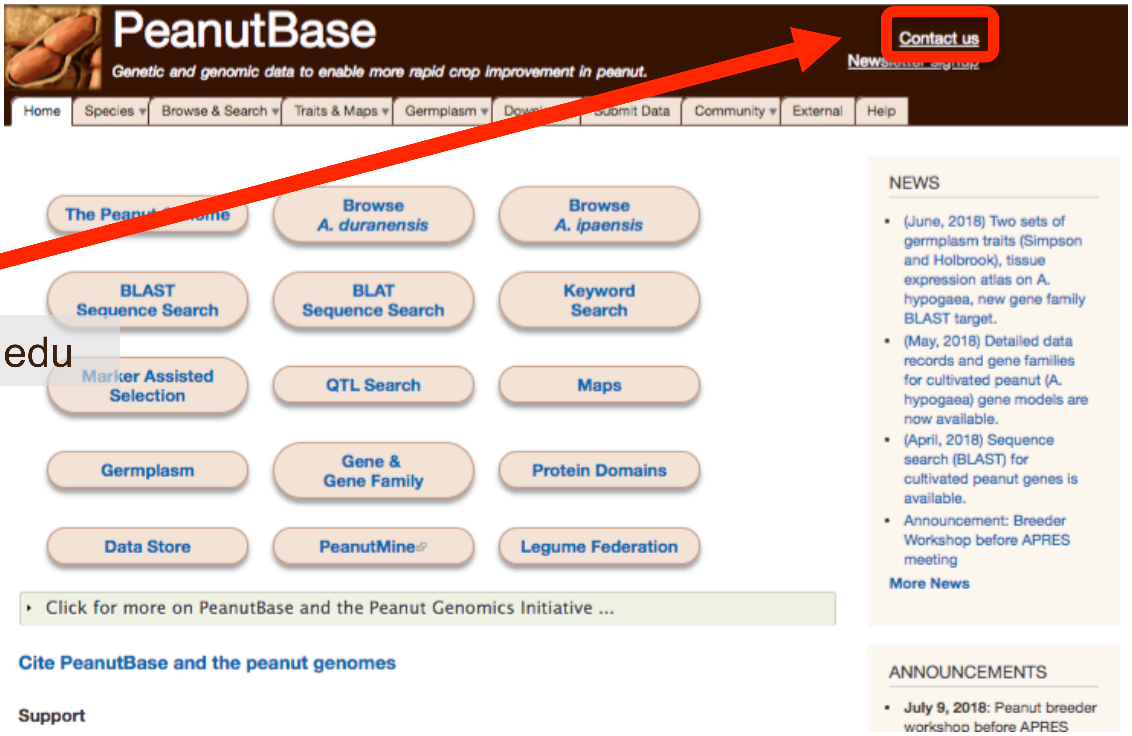
PeanutBase Resources for Breeders

PeanutBase.org

Ethy Cannon
Iowa State University
July 9th, 2018

Talk Overview

PeanutBase is a community resource that exists to serve the peanut breeding and research community.



PeanutBase

Genetic and genomic data to enable more rapid crop improvement in peanut.

Contact us

Newsletter signup

Click for more on PeanutBase and the Peanut Genomics Initiative ...

Cite PeanutBase and the peanut genomes

Support

NEWS

- (June, 2018) Two sets of germplasm traits (Simpson and Holbrook), tissue expression atlas on A. hypogaea, new gene family BLAST target.
- (May, 2018) Detailed data records and gene families for cultivated peanut (A. hypogaea) gene models are now available.
- (April, 2018) Sequence search (BLAST) for cultivated peanut genes is available.
- Announcement: Breeder Workshop before APRES meeting

More News

ANNOUNCEMENTS

- **July 9, 2018:** Peanut breeder workshop before APRES

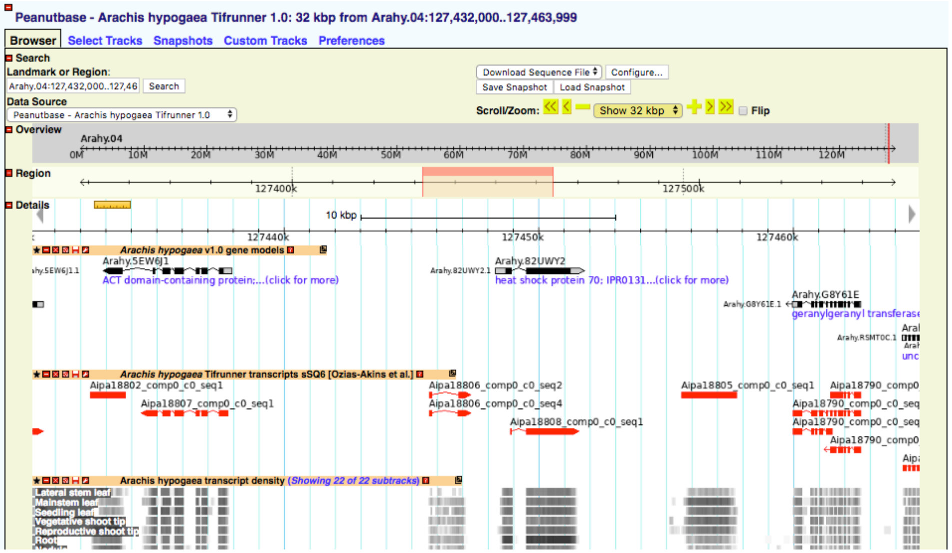
ekcannon@iastate.edu

PeanutBase Resources for Breeders

Genomic resources

- Genome assembly browsers
    - GBrowse and JBrowse
    - ***A. hypogaea*, Tifrunner***
    - *A. duranensis*
    - *A. ipaensis*

*Released in December, 2017 under Fort Lauderdale Agreement

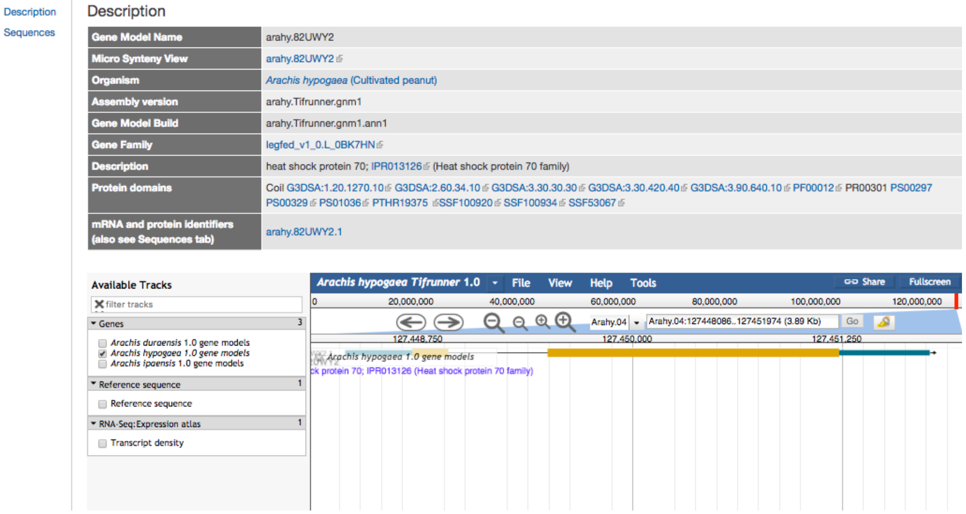


PeanutBase Resources for Breeders

Genomic resources

- Genome assembly browsers
- Gene models
    - ○ ***A. hypogaea*** **Tifrunner***
    - ○ *A. duranensis*
    - ○ *A. ipaensis*

*Released April, 2018; Jacqueline Campbell and Andrew Farmer



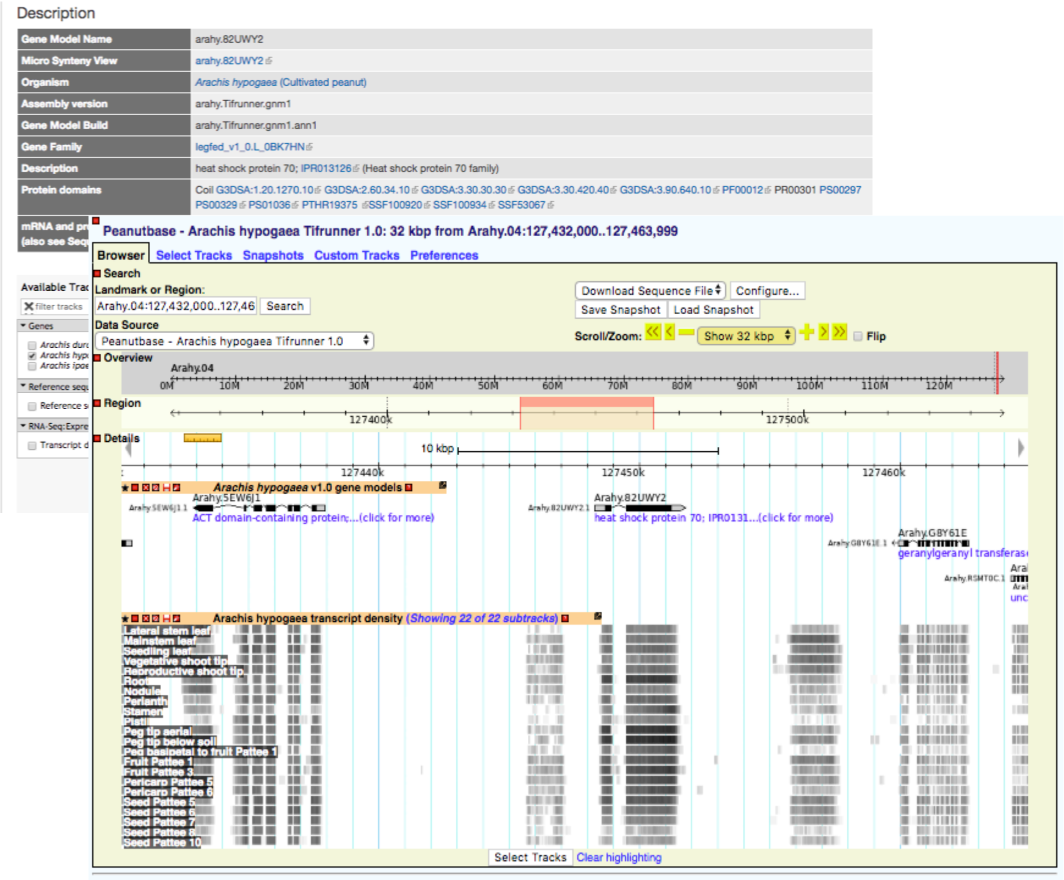
Description

Gene Model Name	arahy.82UWY2
Micro Synteny View	arahy.82UWY2
Organism	*Arachis hypogaea* (Cultivated peanut)
Assembly version	arahy.Tifrunner.gnm1
Gene Model Build	arahy.Tifrunner.gnm1.ann1
Gene Family	legfed_v1_0.L_0BK7HN
Description	heat shock protein 70; IPR013126 (Heat shock protein 70 family)
Protein domains	Coil G3DSA:1.20.1270.10 G3DSA:2.60.34.10 G3DSA:3.30.30.30 G3DSA:3.30.420.40 G3DSA:3.90.640.10 PF00012 PR00301 PS00297 PS00329 PS01036 PTHR19375 SSF100920 SSF100934 SSF53067
mRNA and protein identifiers (also see Sequences tab)	arahy.82UWY2.1

PeanutBase Resources for Breeders

Genomic resources

- Genome assembly browsers
- Gene models
    - Gene function predictions
    - Gene expression



Description

Gene Model Name	arahy.82UWY2
Micro Synteny View	arahy.82UWY2
Organism	*Arachis hypogaea* (Cultivated peanut)
Assembly version	arahy.Tifrunner.gnm1
Gene Model Build	arahy.Tifrunner.gnm1.ann1
Gene Family	legfed_v1_0.L_0BK7HN
Description	heat shock protein 70; IPR013126 (Heat shock protein 70 family)
Protein domains	Coil G3DSA:1.20.1270.10 G3DSA:2.60.34.10 G3DSA:3.30.30.30 G3DSA:3.30.420.40 G3DSA:3.90.640.10 PF00012 PR00301 PS00297 PS00329 PS01036 PTHR19375 SSF100920 SSF100934 SSF53067
mRNA and pr (also see Seq	

Peanutbase - Arachis hypogaea Tifrunner 1.0: 32 kbp from Arahy.04:127,432,000..127,463,999

Landmark or Region: Arahy.04:127,432,000..127,46

Data Source: Peanutbase - Arachis hypogaea Tifrunner 1.0

Scroll/Zoom: Show 32 kbp

PeanutBase Resources for Breeders

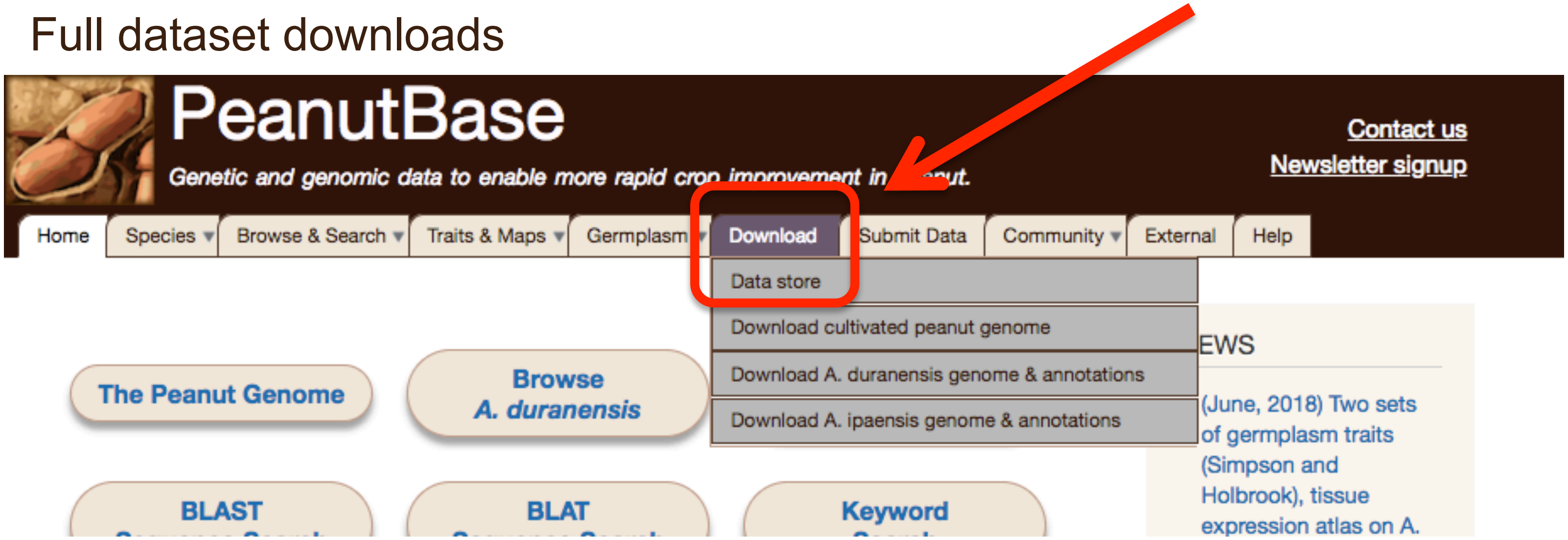
Genomic resources

- Genome assembly browsers
- Gene models
- Markers, including the Affy SNP chip markers.
    - Aligned on diploids, soon on Tiffrunner
    - Searchable in database
    - Download files available

