



MUSATRACT PROJECT

Involving Genoscope, Cirad , and several partners in particular from the Global Musa Genomics Consortium in the framework of the Global Musa Genomics Consortium



PAHANG DOUBLED HAPLOID

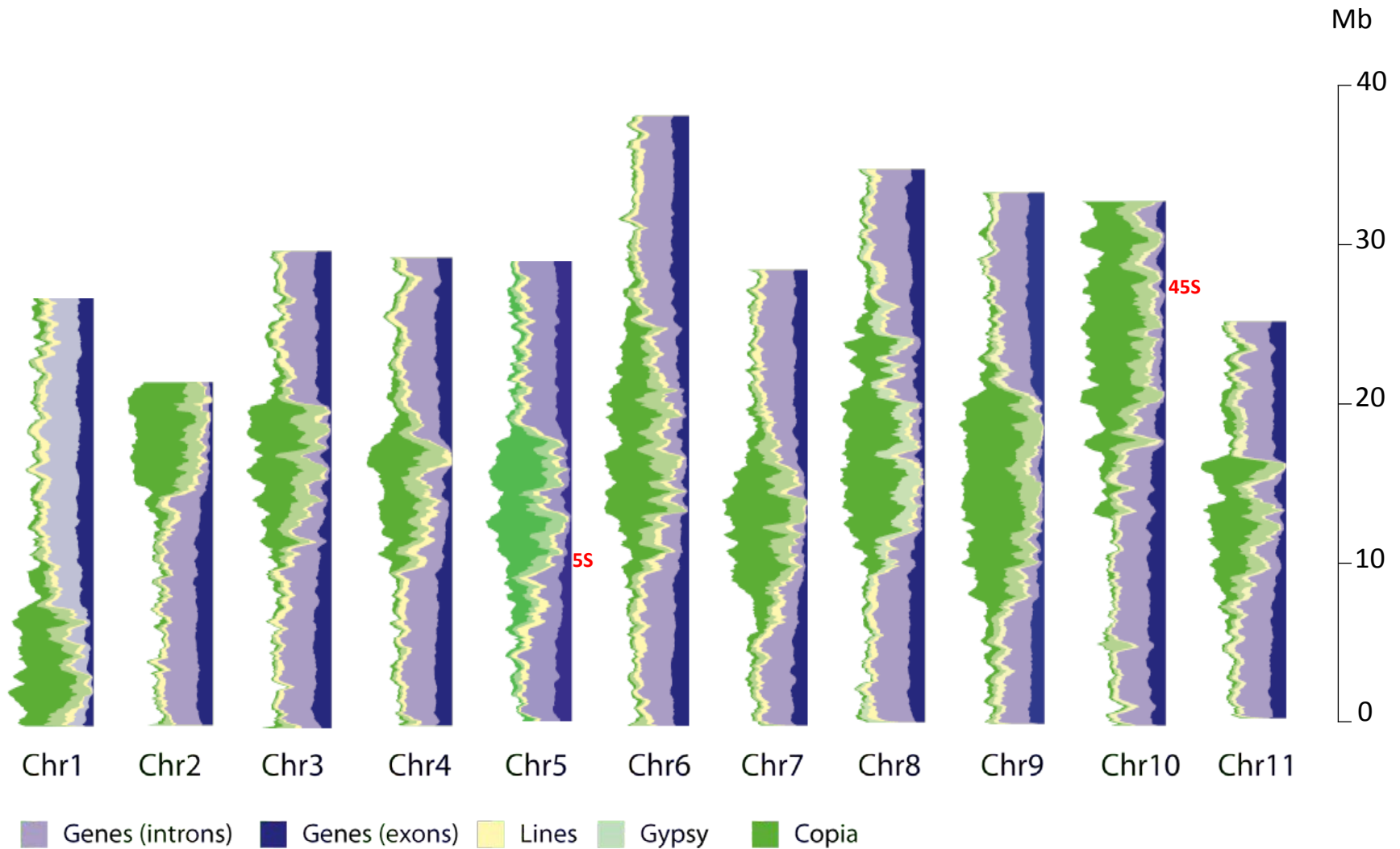
-> Haploids available only for one *M. acuminata* genotype : Pahang



