National Center for Biotechnology Information Resources for Plant Genomics

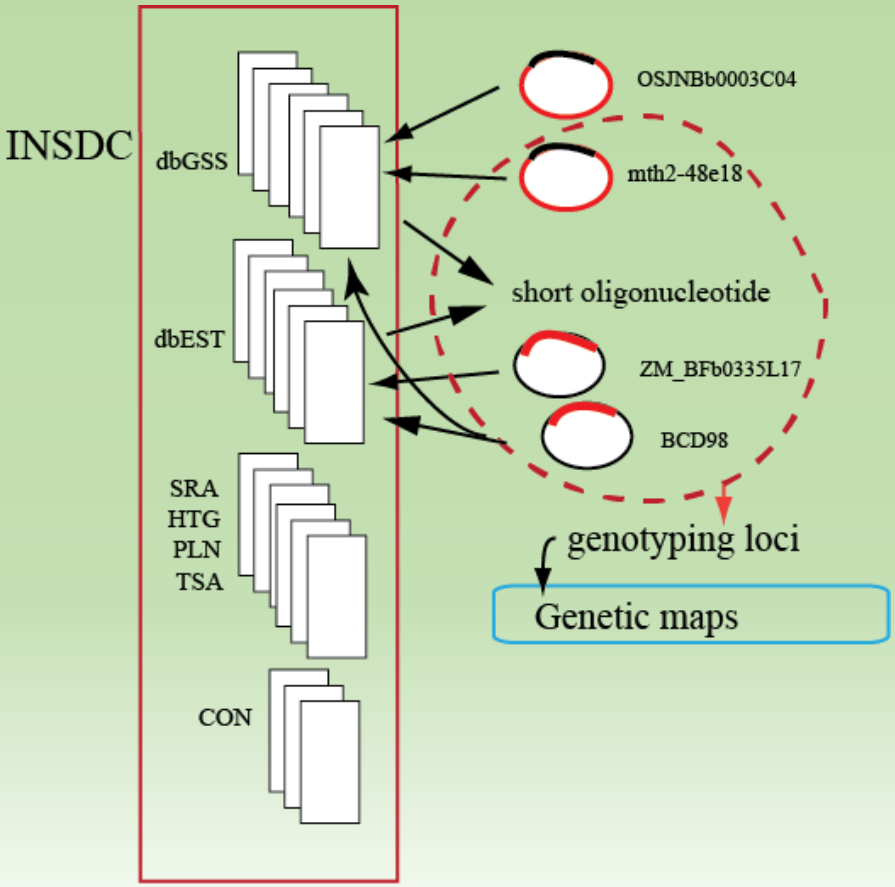
Brian Smith-White

Tuesday 13 January 2015

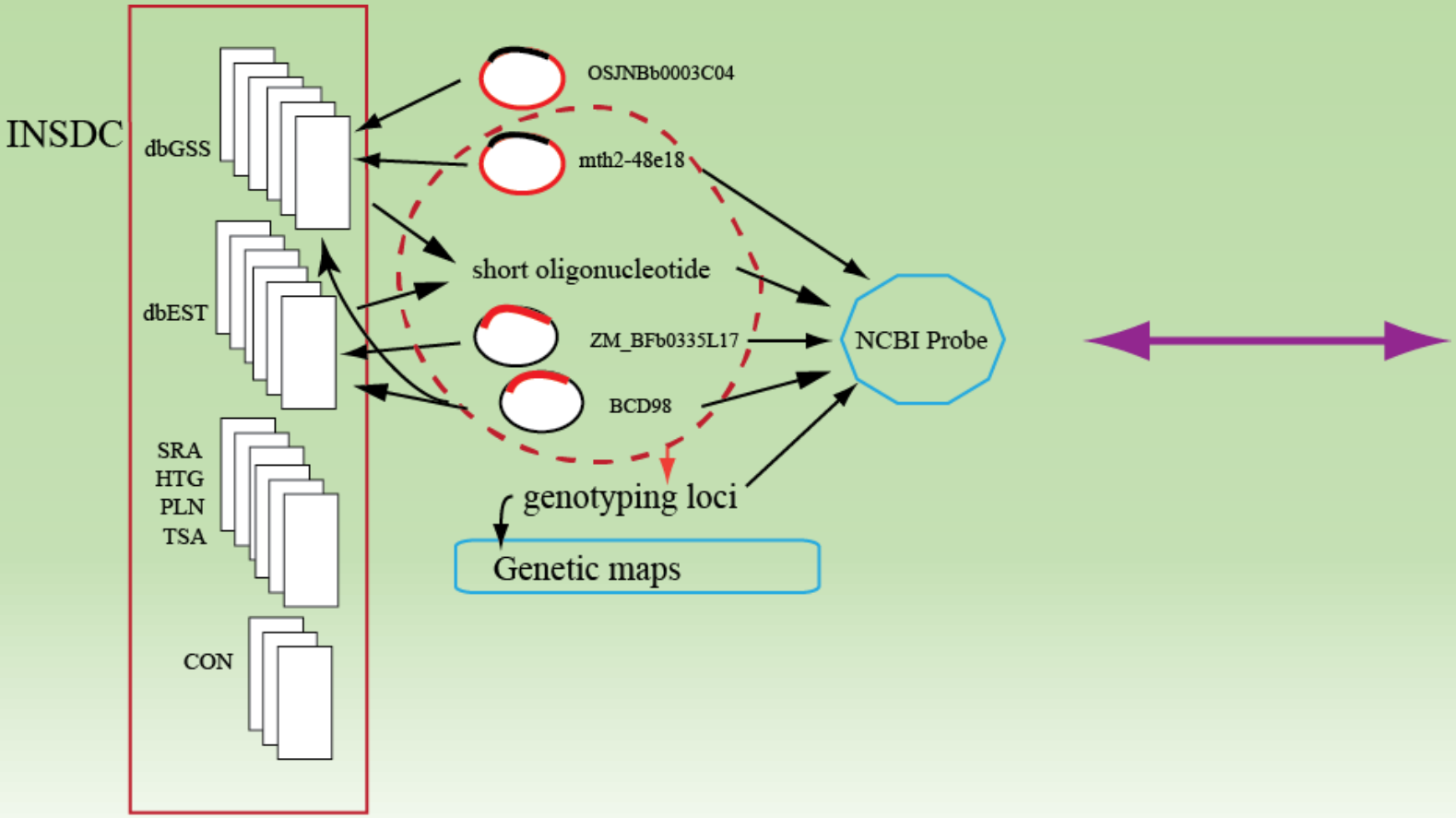
Acknowledgements

- Svetlana Zazvovskaia – NCBI Probe group
- Anjana Raina – RefSeq group
- Terence D. Murphy – NCBI Gene group
- Ilene Mizrachi – NCBI Probe group
- Valerie Schneider – CloneDB group
- Kim D. Pruitt – RefSeq group

Nucleic acid reagents



NCBI Probe - http://www.ncbi.nlm.nih.gov/probe



Granularity of NCBI Probe data – same name, different techniques

NCBI Resources How To

Probe | Probe | TG174

Save search Limits Advanced

Display Settings: Summary Send to:

Results: 3

1. STS probe TG174
   Accession: Pr012790551 ID: 12790551
   Name: TG174
   Type: STS

2. Solanum lycopersicum CAPS probe TG174
   Accession: Pr006097453 ID: 6097453
   Name: TG174
   Type: CAPS
   Application: genotyping
   Target organism: Solanum lycopersicum

3. Solanum lycopersicum RFLP probe TG174
   Accession: Pr002246415 ID: 2246415
   Name: TG174
   Type: RFLP
   Application: genotyping
   Source organism: Solanum lycopersicum
   Target organisms: Capsicum annuum; Solanum lycopersicum; Solanum peruvianum; Solanum pimpinellifolium; Solanum pennellii; Solanum habrochaites; Capsicum chinense; Capsicum annuum x Capsicum chinense

Granularity of NCBI Probe data – same name, different organism

NCBI Resources How To

Probe | Probe | TG174

Save search Limits Advance

Display Settings: Summary

Results: 3

1. STS probe TG174
   Accession: Pr012790551 ID: 12790551
   Name: TG174
   Type: STS

2. Solanum lycopersicum CAPS probe TG174
   Accession: Pr006097453 ID: 6097453
   Name: TG174
   Type: CAPS
   Application: genotyping
   Target organism: Solanum lycopersicum

3. Solanum lycopersicum RFLP probe TG174
   Accession: Pr002246415 ID: 2246415
   Name: TG174
   Type: RFLP
   Application: genotyping
   Source organism: Solanum lycopersicum
   Target organisms: Capsicum annuum; Solanum lycopersicum; Sc
   Solanum habrochaites; Capsicum chinense; Capsicum annuum x Capsicum chinense

NCBI Resources How To

Probe | Probe | pA086

Save search Limits Advanced

Display Settings: Summary Send to:

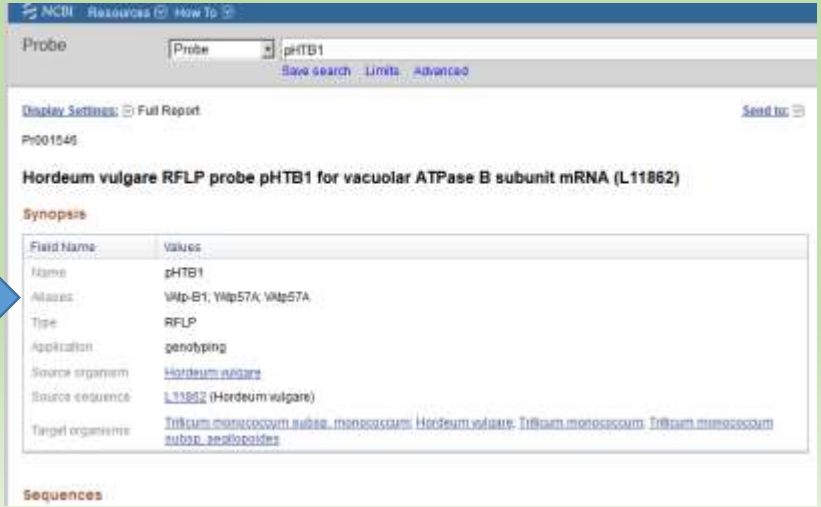
Results: 2

1. Hordeum vulgare RFLP probe **pA086** for cold-regulated mRNA (M60733)
   Accession: Pr004066840 ID: 4066840
   Name: pA086
   Type: RFLP
   Application: genotyping
   Source organism: Hordeum vulgare
   Source sequence: M60733
   Target organism: Hordeum vulgare

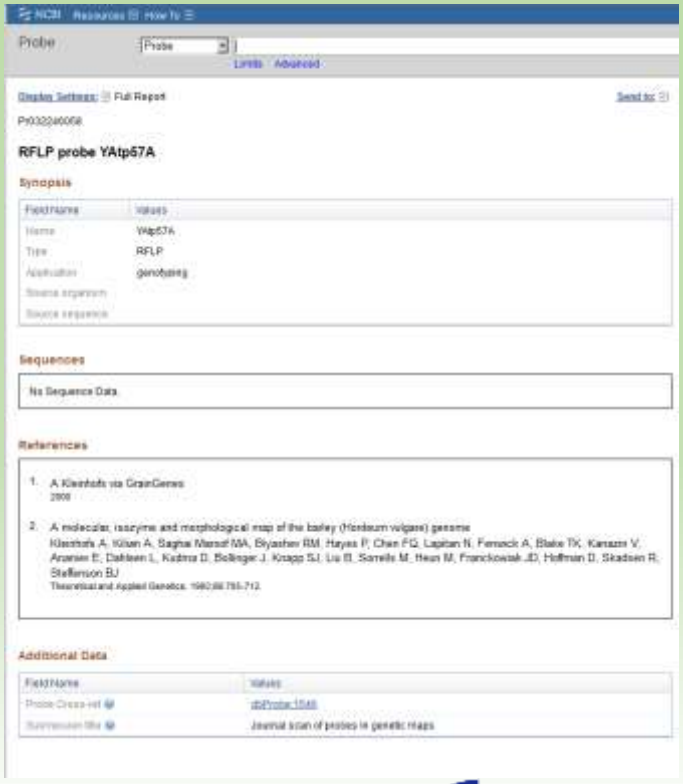
2. Glycine max RFLP probe **pA086** for T134012 Soybean RFLP probe Glycine max genomic clone A086 (AQ841762) and 3 more sequences
   Accession: Pr003647552 ID: 3647552
   Name: pA086
   Type: RFLP
   Application: genotyping
   Source organism: Glycine max
   Source sequences: 4 sequences
   Target organisms: Glycine max; Glycine soja

Display of synonym data

Probe name display



Synonym name display



Display of synonym data – multiple probes with identical synonym

NCBI Resources How To Sign in to NCBI

Probe | Probe | AFLP11 | Search

Save search Limits Advanced Help

Display Settings: Summary Send to:

Results: 4

1. AFLP probe set **AFLP11**
   Accession: Pr031976813 ID: 31976813
   Name: AFLP11
   Type: AFLP

2. Theobroma cacao AFLP probe set E40M6062
   Accession: Pr031905623 ID: 31905623
   Name: E40M6062
   Aliase: AFLP11
   Type: AFLP
   Target organism: Theobroma cacao

