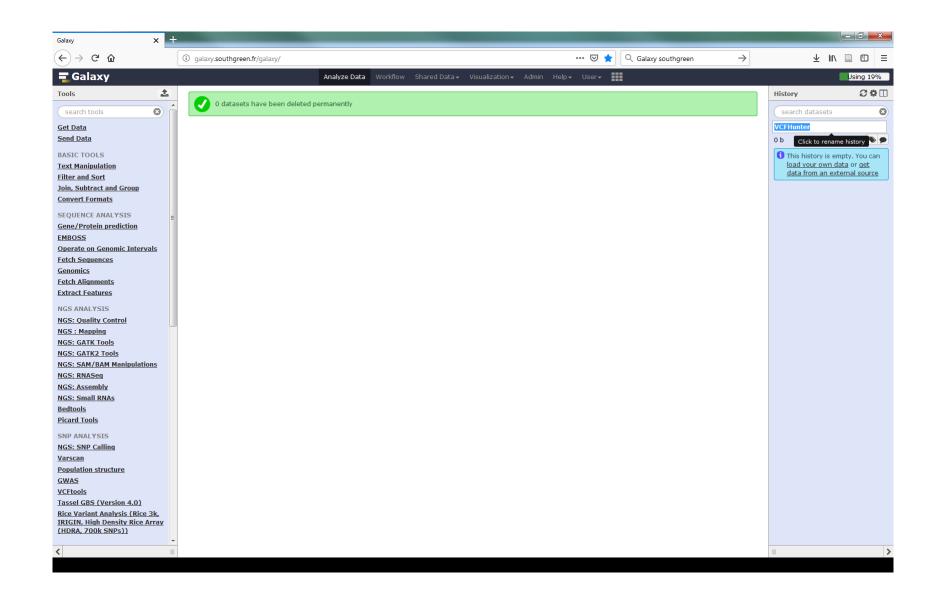
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## Renaming the History (easier to find analysis)









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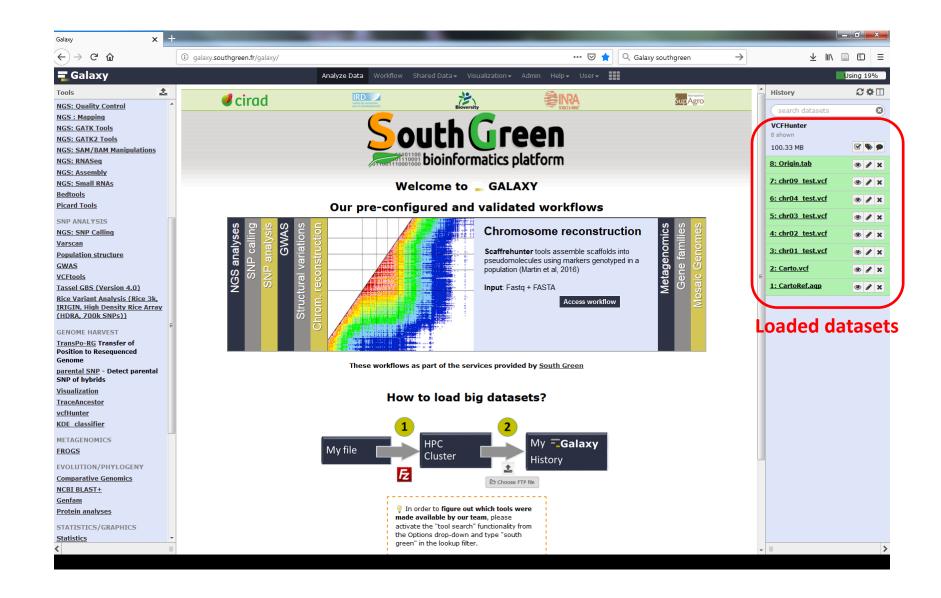
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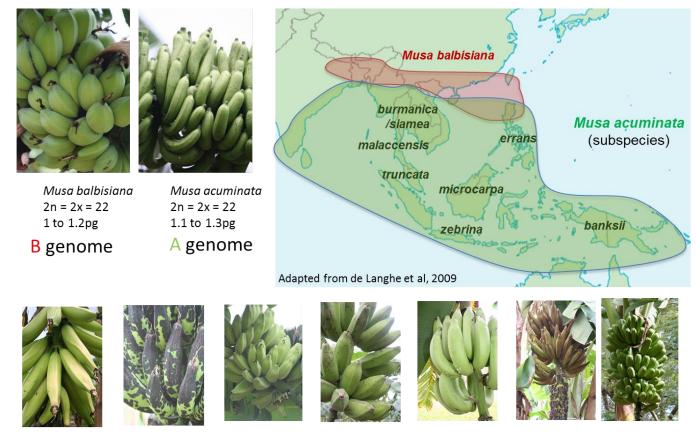


### Going back to history





# **Chromosome painting with vcfHunter tool** Developed to answer banana problematics



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?



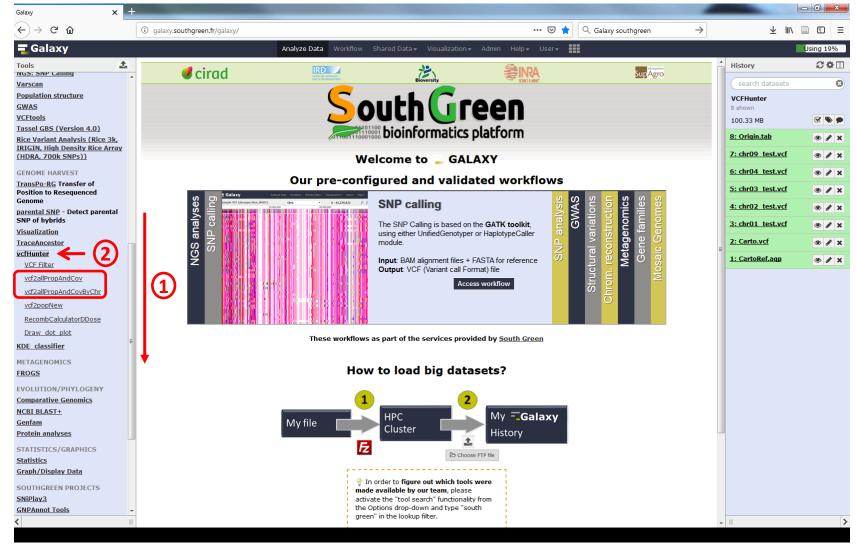
GenomeHarvest

Slide adapted from F.C Baurens

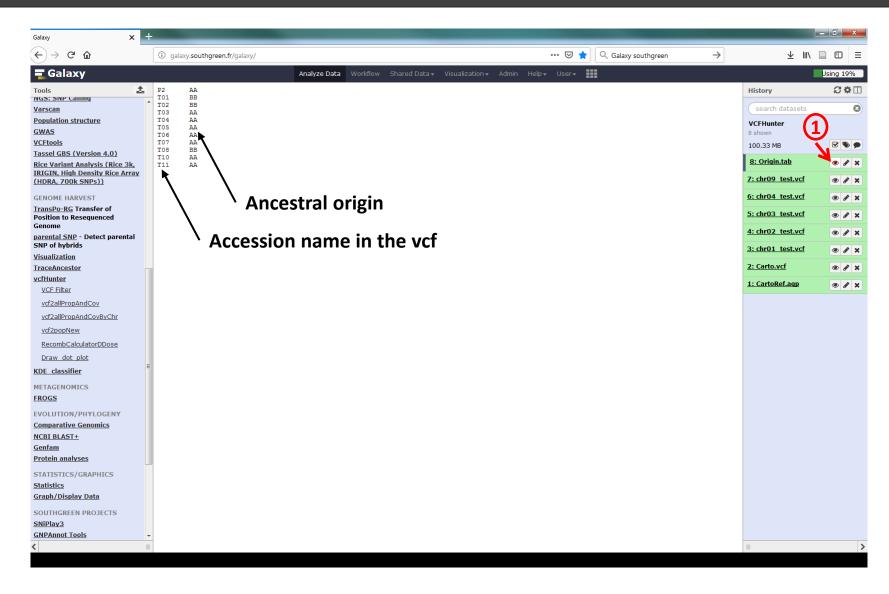
What is the contribution of ancestral genomes along chromosomes of cultivated

hybrids?

Several tools developed under vcfHunter toolbox for this purpose:



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



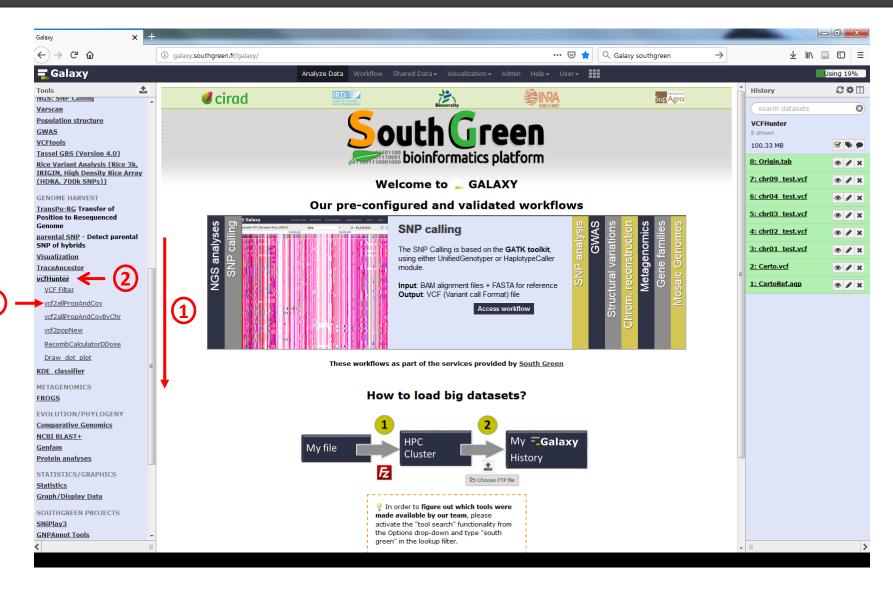


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Used data: Several vcf files containing the genotypes of 15 accessions

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FROGS	This program perform two things based on a vcf.			
EVOLUTION/PHYLOGENY				
Comparative Genomics	<ol> <li>It plots for an accession, the allele coverage alongs its chromosomes.</li> <li>It identify, based on known ancestral accessions in the vcf, the alleles specific to each groups and plot</li> </ol>	ot the alleles proportion at a site in the accession along chromosom	ies.	
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ROGS	Support For any questions about Galaxy integration, please send an e-mail to <u>aurore.comte@ird.fr</u>			
EVOLUTION/PHYLOGENY			_	
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NCBI BLAST+	VCIZAIIFIOPAIIdCOV			
<u>Genfam</u> Protein analyses	E Description			
	This program perform two things based on a vcf.			
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FROGS	<b>Support</b> For any questions about Galaxy integration, please send an e-mail to <u>aurore.comte@ird.fr</u>		• / ×
EVOLUTION/PHYLOGENY Comparative Genomics		4: chr02 test.vcf	
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<u>Graph/Display Data</u>	Inputs:				
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CMAEE tools	102 DD				
<pre></pre>	Outputs:		- III		:



- 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:

GenomeHarvest

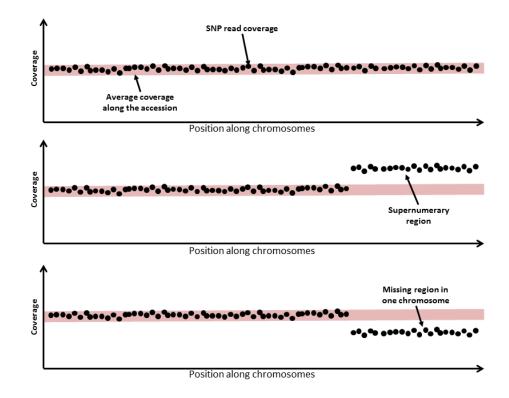
✓ Allele should be present in all member of the ancestral group ("yes" or "no")

		all accessions should have the allele	
		yes	<b>-</b>
$\checkmark$	Missing data are ac	cepted in member of ancestral group ("yes	" or "no")
		ancestral accession can't have missing data	
		no	<b>_</b>

- Calculate, in the studied accession, the proportion of read having this allele
  - Plot this proportion (D) Tetraploid and 2 ancestral origins (C) Triploid and 2 ancestral origins (1 red and 3 green) (A) Diploid and 1 (B) Diploid and 2 (2 red and 1 green) ancestral origin ancestral origins Allele ratio 0.75 0.66 0.33 0.25 Position along chromosomes

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

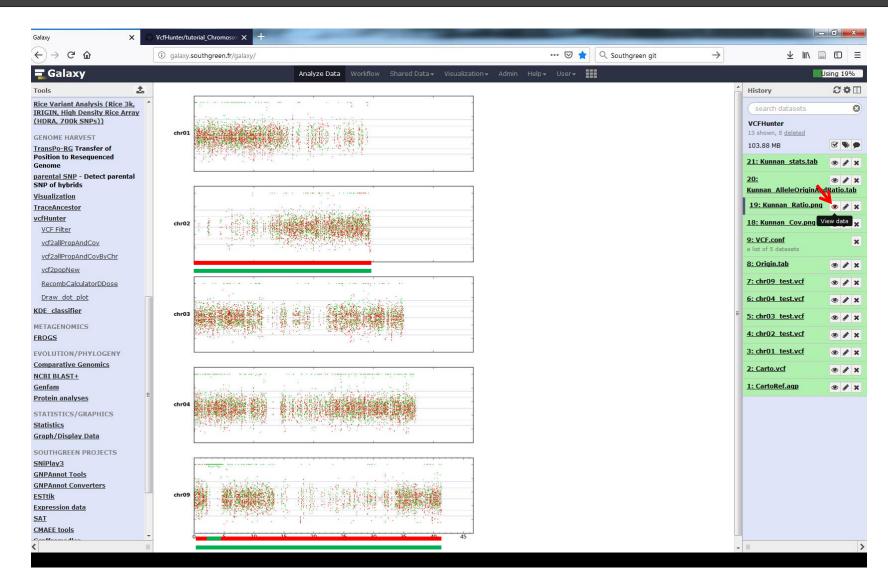
Plot normalized variant site coverage





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Protein analyses	chr04		
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vcf2allPropAndCovByChr	chr02 2432380 A BB	0.59523809 238095	Allele ancestral group	8: Origin.tab	● / ×
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Draw dot plot	chr02 2432383 A AA	0.4285714285714285	Attributed allele	6: chr04 test.vcf	● / ×
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Comparative Genomics	chr02 2447319 T BB	0.4242424242424242425		2: Carto.vcf	⊛ / ×
NCBI BLAST+	chr02 2447319 A AA	0.5757575757575758			
Genfam	chr02 2447328 G BB	0.375		1: CartoRef.agp	👁 🖋 🗙
Protein analyses	chr02 2447328 A AA	0.625			
STATISTICS/GRAPHICS	chr02 2480263 G BB	0.48			
Statistics	chr02 2480263 C AA	0.52			
Graph/Display Data	chr02 2480266 A BB	0.4782608695652174			
	chr02 2487990 G BB chr02 2487990 A AA	0.472222222222222			
SOUTHGREEN PROJECTS SNiPlay3	chr02 2487990 A AA chr02 2575326 T BB	0.527777777777778 0.5714285714285714			
GNPAnnot Tools	chr02 2575326 C AA	0.42857142857142855			
GNPAnnot Tools GNPAnnot Converters	chr02 2696749 T BB	0.6			
ESTtik	chr02 2696749 C AA	0.4			
Expression data	chr02 4387494 C BB	0.5			
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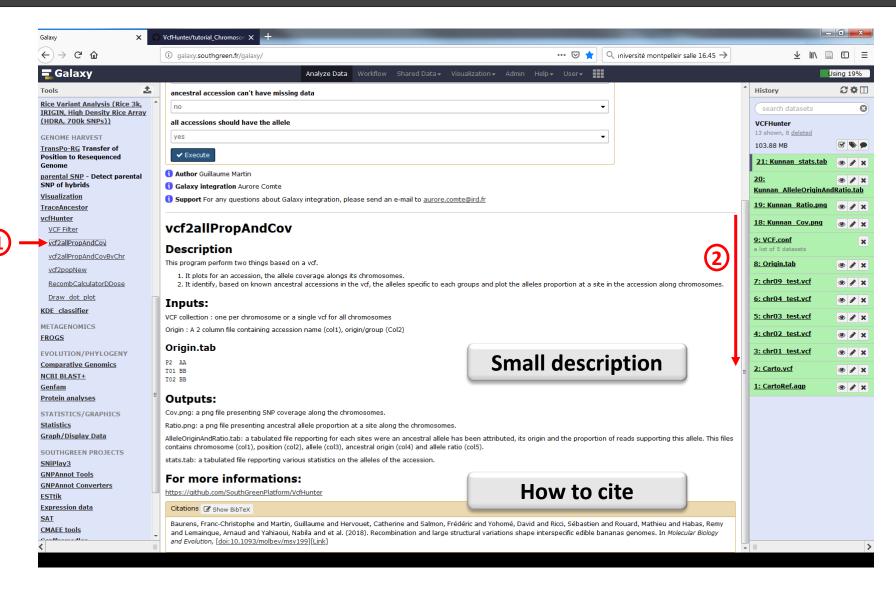
1- Chromosome painting of one accession : To go further

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KDE classifier	Author Guillaume Martin			5: chr03_test.vcf	• / ×
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<u>NCBI BLAST+</u> <u>Genfam</u>	Description			1: CartoRef.agp	⊛ / ×
Protein analyses	This program perform two things based on a vcf.				
STATISTICS/GRAPHICS	1. It plots for an accession, the allele coverage alongs its chromosomes.				
Statistics	2. It identify, based on known ancestral accessions in the vcf, the alleles speci	ic to each groups and plot the alleles proportion at a site i	n the accession along chromosomes.		
<u>Graph/Display Data</u>	Inputs:				
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GNPAnnot Tools	Origin : A 2 column file containing accession name (col1), origin/group (Col2)				
GNPAnnot Converters	Origin.tab				
ESTtik	P2 AA				
Expression data SAT	T01 BB T02 BB				
CMAEE tools					
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Running the analysis with other options, other accessions of the vcf. Other hybrids names in the vcf GP1 (triploid), P1 (tetraploid) and P025 (triploid)



