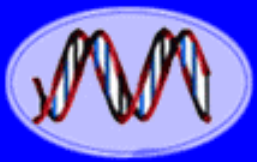


HC70AL Summer 2014

An Introduction to Bioinformatics

**by
Kelli Henry**

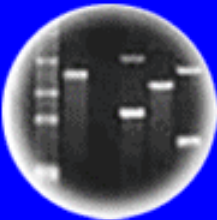
August 14, 2014



DNA
Genetic Code of Life



Entire Genetic Code
of a Bacteria



DNA Fingerprinting



Cloning: Ethical Issues
and Future Consequences



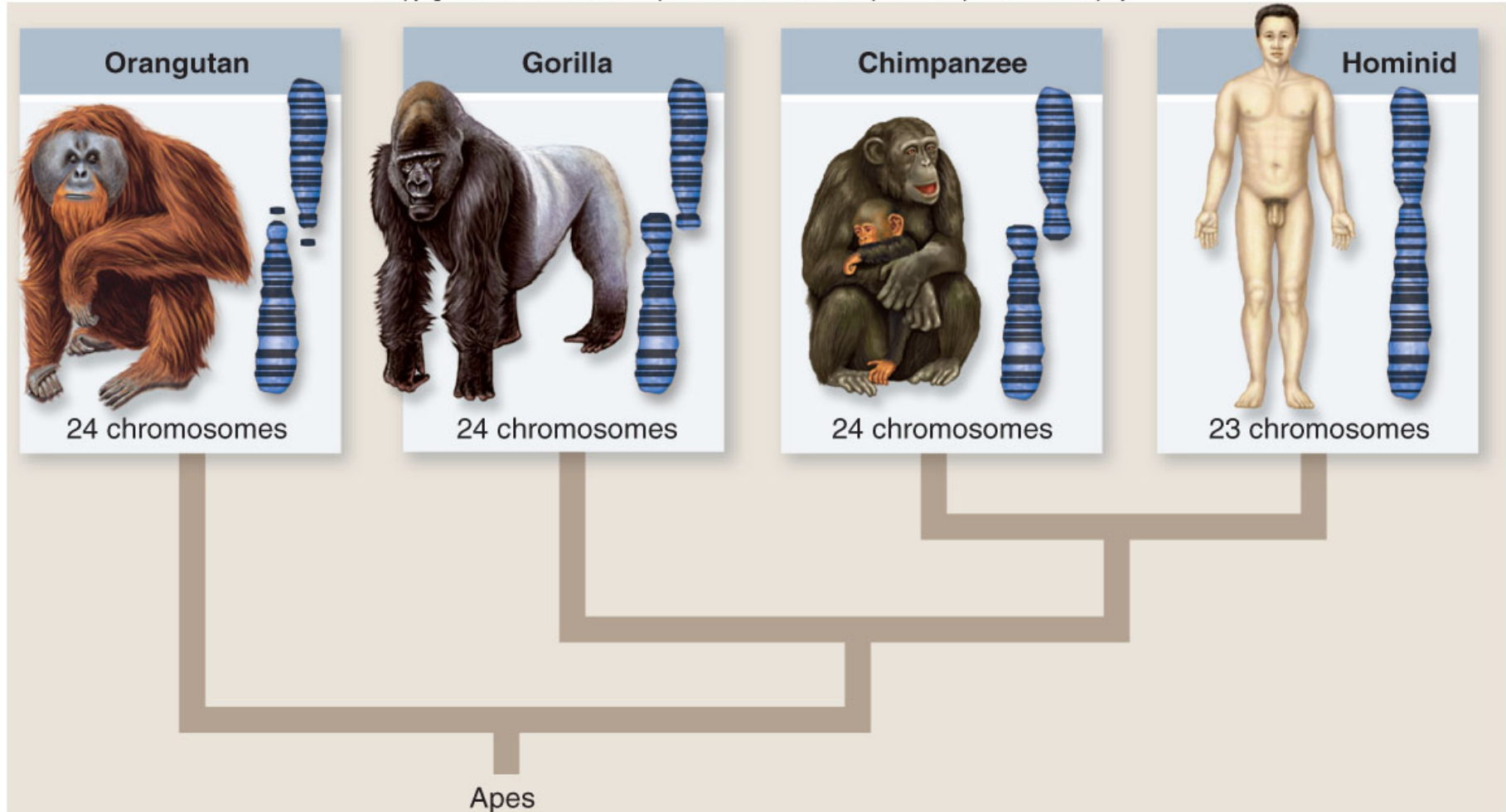
Plants of Tomorrow

A New Comparative Genomics Field Has Emerged Allowing the Comparison of Entire Genomes!

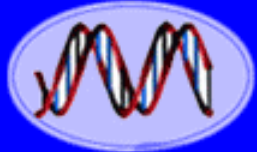


Comparison of Mammalian Genomes Attempts To Determine “What Makes a Man, a Man and a Mouse a Mouse”

Copyright © The McGraw-Hill Companies, Inc. Permission required for reproduction or display.



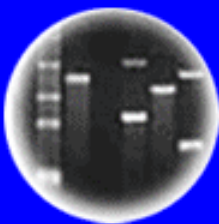
There is <1% Difference Between Human & Chimpanzee DNAs!



DNA
Genetic Code of Life



Entire Genetic Code
of a Bacteria



DNA Fingerprinting

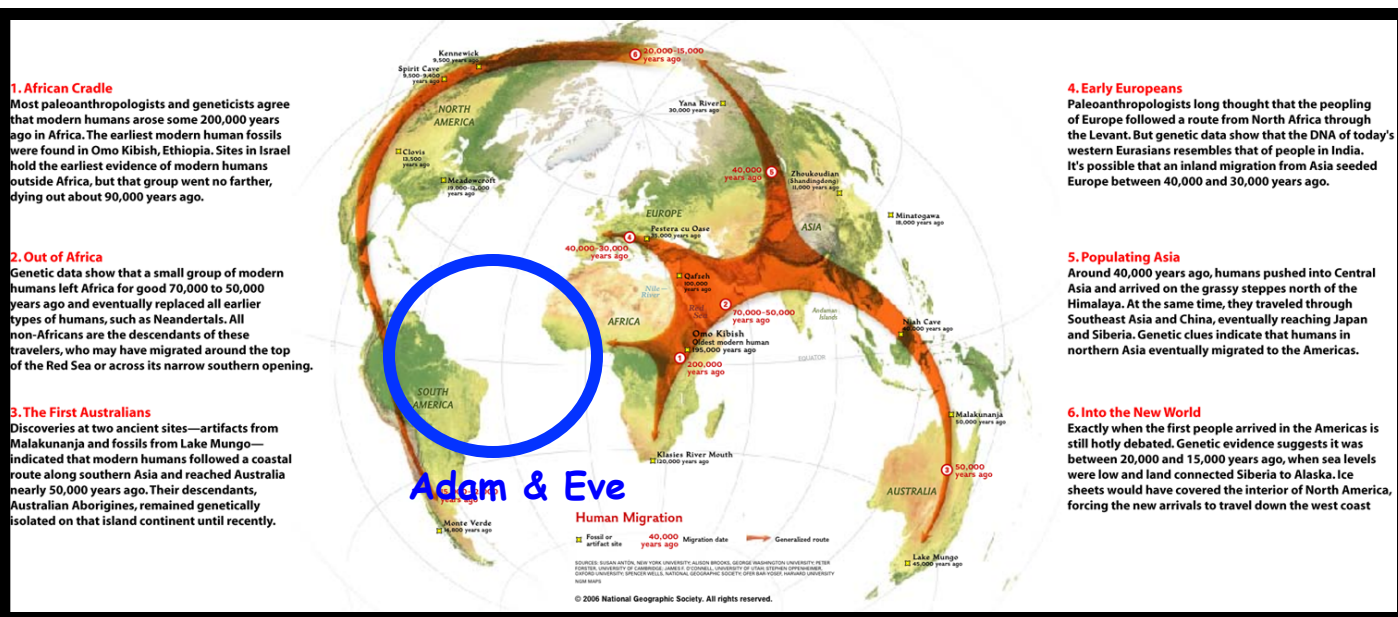
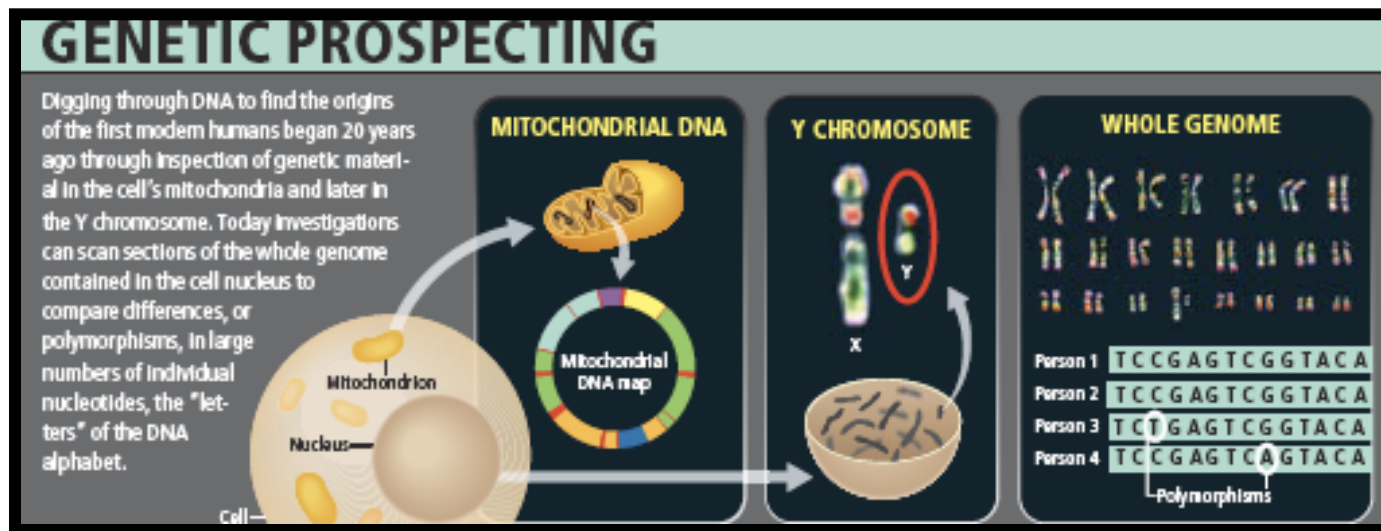


Cloning: Ethical Issues
and Future Consequences



Plants of Tomorrow

SNPS Can Be Used To Trace Human Populations & Origins



The Shaping of Modern Human Immune Systems by Multiregional Admixture with Archaic Humans

www.sciencemag.org SCIENCE VOL 334 7 OCTOBER 2011



Comparing 40,000
Year-Old
Fossil Genomes to
Our Genome
Reveals Ancient
“Matings”
Between Different
Human Ancestor
Lineages!!