3. AFLP probe set **AFLP11**
   Accession: Pr031899717 ID: 31899717
   Name: AFLP11
   Type: AFLP

4. Avena strigosa x Avena wiestii AFLP probe set E34M56
   Accession: Pr031870007 ID: 31870007
   Name: E34M56
   Aliase: AFLP11
   Type: AFLP
   Target organism: Avena strigosa x Avena wiestii

Display Settings: Summary Send to:

Filter your results:
- All (4)
- Variation (0)
- Silencing (0)
- Expression (0)

Manage Filters

Results by taxon

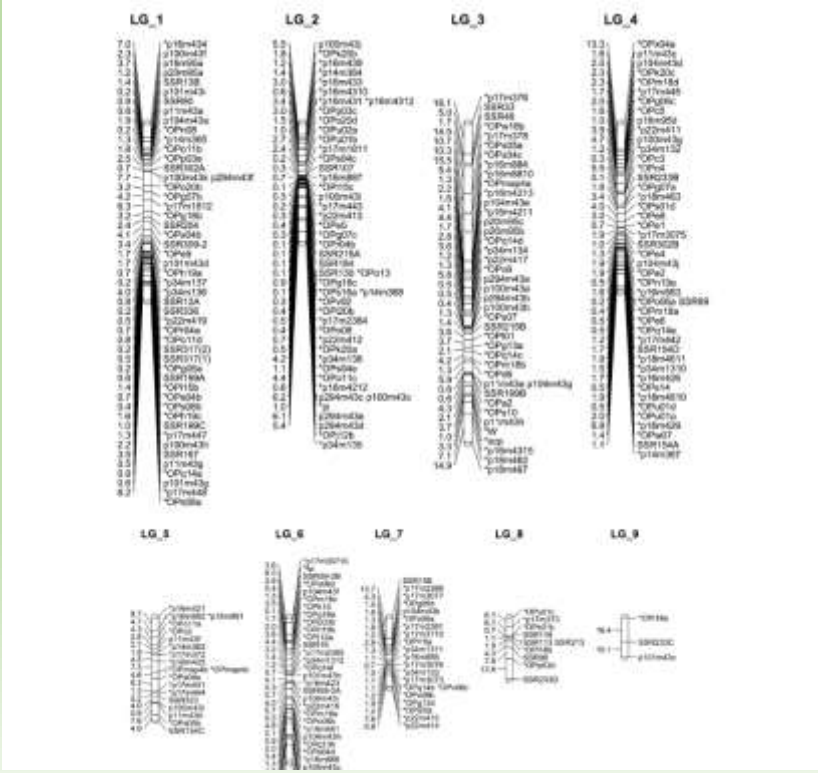
Top Organisms [Tree]
Avena strigosa x Avena wiestii *(1)*
Theobroma cacao *(1)*

