

HC70AL Spring 2011

**An Introduction to Bioinformatics
By**

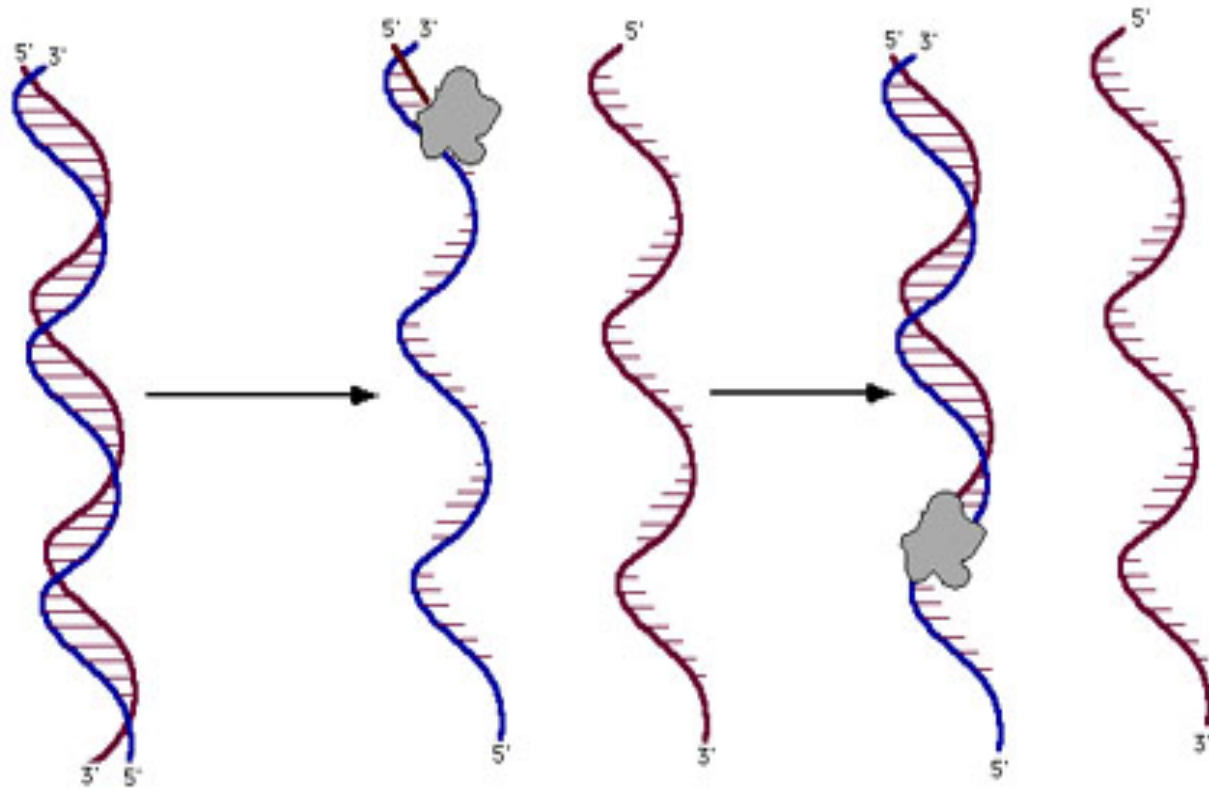
Brandon Le

April 7, 2011

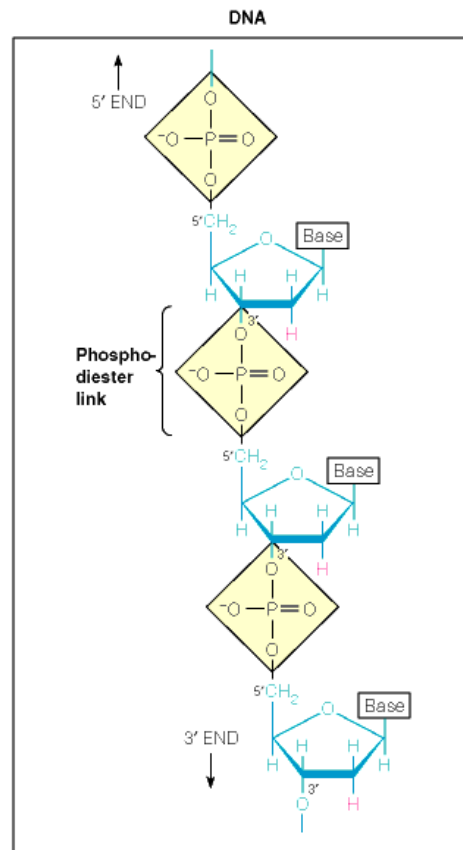
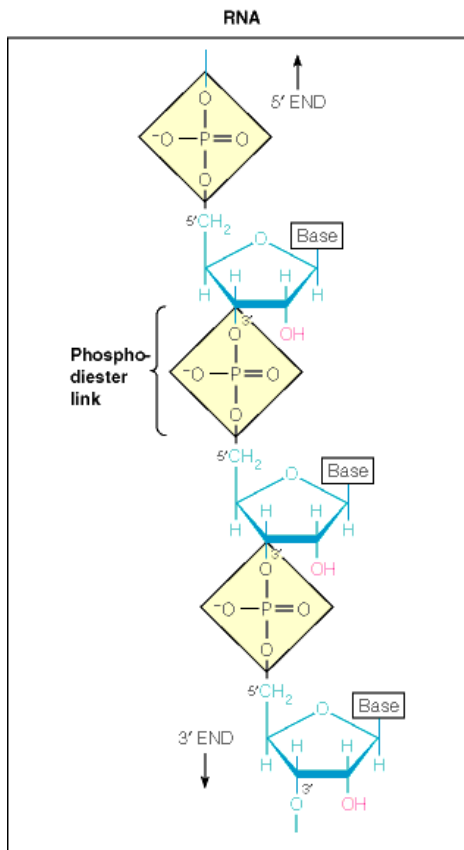
Outline

1. Review of Dideoxy Sequencing
2. Obtaining and Processing DNA Sequences
3. What is a Gene?
4. Sequence Analysis Using BLAST
5. Identifying Knockout Lines from SALK

A Review of Dideoxy Sequencing

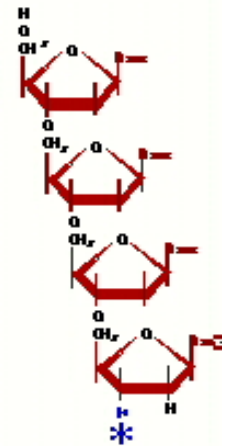
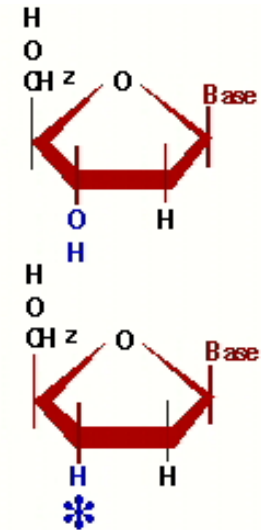


