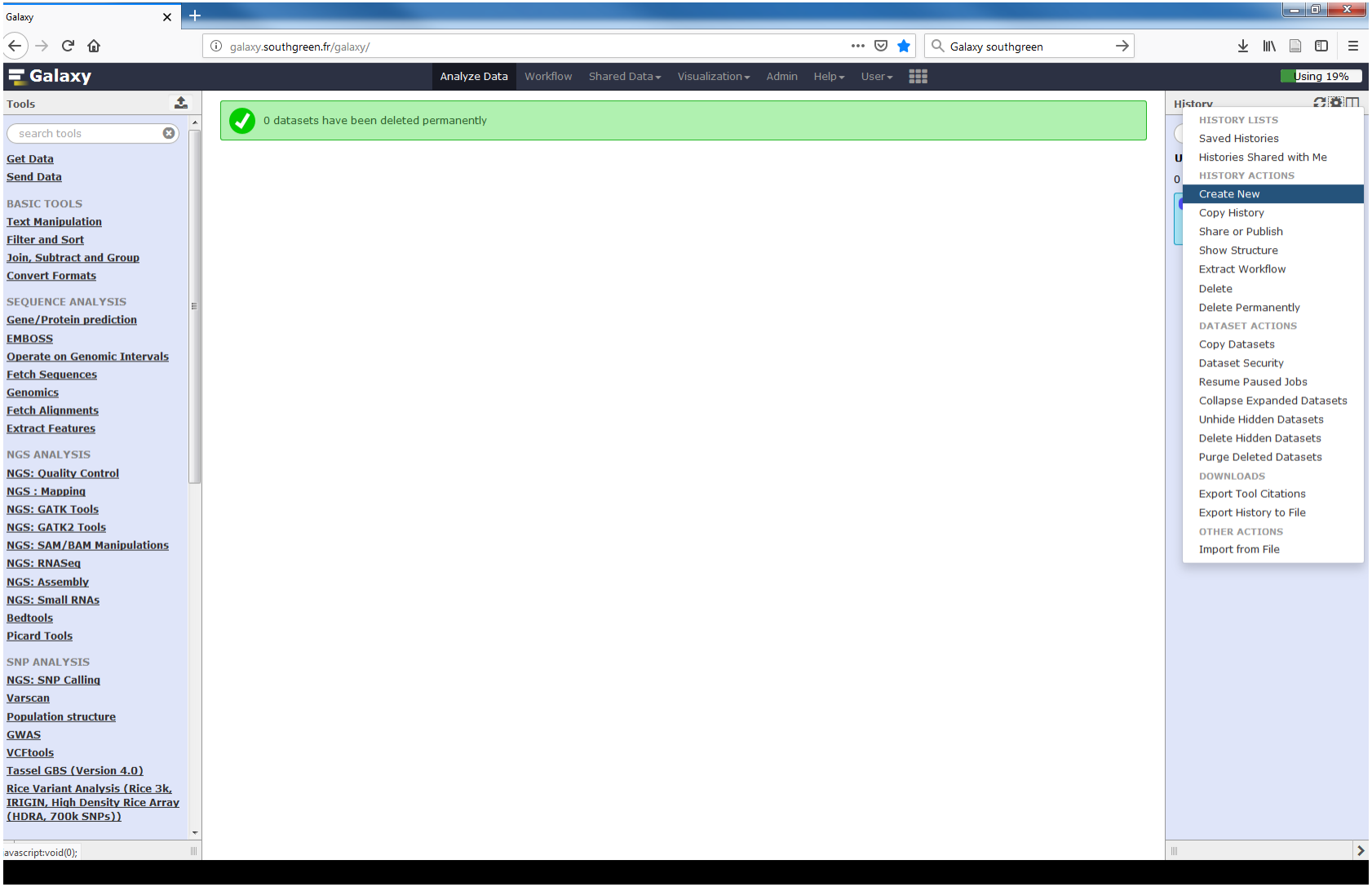
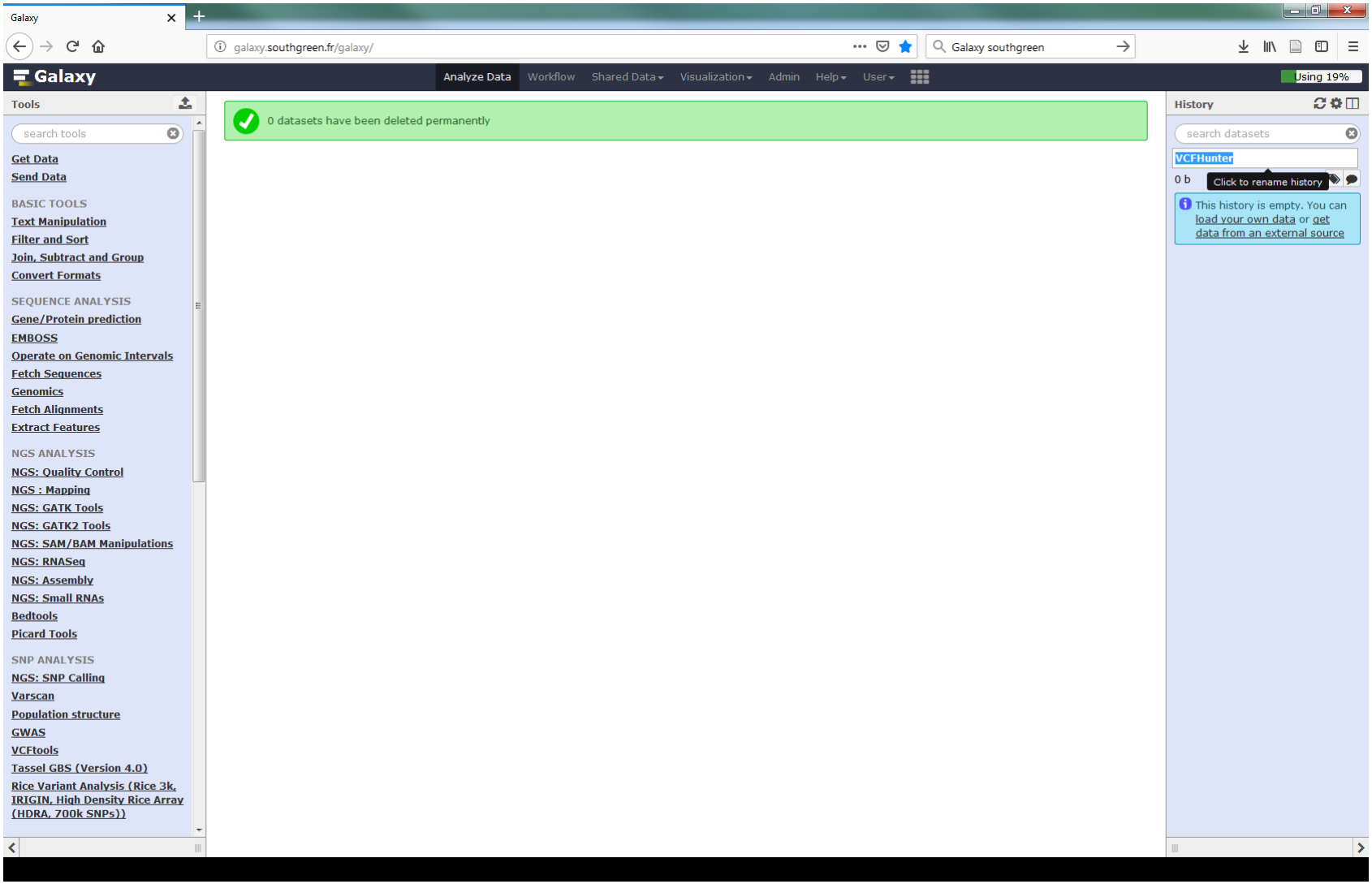
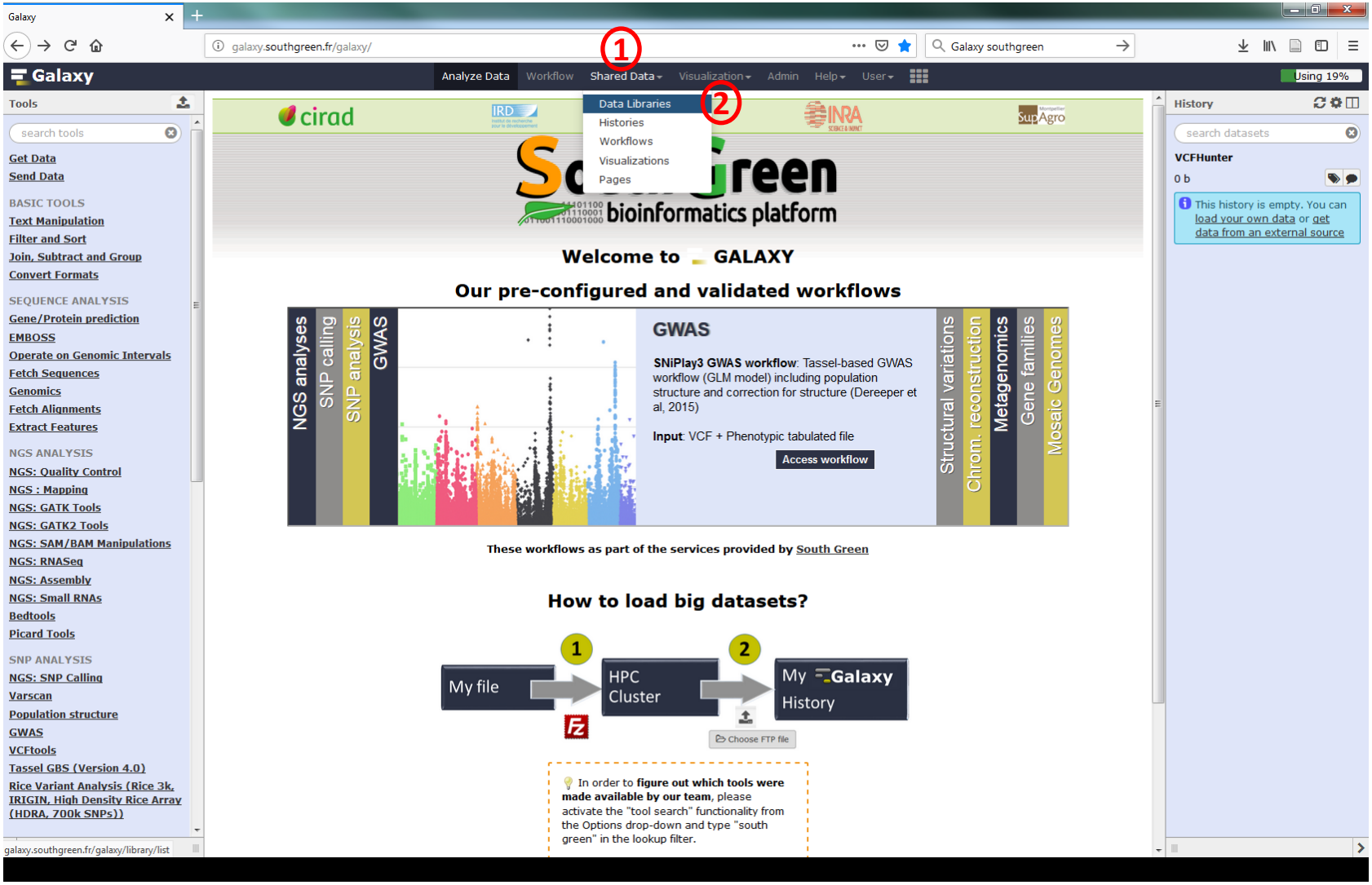
Creating an history: All analysis will be found in this history



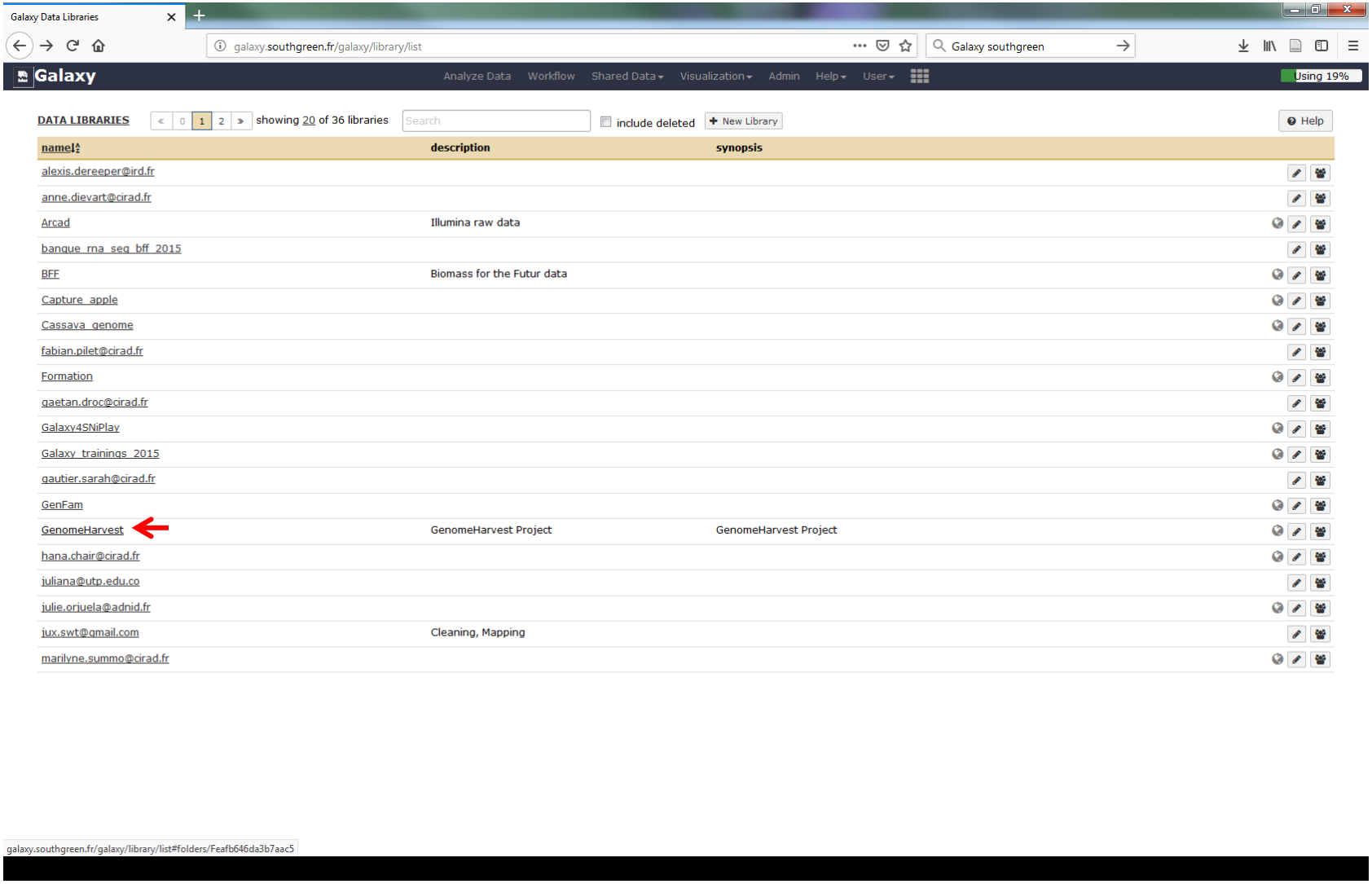
Renaming the History (easier to find analysis)



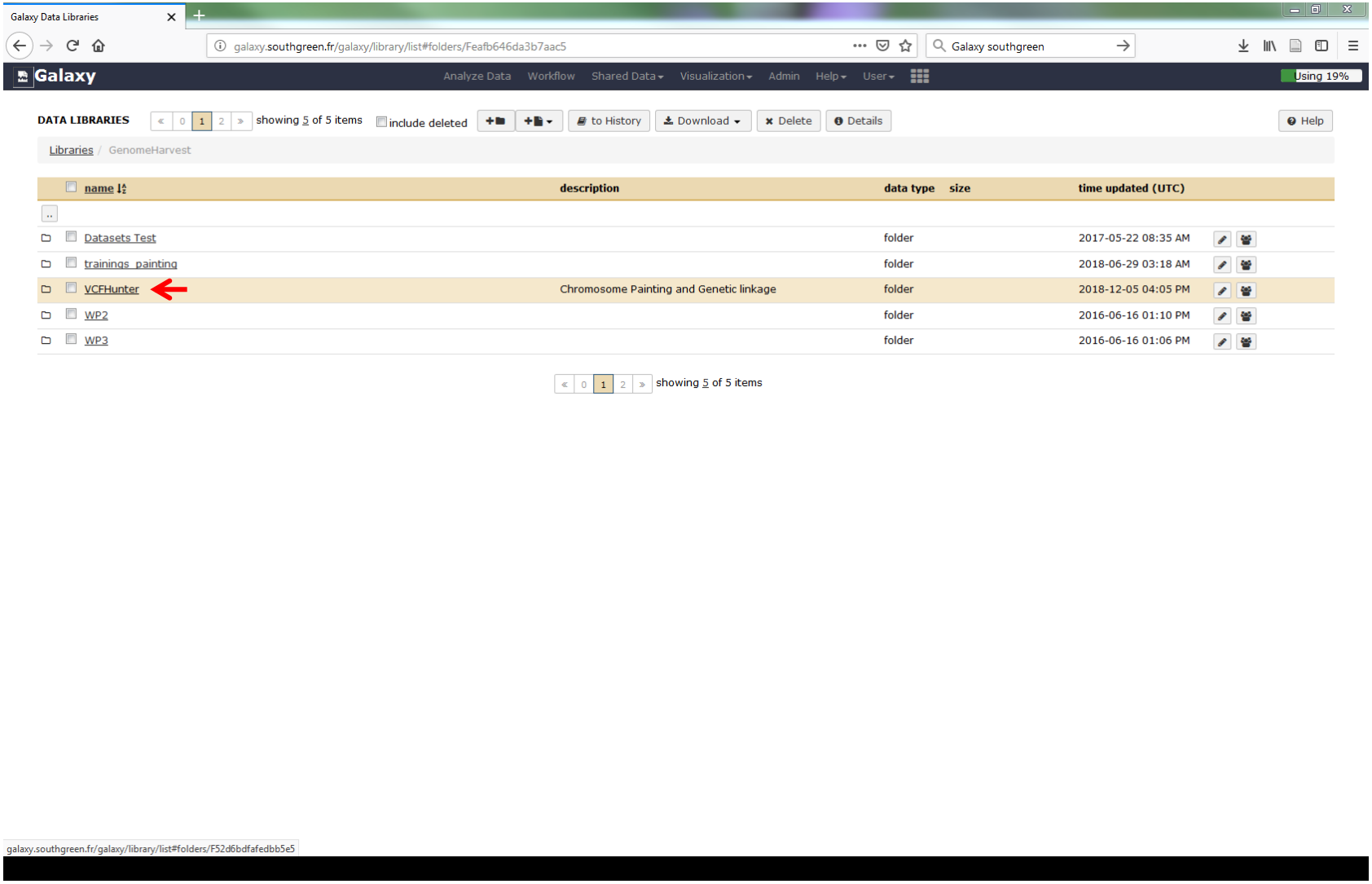
Loading existing dataset: To test tools



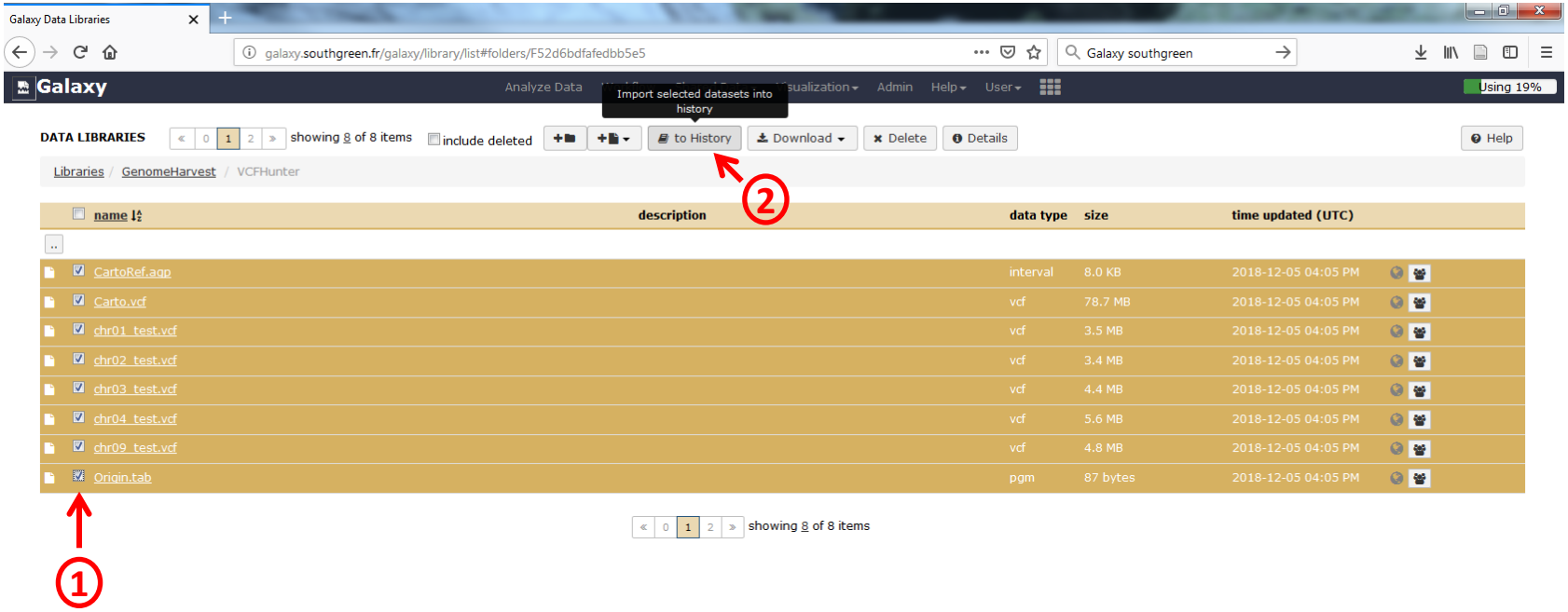
Loading existing dataset: To test tools



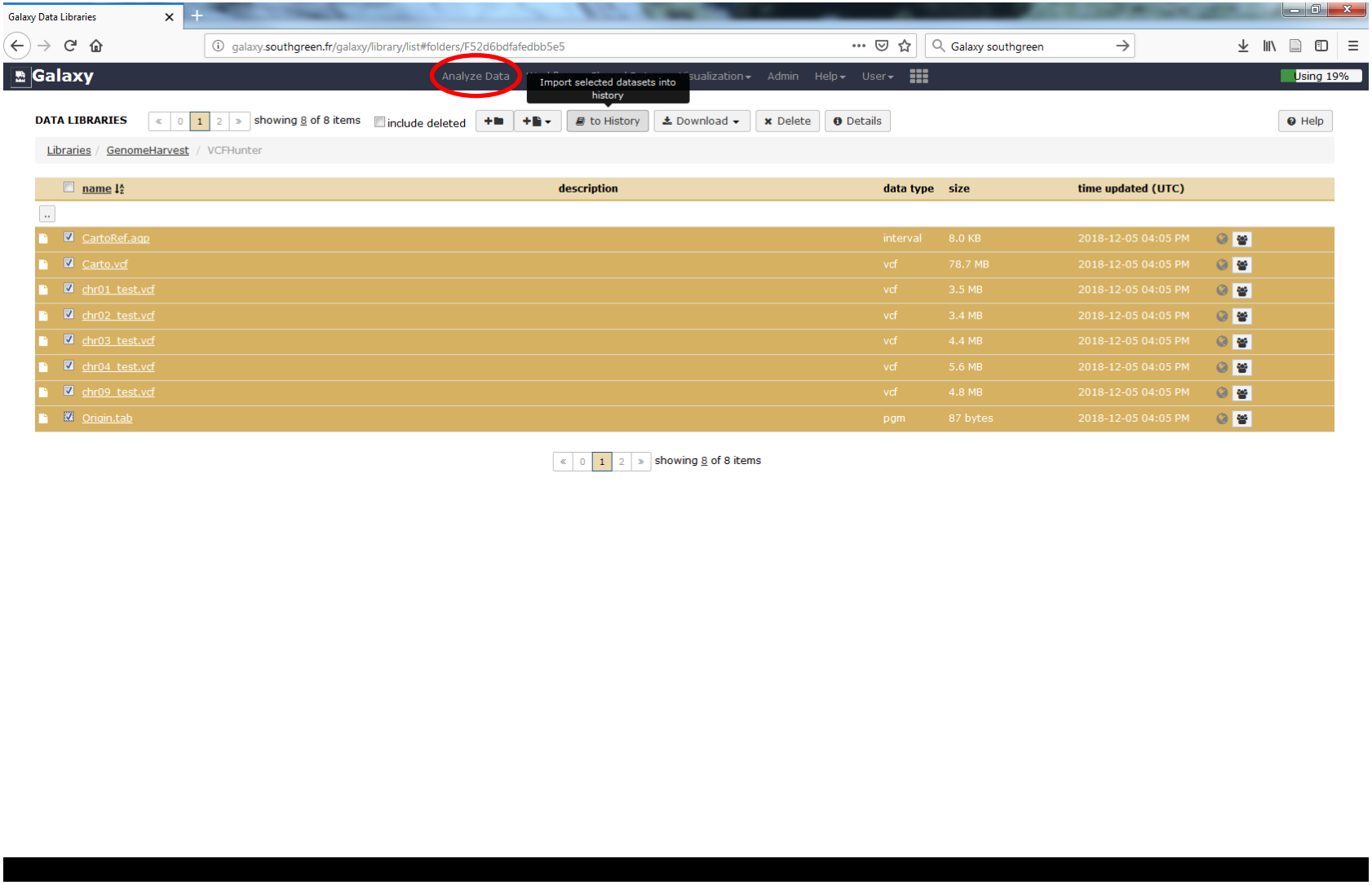
Loading existing dataset: To test tools



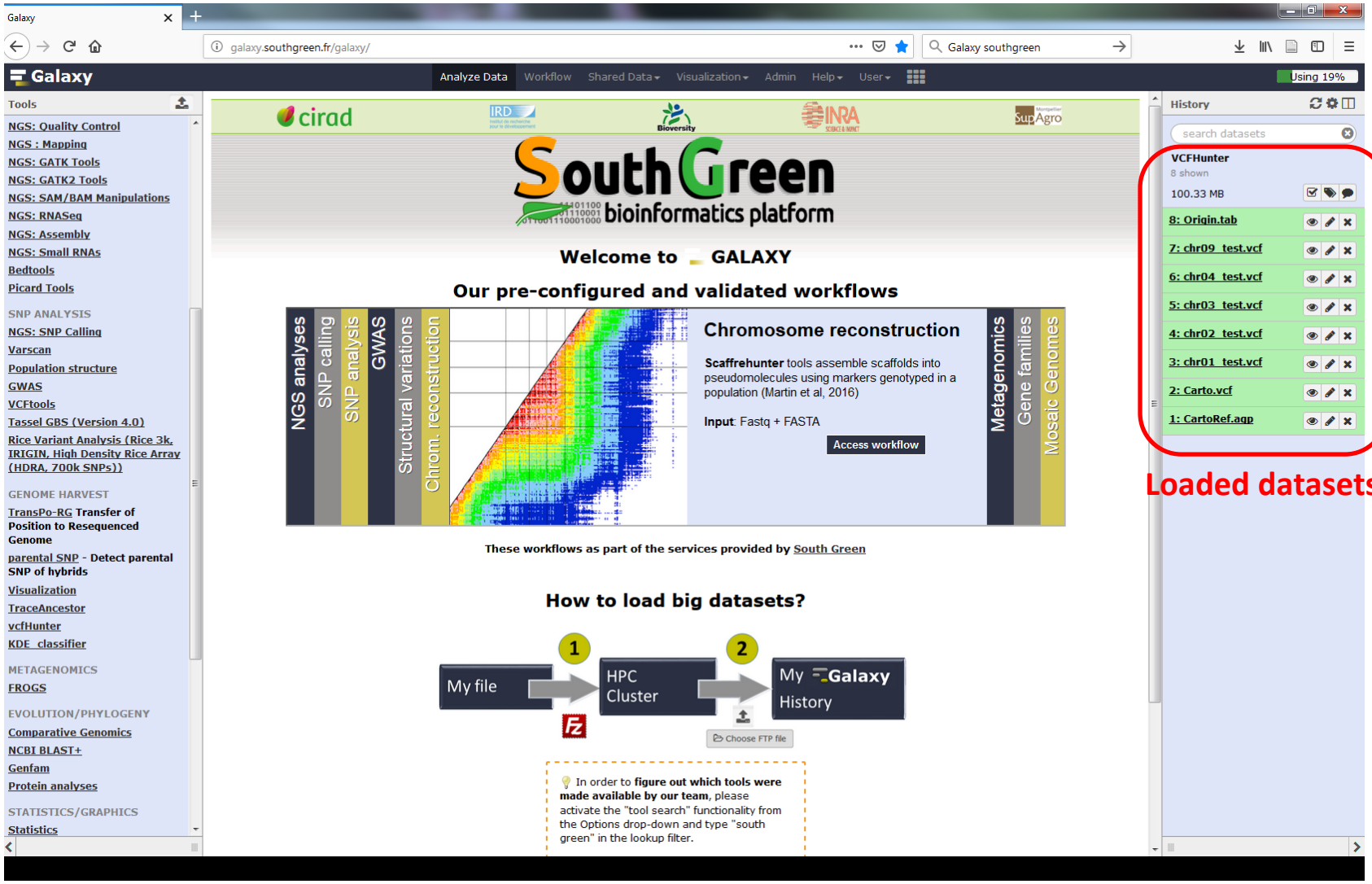
Loading existing dataset: To test tools



Going back to history to analyze data



Going back to history



Loaded datasets

Chromosome painting with vcfHunter tool

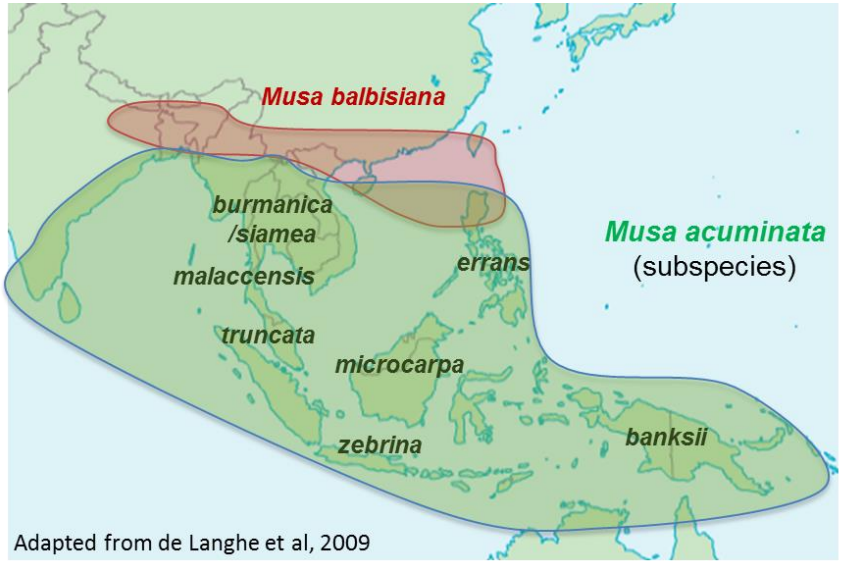
Developed to answer banana problematics

Musa balbisiana
2n = 2x = 22
1 to 1.2pg

B genome

Musa acuminata
2n = 2x = 22
1.1 to 1.3pg

A genome



Nearly half of the banana production worldwide relay on interspecific hybrids of various ploidy (AB, AAB , ABB , AAAB).

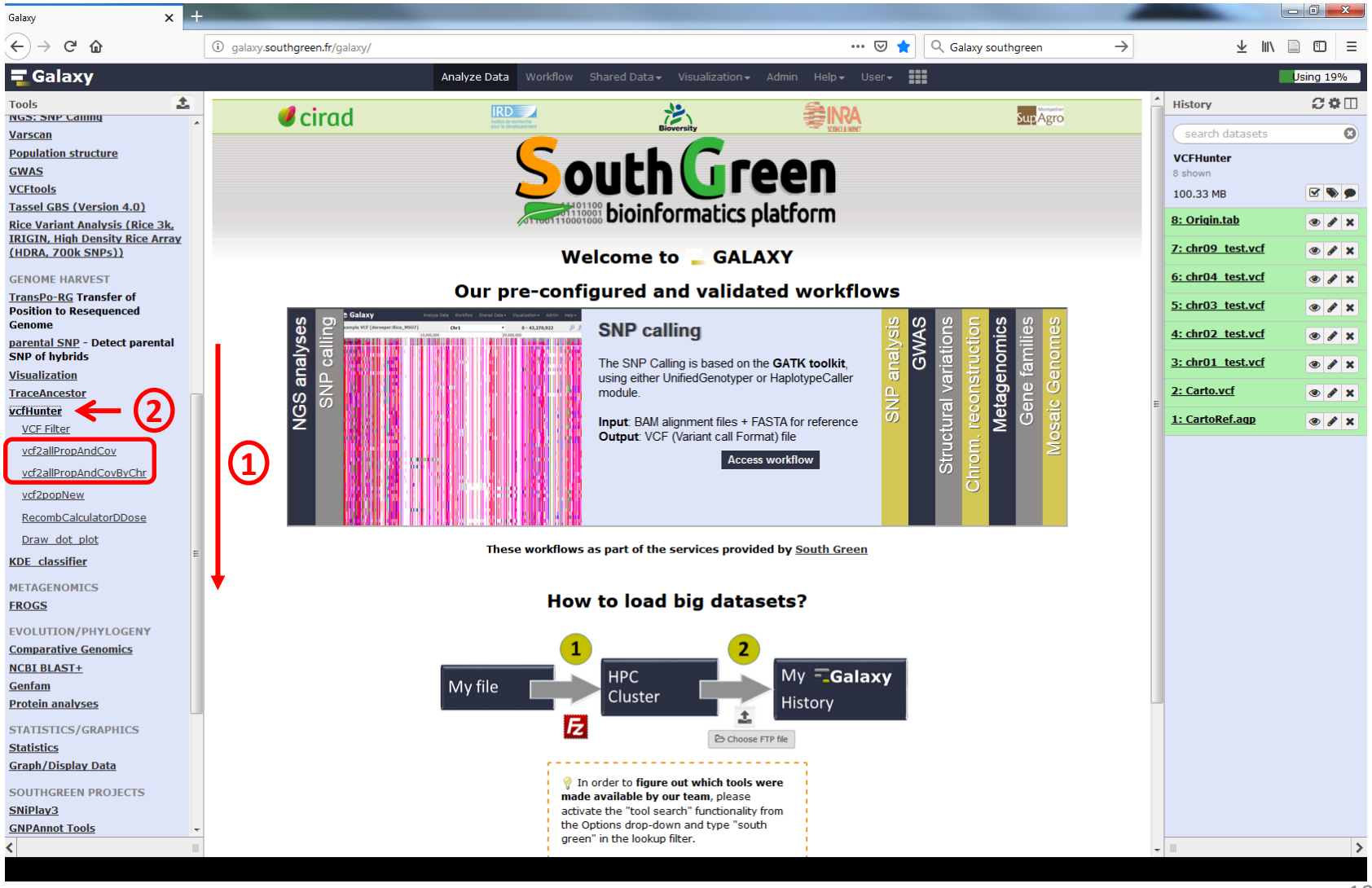
What is the composition of A and B genomes along chromosomes of cultivated banana hybrids?