We Have
Neanderthal &
Denisovan Genes in
Our Chromosomes

It's All in the DNA!

Nature Reviews | Genetics
September, 2011

What is BLAST?

Basic Local Alignment Search Tool (BLAST)

What does BLAST do?

A family of programs that allows you to input a query sequence and compare it to DNA or protein sequences in a database.

What Are the Different BLAST Programs?

Fastest

blastp - protein query vs protein database

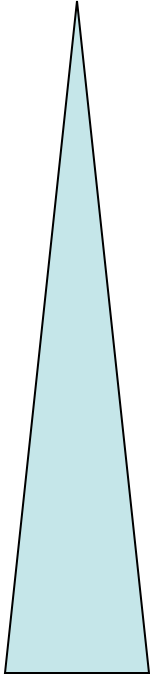
blastn - DNA query vs DNA database

blastx - translated DNA query vs protein database

tblastn - protein query vs translated DNA database

Slowest

tblastx - translated DNA query vs translated DNA database





► NCB/ BLAST Home

BLAST finds regions of similarity between biological sequences. [more...](#)

The Basic Local Alignment Search Tool (BLAST) finds regions of local similarity between sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance of matches. BLAST can be used to infer functional and evolutionary relationships between sequences as well as help identify members of gene families.

BLAST Assembled RefSeq Genomes

Choose a species genome to search, or [list all genomic BLAST databases](#).

- | | | | |
|--|---|--|--|
| <input type="checkbox"/> Human | <input type="checkbox"/> Dog | <input type="checkbox"/> Fruit fly | <input type="checkbox"/> Arabidopsis |
| <input type="checkbox"/> Mouse | <input type="checkbox"/> Rabbit | <input type="checkbox"/> Honey bee | <input type="checkbox"/> Rice |
| <input type="checkbox"/> Rat | <input type="checkbox"/> Chimp | <input type="checkbox"/> Chicken | <input type="checkbox"/> Yeast |
| <input type="checkbox"/> Cow | <input type="checkbox"/> Guinea pig | <input type="checkbox"/> Zebrafish | <input type="checkbox"/> Neurospora crassa |
| <input type="checkbox"/> Pig | <input type="checkbox"/> Sheep | <input type="checkbox"/> Clawed frog | <input type="checkbox"/> Microbes |

Basic BLAST

Choose a BLAST program to run.

[nucleotide blast](#)

Search a **nucleotide** database using a **nucleotide** query
Algorithms: blastn, megablast, discontinuous megablast

[protein blast](#)

Search **protein** database using a **protein** query
Algorithms: blastp, psi-blast, phi-blast, delta-blast

[blastx](#)

Search **protein** database using a **translated nucleotide** query

[tblastn](#)

Search **translated nucleotide** database using a **protein** query

[tblastx](#)

Search **translated nucleotide** database using a **translated nucleotide** query

Note: The Arabidopsis Information Resources (TAIR) (<http://arabidopsis.org/>) has a BLAST program specific to Arabidopsis

<http://blast.st-va.ncbi.nlm.nih.gov/Blast.cgi>

Obtaining Sequences From the UCLA Sequencing Facility

GENOSEQ
UCLA GENOTYPING & SEQUENCING

WebSeq

[Help](#)

[Sequencing & Genotyping
Core Home Page](#)

Welcome to WebSeq

Username:

goldberg_r

Password:

.....

Login

<http://www.genetics.ucla.edu/webseq/>

Selecting Sequence to Download



WebSeq

[Sequencing](#)

[R2R Signup \(List\)](#)

[R2R Signup \(Plate\)](#)

[R2R Lookup](#)

[Full Service Signup](#)

[Full Service Lookup](#)

[Tagman](#)

[Tagman Signup \(384\)](#)

[Tagman Signup \(96\)](#)

[LightCycler 480 Signup](#)

[Genotyping](#)

[Summary](#)

[Password](#)

[Help](#)

[Logout](#)

[Sequencing & Genotyping](#)

[Core Home Page](#)

Sequencing files for Robert B. Goldberg

Filter files: (only files with this string in their name will be displayed)

[Download selected](#) [Select All](#) [Select None](#) [Select Range](#) (?)

Sorted by date - click on column header to sort by that column. **Only the first 1000 files are displayed; to see the full list, filter for "."**

Files older than 90 days will not be available.

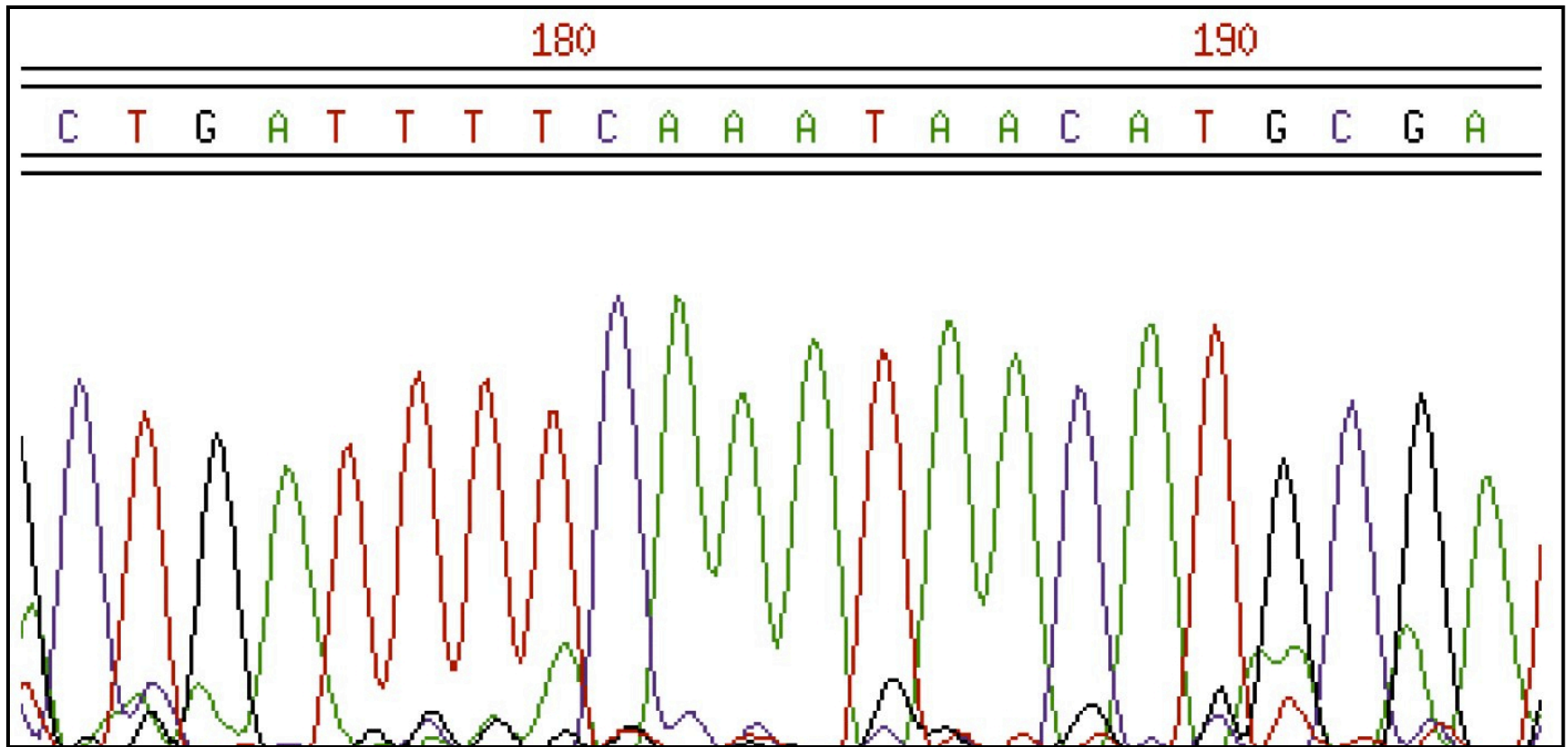
| Select | Filename | Size | Date |
|--------------------------|--|--------|-------------|
| <input type="checkbox"/> | 140545GoldR_KH1658_H10.ab1 | 338999 | 31 Jul 2014 |
| <input type="checkbox"/> | 140545GoldR_KH1659_A12.ab1 | 320996 | 31 Jul 2014 |
| <input type="checkbox"/> | 140328GoldR_KH1657_G04.ab1 | 325580 | 18 Jul 2014 |
| <input type="checkbox"/> | 140258GoldR_KH1655_D03.ab1 | 337431 | 17 Jul 2014 |
| <input type="checkbox"/> | 140258GoldR_KH1656_E03.ab1 | 315046 | 17 Jul 2014 |
| <input type="checkbox"/> | 140034GoldR_KH1651_A12.ab1 | 337078 | 03 Jul 2014 |
| <input type="checkbox"/> | 140034GoldR_KH1652_B12.ab1 | 324386 | 03 Jul 2014 |
| <input type="checkbox"/> | 140034GoldR_KH1653_C12.ab1 | 338397 | 03 Jul 2014 |
| <input type="checkbox"/> | 140034GoldR_KH1654_D12.ab1 | 319160 | 03 Jul 2014 |
| <input type="checkbox"/> | 139943GoldR_KH1647_A12.ab1 | 337773 | 27 Jun 2014 |
| <input type="checkbox"/> | 139943GoldR_KH1648_B12.ab1 | 324774 | 27 Jun 2014 |
| <input type="checkbox"/> | 139943GoldR_KH1649_C12.ab1 | 338079 | 27 Jun 2014 |
| <input type="checkbox"/> | 139943GoldR_KH1650_D12.ab1 | 335365 | 27 Jun 2014 |
| <input type="checkbox"/> | 139887GoldR_KH1637_A11.ab1 | 336985 | 25 Jun 2014 |
| <input type="checkbox"/> | 139887GoldR_KH1638_B11.ab1 | 332496 | 25 Jun 2014 |
| <input type="checkbox"/> | 139887GoldR_KH1639_C11.ab1 | 336603 | 25 Jun 2014 |
| <input type="checkbox"/> | 139887GoldR_KH1640_D11.ab1 | 326932 | 25 Jun 2014 |
| <input type="checkbox"/> | 139887GoldR_KH1641_E11.ab1 | 337227 | 25 Jun 2014 |
| <input type="checkbox"/> | 139887GoldR_KH1642_F11.ab1 | 334507 | 25 Jun 2014 |
| <input type="checkbox"/> | 139887GoldR_KH1643_G11.ab1 | 337335 | 25 Jun 2014 |
| <input type="checkbox"/> | 139887GoldR_KH1644_H11.ab1 | 322988 | 25 Jun 2014 |
| <input type="checkbox"/> | 139887GoldR_KH1645_A12.ab1 | 337273 | 25 Jun 2014 |
| <input type="checkbox"/> | 139887GoldR_KH1646_B12.ab1 | 313747 | 25 Jun 2014 |

Click to
download
your
sequence

[Download selected](#) [Select All](#) [Select None](#) [Select Range](#) (?)

