

TwiTAIR: What's happening at TAIR right now



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www.arabidopsis.org

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Outline

- Philippe Lamesch
- Introduction
- TAIR10 genome annotation
- TAIR gene confidence ranking
- TAIR genome analysis tools
- Donghui Li
- Accessing gene function information at TAIR
- Arabidopsis community curation effort

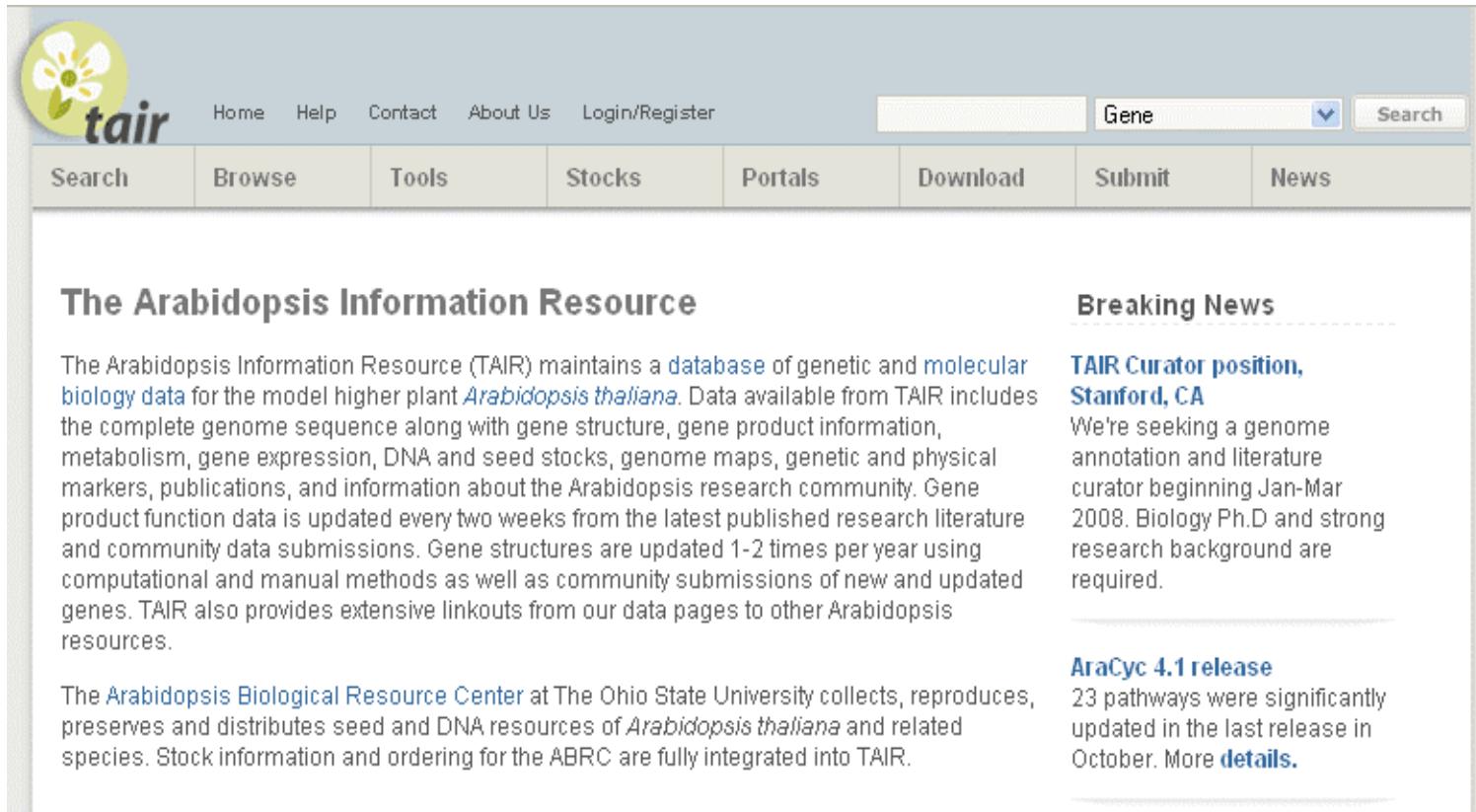


Outline

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- **Introduction**
- TAIR10 genome annotation
- TAIR gene confidence ranking
- TAIR genome analysis tools

TAIR: The Arabidopsis Information Resource

- collect, curate and distribute information on Arabidopsis
- information freely available from arabidopsis.org



The screenshot shows the homepage of the TAIR website. At the top left is the logo featuring a stylized flower inside a green circle with the word "tair" below it. The top navigation bar includes links for Home, Help, Contact, About Us, and Login/Register. A search bar is present with a dropdown menu set to "Gene" and a "Search" button. Below the header is a horizontal menu bar with links for Search, Browse, Tools, Stocks, Portals, Download, Submit, and News. The main content area features a section titled "The Arabidopsis Information Resource" which describes the database's scope and update frequency. It also mentions the integration with the Arabidopsis Biological Resource Center. To the right, there is a "Breaking News" sidebar with two entries: one about a curator position at Stanford, CA, and another about the AraCyc 4.1 release.

The Arabidopsis Information Resource

The Arabidopsis Information Resource (TAIR) maintains a [database](#) of genetic and molecular biology data for the model higher plant *Arabidopsis thaliana*. Data available from TAIR includes the complete genome sequence along with gene structure, gene product information, metabolism, gene expression, DNA and seed stocks, genome maps, genetic and physical markers, publications, and information about the Arabidopsis research community. Gene product function data is updated every two weeks from the latest published research literature and community data submissions. Gene structures are updated 1-2 times per year using computational and manual methods as well as community submissions of new and updated genes. TAIR also provides extensive linkouts from our data pages to other Arabidopsis resources.

The [Arabidopsis Biological Resource Center](#) at The Ohio State University collects, reproduces, preserves and distributes seed and DNA resources of *Arabidopsis thaliana* and related species. Stock information and ordering for the ABRC are fully integrated into TAIR.

Breaking News

TAIR Curator position, Stanford, CA
We're seeking a genome annotation and literature curator beginning Jan-Mar 2008. Biology Ph.D and strong research background are required.

AraCyc 4.1 release
23 pathways were significantly updated in the last release in October. More [details](#).

Slides available from TAIR

www.arabidopsis.org

The screenshot shows the TAIR website's navigation bar at the top, featuring a logo with a flower, and links for Home, Help, Contact, About Us, and Login/Register. Below the navigation is a horizontal menu bar with links for Search, Browse, Tools, Stocks, Portals, Download, Submit, and News. The main content area displays a sidebar on the left with links to various resources like About Arabidopsis, Search Arabidopsis Protocols and Manuals, Science Education and Outreach Programs, Teaching Resources, Funding for Education and Outreach, Plant Biology Education Newsgroups, TAIR Presentations (ppt), and TAIR Help. The main content area shows the 'Portals Overview' page for the ICAR Workshop 2009. It includes a breadcrumb trail (Home > Portals > Education), a title 'ICAR Workshop 2009', and a summary of the workshop. A list of resources is provided, categorized into 'Part I: Tips and strategies' and 'Part II: Hands-on exercises and individual help'. The 'Part I' list includes: Date: July 2, 2009; Time: 4:30 - 6:00; Location: Kilsyth; Conference site: [http://min.us/u/Tair](#). The 'Part II' list includes: TAIR ICAR Workshop Resource Guide; TAIR ICAR Workshop Practice Questions; TAIR workshop - part 2 - data file (Microarray / OMICs viewer data file for Question #1); TAIR ICAR Workshop Practice Questions with Answers.

Home > Portals > Education

ICAR Workshop 2009

TAIR gave a workshop at the 2009 International Congress of Arabidopsis Research (ICAR) in Kilsyth, Victoria, Australia.

Putting TAIR to work for you - Part I: Tips and strategies

- Date: July 2, 2009
- Time: 4:30 - 6:00
- Location: Kilsyth
- Conference site: [http://min.us/u/Tair](#)

Part I: Tips and strategies

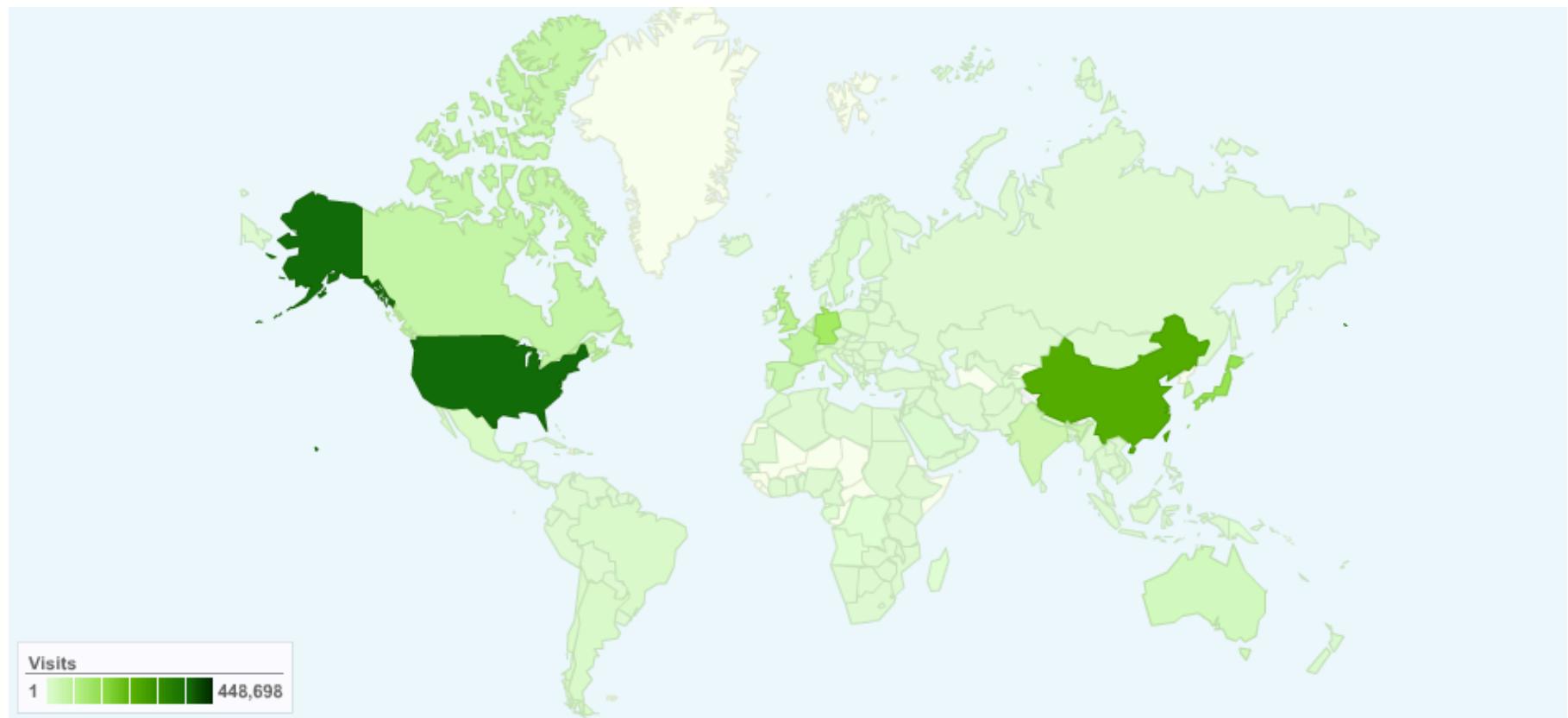
- Gene searches and the locus page (*presented by Eva Huala*)
- TAIR9, GBrowse, and confidence scores (*presented by Dave Swarbreck*)
- Generating and working with data sets (*presented by Kate Dreher*)

- TAIR ICAR Workshop Resource Guide

Part II: Hands-on exercises and individual help (*presenters and participants*)

- TAIR ICAR Workshop Practice Questions
- TAIR workshop - part 2 - data file (Microarray / OMICs viewer data file for Question #1)
- TAIR ICAR Workshop Practice Questions with Answers

TAIR visitors in 2010-2011



1,800,907 visits came from 177 countries/territories

TAIR visitors in 2010-2011

	Detail Level: Country/Territory <input type="button" value="▼"/>	Visits ↓	Pages/Visit	Avg. Time on Site	% New Visits	Bounce Rate
1.	United States	448,698	6.21	00:08:07	18.94%	36.71%
2.	China	280,121	8.11	00:11:23	17.64%	23.17%
3.	Japan	166,599	6.12	00:07:53	9.94%	39.25%
4.	Germany	143,270	5.59	00:07:46	17.86%	31.07%
5.	United Kingdom	86,703	5.35	00:07:25	16.79%	39.74%
6.	France	71,606	5.60	00:07:58	18.15%	33.96%
7.	South Korea	65,350	6.95	00:08:29	14.85%	29.02%
8.	Canada	62,183	6.28	00:08:04	23.84%	36.11%
9.	Spain	49,653	6.15	00:09:14	17.75%	33.06%
10.	India	46,652	5.73	00:07:47	37.33%	40.13%

Filter Country/Territory: [Advanced Filter](#) Go to: Show rows: 1 - 10 of 177

Steady increase of TAIR users over the last 4 years



What TAIR does:

(1) Arabidopsis genome annotation



What TAIR does: (2) manual literature curation

- Controlled vocabulary annotations

Gene Ontology (GO) <http://www.geneontology.org/>

Plant Ontology (PO) <http://www.plantontology.org/>

- Gene name, symbol
- Allele, phenotype
- Summary statement composition

Who we partner with:

PMN (Plant Metabolic Network) and PlantCyc

A comprehensive plant biochemical pathway database, containing curated information from the literature and computational analyses about the genes, enzymes, compounds, reactions, and pathways involved in primary and secondary metabolism

Who we partner with: ABRC

Distribution of biological research materials

For requests email: <http://abrc.osu.edu/>

The screenshot shows the homepage of the ABRC. At the top left is the Ohio State University logo. To its right is the text "Arabidopsis Biological Resource Center" above a photograph of many small green Arabidopsis plants. A yellow oval logo with a stylized plant icon and the letters "ABRC" is overlaid on the plants. Below the header is a navigation menu with links like "ABRC Home Page", "Search Seed Stocks", and "DNA Stock Handling". The main content area features a red title "Arabidopsis Biological Resource Center" and a paragraph about the center's history and mission. It also includes a bio of the Director, Dr. Randy Scholl, and descriptions of seed and DNA donation processes.