1- Chromosome painting of one accession : Additional information

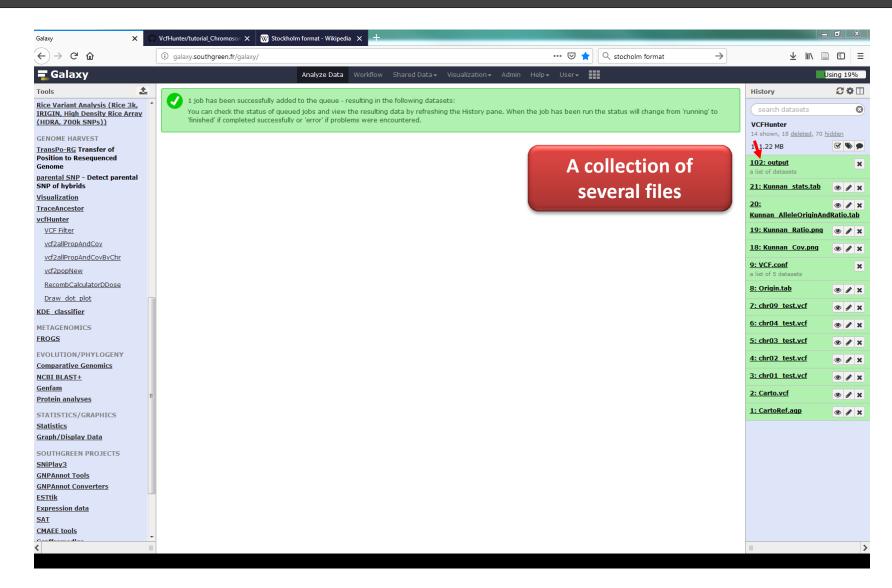




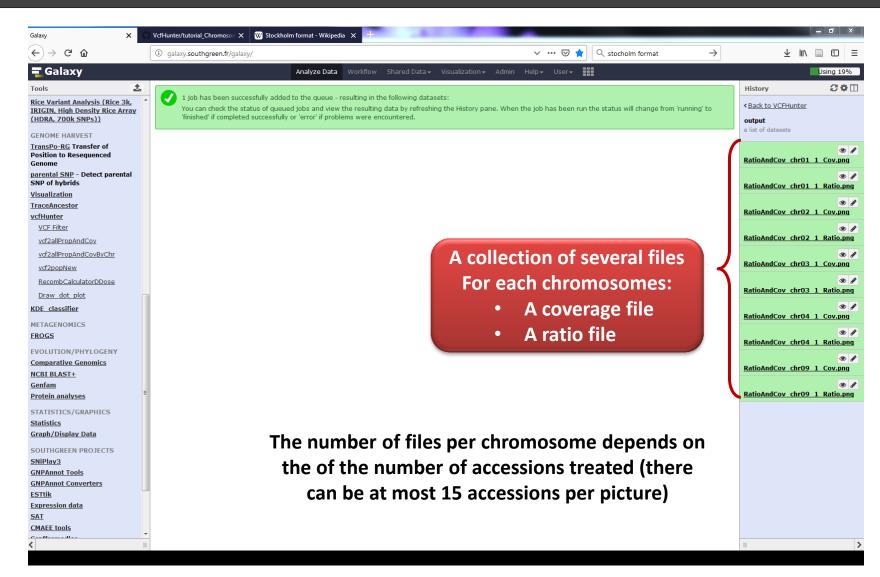
2- Comparison of several accessions

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parental SNP - Detect parental SNP of hybrids	accessions to work with	004 D	
Visualization	T04,T02,Kunnan,GP1,P025,P1 3 T04,T02,Kur	inan,GP1,P	025,P1
TraceAncestor	Several accession names should be separated by a , . If this parameter is omitted, the picture will be drawn for all accessions found in the vcf	Kunnan AlleleOrigin/	and Datio tab
vcfHunter	ploidy of accessions	Kunnan AlleleOriginA	AndKatio.tab
VCF Filter	ع (triploid -۱) 3 (triploid -۱	not verv im	nortant
vcf2allPropAndCov	ancestral accessions can't have missing data		portain
vcf2allPropAndCovByChr vcf2popNew		<u>9: VCF.conf</u>	×
RecombCalculatorDDose	all accessions should have the allele	a list of 5 datasets	
Draw dot plot		8: Origin.tab	
KDE classifier		7: chr09 test.vcf	👁 🖋 🗙
METAGENOMICS		6: chr04 test.vcf	• / ×
FROGS	<b>3</b> Author Guillaume MARTIN : <u>guillaume.martin@cirad.fr</u> , Marion Dupouy : <u>marion.dupouy@cirad.fr</u> , Franc-Christophe Baurens: <u>baurens@cirad.fr</u>	5: chr03 test.vcf	● / ×
EVOLUTION/PHYLOGENY	Galaxy integration Aurore Comte     Galaxy integration, please send an e-mail to aurore.comte@ird.fr     Support For any questions about Galaxy integration, please send an e-mail to aurore.comte@ird.fr	<u>4: chr02_test.vcf</u>	
Comparative Genomics	Support For any questions about Galaxy integration, please send an e-mail to <u>autore.comte@ird.ir</u>		
NCBI BLAST+	vert2allDreanAndCov/Dv/Chr	<u>3: chr01_test.vcf</u>	
<u>Genfam</u> <u>Protein analyses</u>	vcf2allPropAndCovByChr	2: Carto.vcf	👁 🖋 🗙
STATISTICS/GRAPHICS	Description	1: CartoRef.agp	● # ×
Statistics	This program perform two things based on a vcf.		
Graph/Display Data	<ol> <li>It plots for a chromosome of all accessions in a vcf, the allele coverage alongs its chromosomes.</li> <li>It identify,based on known ancestral accessions in the vcf, the alleles specific to each groups and plot the alleles proportion at a site along chromosomes for all accessions.</li> </ol>		
SOUTHGREEN PROJECTS	2. A defininguased on known anceston and ecessions in the volume ances specific to each groups and procure aneles proportion at a size along chromosomes for an accessions.		
<u>SNiPlay3</u>	Inputs:		
<u>GNPAnnot Tools</u> <u>GNPAnnot Converters</u>	VCF collection : one per chromosome or a single vcf for all chromosomes		
ESTtik	Origin : A 2 column file containing accession name (col1), origin/group (Col2)		
Expression data	Origin.tab		
SAT	P2 AA		
Contraction	TO1 BB TO2 BB		
<		• III	>

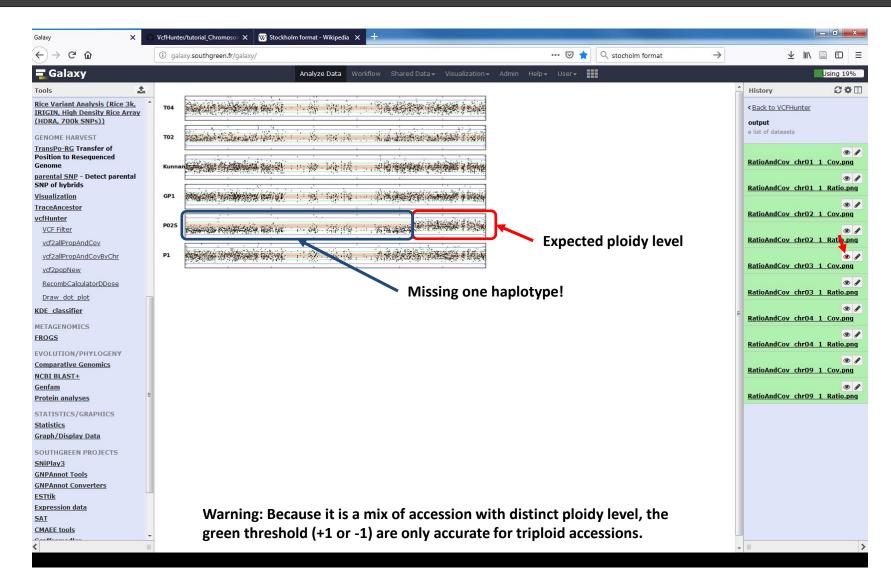




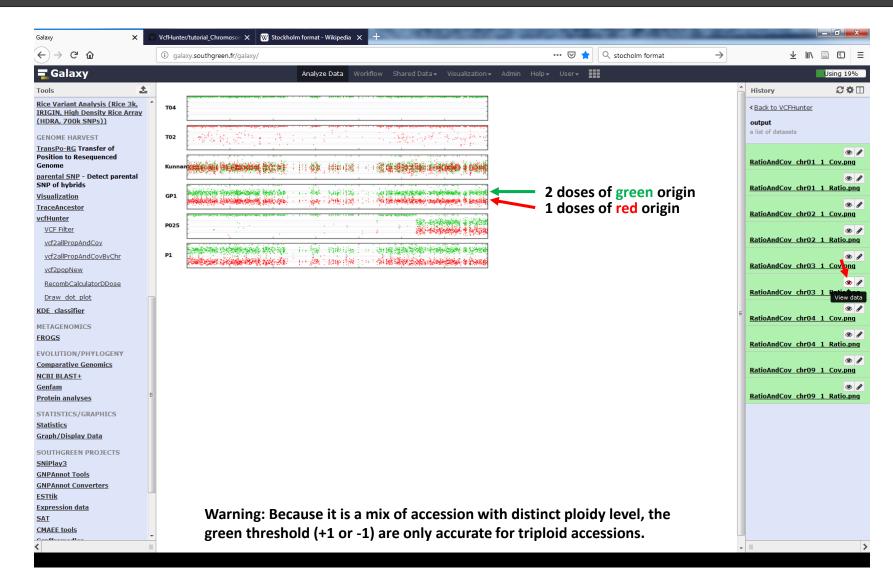






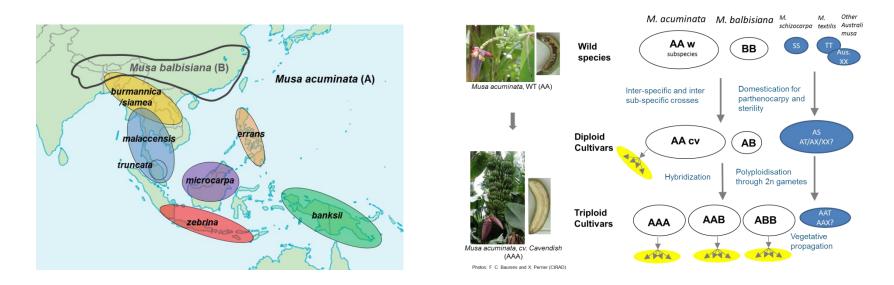








# Genetic mapping analysis with vcfHunter tool Developed to answer banana problematics



 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?



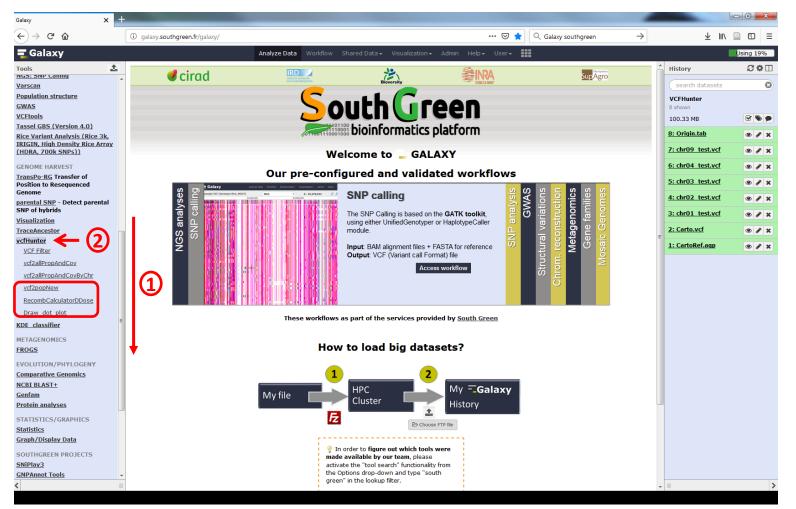
## Genetic mapping analysis with vcfHunter tool

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

Tools       Image: Construct of the second sec	Jsing 19%
Tools       Image: Search tools <td< th=""><th>CONTRACTOR</th></td<>	CONTRACTOR
search tools       Image: Control of the search dataset is large and only the first megabyte is shown below.       Search datasets         Search data         Send Data         BASIC TOOLS         Iext Manipulation         Fifther and Sort         HORNAT - (ID=C), Number=., Type=Integer, Description="Read Depth">         HORNAT - (ID=C), Number=., Type=Integer, Description="Converge For the ref and alt alleles in the order listed">         HORNAT - (ID=C), Number=., Type=Integer, Description="Converge For the ref and alt alleles in the order listed">         HORNAT - (ID=C), Number=., Type=Integer, Description="Converge For the ref and alt alleles in the order listed">         HORNAT - (ID=C), Number=., Type=Integer, Description="Converge For the ref and alt alleles in the order listed">         HORNAT - (ID=C), Number=., Type=Integer, Description="Converge For the ref and alt alleles in the order listed">         HORNAT - (ID=C), Number=., Type=Integer, Description="Converge For the ref and alt alleles in the order listed">         HORN	
search tools       Show all   Save       search datasets         Get Data       **fileformat=VCFV4.2       **fileformat=VCFV4.2         *#fileformat=VCFV4.2       **fileformat=VCFV4.2       **fileformat=VCFV4.2         #fileformat=VCFV4.2	hidden V V V X V X V X
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Iext Manipulation       ##FORMAT       ##FORMAT       Image: Im	• # ×
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Filed and Soft       ##FORMAT=(1)=CT, Numbe=1, Type=Strin, Description="Genotype">       21: Kunnan stats.tat         Join, Subtract and Group       ##GATKCommandLine.ViriantFiltration, CommandLineOptions="analysis_type=VariantFiltration input_file=[] showFullBamList=false read_buffer_size=1       21: Kunnan stats.tat         Convert Formats       ##Additionnal.filter=(ID=TAGRemoval, Description="WariantShpCluster are removed", Date="2018-01-08 14:37:19.913025">       21: Kunnan stats.tat         SEQUENCE ANALYSIS       ##Additionnal.filter=(ID=ChrOil, length=29070452>       ##Additionnal.filter=(ID=chrOil, length=29070452>       20:         #encl/Protein prediction       #econtig=(ID=chrOil, length=29070452>       #econtig=(ID=chrOil, length=29070452>       19: Kunnan AlleleOrigin/         #econtig=(ID=chrOil, length=29070452)       #econtig=(ID=chrOil, length=29070452)       19: Kunnan Ratio.pm         #econtig=(ID=chrOil, length=29070452)       #econtig=(ID=chrOil, length=35020413)       19: Kunnan Cov.pmg         Operate on Genomic Intervals       CREM POS ID REF ALI QUAL FILTER INFO FORMAT F191 F134 F135 F136 F137 F039 F038 F132 F133 F035 F034 F037       18: Kunnan Cov.pmg	۰ ک ×
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chr01 5163 . A C . PASS . GT:AD:DP:GC 0/0/0:58:0:58:3.26470499283e+18 0/0/1:71,11:82:5.03108366703e+12 0/0/1:53,7:	👁 🖋 🗙
Peter sequences	×
Centrol 8846 . A C . PASS . GT:AD:DP:GC 0/0/0:51,0:51:1.27000083428e+16 0/0/1:56,6:62:193.526687819 0/0/1:43,5:48:1405.	· ·
Fetch Alignments         chro1         8858         C         A         PASS         GT:AD:DP:GC         0/0/1:40,11:51:2.88230376152e+17         0/0/1:50,12:62:1.65030130534e+21         0/0           Extends Factures         chro1         8888         T         G         PASS         GT:AD:DP:GC         0/0/1:44,7:51:55522078.414         0/0/0:63:1.7344819115e+20         0/0/0:45,3:48:4393.1         8: Origin tab	
Extract Features         chr01         8888         T         G         PASS         GT:AD:DP:GC         0/0/1:44,7:51:55252078.414         0/0/0:63;1,7344819115e+20         0/0/0:45,3:48:4393.1         8: Origin.tab           chr01         8905         T         A         PASS         GT:AD:DP:GC         0/0/0:51,1:27000083428e+16         0/0/0:59,4:63:74842.0551806         0/0/1:42,5:47:2832.1	👁 🖋 🗙
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NGS: Quality Control chr01 17228 . A T . PASS . GT:AD:DP:GC 0/0/0:47,0:47:5.26129332617e+14 0/0/1:59,21:80:7.55578637259e+22 0/0/1:57,23	
chr01 20888 . G A . PASS . GT:AD:DP:GC 0/0/1:39,7:46:13301352470.1 0/0/0:53,0:53:6.07605004837e+16 0/0/0:60:1.598: 6:chr04 test.vcf	👁 🥖 🗙
NGS: GATK Tools         chr01         20916         T         C         PASS         GT:AD:DP:GC         0/0/0146,0:46:2.43891551199e+14         0/0/1:36,16:52:1.09951162778e+12         0/0/1:44,15           NGS: GATK2 Tools         chr01         20934         G         A         PASS         GT:AD:DP:GC         0/0/1:34,12:46:1.75921860444e+13         0/0/0:51,0:51:1.27000083428e+16         0/0/0:59,0:1	👁 🖋 🗙
NGS: SAMK 10003         chroll 21019         A         G         PASS         GT And DEGG         0/0/1349,25:7412,21474976711e+14         0/0/053,0:53:6.07608004837e+16         4: chr02 test.vc           NGS: SAM/BAM Manipulations         b         Employee         GT And DEGG         0/0/1:49,25:7412,21474976711e+14         0/0/0/053,0:53:6.07608004837e+16         0/0/0/055,0::         4: chr02 test.vc	• / ×
NGS. SAM/DAM Manufulduons chro1 29287 . C A . PASS . GT:AD:DP:GC 0/1/1:19,22:41:64.0 0/0/0:47,1:48:98747997863.5 0/0/1:47,12:59:1.1805916207:	
NGS: RNASeq         chro1         29391         A         T         PASS         GT:AD:DP:GC         0/0/0:41,0:41:4.62632016737e+12         0/0/1:63,9:72:1432921316.62         0/0/1:52,10:62:1.31         3: chr01         test.vcf           NGS: Assembly         chr01         29415         T         G         PASS         GT:AD:DP:GC         0/0/0:41,0:41:4.62632016737e+12         0/0/0:69,0:69:2.0563920187e+22         0/0/0:59;0:59:7.102         3: chr01         test.vcf	👁 🖋 🗙
NGS: Small RNAs chr01 37131 . C T . PASS . GT:AD:DP:GC 0/0/1:33,13:46:1.09951162778e+12 0/1/1:32,41:73:262144.0 0/0/1:47,18:6512.88:	🤏 🖋 🗙
Bedtools         chr01 37155         C         T         PASS         GT:AD:DP:GC         0/0/1:33,13:46:1.09951162778e+12         0/1/1:32,41:73:262144.0         0/0/1:44,18:62:4.50         1: CartoRef.agp	👁 🥒 🗙
Picard Tools         chr01         50285         T         C         FASS         GT:AD:DP:GC         0/0/0:47,0:47:5.26129332617e+14         0/0/1:68,12:80:2.70381667849e+16         0/0/1:30,12	
SNP ANALYSIS         Chrol         50313         T         C         PASS         GT:AD:DP:GC         0/0/01:47,0:47:5.26129332617e+14         0/0/1:67,12:79:5.04415731515e+16         0/0/1:31,12           SNP ANALYSIS         chrol         50330         G         A         PASS         GT:AD:DP:GC         0/0/1:32,15:47:17179869184.0         0/0/1:41,38:79:64.0         0/0/1:34,9:43:1.12589990684	
NGS: SNP Calling Chr01 53409 . C G . PAS5 . GTAD.DF:GC 0/0/0161.01611353489552419 0/01/14.155644.5035962737e415 0/0/139.11	
Varsran C G . PASS . GT:AD:DP:GC 0/0/1:44,16:60:7.20575940379e+16 0/0/0:56,0:56:6.56046544339e+17 0/0/1:37,14	
chro1 59316 . G A . PASS . GT:AD:DP:GC 0/0/1:35,23:58:16777216.0 0/0/0:58:3.26470499283e+18 0/0/1:55,22:77:7.37	
Population structure         chro1         59428         T         C         PASS         GT:AD:DP:GC         0/0/1:40,11:51:2.88230376152e+17         0/0/1:47,27:74:1.09951162778e+12         0/0,           GWAS         chro1         67413         T         A         PASS         GT:AD:DP:GC         0/0/01:50,0158:3.26470499283e+18         0/0/1:61,19:80:1.93428131138e+25         0/0/1:55,17	
GWAS         Child 0/413         I         A         PASS         G1:Ab/DF/GC         0/0/053,05532264/0592635410 0/01(3;15:041:554263131644:53         0/0/153,17           VCFtools         chr01         67461         G         A         PASS         G1:Ab/DF/GC         0/0/058,05532264/0592636410 0/01(3;15:041:554263131664:53         0/0/153,17	
chr01 67517 . C A . PASS . GT:AD:DP:GC 0/0/1:36,14:50:1.75921860444e+13 0/0/0:58,1:59:4.82026012455e+14 0/0/1:53,8:	
Tassel GBS (Version 4.0)         chro1         67527         T         G         PASS         GT:AD:DP:GC         0/0/0:50,0:50:5.64444815235e+15         0/0/1:48,11:59:9.29162287927e+18         0/0/1:50,11	
Rice Variant Analysis (Rice 3k, IRIGIN, High Density Rice Array         chr01         67556         T         C         PASS         GT:AD:DP:GC         0/0/0:50,0:50:5.64444815235e+15         0/0/0:57,2:59:66552899445.0         0/0/0:55,5:60:3.011           IRIGIN, High Density Rice Array         chr01         89901         A         C         PASS         GT:AD:DP:GC         0/0/0:52,0:52:2.80333245379e+16         0/0/0:41,0:41:4.62632016737e+12         0/0/0:36:93382-	
IRIGIN, High Density Rice Array         chr01         89901         A         C         PASS         GT:AD:DP:GC         0/0/0:52,0:52:2.80333245379e+16         0/0/0:41,0:41:4.62632016737e+12         0/0/0:36;93382           (HDRA, 700k SNPs))         chr01         89911         T         C         PASS         GT:AD:DP:GC         0/0/0:52,0:52:2.80333245379e+16         0/0/0:41,0:41:4.62632016737e+12         0/0/0:36;93382	
v         chr01         89917         C         T         .         PASS         .         GT:AD:DD:GC         0/0/0:52,0:52:2.80333245379e+16         0/0/1:41,12:53:2.88230376152e+17         0/0/1:37,12	
chroll 89923 G T - PASS GTLAD:DP:GC 0/0/0152.0155/2.6033245379e16 0/0/1140.121527.7.20575940379e16 0/0/1137.12	