A Review of Dideoxy Sequencing



Normal nucleotides:

Dideoxy Chain Terminators:



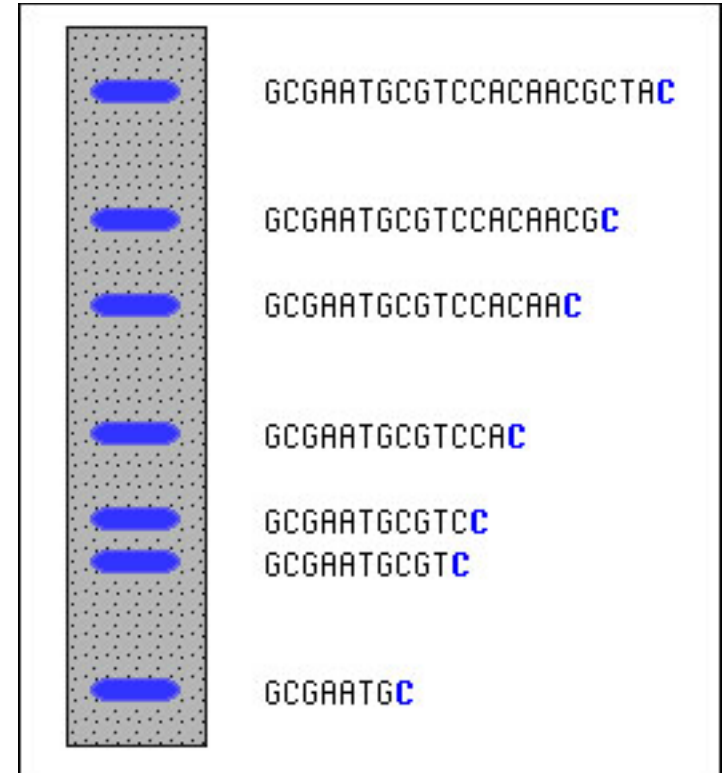
A Review of Dideoxy Sequencing

DNA Polymerase reads the template strand and synthesizes a new second strand to match:

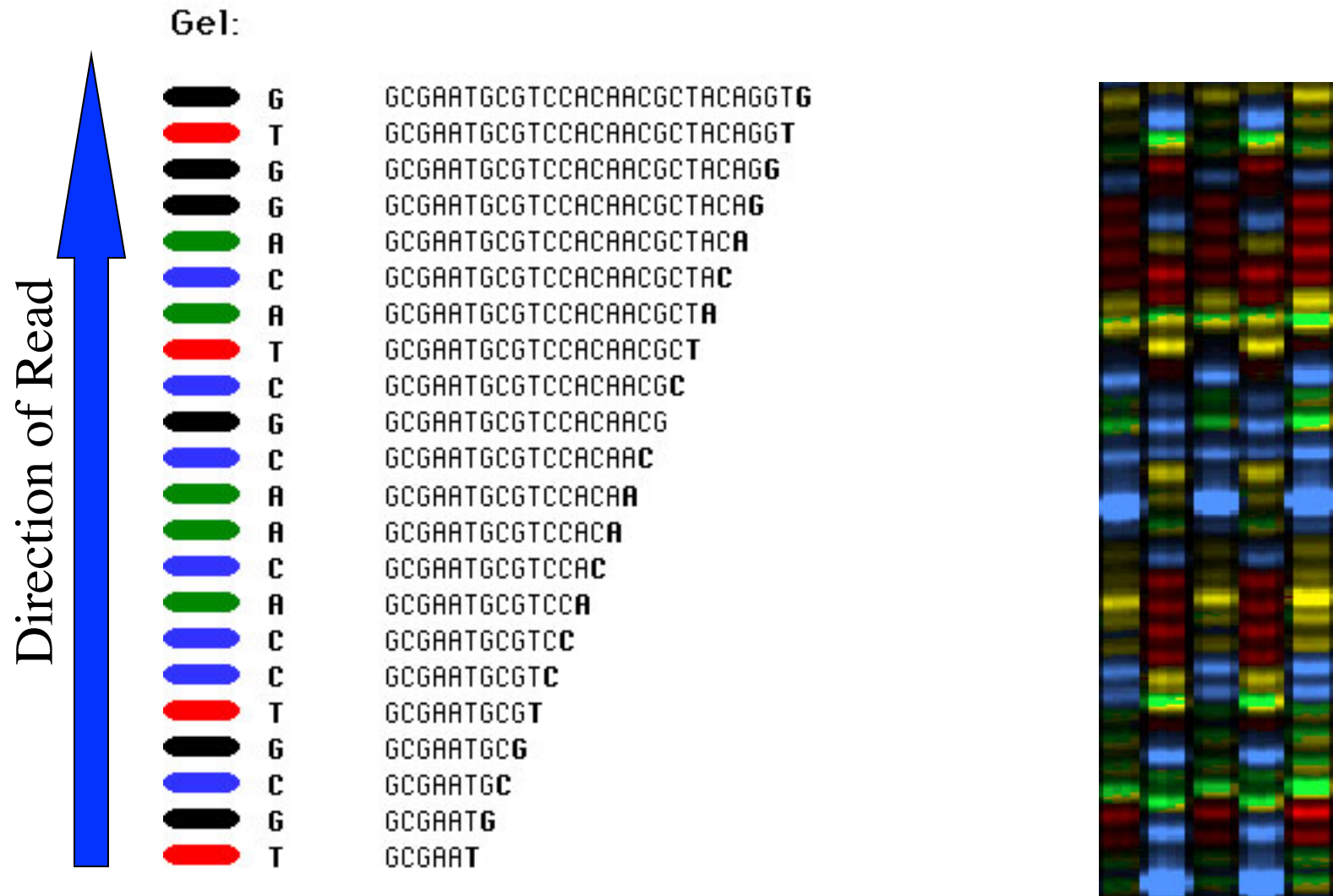


IF 5% of the T nucleotides are actually dideoxy T, then each strand will terminate when it gets a ddT on its growing end:

5' - TACGCGGTACGGTATGTTGACCGTTTAGCTACCGAT•
 5' - TACGCGGTACGGTATGTTGACCGTTTAGCT•
 5' - TACGCGGTACGGTATGTTGACCGTTT•
 5' - TACGCGGTACGGTATGTTGACCGTT•
 5' - TACGCGGTACGGTATGTTGACCGT•
 5' - TACGCGGTACGGTATGTT•
 5' - TACGCGGTACGGTATGT•
 5' - TACGCGGTACGGTAT•
 5' - TACGCGGTACGGT•
 5' - TACGCGGT•

