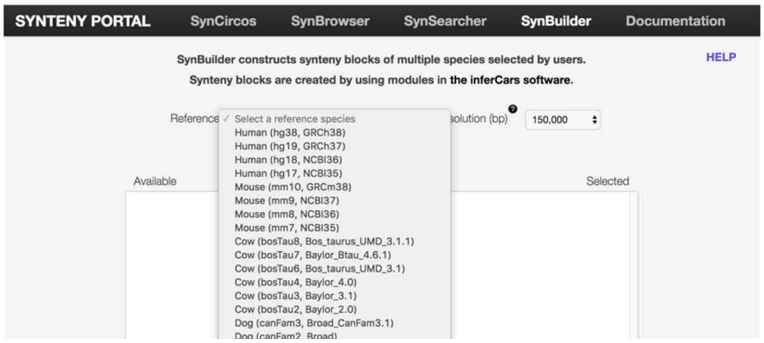
4. SynBuilder

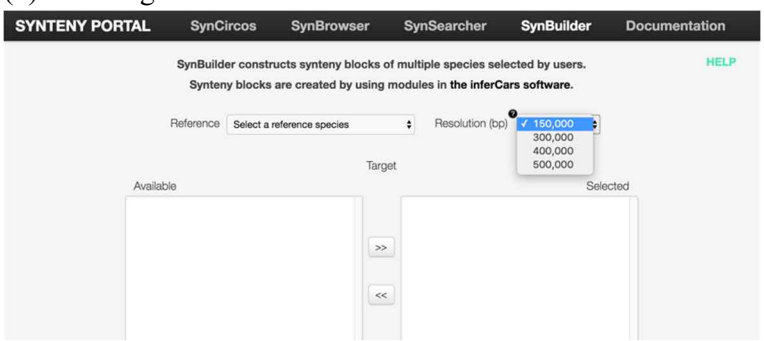
SynBuilder constructs synteny blocks of multiple species selected by users by using prebuilt whole-genome sequence alignments collected from the UCSC genome browser database.

(1) Selecting a reference species



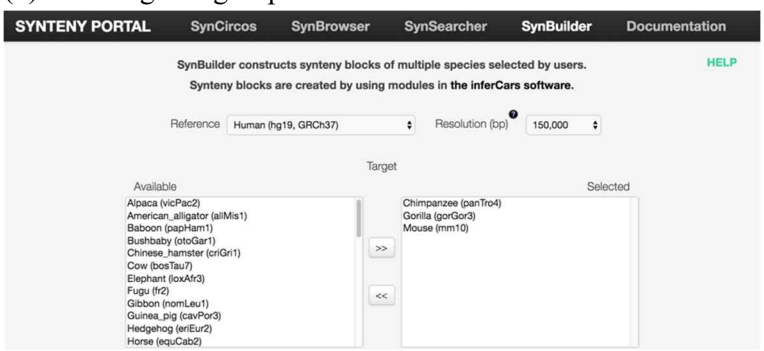
- Selecting a reference species and its assembly version.

(2) Selecting a resolution



- Selecting a resolution for building synteny blocks.

(3) Selecting a target species

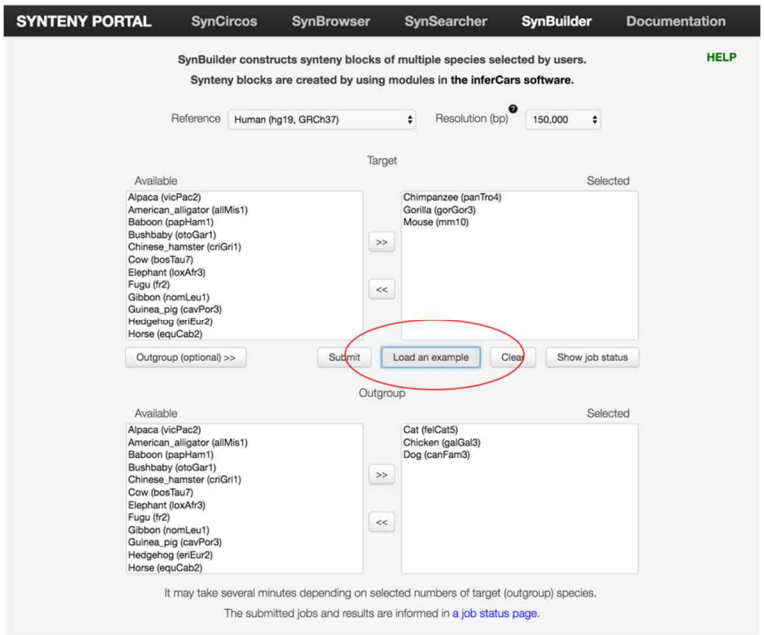


- Users can select target species and their assembly versions by using the '>>' button.
- Also, the selected target species can be unselected by using the '<<' button.