Find related data

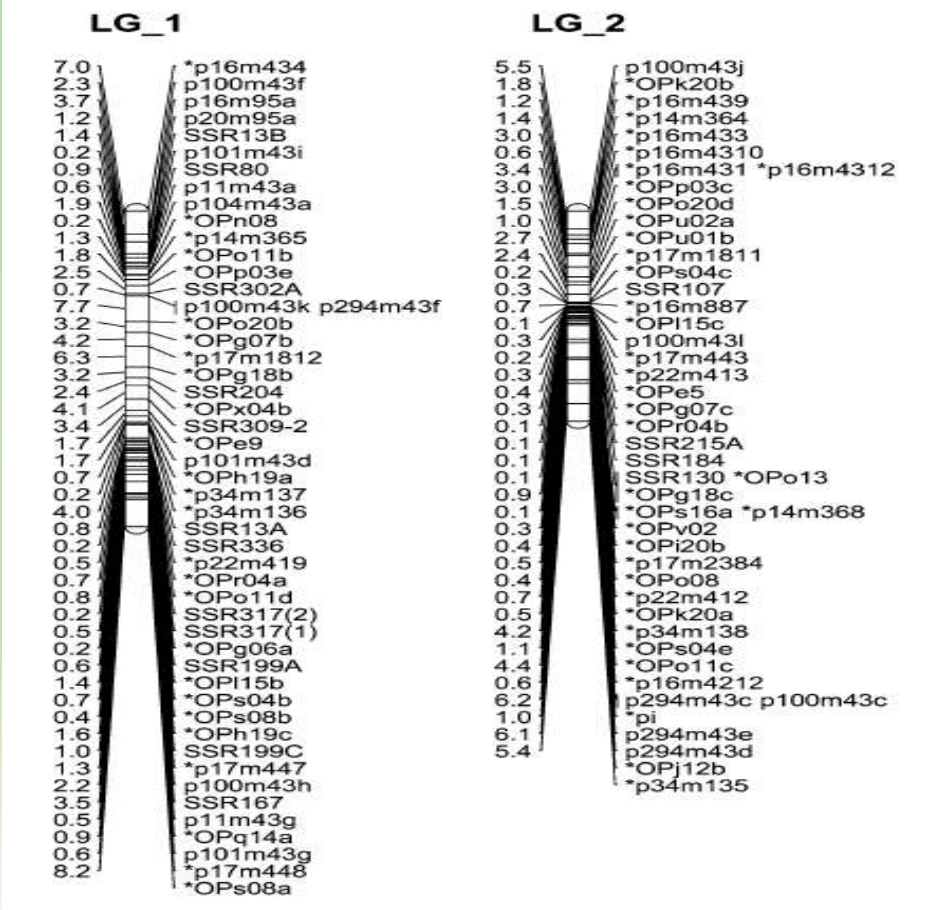
Search details

Recent activity

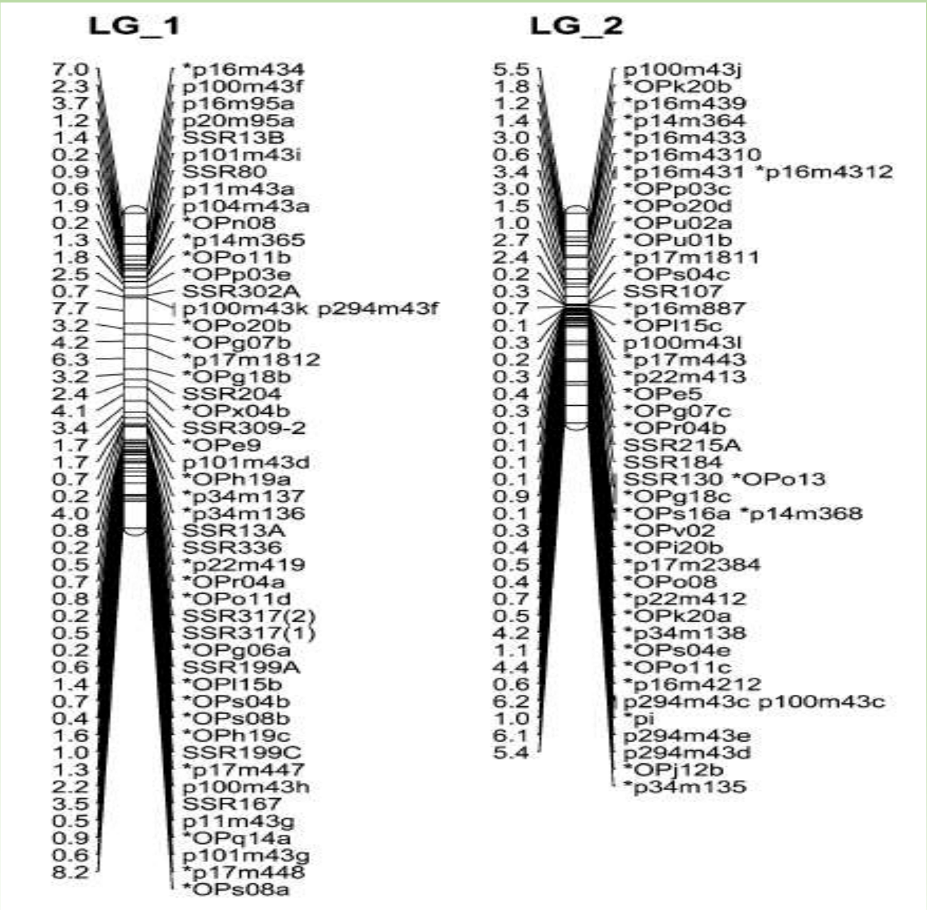
Genetic map processing



Genetic map processing

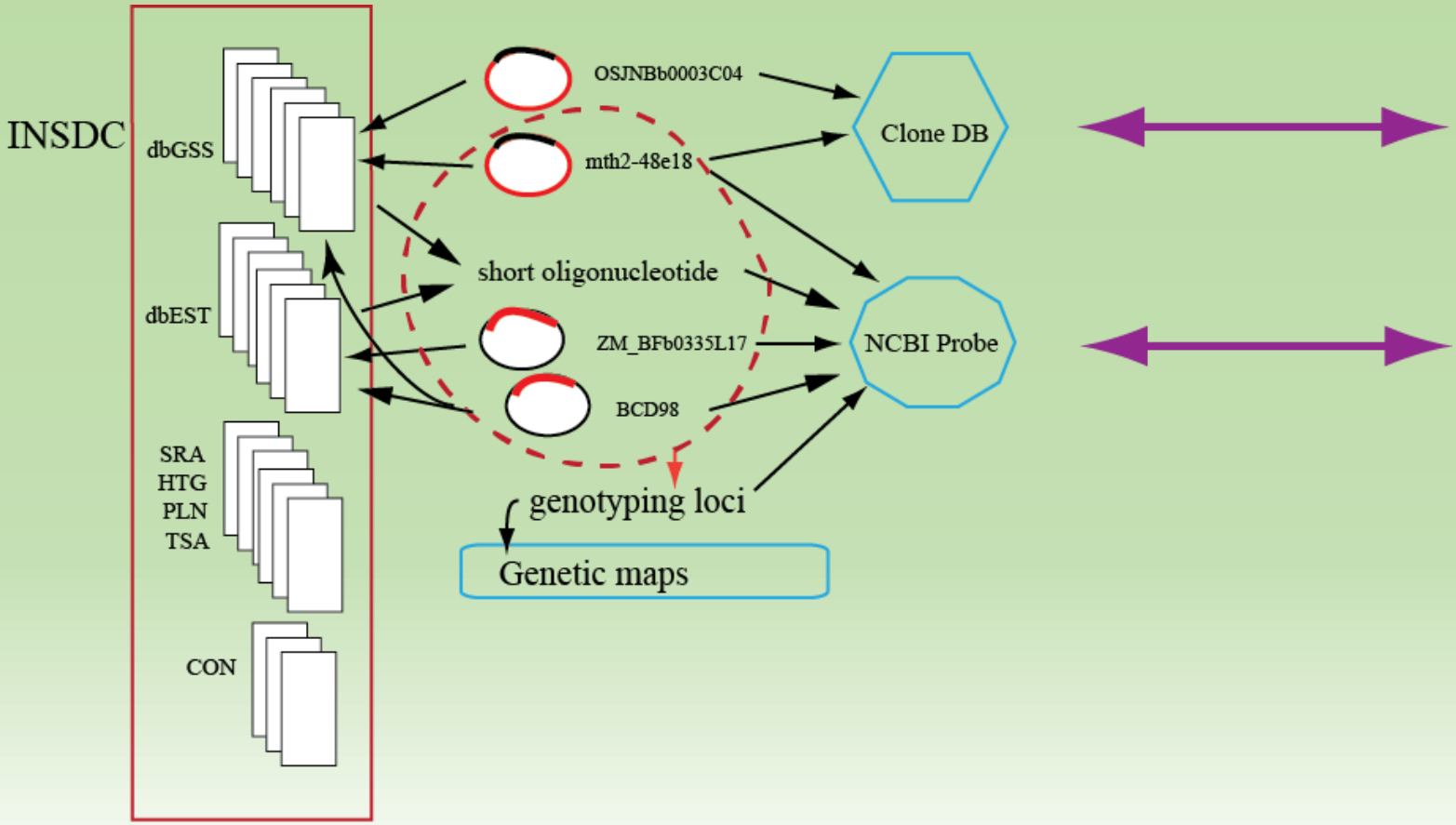


Genetic map processing

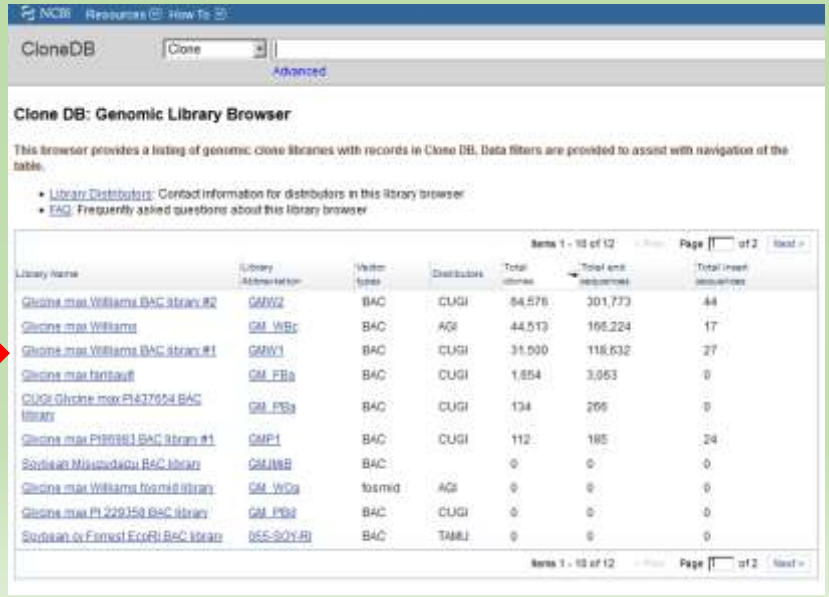



```
        <PROBESET_TRQ>AFLP_set:126609</PROBESET_TRQ>
</row>
<row>
        <MAP_MARKER_NAME>SSR167</MAP_MARKER_NAME>
        <MAP_CHROM>LG1</MAP_CHROM>
        <MAP_POS>75.7</MAP_POS>
        <PROBE_TRQ>SSR:11928</PROBE_TRQ>
</row>
<row>
        <MAP_MARKER_NAME>p11m43g</MAP_MARKER_NAME>
        <MAP_CHROM>LG1</MAP_CHROM>
        <MAP_POS>79.2</MAP_POS>
        <PROBESET_TRQ>AFLP_set:14771</PROBESET_TRQ>
</row>
<row>
        <MAP_MARKER_NAME>OPq14a</MAP_MARKER_NAME>
        <MAP_CHROM>LG1</MAP_CHROM>
        <MAP_POS>79.7</MAP_POS>
        <PROBE_TRQ>RAPD:1294</PROBE_TRQ>
</row>
<row>
        <MAP_MARKER_NAME>p101m43g</MAP_MARKER_NAME>
        <MAP_CHROM>LG1</MAP_CHROM>
        <MAP_POS>80.6</MAP_POS>
        <PROBESET_TRQ>AFLP_set:126700</PROBESET_TRQ>
</row>
<row>
        <MAP_MARKER_NAME>p17m448</MAP_MARKER_NAME>
        <MAP_CHROM>LG1</MAP_CHROM>
        <MAP_POS>81.2</MAP_POS>
        <PROBESET_TRQ>AFLP_set:15270</PROBESET_TRQ>
</row>
<row>
        <MAP_MARKER_NAME>OPs08a</MAP_MARKER_NAME>
        <MAP_CHROM>LG1</MAP_CHROM>
        <MAP_POS>89.4</MAP_POS>
        <PROBE_TRQ>RAPD:330</PROBE_TRQ>
</row>
<row>
        <MAP_MARKER_NAME>p100m43j</MAP_MARKER_NAME>
        <MAP_CHROM>LG2</MAP_CHROM>
        <MAP_POS>0</MAP_POS>
        <PROBESET_TRQ>AFLP_set:126609</PROBESET_TRQ>
</row>
<row>
        <MAP_MARKER_NAME>OPk20b</MAP_MARKER_NAME>
        <MAP_CHROM>LG2</MAP_CHROM>
        <MAP_POS>5.5</MAP_POS>
        <PROBE_TRQ>RAPD:222</PROBE_TRQ>
</row>
<row>
        <MAP_MARKER_NAME>p16m439</MAP_MARKER_NAME>
        <MAP_CHROM>LG2</MAP_CHROM>
        <MAP_POS>7.3</MAP_POS>
        <PROBESET_TRQ>AFLP_set:15184</PROBESET_TRQ>
</row>
<row>
        <MAP_MARKER_NAME>p14m364</MAP_MARKER_NAME>
        <MAP_CHROM>LG2</MAP_CHROM>
        <MAP_POS>8.5</MAP_POS>
        <PROBESET_TRQ>AFLP_set:15007</PROBESET_TRQ>
</row>
<row>
        <MAP_MARKER_NAME>p16m433</MAP_MARKER_NAME>
        <MAP_CHROM>LG2</MAP_CHROM>
        <MAP_POS>9.9</MAP_POS>
        <PROBESET_TRQ>AFLP_set:15184</PROBESET_TRQ>
```

CloneDB - http://www.ncbi.nlm.nih.gov/clone/



CloneDB – metadata and placement



CloneDB – metadata and placement

Glycine max Williams BAC library #1

Library Summary

Library Abbreviation:	GMW1
Organism:	Glycine max
Vector type(s):	BAC
# clones Clone DB:	31,600
# end sequences Clone DB:	116,632
# insert sequences Clone DB:	27
# clones with both ends sequenced:	27,796

Library Details

DNA Source | Library Construction | Library Statistics | Alternate Library Names | Distributors

Library segment	Cultivar	Sex	Tissue
ALL	Williams 82	hermaphrodite	etiolated leaf

DNA Source | Library Construction | Library Statistics | Alternate Library Names | Distributors

Library segment	Vector Name	Vector Cloning Site(s)	Insert Cloning Site(s)	Vector Selection	Insert Prep Method	Lab Host	Vector Delivery Method
1	pBeloBAC11	HindIII	HindIII	chloramphenicol	Partial digestion	DH10B	electroporation

DNA Source | Library Construction | Library Statistics | Alternate Library Names | Distributors

Library segment	Avg insert(kb)	Coverage	Plate range(s)	% Plated
1	150	5.42	1 to 105	1

DNA Source | Library Construction | Library Statistics | Alternate Library Names | Distributors

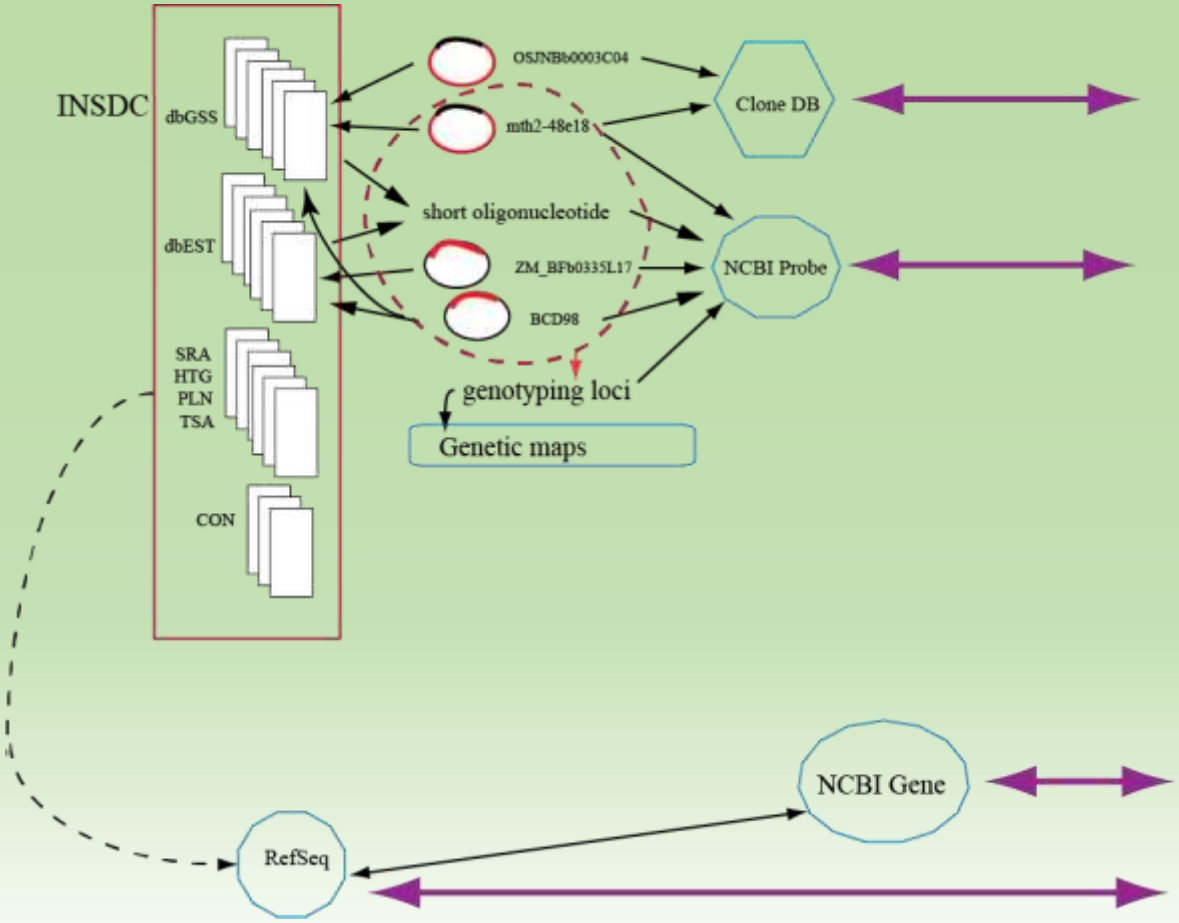
Alternate library name(s)	Alternate library abbreviation(s)
ISU Hindi BAC library	GM_Willa, Williams 82, Gm_ISU001

DNA Source | Library Construction | Library Statistics | Alternate Library Names | Distributors

Distributor Logo	Distributor Type	Contact	More Info
CUGI	Creator Academic	Clemson University Genomics Institute (CUGI) Email: orders@genome.clemson.edu	Address

CloneDB – metadata and placement

NCBI RefSeq - http://www.ncbi.nlm.nih.gov/refseq/



Single source, multiple sources

Nucleotide | Nucleotide | Advanced

Display Settings: GenBank | Send:

Zea mays CASP-like protein 13 (LOC100276350), mRNA

NCBI Reference Sequence: NM_001150159.1

FASTA Graphics

Go to:

```
LOCUS       NM_001150159            872 bp    mRNA    linear   PLN 12-OCT-2014
DEFINITION  Zea mays CASP-like protein 13 (LOC100276350), mRNA.
ACCESSION   NM_001150159
VERSION     NM_001150159.1  GI:226508149
KEYWORDS    RefSeq.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACMAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 872)
  AUTHORS   Alexandrov NN, Brover VV, Freidin S, Troukhan ME, Tatarinova TV,
            Zhang H, Swaller TJ, Lu YP, Bouck J, Flavell RB and Feldmann KA.
  TITLE     Insights into corn genes derived from large-scale cDNA sequencing
  JOURNAL   Plant Mol. Biol. 69 (1-2), 179-194 (2009)
   PUBMED   18937034
COMMENT     PROVISIONAL REFSEQ: This record has not yet been subject to final
            NCBI review. The reference sequence was derived from EU961555.1.

            ##Evidence-Data-START##
            Transcript exon combination :: EU961555.1 [ECO:0000332]
            ##Evidence-Data-END##
```

Nucleotide | Nucleotide | Advanced

Display Settings: GenBank | Send:

Homo sapiens toll-like receptor 4 (TLR4), transcript variant 3, mRNA

NCBI Reference Sequence: NM_003266.3

FASTA Graphics

Go to:

```
LOCUS       NM_003266               5781 bp    mRNA    linear   PRI 25-MAY-2014
DEFINITION  Homo sapiens toll-like receptor 4 (TLR4), transcript variant 3,
            mRNA.
ACCESSION   NM_003266 NR_024168
VERSION     NM_003266.3  GI:373432601
KEYWORDS    RefSeq.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 5781)
  AUTHORS   Chen YF, Shiau AL, Wang SM, Yang JJ, Chang SJ, Wu CL and Wu IS.
  TITLE     Zhankuic acid A isolated from Taiwanofungus camphoratus is a novel
            selective TLR4/MD-2 antagonist with anti-inflammatory properties
  JOURNAL   J. Immunol. 192 (6), 2778-2786 (2014)
```