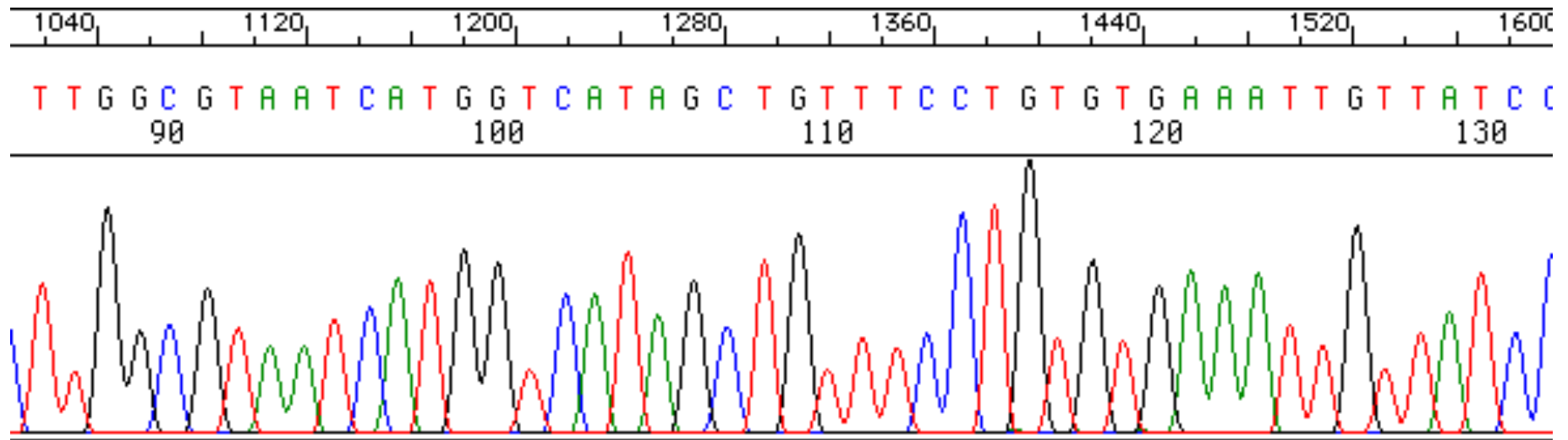


A Review of Dideoxy Sequencing



Each Lane is One DNA Sequence

A Review of Dideoxy Sequencing



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>



Goldberg EST-DB

Current disk usage: 15G free (43% used) / 0.18,0.21,0.09 / [Jobs](#)

Process

Process trace files, either existing remotely via an FTP server or provided by an outside source and uploaded to this server. Or, input a new sequence manually, without processing any trace files.

Summary, Search & Select

Obtain summaries, search the database, select specific sets of sequences on which to perform actions.

Browse/manipulate datasets

Browse the cap3 analysis data or the databases available for BLAST. Manually update these datasets, or delete custom blast databases. To create a BLAST database, use the [Search form](#) to first select the desired sequences, then use the "Make Blast DB" action.

Preferences

Update database entries such as projects, function groups, etc.

Help

Online help manual

Links

Links to some useful software.

<http://estdb.biology.ucla.edu/~goldberg>

Processing Sequence Files - PART I



Goldberg EST-DB

Current disk usage: 15G free (43% used) / 0.06,0.16,0.08 / [Jobs](#)

Process files from UCLA sequencing facility

In order to process files from the UCLA sequencing facility, you must first download the files from [WebSeq](#). The file, containing all of the sequences you wish to process should be called "webseq.zip". Please use the following to upload ~~your webseq~~ webseq.zip to estdb for processing by clicking the "Browse" button, then navigating to the location of webseq.zip on your computer. Please note that the upload and unzipping process may take a bit of time. Please be patient and do not cancel the process prematurely.

You may also use this form to upload a single (non-zipped) sequence file.

no file selected

Process local files

Select this item if you wish to process files not located at UCLA's sequencing facility. These files should have been uploaded to estdb.biology.ucla.edu via ftp prior to selecting this option.

Obtaining Sequences From UCLA Sequencing Facility



UCLA Sequencing
& Genotyping Core

[Help](#)

[Sequencing & Genotyping
Core Home Page](#)

WebSeq

Welcome to WebSeq

Username:

Password:

Login

Copyright (C) 2002-2004 UCLA Human Genetics
Last modified 20 January 2004 14:44:07.

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

Selecting Sequence to Download

WebSeq - Sequencing

http://www.genetics.ucla.edu/webseq/user?show=sequencing&sort=date&i

Lab Lab HC70A HC70A Bioinformatics FIRE IClust Bioinformatics BioWareDB GDR CAP3

WebSeq - Sequencing

GENOSEQ
UCLA GENOTYPING & SEQUENCING

WebSeq

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.

Select	Filename	Size	Date
<input type="checkbox"/>	59786GoldR_RY-8R.ab1	315947	04 Apr 2008
<input type="checkbox"/>	59786GoldR_KG-F.ab1	296816	04 Apr 2008
<input type="checkbox"/>	59786GoldR_KG-R.ab1	297936	04 Apr 2008
<input type="checkbox"/>	59786GoldR_KT-F.ab1	309632	04 Apr 2008
<input type="checkbox"/>	59786GoldR_KT-R.ab1	301912	04 Apr 2008
<input type="checkbox"/>	59786GoldR_MG-7F.ab1	311146	04 Apr 2008
<input type="checkbox"/>	59786GoldR_MG-7R.ab1	311146	04 Apr 2008
<input type="checkbox"/>	59786GoldR_MT-2F.ab1	296027	04 Apr 2008
<input type="checkbox"/>	59786GoldR_MT-2R.ab1	296363	04 Apr 2008
<input type="checkbox"/>	59786GoldR_AC-9R.ab1	304835	04 Apr 2008
<input type="checkbox"/>	59786GoldR_AC-9F.ab1	306635	04 Apr 2008

Choose File to Upload to ESTDB


webseq.zip




Goldberg EST-DB

Current disk usage: 15G free (43% used) / 0.06,0.16,0.08 / [Jobs](#)


Process files from UCLA sequencing facility

In order to process files from the UCLA sequencing facility, you must first download the files from [WebSeq](#). The file, containing all of the sequences you wish to process should be called "webseq.zip". Please use the following to upload your webseq.zip to estdb for processing by clicking the "Browse" button, then navigating to the location of webseq.zip on your computer. Please note that the upload and unzipping process make take a bit of time. Please be patient and do not cancel the process prematurely.

You may also use this form to upload a single (non-zipped) sequence file.

 webseq.zip

Select Individual Files to Process in ESTDB



Goldberg EST-DB

Current disk usage: 15G free (43% used) / 0.00,0.05,0.05 / [Jobs](#)

:: process sequence trace files into the database

File selection

Directory: /home/goldberg/tmp/12755102524090db5f13178

Which of the following files should be processed?

☐ 11012GoldR_F-JW_083.ab1
☐ 11012GoldR_R-JW_091.ab1
[Select All](#) | [Deselect All](#)

Continue with selected

Renaming and Initial Annotation of Files



Renaming and initial annotation

Below is a list of the sequences selected from the **8810816084090df4038ca0** directory. Please review it before providing initial annotation and inputing new names for these files. Once complete, click the continue button at the bottom.

Project: Primer: Vector: Sequenced from end

Original Name	New Name
8966GoldR_EM-K16JL_008.ab1	<input type="text" value="Gene_Superpool_JL202"/>
8966GoldR_EM-K16RV_007.ab1	<input type="text" value="Gene_Superpool_Rv"/>

Base name :
Starting number :

Use the above two fields ("Base name" and "Starting number") to automatically fill a basename plus a starting number in the rename fields to the left. This does not finalize this form- you have to click the continue button at the bottom- but eases repetitive entry.

