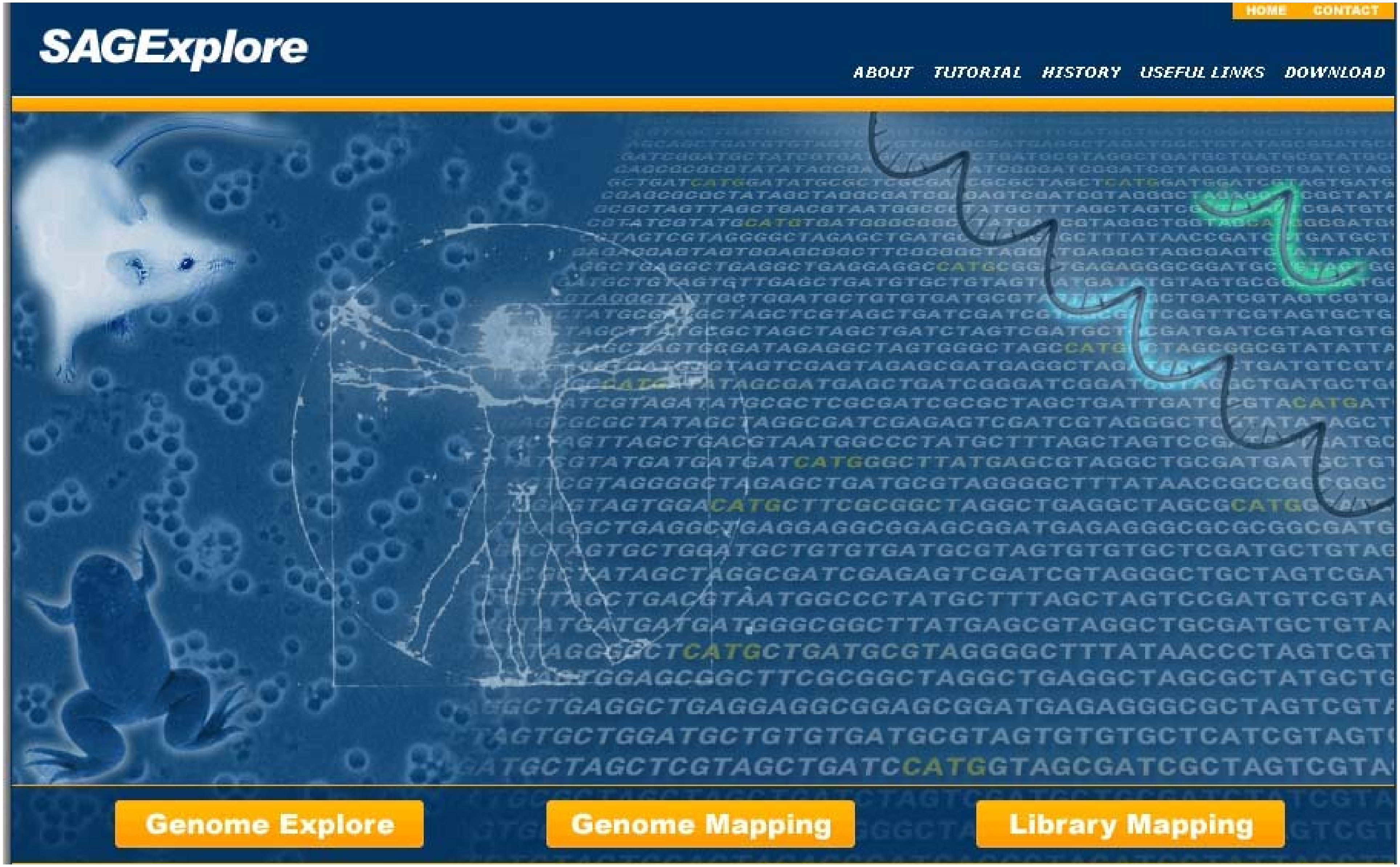
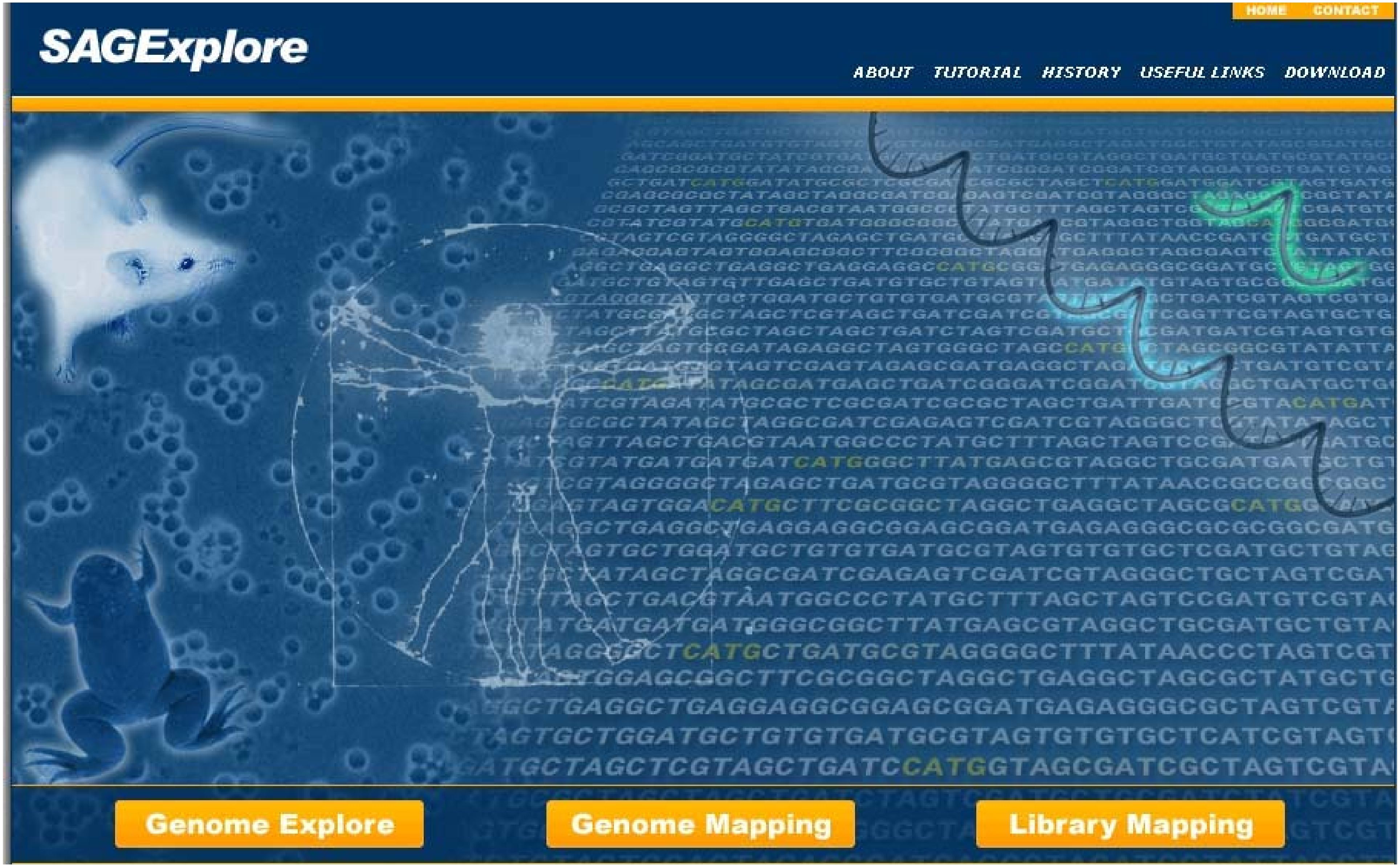
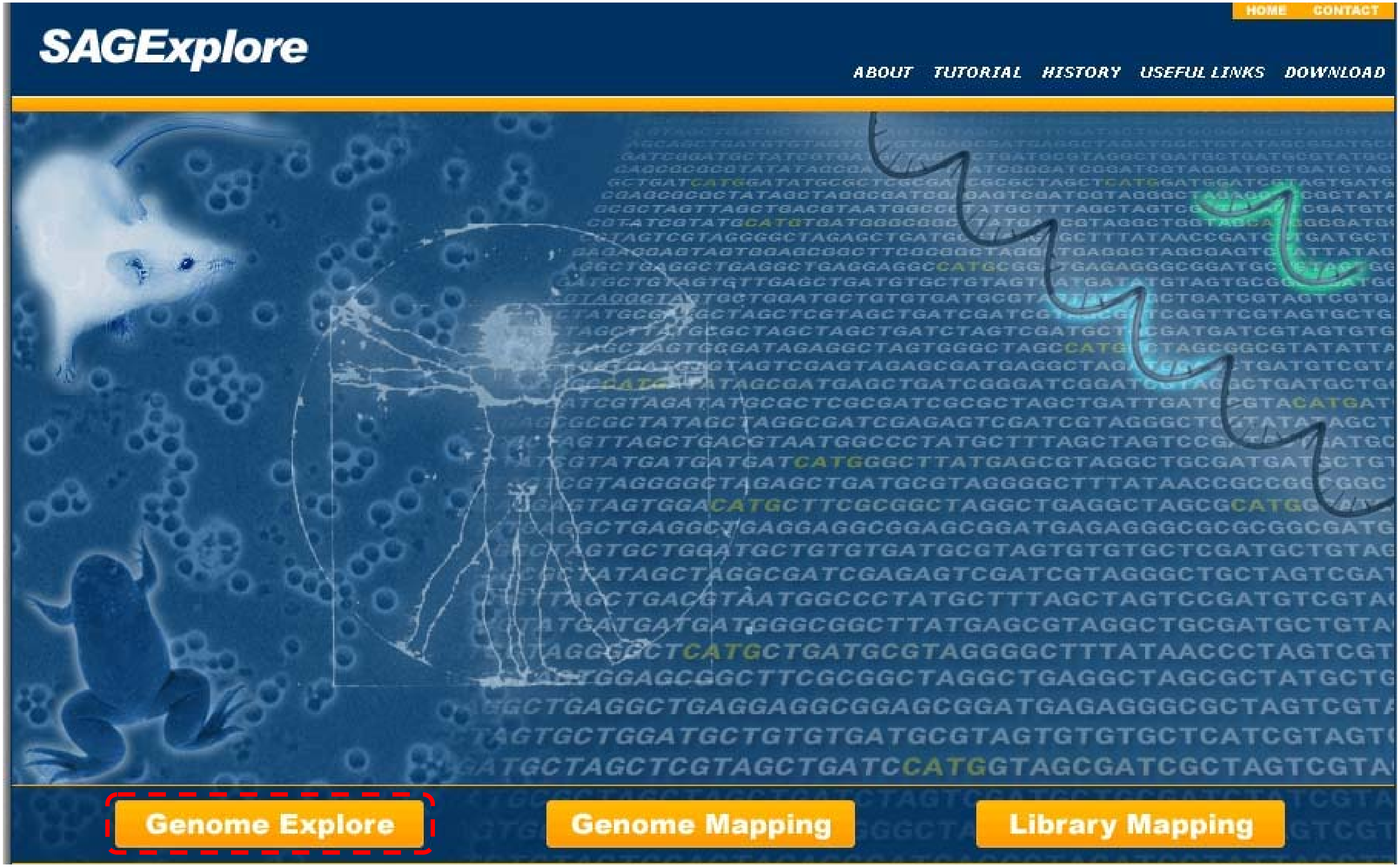


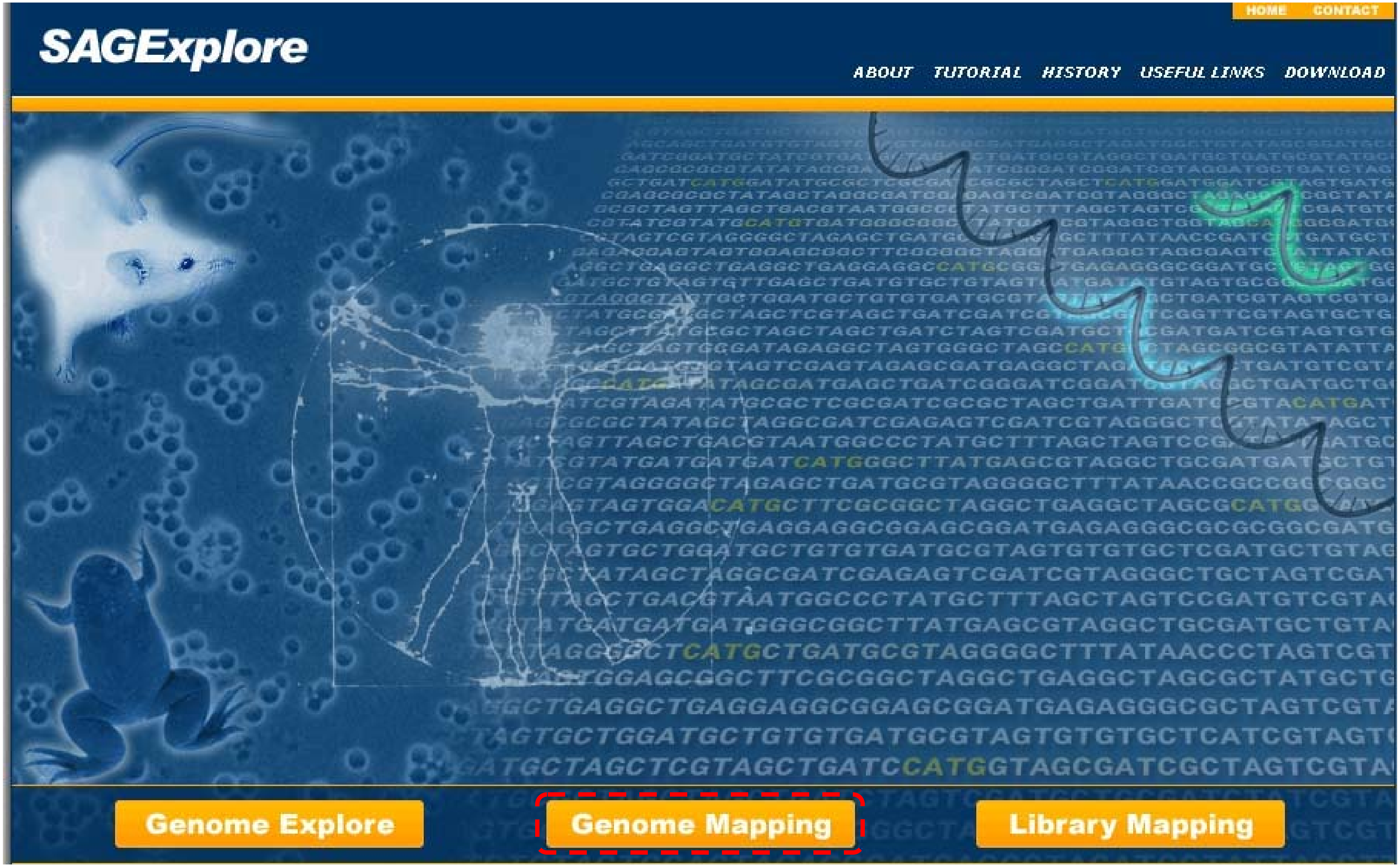
SAGExplore web server tutorial



The SAGExplore server has three different modules …

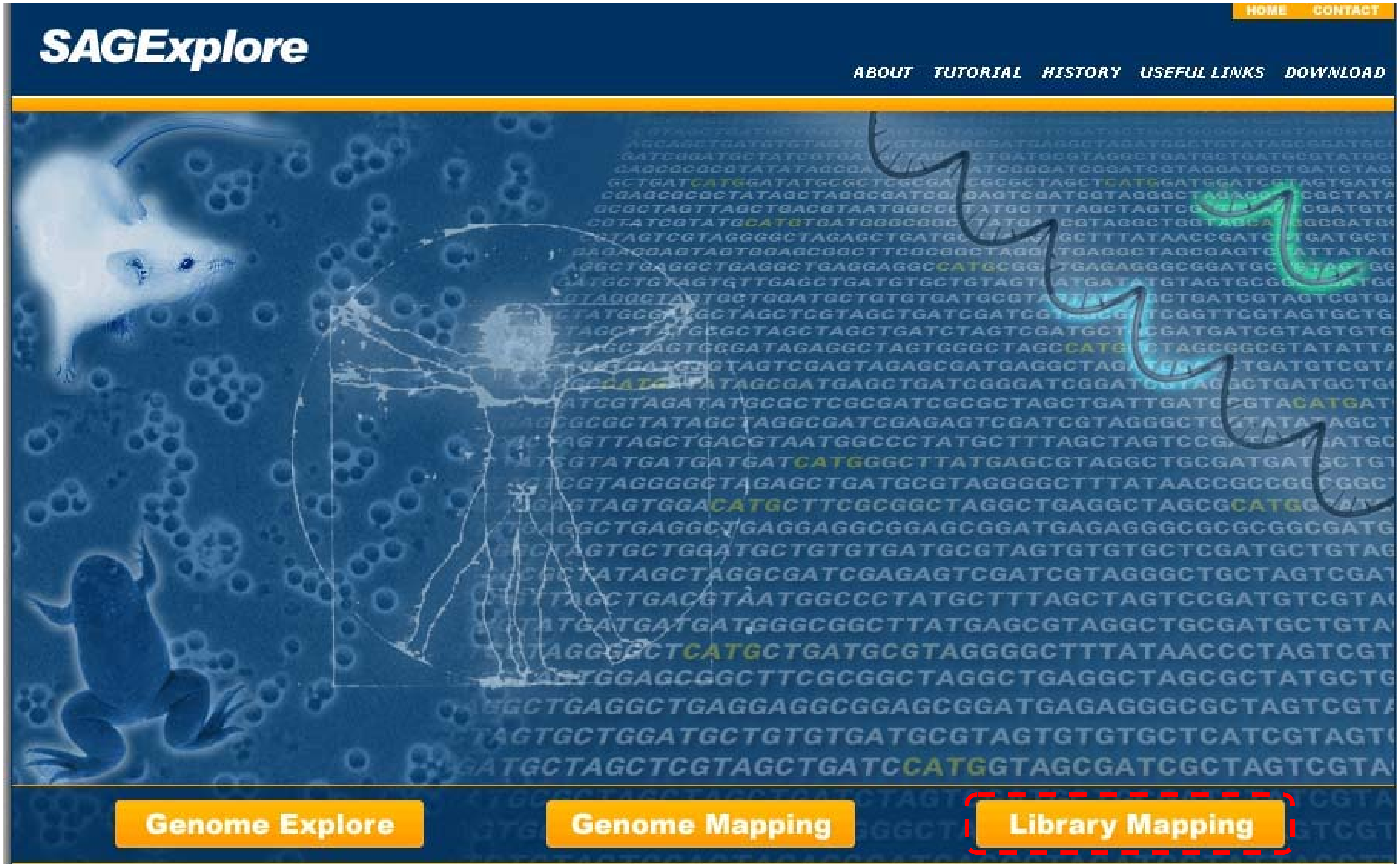


I.- Genome Explore Module: This module allows the user to browse and explore a genome, in terms of the context where potential or virtual SAGE tags are found for a given anchoring-tagging enzyme pair.



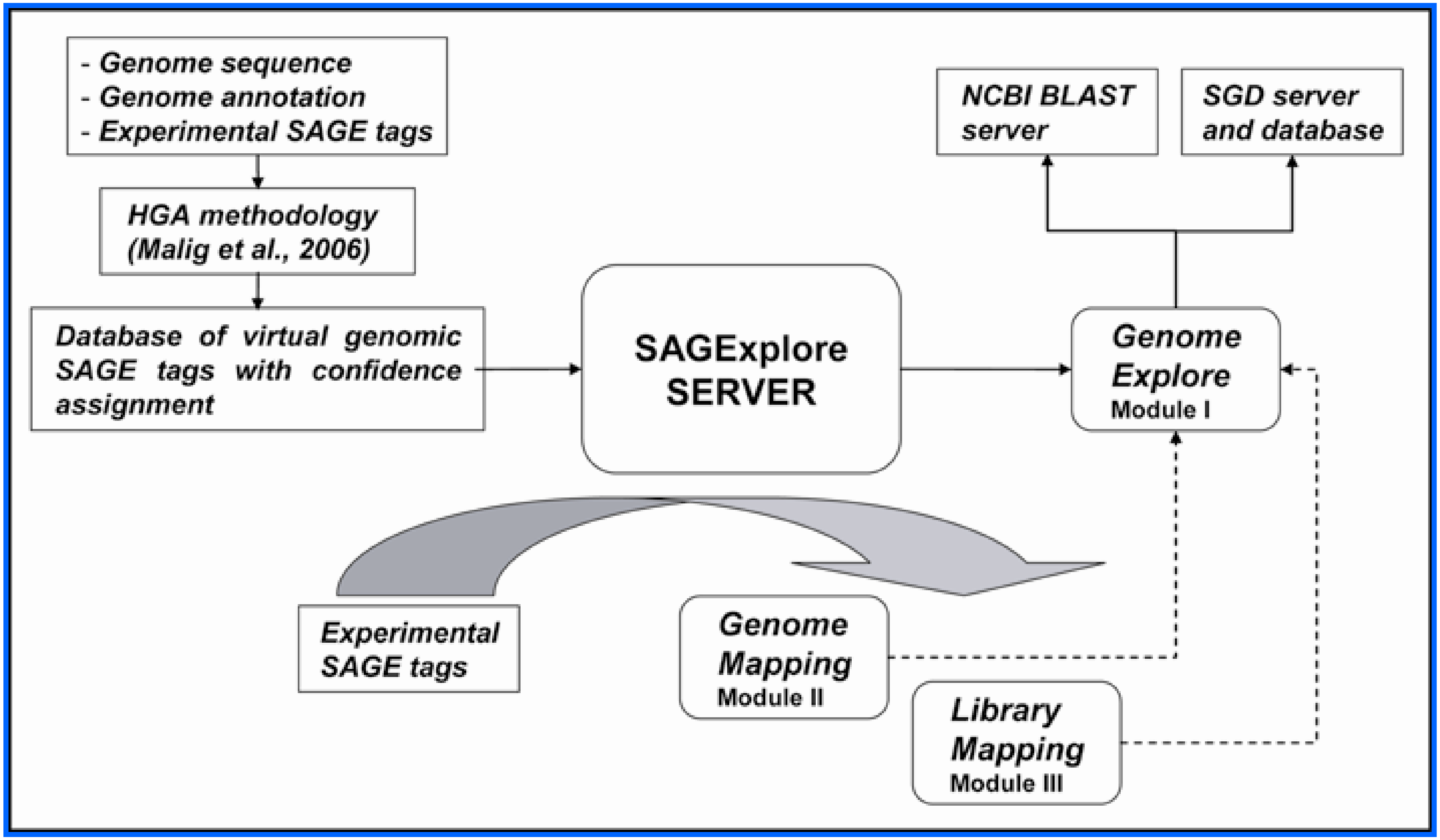
II.- Genome Mapping Module:

This module allows the user to map experimental tags against the genome.



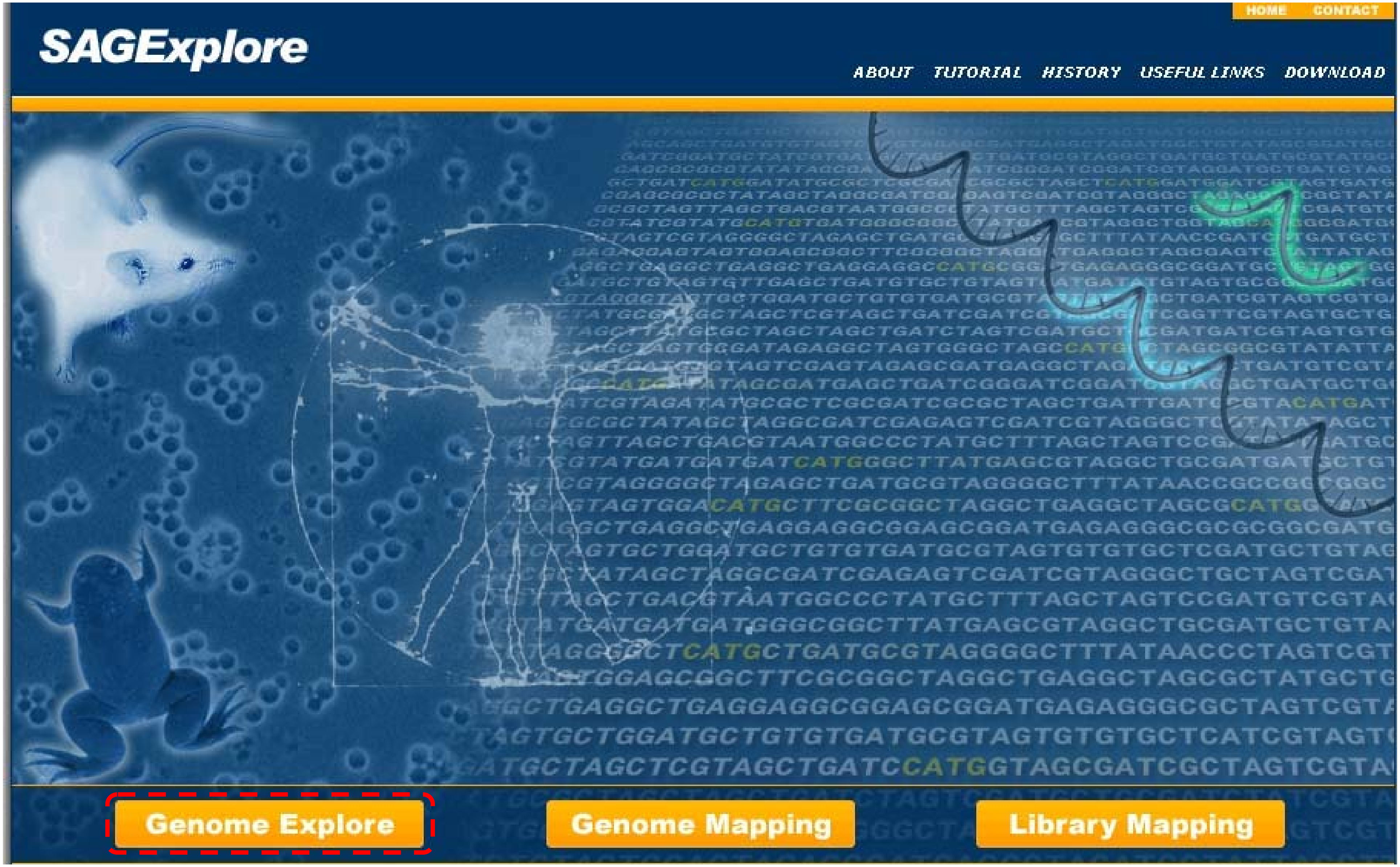
III.- Library Mapping Module:

This module allows the user to map experimental tags against known experimental libraries of SAGE tags.

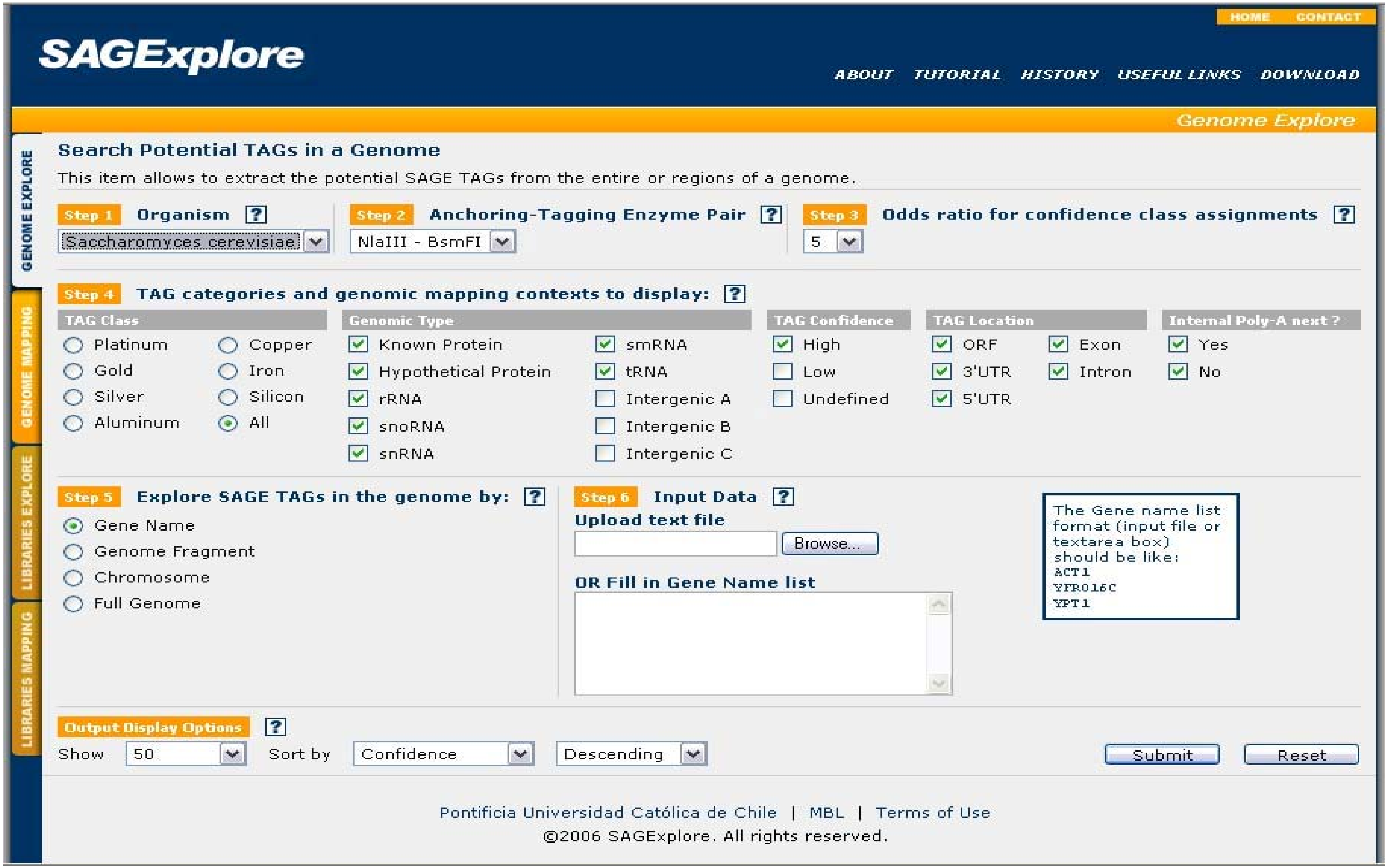


Layout and flowchart of the SAGExplore server.

The core of the server is a MySQL database of virtual genomic SAGE tags with confidence assignments The module I is linked to NCBI BLAST server and to the Saccharomyces Genome Database (SGD) and does not require any input from the user. The modules II and III requires experimental tag sequences and their counts (optional) as input, and are linked to the module I and, through this, to the external servers and databases.



I.- Tutorial Genome Explore Module.



Search Potential TAGs in a Genome

This item allows to extract the potential SAGE TAGs from the entire or regions of a genome.

Step 1 Organism [?]: Saccharomyces cerevisiae

Step 2 Anchoring-Tagging Enzyme Pair [?]: NlaIII - BsmFI

Step 3 Odds ratio for confidence class assignments [?]: 5

Step 4 TAG categories and genomic mapping contexts to display: [?]

TAG Class
- ○ Platinum
- ○ Gold
- ○ Silver
- ○ Aluminum
- ○ Copper
- ○ Iron
- ○ Silicon
- ● All

Genomic Type
- ☑ Known Protein
- ☑ Hypothetical Protein
- ☑ rRNA
- ☑ snoRNA
- ☑ snRNA
- ☑ smRNA
- ☑ tRNA
- ☐ Intergenic A
- ☐ Intergenic B
- ☐ Intergenic C

TAG Confidence
- ☑ High
- ☐ Low
- ☐ Undefined

TAG Location
- ☑ ORF
- ☑ 3'UTR
- ☑ 5'UTR
- ☑ Exon
- ☑ Intron

Internal Poly-A next ?
- ☑ Yes
- ☑ No

Step 5 Explore SAGE TAGs in the genome by: [?]
- ● Gene Name
- ○ Genome Fragment
- ○ Chromosome
- ○ Full Genome

Step 6 Input Data [?]

Upload text file

OR Fill in Gene Name list

The Gene name list format (input file or textarea box) should be like:
ACT1
YFR016C
YPT1

Output Display Options [?]

Show 50 Sort by Confidence Descending

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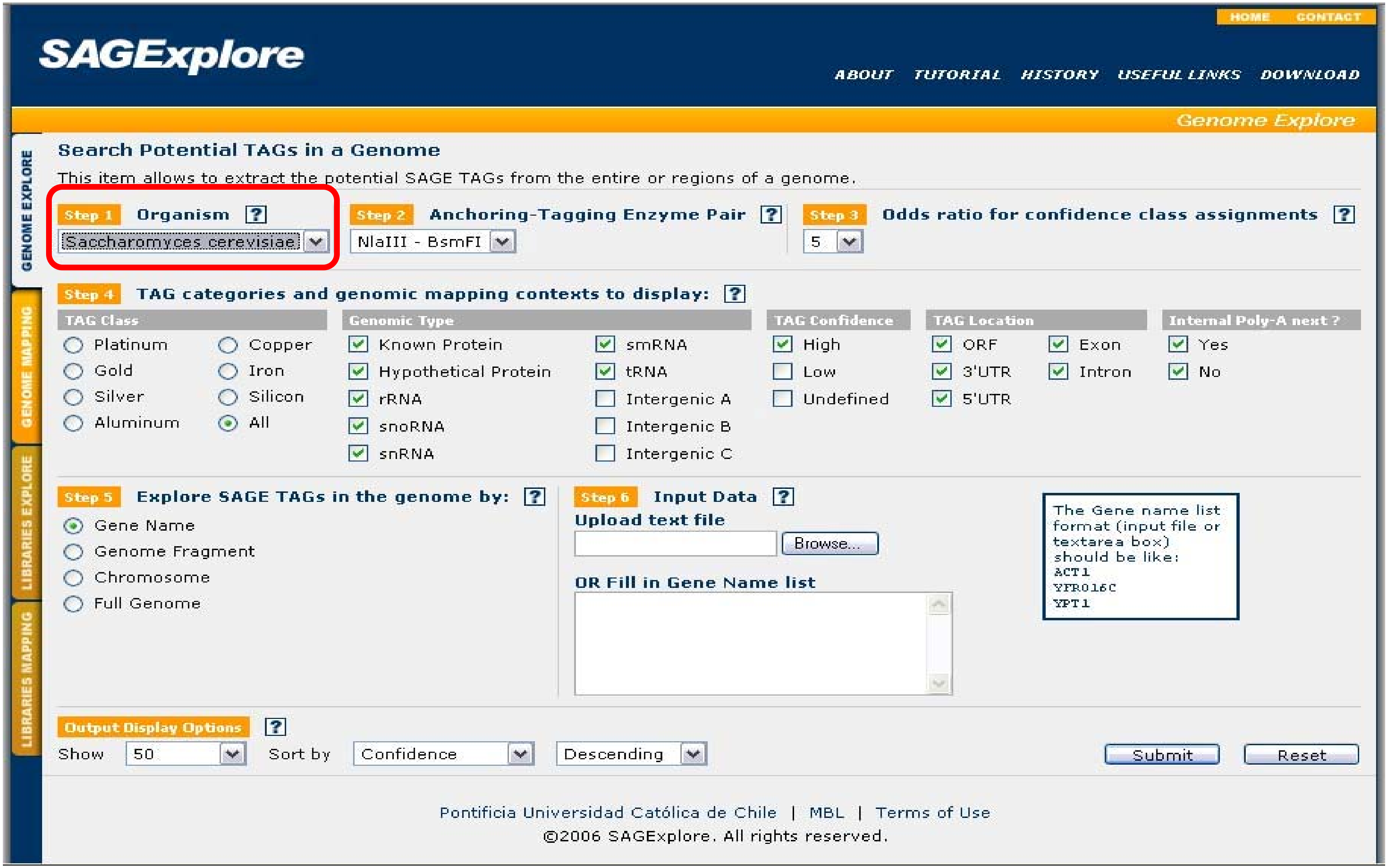
I.- Genome Explore Module Form: The user must follow six sequential steps in this form. Online help with the relevant details is provided for each step.



Search Potential TAGs in a Genome

This item allows to extract the potential SAGE TAGs from the entire or regions of a genome.

Step 1 Organism ?: Saccharomyces cerevisiae

Step 2 Anchoring-Tagging Enzyme Pair ?: NlaIII - BsmFI

Step 3 Odds ratio for confidence class assignments ?: 5

Step 4 TAG categories and genomic mapping contexts to display: ?

TAG Class:
- ○ Platinum
- ○ Gold
- ○ Silver
- ○ Aluminum
- ○ Copper
- ○ Iron
- ○ Silicon
- ● All

Genomic Type:
- ☑ Known Protein
- ☑ Hypothetical Protein
- ☑ rRNA
- ☑ snoRNA
- ☑ snRNA
- ☑ smRNA
- ☑ tRNA
- ☐ Intergenic A
- ☐ Intergenic B
- ☐ Intergenic C

TAG Confidence:
- ☑ High
- ☐ Low
- ☐ Undefined

TAG Location:
- ☑ ORF
- ☑ 3'UTR
- ☑ 5'UTR
- ☑ Exon
- ☑ Intron

Internal Poly-A next ?:
- ☑ Yes
- ☑ No

Step 5 Explore SAGE TAGs in the genome by: ?
- ● Gene Name
- ○ Genome Fragment
- ○ Chromosome
- ○ Full Genome

Step 6 Input Data ?

Upload text file [Browse...]

OR Fill in Gene Name list

The Gene name list format (input file or textarea box) should be like:
ACT1
YFR016C
YPT1

Output Display Options ?

Show 50 Sort by Confidence Descending

[Submit] [Reset]

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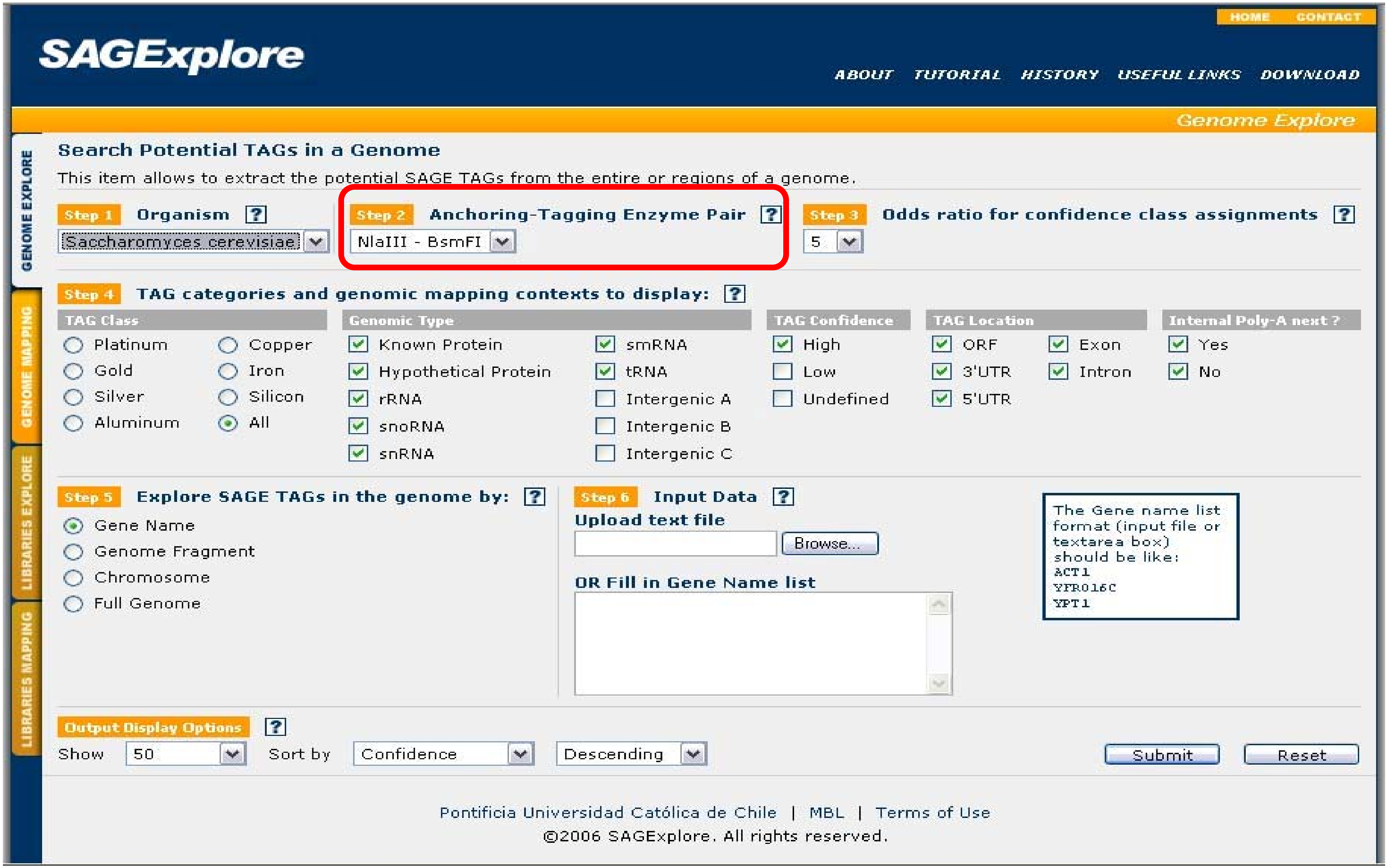
Step 1: The user must select the organism of interest. Currently, only *Saccharomyces cerevisiae* is available. In the near future, other organisms will be added.



Search Potential TAGs in a Genome

This item allows to extract the potential SAGE TAGs from the entire or regions of a genome.

Step 1 Organism: Saccharomyces cerevisiae

Step 2 Anchoring-Tagging Enzyme Pair: NlaIII - BsmFI

Step 3 Odds ratio for confidence class assignments: 5

Step 4 TAG categories and genomic mapping contexts to display:

TAG Class: ○ Platinum ○ Gold ○ Silver ○ Aluminum ○ Copper ○ Iron ○ Silicon ● All

Genomic Type: ☑ Known Protein ☑ Hypothetical Protein ☑ rRNA ☑ snoRNA ☑ snRNA ☑ smRNA ☑ tRNA ☐ Intergenic A ☐ Intergenic B ☐ Intergenic C

TAG Confidence: ☑ High ☐ Low ☐ Undefined

TAG Location: ☑ ORF ☑ 3'UTR ☑ 5'UTR ☑ Exon ☑ Intron

Internal Poly-A next ?: ☑ Yes ☑ No

Step 5 Explore SAGE TAGs in the genome by: ● Gene Name ○ Genome Fragment ○ Chromosome ○ Full Genome

Step 6 Input Data

Upload text file [Browse...]

OR Fill in Gene Name list

The Gene name list format (input file or textarea box) should be like:
ACT1
YFR016C
YPT1

Output Display Options

Show 50 Sort by Confidence Descending

[Submit] [Reset]

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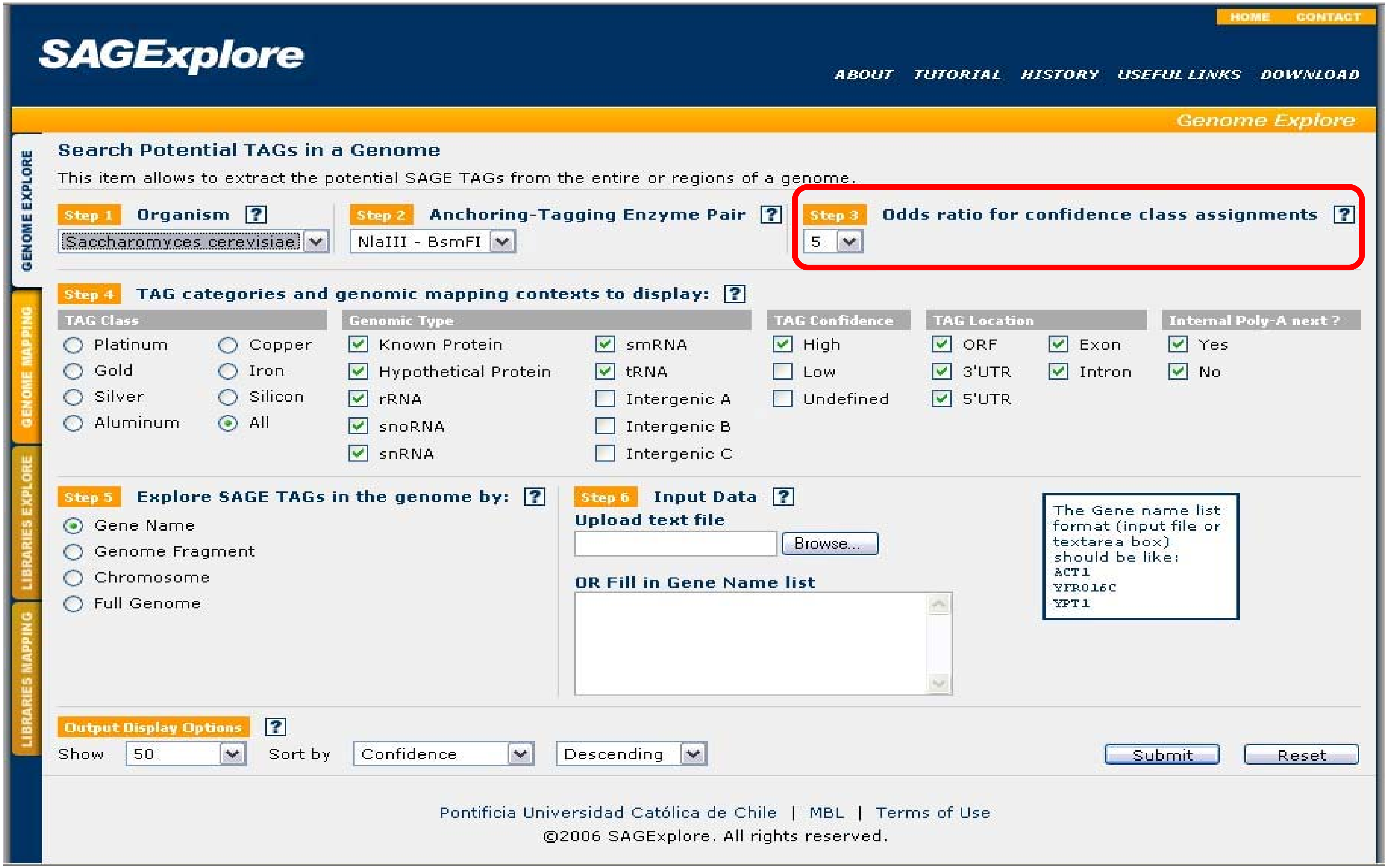
Step 2: The user must select the anchoring-tagging enzyme pair used in SAGE. Currently, only the pair NlaIII-BsmFI is available. In the near future, other enzyme pairs such as the one used in Long-SAGE will be added.



Search Potential TAGs in a Genome

This item allows to extract the potential SAGE TAGs from the entire or regions of a genome.

Step 1 **Organism** ?
Saccharomyces cerevisiae

Step 2 **Anchoring-Tagging Enzyme Pair** ?
NlaIII - BsmFI

Step 3 **Odds ratio for confidence class assignments** ?
5

Step 4 **TAG categories and genomic mapping contexts to display:** ?

TAG Class
- ○ Platinum
- ○ Gold
- ○ Silver
- ○ Aluminum
- ○ Copper
- ○ Iron
- ○ Silicon
- ● All

Genomic Type
- ☑ Known Protein
- ☑ Hypothetical Protein
- ☑ rRNA
- ☑ snoRNA
- ☑ snRNA
- ☑ smRNA
- ☑ tRNA
- ☐ Intergenic A
- ☐ Intergenic B
- ☐ Intergenic C

TAG Confidence
- ☑ High
- ☐ Low
- ☐ Undefined

TAG Location
- ☑ ORF
- ☑ 3'UTR
- ☑ 5'UTR
- ☑ Exon
- ☑ Intron

Internal Poly-A next ?
- ☑ Yes
- ☑ No

Step 5 **Explore SAGE TAGs in the genome by:** ?
- ● Gene Name
- ○ Genome Fragment
- ○ Chromosome
- ○ Full Genome

Step 6 **Input Data** ?

Upload text file

OR Fill in Gene Name list

The Gene name list format (input file or textarea box) should be like:
ACT1
YFR016C
YPT1

Output Display Options ?
Show 50 Sort by Confidence Descending

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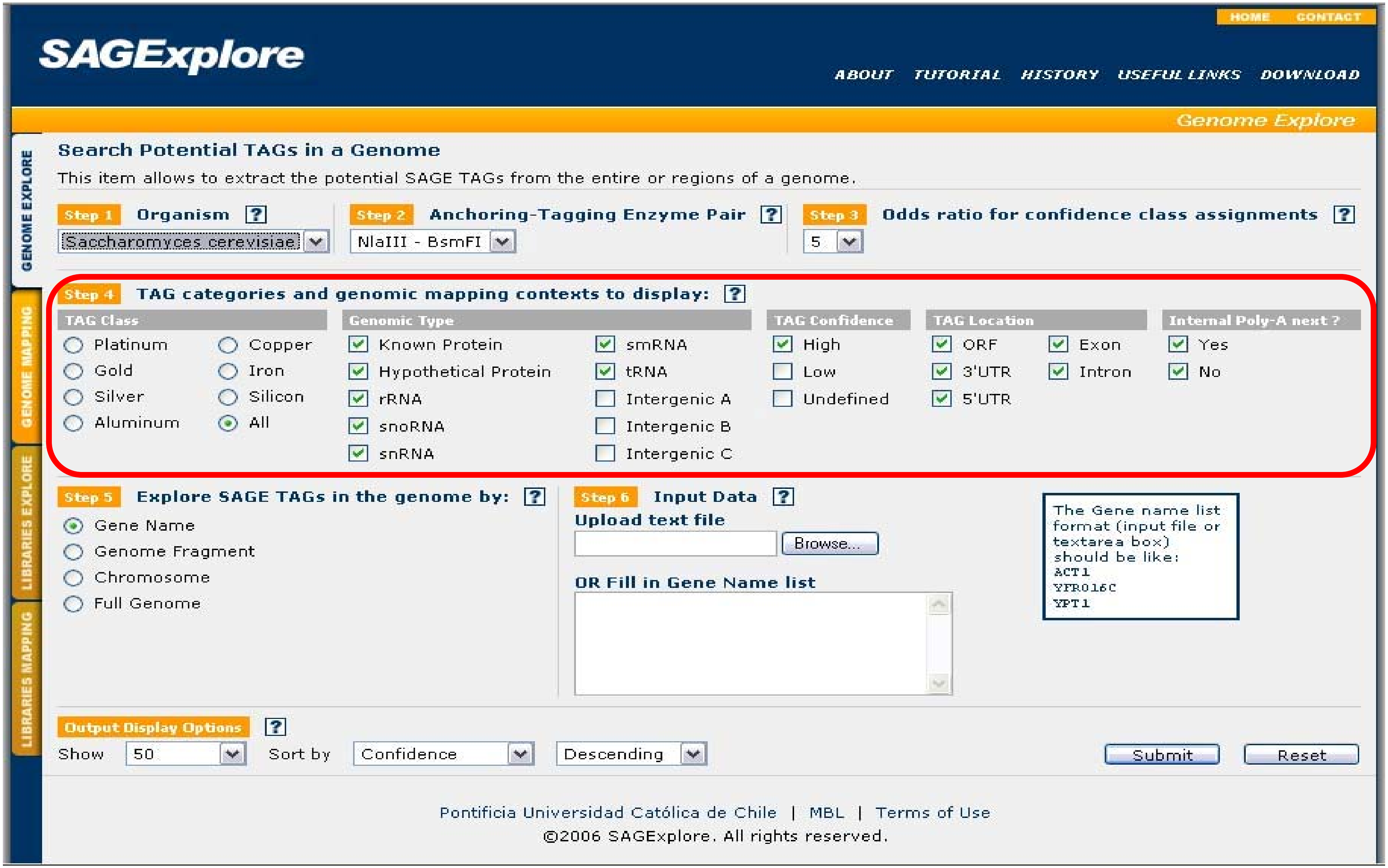
Step 3: The user must select the odds ratio used to assign the confidence classes to the different genomic tags. For details see: Malig, R., Varela, C., Agosin, E. and Melo, F. (2006) Accurate and unambiguous tag-to-gene mapping in SAGE by a hierarchical gene assignment procedure. *BMC Bioinformatics*, **7,** 487-507.



Search Potential TAGs in a Genome

This item allows to extract the potential SAGE TAGs from the entire or regions of a genome.

Step 1 Organism [?]: Saccharomyces cerevisiae

Step 2 Anchoring-Tagging Enzyme Pair [?]: NlaIII - BsmFI

Step 3 Odds ratio for confidence class assignments [?]: 5

Step 4 TAG categories and genomic mapping contexts to display: [?]

TAG Class		Genomic Type		TAG Confidence	TAG Location		Internal Poly-A next ?
○ Platinum	○ Copper	☑ Known Protein	☑ smRNA	☑ High	☑ ORF	☑ Exon	☑ Yes
○ Gold	○ Iron	☑ Hypothetical Protein	☑ tRNA	☐ Low	☑ 3'UTR	☑ Intron	☑ No
○ Silver	○ Silicon	☑ rRNA	☐ Intergenic A	☐ Undefined	☑ 5'UTR		
○ Aluminum	● All	☑ snoRNA	☐ Intergenic B				
		☑ snRNA	☐ Intergenic C				

Step 5 Explore SAGE TAGs in the genome by: [?]

● Gene Name
○ Genome Fragment
○ Chromosome
○ Full Genome

Step 6 Input Data [?]

Upload text file

OR Fill in Gene Name list

The Gene name list format (input file or textarea box) should be like:
ACT1
YFR016C
YPT1

Output Display Options [?]

Show 50 Sort by Confidence Descending

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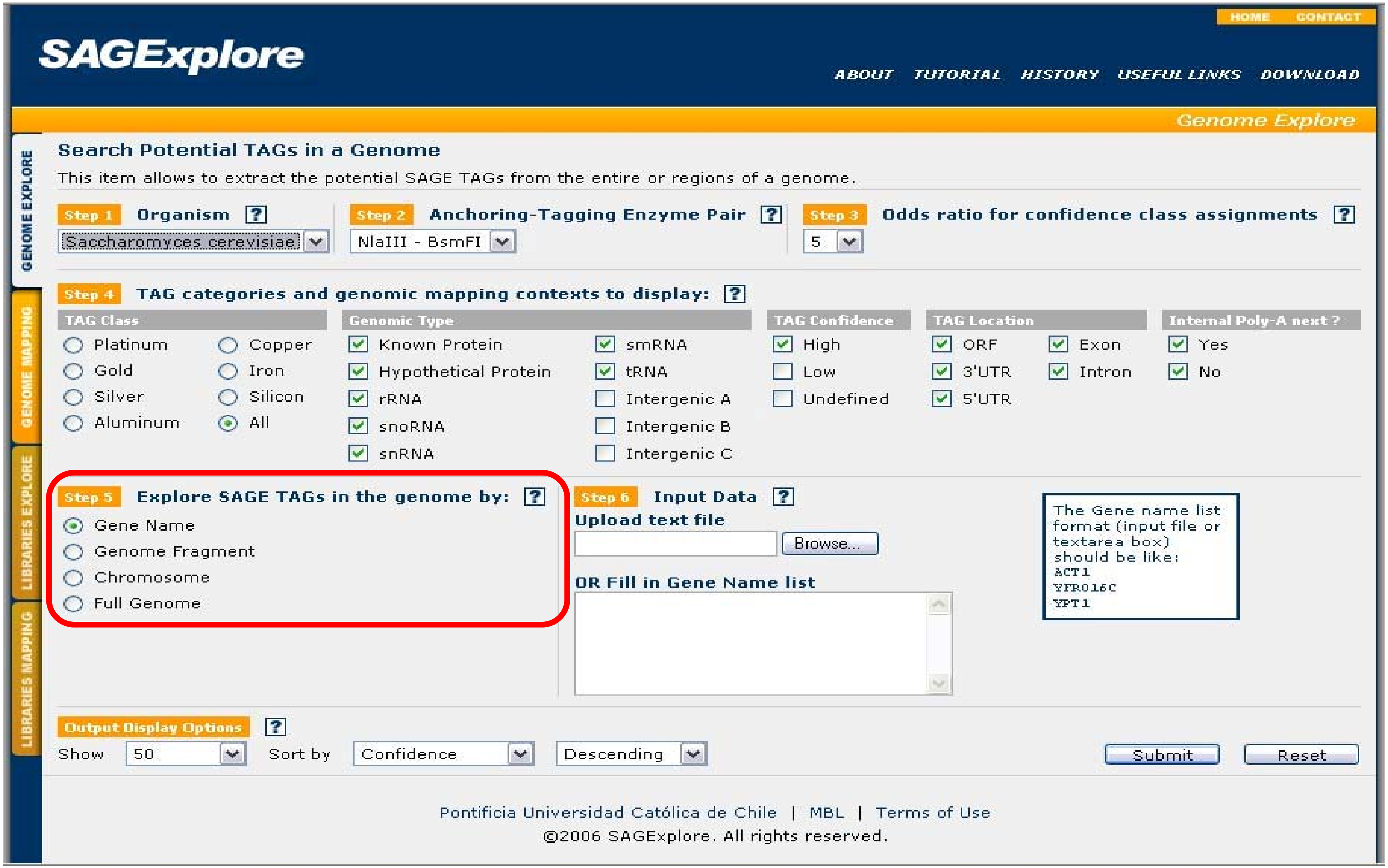
Step 4: The user can choose to display subsets of tags upon a large amount of different features. For details see the help links or: Malig, R., Varela, C., Agosin, E. and Melo, F. (2006) Accurate and unambiguous tag-to-gene mapping in SAGE by a hierarchical gene assignment procedure. *BMC Bioinformatics*, **7,** 487-507.



Search Potential TAGs in a Genome

This item allows to extract the potential SAGE TAGs from the entire or regions of a genome.

Step 1 Organism [?]: Saccharomyces cerevisiae

Step 2 Anchoring-Tagging Enzyme Pair [?]: NlaIII - BsmFI

Step 3 Odds ratio for confidence class assignments [?]: 5

Step 4 TAG categories and genomic mapping contexts to display: [?]

TAG Class
- ○ Platinum
- ○ Gold
- ○ Silver
- ○ Aluminum
- ○ Copper
- ○ Iron
- ○ Silicon
- ● All

Genomic Type
- ☑ Known Protein
- ☑ Hypothetical Protein
- ☑ rRNA
- ☑ snoRNA
- ☑ snRNA
- ☑ smRNA
- ☑ tRNA
- ☐ Intergenic A
- ☐ Intergenic B
- ☐ Intergenic C

TAG Confidence
- ☑ High
- ☐ Low
- ☐ Undefined

TAG Location
- ☑ ORF
- ☑ 3'UTR
- ☑ 5'UTR
- ☑ Exon
- ☑ Intron

Internal Poly-A next ?
- ☑ Yes
- ☑ No

Step 5 Explore SAGE TAGs in the genome by: [?]
- ● Gene Name
- ○ Genome Fragment
- ○ Chromosome
- ○ Full Genome

Step 6 Input Data [?]

Upload text file

OR Fill in Gene Name list

The Gene name list format (input file or textarea box) should be like:
ACT1
YFR016C
YPT1

Output Display Options [?]

Show 50 Sort by Confidence Descending

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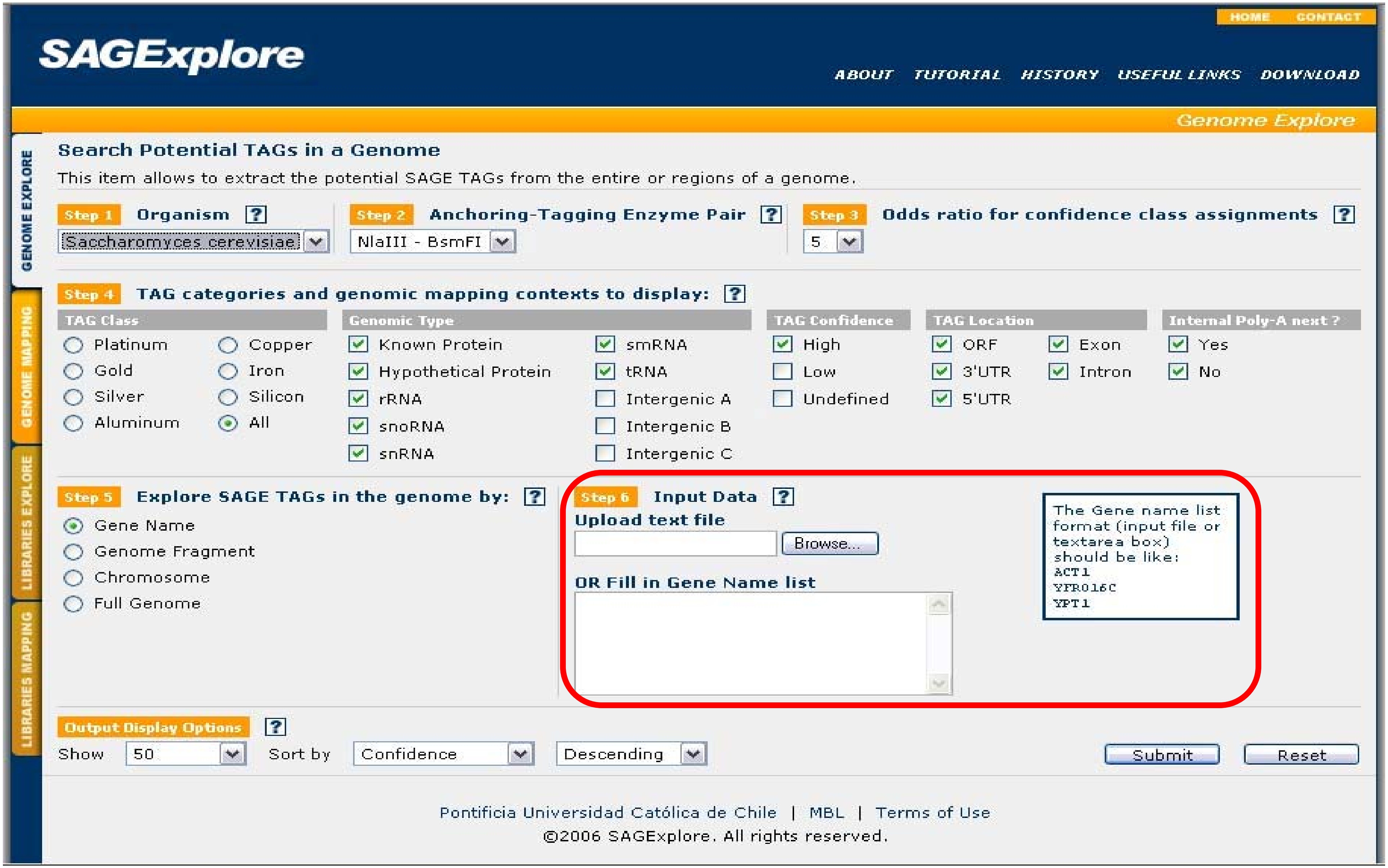
Step 5: The user must select the type of input that will be provided in the next step. Four options are available.



Search Potential TAGs in a Genome

This item allows to extract the potential SAGE TAGs from the entire or regions of a genome.

Step 1 Organism [?]: Saccharomyces cerevisiae

Step 2 Anchoring-Tagging Enzyme Pair [?]: NlaIII - BsmFI

Step 3 Odds ratio for confidence class assignments [?]: 5

Step 4 TAG categories and genomic mapping contexts to display: [?]

TAG Class		Genomic Type		TAG Confidence	TAG Location		Internal Poly-A next ?
○ Platinum	○ Copper	☑ Known Protein	☑ smRNA	☑ High	☑ ORF	☑ Exon	☑ Yes
○ Gold	○ Iron	☑ Hypothetical Protein	☑ tRNA	☐ Low	☑ 3'UTR	☑ Intron	☑ No
○ Silver	○ Silicon	☑ rRNA	☐ Intergenic A	☐ Undefined	☑ 5'UTR		
○ Aluminum	● All	☑ snoRNA	☐ Intergenic B				
		☑ snRNA	☐ Intergenic C				

Step 5 Explore SAGE TAGs in the genome by: [?]