Please consult [detailed help](#) for assistance using WebSeq. To contact us regarding WebSeq, please email webseq@genetics.ucla.edu

Reading the DNA Sequence



FINCH TV

MAC - <http://mac.softpedia.com/get/Math-Scientific/FinchTV.shtml>

PC - <http://www.softpedia.com/get/Science-CAD/FinchTV.shtml>

4Peaks

MAC - <http://www.mekentosj.com/science/4peaks>

What Gene Are You Working With?

Task: Use the DNA sequence you've obtained from sequencing with your gene-specific salk primer to identify your gene

Tools: The Arabidopsis Information Resources (TAIR)
(<http://arabidopsis.org/>)

Procedure:

1. Go to the TAIR BLAST page (<http://arabidopsis.org/Blast/index.jsp>)
2. Select BLASTN
3. For Dataset, Select "TAIR10 Genes"
4. Paste your sequence
5. Run BLAST

Results/Question:

1. What is the gene that you're working with?

How to Perform a BLAST Search for Arabidopsis

The screenshot shows the TAIR BLAST 2.2.8 web interface. At the top is the TAIR logo and navigation links: Home, Help, Contact, About Us, Login/Register. Below this is a menu bar with Search, Browse, Tools, Portals, Download, Submit, News, and ABRC Stocks. The main content area shows the path Home > Tools > BLAST and the title TAIR BLAST 2.2.8. A note states: "Please note that this form uses NCBI BLAST2.2.8, and NOT WU-BLAST2.0." The BLAST form includes a dropdown for the BLAST program (set to "BLASTN: NT query, NT db"), a dropdown for the dataset (set to "TAIR10 Genes (+introns, +UTRs) (DNA)"), and a text input box for the query sequence containing a DNA sequence. Red arrows point to these three elements with labels: "Select BLAST program", "Select dataset", and "Paste sequence of interest into BLAST input box". Below the input box is a "Choose File" button and the text "no file selected". There is also a checkbox for "Filter query" which is checked. The form has sections for "Advanced BLAST™ Parameter Options" and "Results Return Options". The "Results Return Options" section includes fields for "Output Title", "E-mail address:", "Return Results:" (set to "To your web browser"), and "Result Format:" (set to "HTML hypertext"). At the bottom, there is a "Reset" button and a "Run BLAST" button, with a red arrow pointing to the latter and the label "Run BLAST". A disclaimer at the bottom states: "Please be patient. Replies directly to your browser may take a minute or two. Selecting an e-mail reply allows you to immediately request more searches."

Home > Tools > BLAST

TAIR BLAST 2.2.8

Please note that this form uses NCBI BLAST2.2.8, and NOT WU-BLAST2.0.

Blast

BLAST™ program: BLASTN: NT query, NT db

Datasets: TAIR10 Genes (+introns, +UTRs) (DNA)

Input: ☒ query sequence
☐ locus name (At1g01030)

ATGAAGAGGAAATCGCCACTACAAGTTCAAGCTCTTGAGGGTT
TTTATTTGGAGCAAATGTATCCGACTCCTAAGGAAATGGAGGA
CTTGGGGAAGTCTTTAGGGTTAACATTGAAGGAAGTACGTGGA
TGGTTCAAGAGAAGAGGAGTAGAGGGAAGGTGTAAATCCA
TGGCAATGATGGGTTGGGAGCAAAGAATCCTCAGTTATACGA

Upload a file: Choose File no file selected

Raw, FASTA, GCG and RSF formats accepted.
☒ Filter query

Advanced BLAST™ Parameter Options

Results Return Options

Output Title: optional, will be added to output for your use

E-mail address:

Return Results: To your web browser

Result Format: HTML hypertext

Please be patient. Replies directly to your browser may take a minute or two.
Selecting an e-mail reply allows you to immediately request more searches.

Reset Run BLAST

<http://www.arabidopsis.org/Blast/index.jsp>

Anatomy of a BLAST Result -- Part I

BLAST query on TAIR10 Genes (+introns, +UTRs) (DNA) sequences

Query performed by the [The Arabidopsis Information Resource \(TAIR\)](#) for full BLAST options and parameters, refer to the [NCBI BLAST Documentation](#)

Your comments and suggestions are requested: Send a Message to [TAIR](#)

BLASTN 2.2.24 [Aug-08-2010]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= user-submitted sequence
(3396 letters)

Database: TAIR10 Genes (+introns, +UTRs) (DNA)
41,671 sequences; 93,974,285 total letters

Searching.....done

Arabidopsis Gene
Identification (AGI)
number

Gene description

E value -

Sequences producing significant alignments:

| | | | Score (bits) | E Value |
|--|--|--|-----------------|------------|
|--|--|--|-----------------|------------|

Top hit

| | | | | |
|-----------------------------|----------|---|----------------------|-------|
| AT4G12750.1 | Symbols: | Homeodomain-like transcriptional ... | 1193 | 0.0 |
| AT2G01670.1 | Symbols: | atnudt17, NUDT17 nudix hydrolase h... | 48 | 0.001 |
| AT2G35020.1 | Symbols: | GlcNAc1pUT2 N-acetylglucosamine-1-... | 44 | 0.017 |
| AT2G38370.1 | Symbols: | Plant protein of unknown function... | 42 | 0.066 |
| AT2G25800.1 | Symbols: | Protein of unknown function (DUF8... | 40 | 0.26 |
| AT5G13370.1 | Symbols: | Auxin-responsive GH3 family prote... | 38 | 1.0 |
| AT5G44230.1 | Symbols: | Pentatricopeptide repeat (PPR) su... | 38 | 1.0 |
| AT1G12560.1 | Symbols: | ATEXPA7, EXP7, ATEXP7, ATHEXP ALPHA ... | 38 | 1.0 |
| AT1G43830.1 | Symbols: | transposable element gene chr1:... | 38 | 1.0 |
| AT5G27395.2 | Symbols: | Mitochondrial inner membrane tran... | 36 | 4.1 |
| AT5G23510.2 | Symbols: | unknown protein; LOCATED IN: cell... | 36 | 4.1 |
| AT5G27395.1 | Symbols: | Mitochondrial inner membrane tran... | 36 | 4.1 |
| AT5G23510.1 | Symbols: | unknown protein; BEST Arabidopsis... | 36 | 4.1 |
| AT5G20350.1 | Symbols: | TIP1 Ankyrin repeat family protein... | 36 | 4.1 |

Anatomy of a BLAST Result -- Part II

Arabidopsis Gene
Identification (AGI) number

Gene Description

Click AGI to go to
the Locus Detail
page and get
more information
about your gene

→ [>AT4G12750.1](#) | Symbols: | Homeodomain-like transcriptional regulator |
chr4:7497814-7504716 REVERSE LENGTH=6903
Length = 6903 ← The size of your gene in bp
Score = 1193 bits (602), Expect = 0.0 ← E value
Identities = 602/602 (100%)
Strand = Plus / Plus

Your input sequence

Sequence from
the dataset

Sequence
alignment

```
Query: 2444 aggcctttgcgggcgctgttgtcagttttggacgataggggcagacgggaagctcgtctta 2503
          |||
Sbjct: 5340 aggcctttgcgggcgctgttgtcagttttggacgataggggcagacgggaagctcgtctta 5399

Query: 2504 ttgagtcgttggagaaacgagaaagttttctttgtcaagccatgctgagtagacaggtga 2563
          |||
Sbjct: 5400 ttgagtcgttggagaaacgagaaagttttctttgtcaagccatgctgagtagacaggtga 5459

Query: 2564 cccagtcggagacagcccatttcacagatatagttagagaggacagttcttcacctgttt 2623
          |||
Sbjct: 5460 cccagtcggagacagcccatttcacagatatagttagagaggacagttcttcacctgttt 5519

Query: 2624 ctgatatagacaacaacctatgtctgaatgaaattgccaatgatcaattctcctcgcaac 2683
          |||
Sbjct: 5520 ctgatatagacaacaacctatgtctgaatgaaattgccaatgatcaattctcctcgcaac 5579

Query: 2684 atgcggtatagtatatttgagattggaagtaagcgggagaaaagcttattgtggagcctta 2743
          |||
Sbjct: 5580 atgcggtatagtatatttgagattggaagtaagcgggagaaaagcttattgtggagcctta 5639
```

Genes Have a Unique Position in the Genome!

Task: Where is your gene located in the genome?

Tools: The Arabidopsis Information Resources (TAIR)
(<http://www.arabidopsis.org>)

Procedure:

1. Go to the Locus Detail page for your gene
2. Under Map Links, select Sequence Viewer
2. Hover your mouse over your highlighted AGI number.
A Locus box appears.
3. Select nucleotide seq view at the bottom of the box.

Results/Question:

1. What chromosome is your gene in?
2. What other genes/markers are next to your gene?
3. What is the exact position of your gene in the genome?

<http://www.arabidopsis.org>

Enter your Arabidopsis Gene
Identification (AGI) number

Search



[Home](#) [Help](#) [Contact](#) [About Us](#) [Login/Register](#)

AT4G12750

Gene

Search

[Search](#)

[Browse](#)

[Tools](#)

[Portals](#)

[Download](#)

[Submit](#)

[News](#)

[ABRC Stocks](#)

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, 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 week from the latest published research literature and community data submissions. 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.



TAIR is located at [Phoenix Bioinformatics](#) and funded by [subscriptions](#).

Full access to TAIR requires a subscription. ABRC catalog, stock and ordering pages hosted at TAIR will remain freely accessible. Please see our [subscription page](#) for further details.

- [Subscribe to news feed](#)
- [Follow our Twitter feed](#)
- [Join our Facebook group](#)

Breaking News

TAIR is going to ICAR2014.

[July 23, 2014]


We're looking forward to seeing you in Vancouver. Bring your questions to our workshop (M, 7/28, 4:30-5:30 pm) or our booth.