Slide adapted from F.C Baurens

Chromosome painting with vcfHunter tool

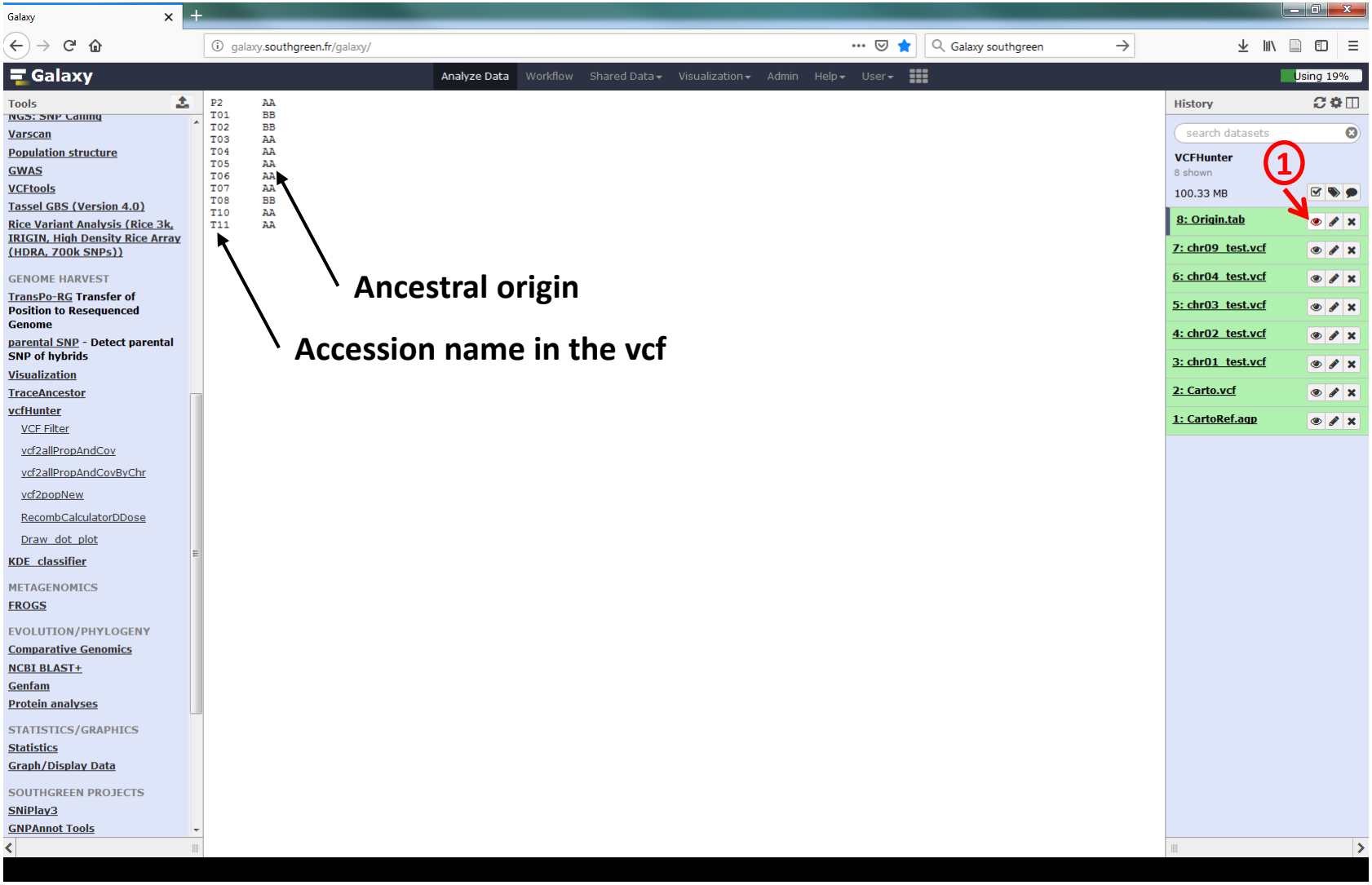
What is the contribution of ancestral genomes along chromosomes of cultivated hybrids?

Several tools developed under vcfHunter toolbox for this purpose:



