

SSRome Manual

SSRome Main-Bar Overview



An Integrated Database and Pipelines for Exploring
Microsatellites in All Organisms

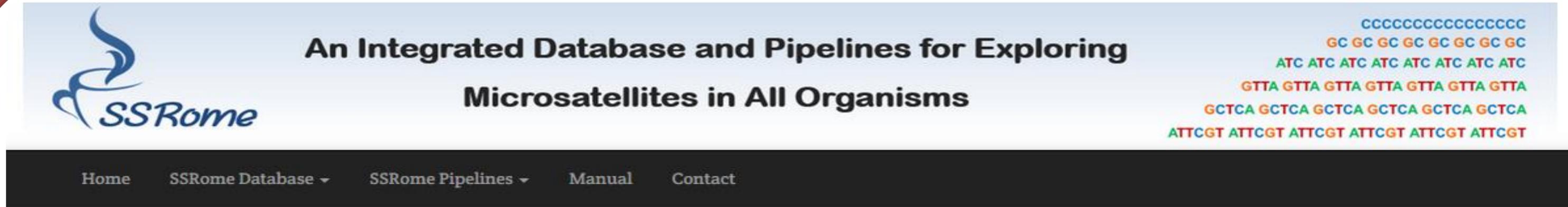
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GC GC GC GC GC GC GC GC
ATC ATC ATC ATC ATC ATC ATC ATC
GTTA GTTA GTTA GTTA GTTA GTTA GTTA
GCTCA GCTCA GCTCA GCTCA GCTCA GCTCA
ATTCGT ATTCGT ATTCGT ATTCGT ATTCGT ATTCGT

[Home](#) [SSRome Database](#) [SSRome Pipelines](#) [Manual](#) [Contact](#)

- **Home:** Navigation Bar; About SSRome; SSRome Genomic Pipeline; SSRome Transcriptomic Pipeline; SSRome Comparative Analysis Pipeline; Analyzed Genomes in SSRome Database; Analyzed ESTs in SSRome Database; Analyzed Organelle Genome's in SSRome Database; Valuable Resources, Useful Links; How to cite.
- **SSRome Database:** Statistics; Download; Database Search; SSRome Comparisons.
- **SSRome Pipelines:** SSRome Upload Files; SSRome Genomic Pipeline; SSRome Transcriptomic Pipeline; SSRome Comparative Analysis Pipeline.
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Home Page

- About SSRome



**An Integrated Database and Pipelines for Exploring
Microsatellites in All Organisms**

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About SSRome

Microsatellites, also referred to as simple sequence repeats (SSRs) or short tandem repeats (STRs) - are co-dominant molecular markers universally scattered within all organisms genomes. Microsatellites markers are highly popular due to their abundance, hyper-variability, multi-allelic, highly reproducibility and detection simplicity. Over past decades, they are extensively used in a variety of fundamental and applied biological sciences for prokaryotes, plants and animals studies. Microsatellites are also have extensively been exploited as genetic markers for diverse applications including genome mapping, genetic material characterization, population genetics and genome evolution studies.

SSRome is a comprehensive, integrated database and pipelines for microsatellites mining, classification, comparative analysis and markers development across all organisms.

Nowadays, with the development of genome sequencing technologies, hundreds of genome sequences have been decoded and released. This published genomes data and the availability of bioinformatics tools provides an important opportunity for scientists to identify simple sequence repeats that could be used to develop useful SSR markers. These markers can be used subsequently in different studies such as; variety identification, genetic diversity evaluation, construction of genetic linkage maps, association mapping, and marker-assisted selection.

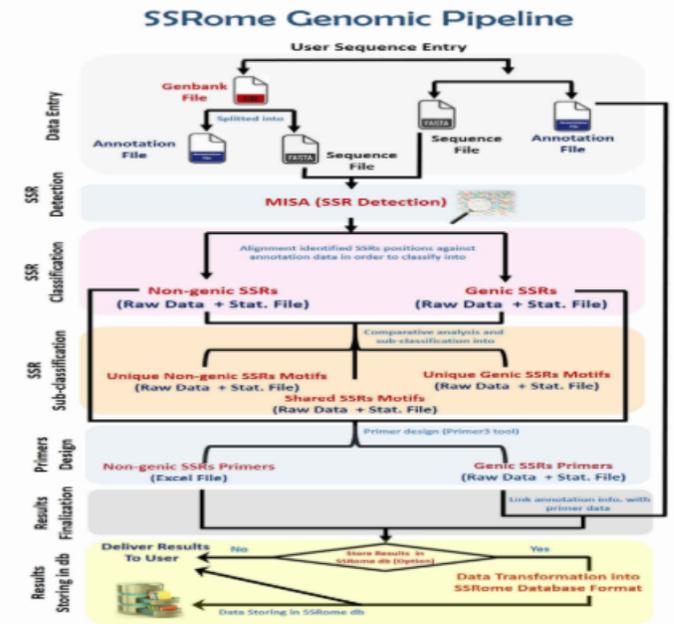
Home Page

- SSRome Genomic Pipeline



SSRome Genomic Pipeline (SGP)

SSRome Genomic Pipeline (SGP) is a user-friendly tool can help scientists to identify and localize microsatellites at the Genome-wide level. The SGP tool can classify generated results into 'SSR repeats unique to genic regions', 'SSR repeats unique to intergenic regions' and 'SSR repeats overlapped between genic and intergenic regions'. In addition, SSRome Genomic Pipeline includes adjustable SSR repeat unit and primer design parameters and user selectivity to design SSR primers in genic regions only, or in intergenic regions only or in both across the whole genomic regions.