For example, if you want the first sequence on the left (**8966GoldR_EM-K16JL_008.ab1**) to be named **PCEP00100**, you would type in "PCEP00" for the base name, and "100" for the starting number, then click the "Fill In" button.

Interpreting Sequence Chromatogram Information



Goldberg EST-DB

Current disk usage: 15G free (43% used) / 0.00,0.02,0.03 / [Jobs](#)

Rename sequences

The files will now be renamed. **Do not interrupt this process.**

Please wait till transfer is complete before reviewing and selecting an option at the bottom.

```
Trying to make /home/goldberg/tmp/2da08cbf25b0588d96fe66cd57176513...OK
Moving /home/goldberg/tmp/12755102524090db5f13178/11012GoldR_F-JW_083.ab1 to /home/goldberg/tmp/2da08cbf2!
Moving /home/goldberg/tmp/12755102524090db5f13178/11012GoldR_R-JW_091.ab1 to /home/goldberg/tmp/2da08cbf2!
```

Next step: base call with phred

CATTATGGCCGGG	: Tell phred to trim
12	: Hilite poly-A of length
	: Other sequences to highlight (separate multiple with commas)
	: Omit sequences less than or equal to this length

Start phred

Successful Interpretation of Chromatogram

Base Calling with Phred

The files are now being base called.

Do not interrupt this process or click on a link until the reads are done- wait until this is complete before reviewing and selecting an option at the bottom.

```
LEN : length of sequence read, after trimming
PRET : length of sequence read, pre-trimming
Ns : number of Ns in sequence read
STAT : status
      OMIT : sequence was omitted due to short read; sequence not inputted into database
      ERR! : an error occurred during base calling by phred; sequence not inputted into database
      A : when an A occurs, a poly A sequence greater than or equal to 12 in length was found
      M : when an M occurs, a match to one of given sequences was found (none given)
```

Trying to make /home/goldberg/tmp/9fb2c99b2e9f5edc660880ec4a283858-phred...OK

NAME	LEN	PRET	Ns	STAT	+	10	20	30	40	50
Gene_Superpool_JL202	420	909	0	----	TTCTTTTCTCCTATTGACCATCATACTCATTTGCTGATCCATGTAGATTTCCCGGACAT					
Gene_Superpool_Rv	568	883	0	----	AAGACTCGAATGAAATAACAAAAAGTTCCAAGTCCAACAATGACAAGGAAACCAAGAC					

Deleting temp directory for sequence reads... OK

```
SUMMARY :
Sequences added to database : 2 (avg length 494.00000000000000)
Sequences omitted/too short : 0
Sequences generating errors : 0
```

The sequences above, unless marked as **OMIT** or **ERR!**, were read and entered into the database.

You may edit or delete a sequence at this point by clicking on it. Sequence editing will occur in a separate window. Trace download is not available until the next step.

<input type="button" value="Discard reads"/>	Select this option if you wish to discard all of the reads performed above. If you wish to change the parameters passed to phred on the previous page, select this option before using the Back button to go to the previous page.
<input type="button" value="Continue"/>	Select this option if you wish to continue with the sequences above, as edited, and configure the blast runs with them. Do not use the back button after you have used this option.

Sequence Record Information

Edit Sequence Record for Gene_Superpool_JL202

[Show BLAST/PFAM data](#)

Perform action:

```
TTCTTTTCTCCTATTGACCATCATACTCATTGCTGATCCATGTAGA
TTTCCCGGACATGAAGCCATTTACAATTGAATATACTATAACATAT
ATTAGGTCAGGTGTGTAATTAATGACCTGTATTTGCAAATCTGTG
GTCAACAATGTTTGCCGGAATTGTTGGTAGAGCCAGGACTCATGAA
CAGATAATGGCTGATGCTGCTGGAACTTCAATGGAAATCTCCAAA
TAGTAAGTCTTCTACACTAATATAGAGTTATACAAAGAAAAAAAC
AATACTTGTTTGATATATAAAAGTTTAACCAATTAATATTGTTCTTA
TTCATAGATGAGTGCTGAGTACCAAGTGCTTTCCCGCTAGTCACA
ACCCGCGAAAGCTACTTCGTCCGCTACTGAAAGCAACAAGGAGAG
GGTTT
```

Length : 420

Ns : 0

Date entered : 04/29/2004

Date modified : 04/29/2004

Session : 9fb2c99b2e9f5edc660880ec4a283858

Project	<input type="text" value="Manual Sequencing and Others"/>
Vector	<input type="text" value="n.d."/>
Primer	<input type="text" value="n.d."/>
Sequenced from	<input type="text" value="3'"/> end
cDNA size	<input type="text"/>
Function group	<input type="text" value="No Significant Hits"/>
Most homologous	<input type="text"/>
Origin	<input type="text" value="n.a."/>
Arabidopsis hit?	<input type="radio"/> Yes <input checked="" type="radio"/> No
poly-A tail?	<input type="radio"/> Yes <input checked="" type="radio"/> No
Accession #	(none)
DBESTID	(none)

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 db.

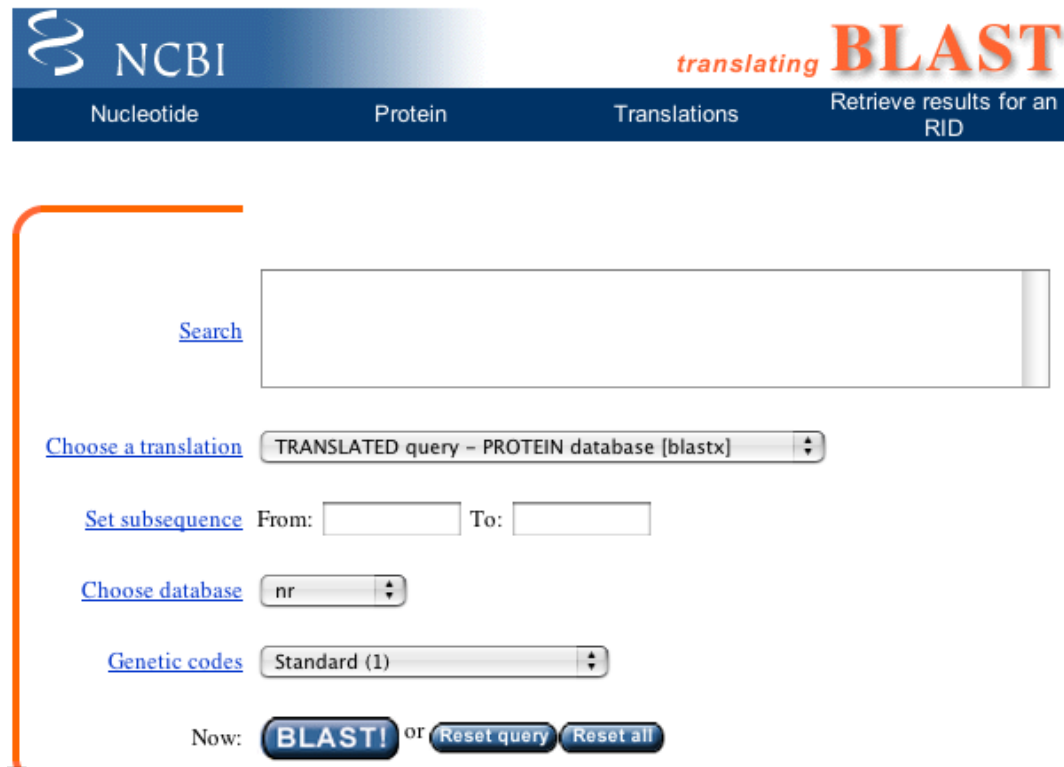
What are the steps to performing BLAST search?