● Gene Name
○ Genome Fragment
○ Chromosome
○ Full Genome

Step 6 Input Data [?]

Upload text file

OR Fill in Gene Name list

The Gene name list format (input file or textarea box) should be like:
ACT1
YFR016C
YPT1

Output Display Options [?]

Show 50 Sort by Confidence Descending

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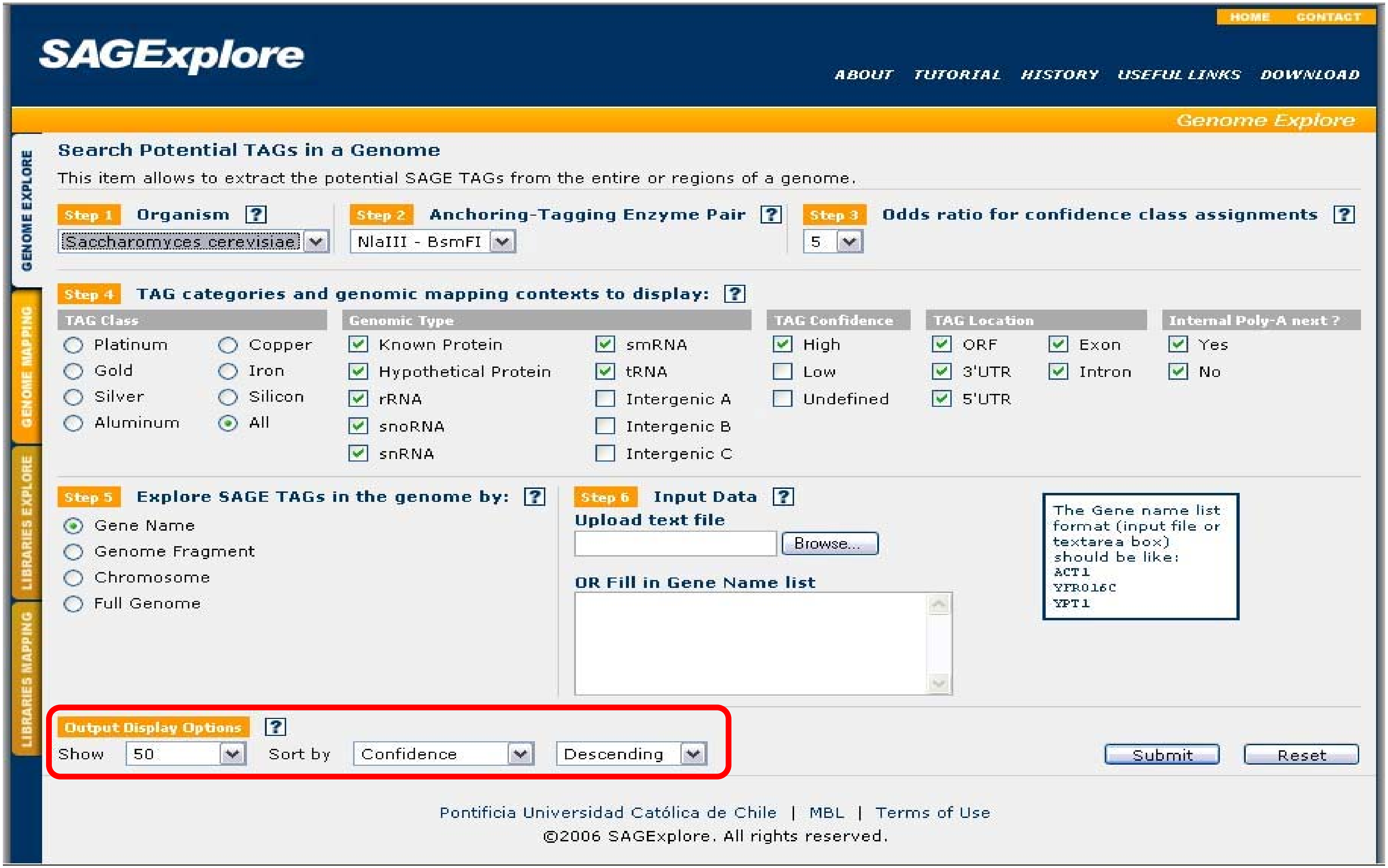
Step 6: The user must provide the list of genes, genome fragments or chromosomes to explore. In the case of the full genome option, no input is required here. The window in the right explains the input format required for each case.



Search Potential TAGs in a Genome

This item allows to extract the potential SAGE TAGs from the entire or regions of a genome.

Step 1 Organism: Saccharomyces cerevisiae

Step 2 Anchoring-Tagging Enzyme Pair: NlaIII - BsmFI

Step 3 Odds ratio for confidence class assignments: 5

Step 4 TAG categories and genomic mapping contexts to display:

TAG Class: ○ Platinum ○ Gold ○ Silver ○ Aluminum ○ Copper ○ Iron ○ Silicon ● All

Genomic Type: ☑ Known Protein ☑ Hypothetical Protein ☑ rRNA ☑ snoRNA ☑ snRNA ☑ smRNA ☑ tRNA ☐ Intergenic A ☐ Intergenic B ☐ Intergenic C

TAG Confidence: ☑ High ☐ Low ☐ Undefined

TAG Location: ☑ ORF ☑ 3'UTR ☑ 5'UTR ☑ Exon ☑ Intron

Internal Poly-A next ?: ☑ Yes ☑ No

Step 5 Explore SAGE TAGs in the genome by: ● Gene Name ○ Genome Fragment ○ Chromosome ○ Full Genome

Step 6 Input Data

Upload text file

OR Fill in Gene Name list

The Gene name list format (input file or textarea box) should be like:
ACT1
YFR016C
YPT1

Output Display Options

Show: 50 Sort by: Confidence Descending

Submit Reset

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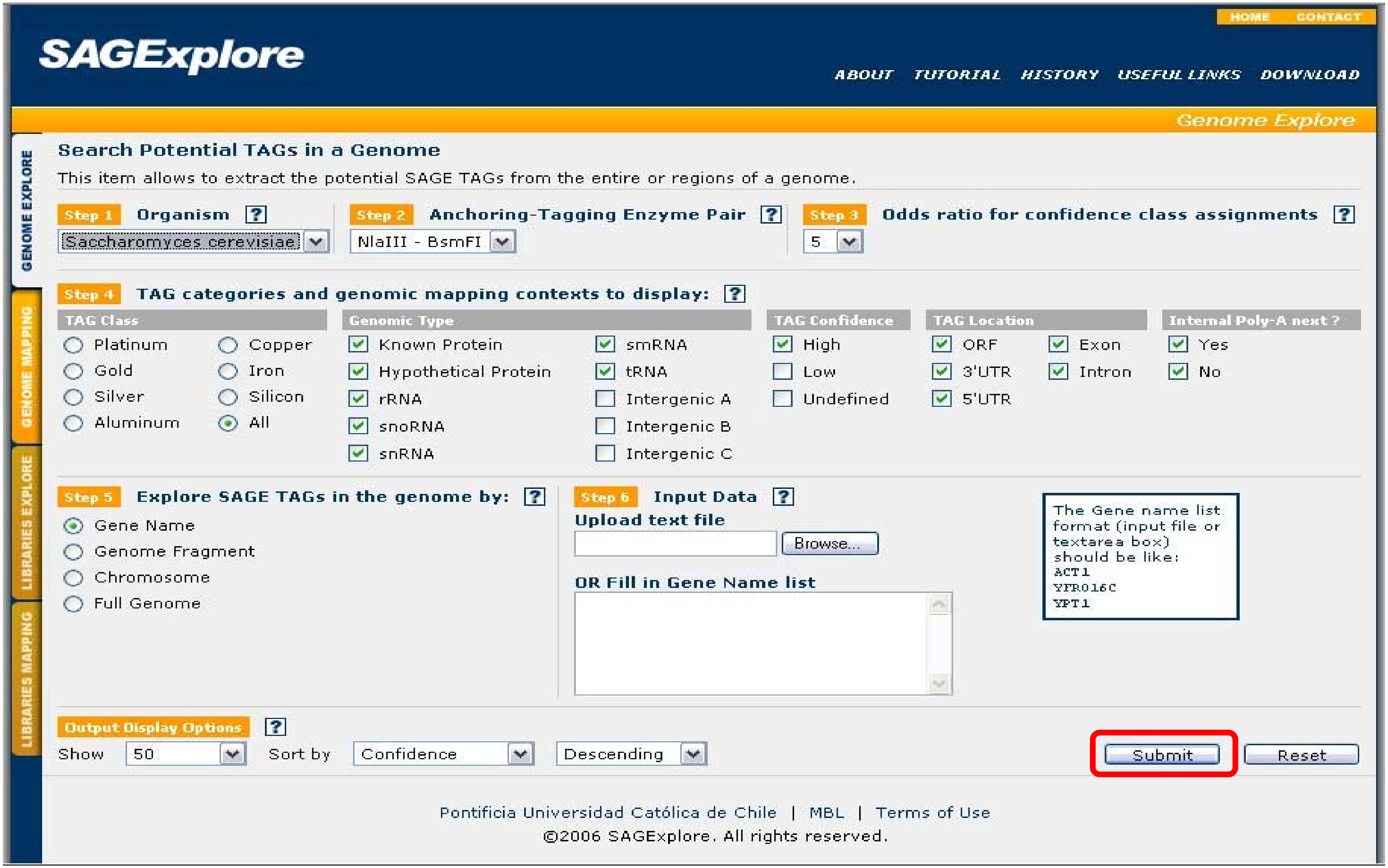
Pre-submit: Before submitting the query, the user can choose the number of rows to display per page and also how to sort the results.



Search Potential TAGs in a Genome

This item allows to extract the potential SAGE TAGs from the entire or regions of a genome.

Step 1 **Organism** ? Saccharomyces cerevisiae

Step 2 **Anchoring-Tagging Enzyme Pair** ? NlaIII - BsmFI

Step 3 **Odds ratio for confidence class assignments** ? 5

Step 4 **TAG categories and genomic mapping contexts to display:** ?

TAG Class
- ○ Platinum
- ○ Gold
- ○ Silver
- ○ Aluminum
- ○ Copper
- ○ Iron
- ○ Silicon
- ● All

Genomic Type
- ☑ Known Protein
- ☑ Hypothetical Protein
- ☑ rRNA
- ☑ snoRNA
- ☑ snRNA
- ☑ smRNA
- ☑ tRNA
- ☐ Intergenic A
- ☐ Intergenic B
- ☐ Intergenic C

TAG Confidence
- ☑ High
- ☐ Low
- ☐ Undefined

TAG Location
- ☑ ORF
- ☑ 3'UTR
- ☑ 5'UTR
- ☑ Exon
- ☑ Intron

Internal Poly-A next ?
- ☑ Yes
- ☑ No

Step 5 **Explore SAGE TAGs in the genome by:** ?
- ● Gene Name
- ○ Genome Fragment
- ○ Chromosome
- ○ Full Genome

Step 6 **Input Data** ?

Upload text file

OR Fill in Gene Name list

The Gene name list format (input file or textarea box) should be like:
ACT1
YFR016C
YPT1

Output Display Options ?

Show 50 Sort by Confidence Descending

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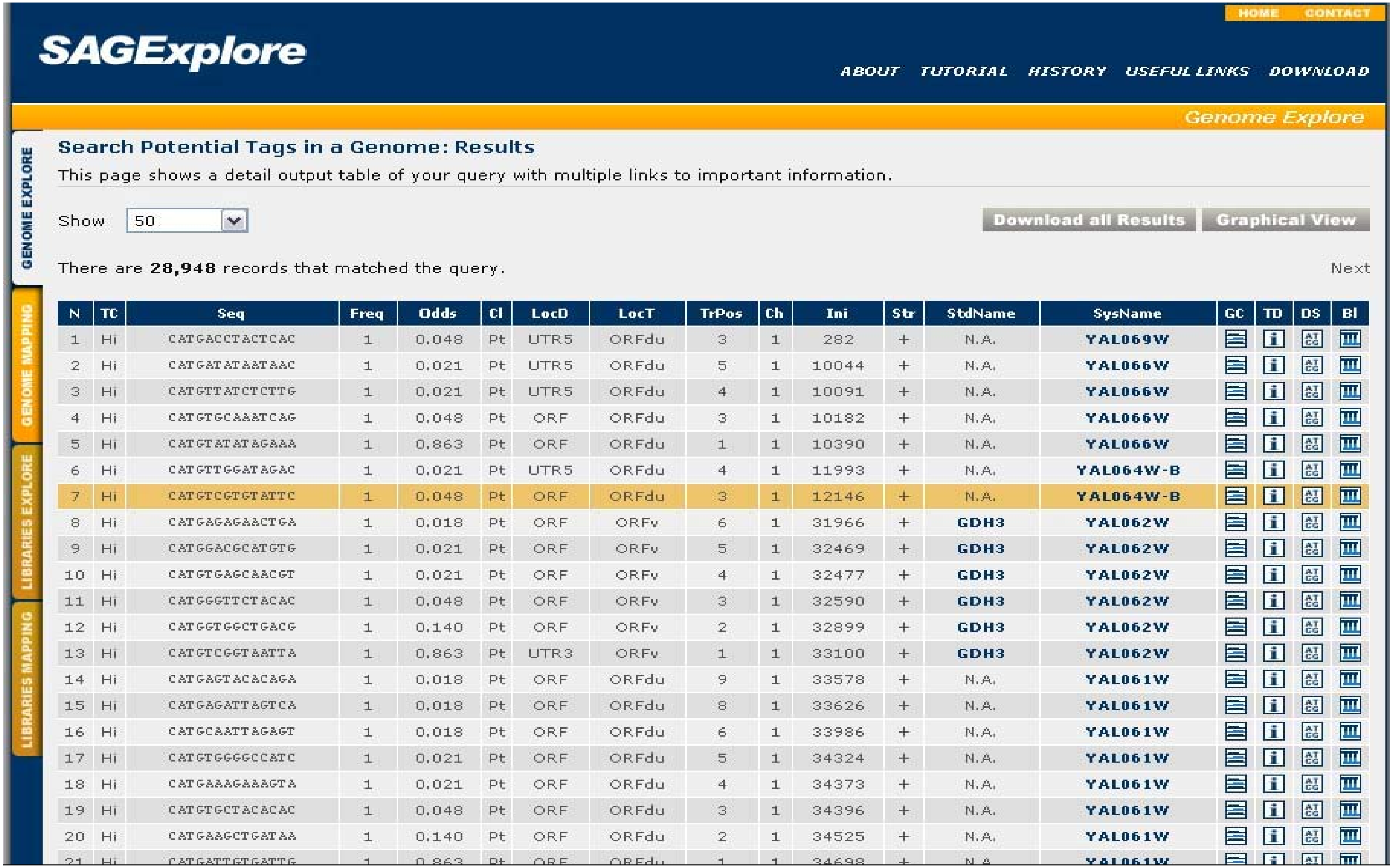
Submit: The user is ready to submit the query to the server.



Search Potential Tags in a Genome: Results

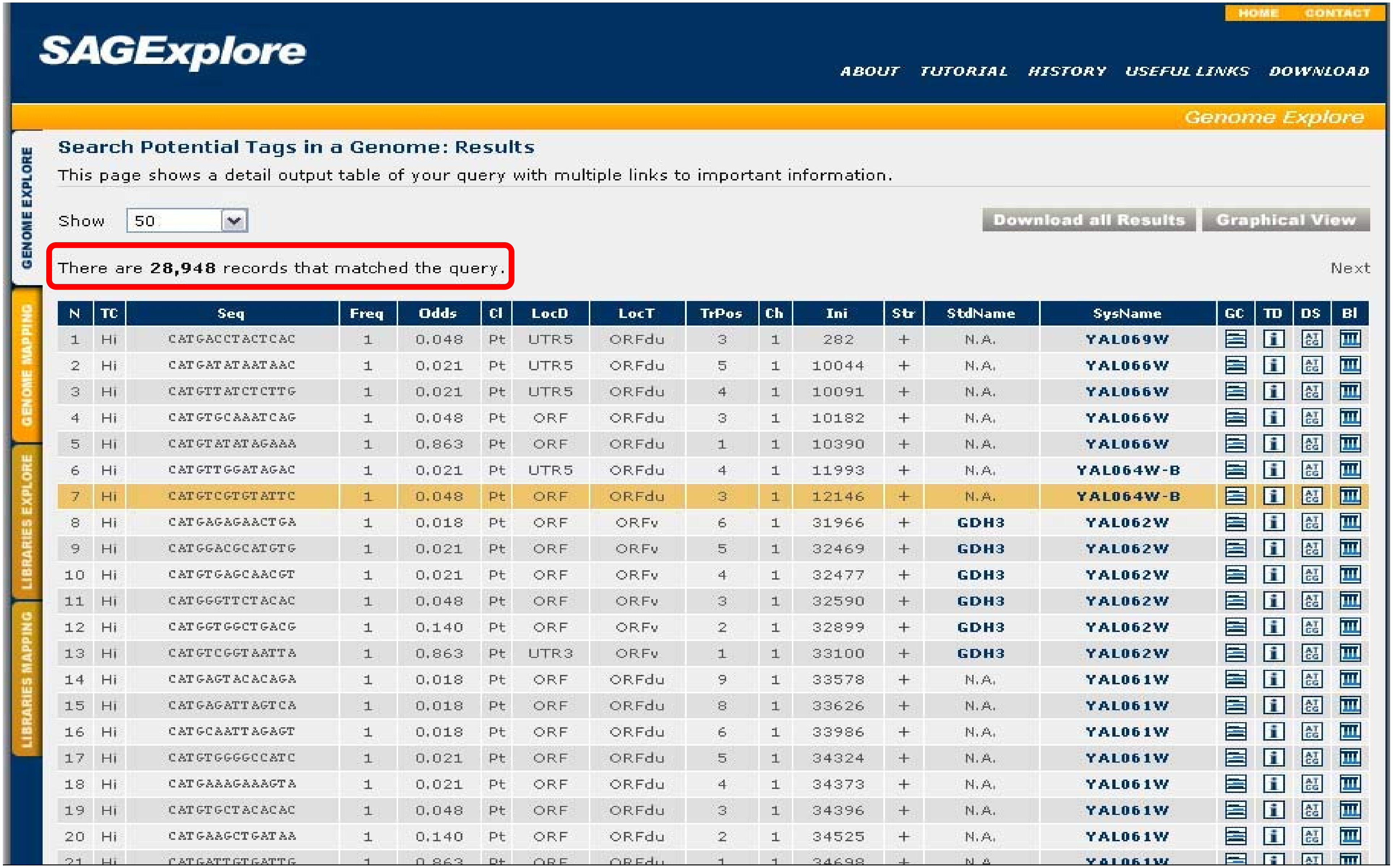
This page shows a detail output table of your query with multiple links to important information.

Show 50

There are **28,948** records that matched the query.

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	BI
1	Hi	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	3	1	282	+	N.A.	YAL069W	☰	ℹ	▦	▥
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W	☰	ℹ	▦	▥
3	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W	☰	ℹ	▦	▥
4	Hi	CATGTGCAAATCAG	1	0.048	Pt	ORF	ORFdu	3	1	10182	+	N.A.	YAL066W	☰	ℹ	▦	▥
5	Hi	CATGTATATAGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W	☰	ℹ	▦	▥
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B	☰	ℹ	▦	▥
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	3	1	12146	+	N.A.	YAL064W-B	☰	ℹ	▦	▥
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	GDH3	YAL062W	☰	ℹ	▦	▥
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W	☰	ℹ	▦	▥
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W	☰	ℹ	▦	▥
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	3	1	32590	+	GDH3	YAL062W	☰	ℹ	▦	▥
12	Hi	CATGGTGGCTGACG	1	0.140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W	☰	ℹ	▦	▥
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W	☰	ℹ	▦	▥
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W	☰	ℹ	▦	▥
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W	☰	ℹ	▦	▥
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W	☰	ℹ	▦	▥
17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W	☰	ℹ	▦	▥
18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W	☰	ℹ	▦	▥
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	3	1	34396	+	N.A.	YAL061W	☰	ℹ	▦	▥
20	Hi	CATGAAGCTGATAA	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W	☰	ℹ	▦	▥
21	Hi	CATGATTGTGATTG	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	YAL061W	☰	ℹ	▦	▥

Query Results: Typical output of the Genome Explore Form.



Search Potential Tags in a Genome: Results

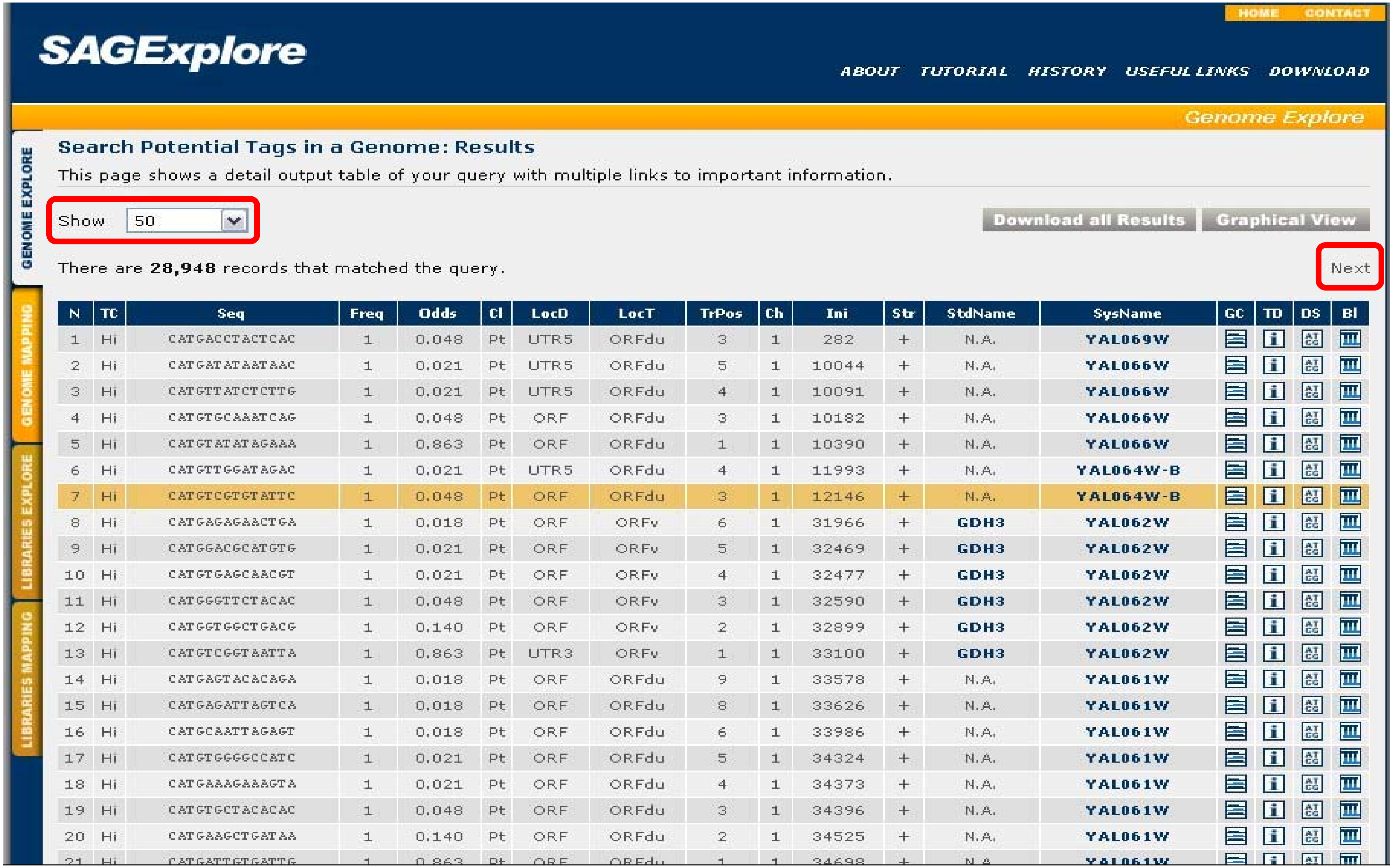
This page shows a detail output table of your query with multiple links to important information.

Show 50

There are **28,948** records that matched the query.

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	Bl
1	Hi	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	3	1	282	+	N.A.	YAL069W	☰	ℹ	AT CG	▥
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W	☰	ℹ	AT CG	▥
3	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W	☰	ℹ	AT CG	▥
4	Hi	CATGTGCAAATCAG	1	0.048	Pt	ORF	ORFdu	3	1	10182	+	N.A.	YAL066W	☰	ℹ	AT CG	▥
5	Hi	CATGTATATAGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W	☰	ℹ	AT CG	▥
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B	☰	ℹ	AT CG	▥
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	3	1	12146	+	N.A.	YAL064W-B	☰	ℹ	AT CG	▥
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	GDH3	YAL062W	☰	ℹ	AT CG	▥
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W	☰	ℹ	AT CG	▥
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W	☰	ℹ	AT CG	▥
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	3	1	32590	+	GDH3	YAL062W	☰	ℹ	AT CG	▥
12	Hi	CATGGTGGCTGACG	1	0.140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W	☰	ℹ	AT CG	▥
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W	☰	ℹ	AT CG	▥
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W	☰	ℹ	AT CG	▥
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W	☰	ℹ	AT CG	▥
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W	☰	ℹ	AT CG	▥
17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W	☰	ℹ	AT CG	▥
18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W	☰	ℹ	AT CG	▥
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	3	1	34396	+	N.A.	YAL061W	☰	ℹ	AT CG	▥
20	Hi	CATGAAGCTGATAA	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W	☰	ℹ	AT CG	▥
21	Hi	CATGATTGTGATTG	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	YAL061W	☰	ℹ	AT CG	▥

Query Results: The total number of records that matched the query are reported.



Search Potential Tags in a Genome: Results

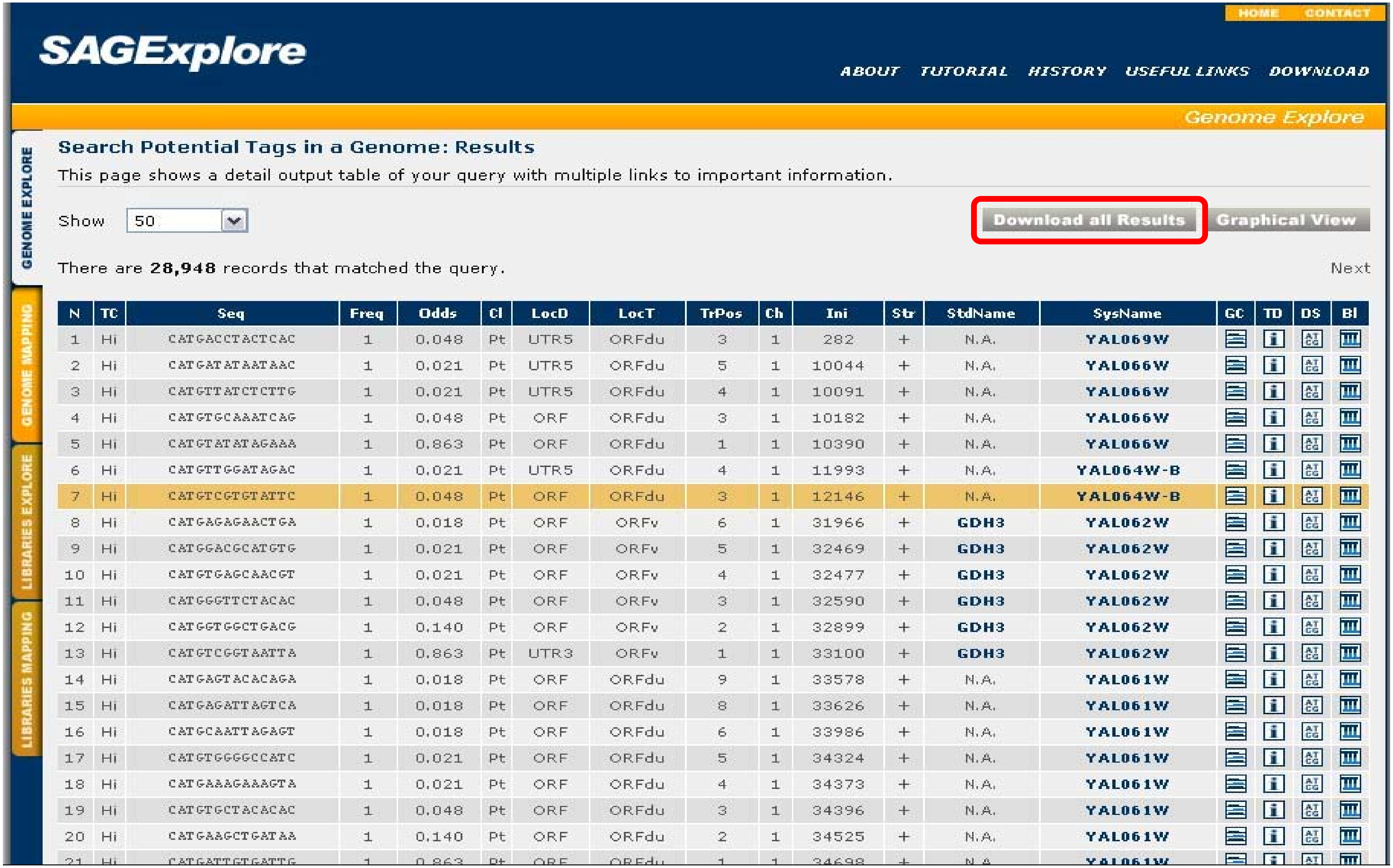
This page shows a detail output table of your query with multiple links to important information.

Show 50

There are **28,948** records that matched the query.

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	BI
1	Hi	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	3	1	282	+	N.A.	**YAL069W**	☰	ℹ	AT CG	▥
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	**YAL066W**	☰	ℹ	AT CG	▥
3	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	**YAL066W**	☰	ℹ	AT CG	▥
4	Hi	CATGTGCAAATCAG	1	0.048	Pt	ORF	ORFdu	3	1	10182	+	N.A.	**YAL066W**	☰	ℹ	AT CG	▥
5	Hi	CATGTATATAGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	**YAL066W**	☰	ℹ	AT CG	▥
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	**YAL064W-B**	☰	ℹ	AT CG	▥
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	3	1	12146	+	N.A.	**YAL064W-B**	☰	ℹ	AT CG	▥
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	**GDH3**	**YAL062W**	☰	ℹ	AT CG	▥
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	**GDH3**	**YAL062W**	☰	ℹ	AT CG	▥
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	**GDH3**	**YAL062W**	☰	ℹ	AT CG	▥
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	3	1	32590	+	**GDH3**	**YAL062W**	☰	ℹ	AT CG	▥
12	Hi	CATGGTGGCTGACG	1	0.140	Pt	ORF	ORFv	2	1	32899	+	**GDH3**	**YAL062W**	☰	ℹ	AT CG	▥
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	**GDH3**	**YAL062W**	☰	ℹ	AT CG	▥
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	**YAL061W**	☰	ℹ	AT CG	▥
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	**YAL061W**	☰	ℹ	AT CG	▥
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	**YAL061W**	☰	ℹ	AT CG	▥
17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	**YAL061W**	☰	ℹ	AT CG	▥
18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	**YAL061W**	☰	ℹ	AT CG	▥
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	3	1	34396	+	N.A.	**YAL061W**	☰	ℹ	AT CG	▥
20	Hi	CATGAAGCTGATAA	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	**YAL061W**	☰	ℹ	AT CG	▥
21	Hi	CATGATTGTGATTG	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	**YAL061W**	☰	ℹ	AT CG	▥

Query Results: Only a fraction of the results is displayed. This option can be easily changed by selecting a different number of rows to display or the next button used to go to the next page.



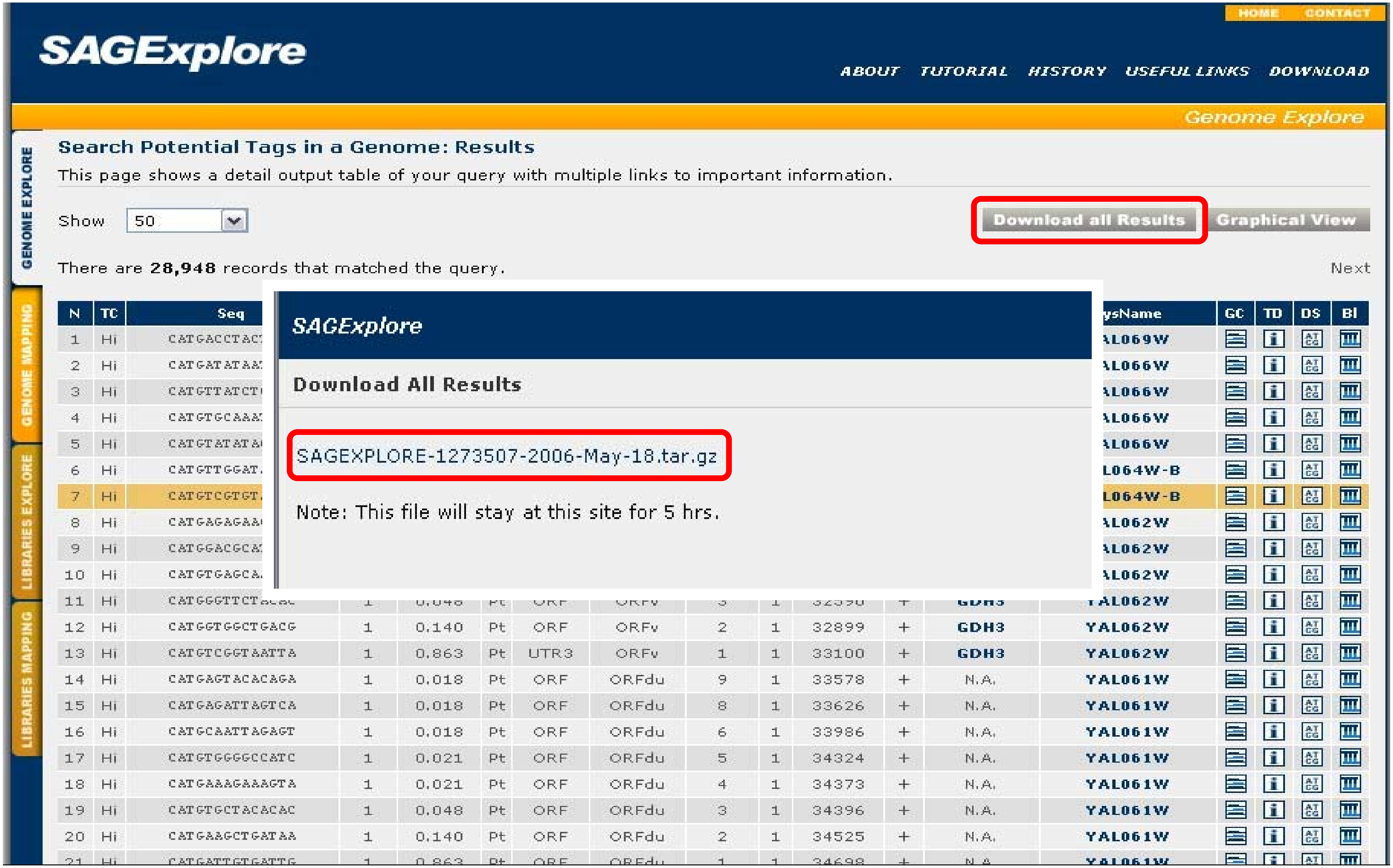
Search Potential Tags in a Genome: Results

This page shows a detail output table of your query with multiple links to important information.

There are **28,948** records that matched the query.

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	Bl
1	Hi	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	3	1	282	+	N.A.	YAL069W	☰	ℹ	▦	▥
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W	☰	ℹ	▦	▥
3	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W	☰	ℹ	▦	▥
4	Hi	CATGTGCAAATCAG	1	0.048	Pt	ORF	ORFdu	3	1	10182	+	N.A.	YAL066W	☰	ℹ	▦	▥
5	Hi	CATGTATATAGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W	☰	ℹ	▦	▥
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B	☰	ℹ	▦	▥
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	3	1	12146	+	N.A.	YAL064W-B	☰	ℹ	▦	▥
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	GDH3	YAL062W	☰	ℹ	▦	▥
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W	☰	ℹ	▦	▥
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W	☰	ℹ	▦	▥
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	3	1	32590	+	GDH3	YAL062W	☰	ℹ	▦	▥
12	Hi	CATGGTGGCTGACG	1	0.140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W	☰	ℹ	▦	▥
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W	☰	ℹ	▦	▥
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W	☰	ℹ	▦	▥
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W	☰	ℹ	▦	▥
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W	☰	ℹ	▦	▥
17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W	☰	ℹ	▦	▥
18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W	☰	ℹ	▦	▥
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	3	1	34396	+	N.A.	YAL061W	☰	ℹ	▦	▥
20	Hi	CATGAAGCTGATAA	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W	☰	ℹ	▦	▥
21	Hi	CATGATTGTGATTG	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	YAL061W	☰	ℹ	▦	▥

Query Results: The full table can be downloaded as tab-delimited text (compressed file or tar.gzipped).



Search Potential Tags in a Genome: Results

This page shows a detail output table of your query with multiple links to important information.

Show 50

There are **28,948** records that matched the query.

SAGExplore

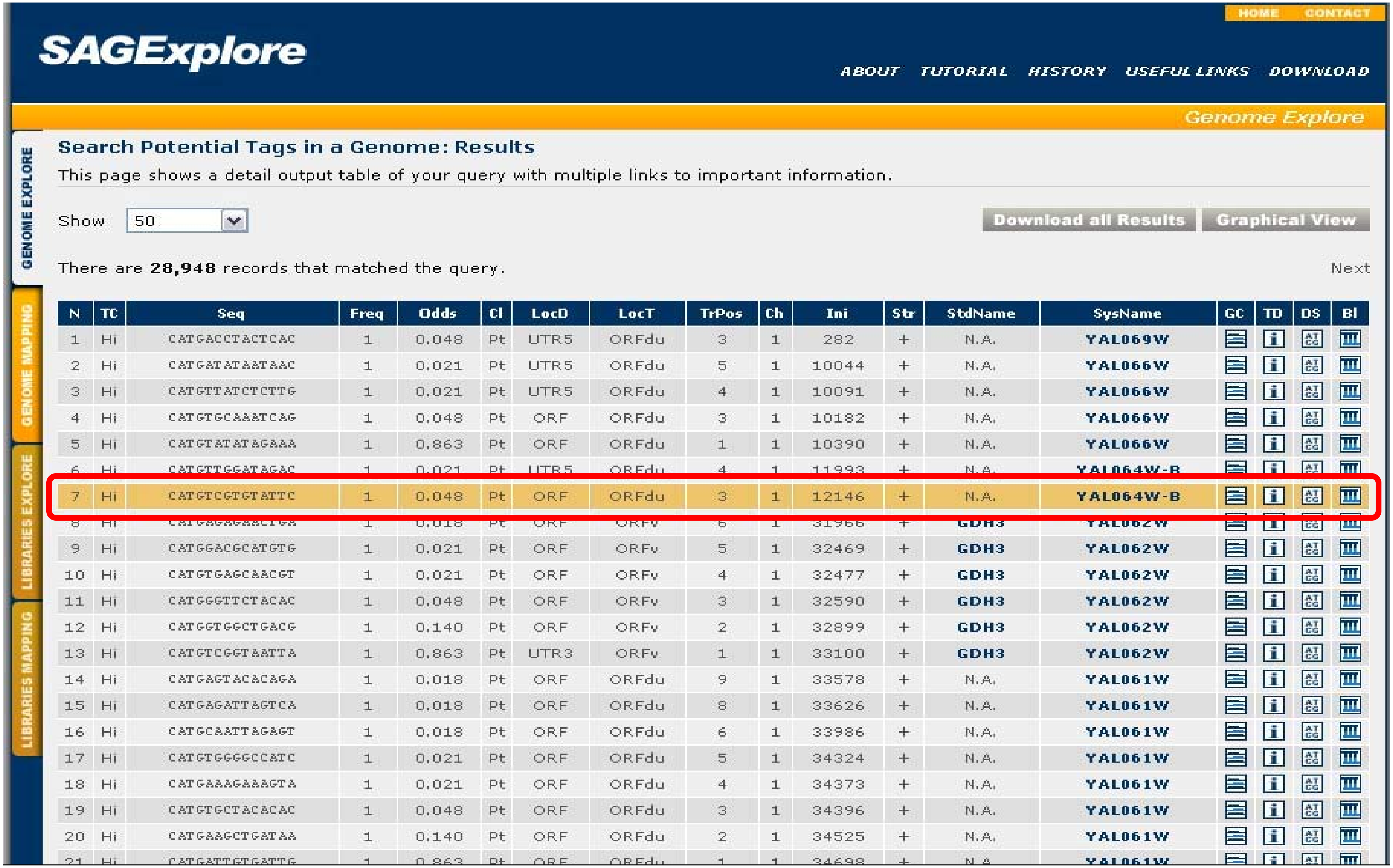
Download All Results

SAGEXPLORE-1273507-2006-May-18.tar.gz

Note: This file will stay at this site for 5 hrs.

N	TC	Seq											ysName	GC	TD	DS	BI
1	Hi	CATGACCTAC											AL069W				
2	Hi	CATGATATAA											AL066W				
3	Hi	CATGTTATCT											AL066W				
4	Hi	CATGTGCAAA											AL066W				
5	Hi	CATGTATATA											AL066W				
6	Hi	CATGTTGGAT											L064W-B				
7	Hi	CATGTCGTGT											L064W-B				
8	Hi	CATGAGAGAA											AL062W				
9	Hi	CATGGACGCA											AL062W				
10	Hi	CATGTGAGCA											AL062W				
11	Hi	CATGGGTTCTacac	1	0.048	Pt	ORF	ORFv	3	1	32590	+	GDH3	YAL062W				
12	Hi	CATGGTGGCTGACG	1	0.140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W				
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W				
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W				
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W				
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W				
17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W				
18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W				
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	3	1	34396	+	N.A.	YAL061W				
20	Hi	CATGAAGCTGATAA	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W				
21	Hi	CATGATTGTGATTG	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	YAL061W				

Query Results: Compressed files for download are kept for 5 hours at the server and then deleted. By clicking on the filename, the file is downloaded.



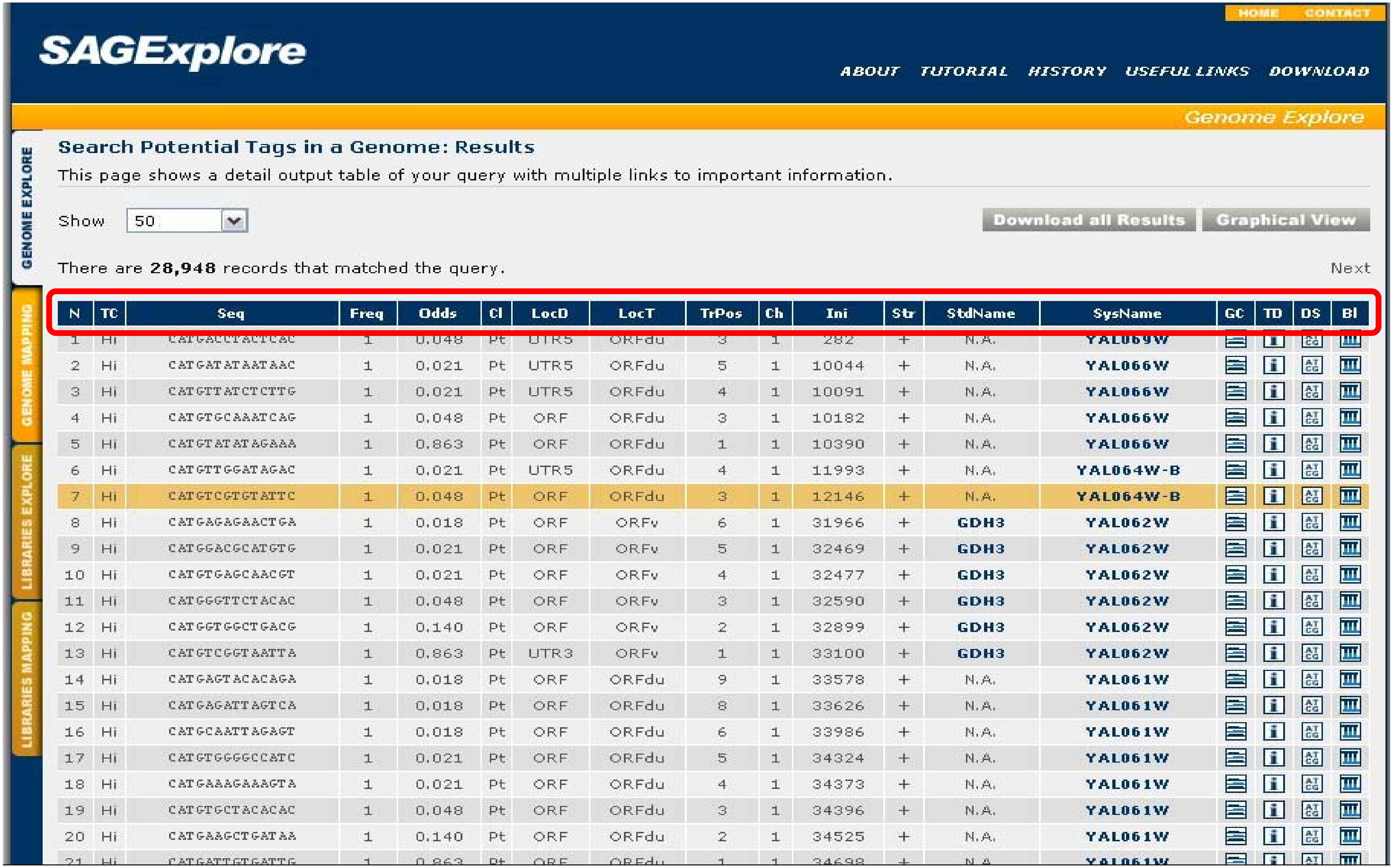
Search Potential Tags in a Genome: Results

This page shows a detail output table of your query with multiple links to important information.

There are **28,948** records that matched the query.

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	Bl
1	Hi	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	3	1	282	+	N.A.	**YAL069W**	☰	ℹ	▦	▥
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	**YAL066W**	☰	ℹ	▦	▥
3	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	**YAL066W**	☰	ℹ	▦	▥
4	Hi	CATGTGCAAATCAG	1	0.048	Pt	ORF	ORFdu	3	1	10182	+	N.A.	**YAL066W**	☰	ℹ	▦	▥
5	Hi	CATGTATATAGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	**YAL066W**	☰	ℹ	▦	▥
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	**YAL064W-B**	☰	ℹ	▦	▥
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	3	1	12146	+	N.A.	**YAL064W-B**	☰	ℹ	▦	▥
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	**GDH3**	**YAL062W**	☰	ℹ	▦	▥
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	**GDH3**	**YAL062W**	☰	ℹ	▦	▥
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	**GDH3**	**YAL062W**	☰	ℹ	▦	▥
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	3	1	32590	+	**GDH3**	**YAL062W**	☰	ℹ	▦	▥
12	Hi	CATGGTGGCTGACG	1	0.140	Pt	ORF	ORFv	2	1	32899	+	**GDH3**	**YAL062W**	☰	ℹ	▦	▥
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	**GDH3**	**YAL062W**	☰	ℹ	▦	▥
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	**YAL061W**	☰	ℹ	▦	▥
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	**YAL061W**	☰	ℹ	▦	▥
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	**YAL061W**	☰	ℹ	▦	▥
17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	**YAL061W**	☰	ℹ	▦	▥
18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	**YAL061W**	☰	ℹ	▦	▥
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	3	1	34396	+	N.A.	**YAL061W**	☰	ℹ	▦	▥
20	Hi	CATGAAGCTGATAA	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	**YAL061W**	☰	ℹ	▦	▥
21	Hi	CATGATTGTGATTG	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	**YAL061W**	☰	ℹ	▦	▥

Query Results: Moving the mouse pointer over the table highlights the current row.



Search Potential Tags in a Genome: Results

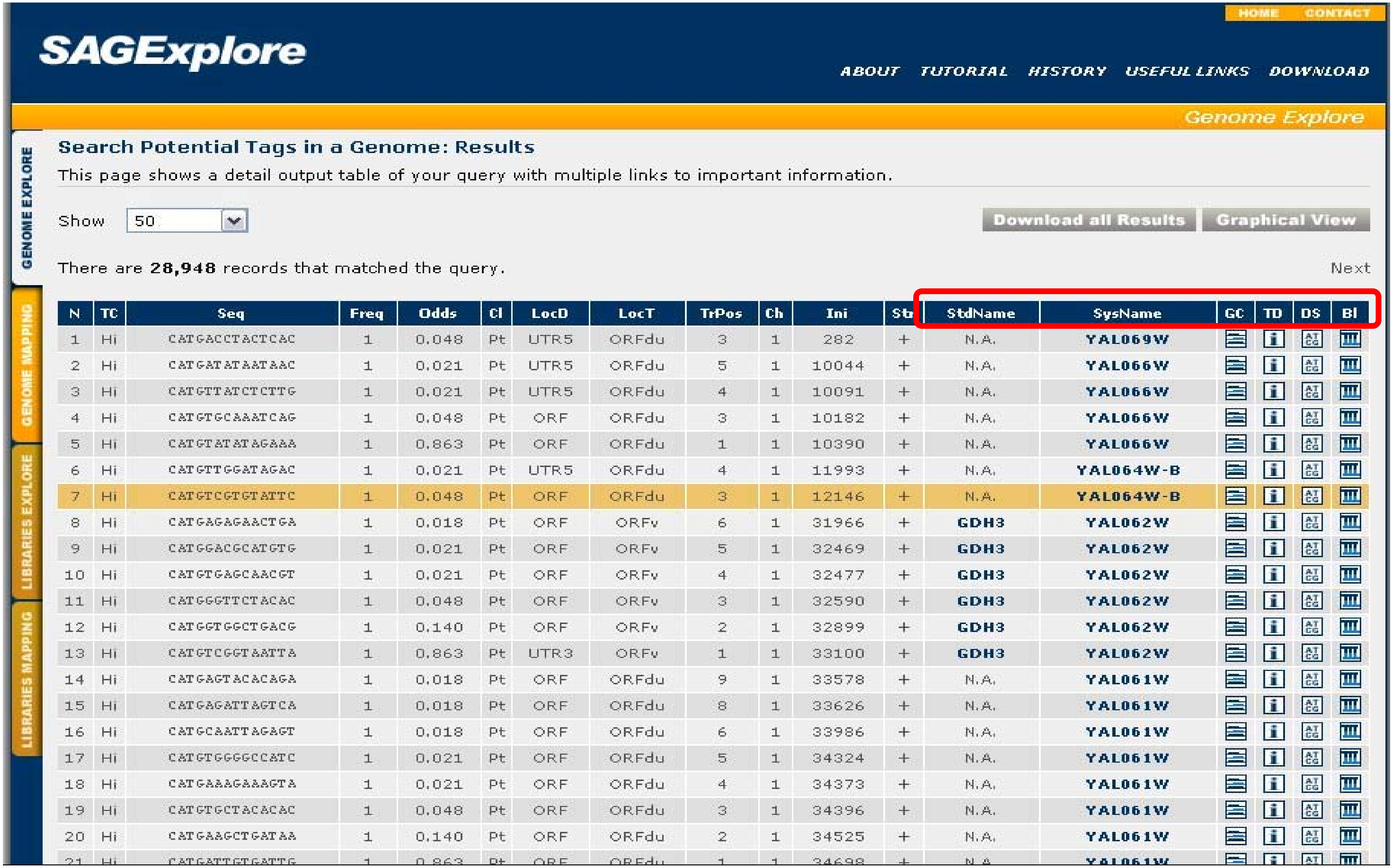
This page shows a detail output table of your query with multiple links to important information.

Show 50

There are **28,948** records that matched the query.

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	BI
1	Hi	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	3	1	282	+	N.A.	YAL069W	☰	ℹ	AT CG	Ⅲ
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W	☰	ℹ	AT CG	Ⅲ
3	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W	☰	ℹ	AT CG	Ⅲ
4	Hi	CATGTGCAAATCAG	1	0.048	Pt	ORF	ORFdu	3	1	10182	+	N.A.	YAL066W	☰	ℹ	AT CG	Ⅲ
5	Hi	CATGTATATAGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W	☰	ℹ	AT CG	Ⅲ
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B	☰	ℹ	AT CG	Ⅲ
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	3	1	12146	+	N.A.	YAL064W-B	☰	ℹ	AT CG	Ⅲ
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	GDH3	YAL062W	☰	ℹ	AT CG	Ⅲ
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W	☰	ℹ	AT CG	Ⅲ
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W	☰	ℹ	AT CG	Ⅲ
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	3	1	32590	+	GDH3	YAL062W	☰	ℹ	AT CG	Ⅲ
12	Hi	CATGGTGGCTGACG	1	0.140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W	☰	ℹ	AT CG	Ⅲ
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W	☰	ℹ	AT CG	Ⅲ
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W	☰	ℹ	AT CG	Ⅲ
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W	☰	ℹ	AT CG	Ⅲ
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W	☰	ℹ	AT CG	Ⅲ
17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W	☰	ℹ	AT CG	Ⅲ
18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W	☰	ℹ	AT CG	Ⅲ
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	3	1	34396	+	N.A.	YAL061W	☰	ℹ	AT CG	Ⅲ
20	Hi	CATGAAGCTGATAA	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W	☰	ℹ	AT CG	Ⅲ
21	Hi	CATGATTGTGATTG	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	YAL061W	☰	ℹ	AT CG	Ⅲ

Query Results: Online help explaining the meaning of each column is obtained by left-clicking with the mouse over the column headers.



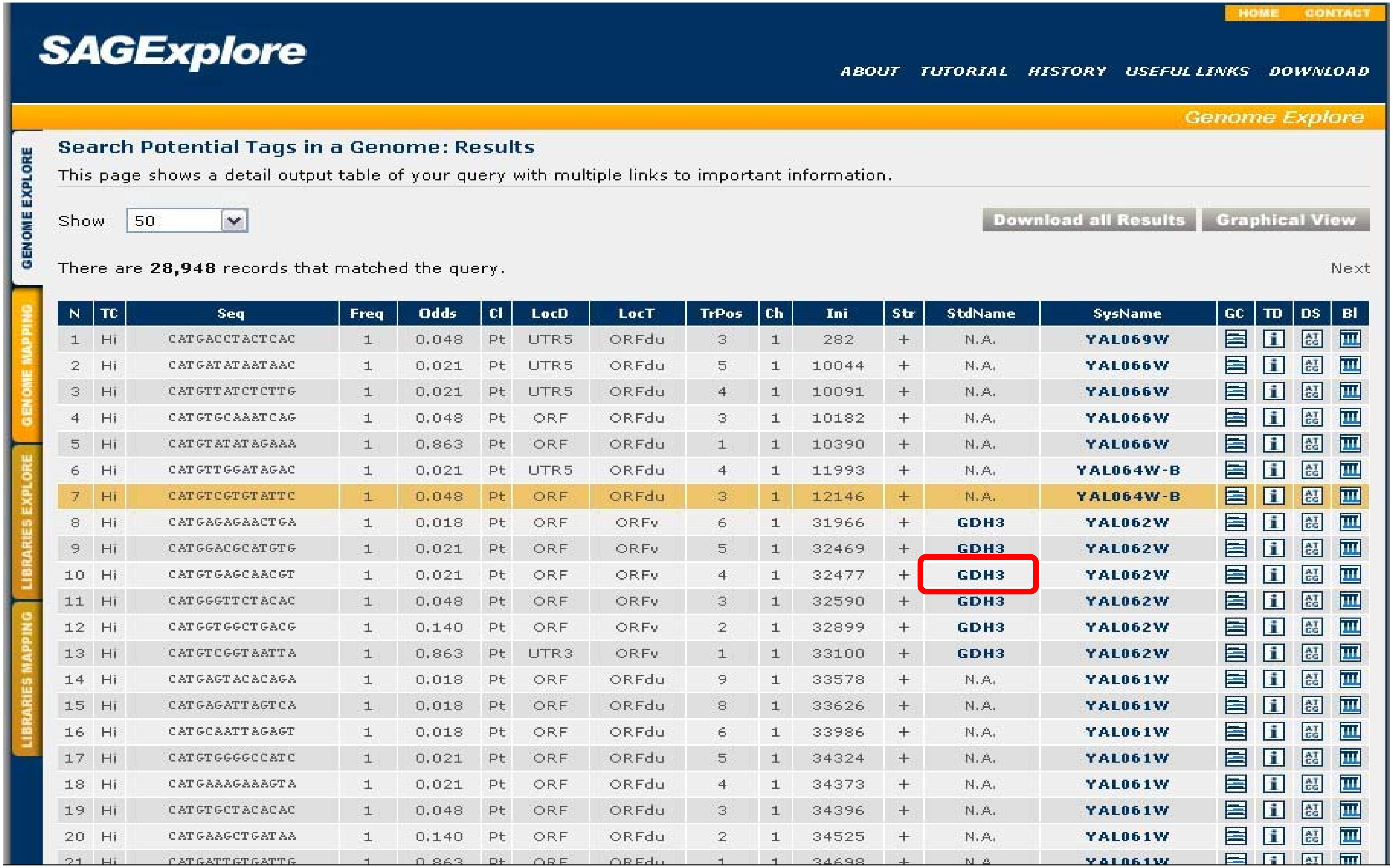
Search Potential Tags in a Genome: Results

This page shows a detail output table of your query with multiple links to important information.

There are **28,948** records that matched the query.

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	St	StdName	SysName	GC	TD	DS	BI
1	Hi	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	3	1	282	+	N.A.	YAL069W				
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W				
3	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W				
4	Hi	CATGTGCAAATCAG	1	0.048	Pt	ORF	ORFdu	3	1	10182	+	N.A.	YAL066W				
5	Hi	CATGTATATAGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W				
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B				
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	3	1	12146	+	N.A.	YAL064W-B				
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	GDH3	YAL062W				
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W				
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W				
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	3	1	32590	+	GDH3	YAL062W				
12	Hi	CATGGTGGCTGACG	1	0.140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W				
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W				
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W				
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W				
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W				
17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W				
18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W				
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	3	1	34396	+	N.A.	YAL061W				
20	Hi	CATGAAGCTGATAA	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W				
21	Hi	CATGATTGTGATTG	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	YAL061W				

Query Results: These 6 columns contain linked fields.



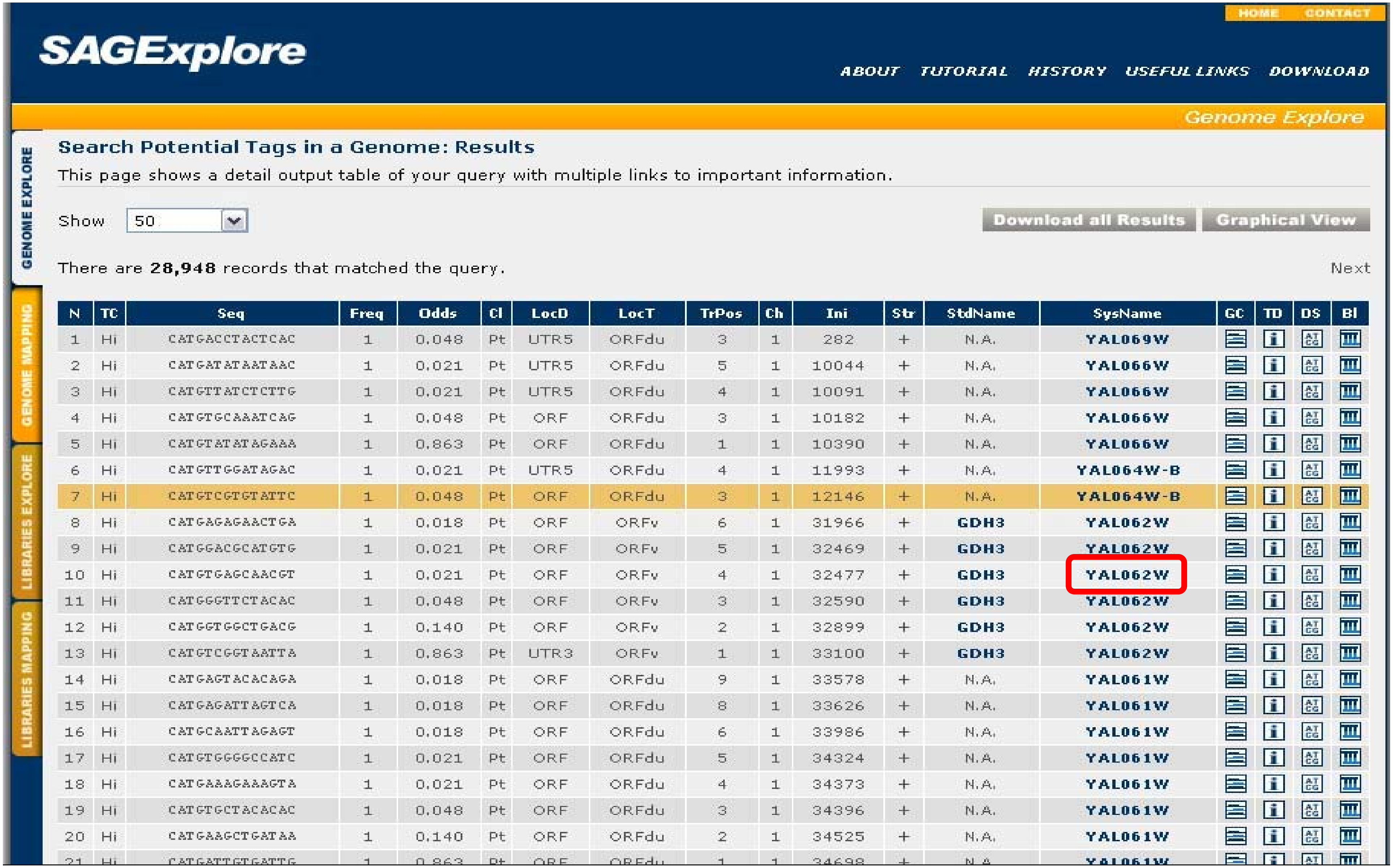
Search Potential Tags in a Genome: Results

This page shows a detail output table of your query with multiple links to important information.

There are **28,948** records that matched the query.

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	BI
1	Hi	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	3	1	282	+	N.A.	**YAL069W**				
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	**YAL066W**				
3	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	**YAL066W**				
4	Hi	CATGTGCAAATCAG	1	0.048	Pt	ORF	ORFdu	3	1	10182	+	N.A.	**YAL066W**				
5	Hi	CATGTATATAGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	**YAL066W**				
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	**YAL064W-B**				
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	3	1	12146	+	N.A.	**YAL064W-B**				
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	**GDH3**	**YAL062W**				
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	**GDH3**	**YAL062W**				
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	**GDH3**	**YAL062W**				
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	3	1	32590	+	**GDH3**	**YAL062W**				
12	Hi	CATGGTGGCTGACG	1	0.140	Pt	ORF	ORFv	2	1	32899	+	**GDH3**	**YAL062W**				
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	**GDH3**	**YAL062W**				
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	**YAL061W**				
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	**YAL061W**				
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	**YAL061W**				
17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	**YAL061W**				
18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	**YAL061W**				
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	3	1	34396	+	N.A.	**YAL061W**				
20	Hi	CATGAAGCTGATAA	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	**YAL061W**				
21	Hi	CATGATTGTGATTG	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	**YAL061W**				

Query Results: By clicking over the standard gene name, a query to the Saccharomyces Genome Database is launched. Thus, the user can obtain a large amount of data about a given gene.