Arabidopsis Biological Resource Center

The Arabidopsis Biological Resource Center (ABRC) was established at [The Ohio State University](#) in September, 1991. Primary support for the ABRC is provided by a [National Science Foundation](#) grant. The mission of the ABRC is to acquire, preserve and distribute seed and DNA resources that are useful to the Arabidopsis research community.

[Dr. Randy Scholl](#) is the Director of the Center, and Associate Professor in the Department of Plant Cellular and Molecular Biology.

New seed and DNA enter ABRC through donation by national and international researchers. An identifying number is assigned to each stock. The stock is then evaluated, documented and made available for distribution. The preservation of seed and DNA stocks is conducted according to strict, defined protocols. Backups of stocks are maintained to ensure preservation.

The ABRC's holdings and stock distribution rates have increased rapidly so that presently hundreds of thousands of stocks are available. More than 100,000 stocks are shipped annually to researchers in more than 60 countries, and modest fees for stocks are charged.

- [ABRC Home Page](#)
- [Search Seed Stocks](#)
- [Search DNA Stocks](#)
- [Browse Catalog](#)
- [Charging System](#)
- [How to Make Payments](#)
- [Order Stocks](#)
- [Search Order History](#)
- [Stock Donation Forms](#)
- [DNA Stock Handling](#)
- [Plant and Seed Handling](#)
- [Stock Acquisition/ Deacquisition Policy](#)
- [ABRC Personnel](#)
- [Advisory Committee](#)
- [Seed and DNA Facilities](#)
- [FAQ's](#)
- [Links to other Resources](#)
- [PCMB Home Page](#)
- [Contact Us](#)

Arabidopsis genome annotation

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Arabidopsis genome annotation

- Arabidopsis genome sequenced ~ 11 years ago
- High quality sequence with few gaps
- TIGR did initial genome annotation
- TAIR took over responsibility in 2005
- TAIR has since released 5 genome annotations: TAIR6-TAIR10



Arabidopsis genome annotation



Genome annotation at TAIR

Add novel genes

Update exon/intron structures of existing genes

Delete mispredicted genes

Merge and split genes

Change gene types

Add splice-variants

Genome annotation at TAIR

- Add novel genes
- Update exon/intron structures of existing genes
- Delete mispredicted genes
- Merge and split genes
- Change gene types
- Add splice-variants
- Annotate ‘atypical’ gene classes

 Short protein-coding genes

 Trans. element  Transposable element genes

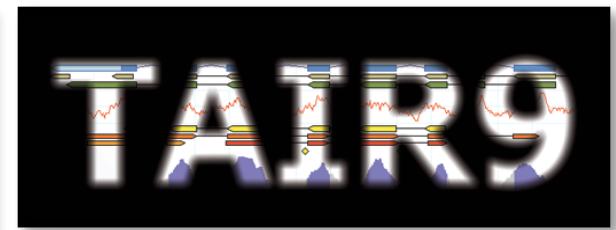
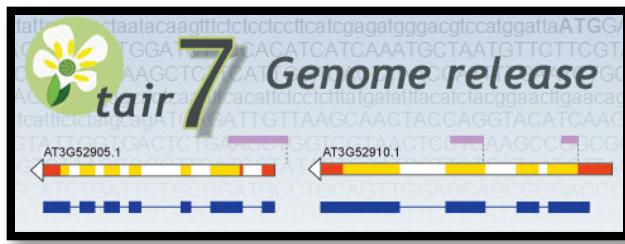
 * * * * * * Pseudogenes

 uORFs (genes within UTR of other genes)



Arabidopsis gene structure annotation A new approach

TAIR6-TAIR9: Use ESTs and cDNAs and a assembly tool called PASA to improve gene structures

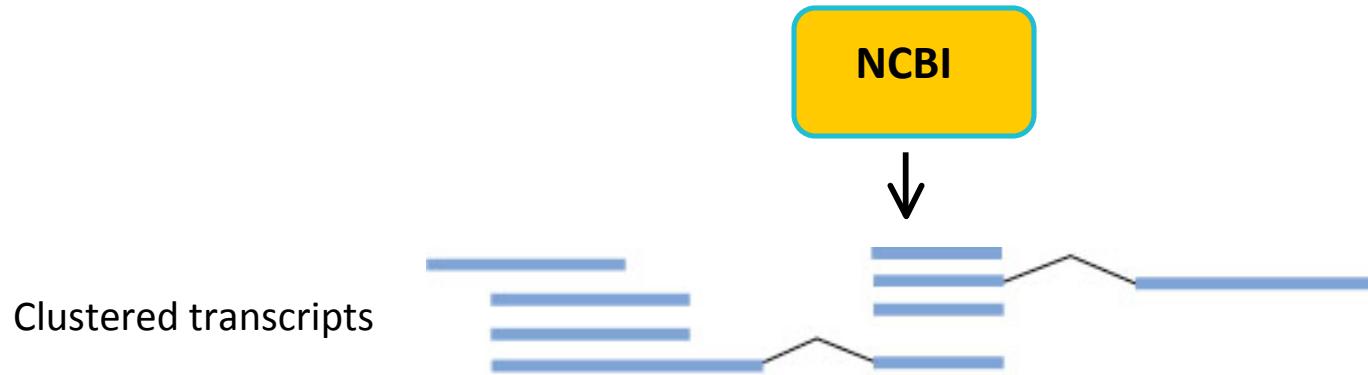


TAIR10: Use new experimental data and new prediction tools to further improve gene structure predictions



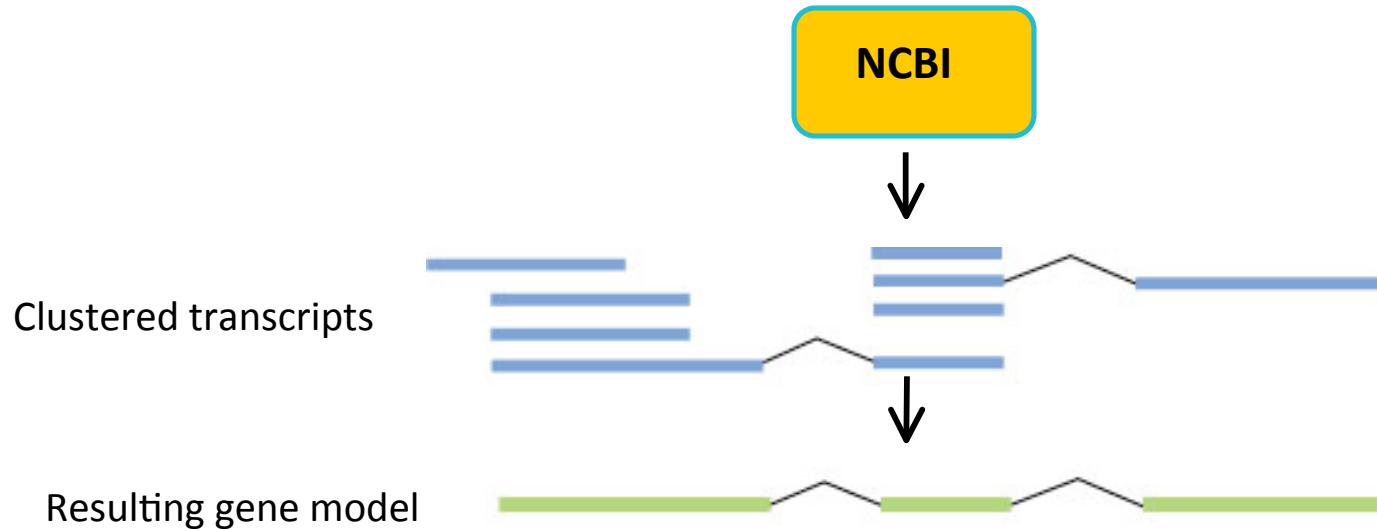
Genome annotation TAIR6-TAIR9

Using PASA and ESTs/cDNAs



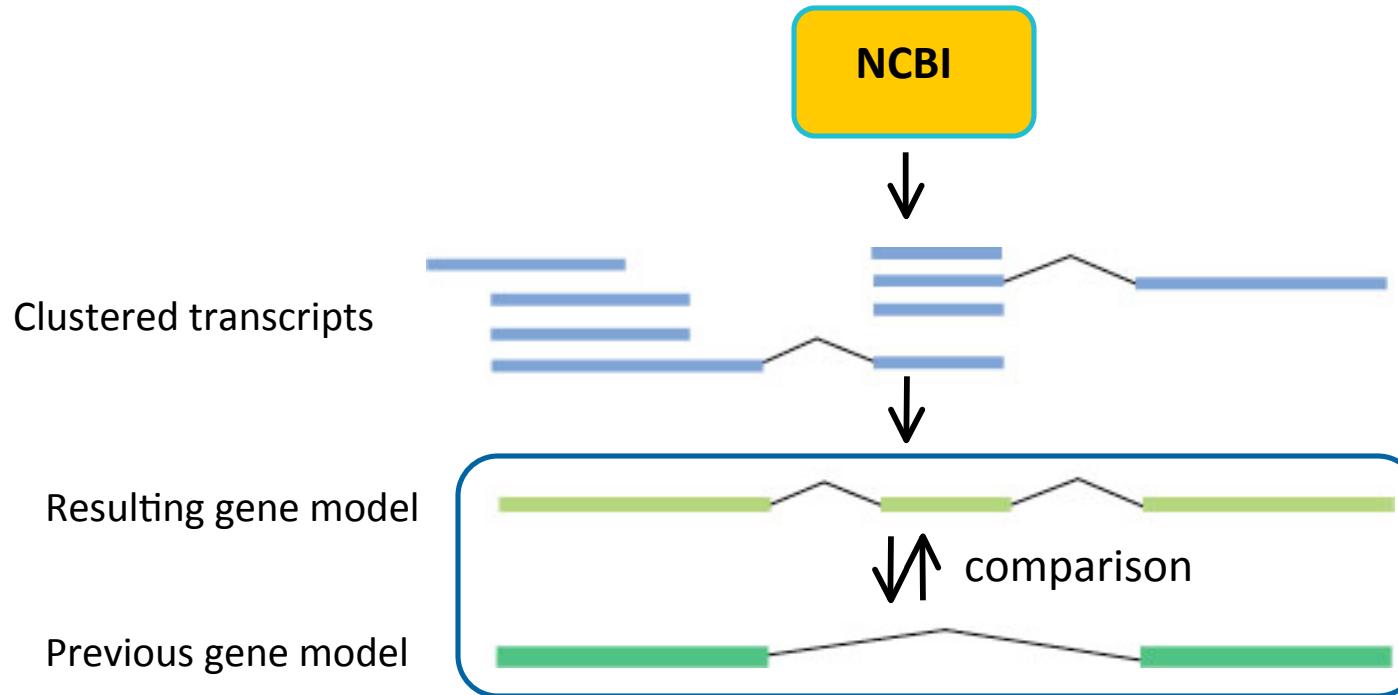
Genome annotation TAIR6-TAIR9

Using PASA and ESTs/cDNAs



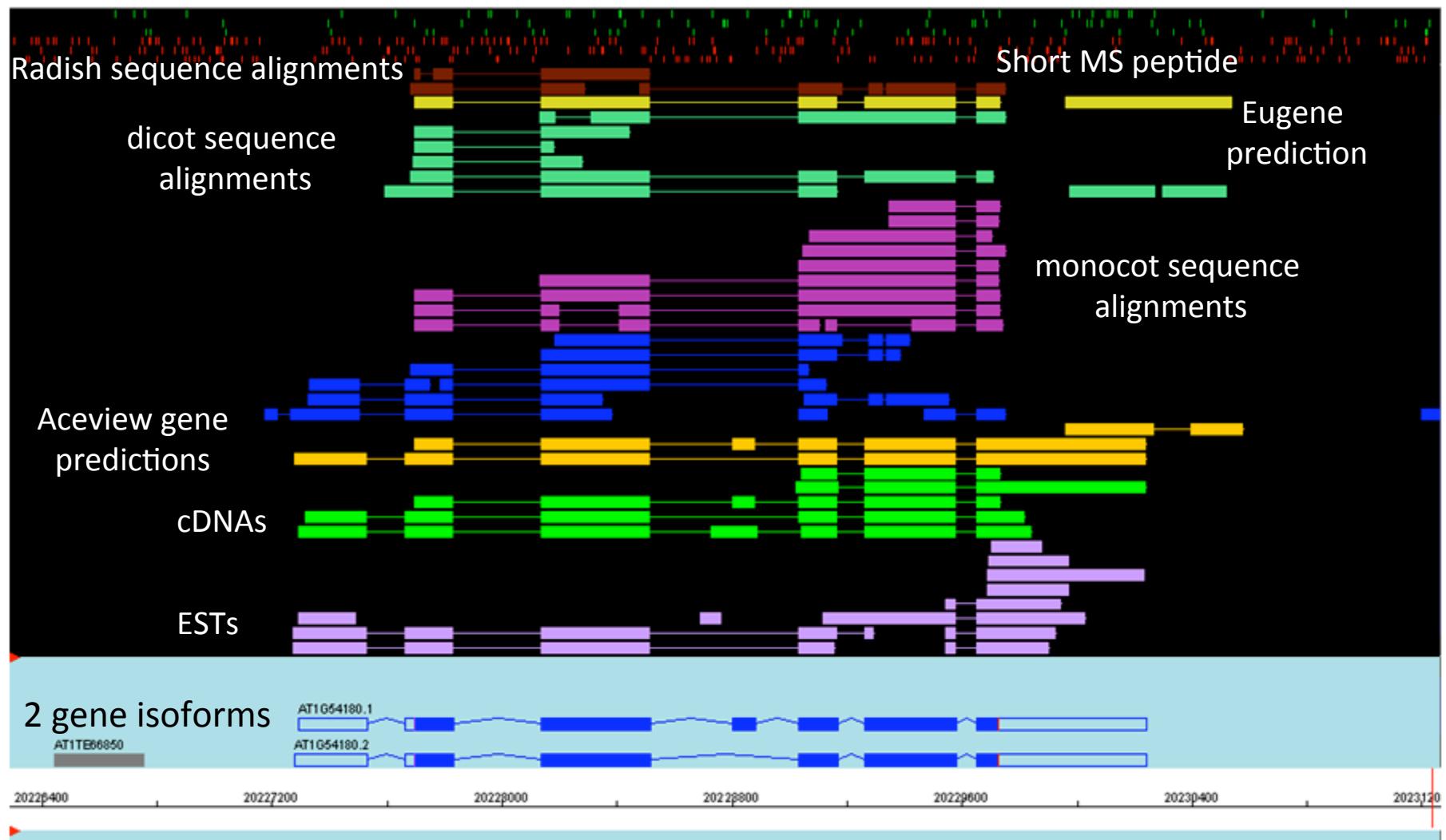
Genome annotation TAIR6-TAIR9

Using PASA and ESTs/cDNAs



- Novel genes
- New Splice-variants
- Gene structure updates

Manual annotation at TAIR: Apollo



TAIR10: using proteomics and RNA-seq data to improve genome annotation

4-step process:

- 1.Mapping RNA seq & Peptides**
- 2.Assembly/Gene built**
- 3.Manual review**
- 4.Integration (genome release/Gbrowse)**



Mapping and Assembly

1. Mapping

- RNA-seq sequences (**Tophat** (C. Trapnell),
Supersplat (T.C. Mockler))
- Peptides (6-frame translation, spliced exon graph)

2. Assembly approaches

- **Augustus** (M. Stanke)
 - Uses spliced RNA seq reads, peptides
 - Aim: Identify additional splice-variants, update existing genes
- **TAU** (T.C. Mockler)
 - Uses spliced RNA seq reads
 - Aim: Identify additional splice-variants
- **Cufflinks** (C. Trapnell)
 - Uses spliced and unspliced RNA seq data
 - Aim: Identify novel genes

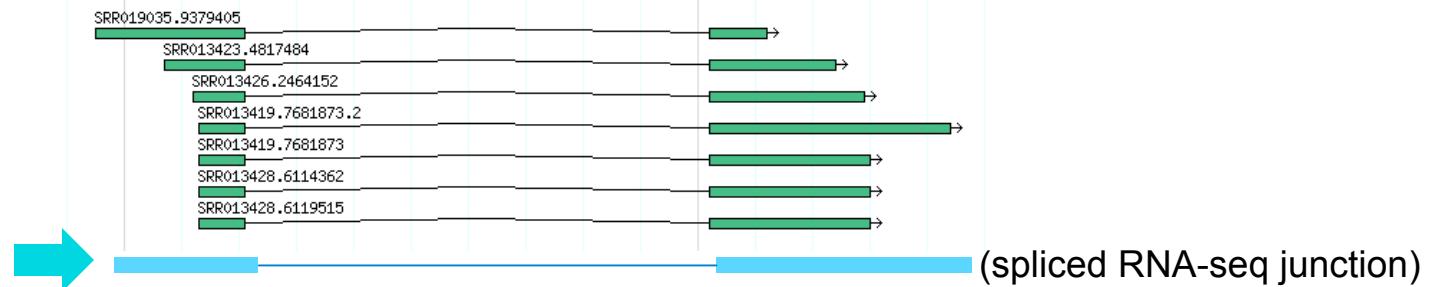


Tophat/Supersplat transcript mapping

RNA-seq datasets (Mockler Lab, Ecker Lab)

TopHat, SuperSplat

200 Million aligned RNA-seq reads
203,000 clustered **spliced** RNA-seq junctions



145,000 RNA-seq junctions based on >1 read

Augustus Gene Built

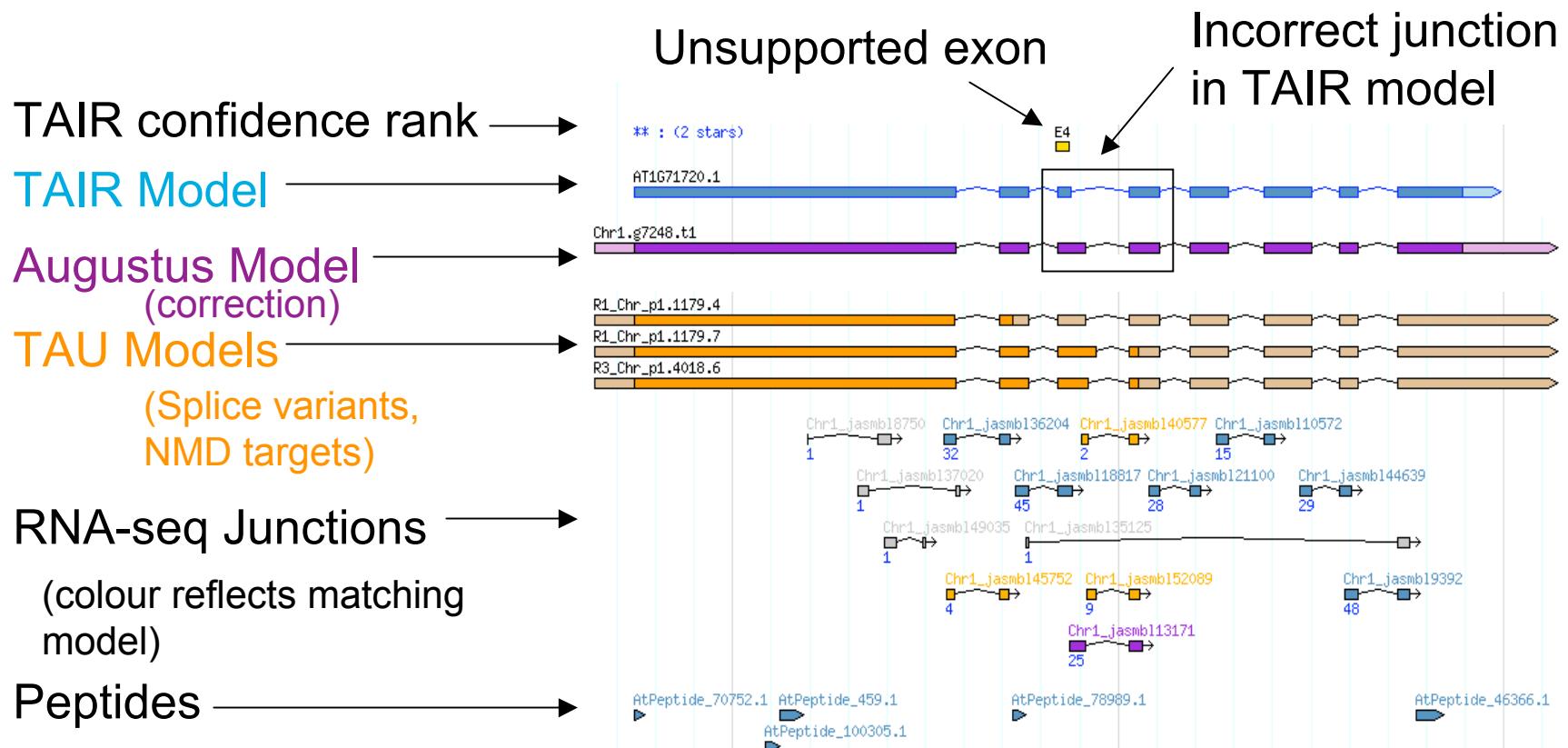
145,000 RNA-seq junctions based on **>1** read
260,000 peptides (Baerenfaller et al, Castellana et al)
+ ESTs & cDNAs
+ AGI models

Augustus gene prediction

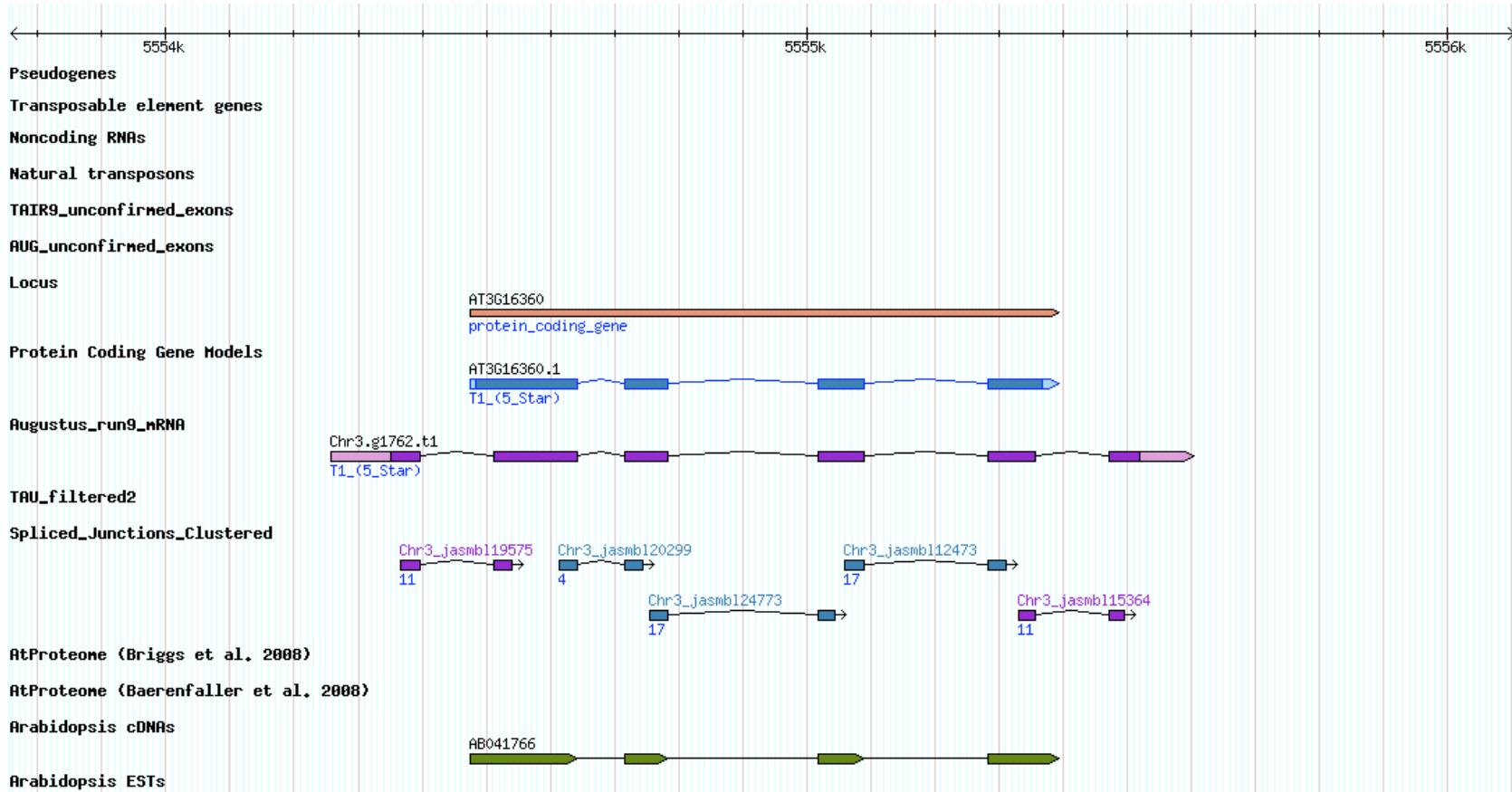
11% of RNA-seq junctions incorporated into Augustus models
64% of peptide sequences incorporated into Augustus models

