

Visualizing the IWGSC Refseq v1.0 Wheat Assembly in Ensembl Plants



Guy Naamati

IWGSC – Wheat Genome Manual and Functional Annotation

PAG XXVII

Jan 15 2018



What I will talk about

- The European Bioinformatics Institute and **Ensembl Plants**
- Ensembl Plants Genome Browser
- Comparative analysis and the Ensembl Gene Tree
- Variation and the **TILLING** population in Ensembl
- 10+ genome project



What we do in the European Bioinformatics Institute (EBI-EMBL)

Cambridge (UK)



Hinxton



We provide freely available data and bioinformatics services to the scientific community.



Heidelberg



Barcelona

Ensembl Plants

Search: All species for

e.g. Carboxy* or chx28

All genomes

-- Select a species --

- [View full list of all Ensembl Plants species](#)
- [Edit your favourites](#)

Favourite genomes



Arabidopsis thaliana
TAIR10



Oryza sativa Japonica Group
IRGSP-1.0



Triticum aestivum
IWGSC



Hordeum vulgare
IBSC_v2



Zea mays
B73_RefGen_v4

New wheat assembly

This release of Ensembl Plants hosts the [latest wheat assembly](#) from the IWGSC (RefSeq v1.0). Current data includes:

- The IWGSC RefSeq v1.1 gene annotation.
- Alignment of 98,270 high confidence genes from the TGACv1 annotation.
- The Axiom 820K SNP Array from CerealsDB.
- EMS-induced mutations from sequenced TILLING populations (Kronos and Cadensa).
- Assembly to assembly mapping and gene ID mapping to the previous TGAC v1 assembly and annotation.
- Whole genome alignments to rice, brachypodium and barley.
- The TGACv1 assembly will still be available via the [Ensembl Plants archive site](#).

Polyploid View Enabled

Polyploid view for [wheat](#) has been enabled, allowing users to view alignments between the three wheat components [simultaneously](#).

Funding

Ensembl Plants datasets are constructed in a direct collaboration with the [Gramene](#) resource, funded by the United States [National Science Foundation](#) award #1127112. Read [more about our collaboration with Gramene](#).



The development of resources for wheat is funded by the BBSRC-funded [Designing Future Wheat ISP](#).

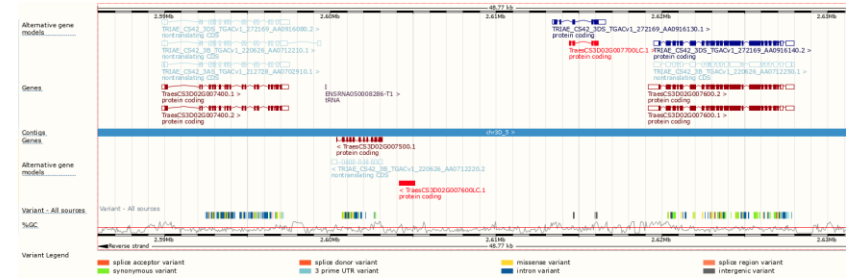


<https://plants.ensembl.org>

Free and open source

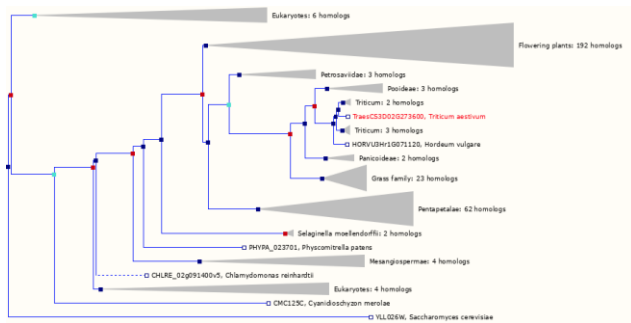
API, VEP, Archive Site, Bulk Download, Release Cycle, Polyploid View, User tracks...

Genome Browser for nearly 60 plants species



Comparative Genomics

Variation Data



Science

\$15
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AAAS



ROAD MAP FOR WHEAT

Ordered sequence will
speed research pp. 635, 661, & 662

Introducing the new IWGSC wheat genome assembly

18TH JULY 2018 BY ERIN (OUTREACH) · COMMENTS OFF



One of the biggest highlights of the new [Ensembl Plants release 40](#) is the inclusion of the new Wheat (RefSeq v1.0) genome from the International Wheat Genome Sequencing Consortium (IWGSC).

The path to sequencing the wheat genome has been no easy ride, due to its large and highly repetitive genome. This new assembly from the IWGSC bridges many gaps from the initial genome sequencing effort. Read on to find out more about this

exciting new genome assembly!



Latest wheat assembly now available in
[Ensembl](#)



About *Triticum aestivum*

Triticum aestivum (bread wheat) is a major global cereal grain essential to human nutrition. Wheat was one of the first cereals to be domesticated, originating in the [fertile crescent](#) around 7000 years ago. Bread wheat is hexaploid, with a genome size estimated at ~17 Gbp, composed of three closely-related and independently maintained genomes that are the result of a series of naturally occurring hybridization events. The ancestral progenitor genomes are considered to be [Triticum urartu](#) (the A-genome donor) and an unknown grass thought to be related to [Aegilops speltoides](#) (the B-genome donor). This first hybridization event produced tetraploid emmer wheat (AABB, *T. dicoccoides*) which hybridized again with [Aegilops tauschii](#) (the D-genome donor) to produce modern bread wheat.

Taxonomy ID [4565](#)

Data source [International Wheat Genome Sequencing Consortium](#)

[More information and statistics](#)

Genome assembly: [IWGSC](#)

[More information and statistics](#)

[Download DNA sequence \(FASTA\)](#)

[Convert your data to IWGSC coordinates](#)

[Display your data in Ensembl Plants](#)



[View karyotype](#)



[Example region](#)

Gene annotation

What can I find? Protein-coding and non-coding genes, splice variants, cDNA and protein sequences, non-coding RNAs.

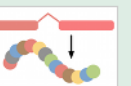
[More about this genebuild](#)

[Download genes, cDNAs, ncRNA, proteins - FASTA - GFF3](#)

[Update your old Ensembl IDs](#)



[Example gene](#)



[Example transcript](#)

Comparative genomics

What can I find? Homologues, gene trees, and whole genome alignments across multiple species.

[More about comparative analyses](#)

[Phylogenetic overview of gene families](#)

[Download alignments \(EMF\)](#)

[Genomic alignments \[5\] \[Show»\]](#)



[Example gene tree](#)

Variation

What can I find? Short sequence variants.

