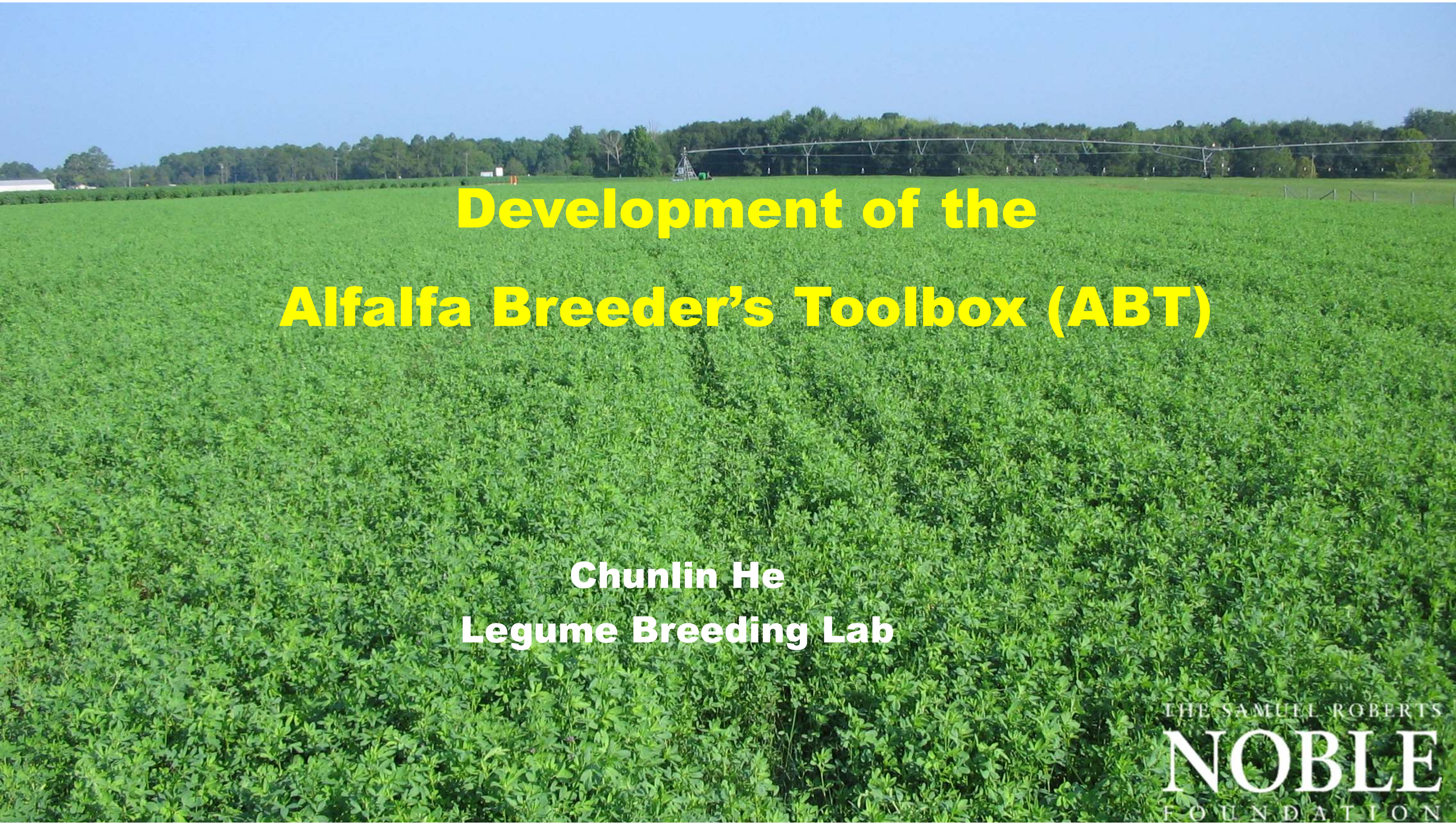


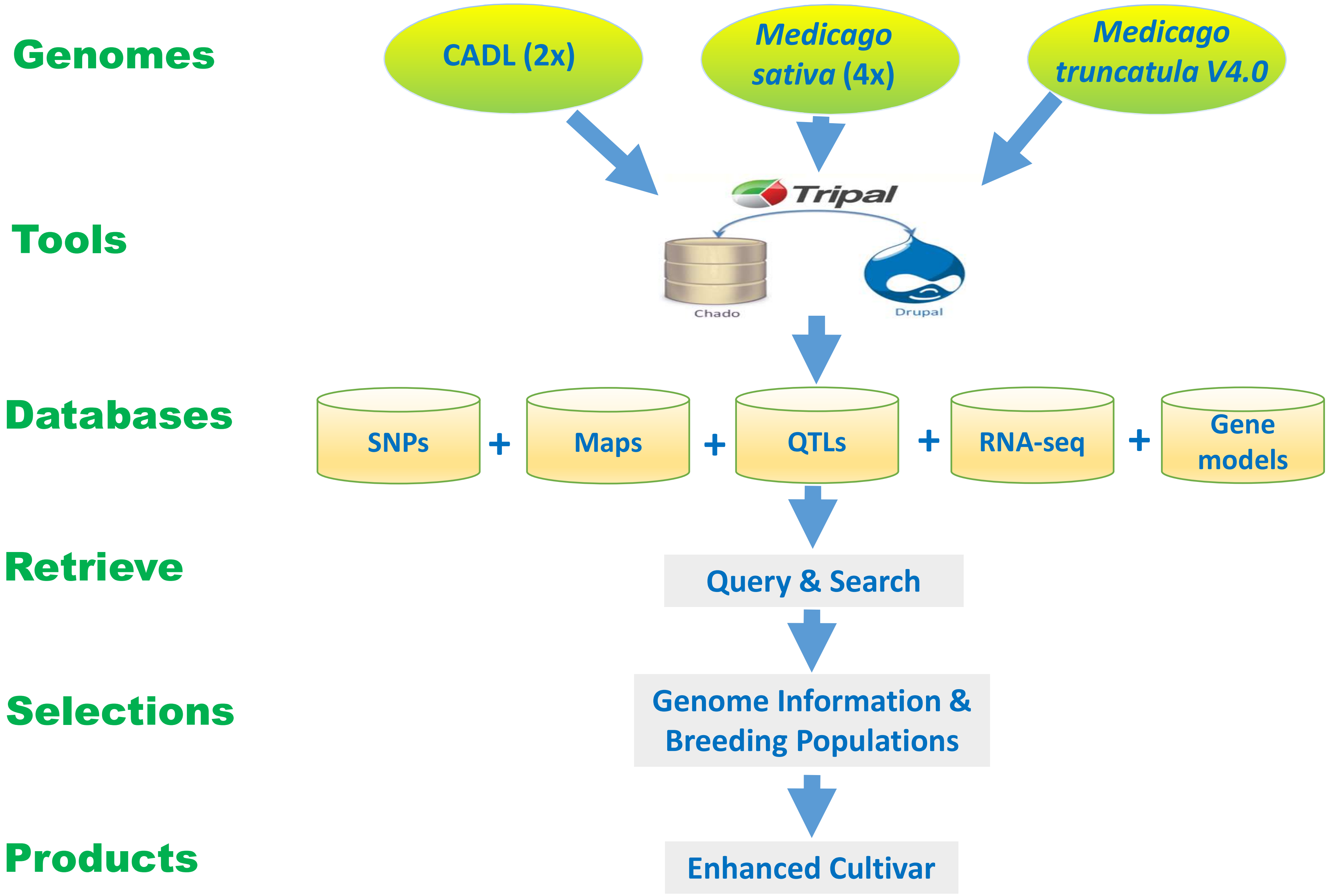
Development of the Alfalfa Breeder's Toolbox (ABT)

Chunlin He
Legume Breeding Lab

THE SAMUEL ROBERTS
NOBLE
FOUNDATION

Objectives of the Alfalfa Breeder's Toolbox (ABT)

- ☐ Generate a resource of breeder-friendly tools that integrates genomic, genetic and phenotypic information
- ☐ Provide breeders with web-accessible data resource for molecular breeding to enhance efficiencies and result in shorter timelines to develop new cultivars



Genomes

CADL (2x)

Medicago sativa (4x)

Medicago truncatula V4.0

Tools

Databases

SNPs + Maps + QTLs + RNA-seq + Gene models

Retrieve

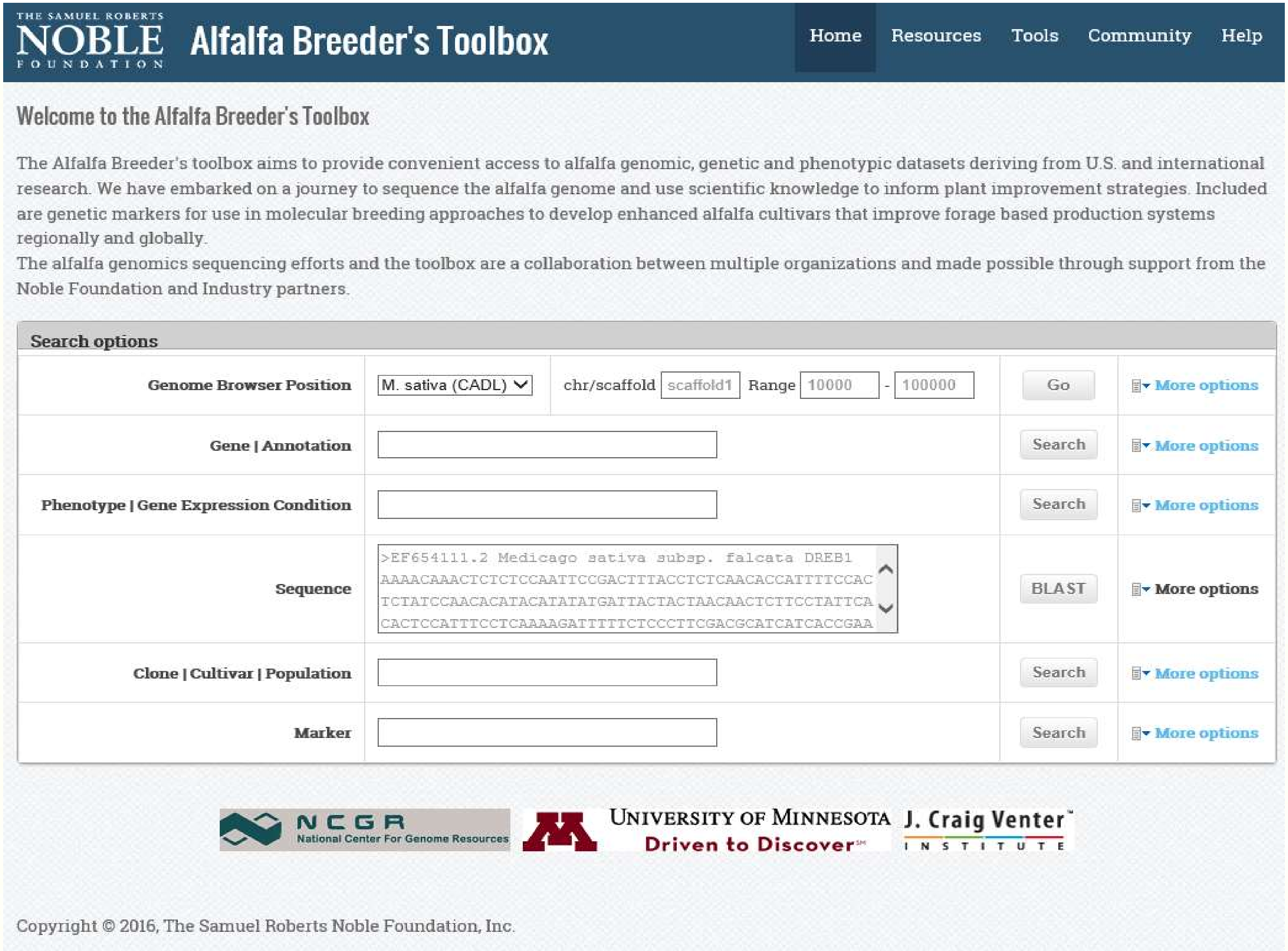
Query & Search

Selections

Genome Information & Breeding Populations

Products

Enhanced Cultivar



Welcome to the Alfalfa Breeder's Toolbox

The Alfalfa Breeder's toolbox aims to provide convenient access to alfalfa genomic, genetic and phenotypic datasets deriving from U.S. and international research. We have embarked on a journey to sequence the alfalfa genome and use scientific knowledge to inform plant improvement strategies. Included are genetic markers for use in molecular breeding approaches to develop enhanced alfalfa cultivars that improve forage based production systems regionally and globally.

The alfalfa genomics sequencing efforts and the toolbox are a collaboration between multiple organizations and made possible through support from the Noble Foundation and Industry partners.

Search options

Genome Browser Position M. sativa (CADL) chr/scaffold scaffold1 Range 10000 - 100000

Sequence

```
>EF654111.2 Medicago sativa subsp. falcata DREB1
AAAACAAACTCTCTCCAATTCCGACTTTACCTCTCAACACCATTTTCCAC
TCTATCCAACACATACATATATGATTACTACTAACAACTCTTCCTATTCA
CACTCCATTTCCTCAAAAGATTTTTCTCCCTTCGACGCATCATCACCGAA
```

Questions for Practical Molecular Breeding

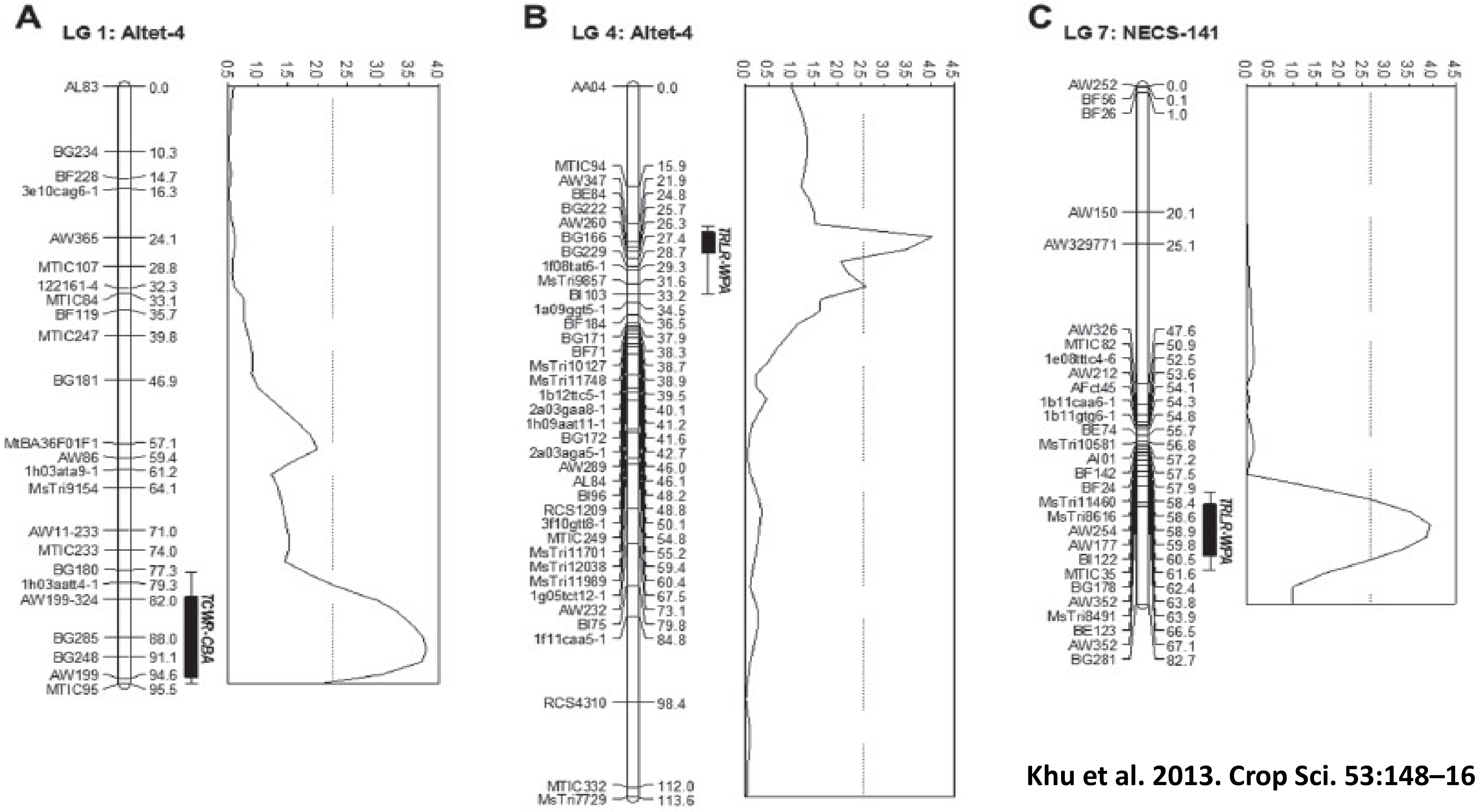
Test Case 1:

I have identified QTLs for aluminum tolerance in alfalfa.