⋮

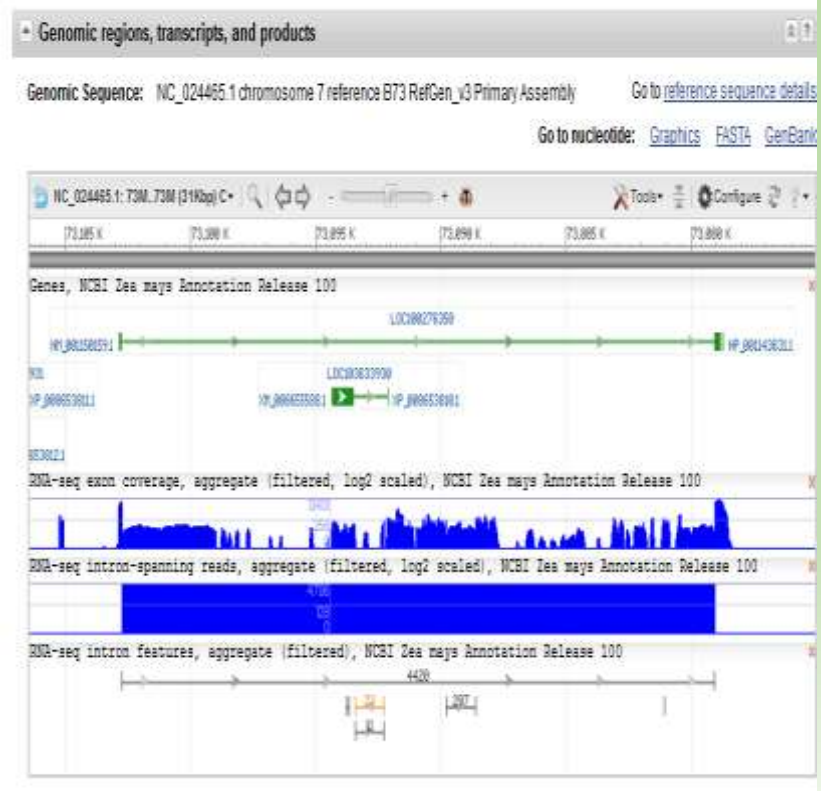
```
  AUTHORS   Rock FL, Hardiman G, Timans JC, Kastelein RA and Bazan JF.
  TITLE     A family of human receptors structurally related to Drosophila Toll
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 95 (2), 588-593 (1998)
   PUBMED   9435236
REFERENCE   10  (bases 1 to 5781)
  AUTHORS   Medzhitov R, Preston-Hurlburt P and Janeway CA Jr.
  TITLE     A human homologue of the Drosophila Toll protein signals activation
            of adaptive immunity
  JOURNAL   Nature 388 (6643), 394-397 (1997)
   PUBMED   9237759
COMMENT     REVIEWED REFSEQ: This record has been curated by NCBI staff. The
            reference sequence was derived from DA187988.1, BC143841.1,
            BC025294.1, AK228155.1, BG622357.1 and DR218008.1.
            On or before Jan 21, 2012 this sequence version replaced
            gi:207028451, gi:19924147.

            Summary: The protein encoded by this gene is a member of the
            Toll-like receptor (TLR) family which plays a fundamental role in
            pathogen recognition and activation of innate immunity. TLRs are
            highly conserved from Drosophila to humans and share structural and
            functional similarities. They recognize pathogen-associated
            molecular patterns that are expressed on infectious agents, and
```

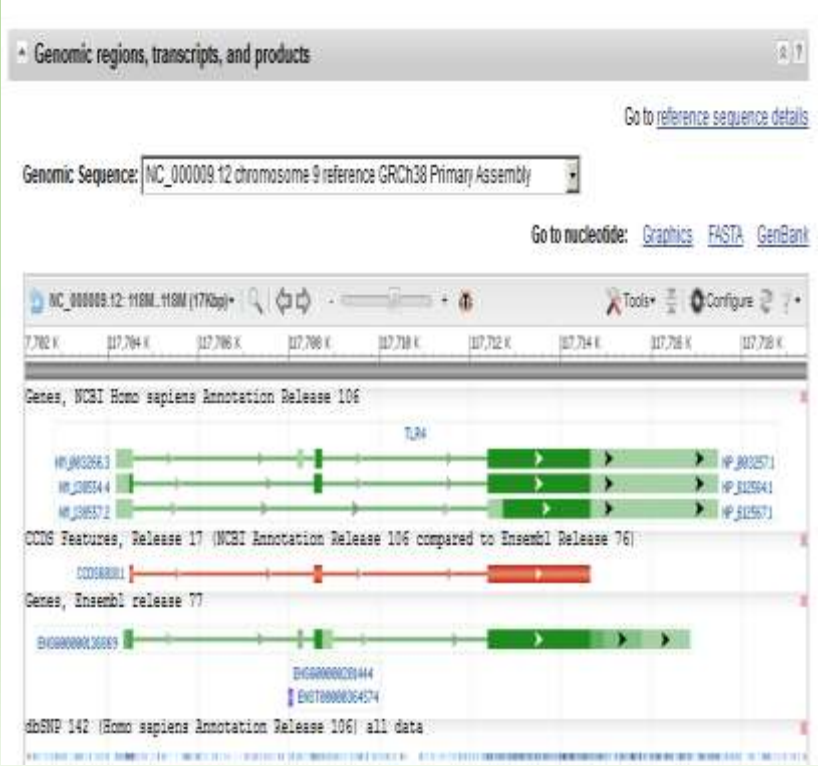
Single source, multiple sources

```
##Evidence-Data-END##
FEATURES             Location/Qualifiers
     source          1..872
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /db_xref="taxon:4577"
                     /chromosome="7"
     gene            1..872
                     /gene="LOC100276350"
                     /note="CASP-like protein 13"
                     /db_xref="GeneID:100276350"
                     /gene="LOC100276350"
                     /note="zmCASPL5B3"
                     /codon_start=1
                     /product="CASP-like protein 5B3"
                     /protein_id="NP_001143631.1"
                     /db_xref="GI:226508150"
                     /db_xref="GeneID:100276350"
                     /translation="MKDVVGSPGTWSGMALRLSQCVSAGASMGAMAIAYGFSNYTAFC
                     YLIASMGLQLLWSFGLACLDVYSLKTKRDLRNPVLVSLFVVGDWVTAILSFAAASASA
                     GVTILFERDVSFCRMYPQLSCGRYALSVVLAFITWSFIATSAVSMFWLLPSL"
     misc_feature    215..283
                     /gene="LOC100276350"
                     /experiment="experimental evidence, no additional details
                     recorded"
                     /note="propagated from UniProtKB/Swiss-Prot (B6T990.1);
                     transmembrane region"
     misc_feature    299..361
                     /gene="LOC100276350"
                     /experiment="experimental evidence, no additional details
```

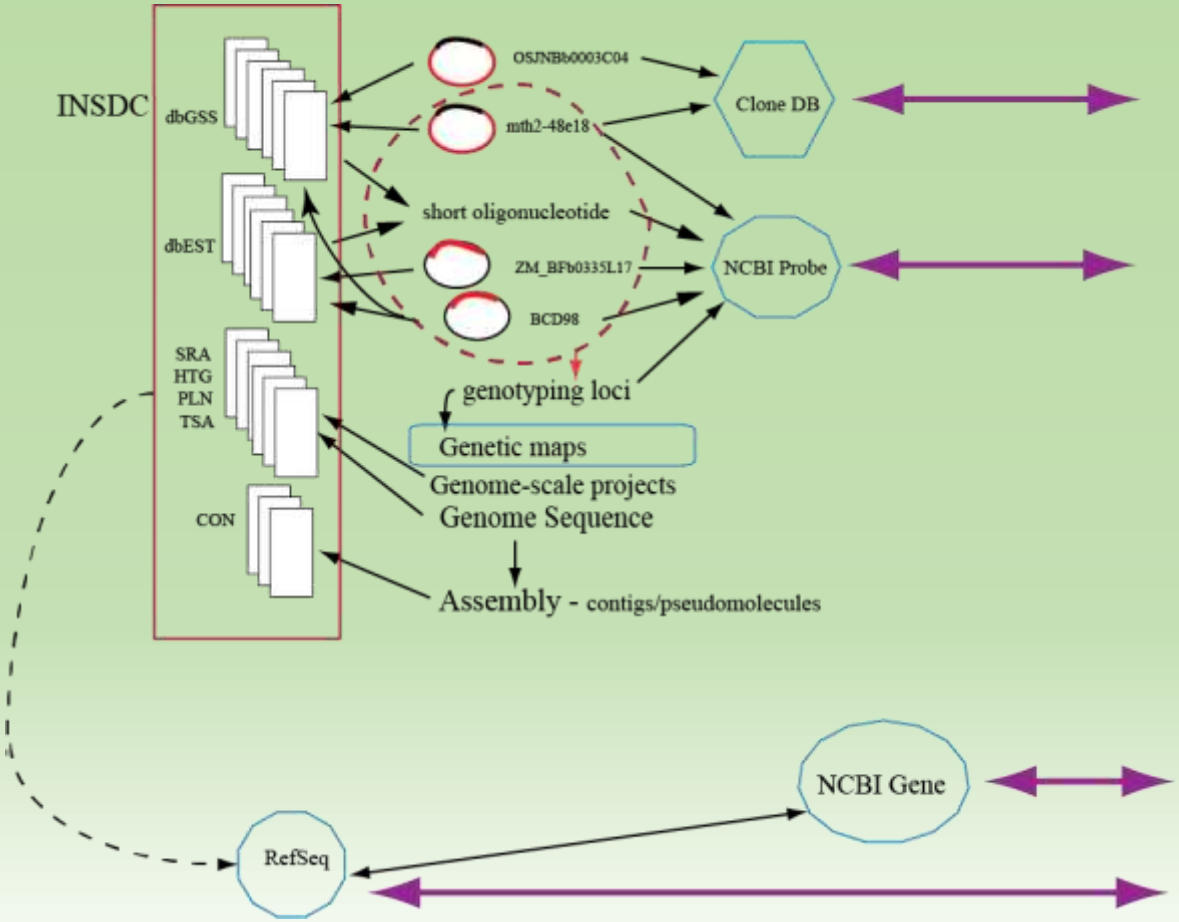
```
                                   ERS025082, ERS025084 [ECO:0000348]
          ##Evidence-Data-END##
          COMPLETENESS: complete on the 3' end.
PRIMARY   REFSEQ_SPAN        PRIMARY_IDENTIFIER PRIMARY_SPAN      COMP
          1-278              DA187988.1         1-278
          279-2980           BC143841.1         1-2702
          2981-3242          BC025294.1         2480-2741
          3243-5161          AK226155.1         2998-4916
          5162-5608          BG622357.1         121-567
          5609-5781          DA218006.1         386-558
FEATURES             Location/Qualifiers
     source          1..5781
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="9"
                     /map="9q33.1"
     gene            1..5781
                     /gene="TLR4"
                     /gene_synonym="ARMD10; CD284; TLR-4; TOLL"
                     /note="toll-like receptor 4"
                     /db_xref="GeneID:7099"
                     /db_xref="HGNC:HGNC:11850"
                     /db_xref="MIM:603030"
                     /gene="TLR4"
                     /gene_synonym="ARMD10; CD284; TLR-4; TOLL"
                     /inference="alignment:Splign:1.39.8"
     exon            392..511
                     /gene="TLR4"
                     /gene_synonym="ARMD10; CD284; TLR-4; TOLL"
                     /inference="alignment:Splign:1.39.8"
     misc_feature    401..403
                     /gene="TLR4"
                     /gene_synonym="ARMD10; CD284; TLR-4; TOLL"
                     /note="upstream in-frame stop codon"
     exon            512..678
                     /gene="TLR4"
                     /gene_synonym="ARMD10; CD284; TLR-4; TOLL"
molecular patterns that are expressed on infectious agents, and
```