[More about variation in Triticum aestivum](#)

[More about variation in Ensembl Plants](#)

[Download all variants - GVF - VCF - VEP](#)

[Variant Effect Predictor](#)







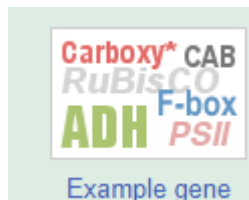
[Example variant](#)

<https://plants.ensembl.org/wheat>

A closer look and examples




Genome assembly: [IWGSC](#)

-  [More information and statistics](#)
-  [Download DNA sequence \(FASTA\)](#)
-  [Convert your data to IWGSC coordinates](#)
-  [Display your data in Ensembl Plants](#)







Gene annotation

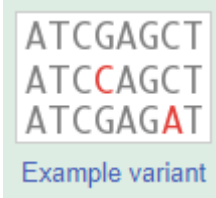
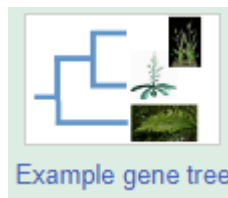
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-  [Download alignments \(EMF\)](#)
-  [Genomic alignments \[5\] \[Show» \]](#)



Variation

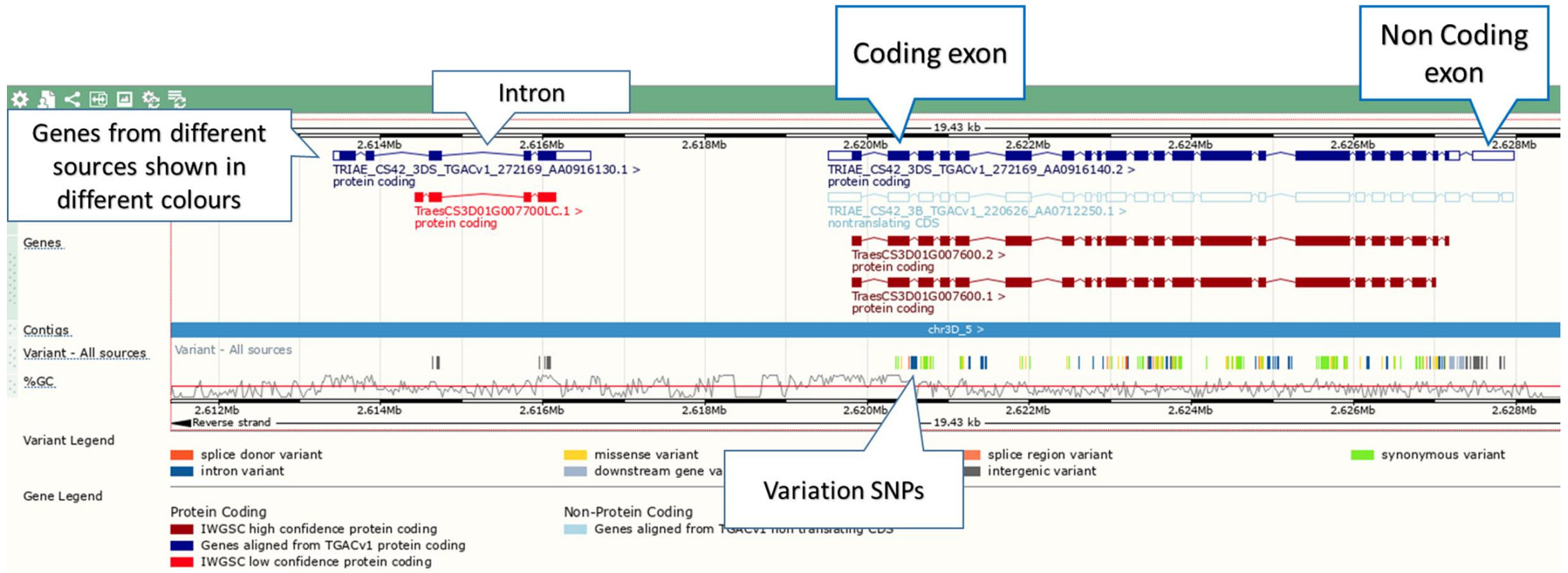
What can I find? Short sequence variants.

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-  [More about variation in Ensembl Plants](#)
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Variant Effect Predictor



The Ensembl Plants Genome Browser



From Genome Browser to Gene

Gene: TraesCS3D02G273600

Description Heat shock protein 101 [Source:UniProtKB/TrEMBL;Acc:Q9SPH4]

Location [Chromosome 3D: 379,535,906-379,539,827](#) reverse strand.

About this gene This gene has 2 transcripts ([splice variants](#)), [80 orthologues](#) and [21 paralogues](#).

Transcripts

Hide transcript table

Gene info

Name	Transcript ID	bp	Protein	Biotype	UniProt	Flags
Novel	TraesCS3D02G273600.1	3297	913aa	Protein coding	Q9SPH4	
Novel	TraesCS3D02G273600.2	2901	895aa	Protein coding	-	

Transcript info

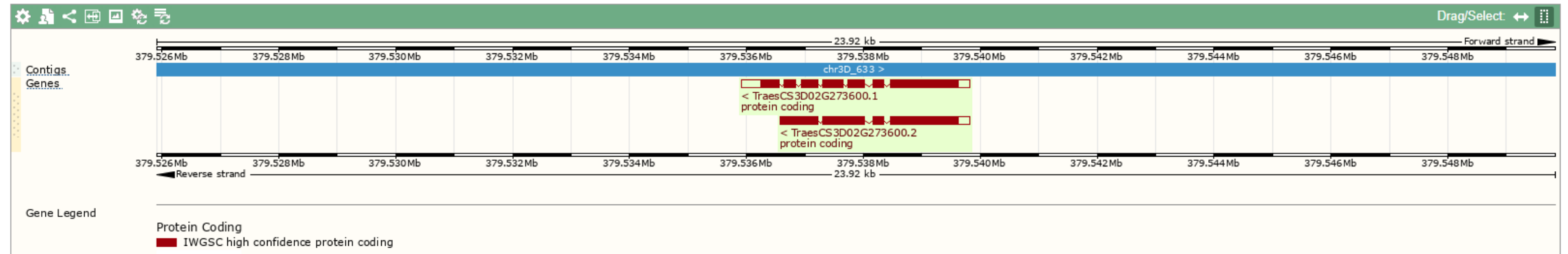
Summary

Gene type Protein coding

Annotation method Genes annotated with high confidence by IWGSC

Genome Browser

Go to Region in Detail for more tracks and navigation options (e.g. zooming)



From Gene to Transcript

Sequence information

- Transcript-based displays
 - Summary
 - Sequence
 - Exons
 - cDNA
 - Protein
 - Protein Information
 - Protein summary
 - Domains & features
 - Variants
 - Genetic Variation
 - Variant table
 - Variant image
 - Population comparison
 - Comparison image
 - External References
 - General identifiers
 - Oligo probes
 - Supporting evidence
 - ID History
 - Transcript history
 - Protein history

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Ensembl Plants is produced in collaboration with Gramene

Transcript: TraesCS3D02G273600.1

Description Heat shock protein 101 [Source:UniProtKB/TrEMBL;Acc:Q9SPH4]

Location Chromosome 3D: 379,535,906-379,539,827 reverse strand.

