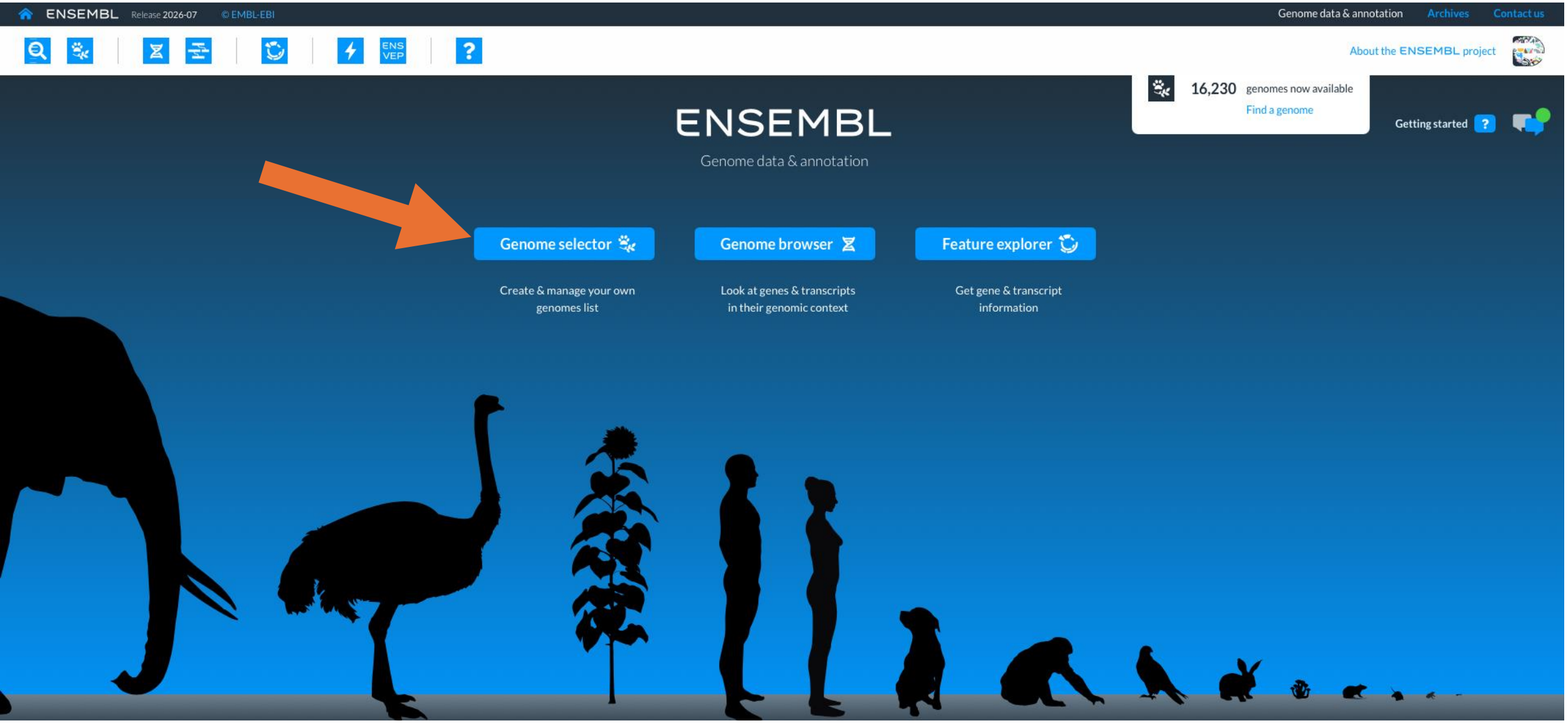
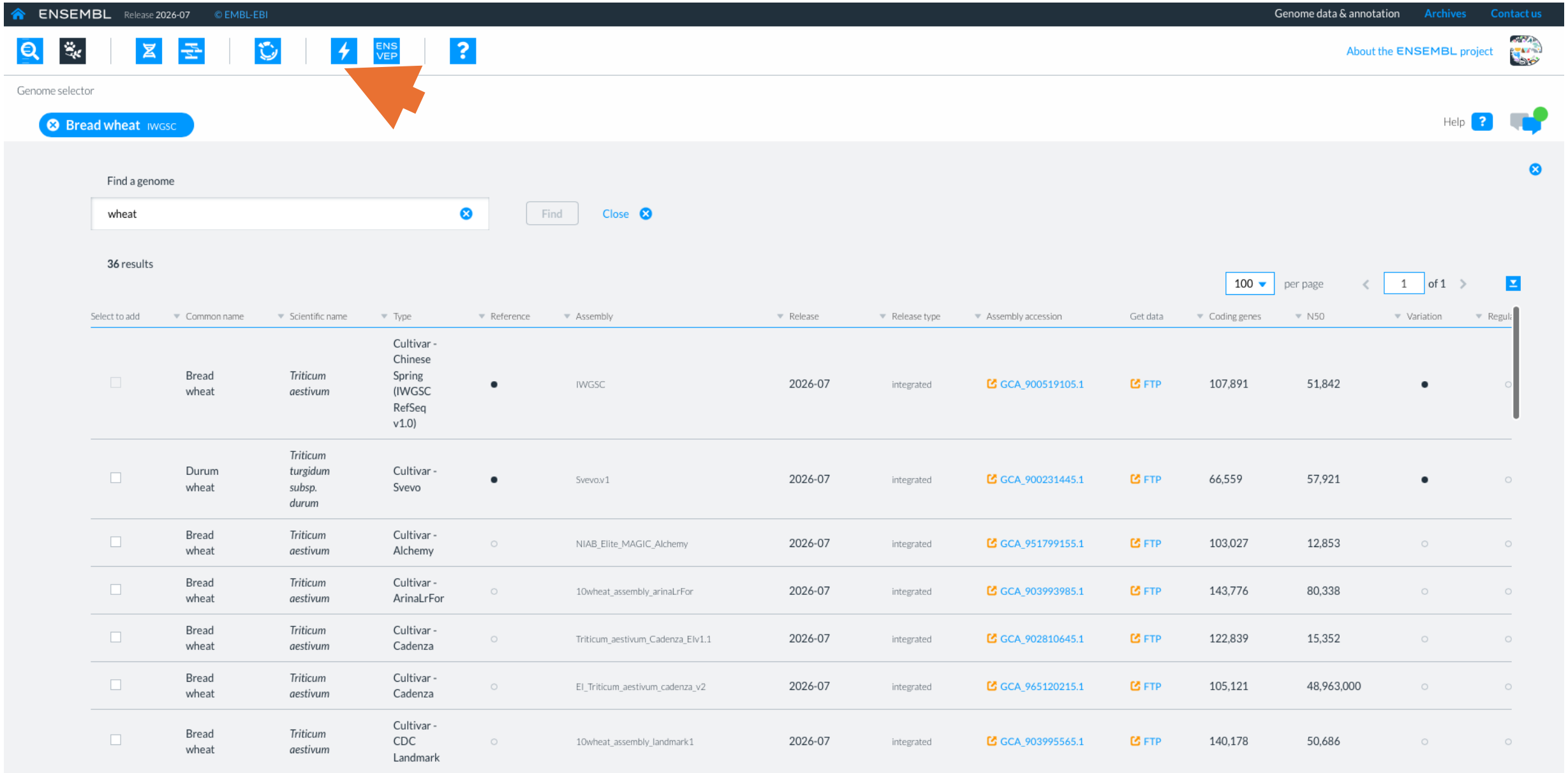
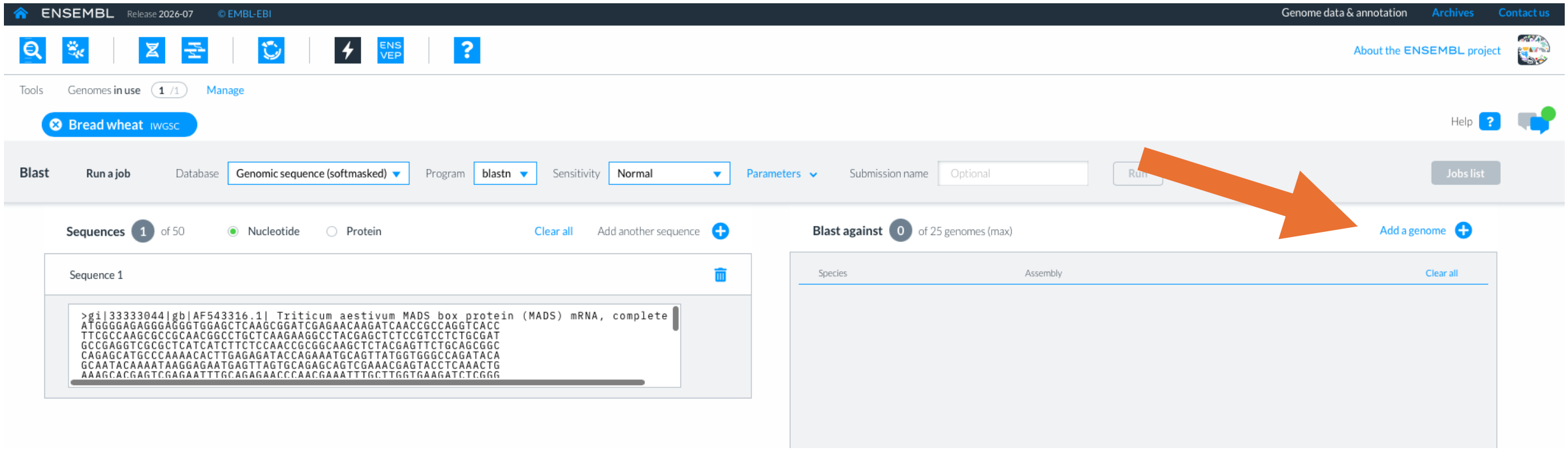
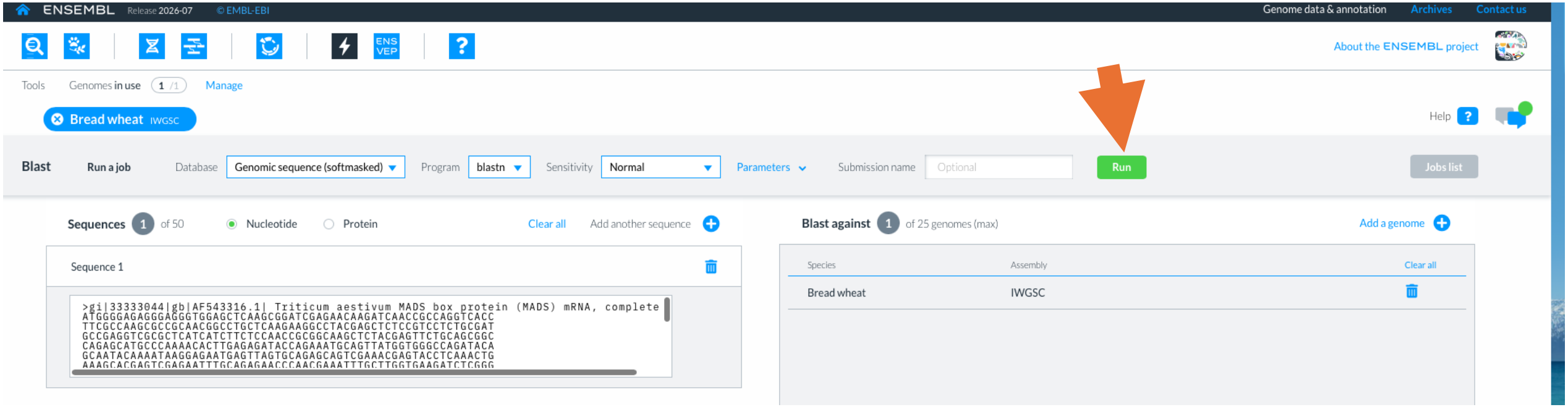