Search Potential Tags in a Genome: Results

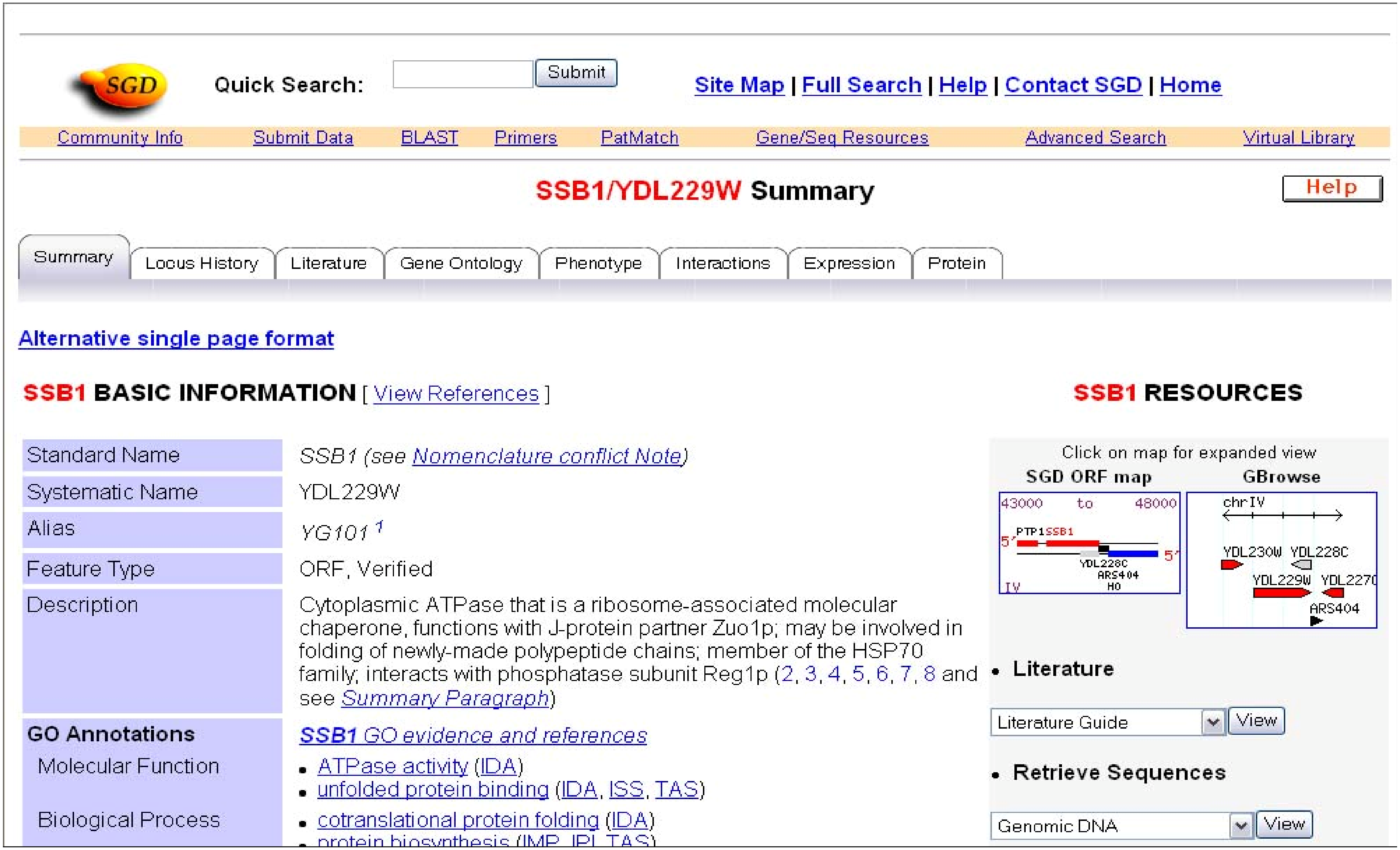
This page shows a detail output table of your query with multiple links to important information.

Show 50

There are **28,948** records that matched the query.

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	BI
1	Hi	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	3	1	282	+	N.A.	YAL069W				
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	YAL066W				
3	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W				
4	Hi	CATGTGCAAATCAG	1	0.048	Pt	ORF	ORFdu	3	1	10182	+	N.A.	YAL066W				
5	Hi	CATGTATATAGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W				
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B				
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	3	1	12146	+	N.A.	YAL064W-B				
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	GDH3	YAL062W				
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W				
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W				
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	3	1	32590	+	GDH3	YAL062W				
12	Hi	CATGGTGGCTGACG	1	0.140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W				
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W				
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	YAL061W				
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W				
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W				
17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W				
18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W				
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	3	1	34396	+	N.A.	YAL061W				
20	Hi	CATGAAGCTGATAA	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W				
21	Hi	CATGATTGTGATTG	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	YAL061W				

Query Results: By clicking over the systematic gene name, a query to the Saccharomyces Genome Database is launched. Thus, the user can obtain a large amount of data about a given gene.



SSB1/YDL229W Summary

Alternative single page format

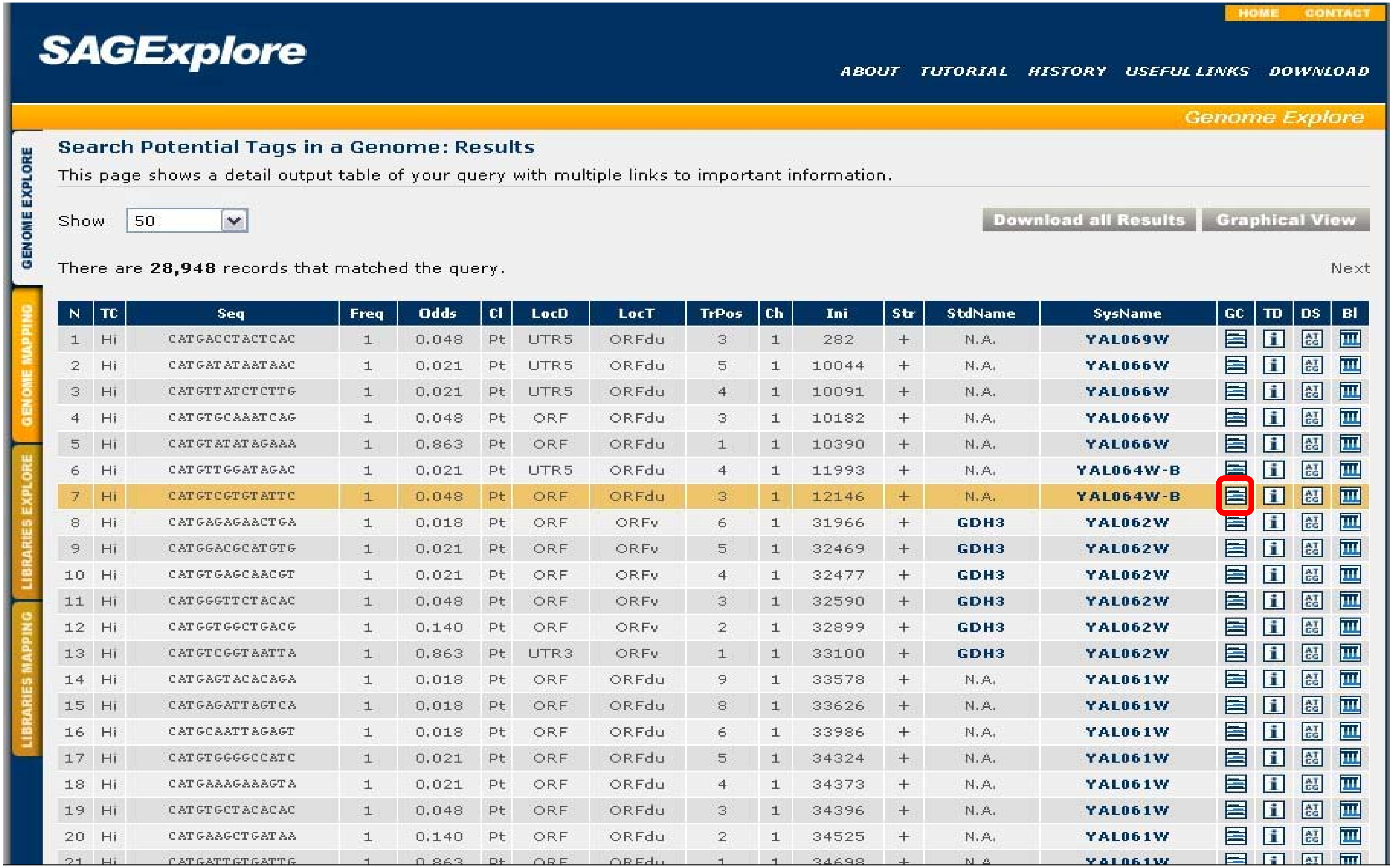
SSB1 BASIC INFORMATION [View References]

SSB1 RESOURCES

Standard Name	*SSB1 (see Nomenclature conflict Note)*
Systematic Name	YDL229W
Alias	*YG101* [1]
Feature Type	ORF, Verified
Description	Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p (2, 3, 4, 5, 6, 7, 8 and see *Summary Paragraph*)
GO Annotations	*SSB1 GO evidence and references*
Molecular Function	ATPase activity (IDA) unfolded protein binding (IDA, ISS, TAS)
Biological Process	cotranslational protein folding (IDA) protein biosynthesis (IMP, IPI, TAS)

- **Literature**
- **Retrieve Sequences**

SGD Query: An example of the results obtained when quering the Saccharomyces Genome Database by standard or systematic gene name.



Search Potential Tags in a Genome: Results

This page shows a detail output table of your query with multiple links to important information.

There are **28,948** records that matched the query.

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	Bl
1	Hi	CATGACCTACTCAC	1	0.048	Pt	UTR5	ORFdu	3	1	282	+	N.A.	**YAL069W**	☰	ℹ	▦	▥
2	Hi	CATGATATAATAAC	1	0.021	Pt	UTR5	ORFdu	5	1	10044	+	N.A.	**YAL066W**	☰	ℹ	▦	▥
3	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	**YAL066W**	☰	ℹ	▦	▥
4	Hi	CATGTGCAAATCAG	1	0.048	Pt	ORF	ORFdu	3	1	10182	+	N.A.	**YAL066W**	☰	ℹ	▦	▥
5	Hi	CATGTATATAGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	**YAL066W**	☰	ℹ	▦	▥
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	**YAL064W-B**	☰	ℹ	▦	▥
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	3	1	12146	+	N.A.	**YAL064W-B**	☰	ℹ	▦	▥
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	**GDH3**	**YAL062W**	☰	ℹ	▦	▥
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	**GDH3**	**YAL062W**	☰	ℹ	▦	▥
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	**GDH3**	**YAL062W**	☰	ℹ	▦	▥
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	3	1	32590	+	**GDH3**	**YAL062W**	☰	ℹ	▦	▥
12	Hi	CATGGTGGCTGACG	1	0.140	Pt	ORF	ORFv	2	1	32899	+	**GDH3**	**YAL062W**	☰	ℹ	▦	▥
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	**GDH3**	**YAL062W**	☰	ℹ	▦	▥
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	**YAL061W**	☰	ℹ	▦	▥
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	**YAL061W**	☰	ℹ	▦	▥
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	**YAL061W**	☰	ℹ	▦	▥
17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	**YAL061W**	☰	ℹ	▦	▥
18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	**YAL061W**	☰	ℹ	▦	▥
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	3	1	34396	+	N.A.	**YAL061W**	☰	ℹ	▦	▥
20	Hi	CATGAAGCTGATAA	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	**YAL061W**	☰	ℹ	▦	▥
21	Hi	CATGATTGTGATTG	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	**YAL061W**	☰	ℹ	▦	▥

Query Results: The genomic context where a tag matches can be obtained by clicking on this field.

SAGExplore

Genomic Context

Organism: *Sacharomyces cerevisiae*
Fragment Displayed: 1 - 6,000

100 Kb Chromosome: 1 Length: 230,208 bp

Keys:

Chromosome:
Watson (+) Strand
Crick (-) Strand
Fragment Displayed
Centromer
TAG of High Confidence
TAG of Undefined Confidence
TAG of Low Confidence

Shape:
Strand
Transcript
Intron
TAG

Color:
UTR5'-ORF-UTR3'
ORF Verified
ORF Uncharacterized
ORF Dubious
tRNA
rRNA
snoRNA
snRNA
ncRNA
TAG of High Confidence
TAG of Undefined Confidence
TAG of Low Confidence

Genomic Context: The selected tag is shown with a vertical arrow head.

SAGExplore

Genomic Context

Organism: *Sacharomyces cerevisiae*
Fragment Displayed: 1 - 6,000

100 Kb **Chromosome: 1** **Length: 230,208 bp**

Keys:

Chromosome:

- ■ Watson (+) Strand
- ■ Crick (-) Strand
- Fragment Displayed
- Centromer
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

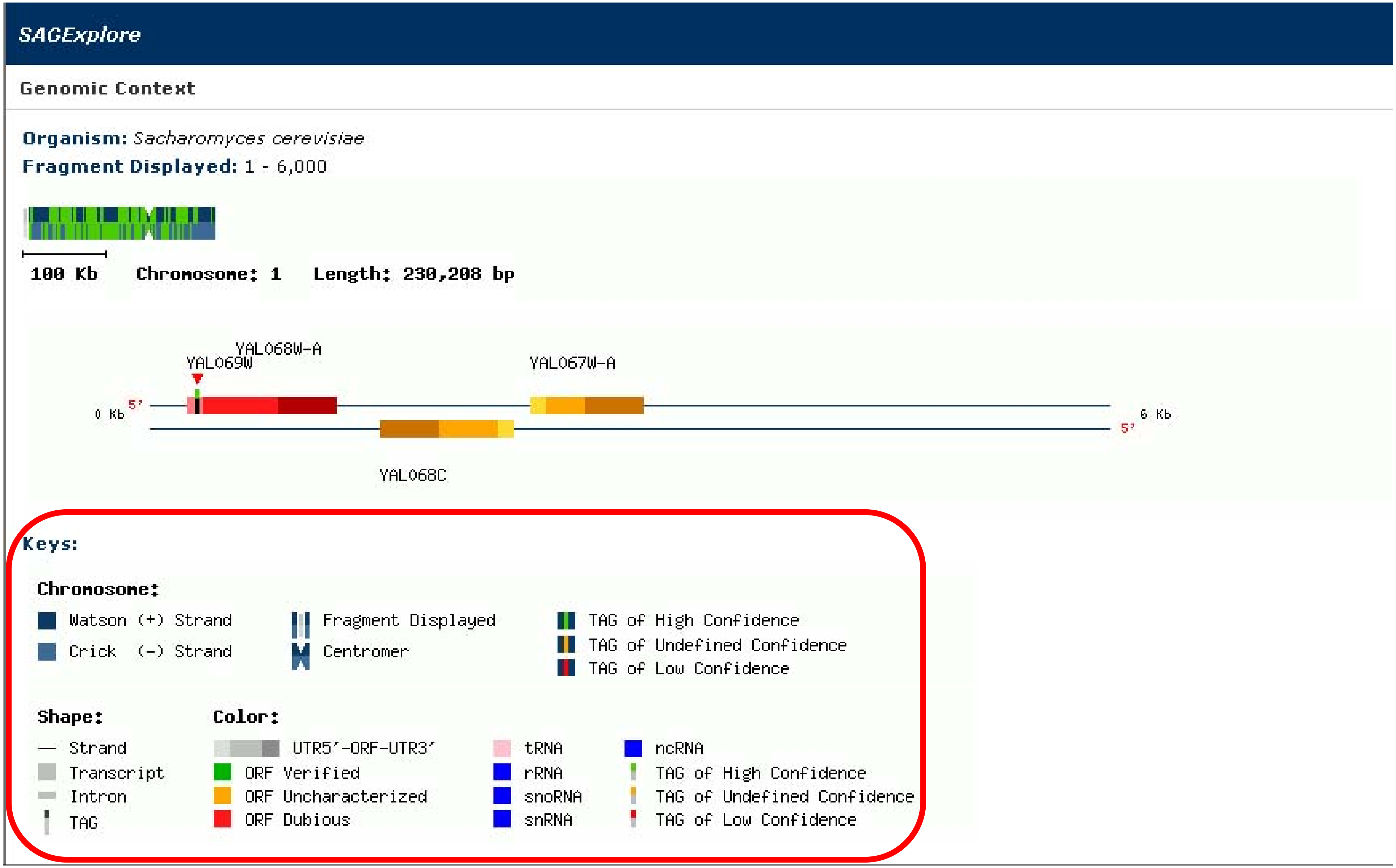
Shape:

- — Strand
- ■ Transcript
- ▬ Intron
- ❘ TAG

Color:

- ▨ UTR5’-ORF-UTR3’
- 🟩 ORF Verified
- 🟧 ORF Uncharacterized
- 🟥 ORF Dubious
- ■ tRNA
- 🟦 rRNA
- 🟦 snoRNA
- 🟦 snRNA
- 🟦 ncRNA
- ❘ TAG of High Confidence
- ❘ TAG of Undefined Confidence
- ❘ TAG of Low Confidence

Genomic Context: Gene names are linked to the Saccharomyces Genome Database.



SAGExplore

Genomic Context

Organism: *Sacharomyces cerevisiae*
Fragment Displayed: 1 - 6,000

100 Kb **Chromosome: 1** **Length: 230,208 bp**

Keys:

Chromosome:

- 🟦 Watson (+) Strand
- 🟦 Crick (-) Strand
- Fragment Displayed
- Centromer
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

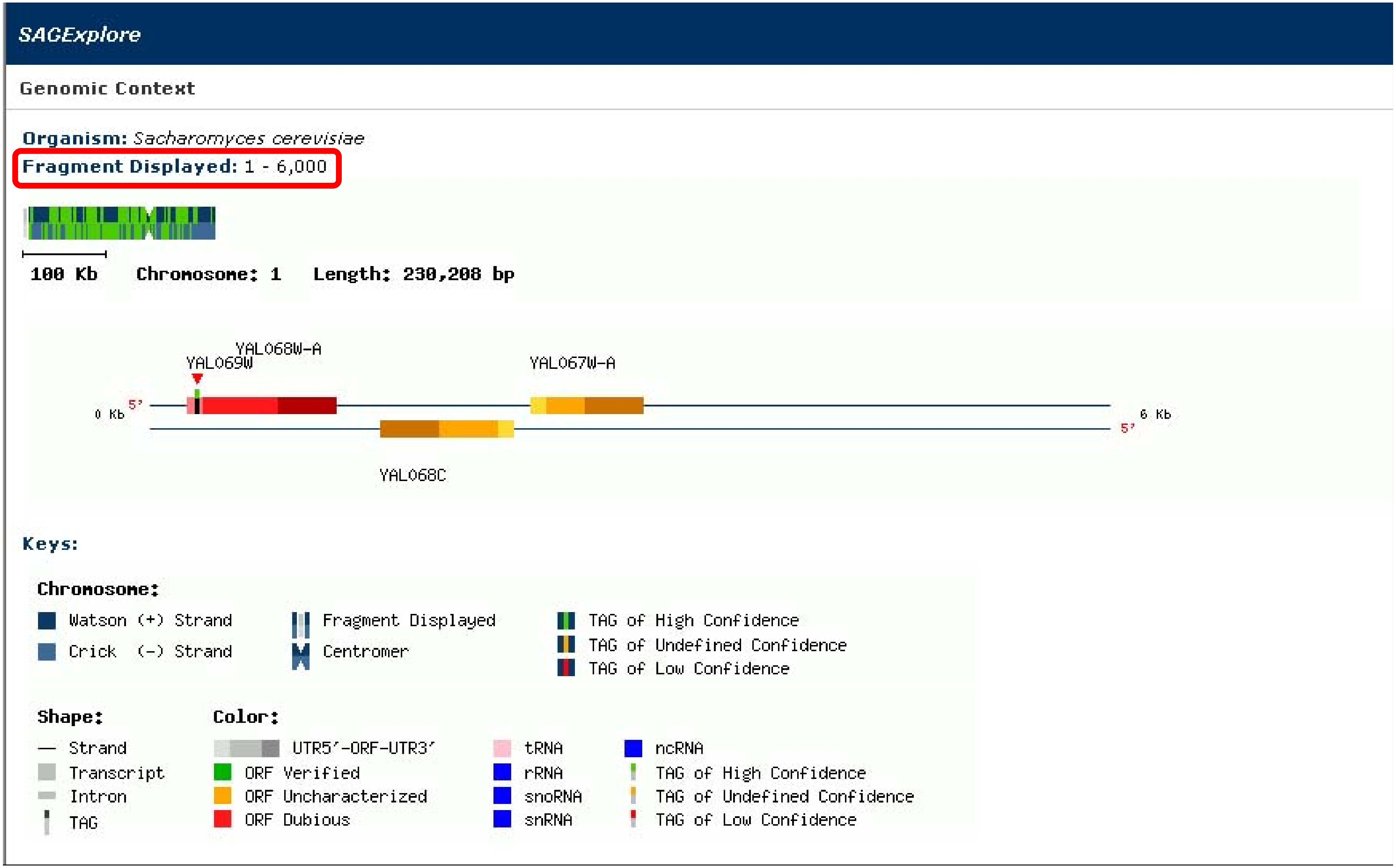
Shape:

- — Strand
- Transcript
- Intron
- TAG

Color:

- UTR5'-ORF-UTR3'
- 🟩 ORF Verified
- 🟧 ORF Uncharacterized
- 🟥 ORF Dubious
- tRNA
- 🟦 rRNA
- 🟦 snoRNA
- 🟦 snRNA
- 🟦 ncRNA
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Genomic Context: Keys of the graphical elements displayed above are provided.



SAGExplore

Genomic Context

Organism: *Sacharomyces cerevisiae*

Fragment Displayed: 1 - 6,000

100 Kb **Chromosome: 1** **Length: 230,208 bp**

Keys:

Chromosome:

Watson (+) Strand
Crick (-) Strand
Fragment Displayed
Centromer
TAG of High Confidence
TAG of Undefined Confidence
TAG of Low Confidence

Shape:

— Strand
Transcript
Intron
TAG

Color:

UTR5'-ORF-UTR3'
🟩 ORF Verified
🟧 ORF Uncharacterized
🟥 ORF Dubious
tRNA
🟦 rRNA
🟦 snoRNA
🟦 snRNA
🟦 ncRNA
TAG of High Confidence
TAG of Undefined Confidence
TAG of Low Confidence

Genomic Context: The fragment of the chromosome being displayed is specified.

SAGExplore

Genomic Context

Organism: *Sacharomyces cerevisiae*

Fragment Displayed: 1 - 6,000

100 Kb **Chromosome: 1** **Length: 230,208 bp**

Keys:

Chromosome:

Watson (+) Strand
Crick (-) Strand
Fragment Displayed
Centromer
TAG of High Confidence
TAG of Undefined Confidence
TAG of Low Confidence

Shape:

— Strand
Transcript
Intron
TAG

Color:

UTR5'-ORF-UTR3'
ORF Verified
ORF Uncharacterized
ORF Dubious
tRNA
rRNA
snoRNA
snRNA
ncRNA
TAG of High Confidence
TAG of Undefined Confidence
TAG of Low Confidence

Genomic Context: In this case corresponds to the 5' end of the chromosome. The user can click on this graphical chromosome to select and display a different region.

SAGExplore

Genomic Context

Organism: *Sacharomyces cerevisiae*

Fragment Displayed: 1 - 6,000

100 Kb **Chromosome: 1** **Length: 230,208 bp**

Keys:

Chromosome:

- Watson (+) Strand
- Crick (-) Strand
- Fragment Displayed
- Centromer
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

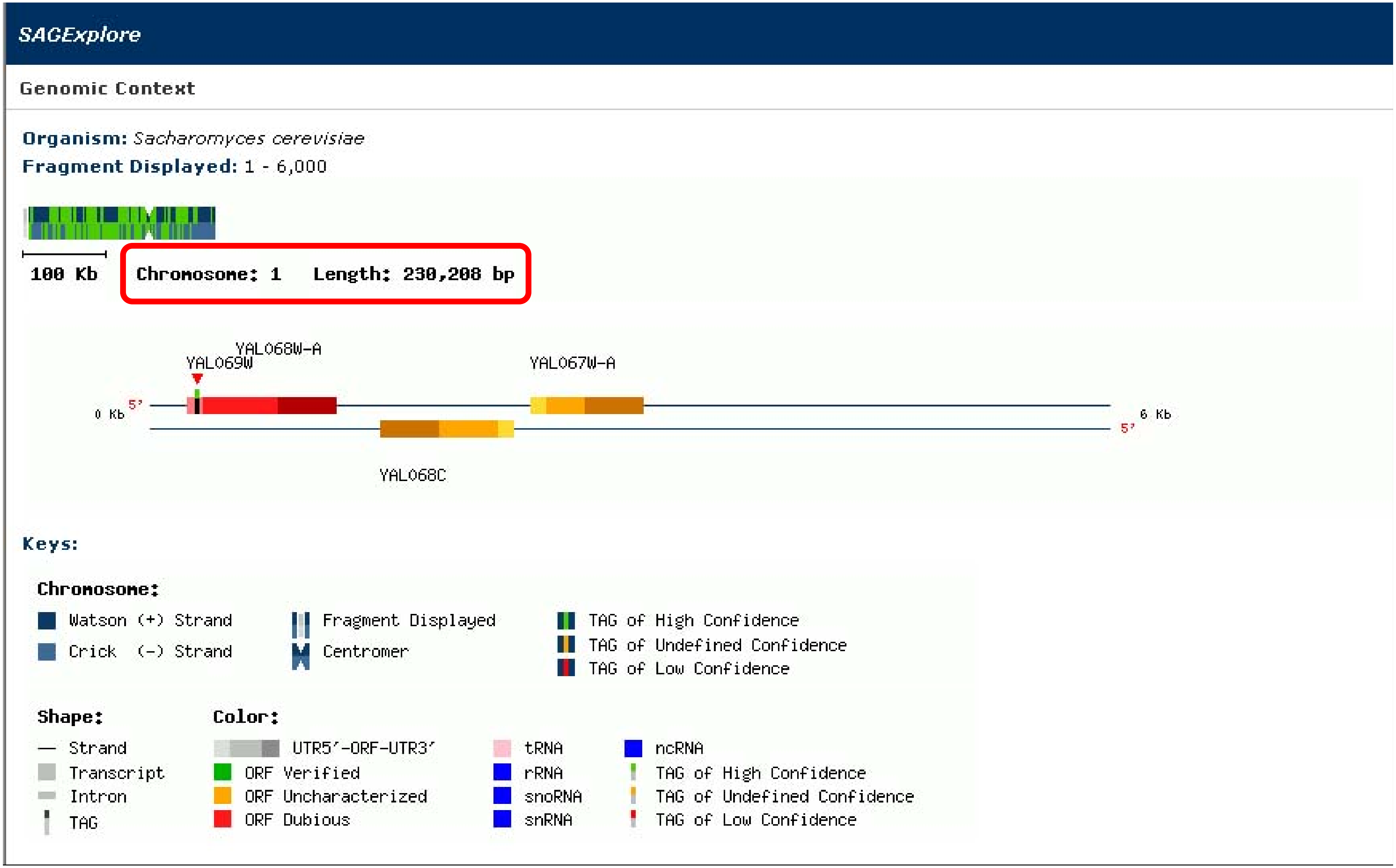
Shape:

- Strand
- Transcript
- Intron
- TAG

Color:

- UTR5'-ORF-UTR3'
- ORF Verified
- ORF Uncharacterized
- ORF Dubious
- tRNA
- rRNA
- snoRNA
- snRNA
- ncRNA
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Genomic Context: The chromosome scale in base pairs is also shown.



Genomic Context

Organism: *Sacharomyces cerevisiae*
Fragment Displayed: 1 - 6,000

100 Kb

Chromosome: 1 Length: 230,208 bp

Keys:

Chromosome:

- Watson (+) Strand
- Crick (-) Strand
- Fragment Displayed
- Centromer
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Shape:

- Strand
- Transcript
- Intron
- TAG

Color:

- UTR5’-ORF-UTR3’
- ORF Verified
- ORF Uncharacterized
- ORF Dubious
- tRNA
- rRNA
- snoRNA
- snRNA
- ncRNA
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Genomic Context: The current chromosome number and size are given.

SAGExplore

Genomic Context

Organism: *Sacharomyces cerevisiae*

Fragment Displayed: 1 - 6,000

100 Kb **Chromosome: 1** **Length: 230,208 bp**

Genomic Context: The 5' and 3' positions of the chromosome fragment displayed are also shown.

SAGExplore

Genomic Context

Organism: *Sacharomyces cerevisiae*

Fragment Displayed: 1 - 6,000

100 Kb Chromosome: 1 Length: 230,208 bp

Keys:

Chromosome:

- Watson (+) Strand
- Crick (-) Strand
- Fragment Displayed
- Centromer
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

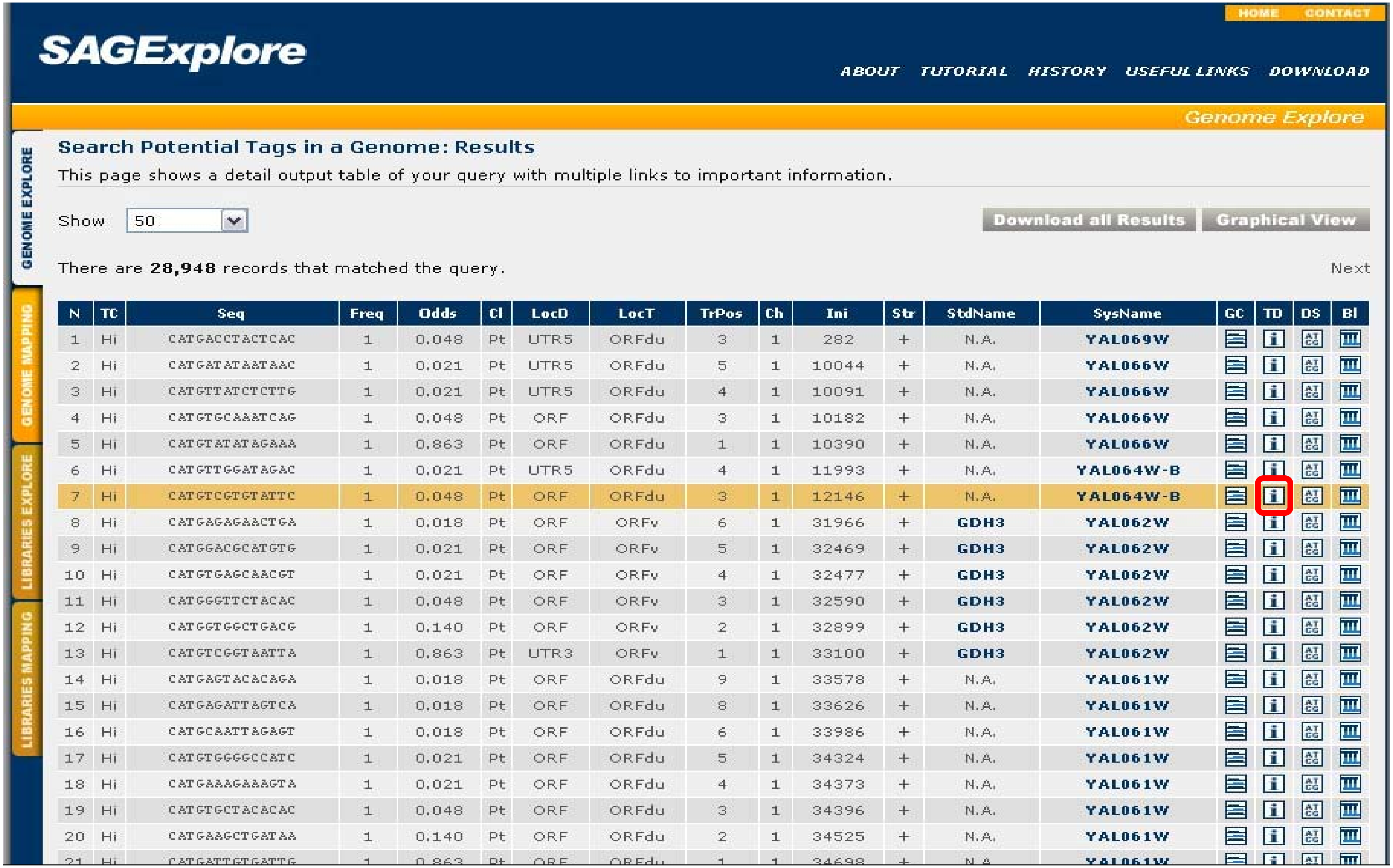
Shape:

- — Strand
- Transcript
- Intron
- TAG

Color:

- UTR5'-ORF-UTR3'
- 🟩 ORF Verified
- 🟧 ORF Uncharacterized
- 🟥 ORF Dubious
- tRNA
- 🟦 rRNA
- 🟦 snoRNA
- 🟦 snRNA
- 🟦 ncRNA
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Genomic Context: Clicking on the tag will display a pop-up window with several details about this tag. This pop-up window can also be launched from the main results table and thus it will be explained next from there.



Search Potential Tags in a Genome: Results

This page shows a detail output table of your query with multiple links to important information.

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3	Hi	CATGTTATCTCTTG	1	0.021	Pt	UTR5	ORFdu	4	1	10091	+	N.A.	YAL066W				
4	Hi	CATGTGCAAATCAG	1	0.048	Pt	ORF	ORFdu	3	1	10182	+	N.A.	YAL066W				
5	Hi	CATGTATATAGAAA	1	0.863	Pt	ORF	ORFdu	1	1	10390	+	N.A.	YAL066W				
6	Hi	CATGTTGGATAGAC	1	0.021	Pt	UTR5	ORFdu	4	1	11993	+	N.A.	YAL064W-B				
7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	3	1	12146	+	N.A.	YAL064W-B				
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	GDH3	YAL062W				
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W				
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W				
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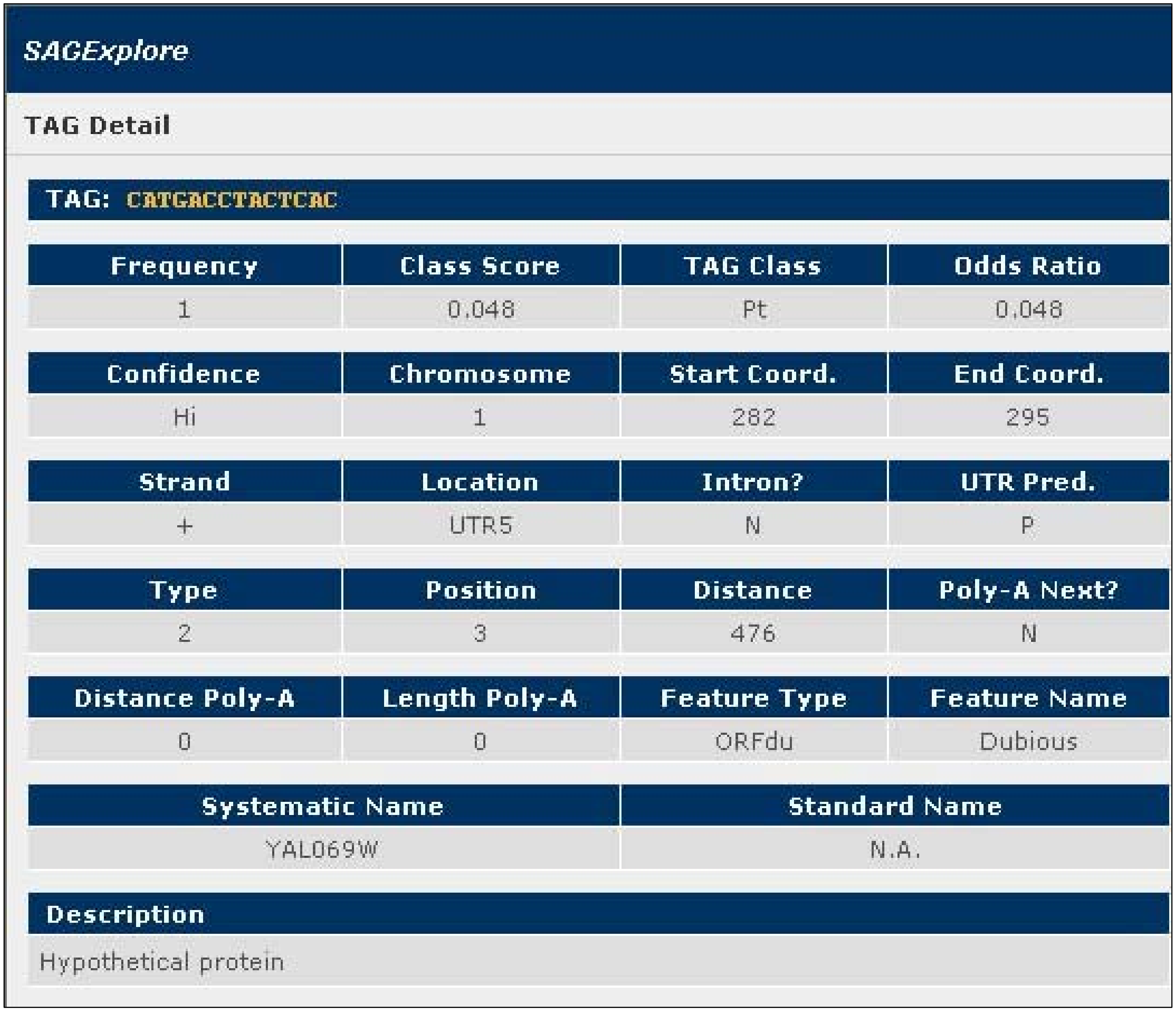
15	Hi	CATGAGATTAGTCA	1	0.018	Pt	ORF	ORFdu	8	1	33626	+	N.A.	YAL061W				
16	Hi	CATGCAATTAGAGT	1	0.018	Pt	ORF	ORFdu	6	1	33986	+	N.A.	YAL061W				
17	Hi	CATGTGGGGCCATC	1	0.021	Pt	ORF	ORFdu	5	1	34324	+	N.A.	YAL061W				
18	Hi	CATGAAAGAAAGTA	1	0.021	Pt	ORF	ORFdu	4	1	34373	+	N.A.	YAL061W				
19	Hi	CATGTGCTACACAC	1	0.048	Pt	ORF	ORFdu	3	1	34396	+	N.A.	YAL061W				
20	Hi	CATGAAGCTGATAA	1	0.140	Pt	ORF	ORFdu	2	1	34525	+	N.A.	YAL061W				
21	Hi	CATGATTGTGATTG	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	YAL061W				

Query Results: A record with several tag details can be obtained by clicking on this field.



SAGExplore

TAG Detail

TAG: CATGACCTACTCAC

Frequency	Class Score	TAG Class	Odds Ratio
1	0.048	Pt	0.048

Confidence	Chromosome	Start Coord.	End Coord.
Hi	1	282	295

Strand	Location	Intron?	UTR Pred.
+	UTR5	N	P

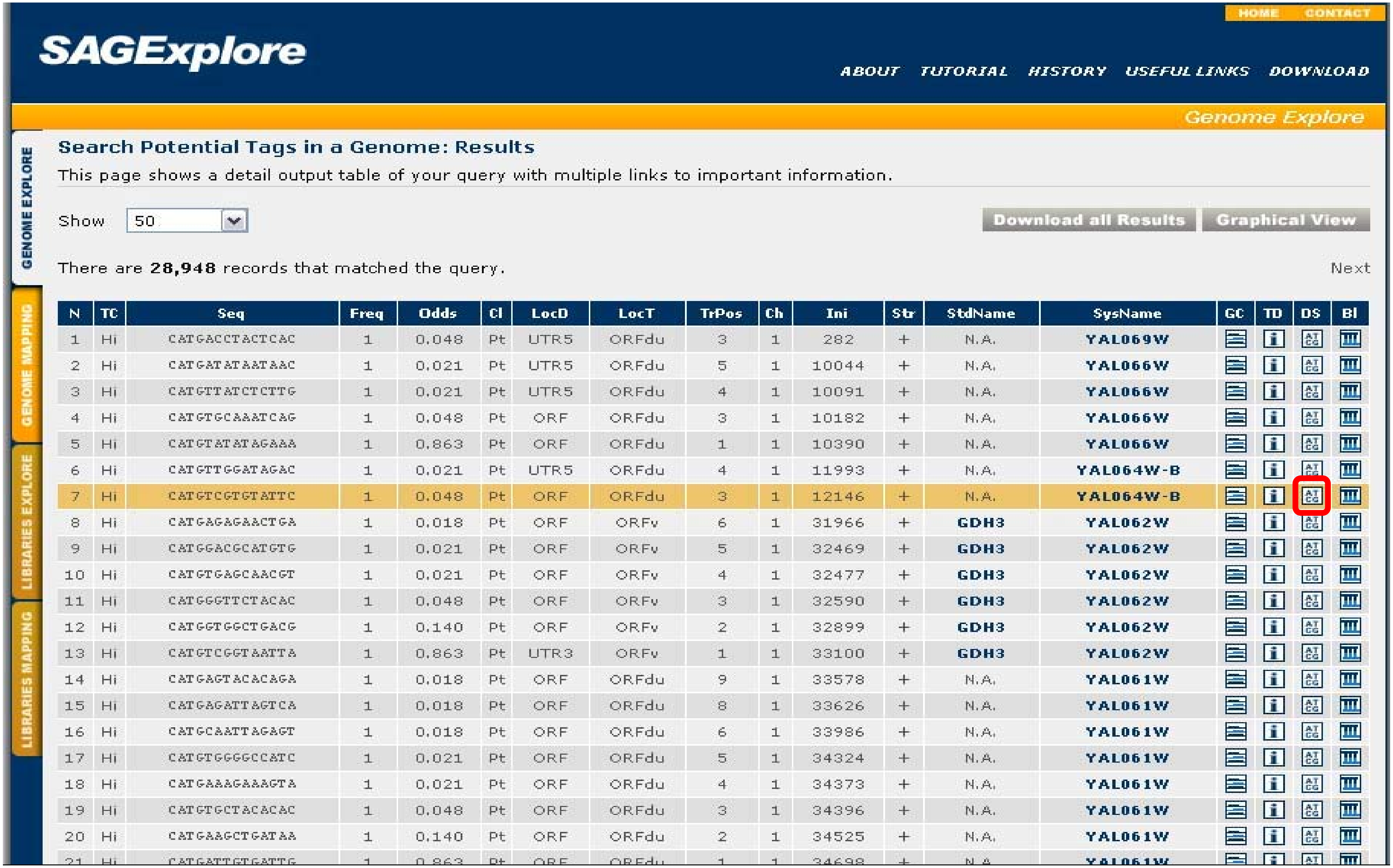
Type	Position	Distance	Poly-A Next?
2	3	476	N

Distance Poly-A	Length Poly-A	Feature Type	Feature Name
0	0	ORFdu	Dubious

Systematic Name	Standard Name
YAL069W	N.A.

Description
Hypothetical protein

Tag details: Many details about the tag are provided here. See the online help for an explanation of each field meaning.



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12	Hi	CATGGTGGCTGACG	1	0.140	Pt	ORF	ORFv	2	1	32899	+	GDH3	YAL062W	☰	ℹ	▦	▥
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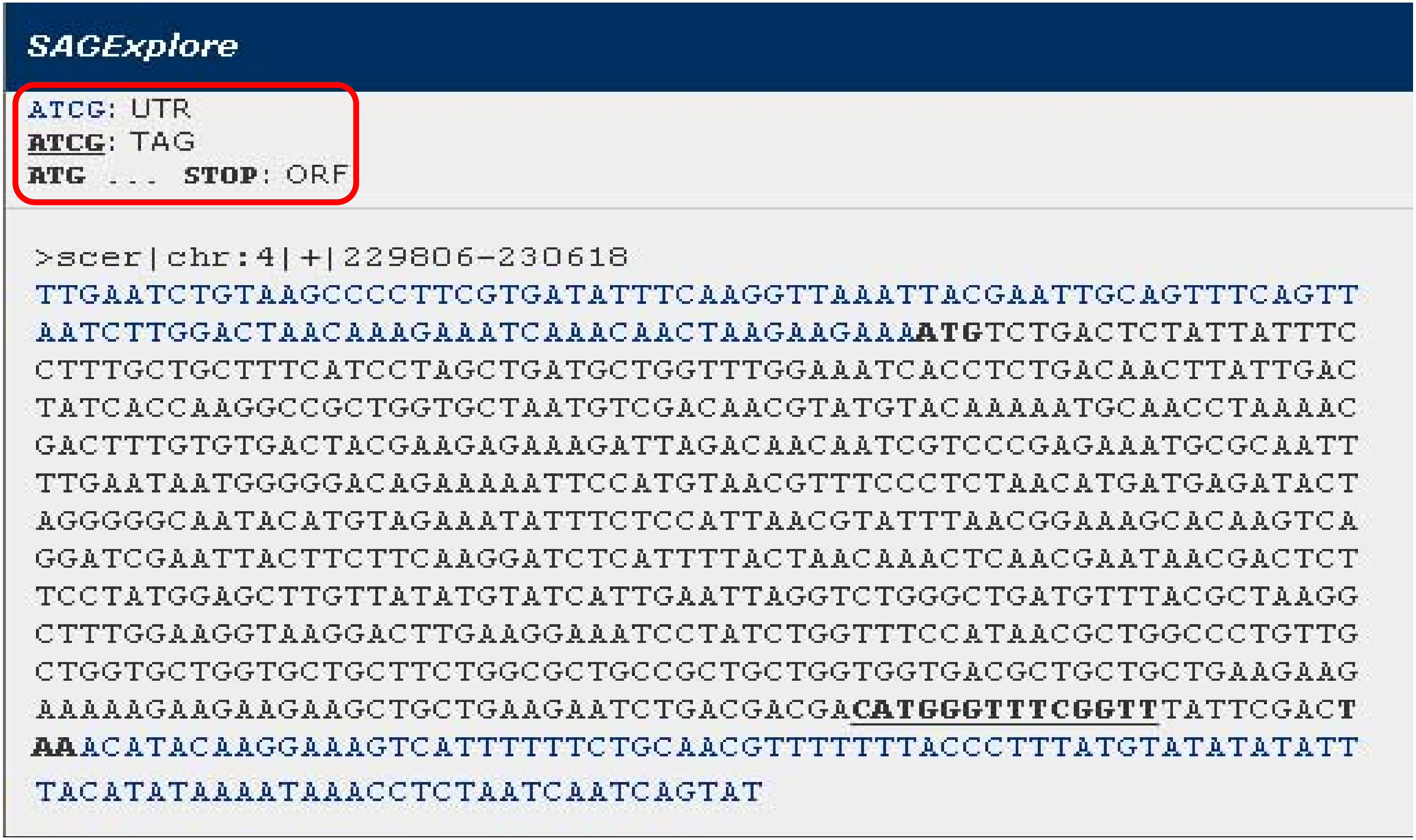
21	Hi	CATGATTGTGATTG	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	YAL061W	☰	ℹ	▦	▥

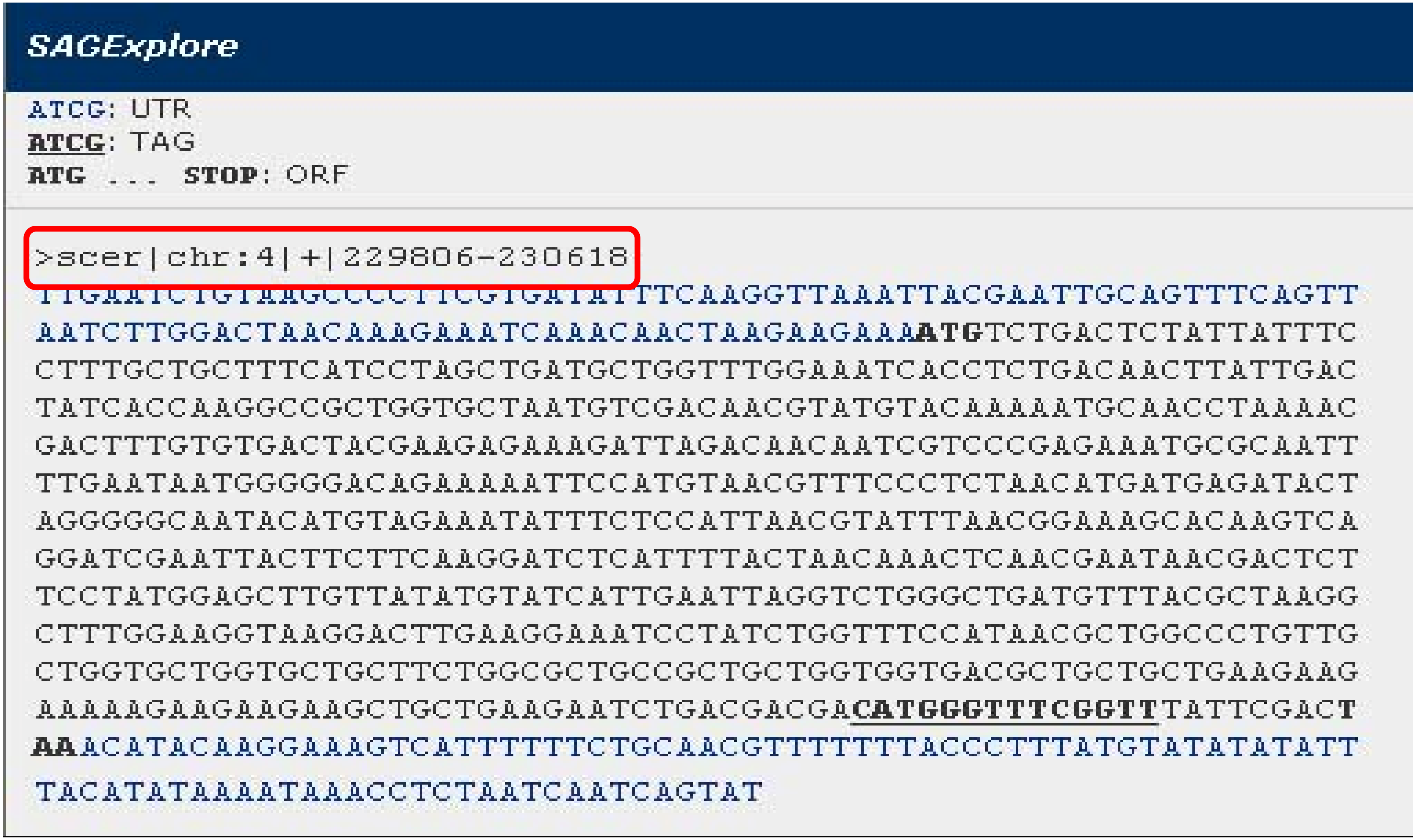
Query Results: The genomic sequence context where the tag matches can be downloaded by clicking on this field.



ATCG: UTR
ATCG: TAG
ATG ... **STOP**: ORF

```
>scer|chr:4|+|229806-230618
TTGAATCTGTAAGCCCCTTCGTGATATTTCAAGGTTAAATTACGAATTGCAGTTTCAGTT
AATCTTGGACTAACAAAGAAATCAAACAACTAAGAAGAAAATGTCTGACTCTATTATTTC
CTTTGCTGCTTTCATCCTAGCTGATGCTGGTTTGGAAATCACCTCTGACAACTTATTGAC
TATCACCAAGGCCGCTGGTGCTAATGTCGACAACGTATGTACAAAAATGCAACCTAAAAC
GACTTTGTGTGACTACGAAGAGAAAGATTAGACAACAATCGTCCCGAGAAATGCGCAATT
TTGAATAATGGGGGACAGAAAAATTCCATGTAACGTTTCCCTCTAACATGATGAGATACT
AGGGGGCAATACATGTAGAAATATTTCTCCATTAACGTATTTAACGGAAAGCACAAGTCA
GGATCGAATTACTTCTTCAAGGATCTCATTTTACTAACAAACTCAACGAATAACGACTCT
TCCTATGGAGCTTGTTATATGTATCATTGAATTAGGTCTGGGCTGATGTTTACGCTAAGG
CTTTGGAAGGTAAGGACTTGAAGGAAATCCTATCTGGTTTCCATAACGCTGGCCCTGTTG
CTGGTGCTGGTGCTGCTTCTGGCGCTGCCGCTGCTGGTGGTGACGCTGCTGCTGAAGAAG
AAAAAGAAGAAGAAGCTGCTGAAGAATCTGACGACGACATGGGTTTCGGTTTATTCGACT
AAACATACAAGGAAAGTCATTTTTTCTGCAACGTTTTTTTACCCTTTATGTATATATATT
TACATATAAAATAAACCTCTAATCAATCAGTAT
```

Download Sequence: If the tag matches an ORF (as it is in this example), the transcript sequence is given. The 5' and 3' UTRs, the start and stop codons, and the tag sequence are all highlighted. If the tag matches an intergenic region, the 500 flanking nucleotides upstream and downstrem the tag are provided. In this case, neighbor elements such as UTRs from other genes are also highlighted if present.



SAGExplore

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ATCG: TAG
ATG ... **STOP**: ORF

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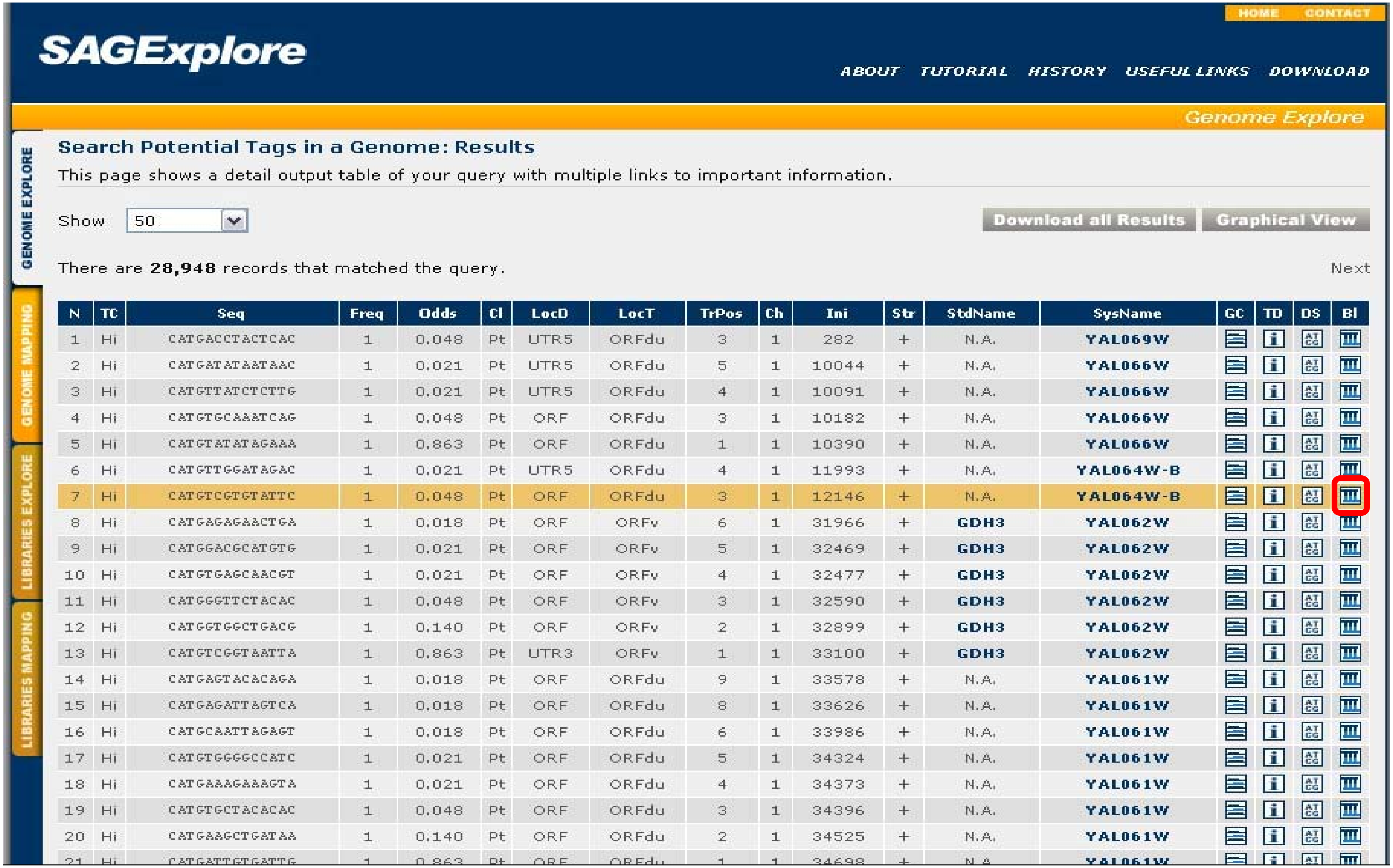
AATCTTGGACTAACAAAGAAATCAAACAACTAAGAAGAAAATGTCTGACTCTATTATTTC
CTTTGCTGCTTTCATCCTAGCTGATGCTGGTTTGGAAATCACCTCTGACAACTTATTGAC
TATCACCAAGGCCGCTGGTGCTAATGTCGACAACGTATGTACAAAAATGCAACCTAAAAC
GACTTTGTGTGACTACGAAGAGAAAGATTAGACAACAATCGTCCCGAGAAATGCGCAATT
TTGAATAATGGGGGACAGAAAAATTCCATGTAACGTTTCCCTCTAACATGATGAGATACT
AGGGGGCAATACATGTAGAAATATTTCTCCATTAACGTATTTAACGGAAAGCACAAGTCA
GGATCGAATTACTTCTTCAAGGATCTCATTTTACTAACAAACTCAACGAATAACGACTCT
TCCTATGGAGCTTGTTATATGTATCATTGAATTAGGTCTGGGCTGATGTTTACGCTAAGG
CTTTGGAAGGTAAGGACTTGAAGGAAATCCTATCTGGTTTCCATAACGCTGGCCCTGTTG
CTGGTGCTGGTGCTGCTTCTGGCGCTGCCGCTGCTGGTGGTGACGCTGCTGCTGAAGAAG
AAAAAGAAGAAGAAGCTGCTGAAGAATCTGACGACGACATGGGTTTCGGTTTATTCGACT
AAACATACAAGGAAAGTCATTTTTTCTGCAACGTTTTTTTACCCTTTATGTATATATATT
TACATATAAAATAAACCTCTAATCAATCAGTAT
```

Download Sequence: The FASTA header indicates the exact region of the sequence displayed.



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7	Hi	CATGTCGTGTATTC	1	0.048	Pt	ORF	ORFdu	3	1	12146	+	N.A.	**YAL064W-B**				
8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	**GDH3**	**YAL062W**				
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	**GDH3**	**YAL062W**				
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	**GDH3**	**YAL062W**				
11	Hi	CATGGGTTCTACAC	1	0.048	Pt	ORF	ORFv	3	1	32590	+	**GDH3**	**YAL062W**				
12	Hi	CATGGTGGCTGACG	1	0.140	Pt	ORF	ORFv	2	1	32899	+	**GDH3**	**YAL062W**				
13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	**GDH3**	**YAL062W**				
14	Hi	CATGAGTACACAGA	1	0.018	Pt	ORF	ORFdu	9	1	33578	+	N.A.	**YAL061W**				
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21	Hi	CATGATTGTGATTG	1	0.863	Pt	ORF	ORFdu	1	1	34698	+	N.A.	**YAL061W**				

Query Results: A query to the BLAST server at the NCBI is launched with the previosuly described sequence by clicking on this field. In the case of tags matching an intergenic region, this option is very useful to aid the process of gene discovery.

Search

