Когда известно название гена

Search: All species for VIT_01s0011g00960 Go

e.g. Carboxy* or chx28

Favourite genomes

Arabidopsis thaliana
TAIR10

Oryza sativa Japonica
IRGSP-1.0

Triticum aestivum
TGACv1

Hordeum vulgare
ASM32608v1

Zea mays
AGPv4

Physcomitrella patens
ASM242v1

Edit favourites

All genomes

-- Select a species --

View full list of all Ensembl Plants species

What's New in Release 35

- Updated genomes

New Bread Wheat Genome Assembly

A new genome assembly of *Triticum aestivum* cv. Chinese Spring is now available in Ensembl Plants. The assembly (TGACv1) and it's accompanying annotation was produced by the Earlham Institute, formerly The Centre for Genome Analysis (TGAC), as part of the Triticeae Genomics for Sustainable Agriculture project.

The assembly has a scaffold N50 of 88 Kbp and a total length of 13.4 Gbp in contigs greater than 500 bp (read more). The gene model annotation consists of 217,907 loci and 273,739 transcripts. A total of 104,09 protein coding genes (154,798 transcripts) and 10,156 long ncRNAs have been annotated with high confidence (read more). Approximately 99,000 genes (99% of the total) annotated on the previous IWGSC CSS assembly (MIPS) have been mapped to the new assembly.

The Axiom 35k and 820k SNP marker sets have been provided by CerealsDB and located on the new assembly (read more).

Ensembl Plants Archive Site

Alongside release 32 we have launched a new archive site, where we will keep selected previous releases of Ensembl Plants publicly available. The first release available on the archive site is release 31, and includes the previous assemblies for wheat and maize.

Ensembl Plants is developed in coordination with other plant genomics and bioinformatics groups via the EBI's role in the transPLANT consortium. The transPLANT project is funded by the European Commission within its 7th Framework Programme, under the thematic area "Infrastructures", contract number 283496.

Part of the transPLANT European Plant Genomics Infrastructure

Search Ensembl Plants
- New Search
- Gene (1)
  - Ensembl Plants (1)

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Ensembl Plants is produced in collaboration with Gramene

Search results for 'VIT_01s0011g00960'

Showing 1 Gene found in Ensembl Plants

VIT_01s0011g00960

Description	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F6HEY8]
Gene ID	VIT_01s0011g00960
Species	Vitis vinifera
Location	1:812008-816090
Gene trees	EPIGT00820000103231 (Plant Compara) EGGT00130000085269 (Pan-taxonomic Compara)

Ensembl Plants release 35 - April 2017 © EMBL-EBI

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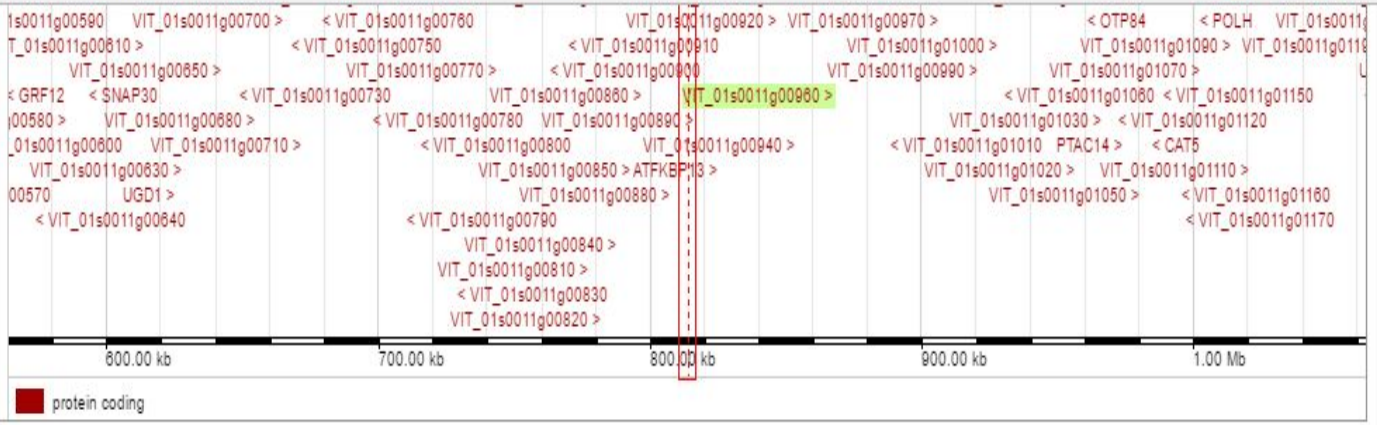
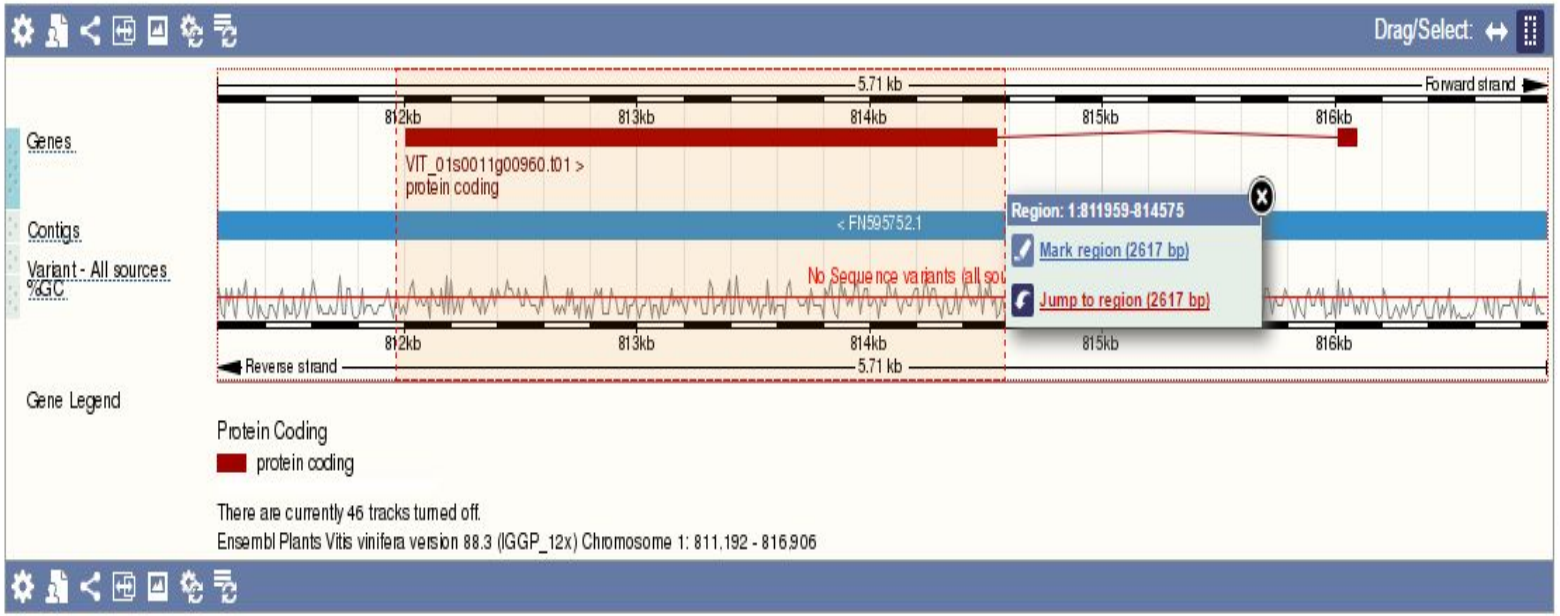


