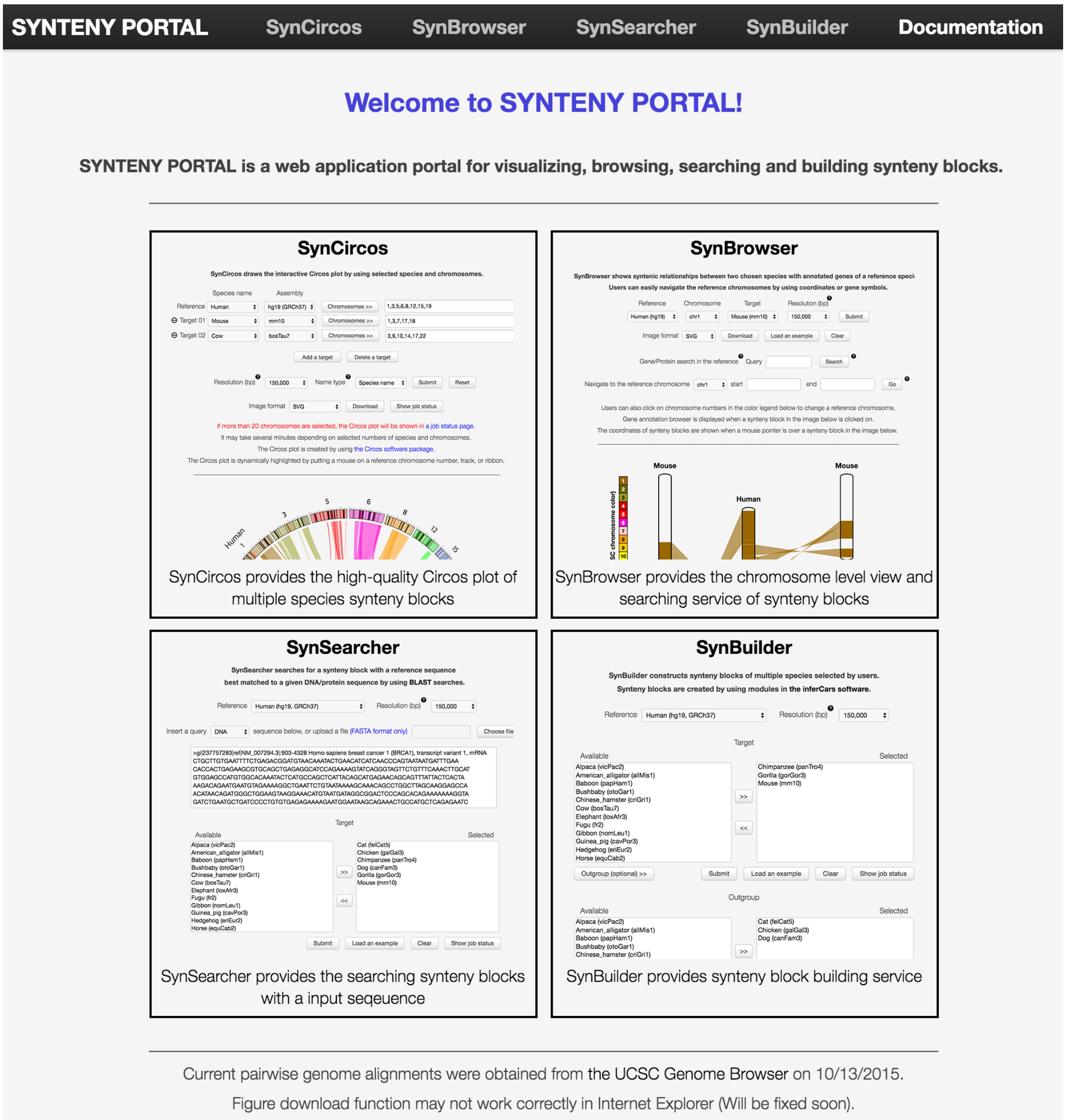
Synteny Portal Documentation

Synteny Portal is a web application portal for visualizing, browsing, searching and building synteny blocks. Synteny Portal provides four main web applications: SynCircos, SynBrowser, SynSearcher, and SynBuilder. SynCircos visualizes synteny blocks constructed from a user-selected reference and target species. SynBrowser displays more details of synteny blocks with annotated reference genes. SynSearcher processes a query sequence to find its syntenic regions in other species. Finally, SynBuilder constructs synteny blocks from chosen multiple species by using prebuilt whole-genome alignments collected from the UCSC genome browser database. The Synteny Portal website was implemented by using HTML5 and JavaScript libraries, such as jQuery (http://jquery.com) and d3.js (http://d3js.org/). Synteny Portal also provides synteny block information as text files and high-quality images to users.



Welcome to SYNTENY PORTAL!

SYNTENY PORTAL is a web application portal for visualizing, browsing, searching and building synteny blocks.

SynCircos

SynCircos draws the interactive Circos plot by using selected species and chromosomes.

	Species name	Assembly		
Reference	Human	hg19 (GRCh37)	Chromosomes >>	1,3,5,6,8,12,15,19
⊖ Target 01	Mouse	mm10	Chromosomes >>	1,3,7,17,18
⊖ Target 02	Cow	bosTau7	Chromosomes >>	3,9,10,14,17,22

Resolution (bp) 150,000

Name type Species name

Image format SVG

If more than 20 chromosomes are selected, the Circos plot will be shown in a job status page.

It may take several minutes depending on selected numbers of species and chromosomes.

The Circos plot is created by using the Circos software package.

The Circos plot is dynamically highlighted by putting a mouse on a reference chromosome number, track, or ribbon.

SynCircos provides the high-quality Circos plot of multiple species synteny blocks

SynBrowser

SynBrowser shows syntenic relationships between two chosen species with annotated genes of a reference speci

Users can easily navigate the reference chromosomes by using coordinates or gene symbols.

Reference Human (hg19)

Chromosome chr1

Target Mouse (mm10)

Resolution (bp) 150,000

Image format SVG

Gene/Protein search in the reference Query

Navigate to the reference chromosome chr1 start end

Users can also click on chromosome numbers in the color legend below to change a reference chromosome.

Gene annotation browser is displayed when a synteny block in the image below is clicked on.

The coordinates of synteny blocks are shown when a mouse pointer is over a synteny block in the image below.

SynBrowser provides the chromosome level view and searching service of synteny blocks

SynSearcher

SynSearcher searches for a synteny block with a reference sequence best matched to a given DNA/protein sequence by using BLAST searches.

Reference Human (hg19, GRCh37)

Resolution (bp) 150,000

Insert a query DNA sequence below, or upload a file (FASTA format only)

```
>gi|237757283|ref|NM_007294.3|:903-4328 Homo sapiens breast cancer 1 (BRCA1), transcript variant 1, mRNA
CTGCTTGTGAATTTTCTGAGACGGATGTAACAAATACTGAACATCATCAACCCAGTAATAATGATTTGAA
CACCACTGAGAAGCGTGCAGCTGAGAGGCATCCAGAAAAGTATCAGGGTAGTTCTGTTTCAAACTTGCAT
GTGGAGCCATGTGGCACAAATACTCATGCCAGCTCATTACAGCATGAGAACAGCAGTTTATTACTCACTA
AAGACAGAATGAATGTAGAAAAGGCTGAATTCTGTAATAAAAGCAAACAGCCTGGCTTAGCAAGGAGCCA
ACATAACAGATGGGCTGGAAGTAAGGAAACATGTAATGATAGGCGGACTCCCAGCACAGAAAAAAAGGTA
GATCTGAATGCTGATCCCCTGTGTGAGAGAAAAGAATGGAATAAGCAGAAACTGCCATGCTCAGAGAATC
```

Target

Available	Selected
Alpaca (vicPac2) American_alligator (allMis1) Baboon (papHam1) Bushbaby (otoGar1) Chinese_hamster (criGri1) Cow (bosTau7) Elephant (loxAfr3) Fugu (fr2) Gibbon (nomLeu1) Guinea_pig (cavPor3) Hedgehog (eriEur2) Horse (equCab2)	Cat (felCat5) Chicken (galGal3) Chimpanzee (panTro4) Dog (canFam3) Gorilla (gorGor3) Mouse (mm10)

SynSearcher provides the searching synteny blocks with a input seqeuence

SynBuilder

SynBuilder constructs synteny blocks of multiple species selected by users.

Synteny blocks are created by using modules in the inferCars software.

Reference Human (hg19, GRCh37)

Resolution (bp) 150,000

Target

Available	Selected
Alpaca (vicPac2) American_alligator (allMis1) Baboon (papHam1) Bushbaby (otoGar1) Chinese_hamster (criGri1) Cow (bosTau7) Elephant (loxAfr3) Fugu (fr2) Gibbon (nomLeu1) Guinea_pig (cavPor3) Hedgehog (eriEur2) Horse (equCab2)	Chimpanzee (panTro4) Gorilla (gorGor3) Mouse (mm10)

Outgroup

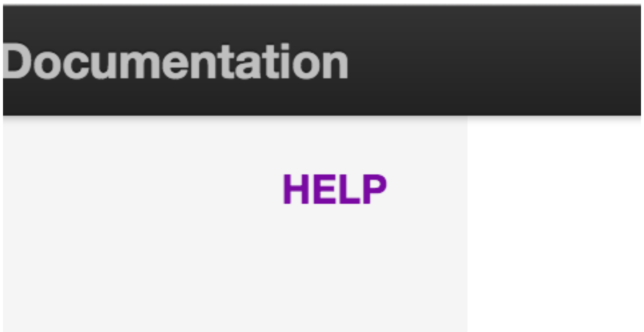
Available	Selected
Alpaca (vicPac2) American_alligator (allMis1) Baboon (papHam1) Bushbaby (otoGar1) Chinese_hamster (criGri1)	Cat (felCat5) Chicken (galGal3) Dog (canFam3)

SynBuilder provides synteny block building service

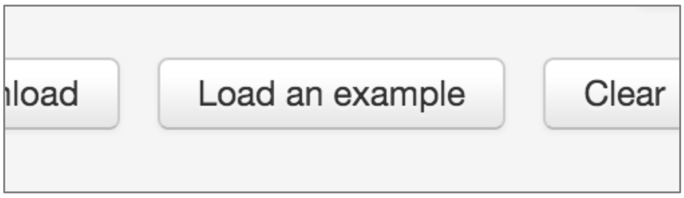
Current pairwise genome alignments were obtained from the UCSC Genome Browser on 10/13/2015.

