GrainGenes: Improved BLAST Services and Genome Browsers to Navigate IWGSC Data

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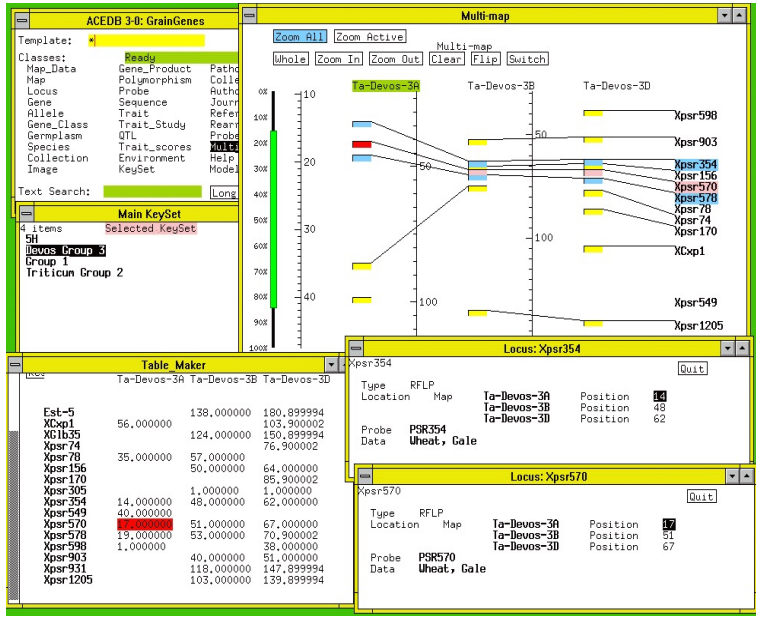
This presentation has been adapted from the one presented at the virtual IWGSC workshop at the Plant and Animal Genome Conference, Jan 11, 2022.

All animations have been parsed into individual frames with relevant points.

GrainGenes : From gene-centric to genome-centric

...but genes are still really important!



The 1990's – ACeDB database is object oriented and very flexible for a limited amount of data.

The 2000's – MySQL relational database can handle a LOT more data. Manually intensive Web site

The GrainGenes project began in Olin Anderson's lab at the USDA/ARS's Western Regional Research Center (WRRC) in the early 1990s. It remains an active part of the US small grains research community as a data hub and permanent repository.

The 2010-20's – MySQL remains stable. Drupel Web Management Genome Browsers and BLAST services

GrainGenes Updates

- December 2021: Rye Weining genome browser and BLAST are available
- December 2021: Wheat Fielder genome browser and BLAST are available
- October 2021: PepsiCo releases annotated gene set and associated files for OT3098 v2 genome in partnership with GrainGenes
- October 2021 : More MASWheat Quality Genes Curated
- October 2021: Aegilops tauschii Aet v5.0 genome browser and BLAST are available
- September 2021: Black awns gene class curated from Wheat Gene Catalogue
- September 2021: WAPO1, a candidate 'spikelet number per spike' gene.
- September 2021: Polyphenol oxidase genes updated with links to MASWheat and the WGC
- September 2021: Quick Links on GrainGenes' homepage are enriched
- August 2021: Historical (1960-1969) hard red spring wheat performance nursery reports added
- August 2021: Glume color genes curated from the WGC
- August 2021: Lipoxygenase genes updated with links to MASWheat and the WGC

more updates....

Check GrainGenes Updates for new content:

- new genome browsers
- large curation projects
- community contributions
- overall improvements to the project

GrainGenes
A Database for Triticeae and Avena

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October 2021 : More MASWheat Quality Genes Curated

Share this on: SHARE

Genes for 'Quality and Yield' traits with protocols at MASWheat were curated for:

- Reduced cadmium concentration
- Thousand Grain Weight and Grain Size gene TaGW2-A1
- Starch properties. Waxy mutants

New genes and alleles were also linked to the Catalogue of Gene Symbols for Wheat at Komugi.

Genes and alleles below have been newly curated or updated with references and links.

Cdu1 (Triticum)

TaGW-A2 (Triticum)

Wx-A1 (Triticum)

- Wx-A1a (Triticum)
- Wx-A1b (Triticum)
- Wx-A1c (Triticum)
- Wx-A1d (Triticum)
- Wx-A1e (Triticum)
- Wx-A1f (Triticum)
- Wx-A1g (Triticum)
- Wx-A1h (Triticum)

'Drupel' pages for GrainGenes Updates are created to support announcements with narrative, metadata, and links to new data records.

GrainGenes strongly supports the MASWheat project at UC Davis (maswheat.org; Dubcovsky Lab), with links to method pages from gene records.

GrainGenes is a digital platform that serves small grains research community as a centralized repository for peer-reviewed and curated data, and as a facilitator for community activities. GrainGenes has been hard-funded by the U.S. Department of Agriculture-Agricultural Research Service to ensure long-term data sustainability through a functional and integrated web interface for wheat, barley, oat, and rye. Please let us know how GrainGenes can improve its interface, tools, and services by using the Feedback button. Please cite us: Blake et al, Database, 2019.

Follow Us

PepsiCo OT3098 Hexaploid Oat Version 2 Genome Assembly Release in collaboration with GrainGenes

PepsiCo releases version 2 of OT3098 reference genome [April 2021]
By: Dr. Mandy Waters, PepsiCo

Method comparison between OT3098 v1 and v2:
Written by Dr. Kevin Fengler, Corteva Agrisciences

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GrainGenes Updates

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- August 2021: Lipoxygenase genes updated with links to MASWheat and the WGC

more updates....

AN INTERNATIONAL, COLLABORATIVE RESEARCH CONSORTIUM

Established in 2005 by a group of wheat growers, plant scientists, and public and private breeders

MISSION

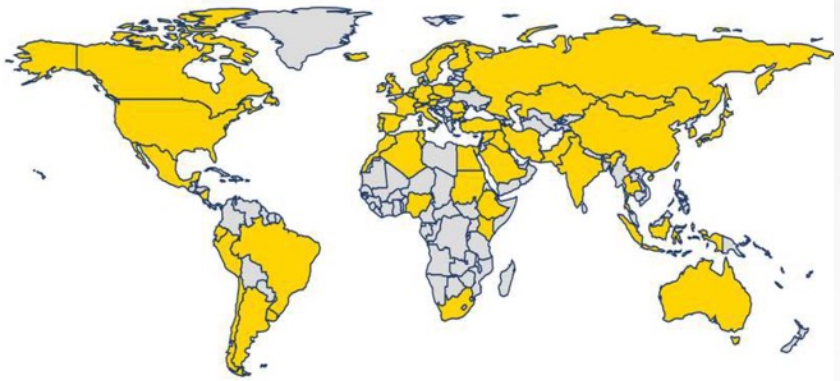
Make a high quality genome sequence of bread wheat publicly available

VISION

Lay a foundation for basic research that will enable breeders to develop improved wheat varieties

Visit IWGSC at www.wheatgenome.org

2,400 MEMBERS IN 68 COUNTRIES



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International Wheat Genome Sequencing Consortium

Generating a high quality genome sequence of bread wheat

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Press Releases

7 December 2021 - Curio Genomics joins the IWGSC

The IWGSC is pleased to announce that the bioinformatics company Curio Genomics has joined the organization as a sponsoring partner.

Curio Genomics provides a fully integrated, modern big data platform explicitly designed to rapidly and seamlessly analyze large and complex plant genomes, such as wheat. The Curio® platform is biologist-friendly, providing dynamic real-time data visualizations that empower researchers to ask more questions, leading to faster discovery.

Read More

Early Career Award

Ellie Taagen, PhD candidate at Cornell University (USA), was awarded the 2022 IWGSC and Catherine Feuillet Early Career Award. She will present a talk during the IWGSC main workshop at the Plant & Animal Genome Conference XXIX (PAG) in January 2022

Ellie's research is broadly focused on the biological constraints of meiotic recombination in a plant breeding context and aims to improve causal variant and prediction-based breeding decisions.

Read her profile and

PAG 2022

Join us at PAG 2022 - Virtual Event

Saturday 8 January: IWGSC Main workshop

- 8:00 to 10:10am Pacific Time
- Program
- Speaker Profiles

Tuesday 11 January 2022: From Structural to Functional Wheat Genomics Workshop

- 1:30 to 3:40 pm Pacific Time
- Program

41588_2012_BFng2447_MOESM12_ESM (version 1).xlsb - AutoRecovered

GrainGenes supports the IWGSC by providing genome browsers with a rich array of annotated tracks and curated data within the database.

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A Database for Triticeae and Avena

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GrainGenes Class Browser

Query (optional) *TraesCS*01G* in Class All GO

Use an asterisk -- * -- as a wildcard. For example, AA*1a will find Aadh-A1a (Triticum) and Aadh-B1a (Triticum). If you do not use any wild cards, they will be added to the beginning and end of the search text automatically for strings longer than a single character. Searching for a1a will automatically search for *a1a*.

This is a search of the GrainGenes database. To perform a more comprehensive, Google-powered, search of the entire GrainGenes website, click here.

Results: 357591 Records matching *TraesCS*01G* in 3 Classes

Class	Records
Locus	109995
Probe	110759
Sequence	136837

GrainGenes Class Browser

Query (optional) *TraesCS*02G* in Class All GO

Use an asterisk -- * -- as a wildcard. For example, AA*1a will find Aadh-A1a (Triticum) and Aadh-B1a (Triticum). If you do not use any wild cards, they will be added to the beginning and end of the search text automatically for strings longer than a single character. Searching for a1a will automatically search for *a1a*.

This is a search of the GrainGenes database. To perform a more comprehensive, Google-powered, search of the entire GrainGenes website, click here.

Results: 374006 Records matching *TraesCS*02G* in 3 Classes

Class	Records
Locus	132370
Probe	107891
Sequence	133745

Annotated records from the IWGSC RefSeq v1.1 and v1.2 are in the GrainGenes MySQL database. All have links to the genome browsers from the probe (methods) records.

Data types for IWGSC data in GrainGenes

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A Database for Triticeae and Avena

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Query (optional) in Class Locus GO

GrainGenes Locus Report: TraesCS1A01G002000.1
[Submit comment/correction] [What is a locus?]

Type	Gene
Probe	TraesCS1A01G002000
Chromosome	1A
Map Data	Wheat, 2018, IWGSC CS RefSeq v1.0 TraesCS1A01G002000
Species	Triticum aestivum
Reference	IWGSC et al. (2018) Shifting the limits in wheat research and breeding using a fully annotated reference genome Science 361.
Remark	BLAST Hit Accession: tr|A0A072UPV9|A0A072UPV9_MEDTR Human Readable Description: RING-finger ubiquitin ligase Pfam IDs Description: PF13639: Ring finger domain InterPro IDs Description: IPR001841: Zinc finger, RING-type; IPR013083: Zinc finger, RING/FYV GO IDs Description via InterPro: GO:0005515 MF: protein binding; GO:0008270 MF: zinc ion bi

Locus names have numerical extensions indicating the transcript.

Query (optional) *TraesCS*01G*2000* in Class Probe GO

GrainGenes Probe Report: TraesCS1A01G002000
[Submit comment/correction] [What is a probe?]

Probe	TraesCS1A01G002000
Browser	View in JBrowse
Locus	TraesCS1A01G002000.1
URL	[*Hide all but 1 of 6*] Pfam PF13639 InterPro IPR001841 InterPro IPR013083 Gene Ontology GO:0005515 Gene Ontology GO:0008270 Gene expression at wheat-expression.com (expVIP)
Reference	IWGSC et al. (2018) Shifting the limits in wheat research and breeding using a fully annotated reference genome Science 361.
General Remarks	BLAST Hit Accession: tr|A0A072UPV9|A0A072UPV9_MEDTR Human Readable Description: RING-finger ubiquitin ligase Pfam IDs Description: PF13639: Ring finger domain InterPro IDs Description: IPR001841: Zinc finger, RING-type; IPR013083: Zinc finger, RING/FYVE/PHD-type GO IDs Description via InterPro: GO:0005515 MF: protein binding; GO:0008270 MF: zinc ion binding
Type	Genomic
Sequence	TraesCS1A01G002000.1
Source Species	Triticum aestivum
Source Germplasm	Chinese Spring

Probes are 'methods'. Records have functional annotations, links to external resources, and links to the browser, locus, and sequences. Genes with multiple transcripts will have a single probe record.