```
TCACCAGTGTTAGGGTCAAGAACAACTGCATCAATACCGAAGAAGGGGAATGAGGCAGA
ACCCGGTTTCATTGGTGTAACACCACCAGCCAGCGGGGTGACCAGATGCGAACCAGATT
CTGTTTGCCAGTAGGTGTCTACAATGGGGATTTCATTTTTACCTATTTTTTCAGAGTAC
CACTCCCAAACTTCAGCAGCAATTGGCTCACCGACCGAACCCAAGCAACGCAAAGATTT
TAAGGAATGATTTTCGATGTAGGAATCACCAGCTCTTTTCAACAAACGCAAAGCAGTTG
```

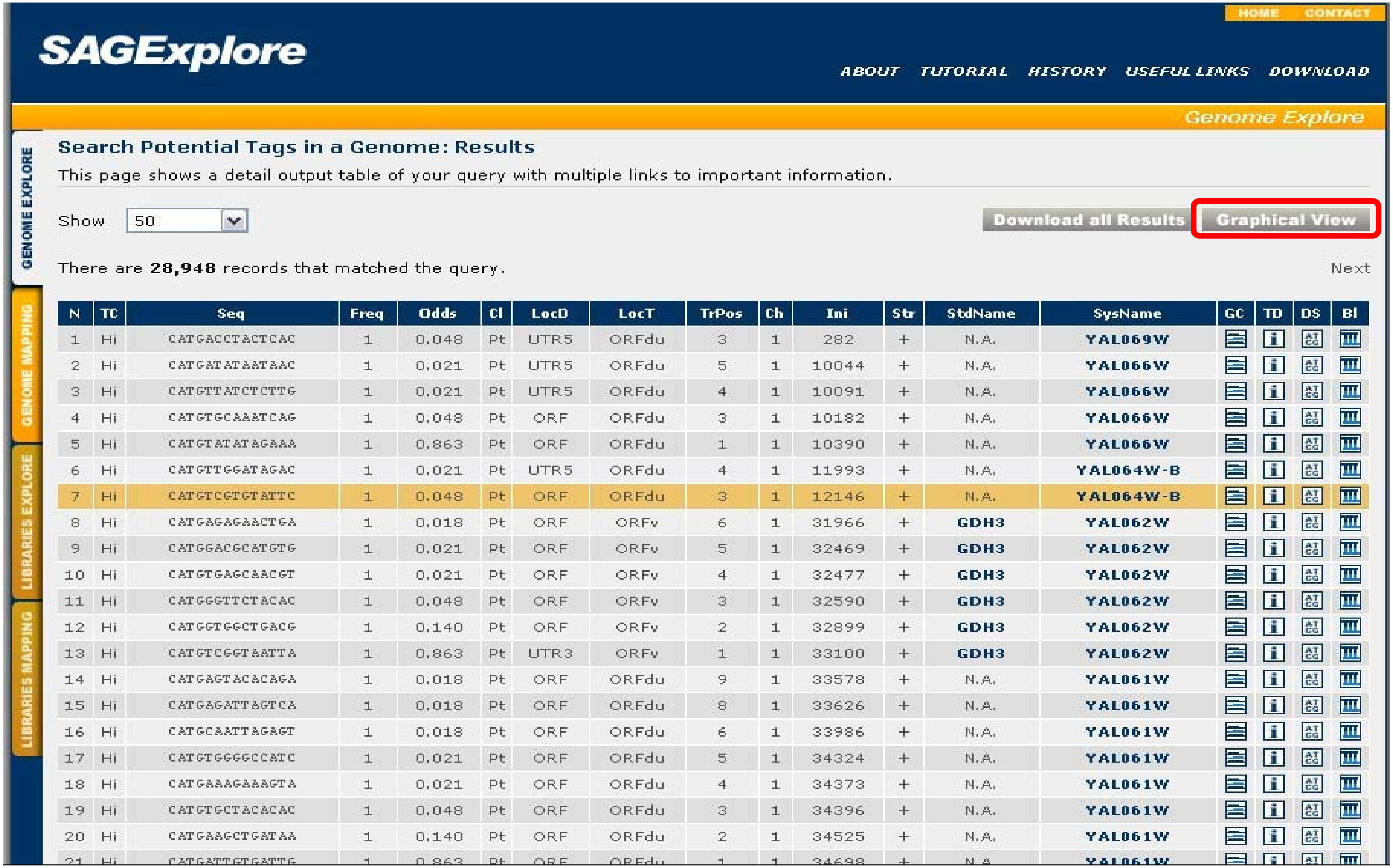
Choose a translation: TRANSLATED query - PROTEIN database [blastx]

Set subsequence From: To:

Choose database: nr

Genetic codes: Standard (1)

BLAST Query: A query to the BLAST server at the NCBI is automatically launched with the flanking sequence that contains the tag. In the case of intergenic tags, BLASTX is launched (this example). In the case of tags matching an ORF, BLASTP is used.



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8	Hi	CATGAGAGAACTGA	1	0.018	Pt	ORF	ORFv	6	1	31966	+	GDH3	YAL062W	☰	ℹ	▦	▥
9	Hi	CATGGACGCATGTG	1	0.021	Pt	ORF	ORFv	5	1	32469	+	GDH3	YAL062W	☰	ℹ	▦	▥
10	Hi	CATGTGAGCAACGT	1	0.021	Pt	ORF	ORFv	4	1	32477	+	GDH3	YAL062W	☰	ℹ	▦	▥
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13	Hi	CATGTCGGTAATTA	1	0.863	Pt	UTR3	ORFv	1	1	33100	+	GDH3	YAL062W	☰	ℹ	▦	▥
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Query Results: A graphical view with all the tags from the results table is also available.

SAGExplore

Graphical View

Organism: *Sacharomyces cerevisiae*

100 Kb Chromosome: 1 Length: 230,208 bp

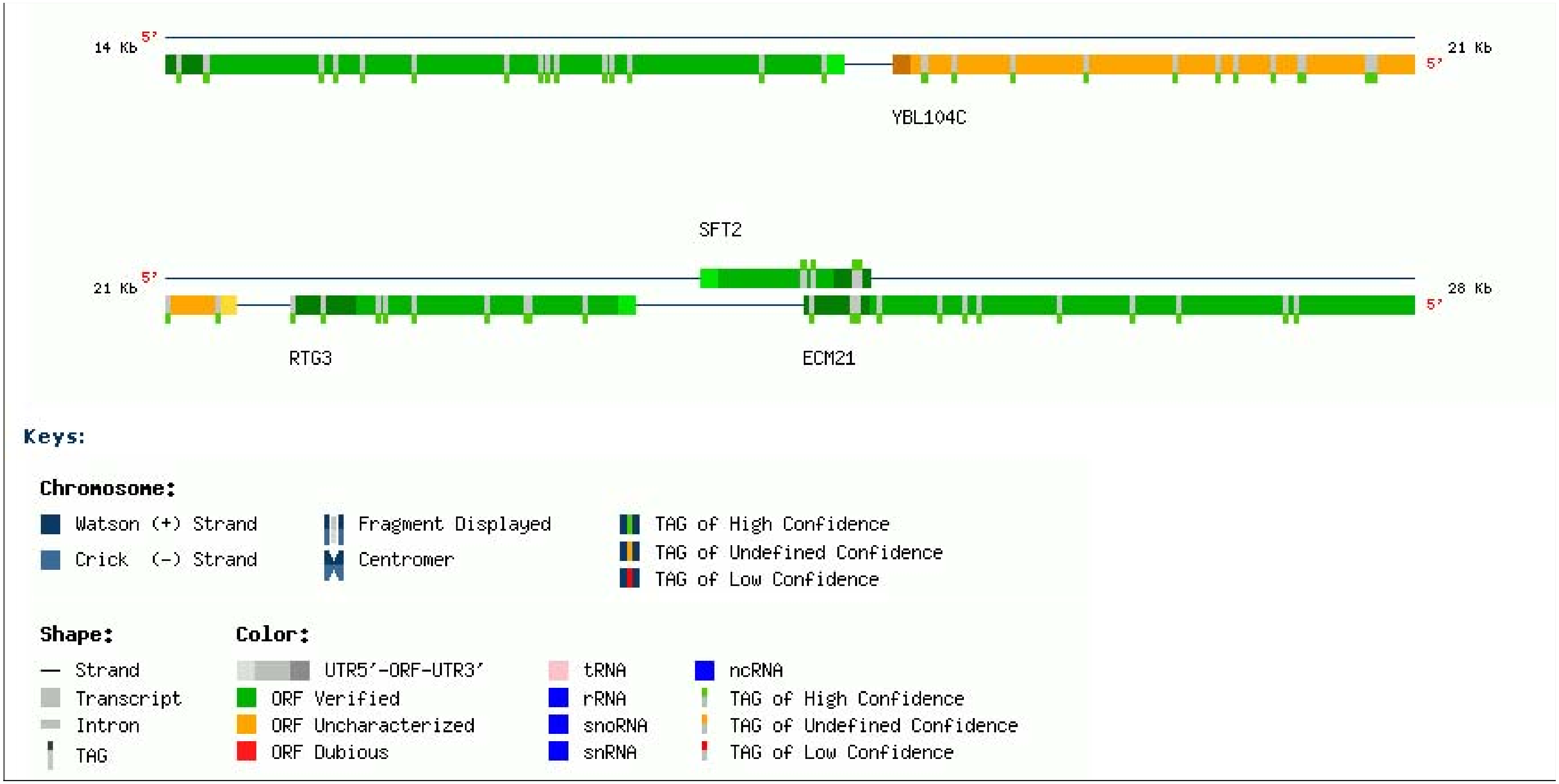
100 Kb Chromosome: 2 Length: 813,178 bp

100 Kb Chromosome: 3 Length: 316,616 bp

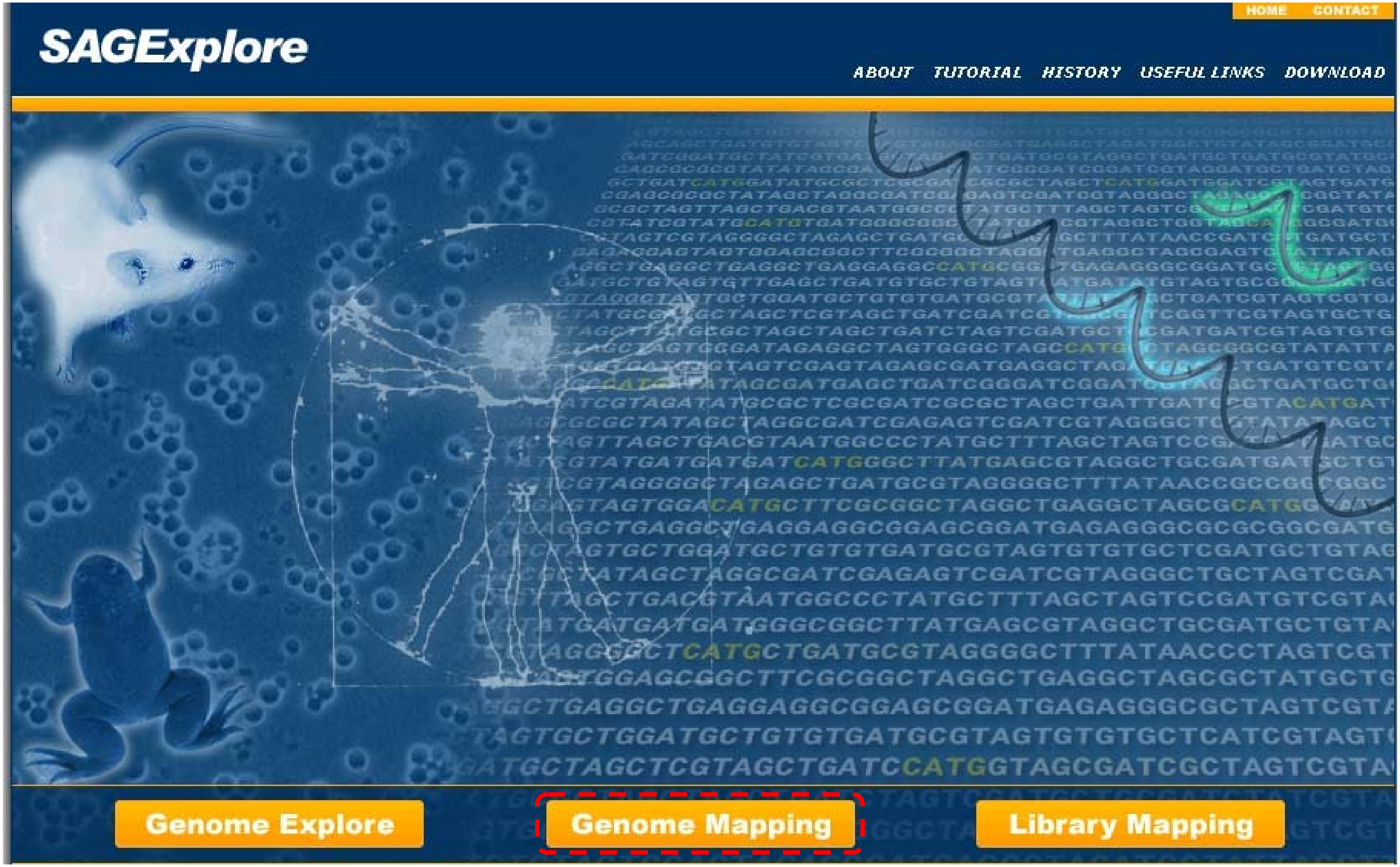
100 Kb Chromosome: 4 Length: 1,531,916 bp

100 Kb Chromosome: 5 Length: 576,869 bp

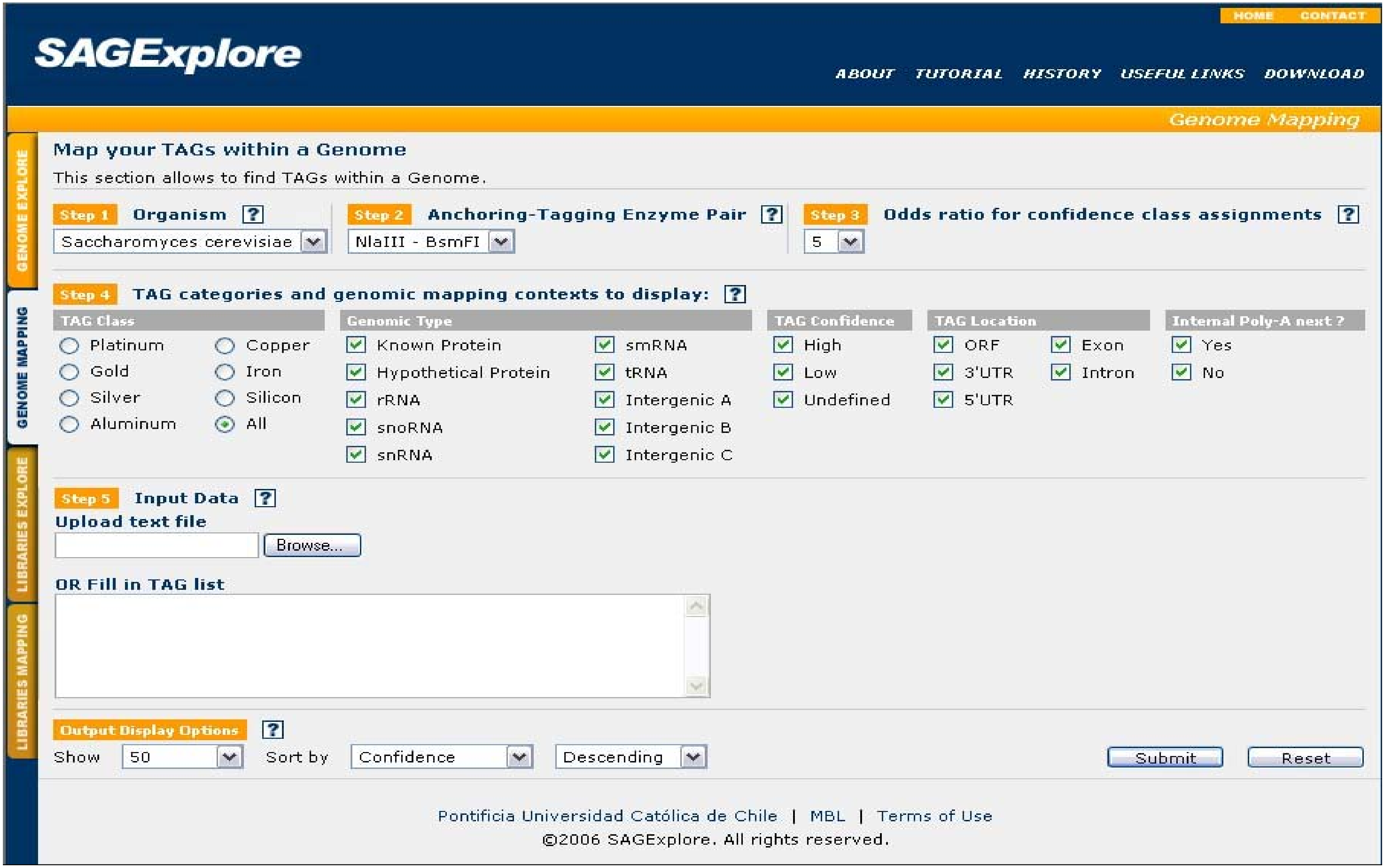
Graphical View: All chromosomes that contain a tag from the results table are shown. Tags are represented graphically on the chromosomes. By clicking on a chromosome, a new pop-up window will emerge with the details of that chromosome region in the context of the current query.



Graphical View: An example showing all high confidence tags mapping into ORFs is shown here.



II.- Tutorial Genome Mapping Module.



Map your TAGs within a Genome

This section allows to find TAGs within a Genome.

Step 1 **Organism** [?]
Saccharomyces cerevisiae

Step 2 **Anchoring-Tagging Enzyme Pair** [?]
NlaIII - BsmFI

Step 3 **Odds ratio for confidence class assignments** [?]
5

Step 4 **TAG categories and genomic mapping contexts to display:** [?]

TAG Class
○ Platinum
○ Gold
○ Silver
○ Aluminum
○ Copper
○ Iron
○ Silicon
● All

Genomic Type
☑ Known Protein
☑ Hypothetical Protein
☑ rRNA
☑ snoRNA
☑ snRNA
☑ smRNA
☑ tRNA
☑ Intergenic A
☑ Intergenic B
☑ Intergenic C

TAG Confidence
☑ High
☑ Low
☑ Undefined

TAG Location
☑ ORF
☑ 3'UTR
☑ 5'UTR
☑ Exon
☑ Intron

Internal Poly-A next ?
☑ Yes
☑ No

Step 5 **Input Data** [?]

Upload text file

OR Fill in TAG list

Output Display Options [?]
Show 50 Sort by Confidence Descending

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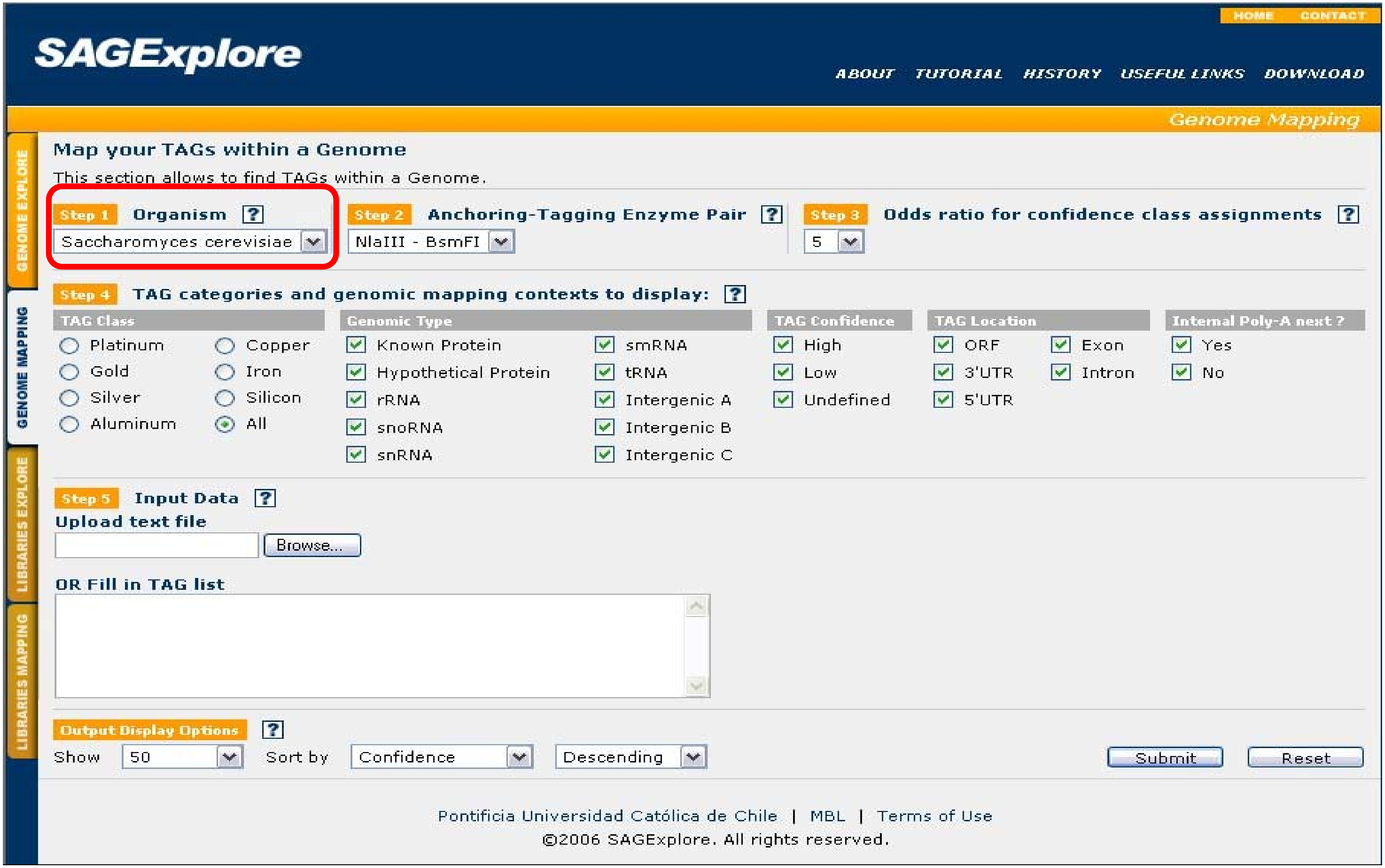
I.- Genome Mapping Module Form: The user must follow five sequential steps in this form. Online help with the relevant details is provided for each step.



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NlaIII - BsmFI

Step 3 **Odds ratio for confidence class assignments** ?
5

Step 4 **TAG categories and genomic mapping contexts to display:** ?

TAG Class		Genomic Type		TAG Confidence	TAG Location		Internal Poly-A next ?
○ Platinum	○ Copper	☑ Known Protein	☑ smRNA	☑ High	☑ ORF	☑ Exon	☑ Yes
○ Gold	○ Iron	☑ Hypothetical Protein	☑ tRNA	☑ Low	☑ 3'UTR	☑ Intron	☑ No
○ Silver	○ Silicon	☑ rRNA	☑ Intergenic A	☑ Undefined	☑ 5'UTR		
○ Aluminum	● All	☑ snoRNA	☑ Intergenic B				
		☑ snRNA	☑ Intergenic C				

Step 5 **Input Data** ?

Upload text file

OR Fill in TAG list

Output Display Options ?

Show 50 Sort by Confidence Descending

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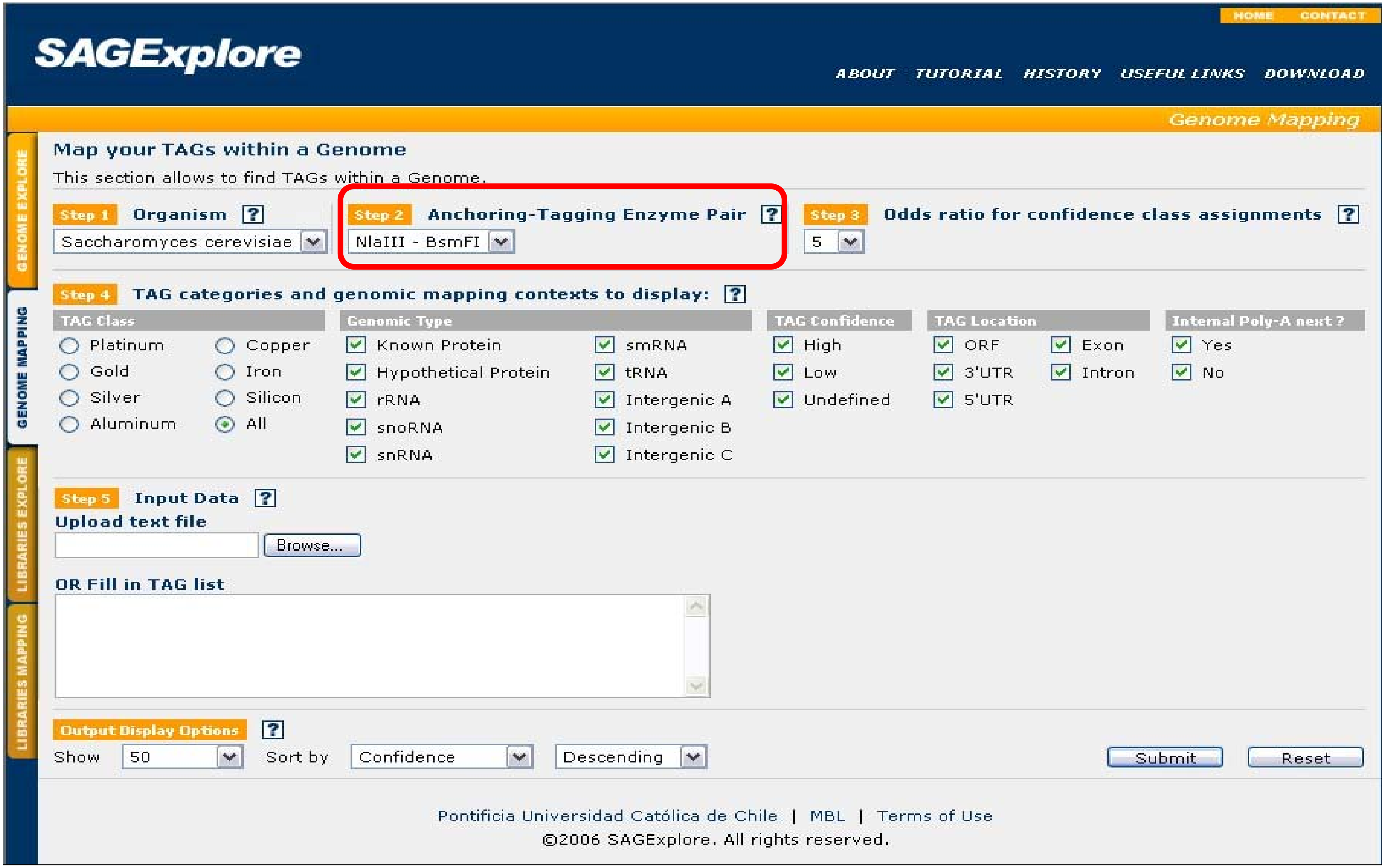
Step 1: The user must select the organism of interest. Currently, only *Saccharomyces cerevisiae* is available. In the near future, other organisms will be added.



Map your TAGs within a Genome

This section allows to find TAGs within a Genome.

Step 1 Organism: Saccharomyces cerevisiae

Step 2 Anchoring-Tagging Enzyme Pair: NlaIII - BsmFI

Step 3 Odds ratio for confidence class assignments: 5

Step 4 TAG categories and genomic mapping contexts to display:

TAG Class		Genomic Type		TAG Confidence	TAG Location		Internal Poly-A next ?
○ Platinum	○ Copper	☑ Known Protein	☑ smRNA	☑ High	☑ ORF	☑ Exon	☑ Yes
○ Gold	○ Iron	☑ Hypothetical Protein	☑ tRNA	☑ Low	☑ 3'UTR	☑ Intron	☑ No
○ Silver	○ Silicon	☑ rRNA	☑ Intergenic A	☑ Undefined	☑ 5'UTR		
○ Aluminum	● All	☑ snoRNA	☑ Intergenic B				
		☑ snRNA	☑ Intergenic C				

Step 5 Input Data

Upload text file

OR Fill in TAG list

Output Display Options

Show: 50 Sort by: Confidence, Descending

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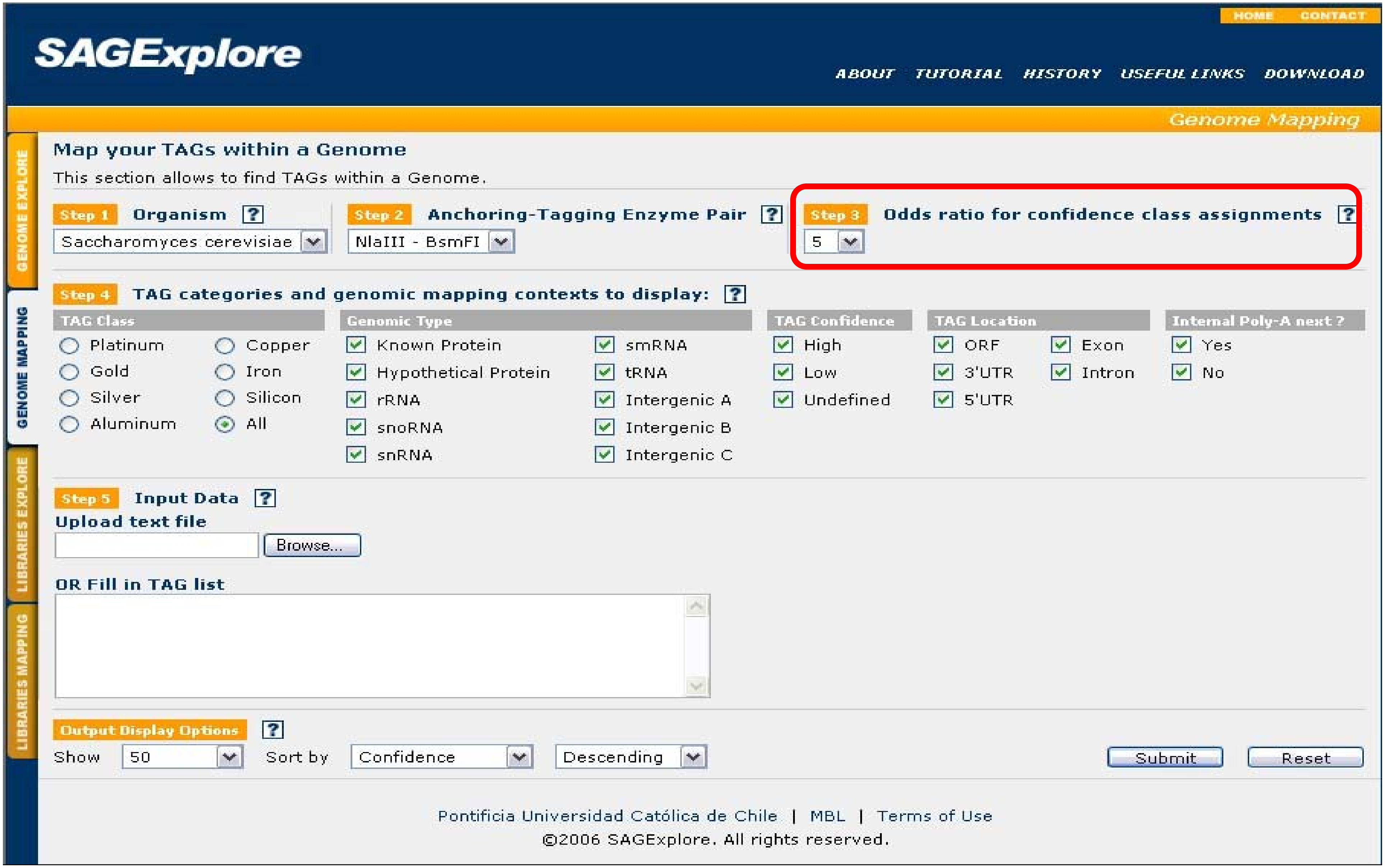
Step 2: The user must select the anchoring-tagging enzyme pair used in SAGE. Currently, only the pair NlaIII-BsmFI is available. In the near future, other enzyme pairs such as the one used in Long-SAGE will be added.



Map your TAGs within a Genome

This section allows to find TAGs within a Genome.

Step 1 Organism [?]: Saccharomyces cerevisiae

Step 2 Anchoring-Tagging Enzyme Pair [?]: NlaIII - BsmFI

Step 3 Odds ratio for confidence class assignments [?]: 5

Step 4 TAG categories and genomic mapping contexts to display: [?]

TAG Class
○ Platinum ○ Copper
○ Gold ○ Iron
○ Silver ○ Silicon
○ Aluminum ● All

Genomic Type
☑ Known Protein ☑ smRNA
☑ Hypothetical Protein ☑ tRNA
☑ rRNA ☑ Intergenic A
☑ snoRNA ☑ Intergenic B
☑ snRNA ☑ Intergenic C

TAG Confidence
☑ High
☑ Low
☑ Undefined

TAG Location
☑ ORF ☑ Exon
☑ 3'UTR ☑ Intron
☑ 5'UTR

Internal Poly-A next ?
☑ Yes
☑ No

Step 5 Input Data [?]

Upload text file

OR Fill in TAG list

Output Display Options [?]

Show 50 Sort by Confidence Descending

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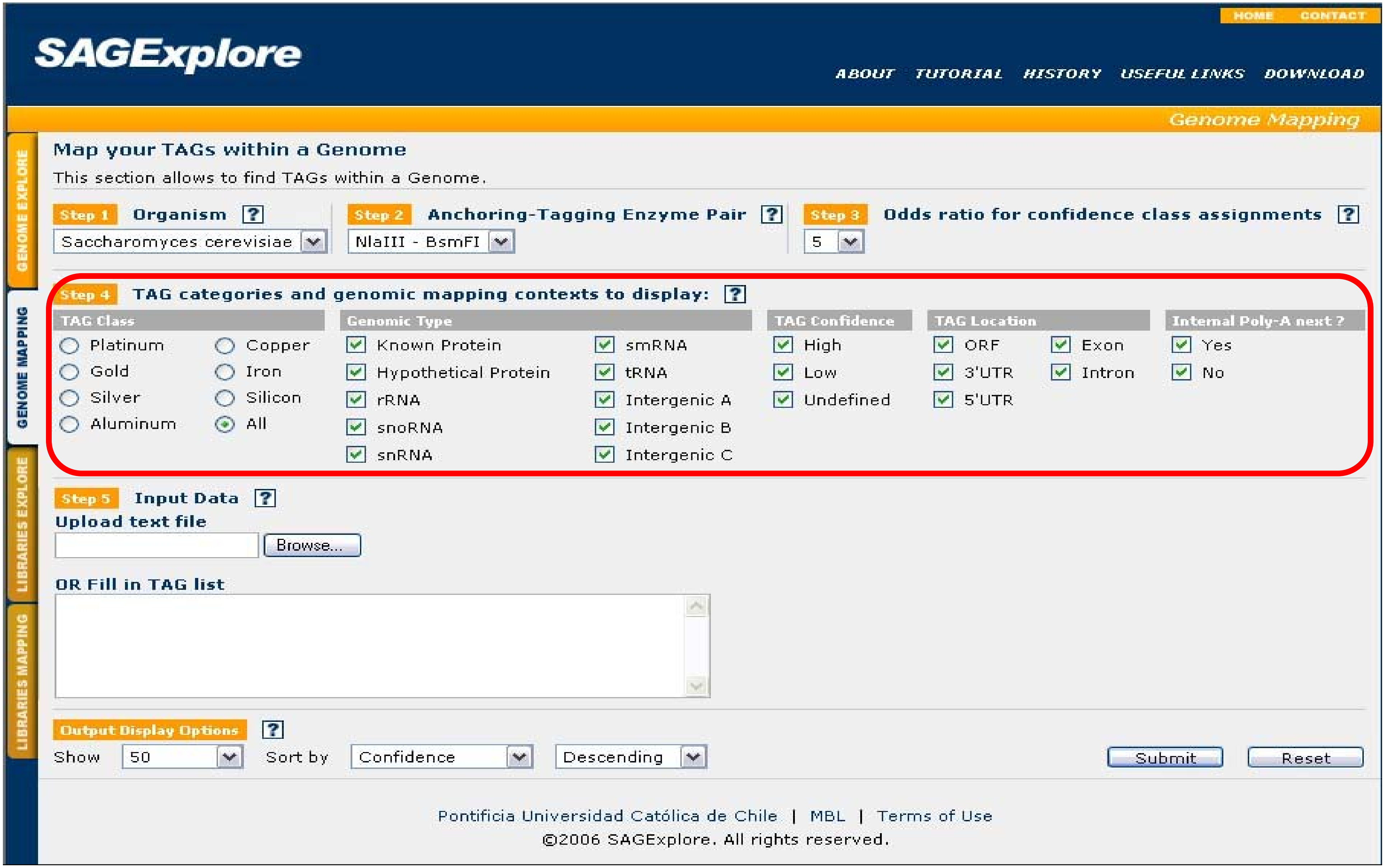
Step 3: The user must select the odds ratio used to assign the confidence classes to the different genomic tags. For details see: Malig, R., Varela, C., Agosin, E. and Melo, F. (2006) Accurate and unambiguous tag-to-gene mapping in SAGE by a hierarchical gene assignment procedure. *BMC Bioinformatics*, **7,** 487-507.



Map your TAGs within a Genome

This section allows to find TAGs within a Genome.

Step 1 Organism: Saccharomyces cerevisiae

Step 2 Anchoring-Tagging Enzyme Pair: NlaIII - BsmFI

Step 3 Odds ratio for confidence class assignments: 5

Step 4 TAG categories and genomic mapping contexts to display:

TAG Class: ○ Platinum ○ Gold ○ Silver ○ Aluminum ○ Copper ○ Iron ○ Silicon ● All

Genomic Type: ☑ Known Protein ☑ Hypothetical Protein ☑ rRNA ☑ snoRNA ☑ snRNA ☑ smRNA ☑ tRNA ☑ Intergenic A ☑ Intergenic B ☑ Intergenic C

TAG Confidence: ☑ High ☑ Low ☑ Undefined

TAG Location: ☑ ORF ☑ 3'UTR ☑ 5'UTR ☑ Exon ☑ Intron

Internal Poly-A next ?: ☑ Yes ☑ No

Step 5 Input Data

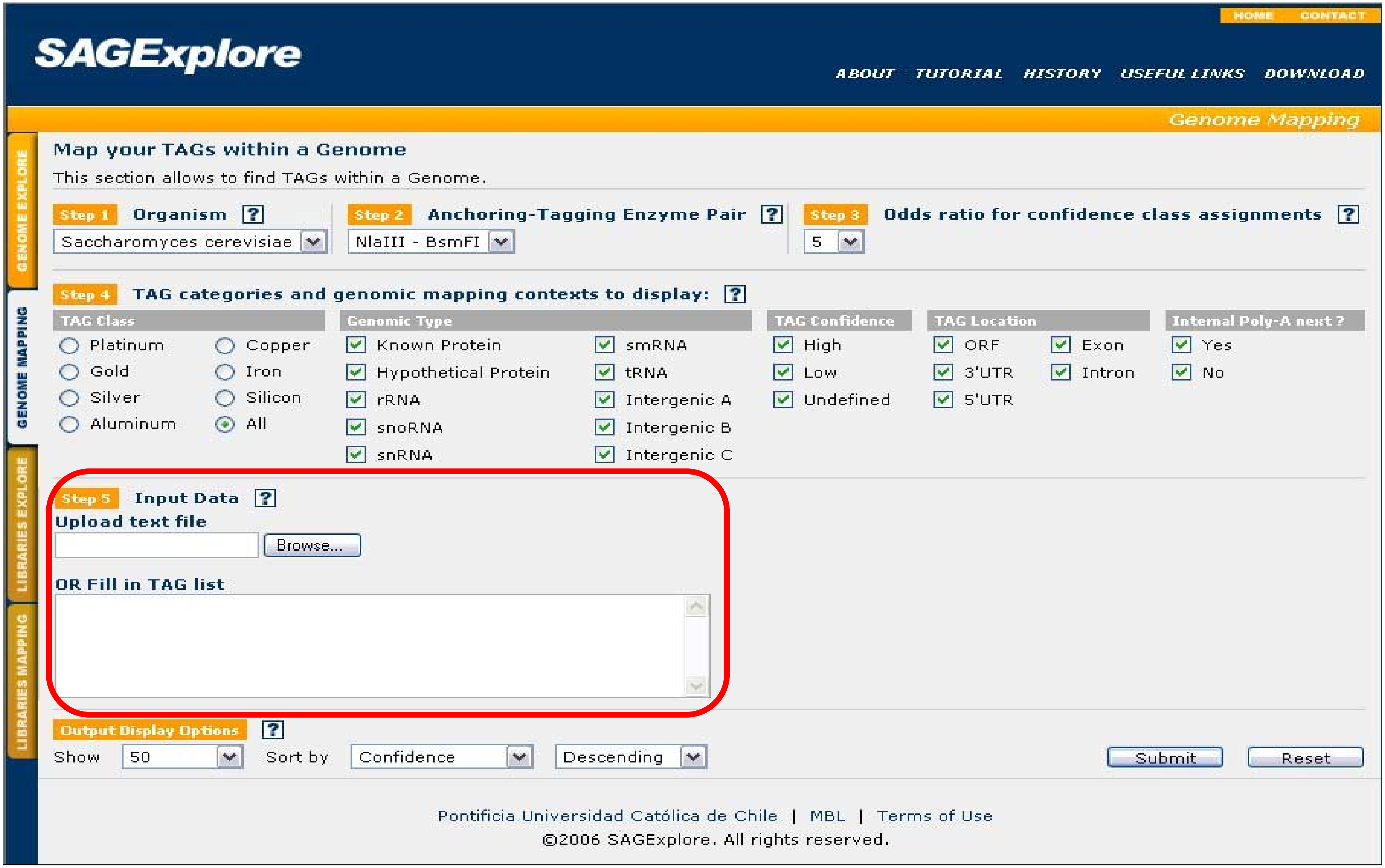
Upload text file

OR Fill in TAG list

Output Display Options

Show 50 Sort by Confidence Descending

Step 4: The user can choose to map the experimental tags against a subset of genomic tags upon a large amount of different features. For details see the help links or: Malig, R., Varela, C., Agosin, E. and Melo, F. (2006) Accurate and unambiguous tag-to-gene mapping in SAGE by a hierarchical gene assignment procedure. *BMC Bioinformatics*, **7,** 487-507.



Map your TAGs within a Genome

This section allows to find TAGs within a Genome.

Step 1 **Organism** ?
Saccharomyces cerevisiae

Step 2 **Anchoring-Tagging Enzyme Pair** ?
NlaIII - BsmFI

Step 3 **Odds ratio for confidence class assignments** ?
5

Step 4 **TAG categories and genomic mapping contexts to display:** ?

TAG Class		Genomic Type		TAG Confidence	TAG Location		Internal Poly-A next ?
○ Platinum	○ Copper	☑ Known Protein	☑ smRNA	☑ High	☑ ORF	☑ Exon	☑ Yes
○ Gold	○ Iron	☑ Hypothetical Protein	☑ tRNA	☑ Low	☑ 3'UTR	☑ Intron	☑ No
○ Silver	○ Silicon	☑ rRNA	☑ Intergenic A	☑ Undefined	☑ 5'UTR		
○ Aluminum	● All	☑ snoRNA	☑ Intergenic B				
		☑ snRNA	☑ Intergenic C				

Step 5 **Input Data** ?

Upload text file

Browse...

OR Fill in TAG list

Output Display Options ?

Show 50 Sort by Confidence Descending

Submit Reset

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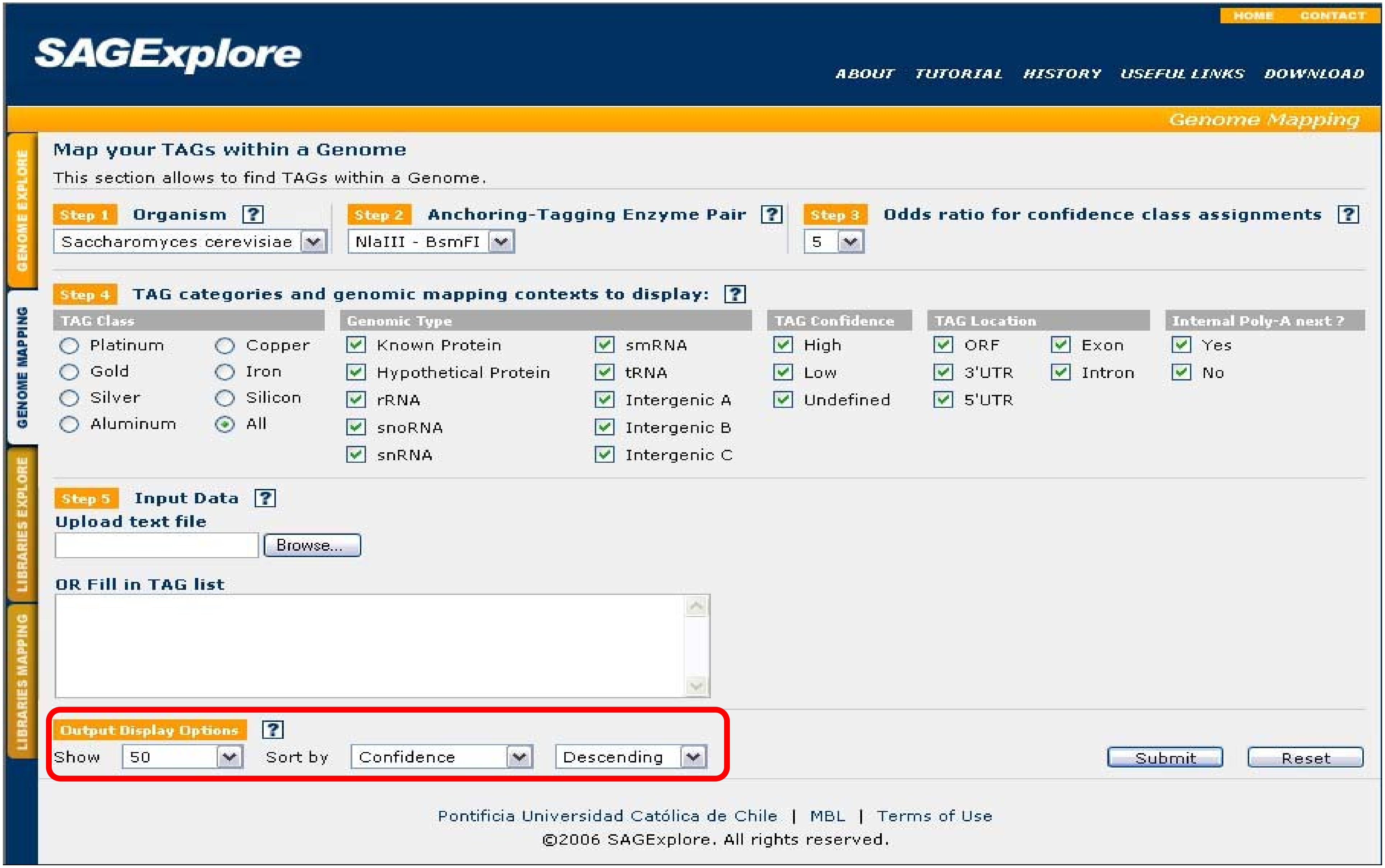
Step 5: The user must provide a list of experimental tags to map against the genome-based annotation of virtual or potential tags. A text file can be uploaded or the data directly pasted into the textarea. The input format is explained in the help link for this step. Full tag sequences must be provided (ie. including CATG).



Map your TAGs within a Genome

This section allows to find TAGs within a Genome.

Step 1 **Organism** ?: Saccharomyces cerevisiae

Step 2 **Anchoring-Tagging Enzyme Pair** ?: NlaIII - BsmFI

Step 3 **Odds ratio for confidence class assignments** ?: 5

Step 4 **TAG categories and genomic mapping contexts to display:** ?

TAG Class		Genomic Type		TAG Confidence	TAG Location		Internal Poly-A next ?
○ Platinum	○ Copper	☑ Known Protein	☑ smRNA	☑ High	☑ ORF	☑ Exon	☑ Yes
○ Gold	○ Iron	☑ Hypothetical Protein	☑ tRNA	☑ Low	☑ 3'UTR	☑ Intron	☑ No
○ Silver	○ Silicon	☑ rRNA	☑ Intergenic A	☑ Undefined	☑ 5'UTR		
○ Aluminum	● All	☑ snoRNA	☑ Intergenic B				
		☑ snRNA	☑ Intergenic C				

Step 5 **Input Data** ?

Upload text file

OR Fill in TAG list

Output Display Options ?

Show 50 Sort by Confidence Descending

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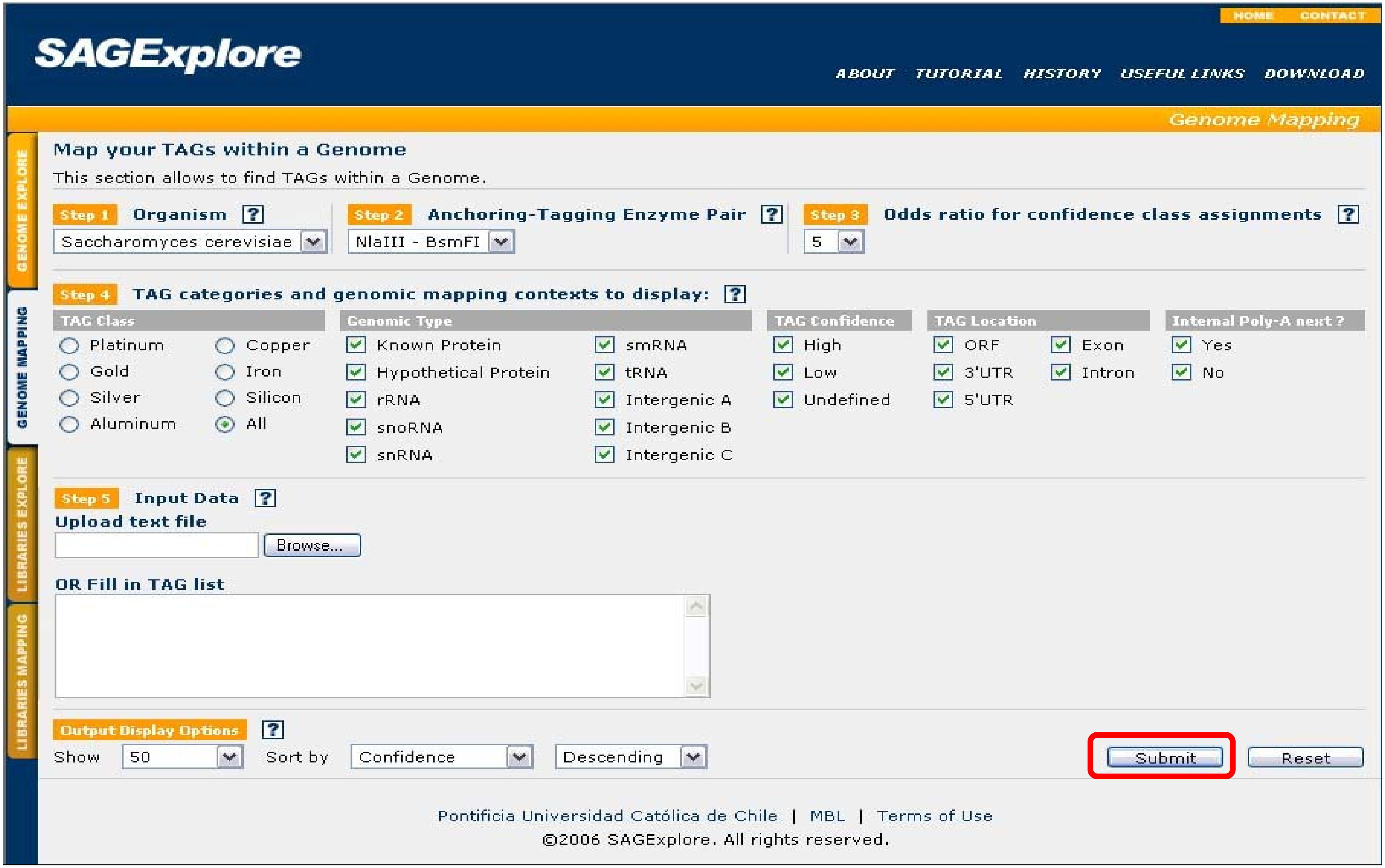
Pre-submit: Before submitting the query, the user can choose the number of rows to display per page and also how to sort the results.



Map your TAGs within a Genome

This section allows to find TAGs within a Genome.

Step 1 Organism [?]: Saccharomyces cerevisiae

Step 2 Anchoring-Tagging Enzyme Pair [?]: NlaIII - BsmFI

Step 3 Odds ratio for confidence class assignments [?]: 5

Step 4 TAG categories and genomic mapping contexts to display: [?]

TAG Class:
○ Platinum
○ Gold
○ Silver
○ Aluminum
○ Copper
○ Iron
○ Silicon
● All

Genomic Type:
☑ Known Protein
☑ Hypothetical Protein
☑ rRNA
☑ snoRNA
☑ snRNA
☑ smRNA
☑ tRNA
☑ Intergenic A
☑ Intergenic B
☑ Intergenic C

TAG Confidence:
☑ High
☑ Low
☑ Undefined

TAG Location:
☑ ORF
☑ 3'UTR
☑ 5'UTR
☑ Exon
☑ Intron

Internal Poly-A next ?:
☑ Yes
☑ No

Step 5 Input Data [?]

Upload text file

OR Fill in TAG list

Output Display Options [?]

Show 50 Sort by Confidence Descending

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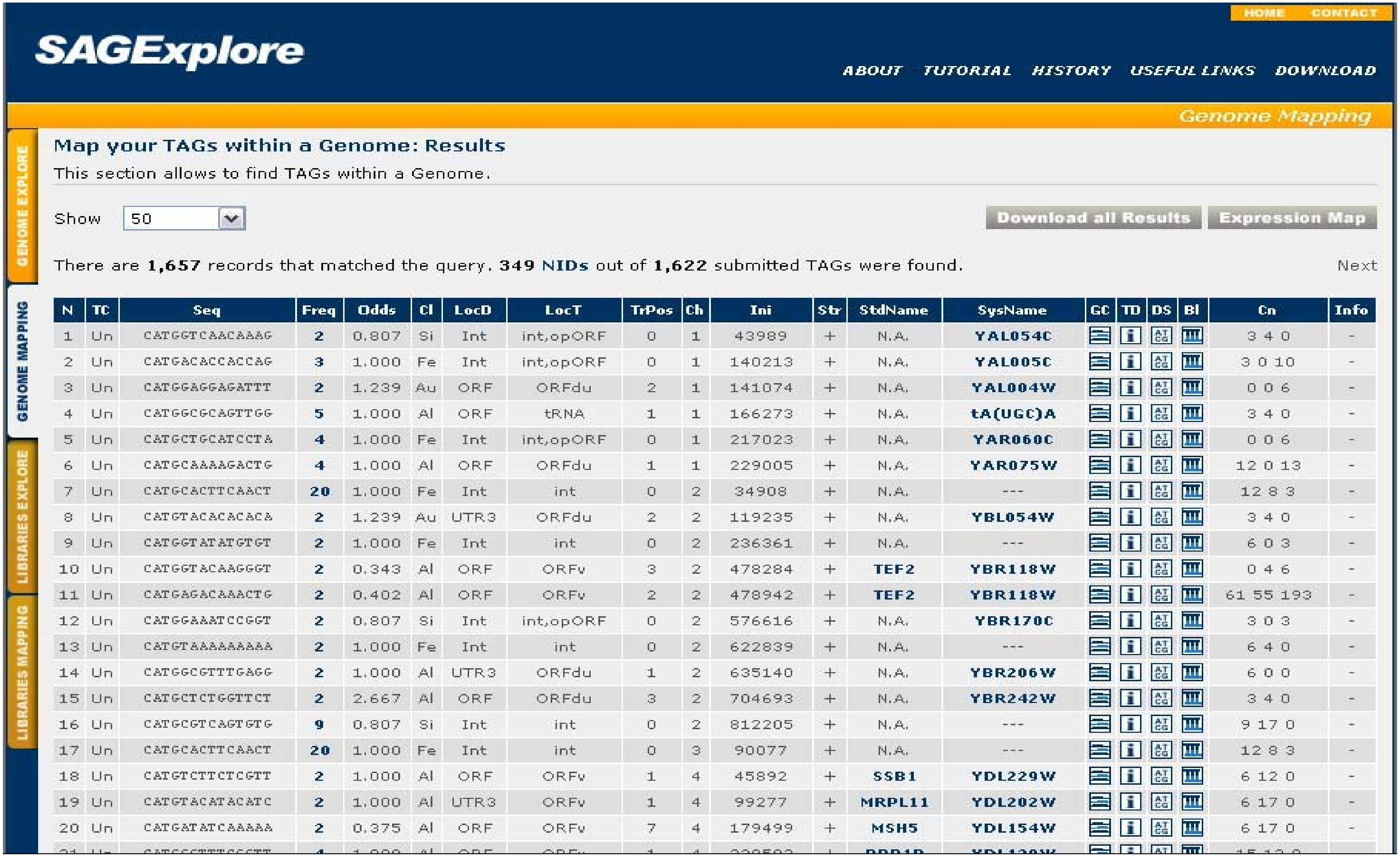
Submit: The user is ready to submit the query to the server.



Map your TAGs within a Genome: Results

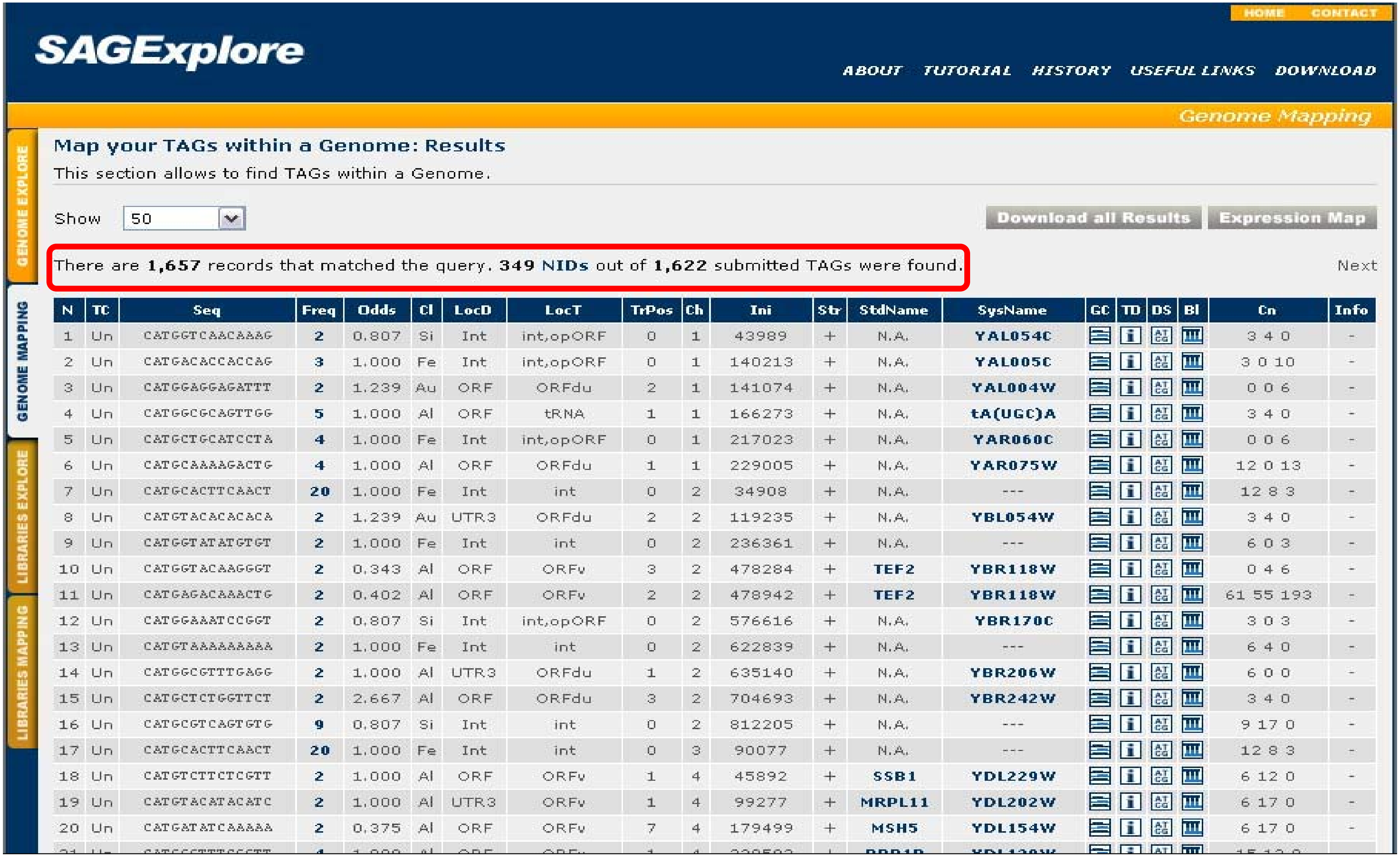
This section allows to find TAGs within a Genome.

Show 50

There are **1,657** records that matched the query. **349 NIDs** out of **1,622** submitted TAGs were found.

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	Bl	Cn	Info
1	Un	CATGGTCAACAAAG	**2**	0.807	Si	Int	int,opORF	0	1	43989	+	N.A.	**YAL054C**	☰	ℹ	AT CG	▥	3 4 0	-
2	Un	CATGACACCACCAG	**3**	1.000	Fe	Int	int,opORF	0	1	140213	+	N.A.	**YAL005C**	☰	ℹ	AT CG	▥	3 0 10	-
3	Un	CATGGAGGAGATTT	**2**	1.239	Au	ORF	ORFdu	2	1	141074	+	N.A.	**YAL004W**	☰	ℹ	AT CG	▥	0 0 6	-
4	Un	CATGGCGCAGTTGG	**5**	1.000	Al	ORF	tRNA	1	1	166273	+	N.A.	**tA(UGC)A**	☰	ℹ	AT CG	▥	3 4 0	-
5	Un	CATGCTGCATCCTA	**4**	1.000	Fe	Int	int,opORF	0	1	217023	+	N.A.	**YAR060C**	☰	ℹ	AT CG	▥	0 0 6	-
6	Un	CATGCAAAAGACTG	**4**	1.000	Al	ORF	ORFdu	1	1	229005	+	N.A.	**YAR075W**	☰	ℹ	AT CG	▥	12 0 13	-
7	Un	CATGCACTTCAACT	**20**	1.000	Fe	Int	int	0	2	34908	+	N.A.	---	☰	ℹ	AT CG	▥	12 8 3	-
8	Un	CATGTACACACACA	**2**	1.239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	**YBL054W**	☰	ℹ	AT CG	▥	3 4 0	-
9	Un	CATGGTATATGTGT	**2**	1.000	Fe	Int	int	0	2	236361	+	N.A.	---	☰	ℹ	AT CG	▥	6 0 3	-
10	Un	CATGGTACAAGGGT	**2**	0.343	Al	ORF	ORFv	3	2	478284	+	**TEF2**	**YBR118W**	☰	ℹ	AT CG	▥	0 4 6	-
11	Un	CATGAGACAAACTG	**2**	0.402	Al	ORF	ORFv	2	2	478942	+	**TEF2**	**YBR118W**	☰	ℹ	AT CG	▥	61 55 193	-
12	Un	CATGGAAATCCGGT	**2**	0.807	Si	Int	int,opORF	0	2	576616	+	N.A.	**YBR170C**	☰	ℹ	AT CG	▥	3 0 3	-
13	Un	CATGTAAAAAAAAA	**2**	1.000	Fe	Int	int	0	2	622839	+	N.A.	---	☰	ℹ	AT CG	▥	6 4 0	-
14	Un	CATGGCGTTTGAGG	**2**	1.000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	**YBR206W**	☰	ℹ	AT CG	▥	6 0 0	-
15	Un	CATGCTCTGGTTCT	**2**	2.667	Al	ORF	ORFdu	3	2	704693	+	N.A.	**YBR242W**	☰	ℹ	AT CG	▥	3 4 0	-
16	Un	CATGCGTCAGTGTG	**9**	0.807	Si	Int	int	0	2	812205	+	N.A.	---	☰	ℹ	AT CG	▥	9 17 0	-
17	Un	CATGCACTTCAACT	**20**	1.000	Fe	Int	int	0	3	90077	+	N.A.	---	☰	ℹ	AT CG	▥	12 8 3	-
18	Un	CATGTCTTCTCGTT	**2**	1.000	Al	ORF	ORFv	1	4	45892	+	**SSB1**	**YDL229W**	☰	ℹ	AT CG	▥	6 12 0	-
19	Un	CATGTACATACATC	**2**	1.000	Al	UTR3	ORFv	1	4	99277	+	**MRPL11**	**YDL202W**	☰	ℹ	AT CG	▥	6 17 0	-
20	Un	CATGATATCAAAAA	**2**	0.375	Al	ORF	ORFv	7	4	179499	+	**MSH5**	**YDL154W**	☰	ℹ	AT CG	▥	6 17 0	-

Query Results: Typical output of the Genome Mapping Form.



Map your TAGs within a Genome: Results

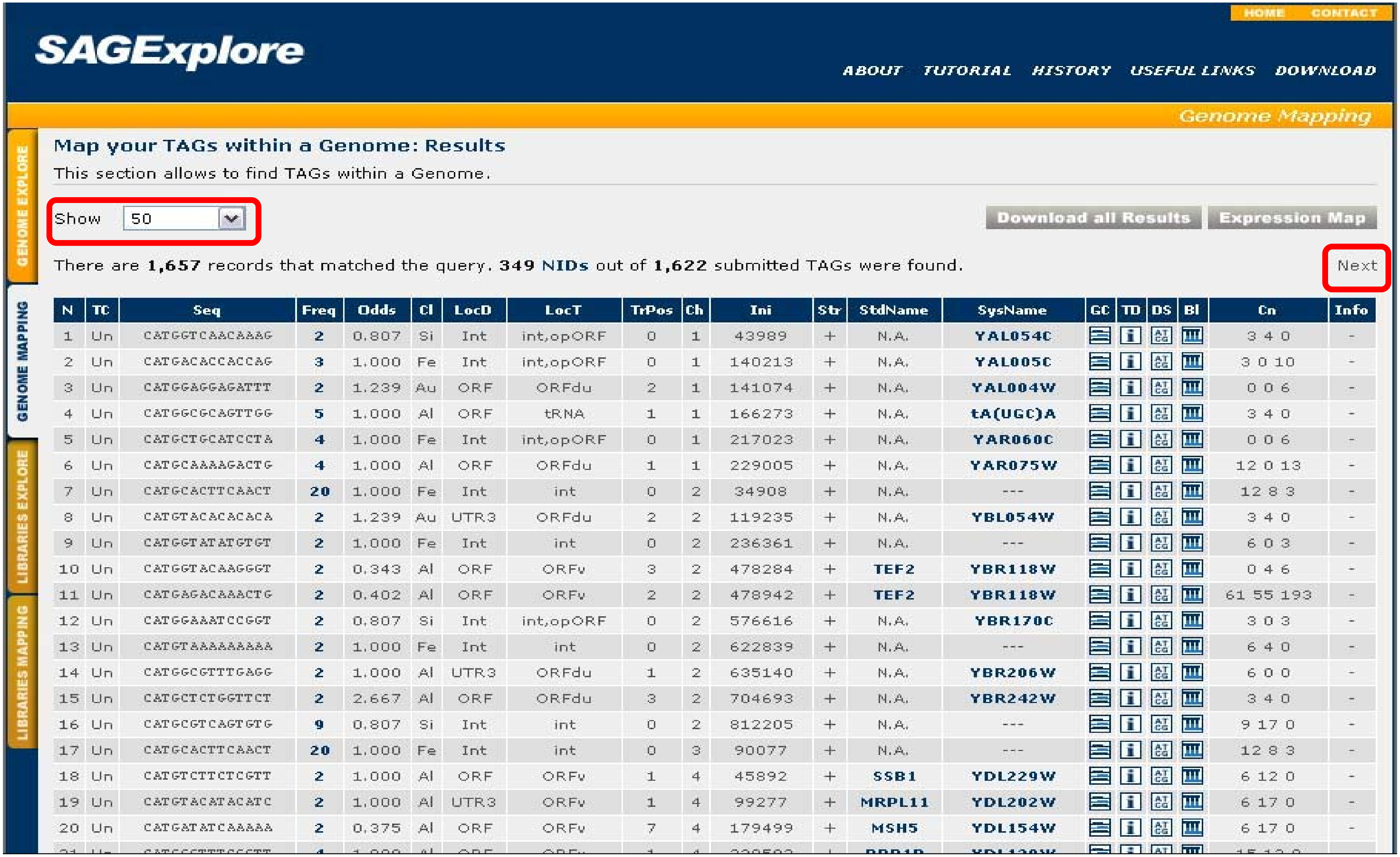
This section allows to find TAGs within a Genome.

Show 50

There are **1,657** records that matched the query. **349 NIDs** out of **1,622** submitted TAGs were found.

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	BI	Cn	Info
1	Un	CATGGTCAACAAAG	**2**	0.807	Si	Int	int,opORF	0	1	43989	+	N.A.	**YAL054C**	☰	ℹ	▦	▥	3 4 0	-
2	Un	CATGACACCACCAG	**3**	1.000	Fe	Int	int,opORF	0	1	140213	+	N.A.	**YAL005C**	☰	ℹ	▦	▥	3 0 10	-
3	Un	CATGGAGGAGATTT	**2**	1.239	Au	ORF	ORFdu	2	1	141074	+	N.A.	**YAL004W**	☰	ℹ	▦	▥	0 0 6	-
4	Un	CATGGCGCAGTTGG	**5**	1.000	Al	ORF	tRNA	1	1	166273	+	N.A.	**tA(UGC)A**	☰	ℹ	▦	▥	3 4 0	-
5	Un	CATGCTGCATCCTA	**4**	1.000	Fe	Int	int,opORF	0	1	217023	+	N.A.	**YAR060C**	☰	ℹ	▦	▥	0 0 6	-
6	Un	CATGCAAAAGACTG	**4**	1.000	Al	ORF	ORFdu	1	1	229005	+	N.A.	**YAR075W**	☰	ℹ	▦	▥	12 0 13	-
7	Un	CATGCACTTCAACT	**20**	1.000	Fe	Int	int	0	2	34908	+	N.A.	---	☰	ℹ	▦	▥	12 8 3	-
8	Un	CATGTACACACACA	**2**	1.239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	**YBL054W**	☰	ℹ	▦	▥	3 4 0	-
9	Un	CATGGTATATGTGT	**2**	1.000	Fe	Int	int	0	2	236361	+	N.A.	---	☰	ℹ	▦	▥	6 0 3	-
10	Un	CATGGTACAAGGGT	**2**	0.343	Al	ORF	ORFv	3	2	478284	+	**TEF2**	**YBR118W**	☰	ℹ	▦	▥	0 4 6	-
11	Un	CATGAGACAAACTG	**2**	0.402	Al	ORF	ORFv	2	2	478942	+	**TEF2**	**YBR118W**	☰	ℹ	▦	▥	61 55 193	-
12	Un	CATGGAAATCCGGT	**2**	0.807	Si	Int	int,opORF	0	2	576616	+	N.A.	**YBR170C**	☰	ℹ	▦	▥	3 0 3	-
13	Un	CATGTAAAAAAAAA	**2**	1.000	Fe	Int	int	0	2	622839	+	N.A.	---	☰	ℹ	▦	▥	6 4 0	-
14	Un	CATGGCGTTTGAGG	**2**	1.000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	**YBR206W**	☰	ℹ	▦	▥	6 0 0	-
15	Un	CATGCTCTGGTTCT	**2**	2.667	Al	ORF	ORFdu	3	2	704693	+	N.A.	**YBR242W**	☰	ℹ	▦	▥	3 4 0	-
16	Un	CATGCGTCAGTGTG	**9**	0.807	Si	Int	int	0	2	812205	+	N.A.	---	☰	ℹ	▦	▥	9 17 0	-
17	Un	CATGCACTTCAACT	**20**	1.000	Fe	Int	int	0	3	90077	+	N.A.	---	☰	ℹ	▦	▥	12 8 3	-
18	Un	CATGTCTTCTCGTT	**2**	1.000	Al	ORF	ORFv	1	4	45892	+	**SSB1**	**YDL229W**	☰	ℹ	▦	▥	6 12 0	-
19	Un	CATGTACATACATC	**2**	1.000	Al	UTR3	ORFv	1	4	99277	+	**MRPL11**	**YDL202W**	☰	ℹ	▦	▥	6 17 0	-
20	Un	CATGATATCAAAAA	**2**	0.375	Al	ORF	ORFv	7	4	179499	+	**MSH5**	**YDL154W**	☰	ℹ	▦	▥	6 17 0	-

Query Results: The total number of records that matched the query are reported. Also, the total number of unmatched tags (NIDs or Non-Identified Tags) out of the total number of submitted tags is given.



Map your TAGs within a Genome: Results

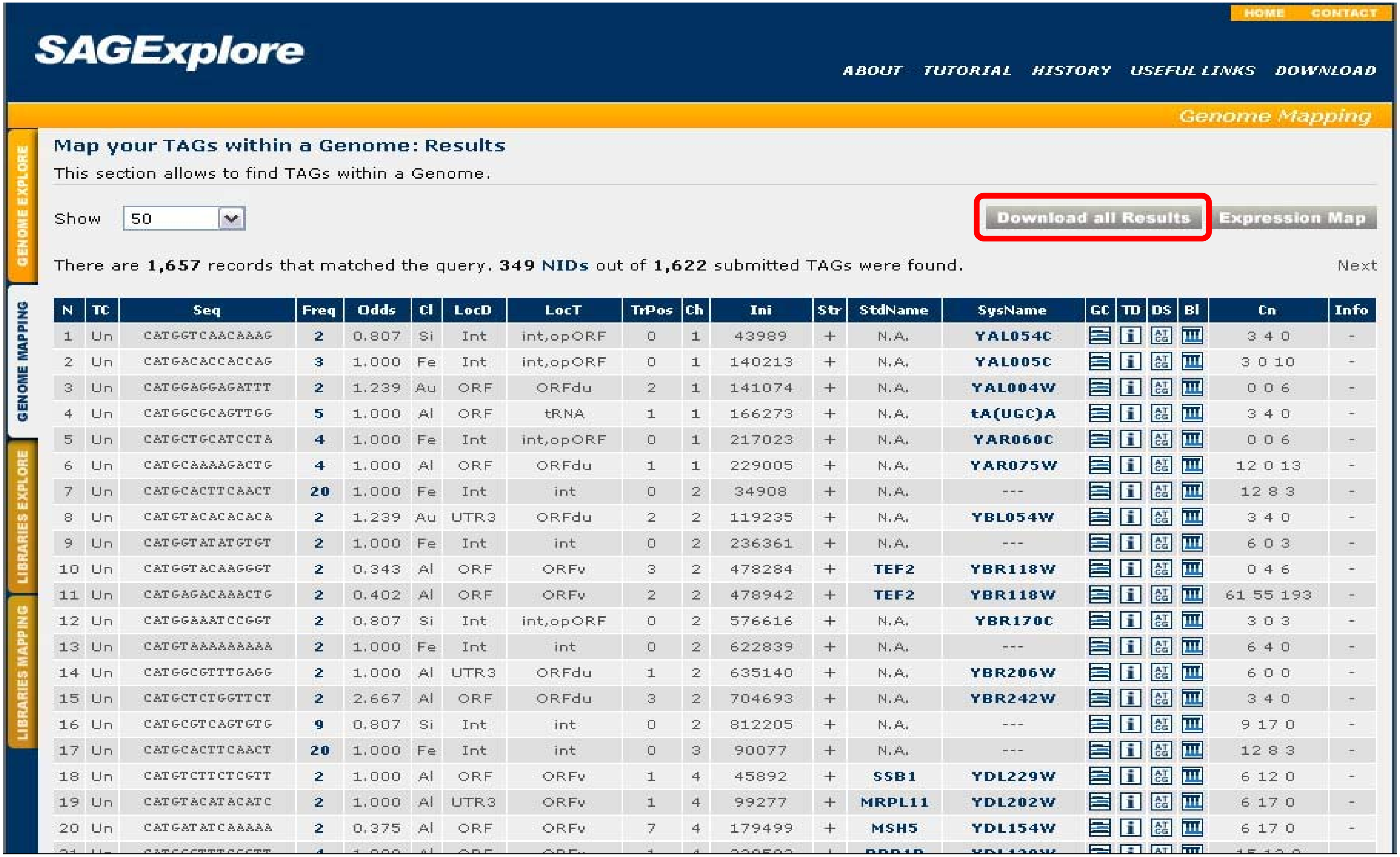
This section allows to find TAGs within a Genome.

Show 50

There are **1,657** records that matched the query. **349 NIDs** out of **1,622** submitted TAGs were found.

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	BI	Cn	Info
1	Un	CATGGTCAACAAAG	**2**	0.807	Si	Int	int,opORF	0	1	43989	+	N.A.	**YAL054C**	☰	ℹ	AT CG	Ⅲ	3 4 0	-
2	Un	CATGACACCACCAG	**3**	1.000	Fe	Int	int,opORF	0	1	140213	+	N.A.	**YAL005C**	☰	ℹ	AT CG	Ⅲ	3 0 10	-
3	Un	CATGGAGGAGATTT	**2**	1.239	Au	ORF	ORFdu	2	1	141074	+	N.A.	**YAL004W**	☰	ℹ	AT CG	Ⅲ	0 0 6	-
4	Un	CATGGCGCAGTTGG	**5**	1.000	Al	ORF	tRNA	1	1	166273	+	N.A.	**tA(UGC)A**	☰	ℹ	AT CG	Ⅲ	3 4 0	-
5	Un	CATGCTGCATCCTA	**4**	1.000	Fe	Int	int,opORF	0	1	217023	+	N.A.	**YAR060C**	☰	ℹ	AT CG	Ⅲ	0 0 6	-
6	Un	CATGCAAAAGACTG	**4**	1.000	Al	ORF	ORFdu	1	1	229005	+	N.A.	**YAR075W**	☰	ℹ	AT CG	Ⅲ	12 0 13	-
7	Un	CATGCACTTCAACT	**20**	1.000	Fe	Int	int	0	2	34908	+	N.A.	---	☰	ℹ	AT CG	Ⅲ	12 8 3	-
8	Un	CATGTACACACACA	**2**	1.239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	**YBL054W**	☰	ℹ	AT CG	Ⅲ	3 4 0	-
9	Un	CATGGTATATGTGT	**2**	1.000	Fe	Int	int	0	2	236361	+	N.A.	---	☰	ℹ	AT CG	Ⅲ	6 0 3	-