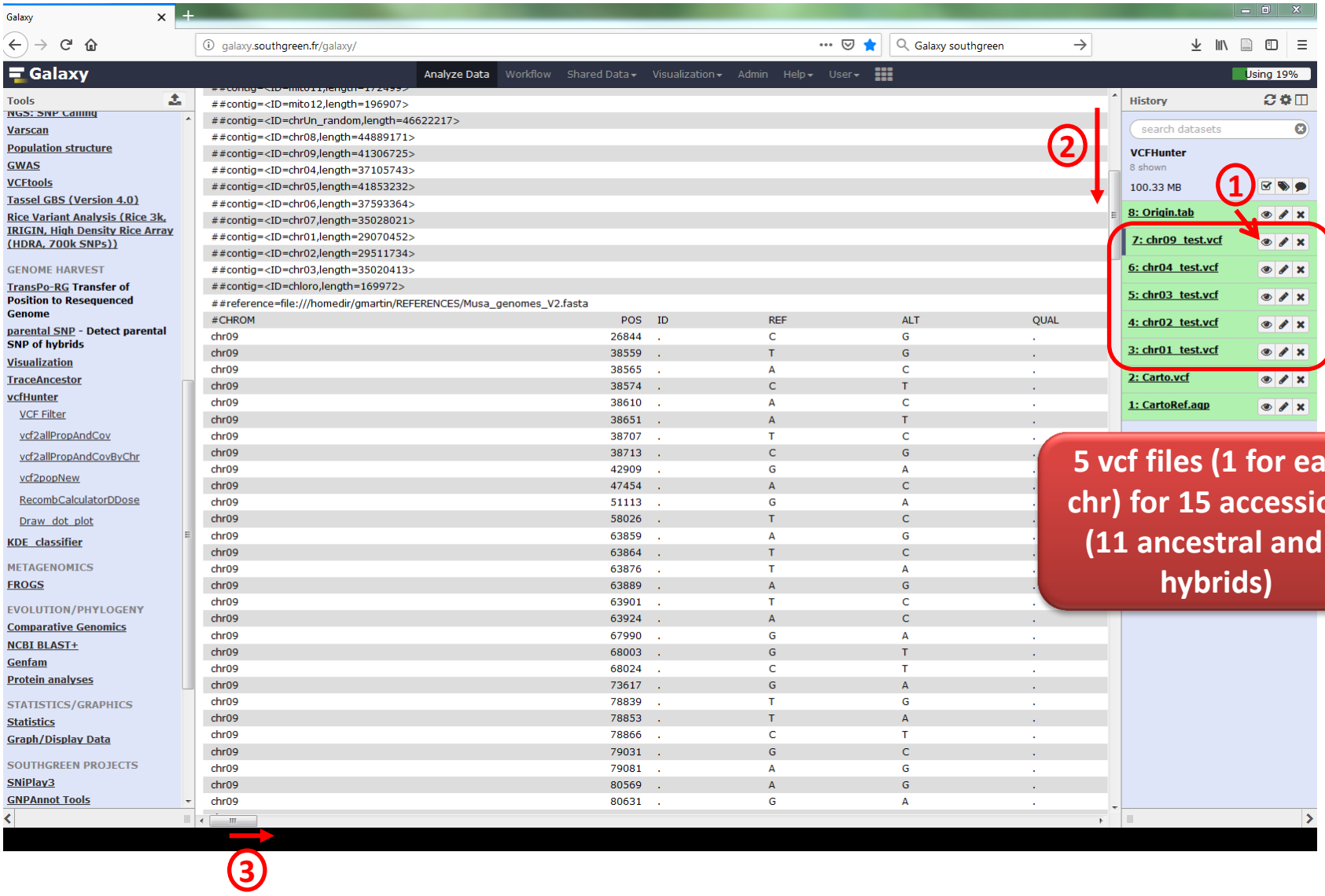
Chromosome painting with vcfHunter tool

Used data: A file containing ancestral (non admixed) accession origin



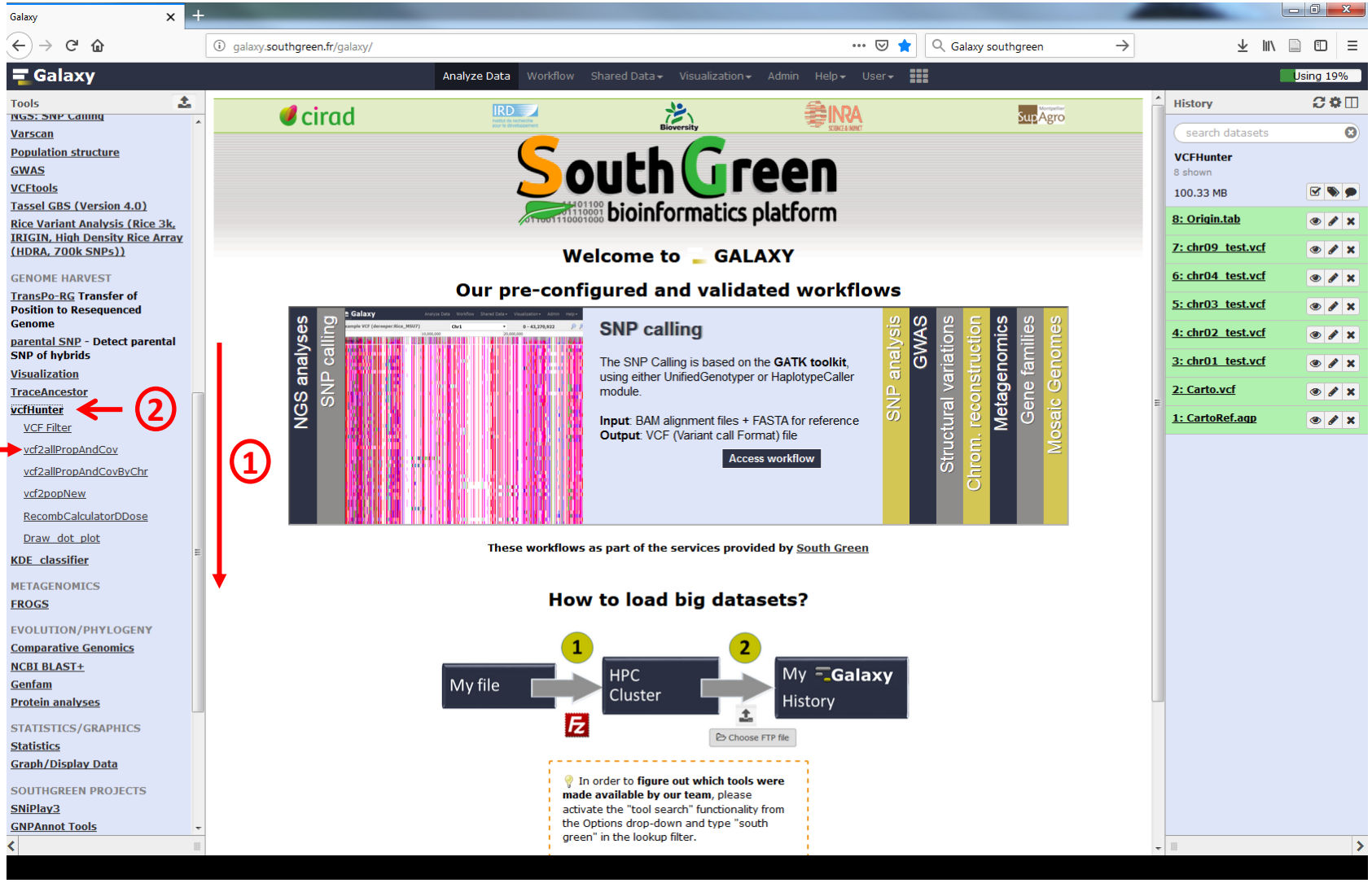
Chromosome painting with vcfHunter tool

Used data: Several vcf files containing the genotypes of 15 accessions



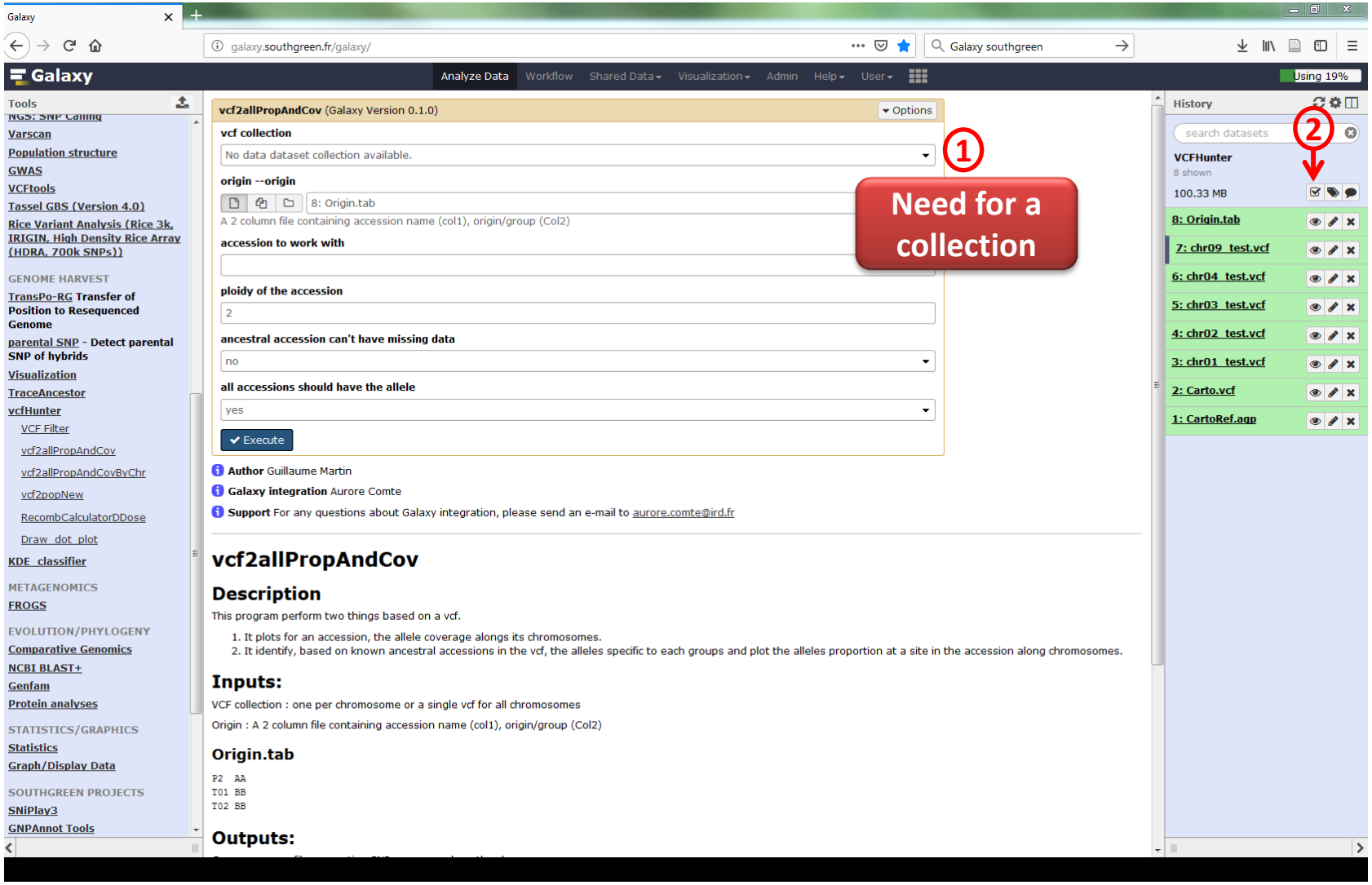
Chromosome painting with vcfHunter tool

1- Chromosome painting of one accession



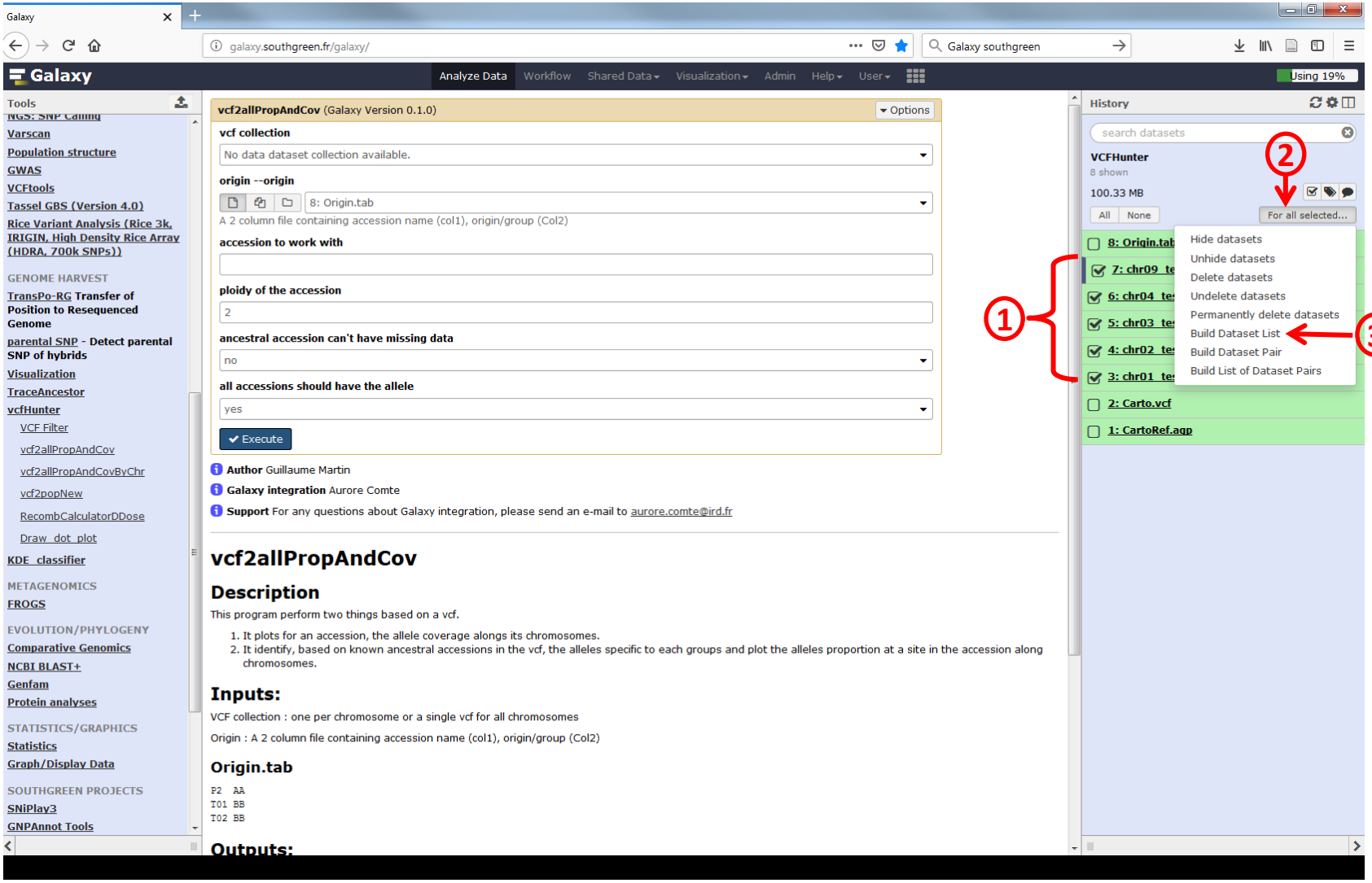
Chromosome painting with vcfHunter tool

1- Chromosome painting of one accession



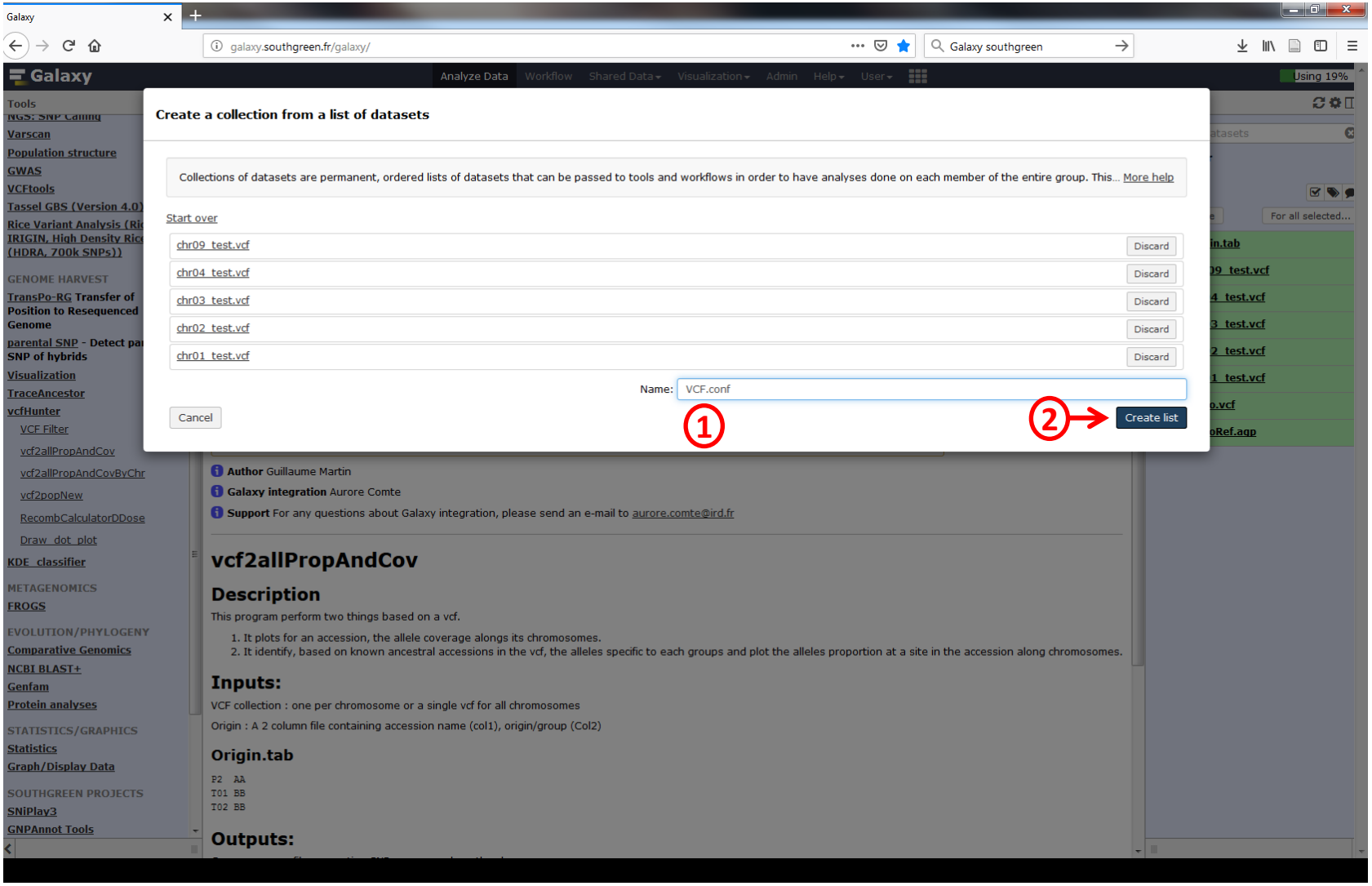
Chromosome painting with vcfHunter tool

1- Chromosome painting of one accession



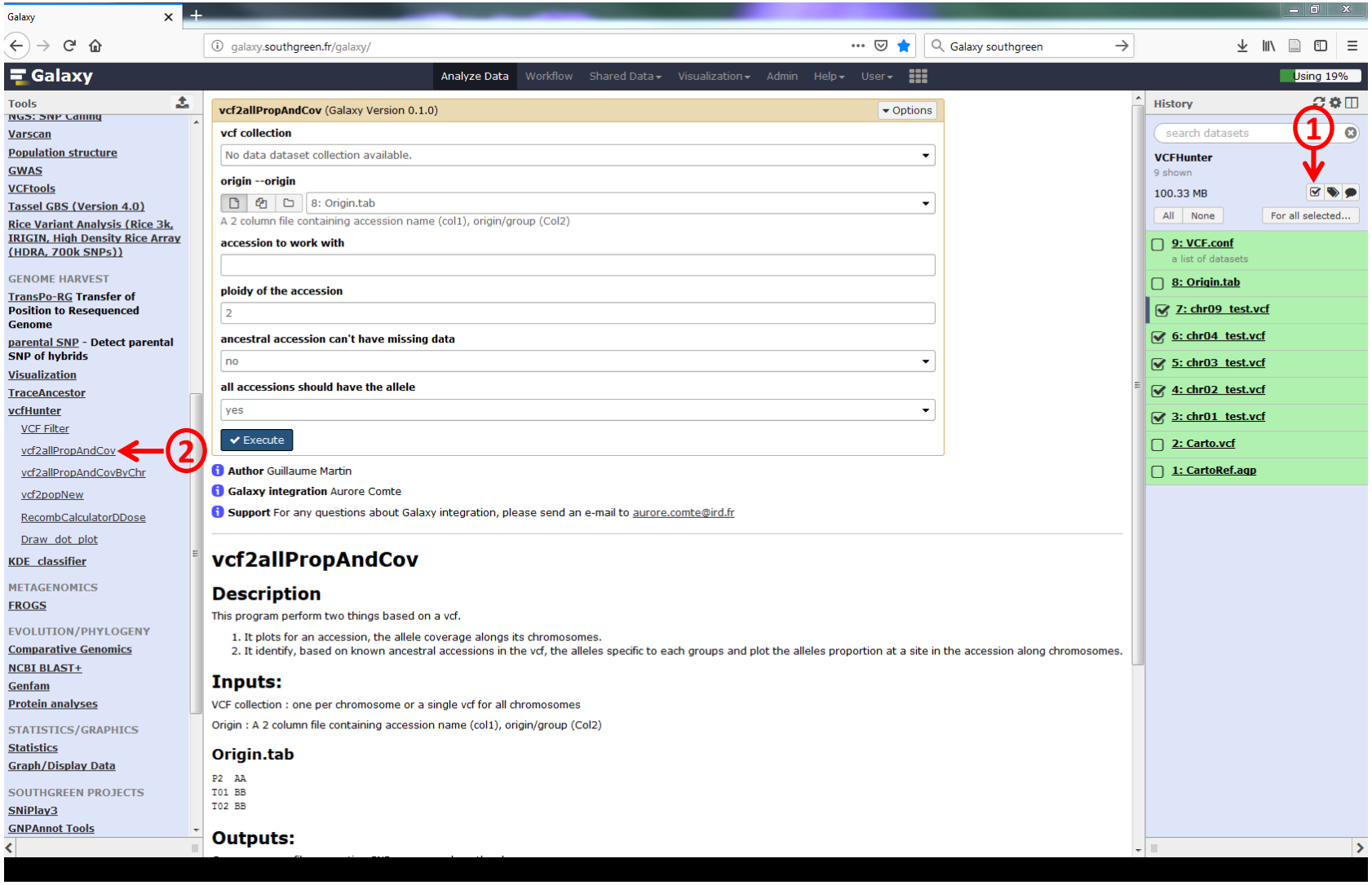
Chromosome painting with vcfHunter tool

1- Chromosome painting of one accession



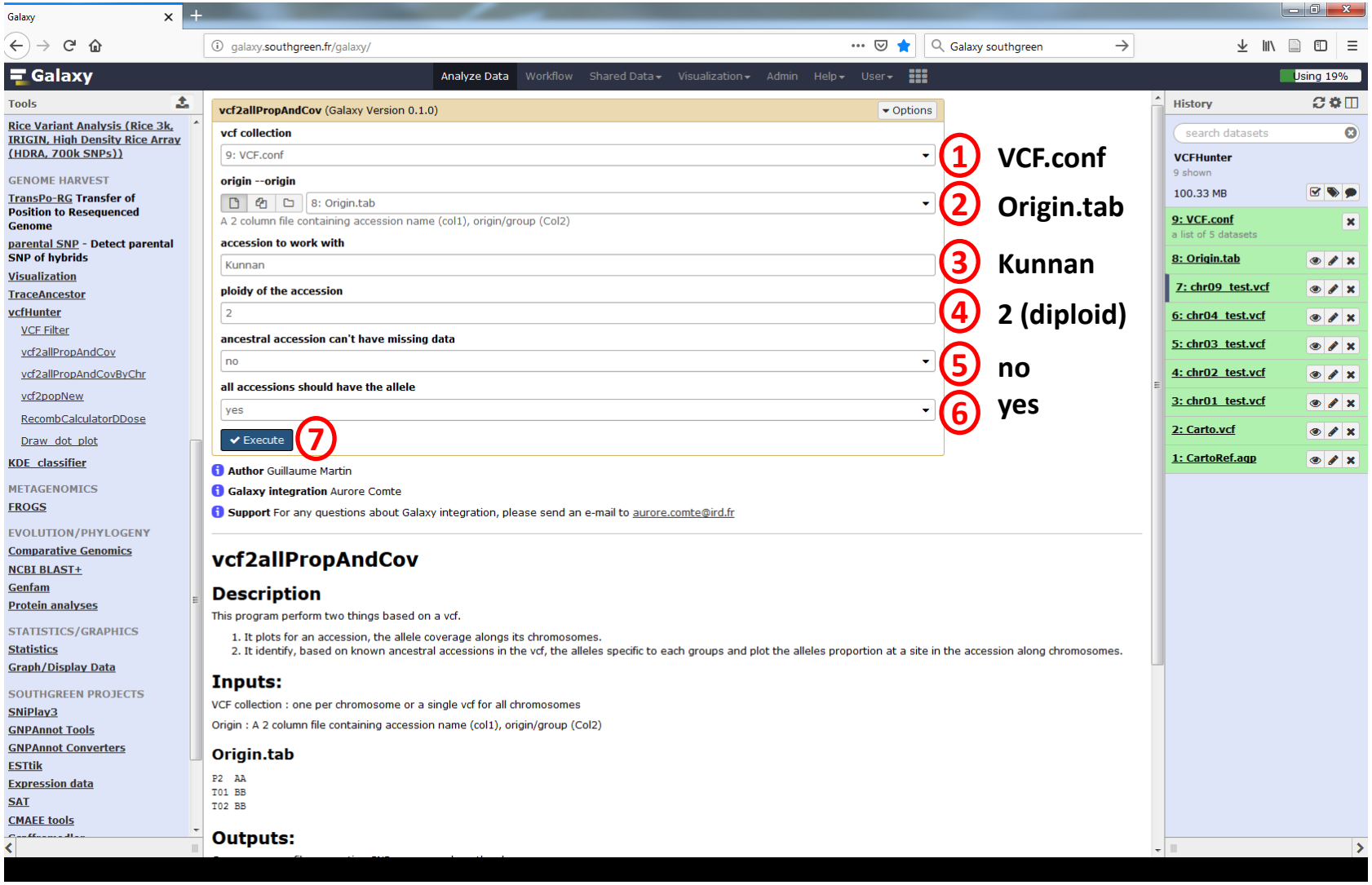
Chromosome painting with vcfHunter tool

1- Chromosome painting of one accession



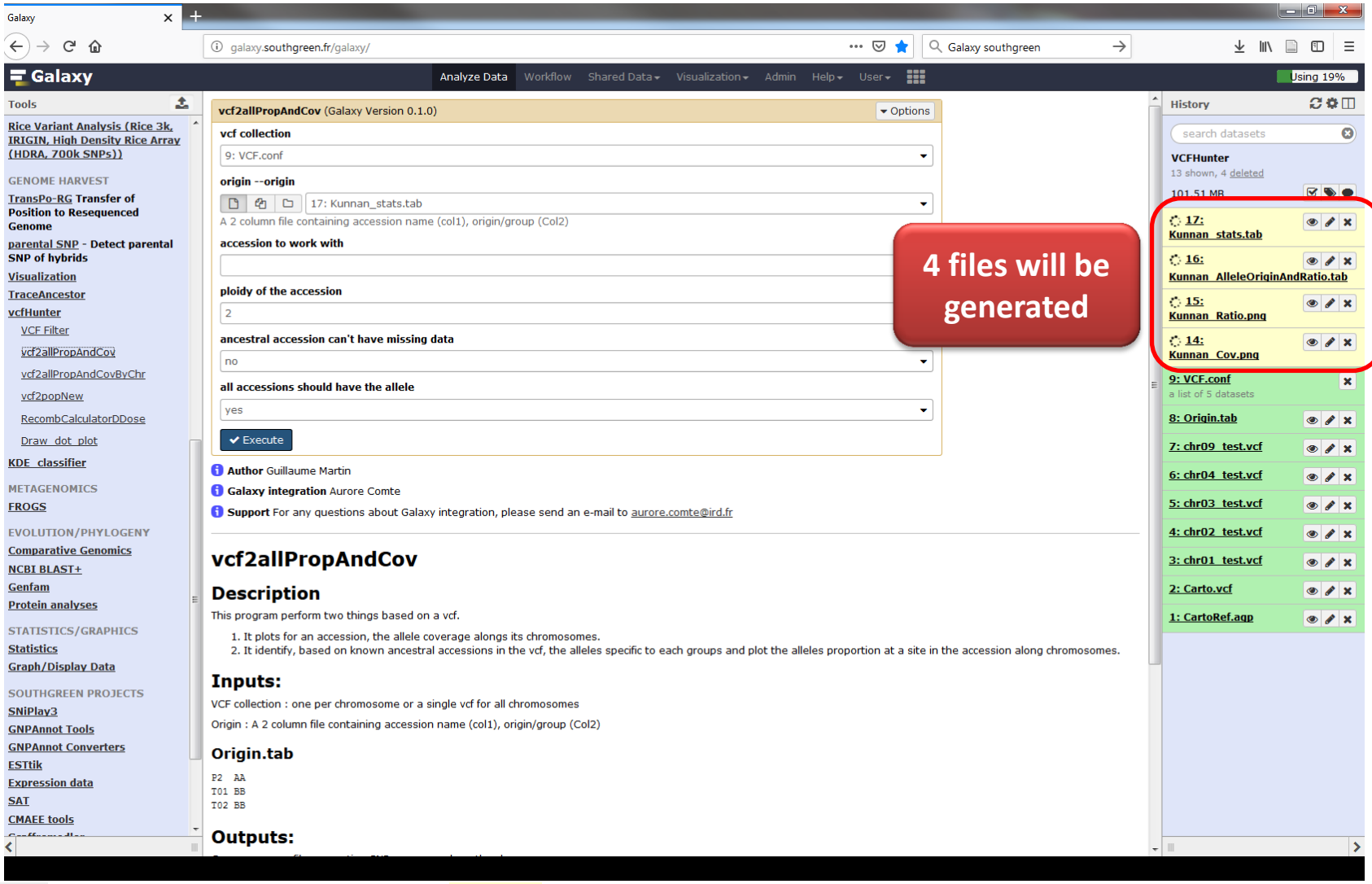
Chromosome painting with vcfHunter tool

1- Chromosome painting of one accession



Chromosome painting with vcfHunter tool

1- Chromosome painting of one accession



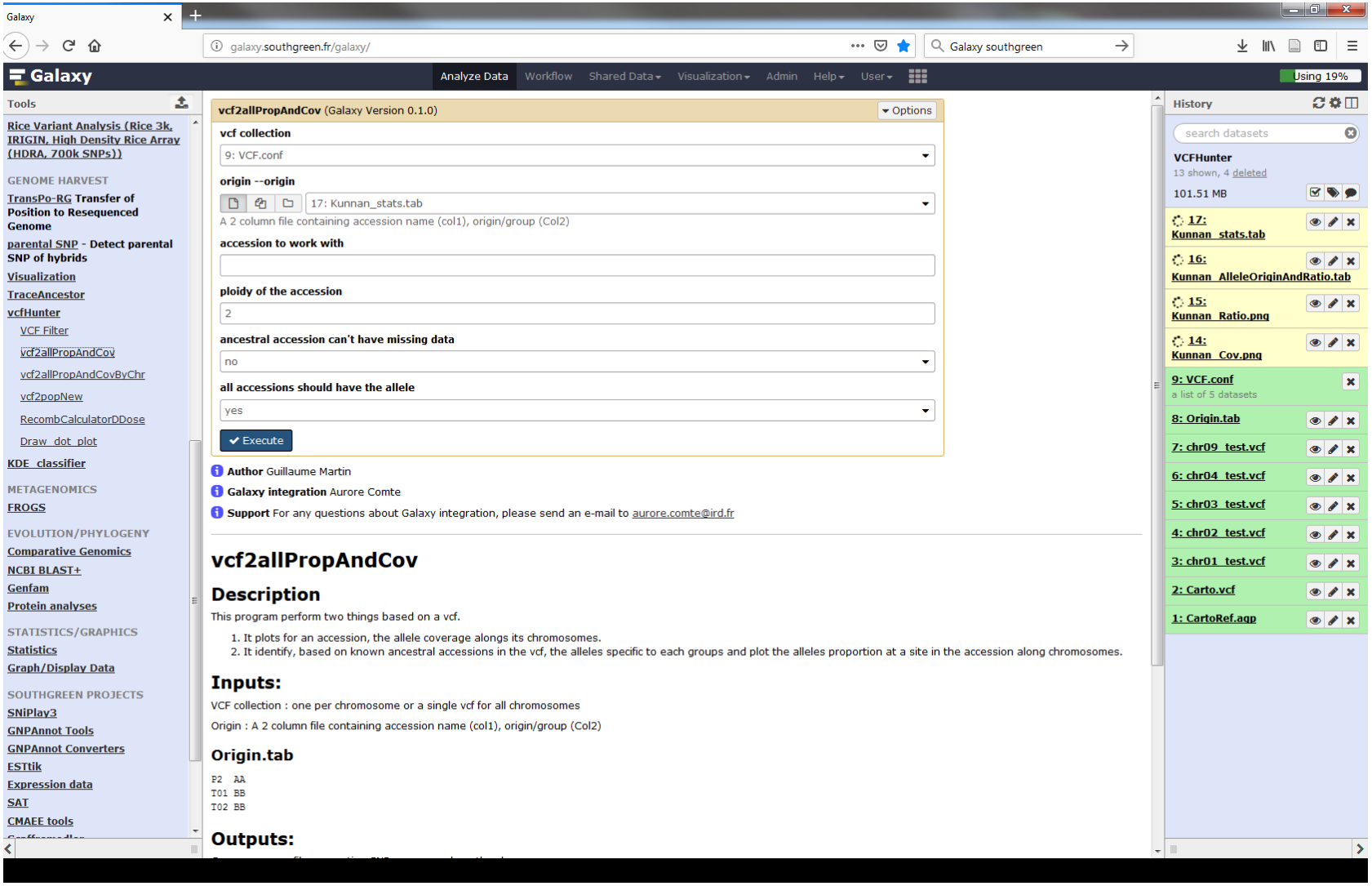
Send to cluster

Running on cluster

21: Finished

Chromosome painting with vcfHunter tool

1- Chromosome painting of one accession



Chromosome painting with vcfHunter tool

1- Chromosome painting of one accession : How the program work?

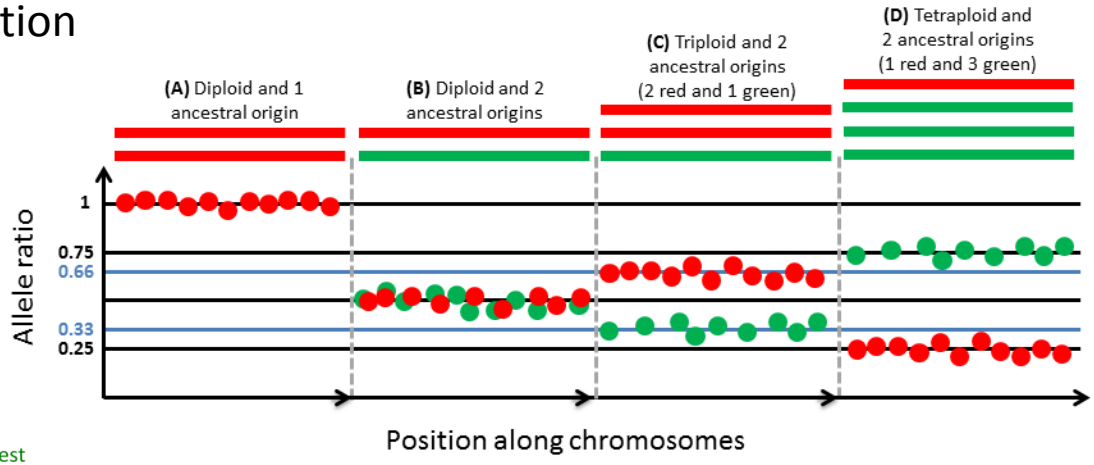
- Based on the origin.tab file, attribute an allele to an ancestral group according to the following rule:
  - ✓ If the allele is found **only** in member of an ancestral group (*i.e.* absent from all member of the other(s) group(s)), then the allele is attributed to this group.

- Possible variants to the rule:
  - ✓ Allele should be present in all member of the ancestral group (“yes” or “no”)

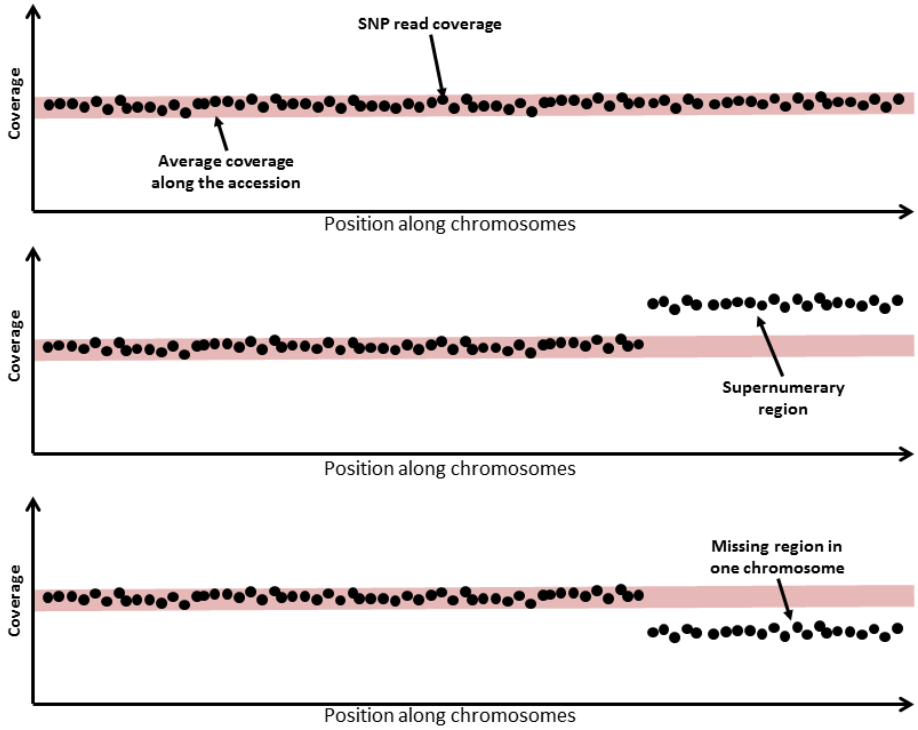
  - ✓ Missing data are accepted in member of ancestral group (“yes” or “no”)

- Calculate, in the studied accession, the proportion of read having this allele

- Plot this proportion

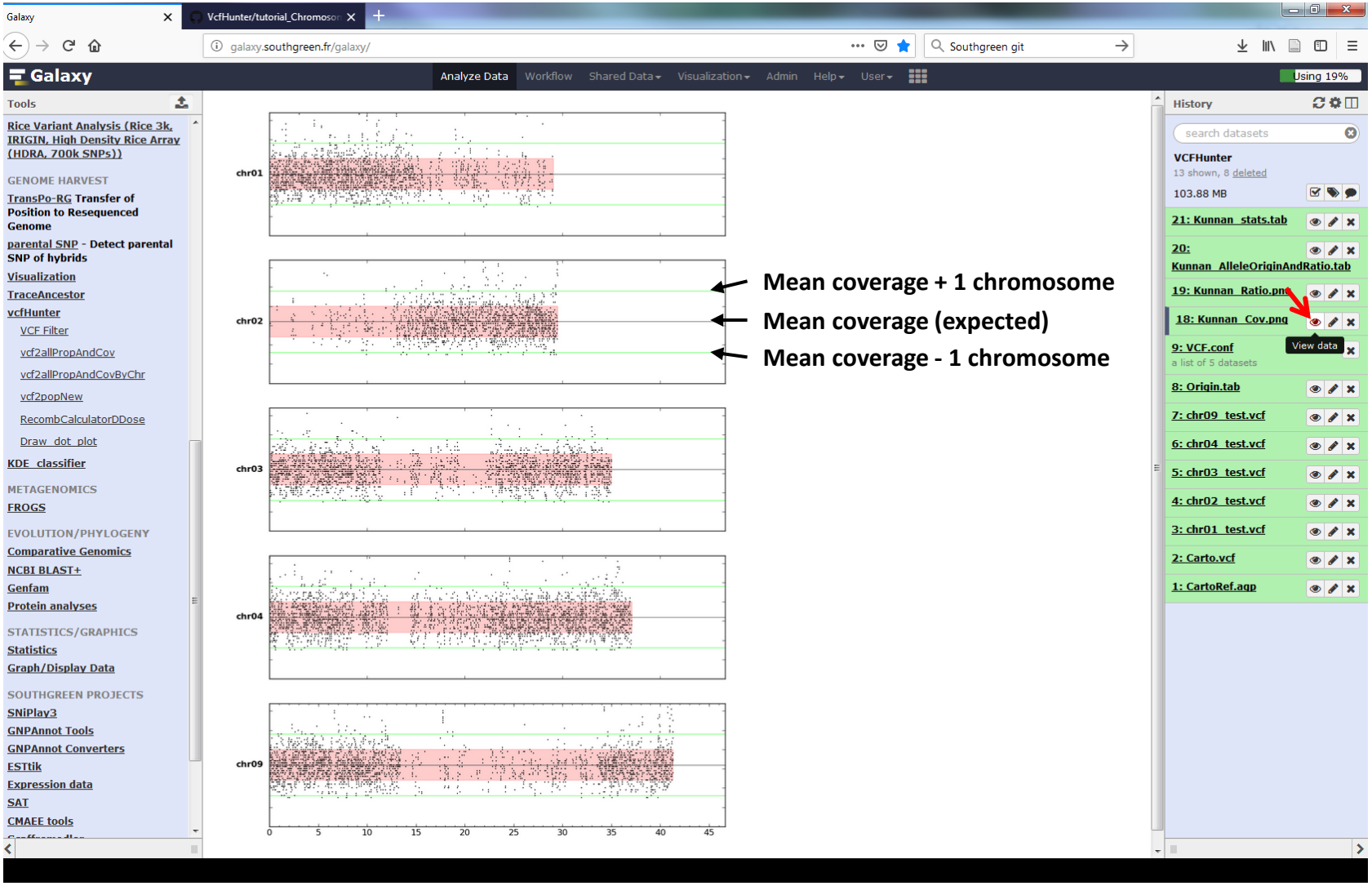


- Plot normalized variant site coverage



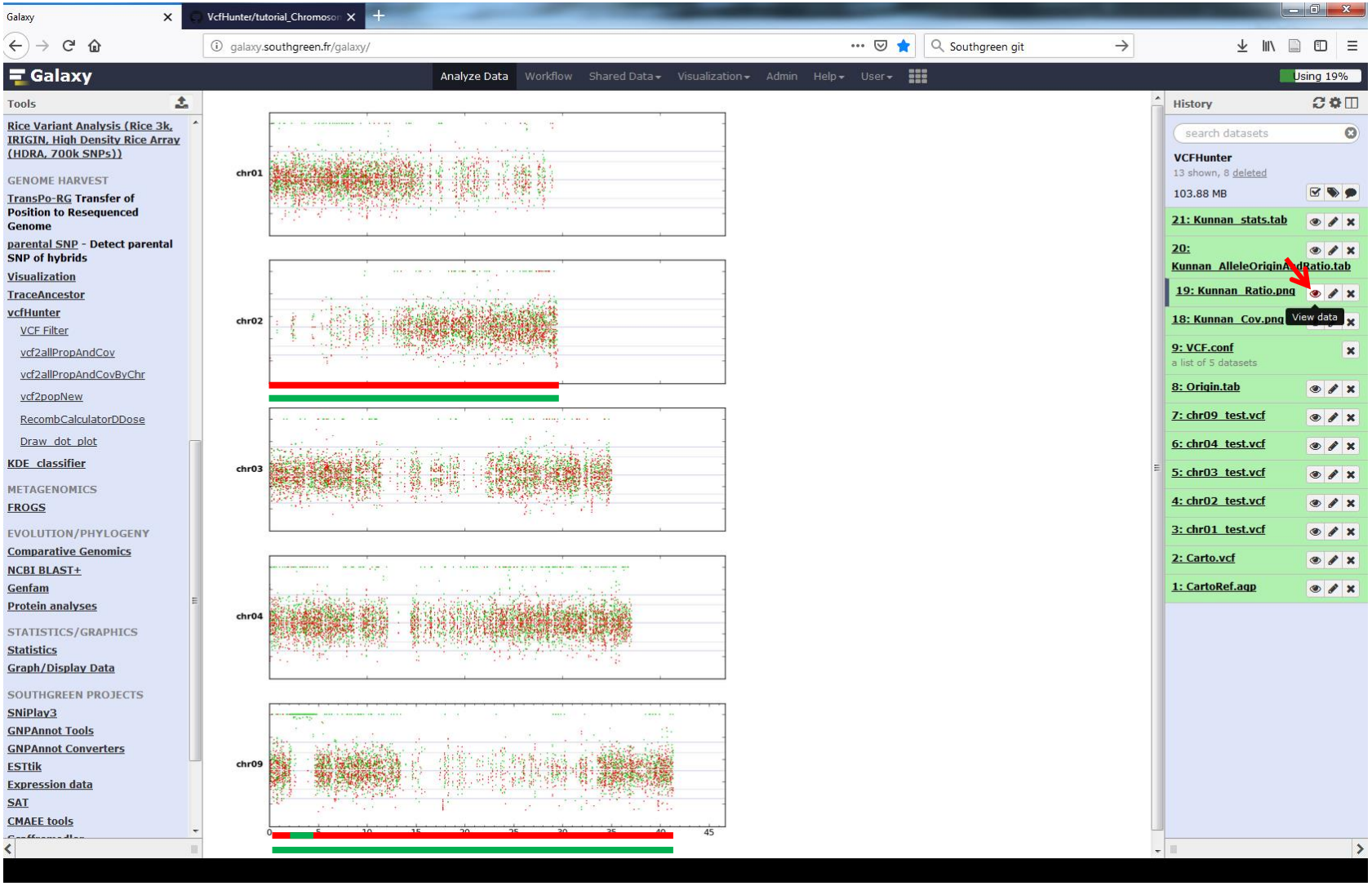
Chromosome painting with vcfHunter tool

1- Chromosome painting of one accession : Outputs description



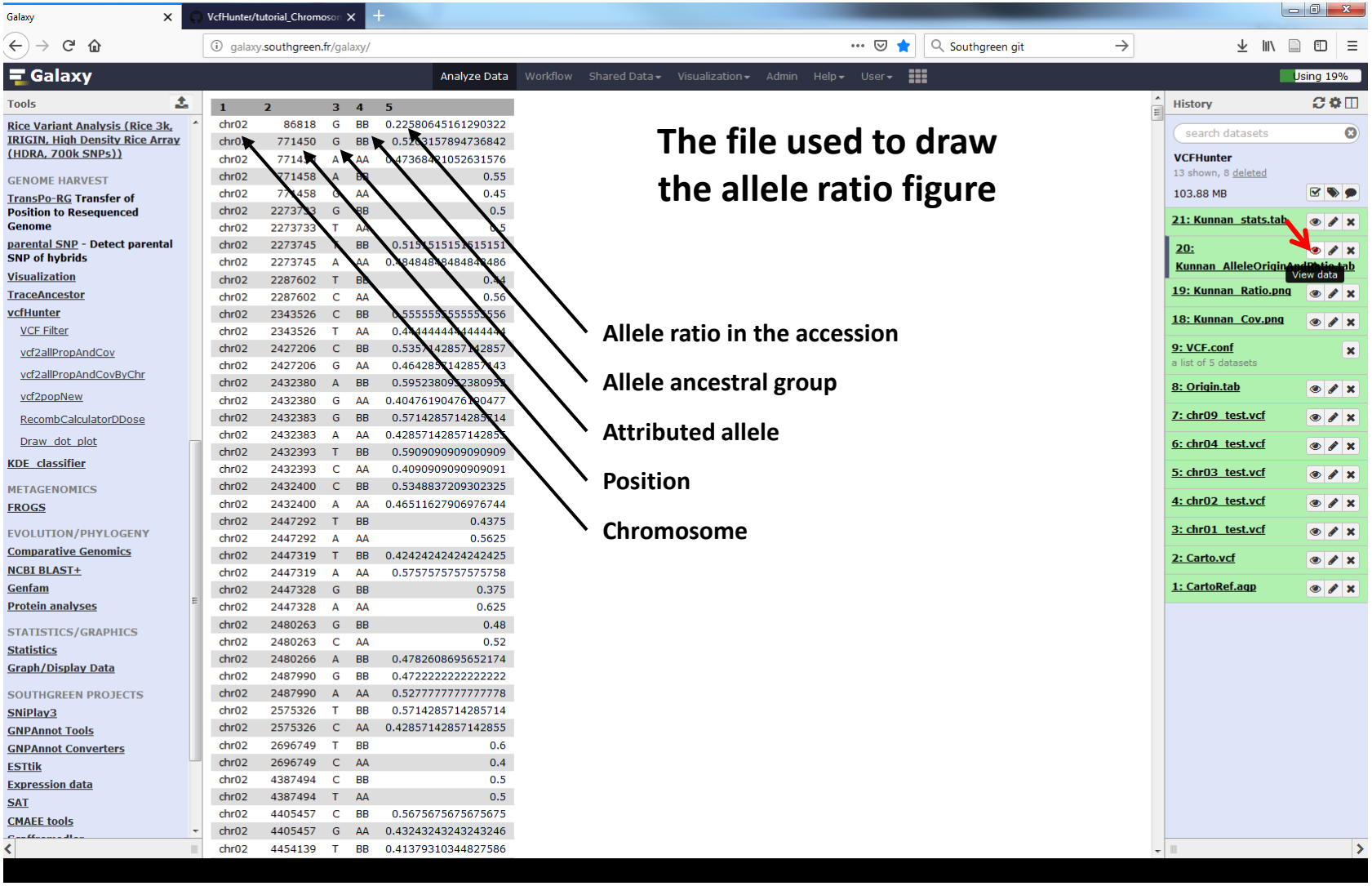
Chromosome painting with vcfHunter tool

1- Chromosome painting of one accession : Outputs description



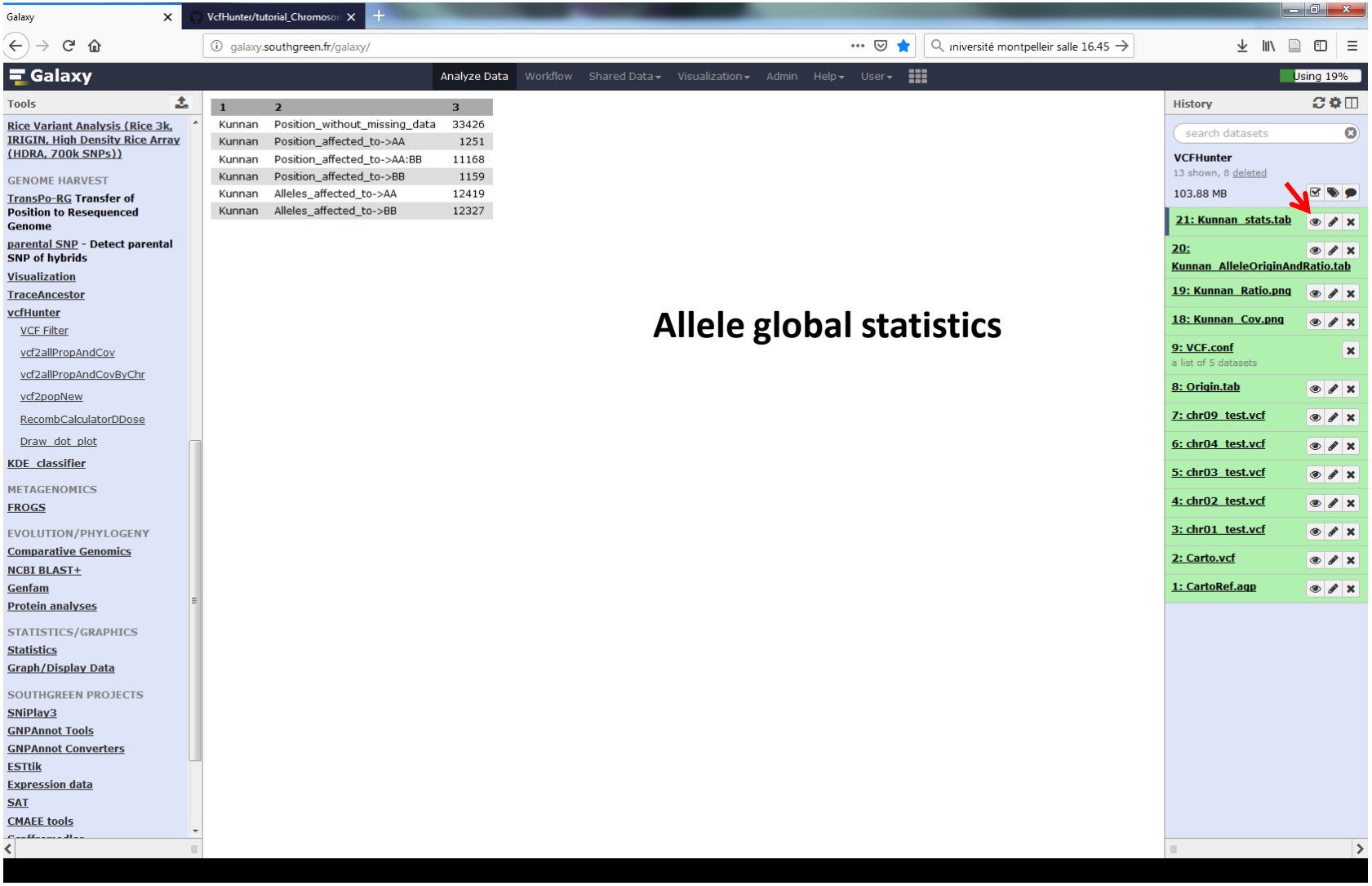
Chromosome painting with vcfHunter tool

1- Chromosome painting of one accession : Outputs description



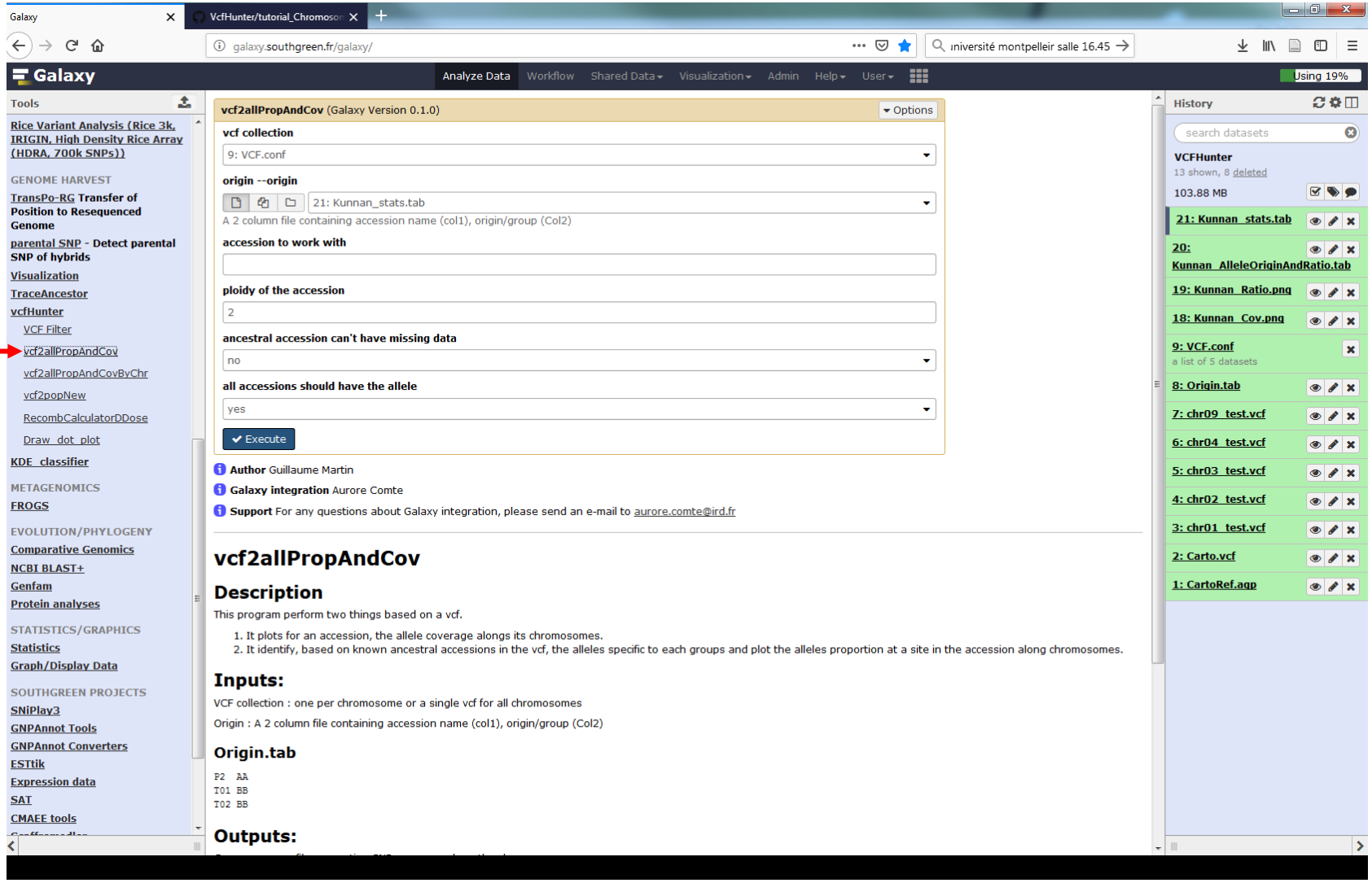
Chromosome painting with vcfHunter tool

1- Chromosome painting of one accession : Outputs description



Chromosome painting with vcfHunter tool

1- Chromosome painting of one accession : To go further



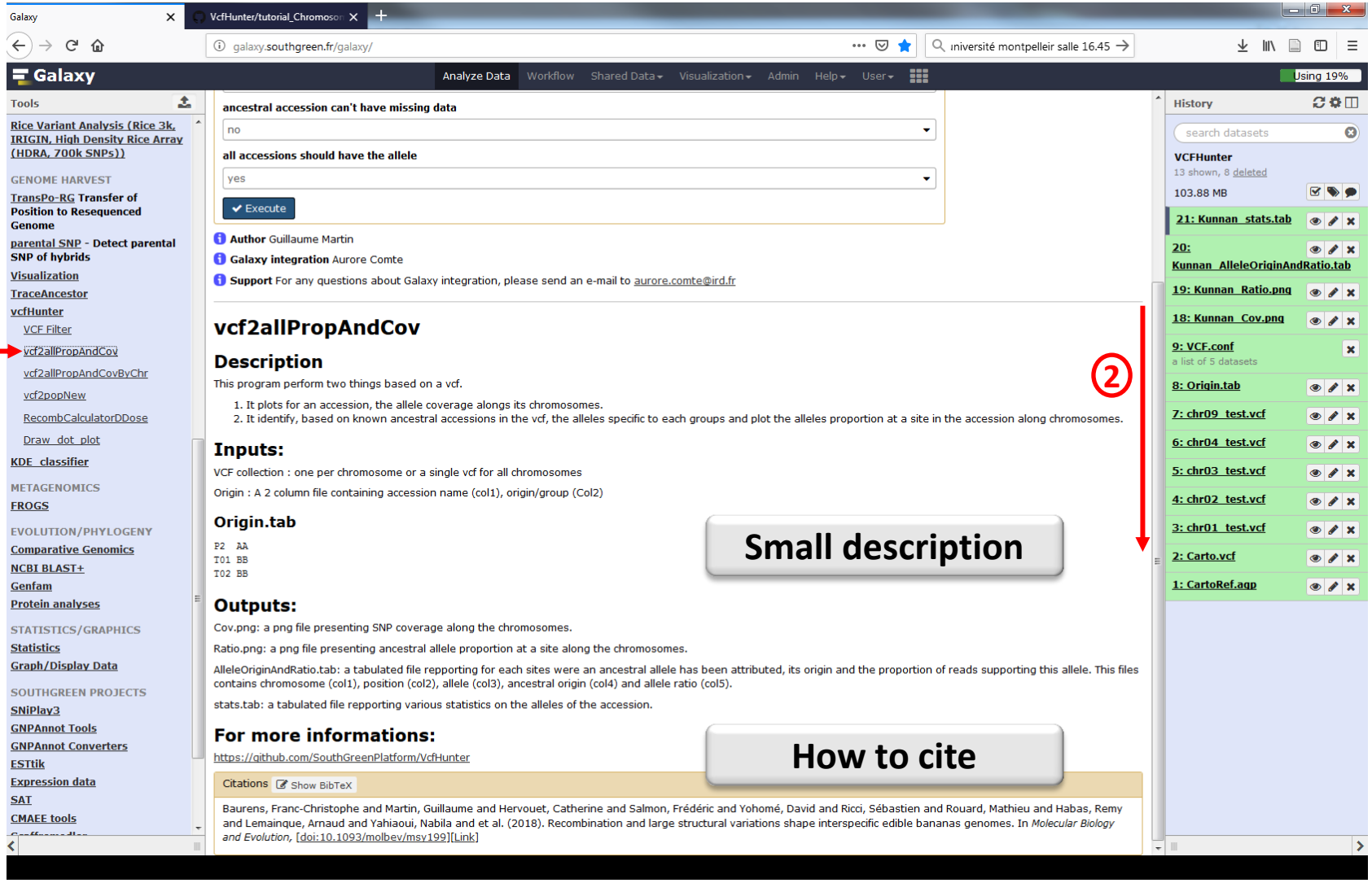
①

Running the analysis with other options, other accessions of the vcf.