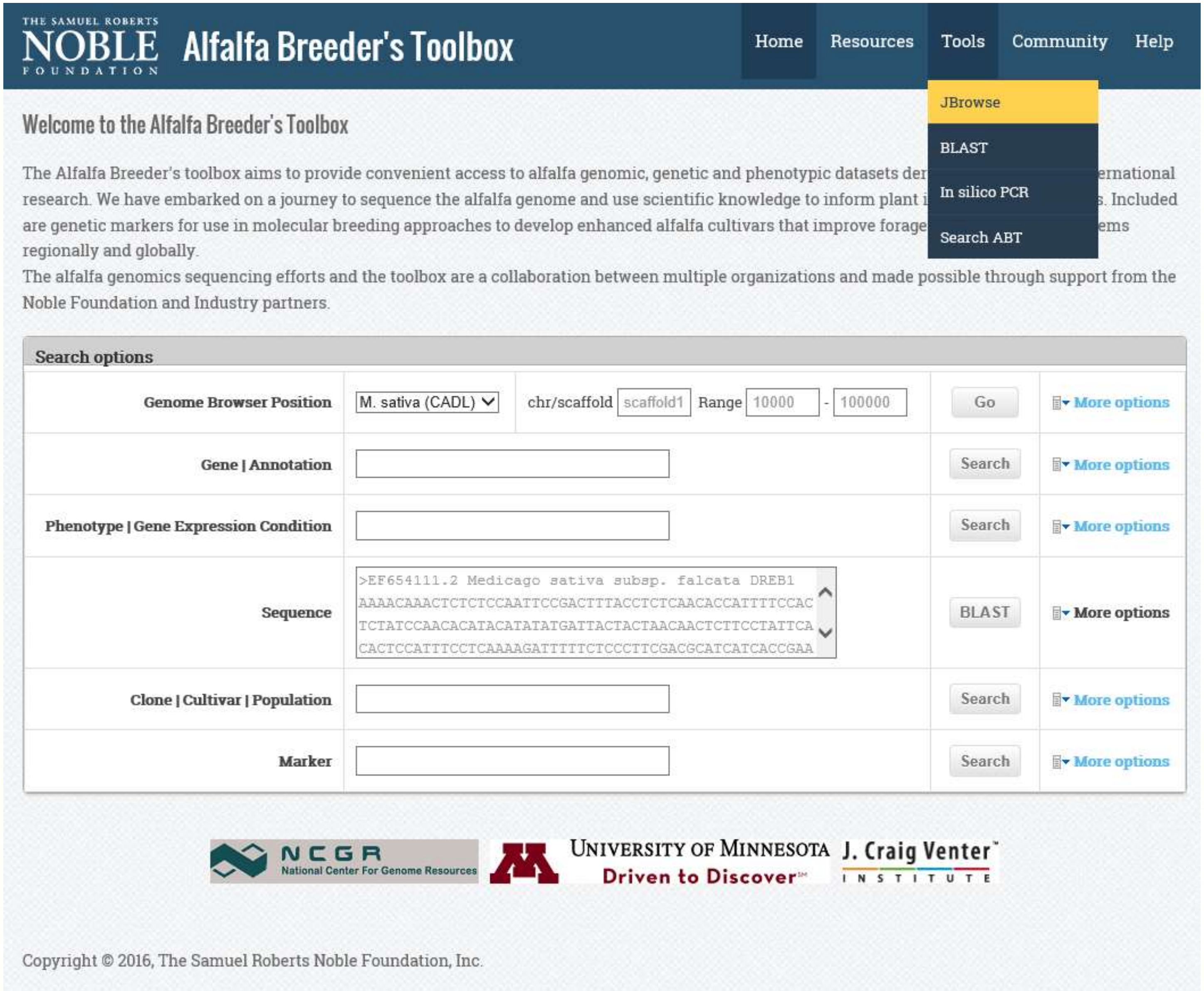
Questions

1. **What are some relevant candidate genes in the area?**
2. **Are SNPs in the region(s) available for use or do I need to develop additional SNPs?**
3. **What markers can I use for marker-assisted selection?**

QTL for Aluminum Tolerance



Khu et al. 2013. Crop Sci. 53:148–163.



Welcome to the Alfalfa Breeder's Toolbox

The Alfalfa Breeder's toolbox aims to provide convenient access to alfalfa genomic, genetic and phenotypic datasets der ernational research. We have embarked on a journey to sequence the alfalfa genome and use scientific knowledge to inform plant i s. Included are genetic markers for use in molecular breeding approaches to develop enhanced alfalfa cultivars that improve forage ems regionally and globally.

The alfalfa genomics sequencing efforts and the toolbox are a collaboration between multiple organizations and made possible through support from the Noble Foundation and Industry partners.

Search options

Genome Browser Position: M. sativa (CADL) chr/scaffold scaffold1 Range 10000 - 100000

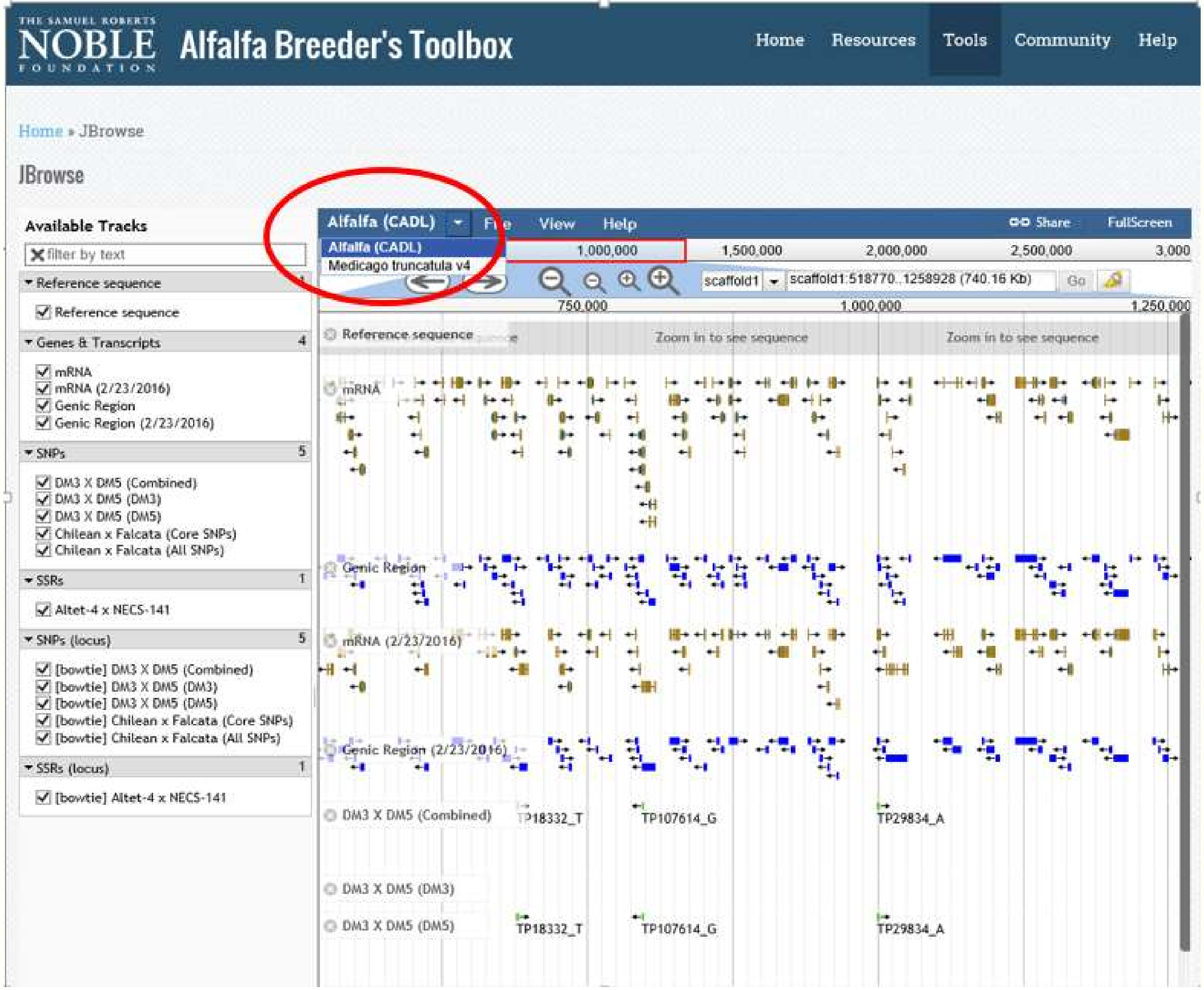
Gene | Annotation

Phenotype | Gene Expression Condition

Sequence:
```
>EF654111.2 Medicago sativa subsp. falcata DREB1
AAAACAAACTCTCTCCAATTCCGACTTTACCTCTCAACACCATTTTCCAC
TCTATCCAACACATACATATATGATTACTACTAACAACTCTTCCTATTCA
CACTCCATTTCCTCAAAAGATTTTTCTCCCTTCGACGCATCATCACCGAA
```

Clone | Cultivar | Population

Marker



Available Tracks

filter by text

Reference sequence
- ☑ Reference sequence

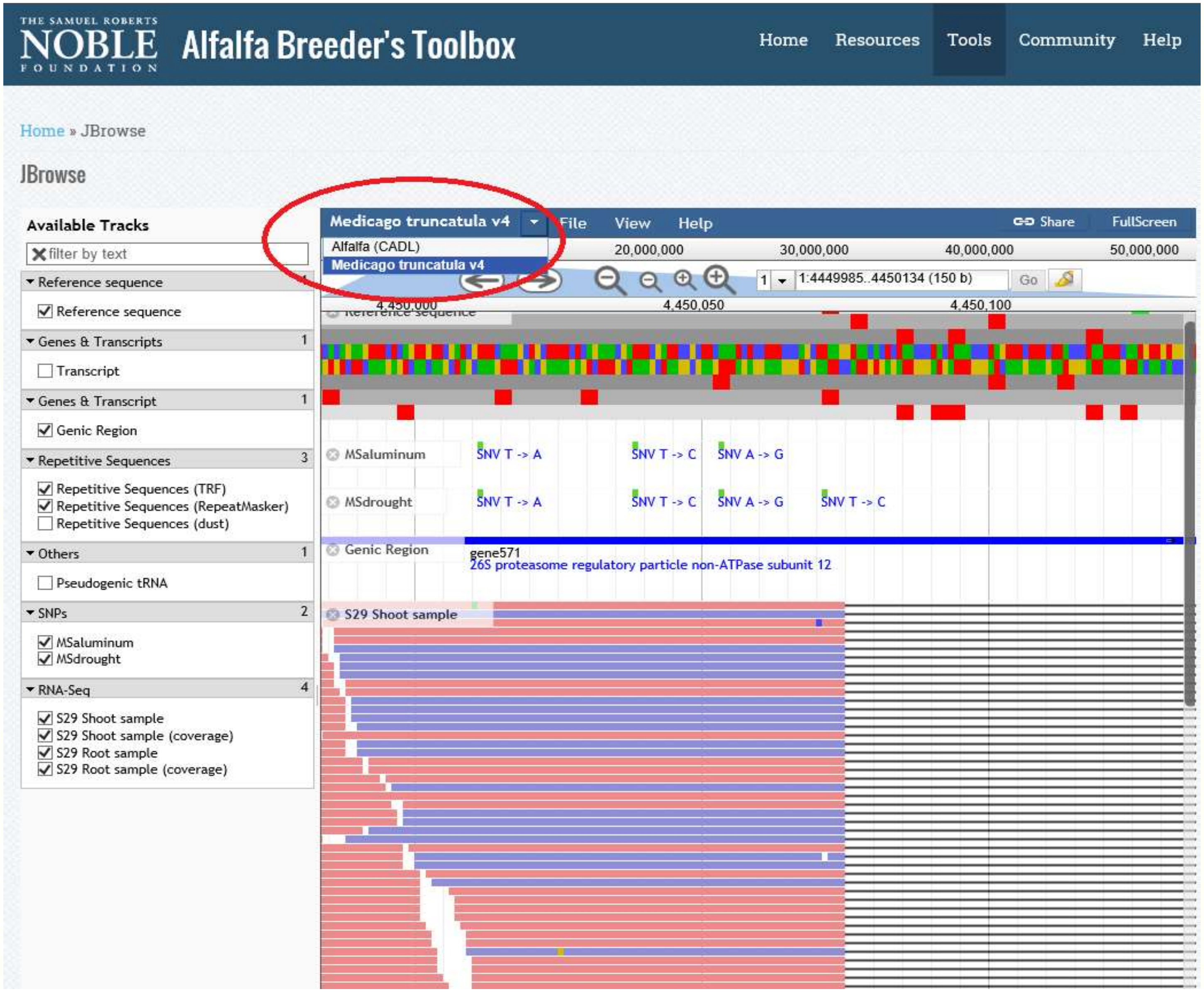
Genes & Transcripts 4
- ☑ mRNA
- ☑ mRNA (2/23/2016)
- ☑ Genic Region
- ☑ Genic Region (2/23/2016)

SNPs 5
- ☑ DM3 X DM5 (Combined)
- ☑ DM3 X DM5 (DM3)
- ☑ DM3 X DM5 (DM5)
- ☑ Chilean x Falcata (Core SNPs)
- ☑ Chilean x Falcata (All SNPs)

SSRs 1
- ☑ Altet-4 x NECS-141

SNPs (locus) 5
- ☑ [bowtie] DM3 X DM5 (Combined)
- ☑ [bowtie] DM3 X DM5 (DM3)
- ☑ [bowtie] DM3 X DM5 (DM5)
- ☑ [bowtie] Chilean x Falcata (Core SNPs)
- ☑ [bowtie] Chilean x Falcata (All SNPs)