## **Genetic mapping analysis with vcfHunter tool** Used data: An agp file locating scaffolds in the reference assembly

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ools 🛃		1	2	3	4	5	6	7	8	9		- Histo	ory	C
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Cat Data		chr01	1	10853	1	W	scaffold1006	1	10853	+		VCE	lunter	
<u>Set Data</u> Send Data		chr01 chr01	10854 10954	10953 14478003	2	N W	100 scaffold3	fragment 1	no 14467050	-			own, 18 <u>deleted</u> , 80	hidder
enu Data		chr01	14478004	14478103	4	N	100	fragment	no				22 MB	8
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ext Manipulation		chr01	15769261	15769360	6	N	100	fragment	no				output	
Iter and Sort		chr01	15769361	15814576	7	w	scaffold551	1	45216	+		a list	of 10 datasets	
oin, Subtract and Group		chr01	15814577	15814676	8	N	100	fragment	no			21: 1	<u>Cunnan stats.tab</u>	۲
onvert Formats		chr01	15814677	17019194	9	w	scaffold63	1	1204518	-		201		
EQUENCE ANALYSIS		chr01	17019195	17019294	10	N	100	fragment	no			<u>20:</u>	an AlleleOriginAr	ک tenha
Sene/Protein prediction	=	chr01	17019295	17819353	11	w	scaffold100	1	800059	+		Kunn		lukati
MBOSS		chr01	17819354	17819453	12	N	100	fragment	no			<u>19: F</u>	Cunnan Ratio.png	۲
)perate on Genomic Intervals		chr01	17819454	18738040	13	w	scaffold84	1	918587	+		10-1	unnan Cov.png	
etch Sequences		chr01	18738041	18738140	14	N	100	fragment	no			10.1	Cov.pig	۲
enomics		chr01	18738141	20132513	15	w	scaffold50	1	1394373	-		<u>9: V</u>	F.conf	
etch Alignments	Ш.	chr01	20132514	20132613	16	N	100	fragment	no			a list	of 5 datasets	
xtract Features		chr01	20132614	20699287	17	w	scaffold152	1	566674	-		8: 0	igin.tab	۲
		chr01	20699288	20699387	18	N	100	fragment	no					
IGS ANALYSIS		chr01	20699388	20894093	19	W	scaffold290	1	194706	-		<u>7: ch</u>	r09_test.vcf	۲
IGS: Quality Control		chr01	20894094	20894193	20	N	100	fragment	no			6: ch	r04 test.vcf	۲
IGS : Mapping		chr01	20894194	21247679	21	W	scaffold216	1	353486	+		<u></u>		•
IGS: GATK Tools		chr01	21247680	21247779	22	N W	100	fragment	N0			<u>5: ch</u>	r03 test.vcf	۲
IGS: GATK2 Tools		chr01 chr01	21247780 22417286	22417285 22417385	23 24	N	scaffold65 100	1	1169506 no	+				
IGS: SAM/BAM Manipulations		chr01	22417286	22652210	24	W	scaffold267	fragment 1	234825	+		<u>4: cn</u>	r02_test.vcf	۲
GS: RNASeq		chr01	22652211	22652310	25	N	100	fragment	23462J NO	+		<u>3: ch</u>	r01 test.vcf	۲
GS: Assembly		chr01	22652311	23188813	27	W	scaffold157	1	536503	+				/
IGS: Small RNAs		chr01	23188814	23188913	28	N	100	fragment	no			<u>2: Ca</u>	rto.vcf	۲
edtools		chr01	23188914	24583804	29	w	scaffold51	1	1394891	-		1:0	artoRef.agp	
icard Tools		chr01	24583805	24583904	30	N	100	fragment	no					•
NP ANALYSIS		chr01	24583905	24963756	31	w	scaffold209	1	379852	-				
IGS: SNP Calling		chr01	24963757	24963856	32	N	100	fragment	no					
/arscan		chr01	24963857	25777628	33	W	scaffold99	1	813772	+				
opulation structure		chr01	25777629	25777728	34	N	100	fragment	no					
WAS		chr01	25777729	25974873	35	W	scaffold288	1	197145	+				
CFtools		chr01	25974874	25974973	36	N	100	fragment	no					
assel GBS (Version 4.0)		chr01	25974974	26399442	37	W	scaffold188	1	424469	+				
ice Variant Analysis (Rice 3k,		chr01	26399443	26399542	38	Ν	100	fragment	no					
RIGIN, High Density Rice Array		chr01	26399543	26446166	39	W	scaffold545	1	46624	+				
IDRA, 700k SNPs))		chr01	26446167	26446266	40	Ν	100	fragment	no					
	*	chr01	26446267	26479156	41	W	scaffold655	1	32890	-				
		chr01	26479157	26479256	42	N	100	fragment	no			<b>+</b>		



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<b>=</b> Galaxy	Analyze Data Workflow Shared Data + Visualization + Admin Help + User +		Using 19%
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Tassel GBS (Version 4.0)	The vcf filevcf		< Back to VCFHunter
<u>Rice Variant Analysis (Rice 3k,</u> IRIGIN, High Density Rice Array (HDRA, 700k SNPs))		•	output a list of datasets
	Segregation testedseg		
GENOME HARVEST TransPo-RG Transfer of	Several segregations can be passed and should be separated by /. A segregation should look like as follows:		RatioAndCov chr01 1 Cov.png
Position to Resequenced Genome	Name:Parents:MarkerCoding:MarkerSegregation: DvalueForTest: With a real example: SimpleDose:P1,P2:Ho,He@nn,np:0.5,0.5:1e- 5/Bridge:P1,P2:Ho,He,Ho@hh,hk,kk:0.25,0.5,0.25:1e-5 (Ho for homozygous, He for heterozygous)		•
parental SNP - Detect parental SNP of hybrids	Minimal read coverage for a marker in an accessionMinCOv		RatioAndCov chr01 1 Ratio.png
Visualization	10	E	RatioAndCov chr02 1 Cov.png
TraceAncestor	If a lower value is found data point is converted to missing.		
<u>vcfHunter</u>	Maximal read coverage for a marker in an accessionMaxCov		RatioAndCov chr02 1 Ratio.png
<u>VCF Filter</u>	1000		
vcf2allPropAndCov	If a greater value is found data point is converted to missing.		RatioAndCov chr03 1 Cov.png
vcf2allPropAndCovByChr	Window for minority allele coverage frequency to be insufficient to call a heterozygous but to high to call an homozygousWinFree	q	
vcf2popNew	0.01:0.1		RatioAndCov chr03 1 Ratio.pnq
RecombCalculatorDDose	(example: "0.05:0.1"). With the example if minority allele is in ]0.05:0.1] calling will become missing for this data point.		
Draw dot plot	Minimal read number of minor allele to call variant heterozygousMinAlCov	_	RatioAndCov chr04 1 Cov.png
KDE_classifier	1		
METAGENOMICS	Maximal missing data proportion in the progeny (Excluding parents)miss		RatioAndCov chr04 1 Ratio.png
FROGS	0.1		۲
EVOLUTION/PHYLOGENY	greater missing proportion will result in removing the marker.		RatioAndCov chr09 1 Cov.png
Comparative Genomics	Add allele coverage information to genotype fileaddcov		
NCBI BLAST+	no	-	RatioAndCov chr09 1 Ratio.png
<u>Genfam</u> Protein analyses	If this option is passed, in addition to genotypes, alleles coverage information is also filled.		
	accessions to exclude from the filtrationNoUsed		
STATISTICS/GRAPHICS	D 🙆 C Nothing selected	-	
<u>Statistics</u> <u>Graph/Display Data</u>	A tabultated file containing in one column, names of accessions to exclude from the filtration (based on missing data and p-value) but which will be kept in final files.		
SOUTHGREEN PROJECTS	accessions to exclude from the analysisexclude		
SNiPlay3	C 2 C Nothing selected	-	
GNPAnnot Tools	A tabultated file containing in one column, names of accessions to exclude from the analysis and the files.	_	
GNPAnnot Converters	The reference fasta fileref		
ESTtik	C 2 Nothing selected	-	
Expression data SAT	If passed, a tag associated to the marker will be outpouted in a fasta file. This tag will contained 125 bases before the marker and 125		
-	bases after.		
	remove	-	· · · · · · · · · · · · · · · · · · ·



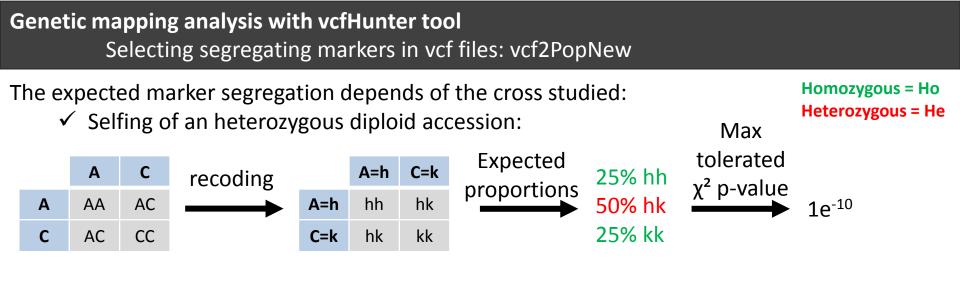
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$\leftrightarrow$ > C $\textcircled{a}$	(	🛈 galaxy.southgreen.fr/galaxy/ 🚥 🖂 🕇	२ southgreen git —	∢	<u>↓</u> III\ 📄 🗊 🗏
<b>=</b> Galaxy		Analyze Data Workflow Shared Data - Visualization - Admin Help - User -			Using 19%
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Tassel GBS (Version 4.0)	^	The vcf filevcf			< Back to VCFHunter
Rice Variant Analysis (Rice 3k,		C 2 119: chr09_test.vcf			output
<u>IRIGIN, High Density Rice Array</u> (HDRA, 700k SNPs))		Segregation tes			a list of datasets
GENOME HARVEST		119: chr09_test.vcf			<b>()</b>
TransPo-RG Transfer of		Several segrega 118: chr04_test.vcf			RatioAndCov chr01 1 Cov.png
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parental SNP - Detect parental		Minimal read co			RatioAndCov chr01 1 Ratio.png
SNP of hybrids		10 115: chr01_test.vcf			
Visualization		114: Carto.vcf	Carto.vcf		RatioAndCov chr02 1 Cov.png
TraceAncestor		If a lower value is round and point to conversed to microing.			. /
vcfHunter		Maximal read coverage for a marker in an accessionMaxCov			RatioAndCov chr02 1 Ratio.png
VCF Filter		1000			
vcf2allPropAndCov		If a greater value is found data point is converted to missing.			RatioAndCov chr03 1 Cov.png
vcf2allPropAndCovByChr		Window for minority allele coverage frequency to be insufficient to call a heterozygous but to high to call an homozygousWinFreq			
<u>vcf2popNew</u>		0.01:0.1			RatioAndCov chr03 1 Ratio.png
RecombCalculatorDDose		(example: "0.05:0.1"). With the example if minority allele is in ]0.05:0.1] calling will become missing for this data point.			
Draw dot plot		Minimal read number of minor allele to call variant heterozygousMinAlCov			RatioAndCov chr04 1 Cov.png
KDE_classifier	L	1			
METAGENOMICS	L	Maximal missing data proportion in the progeny (Excluding parents)miss			RatioAndCov chr04 1 Ratio.png
FROGS		0.1			۲ (
EVOLUTION/PHYLOGENY		greater missing proportion will result in removing the marker.			RatioAndCov chr09 1 Cov.png
Comparative Genomics	-	Add allele coverage information to genotype fileaddcov			۵ (
NCBI BLAST+	-	no			RatioAndCov chr09 1 Ratio.png
<u>Genfam</u> Brotein analyses		If this option is passed, in addition to genotypes, alleles coverage information is also filled.			
<u>Protein analyses</u>		accessions to exclude from the filtrationNoUsed			
STATISTICS/GRAPHICS		C 2 Nothing selected			
Statistics		A tabultated file containing in one column, names of accessions to exclude from the filtration (based on missing data and p-value) but			
<u>Graph/Display Data</u>		which will be kept in final files.			
SOUTHGREEN PROJECTS		accessions to exclude from the analysisexclude			
<u>SNiPlay3</u>		C 4 D Nothing selected			
GNPAnnot Tools		A tabultated file containing in one column, names of accessions to exclude from the analysis and the files.			
<u>GNPAnnot Converters</u> <u>ESTtik</u>		The reference fasta fileref			
Expression data		C 2 Nothing selected			
<u>SAT</u>	-	If passed, a tag associated to the marker will be outpouted in a fasta file. This tag will contained 125 bases before the marker and 125 bases after.			
<					-
		remove			



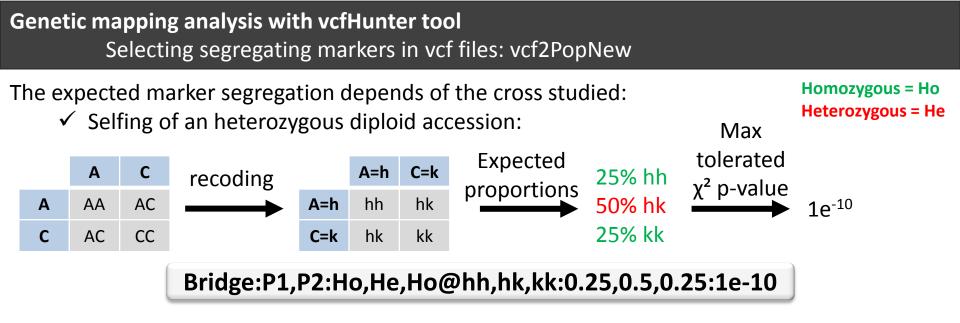
Selecting segregating markers in vcf files: vcf2PopNew

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<b>=</b> Galaxy	Analyze Data Workflow Shared Data + Visualization + Admin H	lelp + User +	Using 19%
Tools	vcf2popNew (Galaxy Version 0.1.0)	✓ Options	🔒 History 🛛 🕄 🗘 🔲
Tassel GBS (Version 4.0)	The vcf filevcf	• Options	< Back to VCFHunter
Rice Variant Analysis (Rice 3k,	• • • • • • • • • • • • • • •		output
IRIGIN, High Density Rice Array (HDRA, 700k SNPs))	Segregation testedseg		a list of datasets
GENOME HARVEST	Segregation testedseg		
TransPo-RG Transfer of	Several segregations can be passed and should be separated by /. A segregation should look like as follows:		RatioAndCov chr01 1 Cov.png
Position to Resequenced Genome	Name:Parents:MarkerCoding:MarkerSegregation:PvalueForTest. With a real example: SimpleDose:P1,P2:Ho,He@nn,r 5/Bridge:P1,P2:Ho,He,Ho@hh,hk,kk:0.25,0.5,0.25:1e-5 (Ho for homozygous, He for heterozygous)	np:0.5,0.5:1e-	• /
parental SNP - Detect parental	Minimal read coverage for a marker in an accessionMinCOv		RatioAndCov chr01 1 Ratio.png
SNP of hybrids	10	Marker	۲ ک
Visualization TraceAncestor	If a lower value is found data point is converted to missing.		atioAndCov_chr02_1_Cov.png
vcfHunter	Maximal read coverage for a marker in an accessionMaxCov	segregation(s) tested	۲ ا
VCF Filter	1000		atioAndCov_chr02_1_Ratio.png
vcf2allPropAndCov	If a greater value is found data point is converted to missing.	to select markers	
vcf2allPropAndCovByChr	Window for minority allele coverage frequency to be insufficient to call a heterozygous but to high to call an hor	nozygouswinFreq	katioAndCov chr03 1 Cov.png
<u>vcf2popNew</u>	0.01:0.1		RatioAndCov chr03 1 Ratio.png
RecombCalculatorDDose	(example: "0.05:0.1"). With the example if minority allele is in ]0.05:0.1] calling will become missing for this data point	t.	
Draw dot plot	Minimal read number of minor allele to call variant heterozygousMinAlCov		RatioAndCov chr04 1 Cov.png
KDE classifier	1		
METAGENOMICS	Maximal missing data proportion in the progeny (Excluding parents)miss		RatioAndCov chr04 1 Ratio.png
FROGS	0.1		•
EVOLUTION/PHYLOGENY	greater missing proportion will result in removing the marker.		RatioAndCov chr09 1 Cov.png
Comparative Genomics	Add allele coverage information to genotype fileaddcov		۲ ک
NCBI BLAST+ Genfam		<b>~</b>	RatioAndCov chr09 1 Ratio.png
Protein analyses	If this option is passed, in addition to genotypes, alleles coverage information is also filled.		
STATISTICS/GRAPHICS	accessions to exclude from the filtrationNoUsed		
Statistics	A tabultated file containing in one column, names of accessions to exclude from the filtration (based on missing data	and p-value) but	
<u>Graph/Display Data</u>	which will be kept in final files.		
SOUTHGREEN PROJECTS	accessions to exclude from the analysisexclude		
SNiPlay3	C 4 D Nothing selected	<b></b>	
GNPAnnot Tools GNPAnnot Converters	A tabultated file containing in one column, names of accessions to exclude from the analysis and the files.		
ESTtik	The reference fasta file ref		
Expression data	C Nothing selected     If passed, a tag associated to the marker will be outpouted in a fasta file. This tag will contained 125 bases before the second	the marker and 125	
SAT	bases after.		
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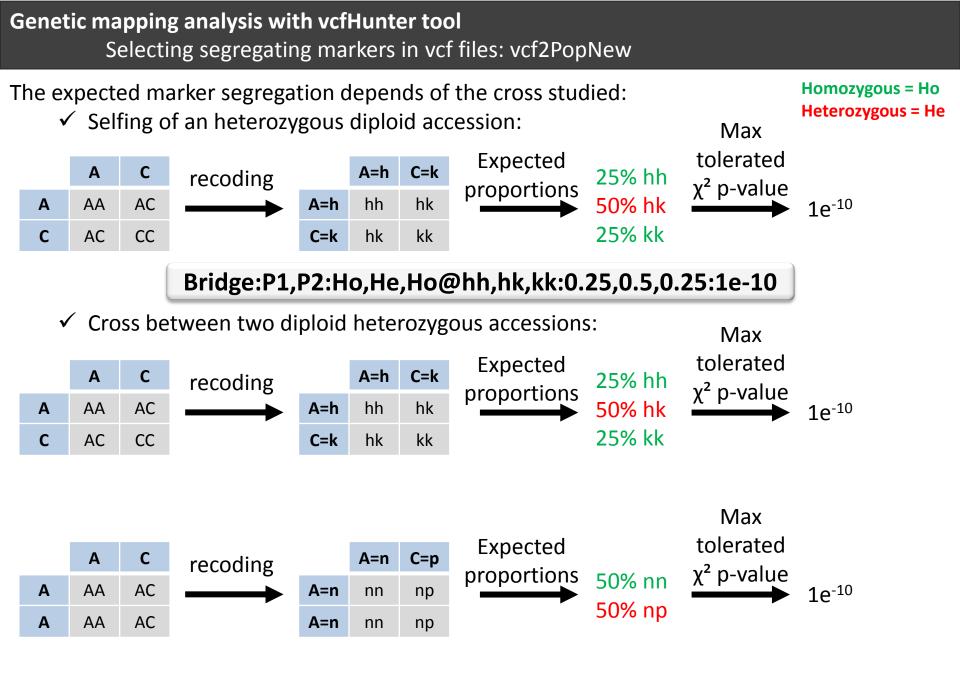




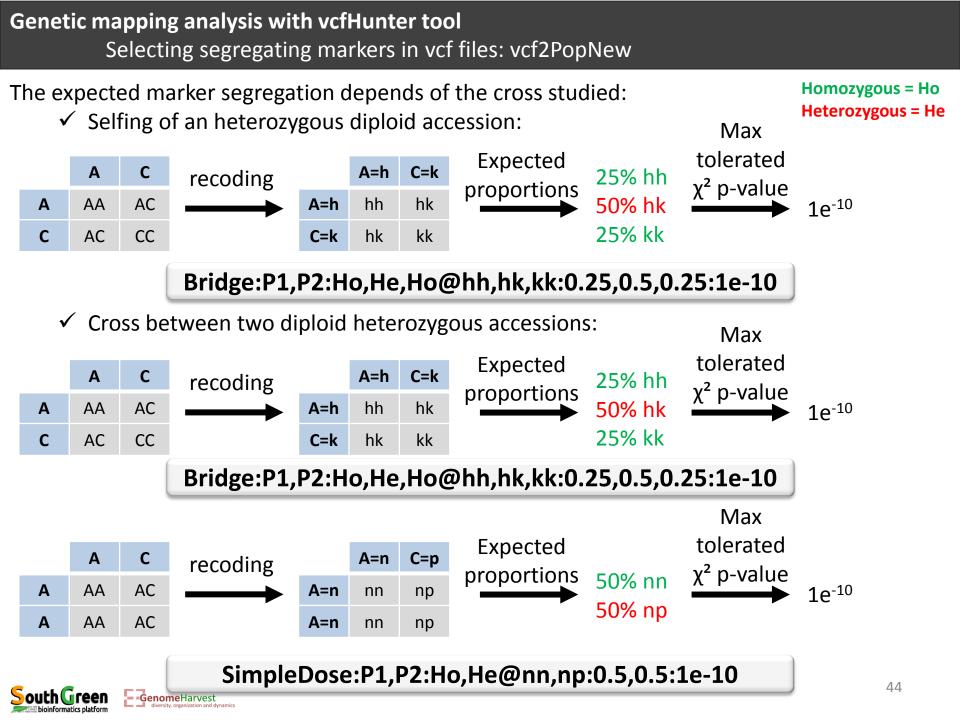












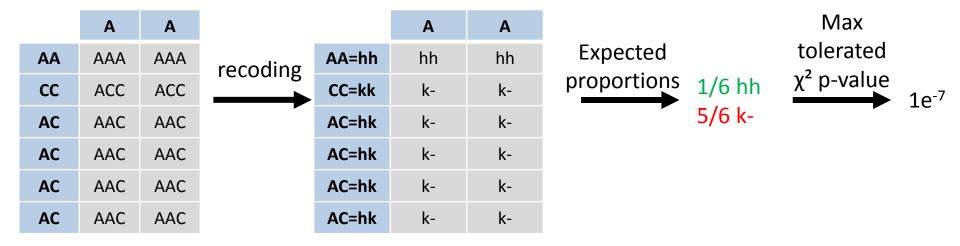
The expected marker segregation depends of the cross studied:

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

Homozygous = Ho

Heterozygous = He

45

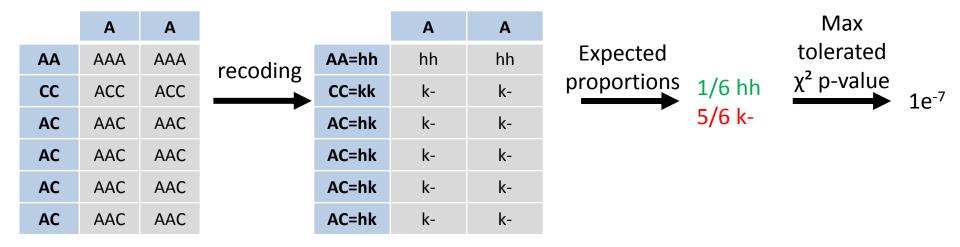


Homozygous = Ho

Heterozygous = He

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 (e.g: P2 genotype = A/A/C/C, P1 genotype = C/C)

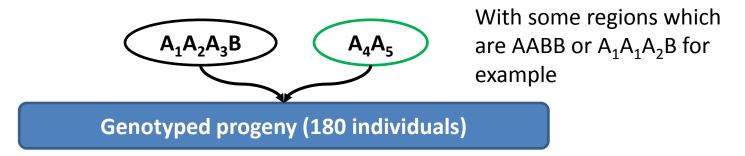


DoubleDose:P1,P2:Ho,He@hh,k-:0.1667,0.8333:1e-7



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!