PeanutBase Resources for Breeders

Genomic resources

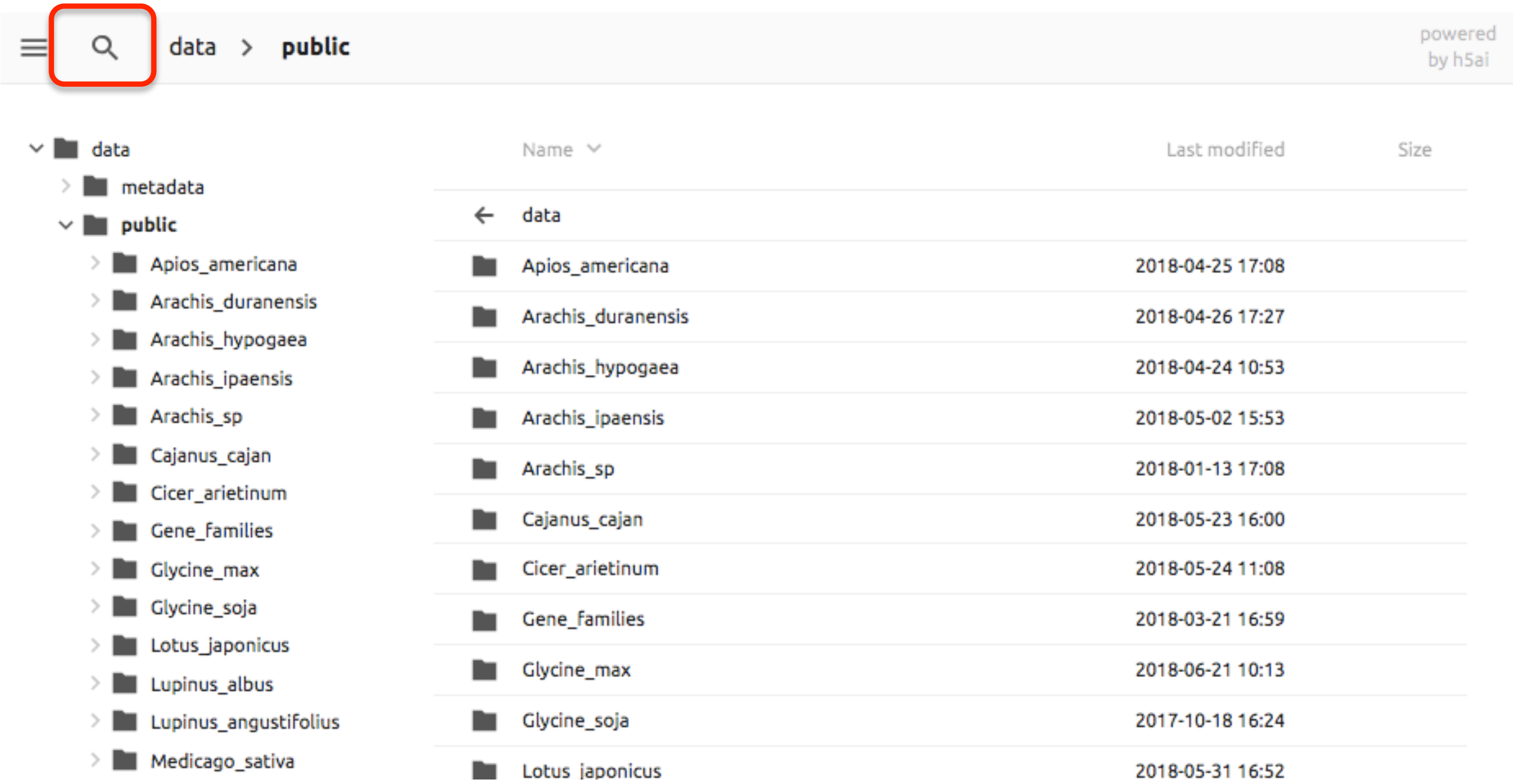
- Genome assembly browsers
- Gene models
- Markers, including the Affy SNP chip markers
- Full dataset downloads



(June, 2018) Two sets of germplasm traits (Simpson and Holbrook), tissue expression atlas on A.

PeanutBase Resources for Breeders

Data Store

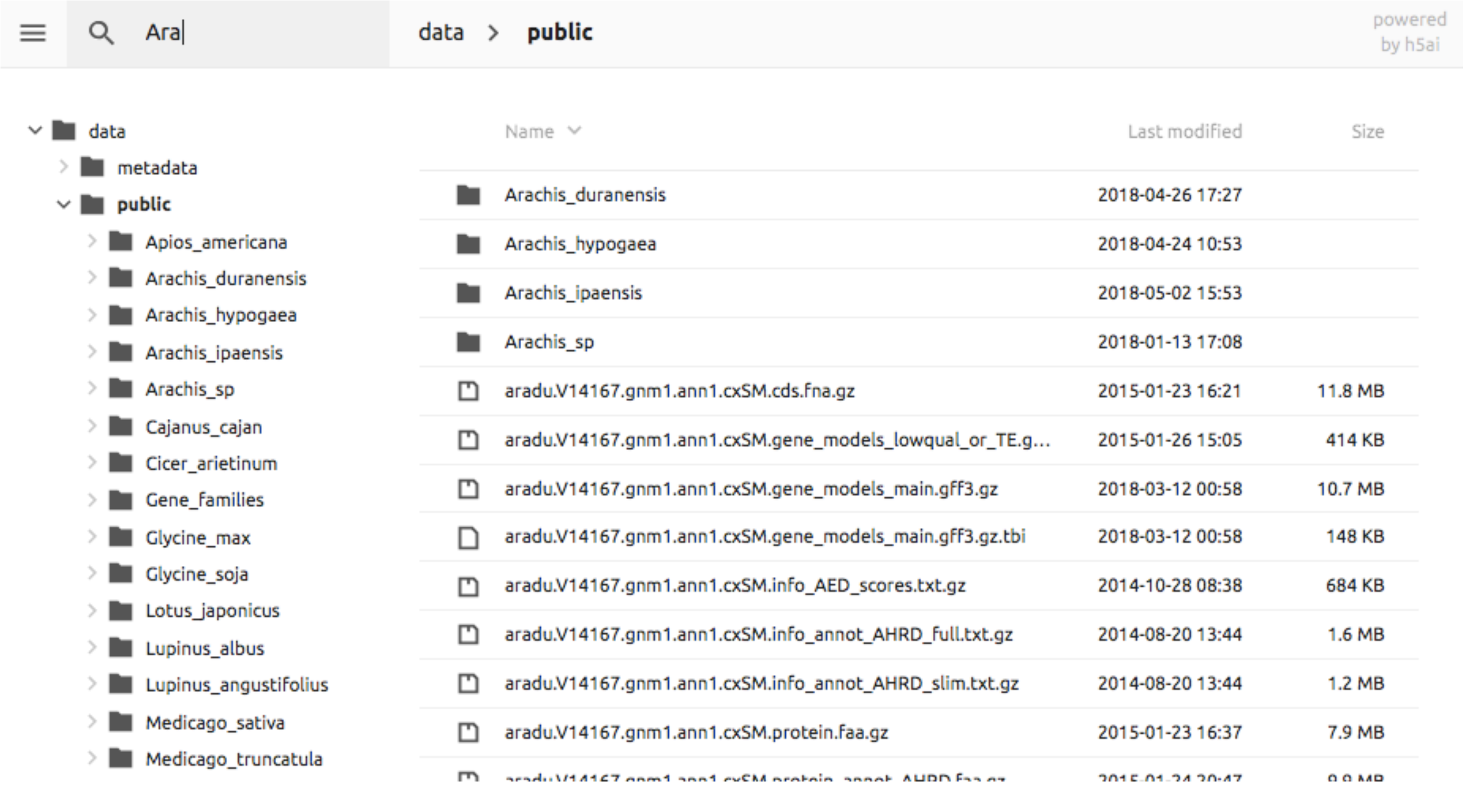


- data
  - metadata
  - public
    - Apios_americana
    - Arachis_duranensis
    - Arachis_hypogaea
    - Arachis_ipaensis
    - Arachis_sp
    - Cajanus_cajan
    - Cicer_arietinum
    - Gene_families
    - Glycine_max
    - Glycine_soja
    - Lotus_japonicus
    - Lupinus_albus
    - Lupinus_angustifolius
    - Medicago_sativa

Name	Last modified	Size
← data		
Apios_americana	2018-04-25 17:08	
Arachis_duranensis	2018-04-26 17:27	
Arachis_hypogaea	2018-04-24 10:53	
Arachis_ipaensis	2018-05-02 15:53	
Arachis_sp	2018-01-13 17:08	
Cajanus_cajan	2018-05-23 16:00	
Cicer_arietinum	2018-05-24 11:08	
Gene_families	2018-03-21 16:59	
Glycine_max	2018-06-21 10:13	
Glycine_soja	2017-10-18 16:24	
Lotus_japonicus	2018-05-31 16:52	

PeanutBase Resources for Breeders

Data Store

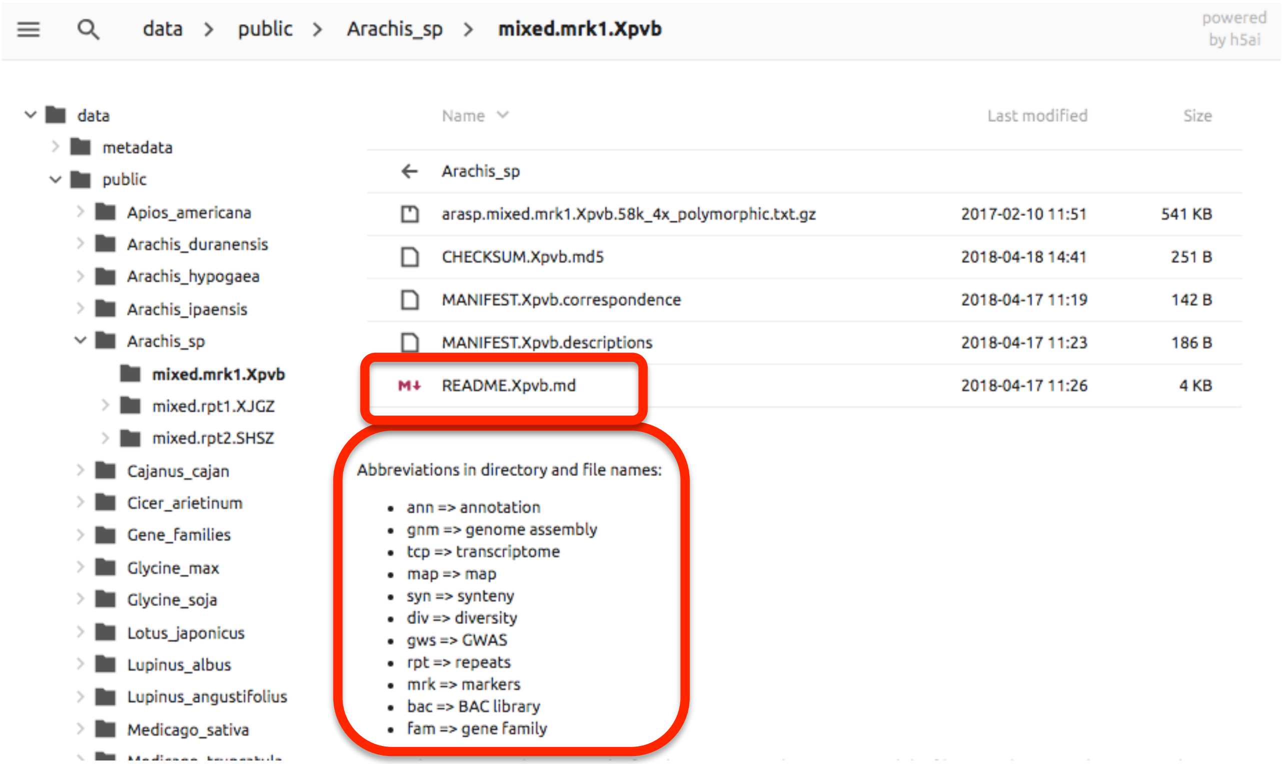


- data
  - metadata
  - public
    - Apios_americana
    - Arachis_duranensis
    - Arachis_hypogaea
    - Arachis_ipaensis
    - Arachis_sp
    - Cajanus_cajan
    - Cicer_arietinum
    - Gene_families
    - Glycine_max
    - Glycine_soja
    - Lotus_japonicus
    - Lupinus_albus
    - Lupinus_angustifolius
    - Medicago_sativa
    - Medicago_truncatula

Name	Last modified	Size
Arachis_duranensis	2018-04-26 17:27	
Arachis_hypogaea	2018-04-24 10:53	
Arachis_ipaensis	2018-05-02 15:53	
Arachis_sp	2018-01-13 17:08	
aradu.V14167.gnm1.ann1.cxSM.cds.fna.gz	2015-01-23 16:21	11.8 MB
aradu.V14167.gnm1.ann1.cxSM.gene_models_lowqual_or_TE.g...	2015-01-26 15:05	414 KB
aradu.V14167.gnm1.ann1.cxSM.gene_models_main.gff3.gz	2018-03-12 00:58	10.7 MB
aradu.V14167.gnm1.ann1.cxSM.gene_models_main.gff3.gz.tbi	2018-03-12 00:58	148 KB
aradu.V14167.gnm1.ann1.cxSM.info_AED_scores.txt.gz	2014-10-28 08:38	684 KB
aradu.V14167.gnm1.ann1.cxSM.info_annot_AHRD_full.txt.gz	2014-08-20 13:44	1.6 MB
aradu.V14167.gnm1.ann1.cxSM.info_annot_AHRD_slim.txt.gz	2014-08-20 13:44	1.2 MB
aradu.V14167.gnm1.ann1.cxSM.protein.faa.gz	2015-01-23 16:37	7.9 MB

PeanutBase Resources for Breeders

Data Store



data > public > Arachis_sp > **mixed.mrk1.Xpvb**

- data
  - metadata
  - public
    - Apios_americana
    - Arachis_duranensis
    - Arachis_hypogaea
    - Arachis_ipaensis
    - Arachis_sp
      - **mixed.mrk1.Xpvb**
      - mixed.rpt1.XJGZ
      - mixed.rpt2.SHSZ
    - Cajanus_cajan
    - Cicer_arietinum
    - Gene_families
    - Glycine_max
    - Glycine_soja
    - Lotus_japonicus
    - Lupinus_albus
    - Lupinus_angustifolius
    - Medicago_sativa

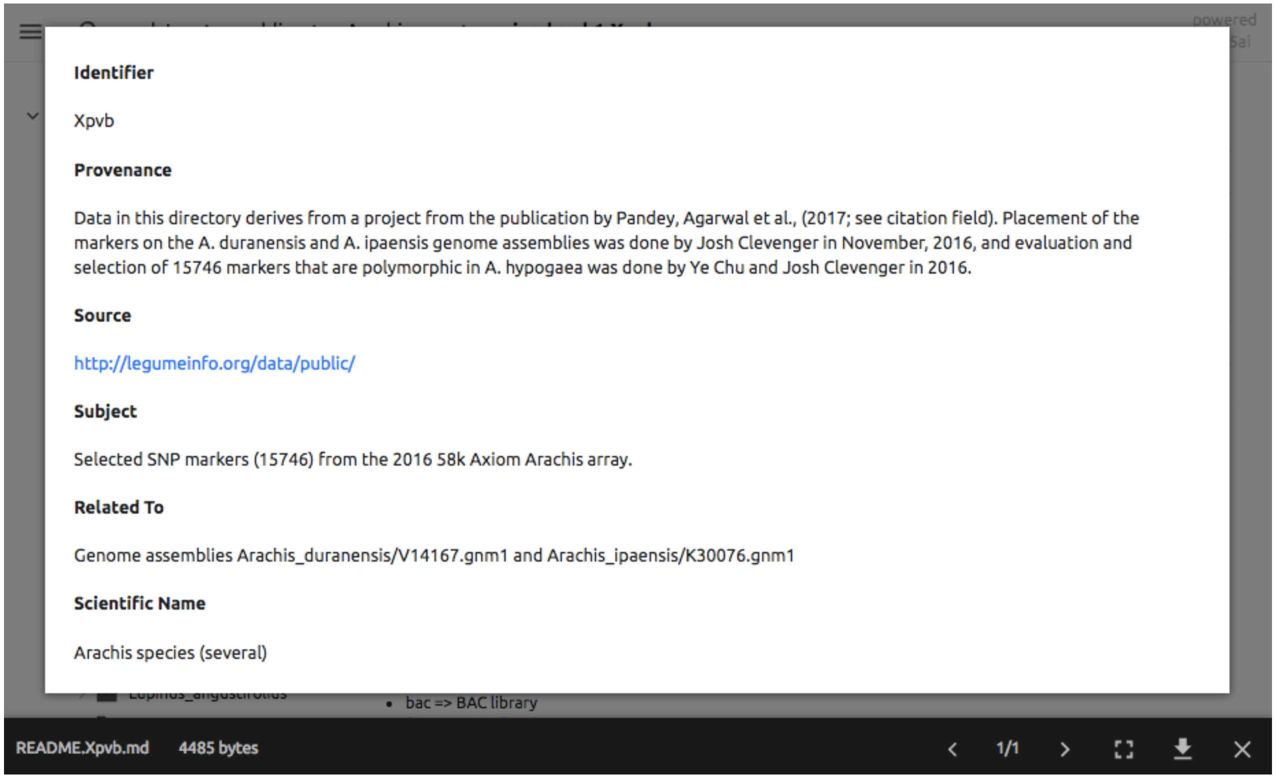
Name	Last modified	Size
← Arachis_sp		
arasp.mixed.mrk1.Xpvb.58k_4x_polymorphic.txt.gz	2017-02-10 11:51	541 KB
CHECKSUM.Xpvb.md5	2018-04-18 14:41	251 B
MANIFEST.Xpvb.correspondence	2018-04-17 11:19	142 B
MANIFEST.Xpvb.descriptions	2018-04-17 11:23	186 B
README.Xpvb.md	2018-04-17 11:26	4 KB

Abbreviations in directory and file names:

- ann => annotation
- gnm => genome assembly
- tcp => transcriptome
- map => map
- syn => synteny
- div => diversity
- gws => GWAS
- rpt => repeats
- mrk => markers
- bac => BAC library
- fam => gene family

PeanutBase Resources for Breeders

Data Store



Identifier

Xpvb

Provenance

Data in this directory derives from a project from the publication by Pandey, Agarwal et al., (2017; see citation field). Placement of the markers on the A. duranensis and A. ipaensis genome assemblies was done by Josh Clevenger in November, 2016, and evaluation and selection of 15746 markers that are polymorphic in A. hypogaea was done by Ye Chu and Josh Clevenger in 2016.