Location: 1:811192-816906 Go Gene: Go



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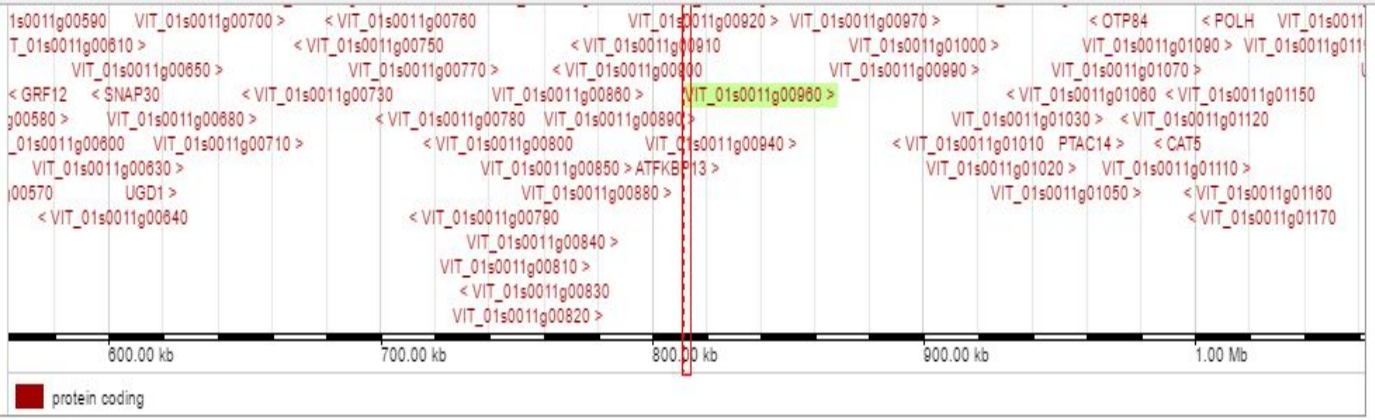
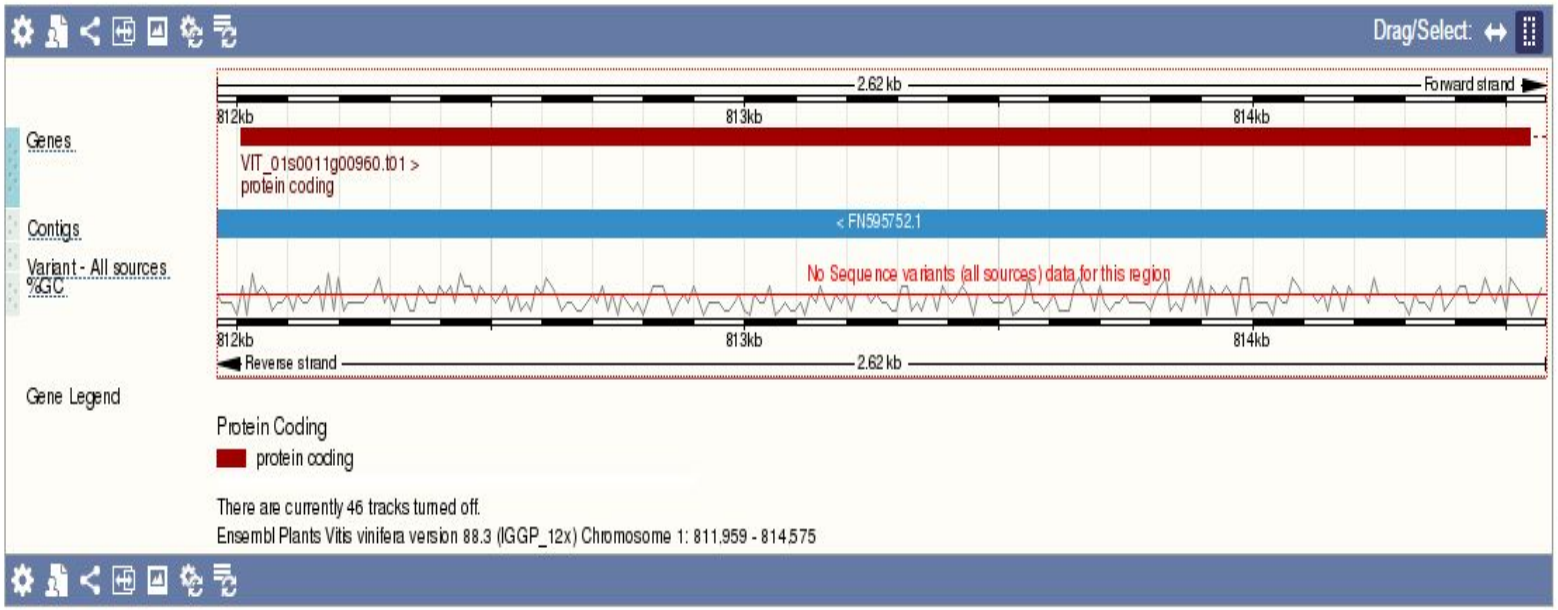
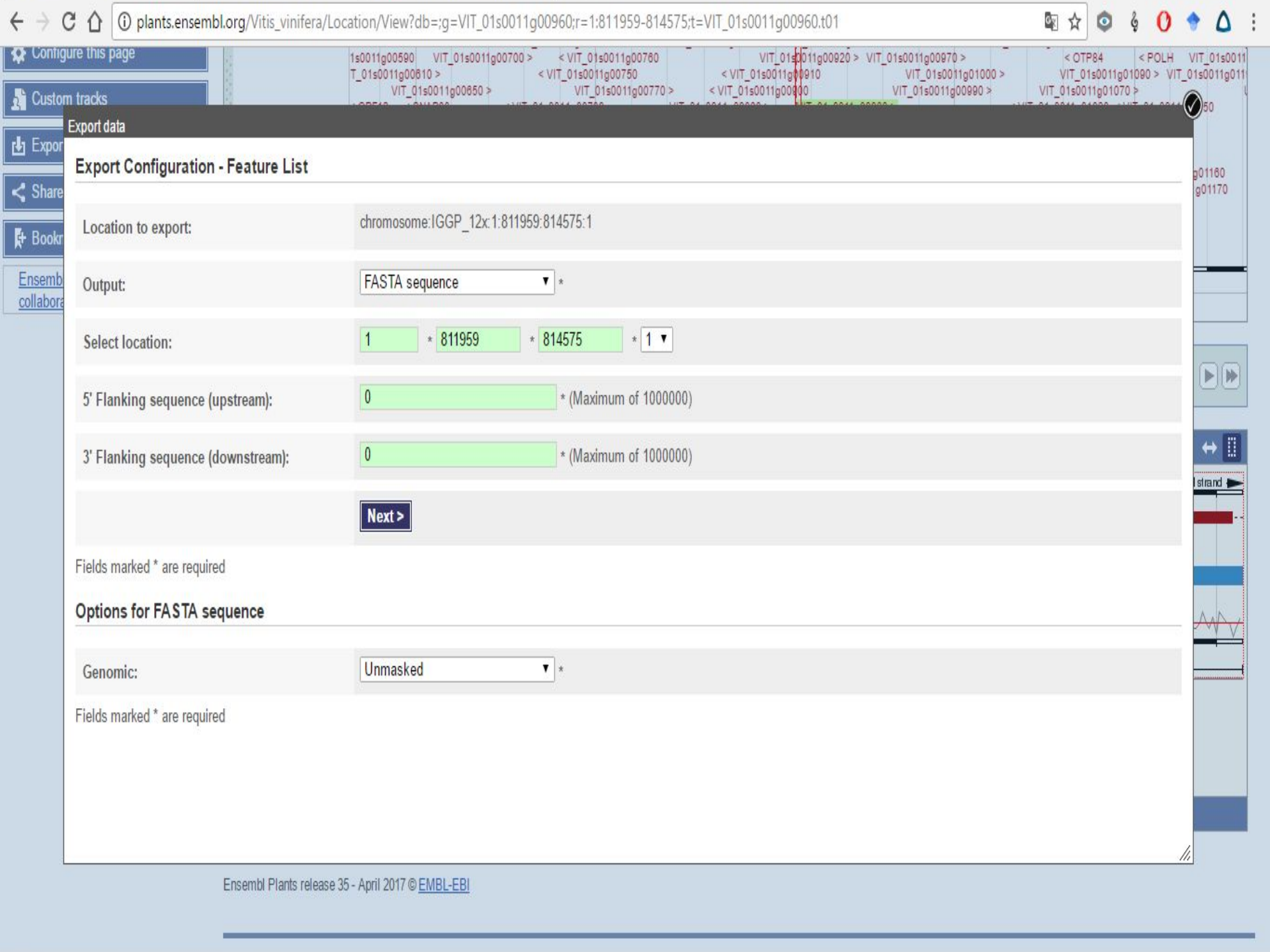
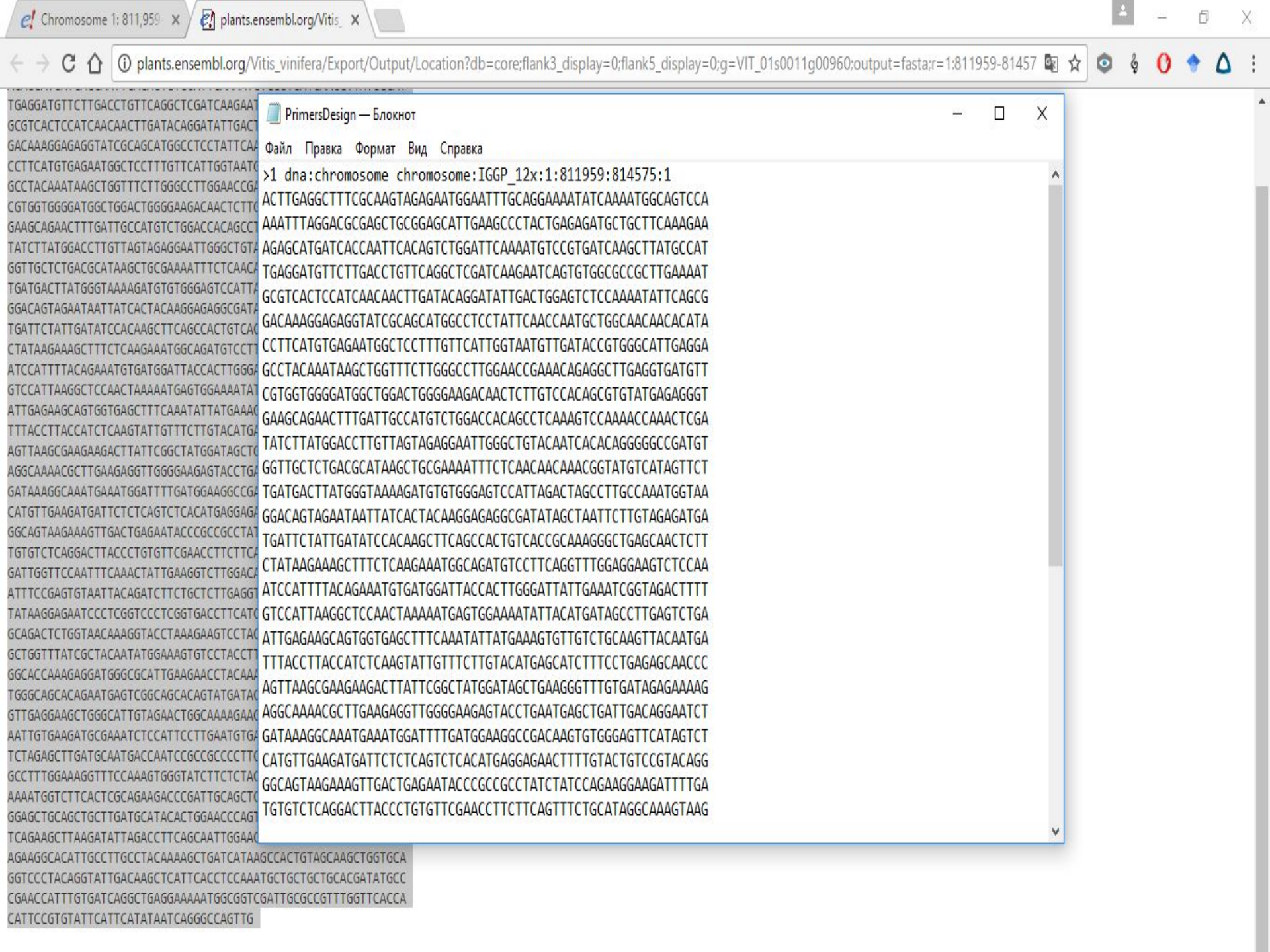