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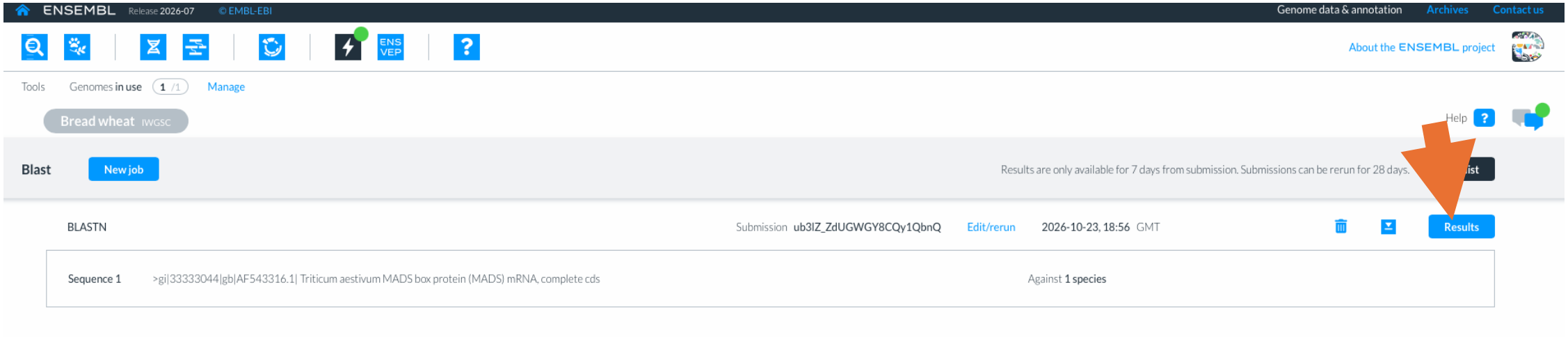
Select the IWGSC genome. Then go to the thunderbolt (orange arrow)