Figure download function may not work correctly in Internet Explorer (Will be fixed soon).

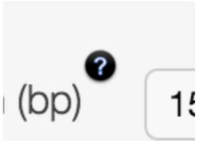
This document can be always accessed through the ‘HELP’ link at the right-top corner of each page as shown below.



Users can test the four applications by using example datasets. Users can automatically insert the example datasets when the ‘Load an example’ button is clicked on at SynBrowser, SynSearcher, and SynBuilder as shown below. In SynCircos, an example dataset is displayed as a default.



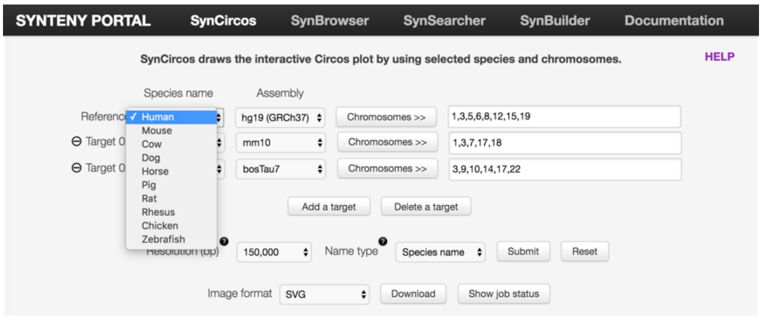
User can easily see the definition or additional information of menus when a mouse pointer moves on or a mouse button is click on the ‘?’ image as shown below.



1. SynCircos

SynCircos draws the interactive Circos plot by using selected species and chromosomes.

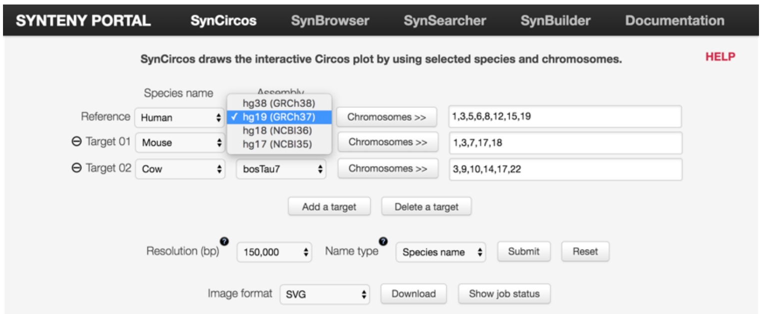
(1) Selecting reference species and assembly version



SynCircos draws the interactive Circos plot by using selected species and chromosomes.

Reference: Human, hg19 (GRCh37), 1,3,5,6,8,12,15,19
Target 01: mm10, 1,3,7,17,18
Target 02: bosTau7, 3,9,10,14,17,22
Resolution (bp): 150,000
Name type: Species name
Image format: SVG

- Selecting a reference species.

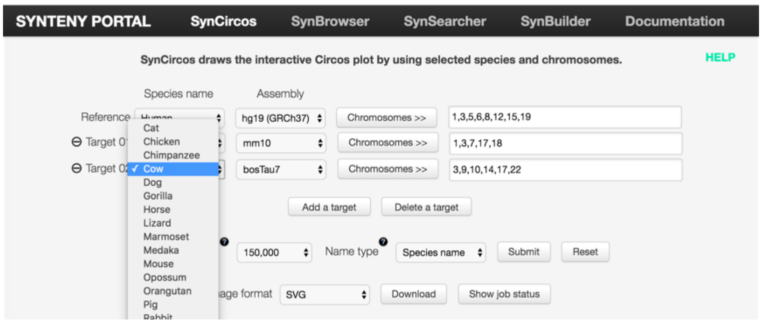


SynCircos draws the interactive Circos plot by using selected species and chromosomes.

Reference: Human, hg19 (GRCh37), 1,3,5,6,8,12,15,19
Target 01: Mouse, 1,3,7,17,18
Target 02: Cow, bosTau7, 3,9,10,14,17,22
Resolution (bp): 150,000
Name type: Species name
Image format: SVG

- Selecting the assembly version of the selected reference species.

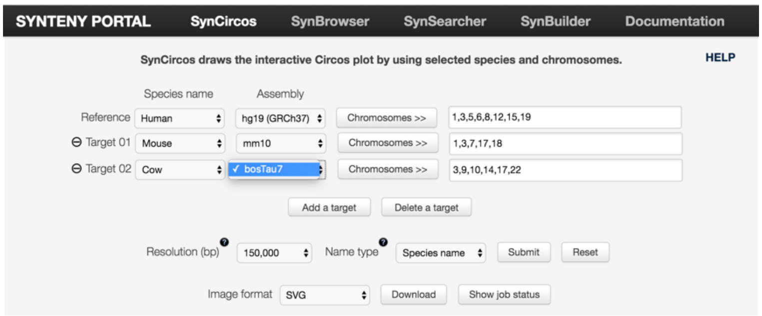
(2) Selecting a target species and assembly version



SynCircos draws the interactive Circos plot by using selected species and chromosomes.

Reference: Human, hg19 (GRCh37), 1,3,5,6,8,12,15,19
Target 01: mm10, 1,3,7,17,18
Target 02: bosTau7, 3,9,10,14,17,22
Name type: Species name
Image format: SVG

- Selecting a target species.

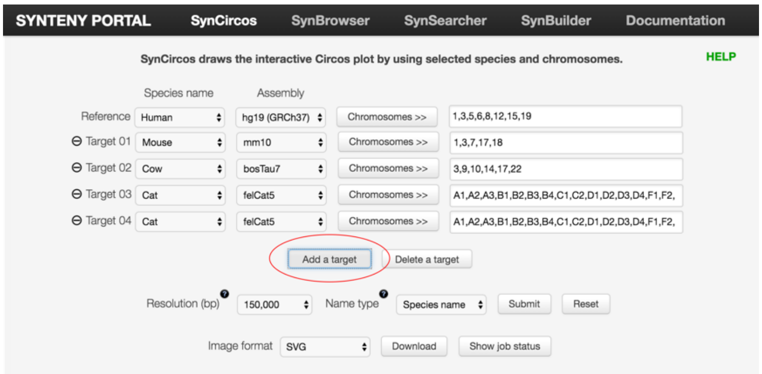


SynCircos draws the interactive Circos plot by using selected species and chromosomes.

Reference: Human, hg19 (GRCh37), 1,3,5,6,8,12,15,19
Target 01: Mouse, mm10, 1,3,7,17,18
Target 02: Cow, bosTau7, 3,9,10,14,17,22
Resolution (bp): 150,000
Name type: Species name
Image format: SVG

- Selecting the assembly version of the selected target species.

(3) Adding target species



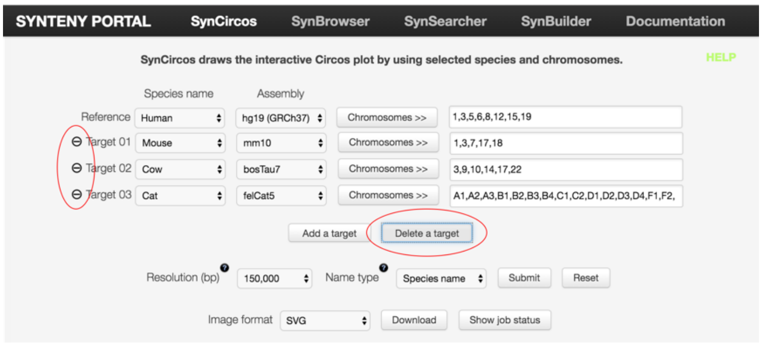
SynCircos draws the interactive Circos plot by using selected species and chromosomes.

	Species name	Assembly		
Reference	Human	hg19 (GRCh37)	Chromosomes >>	1,3,5,6,8,12,15,19
⊖ Target 01	Mouse	mm10	Chromosomes >>	1,3,7,17,18
⊖ Target 02	Cow	bosTau7	Chromosomes >>	3,9,10,14,17,22
⊖ Target 03	Cat	felCat5	Chromosomes >>	A1,A2,A3,B1,B2,B3,B4,C1,C2,D1,D2,D3,D4,F1,F2,
⊖ Target 04	Cat	felCat5	Chromosomes >>	A1,A2,A3,B1,B2,B3,B4,C1,C2,D1,D2,D3,D4,F1,F2,

Resolution (bp): 150,000
Name type: Species name
Image format: SVG

- Users can add target species by clicking on the ‘Add a target’ button.