Source

http://legumeinfo.org/data/public/

Subject

Selected SNP markers (15746) from the 2016 58k Axiom Arachis array.

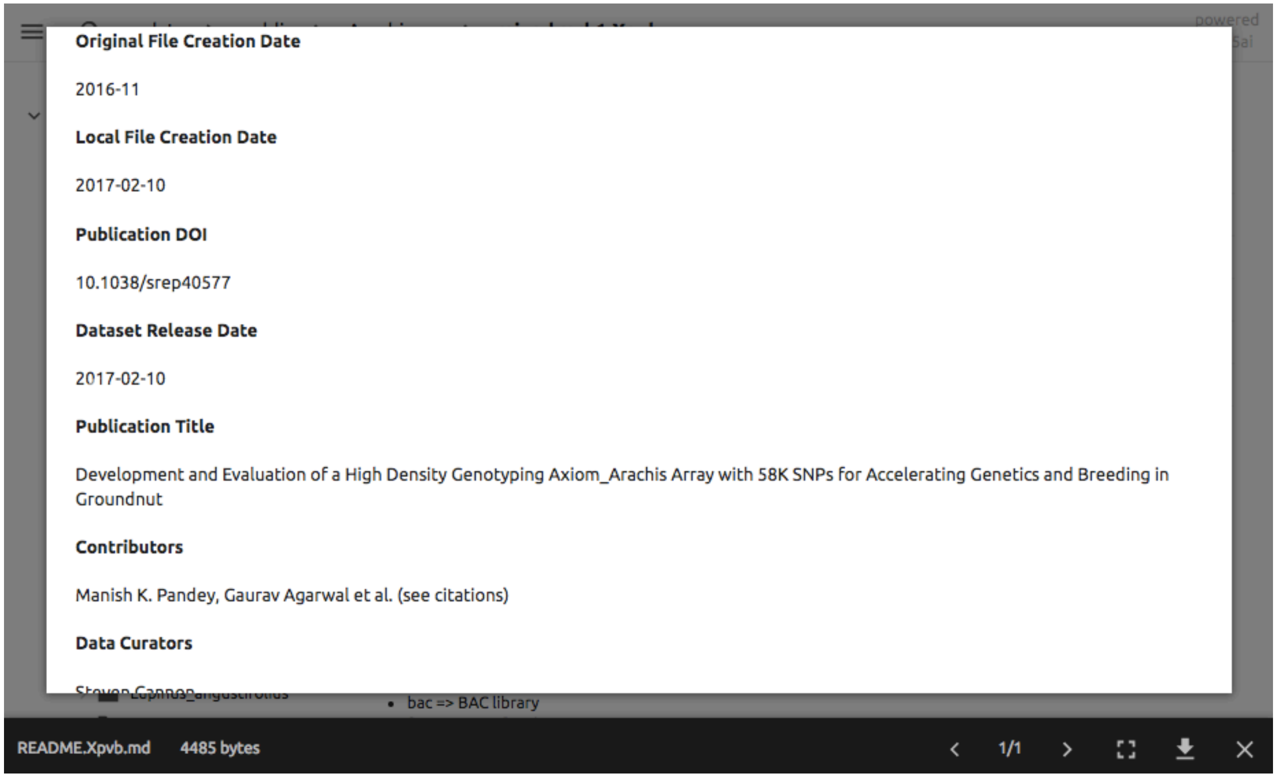
Related To

Genome assemblies Arachis_duranensis/V14167.gnm1 and Arachis_ipaensis/K30076.gnm1

Scientific Name

Arachis species (several)

Data Store



Original File Creation Date

2016-11

Local File Creation Date

2017-02-10

Publication DOI

10.1038/srep40577

Dataset Release Date

2017-02-10

Publication Title

Development and Evaluation of a High Density Genotyping Axiom_Arachis Array with 58K SNPs for Accelerating Genetics and Breeding in Groundnut

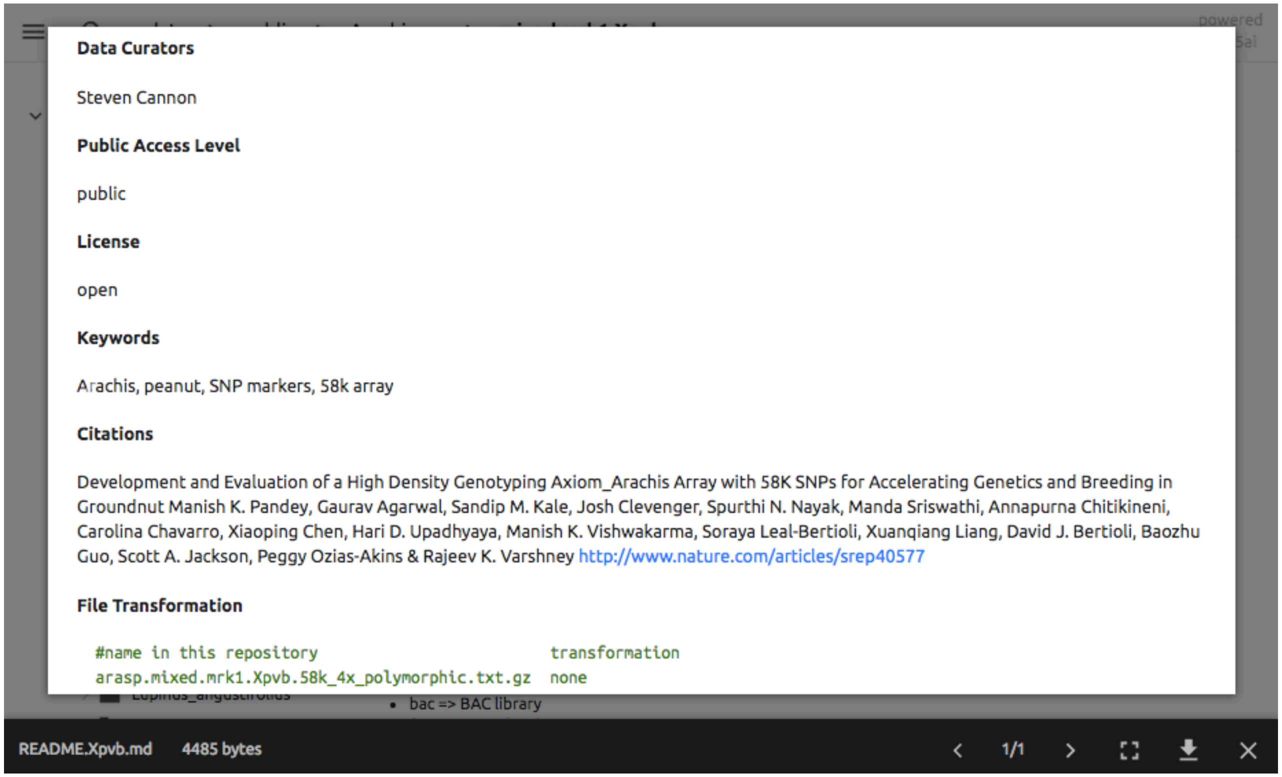
Contributors

Manish K. Pandey, Gaurav Agarwal et al. (see citations)

Data Curators

Steven Cannon

Data Store



Data Curators

Steven Cannon

Public Access Level

public

License

open

Keywords

Arachis, peanut, SNP markers, 58k array

Citations

Development and Evaluation of a High Density Genotyping Axiom_Arachis Array with 58K SNPs for Accelerating Genetics and Breeding in Groundnut Manish K. Pandey, Gaurav Agarwal, Sandip M. Kale, Josh Clevenger, Spurthi N. Nayak, Manda Sriswathi, Annapurna Chitikineni, Carolina Chavarro, Xiaoping Chen, Hari D. Upadhyaya, Manish K. Vishwakarma, Soraya Leal-Bertioli, Xuanqiang Liang, David J. Bertioli, Baozhu Guo, Scott A. Jackson, Peggy Ozias-Akins & Rajeev K. Varshney http://www.nature.com/articles/srep40577

File Transformation

```
#name in this repository                         transformation
arasp.mixed.mrk1.Xpvb.58k_4x_polymorphic.txt.gz  none
```

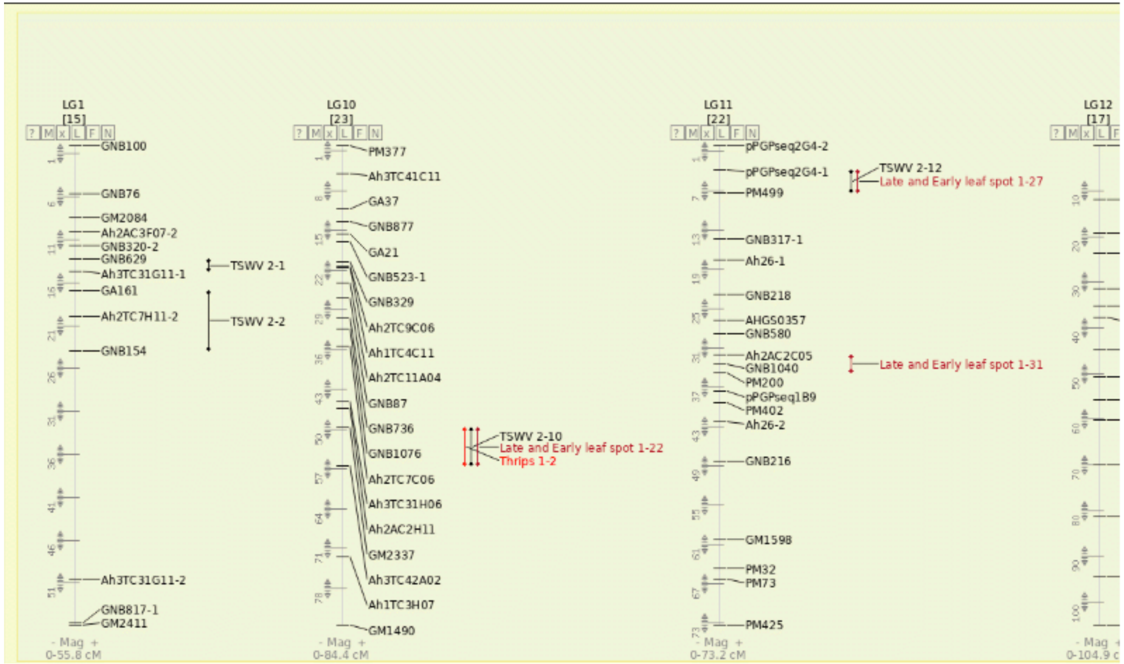
- bac => BAC library

PeanutBase Resources for Breeders

Genetic resources

- Genetic maps collected from literature

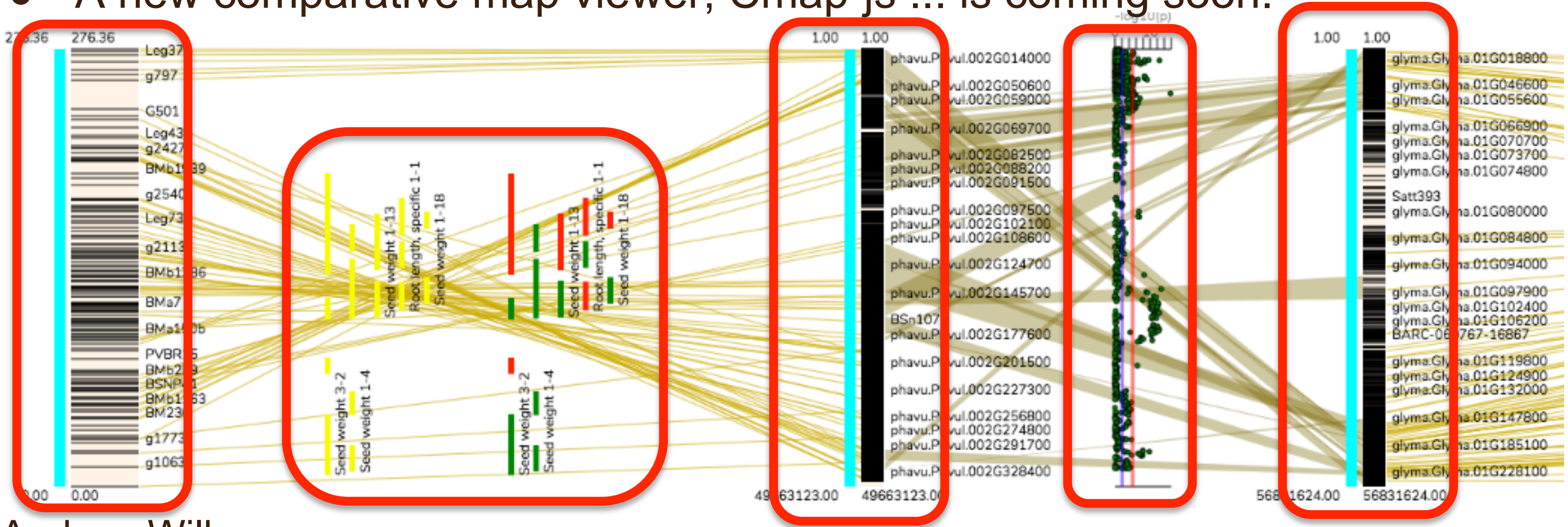
cMap



PeanutBase Resources for Breeders

Genetic resources

- Genetic maps collected from literature
- A new comparative map viewer, Cmap-js ... is coming soon.*