✓ We will select markers for several segregations

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

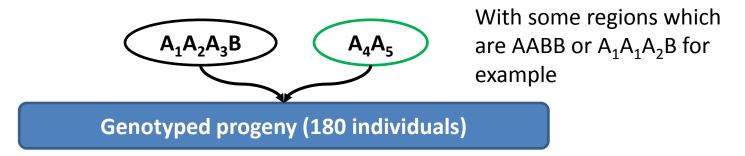
Bridge:P1,P2:Ho,He,Ho@hh,hk,kk:0.25,0.5,0.25:1e-10

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



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!



✓ 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



Selecting segregating markers in vcf files: vcf2PopNew

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<b>=</b> Galaxy		Analyze Data 🛛 Workflow Shared Data 🗸 Visualization 🗸 Admin Help 🗸 User 🗸 🌉	Using 19%
Tools	vcf2popNew (Galaxy Version 0.1.0)	▼ Options	🔒 History 😂 🕸 🖽
Tassel GBS (Version 4.0)	The vcf filevcf		< Back to VCFHunter
Rice Variant Analysis (Rice 3k,	114: Carto.vcf		output
IRIGIN, High Density Rice Array (HDRA, 700k SNPs))	Segregation testedseg		a list of datasets
GENOME HARVEST			۵ ۵
TransPo-RG Transfer of		nould be separated by /. A segregation should look like as follows: ation:PvalueForTest. With a real example: SimpleDose:P1.P2:Ho.He@nn.np:0.5.0.5:1e-	RatioAndCov chr01 1 Cov.png
Position to Resequenced Genome		5,0.25:1e-5 (Ho for homozygous, He for heterozygous)	<b>()</b>
parental SNP - Detect parental SNP of hybrids	Minimal read coverage for a marker in		atio.png
Visualization	10	SimpleDose:P1,P2:Ho,He@nn,np:0	.5,0.5:1e-
TraceAncestor	If a lower value is found data point is co	· · · · · · · · · · · · · · · · · · ·	
vcfHunter	Maximal read coverage for a marker in	10/Bridge:P1,P2:Ho,He,Ho@hh,hk,kk:0.	25,0.5,0.25:1e-
VCF Filter	1000		
vcf2allPropAndCov	If a greater value is found data point is (	10/DoubleDose:P1,P2:Ho,He@hh,k-:0.16	067,0.8333:1e-7
vcf2allPropAndCovByChr	Window for minority allele coverage fr		
vcf2popNew	0.01:0.1	ninority allele is in ]0.05:0.1] calling will become missing for this data point.	RatioAndCov chr03 1 Ratio.png
<u>RecombCalculatorDDose</u> Draw dot plot	Minimal read number of minor allele to ca		۲ ا
KDE classifier			RatioAndCov chr04 1 Cov.png
METAGENOMICS		· · · · · · · · · · · · · · · · · · ·	•
FROGS	Maximal missing data proportion in the pr	ogeny (Excluding parents)miss	RatioAndCov chr04 1 Ratio.png
EVOLUTION/PHYLOGENY	0.1 greater missing proportion will result in rem	oving the marker.	RatioAndCov chr09 1 Cov.png
Comparative Genomics	Add allele coverage information to genoty		
NCBI BLAST+	E no	· ·	RatioAndCov chr09 1 Ratio.png
<u>Genfam</u>	If this option is passed, in addition to genot	ypes, alleles coverage information is also filled.	
<u>Protein analyses</u>	accessions to exclude from the filtration -	NoUsed	
STATISTICS/GRAPHICS Statistics	🗋 省 🗅 Nothing selected	▼	
<u>Graph/Display Data</u>	A tabultated file containing in one column, n which will be kept in final files.	ames of accessions to exclude from the filtration (based on missing data and p-value) but	
SOUTHGREEN PROJECTS	accessions to exclude from the analysis	exclude	
<u>SNiPlay3</u>	Nothing selected	<b></b>	
GNPAnnot Tools	A tabultated file containing in one column, n	ames of accessions to exclude from the analysis and the files.	
<u>GNPAnnot Converters</u> ESTtik	The reference fasta fileref		
ESTUR Expression data	D 2 D Nothing selected	<b>~</b>	
<u>SAT</u>	<ul> <li>If passed, a tag associated to the marker w bases after.</li> </ul>	ill be outpouted in a fasta file. This tag will contained 125 bases before the marker and 125	
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<b>=</b> Galaxy		Analyze Data Workflow Shared Data - Visualization - Admin Help - Us	ser <b>-</b>					Using 19%
	<b>1</b>	vcf2popNew (Galaxy Version 0.1.0)	▼ Options	1		- Hist	ory	<b>2</b> ‡⊡
Tassel GBS (Version 4.0)	^	The vcf filevcf				Se	earch datasets	8
Rice Variant Analysis (Rice 3k,		C 2 I14: Carto.vcf	-				Hunter	
IRIGIN, High Density Rice Array (HDRA, 700k SNPs))	2	Segregation testedseg					hown, 112 <u>deleted</u> , 1	0 <u>hidden</u>
GENOME HARVEST		:Ho,He@nn,np:0.5,0.5:1e-10/Bridge:P1,P2:Ho,He,Ho@hh,hk,kk:0.25,0.5,0.25:1e-10/DoubleDose:P1,P2:Ho,He@hh,k-:0.1667,0	0.8333:1e-7			102.	.91 MB	<b>S D</b>
TransPo-RG Transfer of		Several segregations can be passed and should be separated by /. A segregation should look like as follows:					: output	×
Position to Resequenced Genome		Name:Parents:MarkerCoding:MarkerSegregation:PvalueForTest. With a real example: SimpleDose:P1,P2:Ho,He@nn,np:0.5,0.5: 5/Bridge:P1,P2:Ho,He,Ho@hh,hk,kk:0.25,0.5,0.25:1e-5 (Ho for homozygous, He for heterozygous)	:1e-				of datasets	
parental SNP - Detect parental		Minimal read coverage for a marker in an accessionMinCOv				125	: Kunnan stats.tal	b 💿 🖋 🗙
SNP of hybrids <u>Visualization</u>		15		(1)	15	≡ <u>124</u>		🗶 🖋 🗙
TraceAncestor		If a lower value is found data point is converted to missing.					nan AlleleOriginA	
vcfHunter		Maximal read coverage for a marker in an accessionMaxCov				<u>123:</u> Kuni	<u>:</u> nan Ratio.png	● # ×
VCF Filter		300		(2)	300	122	: Kunnan Cov.png	l 🕑 🥒 🗙
vcf2allPropAndCov		If a greater value is found data point is converted to missing.						
vcf2allPropAndCovByChr		Window for minority allele coverage frequency to be insufficient to call a heterozygous but to high to call an homozygous	WinFreq				: vcf.conf of 5 datasets	×
<u>vcf2popNew</u>		0.01:0.1		(3)	0.01:0.1	120	: Origin.tab	• / ×
RecombCalculatorDDose		(example: "0.05:0.1"). With the example if minority allele is in ]0.05:0.1] calling will become missing for this data point.		$\sim$				
Draw dot plot		Minimal read number of minor allele to call variant heterozygousMinAlCov			•	<u>119</u>	: chr09 test.vcf	• / ×
KDE classifier		3		4	3	<u>118</u>	<u>: chr04 test.vcf</u>	👁 🖋 🗙
METAGENOMICS		Maximal missing data proportion in the progeny (Excluding parents)miss				117	: chr03 test.vcf	👁 🥒 🗙
FROGS		0.05		(5)	0.05	116	: chr02 test.vcf	⊛ / ×
EVOLUTION/PHYLOGENY Comparative Genomics		greater missing proportion will result in removing the marker.		$\sim$				
NCBI BLAST+	Ε	Add allele coverage information to genotype fileaddcov		$\bigcirc$		115	: chr01 test.vcf	
Genfam		no If this option is passed, in addition to genotypes, alleles coverage information is also filled.		$\mathbf{b}$	no	114	: Carto.vcf	👁 🖋 🗙
Protein analyses		accessions to exclude from the filtrationNoUsed				113	: CartoRef.agp	👁 🖋 🗙
STATISTICS/GRAPHICS		C 2 Nothing selected	-					
Statistics		A tabultated file containing in one column, names of accessions to exclude from the filtration (based on missing data and p-value	ue) but					
<u>Graph/Display Data</u>		which will be kept in final files.						
SOUTHGREEN PROJECTS		accessions to exclude from the analysisexclude						
<u>SNiPlay3</u> GNPAnnot Tools		A tabultated file containing in one column, names of accessions to exclude from the analysis and the files.	-					
GNPAnnot Converters		The reference fasta fileref						
ESTtik		C & C Nothing selected	•					
Expression data SAT		If passed, a tag associated to the marker will be outpouted in a fasta file. This tag will contained 125 bases before the marker	and 125					
<u>341</u>	*	bases after.						3
		remove				<b>T</b>		1

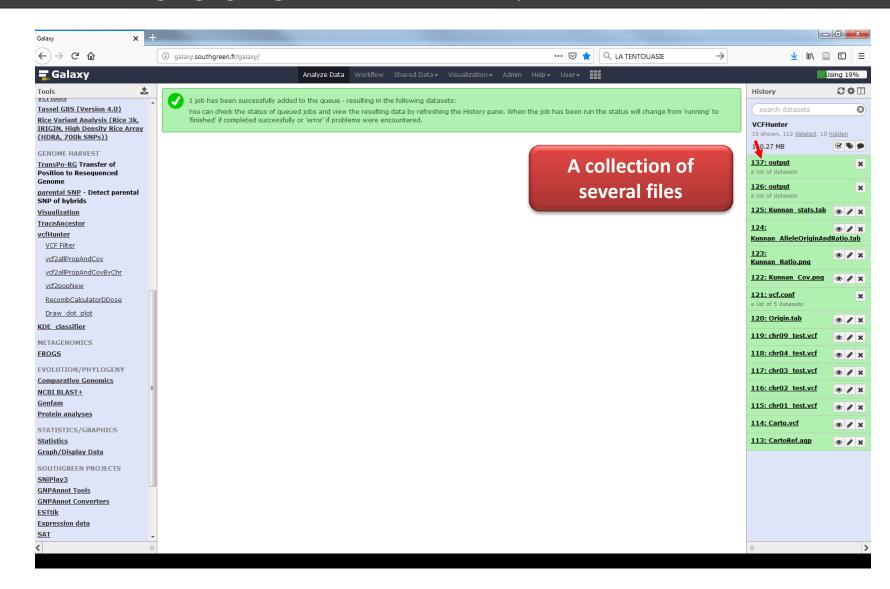


Selecting segregating markers in vcf files: vcf2PopNew

Galaxy 🗙	+	
← → ♂ û	① galaxy.southgreen.fr/galaxy/ ···· ▽ ★ Q google translate →	⊻ II\ 🗎 🗊 =
<b>=</b> Galaxy	Analyze Data Workflow Shared Data - Visualization - Admin Help - User -	Using 19%
Tools	1 If passed, a tag associated to the marker will be outpouted in a fasta file. This tag will contained 125 bases before the marker and 125	^ History C ♥ □
Tassel GBS (Version 4.0)	bases after.	search datasets
Rice Variant Analysis (Rice 3k		VCFHunter
IRIGIN, High Density Rice Arra (HDRA, 700k SNPs))	For some programs, marker name length is limited. This option helps you to reduce marker names. By default marker name is chromosome	14 shown, 112 <u>deleted</u> , 10 <u>hidden</u>
GENOME HARVEST	name+M+site position. A string can be passed that will be searched and removed from all marker name. This is not neccessary if your	102.91 MB
TransPo-RG Transfer of	chromosome name is not to long.	126: output ×
Position to Resequenced Genome		a list of datasets
parental SNP - Detect parental	1 Author Guillaume MARTIN (quillaume.martin@cirad.fr), Franc-Christophe BAURENS (franc-christophe.baurens@cirad.fr) and Olivier GARSMEUR (olivier.qarsmeur@cirad.fr)	125: Kunnan stats.tab 💿 🖋 🗙
SNP of hybrids	() Galaxy integration Aurore Comte	<u>124:</u> (9) 🖋 🗙
<u>Visualization</u> TraceAncestor	Support For any questions about Galaxy integration, please send an e-mail to <u>aurore.comte@ird.fr</u>	Kunnan AlleleOriginAndRatio.tab
vcfHunter		<u>123:</u> <u>Kunnan Ratio.png</u> ♥ ★
VCF Filter	vcf2popNew	
vcf2allPropAndCov	Description	122: Kunnan Cov.pnq 💿 🖋 🗙
vcf2allPropAndCovByChr	Description This program will select markers for genetical mapping analysis from a vcf file based on several criterias including segregation ratio. It will outpout coded markers as requested by	121: vcf.conf a list of 5 datasets
vcf2popNew	This program will select markets for genetical mapping analysis from a voline based on several citizensi including segregation ratio. It will outpout coded markets as requested by the user	
RecombCalculatorDDose	Inputs:	120: Origin.tab
Draw dot plot	VCF : vcf to work on (1)	<u>119: chr09_test.vcf</u> (*) * *
KDE classifier		<u>118: chr04_test.vcf</u>
METAGENOMICS	Outputs:	117: chr03 test.vcf 💿 🖋 🗙
FROGS	Pop_tab_Bridge.tab: A .tab file correponding to a simplified joinmap format that contained bridge markers.	116: chr02 test.vcf (*) / ×
EVOLUTION/PHYLOGENY	Pop_tab_SegregationName_Parent.tab: Two .tab filecorreponding to a simplified joinmap format that contained parent1 and parent2 markers respectively. Only if parent option is filled.	
Comparative Genomics NCBI BLAST+	Pop_tab_unknown.tab: A .tab file correponding to a simplified joinmap format that contained unknown parent markers (missing data for both parents). Only if parent option is filled	<u>115: chr01 test.vcf</u>
Genfam	Pop_report.tab: A file report.	<u>114: Carto.vcf</u>
Protein analyses	Pop_sub.vcf: A sub vcf corresponding to the original vcf with only lines corresponding toconserved markers (no filtering applied in this vcf).	113: CartoRef.agp 💿 🥒 🗙
STATISTICS/GRAPHICS Statistics	Pop.tab: A file containing for aech selected marker, the genotype of each accessions based on filter applied. Two additional values are added at the end of the file: the Khi-Square value and the P-value of the test.	E
<u>Statistics</u> Graph/Display Data	Pop_tags.fasta: A fasta file containing marker tags (to align against another reference genome for example). Only ifref option is filled.	
SOUTHGREEN PROJECTS	Pop_tab_unknown.tab: is a marker coded file corresponding to selected marker that cannot be attributed to one of the two parent.	
SNiPlay3	For more informations:	
GNPAnnot Tools	https://qithub.com/SouthGreenPlatform/VdfHunter	
GNPAnnot Converters	Citations & show BibTeX	
ESTtik Expression data		
SAT	Baurens, Franc-Christophe and Martin, Guillaume and Hervouet, Catherine and Salmon, Frédéric and Yohomé, David and Ricci, Sébastien and Rouard, Mathieu and Habas, Remy and Lemainque, Arnaud and Yahiaoui, Nabila and et al. (2018). Recombination and large structural variations shape interspecific edible bananas genomes. In Molecular Biology	
<	and Evolution, [doi:10.1093/molbev/msy199][Link]	-