(4) Removing target species



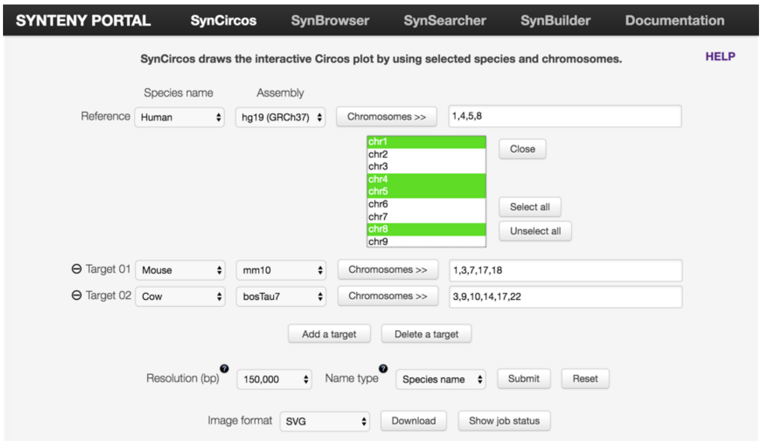
SynCircos draws the interactive Circos plot by using selected species and chromosomes.

	Species name	Assembly		
Reference	Human	hg19 (GRCh37)	Chromosomes >>	1,3,5,6,8,12,15,19
⊖ Target 01	Mouse	mm10	Chromosomes >>	1,3,7,17,18
⊖ Target 02	Cow	bosTau7	Chromosomes >>	3,9,10,14,17,22
⊖ Target 03	Cat	felCat5	Chromosomes >>	A1,A2,A3,B1,B2,B3,B4,C1,C2,D1,D2,D3,D4,F1,F2,

Resolution (bp): 150,000
Name type: Species name
Image format: SVG

- Users can delete target species by clicking on the ‘Delete a target’ button or the ‘-’ symbol in front of the label ‘Target XX’.
- When Users press ‘Delete a target’ button, the last target is removed.

(5) Selecting specific chromosomes



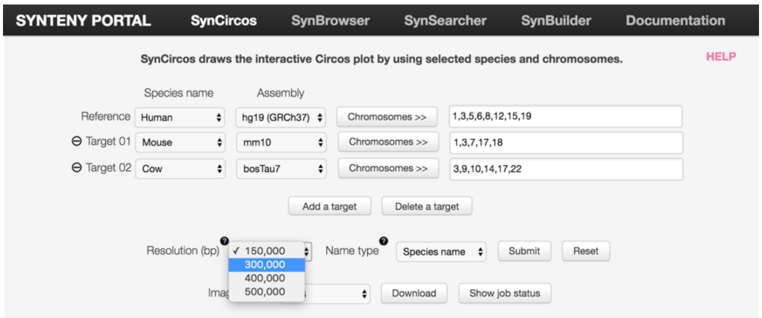
SynCircos draws the interactive Circos plot by using selected species and chromosomes.

	Species name	Assembly		
Reference	Human	hg19 (GRCh37)	Chromosomes >>	1,4,5,8
⊖ Target 01	Mouse	mm10	Chromosomes >>	1,3,7,17,18
⊖ Target 02	Cow	bosTau7	Chromosomes >>	3,9,10,14,17,22

Resolution (bp): 150,000
Name type: Species name
Image format: SVG

- The specific chromosomes of a reference and target species can be selected.
- The chromosome selection menu is opened when user click on the ‘Chromosomes >>’ button.
- It is possible to select multiple chromosomes at once by clicks with the ‘Ctrl’ or ‘Shift’ key.
- All chromosomes can be selected or unselected by using the ‘Select all’ and ‘Unselect all’ buttons respectively.

(6) Selecting a resolution



SynCircos draws the interactive Circos plot by using selected species and chromosomes.

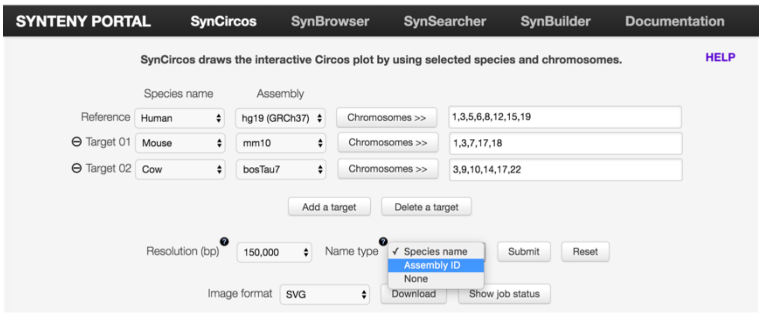
	Species name	Assembly	
Reference	Human	hg19 (GRCh37)	1,3,5,6,8,12,15,19
⊖ Target 01	Mouse	mm10	1,3,7,17,18
⊖ Target 02	Cow	bosTau7	3,9,10,14,17,22

Resolution (bp): ✓ 150,000 / 300,000 / 400,000 / 500,000

Name type: Species name

- Selecting a resolution of synteny blocks.

(7) Selecting a name type



SynCircos draws the interactive Circos plot by using selected species and chromosomes.

	Species name	Assembly	
Reference	Human	hg19 (GRCh37)	1,3,5,6,8,12,15,19
⊖ Target 01	Mouse	mm10	1,3,7,17,18
⊖ Target 02	Cow	bosTau7	3,9,10,14,17,22

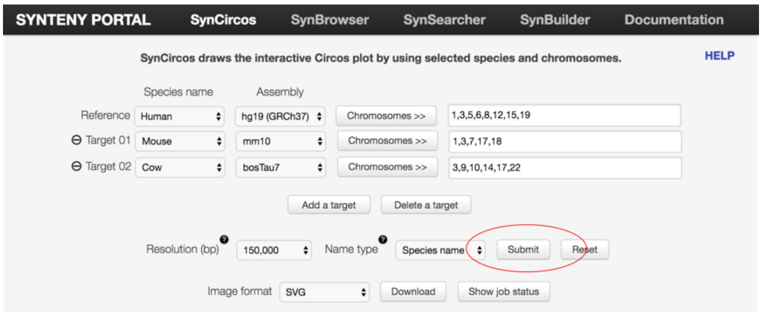
Resolution (bp): 150,000

Name type: ✓ Species name / Assembly ID / None

Image format: SVG

- Selecting the name type of a reference and target species which will be used in the output Circos plot.
- ‘Species name’ is a human-friendly species name, such as human, mouse, and cow.
- ‘Assembly ID’ is a genome assembly identifier, such as hg19, mm10, and bosTau7, used in the UCSC genome browser.
- When users select ‘None’, a name is not shown in the output Circos plot.

(8) Clicking the ‘Submit’ button for drawing the Circos plot



SynCircos draws the interactive Circos plot by using selected species and chromosomes.

	Species name	Assembly	
Reference	Human	hg19 (GRCh37)	1,3,5,6,8,12,15,19
⊖ Target 01	Mouse	mm10	1,3,7,17,18
⊖ Target 02	Cow	bosTau7	3,9,10,14,17,22

Resolution (bp): 150,000

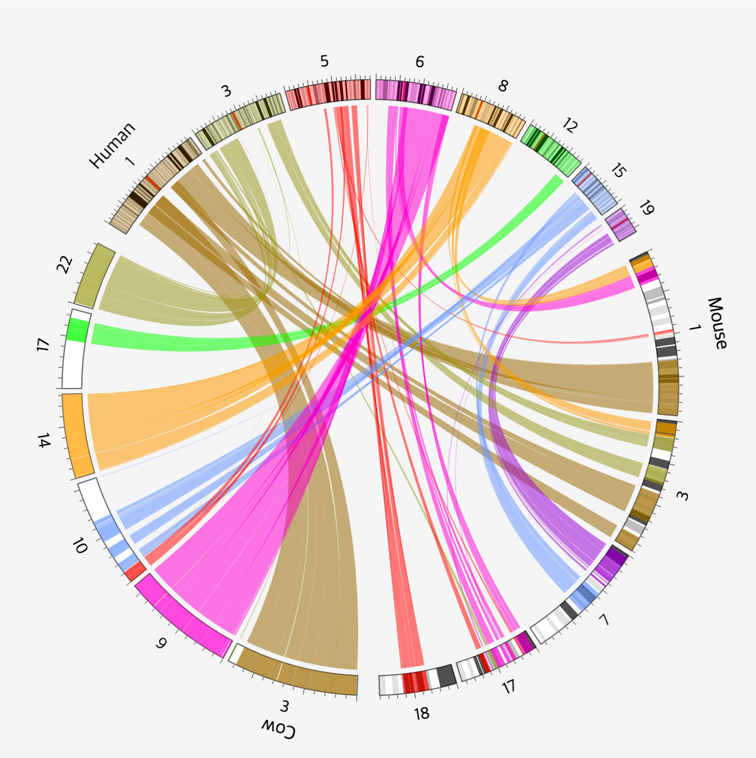
Name type: Species name

Image format: SVG

- The Circos plot is drawn in the current page when the total number of selected chromosomes is less than 20. → (9-1)
- Otherwise, the Circos plot is drawn in a separated result page. → (9-2)

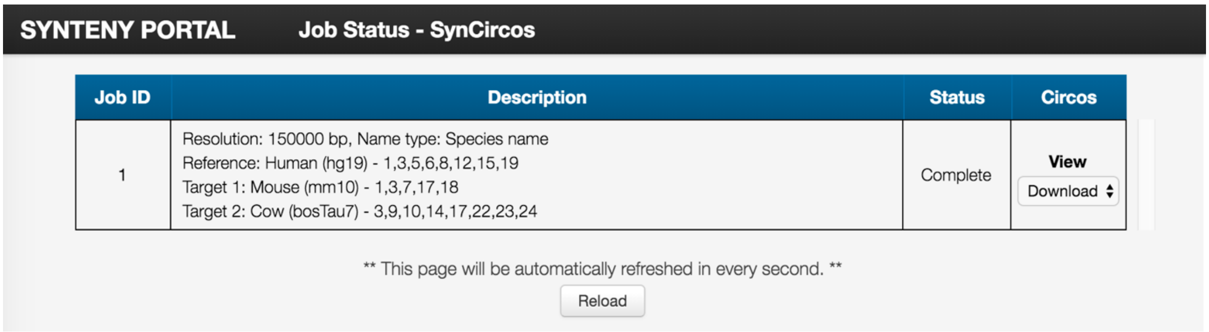
(9-1) An example of SynCircos

The following Circos plot is created by using the Circos software package.