Predicted Augustus models:
5461 updated gene models
1596 novel gene models

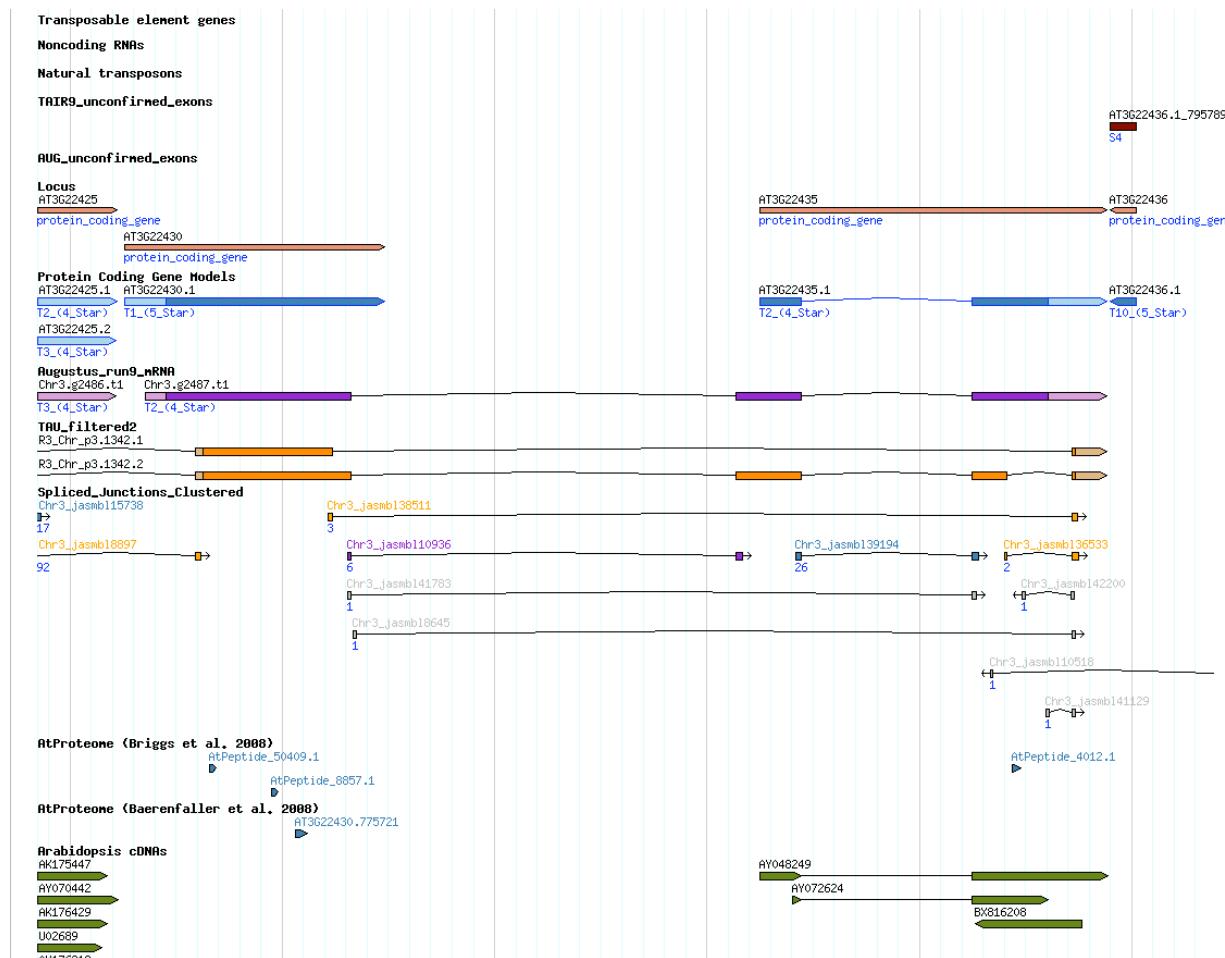
Categorisation/Review



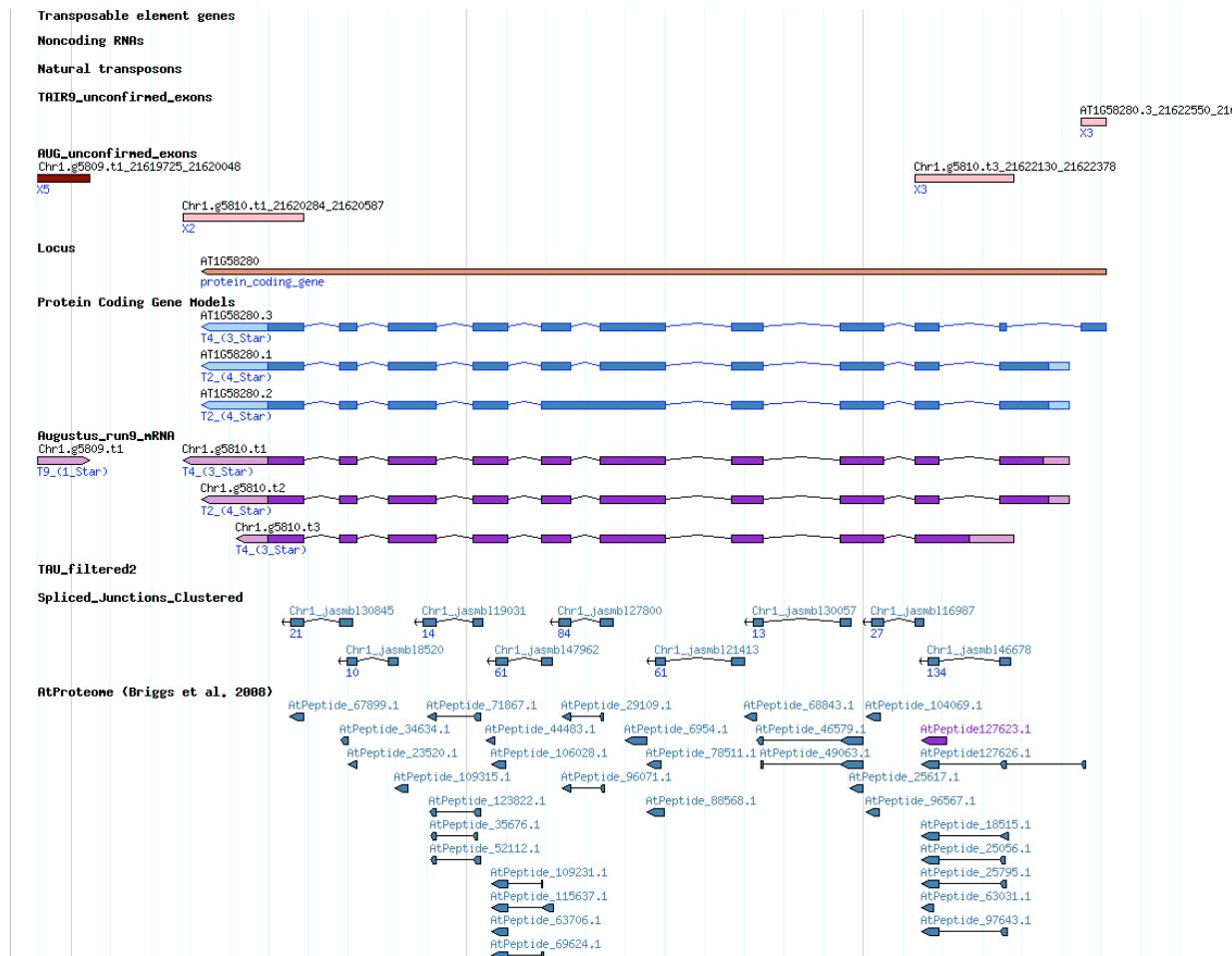
Example Augustus splice variant



Example Augustus update



Example 2 August splice variant



TAIR 10 Results

Total gene loci	33,602
Protein coding genes	27,416
Pseudo/Transposons	4827
Noncoding RNAs	1359

TAIR 10 Results

Total gene loci	33,602
Protein coding genes	27,416
Pseudo/Transposons	4827
Noncoding RNAs	1359
Novel gene loci	126
Novel gene models	2099
Updated gene models	1184
Splice-variants	5885 (18% of all loci)



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- **TAIR gene confidence ranking**
- TAIR genome analysis tools

Gene Confidence Rank

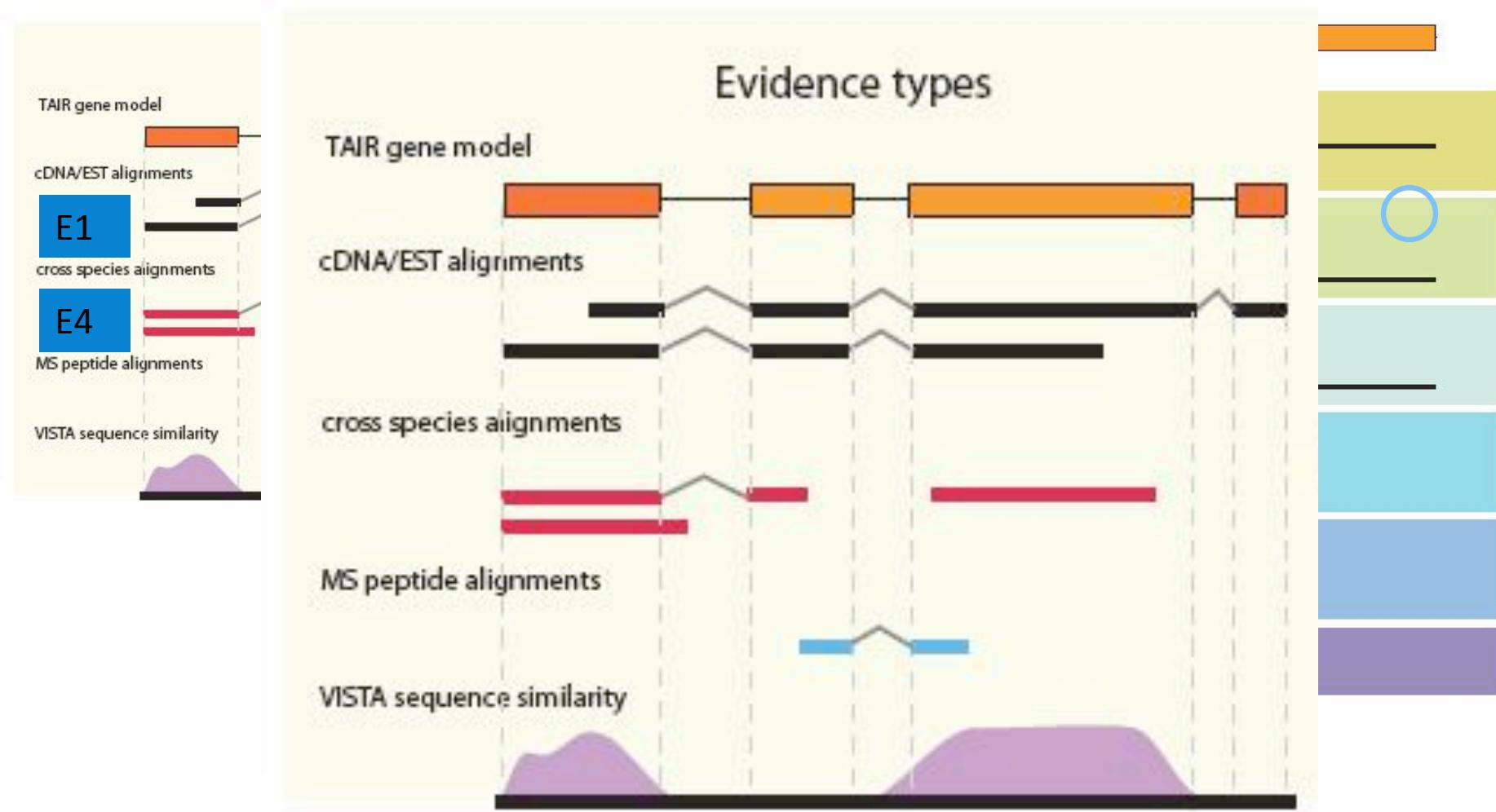
- Attributes confidence scores to all exons and gene models based on different types of experimental and computational evidence

TYPES OF EXPERIMENTAL & COMPUTATIONAL DATA USED

We used 4 types of experimental evidence to generate confidence scores:

- 1) **Arabidopsis transcript data** (ESTs, cDNAs, fragmented mRNAs from Ecker lab: *Lister et al Cell 2008*)
- 2) **Proteomics data** (*Castellana et al PNAS 2008; Baerenfaller et al Science 2008*)
- 3) **X-species alignments** (Brassica, Radish, + 5 other dicot (Glycine max, Solanum tuberosum, Malus x domestica, Gossypium hirsutum and Vitis vinifera) and 5 other monocot (Triticum aestivum, Zea mays, Oryza sativa, Saccharum officinarum and Hordeum vulgare) sequences from JCVI <http://plantta.jcvi.org/index.shtml>)
- 4) **Vista genomic conservation** (*Shah et al Bioinformatics 2004*)

Assigning A Confidence Rank



Full support

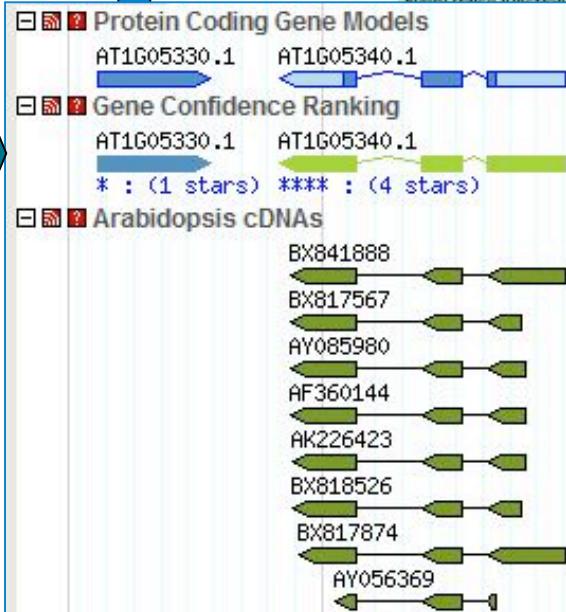
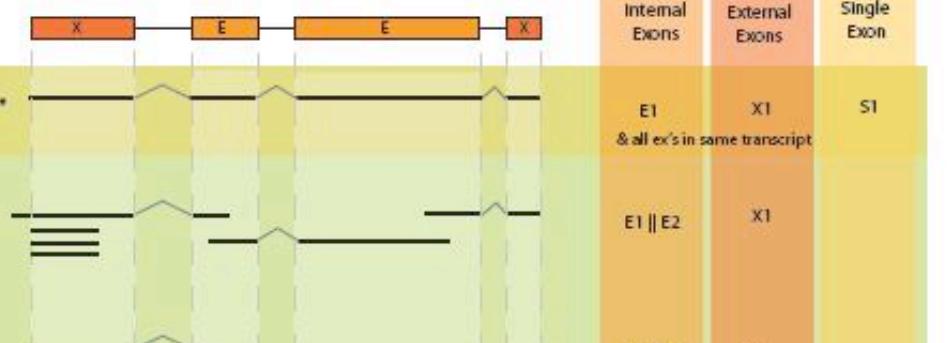
Gene All on All off
 CDS
 Gene Confidence Ranking

Gene Models

1 *****

Every Splice junction * & complete coverage **
by a single piece of evidence

2 **** *



AT1G05350.1

AT1G05350.1

** : (2 stars)

No support

9 *****

No Splice junctions

10*****

No experimental evidence

E5

E6

X4

X5

S3

S4

*except for single exon genes

** Transcript may extend beyond end of genemodel



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 - **N-Browse**
 - GBrowse for 10 plant genomes



N-Browse

- N-Browse (in collaboration with the Kris Gunsalus Lab, NYU)
- > 7,000 experimental interactions
- Interactions curated by TAIR, IntAct & BioGrid
- Tutorial at <http://www.arabidopsis.org/tools/nbrowse.jsp#nb-tut>

N-Browse

1 Search New Gene: HY5 From DB TAIR in species Arabidopsis(A.thaliana) GO Locate Gene:

2

3

4

Node systematic ID : AT4G10180
Node Common Synonym : DET1
Other Names: ATDET1,
DE-ETIOLATED 1, FUS2, FUSCA 2

Description : Encodes a nuclear-localized protein that acts as a repressor of photomorphogenesis and may be involved

step 1; gene(s): HY5 (nodes 10, edges 41);

Multi-Edge Only

Biochemical assays

Affinity technology

Enzymatic study

Chromatography technology

Comigration in gel electroph.

