

SSRome Manual

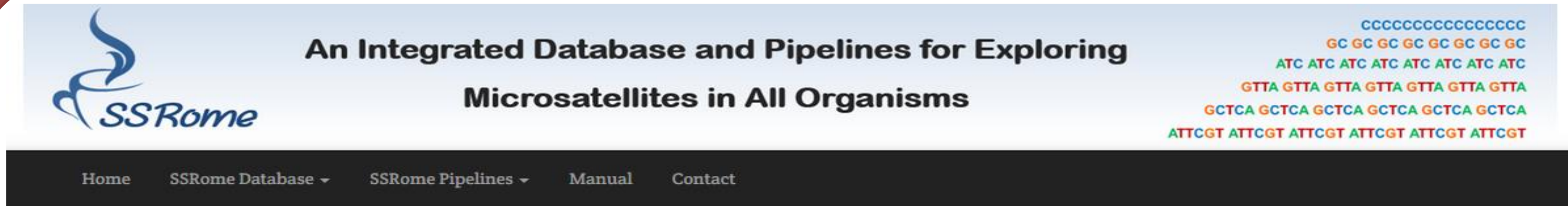
SSRome Main-Bar Overview



- **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.
- **Manual**
- **Contact**

Home Page

- About SSRome



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.

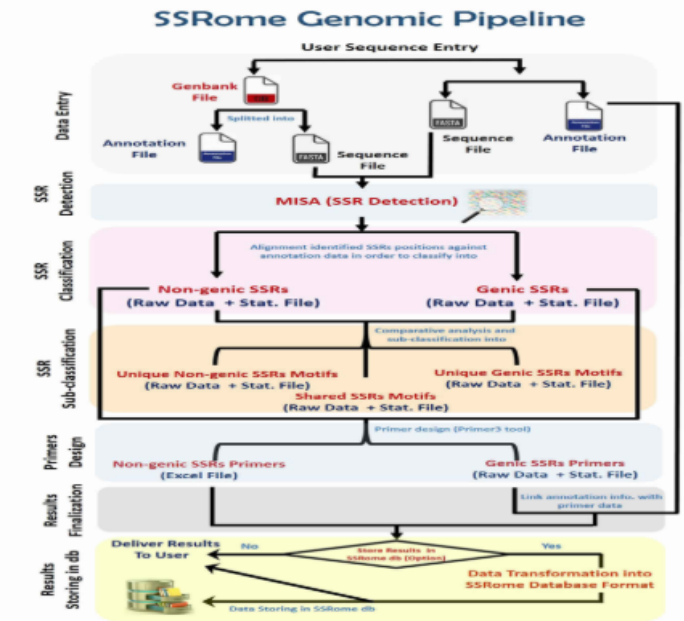
Home Page

■ 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.

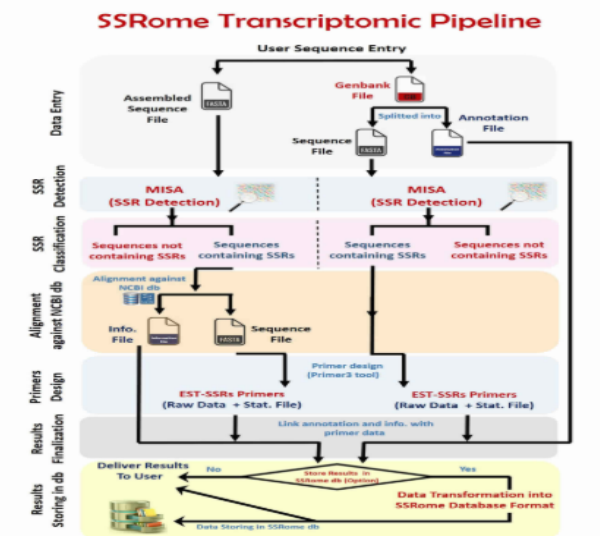


■ SSRome Transcriptomic Pipeline



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.

