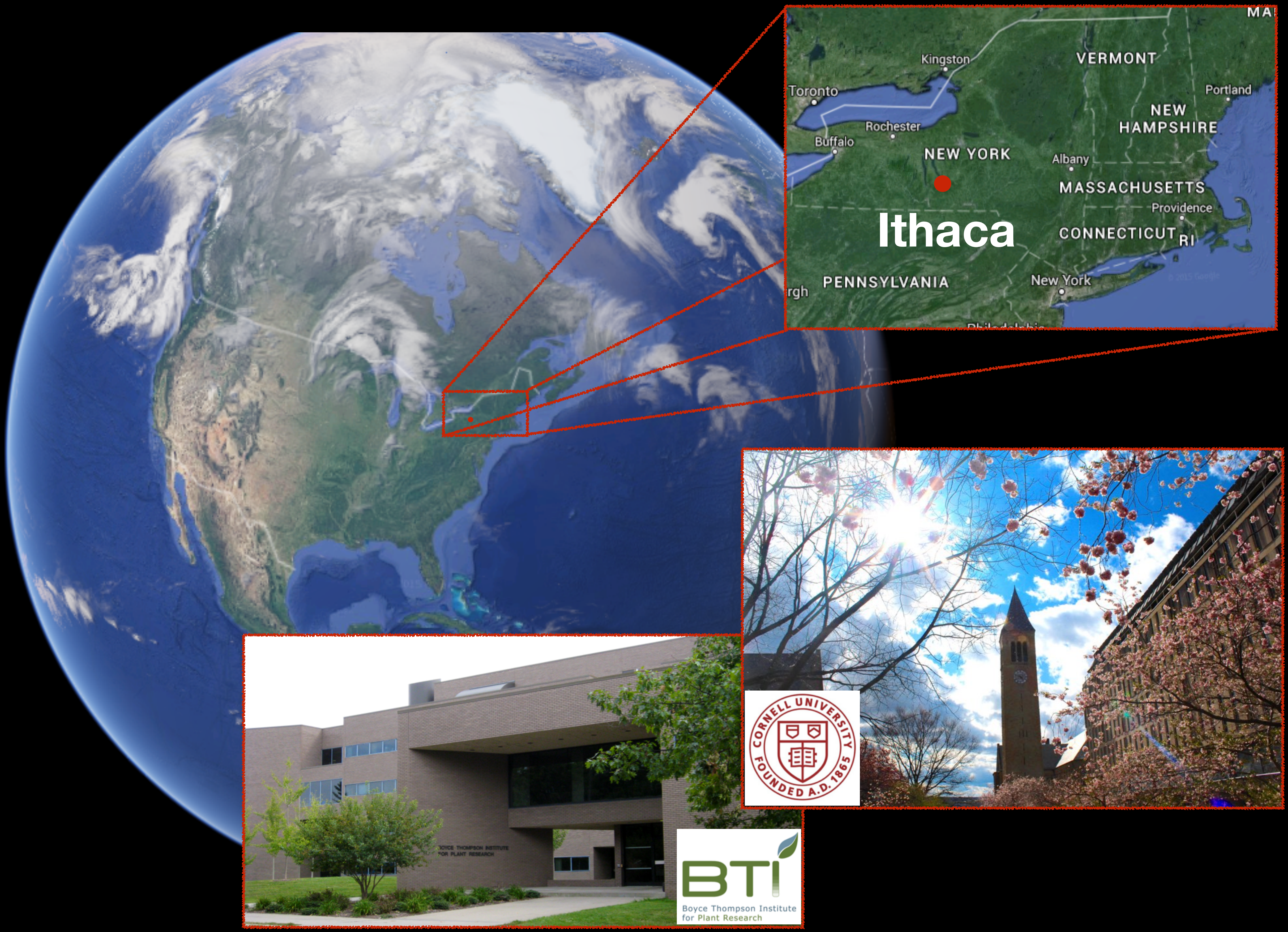
The Sol Genomics Network
bioinformatics tools for genomics and breeding

UPLB January, 2016

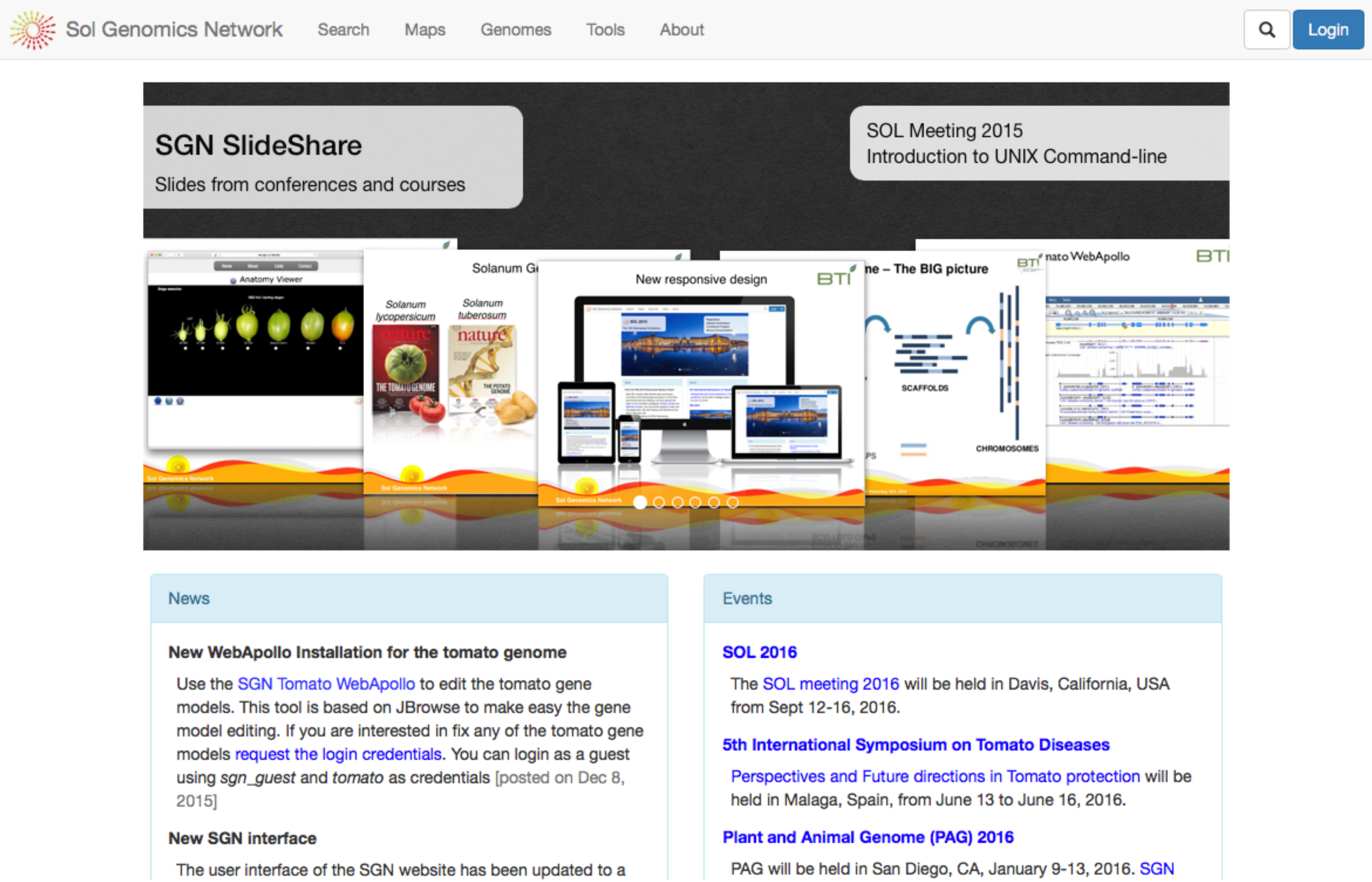
Noe Fernandez-Pozo

Sol Genomics Network


MA
VERMONT
Kingston
Toronto
Portland
NEW
HAMPSHIRE
Rochester
Buffalo
NEW YORK
Albany
MASSACHUSETTS
Providence
Ithaca
CONNECTICUT
RI
PENNSYLVANIA
New York
rgh
BOYCE THOMPSON INSTITUTE FOR PLANT RESEARCH
BTI
Boyce Thompson Institute for Plant Research
CORNELL UNIVERSITY FOUNDED A.D. 1865


NDE

Sol Genomics Network



SGN SlideShare

Slides from conference and courses

SOL Meeting 2015
Introduction to UNIX Command-line

News

New WebApollo Installation for the tomato genome

Use the SGN Tomato WebApollo to edit the tomato gene models. This tool is based on JBrowse to make easy the gene model editing. If you are interested in fix any of the tomato gene models request the login credentials. You can login as a guest using *sgn_guest* and *tomato* as credentials [posted on Dec 8, 2015]

New SGN interface

The user interface of the SGN website has been updated to a

Events

SOL 2016

The SOL meeting 2016 will be held in Davis, California, USA from Sept 12-16, 2016.

5th International Symposium on Tomato Diseases

Perspectives and Future directions in Tomato protection will be held in Malaga, Spain, from June 13 to June 16, 2016.

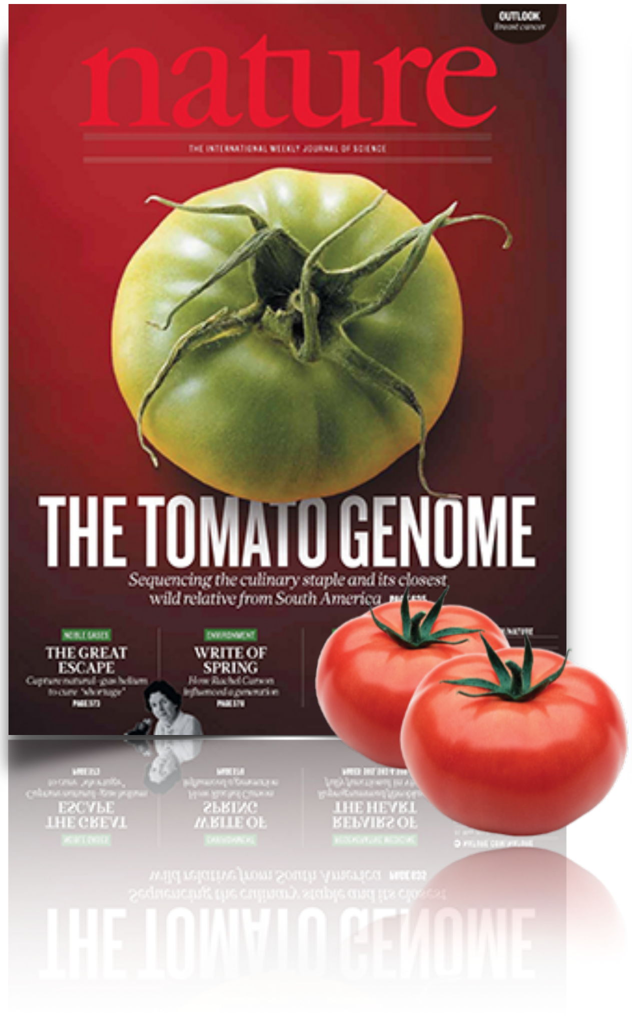
Plant and Animal Genome (PAG) 2016

PAG will be held in San Diego, CA, January 9-13, 2016. SGN

https://solgenomics.net

Solanum Genomes

Solanum lycopersicum



OUTLOOK

nature

THE INTERNATIONAL WEEKLY JOURNAL OF SCIENCE

THE TOMATO GENOME

Sequencing the culinary staple and its closest wild relative from South America

THE GREAT ESCAPE

Capture natural-gas helium to cure "shortage"

WRITE OF SPRING

How Rachel Carson influenced a generation

Solanum tuberosum

OUTLOOK

Alzheimer's disease

nature

THE INTERNATIONAL WEEKLY JOURNAL OF SCIENCE

The DNA sequence of the South American tuber eaten around the world PAGE 189

THE POTATO GENOME

HISTORY

PURE JOY

Arcane mathematics that changed the world

PAGE 166

EVOLUTION

GIANT DINOSAURS

Seeds of greatness in small sauropod ancestors

PAGE 159

NEUROSCIENCE

SPINAL CORD REGENERATIO

Restoring breath co after neck inju

PAGES 178 & 19

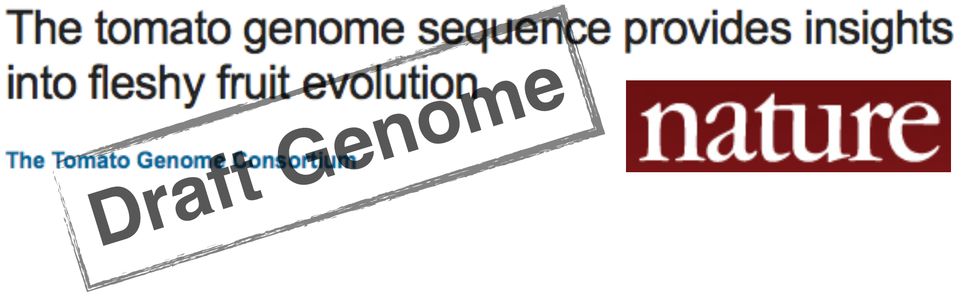
Solanum pennellii

The genome of the stress-tolerant wild tomato species *Solanum pennellii*

Anthony Bolger, Federico Scossa, Marie E Bolger, Christa

nature genetics

Solanum pimpinellifolium



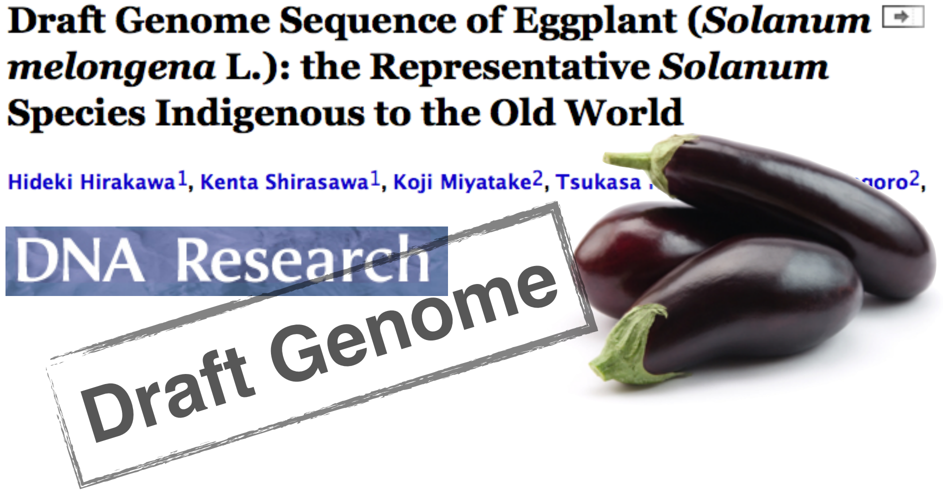
The tomato genome sequence provides insights into fleshy fruit evolution

The Tomato Genome Consortium

nature

Draft Genome

Solanum melongena



Draft Genome Sequence of Eggplant (*Solanum melongena* L.): the Representative *Solanum* Species Indigenous to the Old World

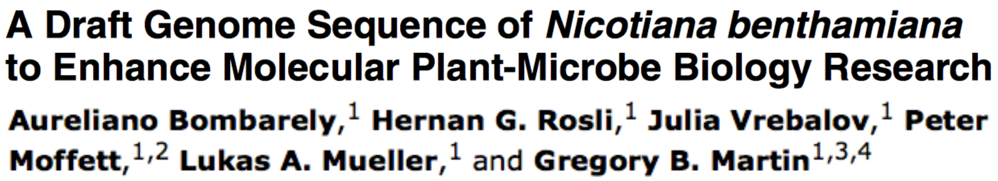
Hideki Hirakawa[1], Kenta Shirasawa[1], Koji Miyatake[2], Tsukasa

DNA Research

Draft Genome

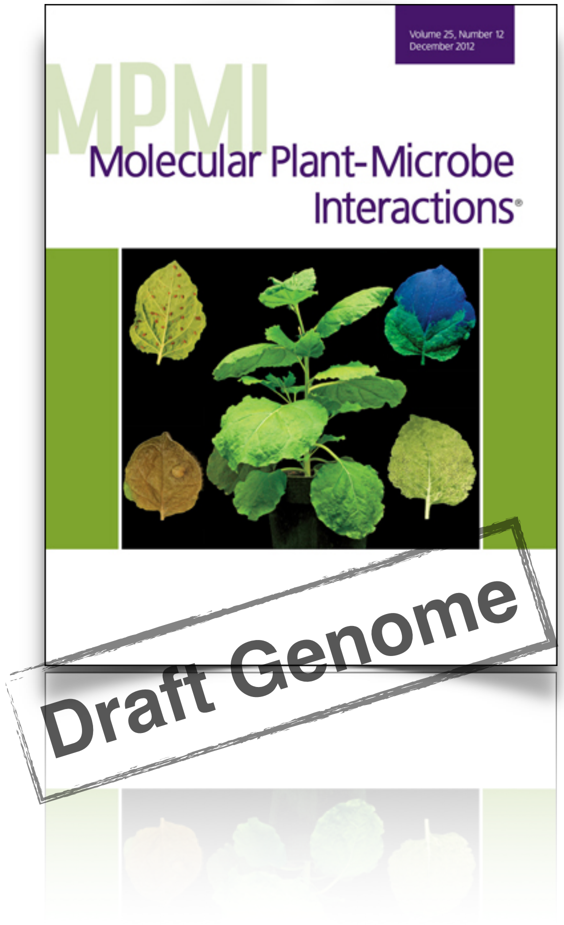
Nicotiana Genomes

Nicotiana benthamiana



A Draft Genome Sequence of *Nicotiana benthamiana* to Enhance Molecular Plant-Microbe Biology Research

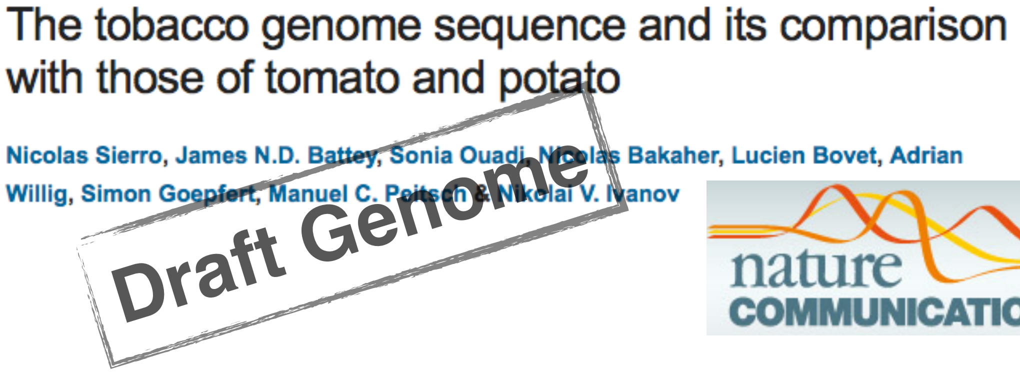
Aureliano Bombarely,[1] **Hernan G. Rosli,**[1] **Julia Vrebalov,**[1] **Peter Moffett,**[1,2] **Lukas A. Mueller,**[1] and **Gregory B. Martin**[1,3,4]



Draft Genome

Nicotiana tabacum

N. tabacum K326 (Flue-cured)
N. tabacum TN90 (Burley)
N. tabacum Basma Xanthi (BX, Oriental)



The tobacco genome sequence and its comparison with those of tomato and potato

Nicolas Sierro, James N.D. Battey, Sonia Ouadi, Nicolas Bakaher, Lucien Bovet, Adrian Willig, Simon Goepfert, Manuel C. Peitsch & Nikolai V. Ivanov

Draft Genome

nature COMMUNICATIONS

Nicotiana sylvestris & *Nicotiana tomentosiformis*

Reference genomes and transcriptomes of *Nicotiana sylvestris* and *Nicotiana tomentosiformis*

Nicolas Sierro, James ND Battey, Sonia Ouadi, Lucien Bovet, Simon Goepfert, Nicolas Bakaher, Manuel C Peitsch and Nikolai V Ivanov*

Genome Biology

Draft Genome

Other Genomes

Capsicum annuum

Capsicum annuum cv. CM334
Capsicum chinense

Genome sequence of the hot pepper provides insights into the evolution of pungency in *Capsicum* species

Seungill Kim, Minkyu Park, Seon-In Yeom, Yong-Min Kim, Je Min Lee,

nature genetics

Capsicum annuum Zunla-1
Capsicum annuum var. glabriusculum

Whole-genome sequencing of cultivated and wild peppers provides insights into *Capsicum* domestication and specialization

Cheng Qin[a,b,c,1], Changshui Yu[b,1], Yaou Shen[a,1], Xiaodong Fang[d,e,1], Lang Chen[b,1], Jiumeng Min[d,1],

PNAS

Petunia spp.

Coming soon …

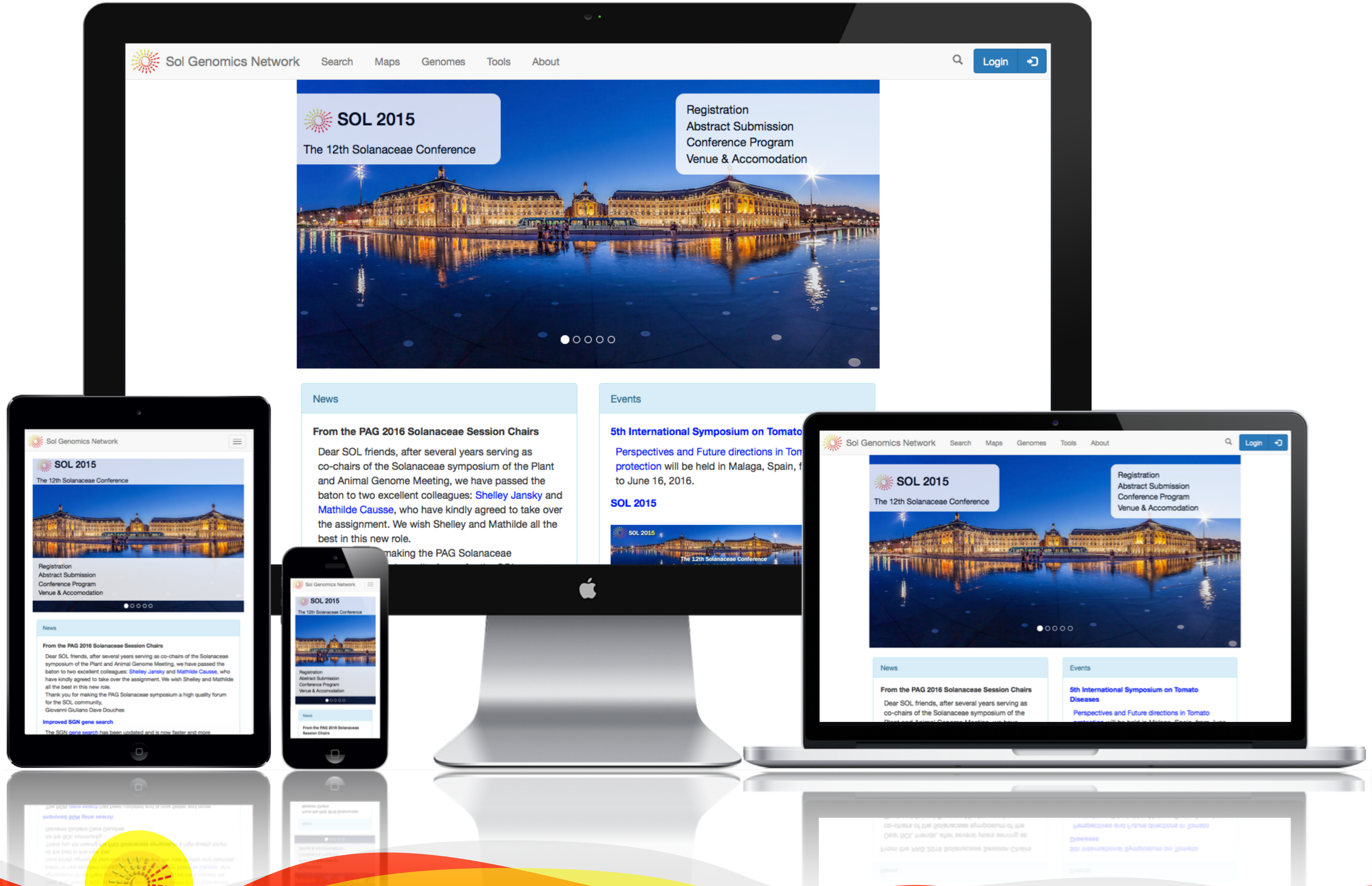
Coffea canephora

The coffee genome provides insight into the convergent evolution of caffeine biosynthesis

France Denoeud[1,2,3], Lorenzo Carretero-Paulet[4], Alexis Dereeper[5], Gaëtan Droc[6], Romain Guyot[7],

Science
AAAS

New responsive design



SOL 2015

The 12th Solanaceae Conference

Registration
Abstract Submission
Conference Program
Venue & Accomodation

News

From the PAG 2016 Solanaceae Session Chairs

Dear SOL friends, after several years serving as co-chairs of the Solanaceae symposium of the Plant and Animal Genome Meeting, we have passed the baton to two excellent colleagues: Shelley Jansky and Mathilde Causse, who have kindly agreed to take over the assignment. We wish Shelley and Mathilde all the best in this new role.

Thank you for making the PAG Solanaceae symposium a high quality forum for the SOL community.
Giovanni Giuliano Dave Douches

Improved SGN gene search

Events

5th International Symposium on Tomato Diseases

Perspectives and Future directions in Tomato protection will be held in Malaga, Spain, from June 13 to June 16, 2016.

SOL 2015

The SGN carousel

linked to the
genome paper

Direct access to JBrowse,
BLAST, and the genome data

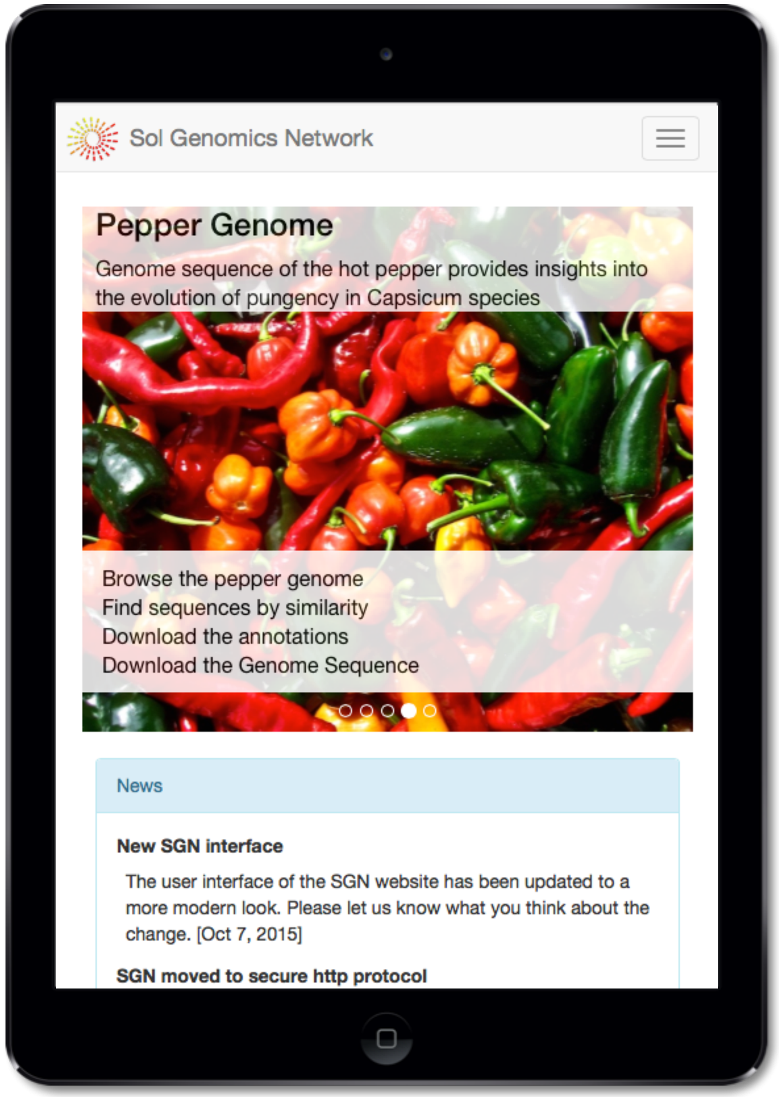
Pepper Genome

Genome sequence of the hot pepper provides insights into the evolution of pungency in Capsicum species

Browse the pepper genome
Find sequences by similarity
Download the annotations
Download the Genome Sequence

More visibility for
news, events and
biological data

The SGN carousel



Sol Genomics Network

Pepper Genome

Genome sequence of the hot pepper provides insights into the evolution of pungency in Capsicum species

Browse the pepper genome
Find sequences by similarity
Download the annotations
Download the Genome Sequence

○○○●○

News

New SGN interface

The user interface of the SGN website has been updated to a more modern look. Please let us know what you think about the change. [Oct 7, 2015]

SGN moved to secure http protocol

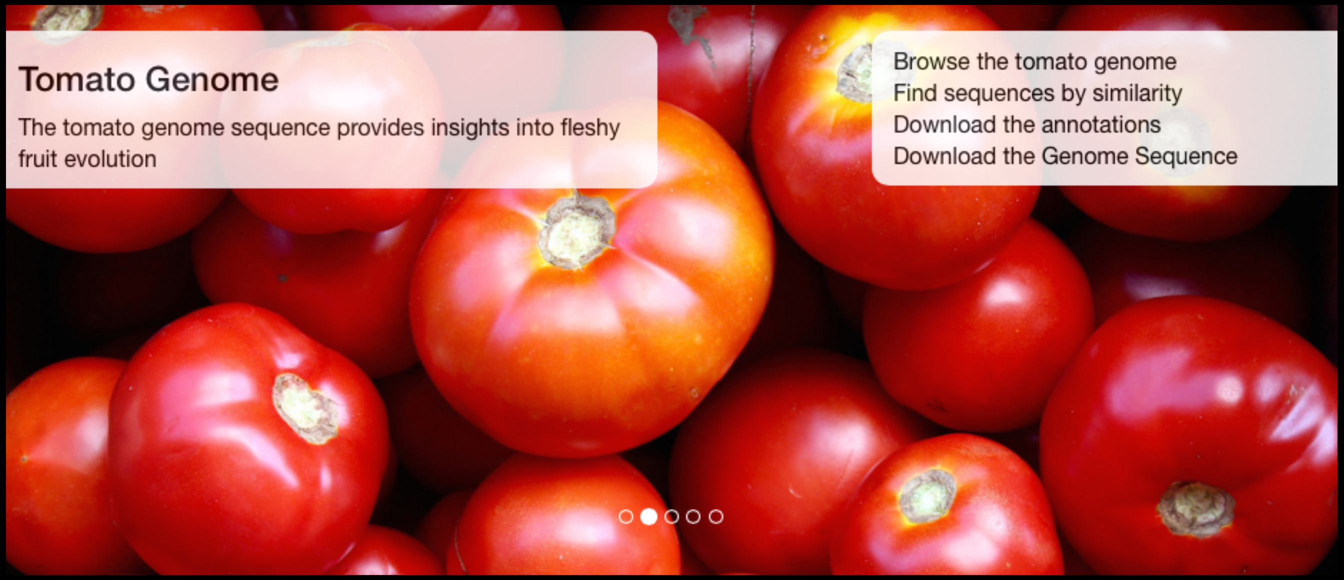
Pepper Genome

Genome sequence of the hot pepper provides insights into the evolution of pungency in Capsicum species

Browse the pepper genome
Find sequences by similarity
Download the annotations
Download the Genome Sequence

○○○●○

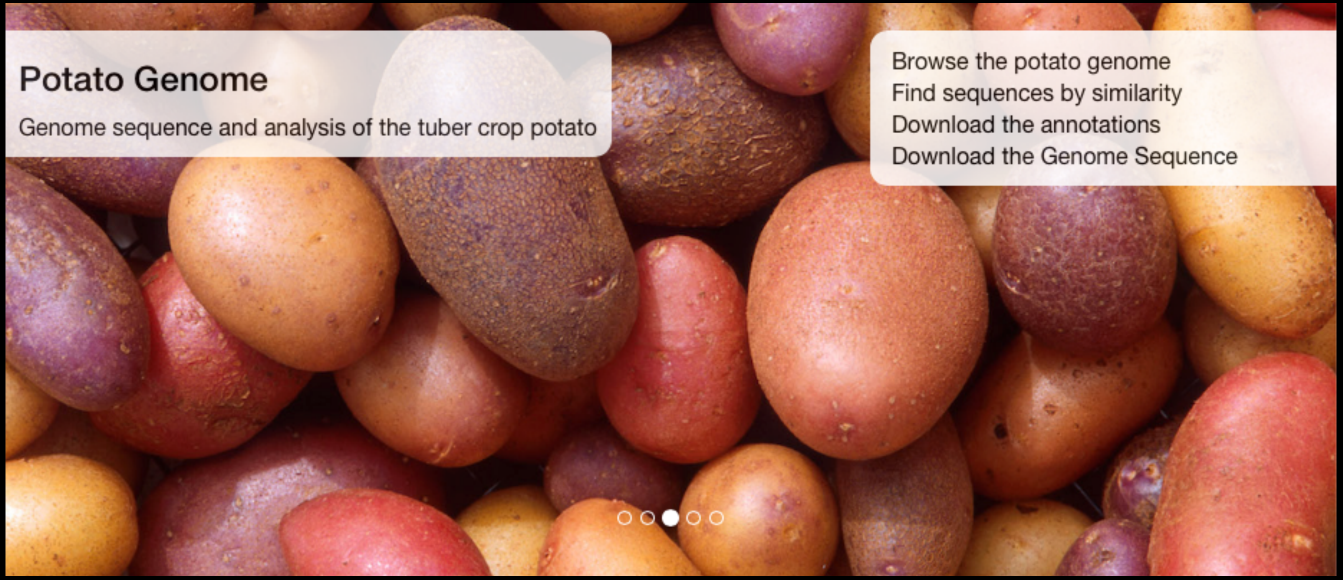
The SGN carousel



Tomato Genome

The tomato genome sequence provides insights into fleshy fruit evolution

- Browse the tomato genome
- Find sequences by similarity
- Download the annotations
- Download the Genome Sequence



Potato Genome

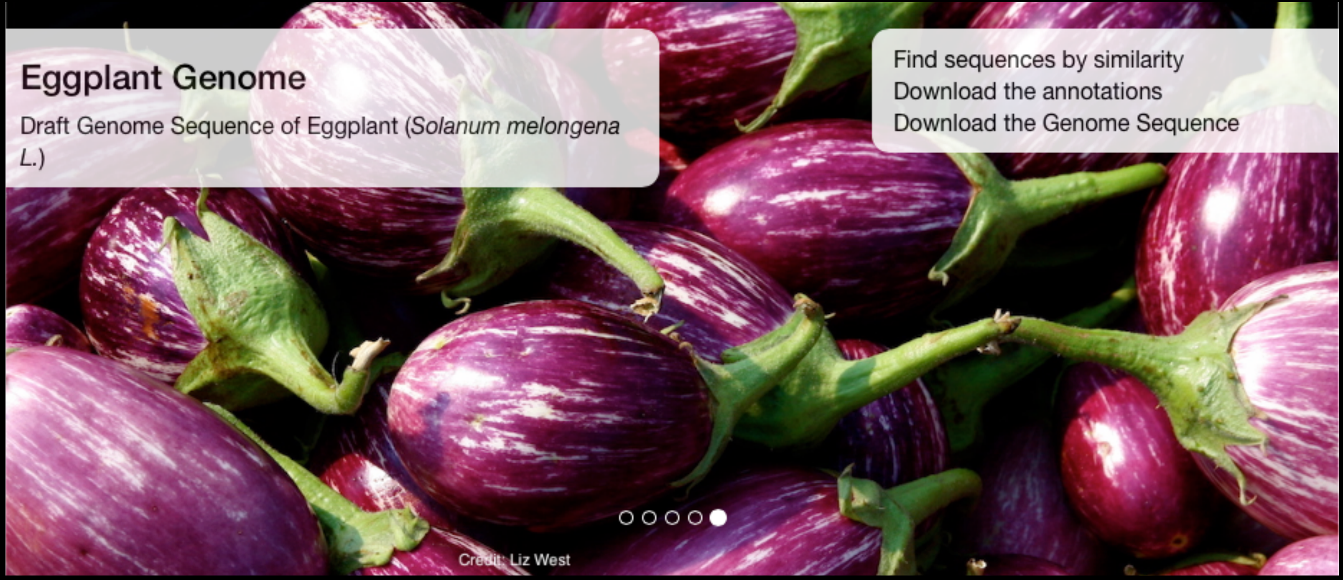
Genome sequence and analysis of the tuber crop potato

- Browse the potato genome
- Find sequences by similarity
- Download the annotations
- Download the Genome Sequence

Pepper Genome

Genome sequence of the hot pepper provides insights into the evolution of pungency in Capsicum species

- Browse the pepper genome
- Find sequences by similarity
- Download the annotations
- Download the Genome Sequence



Eggplant Genome

Draft Genome Sequence of Eggplant (*Solanum melongena* L.)

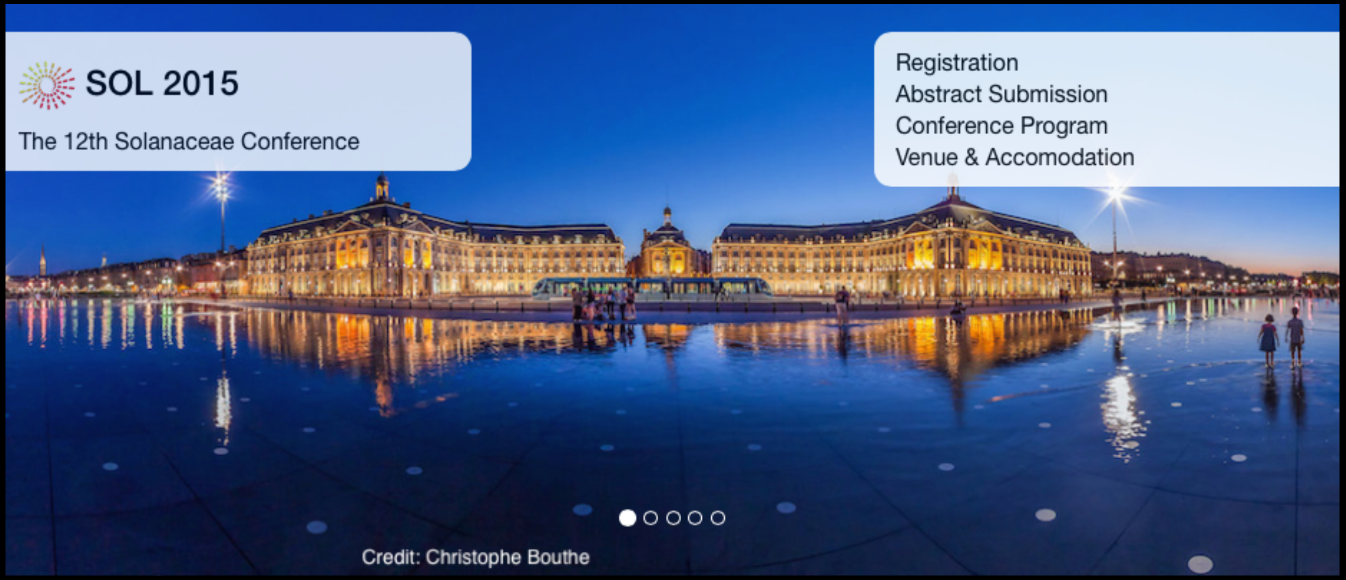
- Find sequences by similarity
- Download the annotations
- Download the Genome Sequence

Credit: Liz West

SGN SlideShare

Slides from conferences and courses

- SOL Meeting 2015
- Introduction to UNIX Command-line



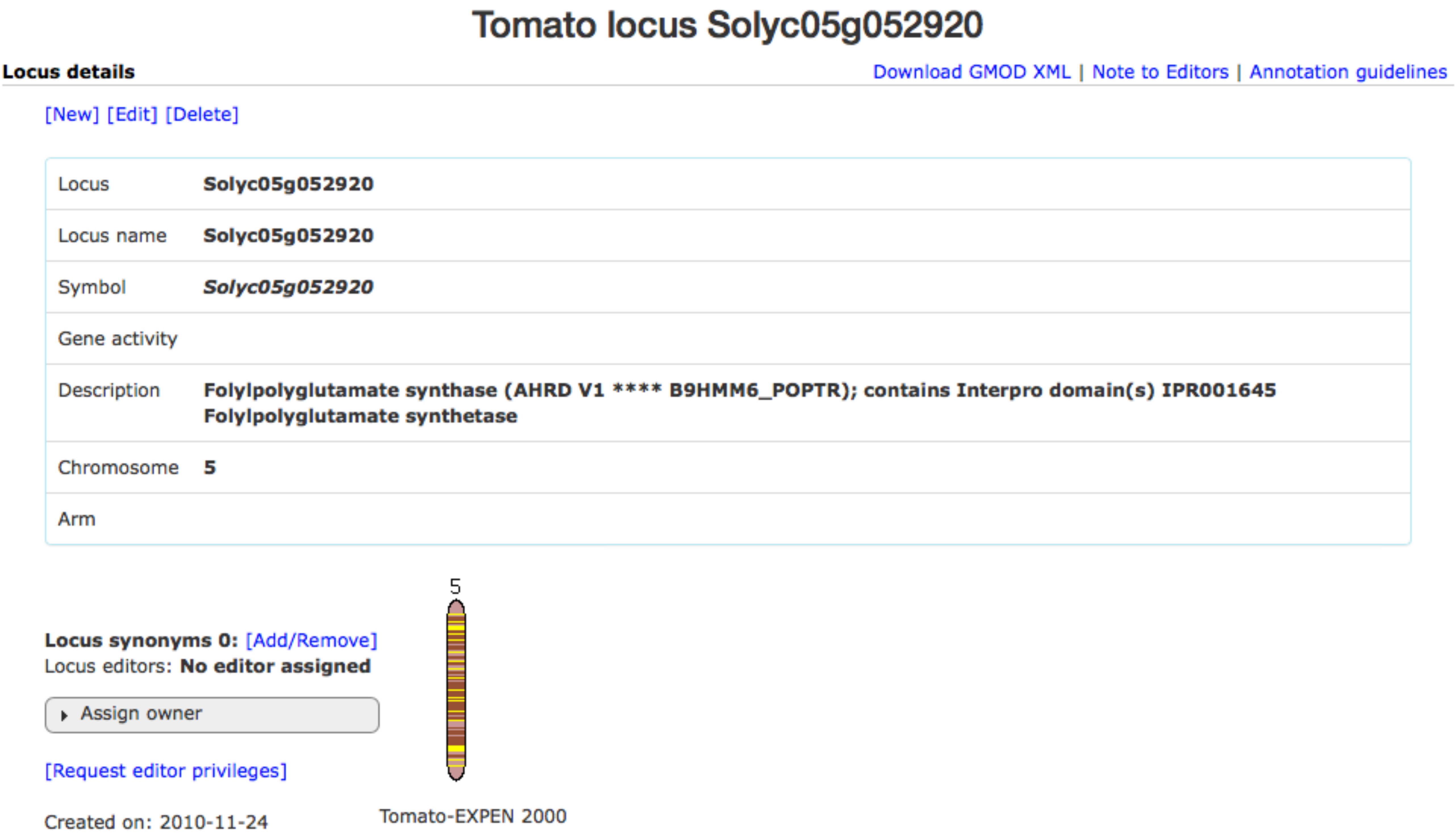
SOL 2015

The 12th Solanaceae Conference

- Registration
- Abstract Submission
- Conference Program
- Venue & Accomodation

Credit: Christophe Bouthe

Locus editors



Tomato locus Solyc05g052920

Locus details

Download GMOD XML | Note to Editors | Annotation guidelines

[New] [Edit] [Delete]

Locus	**Solyc05g052920**
Locus name	**Solyc05g052920**
Symbol	***Solyc05g052920***
Gene activity	
Description	**Folylpolyglutamate synthase (AHRD V1 **** B9HMM6_POPTR); contains Interpro domain(s) IPR001645 Folylpolyglutamate synthetase**
Chromosome	**5**
Arm	

Locus synonyms 0: [Add/Remove]

Locus editors: **No editor assigned**

[Request editor privileges]

Created on: 2010-11-24

Sol Genomics Network

https://solgenomics.net

SGN SlideShare
Slides from conferences and courses

SOL Meeting 2015
Introduction to UNIX Command-line

News

New WebApollo Installation for the to
Use the SGN Tomato WebApollo to ed
models. This tool is based on JBrowse
model editing. If you are interested in
gene models request the login credent

New SGN interface
The user interface of the SGN website
more modern look. Please let us know
the change. [Oct 7, 2015]

SGN moved to secure http protocol

will be held in Davis, California, USA

osium on Tomato Diseases
e directions in Tomato protection will
n, from June 13 to June 16, 2016.
me (PAG) 2016
PAG will be held in San Diego, CA, January 9-13, 2016. SGN and RTB databases workshop will be on Jan 12, 2016.

SGN

https://github.com/solgenomics

Sol Genomics Network

https://solgenomics.net

SGN SlideShare
Slides from conferences and courses

SOL Meeting 2015
Introduction to UNIX Command-line

News

New WebApollo Installation for the to

Use the SGN Tomato WebApollo to ed models. This tool is based on JBrowse model editing. If you are interested in f gene models request the login credent

New SGN interface

The user interface of the SGN website more modern look. Please let us know the change. [Oct 7, 2015]

SGN moved to secure http protocol

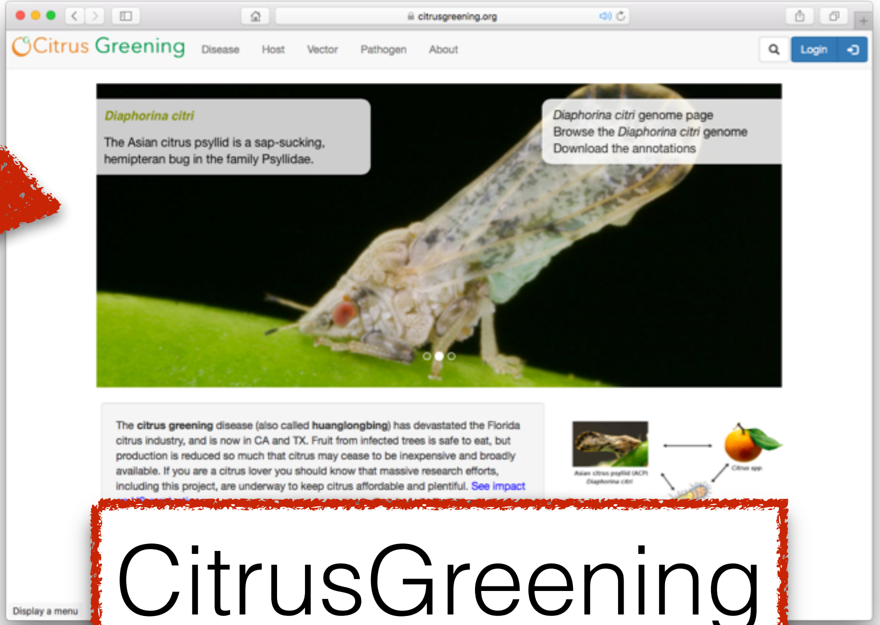
will be held in Davis, California, USA

FAG will be held in San Diego, CA, January 9-13, 2016. and RTB databases workshop will be on Jan 12, 2016.

SGN

GitHub https://github.com/solgenomics

Citrus Greening



Diaphorina citri

The Asian citrus psyllid is a sap-sucking, hemipteran bug in the family Psyllidae.

Diaphorina citri genome page
Browse the *Diaphorina citri* genome
Download the annotations

The **citrus greening** disease (also called **huanglongbing**) has devastated the Florida citrus industry, and is now in CA and TX. Fruit from infected trees is safe to eat, but production is reduced so much that citrus may cease to be inexpensive and broadly available. If you are a citrus lover you should know that massive research efforts, including this project, are underway to keep citrus affordable and plentiful. See impact

CitrusGreening

https://citrusgreening.org

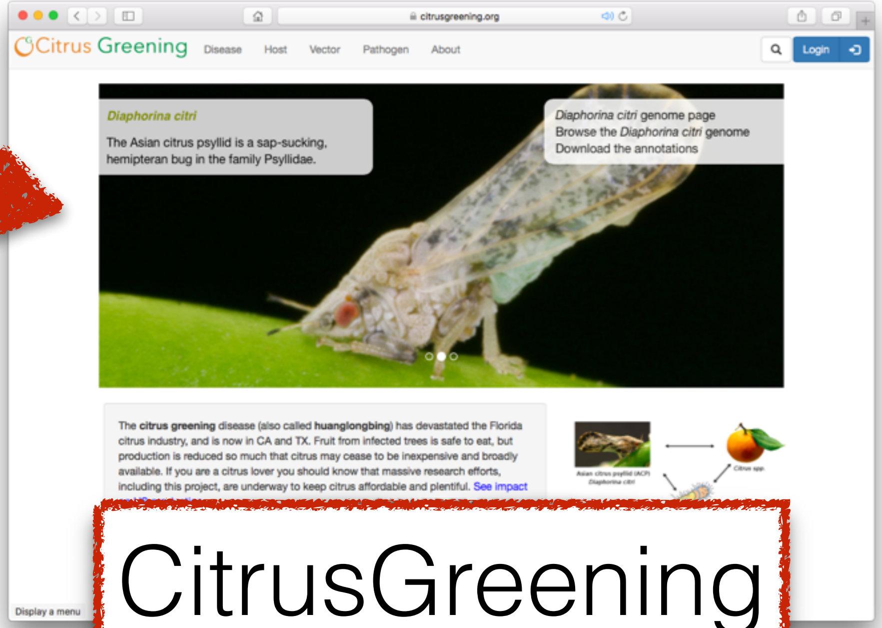
Sol Genomics Network

https://solgenomics.net

SGN

GitHub https://github.com/solgenomics

Citrus Greening



CitrusGreening

https://citrusgreening.org

CASSAVABASE

https://cassavabase.org

CassavaBase

Sol Genomics Network

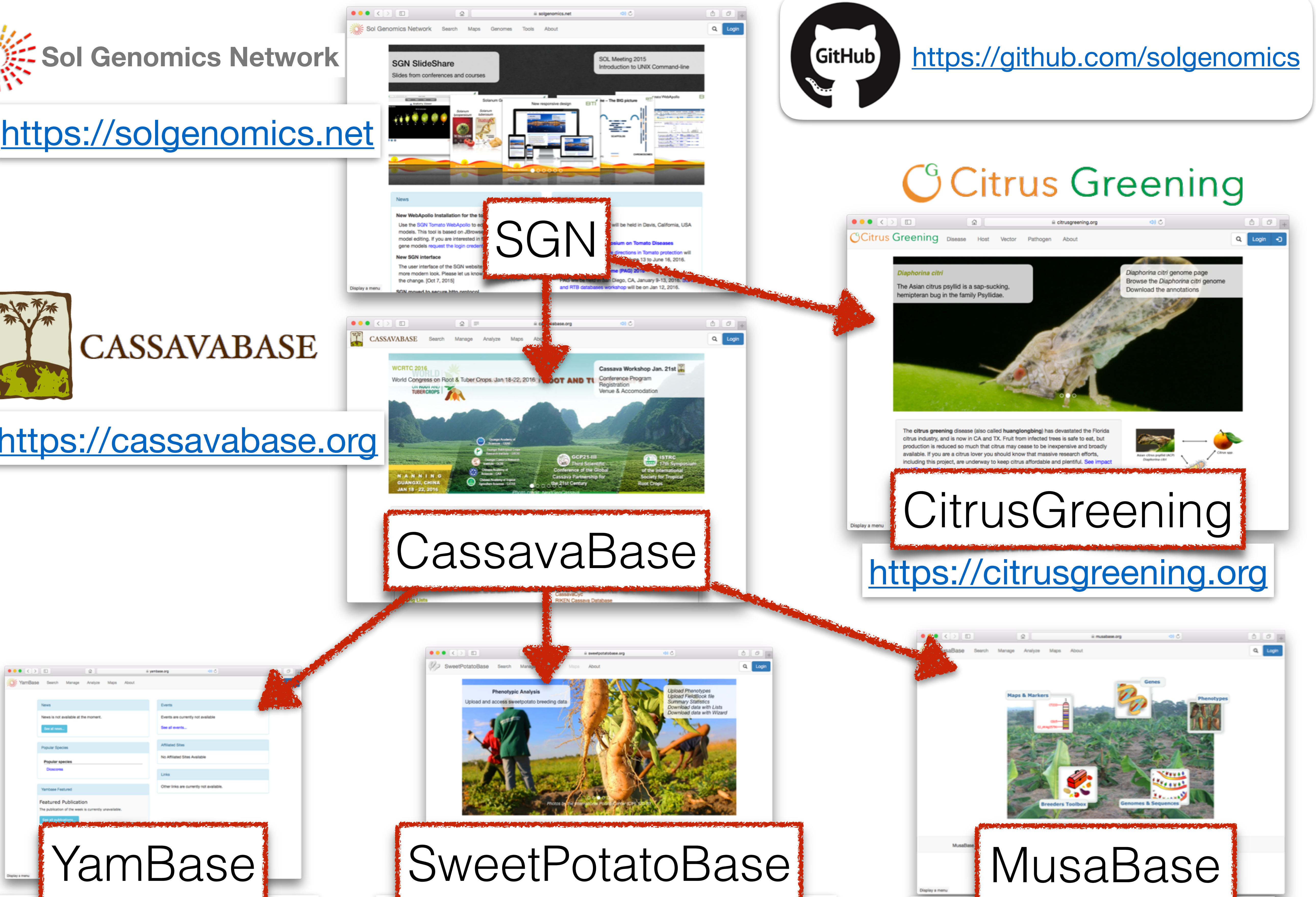
https://solgenomics.net

GitHub https://github.com/solgenomics

Citrus Greening

CASSAVABASE

https://cassavabase.org



SGN

CassavaBase

CitrusGreening

https://citrusgreening.org

YamBase

https://yambase.org

SweetPotatoBase

https://sweetpotatobase.org

MusaBase

https://musabase.org

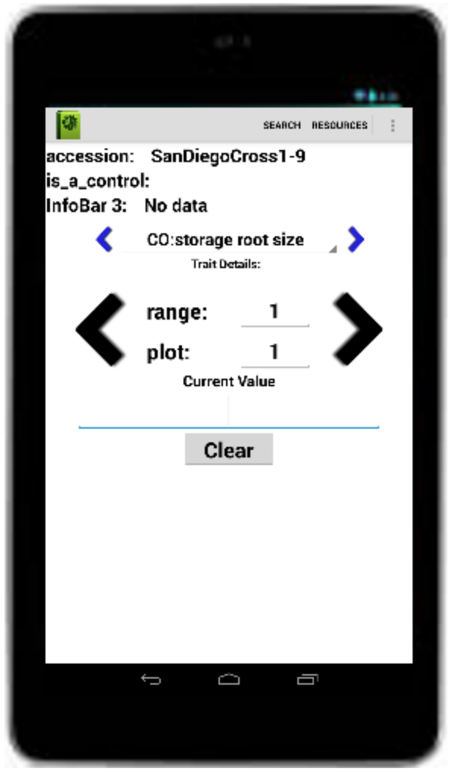
Breeding Informatics

Genotyping Data
(GBS)

CassavaBase

Breeding Decisions

Android FieldBook



accession: SanDiegoCross1-9

is_a_control:

InfoBar 3: No data

CO:storage root size

range: 1

plot: 1

Phenotyping Data

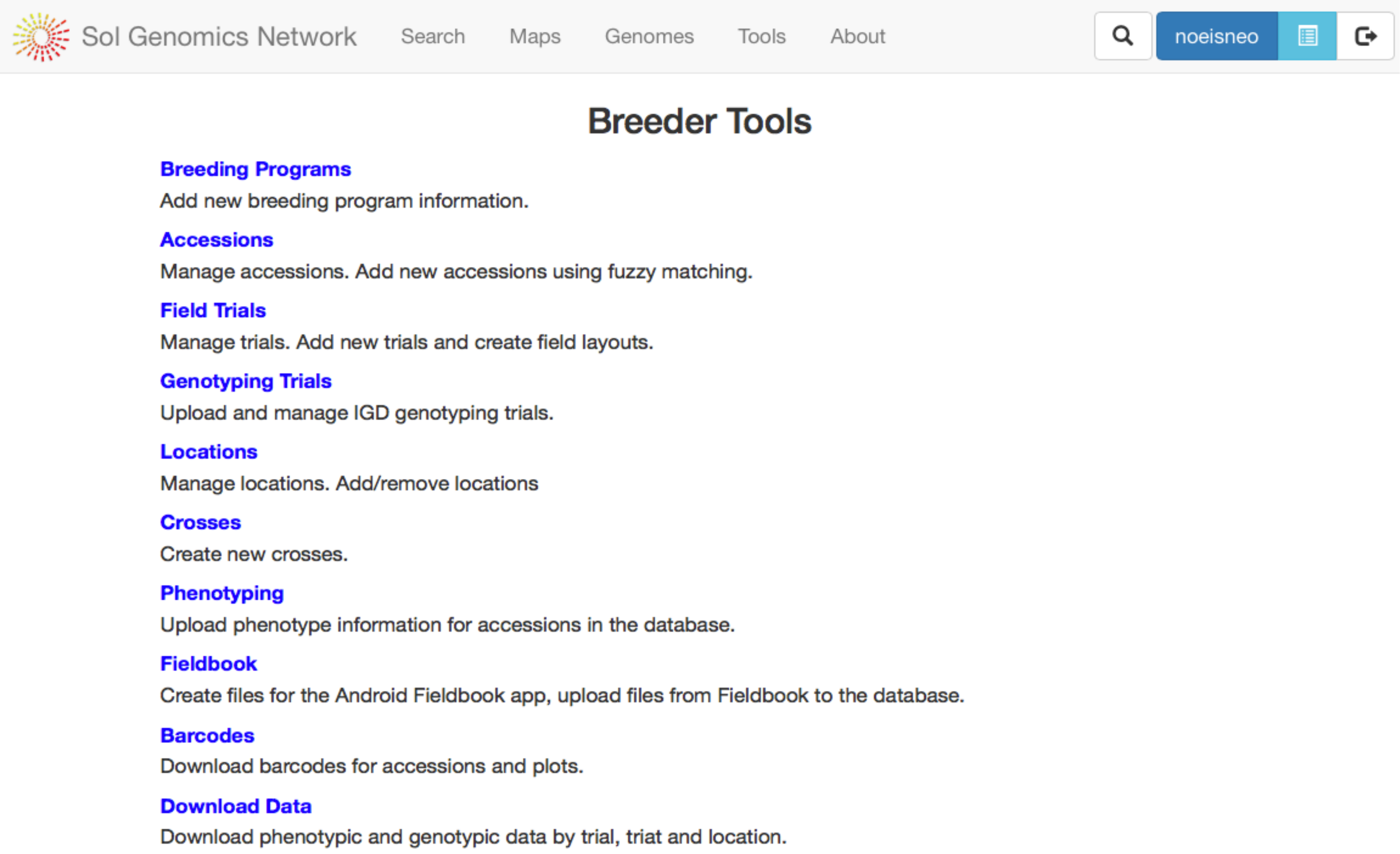
Cassava Crop

- Tropical and subtropical regions
- Mainly grown for starchy roots
- Native to South America
- Major crop in Africa
- Food for 500 million people around the world
- Clonally propagated
- Accumulates toxic cyanogenic glucosides
- Requires processing before consumption

BILL & MELINDA GATES foundation

CassavaBase Data

- 80,000 accessions
- 1,500 trials
- 7,800,000 phenotypic observations
- ~12,000 genotypes
- ~2,000,000,000 marker scores



Breeder Tools

Breeding Programs
Add new breeding program information.