ABRC discontinuing distribution of ESTs.

[July 21, 2014]

ABRC will no longer be distributing ESTs after July 31, 2014. Individual stock detail

Gene Search Results



Home Help Contact About Us Login/Register

Search Browse Tools Portals Download Submit News ABRC Stocks

new search
new gene search

download all
download all results
get all sequences

download checked
check the boxes below and download results
get checked sequences

Your query for genes where gene name, description, phenotype, locus name, uniprot id or GenBank accession contains the term **AT4G12750** resulted in 2 loci matches with 2 distinct gene models.

Displaying 1 - 2.

To see ESTs associated with your gene of interest, click on the Locus link.

Check All Uncheck All

| Locus ? | Description ? | Gene Model(s) ? | Other Names ? | Keywords ? |
|---|---|-----------------------------|---------------|---|
| 1 AT4G12750 <input type="checkbox"/> | Homeodomain-like transcriptional regulator; FUNCTIONS IN: sequence-specific DNA binding, DNA binding, sequence-specific DNA b.... | AT4G12750.1 | | DNA-dependent, nucleus, regulation of transcription, regulation of transcription, DNA-dependent, sequence-specific DNA binding, sequence- |

Click AGI to go to the Locus Detail page and get more information about your gene

Locus Detail Page

Click to get DNA sequence
(including exons, introns and UTRs)

Locus: AT4G12750

Date last modified: 2013-02-11

TAIR Accession: Locus:2135838

Representative Gene Model: **AT4G12750.1**

Gene Model Type: protein_coding

Other names:

Description: Homeodomain-like transcriptional regulator; FUNCTIONS IN: sequence-specific DNA binding, DNA binding, sequence-specific DNA binding transcription factor activity; INVOLVED IN: regulation of transcription, DNA-dependent, regulation of transcription; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: DDT domain superfamily (InterPro:IPR018501), Homeobox (InterPro:IPR01356), Homeodomain-like (InterPro:IPR009057), DDT domain (InterPro:IPR004022), DDT domain, subgroup (InterPro:IPR018500), Homeodomain-related (InterPro:IPR012287); BEST Arabidopsis thaliana protein match is: Homeodomain-like transcriptional regulator (TAIR:AT5G44180.1); Has 164 Blast hits to 146 proteins in 22 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 4; Plants - 152; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLINK).

Map Detail Image

Chr4:7497814..7504716

Protein Coding Gene Models

AT4G12750.1 (T6_2_Star)

Chromosome number, nucleotide coordinates and orientation of your gene

Cartoon of your gene's structure (exons, introns, UTRs)

Publications containing information about your gene

Nucleotide Sequence: full length CDS full length cDNA full length genomic

Protein Data

| name | length(aa) | molecular weight | isoelectric point | domains(# of domains) |
|-------------|------------|------------------|-------------------|--|
| AT4G12750.1 | 1131 | 127804.0 | 7.93 | DDT domain:IPR004022(1) Homeobox:IPR01356(3) DDT domain, subgroup:IPR018500(1) Homeodomain-related:IPR012287(1) Homeodomain-like:IPR009057(1) DDT domain superfamily:IPR018501(1) |

Click to get protein sequence

Map Locations

| chrom | map | map type | coordinates | orientation | attrib |
|-------|--------|---------------|----------------------|-------------|---------|
| 4 | AGI | nuc_sequence | 7497814 - 7504716 bp | reverse | details |
| 4 | T20K18 | assembly_unit | 28330 - 35232 bp | reverse | |

Map Links: Map Viewer Sequence Viewer GBrowse

Polymorphism

| name | type | polymorphism site | allele type |
|------------------|--------------|-------------------|-------------|
| FLAG_583D05 | insertion | exon | unknown |
| GK-192H03-014647 | insertion | intron | unknown |
| GK-192H03-014648 | insertion | intron | unknown |
| GK-361A12-016993 | insertion | intron | unknown |
| GK-361A12-016997 | insertion | intron | unknown |
| GK-378A12-017230 | insertion | intron | unknown |
| GK-383A12-017270 | insertion | intron | unknown |
| ossowski_1210086 | deletion | intron | unknown |
| ossowski_1210087 | deletion | intron | unknown |
| ossowski_742989 | substitution | intron | unknown |
| ossowski_742990 | substitution | coding_region | unknown |
| ossowski_742992 | substitution | intron | unknown |
| ossowski_742993 | substitution | intron | unknown |
| ossowski_742995 | substitution | intron | unknown |
| ossowski_742997 | substitution | intron | unknown |

Germplasm

| name | polymorphisms | background | stock name | select |
|-------------|---------------|------------|-------------|--------------------------|
| SALK_004151 | SALK_004151 | | SALK_004151 | <input type="checkbox"/> |

images: None available

phenotypes: None available

List of available seed stocks (including SALK lines) with a mutation in your gene

| Publication | title | source | associated loci | date |
|-------------|--|--------------|---|------|
| | Comparative analysis of an unusual gene arrangement in the human chromosome 1. | GENE | AT4G12750 AT5G06290 | 2008 |
| | Comparative mapping of Brassica juncea and Arabidopsis thaliana using Intron Polymorphism (IP) markers: homeologous relationships, diversification and evolution of the A, B and C Brassica genomes. | BMC GENOMICS | AT1G01290 AT1G01560 AT1G01910 AT1G02410 AT1G02870 AT1G03180 AT1G03330 AT1G03687 AT1G03910 AT1G04950 AT1G05055 AT1G05205 AT1G05720 AT1G07210 AT1G07980 AT1G09760 AT1G10840 AT1G11240 AT1G11880 AT1G12230 more... | 2008 |

SeqViewer

SeqViewer Close-up View [SeqViewer Home](#) | [Release Note](#) | [Print Version](#)

☒ Markers
☒ Polymorphisms
☒ T-DNA/Tn
☒ Gene Models
☒ Transcripts
☒ Annotation Units

update

The new view will: ☒ insert above the current view(s) ☐ or replace the view

☒ show 3 data rows
☐ show all data [help](#)

Some data objects may be hidden from view
Choose "show all data" and zoom to 200kb or lower to see up to 100 rows of each object type.

Closeup View # 2, Chromosome 4 [Remove](#)

show legend

Zoom to: 200 Kb

Find

Search by name (e.g. UFO)

Go

Select range (e.g. 1500-2500)

List Genes In Range

[See this region in GBrowse](#)

Click here to recentre the view

Sequence ruler - click here to open 10 kb sequence window

7,400,000 7,500,000 7,600,000

AT4G12470.1 AT4G12545.1 AT4G12650.1 AT4G12750.1 AT4G12820.1 AT4G12915.1 AT4G13020.1

AT4G12480.1 AT4G12550.1 AT4G12670.1 AT4G12750.1 AT4G12820.1 AT4G12915.1 AT4G13020.1

AT4G12490.1 AT4G12560.1 AT4G12680.1 AT4G12750.1 AT4G12820.1 AT4G12915.1 AT4G13020.1

MP12P771G172Q (5-PRIME) S0186C07F (3') 10306XP

R17349 RAFL14-06-I23 067573_0865_1842 113115X

EB3R0DY02GTSPR EB3R0DY01CL345 143834_0265_2220

T1P17

T20K18

AT4G12750.1: Homeodomain-like transcriptional regulator; FUNCTIONS IN: sequence-specific DNA binding, DNA binding, sequence-specific DNA binding transcription factor activity; INVOLVED IN: regulation of transcription, DNA-dependent, regulation of transcription; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: DDT domain superfamily (InterPro:IPR018501), Homeobox (InterPro:IPR001356), Homeodomain-like (InterPro:IPR009057), DDT domain (InterPro:IPR004022), DDT domain, subgroup (InterPro:IPR018500), Homeodomain-related (InterPro:IPR012287); BEST Arabidopsis thaliana protein match is: Homeodomain-like transcriptional regulator (TAIR:AT5G44180.1); Has 164 Blast hits to 146 proteins in 22 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 4; Plants - 152; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLINK)

[nucleotide seq view](#)

Closeup View # 1, Chromosome 4 [Remove](#)

show legend

Zoom to: 200 Kb

Find

Search by name (e.g. UFO)

Go

Select range (e.g. 1500-2500)

List Genes In Range

Click here to recentre the view

Sequence ruler - click here to open 10 kb sequence window

7,400,000 7,500,000 7,600,000

AT4G12470.1 AT4G12545.1 AT4G12650.1 AT4G12750.1 AT4G12820.1 AT4G12915.1 AT4G13020.1

AT4G12480.1 AT4G12550.1 AT4G12670.1 AT4G12750.1 AT4G12820.1 AT4G12915.1 AT4G13020.1

AT4G12490.1 AT4G12560.1 AT4G12680.1 AT4G12750.1 AT4G12820.1 AT4G12915.1 AT4G13020.1

MP12P771G172Q (5-PRIME) S0186C07F (3') 10306XP

R17349 RAFL14-06-I23 067573_0865_1842 113115X

EB3R0DY02GTSPR EB3R0DY01CL345 143834_0265_2220

T1P17

T20K18

AT4G12750.1: Homeodomain-like transcriptional regulator; FUNCTIONS IN: sequence-specific DNA binding, DNA binding, sequence-specific DNA binding transcription factor activity; INVOLVED IN: regulation of transcription, DNA-dependent, regulation of transcription; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: DDT domain superfamily (InterPro:IPR018501), Homeobox (InterPro:IPR001356), Homeodomain-like (InterPro:IPR009057), DDT domain (InterPro:IPR004022), DDT domain, subgroup (InterPro:IPR018500), Homeodomain-related (InterPro:IPR012287); BEST Arabidopsis thaliana protein match is: Homeodomain-like transcriptional regulator (TAIR:AT5G44180.1); Has 164 Blast hits to 146 proteins in 22 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 4; Plants - 152; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLINK)

[nucleotide seq view](#)

Click view your gene sequence on the chromosome

Nucleotide Sequence Viewer



SeqViewer Nucleotide View

[SeqViewer Home](#) | [Release Note](#)