Location: 1:811959-814575 Go Gene: Go




plants.ensembl.org/Vitis_vinifera/Location/View?db=:g=VIT_01s0011g00960;r=1:811959-814575;t=VIT_01s0011g00960.t01
Configure this page
Custom tracks
Export data
Export Configuration - Feature List
Location to export:
chromosome:IGGP_12x:1:811959:814575:1
Output:
FASTA sequence
Select location:
1
811959
814575
1
5' Flanking sequence (upstream):
0
(Maximum of 1000000)
3' Flanking sequence (downstream):
0
(Maximum of 1000000)
Next >
Fields marked * are required
Options for FASTA sequence
Genomic:
Unmasked
Fields marked * are required
Ensembl Plants release 35 - April 2017 © EMBL-EBI


Chromosome 1: 811,959
plants.ensembl.org/Vitis_
plants.ensembl.org/Vitis_vinifera/Export/Output/Location?db=core;flank3_display=0;flank5_display=0;g=VIT_01s0011g00960;output=fasta;r=1:811959-81457
PrimersDesign — Блокнот
Файл Правка Формат Вид Справка
>1 dna:chromosome chromosome:IGGP_12x:1:811959:814575:1
ACTTGAGGCTTTCGCAAGTAGAGAATGGAATTTGCAGGAAAATATCAAAATGGCAGTCCA
AAATTTAGGACGCGAGCTGCGGAGCATTGAAGCCCTACTGAGAGATGCTGCTTCAAAGAA
AGAGCATGATCACCAATTCACAGTCTGGATTCAAAATGTCCGTGATCAAGCTTATGCCAT
TGAGGATGTTCTTGACCTGTTCAGGCTCGATCAAGAATCAGTGTGGCGCCGCTTGAAAAT
GCGTCACTCCATCAACAACTTGATACAGGATATTGACTGGAGTCTCCAAAATATTCAGCG
GACAAAGGAGAGGTATCGCAGCATGGCCTCCTATTCAACCAATGCTGGCAACAACACATA
CCTTCATGTGAGAATGGCTCCTTTGTTCATTGGTAATGTTGATACCGTGGGCATTGAGGA
GCCTACAAATAAGCTGGTTTCTTGGGCCTTGGAACCGAAACAGAGGCTTGAGGTGATGTT
CGTGGTGGGGATGGCTGGACTGGGGAAGACAACTCTTGTCCACAGCGTGTATGAGAGGGT
GAAGCAGAACTTTGATTGCCATGTCTGGACCACAGCCTCAAAGTCCAAAACCAAACTCGA
TATCTTATGGACCTTGTTAGTAGAGGAATTGGGCTGTACAATCACACAGGGGGCCGATGT
GGTTGCTCTGACGCATAAGCTGCGAAAATTTCTCAACAACAAACGGTATGTCATAGTTCT
TGATGACTTATGGGTAAAAGATGTGTGGGAGTCCATTAGACTAGCCTTGCCAAATGGTAA
GGACAGTAGAATAATTATCACTACAAGGAGAGGCGATATAGCTAATTCTTGTAGAGATGA
TGATTCTATTGATATCCACAAGCTTCAGCCACTGTCACCGCAAAGGGCTGAGCAACTCTT
CTATAAGAAAGCTTTCTCAAGAAATGGCAGATGTCCTTCAGGTTTGGAGGAAGTCTCCAA
ATCCATTTTACAGAAATGTGATGGATTACCACTTGGGATTATTGAAATCGGTAGACTTTT
GTCCATTAAGGCTCCAACTAAAAATGAGTGGAAAATATTACATGATAGCCTTGAGTCTGA
ATTGAGAAGCAGTGGTGAGCTTTCAAATATTATGAAAGTGTTGTCTGCAAGTTACAATGA
TTTACCTTACCATCTCAAGTATTGTTTCTTGTACATGAGCATCTTTCCTGAGAGCAACCC
AGTTAAGCGAAGAAGACTTATTCGGCTATGGATAGCTGAAGGGTTTGTGATAGAGAAAAG
AGGCAAAACGCTTGAAGAGGTTGGGGAAGAGTACCTGAATGAGCTGATTGACAGGAATCT
GATAAAGGCAAATGAAATGGATTTTGATGGAAGGCCGACAAGTGTGGGAGTTCATAGTCT
CATGTTGAAGATGATTCTCTCAGTCTCACATGAGGAGAACTTTTGTACTGTCCGTACAGG
GGCAGTAAGAAAGTTGACTGAGAATACCCGCCGCCTATCTATCCAGAAGGAAGATTTTGA
TGTGTCTCAGGACTTACCCTGTGTTCGAACCTTCTTCAGTTTCTGCATAGGCAAAGTAAG

Primer3 (v. 0.4.0) Pick primers from a DNA sequence.