- The specific syntenic relationship shown as a ribbon can be highlighted by a mouse over the specific reference chromosome number, track or ribbon.

(9-2) An example of SynCircos in a separated result page

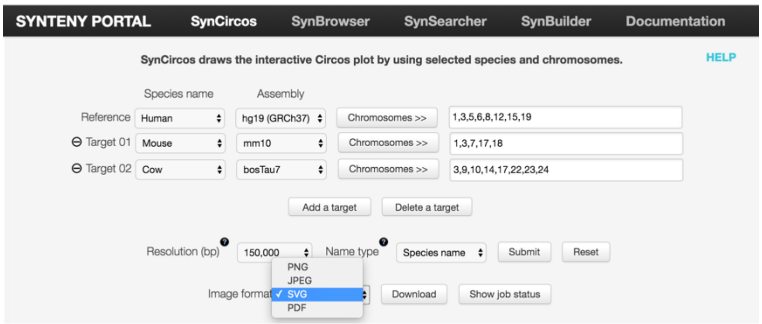


Job ID	Description	Status	Circos
1	Resolution: 150000 bp, Name type: Species name Reference: Human (hg19) - 1,3,5,6,8,12,15,19 Target 1: Mouse (mm10) - 1,3,7,17,18 Target 2: Cow (bosTau7) - 3,9,10,14,17,22,23,24	Complete	View Download

** This page will be automatically refreshed in every second. **

- When the total number of selected chromosomes is larger than 20, the drawing job is submitted to our job scheduler.
- The description and status of submitted jobs are shown in a table as shown above.
- When the job status is changed to ‘Complete’, click ‘View’ button for visualizing the resulting Circos plot.
- The output Circos plot can be downloaded by using the ‘Download’ select box as PNG, JPEG, SVG, or PDF format.

(10) Selecting an image format for downloading the output Circos plot.



SynCircos draws the interactive Circos plot by using selected species and chromosomes.

	Species name	Assembly	
Reference	Human	hg19 (GRCh37)	1,3,5,6,8,12,15,19
⊖ Target 01	Mouse	mm10	1,3,7,17,18
⊖ Target 02	Cow	bosTau7	3,9,10,14,17,22,23,24

Resolution (bp): 150,000

Name type: Species name

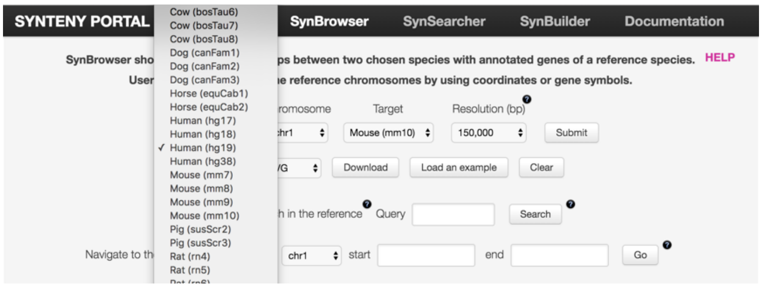
Image format: ✓ SVG

- User can also download the Circos plot drawn in the default page as an image file in four different image formats (PNG, JPEG, SVG, and PDF).

2. SynBrowser

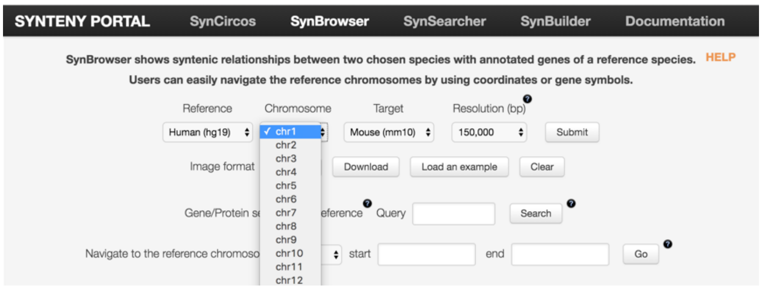
SynBrowser shows syntenic relationships between two chosen species with annotated genes of a reference species. Users can easily navigate the reference chromosomes by using coordinates or genes.

(1) Selecting a reference species



- Selecting a reference species and its assembly version.

(2) Selecting a reference chromosome

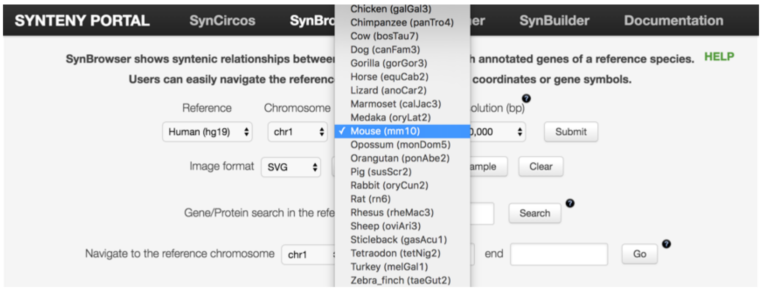


SynBrowser shows syntenic relationships between two chosen species with annotated genes of a reference species.

Users can easily navigate the reference chromosomes by using coordinates or gene symbols.

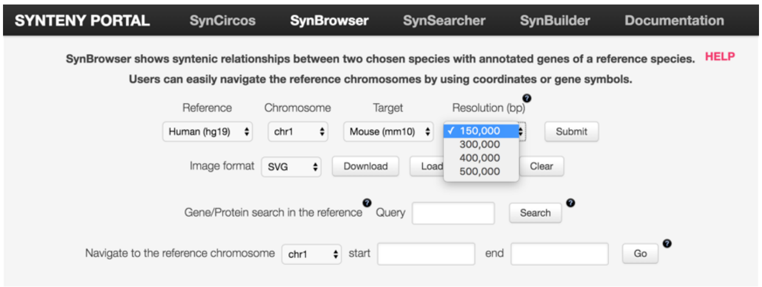
- Selecting a reference chromosome.

(3) Selecting a target species



- Selecting a target species and its assembly version.

(4) Selecting a resolution

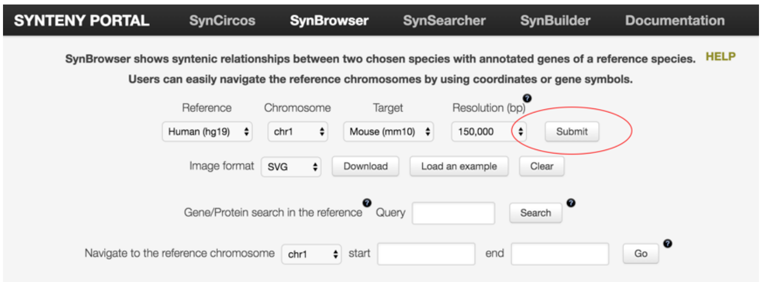


SynBrowser shows syntenic relationships between two chosen species with annotated genes of a reference species.

Users can easily navigate the reference chromosomes by using coordinates or gene symbols.

- Selecting a resolution of synteny blocks.

(5) Clicking the ‘Submit’ button for drawing syntenic relationships

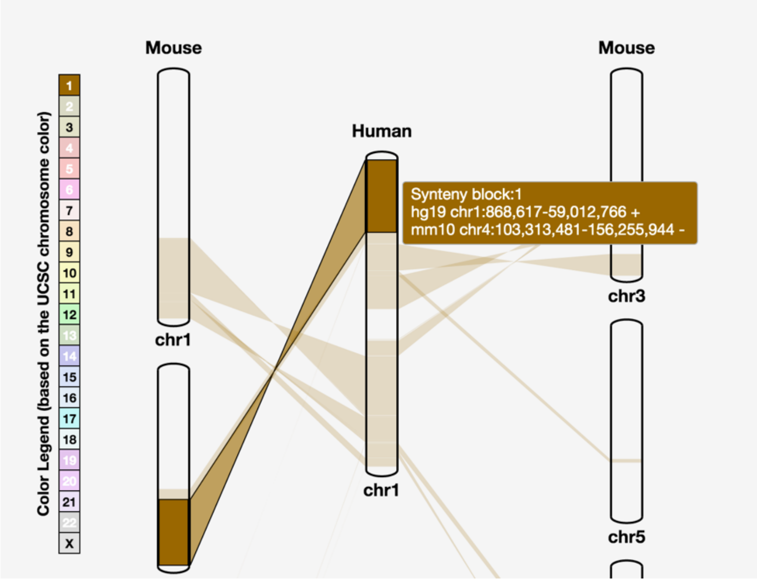


SynBrowser shows syntenic relationships between two chosen species with annotated genes of a reference species. Users can easily navigate the reference chromosomes by using coordinates or gene symbols.

Reference: Human (hg19)
Chromosome: chr1
Target: Mouse (mm10)
Resolution (bp): 150,000
Image format: SVG
Navigate to the reference chromosome: chr1

- The pairwise syntenic information appears in the bottom section as shown below.