Crosslinking study

Cosedimentation

Other biochemical methods

Biophysical assays

Fluorescence technology

Surface plasmon resonance

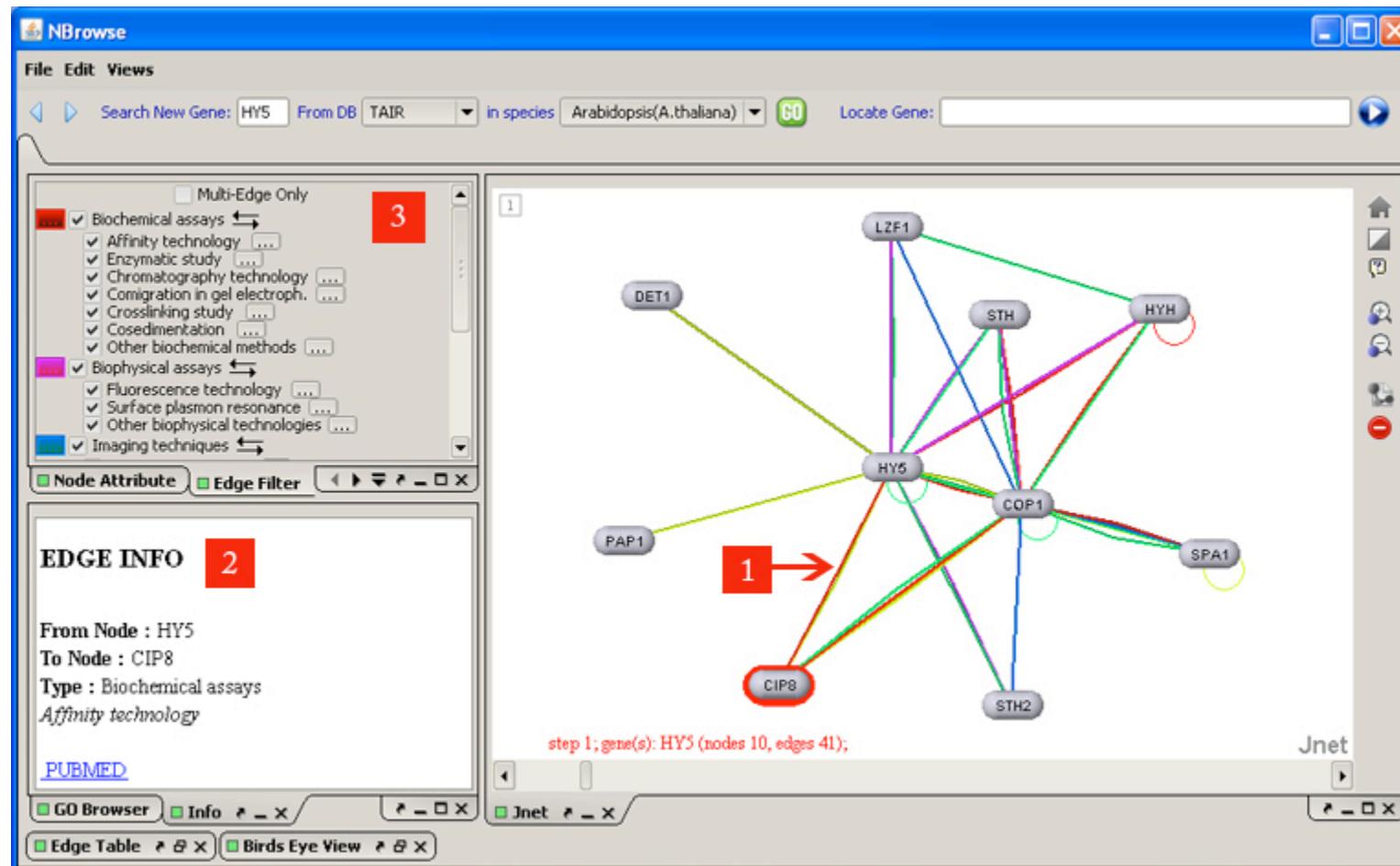
Other biophysical technologies

Node Attribute Edge Filter

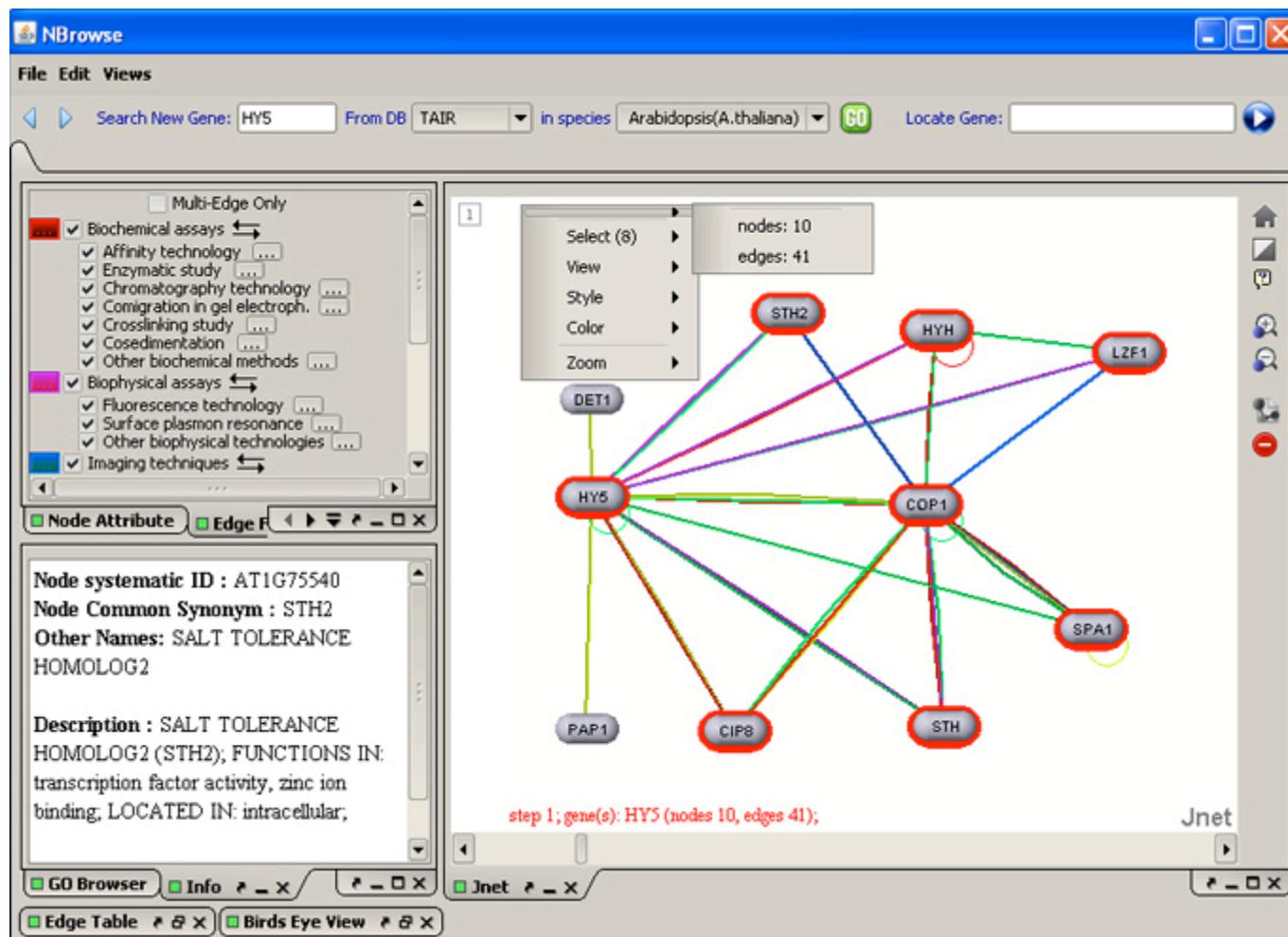
GO Browser Info Jnet

Edge Table Birds Eye View

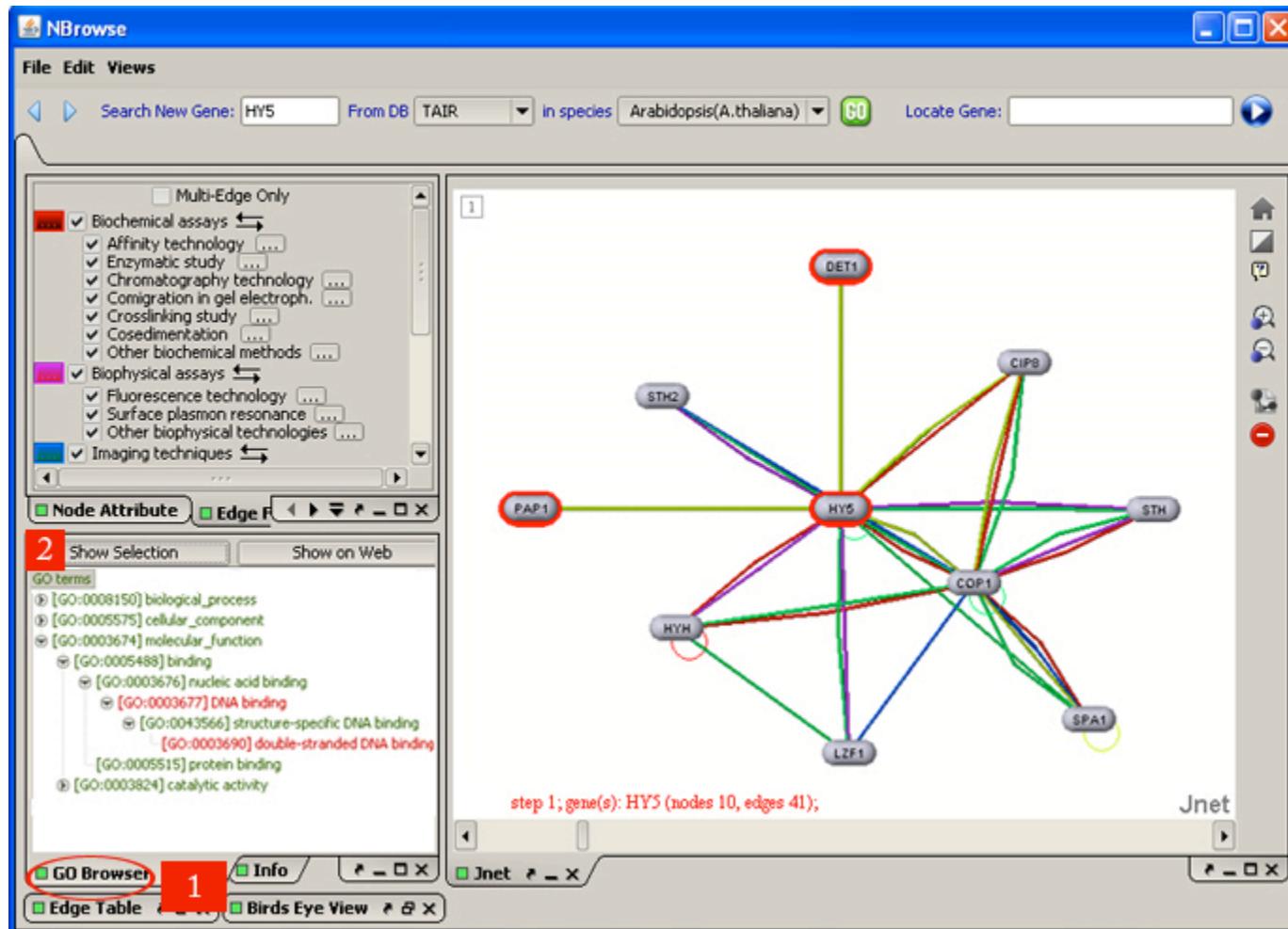
N-Browse: Finding information about edges (interactions)