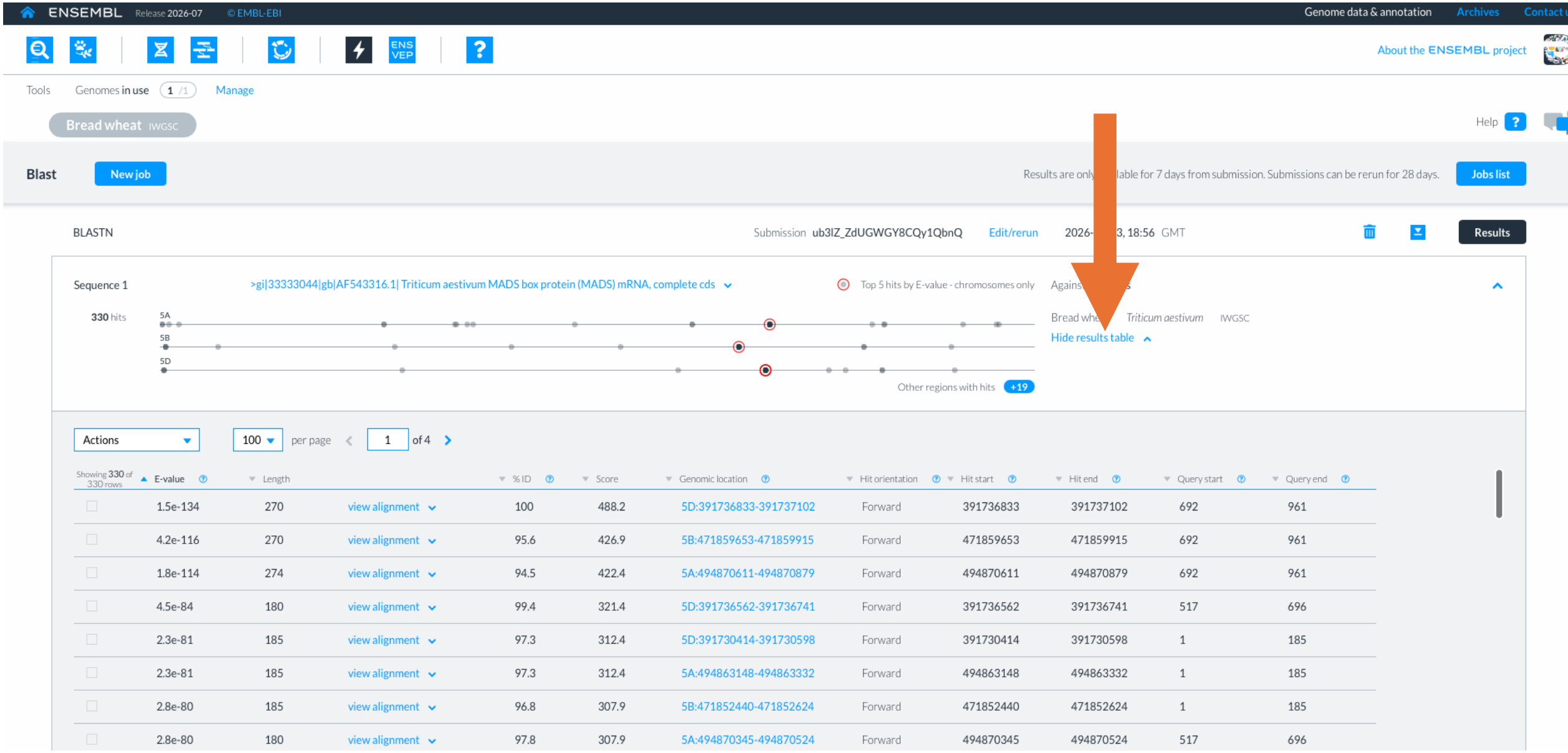
Paste the sequence and then go to “Add a Genome” (arrow)