SSRs (locus) 1
- ☑ [bowtie] Altet-4 x NECS-141



Available Tracks

Reference sequence
- ☑ Reference sequence

Genes & Transcripts 1
- ☐ Transcript

Genes & Transcript 1
- ☑ Genic Region

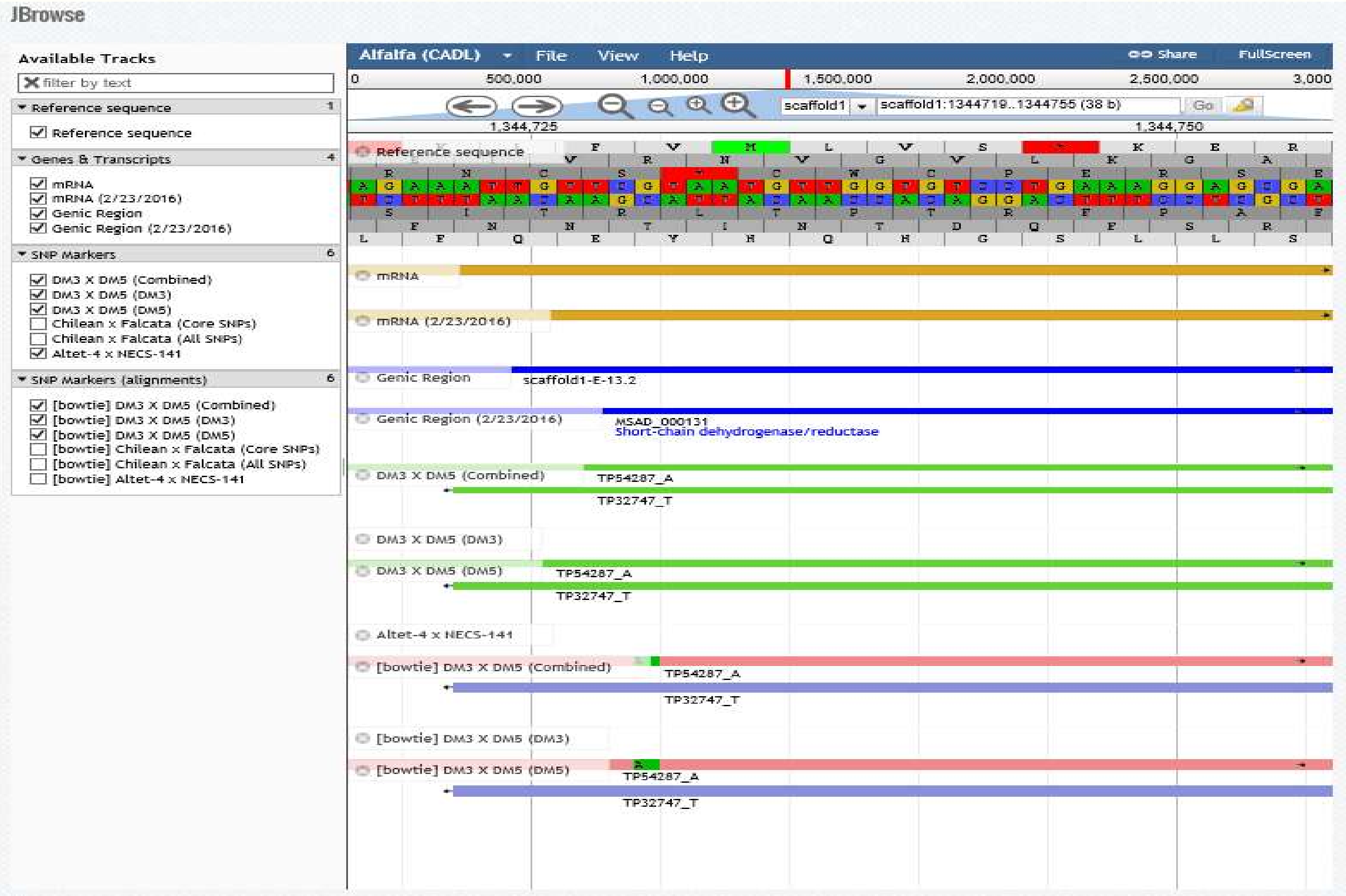
Repetitive Sequences 3
- ☑ Repetitive Sequences (TRF)
- ☑ Repetitive Sequences (RepeatMasker)
- ☐ Repetitive Sequences (dust)

Others 1
- ☐ Pseudogenic tRNA

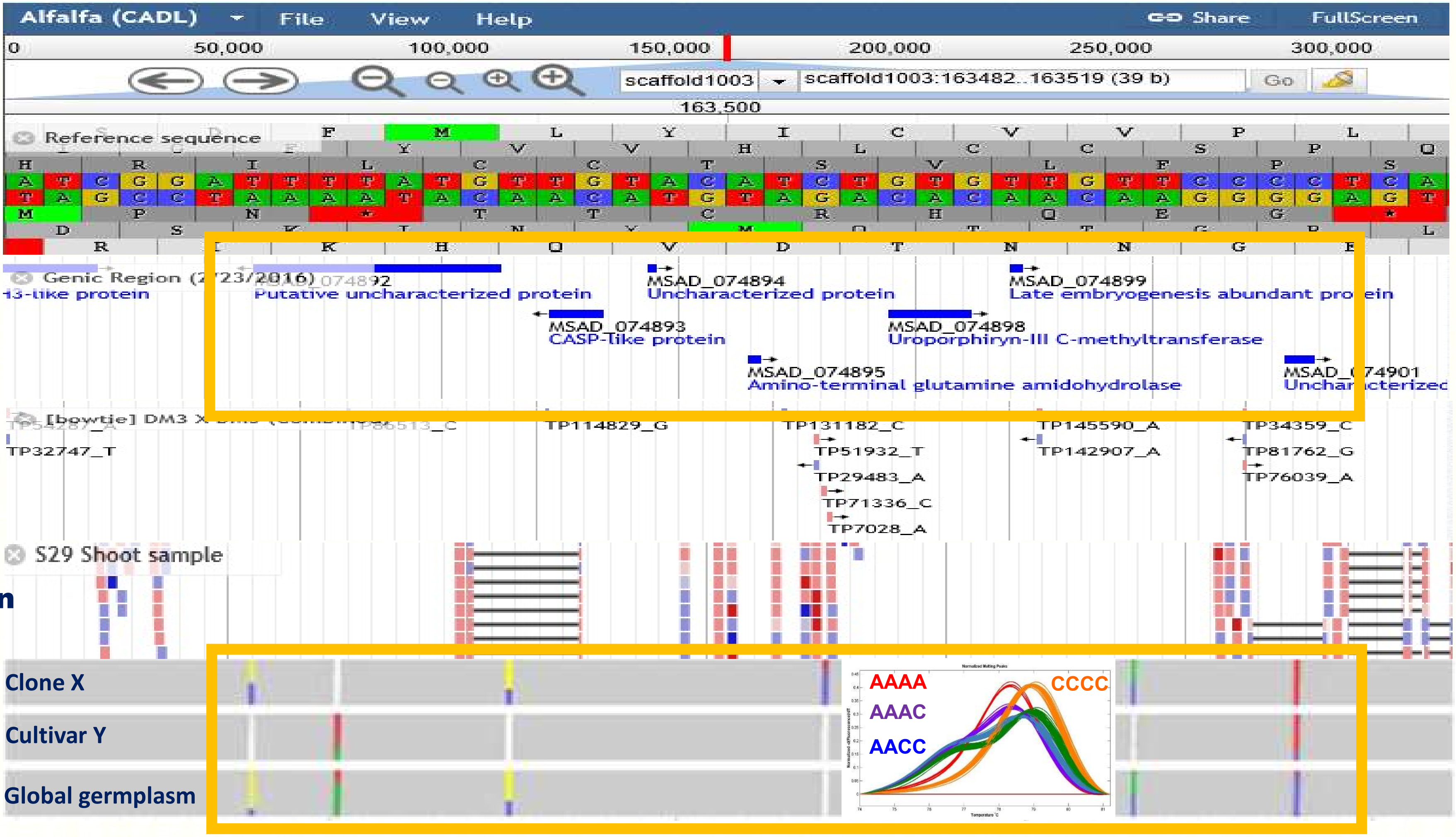
SNPs 2
- ☑ MSaluminum
- ☑ MSdrought

RNA-Seq 4
- ☑ S29 Shoot sample
- ☑ S29 Shoot sample (coverage)
- ☑ S29 Root sample
- ☑ S29 Root sample (coverage)

Alignment of SNP markers to the CADL Genome



Display Genotypic Data as Allele Frequencies



Ref-seq

Gene model

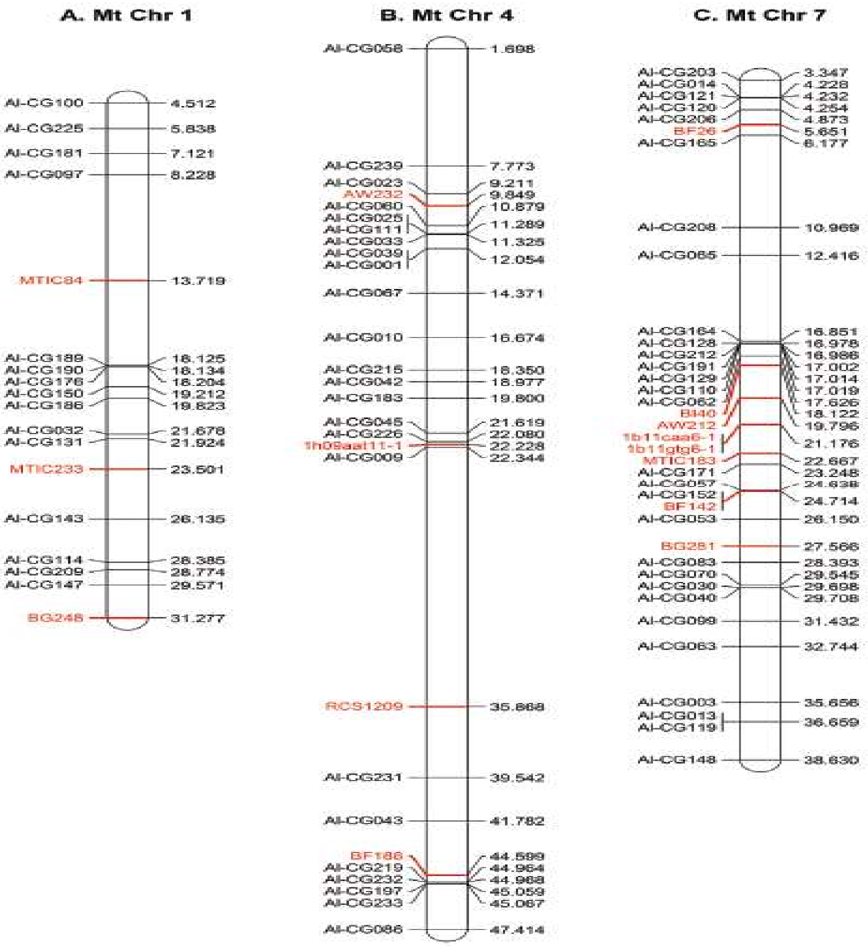
SNPs

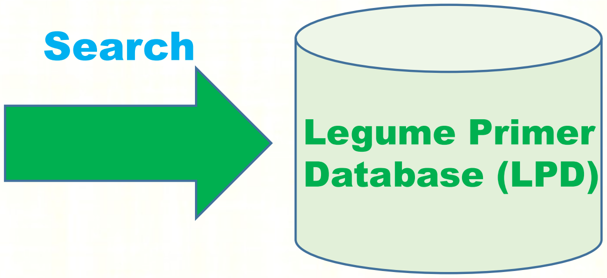
Gene expression

Allele freq

A = Green C = Blue G = Yellow T = Red Gray = Monomorphic

Physical Location of Markers Associated with Aluminum Tolerance QTLs

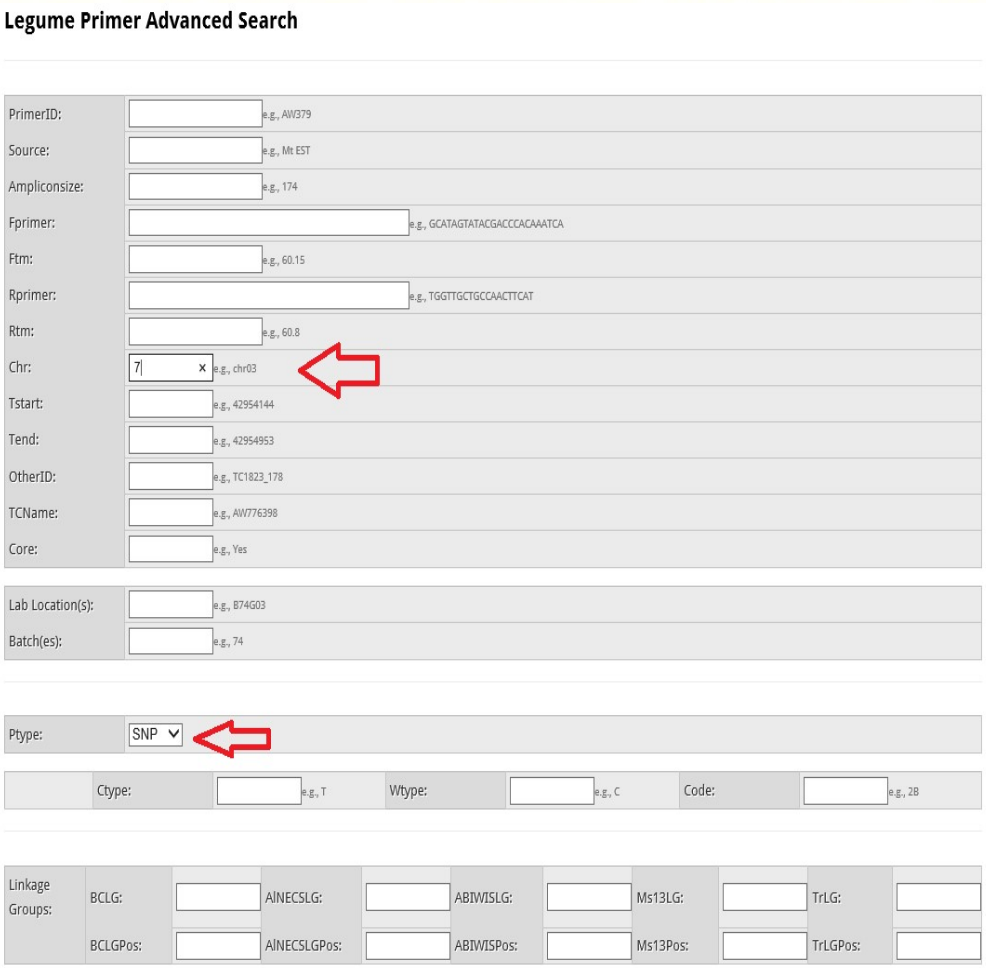




Search

Legume Primer Database (LPD)

Searching the Legume Primer Database (LPD)