There is a newer version of Primer3 available at http://primer3.ut.ee

Paste source sequence below (5'->3', string of ACGTNacgtn -- other letters treated as N -- numbers and blanks ignored). FASTA format ok. Please N-out undesirable sequence (vector, ALUs, LINEs, etc.) or use a Mispriming Library (repeat library): NONE

```
ACTTGAGGCTTTCGCAAGTAGAGAATGGAATTTGCAGGAAAATATCAAAATGGCAGTCCA
AAATTTAGGACGCGAGCTGCGGAGCATTGAAGCCCTACTGAGAGATGCTGCTTCAAAGAA
AGAGCATGATCACCAATTCACAGTCTGGATTCAAAATGTCCGTGATCAAGCTTATGCCAT
TGAGGATGTTCTTGACCTGTTCAGGCTCGATCAAGAATCAGTGTGGCGCCGCTTGAAAAT
GCGTCACTCCATCAACAACTTGATACAGGATATTGACTGGAGTCTCCAAAATATTCAGCG
GACAAAGGAGAGGTATCGCAGCATGGCCTCCTATTCAACCAATGCTGGCAACAACACATA
```

Pick left primer, or use left primer below:	Pick hybridization probe (internal oligo), or use oligo below:	Pick right primer, or use right primer below (5' to 3' on opposite strand):

Pick Primers | Reset Form

Sequence Id: A string to identify your output.

Targets: E.g. 50,2 requires primers to surround the 2 bases at positions 50 and 51. Or mark the source sequence with [and]: e.g. ...ATCT[CCCC]TCAT.. means that primers must flank the central CCCC.

Excluded Regions: E.g. 401,7 68,3 forbids selection of primers in the 7 bases starting at 401 and the 3 bases at 68. Or mark the source sequence with < and >: e.g. ...ATCT<CCCC>TCAT.. forbids primers in the central CCCC.

Product Size Ranges: 1900-2100

Number To Return	5	Max 3' Stability	9.0
Max Repeat Mispriming	12.00	Pair Max Repeat Mispriming	24.00
Max Template Mispriming	12.00	Pair Max Template Mispriming	24.00

Pick Primers | Reset Form

2521 CGAACCATTTGTGATCAGGCTGAGGAAAAATGGCGGTCGATTGCGCCGTTTGGTTCACCA

2581 CATTCCGTGTATTCATTCATATAATCAGGGCCAGTTG

KEYS (in order of precedence):
>>>>>> left primer
<<<<<< right primer

ADDITIONAL OLIGOS

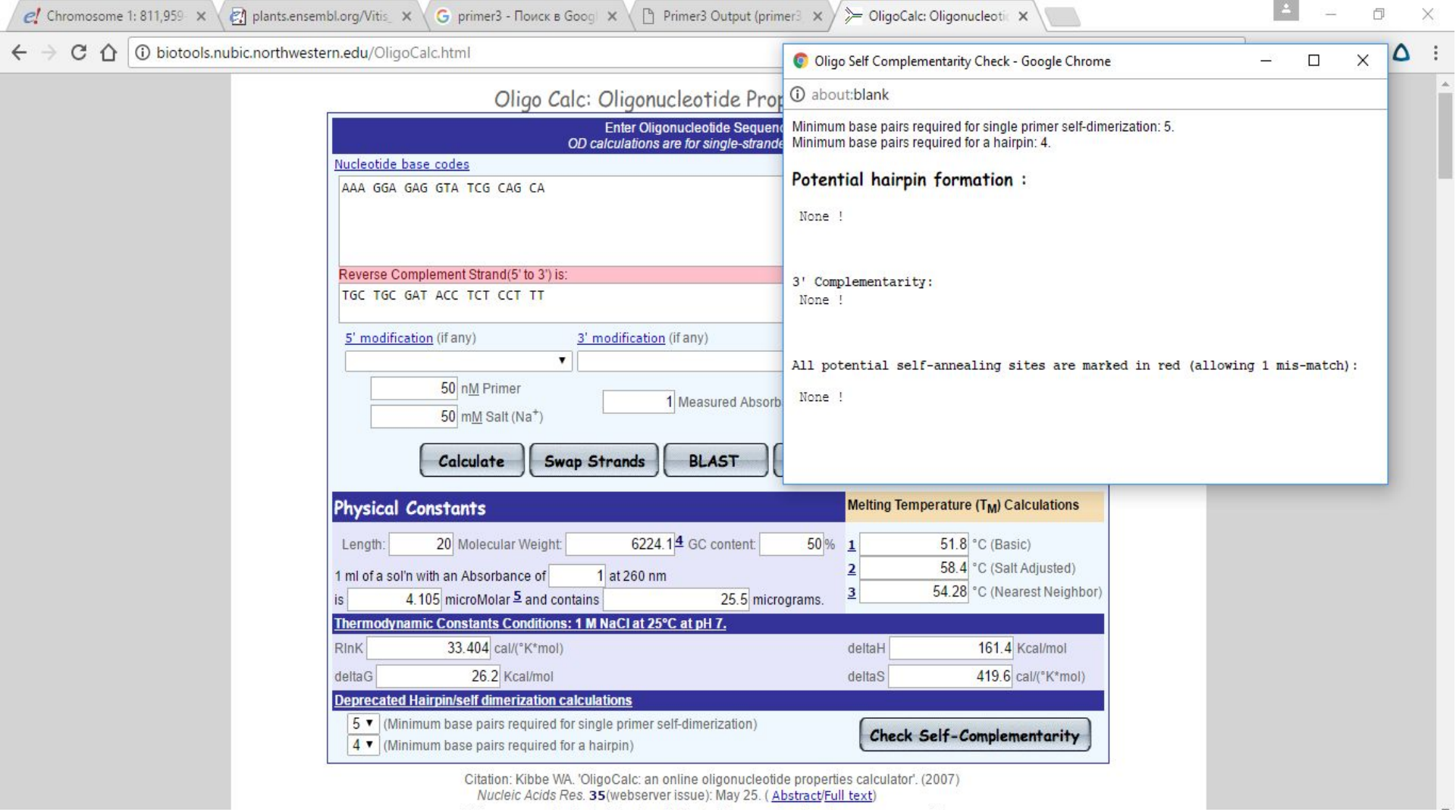
	start	len	tm	gc%	any	3'	seq
1 LEFT PRIMER	304	20	59.98	50.00	3.00	1.00	AAAGGAGAGGTATCGCAGCA
RIGHT PRIMER	2344	20	60.04	45.00	7.00	1.00	CTGAAATTTTCCCGACCTGA
PRODUCT SIZE: 2041, PAIR ANY COMPL: 4.00, PAIR 3' COMPL: 1.00							
2 LEFT PRIMER	304	20	59.98	50.00	3.00	1.00	AAAGGAGAGGTATCGCAGCA
RIGHT PRIMER	2345	20	60.04	45.00	7.00	1.00	TCTGAAATTTTCCCGACCTG
PRODUCT SIZE: 2042, PAIR ANY COMPL: 4.00, PAIR 3' COMPL: 2.00							
3 LEFT PRIMER	374	20	59.93	45.00	3.00	2.00	ATGGCTCCTTTGTTCATTGG
RIGHT PRIMER	2383	20	59.99	45.00	6.00	1.00	CAGCTGTTCCAATTGCTGAA
PRODUCT SIZE: 2010, PAIR ANY COMPL: 5.00, PAIR 3' COMPL: 3.00							
4 LEFT PRIMER	396	20	60.08	45.00	3.00	1.00	ATGTTGATACCGTGGGCATT
RIGHT PRIMER	2383	20	59.99	45.00	6.00	1.00	CAGCTGTTCCAATTGCTGAA
PRODUCT SIZE: 1988, PAIR ANY COMPL: 3.00, PAIR 3' COMPL: 2.00							