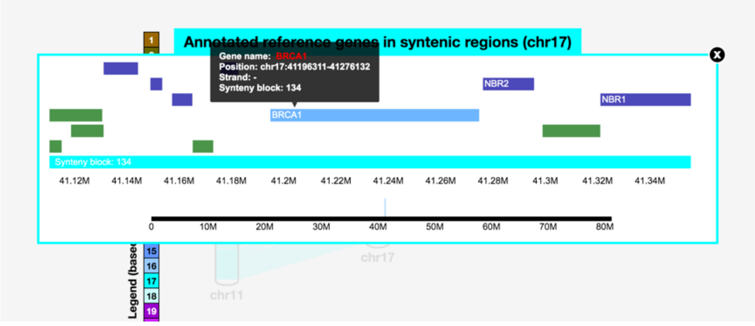
(6) Putting a mouse pointer on a synteny block for seeing the details of the synteny block.



Synteny block:1
hg19 chr1:868,617-59,012,766 +
mm10 chr4:103,313,481-156,255,944 -

- User can easily see the details of synteny blocks with moving a mouse pointer on a specific synteny block.
- The information includes a synteny block number, the coordinates of reference and target genome.

(7) Browsing gene annotations

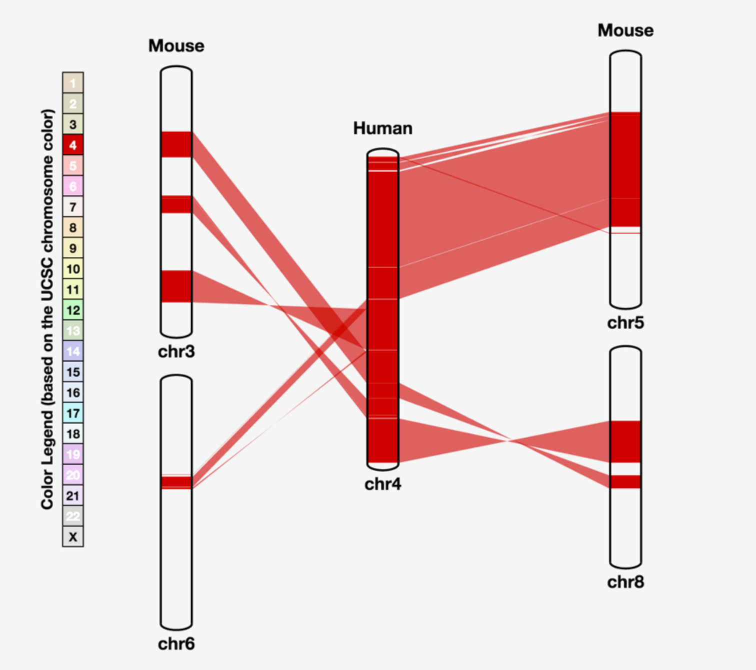


Gene name: BRCA1
Position: chr17:41196311-41276132
Strand: -
Synteny block: 134

- The gene annotation browser is opened when a specific synteny block is clicked on.
- The blue and green blocks represent the plus and minus strand genes, respectively.
- The names and simple information of the genes appear when a mouse pointer moves on the block.
- The color of a synteny block track (light blue in the figure) represents the reference chromosome color.
- The black scale bar at the bottom of the figure represents a selected reference chromosome.

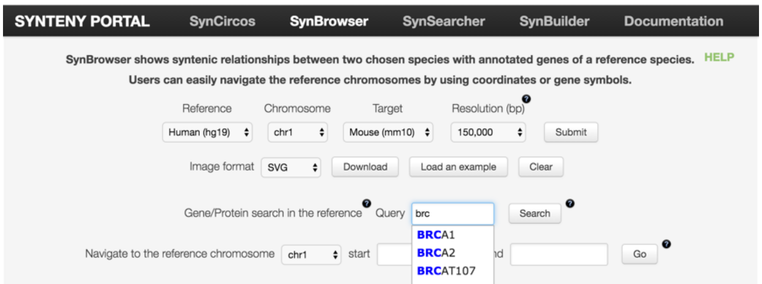
- The blue box on the black scale bar represents the selected region in the selected reference chromosome.
- Users can browse and move the tracks by mouse drags and wheels.
  - Mouse click and drag → Move track
  - Mouse wheel up/down → Zoom in/out
- Users also can move the tracks by dragging the blue box on the black scale.
- Users can resize the visible region by resizing the blue box on the black scale bar.
- When users clicks on a specific gene, the UCSC genome browser is shown.

(8) Selecting a reference chromosome in the left panel



- A reference chromosome can be changed when a chromosome number in the left panel is clicked on.

(9) Searching a query gene

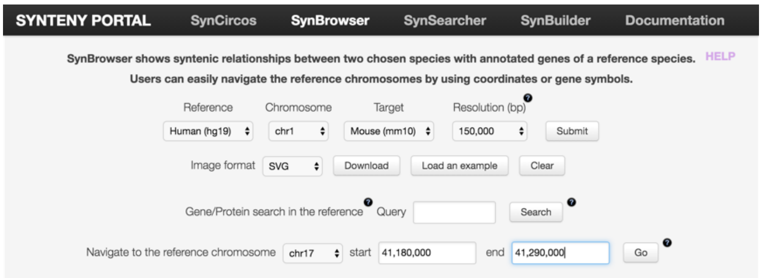


SynBrowser shows syntenic relationships between two chosen species with annotated genes of a reference species.
Users can easily navigate the reference chromosomes by using coordinates or gene symbols.

Reference: Human (hg19)
Chromosome: chr1
Target: Mouse (mm10)
Resolution (bp): 150,000
Image format: SVG
Gene/Protein search in the reference Query: brc
BRCA1
BRCA2
BRCAT107
Navigate to the reference chromosome: chr1 start

- Users can search for a query gene/protein of the selected reference species by entering a query gene/protein name or identifier.
- We support WIKIGENE (e.g. BRCA1, TP53), REFSEQ_MRNA (e.g. NM_007300, NM_001276760), Ensembl gene (e.g. ENSG00000012048, ENSG00000124251), Ensembl protein (e.g. ENSP00000350283, ENSP00000361811), Ensembl transcript (e.g. ENST00000357654, ENST00000372726), ENTREZGENE (e.g. 672, 27296), and PROTEIN_ID (e.g. AAI15038, AAH36785).
- The query is auto-completed based on gene identifiers in WIKIGENE.

(10) Searching a specific position of synteny blocks



SynBrowser shows syntenic relationships between two chosen species with annotated genes of a reference species. Users can easily navigate the reference chromosomes by using coordinates or gene symbols.

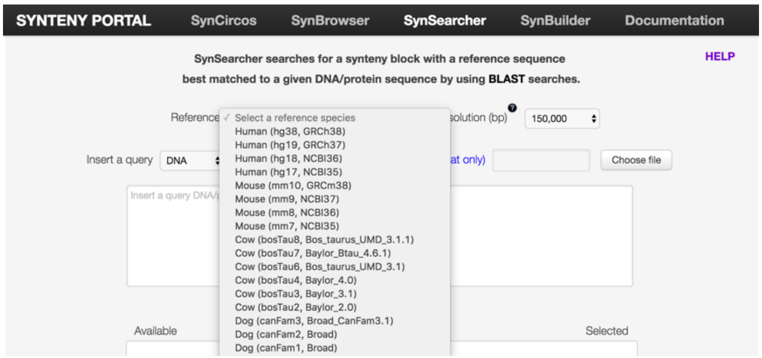
Reference: Human (hg19)
Chromosome: chr1
Target: Mouse (mm10)
Resolution (bp): 150,000
Image format: SVG
Gene/Protein search in the reference Query:
Navigate to the reference chromosome: chr17 start 41,180,000 end 41,290,000

- Users can search a specific region of the selected reference species in the browser by specifying a chromosome number, start and end positions.

3. SynSearcher

SynSearcher searches for a synteny block with a reference sequence best matched to a given DNA or protein sequence by using BLAST searches.

(1) Selecting a reference species



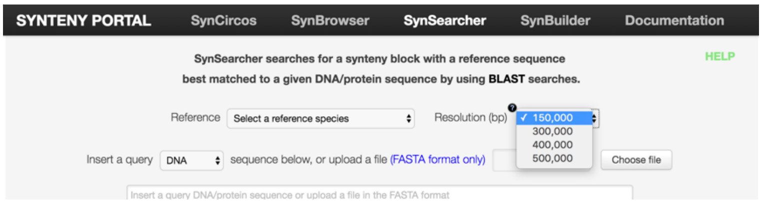
SynSearcher searches for a synteny block with a reference sequence
best matched to a given DNA/protein sequence by using **BLAST** searches.

Resolution (bp): 150,000

Insert a query: DNA

- Selecting a reference and its assembly version.

(2) Selecting a resolution



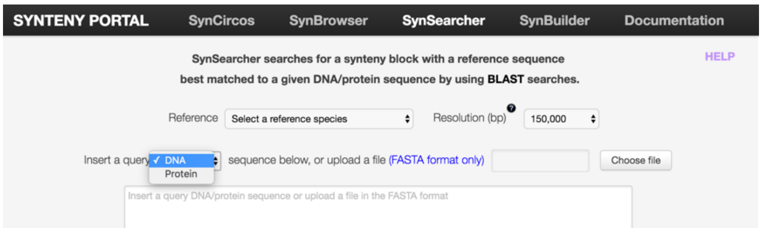
SynSearcher searches for a synteny block with a reference sequence
best matched to a given DNA/protein sequence by using **BLAST** searches.

Reference: Select a reference species

Insert a query: DNA sequence below, or upload a file (FASTA format only)

- Selecting a resolution of synteny blocks.

