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PeanutBase provides peanut researchers and breeders with trait, genetic and genomic data for *Arachis* and provides means for connecting peanut data to closely related plants with more developed datasets, for example, soybean and common bean.

PeanutBase is being developed in collaboration with the Legume Information System (LIS; <http://legumeinfo.org>)

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

Home Species Browse & Search Traits & Maps Download Submit Data Community External Resources Help

Marker Assisted Selection **Browse A. duranensis** **Browse A. ipaensis**

BLAST Sequence Search **BLAT Sequence Search** **Keyword Search**

QTL **Maps** **Genome & Gene Sequences**

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

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 for the Peanut Genomics Initiative. Additional support from USDA-ARS. Database developed and hosted by the USDA-ARS SoyBase and Legume Clade Database group at Ames, IA, with NCGR and other participants.

NEWS

- (Nov 2014) Diploid gene models in genome browser, new sequence search utility, reorganization of site and more QTL data ...
- (Oct 2014) Oil quality, nematode and rust resistance traits have been added to Marker Assisted Selection list.
- (Sep 2014) The BLAST sequence search tool has been refined at PeanutBase.
- (Sep 2014) A prototype Marker Assisted Selection (MAS) page.

ANNOUNCEMENTS

AAGB-2014
7th International Conference on Advances in Arachis through Genomics and Biotechnology
November 11-14, 2014, Savannah, GA
More details ...

Marker Assisted Selection (MAS)

MAS pages are being created with help from experts in the community on particular traits of interest. Each page combines information and data pertaining to a particular trait.

Submitted by sdash on Fri, 09/19/2014 - 1

Trait: Rust, Puccinia

Trait Symbol: Leaf Rust

Page Contributors: PeanutBase (Jugpreet Singh)

Major Information Sources: Varshney, RajeevK., Pandey, ManishK., Janila, Pasupuleti, Nigam, ShyamN., Sudini, Harikishan, Gowda, M.V.C.,

Markers associated with this trait

- ♦ **IPAHM103** ♦ **GM1536** ♦ **GM2301** ♦ **GM2079**
- ♦ **TE 360** ♦ **TE 498**
- ♦ **SSR_GO340445** ♦ **SSR_HO115759**

Genotypes: Accession (DBSN) Susceptibility Allele Pedigree Plant Type Accession Source

VG 8014 Resistant B 00 F X A (selfed) Shuhua, Harbin Research Center, Tianjin, China

T60 24 Susceptible A T082 X T081 Spanish Bush

Traits, Maps and Markers

PeanutBase curators are developing a consistent trait vocabulary and collecting map, marker, and QTL data from the literature. Direct contributions from the community are welcome!

Traits and QTL maps - TSWV example

QTL Overview

QTL Name: TSWV 2-20

Trait Information:
Trait name: Tomato Spotted Wilt Virus (TSWV) reaction
Trait Description: Reaction of the plant or plant part to infection by Tomato Spotted Wilt Virus (TSWV).
Trait Class: Viral

QTL Information:
Trait Unit: 0 to 5 scale
Treatment: shFRD2R
Organism: *Arachis hypogaea* (peanut)
Map(s): TT_Tifrunner_x_GT-C20_a [CMap:†] (linkage group: LG19 [CMap:†])