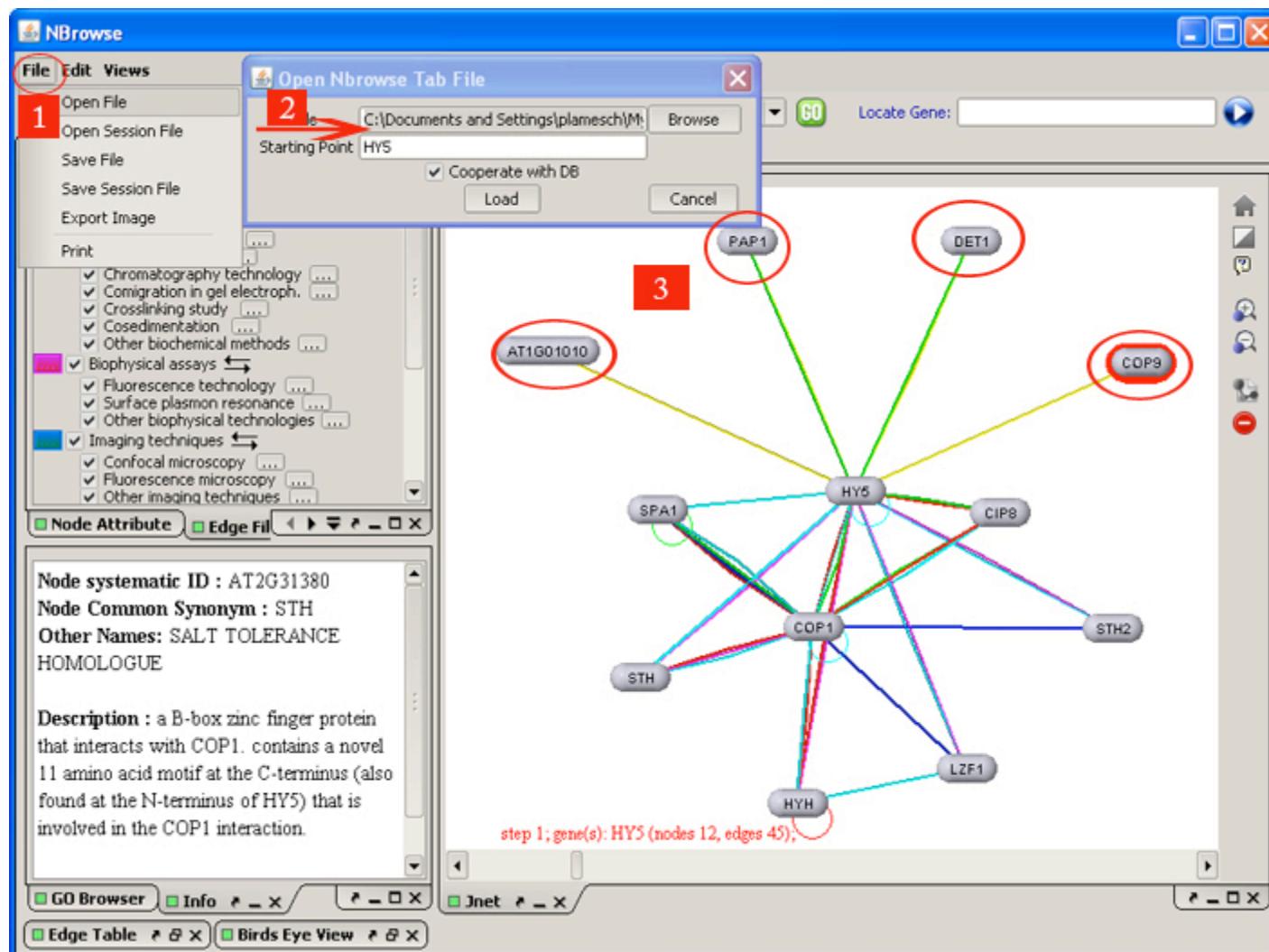
N-Browse: How to select and move nodes



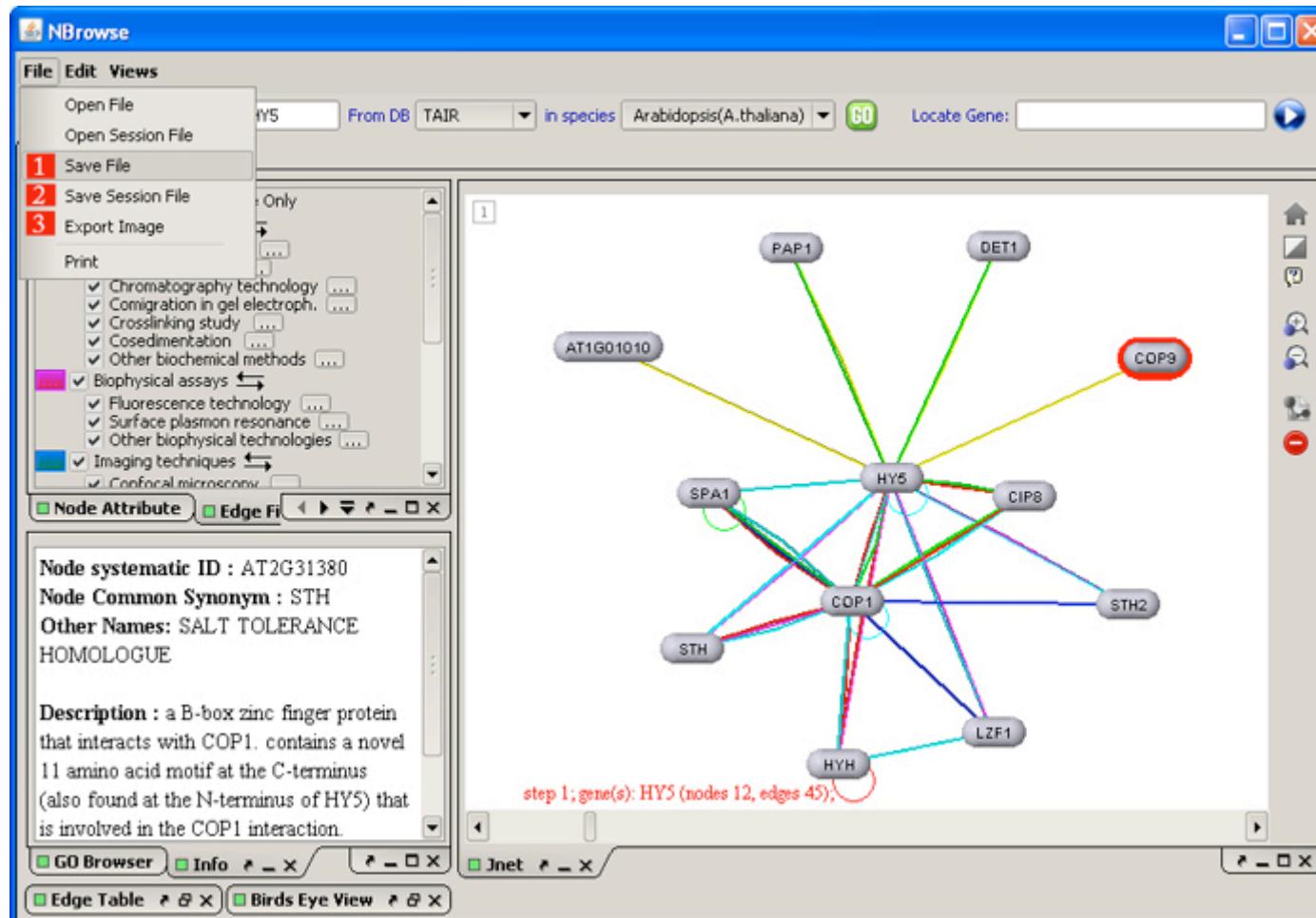
N-Browse: How to visualize GO terms from a selected set of nodes



N-Browse: How to load your own file and overlay it with the curated interaction data



N-Browse: How to save your session and export your data



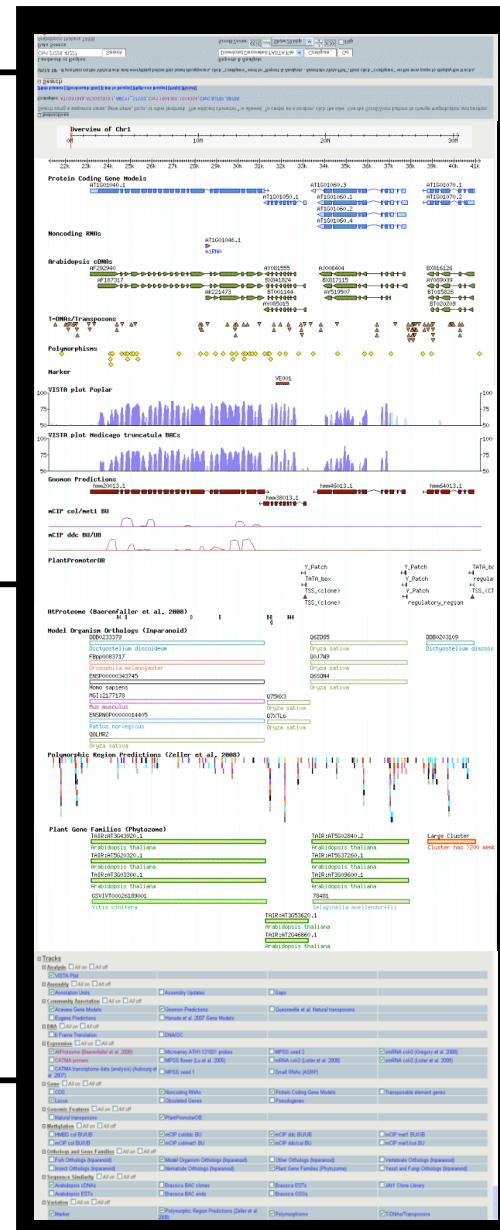


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GBrowse

Header

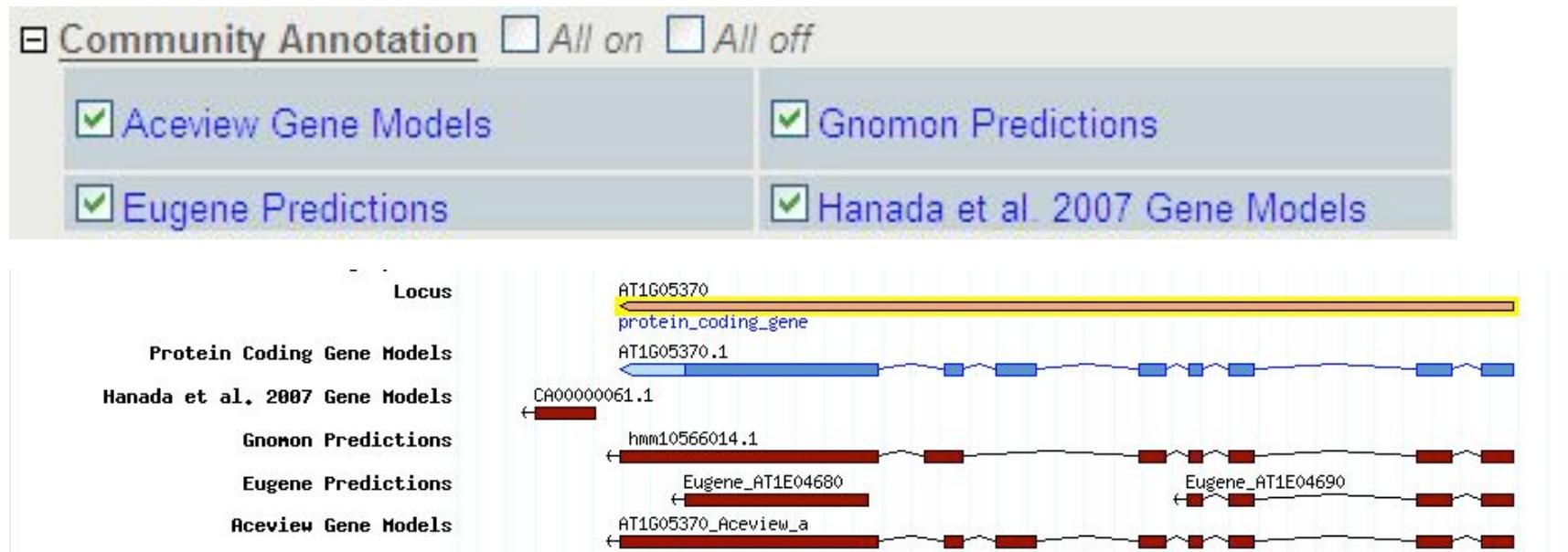


Main Browser Window

Track Menu

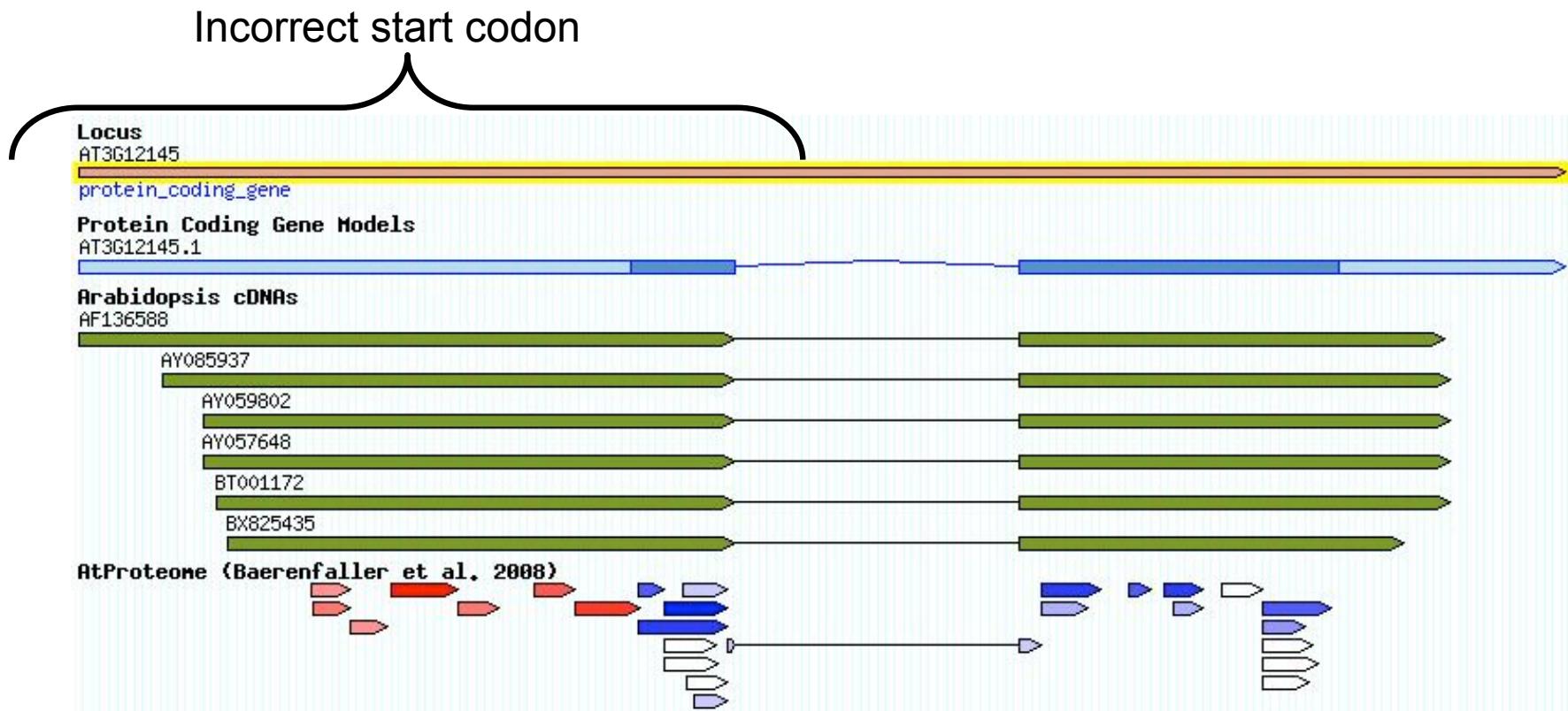
Alternative gene annotations

- Eugene (transcript, proteins +) Thierry-Mieg (NCBI)
- Gnomon (transcript, proteins) Souvorov (NCBI)
- Aceview (transcript) Sebastien Aubourg
- Hanada et al 2007 (3633 predicted genes)