Other hybrids names in the vcf GP1 (triploid), P1 (tetraploid) and P025 (triploid)

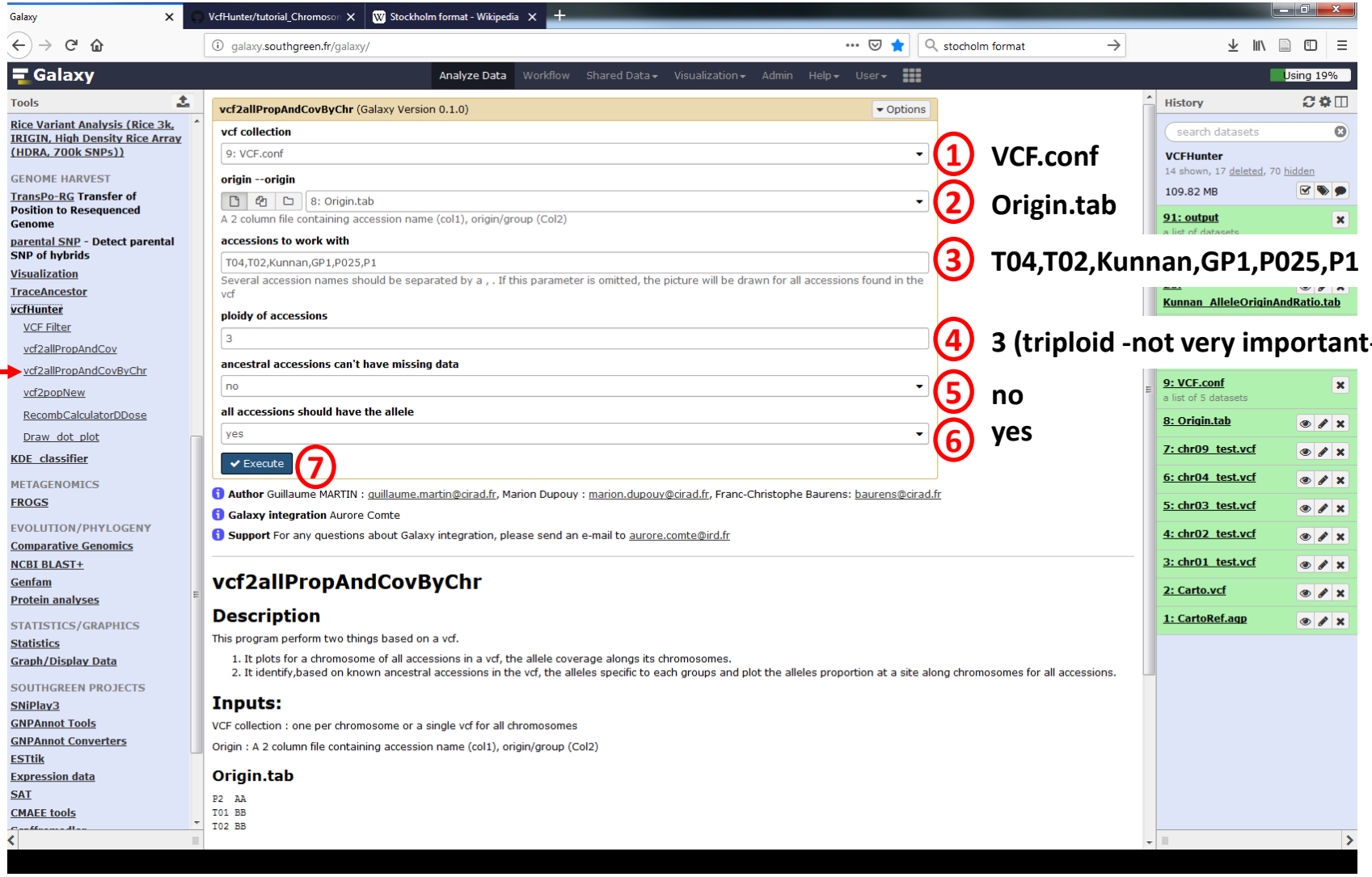
Chromosome painting with vcfHunter tool

1- Chromosome painting of one accession : Additional information



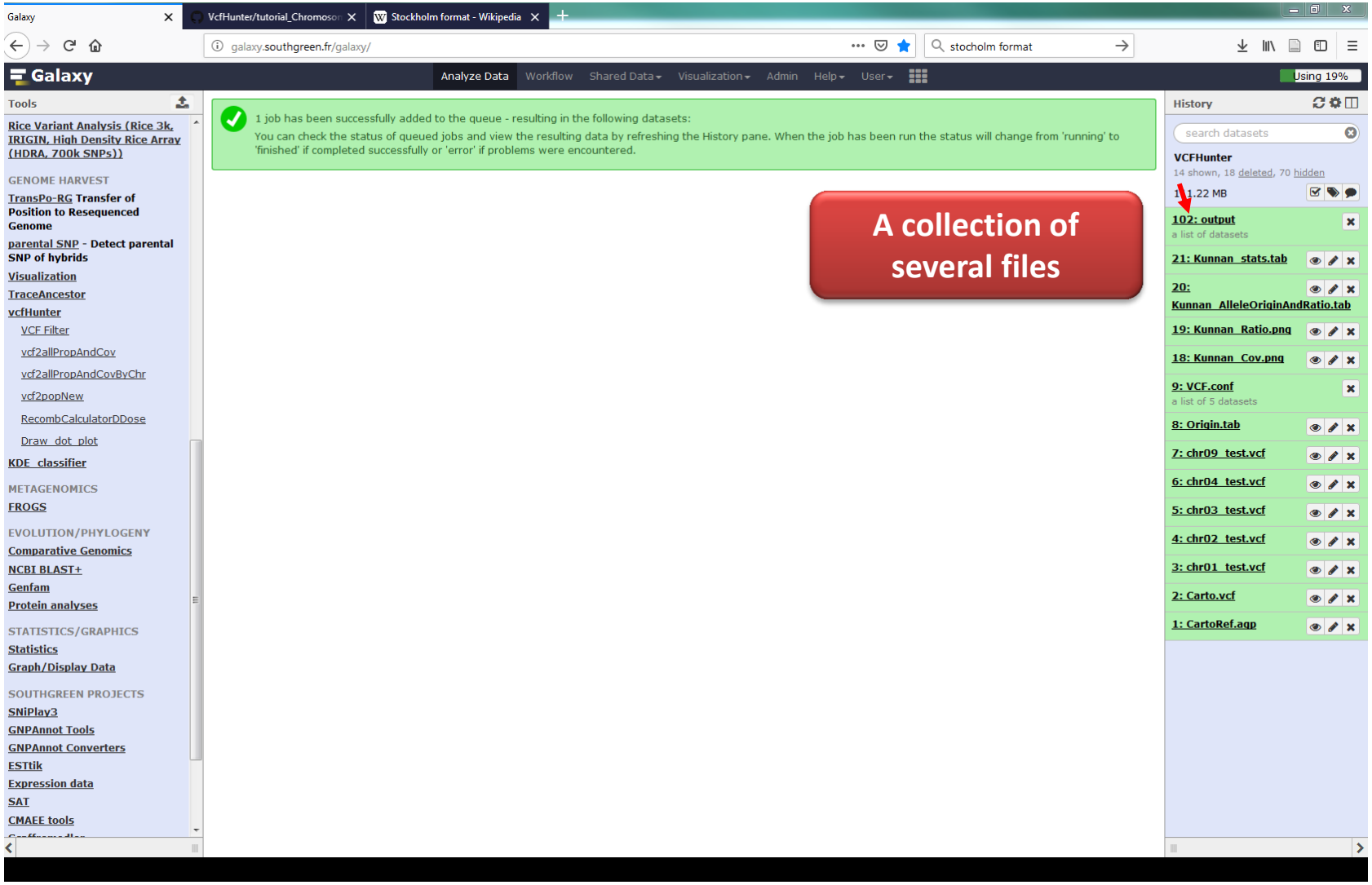
Chromosome painting with vcfHunter tool

2- Comparison of several accessions



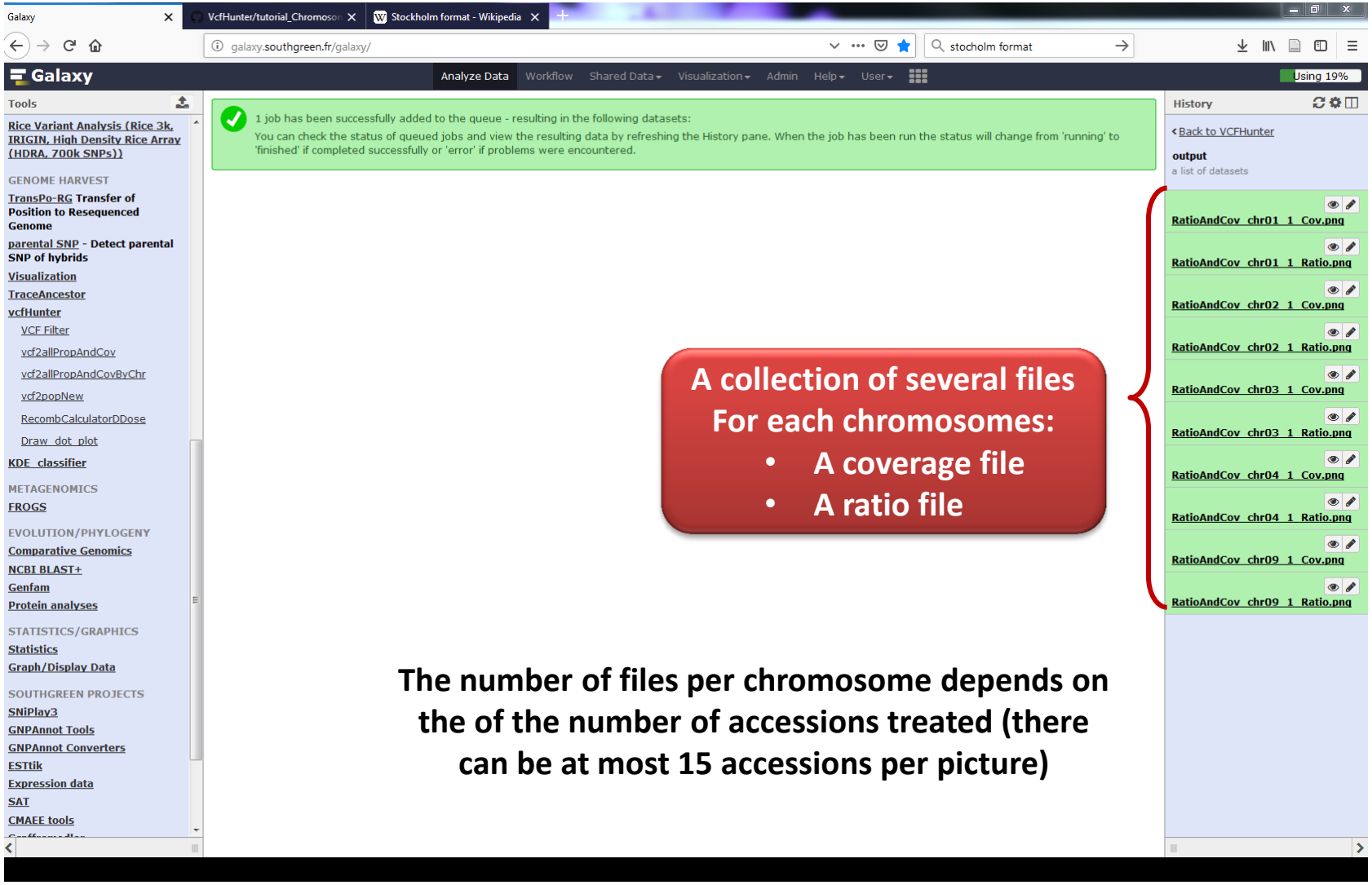
Chromosome painting with vcfHunter tool

2- Comparison of several accessions: output description



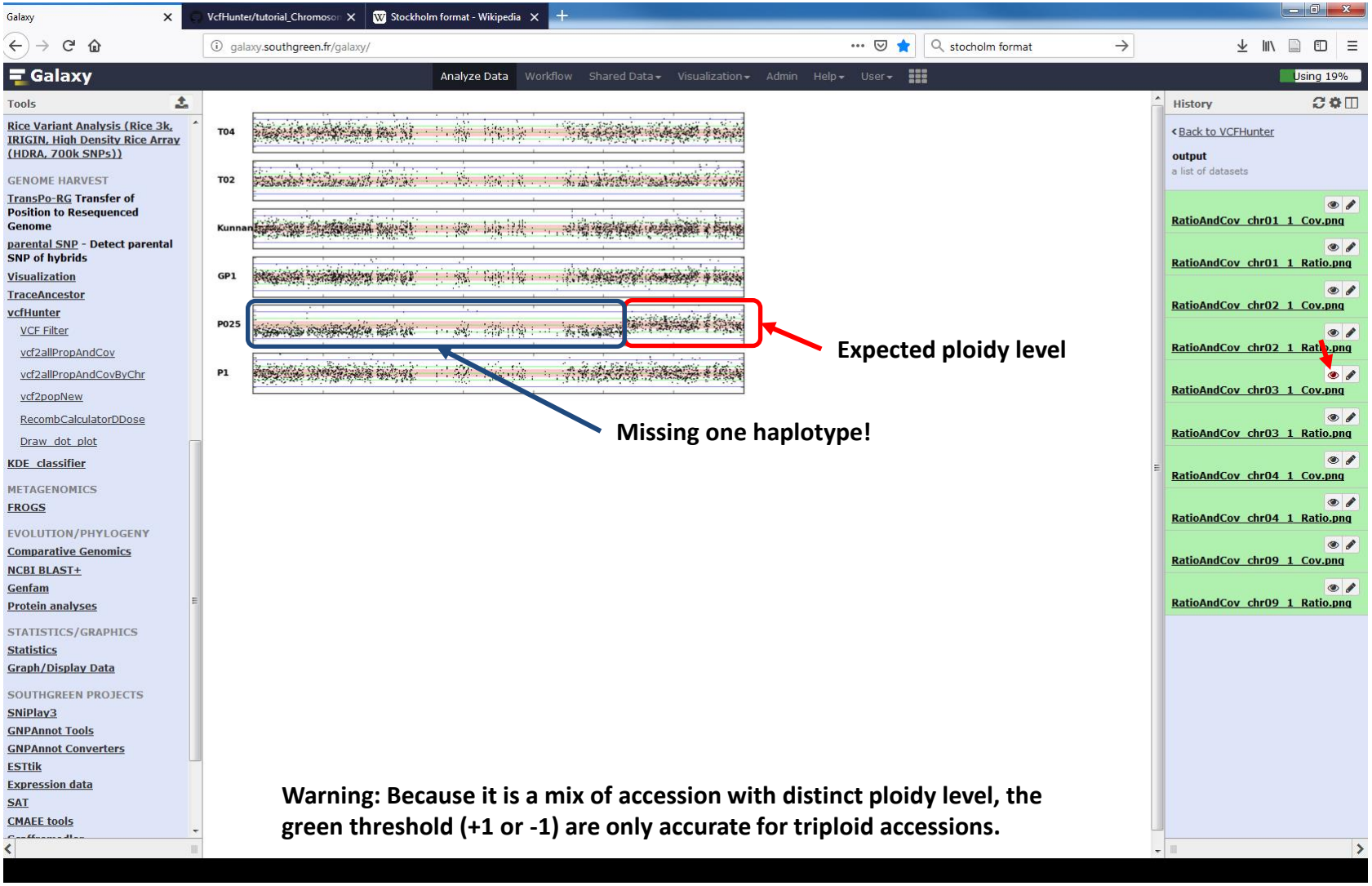
Chromosome painting with vcfHunter tool

2- Comparison of several accessions: output description



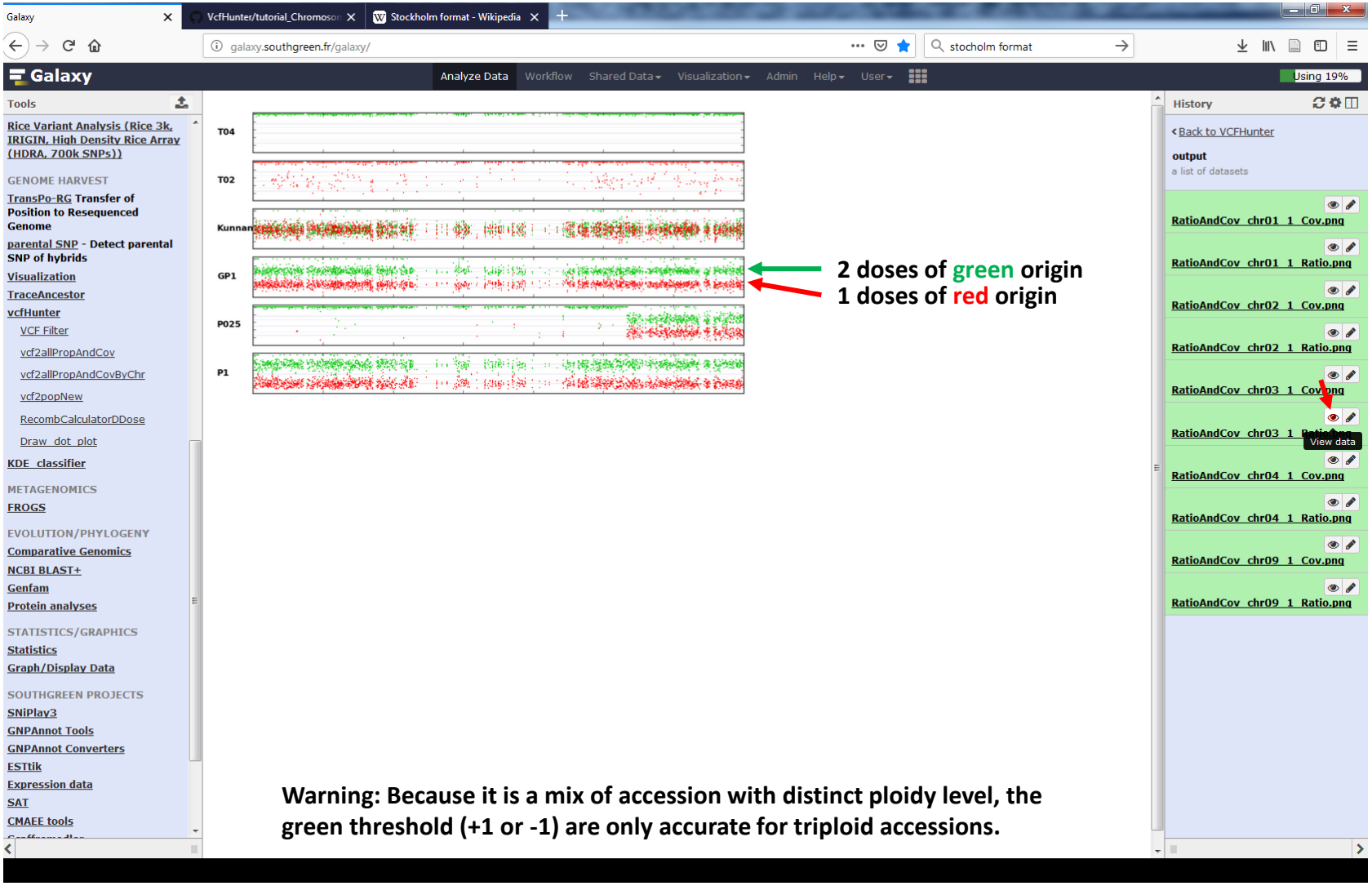
Chromosome painting with vcfHunter tool

2- Comparison of several accessions: output description



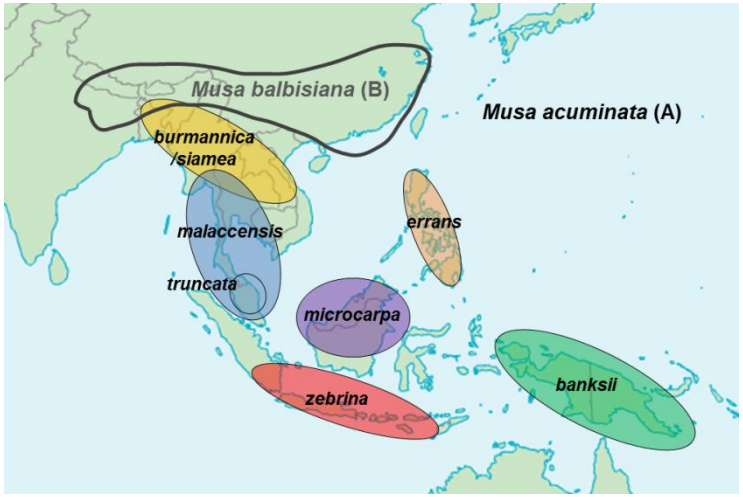
Chromosome painting with vcfHunter tool

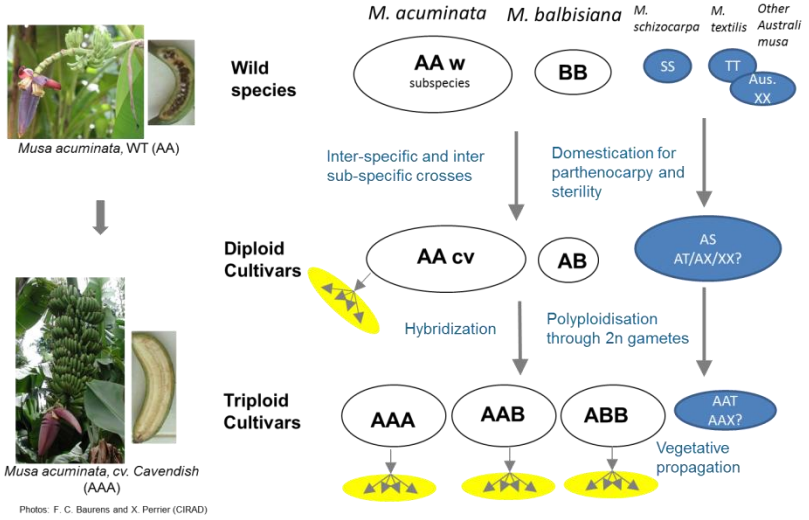
2- Comparison of several accessions: output description



Genetic mapping analysis with vcfHunter tool

Developed to answer banana problematics





- Cultivated banana are hybrids between distinct species and subspecies showing chromosomal structural rearrangements

What are the chromosomal structures of species and subspecies implicated in cultivated bananas?

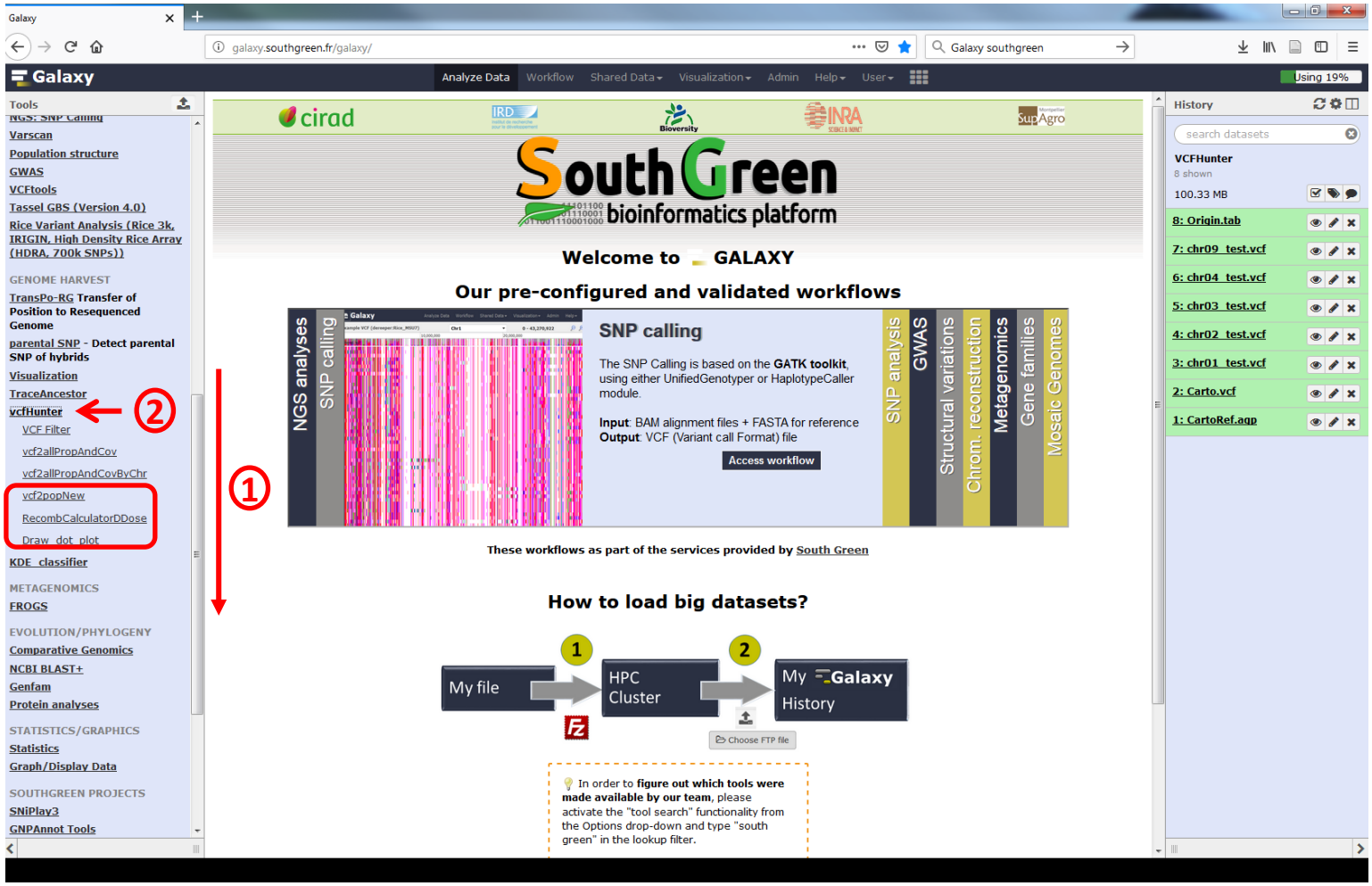
What are the consequences of these structural variations on chromosomal pairing, recombination and segregation?

Genetic mapping analysis with vcfHunter tool

What are the chromosomal structures of plants?

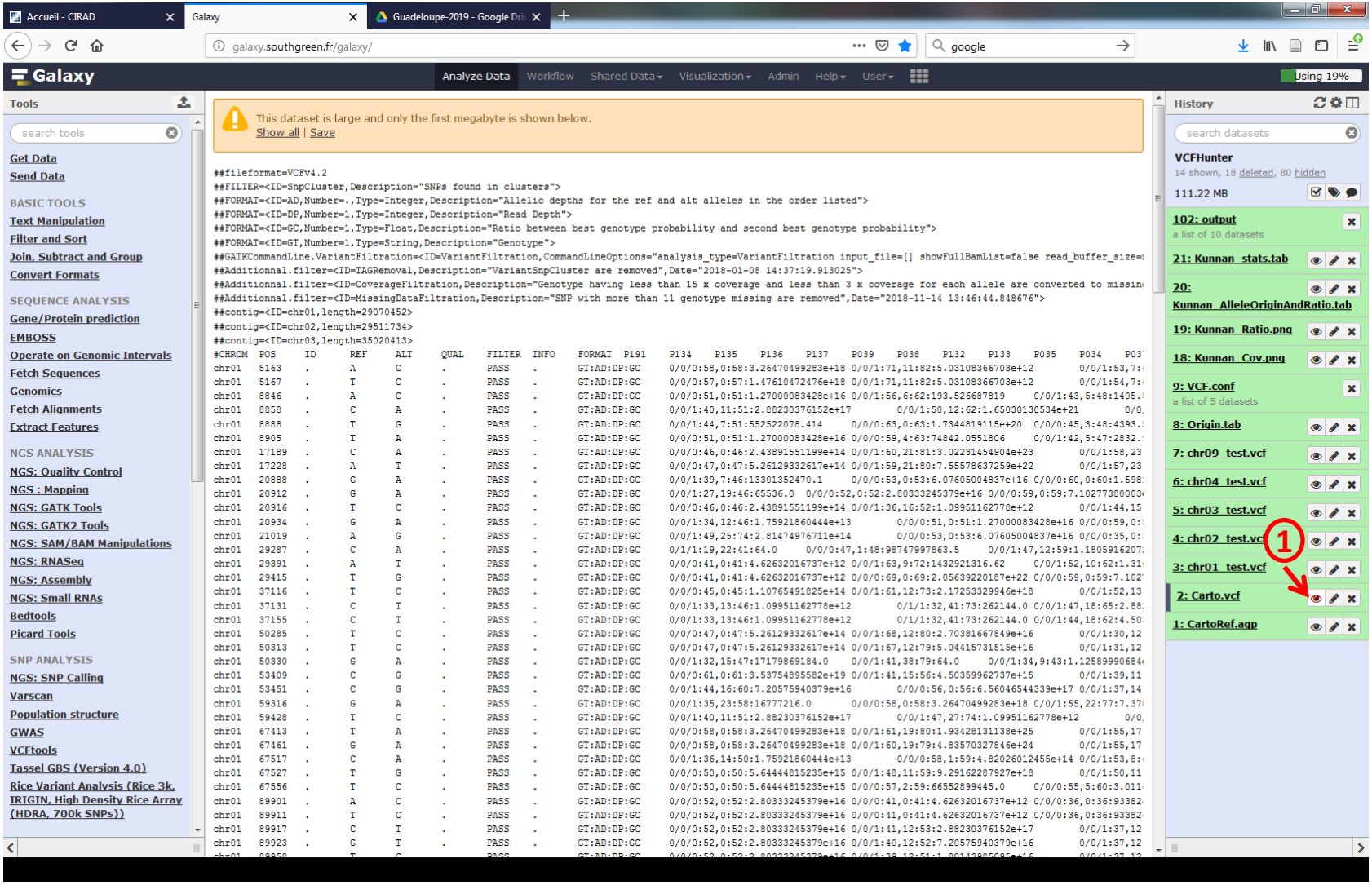
What are the consequences of these structural variations on chromosomal pairing, recombination and segregation

Several tools developed under vcfHunter toolbox for this purpose:



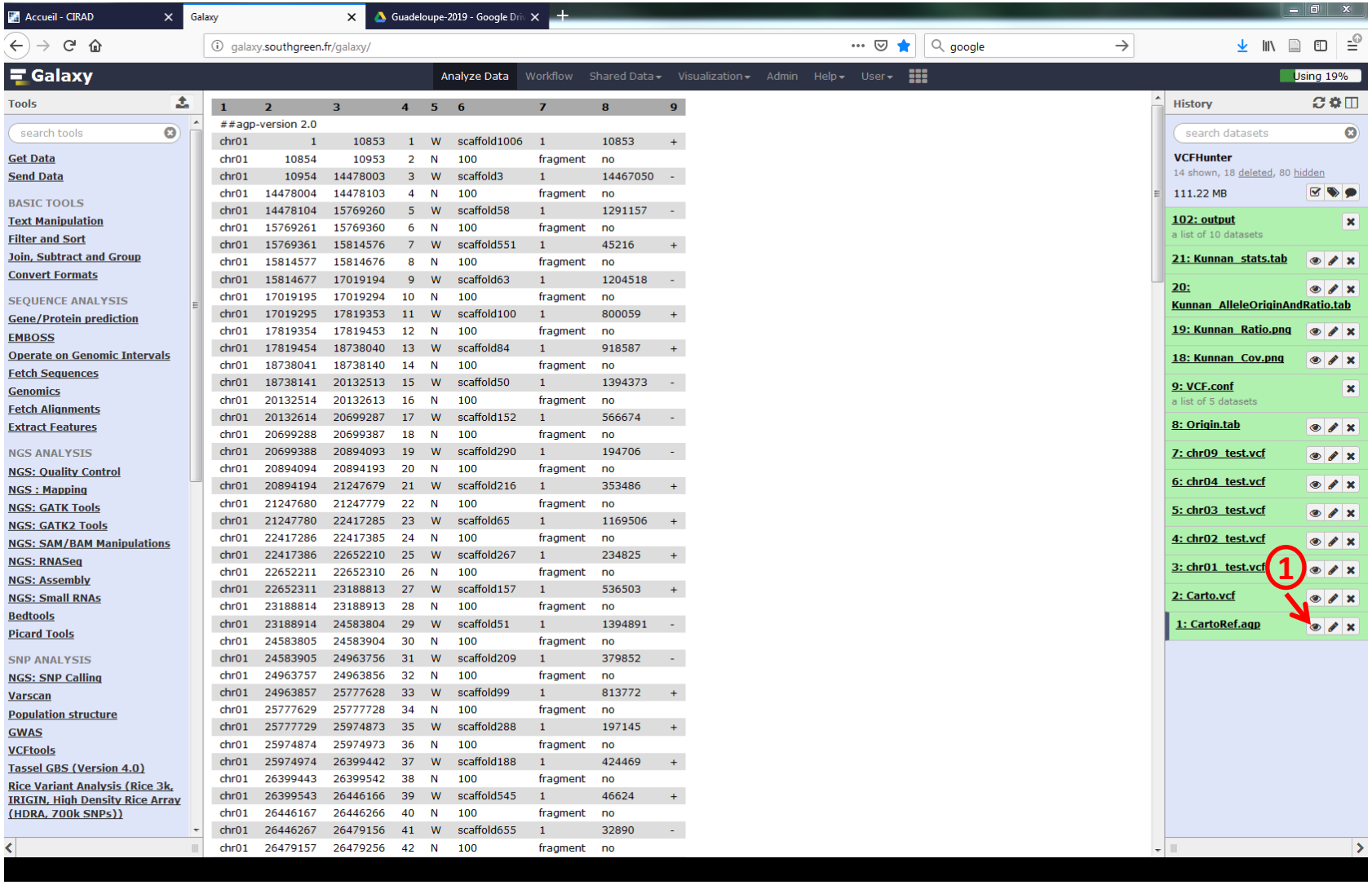
Genetic mapping analysis with vcfHunter tool

Used data: A vcf file containing genotypes for each individuals of a mapping population



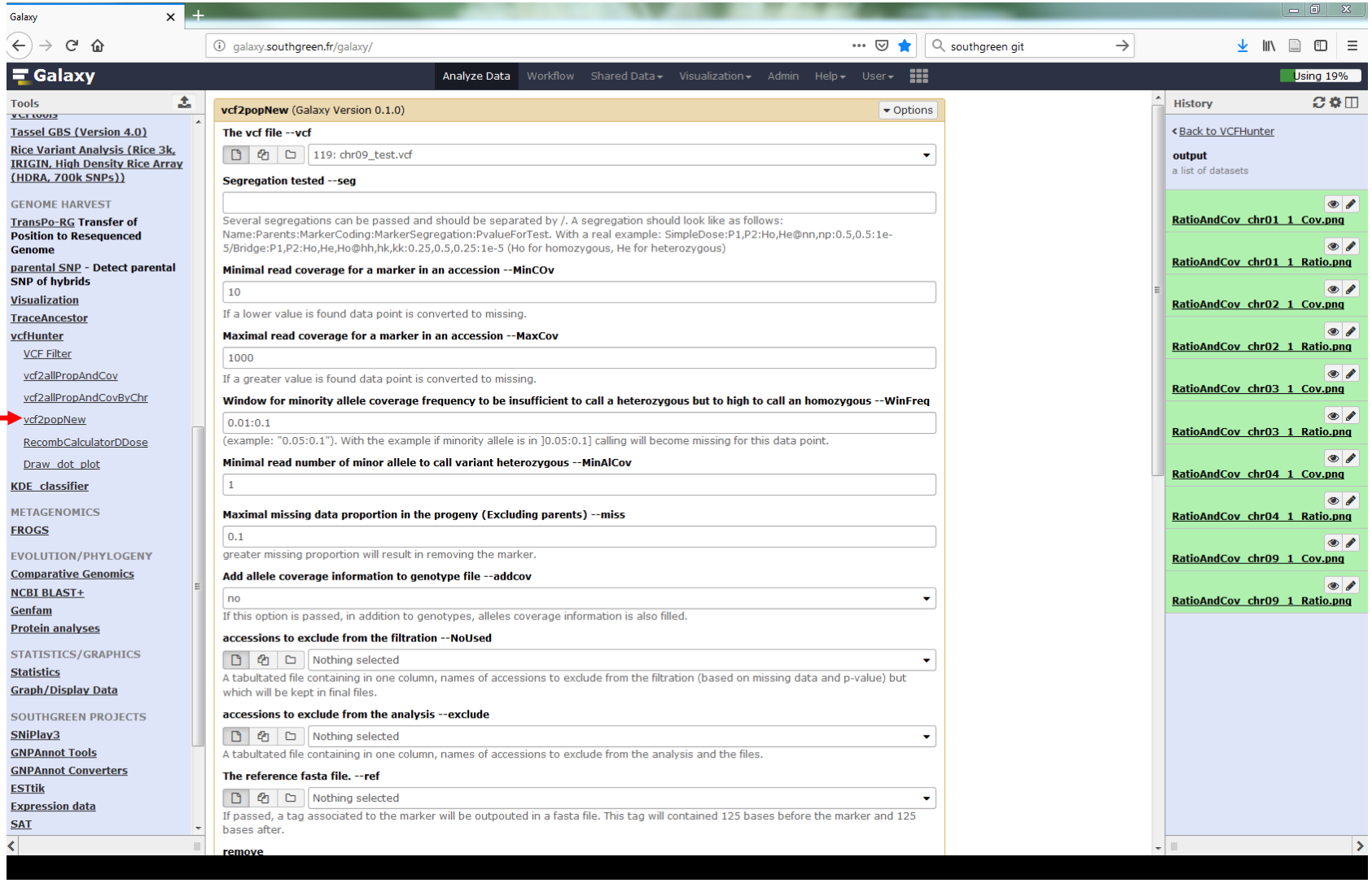
Genetic mapping analysis with vcfHunter tool