Selecting segregating markers in vcf files: outputs





Selecting segregating markers in vcf files: outputs

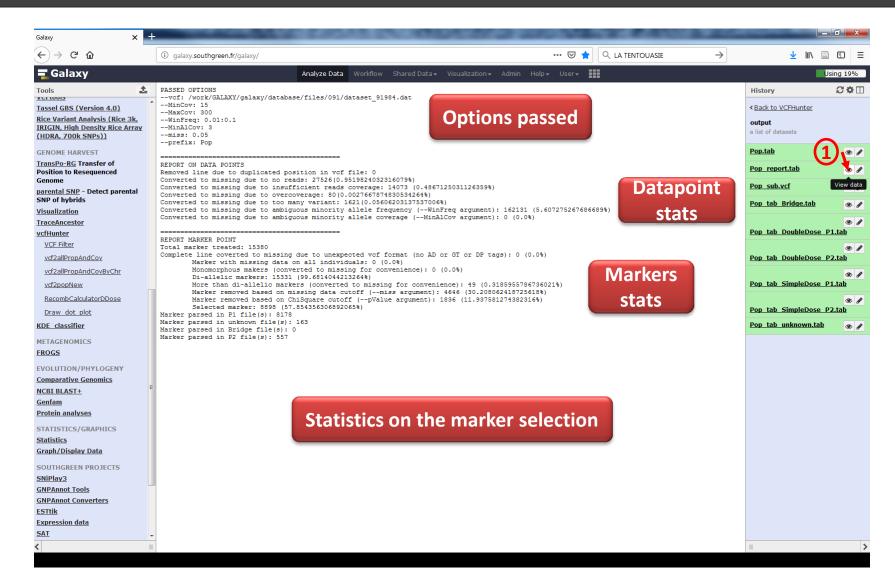
Galaxy X	+				_	_												_			_ 0 <mark>_</mark> X
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Galaxy				Anal	yze Data	Workfle	ow Sha	ared Data	ı∓ Visı	ualization	- Adm	in Help	I <del>▼</del> Use	r <b>- 11</b>							Using 19%
Tools																				History	C 🕸 🛛
Tassel GBS (Version 4.0)		dataset is l <u>1 all</u>   <u>Save</u>	large and only	the first m	egabyte is	s shown t	below.													< Back to VCFHunt	<u>er</u>
Rice Variant Analysis (Rice 3k,		·																		output	6
IRIGIN, High Density Rice Array (HDRA, 700k SNPs))	chom	osome	position	P191	P134	P135	P136	P137	P039	P038	P132	P133	P035	P034	P037	P036	P031	P030	P03:	a list of datasets	UN.
	417228 Chiro1M20912	chr01 chr01	17228 A/ 20912 G/		A/T G/G	A/T G/G	A/A G/A	A/T G/A	A/A G/G	./. G/A	A/T G/A	A/T G/G	A/T G/G	A/A G/G	A/A G/A	A/T G/G	A/A G/G	A/A G/G	A/T G/G	Des tab	
SENOME HARVEST	chr01M20912	chr01	20912 G/ 20916 T/		T/C	T/C	T/T	T/C	I/I	T/T	T/C	T/C	T/C	T/T	T/T	T/C	T/T	T/T	T/C	Pop.tab	۲
<u>FransPo-RG</u> Transfer of Position to Resequenced	chr01M29287	chr01	29287 C/	A ./.	C/A	C/C	C/A	C/C	C/C	C/A	C/A	C/C	C/A	c/c	C/A	C/A	C/A	C/C	C/A	Pop report.tab	View da
Genome	chr01M37116	chr01	37116 T/		T/C	T/C	T/T	T/C	T/T	T/T	T/C	T/C	T/C	T/T	T/T	T/C	T/T	T/T	T/C		
arental SNP - Detect parental	chr01M37131 chr01M37155	chr01 chr01	37131 C/ 37155 C/		C/T C/T	C/T C/T	./. ./.	C/T C/T	C/T C/T	C/T C/T	C/C C/C	C/T C/T	C/C	C/T C/T	c/c c/c	C/T C/T	C/T C/T	C/T C/T	C/C C/C	Pop_sub.vcf	۲
SNP of hybrids	chr01M50285	chr01	50285 T/		T/C	T/C	T/T	T/C	T/T	T/T	T/C	T/C	T/C	T/T	T/T	T/C	T/T	T/T	T/C	Pop tab Bridge.	tab 💿 d
/isualization	chr01M50313	chr01	50313 T/		T/C	T/C	T/T	T/C	T/T	T/T	T/C	T/C	T/C	T/T	T/T	T/C	T/T	T/T	T/C	Top tub bridge.	
<b>FraceAncestor</b>	chr01M50330 chr01M53409	chr01 chr01	50330 G/ 53409 C/		G/A C/G	G/A C/G	G/G C/C	G/A C/G	G/A ./.	G/A C/C	G/G C/G	G/A C/G	G/G C/G	G/A ./.	G/G C/C	G/A C/G	G/A C/C	G/A C/C	G/G C/G		ی ک
vcfHunter	chr01M53451	chr01	53409 C/ 53451 C/		C/G	C/G C/C	C/C C/G	C/G C/C	c/c	C/C C/G	C/G	./.	C/G	./.	C/C C/G	C/G	C/C C/G	C/C	C/G	Pop tab Double	Dose P1.tab
VCF Filter	chr01M59316	chr01	59316 G/		G/A	G/G	G/A	G/G	G/G	G/A	G/A	G/G	G/A	G/G	G/A	G/A	G/A	G/G	G/A		۲
vcf2allPropAndCov	chr01M59428	chr01	59428 T/		T/C	T/C	T/T	T/C	T/C	T/C	T/T	T/C	T/T	T/C	T/T	T/C	T/C	T/C	T/T	Pop tab Double	
	chr01M67527 chr01M89917	chr01 chr01	67527 T/ 89917 C/		T/G C/T	T/G C/T	./. c/c	T/G C/T	T/T C/C	T/T C/C	T/G C/T	T/G C/T	T/G C/T	T/T C/C	T/T C/C	T/G C/T	T/T C/C	T/T C/C	T/G C/T		
vcf2allPropAndCovByChr	chr01M89923	chr01	89923 G/		G/T	G/T	G/G	G/T	G/G	G/G	G/T	G/T	G/T	G/G	G/G	G/T	G/G	G/G	G/T		ی ک
<u>vcf2popNew</u>	chr01M105158	chr01	105158 C/		C/T	C/C	C/T	C/C	C/C	C/T	C/T	C/C	C/T	C/C	C/T	C/T	C/T	C/C	C/T	Pop tab Simple	<u>Dose P1.tab</u>
RecombCalculatorDDose	chr01M127702 chr01M144740	chr01	127702 T/	G T/T	T/G	T/T	T/G	T/T	T/T	T/G	T/G	T/T	T/G	T/T	T/G	T/G	T/G	T/T	T/G A/A		٠ (
Draw dot plot	chr01M144740		1447															A/C G/G	G/A	Pop tab Simplet	Dose P2.tab
KDE classifier	chr01M157399		157	• •	~	•				•								T/T	T/C	Pop tab unknow	m.tab 💿 🖉
	chr01M165977	chr01	165	list c	Dt Va	aria	nt l	line	pa	ssir	ng n	niss	sing	i da	ta i	ilte	r	T/T	T/G		
METAGENOMICS	chr01M165990 chr01M182847	chr01 chr01	100															C/C G/A	C/T G/A		
FROGS	chr01M186534	chr01	186	(not	lise	s he	afte	r in	th	is ti	itoi	rial	hui	t ca	n h	e 0'	f	A/A	A/G		
EVOLUTION/PHYLOGENY	chr01M186547	chr01	100	(1100	ast	- 4 0						Iui	Nat	. cu				T/C	T/T		
Comparative Genomics	chr01M186553		186				ro	<b>~</b> ~~	rch	or i	nto	roc	+\					A/T C/C	A/A		
NCBI BLAST+	chr01M192113 E chr01M192120	chr01 chr01	192 192				re	sea	ICII	eri	nte	res	L)					I/I	C/G T/G		
Genfam	chr01M192136		192															G/G	G/A		
Protein analyses	chr01M226490	chr01	22649															G/G	G/T		
rotem analyses	chr01M235828 chr01M246911	chr01 chr01	235828 A/ 246911 T/		A/G T/C	A/G T/C	A/A T/T	A/G T/C	A/A T/C	A/A T/C	A/G T/T	A/G T/C	A/G T/T	./. T/C	A/A T/T	A/G T/C	A/A T/C	A/A T/C	A/G		
STATISTICS/GRAPHICS	chr01M251887	chr01	251887 C/		C/G	C/G	C/C	C/G	./.	C/C	C/G	C/G	C/G	c/c	c/c	C/G	C/C	C/C	C/G		
		chr01	251913 C/	C C/A	C/A	C/A	C/C	C/A	./.	C/C	C/A	C/A	C/A	C/C	C/C	C/A	C/C	C/C	C/A		
Statistics	chr01M251913					/	G/G	G/G	G/G	G/G A/A	G/G	G/A	G/A	G/G	G/G	G/A	G/G	G/G	G/A		
<u>Statistics</u> Graph/Display Data	chr01M251923	chr01	251923 G/		G/G	./.	2.02	3.40			A/G	A/G	A/G	A/A	A/A	A/G	A/A	A/A	A/G		
Graph/Display Data	chr01M251923 chr01M310320	chr01	310320 A/	A A/G	A/G	A/G	A/A A/A	A/G A/C	A/A A/A		A/C	A/C	A/C	A/A	A/A	A/C	A/A	A/A	A/C		
G <mark>raph/Display Data</mark> GOUTHGREEN PROJECTS	chr01M251923			A A/G A A/C			A/A A/A G/G	A/G A/C G/T	A/A A/A G/G	A/A G/G	A/C G/T	A/C G/T	A/C G/T	A/A G/G	A/A G/G	A/C G/T	A/A G/G	A/A G/G	A/C G/T		
Graph/Display Data GOUTHGREEN PROJECTS INIPlay3	chr01M251923 chr01M310320 chr01M310368 chr01M326767 chr01M340656	chr01 chr01 chr01 chr01	310320 A/ 310368 A/ 326767 G/ 340656 C/	A A/G A A/C G G/T C C/G	A/G A/C G/T C/G	A/G A/C G/T C/G	A/A G/G C/C	A/C G/T C/G	A/A G/G C/C	A/A G/G C/C	G/T C/G	G/T C/G	G/T C/G	G/G C/C	G/G C/C	G/T C/G	G/G C/C	G/G C/C	G/T C/G		
Graph/Display Data GOUTHGREEN PROJECTS SNIPlay3 GNPAnnot Tools	chr01M251923 chr01M310320 chr01M310368 chr01M326767 chr01M340656 chr01M381756	chr01 chr01 chr01 chr01 chr01	310320 A/ 310368 A/ 326767 G/ 340656 C/ 381756 T/	A A/G A A/C G G/T C C/G T T/A	A/G A/C G/T C/G T/A	A/G A/C G/T C/G T/A	A/A G/G C/C T/T	A/C G/T C/G T/A	A/A G/G C/C T/T	A/A G/G C/C T/T	G/T C/G T/A	G/T C/G T/A	G/T C/G T/A	G/G C/C T/T	G/G C/C T/T	G/T C/G T/A	G/G C/C T/T	G/G C/C T/T	G/T C/G T/A		
Graph/Display Data SOUTHGREEN PROJECTS SNIPlay3 GNPAnnot Tools GNPAnnot Converters	chr01M251923 chr01M310320 chr01M310368 chr01M326767 chr01M340656	chr01 chr01 chr01 chr01 chr01 chr01	310320 A/ 310368 A/ 326767 G/ 340656 C/	A A/G A A/C G G/T C C/G T T/A C C/T	A/G A/C G/T C/G	A/G A/C G/T C/G	A/A G/G C/C	A/C G/T C/G	A/A G/G C/C	A/A G/G C/C	G/T C/G	G/T C/G	G/T C/G	G/G C/C	G/G C/C	G/T C/G	G/G C/C	G/G C/C	G/T C/G		
Graph/Display Data SOUTHGREEN PROJECTS SNIPlay3 GNPAnnot Tools GNPAnnot Converters ESTtik	chr01M251923 chr01M310320 chr01M310368 chr01M326767 chr01M340656 chr01M381756 chr01M389536	chr01 chr01 chr01 chr01 chr01 chr01	310320 A/ 310368 A/ 326767 G/ 340656 C/ 381756 T/ 389536 C/	A         A/G           A         A/C           G         G/T           C         C/G           T         T/A           C         C/T           G         G/A	A/G A/C G/T C/G T/A C/T	A/G A/C G/T C/G T/A C/T	A/A G/G C/C T/T	A/C G/T C/G T/A C/T	A/A G/G C/C T/T C/C	A/A G/G C/C T/T C/C G/G	G/T C/G T/A	G/T C/G T/A C/T	G/T C/G T/A C/T	G/G C/C T/T C/C	G/G C/C T/T C/C	G/T C/G T/A C/T	G/G C/C T/T C/C	G/G C/C T/T C/C	G/T C/G T/A C/T		
Graph/Display Data SOUTHGREEN PROJECTS SNIPlay3 GNPAnnot Tools GNPAnnot Converters ESTtik Expression data	chr01M251923 chr01M310320 chr01M310365 chr01M326767 chr01M340656 chr01M309556 chr01M309556 chr01M408718 chr01M415461 chr01M456101	chr01 chr01 chr01 chr01 chr01 chr01 chr01 chr01 chr01	310320 A/ 310368 A/ 326767 G/ 340656 C/ 381756 T/ 389536 C/ 408718 G/ 415461 C/ 466101 C/	A         A/G           A         A/C           G         G/T           C         C/G           T         T/A           C         C/T           G         G/A           C         C/T           C         C/T           C         C/T	A/G A/C G/T C/G T/A C/T G/A C/T C/T	A/G A/C G/T C/G T/A C/T G/A C/T C/T	A/A G/G C/C I/T ./. G/G C/C C/C	A/C G/T C/G T/A C/T G/A C/T C/T	A/A G/G C/C I/T C/C G/G C/C C/C	A/A G/G C/C T/T C/C G/G C/C	G/T C/G T/A C/T C/T T /T	G/T C/G T/A C/T G/A C/T C/T	G/T C/G T/A C/T G/A C/T C/T	G/G C/C T/T C/C G/G C/C C/C	G/G C/C T/T C/C G/G C/C C/C	G/T C/G T/A C/T G/A C/T C/T	G/G C/C T/T C/C G/G C/C C/C	G/G C/C T/T C/C G/G C/C C/C	G/T C/G T/A C/T G/A C/T C/T		
Graph/Display Data SOUTHGREEN PROJECTS SNIPlay3 GNPAnnot Tools GNPAnnot Converters ESTtik	chr01M251923 chr01M310320 chr01M310368 chr01M326767 chr01M340656 chr01M381756 chr01M389536 chr01M489718 chr01M415461	chr01 chr01 chr01 chr01 chr01 chr01 chr01 chr01 chr01 chr01	310320 A/ 310368 A/ 326767 G/ 340656 C/ 381756 T/ 389536 C/ 408718 G/ 415461 C/	A         A/G           A         A/C           G         G/T           C         C/G           T         T/A           C         C/T           G         G/A           C         C/T           C         C/T           T         T/G	A/G A/C G/T C/G T/A C/T G/A C/T	A/G A/C G/T C/G T/A C/T G/A C/T	A/A G/G C/C T/T ./. G/G C/C	A/C G/T C/G T/A C/T G/A C/T	A/A G/G C/C T/T C/C G/G C/C	A/A G/G C/C T/T C/C G/G C/0	G/T C/G T/A C/T G/A	G/T C/G T/A C/T G/A C/T	G/T C/G T/A C/T G/A C/T	G/G C/C T/T C/C G/G C/C	G/G C/C T/T C/C G/G C/C	G/T C/G T/A C/T G/A C/T	G/G C/C T/T C/C G/G C/C	G/G C/C T/T C/C G/G C/C	G/T C/G T/A C/T G/A C/T		



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Galaxy						Analyze	Data W	/orkflow	Shared D	ata <del>v</del> Vis	sualization	👻 Admi	n Help <del>-</del> User -				Using 19
ols 🛃	19	P148	P022	P023	P020	P021	P026	P027	P024	P025	P028	P029	P118 P-value ChiSq		^	History	C 🕯
	-	A/T G/A	A/A G/A	A/T G/A	A/T G/G	A/T G/G	A/T G/A	A/T G/G	A/A G/G	A/A G/A	A/T G/G	A/A G/G	0.3574985362366353 0.242410153454242	2.0572480225988703 0.1756480446927373			
ssel GBS (Version 4.0)	2	T/C	T/T	T/C	T/C	T/C	T/C	T/C	T/T	T/T	T/C	T/T	2.6181543848150135	0. 620340782122905		< Back to VCFHunter	
<u>e Variant Analysis (Rice 3k,</u> IGIN, High Density Rice Array	E.	C/A T/C	C/A T/T	C/C T/C	C/C T/C	C/C T/C						C T	0.2224172220150283 0.3574985362366353	3 0064005649717513 .0572480225988703		output	
DRA, 700k SNPs))	1	C/T	C/C	C/T	C/T	C/T						Ť	0.6188652157518436	0.9597355503159057		a list of datasets	
	E	C/T T/C	C/C T/T	C/T	C/T T/C	C/T T/C		- X <sup>2</sup>	b-v	valu	2		0.6188652157518436 0.7884679191557895	0.9597355503159057 0.4753271186440678			
NOME HARVEST	-	T/C	T/T	./.	T/C	T/C					-	Ť	0.7884679191557895	0.4753271186440678		Pop.tab	۹
ansPo-RG Transfer of	4	G/A	./.	G/A	G/A	G/A						A	0.8892865927771468	0.2346714376863562		Pop report.tab	
sition to Resequenced nome	2	C/G C/G	C/C C/G	C/G C/C	C/G C/C	C/G C/C	c/c	C/G	c/c	c/c	C/G	c/c	0.4381323782633934 0.22613940552171512	1.650468361581921 2.9732072625698325			
	Ę.	G/A	G/A	G/G	G/G	G/G	G/G	G/A	G/G	G/G	G/A	G/G	0.1762997977067575	3.471138674033149		Pop_sub.vcf	۲
rental <u>SNP</u> - Detect parental IP of hybrids	E	T/C	T/T	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	0.51706080080527.84	1.319189616566847			
sualization	ŀ	T/G C/T	T/T C/C	T/G C/T	T/G C/T	T/G C/T	T/G C/T	T/G C/T	T/T C/C	T/T ./.	T/G C/T	T/T C/C	0.5715165725947204 0.43813237826739346	1.118923595505618 1.650468361581921		<u>Pop tab Bridge.tab</u>	٩
	1	G/T	G/G	G/T	G/T	G/T	G/T	G/T	G/G	./.	G/T	G/G	0.43813237829339346	1.650468361581921			٩
aceAncestor	2	C/T T/G	C/T T/G	C/C T/T	C/C T/T	C/C T/T	C/C T/T	C/T T/G	c/c	c/c	C/T	c/c	0.22613940552171552	2.9732072625698325 3.7324857142857146		Pop tab DoubleDose	
Hunter	-	A/C	A/A	A/C	A/C	A/C	A/C	A/C					18965586475	0.5176065197018618		rop tab boablebose	. <b>F1.tub</b>
VCF Filter	5	G/A	G/A	G/G	G/G	G/G	G/G	G/A		3			19/307562853	4.422294382022472			4
rcf2allPropAndCov		T/C T/G	T/C T/T	T/T T/G	T/T T/G	T/T T/G	./. T/G	T/C T/G		- X2	val	ue	73534805258	3.5095201117318435 0.470413966480447		Pop tab DoubleDose	P2.tab
cf2allPropAndCovByChr	-	C/T	c/c	C/T	C/T	C/T	C/T	C/T					72316463274	0.470413966480447			
	È.	G/A A/G	./. A/A	G/A A/G	G/A A/G	G/A A/G	G/A A/G	G/A A/G					8464888715e-05 73612478361			Pop tab SimpleDose	
vcf2popNew		T/C	T/T	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	0.8112117096960386	0.9725022598870057 0.4184524224395379		rop tab Simplebose	FILLOD
<u>RecombCalculatorDDose</u>	1	A/T	A/A	A/T	A/T	A/T	A/T	A/T	A/T	A/T	A/T	A/T	0.8112117096960386	0.4184524224395379			0
Draw dot plot		C/G T/G	C/C T/T	C/G T/G	C/G T/G	C/G T/G	C/G T/G	C/G T/G	C/C T/T	C/C T/T	C/G T/G	C/C T/T	0.7941670293722387 0.7941670293722387	0.4609229508196721 0.4609229508196721		Pop tab SimpleDose	P2.tab
Г ;Кі	L.	G/A	G/G	G/A	G/A	G/A	G/A	G/A	G/G	G/G	G/A	G/G	0.7528981835562427	0.5676505494505495		Pop tab unknown.ta	h (
<u>E classifier</u>	E	G/T	./.	G/T	G/T	G/T	G/T	G/T	G/G	G/G	G/T	G/G	0.5249547448776666	1.288886440677966			<u>b</u>
TAGENOMICS		A/G ./.	A/A T/T	A/G T/C	A/G T/C	A/G T/C	A/G T/C	A/G T/C	A/A T/C	A/A T/C	A/G T/C	A/A T/C	0.5249547448776666 0.9366257998724724	1.288886440677966 0.1309428726073232			
DGS	1	C/G	c/c	C/G	C/G	C/G	C/G	C/G	C/C	C/C	C/G	C/C	0.5249547448776666	1.288886440677966			
	È.	C/A	c/c	C/A	C/A	C/A	C/A	C/A	C/C	c/c	C/A	C/C	0.5249547448776666	1.288886440677966			
DLUTION/PHYLOGENY	2	G/A A/G	G/G A/A	G/G A/G	G/A A/G	./. A/G	G/G A/G	G/A A/G	G/G A/A	G/G A/A	G/G A/G	G/G A/A	1.8989378722328712e-1 0.6181543848150135	.0 44.76911242937853 0.9620340782122905			
nparative Genomics	_ :	A/C	A/A	A/C	A/C	A/C	A/C	A/C	A/A	A/A	A/C	A/A	0.6643142323222169	0.818000000000000			
BI BLAST+	=	G/T C/G	G/G C/C	G/T C/G	G/T C/G	G/T C/G	G/T C/G	G/T C/G	G/G ./.	G/G C/C	G/T C/G	G/G C/C	0.7068485671129155 0.7506785277537805	0.693877653631285 0.5735555555555556			
<u>ıfam</u>	ĺ.	T/A	T/T	T/A	T/A	T/A	T/A	T/A	T/T	T/T	T/A	T/T	0.7068485671129155	0.693877653631285			
tein analyses		C/T	c/c	C/T	C/T	C/T	C/T	./.	c/c	c/c	C/T	c/c	0.8280553484317711	0.3773505617977528			
TIETICE COMPUTCE	1	G/A C/T	G/G C/C	G/A C/T	G/A C/T	G/A C/T	G/A C/T	G/A C/T	./. c/c	G/G C/C	G/A C/T	G/G C/C	0.6149273612478361 0.6614013865683321	0.9725022598870057 0.8267887640449438			
TISTICS/GRAPHICS		C/T	c/c	C/T	C/T	C/T	C/T	C/T	C/C	C/C	C/T	c/c	0.7042246211332313	0.7013158192090396			
tistics		T/G G/T	T/T G/G	T/G G/T	T/G G/T	T/G G/T	T/G G/T	T/G G/T	T/T G/G	T/T G/G	T/G G/T	T/T G/G	0.7068485671129155 0.6614013865683321	0.693877653631285 0.8267887640449438			
ph/Display Data	L.	G/T G/A	G/G G/G	G/T G/A	G/T G/A	G/T G/A	G/T G/A	G/T G/A	G/G G/G	G/G G/G	G/T G/A	G/G G/G	0.6149273612478361	0.8267887640449438			
JTHGREEN PROJECTS	5	A/G	A/A	A/G	A/G	A/G	A/G	A/G	A/A	A/A	A/G	A/A	0.6614013865683321	0.8267887640449438			
Play3		T/C T/A	T/T T/T	T/C T/A	T/C T/A	T/C T/A	T/C T/A	T/C T/A	T/T T/T	T/T T/T	T/C T/A	T/T T/T	0.7068485671129155 0.7506785277537805	0.693877653631285 0.573555555555556			
PAnnot Tools		A/G	A/G	A/G	A/A	A/A	A/G	A/G	A/A	A/G	A/G	A/G	0.9860436840357866	0.028109242129956746			
	÷	G/A	G/G	G/A	G/A	G/A	G/A	G/A	G/A	G/G	G/A	G/G	0.3302183756773579	2.216002197802198			
PAnnot Converters	E	C/T A/C	C/C A/A	C/C A/C	C/T A/C	C/T A/C	C/T A/C	C/T A/C	C/T A/A	C/C A/A	C/C A/C	C/T ./.	0.482873229976734 0.5715165725941204	1.4560022471910112 1.118923595505618			
<u>ítik</u>	5	A/G	A/A	A/G	A/G	A/G	A/G	A/G	A/A	A/A	A/G	A/A	0.6643142323222169	0.8180000000000001			
oression data	E	C/T	./.	C/T	C/T	C/T	C/T	C/T	c/c	c/c	C/T	C/C	0.5249547448776666	1.288886440677966			
Γ	-	G/A G/A	./. G/G	G/A G/A	G/A G/A	G/A G/A	G/A G/A	G/A G/A	./. G/G	G/G ./.	G/A G/A	G/G G/G	0.5249547448776666 0.6181543848150135	1.288886440677966 0.9620340782122905	-		
	1																