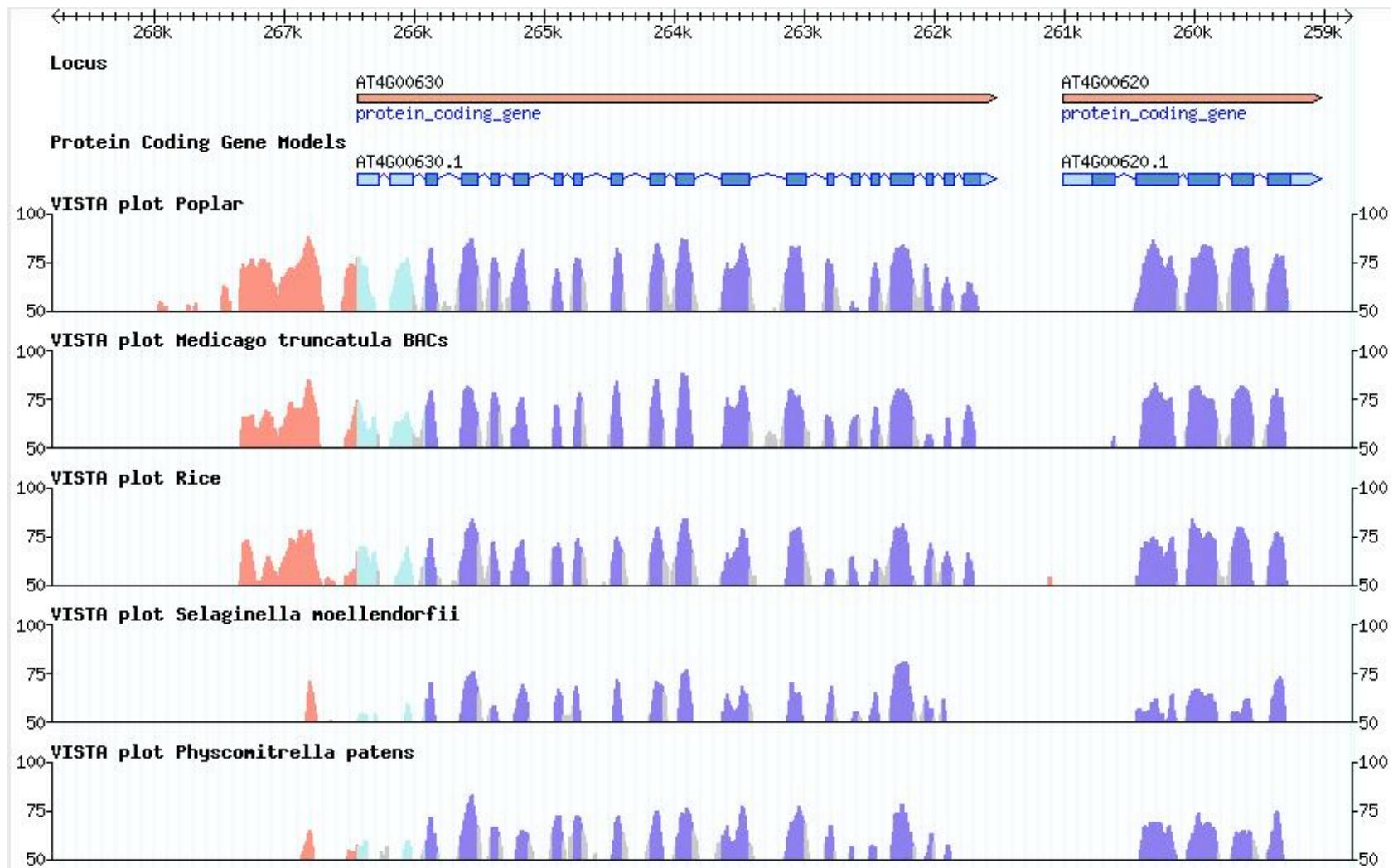


Proteomic Data

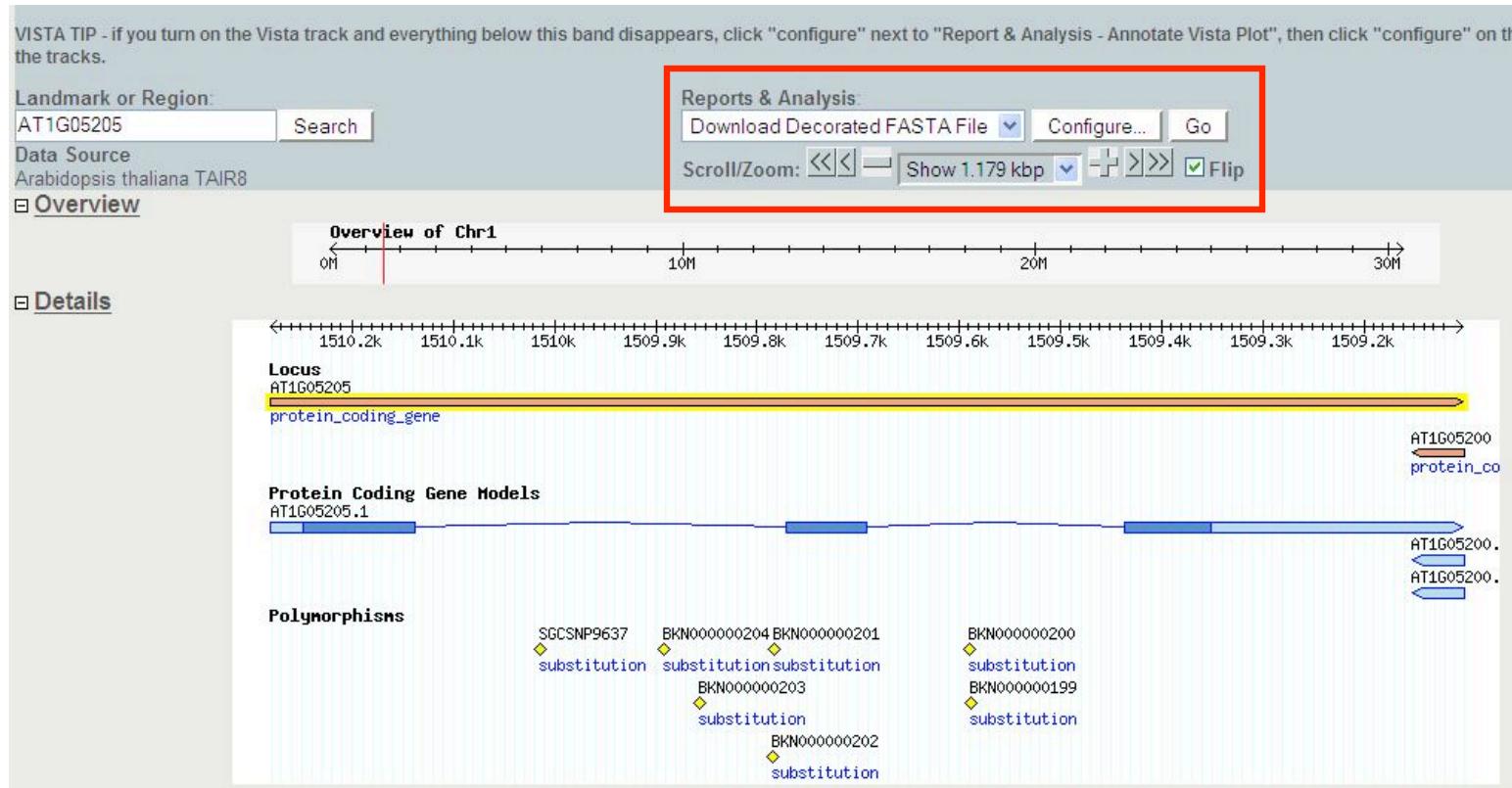
- High-density *Arabidopsis* proteome map (Baerenfaller. 2008)



VISTA plot Gbrowse track



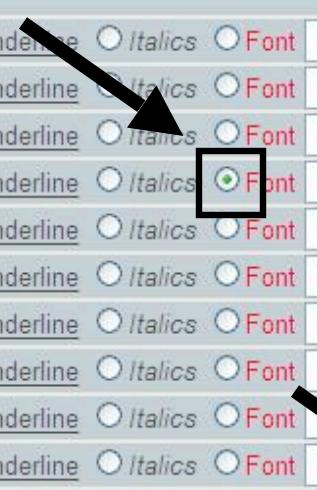
Decorated Fasta file



Decorated Fasta file

Configure... Decorated FASTA File

Output	<input type="radio"/> text <input checked="" type="radio"/> html
Orientation	<input type="checkbox"/> Flip
Chromosome	<input type="radio"/> None <input type="radio"/> CAPS <input type="radio"/> Bold <input type="radio"/> Underline <input type="radio"/> Italics <input type="radio"/> Font red <input type="button" value="▼"/>
Annotation Units	<input type="radio"/> None <input type="radio"/> CAPS <input type="radio"/> Bold <input type="radio"/> Underline <input type="radio"/> Italics <input type="radio"/> Font red <input type="button" value="▼"/>
Locus	<input type="radio"/> None <input type="radio"/> CAPS <input type="radio"/> Bold <input type="radio"/> Underline <input type="radio"/> Italics <input type="radio"/> Font red <input type="button" value="▼"/>
Protein Coding Gene Models	<input type="radio"/> None <input type="radio"/> CAPS <input type="radio"/> Bold <input type="radio"/> Underline <input type="radio"/> Italics <input checked="" type="radio"/> Font red <input type="button" value="▼"/>
CDS	<input type="radio"/> None <input type="radio"/> CAPS <input type="radio"/> Bold <input type="radio"/> Underline <input type="radio"/> Italics <input type="radio"/> Font red <input type="button" value="▼"/>
Pseudogenes	<input type="radio"/> None <input type="radio"/> CAPS <input type="radio"/> Bold <input type="radio"/> Underline <input type="radio"/> Italics <input type="radio"/> Font red <input type="button" value="▼"/>
Noncoding RNAs	<input type="radio"/> None <input type="radio"/> CAPS <input type="radio"/> Bold <input type="radio"/> Underline <input type="radio"/> Italics <input type="radio"/> Font red <input type="button" value="▼"/>
Hanada et al. 2007 Gene Models	<input type="radio"/> None <input type="radio"/> CAPS <input type="radio"/> Bold <input type="radio"/> Underline <input type="radio"/> Italics <input type="radio"/> Font red <input type="button" value="▼"/>
cDNAs	<input type="radio"/> None <input type="radio"/> CAPS <input type="radio"/> Bold <input type="radio"/> Underline <input type="radio"/> Italics <input type="radio"/> Font red <input type="button" value="▼"/>
ESTs	<input type="radio"/> None <input type="radio"/> CAPS <input type="radio"/> Bold <input type="radio"/> Underline <input type="radio"/> Italics <input type="radio"/> Font red <input type="button" value="▼"/>
T-DNA/Transposons	<input type="radio"/> None <input type="radio"/> CAPS <input type="radio"/> Bold <input type="radio"/> Underline <input type="radio"/> Italics <input type="radio"/> Font red <input type="button" value="▼"/>
Polymorphisms	<input type="radio"/> None <input type="radio"/> CAPS <input type="radio"/> Bold <input type="radio"/> Underline <input type="radio"/> Italics <input type="radio"/> Font red <input type="button" value="▼"/>
Marker	<input type="radio"/> None <input type="radio"/> CAPS <input type="radio"/> Bold <input type="radio"/> Underline <input type="radio"/> Italics <input type="radio"/> Font red <input type="button" value="▼"/>

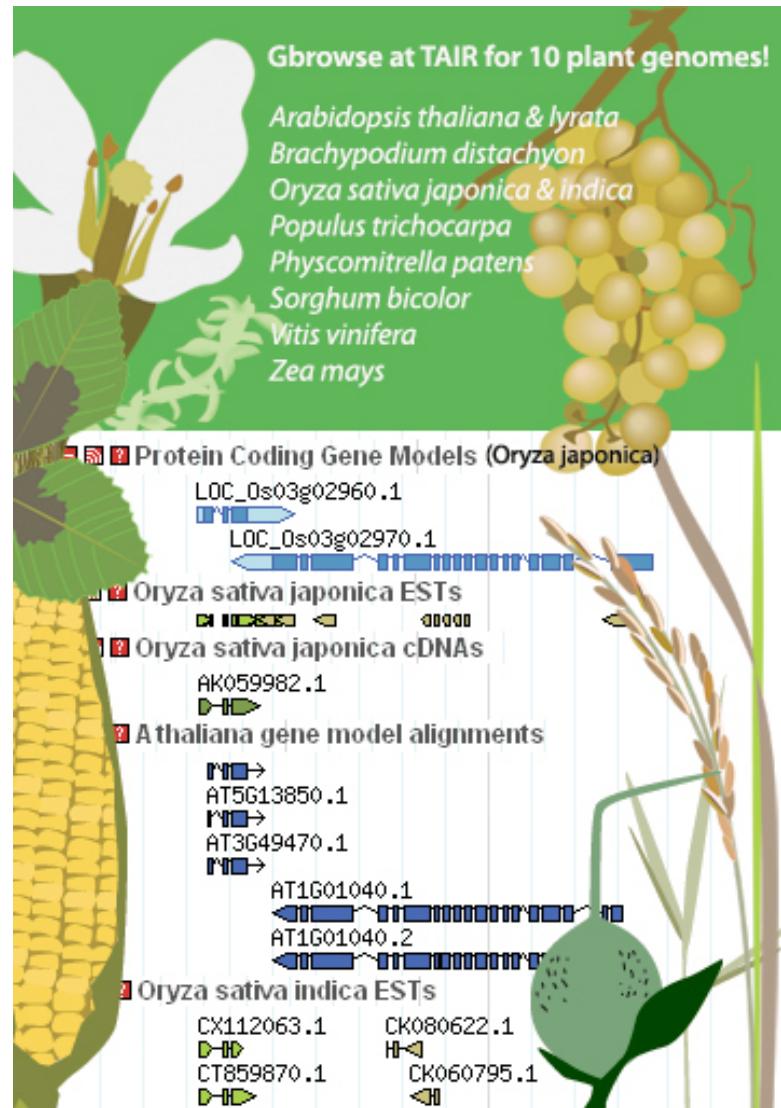


Decorated Fasta file

Chr1:1509102..1510280 (reverse complemented)

>Chr1:1509102..1510280 (reverse complemented)
gcgtttgagatttaccaggagaagaaatggcgacgacgacccatgtccggagga
gagagagtccatgggttaccggaaagggtcaccgtgagccccaaagctcaccgctgcaacg
atcgtgttgaagacgttatccagggttctcaccatcccttcgtttcaatttaaaaag
ttccatTTTCTGATAAACCTTGGAGAGATCTCTCTTAGATAACAGCAGAGA
TTCACTGTAAATCAATTAGGGTTTCAGGGTTCTGTACTTTCTATAATGTGGGGAGG
ATGATGGTTAATGGCATTGATCATGAACGATTAATACCTAAATTCTGGCTTTATGA
ATCTATTCTTCAATTGTTGTTGAAGCGTGTATCAGCTTATTGACTTGTTCATGG
AAGAACTAAAATTGCTTGGTTGGGCCATGATTGTTGAAAAGTATCCTCTTGATCTATT
CATATCATAGTATTAGTAACTTTCTAGGGCTTATTGAGGGAAACCCATTCAAGACA
GTTCCAGGACCTTCAAACACTCTTCTACCGATGTATGCGCTCTAAGCCAGGGTATGTGAA
TTTCATACTTTATCATAACCATCAAGTGTGTTGATACTAAGCTGCAGAACTTTGCTGC
TTGTTCCATTGCCACTGAATGAATGGTTCTTAATTCTTGTCCACCAGCTATTGTTCCCG
CTAAACCAAGTTCTCGTCTTTTATTAAACAATAGACAGACAGCTTAGCCTTCTGCTT
TCTTGTGTTGGTTATTACTAGATCTGGAGGGCTGAACCATTCACCTTTAT
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GTTAAACTGAAGAAGCAGCTTGAGTAAAGTGTATTCACCTCCCTTTATTCTGC
ATACCTTTAGCTGAGCGTGTAAAGCGCCATCACTGTGATTAAAGTTACCTTCAATATG
TGTCAACAAACATCTTATTCTCTTAATAAAAATTGATACTCGGAGGTTCTGATT
ATCTATTGCTTAATCTGTTCACTTGCAAGCTCTGTGAATGTGAACCTGTGATGAAGAT
GCTTTTCTTACGACTCAGAAAAAGATTACAATT

GBrowse for 10 new plant genomes



GBrowse for 10 new plant genomes

<http://gbrowse.arabidopsis.org/cgi-bin/gbrowse/arabidopsis/>

The screenshot shows the Tair GBrowse interface. At the top, there is a navigation bar with links for Home, Help, Contact, About Us, Login/Register, and Logout. Below the navigation bar is a search bar with dropdown menus for "Gene" and "Search". A logo for "tair" is on the left.