Accessions
Manage accessions. Add new accessions using fuzzy matching.

Field Trials
Manage trials. Add new trials and create field layouts.

Genotyping Trials
Upload and manage IGD genotyping trials.

Locations
Manage locations. Add/remove locations

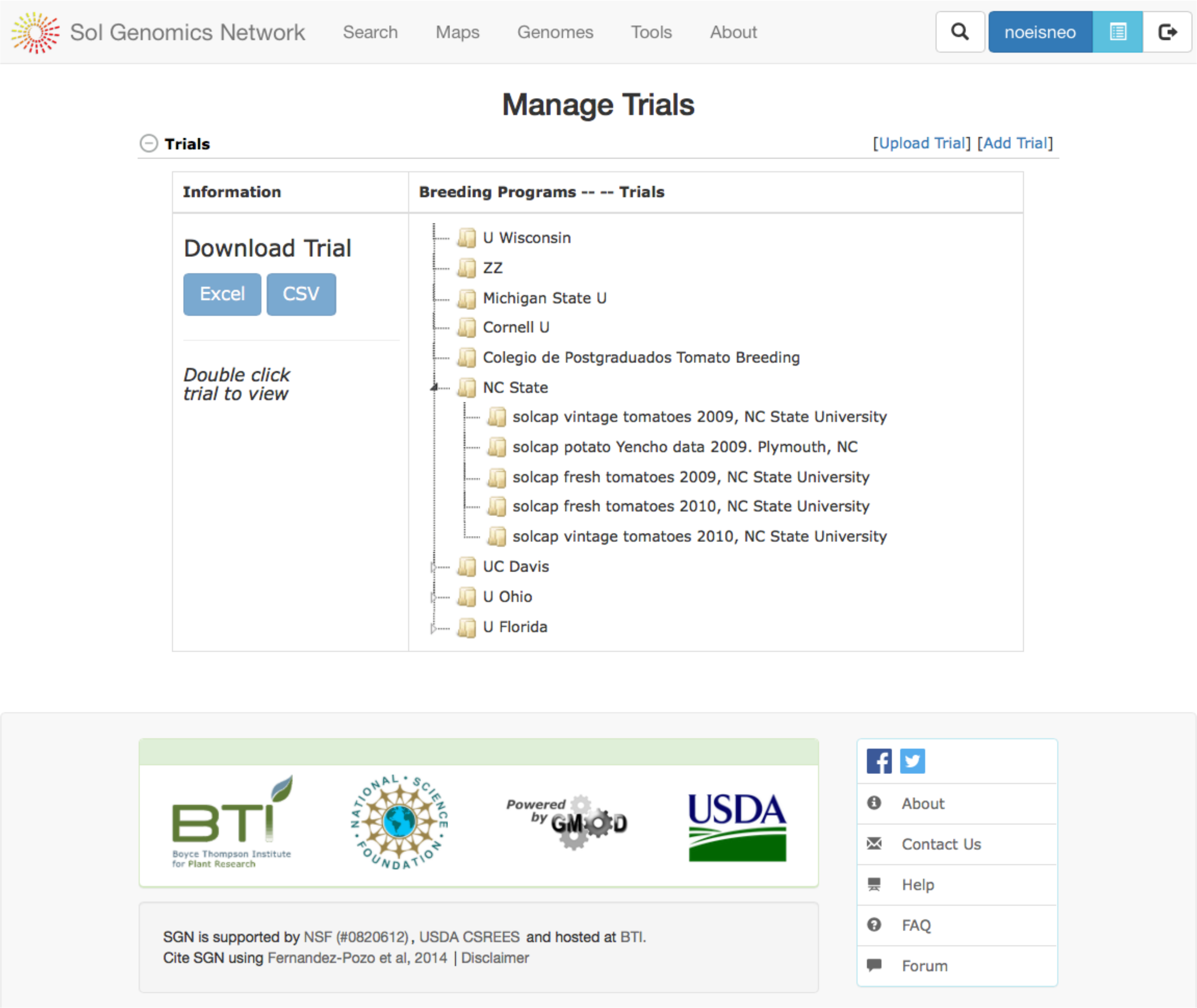
Crosses
Create new crosses.

Phenotyping
Upload phenotype information for accessions in the database.

Fieldbook
Create files for the Android Fieldbook app, upload files from Fieldbook to the database.

Barcodes
Download barcodes for accessions and plots.

Download Data
Download phenotypic and genotypic data by trial, triat and location.



Manage Trials

Trials [Upload Trial] [Add Trial]

Information

Download Trial

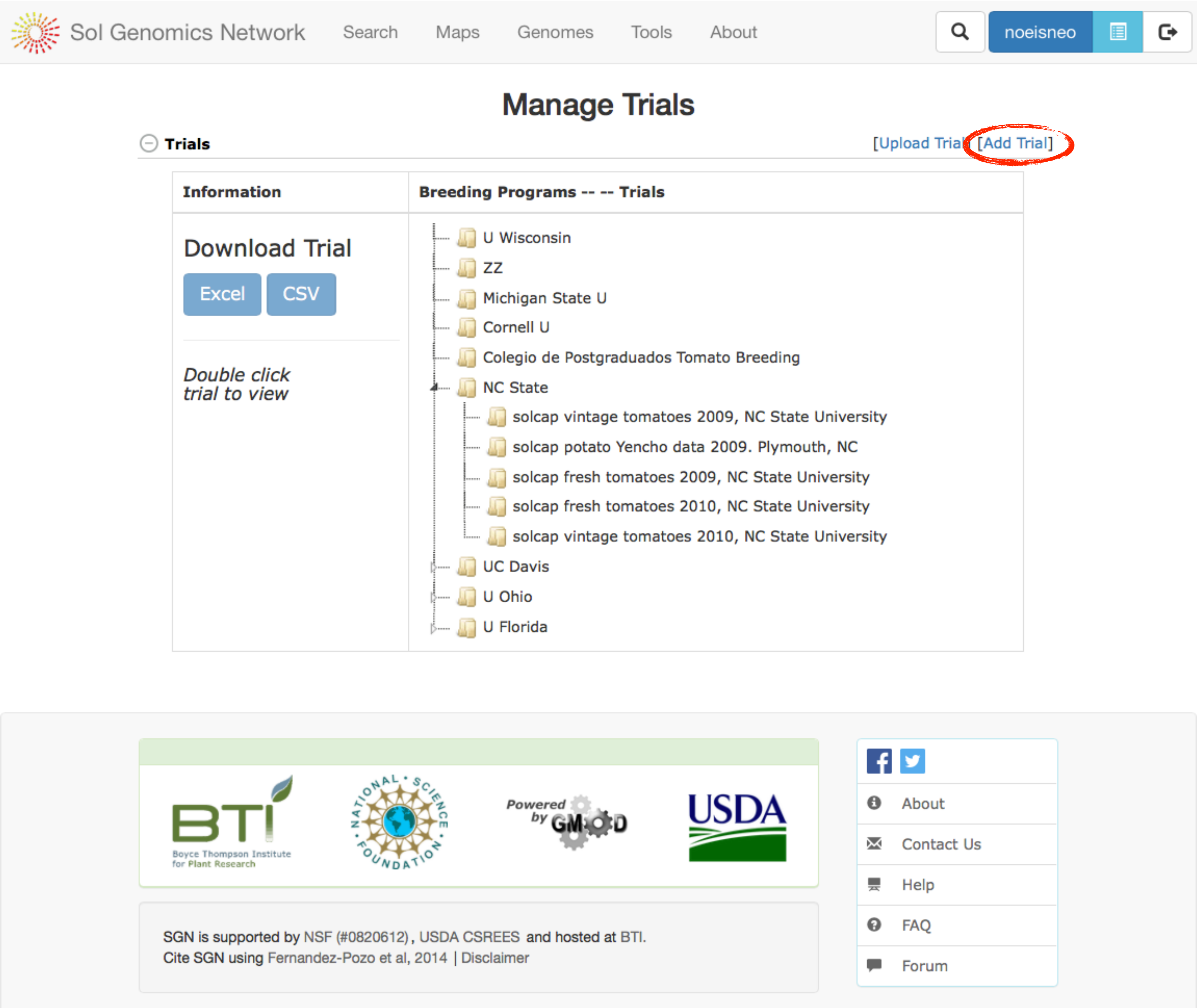
Double click trial to view

Breeding Programs -- -- Trials

- U Wisconsin
- ZZ
- Michigan State U
- Cornell U
- Colegio de Postgraduados Tomato Breeding
- NC State
  - solcap vintage tomatoes 2009, NC State University
  - solcap potato Yencho data 2009. Plymouth, NC
  - solcap fresh tomatoes 2009, NC State University
  - solcap fresh tomatoes 2010, NC State University
  - solcap vintage tomatoes 2010, NC State University
- UC Davis
- U Ohio
- U Florida

SGN is supported by NSF (#0820612), USDA CSREES and hosted at BTI.
Cite SGN using Fernandez-Pozo et al, 2014 | Disclaimer

Sol Genomics Network

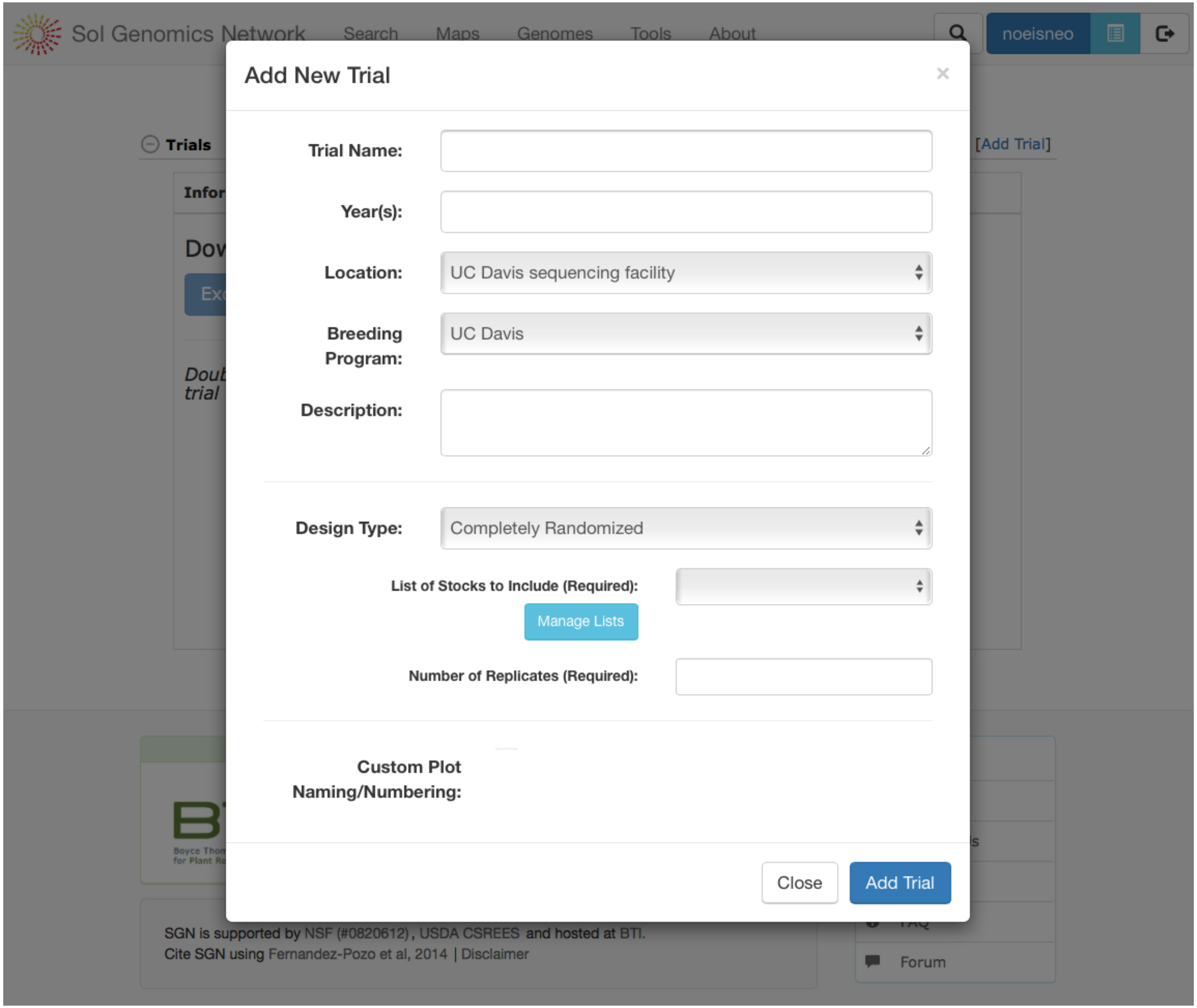


Manage Trials

Trials [Upload Trial] [Add Trial]

Information	Breeding Programs -- -- Trials
Download Trial Excel CSV *Double click trial to view*	U Wisconsin ZZ Michigan State U Cornell U Colegio de Postgraduados Tomato Breeding NC State solcap vintage tomatoes 2009, NC State University solcap potato Yencho data 2009. Plymouth, NC solcap fresh tomatoes 2009, NC State University solcap fresh tomatoes 2010, NC State University solcap vintage tomatoes 2010, NC State University UC Davis U Ohio U Florida

SGN is supported by NSF (#0820612), USDA CSREES and hosted at BTI.
Cite SGN using Fernandez-Pozo et al, 2014 | Disclaimer



Add New Trial

Trial Name:

Year(s):

Location: UC Davis sequencing facility

Breeding Program: UC Davis

Description:

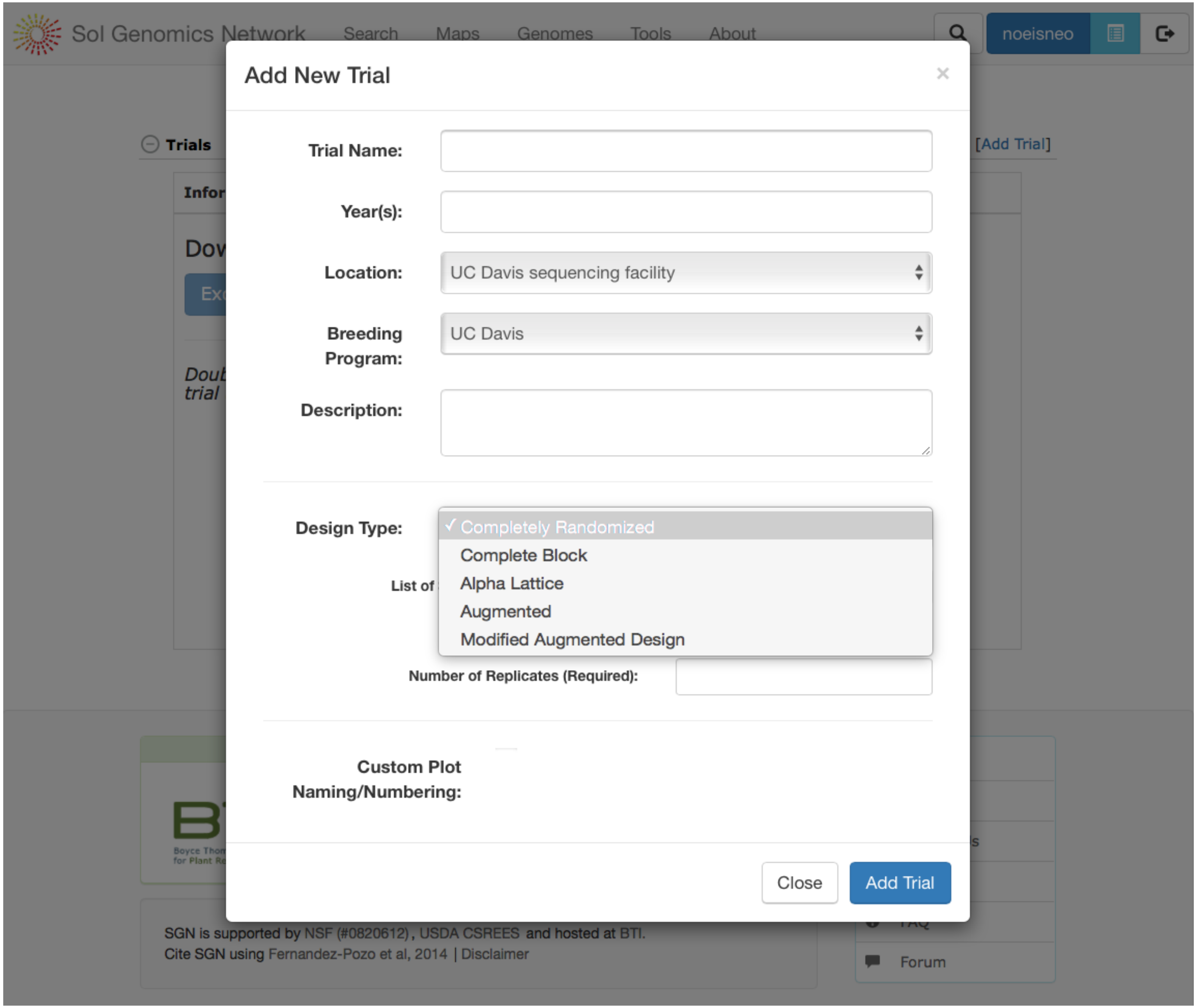
Design Type: Completely Randomized

List of Stocks to Include (Required):

Number of Replicates (Required):

Custom Plot Naming/Numbering:

SGN is supported by NSF (#0820612), USDA CSREES and hosted at BTI.
Cite SGN using Fernandez-Pozo et al, 2014 | Disclaimer



Add New Trial

Trial Name:

Year(s):

Location: UC Davis sequencing facility

Breeding Program: UC Davis

Description:

Design Type:

- ✓ Completely Randomized
- Complete Block
- Alpha Lattice
- Augmented
- Modified Augmented Design

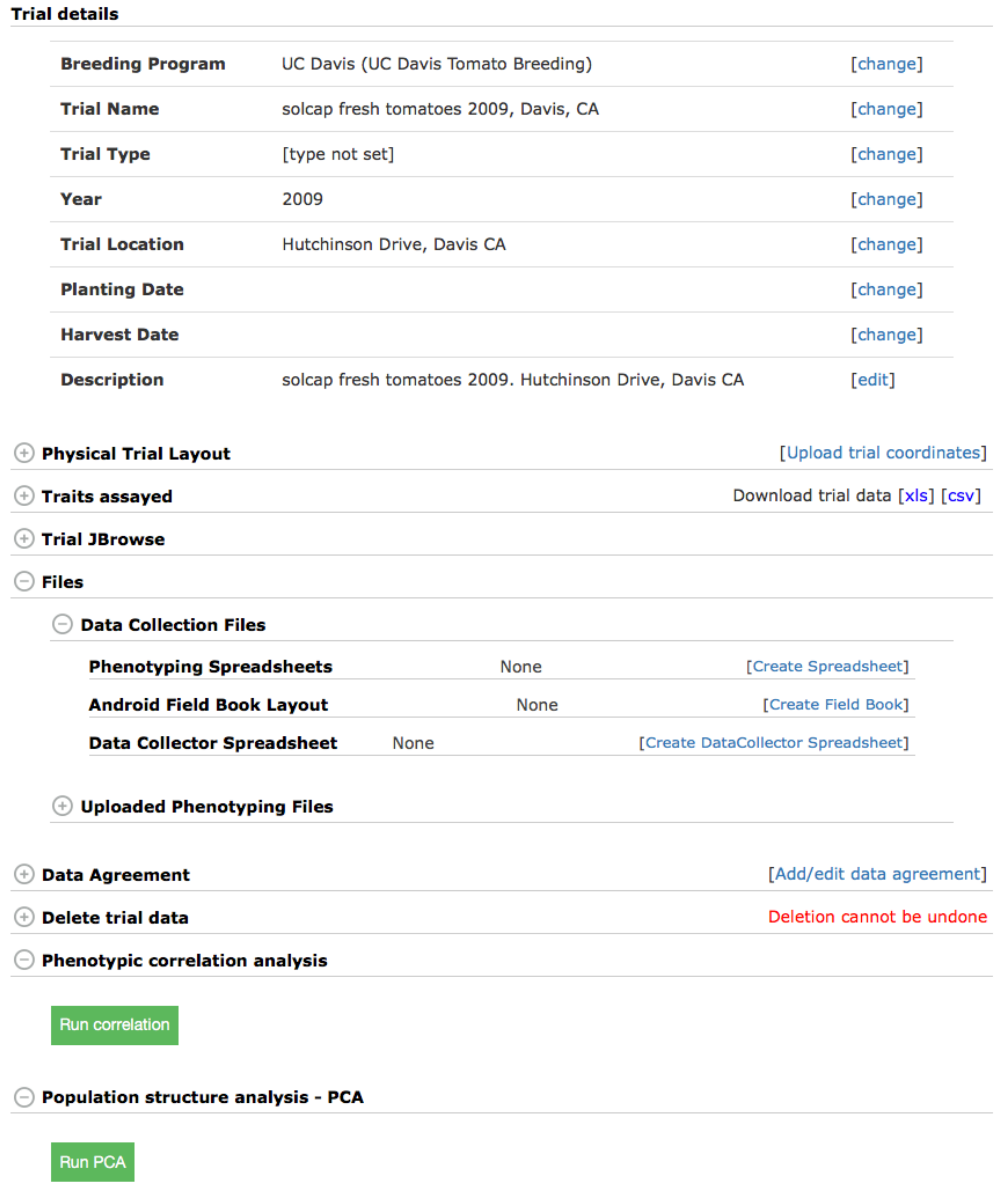
Number of Replicates (Required):

Custom Plot Naming/Numbering:

SGN is supported by NSF (#0820612), USDA CSREES and hosted at BTI.
Cite SGN using Fernandez-Pozo et al, 2014 | Disclaimer

Sol Genomics Network

Trial detail for solcap fresh tomatoes 2009, Davis, CA



Trial details

Breeding Program	UC Davis (UC Davis Tomato Breeding)	[change]
Trial Name	solcap fresh tomatoes 2009, Davis, CA	[change]
Trial Type	[type not set]	[change]
Year	2009	[change]
Trial Location	Hutchinson Drive, Davis CA	[change]
Planting Date		[change]
Harvest Date		[change]
Description	solcap fresh tomatoes 2009. Hutchinson Drive, Davis CA	[edit]

⊕ **Physical Trial Layout** [Upload trial coordinates]

⊕ **Traits assayed** Download trial data [xls] [csv]

⊕ **Trial JBrowse**

⊖ **Files**

⊖ **Data Collection Files**

Phenotyping Spreadsheets	None	[Create Spreadsheet]
Android Field Book Layout	None	[Create Field Book]
Data Collector Spreadsheet	None	[Create DataCollector Spreadsheet]

⊕ **Uploaded Phenotyping Files**

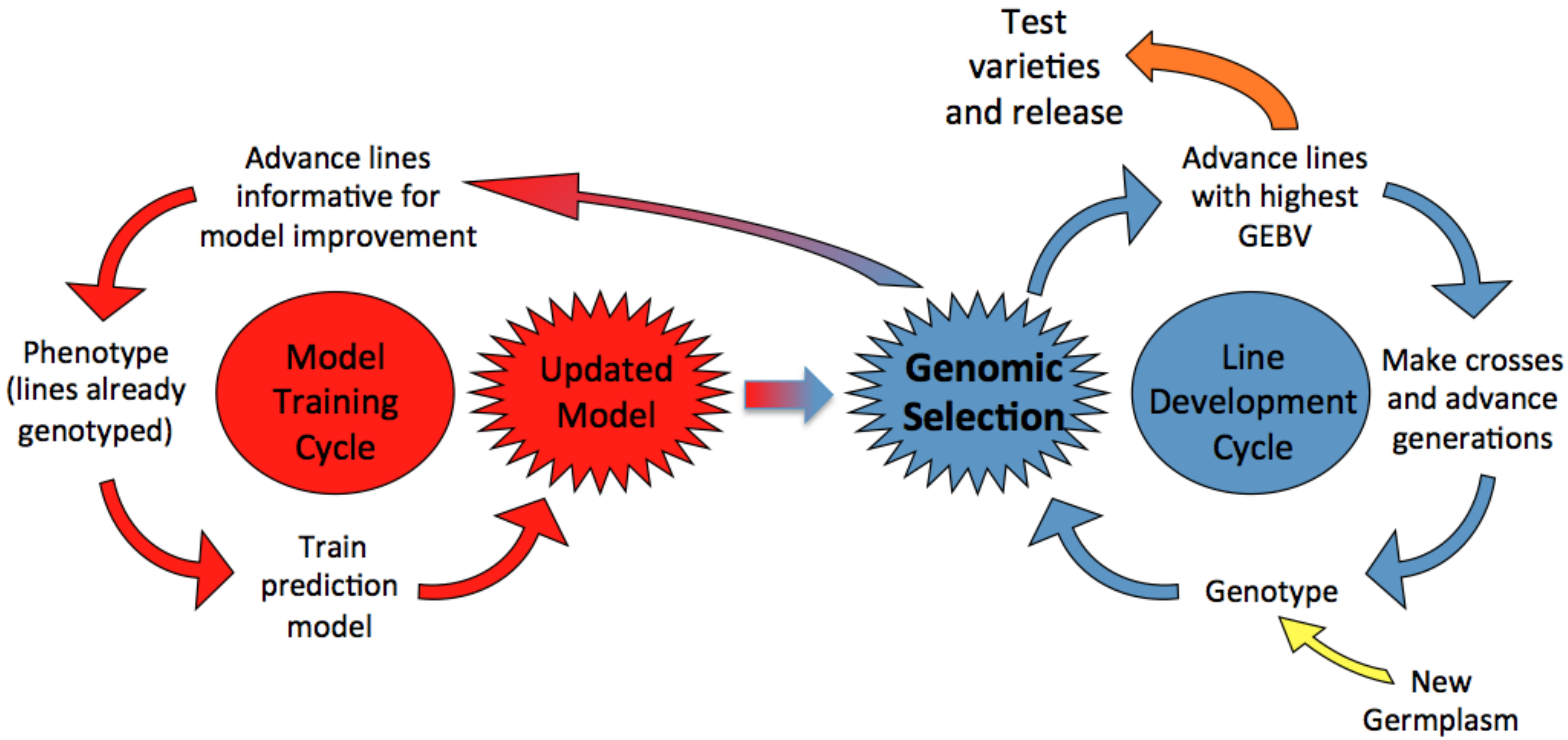
⊕ **Data Agreement** [Add/edit data agreement]

⊕ **Delete trial data** Deletion cannot be undone

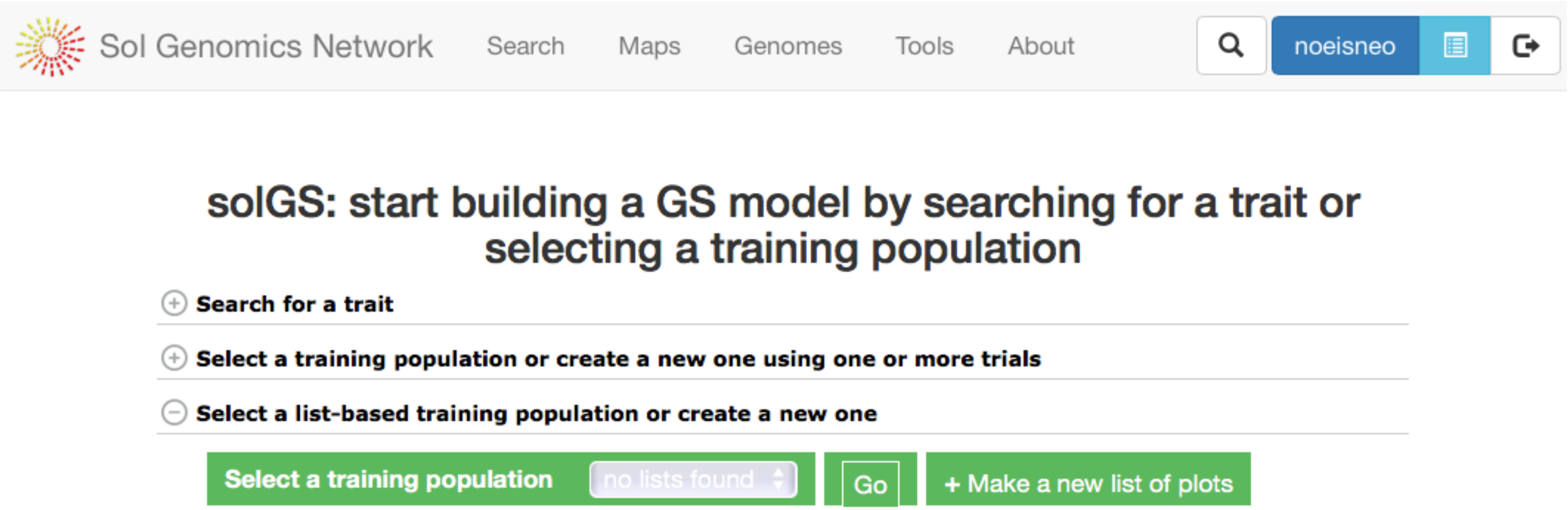
⊖ **Phenotypic correlation analysis**

⊖ **Population structure analysis - PCA**

Genomic Selection



Genomic Selection Tool

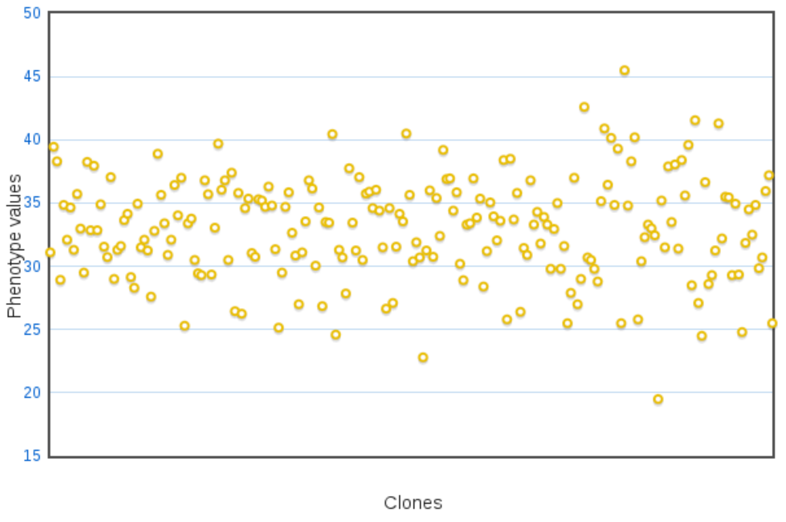


solGS: start building a GS model by searching for a trait or selecting a training population

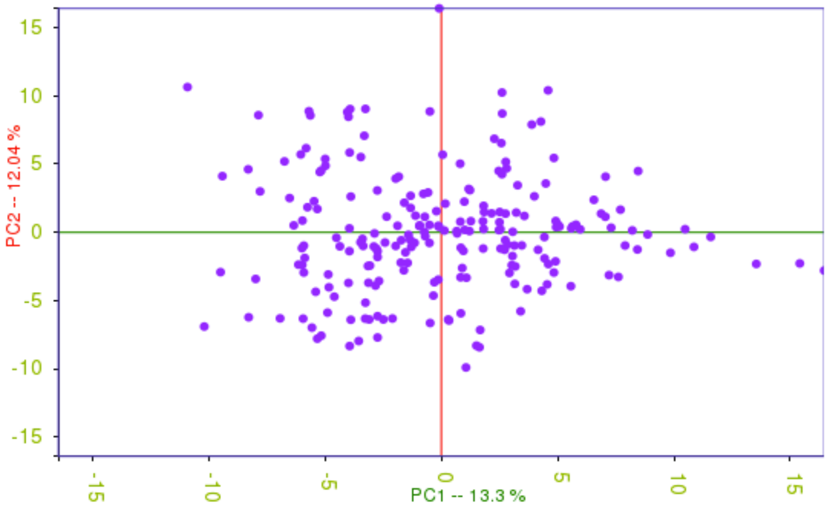
⊕ **Search for a trait**

⊕ **Select a training population or create a new one using one or more trials**

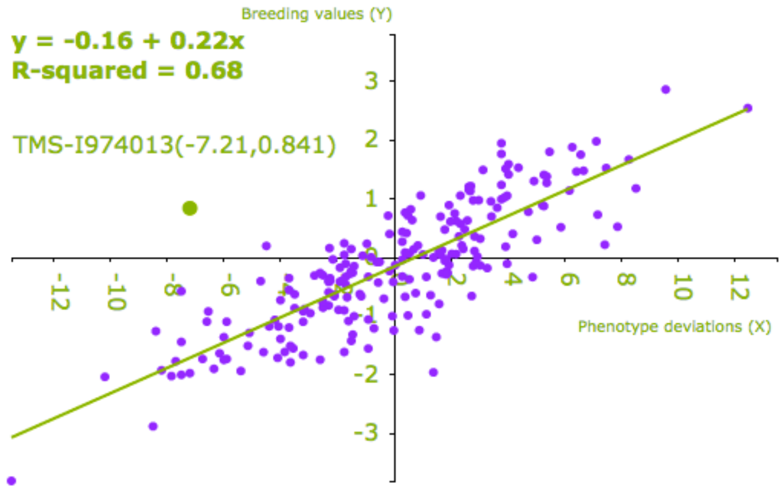
⊖ **Select a list-based training population or create a new one**



Phenotypic values

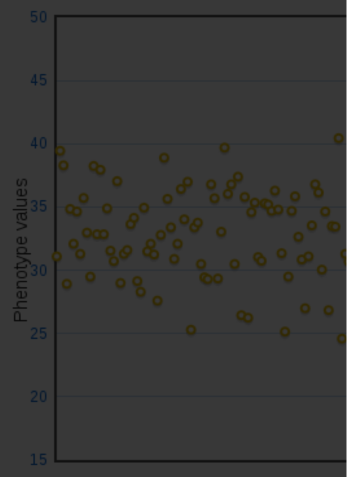


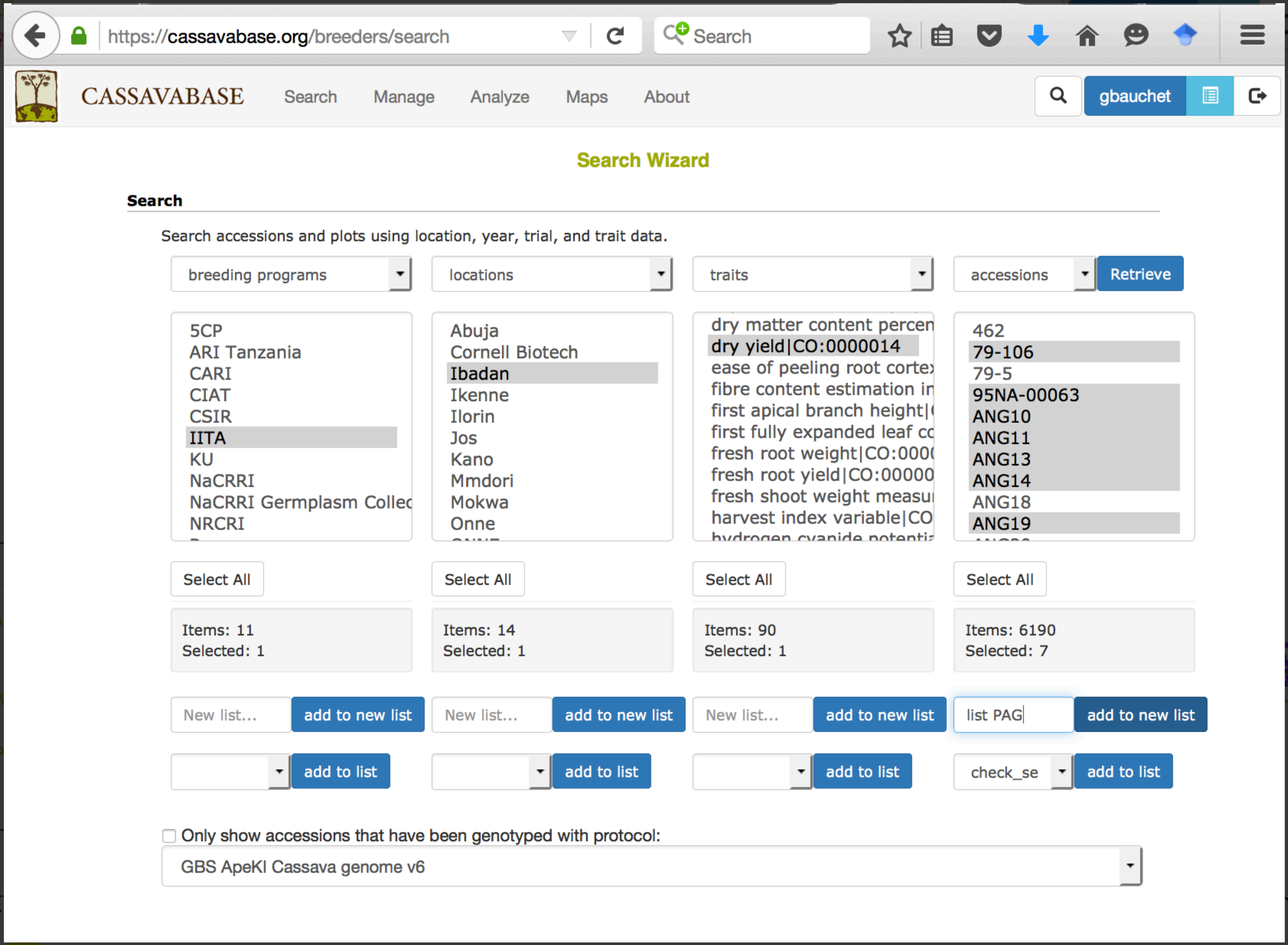
Population Structure



GEBV vs phenotypes

Genomic Selection Tool





Search Wizard

Search

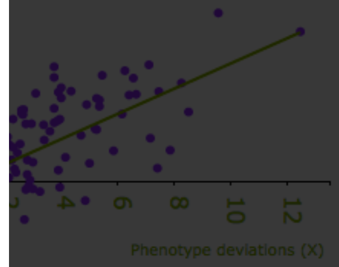
Search accessions and plots using location, year, trial, and trait data.

breeding programs	locations	traits	accessions
5CP ARI Tanzania CARI CIAT CSIR IITA KU NaCRRI NaCRRI Germplasm Collec NRCRI	Abuja Cornell Biotech Ibadan Ikenne Ilorin Jos Kano Mmdori Mokwa Onne	dry matter content percen dry yield|CO:0000014 ease of peeling root cortex fibre content estimation in first apical branch height| first fully expanded leaf co fresh root weight|CO:000 fresh root yield|CO:00000 fresh shoot weight measu harvest index variable|CO hydrogen cyanide potentia	462 79-106 79-5 95NA-00063 ANG10 ANG11 ANG13 ANG14 ANG18 ANG19
Select All	Select All	Select All	Select All
Items: 11 Selected: 1	Items: 14 Selected: 1	Items: 90 Selected: 1	Items: 6190 Selected: 7
New list... add to new list	New list... add to new list	New list... add to new list	list PAG add to new list
add to list	add to list	add to list	check_se add to list

Retrieve

☐ Only show accessions that have been genotyped with protocol:

GBS ApeKI Cassava genome v6



Phenot

notypes

Sol Genomics Network

GMOD Tools

GMOD

The **Generic Model Organism Database** project, a collection of open source software tools for managing, visualizing, storing, and disseminating genetic and genomic data.

CHADO

CMap

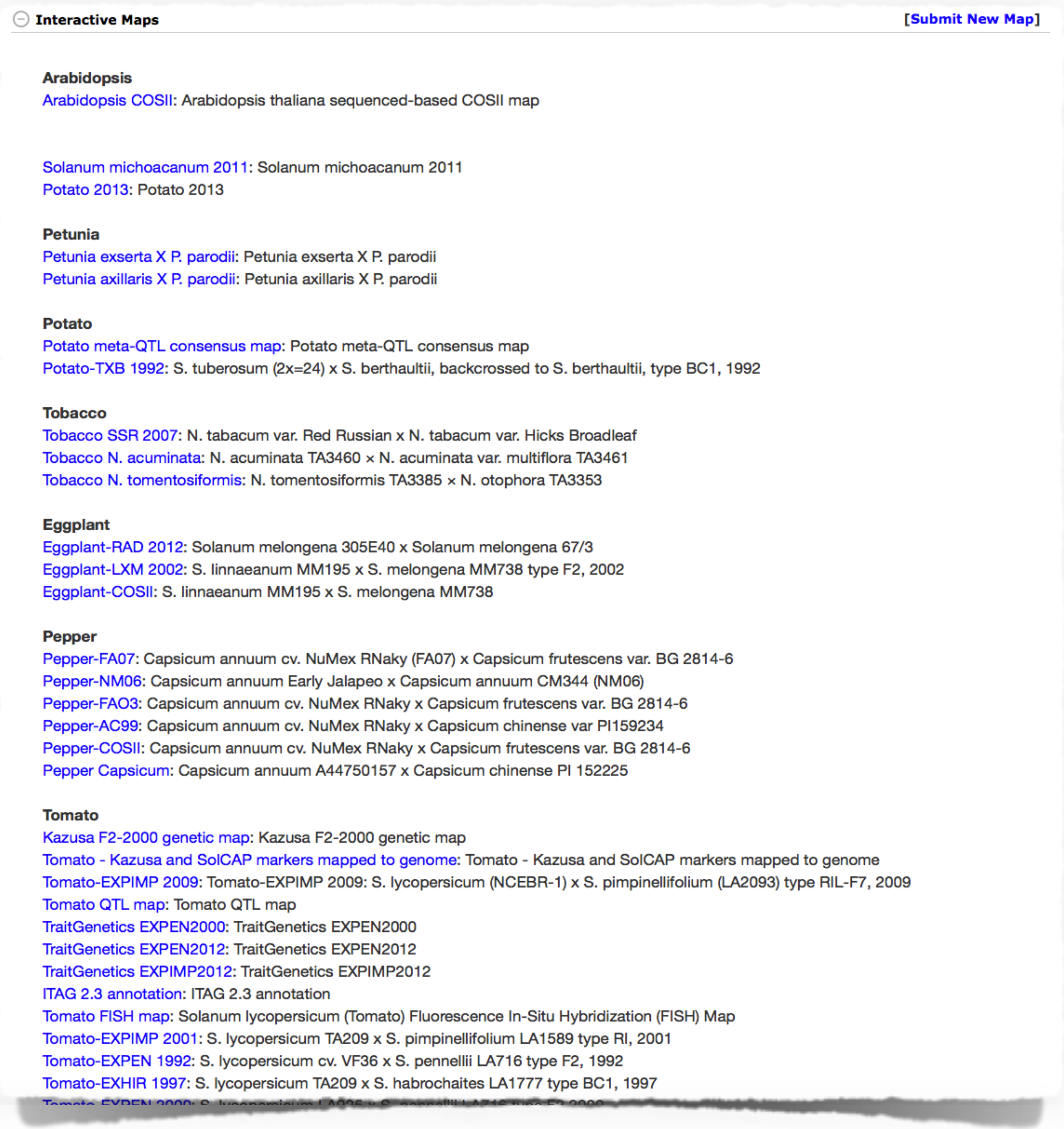
Pathway Tools

~~GBrowse~~

JBrowse

Web Apollo

Maps



Arabidopsis
Arabidopsis COSII: Arabidopsis thaliana sequenced-based COSII map

Solanum michoacanum 2011: Solanum michoacanum 2011
Potato 2013: Potato 2013

Petunia
Petunia exserta X P. parodii: Petunia exserta X P. parodii
Petunia axillaris X P. parodii: Petunia axillaris X P. parodii

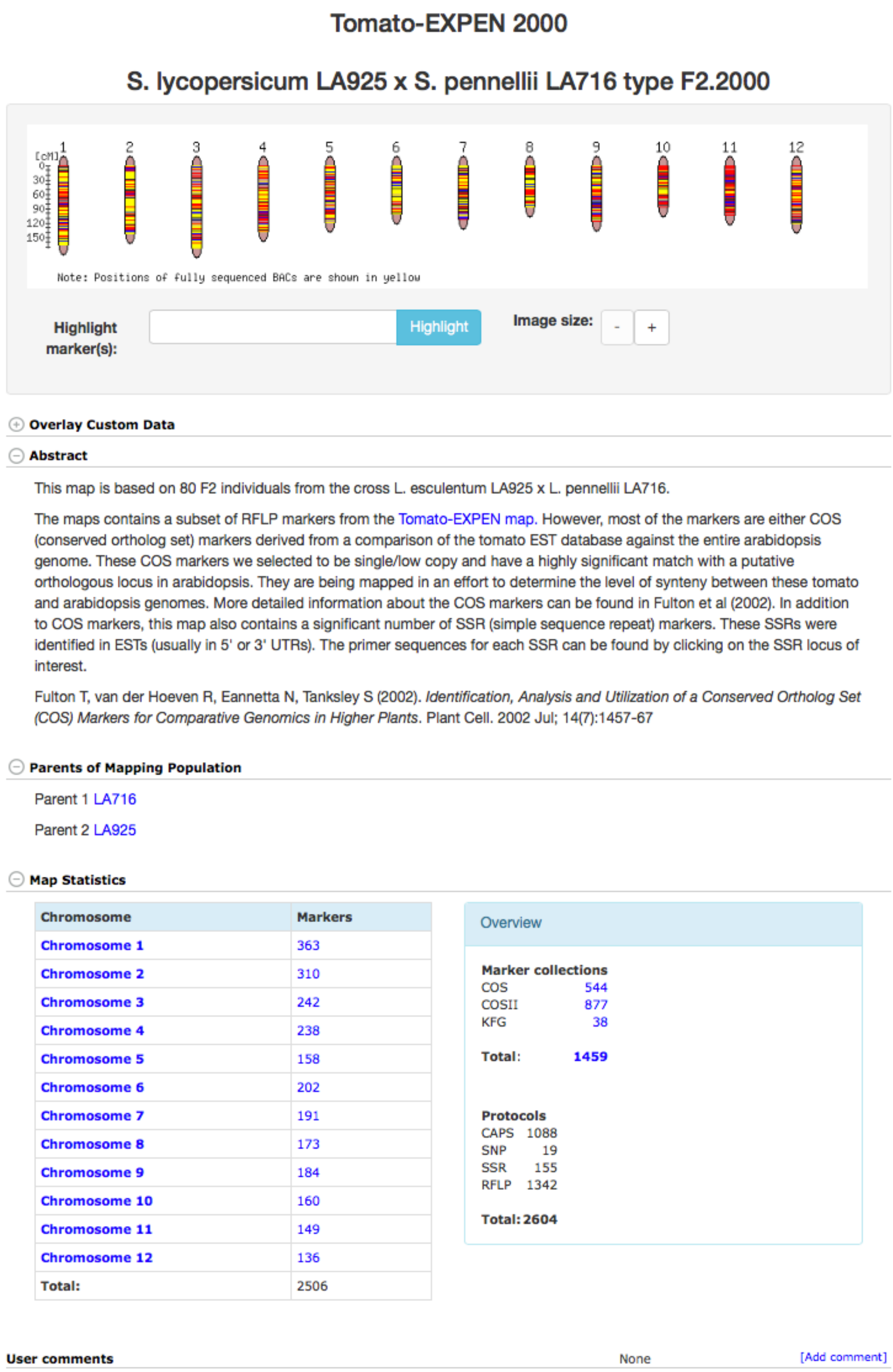
Potato
Potato meta-QTL consensus map: Potato meta-QTL consensus map
Potato-TXB 1992: S. tuberosum (2x=24) x S. berthaultii, backcrossed to S. berthaultii, type BC1, 1992

Tobacco
Tobacco SSR 2007: N. tabacum var. Red Russian x N. tabacum var. Hicks Broadleaf
Tobacco N. acuminata: N. acuminata TA3460 × N. acuminata var. multiflora TA3461
Tobacco N. tomentosiformis: N. tomentosiformis TA3385 × N. otophora TA3353

Eggplant
Eggplant-RAD 2012: Solanum melongena 305E40 x Solanum melongena 67/3
Eggplant-LXM 2002: S. linnaeanum MM195 x S. melongena MM738 type F2, 2002
Eggplant-COSII: S. linnaeanum MM195 x S. melongena MM738

Pepper
Pepper-FA07: Capsicum annuum cv. NuMex RNaky (FA07) x Capsicum frutescens var. BG 2814-6
Pepper-NM06: Capsicum annuum Early Jalapeo x Capsicum annuum CM344 (NM06)
Pepper-FAO3: Capsicum annuum cv. NuMex RNaky x Capsicum frutescens var. BG 2814-6
Pepper-AC99: Capsicum annuum cv. NuMex RNaky x Capsicum chinense var PI159234
Pepper-COSII: Capsicum annuum cv. NuMex RNaky x Capsicum frutescens var. BG 2814-6
Pepper Capsicum: Capsicum annuum A44750157 x Capsicum chinense PI 152225

Tomato
Kazusa F2-2000 genetic map: Kazusa F2-2000 genetic map
Tomato - Kazusa and SolCAP markers mapped to genome: Tomato - Kazusa and SolCAP markers mapped to genome
Tomato-EXPIMP 2009: Tomato-EXPIMP 2009: S. lycopersicum (NCEBR-1) x S. pimpinellifolium (LA2093) type RIL-F7, 2009
Tomato QTL map: Tomato QTL map
TraitGenetics EXPEN2000: TraitGenetics EXPEN2000
TraitGenetics EXPEN2012: TraitGenetics EXPEN2012
TraitGenetics EXPIMP2012: TraitGenetics EXPIMP2012
ITAG 2.3 annotation: ITAG 2.3 annotation
Tomato FISH map: Solanum lycopersicum (Tomato) Fluorescence In-Situ Hybridization (FISH) Map
Tomato-EXPIMP 2001: S. lycopersicum TA209 x S. pimpinellifolium LA1589 type RI, 2001
Tomato-EXPEN 1992: S. lycopersicum cv. VF36 x S. pennellii LA716 type F2, 1992
Tomato-EXHIR 1997: S. lycopersicum TA209 x S. habrochaites LA1777 type BC1, 1997
Tomato-EXPEN 2000: S. lycopersicum LA925 x S. pennellii LA716 type F2.2000



Tomato-EXPEN 2000

S. lycopersicum LA925 x S. pennellii LA716 type F2.2000

Note: Positions of fully sequenced BACs are shown in yellow

Abstract

This map is based on 80 F2 individuals from the cross L. esculentum LA925 x L. pennellii LA716.

The maps contains a subset of RFLP markers from the Tomato-EXPEN map. However, most of the markers are either COS (conserved ortholog set) markers derived from a comparison of the tomato EST database against the entire arabidopsis genome. These COS markers we selected to be single/low copy and have a highly significant match with a putative orthologous locus in arabidopsis. They are being mapped in an effort to determine the level of synteny between these tomato and arabidopsis genomes. More detailed information about the COS markers can be found in Fulton et al (2002). In addition to COS markers, this map also contains a significant number of SSR (simple sequence repeat) markers. These SSRs were identified in ESTs (usually in 5' or 3' UTRs). The primer sequences for each SSR can be found by clicking on the SSR locus of interest.