Pahang **Doubled-Haploid**
from anther culture
Genome size : **520 Mb**

Pahang
Wild diploid ($2n=22$)
Species: M. acuminata
Subspecies: malaccencis

GENE AND TE DISTRIBUTION



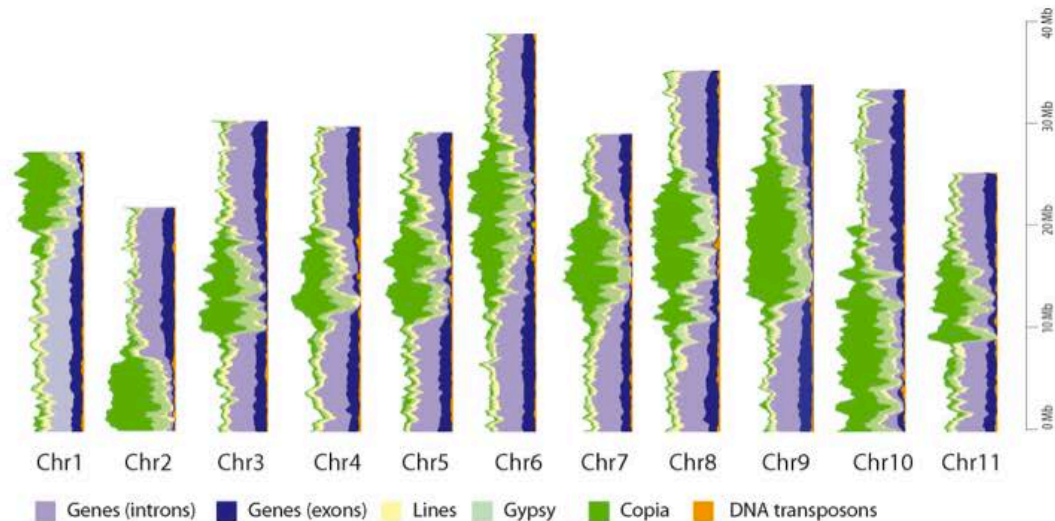
<http://banana-genome.cirad.fr>

Banana Genome Hub

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The **Musa genome sequence** results from collaboration between Genoscope and Cirad (UMR AGAP) funded by ANR. The sequenced genotype is a doubled-haploid ($2n=22$, $1C=523$ Mb) from the species *Musa acuminata* (A genome) subspecies *malaccensis*. The doubled-haploid (DH-Pahang) was produced at Cirad through anther culture of the wild diploid accession Pahang and spontaneous chromosomes doubling. The wild Pahang accession originated from Central Malaysia.

The sequence was analysed in collaboration with several teams in particular of the Global Musa Genomics Consortium and was published in : "The banana (*Musa acuminata*) genome and the evolution of monocotyledonous plants". D'Hont et al. 2012. Nature



Supported by:



The **Banana Genome Hub** centralises databases of genetic and genomic data for the *Musa acuminata* crop Hub developed by Cirad and Biodiversity and supported by the South Green Bioinformatics platform. Data available are the complete genome sequence along with gene structure, gene product information, metabolism, gene families, transcriptomics (ESTs, RNA-Seq), genetic markers (SSR, DArT, SNPs) and genetic maps.

Sequence Contact:

dhont@cirad.fr

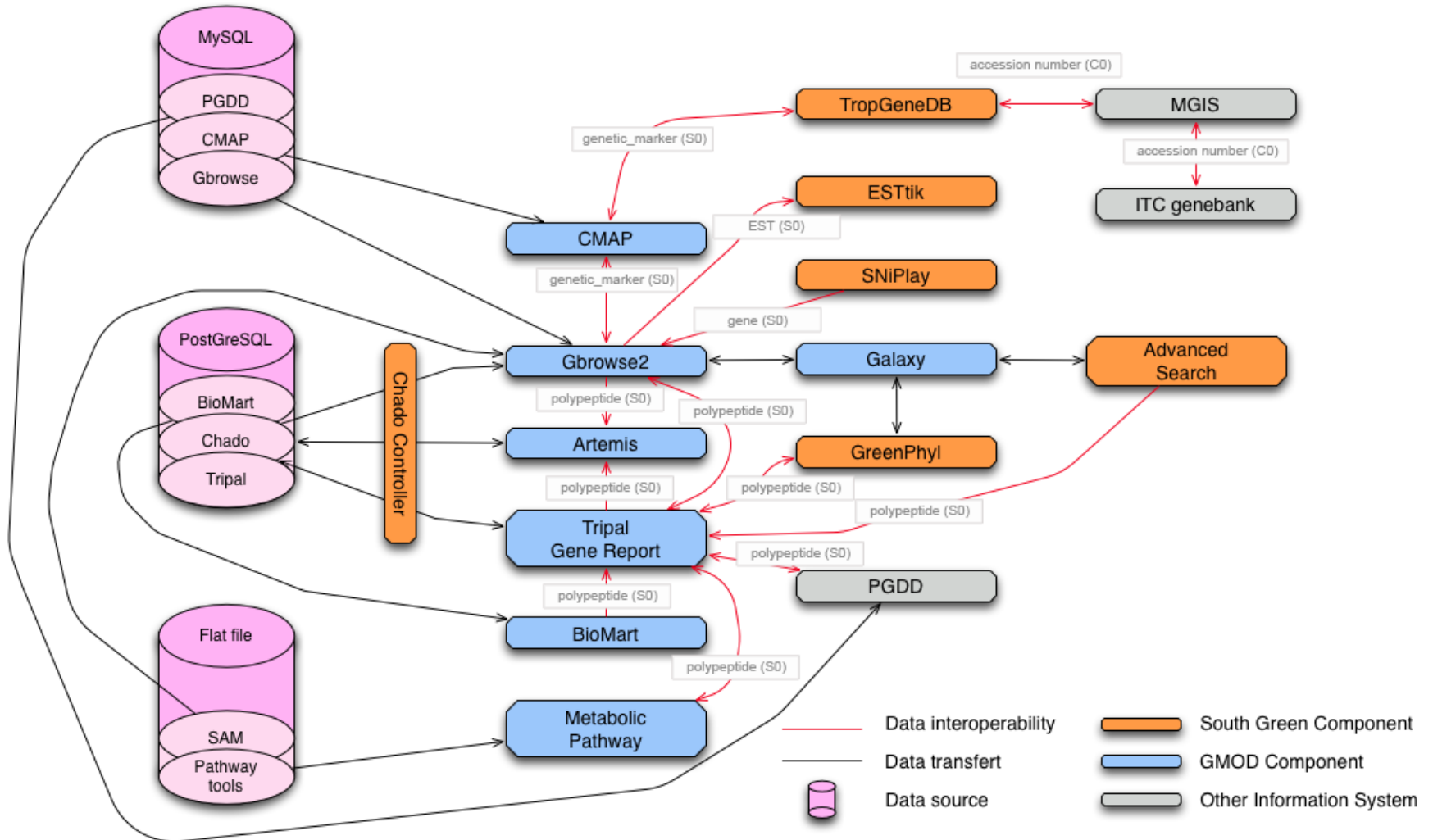
wincker@genoscope.cns.fr

Hub Contact:

droc@cirad.fr



ARCHITECTURE



GENE REPORT VIA TRIPAL

GSMUA_Achr10P01390_001 (polypeptide) *Musa acuminata*

Feature Details

Name	GSMUA_Achr10P01390_001
Unique Name	GSMUA_Achr10P01390_001
Length	247
Product	BI1-like protein
Evidence code	ISS
Status	in_progress
Location	chr10:3380912..3386947
Organism	<i>Musa acuminata</i> (Banana)

Resources

- [Feature Details](#)
- [Sequence](#)
- [Relationships](#)
- [Cross References](#)
- [Controlled vocabularies Assignments](#)
- [InterPro Report 2012-08-10](#)
- [TIGR Homologs](#)
- [SwissProt Homologs](#)
- [TrEMBL Homologs](#)
- [Analyses](#)

External Link

- [View in Gbrowse](#)
- [GreenPhyl Report](#)
- [Edit with Artemis](#)
- [MusaCyc Report](#)
- [CoGe Report](#)

GENE REPORT VIA TRIPAL

GSMUA_Achr10P01390_001 (polypeptide) *Musa acuminata*

Controlled vocabularies Assignments

This polypeptide is annotated with the following Controlled vocabularies terms.