Statistics

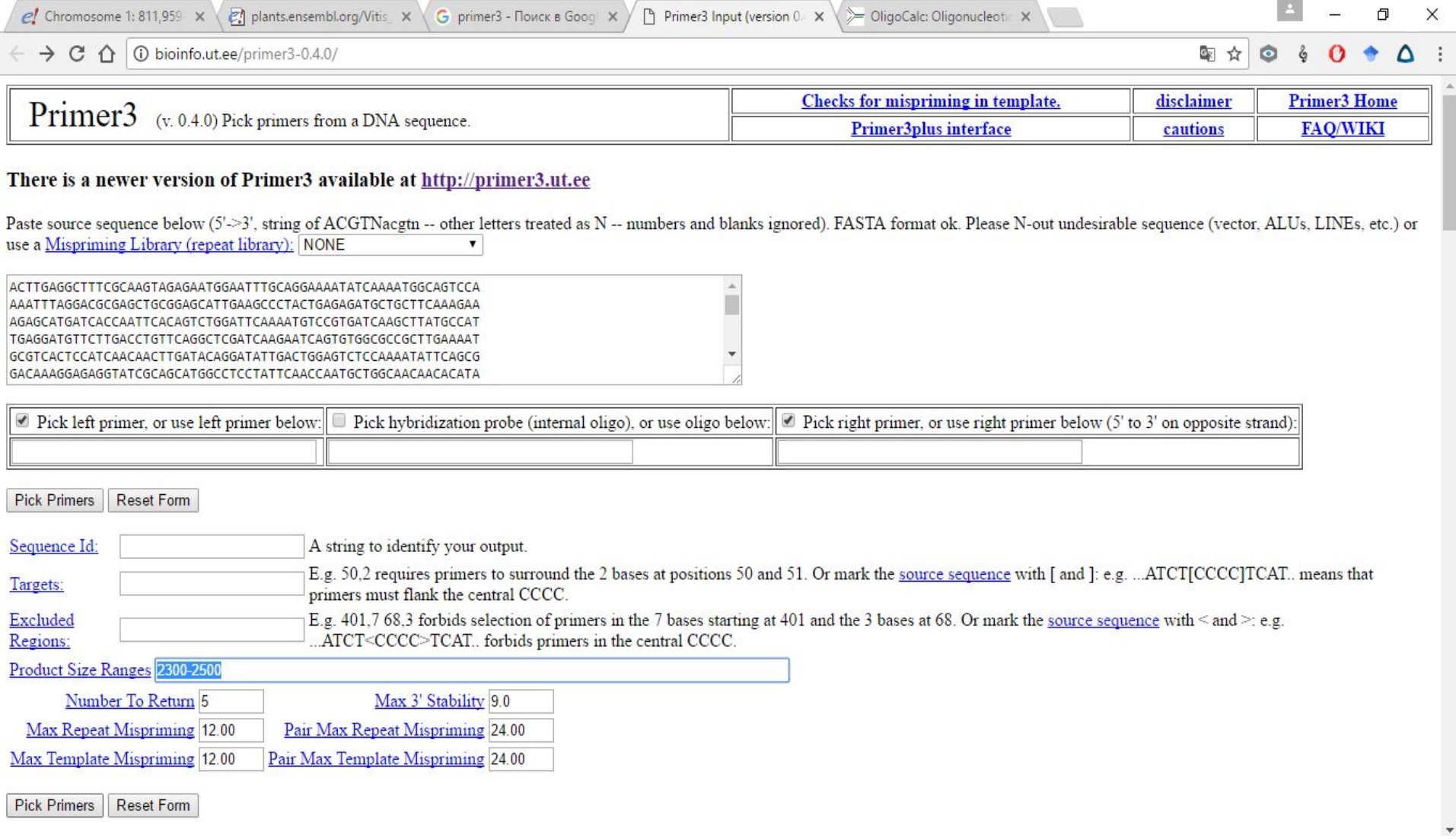
	con sidered	too many Ns	in tar get	in excl reg	bad GC%	no GC clamp	tm too low	tm too high	high any compl	high 3' compl	poly X	high end stab	ok
Left	6394	0	0	0	0	0	1828	2695	0	1	0	105	1765
Right	6294	0	0	0	2	0	1825	2762	0	2	0	114	1589

Pair Stats:
considered 52, unacceptable product size 44, ok 8
primer3 release 1.1.4

(primer3_results.cgi release 0.4.0)



Со всеми обратным праймерами проблемы, поэтому нужно подобрать другие им на замену.