GrainGenes Sequence Report: TraesCS1A01G002000.1
[Submit comment/correction]

Sequence	TraesCS1A01G002000.1
Germplasm	Chinese Spring
Species	Triticum aestivum
Probe	TraesCS1A01G002000
Gene Product	RING-finger ubiquitin ligase *New!*
Reference	IWGSC et al. (2018) Shifting the limits in wheat research and breeding using a fully annotated reference genome Science 361.
DNA	ATGGCGATGCGGGGCGTCGATTTCAAGTGGTACGACGGCTTCTTCCTCTC CATGCTCGCCACCAGCGTAATCATCGTGTCCATCAACTGGAGGAGGTACC GCCTCTGCGCCCACCCGCTCCACATATGGATCGTCGTCGACTACACCACC GTCTTCGTCTTCCGCCTCCTCATGTTCCTCGACAACGGACTCGCAGCAGG GATGGGGCTGGATCTTGGATGGCAACAGAGATATACTCGTTTCTGTGGGA GGATAGTTGTTCTGTCAGTCCTTGTTCTTCTTCTGTACCCCTTCCTGTGG GTTTGGACTGTGATAGGAACATTGTGGTTTAACAGTGCAAGGAGCTGCCT GCCAGAGGAAGGACAAAAATGGGGCTTCCTGATATGGCTGCTTTTCAGTT ACTGTGGCCTCGCCTGTATTGCATGCGTGGCTGTTGGAAAGTGGCTAAAC CGAAGGCACGCACTCCGCCTGAGGGCACAGCAGGGGATTCCGGTCTCTGA ATACGGGGTTTTGGTTGACATGATTCGTGTGCCTGACTGGGCATTTGAGG CGGTCGGCTTGGAACTGAGAGGAATGGGCCAGGACACTGCATACCATCCT GGTCTTTATCTGACAGCAGCCCAGAGAGAAGCTGTGGAGGCTCTTATCCA GGAGCTCCCCAAGTTCATGCTGAAAGCCGTCCCAACAGACTGCAGCGAGT GCCCGATCTGCCTGGAGGAGTTCAAGGTGGGCAACGAGGTGCGGGGGCTC CCCTGCGCGCACAACTTCCACGTGGAGTGCATCGACCAGTGGCTGCGGCT GAACGTCAAGTGCCCGCGCTGCCGCTGCTCCGTGTTCCCCAACCTGGACC TGAGCGCGCTCAACGGCATCCGCTCCAGCAGCGAGATGCTGCAGCAGGAC CGCCCCTCAGGGAGCAGCGGTGGAGAGGCGGTGGTGAGCCGGTACGTGGG GCCACAGCCGGGGCCGGGGCAGAGCTACCTGGTGCGGCTGCAGGGCCTGC TGCTCCGGCCCGTGGTGGGGCATCACGGCGGTGATGACGCTGAGGGCGGG CGAGCGGTGGTCGTTGATGGGGCTGAGGTGGCGGGCGGCGTGGTGGTGGT GGTTGAAGATGGGCATGAGCTGCGGGATCGCTGA

BLAST this sequence

Sequence records in GrainGenes now have a 'gene product' tag, which groups all genes with the same BLAST human readable description and is searchable in MySQL.

A link to the GrainGenes BLAST tool will automatically load the sequence into the interface.

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Query (optional) in Class Map Data GO

GrainGenes Map Data Report: Wheat, 2018, IWGSC CS RefSeq v1.0
[Submit comment/correction]

Map Data	Wheat, 2018, IWGSC CS RefSeq v1.0
Species	Triticum aestivum
Parent	Chinese Spring
Type	Physical
Map Units	bp
Reference	IWGSC et al. (2018) Shifting the limits in wheat research and breeding using a fully annotated reference genome Science 361.
URL	https://wheat.pw.usda.gov/jb?data=/ggds/whe-iwgsc2018 JBrowse Genome Browser for the v1.0 and v1.1 assemblies
Remarks	High Confidence genes from RefSeq v1.0 from Chinese Spring produced by the IWGSC. For functional annotations click on a locus link below or the probe record (2nd column in the locus list) for a record with a link to that gene on the browser.
Data Curator	Blake, Victoria Carollo
Locus	TraesCS1A01G000100.1 TraesCS1A01G000100 [*Show all 107501*]

Mapdata records in GrainGenes contain metadata and links to all loci.

Functional Annotations of IWGSC genes in GG

RefSeq v1.0

Locus : **TraesCS1A01G002000.1 –** Annotations (ex. Human Readable Description: RING-finger ubiquitin ligase)
- Link to Probe

Probe: **TraesCS1A01G002000 –** Annotations (ex. Human Readable Description: RING-finger ubiquitin ligase)
- links to Pfam, Interpro, GO
- Links to JBrowse

Sequence : **TraesCS1A01G002000.1 –** ***new!*** Gene Product added from BLAST description. Searchable in MySQL.
- BLAST into any collection or browser.

RefSeq v1.1 (gene numbers the same)

Locus : **TraesCS1A02G002000.1** – Link to Probe

Probe : **TraesCS1A02G002000** - Link to JBrowse
- Link to previous name (01G) for annotations, but not reciprocal (*to do list*)

RefSeq v2.1 (gene numbers are **NOT** the same)

- Not curated in GG MySQL

Hexaploid wheat BLAST databases

- databases with corresponding genome browsers

Wheat ABD Collections [Select all]

- Wheat Fielder pseudomolecules, Sato (Jun 2021)
- Wheat Chinese Spring IWGSC RefSeq v2.1 genome assembly (2021)
- 10+ Genome - ArinaLrFor v3.0 pseudomolecules (2020)
- 10+ Genome - Jagger v1.0 pseudomolecules (2020)
- 10+ Genome - Julius v1.0 pseudomolecules (2020)
- 10+ Genome - LongReach Lancer v1.0 (2020)
- 10+ Genome - CDC Landmark v1.0 pseudomolecules (2020)
- 10+ Genome - Mace v1.0 pseudomolecules (2020)
- 10+ Genome - SY Mattis v1.0 pseudomolecules (2020)
- 10+ Genome - Norin61 v1.1 pseudomolecules (2020)
- 10+ Genome - Triticum spelta PI190962 v1.0 pseudomolecules (2020)
- 10+ Genome - CDC Stanley v1.2 stanley (2020)
- Wheat Chinese Spring IWGSC RefSeq v1.0 genome assembly (2018)
- Hexaploid Wheat Pangenome, Montenegro (2017)
- Chinese Spring WGA pseudomolecules v1, all data (Oct 2016) [Toronto Agmt]

...

...

- Chinese Spring WGA pseudomolecules v1, mapped data (Oct 2016) [Toronto Agmt]
- IWGSCv1 Chinese Spring WGA pseudomolecules, unmapped (Oct 2016) [see Toronto Agmt]
- Chinese Spring (released runs), 5X coverage - UK Roche 454 sequencing (Sep 2010)
- IWGSC2 Triticum aestivum pseudomolecules rel25, all data (Nov 2014)
- IWGSC2 Triticum aestivum pseudomolecules rel25, formal map (Nov 2014)
- IWGSC2 Triticum aestivum pseudomolecules rel-25 scaffolds (Nov 2014)
- IWGSC2 Triticum aestivum pseudomolecules rel-25 organelle (Nov 2014)
- IWGSC Triticum aestivum pseudomolecule rel30, all data (Jan 2016)
- IWGSC Triticum aestivum pseudomolecules rel30, formal map (Jan 2016)
- IWGSC Triticum aestivum pseudomolecule rel-30 scaffolds (Jan 2016)
- IWGSC Triticum aestivum pseudomolecule rel-30 organelle (Jan 2016)
- IWGSC Triticum aestivum pseudomolecules rel31, all data (Mar 2016)
- IWGSC Triticum aestivum pseudomolecules rel31, formal map (Mar 2016)
- IWGSC Triticum aestivum pseudomolecule rel-31 scaffolds (Mar 2016)
- IWGSC Triticum aestivum pseudomolecule rel-31 organelle (March 2016)
- Triticum aestivum cv. Chinese Spring NCBI WGA 3.1, Zimin (2017)
- Triticum aestivum cv. Claire Earlham Inst. v1 scaffolds, winter wheat (Jan 2017)
- Triticum aestivum cv. Paragon Earlham Inst. v1 scaffolds, spring wheat (Jan 2017)
- Triticum aestivum cv. Robigus Earlham Inst. v1 scaffolds, winter wheat (Jan 2017)

Wheat AB Collections [Select all]

- Wild Emmer Wheat Zavitan WEWSeq v2.0 pseudomolecules (2019)
- Triticum turgidum Durum Wheat Svevo Rel. 1.0 pseudomolecules (2019)
- Wild Emmer Wheat Zavitan WEWSeq v1.0 pseudomolecules (2017)
- Zavitan RefSeq v1 mapped gene set (Apr 2017)
- Zavitan RefSeq v1 unmapped gene set (Apr 2017)
- Triticum turgidum ssp. durum cv. Svevo pseudomolecules (Feb 2019)
- Triticum turgidum subsp. durum cv. Kronos Earlham Inst. v1 scaffolds (Jan 2017)

Wheat A Collections [Select all]

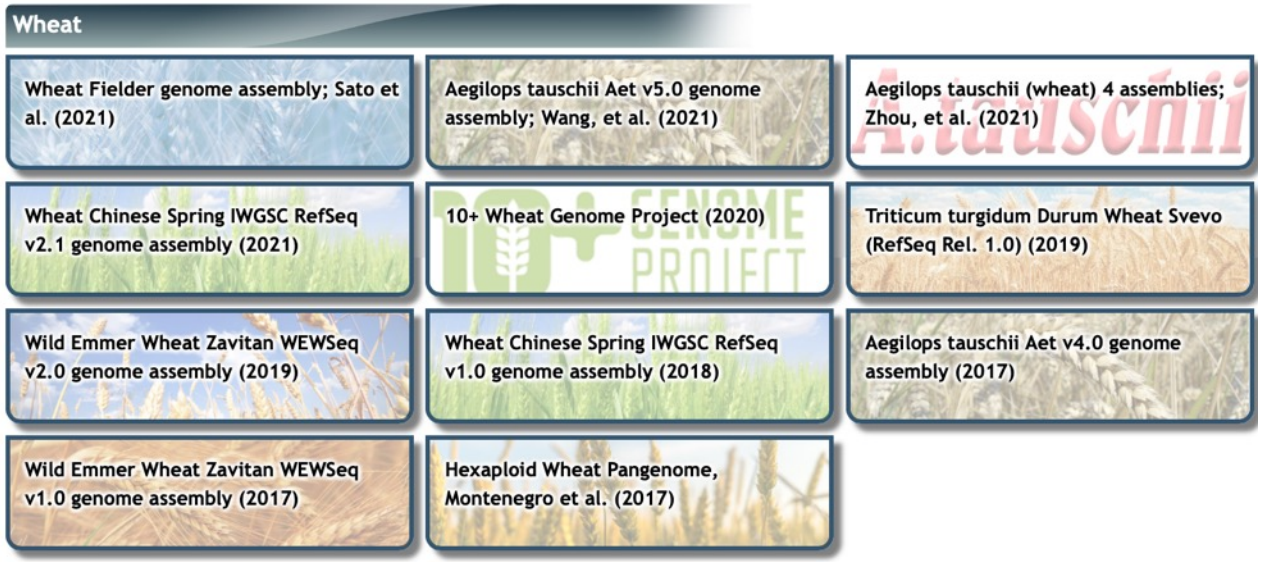
- Triticum dicoccoides cv. Zavitan v1, A-genome (May 2017)
- Triticum dicoccoides cv. Zavitan RefSeq v.1.0, B-genome (May 2017)
- Triticum monococcum cv. DV92 RNA-Seq transcriptome - OSU - Jaiswal (Aug 2012)

Wheat D Collections [Select all]

- Aegilops tauschii (Aet 5.0) pseudomolecules, Wang et al. (2021)
- Aegilops tauschii AY17, wheat pseudomolecules, Zhou et al. (2021)
- Aegilops tauschii AY61, wheat pseudomolecules, Zhou et al. (2021)
- Aegilops tauschii T093, wheat pseudomolecules, Zhou et al. (2021)
- Aegilops tauschii XJ02, wheat pseudomolecules, Zhou et al. (2021)
- Aegilops tauschii Aet v4.0 pseudomolecules, Luo et al. (2017)
- Aegilops tauschii BGI - Assembly from whole genome shotgun (Feb 2013)

diploid and tetraploid wheat BLAST databases

- databases with corresponding genome browsers



The Wheat genome browsers links are shown here.

The 10+ Wheat Genome Project link expands to links for the individual browsers.

The newest browser for cv. Fielder was done with PacBio long reads.

Wheat Browsers and Annotations

Fielder	**Sato** et al. (2021) annotated genes for cv. Fielder.
***Ae. tauschii* v5.0**	**Wang** et al. (2021) high & low conf. genes, RGA, community annotations for AL8/78
***Ae. tauschii*, 4 assemblies**	**Zhao** et al. (2021) annotations from TO93, AY61, XJ02, AY17
Chinese Spring IWGSC v2.1	**Zhu** et al. (2021) high & low conf. genes, TE, official markers, IWGSC annotations
10+ Genomes	**Walkowiak** et al. (2020) Genes, LTR retrotransposons, and TEs for: ArinaLrFor, Jagger, Julius, LongReach Lancer, CDC Landmark, Mace, SY Mattis, Norin61, PI90962, CDC Stanley
***T.turgidum* Svevo**	**Maccaferri** et al. (2019) high & low conf. genes, markers, QTL
Wild Emmer Zavitan v2.0	**Zhu** et al. (2019) gene annotations. **Scott** et al. (2019) Ancient Egyptian emmer SNPs
Chinese Spring IWGSC v1.0	**IWGSC** et al. (2018) high, low conf., manually-curated genes, TE, RNA
	T3 GWAS (https://wheat.triticeaetoolbox.org). **He** et al. (2018) 1000 Exomes
	Krasileva et al. (2017) TILLING mutants. **Jordan** et al. (2015) Hapmap variants
	Pont et al. (2019) WHEALBI variants. **Dubcovsky** EMS Mutations (https://dubcovskylab.ucdavis.edu).
	Cagirici et al. (2020) G-quadruplexes. **Jordan** et al. (2020) MNase chromatin states
	IPK 10+ Genome Project. genes, TE, LTR retrotransposons (https://www.ipk-gatersleben.de)
	Fauteux et al. (2019) expression QTL, seedling and spike SNPs
	Aknunov and **Dubcovsky**. Varietal SNPs (https://dubcovskylab.ucdavis.edu).
***Ae. tauschii* v4.0**	**Luo** et al. (2017) high & low conf. genes, mRNA
Wild Emmer Zavitan v1.0	**Avni** et al. (2017) high & low conf. genes, CDS, LTRs, homologs, mRNA
Hexaploid Pangenome	**Montenegro** et al. (2017) gene annotations, presence/absence variation (PAVs), SNPs

Example 1. Where can I find a gene / gene family on the 2021 IWGSC v2.1 genome browser?