About this transcript This transcript has [7 exons](#), is annotated with [32 domains and features](#) and is associated with [130 variations](#).

Gene This transcript is a product of gene [TraesCS3D02G273600](#) [Hide transcript table](#)

Show/hide columns (1 hidden)		Filter				
Name	Transcript ID	bp	Protein	Biotype	UniProt	Flags
Novel	TraesCS3D02G273600.1	3297	913aa	Protein coding	Q9SPH4	
Novel	TraesCS3D02G273600.2	2901	895aa	Protein coding	-	

External links

Summary



Statistics Exons: 7, Coding exons: 7, Transcript length: 3,297 bps, Translation length: 913 residues

Version TraesCS3D02G273600.1.

Type Protein coding

Annotation Method Genes annotated with high confidence by IWGSC

From Transcript to Exon Sequence

Exons ?

Download sequence

Exons/ Introns Translated sequence Flanking sequence Intron sequence UTR

Variants 3 prime UTR Missense Stop gained Synonymous

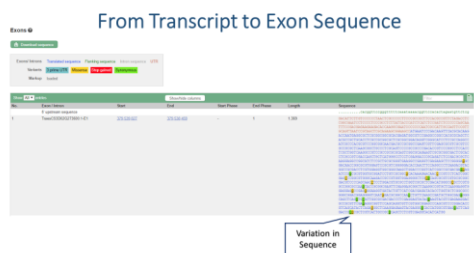
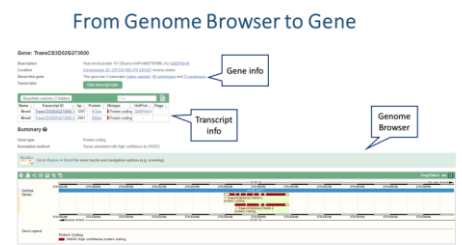
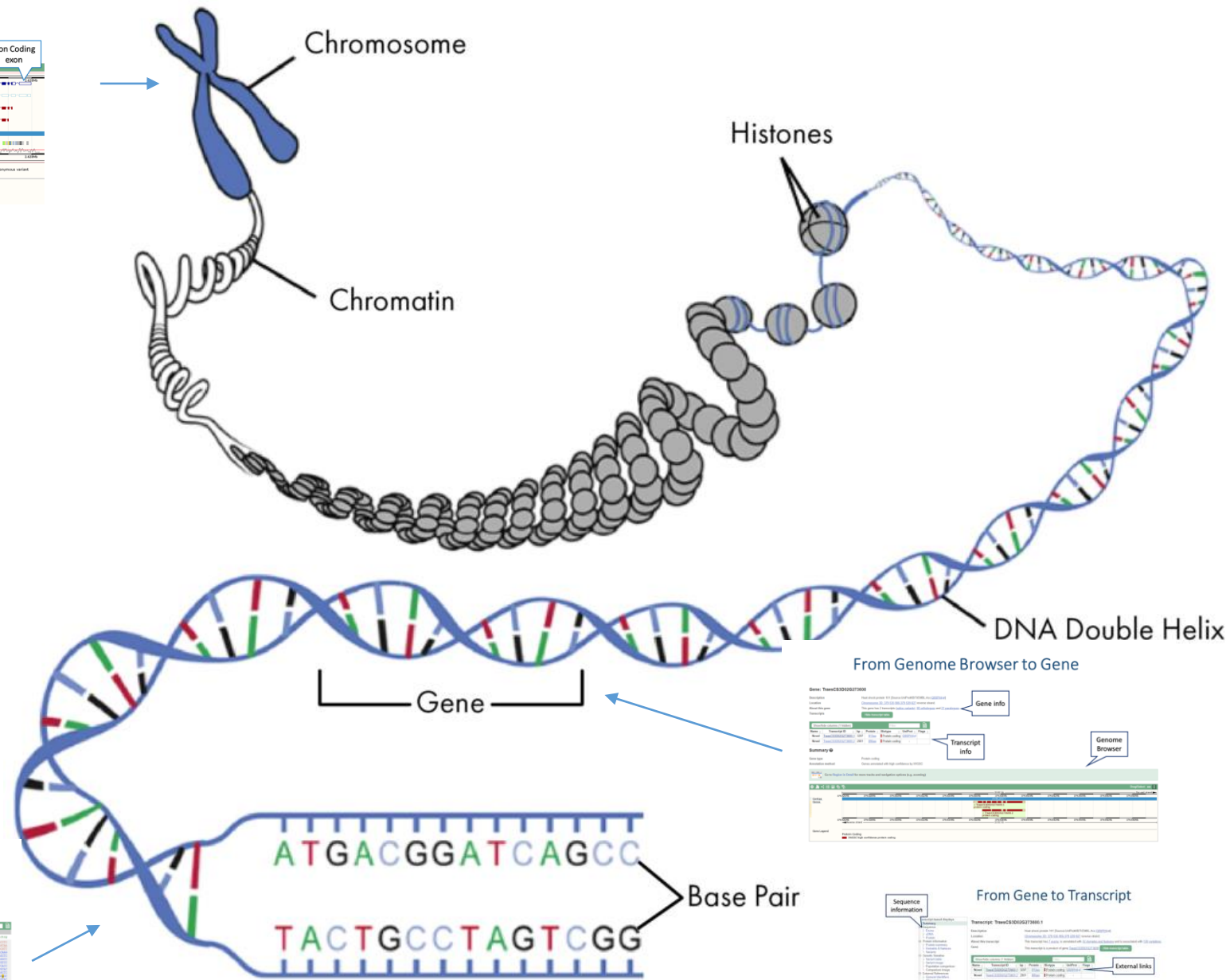
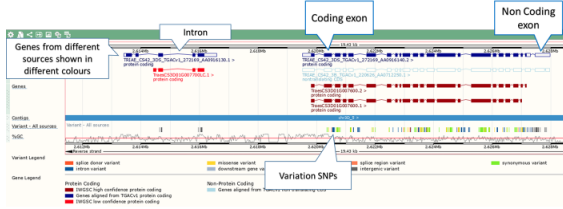
Markup loaded