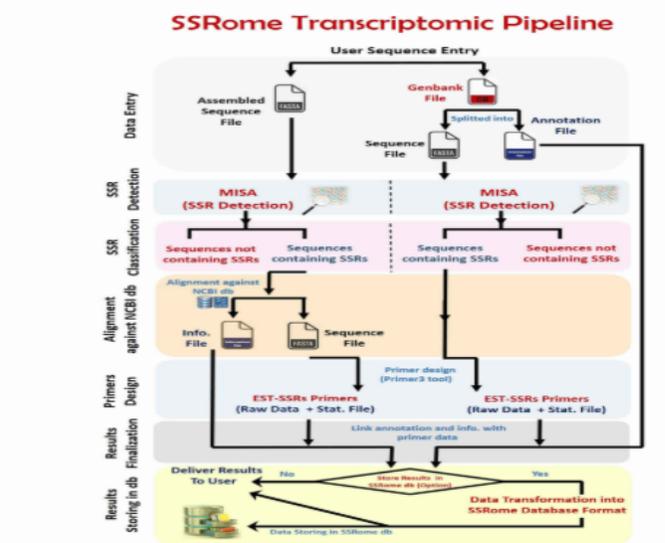


- SSRome Transcriptomic Pipeline



SSRome Transcriptomic Pipeline (STP)

SSRome Transcriptomic Pipeline (STP) is a user-friendly tool can identify and localize microsatellites at whole Transcriptomic-wide level (RNA-Seq data) or short cDNA sequences. The STP pipeline can perform SSRs mining at both assembled RNA Sequences with or without annotation information. In the case of providing STP with RNA Sequences without annotation information, STP will BLAST the RNA-sequences against local NCBI database to elucidate their best matching. In addition, SSRome Transcriptomic Pipeline includes adjustable SSR repeat unit and primer design parameters.

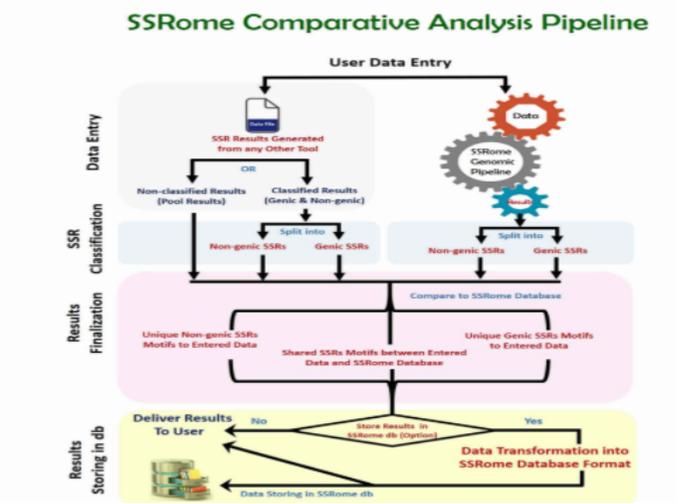


- SSRome Comparative Analysis Pipeline



SSRome Comparative Analysis Pipeline (SCAP)

SSRome Comparative Analysis Pipeline (SCAP) is a user-friendly pipeline can compare identified SSR motifs of any organism as generated using SSRome pipelines or any other SSR detection tools against the SSRome database. The SCAP pipeline will deliver comparing results in form of unique SSR motifs of submitted sequence (if found) and full comparative profile of this sequence in relevant of other organisms available in SSRome database.



Home Page

Analyzed Genomes in SSRome Database

Analyzed Genomes in SSRome Database

- Metazoa
- Plant
- Archaea
- Bacteria
- Virus
- Fungi
- Protozoa

 Amphimedon queenslandica Search page	 Acanthaster planci Search page	 Acropora digitifera Search page
 Acyrtosiphon pisum Search page	 Amphimedon queenslandica Search page	 Anas platyrhynchos Search page
 Anolis carolinensis Search page	 Anopheles gambiae Search page	 Apis mellifera Search page

Select one of this genera

Organism Scientific Name

Click to go to the Organism Specific Search Page

*** the Organism Specific Search Page Layout**

* Please enter the SSRome primer Id in Primer Id field "Optional".
* Please select SSR repeat type from Repeat Type drop down menu "Optional".
* Select one or all options, then press "Search" to get your results from SSRome Apis mellifera database.

Apis mellifera Genic SSRs

Repeat Sequence Gene symbol or Locus tag Organism Name Repeat Type

Apis mellifera Non-Genic SSRs

Primer Id Repeat Sequence Organism Name Repeat Type

Home Page

- Analyzed ESTs in SSRome Database

Analyzed ESTs in SSRome Database

ALL NCBI PLANT ESTS	Plant ESTs Plants ESTs available in NCBI ESTdb till March 2018 Search page	ALL NCBI METAZOEA ESTS	Metazoa ESTs Animals ESTs available in NCBI ESTdb till March 2018 Search page	ALL NCBI OTHERS ESTS	Others ESTs Others ESTs available in NCBI ESTdb till March 2018 Search page
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- Analyzed Organelles Genomes in SSRome Database

Analyzed Organelles in SSRome Database

MITOCHONDRIA 120 PLANT GENOME	Plant Mitochondria Plants mitochondria available in NCBI organelle genome resources till March 2018 Search page	MITOCHONDRIA 2669 METAZOEA GENOME	Metazoa Mitochondria Animals mitochondria available in NCBI organelle genome resources till March 2018 Search page	CHLOROPLAST 1034 PLANT GENOME	Plant Chloroplast Plants chloroplast available in NCBI organelle genome resources till March 2018 Search page
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Click to go to the Search Page for each category

Click to go to the Search Page for each category



An Integrated Database and Pipelines for Exploring Microsatellites in All Organisms

CCCCCCCCCCCCCCCC
GC GC GC GC GC GC GC GC
ATC ATC ATC ATC ATC ATC ATC
GTTA GTTA GTTA GTTA GTTA GTTA
GCTCA GCTCA GCTCA GCTCA GCTCA
ATTCGT ATTCGT ATTCGT ATTCGT ATTCGT