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Genomic sequence (softmasked)
Program
blastn
Sensitivity
Normal
Parameters
Submission name
Optional
Run
Jobs list
Sequences 1 of 50
Nucleotide
Protein
Clear all
Add another sequence
Sequence 1
>gi|33333044|gb|AF543316.1| Triticum aestivum MADS box protein (MADS) mRNA, complete
ATGGGGAGAGGGAGGGTGGAGCTCAAGCGGATCGAGAACAAGATCAACCGCCAGGTCACC
TTCGCCAAGCGCCGCAACGGCCTGCTCAAGAAGGCCTACGAGCTCTCCGTCCTCTGCGAT
GCCGAGGTCGCGCTCATCATCTTCTCCAACCGCGGCAAGCTCTACGAGTTCTGCAGCGGC
CAGAGCATGCCCAAAACACTTGAGAGATACCAGAAATGCAGTTATGGTGGGCCAGATACA
GCAATACAAAATAAGGAGAATGAGTTAGTGCAGAGCAGTCGAAACGAGTACCTCAAACTG
AAAGCACGAGTCGAGAATTTGCAGAGAACCCAACGAAATTTGCTTGGTGAAGATCTCGGG
Blast against 1 of 25 genomes (max)
Add a genome
Species
Assembly
Clear all
Bread wheat
IWGSC