Show All entries Show/hide columns Filter

No.	Exon / Intron	Start	End	Start Phase	End Phase	Length	Sequence
	5' upstream sequence					caaggttccgggtttttcaaataaaacggttccacactagaatgttctcg
1	TraesCS3D02G273600.1-E1	379,539,827	379,538,459	-	1	1,369	GACATTCTTGTCCCCCTAACTCGCCCCCTTCCGCGCGTTCACGCGGTTCTAGACCTC CGGCGAATCCTCCCCTCCCGCCTCTTATTACCCATCTCATCTCCGATCTCCCCAGCAA TTTCCGACGAGAAGAAGACACCAAGGCGAATCCCCCAATCGCCATTGCCAGTTCGGTT GCAGTTAATCCGTAGCTCGCAGAAGCGAAGCCATGAATCCCGACAAGTTCACGCAAG ACCAATGAGGCGCTCGCGCGGCGCACGAGATGGCGTCCGAGGCGGCCACGCGCAGCTC ACGCGCTGCACCTCGCGCGGCGCTCGCGGCGGACAGGTCGGGCATCCTCCGCCAGGCC ATCGCCACGCGTCCGGCGGCAACGACGCGCGCGCGAGTCGTTGAGGCGCTCGCGTCC GCCGCGCTCAAGCGGCTGCCCTCGCAGTCCCCGCGCCGACACCGTCCCCGCCCTCCACC TCGCTGTCAGGCGGTCGCGCGCGCGCAGTCGGCGCAGAAGTCGCGCGGCGACTCGCAC CTCGCGTCGACAGCTGCTCATGGCCCTCCTCGAGGACCCGAGATCTCCGACGCGCTC AAGGAGGCGCGCATCTCCGCTGCGCGGTTAAGGCGGAGTCCGAGAAGCTCCGGGAGGC GACACCGGCGGTTGGAGTCCGCGTCCGGGACACCAACTCCAGGCCCTCAAGAGCTAC GGCCGCGACTCGTGGAGTGGCGGGCAAGCTGGACCCGGTTCATCGGCGCGACGAGAG ATCCCGCGTGGTCCGATCCTGTCCGCGCCACAAAGAACCAACCGTCTCATCGCG GAGCCCGGCGTGGCAAGACCCCGTGGTGGAGGGGCTCGCCAGCGCTCGTGGCGCGC GACGTCCCAGCAACTCCTGGACGTCGCGCTGGTCCGCTCGACATGGGCGGCTCGTGTG GCCGCGCCAACTACCGCGGCGAGTTCGAGGAGCGGCTCAAGGCGGTGCTCRAAGGAGTG GAGGAGCCGAGGGAAGGTGATACTGTTTCATCGACGAGATACACCTGGTGTCCGGCGCC GGCGGACGGAGGGGTCAATGACCGCGCCATCTGTTCAAGCCGATGCTGGCGAGGGG CAGCTCAGTGTATTGGCGGACGACCTCGAGGAGTACAGGAGTACGTCGAGAGGAC GCCGCGTTCGAGAGGCGGTTCCAGCAGGTGTTGTTGGCGGAGCCGAGCGTCCCGGACCC GTCAGCATACTCAGAGGCTCAAGGAGAAGTACGAGGCGCACCATGGCGTGAATTCAG GACCGCGCGCTCGTTCATTCGCGCCAGCTCTCGTGGATACATCATGG

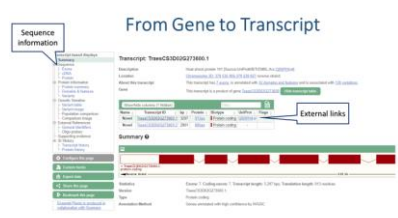
Variation in Sequence

The Ensembl Plants Genome Browser



ATGACGGATCAGCC
TACTGCCTAGTCGG

Base Pair

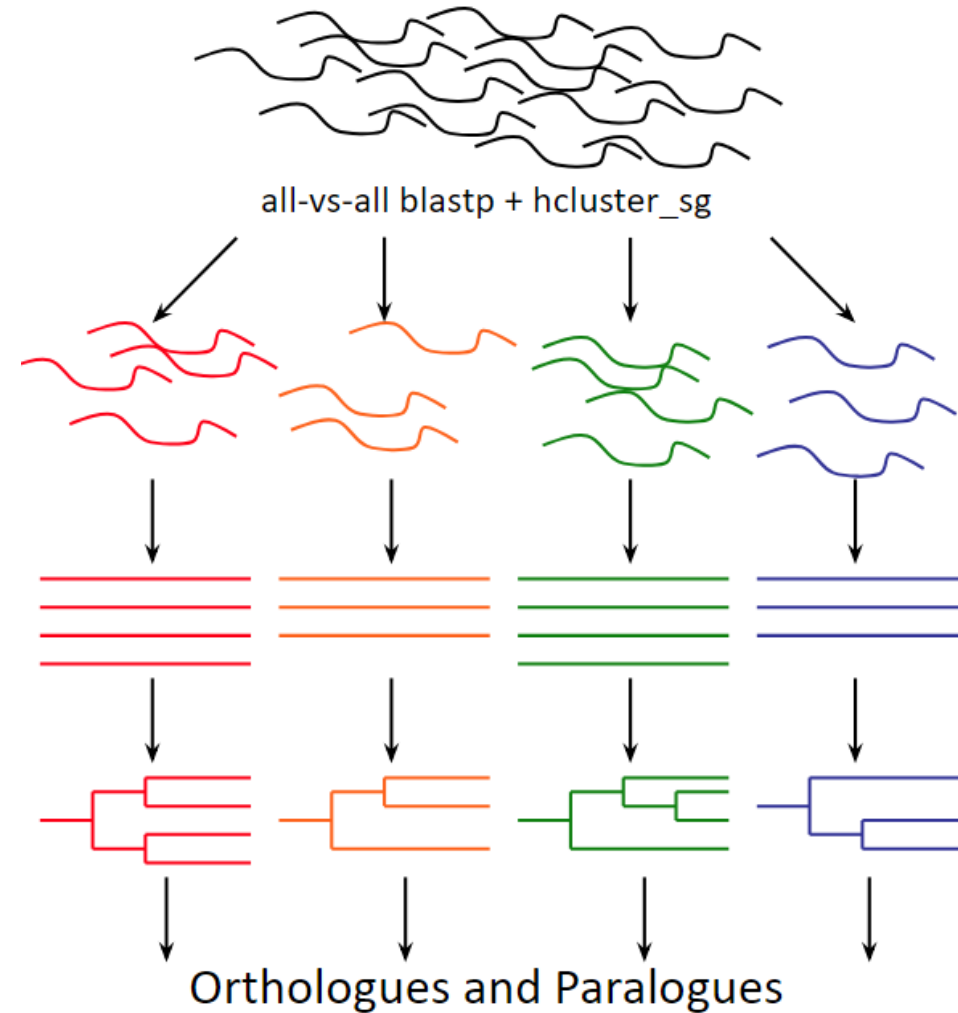


What I will talk about

- ✓ The European Bioinformatics Institute and Ensembl Plants
- ✓ Ensembl Plants Genome Browser
 - Comparative analysis and gene tree
 - Variation and the TILLING population in Ensembl
 - 10+ genome project



