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

Victoria Carollo Blake[1], Eric Yao[2], Gerard R. Lazo[3], Laurel Cooper[4], Halise Busra Cagirici[3], Steve L. Michel[3], and Taner Z. Sen[3]

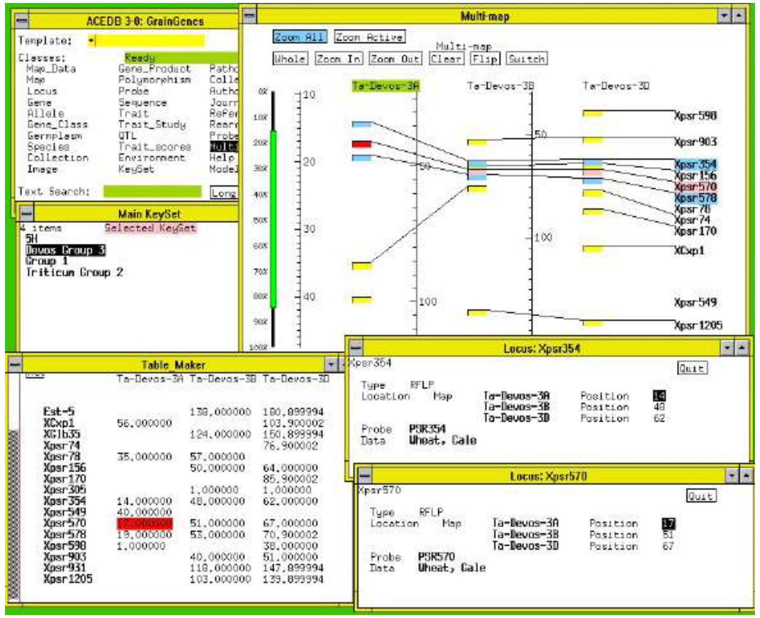
(1)Montana State University, Bozeman, MT (2)University of California, Berkeley, CA
(3)USDA ARS, Albany, CA (4) Oregon State University, Corvallis, OR

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

Barleymap MorexV3 2021 release

Barleymap (https://floresta.eead.csic.es/barleymap), a Web tool for mapping the position of genetic markers along the physical and genetic maps of the barley genome, has been updated and now it supports the Morex V3 genome.

PepsiCo releases annotated gene set and associated files for OT3098 v2 genome in partnership with GrainGenes

[October 19, 2021]

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By: Dr. Mandy Waters, PepsiCo

Aegilops tauschii genome assembly Aet v5.0 paper was published

[Update on October 13, 2021]
Aegilops tauschii Aet v5.0 genome browser and BLAST service were created at GrainGenes based on Wang et al., G3, 2021

Aet v5.0 genome browser: https://wheat.pw.usda.gov/jb?data=/ggds/whe-aet5
Aet v5.0 BLAST service: https://wheat.pw.usda.gov/blast/

IWGSC RefSeq v2.1 Assembly and Annotation now freely available at URGI and NCBI [and GrainGenes]

[Update on May 18, 2021]

IWGSC RefSeq v2.1 assembly and annotations & BLAST are available at GrainGenes.

• Genome Browser: https://wheat.pw.usda.gov/jb?data=/ggds/whe-iwgsc2
• BLAST: https://wheat.pw.usda.gov/blast/ (select "Wheat Chinese Spring IWGSC RefSeq v2.1 genome assembly (2021)
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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

Search

- Search & Browse GrainGenes
- Genetic Maps at GrainGenes

Submit Your Data to GrainGenes

- Submit Your Data to GrainGenes
- GrainGenes Data Formats

Community Services

- Calendar
- Current Hot Topics
- Data Download
- GrainGenes Mailing List
- Job Listings
- Oatmail Mailing List
- Tutorials

Species Portals on GrainGenes

- Wheat Gene Catalogue
- Annual Wheat Newsletter
- Barley Boulevard
- Barley Genetics Newsletter
- Oat Newsletter
- Oat Nomenclature

Upcoming Events

- Plant and Animal Genome Conference in San Diego, California
  Jan 8 2022 to Jan 12 2022
- Genomic selection in plant breeding. A hands-on short course in R
  Mar 14 2022 to Mar 18 2022
- International Cereal Rusts and Powdery Mildews Conference 2022 in Cambridge, UK
  Apr 6 2022 to Apr 8 2022
- 13th International Barley Genetics Symposium (IBGS13) in Riga, Latvia
  Jul 3 2022 to Jul 7 2022
- 2nd International Wheat Congress in Beijing, China
  Sep 12 2022 to Sep 16 2022
- The 11th International Oat Conference in Perth, Western Australia
  Oct 10 2022 to Oct 13 2022
- International Wheat Congress in Adelaide, Australia
  Sep 1 2024

About GrainGenes

GrainGenes is a digital platform that serves small grains research communities as a centralized repository for peer-reviewed and curated data, and as a facilitator for community activities. It 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.

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Quick Links

Hot Topics

Barleymap MorexV3 2021 release

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more updates....

@GrainGenes Tweets

Tweets by @GrainGenes

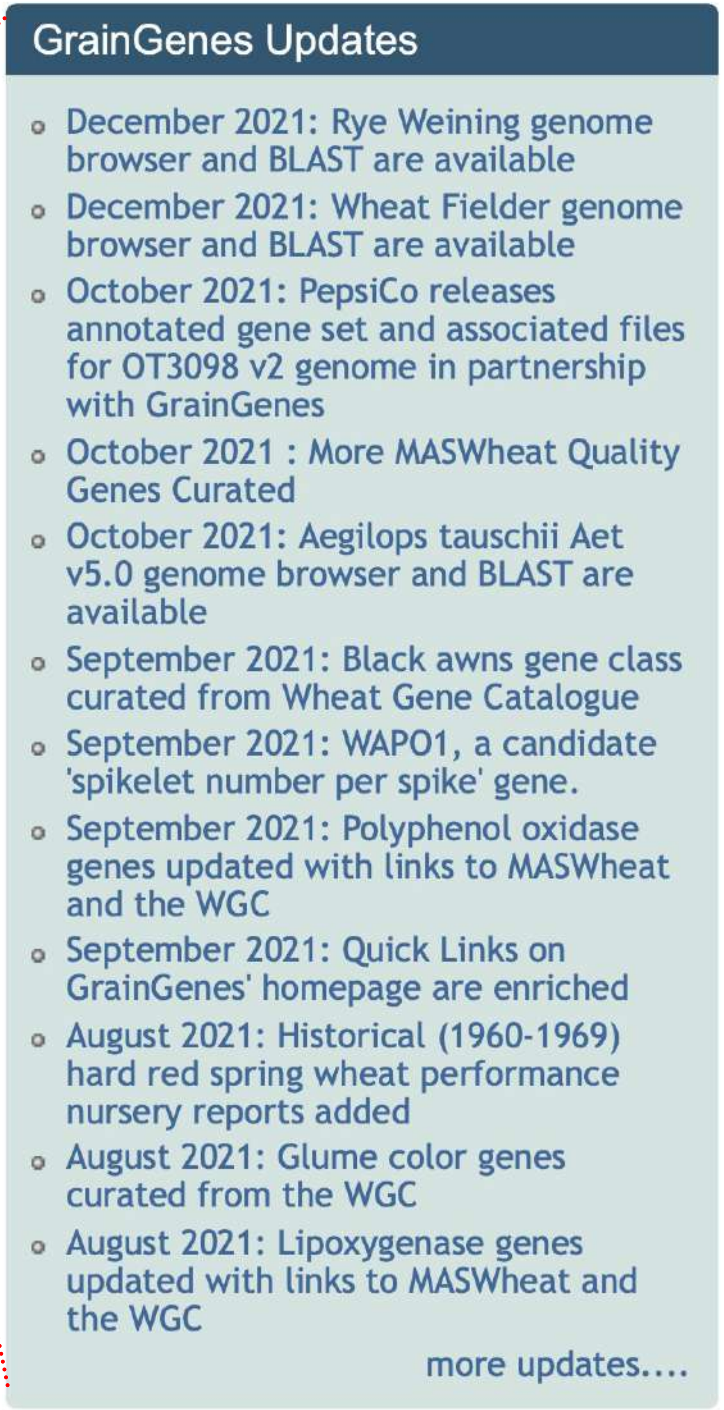
GrainGenes
@GrainGenes

Open position (citizenship restrictions apply): Postdoctoral Research Geneticist in Wheat at USDA-ARS at the University of Nebraska-Lincoln
wheat.pw.usda.gov/GG3/content/po...
@WheatInitiative

Dec 15, 2021

GrainGenes
@GrainGenes

Open position (US citizenship required): Research Geneticist (wheat and oat improvement) at USDA-ARS in St. Paul, Minnesota
wheat.pw.usda.gov/GG3/content/re...
@WheatInitiative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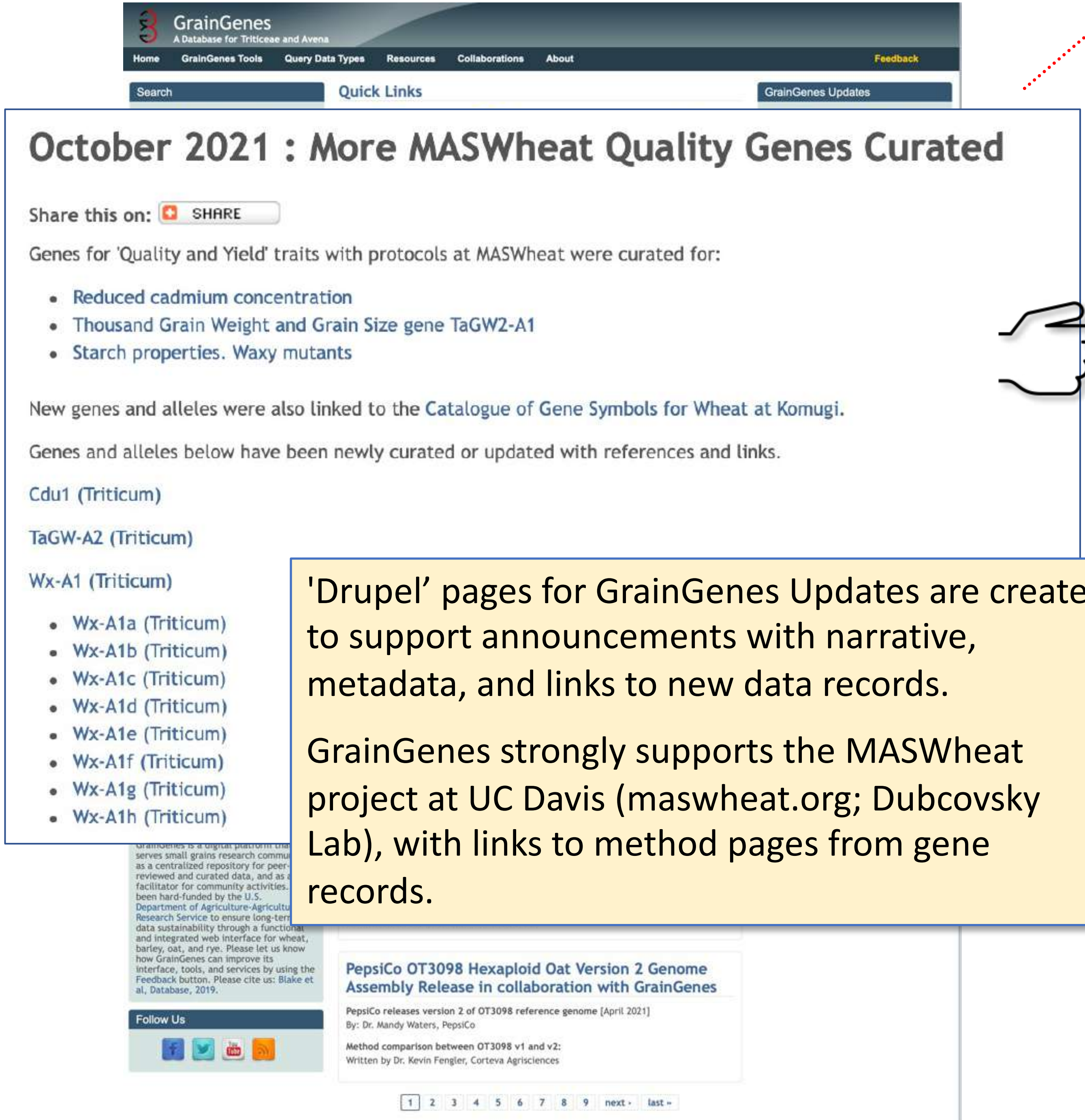
more updates....

Check GrainGenes Updates for new content:

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



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)

serves small grains research commu
as a centralized repository for peer-
reviewed and curated data, and as a
facilitator for community activities.
been hard-funded by the U.S.
Department of Agriculture-Agricultu
Research Service to ensure long-ter
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.

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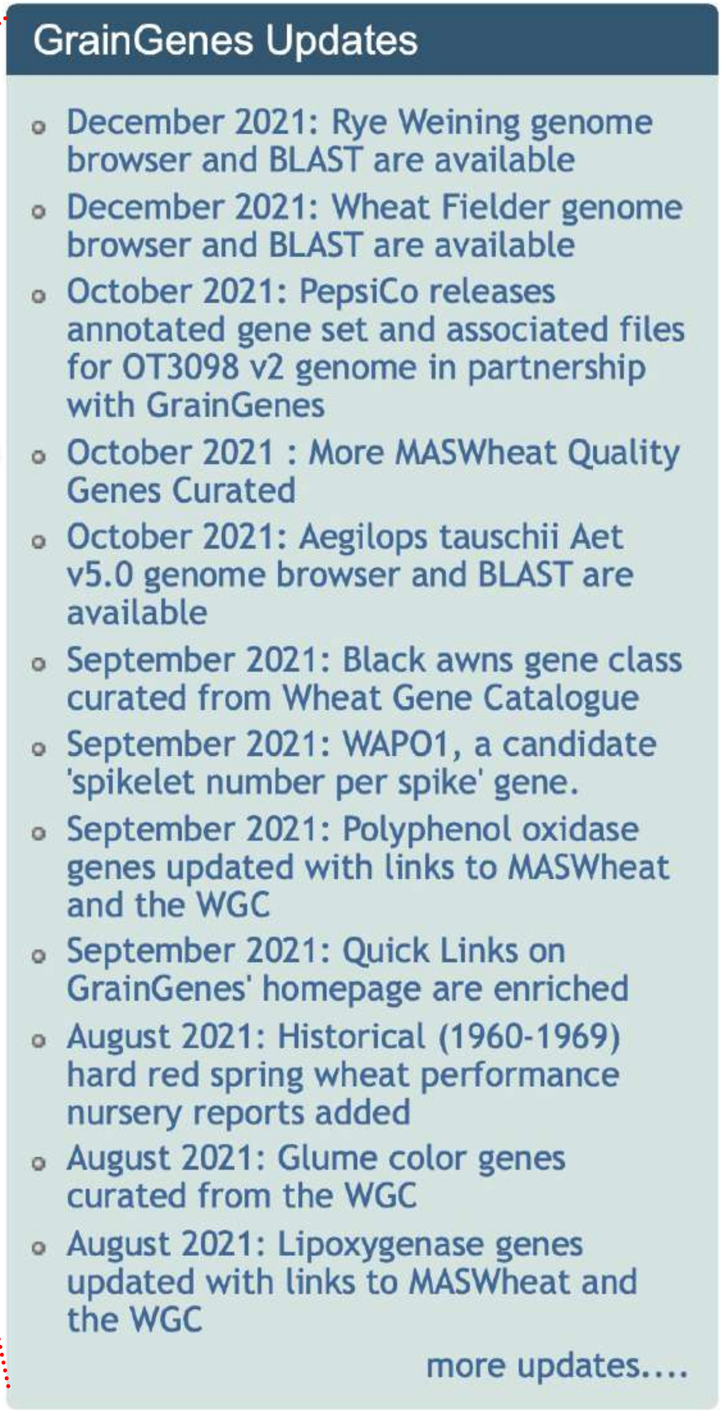
'Drupel' pages for GrainGenes Updates are created to support announcements with narrative, metadata, and links to new data records.

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



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more updates....