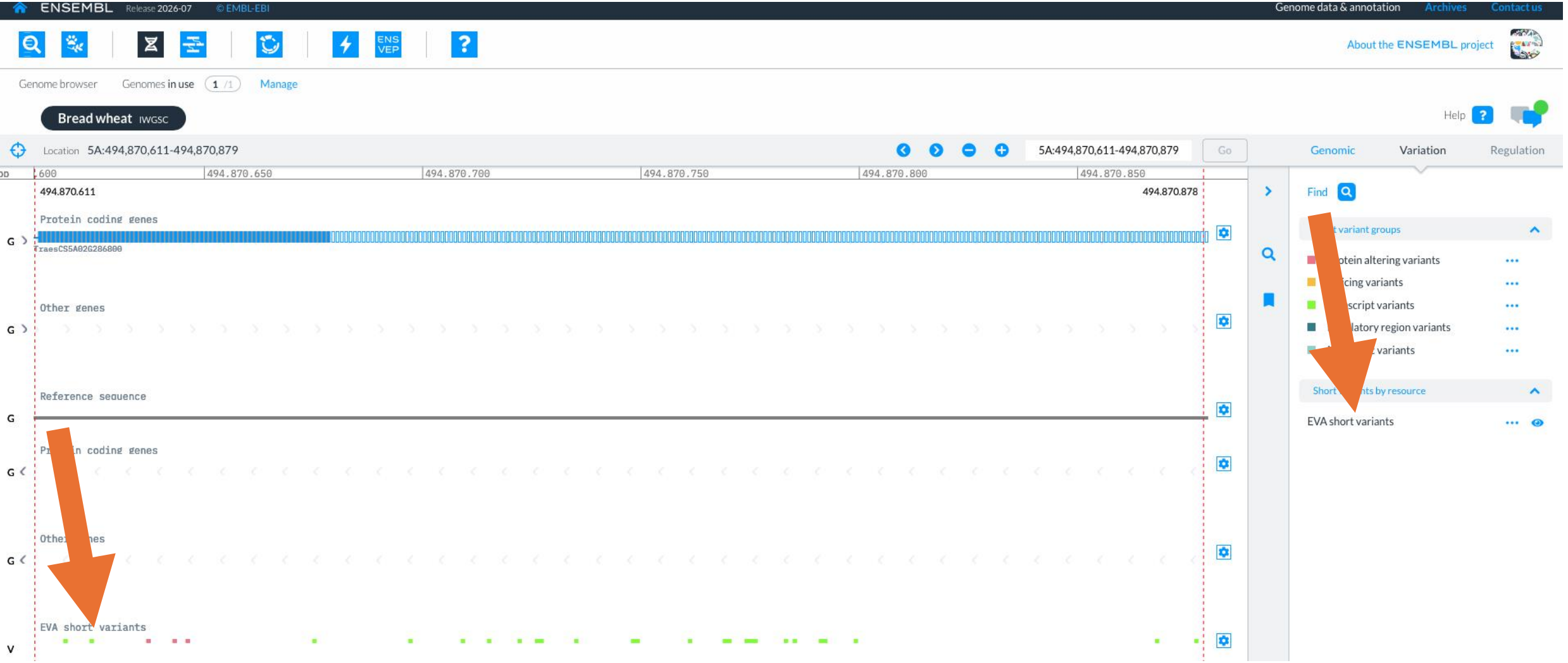
Press Run



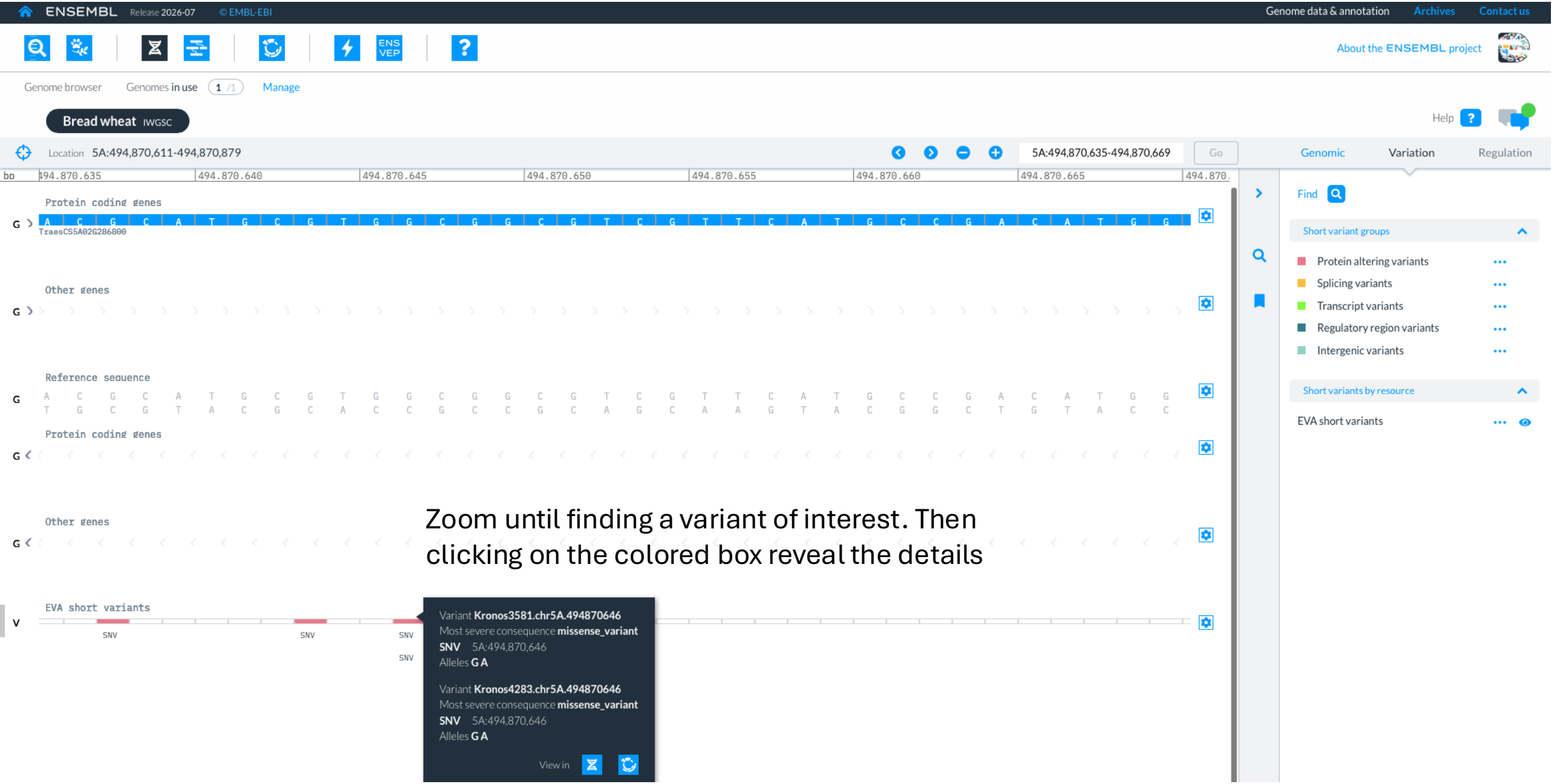
Go to Results



Expand to result table. Choose the genomic location



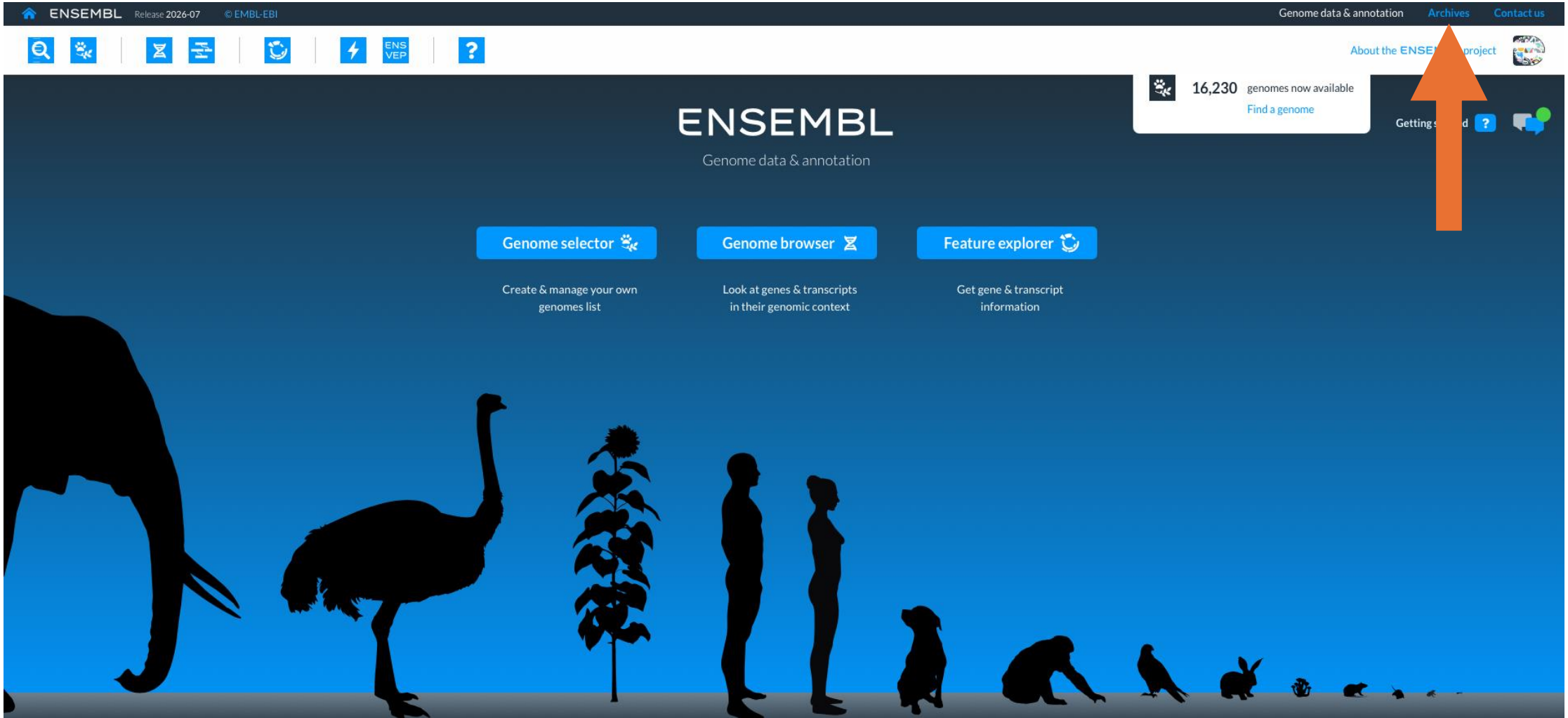
Make sure the EVA short variant is visible