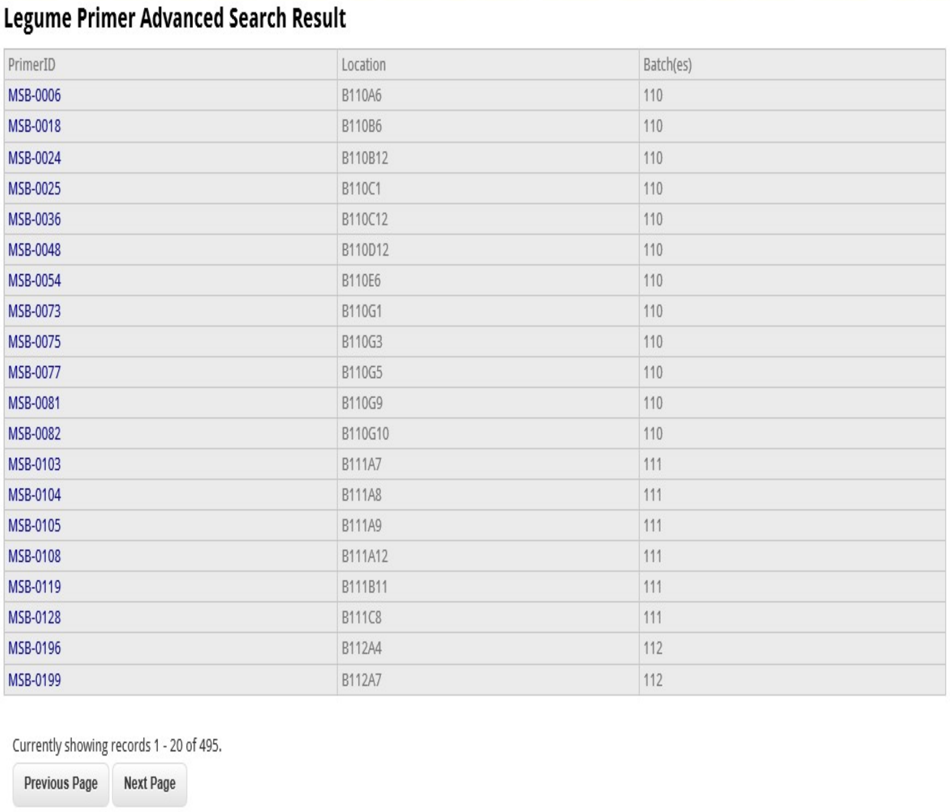


Legume Primer Advanced Search

PrimerID:		e.g., AW379
Source:		e.g., Mt EST
Ampliconsize:		e.g., 174
Fprimer:		e.g., GCATAGTATACGACCCACAAATCA
Ftm:		e.g., 60.15
Rprimer:		e.g., TGGTTGCTGCCAACTTCAT
Rtm:		e.g., 60.8
Chr:	7	e.g., chr03
Tstart:		e.g., 42954144
Tend:		e.g., 42954953
OtherID:		e.g., TC1823_178
TCName:		e.g., AW776398
Core:		e.g., Yes
Lab Location(s):		e.g., B74G03
Batch(es):		e.g., 74
Ptype:	SNP	

Ctype: e.g., T
Wtype: e.g., C
Code: e.g., 2B

Linkage Groups:
BCLG: AlNECSLG: ABIWISLG: Ms13LG: TrLG:
BCLGPos: AlNECSLGPos: ABIWISPos: Ms13Pos: TrLGPos:

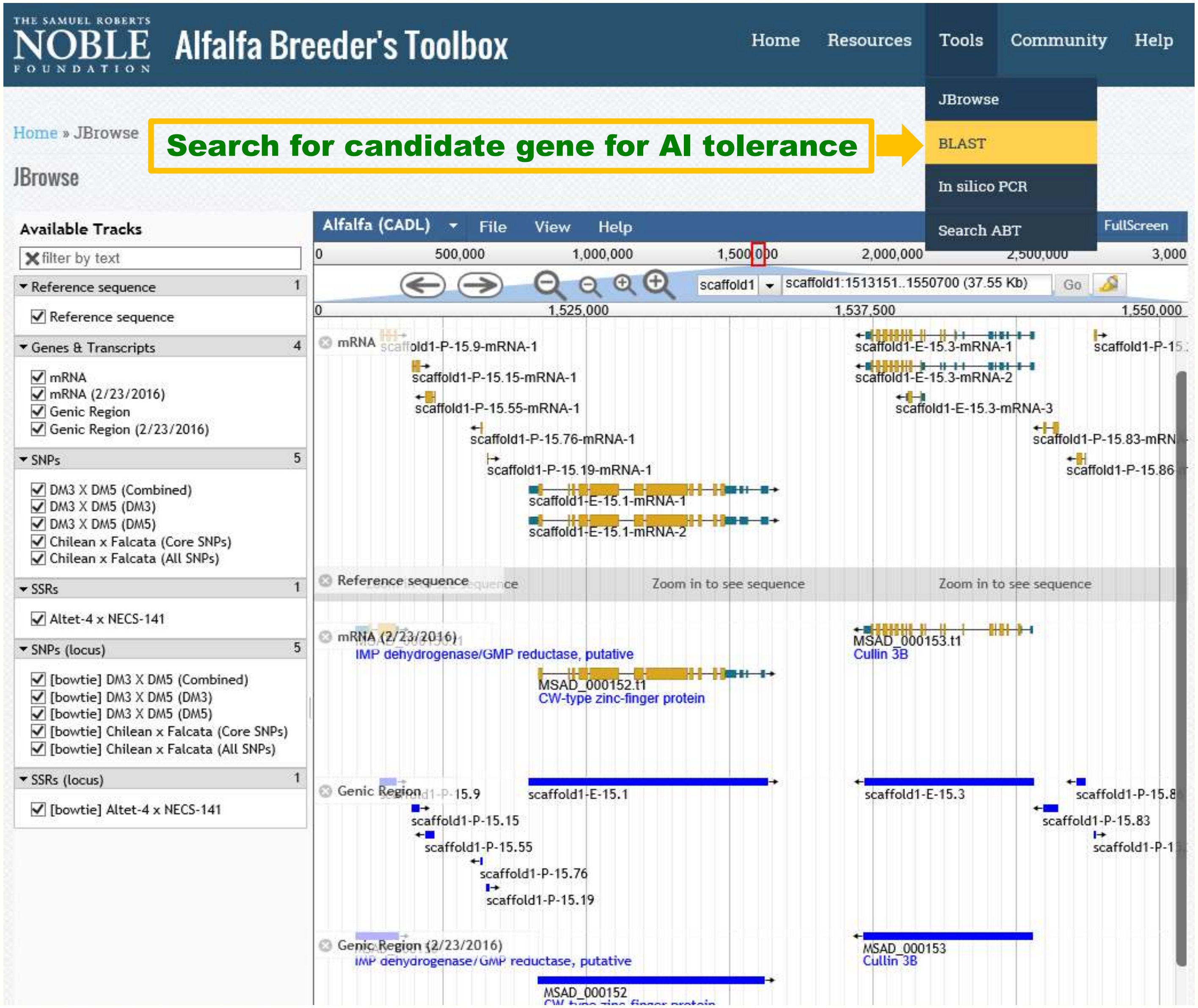


Legume Primer Advanced Search Result

PrimerID	Location	Batch(es)
MSB-0006	B110A6	110
MSB-0018	B110B6	110
MSB-0024	B110B12	110
MSB-0025	B110C1	110
MSB-0036	B110C12	110
MSB-0048	B110D12	110
MSB-0054	B110E6	110
MSB-0073	B110G1	110
MSB-0075	B110G3	110
MSB-0077	B110G5	110
MSB-0081	B110G9	110
MSB-0082	B110G10	110
MSB-0103	B111A7	111
MSB-0104	B111A8	111
MSB-0105	B111A9	111
MSB-0108	B111A12	111
MSB-0119	B111B11	111
MSB-0128	B111C8	111
MSB-0196	B112A4	112
MSB-0199	B112A7	112

Currently showing records 1 - 20 of 495.

Search for candidate gene for Al tolerance



scaffold1:1513151..1550700 (37.55 Kb)

Reference sequence 1
- ☑ Reference sequence

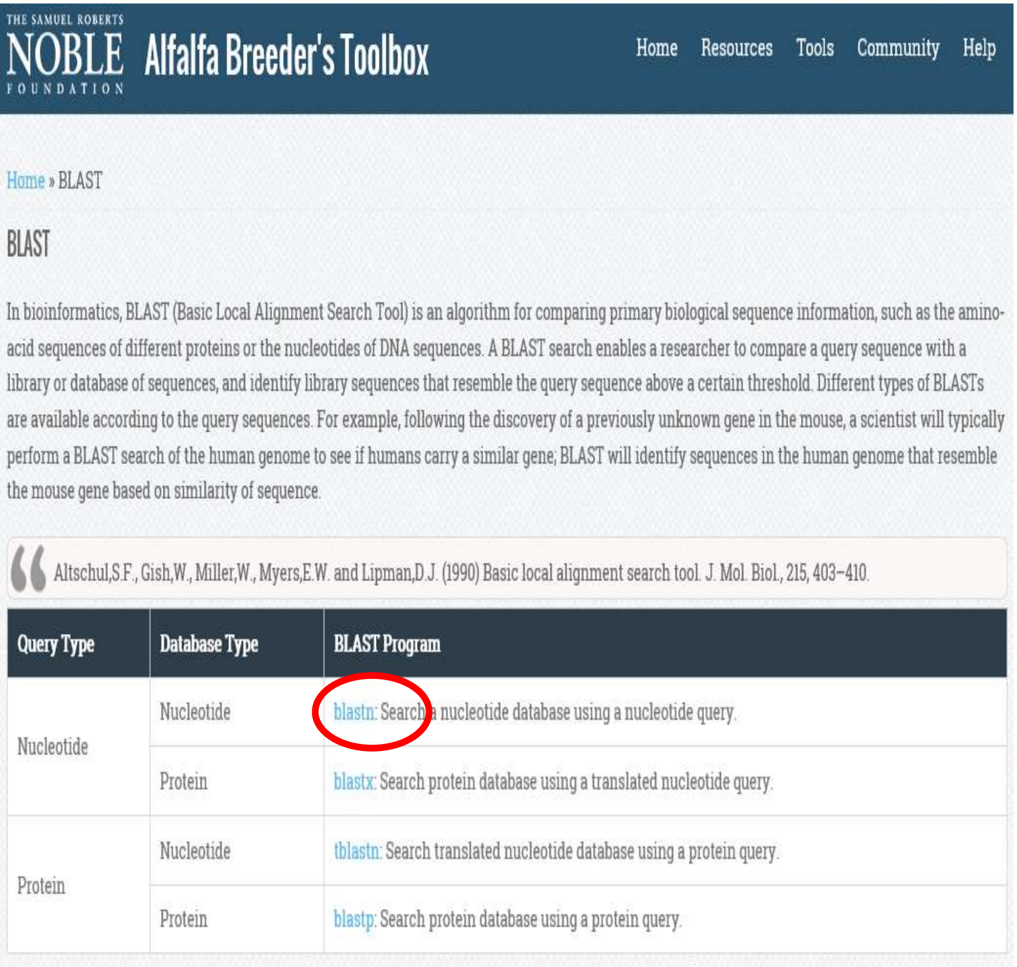
Genes & Transcripts 4
- ☑ mRNA
- ☑ mRNA (2/23/2016)
- ☑ Genic Region
- ☑ Genic Region (2/23/2016)

SNPs 5
- ☑ DM3 X DM5 (Combined)
- ☑ DM3 X DM5 (DM3)
- ☑ DM3 X DM5 (DM5)
- ☑ Chilean x Falcata (Core SNPs)
- ☑ Chilean x Falcata (All SNPs)

SSRs 1
- ☑ Altet-4 x NECS-141

SNPs (locus) 5
- ☑ [bowtie] DM3 X DM5 (Combined)
- ☑ [bowtie] DM3 X DM5 (DM3)
- ☑ [bowtie] DM3 X DM5 (DM5)
- ☑ [bowtie] Chilean x Falcata (Core SNPs)
- ☑ [bowtie] Chilean x Falcata (All SNPs)

SSRs (locus) 1
- ☑ [bowtie] Altet-4 x NECS-141



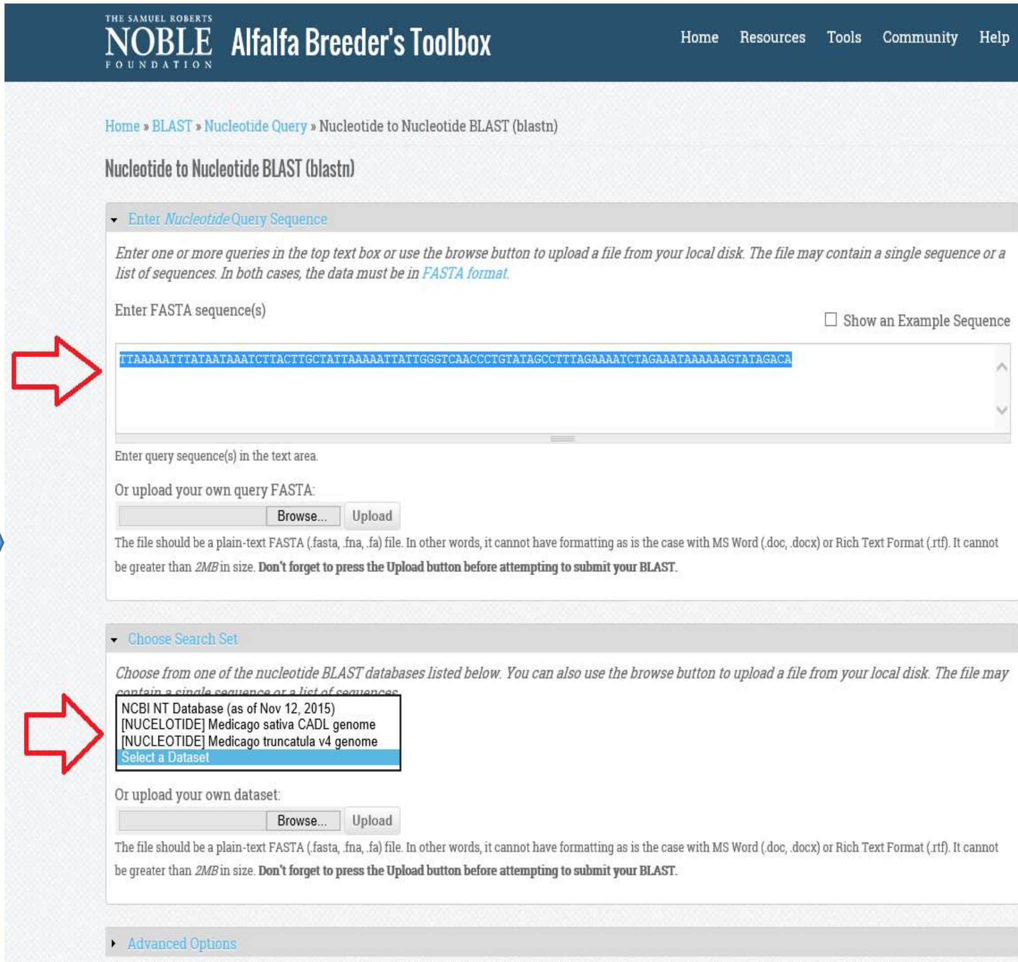
Home » BLAST

BLAST

In bioinformatics, BLAST (Basic Local Alignment Search Tool) is an algorithm for comparing primary biological sequence information, such as the amino-acid sequences of different proteins or the nucleotides of DNA sequences. A BLAST search enables a researcher to compare a query sequence with a library or database of sequences, and identify library sequences that resemble the query sequence above a certain threshold. Different types of BLASTs are available according to the query sequences. For example, following the discovery of a previously unknown gene in the mouse, a scientist will typically perform a BLAST search of the human genome to see if humans carry a similar gene; BLAST will identify sequences in the human genome that resemble the mouse gene based on similarity of sequence.