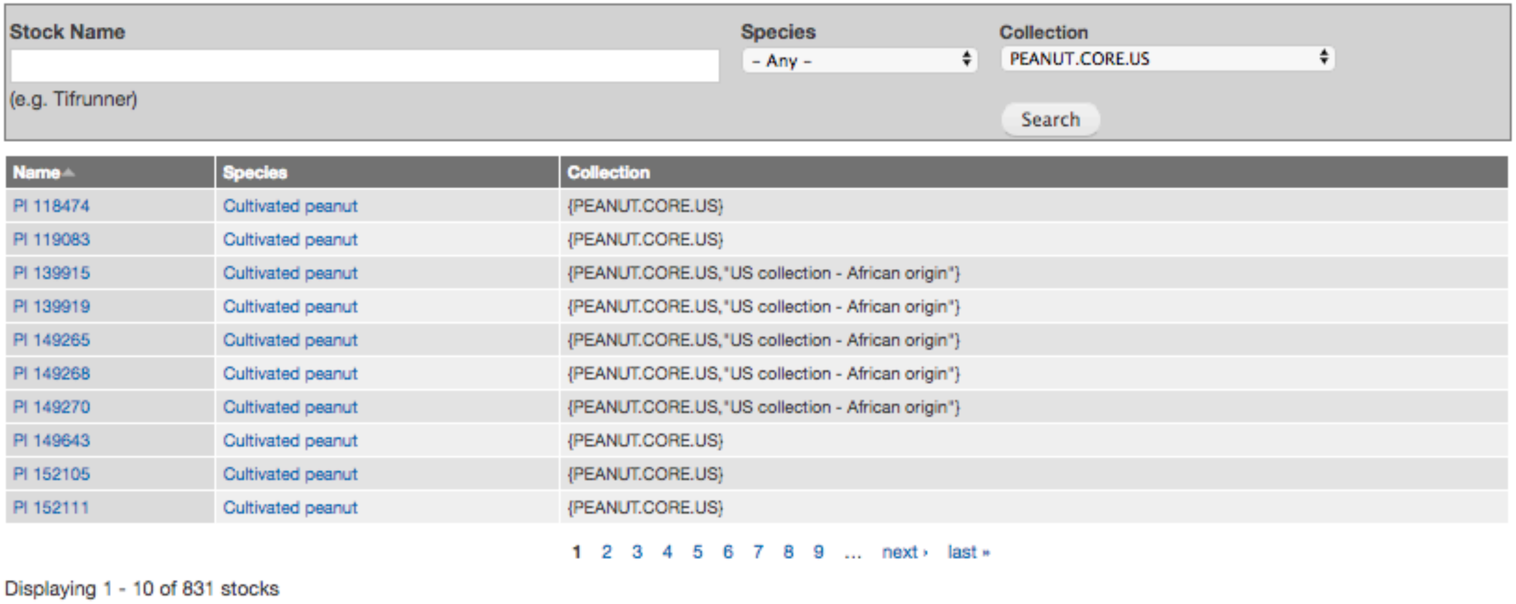


*Andrew Wilkey

PeanutBase Resources for Breeders

Germplasm data

- All GRIN germplasm and trait data mirrored at PeanutBase



Name	Species	Collection
PI 118474	Cultivated peanut	{PEANUT.CORE.US}
PI 119083	Cultivated peanut	{PEANUT.CORE.US}
PI 139915	Cultivated peanut	{PEANUT.CORE.US,"US collection - African origin"}
PI 139919	Cultivated peanut	{PEANUT.CORE.US,"US collection - African origin"}
PI 149265	Cultivated peanut	{PEANUT.CORE.US,"US collection - African origin"}
PI 149268	Cultivated peanut	{PEANUT.CORE.US,"US collection - African origin"}
PI 149270	Cultivated peanut	{PEANUT.CORE.US,"US collection - African origin"}
PI 149643	Cultivated peanut	{PEANUT.CORE.US}
PI 152105	Cultivated peanut	{PEANUT.CORE.US}
PI 152111	Cultivated peanut	{PEANUT.CORE.US}

Displaying 1 - 10 of 831 stocks

PeanutBase Resources for Breeders

Germplasm data

- All GRIN germplasm and trait data mirrored at PeanutBase
- GIS view of germplasm origins

Results: 200 Your max # of results are listed below, but may appear to be clustered at the center of the map. Try zooming the map in, change search parameters, or increase the max # of results. ×

accession	taxon	crop name	orig country		collection site	acq date	elev (m.)
PI 475871	● Arachis hypogaea var. hypogaea		BRA		Farm, Guajara-Mirim	1981-12-01	140
PI 590516	● Arachis hypogaea var. fastigiata	Valencia peanut	BRA		Cruizeiro do Sul. Cultivated upriver in ...	1993-12-09	300
PI [illegible]	● Arachis hypogaea var. fastigiata	Valencia peanut	BRA		Cruzeiro do Sul. Cultivated upriver in t	1993-12-09	300

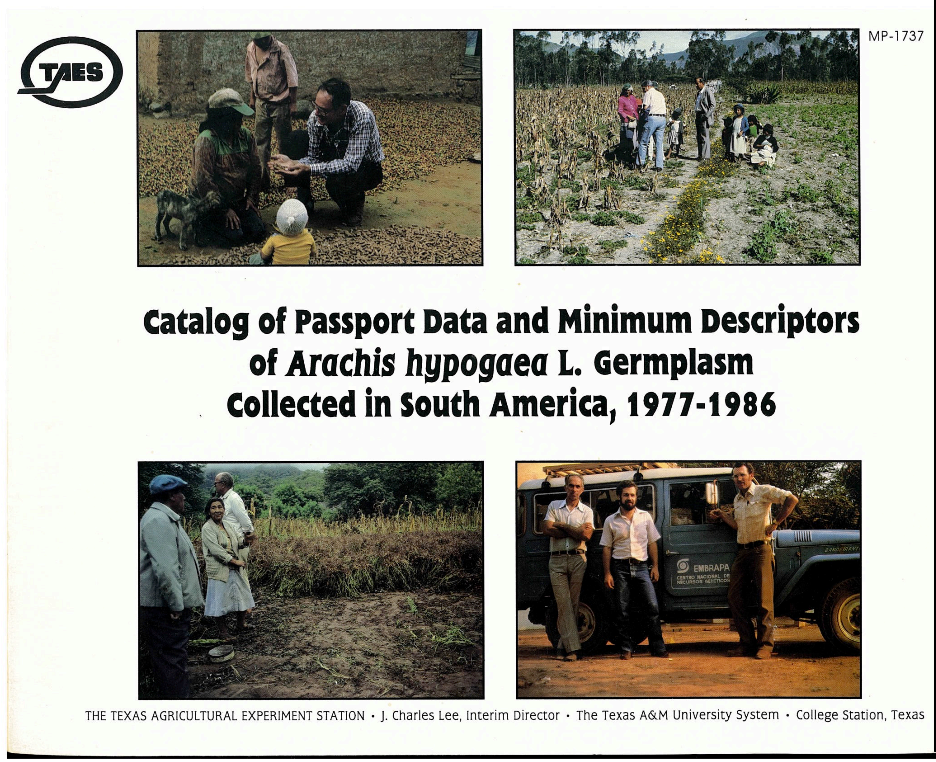
PeanutBase Resources for Breeders

Germplasm data

- All GRIN germplasm and trait data mirrored at PeanutBase
- GIS view of germplasm origins
- Traits from multiple studies attached to germplasm

PeanutBase Resources for Breeders

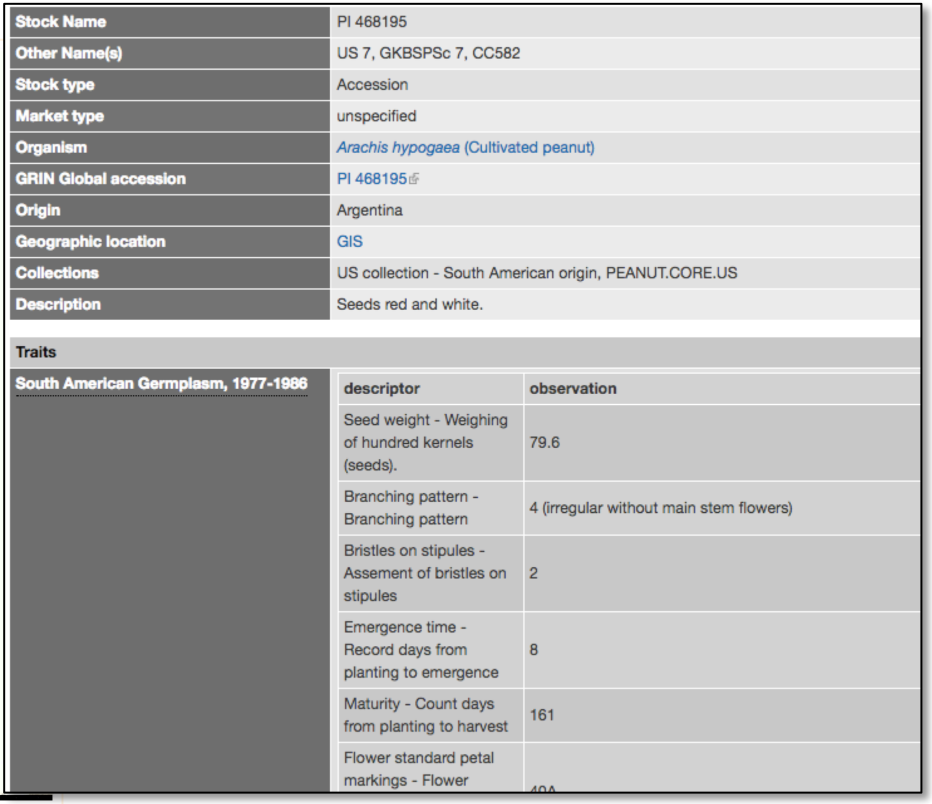
Traits collected by Charles Simpson and colleagues in 1980s



MP-1737

Catalog of Passport Data and Minimum Descriptors of *Arachis hypogaea* L. Germplasm Collected in South America, 1977-1986

THE TEXAS AGRICULTURAL EXPERIMENT STATION • J. Charles Lee, Interim Director • The Texas A&M University System • College Station, Texas



Stock Name	PI 468195
Other Name(s)	US 7, GKBSPSc 7, CC582
Stock type	Accession
Market type	unspecified
Organism	*Arachis hypogaea* (Cultivated peanut)
GRIN Global accession	PI 468195
Origin	Argentina
Geographic location	GIS
Collections	US collection - South American origin, PEANUT.CORE.US
Description	Seeds red and white.

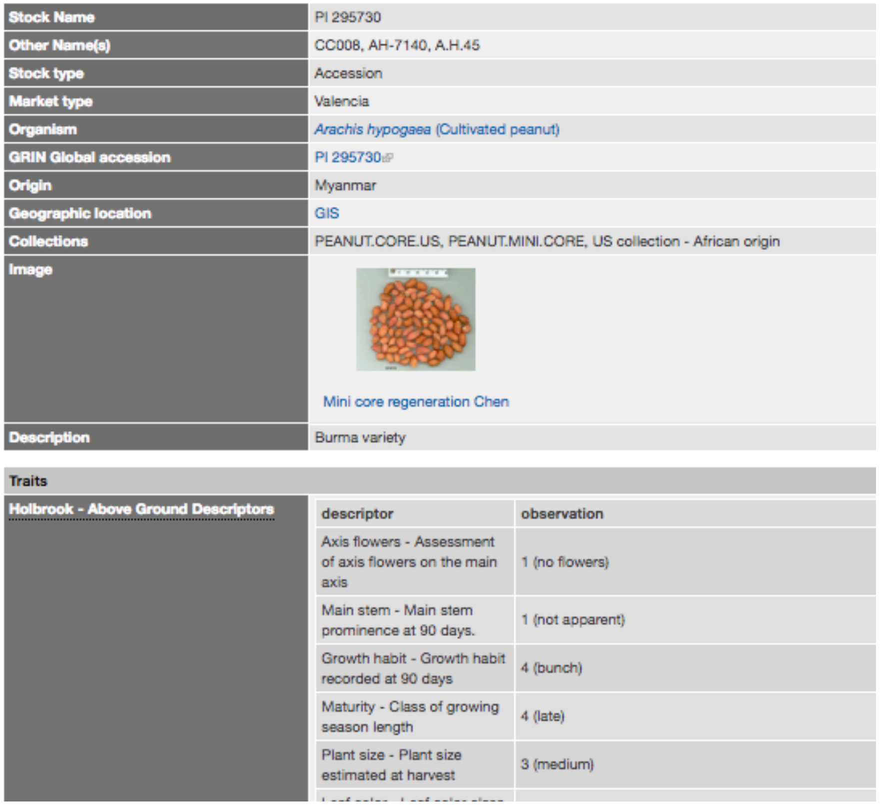
Traits

South American Germplasm, 1977-1986

descriptor	observation
Seed weight - Weighing of hundred kernels (seeds).	79.6
Branching pattern - Branching pattern	4 (irregular without main stem flowers)
Bristles on stipules - Assement of bristles on stipules	2
Emergence time - Record days from planting to emergence	8
Maturity - Count days from planting to harvest	161
Flower standard petal markings - Flower	40A

PeanutBase Resources for Breeders

Above and below ground traits for mini core collected by Corley Holbrook in the 1990s



Stock Name	PI 295730
Other Name(s)	CC008, AH-7140, A.H.45
Stock type	Accession
Market type	Valencia
Organism	*Arachis hypogaea* (Cultivated peanut)
GRIN Global accession	PI 295730
Origin	Myanmar
Geographic location	GIS
Collections	PEANUT.CORE.US, PEANUT.MINI.CORE, US collection - African origin
Image	Mini core regeneration Chen
Description	Burma variety

Traits

Holbrook - Above Ground Descriptors

descriptor	observation
Axis flowers - Assessment of axis flowers on the main axis	1 (no flowers)
Main stem - Main stem prominence at 90 days.	1 (not apparent)
Growth habit - Growth habit recorded at 90 days	4 (bunch)
Maturity - Class of growing season length	4 (late)
Plant size - Plant size estimated at harvest	3 (medium)

PeanutBase Resources for Breeders

Germplasm traits/phenotypes

- Working on peanut trait names with Crop Ontology and Planteome groups.
  - PeanutBase trait terms linked to the Crop Ontology.
  - Will link GRIN trait terms to the Crop Ontology
  - Use of Crop Ontology terms will enable integration with other resources

PeanutBase Resources for Breeders

Germplasm traits/phenotypes

- Working with Crop Ontology group to create standard trait names.
- Working with the Integrated Breeding Platform group to integrate PeanutBase with the BMS.
  - Data exchange via standard trait terms (Crop Ontology)
  - PeanutBase marker data first
  - Germplasm data also a candidate for sharing

PeanutBase Resources for Breeders

Germplasm traits/phenotype

- Working with Crop Ontology group to create standard trait names.
- Working with the Integrated Breeding Platform group
- Data templates, loaders, and display for germplasm trait data.

PeanutBase Resources for Breeders

Germplasm traits/phenotype

- Working with Crop Ontology group to create standard trait names.
- Working with the Integrated Breeding Platform group
- Data templates, loaders, and display for germplasm trait/phenotype data.
- Work with us early to ensure sufficient information is collected.
    - Consider using our data templates as a base for your data collection.
    - Complete definitions of traits and how they are measured is essential.

PeanutBase Resources for Breeders

Marker - trait associations

- Collecting markers and marker-trait data from literature.

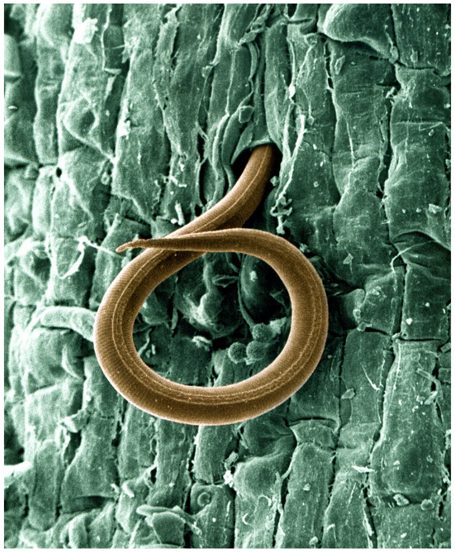
PeanutBase Resources for Breeders

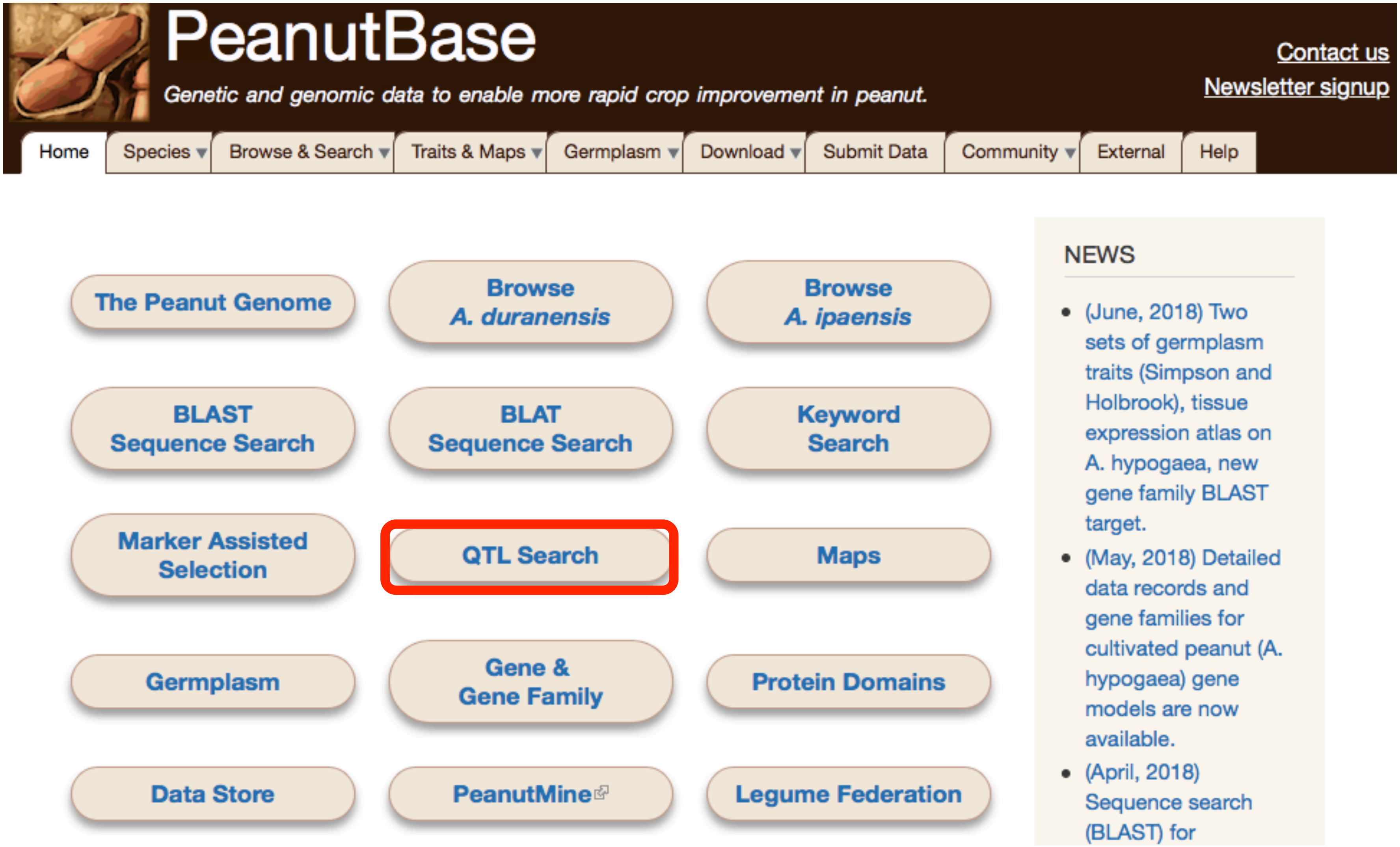
Marker - trait associations

- Collecting markers and marker-trait data from literature.
- Marker Assisted Selection pages on traits of high importance.
    - Late leaf spot (Phaeoisariopsis personata infection)
    - Peanut root-knot nematode
    - Seed oleic acid to linoleic acid ratio
    - Rust, Puccinia