Paste sequence of interest into BLAST input box

Select BLAST program

Select db

Select Optional Parameters



The screenshot shows the NCBI translating BLAST web interface. At the top, the NCBI logo is on the left, and the text "translating BLAST" is on the right. Below the logo, there are four tabs: "Nucleotide", "Protein", "Translations", and "Retrieve results for an RID". The "Translations" tab is selected. Below the tabs, there is a large text input box for the query sequence. To the left of this box is a "Search" link. Below the input box, there is a "Choose a translation" link and a dropdown menu showing "TRANSLATED query - PROTEIN database [blastx]". Below this, there is a "Set subsequence" link and two input boxes for "From:" and "To:". Below that, there is a "Choose database" link and a dropdown menu showing "nr". Below that, there is a "Genetic codes" link and a dropdown menu showing "Standard (1)". At the bottom, there is a "Now:" label followed by a "BLAST!" button, an "or" label, and two buttons: "Reset query" and "Reset all".

NCBI

translating **BLAST**

Nucleotide Protein Translations Retrieve results for an RID

[Search](#)

[Choose a translation](#) TRANSLATED query - PROTEIN database [blastx]

[Set subsequence](#) From: To:

[Choose database](#) nr

[Genetic codes](#) Standard (1)

Now: **BLAST!** or [Reset query](#) [Reset all](#)

What are the different BLAST Programs?

Fastest

blastp - protein query vs protein db

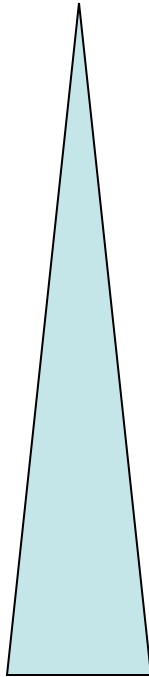
blastn - DNA query vs DNA db

blastx - translated DNA query vs protein db

tblastn - protein query vs translated DNA db

Slowest

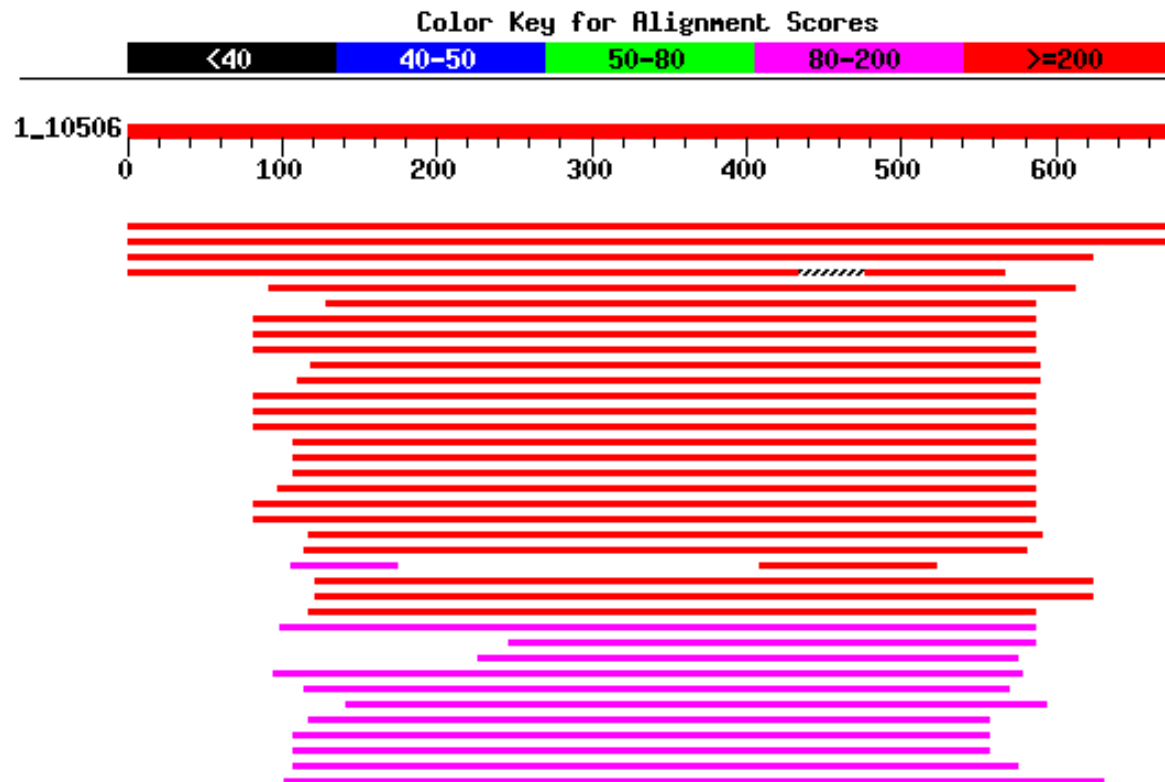
tblastx - translated DNA query vs translated DNA db



Anatomy of a BLAST Result -- Part I

Distribution of 339 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Anatomy of a BLAST Result -- Part II

Sequences producing significant alignments:			Score (bits)	E-Value	
gi 14532716 gb AAK64159.1 	unknown protein [Arabidopsis tha...	1206	0.0		
gi 18394588 ref NP_564049.1 	suppressor of lin-12-like prot...	1209	0.0		
gi 15219499 ref NP_177498.1 	suppressor of lin-12-like prot...	877	0.0		
gi 11120786 gb AAG30966.1 	hypothetical protein, 3' partial...	426	e-118		
gi 41151276 ref XP_046437.5 	chromosome 20 open reading fra...	291	3e-77		L
gi 13559241 emb CAB65792.2 	dJ842G6.2 (novel protein imilar...	282	2e-74		L
gi 19923669 ref NP_005056.3 	sel-1 suppressor of lin-12-lik...	268	4e-70		L
gi 6851089 gb AAF29413.1 	SEL1L [Homo sapiens] >gi 17646138...	268	4e-70		L
gi 9967440 dbj BAB12403.1 	SEL1L [Mesocricetus auratus]	264	4e-69		
gi 31203035 ref XP_310466.1 	ENSANGP00000019196 [Anopheles ...	263	1e-68		
gi 21355295 ref NP_651179.1 	CG10221-PA [Drosophila melanog...	263	1e-68		L
gi 20857527 ref XP_127076.1 	Sell (suppressor of lin-12) 1 ...	261	4e-68		L
gi 4159995 gb AAD05210.1 	SEL1L [Mus musculus] >gi 20073079...	259	1e-67		L
gi 29336095 ref NP_808794.1 	Sell (suppressor of lin-12) 1 ...	259	2e-67		L
gi 29612522 gb AAH49959.1 	Sellh protein [Mus musculus]	258	4e-67		L
gi 17563256 ref NP_506144.1 	Suppressor/Enhancer of Lin-12 ...	247	9e-64		L
gi 1255199 gb AAC47112.1 	sel-1 gene product	247	9e-64		L