10	Un	CATGGTACAAGGGT	**2**	0.343	Al	ORF	ORFv	3	2	478284	+	**TEF2**	**YBR118W**	☰	ℹ	AT CG	Ⅲ	0 4 6	-
11	Un	CATGAGACAAACTG	**2**	0.402	Al	ORF	ORFv	2	2	478942	+	**TEF2**	**YBR118W**	☰	ℹ	AT CG	Ⅲ	61 55 193	-
12	Un	CATGGAAATCCGGT	**2**	0.807	Si	Int	int,opORF	0	2	576616	+	N.A.	**YBR170C**	☰	ℹ	AT CG	Ⅲ	3 0 3	-
13	Un	CATGTAAAAAAAAA	**2**	1.000	Fe	Int	int	0	2	622839	+	N.A.	---	☰	ℹ	AT CG	Ⅲ	6 4 0	-
14	Un	CATGGCGTTTGAGG	**2**	1.000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	**YBR206W**	☰	ℹ	AT CG	Ⅲ	6 0 0	-
15	Un	CATGCTCTGGTTCT	**2**	2.667	Al	ORF	ORFdu	3	2	704693	+	N.A.	**YBR242W**	☰	ℹ	AT CG	Ⅲ	3 4 0	-
16	Un	CATGCGTCAGTGTG	**9**	0.807	Si	Int	int	0	2	812205	+	N.A.	---	☰	ℹ	AT CG	Ⅲ	9 17 0	-
17	Un	CATGCACTTCAACT	**20**	1.000	Fe	Int	int	0	3	90077	+	N.A.	---	☰	ℹ	AT CG	Ⅲ	12 8 3	-
18	Un	CATGTCTTCTCGTT	**2**	1.000	Al	ORF	ORFv	1	4	45892	+	**SSB1**	**YDL229W**	☰	ℹ	AT CG	Ⅲ	6 12 0	-
19	Un	CATGTACATACATC	**2**	1.000	Al	UTR3	ORFv	1	4	99277	+	**MRPL11**	**YDL202W**	☰	ℹ	AT CG	Ⅲ	6 17 0	-
20	Un	CATGATATCAAAAA	**2**	0.375	Al	ORF	ORFv	7	4	179499	+	**MSH5**	**YDL154W**	☰	ℹ	AT CG	Ⅲ	6 17 0	-

Query Results: Only a fraction of the results is displayed. This option can be easily changed by selecting a different number of rows to display or the next button used to go to the next page.



Map your TAGs within a Genome: Results

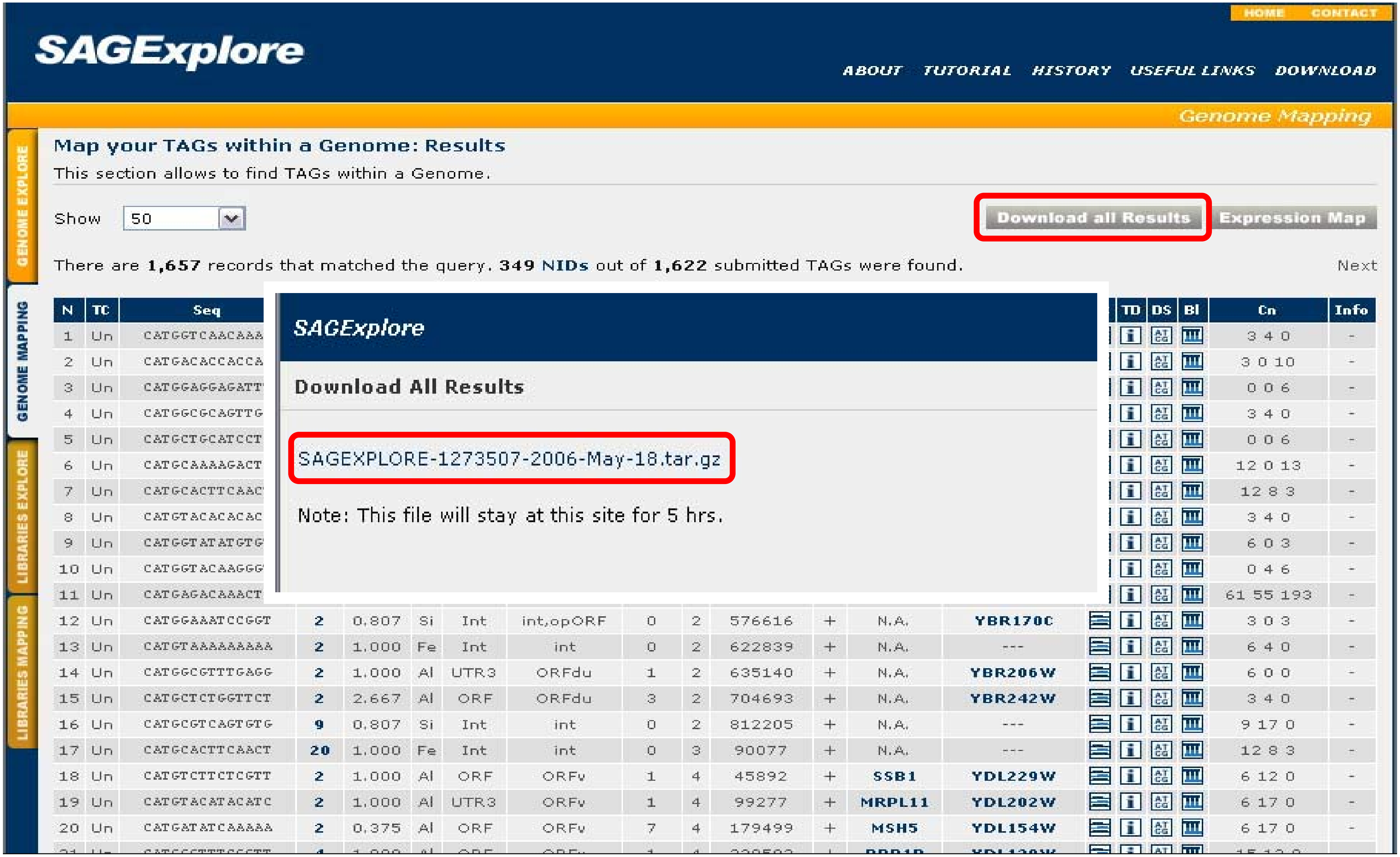
This section allows to find TAGs within a Genome.

Show 50

There are **1,657** records that matched the query. **349 NIDs** out of **1,622** submitted TAGs were found.

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	Bl	Cn	Info
1	Un	CATGGTCAACAAAG	**2**	0.807	Si	Int	int,opORF	0	1	43989	+	N.A.	**YAL054C**					3 4 0	-
2	Un	CATGACACCACCAG	**3**	1.000	Fe	Int	int,opORF	0	1	140213	+	N.A.	**YAL005C**					3 0 10	-
3	Un	CATGGAGGAGATTT	**2**	1.239	Au	ORF	ORFdu	2	1	141074	+	N.A.	**YAL004W**					0 0 6	-
4	Un	CATGGCGCAGTTGG	**5**	1.000	Al	ORF	tRNA	1	1	166273	+	N.A.	**tA(UGC)A**					3 4 0	-
5	Un	CATGCTGCATCCTA	**4**	1.000	Fe	Int	int,opORF	0	1	217023	+	N.A.	**YAR060C**					0 0 6	-
6	Un	CATGCAAAAGACTG	**4**	1.000	Al	ORF	ORFdu	1	1	229005	+	N.A.	**YAR075W**					12 0 13	-
7	Un	CATGCACTTCAACT	**20**	1.000	Fe	Int	int	0	2	34908	+	N.A.	---					12 8 3	-
8	Un	CATGTACACACACA	**2**	1.239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	**YBL054W**					3 4 0	-
9	Un	CATGGTATATGTGT	**2**	1.000	Fe	Int	int	0	2	236361	+	N.A.	---					6 0 3	-
10	Un	CATGGTACAAGGGT	**2**	0.343	Al	ORF	ORFv	3	2	478284	+	**TEF2**	**YBR118W**					0 4 6	-
11	Un	CATGAGACAAACTG	**2**	0.402	Al	ORF	ORFv	2	2	478942	+	**TEF2**	**YBR118W**					61 55 193	-
12	Un	CATGGAAATCCGGT	**2**	0.807	Si	Int	int,opORF	0	2	576616	+	N.A.	**YBR170C**					3 0 3	-
13	Un	CATGTAAAAAAAAA	**2**	1.000	Fe	Int	int	0	2	622839	+	N.A.	---					6 4 0	-
14	Un	CATGGCGTTTGAGG	**2**	1.000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	**YBR206W**					6 0 0	-
15	Un	CATGCTCTGGTTCT	**2**	2.667	Al	ORF	ORFdu	3	2	704693	+	N.A.	**YBR242W**					3 4 0	-
16	Un	CATGCGTCAGTGTG	**9**	0.807	Si	Int	int	0	2	812205	+	N.A.	---					9 17 0	-
17	Un	CATGCACTTCAACT	**20**	1.000	Fe	Int	int	0	3	90077	+	N.A.	---					12 8 3	-
18	Un	CATGTCTTCTCGTT	**2**	1.000	Al	ORF	ORFv	1	4	45892	+	**SSB1**	**YDL229W**					6 12 0	-
19	Un	CATGTACATACATC	**2**	1.000	Al	UTR3	ORFv	1	4	99277	+	**MRPL11**	**YDL202W**					6 17 0	-
20	Un	CATGATATCAAAAA	**2**	0.375	Al	ORF	ORFv	7	4	179499	+	**MSH5**	**YDL154W**					6 17 0	-

Query Results: The full table can be downloaded as tab-delimited text (compressed file or tar.gzipped).



Map your TAGs within a Genome: Results

This section allows to find TAGs within a Genome.

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SAGExplore

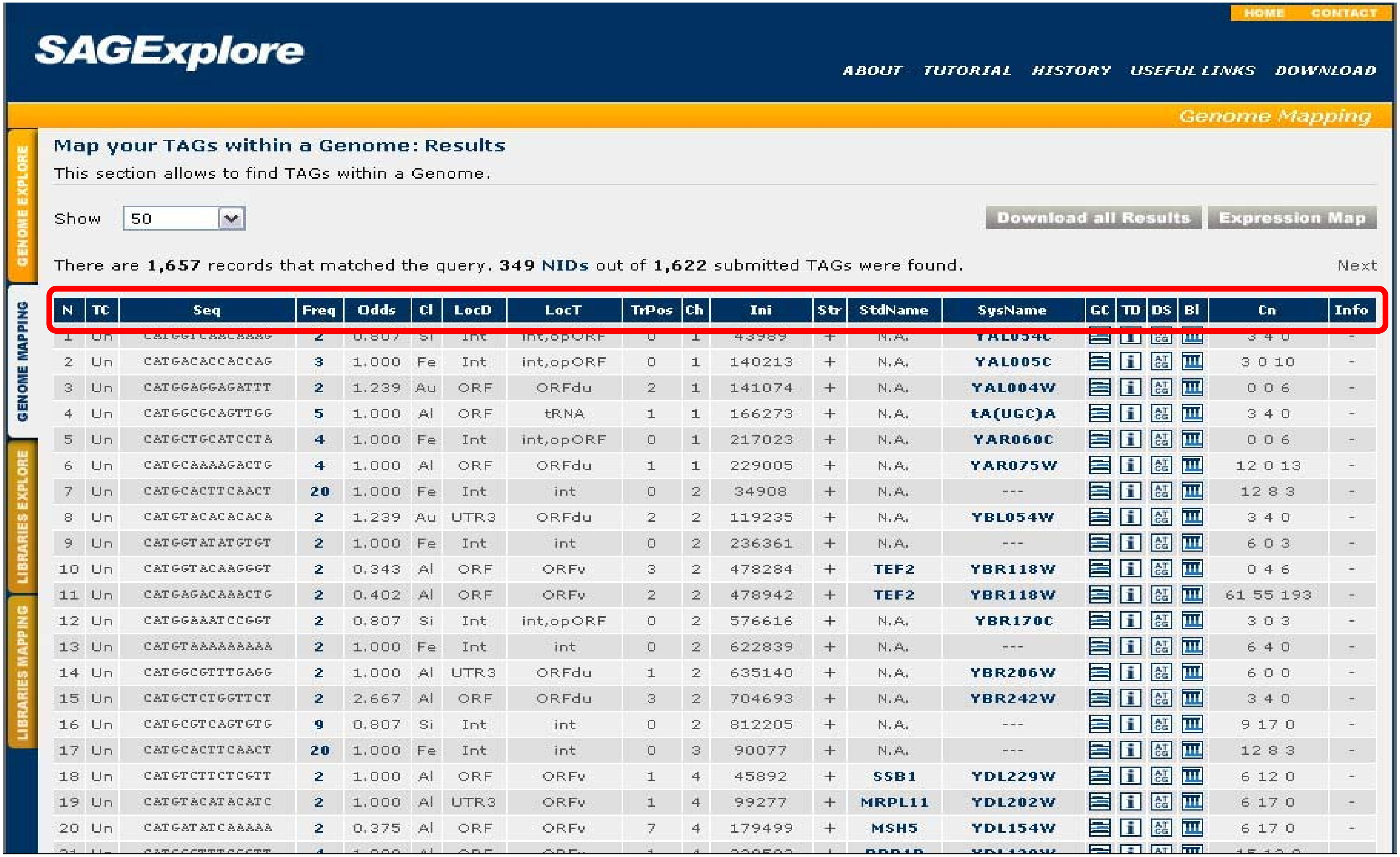
Download All Results

SAGEXPLORE-1273507-2006-May-18.tar.gz

Note: This file will stay at this site for 5 hrs.

N	TC	Seq													TD	DS	Bl	Cn	Info
1	Un	CATGGTCAACAAA													ℹ	AT CG	▥	3 4 0	-
2	Un	CATGACACCACCA													ℹ	AT CG	▥	3 0 10	-
3	Un	CATGGAGGAGATT													ℹ	AT CG	▥	0 0 6	-
4	Un	CATGGCGCAGTTG													ℹ	AT CG	▥	3 4 0	-
5	Un	CATGCTGCATCCT													ℹ	AT CG	▥	0 0 6	-
6	Un	CATGCAAAAGACT													ℹ	AT CG	▥	12 0 13	-
7	Un	CATGCACTTCAAC													ℹ	AT CG	▥	12 8 3	-
8	Un	CATGTACACACAC													ℹ	AT CG	▥	3 4 0	-
9	Un	CATGGTATATGTG													ℹ	AT CG	▥	6 0 3	-
10	Un	CATGGTACAAGGG													ℹ	AT CG	▥	0 4 6	-
11	Un	CATGAGACAAACT													ℹ	AT CG	▥	61 55 193	-
12	Un	CATGGAAATCCGGT	2	0.807	Si	Int	int,opORF	0	2	576616	+	N.A.	YBR170C	☰	ℹ	AT CG	▥	3 0 3	-
13	Un	CATGTAAAAAAAAA	2	1.000	Fe	Int	int	0	2	622839	+	N.A.	---	☰	ℹ	AT CG	▥	6 4 0	-
14	Un	CATGGCGTTTGAGG	2	1.000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	YBR206W	☰	ℹ	AT CG	▥	6 0 0	-
15	Un	CATGCTCTGGTTCT	2	2.667	Al	ORF	ORFdu	3	2	704693	+	N.A.	YBR242W	☰	ℹ	AT CG	▥	3 4 0	-
16	Un	CATGCGTCAGTGTG	9	0.807	Si	Int	int	0	2	812205	+	N.A.	---	☰	ℹ	AT CG	▥	9 17 0	-
17	Un	CATGCACTTCAACT	20	1.000	Fe	Int	int	0	3	90077	+	N.A.	---	☰	ℹ	AT CG	▥	12 8 3	-
18	Un	CATGTCTTCTCGTT	2	1.000	Al	ORF	ORFv	1	4	45892	+	SSB1	YDL229W	☰	ℹ	AT CG	▥	6 12 0	-
19	Un	CATGTACATACATC	2	1.000	Al	UTR3	ORFv	1	4	99277	+	MRPL11	YDL202W	☰	ℹ	AT CG	▥	6 17 0	-
20	Un	CATGATATCAAAAA	2	0.375	Al	ORF	ORFv	7	4	179499	+	MSH5	YDL154W	☰	ℹ	AT CG	▥	6 17 0	-

Query Results: Compressed files for download are kept for 5 hours at the server and then deleted. By clicking on the filename, the file is downloaded.



Map your TAGs within a Genome: Results

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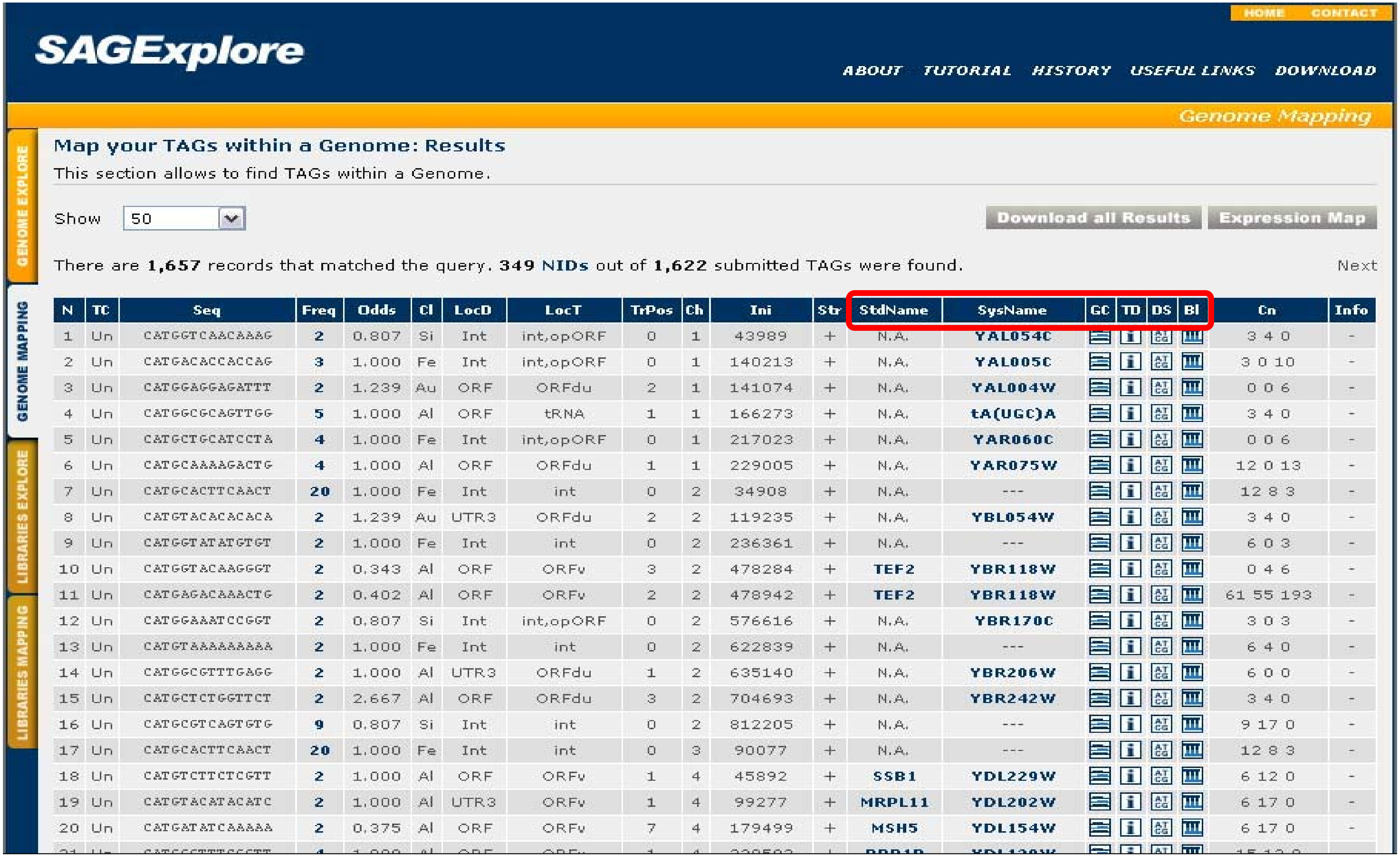
Show 50

There are **1,657** records that matched the query. **349 NIDs** out of **1,622** submitted TAGs were found.

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	BI	Cn	Info
1	Un	CATGGTCAACAAAG	**2**	0.807	Si	Int	int,opORF	0	1	43989	+	N.A.	**YAL054C**	☰	ℹ	▦	Ⅲ	3 4 0	-
2	Un	CATGACACCACCAG	**3**	1.000	Fe	Int	int,opORF	0	1	140213	+	N.A.	**YAL005C**	☰	ℹ	▦	Ⅲ	3 0 10	-
3	Un	CATGGAGGAGATTT	**2**	1.239	Au	ORF	ORFdu	2	1	141074	+	N.A.	**YAL004W**	☰	ℹ	▦	Ⅲ	0 0 6	-
4	Un	CATGGCGCAGTTGG	**5**	1.000	Al	ORF	tRNA	1	1	166273	+	N.A.	**tA(UGC)A**	☰	ℹ	▦	Ⅲ	3 4 0	-
5	Un	CATGCTGCATCCTA	**4**	1.000	Fe	Int	int,opORF	0	1	217023	+	N.A.	**YAR060C**	☰	ℹ	▦	Ⅲ	0 0 6	-
6	Un	CATGCAAAAGACTG	**4**	1.000	Al	ORF	ORFdu	1	1	229005	+	N.A.	**YAR075W**	☰	ℹ	▦	Ⅲ	12 0 13	-
7	Un	CATGCACTTCAACT	**20**	1.000	Fe	Int	int	0	2	34908	+	N.A.	---	☰	ℹ	▦	Ⅲ	12 8 3	-
8	Un	CATGTACACACACA	**2**	1.239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	**YBL054W**	☰	ℹ	▦	Ⅲ	3 4 0	-
9	Un	CATGGTATATGTGT	**2**	1.000	Fe	Int	int	0	2	236361	+	N.A.	---	☰	ℹ	▦	Ⅲ	6 0 3	-
10	Un	CATGGTACAAGGGT	**2**	0.343	Al	ORF	ORFv	3	2	478284	+	**TEF2**	**YBR118W**	☰	ℹ	▦	Ⅲ	0 4 6	-
11	Un	CATGAGACAAACTG	**2**	0.402	Al	ORF	ORFv	2	2	478942	+	**TEF2**	**YBR118W**	☰	ℹ	▦	Ⅲ	61 55 193	-
12	Un	CATGGAAATCCGGT	**2**	0.807	Si	Int	int,opORF	0	2	576616	+	N.A.	**YBR170C**	☰	ℹ	▦	Ⅲ	3 0 3	-
13	Un	CATGTAAAAAAAAA	**2**	1.000	Fe	Int	int	0	2	622839	+	N.A.	---	☰	ℹ	▦	Ⅲ	6 4 0	-
14	Un	CATGGCGTTTGAGG	**2**	1.000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	**YBR206W**	☰	ℹ	▦	Ⅲ	6 0 0	-
15	Un	CATGCTCTGGTTCT	**2**	2.667	Al	ORF	ORFdu	3	2	704693	+	N.A.	**YBR242W**	☰	ℹ	▦	Ⅲ	3 4 0	-
16	Un	CATGCGTCAGTGTG	**9**	0.807	Si	Int	int	0	2	812205	+	N.A.	---	☰	ℹ	▦	Ⅲ	9 17 0	-
17	Un	CATGCACTTCAACT	**20**	1.000	Fe	Int	int	0	3	90077	+	N.A.	---	☰	ℹ	▦	Ⅲ	12 8 3	-
18	Un	CATGTCTTCTCGTT	**2**	1.000	Al	ORF	ORFv	1	4	45892	+	**SSB1**	**YDL229W**	☰	ℹ	▦	Ⅲ	6 12 0	-
19	Un	CATGTACATACATC	**2**	1.000	Al	UTR3	ORFv	1	4	99277	+	**MRPL11**	**YDL202W**	☰	ℹ	▦	Ⅲ	6 17 0	-
20	Un	CATGATATCAAAAA	**2**	0.375	Al	ORF	ORFv	7	4	179499	+	**MSH5**	**YDL154W**	☰	ℹ	▦	Ⅲ	6 17 0	-

Query Results: Online help explaining the meaning of each column is obtained by left-clicking with the mouse over the column headers.



Map your TAGs within a Genome: Results

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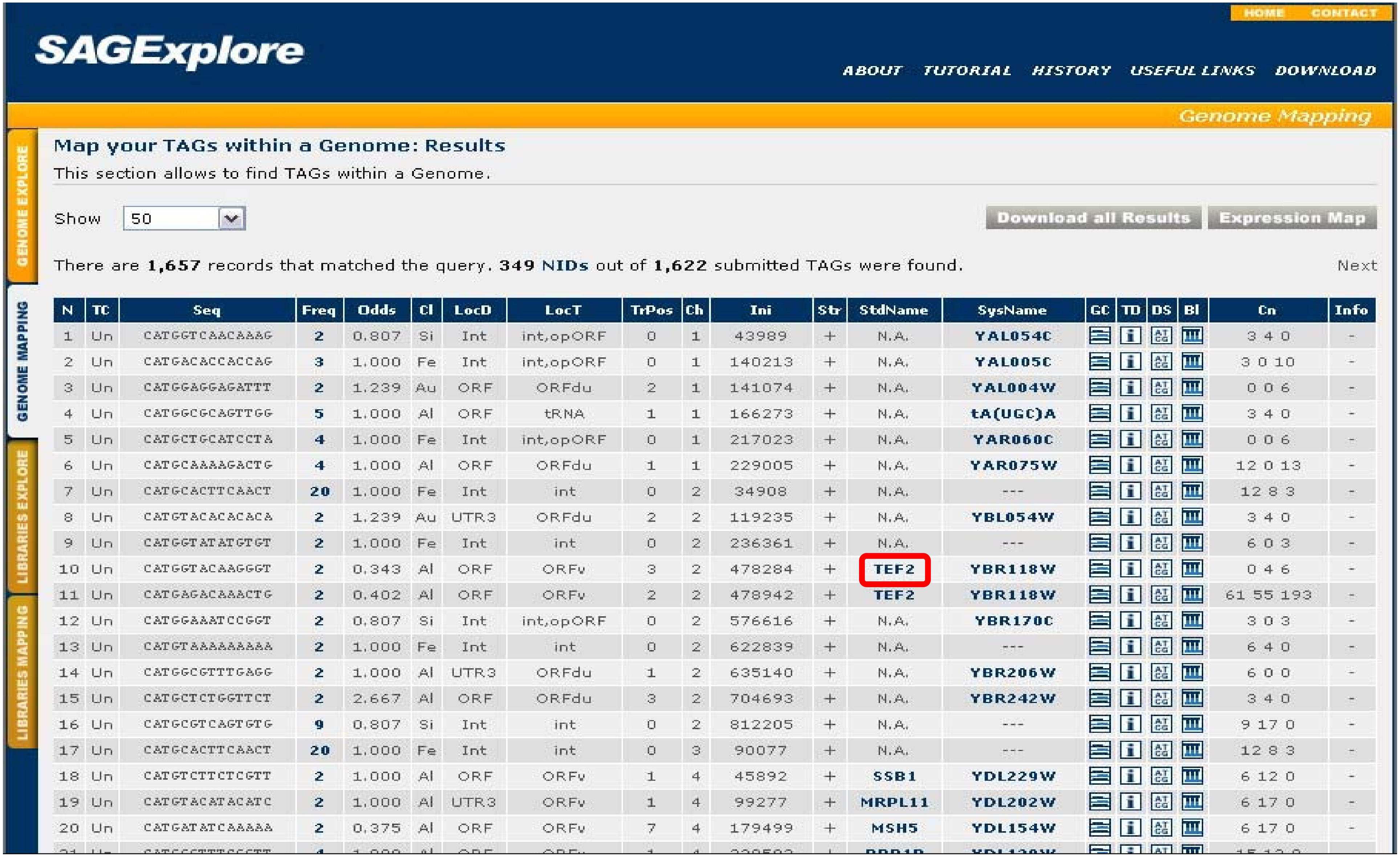
Show 50

There are **1,657** records that matched the query. **349 NIDs** out of **1,622** submitted TAGs were found.

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	BI	Cn	Info
1	Un	CATGGTCAACAAAG	**2**	0.807	Si	Int	int,opORF	0	1	43989	+	N.A.	**YAL054C**	☰	ℹ	AT CG	▥	3 4 0	-
2	Un	CATGACACCACCAG	**3**	1.000	Fe	Int	int,opORF	0	1	140213	+	N.A.	**YAL005C**	☰	ℹ	AT CG	▥	3 0 10	-
3	Un	CATGGAGGAGATTT	**2**	1.239	Au	ORF	ORFdu	2	1	141074	+	N.A.	**YAL004W**	☰	ℹ	AT CG	▥	0 0 6	-
4	Un	CATGGCGCAGTTGG	**5**	1.000	Al	ORF	tRNA	1	1	166273	+	N.A.	**tA(UGC)A**	☰	ℹ	AT CG	▥	3 4 0	-
5	Un	CATGCTGCATCCTA	**4**	1.000	Fe	Int	int,opORF	0	1	217023	+	N.A.	**YAR060C**	☰	ℹ	AT CG	▥	0 0 6	-
6	Un	CATGCAAAAGACTG	**4**	1.000	Al	ORF	ORFdu	1	1	229005	+	N.A.	**YAR075W**	☰	ℹ	AT CG	▥	12 0 13	-
7	Un	CATGCACTTCAACT	**20**	1.000	Fe	Int	int	0	2	34908	+	N.A.	---	☰	ℹ	AT CG	▥	12 8 3	-
8	Un	CATGTACACACACA	**2**	1.239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	**YBL054W**	☰	ℹ	AT CG	▥	3 4 0	-
9	Un	CATGGTATATGTGT	**2**	1.000	Fe	Int	int	0	2	236361	+	N.A.	---	☰	ℹ	AT CG	▥	6 0 3	-
10	Un	CATGGTACAAGGGT	**2**	0.343	Al	ORF	ORFv	3	2	478284	+	**TEF2**	**YBR118W**	☰	ℹ	AT CG	▥	0 4 6	-
11	Un	CATGAGACAAACTG	**2**	0.402	Al	ORF	ORFv	2	2	478942	+	**TEF2**	**YBR118W**	☰	ℹ	AT CG	▥	61 55 193	-
12	Un	CATGGAAATCCGGT	**2**	0.807	Si	Int	int,opORF	0	2	576616	+	N.A.	**YBR170C**	☰	ℹ	AT CG	▥	3 0 3	-
13	Un	CATGTAAAAAAAAA	**2**	1.000	Fe	Int	int	0	2	622839	+	N.A.	---	☰	ℹ	AT CG	▥	6 4 0	-
14	Un	CATGGCGTTTGAGG	**2**	1.000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	**YBR206W**	☰	ℹ	AT CG	▥	6 0 0	-
15	Un	CATGCTCTGGTTCT	**2**	2.667	Al	ORF	ORFdu	3	2	704693	+	N.A.	**YBR242W**	☰	ℹ	AT CG	▥	3 4 0	-
16	Un	CATGCGTCAGTGTG	**9**	0.807	Si	Int	int	0	2	812205	+	N.A.	---	☰	ℹ	AT CG	▥	9 17 0	-
17	Un	CATGCACTTCAACT	**20**	1.000	Fe	Int	int	0	3	90077	+	N.A.	---	☰	ℹ	AT CG	▥	12 8 3	-
18	Un	CATGTCTTCTCGTT	**2**	1.000	Al	ORF	ORFv	1	4	45892	+	**SSB1**	**YDL229W**	☰	ℹ	AT CG	▥	6 12 0	-
19	Un	CATGTACATACATC	**2**	1.000	Al	UTR3	ORFv	1	4	99277	+	**MRPL11**	**YDL202W**	☰	ℹ	AT CG	▥	6 17 0	-
20	Un	CATGATATCAAAAA	**2**	0.375	Al	ORF	ORFv	7	4	179499	+	**MSH5**	**YDL154W**	☰	ℹ	AT CG	▥	6 17 0	-

Query Results: These 6 columns contain linked fields.



Map your TAGs within a Genome: Results

This section allows to find TAGs within a Genome.

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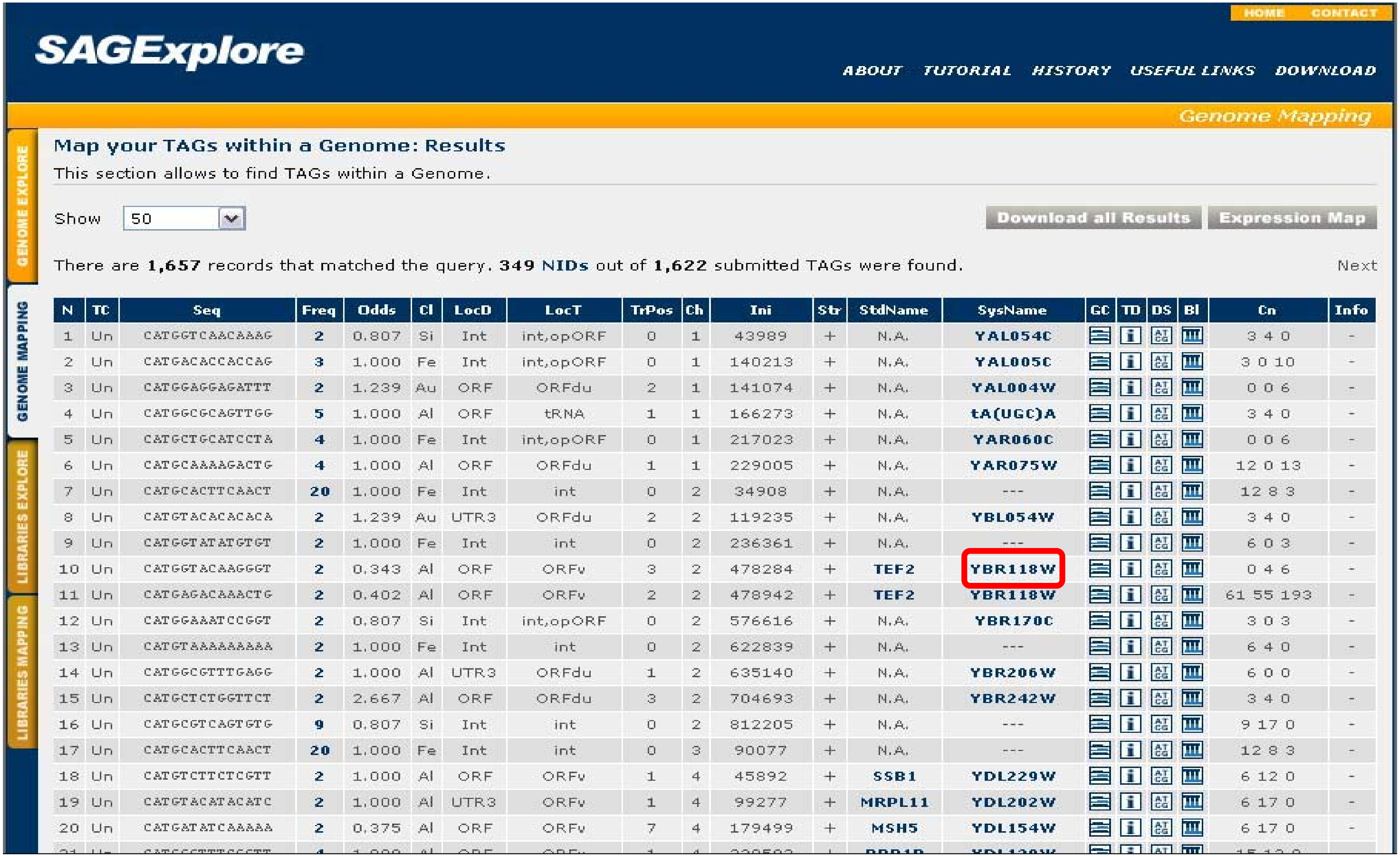
N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	BI	Cn	Info
1	Un	CATGGTCAACAAAG	**2**	0.807	Si	Int	int,opORF	0	1	43989	+	N.A.	**YAL054C**	☰	ℹ	▦	▥	3 4 0	-
2	Un	CATGACACCACCAG	**3**	1.000	Fe	Int	int,opORF	0	1	140213	+	N.A.	**YAL005C**	☰	ℹ	▦	▥	3 0 10	-
3	Un	CATGGAGGAGATTT	**2**	1.239	Au	ORF	ORFdu	2	1	141074	+	N.A.	**YAL004W**	☰	ℹ	▦	▥	0 0 6	-
4	Un	CATGGCGCAGTTGG	**5**	1.000	Al	ORF	tRNA	1	1	166273	+	N.A.	**tA(UGC)A**	☰	ℹ	▦	▥	3 4 0	-
5	Un	CATGCTGCATCCTA	**4**	1.000	Fe	Int	int,opORF	0	1	217023	+	N.A.	**YAR060C**	☰	ℹ	▦	▥	0 0 6	-
6	Un	CATGCAAAAGACTG	**4**	1.000	Al	ORF	ORFdu	1	1	229005	+	N.A.	**YAR075W**	☰	ℹ	▦	▥	12 0 13	-
7	Un	CATGCACTTCAACT	**20**	1.000	Fe	Int	int	0	2	34908	+	N.A.	---	☰	ℹ	▦	▥	12 8 3	-
8	Un	CATGTACACACACA	**2**	1.239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	**YBL054W**	☰	ℹ	▦	▥	3 4 0	-
9	Un	CATGGTATATGTGT	**2**	1.000	Fe	Int	int	0	2	236361	+	N.A.	---	☰	ℹ	▦	▥	6 0 3	-
10	Un	CATGGTACAAGGGT	**2**	0.343	Al	ORF	ORFv	3	2	478284	+	**TEF2**	**YBR118W**	☰	ℹ	▦	▥	0 4 6	-
11	Un	CATGAGACAAACTG	**2**	0.402	Al	ORF	ORFv	2	2	478942	+	**TEF2**	**YBR118W**	☰	ℹ	▦	▥	61 55 193	-
12	Un	CATGGAAATCCGGT	**2**	0.807	Si	Int	int,opORF	0	2	576616	+	N.A.	**YBR170C**	☰	ℹ	▦	▥	3 0 3	-
13	Un	CATGTAAAAAAAAA	**2**	1.000	Fe	Int	int	0	2	622839	+	N.A.	---	☰	ℹ	▦	▥	6 4 0	-
14	Un	CATGGCGTTTGAGG	**2**	1.000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	**YBR206W**	☰	ℹ	▦	▥	6 0 0	-
15	Un	CATGCTCTGGTTCT	**2**	2.667	Al	ORF	ORFdu	3	2	704693	+	N.A.	**YBR242W**	☰	ℹ	▦	▥	3 4 0	-
16	Un	CATGCGTCAGTGTG	**9**	0.807	Si	Int	int	0	2	812205	+	N.A.	---	☰	ℹ	▦	▥	9 17 0	-
17	Un	CATGCACTTCAACT	**20**	1.000	Fe	Int	int	0	3	90077	+	N.A.	---	☰	ℹ	▦	▥	12 8 3	-
18	Un	CATGTCTTCTCGTT	**2**	1.000	Al	ORF	ORFv	1	4	45892	+	**SSB1**	**YDL229W**	☰	ℹ	▦	▥	6 12 0	-
19	Un	CATGTACATACATC	**2**	1.000	Al	UTR3	ORFv	1	4	99277	+	**MRPL11**	**YDL202W**	☰	ℹ	▦	▥	6 17 0	-
20	Un	CATGATATCAAAAA	**2**	0.375	Al	ORF	ORFv	7	4	179499	+	**MSH5**	**YDL154W**	☰	ℹ	▦	▥	6 17 0	-

Query Results: By clicking over the standard gene name, a query to the Saccharomyces Genome Database is launched. Thus, the user can obtain a large amount of data about a given gene.



Map your TAGs within a Genome: Results

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Show: 50

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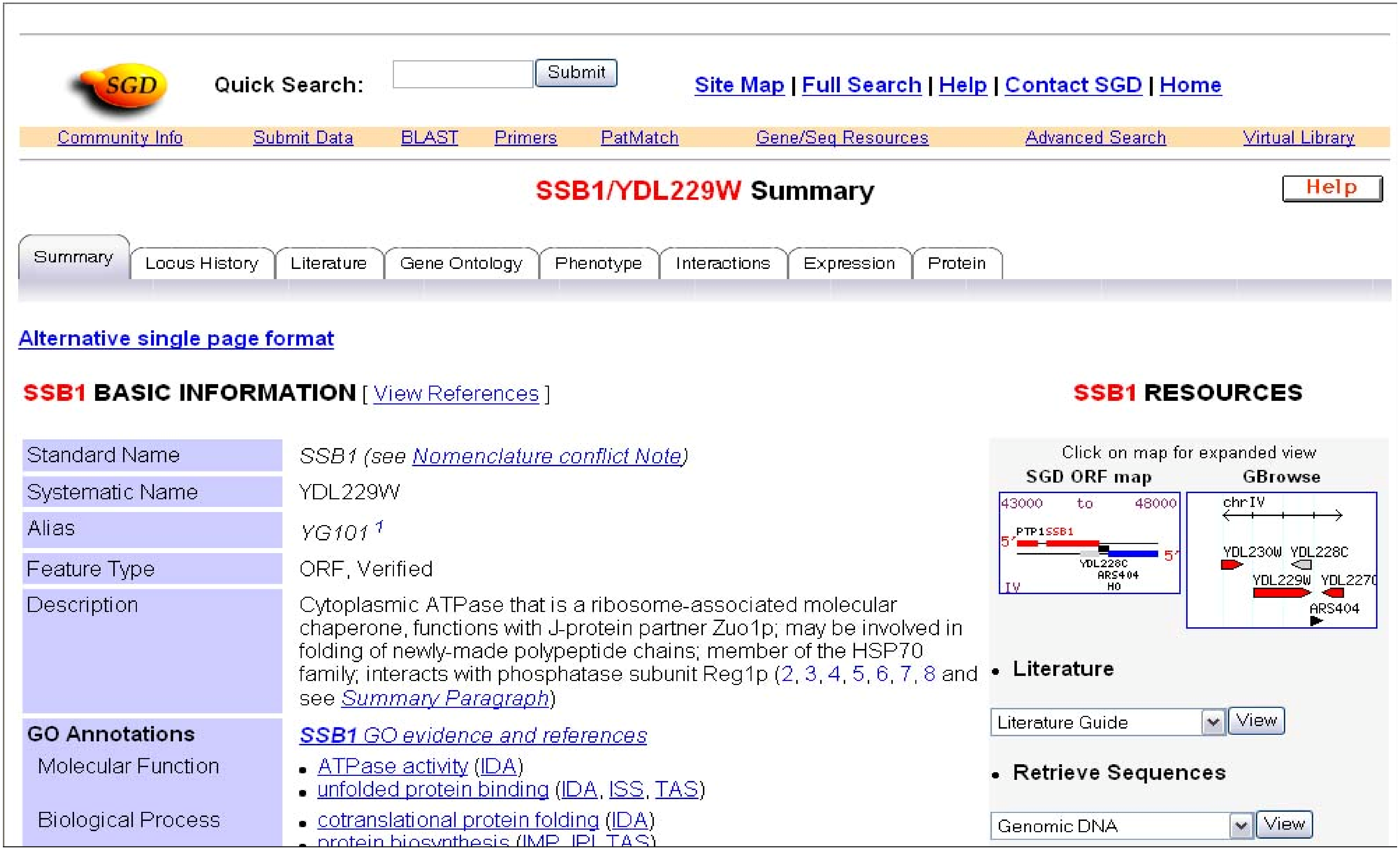
N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	BI	Cn	Info
1	Un	CATGGTCAACAAAG	2	0.807	Si	Int	int,opORF	0	1	43989	+	N.A.	YAL054C	☰	ℹ	AT CG	▥	3 4 0	-
2	Un	CATGACACCACCAG	3	1.000	Fe	Int	int,opORF	0	1	140213	+	N.A.	YAL005C	☰	ℹ	AT CG	▥	3 0 10	-
3	Un	CATGGAGGAGATTT	2	1.239	Au	ORF	ORFdu	2	1	141074	+	N.A.	YAL004W	☰	ℹ	AT CG	▥	0 0 6	-
4	Un	CATGGCGCAGTTGG	5	1.000	Al	ORF	tRNA	1	1	166273	+	N.A.	tA(UGC)A	☰	ℹ	AT CG	▥	3 4 0	-
5	Un	CATGCTGCATCCTA	4	1.000	Fe	Int	int,opORF	0	1	217023	+	N.A.	YAR060C	☰	ℹ	AT CG	▥	0 0 6	-
6	Un	CATGCAAAAGACTG	4	1.000	Al	ORF	ORFdu	1	1	229005	+	N.A.	YAR075W	☰	ℹ	AT CG	▥	12 0 13	-
7	Un	CATGCACTTCAACT	20	1.000	Fe	Int	int	0	2	34908	+	N.A.	---	☰	ℹ	AT CG	▥	12 8 3	-
8	Un	CATGTACACACACA	2	1.239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	YBL054W	☰	ℹ	AT CG	▥	3 4 0	-
9	Un	CATGGTATATGTGT	2	1.000	Fe	Int	int	0	2	236361	+	N.A.	---	☰	ℹ	AT CG	▥	6 0 3	-
10	Un	CATGGTACAAGGGT	2	0.343	Al	ORF	ORFv	3	2	478284	+	TEF2	YBR118W	☰	ℹ	AT CG	▥	0 4 6	-
11	Un	CATGAGACAAACTG	2	0.402	Al	ORF	ORFv	2	2	478942	+	TEF2	YBR118W	☰	ℹ	AT CG	▥	61 55 193	-
12	Un	CATGGAAATCCGGT	2	0.807	Si	Int	int,opORF	0	2	576616	+	N.A.	YBR170C	☰	ℹ	AT CG	▥	3 0 3	-
13	Un	CATGTAAAAAAAAA	2	1.000	Fe	Int	int	0	2	622839	+	N.A.	---	☰	ℹ	AT CG	▥	6 4 0	-
14	Un	CATGGCGTTTGAGG	2	1.000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	YBR206W	☰	ℹ	AT CG	▥	6 0 0	-
15	Un	CATGCTCTGGTTCT	2	2.667	Al	ORF	ORFdu	3	2	704693	+	N.A.	YBR242W	☰	ℹ	AT CG	▥	3 4 0	-
16	Un	CATGCGTCAGTGTG	9	0.807	Si	Int	int	0	2	812205	+	N.A.	---	☰	ℹ	AT CG	▥	9 17 0	-
17	Un	CATGCACTTCAACT	20	1.000	Fe	Int	int	0	3	90077	+	N.A.	---	☰	ℹ	AT CG	▥	12 8 3	-
18	Un	CATGTCTTCTCGTT	2	1.000	Al	ORF	ORFv	1	4	45892	+	SSB1	YDL229W	☰	ℹ	AT CG	▥	6 12 0	-
19	Un	CATGTACATACATC	2	1.000	Al	UTR3	ORFv	1	4	99277	+	MRPL11	YDL202W	☰	ℹ	AT CG	▥	6 17 0	-
20	Un	CATGATATCAAAAA	2	0.375	Al	ORF	ORFv	7	4	179499	+	MSH5	YDL154W	☰	ℹ	AT CG	▥	6 17 0	-

Query Results: By clicking over the systematic gene name, a query to the Saccharomyces Genome Database is launched. Thus, the user can obtain a large amount of data about a given gene.



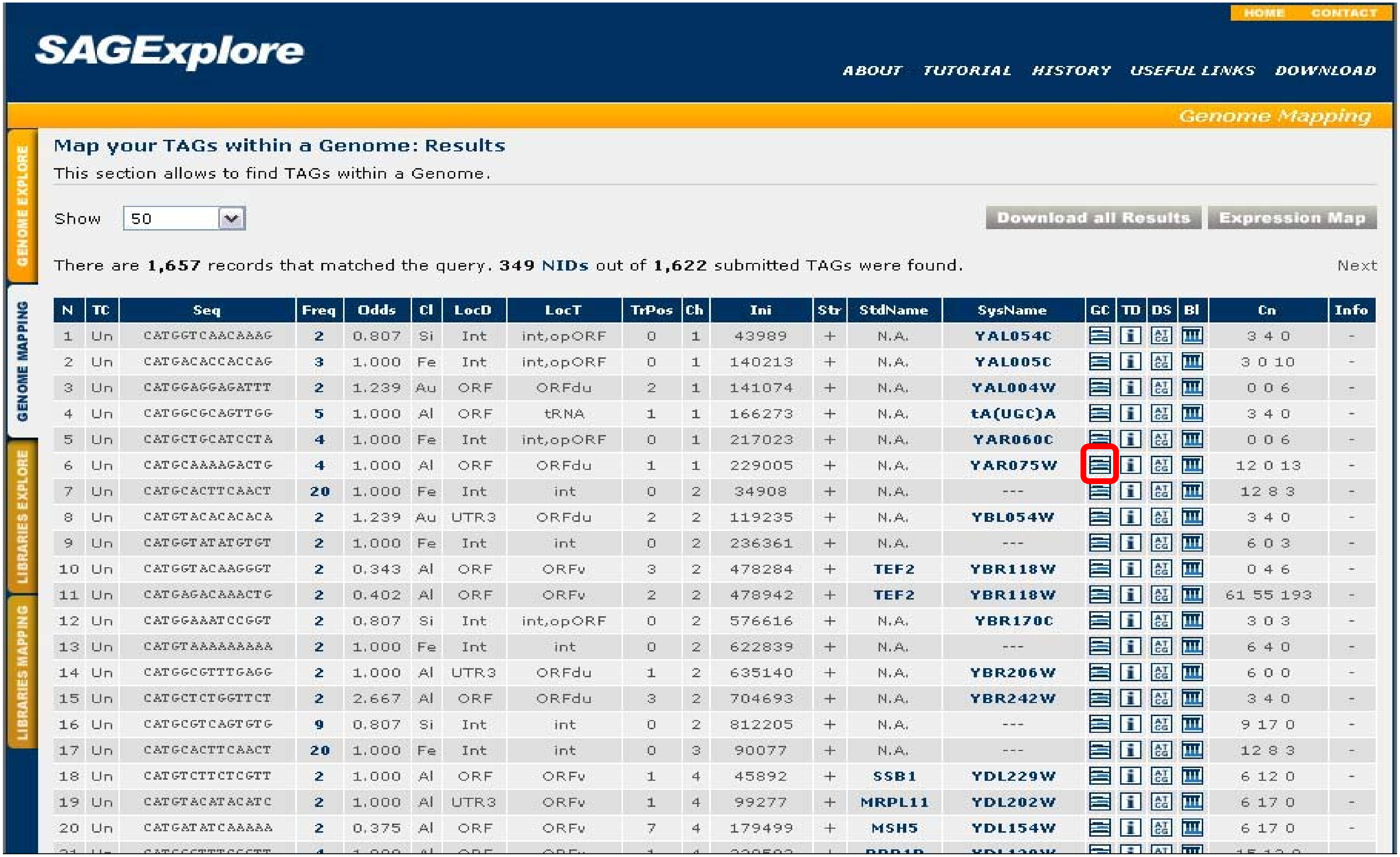
SSB1/YDL229W Summary

SSB1 BASIC INFORMATION [View References]

SSB1 RESOURCES

Standard Name	*SSB1* (see Nomenclature conflict Note)
Systematic Name	YDL229W
Alias	*YG101* [1]
Feature Type	ORF, Verified
Description	Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p (2, 3, 4, 5, 6, 7, 8 and see Summary Paragraph)
GO Annotations	*SSB1 GO evidence and references*
Molecular Function	ATPase activity (IDA) unfolded protein binding (IDA, ISS, TAS)
Biological Process	cotranslational protein folding (IDA) protein biosynthesis (IMP, IPI, TAS)

SGD Query: An example of the results obtained when quering the Saccharomyces Genome Database by standard or systematic gene name.



Map your TAGs within a Genome: Results

This section allows to find TAGs within a Genome.

There are **1,657** records that matched the query. **349 NIDs** out of **1,622** submitted TAGs were found.

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	BI	Cn	Info
1	Un	CATGGTCAACAAAG	**2**	0.807	Si	Int	int,opORF	0	1	43989	+	N.A.	**YAL054C**	☰	ℹ	AT CG	▥	3 4 0	-
2	Un	CATGACACCACCAG	**3**	1.000	Fe	Int	int,opORF	0	1	140213	+	N.A.	**YAL005C**	☰	ℹ	AT CG	▥	3 0 10	-
3	Un	CATGGAGGAGATTT	**2**	1.239	Au	ORF	ORFdu	2	1	141074	+	N.A.	**YAL004W**	☰	ℹ	AT CG	▥	0 0 6	-
4	Un	CATGGCGCAGTTGG	**5**	1.000	Al	ORF	tRNA	1	1	166273	+	N.A.	**tA(UGC)A**	☰	ℹ	AT CG	▥	3 4 0	-
5	Un	CATGCTGCATCCTA	**4**	1.000	Fe	Int	int,opORF	0	1	217023	+	N.A.	**YAR060C**	☰	ℹ	AT CG	▥	0 0 6	-
6	Un	CATGCAAAAGACTG	**4**	1.000	Al	ORF	ORFdu	1	1	229005	+	N.A.	**YAR075W**	☰	ℹ	AT CG	▥	12 0 13	-
7	Un	CATGCACTTCAACT	**20**	1.000	Fe	Int	int	0	2	34908	+	N.A.	---	☰	ℹ	AT CG	▥	12 8 3	-
8	Un	CATGTACACACACA	**2**	1.239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	**YBL054W**	☰	ℹ	AT CG	▥	3 4 0	-
9	Un	CATGGTATATGTGT	**2**	1.000	Fe	Int	int	0	2	236361	+	N.A.	---	☰	ℹ	AT CG	▥	6 0 3	-
10	Un	CATGGTACAAGGGT	**2**	0.343	Al	ORF	ORFv	3	2	478284	+	**TEF2**	**YBR118W**	☰	ℹ	AT CG	▥	0 4 6	-
11	Un	CATGAGACAAACTG	**2**	0.402	Al	ORF	ORFv	2	2	478942	+	**TEF2**	**YBR118W**	☰	ℹ	AT CG	▥	61 55 193	-
12	Un	CATGGAAATCCGGT	**2**	0.807	Si	Int	int,opORF	0	2	576616	+	N.A.	**YBR170C**	☰	ℹ	AT CG	▥	3 0 3	-
13	Un	CATGTAAAAAAAAA	**2**	1.000	Fe	Int	int	0	2	622839	+	N.A.	---	☰	ℹ	AT CG	▥	6 4 0	-