Statistics Page

Home SSRome Database ▾ SSRome Pipelines ▾ Manual Contact

- Statistics
- Download
- Database Search
- SSRome Comparisons



An Integrated Database and Pipelines for Exploring Microsatellites in All Organisms

CCCCCCCCCCCCCCCC
GC GC GC GC GC GC GC GC
ATC ATC ATC ATC ATC ATC ATC
GTTA GTTA GTTA GTTA GTTA GTTA
GCTCA GCTCA GCTCA GCTCA GCTCA
ATTCGT ATTCGT ATTCGT ATTCGT ATTCGT

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Genomic

Plant Statistics

Name	No. of designed primers	Name	No. of designed primers	Name	No. of designed primers
Arabidopsis thaliana	33180	Beta vulgaris	120097	Brachypodium	72818
Brassica napus	100394	Brassica oleracea	169334	Brassica rapa	115949
Camelina sativa	237970	Cicer arietinum	97342	Citrus sinensis	123012
Cucumis sativus	87547	Elaeis guineensis	311047	Fragaria vesca	87726
Glycine max	255245	Gossypium arboreum	193797	Malus domestica	124084
Oryza brachyantha	98923	Oryza sativa Japonica	91306	Solanum lycopersicum	130415
Solanum tuberosum	145977	Vitis vinifera	120734		

Move from one to another Genra by "Click" to view statistics table

Statistics Categories

Metazoa Statistics

Others Statistics

Transcriptomic

Plant Statistics

Metazoa Statistics

Others Statistics

Mitochondria

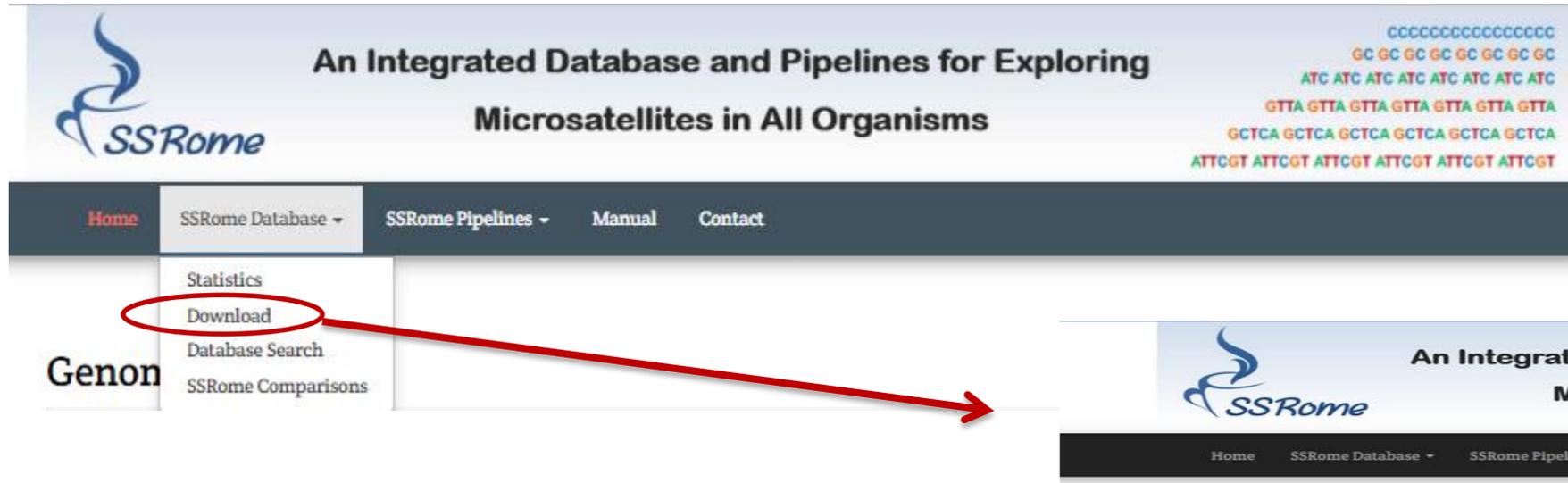
Plant Statistics

Metazoa Statistics

Chloroplast

Plant Statistics

Download Page



- Plant
- Metazoa**
- Others

Click to view all analyzed Plant results available in SSRome

Click to view all analyzed Metazoa results available in SSRome

Click to view all Others organisms results available in SSRome

Organism	Genic SSR	Genic SSR Stat	Uniqe Genic SSR	Genic SSR Primers	Non-genic SSR	Non-genic SSR Stat	Uniqe Non-genic SSR	Non-genic SSR Primers	SSR Overlap
Arabidopsis thaliana	Genic SSR	Genic SSR Stat	Uniqe Genic SSR	Genic SSR Primers	Non-genic SSR	Non-genic SSR Stat	Uniqe Non-genic SSR	Non-genic SSR Primers	SSR Overlap
Beta vulgaris	Genic SSR	Genic SSR Stat	Uniqe Genic SSR	Genic SSR Primers	Non-genic SSR	Non-genic SSR Stat	Uniqe Non-genic SSR	Non-genic SSR Primers	SSR Overlap
Brachypodium distachyon	Genic SSR	Genic SSR Stat	Uniqe Genic SSR	Genic SSR Primers	Non-genic SSR	Non-genic SSR Stat	Uniqe Non-genic SSR	Non-genic SSR Primers	SSR Overlap
Brassica napus	Genic SSR	Genic SSR Stat	Uniqe Genic SSR	Genic SSR Primers	Non-genic SSR	Non-genic SSR Stat	Uniqe Non-genic SSR	Non-genic SSR Primers	SSR Overlap
Brassica oleracea	Genic SSR	Genic SSR Stat	Uniqe Genic SSR	Genic SSR Primers	Non-genic SSR	Non-genic SSR Stat	Uniqe Non-genic SSR	Non-genic SSR Primers	SSR Overlap
Brassica rapa	Genic SSR	Genic SSR Stat	Uniqe Genic SSR	Genic SSR Primers	Non-genic SSR	Non-genic SSR Stat	Uniqe Non-genic SSR	Non-genic SSR Primers	SSR Overlap
Musa acuminata	Genic SSR	Genic SSR Stat	Uniqe Genic SSR	Genic SSR Primers	Non-genic SSR	Non-genic SSR Stat	Uniqe Non-genic SSR	Non-genic SSR Primers	SSR Overlap
Solanum lycopersicum	Genic SSR	Genic SSR Stat	Uniqe Genic SSR	Genic SSR Primers	Non-genic SSR	Non-genic SSR Stat	Uniqe Non-genic SSR	Non-genic SSR Primers	SSR Overlap
Solanum tuberosum	Genic SSR	Genic SSR Stat	Uniqe Genic SSR	Genic SSR Primers	Non-genic SSR	Non-genic SSR Stat	Uniqe Non-genic SSR	Non-genic SSR Primers	SSR Overlap
Vitis vinifera	Genic SSR	Genic SSR Stat	Uniqe Genic SSR	Genic SSR Primers	Non-genic SSR	Non-genic SSR Stat	Uniqe Non-genic SSR	Non-genic SSR Primers	SSR Overlap