Selecting segregating markers in vcf files: outputs





Selecting segregating markers in vcf files: outputs

Galaxy 🗙 🗧	
↔ ∀ ♀	① galaxy.southgreen.fr/galaxy/ ♥ ★ Q. LA TENTOUASIE → 보 III □ ①
Galaxy	Analyze Data Workflow Shared Data - Visualization - Admin Help - User -
Fools	History 🗸
CT 10015	A This dataset is large and only the first megabyte is shown below.     Show all I Save     (Back to VCFHunter)
<u>Fassel GBS (Version 4.0)</u> Rice Variant Analysis (Rice 3k,	
(RIGIN, High Density Rice Array	a list of datasets
(HDRA, 700k SNPs))	<pre>##fileformat=VCFv4.2 ##FILTER=<id=snpcluster,description="snps clusters"="" found="" in=""></id=snpcluster,description="snps></pre>
GENOME HARVEST	#FTORMAT=<1D=AD_Number=., Type=Integer, Description="Allelic depths for the ref and alt alleles in the order listed">
FransPo-RG Transfer of	+#FORMAI= <id=dp,number=1,type=integer,description="read depth"=""></id=dp,number=1,type=integer,description="read>
Position to Resequenced	##FORMAT= <id=gc,number=1,type=float,description="ratio and="" best="" between="" genotype="" probability="" probability"="" second=""> Pop report.tab ##FORMAT=<id=gt,number=1,type=string,description="genotype"></id=gt,number=1,type=string,description="genotype"></id=gc,number=1,type=float,description="ratio>
Genome	##GATKCommandline.VariantFiltration_TD=VariantFiltration_CommandLineOptions="analysis_type=VariantFiltration input_file=[] showFullBamList=false read_buffer_size=  Pop_sub.vcf
Darental SNP - Detect parental	##Additionnal.filter=(TD=TAGRemoval,Description="VariantSnpCluster are removed",Date="2018-01-08 14:37:19.913025">
GNP of hybrids /isualization	##Additionnal.filter= <id=coveragefiltration,description="genotype #="" ##additionnal.filter='&lt;ID=MissingDataFiltration,Description="SNP' 11="" 15="" 3="" allele="" and="" are="" bridge.tab="" converted="" coverage="" each="" for="" genotype="" having="" less="" missin="" missing="" more="" pop="" removed",date="2018-11-14 13:46:44.848676" tab="" than="" to="" view="" with="" x=""></id=coveragefiltration,description="genotype>
	#contig=tD=chr01,length=29070452>
<u>rraceAncestor</u> /cfHunter	##contig= <id=chr02,length=29511734></id=chr02,length=29511734>
VCF Filter	##contig= <id=chr03,length=35020413> #CHROM POS ID REF ALT QUAL FILTER INFO FORMAT P191 P134 P135 P136 P137 P039 P038 P132 P133 P035 P034 P03'</id=chr03,length=35020413>
	chr01 17228 . A T . PASS . GT:AD:DP:GC 0/0/0:47.0:47:5.26129332617e+14 0/0/1:59.21:80:7.55578637259e+22 0/0/1:57.23
<u>vcf2allPropAndCov</u>	chr01 20912 . G A . PAS . GT:AD:DP:GC 0/0/1:27,19:46:65536.0 0/0/0:52,0:52:2.80333245379e+16 0/0/0:59,0:59:7.10277380003
vcf2allPropAndCovByChr	chroll 20916 . T C . PASS . GT:AD:DP:GC 0/0/01:46;2:43891551199e+14 0/0/1:36,16:52:11.09951162778e+12 0/0/1:44,15
vcf2popNew	chr01 29287 . C A . PASS . GT:AD:DP:GC 0/1/1:19,22:41:64.0 0/0/0:47,1:48:98747997863.5 0/0/1:47,12:59:1.1805916207: chr01 37116 . T C . PASS . GT:AD:DP:GC 0/0/0:45,0:45:1.10765491825e+14 0/0/1:61,12:73:2.17253329946e+18 0/0/1:52,13
RecombCalculatorDDose	chr01 37131 . C T . PASS . GT:AD:DP:GC 0/0/1:33.13:46:1.09951162778e+12 0/1/1:32.41:73:262144.0 0/0/1:47.18:65:2.88:
	chr01 37155 . C chr01 5025 . T 0/0/(1:30.12 Pop tab SimpleDose P2.tab
<u>Draw dot plot</u>	
<u>KDE_classifier</u>	Chrol 50330 : G Vcf containing variant line passing missing
METAGENOMICS	
FROGS	chroit 53451 c doto filton (not used often in this tutonic) but <sup>1</sup> 0/0/1:37,14
	chrol 59316 G data filter (not used after in this tutorial but 55,22:77:7.37)
EVOLUTION/PHYLOGENY	
Comparative Genomics	chroi 89917 c can be of researcher interest)
NCBI BLAST+	CHICI 83923 . 6 0/0/1:37,12
<u>Genfam</u>	chr01 105158 . C 7 0/0/1:33,10 chr01 127702 . T 7 153,14:67:3.02
Protein analyses	chr01 144740 . A C . PASS . GT:AD:DP:GC 0/0/1:19,15:34:256.0 0/0/1:41,26:67:1073741824.0 0/0/1:49,7:56:21425805.5722
STATISTICS/GRAPHICS	chr01 152926 . G A . PASS . GT:AD:DP:GC 0/0/1:25,15:40:1048576.0 0/0/0:60,0:60:1.59812410501e+19 0/0/1:44,12:56:1.84 chr01 157399 . T C . PASS . GT:AD:DP:GC 0/0/1:17,15:32:16.0 0/0/0:38.0:38:4.36927180114e+11 0/0/1:19.14:33:1024.0 0/0
Statistics	chr01 157399 . T C . PASS . GT:AD:DP:GC 0/0/1:17,15:32:16.0 0/0/0:38,0:38:4.36927180114e+11 0/0/1:19,14:33:1024.0 0/0. chr01 165977 . T G . PASS . GT:AD:DP:GC 0/0/0:51,0:51:1.27000083428e+16 0/0/1:44,17:61:1.80143985095e+16 0/0/1:34,13
Graph/Display Data	chrol 16599 . C T . PASS . GT:AD:DF:GC 0/0/0151,0:5011.127000083428+16 0/0/1:42,17:59:1.12589990684+15 0/0/1:43,13
	chr01 182847 . G A . PASS . GT:AD:DP:GC 0/0/1:30,14:44:4294967296.0 0/1/1:18,50:68:1.84467440737e+19 0/1/1:27,36
SOUTHGREEN PROJECTS	chrol 186534 A G PASS GT:AD:DP:GC 0/0/052.05212.8033245379e+16 0/0/1:44,15:59:2.88230376152e+17 0/0/1:41,14
SNiPlay3	chr01 186547 . T C . PASS . GT:AD:DP:GC 0/0/1:38,14:52:2.81474976711e+14 0/0/1:30,29:59:4.0 0/0/1:35,19:54:4294 chr01 186553 . A T . PASS . GT:AD:DP:GC 0/0/1:38,14:52:2.81474976711e+14 0/0/1:30,29:59:4.0 0/0/1:34,19:53:1073
<u>GNPAnnot Tools</u>	chr01 192113 . C G . PASS . GT:AD:DP:GC 0/0/0:36,0:36:93382422010.7 0/0/1:32,8:40:2.81474976711e+14 0/0/1:38,10:48:7.20
SNPAnnot Converters	chr01 192120 . T G . PASS . GT:AD:DP:GC 0/0/0:36,0:36:93382422010.7 0/0/1:31,8:39:7.03687441777e+13 0/0/1:38,10:48:7.20
STtik	chr01 192136 . G A . PASS . GT:AD:DP:GC 0/0/0:36,0:36:93382422010.7 0/0/1:31,8:39:7.03687441777e+13 0/0/1:39,10:49:2.88: chr01 226490 . G T . PASS . GT:AD:DP:GC 0/0/0:42,0:42:1.04092203766e+13 0/0/1:52,21:73:4.61168601843e+18 0/0/1:48,17
Expression data	CHICU 226490 . G I . PASS . GITADIDE'G U/U/142,114211.0402203/066413 U/U/152,211/314.01160016436418 U/U/1146,11 CHICU 25828 A T,G . PASS . GITADIDE'G U/U/142,1175986614.41 U/U/2152395351.5 (0/0/2140,016/56:63)
SAT	Chr01 246911 . T C . PASS . GT:AD:DP:GC 0/0/1:35,10:45:1.12589990684e+15 0/0/1:32,21:53:4194304.0 0/0/1:42,17
	chr01 251887 . C G . PASS . GT:AD:DP:GC 0/0/0:52,0:52:2.80333245379e+16 0/0/1:56,13:69:2.76454365653e+22 0/0/1:36,12



Galaxy X																			
←)→ ୯ û	(i) galaxy	.southgre	en.fr/gala	xy/								•••	⊴ 📩	Q git south	igreen	$\rightarrow$		<u>↓</u> III\	
<b>=</b> Galaxy					Analyze Dat	a Workfl							er <del>-</del>						Using 19
Fools	Marker	coding	ratio	rephased	P191	P134	P135	P136	P137	P039	P038	P132	P133	P035	P034 P03	7 P036	P03 History	r	20
Tassel GBS (Version 4.0)																	< Back to	o VCFHunter	
<u>Rice Variant Analysis (Rice 3k,</u> IRIGIN, High Density Rice Array (HDRA, 700k SNPs))																	a list of a	datasets	
GENOME HARVEST																	Pop.tab	2	۲
<u>TransPo-RG</u> Transfer of Position to Resequenced																	Pop re	port.tab	۲
Genome																			<b>A</b>
<u>parental SNP</u> - Detect parental SNP of hybrids																	Pop su Pop tal	<u>b. Bridge.tal</u>	Ш
/isualization																			(0)
<u>rraceAncestor</u> /cfHunter																	Pop ta	b DoubleDo	_
VCF Filter				Thi	s is tł	o fi		hick	a ch	ould		ntai	n h	ridaa					
vcf2allPropAndCov					5 15 11	ie ii			1 511	ouit		IIIa		luge			Pop ta	b DoubleDo	ی <u>se P2.tab</u>
vcf2allPropAndCovByChr				n	narke	rs is	em	ntv	hec	aus	e th	ere	are	no					۲
vcf2popNew													are				Pop ta	b SimpleDo	
RecombCalculatorDDose							br	idge	e ma	arke	rs								۲
Draw dot plot																	Pop tal	b SimpleDo	se P2.tab
<u>DE classifier</u>																	Pop ta	b unknown.	tab 🎯
IETAGENOMICS																			
ROGS																			
VOLUTION/PHYLOGENY																			
comparative Genomics																			
CBI BLAST+																			
Senfam																			
<u>rotein analyses</u>																			
TATISTICS/GRAPHICS																			
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OUTHGREEN PROJECTS																			
<u>SNiPlay3</u> SNPAnnot Tools	J																		
GNPAnnot Converters																			
STtik																			
xpression data																			
SAT -																			
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Selecting segregating markers in vcf files: outputs

Galaxy X -	ł				
← → ♂ ଢ	(i) galaxy.southgreen.fr/galaxy/		🗟 🕇	$\bigcirc$ cirad $\rightarrow$	<u>↓</u> II\ 🗎 🗊 Ξ
<b>=</b> Galaxy		Analyze Data Workflow Share	d Data 🗸 Visualization 🗸 Admin Help 🕇 User 🗸 🚺		Using 19%
Tools 2	This dataset is large and only th	e first megabyte is shown below.			History C C C
<u>Rice Variant Analysis (Rice 3k,</u> IRIGIN, High Density Rice Array (HDRA, 700k SNPs))	Marker coding ratio rephased chr01M37131 hh,k- 0.1667,0.8333	0 k- k- k-	P137 P039 P038 P132 P133 P035 P034 k k- k- k- hh k-	P037 P036 P031 P030 P03: hh k- hh k- k-	output a list of datasets
GENOME HARVEST <u>TransPo-RG</u> Transfer of	chr01M37155 hh,k- 0.1667,0.8333 chr01M50330 hh,k- 0.1667,0.8333 chr01M59428 hh,k- 0.1667,0.8333	0 k- k- k-	k k- k- k- hh k- k- hh k- k- k- hh k- k- hh k- k- k- hh k-	hh k- hh k- k- hh k- hh k- k- hh k- hh k- k-	Pop.tab (1) (2) (2) (2) (2) (2) (2) (2) (2) (2) (2
Position to Resequenced Genome <u>parental SNP</u> - Detect parental	chr01M144740 hh,k- 0.1667,0.8333 chr01M182847 hh,k- 0.1667,0.8333	0 k- k- k- 0 k- k- k-	k- hh k- k- k- hh k- k- hh k- k- k- k- k-	hh k- hh k- k- k- k- hh k- k-	Pop report.tab (%) a Pop sub.vcf (%) a
SNP of hybrids Visualization	chr01M186547 hh,k- 0.1667,0.8333 chr01M186553 hh,k- 0.1667,0.8333 chr01M246911 hh,k- 0.1667,0.8333	0 k- k- k- 0 k- k- k-	k- hh k- k- k- hh k- k- hh k- k- k- hh k- k- hh k- k- k- hh k-	hh k- hh k- k- hh k- hh k- k- hh k- hh k- k-	Pop tab Bridge.tal
<u>TraceAncestor</u> vcfHunter	chr01M502178 hh,k- 0.1667,0.8333 chr01M664756 hh,k- chr01M664790 hh,k-	0 k- k- k-	k- k- hh k- k- k- k-	k- k- k- k- - k- k- k- k-	Pop tab DoubleDose P1 tab
<u>VCF Filter</u> <u>vcf2allPropAndCov</u>	chr01M664806 hh,k-	his file contai	ned double dose mark	k- k-	Pop tab DoubleDose P2.tab
vcf2allPropAndCovByChr vcf2popNew	chr01M681020 hh,k- chr01M681026 hh,k-			k- k-	Pop tab SimpleDose P1.tab
RecombCalculatorDDose	_ chr01M708929 hh,k- chr01M768075 hh,k- chr01M768195 hh,k-	which are net	terozygous in parent F	k- k- k- k-	Pop tab SimpleDose P2.tab
<u>Draw dot plot</u> KDE classifier	chr01M797138 hh,k- chr01M811010 hh,k- 0.1007,0.0000 chr01M811013 hh,k- 0.1667,0.8333		x- x- x- mi mi x- mi	A k- k- x- x- k- k- k-	Don tob unknown tob
METAGENOMICS FROGS	chr01M811045 hh,k- 0.1667,0.8333 chr01M823679 hh,k- 0.1667,0.8333 chr01M870753 hh,k- 0.1667,0.8333		e information (1 = m	harker has bee	en rephased)
EVOLUTION/PHYLOGENY	chr01M870772 hh,k- 0.1667,0.833 chr01M894164 hh,k- 0.1667,0.8333 chr01M894199 hh,k- 0.1667,0.8333		x- x- x- nn nn x k- k- k- hh hh k- hh k-	x- x- x- x- x- k- k- k- k- k- k- k- k-	
NCBI BLAST+ Genfam	<pre>chr01M901388 hh, 0.1667,0.8333 chr01M900033 hh,k- 0.1667,0.8333</pre>	0 hh k- k- 0 hh k- k-	Expected propo	ortion k- k- k-	
Protein analyses	chr01M94435 hh,k- 0.1667,0.8333 chr01M951781 hh,k- 0.1667,0.8333 chr01M1048549 hh,k- 0.1667,0.8333	0 hh <del>k- k-</del> 0 k- k-	k- k- k- k- hh hh k k- k hh k	k- k- k- k- k- k- k- k- k- k- k-	
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tecombCalculatorDDose oraw dot plot E classifier TAGENOMICS DG <mark>S</mark>	chr01M4032506 chr01M4047381 chr01M4047390 chr01M4053672 chr01M415915 chr01M415915 chr01M416915 chr01M4167055 chr01M422080 chr01M4235526	nn, n nn, n nn, n nn, n nn, n nn, np nn, np nn, np nn, np nn, np nn, np	U.S, U.S U 0.5, 0.5 0 0.5, 0.5 0 0.5, 0.5 0 0.5, 0.5 0	which	nare np np nn nn	e he	np n nn n np n np n	ygou p nn p nn n np n np	np nn nn np np	nn np np nn nn	nn np np nn nn	nn np nn nn nn	nn np np	nn nn nn np np nn nn	np np np nn nn nn np np nn nn	2 2 2 2 2 2	Pop tab SimpleDos	e P2 tab View
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ecombCalculatorDDose Draw dot plot E classifier TAGENOMICS DGS DLUTION/PHYLOGENY INPARATIVE GENOMICS	chr01M4032506 chr01M4047381 chr01M4047390 chr01M4047390 chr01M4127313 chr01M4127313 chr01M4150482 chr01M4150482 chr01M4167085 chr01M4185588 chr01M423526 chr01M4242784	nn, n nn, n nn, n nn, n nn, n nn, n nn, np nn, np nn, np nn, np nn, np nn, np nn, np	U.S, 0.S 0 0.5, 0.5 0 0.5, 0.5 0 0.5, 0.5 0 0.5, 0.5 0 0.5, 0.5 0 0.5, 0.5 0	which	nn are np np nn nn np np np	e he	np n nn n np n np n np n	ygou p nn p nn n np n np p nn p nn	np nn nn np nn nn nn nn	pare	nn np np nn nn np np np	P2	nn np  	nn nn nn np np nn nn np nn np	np np np nn nn nn np np nn np nn np np	2 2 2 2 2 2	Pop tab SimpleDos	e P2 tab View
ecombCalculatorDDose raw dot plot : classifier IAGENOMICS JGS DLUTION/PHYLOGENY aparative Genomics BI BLAST+	chr01M4032506 chr01M4047391 chr01M4047390 chr01M4053672 chr01M4127313 chr01M4145915 chr01M4163170 chr01M4165188 chr01M4185588 chr01M4185588 chr01M4222080 chr01M4242788	nn, n nn, n nn, n nn, n nn, n nn, np nn, np nn, np nn, np nn, np nn, np nn, np nn, np nn, np	0.5,0.5 0.5,0.5 0.5,0.5 0.5,0.5 0.5,0.5 0.5,0.5 0.5,0.5 0	which	n are	nn np nn nn nn np	np n nn n np n np n np n nn n	ygou p nn p nn n np n np p nn n np n np	np nn nn np np nn nn nn np	nn np np nn nn np	nn np np nn nn np	P2	nn np np  np	nn nn nn np np nn nn nn np	np np np nn nn nn np np nn nn np	2 2 2 2 2 2	Pop tab SimpleDos	e P2 tab View
RecombCalculatorDDose Praw dot plot E classifier TAGENOMICS DES DLUTION/PHYLOGENY mparative Genomics BI BLAST+	chr01M4032506 chr01M4047391 chr01M4047390 chr01M4053672 chr01M4127313 chr01M4145915 chr01M4163170 chr01M4163170 chr01M4163170 chr01M4185588 chr01M4222080 chr01M4235526 chr01M4242788 chr01M4242788 chr01M4242788	nn, n nn, n nn, n nn, n nn, n nn, n nn, np nn, np nn, np nn, np nn, np nn, np nn, np	U.S, U.S 0 0.5, 0.5 0 0.5, 0.5 0 0.5, 0.5 0 0.5, 0.5 0 0.5, 0.5 0 0.5, 0.5 0	which	nn np np nn nn np np nn	nm np nn nn nn np nn nn np nn	np n nn n np n np n nn n np n nn n np n	ygou p nn p nn n np n np p nn n np n np	np nn nn np nn nn nn nn	nn np nn nn np nn np nn	nn np np nn nn np np np nn	P2	nn np  	nn nn nn np np nn nn np np np np	np np np nn nn nn np np nn nn nn nn	2 2 2 2 2 2	Pop tab SimpleDos	e P2 tab
ecombCalculatorDDose raw_dot_plot :_classifier rAGENOMICS 2GS DLUTION/PHYLOGENY nparative Genomics 3I BLAST+ fam	chr01M4032506 chr01M4047381 chr01M4047380 chr01M4047381 chr01M4127313 chr01M4127313 chr01M4150482 chr01M4167085 chr01M4167085 chr01M4222080 chr01M4242784 chr01M4242784 chr01M4242799 chr01M4242794 chr01M4242794	nn, n nn, n nn, n nn, n nn, n nn, np nn, np nn, np nn, np nn, np nn, np nn, np nn, np	U 0.5,0.5 0 0.5,0.5 0 0.5,0.5 0 0.5,0.5 0 0.5,0.5 0 0.5,0.5 0 0.5,0.5 0 0.5,0.5 0 0.5,0.5 0 0.5,0.5 0	which	nn np nn nn np nn nn nn nn nn	e he	np nn nn nn np nn nn np nn nn np nn nn n	ygou p nn p nn n np p nn p nn n np	np nn nn np nn nn np nn nn np np nn	pare	nn np np nn nn np np nn nn nn	P2	nn np  np np np	nn nn nn np np nn np np nn np np nn np np	np np np nn nn nn np np np np np np np n	2 2 2 2 2 2	Pop tab SimpleDos	e P2 tab View
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ce Variant Analysis (Rice 3k,	chr01M3288418	hh,k-	0.1667,0.8333	0	k-	k-	k-		- k-	hh	k-	k-	k-	k-	k-	1			
IGIN, High Density Rice Array	chr01M3592725	hh, k-	0.1667,0.8333	ō		k-	k-	k- k		k-	hh	k-	hh	k-	k-	1	output		
DRA, 700k SNPs))	chr01M3603814	hh, k-	0.1667,0.8333	0	hh	k-	k-	k- k	- k-	k-	hh	k-	hh	k-	k-	1	a list of datasets		
	chr01M3603846	hh,k-	0.1667,0.8333	0	hh	k-	k-	k- k		k-	hh	k-	hh	k-	k-	1			
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ansPo-RG Transfer of	chr01M4325104 chr01M4372486	hh,k- hh,k-	0.1667,0.8333 0.1667,0.8333	0	hh k-	k-	k-		- x- - k-	k-	k-	k- hh	hh k-	k-	k- k-				
sition to Resequenced	chr01M4491444	hh, k-	0.1667,0.8333	0	hh	k-	k-		- k-	k-	hh	k-	hh	k-	k-	E	Pop report.tab		4
enome	chr01M4537232	hh, k-	0.1667,0.8333	0	hh	k-	k-	k- k		k-	hh	k-		k-	k-	1			
wental CND Detect parental	chr01M4537284	hh, k-	0.1667,0.8333	0	hh	k-	k-	k- k	- k-	k-	hh	k-		k-	k-	1	Pop_sub.vcf		4
<u>rental SNP</u> - Detect parental IP of hybrids	chr01M4630303	hh,k-	0.1667,0.8333	0	hh	k-	k-	k- k		k-	hh	k-		k-	k-	1			
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sualization	chr01M4674927 chr01M4848289	hh,k-	0.1667,0.8333	0	hh	k-	k-	k- k	:- k-	k-	hh	k-	hh	k-	k- k-	-			
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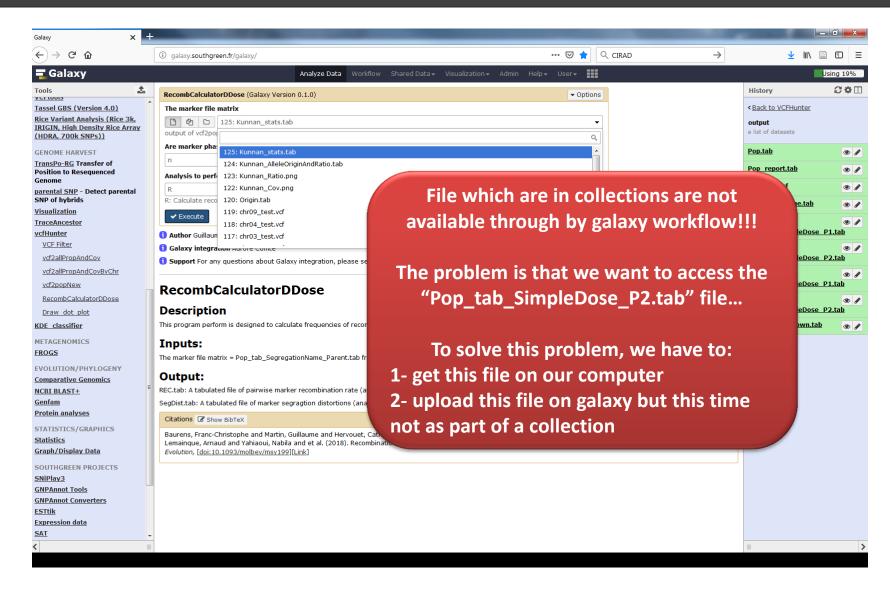