AN INTERNATIONAL, COLLABORATIVE RESEARCH CONSORTIUM

I W G S C

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

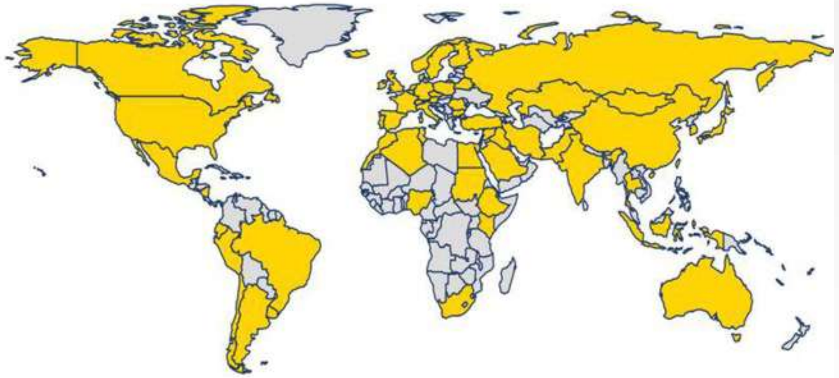
MISSION

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

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

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

Join us at PAG 2022 - Virtual Event

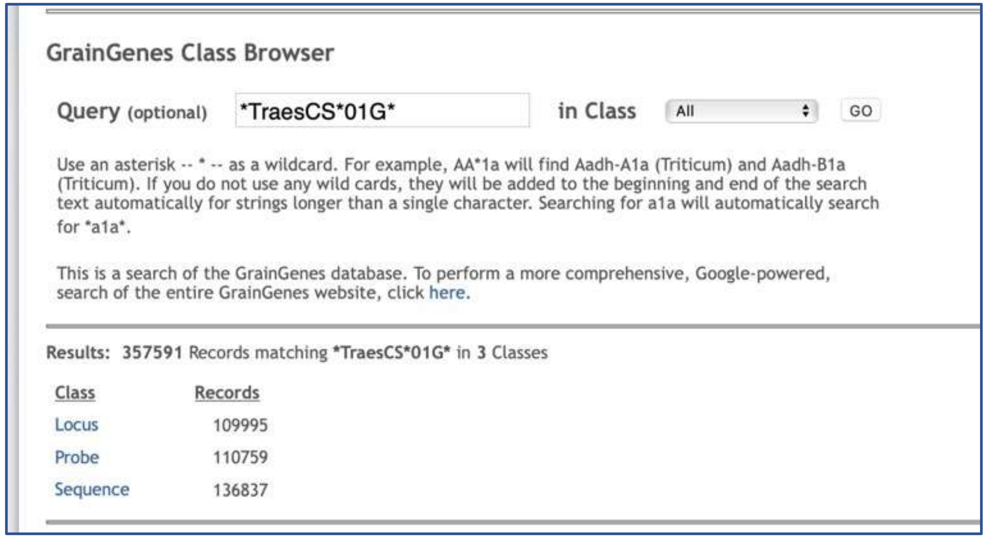
Saturday 8 January: IWGSC Main workshop

- 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

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



GrainGenes Class Browser

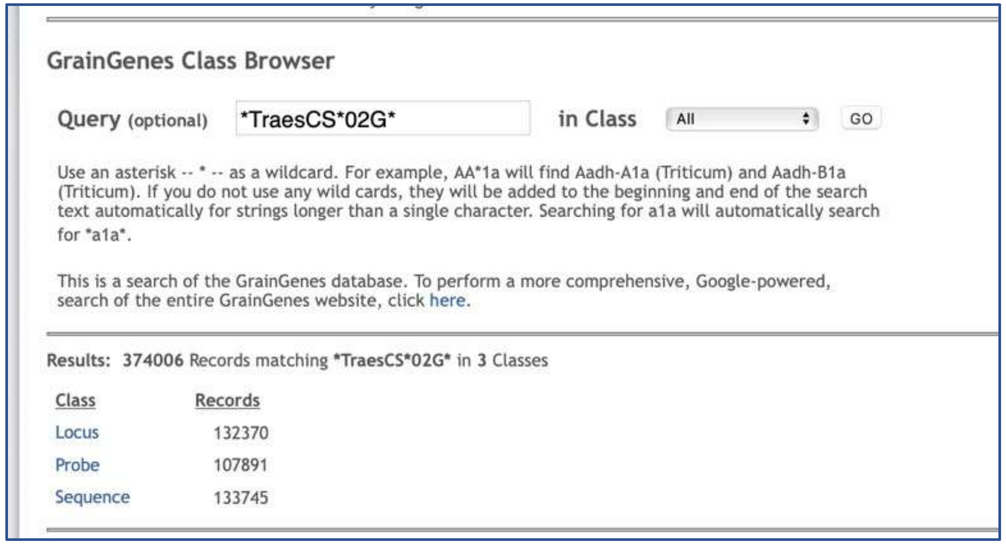
Query (optional) *TraesCS*01G* in Class All GO

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



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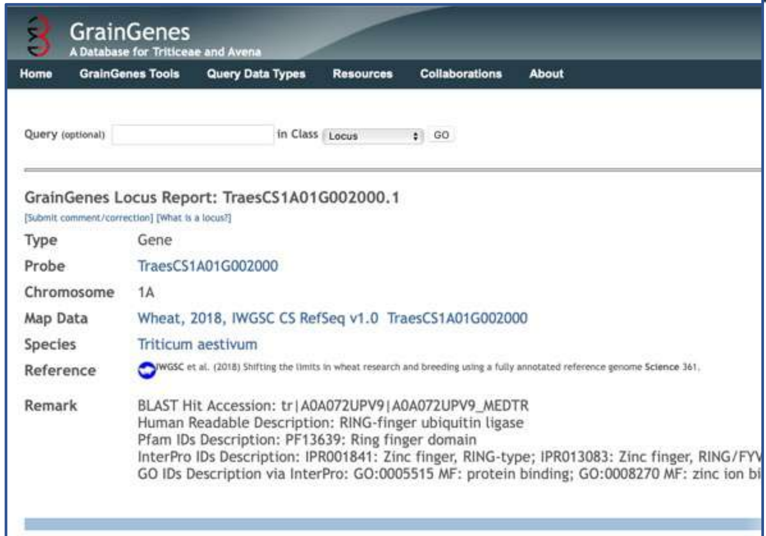
This is a search of the GrainGenes database. To perform a more comprehensive, Google-powered, search of the entire GrainGenes website, click here.

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



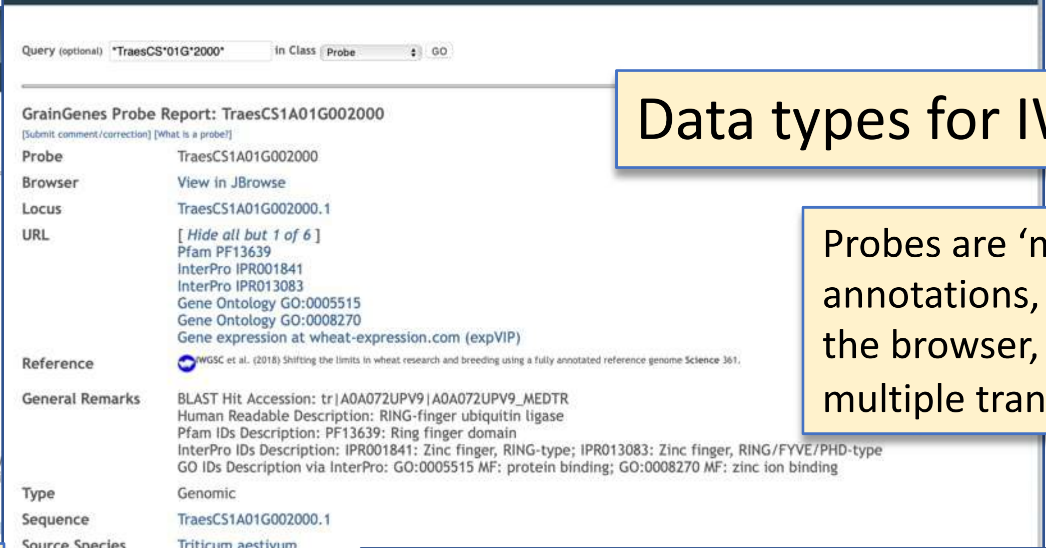
Query (optional) in Class Locus GO

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.



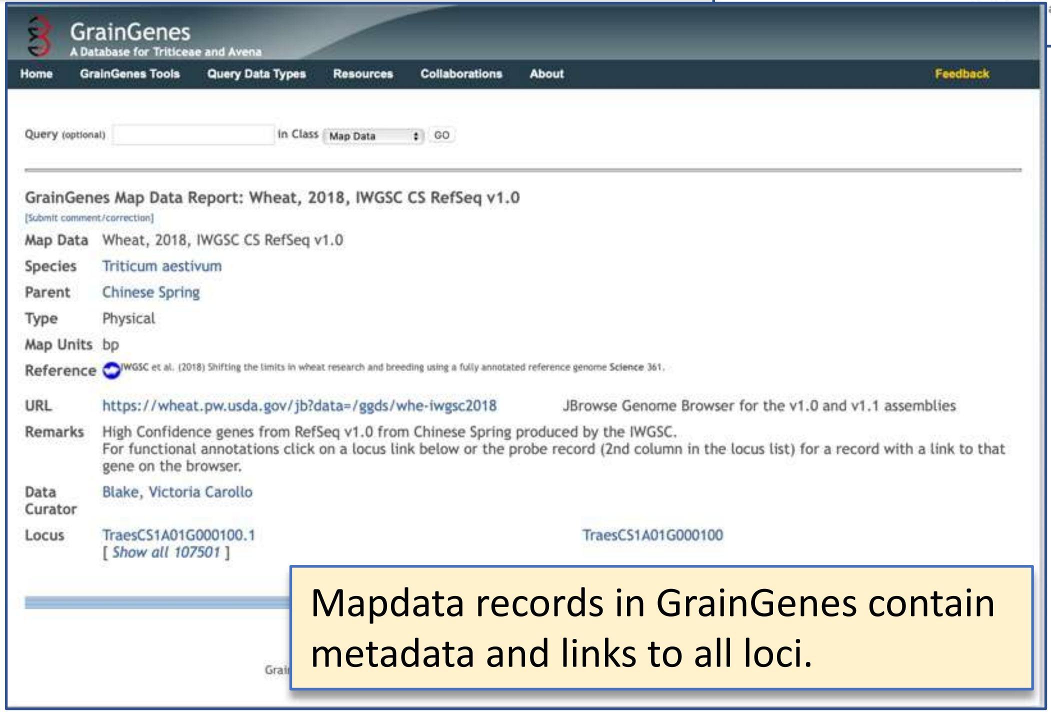
Query (optional) *TraesCS*01G*2000* in Class Probe GO

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.



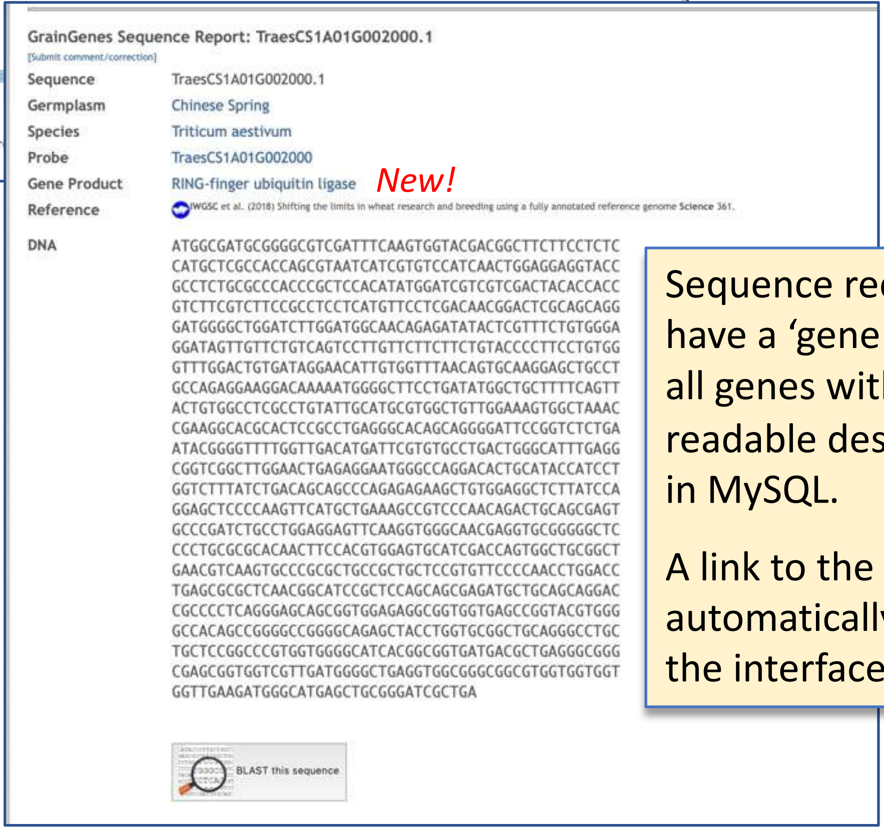
Query (optional) in Class Map Data GO

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.