Genomic download part

Organelles download part

Transcriptomic download part

Organelles Downloads

All Plant Chloroplasts	Genic SSR	Genic SSR Stat	Uniqe Genic SSR	Genic SSR Primers	Intergenic SSR	Intergenic SSR Stat	Uniqe Intergenic SSR	Intergenic SSR Primers	SSR Overlap
All Plant Mitochondria genes	Genic SSR	Genic SSR Stat	Uniqe Genic SSR	Genic SSR Primers	Intergenic SSR	Intergenic SSR Stat	Uniqe Intergenic SSR	Intergenic SSR Primers	SSR Overlap

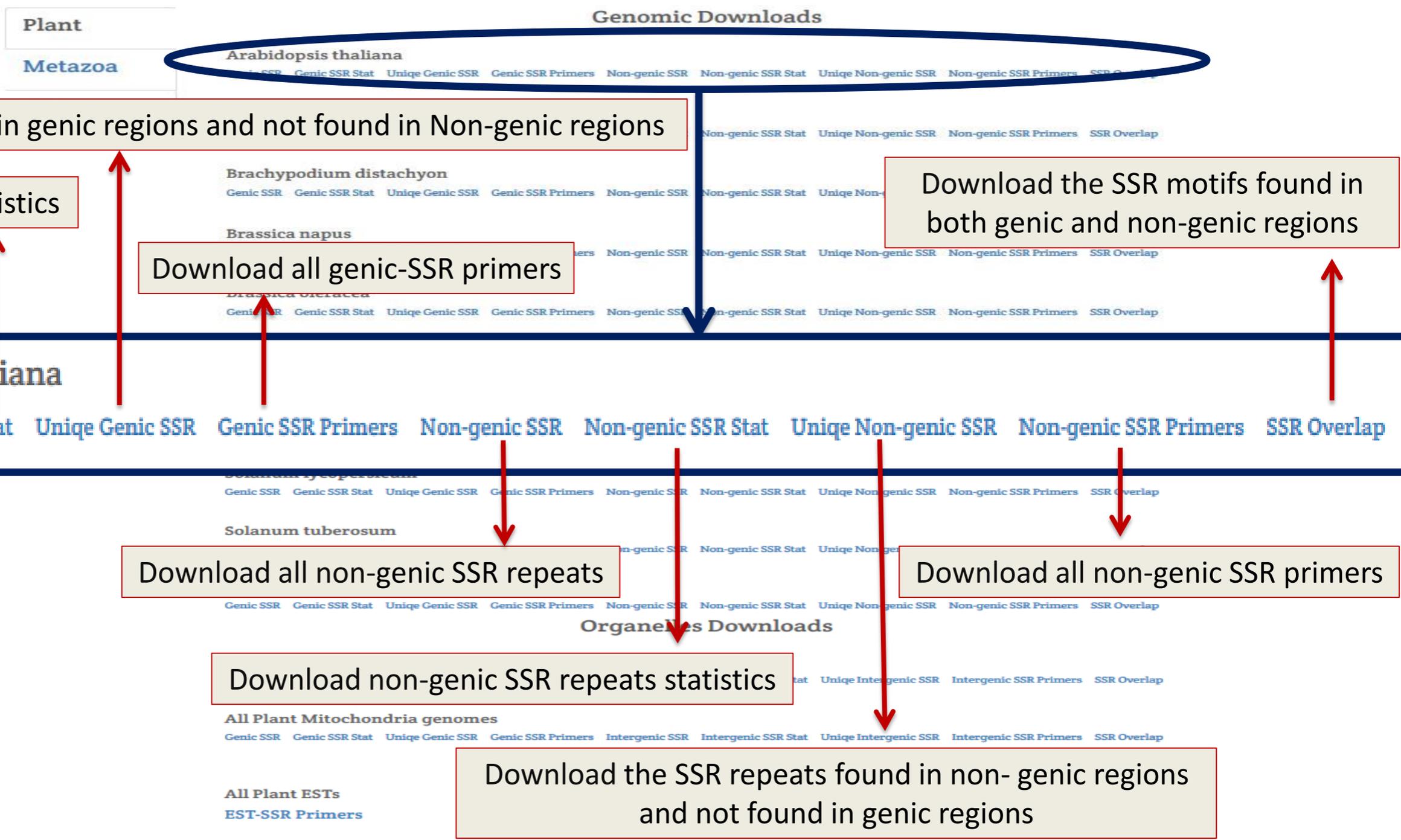
Transcriptomic Downloads

All Plant ESTs	EST-SSR Primers
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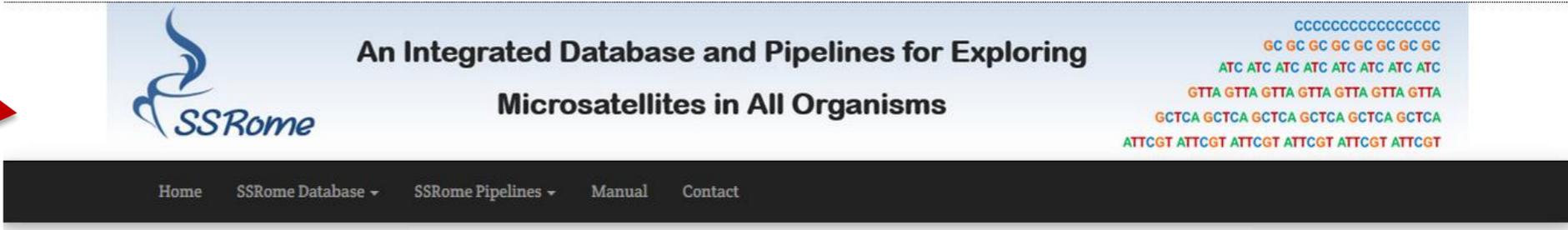
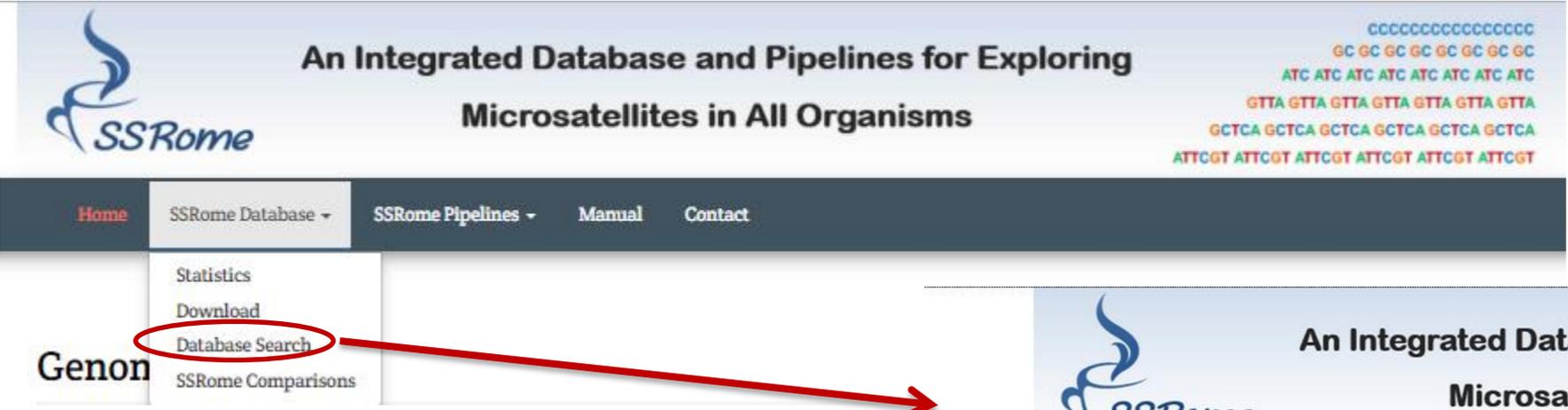
Download Page



```
CCCCCCCCCCCCCCCC  
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ATC ATC ATC ATC ATC ATC ATC  
GTTA GTTA GTTA GTTA GTTA GTTA  
GCTCA GCTCA GCTCA GCTCA GCTCA  
ATTCGT ATTCGT ATTCGT ATTCGT ATTCGT
```



Search Page



Move from one to another Search Page by "Click"

- Plant
- Metazoa
- Others
- Comparative

- Plant
- Metazoa
- Others

*** the Plant Search Page Layout**

SSRome Genomic Database

Plant Genic Region

Repeat Sequence Gene symbol or Locus tag Organism Name Repeat Type

Plant Non-genic Region

Primer Id Repeat Sequence Organism Name Repeat Type

Search Categories

Search Page



An Integrated Database and Pipelines for Exploring
Microsatellites in All Organisms

CCCCCCCCCCCCCCCC
GC GC GC GC GC GC GC
ATC ATC ATC ATC ATC ATC ATC
GTTA GTTA GTTA GTTA GTTA GTTA
GCTCA GCTCA GCTCA GCTCA GCTCA GCTCA
ATTCGT ATTCGT ATTCGT ATTCGT ATTCGT ATTCGT

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SSRome Database Search



Please enter (write) the Gene Symbol or Locus Tag of sequence you looking for. **Optional**