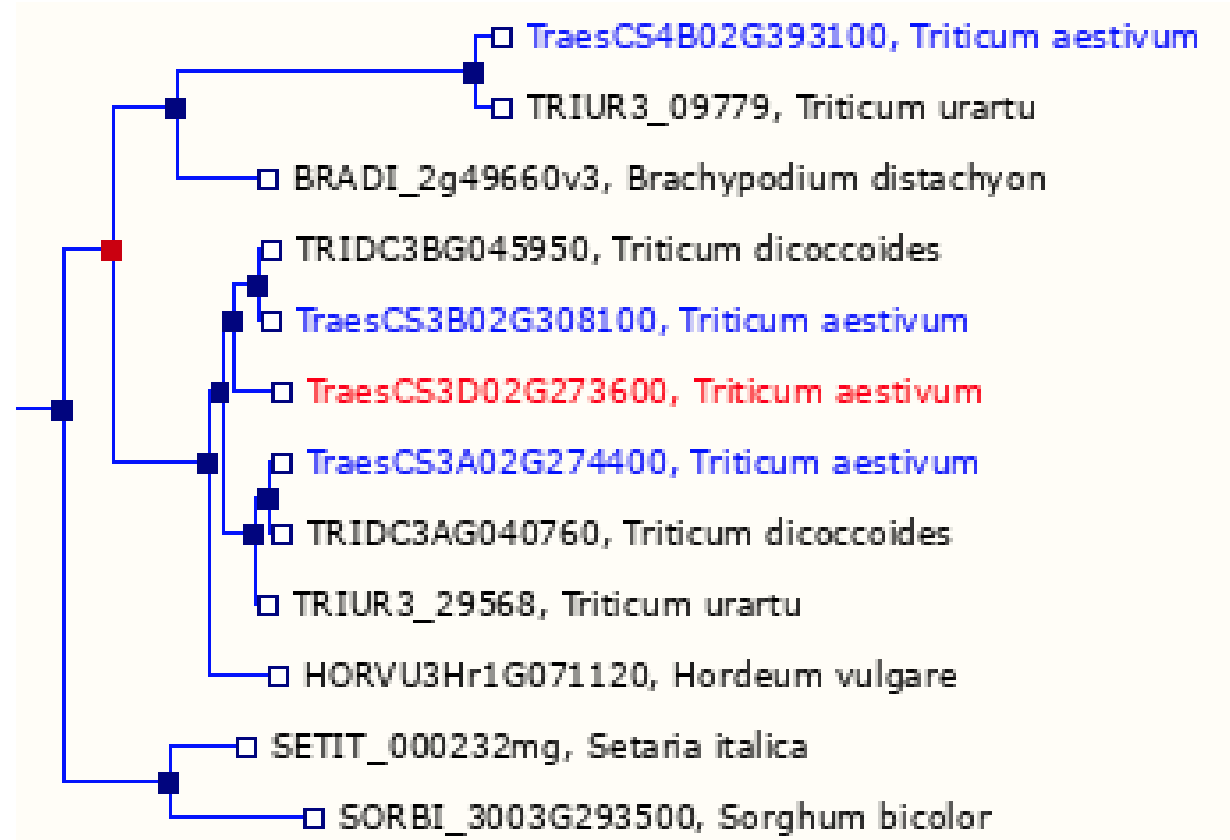
Creating the Comparative Analysis Gene Tree



Gene tree for TraesCS3D02G273600 (Heat shock protein)



Gene tree for TraesCS3D02G273600 (Heat shock protein)



Orthologues


 Download orthologues

Summary of orthologues of this gene [Hide](#)

Click on 'Show details' to display the orthologues for one or more groups of species. Alternatively, click on 'Configure this page' to choose a custom list of species.

Species set	Show details	<u>With 1:1 orthologues</u>	<u>With 1:many orthologues</u>	<u>With many:many orthologues</u>	<u>Without orthologues</u>
All (49 species)	<input type="checkbox"/>	4	10	14	21
Amborellales (1 species)	<input type="checkbox"/>	0	1	0	0
Bryophyta (1 species)	<input type="checkbox"/>	0	1	0	0
Chlorophyta (2 species)	<input type="checkbox"/>	0	1	0	1
Liliopsida (20 species)	<input type="checkbox"/>	4	0	1	15
Lycopodiophyta (1 species)	<input type="checkbox"/>	0	0	1	0
Rhodophyta (3 species)	<input type="checkbox"/>	0	2	0	1
Eudicotyledons (16 species)	<input type="checkbox"/>	0	5	11	0

Selected orthologues [Hide](#)

Show All entries		Show/hide columns		Filter				
Species	Type	Orthologue	dN/dS	Target %id	Query %id	GOC Score	WGA Coverage	High Confidence
Amborella trichopoda	1-to-many View Gene Tree	AMTR_s00086p00119290 Compare Regions (AmTr_v1.0_scaffold00086:1,562,078-1,566,063:-1) View Sequence Alignments	n/a	83.75 %	83.57 %	n/a	n/a	n/a
Arabidopsis lyrata	Many-to-many View Gene Tree	ATHSP101 (fgenesh2_kg.2_1695_AT1G74310.1) Compare Regions (2:16,230,526-16,234,220:-1) View Sequence Alignments	n/a	83.42 %	83.24 %	n/a	n/a	n/a
Arabidopsis lyrata	Many-to-many View Gene Tree	fgenesh2_kg.7_2872_AT4G14670.1 Compare Regions (7:13,781,642-13,783,448:-1) View Sequence Alignments	n/a	75.88 %	44.80 %	n/a	n/a	n/a
Arabidopsis lyrata	Many-to-many View Gene Tree	scaffold_102080.1 Compare Regions (1:7,827,877-7,830,479:-1)	n/a	72.09 %	54.87 %	n/a	n/a	n/a

- Gene-based displays
 - Summary
 - Splice variants
 - Transcript comparison
 - Gene alleles
 - Sequence
 - Secondary Structure
 - Gene families
 - Literature
 - Plant Compara
 - Genomic alignments
 - Gene tree
 - Gene gain/loss tree
 - Orthologues
 - Paralogues
 - Homoeologues**
 - Pan-taxonomic Compara
 - Gene Tree
 - Orthologues
 - Ontologies
 - GO: Molecular function
 - GO: Biological process
 - GO: Cellular component
 - Phenotypes
 - Genetic Variation
 - Variant table
 - Variant image
 - Structural variants
 - Gene expression
 - Pathway
 - Regulation
 - External references
 - Supporting evidence
 - ID History
 - Gene history

Gene: TraesCS3D02G273600

Description Heat shock protein 101 [Source:UniProtKB/TrEMBL;Acc:[Q9SPH4](#)]

Location [Chromosome 3D: 379,535,906-379,539,827](#) reverse strand.