GrainGenes Class Browser

Query (optional) RING-finger ubiquitin ligase in Class All GO

Use an asterisk -- * -- as a wildcard. For example, AA*1a will find Aadh-A1a (Triticum) and Aadh-B1a (Triticum). If you do not use any wild cards, they will be added to the beginning and end of the search text automatically for strings longer than a single character. Searching for a1a will automatically search for *a1a*.

This is a search of the GrainGenes database. To perform a more comprehensive, Google-powered, search of the entire GrainGenes website, click here.

Seven genes from the IWGSC v1.0 assembly are annotated with the exact phrase “RING-finger ubiquitin ligase”.

Users are encouraged to browse the data class and try other forms of this term for better coverage.

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Query (optional) in Class Gene Product GO

GrainGenes Gene Product Report: RING-finger ubiquitin ligase

[Submit comment/correction]

Gene Product	RING-finger ubiquitin ligase
Sequence	[*Hide all but 1 of 7*] TraesCS1A01G002000.1 TraesCS1B01G000900.1 TraesCS1D01G004000.1 TraesCS4B01G381000.1 TraesCS6A01G298300.1 TraesCS6B01G327800.1 TraesCS6D01G278100.1

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Query (optional) in Class Sequence GO

GrainGenes Sequence Report: TraesCS1A01G002000.1

[Submit comment/correction]

Sequence	TraesCS1A01G002000.1
Germplasm	Chinese Spring
Species	Triticum aestivum
Probe	TraesCS1A01G002000
Gene Product	RING-finger ubiquitin ligase
Reference	IWGSC et al. (2018) Shifting the limits in wheat research and breeding using a fully annotated reference genome **Science** 361.

DNA

```
ATGGCGATGCGGGGCGTCGATTTCAAGTGGTACGACGGCTTCTTCCTCTC
CATGCTCGCCACCAGCGTAATCATCGTGTCCATCAACTGGAGGAGGTACC
GCCTCTGCGCCCACCCGCTCCACATATGGATCGTCGTCGACTACACCACC
GTCTTCGTCTTCCGCCTCCTCATGTTCCTCGACAACGGACTCGCAGCAGG
GATGGGGCTGGATCTTGGATGGCAACAGAGATATACTCGTTTCTGTGGGA
GGATAGTTGTTCTGTCAGTCCTTGTTCTTCTTCTGTACCCCTTCCTGTGG
GTTTGGACTGTGATAGGAACATTGTGGTTTAACAGTGCAAGGAGCTGCCT
GCCAGAGGAAGGACAAAAATGGGGCTTCCTGATATGGCTGCTTTTCAGTT
ACTGTGGCCTCGCCTGTATTGCATGCGTGGCTGTTGGAAAGTGGCTAAAC
CGAAGGCACGCACTCCGCCTGAGGGCACAGCAGGGGATTCCGGTCTCTGA
ATACGGGGTTTTGGTTGACATGATTCGTGTGCCTGACTGGGCATTTGAGG
CGGTCGGCTTGGAACTGAGAGGAATGGGCCAGGACACTGCATACCATCCT
GGTCTTTATCTGACAGCAGCCCAGAGAGAAGCTGTGGAGGCTCTTATCCA
GGAGCTCCCCAAGTTCATGCTGAAAGCCGTCCCAACAGACTGCAGCGAGT
GCCCGATCTGCCTGGAGGAGTTCAAGGTGGGCAACGAGGTGCGGGGGCTC
CCCTGCGCGCACAACTTCCACGTGGAGTGCATCGACCAGTGGCTGCGGCT
GAACGTCAAGTGCCCGCGCTGCCGCTGCTCCGTGTTCCCCAACCTGGACC
TGAGCGCGCTCAACGGCATCCGCTCCAGCAGCGAGATGCTGCAGCAGGAC
CGCCCCTCAGGGAGCAGCGGTGGAGAGGCGGTGGTGAGCCGGTACGTGGG
GCCACAGCCGGGGCCGGGGCAGAGCTACCTGGTGCGGCTGCAGGGCCTGC
TGCTCCGGCCCGTGGTGGGGCATCACGGCGGTGATGACGCTGAGGGCGGG
CGAGCGGTGGTCGTTGATGGGGCTGAGGTGGCGGGCGGCGTGGTGGTGGT
GGTTGAAGATGGGCATGAGCTGCGGGATCGCTGA
```

BLAST this sequence

Sequence records have links to the BLAST tool. By BLASTing into the 2021 assembly, we can map this gene on the new genome.

wheat.pw.usda.gov/blast/

Examples: Wheat | Barley | Oat | Rye | Multi Sequence

```
ATGGCGATGCGGGGCGTCGATTTCAAGTGGTACGACGGCTTCTTCCTCTCCATGCTCGCCACCAGCGTAATCATCGTGTCCATCAACTGGAGGAGGTACCGCCTCTGCGCCCACCCGCTCCACATATGGATCGTCGTCGACTACACCACCGTCT
TCTTCCGCCTCCTCATGTTCCTCGACAACGGACTCGCAGCAGGGATGGGGCTGGATCTTGGATGGCAACAGAGATATACTCGTTTCTGTGGGAGGATAGTTGTTCTGTCAGTCCTTGTTCTTCTTCTGTACCCCTTCCTGTGGGTTTGGACTGT
AGGAACATTGTGGTTTAACAGTGCAAGGAGCTGCCTGCCAGAGGAAGGACAAAAATGGGGCTTCCTGATATGGCTGCTTTTCAGTTACTGTGGCCTCGCCTGTATTGCATGCGTGGCTGTTGGAAAGTGGCTAAACCGAAGGCACGCACTCCGCCTG
AGGGCACAGCAGGGGATTCCGGTCTCTGAATACGGGGTTTTGGTTGACATGATTCGTGTGCCTGACTGGGCATTTGAGGCGGTCGGCTTGGAACTGAGAGGAATGGGCCAGGACACTGCATACCATCCTGGTCTTTATCTGACAGCAGCCCAGAGAG
AAGCTGTGGAGGCTCTTATCCAGGAGCTCCCCAAGTTCATGCTGAAAGCCGTCCCAACAGACTGCAGCGAGTGCCCGATCTGCCTGGAGGAGTTCAAGGTGGGCAACGAGGTGCGGGGGCTCCCCTGCGCGCACAACTTCCACGTGGAGTGCATCGA
CCAGTGGCTGCGGCTGAACGTCAAGTGCCCGCGCTGCCGCTGCTCCGTGTTCCCCAACCTGGACCTGAGCGCGCTCAACGGCATCCGCTCCAGCAGCGAGATGCTGCAGCAGGACCGCCCCTCAGGGAGCAGCGGTGGAGAGGCGGTGGTGAGCCGG
TACGTGGGGCCACAGCCGGGGCCGGGGCAGAGCTACCTGGTGCGGCTGCAGGGCCTGCTGCTCCGGCCCGTGGTGGGGCATCACGGCGGTGATGACGCTGAGGGCGGGCGAGCGGTGGTCGTTGATGGGGCTGAGGTGGCGGGCGGCGTGGTGGTGG
TGGTTGAAGATGGGCATGAGCTGCGGGATCGCTGA
```

Detected: nucleotide sequence(s).

- databases with corresponding genome browsers

Wheat ABD Nucleotide Collections [Select all]

- Wheat Fielder pseudomolecules, Sato (Jun 2021)
- Wheat Chinese Spring IWGSC RefSeq v2.1 genome assembly (2021)
- 10+ Genome - ArinaLrFor v3.0 pseudomolecules (2020)
- 10+ Genome - Jagger v1.0 pseudomolecules (2020)
- 10+ Genome - Julius v1.0 pseudomolecules (2020)
- lecules (2020)
- 020)
- s (2020)
- (2020)
- pseudomolecules (2020)
-)
- ome assembly (2018)
- 017)
- ta (Oct 2016) [Toronto Agmt]
- ed data (Oct 2016) [Toronto Agmt]
- , unmapped (Oct 2016) [see Toronto Agmt]
- Chinese Spring (released runs), 5X coverage - OK Roche 454 sequencing (Sep 2010)
- IWGSC2 Triticum aestivum pseudomolecules rel25, all data (Nov 2014)
- IWGSC2 Triticum aestivum pseudomolecules rel25, formal map (Nov 2014)
- IWGSC2 Triticum aestivum pseudomolecules rel-25 scaffolds (Nov 2014)

Wheat AB Nucleotide Collections [Select all]

- Wild Emmer Wheat Zavitan WEWSeq v2.0 pseudomolecules (2019)
- Triticum turgidum Durum Wheat Svevo Rel. 1.0 pseudomolecules (2019)
- Wild Emmer Wheat Zavitan WEWSeq v1.0 pseudomolecules (2017)
- Zavitan RefSeq v1 mapped gene set (Apr 2017)
- Zavitan RefSeq v1 unmapped gene set (Apr 2017)
- Triticum turgidum ssp. durum cv. Svevo pseudomolecules (Feb 2019)
- Triticum turgidum subsp. durum cv. Kronos Earlham Inst. v1 scaffolds (Jan 2017)

Wheat A Nucleotide Collections [Select all]

- Triticum dicoccoides cv. Zavitan v1, A-genome (May 2017)
- Triticum dicoccoides cv. Zavitan RefSeq v.1.0, B-genome (May 2017)
- Triticum monococcum cv. DV92 RNA-Seq transcriptome - OSU - Jaiswal (Aug 2012)

Wheat D Collections [Select all]

- Aegilops tauschii (Aet 5.0) pseudomolecules, Wang et al. (2021)
- Aegilops tauschii AY17, wheat pseudomolecules, Zhou et al. (2021)
- Aegilops tauschii AY61, wheat pseudomolecules, Zhou et al. (2021)
- Aegilops tauschii T093, wheat pseudomolecules, Zhou et al. (2021)
- Aegilops tauschii XJ02, wheat pseudomolecules, Zhou et al. (2021)
- Aegilops tauschii Aet v4.0 pseudomolecules, Luo et al. (2017)
- Aegilops tauschii BGI - Assembly from whole genome shotgun (Feb 2013)

The sequence will automatically populate the input text box.

Here I selected the IWGSC v2.1 RefSeq BLAST database

Note that BLAST databases with the GG logo have individual genome browsers.

GrainGenes
BLAST Service BETA

Legacy BLAST service

New BLAST Query

Download FASTA, XML, TSV

FASTA of all hits

FASTA of selected hit(s)

Alignment of all hits

Alignment of selected hit(s)

Standard tabular report

Full tabular report

Full XML report

SequenceServer 2.0.0.rc4 using **BLASTN 2.12.0+**, query submitted on 2022-01-11 15:40:21 UTC

Databases: Wheat Chinese Spring IWGSC RefSeq v2.1 genome assembly (2021) (22 sequences, 14577412364 characters)

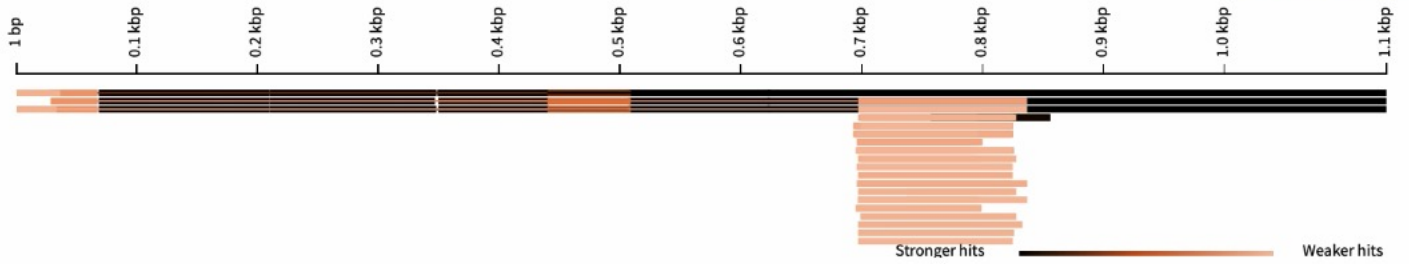
Parameters: task blastn, evalue 1e-05, sc-match 2, sc-mismatch -3, gap-open 5, gap-extend 2, filter L;m;

Please cite: https://doi.org/10.1093/molbev/msz185

Queries and their top hits: chord diagram

Query= Query_1 length: 1,134

Graphical overview of hits SVG | PNG



Length distribution of hits

Summary table of hits

#	Similar sequences	Query coverage (%)	Total score	E value	Identity (%)
1.	gnl|ta-IWGSCv2|Chr1A	100	2299	0	99
2.	gnl|ta-IWGSCv2|Chr1D	97	2066	0	92
3.	gnl|ta-IWGSCv2|Chr1B	99	2151	0	93
4.	gnl|ta-IWGSCv2|Chr7B	14	563	9.11×10^{-37}	80
5.	gnl|ta-IWGSCv2|Chr5A	12	296	2.98×10^{-11}	72
6.	gnl|ta-IWGSCv2|Chr5D	12	449	1.04×10^{-10}	73
7.	gnl|ta-IWGSCv2|Chr5B	9	147	5.39×10^{-8}	74
8.	gnl|ta-IWGSCv2|Chr2A	12	208	1.88×10^{-7}	72
9.	gnl|ta-IWGSCv2|Chr7A	12	209	6.56×10^{-7}	72
10.	gnl|ta-IWGSCv2|Chr4D	11	137	6.56×10^{-7}	71
11.	gnl|ta-IWGSCv2|Chr4B	11	71	6.56×10^{-7}	72
12.	gnl|ta-IWGSCv2|Chr4A	13	141	6.56×10^{-7}	71
13.	gnl|ta-IWGSCv2|Chr3A	12	139	6.56×10^{-7}	73
14.	gnl|ta-IWGSCv2|Chr3B	12	272	6.56×10^{-7}	75
15.	gnl|ta-IWGSCv2|ChrUnknown	9	138	2.29×10^{-6}	73
16.	gnl|ta-IWGSCv2|Chr7D	11	69	2.29×10^{-6}	70
17.	gnl|ta-IWGSCv2|Chr3D	12	68	2.29×10^{-6}	70
18.	gnl|ta-IWGSCv2|Chr2D	11	68	2.29×10^{-6}	72
19.	gnl|ta-IWGSCv2|Chr2B	11	66	7.99×10^{-6}	71

There are a lot of BLAST hits.