Please enter the SSRome primer-Id in Primer Id field **Optional**

Please enter (write) the repeat sequence you looking for. **Optional**

Please select the organism name from Organism Name drop down menu

Please select SSR repeat type from Repeat Type drop down menu

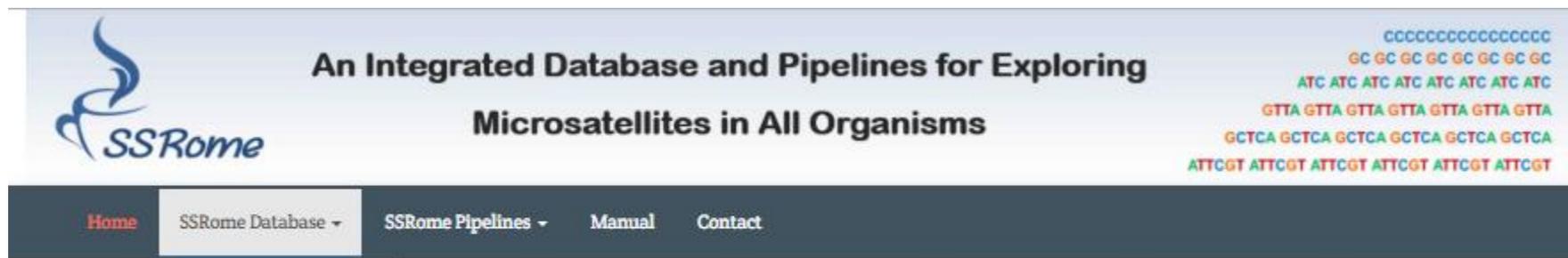
Plant Genic Region

Repeat Sequence Gene symbol or Locus tag Organism Name Repeat Type

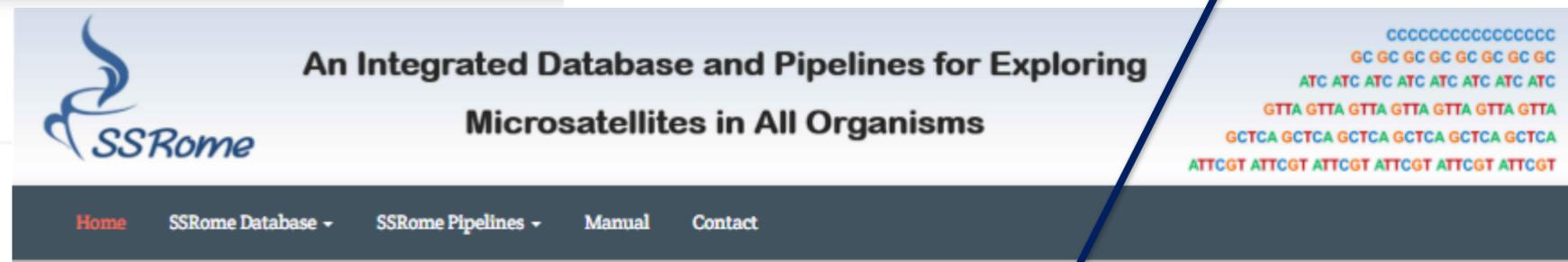
Plant Non-genic Region

Primer Id Repeat Sequence Organism Name Repeat Type

Comparisons Page



Please select SSR repeat type from Repeat Type drop down menu



Move from one to another Genra Comparisons Page by "Click"



Search for SSR motifs overlapped between genic and non-genic regions

View genic SSR motifs statistics

View non-genic SSR motifs statistics

View SSR unique motifs to genic regions

View SSR unique motifs to non-genic regions

SSRome Comparisons *Plant*

Genic and Non-Genic Overlap

Organism Name Repeat Type Search

Genic Statistics

Organism Name Repeat Type Search

Non-Genic Statistics

Organism Name Repeat Type Search

Unique to Genic

Organism Name Repeat Type Search

Unique to Non-Genic

Organism Name Repeat Type Search

Please select the organism name from Organism Name drop down menu

SSRome Upload Files page



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Microsatellites in All Organisms

CCCCCCCCCCCCCCCC
GC GC GC GC GC GC GC GC
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GTTA GTTA GTTA GTTA GTTA GTTA
GCTCA GCTCA GCTCA GCTCA GCTCA
ATTTCGT ATTTCGT ATTTCGT ATTTCGT ATTTCGT

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SSRome Upload Files

SSRome Genomic Pipeline
SSRome Transcriptomic Pipeline
SSRome Comparative Analysis Pipeline



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Microsatellites in All Organisms

CCCCCCCCCCCCCCCC
GC GC GC GC GC GC GC GC
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GTTA GTTA GTTA GTTA GTTA GTTA
GCTCA GCTCA GCTCA GCTCA GCTCA
ATTTCGT ATTTCGT ATTTCGT ATTTCGT ATTTCGT

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For Small Sized Files :

Note: If you have **more than one fasta/genbank file** (each chromosome in separate file or your genome existed in separate contig files) you should **put all files in one folder, then, compress it** before upload it.

* In case the upload process wasn't done successfully; please use the SSRome FTP account "**available for free**" [Here](#) to upload your file(s).

Choose a file to upload:

No file selected.

For "huge sized file(s)" please create the SSRome FTP account "available for free" .

For "small sized file(s)" select file from your computer and click "upload"

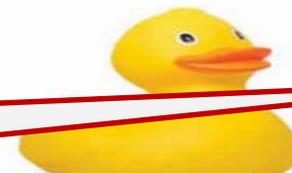
For Huge Sized Files :

Note: In case you try to upload large sized files you should use this part.

We suggest to use any of the following tools to upload your files.

Cyberduck

[Download Cyberduck Client](#)



FileZilla

[Download FileZilla](#)



CoffeeCup FTP

[Download CoffeeCup Client](#)



For "huge sized files", We suggest to use one of the following tools to upload your files.

SSRome Genomic Pipeline page (Part-1)



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CCCCCCCCCCCCCCCC
GC GC GC GC GC GC GC GC
ATC ATC ATC ATC ATC ATC ATC
GTTA GTTA GTTA GTTA GTTA GTTA
GCTCA GCTCA GCTCA GCTCA GCTCA
ATTCGT ATTCGT ATTCGT ATTCGT ATTCGT

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- SSRome Upload Files
- SSRome Genomic Pipeline
- SSRome Transcriptomic Pipeline
- SSRome Comparative Analysis Pipeline



An Integrated Database and Pipelines for Exploring
Microsatellites in All Organisms

CCCCCCCCCCCCCCCC
GC GC GC GC GC GC GC GC
ATC ATC ATC ATC ATC ATC ATC
GTTA GTTA GTTA GTTA GTTA GTTA
GCTCA GCTCA GCTCA GCTCA GCTCA
ATTCGT ATTCGT ATTCGT ATTCGT ATTCGT

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SSRome Genomic Pipeline

Note: To use SSRome Genomic Pipeline you should **upload all your data/files at first**, then you can use SSRome Genomic Pipeline to analysis your uploaded data, [See Manual](#), [SSRome Upload Files](#).