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
```

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.

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)

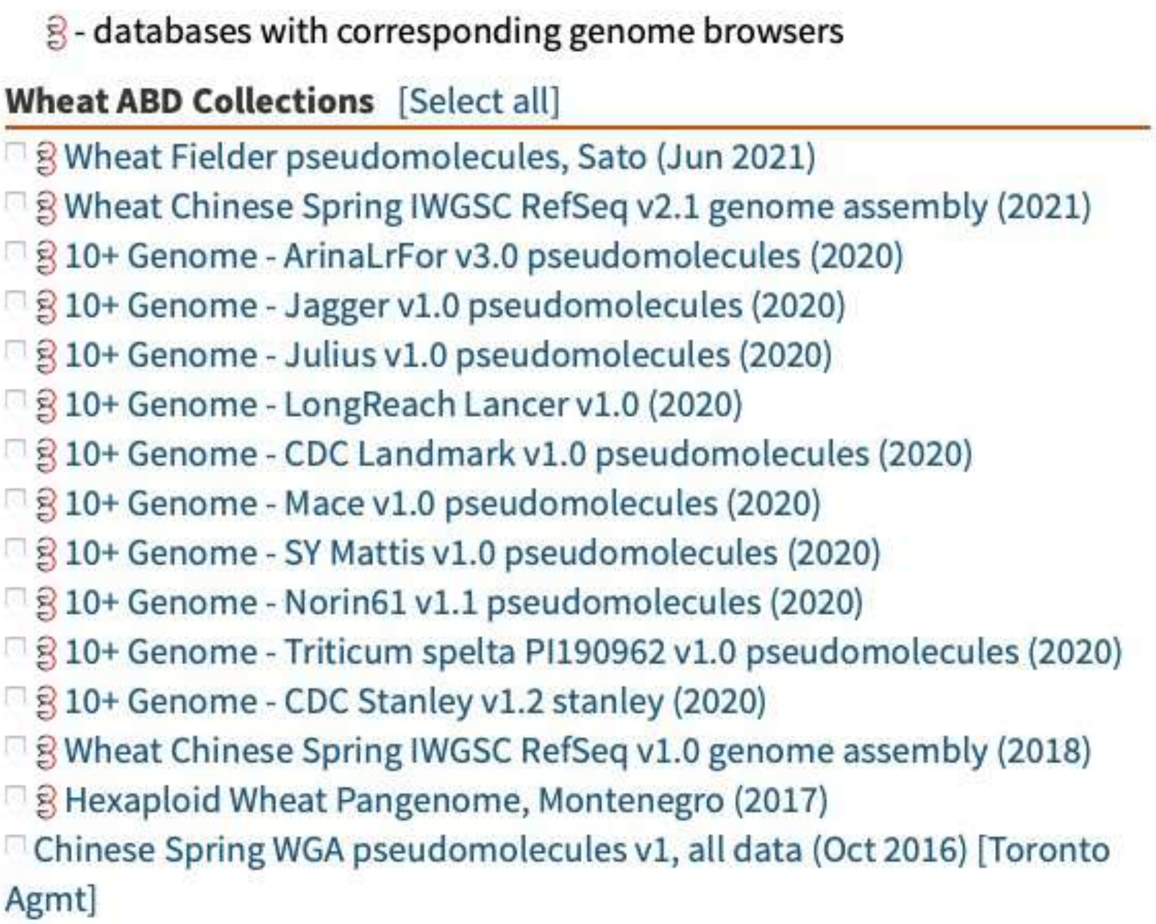
Locus : **TraesCS1A02G002000.1** – Link to Probe

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]

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- ☐ 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)

diploid and tetraploid wheat BLAST databases

🧬 - databases with corresponding genome browsers

Wheat AB Collections [Select all]

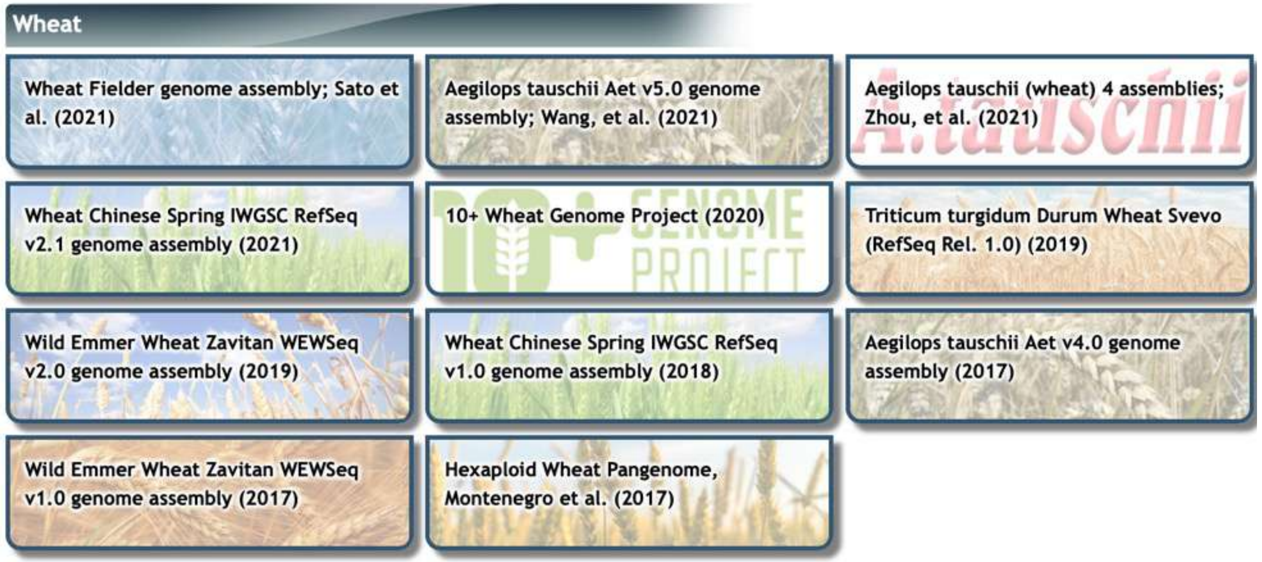
- ☐ 🧬 Wild Emmer Wheat Zavitan WEWSeq v2.0 pseudomolecules (2019)
- ☐ 🧬 Triticum turgidum Durum Wheat Svevo Rel. 1.0 pseudomolecules (2019)
- ☐ 🧬 Wild Emmer Wheat Zavitan WEWSeq v1.0 pseudomolecules (2017)
- ☐ Zavitan RefSeq v1 mapped gene set (Apr 2017)
- ☐ Zavitan RefSeq v1 unmapped gene set (Apr 2017)
- ☐ 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)


Wheat

Wheat Fielder genome assembly; Sato et al. (2021)

Aegilops tauschii Aet v5.0 genome assembly; Wang, et al. (2021)

Aegilops tauschii (wheat) 4 assemblies; Zhou, et al. (2021)

Wheat Chinese Spring IWGSC RefSeq v2.1 genome assembly (2021)

10+ Wheat Genome Project (2020)

Triticum turgidum Durum Wheat Svevo (RefSeq Rel. 1.0) (2019)

Wild Emmer Wheat Zavitan WEWSeq v2.0 genome assembly (2019)

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

Aegilops tauschii Aet v4.0 genome assembly (2017)

Wild Emmer Wheat Zavitan WEWSeq v1.0 genome assembly (2017)

Hexaploid Wheat Pangenome, Montenegro et al. (2017)

The Wheat genome browsers links are shown here.

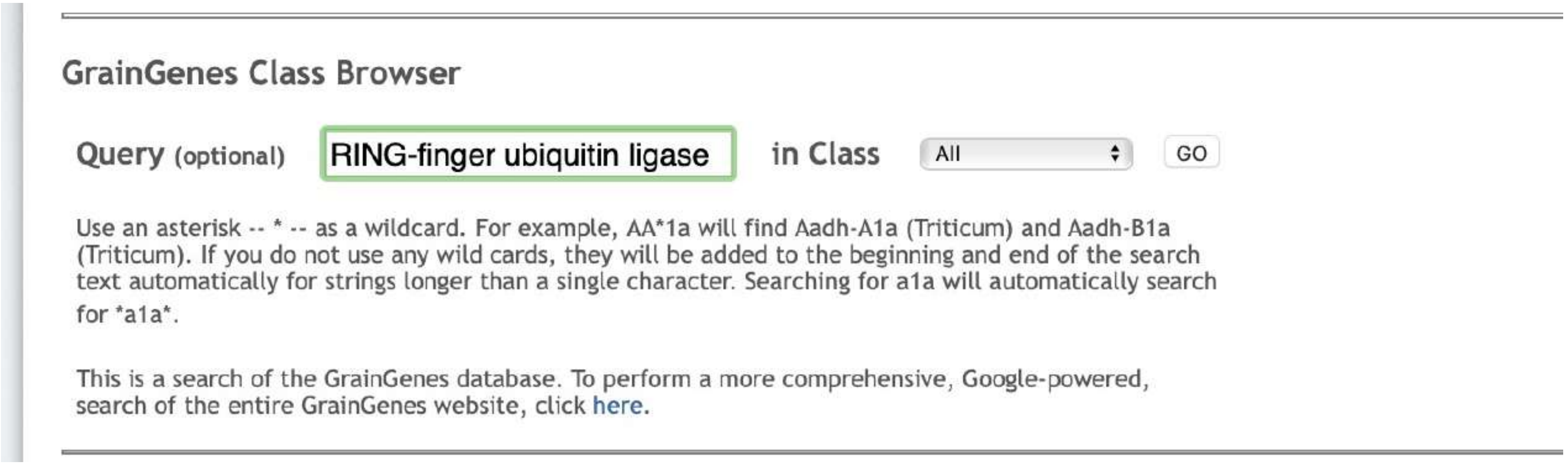
The 10+ Wheat Genome Project link expands to links for the individual browsers.

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

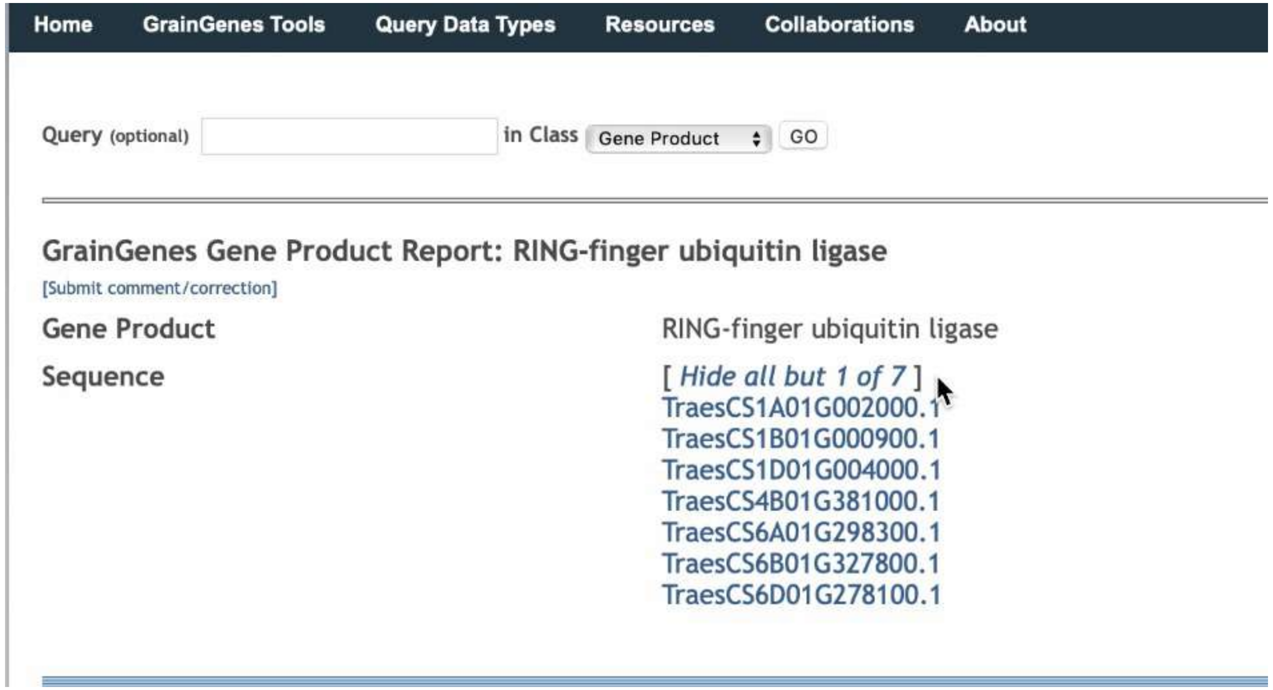
Query (optional): RING-finger ubiquitin ligase in Class: All

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”.

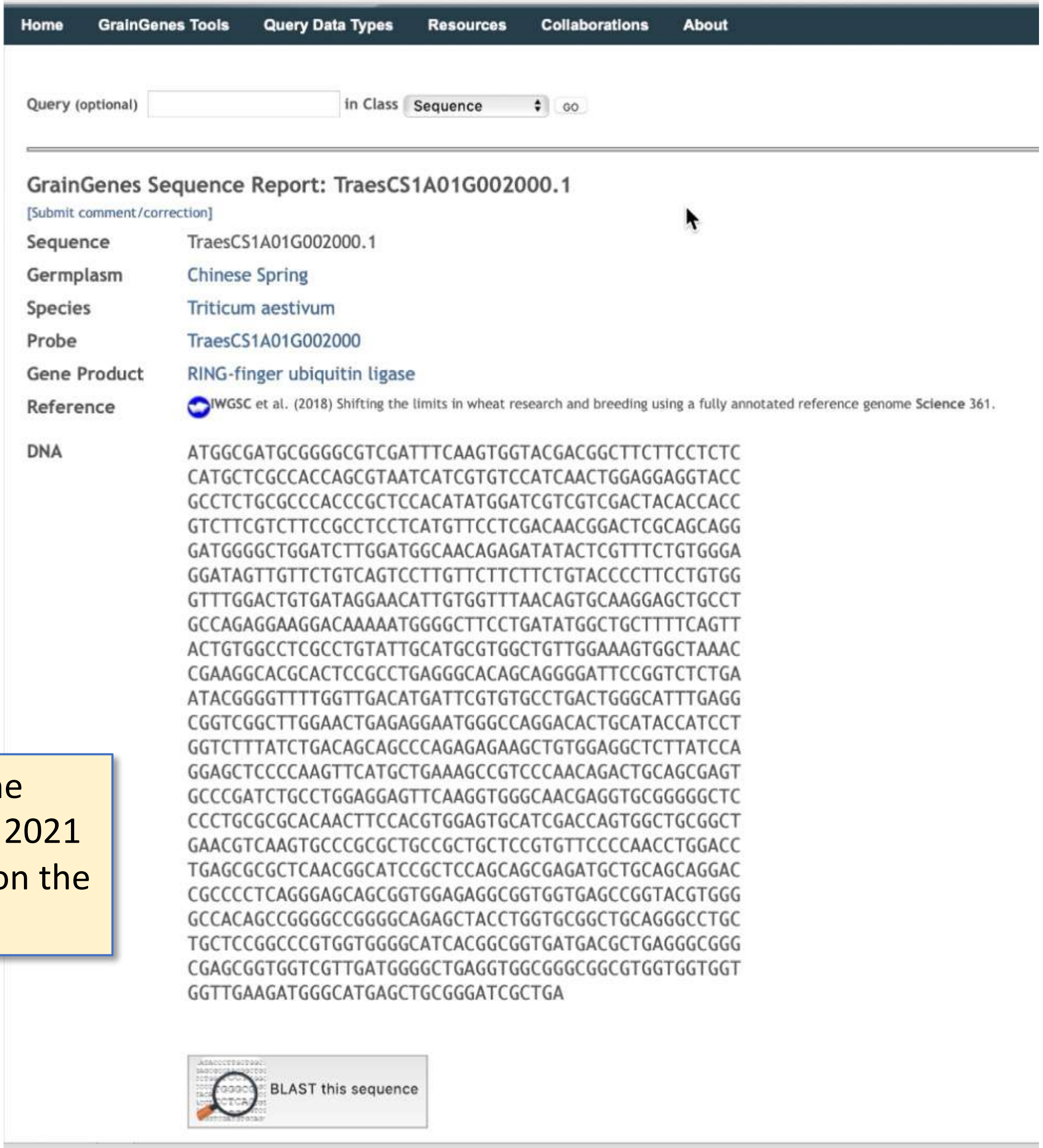
Users are encouraged to browse the data class and try other forms of this term for better coverage.



Query (optional): in Class: Gene Product

GrainGenes Gene Product Report: RING-finger ubiquitin ligase

Gene Product	RING-finger ubiquitin ligase
Sequence	TraesCS1A01G002000.1 TraesCS1B01G000900.1 TraesCS1D01G004000.1 TraesCS4B01G381000.1 TraesCS6A01G298300.1 TraesCS6B01G327800.1 TraesCS6D01G278100.1



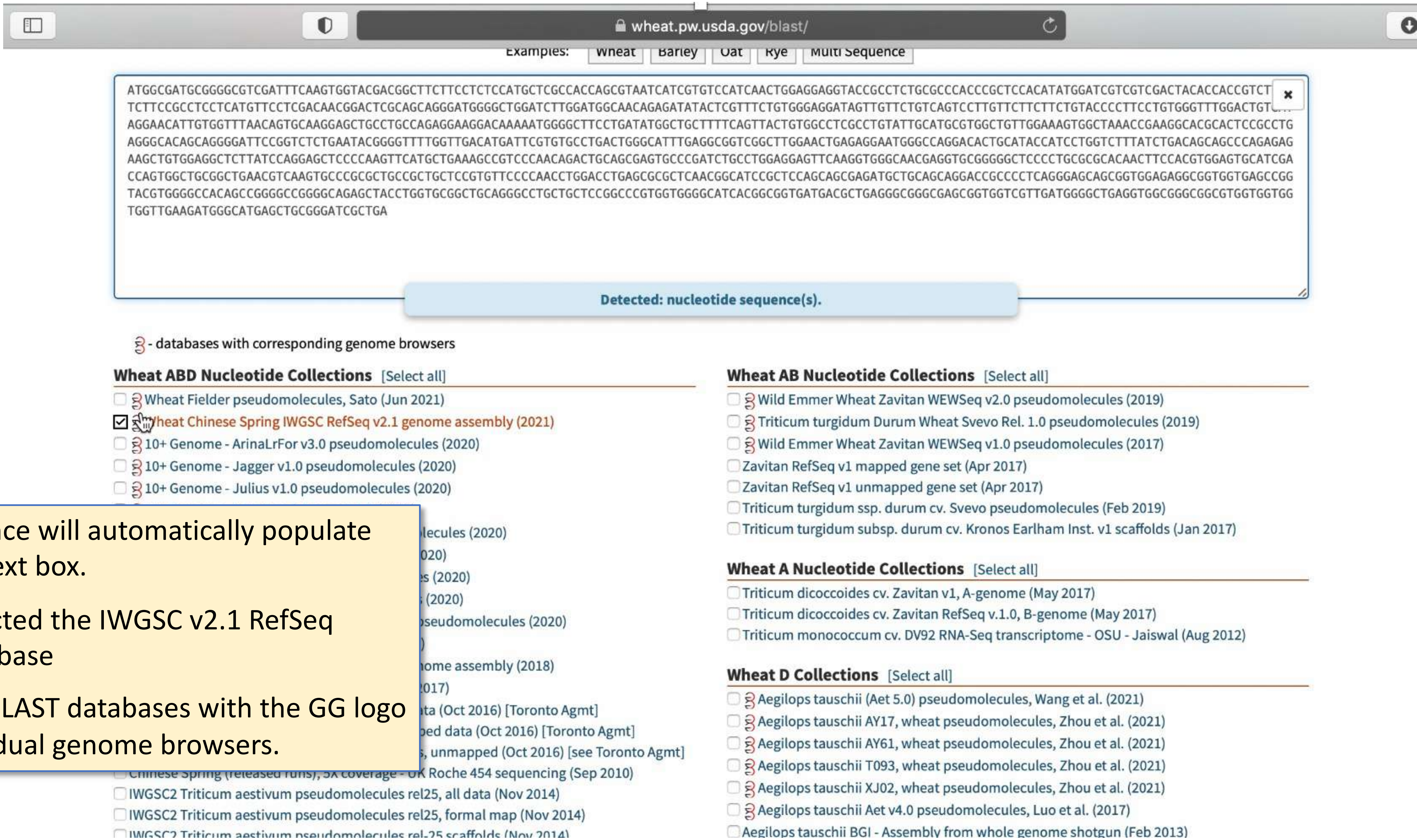
GrainGenes Sequence Report: TraesCS1A01G002000.1

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
```