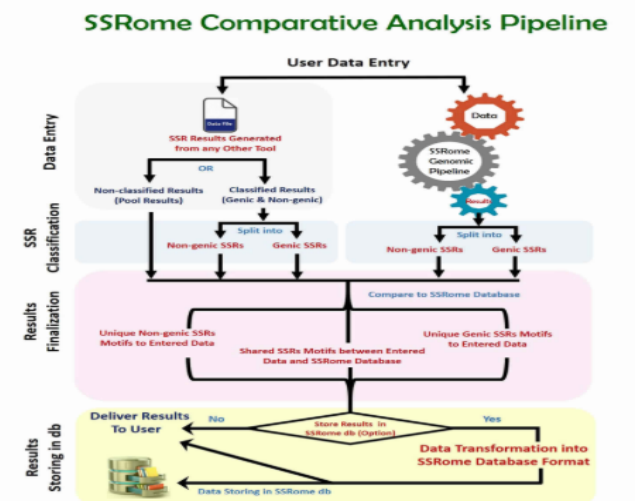


■ SSRome Comparative Analysis Pipeline



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

Select one of this
genra

Metazoa

Plant

Archaea


Bacteria

Virus

Fungi


Protozoa

Analyzed Genomes in SSRome Database




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

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 resluts from SSRome Apis mellifera database.

Apis mellifera Genic SSRs

Repeat Sequence

[TGA]5

Gene symbol or Locus tag

Organism Name

Apis mellifera

Repeat Type

Mono

Search

Apis mellifera Non-Genic SSRs

Primer Id

SSRome Primer Id

Repeat Sequence

[TGA]5

Organism Name

Apis mellifera

Repeat Type

Di

Search

Home Page

- Analyzed ESTs in SSRome Database

Analyzed ESTs in SSRome Database

<div>ALL NCBI PLANT ESTS</div>	<div>Plant ESTs</div> <div>Plants ESTs available in NCBI ESTdb till March 2018</div> <div>Search page</div>	<div>ALL NCBI METAZOA ESTS</div>	<div>Metazoa ESTs</div> <div>Animals ESTs available in NCBI ESTdb till March 2018</div> <div>Search page</div>	<div>ALL NCBI OTHERS ESTS</div>	<div>Others ESTs</div> <div>Others ESTs available in NCBI ESTdb till March 2018</div> <div>Search page</div>
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Click to go to the Search Page for each category

- Analyzed Organelles Genomes in SSRome Database

Analyzed Organelles in SSRome Database

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

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	Prunus avium	130415
Solanum tuberosum	145977	Vitis vinifera	120734		

Metazoa Statistics

Others Statistics

Transcriptomic

Plant Statistics

Metazoa Statistics

Others Statistics

Mitochondria

Plant Statistics

Metazoa Statistics


Chloroplast

Plant Statistics

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

Statistics Categories

Download Page



An Integrated Database and Pipelines for Exploring
Microsatellites in All Organisms

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[Statistics](#) [Download](#) [Database Search](#) [SSRome Comparisons](#)

Genome



An Integrated Database and Pipelines for Exploring
Microsatellites in All Organisms

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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

- Plant
- Metazoa
- Others

Genomic Downloads

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

Organelles download part

Transcriptomic download part


Organelles Downloads

All Plant Chloroplasts	Genic SSR	Genic SSR Stat	Unique Genic SSR	Genic SSR Primers	Intergenic SSR	Intergenic SSR Stat	Unique Intergenic SSR	Intergenic SSR Primers	SSR Overlap
All Plant Mitochondria genomes	Genic SSR	Genic SSR Stat	Unique Genic SSR	Genic SSR Primers	Intergenic SSR	Intergenic SSR Stat	Unique Intergenic SSR	Intergenic SSR Primers	SSR Overlap

Transcriptomic Downloads

All Plant ESTs
EST-SSR Primers

Download Page



An Integrated Database and Pipelines for Exploring
Microsatellites in All Organisms

HomeSSRome Database ▾SSRome Pipelines ▾ManualContact

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

Genomic Downloads

Plant
Metazoa

Arabidopsis thaliana

Genic SSR Genic SSR Stat Unique Genic SSR Genic SSR Primers Non-genic SSR Non-genic SSR Stat Unique Non-genic SSR Non-genic SSR Primers SSR Overlap

Brachypodium distachyon

Genic SSR Genic SSR Stat Unique Genic SSR Genic SSR Primers Non-genic SSR Non-genic SSR Stat Unique Non-genic SSR Non-genic SSR Primers SSR Overlap

Brassica napus

Genic SSR Genic SSR Stat Unique Genic SSR Genic SSR Primers Non-genic SSR Non-genic SSR Stat Unique Non-genic SSR Non-genic SSR Primers SSR Overlap