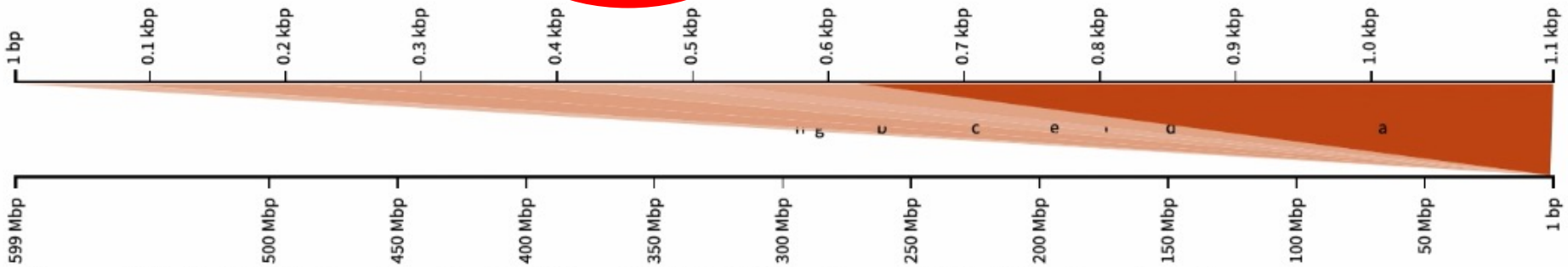
TraesCS1A01G002000.1 is on chromosome 1A, and the 1A BLAST hit is the strongest, as expected (hoped for).

13.	gnl|ta-IWGSCv2|Chr3A	12	139	6.56×10^{-7}	73
14.	gnl|ta-IWGSCv2|Chr3B	12	272	6.56×10^{-7}	75
15.	gnl|ta-IWGSCv2|ChrUnknown	9	138	2.29×10^{-6}	73
16.	gnl|ta-IWGSCv2|Chr7D	11	69	2.29×10^{-6}	70
17.	gnl|ta-IWGSCv2|Chr3D	12	68	2.29×10^{-6}	70
18.	gnl|ta-IWGSCv2|Chr2D	11	68	2.29×10^{-6}	72
19.	gnl|ta-IWGSCv2|Chr2B	11	66	7.99×10^{-6}	71

gnl|ta-IWGSCv2|Chr1A hit 1, length: 598,660,471

Select | Sequence | FASTA | Alignment | JBrowse

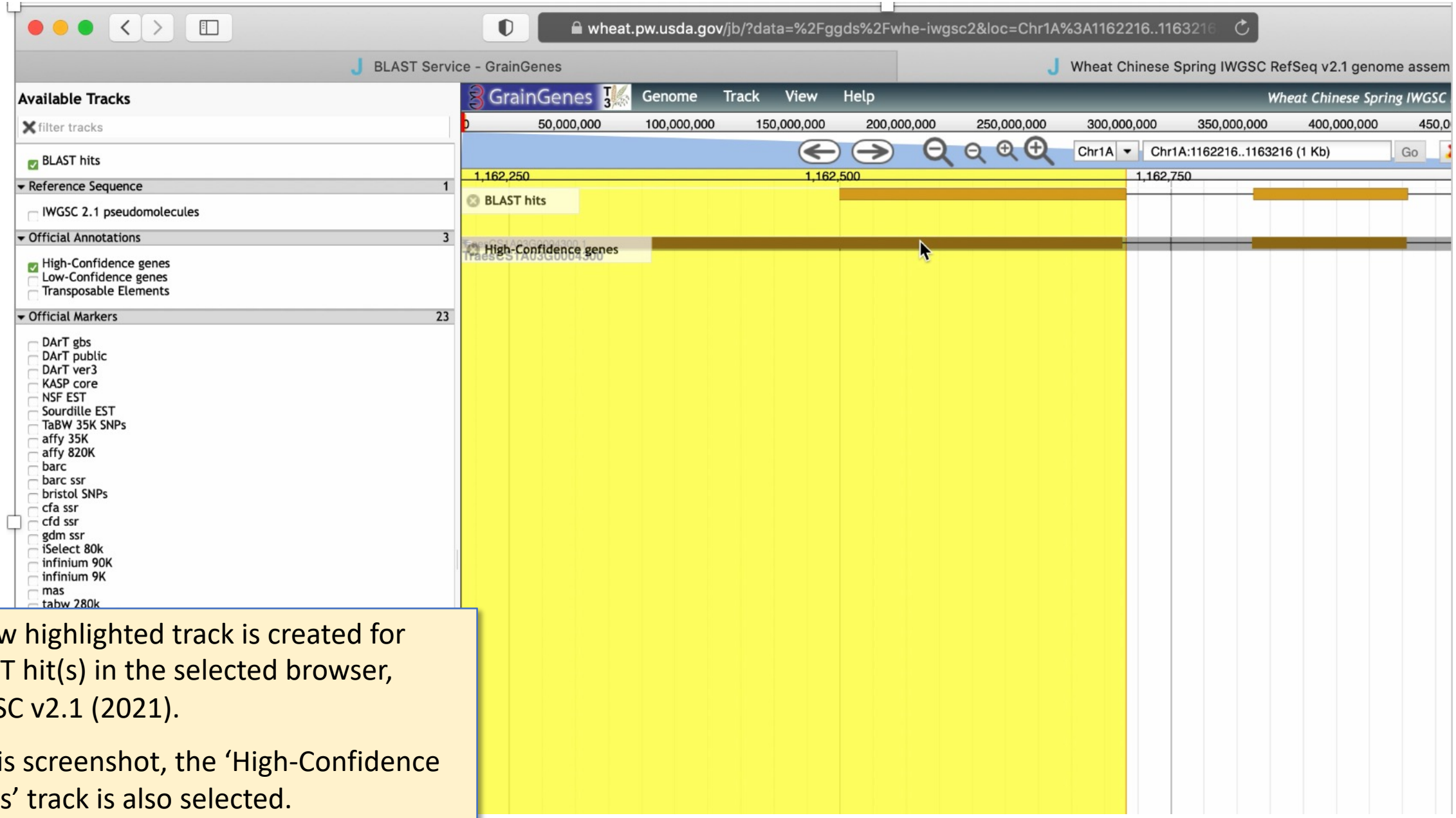
Graphical overview of aligning region(s) SVG | PNG




```
a. Score: 926.41 (1026), E value: 0, Identity: 513/513 (100%), Gaps: 0/513 (0%), Strand: + / -
                 AAGCTGTGGAGGCTCTTATCCAGGAGCTCCCCAAGTTCATGCTGAAAGCCGTCCCAACAGACTGCAGCGAGTGCCCGAT 707
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                 AAGCTGTGGAGGCTCTTATCCAGGAGCTCCCCAAGTTCATGCTGAAAGCCGTCCCAACAGACTGCAGCGAGTGCCCGAT 1162631
                 GAGGAGTTCAAGGTGGGCAACGAGGTGCGGGGGCTCCCCTGCGCGCACAACTTCCACGTGGAGTGCATCGACCAGTGGC 793
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                 GAGGAGTTCAAGGTGGGCAACGAGGTGCGGGGGCTCCCCTGCGCGCACAACTTCCACGTGGAGTGCATCGACCAGTGGC 1162545
                 GAACGTCAAGTGCCCGCGCTGCCGCTGCTCCGTGTTCCCCAACCTGGACCTGAGCGCGCTCAACGGCATCCGCTCCAGC 879
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                 GAACGTCAAGTGCCCGCGCTGCCGCTGCTCCGTGTTCCCCAACCTGGACCTGAGCGCGCTCAACGGCATCCGCTCCAGC 1162459
Query        880 AGCGAGATGCTGCAGCAGGACCGCCCCTCAGGGAGCAGCGGTGGAGAGGCGGTGGTGAGCCGGTACGTGGGGCCACAGCCGGGGCC 965
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Subject 1162458  AGCGAGATGCTGCAGCAGGACCGCCCCTCAGGGAGCAGCGGTGGAGAGGCGGTGGTGAGCCGGTACGTGGGGCCACAGCCGGGGCC 1162373
Query        966 GGGGCAGAGCTACCTGGTGCGGCTGCAGGGCCTGCTGCTCCGGCCCGTGGTGGGGCATCACGGCGGTGATGACGCTGAGGGCGGGC 1051
                 ''''''''''''''''''''''''''''''''''''''''''''''''''''''''''''''''''''''''''''''''''''''
```

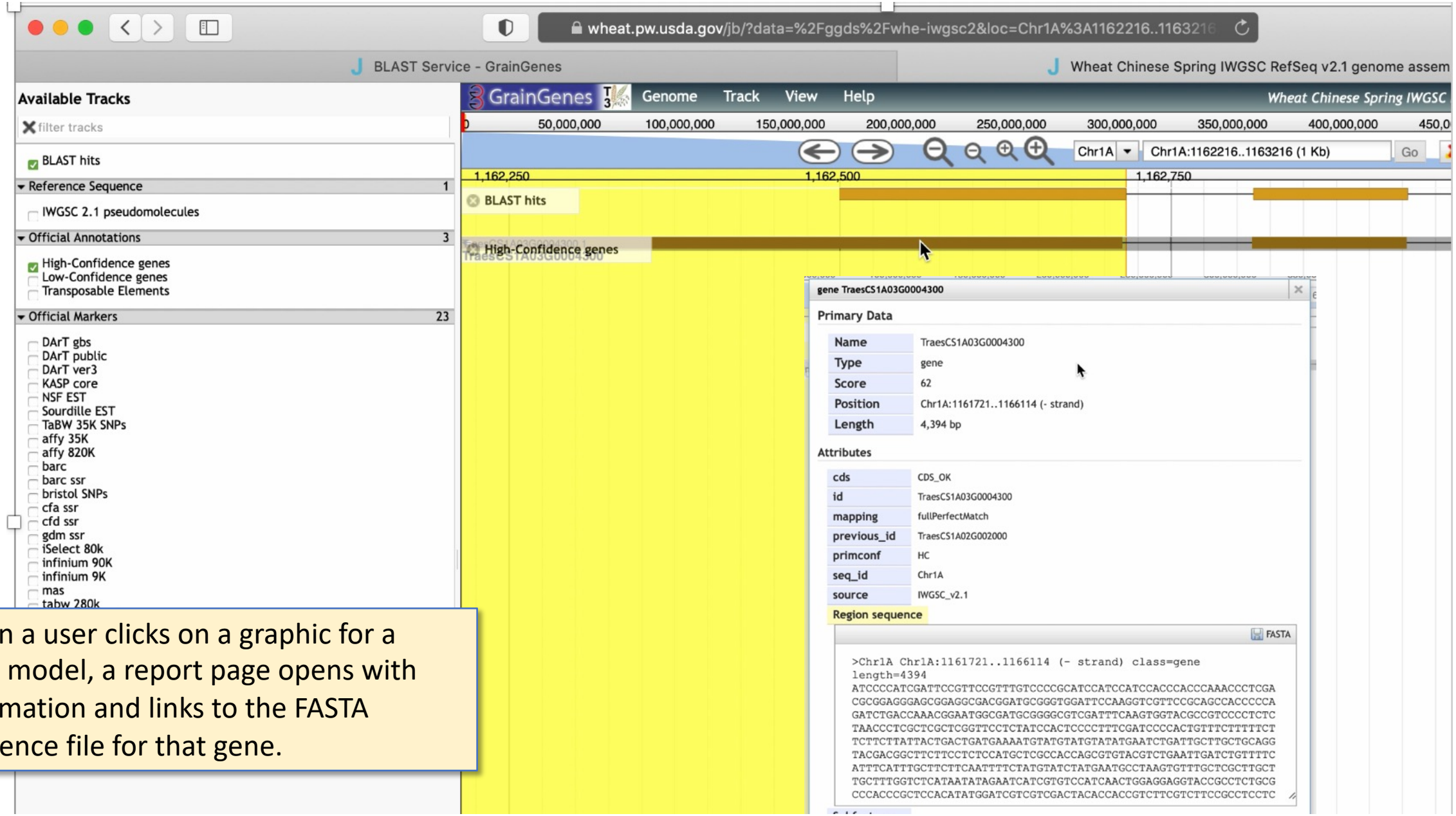
BLAST results are now presented in a graphical view.