An example

Look for markers associated with resistance to root-knot nematode

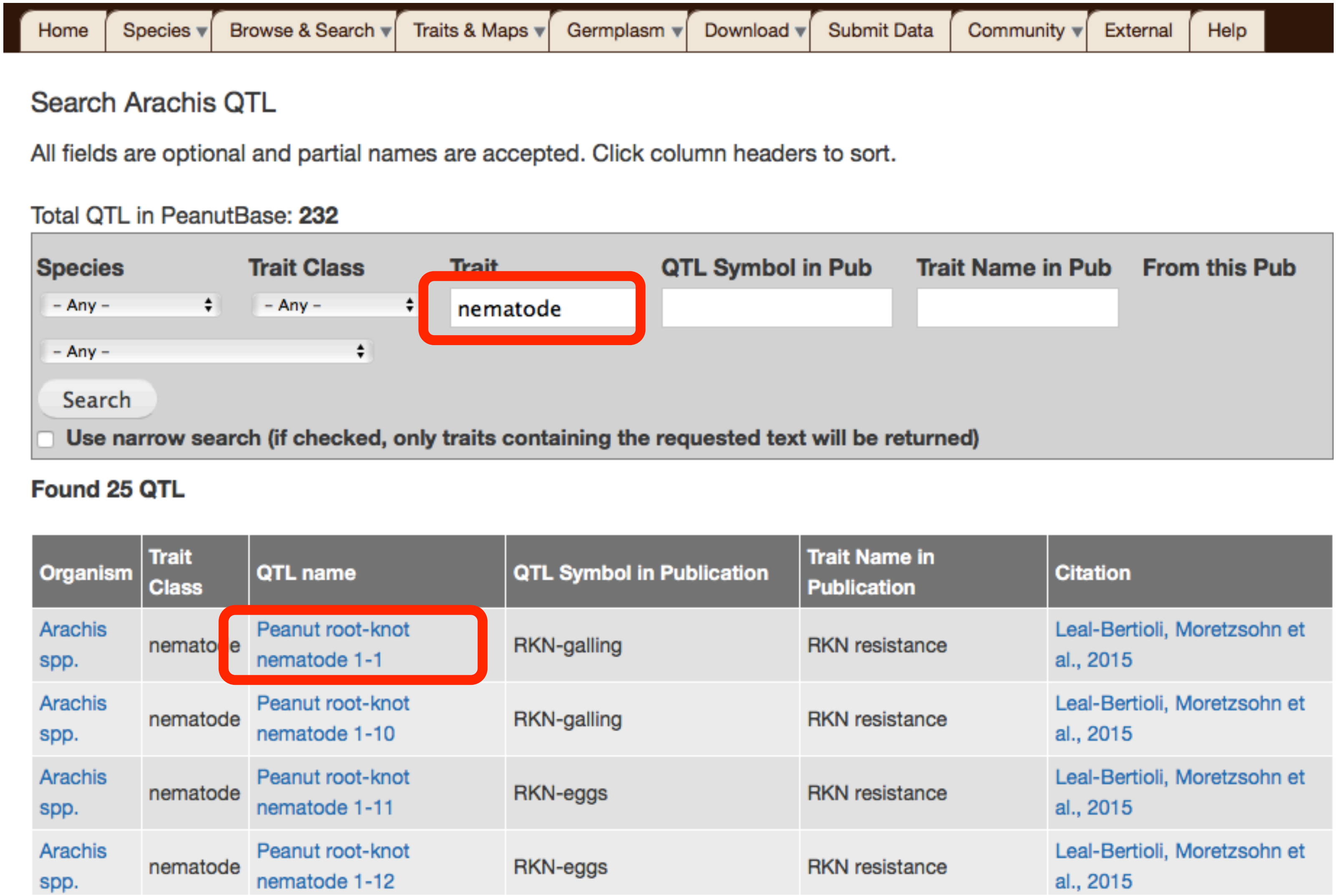




Genetic and genomic data to enable more rapid crop improvement in peanut.

NEWS

- (June, 2018) Two sets of germplasm traits (Simpson and Holbrook), tissue expression atlas on A. hypogaea, new gene family BLAST target.
- (May, 2018) Detailed data records and gene families for cultivated peanut (A. hypogaea) gene models are now available.
- (April, 2018) Sequence search (BLAST) for



Search Arachis QTL

All fields are optional and partial names are accepted. Click column headers to sort.

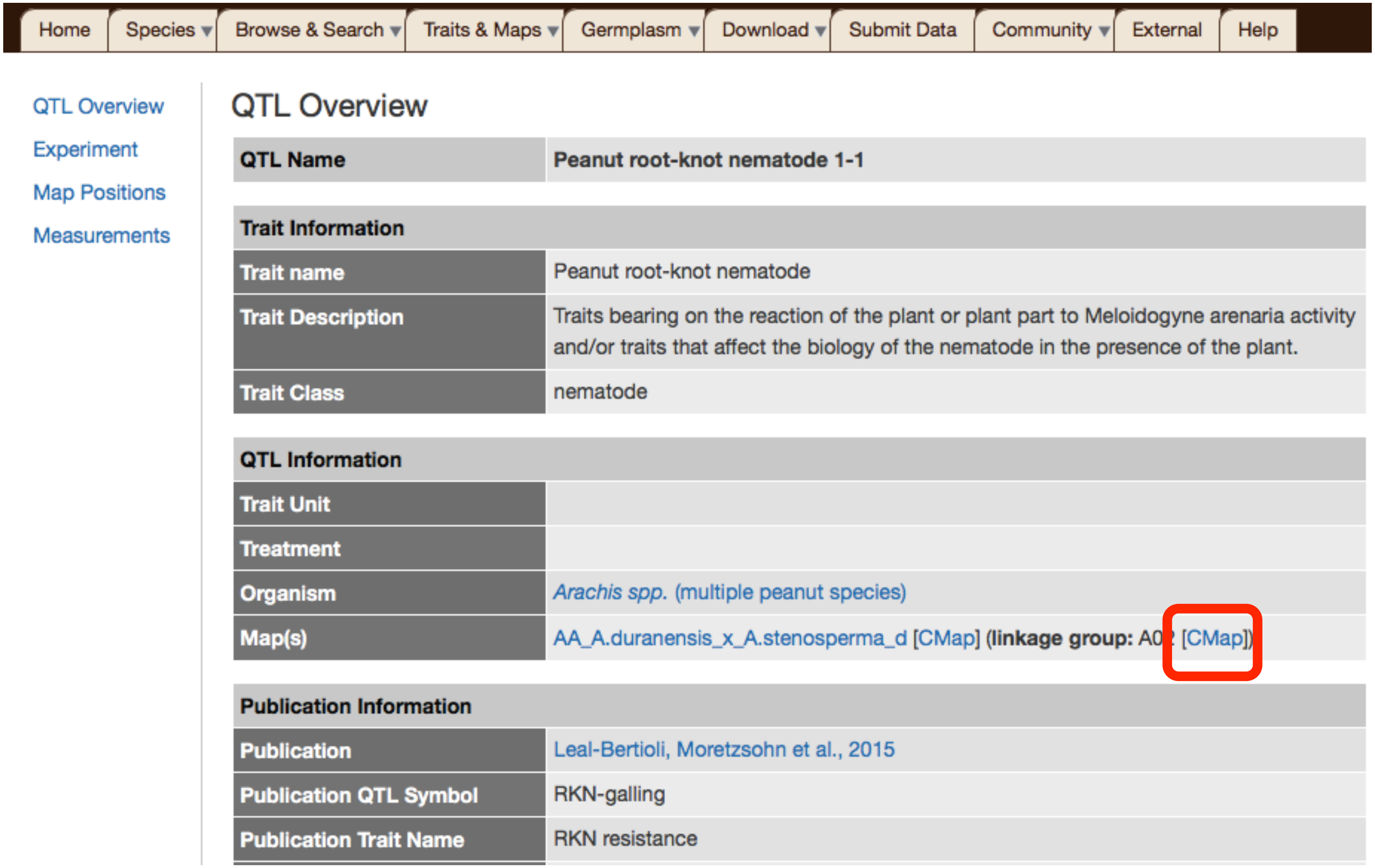
Total QTL in PeanutBase: **232**

Species: – Any –
Trait Class: – Any –
Trait: nematode
QTL Symbol in Pub:
Trait Name in Pub:
From this Pub: – Any –

☐ **Use narrow search (if checked, only traits containing the requested text will be returned)**

Found 25 QTL

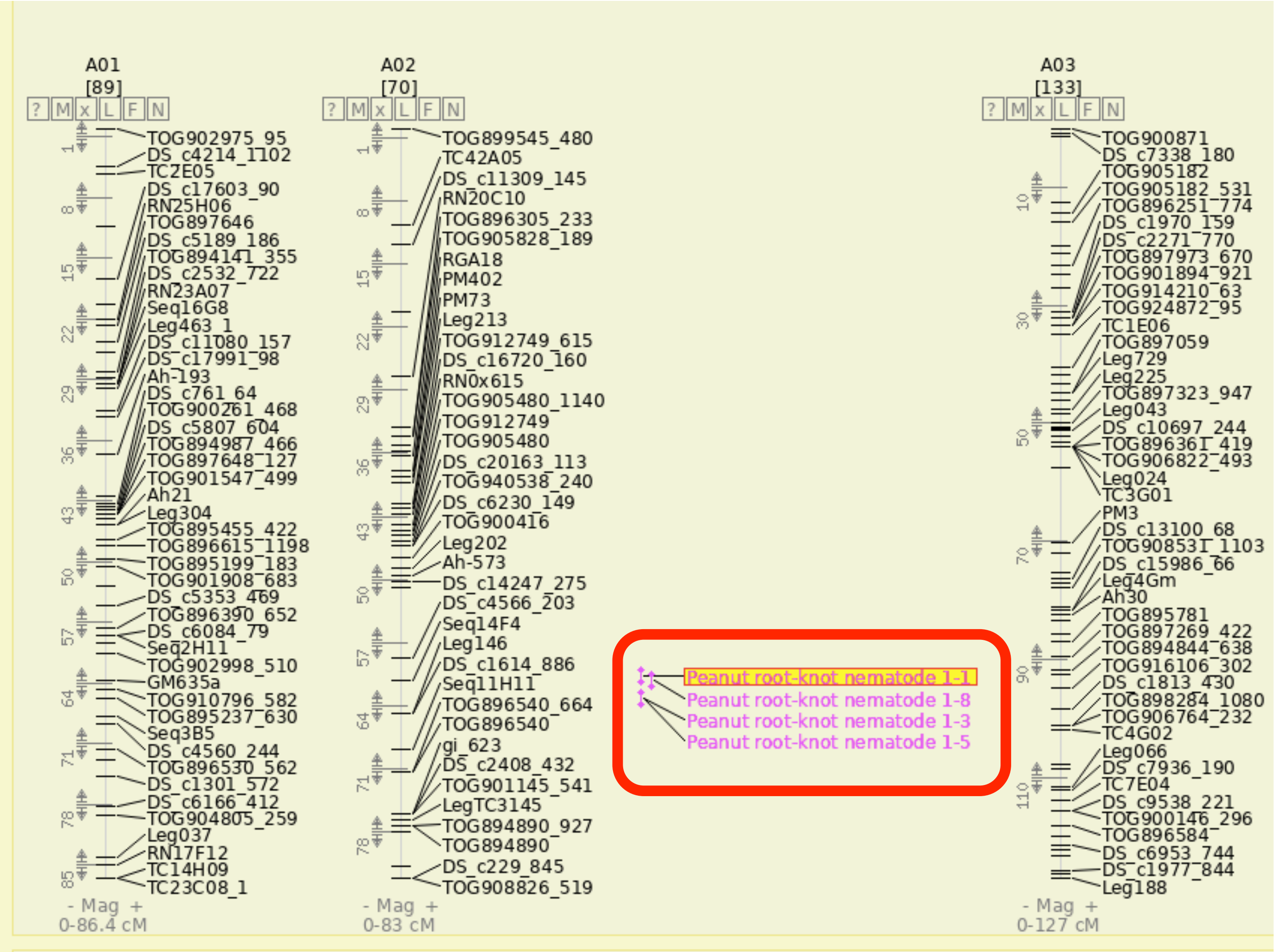
Organism	Trait Class	QTL name	QTL Symbol in Publication	Trait Name in Publication	Citation
Arachis spp.	nemato e	Peanut root-knot nematode 1-1	RKN-galling	RKN resistance	Leal-Bertioli, Moretzsohn et al., 2015
Arachis spp.	nematode	Peanut root-knot nematode 1-10	RKN-galling	RKN resistance	Leal-Bertioli, Moretzsohn et al., 2015
Arachis spp.	nematode	Peanut root-knot nematode 1-11	RKN-eggs	RKN resistance	Leal-Bertioli, Moretzsohn et al., 2015
Arachis spp.	nematode	Peanut root-knot nematode 1-12	RKN-eggs	RKN resistance	Leal-Bertioli, Moretzsohn et al., 2015