Category	Term Name
CC_EC_number	no_EC_number
CC_evidence	automatic
CC_evidence_code	ISS
CC_functional_completeness	complete
CC_gene	At4g15470
CC_gene	Cj0236c
CC_gene	FAIM2
CC_gene	SPCC576.04
CC_gene	tmbi-4
CC_gene	Tmbim4
CC_gene	TMBIM4
CC_status	in_progress
genedb_products	BI1-like protein

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GENE REPORT VIA TRIPAL

GSMUA_Achr10P01390_001 (polypeptide) *Musa acuminata*

InterPro Report 2012-08-10

Analysis name: InterProScan

Date Performed: 2012-08-10

Summary of Annotated IPR terms

Term	Name
IPR006214	Inhibitor of apoptosis-promoting Bax1 related

Analysis Details

ORF: GSMUA_Achr10P01390_001, Length: 246

IPR Term: IPR006214 Inhibitor of apoptosis-promoting Bax1 related (Family)

Method	Identifier	Description	Matches*
PANTHER	PTHR23291	BAX INHIBITOR-RELATED	9.3e-111 [14-243] T
PFAM	PF01027	UPF0005	3.9e-51 [37-240] T

* score [start-end] status

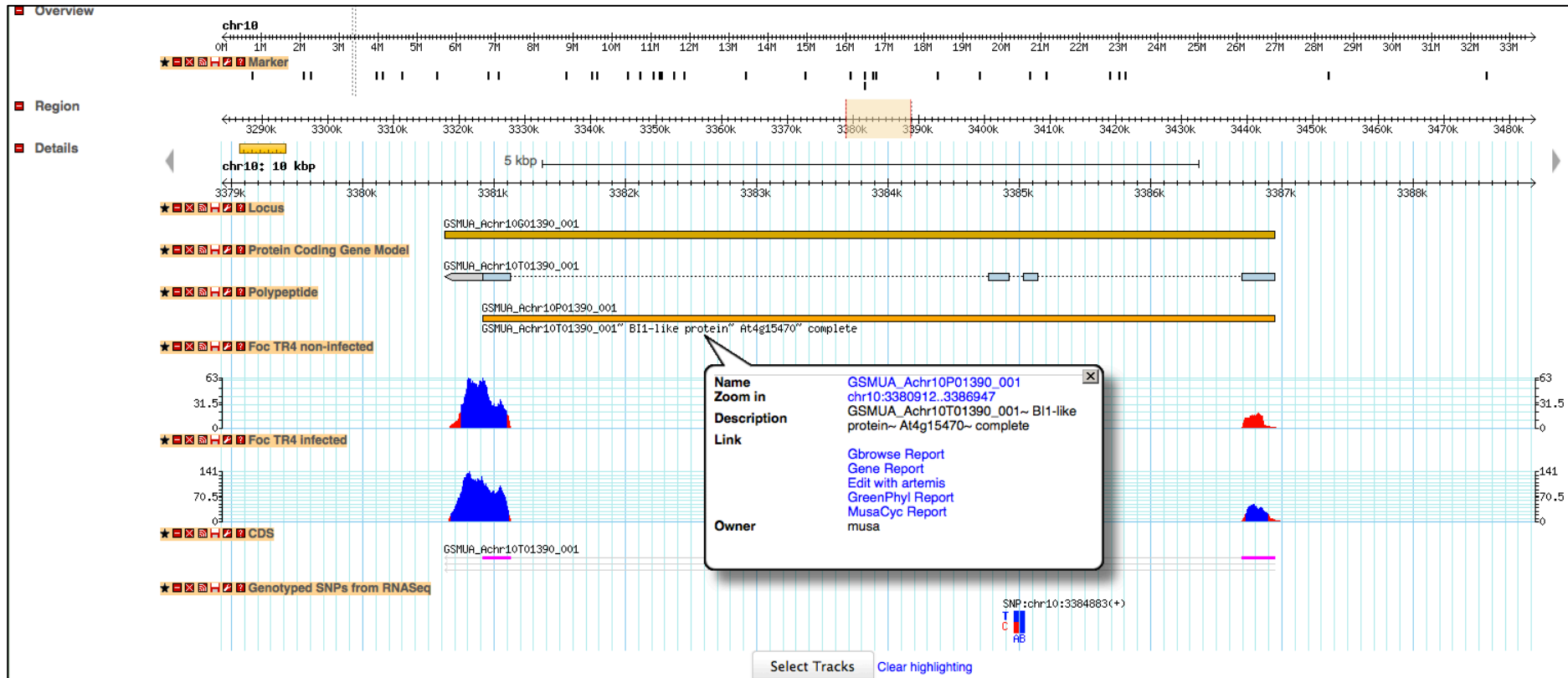
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GBROWSE2