Calculating marker segregation distortion on parent P2 simple dose markers

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isualization	✓ Execute				
<u>aceAncestor</u> :fHunter				Pop tab DoubleDose	P1.tab
VCF Filter	Author Guillaume MARTIN ( <u>quillaume.martin@cirad.fr</u> )     Galaxy integration Aurore Comte				
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omparative Genomics	Output:				
CBI BLAST+	REC.tab: A tabulated file of pairwise marker recombination rate (analysis to perform R	).			
<u>enfam</u> rotein analyses	SegDist.tab: A tabulated file of marker segragtion distortions (analysis to perform S).				
TATISTICS/GRAPHICS	Citations Show BibTeX				
tatistics	Baurens, Franc-Christophe and Martin, Guillaume and Hervouet, Catherine and Salm Lemainque, Arnaud and Yahiaoui, Nabila and et al. (2018). Recombination and large				
aph/Display Data	Evolution, [doi:10.1093/molbev/msy199][Link]	su decarar variations snape interspecific edible Dallallas gel	nomes, in molecular biology allu		
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Calculating marker segregation distortion on parent P2 simple dose markers





1- Downloading the Pop\_tab\_SimpleDose\_P2.tab

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<b>=</b> Galaxy	Analyze Data Workflow Shared Data	- Visualization - Admin Help - User -	l	Using 19%
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SENOME HARVEST	Are marker phased?		Pop.tab	۲
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<u>/isualization</u> <u>FraceAncestor</u> /cfHunter	Execute     Author Guillaume MARTIN (quillaume.martin@cirad.fr)		Pop tab DoubleDos	٠
VCF Filter	Galaxy integration Aurore Comte			۲
vcf2allPropAndCov vcf2allPropAndCovByChr	Galaxy integration Active Contee     Support For any questions about Galaxy integration, please send an e-mail to <u>auron</u>	re.comte@ird.fr	Pop tab DoubleDos	se P2.tab
vcf2popNew RecombCalculatorDDose Draw_dot_plot	RecombCalculatorDDose Description		Pop tab SimpleDos	() <u>se P1.tab</u> () <u>se P2.tab</u>
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EVOLUTION/PHYLOGENY Comparative Genomics	Output:			
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Protein analyses	Citations Show BibTeX			
STATISTICS/GRAPHICS <u>Statistics</u> <u>Graph/Display Data</u>		n, Frédéric and Yohomé, David and Ricci, Sébastien and Rouard, Mathieu and Habas, Rem tructural variations shape interspecific edible bananas genomes. In <i>Molecular Biology and</i>		
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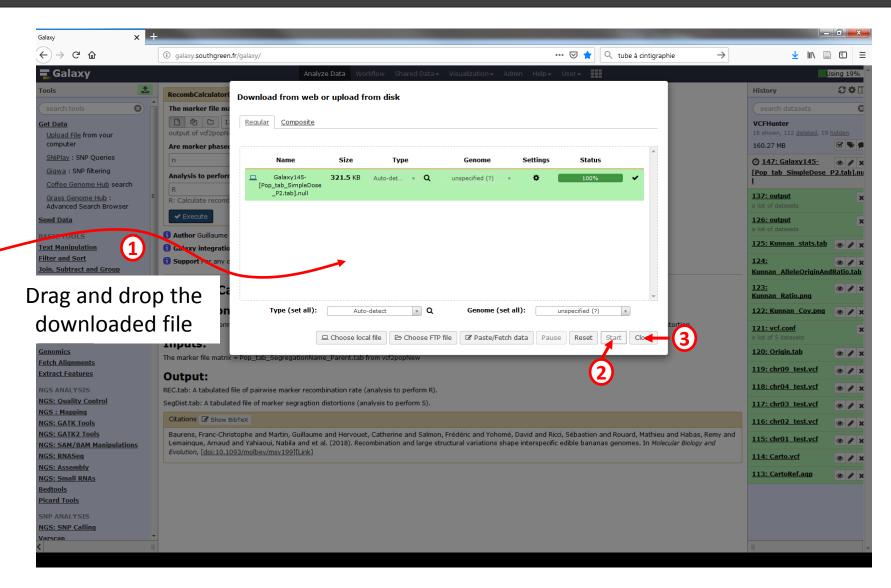


1- Uploading the Pop\_tab\_SimpleDose\_P2.tab onto Galaxy

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Galaxy	Analyze Data Workflow Shared Data - Visualization - Admin Help - User -		Jsing 19%
Tools	RecombCalculatorDDose (Galaxy Version 0.1.0)	History	<b>2 \$</b> []
search tools	C) The marker file matrix	< Back to VCFHunter	
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<u>Grass Genome Hub</u> : Advanced Search Browser	R: Calculate recombination rate / S: Calculate segregation distortions	Pop tab Bridge.tab	۲
Send Data	✓ Execute		۲
BASIC TOOLS	Author Guillaume MARTIN (quillaume.martin@cirad.fr)	Pop tab DoubleDose I	
Text Manipulation	<b>1</b> Galaxy integration Aurore Comte		۲
Filter and Sort	Support For any questions about Galaxy integration, please send an e-mail to <u>aurore.comte@ird.fr</u>	Pop tab DoubleDose I	P2.tab
Join, Subtract and Group		_	۲
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SEQUENCE ANALYSIS			۲ ک
Gene/Protein prediction EMBOSS	Description	Pop tab SimpleDose I	P2.tab
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NGS: Quality Control	SegDist.tab: A tabulated file of marker segraption distortions (analysis to perform S).		
NGS : Mapping			
NGS: GATK Tools	Citations & Show BibTeX		
NGS: GATK2 Tools NGS: SAM/BAM Manipulation	Baurens, Franc-Christophe and Martin, Guillaume and Hervouet, Catherine and Salmon, Frédéric and Yohomé, David and Ricci, Sébastien and Rouard, Mathieu and Habas, Remy and Lemainque, Arnaud and Yahiaoui, Nabila and et al. (2018). Recombination and large structural variations shape interspecific edible bananas genomes. In Molecular Biology and		
NGS: RNASeq	Evolution, [doi:10.1093/molbev/msy199][Link]		
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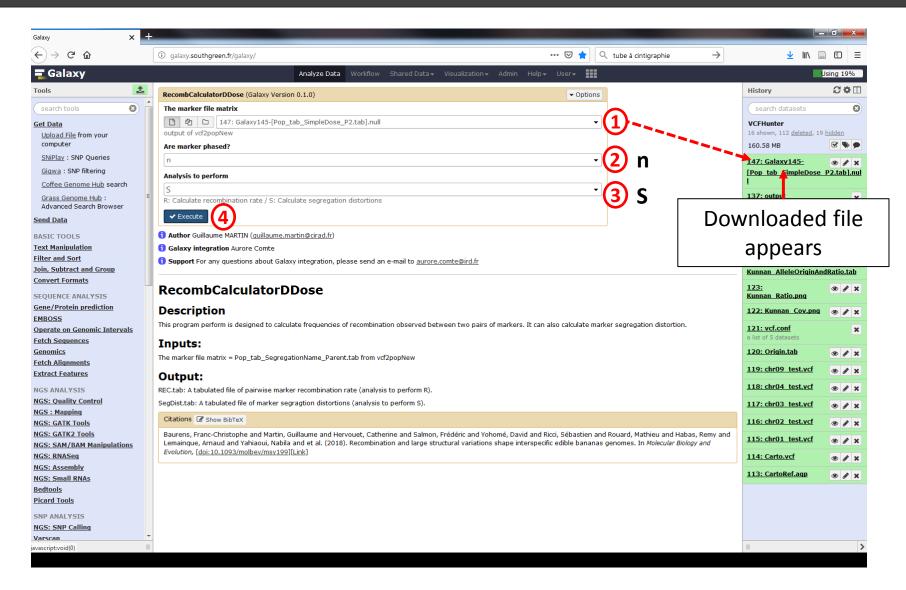


1- Uploading the Pop\_tab\_SimpleDose\_P2.tab onto Galaxy





Calculating marker segregation distortion on parent P2 simple dose markers





Calculating marker segregation distortion : output

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enome	chr01M3417999 1.0	0675463526216225	1- marker name			147: Galaxy145-	٠
arental SNP - Detect parental	chr01M3493115 0.9	9336553965234122				[Pop tab SimpleDose	P2.ta
NP of hybrids	chr01M3507847 0.5	5276568002953714	2- marker segreg	ation distortion		1	
sualization		5726718245857745				137: output	
aceAncestor		9336553965234122			_	a list of 9 datasets	
<u>fHunter</u>		0675463526216225				136. output	
VCF Filter		4098131172920304				126: output a list of 10 datasets	
vcf2allPropAndCov		5276568002953714					
		3051680529937114				125: Kunnan stats.tab	b 👁
vcf2allPropAndCovByChr		)587658909783821				<u>124:</u>	-
vcf2popNew		4763798150217415				Kunnan AlleleOriginAn	ک dPati
RecombCalculatorDDose		.523767198186683				Kullian Aneleonginan	Iunati
Draw dot plot		.523767198186683				<u>123:</u>	۲
		1763798150217415				Kunnan Ratio.png	
<u>E classifier</u>		3594678641097688				122: Kunnan Cov.png	I 💿
TAGENOMICS		.995462582229307					
DGS		4763798150217415				121: vcf.conf	
		3080719000803791				a list of 5 datasets	
DLUTION/PHYLOGENY		0587658909783821				120: Origin.tab	۲
nparative Genomics		1424366088102702					
BI BLAST+		1424366088102702				<u>119: chr09_test.vcf</u>	۲
<u>nfam</u>		1328964223140199				118: chr04 test.vcf	۲
otein analyses		1798874785587451					
ATISTICS/GRAPHICS		5276568002953714				117: chr03 test.vcf	۲
		.523767198186683				116, shr02, tast usf	
<u>itistics</u> 1ph/Display Data		5277828140473716				116: chr02 test.vcf	۲
Ipit/Display Data		1328964223140199				115: chr01 test.vcf	۲
UTHGREEN PROJECTS		.123551035124867					
Play3		0.63257328864087				114: Carto.vcf	۲
PAnnot Tools		7454217266286189				113: CartoRef.agp	
PAnnot Converters		.995462582229307				<u>xx3. cartokenadp</u>	۲
<u>Ttik</u>		0675463526216225					
pression data		5276568002953714					
Ī		5276568002953714					
		.050163073656123					
	chr01M4325073 0.4	1798874785587451				• III	



Calculating marker segregation distortion : output

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<b>_</b> Galaxy		Analyze D	ta Workflow Shared Data 🗸 Visualization 🗸 Admin	Help∓ User∓			Using 19
ools 🍰	1 2					History	C \$
assel GBS (Version 4.0)	chr01M2909259 1.0	0675463526216225				search datasets	
ice Variant Analysis (Rice 3k,	chr01M3084769 1.0	0587658909783821				- Search datasets	
RIGIN, High Density Rice Array	chr01M3230825 1.	.123551035124867			ŀ	VCFHunter	
HDRA, 700k SNPs))	chr01M3284968 0.4	1798874785587451				17 shown, 112 <u>deletsu</u> , 19	9 <u>hidden</u>
ENOME HARVEST	chr01M3285013 0.5	5276568002953714	A two column file wit	h•		160.6 MB	
ransPo-RG Transfer of	chr01M3358254 0.8	3080719000803791				148: SegDist.tab	
osition to Resequenced	chr01M3395458 1.1	1328964223140199				140. 36qDist.tab	•
enome	chr01M3417999 1.0	0675463526216225	1- marker name			147: Galaxy145-	٠
arental SNP - Detect parental	chr01M3493115 0.9	9336553965234122				[Pop tab SimpleDose	P2.ta
NP of hybrids	chr01M3507847 0.5	5276568002953714	2- marker segreg	ation distortion		1	
sualization		5726718245857745				137: output	
aceAncestor		9336553965234122			_	a list of 9 datasets	
<u>fHunter</u>		0675463526216225				136. output	
VCF Filter		4098131172920304				126: output a list of 10 datasets	
vcf2allPropAndCov		5276568002953714					
		3051680529937114				125: Kunnan stats.tab	b 👁
vcf2allPropAndCovByChr		)587658909783821				<u>124:</u>	-
vcf2popNew		4763798150217415				Kunnan AlleleOriginAn	ک dPati
RecombCalculatorDDose		.523767198186683				Kullian Aneleonginan	Iunati
Draw dot plot		.523767198186683				<u>123:</u>	۲
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TAGENOMICS		.995462582229307					
DGS		4763798150217415				121: vcf.conf	
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nparative Genomics		1424366088102702					
BI BLAST+		1424366088102702				<u>119: chr09_test.vcf</u>	۲
<u>nfam</u>		1328964223140199				118: chr04 test.vcf	۲
otein analyses		1798874785587451					
ATISTICS/GRAPHICS		5276568002953714				117: chr03 test.vcf	۲
		.523767198186683				116, shr02, tast usf	
<u>itistics</u> 1ph/Display Data		5277828140473716				116: chr02 test.vcf	۲
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Play3		0.63257328864087				114: Carto.vcf	۲
PAnnot Tools		7454217266286189				113: CartoRef.agp	
PAnnot Converters		.995462582229307				<u>xx3. cartokenadp</u>	۲
<u>Ttik</u>		0675463526216225					
pression data		5276568002953714					
Ī		5276568002953714					
		.050163073656123					
	chr01M4325073 0.4	1798874785587451				+ III	



Calculating pairwise marker recombination rate on P2 simple dose

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				History	
<u>VCI (0015</u>	Recompcateuratorbbose (Galaxy Version 0.1.0)	- Options			~
Tassel GBS (Version 4.0)	The marker file matrix			< Back to VCFHunter	
<u>Rice Variant Analysis (Rice 3k,</u> IRIGIN, High Density Rice Array	125: Kunnan_stats.tab	•		output	
(HDRA, 700k SNPs))	output of vcf2popNew			a list of datasets	
GENOME HARVEST	Are marker phased?			Pop.tab	۲
TransPo-RG Transfer of	n			Pop report.tab	
Position to Resequenced Genome	Analysis to perform				٥
parental SNP - Detect parental	R	•		Pop_sub.vcf	ه ک
SNP of hybrids	R: Calculate recombination rate / S: Calculate segregation distortions			Pop tab Bridge.tab	۲
<u>Visualization</u>	✓ Execute				
TraceAncestor				Pop tab DoubleDose	D1 tab
vcfHunter VCF Filter	Author Guillaume MARTIN ( <u>quillaume.martin@cirad.fr</u> )			Pop tab DoubleDose	
	<b>i</b> Galaxy integration Aurore Comte			Pan tah DaubleDece	() () () () () () () () () () () () () () () (
vcf2allPropAndCov	<b>()</b> Support For any questions about Galaxy integration, please send an e-mail to <u>aurore.comtec</u>	<u>pird.fr</u>		Pop tab DoubleDose	P2.1dD
vcf2allPropAndCovByChr					٠
vcf2popNew	RecombCalculatorDDose			Pop tab SimpleDose	<u>P1.tab</u>
RecombCalculatorDDose					۰ ک
<u>Draw dot plot</u>	Description			Pop tab SimpleDose	
KDE classifier	This program perform is designed to calculate frequencies of recombination observed between t	wo pairs of markers. It can also calculate marker segre	egation distortion.	Pop tab unknown.tab	ی ک
METAGENOMICS	Inputs:				
FROGS	The marker file matrix = Pop_tab_SegregationName_Parent.tab from vcf2popNew				
EVOLUTION/PHYLOGENY					
Comparative Genomics	Output:				
NCBI BLAST+	REC.tab: A tabulated file of pairwise marker recombination rate (analysis to perform R).				
Genfam	SegDist.tab: A tabulated file of marker segragtion distortions (analysis to perform S).				
<u>Protein analyses</u>	Citations & Show BibTeX				
STATISTICS/GRAPHICS	Baurens, Franc-Christophe and Martin, Guillaume and Hervouet, Catherine and Salmon, Frédér	ic and Yohomé. David and Ricci. Sébastien and Rouard	Mathieu and Habas, Remy and		
Statistics	Lemainque, Arnaud and Yahiaoui, Nabila and et al. (2018). Recombination and large structural				
<u>Graph/Display Data</u>	Evolution, [doi:10.1093/molbev/msy199][Link]				
SOUTHGREEN PROJECTS					
<u>SNiPlay3</u>					
GNPAnnot Tools					
<u>GNPAnnot Converters</u> ESTtik					
Expression data					
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Calculating pairwise marker recombination rate on P2 simple dose