Enter your analysis name

Enter your Email address to notify you when your analysis complete.

“Check” to customize your analysis parameters

Project Information

Analysis Name

Analysis Name

Email

Email

Sequence Information

Sequence with annotation information (Genbanke format) [See Example](#).

Separate sequence in fasta format [See Example](#).

Note: If you select "Separate sequence in fasta format" option you could also select "Separate annotation file" option to provide annotation information of your sequence.

Note: If you select "Separate sequence in fasta format" option you could also select "Separate annotation file" option to provide annotation information of your sequence.

Separate annotation file.

SSRome Genomic Pipeline page (Part-2)

Enter the name of Genbank File you uploaded through "SSRome Upload Files" page. Or write "None" in case of no file uploaded.

Enter the name of Fasta File you uploaded through "SSRome Upload Files" page. Or write "None" in case of no file uploaded.

Enter the name of Annotation File you uploaded through "SSRome Upload Files" page. Or write "None" in case of no file uploaded.

Customize SSR Mining Parameters

"Check" to customize your SSR classification parameters

Customize your SSR primer design options

Input Data

Genbank File
Genbank File Name OR None
Note: Please provide the name of Genbank File you uploaded through "SSRome Upload Files" page. Or write "None" in case of no file uploaded.

OR

Fasta File
Fasta File Name OR None
Note: Please provide the name of Fasta File you uploaded through "SSRome Upload Files" page. Or write "None" in case of no file uploaded.

And

Annotation File
Annotation File Name OR None
Note: Please provide the name of Annotation File you uploaded through "SSRome Upload Files" page. Or write "None" in case of no file uploaded.

Parameters

SSR Mining Parameters
Mon ≥ 10 Di ≥ 6 Tri ≥ 5 Tetra ≥ 4 Penta ≥ 3 Hexa ≥ 3

SSR Classification Options

Classify SSR repeats to genic and intergenic.
Note: If you didn't feed SSRome Genomic Pipeline with your annotation information, please don't select this option.

Determine the SSR repeats unique to genic regions.
Note: This option to determine the SSR repeats found in genic regions and not found in intergenic regions.

Determine the SSR repeats unique to intergenic regions.
Note: This option to determine the SSR repeats found in intergenic regions and not found in genic regions.

Determine the SSR repeats overlapped between genic and intergenic regions.
Note: This option to determine the SSR repeats found in both genic and intergenic regions.

SSR primer design options

Design SSR primers in genic regions.
Note: If you didn't feed SSRome Genomic Pipeline with your annotation information, please don't select this option.

Design SSR primers in intergenic regions.
Note: If you didn't feed SSRome Genomic Pipeline with your annotation information, please don't select this option.

Design SSR primers in all genomic regions.
Note: select this option if you didn't feed SSRome Genomic Pipeline with annotation information.

Primer size
Min 18 Opt 20 Max 22

Primer Tm
Min 57.0 Opt 59.0 Max 62.0

Primer GC%
Min 30.0 Opt 50.0 Max 70.0

Product Size Ranges
Size 100-500

SSRome Genomic Pipeline page (Part-3)

Select this option if you want to compare your results (identified SSR repeats) with SSRome Database to determine the unique repeats to your organism

If you selected previous option you should feed SSRome Comparative Analysis Pipeline with your organism scientific name. Or write "None" if you don't select this option.

Customize your SSRome Genomic Pipeline Results options

If you agree to Store your results in SSRome database, please provide us the date you want to make it available freely online

Enter your comment(S)

Click "submit" to run your analysis

SSRome Comparative Analysis

Compare your SSR repeats with SSRome Database.

Note1: select this option if you want to compare your results (identified SSR repeats) with SSRome Database to determine the unique repeats to your organism.

Note2: If you selected this option you should provide SSRome Comparative Analysis Pipeline with your organism scientific name.Or write "None" if you don't select this option.

Your organism scientific name

SSRome Genomic Pipeline Results

Availability of SSRome Genomic Pipeline Results

Store your results in SSRome database.

* Store your results in SSRome database and make it available free online.

Don't store my results in SSRome database.

* If you agree to Store your results in SSRome database, please provide us the date you want make it available free online

Available free online date

Comment

SSRome Transcriptomic Pipeline (Part-1)



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CCCCCCCCCCCCCCCC
GC GC GC GC GC GC GC GC
ATC ATC ATC ATC ATC ATC ATC
GTTA GTTA GTTA GTTA GTTA GTTA
GCTCA GCTCA GCTCA GCTCA GCTCA
ATTCGT ATTCGT ATTCGT ATTCGT ATTCGT

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- SSRome Upload Files
- SSRome Genomic Pipeline
- SSRome Transcriptomic Pipeline
- SSRome Comparative Analysis Pipeline



An Integrated Database and Pipelines for Exploring
Microsatellites in All Organisms

CCCCCCCCCCCCCCCC
GC GC GC GC GC GC GC GC
ATC ATC ATC ATC ATC ATC ATC
GTTA GTTA GTTA GTTA GTTA GTTA
GCTCA GCTCA GCTCA GCTCA GCTCA
ATTCGT ATTCGT ATTCGT ATTCGT ATTCGT

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SSRome Transcriptomic Pipeline

Note: To use SSRome Transcriptomic Pipeline you should **upload all your data/files at first**, then you can use SSRome Transcriptomic Pipeline to analyze your uploaded data, [See Manual](#), [SSRome Upload Files](#).

Enter your analysis name

Enter your Email address to notify you when your analysis complete.