A new feature is a direct link to the BLAST result on the genome browser. Look for the JBrowse link. (circled above)



A new highlighted track is created for BLAST hit(s) in the selected browser, IWGSC v2.1 (2021).

In this screenshot, the ‘High-Confidence genes’ track is also selected.



When a user clicks on a graphic for a gene model, a report page opens with information and links to the FASTA sequence file for that gene.

Example 2. How can one observe GWAS / QTL results in a genomic context?

Plant Biotechnology Journal
Open Access

Research Article | Open Access

Overexpression of *TaSTT3b-2B* improves resistance to sharp eyespot and increases grain weight in wheat

Xiuliang Zhu, Wei Rong, Kai Wang, Wei Guo, Miaoping Zhou, Jizhong Wu, Xingguo Ye, Xuening Wei, Zengyan Zhang

First published: 07 December 2021 | https://doi.org/10.1111/pbi.13760

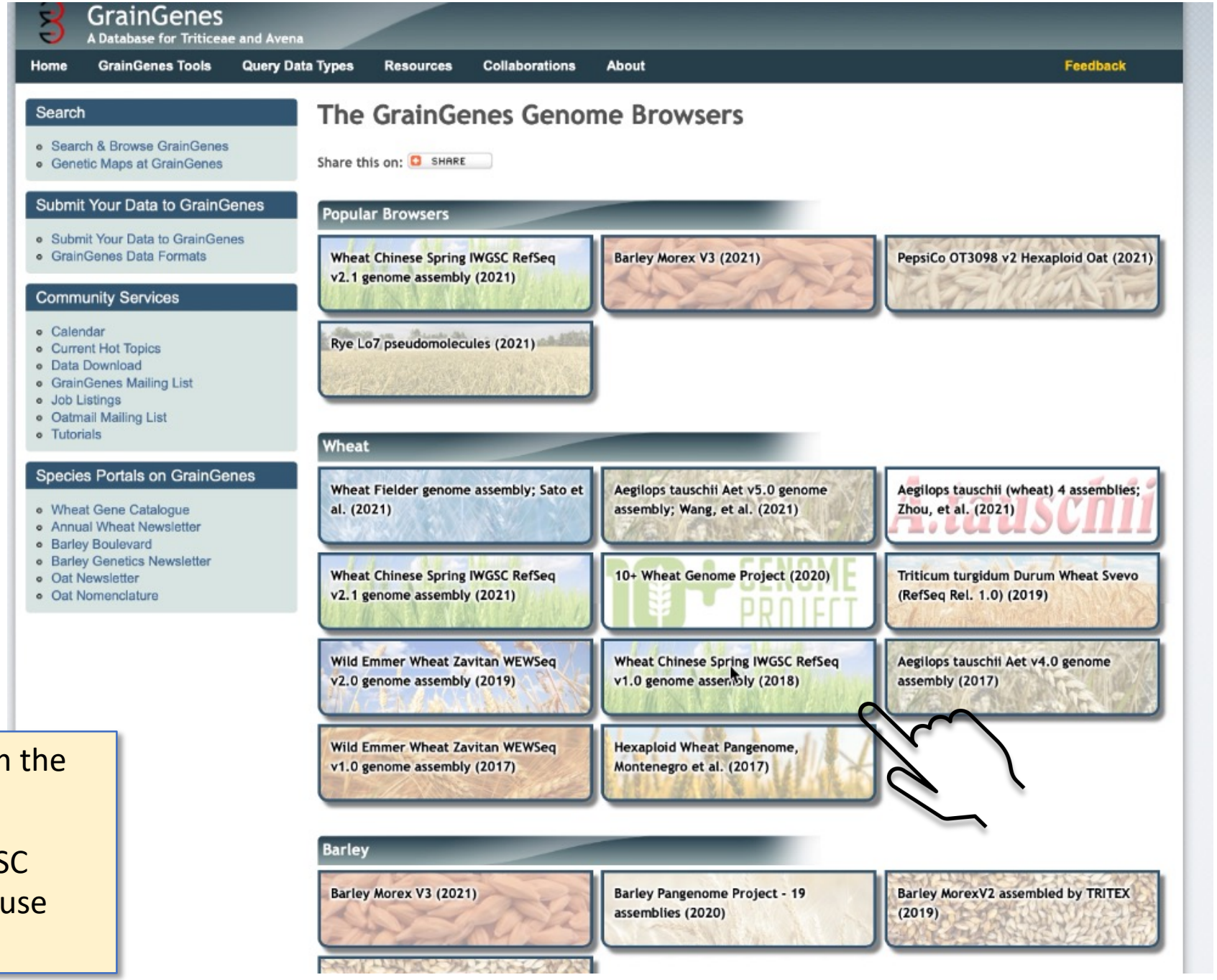
TraesCS1A02G340400.1

- Traes: Abbrev. for Triticum aestivum
- CS: Chinese Spring
- 1A: Chromosome 1A
- 02: 2nd genome assembly
- G340400: Gene number

Results

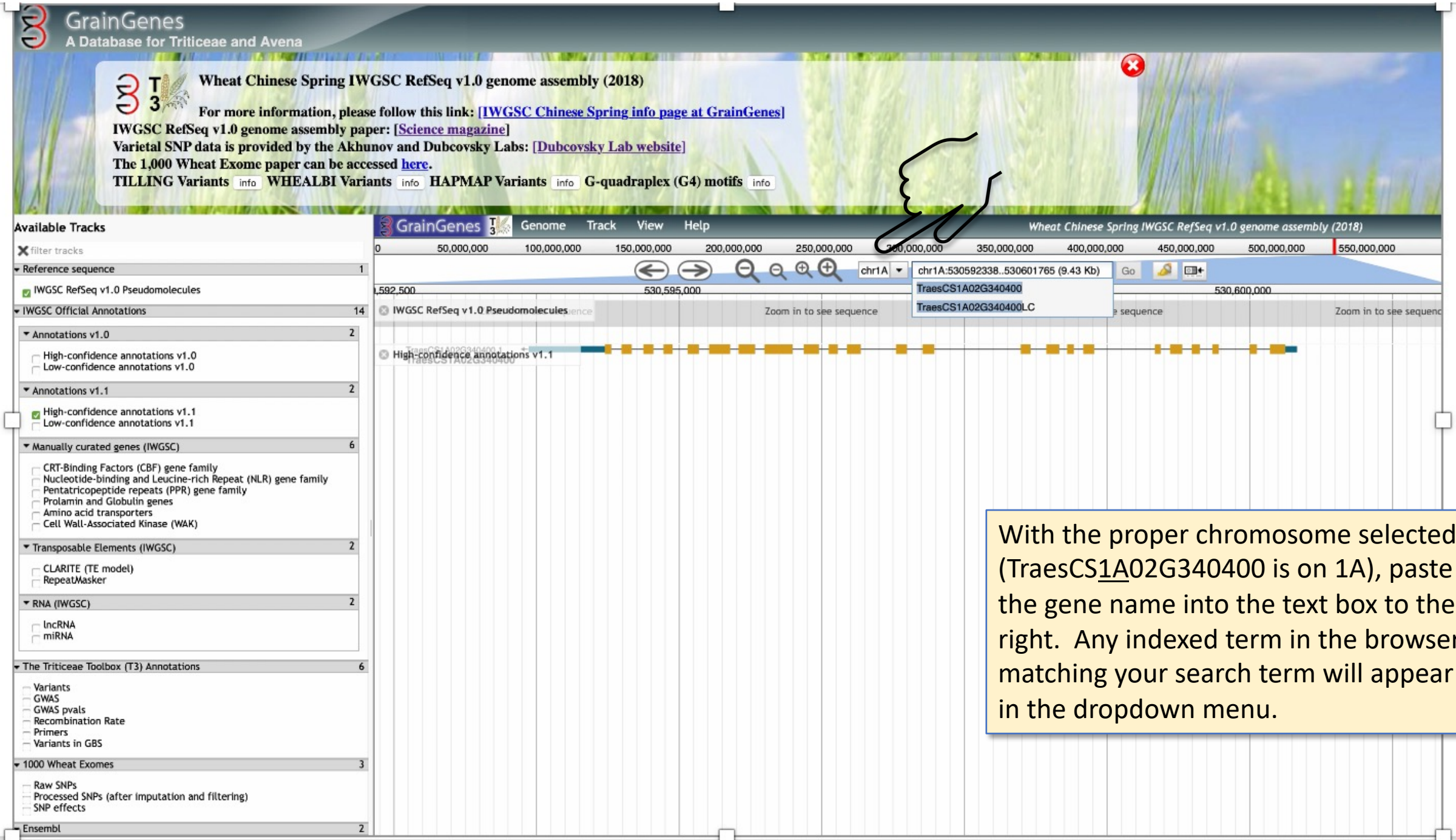
Identification and expression patterns of *TaSTT3a* and *TaSTT3b* genes in common wheat

STT3 plays important roles in abiotic stress tolerance of the host plants (Jiang *et al*., 2015; Jiao *et al*., 2020; Koiwa *et al*., 2003). Here, we explored whether STT3 in common wheat is involved in defense response to biotic stress. To obtain the sequences of *STT3* genes in wheat, we conducted BLAST searches against IWGSC Survey Sequence Assemblies using the amino acid sequences of STT3a (AAL07040.1) and STT3b (NP_174675.2) in Arabidopsis as seed sequences. Six highly conserved, full sequences (TraesCS1A02G340400.1, TraesCS1B02G352700.1, and TraesCS1D02G342400.1 conserved to STT3a; and TraesCS2A02G555600.1, TraesCS2B02G587900.1, and TraesCS2D02G558800.1 conserved to STT3b) were obtained, indicating that the wheat *STT3a* and *STT3b* genes each had three homologous loci (named as *TaSTT3a-1A*, *TaSTT3a-1B*, *TaSTT3a-1D*, *TaSTT3b-2A*, *TaSTT3b-2B*, and *TaSTT3b-2D* in this study) on the A, B, and D chromosomes. To investigate the role of STT3 in wheat defense against pathogen infection, we detected the expression profiles of *TaSTT3a* and *TaSTT3b* in wheat after *R. cerealis* infection using real-time quantitative PCR (qRT-PCR). The results showed that the transcriptional abundance of *TaSTT3b* was significantly elevated after *R. cerealis* infection, and the induced level of *TaSTT3b-2B* was the highest at 10 days post infection (dpi) with *R. cerealis* (Figure 1a). While transcriptional levels of *TaSTT3a* were only up-regulated at 10 dpi and 21 dpi, the induction degree was relatively weaker than that of *TaSTT3b-2B* (Figure S1).



The first gene to investigate from the paper is TraesCS1A02G340400.1

This is mapped in the 2018 IWGSC RefSeq v1.2 (we know this because 02G is in the gene name).



With the proper chromosome selected (TraesCS1A02G340400 is on 1A), paste the gene name into the text box to the right. Any indexed term in the browser matching your search term will appear in the dropdown menu.