Fulton T, van der Hoeven R, Eannetta N, Tanksley S (2002). *Identification, Analysis and Utilization of a Conserved Ortholog Set (COS) Markers for Comparative Genomics in Higher Plants*. Plant Cell. 2002 Jul; 14(7):1457-67

Parents of Mapping Population

Parent 1 LA716

Parent 2 LA925

Map Statistics

Chromosome	Markers
Chromosome 1	363
Chromosome 2	310
Chromosome 3	242
Chromosome 4	238
Chromosome 5	158
Chromosome 6	202
Chromosome 7	191
Chromosome 8	173
Chromosome 9	184
Chromosome 10	160
Chromosome 11	149
Chromosome 12	136
Total:	2506

Overview

Marker collections

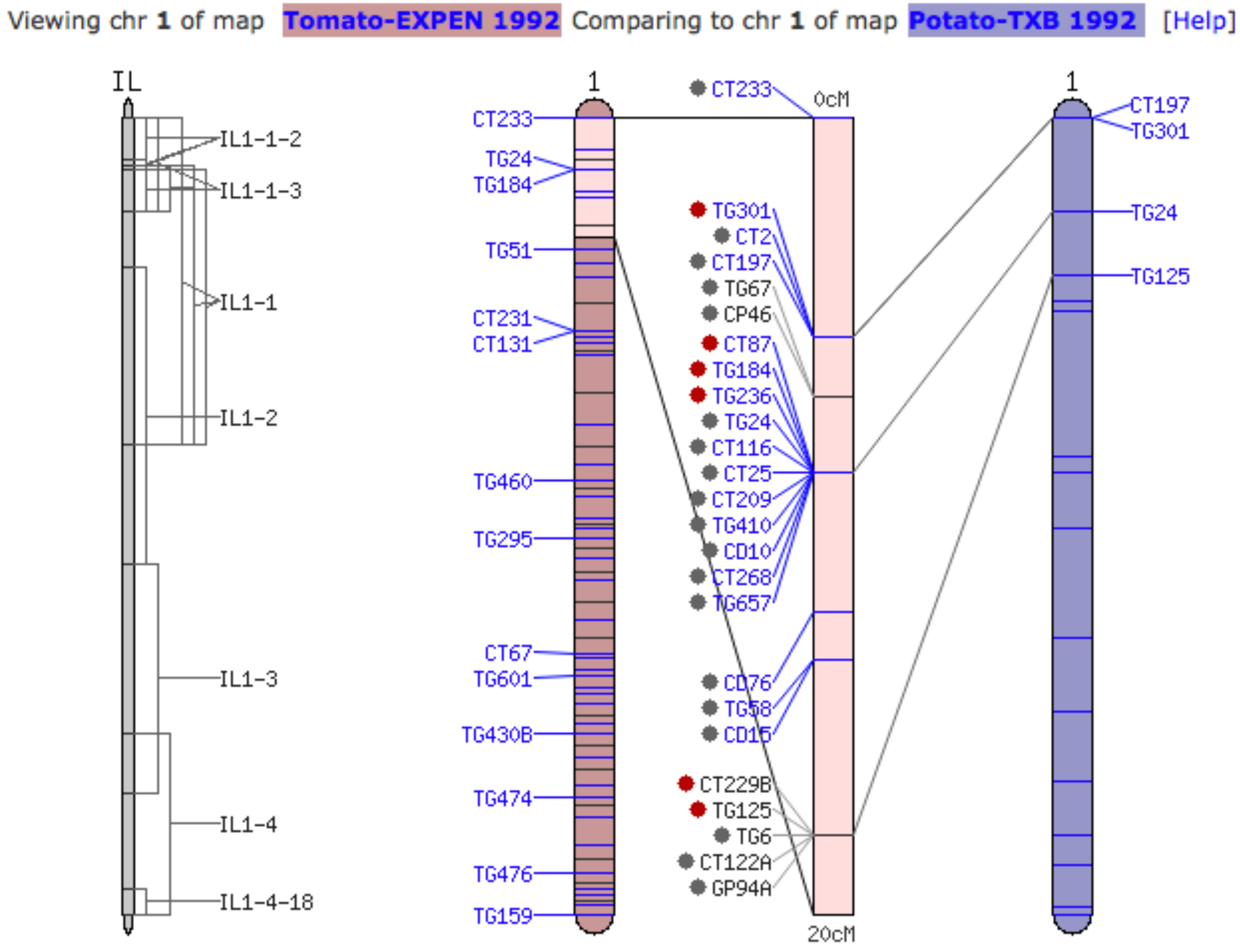
COS	544
COSII	877
KFG	38
Total:	**1459**

Protocols

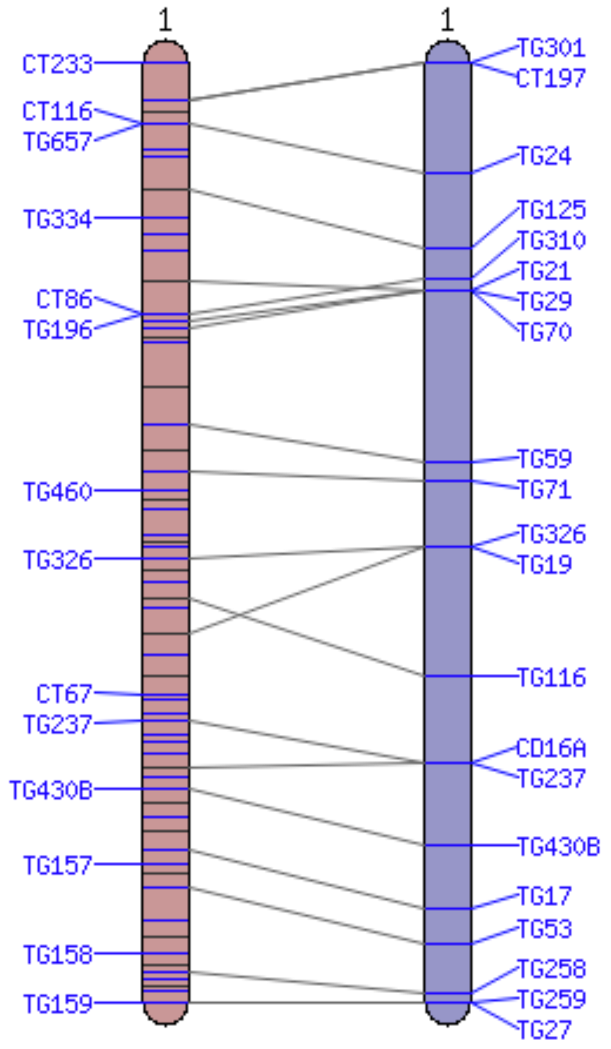
CAPS	1088
SNP	19
SSR	155
RFLP	1342
Total:	**2604**

User comments None [Add comment]

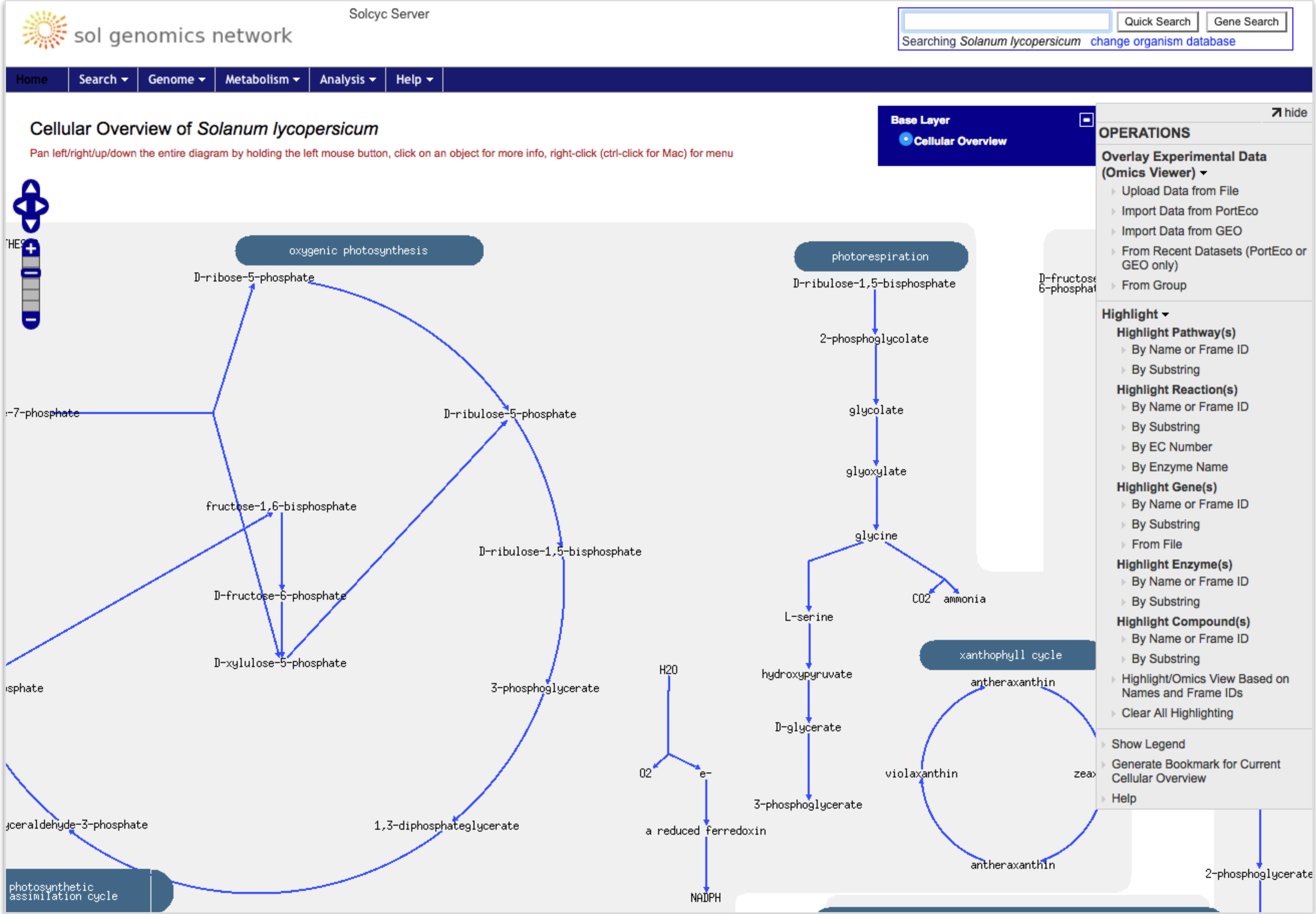
Maps



Viewing chr **1** of map **Tomato-EXPEN 1992** Comparing to chr **1** of map **Potato-TXB 1992** [Help]



Pathway Tools



Solcyc Server

Searching *Solanum lycopersicum* change organism database

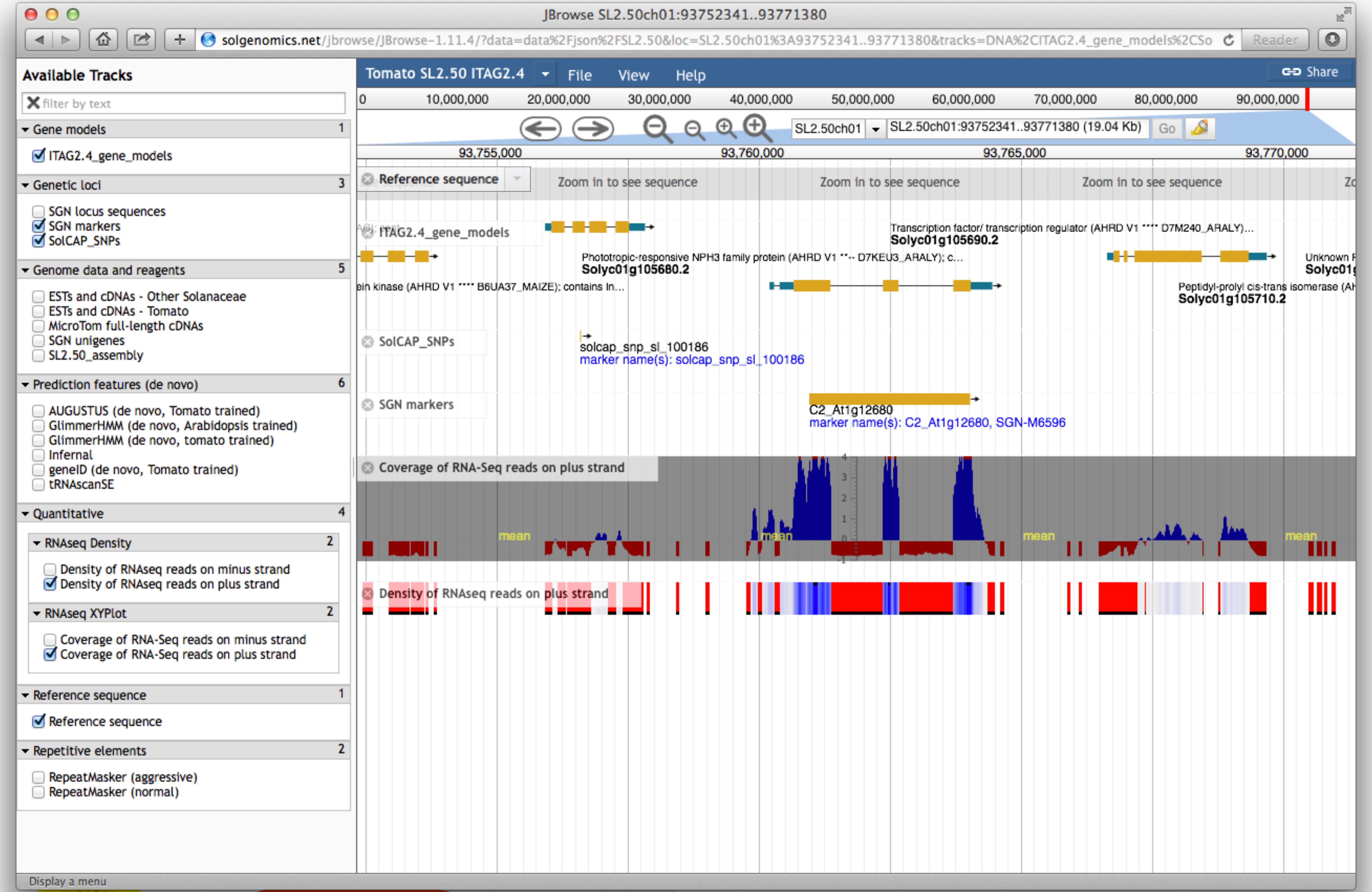
Cellular Overview of *Solanum lycopersicum*

Pan left/right/up/down the entire diagram by holding the left mouse button, click on an object for more info, right-click (ctrl-click for Mac) for menu

Sol Genomics Network

JBrowse

BTI



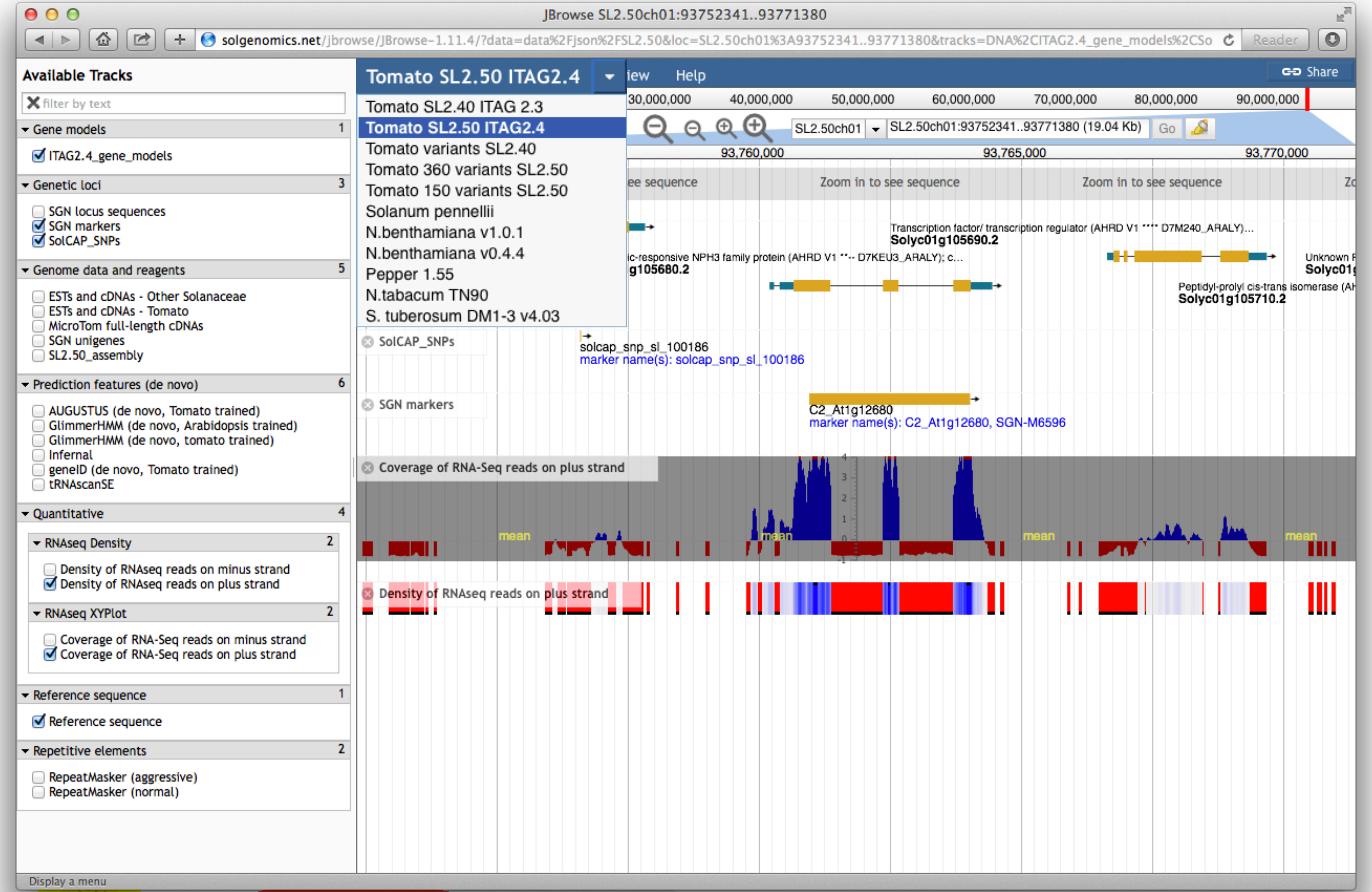
JBrowse SL2.50ch01:93752341..93771380

solgenomics.net/jbrowse/JBrowse-1.11.4/?data=data%2Fjson%2FSL2.50&loc=SL2.50ch01%3A93752341..93771380&tracks=DNA%2CITAG2.4_gene_models%2CSo

Available Tracks

- Gene models 1
  - ☑ ITAG2.4_gene_models
- Genetic loci 3
  - ☐ SGN locus sequences
  - ☑ SGN markers
  - ☑ SolCAP_SNPs
- Genome data and reagents 5
  - ☐ ESTs and cDNAs - Other Solanaceae
  - ☐ ESTs and cDNAs - Tomato
  - ☐ MicroTom full-length cDNAs
  - ☐ SGN unigenes
  - ☐ SL2.50_assembly
- Prediction features (de novo) 6
  - ☐ AUGUSTUS (de novo, Tomato trained)
  - ☐ GlimmerHMM (de novo, Arabidopsis trained)
  - ☐ GlimmerHMM (de novo, tomato trained)
  - ☐ Infernal
  - ☐ geneID (de novo, Tomato trained)
  - ☐ tRNAscanSE
- Quantitative 4
  - RNAseq Density 2
    - ☐ Density of RNAseq reads on minus strand
    - ☑ Density of RNAseq reads on plus strand
  - RNAseq XYPlot 2
    - ☐ Coverage of RNA-Seq reads on minus strand
    - ☑ Coverage of RNA-Seq reads on plus strand
- Reference sequence 1
  - ☑ Reference sequence
- Repetitive elements 2
  - ☐ RepeatMasker (aggressive)
  - ☐ RepeatMasker (normal)

SL2.50ch01 SL2.50ch01:93752341..93771380 (19.04 Kb)



JBrowse SL2.50ch01:93752341..93771380

solgenomics.net/jbrowse/JBrowse-1.11.4/?data=data%2Fjson%2FSL2.50&loc=SL2.50ch01%3A93752341..93771380&tracks=DNA%2CITAG2.4_gene_models%2CSo

Available Tracks

filter by text

Gene models 1

- ☑ ITAG2.4_gene_models

Genetic loci 3

- ☐ SGN locus sequences
- ☑ SGN markers
- ☑ SolCAP_SNPs

Genome data and reagents 5

- ☐ ESTs and cDNAs - Other Solanaceae
- ☐ ESTs and cDNAs - Tomato
- ☐ MicroTom full-length cDNAs
- ☐ SGN unigenes
- ☐ SL2.50_assembly

Prediction features (de novo) 6

- ☐ AUGUSTUS (de novo, Tomato trained)
- ☐ GlimmerHMM (de novo, Arabidopsis trained)
- ☐ GlimmerHMM (de novo, tomato trained)
- ☐ Infernal
- ☐ geneID (de novo, Tomato trained)
- ☐ tRNAscanSE

Quantitative 4

RNAseq Density 2

- ☐ Density of RNAseq reads on minus strand
- ☑ Density of RNAseq reads on plus strand

RNAseq XYPlot 2

- ☐ Coverage of RNA-Seq reads on minus strand
- ☑ Coverage of RNA-Seq reads on plus strand

Reference sequence 1

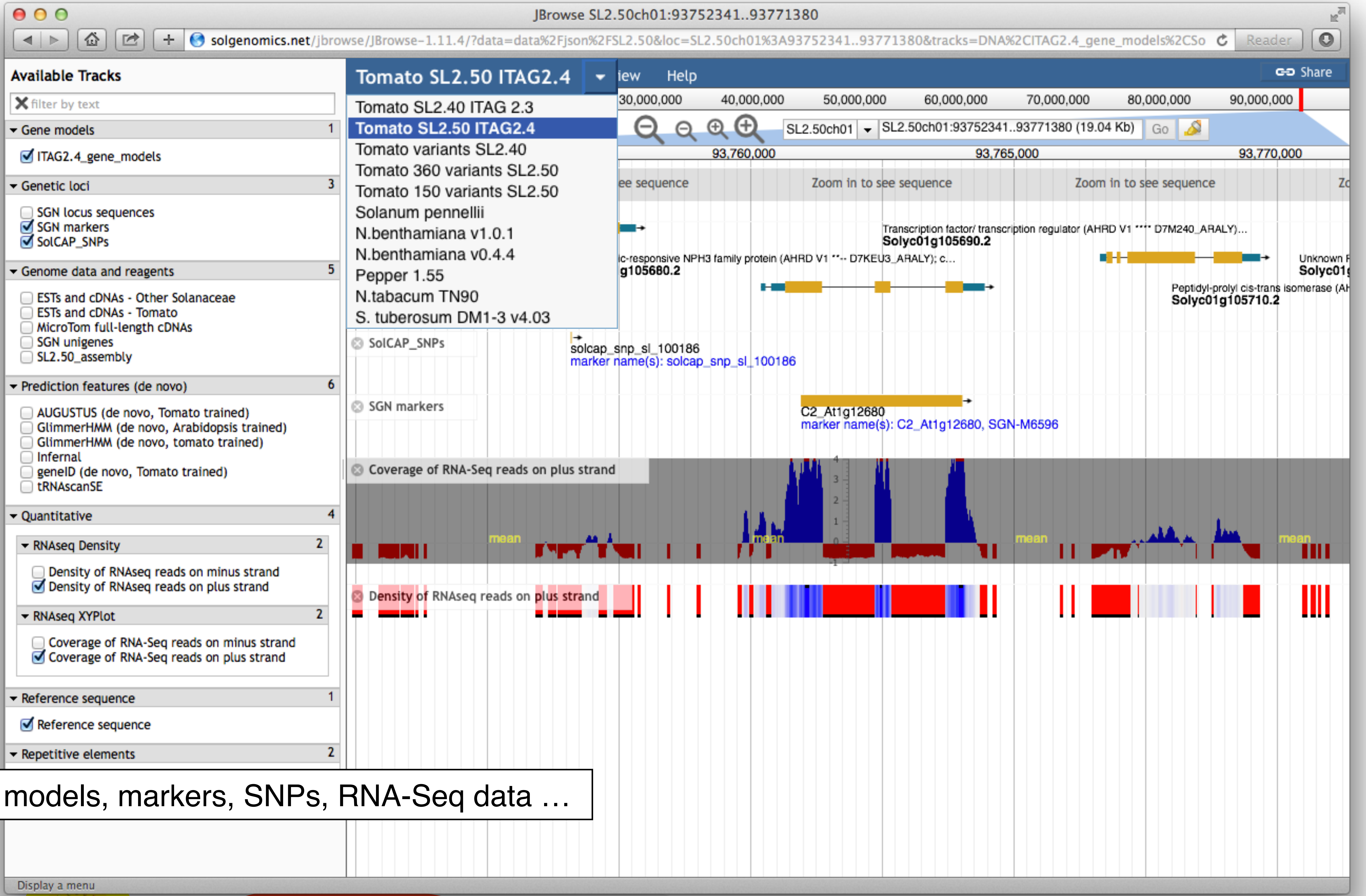
- ☑ Reference sequence

Repetitive elements 2

- ☐ RepeatMasker (aggressive)
- ☐ RepeatMasker (normal)

Display a menu

SL2.50ch01 SL2.50ch01:93752341..93771380 (19.04 Kb) Go



JBrowse SL2.50ch01:93752341..93771380

solgenomics.net/jbrowse/JBrowse-1.11.4/?data=data%2Fjson%2FSL2.50&loc=SL2.50ch01%3A93752341..93771380&tracks=DNA%2CITAG2.4_gene_models%2CSo

Available Tracks

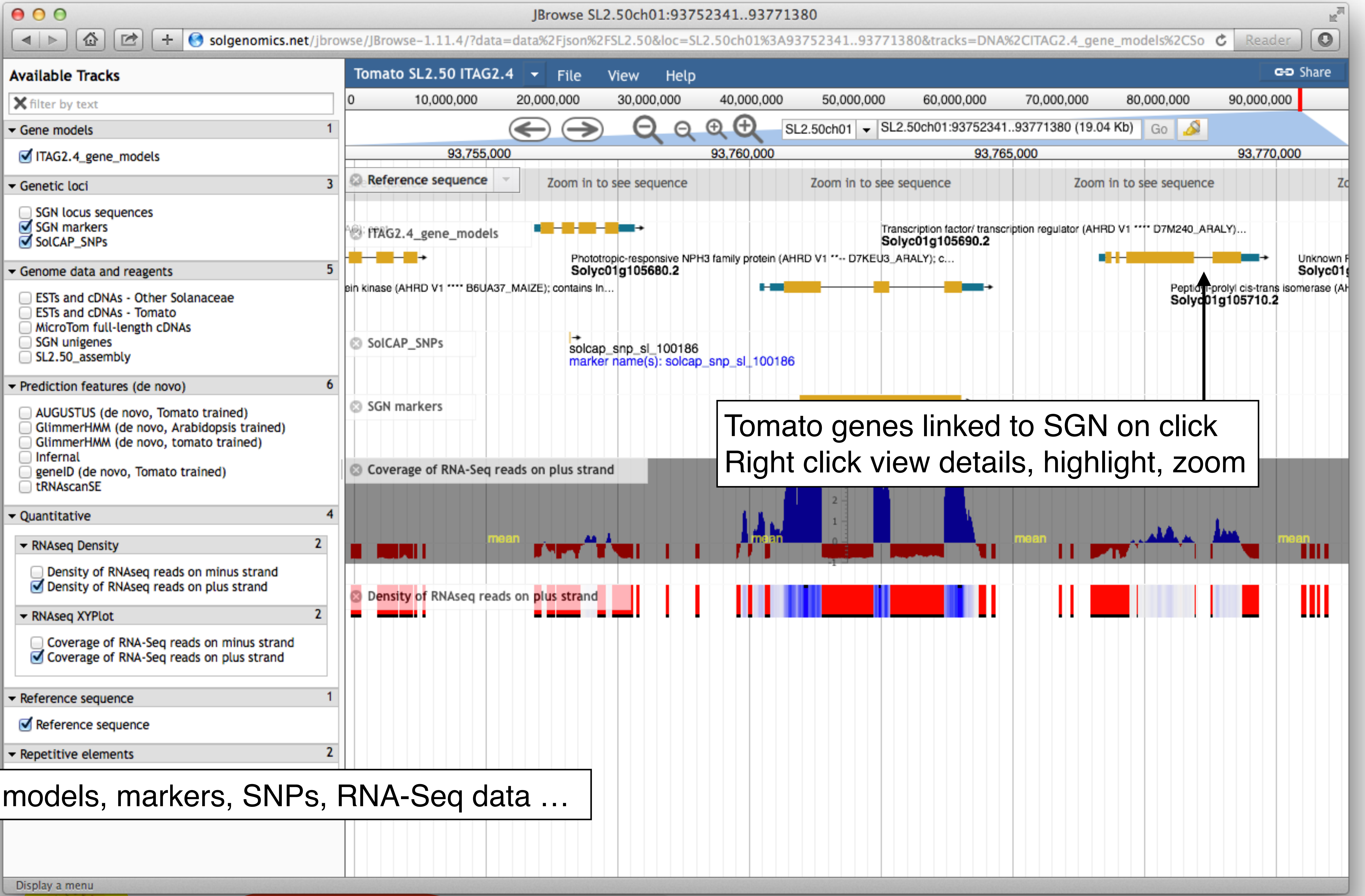
- Gene models 1
  - ☑ ITAG2.4_gene_models
- Genetic loci 3
  - ☐ SGN locus sequences
  - ☑ SGN markers
  - ☑ SolCAP_SNPs
- Genome data and reagents 5
  - ☐ ESTs and cDNAs - Other Solanaceae
  - ☐ ESTs and cDNAs - Tomato
  - ☐ MicroTom full-length cDNAs
  - ☐ SGN unigenes
  - ☐ SL2.50_assembly
- Prediction features (de novo) 6
  - ☐ AUGUSTUS (de novo, Tomato trained)
  - ☐ GlimmerHMM (de novo, Arabidopsis trained)
  - ☐ GlimmerHMM (de novo, tomato trained)
  - ☐ Infernal
  - ☐ geneID (de novo, Tomato trained)
  - ☐ tRNAscanSE
- Quantitative 4
  - RNAseq Density 2
    - ☐ Density of RNAseq reads on minus strand
    - ☑ Density of RNAseq reads on plus strand
  - RNAseq XYPlot 2
    - ☐ Coverage of RNA-Seq reads on minus strand
    - ☑ Coverage of RNA-Seq reads on plus strand
- Reference sequence 1
  - ☑ Reference sequence
- Repetitive elements 2

Tomato SL2.50 ITAG2.4

- Tomato SL2.40 ITAG 2.3
- Tomato SL2.50 ITAG2.4
- Tomato variants SL2.40
- Tomato 360 variants SL2.50
- Tomato 150 variants SL2.50
- Solanum pennellii
- N.benthamiana v1.0.1
- N.benthamiana v0.4.4
- Pepper 1.55
- N.tabacum TN90
- S. tuberosum DM1-3 v4.03

SL2.50ch01:93752341..93771380 (19.04 Kb)

gene models, markers, SNPs, RNA-Seq data …



Available Tracks

filter by text

Gene models 1

☑ ITAG2.4_gene_models

Genetic loci 3

☐ SGN locus sequences
☑ SGN markers
☑ SolCAP_SNPs

Genome data and reagents 5

☐ ESTs and cDNAs - Other Solanaceae
☐ ESTs and cDNAs - Tomato
☐ MicroTom full-length cDNAs
☐ SGN unigenes
☐ SL2.50_assembly

Prediction features (de novo) 6

☐ AUGUSTUS (de novo, Tomato trained)
☐ GlimmerHMM (de novo, Arabidopsis trained)
☐ GlimmerHMM (de novo, tomato trained)
☐ Infernal
☐ geneID (de novo, Tomato trained)
☐ tRNAscanSE

Quantitative 4

RNAseq Density 2

☐ Density of RNAseq reads on minus strand
☑ Density of RNAseq reads on plus strand

RNAseq XYPlot 2

☐ Coverage of RNA-Seq reads on minus strand
☑ Coverage of RNA-Seq reads on plus strand

Reference sequence 1

☑ Reference sequence

Repetitive elements 2

Transcription factor/ transcription regulator (AHRD V1 **** D7M240_ARALY)...
Solyc01g105690.2

Phototropic-responsive NPH3 family protein (AHRD V1 **-- D7KEU3_ARALY); c...
Solyc01g105680.2

ein kinase (AHRD V1 **** B6UA37_MAIZE); contains In...

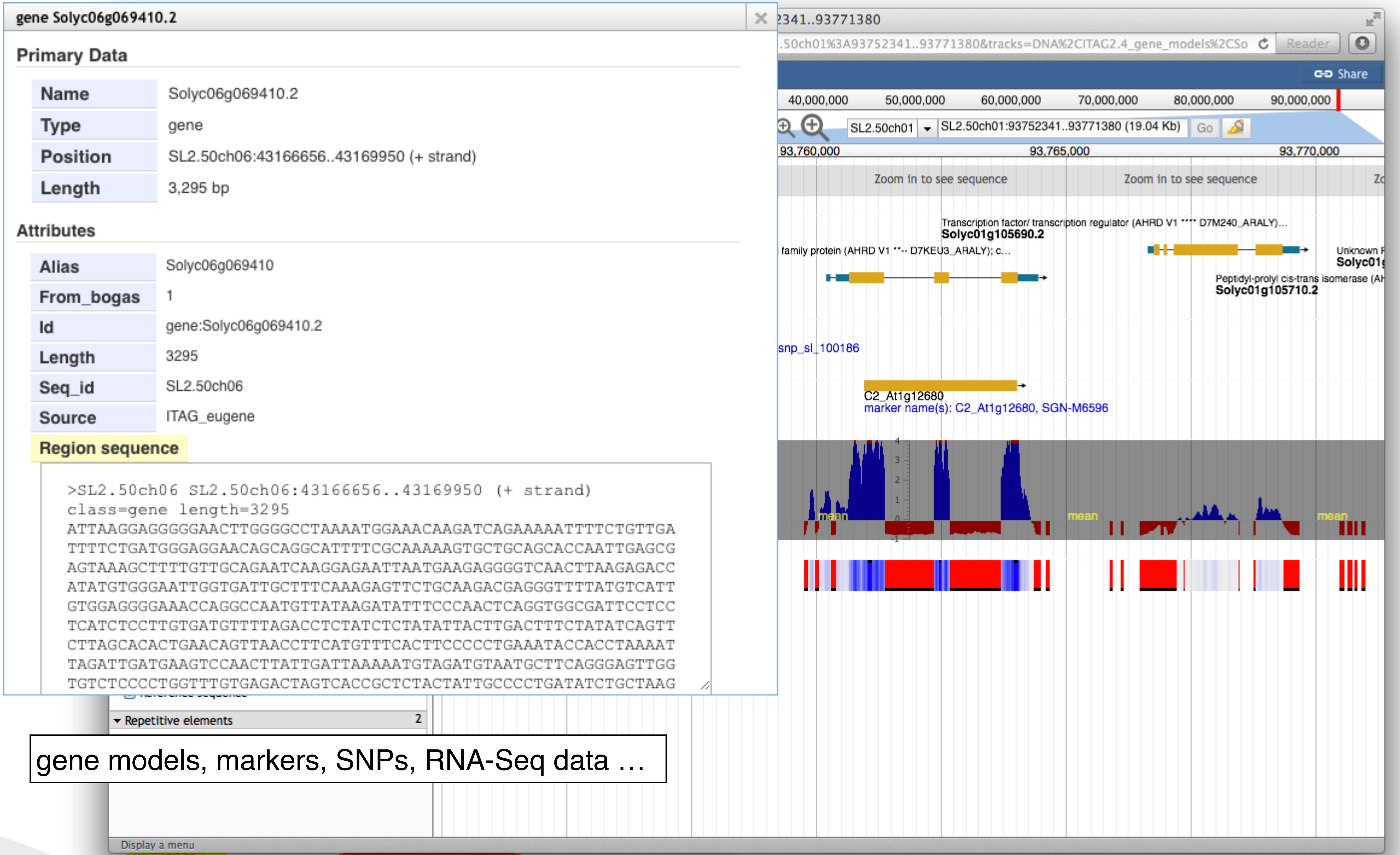
Peptidyl-prolyl cis-trans isomerase (AH
Solyc01g105710.2

Unknown F
Solyc01g

solcap_snp_sl_100186
marker name(s): solcap_snp_sl_100186

Tomato genes linked to SGN on click
Right click view details, highlight, zoom

gene models, markers, SNPs, RNA-Seq data …



gene Solyc06g069410.2

Primary Data

Name	Solyc06g069410.2
Type	gene
Position	SL2.50ch06:43166656..43169950 (+ strand)
Length	3,295 bp

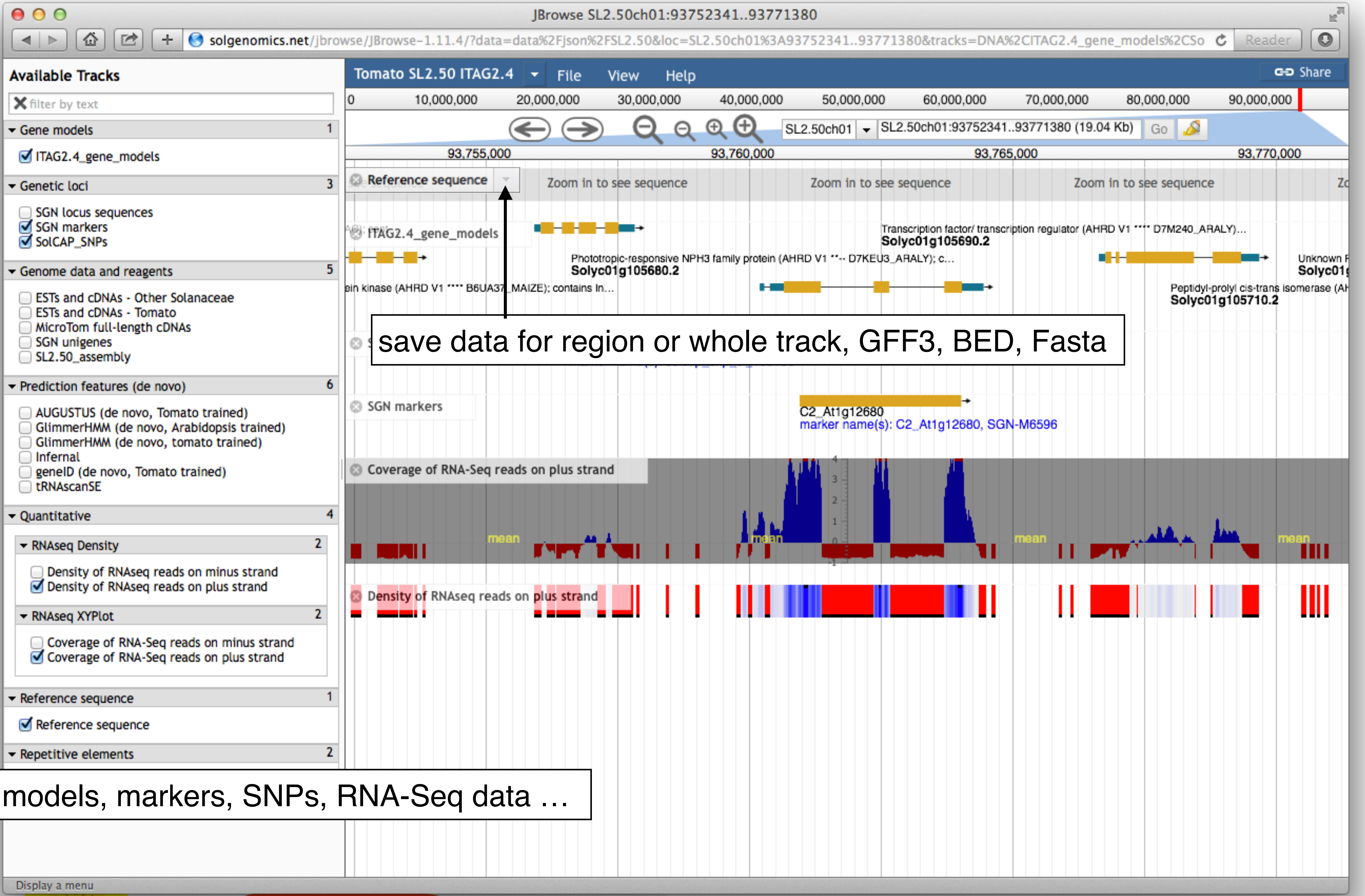
Attributes

Alias	Solyc06g069410
From_bogas	1
Id	gene:Solyc06g069410.2
Length	3295
Seq_id	SL2.50ch06
Source	ITAG_eugene

Region sequence

```
>SL2.50ch06 SL2.50ch06:43166656..43169950 (+ strand)
class=gene length=3295
ATTAAGGAGGGGGAACTTGGGGCCTAAAATGGAAACAAGATCAGAAAAATTTTCTGTTGA
TTTTCTGATGGGAGGAACAGCAGGCATTTTCGCAAAAAGTGCTGCAGCACCAATTGAGCG
AGTAAAGCTTTTGTTGCAGAATCAAGGAGAATTAATGAAGAGGGGTCAACTTAAGAGACC
ATATGTGGGAATTGGTGATTGCTTTCAAAGAGTTCTGCAAGACGAGGGTTTTATGTCATT
GTGGAGGGGAAACCAGGCCAATGTTATAAGATATTTCCCAACTCAGGTGGCGATTCCTCC
TCATCTCCTTGTGATGTTTTAGACCTCTATCTCTATATTACTTGACTTTCTATATCAGTT
CTTAGCACACTGAACAGTTAACCTTCATGTTTCACTTCCCCCTGAAATACCACCTAAAAT
TAGATTGATGAAGTCCAACTTATTGATTAAAAATGTAGATGTAATGCTTCAGGGAGTTGG
TGTCTCCCCTGGTTTGTGAGACTAGTCACCGCTCTACTATTGCCCCTGATATCTGCTAAG
```

gene models, markers, SNPs, RNA-Seq data …



Available Tracks

filter by text

Gene models 1
- ☑ ITAG2.4_gene_models

Genetic loci 3
- ☐ SGN locus sequences
- ☑ SGN markers
- ☑ SolCAP_SNPs

Genome data and reagents 5
- ☐ ESTs and cDNAs - Other Solanaceae
- ☐ ESTs and cDNAs - Tomato
- ☐ MicroTom full-length cDNAs
- ☐ SGN unigenes
- ☐ SL2.50_assembly

Prediction features (de novo) 6
- ☐ AUGUSTUS (de novo, Tomato trained)
- ☐ GlimmerHMM (de novo, Arabidopsis trained)
- ☐ GlimmerHMM (de novo, tomato trained)
- ☐ Infernal
- ☐ geneID (de novo, Tomato trained)
- ☐ tRNAscanSE

Quantitative 4
- RNAseq Density 2
  - ☐ Density of RNAseq reads on minus strand
  - ☑ Density of RNAseq reads on plus strand
- RNAseq XYPlot 2
  - ☐ Coverage of RNA-Seq reads on minus strand
  - ☑ Coverage of RNA-Seq reads on plus strand

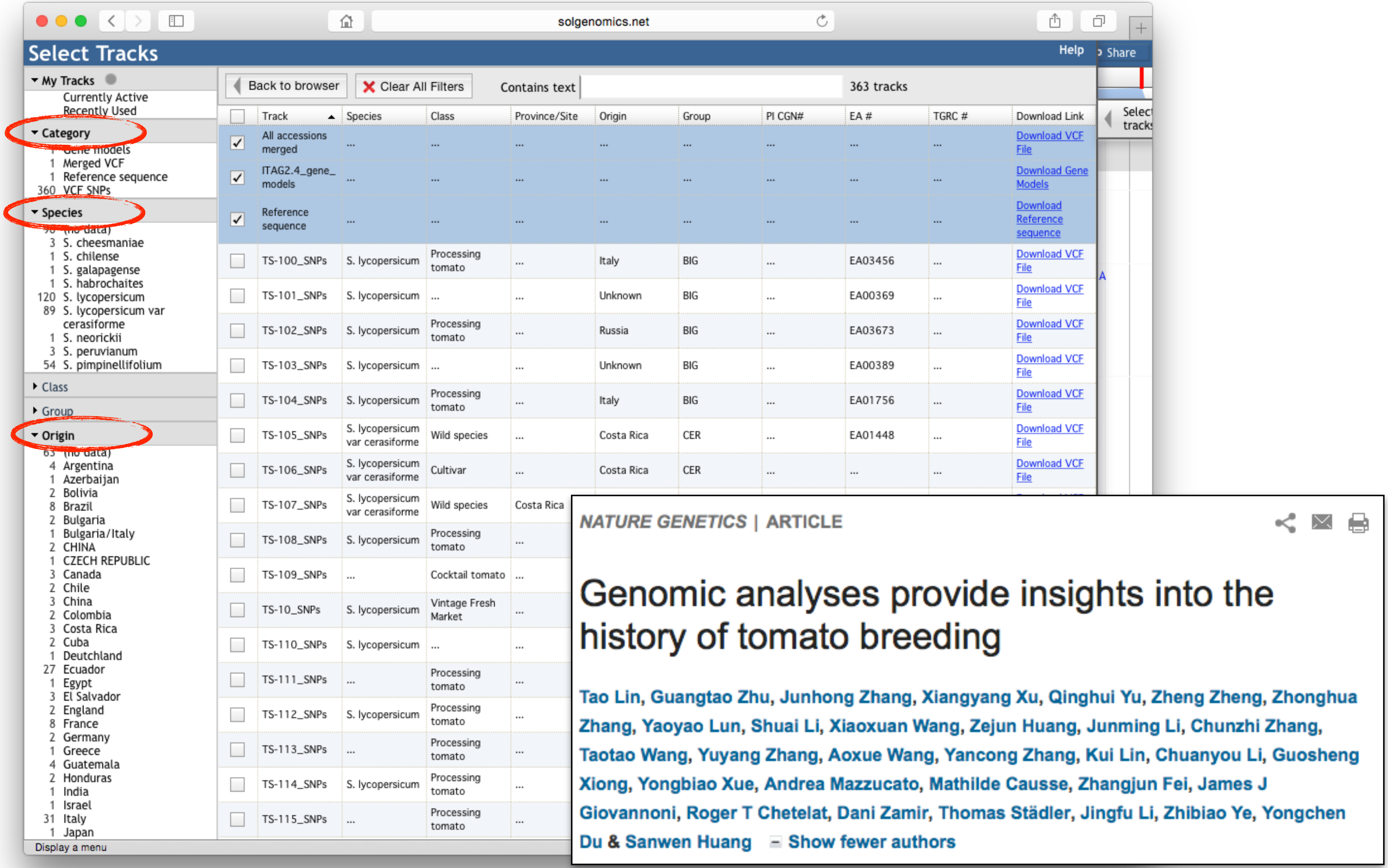
Reference sequence 1
- ☑ Reference sequence

Repetitive elements 2

save data for region or whole track, GFF3, BED, Fasta

gene models, markers, SNPs, RNA-Seq data …

360 Tomato variants



Select Tracks

My Tracks
Currently Active
Recently Used

Category
1 Gene models
1 Merged VCF
1 Reference sequence
360 VCF SNPs

Species
90 (no data)
3 S. cheesmaniae
1 S. chilense
1 S. galapagense
1 S. habrochaites
120 S. lycopersicum
89 S. lycopersicum var cerasiforme
1 S. neorickii
3 S. peruvianum
54 S. pimpinellifolium

Class

Group

Origin
63 (no data)
4 Argentina
1 Azerbaijan
2 Bolivia
8 Brazil
2 Bulgaria
1 Bulgaria/Italy
2 CHINA
1 CZECH REPUBLIC
3 Canada
2 Chile
3 China
2 Colombia
3 Costa Rica
2 Cuba
1 Deutchland
27 Ecuador
1 Egypt
3 El Salvador
2 England
8 France
2 Germany
1 Greece
4 Guatemala
2 Honduras
1 India
1 Israel
31 Italy
1 Japan

Back to browser | Clear All Filters | Contains text | 363 tracks

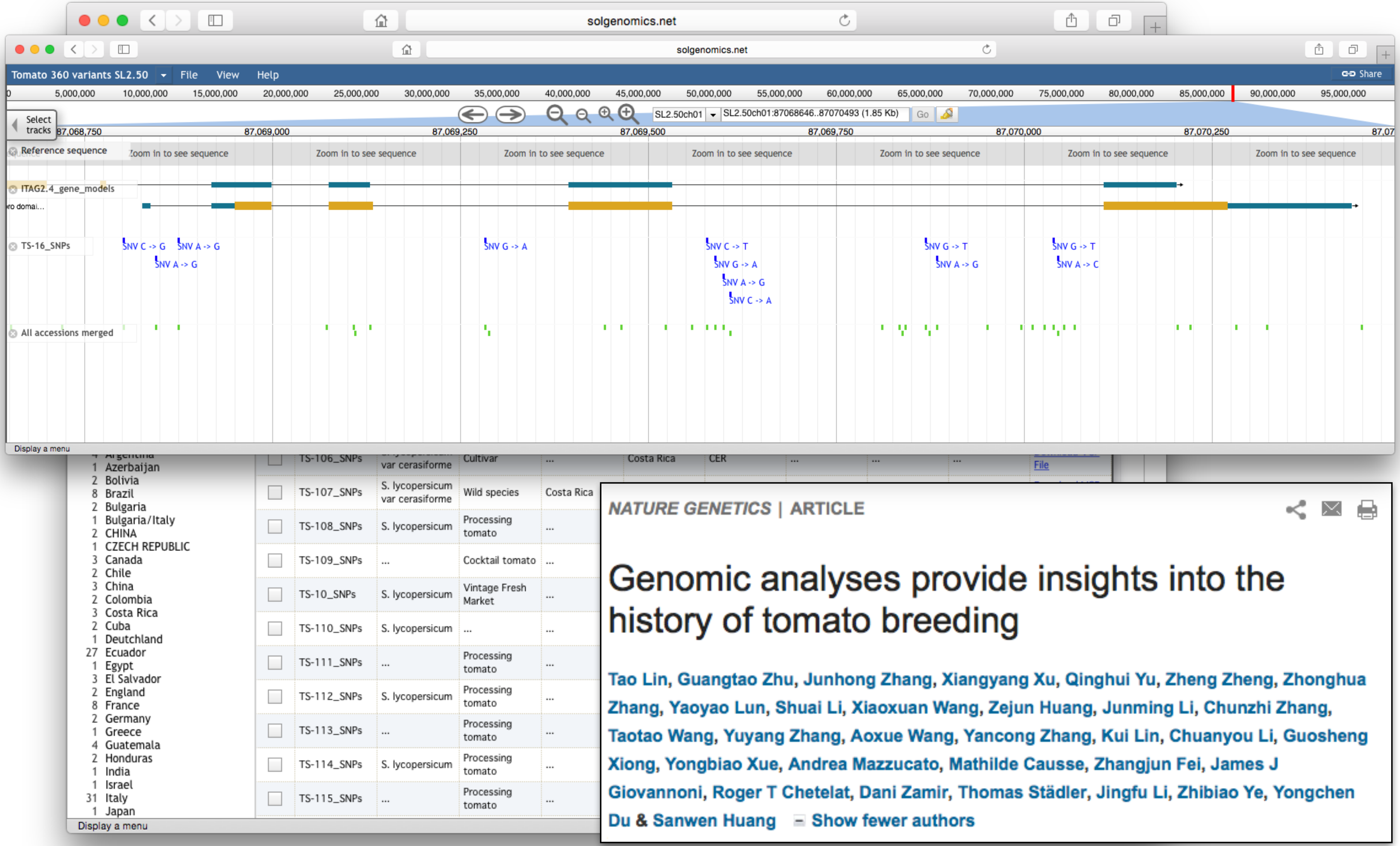
☐	Track	Species	Class	Province/Site	Origin	Group	PI CGN#	EA #	TGRC #	Download Link
☑	All accessions merged	...	...	...	...	...	...	...	...	Download VCF File
☑	ITAG2.4_gene_models	...	...	...	...	...	...	...	...	Download Gene Models
☑	Reference sequence	...	...	...	...	...	...	...	...	Download Reference sequence
☐	TS-100_SNPs	S. lycopersicum	Processing tomato	...	Italy	BIG	...	EA03456	...	Download VCF File
☐	TS-101_SNPs	S. lycopersicum	...	...	Unknown	BIG	...	EA00369	...	Download VCF File
☐	TS-102_SNPs	S. lycopersicum	Processing tomato	...	Russia	BIG	...	EA03673	...	Download VCF File
☐	TS-103_SNPs	S. lycopersicum	...	...	Unknown	BIG	...	EA00389	...	Download VCF File
☐	TS-104_SNPs	S. lycopersicum	Processing tomato	...	Italy	BIG	...	EA01756	...	Download VCF File
☐	TS-105_SNPs	S. lycopersicum var cerasiforme	Wild species	...	Costa Rica	CER	...	EA01448	...	Download VCF File
☐	TS-106_SNPs	S. lycopersicum var cerasiforme	Cultivar	...	Costa Rica	CER	...	...	...	Download VCF File
☐	TS-107_SNPs	S. lycopersicum var cerasiforme	Wild species	Costa Rica						
☐	TS-108_SNPs	S. lycopersicum	Processing tomato	...						
☐	TS-109_SNPs	...	Cocktail tomato	...						
☐	TS-10_SNPs	S. lycopersicum	Vintage Fresh Market	...						
☐	TS-110_SNPs	S. lycopersicum	...	...						
☐	TS-111_SNPs	...	Processing tomato	...						
☐	TS-112_SNPs	S. lycopersicum	Processing tomato	...						
☐	TS-113_SNPs	...	Processing tomato	...						
☐	TS-114_SNPs	S. lycopersicum	Processing tomato	...						
☐	TS-115_SNPs	...	Processing tomato	...						

NATURE GENETICS | ARTICLE

Genomic analyses provide insights into the history of tomato breeding

Tao Lin, Guangtao Zhu, Junhong Zhang, Xiangyang Xu, Qinghui Yu, Zheng Zheng, Zhonghua Zhang, Yaoyao Lun, Shuai Li, Xiaoxuan Wang, Zejun Huang, Junming Li, Chunzhi Zhang, Taotao Wang, Yuyang Zhang, Aoxue Wang, Yancong Zhang, Kui Lin, Chuanyou Li, Guosheng Xiong, Yongbiao Xue, Andrea Mazzucato, Mathilde Causse, Zhangjun Fei, James J Giovannoni, Roger T Chetelat, Dani Zamir, Thomas Städler, Jingfu Li, Zhibiao Ye, Yongchen Du & Sanwen Huang − Show fewer authors

360 Tomato variants



1	Azerbaijan
2	Bolivia
8	Brazil
2	Bulgaria
1	Bulgaria/Italy
2	CHINA
1	CZECH REPUBLIC
3	Canada
2	Chile
3	China
2	Colombia
3	Costa Rica
2	Cuba
1	Deutchland
27	Ecuador
1	Egypt
3	El Salvador
2	England
8	France
2	Germany
1	Greece
4	Guatemala
2	Honduras
1	India
1	Israel
31	Italy
1	Japan

☐	TS-106_SNPs	var cerasiforme	Cultivar	...	Costa Rica	CER	...	...	...	File
☐	TS-107_SNPs	S. lycopersicum var cerasiforme	Wild species	Costa Rica						
☐	TS-108_SNPs	S. lycopersicum	Processing tomato	...						
☐	TS-109_SNPs	...	Cocktail tomato	...						
☐	TS-10_SNPs	S. lycopersicum	Vintage Fresh Market	...						
☐	TS-110_SNPs	S. lycopersicum	...	...						
☐	TS-111_SNPs	...	Processing tomato	...						
☐	TS-112_SNPs	S. lycopersicum	Processing tomato	...						
☐	TS-113_SNPs	...	Processing tomato	...						
☐	TS-114_SNPs	S. lycopersicum	Processing tomato	...						
☐	TS-115_SNPs	...	Processing tomato	...						

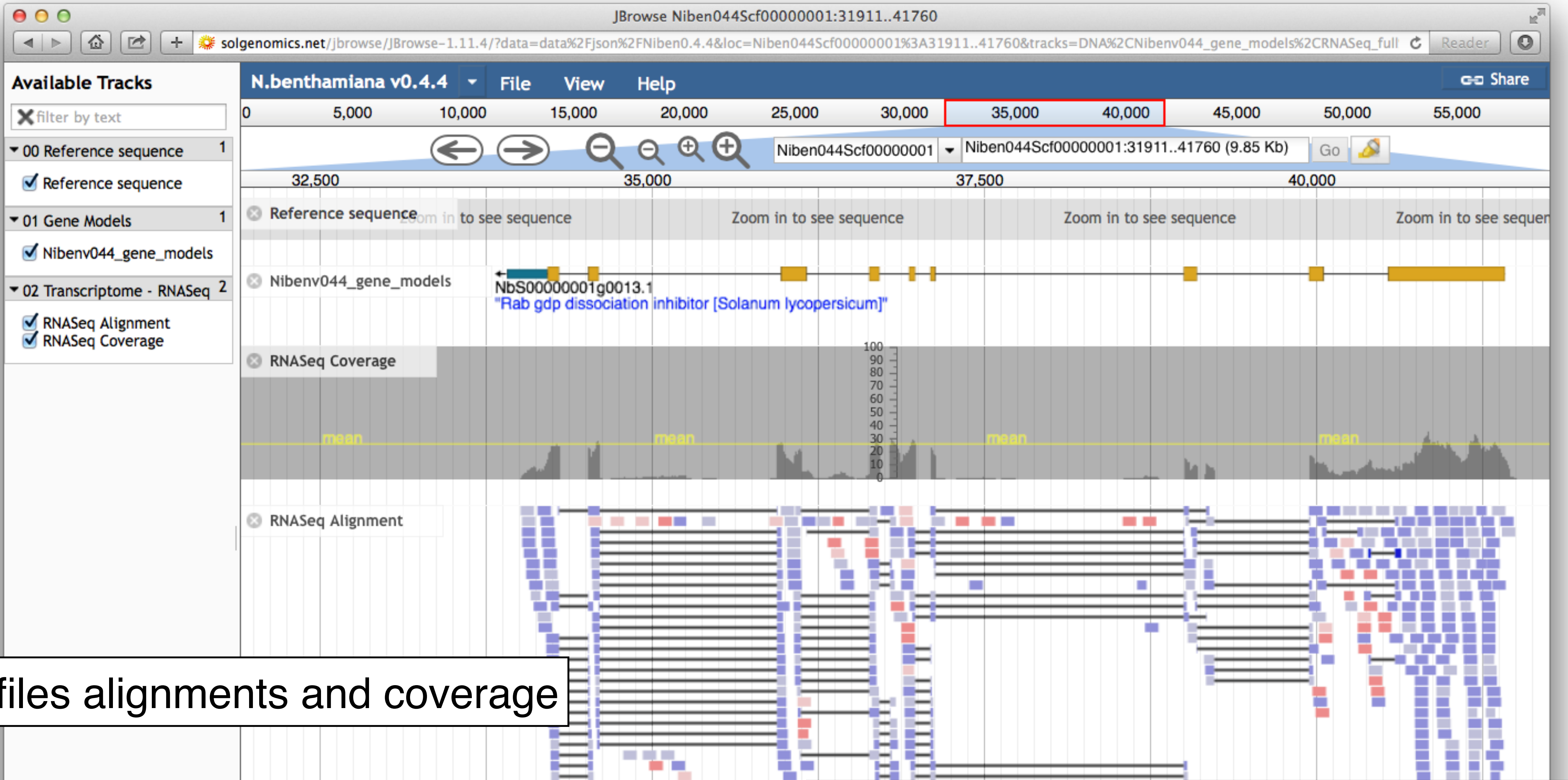
Display a menu

NATURE GENETICS | ARTICLE

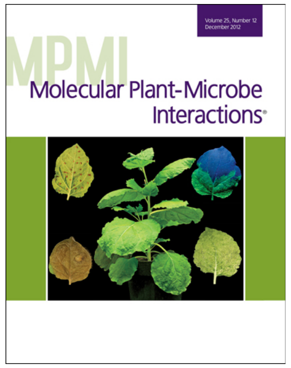
Genomic analyses provide insights into the history of tomato breeding

Tao Lin, Guangtao Zhu, Junhong Zhang, Xiangyang Xu, Qinghui Yu, Zheng Zheng, Zhonghua Zhang, Yaoyao Lun, Shuai Li, Xiaoxuan Wang, Zejun Huang, Junming Li, Chunzhi Zhang, Taotao Wang, Yuyang Zhang, Aoxue Wang, Yancong Zhang, Kui Lin, Chuanyou Li, Guosheng Xiong, Yongbiao Xue, Andrea Mazzucato, Mathilde Causse, Zhangjun Fei, James J Giovannoni, Roger T Chetelat, Dani Zamir, Thomas Städler, Jingfu Li, Zhibiao Ye, Yongchen Du & Sanwen Huang − Show fewer authors

JBrowse: *Nicotiana benthamiana*



bam files alignments and coverage



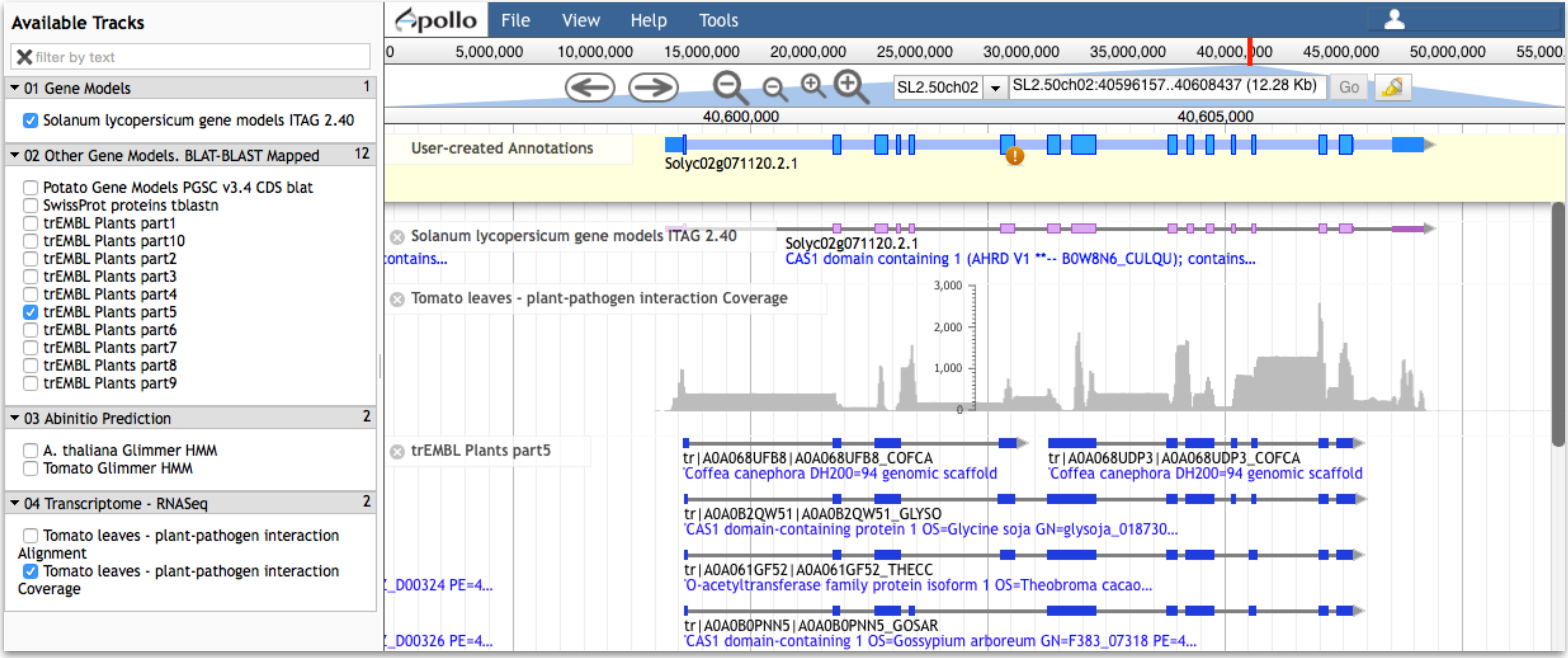
Nicotiana benthamiana

A Draft Genome Sequence of *Nicotiana benthamiana* to Enhance Molecular Plant-Microbe Biology Research

Aureliano Bombarely,[1] Hernan G. Rosli,[1] Julia Vrebalov,[1] Peter Moffett,[1,2] Lukas A. Mueller,[1] and **Gregory B. Martin[1,3,4]**

Sol Genomics Network

Web Apollo



Available Tracks

filter by text

- 01 Gene Models 1
  - ☑ Solanum lycopersicum gene models ITAG 2.40
- 02 Other Gene Models. BLAT-BLAST Mapped 12
  - ☐ Potato Gene Models PGSC v3.4 CDS blat
  - ☐ SwissProt proteins tblastn
  - ☐ trEMBL Plants part1
  - ☐ trEMBL Plants part10
  - ☐ trEMBL Plants part2
  - ☐ trEMBL Plants part3
  - ☐ trEMBL Plants part4
  - ☑ trEMBL Plants part5
  - ☐ trEMBL Plants part6
  - ☐ trEMBL Plants part7
  - ☐ trEMBL Plants part8
  - ☐ trEMBL Plants part9
- 03 Abinitio Prediction 2
  - ☐ A. thaliana Glimmer HMM
  - ☐ Tomato Glimmer HMM
- 04 Transcriptome - RNASeq 2
  - ☐ Tomato leaves - plant-pathogen interaction Alignment
  - ☑ Tomato leaves - plant-pathogen interaction Coverage

SL2.50ch02:40596157..40608437 (12.28 Kb)

User-created Annotations

Solyc02g071120.2.1

Solanum lycopersicum gene models ITAG 2.40

Solyc02g071120.2.1
CAS1 domain containing 1 (AHRD V1 **-- B0W8N6_CULQU); contains...

contains...