- Ничего страшного. Просто расширяем зону поиска сайтов посадки праймеров.

```
 2521 CGAACCATTTGTGATCAGGCTGAGGAAAAATGGCGGTCGATTGCGCCGTTTGGTTCACCA


 2581 CATTCCGTGTATTCATTCATATAATCAGGGCCAGTTG


KEYS (in order of precedence):
>>>>>> left primer
<<<<<< right primer

ADDITIONAL OLIGOS
                  start  len      tm      gc%   any   3'  seq

 1 LEFT PRIMER        81   20   59.84   55.00  3.00  1.00 GGAGCATTGAAGCCCTACTG
   RIGHT PRIMER     2414   20   60.08   45.00  4.00  1.00 GCAATGTGCCTTCTTCCATT
   PRODUCT SIZE: 2334, PAIR ANY COMPL: 5.00, PAIR 3' COMPL: 2.00

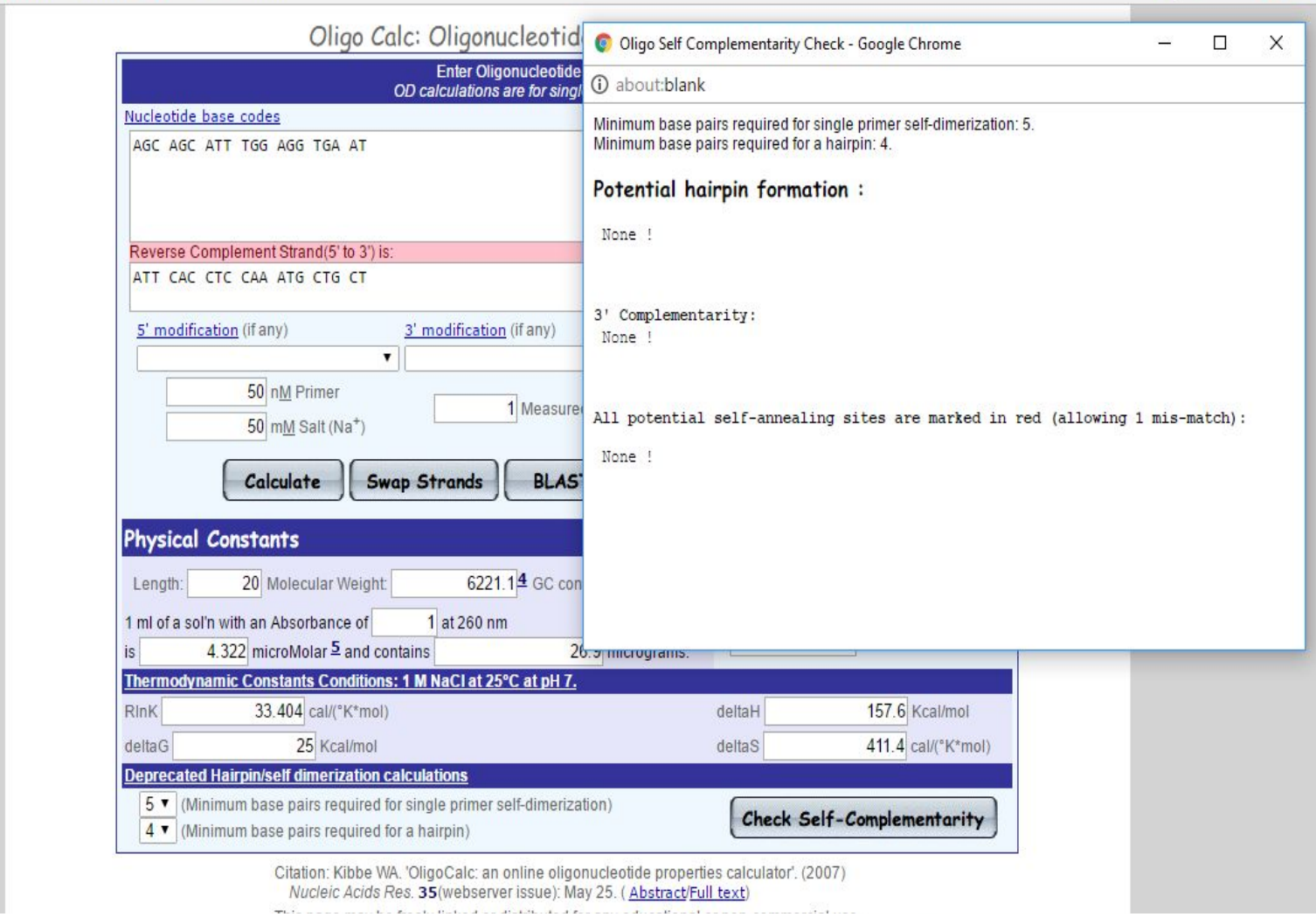
 2 LEFT PRIMER       146   20   59.90   40.00  4.00  2.00 TGGATTCAAAATGTCCGTGA
   RIGHT PRIMER     2505   20   59.70   45.00  3.00  2.00 AGCAGCATTTGGAGGTGAAT
   PRODUCT SIZE: 2360, PAIR ANY COMPL: 6.00, PAIR 3' COMPL: 1.00

 3 LEFT PRIMER        81   20   59.84   55.00  3.00  1.00 GGAGCATTGAAGCCCTACTG
   RIGHT PRIMER     2426   20   59.73   45.00  3.00  2.00 TTTGTAGGCAAGGCAATGTG
   PRODUCT SIZE: 2346, PAIR ANY COMPL: 5.00, PAIR 3' COMPL: 1.00

 4 LEFT PRIMER       146   20   59.90   40.00  4.00  2.00 TGGATTCAAAATGTCCGTGA
   RIGHT PRIMER     2532   20   59.65   45.00  4.00  2.00 ACAAATGGTTCGGGCATATC
   PRODUCT SIZE: 2387, PAIR ANY COMPL: 5.00, PAIR 3' COMPL: 2.00

Statistics
         con   too    in    in          no    tm    tm  high  high        high
         sid  many   tar  excl   bad    GC   too   too   any    3'  poly   end
        ered    Ns   get   reg   GC% clamp   low  high compl compl     X  stab    ok
Left    2886     0     0     0     0     0   821  1190     1     4     0    39   831
Right   2839     0     0     0     2     0   795  1277     0     2     0    45   718
Pair Stats:
considered 329, unacceptable product size 304, high end compl 6, ok 19
primer3 release 1.1.4


(primer3_results.cgi release 0.4.0)
```



- Остальные два праймера тоже хорошо подходят, но тут нужно выбирать в зависимости от цели, какой длины ПЦР продукт нужен.

Primer-BLAST

A tool for finding specific primers

NCBI/ Primer-BLAST: Finding primers specific to your PCR template (using Primer3 and BLAST).

Reset page | Save search parameters | Retrieve recent results | Publication | Tips for finding specific primers

PCR Template

Enter accession, gi, or FASTA sequence (A refseq record is preferred) Clear

```
ACTTGAGGCTTTCGCAAGTAGAGAATGGAATTTGCAGGAAAATATCAAAATGGCAGTCCA
AAATTTAGGACGCGAGCTGCGGAGCATTGAAGCCCTACTGAGAGATGCTGCTTCAAAGAA
AGAGCATGATCACCAATTCACAGTCTGGATTCAAAATGTCCGTGATCAAGCTTATGCCAT
TGAGGATGTTCTTGACCTGTTCAGGCTCGATCAAGAATCAGTGTGGCGCCGCTTGAAAAT
GCGTCACTCCATCAACAACTTGATACAGGATATTGACTGGAGTCTCCAAAATATTCAGCG
```

Range

	From	To	
Forward primer			Clear
Reverse primer			

Or, upload FASTA file: Выберите файл — Файл не выбран

Primer Parameters

Use my own forward primer (5'->3' on plus strand)	AAAGGAGAGGTATCGCAGCA	Clear
Use my own reverse primer (5'->3' on minus strand)	AGCAGCATTTGGAGGTGAAT	Clear

	Min	Max
PCR product size	70	1000
# of primers to return	10	

	Min	Opt	Max	Max Tm difference
Primer melting temperatures (Tm)	57.0	60.0	63.0	3

Exon/intron selection

A refseq mRNA sequence as PCR template input is required for options in the section

Exon junction span: No preference

Exon junction match

Exon at 5' side	Exon at 3' side
7	4

Minimal number of bases that must anneal to exons at the 5' or 3' side of the junction

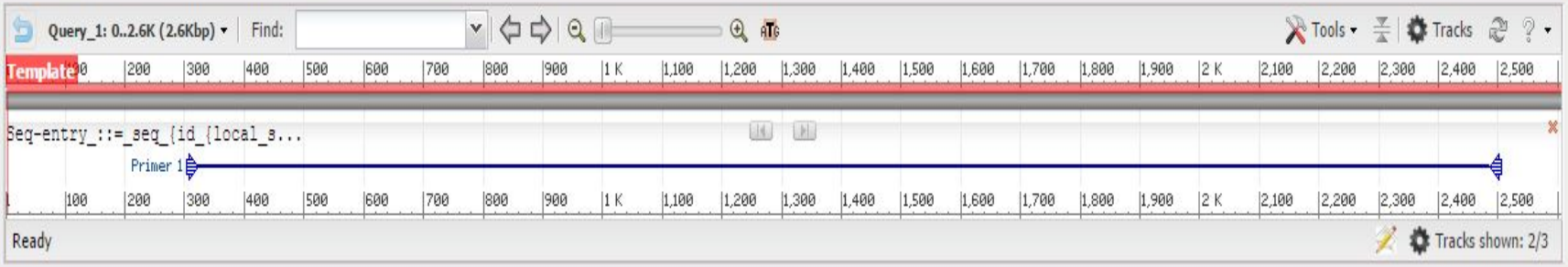
Intron inclusion: Primer pair must be separated by at least one intron on the corresponding genomic DNA

Intron length range

Min	Max
1000	1000000

Input PCR template
Range 1 - 2617
Specificity of primers primers may **not** be specific to the input PCR template as targets were found in selected database:Refseq mRNA (Organism limited to Homo sapiens)...help on specific primers
Other reports Search Summary

Graphical view of primer pairs



Detailed primer reports

Primer pair 1

	Sequence (5'->3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	AAAGGAGAGGTATCGCAGCA	Plus	20	304	323	58.80	50.00	3.00	1.00
Reverse primer	AGCAGCATTTGGAGGTGAAT	Minus	20	2505	2486	57.77	45.00	3.00	2.00
Product length	2202								