ATG = Translational Start/Stop

ATGC = Exon

atgc = Annotation on other strand [Hide](#)

atgc = UTR

atgc = Intron

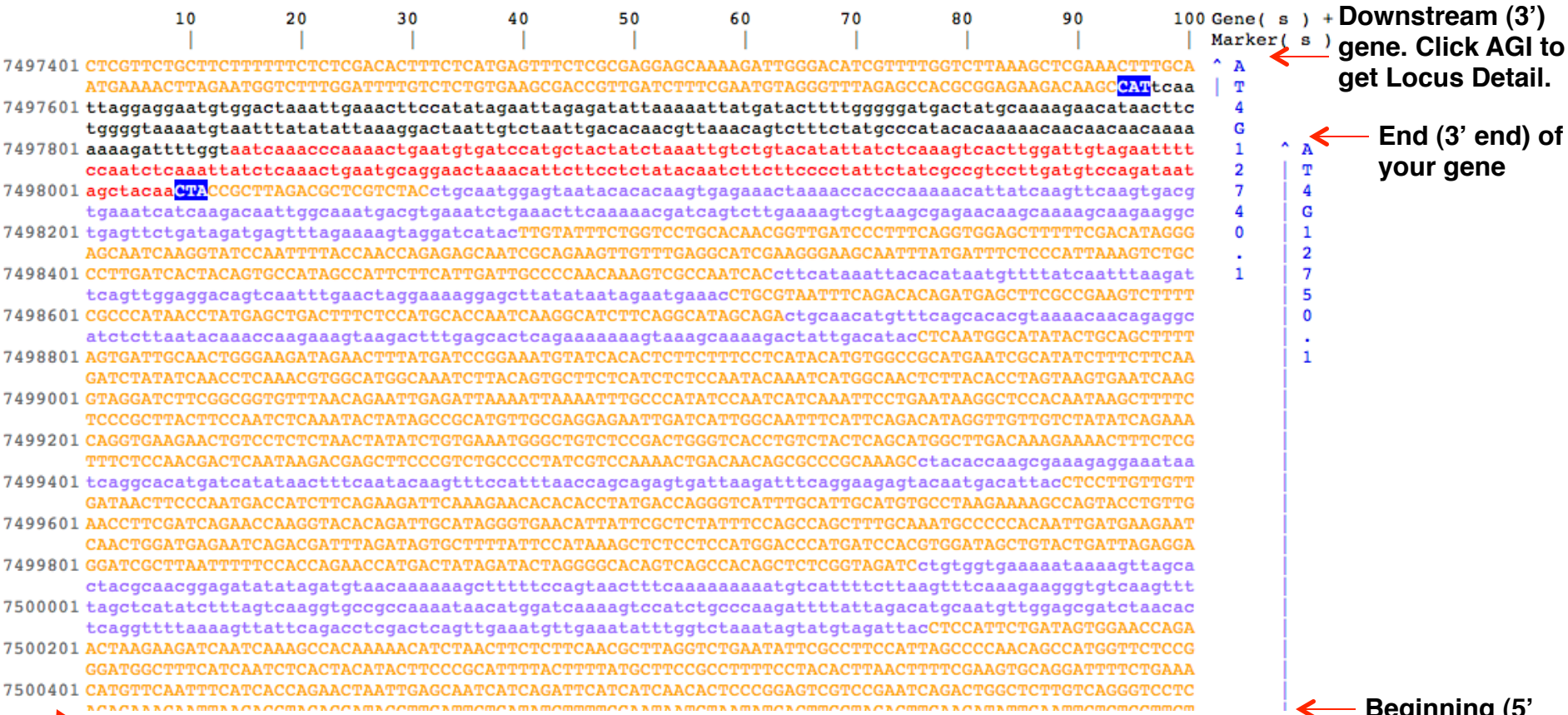
Choose strand to view:

Forward Strand

Choose objects to be highlighted:

Genes

Clicking on the arrows will shift the view by 5 kb



Nucleotide position on the chromosome.
Note that Arabidopsis has 5 chromosomes.

Beginning (5')
end) of your
gene

Where Do Your Primers Anneal?

Task: Where do your gene-specific salk primers anneal relative to your gene?

Tools: The Arabidopsis Information Resources (TAIR)
(<http://arabidopsis.org/>)

Procedure:

1. Go to the TAIR BLAST page (<http://arabidopsis.org/Blast/index.jsp>)
2. Select BLASTN
3. For Dataset, select “TAIR10 Genes”
4. Paste your primer sequence
5. Run BLAST

Note: If there are no BLAST results, try selecting a different dataset, such as Upstream Sequences.

Results/Question:

1. Where do your gene-specific salk forward and reverse primers anneal relative to your gene?

Where Is the T-DNA Located in Your Gene?

Task: Where is the T-DNA inserted relative to your gene?

Tools: The Arabidopsis Information Resources (TAIR)
(<http://arabidopsis.org/>)

Procedure:

1. Go to the TAIR BLAST page (<http://arabidopsis.org/Blast/index.jsp>)
2. Select BLASTN
3. For Dataset, select “TAIR10 Genes”
4. Paste your sequence
5. Run BLAST

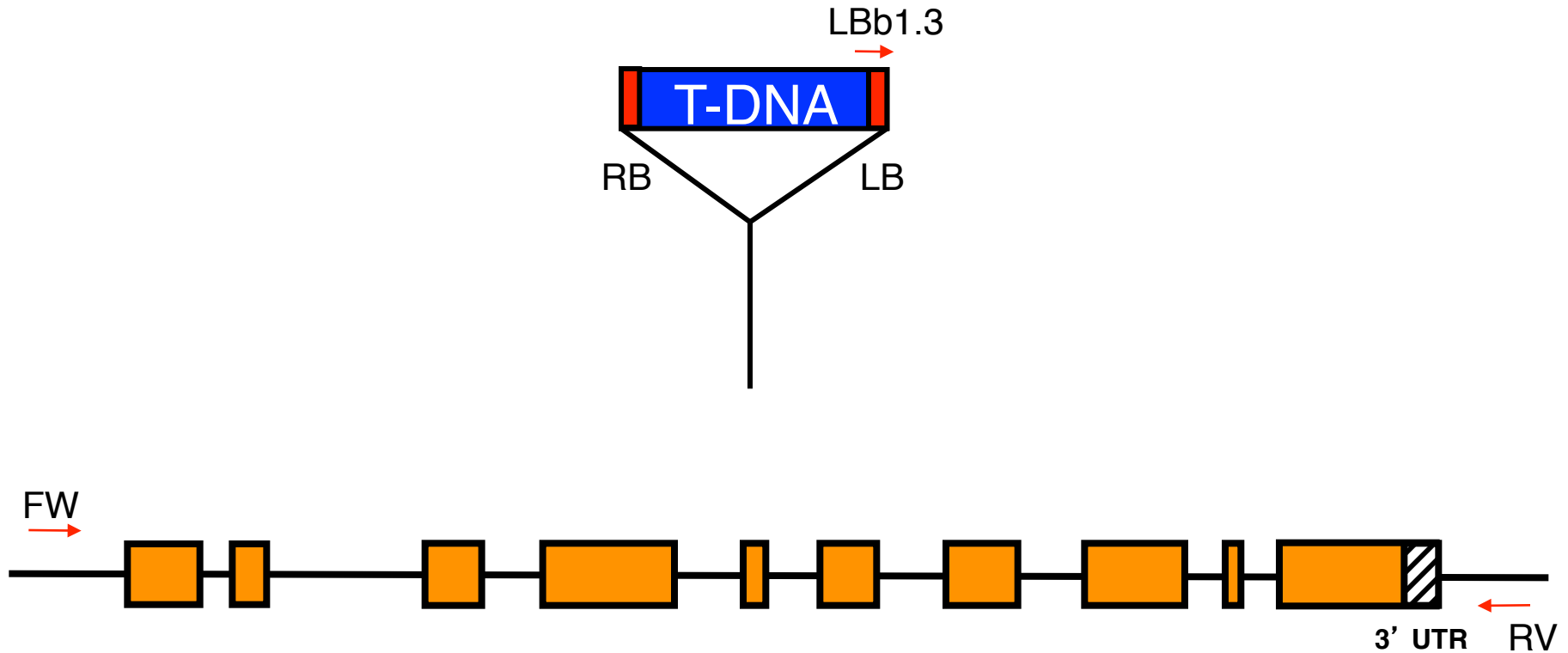
Note: If there are no BLAST results, try selecting a different dataset, such as Upstream Sequences.

Results/Question:

1. At what position in your gene is the T-DNA inserted?
2. Is the T-DNA inserted in an exon? Intron? UTR? Upstream sequence?
3. What is the orientation of the T-DNA relative to your gene?

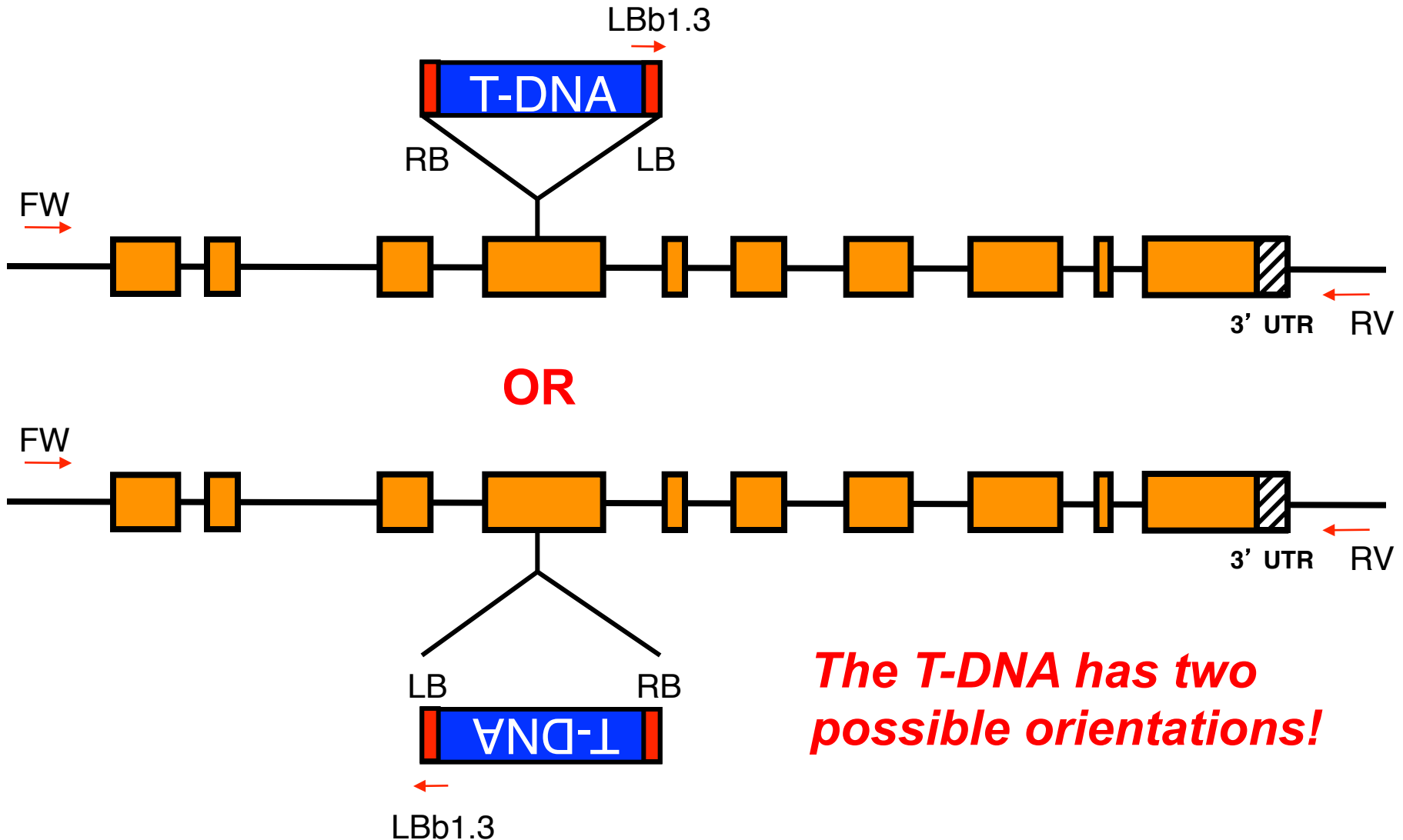
SALK T-DNA Lines

How Were T-DNA Lines Created?