Brassica oleracea

Genic SSR Genic SSR Stat Unique Genic SSR Genic SSR Primers Non-genic SSR Non-genic SSR Stat Unique Non-genic SSR Non-genic SSR Primers SSR Overlap

Arabidopsis thaliana

Genic SSR Genic SSR Stat Unique Genic SSR Genic SSR Primers Non-genic SSR Non-genic SSR Stat Unique Non-genic SSR Non-genic SSR Primers SSR Overlap

Solanum lycopersicum

Genic SSR Genic SSR Stat Unique Genic SSR Genic SSR Primers Non-genic SSR Non-genic SSR Stat Unique Non-genic SSR Non-genic SSR Primers SSR Overlap

Solanum tuberosum

Genic SSR Genic SSR Stat Unique Genic SSR Genic SSR Primers Non-genic SSR Non-genic SSR Stat Unique Non-genic SSR Non-genic SSR Primers SSR Overlap

Organelles Downloads

All Plant Mitochondria genomes

Genic SSR Genic SSR Stat Unique Genic SSR Genic SSR Primers Intergenic SSR Intergenic SSR Stat Unique Intergenic SSR Intergenic SSR Primers SSR Overlap

All Plant ESTs

EST-SSR Primers

Download the SSR repeats found in genic regions and not found in Non-genic regions

Download genic-SSR repeats statistics

Download all genic-SSR repeats

Download all genic-SSR primers

Download the SSR motifs found in both genic and non-genic regions

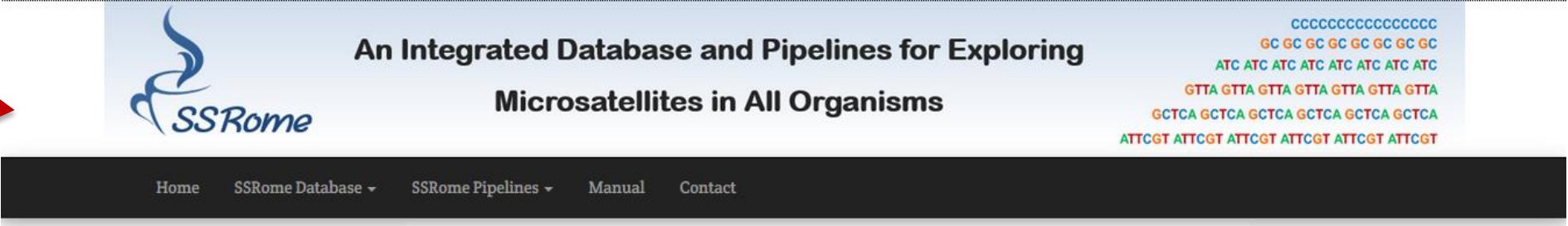
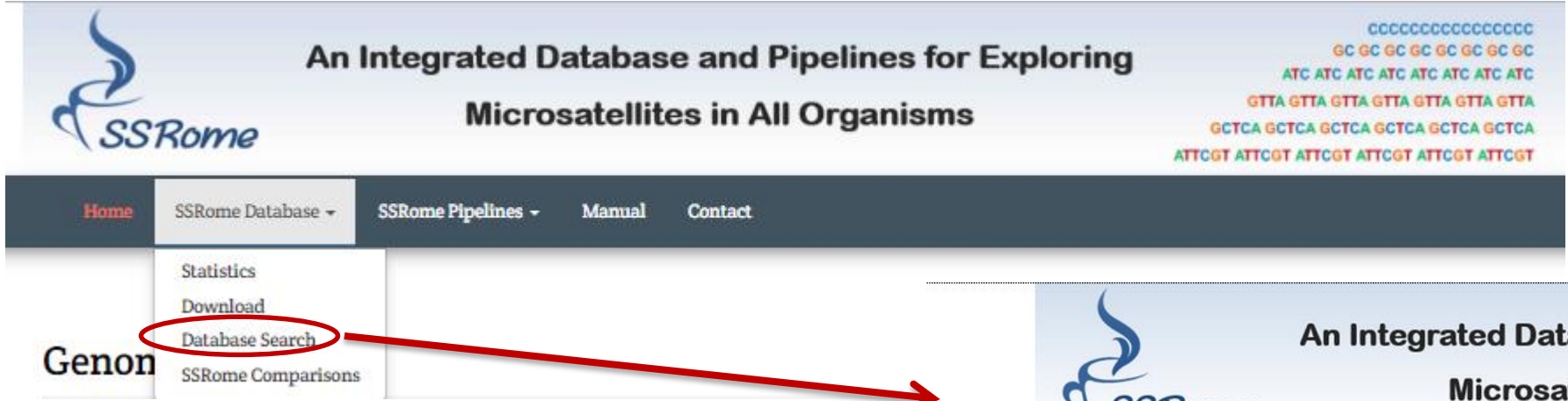
Download all non-genic SSR repeats