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<b>=</b> Galaxy	Analyze Data Workflow Shared Data - Visualization - Admin	in Help+ User+		Using 19%
Tools	RecombCalculatorDDose (Galaxy Version 0.1.0)	- Options	History	<b>2</b> \$[
search tools	The marker file matrix		search datasets	6
<u>Get Data</u> <u>Upload File</u> from your computer	Image: Constraint of the state of the s	· (1)	VCFHunter 16 shown, 112 <u>deleted</u> , 19 160.58 MB	9 <u>hidden</u>
SNiPlay : SNP Queries	n	-(2) n	147: Galaxy145-	(a)
Gigwa : SNP filtering	Analysis to perform		[Pop tab SimpleDose	
Coffee Genome Hub search	R		1	
<u>Grass Genome Hub</u> : Advanced Search Browser	R: Calculate recombination rate / S: Calculate segregation distortions	3 R	a list of datasets	3
Send Data	Execute 4		126: output a list of datasets	3
BASIC TOOLS	3 Author Guillaume MARTIN ( <u>quillaume.martin@cirad.fr</u> )		125: Kunnan stats.tab	
Text Manipulation	<b>1</b> Galaxy integration Aurore Comte		123. Kuman Stats.tab	• • • •
<u>Filter and Sort</u> Join, Subtract and Group	<b>3</b> Support For any questions about Galaxy integration, please send an e-mail to <u>aurore.comte@ird.fr</u>		<u>124:</u> <u>Kunnan AlleleOriginAn</u>	و 🖋 ک ndRatio.tab
Convert Formats SEQUENCE ANALYSIS	RecombCalculatorDDose		<u>123:</u> <u>Kunnan Ratio.pnq</u>	• / >
Gene/Protein prediction EMBOSS	Description		122: Kunnan Cov.png	• / >
Operate on Genomic Intervals	This program perform is designed to calculate frequencies of recombination observed between two pairs of market	ers. It can also calculate marker segregation distortion.	121: vcf.conf	3
Fetch Sequences	Inputs:		a list of 5 datasets	
Genomics	The marker file matrix = Pop_tab_SegregationName_Parent.tab from vcf2popNew		120: Origin.tab	۲ 🖉 👁
Fetch Alignments Extract Features	Output:		119: chr09_test.vcf	۰ 🆋 ک
NGS ANALYSIS	REC.tab: A tabulated file of pairwise marker recombination rate (analysis to perform R).		118: chr04 test.vcf	۰ 🇨 ک
NGS: Quality Control	SegDist.tab: A tabulated file of marker segragtion distortions (analysis to perform S).		117: chr03_test.vcf	۰ 🇨 ک
<u>NGS : Mappinq</u> NGS: GATK Tools	Citations & Show BibTeX		116: chr02 test.vcf	
NGS: GATK2 Tools	Baurens, Franc-Christophe and Martin, Guillaume and Hervouet, Catherine and Salmon, Frédéric and Yohomé, D	David and Ricci, Sébastien and Rouard, Mathieu and Habas, Remy and		• / >
NGS: SAM/BAM Manipulations	Lemainque, Arnaud and Yahiaoui, Nabila and et al. (2018). Recombination and large structural variations shape		115: chr01_test.vcf	• / >
NGS: RNASeq	Evolution, [doi:10.1093/molbev/msy199][Link]		114: Carto.vcf	۰ 🖋 ک
<u>NGS: Assembly</u> NGS: Small RNAs			113: CartoRef.agp	۰ / ۱
Bedtools				
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SNP ANALYSIS				
NGS: SNP Calling				
Varscan avascript:void(0)				
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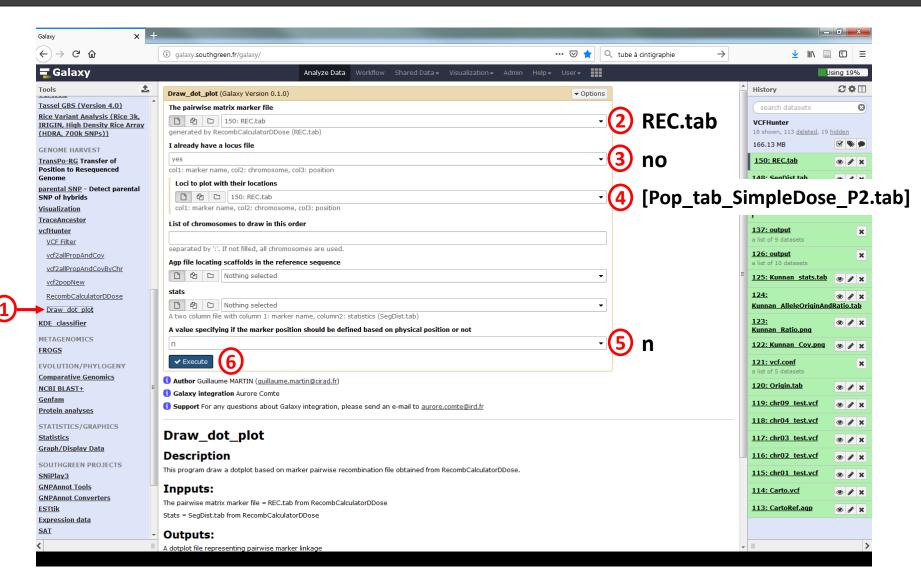


Calculating pairwise marker recombination rate: output

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<b>_</b> Galaxy			Analyze Data Workflo	ow Shared Data <del>-</del> Visu	ualization <del> -</del> Admin Hel	p∓ User∓ <b>III</b>				Using 19%
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assel GBS (Version 4.0)		taset is large and only the	first megabyte is shown b	elow.					Caraceter distances	
tice Variant Analysis (Rice 3k,	SHOW a	II   <u>Save</u>							search datasets	
RIGIN, High Density Rice Array HDRA, 700k SNPs))		2909259 chr01M3084769		13284968 chr01M3285013		M3395458 chr01M3417999			VCFHunter 18 shown, 113 deletation	9 <u>hidden</u>
	chr01M2909259 chr01M3084769	0.0 0.010909090909 0.01090909090909091	09091 0.021897810218 0.0 0.010791366906						166.13 MB	. 🗹 🔊
ENOME HARVEST	chr01M3230825	0.021897810218978103	0.01079136690647482	0.0 0.01142857142					150: REC.tab	
ransPo-RG Transfer of position to Resequenced	chr01M3284968	0.046511627906976744	0.028735632183908046	0.011428571428571429	0.0 0.0 0.0	0.005780346820809248	0.005813953488372093	0.0	150: KEC.Idb	<b>S</b>
enome	chr01M3285013	0.046242774566473986	0.02857142857142857	0.01136363636363636364	0.0 0.0 0.0	0.005747126436781609	0.005780346820809248	0.0	148: SegDist.tab	View data
arental SNP - Detect parental	chr01M3358254 chr01M3395458	0.05202312138728324 0.025830258302583026	0.034482758620689655 0.01454545454545454545	0.017142857142857144 0.0035971223021582736	0.0 0.0 0.0 0.005780346820809248	0.011560693641618497 0.005747126436781609	0.011627906976744186 0.011560693641618497	0.0:		
NP of hybrids	chr01M3395458 chr01M3417999	0.025830258302583026	0.0145454545454545454545454545	0.0035971223021582736	0.005780346820809248	0.005780346820809248	0.011560693641618497	0.0	147: Galaxy145-	۲
sualization	chr01M3493115	0.026022304832713755	0.014652014652014652	0.0036231884057971015	0.005813953488372093	0.005780346820809248	0.011627906976744186	0.0	Pop tab SimpleDose	P2.tab].r
aceAncestor	chr01M3507847	0.05202312138728324	0.03428571428571429	0.01694915254237288	0.0 0.0 0.0	0.011494252873563218	0.011560693641618497	0.0:	1	
fHunter	chr01M3580672	0.056818181818181816	0.03932				0.00392156862745098	0.0:	137: output	
VCF Filter	chr01M3758744 chr01M3775407	0.0449438202247191 0.04477611940298507	0.0332:				0.040697674418604654 0.040697674418604654	0.0:	a list of 9 datasets	
	chr01M3775423	0.08092485549132948	0.06288	square m	atrix of m	arkor	0.0199203187250996	0.0	120	
vcf2allPropAndCov	chr01M3837583	0.08670520231213873	0.0685	square m		anker	0.024 0.045977011494		a list of 10 datasets	
vcf2allPropAndCovByChr	chr01M3837669	0.07514450867052024	0.0628				0.024 0.045977011494			
vcf2popNew	chr01M3847042	0.04797047970479705	0.0366:	rwise rec	ombinatio	on rate	4285714 0.021897810218		125: Kunnan stats.tab	2 💿 🥒 :
	chr01M3856981	0.08045977011494253	0.0625				9523808 0.045714285714			
<u>RecombCalculatorDDose</u>	chr01M3881851 chr01M3901090	0.08571428571428572 0.08522727272727272	0.06779				0.02390438247011952	0.0	<u>124:</u>	۲ 🖉 🕐
Draw dot plot	chr01M3901141	0.08571428571428572	0.0681818181818181818	0.05084745762711865	0.023715415019762844	0.023622047244094488	0.023 0.045714285714		Kunnan AlleleOriginAr	ndRatio.tal
DE classifier	chr01M3913984	0.05185185185185185	0.04 0.028985507246	5376812 0.045714285714					<u>123:</u>	۲
	chr01M3926703	0.05223880597014925	0.04044117647058824	0.029197080291970802	0.046242774566473986	0.04597701149425287	0.05202312138728324	0.0:	Kunnan Ratio.png	
ETAGENOMICS	chr01M3958080	0.08620689655172414	0.0738636363636363637	0.05649717514124294	0.02766798418972332	0.027559055118110236	0.028 0.051428571428		100: Kunnan, Courne	
ROGS	chr01M4015771 chr01M4032506	0.052830188679245285 0.04814814814814815	0.040892193308550186 0.03676470588235294	0.02952029520295203 0.025362318840579712	0.046511627906976744 0.04597701149425287	0.046242774566473986 0.045714285714285714	0.05232558139534884 0.05142857142857143	0.0:	122: Kunnan Cov.pnq	۲
	chr01M4032506	0.05639097744360902	0.04460966542750929	0.03308823529411765	0.05232558139534884	0.05202312138728324	0.05232558139534884	0.0:	121: vcf.conf	
OLUTION/PHYLOGENY	chr01M4047390	0.05639097744360902	0.04460966542750929	0.03308823529411765	0.05232558139534884	0.05202312138728324	0.05232558139534884	0.0:	a list of 5 datasets	-
omparative Genomics	chr01M4053672	0.052434456928838954	0.04059040590405904	0.0290909090909090909	0.046242774566473986	0.04597701149425287	0.05202312138728324	0.0:	120: Origin tab	
CBI BLAST+	E chr01M4127313	0.10465116279069768	0.08620689655172414	0.06857142857142857	0.035856573705179286	0.035856573705179286	0.03643724696356275	0.0	<u>120: Origin.tab</u>	۲
<u>enfam</u>	chr01M4145915	0.10404624277456648	0.08571428571428572	0.0681818181818181818	0.03571428571428571	0.03571428571428571	0.036290322580645164 0.04 0.068181818181	0.0	119: chr09 test.vcf	۲
rotein analyses	chr01M4150482 chr01M4163170	0.10857142857142857 0.10285714285714286	0.0903954802259887 0.0847457627118644	0.07303370786516854 0.06741573033707865	0.03543307086614173 0.03557312252964427	0.0392156862745098 0.03543307086614173	0.04 0.068181818181 0.036 0.0625 0.0628			
ATISTICS (CRADUICS	chr01M4167085	0.0599250936329588	0.04814814814814814815	0.03663003663003663	0.05747126436781609	0.05714285714285714	0.057803468208092484	0.0:	118: chr04 test.vcf	۲
TATISTICS/GRAPHICS	chr01M4185588	0.05904059040590406	0.04744525547445255	0.036231884057971016	0.05714285714285714	0.056818181818181818	0.06285714285714286	0.0:		
atistics	chr01M4222080	0.10404624277456648	0.08571428571428572	0.06779661016949153	0.035856573705179286	0.03571428571428571	0.036290322580645164	0.0	<u>117: chr03_test.vcf</u>	۲
raph/Display Data	chr01M4235526	0.09770114942528736					47126436781609 0.0578		116: chr02_test.vcf	
OUTHGREEN PROJECTS	chr01M4242788 chr01M4242794	0.06037735849056604 0.06060606060606061	0.04814814814814815 0.048327137546468404	0.03676470588235294 0.03690036900369004	0.057803468208092484 0.05813953488372093	0.05747126436781609 0.057803468208092484	0.06358381502890173 0.06395348837209303	0.0:	110. Chi Oz (est.VCI	۲
NiPlay3	chr01M4269479	0.10404624277456648	0.08571428571428572	0.0681818181818181818	0.035856573705179286	0.03571428571428571	0.036290322580645164	0.0	115: chr01 test.vcf	۲
NPAnnot Tools	chr01M4288400	0.09826589595375723	0.08 0.0625 0.0318				47126436781609 0.0578	03468:		~ 0
	chr01M4288430	0.05904059040590406	0.0472727272727272727	0.036101083032490974	0.056818181818181818	0.05649717514124294	0.0625 0.032608695652		114: Carto.vcf	۲
NPAnnot Converters	chr01M4325073	0.10465116279069768	0.08620689655172414	0.06857142857142857	0.035856573705179286	0.03571428571428571	0.03643724696356275	0.0	112: CarteBof acr	
<u>STtik</u>	chr01M4334576 chr01M4366480	0.055970149253731345 0.09883720930232558	0.04411764705882353 0.08620689655172414	0.03296703296703297 0.06857142857142857	0.05232558139534884 0.035856573705179286	0.05202312138728324 0.035856573705179286	0.057803468208092484 0.036290322580645164	0.0:	113: CartoRef.agp	۲
xpression data	chr01M4366480	0.09883720930232558	0.08045977011494253	0.06285714285714286	0.036 0.03585657370		7551024 0.057803468208			
<u>AT</u>	<ul> <li>chr01M4426367</li> </ul>	0.09714285714285714	0.0847457627118644	0.06741573033707865	0.03529411764705882	0.03529411764705882	0.036 0.0625 0.0628			
		0.09714285714285714	0.0847457627118644	0.06741573033707865	0.03529411764705882	0.03529411764705882	0.036 0.0625 0.0628		-	
	ab m01M4425206	0 05035035035035036	0 0472727272727272727	0 02507122202159272	0 05601010101010101016	0.05640717514124204	0 0625 0 022727272727	12121		

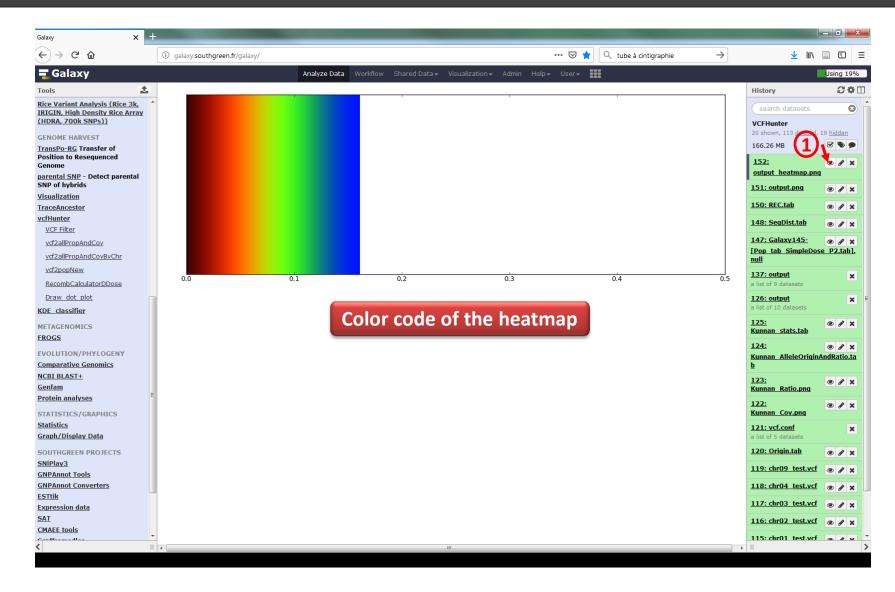


Plotting pairwise recombination



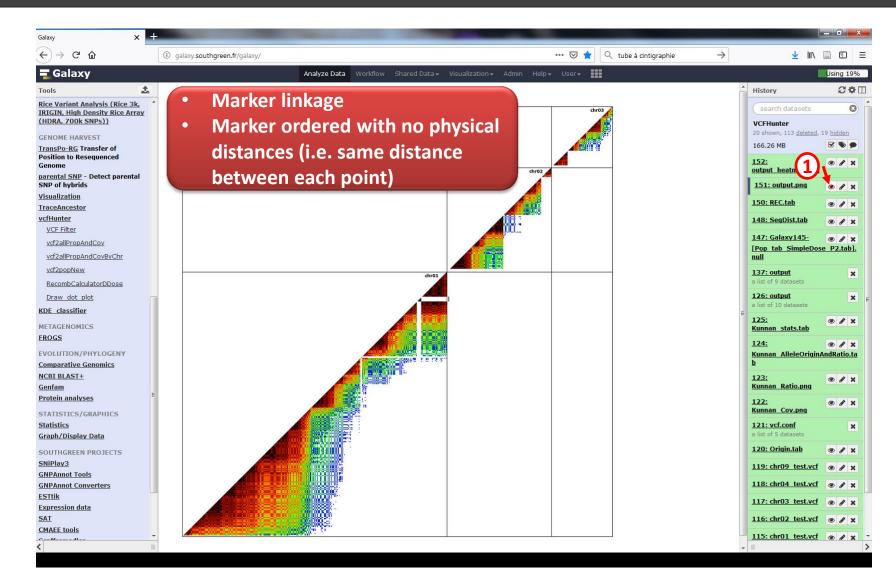


Plotting pairwise recombination: outputs



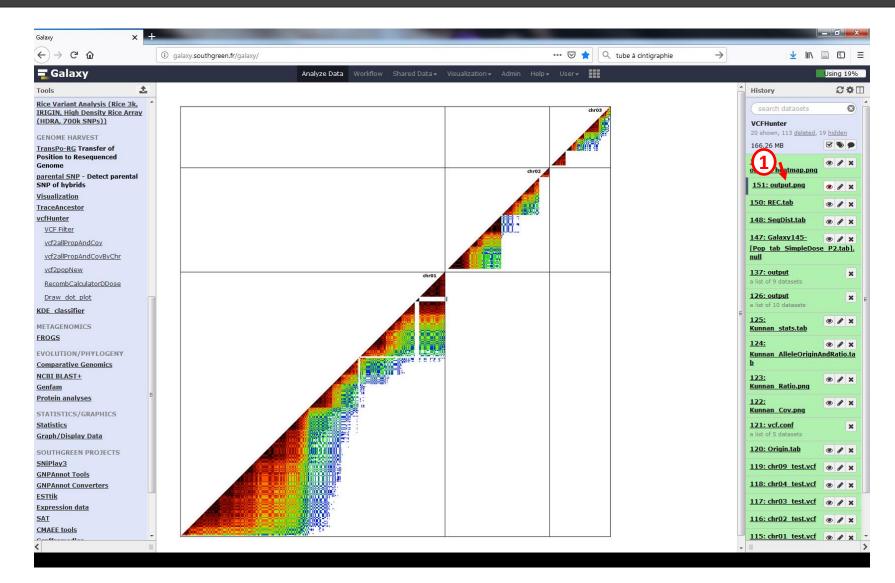


Plotting pairwise recombination: outputs





Plotting pairwise recombination with other options





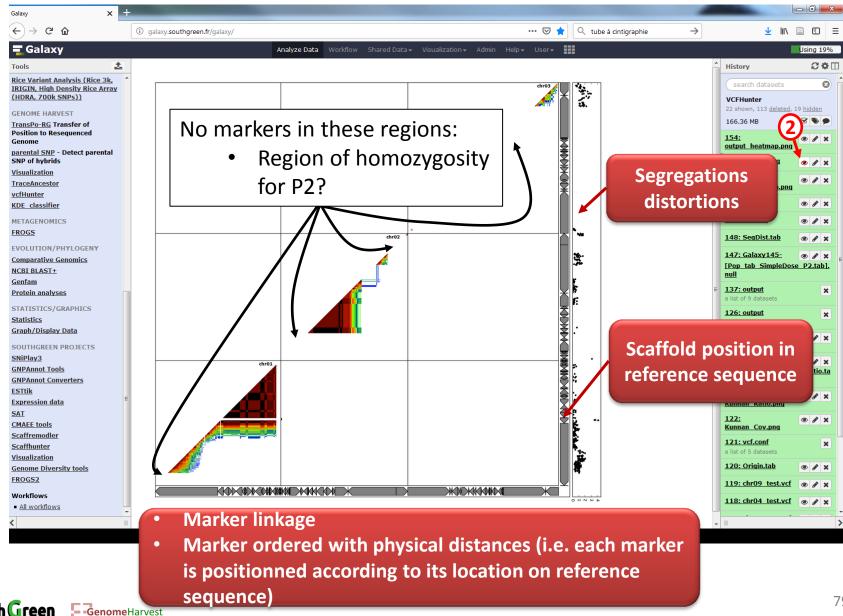
Plotting pairwise recombination with other options

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IGIN, High Density Rice Arı IDRA, 700k SNPs))	av 150: REC.tab	<b>_</b>	25 26	
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cf2popNew	Agp file locating scaffolds in the reference sequence			
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enfam	<b>i</b> Author Guillaume MARTIN ( <u>quillaume.martin@cirad.fr</u> )		56 57	
otein analyses	Galaxy integration Aurore Comte		58	
ATISTICS/GRAPHICS	<b>1</b> Support For any questions about Galaxy integration, please send an e-mail to <u>aurore.comte@ird.fr</u>			
atistics				
raph/Display Data	Draw_dot_plot		63	
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IPAnnot Tools	This program draw a dotplot based on marker pairwise recombination file obtained from RecombCalculatorDDose.		Image in png format	:
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MAEE tools	- Outputs:		[Pop tab Simp	
ff	A dotplot file representing pairwise marker linkage			



bioinformatics platform

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