SALK T-DNA Lines

How Were T-DNA Lines Created?



Where Is the T-DNA Located in Your Gene?

Locus Detail

 Home Help Contact About Us Login/Register

Search Browse Tools Portals Download Submit News ABRC Stocks

Locus: AT4G12750

| Germplasm | name | polymorphisms | background | stock name | select |
|-----------------------------|---------------------------------------|-----------------------------|-----------------------------|-----------------------------|--------------------------|
| Showing 9 of 9 entries | SALK_004151 | SALK_004151 | | SALK_004151 | <input type="checkbox"/> |
| | images None available | | | | |
| | phenotypes ⓘ None available | | | | |
| | <hr/> | | | | |
| | SALK_009964 | SALK_009964 | | SALK_009964 | <input type="checkbox"/> |
| | images None available | | | | |
| | phenotypes ⓘ None available | | | | |
| <hr/> | | | | | |
| SALK_052476 | SALK_052476.31.35.x | | SALK_052476 | <input type="checkbox"/> | |
| | images None available | | | | |
| | phenotypes ⓘ None available | | | | |
| <hr/> | | | | | |
| SALK_067532 | SALK_067532.56.00.x | | SALK_067532 | not available | |
| | images None available | | | | |
| | phenotypes ⓘ None available | | | | |
| <hr/> | | | | | |
| SALK_130161 | SALK_130161.42.70.x | | SALK_130161 | not available | |
| | images None available | | | | |
| | phenotypes ⓘ None available | | | | |

List of available
seed stocks
(including SALK
lines) with a
mutation in your
gene

Click to view PolyAllele Detail

Where Is the T-DNA Located in Your Gene?

PolyAllele Detail

| Search | Browse | Tools | Portals | Download | Submit | News | ABRC Stocks |
|-----------------------------------|--|---|----------------------|----------------------|-----------------------|---------|-------------|
| Polymorphism: SALK_052476.31.35.x | | | | | | | |
| Name | SALK_052476.31.35.x | | | | | | |
| Date last modified | 2009-10-08 | | | | | | |
| Tair Accession | Polymorphism:1005459901 | | | | | | |
| Type | insertion | Insertion Type | T-DNA | | | | |
| Chromosome | 4 | | | | | | |
| Construct Type | simple_insert | | | | | | |
| Associated Genes | Gene Model | Locus | Polymorphism site | | Association Type | | |
| | AT4G12750.1 | AT4G12750 | intron | | is an allele of | | |
| | Description | Homeodomain-like transcriptional regulator; FUNCTIONS IN: sequence-specific DNA binding, DNA binding, sequence-specific DNA binding transcription factor activity; INVOLVED IN: regulation of transcription, DNA-dependent, regulation of transcription; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: DDT domain superfamily (InterPro:IPR018501), Homeobox (InterPro:IPR001356), Homeodomain-like (InterPro:IPR009057), DDT domain (InterPro:IPR004022), DDT domain, subgroup (InterPro:IPR018500), Homeodomain-related (InterPro:IPR012287); BEST Arabidopsis thaliana protein match is: Homeodomain-like transcriptional regulator (TAIR:AT5G44180.1); Has 164 Blast hits to 146 proteins in 22 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 4; Plants - 152; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLINK). | | | | | |
| Associated Loci | AT4G12750 | | | | | | |
| Mutagen | T-DNA insertion | | | | | | |
| Mutation Site | gene | | | | | | |
| Description | PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html | | | | | | |
| Associated Polymorphisms | | | | | | | |
| Insertion | Species Variant (attribution) | Length | Polymorphic Sequence | | Polymorphism Verified | | |
| | Col | unknown | | | unknown | | |
| Associated Nucleotide Sequences | | | | | | | |
| Insertion Flanking Sequence | TAATAGTCAATTTTTCAGAAAACCCCTAGCCTTCTTCATTAGACAGGTTTTATATTGCGATGTAGCGATTAAACGGGGATATACCTTTGCGAGCTCCAGACCGGAGATGATCAAATTCAGAA CCAATCGATGGACCATCCTTTTCGAATAACTTTAGCCTCAATGTGTGATGAAGGCCAACAAAG TTTTGACAACCTGGCCTTCTCTGTTCCCAACAATACATCTTTCTCAACAGCTACTCCAAACG CATCTGGAAGATGTGGAACCTCCTCGTGAGGGATCTATCGTATAACTGAGGATTCCTTTGCT CCCAACCCCAACATTGCGCATGGATTTTACAACATGGCCTCAACTCCTTCTCTCGTGAAC CAACGACGTACTGCTTCAACGTTAAACCTAAAGACTTCCCCAAGTCCGCCATTTC (Length:416) | | | | | | |
| | GenBank Accession | | CC054042 | | | | |
| Map Locations | chrom | map | map type | coordinates | orientation | attrib | |
| | 4 | AGI | nuc_sequence | 7503231 - 7503646 bp | forward | details | |
| | 4 | T20K18 | assembly_unit | 33747 - 34162 bp | forward | | |
| Map Links | Sequence Viewer | | GBrowse | | | | |
| Germplasm | Name/Image | Polymorphisms | Background | Stock Name | Select | | |

Click Sequence Viewer to see Close Up View



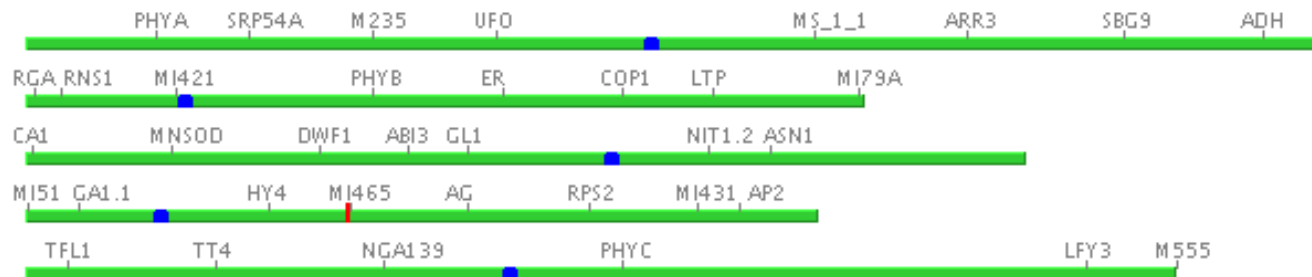
Where Is the T-DNA Located in Your Gene?



SeqViewer Close-up View

[SeqViewer Home](#) | [Release Note](#) | [Print Version](#)

- ☒ Markers
- ☒ Polymorphisms
- ☒ T-DNA/Tn
- ☒ Gene Models
- ☒ Transcripts
- ☒ Annotation Units



The new view will: ☒ insert above the current view(s) ☐ or replace the view

- ☒ show 3 data rows
☐ show all data [help](#)

Some data objects may be hidden from view
Choose "show all data" and zoom to 200kb or lower to see up to 100 rows of each object type.

Closeup View # 3, Chromosome 4

[Remove](#)

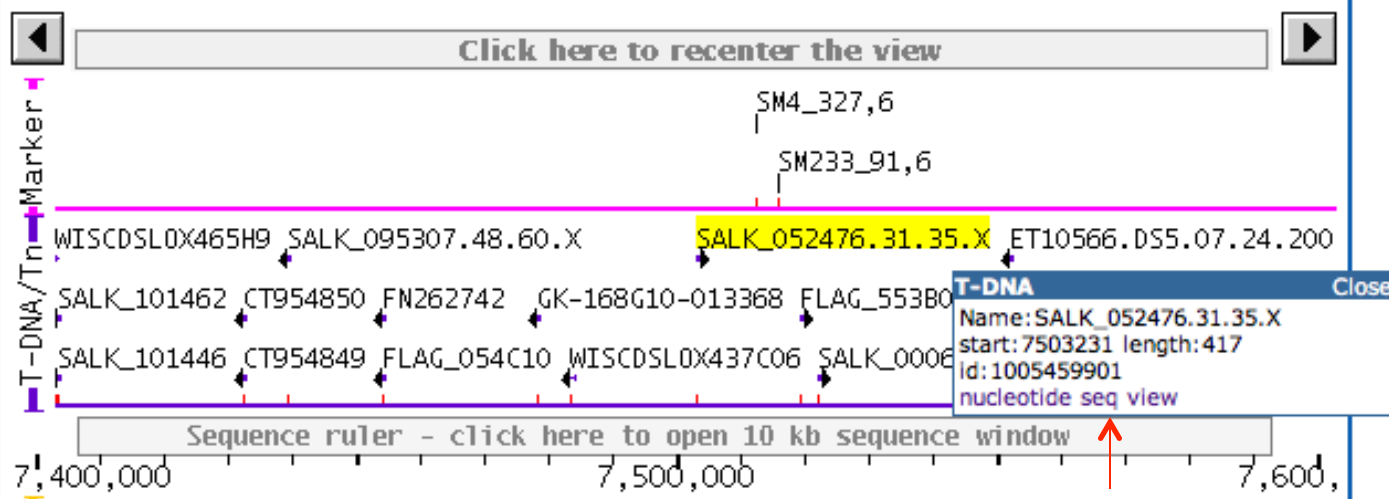
[show legend](#)

Zoom to:

Search by name (e.g. UFO)

Select range (e.g. 1500-2500)

[See this region in](#)



[Click to view SeqViewer Nucleotide view](#)

Where Is the T-DNA Located in Your Gene?