Download all non-genic SSR primers

Download non-genic SSR repeats statistics

Download the SSR repeats found in non- genic regions and not found in genic regions

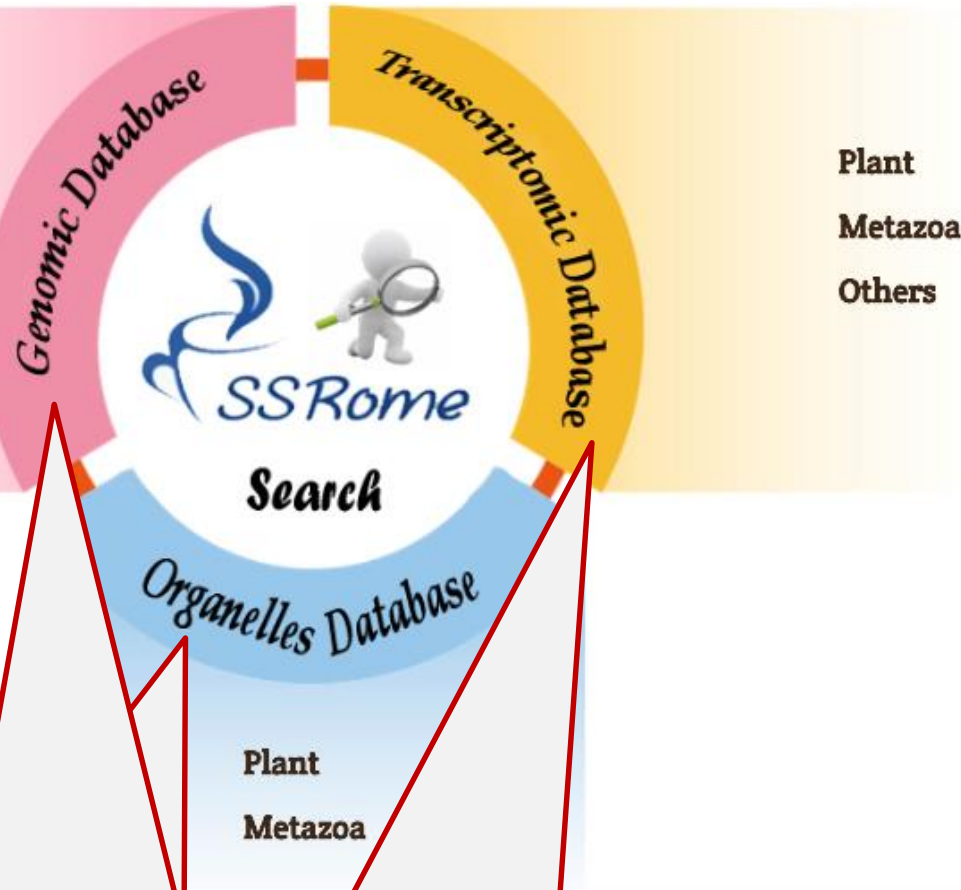
Search Page



Move from one to another Search Page by “Click”