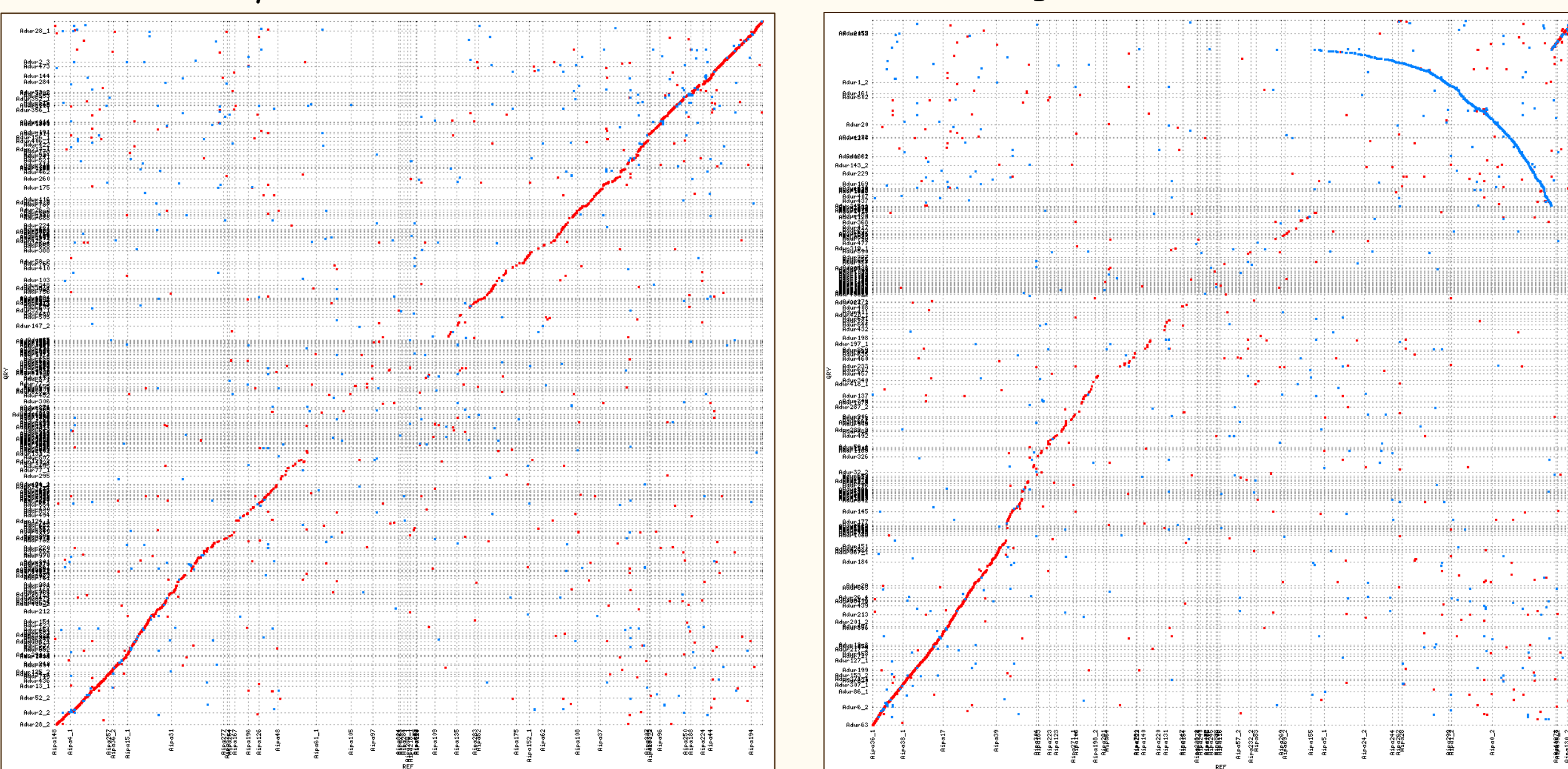
Map Positions

Map Position 1
Map: TT_Tifrunner_x_GT-C20_a [CMap:†]
Linkage Group: LG19 [CMap:†]
QTL Peak: 0
Start Position: 18.39
End Position: 18.39
Mapping Population: TT_Tifrunner_x_GT-C20_a
Parent1: Tifrunner
Parent2: GT-C20
Interval Calculation Method: cM from experiment markers