14	Un	CATGGCGTTTGAGG	**2**	1.000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	**YBR206W**	☰	ℹ	AT CG	▥	6 0 0	-
15	Un	CATGCTCTGGTTCT	**2**	2.667	Al	ORF	ORFdu	3	2	704693	+	N.A.	**YBR242W**	☰	ℹ	AT CG	▥	3 4 0	-
16	Un	CATGCGTCAGTGTG	**9**	0.807	Si	Int	int	0	2	812205	+	N.A.	---	☰	ℹ	AT CG	▥	9 17 0	-
17	Un	CATGCACTTCAACT	**20**	1.000	Fe	Int	int	0	3	90077	+	N.A.	---	☰	ℹ	AT CG	▥	12 8 3	-
18	Un	CATGTCTTCTCGTT	**2**	1.000	Al	ORF	ORFv	1	4	45892	+	**SSB1**	**YDL229W**	☰	ℹ	AT CG	▥	6 12 0	-
19	Un	CATGTACATACATC	**2**	1.000	Al	UTR3	ORFv	1	4	99277	+	**MRPL11**	**YDL202W**	☰	ℹ	AT CG	▥	6 17 0	-
20	Un	CATGATATCAAAAA	**2**	0.375	Al	ORF	ORFv	7	4	179499	+	**MSH5**	**YDL154W**	☰	ℹ	AT CG	▥	6 17 0	-

Query Results: The genomic context where a tag matches can be obtained by clicking on this field.

SAGExplore

Genomic Context

Organism: *Sacharomyces cerevisiae*

Fragment Displayed: 1 - 6,000

100 Kb **Chromosome: 1** **Length: 230,208 bp**

Keys:

Chromosome:

🟦 Watson (+) Strand

🟦 Crick (-) Strand

Fragment Displayed

Centromer

TAG of High Confidence

TAG of Undefined Confidence

TAG of Low Confidence

Shape:

— Strand

Transcript

Intron

TAG

Color:

UTR5'-ORF-UTR3'

🟩 ORF Verified

🟧 ORF Uncharacterized

🟥 ORF Dubious

tRNA

🟦 rRNA

🟦 snoRNA

🟦 snRNA

🟦 ncRNA

TAG of High Confidence

TAG of Undefined Confidence

TAG of Low Confidence

Genomic Context: The selected tag is shown with a vertical arrow head.

SAGExplore

Genomic Context

Organism: *Sacharomyces cerevisiae*
Fragment Displayed: 1 - 6,000

100 Kb **Chromosome: 1** **Length: 230,208 bp**

Keys:

Chromosome:

- Watson (+) Strand
- Crick (-) Strand
- Fragment Displayed
- Centromer
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

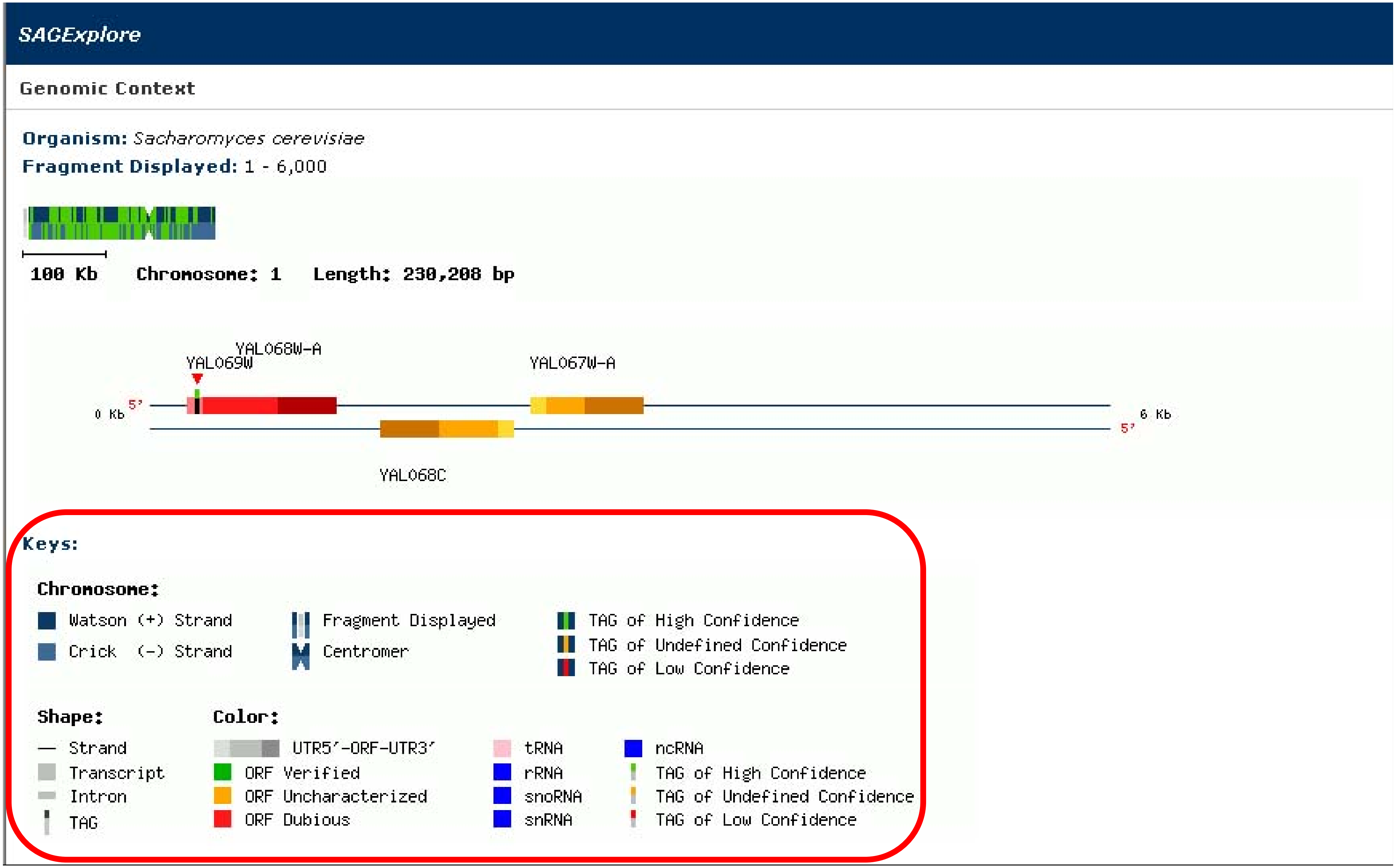
Shape:

- Strand
- Transcript
- Intron
- TAG

Color:

- UTR5'-ORF-UTR3'
- ORF Verified
- ORF Uncharacterized
- ORF Dubious
- tRNA
- rRNA
- snoRNA
- snRNA
- ncRNA
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Genomic Context: Gene names are linked to the Saccharomyces Genome Database.



SAGExplore

Genomic Context

Organism: *Sacharomyces cerevisiae*
Fragment Displayed: 1 - 6,000

100 Kb **Chromosome: 1** **Length: 230,208 bp**

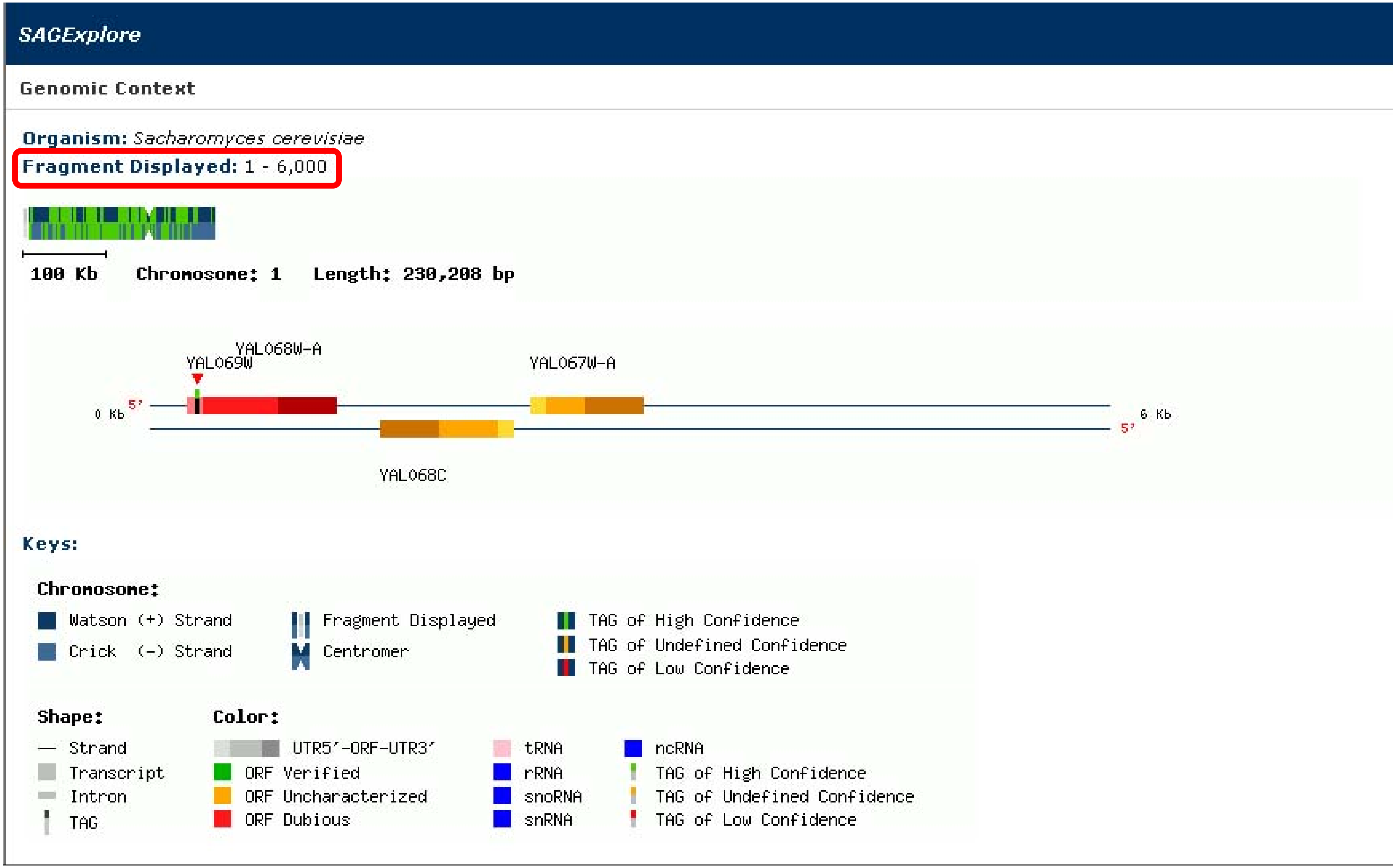
Keys:

Chromosome:
- Watson (+) Strand
- Crick (-) Strand
- Fragment Displayed
- Centromer
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Shape:
- — Strand
- Transcript
- Intron
- TAG

Color:
- UTR5'-ORF-UTR3'
- 🟩 ORF Verified
- 🟧 ORF Uncharacterized
- 🟥 ORF Dubious
- tRNA
- 🟦 rRNA
- 🟦 snoRNA
- 🟦 snRNA
- 🟦 ncRNA
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Genomic Context: Keys of the graphical elements displayed above are provided.



SAGExplore

Genomic Context

Organism: *Sacharomyces cerevisiae*

Fragment Displayed: 1 - 6,000

100 Kb   Chromosome: 1   Length: 230,208 bp

Keys:

Chromosome:

- Watson (+) Strand
- Crick (-) Strand
- Fragment Displayed
- Centromer
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Shape:

- Strand
- Transcript
- Intron
- TAG

Color:

- UTR5'-ORF-UTR3'
- 🟩 ORF Verified
- 🟧 ORF Uncharacterized
- 🟥 ORF Dubious
- tRNA
- 🟦 rRNA
- 🟦 snoRNA
- 🟦 snRNA
- 🟦 ncRNA
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Genomic Context: The fragment of the chromosome being displayed is specified.

SAGExplore

Genomic Context

Organism: *Sacharomyces cerevisiae*
Fragment Displayed: 1 - 6,000

100 Kb **Chromosome: 1** **Length: 230,208 bp**

Keys:

Chromosome:
Watson (+) Strand
Crick (-) Strand
Fragment Displayed
Centromer
TAG of High Confidence
TAG of Undefined Confidence
TAG of Low Confidence

Shape:
Strand
Transcript
Intron
TAG

Color:
UTR5'-ORF-UTR3'
ORF Verified
ORF Uncharacterized
ORF Dubious
tRNA
rRNA
snoRNA
snRNA
ncRNA
TAG of High Confidence
TAG of Undefined Confidence
TAG of Low Confidence

Genomic Context: In this case corresponds to the 5' end of the chromosome. The user can click on this graphical chromosome to select and display a different region.

SAGExplore

Genomic Context

Organism: *Sacharomyces cerevisiae*

Fragment Displayed: 1 - 6,000

100 Kb **Chromosome: 1** **Length: 230,208 bp**

Keys:

Chromosome:

- Watson (+) Strand
- Crick (-) Strand
- Fragment Displayed
- Centromer
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

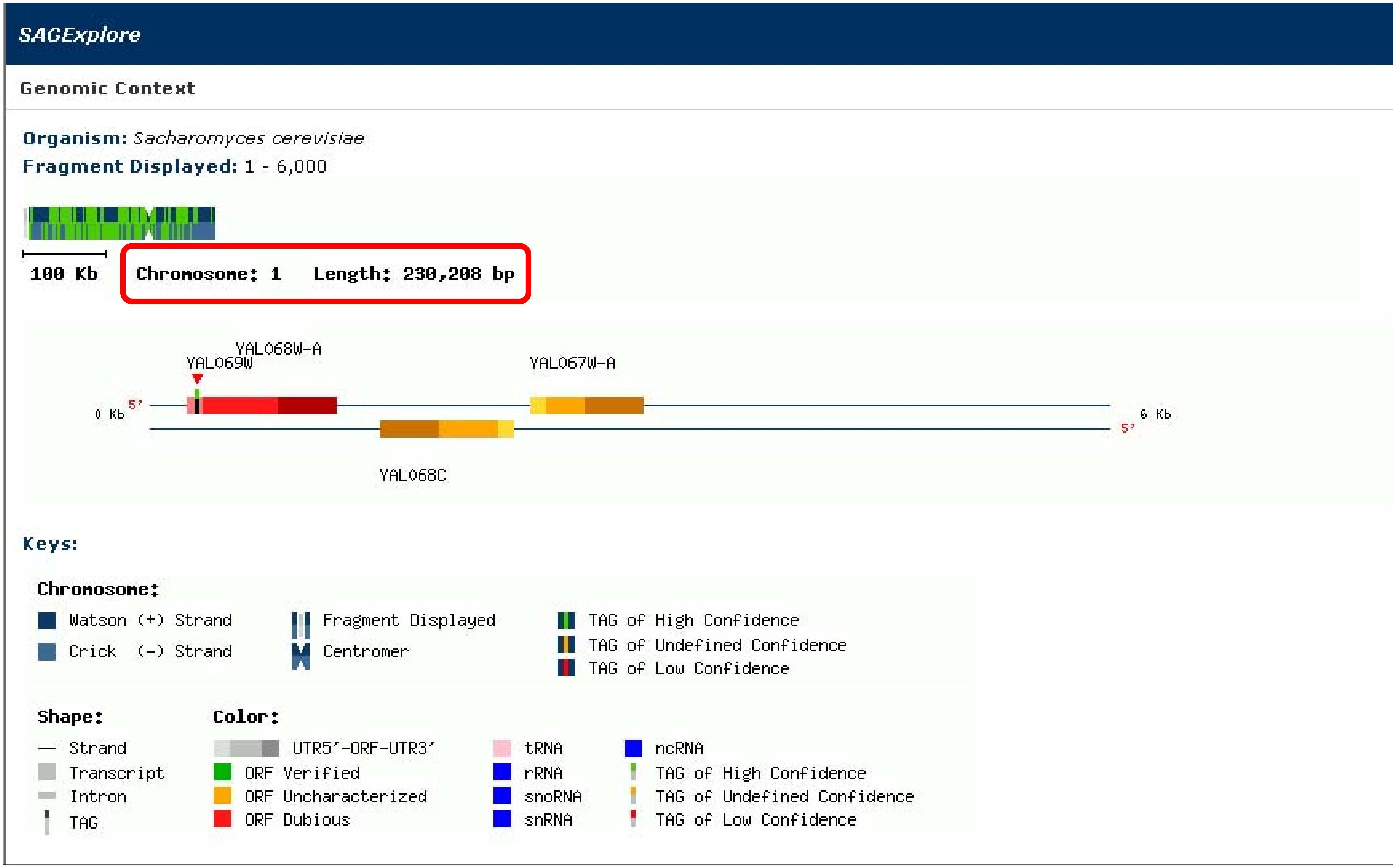
Shape:

- Strand
- Transcript
- Intron
- TAG

Color:

- UTR5'-ORF-UTR3'
- ORF Verified
- ORF Uncharacterized
- ORF Dubious
- tRNA
- rRNA
- snoRNA
- snRNA
- ncRNA
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Genomic Context: The chromosome scale in base pairs is also shown.



SAGExplore

Genomic Context

Organism: *Sacharomyces cerevisiae*

Fragment Displayed: 1 - 6,000

100 Kb

Chromosome: 1 Length: 230,208 bp

Keys:

Chromosome:

- Watson (+) Strand
- Crick (-) Strand
- Fragment Displayed
- Centromer
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Shape:

- — Strand
- Transcript
- Intron
- TAG

Color:

- UTR5'-ORF-UTR3'
- 🟩 ORF Verified
- 🟧 ORF Uncharacterized
- 🟥 ORF Dubious
- tRNA
- 🟦 rRNA
- 🟦 snoRNA
- 🟦 snRNA
- 🟦 ncRNA
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Genomic Context: The current chromosome number and size are given.

SAGExplore

Genomic Context

Organism: *Sacharomyces cerevisiae*

Fragment Displayed: 1 - 6,000

100 Kb **Chromosome: 1** **Length: 230,208 bp**

Keys:

Chromosome:

- 🟦 Watson (+) Strand
- 🟦 Crick (-) Strand
- Fragment Displayed
- Centromer
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Shape:

- — Strand
- Transcript
- Intron
- TAG

Color:

- UTR5'-ORF-UTR3'
- 🟩 ORF Verified
- 🟧 ORF Uncharacterized
- 🟥 ORF Dubious
- tRNA
- 🟦 rRNA
- 🟦 snoRNA
- 🟦 snRNA
- 🟦 ncRNA
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Genomic Context: The 5’ and 3’ positions of the chromosome fragment displayed are also shown.

SAGExplore

Genomic Context

Organism: *Sacharomyces cerevisiae*

Fragment Displayed: 1 - 6,000

100 Kb **Chromosome: 1** **Length: 230,208 bp**

Keys:

Chromosome:

- Watson (+) Strand
- Crick (-) Strand
- Fragment Displayed
- Centromer
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

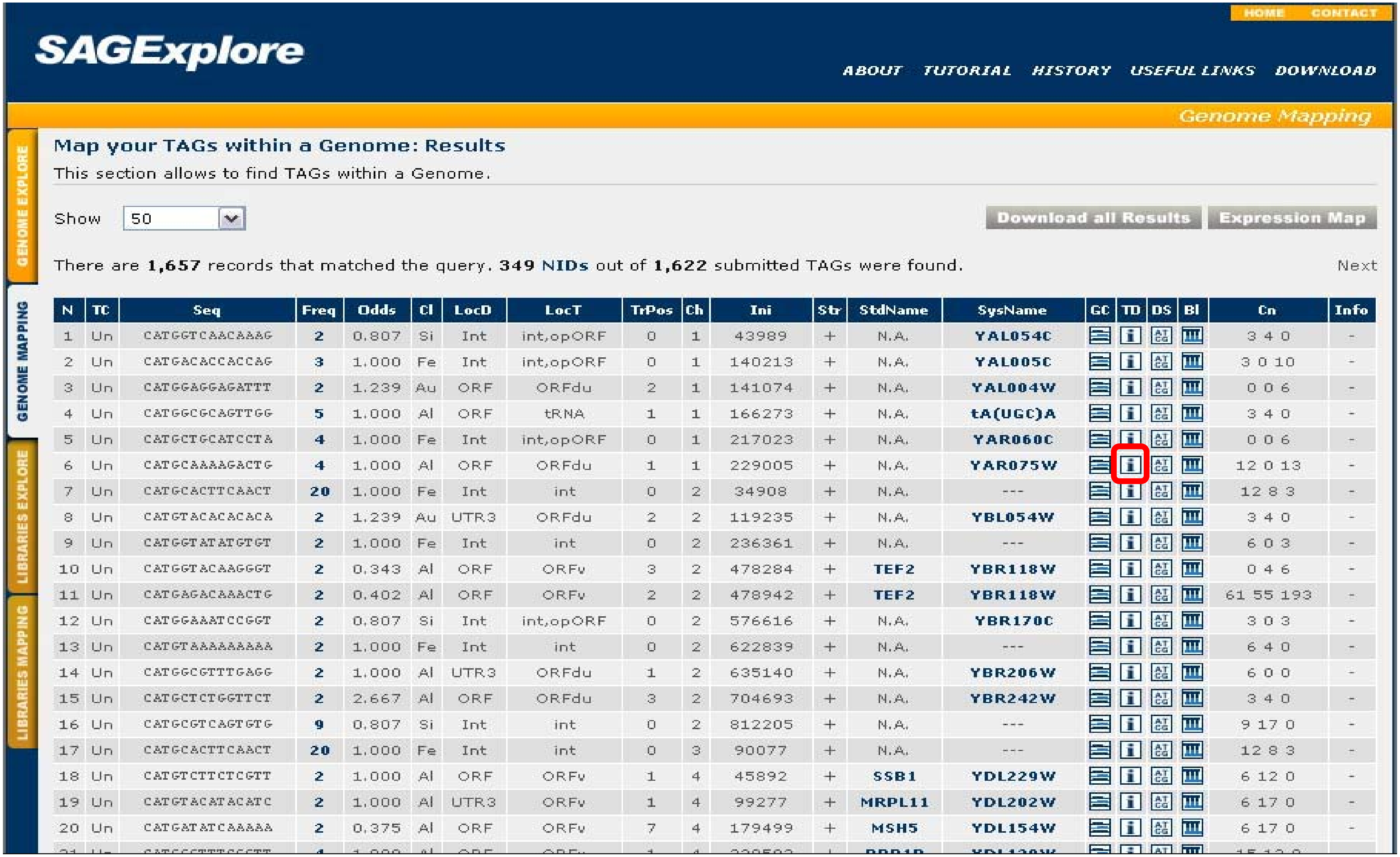
Shape:

- — Strand
- Transcript
- Intron
- TAG

Color:

- UTR5'-ORF-UTR3'
- 🟩 ORF Verified
- 🟧 ORF Uncharacterized
- 🟥 ORF Dubious
- tRNA
- 🟦 rRNA
- 🟦 snoRNA
- 🟦 snRNA
- 🟦 ncRNA
- TAG of High Confidence
- TAG of Undefined Confidence
- TAG of Low Confidence

Genomic Context: Clicking on the tag will display a pop-up window with several details about this tag. This pop-up window can also be launched from the main results table and thus it will be explained next from there.



Map your TAGs within a Genome: Results

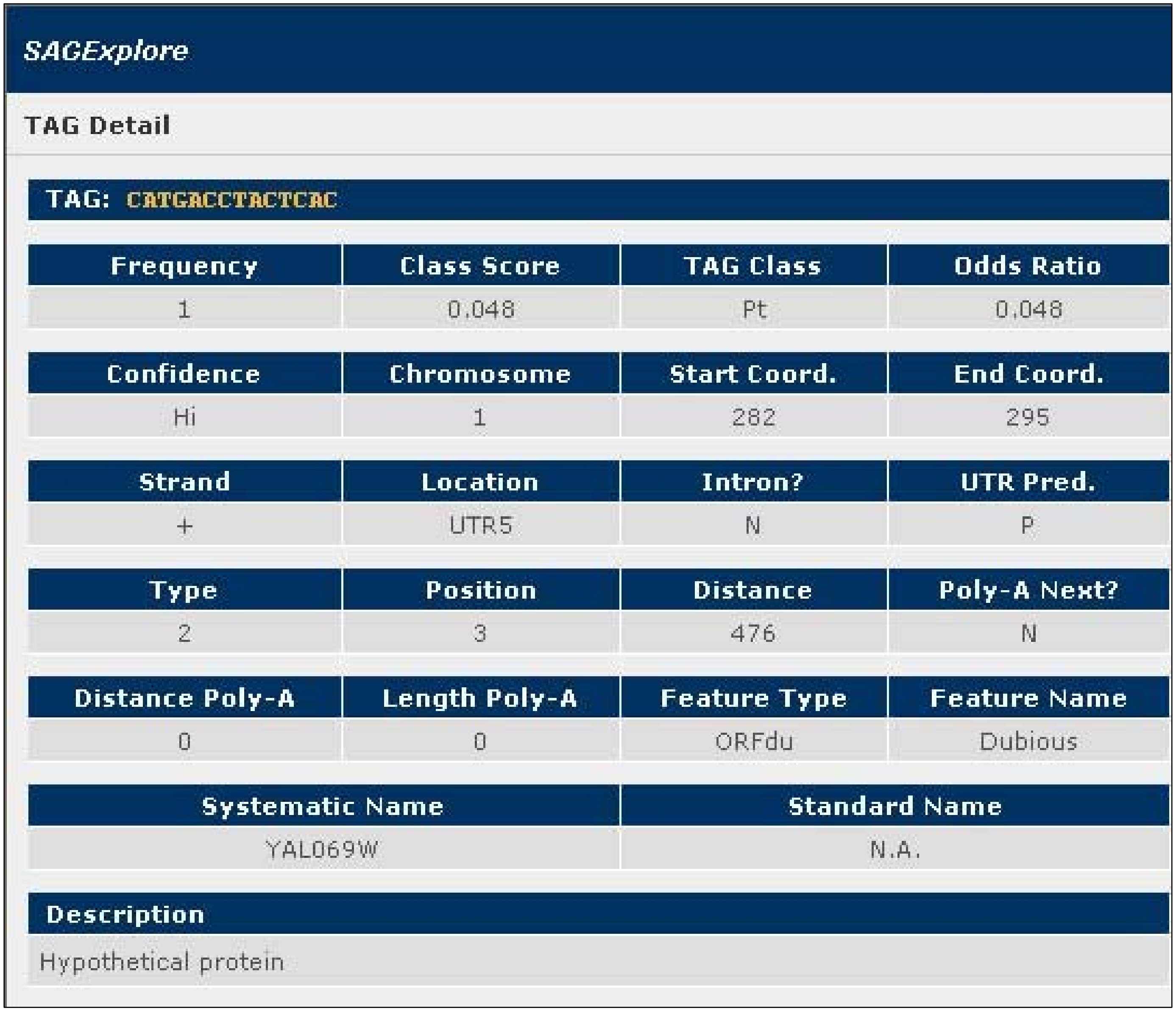
This section allows to find TAGs within a Genome.

Show 50

There are **1,657** records that matched the query. **349 NIDs** out of **1,622** submitted TAGs were found.

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	BI	Cn	Info
1	Un	CATGGTCAACAAAG	**2**	0.807	Si	Int	int,opORF	0	1	43989	+	N.A.	**YAL054C**	☰	ℹ	AT CG	▥	3 4 0	-
2	Un	CATGACACCACCAG	**3**	1.000	Fe	Int	int,opORF	0	1	140213	+	N.A.	**YAL005C**	☰	ℹ	AT CG	▥	3 0 10	-
3	Un	CATGGAGGAGATTT	**2**	1.239	Au	ORF	ORFdu	2	1	141074	+	N.A.	**YAL004W**	☰	ℹ	AT CG	▥	0 0 6	-
4	Un	CATGGCGCAGTTGG	**5**	1.000	Al	ORF	tRNA	1	1	166273	+	N.A.	**tA(UGC)A**	☰	ℹ	AT CG	▥	3 4 0	-
5	Un	CATGCTGCATCCTA	**4**	1.000	Fe	Int	int,opORF	0	1	217023	+	N.A.	**YAR060C**	☰	ℹ	AT CG	▥	0 0 6	-
6	Un	CATGCAAAAGACTG	**4**	1.000	Al	ORF	ORFdu	1	1	229005	+	N.A.	**YAR075W**	☰	ℹ	AT CG	▥	12 0 13	-
7	Un	CATGCACTTCAACT	**20**	1.000	Fe	Int	int	0	2	34908	+	N.A.	---	☰	ℹ	AT CG	▥	12 8 3	-
8	Un	CATGTACACACACA	**2**	1.239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	**YBL054W**	☰	ℹ	AT CG	▥	3 4 0	-
9	Un	CATGGTATATGTGT	**2**	1.000	Fe	Int	int	0	2	236361	+	N.A.	---	☰	ℹ	AT CG	▥	6 0 3	-
10	Un	CATGGTACAAGGGT	**2**	0.343	Al	ORF	ORFv	3	2	478284	+	**TEF2**	**YBR118W**	☰	ℹ	AT CG	▥	0 4 6	-
11	Un	CATGAGACAAACTG	**2**	0.402	Al	ORF	ORFv	2	2	478942	+	**TEF2**	**YBR118W**	☰	ℹ	AT CG	▥	61 55 193	-
12	Un	CATGGAAATCCGGT	**2**	0.807	Si	Int	int,opORF	0	2	576616	+	N.A.	**YBR170C**	☰	ℹ	AT CG	▥	3 0 3	-
13	Un	CATGTAAAAAAAAA	**2**	1.000	Fe	Int	int	0	2	622839	+	N.A.	---	☰	ℹ	AT CG	▥	6 4 0	-
14	Un	CATGGCGTTTGAGG	**2**	1.000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	**YBR206W**	☰	ℹ	AT CG	▥	6 0 0	-
15	Un	CATGCTCTGGTTCT	**2**	2.667	Al	ORF	ORFdu	3	2	704693	+	N.A.	**YBR242W**	☰	ℹ	AT CG	▥	3 4 0	-
16	Un	CATGCGTCAGTGTG	**9**	0.807	Si	Int	int	0	2	812205	+	N.A.	---	☰	ℹ	AT CG	▥	9 17 0	-
17	Un	CATGCACTTCAACT	**20**	1.000	Fe	Int	int	0	3	90077	+	N.A.	---	☰	ℹ	AT CG	▥	12 8 3	-
18	Un	CATGTCTTCTCGTT	**2**	1.000	Al	ORF	ORFv	1	4	45892	+	**SSB1**	**YDL229W**	☰	ℹ	AT CG	▥	6 12 0	-
19	Un	CATGTACATACATC	**2**	1.000	Al	UTR3	ORFv	1	4	99277	+	**MRPL11**	**YDL202W**	☰	ℹ	AT CG	▥	6 17 0	-
20	Un	CATGATATCAAAAA	**2**	0.375	Al	ORF	ORFv	7	4	179499	+	**MSH5**	**YDL154W**	☰	ℹ	AT CG	▥	6 17 0	-

Query Results: A record with several tag details can be obtained by clicking on this field.



SAGExplore

TAG Detail

TAG: CATGACCTACTCAC

Frequency	Class Score	TAG Class	Odds Ratio
1	0.048	Pt	0.048

Confidence	Chromosome	Start Coord.	End Coord.
Hi	1	282	295

Strand	Location	Intron?	UTR Pred.
+	UTR5	N	P

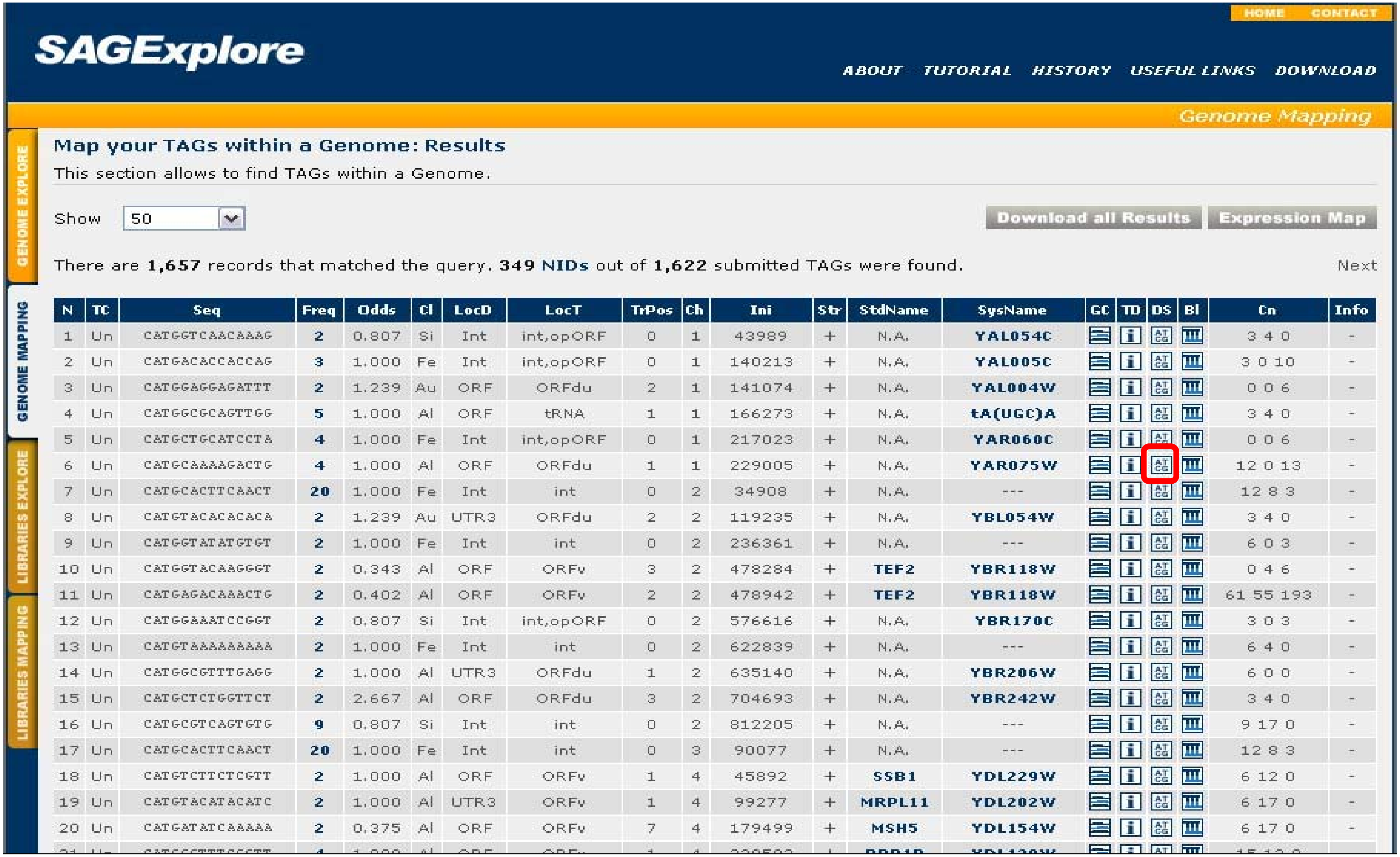
Type	Position	Distance	Poly-A Next?
2	3	476	N

Distance Poly-A	Length Poly-A	Feature Type	Feature Name
0	0	ORFdu	Dubious

Systematic Name	Standard Name
YAL069W	N.A.

Description
Hypothetical protein

Tag details: Many details about the tag are provided here. See the online help for an explanation of each field meaning.



Map your TAGs within a Genome: Results

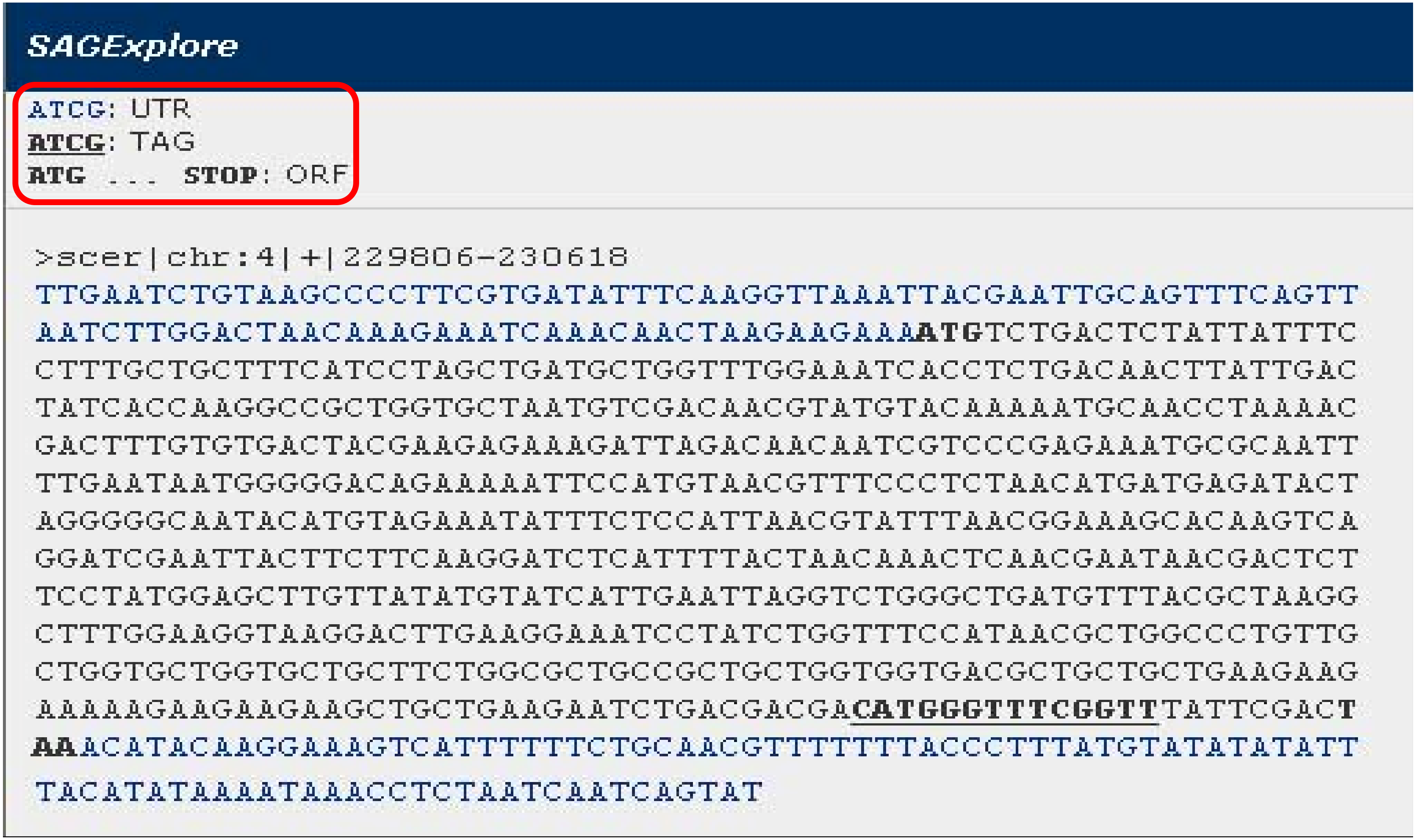
This section allows to find TAGs within a Genome.

Show 50

There are **1,657** records that matched the query. **349 NIDs** out of **1,622** submitted TAGs were found.

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	BI	Cn	Info
1	Un	CATGGTCAACAAAG	**2**	0.807	Si	Int	int,opORF	0	1	43989	+	N.A.	**YAL054C**	☰	ℹ	ATCG	▥	3 4 0	-
2	Un	CATGACACCACCAG	**3**	1.000	Fe	Int	int,opORF	0	1	140213	+	N.A.	**YAL005C**	☰	ℹ	ATCG	▥	3 0 10	-
3	Un	CATGGAGGAGATTT	**2**	1.239	Au	ORF	ORFdu	2	1	141074	+	N.A.	**YAL004W**	☰	ℹ	ATCG	▥	0 0 6	-
4	Un	CATGGCGCAGTTGG	**5**	1.000	Al	ORF	tRNA	1	1	166273	+	N.A.	**tA(UGC)A**	☰	ℹ	ATCG	▥	3 4 0	-
5	Un	CATGCTGCATCCTA	**4**	1.000	Fe	Int	int,opORF	0	1	217023	+	N.A.	**YAR060C**	☰	ℹ	ATCG	▥	0 0 6	-
6	Un	CATGCAAAAGACTG	**4**	1.000	Al	ORF	ORFdu	1	1	229005	+	N.A.	**YAR075W**	☰	ℹ	ATCG	▥	12 0 13	-
7	Un	CATGCACTTCAACT	**20**	1.000	Fe	Int	int	0	2	34908	+	N.A.	---	☰	ℹ	ATCG	▥	12 8 3	-
8	Un	CATGTACACACACA	**2**	1.239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	**YBL054W**	☰	ℹ	ATCG	▥	3 4 0	-
9	Un	CATGGTATATGTGT	**2**	1.000	Fe	Int	int	0	2	236361	+	N.A.	---	☰	ℹ	ATCG	▥	6 0 3	-
10	Un	CATGGTACAAGGGT	**2**	0.343	Al	ORF	ORFv	3	2	478284	+	**TEF2**	**YBR118W**	☰	ℹ	ATCG	▥	0 4 6	-
11	Un	CATGAGACAAACTG	**2**	0.402	Al	ORF	ORFv	2	2	478942	+	**TEF2**	**YBR118W**	☰	ℹ	ATCG	▥	61 55 193	-
12	Un	CATGGAAATCCGGT	**2**	0.807	Si	Int	int,opORF	0	2	576616	+	N.A.	**YBR170C**	☰	ℹ	ATCG	▥	3 0 3	-
13	Un	CATGTAAAAAAAAA	**2**	1.000	Fe	Int	int	0	2	622839	+	N.A.	---	☰	ℹ	ATCG	▥	6 4 0	-
14	Un	CATGGCGTTTGAGG	**2**	1.000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	**YBR206W**	☰	ℹ	ATCG	▥	6 0 0	-
15	Un	CATGCTCTGGTTCT	**2**	2.667	Al	ORF	ORFdu	3	2	704693	+	N.A.	**YBR242W**	☰	ℹ	ATCG	▥	3 4 0	-
16	Un	CATGCGTCAGTGTG	**9**	0.807	Si	Int	int	0	2	812205	+	N.A.	---	☰	ℹ	ATCG	▥	9 17 0	-
17	Un	CATGCACTTCAACT	**20**	1.000	Fe	Int	int	0	3	90077	+	N.A.	---	☰	ℹ	ATCG	▥	12 8 3	-
18	Un	CATGTCTTCTCGTT	**2**	1.000	Al	ORF	ORFv	1	4	45892	+	**SSB1**	**YDL229W**	☰	ℹ	ATCG	▥	6 12 0	-
19	Un	CATGTACATACATC	**2**	1.000	Al	UTR3	ORFv	1	4	99277	+	**MRPL11**	**YDL202W**	☰	ℹ	ATCG	▥	6 17 0	-
20	Un	CATGATATCAAAAA	**2**	0.375	Al	ORF	ORFv	7	4	179499	+	**MSH5**	**YDL154W**	☰	ℹ	ATCG	▥	6 17 0	-

Query Results: The genomic sequence context where the tag matches can be downloaded by clicking on this field.



ATCG: UTR

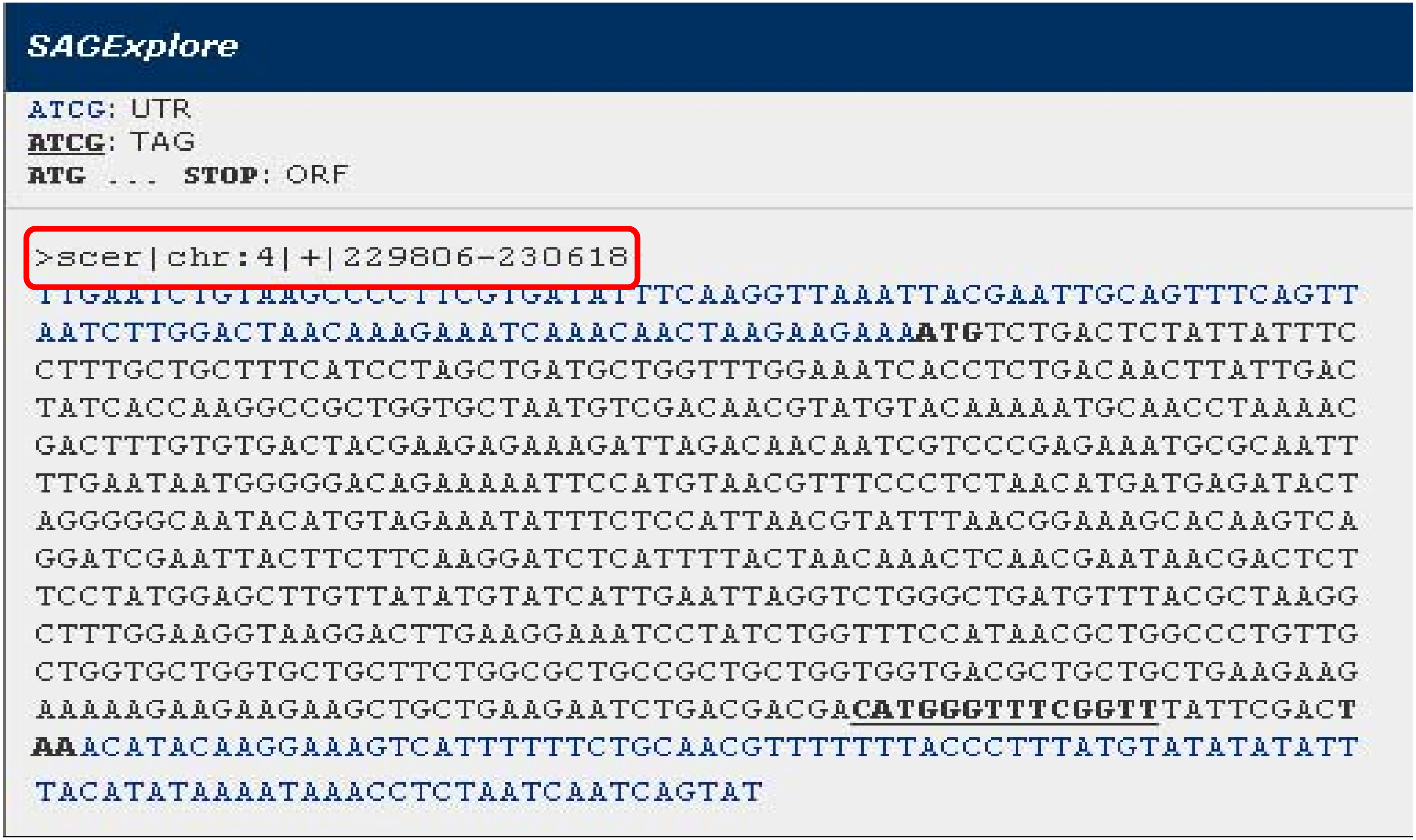
ATCG: TAG

ATG ... **STOP**: ORF

\>scer|chr:4|+|229806-230618

TTGAATCTGTAAGCCCCTTCGTGATATTTCAAGGTTAAATTACGAATTGCAGTTTCAGTT
AATCTTGGACTAACAAAGAAATCAAACAACTAAGAAGAAA**ATG**TCTGACTCTATTATTTC
CTTTGCTGCTTTCATCCTAGCTGATGCTGGTTTGGAAATCACCTCTGACAACTTATTGAC
TATCACCAAGGCCGCTGGTGCTAATGTCGACAACGTATGTACAAAAATGCAACCTAAAAC
GACTTTGTGTGACTACGAAGAGAAAGATTAGACAACAATCGTCCCGAGAAATGCGCAATT
TTGAATAATGGGGGACAGAAAAATTCCATGTAACGTTTCCCTCTAACATGATGAGATACT
AGGGGGCAATACATGTAGAAATATTTCTCCATTAACGTATTTAACGGAAAGCACAAGTCA
GGATCGAATTACTTCTTCAAGGATCTCATTTTACTAACAAACTCAACGAATAACGACTCT
TCCTATGGAGCTTGTTATATGTATCATTGAATTAGGTCTGGGCTGATGTTTACGCTAAGG
CTTTGGAAGGTAAGGACTTGAAGGAAATCCTATCTGGTTTCCATAACGCTGGCCCTGTTG
CTGGTGCTGGTGCTGCTTCTGGCGCTGCCGCTGCTGGTGGTGACGCTGCTGCTGAAGAAG
AAAAAGAAGAAGAAGCTGCTGAAGAATCTGACGACGA**CATGGGTTTCGGTT**TATTCGAC**T**
AAACATACAAGGAAAGTCATTTTTTCTGCAACGTTTTTTTACCCTTTATGTATATATATT
TACATATAAAATAAACCTCTAATCAATCAGTAT

Download Sequence: If the tag matches an ORF (as it is in this example), the transcript sequence is given. The 5' and 3' UTRs, the start and stop codons, and the tag sequence are all highlighted. If the tag matches an intergenic region, the 500 flanking nucleotides upstream and downstrem the tag are provided. In this case, neighbor elements such as UTRs from other genes are also highlighted if present.

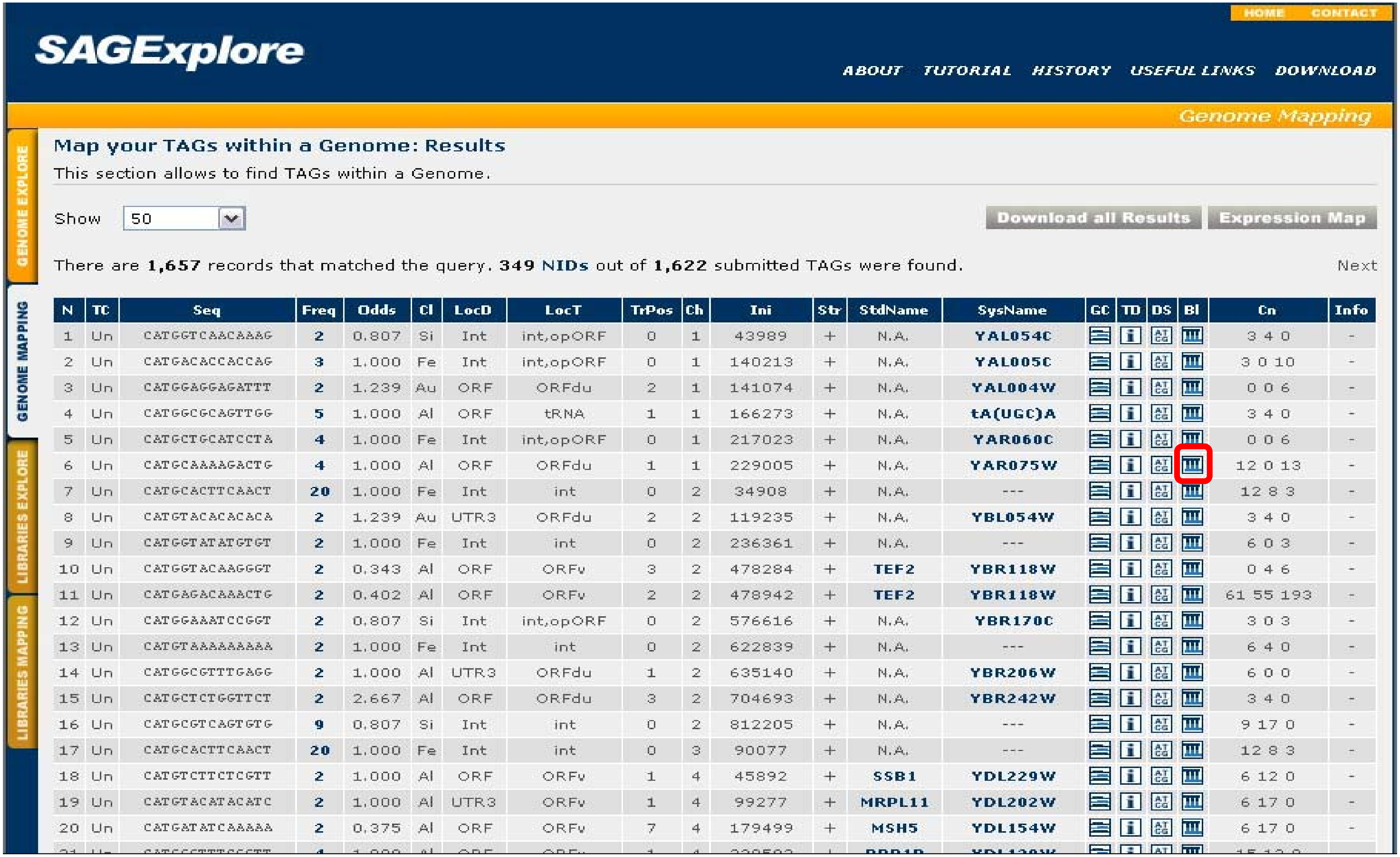


SAGExplore

ATCG: UTR
ATCG: TAG
ATG ... **STOP**: ORF

>scer|chr:4|+|229806-230618
TTGAATCTGTAAGCCCCTTCGTGATATTTCAAGGTTAAATTACGAATTGCAGTTTCAGTT
AATCTTGGACTAACAAAGAAATCAAACAACTAAGAAGAAA**ATG**TCTGACTCTATTATTTC
CTTTGCTGCTTTCATCCTAGCTGATGCTGGTTTGGAAATCACCTCTGACAACTTATTGAC
TATCACCAAGGCCGCTGGTGCTAATGTCGACAACGTATGTACAAAAATGCAACCTAAAAC
GACTTTGTGTGACTACGAAGAGAAAGATTAGACAACAATCGTCCCGAGAAATGCGCAATT
TTGAATAATGGGGGACAGAAAAATTCCATGTAACGTTTCCCTCTAACATGATGAGATACT
AGGGGGCAATACATGTAGAAATATTTCTCCATTAACGTATTTAACGGAAAGCACAAGTCA
GGATCGAATTACTTCTTCAAGGATCTCATTTTACTAACAAACTCAACGAATAACGACTCT
TCCTATGGAGCTTGTTATATGTATCATTGAATTAGGTCTGGGCTGATGTTTACGCTAAGG
CTTTGGAAGGTAAGGACTTGAAGGAAATCCTATCTGGTTTCCATAACGCTGGCCCTGTTG
CTGGTGCTGGTGCTGCTTCTGGCGCTGCCGCTGCTGGTGGTGACGCTGCTGCTGAAGAAG
AAAAAGAAGAAGAAGCTGCTGAAGAATCTGACGACGA**CATGGGTTTCGGTT**TATTCGAC**T**
AAACATACAAGGAAAGTCATTTTTTCTGCAACGTTTTTTTACCCTTTATGTATATATATT
TACATATAAAATAAACCTCTAATCAATCAGTAT

Download Sequence: The FASTA header indicates the exact region of the sequence displayed.



Map your TAGs within a Genome: Results

This section allows to find TAGs within a Genome.

Show 50

There are **1,657** records that matched the query. **349 NIDs** out of **1,622** submitted TAGs were found.

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	Bl	Cn	Info
1	Un	CATGGTCAACAAAG	**2**	0.807	Si	Int	int,opORF	0	1	43989	+	N.A.	**YAL054C**	☰	ℹ	AT CG	▥	3 4 0	-
2	Un	CATGACACCACCAG	**3**	1.000	Fe	Int	int,opORF	0	1	140213	+	N.A.	**YAL005C**	☰	ℹ	AT CG	▥	3 0 10	-
3	Un	CATGGAGGAGATTT	**2**	1.239	Au	ORF	ORFdu	2	1	141074	+	N.A.	**YAL004W**	☰	ℹ	AT CG	▥	0 0 6	-
4	Un	CATGGCGCAGTTGG	**5**	1.000	Al	ORF	tRNA	1	1	166273	+	N.A.	**tA(UGC)A**	☰	ℹ	AT CG	▥	3 4 0	-
5	Un	CATGCTGCATCCTA	**4**	1.000	Fe	Int	int,opORF	0	1	217023	+	N.A.	**YAR060C**	☰	ℹ	AT CG	▥	0 0 6	-
6	Un	CATGCAAAAGACTG	**4**	1.000	Al	ORF	ORFdu	1	1	229005	+	N.A.	**YAR075W**	☰	ℹ	AT CG	▥	12 0 13	-
7	Un	CATGCACTTCAACT	**20**	1.000	Fe	Int	int	0	2	34908	+	N.A.	---	☰	ℹ	AT CG	▥	12 8 3	-
8	Un	CATGTACACACACA	**2**	1.239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	**YBL054W**	☰	ℹ	AT CG	▥	3 4 0	-
9	Un	CATGGTATATGTGT	**2**	1.000	Fe	Int	int	0	2	236361	+	N.A.	---	☰	ℹ	AT CG	▥	6 0 3	-
10	Un	CATGGTACAAGGGT	**2**	0.343	Al	ORF	ORFv	3	2	478284	+	**TEF2**	**YBR118W**	☰	ℹ	AT CG	▥	0 4 6	-
11	Un	CATGAGACAAACTG	**2**	0.402	Al	ORF	ORFv	2	2	478942	+	**TEF2**	**YBR118W**	☰	ℹ	AT CG	▥	61 55 193	-
12	Un	CATGGAAATCCGGT	**2**	0.807	Si	Int	int,opORF	0	2	576616	+	N.A.	**YBR170C**	☰	ℹ	AT CG	▥	3 0 3	-
13	Un	CATGTAAAAAAAAA	**2**	1.000	Fe	Int	int	0	2	622839	+	N.A.	---	☰	ℹ	AT CG	▥	6 4 0	-
14	Un	CATGGCGTTTGAGG	**2**	1.000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	**YBR206W**	☰	ℹ	AT CG	▥	6 0 0	-
15	Un	CATGCTCTGGTTCT	**2**	2.667	Al	ORF	ORFdu	3	2	704693	+	N.A.	**YBR242W**	☰	ℹ	AT CG	▥	3 4 0	-
16	Un	CATGCGTCAGTGTG	**9**	0.807	Si	Int	int	0	2	812205	+	N.A.	---	☰	ℹ	AT CG	▥	9 17 0	-
17	Un	CATGCACTTCAACT	**20**	1.000	Fe	Int	int	0	3	90077	+	N.A.	---	☰	ℹ	AT CG	▥	12 8 3	-
18	Un	CATGTCTTCTCGTT	**2**	1.000	Al	ORF	ORFv	1	4	45892	+	**SSB1**	**YDL229W**	☰	ℹ	AT CG	▥	6 12 0	-
19	Un	CATGTACATACATC	**2**	1.000	Al	UTR3	ORFv	1	4	99277	+	**MRPL11**	**YDL202W**	☰	ℹ	AT CG	▥	6 17 0	-
20	Un	CATGATATCAAAAA	**2**	0.375	Al	ORF	ORFv	7	4	179499	+	**MSH5**	**YDL154W**	☰	ℹ	AT CG	▥	6 17 0	-

Query Results: A query to the BLAST server at the NCBI is launched with the previosuly described sequence by clicking on this field. In the case of tags matching an intergenic region, this option is very useful to aid the process of gene discovery.

Search

