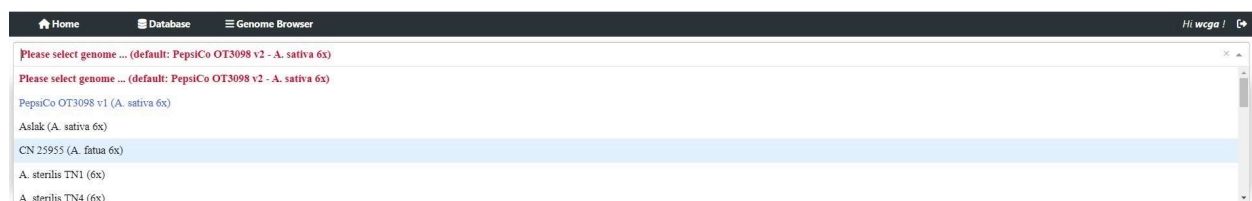


I. Oat genome browser tutorials

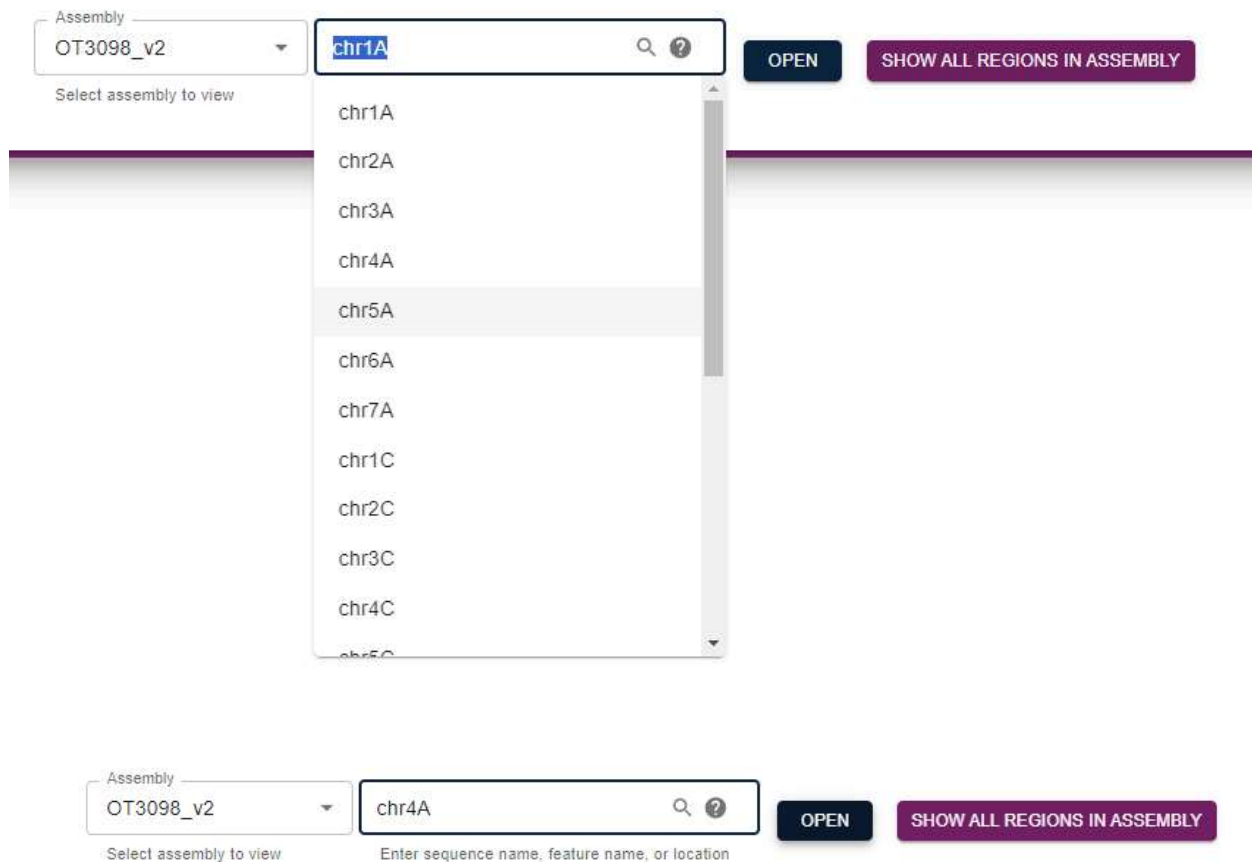
1. The genome browsers can be accessed using the following link