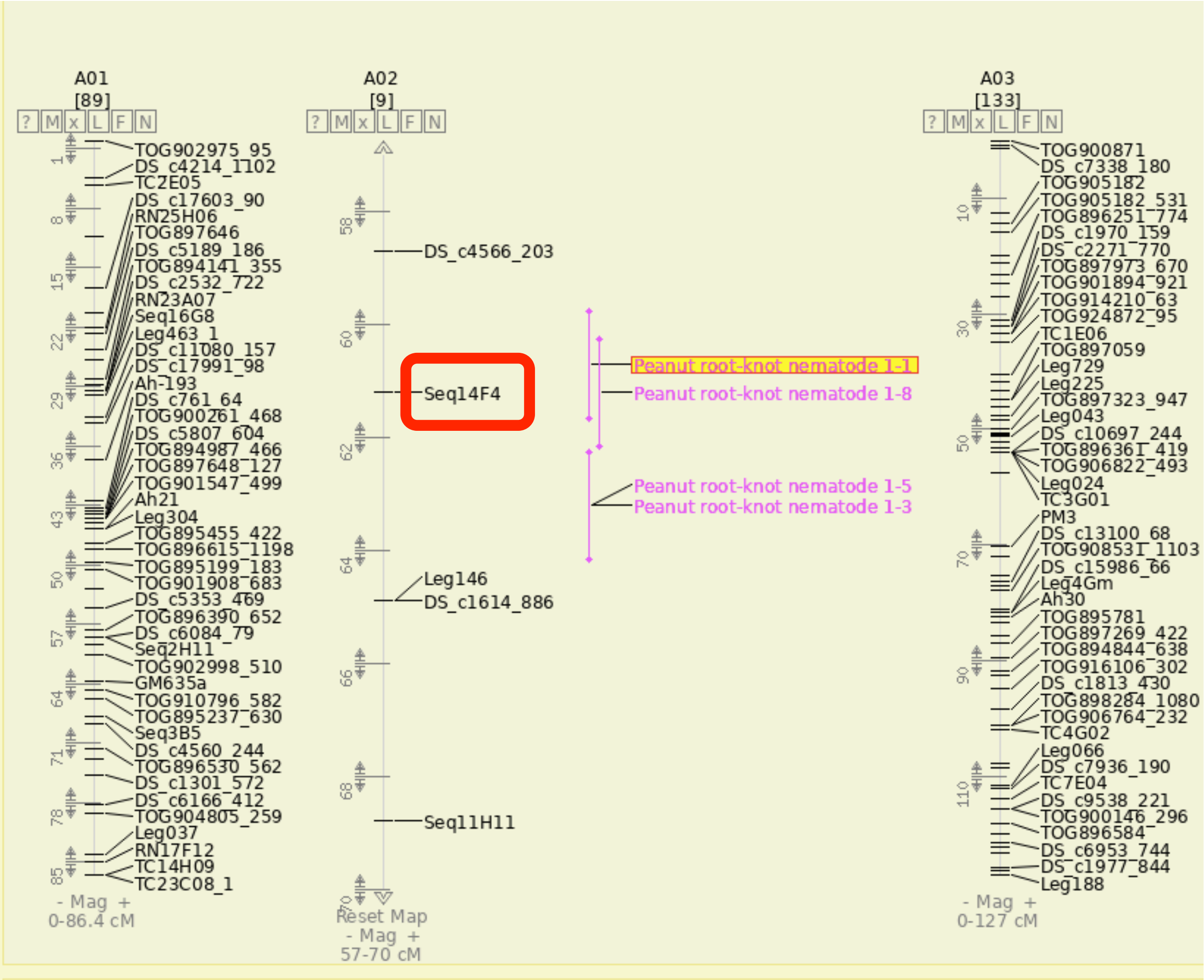
QTL Overview

QTL Name	**Peanut root-knot nematode 1-1**
Trait Information	
Trait name	Peanut root-knot nematode
Trait Description	Traits bearing on the reaction of the plant or plant part to Meloidogyne arenaria activity and/or traits that affect the biology of the nematode in the presence of the plant.
Trait Class	nematode
QTL Information	
Trait Unit	
Treatment	
Organism	*Arachis spp.* (multiple peanut species)
Map(s)	AA_A.duranensis_x_A.stenosperma_d [CMap] (**linkage group:** A02 [CMap])
Publication Information	
Publication	Leal-Bertioli, Moretzsohn et al., 2015
Publication QTL Symbol	RKN-galling
Publication Trait Name	RKN resistance

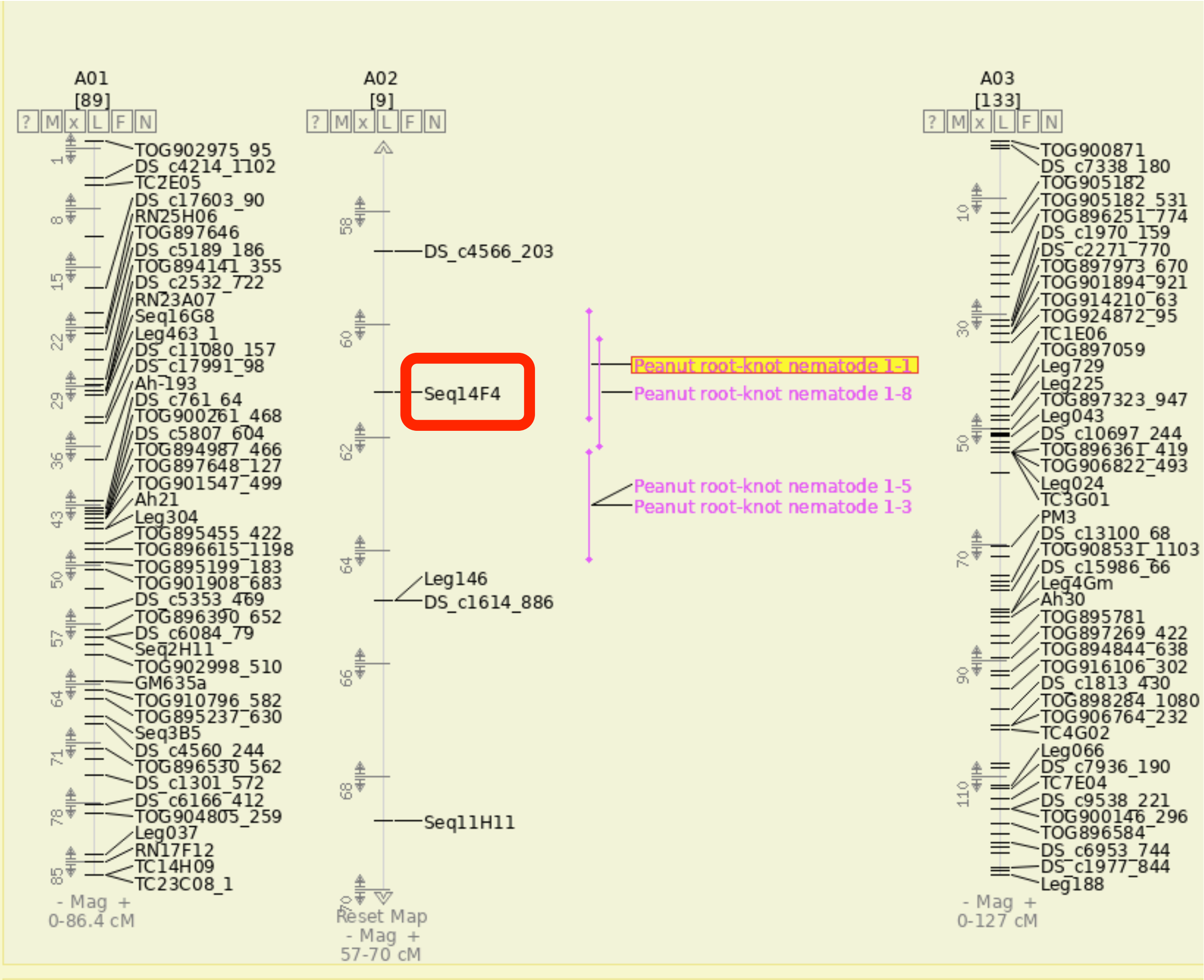
QTL displayed on cMap

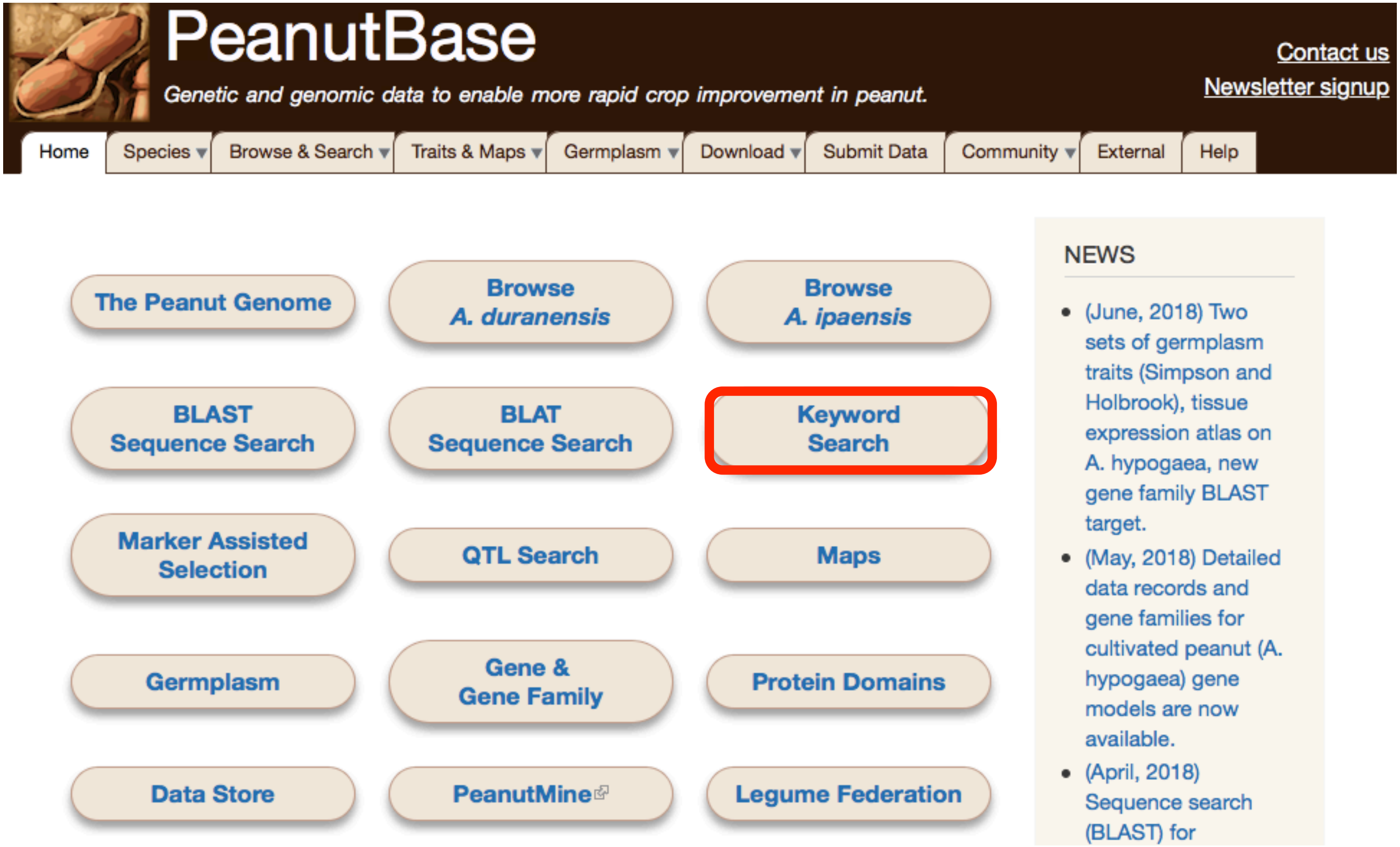


QTL displayed on cMap

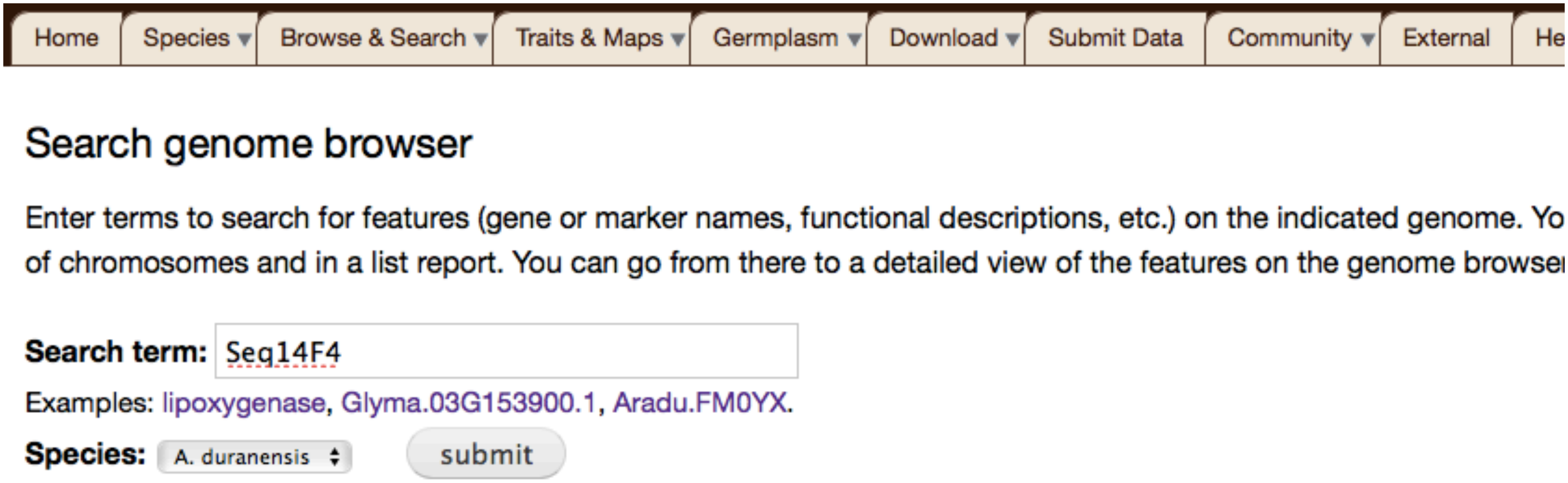


Search for marker **Seq14F4** at the “keyword search” page





- (June, 2018) Two sets of germplasm traits (Simpson and Holbrook), tissue expression atlas on A. hypogaea, new gene family BLAST target.
- (May, 2018) Detailed data records and gene families for cultivated peanut (A. hypogaea) gene models are now available.
- (April, 2018) Sequence search (BLAST) for



Search genome browser

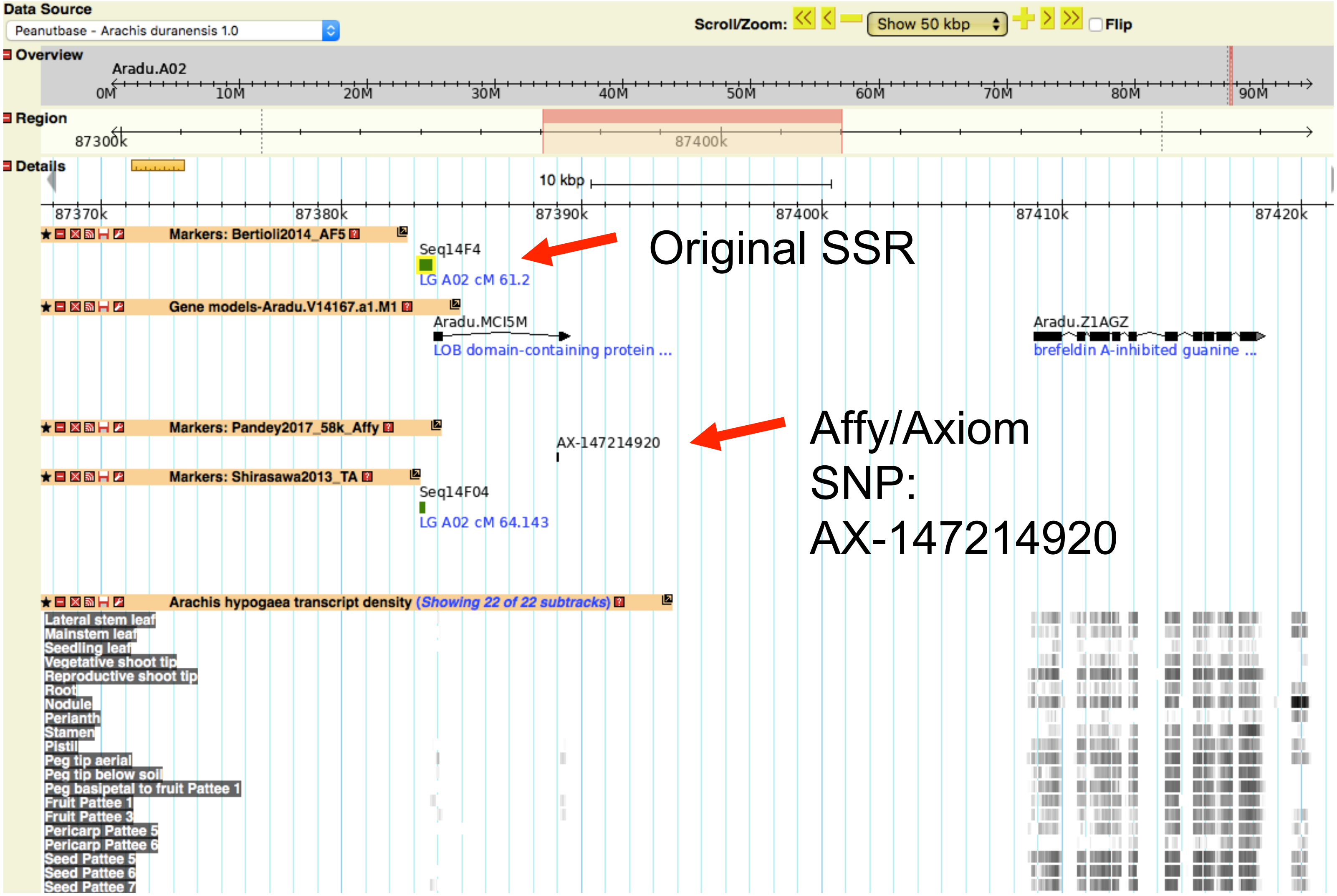
Enter terms to search for features (gene or marker names, functional descriptions, etc.) on the indicated genome. Yo
of chromosomes and in a list report. You can go from there to a detailed view of the features on the genome browse

Search term: Seq14F4

Examples: lipoxygenase, Glyma.03G153900.1, Aradu.FM0YX.