(3) Selecting a query sequence type



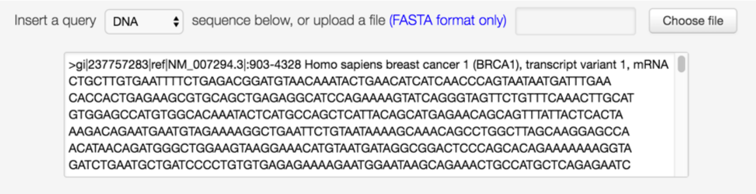
SynSearcher searches for a synteny block with a reference sequence
best matched to a given DNA/protein sequence by using **BLAST** searches.

Reference: Select a reference species

Resolution (bp): 150,000

- Selecting a query sequence type (DNA or protein).

(4) Inserting a query sequence

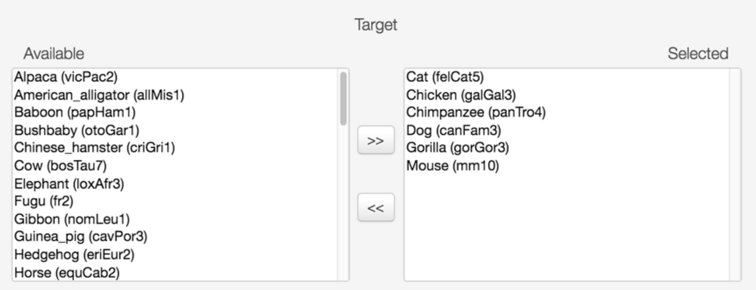


Insert a query: DNA sequence below, or upload a file (FASTA format only)

```
>gi|237757283|ref|NM_007294.3|:903-4328 Homo sapiens breast cancer 1 (BRCA1), transcript variant 1, mRNA
CTGCTTGTGAATTTTCTGAGACGGATGTAACAAATACTGAACATCATCAACCCAGTAATAATGATTTGAA
CACCACTGAGAAGCGTGCAGCTGAGAGGCATCCAGAAAAGTATCAGGGTAGTTCTGTTTCAAACTTGCAT
GTGGAGCCATGTGGCACAAATACTCATGCCAGCTCATTACAGCATGAGAACAGCAGTTTATTACTCACTA
AAGACAGAATGAATGTAGAAAAGGCTGAATTCTGTAATAAAAGCAAACAGCCTGGCTTAGCAAGGAGCCA
ACATAACAGATGGGCTGGAAGTAAGGAAACATGTAATGATAGGCGGACTCCCAGCACAGAAAAAAAGGTA
GATCTGAATGCTGATCCCCTGTGTGAGAGAAAAGAATGGAATAAGCAGAAACTGCCATGCTCAGAGAATC
```

- Entering the query sequence in the text box by self-typing, copy and paste, or uploading a file.
- The query sequence must be in the FASTA format.

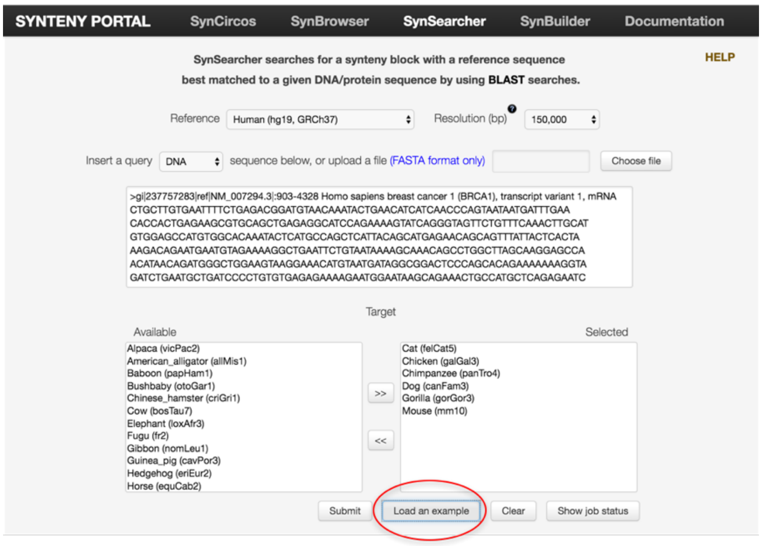
(5) Selecting a target species



Cat (felCat5)
Chicken (galGal3)
Chimpanzee (panTro4)
Dog (canFam3)
Gorilla (gorGor3)
Mouse (mm10)

- Selecting target species and their assembly versions for searching the query gene sequence.
- ‘>>’ button is used for adding target species.
- ‘<<’ button is used for deleting target species.

(5) An example of a query sequence and chosen species



SynSearcher searches for a synteny block with a reference sequence best matched to a given DNA/protein sequence by using **BLAST** searches.

Reference: Human (hg19, GRCh37)
Resolution (bp): 150,000

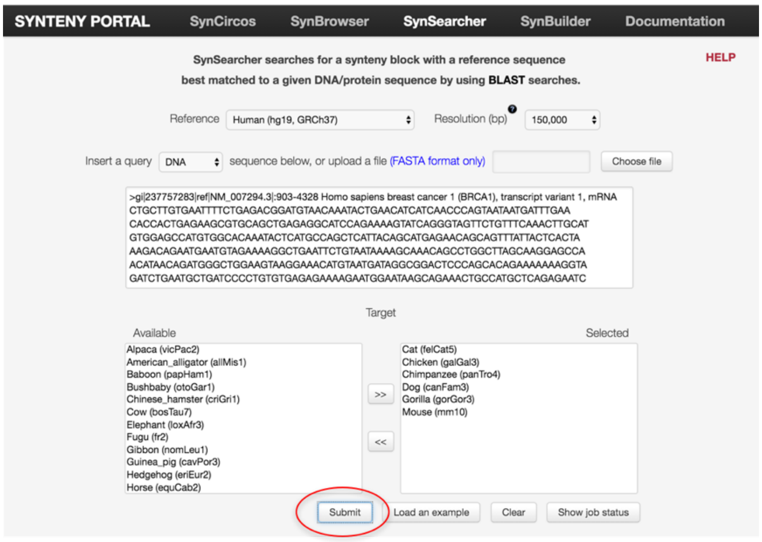
Insert a query: DNA sequence below, or upload a file (FASTA format only)

```
>gi|237757283|ref|NM_007294.3|:903-4328 Homo sapiens breast cancer 1 (BRCA1), transcript variant 1, mRNA
CTGCTTGTGAATTTTCTGAGACGGATGTAACAAATACTGAACATCATCAACCCAGTAATAATGATTTGAA
CACCACTGAGAAGCGTGCAGCTGAGAGGCATCCAGAAAAGTATCAGGGTAGTTCTGTTTCAAACTTGCAT
GTGGAGCCATGTGGCACAAATACTCATGCCAGCTCATTACAGCATGAGAACAGCAGTTTATTACTCACTA
AAGACAGAATGAATGTAGAAAAGGCTGAATTCTGTAATAAAAGCAAACAGCCTGGCTTAGCAAGGAGCCA
ACATAACAGATGGGCTGGAAGTAAGGAAACATGTAATGATAGGCGGACTCCCAGCACAGAAAAAAAGGTA
GATCTGAATGCTGATCCCCTGTGTGAGAGAAAAGAATGGAATAAGCAGAAACTGCCATGCTCAGAGAATC
```

Selected:
Cat (felCat5)
Chicken (galGal3)
Chimpanzee (panTro4)
Dog (canFam3)
Gorilla (gorGor3)
Mouse (mm10)

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

(6) Job submission



SynSearcher searches for a synteny block with a reference sequence best matched to a given DNA/protein sequence by using **BLAST** searches.

Reference: Human (hg19, GRCh37)
Resolution (bp): 150,000

Insert a query: DNA sequence below, or upload a file (FASTA format only)

```
>gi|237757283|ref|NM_007294.3|:903-4328 Homo sapiens breast cancer 1 (BRCA1), transcript variant 1, mRNA
CTGCTTGTGAATTTTCTGAGACGGATGTAACAAATACTGAACATCATCAACCCAGTAATAATGATTTGAA
CACCACTGAGAAGCGTGCAGCTGAGAGGCATCCAGAAAAGTATCAGGGTAGTTCTGTTTCAAACTTGCAT
GTGGAGCCATGTGGCACAAATACTCATGCCAGCTCATTACAGCATGAGAACAGCAGTTTATTACTCACTA
AAGACAGAATGAATGTAGAAAAGGCTGAATTCTGTAATAAAAGCAAACAGCCTGGCTTAGCAAGGAGCCA
ACATAACAGATGGGCTGGAAGTAAGGAAACATGTAATGATAGGCGGACTCCCAGCACAGAAAAAAAGGTA
GATCTGAATGCTGATCCCCTGTGTGAGAGAAAAGAATGGAATAAGCAGAAACTGCCATGCTCAGAGAATC
```

Selected:
Cat (felCat5)
Chicken (galGal3)
Chimpanzee (panTro4)
Dog (canFam3)
Gorilla (gorGor3)
Mouse (mm10)

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

(7) Result page

Job ID	Description	Status	Result	Circos
1	Input sequence: Click, Sequence type: DNA Resolution: 150000 bp Reference: Human (hg19) Target species: Cat (felCat5), Chicken (galGal3), Chimpanzee (panTro4), Dog (canFam 3), Gorilla (gorGor3), Mouse (mm10)	Complete	View Download	View Download ⇕