> Altschul,S.F., Gish,W., Miller,W., Myers,E.W. and Lipman,D.J. (1990) Basic local alignment search tool. J. Mol. Biol., 215, 403–410.

Query Type	Database Type	BLAST Program
Nucleotide	Nucleotide	blastn: Search a nucleotide database using a nucleotide query.
	Protein	blastx: Search protein database using a translated nucleotide query.
Protein	Nucleotide	tblastn: Search translated nucleotide database using a protein query.
	Protein	blastp: Search protein database using a protein query.



Home » BLAST » Nucleotide Query » Nucleotide to Nucleotide BLAST (blastn)

Nucleotide to Nucleotide BLAST (blastn)

Enter *Nucleotide* Query Sequence

Enter one or more queries in the top text box or use the browse button to upload a file from your local disk. The file may contain a single sequence or a list of sequences. In both cases, the data must be in FASTA format.

Enter FASTA sequence(s)

☐ Show an Example Sequence

```
TTAAAAATTTATAATAAATCTTACTTGCTATTAAAAATTATTGGGTCAACCCTGTATAGCCTTTAGAAAATCTAGAAATAAAAAAGTATAGACA
```

Enter query sequence(s) in the text area.

Or upload your own query FASTA:

The file should be a plain-text FASTA (.fasta, .fna, .fa) file. In other words, it cannot have formatting as is the case with MS Word (.doc, .docx) or Rich Text Format (.rtf). It cannot be greater than *2MB* in size. **Don't forget to press the Upload button before attempting to submit your BLAST.**

Choose Search Set

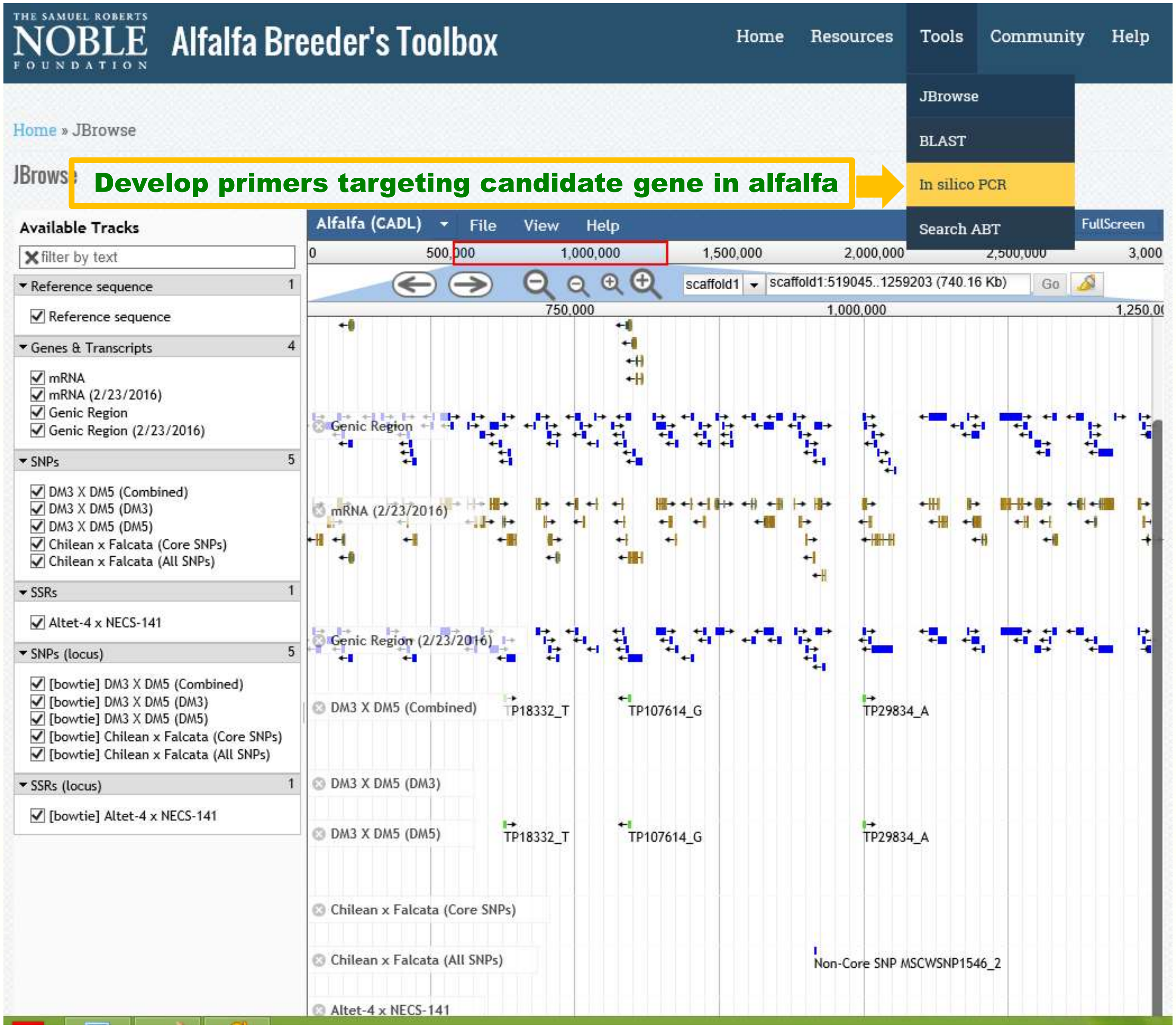
Choose from one of the nucleotide BLAST databases listed below. You can also use the browse button to upload a file from your local disk. The file may contain a single sequence or a list of sequences.

NCBI NT Database (as of Nov 12, 2015)
[NUCELOTIDE] Medicago sativa CADL genome
[NUCLEOTIDE] Medicago truncatula v4 genome
Select a Dataset

Or upload your own dataset:

The file should be a plain-text FASTA (.fasta, .fna, .fa) file. In other words, it cannot have formatting as is the case with MS Word (.doc, .docx) or Rich Text Format (.rtf). It cannot be greater than *2MB* in size. **Don't forget to press the Upload button before attempting to submit your BLAST.**

Advanced Options



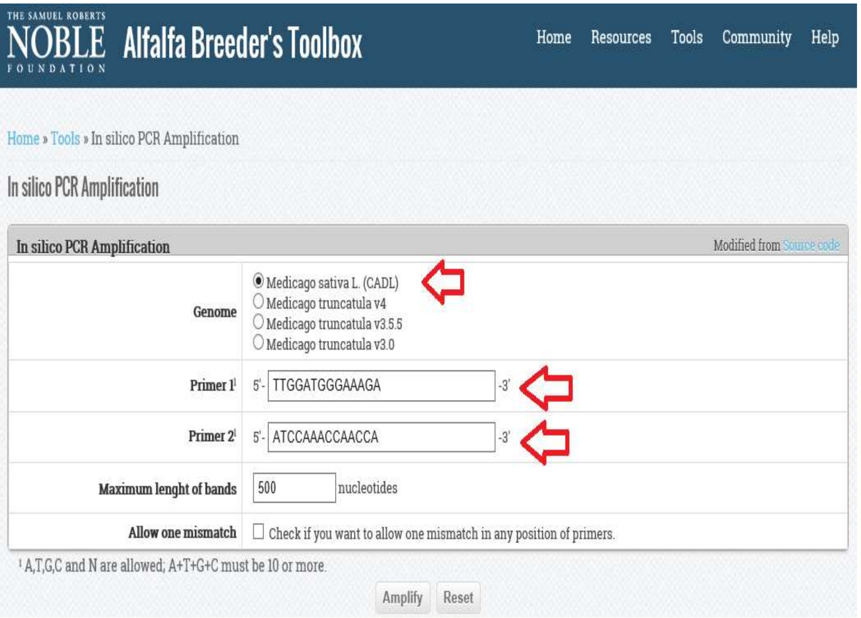
Develop primers targeting candidate gene in alfalfa

scaffold1:519045..1259203 (740.16 Kb)

Available Tracks

filter by text

- Reference sequence 1
  - ☑ Reference sequence
- Genes & Transcripts 4
  - ☑ mRNA
  - ☑ mRNA (2/23/2016)
  - ☑ Genic Region
  - ☑ Genic Region (2/23/2016)
- SNPs 5
  - ☑ DM3 X DM5 (Combined)
  - ☑ DM3 X DM5 (DM3)
  - ☑ DM3 X DM5 (DM5)
  - ☑ Chilean x Falcata (Core SNPs)
  - ☑ Chilean x Falcata (All SNPs)
- SSRs 1
  - ☑ Altet-4 x NECS-141
- SNPs (locus) 5
  - ☑ [bowtie] DM3 X DM5 (Combined)
  - ☑ [bowtie] DM3 X DM5 (DM3)
  - ☑ [bowtie] DM3 X DM5 (DM5)
  - ☑ [bowtie] Chilean x Falcata (Core SNPs)
  - ☑ [bowtie] Chilean x Falcata (All SNPs)
- SSRs (locus) 1
  - ☑ [bowtie] Altet-4 x NECS-141

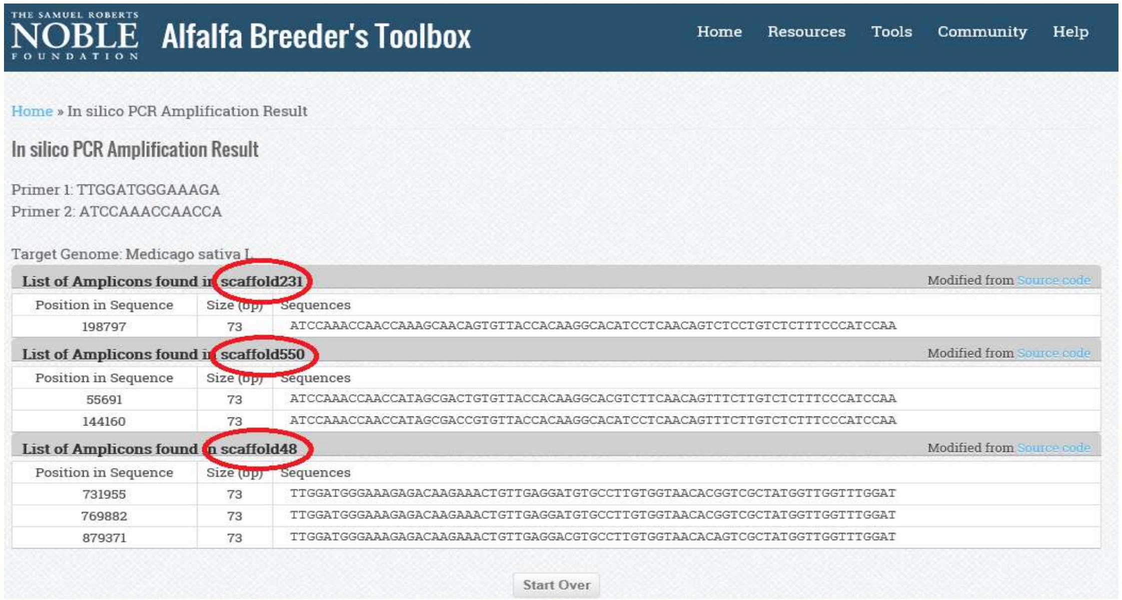


In silico PCR Amplification

In silico PCR Amplification — Modified from Source code

Genome	● Medicago sativa L. (CADL) ○ Medicago truncatula v4 ○ Medicago truncatula v3.5.5 ○ Medicago truncatula v3.0
Primer 1[1]	5'- TTGGATGGGAAAGA -3'
Primer 2[1]	5'- ATCCAAACCAACCA -3'
Maximum lenght of bands	500 nucleotides
Allow one mismatch	☐ Check if you want to allow one mismatch in any position of primers.

[1] A,T,G,C and N are allowed; A+T+G+C must be 10 or more.



In silico PCR Amplification Result

Primer 1: TTGGATGGGAAAGA
Primer 2: ATCCAAACCAACCA

Target Genome: Medicago sativa L.

List of Amplicons found in scaffold231 — Modified from Source code

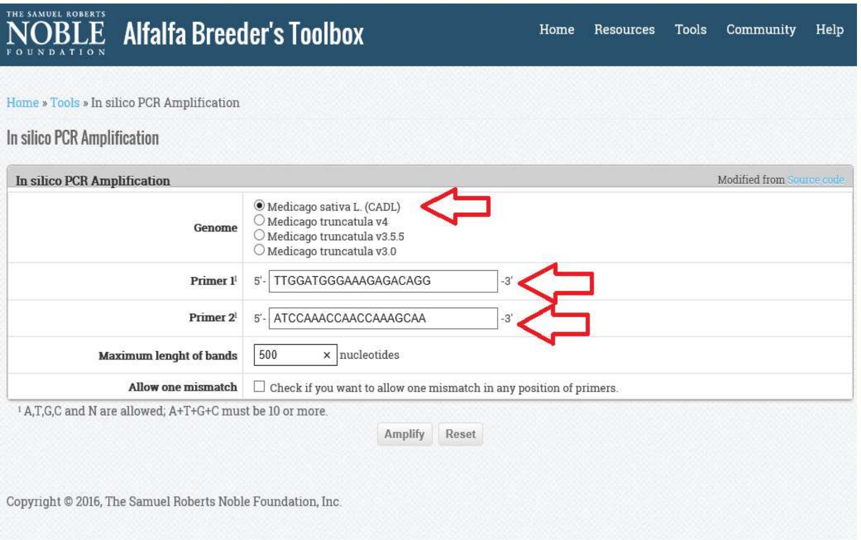
Position in Sequence	Size (bp)	Sequences
198797	73	ATCCAAACCAACCAAAGCAACAGTGTTACCACAAGGCACATCCTCAACAGTCTCCTGTCTCTTTCCCATCCAA

List of Amplicons found in scaffold550 — Modified from Source code

Position in Sequence	Size (bp)	Sequences
55691	73	ATCCAAACCAACCATAGCGACTGTGTTACCACAAGGCACGTCTTCAACAGTTTCTTGTCTCTTTCCCATCCAA
144160	73	ATCCAAACCAACCATAGCGACCGTGTTACCACAAGGCACATCCTCAACAGTTTCTTGTCTCTTTCCCATCCAA

List of Amplicons found in scaffold48 — Modified from Source code

Position in Sequence	Size (bp)	Sequences
731955	73	TTGGATGGGAAAGAGACAAGAAACTGTTGAGGATGTGCCTTGTGGTAACACGGTCGCTATGGTTGGTTTGGAT
769882	73	TTGGATGGGAAAGAGACAAGAAACTGTTGAGGATGTGCCTTGTGGTAACACGGTCGCTATGGTTGGTTTGGAT
879371	73	TTGGATGGGAAAGAGACAAGAAACTGTTGAGGACGTGCCTTGTGGTAACACAGTCGCTATGGTTGGTTTGGAT



In silico PCR Amplification

In silico PCR Amplification — Modified from Source code

Genome	● Medicago sativa L. (CADL) ○ Medicago truncatula v4 ○ Medicago truncatula v3.5.5 ○ Medicago truncatula v3.0
Primer 1[1]	5'- TTGGATGGGAAAGAGACAGG -3'
Primer 2[1]	5'- ATCCAAACCAACCAAAGCAA -3'
Maximum lenght of bands	500 × nucleotides
Allow one mismatch	☐ Check if you want to allow one mismatch in any position of primers.