Species: A. duranensis

There are markers from several map sets



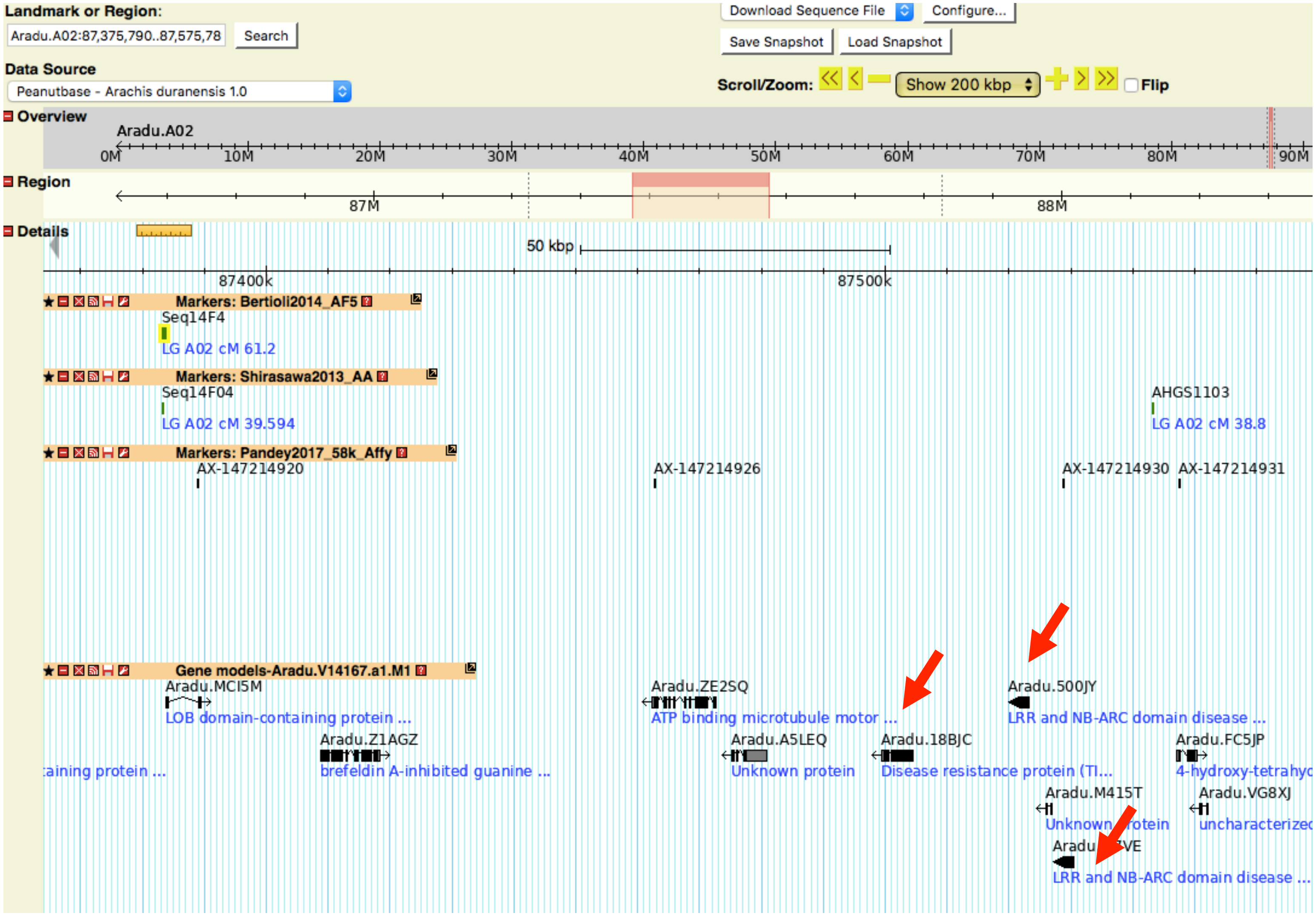
Data Source: Peanutbase - Arachis duranensis 1.0

Scroll/Zoom: Show 50 kbp

Original SSR

Affy/Axiom SNP: AX-147214920

Nearby are several disease-resistance genes (possible candidates for nematode resistance)



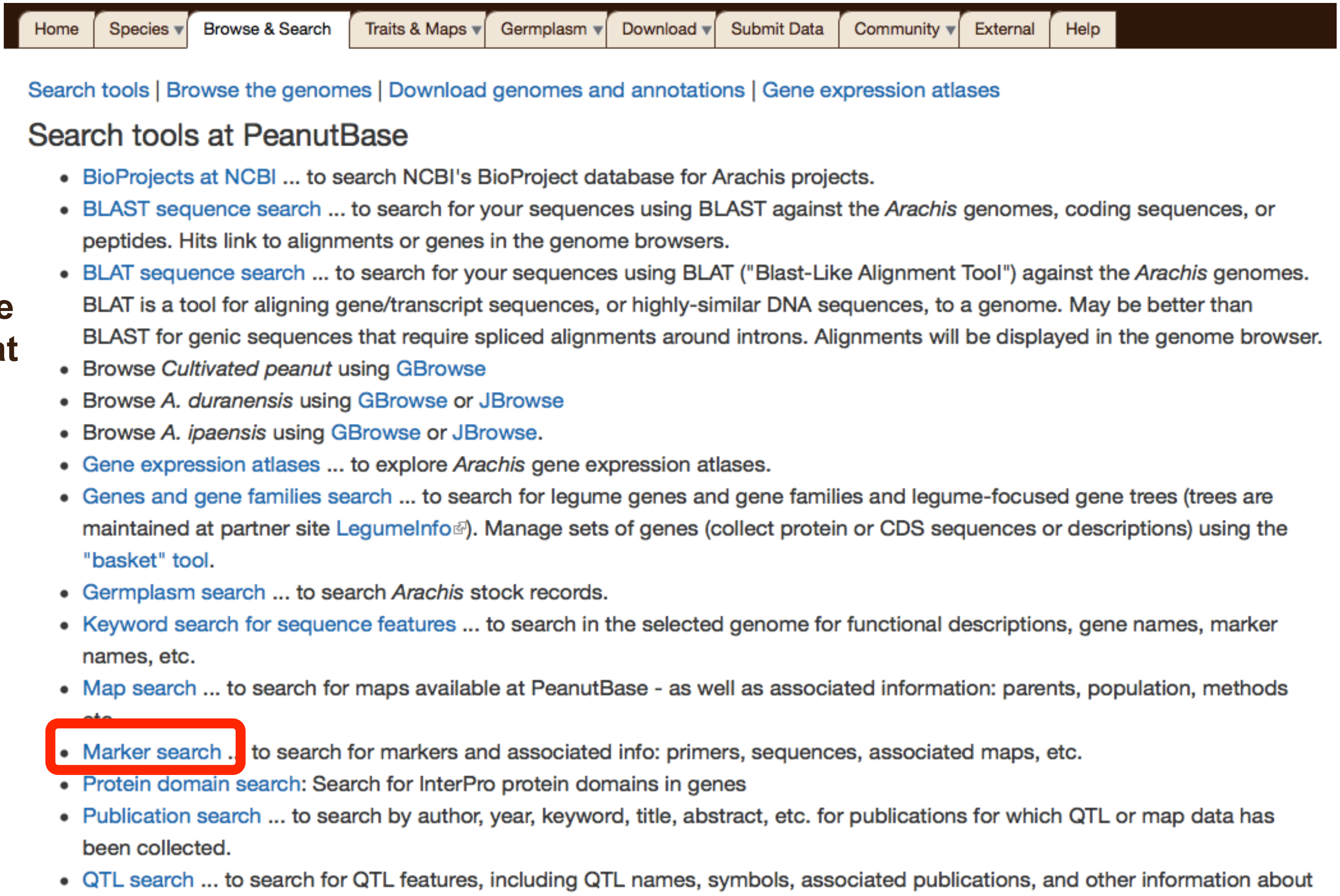
Landmark or Region: Aradu.A02:87,375,790..87,575,78

Data Source: Peanutbase - Arachis duranensis 1.0

Scroll/Zoom: Show 200 kbp

☐ Flip

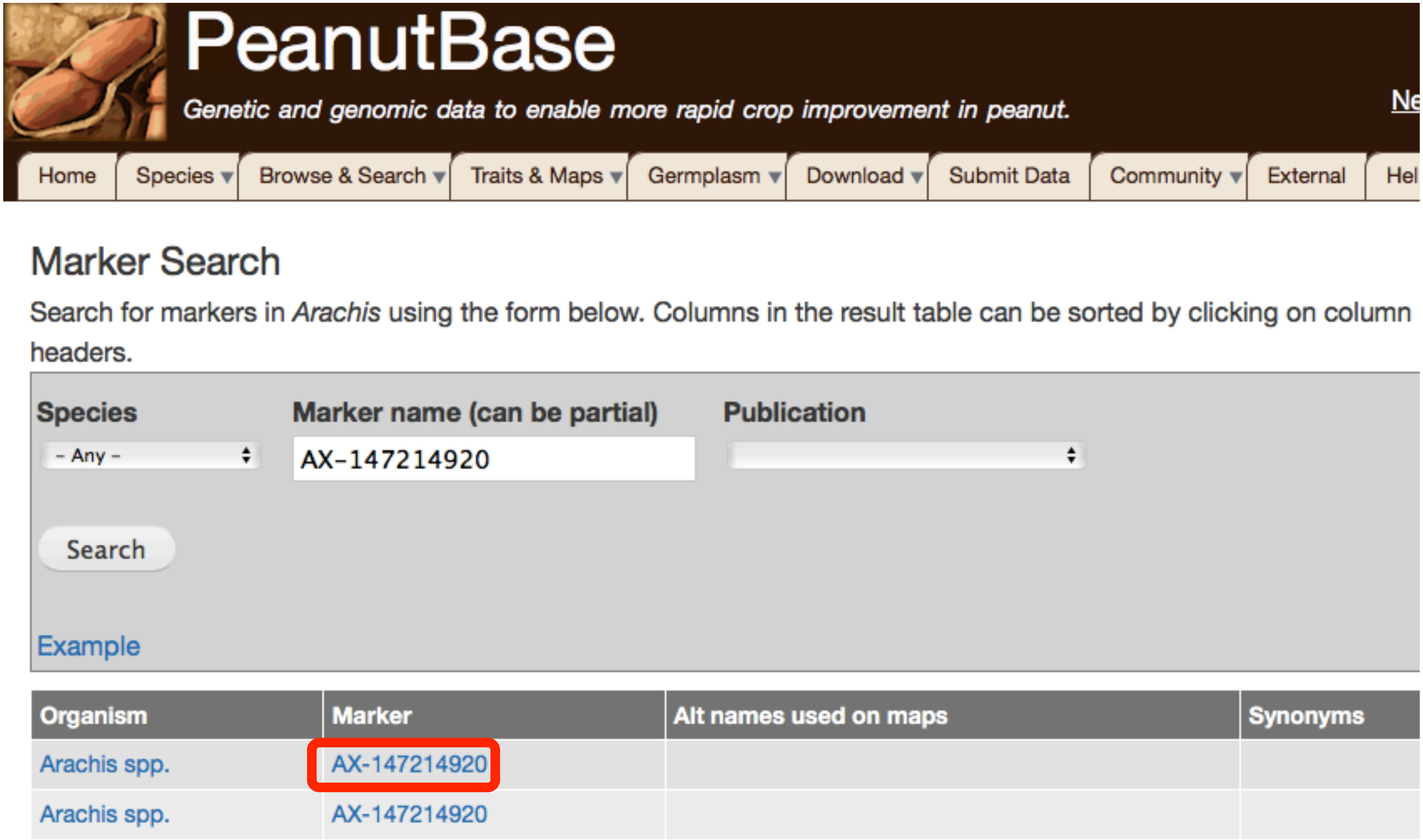
Search for the SNP marker at the marker search page



Search tools | Browse the genomes | Download genomes and annotations | Gene expression atlases

Search tools at PeanutBase

- BioProjects at NCBI ... to search NCBI's BioProject database for Arachis projects.
- BLAST sequence search ... to search for your sequences using BLAST against the *Arachis* genomes, coding sequences, or peptides. Hits link to alignments or genes in the genome browsers.
- BLAT sequence search ... to search for your sequences using BLAT ("Blast-Like Alignment Tool") against the *Arachis* genomes. BLAT is a tool for aligning gene/transcript sequences, or highly-similar DNA sequences, to a genome. May be better than BLAST for genic sequences that require spliced alignments around introns. Alignments will be displayed in the genome browser.
- Browse *Cultivated peanut* using GBrowse
- Browse *A. duranensis* using GBrowse or JBrowse
- Browse *A. ipaensis* using GBrowse or JBrowse.
- Gene expression atlases ... to explore *Arachis* gene expression atlases.
- Genes and gene families search ... to search for legume genes and gene families and legume-focused gene trees (trees are maintained at partner site LegumeInfo). Manage sets of genes (collect protein or CDS sequences or descriptions) using the "basket" tool.
- Germplasm search ... to search *Arachis* stock records.
- Keyword search for sequence features ... to search in the selected genome for functional descriptions, gene names, marker names, etc.
- Map search ... to search for maps available at PeanutBase - as well as associated information: parents, population, methods etc.
- Marker search ... to search for markers and associated info: primers, sequences, associated maps, etc.
- Protein domain search: Search for InterPro protein domains in genes
- Publication search ... to search by author, year, keyword, title, abstract, etc. for publications for which QTL or map data has been collected.
- QTL search ... to search for QTL features, including QTL names, symbols, associated publications, and other information about



Marker Search

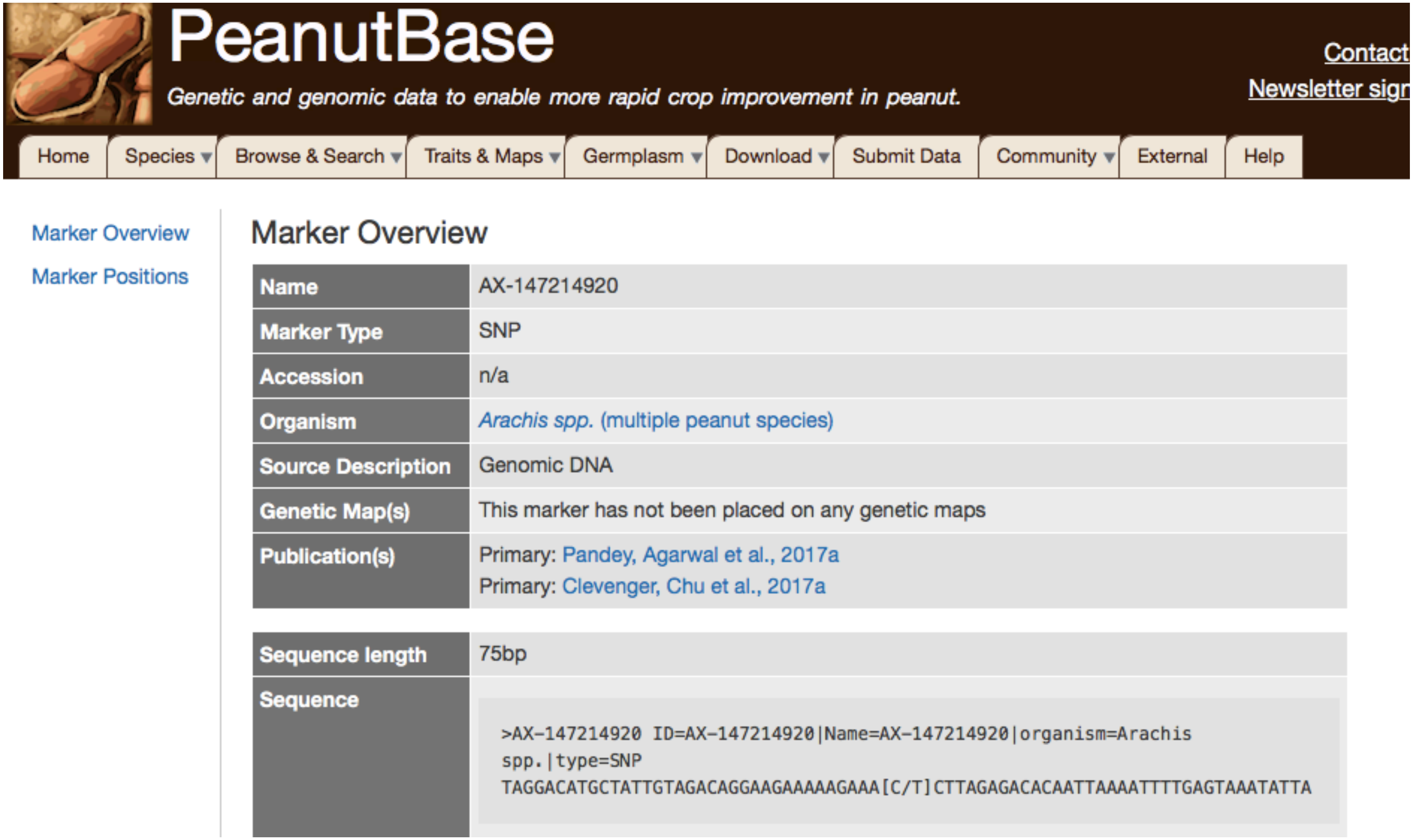
Search for markers in *Arachis* using the form below. Columns in the result table can be sorted by clicking on column headers.