About this gene This gene has 2 transcripts ([splice variants](#)), [80 orthologues](#) and [21 paralogues](#).

Transcripts [Hide transcript table](#)

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Novel	TraesCS3D02G273600.2	2901	895aa	Protein coding	-	

Homoeologues

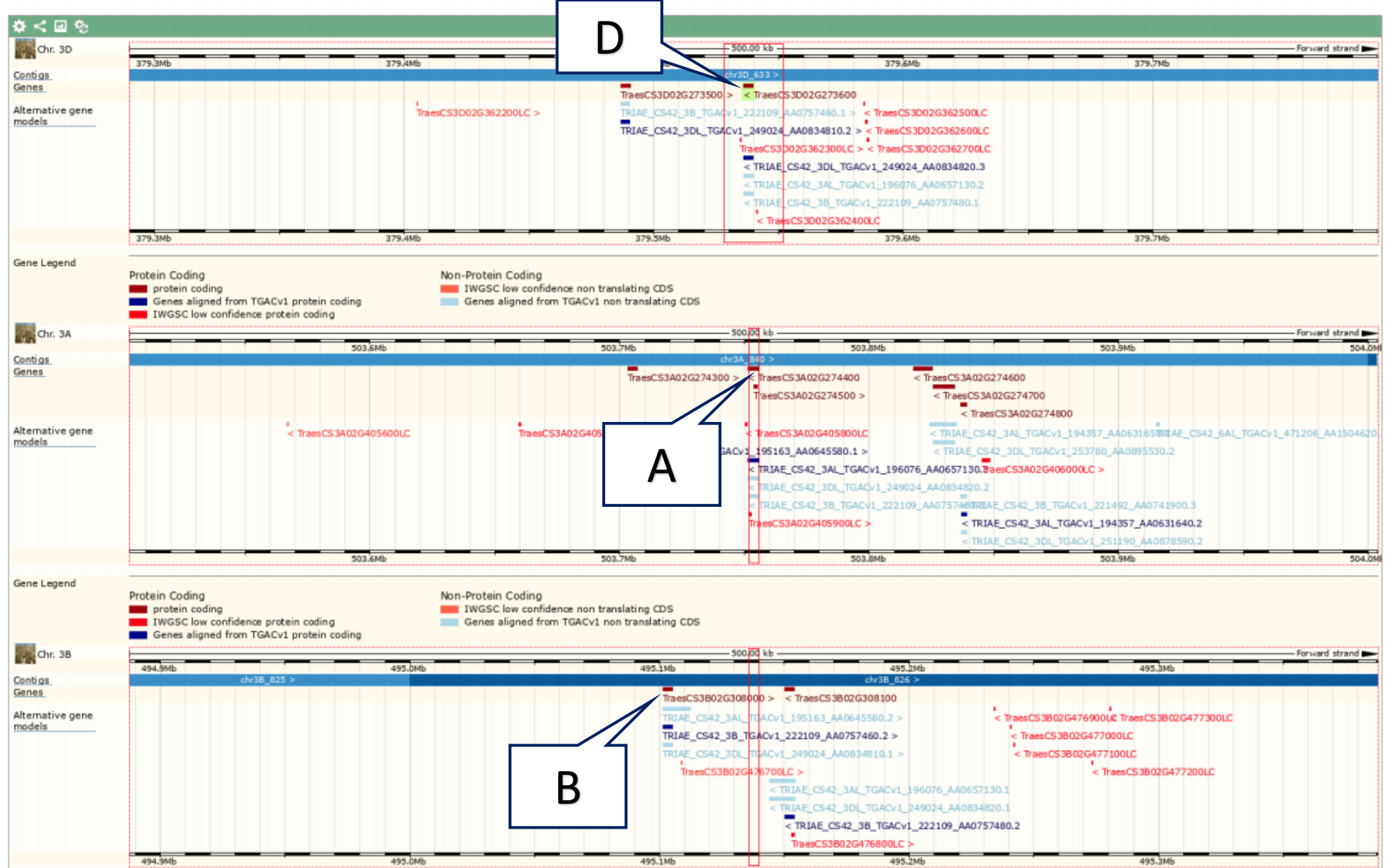
[Download homoeologues](#)

Show/hide columns		
Species	Type	Homoeologue
Triticum aestivum	1-to-1	TraesCS3A02G274400
	View Gene Tree	Compare Regions (3A:503,751,497-503,755,373:-1)
		View Sequence Alignments
Triticum aestivum	1-to-1	TraesCS3B02G308100
	View Gene Tree	Compare Regions (3B:495,150,368-495,154,251:-1)
		View Sequence Alignments

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Polyploid view



A closer look and examples




Genome assembly: [IWGSC](#)

-  [More information and statistics](#)
-  [Download DNA sequence \(FASTA\)](#)
-  [Convert your data to IWGSC coordinates](#)
-  [Display your data in Ensembl Plants](#)







Gene annotation

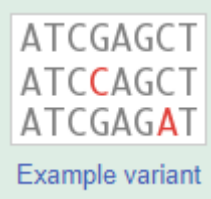
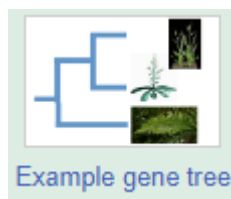
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-  [Download alignments \(EMF\)](#)
-  [Genomic alignments \[5\] \[Show» \]](#)



Variation

What can I find? Short sequence variants.

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-  [More about variation in Ensembl Plants](#)
-  [Download all variants - GVF - VCF - VEP](#)

Variant Effect Predictor



Variation SNP (820K SNP Array)

BA00249348 SNP

Most severe consequence

missense variant | [See all predicted consequences](#)

Alleles

T/C | Highest population MAF: 0.09

Location

[Chromosome 4A:714193714](#) (forward strand) | VCF: 4A 714193714 BA00249348 T C

HGVS names

This variant has 3 HGVS names - [Hide](#) ▾

- [4A:g.714193714T>C](#)
- [TraesCS4A01G446800.1:c.695A>G](#)
- [TraesCS4A01G446800.1:p.Lys232Arg](#)

Synonyms

CerealsDB AX-94599889

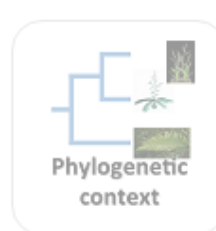
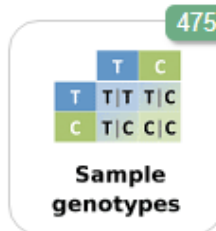
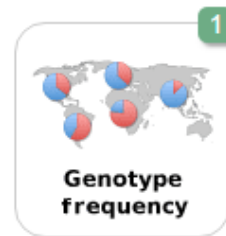
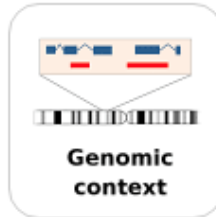
Original source

Markers from 820k SNP Array provided by [CerealsDB](#)

[About this variant](#)

This variant overlaps [1 transcript](#) and has [475 sample genotypes](#).