[1] A,T,G,C and N are allowed; A+T+G+C must be 10 or more.

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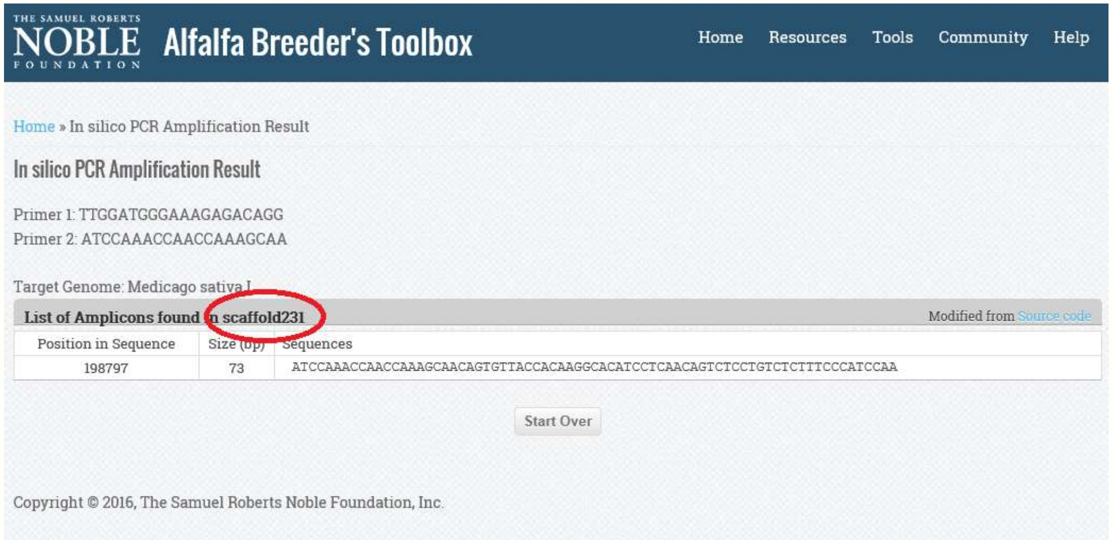

In silico PCR Amplification Result

Primer 1: TTGGATGGGAAAGAGACAGG
Primer 2: ATCCAAACCAACCAAAGCAA

Target Genome: Medicago sativa L.

List of Amplicons found in scaffold231 — Modified from Source code

Position in Sequence	Size (bp)	Sequences
198797	73	ATCCAAACCAACCAAAGCAACAGTGTTACCACAAGGCACATCCTCAACAGTCTCCTGTCTCTTTCCCATCCAA

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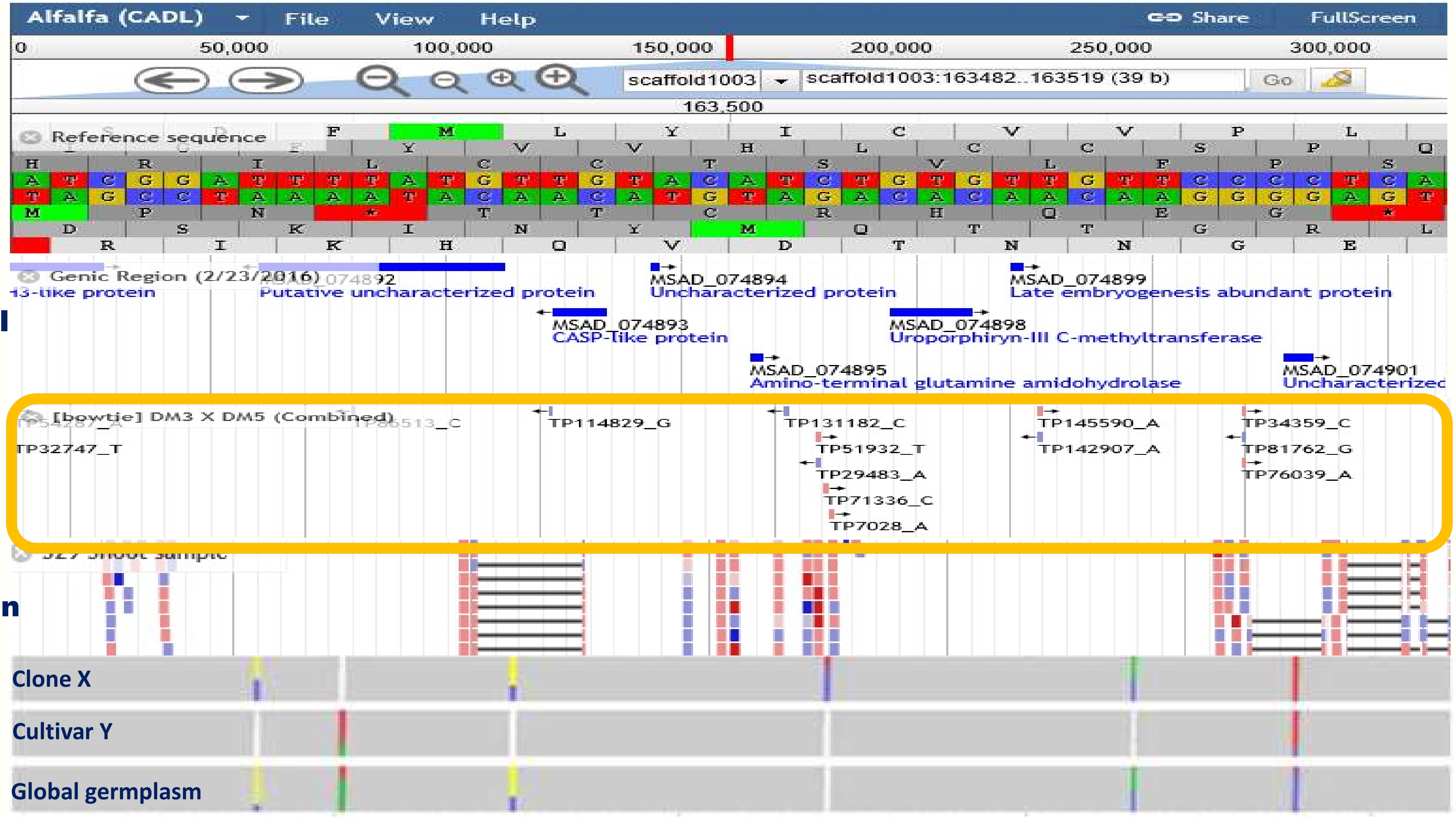
Display Markers across the Genome



Ref-seq

Gene model

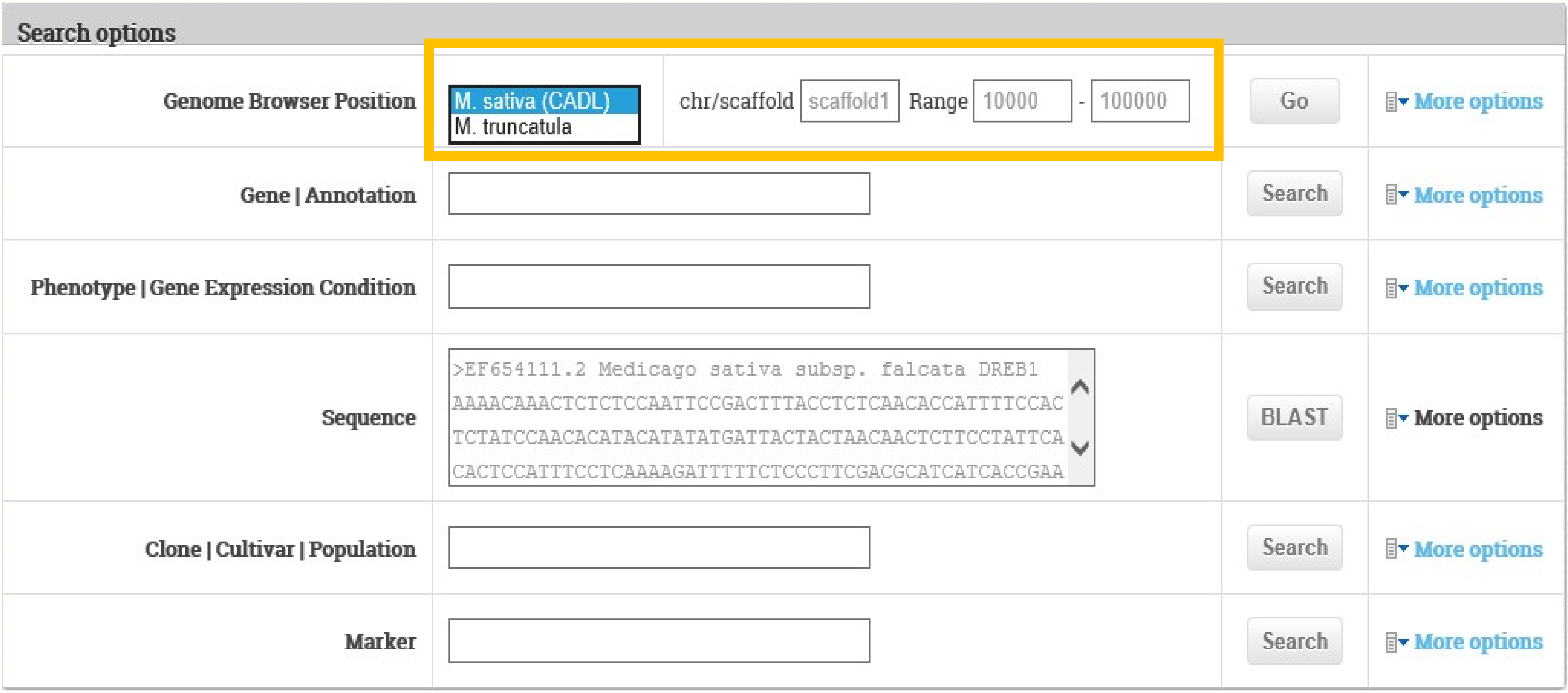
SNPs

Gene expression

Allele freq

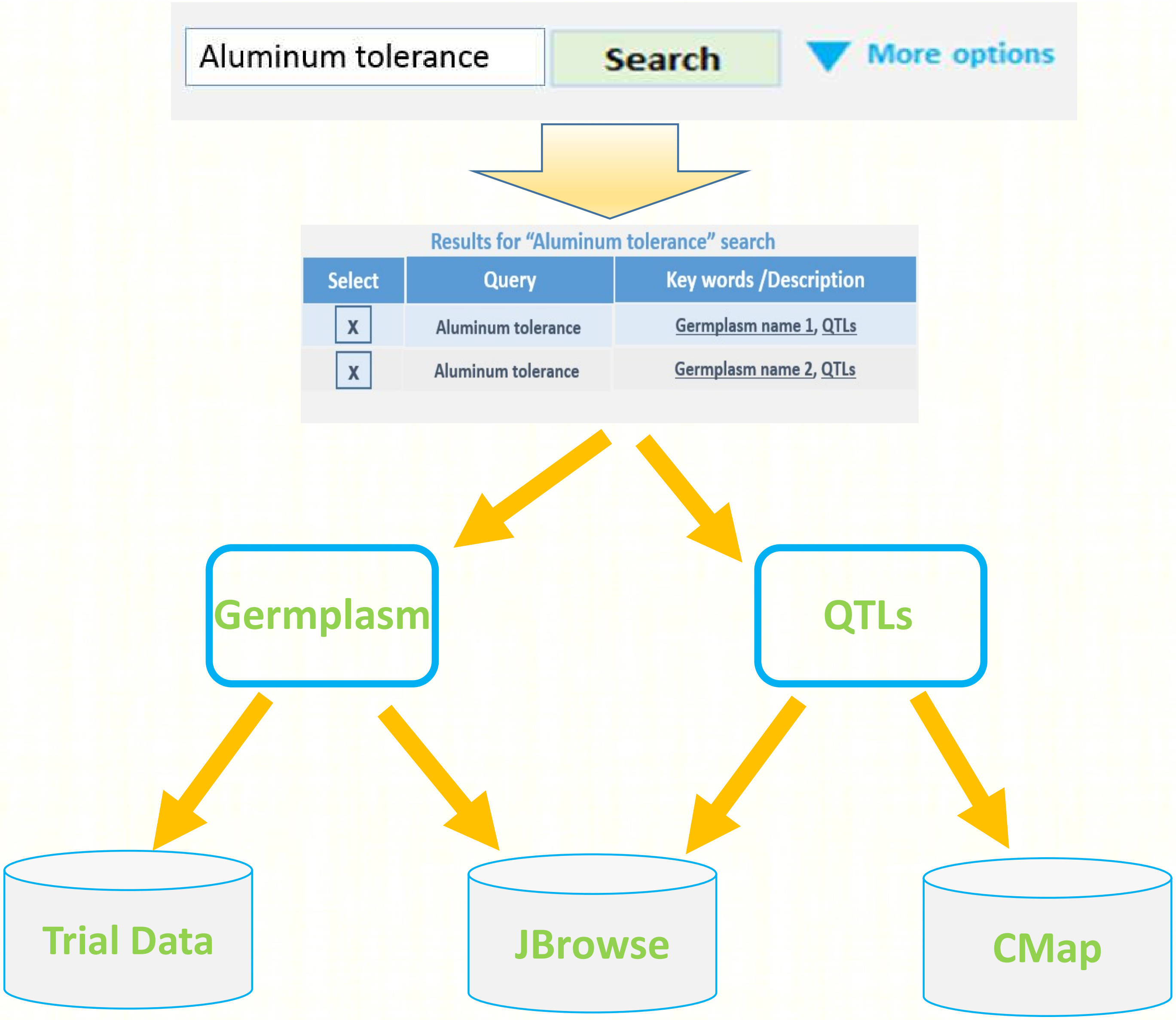
A = Green   C = Blue   G = Yellow   T = Red   Gray = Monomorphic

Additional Approach:
Retrieve Genomic Information from the Homepage



Search options

Genome Browser Position	M. sativa (CADL) M. truncatula	chr/scaffold scaffold1 Range 10000 - 100000	Go	More options
Gene | Annotation			Search	More options
Phenotype | Gene Expression Condition			Search	More options
Sequence	>EF654111.2 Medicago sativa subsp. falcata DREB1 AAAACAAACTCTCTCCAATTCCGACTTTACCTCTCAACACCATTTTCCAC TCTATCCAACACATACATATATGATTACTACTAACAACTCTTCCTATTCA CACTCCATTTCCTCAAAAGATTTTTCTCCCTTCGACGCATCATCACCGAA		BLAST	More options
Clone | Cultivar | Population			Search	More options
Marker			Search	More options



