

Tutorial: How to use BLAST with Eco TILLING database

1. Visit <https://triticeaetoolbox.org/wheat/>
2. Login, your account must be registered as CAP participant.

Quick Links

[Login/Register](#)

Current selections:
[Lines: 0](#)
[Markers: All](#)
[Traits: 0](#)
[Phenotype Trials](#)
[Genotype Experiments](#)

What's New

Breeders Datafarm Data

The Wheat Breeders Datafarm has been retired. Each of the 884 phenotype trials have been copied across to T3/Wheat.

Reports

[Variation Effects list SIFT](#)
score and consequences for

Login/Register

Why Register?

Participants

- have pre-release access to all phenotype and genotype data from the project.

All Registered Users

- can create private germplasm line panels. ([Tutorial](#))
- can use the "Current Selections" they created during the previous session.

What is your email address?

My email address is:

Do you have a password?

Yes, I have a password:

No, I am a new user.

I forgot my password.

I want to change my password.

3. Select Analyze – BLAST

Basic Search - using default BLAST parameter settings

Enter query sequences here in [Fasta format](#)

Or upload sequence fasta file: No file chosen

Program

Database(s)
Wheat TGACv1
Wheat Pangenome
RefSeq_v1

And/or upload sequence fasta file: No file chosen

- Paste nucleotide sequence into text area
- Select Database "RefSeq_v1"

Basic Search - using default BLAST parameter settings

Enter query sequences here in Fasta format

```
AGACGGTGCCCTAGACCCTGTTGTATCCCACGTTTTTACTGAACAGGCGGCGGAT
GTAACGACTTGCAACGCACTGGCGCCATGAAAGCCGCGTACTCT
```

Or upload sequence fasta file: No file chosen

Program Database(s)

And/or upload sequence fasta file: No file chosen

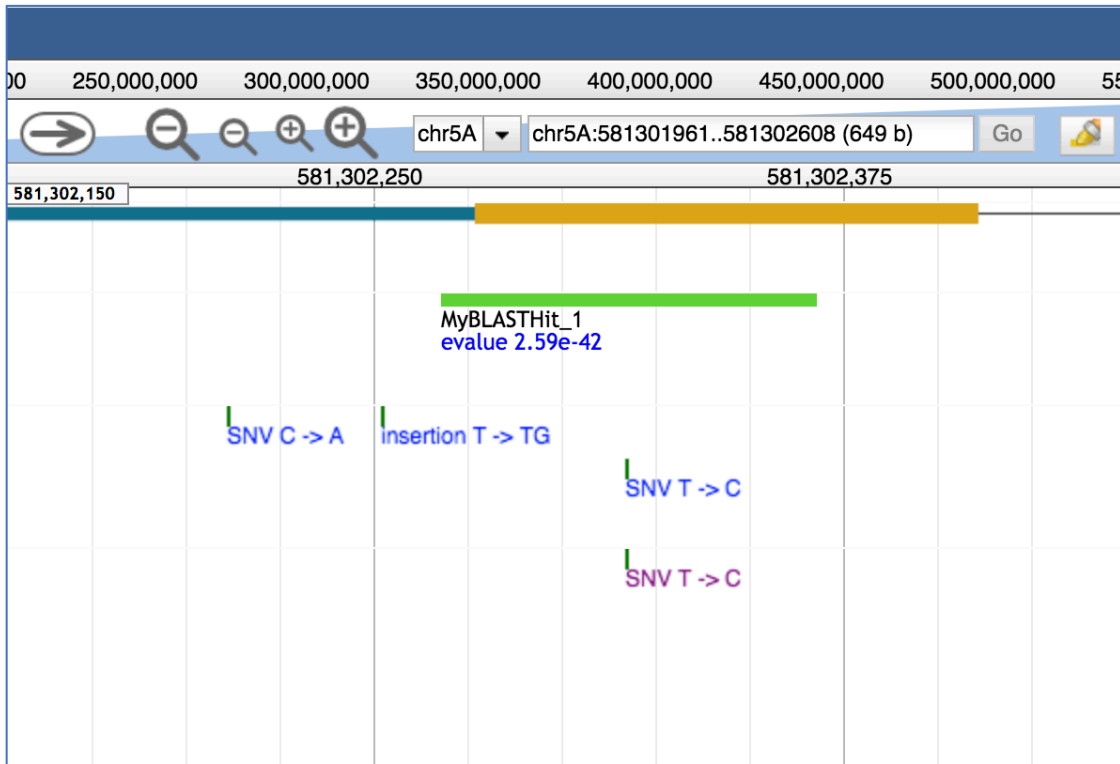
- Select "Basic search"
- The results of the analysis will be similar to the screen below.

Distribution of 3 Blast Hits on the Query Sequence
Color keys for alignment scores

Select/Deselect all

Query	Subject	Score	Identities (Query length)	Percentage	Expect	Start	End	T3 JBrowse	URGI JBrowse
Query1	<input type="checkbox"/> chr5A	<u>178</u>	100/101 (101)	99.01	3e-42	581302267	581302367	chr5A	chr5A
Query1	<input type="checkbox"/> chr5B	<u>172</u>	98/100 (101)	98.00	1e-40	567155439	567155538	chr5B	chr5B
Query1	<input type="checkbox"/> chr5D	<u>165</u>	97/101 (101)	96.04	2e-38	461214890	461214990	chr5D	chr5D

- Select the link under T3 JBrowse to view the match. Under “Available Tracks” you should check the “BlastHSP Results”. This shows you the BLAST match.



- Also select either “All Accessions with SNPEff” or “Combined Dubcovsky” to view the SNP’s for each of the TILLING lines.

- Click on a SNP from these two tracks to display lines containing the SNPs.

SNV

BaseQRankSum	-2.346
DP	721
Dels	0.00
ExcessHet	0.0000
FS	1.100
HaplotypeScore	0.3229
InbreedingCoeff	0.8760
MLEAC	66
MLEAF	0.579
MQ	60.00
MQ0	0
MQRankSum	0.000
QD	25.01
ReadPosRankSum	6.246
SOR	0.620
alternative_alleles	C
description	SNV T -> C
reference_allele	T
seq_id	chr5A

Genotypes (60)

non-variant	25	41.67%
homozygous for reference	22	36.67%
no call	3	5%
variant	35	58.33%
homozygous	33	55%
C variant	33	55%
heterozygous	2	3.33%
Total	60	100%

Name	GT	AD	DP	GQ	PL
16REG01643	C / C	0 2	2	6	51 6 0
16REG01644	C / C	0 3	3	9	92 9 0
2045A	ref (T) / ref (T)	32 0	32	60	0 60 788
26R61	C / C	0 10	10	30	276 30 0

OK