Zoom until finding a variant of interest. Then clicking on the colored box reveal the details

To access the historic variant table

https://eg63-plants.ensembl.org/



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Overview Getting started Using Ensembl Ensembl data

Ensembl data > Release information > Archives

Ensembl archives and previous sites

This Ensembl site uses a different versioning system and release cycle to that of previous Ensembl versions. Ensembl versions released prior to July 2026 were numbered numerically following a 3-4 month long release cycle.

The legacy Ensembl archives for versions 116 and Ensembl Genomes version 63

These archives have enhanced tool functionality and features compared to older archive sites. Use these sites if you are searching for a feature or view which is unavailable in the new Ensembl.

- Ensembl 116: Jun 2026
- Ensembl Plants eg63: Jun 2026

Choose Ensembl Plant

Search: All species for
Go
e.g. **Carboxy*** or **chx28**

All genomes

-- Select a species --

View full list of all species

Favourite genomes



Arabidopsis thaliana
TAIR10



Oryza sativa Japonica Group
IRGSP-1.0



Triticum aestivum
IWGSC



Hordeum vulgare
MorexV3_pseudomolecules_assembly



Zea mays
Zm-B73-REFERENCE-NAM-5.0



Physcomitrium patens
Phypa_V3

Wheat assemblies

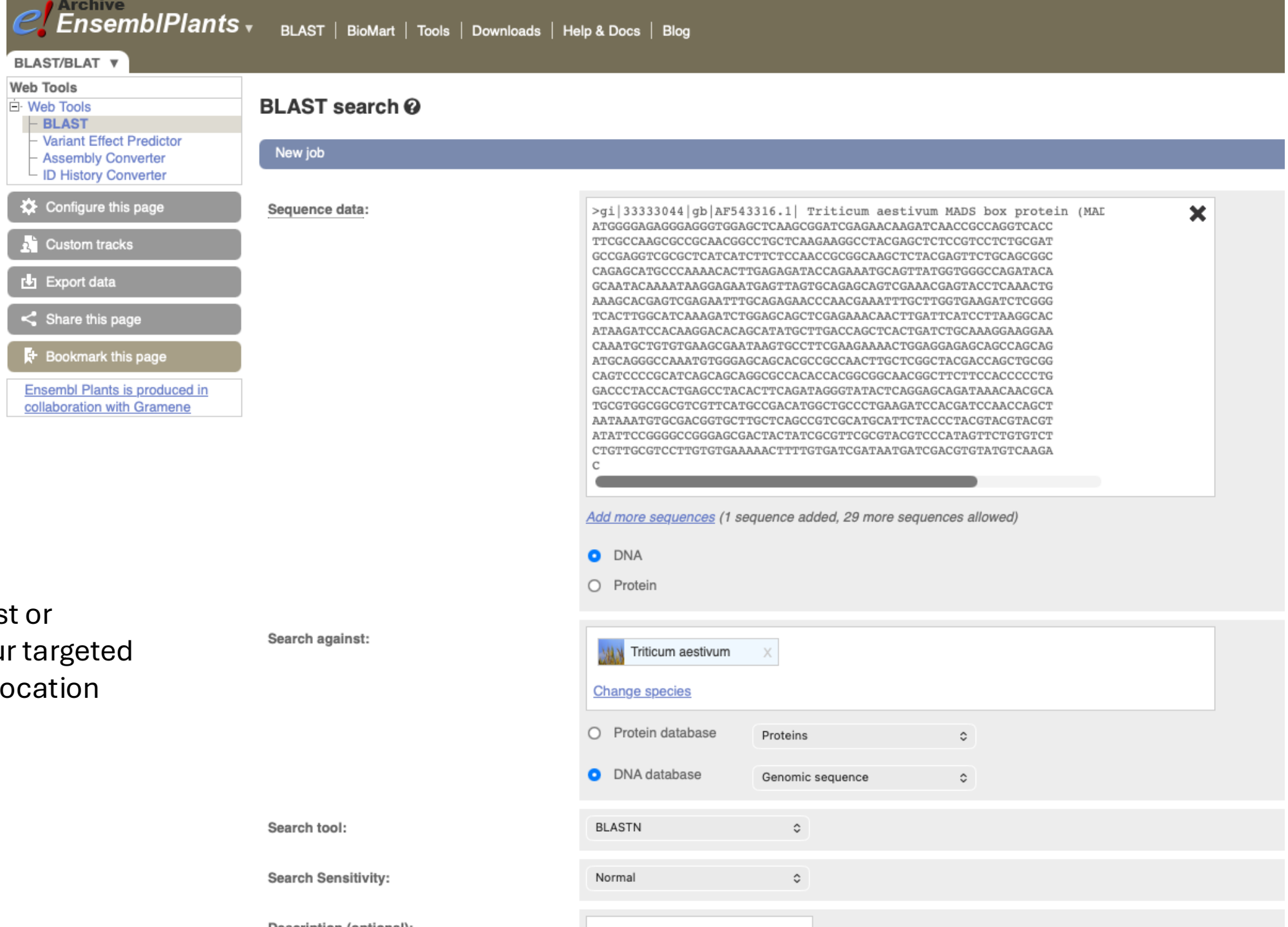
Ensembl Plants hosts the RefSeq v1.0 assembly from the IWGSC, including:

- The IWGSC RefSeq v1.1 gene annotation, with links to wheat expression browser and KnetMiner
- 19 wheat cultivars from the 10+ genome project and other sources including comparative analysis across the different lines
- ~90 million variants from the Watkins Landrace Wheat Collection
- Variants were loaded from the *Triticum aestivum* Next GenerationTaNG array derived from 204 elite wheat lines and 111 wheat landraces from the Watkins 'Core Collection'
- Axiom 35K, 820K SNP arrays from CerealsDB, including QTL links in selected cases and Linkage Disequilibrium display - see QTL example here. 820K variants have been lifted over to the chromosomal level 10+ wheat cultivars
- EMS-induced mutations from sequenced TILLING populations of Cadenza (coding regions) and Kronos (coding regions and promoters)
- Inter-Homeologous Variants (IHVs) between the A, B and D genome components
- Chromosome specific KASP markers from the Nottingham BBSRC Wheat Research Centre
- brachypodium and barley
- Polyploid view enabled, allowing users to view alignments among multiple wheat components simultaneously
- Durum wheat 35K, 90K, 820K and TaBW280K variants
- Chromosome and centromere data can be viewed here
- AlphaFold protein predictions have been added to all transcripts - see an example here

Pangenomes

Ensembl Plants hosts the following four pangenomes:

- The barley pangenome comprises 77 wild and domesticated barley accessions
- The oat pangenome that includes 33 wild and domesticated oat lines
- The rice pangenome consists of 26 *Oryza* genomes including 16 *Oryza sativa* cultivars
- The wheat pangenome consists of 24 *Triticum* genomes including 19 *Triticum aestivum* cultivars



Run a blast or
select your targeted
genomic location

Web Tools
- Web Tools
  - BLAST
    - Ticket
      - gil33333044lgblAF543316.
  - Variant Effect Predictor
  - Assembly Converter
  - ID History Converter

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Results for gil33333044lgblAF543316.1l Triticum aestivum MADS box protein (MADS) mRNA, complete cds

Job details

Job name gil33333044lgblAF543316.1l Triticum aestivum MADS box protein (MADS) mRNA, complete cds

Species Triticum aestivum

Assembly IWGSC

Search type BLASTN (NCBI BLAST)

Download results file | New job

Results table

Show All entries | Show/hide columns (4 hidden) | Filter

Genomic Location	Overlapping Gene(s)	Orientation	Length	Score	E-val	%ID
5D:391736833-391737102 [Sequence]	MADS	Forward	270 [Sequence]	270	7.3e-149	100.0 [Alignment]
5D:391736565-391736741 [Sequence]	MADS	Forward	177 [Sequence]	177	2.3e-93	100.0 [Alignment]
5D:391730427-391730598 [Sequence]	MADS	Forward	172 [Sequence]	168	5.4e-88	99.4 [Alignment]
5A:494863161-494863332 [Sequence]	MADS	Forward	172 [Sequence]	168	5.4e-88	99.4 [Alignment]
5A:[illegible] [Sequence]	MADS	Forward	177 [Sequence]	165	3.3e-86	98.3 [Alignment]
5B:[illegible] [Sequence]	TraesCS5B02G286100	Forward	172 [Sequence]	164	1.3e-85	98.8 [Alignment]
5B:471859391-471859567 [Sequence]	TraesCS5B02G286100	Forward	177 [Sequence]	153	4.8e-79	96.6 [Alignment]
7D:237610173-237610349 [Sequence]	WSEP-D	Forward	177 [Sequence]	145	2.9e-74	95.5 [Alignment]
7A:253427929-253428105 [Sequence]	WSEP-A	Forward	177 [Sequence]	145	2.9e-74	95.5 [Alignment]
7B:215001224-215001400 [Sequence]	WSEP-B	Forward	177 [Sequence]	141	7e-72	94.9 [Alignment]
6B:516075219-516075396 [Sequence]	TraesCS6B02G286400	Forward	178 [Sequence]	130	2.6e-65	93.3 [Alignment]
6A:481737160-481737337 [Sequence]	TraesCS6A02G259000	Forward	178 [Sequence]	126	6.3e-63	92.7 [Alignment]
6D:341645548-341645725 [Sequence]	TraesCS6D02G240200	Forward	178 [Sequence]	126	6.3e-63	92.7 [Alignment]
5A:494870611-494870735 [Sequence]	MADS	Forward	125 [Sequence]	117	1.5e-57	98.4 [Alignment]
5B:471859653-471859777 [Sequence]	TraesCS5B02G286100	Forward	125 [Sequence]	109	8.7e-53	96.8 [Alignment]
7D:74607627-74607768 [Sequence]	WM20	Reverse	142 [Sequence]	94	7.8e-44	91.5 [Alignment]
5B:574061062-574061183 [Sequence]	TraesCS5B02G396700	Reverse	122 [Sequence]	94	7.8e-44	94.3 [Alignment]

Region in Detail

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Triticum aestivum (IWGSC) ▾

Location: 5A:494,863,152-494,863,340 | BLAST/BLAT results ▾

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- Whole genome
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- Region overview
- Region in detail
- Comparative Genomics
  - Synteny
  - Alignments (image)
  - Alignments (text)
  - Region Comparison
  - Polyploid view
- Genetic Variation
  - Variant table
  - Resequencing
  - Linkage Data
- Markers