Gene to RefSeq
one-to-one or one-to-many

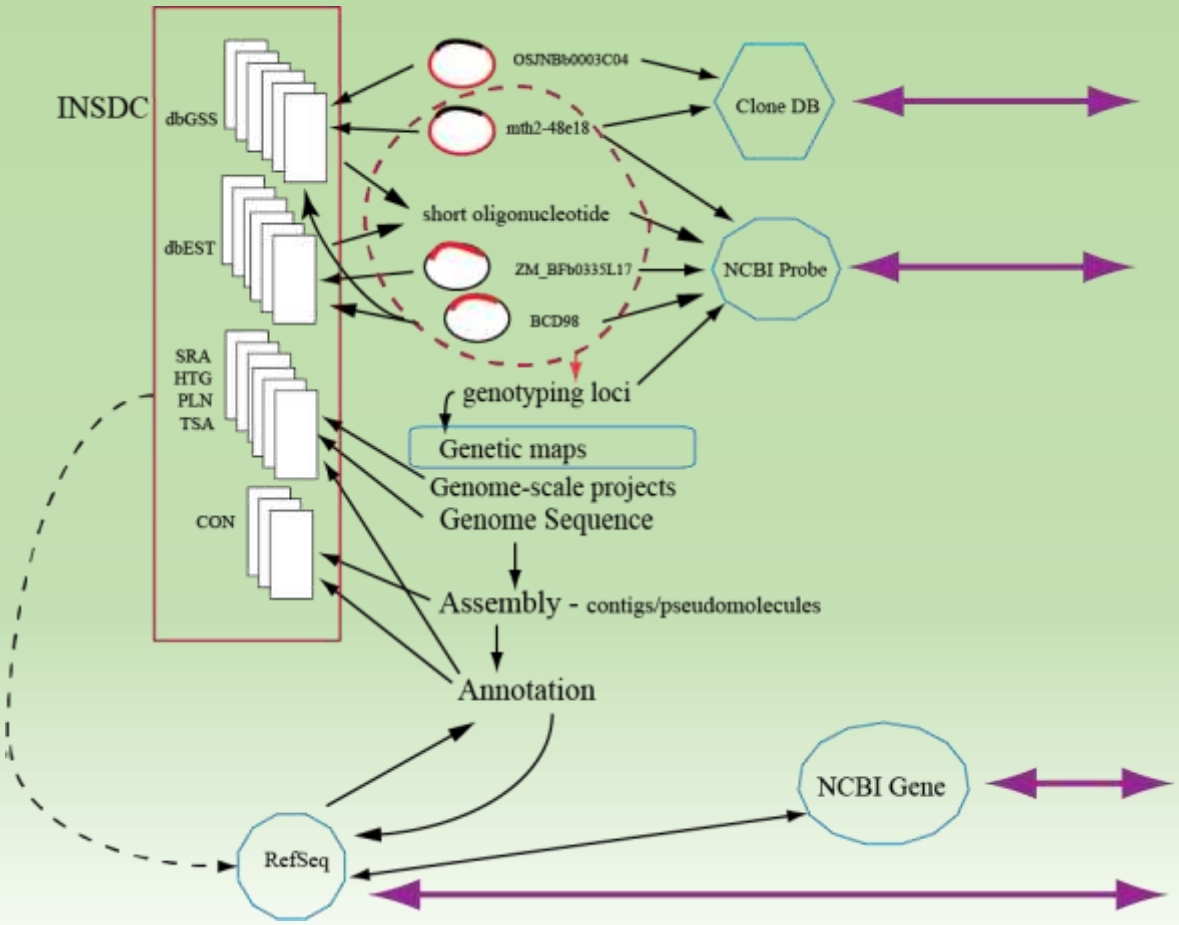




Genome sequence



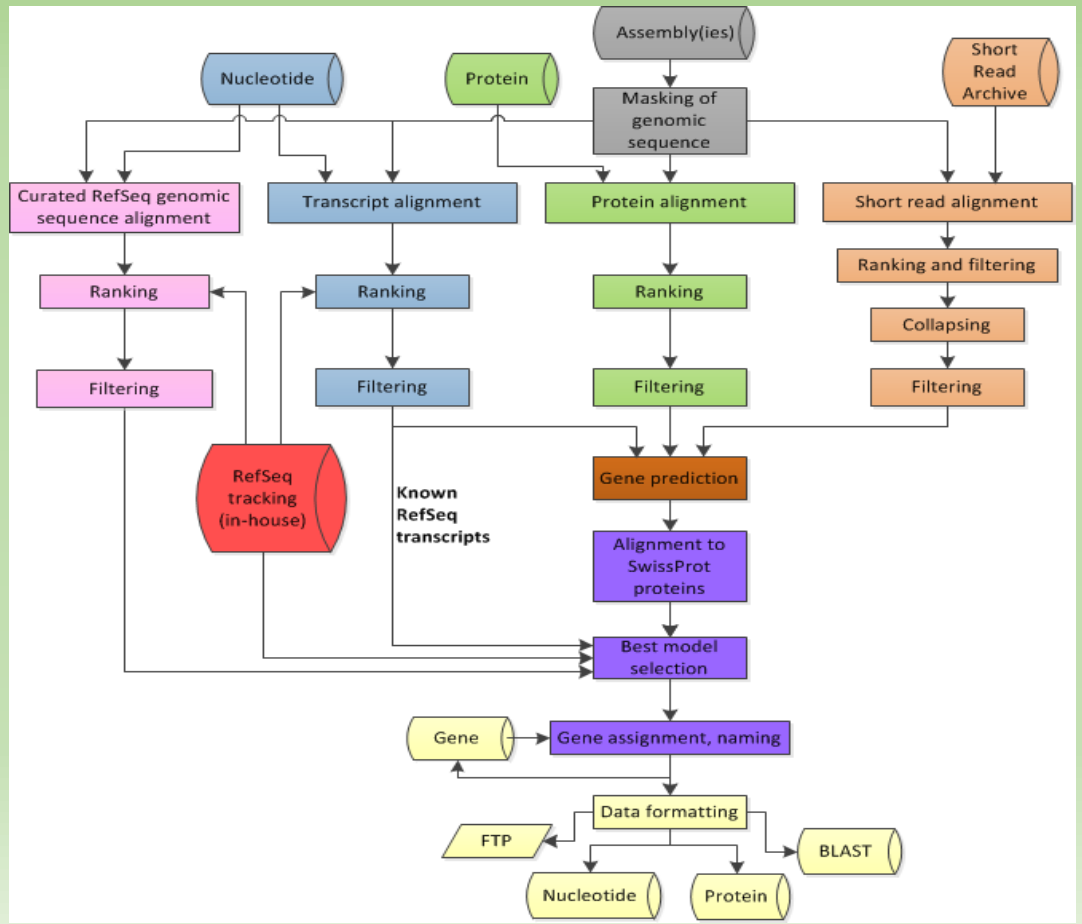
Annotation


INSDC
dbGSS
dbEST
SRA
HTG
PLN
TSA
CON
OSJNBb0003C04
mth2-48e18
short oligonucleotide
ZM_BFb0335L17
BCD98
Clone DB
NCBI Probe
genotyping loci
Genetic maps
Genome-scale projects
Genome Sequence
Assembly - contigs/pseudomolecules
Annotation
NCBI Gene
RefSeq

Eukaryotic Genome Annotation

- Input “substrate” is a RefSeq genome (contigs or chromosomes)
- Input “reagents” are sequence records:
  - INSDC mRNA
  - INSDC protein
  - EST
  - RNA-seq
  - NM/NP RefSeq
- Output is a collection of RefSeq nuc/prot pairs, each pair belonging to an associated NCBI Gene record

Eukaryotic Genome Annotation



Reagents
- RefSeqs, GenBank transcripts and proteins
- RNA-seq data

Alignments
- Splign and proSplign

Best Alignments
- Filter to obtain best alignments

Predict Models
- Gnomon predicts gene models, best models added to RefSeq set (XM_/XP, XR_)

Ortholog calls
- Based on protein identity and synteny calculation

Assign gene IDs and names
- Orthology used to assign names and locus types

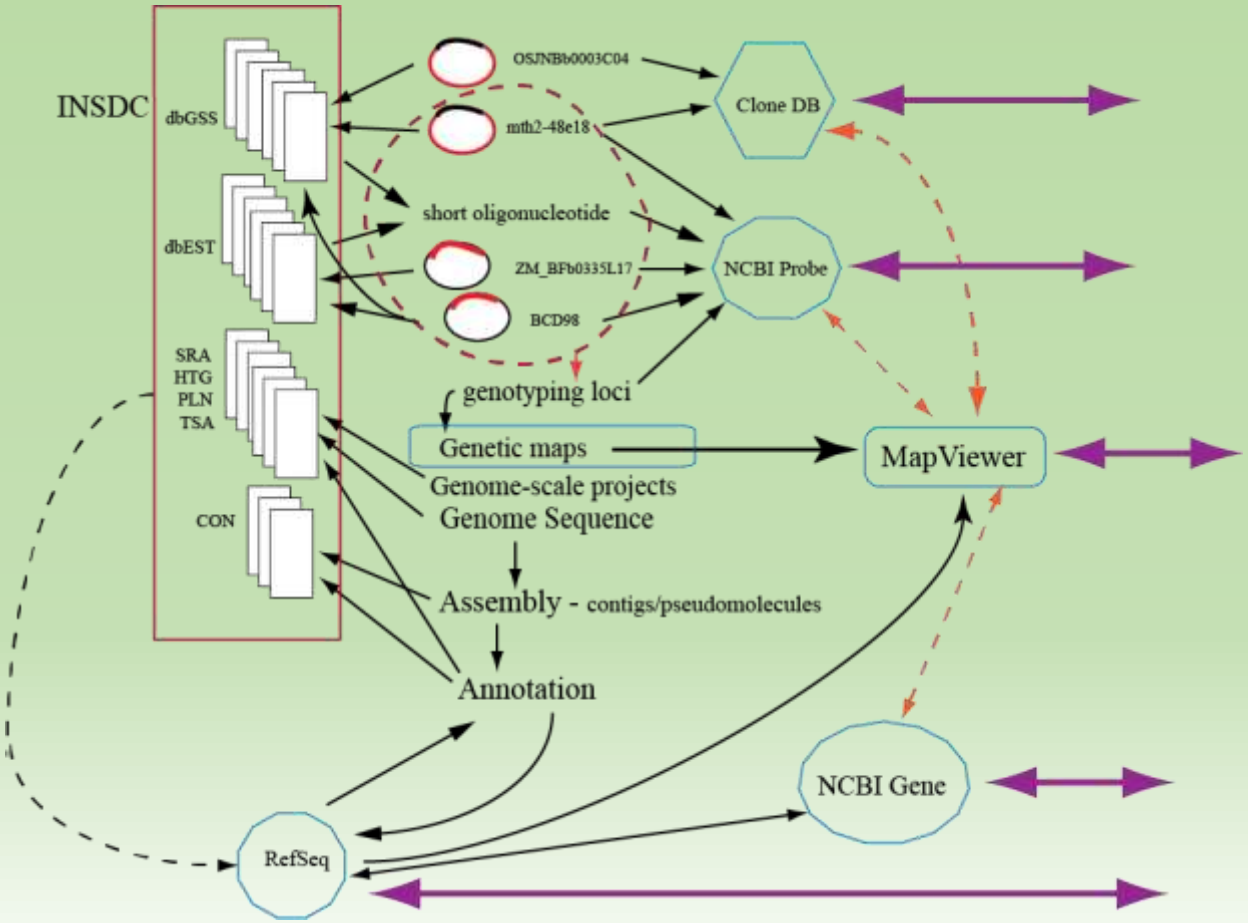
*Speed (5-10 days), *RNA-seq data for gene prediction, *using aligned transcripts for 'gap-filling', *enhanced public reports

Visit Poster P0051 for more on genome annotation

Plant genomes – as of 2015

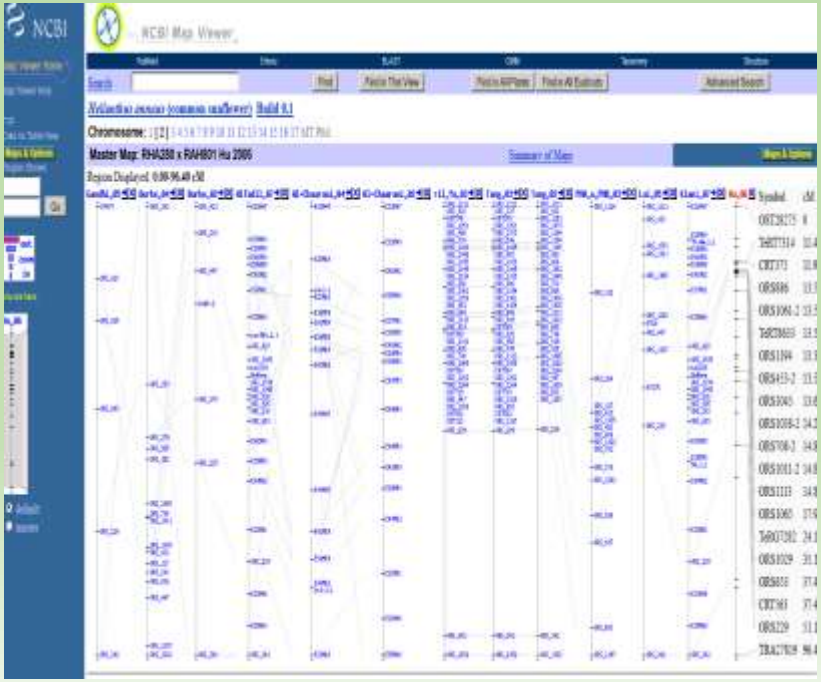
- 146 plants have 246 nuclear genomes submitted
  - 43 of these plants have chromosome assemblies
- 561 plants have only organelle genomes submitted
- 31 plants have annotated genomes
  - 4 are presented with the submission annotation