Used data: An agp file locating scaffolds in the reference assembly



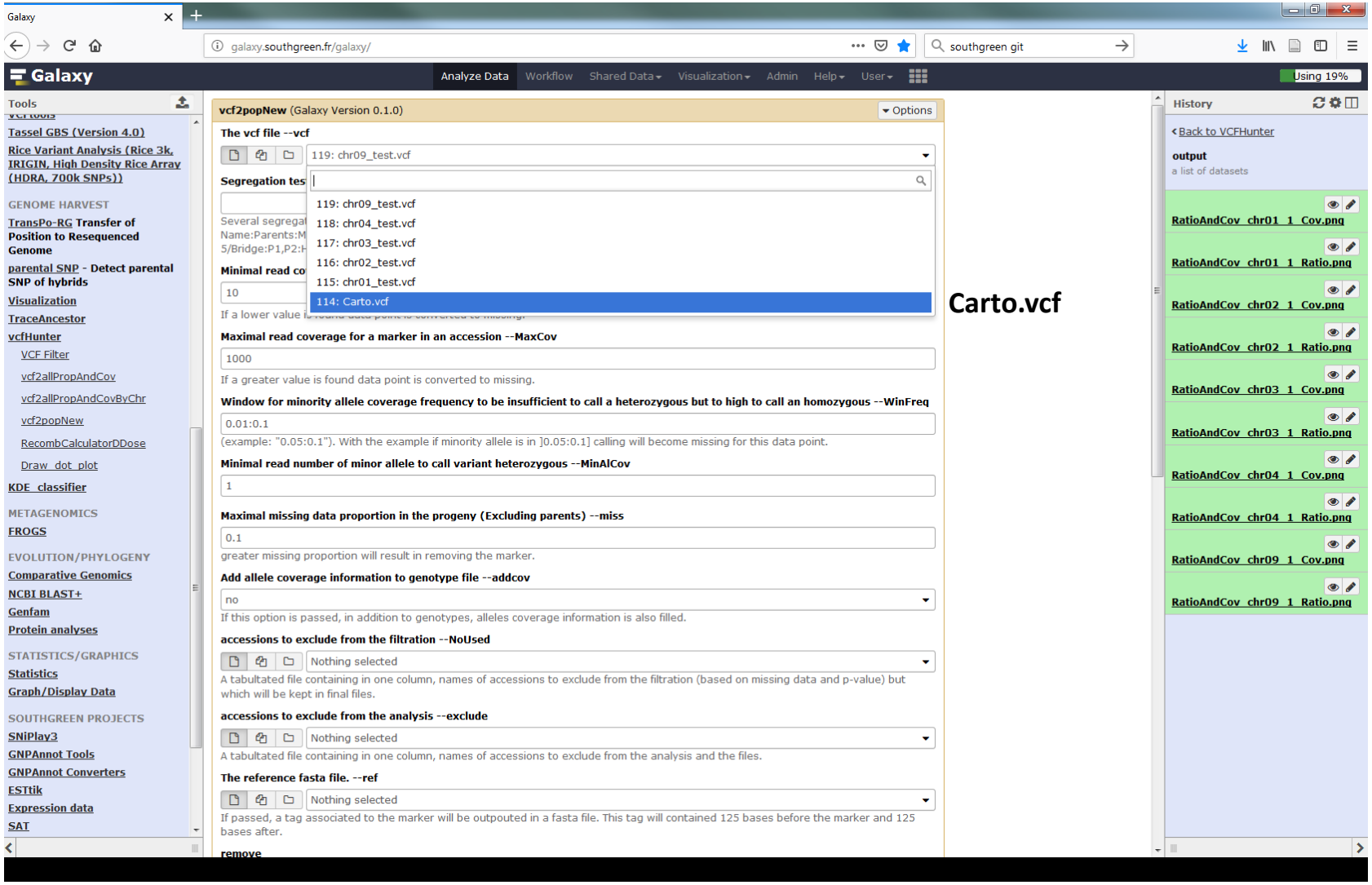
Genetic mapping analysis with vcfHunter tool

Selecting segregating markers in vcf files: vcf2PopNew



Genetic mapping analysis with vcfHunter tool

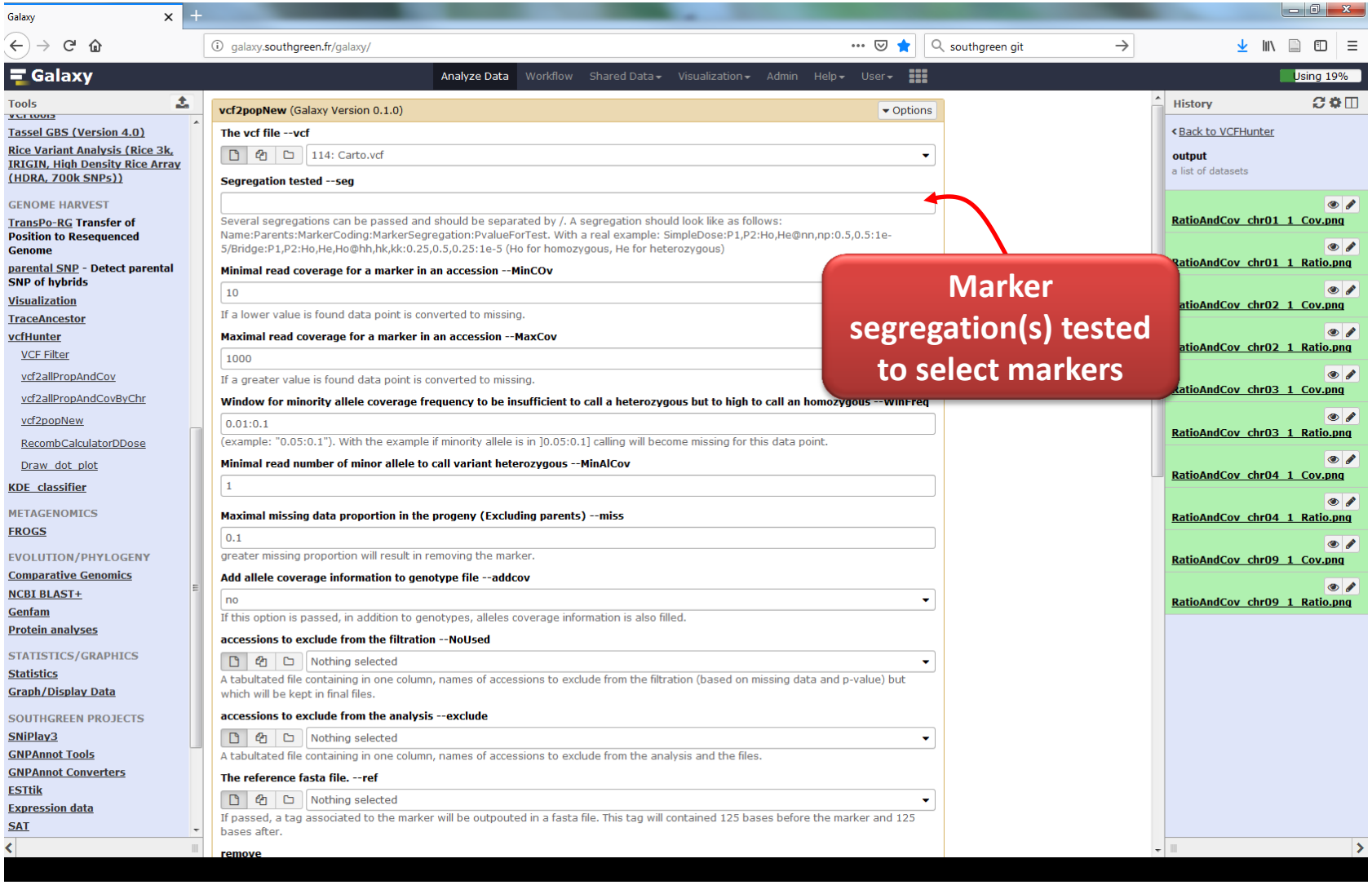
Selecting segregating markers in vcf files: vcf2PopNew



Carto.vcf

Genetic mapping analysis with vcfHunter tool

Selecting segregating markers in vcf files: vcf2PopNew



The expected marker segregation depends of the cross studied:

- ✓ Selfing of an heterozygous diploid accession:

	A	**C**
A	AA	AC
C	AC	CC

recoding →

	A=h	**C=k**
A=h	hh	hk
C=k	hk	kk

Expected proportions →

25% hh
50% hk
25% kk

Max tolerated χ^2 p-value →

$1e^{-10}$

Homozygous = Ho
Heterozygous = He

The expected marker segregation depends of the cross studied:

- ✓ Selfing of an heterozygous diploid accession:

Homozygous = Ho
Heterozygous = He

	A	**C**
A	AA	AC
C	AC	CC

recoding →

	A=h	**C=k**
A=h	hh	hk
C=k	hk	kk

Expected proportions →
25% hh
50% hk
25% kk

Max tolerated χ^2 p-value → $1e^{-10}$

Bridge:P1,P2:Ho,He,Ho@hh,hk,kk:0.25,0.5,0.25:1e-10

The expected marker segregation depends of the cross studied:

Homozygous = Ho
Heterozygous = He

✓ Selfing of an heterozygous diploid accession:

	A	C
A	AA	AC
C	AC	CC

recoding →

	A=h	C=k
A=h	hh	hk
C=k	hk	kk

Expected proportions →
25% hh
50% hk
25% kk

Max tolerated χ^2 p-value → $1e^{-10}$

Bridge:P1,P2:Ho,He,Ho@hh,hk,kk:0.25,0.5,0.25:1e-10

✓ Cross between two diploid heterozygous accessions:

	A	C
A	AA	AC
C	AC	CC

recoding →

	A=h	C=k
A=h	hh	hk
C=k	hk	kk

Expected proportions →
25% hh
50% hk
25% kk

Max tolerated χ^2 p-value → $1e^{-10}$

	A	C
A	AA	AC
A	AA	AC

recoding →

	A=n	C=p
A=n	nn	np
A=n	nn	np

Expected proportions →
50% nn
50% np

Max tolerated χ^2 p-value → $1e^{-10}$

The expected marker segregation depends of the cross studied:

Homozygous = Ho
Heterozygous = He

✓ Selfing of an heterozygous diploid accession:

	A	C
A	AA	AC
C	AC	CC

recoding →

	A=h	C=k
A=h	hh	hk
C=k	hk	kk

Expected proportions →
25% hh
50% hk
25% kk

Max tolerated χ^2 p-value → $1e^{-10}$

Bridge:P1,P2:Ho,He,Ho@hh,hk,kk:0.25,0.5,0.25:1e-10

✓ Cross between two diploid heterozygous accessions:

	A	C
A	AA	AC
C	AC	CC

recoding →

	A=h	C=k
A=h	hh	hk
C=k	hk	kk

Expected proportions →
25% hh
50% hk
25% kk

Max tolerated χ^2 p-value → $1e^{-10}$

Bridge:P1,P2:Ho,He,Ho@hh,hk,kk:0.25,0.5,0.25:1e-10

	A	C
A	AA	AC
A	AA	AC

recoding →

	A=n	C=p
A=n	nn	np
A=n	nn	np

Expected proportions →
50% nn
50% np

Max tolerated χ^2 p-value → $1e^{-10}$

SimpleDose:P1,P2:Ho,He@nn,np:0.5,0.5:1e-10

The expected marker segregation depends of the cross studied:

Homozygous = Ho
Heterozygous = He

- ✓ Selfing of an heterozygous diploid accession with an heterozygous tetraploid accession: An additional segregation tested: double dose markers (e.g: P2 genotype = A/A/C/C, P1 genotype = C/C)

	A	A
AA	AAA	AAA
CC	ACC	ACC
AC	AAC	AAC
AC	AAC	AAC
AC	AAC	AAC
AC	AAC	AAC

recoding →

	A	A
AA=hh	hh	hh
CC=kk	k-	k-
AC=hk	k-	k-
AC=hk	k-	k-
AC=hk	k-	k-
AC=hk	k-	k-

Expected proportions → 1/6 hh, 5/6 k-

Max tolerated χ^2 p-value → $1e^{-7}$

The expected marker segregation depends of the cross studied:

Homozygous = Ho
Heterozygous = He

- ✓ Selfing of an heterozygous diploid accession with an heterozygous tetraploid accession: An additional segregation tested: double dose markers (e.g: P2 genotype = A/A/C/C, P1 genotype = C/C)

	A	A
AA	AAA	AAA
CC	ACC	ACC
AC	AAC	AAC
AC	AAC	AAC
AC	AAC	AAC
AC	AAC	AAC

recoding →

	A	A
AA=hh	hh	hh
CC=kk	k-	k-
AC=hk	k-	k-
AC=hk	k-	k-
AC=hk	k-	k-
AC=hk	k-	k-

Expected proportions → 1/6 hh, 5/6 k-

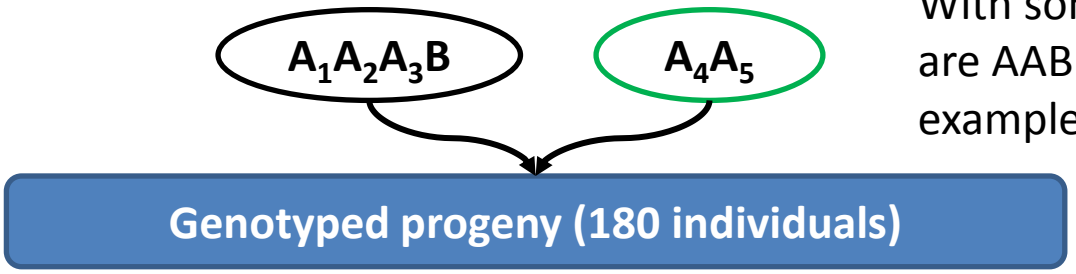
Max tolerated χ^2 p-value → $1e^{-7}$

DoubleDose:P1,P2:Ho,He@hh,k-:0.1667,0.8333:1e-7

The expected marker segregation depends of the cross studied:

- ✓ Selfing of an heterozygous diploid accession with an heterozygous tetraploid accession: An additional segregation tested: double dose markers

- ✓ This is the type of cross we have in our example!



With some regions which are AABB or $A_1A_1A_2B$ for example

- ✓ We will select markers for several segregations

DoubleDose:P1,P2:Ho,He@hh,k-:0.1667,0.8333:1e-7

Bridge:P1,P2:Ho,He,Ho@hh,hk,kk:0.25,0.5,0.25:1e-10

SimpleDose:P1,P2:Ho,He@nn,np:0.5,0.5:1e-10

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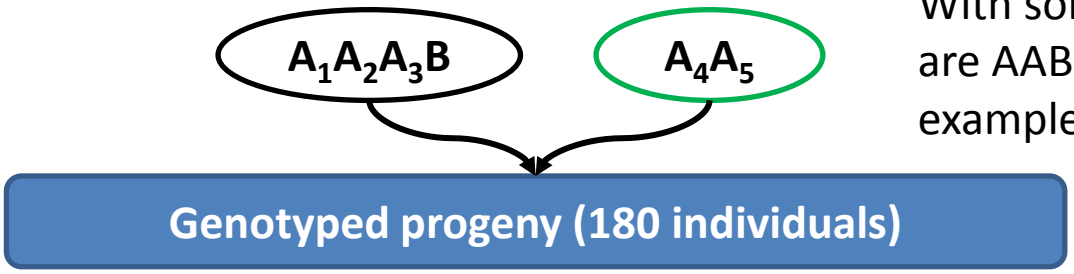

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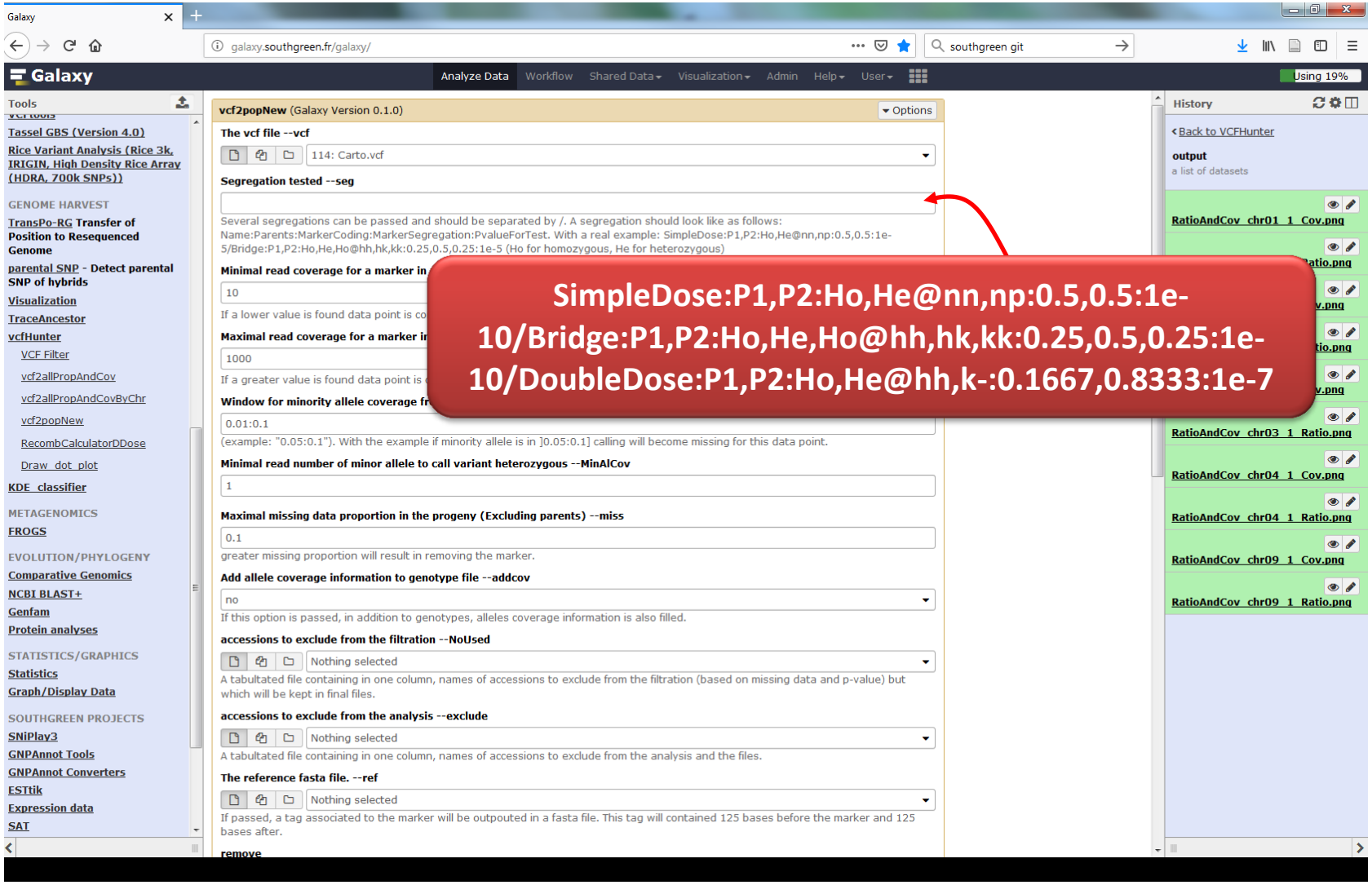
Genetic mapping analysis with vcfHunter tool

Selecting segregating markers in vcf files: vcf2PopNew



Genetic mapping analysis with vcfHunter tool

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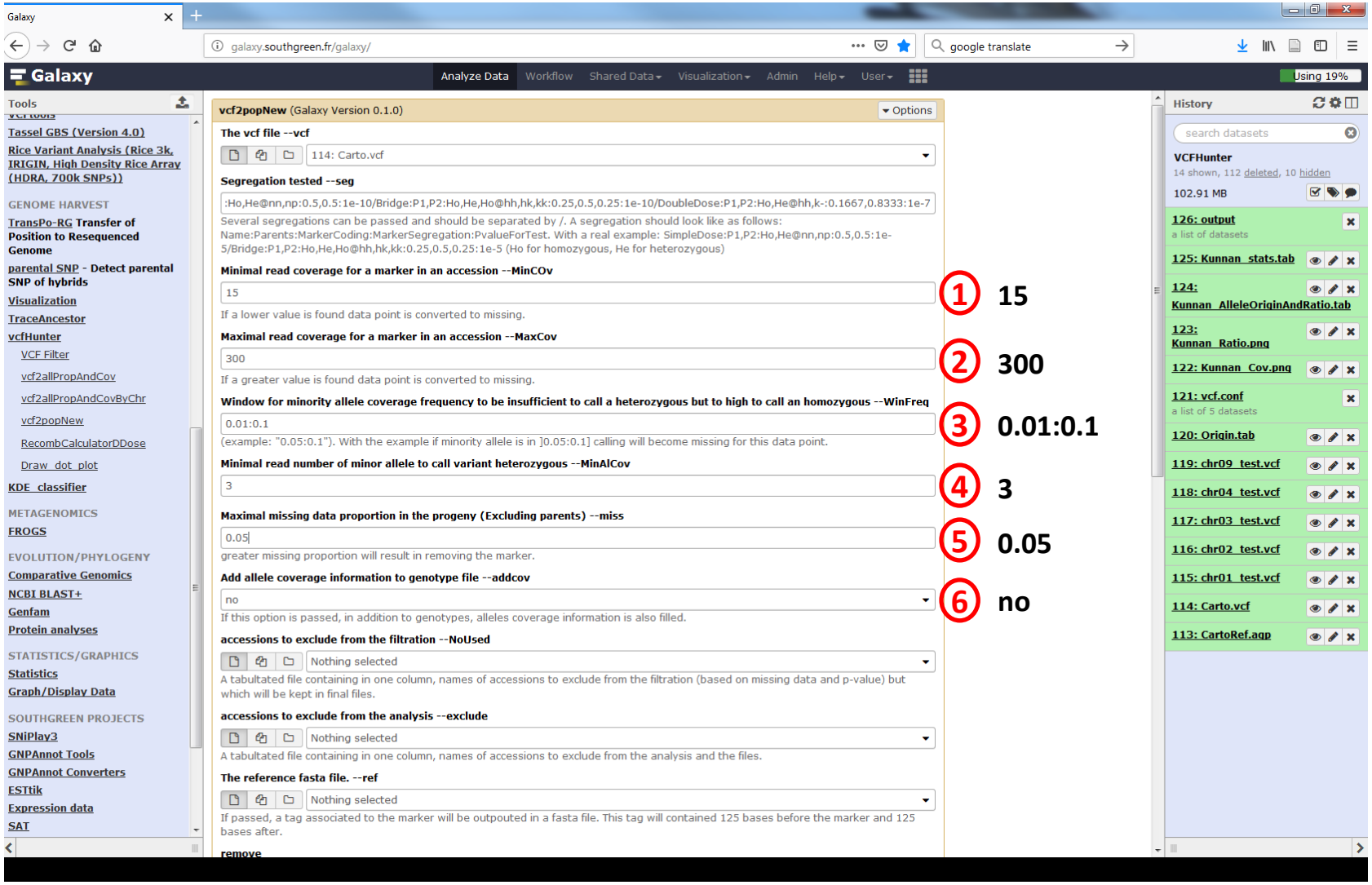

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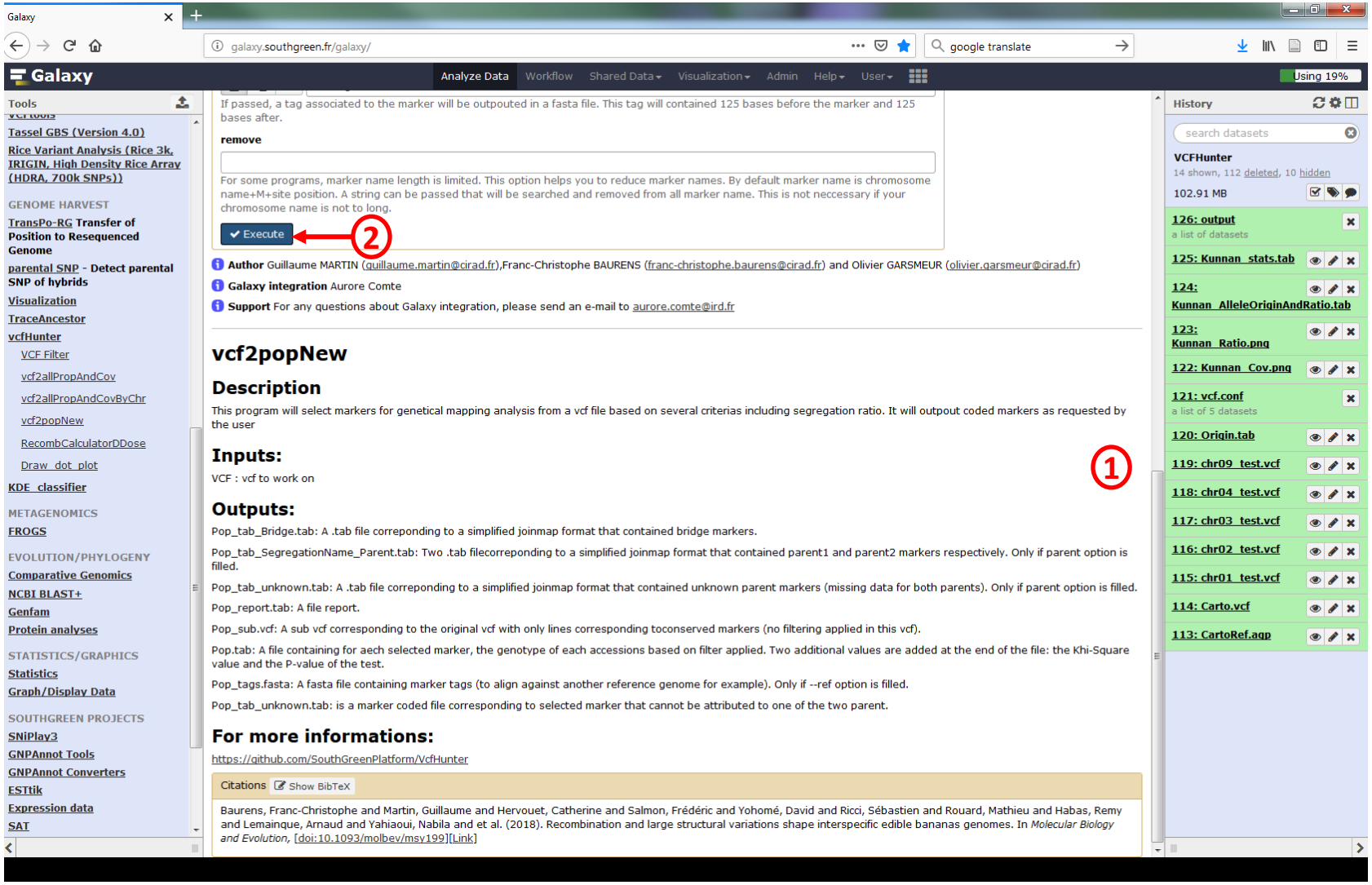
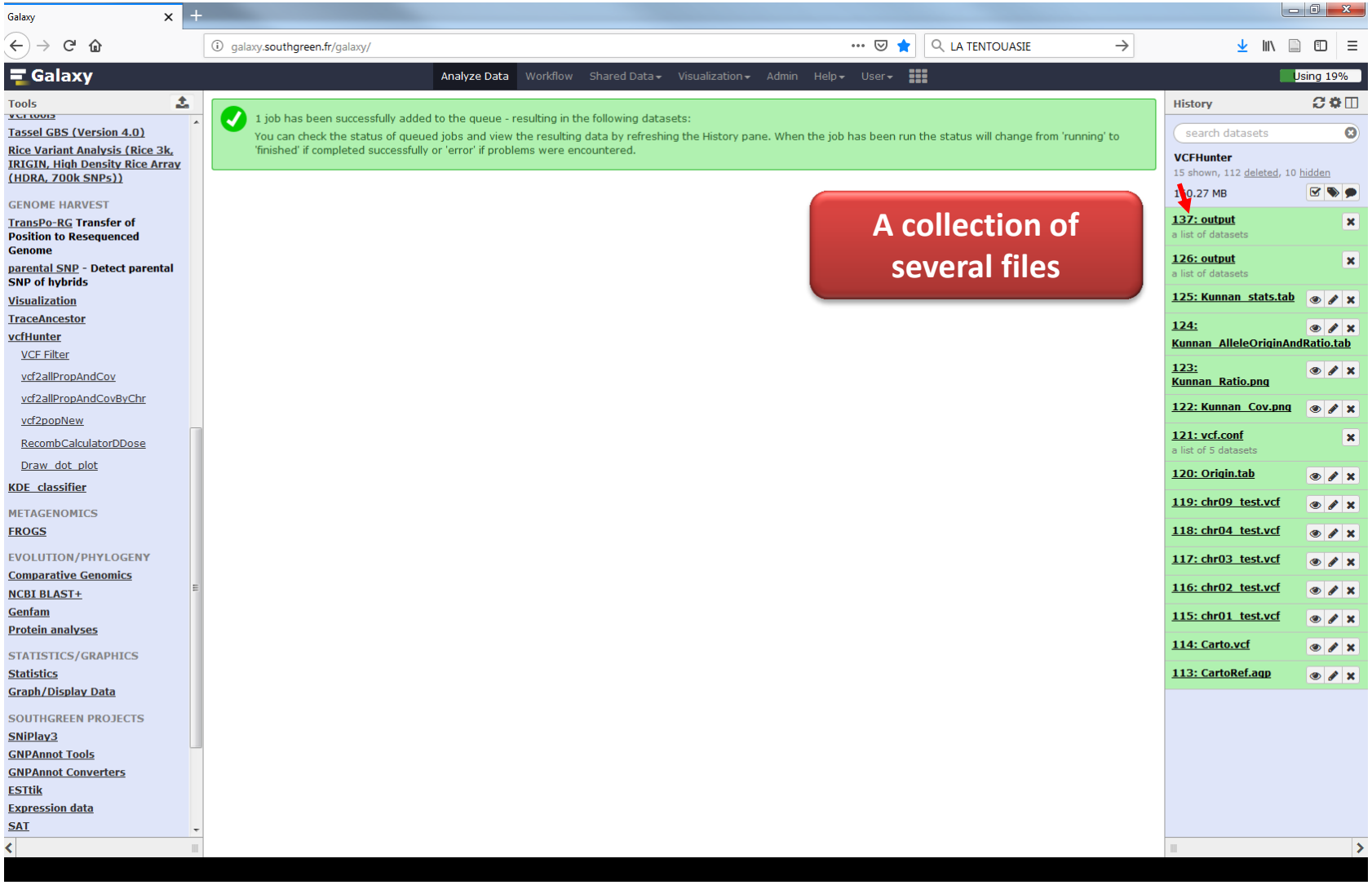


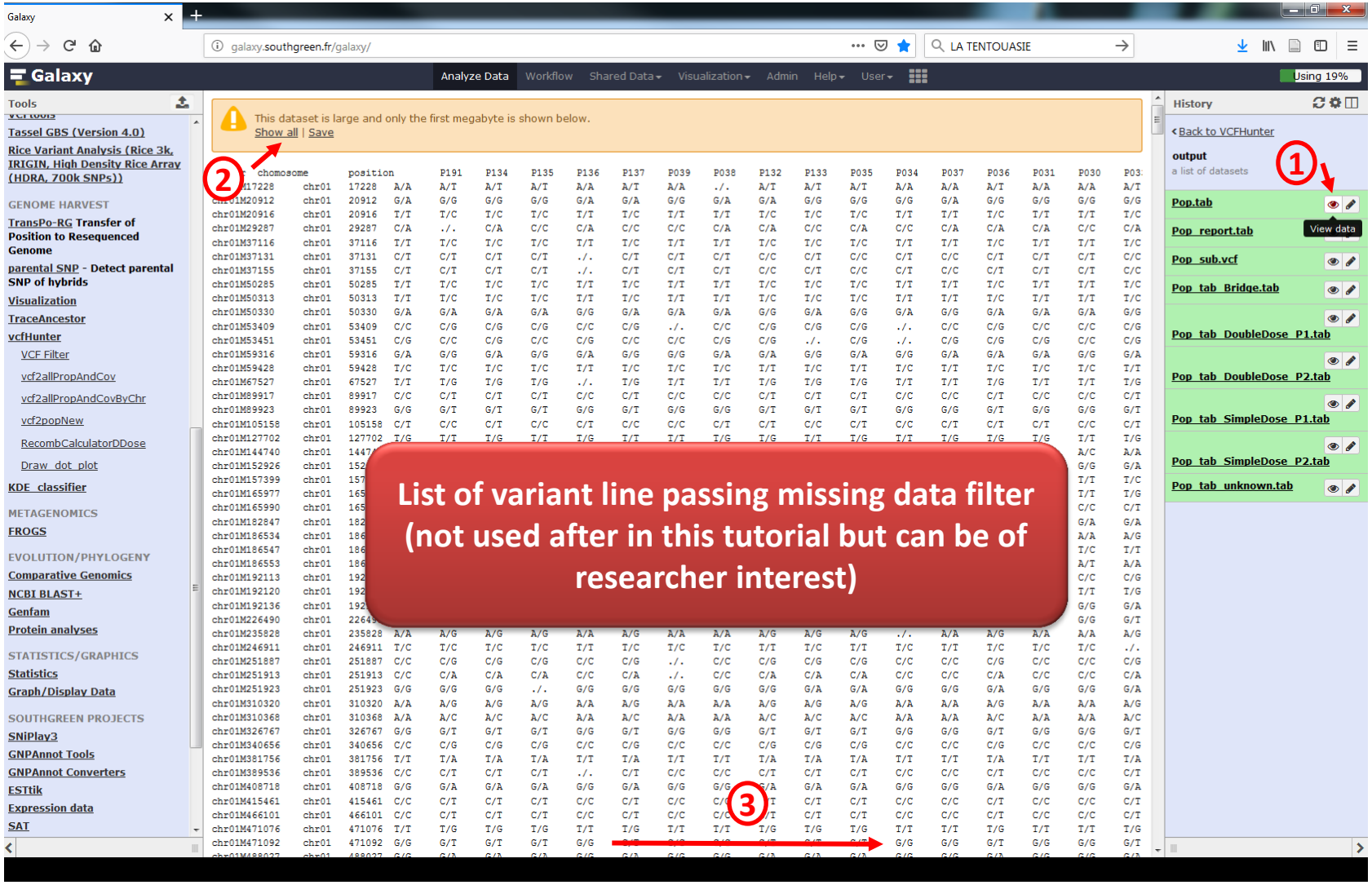
Genetic mapping analysis with vcfHunter tool