Anatomy of a BLAST Result -- Part III

```
>gi|14532716|gb|AAK64159.1| unknown protein [Arabidopsis thaliana]
      Length = 678

Score = 1206 bits (3120), Expect = 0.0
Identities = 614/678 (90%), Positives = 614/678 (90%)

Query: 1   MRILSYGIVILSLLVFSFIEFGVHARPVVLVXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 60
          MRILSYGIVILSLLVFSFIEFGVHARPVVLV                               V
Sbjct: 1   MRILSYGIVILSLLVFSFIEFGVHARPVVLVLSNDDLNSGGDDNGVGESSDFDEFGESEP 60

Query: 61  XXXXXLDPGSWRSIFEPDDSTVQAASPQYYSGLKKILSAASEGNFRLMEEAVDEIEAASS 120
          LDPGSWRSIFEPDDSTVQAASPQYYSGLKKILSAASEGNFRLMEEAVDEIEAASS
Sbjct: 61  KSEEELDPGSWRSIFEPDDSTVQAASPQYYSGLKKILSAASEGNFRLMEEAVDEIEAASS 120

Query: 121 AGDPHAQSIMGFVYGIGMMREKSKSKSFLHHNFAAAGGNMQSKMALAFTYLRQDMHDKAV 180
          AGDPHAQSIMGFVYGIGMMREKSKSKSFLHHNFAAAGGNMQSKMALAFTYLRQDMHDKAV
Sbjct: 121 AGDPHAQSIMGFVYGIGMMREKSKSKSFLHHNFAAAGGNMQSKMALAFTYLRQDMHDKAV 180

Query: 181 QLYAELAETAVNSFLISKDSPVVEPTRIHSgteENKGALRKSRGEEDEDfQILEYQAQKG 240
          QLYAELAETAVNSFLISKDSPVVEPTRIHSgteENKGALRKSRGEEDEDfQILEYQAQKG
Sbjct: 181 QLYAELAETAVNSFLISKDSPVVEPTRIHSgteENKGALRKSRGEEDEDfQILEYQAQKG 240

Query: 241 NANAMYKIGLFYYFGLRGLRRDHTKALHWFLKAVDKGEPRSMELLGEIYARGAGVERNYT 300
          NANAMYK GLFYYFGLRGLRRDHTKALHWFLKAVDKGEPRSMELLGEIYARGAGVERNYT
Sbjct: 241 NANAMYKNGLFYYFGLRGLRRDHTKALHWFLKAVDKGEPRSMELLGEIYARGAGVERNYT 300
```

What is a Gene?

An ordered sequence of nucleotides

What are the 4 Nucleotides in DNA?

A - Adenine

T - Thymine

C - Cytosine

G - Guanine

What are the Characteristics of a Gene?

- An ordered sequence of nucleotides
- A unique position/location in the genome
- Polarity (5' to 3')
- Exons and/or Introns

What are the Anatomical Features of Genes?

- Discrete beginning and discrete end
- Two strands of DNA
- Double helical
- Strand one (5' to 3')
- Strand two (3' to 5')
- Sense strand (5' to 3')
 - specifies the trait
- Nonsense strand (3' to 5')
 - template for transcription

Sense Strand

5'	-	ACGTCAGTCGATGCATGCTAGCTAGC	-	3'
3'	-	TGCAGTCAGCTACGTACGATCGATCG	-	5'

Nonsense Strand

What Gene Are You Working With?

Task: Use the DNA sequence you've obtained from the sequencing facility 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. Run BLAST

Results/Question:

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

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. **Select Seqviewer**
2. **Enter gene number (ex. AT2G26320)**
3. **Submit**

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?**

Genes Have a Unique Order of Nucleotides!

Task: What is the order of nucleotides for your gene?

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

Procedure: (Continue from previous slide)

1. Click on Location

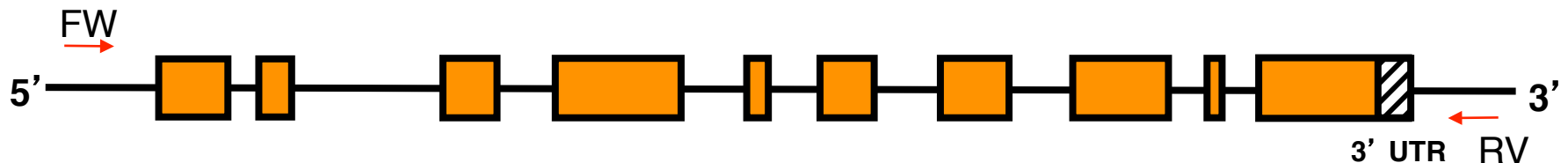
Results/Question:

1. What are your neighbor genes?
2. What is the orientation of your gene?
3. How big is your gene?

Genes Have Exons and/or Introns!

Task: How many exons and/or introns does your gene have?

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



Procedure: (Continue from previous slide)

1. Click on gene information on the right

Results/Question:

1. How many exons/introns in your gene?
2. What are exons?
3. What are introns?

A Gene Encodes a Protein

Task: Determine the protein encoded by your gene

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

Results/Question:

1. How large is your protein?
2. What are the anatomy of a protein?



What is the identity of your gene?

Task: What does your gene code for?

Tools: TAIR

<http://arabidopsis.org>

NCBI Pubmed

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

PubMed - Endless Resources

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

The screenshot shows the PubMed website interface. At the top, there are logos for NCBI, PubMed, and the National Library of Medicine (NLM). Below the logos is a navigation bar with links to Entrez, PubMed, Nucleotide, Protein, Genome, Structure, and OMIM. The main search area features a search bar with the text 'PubMed' and a 'Go' button. Below the search bar are links for Limits, Preview/Index, History, Clipboard, and Details. On the left side, there is a sidebar with links to About Entrez, Text Version, Entrez PubMed, Overview, Help | FAQ, Tutorial, New/Noteworthy, E-Utilities, PubMed Services, Journals Database, MeSH Database, and Single Citation. In the center, there is a list of search instructions:

- Enter one or more search terms, or click [Preview/Index](#) for advanced searching.
- Enter [author names](#) as smith jc. Initials are optional.
- Enter [journal titles](#) in full or as MEDLINE abbreviations. Use the [Journals Database](#) to find journal titles.