**Expected T-DNA insertion site for
SALK line SALK_052476**

10 20 30 40 50 60 70 80 90 100 Gene(s) +
| Marker(s)

7502801 TACACGCCATACAGTCATCAAACCCCTTCCAAATACCATGTTTCATCACAGTAGCATTTCTCTTGAATGCAATCCTGACTGGTATGATCCATCAGCTCAGAA ^ A
ATctaaagaaaattaagatcagggactaagtaacttagcgatccaggtaaaactaccttatgaaacaacacatatccactacCTTCTCTTTTCTTGCCA | T
7503001 CTTTCTGTTTCTGTTGACCGACAGAAGAAGTGCCAGCCAAGAAGctagcacaagagaaagaagtccacgttagaatcaatataactatacgatacttct 4
tgaagtcatacaaaatcaagtcgcgactca↓ccagagtccaattatccagtcatgcatatttttcattagaaaaatcaataactaatatgaaagcattaat G
7503201 ttcatagtcacattataaaaagcttgggtgtaatatagtcgaatttttcagaaaccctagccttcttcattatacagggtttttatattgcgatgtagcgataa 1
|=====SALK_052476.31.35.X===== 2
aggtggatatacCTTTGCGAGCTCCAGACGGGAGATGATCAAATTCAGAACCAGCGATGGACCATCCTTTTCGAAAAAAGTTTAGCCAAAATGTGTGATGA 7
=====SALK_052476.31.35.X===== 5
7503401 AGGCAACAAGTTTTGACAACTGGCCTTCCTTGTTCACCAATACATCTTTCTCTCAACAGCTACTCCAACGCATCTGGAAGATGTGGAAGCTCCTCATGAGG 0
=====SALK_052476.31.35.X===== .
GATCTATCGTATAACTGAGGATTCTTTGCTCCCAACCCATCATTGCGCATGGATTTTACACCTTTCCCTCTACTCCTTCTTCTCTTGAACCATCCACGTA 1
=====SALK_052476.31.35.X=====

7503601 CTTCTTCAATGTTAACCCTAAAGACTTCCCAAGTCTCCATTTCTTCTAGGAGTCGGATACATTTGCTctgctttcacaaatcagatagctatcagtga
=====SALK_052476.31.35.X===== ->
cagcaaaagaaaacgaaaaacccaaaagagaaatataacccaaaagtaaaccatatccaaaaagctaccacaggaggccaattctagagatatctttacaag
7503801 atgatcaacacaaaactaacatatcatcttatgtatgttactacaaatagaaaaagaaaaatcgacCCAAATAAAAACCTCAAGAGCTTGAAGCTTGT
AGTGGCGATTTCCTCTTCATctccacttaataaaacttcagaaaaactcttactctctcttaaggtatcaaaaccaggcgcataaatagttaaagcgtct
7504001 ccaacatttctgcaacatcaagcaatcaattatcttcatcatcattatcccatataaaactgatcaaaaatcataaagctatcagaccacaagaggaagaa
<-----SALK_009964-----
gcgatcaccactgatcacttaaatcgctacgcttcaatacaacaaatccaaaattaccggaaatgaattcaaaacaaatgaattcaacccaataatcgca
=====SALK_009964=====
<=====
<=====


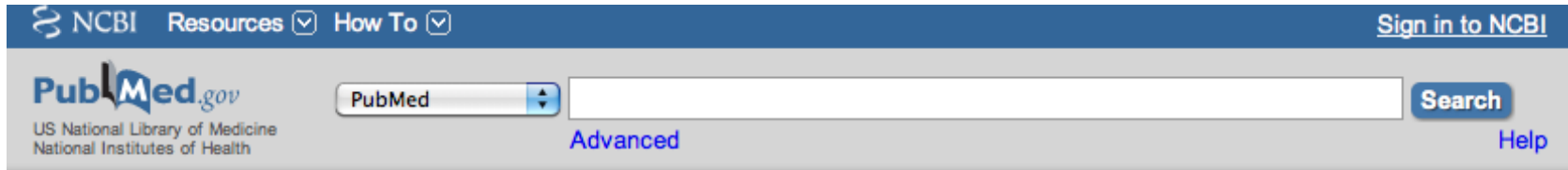
7504201 tcaaatgatgaacacacgaaatcaaaaaagaattaccagaaacttagatttccatagtggttagacacactaaaatgaagcgatacacaacagtagaa
=====SALK_009964=====
=====SALK_067532.56.00.X=====
=====SALK_009964.47.90.X=====
gtacaattaaaagcaaagagcaaagtcaattcacaaaaaccattagaattgaagataccggaatctcagtttcagcgaaattgatggaaaaaacacaa

This sequence should align to your LBb1.3 sequencing reaction

**This
sequence
should align
to your
LBb1.3
sequencing
reaction**

PubMed - Endless Resources

<http://www.ncbi.nlm.nih.gov/pubmed>



PubMed

PubMed comprises more than 24 million citations for biomedical literature from MEDLINE, life science journals, and online books. Citations may include links to full-text content from PubMed Central and publisher web sites.

PubMed COMMONS



Featured comment - Aug 10

Recasting the net: R Pazoki suggests searching additional eQTL databases to ID other potential gene associations.

1.usa.gov/V0GK70

Using PubMed

[PubMed Quick Start Guide](#)

[Full Text Articles](#)

[PubMed FAQs](#)

[PubMed Tutorials](#)

[New and Noteworthy](#) 

PubMed Tools

[PubMed Mobile](#)

[Single Citation Matcher](#)

[Batch Citation Matcher](#)

[Clinical Queries](#)

[Topic-Specific Queries](#)

More Resources

[MeSH Database](#)

[Journals in NCBI Databases](#)

[Clinical Trials](#)

[E-Utilities \(API\)](#)

[LinkOut](#)

Ex. Author search: Goldberg RB, Harada JJ

Keyword: Arabidopsis T-DNA Mutagenesis, etc...

Note: If you are off campus, use VPN to access journal articles.

Where Is Your Gene Expressed?

Task: When during seed development and in which part of the seed is your gene transcribed?

Tools: Seed Gene Network
(<http://seedgenenetwork.net/arabidopsis>)

Procedure:

1. Select Analyze GeneChip Data
2. Select Browse
3. Enter your AGI Locus ID
4. Click Submit
5. Click on the Probe Set identifier

Results/Question:

1. When during seed development and in which part of the seed is your gene transcribed?

GENE NETWORKS IN SEED DEVELOPMENT

Identifying all the genes and gene networks required to "make a seed"

[Home](#) [Soybean GeneChip Experiments](#) [Arabidopsis GeneChip Experiments](#) [GeneChip Annotations](#) [Sequencing](#) [RNAi](#) [People](#)

[Data & Resources](#) [Genome Browsers](#)

GeneChip Experiment

GeneChip Validation

Analyze GeneChip Data

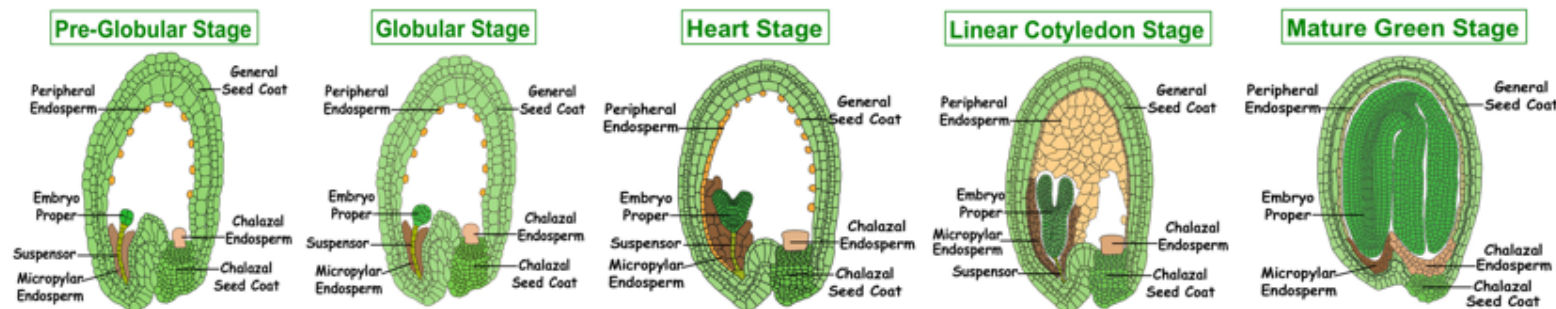
Procedures

Figures

Arabidopsis Seed Tissues/Compartments GeneChip Experiments.

We completed **65** GeneChip experiments of **31** tissues/compartments throughout *Arabidopsis* seed development using Affymetrix Arabidopsis ATH1 array ([Click here to view our annotation of Arabidopsis ATH1 array](#)).

Figure. Tissues/Compartments Studied Throughout Arabidopsis Seed Development (All images were illustrated by Meryl Hashimoto. The images are not to scale. [Click on the image to enlarge](#).)



Click on the name of *Arabidopsis* seed tissues/compartments listed below to find the detail information about GeneChip experiments of *Arabidopsis* seed tissues/compartments. The information includes:

Analyze GeneChip Data

Supported by:



GENE NETWORKS IN SEED DEVELOPMENT

Identifying all the genes and gene networks required to "make a seed"

[Home](#) [Soybean GeneChip Experiments](#) [Arabidopsis GeneChip Experiments](#) [GeneChip Annotations](#) [Sequencing](#) [RNAi](#) [People](#)

[Data & Resources](#) [Genome Browsers](#)

[GeneChip Experiment](#)

[GeneChip Validation](#)

[Analyze GeneChip Data](#)

[Procedures](#)

[Figures](#)

***Arabidopsis* Analysis Tools**

Browse

Click to browse the mRNA profiles of compartments during *Arabidopsis* seed development by probe identification, gene ontology, or function category.

Analyze

Click to compare gene activity in different *Arabidopsis* seed compartments at different developmental stages.

Blast

Click to BLAST DNA sequence against target sequences on the Affymetrix *Arabidopsis* ATH1 array and view the seed expression pattern related to your gene-of-interest.