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



```
ATGGCGATGCGGGGCGTCGATTTCAAGTGGTACGACGGCTTCTTCCTCTCCATGCTCGCCACCAGCGTAATCATCGTGTCCATCAACTGGAGGAGGTACCGCCTCTGCGCCCACCCGCTCCACATATGGATCGTCGTCGACTACACCACCGTCT
TCTTCCGCCTCCTCATGTTCCTCGACAACGGACTCGCAGCAGGGATGGGGCTGGATCTTGGATGGCAACAGAGATATACTCGTTTCTGTGGGAGGATAGTTGTTCTGTCAGTCCTTGTTCTTCTTCTGTACCCCTTCCTGTGGGTTTGGACTGT
AGGAACATTGTGGTTTAACAGTGCAAGGAGCTGCCTGCCAGAGGAAGGACAAAAATGGGGCTTCCTGATATGGCTGCTTTTCAGTTACTGTGGCCTCGCCTGTATTGCATGCGTGGCTGTTGGAAAGTGGCTAAACCGAAGGCACGCACTCCGCCTG
AGGGCACAGCAGGGGATTCCGGTCTCTGAATACGGGGTTTTGGTTGACATGATTCGTGTGCCTGACTGGGCATTTGAGGCGGTCGGCTTGGAACTGAGAGGAATGGCCAGGACACTGCATACCATCCTGGTCTTTATCTGACAGCAGCCCAGAGAG
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)
)
nome assembly (2018)
017)
ta (Oct 2016) [Toronto Agmt]
ped data (Oct 2016) [Toronto Agmt]
, 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)

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)

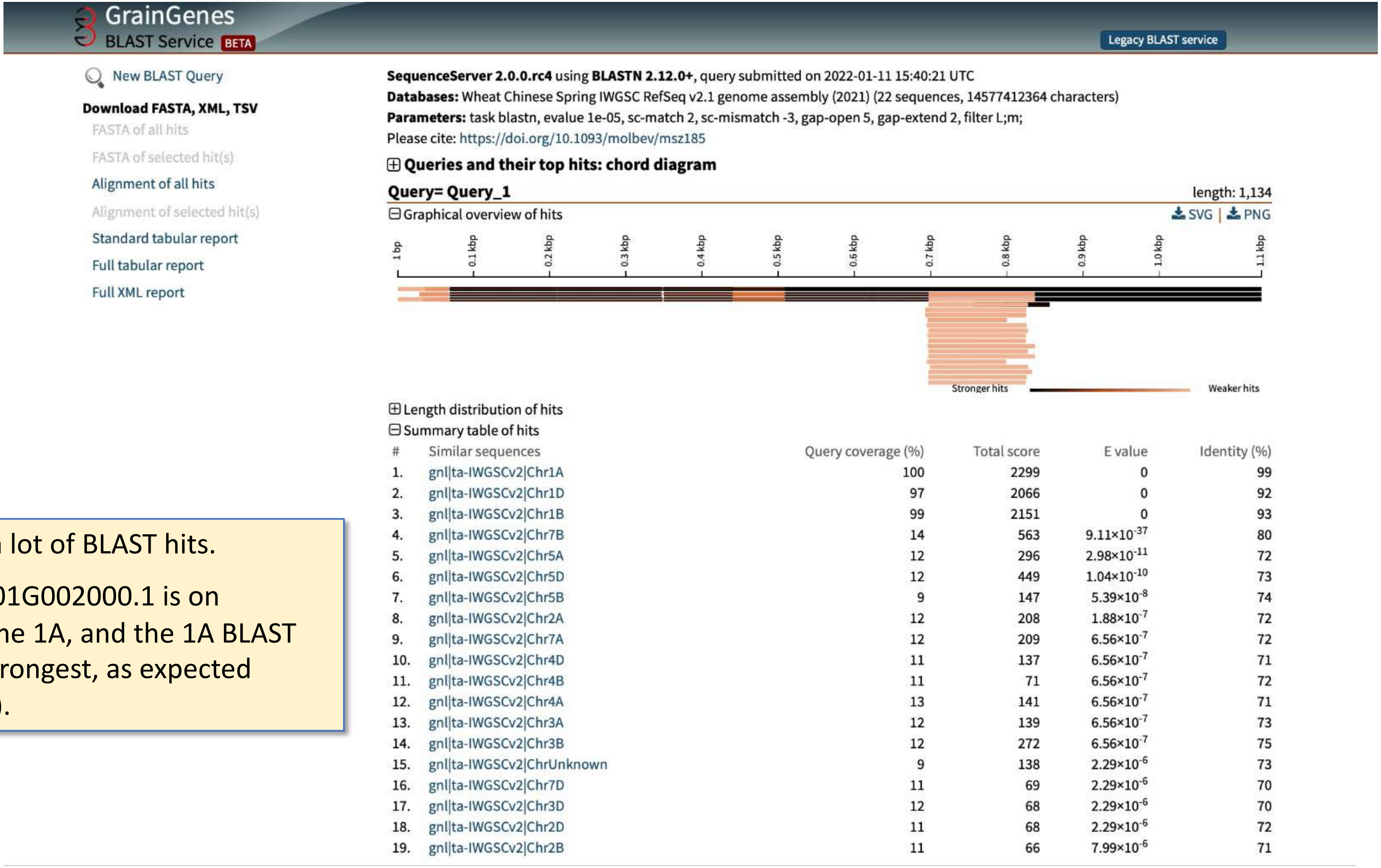
Wheat D Collections [Select all]

☐ 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.



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

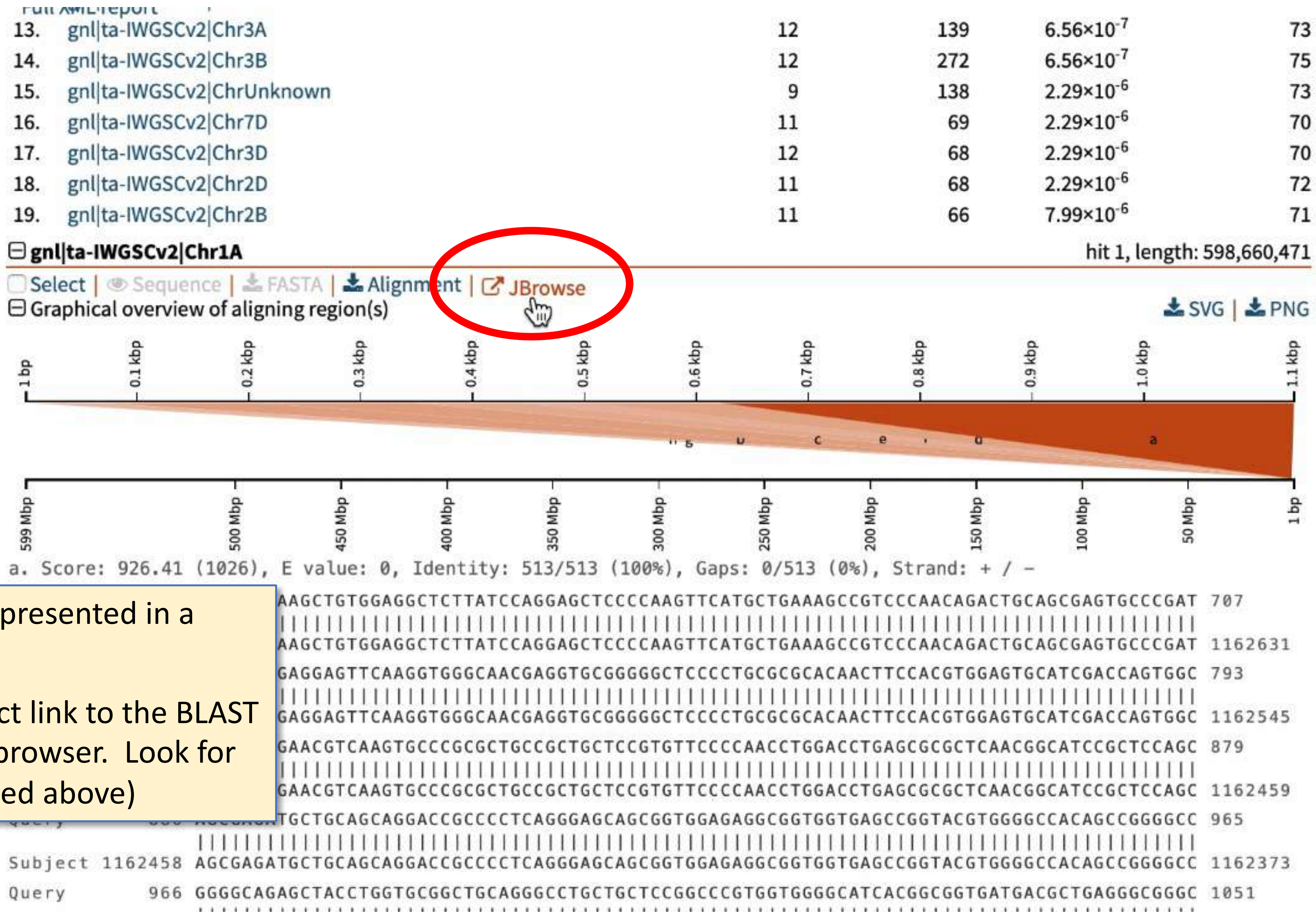
⊞ Length distribution of hits

⊟ 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).



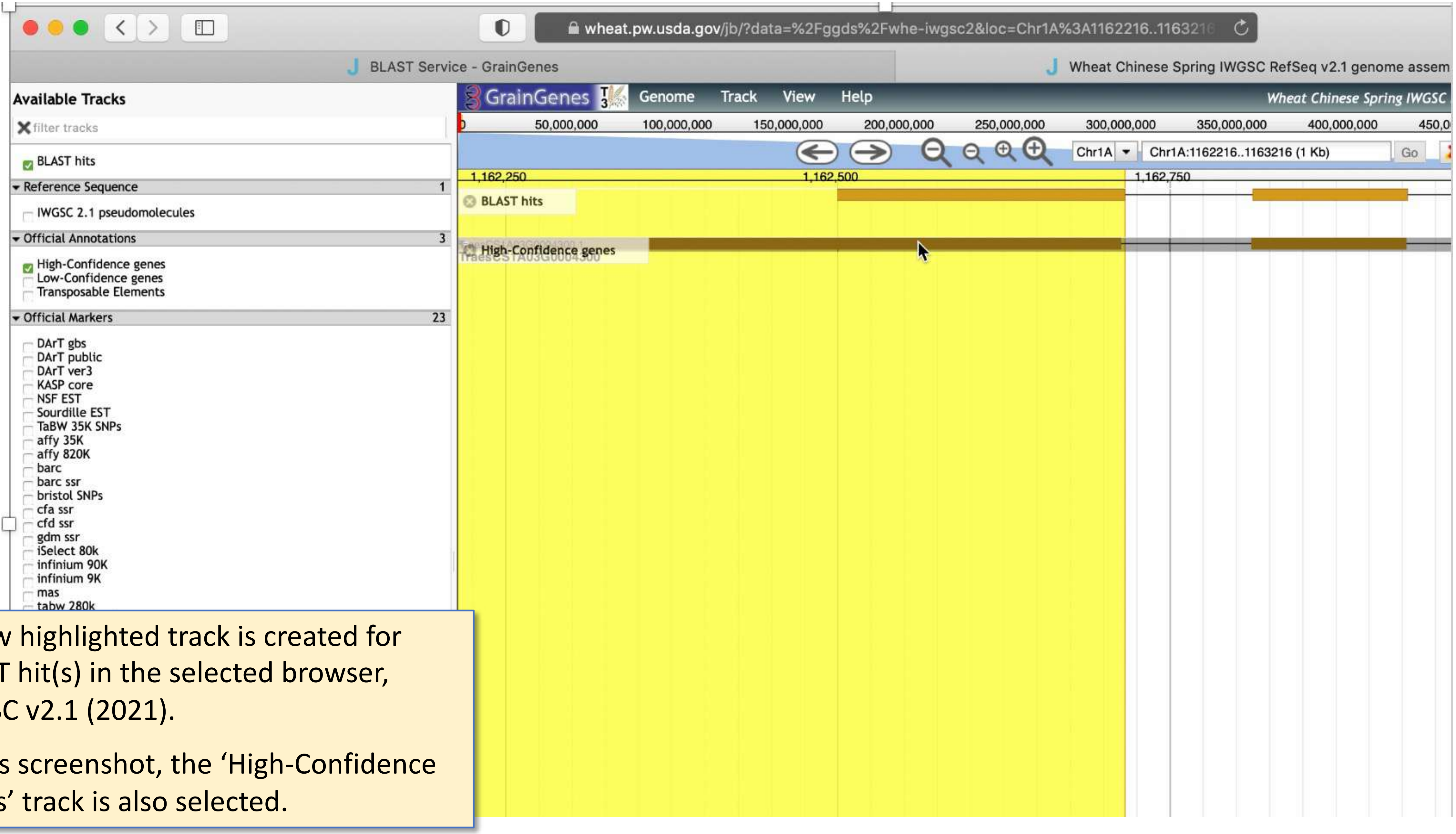
13.	gnl|ta-IWGSCv2|Chr3A	12	139	6.56×10^{-7}	73
14.	gnl|ta-IWGSCv2|Chr3B	12	272	6.56×10^{-7}	75
15.	gnl|ta-IWGSCv2|ChrUnknown	9	138	2.29×10^{-6}	73
16.	gnl|ta-IWGSCv2|Chr7D	11	69	2.29×10^{-6}	70
17.	gnl|ta-IWGSCv2|Chr3D	12	68	2.29×10^{-6}	70
18.	gnl|ta-IWGSCv2|Chr2D	11	68	2.29×10^{-6}	72
19.	gnl|ta-IWGSCv2|Chr2B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

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

```
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
       TGCTGCAGCAGGACCGCCCCTCAGGGAGCAGCGGTGGAGAGGCGGTGGTGAGCCGGTACGTGGGGCCACAGCCGGGGCC 965
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Subject 1162458 AGCGAGATGCTGCAGCAGGACCGCCCCTCAGGGAGCAGCGGTGGAGAGGCGGTGGTGAGCCGGTACGTGGGGCCACAGCCGGGGCC 1162373
Query       966 GGGGCAGAGCTACCTGGTGCGGCTGCAGGGCCTGCTGCTCCGGCCCGTGGTGGGGCATCACGGCGGTGATGACGCTGAGGGCGGGC 1051
```

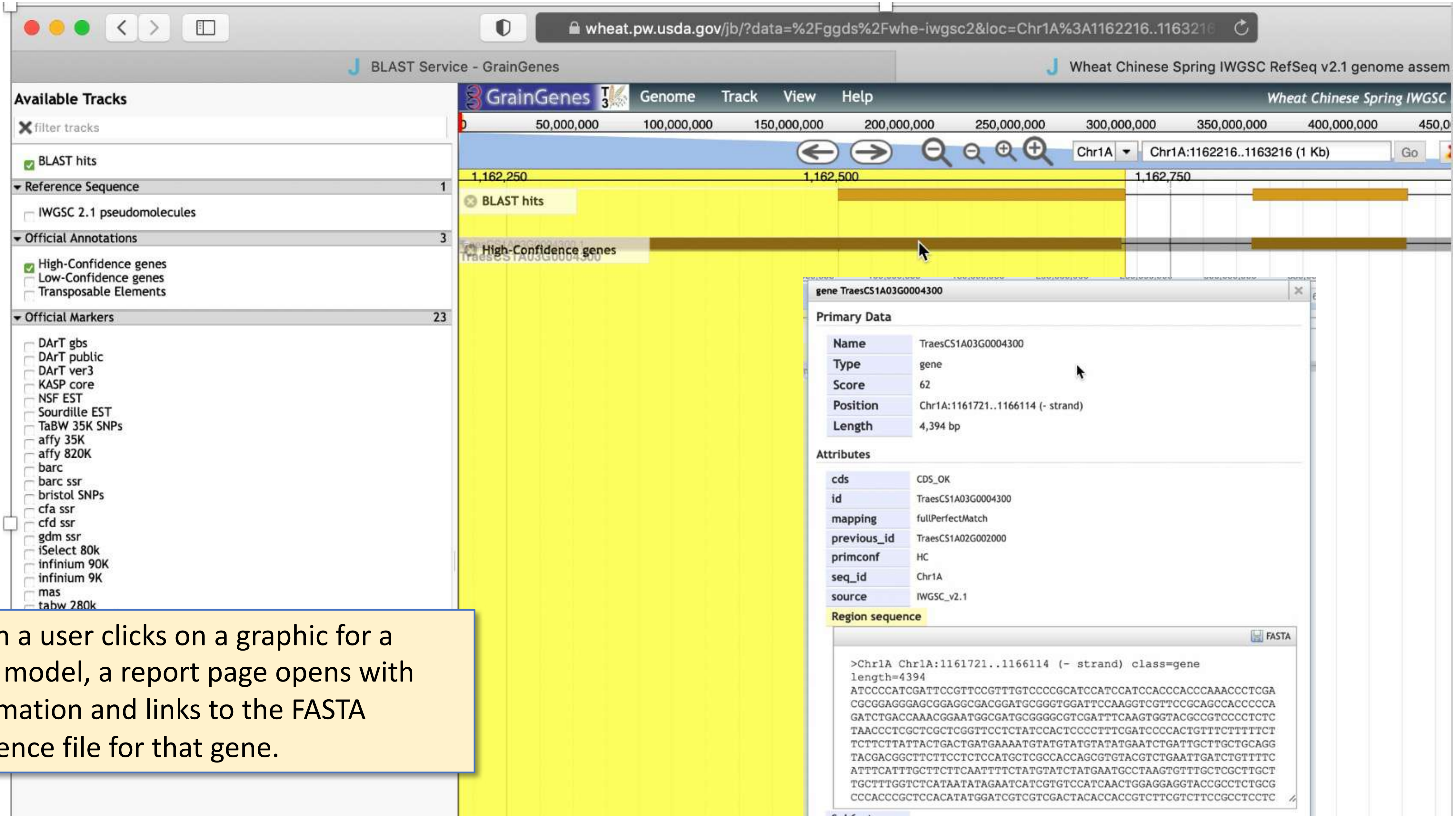
BLAST results are now presented in a graphical view.

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.



gene TraesCS1A03G0004300

Primary Data

Name	TraesCS1A03G0004300
Type	gene
Score	62
Position	Chr1A:1161721..1166114 (- strand)
Length	4,394 bp

Attributes

cds	CDS_OK
id	TraesCS1A03G0004300
mapping	fullPerfectMatch
previous_id	TraesCS1A02G002000
primconf	HC
seq_id	Chr1A
source	IWGSC_v2.1

Region sequence

FASTA