Products on potentially unintended templates

>XM_017024298.1 PREDICTED: Homo sapiens dishevelled segment polarity protein 2 (DVL2), transcript variant X5, mRNA

```
product length = 136
Forward primer  1    AAAGGAGAGGTATCGCAGCA  20
Template        707  TG........G...C.....  688
```

Когда есть «неизвестная» последовательность ДНК

На примере гена NBS-LRR гена детекции патогенов у люцерны (давайте сделаем вид, что сиквенс действительно случайный)

Web Tools
- Web Tools
  - BLAST
  - Variant Effect Predictor
  - Assembly Converter
  - ID History Converter

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BLAST search

Sequence data:

```
>
TTTCAAATGGGTGGATTGCCTTCCAACTTGGCCGACCTTTATATAGAGAATTGCCCAAAA
CTGATTGCTTCAAGAAAGGAGTGGGGTTTGTTCCAACTCAATTCCTTGAAGTCATTCTTC
ATCAGTAATGAGTTTGAAAACGTGGAGTCATTCCCAGAGAAGAATCTGCTGCCACCAACT
CTTCAAACTCTTTGTATTAATGATTGTTCAAAGCTAAGAATAATGAACAACAAGGGTTTT
CTCCACCTCAAATCTCTCATAGAACTACATATTTGGAACTGTCCTATTCTTGAGCGCTTG
CCAGAGGAGGCTCTACCCAACACCCTTACTTCTATTGAAATTTCCGATTGTCCATTAATT
AAAGGGAAGTATGAAAAGGAGGGAGGAGAGAATTGGCATACAATTAGTCACATCCCTCAT
GTGACGATTGACGGAATTGAGCAGAAATGAGCTAA
```

Add more sequences (1 sequence added, 29 more sequences allowed)

- (•) DNA
- ( ) Protein

Search against:

Medicago truncatula X

Add/remove species

- (•) DNA database — Genomic sequence ▾
- ( ) Protein database — Proteins ▾

Search tool: BLASTN ▾

Search Sensitivity: Normal ▾

Web Tools
- Web Tools
  - BLAST
  - Variant Effect Predictor
  - Assembly Converter
  - ID History Converter

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BLAST search

New job

Recent jobs

Refresh

Show/hide columns (1 hidden) Filter

Analysis	Jobs			Submitted at
BLASTN	BLASTN against Medicago truncatula MedtrA17_4.0 (Genomic sequence)	Done: 237 hits found	View results	15/05/2017, 11:07 (BST)

plants.ensembl.org/Multi/Tools/Blast/View?db=core;tl=VPv2HPtFZOqOIgFR-17858918

Web Tools
- Web Tools
  - BLAST
    - Ticket
      - BLASTN against Medicag
  - Variant Effect Predictor
  - Assembly Converter
  - ID History Converter

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Results for BLASTN against Medicago truncatula MedtrA17_4.0 (Genomic sequence)

Job details

Job name: BLASTN against Medicago truncatula MedtrA17_4.0 (Genomic sequence)

Species: Medicago truncatula

Assembly: MedtrA17_4.0

Search type: BLASTN (NCBI BLAST)

Download results file

Results table

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

Genomic Location	Overlapping Gene(s)	Orientation	Length	Score	E-val	%ID
scaffold2053:198-652 [Sequence]	MTR_2053s0010	Forward	455 [Sequence]	455	0.0	100.0 [Alignment]
scaffold1643:3-133 [Sequence]		Reverse	131 [Sequence]	99	1.1E-48	93.9 [Alignment]
3:6733583-6733716 [Sequence]	MTR_3g022600	Reverse	134 [Sequence]	94	1.0E-45	92.5 [Alignment]
3:6941721-6941824 [Sequence]	MTR_3g023020	Reverse	104 [Sequence]	72	1.4E-32	92.3 [Alignment]
3:8571018-8571148 [Sequence]	MTR_3g027420	Forward	131 [Sequence]	67	1.3E-29	87.8 [Alignment]
3:6523624-6523683 [Sequence]	MTR_3g022230	Forward	60 [Sequence]	60	2.0E-25	100.0 [Alignment]
3:6945053-6945156 [Sequence]	MTR_3g023030	Reverse	104 [Sequence]	60	2.0E-25	89.4 [Alignment]
3:6782319-6782389 [Sequence]	MTR_3g022730	Forward	71 [Sequence]	55	1.9E-22	94.4 [Alignment]
3:8469378-8469448 [Sequence]	MTR_3g027250	Reverse	71 [Sequence]	55	1.9E-22	94.4 [Alignment]
3:6782473-6782529 [Sequence]	MTR_3g022730	Forward	57 [Sequence]	53	3.0E-21	98.2 [Alignment]
3:7585704-7585759 [Sequence]	MTR_3g024460	Reverse	56 [Sequence]	52	1.2E-20	98.2 [Alignment]
scaffold0425:9753-9823 [Sequence]	MTR_0425s0020	Forward	71 [Sequence]	51	4.7E-20	93.0 [Alignment]

Nucleotide BLAST: Searc | BLAST Genomic Sequenc
plants.ensembl.org/Medicago_truncatula/Tools/Blast/GenomicSeq?db=core;tl=VPv2HPtFZOqOlgFR-17858918-258471264

Web Tools
- BLAST
  - Ticket
    - BLASTN against Medicago
      - Alignment
      - Query Sequence
      - Genomic Sequence
- Variant Effect Predictor
- Assembly Converter
- ID History Converter

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BLAST Genomic Sequence

BLAST/BLAT type	BLASTN
Query location	Query_1 1 to 455 (+)
Database location	scaffold2053 198 to 652 (+)
Genomic location	scaffold2053 198 to 652 (+)
Alignment score	455
E-value	0.0
Alignment length	455
Percentage identity	100.0