Selecting segregating markers in vcf files: outputs



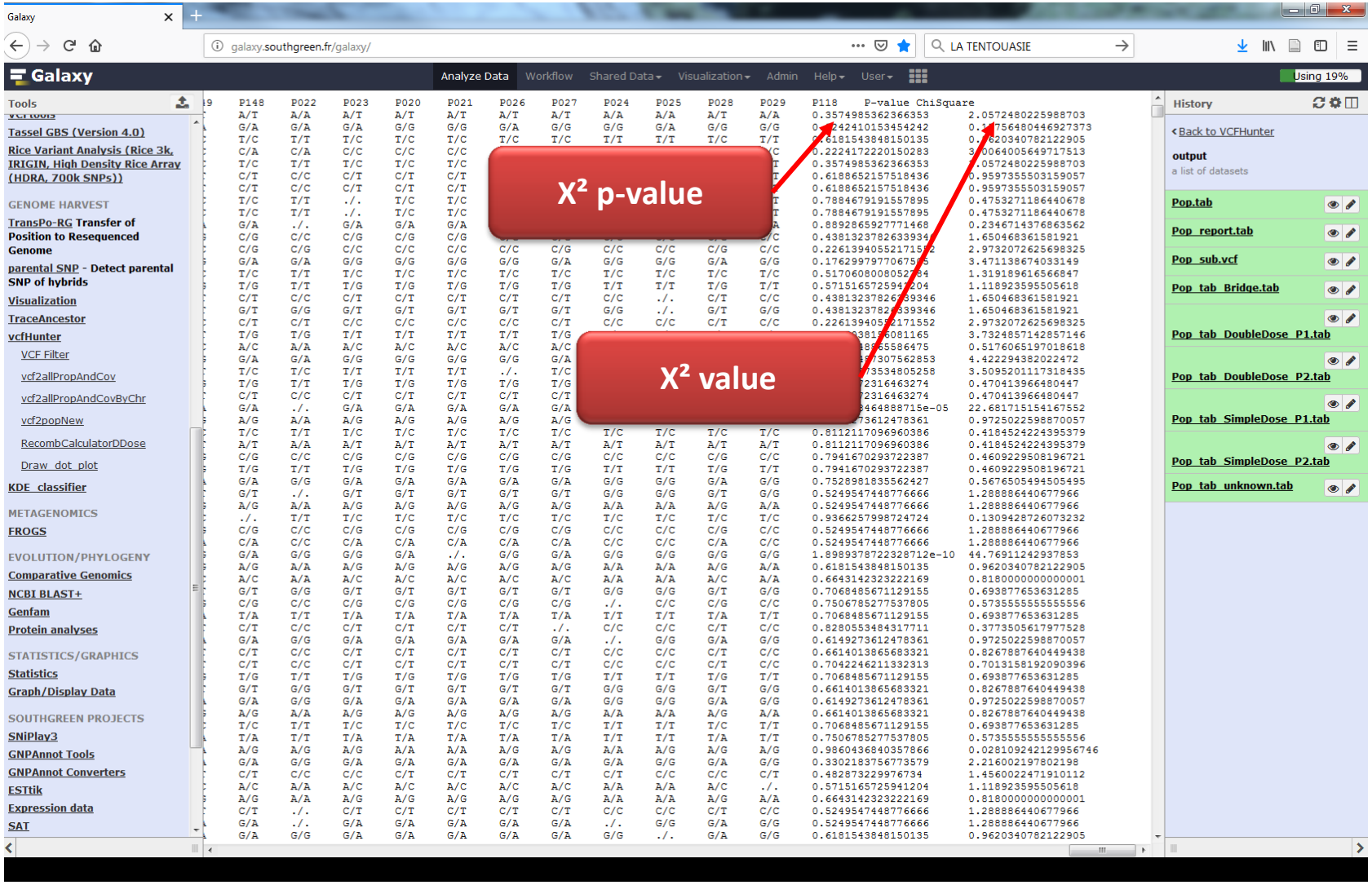
Genetic mapping analysis with vcfHunter tool

Selecting segregating markers in vcf files: outputs



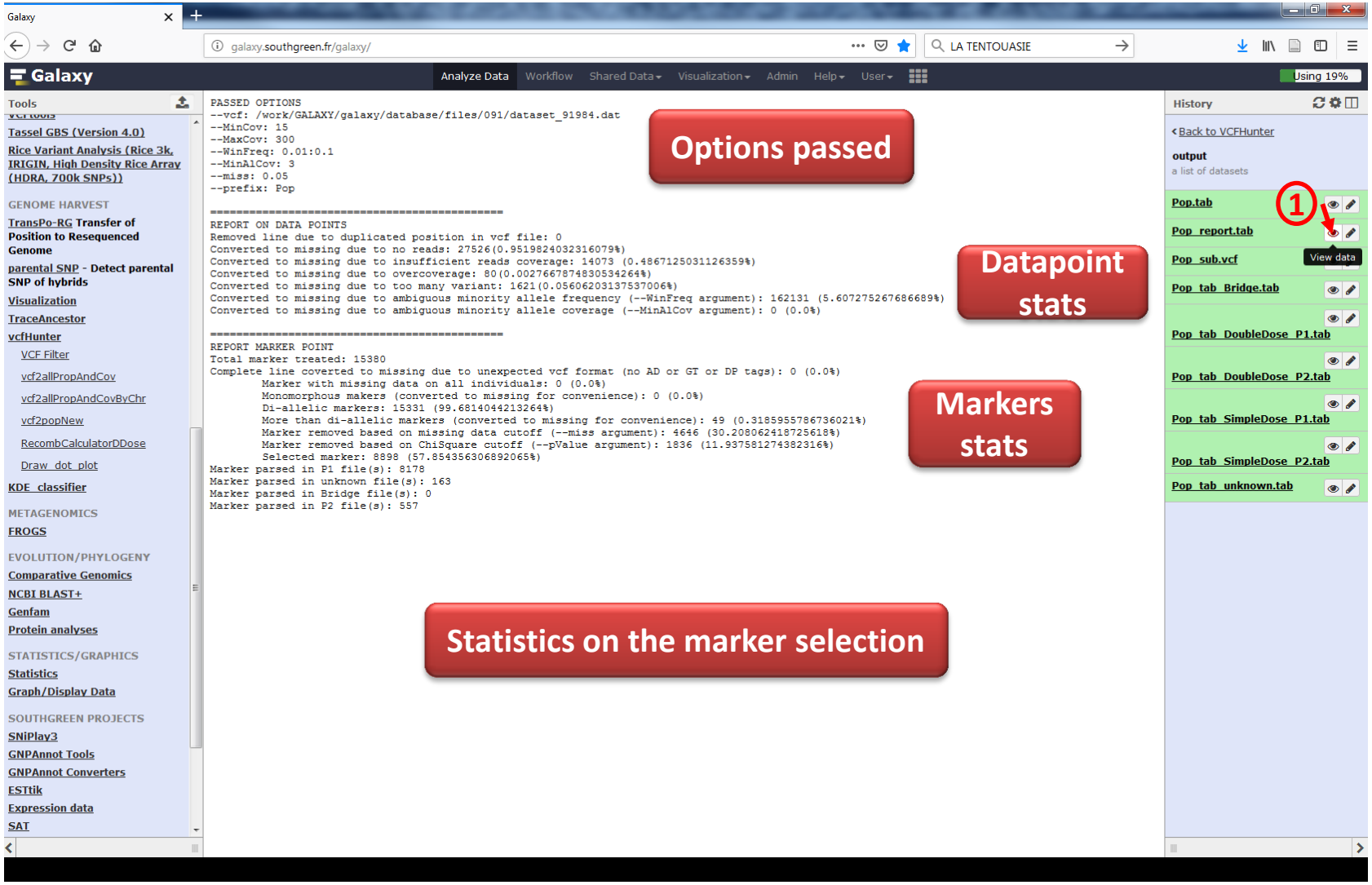
Genetic mapping analysis with vcfHunter tool

Selecting segregating markers in vcf files: outputs



Genetic mapping analysis with vcfHunter tool

Selecting segregating markers in vcf files: outputs



Genetic mapping analysis with vcfHunter tool

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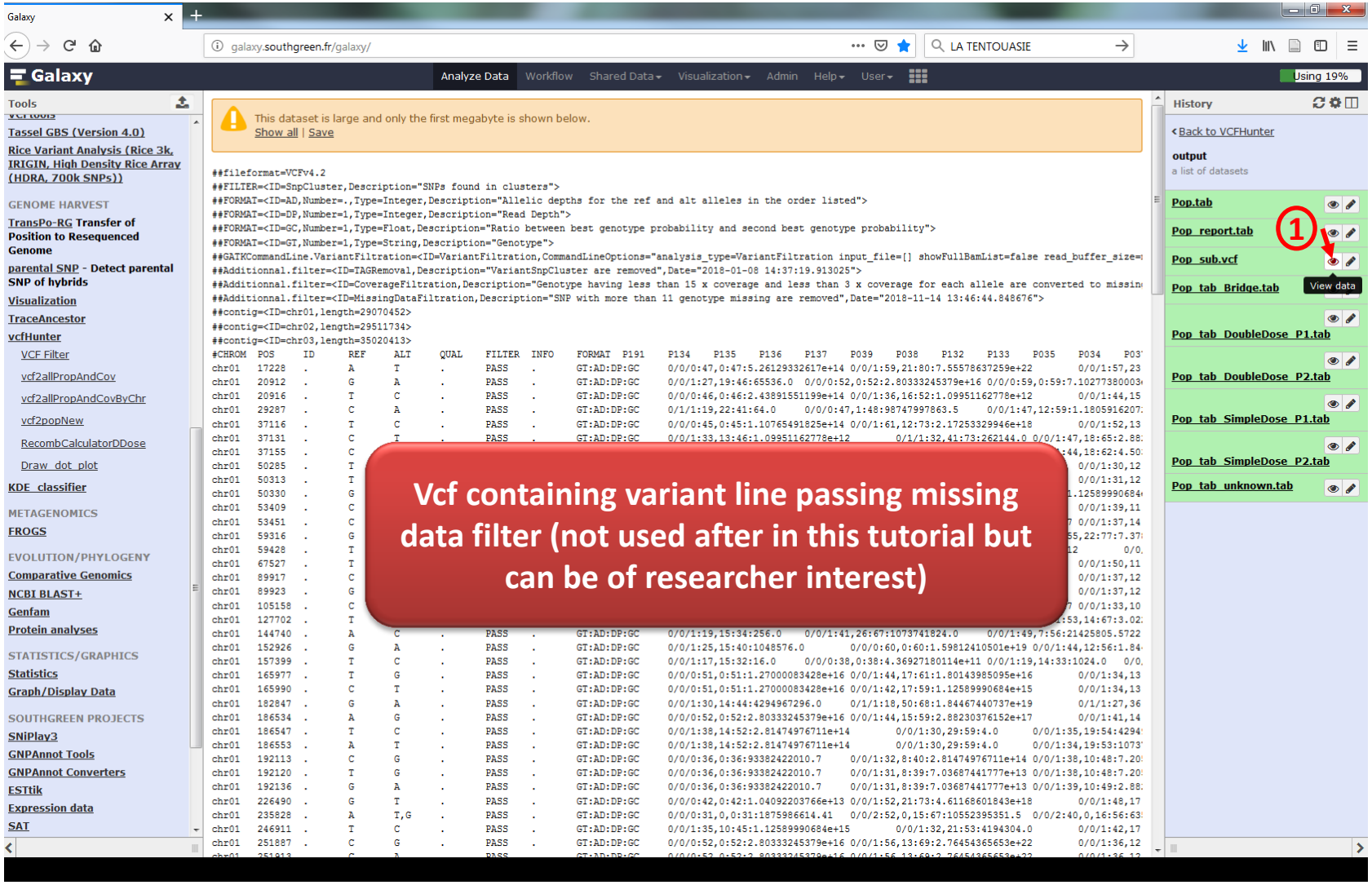

Genetic mapping analysis with vcfHunter tool

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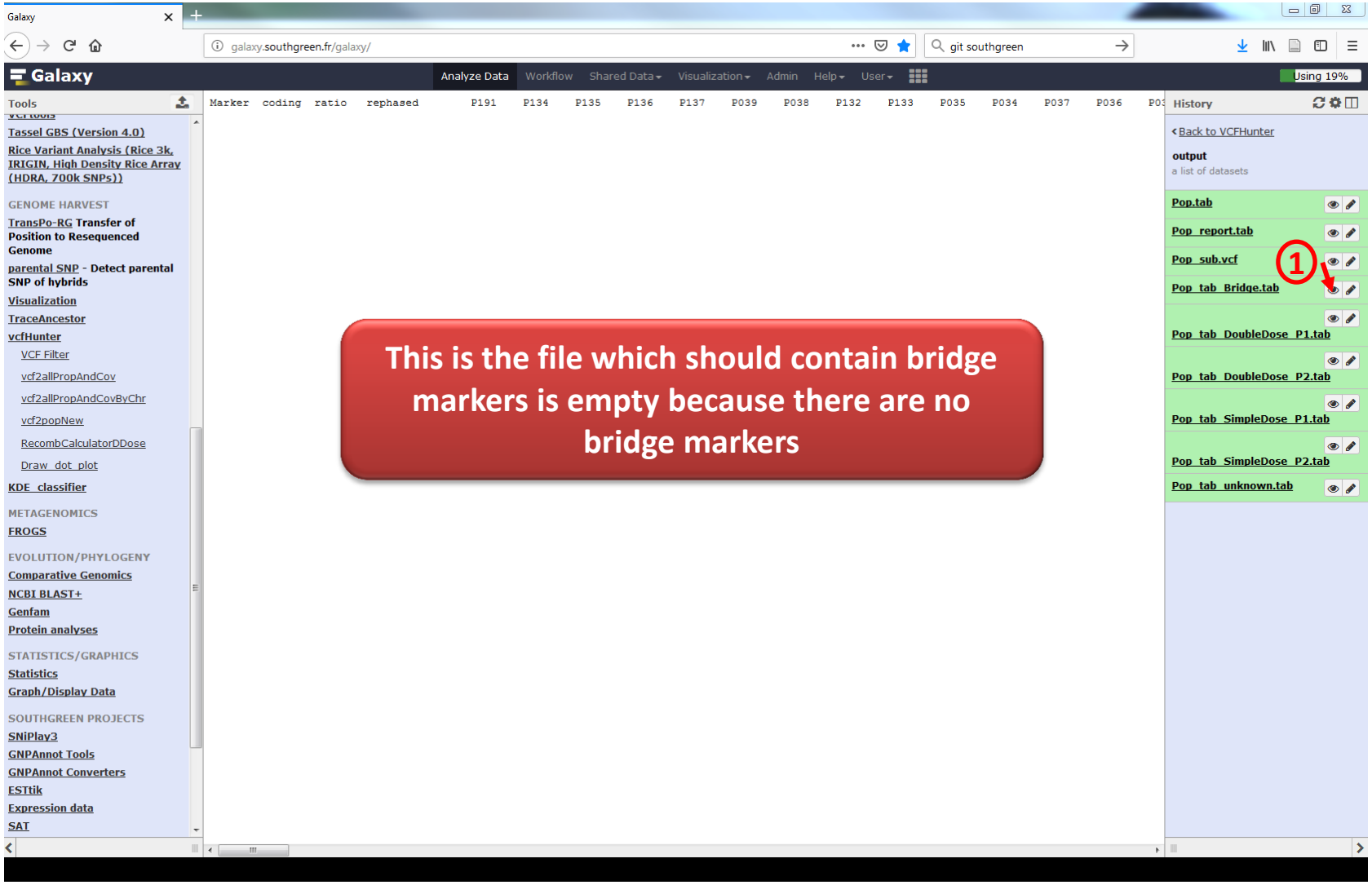
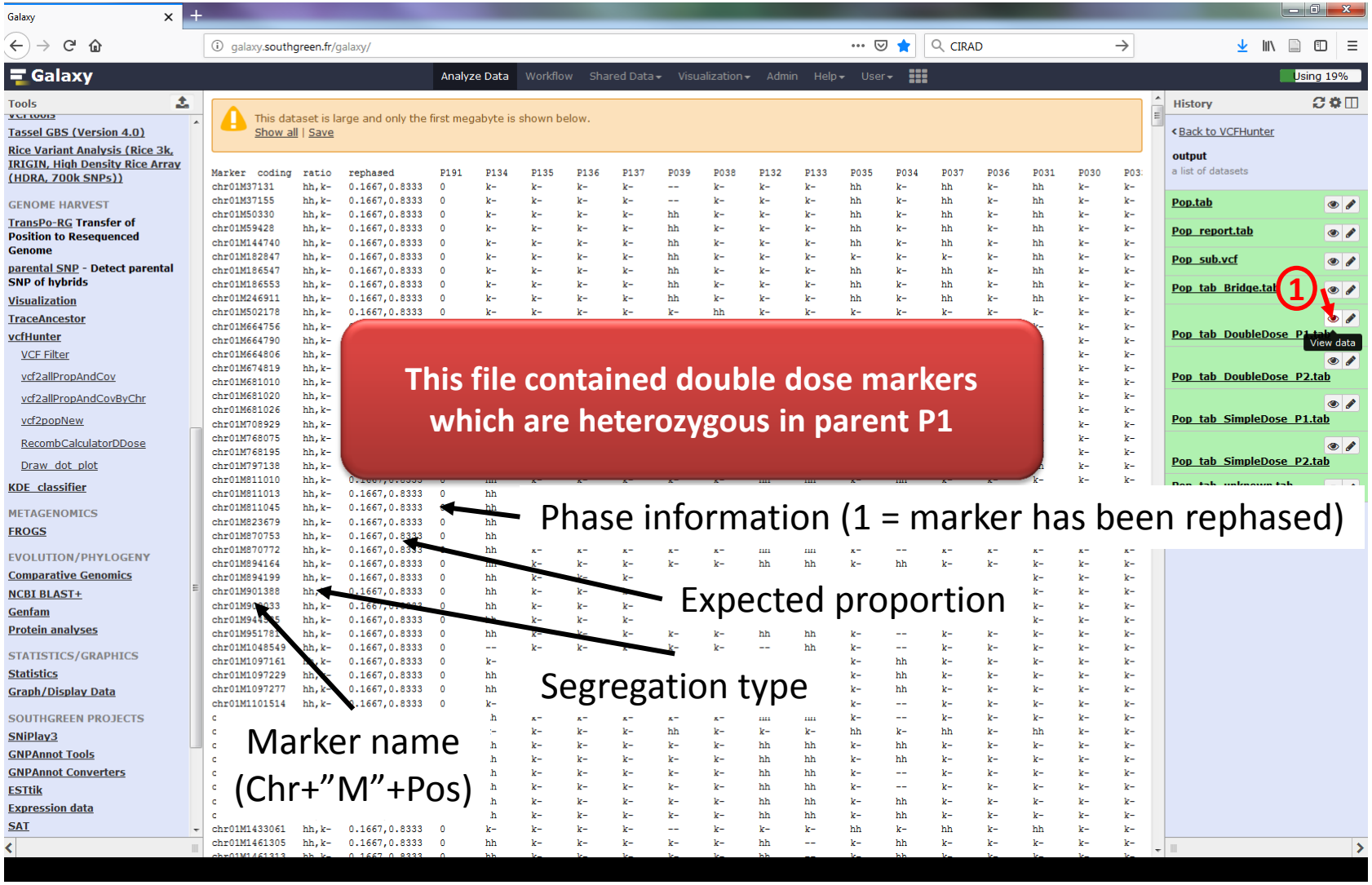


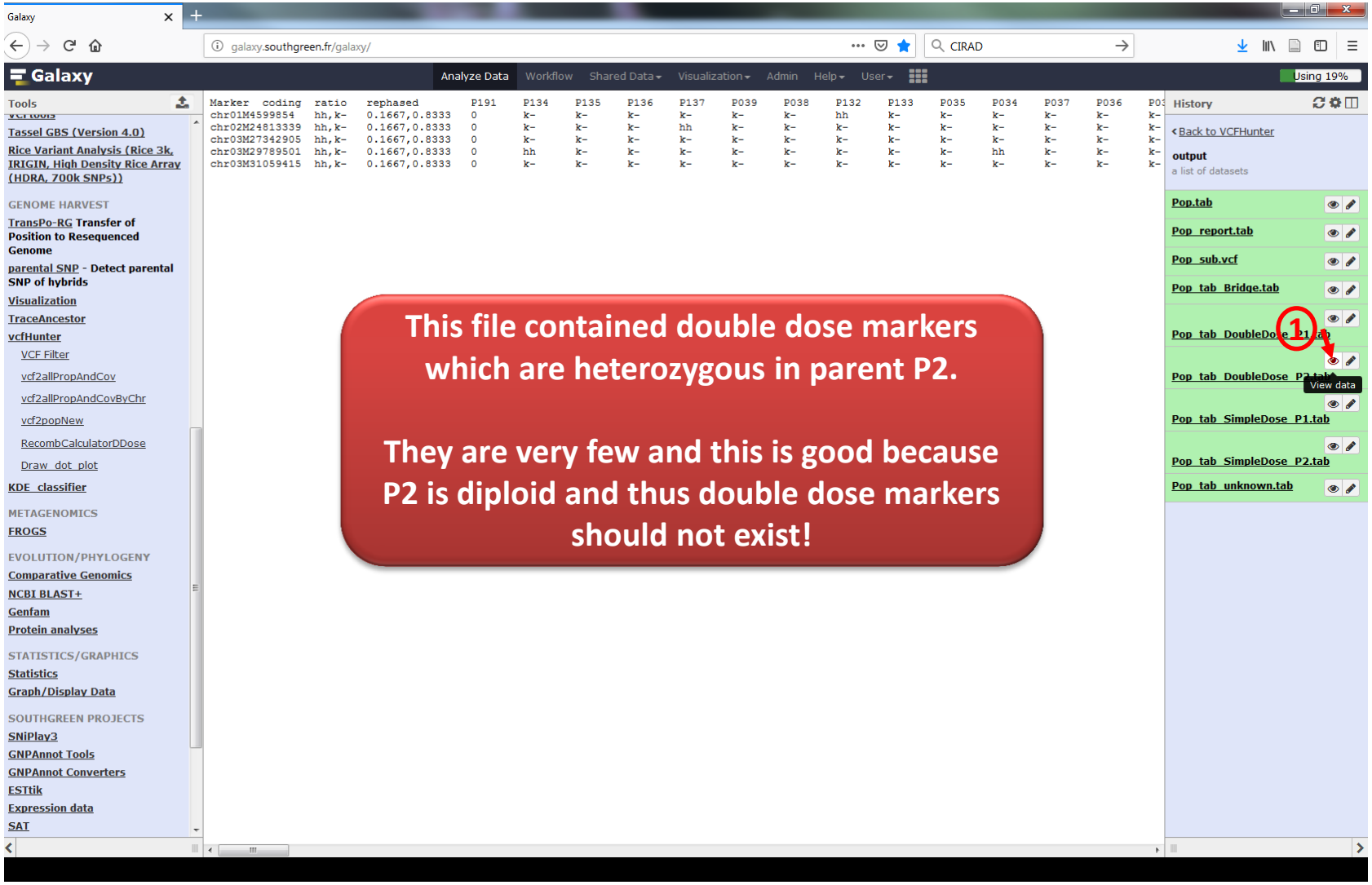
Genetic mapping analysis with vcfHunter tool

Selecting segregating markers in vcf files: outputs



Genetic mapping analysis with vcfHunter tool

Selecting segregating markers in vcf files: outputs



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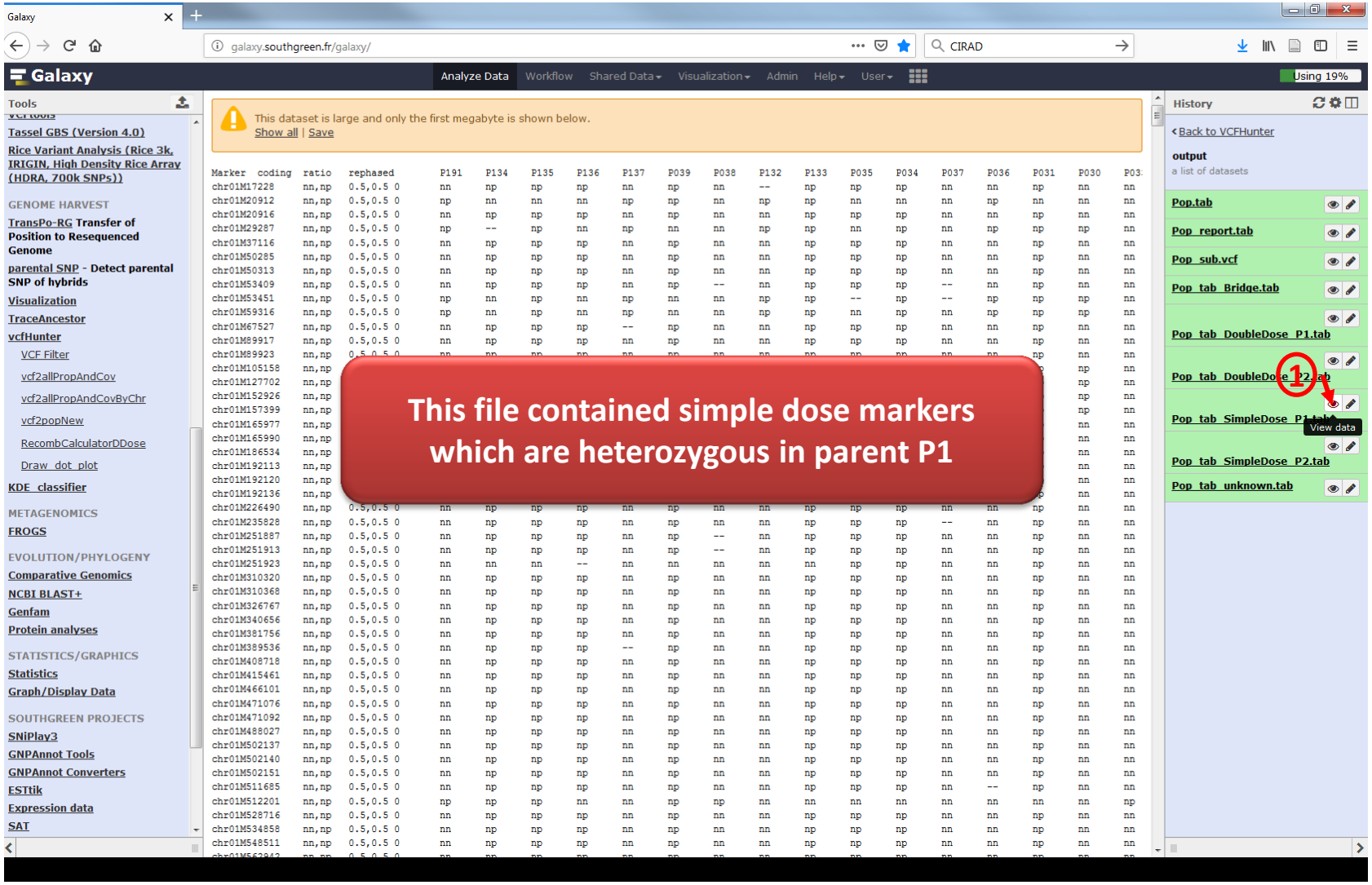
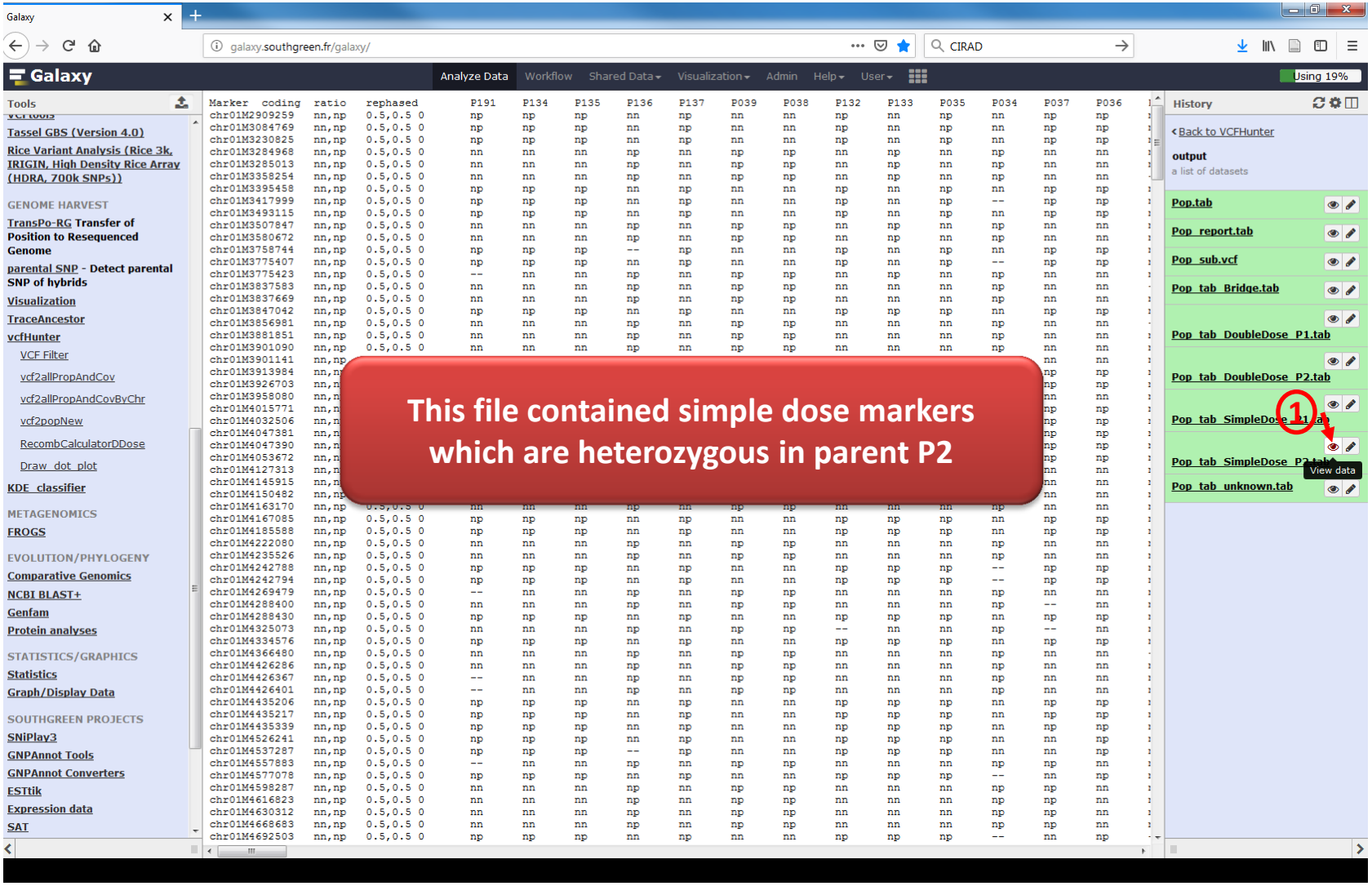
Selecting segregating markers in vcf files: outputs



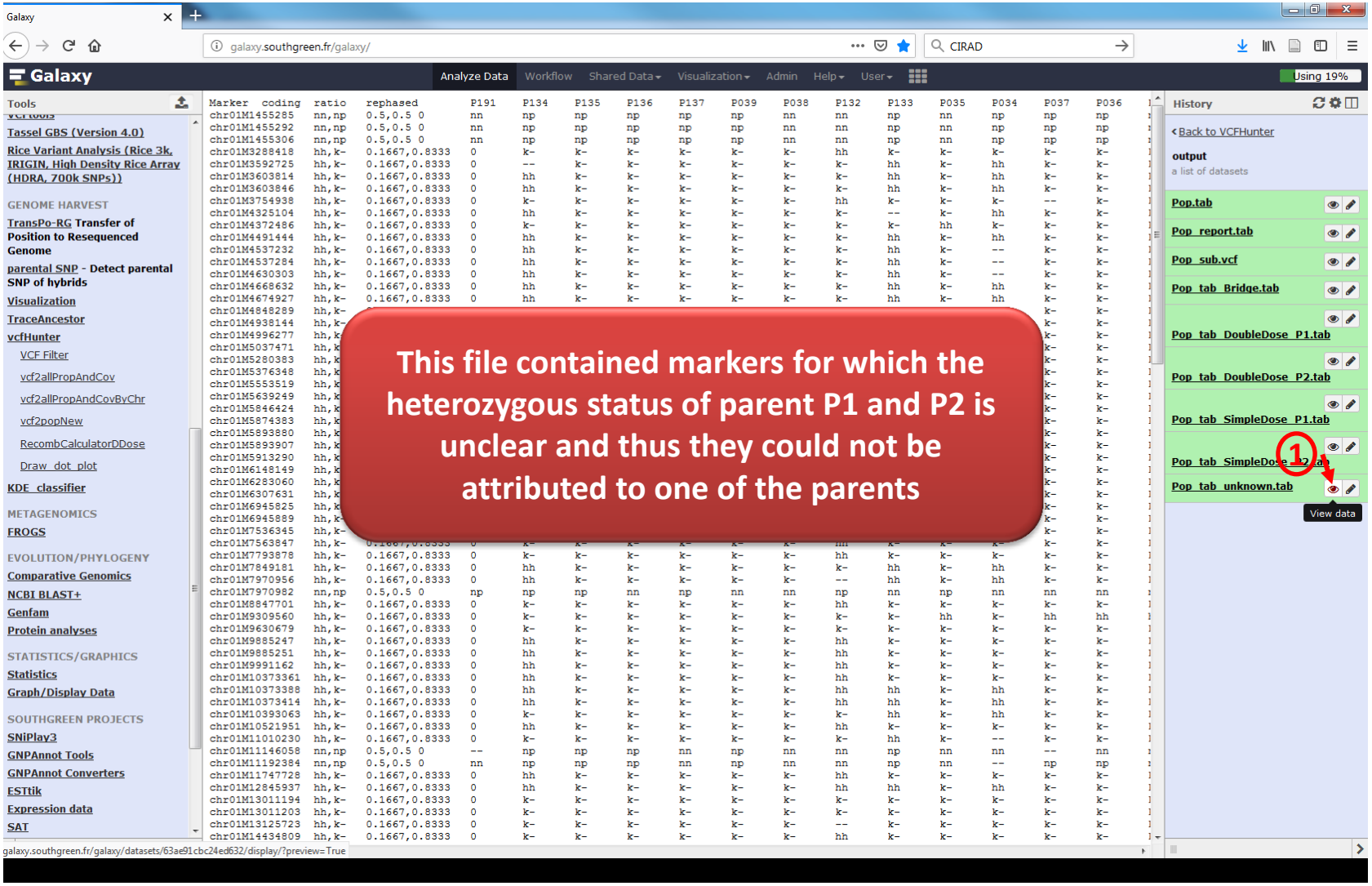
Genetic mapping analysis with vcfHunter tool