Query

Results

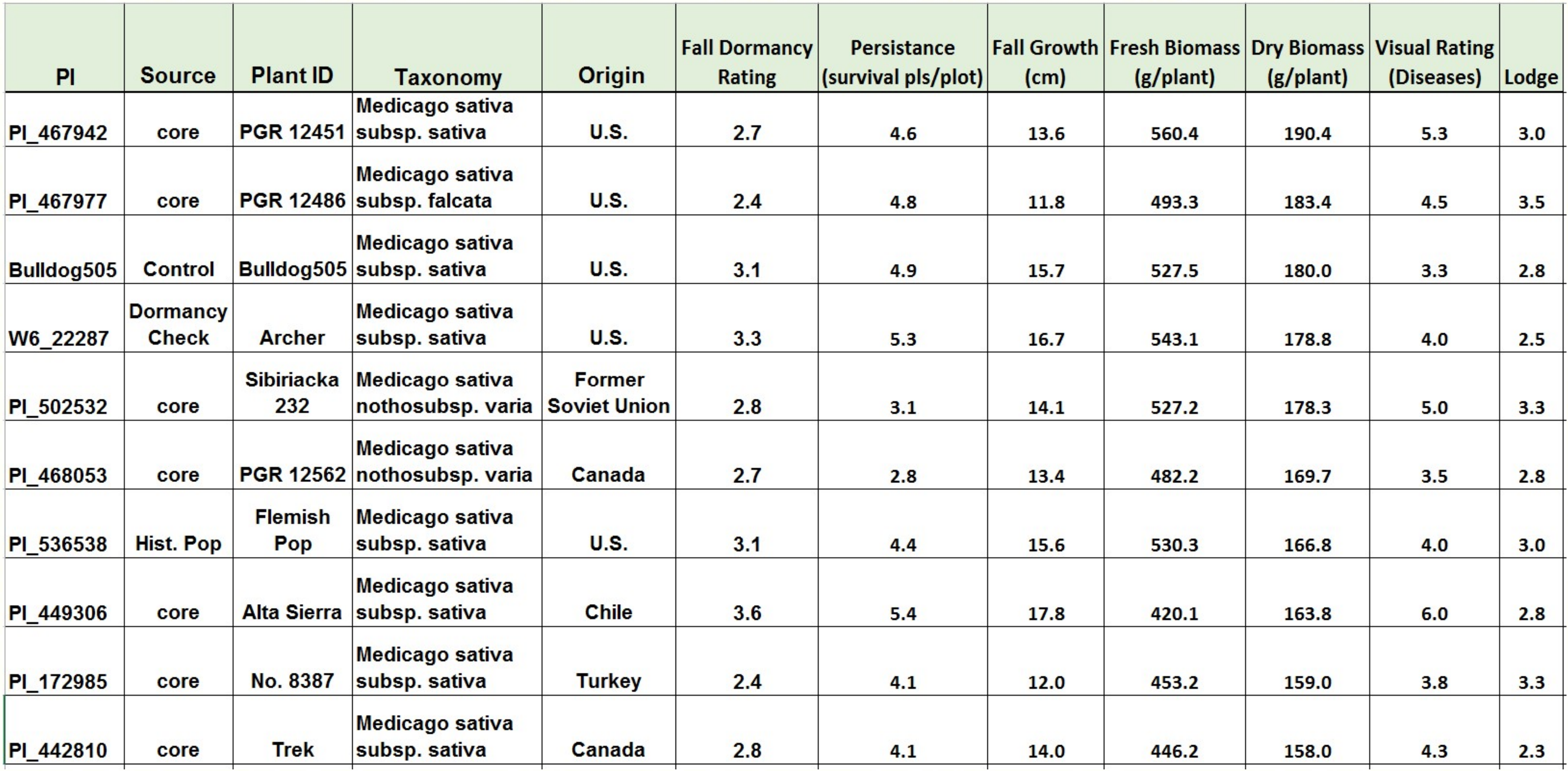
Results for “Aluminum tolerance” search

Select	Query	Key words /Description
X	Aluminum tolerance	Germplasm name 1, QTLs
X	Aluminum tolerance	Germplasm name 2, QTLs

Focus

Databases

Integrate Phenotypic Data from Field Trials

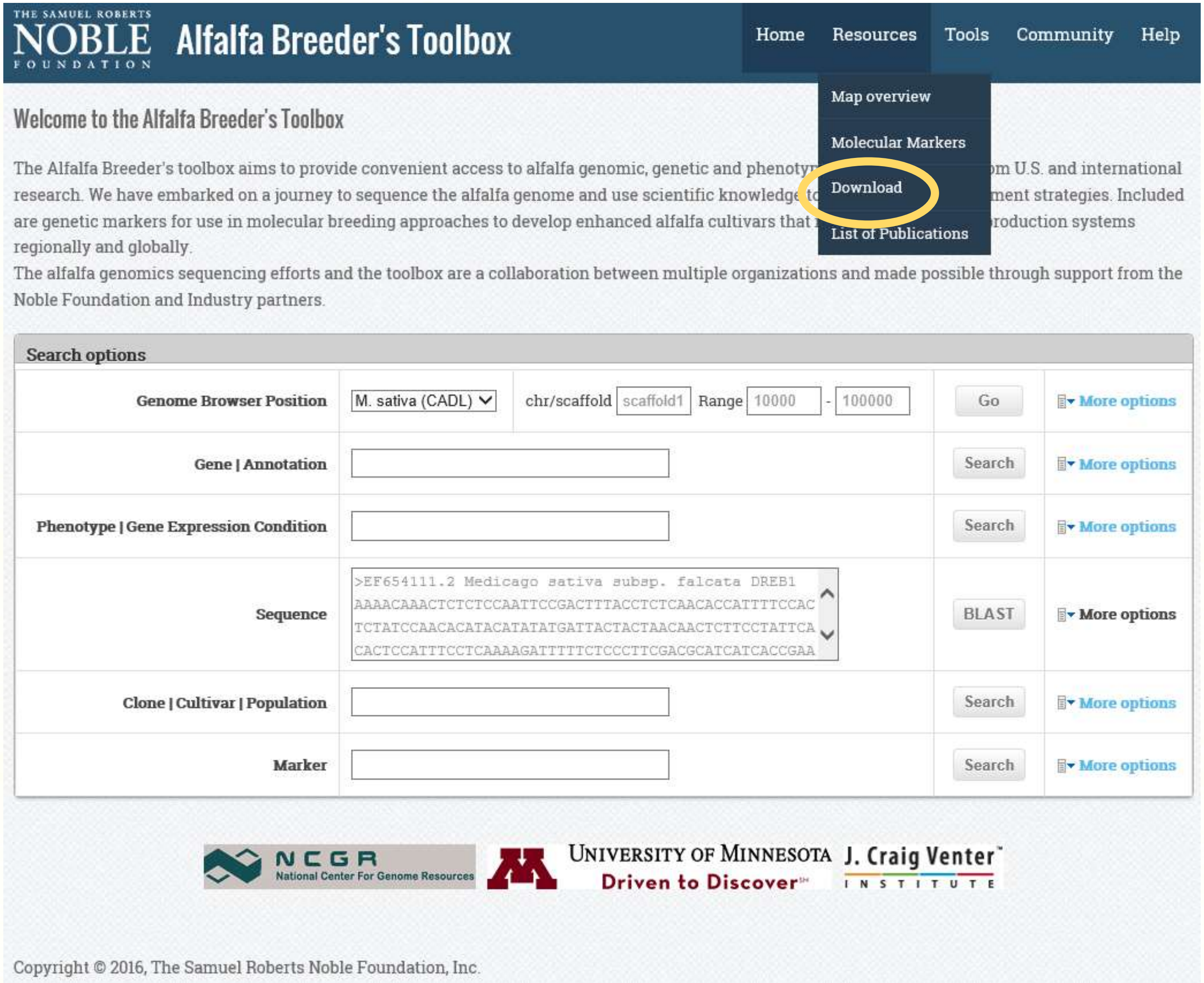


PI	Source	Plant ID	Taxonomy	Origin	Fall Dormancy Rating	Persistance (survival pls/plot)	Fall Growth (cm)	Fresh Biomass (g/plant)	Dry Biomass (g/plant)	Visual Rating (Diseases)	Lodge
PI_467942	core	PGR 12451	Medicago sativa subsp. sativa	U.S.	2.7	4.6	13.6	560.4	190.4	5.3	3.0
PI_467977	core	PGR 12486	Medicago sativa subsp. falcata	U.S.	2.4	4.8	11.8	493.3	183.4	4.5	3.5
Bulldog505	Control	Bulldog505	Medicago sativa subsp. sativa	U.S.	3.1	4.9	15.7	527.5	180.0	3.3	2.8
W6_22287	Dormancy Check	Archer	Medicago sativa subsp. sativa	U.S.	3.3	5.3	16.7	543.1	178.8	4.0	2.5
PI_502532	core	Sibiriacka 232	Medicago sativa nothosubsp. varia	Former Soviet Union	2.8	3.1	14.1	527.2	178.3	5.0	3.3
PI_468053	core	PGR 12562	Medicago sativa nothosubsp. varia	Canada	2.7	2.8	13.4	482.2	169.7	3.5	2.8
PI_536538	Hist. Pop	Flemish Pop	Medicago sativa subsp. sativa	U.S.	3.1	4.4	15.6	530.3	166.8	4.0	3.0
PI_449306	core	Alta Sierra	Medicago sativa subsp. sativa	Chile	3.6	5.4	17.8	420.1	163.8	6.0	2.8
PI_172985	core	No. 8387	Medicago sativa subsp. sativa	Turkey	2.4	4.1	12.0	453.2	159.0	3.8	3.3
PI_442810	core	Trek	Medicago sativa subsp. sativa	Canada	2.8	4.1	14.0	446.2	158.0	4.3	2.3

Integrate Forage Quality Data

PDB = Percent dry biomass

PI	Source	Plant ID	Taxonomy	Origin	Ca (PDB)	P (PDB)	K (PDB)	Mg (PDB)	CP (PDB)	ADF (PDB)	NDF (PDB)	RFV	TDN (PDB)	Lignin (PDB)	IVTDMD (PDB)	dNDF48 (PDB)
PI_467942	core	PGR 12451	Medicago sativa subsp. sativa	U.S.	1.43	0.26	1.87	0.39	21.22	30.67	37.94	164.02	65.01	6.94	76.17	16.03
PI_467977	core	PGR 12486	Medicago sativa subsp. falcata	U.S.	1.34	0.26	1.74	0.39	21.51	30.45	37.62	163.37	65.18	6.99	75.76	15.65
Bulldog505	Control	Bulldog505	Medicago sativa subsp. sativa	U.S.	1.56	0.26	1.76	0.42	21.96	29.51	36.32	173.37	65.91	6.57	76.98	15.37
W6_22287	Dormancy Check	Archer	Medicago sativa subsp. sativa	U.S.	1.45	0.26	1.96	0.39	21.78	28.74	35.48	175.95	66.51	6.29	78.06	15.76
PI_502532	core	Sibiriacka 232	Medicago sativa nothosubsp. varia	Former Soviet Union	1.30	0.26	1.95	0.38	21.17	31.21	38.50	159.02	64.59	6.98	75.89	16.34
PI_468053	core	PGR 12562	Medicago sativa nothosubsp. varia	Canada	1.58	0.26	1.88	0.41	21.87	28.12	34.74	185.46	66.99	6.14	78.68	15.50
PI_536538	Hist. Pop	Flemish Pop	Medicago sativa subsp. sativa	U.S.	1.57	0.25	1.85	0.41	21.08	29.23	36.03	173.19	66.13	6.60	77.32	15.56
PI_449306	core	Alta Sierra	Medicago sativa subsp. sativa	Chile	1.43	0.27	1.78	0.39	21.31	29.94	36.89	168.22	65.58	6.69	76.39	15.43
PI_172985	core	No. 8387	Medicago sativa subsp. sativa	Turkey	1.36	0.26	1.68	0.43	22.21	30.88	38.02	164.41	64.84	7.11	75.86	15.69
PI_442810	core	Trek	Medicago sativa subsp. sativa	Canada	1.40	0.25	1.71	0.40	20.69	28.33	35.09	178.43	66.83	6.16	78.31	15.38



Welcome to the Alfalfa Breeder's Toolbox

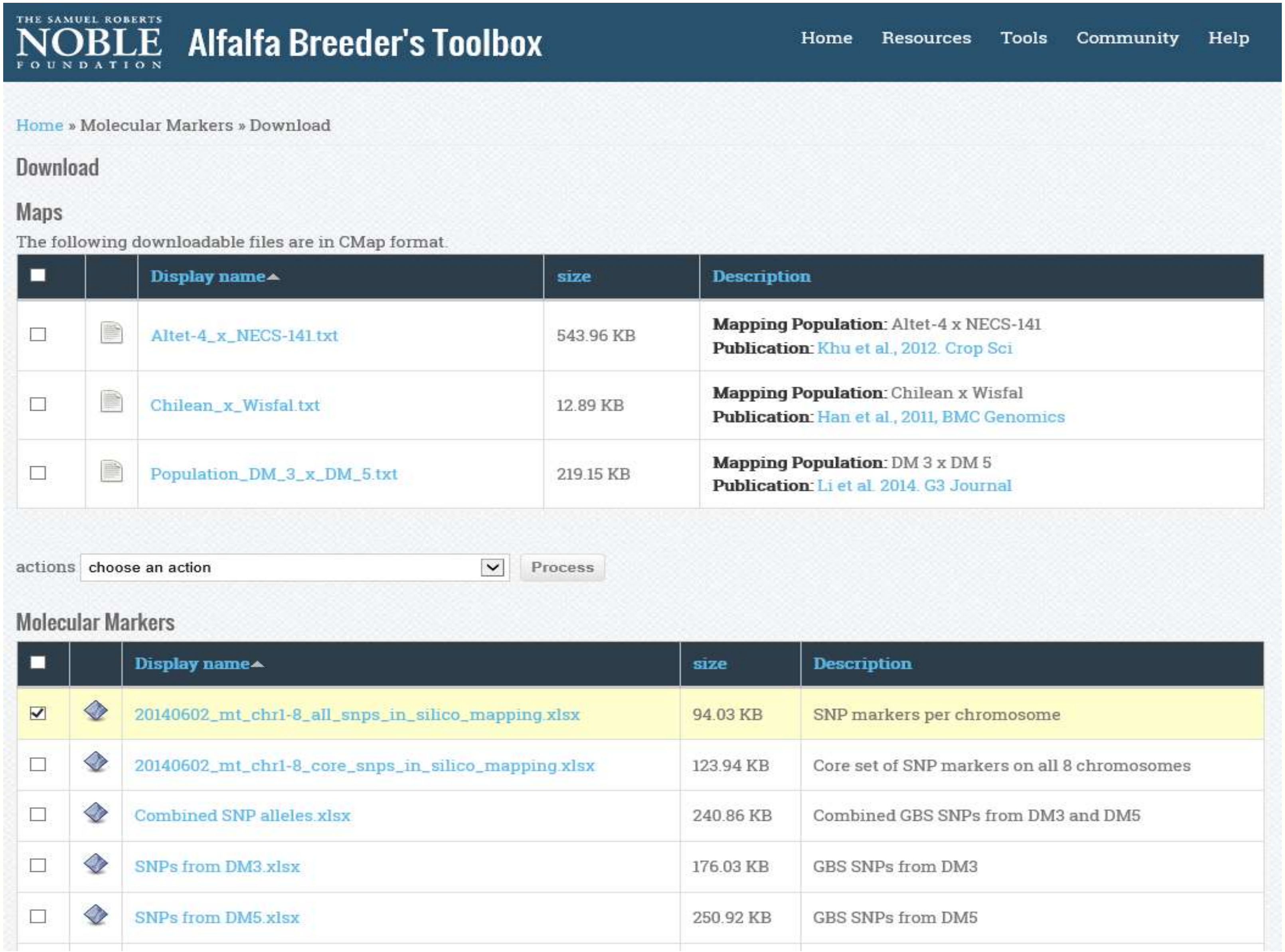
The Alfalfa Breeder's toolbox aims to provide convenient access to alfalfa genomic, genetic and phenotyp om U.S. and international research. We have embarked on a journey to sequence the alfalfa genome and use scientific knowledge to ment strategies. Included are genetic markers for use in molecular breeding approaches to develop enhanced alfalfa cultivars that roduction systems regionally and globally.