Tomato leaves - plant-pathogen interaction Coverage

trEMBL Plants part5

tr|A0A068UFB8|A0A068UFB8_COFCA
Coffea canephora DH200=94 genomic scaffold

tr|A0A068UDP3|A0A068UDP3_COFCA
Coffea canephora DH200=94 genomic scaffold

tr|A0A0B2QW51|A0A0B2QW51_GLYSO
CAS1 domain-containing protein 1 OS=Glycine soja GN=glysoja_018730...

tr|A0A061GF52|A0A061GF52_THECC
O-acetyltransferase family protein isoform 1 OS=Theobroma cacao...

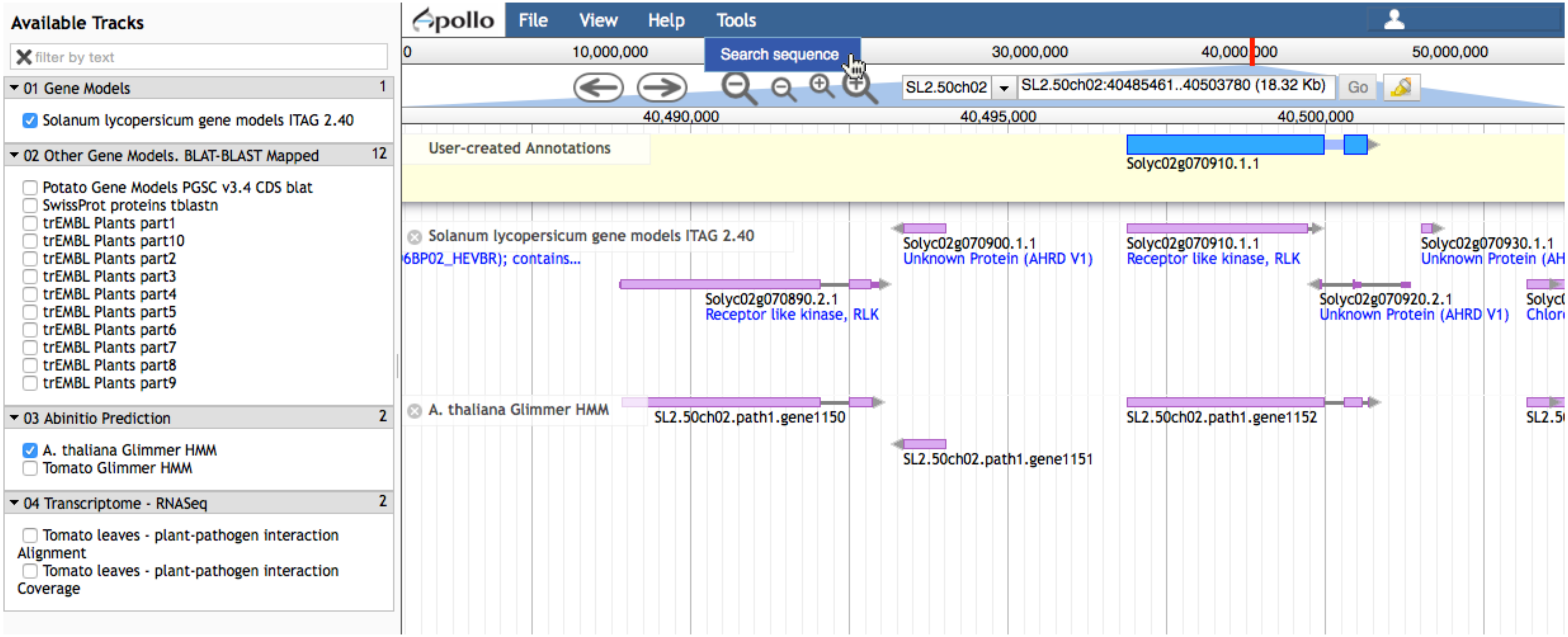
_D00324 PE=4...

tr|A0A0B0PNN5|A0A0B0PNN5_GOSAR
CAS1 domain-containing 1 OS=Gossypium arboreum GN=F383_07318 PE=4...

_D00326 PE=4...

Web Apollo

BTI



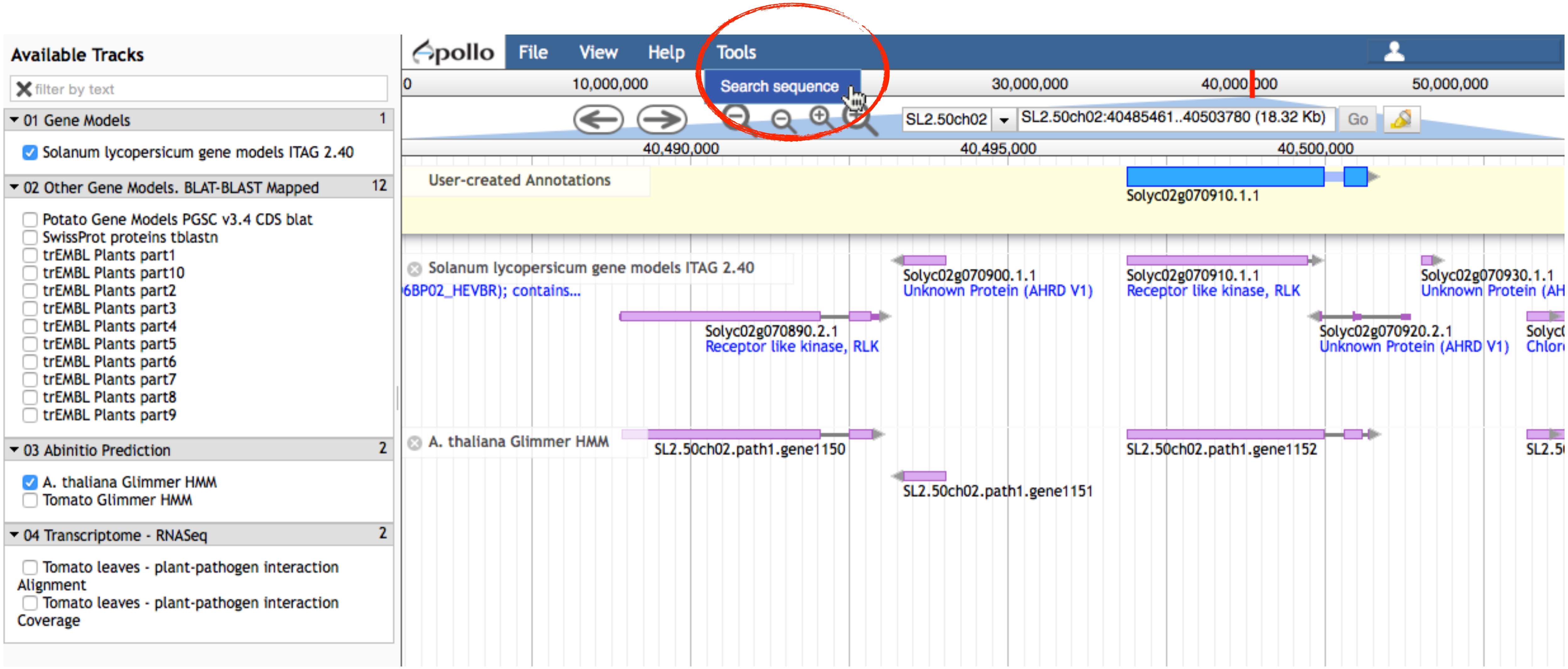
Available Tracks

filter by text

- 01 Gene Models 1
  - ☑ Solanum lycopersicum gene models ITAG 2.40
- 02 Other Gene Models. BLAT-BLAST Mapped 12
  - ☐ Potato Gene Models PGSC v3.4 CDS blat
  - ☐ SwissProt proteins tblastn
  - ☐ trEMBL Plants part1
  - ☐ trEMBL Plants part10
  - ☐ trEMBL Plants part2
  - ☐ trEMBL Plants part3
  - ☐ trEMBL Plants part4
  - ☐ trEMBL Plants part5
  - ☐ trEMBL Plants part6
  - ☐ trEMBL Plants part7
  - ☐ trEMBL Plants part8
  - ☐ trEMBL Plants part9
- 03 Abinitio Prediction 2
  - ☑ A. thaliana Glimmer HMM
  - ☐ Tomato Glimmer HMM
- 04 Transcriptome - RNASeq 2
  - ☐ Tomato leaves - plant-pathogen interaction Alignment
  - ☐ Tomato leaves - plant-pathogen interaction Coverage

SL2.50ch02 SL2.50ch02:40485461..40503780 (18.32 Kb)

Web Apollo



Available Tracks

filter by text

▾ 01 Gene Models 1

☑ Solanum lycopersicum gene models ITAG 2.40

▾ 02 Other Gene Models. BLAT-BLAST Mapped 12

☐ Potato Gene Models PGSC v3.4 CDS blat
☐ SwissProt proteins tblastn
☐ trEMBL Plants part1
☐ trEMBL Plants part10
☐ trEMBL Plants part2
☐ trEMBL Plants part3
☐ trEMBL Plants part4
☐ trEMBL Plants part5
☐ trEMBL Plants part6
☐ trEMBL Plants part7
☐ trEMBL Plants part8
☐ trEMBL Plants part9

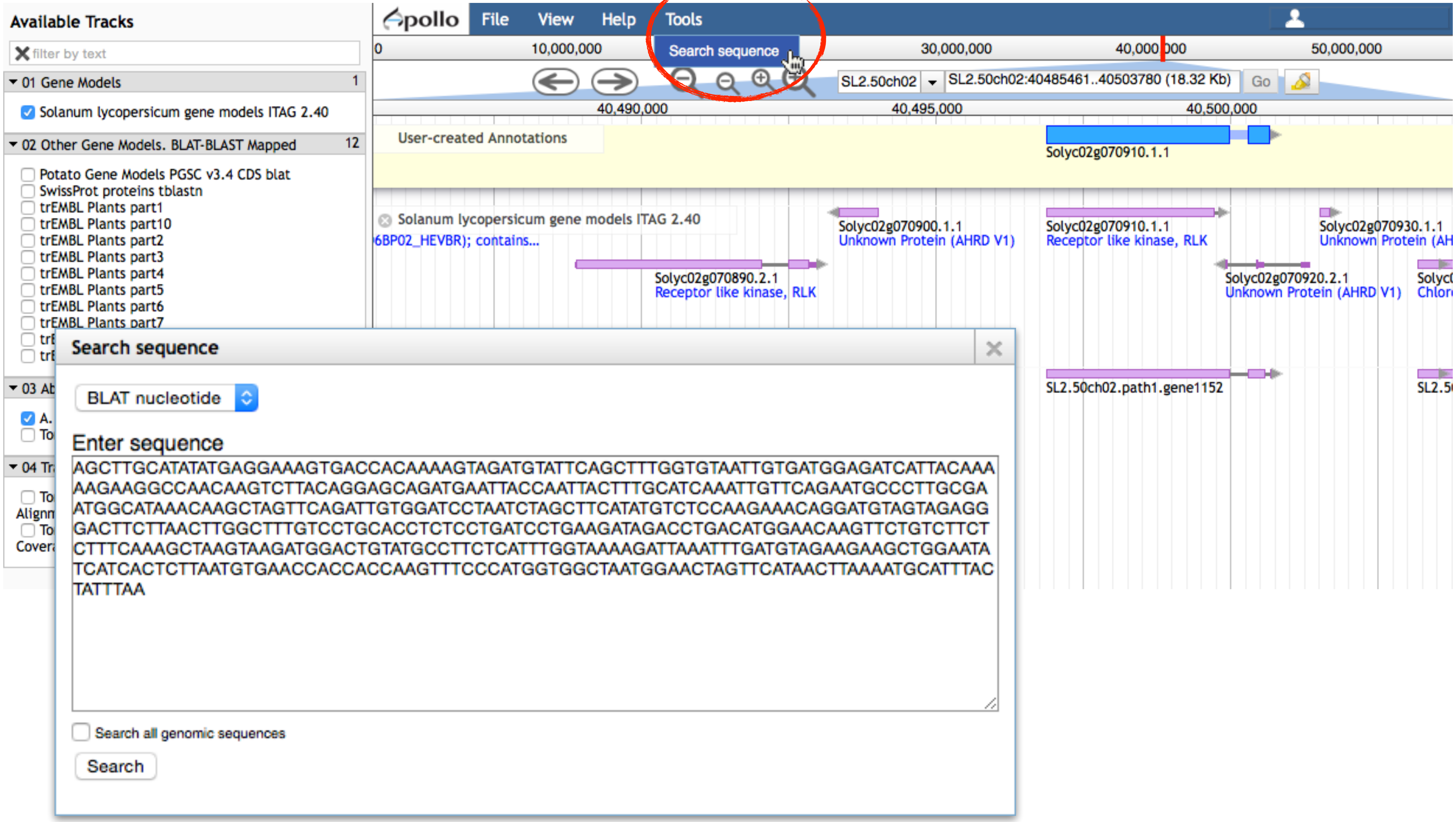
▾ 03 Abinitio Prediction 2

☑ A. thaliana Glimmer HMM
☐ Tomato Glimmer HMM

▾ 04 Transcriptome - RNASeq 2

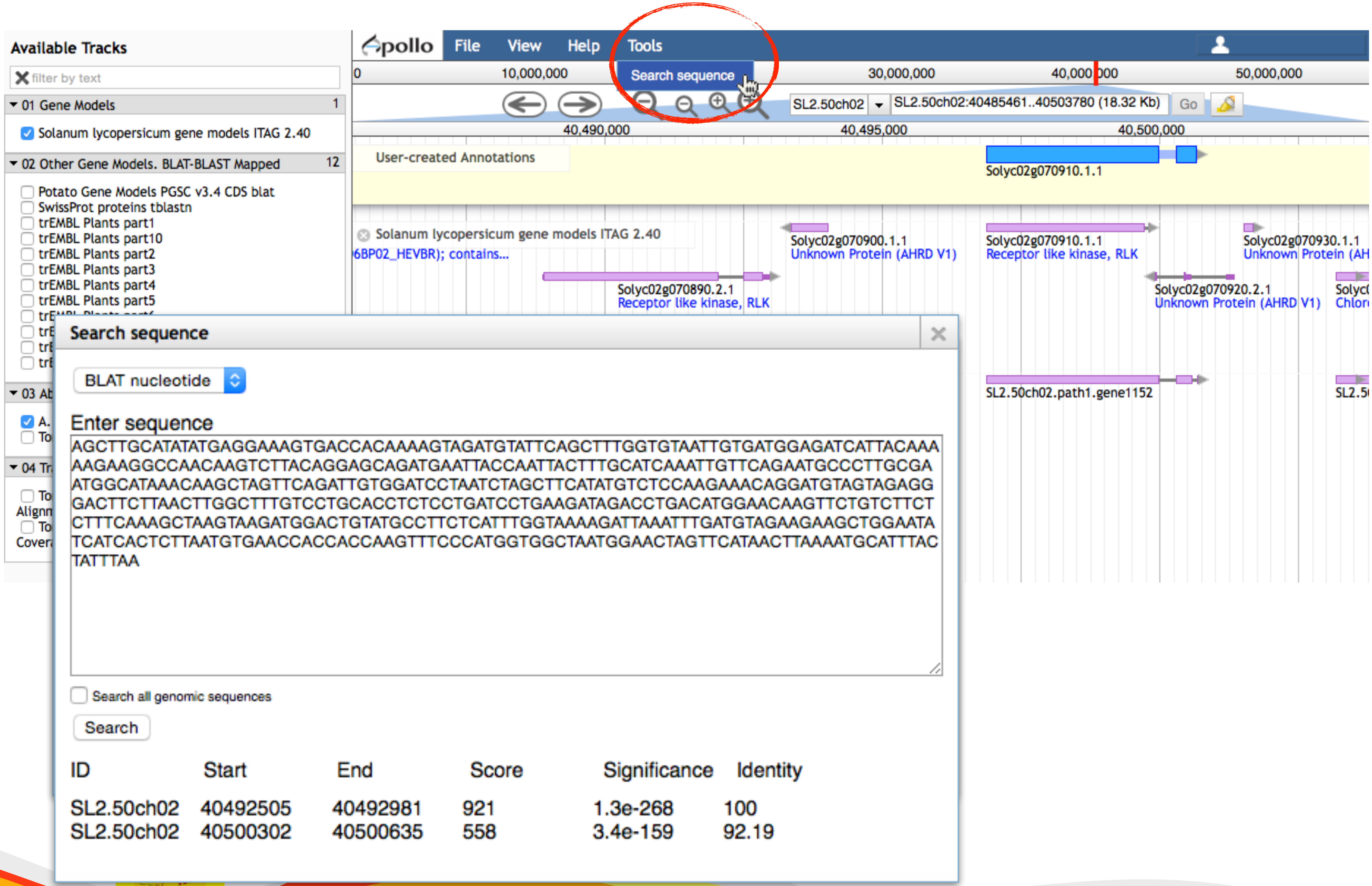
☐ Tomato leaves - plant-pathogen interaction Alignment
☐ Tomato leaves - plant-pathogen interaction Coverage

Web Apollo



```
AGCTTGCATATATGAGGAAAGTGACCACAAAAGTAGATGTATTCAGCTTTGGTGTAATTGTGATGGAGATCATTACAAA
AAGAAGGCCAACAAGTCTTACAGGAGCAGATGAATTACCAATTACTTTGCATCAAATTGTTCAGAATGCCCTTGCGA
ATGGCATAAACAAGCTAGTTCAGATTGTGGATCCTAATCTAGCTTCATATGTCTCCAAGAAACAGGATGTAGTAGAGG
GACTTCTTAACTTGGCTTTGTCCTGCACCTCTCCTGATCCTGAAGATAGACCTGACATGGAACAAGTTCTGTCTTCT
CTTTCAAAGCTAAGTAAGATGGACTGTATGCCTTCTCATTTGGTAAAAGATTAAATTTGATGTAGAAGAAGCTGGAATA
TCATCACTCTTAATGTGAACCACCACCAAGTTTCCCATGGTGGCTAATGGAACTAGTTCATAACTTAAAATGCATTTAC
TATTTAA
```

Web Apollo



Search sequence

BLAT nucleotide

Enter sequence

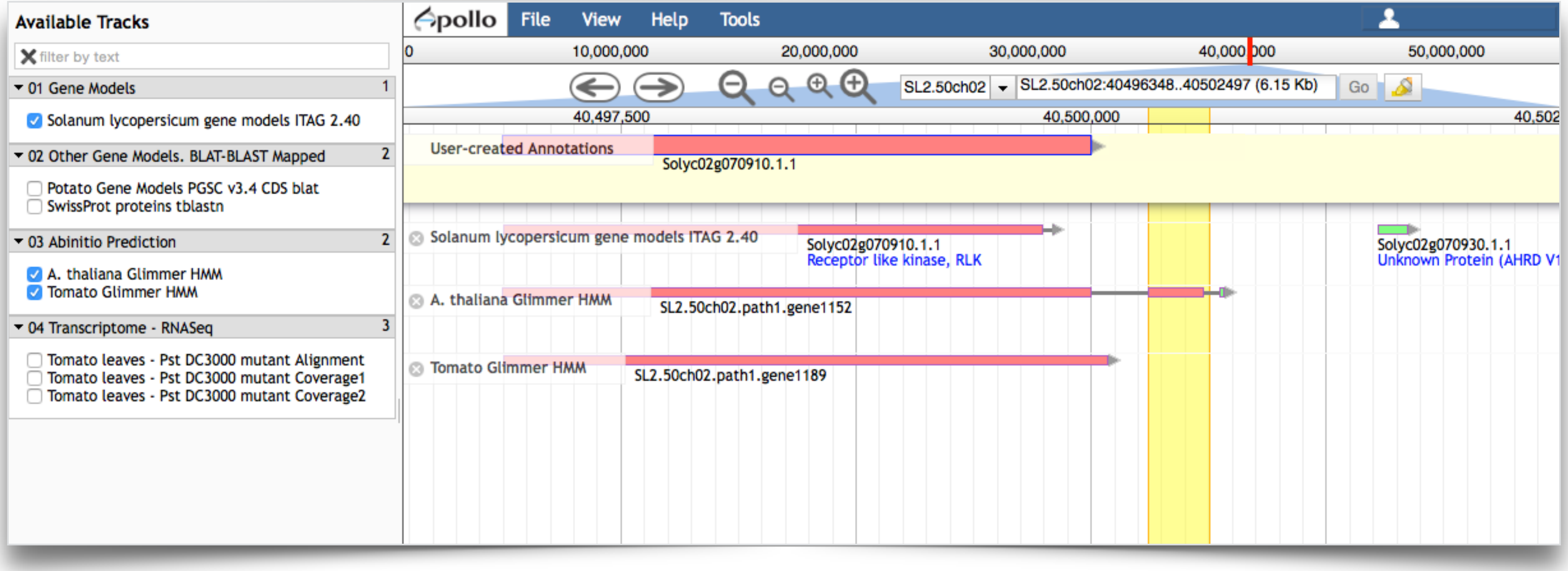
```
AGCTTGCATATATGAGGAAAGTGACCACAAAAGTAGATGTATTCAGCTTTGGTGTAATTGTGATGGAGATCATTACAAA
AAGAAGGCCAACAAGTCTTACAGGAGCAGATGAATTACCAATTACTTTGCATCAAATTGTTCAGAATGCCCTTGCGA
ATGGCATAAACAAGCTAGTTCAGATTGTGGATCCTAATCTAGCTTCATATGTCTCCAAGAAACAGGATGTAGTAGAGG
GACTTCTTAACTTGGCTTTGTCCTGCACCTCTCCTGATCCTGAAGATAGACCTGACATGGAACAAGTTCTGTCTTCT
CTTTCAAAGCTAAGTAAGATGGACTGTATGCCTTCTCATTTGGTAAAAGATTAAATTTGATGTAGAAGAAGCTGGAATA
TCATCACTCTTAATGTGAACCACCACCAAGTTTCCCATGGTGGCTAATGGAACTAGTTCATAACTTAAAATGCATTTAC
TATTTAA
```

☐ Search all genomic sequences

Search

ID	Start	End	Score	Significance	Identity
SL2.50ch02	40492505	40492981	921	1.3e-268	100
SL2.50ch02	40500302	40500635	558	3.4e-159	92.19

Web Apollo



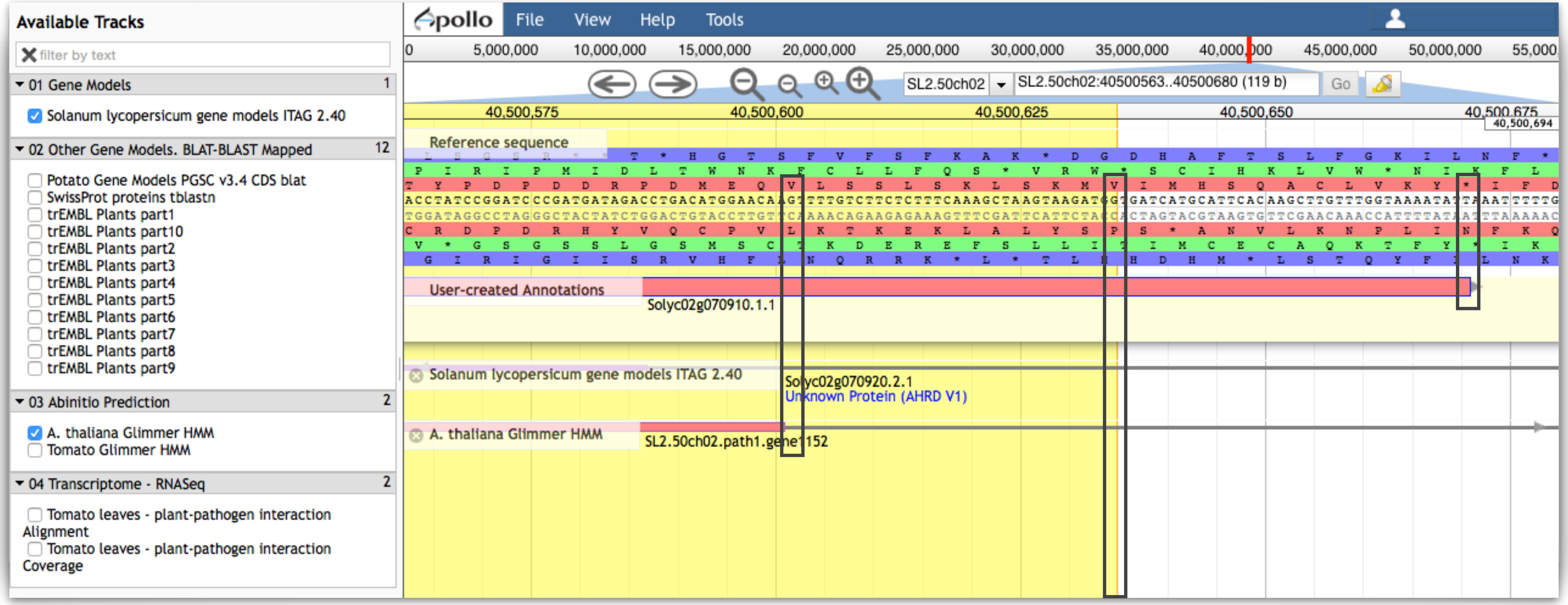
Available Tracks

filter by text

- 01 Gene Models 1
  - ☑ Solanum lycopersicum gene models ITAG 2.40
- 02 Other Gene Models. BLAT-BLAST Mapped 2
  - ☐ Potato Gene Models PGSC v3.4 CDS blat
  - ☐ SwissProt proteins tblastn
- 03 Abinitio Prediction 2
  - ☑ A. thaliana Glimmer HMM
  - ☑ Tomato Glimmer HMM
- 04 Transcriptome - RNASeq 3
  - ☐ Tomato leaves - Pst DC3000 mutant Alignment
  - ☐ Tomato leaves - Pst DC3000 mutant Coverage1
  - ☐ Tomato leaves - Pst DC3000 mutant Coverage2

SL2.50ch02 SL2.50ch02:40496348..40502497 (6.15 Kb)

Web Apollo



Available Tracks

filter by text

01 Gene Models 1

☑ Solanum lycopersicum gene models ITAG 2.40

02 Other Gene Models. BLAT-BLAST Mapped 12

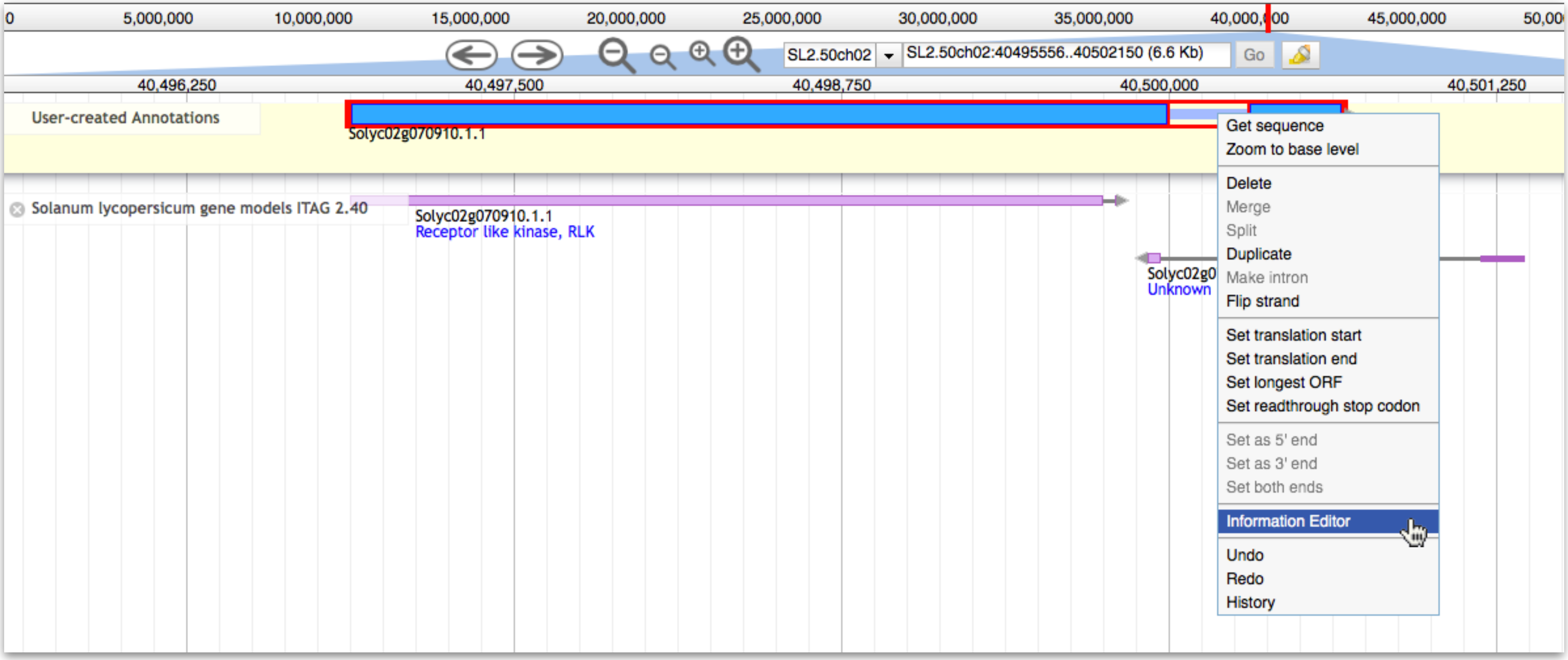
☐ Potato Gene Models PGSC v3.4 CDS blat
☐ SwissProt proteins tblastn
☐ trEMBL Plants part1
☐ trEMBL Plants part10
☐ trEMBL Plants part2
☐ trEMBL Plants part3
☐ trEMBL Plants part4
☐ trEMBL Plants part5
☐ trEMBL Plants part6
☐ trEMBL Plants part7
☐ trEMBL Plants part8
☐ trEMBL Plants part9

03 Abinitio Prediction 2

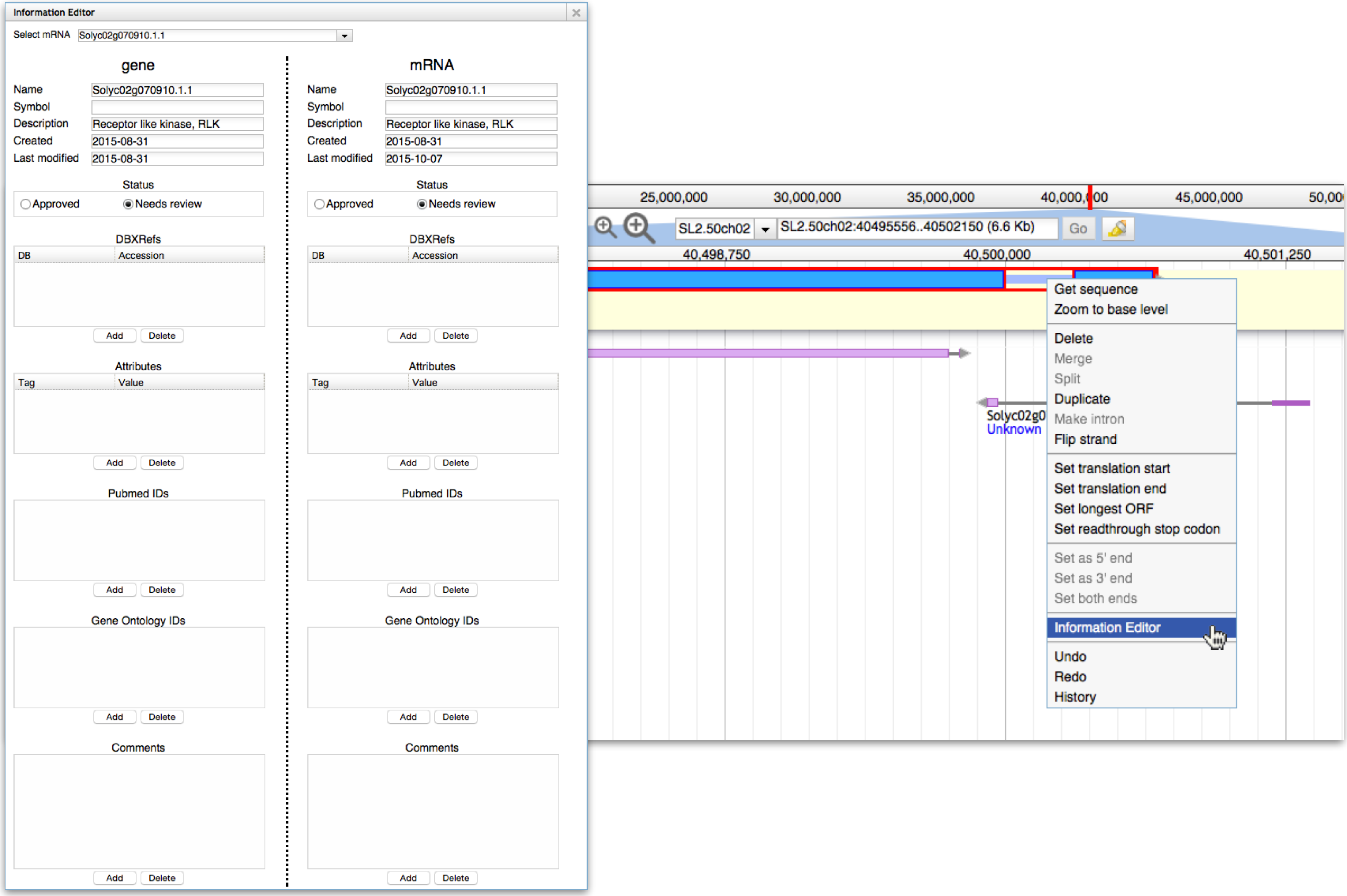
☑ A. thaliana Glimmer HMM
☐ Tomato Glimmer HMM

04 Transcriptome - RNASeq 2

☐ Tomato leaves - plant-pathogen interaction Alignment
☐ Tomato leaves - plant-pathogen interaction Coverage


0
5,000,000
10,000,000
15,000,000
20,000,000
25,000,000
30,000,000
35,000,000
40,000,000
45,000,000
SL2.50ch02
SL2.50ch02:40495556..40502150 (6.6 Kb)
Go
40,496,250
40,497,500
40,498,750
40,500,000
40,501,250
User-created Annotations
Solyc02g070910.1.1
Solanum lycopersicum gene models ITAG 2.40
Solyc02g070910.1.1
Receptor like kinase, RLK
Solyc02g0
Unknown
Get sequence
Zoom to base level
Delete
Merge
Split
Duplicate
Make intron
Flip strand
Set translation start
Set translation end
Set longest ORF
Set readthrough stop codon
Set as 5' end
Set as 3' end
Set both ends
Information Editor
Undo
Redo
History

Web Apollo



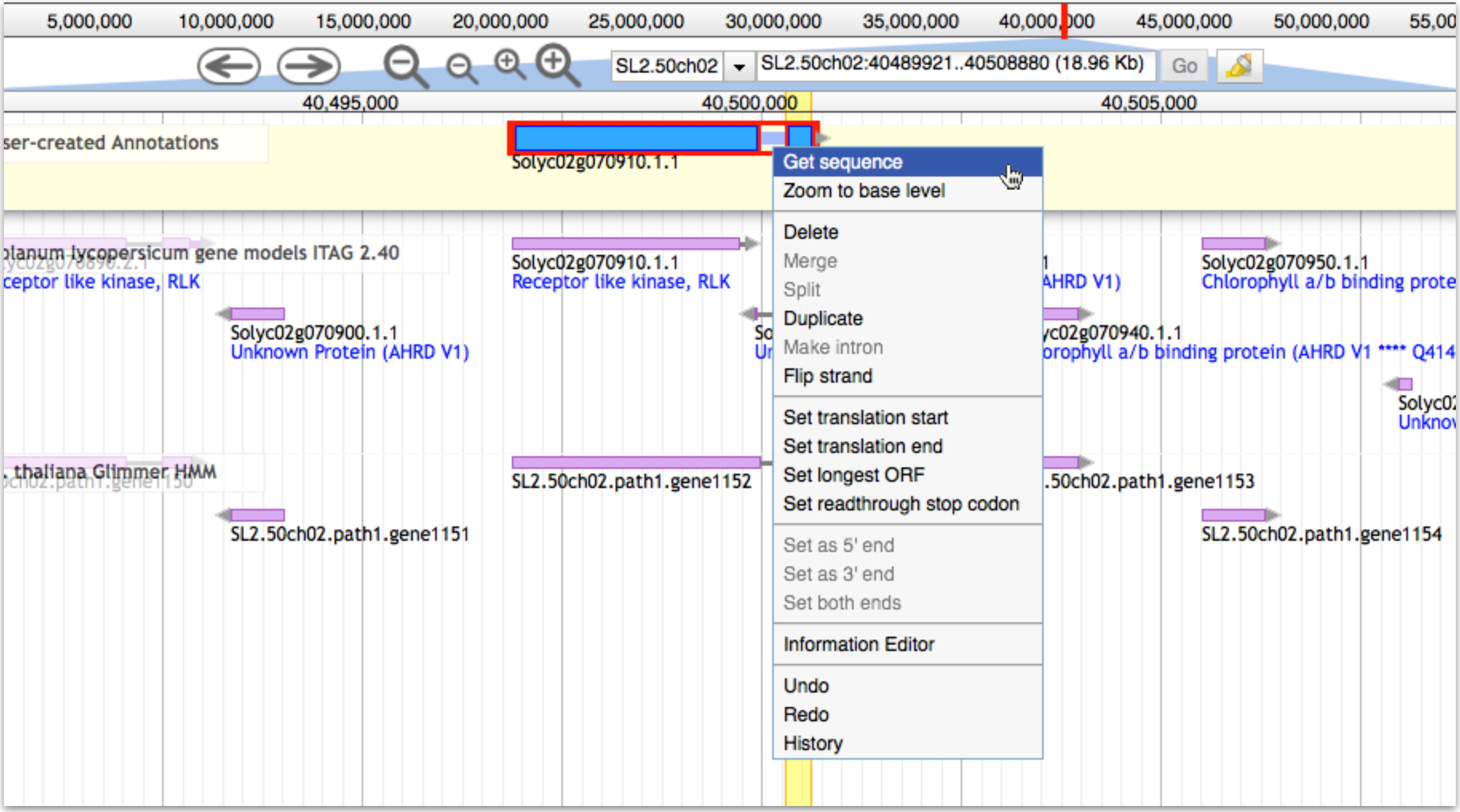
Information Editor

Select mRNA: Solyc02g070910.1.1

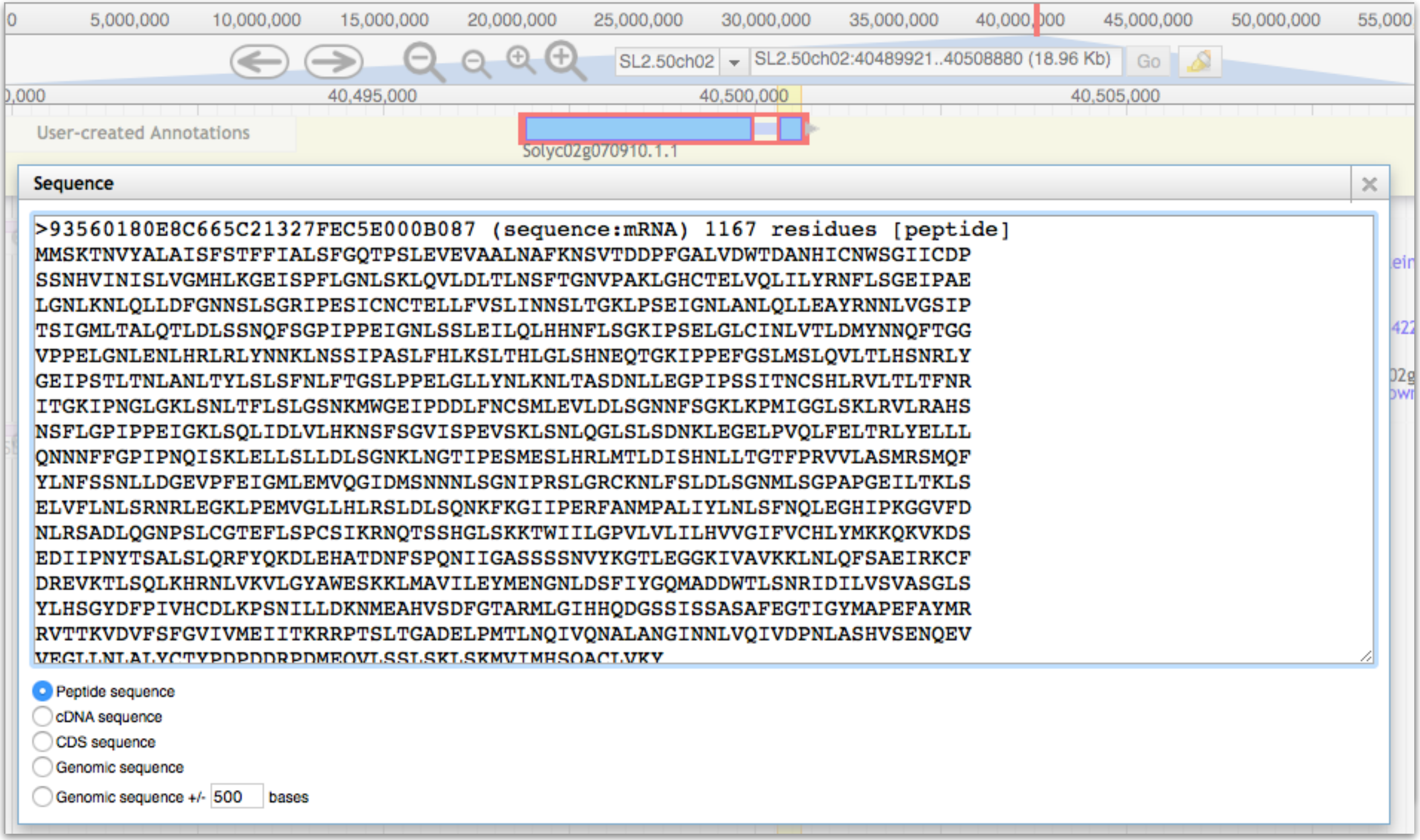
	gene	mRNA
Name	Solyc02g070910.1.1	Solyc02g070910.1.1
Symbol		
Description	Receptor like kinase, RLK	Receptor like kinase, RLK
Created	2015-08-31	2015-08-31
Last modified	2015-08-31	2015-10-07
Status	○ Approved ● Needs review	○ Approved ● Needs review

Web Apollo

BTI



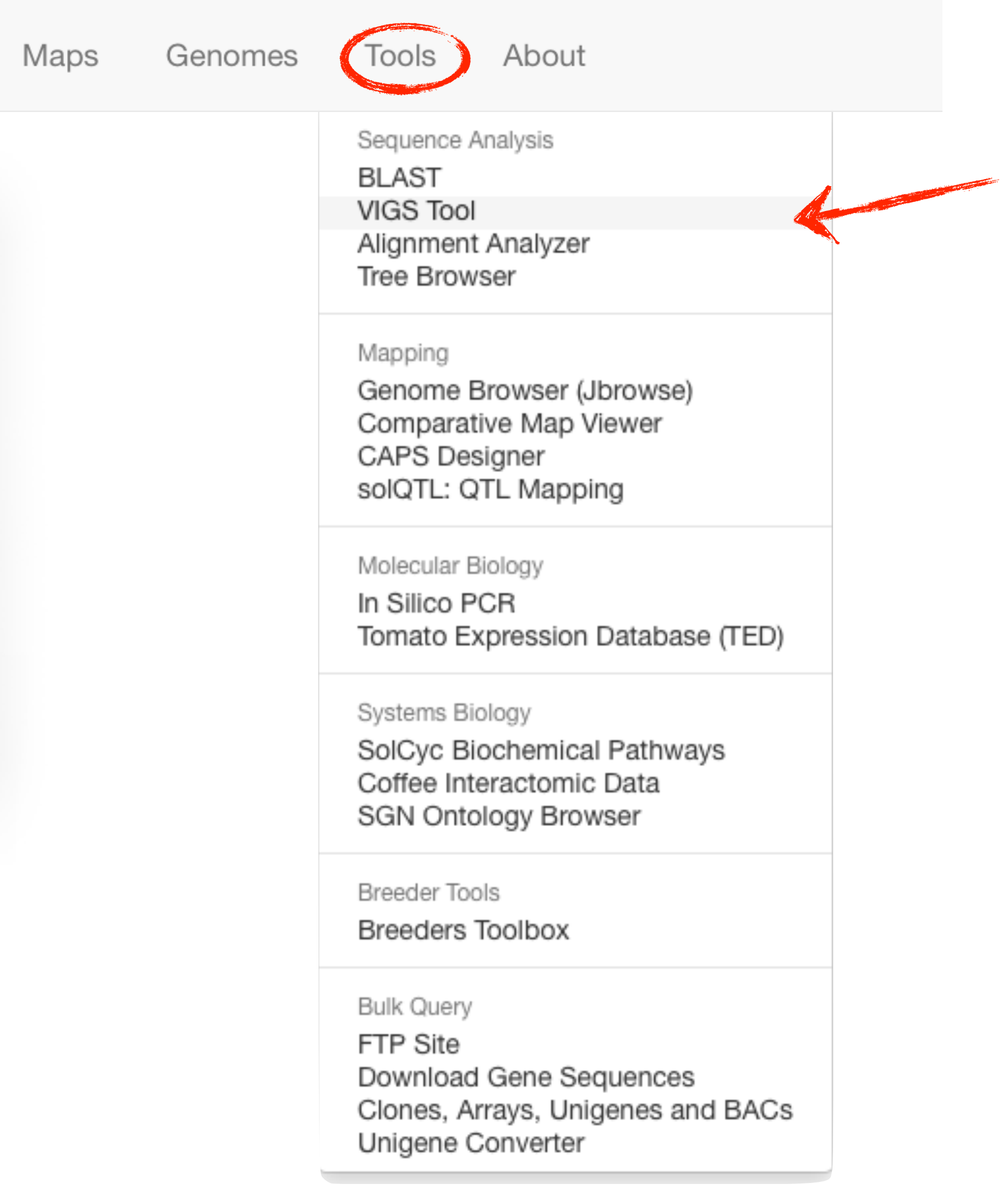
Web Apollo



```
>93560180E8C665C21327FEC5E000B087 (sequence:mRNA) 1167 residues [peptide]
MMSKTNVYALAISFSTFFIALSFGQTPSLEVEVAALNAFKNSVTDDPFGALVDWTDANHICNWSGIICDP
SSNHVINISLVGMHLKGEISPFLGNLSKLQVLDLTLNSFTGNVPAKLGHCTELVQLILYRNFLSGEIPAE
LGNLKNLQLLDFGNNSLSGRIPESICNCTELLFVSLINNSLTGKLPSEIGNLANLQLLEAYRNNLVGSIP
TSIGMLTALQTLDLSSNQFSGPIPPEIGNLSSLEILQLHHNFLSGKIPSELGLCINLVTLDMYNNQFTGG
VPPELGNLENLHRLRLYNNKLNSSIPASLFHLKSLTHLGLSHNEQTGKIPPEFGSLMSLQVLTLHSNRLY
GEIPSTLTNLANLTYLSLSFNLFTGSLPPELGLLYNLKNLTASDNLLEGPIPSSITNCSHLRVLTLTFNR
ITGKIPNGLGKLSNLTFLSLGSNKMWGEIPDDLFNCSMLEVLDLSGNNFSGKLKPMIGGLSKLRVLRAHS
NSFLGPIPPEIGKLSQLIDLVLHKNSFSGVISPEVSKLSNLQGLSLSDNKLEGELPVQLFELTRLYELLL
QNNNFFGPIPNQISKLELLSLLDLSGNKLNGTIPESMESLHRLMTLDISHNLLTGTFPRVVLASMRSMQF
YLNFSSNLLDGEVPFEIGMLEMVQGIDMSNNNLSGNIPRSLGRCKNLFSLDLSGNMLSGPAPGEILTKLS
ELVFLNLSRNRLEGKLPEMVGLLHLRSLDLSQNKFKGIIPERFANMPALIYLNLSFNQLEGHIPKGGVFD
NLRSADLQGNPSLCGTEFLSPCSIKRNQTSSHGLSKKTWIILGPVLVLILHVVGIFVCHLYMKKQKVKDS
EDIIPNYTSALSLQRFYQKDLEHATDNFSPQNIIGASSSSNVYKGTLEGGKIVAVKKLNLQFSAEIRKCF
DREVKTLSQLKHRNLVKVLGYAWESKKLMAVILEYMENGNLDSFIYGQMADDWTLSNRIDILVSVASGLS
YLHSGYDFPIVHCDLKPSNILLDKNMEAHVSDFGTARMLGIHHQDGSSISSASAFEGTIGYMAPEFAYMR
RVTTKVDVFSFGVIVMEIITKRRPTSLTGADELPMTLNQIVQNALANGINNLVQIVDPNLASHVSENQEV
VEGLLNLALYCTYPDPDDRPDMEQVLSSLSKLSKMVIMHSQACLVKY
```

● Peptide sequence
○ cDNA sequence
○ CDS sequence
○ Genomic sequence
○ Genomic sequence +/- 500 bases

SGN VIGS Tools



Sequence Analysis
BLAST
VIGS Tool
Alignment Analyzer
Tree Browser

Mapping
Genome Browser (Jbrowse)
Comparative Map Viewer
CAPS Designer
solQTL: QTL Mapping

Molecular Biology
In Silico PCR
Tomato Expression Database (TED)

Systems Biology
SolCyc Biochemical Pathways
Coffee Interactomic Data
SGN Ontology Browser

Breeder Tools
Breeders Toolbox

Bulk Query
FTP Site
Download Gene Sequences
Clones, Arrays, Unigenes and BACs
Unigene Converter

Molecular Plant

Cell PRESS

Volume 8, Issue 3, 2 March 2015, Pages 486–488

Letter to the Editor

The SGN VIGS Tool: User-Friendly Software to Design Virus-Induced Gene Silencing (VIGS) Constructs for Functional Genomics

Noe Fernandez-Pozo[1], Hernan G. Rosli[1,2], Gregory B. Martin[1,3], Lukas A. Mueller[1]