Browse Arabidopsis mRNAs Profiling Database

GENE NETWORKS IN SEED DEVELOPMENT *Identifying all the genes and gene networks required to "make a seed"*

Home Soybean GeneChip Experiments Arabidopsis GeneChip Experiments GeneChip Annotations Sequencing RNAi People Data & Resources Genome Browsers

Browse Arabidopsis mRNAs Profiling Database

More Tools Analyze Blast

Use the search form below to browse and search the gene expression profile of your gene of interest, then view the seed expression patterns using the following options:

- Type in the Probe Set Identifier, Arabidopsis Genome Initiative (AGI) locus ID, (Please separate multiple IDs by ';'. No Space.), **OR**
- Type in Gene Ontology ID (Multiple IDs are not acceptable), **OR**
- Select Functional Category, **OR**
- Type in the keyword related to the gene of interest.

Those options can be combined to make your selection more specific. Once you set up your searching criteria, click **Submit Query** to start the analysis.

Please be patient and do not cancel the process prematurely. A list of genes matching the criteria you set up on this page will be returned in the "Search Results" page. Click on the probe set identifier to view the gene expression profile. Also you can download the list of genes by clicking the button the top of "Search Results" page as a text-format file.

Browse by Probe Set or Gene ID

Probe Set Identifier: (e.g. 251898_at)

AGI Locus ID (e.g. AT1G21970) ← Enter your AGI

Browse by Gene Ontology Term ID

GO: Biological Processes (e.g. GO:0006355)

GO: Cellular (e.g. GO:0005634)

Components

GO: Molecular Function (e.g. GO:0003677)

Browse by Functional Categories or Keywords

Functional Category: Any

Description/Keyword: (e.g. transcription, CCAAT)

Submit

← Submit

Results for Search by Gene ID

Supported by:



GENE NETWORKS IN SEED DEVELOPMENT

Identifying all the genes and gene networks required to "make a seed"

[Home](#) [Soybean GeneChip Experiments](#) [Arabidopsis GeneChip Experiments](#) [GeneChip Annotations](#) [Sequencing](#)

[RNAi](#) [People](#) [Data & Resources](#) [Genome Browsers](#)

Search results

Showing results where probe is in project *Arabidopsis ATH1 Array*, AGI Locus ID contains *AT4G12750* (**1 total matches**).

Click the button below download GeneChip annotation, data, or both for your search results in text format.

[Download GeneChip Annotation](#)

[Download GeneChip Data](#)

[Download GeneChip Annotation and Data](#)

| | Probe Set | Project | Gene Model | Functional Category | Description |
|---|-----------|------------------------|------------|---------------------|--|
| 1 | 254778_at | Arabidopsis ATH1 Array | AT4G12750 | Transcription | DNA binding / sequence-specific DNA binding / transcription factor |

Click to view
your gene's
mRNA profile
during seed
development



Gene Expression Profile – Part I

Supported by:



GENE NETWORKS IN SEED DEVELOPMENT

Identifying all the genes and gene networks required to "make a seed"

[Home](#) [Soybean GeneChip Experiments](#) [Arabidopsis GeneChip Experiments](#) [GeneChip Annotations](#) [Sequencing](#) [RNAi](#) [People](#) [Data & Resources](#) [Genome Browsers](#)

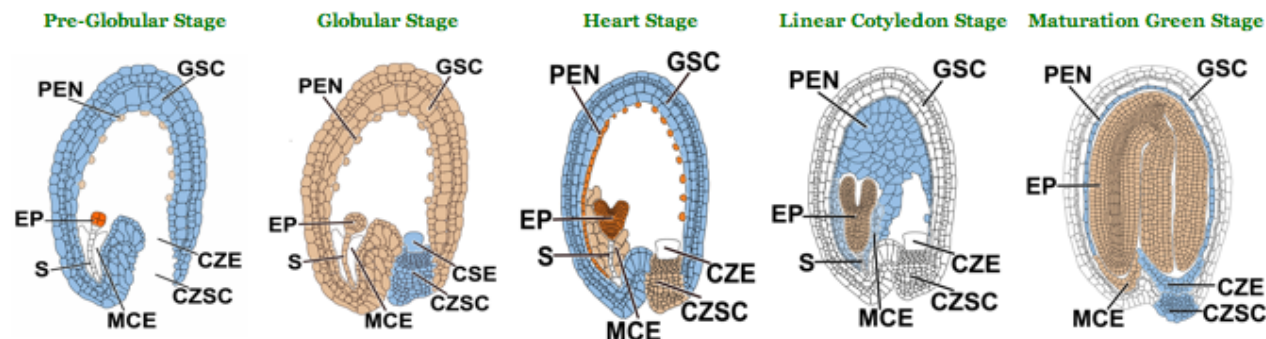
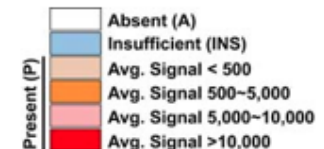
GeneChip Expression Profile for Probe Set - 254778_at

[Expression Profile Summary](#) [Download GeneChip Data](#) [Probe Set Description](#) [View in Genome Browser](#)

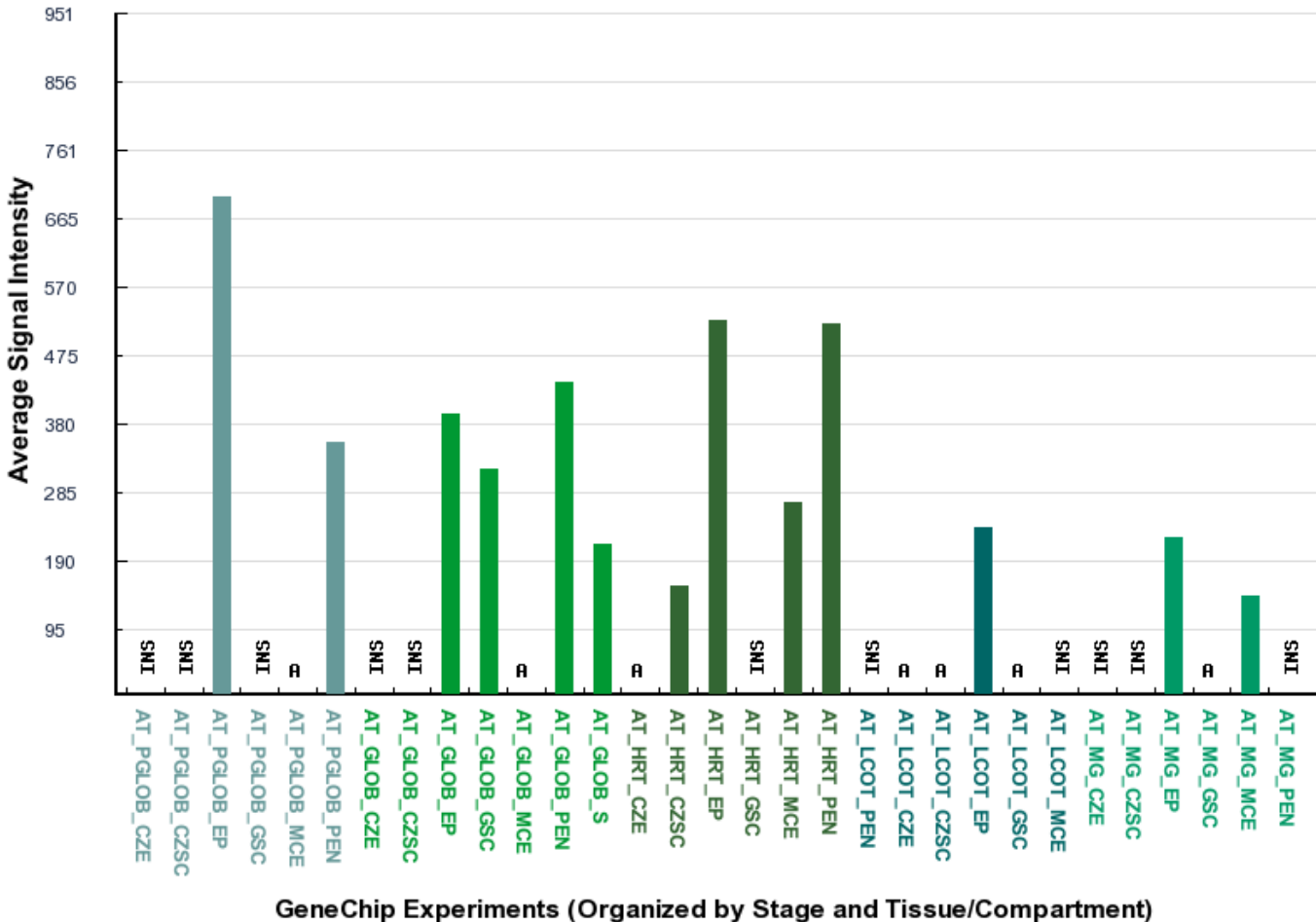
The images below indicate showing where mRNAs related to this probe set accumulated in seeds throughout development. The color corresponds to the average signal intensity of biological replicates (shown in the right).

The plot below displays the average signal intensity of biological replicates for all seed tissues/compartments studied in this project.

- Click the images to enlarge. To save the images and plot, PC users right-click on the image and choose 'save image as'; Mac users hold 'ctrl' key and click on the image, then choose 'save image as'.
- To view the description of this probe set, click "**Probe Set Description**" on the top.
- Click "**Download GeneChip Data**" on the top to get the signal intensities of all GeneChip experiments for this probe set.
- Also, you can view where the probe set aligns in the genome and 454 ESTs that map to corresponding gene using "**Genome Browser**".



Gene Expression Profile – Part II



Abbreviation: A, absent; INS, inconsistent detection call between biological replicas; M, marginal; P, present

Abbreviation of Stage and Tissue/Compartment:

Stage: PGLob - Pre-Globular Stage; GLOB - Globular Stage; HRT - Heart Stage; LCOT - Linear Cotyledon Stage; MG - Maturation Green Stage

Tissue: CZE - Chalazal Endosperm; CZSC - Chalazal Seed Coat; EP - Embryo Proper; GSC - General Seed Coat; MCE - Micropylar Endosperm; PEN - Peripheral Endosperm; S - Suspensor; WS - Whole Seed

Signal intensities (relative mRNA prevalences) and signal detection calls (P, A, or M) were generated using MAS 5.0 algorithm. For comparative purposes, GeneChip data were scaled globally to a target intensity of 500 for all probe sets on the chip using MAS 5.0 default parameters. Each probe set was manually assigned a consensus detection call based on the MAS 5.0 detection calls of both biological replicates of an RNA sample. Probe sets with same signal detection calls in both biological replicates were assigned consensus detection calls of P, A, or M, respectively. By contrast, probe sets with different, or discordant, detection calls for the two biological replicates (e.g., P and A; P and M) were assigned a consensus detection call of Insufficient (INS). Consensus detection calls are used to shown in the plot.