Explore this variant



Welcome to CerealsDB

The CerealsDB web-site was created by members of the Functional Genomics Group at the University of Bristol. The site provides a range of facilities for the study of the wheat genome. The site has been designed with breeders in mind, and we hope that it will be easy and straightforward to use. Principally the site is aimed at those who wish to obtain information about SNP markers; e.g., the sequence upon which they are based, obtain primers used for their identification, identify the haplotypes of common UK varieties. These publicly funded resources are available as an on-line, searchable database (please see "Important Note" box to the right of this page).

The last update to the database was October 2018.

SNPs databases

The information regarding SNP markers is divided by platform:

-

Axiom® 820K and 35K SNP Arrays

Along with researchers at Affymetrix, we have developed both an '820,000' and a '35,000' feature wheat SNP array. The data sets for these (Affymetrix code, Bristol SNP code and probe sequence containing the SNP ambiguity code) can be downloaded [here](#).

-

iSelect Array

The iSelect Array contains over 80,000 SNP loci of which 44,000 have been mapped.

-

KASP probes

Wheat TILLING population

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NEW RESEARCH IN

Physical Sciences

Social Sciences

Uncovering hidden variation in polyploid wheat



Ksenia V. Krasileva, Hans A. Vasquez-Gross, Tyson Howell, Paul Bailey, Francine Paraiso, Leah Clissold, James Simmonds, Ricardo H. Ramirez-Gonzalez, Xiaodong Wang, Philippa Borrill, Christine Fosker, Sarah Ayling, Andrew L. Phillips, Cristobal Uauy, and Jorae Dubcovsky

Wheat TILLING population

- 2,735 wheat mutant lines were sequenced and developed on a public database
- Lines from **Kronos** (tetraploid) and **Cadenza** (hexaploid)
- Database includes more than 10 million EMS induced mutations



Seeds with mutations can be ordered

- Researchers and breeders can study and order seeds with mutation
- A foundation for many wheat experiments and research
- Makes it possible to do **double knockouts** (Kronos) and **triple knockouts** (Cadenza) in a few generations
- Knockouts allows you to uncover **hidden variation**



in silico TILLING mutant resources

Knock-out mutations are available in most wheat genes providing an invaluable resource for characterising gene function.

Targeting Induced Local Lesions In Genomes (TILLING) is a method of inducing and identifying mutations in specific genes. This section will describe how to use the *in silico* wheat TILLING resource (www.wheat-tilling.com).

This resource consists of TILLING populations developed in tetraploid durum wheat cv 'Kronos' and hexaploid bread wheat cv 'Cadenza' as part of a joint project between the University of California Davis, Rothamsted Research, The Earlham Institute, and John Innes Centre.

The exome sequences of 1,535 Kronos and 1,200 Cadenza mutants have been re-sequenced using Illumina next-generation sequencing, the raw data aligned to the IWGSC Chinese Spring chromosome arm survey sequence, mutations identified, and their effects predicted based on the protein annotation available at the Ensembl Plants archive site.

This section will cover the following four topics:



Selecting TILLING Mutants

Designing Genome Specific Primers

Improving Gene Models

Designing Crossing Schemes

<http://www.wheat-training.com/tilling-mutant-resources/>

Cadenza0225.chr3D.379537010 SNP

Most severe consequence	missense variant See all predicted consequences
Alleles	G/A
Location	Chromosome 3D:379537010 (forward strand) VCF: 3D 379537010 Cadenza0225.chr3D.379537010 G A
HGVS names	This variant has 5 HGVS names - Show
Synonyms	Primer metadata Cadenza0225.chr3D.379537010:snp_type=non-homoeologous;total_configs=3;A=tgacctcAaaccttggcgC;B=tgacctcAaaccttggcgT;common=cAcgagcaacctcatCgaA;primer_type=chromosome_specific;product_size=69;EMS-GT=Het
Original source	EMS-induced mutations from sequenced TILLING populations. Seeds can be ordered from UK SeedStor or US Dubcovsky lab . Line identifier is variant name up to dot (e.g Kronos3128).
About this variant	This variant overlaps 2 transcripts .

Gene and Transcript consequences

Gene	Transcript (strand)	Allele (transcript allele)	Consequence Type	Position in transcript	Position in CDS	Position in protein	Amino acid	Codons	SIFT	Detail
TraesCS3D01G273600	TraesCS3D01G273600.1 (-) biotype: protein_coding	A (T)	missense variant	2171 (out of 2742)	2171 (out of 2742)	724 (out of 913)	AV	GCG/GTG	0.01	Show
TraesCS3D01G273600	TraesCS3D01G273600.2 (-) biotype: protein_coding	A (T)	missense variant	2261 (out of 2888)	2261 (out of 2888)	754 (out of 895)	AV	GCG/GTG	deleterious	Show