<http://database.oatpangenome.com/jbrowse/>

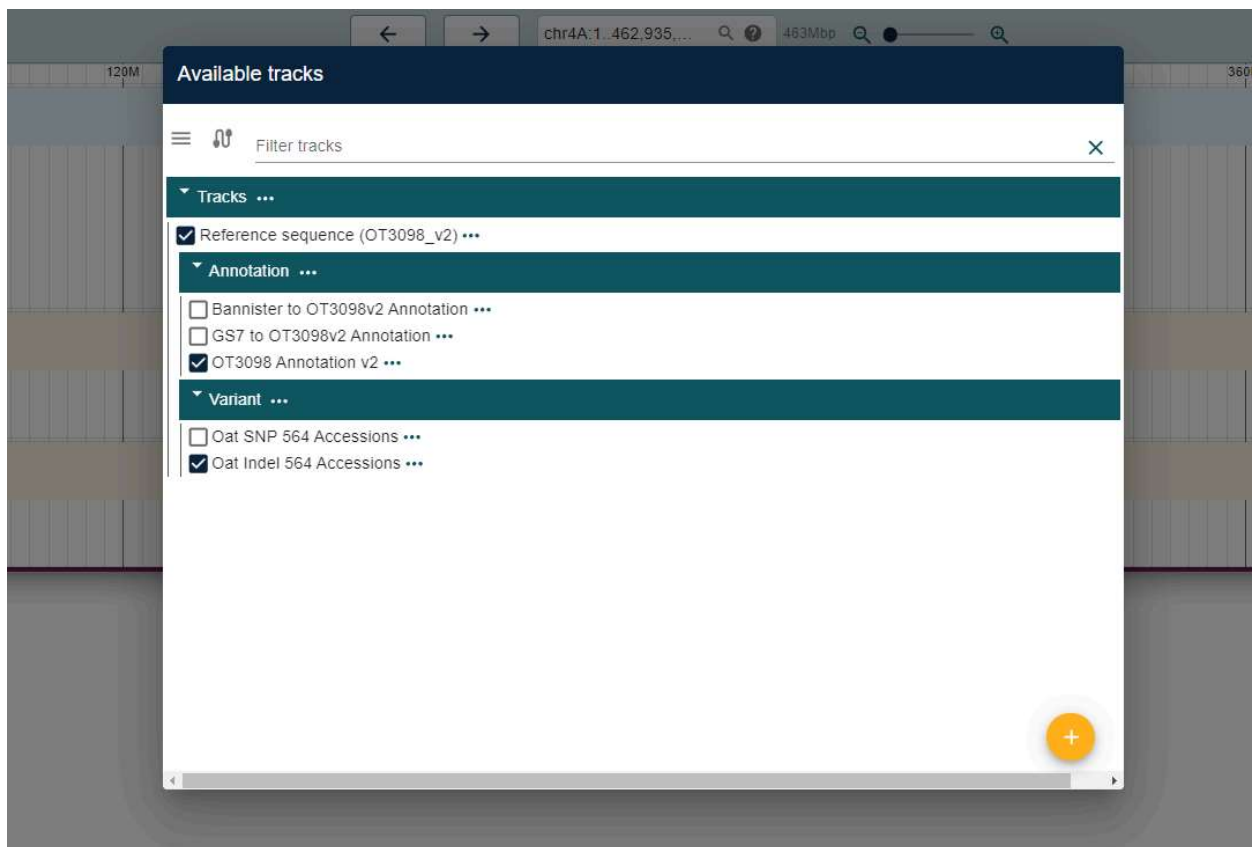
2. First, select the genome from the dropdown list