GrainGenes
A Database for Triticeae and Avena

Wheat Chinese Spring IWGSC RefSeq v1.0 genome assembly (2018)

For more information, please follow this link: [IWGSC Chinese Spring info page at GrainGenes]
IWGSC RefSeq v1.0 genome assembly paper: [Science magazine]
Varietal SNP data is provided by the Akhunov and Dubcovsky Labs: [Dubcovsky Lab website]
The 1,000 Wheat Exome paper can be accessed here.
TILLING Variants info WHEALBI Variants info HAPMAP Variants info G-quadraplex (G4) motifs info

Available Tracks

filter tracks

- Reference sequence 1
  - IWGSC RefSeq v1.0 Pseudomolecules
- IWGSC Official Annotations 14
  - Annotations v1.0 2
    - High-confidence annotations v1.0
    - Low-confidence annotations v1.0
  - Annotations v1.1 2
    - High-confidence annotations v1.1
    - Low-confidence annotations v1.1
  - Manually curated genes (IWGSC) 6
    - CRT-Binding Factors (CBF) gene family
    - Nucleotide-binding and Leucine-rich Repeat (NLR) gene family
    - Pentatricopeptide repeats (PPR) gene family
    - Prolamin and Globulin genes
    - Amino acid transporters
    - Cell Wall-Associated Kinase (WAK)
  - Transposable Elements (IWGSC) 2
    - CLARITE (TE model)
    - RepeatMasker
  - RNA (IWGSC) 2
    - lncRNA
    - miRNA
- The Triticeae Toolbox (T3) Annotations 6
  - Variants
  - GWAS
  - GWAS pvals
  - Recombination Rate
  - Primers
  - Variants in GBS
- 1000 Wheat Exomes 3
  - Raw SNPs
  - Processed SNPs (after imputation and filtering)
  - SNP effects

GrainGenes Genome Track View Help — Wheat Chinese Spring IWGSC RefSeq v1.0 genome assembly (2018)

530,597,500 530,600,000 — Zoom in to see sequence

gene TraesCS1A02G340400

Attributes

Id	TraesCS1A02G340400
Previous_id	TraesCS1A01G340400
Primconf	HC
Seq_id	chr1A
Source	IWGSC_v1.1_201706

Links

expVIP | KnetMiner | PhyloGene | Ensembl

Region sequence

FASTA

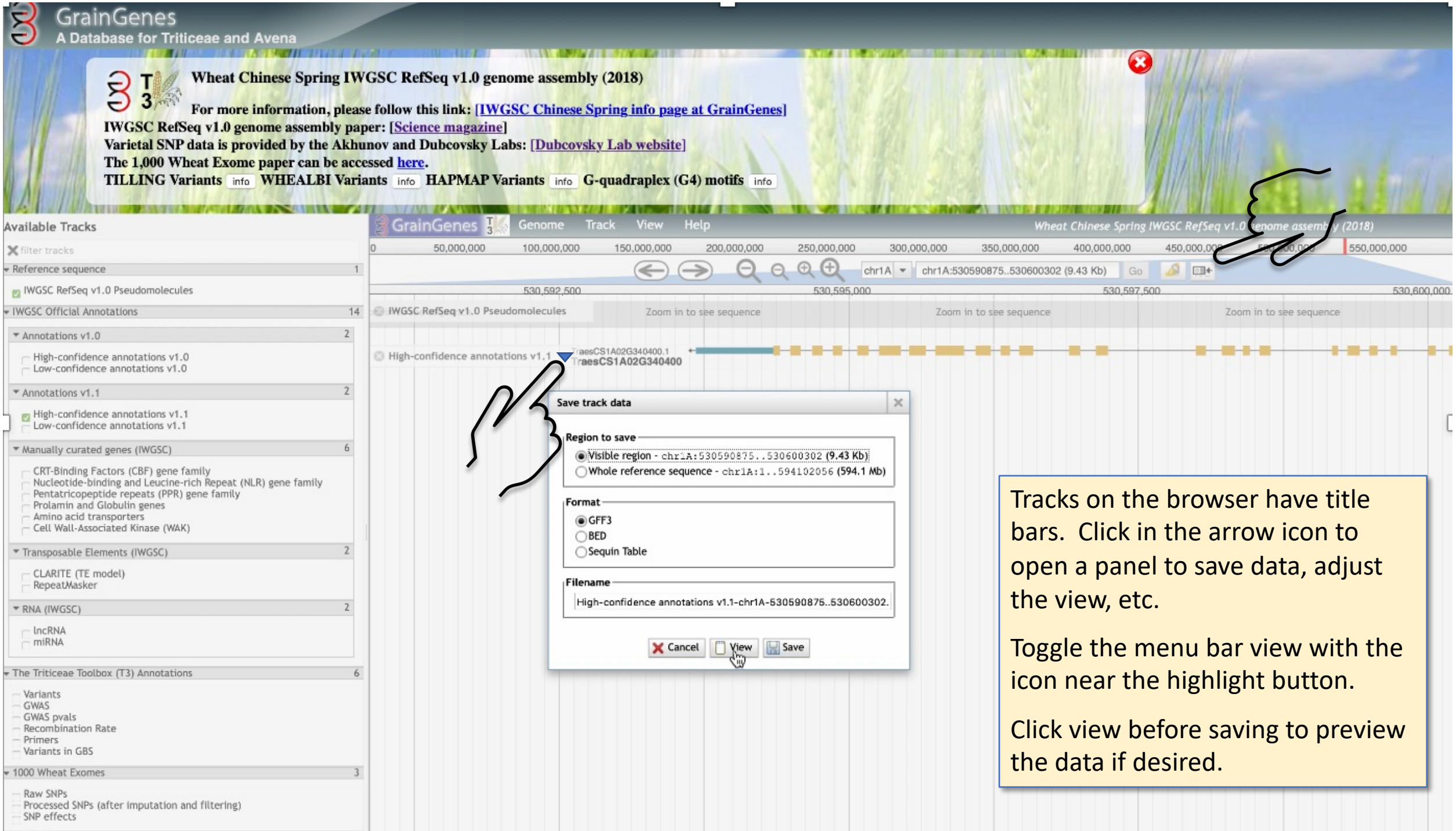
```
>chr1A chr1A:530593686..530600419 (- strand) class=gene
length=6734
CTCGCGATCGGGAGGTCTTCGTCTCCGCCTGGGAACGCCACCGAGATTTCTCCGTCCCTCTC
CCCCCTCCCCCCTCACGCACCCAGCCGCGACTCGGCCGCAATGGCGGAGCCCGTGGCCAACG
CGGCGGCGCCCGCCCCCGCCCCCGGCCGCCTCCGCAACGCCTTCGGCGGCGTGCTCTGCGCC
TTTACCCTCATCCTCATCGGCGTCCtCGCCTTCTCGATCCGCCTCTTCTCCGTAAGATCTGA
TCCGCCCCCCCGCCCCCGTGCCTCCAGATCCGGTCCCGTGTTCGAACAGAGGTTCCGGAATT
GCGTTTTTTTTCTCACGCGTCTCGCCGTTTCGGTGCCGCAGGTGATCAAGTACGAGAGCGTG
ATCCACGAGTTCGACCCCTACTTCAACTTCCGCGTCACTCAGGTTCGATTGCCCGGTTCCAT
TTTGTCGAGTTCTGTTCTGGAGCGCGCGGAATTGGGTTCTCAGCTCTTAGCGGGCTGCATAA
TGTGTTGTTGTGACTTGTGAATCTGGGGGAGGGTTCTGGGTTTTGGAAATTGACCGCTGTCT
```

Subfeatures

Primary Data

Name	TraesCS1A02G340400.1
Type	mRNA

Click on the gene model graphic for the information report. Notice the RefSeq v1.1 genes have links to several external databases providing functional annotations, expression data, etc.



Tracks on the browser have title bars. Click in the arrow icon to open a panel to save data, adjust the view, etc.

Toggle the menu bar view with the icon near the highlight button.

Click view before saving to preview the data if desired.

GrainGenes
A Database for Triticeae and Avena

Wheat Chinese Spring IWGSC RefSeq v1.0 genome assembly (2018)

For more information, please follow this link: [IWGSC Chinese Spring info page at GrainGenes]
IWGSC RefSeq v1.0 genome assembly paper: [Science magazine]
Varietal SNP data is provided by the Akhunov and Dubcovsky Labs: [Dubcovsky Lab website]
The 1,000 Wheat Exome paper can be accessed here.
TILLING Variants info WHEALBI Variants info HAPMAP Variants info G-quadraplex (G4) motifs info

Available Tracks

filter tracks

- Reference sequence 1
  - IWGSC RefSeq v1.0 Pseudomolecules
- IWGSC Official Annotations 14
  - Annotations v1.0 2
    - High-confidence annotations v1.0
    - Low-confidence annotations v1.0
  - Annotations v1.1 2
    - High-confidence annotations v1.1
    - Low-confidence annotations v1.1
  - Manually curated genes (IWGSC) 6
    - CRT-Binding Factors (CBF) gene family
    - Nucleotide-binding and Leucine-rich Repeat (NLR) gene family
    - Pentatricopeptide repeats (PPR) gene family
    - Prolamin and Globulin genes
    - Amino acid transporters
    - Cell Wall-Associated Kinase (WAK)
  - Transposable Elements (IWGSC) 2
    - CLARITE (TE model)
    - RepeatMasker
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  - GWAS pvals
  - Recombination Rate
  - Primers
  - Variants in GBS
- 1000 Wheat Exomes 3
  - Raw SNPs
  - Processed SNPs (after imputation and filtering)
  - SNP effects

GrainGenes Genome Track View Help — Wheat Chinese Spring IWGSC RefSeq v1.0 genome assembly (2018)

0 50,000,000 100,000,000 150,000,000 200,000,000 250,000,000 300,000,000 350,000,000 400,000,000 450,000,000 500,000,000 550,000,000

chr1A chr1A:530590875..530600302 (9.43 Kb) Go

530,592,500 530,595,000 530,597,500 530,600,000

IWGSC RefSeq — Zoom in to see sequence

High-confiden

GFF3 export - chr1A:530590875..530600302 (5.82 Kbytes)

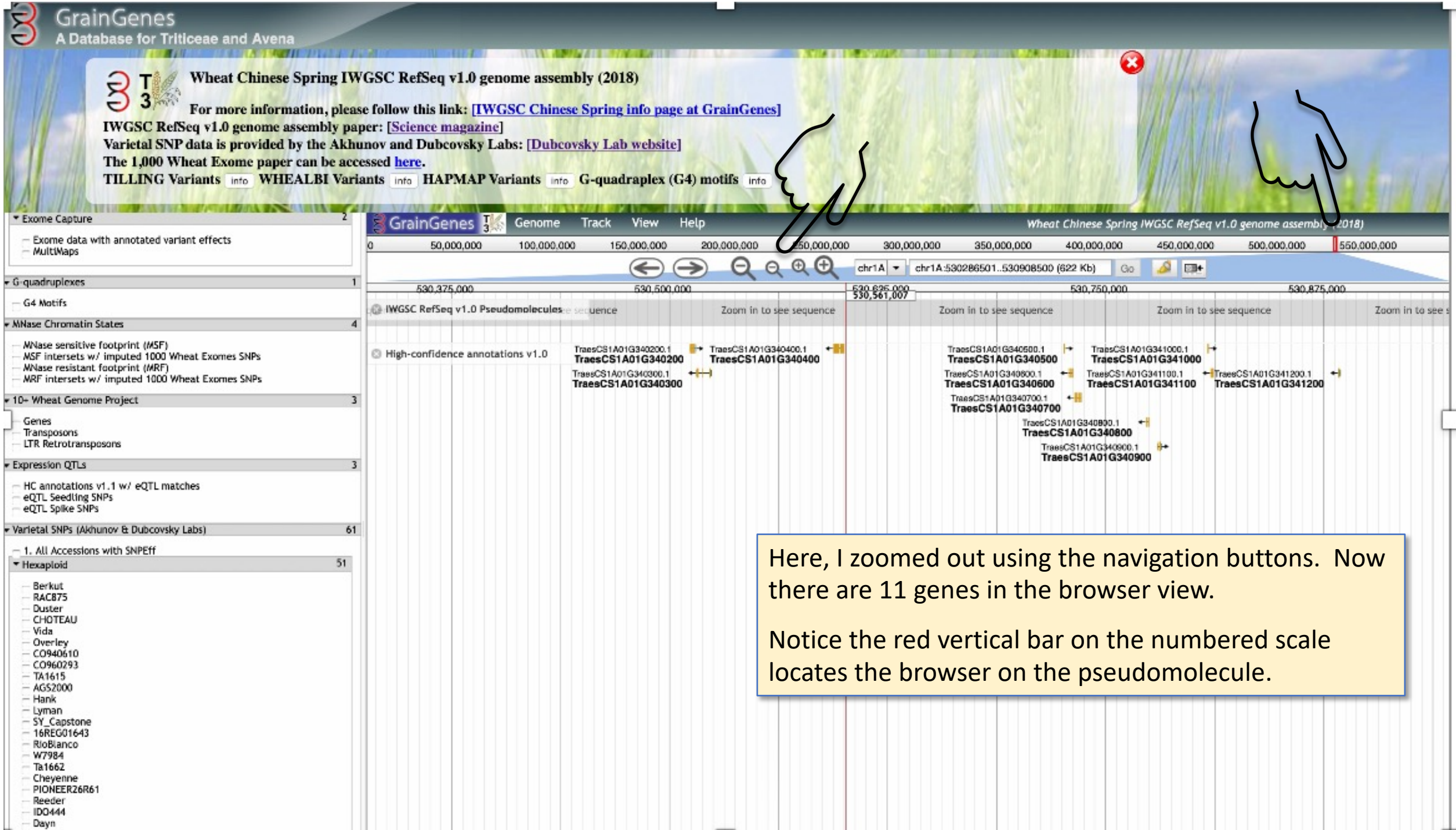
```
##gff-version 3
##sequence-region chr1A 530590875 530600302
chr1A	IWGSC_v1.1_201706	gene	530593686	530600419	62	-	.	ID=TraesCS1A02G34C
chr1A	IWGSC_v1.1_201706	mRNA	530593686	530600419	.	-	.	ID=TraesCS1A02G34C
chr1A	IWGSC_v1.1_201706	five_prime_UTR	530600318	530600419	.	-	.	ID=TraesCS
chr1A	IWGSC_v1.1_201706	CDS 530600183	530600317	.	-	0	ID=TraesCS1A02G340400.
chr1A	IWGSC_v1.1_201706	exon	530600183	530600419	.	-	.	ID=TraesCS1A02G34C
chr1A	IWGSC_v1.1_201706	CDS 530600006	530600068	.	-	0	ID=TraesCS1A02G340400.
chr1A	IWGSC_v1.1_201706	exon	530600006	530600068	.	-	.	ID=TraesCS1A02G34C
chr1A	IWGSC_v1.1_201706	CDS 530599676	530599731	.	-	0	ID=TraesCS1A02G340400.
chr1A	IWGSC_v1.1_201706	exon	530599676	530599731	.	-	.	ID=TraesCS1A02G34C
chr1A	IWGSC_v1.1_201706	CDS 530599494	530599565	.	-	1	ID=TraesCS1A02G340400.
chr1A	IWGSC_v1.1_201706	exon	530599494	530599565	.	-	.	ID=T
chr1A	IWGSC_v1.1_201706	CDS 530599306	530599411	.	-	1	ID=TraesC
chr1A	IWGSC_v1.1_201706	exon	530599306	530599411	.	-	.	ID=T
chr1A	IWGSC_v1.1_201706	exon	530599173	530599223	.	-	.	ID=T
chr1A	IWGSC_v1.1_201706	CDS 530599173	530599223	.	-	0	ID=TraesC
chr1A	IWGSC_v1.1_201706	CDS 530598547	530598642	.	-	0	ID=TraesC
chr1A	IWGSC_v1.1_201706	exon	530598547	530598642	.	-	.	ID=T
chr1A	IWGSC_v1.1_201706	CDS 530598405	530598464	.	-	0	ID=TraesC
chr1A	IWGSC_v1.1_201706	exon	530598405	530598464	.	-	.	ID=T
chr1A	IWGSC_v1.1_201706	CDS 530598223	530598336	.	-	0	ID=TraesCS1A02G340400.
chr1A	IWGSC_v1.1_201706	exon	530598223	530598336	.	-	.	ID=TraesCS1A02G34C
chr1A	IWGSC_v1.1_201706	CDS 530597999	530598085	.	-	0	ID=TraesCS1A02G340400.
chr1A	IWGSC_v1.1_201706	exon	530597999	530598085	.	-	.	ID=TraesCS1A02G34C
chr1A	IWGSC_v1.1_201706	CDS 530597136	530597239	.	-	0	ID=TraesCS1A02G340400.
chr1A	IWGSC_v1.1_201706	exon	530597136	530597239	.	-	.	ID=TraesCS1A02G34C
chr1A	IWGSC_v1.1_201706	CDS 530596904	530596999	.	-	1	ID=TraesCS1A02G340400.
chr1A	IWGSC_v1.1_201706	exon	530596904	530596999	.	-	.	ID=TraesCS1A02G34C
chr1A	IWGSC_v1.1_201706	CDS 530596475	530596595	.	-	1	ID=TraesCS1A02G340400.
chr1A	IWGSC_v1.1_201706	exon	530596475	530596595	.	-	.	ID=TraesCS1A02G34C
```