The alfalfa genomics sequencing efforts and the toolbox are a collaboration between multiple organizations and made possible through support from the Noble Foundation and Industry partners.

Search options

Genome Browser Position: M. sativa (CADL) chr/scaffold scaffold1 Range 10000 - 100000

Sequence:
>EF654111.2 Medicago sativa subsp. falcata DREB1
AAAACAAACTCTCTCCAATTCCGACTTTACCTCTCAACACCATTTTCCAC
TCTATCCAACACATACATATATGATTACTACTAACAACTCTTCCTATTCA
CACTCCATTTCCTCAAAAGATTTTTCTCCCTTCGACGCATCATCACCGAA



Home » Molecular Markers » Download

Download

Maps

The following downloadable files are in CMap format.

☐		Display name▲	size	Description
☐		Altet-4_x_NECS-141.txt	543.96 KB	**Mapping Population:** Altet-4 x NECS-141 **Publication:** Khu et al., 2012. Crop Sci
☐		Chilean_x_Wisfal.txt	12.89 KB	**Mapping Population:** Chilean x Wisfal **Publication:** Han et al., 2011, BMC Genomics
☐		Population_DM_3_x_DM_5.txt	219.15 KB	**Mapping Population:** DM 3 x DM 5 **Publication:** Li et al. 2014. G3 Journal

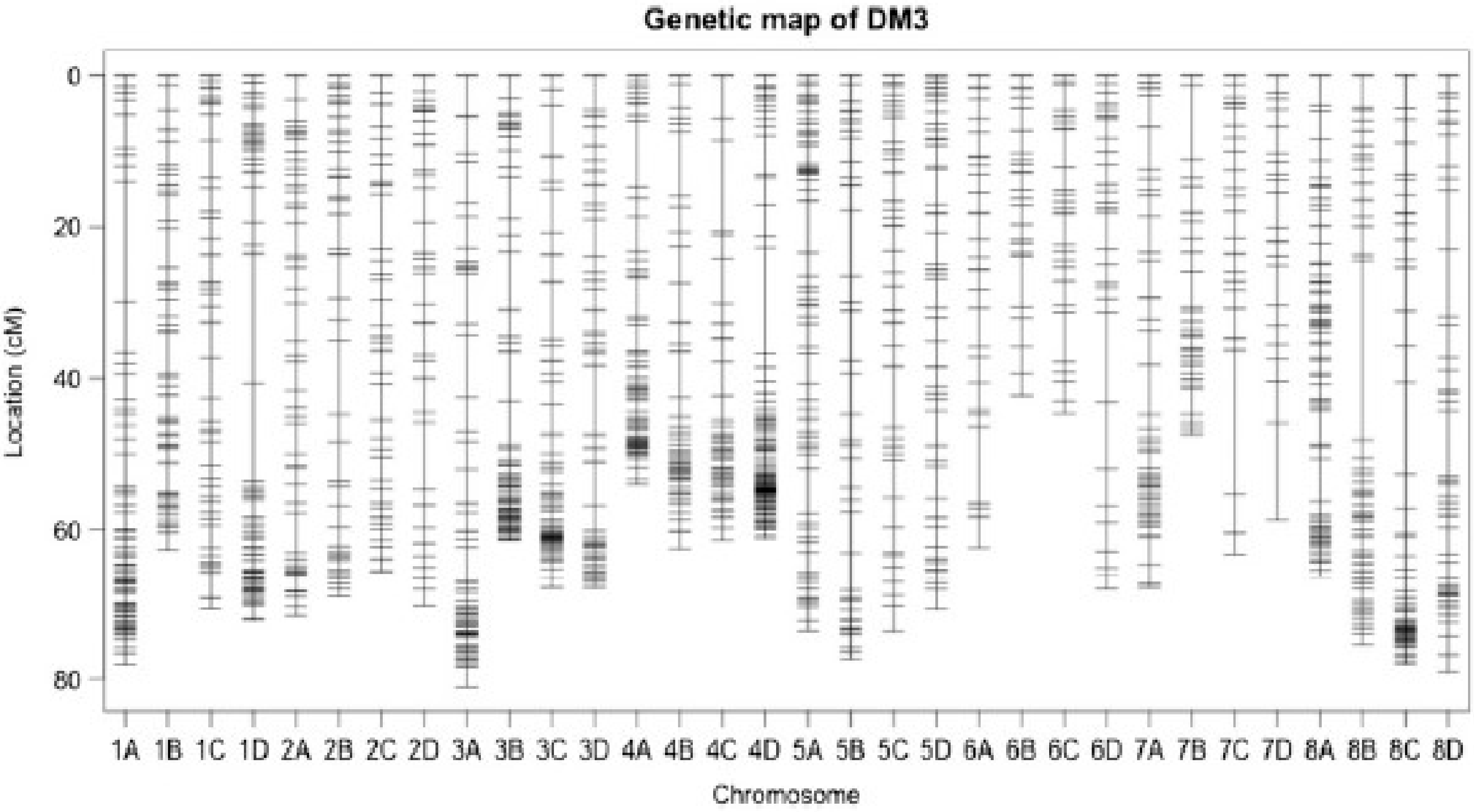
Molecular Markers

☐		Display name▲	size	Description
☑		20140602_mt_chr1-8_all_snps_in_silico_mapping.xlsx	94.03 KB	SNP markers per chromosome
☐		20140602_mt_chr1-8_core_snps_in_silico_mapping.xlsx	123.94 KB	Core set of SNP markers on all 8 chromosomes
☐		Combined SNP alleles.xlsx	240.86 KB	Combined GBS SNPs from DM3 and DM5
☐		SNPs from DM3.xlsx	176.03 KB	GBS SNPs from DM3
☐		SNPs from DM5.xlsx	250.92 KB	GBS SNPs from DM5

Alfalfa Linkage Map Using GBS

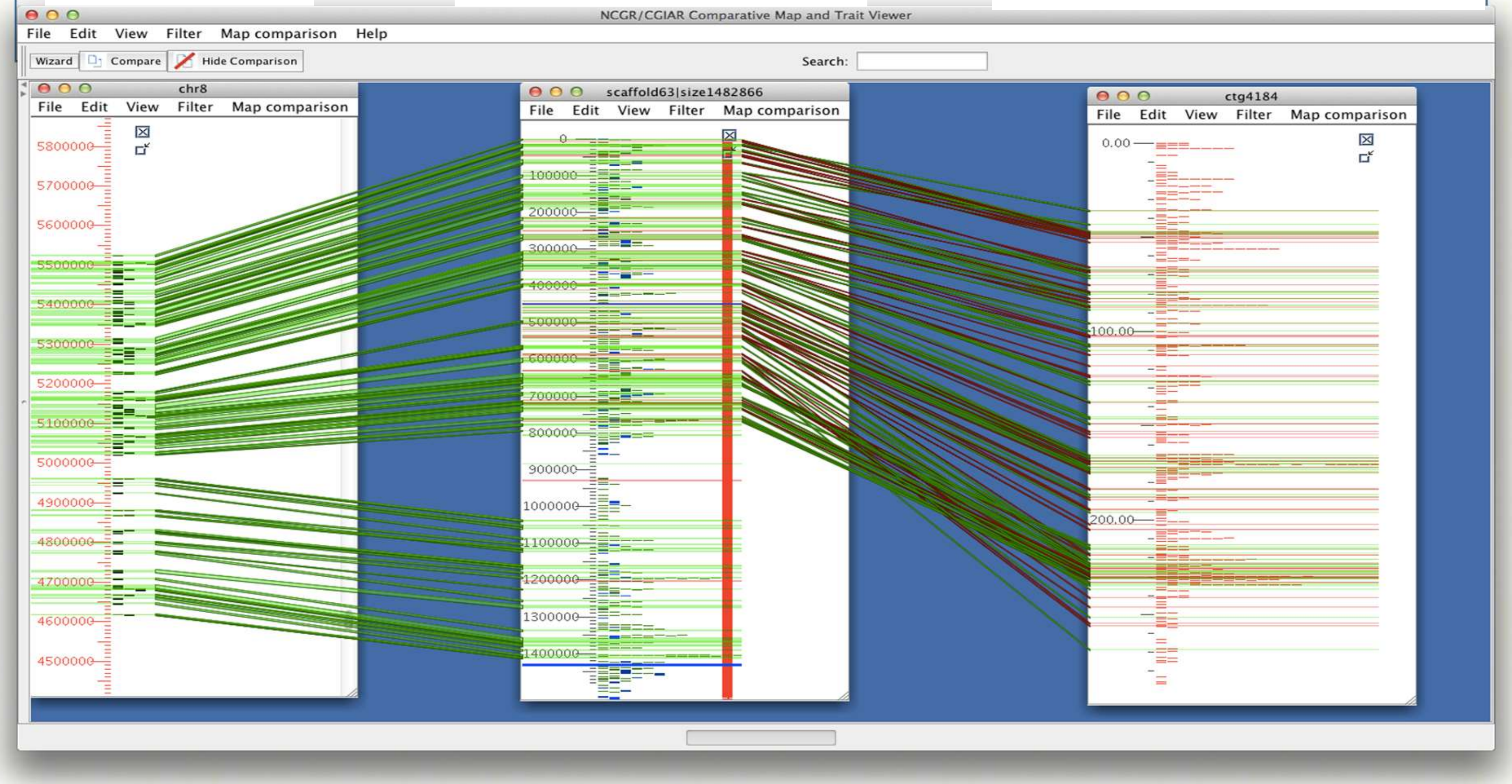
- **Population: DM3 x DM5**
- **A total of 3,591 SNPs**
- ***Ape*KI**

Li et al. 2014. G3-Genes Genomes Genetics. 4(10):1971-9.



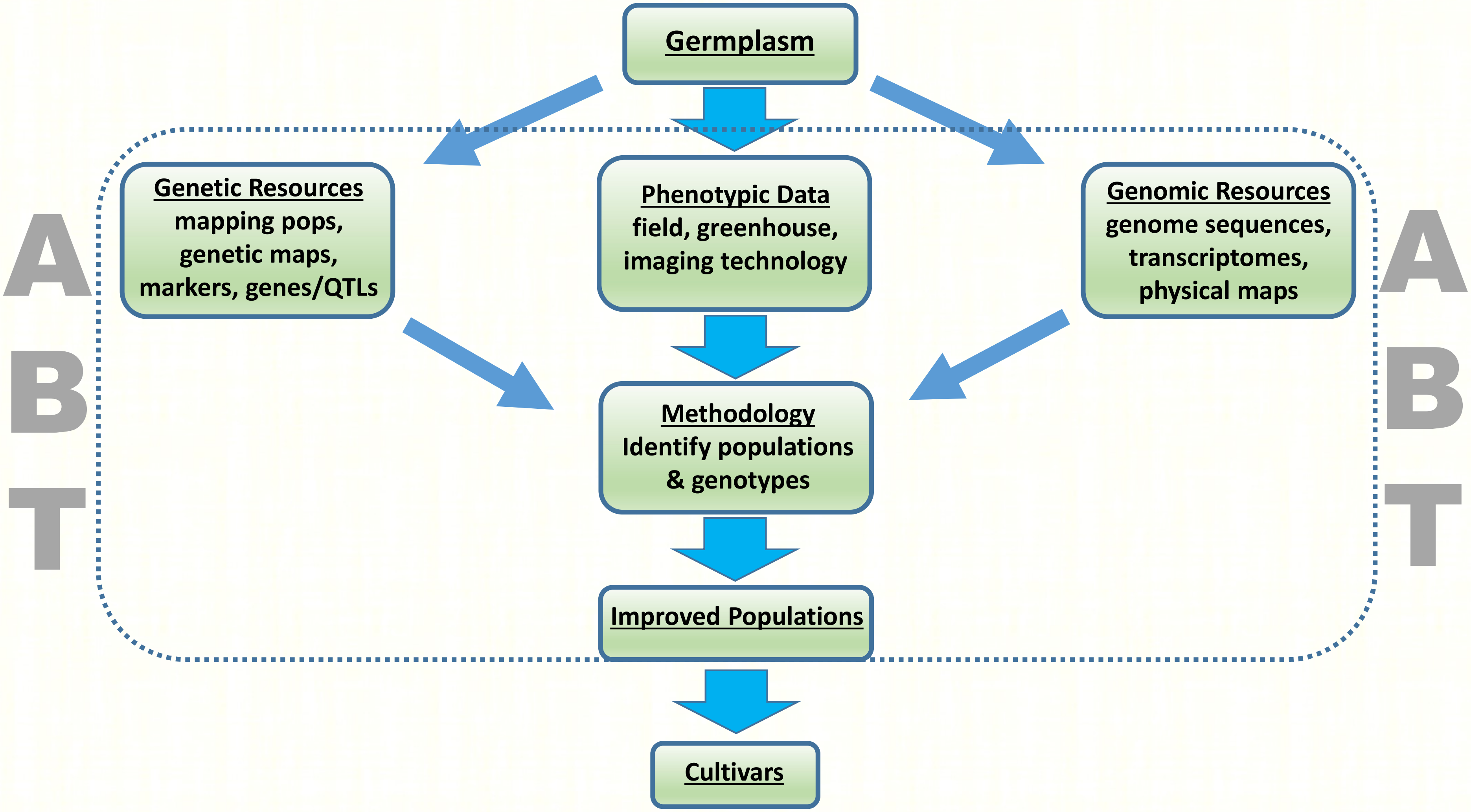
Synteny Between Alfalfa and Other Legumes

Mt 4.0 Csome **CADL 2X alfalfa (100X)** **WGP physical map contig (4X)**



Source: Andrew Farmer at NCGR

Strategy for Alfalfa Improvement



Germplasm

Genetic Resources
mapping pops,
genetic maps,
markers, genes/QTLs

Phenotypic Data
field, greenhouse,
imaging technology

Genomic Resources
genome sequences,
transcriptomes,
physical maps

Methodology
Identify populations
& genotypes

Improved Populations

Cultivars

Summary of Progress and Ongoing Activities

Achievements

- Developed a beta version of the ABT website
- Integrated Mt 4.0 and CADL genomes and the gene models into the JBrowse
- Anchored SNP and SSR markers to the genomes
- Established pipeline for data acquisition, processing, curation and integration

Ongoing

- Integrating the RNA-seq datasets for Al and drought tolerance gene expression atlas (resistant vs. susceptible)
- Continue to develop functionalities for test case scenarios for breeding applications
- Search capability for germplasm and phenotypic data obtained from the field
- Integrate CMap functionalities and syntenic data from other legumes

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- **ABT team members**

  Maria Monteros, Patrick Zhao, Chunlin He, Jaeyoung Choi, Perdeep Mehta, Michael Trammell, Xinbin Dai , Junil Chang, Nick Krom, Christy Motes, Alyssa Nedley, Wenchao Zhang, Yuhong Tang, Malay Saha, Melanie Davis, Justin Vaughn

- **Lab members**

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