3. Select the chromosome you'd like to view then "Open"

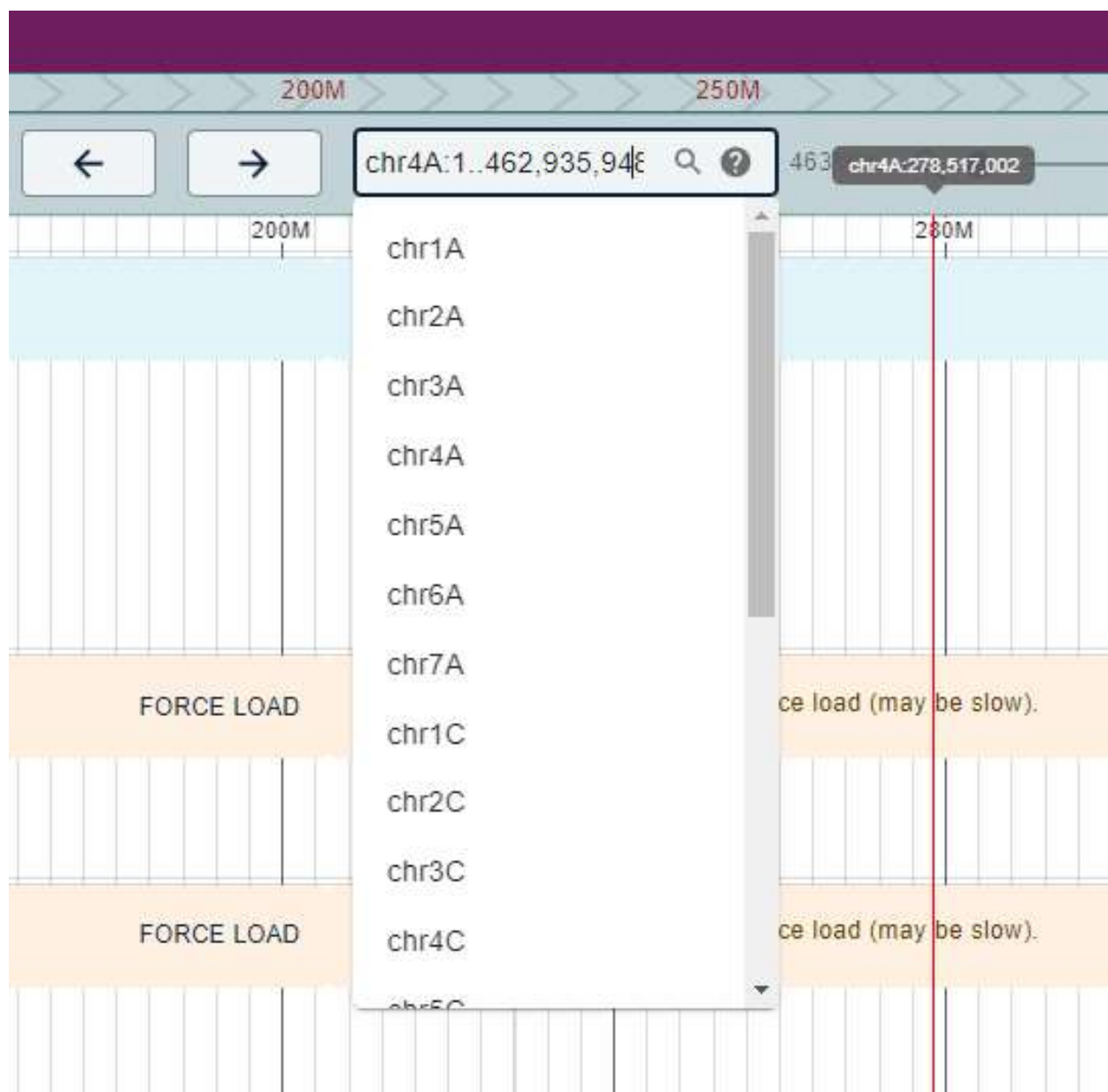


4. Select the tracks using the "Open track selector" button

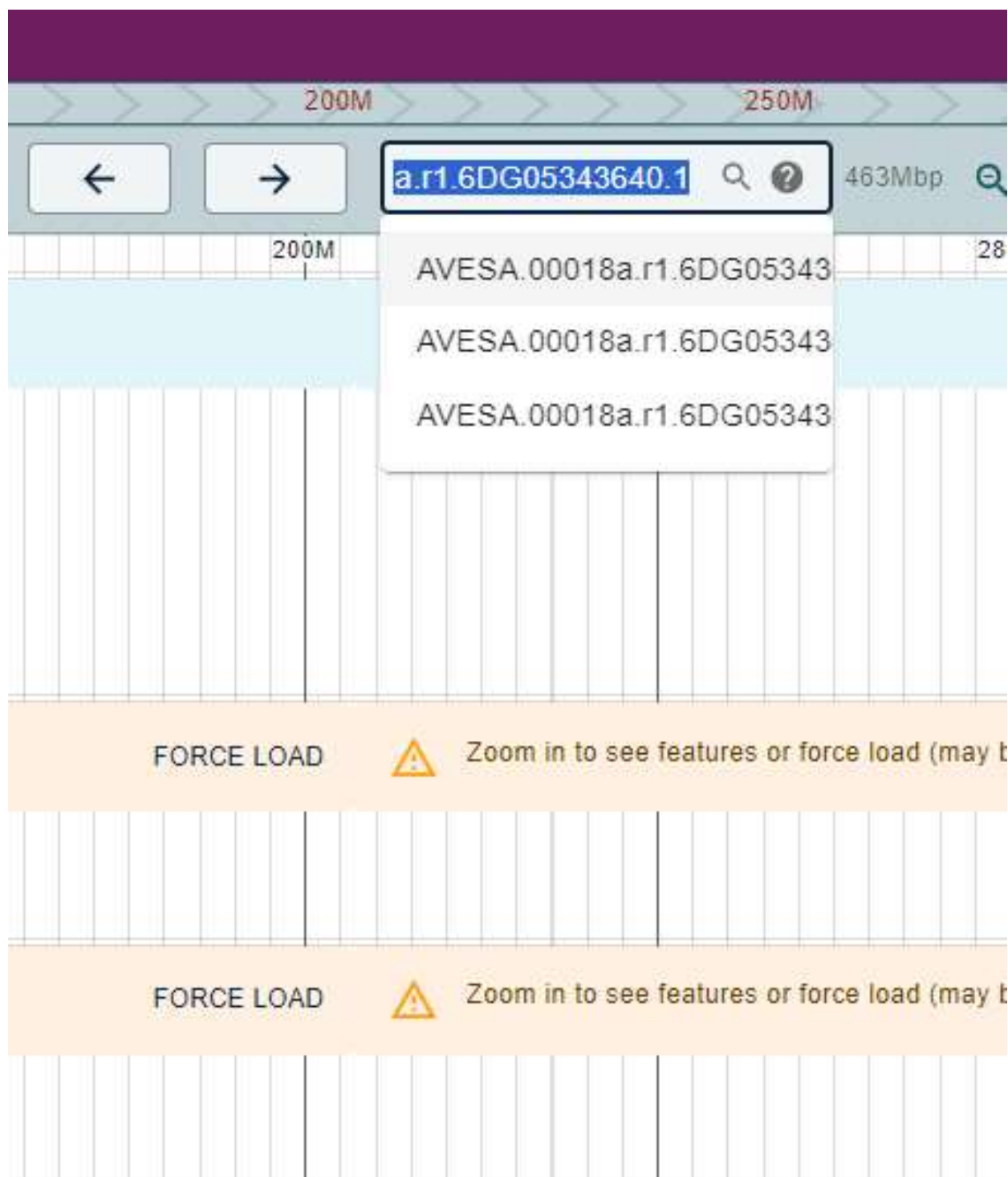


5. You can manually input the region you want to search