Selecting segregating markers in vcf files: outputs



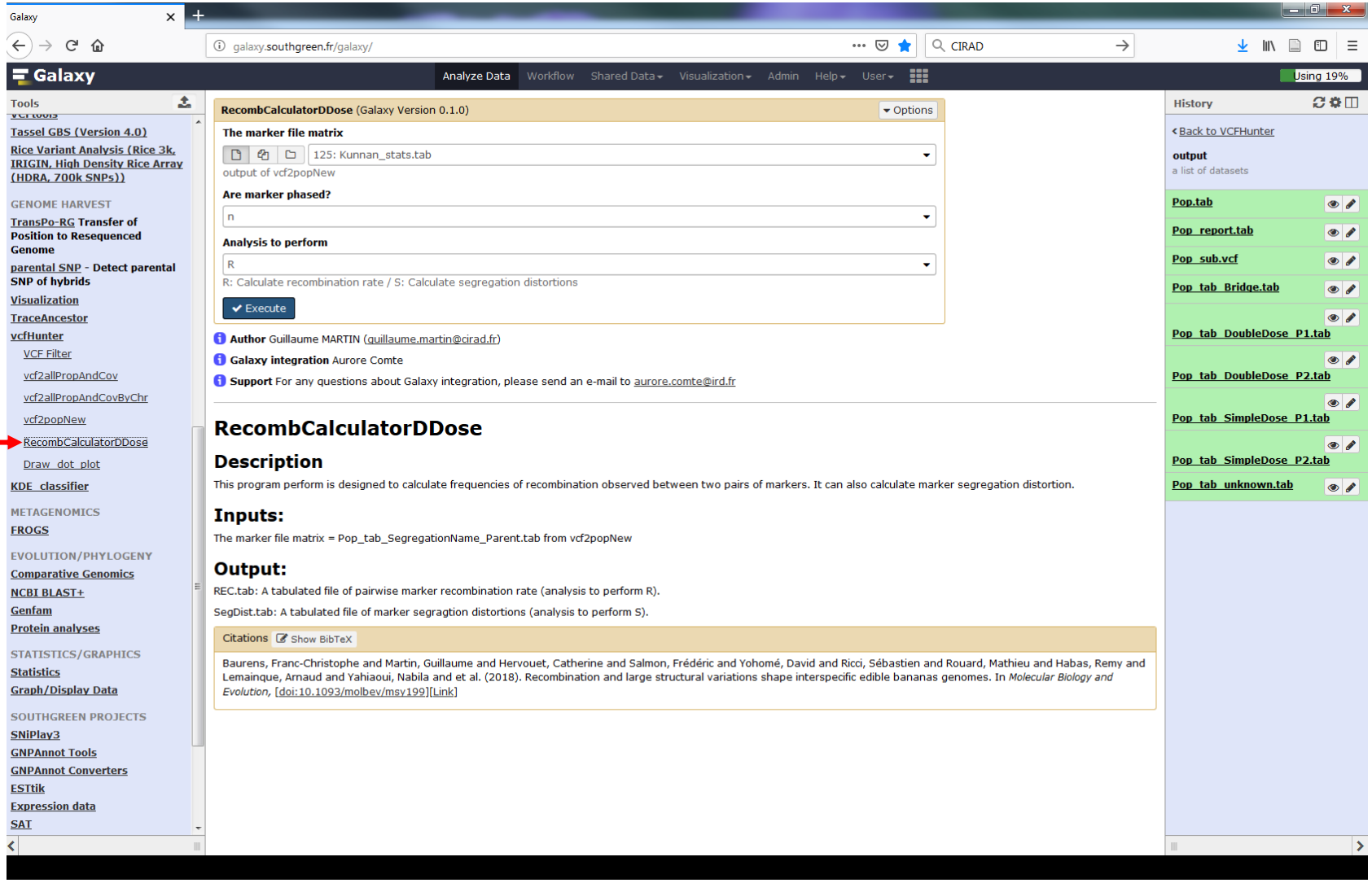
Genetic mapping analysis with vcfHunter tool

Selecting segregating markers in vcf files: outputs



Genetic mapping analysis with vcfHunter tool

Calculating marker segregation distortion on parent P2 simple dose markers



Genetic mapping analysis with vcfHunter tool

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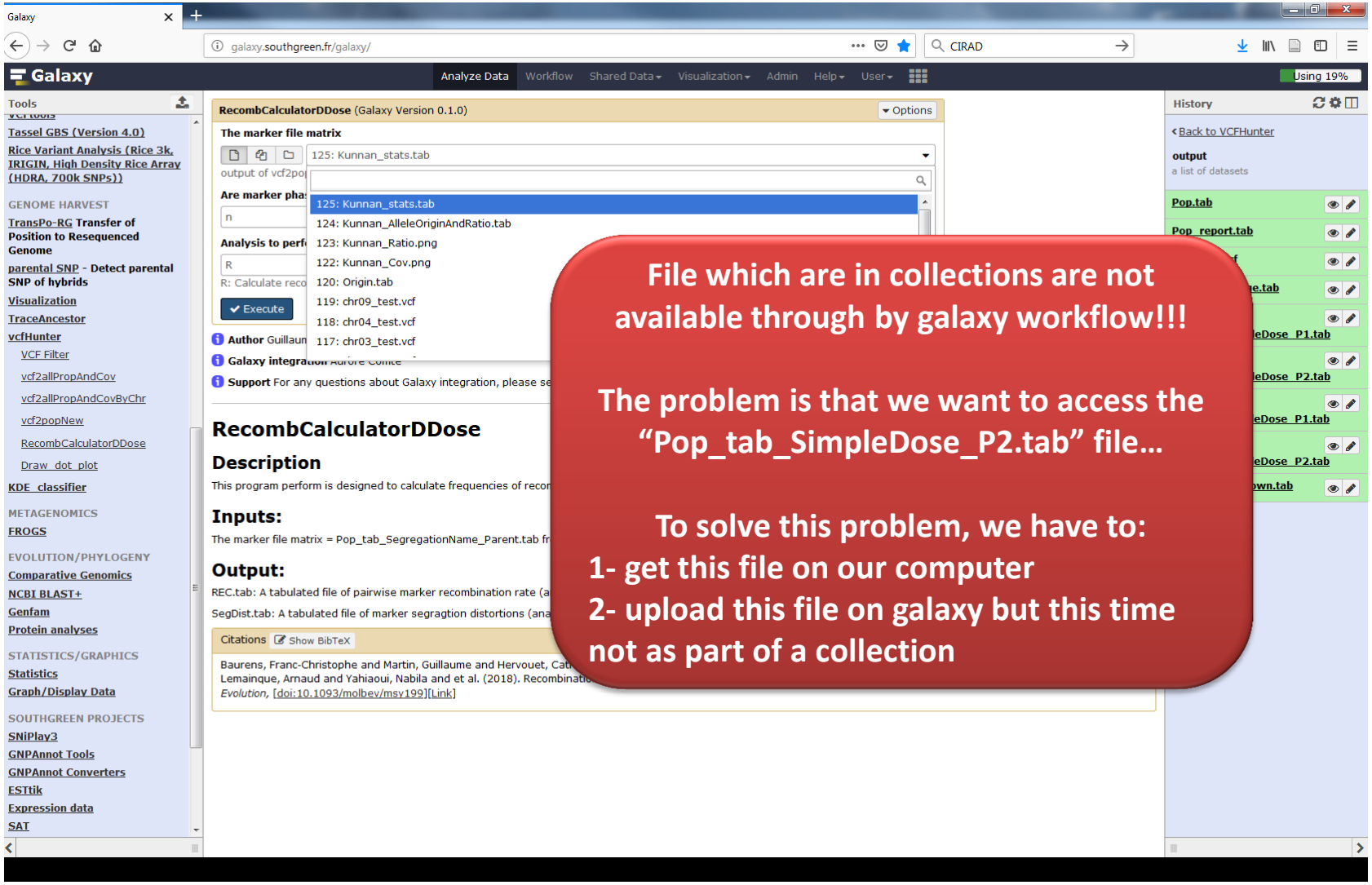
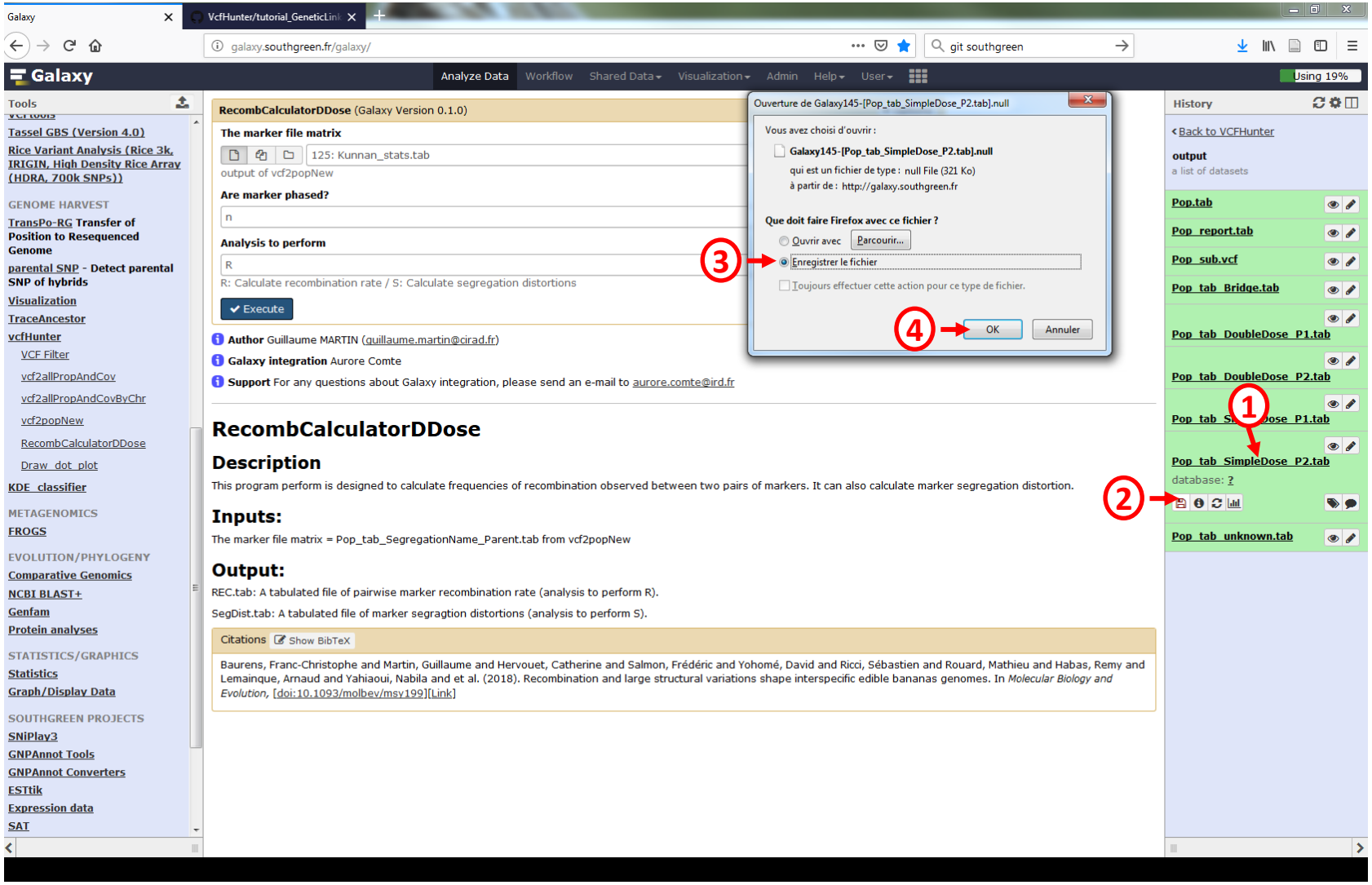


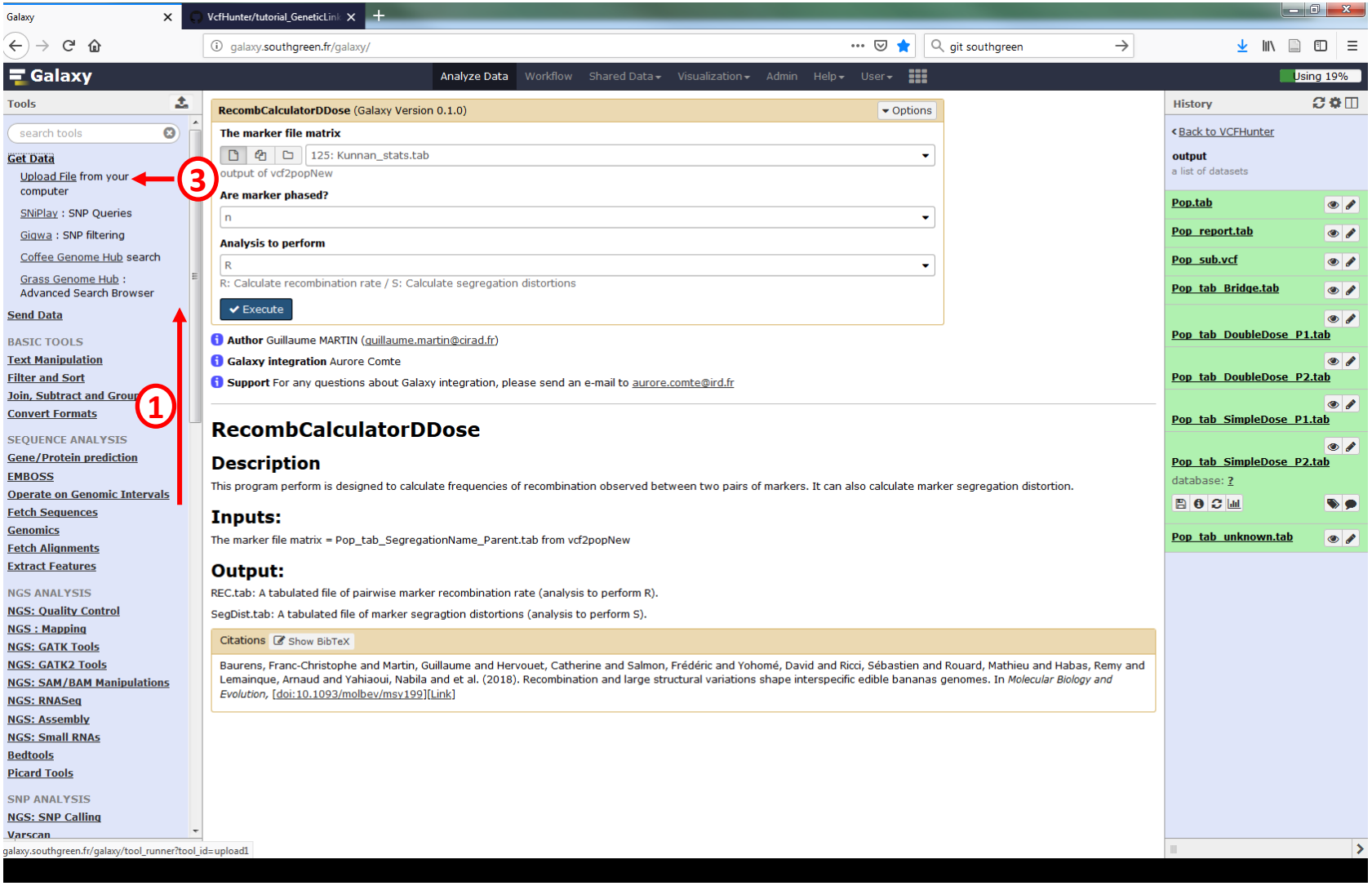
Genetic mapping analysis with vcfHunter tool

1- Downloading the Pop_tab_SimpleDose_P2.tab



Genetic mapping analysis with vcfHunter tool

1- Uploading the Pop_tab_SimpleDose_P2.tab onto Galaxy



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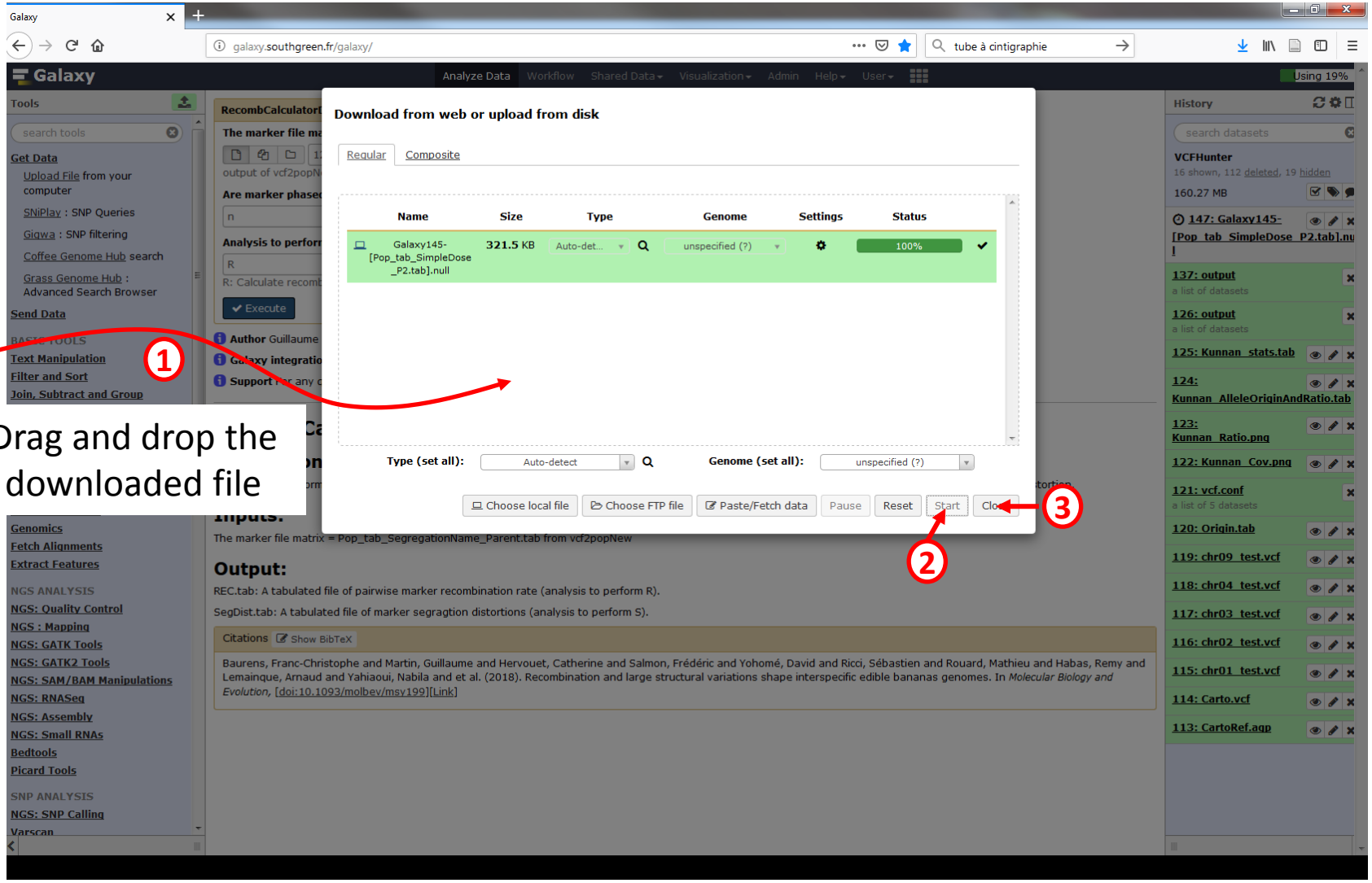

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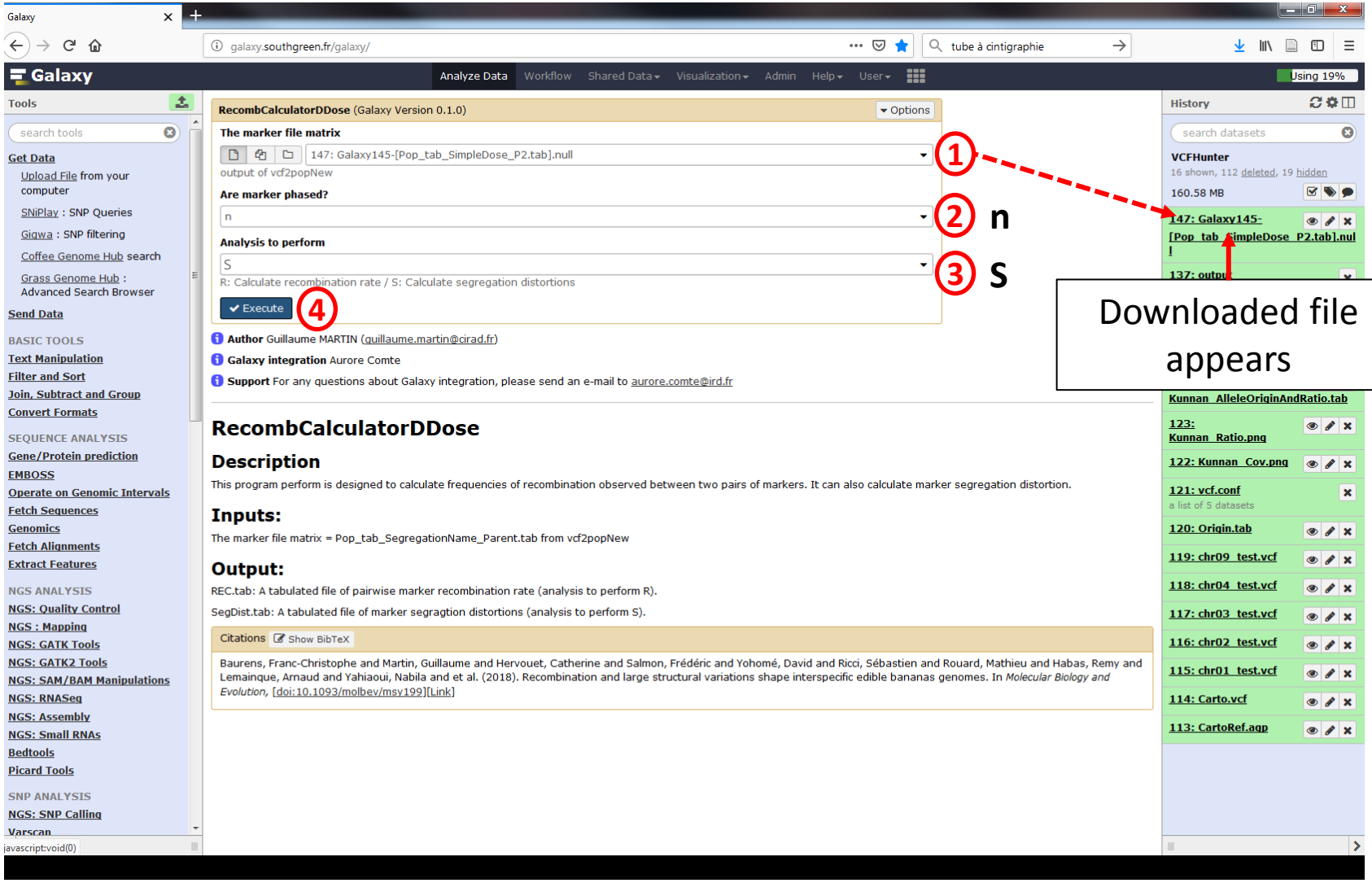
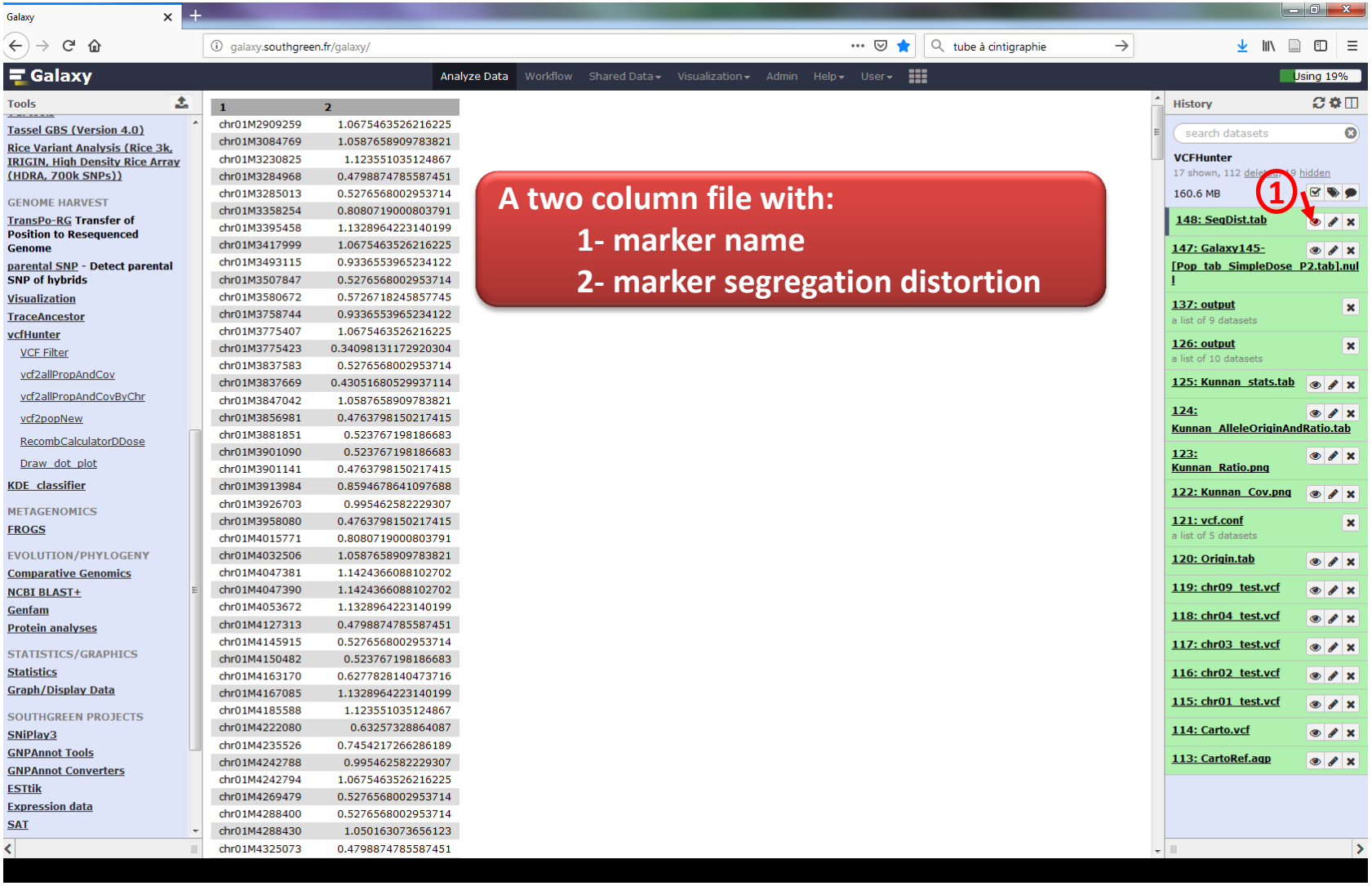


Genetic mapping analysis with vcfHunter tool

Calculating marker segregation distortion : output



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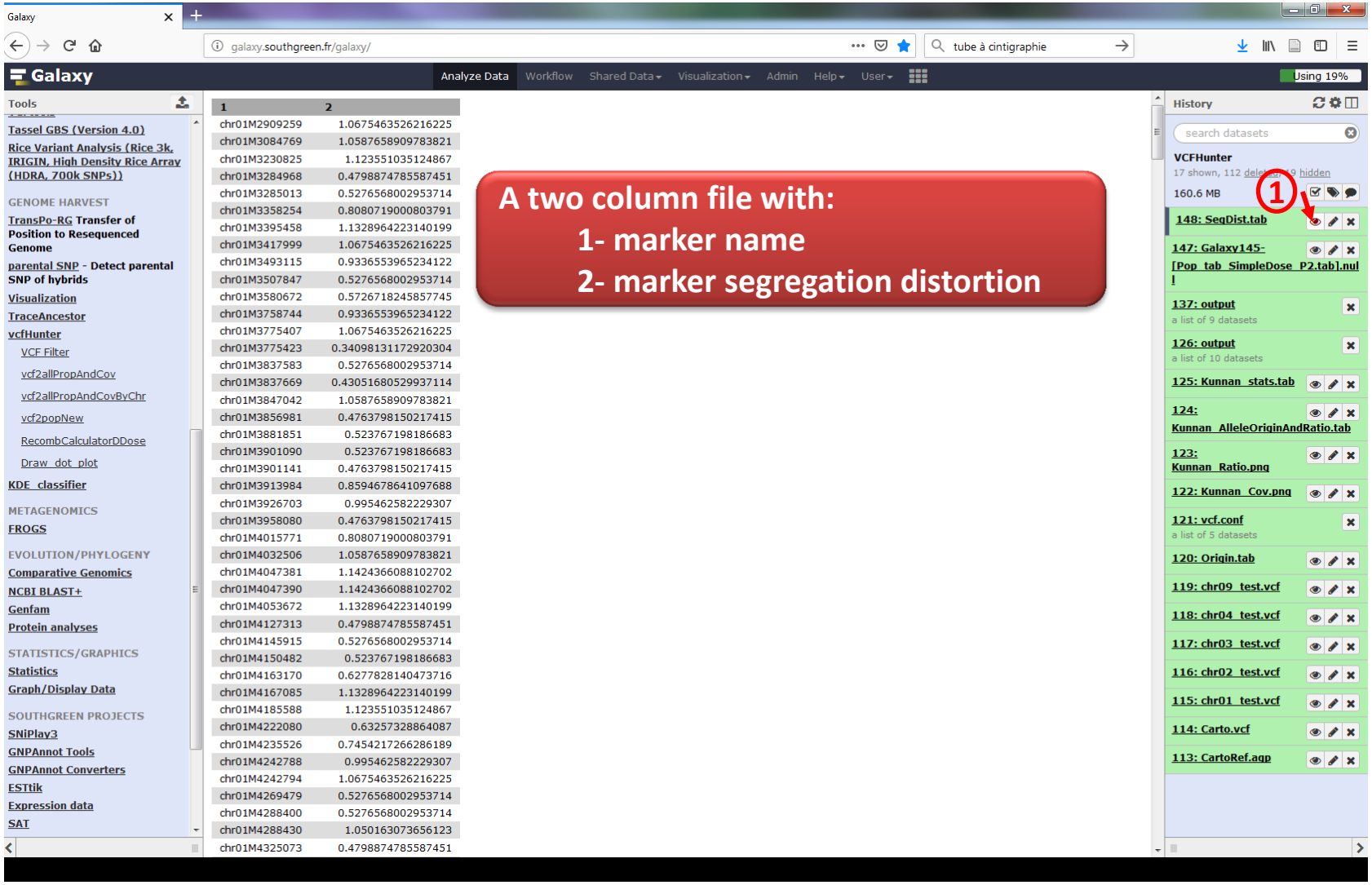
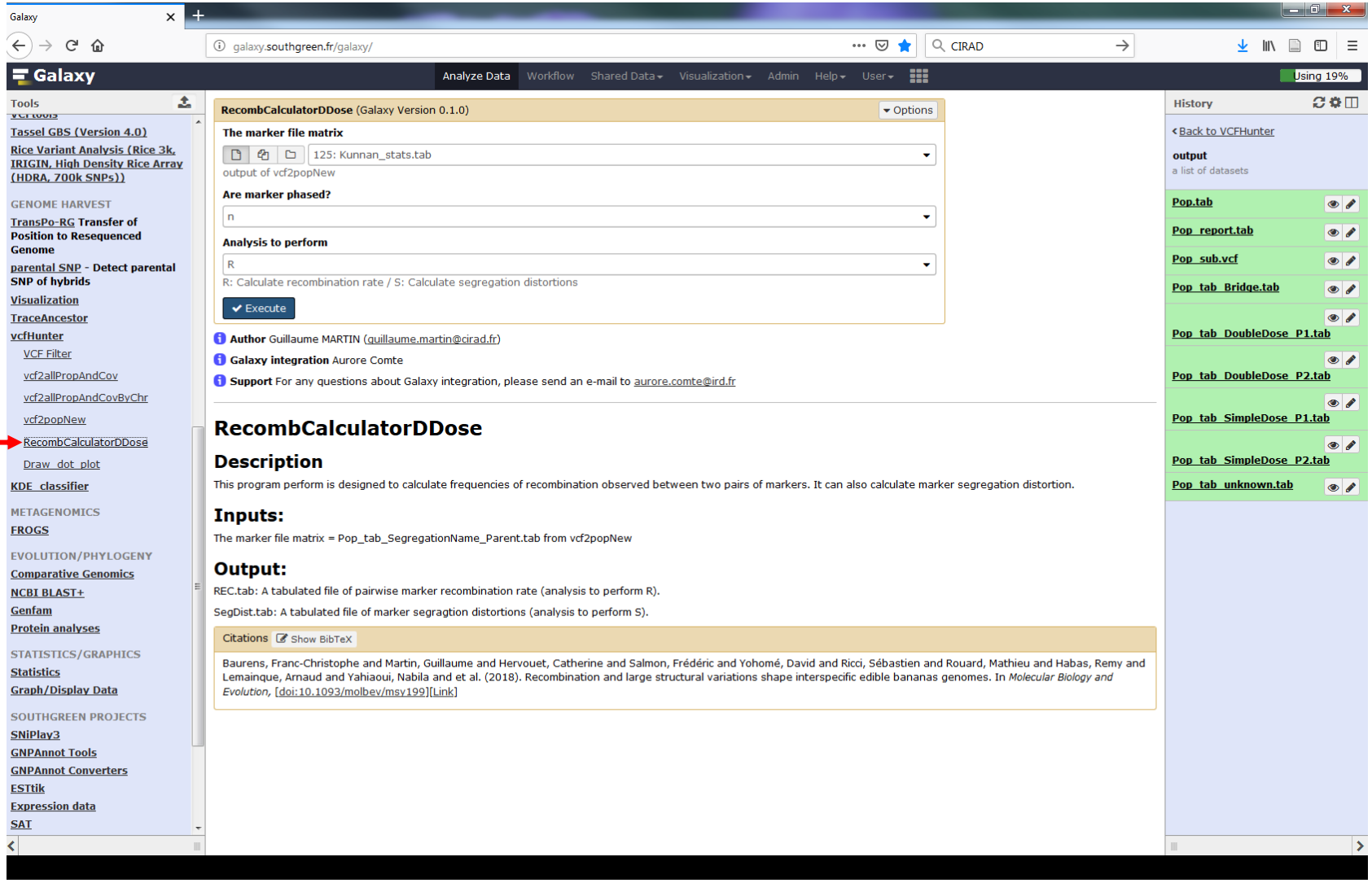