No overlap with Ensembl Regulatory features

SIFT predicts SNP effect on **protein function**

Based on **sequence homology and physical properties** of amino acids

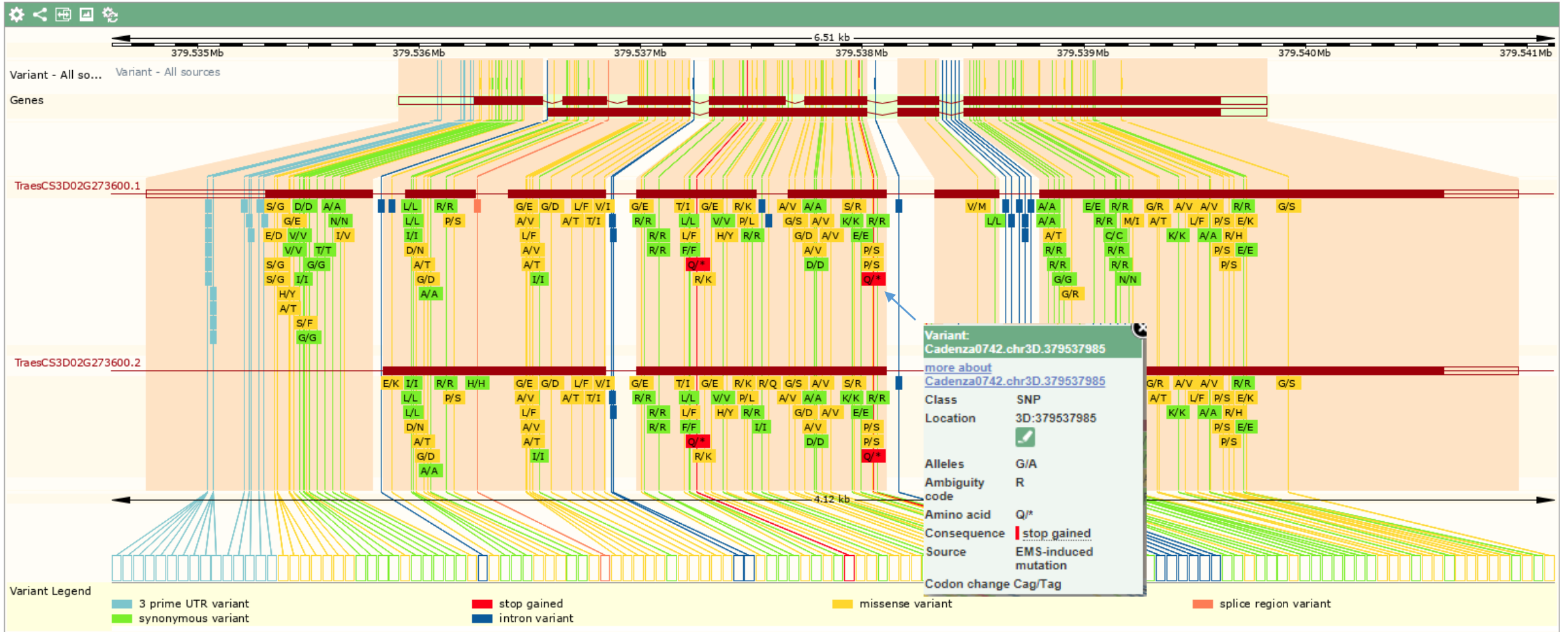
<http://sift.bii.a-star.edu.sg/>

SIFT predictions for all gene variations

Cadenza0455.chr3D.379536699	3D:379536699	C/T	SNP	EMS-induced mutation	-	-	missense variant	A/T	796	0.37	TraesCS3D01G273600.1
Cadenza1723.chr3D.379536710	3D:379536710	C/T	SNP	EMS-induced mutation	-	-	missense variant	G/D	792	0.37	TraesCS3D01G273600.1
Cadenza1241.chr3D.379536718	3D:379536718	G/A	SNP	EMS-induced mutation	-	-	synonymous variant	A	789	-	TraesCS3D01G273600.1
Cadenza1165.chr3D.379536763	3D:379536763	C/T	SNP	EMS-induced mutation	-	-	synonymous variant	R	774	-	TraesCS3D01G273600.1
Cadenza1808.chr3D.379536786	3D:379536786	G/A	SNP	EMS-induced mutation	-	-	missense variant	P/S	767	0.15	TraesCS3D01G273600.1
Cadenza1494.chr3D.379536853	3D:379536853	G/A	SNP	EMS-induced mutation	-	-	splice region variant intron variant	-	-	-	TraesCS3D01G273600.1
Cadenza2068.chr3D.379536992	3D:379536992	C/T	SNP	EMS-induced mutation	-	-	missense variant	G/E	730	0.09	TraesCS3D01G273600.1
Cadenza1819.chr3D.379536995	3D:379536995	G/A	SNP	EMS-induced mutation	-	-	missense variant	A/V	729	0.07	TraesCS3D01G273600.1
Cadenza1793.chr3D.379537002	3D:379537002	G/A	SNP	EMS-induced mutation	-	-	missense variant	L/F	727	0.02	TraesCS3D01G273600.1
Cadenza0225.chr3D.379537010	3D:379537010	G/A	SNP	EMS-induced mutation	-	-	missense variant	A/V	724	0.01	TraesCS3D01G273600.1
Cadenza0844.chr3D.379537011	3D:379537011	C/T	SNP	EMS-induced mutation	-	-	missense variant	A/T	724	0.01	TraesCS3D01G273600.1
Cadenza0726.chr3D.379537030	3D:379537030	G/A	SNP	EMS-induced mutation	-	-	synonymous variant	I	717	-	TraesCS3D01G273600.1

All mutations for a given gene

Variant image



A look into the future



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A background image of a wheat field with golden stalks, overlaid with a semi-transparent dark grey rectangle.

The Wheat 'Pan Genome'

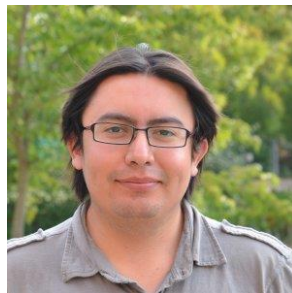
Would you like to know more?

- Our outreach team gives workshops and courses for organizations and institutions
- Minimum of 10 participants
- Workshops are free (just pay for travel and food)
- <http://www.ensembl.org/info/about/outreach/index.html>
- helpdesk@ensemblgenomes.org





Thanks!!!

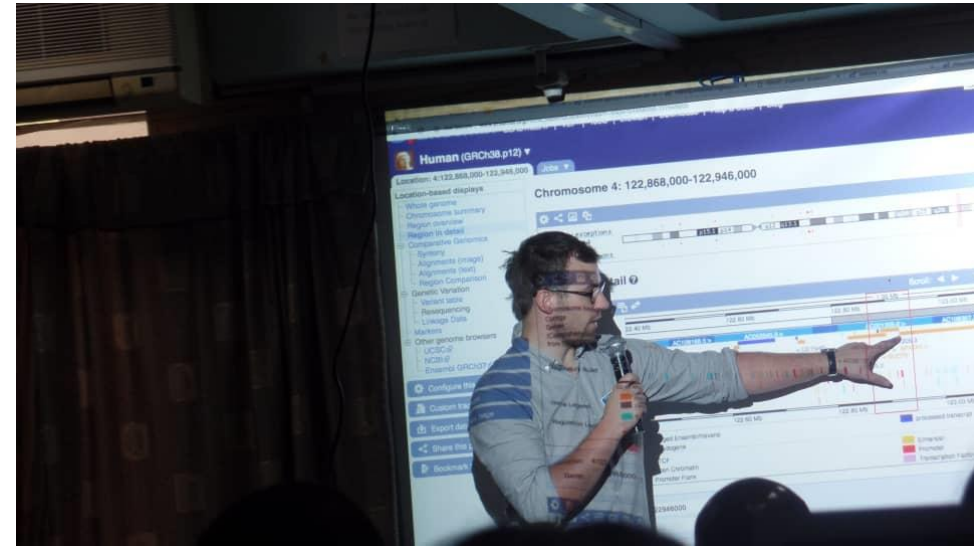


Thanks again!



Ensembl4Breeders Event

Feb 22nd 2019



Experience meeting with Ensembl Plants and the plant breeding community

European Bioinformatics Institute

Hinxton, Cambridge