Exons	All exons
HSP	Location of other alignments Location of selected alignment
Markup	loaded

```
>supercontig:MedtrA17_4.0:scaffold2053:-102:952:1
 -102 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN   -43
  -42 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTCAACAATACCATTCTT    17
   18 GAAGAGTTGAAGTTGGATTTCAGAGGCTGTGTAAACTGTCCCTCTTTGGATTTACGTTGC    77
   78 TATAATTCTCTTTGGAGACTATCAATAAAAGGATGGCACTCATCCTCGTTGCCTTTTTCA   137
  138 CTACACTTGTTCACCAAACTTCATTCTCTGTATCTATACGATTGTCCAGAGCTGGAATGG   197
  198 TTTCAAATGGGTGGATTGCCTTCCAACTTGGCCGACCTTTATATAGAGAATTGCCCAAAA   257
  258 CTGATTGCTTCAAGAAAGGAGTGGGGTTTGTTCCAACTCAATTCCTTGAAGTCATTCTTC   317
  318 ATCAGTAATGAGTTTGAAAACGTGGAGTCATTCCCAGAGAAGAATCTGCTGCCACCAACT   377
  378 CTTCAAACTCTTTGTATTAATGATTGTTCAAAGCTAAGAATAATGAACAACAAGGGTTTT   437
  438 CTCCACCTCAAATCTCTCATAGAACTACATATTTGGAACTGTCCTATTCTTGAGCGCTTG   497
  498 CCAGAGGAGGCTCTACCCAACACCCTTACTTCTATTGAAATTTCCGATTGTCCATTAATT   557
  558 AAAGGGAAGTATGAAAAGGAGGGAGGAGAGAATTGGCATACAATTAGTCACATCCCTCAT   617
  618 GTGACGATTGACGGAATTGAGCAGAAATGAGCTAAATTACCTGAAGTTGTCTTGGAGTTA   677
  678 TTTGTGTTTGTATGTTTTGGGACAGTTTGAGTGATGATTGTGTTAAGAGTGAGTTATTTG   737
  738 TCTTTGTATGTATGATTGTTCCAAGTTAAGAATAATAAACTACACAGGTTTTCTCCACCT   797
  798 TAAATTGGAGTGAGATGTTGCCGCAGGCATACATCCTCTTTTTTGCACATGACCAGTTTG   857
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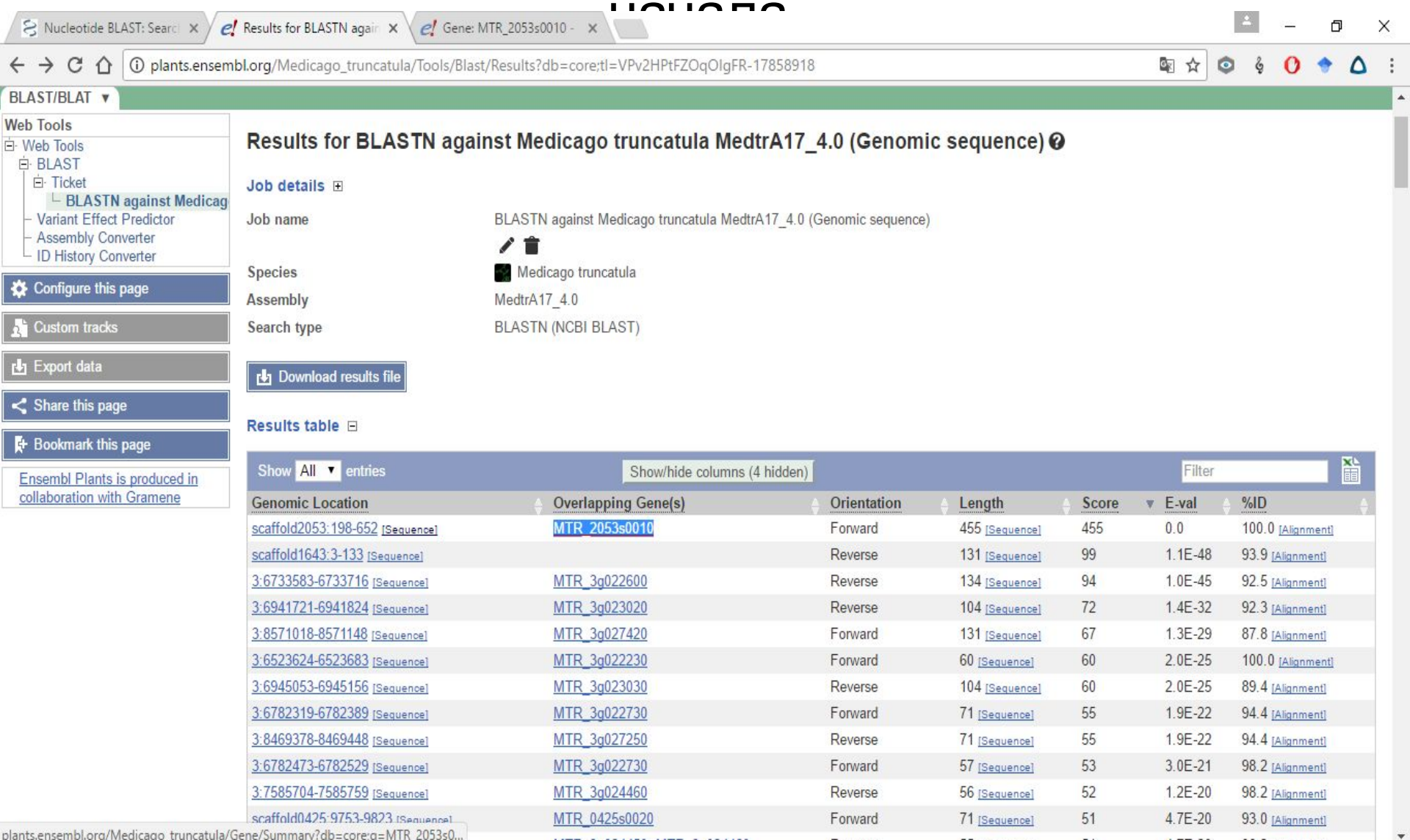
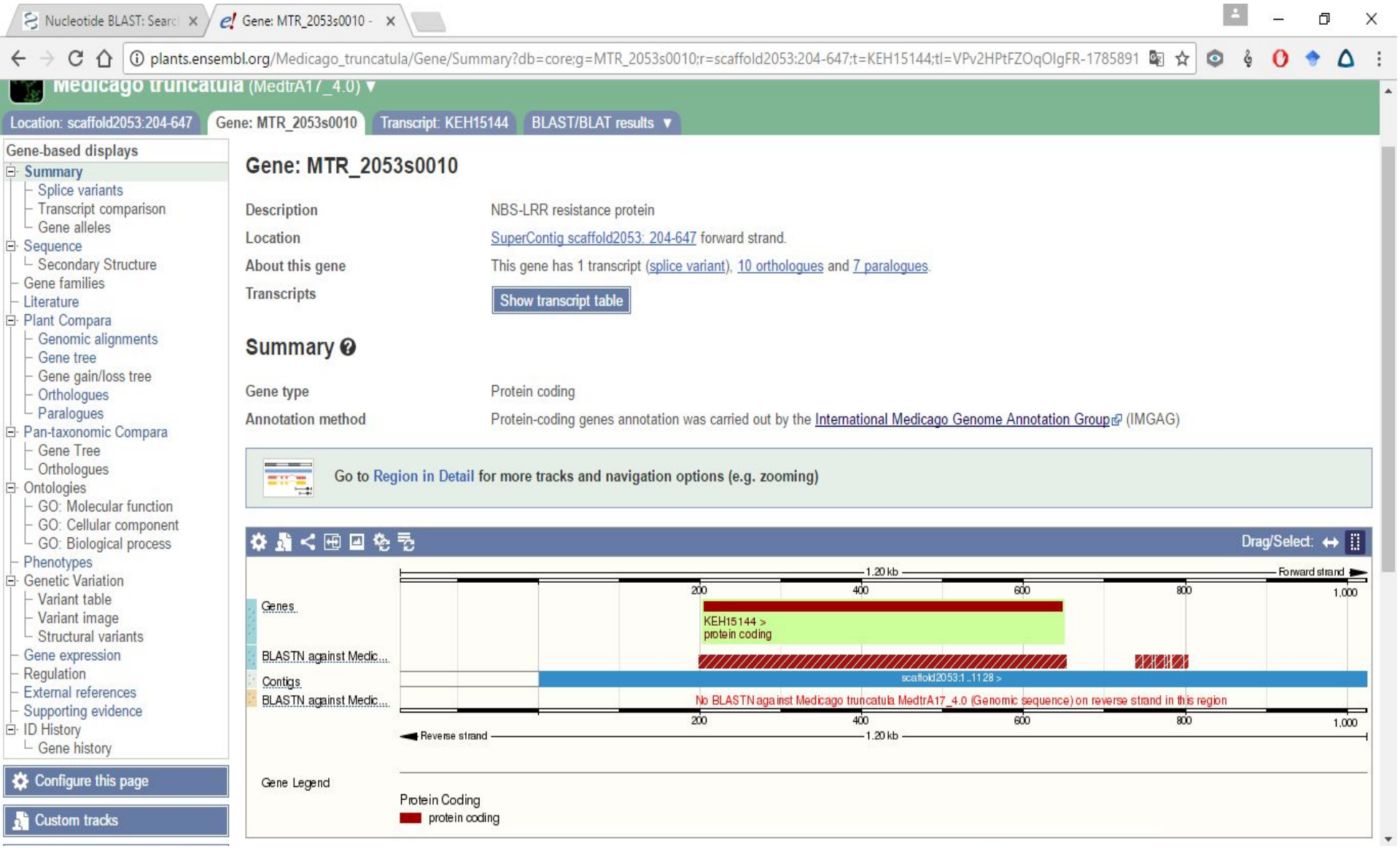
Далее возвращаемся к разделу Primer3 и делаем как делали ранее.

То есть все то же самое, только если бы у Вас не было названия гена, а был какой-то его сиквенс.

Но. Если есть название гена, который пересекается с нашим сиквенсом, то можно сделать точно также, как мы делали с самого начала



Смотрим первый слайд.