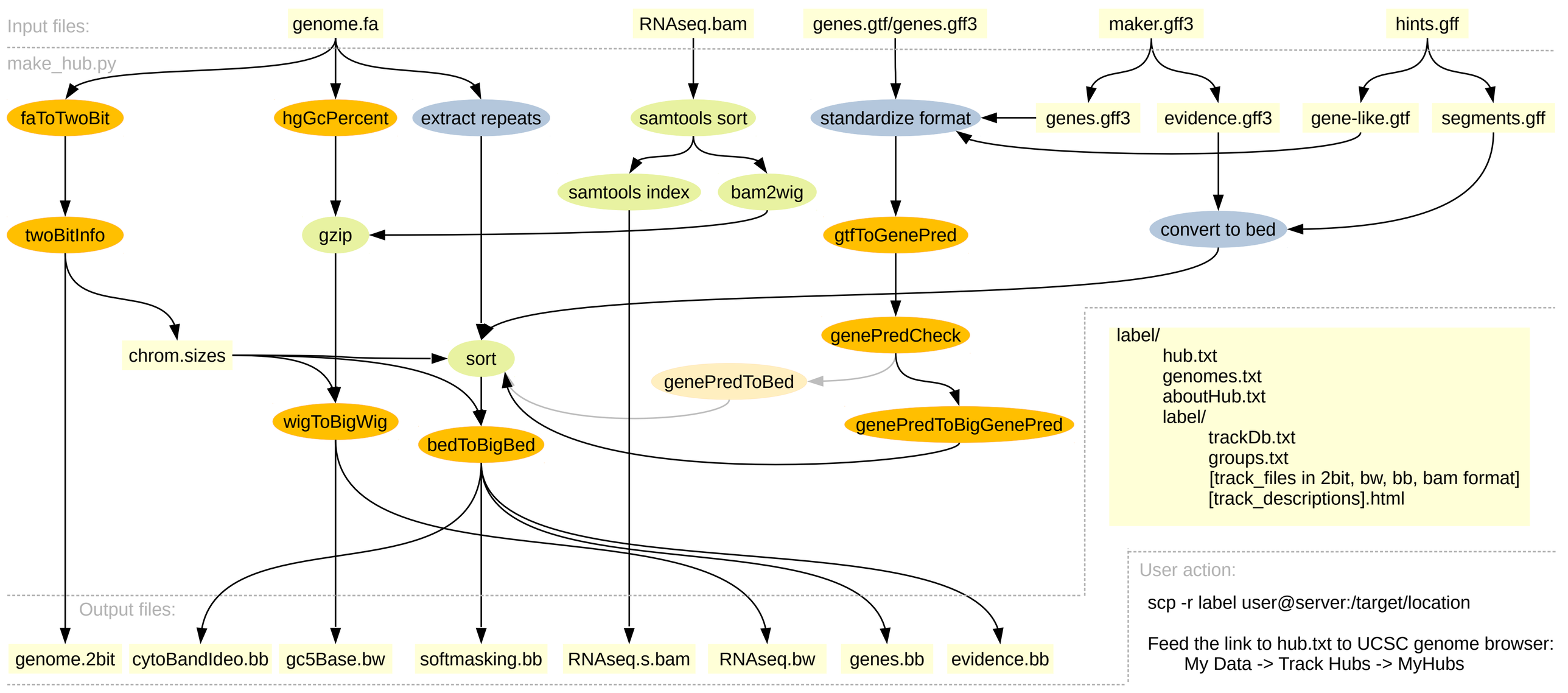
Input files:
genome.fa
RNAseq.bam
genes.gtf/genes.gff3
maker.gff3
hints.gff
make_hub.py
faToTwoBit
hgGcPercent
extract repeats
samtools sort
standardize format
genes.gff3
evidence.gff3
gene-like.gtf
segments.gff
samtools index
bam2wig
twoBitInfo
gzip
gtfToGenePred
convert to bed
genePredCheck
chrom.sizes
sort
genePredToBed
wigToBigWig
bedToBigBed
genePredToBigGenePred
label/
hub.txt
genomes.txt
aboutHub.txt
label/
trackDb.txt
groups.txt
[track_files in 2bit, bw, bb, bam format]
[track_descriptions].html
User action:
scp -r label user@server:/target/location
Feed the link to hub.txt to UCSC genome browser:
My Data -> Track Hubs -> MyHubs
Output files:
genome.2bit
cytoBandIdeo.bb
gc5Base.bw
softmasking.bb
RNAseq.s.bam
RNAseq.bw
genes.bb
evidence.bb