Species: - Any -

Marker name (can be partial): AX-147214920

Publication:

Organism	Marker	Alt names used on maps	Synonyms
Arachis spp.	AX-147214920		
Arachis spp.	AX-147214920		



PeanutBase

Genetic and genomic data to enable more rapid crop improvement in peanut.

Marker Overview

Name	AX-147214920
Marker Type	SNP
Accession	n/a
Organism	*Arachis spp.* (multiple peanut species)
Source Description	Genomic DNA
Genetic Map(s)	This marker has not been placed on any genetic maps
Publication(s)	Primary: Pandey, Agarwal et al., 2017a Primary: Clevenger, Chu et al., 2017a

Sequence length	75bp
Sequence	

```
>AX-147214920 ID=AX-147214920|Name=AX-147214920|organism=Arachis
spp.|type=SNP
TAGGACATGCTATTGTAGACAGGAAGAAAAAGAAA[C/T]CTTAGAGACACAATTAAAATTTTGAGTAAATATTA
```

What we’ve done:

1. Started from a mapped trait (QTL resistance)
2. Found nearby markers
3. Found possible candidate genes, which can be tested
4. Found markers in other maps & marker sets …
5. … which can be used to identify breeding lines, or for MAS

In Progress

Genotyping: PeanutBase is leading genotyping of US Core Collection and exploring software components for browsing and analyzing genotype and phenotype data.

Markers: continuing to collect markers and marker-trait data from literature.

Traits/phenotypes: we can take your germplasm trait data.

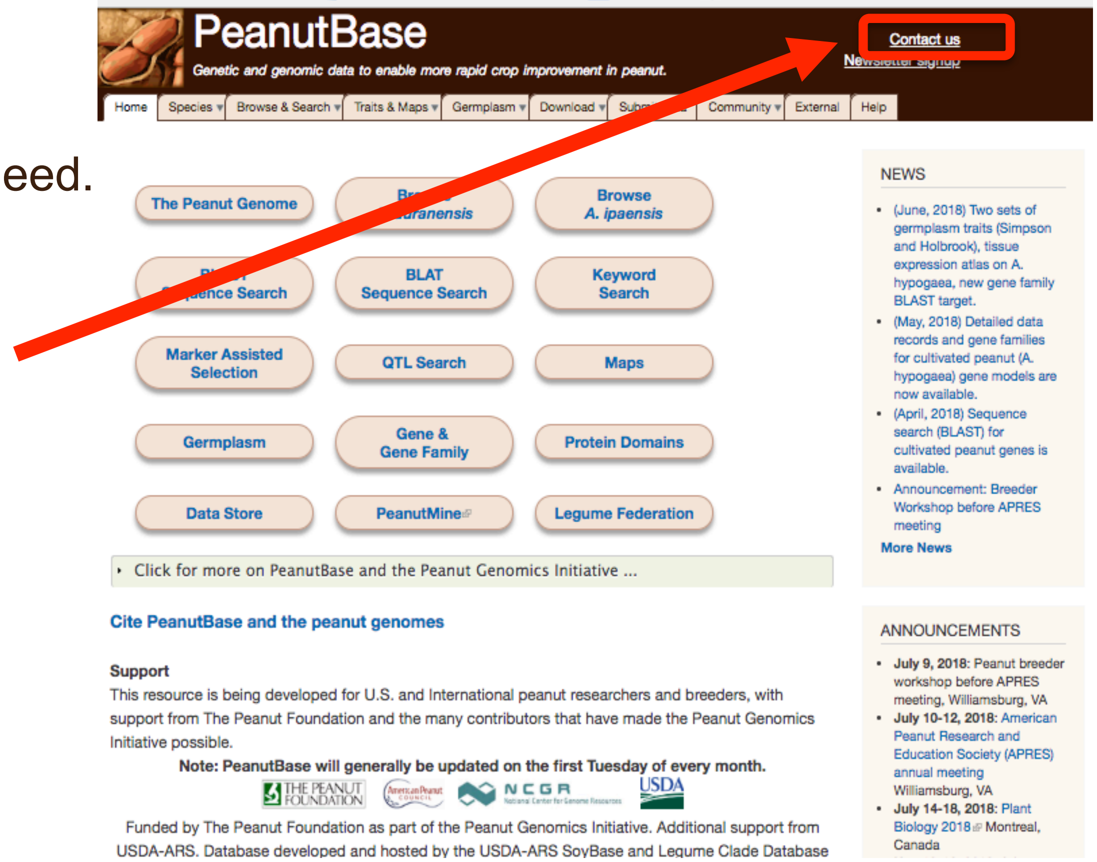
Germplasm: the PeanutBase germplasm data is not limited to GRIN; we can hold information about your germplasm collection too.

Data sharing: Exploring software components to expose marker data to other resources, like the BMS

How You Can Help

How you can help

- Talk with us about what you need.



PeanutBase

Genetic and genomic data to enable more rapid crop improvement in peanut.

Contact us

Newsletter signup

‣ Click for more on PeanutBase and the Peanut Genomics Initiative ...

Cite PeanutBase and the peanut genomes

Support

This resource is being developed for U.S. and International peanut researchers and breeders, with support from The Peanut Foundation and the many contributors that have made the Peanut Genomics Initiative possible.

Note: PeanutBase will generally be updated on the first Tuesday of every month.

Funded by The Peanut Foundation as part of the Peanut Genomics Initiative. Additional support from USDA-ARS. Database developed and hosted by the USDA-ARS SoyBase and Legume Clade Database

NEWS

- (June, 2018) Two sets of germplasm traits (Simpson and Holbrook), tissue expression atlas on A. hypogaea, new gene family BLAST target.
- (May, 2018) Detailed data records and gene families for cultivated peanut (A. hypogaea) gene models are now available.
- (April, 2018) Sequence search (BLAST) for cultivated peanut genes is available.
- Announcement: Breeder Workshop before APRES meeting

More News

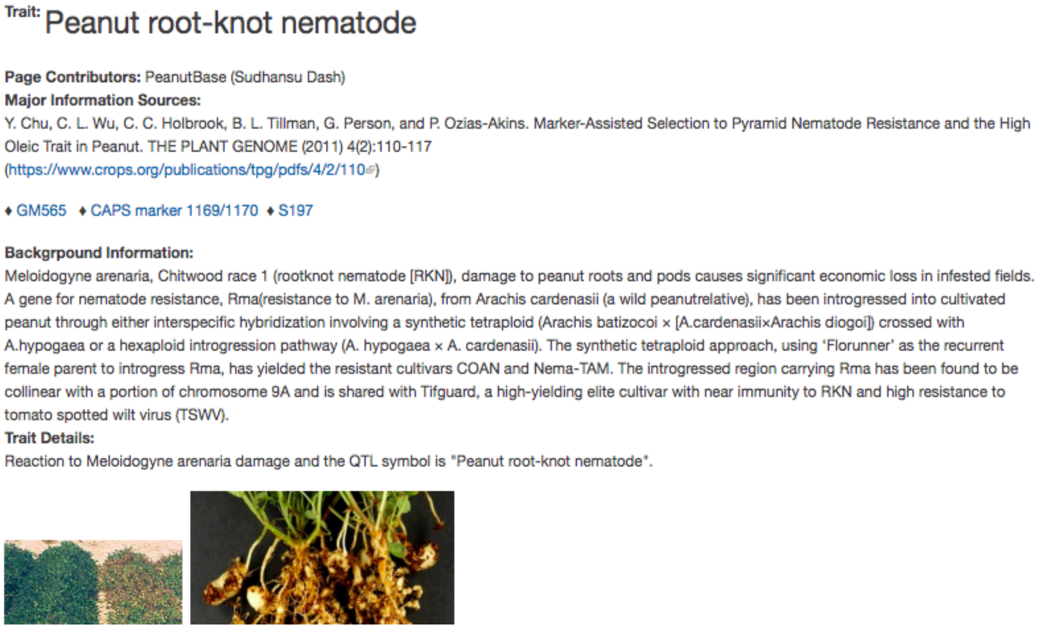
ANNOUNCEMENTS

- **July 9, 2018:** Peanut breeder workshop before APRES meeting, Williamsburg, VA
- **July 10-12, 2018:** American Peanut Research and Education Society (APRES) annual meeting Williamsburg, VA
- **July 14-18, 2018:** Plant Biology 2018 Montreal, Canada

How You Can Help

How you can help

- Talk with us about what you need.
- Help maintain or create new MAS pages.



Trait: Peanut root-knot nematode

Page Contributors: PeanutBase (Sudhansu Dash)
Major Information Sources:
Y. Chu, C. L. Wu, C. C. Holbrook, B. L. Tillman, G. Person, and P. Ozias-Akins. Marker-Assisted Selection to Pyramid Nematode Resistance and the High Oleic Trait in Peanut. THE PLANT GENOME (2011) 4(2):110-117 (https://www.crops.org/publications/tpg/pdfs/4/2/110)

♦ GM565 ♦ CAPS marker 1169/1170 ♦ S197

Backgrpound Information:
Meloidogyne arenaria, Chitwood race 1 (rootknot nematode [RKN]), damage to peanut roots and pods causes significant economic loss in infested fields. A gene for nematode resistance, Rma(resistance to M. arenaria), from Arachis cardenasii (a wild peanutrelative), has been introgressed into cultivated peanut through either interspecific hybridization involving a synthetic tetraploid (Arachis batizocoi × [A.cardenasii×Arachis diogoi]) crossed with A.hypogaea or a hexaploid introgression pathway (A. hypogaea × A. cardenasii). The synthetic tetraploid approach, using 'Florunner' as the recurrent female parent to introgress Rma, has yielded the resistant cultivars COAN and Nema-TAM. The introgressed region carrying Rma has been found to be collinear with a portion of chromosome 9A and is shared with Tifguard, a high-yielding elite cultivar with near immunity to RKN and high resistance to tomato spotted wilt virus (TSWV).
Trait Details:
Reaction to Meloidogyne arenaria damage and the QTL symbol is "Peanut root-knot nematode".

How You Can Help

How you can help

- Talk with us about what you need.
- Help maintain or create new MAS pages.
- Volunteer to collect marker-trait data from literature.
- Recommend papers with data to host at PeanutBase

How You Can Help

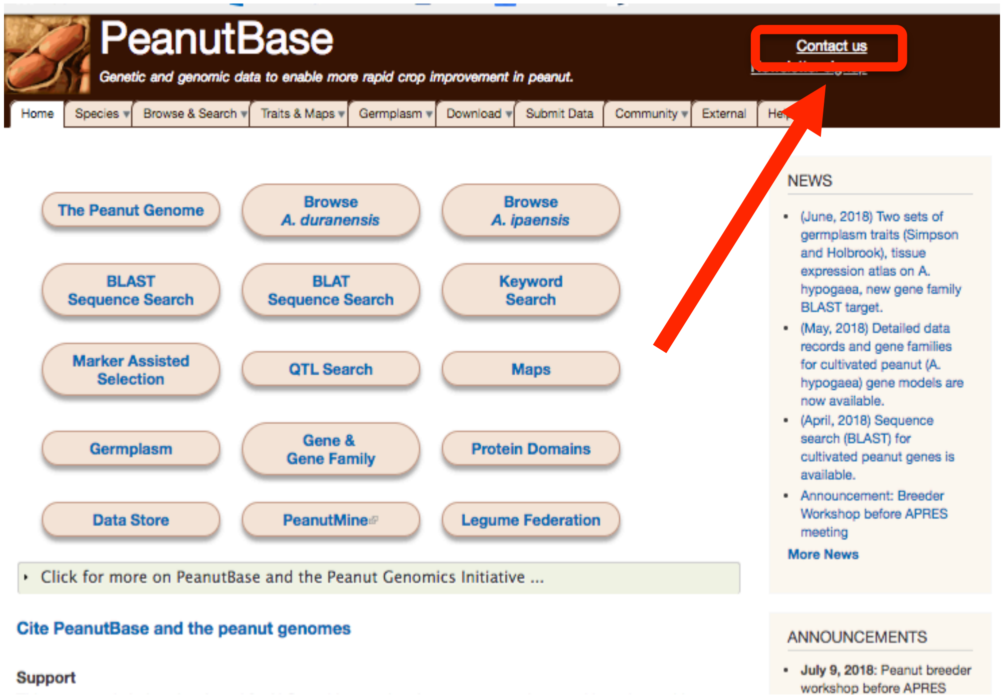
How you can help

- Talk with us about what you need.
- Volunteer to maintain or create new MAS pages.
- Volunteer to collect marker-trait data from literature
- Recommend papers with data to host at PeanutBase
- Share public data: pedigrees, germplasm collections, markers, traits. Work with us early in your research.

What do you need?

Let us know what you need. Talk with me during the conference, use feedback button, send e-mail, arrange a phone call.

ekcannon@iastate.edu



PeanutBase

Genetic and genomic data to enable more rapid crop improvement in peanut.

NEWS

- (June, 2018) Two sets of germplasm traits (Simpson and Holbrook), tissue expression atlas on A. hypogaea, new gene family BLAST target.
- (May, 2018) Detailed data records and gene families for cultivated peanut (A. hypogaea) gene models are now available.
- (April, 2018) Sequence search (BLAST) for cultivated peanut genes is available.
- Announcement: Breeder Workshop before APRES meeting

More News

▸ Click for more on PeanutBase and the Peanut Genomics Initiative ...

Cite PeanutBase and the peanut genomes

Support

ANNOUNCEMENTS

- **July 9, 2018:** Peanut breeder workshop before APRES

Contributors to PeanutBase

Iowa State University/PeanutBase

Ethy Cannon – lead

Wei Huang – computational biologist

Paul Otyama – PhD student

Iowa State University/Legume Federation

Jacqueline Campbell – data curator and outreach

Malachy O'Connell – programmer

USDA-ARS at Ames, IA

Steven Cannon – lead scientist, ARS legume database project

Nathan Weeks – IT specialist and computational biologist

Scott Kalberer – data curator

Andrew Wilkey – programmer

National Center for Genomic Resources

Andrew Farmer – lead, Legume Information System

Sudhansu Dash - geneticist and computational biologist

Alex Rice - programmer

ekcannon@iastate.edu

THE PEANUT FOUNDATION

STATE

NSF

USDA

NCGR
National Center for Genome Resources