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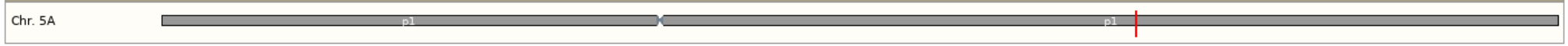
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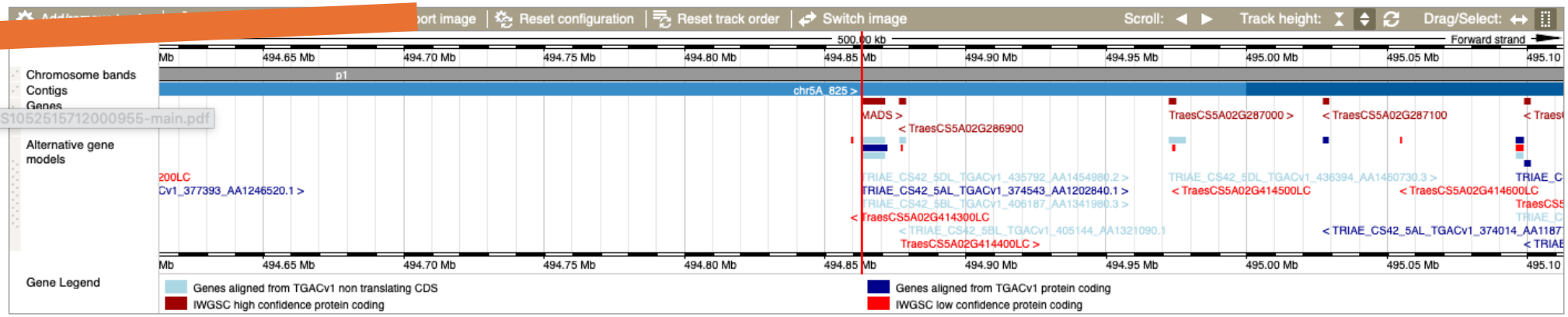
Chromosome 5A: 494,863,152-494,863,340

Add/remove tracks | Share | Export image | Reset configuration



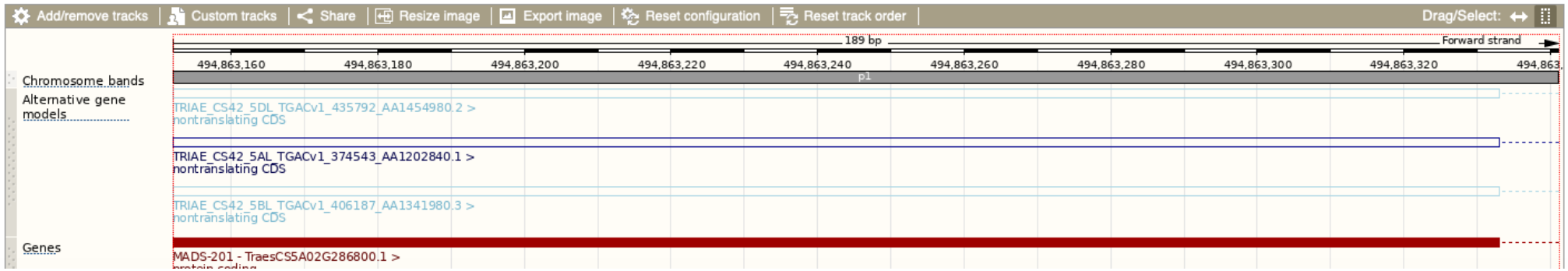
Region in detail

Reset configuration | Reset track order | Switch image | Scroll: | Track height: | Drag/Select:



Location: 5A:494863152-494863340 Go Gene: Go

Add/remove tracks | Custom tracks | Share | Resize image | Export image | Reset configuration | Reset track order | Drag/Select:



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Chromosome 5A: 494,863,058-494,863,435

Variant table

Location: 5A:494863058-494863435 Go Gene: Go

Filter: Class: All | Consequences: All | Filter Other Columns

Show/hide columns Search...

Variant ID	Chr: bp	Alleles	Class	Source	Evidence	ClinVar ID	Consequence	Phenotype
5A_494863069	5A:494863070-494863097	AGGAGGAGGAGGAGGAGG.../AGGAGGAGGAGGAGG...	indel	Watkins-exome-capture	-	-	5 prime UTR variant	-
Kronos3067.chr5A.494863074	5A:494863074	G/A	SNP	EMS-induced mutation	-	-	5 prime UTR variant	-
Cadenza1670.chr5A.494863089	5A:494863089	G/A	SNP	EMS-induced mutation	-	-	5 prime UTR variant	-
Kronos890.chr5A.494863095	5A:494863095	G/A	SNP	EMS-induced mutation	-	-	5 prime UTR variant	-
Cadenza1354.chr5A.494863095	5A:494863095	G/A	SNP	EMS-induced mutation	-	-	5 prime UTR variant	-
Kronos950.chr5A.494863096	5A:494863096	G/A	SNP	EMS-induced mutation	-	-	5 prime UTR variant	-
Kronos481.chr5A.494863097	5A:494863097	G/A	SNP	EMS-induced mutation	-	-	5 prime UTR variant	-
Kronos2469.chr5A.494863112	5A:494863112	C/T	SNP	EMS-induced mutation	-	-	5 prime UTR variant	-
Cadenza1213.chr5A.494863116	5A:494863116	C/T	SNP	EMS-induced mutation	-	-	5 prime UTR variant	-
Cadenza0216.chr5A.494863121	5A:494863121	C/T	SNP	EMS-induced mutation	-	-	5 prime UTR variant	-
Kronos2296.chr5A.494863124	5A:494863124	G/A	SNP	EMS-induced mutation	-	-	5 prime UTR variant	-
Kronos884.chr5A.494863130	5A:494863130	G/A	SNP	EMS-induced mutation	-	-	5 prime UTR variant	-