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

SYNTENY PORTAL	SynCircos	SynBrowser	SynSearcher	SynBuilder	Documentation
	SynSearcher best matched to	searches for a synteny o a given DNA/protein	v block with a reference sequence by using BLA:	sequence ST searches.	HELP
Insert a query	Reference ✓ Select Human DNA ¢ Human Human Mouse Query DNA/t	a reference species (hg38, GRCh38) (hg19, GRCh37) (hg18, NCBI36) (hg17, NCBI35) (mm10, GRCm38) (mm9, NCBI37)	solution (bp) at only)	150,000 €	Choose file
	Mouse Mouse Cow (b Cow (b Cow (b Cow (b	(mm8, NCBI36) (mm7, NCBI35) oosTau8, Bos_taurus_UMD_ oosTau7, Baylor_Btau_4.6.1 oosTau6, Bos_taurus_UMD_ oosTau4, Baylor_4.0)	.3.1.1) 1) 3.1)		
Availa	Cow (b Cow (b Dog (c Dog (c Dog (c	osTau3, Baylor_3.1) osTau2, Baylor_2.0) anFam3, Broad_CanFam3. anFam2, Broad) anFam1, Broad)	1)	Sele	acted

• Selecting a reference and its assembly version.

(2) Selecting a resolution

SYNTENY PORTAL	SynCir	rcos SynBrowser	SynSearcher	SynBuilder	Documentation
	SynSea best mate	archer searches for a synten ched to a given DNA/protein	y block with a referenc sequence by using BL	e sequence AST searches.	HELP
	Reference	Select a reference species	Resolution (bp)	✓ 150,000 300,000 400,000	
Insert a query	DNA \$	sequence below, or upload a fil tein sequence or upload a file in th	e (FASTA format only)	500,000	Choose file

• Selecting a resolution of synteny blocks.

(3) Selecting a query sequence type



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

(4) Inserting a query sequence



- 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

	Target		
Available			Selected
Alpaca (vicPac2) American_alligator (allMis1) Baboon (papHam1) Bushbaby (otoGar1) Chinese_hamster (criGri1) Cow (bosTau7) Elephant (loxAfr3) Fugu (fr2) Glibbon (nomLeu1) Guinea_pig (cavPor3) Hedgehog (eriEur2) Horse (equCab2)	» «	Cat (felCat5) Chicken (galGal3) Chimpanzee (panTro4) Dog (canFam3) Gorilla (gorCor3) 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

SYNTENY PORTAL	SynC	ircos SynBrows	er SynSearc	her SynBuilder	Documentation
	SynSe best ma	earcher searches for a sy tched to a given DNA/pr Human (hg19, GRCh37)	nteny block with a re otein sequence by us Presolu	eference sequence sing BLAST searches. tion (bp) 150,000	+ELP
Insert a query	DNA \$	sequence below, or uploa	d a file (FASTA format o	only)	Choose file
>gl/2 CTGC CACC GTGC AAGJ ACAT GATC	37757283 ref NM CTTGTGAAATTTT CACTGAGAAGC GAGCCATGTGG ACAGAATGAATG AACAGATGGGC TGAATGCTGAT	L007294.3):903-4328 Homo s CTGAGACGGATGTAACAATA GTGCAGGCTAGAGAGGCATCC: CACAAATACTCATGCCAGCT ITAGAAAAGGCTGAATTCTGT; CTGGAAGTAAGGAAACATGTA CCCCTGTGTGAGAGAAAAG/	piens breast cancer 1 (E CTGAACATCATCAACCC GAAAAGTATCAGGGTA ATTACAGCATGAGAGCA ATTACAGCCAGAGACACCC ATGATAAGCCGGACTCCC ATGGAATAAGCAGAAAC Target	IRCA1), transcript variant 1, AGTAATAATGATTTGAA 3TTCTGTTTCAAACTTGAA GGCAGTTATTACTCACTA TGGCTTAGCAAGGAGCCA AGGCACAGAAAAAAAGGTA 2TGCCATGCTCAGAAGAATC	mRINA
Avai	lable			s	Selected
Alpacı Ameri Babob Chine Cow (Elephy Fugu Gibbo Guine Hedge Horse	a (vicPac2) can_aligator (all? on (papHam1) se_hamster (criG bosTau7) ant (loxAfr3) fr2) n (nomLeu1) a,pig (cavPor3) ohog (eriEur2) (equCab2)	Mis1) kd1)	Cat (felCat5) Chicken (galG Chimparzee (r Dog (canFam3 Gorila (gorGor Mouse (mm10	al3) anTro4)) 3)	
		Subm	t Load an example	B Clear Show ju	ob status

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

(6) Job submission

	SynSe	earcher searches for a sy	nteny block v	vith a reference	sequence	HEL
	best ma	tched to a given DNA/pr	otein sequend	e by using BLA	AST searches.	
	Reference	Human (hg19, GRCh37)	\$	Resolution (bp)	●150,000 \$	
Insert a query	DNA \$	sequence below, or uploa	d a file (FASTA	format only)		Choose file
CTGC CACC GTGG AAGA	CTTGTGAATTTR CACTGAGAAGC AGCCATGTGG CAGAATGAATG	CTGAGACGGATGTAACAAATA GTGCAGCTGAGAGGCATCC, CACAAATACTCATGCCAGCT TAGAAAAGGCTGAATTCTGT	CTGAACATCAT AGAAAAGTATCA CATTACAGCATG	CAACCCAGTAATA GGGTAGTTCTGT	ATGATTTGAA TTCAAACTTGCAT TATTACTCACTA	
ACAT/ GATC	AACAGATGGGC TGAATGCTGAT	CCCTGTGTGAGAGAAACATGTA	ATGATAGGCGG ATGATAGGCGG	ACTCCCAGCACA ACTCCCAGCACA AGAAACTGCCAT	IGCAAGGAGCCA IGAAAAAAAGGTA GCTCAGAGAATC	
ACAT/ GATC	AACAGATGGGC	TGGAAGTAAGGAAACATGTA CCCCTGTGTGAGAGAAAAG/	ATGATAGGCGG ATGGAATAAGC Target	CAGCCTGGCTA ACTCCCAGCACA AGAAACTGCCAT	IGCAAGGAGCCA IGAAAAAAAGGTA GCTCAGAGAATC	
ACAT/ GATC Avail:	AACAGATGGGG TGAATGCTGAT able	TGGAAGTAAGGAAACATGTA CCCCTGTGTGAGAGAAAAGA	ATGATAGGCGG ATGGAATAAGC Target		IGCAAGGAGCCA IGAAAAAAAGGTA GCTCAGAGAATC Sele	acted

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

(7) 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 BLAST search result.
 - Waiting \rightarrow Waiting for finishing the job
 - \circ View \rightarrow Viewing the result of the searched syntemy blocks
 - \circ Download \rightarrow Downloading the result of the searched syntemy blocks as a text file.
 - No result \rightarrow Syntenic regions not found.
- The Circos column provides the Circos plot drawn by using found synteny blocks.
 - Waiting \rightarrow Waiting for drawing the Circos plot.
 - View \rightarrow Viewing the Circos plot.
 - \circ Download select box \rightarrow Selecting and downloading the Circos plot.
 - No results \rightarrow 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 \rightarrow The minimum size of a reference block in bp
 - \circ Reference species \rightarrow Selected reference species
 - Target species \rightarrow 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