```
TCACCAGTGTTAGGGTCAAGAACAACTGCATCAATACCGAAGAAGGGGAATGAGGCAGA
ACCCGGTTTCATTGGTGTAACACCACCAGCCAGCGGGGTGACCAGATGCGAACCAGATT
CTGTTTGCCAGTAGGTGTCTACAATGGGGATTTCATTTTTACCTATTTTTTCAGAGTAC
CACTCCCAAACTTCAGCAGCAATTGGCTCACCGACCGAACCCAAGCAACGCAAAGATTT
TAAGGAATGATTTTCGATGTAGGAATCACCAGCTCTTTTCAACAAACGCAAAGCAGTTG
```

Choose a translation: TRANSLATED query - PROTEIN database [blastx]

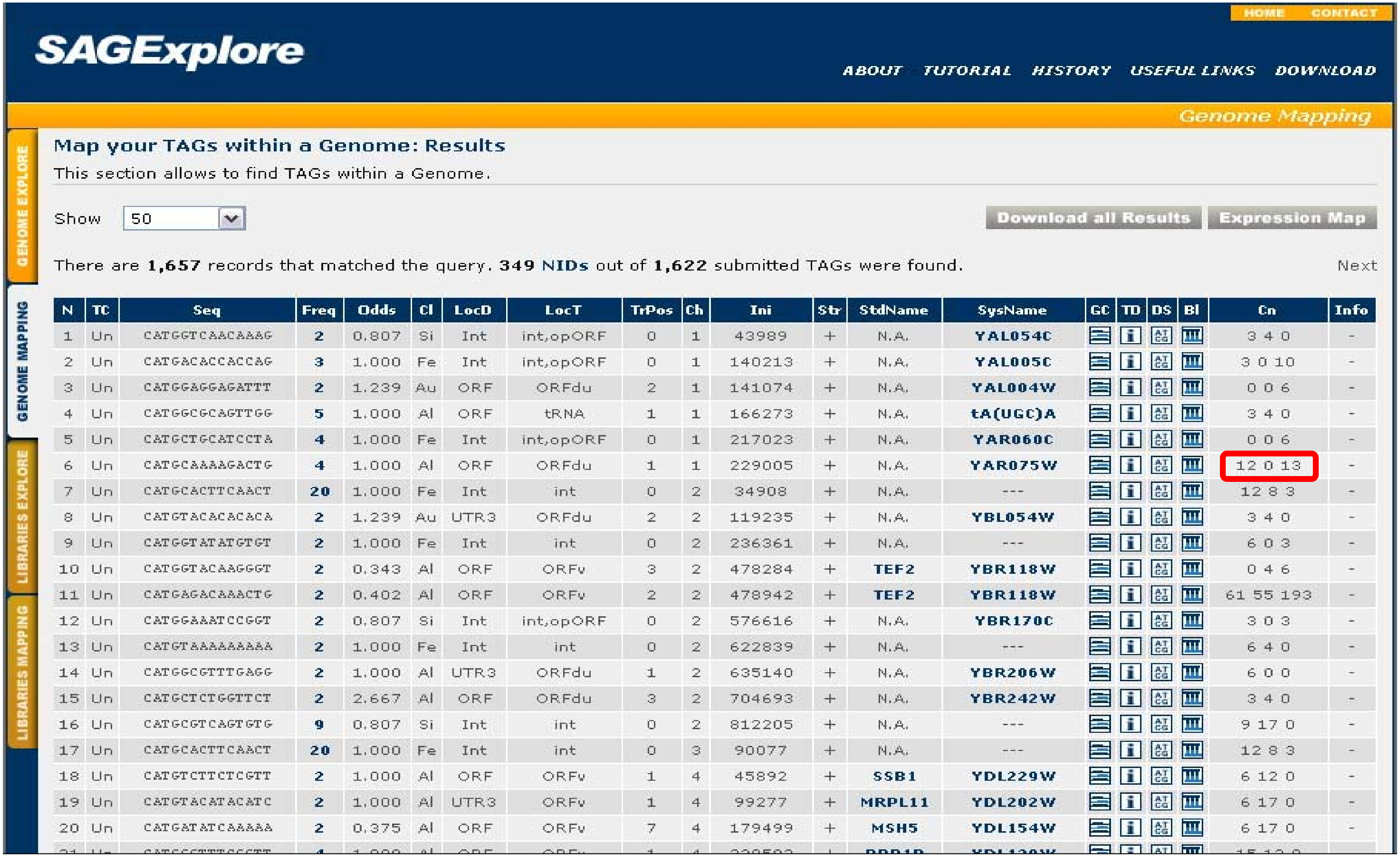
Set subsequence From: To:

Choose database: nr

Genetic codes: Standard (1)

Now:

BLAST Query: A query to the BLAST server at the NCBI is automatically launched with the flanking sequence that contains the tag. In the case of intergenic tags, BLASTX is launched (this example). In the case of tags matching an ORF, BLASTP is used.



Map your TAGs within a Genome: Results

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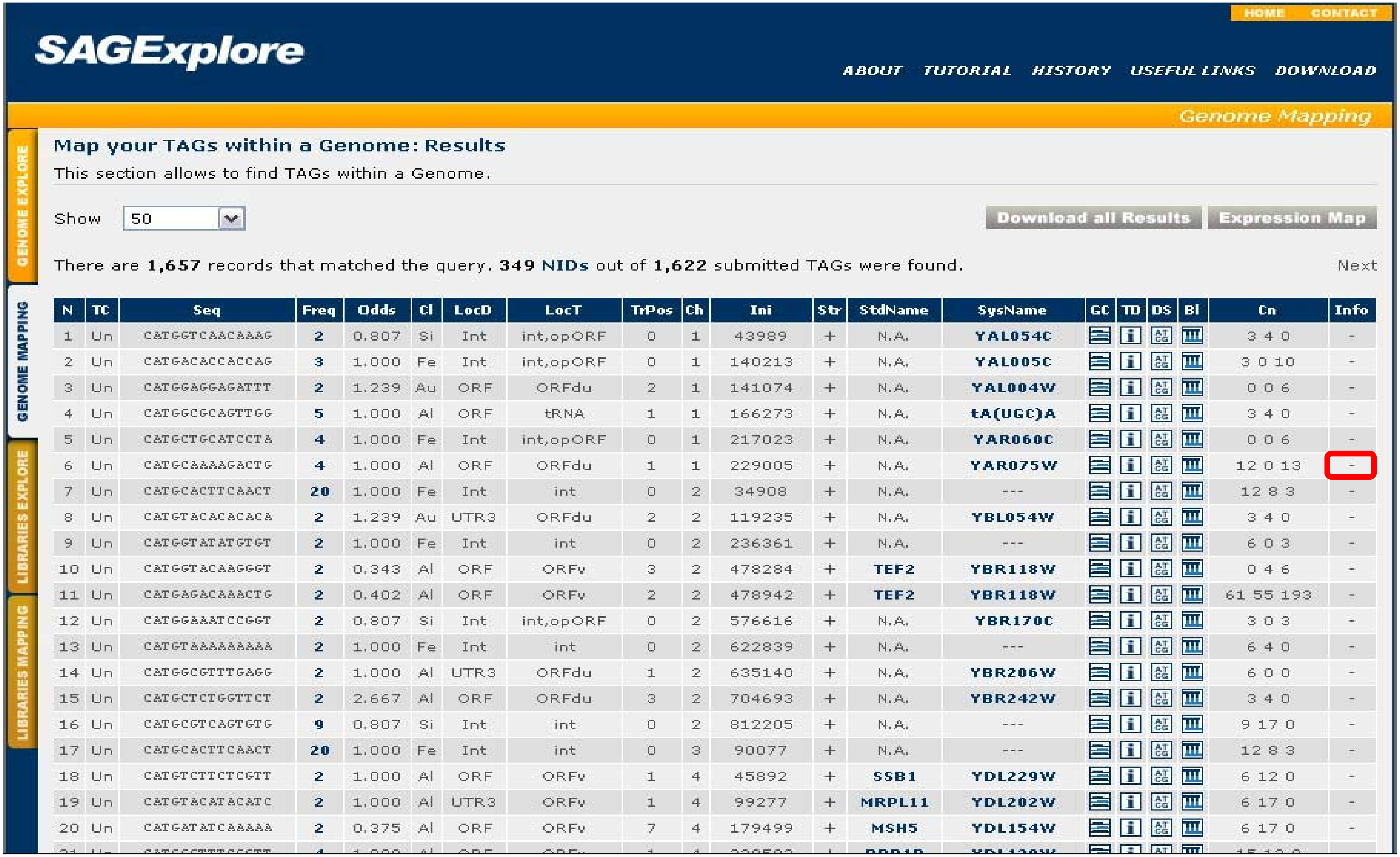
Show 50

There are **1,657** records that matched the query. **349 NIDs** out of **1,622** submitted TAGs were found.

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	BI	Cn	Info
1	Un	CATGGTCAACAAAG	**2**	0.807	Si	Int	int,opORF	0	1	43989	+	N.A.	**YAL054C**	☰	ℹ	AT CG	▥	3 4 0	-
2	Un	CATGACACCACCAG	**3**	1.000	Fe	Int	int,opORF	0	1	140213	+	N.A.	**YAL005C**	☰	ℹ	AT CG	▥	3 0 10	-
3	Un	CATGGAGGAGATTT	**2**	1.239	Au	ORF	ORFdu	2	1	141074	+	N.A.	**YAL004W**	☰	ℹ	AT CG	▥	0 0 6	-
4	Un	CATGGCGCAGTTGG	**5**	1.000	Al	ORF	tRNA	1	1	166273	+	N.A.	**tA(UGC)A**	☰	ℹ	AT CG	▥	3 4 0	-
5	Un	CATGCTGCATCCTA	**4**	1.000	Fe	Int	int,opORF	0	1	217023	+	N.A.	**YAR060C**	☰	ℹ	AT CG	▥	0 0 6	-
6	Un	CATGCAAAAGACTG	**4**	1.000	Al	ORF	ORFdu	1	1	229005	+	N.A.	**YAR075W**	☰	ℹ	AT CG	▥	12 0 13	-
7	Un	CATGCACTTCAACT	**20**	1.000	Fe	Int	int	0	2	34908	+	N.A.	---	☰	ℹ	AT CG	▥	12 8 3	-
8	Un	CATGTACACACACA	**2**	1.239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	**YBL054W**	☰	ℹ	AT CG	▥	3 4 0	-
9	Un	CATGGTATATGTGT	**2**	1.000	Fe	Int	int	0	2	236361	+	N.A.	---	☰	ℹ	AT CG	▥	6 0 3	-
10	Un	CATGGTACAAGGGT	**2**	0.343	Al	ORF	ORFv	3	2	478284	+	**TEF2**	**YBR118W**	☰	ℹ	AT CG	▥	0 4 6	-
11	Un	CATGAGACAAACTG	**2**	0.402	Al	ORF	ORFv	2	2	478942	+	**TEF2**	**YBR118W**	☰	ℹ	AT CG	▥	61 55 193	-
12	Un	CATGGAAATCCGGT	**2**	0.807	Si	Int	int,opORF	0	2	576616	+	N.A.	**YBR170C**	☰	ℹ	AT CG	▥	3 0 3	-
13	Un	CATGTAAAAAAAAA	**2**	1.000	Fe	Int	int	0	2	622839	+	N.A.	---	☰	ℹ	AT CG	▥	6 4 0	-
14	Un	CATGGCGTTTGAGG	**2**	1.000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	**YBR206W**	☰	ℹ	AT CG	▥	6 0 0	-
15	Un	CATGCTCTGGTTCT	**2**	2.667	Al	ORF	ORFdu	3	2	704693	+	N.A.	**YBR242W**	☰	ℹ	AT CG	▥	3 4 0	-
16	Un	CATGCGTCAGTGTG	**9**	0.807	Si	Int	int	0	2	812205	+	N.A.	---	☰	ℹ	AT CG	▥	9 17 0	-
17	Un	CATGCACTTCAACT	**20**	1.000	Fe	Int	int	0	3	90077	+	N.A.	---	☰	ℹ	AT CG	▥	12 8 3	-
18	Un	CATGTCTTCTCGTT	**2**	1.000	Al	ORF	ORFv	1	4	45892	+	**SSB1**	**YDL229W**	☰	ℹ	AT CG	▥	6 12 0	-
19	Un	CATGTACATACATC	**2**	1.000	Al	UTR3	ORFv	1	4	99277	+	**MRPL11**	**YDL202W**	☰	ℹ	AT CG	▥	6 17 0	-
20	Un	CATGATATCAAAAA	**2**	0.375	Al	ORF	ORFv	7	4	179499	+	**MSH5**	**YDL154W**	☰	ℹ	AT CG	▥	6 17 0	-

Query Results: The tag counts provided by the user are shown here (in case the user provided this information). In this case, the counts of three independent experiments were provided and shown.



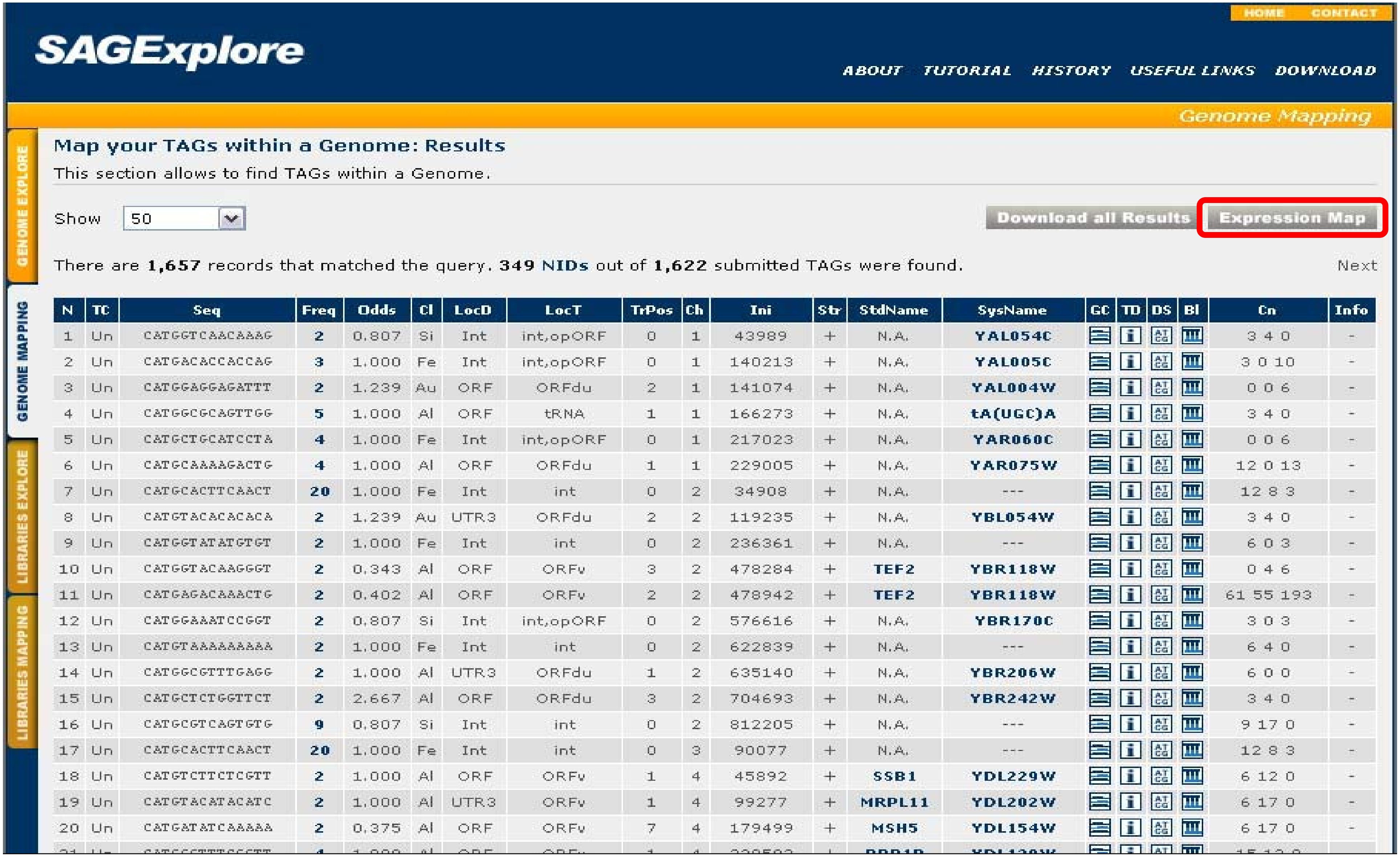
Map your TAGs within a Genome: Results

This section allows to find TAGs within a Genome.

There are **1,657** records that matched the query. **349 NIDs** out of **1,622** submitted TAGs were found.

N	TC	Seq	Freq	Odds	Cl	LocD	LocT	TrPos	Ch	Ini	Str	StdName	SysName	GC	TD	DS	BI	Cn	Info
1	Un	CATGGTCAACAAAG	2	0.807	Si	Int	int,opORF	0	1	43989	+	N.A.	YAL054C	☰	ℹ	▦	▥	3 4 0	-
2	Un	CATGACACCACCAG	3	1.000	Fe	Int	int,opORF	0	1	140213	+	N.A.	YAL005C	☰	ℹ	▦	▥	3 0 10	-
3	Un	CATGGAGGAGATTT	2	1.239	Au	ORF	ORFdu	2	1	141074	+	N.A.	YAL004W	☰	ℹ	▦	▥	0 0 6	-
4	Un	CATGGCGCAGTTGG	5	1.000	Al	ORF	tRNA	1	1	166273	+	N.A.	tA(UGC)A	☰	ℹ	▦	▥	3 4 0	-
5	Un	CATGCTGCATCCTA	4	1.000	Fe	Int	int,opORF	0	1	217023	+	N.A.	YAR060C	☰	ℹ	▦	▥	0 0 6	-
6	Un	CATGCAAAAGACTG	4	1.000	Al	ORF	ORFdu	1	1	229005	+	N.A.	YAR075W	☰	ℹ	▦	▥	12 0 13	-
7	Un	CATGCACTTCAACT	20	1.000	Fe	Int	int	0	2	34908	+	N.A.	---	☰	ℹ	▦	▥	12 8 3	-
8	Un	CATGTACACACACA	2	1.239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	YBL054W	☰	ℹ	▦	▥	3 4 0	-
9	Un	CATGGTATATGTGT	2	1.000	Fe	Int	int	0	2	236361	+	N.A.	---	☰	ℹ	▦	▥	6 0 3	-
10	Un	CATGGTACAAGGGT	2	0.343	Al	ORF	ORFv	3	2	478284	+	TEF2	YBR118W	☰	ℹ	▦	▥	0 4 6	-
11	Un	CATGAGACAAACTG	2	0.402	Al	ORF	ORFv	2	2	478942	+	TEF2	YBR118W	☰	ℹ	▦	▥	61 55 193	-
12	Un	CATGGAAATCCGGT	2	0.807	Si	Int	int,opORF	0	2	576616	+	N.A.	YBR170C	☰	ℹ	▦	▥	3 0 3	-
13	Un	CATGTAAAAAAAAA	2	1.000	Fe	Int	int	0	2	622839	+	N.A.	---	☰	ℹ	▦	▥	6 4 0	-
14	Un	CATGGCGTTTGAGG	2	1.000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	YBR206W	☰	ℹ	▦	▥	6 0 0	-
15	Un	CATGCTCTGGTTCT	2	2.667	Al	ORF	ORFdu	3	2	704693	+	N.A.	YBR242W	☰	ℹ	▦	▥	3 4 0	-
16	Un	CATGCGTCAGTGTG	9	0.807	Si	Int	int	0	2	812205	+	N.A.	---	☰	ℹ	▦	▥	9 17 0	-
17	Un	CATGCACTTCAACT	20	1.000	Fe	Int	int	0	3	90077	+	N.A.	---	☰	ℹ	▦	▥	12 8 3	-
18	Un	CATGTCTTCTCGTT	2	1.000	Al	ORF	ORFv	1	4	45892	+	SSB1	YDL229W	☰	ℹ	▦	▥	6 12 0	-
19	Un	CATGTACATACATC	2	1.000	Al	UTR3	ORFv	1	4	99277	+	MRPL11	YDL202W	☰	ℹ	▦	▥	6 17 0	-
20	Un	CATGATATCAAAAA	2	0.375	Al	ORF	ORFv	7	4	179499	+	MSH5	YDL154W	☰	ℹ	▦	▥	6 17 0	-

Query Results: Each tag can have a label (if the user provided it), which is displayed in this field. This could be useful to highlight some specific tags of interest, or for example, to see the cluster group number of each tag. The user can provide any label here. This field is optional and can be empty (as it is this example case).



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1	Un	CATGGTCAACAAAG	**2**	0.807	Si	Int	int,opORF	0	1	43989	+	N.A.	**YAL054C**	☰	ℹ	ATCG	▥	3 4 0	-
2	Un	CATGACACCACCAG	**3**	1.000	Fe	Int	int,opORF	0	1	140213	+	N.A.	**YAL005C**	☰	ℹ	ATCG	▥	3 0 10	-
3	Un	CATGGAGGAGATTT	**2**	1.239	Au	ORF	ORFdu	2	1	141074	+	N.A.	**YAL004W**	☰	ℹ	ATCG	▥	0 0 6	-
4	Un	CATGGCGCAGTTGG	**5**	1.000	Al	ORF	tRNA	1	1	166273	+	N.A.	**tA(UGC)A**	☰	ℹ	ATCG	▥	3 4 0	-
5	Un	CATGCTGCATCCTA	**4**	1.000	Fe	Int	int,opORF	0	1	217023	+	N.A.	**YAR060C**	☰	ℹ	ATCG	▥	0 0 6	-
6	Un	CATGCAAAAGACTG	**4**	1.000	Al	ORF	ORFdu	1	1	229005	+	N.A.	**YAR075W**	☰	ℹ	ATCG	▥	12 0 13	-
7	Un	CATGCACTTCAACT	**20**	1.000	Fe	Int	int	0	2	34908	+	N.A.	---	☰	ℹ	ATCG	▥	12 8 3	-
8	Un	CATGTACACACACA	**2**	1.239	Au	UTR3	ORFdu	2	2	119235	+	N.A.	**YBL054W**	☰	ℹ	ATCG	▥	3 4 0	-
9	Un	CATGGTATATGTGT	**2**	1.000	Fe	Int	int	0	2	236361	+	N.A.	---	☰	ℹ	ATCG	▥	6 0 3	-
10	Un	CATGGTACAAGGGT	**2**	0.343	Al	ORF	ORFv	3	2	478284	+	**TEF2**	**YBR118W**	☰	ℹ	ATCG	▥	0 4 6	-
11	Un	CATGAGACAAACTG	**2**	0.402	Al	ORF	ORFv	2	2	478942	+	**TEF2**	**YBR118W**	☰	ℹ	ATCG	▥	61 55 193	-
12	Un	CATGGAAATCCGGT	**2**	0.807	Si	Int	int,opORF	0	2	576616	+	N.A.	**YBR170C**	☰	ℹ	ATCG	▥	3 0 3	-
13	Un	CATGTAAAAAAAAA	**2**	1.000	Fe	Int	int	0	2	622839	+	N.A.	---	☰	ℹ	ATCG	▥	6 4 0	-
14	Un	CATGGCGTTTGAGG	**2**	1.000	Al	UTR3	ORFdu	1	2	635140	+	N.A.	**YBR206W**	☰	ℹ	ATCG	▥	6 0 0	-
15	Un	CATGCTCTGGTTCT	**2**	2.667	Al	ORF	ORFdu	3	2	704693	+	N.A.	**YBR242W**	☰	ℹ	ATCG	▥	3 4 0	-
16	Un	CATGCGTCAGTGTG	**9**	0.807	Si	Int	int	0	2	812205	+	N.A.	---	☰	ℹ	ATCG	▥	9 17 0	-
17	Un	CATGCACTTCAACT	**20**	1.000	Fe	Int	int	0	3	90077	+	N.A.	---	☰	ℹ	ATCG	▥	12 8 3	-
18	Un	CATGTCTTCTCGTT	**2**	1.000	Al	ORF	ORFv	1	4	45892	+	**SSB1**	**YDL229W**	☰	ℹ	ATCG	▥	6 12 0	-
19	Un	CATGTACATACATC	**2**	1.000	Al	UTR3	ORFv	1	4	99277	+	**MRPL11**	**YDL202W**	☰	ℹ	ATCG	▥	6 17 0	-
20	Un	CATGATATCAAAAA	**2**	0.375	Al	ORF	ORFv	7	4	179499	+	**MSH5**	**YDL154W**	☰	ℹ	ATCG	▥	6 17 0	-

Query Results: An expression map with the counts of all the mapped tags onto the genome is available by following the highlighted button.

Expression Map

Experimental Condition: All

Expression Level: 0 to 1000 (range: 0-1000)

Y-Axis Scale: Logarithmic

Organism: *Sacharomyces cerevisiae*

Chromosome: 2

Keys:

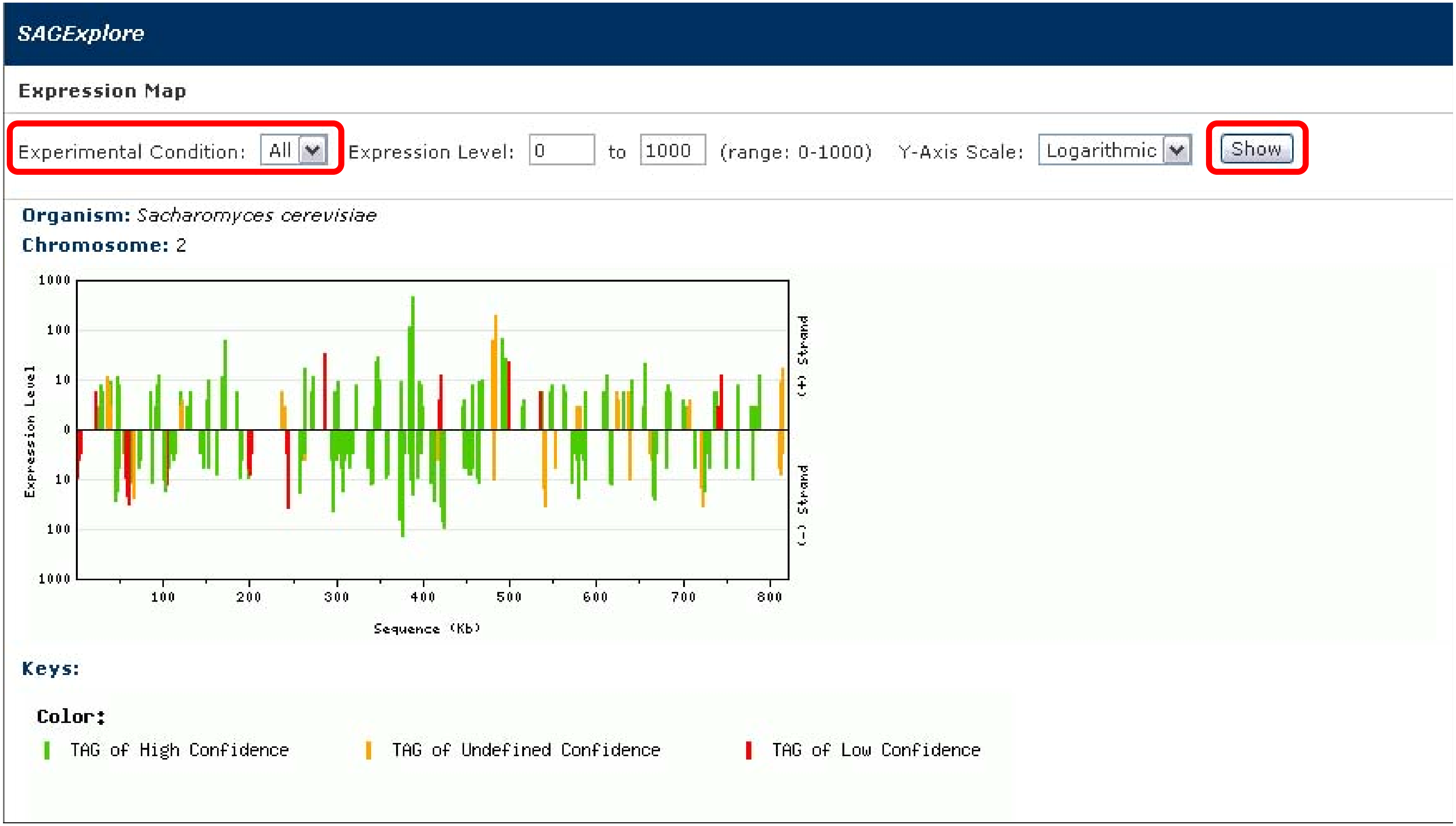
Color:

🟩 TAG of High Confidence

🟧 TAG of Undefined Confidence

🟥 TAG of Low Confidence

Expression Map: An expression map with the counts of all the mapped tags onto the genome is displayed. This is useful to detect transcriptionally active regions in a chromosome.



Experimental Condition: All

Expression Level: 0 to 1000 (range: 0-1000)

Y-Axis Scale: Logarithmic

Organism: *Sacharomyces cerevisiae*

Chromosome: 2

Keys:

Color:

🟩 TAG of High Confidence

🟧 TAG of Undefined Confidence

🟥 TAG of Low Confidence

Expression Map: The user can select a single experimental condition or to display all of them simultaneously (as it is the case in this example). The ‘show’ button on the right must be clicked to make effective any change of parameters.

Expression Map

Experimental Condition: All

Expression Level: 0 to 1000 (range: 0-1000)

Y-Axis Scale: Logarithmic

Organism: *Sacharomyces cerevisiae*

Chromosome: 2

Keys:

Color:

🟩 TAG of High Confidence

🟧 TAG of Undefined Confidence

🟥 TAG of Low Confidence

Expression Map: The user can select a range of expression level. Only the tags which counts belong to this expression range will be displayed. The ‘show’ button on the right must be clicked to make effective any change of parameters.

SAGExplore

Expression Map

Experimental Condition: All

Expression Level: 0 to 1000 (range: 0-1000)

Y-Axis Scale: Logarithmic

Organism: *Sacharomyces cerevisiae*

Chromosome: 2

Keys:

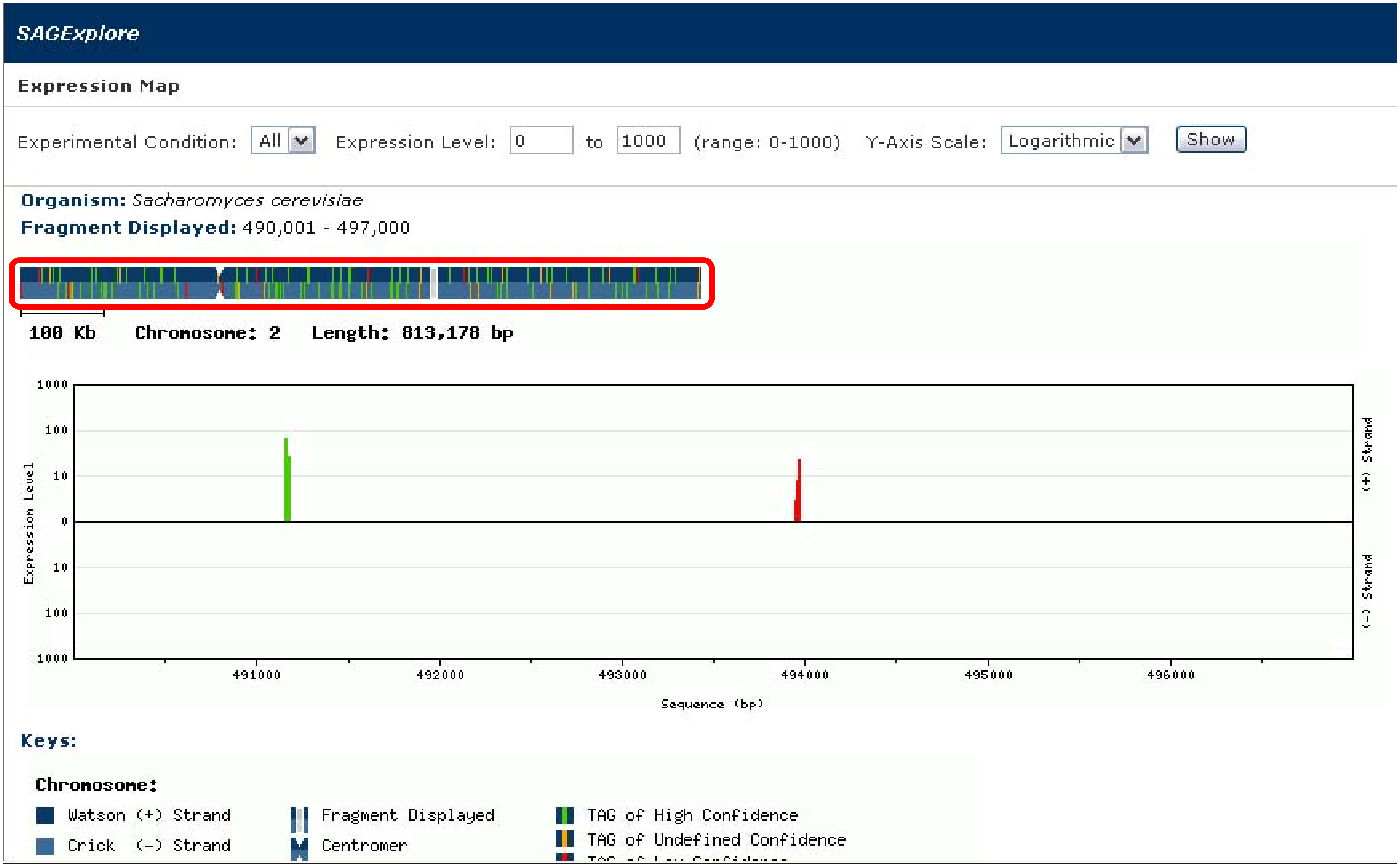
Color:

🟩 TAG of High Confidence

🟧 TAG of Undefined Confidence

🟥 TAG of Low Confidence

Expression Map: The user can select two types of scale for the Y axis of the graph: linear or logarithmic. The ‘show’ button on the right must be clicked to make effective any change of parameters.



SAGExplore

Expression Map

Experimental Condition: All

Expression Level: 0 to 1000 (range: 0-1000)

Y-Axis Scale: Logarithmic

Organism: *Sacharomyces cerevisiae*

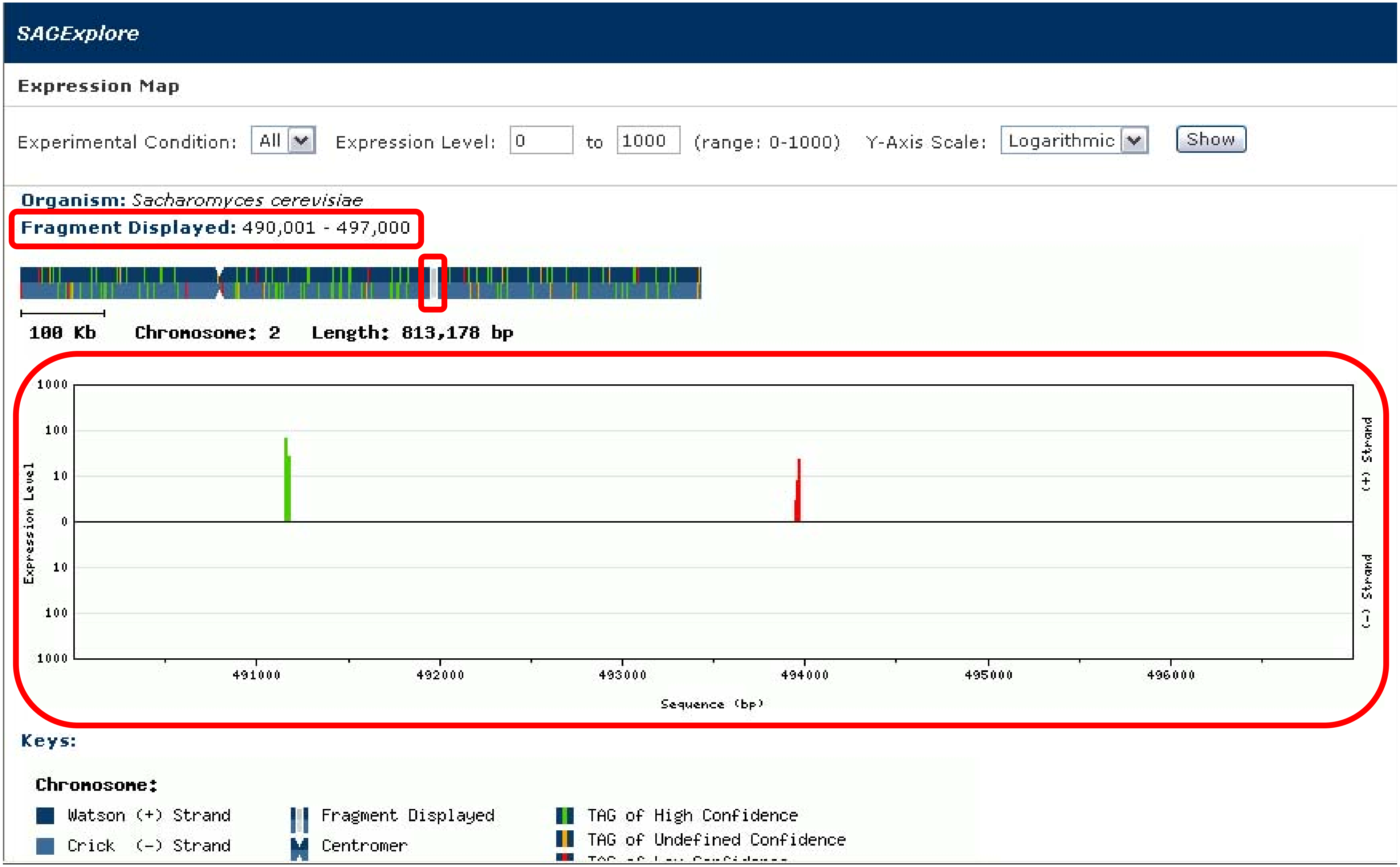
Fragment Displayed: 490,001 - 497,000

Keys:

Chromosome:

- Watson (+) Strand
- Crick (-) Strand
- Fragment Displayed
- Centromer
- TAG of High Confidence
- TAG of Undefined Confidence

Expression Map: The tags mapped are graphically shown in the chromosome.



Experimental Condition: All

Expression Level: 0 to 1000 (range: 0-1000)

Y-Axis Scale: Logarithmic

Organism: *Saccharomyces cerevisiae*

Fragment Displayed: 490,001 - 497,000

100 Kb **Chromosome: 2** **Length: 813,178 bp**

Keys:

Chromosome:

■ Watson (+) Strand	▮ Fragment Displayed	▮ TAG of High Confidence
■ Crick (-) Strand	▮ Centromer	▮ TAG of Undefined Confidence

Expression Map: The start and end coordinates of the chromosome fragment displayed are given. Also, in the chromosome, the selected region is highlighted. The graph below shows the counts of each tag for each experimental condition, as supplied by the user.

SAGExplore

Expression Map

Experimental Condition: All ▾ Expression Level: 0 to 1000 (range: 0-1000) Y-Axis Scale: Logarithmic ▾

Organism: *Sacharomyces cerevisiae*

Fragment Displayed: 490,001 - 497,000

100 Kb **Chromosone: 2** **Length: 813,178 bp**

Keys:

Chromosone:

■ Watson (+) Strand

■ Crick (-) Strand

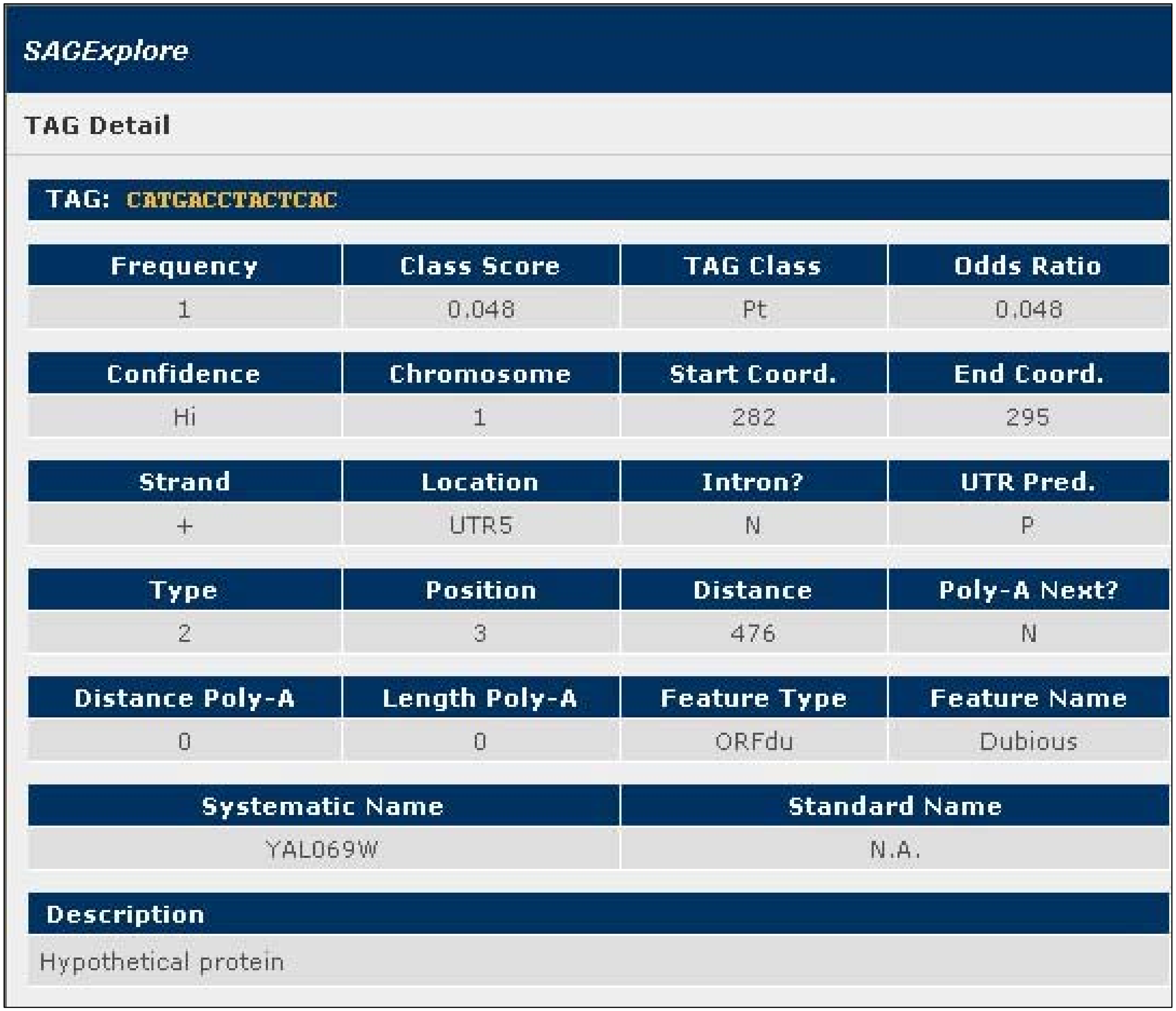
Fragment Displayed

Centromer

TAG of High Confidence

TAG of Undefined Confidence

Expression Map: By clicking on a given tag count, several tag details are given in a pop-up window.



SAGExplore

TAG Detail

TAG: CATGACCTACTCAC

Frequency	Class Score	TAG Class	Odds Ratio
1	0.048	Pt	0.048

Confidence	Chromosome	Start Coord.	End Coord.
Hi	1	282	295

Strand	Location	Intron?	UTR Pred.
+	UTR5	N	P

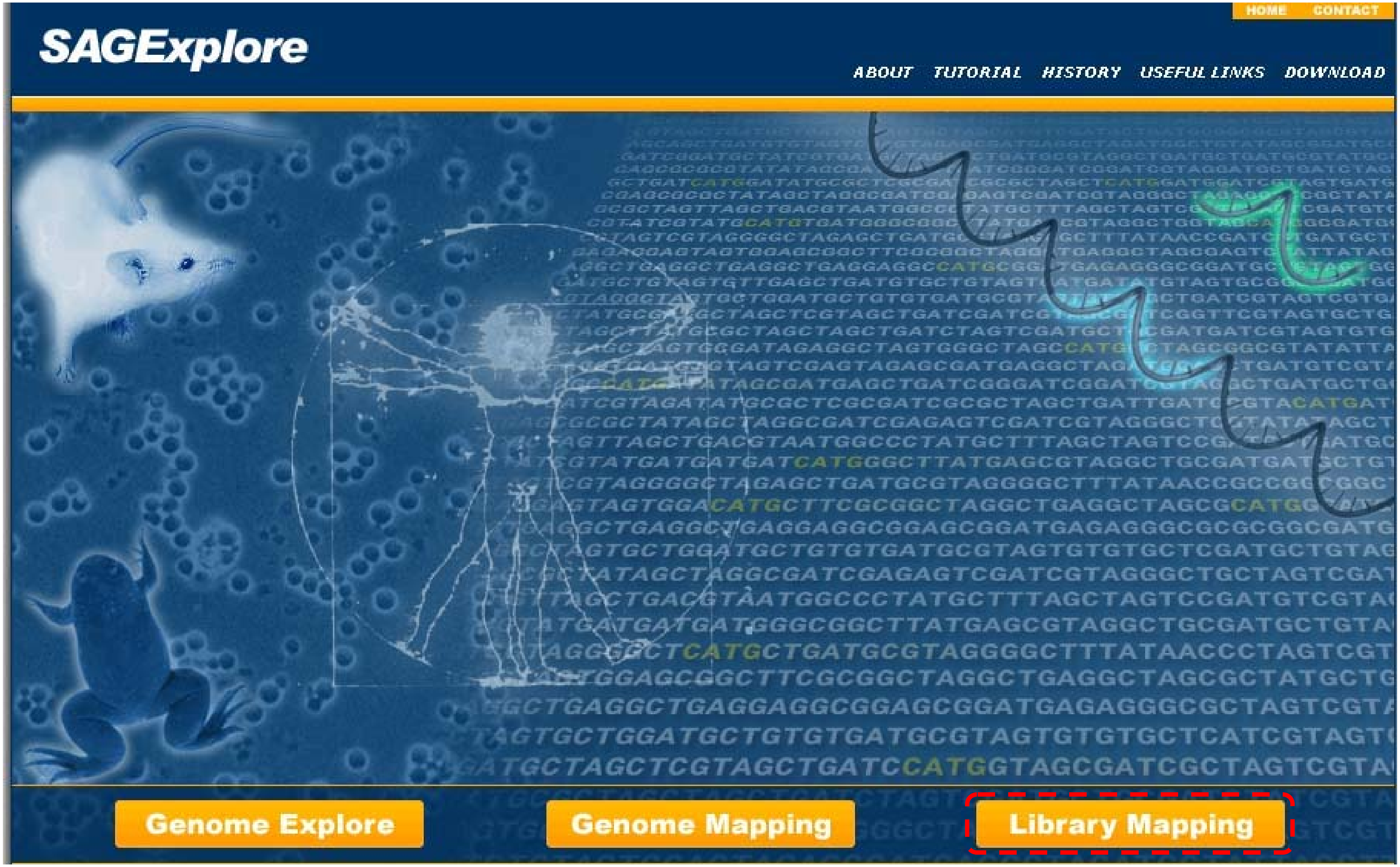
Type	Position	Distance	Poly-A Next?
2	3	476	N

Distance Poly-A	Length Poly-A	Feature Type	Feature Name
0	0	ORFdu	Dubious

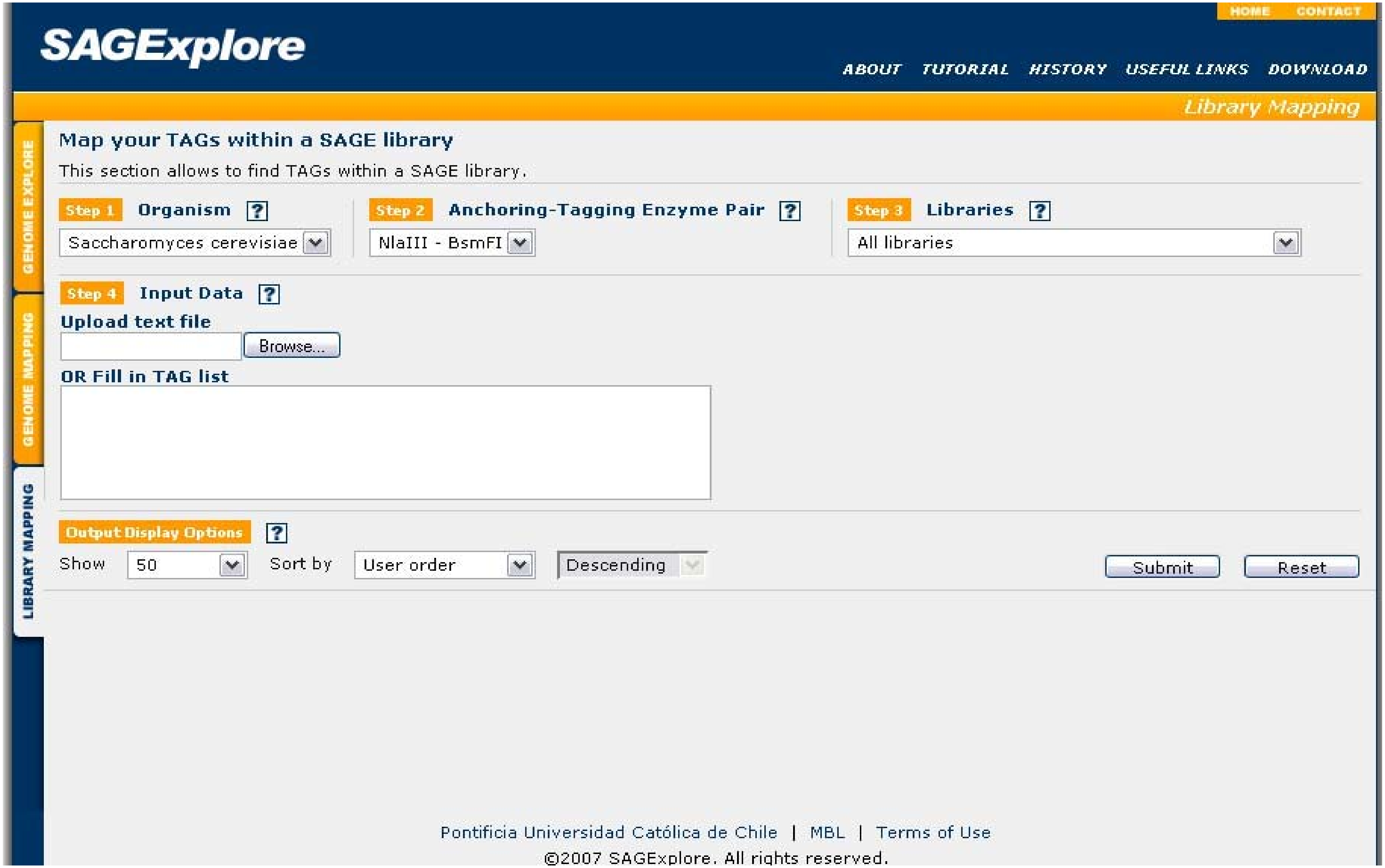
Systematic Name	Standard Name
YAL069W	N.A.

Description
Hypothetical protein

Tag details: Many details about the tag are provided here. See the online help for an explanation of each field meaning.



III.- Tutorial Library Mapping Module.



Map your TAGs within a SAGE library

This section allows to find TAGs within a SAGE library.

Step 1 Organism: Saccharomyces cerevisiae

Step 2 Anchoring-Tagging Enzyme Pair: NlaIII - BsmFI

Step 3 Libraries: All libraries

Step 4 Input Data

Upload text file

OR Fill in TAG list

Output Display Options

Show: 50

Sort by: User order

Descending

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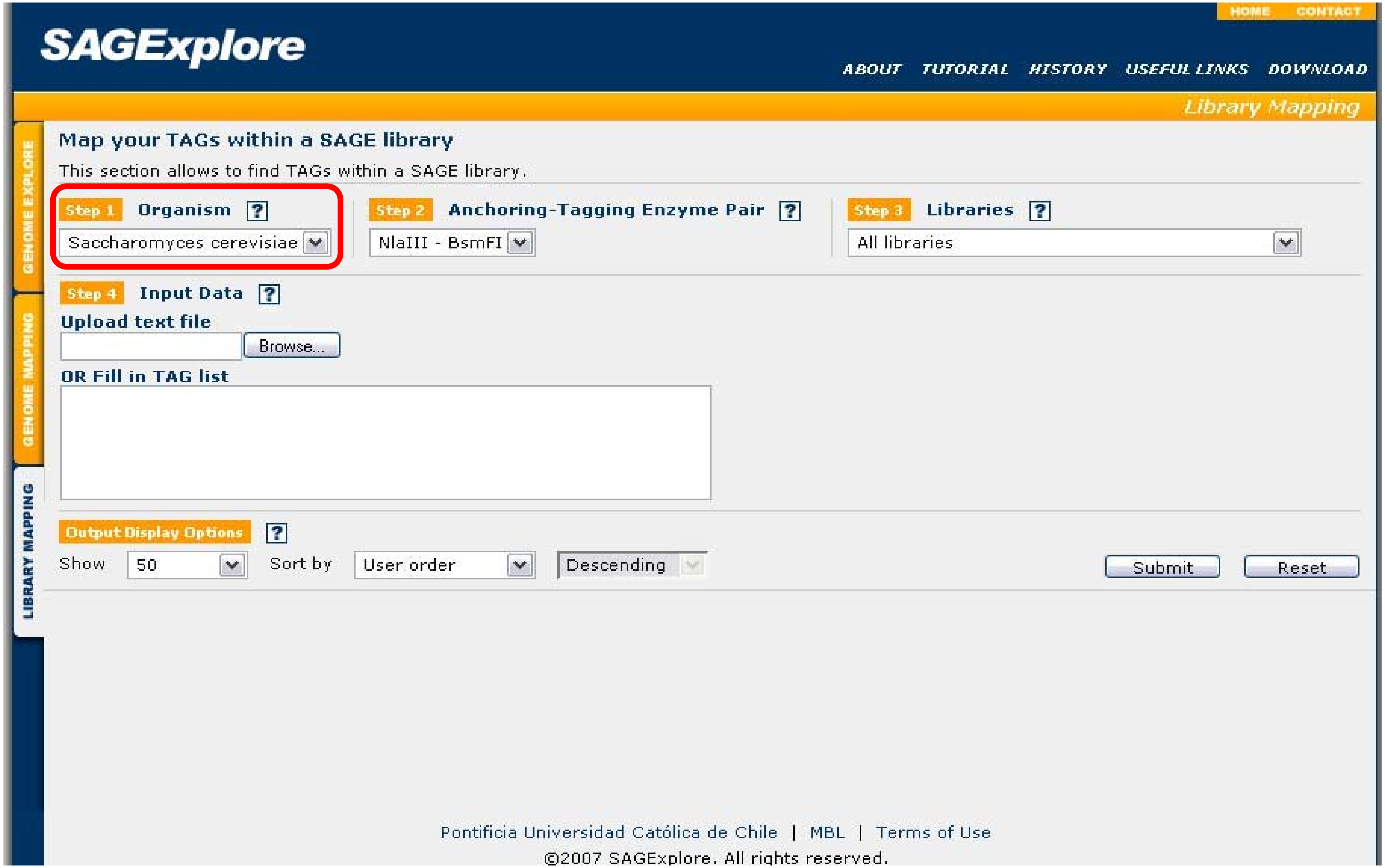
III.- Library Mapping Module Form: The user must follow four sequential steps in this form. Online help with the relevant details is provided for each step.



Map your TAGs within a SAGE library

This section allows to find TAGs within a SAGE library.

Step 1 Organism: Saccharomyces cerevisiae

Step 2 Anchoring-Tagging Enzyme Pair: NlaIII - BsmFI

Step 3 Libraries: All libraries

Step 4 Input Data

Upload text file

OR Fill in TAG list

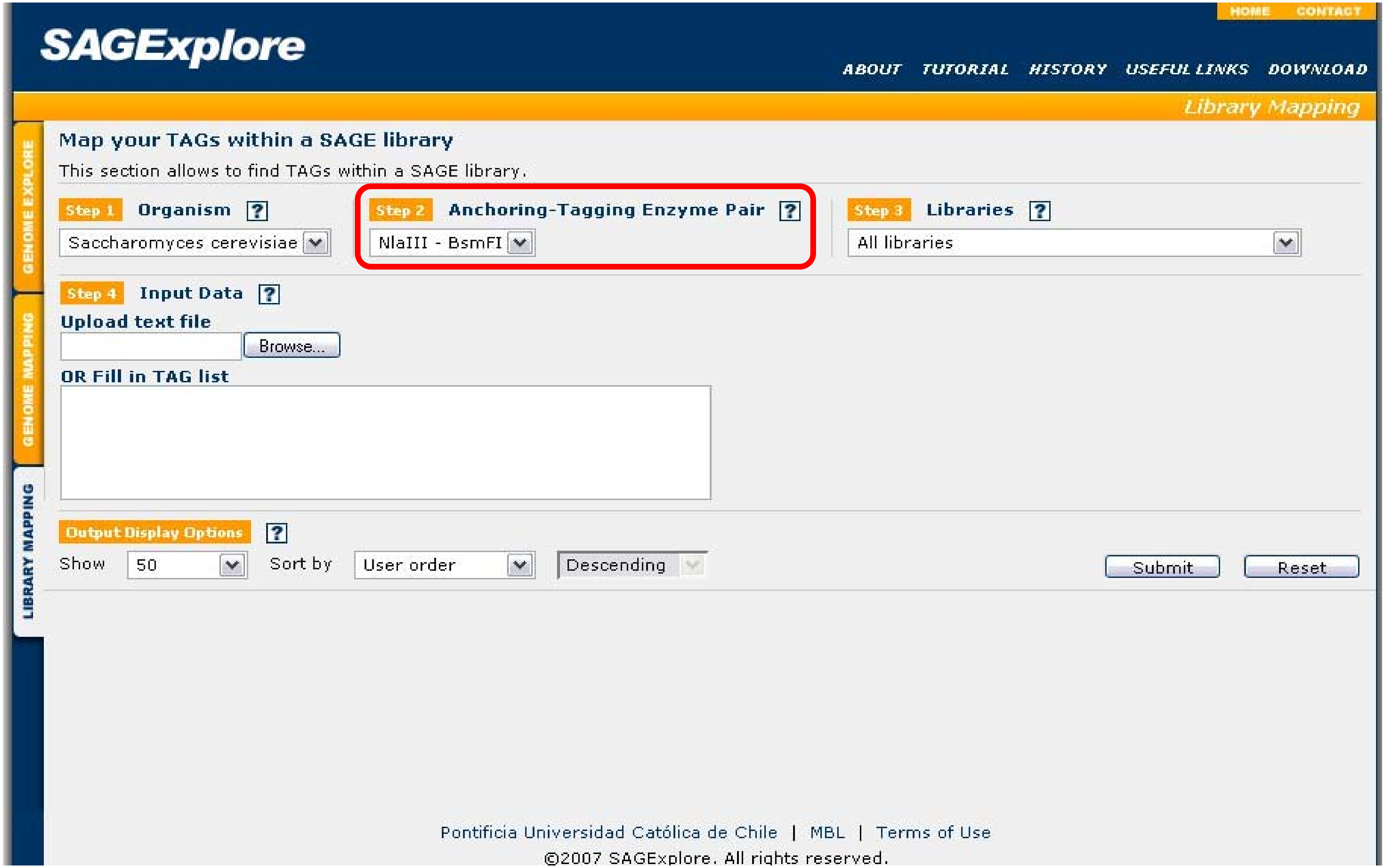
Output Display Options

Show: 50

Sort by: User order

Descending

Step 1: The user must select the organism of interest. Currently, only *Saccharomyces cerevisiae* is available. In the near future, other organisms will be added.



Map your TAGs within a SAGE library

This section allows to find TAGs within a SAGE library.

Step 1 Organism: Saccharomyces cerevisiae

Step 2 Anchoring-Tagging Enzyme Pair: NlaIII - BsmFI

Step 3 Libraries: All libraries

Step 4 Input Data

Upload text file

OR Fill in TAG list

Output Display Options

Show 50 Sort by User order Descending

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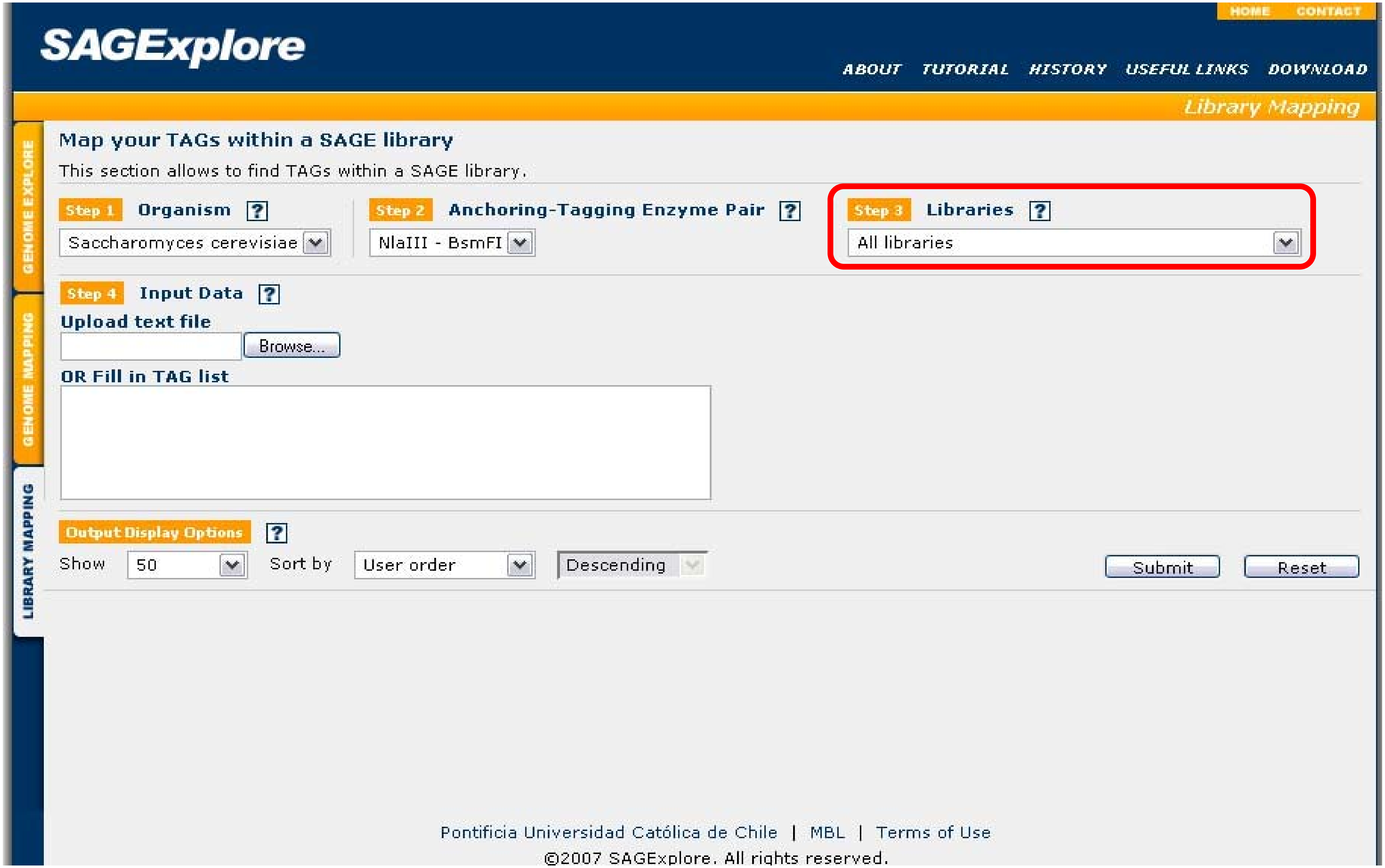
Step 2: The user must select the anchoring-tagging enzyme pair used in SAGE. Currently, only the pair NlaIII-BsmFI is available. In the near future, other enzyme pairs such as the one used in Long-SAGE will be added.



Map your TAGs within a SAGE library