Below the list, there is a yellow box containing text: PubMed, a service of the National Library of Medicine, includes over 14 million citations for biomedical articles back to the 1950's. These citations are from MEDLINE and additional life science journals. PubMed includes links to many sites providing full text articles and other related resources.

Ex. Author search - Goldberg RB, Bui AB

Keyword - T-DNA Mutagenesis, etc...

SALK T-DNA Lines

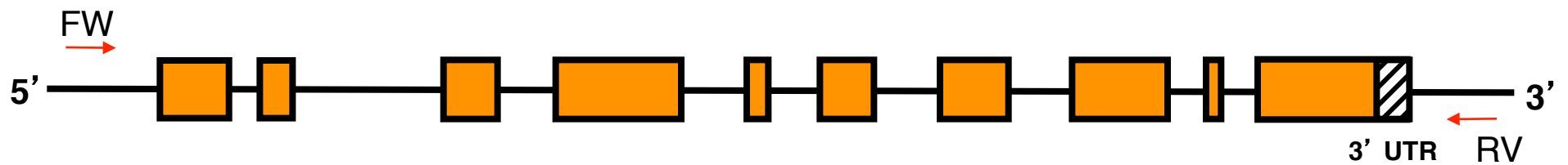
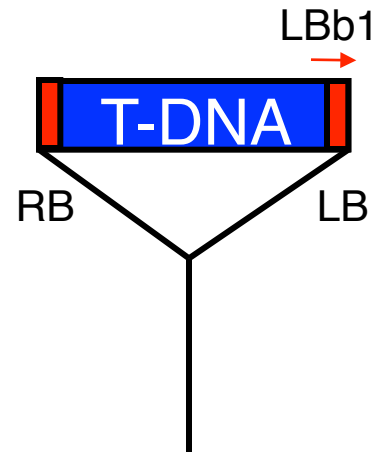
A Collection of T-DNA Mutant Lines



<http://signal.salk.edu/cgi-bin/tdnaexpress>

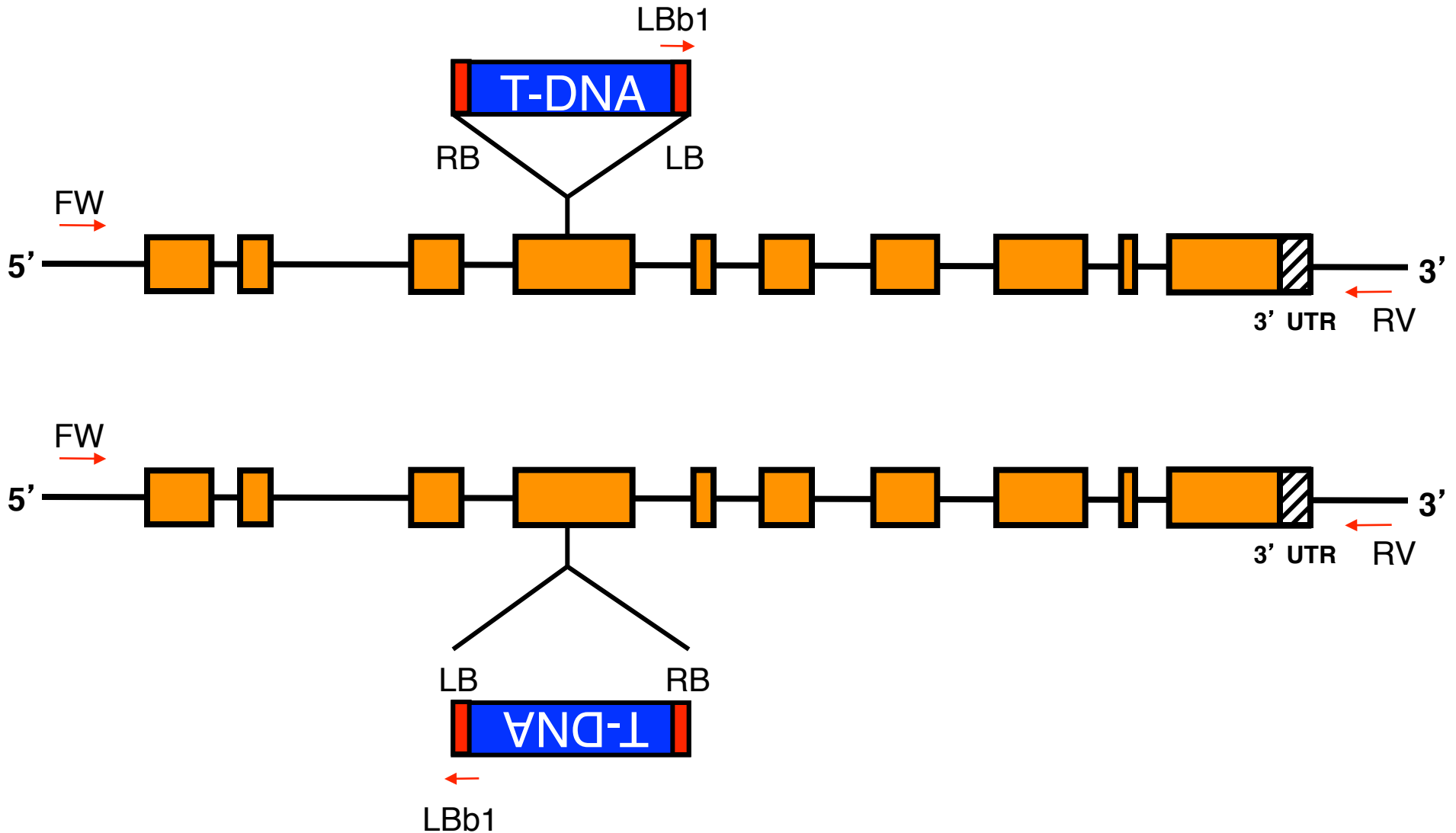
SALK T-DNA Lines

How Were T-DNA Lines Created?