```
>Chr1A Chr1A:1161721..1166114 (- strand) class=gene
length=4394
ATCCCCATCGATTCCGTTCCGTTTGTCCCCGCATCCATCCATCCACCCACCCAAACCCTCGA
CGCGGAGGGAGCGGAGGCGACGGATGCGGGTGGATTCCAAGGTCGTTCCGCAGCCACCCCCA
GATCTGACCAAACGGAATGGCGATGCGGGGCGTCGATTTCAAGTGGTACGCCGTCCCCTCTC
TAACCCTCGCTCGCTCGGTTCCTCTATCCACTCCCCTTTCGATCCCCACTGTTTCTTTTTCT
TCTTCTTATTACTGACTGATGAAAATGTATGTATGTATATGAATCTGATTGCTTGCTGCAGG
TACGACGGCTTCTTCCTCTCCATGCTCGCCACCAGCGTGTACGTCTGAATTGATCTGTTTTC
ATTTCATTTGCTTCTTCAATTTTCTATGTATCTATGAATGCCTAAGTGTTTGCTCGCTTGCT
TGCTTTGGTCTCATAATATAGAATCATCGTGTCCATCAACTGGAGGAGGTACCGCCTCTGCG
CCCACCCGCTCCACATATGGATCGTCGTCGACTACACCACCGTCTTCGTCTTCCGCCTCCTC
```

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

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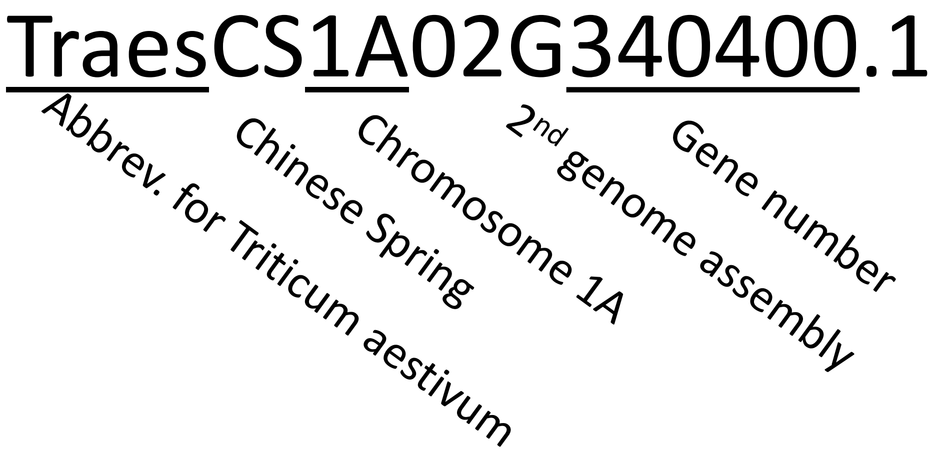


TraesCS1A02G340400.1

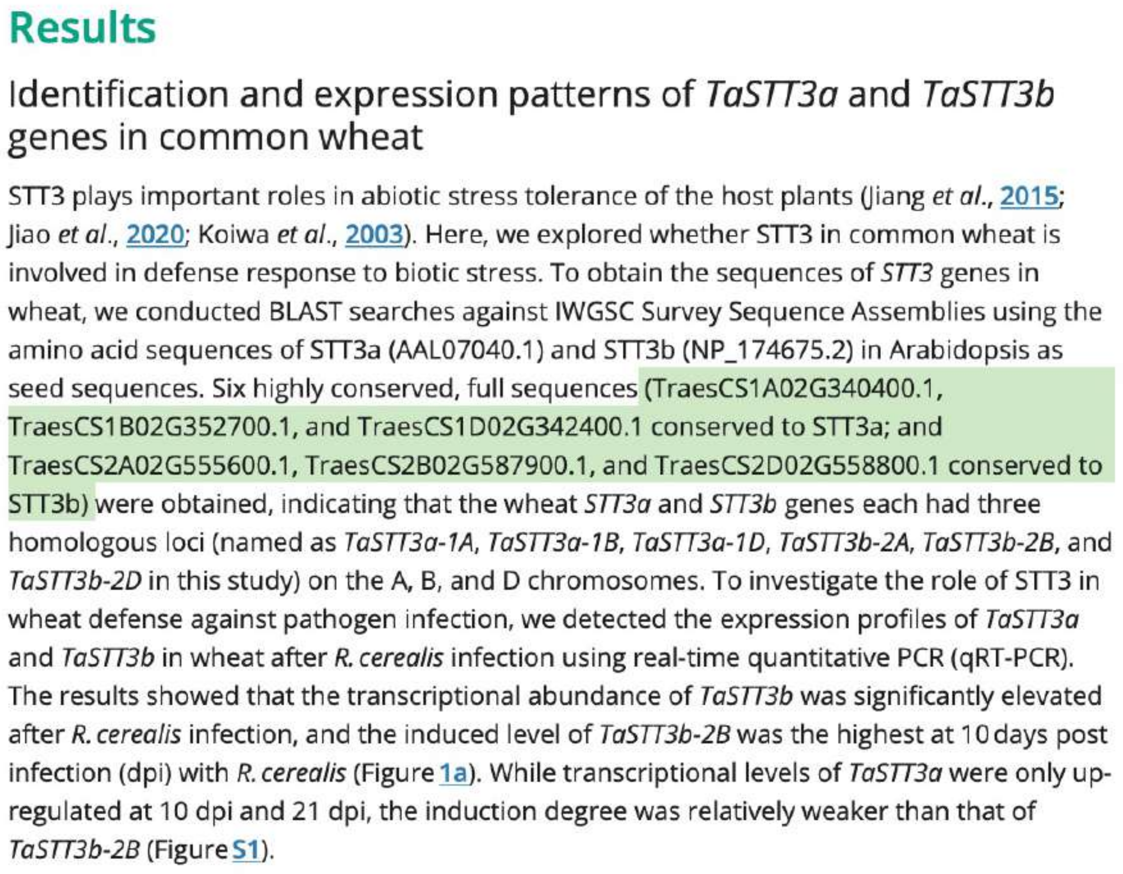
Abbrev. for Triticum aestivum

Chinese Spring

Chromosome 1A

2^{nd} genome assembly

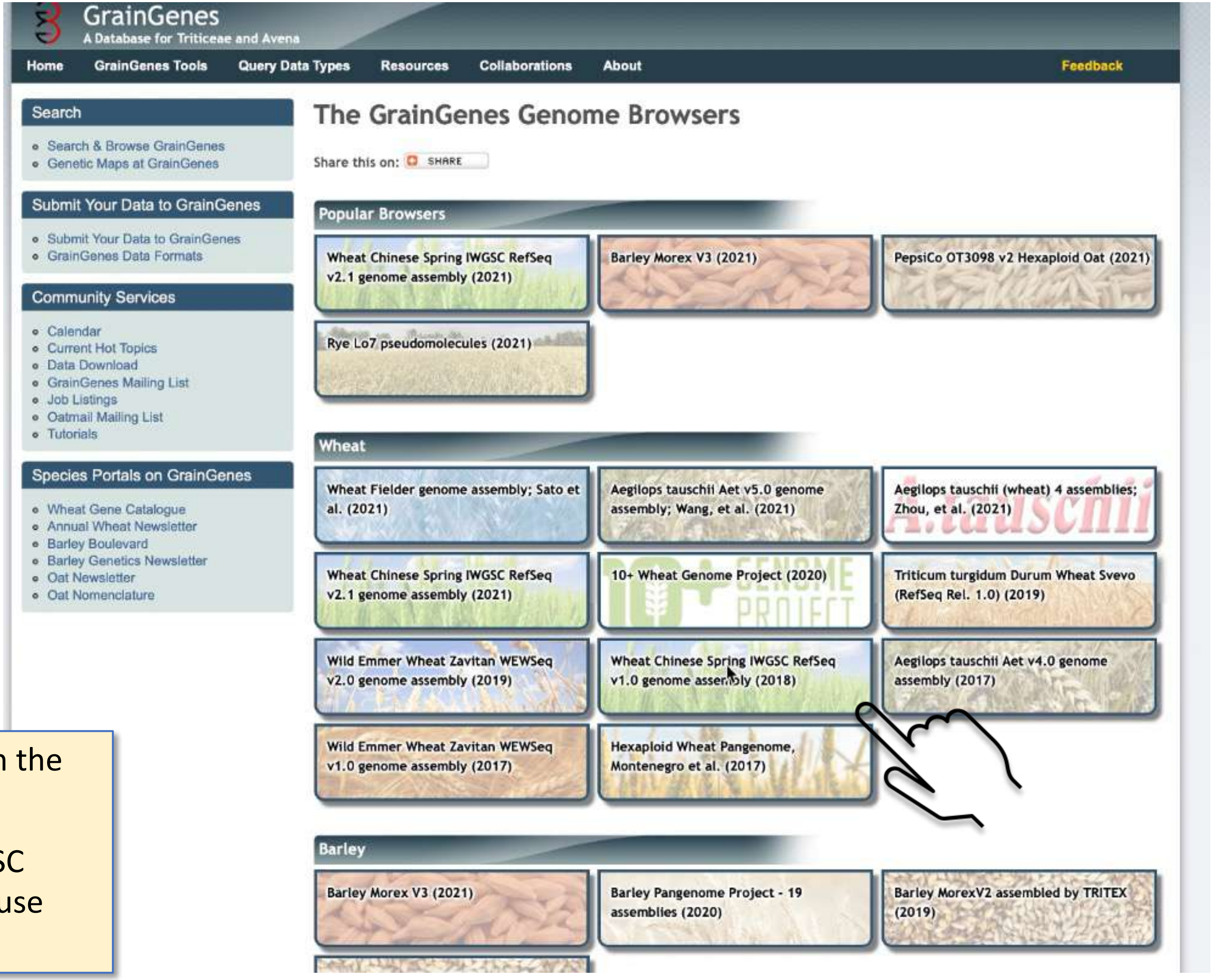
Gene number



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 GrainGenes Genome Browsers

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- Annual Wheat Newsletter
- Barley Boulevard
- Barley Genetics Newsletter
- Oat Newsletter
- Oat Nomenclature

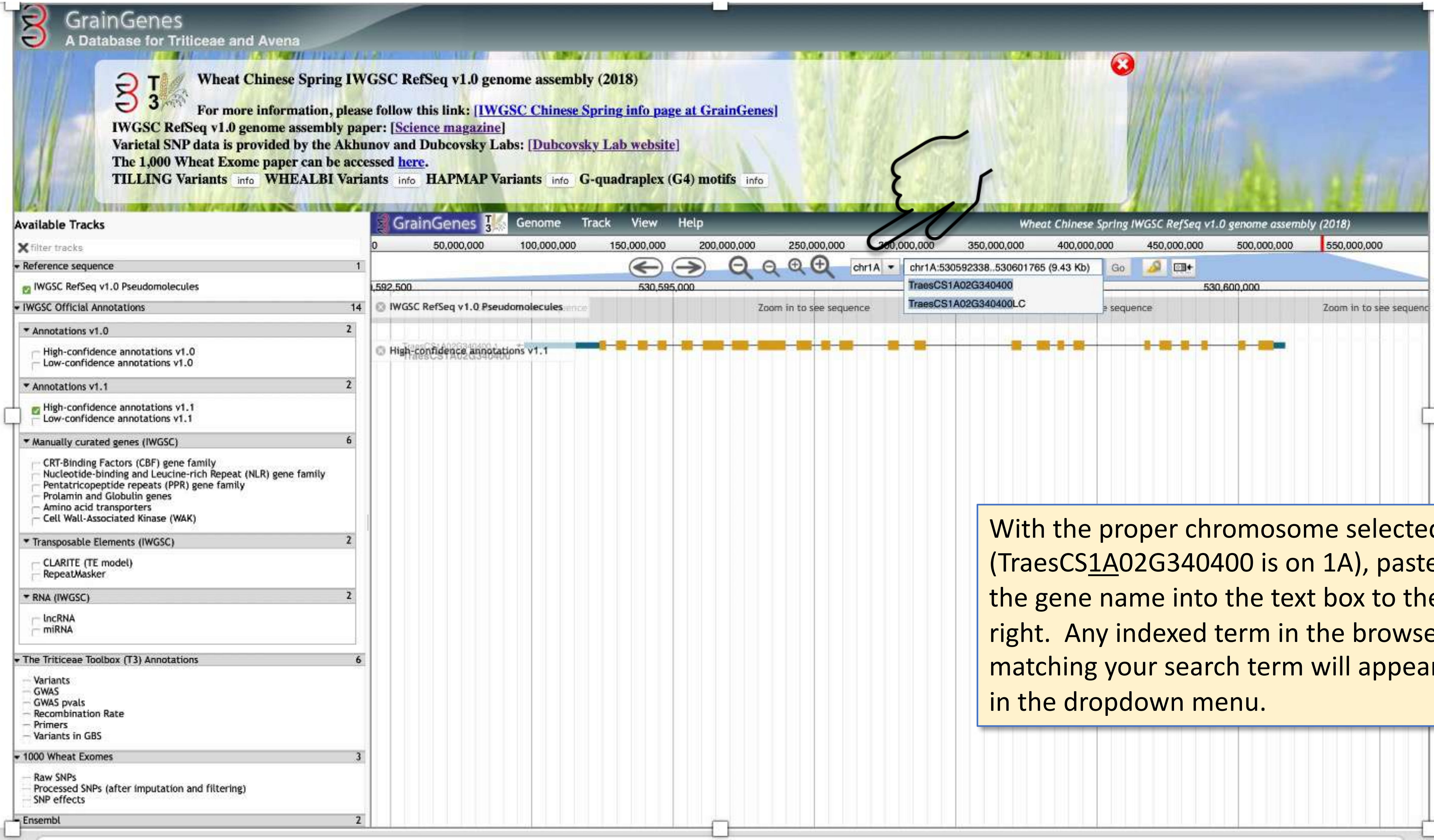
Popular Browsers
- Wheat Chinese Spring IWGSC RefSeq v2.1 genome assembly (2021)
- Barley Morex V3 (2021)
- PepsiCo OT3098 v2 Hexaploid Oat (2021)
- Rye Lo7 pseudomolecules (2021)

Wheat
- Wheat Fielder genome assembly; Sato et al. (2021)
- Aegilops tauschii Aet v5.0 genome assembly; Wang, et al. (2021)
- Aegilops tauschii (wheat) 4 assemblies; Zhou, et al. (2021)
- Wheat Chinese Spring IWGSC RefSeq v2.1 genome assembly (2021)
- 10+ Wheat Genome Project (2020)
- Triticum turgidum Durum Wheat Svevo (RefSeq Rel. 1.0) (2019)
- Wild Emmer Wheat Zavitan WEWSeq v2.0 genome assembly (2019)
- Wheat Chinese Spring IWGSC RefSeq v1.0 genome assembly (2018)
- Aegilops tauschii Aet v4.0 genome assembly (2017)
- Wild Emmer Wheat Zavitan WEWSeq v1.0 genome assembly (2017)
- Hexaploid Wheat Pangenome, Montenegro et al. (2017)

Barley
- Barley Morex V3 (2021)
- Barley Pangenome Project - 19 assemblies (2020)
- Barley MorexV2 assembled by TRITEX (2019)

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).



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]

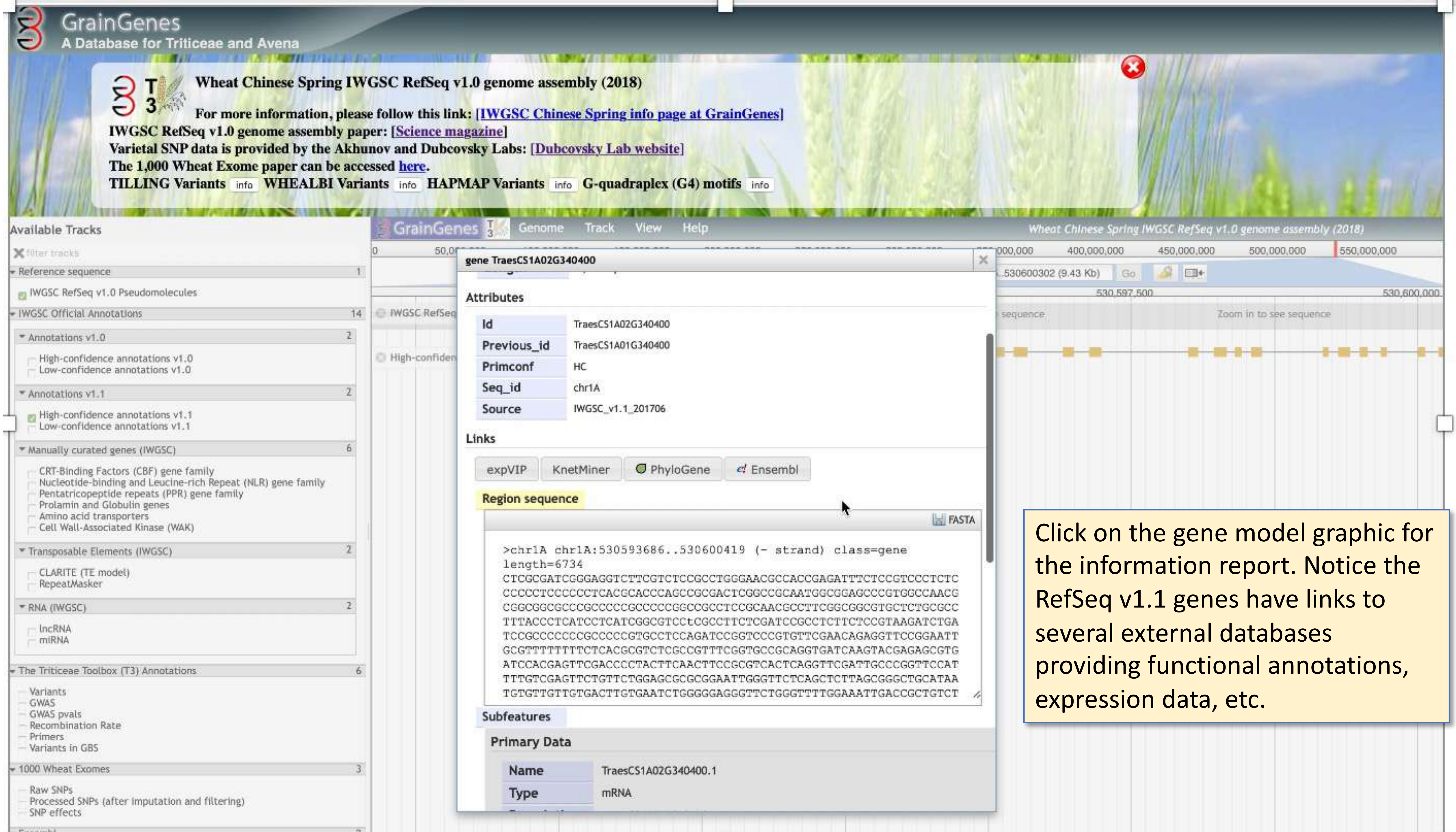
The 1,000 Wheat Exome paper can be accessed here.

chr1A:530592338..530601765 (9.43 Kb)

TraesCS1A02G340400

TraesCS1A02G340400LC

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.



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

gene TraesCS1A02G340400

Attributes

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

Links

Region sequence

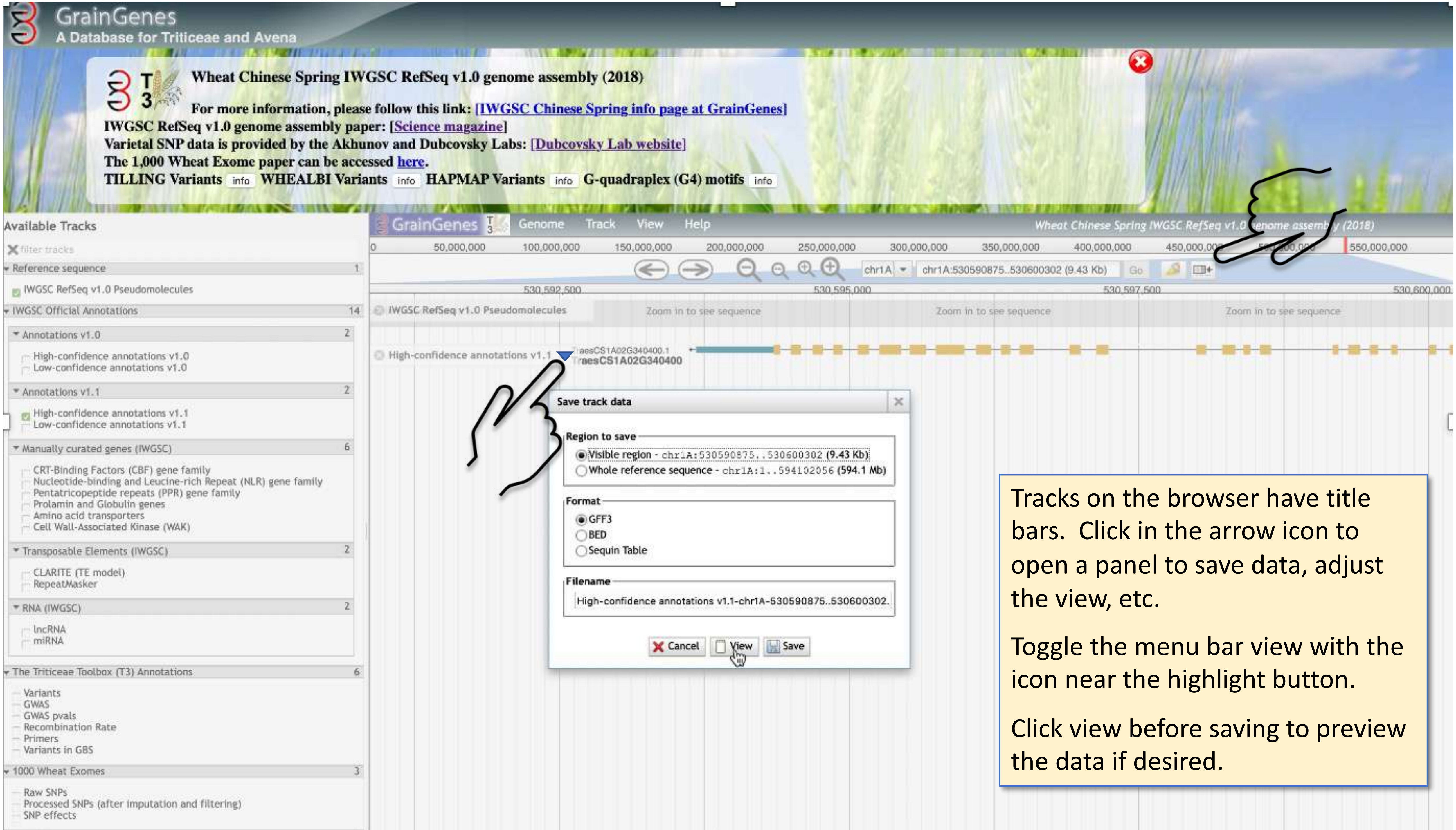
```
>chr1A chr1A:530593686..530600419 (- strand) class=gene
length=6734
CTCGCGATCGGGAGGTCTTCGTCTCCGCCTGGGAACGCCACCGAGATTTCTCCGTCCCTCTC
CCCCCTCCCCCCTCACGCACCCAGCCGCGACTCGGCCGCAATGGCGGAGCCCGTGGCCAACG
CGGCGGCGCCCGCCCCCGCCCCCGGCCGCCTCCGCAACGCCTTCGGCGGCGTGCTCTGCGCC
TTTACCCTCATCCTCATCGGCGTCCtCGCCTTCTCGATCCGCCTCTTCTCCGTAAGATCTGA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



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

Save track data

Region to save
● Visible region - `chr1A:530590875..530600302` (9.43 Kb)
○ Whole reference sequence - `chr1A:1..594102056` (594.1 Mb)

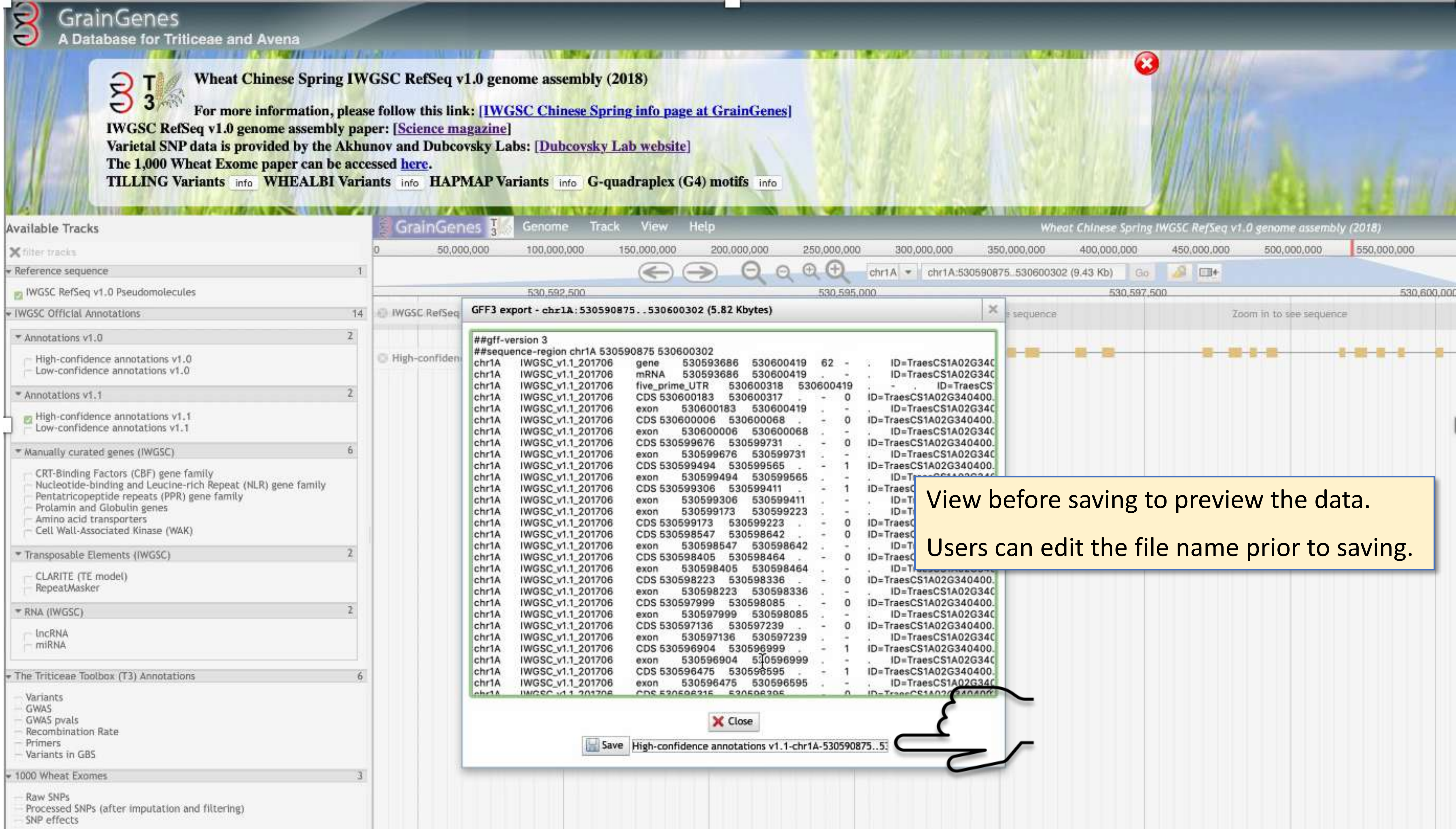
Format
● GFF3
○ BED
○ Sequin Table

Filename
High-confidence annotations v1.1-chr1A-530590875..530600302.