Map Viewer - http://www.ncbi.nlm.nih.gov/mapview/

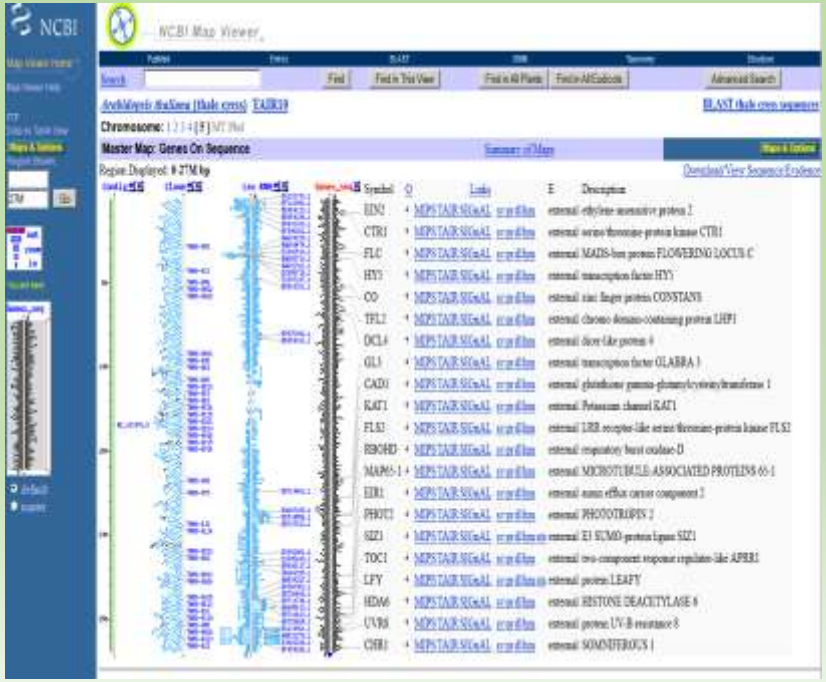


Map Viewer – display tool for genome units

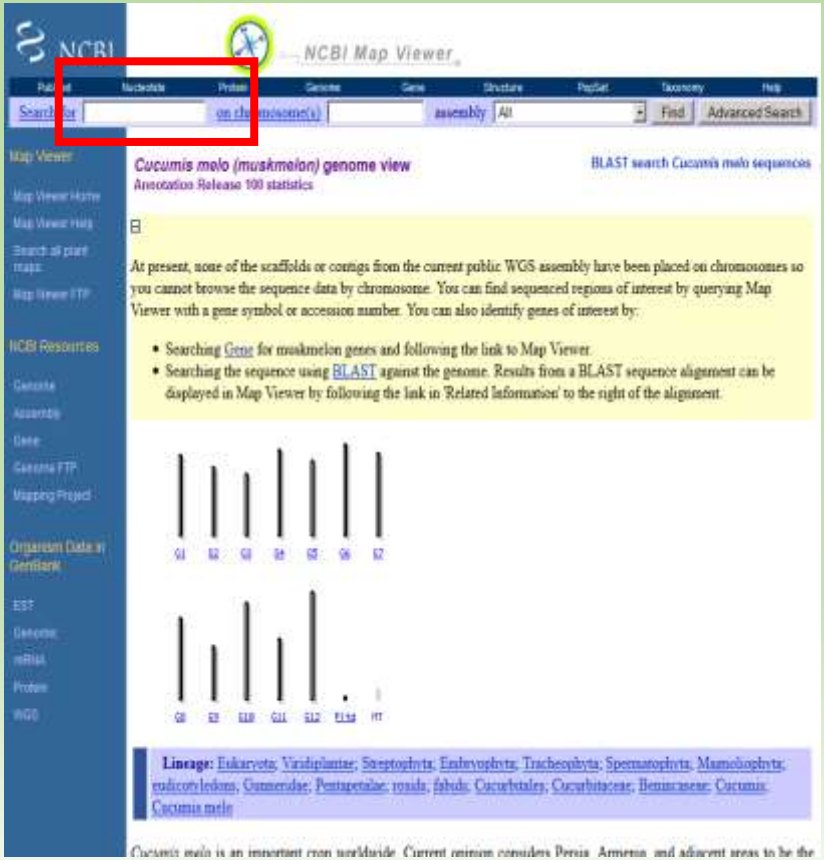
Genetic Maps



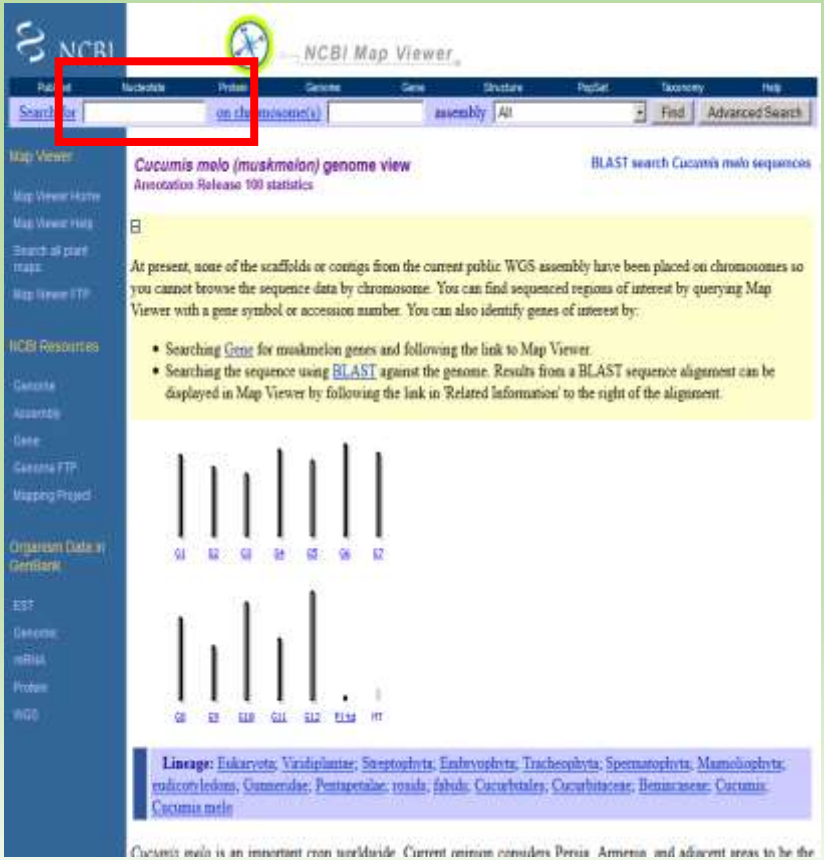
Sequence Maps

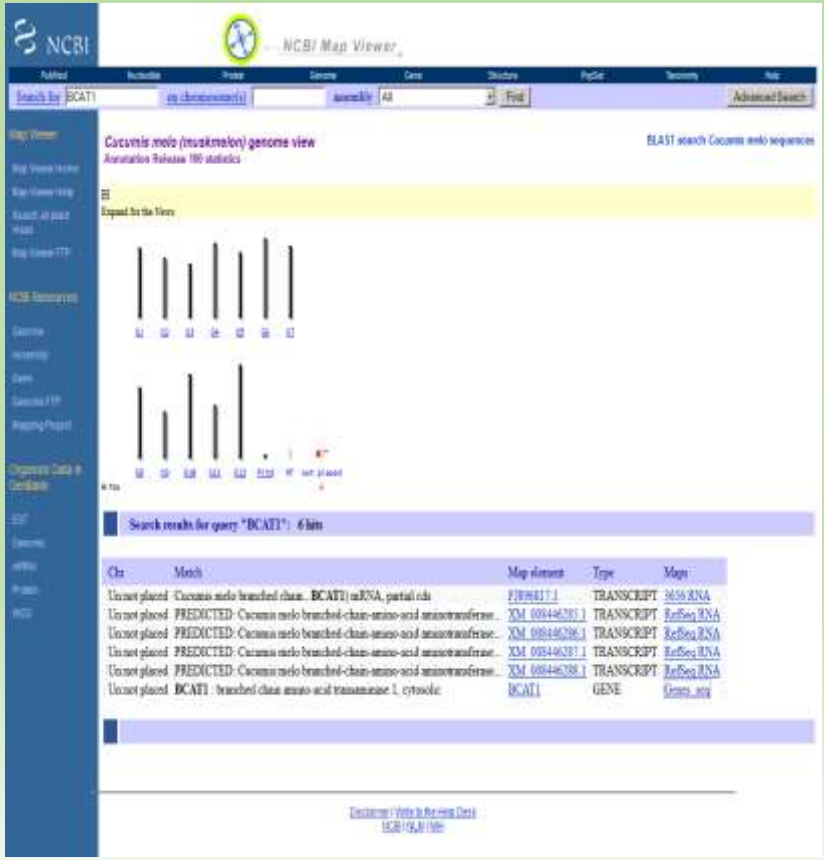


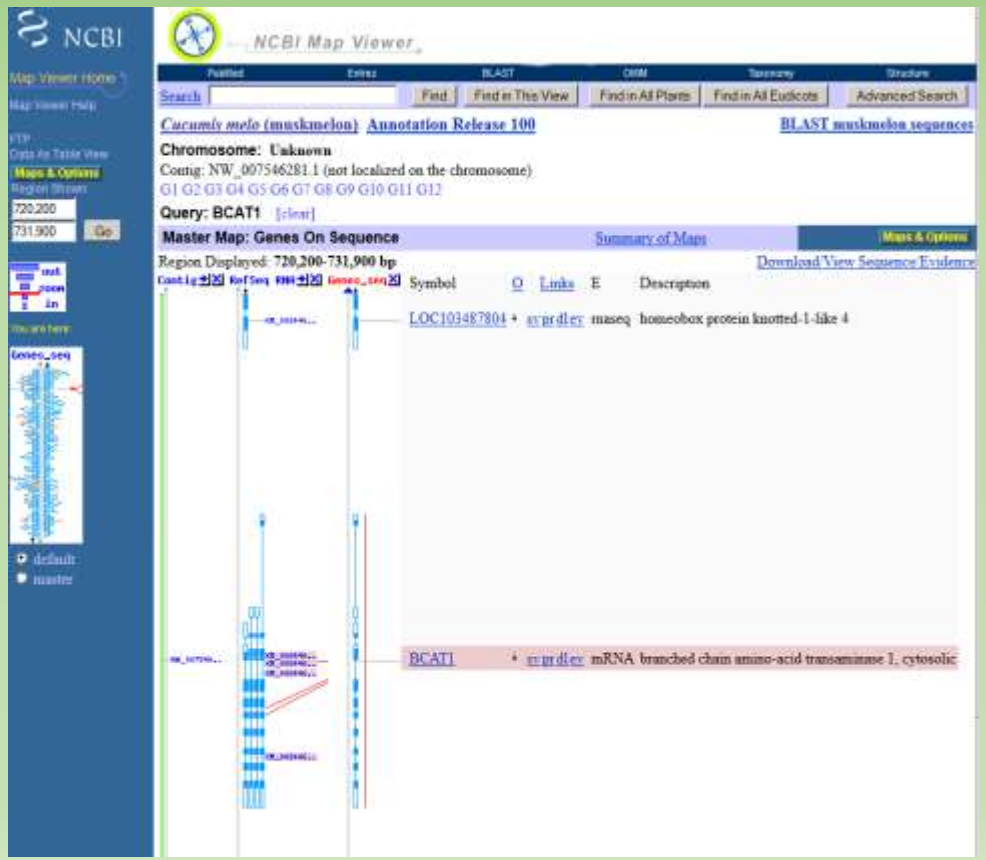
Text search for gene name – the backdoor to unplaced sequence

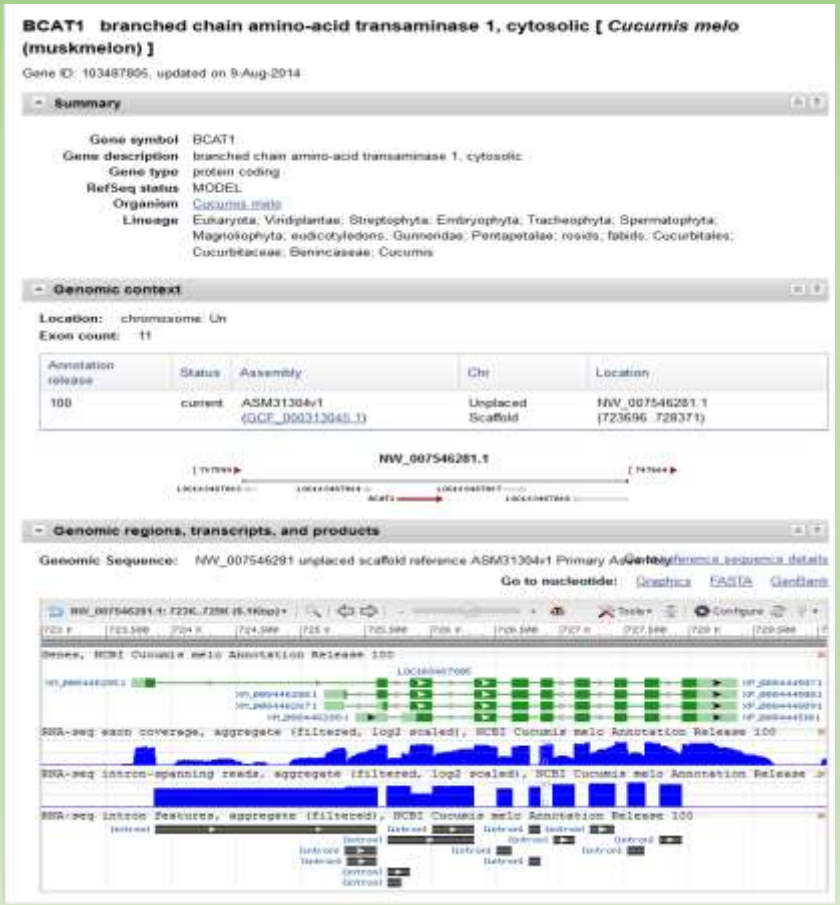


Text search for gene name – the backdoor to unplaced sequence





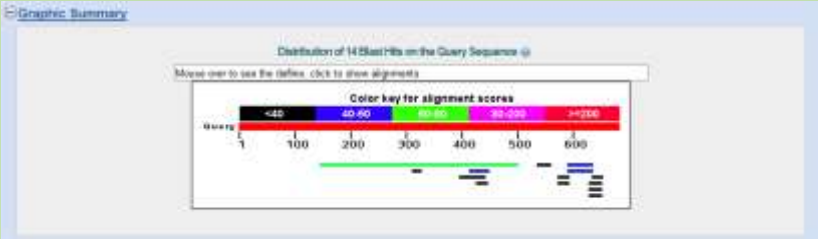

NCBI
NCBI Map Viewer
Search
Find
Find in This View
Find in All Plants
Find in All Eudicots
Advanced Search
Cucumis melo (muskmelon) Annotation Release 100
BLAST muskmelon sequences
Chromosome: Unknown
Contig: NW_007546281.1 (not localized on the chromosome)
G1 G2 G3 G4 G5 G6 G7 G8 G9 G10 G11 G12
Query: BCAT1 [clear]
Master Map: Genes On Sequence
Summary of Maps
Maps & Options
Region Displayed: 720,200-731,900 bp
Download/View Sequence Evidence
Symbol
Links
Description
LOC103487804 + avprdlev maseq homeobox protein knotted-1-like 4
BCAT1 + avprdlev mRNA branched chain amino-acid transaminase 1, cytosolic