(4) Selecting outgroup species

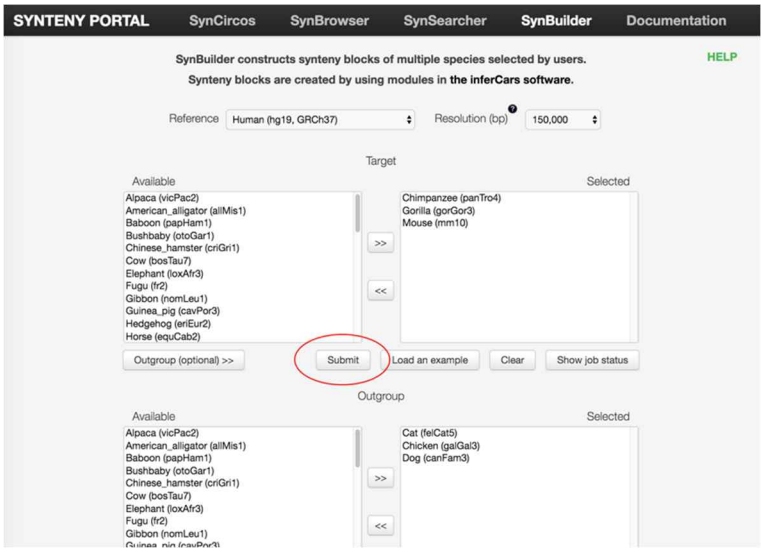
- Users can select outgroup species and their assembly versions by using the '>>' button.
- Also, the selected outgroup species can be unselected by using the '<<' button.

(5) An example of selected species



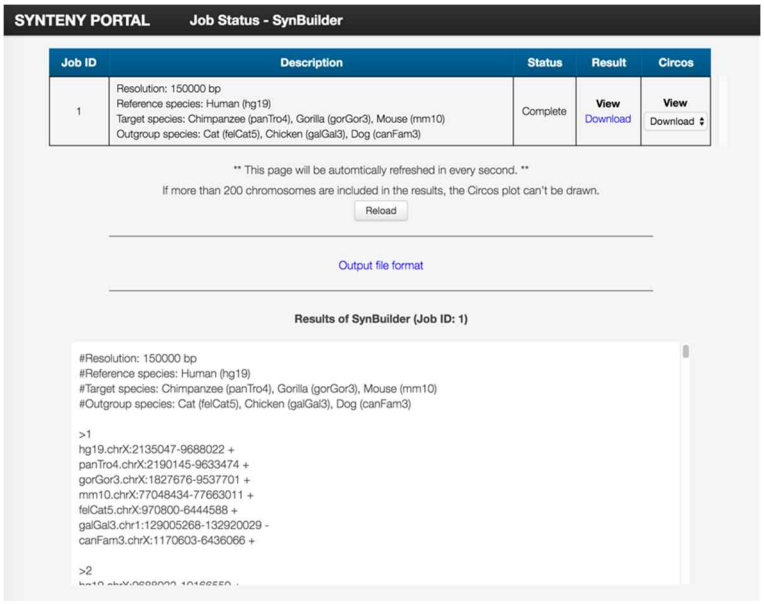
- User can load an example data set by clicking the 'Load an example' button.