Plant
Metazoa
Others
Comparative

SSRome Database Search



* 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

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
Metazoa
Others
Comparative

Plant
Metazoa
Others

Genomic Database

Transcriptomic Database

Search

Organelles Database

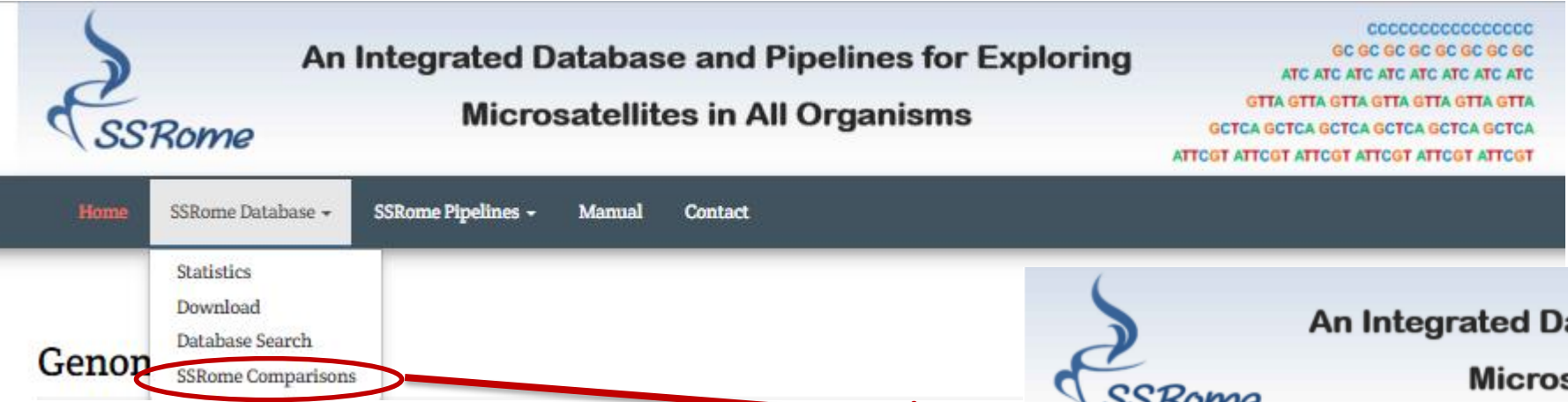
Plant Genic Region

Repeat Sequence Gene symbol or Locus tag Organism Name Repeat Type

Plant Non-genic Region

Primer Id Repeat Sequence Organism Name Repeat Type

Comparisons Page



Please select SSR repeat type from Repeat Type drop down menu

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



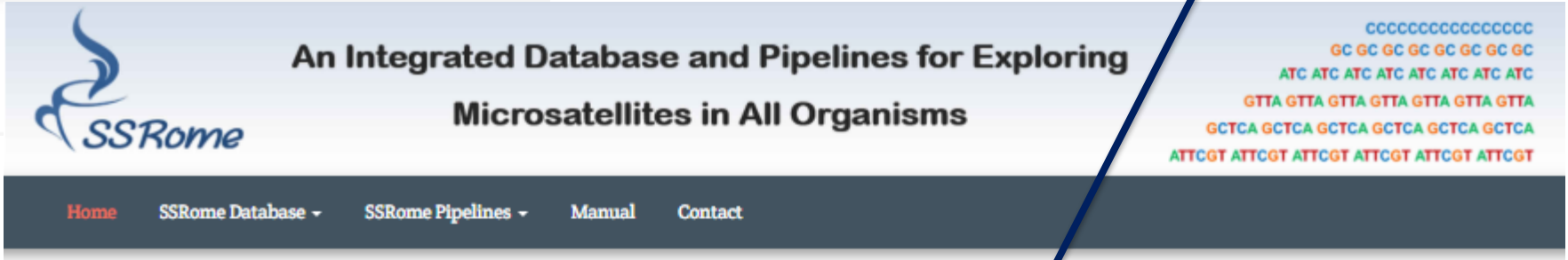
Search for SSR motifs overlapped between genic and non-genic regions

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

Genic Statistics

Organism Name Repeat Type

Non-Genic Statistics

Organism Name Repeat Type

Unique to Genic

Organism Name Repeat Type

Unique to Non-Genic

Organism Name Repeat Type

Please select the organism name from Organism Name drop down menu

SSRome Upload Files page



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 GCTCA
ATTCGT 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 GCTCA
ATTCGT ATTCGT ATTCGT ATTCGT ATTCGT ATTCGT

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SSRome Pipelines ▾

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

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 “small sized file(s)” select file from your computer and click “upload”

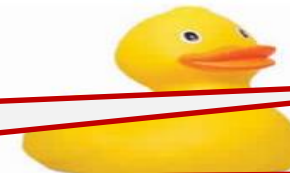
For Huge Sized Files :

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)



An Integrated Database and Pipelines for Exploring Microsatellites in All Organisms

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An Integrated Database and Pipelines for Exploring Microsatellites in All Organisms

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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 ≥ 10Di ≥ 6Tri ≥ 5Tetra ≥ 4Penta ≥ 3Hexa ≥ 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 18Opt 20Max 22