Close

Save High-confidence annotations v1.1-chr1A-530590875..5

View before saving to preview the data.

Users can edit the file name prior to saving.



Here, I zoomed out using the navigation buttons. Now there are 11 genes in the browser view.

Notice the red vertical bar on the numbered scale locates the browser on the pseudomolecule.

GrainGenes
A Database for Triticeae and Avena

Wheat Chinese Spring IWGSC RefSeq v1.0 genome assembly (2018)

For more information, please follow this link: [IWGSC Chinese Spring info page at GrainGenes]
IWGSC RefSeq v1.0 genome assembly paper: [Science magazine]
Varietal SNP data is provided by the Akhunov and Dubcovsky Labs: [Dubcovsky Lab website]
The 1,000 Wheat Exome paper can be accessed here.
TILLING Variants info WHEALBI Variants info HAPMAP Variants info G-quadraplex (G4) motifs info

Annotations v1.0 2
- High-confidence annotations v1.0
- Low-confidence annotations v1.0

Annotations v1.1 2
- High-confidence annotations v1.1
- Low-confidence annotations v1.1

Manually curated genes (IWGSC) 6
- CRT-Binding Factors (CBF) gene family
- Nucleotide-binding and Leucine-rich Repeat (NLR) gene family
- Pentatricopeptide repeats (PPR) gene family
- Prolamin and Globulin genes
- Amino acid transporters
- Cell Wall-Associated Kinase (WAK)

Transposable Elements (IWGSC) 2
- CLARITE (TE model)
- RepeatMasker

RNA (IWGSC) 2
- lncRNA
- miRNA

The Triticeae Toolbox (T3) Annotations 6
- Variants
- GWAS
- GWAS pvals
- Recombination Rate
- Primers
- Variants in GBS

1000 Wheat Exomes 3
- Raw SNPs
- Processed SNPs (after imputation and filtering)
- SNP effects

Ensembl 2
- TILLING Variants (Enaembl Release 46)
- TILLING Consequences of variations (Enaembl Release 46)

HAPMAP 1
- Hapmap WEC SNP (updated)

WHEALBI 2

GrainGenes T3 Genome Track View Help — Wheat Chinese Spring IWGSC RefSeq v1.0 genome assembly (2018)

chr1A chr1A:530286501..530908500 (622 Kb) Go

530,644,507

IWGSC RefSeq v1.0 Pseudomolecules — Zoom in to see sequence

High-confidence annotations v1.0
TraesCS1A01G340200.1 TraesCS1A01G340200
TraesCS1A01G340300.1 TraesCS1A01G340300
TraesCS1A01G340400.1 TraesCS1A01G340400
TraesCS1A01G340500.1 TraesCS1A01G340500
TraesCS1A01G340600.1 TraesCS1A01G340600
TraesCS1A01G340700.1 TraesCS1A01G340700
TraesCS1A01G340800.1 TraesCS1A01G340800
TraesCS1A01G340900.1 TraesCS1A01G340900
TraesCS1A01G341000.1 TraesCS1A01G341000
TraesCS1A01G341100.1 TraesCS1A01G341100
TraesCS1A01G341200.1 TraesCS1A01G341200

1. All Accessions with SNPEff

miRNA
miR1130-3p-391
miR1130-3p-153
miR1130-3p-198
miR1130-3p-322
miR5049-3p-107

TILLING Variants (Enaembl Release 46) — Too much data to show; zoom in to see detail.

Additional tracks were added:

- All Varietal SNPEffects. This track was selected from the left menu, below the current view. This view is 'Collapsed'
- Micro RNAs (miRNAs)
- Tilling mutants. Note there are too many to render.

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TILLING Variants info WHEALBI Variants info HAPMAP Variants info G-quadraplex (G4) motifs info

- Annotations v1.0 (2)
  - High-confidence annotations v1.0
  - Low-confidence annotations v1.0
- Annotations v1.1 (2)
  - High-confidence annotations v1.1
  - Low-confidence annotations v1.1
- Manually curated genes (IWGSC) (6)
  - CRT-Binding Factors (CBF) gene family
  - Nucleotide-binding and Leucine-rich Repeat (NLR) gene family
  - Pentatricopeptide repeats (PPR) gene family
  - Prolamin and Globulin genes
  - Amino acid transporters
  - Cell Wall-Associated Kinase (WAK)
- Transposable Elements (IWGSC) (2)
  - CLARITE (TE model)
  - RepeatMasker
- RNA (IWGSC) (2)
  - lncRNA
  - miRNA
- The Triticeae Toolbox (T3) Annotations (6)
  - Variants
  - GWAS
  - GWAS pvals
  - Recombination Rate
  - Primers
  - Variants in GBS
- 1000 Wheat Exomes (3)
  - Raw SNPs
  - Processed SNPs (after imputation and filtering)
  - SNP effects
- Ensembl (2)
  - TILLING Variants (Enaembl Release 46)
  - TILLING Consequences of variations (Enaembl Release 46)
- HAPMAP (1)
  - Hapmap WEC SNP (updated)

GrainGenes Genome Track View Help — *Wheat Chinese Spring IWGSC RefSeq v1.0 genome assembly (2018)*

0 50,000,000 100,000,000 150,000,000 200,000,000 250,000,000 300,000,000 350,000,000 400,000,000 450,000,000 500,000,000 550,000,000

chr1A chr1A:530566479..530637979 (71.5 Kb) Go

530,575,000 530,587,500 530,591,480 530,600,000 530,612,500 530,625,000

IWGSC RefSeq v1.0 Pseudomolecules — Zoom in to see sequence

High-confidence annotations v1.0 — TraesCS1A01G340400.1 TraesCS1A01G340400

1. All Accessions with SNPEff

miRNA — miR1130-3p-391

TILLING Variants (Enaembl Release 46)

Zooming back into the region near the gene renders the Tilling mutation sites in 'Normal' view, i.e., stacked in a very long track.

GrainGenes
A Database for Triticeae and Avena

Wheat Chinese Spring IWGSC RefSeq v1.0 genome assembly (2018)

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IWGSC RefSeq v1.0 genome assembly paper: [Science magazine]
Varietal SNP data is provided by the Akhunov and Dubcovsky Labs: [Dubcovsky Lab website]
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TILLING Variants info WHEALBI Variants info HAPMAP Variants info G-quadraplex (G4) motifs info

- Annotations v1.0 2
  - High-confidence annotations v1.0
  - Low-confidence annotations v1.0
- Annotations v1.1 2
  - High-confidence annotations v1.1
  - Low-confidence annotations v1.1
- Manually curated genes (IWGSC) 6
  - CRT-Binding Factors (CBF) gene family
  - Nucleotide-binding and Leucine-rich Repeat (NLR) gene family
  - Pentatricopeptide repeats (PPR) gene family
  - Prolamin and Globulin genes
  - Amino acid transporters
  - Cell Wall-Associated Kinase (WAK)
- Transposable Elements (IWGSC) 2
  - CLARITE (TE model)
  - RepeatMasker
- RNA (IWGSC) 2
  - lncRNA
  - miRNA
- The Triticeae Toolbox (T3) Annotations 6
  - Variants
  - GWAS
  - GWAS pvals
  - Recombination Rate
  - Primers
  - Variants in GBS
- 1000 Wheat Exomes 3
  - Raw SNPs
  - Processed SNPs (after imputation and filtering)
  - SNP effects
- Ensembl 2
  - TILLING Variants (Enaembl Release 46)
  - TILLING Consequences of variations (Enaembl Release 46)
- HAPMAP 1

GrainGenes Genome Track View Help — Wheat Chinese Spring IWGSC RefSeq v1.0 genome assembly (2018)

chr1A chr1A:530560674..530632174 (71.5 Kb) Go

IWGSC RefSeq v1.0 Pseudomolecules — Zoom in to see sequence

SNV Cadenza0418.chr1A.530596502

Primary Data

Name	Cadenza0418.chr1A.530596502
Type	SNV
Description	SNV C -> T
Position	chr1A:530596502..530596502
Length	1 bp

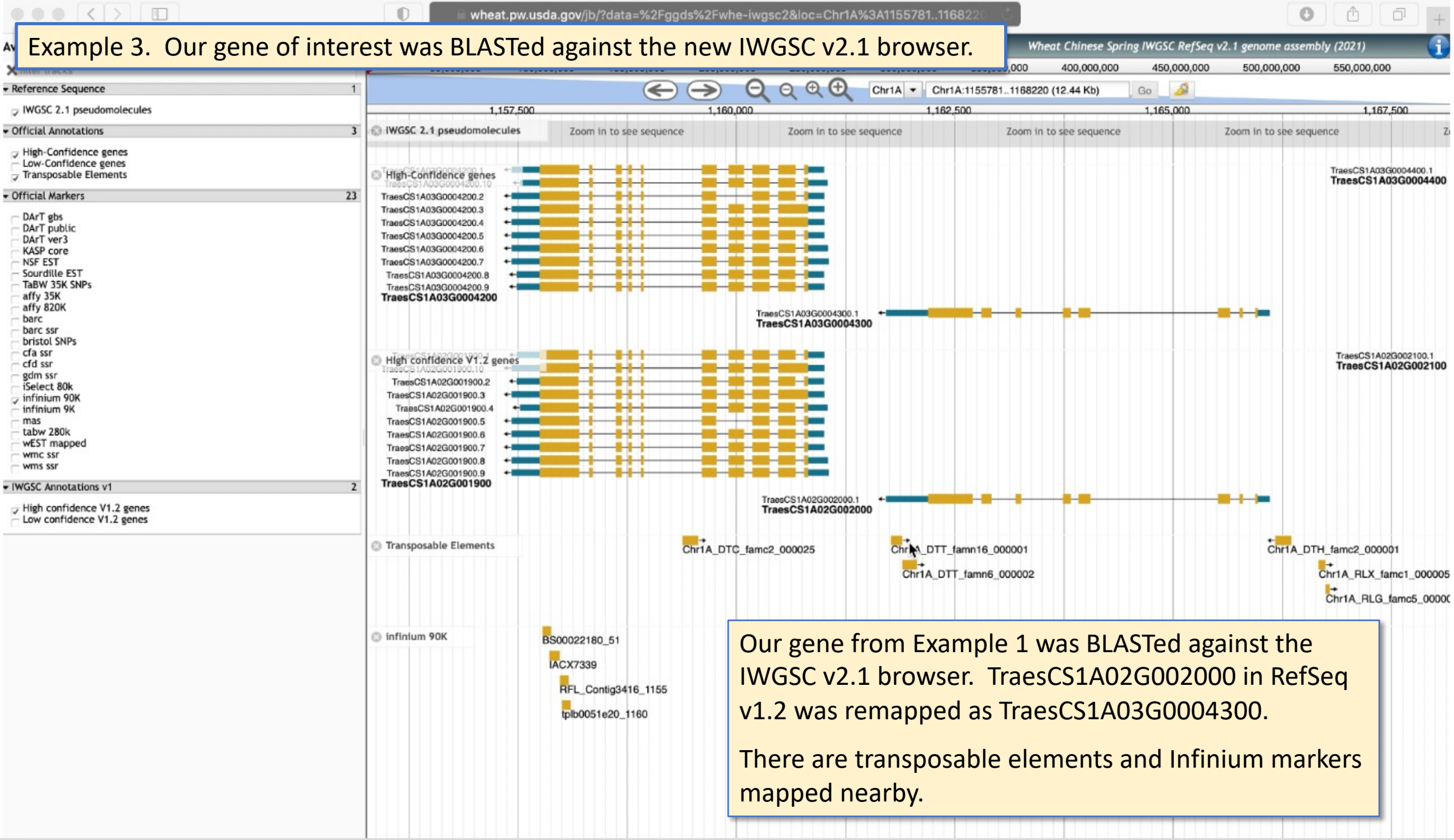
Attributes

EMS-induced mutation	
TSA	SNV
alternative_alleles	T
description	SNV C -> T
reference_allele	C
seq_id	chr1A

The Tilling mutant track view was collapsed.