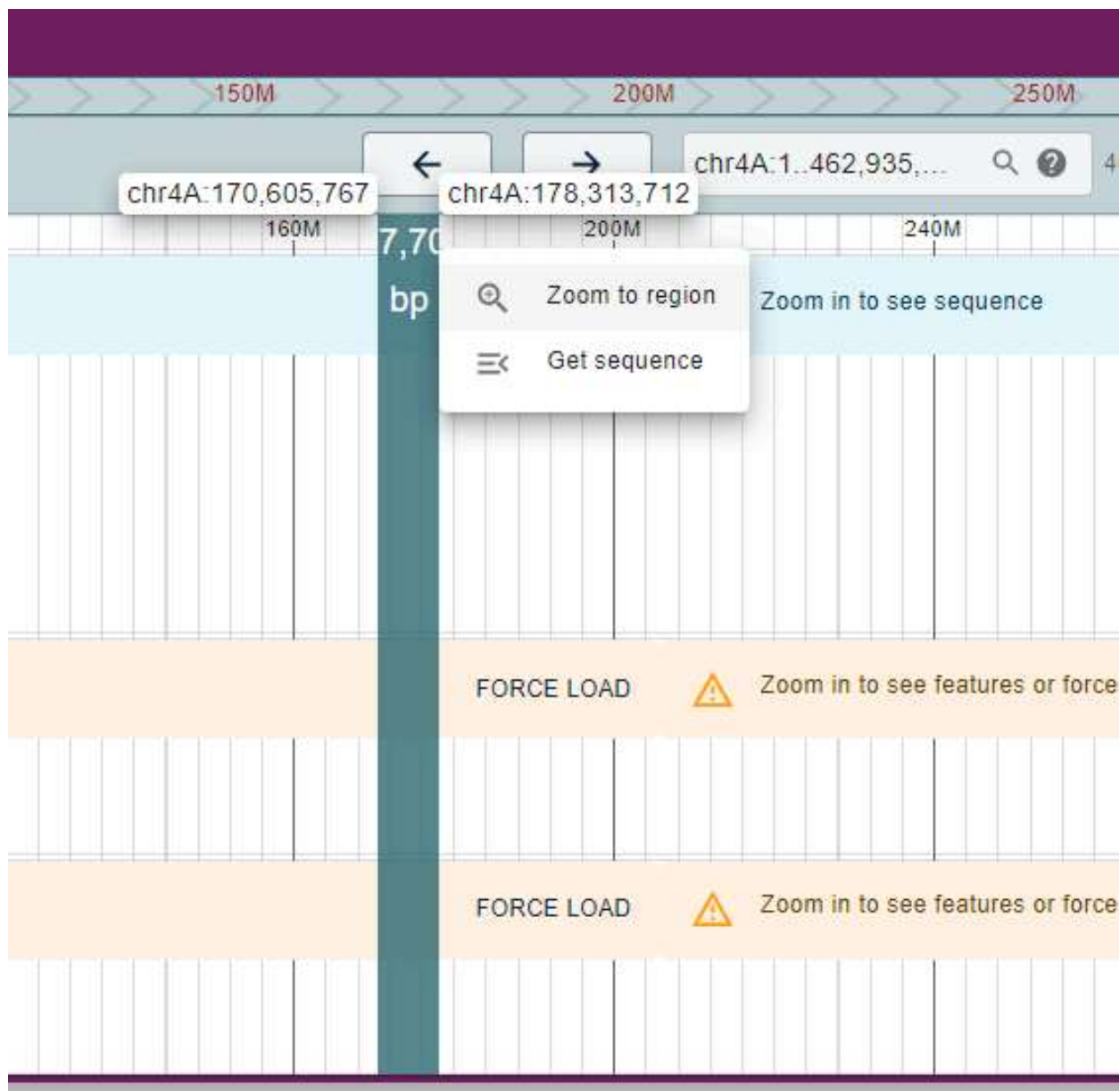
Using the chr1A:123..456 format



Or search using Gene ID *Currently, GeneID of OT3098, GS7 and Bannister is supported for the OT3098v2 browser*

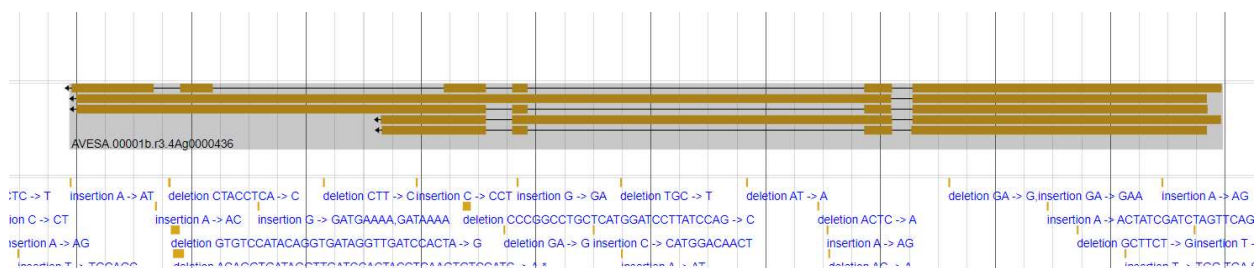


Select the region manually and zoom in



6. Obtain gene sequences

Gene sequences can be obtained by clicking in the gene annotation



Then select the type of sequence you want to get, then hit "Copy as plaintext"