ARTEMIS

Artemis Entry Edit: chr4

Entry: chr4 Commit

3 selected bases on reverse strand: 6900379..6900381 = complement (23151136..23151138)

>>
<<

23152000 | 23152800 | 23153600 | 23154400 | 23155200 | 23156000 | 23156800 | 23157600 | 23158400 | 23159200 | 23160000

MaP04_te0098350 LC MUSAP Angela-scaffold_117_700750_707229
23156800 | 23157600 | 23158400 | 23159200 | 23160000

GSMUA_Achr4G22870_001
MaP04_te0098340 HH MUSAP unclassified-scaffoldc_13_N_13601_5
GSMUA_Achr4G22870_001

<<

C V S A S L D W L L I A Q + K S W H W + Q + S W C R D S * G G A G V G E T G E * R W C R L L
L A Y Q L H W I G C * S H S R S H G T G S S S H G V V T A E E E L E L E K L E S D G G V V F F
L R I S F T G L A A D R T V E V M A L V A V V M V S * Q L R R S W S W R N W R V T V V S S S S
TTGCGTATCAGCTTCACTGGATTGGCTGCTGATCGCACAGTAGAAGTCATGGCACTGGTAGCAGTAGTCATGGTGTGCGTGACAGCTGAGGAGGAGCTGGAGTTGGAGAACTGGAGAGTGACGGTGGTGTGCTCTCTTC
23155520 | 23155540 | 23155560 | 23155580 | 23155600 | 23155620 | 23155640
AACGCATAGTCGAAGTGACCTAACCGACGACTAGCGTGTTCATCTTCAGTACCGTGACCATCGTCATCAGTACCCACAGCACTGTCGACTCCTCCTCGACCTCAACCTCTTTGACCTCTCACTGCCACCACAGCAGAAGAAG
K R I L K V P N A A S R V T S T M A S T A T T M T D H C S L L L Q L Q L F Q L T V T T D D E E
Q T D A E S S Q S S I A C Y F D H C Q Y C Y D H H R S L Q P P A P T P S V P S H R H R R R R R
A Y * S * Q I P Q Q D C L L L * P V P L L L * P T T V A S S S S S S N S F S S L S P P T T K K

<<

gene	23153783	23155588	c	
CDS	23153783	23155588	c	
mRNA	23153783	23155588	c	
polypeptide	23153783	23155588	c	GSMUA_Achr4G22870_001- 9-cis-epoxycarotenoid dioxygenase 1, chloroplastic- NCED1- missing_completeness
gene	23154600	23155588	c	
CDS	23154600	23155588	c	
mRNA	23154600	23155588	c	
polypeptide	23154600	23155588	c	GSMUA_Achr4T22880_001- Hypothetical protein- unknown_gene- missing_functional_completeness
repeat_region	23156080	23156679	c	DNA_transposon- Helitron- Helitron- unclassified_rpt_family- MaP04_te0098340- missing_rpt_type- missin
helitron	23156080	23156679	c	
repeat_region	23156820	23157368	c	Retrotransposon- LTR- Copia- Angela- MaP04_te0098350- missing_rpt_type- missing_rpt_completeness
LTR_retrotransposon	23156820	23157368	c	