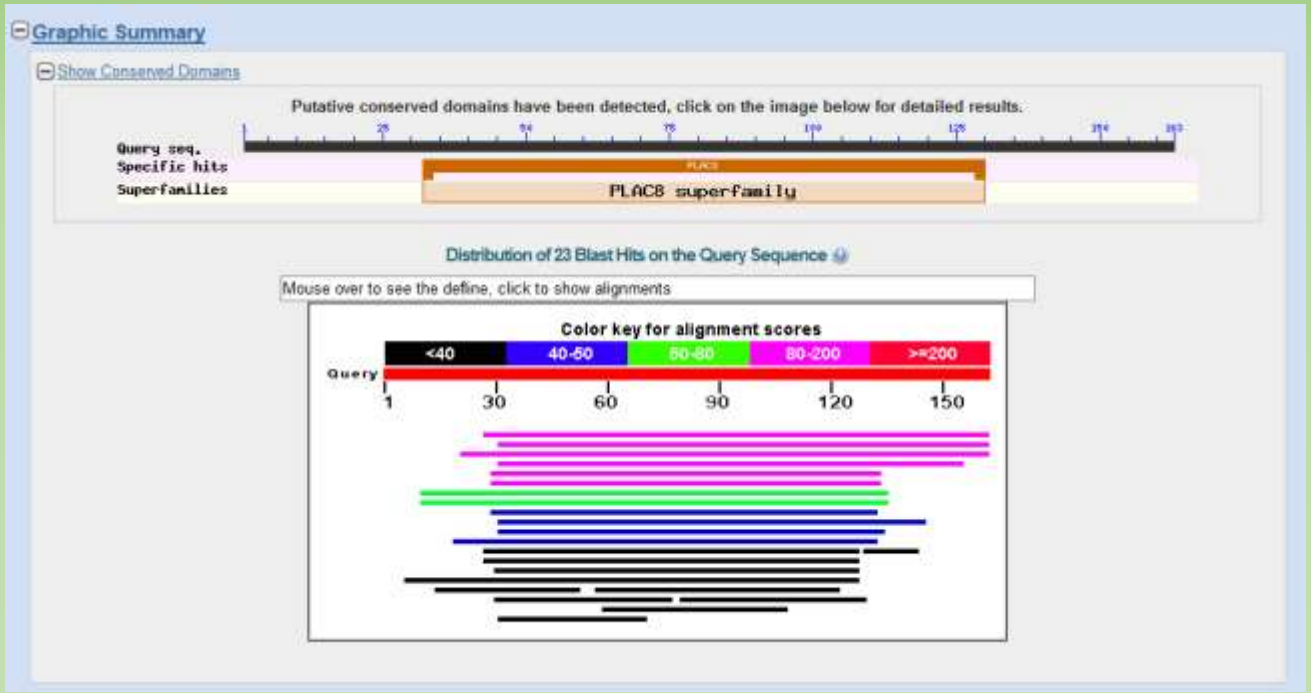

BCAT1 branched chain amino-acid transaminase 1, cytosolic [Cucumis melo (muskmelon)]
Gene ID: 103487806, updated on 9-Aug-2014
Summary
Gene symbol BCAT1
Gene description branched chain amino-acid transaminase 1, cytosolic
Gene type protein coding
RefSeq status MODEL
Organism Cucumis melo
Lineage Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Cucurbitales; Cucurbitaceae; Benincasaeae; Cucumis
Genomic context
Location: chromosome: Un
Exon count: 11
Annotation release
Status
Assembly
Chr
Location
100
current
ASM31304v1
Unplaced Scaffold
NW_007546281.1
(723696..728371)
NW_007546281.1
Genomic regions, transcripts, and products
Genomic Sequence: NW_007546281 unplaced scaffold reference ASM31304v1 Primary Assembly
Go to nucleotide: Graphics FASTA GenBank

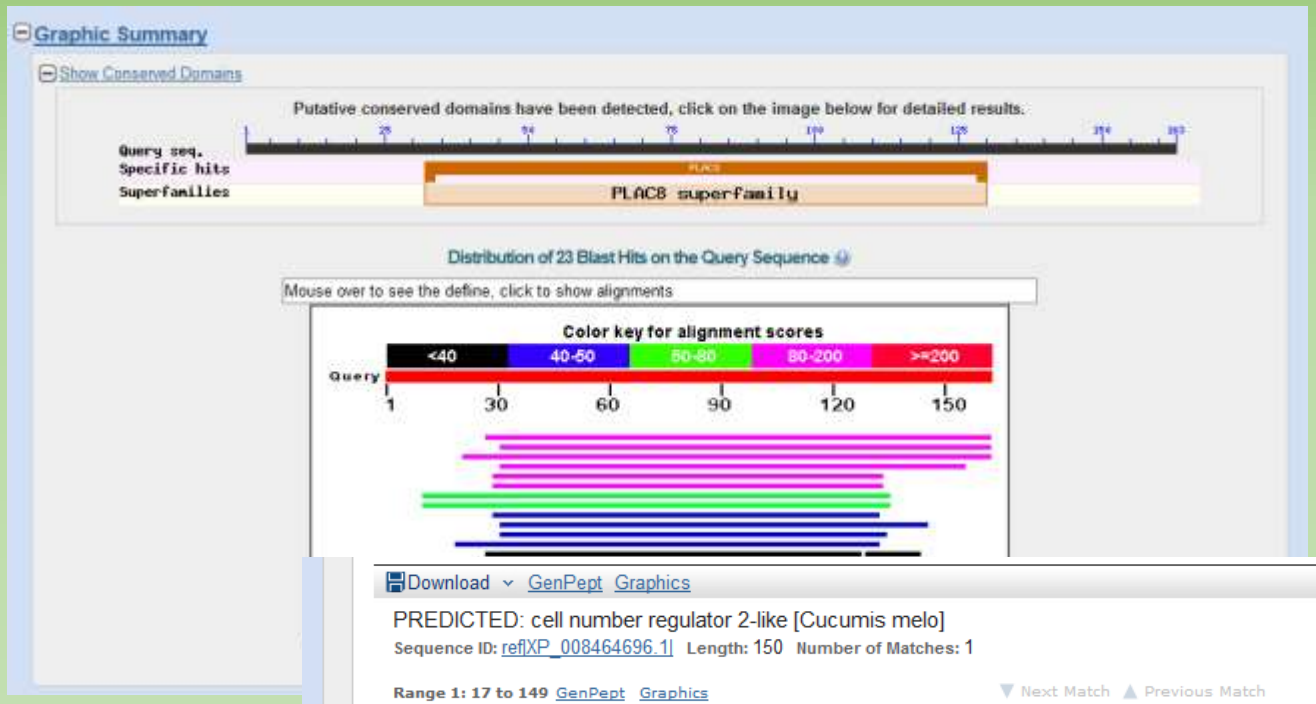
Finding an ortholog and the genome context

- Fruit weight QTL identified in tomato in 1990s
- The tomato gene was cloned in 2000
- Are there fruit weight orthologs in other crops such as apple, melon, or grape?

BLAST of melon RefSeq mRNA with tomato mRNA




Graphic Summary
Show Conserved Domains
Putative conserved domains have been detected, click on the image below for detailed results.
Query seq.
Specific hits
Superfamilies
PLACB superfamily
Distribution of 23 Blast Hits on the Query Sequence
Mouse over to see the define, click to show alignments
Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
30
60
90
120
150



Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: cell number regulator 2-like [Cucumis melo]

Sequence ID: ref|XP_008464696.1| Length: 150 Number of Matches: 1

Range 1: 17 to 149 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
154 bits(388)	3e-47	Compositional matrix adjust.	69/133(52%)	95/133(71%)	1/133(0%)

```
Query  32   WSTGLCHCFDDPANCLVTSVCPCITFGQISEILNKGTTSCGSRGALYCLLG-LTGLPSLY  90
            WS+GLC CF D  +C  T+ CPC+ FGQ SEI+++G+TSC     ++CL+   T    LY
Sbjct  17   WSSGLCDCFSDMGSCCCTTWCPCVPFGQASEIIDEGSTSCFGNALIFCLIASFTPCICLY  76

Query  91   SCFYRSKMRGQYDLEEAPCVDCLVHVFCEPCALCQEYRELKNRGFDMGIGWQANMDRQSR  150
            +C YRS++R +Y+L+E PC DC VH +C  CA+CQEYRELKNRGF+M IGWQ N+ RQ++
Sbjct  77   TCSYRSRLRRKYNLKETPCNDCCVHCWCWSCAMCQEYRELKNRGFNMHIGWQENVQRQNK  136

Query  151  GVTMPPYHAGMTR  163
            G+ +PP   G  +
Sbjct  137  GIEIPPTVPGQMK  149
```

Related Information

Gene - associated gene details

Display Settings: Full Report

Send to:

Filters activated: Current only. Clear all to show 1 items.

LOC103502518 cell number regulator 2-like [*Cucumis melo* (muskmelon)]

Gene ID: 103502518, updated on 9-Aug-2014

Summary

Gene symbol	LOC103502518
Gene description	cell number regulator 2-like
Gene type	protein coding
RefSeq status	MODEL
Organism	Cucumis melo
Lineage	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Cucurbitales; Cucurbitaceae; Benincaseae; Cucumis

Genomic context

Location: chromosome: Un

Exon count: 4

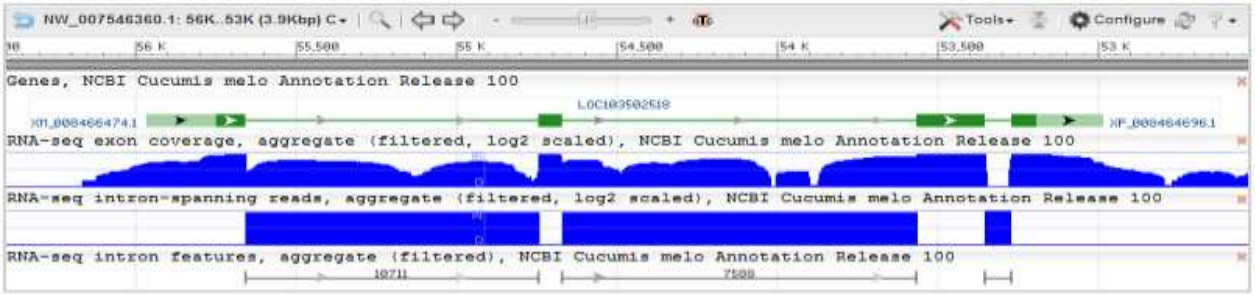
Annotation release	Status	Assembly	Chr	Location
100	current	ASM31304v1 (GCF_000313045.1)	Unplaced Scaffold	NW_007546360.1 (52988..55967, complement)

Genomic regions, transcripts, and products

Genomic Sequence: NW_007546360 unplaced scaffold reference ASM31304v1 Primary Assembly

Go to reference sequence details

Go to nucleotide: Graphics FASTA GenBank



Bibliography

▼ Next ▲ Previous Descriptions

Related Information

Gene - associated gene details

Display Settings: Full Report

Send to:

Filters activated: Current only. Clear all to show 1 items.