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.



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

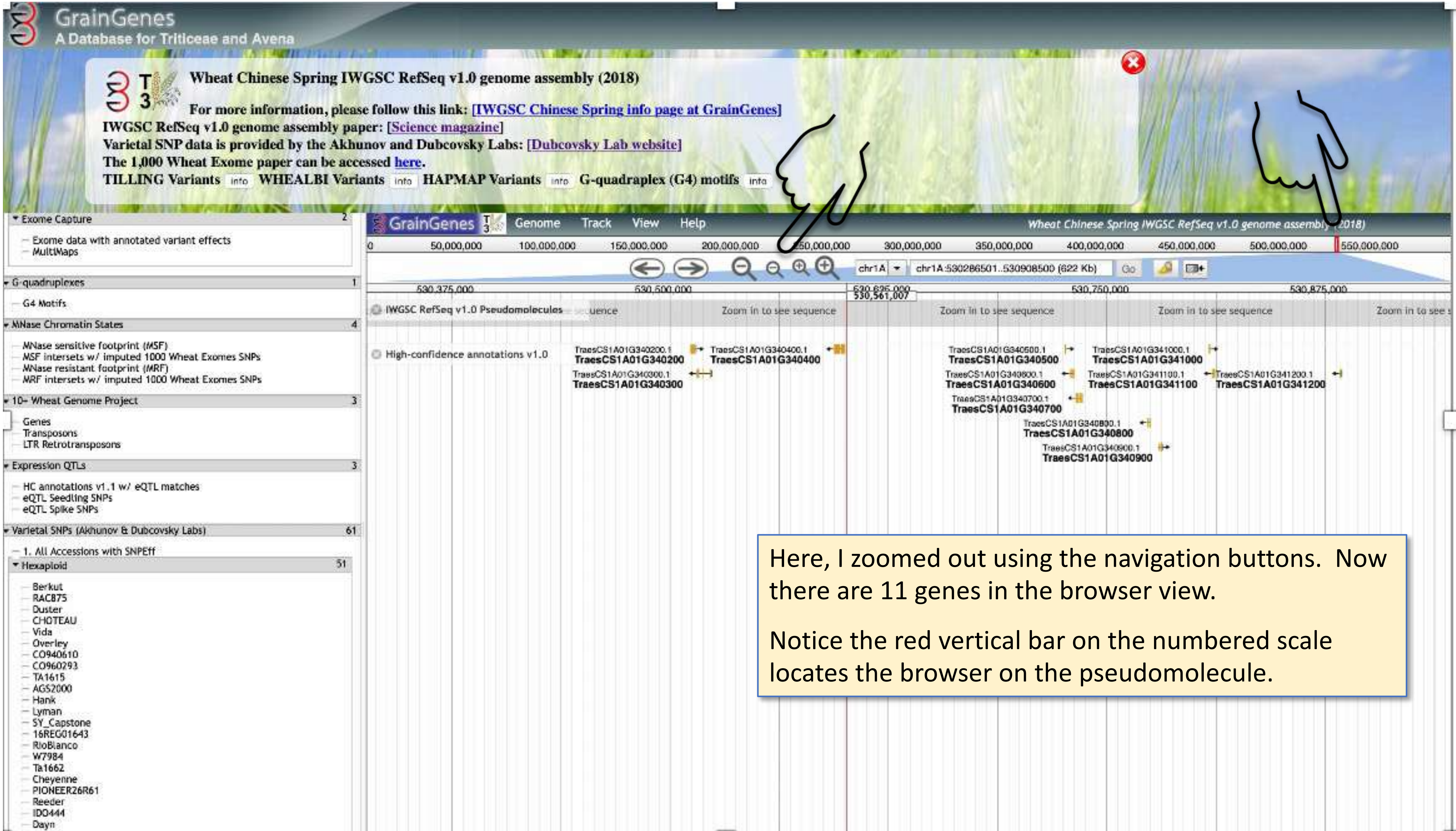
GFF3 export - chr1A:530590875..530600302 (5.82 Kbytes)

```
##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
```

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

View before saving to preview the data.

Users can edit the file name prior to saving.



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]

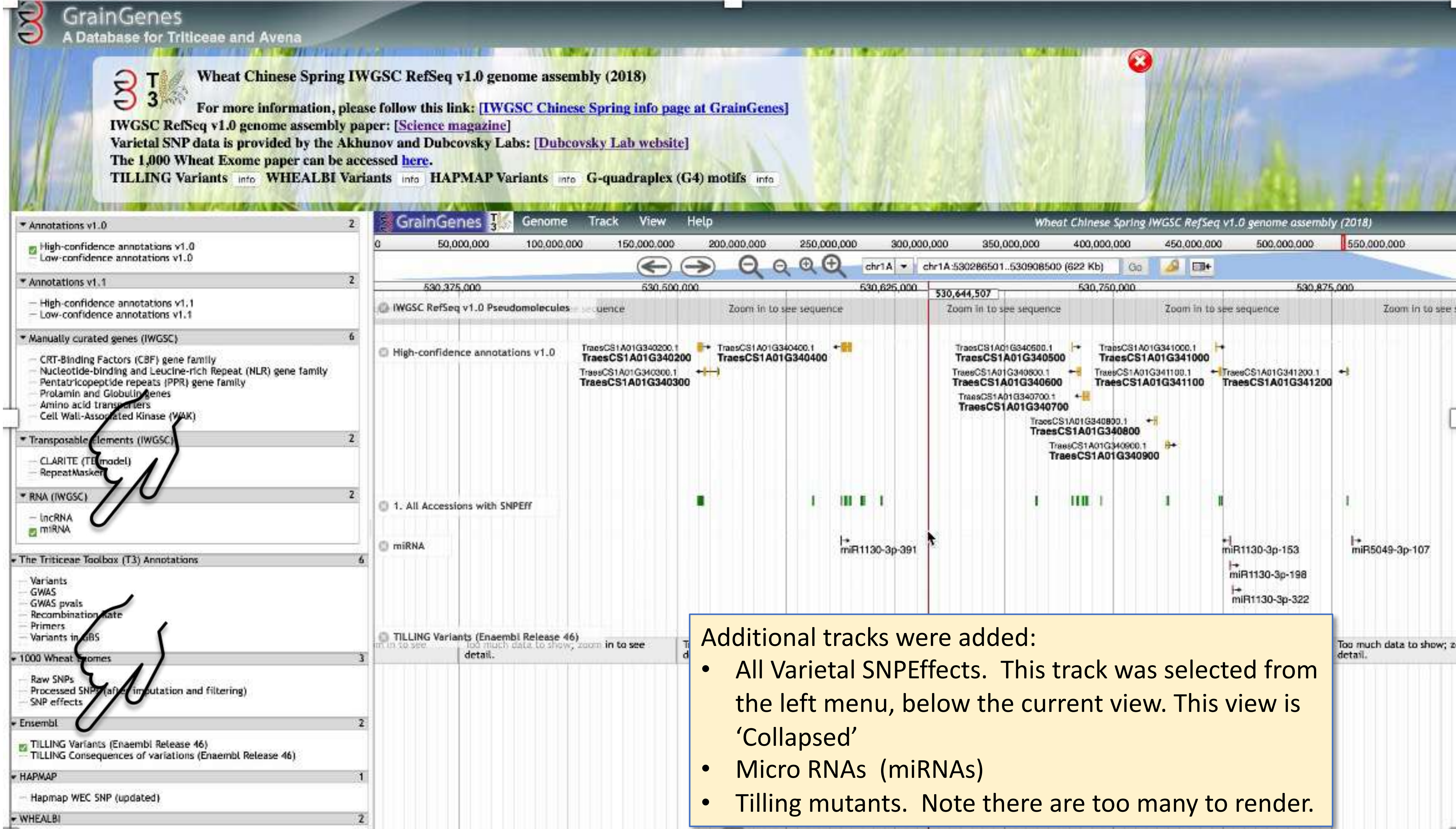
The 1,000 Wheat Exome paper can be accessed here.

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

- Exome Capture 2
  - Exome data with annotated variant effects
  - MultiMaps
- G-quadruplexes 1
  - G4 Motifs
- MNase Chromatin States 4
  - MNase sensitive footprint (MSF)
  - MSF intersets w/ imputed 1000 Wheat Exomes SNPs
  - MNase resistant footprint (MRF)
  - MRF intersets w/ imputed 1000 Wheat Exomes SNPs
- 10+ Wheat Genome Project 3
  - Genes
  - Transposons
  - LTR Retrotransposons
- Expression QTLs 3
  - HC annotations v1.1 w/ eQTL matches
  - eQTL Seedling SNPs
  - eQTL Spike SNPs
- Varietal SNPs (Akhunov & Dubcovsky Labs) 61
  - 1. All Accessions with SNPEff
  - Hexaploid 51
    - Berkut
    - RAC875
    - Duster
    - CHOTEAU
    - Vida
    - Overley
    - CO940610
    - CO960293
    - TA1615
    - AGS2000
    - Hank
    - Lyman
    - SY_Capstone
    - 16REG01643
    - RioBlanco
    - W7984
    - Ta1662
    - Cheyenne
    - PIONEER26R61
    - Reeder
    - IDO444
    - Dayn

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.



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

For more information, please follow this link: [IWGSC Chinese Spring info page at GrainGenes]

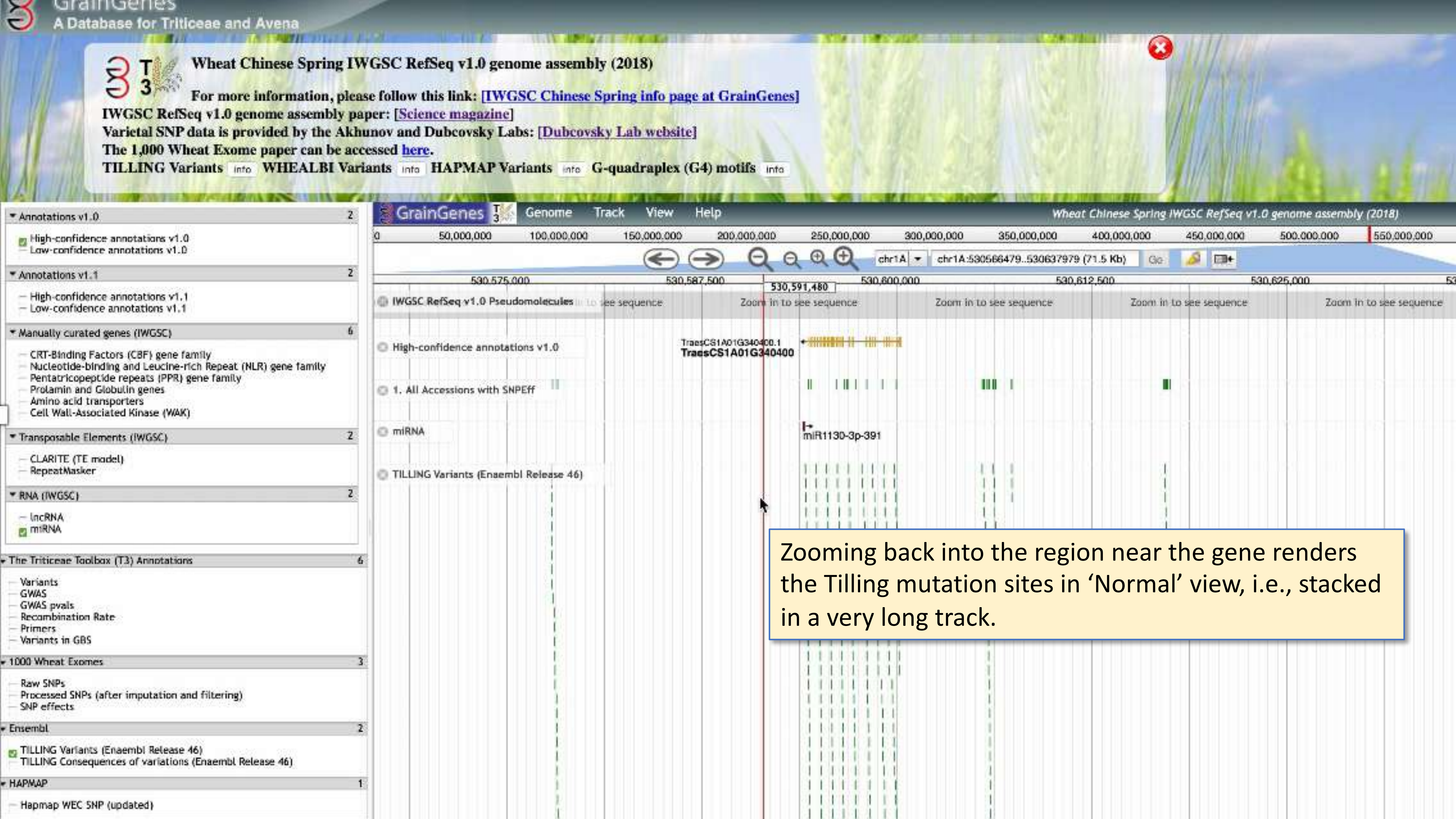
IWGSC RefSeq v1.0 genome assembly paper: [Science magazine]

Varietal SNP data is provided by the Akhunov and Dubcovsky Labs: [Dubcovsky Lab website]

The 1,000 Wheat Exome paper can be accessed here.

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.



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

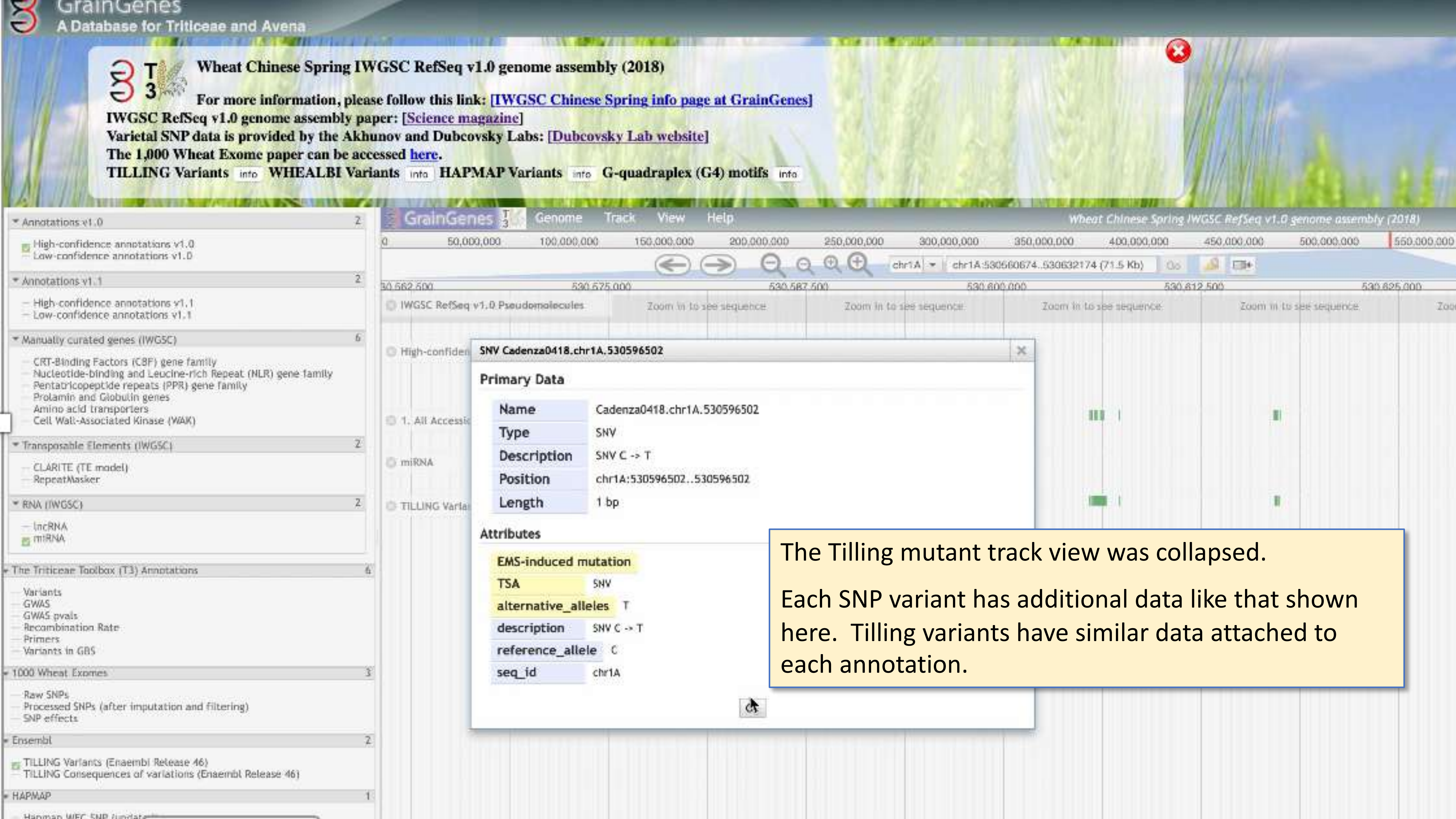
For more information, please follow this link: [IWGSC Chinese Spring info page at GrainGenes]

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.