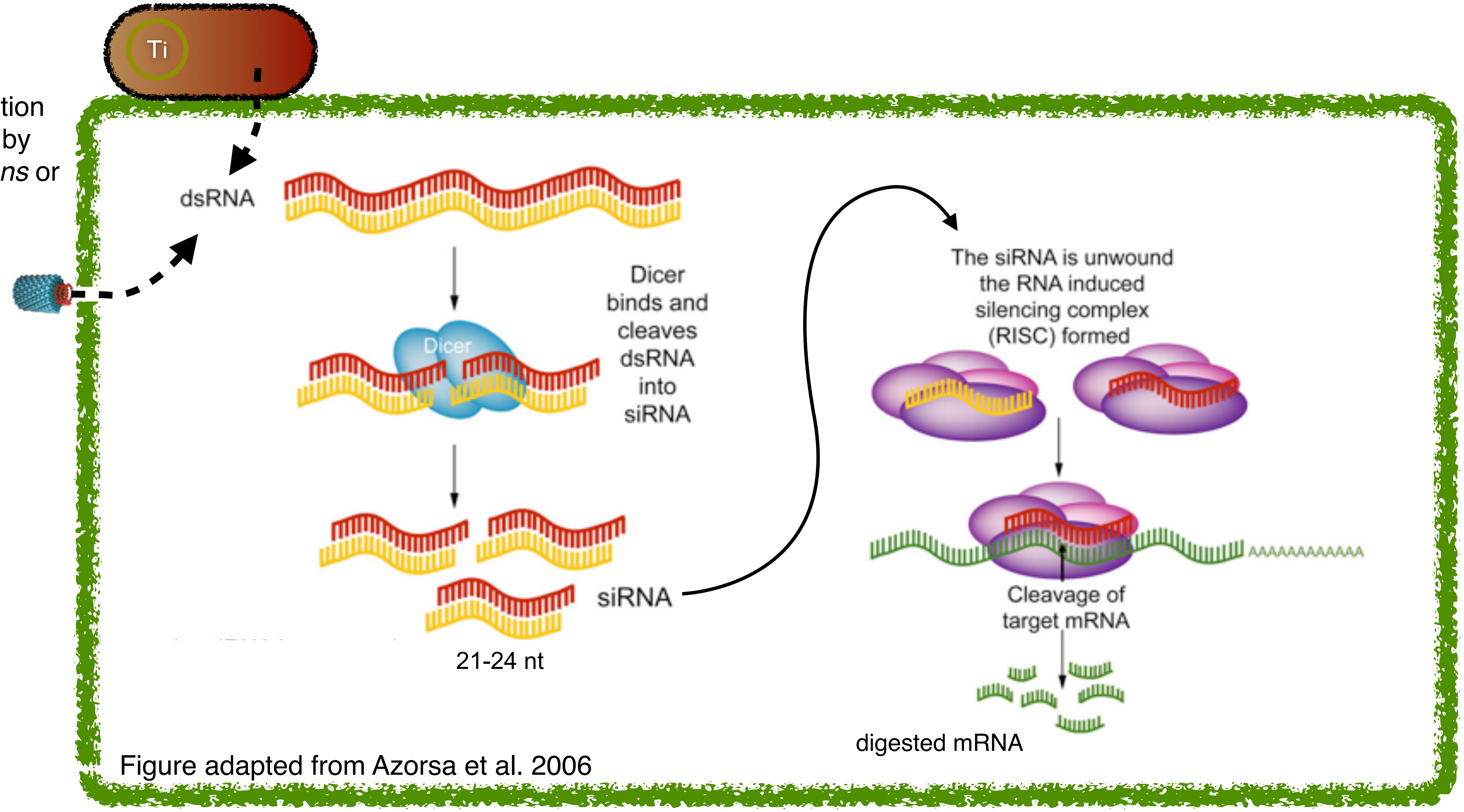
Hernan
Rosli

Gregory
Martin

Lukas
Mueller

http://vigs.solgenomics.net

Virus-Induced Gene Silencing (VIGS)



transformation
mediated by
A.tumefaciens or
virus

Ti

dsRNA

Dicer
binds and
cleaves
dsRNA
into
siRNA

Dicer

siRNA

21-24 nt

The siRNA is unwound
the RNA induced
silencing complex
(RISC) formed

AAAAAAAAAAA

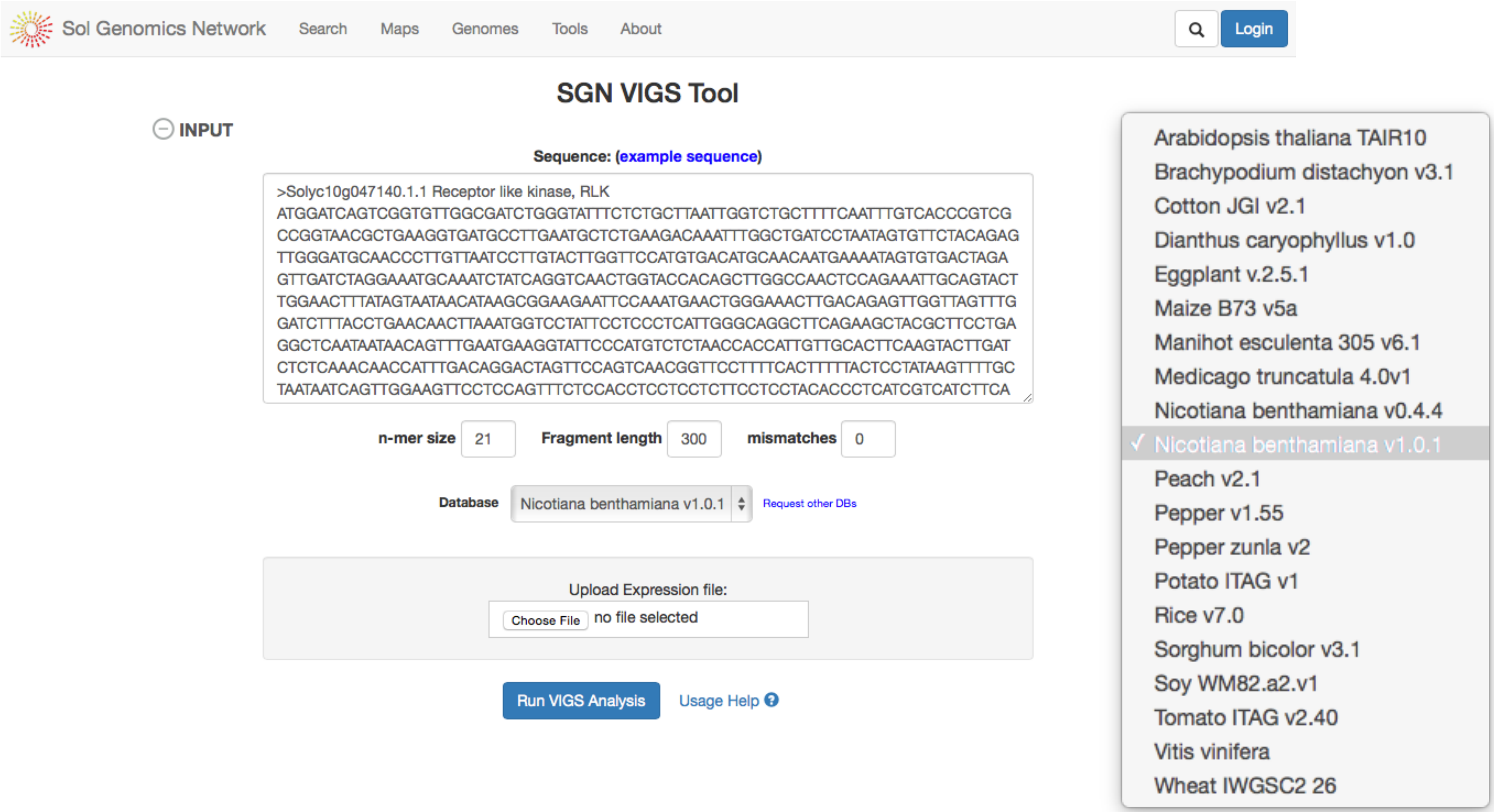
Cleavage of
target mRNA

digested mRNA

Figure adapted from Azorsa et al. 2006

Azorsa D. et al. Gene silencing through RNA interference. (2006). Peptide Nucleic Acids, Morpholinos and Related Antisense Biomolecules. Editors: Janson C.G. and During M.J. pp 252-264

VIGS Tool input



SGN VIGS Tool

INPUT

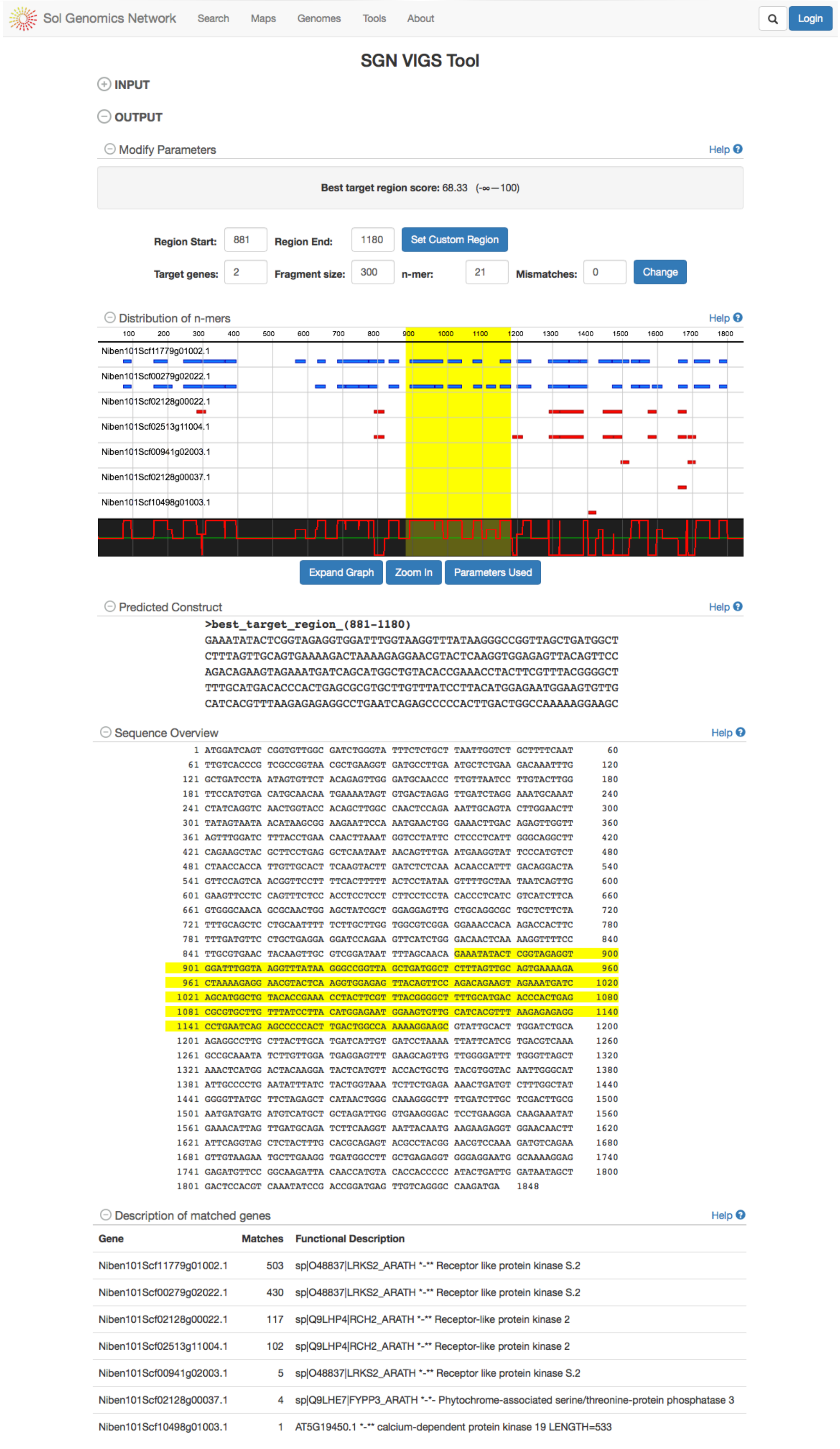
Sequence: (example sequence)

```
>Solyc10g047140.1.1 Receptor like kinase, RLK
ATGGATCAGTCGGTGTTGGCGATCTGGGTATTTCTCTGCTTAATTGGTCTGCTTTTCAATTTGTCACCCGTCG
CCGGTAACGCTGAAGGTGATGCCTTGAATGCTCTGAAGACAAATTTGGCTGATCCTAATAGTGTTCTACAGAG
TTGGGATGCAACCCTTGTTAATCCTTGTACTTGGTTCCATGTGACATGCAACAATGAAAATAGTGTGACTAGA
GTTGATCTAGGAAATGCAAATCTATCAGGTCAACTGGTACCACAGCTTGGCCAACTCCAGAAATTGCAGTACT
TGGAACTTTATAGTAATAACATAAGCGGAAGAATTCCAAATGAACTGGGAAACTTGACAGAGTTGGTTAGTTTG
GATCTTTACCTGAACAACTTAAATGGTCCTATTCCTCCCTCATTGGGCAGGCTTCAGAAGCTACGCTTCCTGA
GGCTCAATAATAACAGTTTGAATGAAGGTATTCCCATGTCTCTAACCACCATTGTTGCACTTCAAGTACTTGAT
CTCTCAAACAACCATTTGACAGGACTAGTTCCAGTCAACGGTTCCTTTTCACTTTTTACTCCTATAAGTTTTGC
TAATAATCAGTTGGAAGTTCCTCCAGTTTCTCCACCTCCTCCTCTTCCTCCTACACCCTCATCGTCATCTTCA
```

n-mer size 21 **Fragment length** 300 **mismatches** 0

Database Nicotiana benthamiana v1.0.1

S Tool output



SGN VIGS Tool

⊕ INPUT

⊖ OUTPUT

⊖ Modify Parameters — Help

Best target region score: 68.33 (-∞—100)

Region Start: 881 **Region End:** 1180 [Set Custom Region]

Target genes: 2 **Fragment size:** 300 **n-mer:** 21 **Mismatches:** 0 [Change]

⊖ Distribution of n-mers — Help

⊖ Predicted Construct — Help

```
>best_target_region_(881-1180)
GAAATATACTCGGTAGAGGTGGATTTGGTAAGGTTTATAAGGGCCGGTTAGCTGATGGCT
CTTTAGTTGCAGTGAAAAGACTAAAAGAGGAACGTACTCAAGGTGGAGAGTTACAGTTCC
AGACAGAAGTAGAAATGATCAGCATGGCTGTACACCGAAACCTACTTCGTTTACGGGGCT
TTTGCATGACACCCACTGAGCGCGTGCTTGTTTATCCTTACATGGAGAATGGAAGTGTTG
CATCACGTTTAAGAGAGAGGCCTGAATCAGAGCCCCCACTTGACTGGCCAAAAAGGAAGC
```

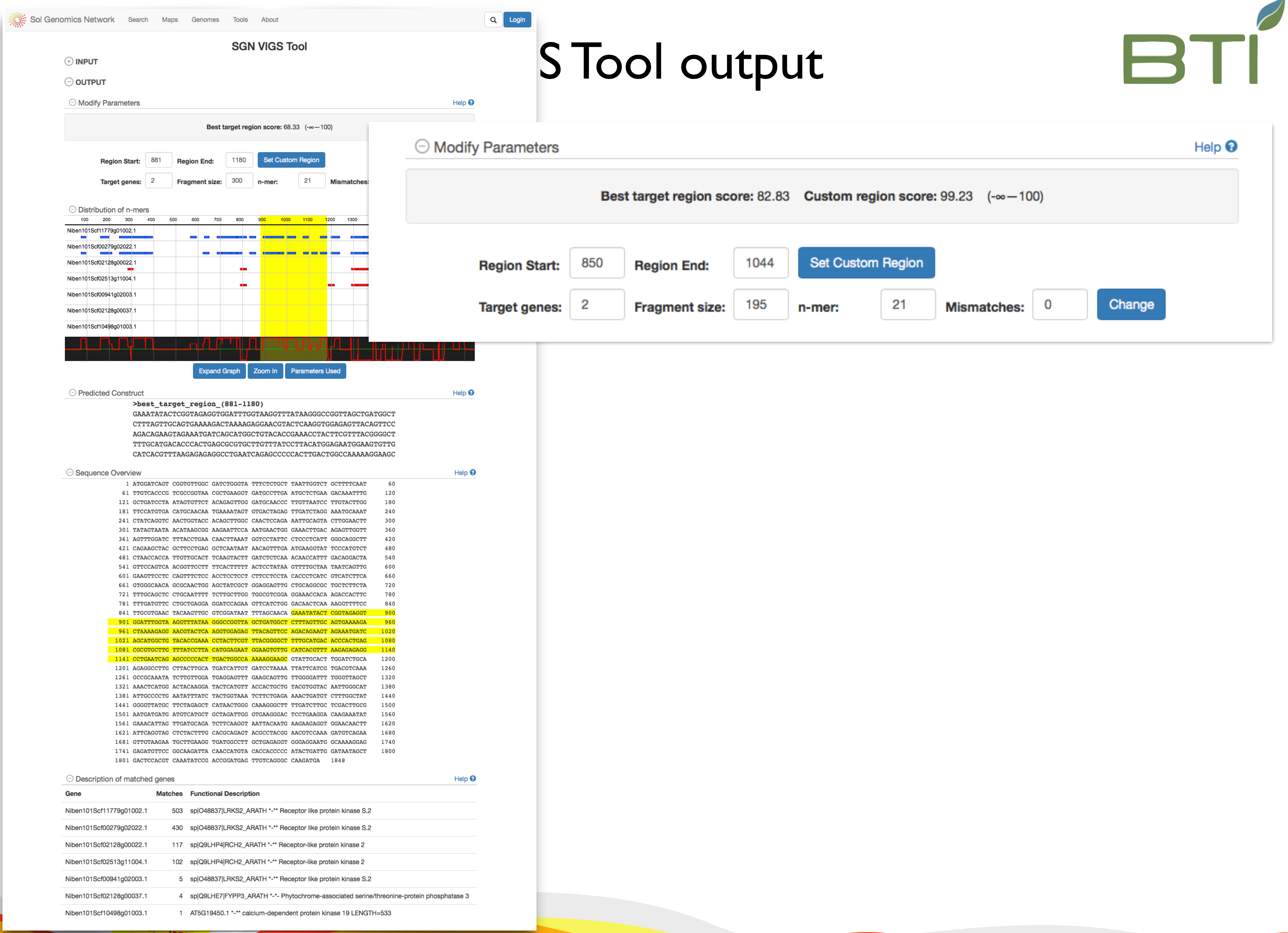
⊖ Sequence Overview — Help

```
   1 ATGGATCAGT CGGTGTTGGC GATCTGGGTA TTTCTCTGCT TAATTGGTCT GCTTTTCAAT     60
  61 TTGTCACCCG TCGCCGGTAA CGCTGAAGGT GATGCCTTGA ATGCTCTGAA GACAAATTTG    120
 121 GCTGATCCTA ATAGTGTTCT ACAGAGTTGG GATGCAACCC TTGTTAATCC TTGTACTTGG    180
 181 TTCCATGTGA CATGCAACAA TGAAAATAGT GTGACTAGAG TTGATCTAGG AAATGCAAAT    240
 241 CTATCAGGTC AACTGGTACC ACAGCTTGGC CAACTCCAGA AATTGCAGTA CTTGGAACTT    300
 301 TATAGTAATA ACATAAGCGG AAGAATTCCA AATGAACTGG GAAACTTGAC AGAGTTGGTT    360
 361 AGTTTGGATC TTTACCTGAA CAACTTAAAT GGTCCTATTC CTCCCTCATT GGGCAGGCTT    420
 421 CAGAAGCTAC GCTTCCTGAG GCTCAATAAT AACAGTTTGA ATGAAGGTAT TCCCATGTCT    480
 481 CTAACCACCA TTGTTGCACT TCAAGTACTT GATCTCTCAA ACAACCATTT GACAGGACTA    540
 541 GTTCCAGTCA ACGGTTCCTT TTCACTTTTT ACTCCTATAA GTTTTGCTAA TAATCAGTTG    600
 601 GAAGTTCCTC CAGTTTCTCC ACCTCCTCCT CTTCCTCCTA CACCCTCATC GTCATCTTCA    660
 661 GTGGGCAACA GCGCAACTGG AGCTATCGCT GGAGGAGTTG CTGCAGGCGC TGCTCTTCTA    720
 721 TTTGCAGCTC CTGCAATTTT TCTTGCTTGG TGGCGTCGGA GGAAACCACA AGACCACTTC    780
 781 TTTGATGTTC CTGCTGAGGA GGATCCAGAA GTTCATCTGG GACAACTCAA AAGGTTTTCC    840
 841 TTGCGTGAAC TACAAGTTGC GTCGGATAAT TTTAGCAACA GAAATATACT CGGTAGAGGT    900
 901 GGATTTGGTA AGGTTTATAA GGGCCGGTTA GCTGATGGCT CTTTAGTTGC AGTGAAAAGA    960
 961 CTAAAAGAGG AACGTACTCA AGGTGGAGAG TTACAGTTCC AGACAGAAGT AGAAATGATC   1020
1021 AGCATGGCTG TACACCGAAA CCTACTTCGT TTACGGGGCT TTTGCATGAC ACCCACTGAG   1080
1081 CGCGTGCTTG TTTATCCTTA CATGGAGAAT GGAAGTGTTG CATCACGTTT AAGAGAGAGG   1140
1141 CCTGAATCAG AGCCCCCACT TGACTGGCCA AAAAGGAAGC GTATTGCACT TGGATCTGCA   1200
1201 AGAGGCCTTG CTTACTTGCA TGATCATTGT GATCCTAAAA TTATTCATCG TGACGTCAAA   1260
1261 GCCGCAAATA TCTTGTTGGA TGAGGAGTTT GAAGCAGTTG TTGGGGATTT TGGGTTAGCT   1320
1321 AAACTCATGG ACTACAAGGA TACTCATGTT ACCACTGCTG TACGTGGTAC AATTGGGCAT   1380
1381 ATTGCCCCTG AATATTTATC TACTGGTAAA TCTTCTGAGA AAACTGATGT CTTTGGCTAT   1440
1441 GGGGTTATGC TTCTAGAGCT CATAACTGGG CAAAGGGCTT TTGATCTTGC TCGACTTGCG   1500
1501 AATGATGATG ATGTCATGCT GCTAGATTGG GTGAAGGGAC TCCTGAAGGA CAAGAAATAT   1560
1561 GAAACATTAG TTGATGCAGA TCTTCAAGGT AATTACAATG AAGAAGAGGT GGAACAACTT   1620
1621 ATTCAGGTAG CTCTACTTTG CACGCAGAGT ACGCCTACGG AACGTCCAAA GATGTCAGAA   1680
1681 GTTGTAAGAA TGCTTGAAGG TGATGGCCTT GCTGAGAGGT GGGAGGAATG GCAAAAGGAG   1740
1741 GAGATGTTCC GGCAAGATTA CAACCATGTA CACCACCCCC ATACTGATTG GATAATAGCT   1800
1801 GACTCCACGT CAAATATCCG ACCGGATGAG TTGTCAGGGC CAAGATGA   1848
```

⊖ Description of matched genes — Help

Gene	Matches	Functional Description
Niben101Scf11779g01002.1	503	sp|O48837|LRKS2_ARATH *-** Receptor like protein kinase S.2
Niben101Scf00279g02022.1	430	sp|O48837|LRKS2_ARATH *-** Receptor like protein kinase S.2
Niben101Scf02128g00022.1	117	sp|Q9LHP4|RCH2_ARATH *-** Receptor-like protein kinase 2
Niben101Scf02513g11004.1	102	sp|Q9LHP4|RCH2_ARATH *-** Receptor-like protein kinase 2
Niben101Scf00941g02003.1	5	sp|O48837|LRKS2_ARATH *-** Receptor like protein kinase S.2
Niben101Scf02128g00037.1	4	sp|Q9LHE7|FYPP3_ARATH *-*- Phytochrome-associated serine/threonine-protein phosphatase 3
Niben101Scf10498g01003.1	1	AT5G19450.1 *-** calcium-dependent protein kinase 19 LENGTH=533

S Tool output



SGN VIGS Tool

⊕ INPUT

⊖ OUTPUT

⊖ Modify Parameters   Help

Best target region score: 68.33 (-∞—100)

Region Start: 881 **Region End:** 1180 Set Custom Region

Target genes: 2 **Fragment size:** 300 **n-mer:** 21 **Mismatches:**

⊖ Distribution of n-mers

⊖ Predicted Construct   Help

```
>best_target_region_(881-1180)
GAAATATACTCGGTAGAGGTGGATTTGGTAAGGTTTATAAGGGCCGGTTAGCTGATGGCT
CTTTAGTTGCAGTGAAAAGACTAAAAGAGGAACGTACTCAAGGTGGAGAGTTACAGTTCC
AGACAGAAGTAGAAATGATCAGCATGGCTGTACACCGAAACCTACTTCGTTTACGGGGCT
TTTGCATGACACCCACTGAGCGCGTGCTTGTTTATCCTTACATGGAGAATGGAAGTGTTG
CATCACGTTTAAGAGAGAGGCCTGAATCAGAGCCCCCACTTGACTGGCCAAAAAGGAAGC
```

⊖ Sequence Overview   Help

```
   1 ATGGATCAGT CGGTGTTGGC GATCTGGGTA TTTCTCTGCT TAATTGGTCT GCTTTTCAAT     60
  61 TTGTCACCCG TCGCCGGTAA CGCTGAAGGT GATGCCTTGA ATGCTCTGAA GACAAATTTG    120
 121 GCTGATCCTA ATAGTGTTCT ACAGAGTTGG GATGCAACCC TTGTTAATCC TTGTACTTGG    180
 181 TTCCATGTGA CATGCAACAA TGAAAATAGT GTGACTAGAG TTGATCTAGG AAATGCAAAT    240
 241 CTATCAGGTC AACTGGTACC ACAGCTTGGC CAACTCCAGA AATTGCAGTA CTTGGAACTT    300
 301 TATAGTAATA ACATAAGCGG AAGAATTCCA AATGAACTGG GAAACTTGAC AGAGTTGGTT    360
 361 AGTTTGGATC TTTACCTGAA CAACTTAAAT GGTCCTATTC CTCCCTCATT GGGCAGGCTT    420
 421 CAGAAGCTAC GCTTCCTGAG GCTCAATAAT AACAGTTTGA ATGAAGGTAT TCCCATGTCT    480
 481 CTAACCACCA TTGTTGCACT TCAAGTACTT GATCTCTCAA ACAACCATTT GACAGGACTA    540
 541 GTTCCAGTCA ACGGTTCCTT TTCACTTTTT ACTCCTATAA GTTTTGCTAA TAATCAGTTG    600
 601 GAAGTTCCTC CAGTTTCTCC ACCTCCTCCT CTTCCTCCTA CACCCTCATC GTCATCTTCA    660
 661 GTGGGCAACA GCGCAACTGG AGCTATCGCT GGAGGAGTTG CTGCAGGCGC TGCTCTTCTA    720
 721 TTTGCAGCTC CTGCAATTTT TCTTGCTTGG TGGCGTCGGA GGAAACCACA AGACCACTTC    780
 781 TTTGATGTTC CTGCTGAGGA GGATCCAGAA GTTCATCTGG GACAACTCAA AAGGTTTTCC    840
 841 TTGCGTGAAC TACAAGTTGC GTCGGATAAT TTTAGCAACA GAAATATACT CGGTAGAGGT    900
 901 GGATTTGGTA AGGTTTATAA GGGCCGGTTA GCTGATGGCT CTTTAGTTGC AGTGAAAAGA    960
 961 CTAAAAGAGG AACGTACTCA AGGTGGAGAG TTACAGTTCC AGACAGAAGT AGAAATGATC   1020
1021 AGCATGGCTG TACACCGAAA CCTACTTCGT TTACGGGGCT TTTGCATGAC ACCCACTGAG   1080
1081 CGCGTGCTTG TTTATCCTTA CATGGAGAAT GGAAGTGTTG CATCACGTTT AAGAGAGAGG   1140
1141 CCTGAATCAG AGCCCCCACT TGACTGGCCA AAAAGGAAGC GTATTGCACT TGGATCTGCA   1200
1201 AGAGGCCTTG CTTACTTGCA TGATCATTGT GATCCTAAAA TTATTCATCG TGACGTCAAA   1260
1261 GCCGCAAATA TCTTGTTGGA TGAGGAGTTT GAAGCAGTTG TTGGGGATTT TGGGTTAGCT   1320
1321 AAACTCATGG ACTACAAGGA TACTCATGTT ACCACTGCTG TACGTGGTAC AATTGGGCAT   1380
1381 ATTGCCCCTG AATATTTATC TACTGGTAAA TCTTCTGAGA AAACTGATGT CTTTGGCTAT   1440
1441 GGGGTTATGC TTCTAGAGCT CATAACTGGG CAAAGGGCTT TTGATCTTGC TCGACTTGCG   1500
1501 AATGATGATG ATGTCATGCT GCTAGATTGG GTGAAGGGAC TCCTGAAGGA CAAGAAATAT   1560
1561 GAAACATTAG TTGATGCAGA TCTTCAAGGT AATTACAATG AAGAAGAGGT GGAACAACTT   1620
1621 ATTCAGGTAG CTCTACTTTG CACGCAGAGT ACGCCTACGG AACGTCCAAA GATGTCAGAA   1680
1681 GTTGTAAGAA TGCTTGAAGG TGATGGCCTT GCTGAGAGGT GGGAGGAATG GCAAAAGGAG   1740
1741 GAGATGTTCC GGCAAGATTA CAACCATGTA CACCACCCCC ATACTGATTG GATAATAGCT   1800
1801 GACTCCACGT CAAATATCCG ACCGGATGAG TTGTCAGGGC CAAGATGA   1848
```

⊖ Description of matched genes   Help

Gene	Matches	Functional Description
Niben101Scf11779g01002.1	503	sp|O48837|LRKS2_ARATH *-** Receptor like protein kinase S.2
Niben101Scf00279g02022.1	430	sp|O48837|LRKS2_ARATH *-** Receptor like protein kinase S.2
Niben101Scf02128g00022.1	117	sp|Q9LHP4|RCH2_ARATH *-** Receptor-like protein kinase 2
Niben101Scf02513g11004.1	102	sp|Q9LHP4|RCH2_ARATH *-** Receptor-like protein kinase 2
Niben101Scf00941g02003.1	5	sp|O48837|LRKS2_ARATH *-** Receptor like protein kinase S.2
Niben101Scf02128g00037.1	4	sp|Q9LHE7|FYPP3_ARATH *-*- Phytochrome-associated serine/threonine-protein phosphatase 3
Niben101Scf10498g01003.1	1	AT5G19450.1 *-** calcium-dependent protein kinase 19 LENGTH=533

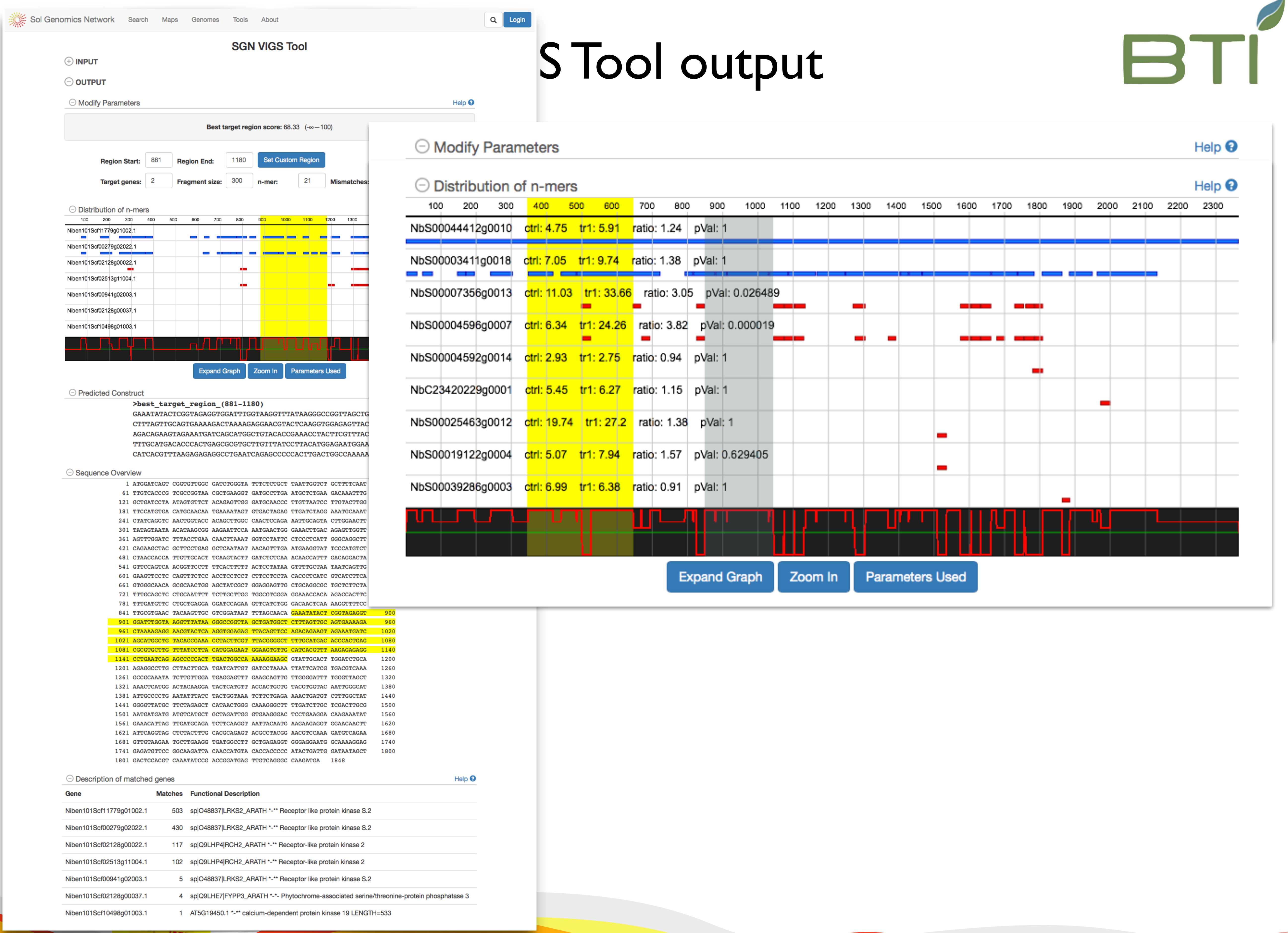
⊖ Modify Parameters   Help

Best target region score: 82.83 **Custom region score:** 99.23 (-∞—100)

Region Start: 850 **Region End:** 1044 Set Custom Region

Target genes: 2 **Fragment size:** 195 **n-mer:** 21 **Mismatches:** 0 Change

S Tool output



SGN VIGS Tool

⊕ INPUT

⊖ OUTPUT

⊖ Modify Parameters

Best target region score: 68.33 (-∞—100)

Region Start: 881 **Region End:** 1180

Target genes: 2 **Fragment size:** 300 **n-mer:** 21 **Mismatches:**

⊖ Distribution of n-mers

⊖ Predicted Construct

```
>best_target_region_(881-1180)
GAAATATACTCGGTAGAGGTGGATTTGGTAAGGTTTATAAGGGCCGGTTAGCTG
CTTTAGTTGCAGTGAAAAGACTAAAAGAGGAACGTACTCAAGGTGGAGAGTTAC
AGACAGAAGTAGAAATGATCAGCATGGCTGTACACCGAAACCTACTTCGTTTAC
TTTGCATGACACCCACTGAGCGCGTGCTTGTTTATCCTTACATGGAGAATGGAA
CATCACGTTTAAGAGAGAGGCCTGAATCAGAGCCCCCACTTGACTGGCCAAAAA
```

⊖ Sequence Overview

```
   1 ATGGATCAGT CGGTGTTGGC GATCTGGGTA TTTCTCTGCT TAATTGGTCT GCTTTTCAAT
  61 TTGTCACCCG TCGCCGGTAA CGCTGAAGGT GATGCCTTGA ATGCTCTGAA GACAAATTTG
 121 GCTGATCCTA ATAGTGTTCT ACAGAGTTGG GATGCAACCC TTGTTAATCC TTGTACTTGG
 181 TTCCATGTGA CATGCAACAA TGAAAATAGT GTGACTAGAG TTGATCTAGG AAATGCAAAT
 241 CTATCAGGTC AACTGGTACC ACAGCTTGGC CAACTCCAGA AATTGCAGTA CTTGGAACTT
 301 TATAGTAATA ACATAAGCGG AAGAATTCCA AATGAACTGG GAAACTTGAC AGAGTTGGTT
 361 AGTTTGGATC TTTACCTGAA CAACTTAAAT GGTCCTATTC CTCCCTCATT GGGCAGGCTT
 421 CAGAAGCTAC GCTTCCTGAG GCTCAATAAT AACAGTTTGA ATGAAGGTAT TCCCATGTCT
 481 CTAACCACCA TTGTTGCACT TCAAGTACTT GATCTCTCAA ACAACCATTT GACAGGACTA
 541 GTTCCAGTCA ACGGTTCCTT TTCACTTTTT ACTCCTATAA GTTTTGCTAA TAATCAGTTG
 601 GAAGTTCCTC CAGTTTCTCC ACCTCCTCCT CTTCCTCCTA CACCCTCATC GTCATCTTCA
 661 GTGGGCAACA GCGCAACTGG AGCTATCGCT GGAGGAGTTG CTGCAGGCGC TGCTCTTCTA
 721 TTTGCAGCTC CTGCAATTTT TCTTGCTTGG TGGCGTCGGA GGAAACCACA AGACCACTTC
 781 TTTGATGTTC CTGCTGAGGA GGATCCAGAA GTTCATCTGG GACAACTCAA AAGGTTTTCC
 841 TTGCGTGAAC TACAAGTTGC GTCGGATAAT TTTAGCAACA GAAATATACT CGGTAGAGGT    900
 901 GGATTTGGTA AGGTTTATAA GGGCCGGTTA GCTGATGGCT CTTTAGTTGC AGTGAAAAGA    960
 961 CTAAAAGAGG AACGTACTCA AGGTGGAGAG TTACAGTTCC AGACAGAAGT AGAAATGATC   1020
1021 AGCATGGCTG TACACCGAAA CCTACTTCGT TTACGGGGCT TTTGCATGAC ACCCACTGAG   1080
1081 CGCGTGCTTG TTTATCCTTA CATGGAGAAT GGAAGTGTTG CATCACGTTT AAGAGAGAGG   1140
1141 CCTGAATCAG AGCCCCCACT TGACTGGCCA AAAAGGAAGC GTATTGCACT TGGATCTGCA   1200
1201 AGAGGCCTTG CTTACTTGCA TGATCATTGT GATCCTAAAA TTATTCATCG TGACGTCAAA   1260
1261 GCCGCAAATA TCTTGTTGGA TGAGGAGTTT GAAGCAGTTG TTGGGGATTT TGGGTTAGCT   1320
1321 AAACTCATGG ACTACAAGGA TACTCATGTT ACCACTGCTG TACGTGGTAC AATTGGGCAT   1380
1381 ATTGCCCCTG AATATTTATC TACTGGTAAA TCTTCTGAGA AAACTGATGT CTTTGGCTAT   1440
1441 GGGGTTATGC TTCTAGAGCT CATAACTGGG CAAAGGGCTT TTGATCTTGC TCGACTTGCG   1500
1501 AATGATGATG ATGTCATGCT GCTAGATTGG GTGAAGGGAC TCCTGAAGGA CAAGAAATAT   1560
1561 GAAACATTAG TTGATGCAGA TCTTCAAGGT AATTACAATG AAGAAGAGGT GGAACAACTT   1620
1621 ATTCAGGTAG CTCTACTTTG CACGCAGAGT ACGCCTACGG AACGTCCAAA GATGTCAGAA   1680
1681 GTTGTAAGAA TGCTTGAAGG TGATGGCCTT GCTGAGAGGT GGGAGGAATG GCAAAAGGAG   1740
1741 GAGATGTTCC GGCAAGATTA CAACCATGTA CACCACCCCC ATACTGATTG GATAATAGCT   1800
1801 GACTCCACGT CAAATATCCG ACCGGATGAG TTGTCAGGGC CAAGATGA   1848
```

⊖ Description of matched genes

Gene	Matches	Functional Description
Niben101Scf11779g01002.1	503	sp|O48837|LRKS2_ARATH *-** Receptor like protein kinase S.2
Niben101Scf00279g02022.1	430	sp|O48837|LRKS2_ARATH *-** Receptor like protein kinase S.2
Niben101Scf02128g00022.1	117	sp|Q9LHP4|RCH2_ARATH *-** Receptor-like protein kinase 2
Niben101Scf02513g11004.1	102	sp|Q9LHP4|RCH2_ARATH *-** Receptor-like protein kinase 2
Niben101Scf00941g02003.1	5	sp|O48837|LRKS2_ARATH *-** Receptor like protein kinase S.2
Niben101Scf02128g00037.1	4	sp|Q9LHE7|FYPP3_ARATH *-*- Phytochrome-associated serine/threonine-protein phosphatase 3
Niben101Scf10498g01003.1	1	AT5G19450.1 *-** calcium-dependent protein kinase 19 LENGTH=533

⊖ Modify Parameters

⊖ Distribution of n-mers

NbS00044412g0010 ctrl: 4.75 tr1: 5.91 ratio: 1.24 pVal: 1

NbS00003411g0018 ctrl: 7.05 tr1: 9.74 ratio: 1.38 pVal: 1

NbS00007356g0013 ctrl: 11.03 tr1: 33.66 ratio: 3.05 pVal: 0.026489

NbS00004596g0007 ctrl: 6.34 tr1: 24.26 ratio: 3.82 pVal: 0.000019

NbS00004592g0014 ctrl: 2.93 tr1: 2.75 ratio: 0.94 pVal: 1

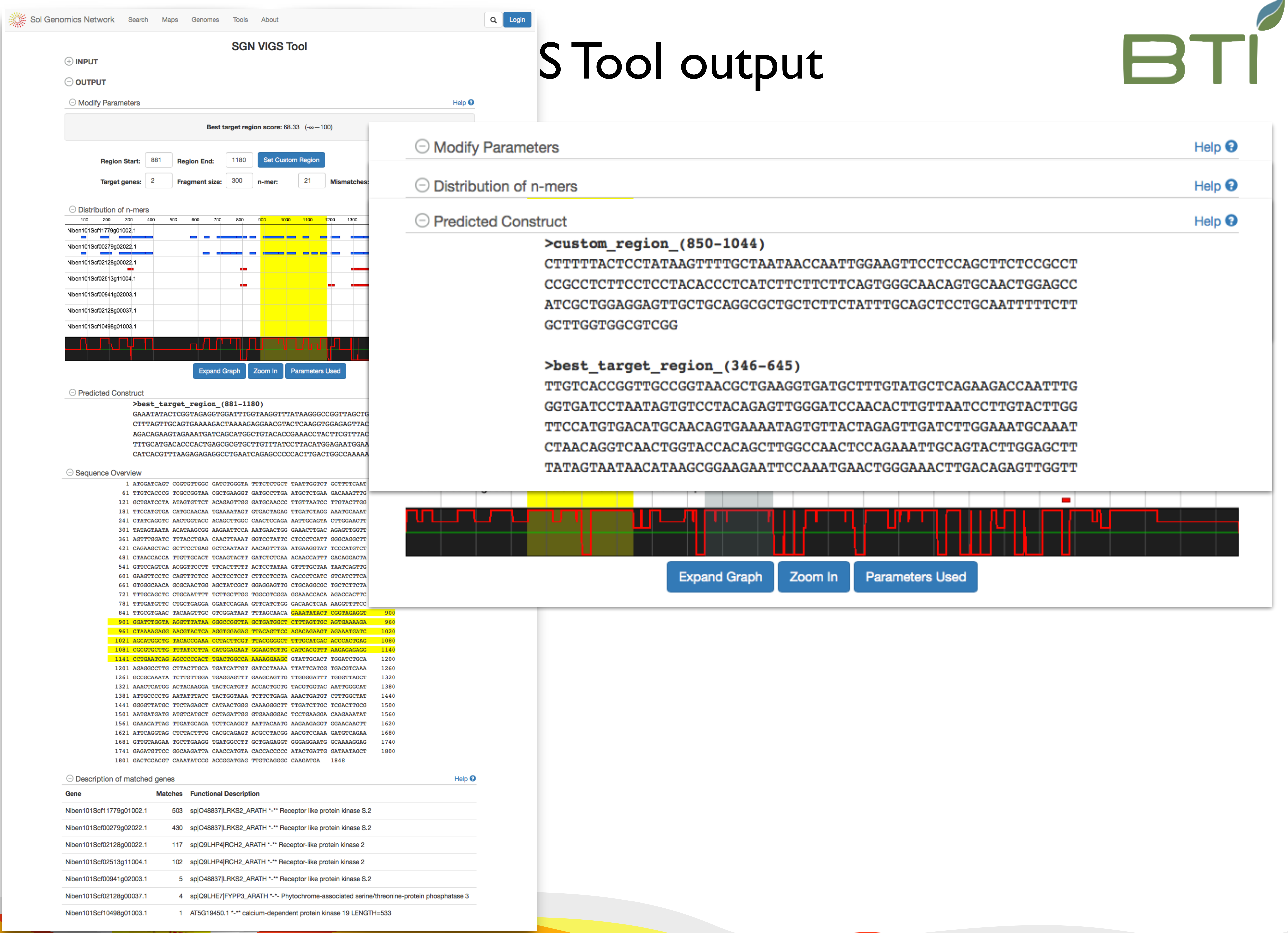
NbC23420229g0001 ctrl: 5.45 tr1: 6.27 ratio: 1.15 pVal: 1

NbS00025463g0012 ctrl: 19.74 tr1: 27.2 ratio: 1.38 pVal: 1

NbS00019122g0004 ctrl: 5.07 tr1: 7.94 ratio: 1.57 pVal: 0.629405

NbS00039286g0003 ctrl: 6.99 tr1: 6.38 ratio: 0.91 pVal: 1

S Tool output



SGN VIGS Tool

⊕ INPUT

⊖ OUTPUT

⊖ Modify Parameters Help

Best target region score: 68.33 (-∞—100)

Region Start: 881 **Region End:** 1180

Target genes: 2 **Fragment size:** 300 **n-mer:** 21 **Mismatches:**

⊖ Distribution of n-mers

⊖ Predicted Construct

```
>best_target_region_(881-1180)
GAAATATACTCGGTAGAGGTGGATTTGGTAAGGTTTATAAGGGCCGGTTAGCTG
CTTTAGTTGCAGTGAAAAGACTAAAAGAGGAACGTACTCAAGGTGGAGAGTTAC
AGACAGAAGTAGAAATGATCAGCATGGCTGTACACCGAAACCTACTTCGTTTAC
TTTGCATGACACCCACTGAGCGCGTGCTTGTTTATCCTTACATGGAGAATGGAA
CATCACGTTTAAGAGAGAGGCCTGAATCAGAGCCCCCACTTGACTGGCCAAAAA
```

⊖ Sequence Overview

```
   1 ATGGATCAGT CGGTGTTGGC GATCTGGGTA TTTCTCTGCT TAATTGGTCT GCTTTTCAAT
  61 TTGTCACCCG TCGCCGGTAA CGCTGAAGGT GATGCCTTGA ATGCTCTGAA GACAAATTTG
 121 GCTGATCCTA ATAGTGTTCT ACAGAGTTGG GATGCAACCC TTGTTAATCC TTGTACTTGG
 181 TTCCATGTGA CATGCAACAA TGAAAATAGT GTGACTAGAG TTGATCTAGG AAATGCAAAT
 241 CTATCAGGTC AACTGGTACC ACAGCTTGGC CAACTCCAGA AATTGCAGTA CTTGGAACTT
 301 TATAGTAATA ACATAAGCGG AAGAATTCCA AATGAACTGG GAAACTTGAC AGAGTTGGTT
 361 AGTTTGGATC TTTACCTGAA CAACTTAAAT GGTCCTATTC CTCCCTCATT GGGCAGGCTT
 421 CAGAAGCTAC GCTTCCTGAG GCTCAATAAT AACAGTTTGA ATGAAGGTAT TCCCATGTCT
 481 CTAACCACCA TTGTTGCACT TCAAGTACTT GATCTCTCAA ACAACCATTT GACAGGACTA
 541 GTTCCAGTCA ACGGTTCCTT TTCACTTTTT ACTCCTATAA GTTTTGCTAA TAATCAGTTG
 601 GAAGTTCCTC CAGTTTCTCC ACCTCCTCCT CTTCCTCCTA CACCCTCATC GTCATCTTCA
 661 GTGGGCAACA GCGCAACTGG AGCTATCGCT GGAGGAGTTG CTGCAGGCGC TGCTCTTCTA
 721 TTTGCAGCTC CTGCAATTTT TCTTGCTTGG TGGCGTCGGA GGAAACCACA AGACCACTTC
 781 TTTGATGTTC CTGCTGAGGA GGATCCAGAA GTTCATCTGG GACAACTCAA AAGGTTTTCC
 841 TTGCGTGAAC TACAAGTTGC GTCGGATAAT TTTAGCAACA GAAATATACT CGGTAGAGGT    900
 901 GGATTTGGTA AGGTTTATAA GGGCCGGTTA GCTGATGGCT CTTTAGTTGC AGTGAAAAGA    960
 961 CTAAAAGAGG AACGTACTCA AGGTGGAGAG TTACAGTTCC AGACAGAAGT AGAAATGATC   1020
1021 AGCATGGCTG TACACCGAAA CCTACTTCGT TTACGGGGCT TTTGCATGAC ACCCACTGAG   1080
1081 CGCGTGCTTG TTTATCCTTA CATGGAGAAT GGAAGTGTTG CATCACGTTT AAGAGAGAGG   1140
1141 CCTGAATCAG AGCCCCCACT TGACTGGCCA AAAAGGAAGC GTATTGCACT TGGATCTGCA   1200
1201 AGAGGCCTTG CTTACTTGCA TGATCATTGT GATCCTAAAA TTATTCATCG TGACGTCAAA   1260
1261 GCCGCAAATA TCTTGTTGGA TGAGGAGTTT GAAGCAGTTG TTGGGGATTT TGGGTTAGCT   1320
1321 AAACTCATGG ACTACAAGGA TACTCATGTT ACCACTGCTG TACGTGGTAC AATTGGGCAT   1380
1381 ATTGCCCCTG AATATTTATC TACTGGTAAA TCTTCTGAGA AAACTGATGT CTTTGGCTAT   1440
1441 GGGGTTATGC TTCTAGAGCT CATAACTGGG CAAAGGGCTT TTGATCTTGC TCGACTTGCG   1500
1501 AATGATGATG ATGTCATGCT GCTAGATTGG GTGAAGGGAC TCCTGAAGGA CAAGAAATAT   1560
1561 GAAACATTAG TTGATGCAGA TCTTCAAGGT AATTACAATG AAGAAGAGGT GGAACAACTT   1620
1621 ATTCAGGTAG CTCTACTTTG CACGCAGAGT ACGCCTACGG AACGTCCAAA GATGTCAGAA   1680
1681 GTTGTAAGAA TGCTTGAAGG TGATGGCCTT GCTGAGAGGT GGGAGGAATG GCAAAAGGAG   1740
1741 GAGATGTTCC GGCAAGATTA CAACCATGTA CACCACCCCC ATACTGATTG GATAATAGCT   1800
1801 GACTCCACGT CAAATATCCG ACCGGATGAG TTGTCAGGGC CAAGATGA   1848
```

⊖ Description of matched genes Help

Gene	Matches	Functional Description
Niben101Scf11779g01002.1	503	sp|O48837|LRKS2_ARATH *-** Receptor like protein kinase S.2
Niben101Scf00279g02022.1	430	sp|O48837|LRKS2_ARATH *-** Receptor like protein kinase S.2
Niben101Scf02128g00022.1	117	sp|Q9LHP4|RCH2_ARATH *-** Receptor-like protein kinase 2
Niben101Scf02513g11004.1	102	sp|Q9LHP4|RCH2_ARATH *-** Receptor-like protein kinase 2
Niben101Scf00941g02003.1	5	sp|O48837|LRKS2_ARATH *-** Receptor like protein kinase S.2
Niben101Scf02128g00037.1	4	sp|Q9LHE7|FYPP3_ARATH *-*- Phytochrome-associated serine/threonine-protein phosphatase 3
Niben101Scf10498g01003.1	1	AT5G19450.1 *-** calcium-dependent protein kinase 19 LENGTH=533

⊖ Modify Parameters Help

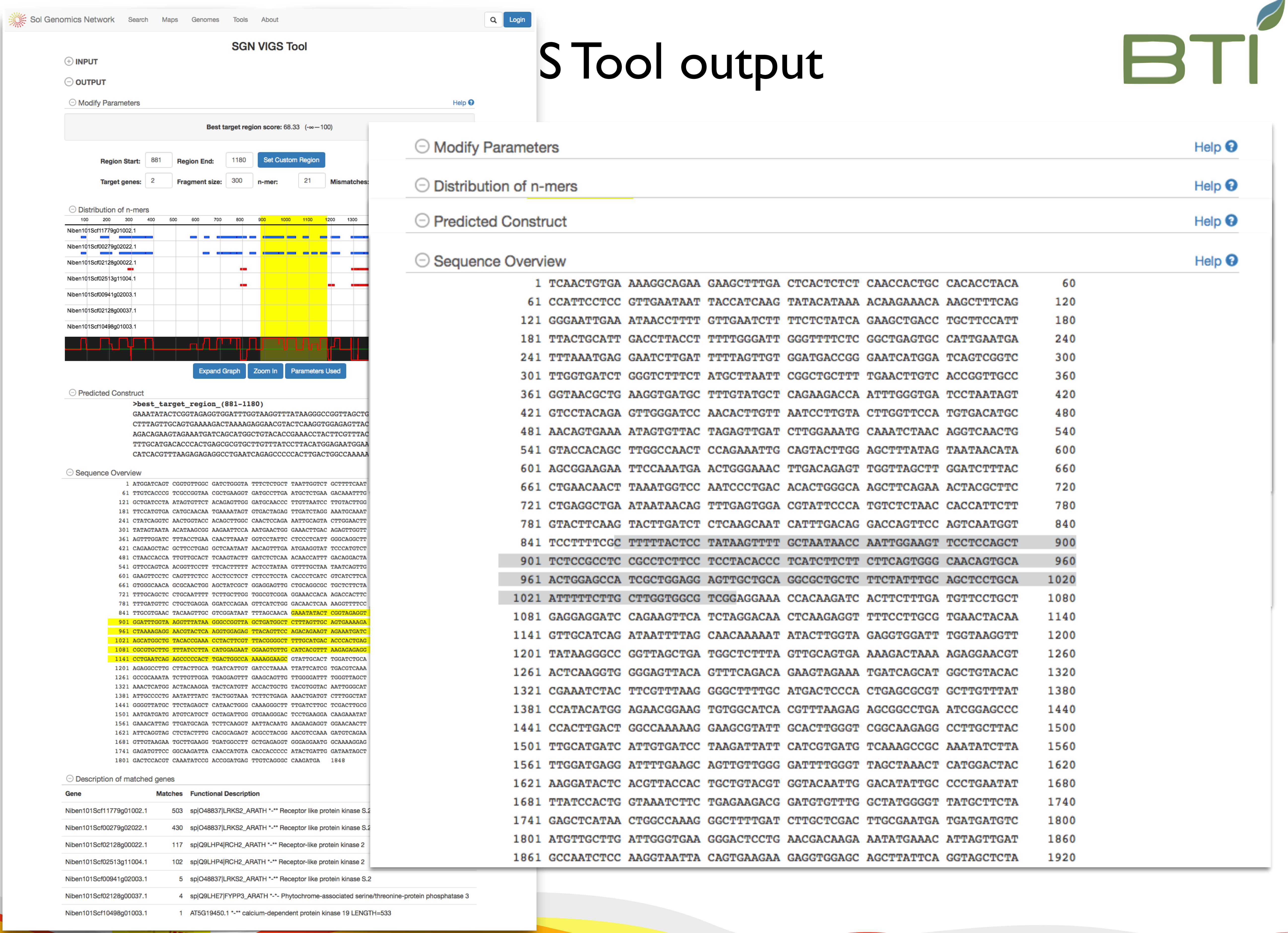
⊖ Distribution of n-mers Help

⊖ Predicted Construct Help

```
>custom_region_(850-1044)
CTTTTTACTCCTATAAGTTTTGCTAATAACCAATTGGAAGTTCCTCCAGCTTCTCCGCCT
CCGCCTCTTCCTCCTACACCCTCATCTTCTTCTTCAGTGGGCAACAGTGCAACTGGAGCC
ATCGCTGGAGGAGTTGCTGCAGGCGCTGCTCTTCTATTTGCAGCTCCTGCAATTTTTCTT
GCTTGGTGGCGTCGG

>best_target_region_(346-645)
TTGTCACCGGTTGCCGGTAACGCTGAAGGTGATGCTTTGTATGCTCAGAAGACCAATTTG
GGTGATCCTAATAGTGTCCTACAGAGTTGGGATCCAACACTTGTTAATCCTTGTACTTGG
TTCCATGTGACATGCAACAGTGAAAATAGTGTTACTAGAGTTGATCTTGGAAATGCAAAT
CTAACAGGTCAACTGGTACCACAGCTTGGCCAACTCCAGAAATTGCAGTACTTGGAGCTT
TATAGTAATAACATAAGCGGAAGAATTCCAAATGAACTGGGAAACTTGACAGAGTTGGTT
```

S Tool output



SGN VIGS Tool

⊕ INPUT

⊖ OUTPUT

⊖ Modify Parameters

Best target region score: 68.33 (-∞—100)

Region Start: 881 **Region End:** 1180 Set Custom Region

Target genes: 2 **Fragment size:** 300 **n-mer:** 21 **Mismatches:**

⊖ Distribution of n-mers

⊖ Predicted Construct

```
>best_target_region_(881-1180)
GAAATATACTCGGTAGAGGTGGATTTGGTAAGGTTTATAAGGGCCGGTTAGCTG
CTTTAGTTGCAGTGAAAAGACTAAAAGAGGAACGTACTCAAGGTGGAGAGTTAC
AGACAGAAGTAGAAATGATCAGCATGGCTGTACACCGAAACCTACTTCGTTTAC
TTTGCATGACACCCACTGAGCGCGTGCTTGTTTATCCTTACATGGAGAATGGAA
CATCACGTTTAAGAGAGAGGCCTGAATCAGAGCCCCCACTTGACTGGCCAAAAA
```