LOC103502518 cell number regulator 2-like [*Cucumis melo* (muskmelon)]

Gene ID: 103502518, updated on 9-Aug-2014

Summary

Gene symbol	LOC103502518
Gene description	cell number regulator 2-like
Gene type	protein coding
RefSeq status	MODEL
Organism	Cucumis melo
Lineage	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Cucurbitales; Cucurbitaceae; Benincaseae; Cucumis

Genomic context

Location: chromosome: Un

Exon count: 4

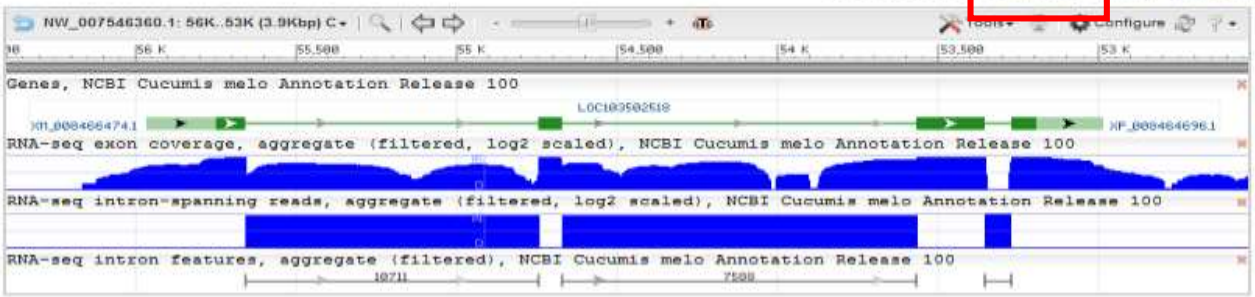
Annotation release	Status	Assembly	Chr	Location
100	current	ASM31304v1 (GCF_000313045.1)	Unplaced Scaffold	NW_007546360.1 (52988..55967, complement)

Genomic regions, transcripts, and products

Genomic Sequence: NW_007546360 unplaced scaffold reference ASM31304v1 Primary Assembly

Go to reference sequence details

Go to nucleotide Graphics FASTA GenBank



Bibliography

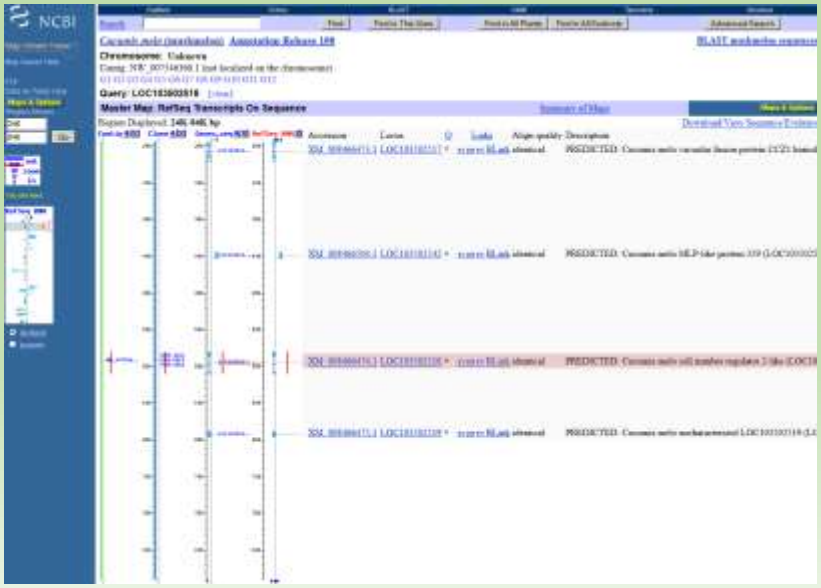
▼ Next ▲ Previous Descriptions

Related Information

Gene - associated gene details

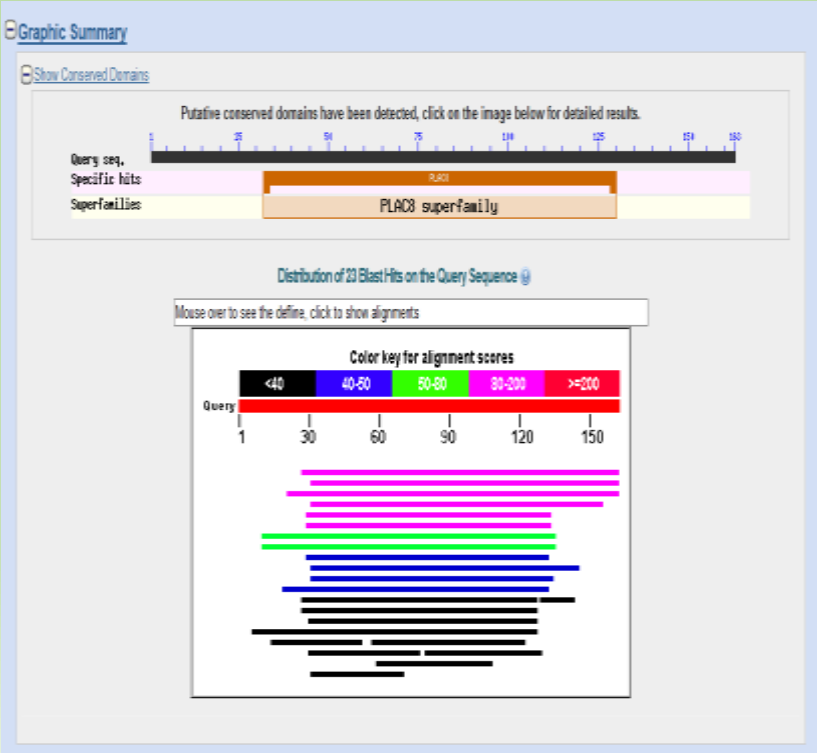
Finding ortholog(s)

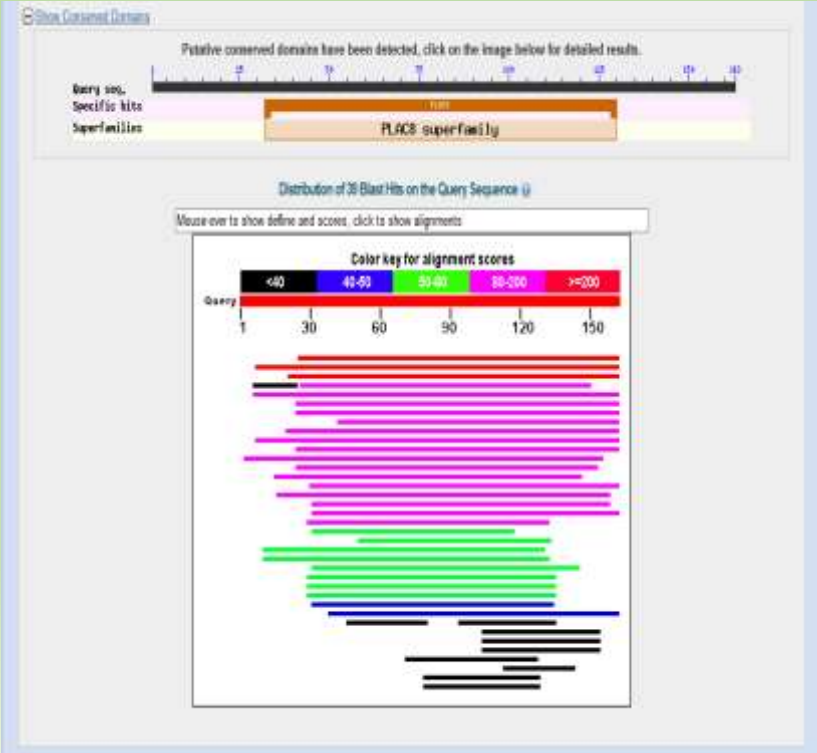
Map Viewer by text search



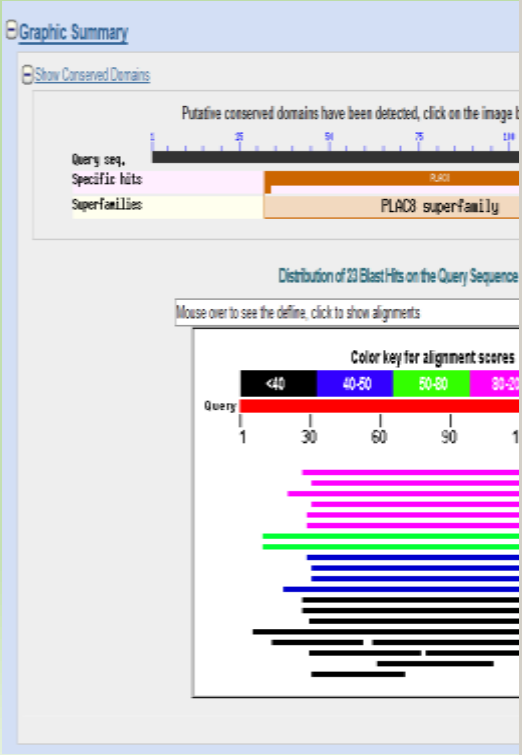
Sequence viewer by URL

Finding ortholog(s)

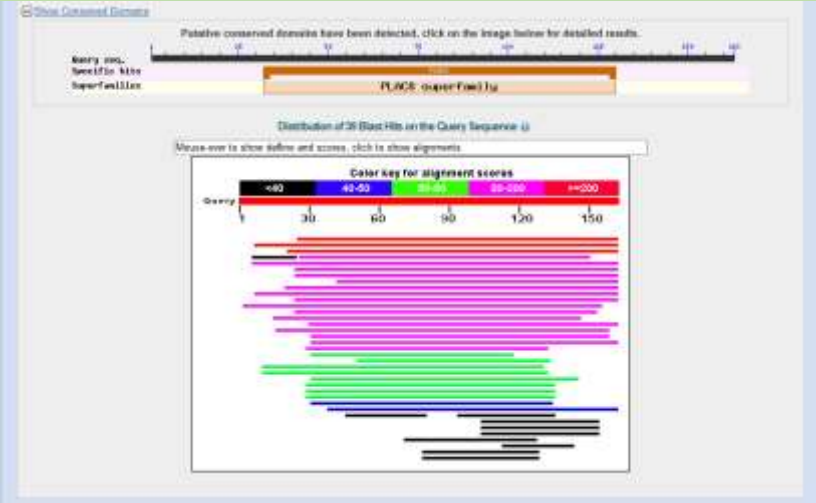


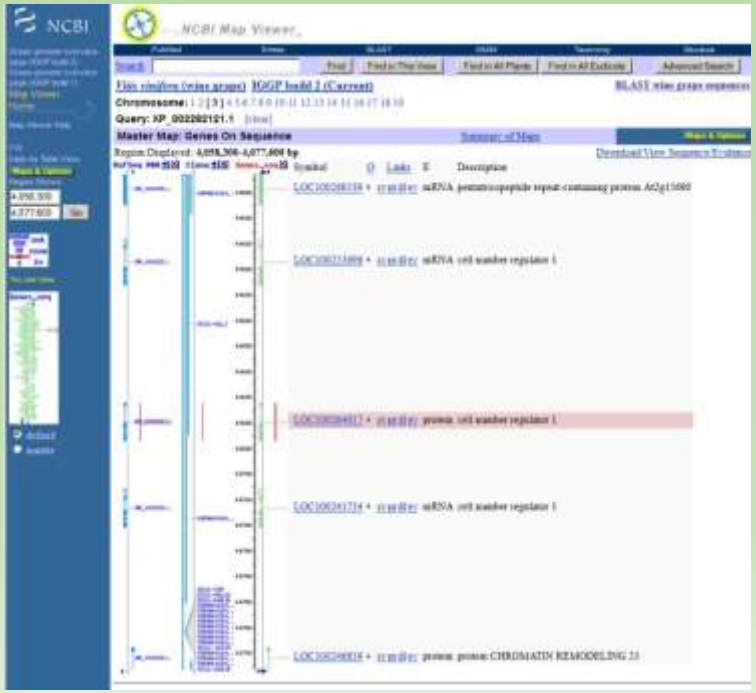


Finding ortholog(s)

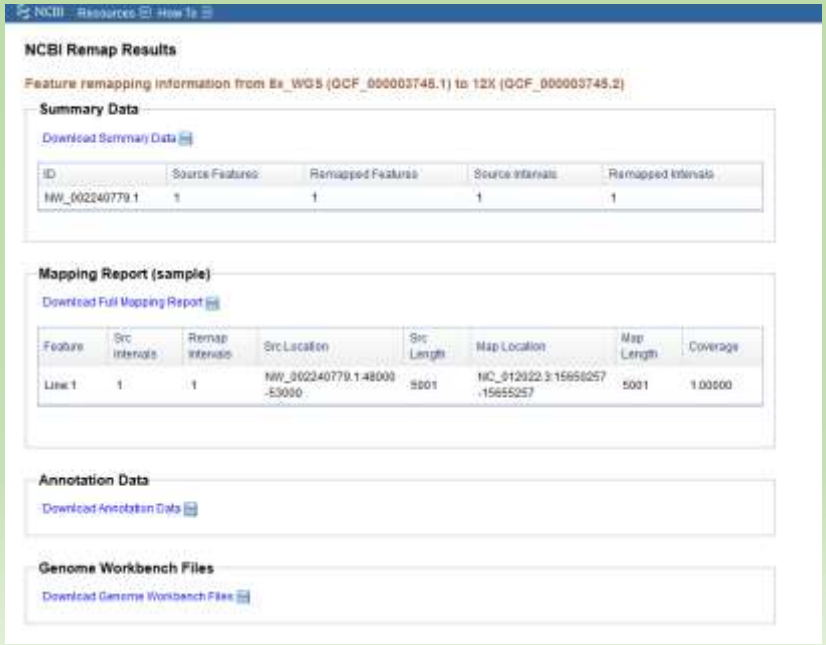


Finding a BAC





Where has my gene gone? – http://www.ncbi.nlm.nih.gov/genome/tools/remap



This software/database/presentation is a "United States Government Work" under the terms of the United States Copyright Act. It was written as part of the author's official duties as a United States Government employee and thus cannot be copyrighted. This software/database/presentation is freely available to the public for use. The National Library of Medicine and the U.S. Government have not placed any restriction on its use or reproduction.

NCBI posters

- P0051: New Developments in the NCBI Eukaryotic Genome Annotation Pipeline
- P0791: Genomic Resources for Arabidopsis Research at NCBI
- P1105: From Genes to Genomes
- P1109: dbSNP and dbVAR
- P1112: Improving the Flow of Data to NCBI Sequence Repositories, SRA and GenBank
- P1115: Annotation of Laurasitheria Genomes by NCBI
- P1120: NCBI Resources for Plant Genomics
- P1142: Sequence Viewer and Genome Workbench