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)

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

SNV Cadenza0418.chr1A.530596502

Primary Data

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

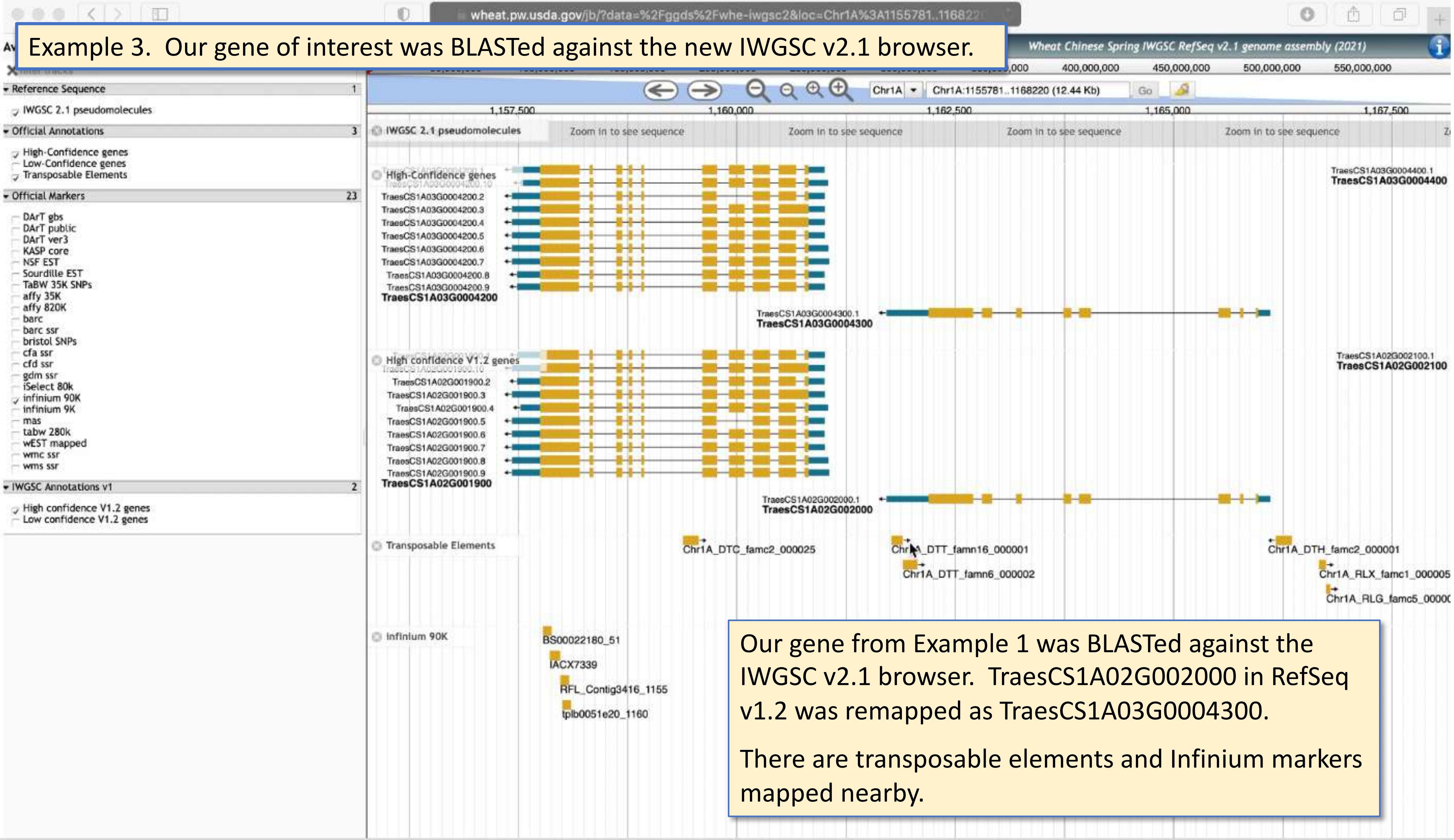
Attributes

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.

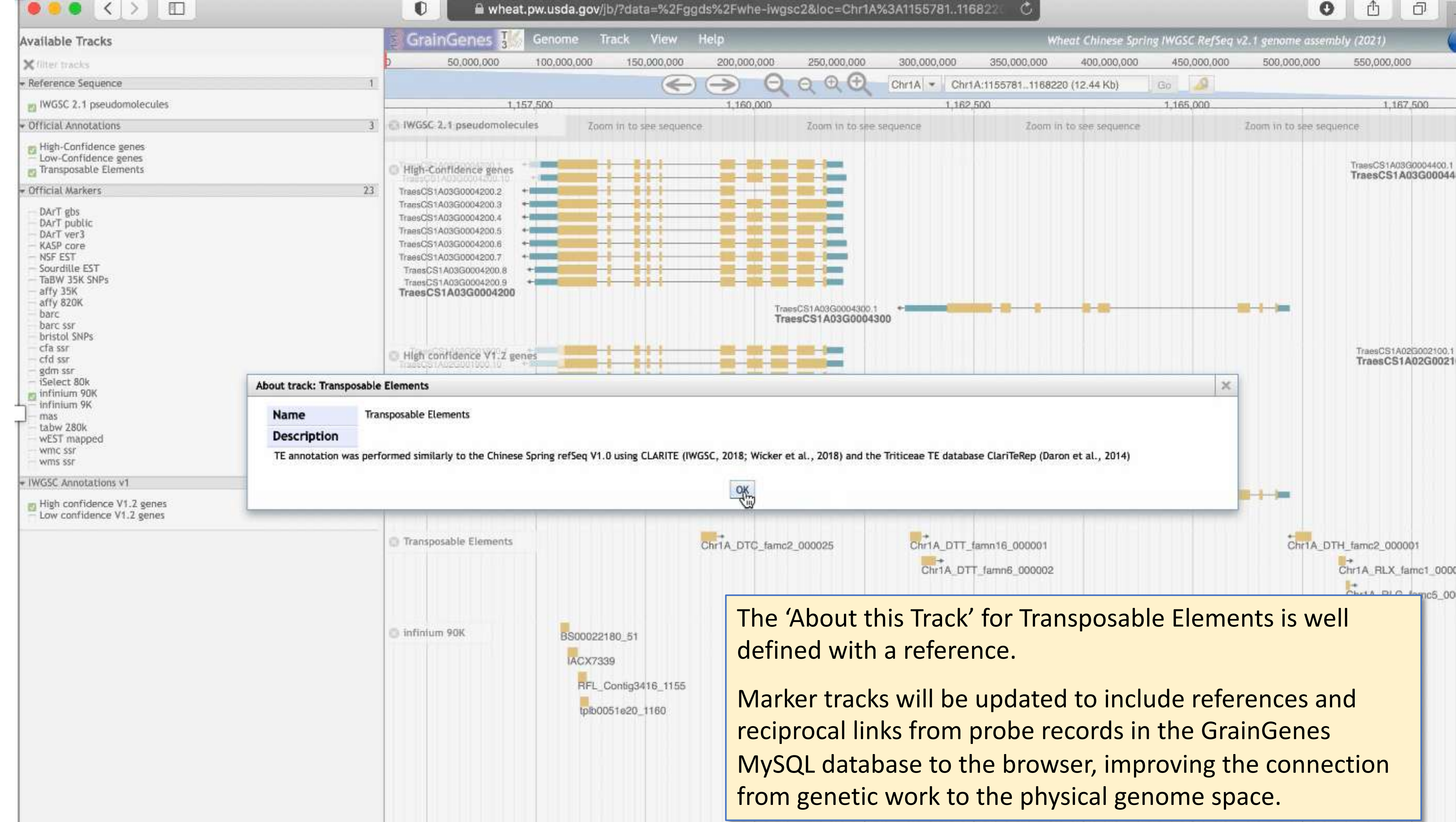
Each SNP variant has additional data like that shown here. Tilling variants have similar data attached to each annotation.

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.



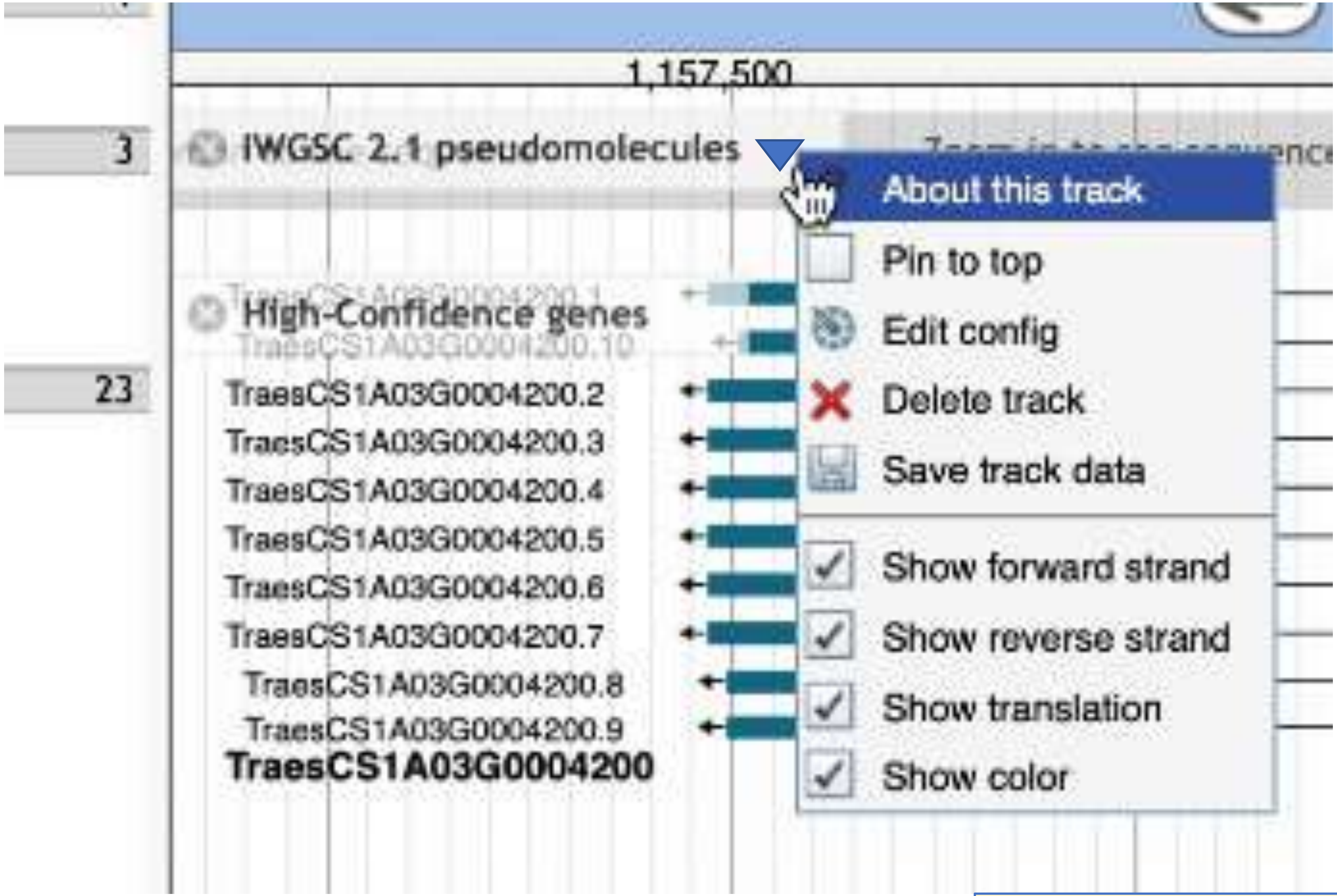
About track: Transposable Elements

Name	Transposable Elements
Description	

TE annotation was performed similarly to the Chinese Spring refSeq V1.0 using CLARITE (IWGSC, 2018; Wicker et al., 2018) and the Triticeae TE database ClariTeRep (Daron et al., 2014)

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.



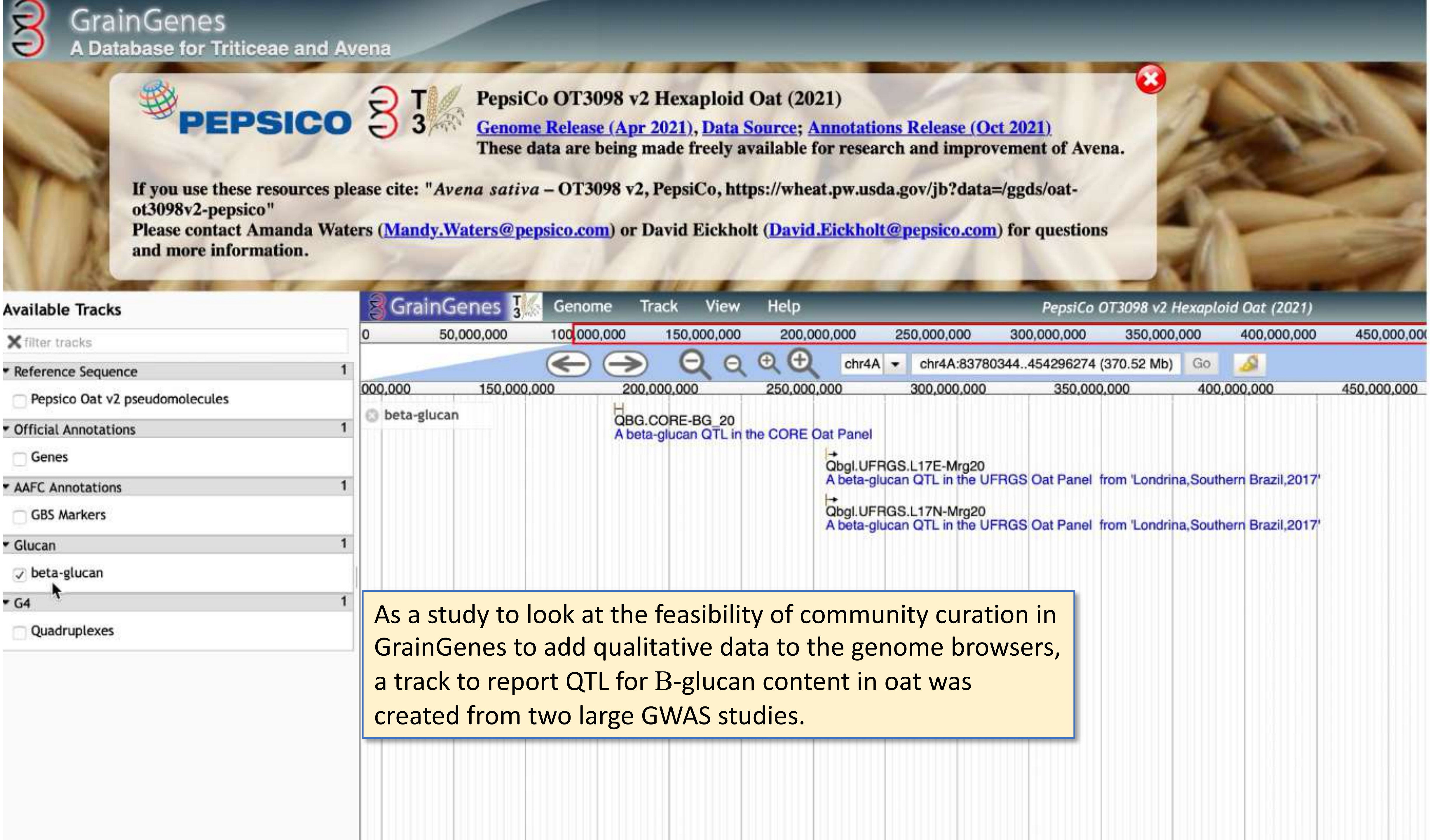
A last note: Save the DNA sequence as a FASTA from any region in the browser by opening the pseudomolecule track and saving the data from the title menu dropdown.

Community Curation / Education Modules in the Future?

User-generated .gff3 tracks

Interactive forms for curators / super-users to enter GWAS results, select a browser, BLAST, then approve results and add annotation to build a .gff3

Module for a genomics course for team-curation



PepsiCo OT3098 v2 Hexaploid Oat (2021)

Genome Release (Apr 2021), Data Source; Annotations Release (Oct 2021)

These data are being made freely available for research and improvement of Avena.

If you use these resources please cite: "*Avena sativa* – OT3098 v2, PepsiCo, https://wheat.pw.usda.gov/jb?data=/ggds/oat-ot3098v2-pepsico"

Please contact Amanda Waters (Mandy.Waters@pepsico.com) or David Eickholt (David.Eickholt@pepsico.com) for questions and more information.

chr4A:83780344..454296274 (370.52 Mb)

QBG.CORE-BG_20

A beta-glucan QTL in the CORE Oat Panel

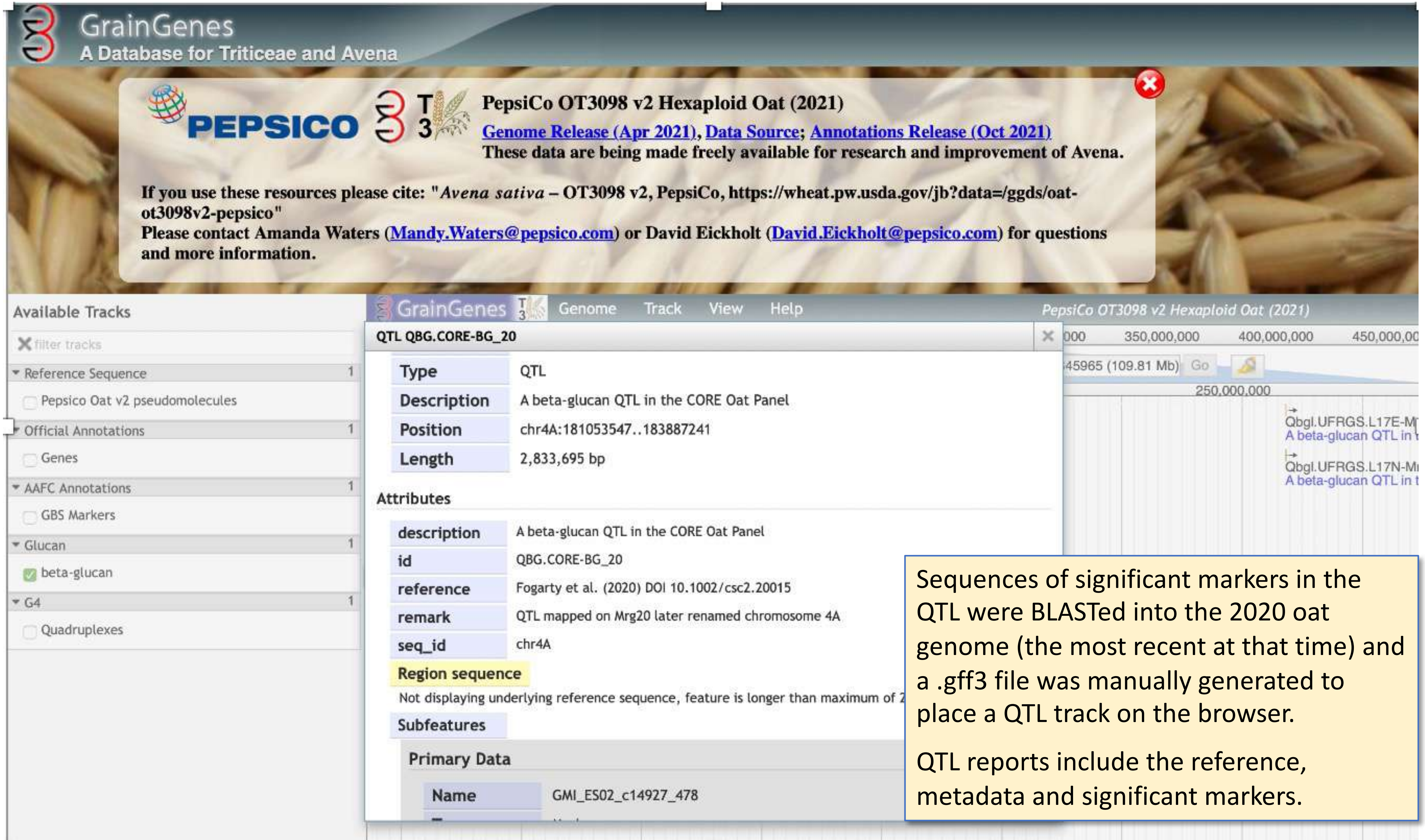
Qbgl.UFRGS.L17E-Mrg20

A beta-glucan QTL in the UFRGS Oat Panel from 'Londrina,Southern Brazil,2017'

Qbgl.UFRGS.L17N-Mrg20

A beta-glucan QTL in the UFRGS Oat Panel from 'Londrina,Southern Brazil,2017'

As a study to look at the feasibility of community curation in GrainGenes to add qualitative data to the genome browsers, a track to report QTL for Β-glucan content in oat was created from two large GWAS studies.