⊖ Sequence Overview

```
   1 ATGGATCAGT CGGTGTTGGC GATCTGGGTA TTTCTCTGCT TAATTGGTCT GCTTTTCAAT
  61 TTGTCACCCG TCGCCGGTAA CGCTGAAGGT GATGCCTTGA ATGCTCTGAA GACAAATTTG
 121 GCTGATCCTA ATAGTGTTCT ACAGAGTTGG GATGCAACCC TTGTTAATCC TTGTACTTGG
 181 TTCCATGTGA CATGCAACAA TGAAAATAGT GTGACTAGAG TTGATCTAGG AAATGCAAAT
 241 CTATCAGGTC AACTGGTACC ACAGCTTGGC CAACTCCAGA AATTGCAGTA CTTGGAACTT
 301 TATAGTAATA ACATAAGCGG AAGAATTCCA AATGAACTGG GAAACTTGAC AGAGTTGGTT
 361 AGTTTGGATC TTTACCTGAA CAACTTAAAT GGTCCTATTC CTCCCTCATT GGGCAGGCTT
 421 CAGAAGCTAC GCTTCCTGAG GCTCAATAAT AACAGTTTGA ATGAAGGTAT TCCCATGTCT
 481 CTAACCACCA TTGTTGCACT TCAAGTACTT GATCTCTCAA ACAACCATTT GACAGGACTA
 541 GTTCCAGTCA ACGGTTCCTT TTCACTTTTT ACTCCTATAA GTTTTGCTAA TAATCAGTTG
 601 GAAGTTCCTC CAGTTTCTCC ACCTCCTCCT CTTCCTCCTA CACCCTCATC GTCATCTTCA
 661 GTGGGCAACA GCGCAACTGG AGCTATCGCT GGAGGAGTTG CTGCAGGCGC TGCTCTTCTA
 721 TTTGCAGCTC CTGCAATTTT TCTTGCTTGG TGGCGTCGGA GGAAACCACA AGACCACTTC
 781 TTTGATGTTC CTGCTGAGGA GGATCCAGAA GTTCATCTGG GACAACTCAA AAGGTTTTCC
 841 TTGCGTGAAC TACAAGTTGC GTCGGATAAT TTTAGCAACA GAAATATACT CGGTAGAGGT
 901 GGATTTGGTA AGGTTTATAA GGGCCGGTTA GCTGATGGCT CTTTAGTTGC AGTGAAAAGA
 961 CTAAAAGAGG AACGTACTCA AGGTGGAGAG TTACAGTTCC AGACAGAAGT AGAAATGATC
1021 AGCATGGCTG TACACCGAAA CCTACTTCGT TTACGGGGCT TTTGCATGAC ACCCACTGAG
1081 CGCGTGCTTG TTTATCCTTA CATGGAGAAT GGAAGTGTTG CATCACGTTT AAGAGAGAGG
1141 CCTGAATCAG AGCCCCCACT TGACTGGCCA AAAAGGAAGC GTATTGCACT TGGATCTGCA
1201 AGAGGCCTTG CTTACTTGCA TGATCATTGT GATCCTAAAA TTATTCATCG TGACGTCAAA
1261 GCCGCAAATA TCTTGTTGGA TGAGGAGTTT GAAGCAGTTG TTGGGGATTT TGGGTTAGCT
1321 AAACTCATGG ACTACAAGGA TACTCATGTT ACCACTGCTG TACGTGGTAC AATTGGGCAT
1381 ATTGCCCCTG AATATTTATC TACTGGTAAA TCTTCTGAGA AAACTGATGT CTTTGGCTAT
1441 GGGGTTATGC TTCTAGAGCT CATAACTGGG CAAAGGGCTT TTGATCTTGC TCGACTTGCG
1501 AATGATGATG ATGTCATGCT GCTAGATTGG GTGAAGGGAC TCCTGAAGGA CAAGAAATAT
1561 GAAACATTAG TTGATGCAGA TCTTCAAGGT AATTACAATG AAGAAGAGGT GGAACAACTT
1621 ATTCAGGTAG CTCTACTTTG CACGCAGAGT ACGCCTACGG AACGTCCAAA GATGTCAGAA
1681 GTTGTAAGAA TGCTTGAAGG TGATGGCCTT GCTGAGAGGT GGGAGGAATG GCAAAAGGAG
1741 GAGATGTTCC GGCAAGATTA CAACCATGTA CACCACCCCC ATACTGATTG GATAATAGCT
1801 GACTCCACGT CAAATATCCG ACCGGATGAG TTGTCAGGGC CAAGATGA   1848
```

⊖ Description of matched genes

Gene	Matches	Functional Description
Niben101Scf11779g01002.1	503	sp|O48837|LRKS2_ARATH *-** Receptor like protein kinase S.2
Niben101Scf00279g02022.1	430	sp|O48837|LRKS2_ARATH *-** Receptor like protein kinase S.2
Niben101Scf02128g00022.1	117	sp|Q9LHP4|RCH2_ARATH *-** Receptor-like protein kinase 2
Niben101Scf02513g11004.1	102	sp|Q9LHP4|RCH2_ARATH *-** Receptor-like protein kinase 2
Niben101Scf00941g02003.1	5	sp|O48837|LRKS2_ARATH *-** Receptor like protein kinase S.2
Niben101Scf02128g00037.1	4	sp|Q9LHE7|FYPP3_ARATH *-*- Phytochrome-associated serine/threonine-protein phosphatase 3
Niben101Scf10498g01003.1	1	AT5G19450.1 *-** calcium-dependent protein kinase 19 LENGTH=533

⊖ Modify Parameters Help

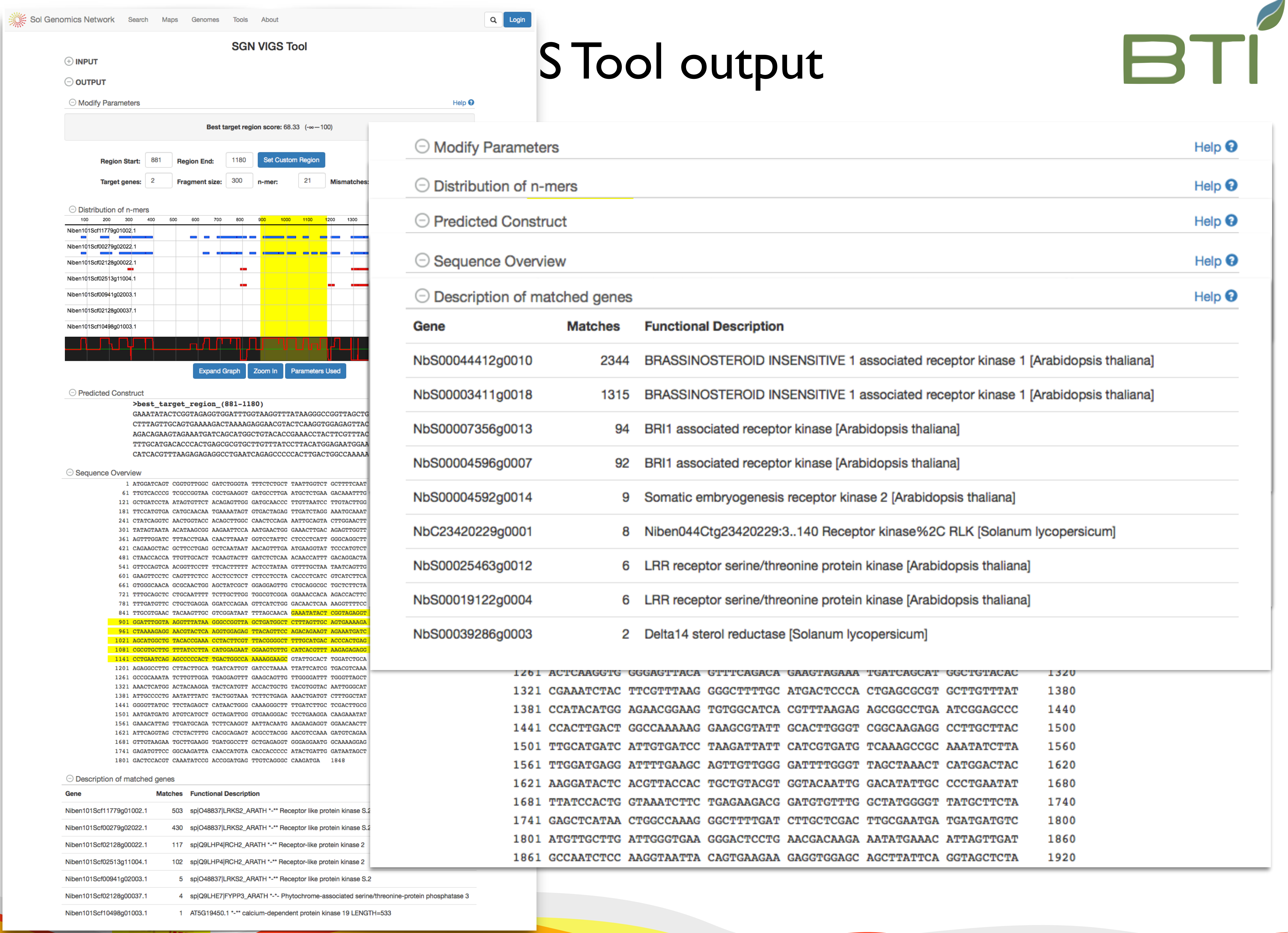
⊖ Distribution of n-mers Help

⊖ Predicted Construct Help

⊖ Sequence Overview Help

```
   1 TCAACTGTGA AAAGGCAGAA GAAGCTTTGA CTCACTCTCT CAACCACTGC CACACCTACA     60
  61 CCATTCCTCC GTTGAATAAT TACCATCAAG TATACATAAA ACAAGAAACA AAGCTTTCAG    120
 121 GGGAATTGAA ATAACCTTTT GTTGAATCTT TTCTCTATCA GAAGCTGACC TGCTTCCATT    180
 181 TTACTGCATT GACCTTACCT TTTTGGGATT GGGTTTTCTC GGCTGAGTGC CATTGAATGA    240
 241 TTTAAATGAG GAATCTTGAT TTTTAGTTGT GGATGACCGG GAATCATGGA TCAGTCGGTC    300
 301 TTGGTGATCT GGGTCTTTCT ATGCTTAATT CGGCTGCTTT TGAACTTGTC ACCGGTTGCC    360
 361 GGTAACGCTG AAGGTGATGC TTTGTATGCT CAGAAGACCA ATTTGGGTGA TCCTAATAGT    420
 421 GTCCTACAGA GTTGGGATCC AACACTTGTT AATCCTTGTA CTTGGTTCCA TGTGACATGC    480
 481 AACAGTGAAA ATAGTGTTAC TAGAGTTGAT CTTGGAAATG CAAATCTAAC AGGTCAACTG    540
 541 GTACCACAGC TTGGCCAACT CCAGAAATTG CAGTACTTGG AGCTTTATAG TAATAACATA    600
 601 AGCGGAAGAA TTCCAAATGA ACTGGGAAAC TTGACAGAGT TGGTTAGCTT GGATCTTTAC    660
 661 CTGAACAACT TAAATGGTCC AATCCCTGAC ACACTGGGCA AGCTTCAGAA ACTACGCTTC    720
 721 CTGAGGCTGA ATAATAACAG TTTGAGTGGA CGTATTCCCA TGTCTCTAAC CACCATTCTT    780
 781 GTACTTCAAG TACTTGATCT CTCAAGCAAT CATTTGACAG GACCAGTTCC AGTCAATGGT    840
 841 TCCTTTTCGC TTTTTACTCC TATAAGTTTT GCTAATAACC AATTGGAAGT TCCTCCAGCT    900
 901 TCTCCGCCTC CGCCTCTTCC TCCTACACCC TCATCTTCTT CTTCAGTGGG CAACAGTGCA    960
 961 ACTGGAGCCA TCGCTGGAGG AGTTGCTGCA GGCGCTGCTC TTCTATTTGC AGCTCCTGCA   1020
1021 ATTTTTCTTG CTTGGTGGCG TCGGAGGAAA CCACAAGATC ACTTCTTTGA TGTTCCTGCT   1080
1081 GAGGAGGATC CAGAAGTTCA TCTAGGACAA CTCAAGAGGT TTTCCTTGCG TGAACTACAA   1140
1141 GTTGCATCAG ATAATTTTAG CAACAAAAAT ATACTTGGTA GAGGTGGATT TGGTAAGGTT   1200
1201 TATAAGGGCC GGTTAGCTGA TGGCTCTTTA GTTGCAGTGA AAAGACTAAA AGAGGAACGT   1260
1261 ACTCAAGGTG GGGAGTTACA GTTTCAGACA GAAGTAGAAA TGATCAGCAT GGCTGTACAC   1320
1321 CGAAATCTAC TTCGTTTAAG GGGCTTTTGC ATGACTCCCA CTGAGCGCGT GCTTGTTTAT   1380
1381 CCATACATGG AGAACGGAAG TGTGGCATCA CGTTTAAGAG AGCGGCCTGA ATCGGAGCCC   1440
1441 CCACTTGACT GGCCAAAAAG GAAGCGTATT GCACTTGGGT CGGCAAGAGG CCTTGCTTAC   1500
1501 TTGCATGATC ATTGTGATCC TAAGATTATT CATCGTGATG TCAAAGCCGC AAATATCTTA   1560
1561 TTGGATGAGG ATTTTGAAGC AGTTGTTGGG GATTTTGGGT TAGCTAAACT CATGGACTAC   1620
1621 AAGGATACTC ACGTTACCAC TGCTGTACGT GGTACAATTG GACATATTGC CCCTGAATAT   1680
1681 TTATCCACTG GTAAATCTTC TGAGAAGACG GATGTGTTTG GCTATGGGGT TATGCTTCTA   1740
1741 GAGCTCATAA CTGGCCAAAG GGCTTTTGAT CTTGCTCGAC TTGCGAATGA TGATGATGTC   1800
1801 ATGTTGCTTG ATTGGGTGAA GGGACTCCTG AACGACAAGA AATATGAAAC ATTAGTTGAT   1860
1861 GCCAATCTCC AAGGTAATTA CAGTGAAGAA GAGGTGGAGC AGCTTATTCA GGTAGCTCTA   1920
```

S Tool output



SGN VIGS Tool

⊕ INPUT

⊖ OUTPUT

⊖ Modify Parameters

Best target region score: 68.33 (-∞—100)

Region Start: 881 **Region End:** 1180

Target genes: 2 **Fragment size:** 300 **n-mer:** 21 **Mismatches:**

⊖ Distribution of n-mers

⊖ Predicted Construct

```
>best_target_region_(881-1180)
GAAATATACTCGGTAGAGGTGGATTTGGTAAGGTTTATAAGGGCCGGTTAGCTG
CTTTAGTTGCAGTGAAAAGACTAAAAGAGGAACGTACTCAAGGTGGAGAGTTAC
AGACAGAAGTAGAAATGATCAGCATGGCTGTACACCGAAACCTACTTCGTTTAC
TTTGCATGACACCCACTGAGCGCGTGCTTGTTTATCCTTACATGGAGAATGGAA
CATCACGTTTAAGAGAGAGGCCTGAATCAGAGCCCCCACTTGACTGGCCAAAAA
```

⊖ Sequence Overview

```
   1 ATGGATCAGT CGGTGTTGGC GATCTGGGTA TTTCTCTGCT TAATTGGTCT GCTTTTCAAT
  61 TTGTCACCCG TCGCCGGTAA CGCTGAAGGT GATGCCTTGA ATGCTCTGAA GACAAATTTG
 121 GCTGATCCTA ATAGTGTTCT ACAGAGTTGG GATGCAACCC TTGTTAATCC TTGTACTTGG
 181 TTCCATGTGA CATGCAACAA TGAAAATAGT GTGACTAGAG TTGATCTAGG AAATGCAAAT
 241 CTATCAGGTC AACTGGTACC ACAGCTTGGC CAACTCCAGA AATTGCAGTA CTTGGAACTT
 301 TATAGTAATA ACATAAGCGG AAGAATTCCA AATGAACTGG GAAACTTGAC AGAGTTGGTT
 361 AGTTTGGATC TTTACCTGAA CAACTTAAAT GGTCCTATTC CTCCCTCATT GGGCAGGCTT
 421 CAGAAGCTAC GCTTCCTGAG GCTCAATAAT AACAGTTTGA ATGAAGGTAT TCCCATGTCT
 481 CTAACCACCA TTGTTGCACT TCAAGTACTT GATCTCTCAA ACAACCATTT GACAGGACTA
 541 GTTCCAGTCA ACGGTTCCTT TTCACTTTTT ACTCCTATAA GTTTTGCTAA TAATCAGTTG
 601 GAAGTTCCTC CAGTTTCTCC ACCTCCTCCT CTTCCTCCTA CACCCTCATC GTCATCTTCA
 661 GTGGGCAACA GCGCAACTGG AGCTATCGCT GGAGGAGTTG CTGCAGGCGC TGCTCTTCTA
 721 TTTGCAGCTC CTGCAATTTT TCTTGCTTGG TGGCGTCGGA GGAAACCACA AGACCACTTC
 781 TTTGATGTTC CTGCTGAGGA GGATCCAGAA GTTCATCTGG GACAACTCAA AAGGTTTTCC
 841 TTGCGTGAAC TACAAGTTGC GTCGGATAAT TTTAGCAACA GAAATATACT CGGTAGAGGT
 901 GGATTTGGTA AGGTTTATAA GGGCCGGTTA GCTGATGGCT CTTTAGTTGC AGTGAAAAGA
 961 CTAAAAGAGG AACGTACTCA AGGTGGAGAG TTACAGTTCC AGACAGAAGT AGAAATGATC
1021 AGCATGGCTG TACACCGAAA CCTACTTCGT TTACGGGGCT TTTGCATGAC ACCCACTGAG
1081 CGCGTGCTTG TTTATCCTTA CATGGAGAAT GGAAGTGTTG CATCACGTTT AAGAGAGAGG
1141 CCTGAATCAG AGCCCCCACT TGACTGGCCA AAAAGGAAGC GTATTGCACT TGGATCTGCA
1201 AGAGGCCTTG CTTACTTGCA TGATCATTGT GATCCTAAAA TTATTCATCG TGACGTCAAA
1261 GCCGCAAATA TCTTGTTGGA TGAGGAGTTT GAAGCAGTTG TTGGGGATTT TGGGTTAGCT
1321 AAACTCATGG ACTACAAGGA TACTCATGTT ACCACTGCTG TACGTGGTAC AATTGGGCAT
1381 ATTGCCCCTG AATATTTATC TACTGGTAAA TCTTCTGAGA AAACTGATGT CTTTGGCTAT
1441 GGGGTTATGC TTCTAGAGCT CATAACTGGG CAAAGGGCTT TTGATCTTGC TCGACTTGCG
1501 AATGATGATG ATGTCATGCT GCTAGATTGG GTGAAGGGAC TCCTGAAGGA CAAGAAATAT
1561 GAAACATTAG TTGATGCAGA TCTTCAAGGT AATTACAATG AAGAAGAGGT GGAACAACTT
1621 ATTCAGGTAG CTCTACTTTG CACGCAGAGT ACGCCTACGG AACGTCCAAA GATGTCAGAA
1681 GTTGTAAGAA TGCTTGAAGG TGATGGCCTT GCTGAGAGGT GGGAGGAATG GCAAAAGGAG
1741 GAGATGTTCC GGCAAGATTA CAACCATGTA CACCACCCCC ATACTGATTG GATAATAGCT
1801 GACTCCACGT CAAATATCCG ACCGGATGAG TTGTCAGGGC CAAGATGA   1848
```

⊖ Description of matched genes

Gene	Matches	Functional Description
Niben101Scf11779g01002.1	503	sp|O48837|LRKS2_ARATH *-** Receptor like protein kinase S.2
Niben101Scf00279g02022.1	430	sp|O48837|LRKS2_ARATH *-** Receptor like protein kinase S.2
Niben101Scf02128g00022.1	117	sp|Q9LHP4|RCH2_ARATH *-** Receptor-like protein kinase 2
Niben101Scf02513g11004.1	102	sp|Q9LHP4|RCH2_ARATH *-** Receptor-like protein kinase 2
Niben101Scf00941g02003.1	5	sp|O48837|LRKS2_ARATH *-** Receptor like protein kinase S.2
Niben101Scf02128g00037.1	4	sp|Q9LHE7|FYPP3_ARATH *-*- Phytochrome-associated serine/threonine-protein phosphatase 3
Niben101Scf10498g01003.1	1	AT5G19450.1 *-** calcium-dependent protein kinase 19 LENGTH=533

⊖ Modify Parameters

⊖ Distribution of n-mers

⊖ Predicted Construct

⊖ Sequence Overview

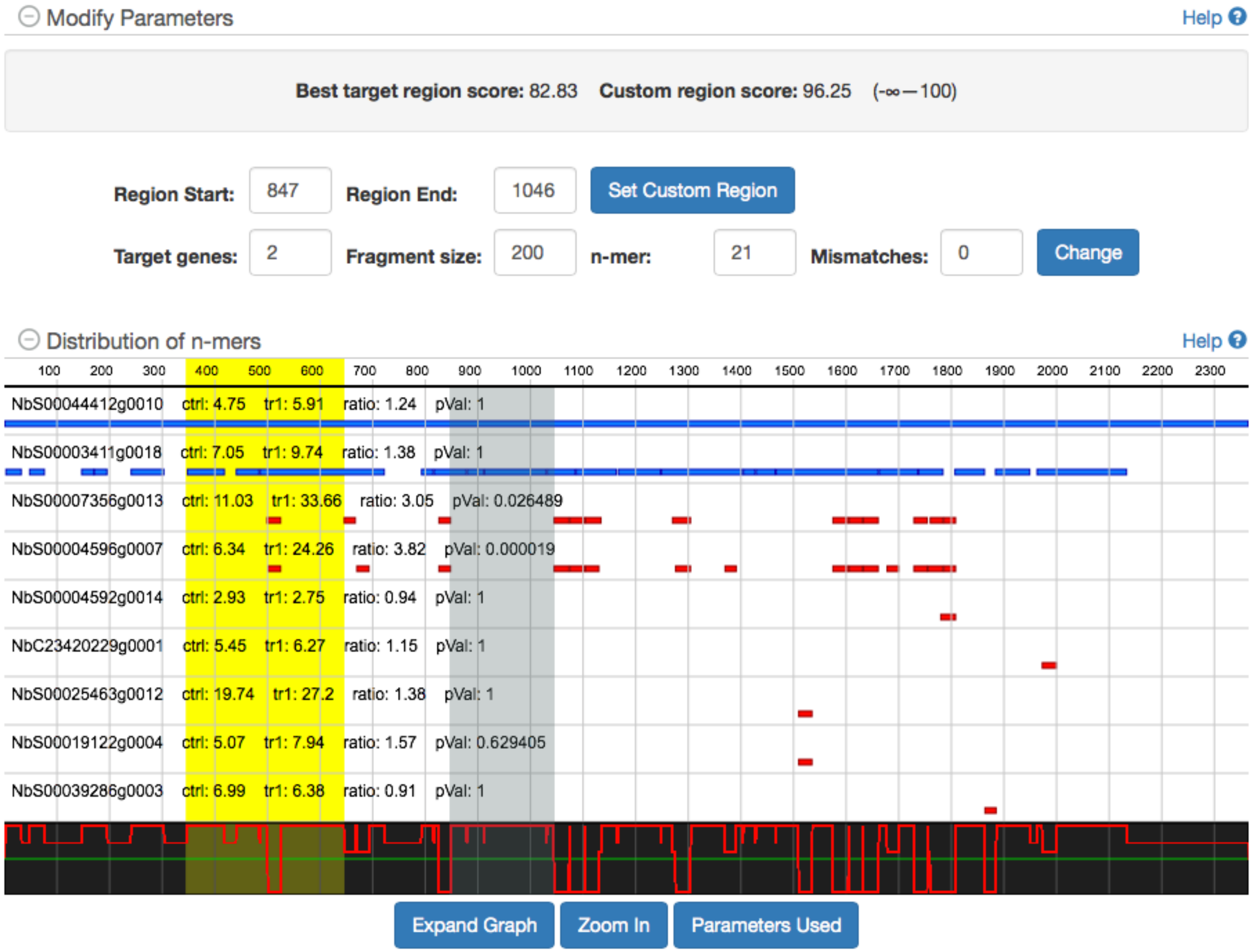
⊖ Description of matched genes

Gene	Matches	Functional Description
NbS00044412g0010	2344	BRASSINOSTEROID INSENSITIVE 1 associated receptor kinase 1 [Arabidopsis thaliana]
NbS00003411g0018	1315	BRASSINOSTEROID INSENSITIVE 1 associated receptor kinase 1 [Arabidopsis thaliana]
NbS00007356g0013	94	BRI1 associated receptor kinase [Arabidopsis thaliana]
NbS00004596g0007	92	BRI1 associated receptor kinase [Arabidopsis thaliana]
NbS00004592g0014	9	Somatic embryogenesis receptor kinase 2 [Arabidopsis thaliana]
NbC23420229g0001	8	Niben044Ctg23420229:3..140 Receptor kinase%2C RLK [Solanum lycopersicum]
NbS00025463g0012	6	LRR receptor serine/threonine protein kinase [Arabidopsis thaliana]
NbS00019122g0004	6	LRR receptor serine/threonine protein kinase [Arabidopsis thaliana]
NbS00039286g0003	2	Delta14 sterol reductase [Solanum lycopersicum]

```
1261 ACTCAAGGTG GGGAGTTACA GTTTCAGACA GAAGTAGAAA TGATCAGCAT GGCTGTACAC   1320
1321 CGAAATCTAC TTCGTTTAAG GGGCTTTTGC ATGACTCCCA CTGAGCGCGT GCTTGTTTAT   1380
1381 CCATACATGG AGAACGGAAG TGTGGCATCA CGTTTAAGAG AGCGGCCTGA ATCGGAGCCC   1440
1441 CCACTTGACT GGCCAAAAAG GAAGCGTATT GCACTTGGGT CGGCAAGAGG CCTTGCTTAC   1500
1501 TTGCATGATC ATTGTGATCC TAAGATTATT CATCGTGATG TCAAAGCCGC AAATATCTTA   1560
1561 TTGGATGAGG ATTTTGAAGC AGTTGTTGGG GATTTTGGGT TAGCTAAACT CATGGACTAC   1620
1621 AAGGATACTC ACGTTACCAC TGCTGTACGT GGTACAATTG GACATATTGC CCCTGAATAT   1680
1681 TTATCCACTG GTAAATCTTC TGAGAAGACG GATGTGTTTG GCTATGGGGT TATGCTTCTA   1740
1741 GAGCTCATAA CTGGCCAAAG GGCTTTTGAT CTTGCTCGAC TTGCGAATGA TGATGATGTC   1800
1801 ATGTTGCTTG ATTGGGTGAA GGGACTCCTG AACGACAAGA AATATGAAAC ATTAGTTGAT   1860
1861 GCCAATCTCC AAGGTAATTA CAGTGAAGAA GAGGTGGAGC AGCTTATTCA GGTAGCTCTA   1920
```

Sol Genomics Network

VIGS Tool output



⊖ Modify Parameters

Best target region score: 82.83 **Custom region score:** 96.25 (-∞—100)

Region Start: 847 **Region End:** 1046

Target genes: 2 **Fragment size:** 200 **n-mer:** 21 **Mismatches:** 0

⊖ Distribution of n-mers

NbS00044412g0010 ctrl: 4.75 tr1: 5.91 ratio: 1.24 pVal: 1

NbS00003411g0018 ctrl: 7.05 tr1: 9.74 ratio: 1.38 pVal: 1

NbS00007356g0013 ctrl: 11.03 tr1: 33.66 ratio: 3.05 pVal: 0.026489

NbS00004596g0007 ctrl: 6.34 tr1: 24.26 ratio: 3.82 pVal: 0.000019

NbS00004592g0014 ctrl: 2.93 tr1: 2.75 ratio: 0.94 pVal: 1

NbC23420229g0001 ctrl: 5.45 tr1: 6.27 ratio: 1.15 pVal: 1

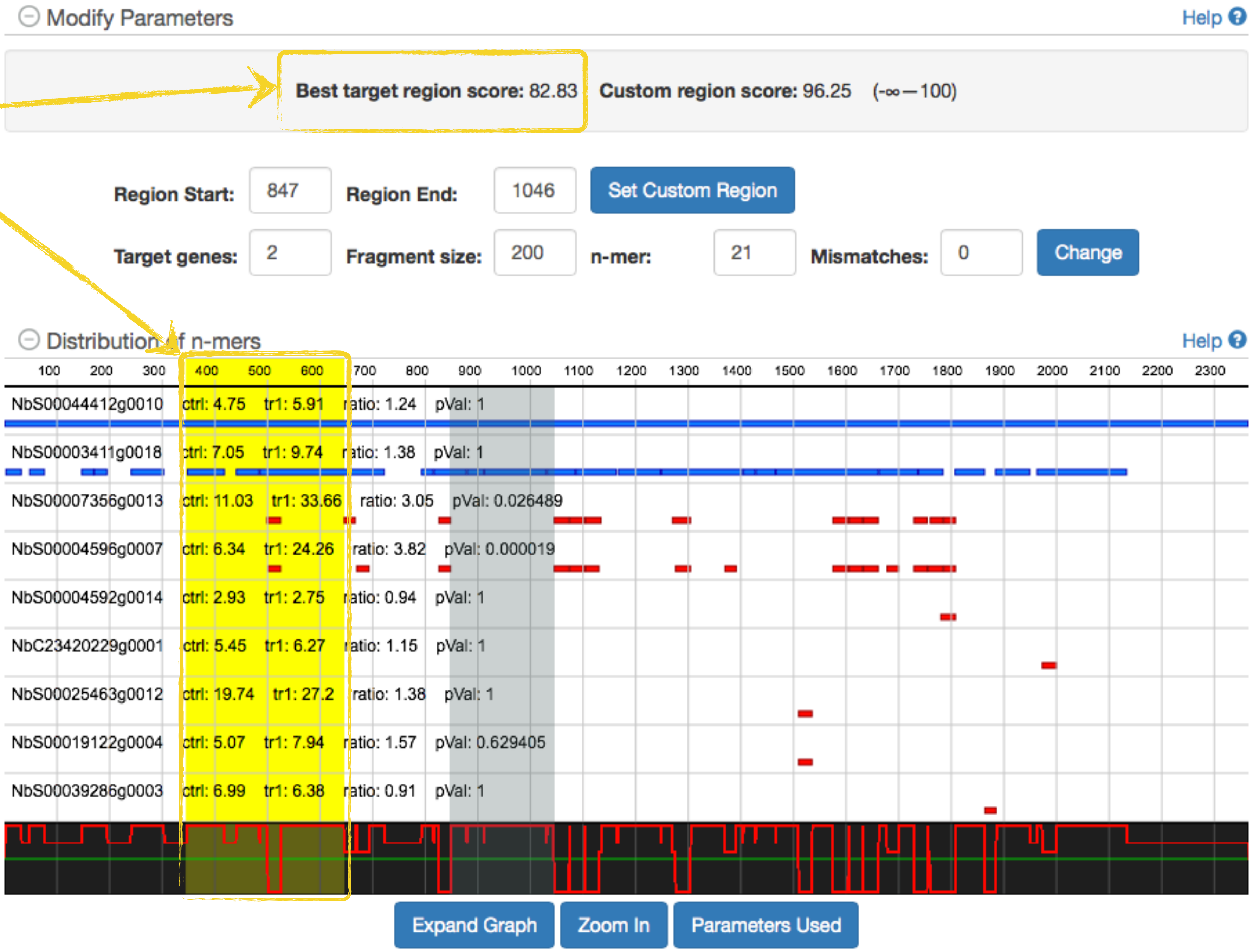
NbS00025463g0012 ctrl: 19.74 tr1: 27.2 ratio: 1.38 pVal: 1

NbS00019122g0004 ctrl: 5.07 tr1: 7.94 ratio: 1.57 pVal: 0.629405

NbS00039286g0003 ctrl: 6.99 tr1: 6.38 ratio: 0.91 pVal: 1

VIGS Tool output

Predicted region



Best target region score: 82.83 **Custom region score:** 96.25 (-∞—100)

Region Start: 847 **Region End:** 1046

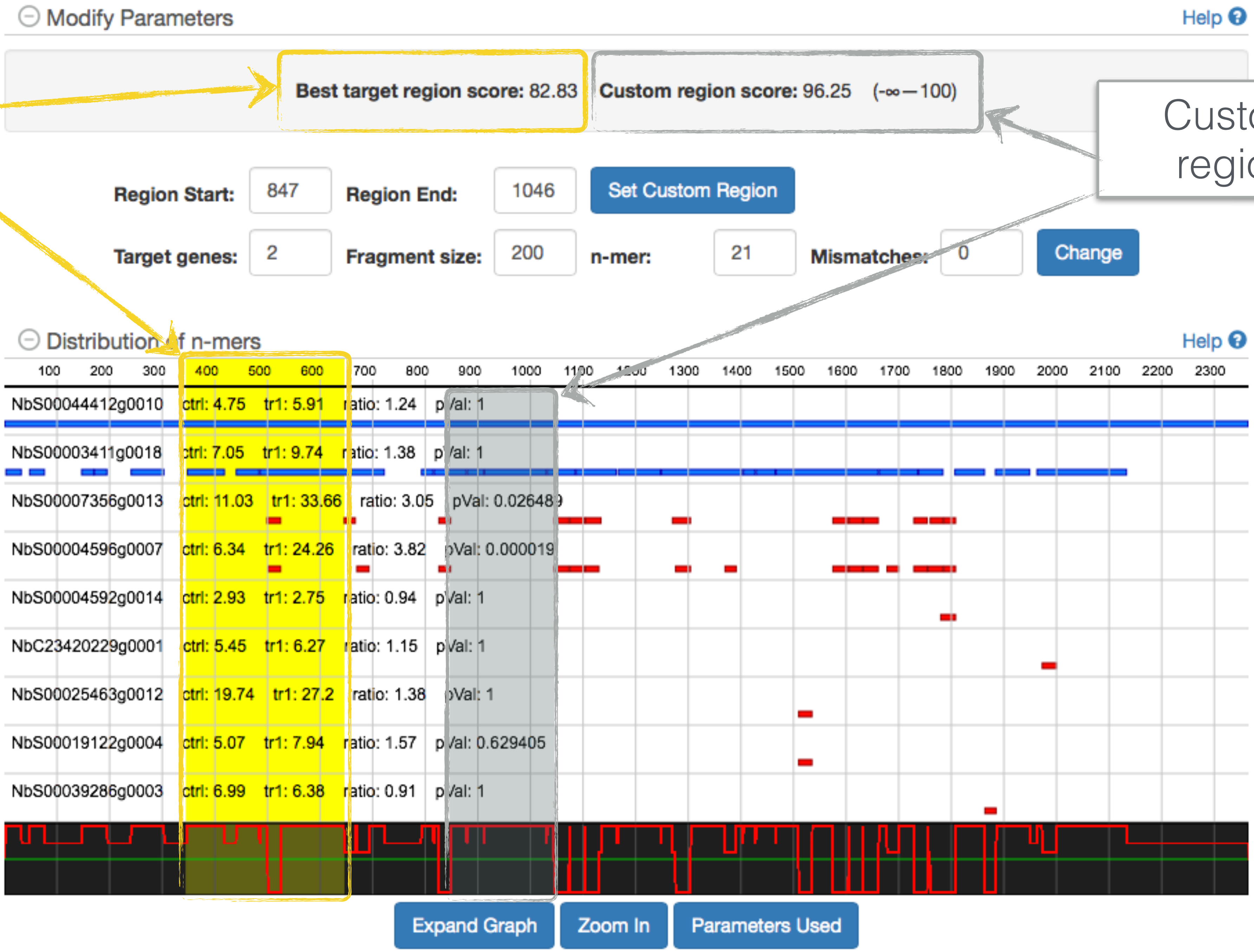
Target genes: 2 **Fragment size:** 200 **n-mer:** 21 **Mismatches:** 0

NbS00044412g0010	ctrl: 4.75	tr1: 5.91	ratio: 1.24	pVal: 1
NbS00003411g0018	ctrl: 7.05	tr1: 9.74	ratio: 1.38	pVal: 1
NbS00007356g0013	ctrl: 11.03	tr1: 33.66	ratio: 3.05	pVal: 0.026489
NbS00004596g0007	ctrl: 6.34	tr1: 24.26	ratio: 3.82	pVal: 0.000019
NbS00004592g0014	ctrl: 2.93	tr1: 2.75	ratio: 0.94	pVal: 1
NbC23420229g0001	ctrl: 5.45	tr1: 6.27	ratio: 1.15	pVal: 1
NbS00025463g0012	ctrl: 19.74	tr1: 27.2	ratio: 1.38	pVal: 1
NbS00019122g0004	ctrl: 5.07	tr1: 7.94	ratio: 1.57	pVal: 0.629405
NbS00039286g0003	ctrl: 6.99	tr1: 6.38	ratio: 0.91	pVal: 1

VIGS Tool output

Predicted region

Custom region



Best target region score: 82.83

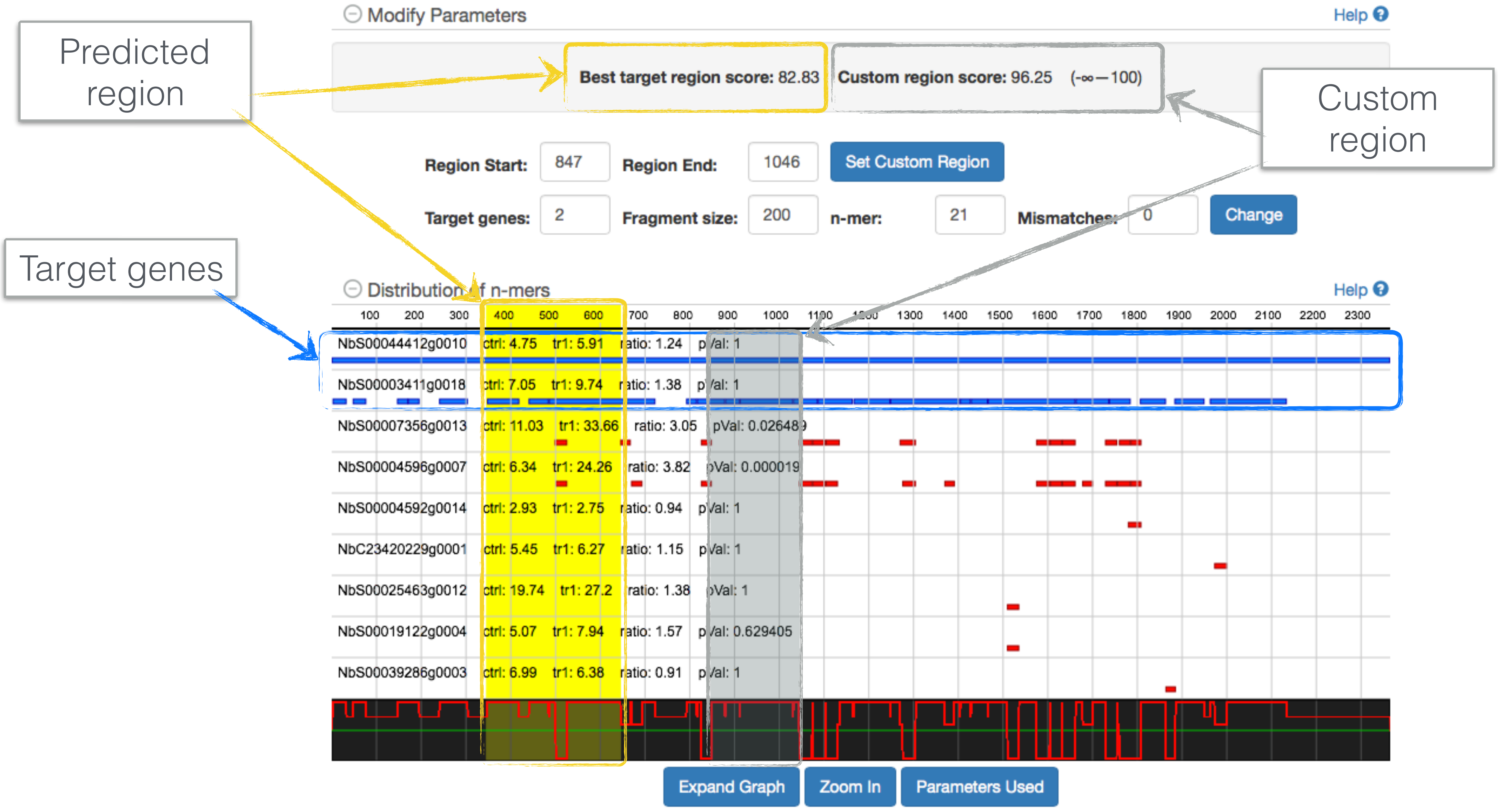
Custom region score: 96.25 (-∞—100)

Region Start: 847 **Region End:** 1046

Target genes: 2 **Fragment size:** 200 **n-mer:** 21 **Mismatches:** 0

NbS00044412g0010	ctrl: 4.75	tr1: 5.91	ratio: 1.24	pVal: 1
NbS00003411g0018	ctrl: 7.05	tr1: 9.74	ratio: 1.38	pVal: 1
NbS00007356g0013	ctrl: 11.03	tr1: 33.66	ratio: 3.05	pVal: 0.026489
NbS00004596g0007	ctrl: 6.34	tr1: 24.26	ratio: 3.82	pVal: 0.000019
NbS00004592g0014	ctrl: 2.93	tr1: 2.75	ratio: 0.94	pVal: 1
NbC23420229g0001	ctrl: 5.45	tr1: 6.27	ratio: 1.15	pVal: 1
NbS00025463g0012	ctrl: 19.74	tr1: 27.2	ratio: 1.38	pVal: 1
NbS00019122g0004	ctrl: 5.07	tr1: 7.94	ratio: 1.57	pVal: 0.629405
NbS00039286g0003	ctrl: 6.99	tr1: 6.38	ratio: 0.91	pVal: 1

VIGS Tool output



Predicted region

Target genes

Custom region

Modify Parameters

Best target region score: 82.83

Custom region score: 96.25 (-∞—100)

Region Start: 847 **Region End:** 1046

Target genes: 2 **Fragment size:** 200 **n-mer:** 21 **Mismatches:** 0

Distribution of n-mers

NbS00044412g0010 ctrl: 4.75 tr1: 5.91 ratio: 1.24 pVal: 1
NbS00003411g0018 ctrl: 7.05 tr1: 9.74 ratio: 1.38 pVal: 1
NbS00007356g0013 ctrl: 11.03 tr1: 33.66 ratio: 3.05 pVal: 0.026489
NbS00004596g0007 ctrl: 6.34 tr1: 24.26 ratio: 3.82 pVal: 0.000019
NbS00004592g0014 ctrl: 2.93 tr1: 2.75 ratio: 0.94 pVal: 1
NbC23420229g0001 ctrl: 5.45 tr1: 6.27 ratio: 1.15 pVal: 1
NbS00025463g0012 ctrl: 19.74 tr1: 27.2 ratio: 1.38 pVal: 1
NbS00019122g0004 ctrl: 5.07 tr1: 7.94 ratio: 1.57 pVal: 0.629405
NbS00039286g0003 ctrl: 6.99 tr1: 6.38 ratio: 0.91 pVal: 1

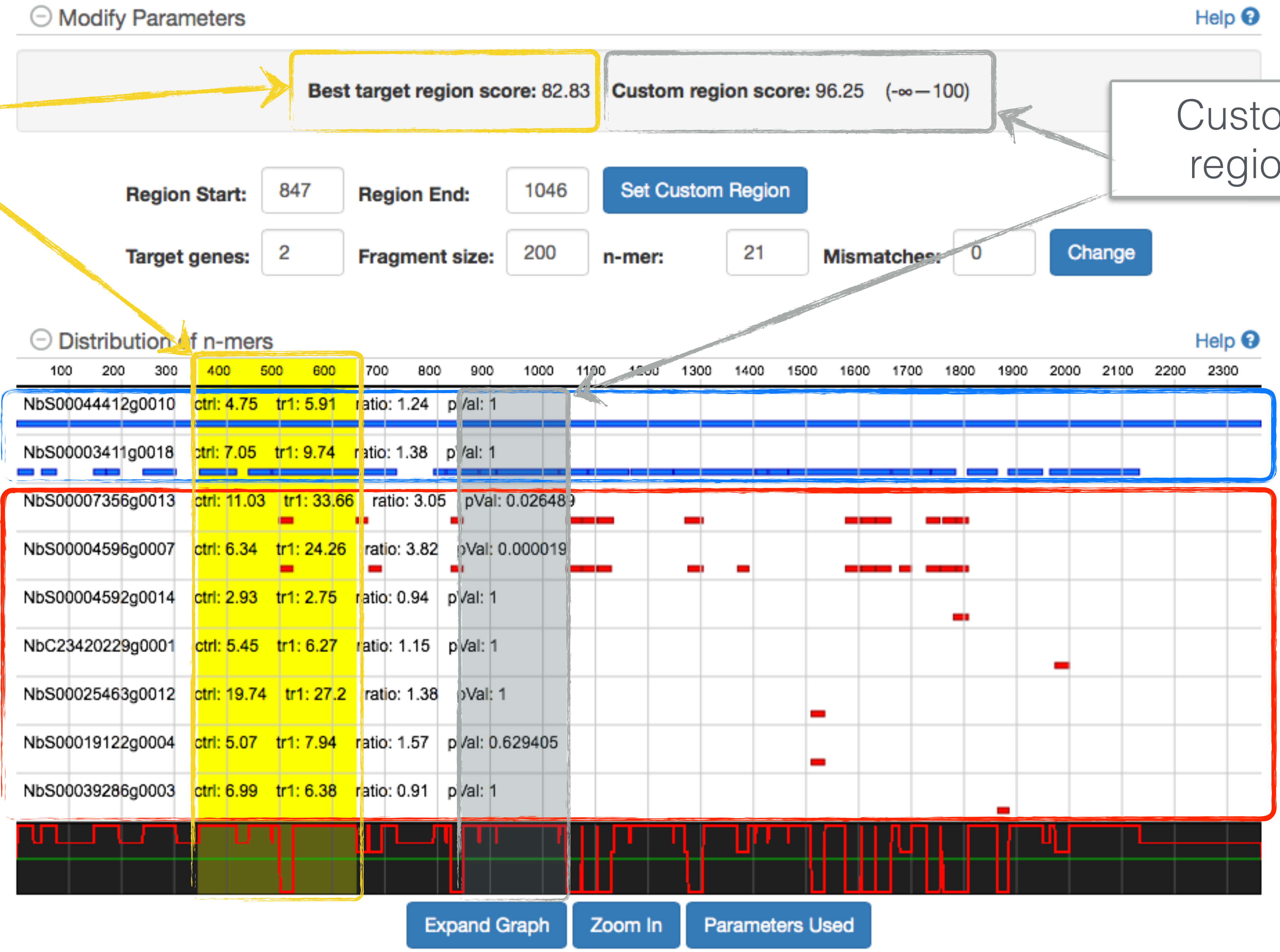
VIGS Tool output

Predicted region

Target genes

Off-Target genes

Custom region



Modify Parameters

Best target region score: 82.83

Custom region score: 96.25 (-∞—100)

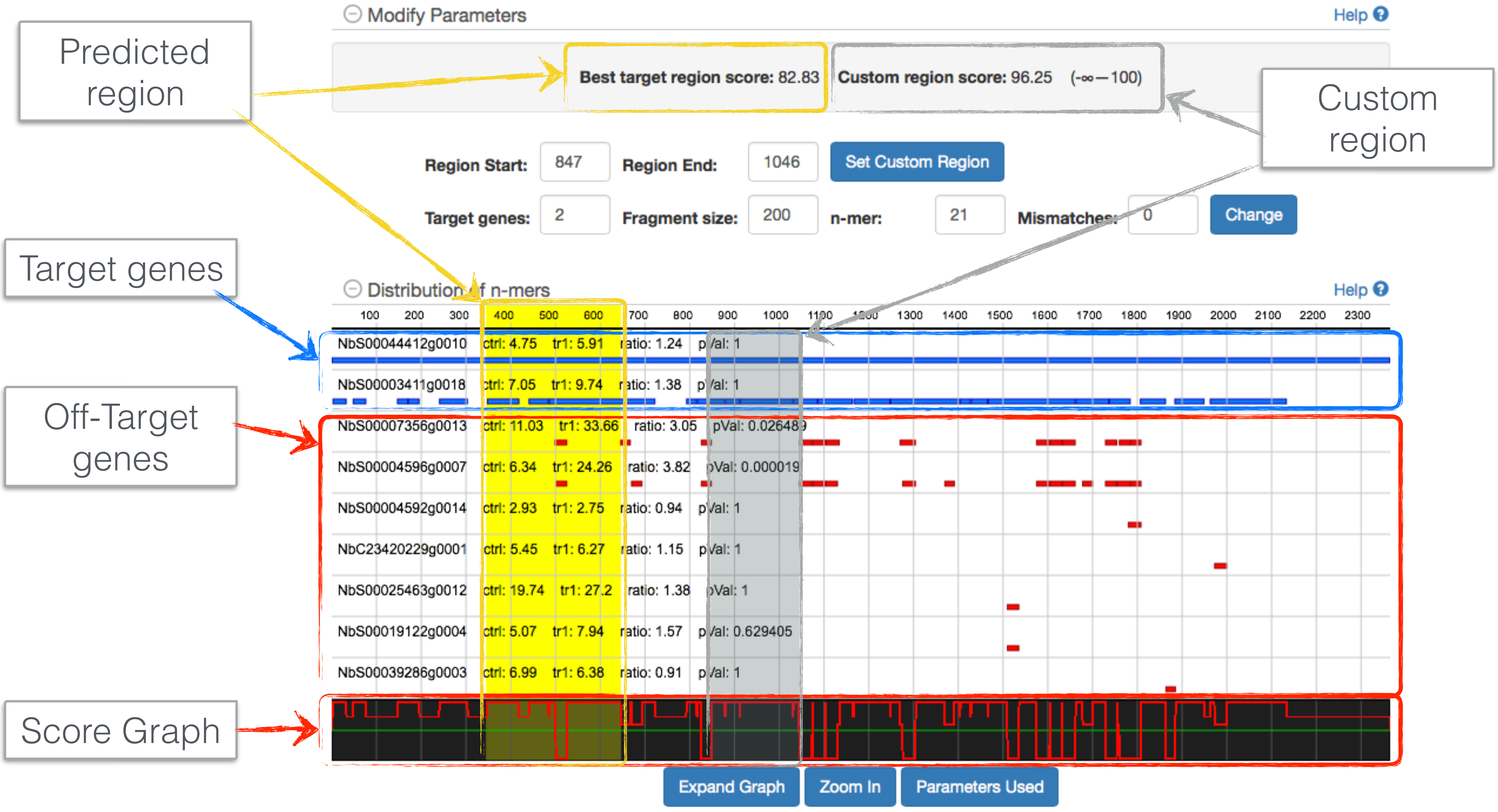
Region Start: 847 **Region End:** 1046

Target genes: 2 **Fragment size:** 200 **n-mer:** 21 **Mismatches:** 0

Distribution of n-mers

```
NbS00044412g0010   ctrl: 4.75    tr1: 5.91    ratio: 1.24   pVal: 1
NbS00003411g0018   ctrl: 7.05    tr1: 9.74    ratio: 1.38   pVal: 1
NbS00007356g0013   ctrl: 11.03   tr1: 33.66   ratio: 3.05   pVal: 0.026489
NbS00004596g0007   ctrl: 6.34    tr1: 24.26   ratio: 3.82   pVal: 0.000019
NbS00004592g0014   ctrl: 2.93    tr1: 2.75    ratio: 0.94   pVal: 1
NbC23420229g0001   ctrl: 5.45    tr1: 6.27    ratio: 1.15   pVal: 1
NbS00025463g0012   ctrl: 19.74   tr1: 27.2    ratio: 1.38   pVal: 1
NbS00019122g0004   ctrl: 5.07    tr1: 7.94    ratio: 1.57   pVal: 0.629405
NbS00039286g0003   ctrl: 6.99    tr1: 6.38    ratio: 0.91   pVal: 1
```

VIGS Tool output



Predicted region

Custom region

Target genes

Off-Target genes

Score Graph

Best target region score: 82.83

Custom region score: 96.25 (-∞—100)

Region Start: 847

Region End: 1046

Target genes: 2

Fragment size: 200

n-mer: 21

Mismatches: 0

NbS00044412g0010 ctrl: 4.75 tr1: 5.91 ratio: 1.24 pVal: 1

NbS00003411g0018 ctrl: 7.05 tr1: 9.74 ratio: 1.38 pVal: 1

NbS00007356g0013 ctrl: 11.03 tr1: 33.66 ratio: 3.05 pVal: 0.026489

NbS00004596g0007 ctrl: 6.34 tr1: 24.26 ratio: 3.82 pVal: 0.000019

NbS00004592g0014 ctrl: 2.93 tr1: 2.75 ratio: 0.94 pVal: 1

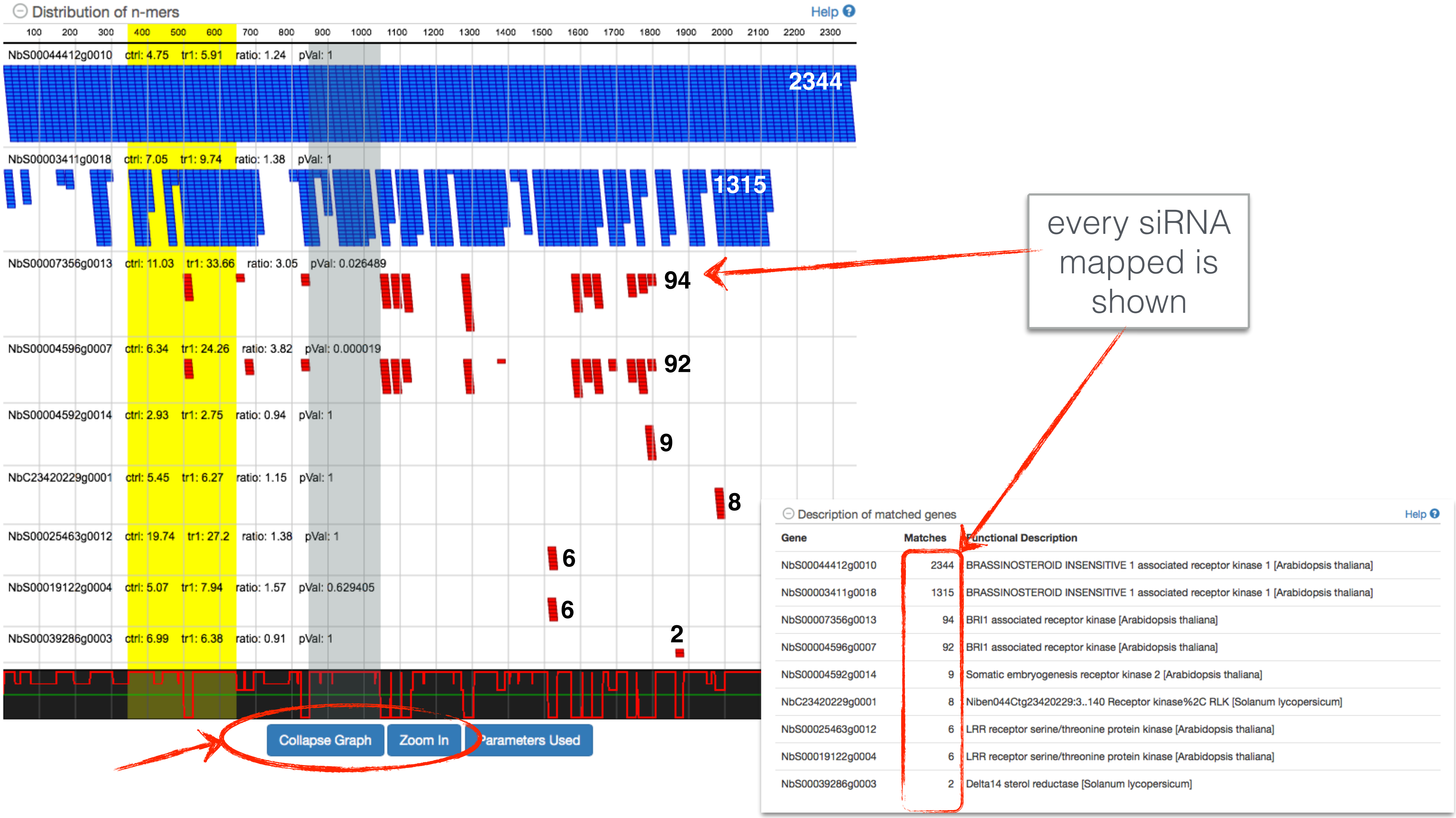
NbC23420229g0001 ctrl: 5.45 tr1: 6.27 ratio: 1.15 pVal: 1