ARTEMIS

Artemis Gene Builder: GSMUA_Achr4G22870_001

Gene Map

GSMUA_Achr4G22870_001

Annotation :: GSMUA_Achr4P22870_001

Key: polypeptide Add Qualifier: EC_number

Location: complement(23153783..23155588)

Complement Refresh Grab Range Remove Range Goto Feature Select Feature TAT ObjectEdit

Properties Core CV References Match

ADD LOOK UP ADD HISTORY

Product WITH/FROM Dbxref

9-cis-epoxycarotenoid dioxygenase 1, chloroplastic

Controlled Curation

Term	Dbxref	Evidence	Qualifier	Date	
1.13.11.51				----/--/--	X
NCED1				----/--/--	X
complete				----/--/--	X
IC_2a				----/--/--	X
curated				----/--/--	X
in_progress				----/--/--	X

Overview Tab View OK Cancel Apply

Annotation Inspector Validation

Validations:

- # Start/Stop codon validation:
- # Sequence validation:
- # Introns validation:
- # Mandatory properties management:
-GSMUA_Achr4G22870_001:
OK
- # Evidence code coherence management:
-GSMUA_Achr4G22870_001:
Evidence Code Management: ERROR: missing GO Term!
- # Gene structure validation:
- # TE structure validation:

Unless you cancel, your changes will be committed to t

Annuler OK

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Advanced Search

▼ Putative Function Search

Example : **WRKY**

Search Text

Output

FASTA file CDS sequences. Does not include intron sequences or UTRs. (ie Coding sequence only)

Translated protein sequences

Action

Send output to Galaxy

▶ Locus Search

▶ InterPro Domain Search

▶ GO Term Search

▶ EC number Search

▶ Location Search

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▼ Blast Search

Input (Load example)

Paste sequence(s)

```
>GSMUA_Achr3G27160_001
ATGTGTGTGCAGGGCAAACATTAGTCCATATGGCTGTAATCTGCCAATGCAGGGCAG
GAAACTTCTCTGAAGAGTGAAGTGGTTCGCGAGCAGTGTCCAAACTTTATGGAAAATGGA
ATGAACAATACACAGTCTCTAAATAACTTTACGTCTTAGGCCATTTGAATATGGGCAT
AATGATAATGATTTAGCTCTCAAACCTTCTAGTCACATTACCCAGTTCAACAAGGAAAT
GCATCCTCCACCAAAGACCTTACCATTCACTTCCCTTCACAAACTCCCTCCAGTTAT
CCCCGCCAAATGTACAAATTCCTGCTGGACATTTCCGCAATGTACTCCAATGAGTCAA
```

Or upload a file

Filter

Program

Database

Expect

Filter query sequence

Number of alignment

Output

FASTA file

CDS sequences. Does not include intron sequences or UTRs. (ie Coding sequence only)

Translated protein sequences.

TOOLS

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3 result(s)

- View BLAST result
- Download Excel file

Query name	Query length	Start Query	End Query	Chromosome	Start Hit	End Hit	Strand	Query coverage	Cumulative HSI	Link
GSMUA_Achr3G27160_001	699	1	699	chr3	26733743	26734635	-	100.00	699	View result on gbrowse
GSMUA_Achr3G27160_001	699	29	542	chr9	28621745	28622258	+	73.39	513	View result on gbrowse
GSMUA_Achr3G27160_001	699	8	522	chr4	8656382	8656896	-	73.53	514	View result on gbrowse

Go to page: Show rows: 1-3 of 3



THANK YOU

Gaëtan Droc, Delphine Larivière, Valentin Guignon, Nabila Yahiaoui, Dominique This, Olivier Garsmeur, Alexis Dereeper, Chantal Hamelin, Xavier Argout, Jean-François Dufayard, Juliette Lengelle, Franc-Christophe Baurens, Alberto Cenci, Bertrand Pitollat, Angélique D'Hont, Manuel Ruiz, Mathieu Rouard, Stéphanie Bocs, The Banana Genome Hub. *Database*: the journal of biological databases and curation, 2013, Submitted revision (manuscript ID DATABASE-2012-0102.R1).

BGH is supported by South Green Bioinformatics Platform <http://southgreen.cirad.fr/>