** This page will be automatically refreshed in every second. **

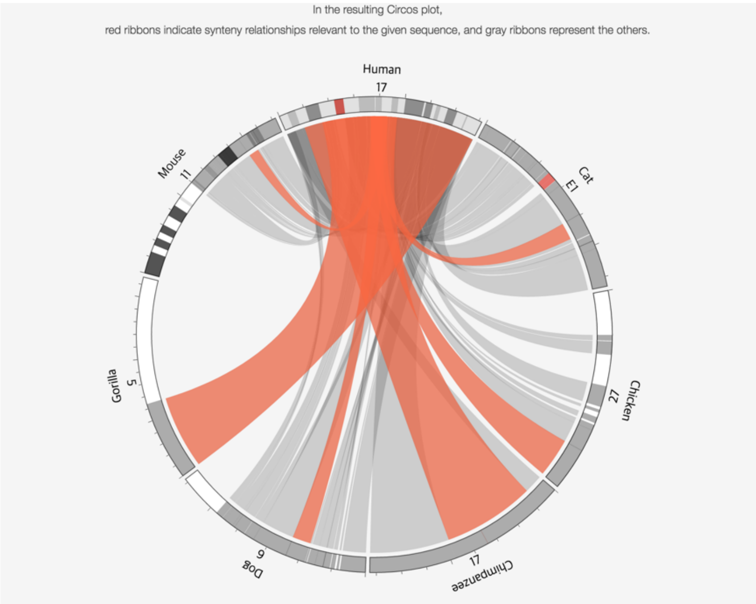
Results of SynSearcher (Job ID: 1)

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

>>Top BLAST search result
RefChr RefStart RefEnd QueryID QueryStart QueryEnd Rawscore Bitscore Evalue
chr17 41246877 41243452 gi|237757283|ref|NM_007294.3|:903-4328 1 3426 3426 6327 0.0

>>Synteny blocks
hg19.chr17:36351207-43543837 +
felCat5.chrE1:39623409-45232369 +

hg19.chr17:36351923-41362932 +
galGal3.chr27:3833709-4830036 +
```


In the resulting Circos plot,

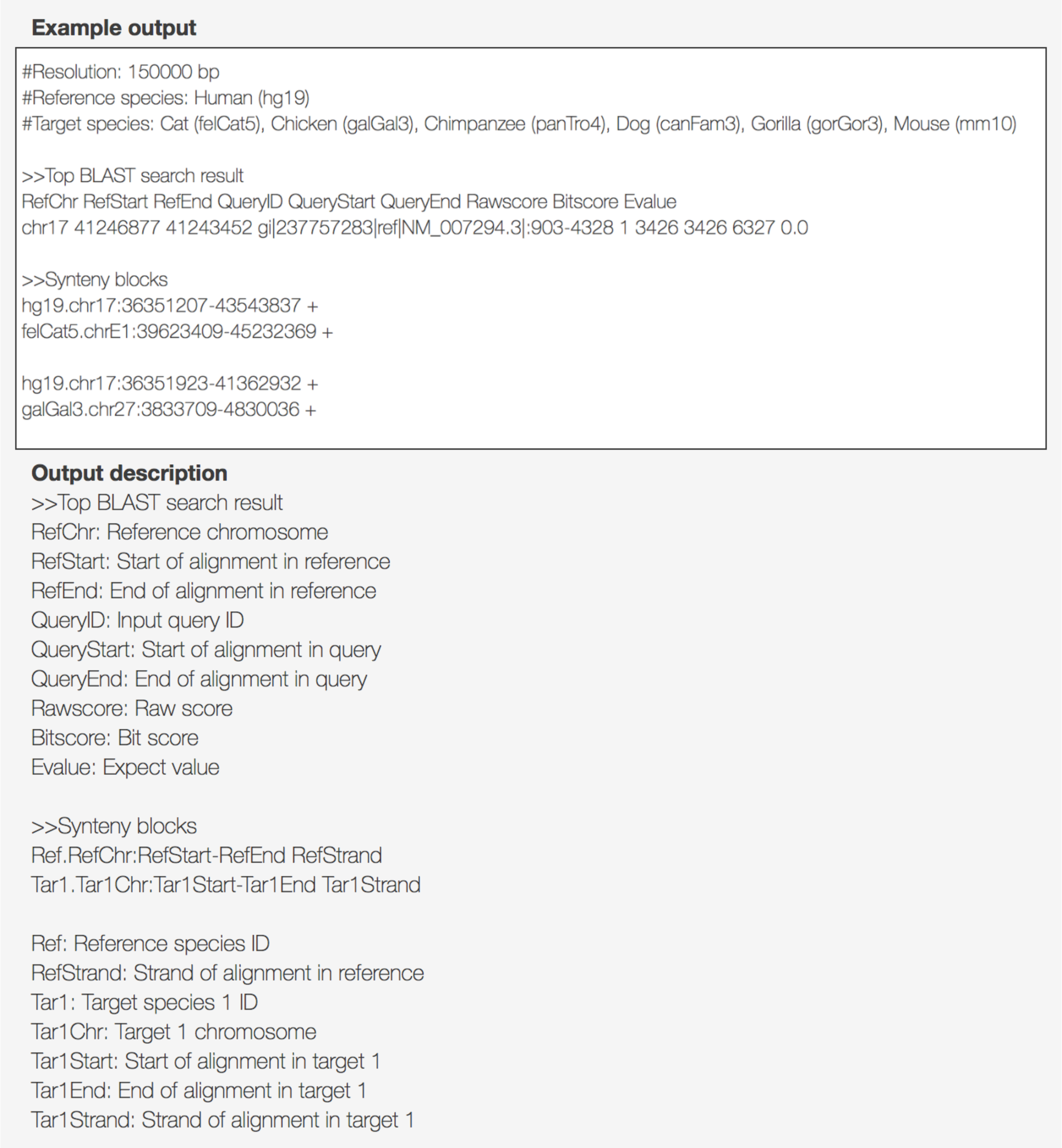
red ribbons indicate synteny relationships relevant to the given sequence, and gray ribbons represent the others.

- 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 BLAST search result.
  - Waiting → Waiting for finishing the job
  - View → Viewing the result of the searched synteny blocks
  - Download → Downloading the result of the searched synteny blocks as a text file.
  - No result → Syntenic regions not found.
- The Circos column provides the Circos plot drawn by using found synteny blocks.
  - Waiting → Waiting for drawing the Circos plot.
  - View → Viewing the Circos plot.
  - Download select box → Selecting and downloading the Circos plot.
  - No results → There is no result for drawing the Circos plot.

- The gray ribbons in the resulting Circos plot represent all syntenic regions between the reference and the selected target species.
- The orange ribbons in the resulting Circos plot represent the matching syntenic regions between the reference and selected target species.

(8) Output file format

- Lines starting with '#' contain parameters of the built synteny blocks.
  - Resolution → The minimum size of a reference block in bp
  - Reference species → Selected reference species
  - Target species → Selected target species
- Top BLAST search result is the best scored result of the BLAST search with a query sequence against the BLAST database of the reference genome.
- Synteny blocks show the pairwise syntenic regions of the reference and targets which contain the BLAST searched region.



Example output

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

>>Top BLAST search result
RefChr RefStart RefEnd QueryID QueryStart QueryEnd Rawscore Bitscore Evalue
chr17 41246877 41243452 gi|237757283|ref|NM_007294.3|:903-4328 1 3426 3426 6327 0.0

>>Synteny blocks
hg19.chr17:36351207-43543837 +
felCat5.chrE1:39623409-45232369 +

hg19.chr17:36351923-41362932 +
galGal3.chr27:3833709-4830036 +
```

Output description

>>Top BLAST search result
RefChr: Reference chromosome
RefStart: Start of alignment in reference
RefEnd: End of alignment in reference
QueryID: Input query ID
QueryStart: Start of alignment in query
QueryEnd: End of alignment in query
Rawscore: Raw score
Bitscore: Bit score
Evalue: Expect value

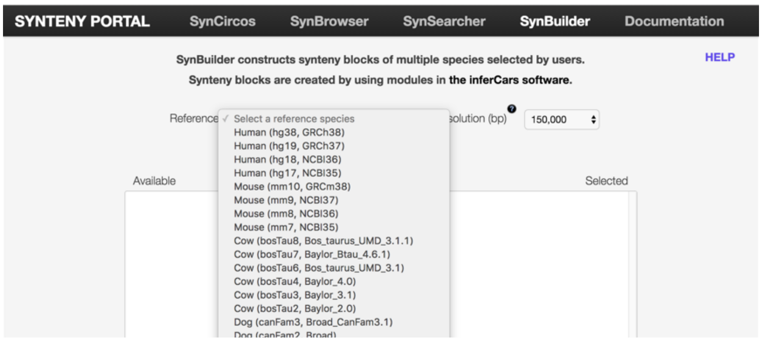
>>Synteny blocks
Ref.RefChr:RefStart-RefEnd RefStrand
Tar1.Tar1Chr:Tar1Start-Tar1End Tar1Strand

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

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

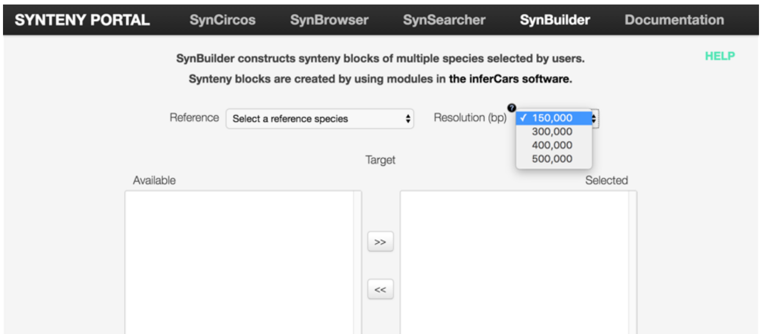


SynBuilder constructs synteny blocks of multiple species selected by users.
Synteny blocks are created by using modules in the inferCars software.