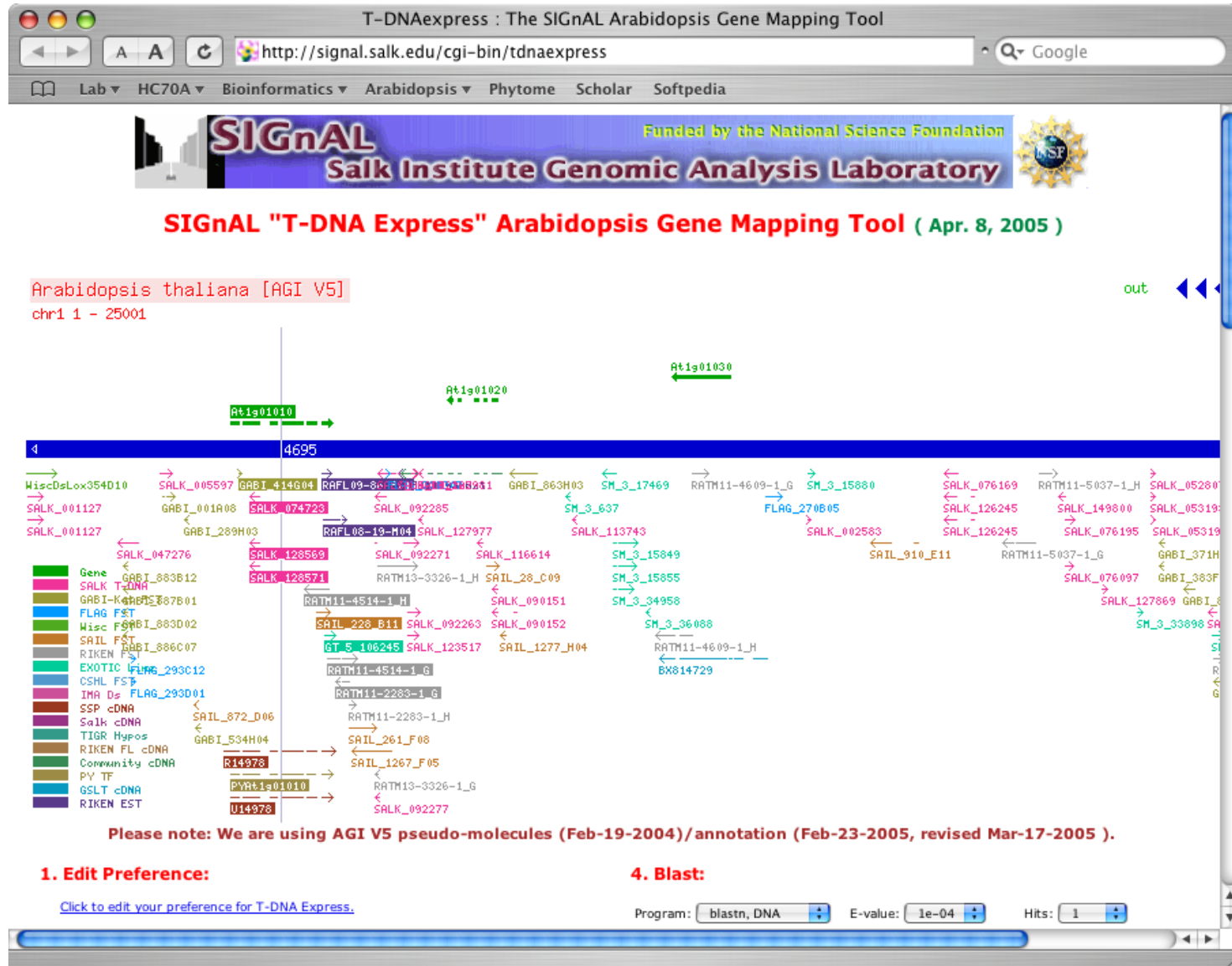


SALK T-DNA Lines

How Were T-DNA Lines Created?



A Collection of T-DNA Mutant Lines



SALK T-DNA Lines

A Collection of T-DNA Mutant Lines

T-DNAexpress : The SIGnAL Arabidopsis Gene Mapping Tool

http://signal.salk.edu/cgi-bin/tdnaexpress

Lab ▾ HC70A ▾ Bioinformatics ▾ Arabidopsis ▾ Phytome ▾ Scholar ▾ Softpedia

[PY11](#) [GSLT cDNA](#) [RIKEN EST](#) [PY11a01010](#) [RATM13-3326-1_G](#) [U14978](#) [SALK_092277](#)

Please note: We are using AGI V5 pseudo-molecules (Feb-19-2004)/annotation (Feb-23-2005, revised Mar-17-2005).

1. Edit Preference:

[Click to edit your preference for T-DNA Express.](#)

2. Search:

Gene name: for example: [At1g01010](#)

or Function: for example: [auxin](#) (Case sensitive)

or cDNA/T-DNA: for example: [SALK_003854](#), [R10047](#)

4. Blast:

Program: E-value: Hits:

Cut and paste your sequence into here.

File : no file selected

3. Locate:

Position: chr1

5. Multiple Search

Search by Gene/Affy/GO/Sequence and plain text return only.

6. SIGnAL iSect Tools

to design primers for T-DNA or your sequences, to retrieve sequences and to compare two lists.

ANNOUNCEMENT : **

- We requested that users include this reference (below) in publications describing the use of SSP gold standard cDNA ORF clones obtained from ABRC. Thanks!
 Kayoko Yamada, Jun Lim, Joseph M. Dale, Huaming Chen, Paul Shinn, Curtis J. Palm, Audrey M. Southwick, Hank C. Wu, Christopher Kim, Michelle Nguyen, Paul Pham, Rosa Cheuk, George Karlin-Newmann, Shirley X. Liu, Bao Lam, Hitomi Sakano, Troy Wu, Guixia Yu, Molly Miranda, Hong L. Quach, Matthew Tripp, Charlie H. Chang, Jeong M. Lee, Mitsue Toriumi, Marie M. H. Chan, Carolyn C. Tang, Courtney S. Onodera, Justine M. Deng, Kenji Akiyama, Yasser Ansari, Takahiro Arakawa, Jenny Banh, Fumika Banno, Leah Bowser, Shelsea Brooks, Piero Carninci, Qimin Chao, Nathan Choy, Akiko Enju, Andrew D. Goldsmith, Mani Gurjal, Nancy F. Hansen, Yoshihide Hayashizaki, Chanda Johnson-Hopson, Vickie W. Hsuan, Kei Iida, Meagan Karnes, Shehnaz Khan, Eric Koesema, Junko Ishida, Paul X. Jiang, Ted Jones, Jun Kawai, Asako Kamiya, Cristina Meyers, Maiko Nakajima, Mari Narusaka, Motoaki Seki, Tetsuya Sakurai, Masakazu Satou, Racquel Tamse, Maria Vaynsberg, Erika K. Wallender, Cecilia Wong, Yuki Yamamura, Shialou Yuan, Kazuo Shinozaki, Ronald W. Davis, Athanasios Theologis, and Joseph R. Ecker (2003) **Empirical Analysis of Transcriptional Activity in the Arabidopsis Genome Science 302: 842-846.**
[\[Abstract \]](#) [\[Full Text \]](#) [\[Supporting data \]](#) [\[Supplementary GEO Analysis Files \]](#)
- We requested that users include this reference (below) in publications describing the use of Salk lines obtained from ABRC or NASC. Thanks!
 José M. Alonso, Anna N. Stepanova, Thomas J. Leisse, Christopher J. Kim, Huaming Chen, Paul Shinn, Denise K. Stevenson, Justin Zimmerman, Pascual Barajas, Rosa Cheuk, Carmelita Gadrinab, Collen Heller, Albert Jeske, Eric Koesema, Cristina C. Meyers, Holly Parker, Lance Prednis, Yasser Ansari, Nathan Choy, Hashim Deen, Michael Geralt, Nisha Hazari, Emily Hom, Meagan Karnes, Celene Mulholland, Ral Ndubaku, Ian Schmidt, Plinio Guzman, Laura Aguilar-Henonin, Markus Schmid, Detlef Weigel, David E. Carter, Trudy

A Collection of T-DNA Mutant Lines