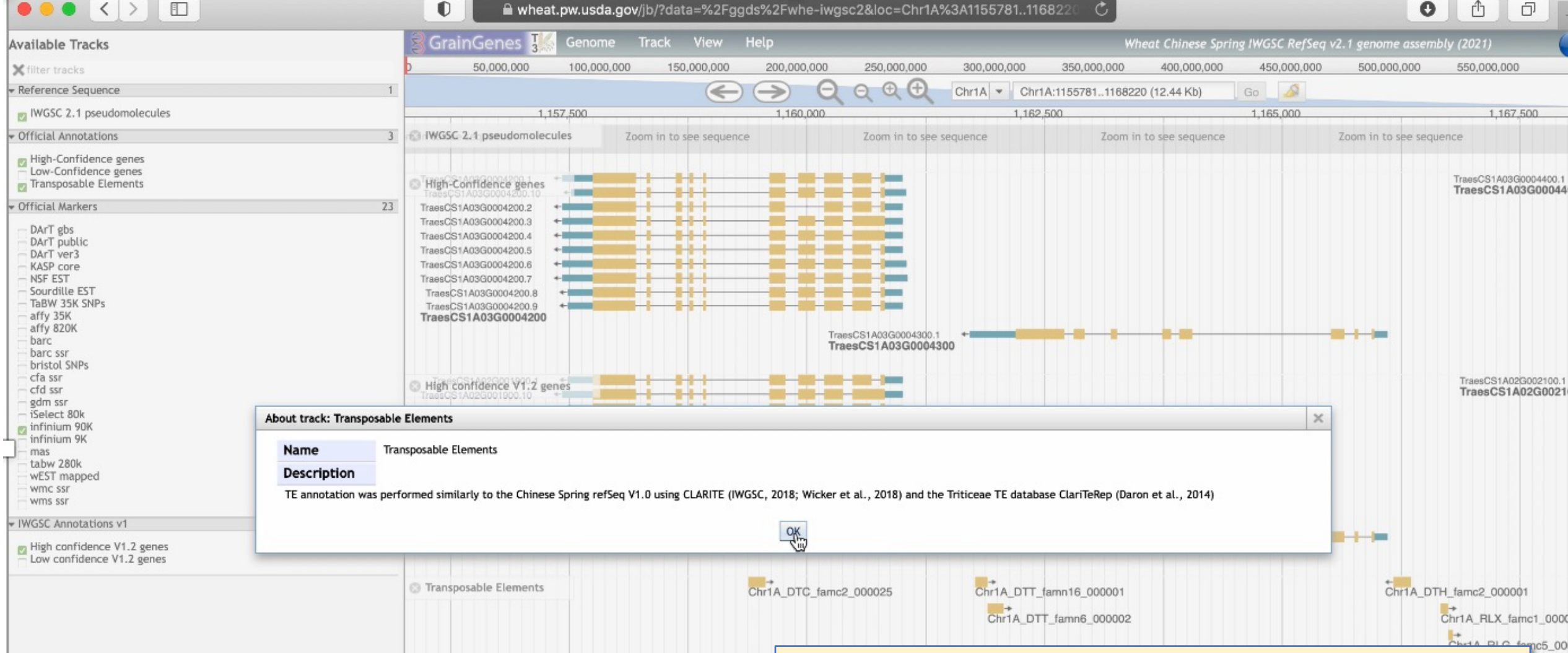
Each SNP variant has additional data like that shown here. Tilling variants have similar data attached to each annotation.

Example 3. Our gene of interest was BLASTed against the new IWGSC v2.1 browser.



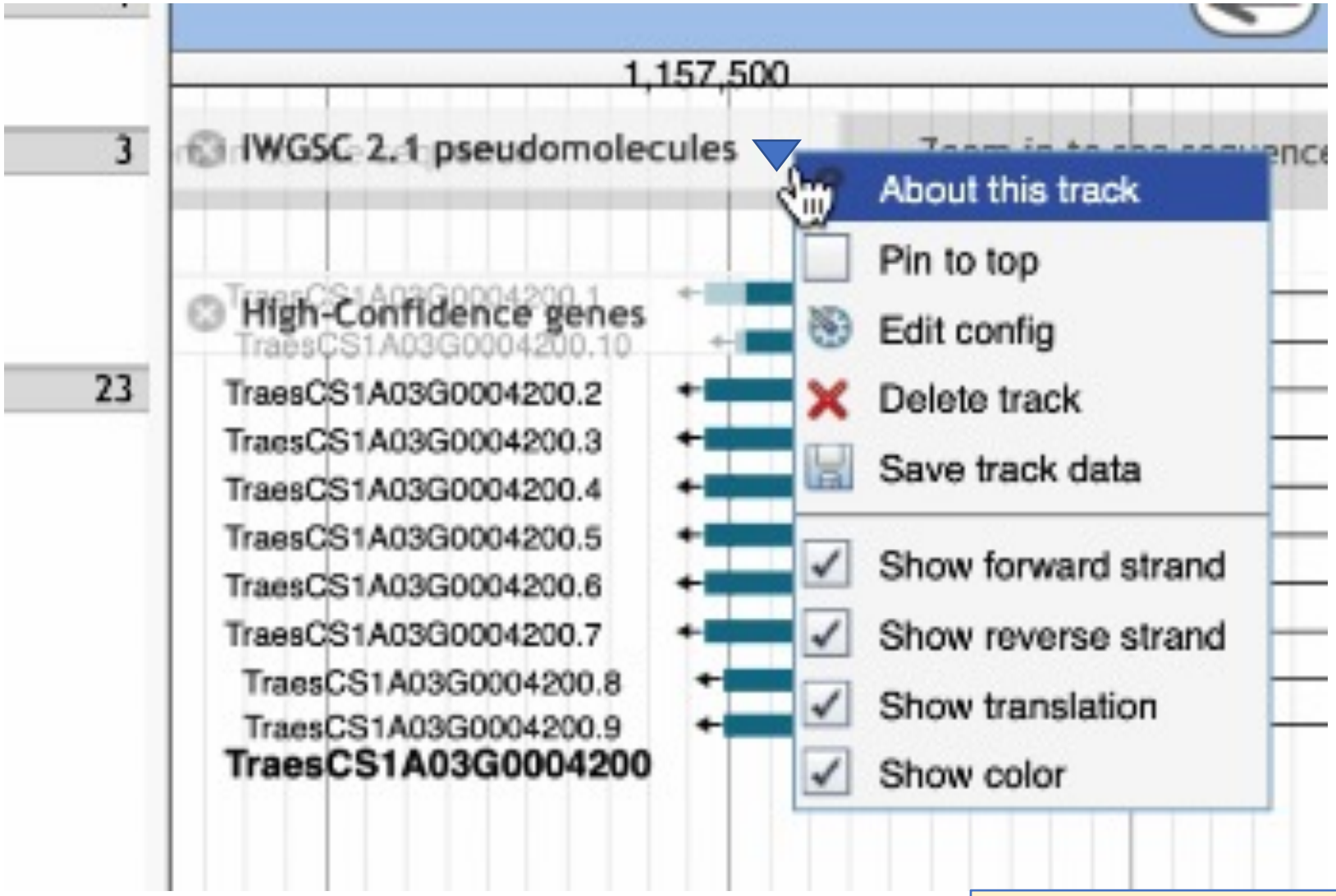
Our gene from Example 1 was BLASTed against the IWGSC v2.1 browser. TraesCS1A02G002000 in RefSeq v1.2 was remapped as TraesCS1A03G0004300.

There are transposable elements and Infinium markers mapped nearby.



The 'About this Track' for Transposable Elements is well defined with a reference.

Marker tracks will be updated to include references and reciprocal links from probe records in the GrainGenes MySQL database to the browser, improving the connection from genetic work to the physical genome space.



A last note: Save the DNA sequence as a FASTA from any region in the browser by opening the pseudomolecule track and saving the data from the title menu dropdown.

Contact us anytime!

The GrainGenes Team

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Crop Improvement and Genetics

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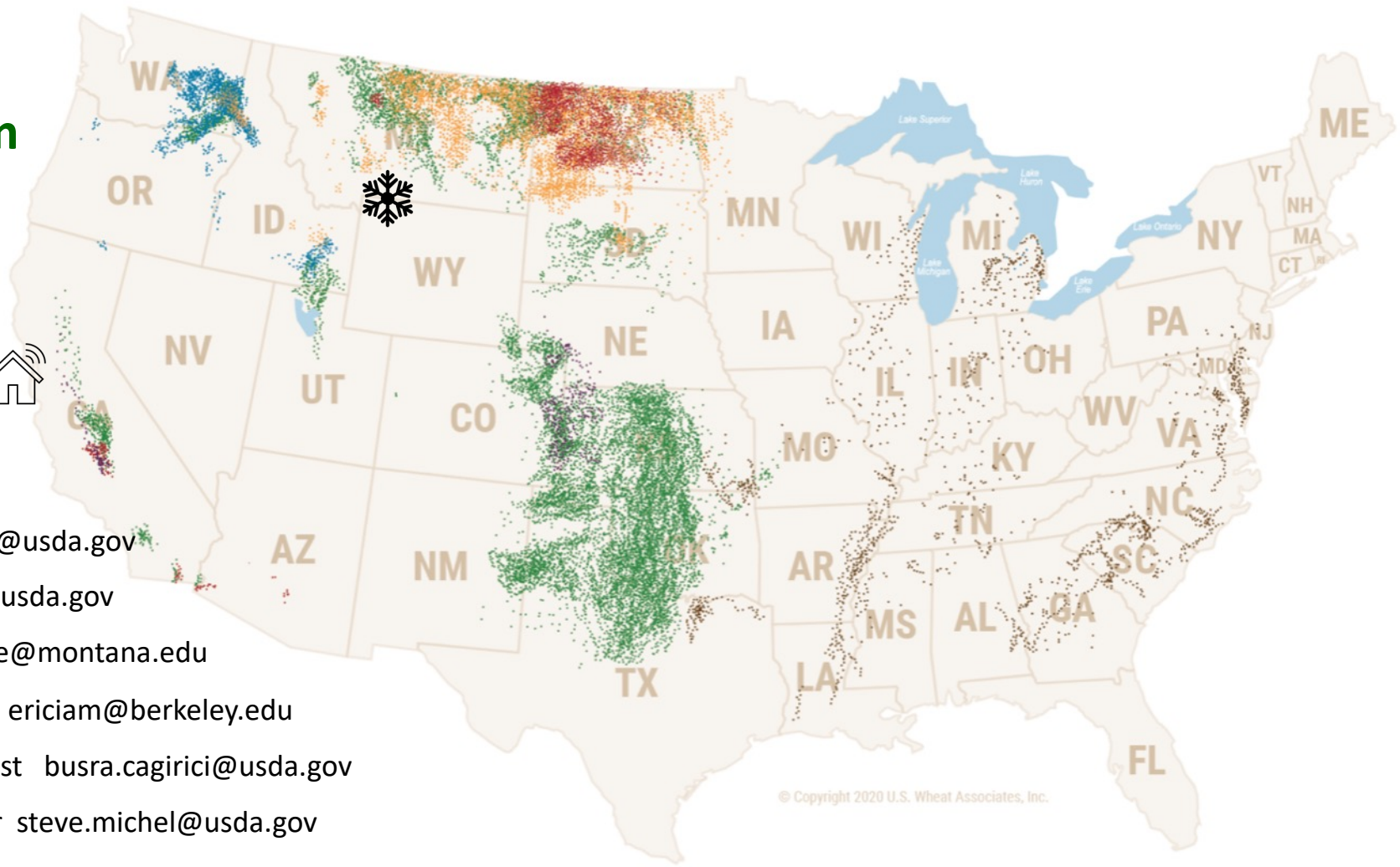
Steve Michel Systems Administrator steve.michel@usda.gov



Hard Red Winter (HRW)

Soft Red Winter (SRW)

Hard White (HW)

Hard Red Spring (HRS)

Soft White (SW)

Durum

map image : https://www.uswheat.org/working-with-buyers/wheat-classes/