NbS00025463g0012 ctrl: 19.74 tr1: 27.2 ratio: 1.38 pVal: 1

NbS00019122g0004 ctrl: 5.07 tr1: 7.94 ratio: 1.57 pVal: 0.629405

NbS00039286g0003 ctrl: 6.99 tr1: 6.38 ratio: 0.91 pVal: 1

VIGS Tool Graph Expanded View



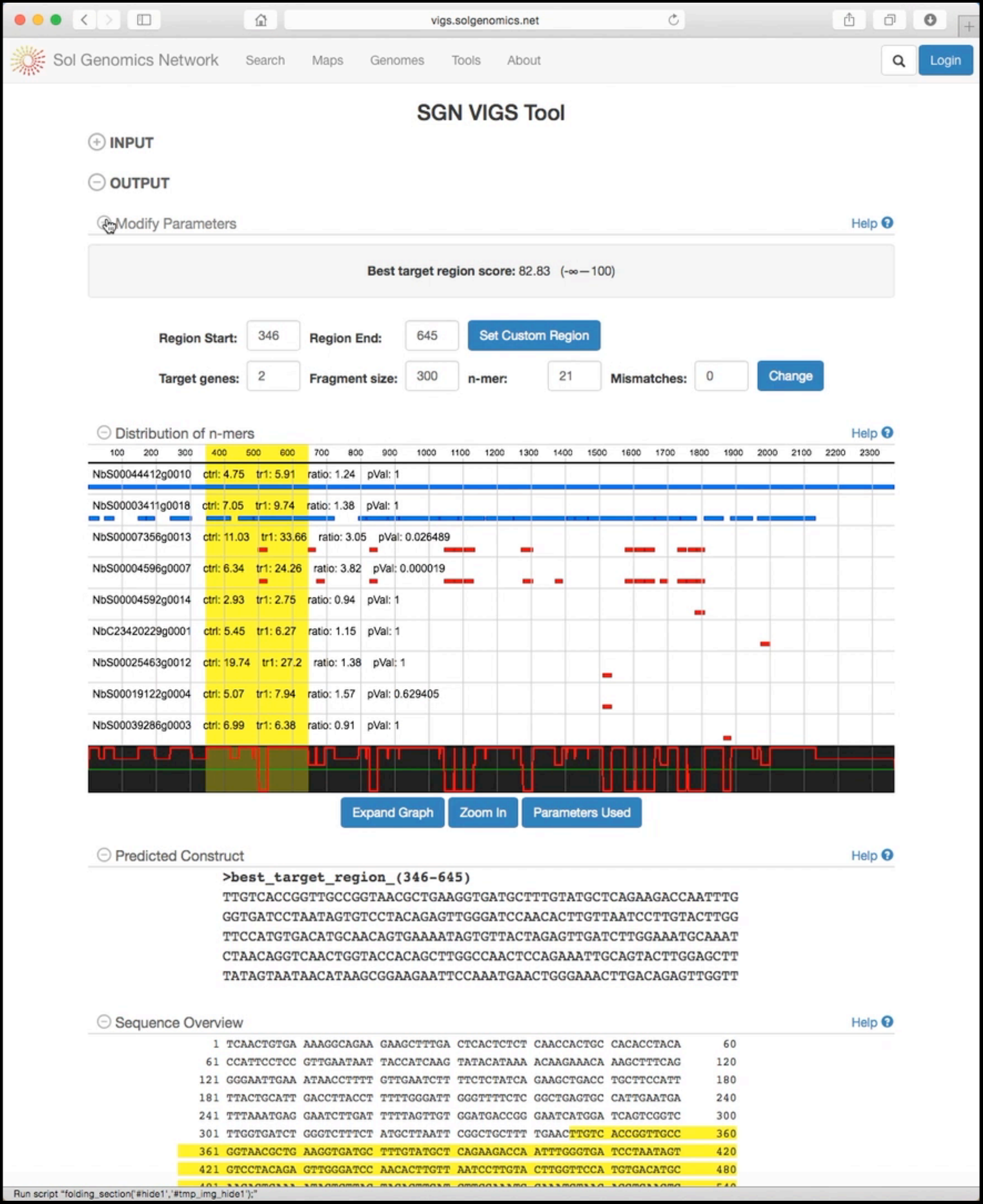
Distribution of n-mers

Gene	ctrl	tr1	ratio	pVal
NbS00044412g0010	4.75	5.91	1.24	1
NbS00003411g0018	7.05	9.74	1.38	1
NbS00007356g0013	11.03	33.66	3.05	0.026489
NbS00004596g0007	6.34	24.26	3.82	0.000019
NbS00004592g0014	2.93	2.75	0.94	1
NbC23420229g0001	5.45	6.27	1.15	1
NbS00025463g0012	19.74	27.2	1.38	1
NbS00019122g0004	5.07	7.94	1.57	0.629405
NbS00039286g0003	6.99	6.38	0.91	1

every siRNA mapped is shown

Description of matched genes

Gene	Matches	Functional Description
NbS00044412g0010	2344	BRASSINOSTEROID INSENSITIVE 1 associated receptor kinase 1 [Arabidopsis thaliana]
NbS00003411g0018	1315	BRASSINOSTEROID INSENSITIVE 1 associated receptor kinase 1 [Arabidopsis thaliana]
NbS00007356g0013	94	BRI1 associated receptor kinase [Arabidopsis thaliana]
NbS00004596g0007	92	BRI1 associated receptor kinase [Arabidopsis thaliana]
NbS00004592g0014	9	Somatic embryogenesis receptor kinase 2 [Arabidopsis thaliana]
NbC23420229g0001	8	Niben044Ctg23420229:3..140 Receptor kinase%2C RLK [Solanum lycopersicum]
NbS00025463g0012	6	LRR receptor serine/threonine protein kinase [Arabidopsis thaliana]
NbS00019122g0004	6	LRR receptor serine/threonine protein kinase [Arabidopsis thaliana]
NbS00039286g0003	2	Delta14 sterol reductase [Solanum lycopersicum]



SGN VIGS Tool

Best target region score: 82.83 (-∞—100)

Region Start: 346 **Region End:** 645

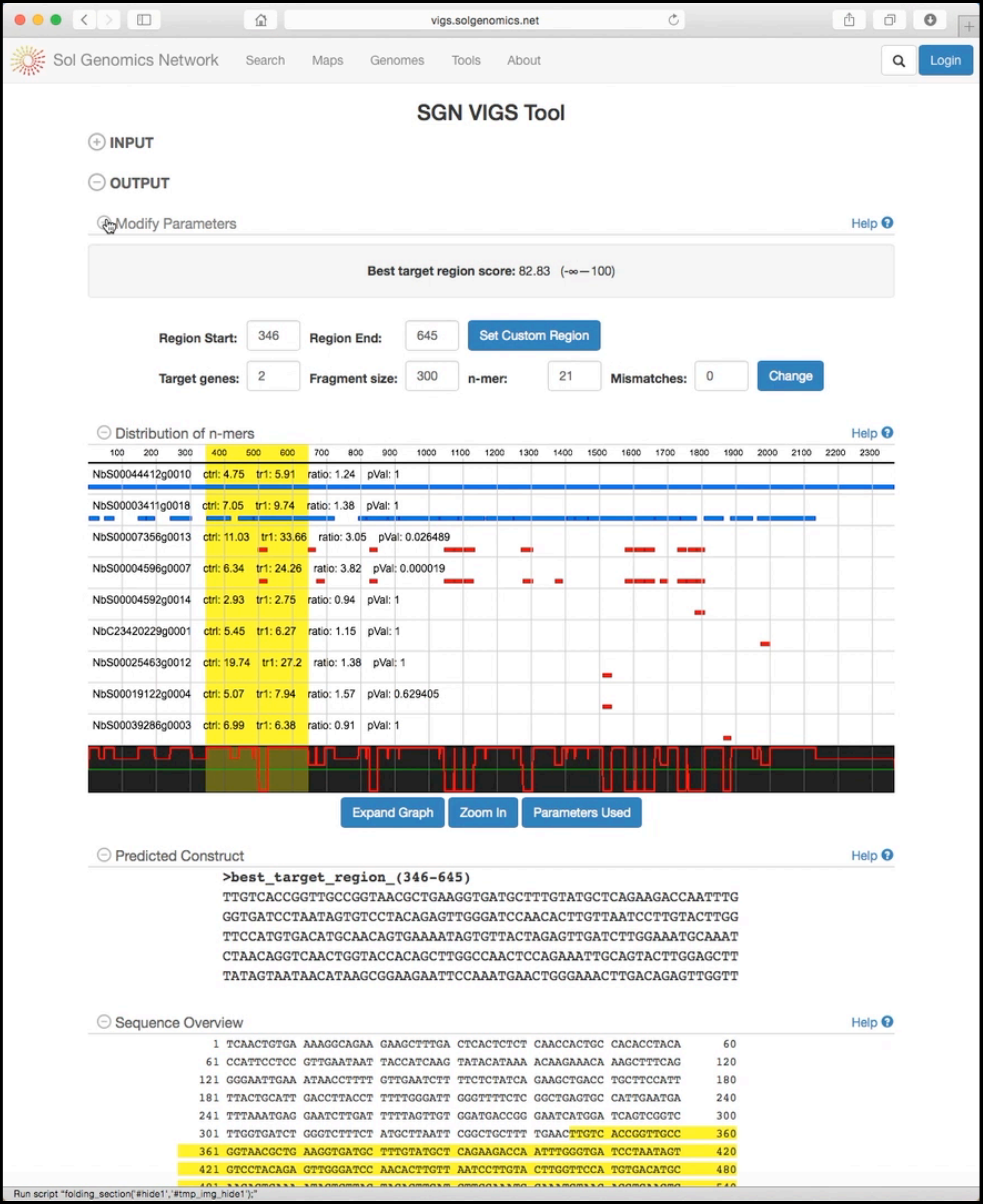
Target genes: 2 **Fragment size:** 300 **n-mer:** 21 **Mismatches:** 0

```
NbS00044412g0010  ctrl: 4.75   tr1: 5.91   ratio: 1.24  pVal: 1
NbS00003411g0018  ctrl: 7.05   tr1: 9.74   ratio: 1.38  pVal: 1
NbS00007356g0013  ctrl: 11.03  tr1: 33.66  ratio: 3.05  pVal: 0.026489
NbS00004596g0007  ctrl: 6.34   tr1: 24.26  ratio: 3.82  pVal: 0.000019
NbS00004592g0014  ctrl: 2.93   tr1: 2.75   ratio: 0.94  pVal: 1
NbC23420229g0001  ctrl: 5.45   tr1: 6.27   ratio: 1.15  pVal: 1
NbS00025463g0012  ctrl: 19.74  tr1: 27.2   ratio: 1.38  pVal: 1
NbS00019122g0004  ctrl: 5.07   tr1: 7.94   ratio: 1.57  pVal: 0.629405
NbS00039286g0003  ctrl: 6.99   tr1: 6.38   ratio: 0.91  pVal: 1
```

```
>best_target_region_(346-645)
TTGTCACCGGTTGCCGGTAACGCTGAAGGTGATGCTTTGTATGCTCAGAAGACCAATTTG
GGTGATCCTAATAGTGTCCTACAGAGTTGGGATCCAACACTTGTTAATCCTTGTACTTGG
TTCCATGTGACATGCAACAGTGAAAATAGTGTTACTAGAGTTGATCTTGGAAATGCAAAT
CTAACAGGTCAACTGGTACCACAGCTTGGCCAACTCCAGAAATTGCAGTACTTGGAGCTT
TATAGTAATAACATAAGCGGAAGAATTCCAAATGAACTGGGAAACTTGACAGAGTTGGTT
```

```
  1 TCAACTGTGA AAAGGCAGAA GAAGCTTTGA CTCACTCTCT CAACCACTGC CACACCTACA    60
 61 CCATTCCTCC GTTGAATAAT TACCATCAAG TATACATAAA ACAAGAAACA AAGCTTTCAG   120
121 GGGAATTGAA ATAACCTTTT GTTGAATCTT TTCTCTATCA GAAGCTGACC TGCTTCCATT   180
181 TTACTGCATT GACCTTACCT TTTTGGGATT GGGTTTTCTC GGCTGAGTGC CATTGAATGA   240
241 TTTAAATGAG GAATCTTGAT TTTTAGTTGT GGATGACCGG GAATCATGGA TCAGTCGGTC   300
301 TTGGTGATCT GGGTCTTTCT ATGCTTAATT CGGCTGCTTT TGAACTTGTC ACCGGTTGCC   360
361 GGTAACGCTG AAGGTGATGC TTTGTATGCT CAGAAGACCA ATTTGGGTGA TCCTAATAGT   420
421 GTCCTACAGA GTTGGGATCC AACACTTGTT AATCCTTGTA CTTGGTTCCA TGTGACATGC   480
```

Run script "folding_section('#hide1','#tmp_img_hide1');"



SGN VIGS Tool

INPUT

OUTPUT

Best target region score: 82.83 (-∞—100)

Region Start: 346 **Region End:** 645

Target genes: 2 **Fragment size:** 300 **n-mer:** 21 **Mismatches:** 0

Distribution of n-mers

```
NbS00044412g0010   ctrl: 4.75   tr1: 5.91   ratio: 1.24   pVal: 1
NbS00003411g0018   ctrl: 7.05   tr1: 9.74   ratio: 1.38   pVal: 1
NbS00007356g0013   ctrl: 11.03   tr1: 33.66   ratio: 3.05   pVal: 0.026489
NbS00004596g0007   ctrl: 6.34   tr1: 24.26   ratio: 3.82   pVal: 0.000019
NbS00004592g0014   ctrl: 2.93   tr1: 2.75   ratio: 0.94   pVal: 1
NbC23420229g0001   ctrl: 5.45   tr1: 6.27   ratio: 1.15   pVal: 1
NbS00025463g0012   ctrl: 19.74   tr1: 27.2   ratio: 1.38   pVal: 1
NbS00019122g0004   ctrl: 5.07   tr1: 7.94   ratio: 1.57   pVal: 0.629405
NbS00039286g0003   ctrl: 6.99   tr1: 6.38   ratio: 0.91   pVal: 1
```

Predicted Construct

```
>best_target_region_(346-645)
TTGTCACCGGTTGCCGGTAACGCTGAAGGTGATGCTTTGTATGCTCAGAAGACCAATTTG
GGTGATCCTAATAGTGTCCTACAGAGTTGGGATCCAACACTTGTTAATCCTTGTACTTGG
TTCCATGTGACATGCAACAGTGAAAATAGTGTTACTAGAGTTGATCTTGGAAATGCAAAT
CTAACAGGTCAACTGGTACCACAGCTTGGCCAACTCCAGAAATTGCAGTACTTGGAGCTT
TATAGTAATAACATAAGCGGAAGAATTCCAAATGAACTGGGAAACTTGACAGAGTTGGTT
```

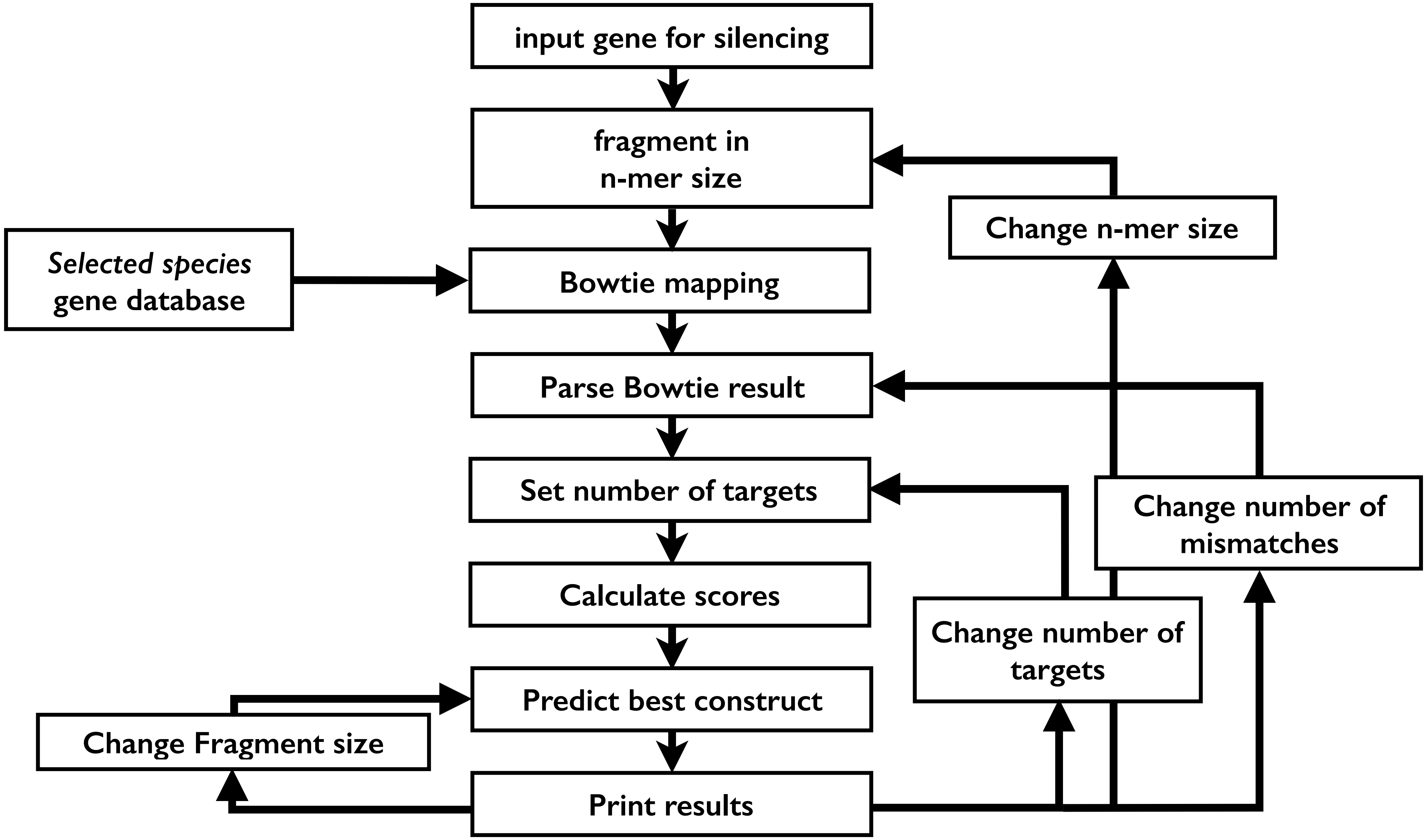
Sequence Overview

```
  1 TCAACTGTGA AAAGGCAGAA GAAGCTTTGA CTCACTCTCT CAACCACTGC CACACCTACA    60
 61 CCATTCCTCC GTTGAATAAT TACCATCAAG TATACATAAA ACAAGAAACA AAGCTTTCAG   120
121 GGGAATTGAA ATAACCTTTT GTTGAATCTT TTCTCTATCA GAAGCTGACC TGCTTCCATT   180
181 TTACTGCATT GACCTTACCT TTTTGGGATT GGGTTTTCTC GGCTGAGTGC CATTGAATGA   240
241 TTTAAATGAG GAATCTTGAT TTTTAGTTGT GGATGACCGG GAATCATGGA TCAGTCGGTC   300
301 TTGGTGATCT GGGTCTTTCT ATGCTTAATT CGGCTGCTTT TGAACTTGTC ACCGGTTGCC   360
361 GGTAACGCTG AAGGTGATGC TTTGTATGCT CAGAAGACCA ATTTGGGTGA TCCTAATAGT   420
421 GTCCTACAGA GTTGGGATCC AACACTTGTT AATCCTTGTA CTTGGTTCCA TGTGACATGC   480
```

Run script "folding_section('#hide1','#tmp_img_hide1');"

VIGS Tool algorithm

The SGN VIGS tool simulates *in silico* the recognition of the mRNA by RISC and the siRNA, and tries to predict the best construct avoiding off-targets



input gene for silencing

fragment in n-mer size

Change n-mer size

Selected species gene database

Bowtie mapping

Parse Bowtie result

Set number of targets

Change number of mismatches

Calculate scores

Change number of targets

Predict best construct

Change Fragment size

Print results

Tomato Expression Atlas

A high resolution map and search tool for tomato genes and their products

Jocelyn Rose

James Giovannoni

Lukas Mueller

Carmen Catala

Zhangjun Fei

Noe Fernandez
Yi Zheng
Philippe Nicolas
Richard Pattison
Laetitia Martin
Stephen Snyder
Yoshi Shinozaki
Yimin Xu

CORNELL UNIVERSITY FOUNDED A.D. 1865

NSF

BTI
Boyce Thompson Institute for Plant Research

Collaborators

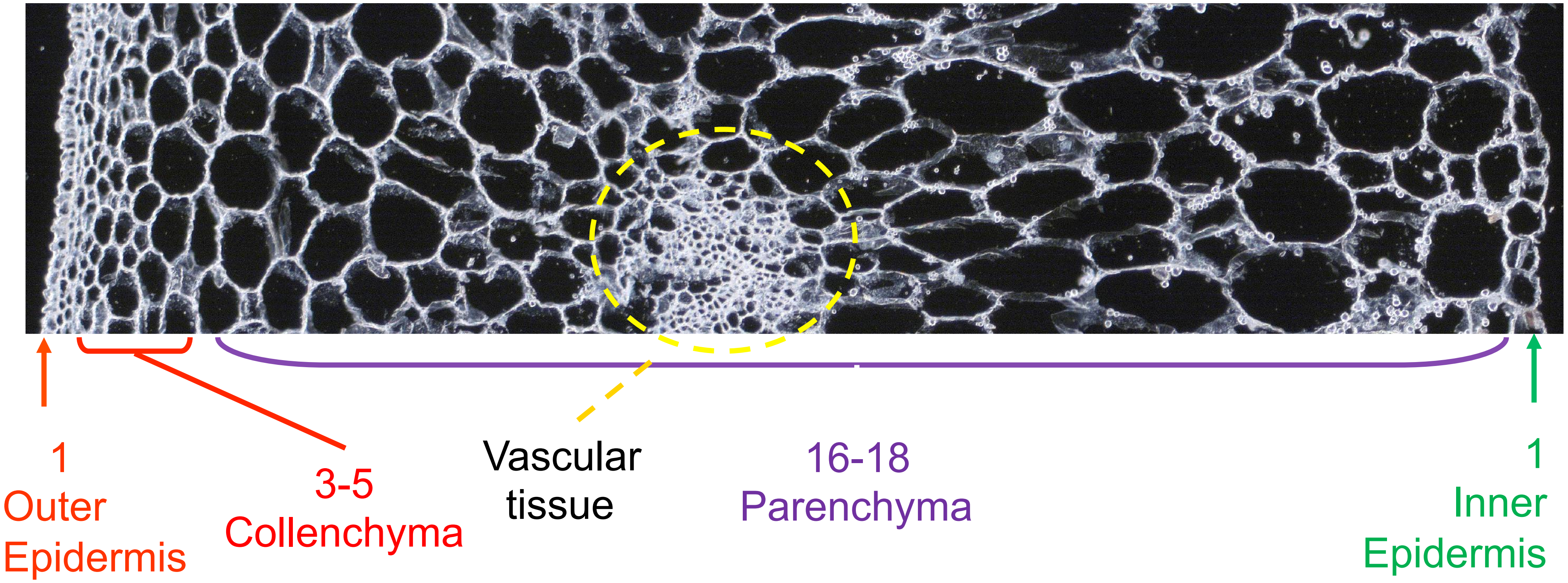
Alisdair Fernie
Max Planck Institute

William Willats
University of Copenhagen

David Domozych
Skidmore College

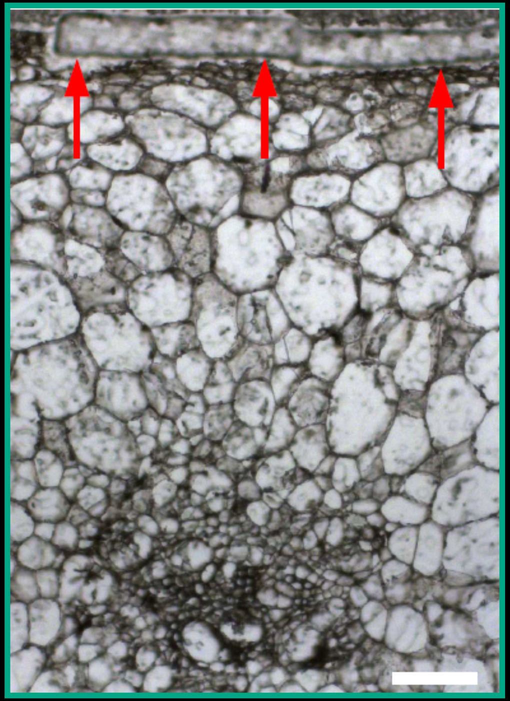
Tissue homogenization

Organ/tissue homogenization:



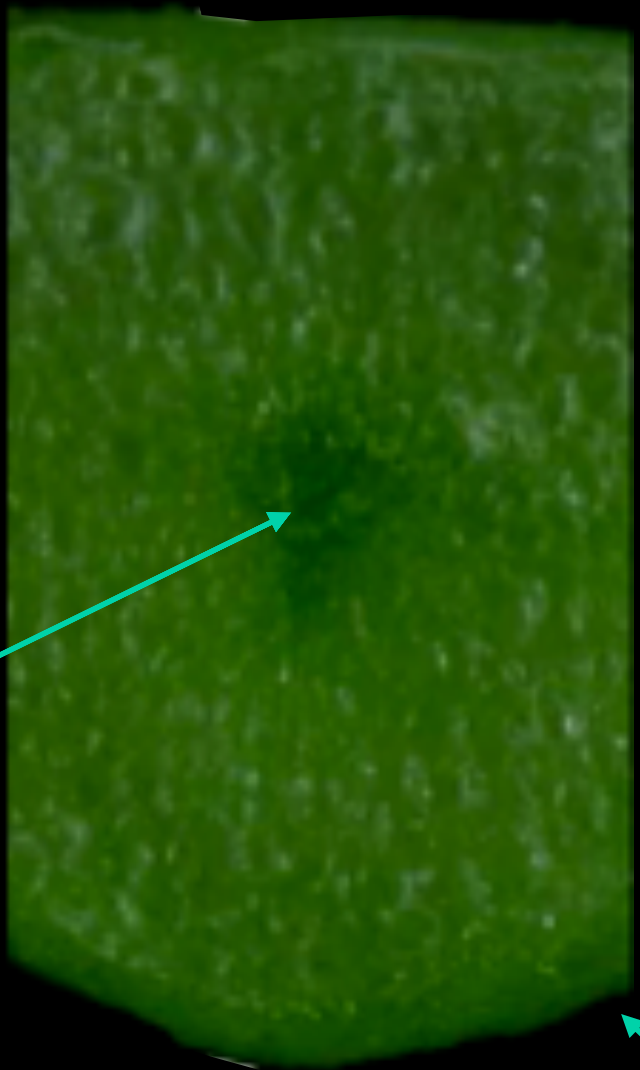
- Significant dilution effects
- Loss of valuable spatial information: biochemical pathway and regulatory networks

Laser Capture Microdissection

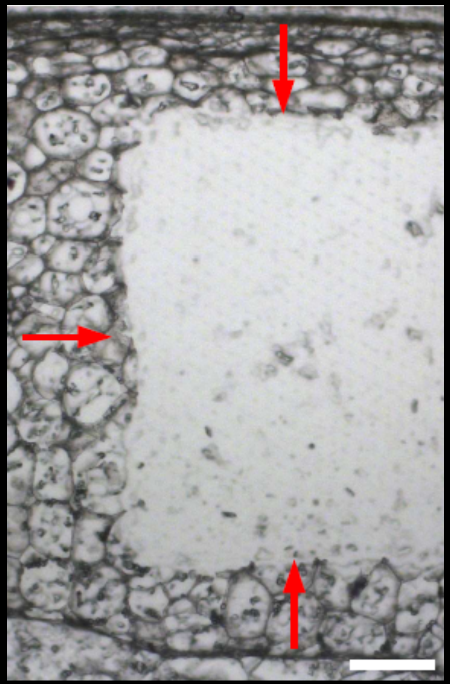


Outer Epidermis

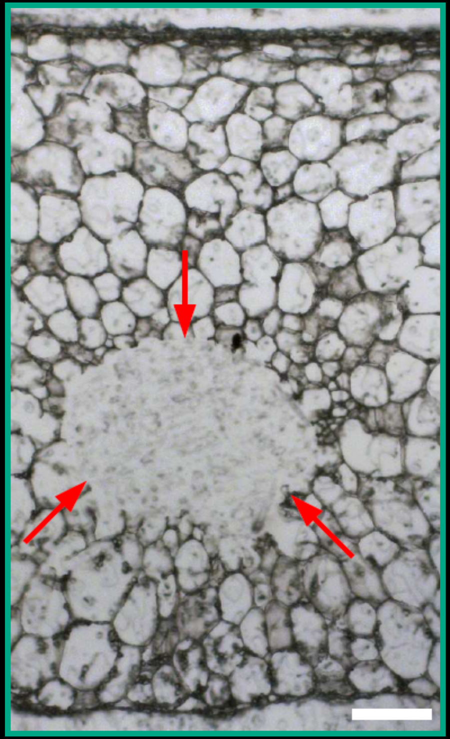
Small green fruit



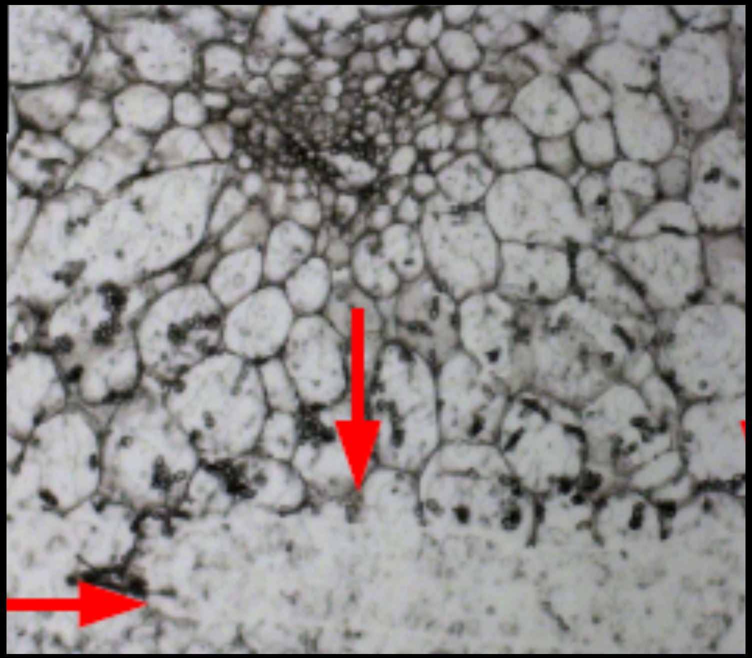
Collenchyma



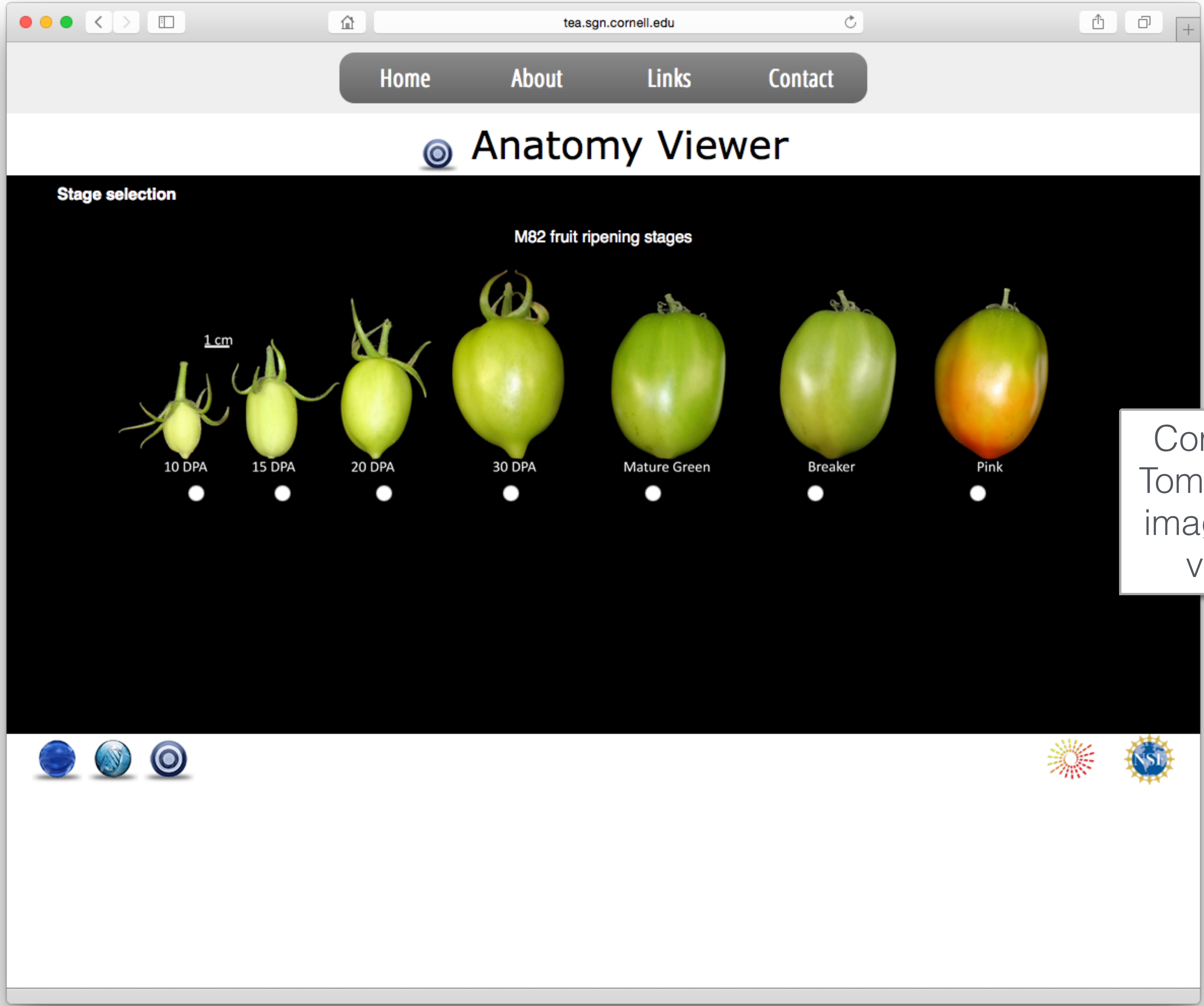
Parenchyma



Vascular Tissue



Inner Epidermis



tea.sgn.cornell.edu

Anatomy Viewer

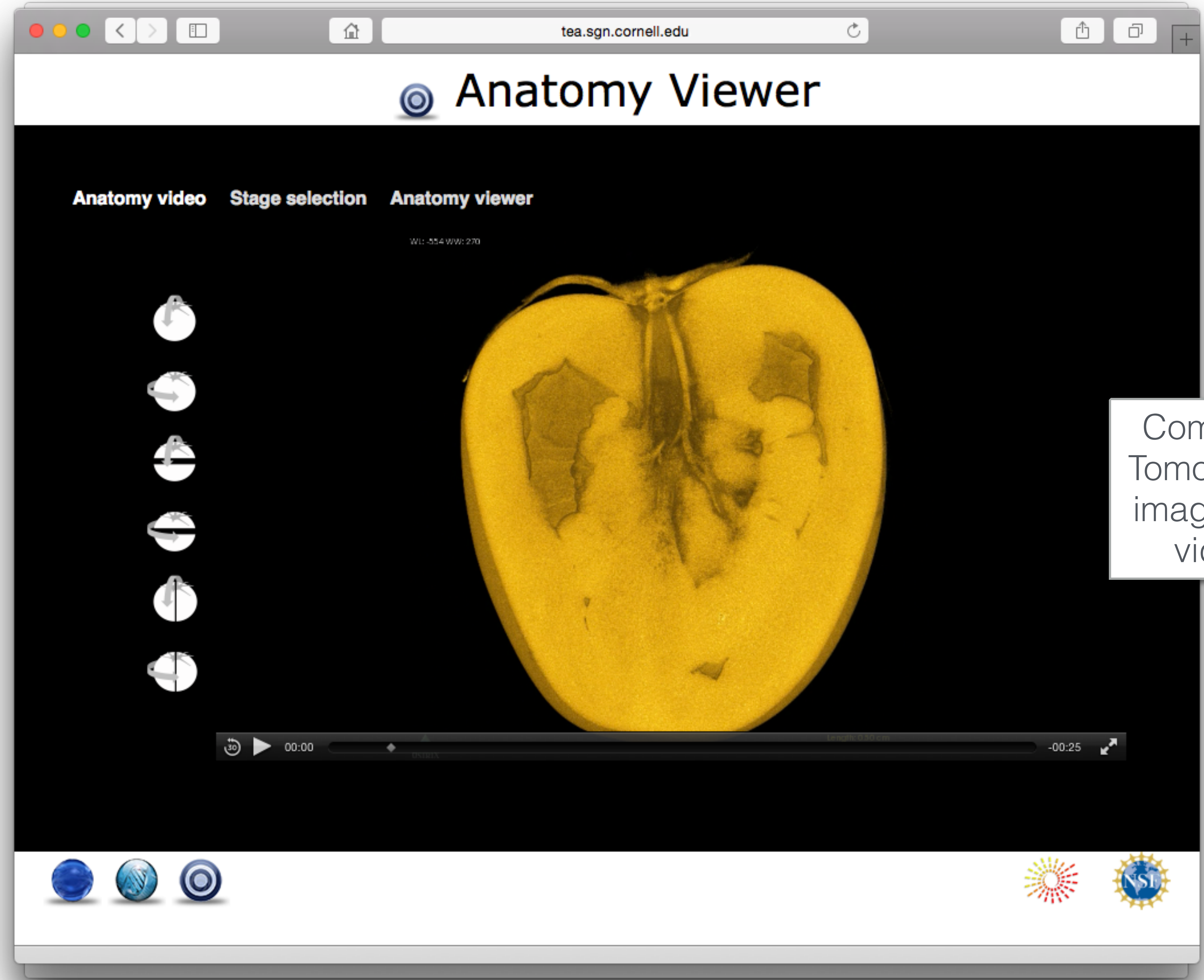
Stage selection

M82 fruit ripening stages

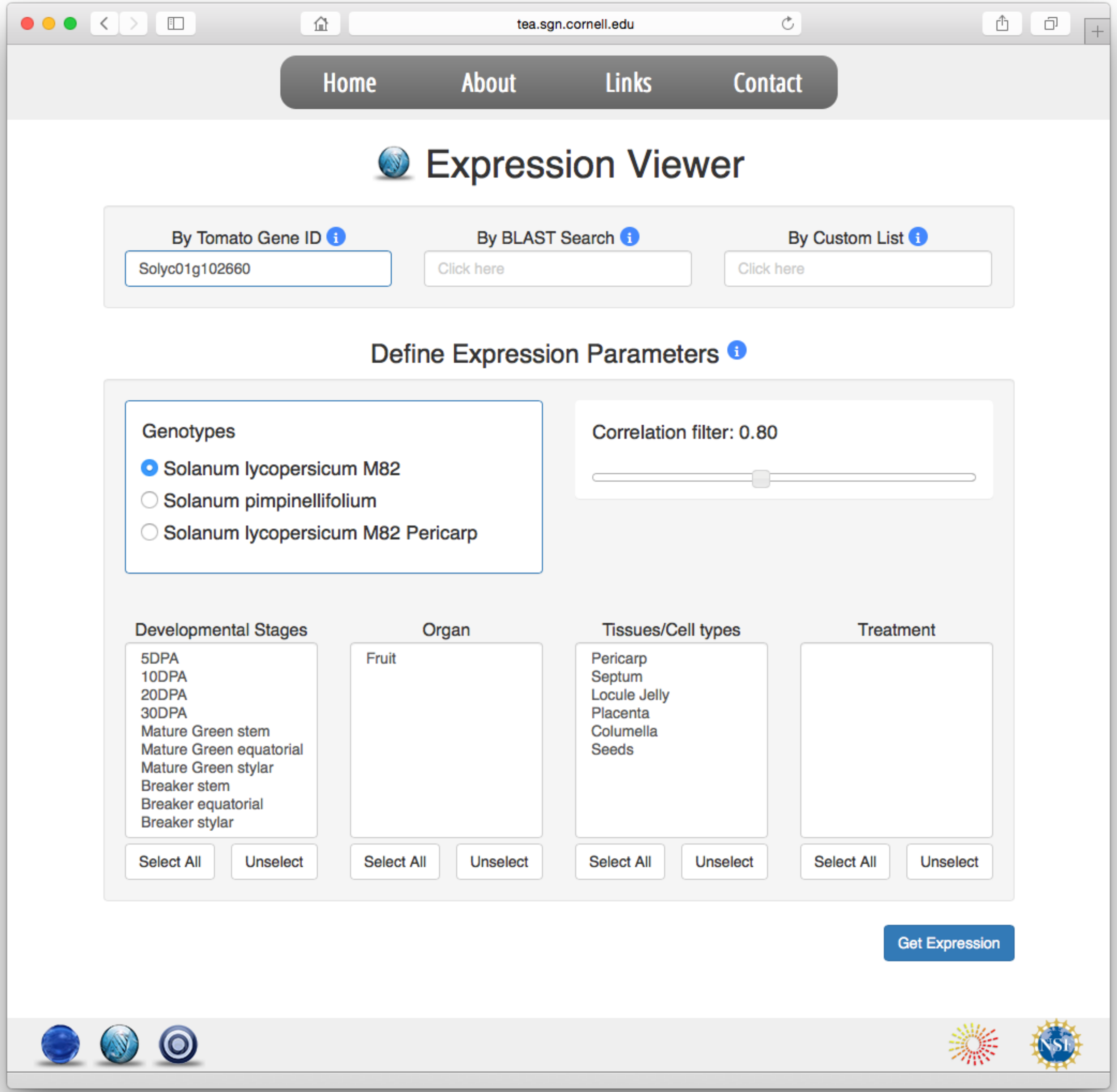
○ 10 DPA ○ 15 DPA ○ 20 DPA ○ 30 DPA ○ Mature Green ○ Breaker ○ Pink

Computed Tomography images and videos

BTI



Computed Tomography images and videos



Expression Viewer

By Tomato Gene ID: Solyc01g102660

By BLAST Search: Click here

By Custom List: Click here

Define Expression Parameters

Genotypes

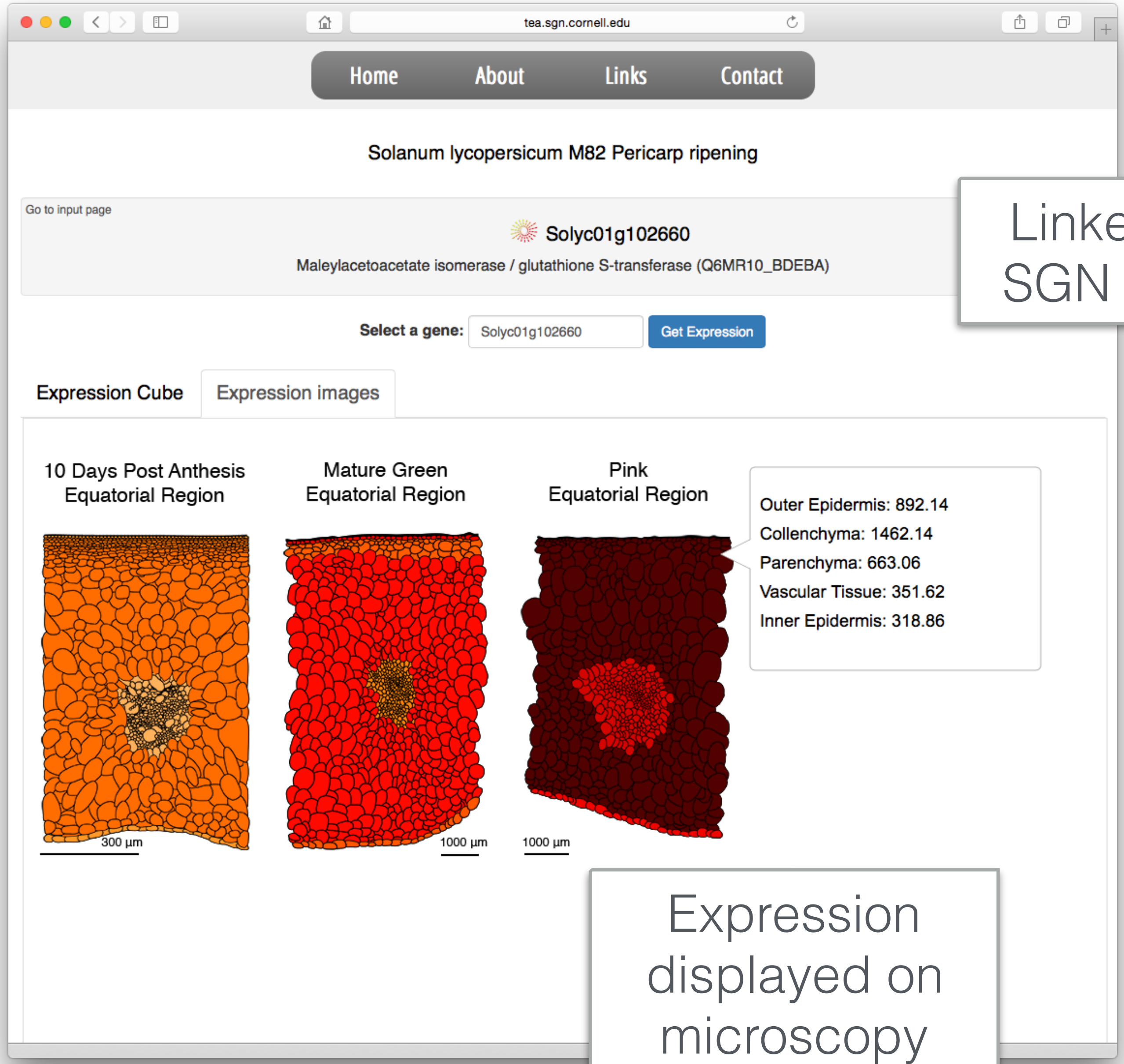
- ● Solanum lycopersicum M82
- ○ Solanum pimpinellifolium
- ○ Solanum lycopersicum M82 Pericarp

Correlation filter: 0.80

Developmental Stages	Organ	Tissues/Cell types	Treatment
5DPA 10DPA 20DPA 30DPA Mature Green stem Mature Green equatorial Mature Green stylar Breaker stem Breaker equatorial Breaker stylar	Fruit	Pericarp Septum Locule Jelly Placenta Columella Seeds	

Sol Genomics Network

Tomato Expression Atlas



Solanum lycopersicum M82 Pericarp ripening

Solyc01g102660

Maleylacetoacetate isomerase / glutathione S-transferase (Q6MR10_BDEBA)

Select a gene: Solyc01g102660

10 Days Post Anthesis Equatorial Region

Mature Green Equatorial Region

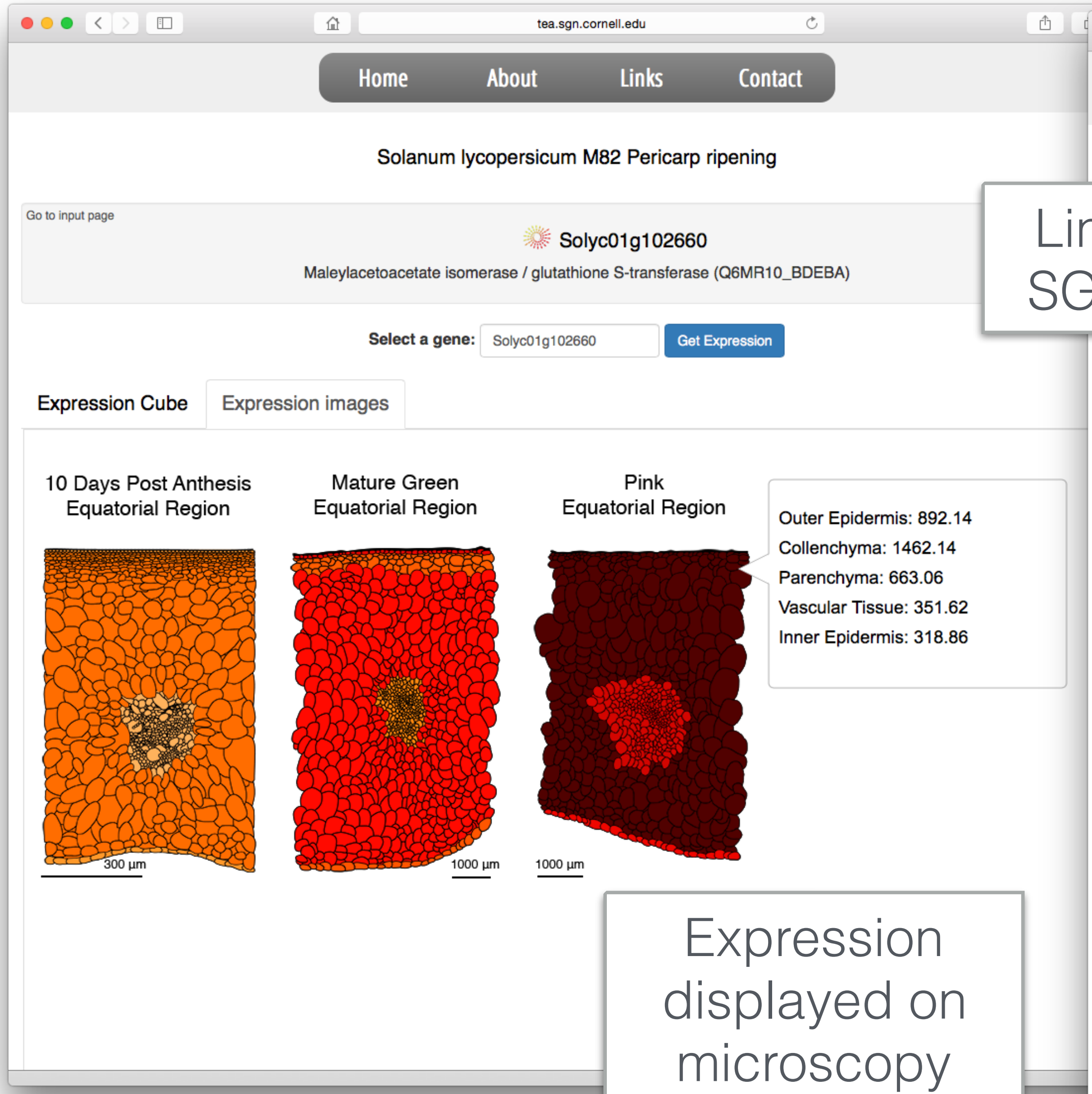
Pink Equatorial Region

Outer Epidermis: 892.14
Collenchyma: 1462.14
Parenchyma: 663.06
Vascular Tissue: 351.62
Inner Epidermis: 318.86

Linked to SGN data

Expression displayed on microscopy images

Tomato Expression Atlas



Solanum lycopersicum M82 Pericarp ripening

Solyc01g102660

Maleylacetoacetate isomerase / glutathione S-transferase (Q6MR10_BDEBA)

Select a gene: Solyc01g102660

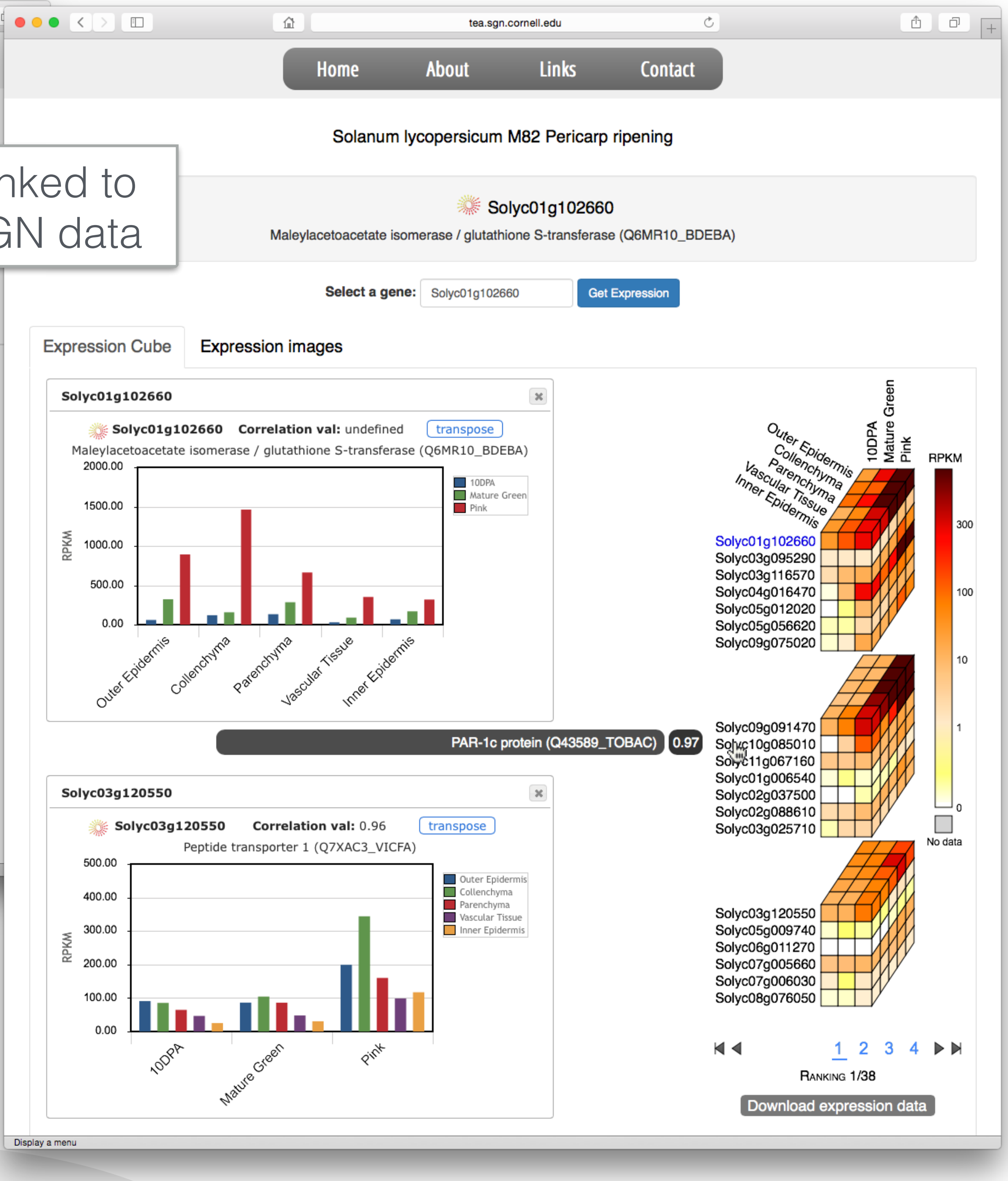
10 Days Post Anthesis Equatorial Region

Mature Green Equatorial Region

Pink Equatorial Region

Outer Epidermis: 892.14
Collenchyma: 1462.14
Parenchyma: 663.06
Vascular Tissue: 351.62
Inner Epidermis: 318.86

Linked to SGN data



Solanum lycopersicum M82 Pericarp ripening

Solyc01g102660

Maleylacetoacetate isomerase / glutathione S-transferase (Q6MR10_BDEBA)

Select a gene: Solyc01g102660

Solyc01g102660

Solyc01g102660 **Correlation val:** undefined

Maleylacetoacetate isomerase / glutathione S-transferase (Q6MR10_BDEBA)

PAR-1c protein (Q43589_TOBAC) 0.97

Solyc03g120550

Solyc03g120550 **Correlation val:** 0.96

Peptide transporter 1 (Q7XAC3_VICFA)

Solyc01g102660
Solyc03g095290
Solyc03g116570
Solyc04g016470
Solyc05g012020
Solyc05g056620
Solyc09g075020

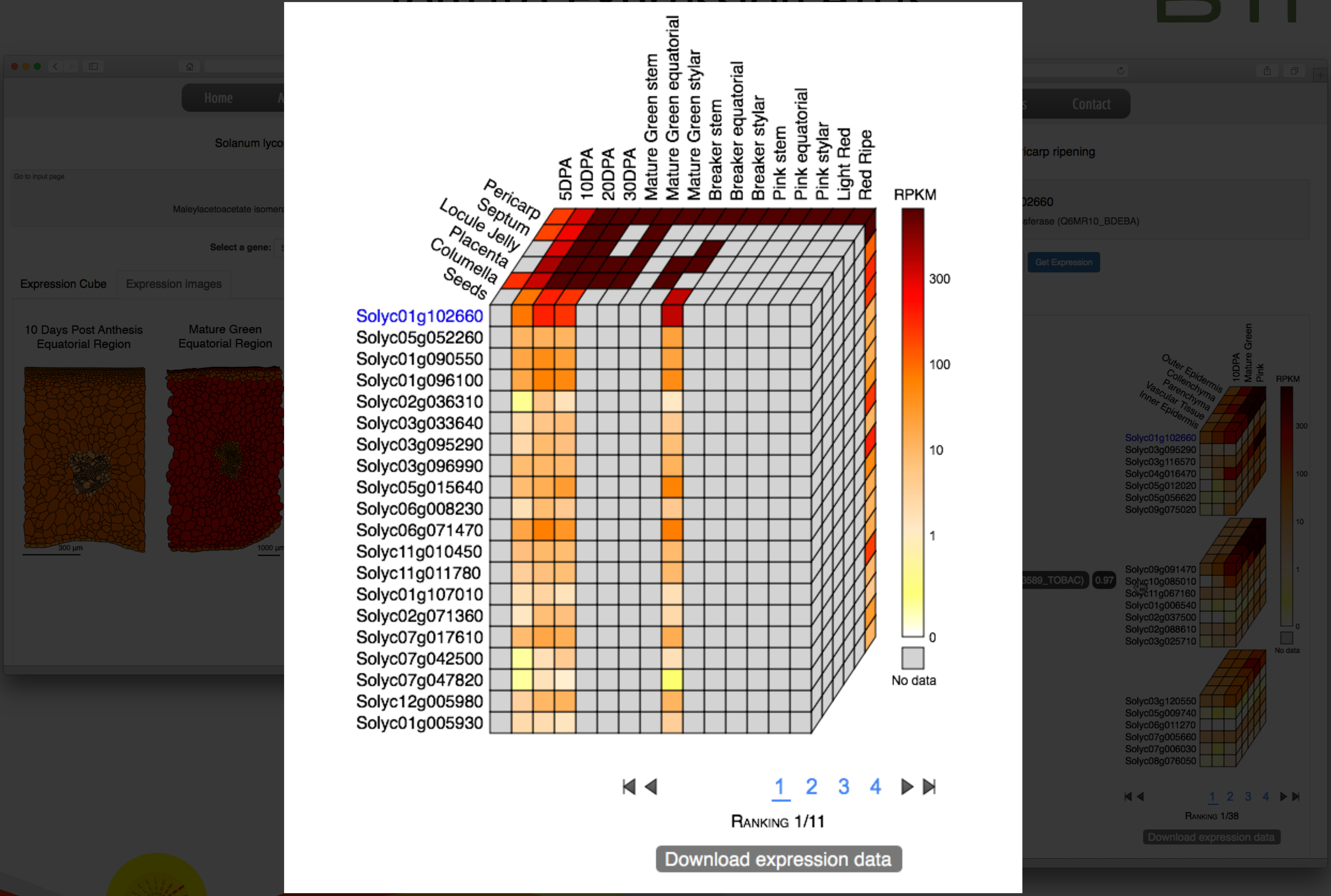
Solyc09g091470
Solyc10g085010
Solyc11g067160
Solyc01g006540
Solyc02g037500
Solyc02g088610
Solyc03g025710