Genetic mapping analysis with vcfHunter tool

Calculating pairwise marker recombination rate on P2 simple dose



Genetic mapping analysis with vcfHunter tool

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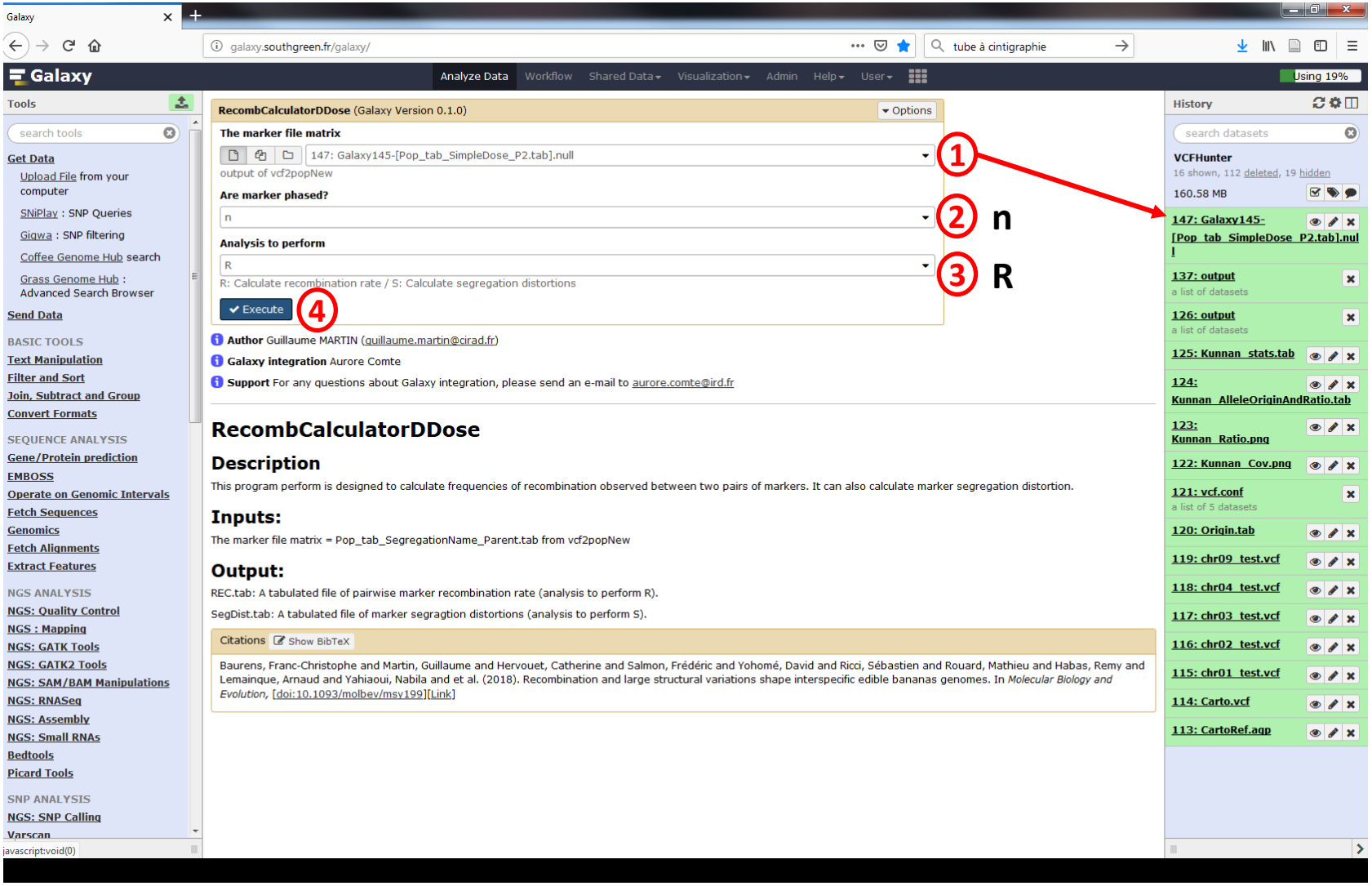

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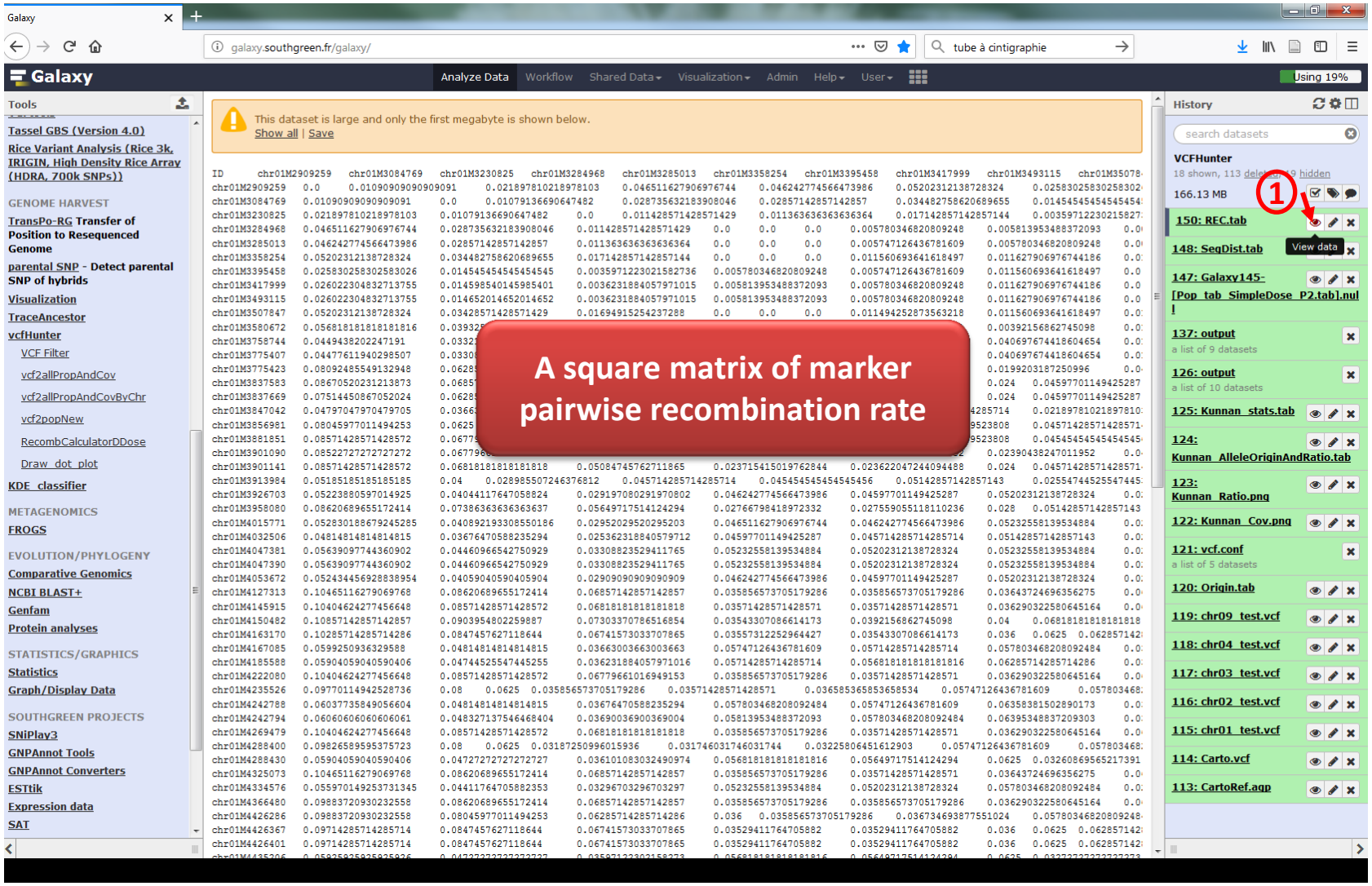
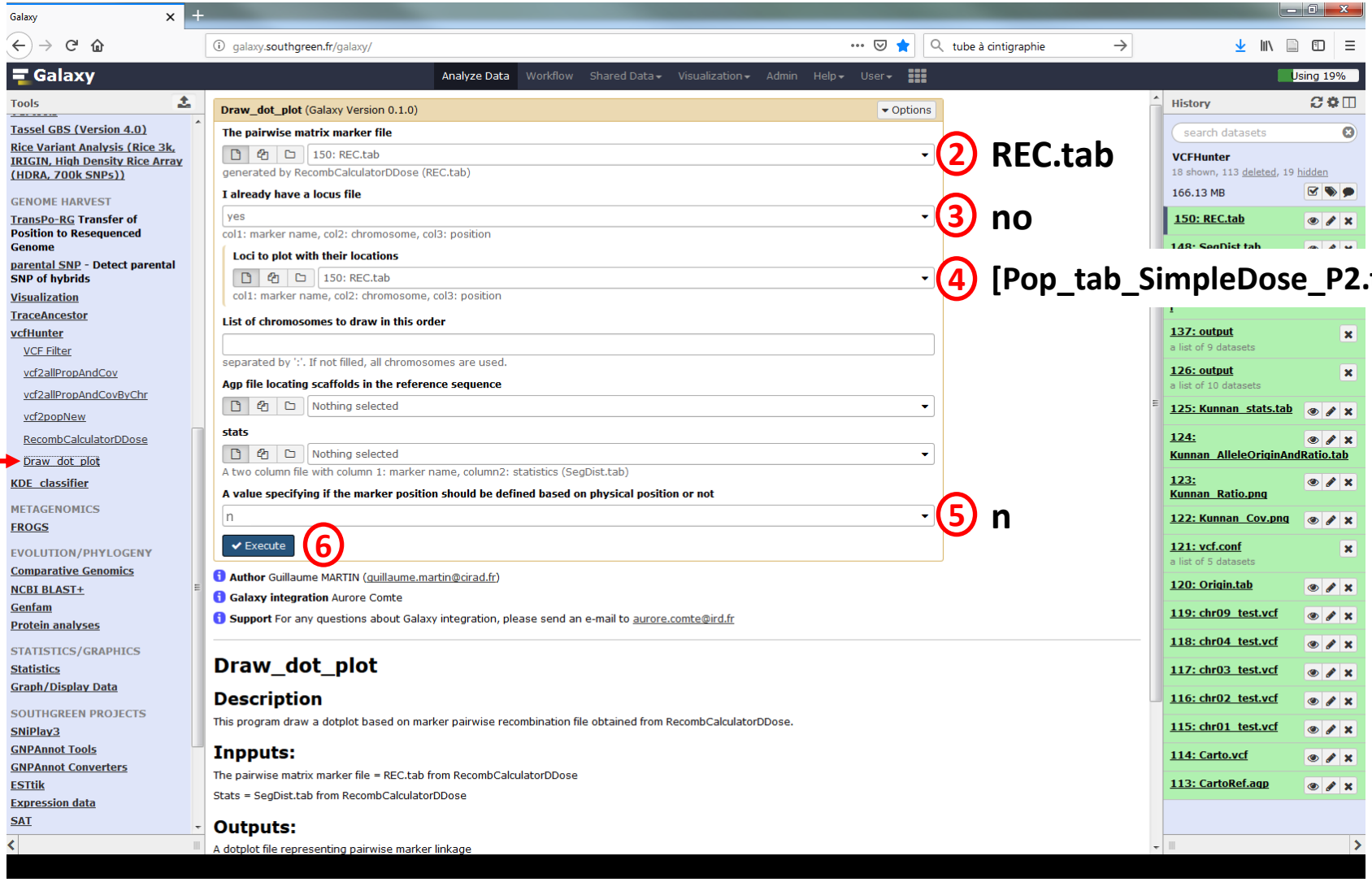
Calculating pairwise marker recombination rate: output



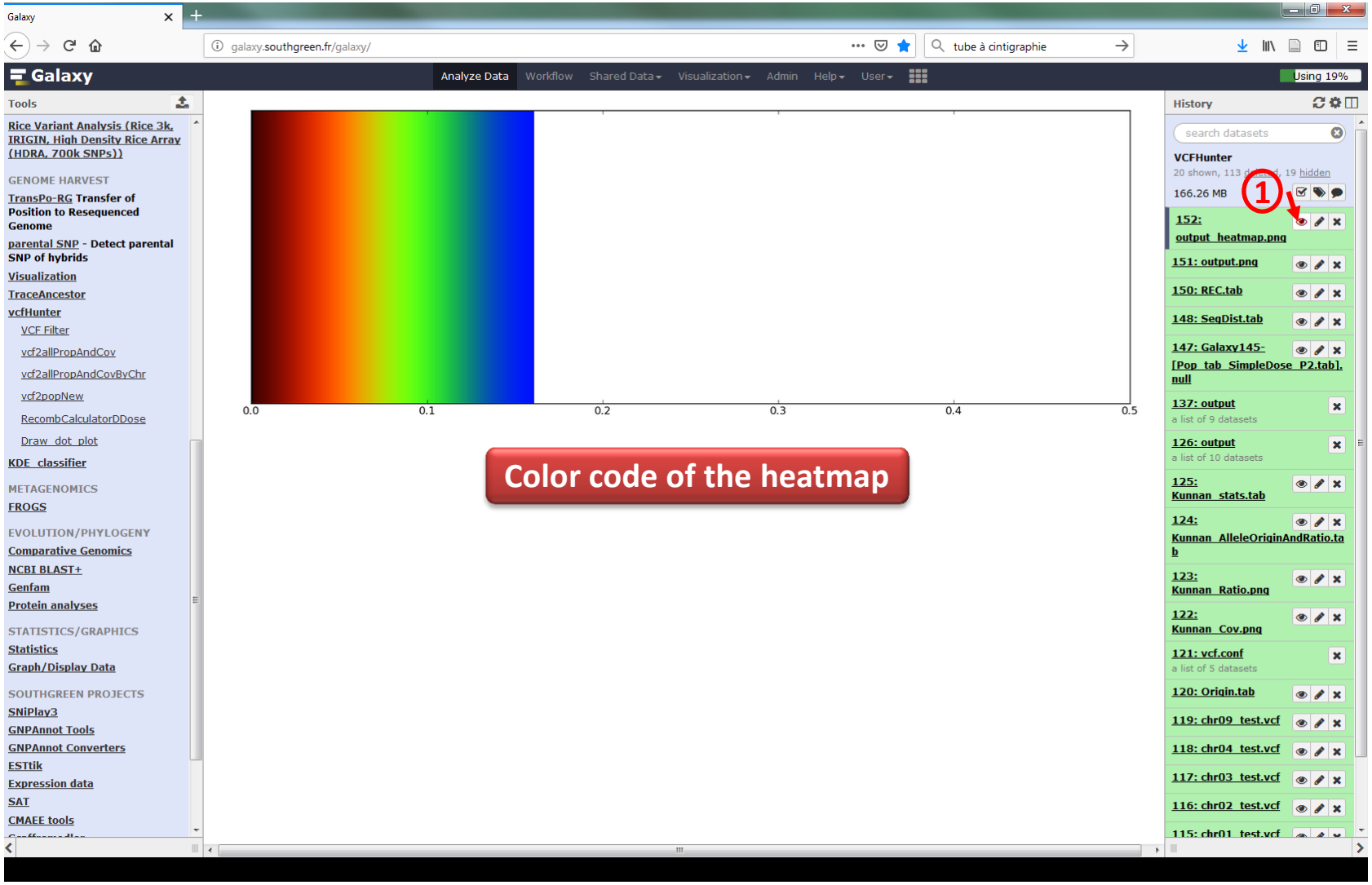
Genetic mapping analysis with vcfHunter tool

Plotting pairwise recombination



Genetic mapping analysis with vcfHunter tool

Plotting pairwise recombination: outputs



Genetic mapping analysis with vcfHunter tool

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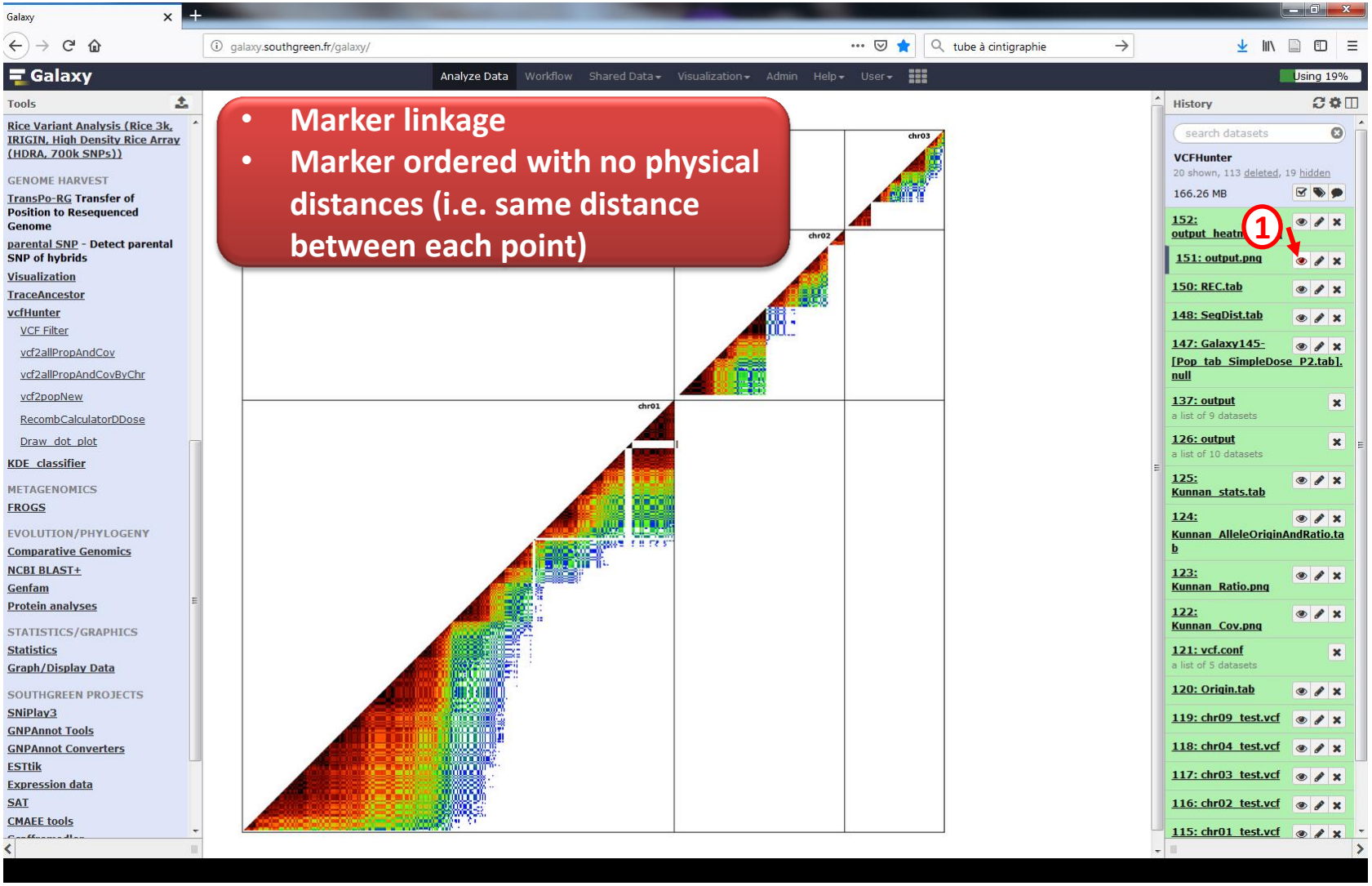
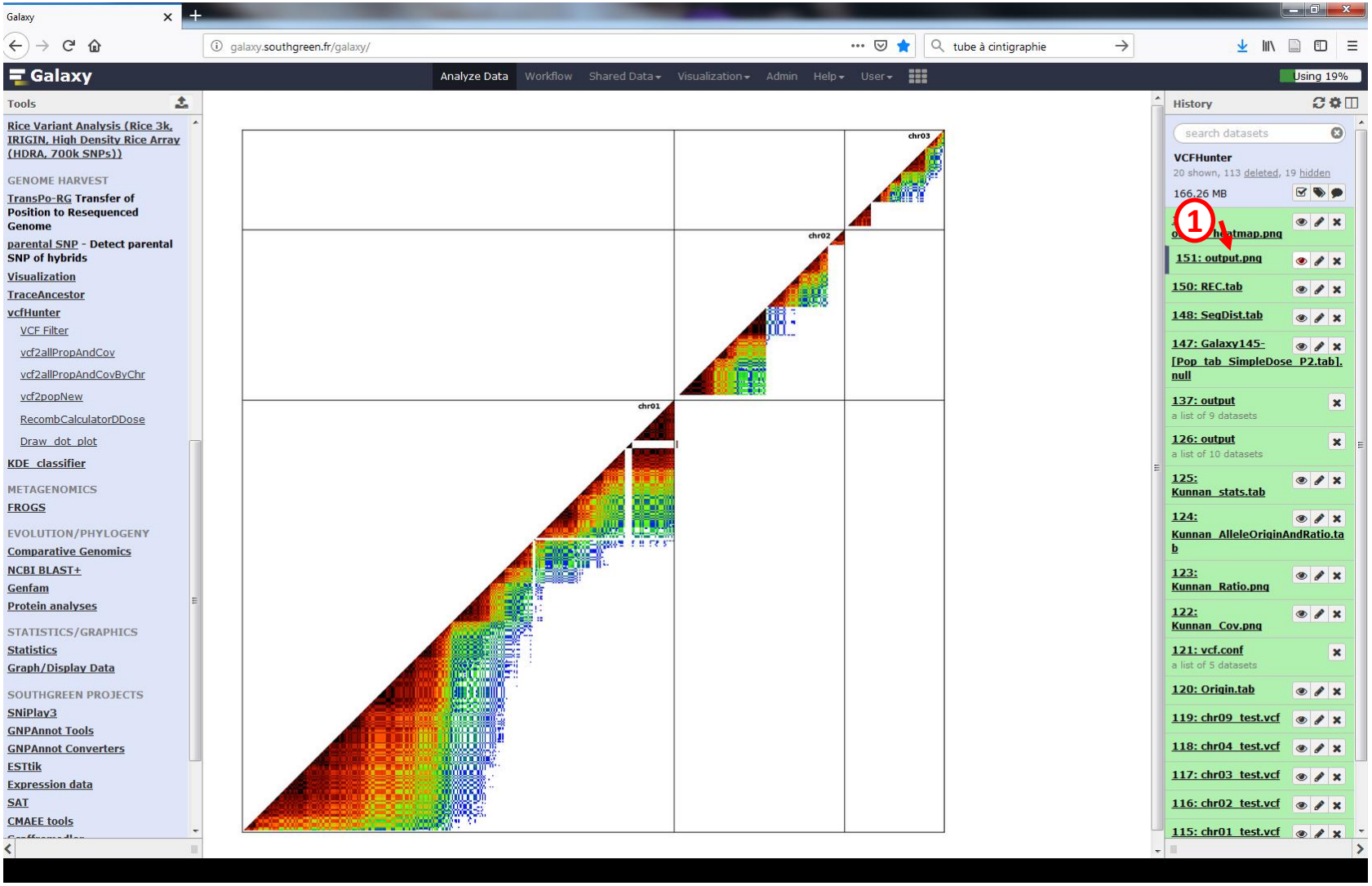


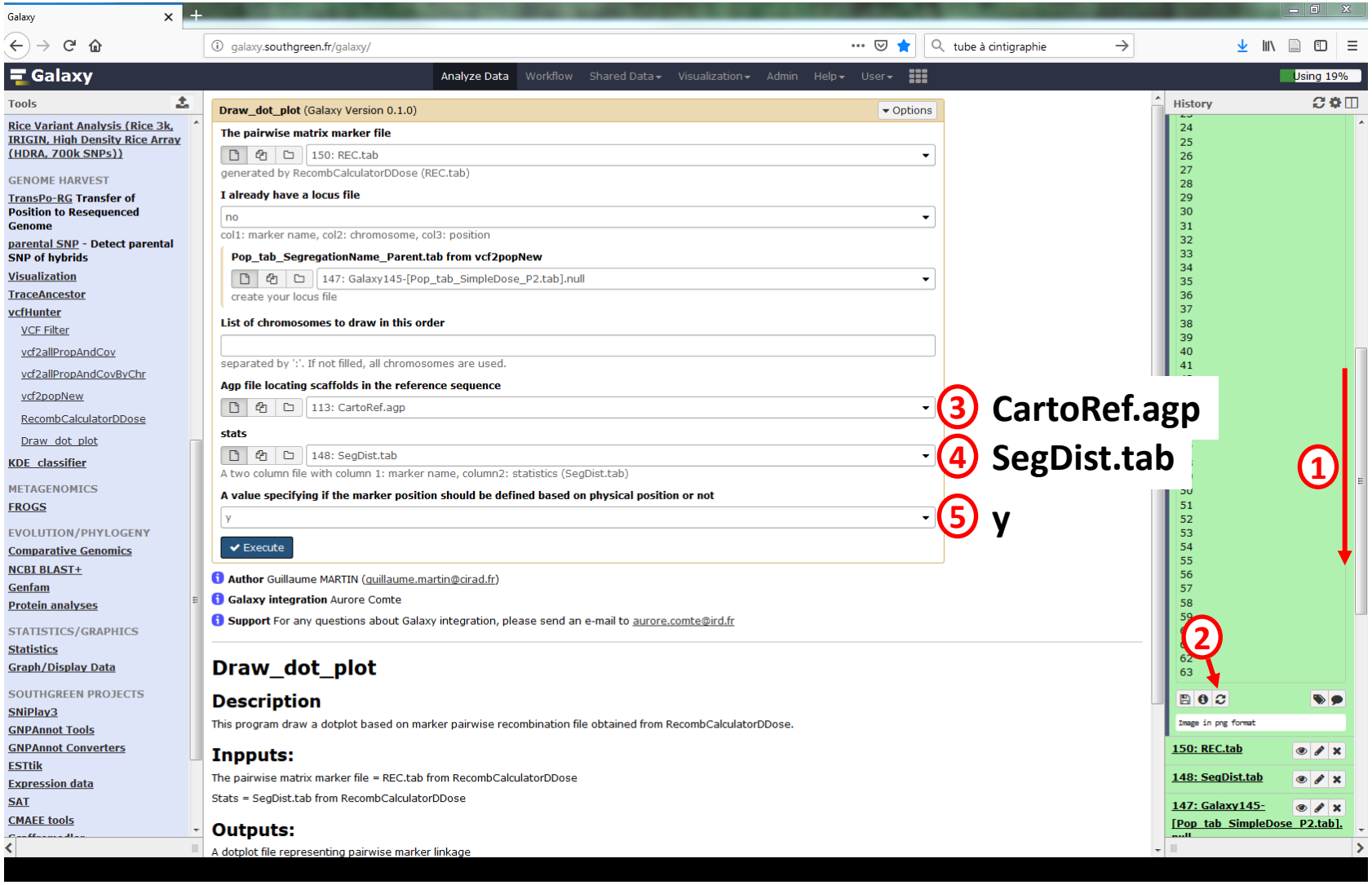
Genetic mapping analysis with vcfHunter tool

Plotting pairwise recombination with other options



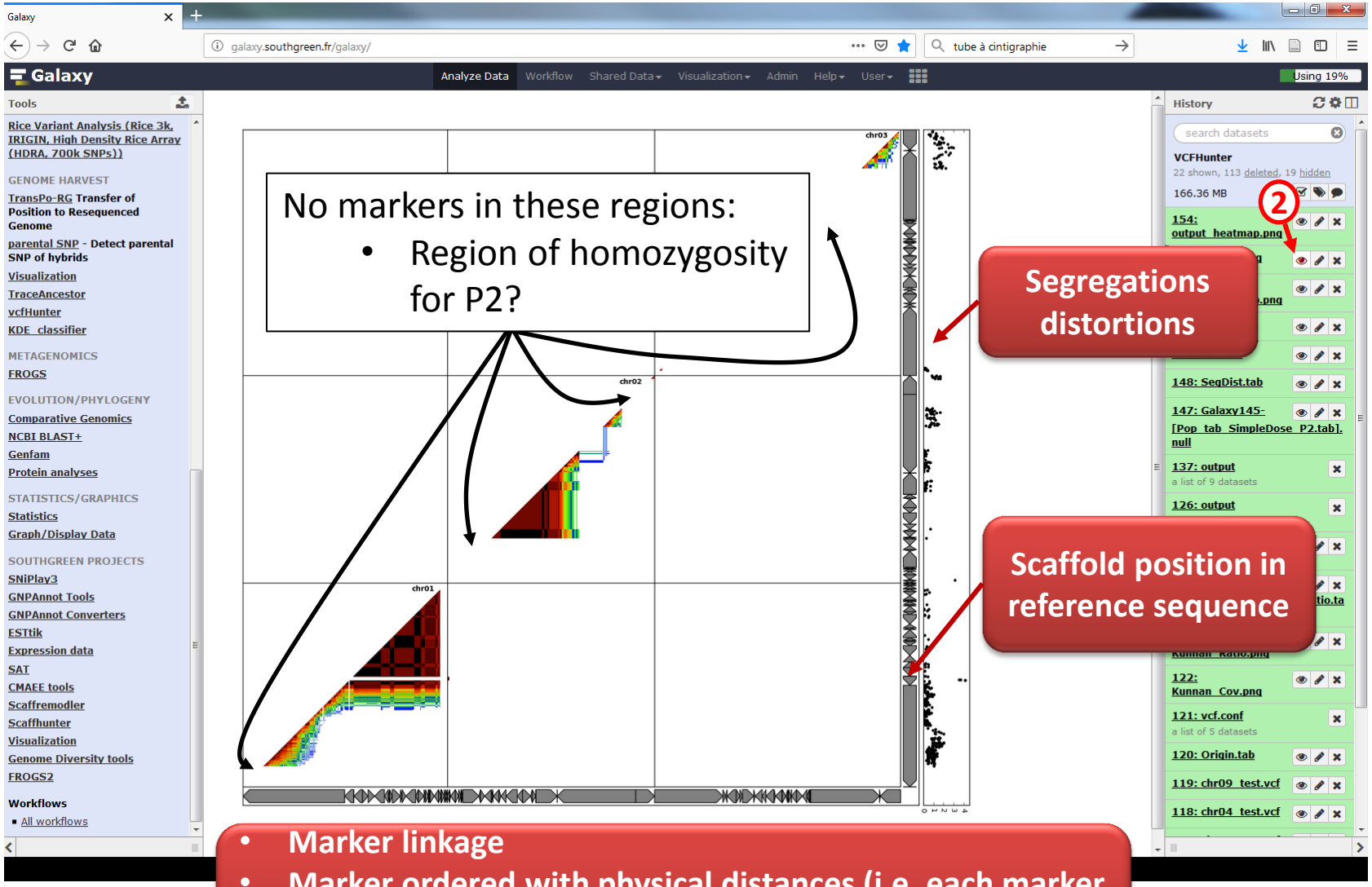
Genetic mapping analysis with vcfHunter tool

Plotting pairwise recombination with other options



Genetic mapping analysis with vcfHunter tool

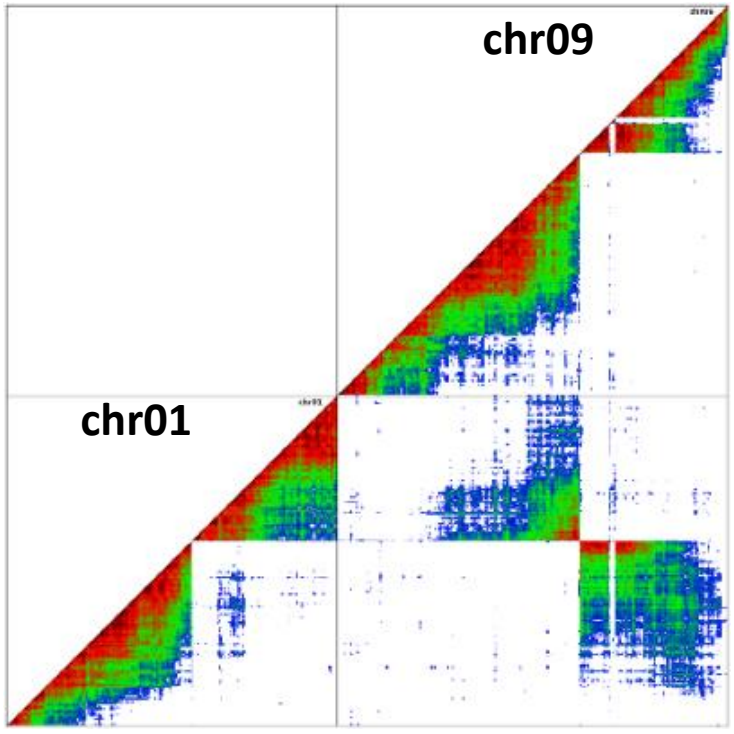
Plotting pairwise recombination with other options



Genetic mapping analysis with vcfHunter tool

Plotting pairwise recombination with other populations

Evidence of reciprocal translocations between chromosome 1 and 9



Evidence for large segregation distortions and inter-chromosomal linkage