PepsiCo OT3098 v2 Hexaploid Oat (2021)

Genome Release (Apr 2021), Data Source; Annotations Release (Oct 2021)

These data are being made freely available for research and improvement of Avena.

If you use these resources please cite: "*Avena sativa* – OT3098 v2, PepsiCo, https://wheat.pw.usda.gov/jb?data=/ggds/oat-ot3098v2-pepsico"

Please contact Amanda Waters (Mandy.Waters@pepsico.com) or David Eickholt (David.Eickholt@pepsico.com) for questions and more information.

QTL QBG.CORE-BG_20

Type	QTL
Description	A beta-glucan QTL in the CORE Oat Panel
Position	chr4A:181053547..183887241
Length	2,833,695 bp

Attributes

description	A beta-glucan QTL in the CORE Oat Panel
id	QBG.CORE-BG_20
reference	Fogarty et al. (2020) DOI 10.1002/csc2.20015
remark	QTL mapped on Mrg20 later renamed chromosome 4A
seq_id	chr4A

Region sequence

Not displaying underlying reference sequence, feature is longer than maximum of 2

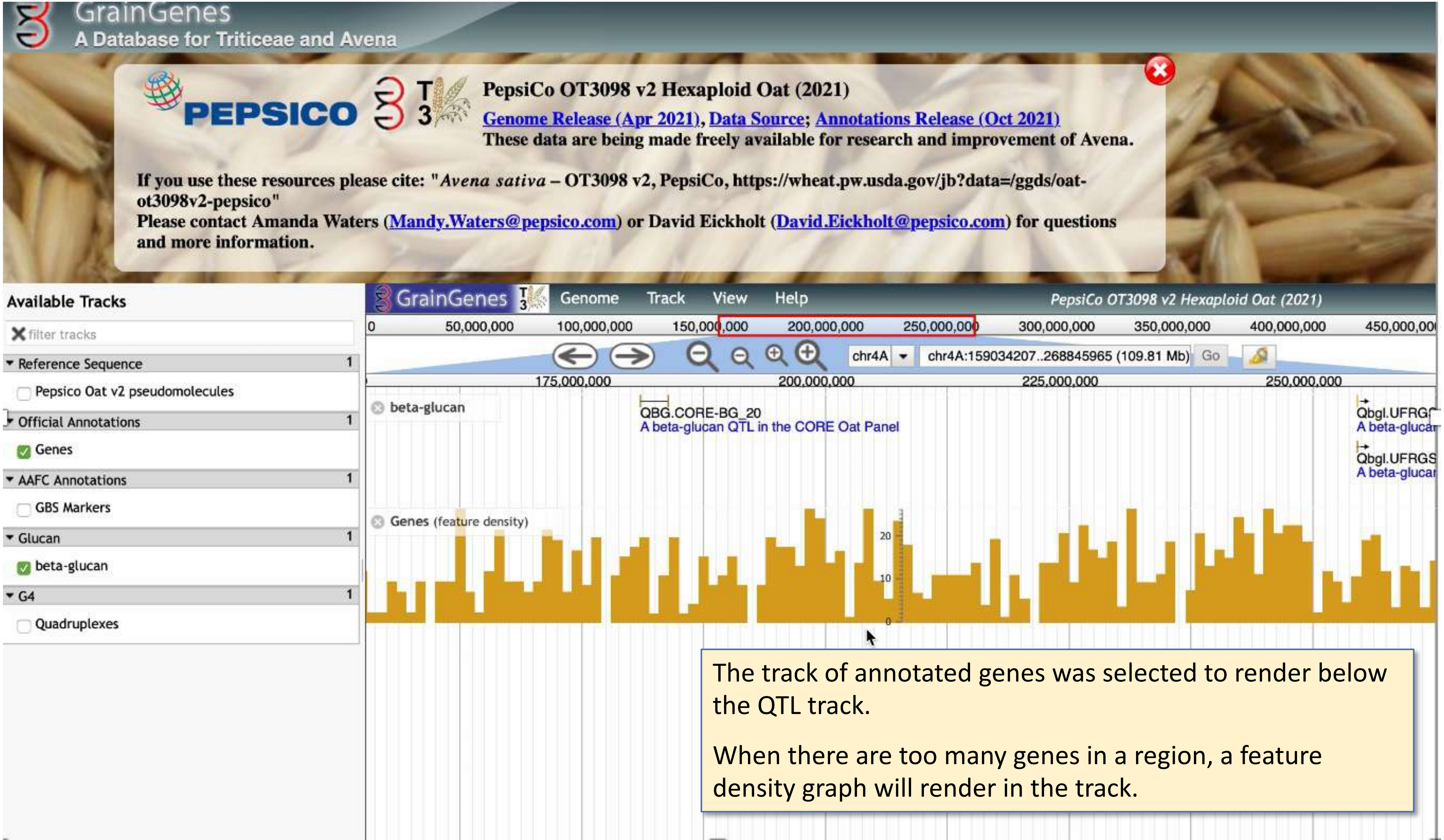
Subfeatures

Primary Data

Name	GMI_ES02_c14927_478

Sequences of significant markers in the QTL were BLASTed into the 2020 oat genome (the most recent at that time) and a .gff3 file was manually generated to place a QTL track on the browser.

QTL reports include the reference, metadata and significant markers.



PepsiCo OT3098 v2 Hexaploid Oat (2021)

Genome Release (Apr 2021), Data Source; Annotations Release (Oct 2021)

These data are being made freely available for research and improvement of Avena.

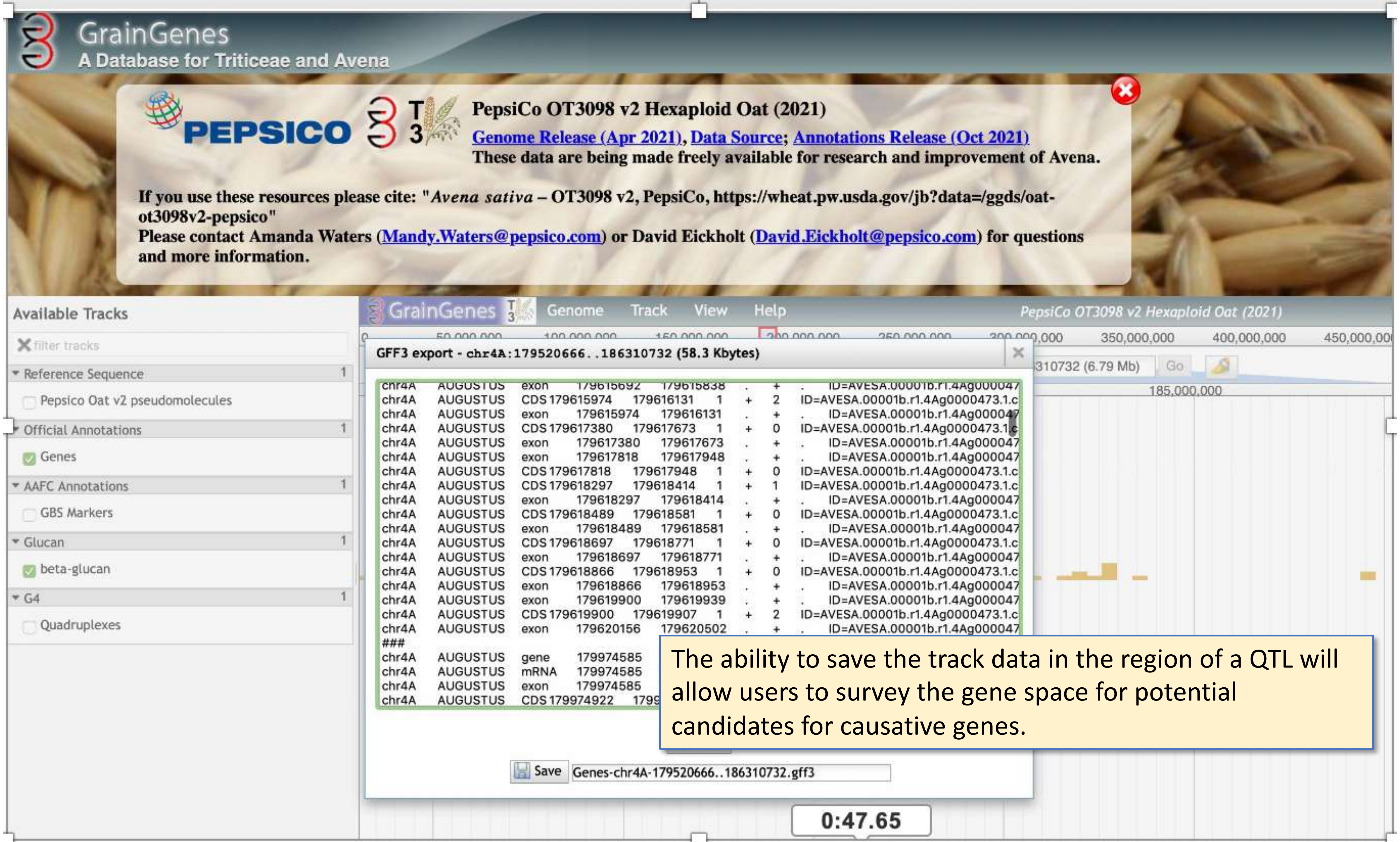
If you use these resources please cite: "*Avena sativa* – OT3098 v2, PepsiCo, https://wheat.pw.usda.gov/jb?data=/ggds/oat-ot3098v2-pepsico"

Please contact Amanda Waters (Mandy.Waters@pepsico.com) or David Eickholt (David.Eickholt@pepsico.com) for questions and more information.

chr4A:159034207..268845965 (109.81 Mb)

The track of annotated genes was selected to render below the QTL track.

When there are too many genes in a region, a feature density graph will render in the track.



PepsiCo OT3098 v2 Hexaploid Oat (2021)

Genome Release (Apr 2021), Data Source; Annotations Release (Oct 2021)

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Please contact Amanda Waters (Mandy.Waters@pepsico.com) or David Eickholt (David.Eickholt@pepsico.com) for questions and more information.

GFF3 export - `chr4A:179520666..186310732` (58.3 Kbytes)

```
chr4A   AUGUSTUS   exon     179615692   179615838   .   +   .   ID=AVESA.00001b.r1.4Ag000047
chr4A   AUGUSTUS   CDS 179615974   179616131   1   +   2   ID=AVESA.00001b.r1.4Ag0000473.1.c
chr4A   AUGUSTUS   exon     179615974   179616131   .   +   .   ID=AVESA.00001b.r1.4Ag000047
chr4A   AUGUSTUS   CDS 179617380   179617673   1   +   0   ID=AVESA.00001b.r1.4Ag0000473.1.c
chr4A   AUGUSTUS   exon     179617380   179617673   .   +   .   ID=AVESA.00001b.r1.4Ag000047
chr4A   AUGUSTUS   exon     179617818   179617948   .   +   .   ID=AVESA.00001b.r1.4Ag000047
chr4A   AUGUSTUS   CDS 179617818   179617948   1   +   0   ID=AVESA.00001b.r1.4Ag0000473.1.c
chr4A   AUGUSTUS   CDS 179618297   179618414   1   +   1   ID=AVESA.00001b.r1.4Ag0000473.1.c
chr4A   AUGUSTUS   exon     179618297   179618414   .   +   .   ID=AVESA.00001b.r1.4Ag000047
chr4A   AUGUSTUS   CDS 179618489   179618581   1   +   0   ID=AVESA.00001b.r1.4Ag0000473.1.c
chr4A   AUGUSTUS   exon     179618489   179618581   .   +   .   ID=AVESA.00001b.r1.4Ag000047
chr4A   AUGUSTUS   CDS 179618697   179618771   1   +   0   ID=AVESA.00001b.r1.4Ag0000473.1.c
chr4A   AUGUSTUS   exon     179618697   179618771   .   +   .   ID=AVESA.00001b.r1.4Ag000047
chr4A   AUGUSTUS   CDS 179618866   179618953   1   +   0   ID=AVESA.00001b.r1.4Ag0000473.1.c
chr4A   AUGUSTUS   exon     179618866   179618953   .   +   .   ID=AVESA.00001b.r1.4Ag000047
chr4A   AUGUSTUS   exon     179619900   179619939   .   +   .   ID=AVESA.00001b.r1.4Ag000047
chr4A   AUGUSTUS   CDS 179619900   179619907   1   +   2   ID=AVESA.00001b.r1.4Ag0000473.1.c
chr4A   AUGUSTUS   exon     179620156   179620502   .   +   .   ID=AVESA.00001b.r1.4Ag000047
###
chr4A   AUGUSTUS   gene     179974585
chr4A   AUGUSTUS   mRNA     179974585
chr4A   AUGUSTUS   exon     179974585
chr4A   AUGUSTUS   CDS 179974922   1799
```

Genes-chr4A-179520666..186310732.gff3

The ability to save the track data in the region of a QTL will allow users to survey the gene space for potential candidates for causative genes.

Contact us anytime!

The GrainGenes Team

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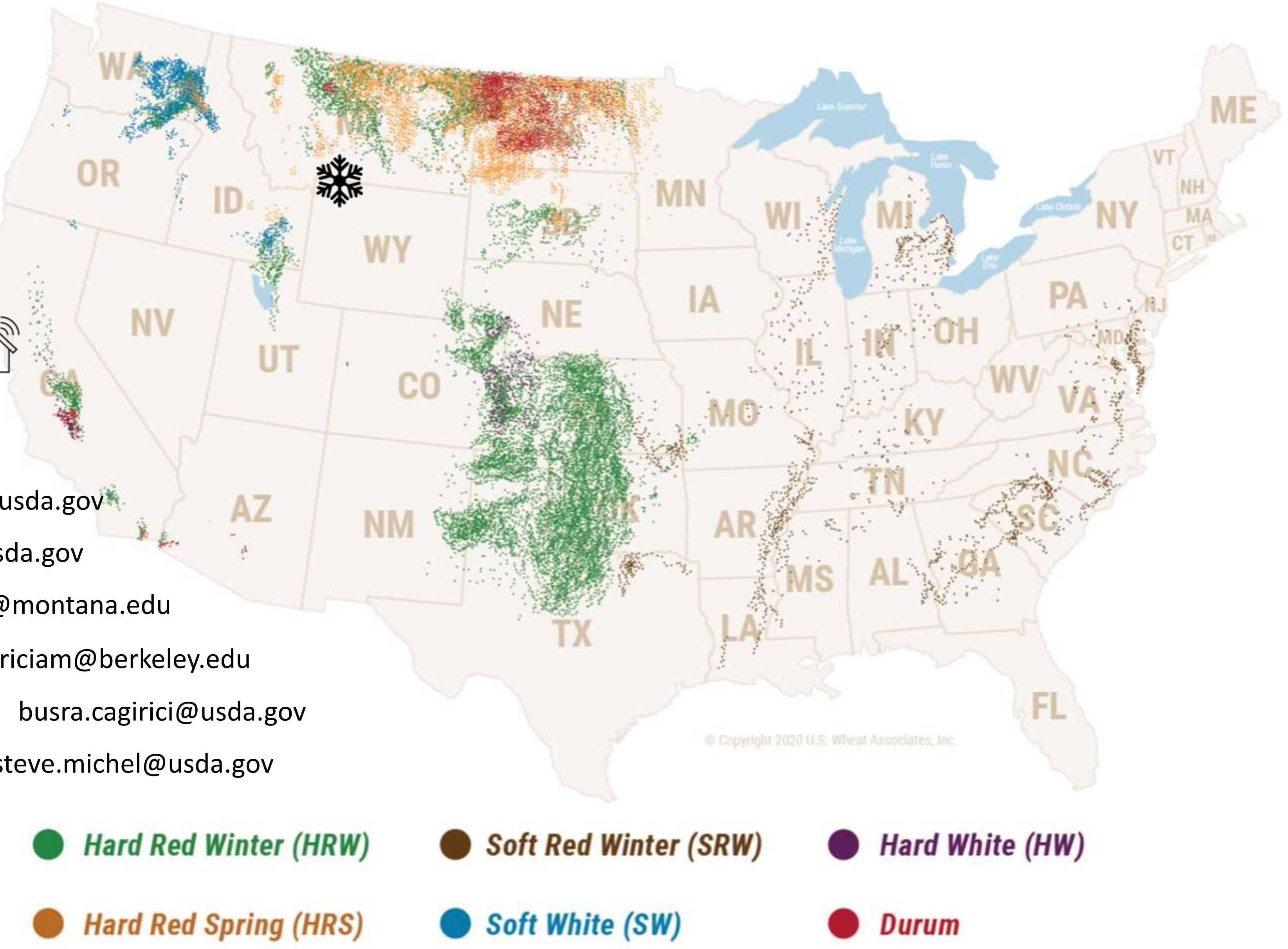

map image : https://www.uswheat.org/working-with-buyers/wheat-classes/