Resolution (bp): 150,000

- Selecting a reference species and its assembly version.

(2) Selecting a resolution

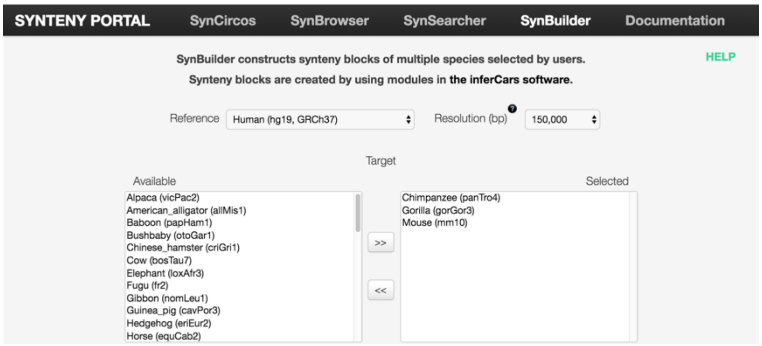


SynBuilder constructs synteny blocks of multiple species selected by users.
Synteny blocks are created by using modules in the inferCars software.

Reference: Select a reference species
Resolution (bp): 150,000

- Selecting a resolution for building synteny blocks.

(3) Selecting a target species



SynBuilder constructs synteny blocks of multiple species selected by users.
Synteny blocks are created by using modules in the inferCars software.

Reference: Human (hg19, GRCh37)
Resolution (bp): 150,000

Selected:
Chimpanzee (panTro4)
Gorilla (gorGor3)
Mouse (mm10)

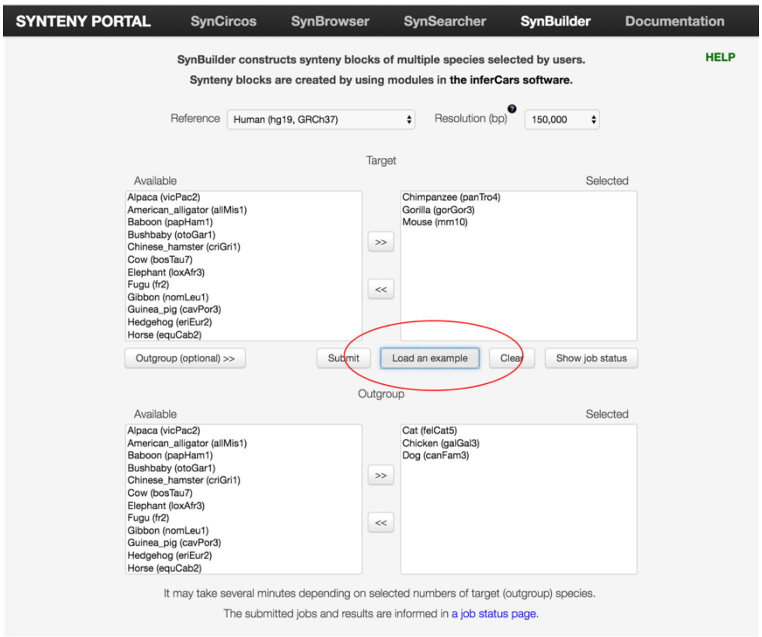
- Users can select target species and their assembly versions by using the ‘>>’ button.
- Also, the selected target species can be unselected by using the ‘<<’ button.

(4) Selecting outgroup species

Cat (felCat5)
Chicken (galGal3)
Dog (canFam3)

- 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



SynBuilder constructs synteny blocks of multiple species selected by users.
Synteny blocks are created by using modules in the inferCars software.

Reference Human (hg19, GRCh37)
Resolution (bp) 150,000

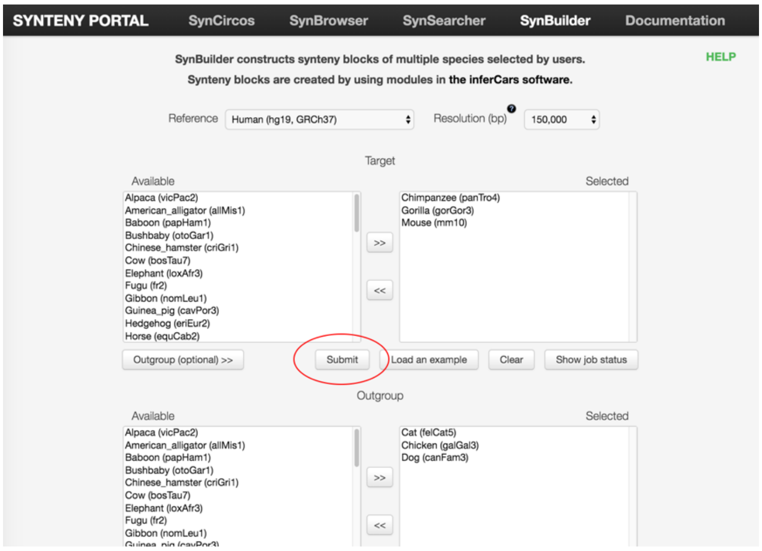
Target selected:
Chimpanzee (panTro4)
Gorilla (gorGor3)
Mouse (mm10)

Outgroup selected:
Cat (felCat5)
Chicken (galGal3)
Dog (canFam3)

It may take several minutes depending on selected numbers of target (outgroup) species.
The submitted jobs and results are informed in a job status page.

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

(6) Job submission



SynBuilder constructs synteny blocks of multiple species selected by users.
Synteny blocks are created by using modules in the inferCars software.

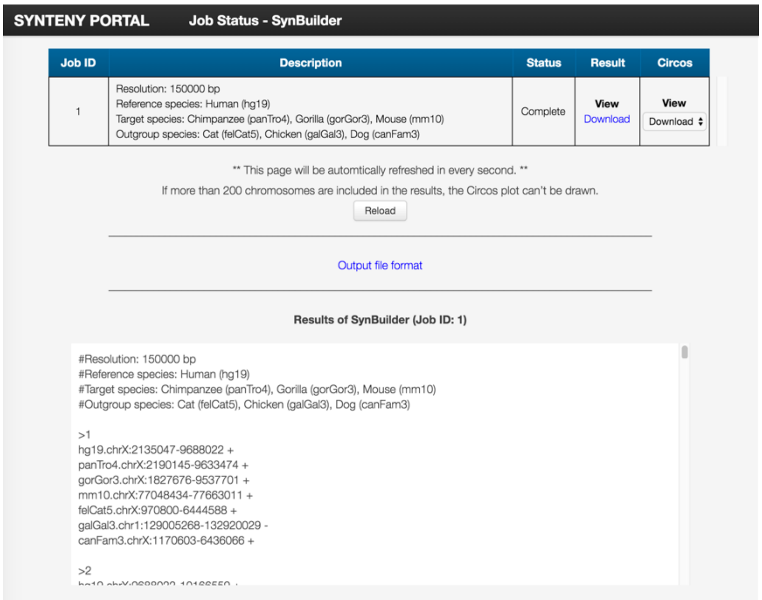
Reference Human (hg19, GRCh37)
Resolution (bp) 150,000

Target selected:
Chimpanzee (panTro4)
Gorilla (gorGor3)
Mouse (mm10)

Outgroup selected:
Cat (felCat5)
Chicken (galGal3)
Dog (canFam3)

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

(6) Result page



Job ID	Description	Status	Result	Circos
1	Resolution: 150000 bp Reference species: Human (hg19) Target species: Chimpanzee (panTro4), Gorilla (gorGor3), Mouse (mm10) Outgroup species: Cat (felCat5), Chicken (galGal3), Dog (canFam3)	Complete	View Download	View Download

** This page will be automtically refreshed in every second. **

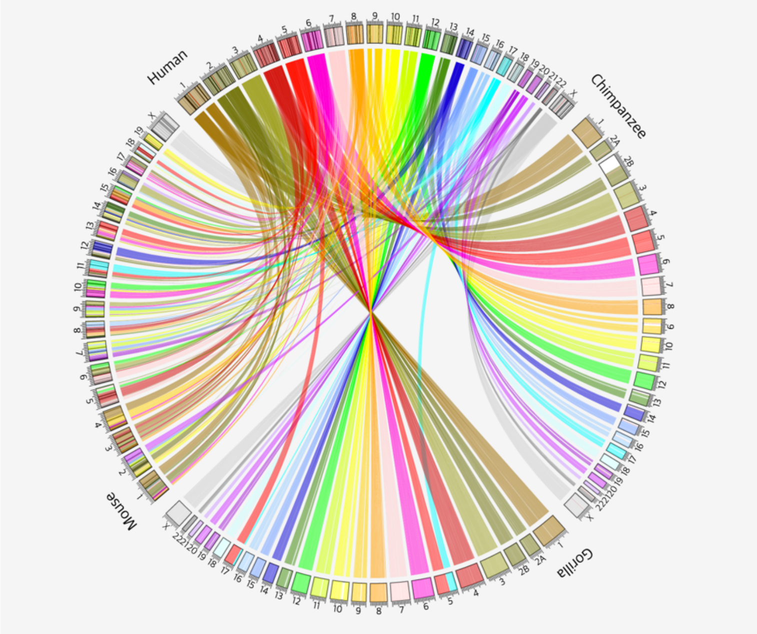
If more than 200 chromosomes are included in the results, the Circos plot can't be drawn.

Results of SynBuilder (Job ID: 1)

```
#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 +

>2
```



- 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