Core details

Position	chr4A:173,627,184..173,631,189 (-)
Length	4,006
Type	gene

Attributes

source	transdecoder
phase	0
id	AVESA.00001b.r3.4Ag0000436

cDNA

>AVESA.00001b.r3.4Ag0000436-cdna

SUBFEATURES

AVESA.00001B.R3.4AG0... - MRNA

Core details

Position	chr4A:173,627,184..173,631,189 (-)
Length	4,006
Type	mRNA

Attributes

source	transdecoder
phase	0
id	AVESA.00001b.r3.4Ag0000436.1
parent	AVESA.00001b.r3.4Ag0000436

cDNA

1-cdna

Gene w/ introns

Gene w/ 10bp of intron

Gene w/ 500bp up+down stream

Gene w/ 500bp up+down stream w/ 10bp intron

cDNA

1-cdna

TCGCCCTCACGCCTCTCACTCCGACCGCCGAATTCGGCCACTGATGACCGTAGCCACCA

GTGGAACCGCCTCCCAACCGGTGTAGCCACCATGTGATCCAGTCTCCACACGCGGATC

CCCTAACCTCCACCGCAGTTCTCAGGGGATGGAGGACCGACGCCCTCCACAAATGGCGACC

ICATGGAGGCCGGATCCGACCTTCCCGGCCCTCGTCTCCCATCTCTCTAATATATTCTC

TTTAGCAGATCTGGAGCAATCAAACCATTTACCATTTGTTACGATTGAAACATGTTTCT

AAATTTGTGCAAAAGGTAGCGATTGGAGAAGCGAGCCCCATCTTTATGTCAGTCCCAAAG

GTGTCATCATCTTGTTCCTCCCTAAGTTTCTGAAGTAGATCGATAGTACAGAGGAGATTG

TGTATATTTTATATTTGTCGATGATGGGTATTTGGTGTGTGCAAAATCTCAGGCATGC

ATAATTTTAATTTACTACCATGTATCAACACGTTTATTGACCATGATGTTGCCATAGTT

TTGGTATAGATTAGTTTAAAAAGAGTCAAGAGTTACACCTACTGACTACAGGTGTTTCTCGGTGTGACCGCATCTTTGTTCTGAG

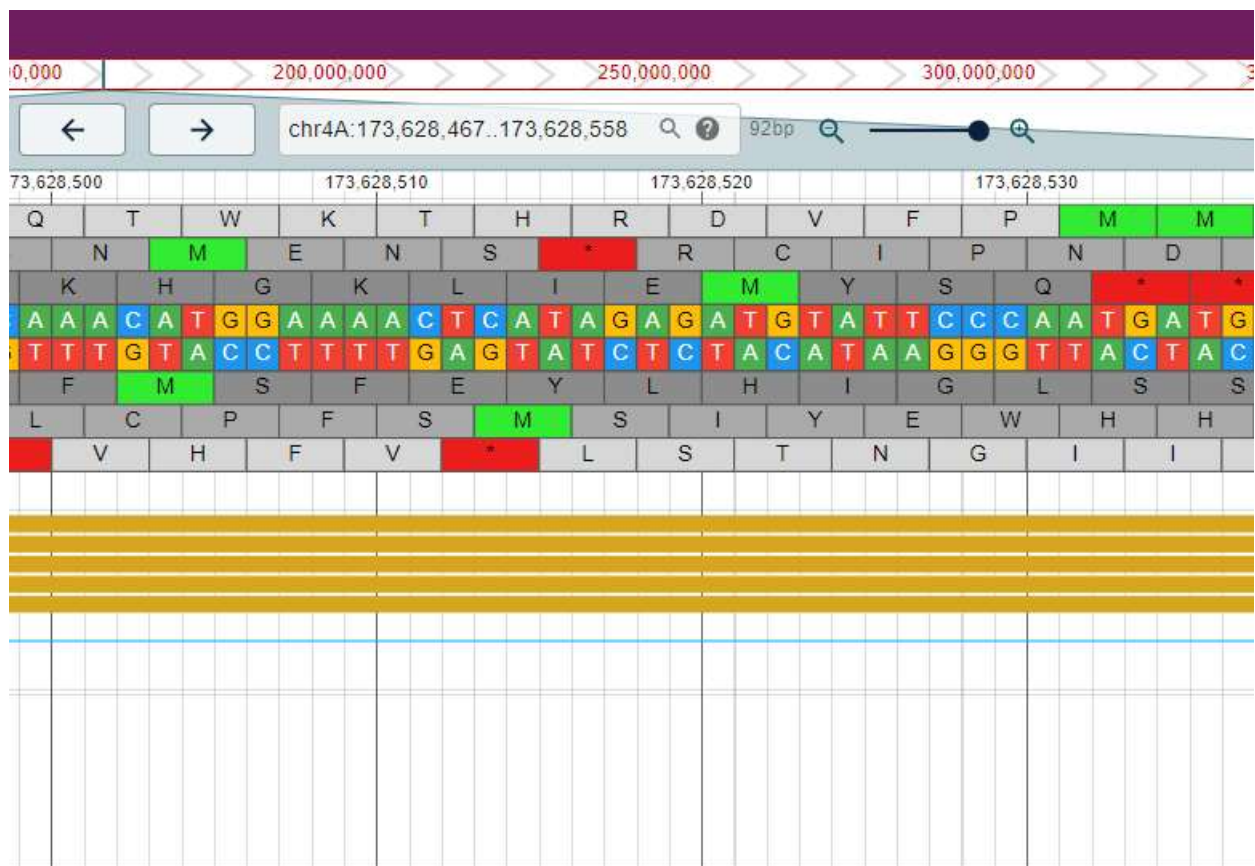
GCTTCCTCTCGGACAAAACCTTGGTTCTGTAGCGTGTGTTTCTTTCTTGTGTTTTTTCATGTGTGCGACTGGCCGTGATCTTCTG