Instructions:
Searching: Search using a sequence name, gene name, locus, or other landmark. The wildcard character * is allowed.
Navigation: Click one of the rulers to center on a location, or click and drag to select a region. Use the Scroll/Zoom buttons to change magnification and position.
Examples: AT1G01040, AT3G52910.1, ABC11_171G2, AtMRP11, Chr1:1504365..1514364, ChrC:63781..68780.

[Help] [Reset]

Search

VISTA TIP - if you turn on the Vista track and everything below this band disappears, click "configure" next to "Report & Analysis - Annotate Vista Plot", then click "configure" on the new page to display the tracks.

Landmark or Region: Search button (circled in red)

Data Source: A dropdown menu showing the following options:

- Arabidopsis thaliana TAIR10 (selected)
- Arabidopsis lyrata (JGI Araly1)
- Arabidopsis thaliana TAIR10
- Arabidopsis thaliana TAIR8
- Arabidopsis thaliana TAIR9
- Brachypodium distachyon (Brachy1.0)
- Oryza sativa indica (BGI 2005-01)
- Oryza sativa japonica (MSU6)
- Physcomitrella patens (JGI Ppatens v1.1)
- Populus trichocarpa (JGI 2004-12)
- Sorghum bicolor (JGI Sb1)
- Vitis vinifera (IGGP 2007-12)
- Zea mays (AGPv1, 2009-03-20)

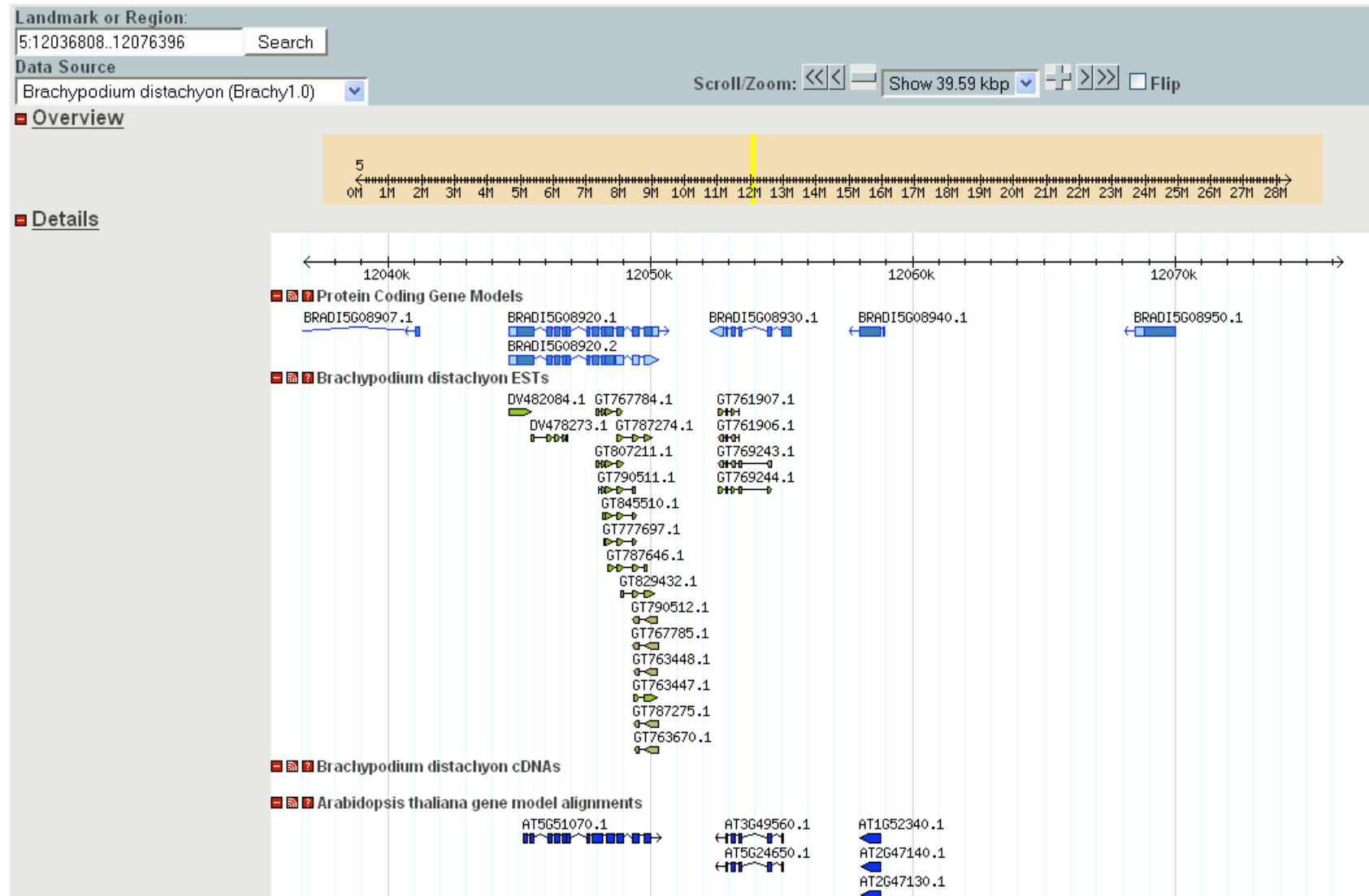
Reports & Analysis: Annotate VISTA Plot, Configure..., Go

Filter Options: These checkboxes are grouped into several categories:

- Assembly Updates, Gaps
- Gnomon Predictions, Hanada et al. 2007 Gene Models, Polyadenylation sites (AtPolyA-DB), Quesneville et al. Natural transposons
- DNA/GC
- AtPeptide (Castellana et al. 2008), CATMA transcriptome data (analysis) (Aubourg et al. 2007), MPSS seed 1, Small RNAs (ASRP)
- AtProteome (Baerenfaller et al. 2008), Microarray ATH1-121501 probes, MPSS seed 2, smRNA col-0 (Gregory et al. 2008)
- CATMA primers, MPSS flower (Lu et al. 2005), mRNA col-0 (Lister et al. 2008), smRNA col-0 (Lister et al. 2008)
- Gene, All on, All off, Blist_gene, Noncoding RNAs, Pseudogenes
- CDS, Obsolete Genes, TAIR10_unconfirmed_exons
- Locus, Protein Coding Gene Models, Transposable element genes
- Genomic Features, DNA replication origins (Costas et al. 2011), Natural transposons, PlantPromoterDB
- Methylation and Phosphorylation, All on, All off

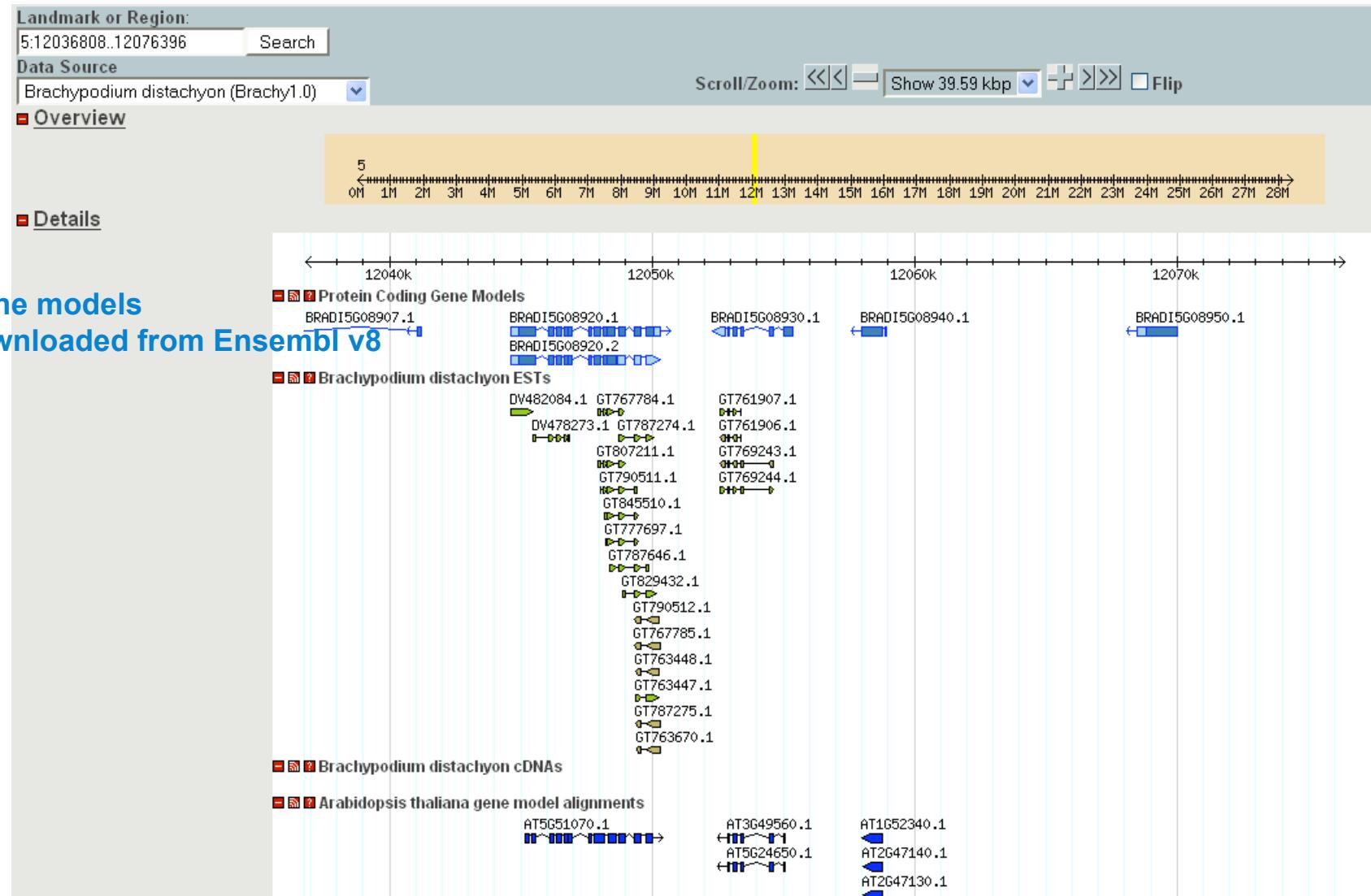
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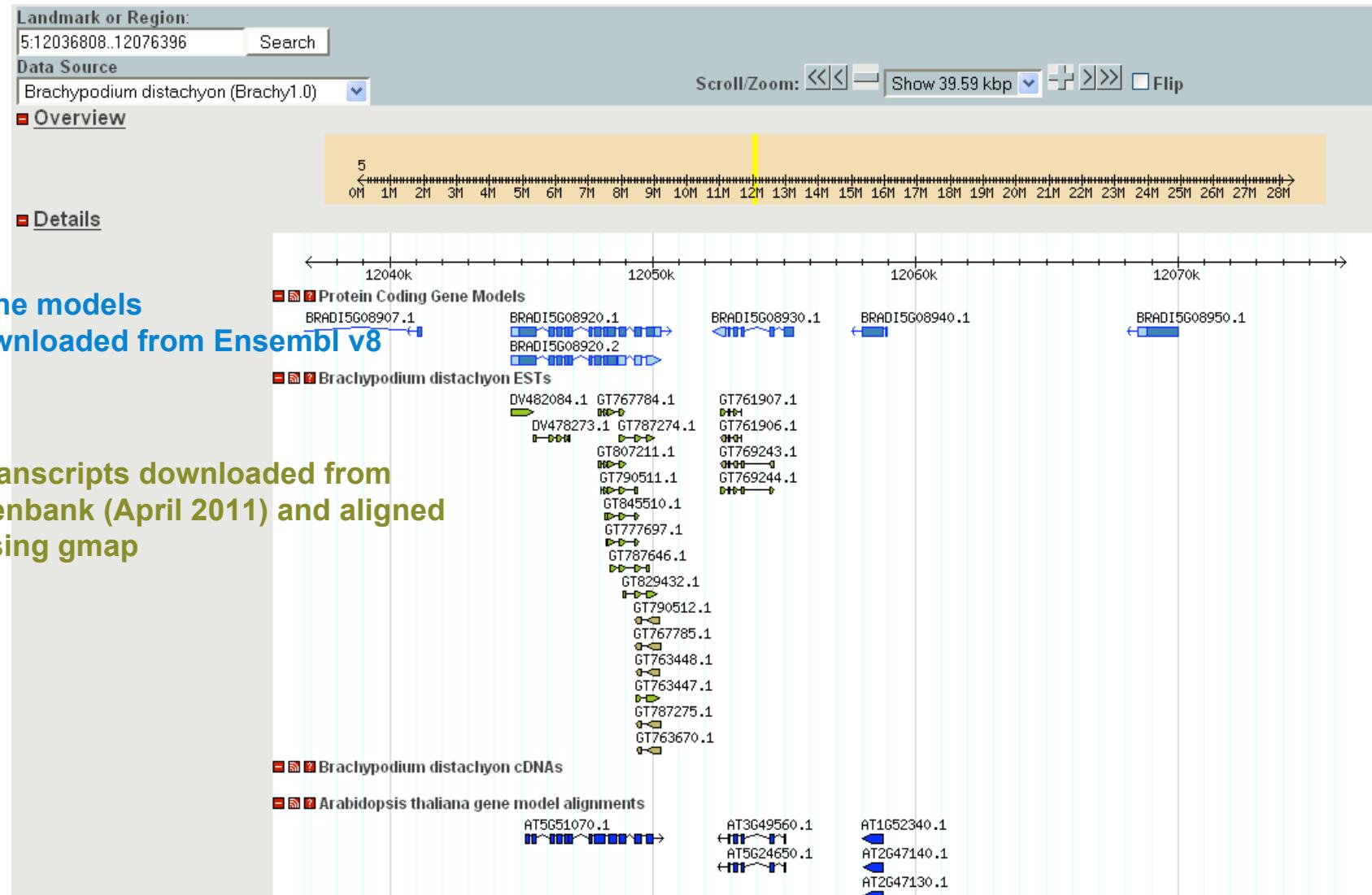
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