Solyc03g120550
Solyc05g009740
Solyc06g011270
Solyc07g005660
Solyc07g006030
Solyc08g076050

Ranking 1/38

Expression displayed on microscopy images

Tomato Expression Atlas



Sol Genomics Network

Solanum lycopersicum M82 Fruit ripening

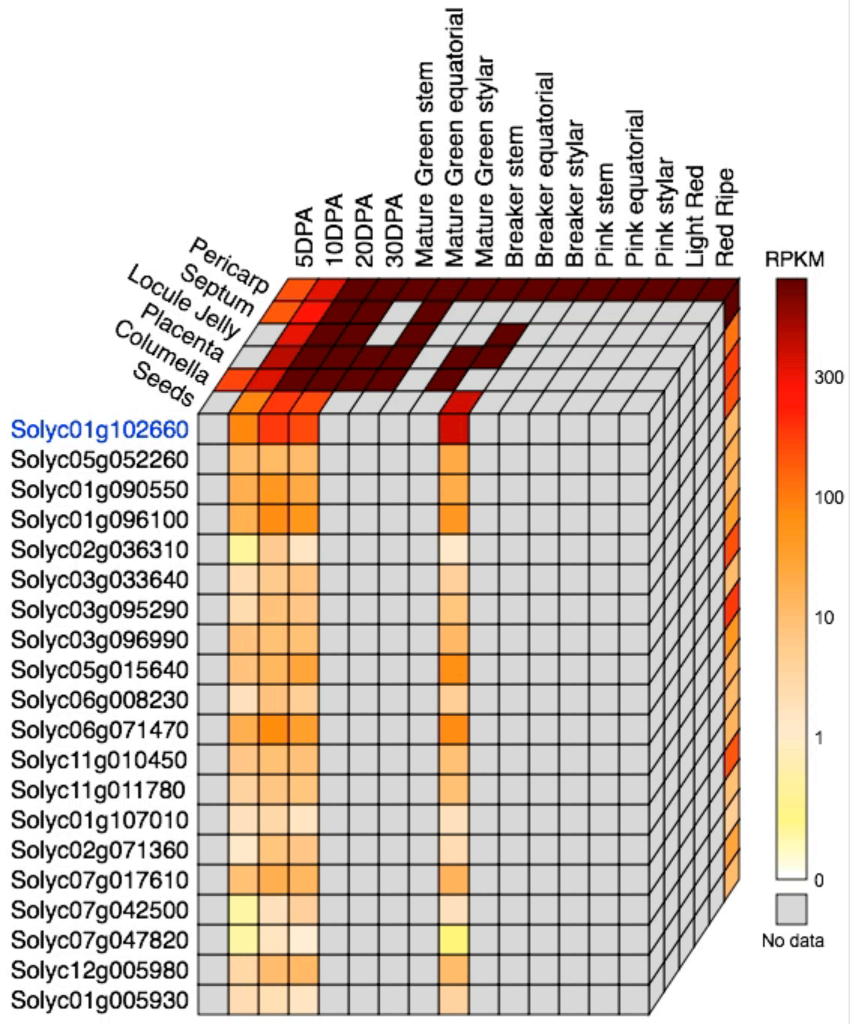
Go to input page

Solyc01g102660

Maleylacetoacetate isomerase / glutathione S-transferase (Q6MR10_BDEBA)

Select a gene: Solyc01g102660 Get Expression

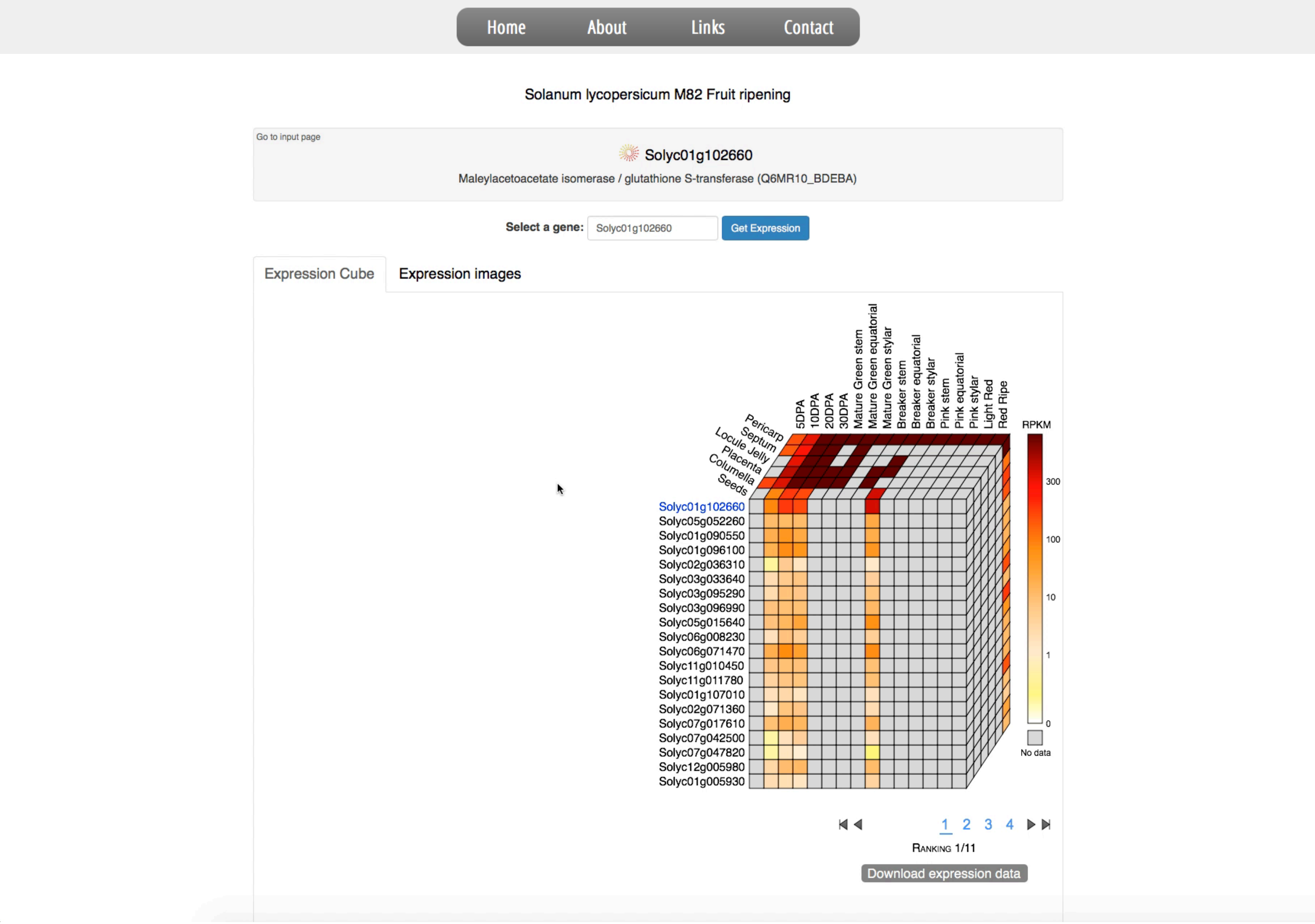
Expression Cube | Expression images



1 2 3 4

Ranking 1/11

Download expression data

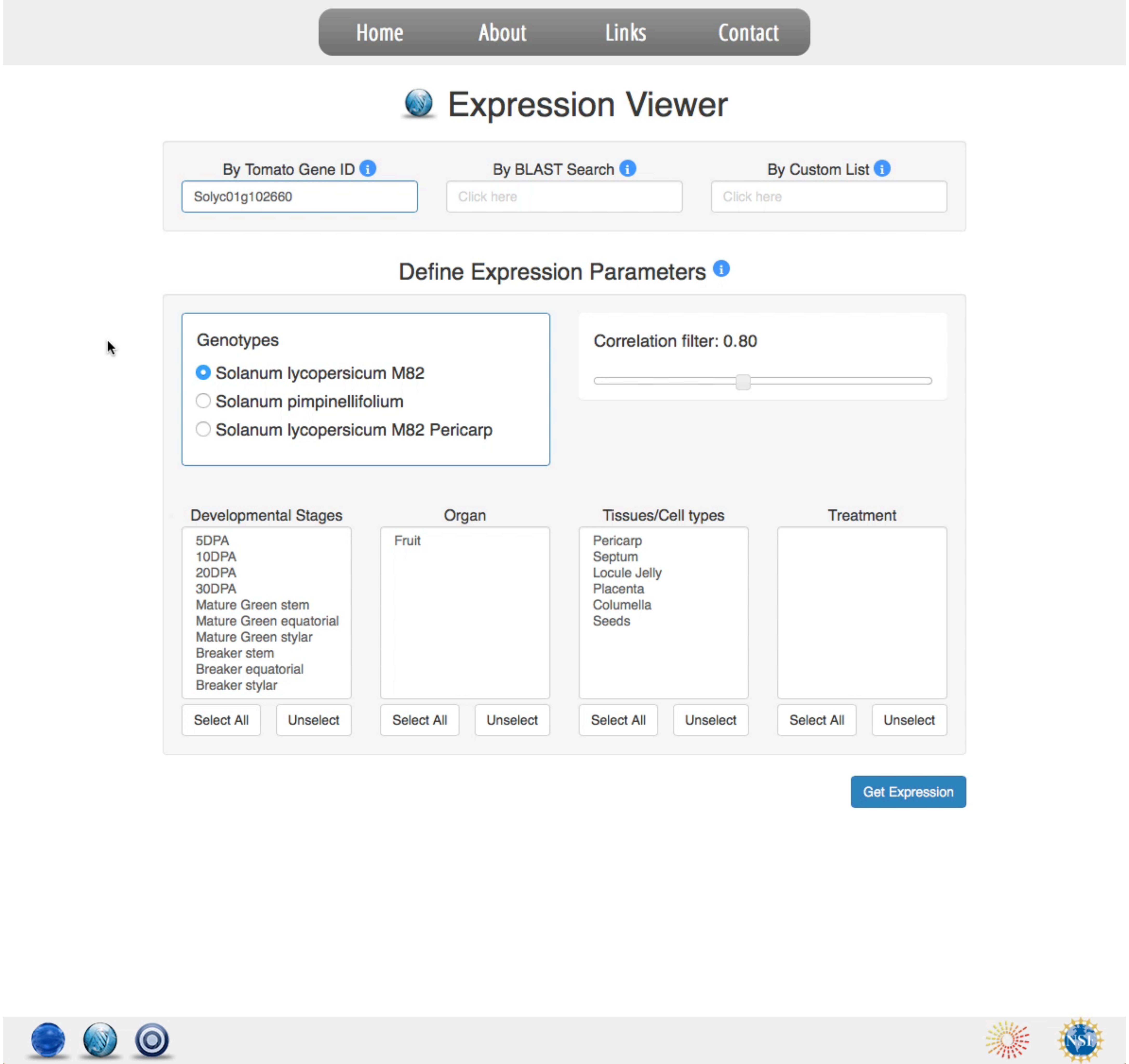


Solanum lycopersicum M82 Fruit ripening

Solyc01g102660

Maleylacetoacetate isomerase / glutathione S-transferase (Q6MR10_BDEBA)

Select a gene: Solyc01g102660



Expression Viewer

By Tomato Gene ID: Solyc01g102660

By BLAST Search: Click here

By Custom List: Click here

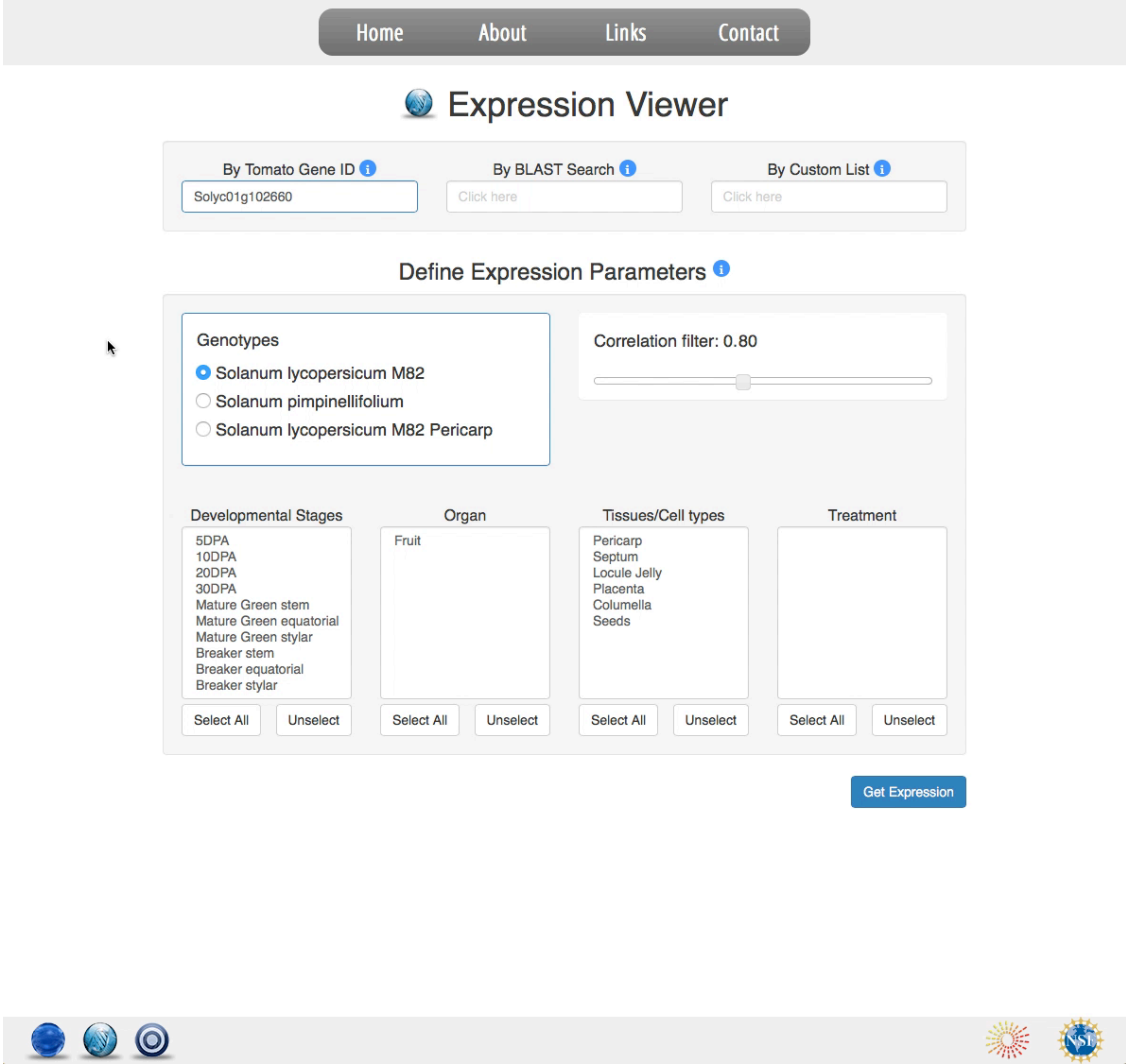
Define Expression Parameters

Genotypes

● Solanum lycopersicum M82
○ Solanum pimpinellifolium
○ Solanum lycopersicum M82 Pericarp

Correlation filter: 0.80

Developmental Stages	Organ	Tissues/Cell types	Treatment
5DPA 10DPA 20DPA 30DPA Mature Green stem Mature Green equatorial Mature Green stylar Breaker stem Breaker equatorial Breaker stylar	Fruit	Pericarp Septum Locule Jelly Placenta Columella Seeds	



Expression Viewer

By Tomato Gene ID: Solyc01g102660

By BLAST Search: Click here

By Custom List: Click here

Define Expression Parameters

Genotypes

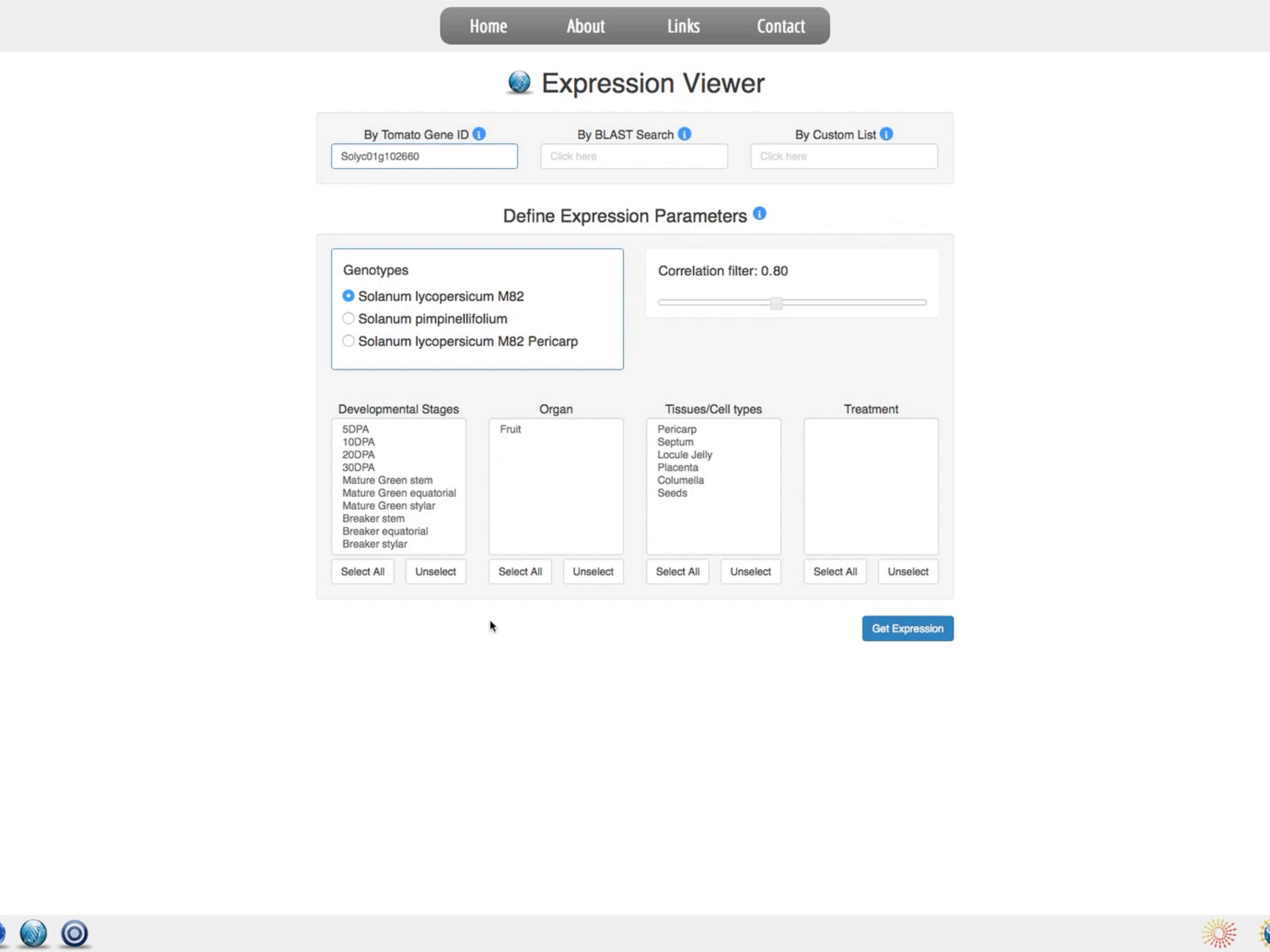
● Solanum lycopersicum M82

○ Solanum pimpinellifolium

○ Solanum lycopersicum M82 Pericarp

Correlation filter: 0.80

Developmental Stages	Organ	Tissues/Cell types	Treatment
5DPA 10DPA 20DPA 30DPA Mature Green stem Mature Green equatorial Mature Green stylar Breaker stem Breaker equatorial Breaker stylar	Fruit	Pericarp Septum Locule Jelly Placenta Columella Seeds	



Expression Viewer

By Tomato Gene ID: Solyc01g102660

By BLAST Search: Click here

By Custom List: Click here

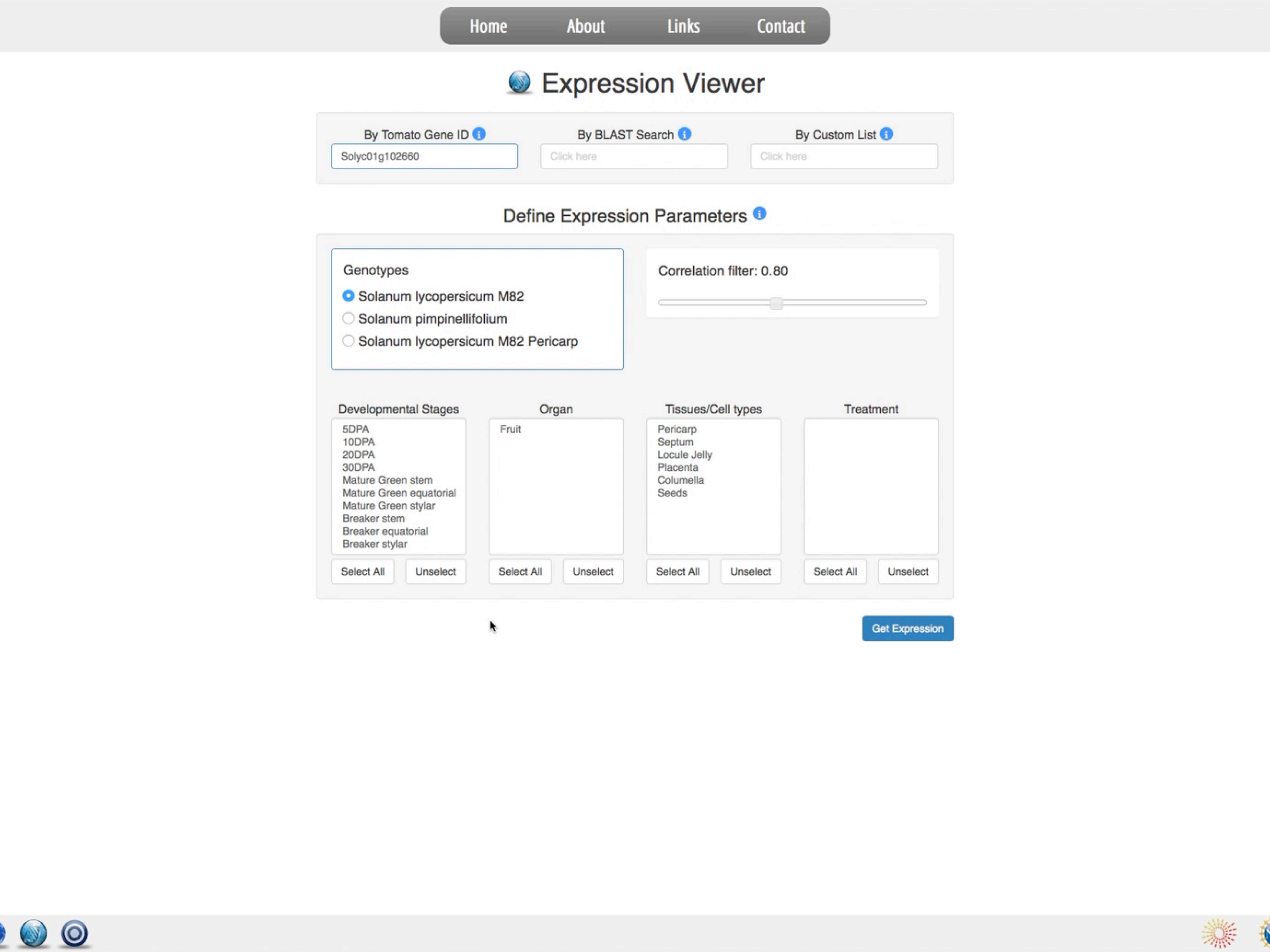
Define Expression Parameters

Genotypes

● Solanum lycopersicum M82
○ Solanum pimpinellifolium
○ Solanum lycopersicum M82 Pericarp

Correlation filter: 0.80

Developmental Stages	Organ	Tissues/Cell types	Treatment
5DPA	Fruit	Pericarp	
10DPA		Septum	
20DPA		Locule Jelly	
30DPA		Placenta	
Mature Green stem		Columella	
Mature Green equatorial		Seeds	
Mature Green stylar			
Breaker stem			
Breaker equatorial			
Breaker stylar			



Expression Viewer

By Tomato Gene ID: Solyc01g102660

By BLAST Search: Click here

By Custom List: Click here

Define Expression Parameters

Genotypes

● Solanum lycopersicum M82
○ Solanum pimpinellifolium
○ Solanum lycopersicum M82 Pericarp

Correlation filter: 0.80

Developmental Stages
- 5DPA
- 10DPA
- 20DPA
- 30DPA
- Mature Green stem
- Mature Green equatorial
- Mature Green stylar
- Breaker stem
- Breaker equatorial
- Breaker stylar

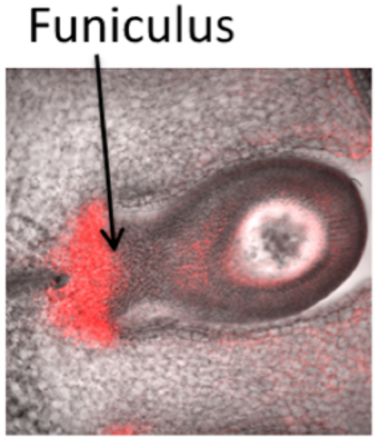
Organ
- Fruit

Tissues/Cell types
- Pericarp
- Septum
- Locule Jelly
- Placenta
- Columella
- Seeds

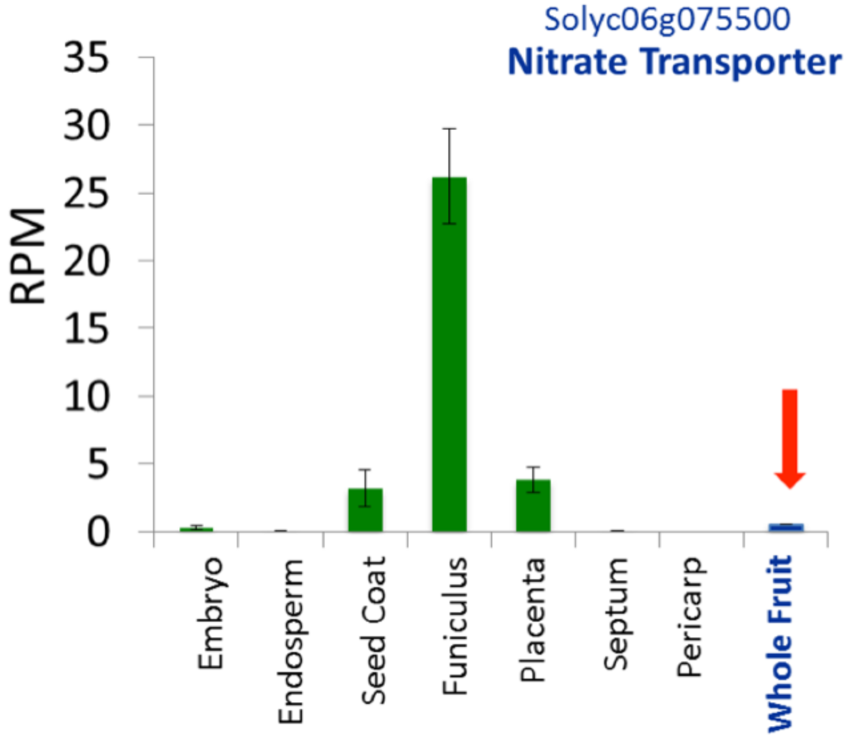
Treatment

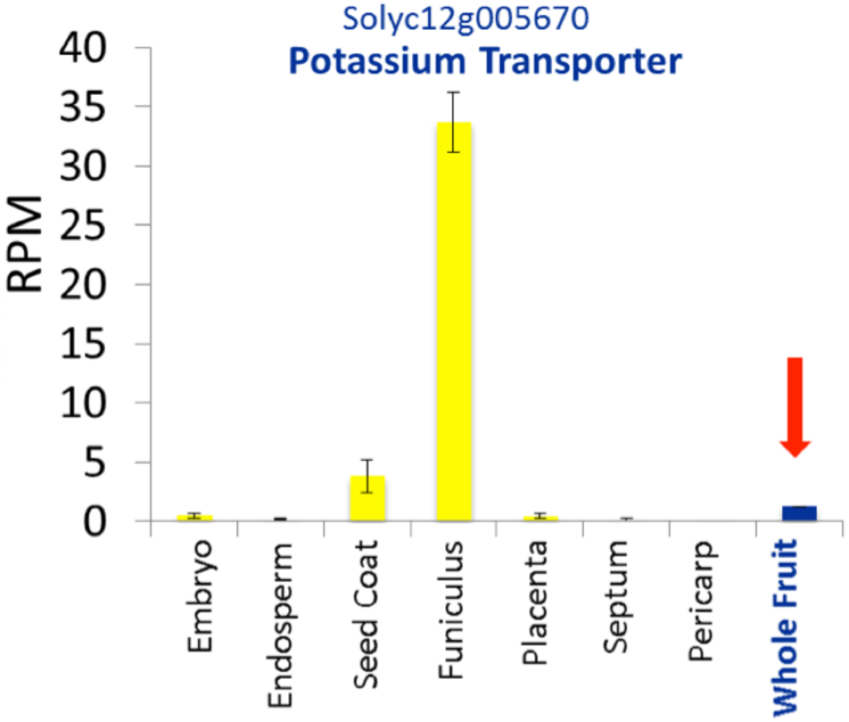
Many genes preferentially expressed in the funiculus are absent from whole fruit RNA-Seq data

Carmen Catala



- Contributes small proportion to total fruit volume
- High transport between seeds and the rest of the fruit

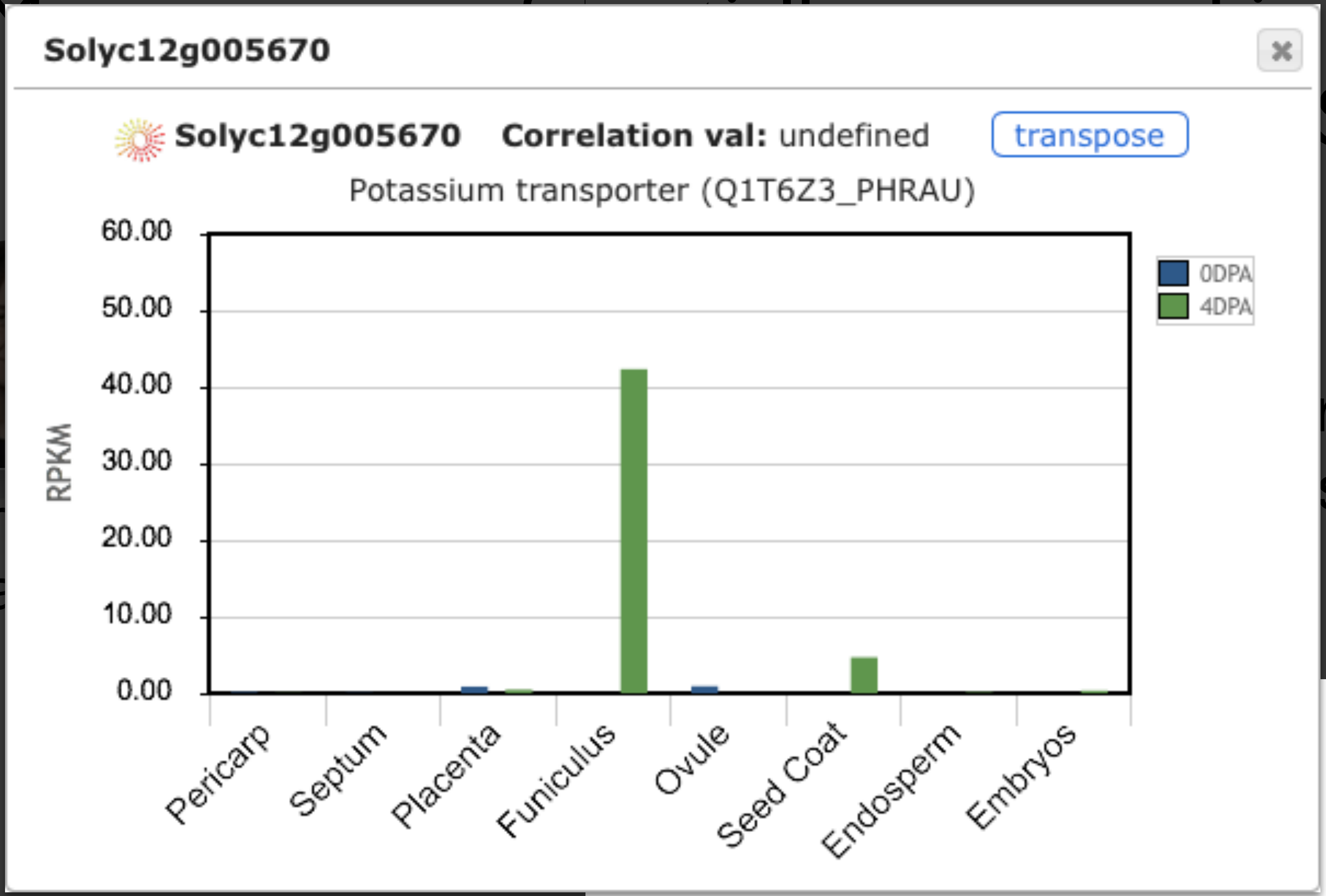




M ... the funiculus ... Seq data

Carm
Cata

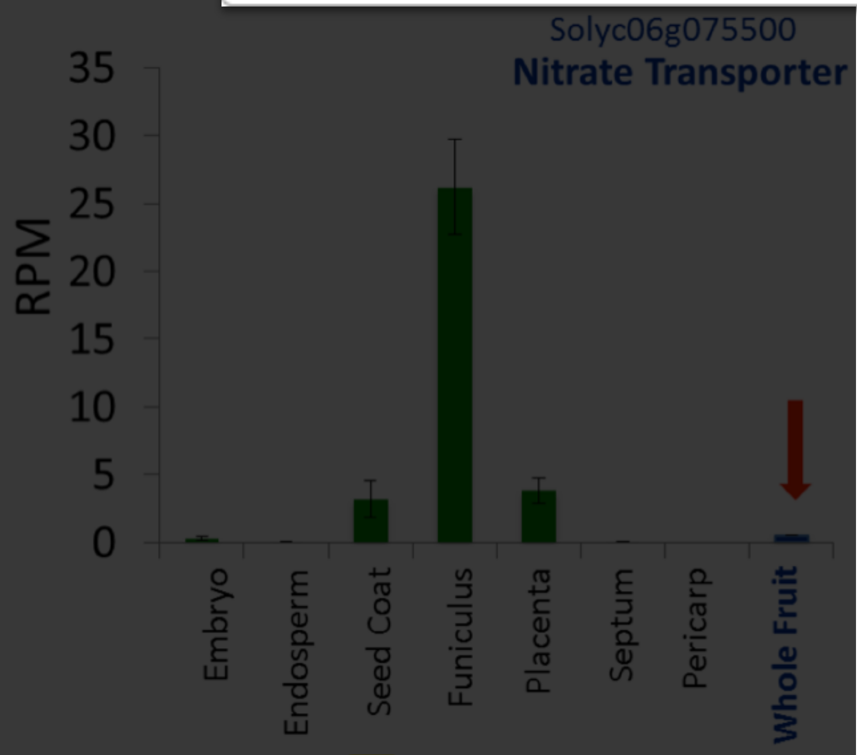
...rtion to total fruit volume
...seeds and the rest of the fruit



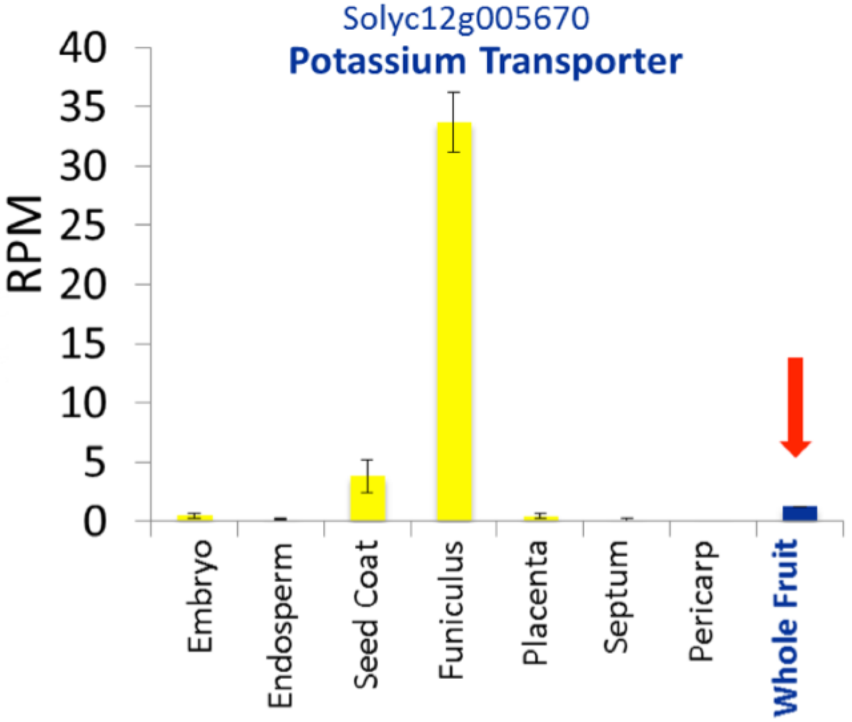
Solyc12g005670

Solyc12g005670 **Correlation val:** undefined

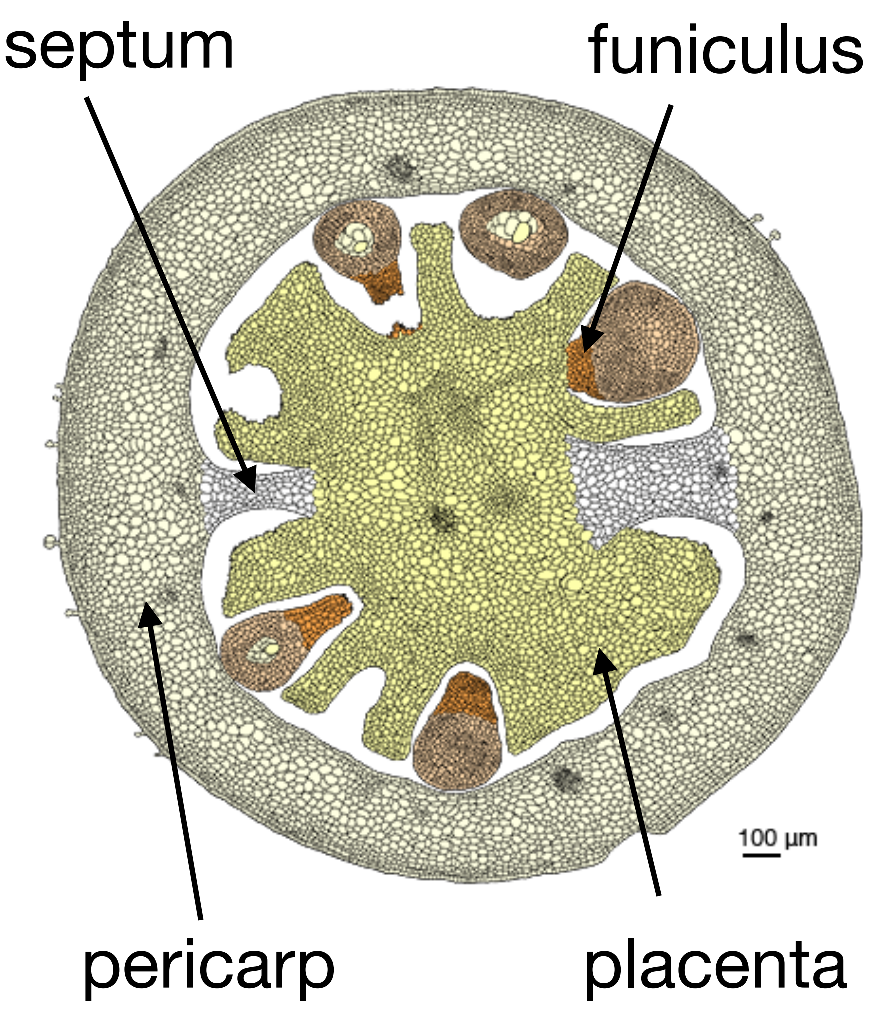
Potassium transporter (Q1T6Z3_PHRAU)



Solyc06g075500
Nitrate Transporter

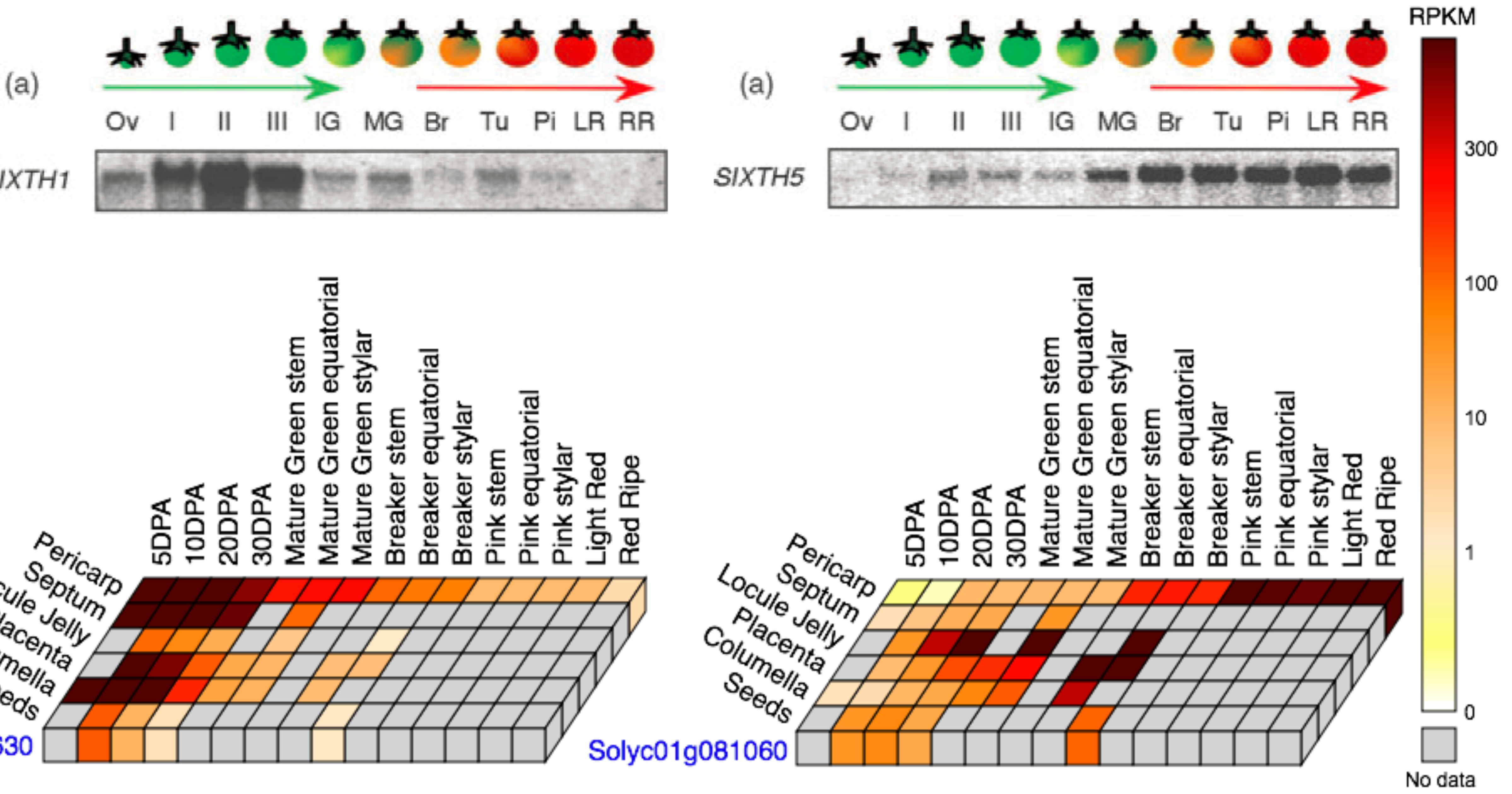


Solyc12g005670
Potassium Transporter

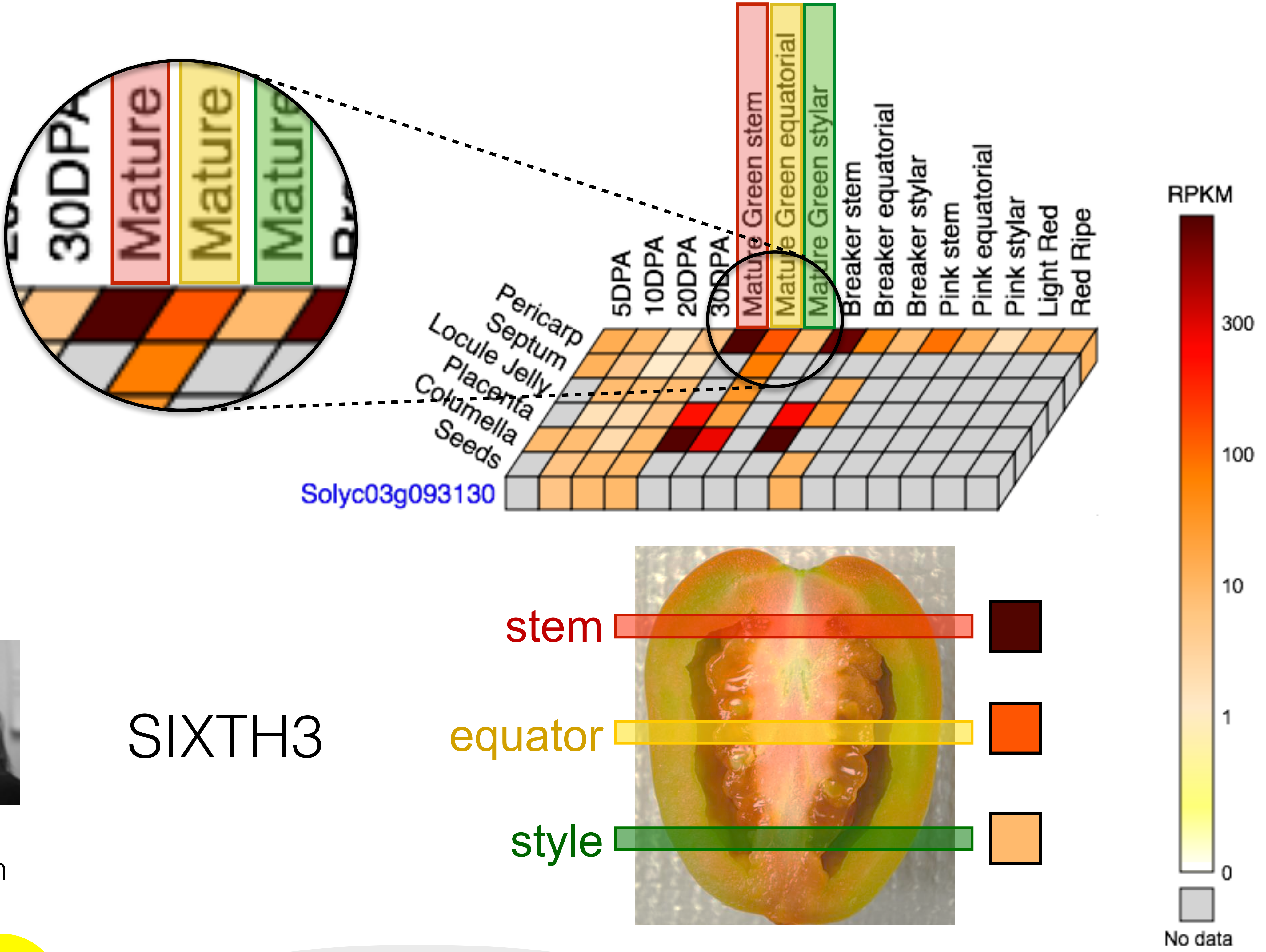


Xyloglucan endotransglucosylase-hydrolases

Iben
Sorensen



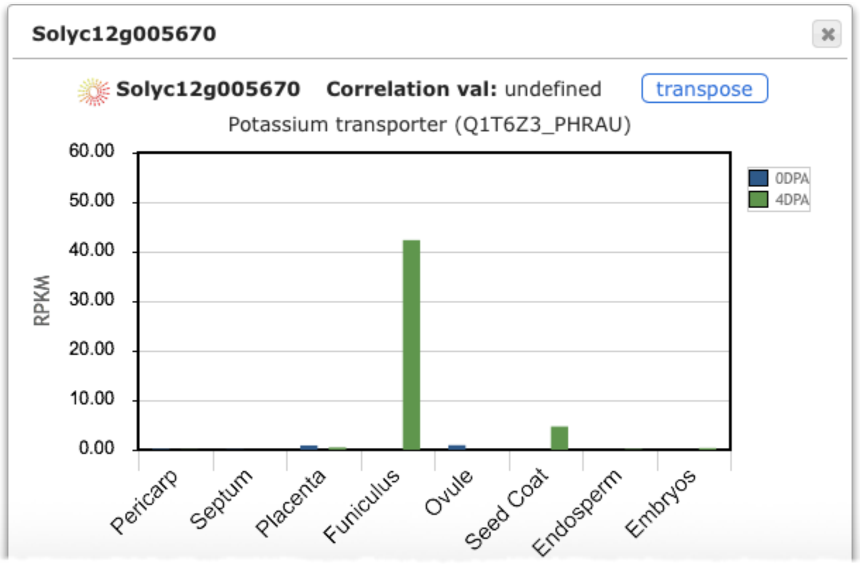
Xyloglucan endotransglucosylase-hydrolases



Iben
Sorensen

SIXTH3

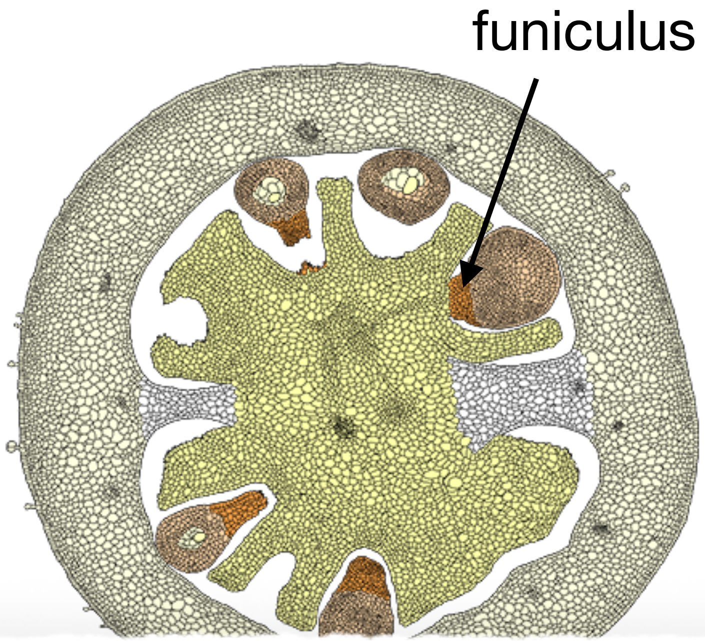
Conclusions



Solyc12g005670

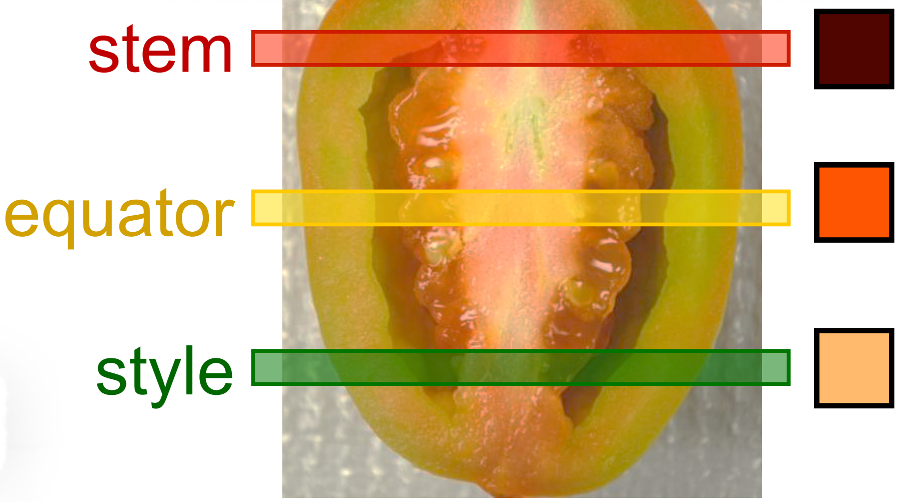
Solyc12g005670 **Correlation val:** undefined transpose

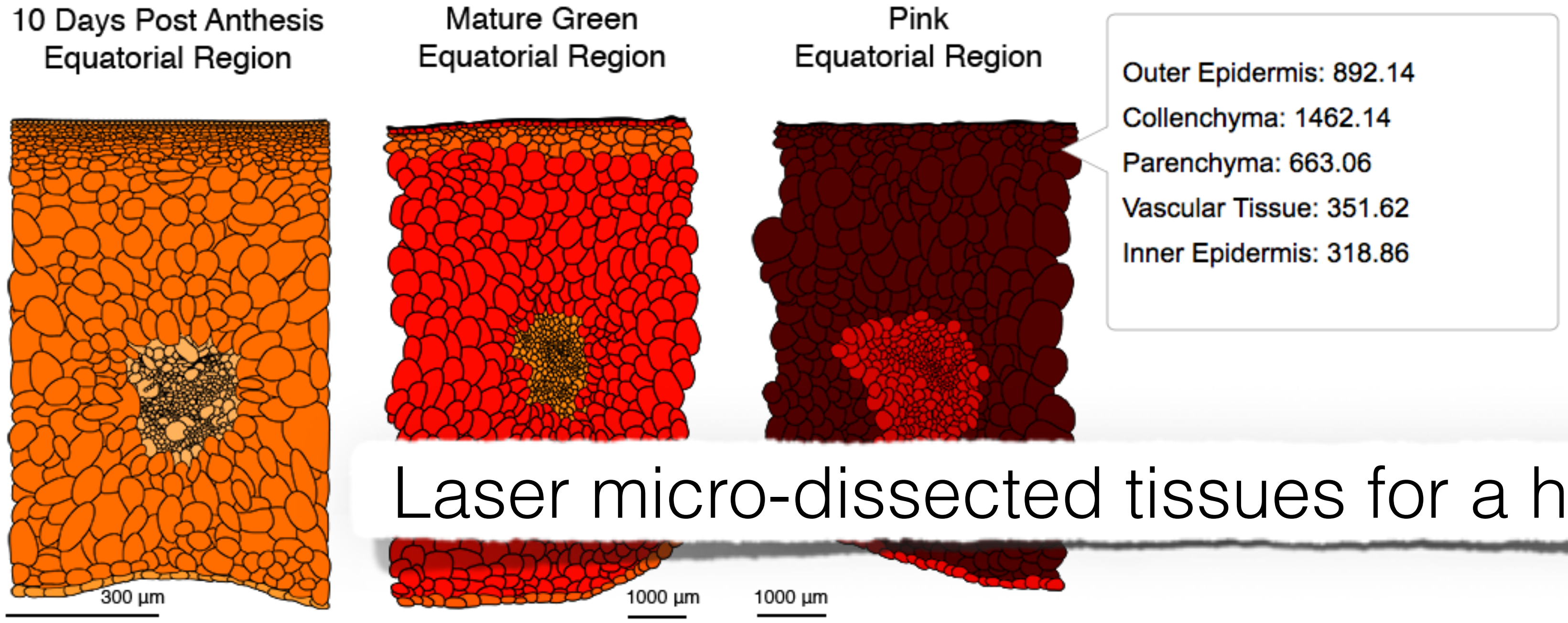
Potassium transporter (Q1T6Z3_PHRAU)



Many tissues for a higher resolution vs Whole fruit

Several fruit sections





10 Days Post Anthesis Equatorial Region

Mature Green Equatorial Region

Pink Equatorial Region

Outer Epidermis: 892.14
Collenchyma: 1462.14
Parenchyma: 663.06
Vascular Tissue: 351.62
Inner Epidermis: 318.86

Laser micro-dissected tissues for a higher resolution

Summary

- **Breeders Tools** to manage breeder programs
- **GMOD Tools** common bioinformatics tools implemented on SGN
- **SGN VIGS Tool** to design VIGS constructs
- **Tomato expression Atlas**, a high resolution expression atlas for tomato fruit developmental stages


BOYCE THOMPSON INSTITUTE
FOR PLANT RESE
533 TOW

Thank you for your attention !