Primer Tm

Min 57.0Opt 59.0Max 62.0

Primer GC%

Min 30.0Opt 50.0Max 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

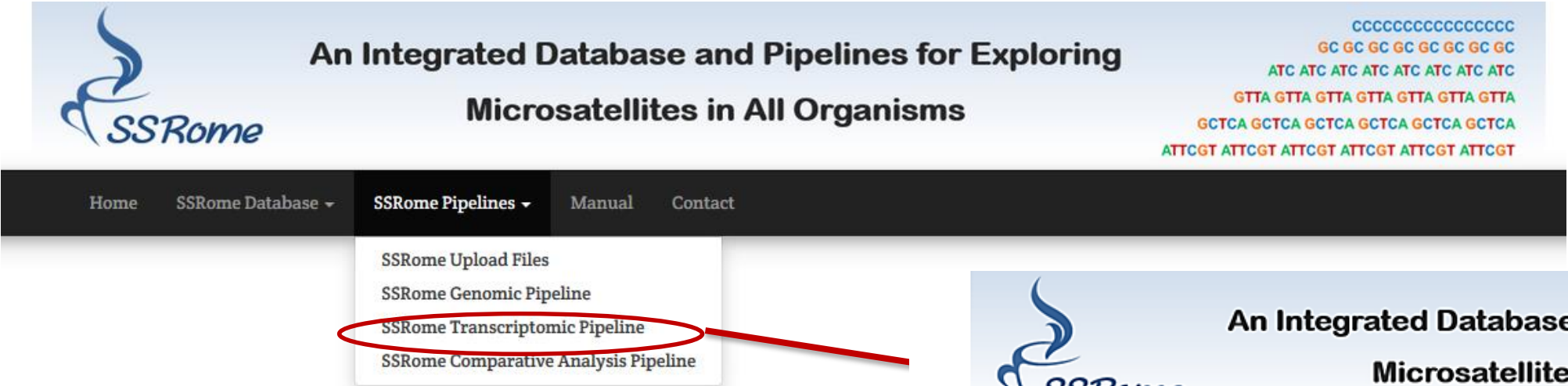
Available free online date

Comment

Comment

Submit

SSRome Transcriptomic Pipeline (Part-1)



The screenshot shows the "SSRome Transcriptomic Pipeline" page. It has the same header as the first image. Below the header, the title "SSRome Transcriptomic Pipeline" is followed by a note: "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](#)." Below the note is a form with two main sections: "Project Information" and "Sequence Information". The "Project Information" section has two input fields: "Analysis Name" and "Email". The "Sequence Information" section has two radio button options: "Assembled RNA Sequences without annotation (Fasta file format)" and "Assembled RNA Sequences with annotation information". Each option has a "See Example" link. Red arrows point from callout boxes on the left to the "Analysis Name" and "Email" fields, and from another callout box to the radio button options.

Enter your analysis name

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

“Check” to customize your analysis parameters

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 Nane

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 Nane

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 ≥ 10Di ≥ 6Tri ≥ 5Tetra ≥ 4Penta ≥ 3Hexa ≥ 3

*

General Primer Designing Conditions

Primer size

Min 18Opt 20Max 22

Primer Tm

Min 57.0Opt 59.0Max 62.0

Primer GC%

Min 30.0Opt 50.0Max 70.0

Product Size Ranges

Size 100-500

*
* 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 Organism scientific name Or None

☐ 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

Submit


SSRome Comparative Analysis Pipeline (Part-1)



An Integrated Database and Pipelines for Exploring Microsatellites in All Organisms

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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](#).

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.

Enter your analysis name

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

“Check” to customize your options

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	
<input type="text" value="Your organism scientific name"/>	
And	
SSR Repeat File	
<input type="text" value="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	
<input type="text" value="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 ≥	<input type="text" value="10"/>
Di ≥	<input type="text" value="6"/>
Tri ≥	<input type="text" value="5"/>
Tetra ≥	<input type="text" value="4"/>
Penta ≥	<input type="text" value="3"/>
Hexa ≥	<input type="text" value="3"/>
Program	
<input type="text" value="MISA"/>	
SSRome Comparative Analysis Pipeline Results	
Availability of SSRome Comparative Analysis Pipeline Results	
<input type="checkbox"/> Store the results in SSRome database.	
* Store your results in SSRome database and make it available free online.	
<input type="checkbox"/> 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	<input type="text" value="1/1/2018"/>
Comment	
<input type="text" value="Comment"/>	
<input type="button" value="Submit"/>	

For any further questions please contact us