Reference peanut TT_Tifrunner_x_GT-C20_a

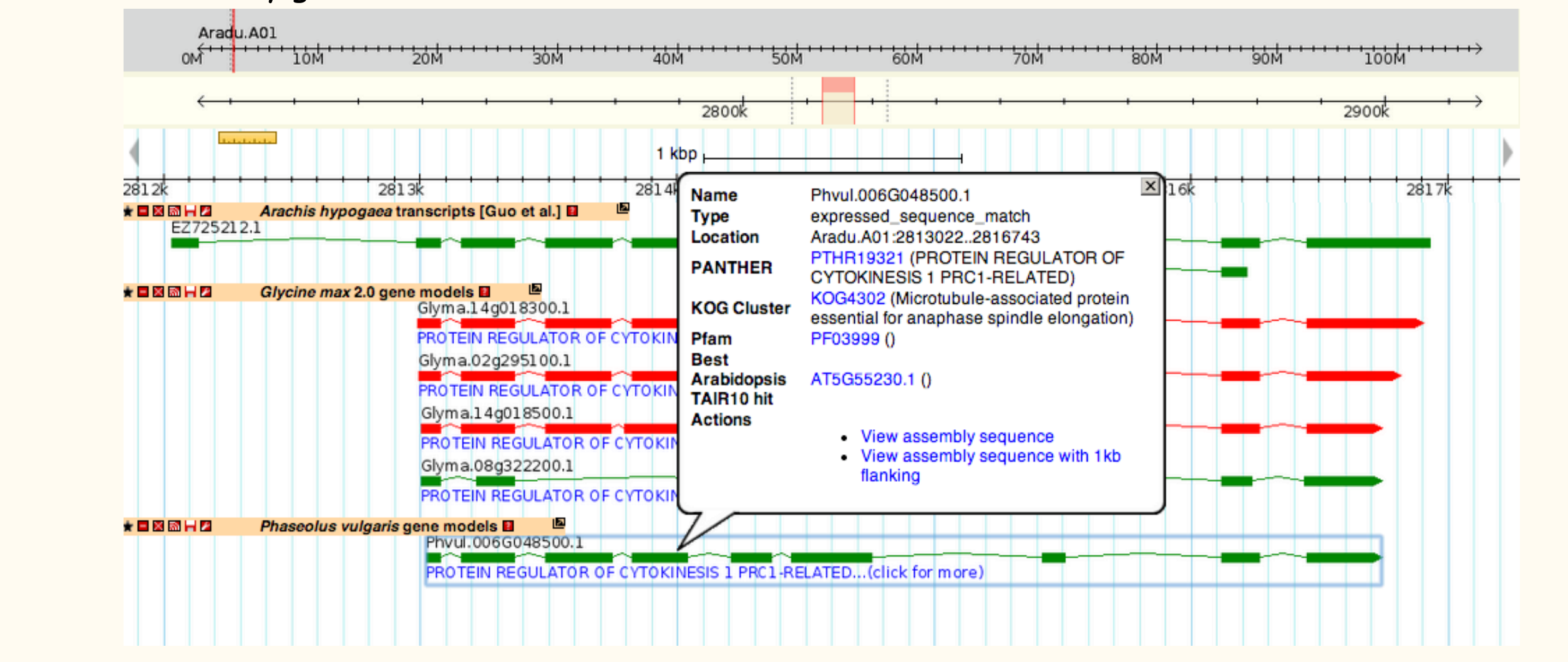
Reference map showing markers: RNS5H04-1500, RC3C07-70, TC506-210, GM2456-800, GM349-2300, ARS768-260, ARS766-210, ARS259-300, ARS766-200, ARS752-300, ARS759-1200, ARS757-350, GM2792-300, ARS751-265, TC1002-280, ARS742-100, GM1847-340, GM2504-1000

A reference genome assembly for *Arachis hypogaea*
Because of the complexity of the tetraploid *A. hypogaea*, its likely diploid progenitor species, *A. duranensis* and *A. ipaensis* were sequenced and assembled first. Although the two species diverged ~ 3 mya, they still maintain significant synteny, although some large rearrangements have occurred. The two progenitor diploid genomes are remarkably similar... ..but there have been some significant rearrangements as well.



Gene models have been created for both *A. duranensis* and *A. ipaensis* using two methods, MAKER-P and GLEAN and are available as genome browser tracks.

Arachis gene models can be compared to *Glycine max* (soybean) and *Phaseolus vulgaris* (common bean) gene models to find likely gene function.



Sequence Search

BLAST and BLAT are available for searching and aligning sequence against the reference assemblies and gene models. Both show the alignments on the reference sequence browsers.

Query Name **Hit Name** **E-Value**

1 partial lipoxigenase Glyma15g03040 Aradu.A08 2.92e-69

2 partial lipoxigenase Glyma15g03040 Aradu.A05 4.66e-42

3 partial lipoxigenase Glyma15g03040 Aradu.A09 3.65e-39

Alignment

HSP 1
Identity= 161/198 (81.31%), Positive= 161/198 (81.31%) Query Matches 451 to 648 Hit Matches = 7359963 to 7359766

Query: 451 ATTATAATCCAGACATATCTTCCAGGAGACACCGCTCACTTCTCAAGTACAGAA 511
BL: 7359963
Query: 512
BL: 7360024
Query: 572
BL: 7360084
Query: 632
BL: 7360144

The following 26 regions match your request.

Name	Type	Position	Match Score
Aradu.A01	BLAT	Aradu.A08:23296925..23300891	99.27
Alignment1	BLAT	Aradu.A08:23276843..23280231	91.15
Alignment2	BLAT	Aradu.A08:4806755..4810412	47.50
Alignment3	BLAT	Aradu.A09:13569732..13624751	45.45
Alignment4	BLAT	Aradu.A09:13562172..13758865	41.01
Alignment5	BLAT	Aradu.A09:7356180..7360291	40.42
Alignment6	BLAT	Aradu.A08:23289238..23271605	39.21
Alignment7	BLAT	Aradu.A08:10829544..10829548	38.20