TTTGACCTGATCGTGATCTTTGTCAGTGTGTTTATTGGTTGAGCAGCGGGTATACAAGAATTGGACAGCAGAATCTTCAGAGGTGGT

TCTGATCTTCAGCAAAATCTCACTGAATCACGCTTCCCTCGGGTAGTATCACGGCCGTCGACGATCTCATCTCTACCCCAATTAGTC

7. Reference genome bases view

Individual base-pair can be view by zooming in the reference tracks



8. Genetic variants view

Genetic variants, including SNP and Indel, can be view by clicking on the variant positions

Home ... (default: PepsiCo OT3098 v2 - A. sativa 6x)

Feature details

INSERTION

Core details

Position	chr4A:173,628,469..173,628,469
Description	insertion A -> ACCATATTAGT
Length	1
Type	insertion

Attributes

CHROM	chr4A
POS	173628469
ALT	ACCATATTAGT
INFO ANN	

ACCATATTAGT[frameshift_variant][HIGH][AVESA.00001b.r3.4Ag0000436][AVESA.00001b.r3.4Ag0000436][transcript][AVESA.00001b.r3.4Ag0000436.2][protein_coding][2/2][c.2595_2596insACTAATATGG][p.Ter866fs(2595/3865;2595/3865/865/1287)][WARNING_TRANSCRIPT_MULTIPLE_STOP_CODONS]

ACCATATTAGT[frameshift_variant][HIGH][AVESA.00001b.r3.4Ag0000436][AVESA.00001b.r3.4Ag0000436][transcript][AVESA.00001b.r3.4Ag0000436.3][protein_coding][4/4][c.1334_1335insACTAATATGG][p.Asn446fs(1334/2603;1334/2603/445/866)][WARNING_TRANSCRIPT_MULTIPLE_STOP_CODONS]

ACCATATTAGT[frameshift_variant][HIGH][AVESA.00001b.r3.4Ag0000436][AVESA.00001b.r3.4Ag0000436][transcript][AVESA.00001b.r3.4Ag0000436.4][protein_coding][3/3][c.2556_2557insACTAATATGG][p.Ter853fs(2556/2765;2556/2765/852/920)][WARNING_TRANSCRIPT_MULTIPLE_STOP_CODONS]

ACCATATTAGT[frameshift_variant][stop_gained][HIGH][AVESA.00001b.r3.4Ag0000436][AVESA.00001b.r3.4Ag0000436][transcript][AVESA.00001b.r3.4Ag0000436.5][protein_coding][4/4][c.1339_1340insACTAATATGG][p.Leu447fs(1339/1545;1339/1545/447/514)][WARNING_TRANSCRIPT_MULTIPLE_STOP_CODONS]

ACCATATTAGT[intron_variant][MODIFIER][AVESA.00001b.r3.4Ag0000436][AVESA.00001b.r3.4Ag0000436][transcript][AVESA.00001b.r3.4Ag0000436.1][protein_coding][4/5][c.1375+11_1375+12insACTAATATGG][WARNING_TRANSCRIPT_MULTIPLE_STOP_CODONS]

INFO LOF (AVESA.00001b.r3.4Ag0000436)[AVESA.00001b.r3.4Ag0000436/5](0.80)

REF A

FILTER PASS

QUAL 31.88

ANN TABLE

Feature	Start	End	Score	Annotation
ACCATATTAGT	173628469	173628470	31.88	insertion A -> ACCATATTAGT