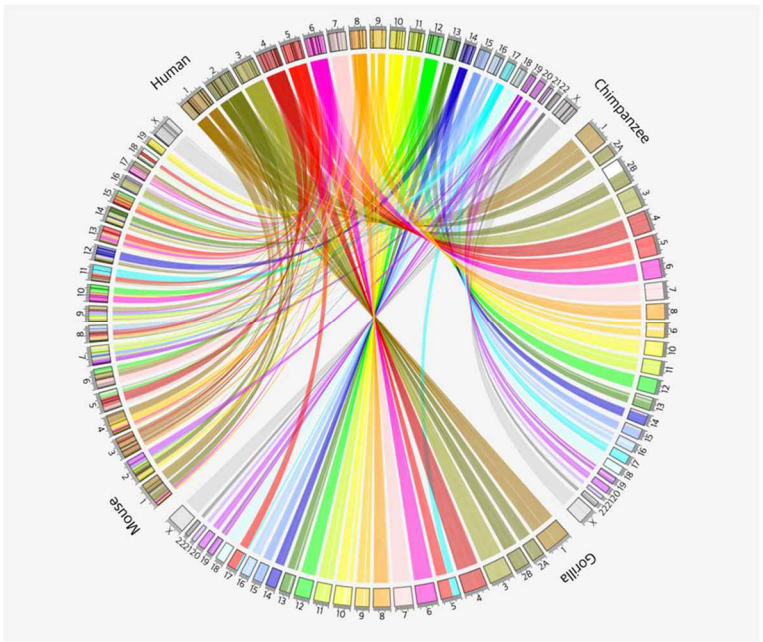
(6) Job submission



- Users can submit a job by clicking the 'Submit' button.

(6) Result page





- Users can check the status of their own jobs in a separated result page, which includes the information of processing and results of searching the synteny blocks and a Circos plot representing syntenic relationships.
- The Job ID column shows the identifier of each submitted job.
- The Description column shows the details of the submitted job.
- The Status column shows the current status of the job.
- The Result column provides the built synteny blocks.
    - Waiting → Waiting for finishing the job
    - View → Viewing the result of the built synteny blocks
    - Download → Downloading the result of the built synteny blocks.
    - No result → Not existing syntenic regions among the selected species.
- Circos column provides a Circos plot drawn by using built synteny blocks (reference and target species).
    - Waiting → Waiting for drawing the Circo plot
    - View → Viewing the Circos plot.

- Download box → Selecting and downloading the Circos plot.
- No results → There is no result for drawing the Circos plot.
  - Not existing syntenic regions among the selected species.
  - If more than 200 chromosomes are included in the results, the Circos plot can't be drawn.

(7) Output file format

- Lines starting with '#' contain parameters of the built synteny blocks.
  - Resolution → Minimum size of a reference block in bp
  - Reference species → Selected reference species
  - Target species → Selected target species
  - Outgroup species → Selected outgroup species
- A number in line started with '>' symbol represents the number of built synteny blocks.
- Other result lines represent syntenic regions within the reference, target, and outgroup species genomes.

Example output

```
#Resolution: 150000 bp
#Reference species: Human (hg19)
#Target species: Chimpanzee (panTro4), Gorilla (gorGor3), Mouse (mm10)
#Outgroup species: Cat (felCat5), Chicken (galGal3), Dog (canFam3)

>1
hg19.chrX:2135047-9688022 +
panTro4.chrX:2190145-9633474 +
gorGor3.chrX:1827676-9537701 +
mm10.chrX:77048434-77663011 +
felCat5.chrX:970800-6444588 +
galGal3.chr1:129005268-132920029 -
canFam3.chrX:1170603-6436066 +
```

Output description

```
>Synteny block number
Ref.RefChr:RefStart-RefEnd RefStrand
Tar1.Tar1Chr:Tar1Start-Tar1End Tar1Strand
Tar2.Tar2Chr:Tar2Start-Tar2End Tar2Strand
…
Out1.Out1Chr:Out1Start-Out1End Out1Strand
Out2.Out2Chr:Out2Start-Out2End Out2Strand
…

Ref: Reference species ID
RefStrand: Strand of alignment in reference
Tar1: Target species 1 ID
Tar1Chr: Target 1 chromosome
Tar1Start: Start of alignment in target 1
Tar1End: End of alignment in target 1
Tar1Strand: Strand of alignment in target 1
Out1: Outgroup species 1 ID
Out1Chr: Target 1 chromosome
Out1Start: Start of alignment in outgroup 1
Out1End: End of alignment in outgroup 1
Out1Strand: Strand of alignment in outgroup 1
```