“Check” to customize your analysis parameters

Project Information

Analysis Name

Analysis Name

Email

Email

Sequence Information

Assembled RNA Sequences without annotation (Fasta file format) [See Example.](#)

Assembled RNA Sequences with annotation information [See Example.](#)

SSRome Transcriptomic Pipeline (Part-2)

In the case your transcriptome (RNA-Seq) sample **without** annotation, Please enter the file name you uploaded through "SSRome Upload Files" page. Or write "None" in case of no file uploaded

In the case your transcriptome (RNA-Seq) sample **with** annotation, Please enter the file name you uploaded through "SSRome Upload Files" page. Or write "None" in case of no file uploaded

Customize SSR Mining Parameters

Customize your SSR primer design Parameters

"Check" to customize your annotation analysis parameters

Input Data

Assembled RNA Sequence without annotation

File Name OR Name

Note: Please provide the name of "Assembled RNA Sequence without annotation" file you uploaded through "SSRome Upload Files" page. Or write "None" in case of no file uploaded.

OR

Assembled RNA Sequence with annotation information

File Name OR Name

Note: Please provide the name of "Assembled RNA Sequence with annotation information" file you uploaded through "SSRome Upload Files" page. Or write "None" in case of no file uploaded.

Parameters

SSR Mining Parameters

Mono ≥ Di ≥ Tri ≥ Tetra ≥ Penta ≥ Hexa ≥

General Primer Designing Conditions

Primer size
Min Opt Max

Primer Tm
Min Opt Max

Primer GC%
Min Opt Max

Product Size Ranges
Size

RNA Annotation Section

Annotate RNA Sequences that successfully designed SSR primers.
Note: Select this option if you don't feed SSRome Transcriptomic Pipeline with annotation information.
Note: If you selected "Annotate RNA Sequences that successfully designed SSR primers" you should feed SSRome Transcriptomic Pipeline with Your sequence source to annotate your sequences. Or write "None"
Your organism scientific name

RNA Sequences already annotated.
Note: If you feed SSRome Transcriptomic Pipeline with annotation information, please select this option.

SSRome Transcriptomic Pipeline (Part-3)

Customize your SSRome Transcriptomic Pipeline Results options

If you agree to Store your results in SSRome database, please provide us the date you want to make it available freely online

Enter your comment(S)

Click "submit" to run your analysis

SSRome Transcriptomic Pipeline Results

Availability of SSRome Transcriptomic Pipeline Results

Store the results in SSRome database.
* Store your results in SSRome database and make it available free online.

Don't store my results in SSRome database.
* If you agree to store your results in SSRome database, please provide us the date you want make it available free online

Available free online date

Comment

Comment

SSRome Comparative Analysis Pipeline (Part-1)



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Microsatellites in All Organisms

CCCCCCCCCCCCCCCC
GC GC GC GC GC GC GC GC
ATC ATC ATC ATC ATC ATC ATC
GTTA GTTA GTTA GTTA GTTA GTTA
GCTCA GCTCA GCTCA GCTCA GCTCA
ATTCGT ATTCGT ATTCGT ATTCGT ATTCGT

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- SSRome Upload Files
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- SSRome Transcriptomic Pipeline
- SSRome Comparative Analysis Pipeline



An Integrated Database and Pipelines for Exploring
Microsatellites in All Organisms

CCCCCCCCCCCCCCCC
GC GC GC GC GC GC GC GC
ATC ATC ATC ATC ATC ATC ATC
GTTA GTTA GTTA GTTA GTTA GTTA
GCTCA GCTCA GCTCA GCTCA GCTCA
ATTCGT ATTCGT ATTCGT ATTCGT ATTCGT

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SSRome Comparative Analysis Pipeline

Note: To use SSRome Comparative Analysis Pipeline you should **upload all your data/files at first**, then you can use SSRome Comparative Analysis Pipeline to analyze your uploaded data, [See Manual](#), [SSRome Upload Files](#).

Enter your analysis name

Enter your Email address to notify you when your analysis complete.

“Check” to customize your options

Project Information

Analysis Name

Analysis Name

Email

Email

Data Information

Submit your SSR results + annotation information (Genbank file) [See SSR results example](#) [See Genbank file example](#).

Note: Please choose this option if you have files contain SSR repeats results identified using any other tool and have Genbank file containing annotation information of your organism.

OR

Submit your SSR results only

Note: Please choose this option if you have only files contain SSR repeats results identified using any other tool.

SSRome Comparative Analysis Pipeline (Part-2)

Enter your organism scientific name

Enter the name of SSR repeat file you uploaded through "SSRome Upload Files" page. Or write "None" in case of no file uploaded.

Enter the name of Genbank file you uploaded through "SSRome Upload Files" page. Or write "None" in case of no file uploaded.

Customize SSR Mining Parameters

Enter the SSR Mining tool name used to determine the SSR repeats

Customize your SSRome Transcriptomic Pipeline Results options

If you agree to Store your results in SSRome database, please provide us the date you want to make it available freely online

Enter your comment(S)

Click "submit" to run your analysis

Input Data

Your organism scientific name
Your organism scientific name

And

SSR Repeat File
SSR Repeat File Name OR None

Note: Please provide the name of SSR repeat file you uploaded through "SSRome Upload Files" page. Or write "None" in case of no file uploaded.

Genbank file
Genbank File Name OR None

Note: Please provide the name of Genbank file you uploaded through "SSRome Upload Files" page. Or write "None" in case of no file uploaded.

Parameters

SSR Mining Parameters

Note: Please provide the SSR mining parameters and the tool name used to determine the SSR repeats.

Mono: 10 Di: 6 Tri: 5 Tetra: 4 Penta: 3 Hexa: 3 Program
name: MISA

SSRome Comparative Analysis Pipeline Results

Availability of SSRome Comparative Analysis Pipeline Results

Store the results in SSRome database.
* Store your results in SSRome database and make it available free online.

Don't store my results in SSRome database.
* If you agree to store the results in SSRome database, please provide us the date you want make it available free online

Available free online date: 1/1/2018

Comment
Comment

Submit

For any further questions please contact us