This section allows to find TAGs within a SAGE library.

Step 1 Organism: Saccharomyces cerevisiae

Step 2 Anchoring-Tagging Enzyme Pair: NlaIII - BsmFI

Step 3 Libraries: All libraries

Step 4 Input Data

Upload text file

OR Fill in TAG list

Output Display Options

Show: 50 Sort by: User order Descending

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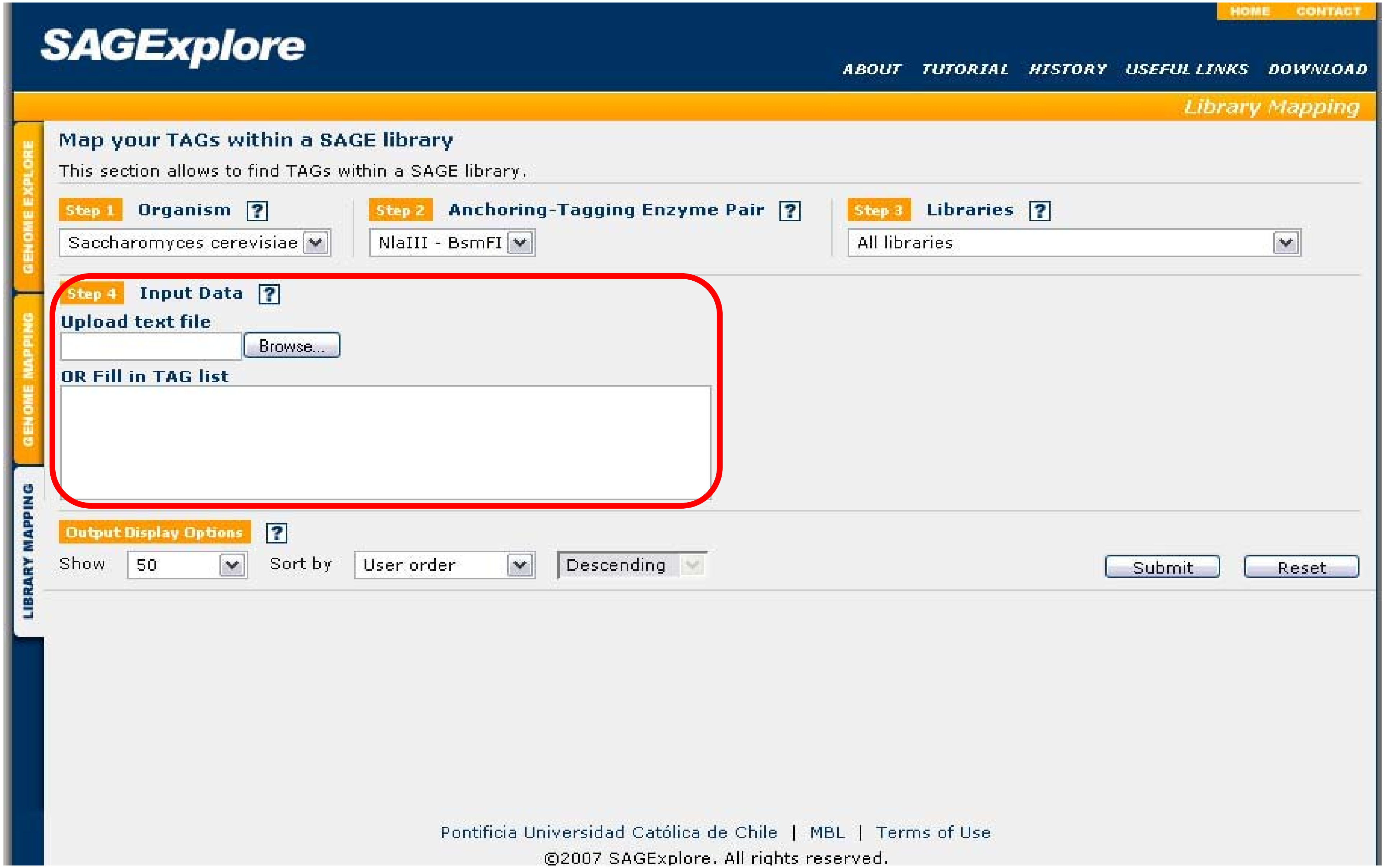
Step 3: The user must select an experimental library of SAGE tags. By default, all libraries will be selected. In the case of Saccharomyces cerevisiae, eight independent libraries have been reported and are included in the server.



Map your TAGs within a SAGE library

This section allows to find TAGs within a SAGE library.

Step 1 **Organism**: Saccharomyces cerevisiae

Step 2 **Anchoring-Tagging Enzyme Pair**: NlaIII - BsmFI

Step 3 **Libraries**: All libraries

Step 4 **Input Data**

Upload text file

OR Fill in TAG list

Output Display Options

Show: 50

Sort by: User order

Descending

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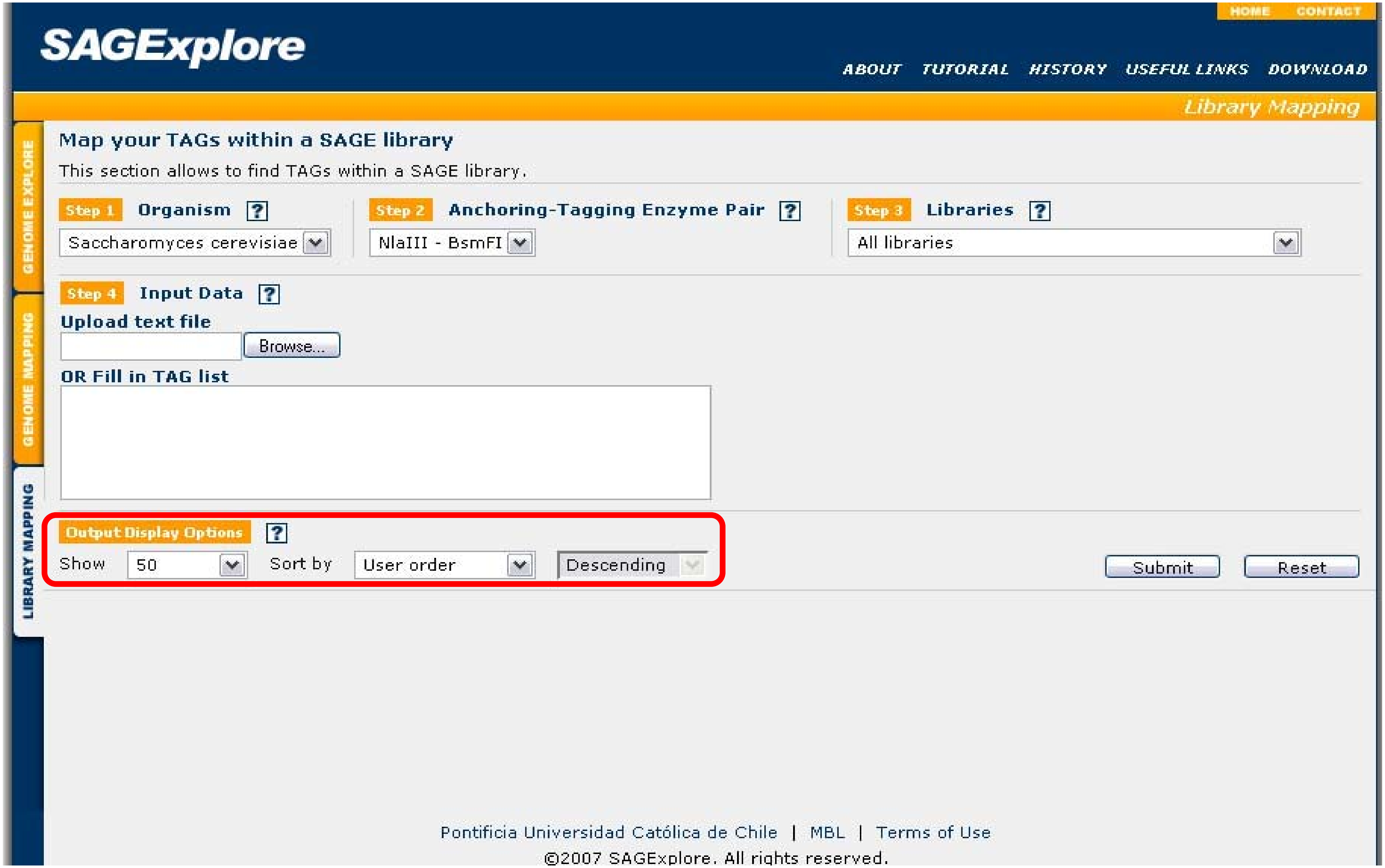
Step 4: The user must provide a list of experimental tags to map against the known experimental libraries of tags. A text file can be uploaded or the data directly pasted into the textarea. The input format is explained in the help link for this step. The full tag sequence must be provided (ie. including the CATG at the 5' end).



Map your TAGs within a SAGE library

This section allows to find TAGs within a SAGE library.

Step 1 **Organism**: Saccharomyces cerevisiae

Step 2 **Anchoring-Tagging Enzyme Pair**: NlaIII - BsmFI

Step 3 **Libraries**: All libraries

Step 4 **Input Data**

Upload text file

OR Fill in TAG list

Output Display Options

Show 50 Sort by User order Descending

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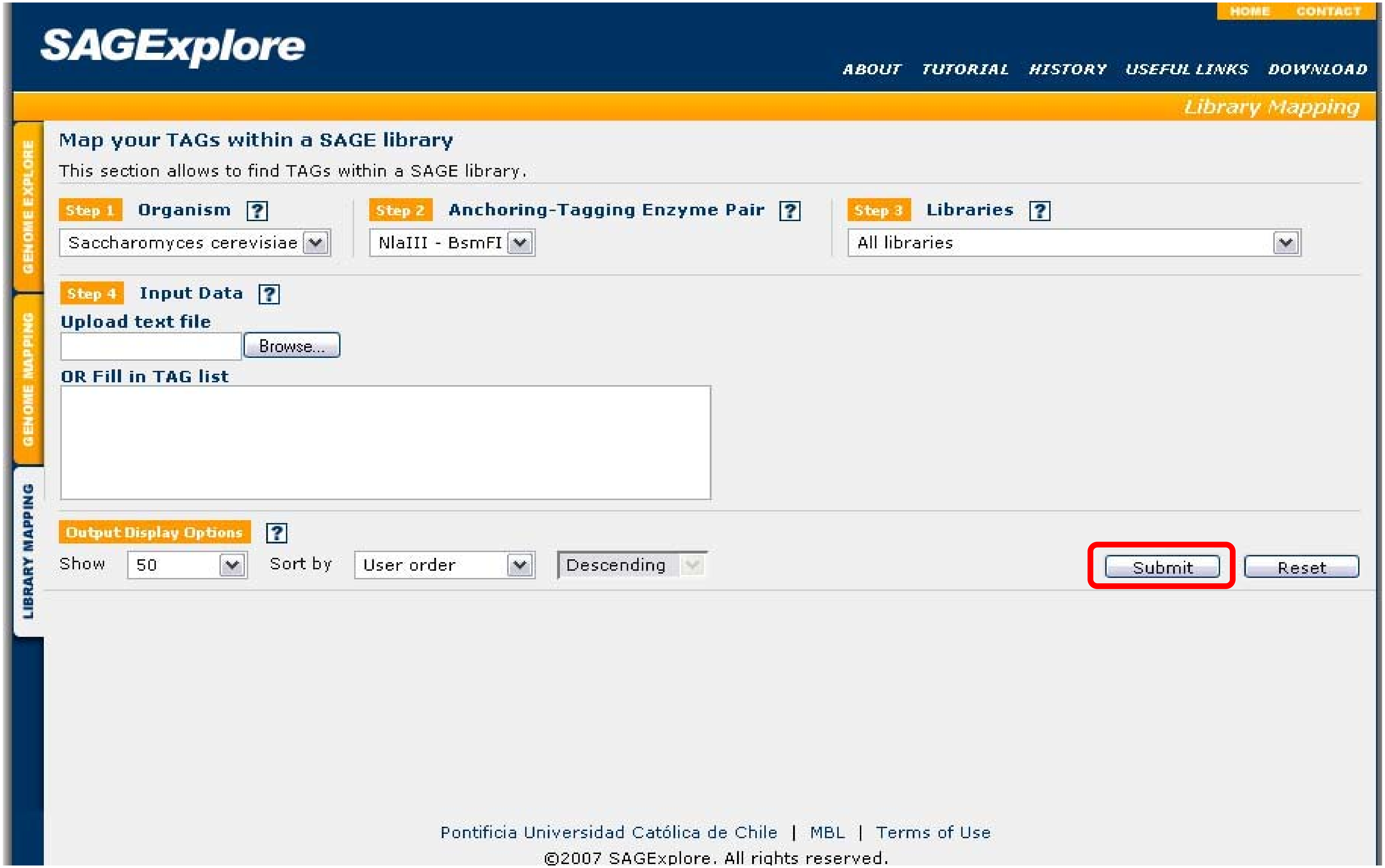
Pre-submit: Before submitting the query, the user can choose the number of rows to display per page and also how to sort the results.



Map your TAGs within a SAGE library

This section allows to find TAGs within a SAGE library.

Step 1 Organism: Saccharomyces cerevisiae

Step 2 Anchoring-Tagging Enzyme Pair: NlaIII - BsmFI

Step 3 Libraries: All libraries

Step 4 Input Data

Upload text file

OR Fill in TAG list

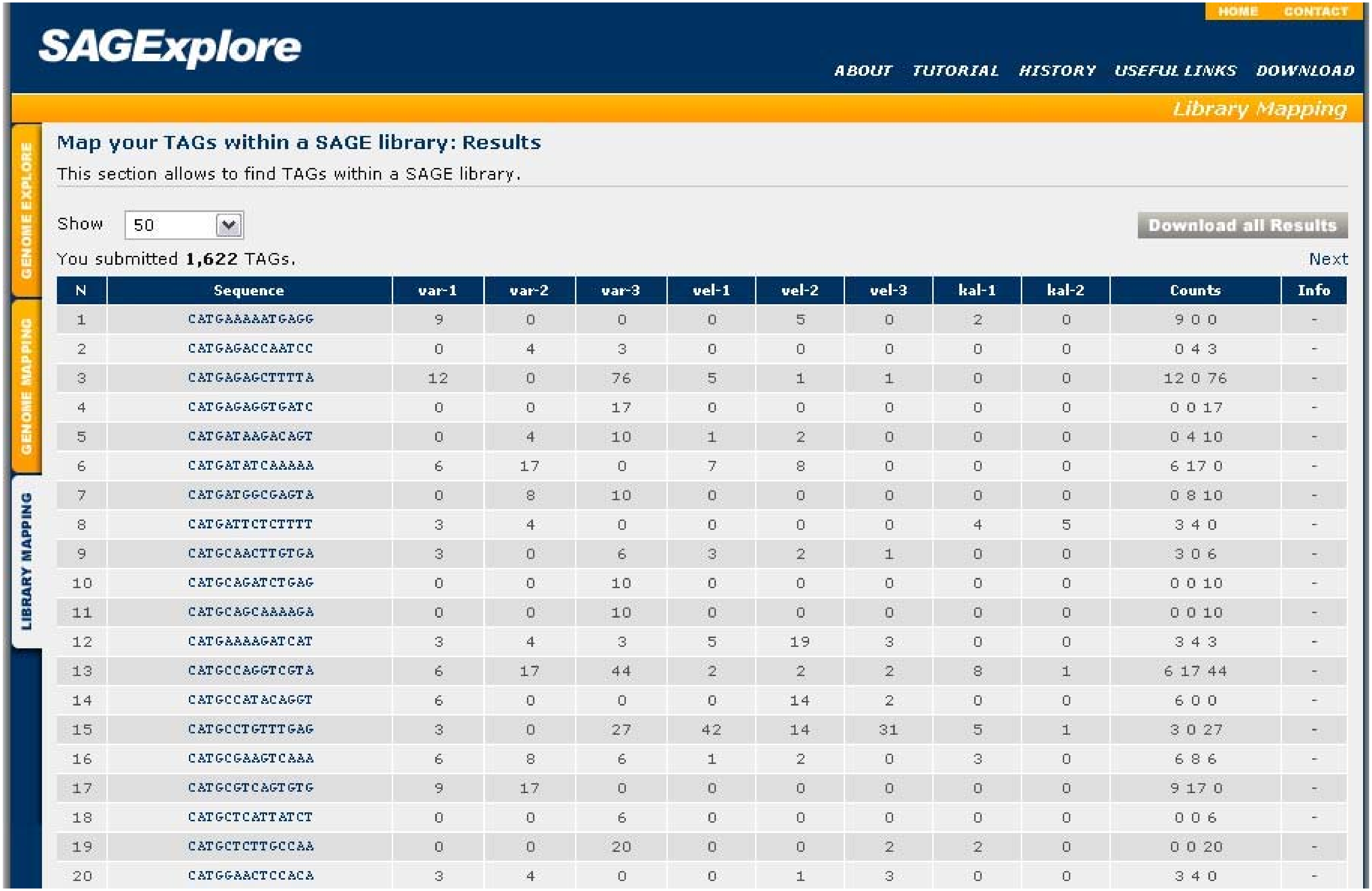
Output Display Options

Show: 50

Sort by: User order

Descending

Submit: The user is ready to submit the query to the server.



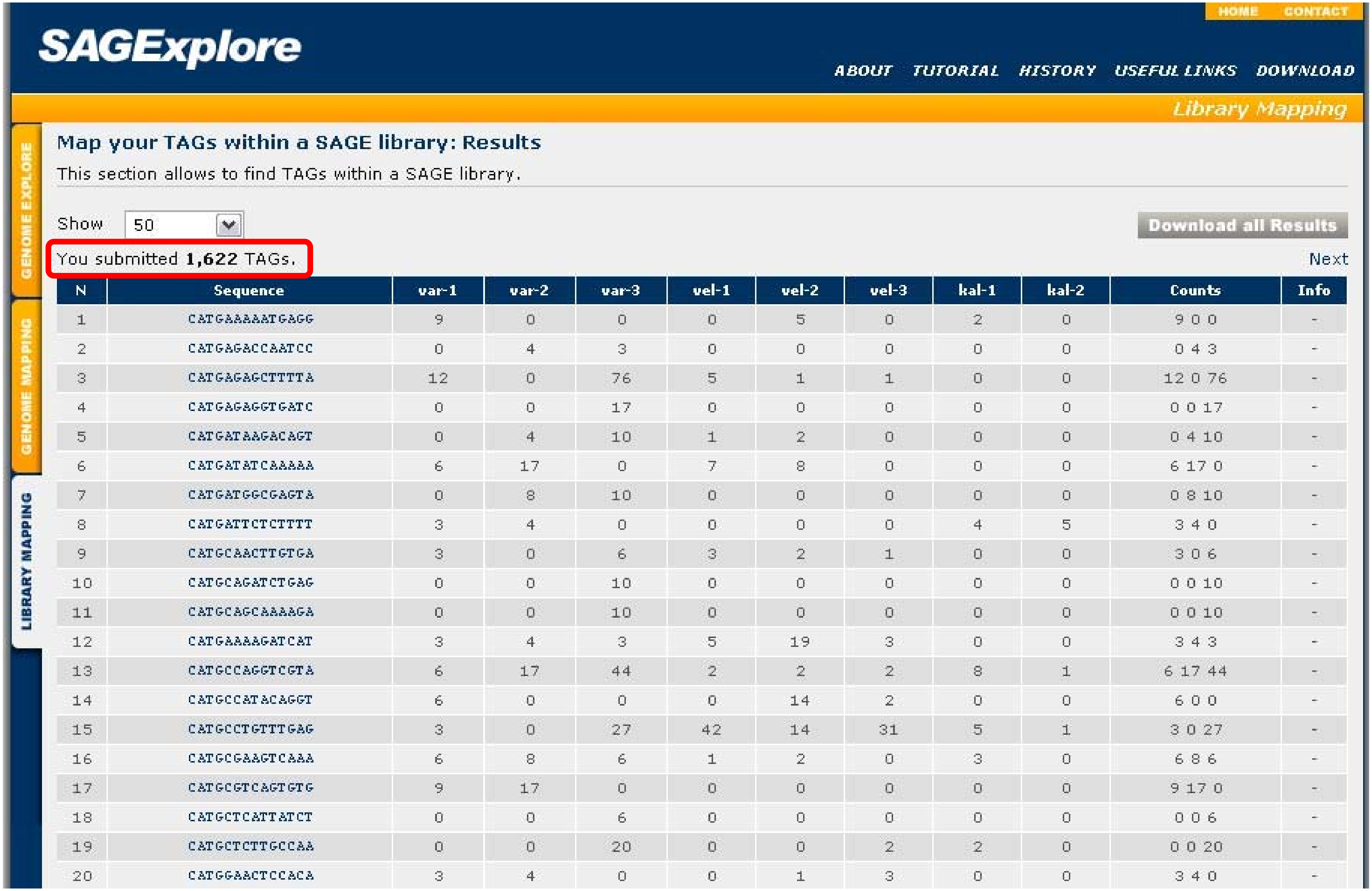
Map your TAGs within a SAGE library: Results

This section allows to find TAGs within a SAGE library.

You submitted **1,622** TAGs.

N	Sequence	var-1	var-2	var-3	vel-1	vel-2	vel-3	kal-1	kal-2	Counts	Info
1	CATGAAAAATGAGG	9	0	0	0	5	0	2	0	9 0 0	-
2	CATGAGACCAATCC	0	4	3	0	0	0	0	0	0 4 3	-
3	CATGAGAGCTTTTA	12	0	76	5	1	1	0	0	12 0 76	-
4	CATGAGAGGTGATC	0	0	17	0	0	0	0	0	0 0 17	-
5	CATGATAAGACAGT	0	4	10	1	2	0	0	0	0 4 10	-
6	CATGATATCAAAAA	6	17	0	7	8	0	0	0	6 17 0	-
7	CATGATGGCGAGTA	0	8	10	0	0	0	0	0	0 8 10	-
8	CATGATTCTCTTTT	3	4	0	0	0	0	4	5	3 4 0	-
9	CATGCAACTTGTGA	3	0	6	3	2	1	0	0	3 0 6	-
10	CATGCAGATCTGAG	0	0	10	0	0	0	0	0	0 0 10	-
11	CATGCAGCAAAAGA	0	0	10	0	0	0	0	0	0 0 10	-
12	CATGAAAAGATCAT	3	4	3	5	19	3	0	0	3 4 3	-
13	CATGCCAGGTCGTA	6	17	44	2	2	2	8	1	6 17 44	-
14	CATGCCATACAGGT	6	0	0	0	14	2	0	0	6 0 0	-
15	CATGCCTGTTTGAG	3	0	27	42	14	31	5	1	3 0 27	-
16	CATGCGAAGTCAAA	6	8	6	1	2	0	3	0	6 8 6	-
17	CATGCGTCAGTGTG	9	17	0	0	0	0	0	0	9 17 0	-
18	CATGCTCATTATCT	0	0	6	0	0	0	0	0	0 0 6	-
19	CATGCTCTTGCCAA	0	0	20	0	0	2	2	0	0 0 20	-
20	CATGGAACTCCACA	3	4	0	0	1	3	0	0	3 4 0	-

Query Results: Typical output of the Library Mapping Form.



Map your TAGs within a SAGE library: Results

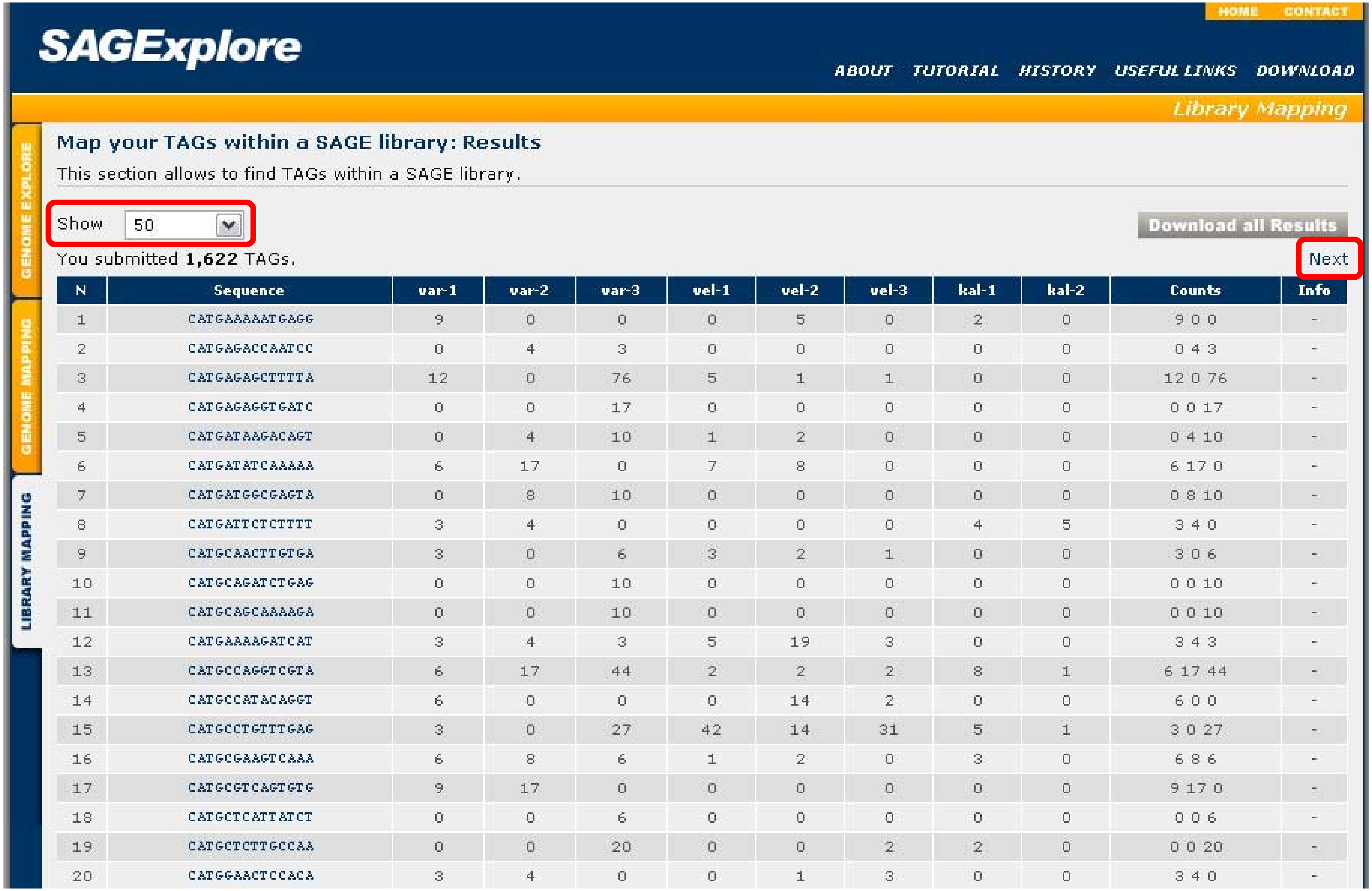
This section allows to find TAGs within a SAGE library.

Show 50

You submitted **1,622** TAGs.

N	Sequence	var-1	var-2	var-3	vel-1	vel-2	vel-3	kal-1	kal-2	Counts	Info
1	CATGAAAAATGAGG	9	0	0	0	5	0	2	0	9 0 0	-
2	CATGAGACCAATCC	0	4	3	0	0	0	0	0	0 4 3	-
3	CATGAGAGCTTTTA	12	0	76	5	1	1	0	0	12 0 76	-
4	CATGAGAGGTGATC	0	0	17	0	0	0	0	0	0 0 17	-
5	CATGATAAGACAGT	0	4	10	1	2	0	0	0	0 4 10	-
6	CATGATATCAAAAA	6	17	0	7	8	0	0	0	6 17 0	-
7	CATGATGGCGAGTA	0	8	10	0	0	0	0	0	0 8 10	-
8	CATGATTCTCTTTT	3	4	0	0	0	0	4	5	3 4 0	-
9	CATGCAACTTGTGA	3	0	6	3	2	1	0	0	3 0 6	-
10	CATGCAGATCTGAG	0	0	10	0	0	0	0	0	0 0 10	-
11	CATGCAGCAAAAGA	0	0	10	0	0	0	0	0	0 0 10	-
12	CATGAAAAGATCAT	3	4	3	5	19	3	0	0	3 4 3	-
13	CATGCCAGGTCGTA	6	17	44	2	2	2	8	1	6 17 44	-
14	CATGCCATACAGGT	6	0	0	0	14	2	0	0	6 0 0	-
15	CATGCCTGTTTGAG	3	0	27	42	14	31	5	1	3 0 27	-
16	CATGCGAAGTCAAA	6	8	6	1	2	0	3	0	6 8 6	-
17	CATGCGTCAGTGTG	9	17	0	0	0	0	0	0	9 17 0	-
18	CATGCTCATTATCT	0	0	6	0	0	0	0	0	0 0 6	-
19	CATGCTCTTGCCAA	0	0	20	0	0	2	2	0	0 0 20	-
20	CATGGAACTCCACA	3	4	0	0	1	3	0	0	3 4 0	-

Query Results: The total number of records that matched the query are reported. Also, the total number of tags that did not match any record in the known libraries out of the total number of submitted tags is given.



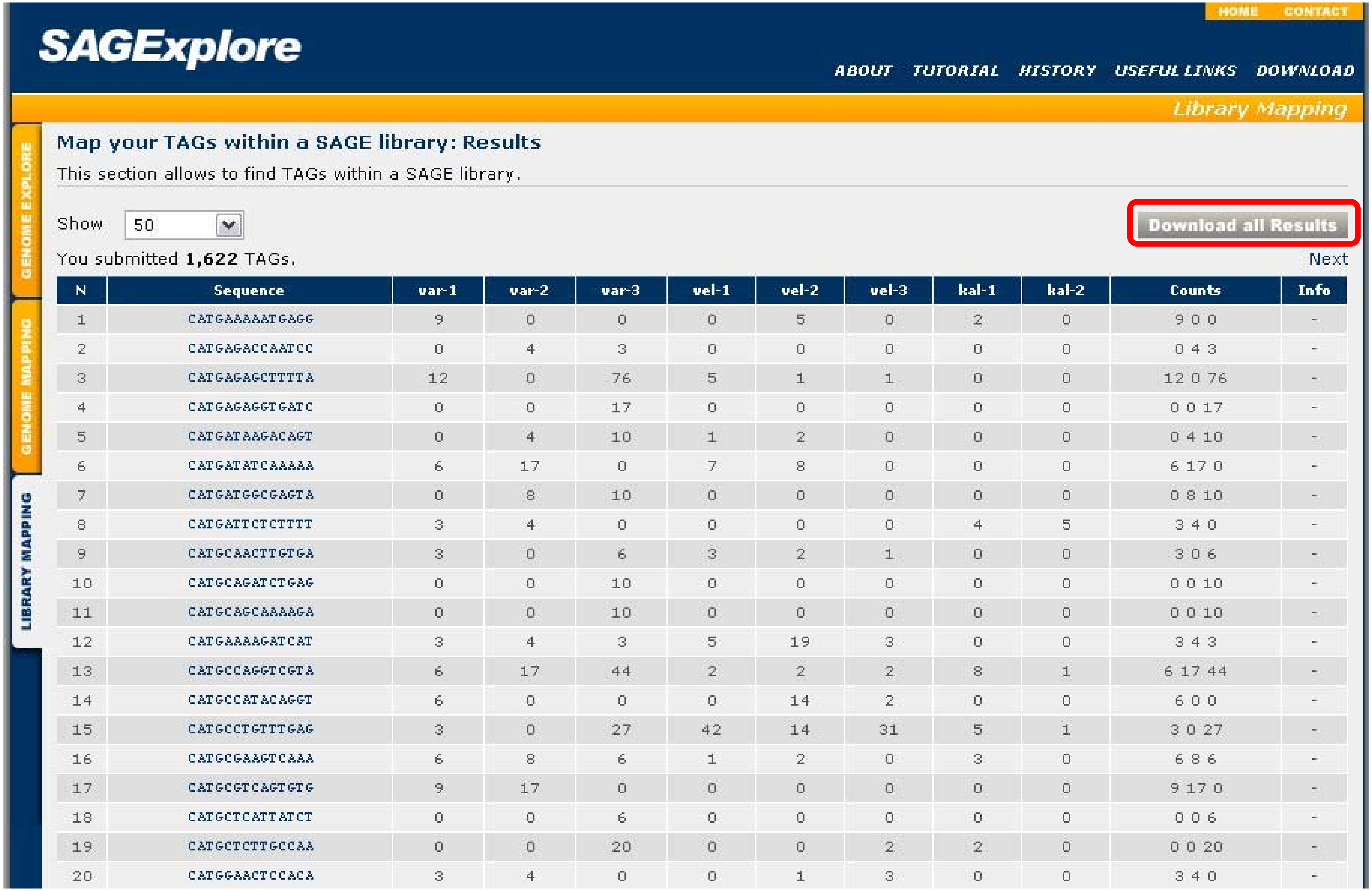
Map your TAGs within a SAGE library: Results

This section allows to find TAGs within a SAGE library.

You submitted **1,622** TAGs.

N	Sequence	var-1	var-2	var-3	vel-1	vel-2	vel-3	kal-1	kal-2	Counts	Info
1	CATGAAAAATGAGG	9	0	0	0	5	0	2	0	9 0 0	-
2	CATGAGACCAATCC	0	4	3	0	0	0	0	0	0 4 3	-
3	CATGAGAGCTTTTA	12	0	76	5	1	1	0	0	12 0 76	-
4	CATGAGAGGTGATC	0	0	17	0	0	0	0	0	0 0 17	-
5	CATGATAAGACAGT	0	4	10	1	2	0	0	0	0 4 10	-
6	CATGATATCAAAAA	6	17	0	7	8	0	0	0	6 17 0	-
7	CATGATGGCGAGTA	0	8	10	0	0	0	0	0	0 8 10	-
8	CATGATTCTCTTTT	3	4	0	0	0	0	4	5	3 4 0	-
9	CATGCAACTTGTGA	3	0	6	3	2	1	0	0	3 0 6	-
10	CATGCAGATCTGAG	0	0	10	0	0	0	0	0	0 0 10	-
11	CATGCAGCAAAAGA	0	0	10	0	0	0	0	0	0 0 10	-
12	CATGAAAAGATCAT	3	4	3	5	19	3	0	0	3 4 3	-
13	CATGCCAGGTCGTA	6	17	44	2	2	2	8	1	6 17 44	-
14	CATGCCATACAGGT	6	0	0	0	14	2	0	0	6 0 0	-
15	CATGCCTGTTTGAG	3	0	27	42	14	31	5	1	3 0 27	-
16	CATGCGAAGTCAAA	6	8	6	1	2	0	3	0	6 8 6	-
17	CATGCGTCAGTGTG	9	17	0	0	0	0	0	0	9 17 0	-
18	CATGCTCATTATCT	0	0	6	0	0	0	0	0	0 0 6	-
19	CATGCTCTTGCCAA	0	0	20	0	0	2	2	0	0 0 20	-
20	CATGGAACTCCACA	3	4	0	0	1	3	0	0	3 4 0	-

Query Results: Only a fraction of the results is displayed. This option can be easily changed by selecting a different number of rows to display or the next button used to go to the next page.



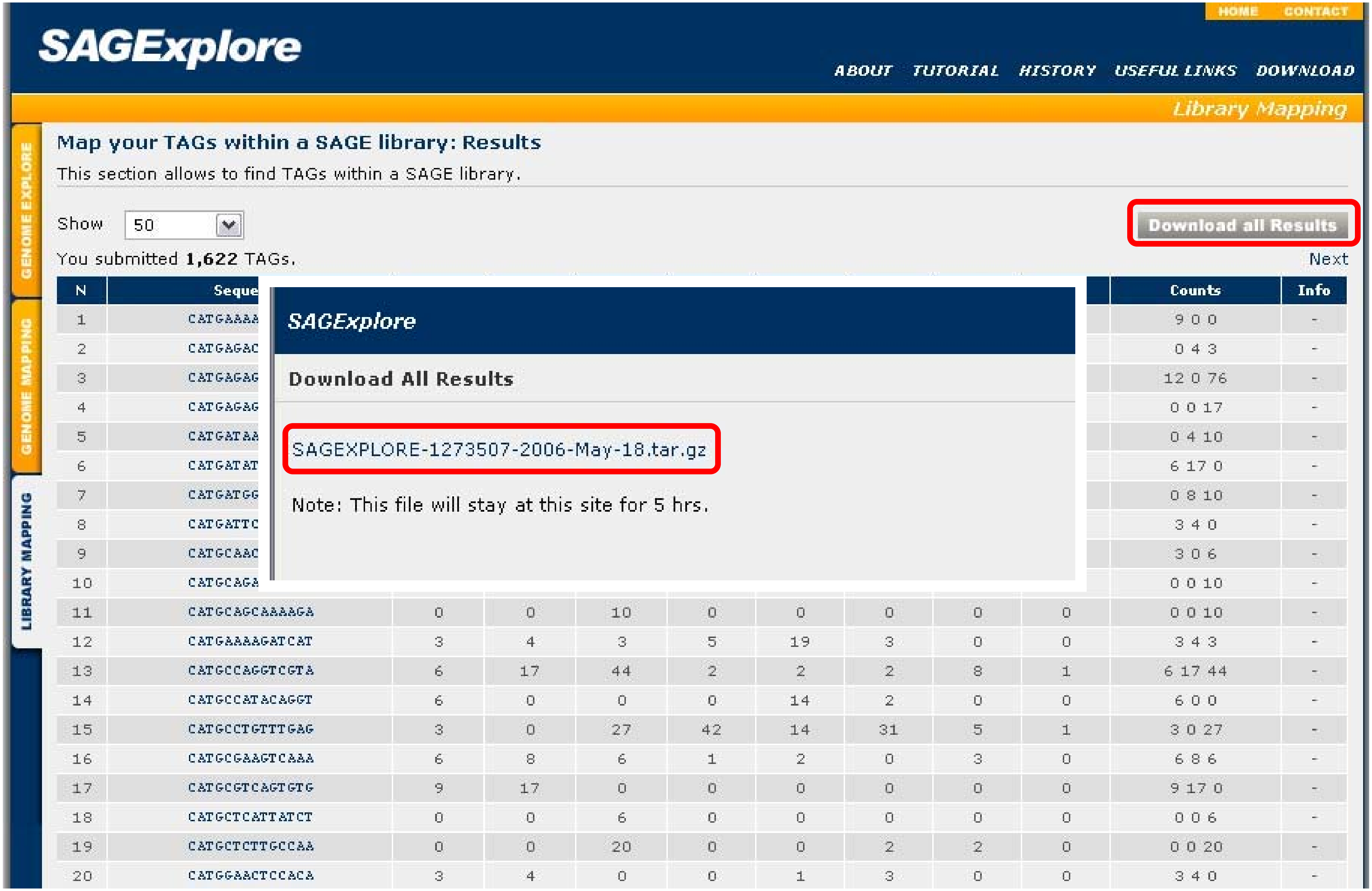
Map your TAGs within a SAGE library: Results

This section allows to find TAGs within a SAGE library.

You submitted **1,622** TAGs.

N	Sequence	var-1	var-2	var-3	vel-1	vel-2	vel-3	kal-1	kal-2	Counts	Info
1	CATGAAAAATGAGG	9	0	0	0	5	0	2	0	9 0 0	-
2	CATGAGACCAATCC	0	4	3	0	0	0	0	0	0 4 3	-
3	CATGAGAGCTTTTA	12	0	76	5	1	1	0	0	12 0 76	-
4	CATGAGAGGTGATC	0	0	17	0	0	0	0	0	0 0 17	-
5	CATGATAAGACAGT	0	4	10	1	2	0	0	0	0 4 10	-
6	CATGATATCAAAAA	6	17	0	7	8	0	0	0	6 17 0	-
7	CATGATGGCGAGTA	0	8	10	0	0	0	0	0	0 8 10	-
8	CATGATTCTCTTTT	3	4	0	0	0	0	4	5	3 4 0	-
9	CATGCAACTTGTGA	3	0	6	3	2	1	0	0	3 0 6	-
10	CATGCAGATCTGAG	0	0	10	0	0	0	0	0	0 0 10	-
11	CATGCAGCAAAAGA	0	0	10	0	0	0	0	0	0 0 10	-
12	CATGAAAAGATCAT	3	4	3	5	19	3	0	0	3 4 3	-
13	CATGCCAGGTCGTA	6	17	44	2	2	2	8	1	6 17 44	-
14	CATGCCATACAGGT	6	0	0	0	14	2	0	0	6 0 0	-
15	CATGCCTGTTTGAG	3	0	27	42	14	31	5	1	3 0 27	-
16	CATGCGAAGTCAAA	6	8	6	1	2	0	3	0	6 8 6	-
17	CATGCGTCAGTGTG	9	17	0	0	0	0	0	0	9 17 0	-
18	CATGCTCATTATCT	0	0	6	0	0	0	0	0	0 0 6	-
19	CATGCTCTTGCCAA	0	0	20	0	0	2	2	0	0 0 20	-
20	CATGGAACTCCACA	3	4	0	0	1	3	0	0	3 4 0	-

Query Results: The full table can be downloaded as tab-delimited text (compressed file or tar.gzipped).



Map your TAGs within a SAGE library: Results

This section allows to find TAGs within a SAGE library.

You submitted **1,622** TAGs.

SAGExplore

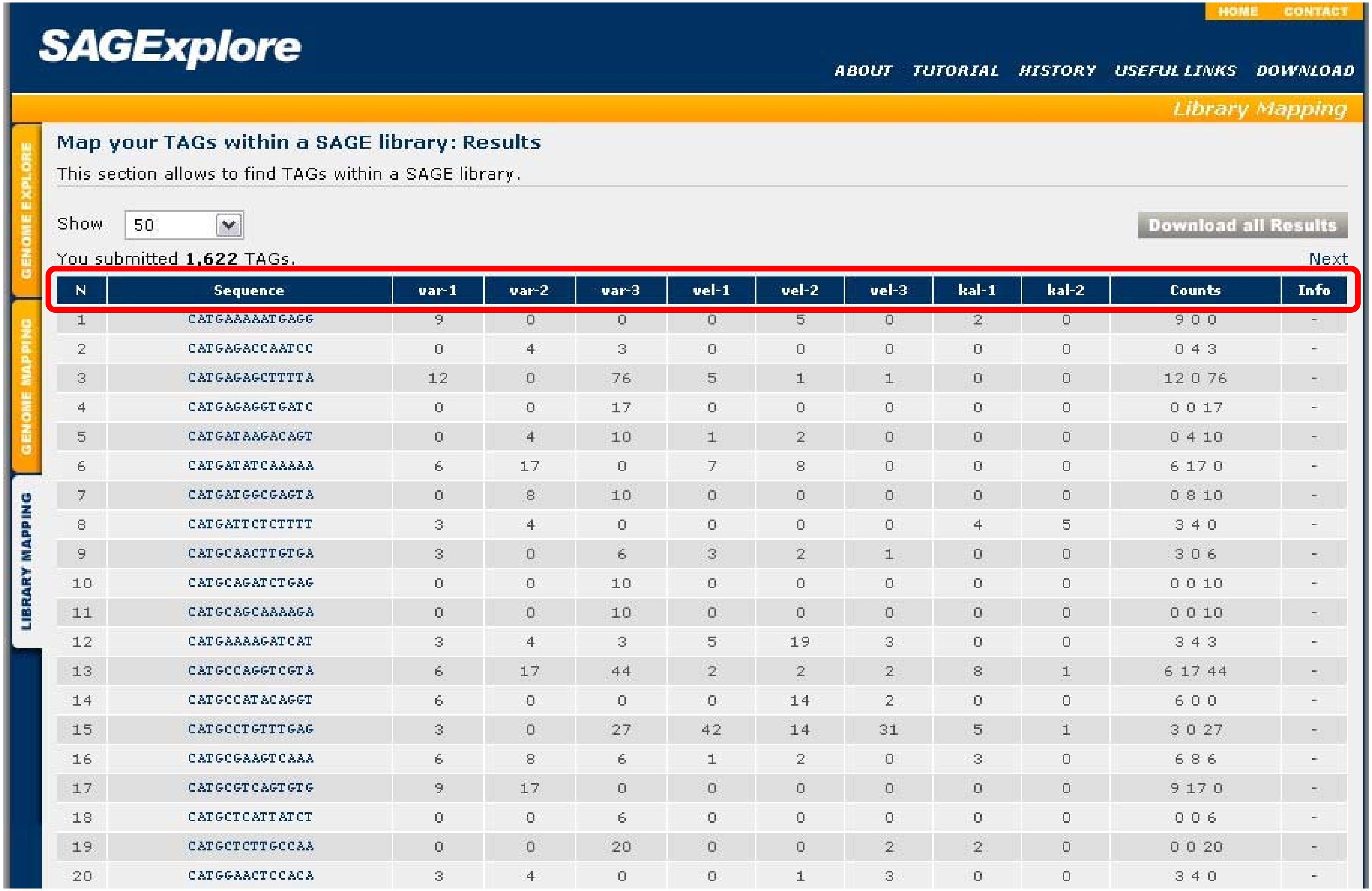
Download All Results

SAGEXPLORE-1273507-2006-May-18.tar.gz

Note: This file will stay at this site for 5 hrs.

N	Seque									Counts	Info
1	CATGAAAA									9 0 0	-
2	CATGAGAC									0 4 3	-
3	CATGAGAG									12 0 76	-
4	CATGAGAG									0 0 17	-
5	CATGATAA									0 4 10	-
6	CATGATAT									6 17 0	-
7	CATGATGG									0 8 10	-
8	CATGATTC									3 4 0	-
9	CATGCAAC									3 0 6	-
10	CATGCAGA									0 0 10	-
11	CATGCAGCAAAAGA	0	0	10	0	0	0	0	0	0 0 10	-
12	CATGAAAAGATCAT	3	4	3	5	19	3	0	0	3 4 3	-
13	CATGCCAGGTCGTA	6	17	44	2	2	2	8	1	6 17 44	-
14	CATGCCATACAGGT	6	0	0	0	14	2	0	0	6 0 0	-
15	CATGCCTGTTTGAG	3	0	27	42	14	31	5	1	3 0 27	-
16	CATGCGAAGTCAAA	6	8	6	1	2	0	3	0	6 8 6	-
17	CATGCGTCAGTGTG	9	17	0	0	0	0	0	0	9 17 0	-
18	CATGCTCATTATCT	0	0	6	0	0	0	0	0	0 0 6	-
19	CATGCTCTTGCCAA	0	0	20	0	0	2	2	0	0 0 20	-
20	CATGGAACTCCACA	3	4	0	0	1	3	0	0	3 4 0	-

Query Results: Compressed files for download are kept for 5 hours at the server and then deleted. By clicking on the filename, the file is downloaded.



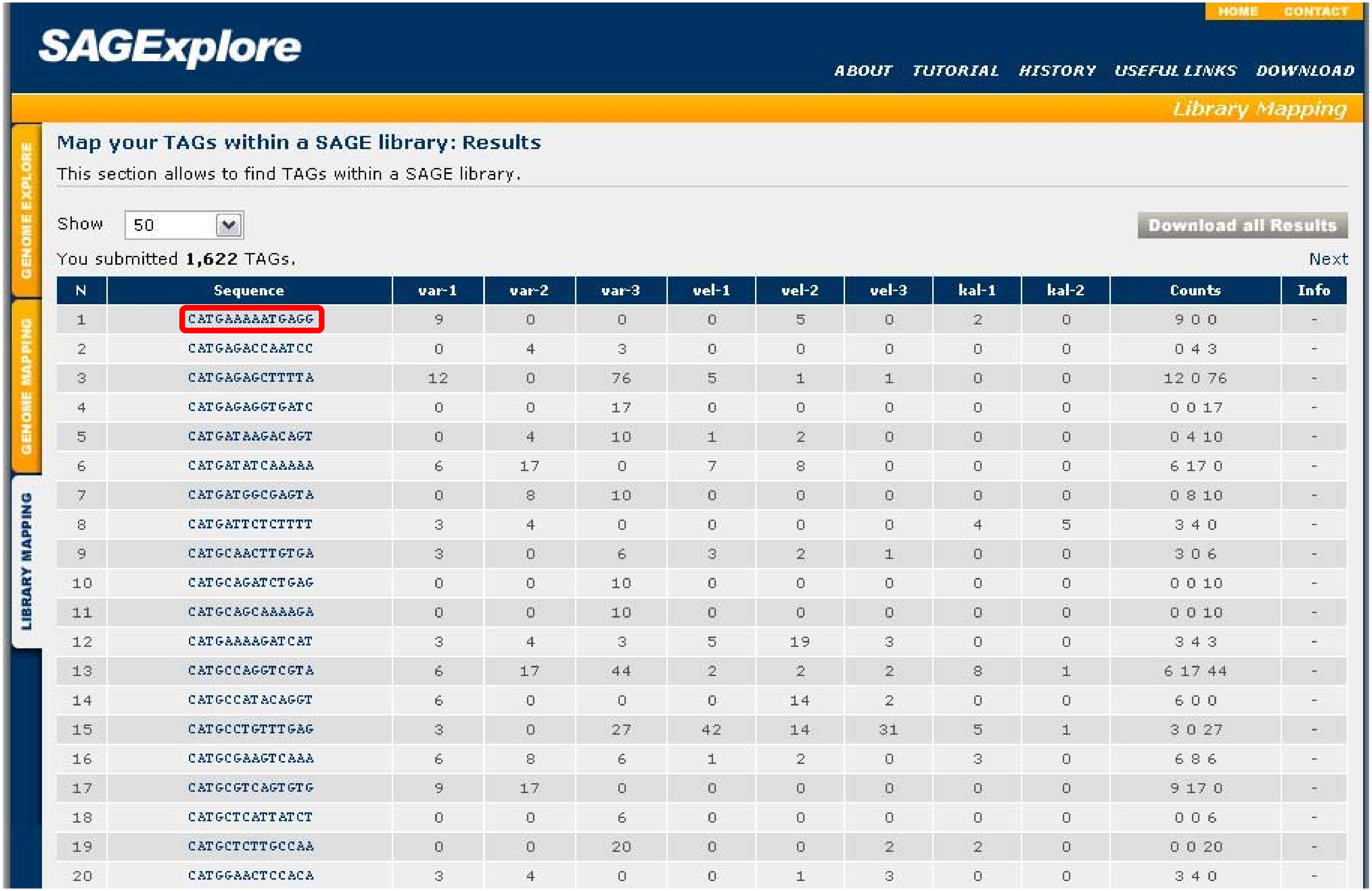
Map your TAGs within a SAGE library: Results

This section allows to find TAGs within a SAGE library.

You submitted **1,622** TAGs.

N	Sequence	var-1	var-2	var-3	vel-1	vel-2	vel-3	kal-1	kal-2	Counts	Info
1	CATGAAAAATGAGG	9	0	0	0	5	0	2	0	9 0 0	-
2	CATGAGACCAATCC	0	4	3	0	0	0	0	0	0 4 3	-
3	CATGAGAGCTTTTA	12	0	76	5	1	1	0	0	12 0 76	-
4	CATGAGAGGTGATC	0	0	17	0	0	0	0	0	0 0 17	-
5	CATGATAAGACAGT	0	4	10	1	2	0	0	0	0 4 10	-
6	CATGATATCAAAAA	6	17	0	7	8	0	0	0	6 17 0	-
7	CATGATGGCGAGTA	0	8	10	0	0	0	0	0	0 8 10	-
8	CATGATTCTCTTTT	3	4	0	0	0	0	4	5	3 4 0	-
9	CATGCAACTTGTGA	3	0	6	3	2	1	0	0	3 0 6	-
10	CATGCAGATCTGAG	0	0	10	0	0	0	0	0	0 0 10	-
11	CATGCAGCAAAAGA	0	0	10	0	0	0	0	0	0 0 10	-
12	CATGAAAAGATCAT	3	4	3	5	19	3	0	0	3 4 3	-
13	CATGCCAGGTCGTA	6	17	44	2	2	2	8	1	6 17 44	-
14	CATGCCATACAGGT	6	0	0	0	14	2	0	0	6 0 0	-
15	CATGCCTGTTTGAG	3	0	27	42	14	31	5	1	3 0 27	-
16	CATGCGAAGTCAAA	6	8	6	1	2	0	3	0	6 8 6	-
17	CATGCGTCAGTGTG	9	17	0	0	0	0	0	0	9 17 0	-
18	CATGCTCATTATCT	0	0	6	0	0	0	0	0	0 0 6	-
19	CATGCTCTTGCCAA	0	0	20	0	0	2	2	0	0 0 20	-
20	CATGGAACTCCACA	3	4	0	0	1	3	0	0	3 4 0	-

Query Results: Online help explaining the meaning of each column is obtained by left-clicking with the mouse over the column headers.



Map your TAGs within a SAGE library: Results

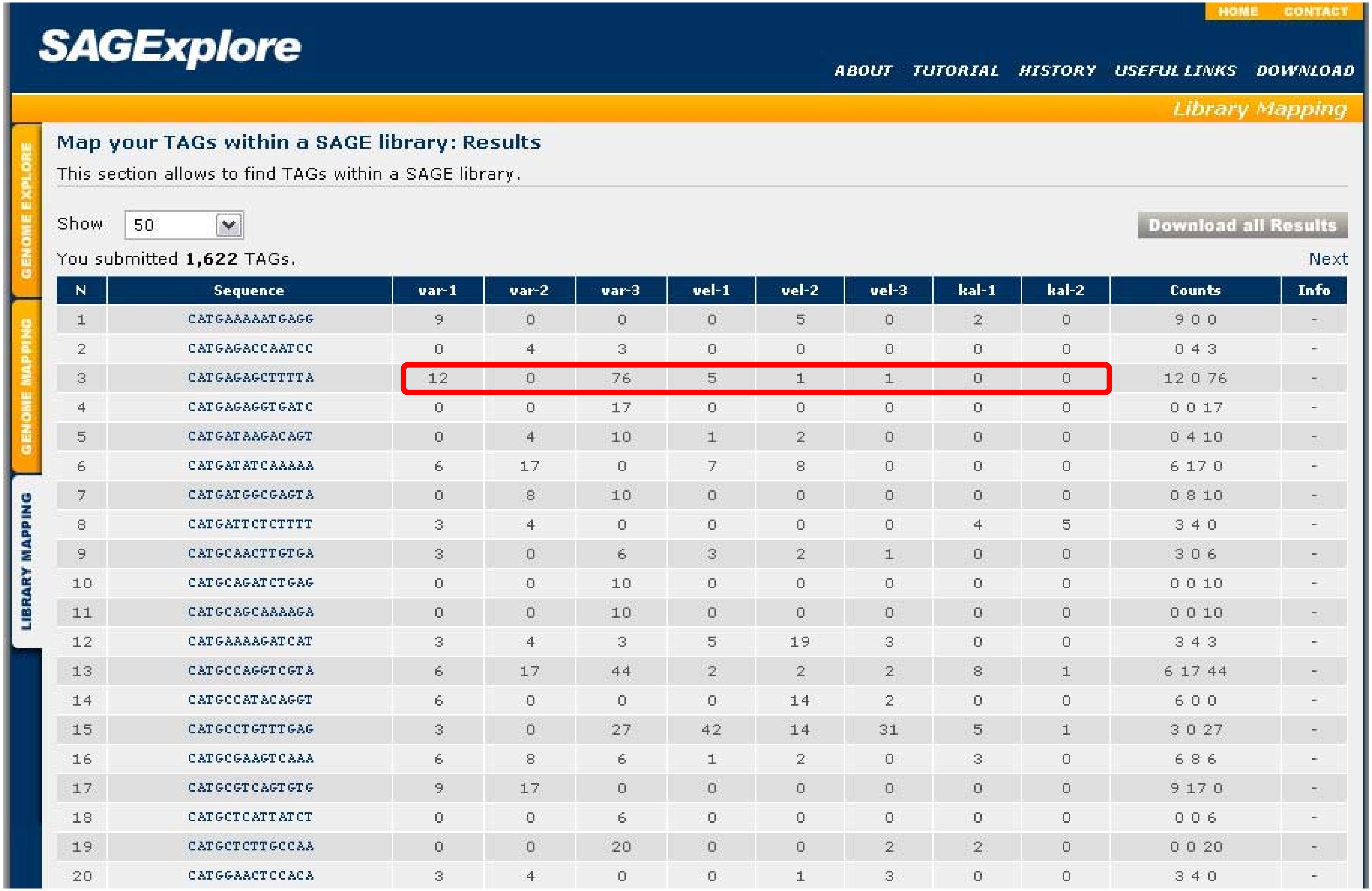
This section allows to find TAGs within a SAGE library.

Show 50

You submitted **1,622** TAGs.

N	Sequence	var-1	var-2	var-3	vel-1	vel-2	vel-3	kal-1	kal-2	Counts	Info
1	CATGAAAAATGAGG	9	0	0	0	5	0	2	0	9 0 0	-
2	CATGAGACCAATCC	0	4	3	0	0	0	0	0	0 4 3	-
3	CATGAGAGCTTTTA	12	0	76	5	1	1	0	0	12 0 76	-
4	CATGAGAGGTGATC	0	0	17	0	0	0	0	0	0 0 17	-
5	CATGATAAGACAGT	0	4	10	1	2	0	0	0	0 4 10	-
6	CATGATATCAAAAA	6	17	0	7	8	0	0	0	6 17 0	-
7	CATGATGGCGAGTA	0	8	10	0	0	0	0	0	0 8 10	-
8	CATGATTCTCTTTT	3	4	0	0	0	0	4	5	3 4 0	-
9	CATGCAACTTGTGA	3	0	6	3	2	1	0	0	3 0 6	-
10	CATGCAGATCTGAG	0	0	10	0	0	0	0	0	0 0 10	-
11	CATGCAGCAAAAGA	0	0	10	0	0	0	0	0	0 0 10	-
12	CATGAAAAGATCAT	3	4	3	5	19	3	0	0	3 4 3	-
13	CATGCCAGGTCGTA	6	17	44	2	2	2	8	1	6 17 44	-
14	CATGCCATACAGGT	6	0	0	0	14	2	0	0	6 0 0	-
15	CATGCCTGTTTGAG	3	0	27	42	14	31	5	1	3 0 27	-
16	CATGCGAAGTCAAA	6	8	6	1	2	0	3	0	6 8 6	-
17	CATGCGTCAGTGTG	9	17	0	0	0	0	0	0	9 17 0	-
18	CATGCTCATTATCT	0	0	6	0	0	0	0	0	0 0 6	-
19	CATGCTCTTGCCAA	0	0	20	0	0	2	2	0	0 0 20	-
20	CATGGAACTCCACA	3	4	0	0	1	3	0	0	3 4 0	-

Query Results: By clicking on the tag sequence, a query with this tag sequence against the genome is carried out (ie. the Genome Mapping Module is invoked). The results displayed correspond to the same described previously for that module.



Map your TAGs within a SAGE library: Results

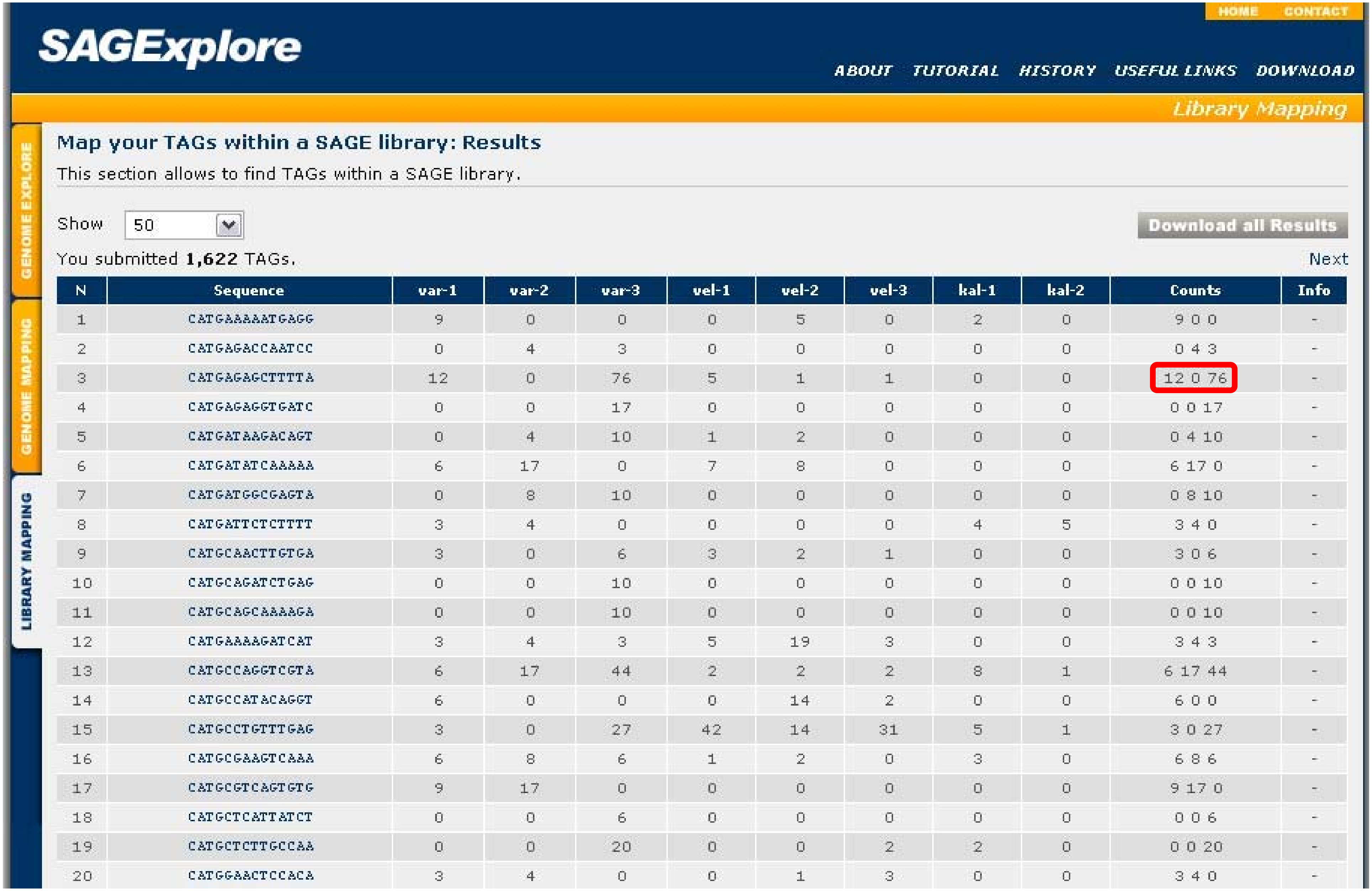
This section allows to find TAGs within a SAGE library.

Show 50

You submitted **1,622** TAGs.

N	Sequence	var-1	var-2	var-3	vel-1	vel-2	vel-3	kal-1	kal-2	Counts	Info
1	CATGAAAAATGAGG	9	0	0	0	5	0	2	0	9 0 0	-
2	CATGAGACCAATCC	0	4	3	0	0	0	0	0	0 4 3	-
3	CATGAGAGCTTTTA	12	0	76	5	1	1	0	0	12 0 76	-
4	CATGAGAGGTGATC	0	0	17	0	0	0	0	0	0 0 17	-
5	CATGATAAGACAGT	0	4	10	1	2	0	0	0	0 4 10	-
6	CATGATATCAAAAA	6	17	0	7	8	0	0	0	6 17 0	-
7	CATGATGGCGAGTA	0	8	10	0	0	0	0	0	0 8 10	-
8	CATGATTCTCTTTT	3	4	0	0	0	0	4	5	3 4 0	-
9	CATGCAACTTGTGA	3	0	6	3	2	1	0	0	3 0 6	-
10	CATGCAGATCTGAG	0	0	10	0	0	0	0	0	0 0 10	-
11	CATGCAGCAAAAGA	0	0	10	0	0	0	0	0	0 0 10	-
12	CATGAAAAGATCAT	3	4	3	5	19	3	0	0	3 4 3	-
13	CATGCCAGGTCGTA	6	17	44	2	2	2	8	1	6 17 44	-
14	CATGCCATACAGGT	6	0	0	0	14	2	0	0	6 0 0	-
15	CATGCCTGTTTGAG	3	0	27	42	14	31	5	1	3 0 27	-
16	CATGCGAAGTCAAA	6	8	6	1	2	0	3	0	6 8 6	-
17	CATGCGTCAGTGTG	9	17	0	0	0	0	0	0	9 17 0	-
18	CATGCTCATTATCT	0	0	6	0	0	0	0	0	0 0 6	-
19	CATGCTCTTGCCAA	0	0	20	0	0	2	2	0	0 0 20	-
20	CATGGAACTCCACA	3	4	0	0	1	3	0	0	3 4 0	-

Query Results: The observed counts of this tag for each known experimental library.are displayed. In those cases where a tag does not match any library, the row is highlighted in red color.



Map your TAGs within a SAGE library: Results

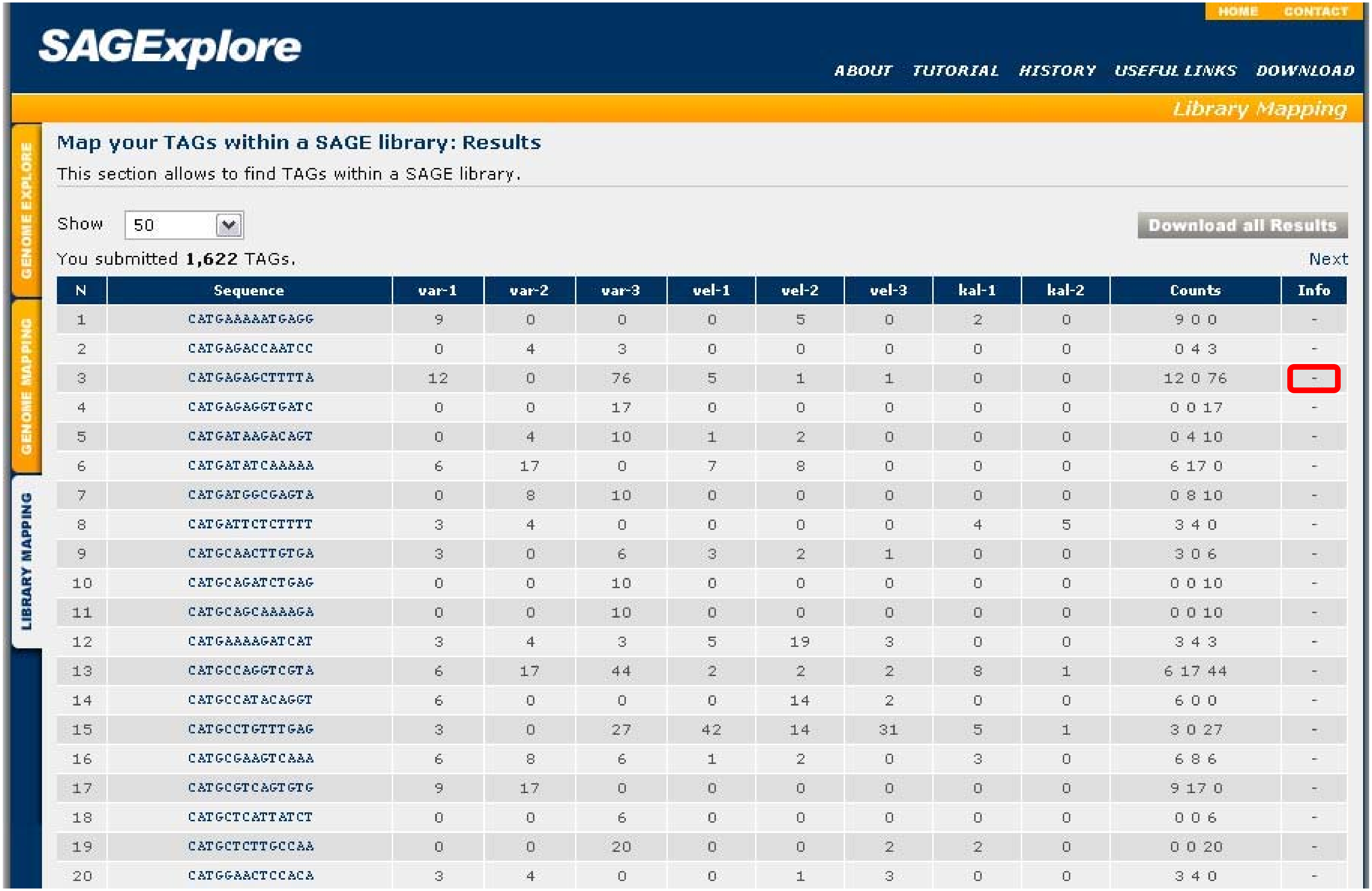
This section allows to find TAGs within a SAGE library.

Show 50

You submitted **1,622** TAGs.

N	Sequence	var-1	var-2	var-3	vel-1	vel-2	vel-3	kal-1	kal-2	Counts	Info
1	CATGAAAAATGAGG	9	0	0	0	5	0	2	0	9 0 0	-
2	CATGAGACCAATCC	0	4	3	0	0	0	0	0	0 4 3	-
3	CATGAGAGCTTTTA	12	0	76	5	1	1	0	0	12 0 76	-
4	CATGAGAGGTGATC	0	0	17	0	0	0	0	0	0 0 17	-
5	CATGATAAGACAGT	0	4	10	1	2	0	0	0	0 4 10	-
6	CATGATATCAAAAA	6	17	0	7	8	0	0	0	6 17 0	-
7	CATGATGGCGAGTA	0	8	10	0	0	0	0	0	0 8 10	-
8	CATGATTCTCTTTT	3	4	0	0	0	0	4	5	3 4 0	-
9	CATGCAACTTGTGA	3	0	6	3	2	1	0	0	3 0 6	-
10	CATGCAGATCTGAG	0	0	10	0	0	0	0	0	0 0 10	-
11	CATGCAGCAAAAGA	0	0	10	0	0	0	0	0	0 0 10	-
12	CATGAAAAGATCAT	3	4	3	5	19	3	0	0	3 4 3	-
13	CATGCCAGGTCGTA	6	17	44	2	2	2	8	1	6 17 44	-
14	CATGCCATACAGGT	6	0	0	0	14	2	0	0	6 0 0	-
15	CATGCCTGTTTGAG	3	0	27	42	14	31	5	1	3 0 27	-
16	CATGCGAAGTCAAA	6	8	6	1	2	0	3	0	6 8 6	-
17	CATGCGTCAGTGTG	9	17	0	0	0	0	0	0	9 17 0	-
18	CATGCTCATTATCT	0	0	6	0	0	0	0	0	0 0 6	-
19	CATGCTCTTGCCAA	0	0	20	0	0	2	2	0	0 0 20	-
20	CATGGAACTCCACA	3	4	0	0	1	3	0	0	3 4 0	-

Query Results: The observed counts of this tag provided by the user are shown in this field.



Map your TAGs within a SAGE library: Results

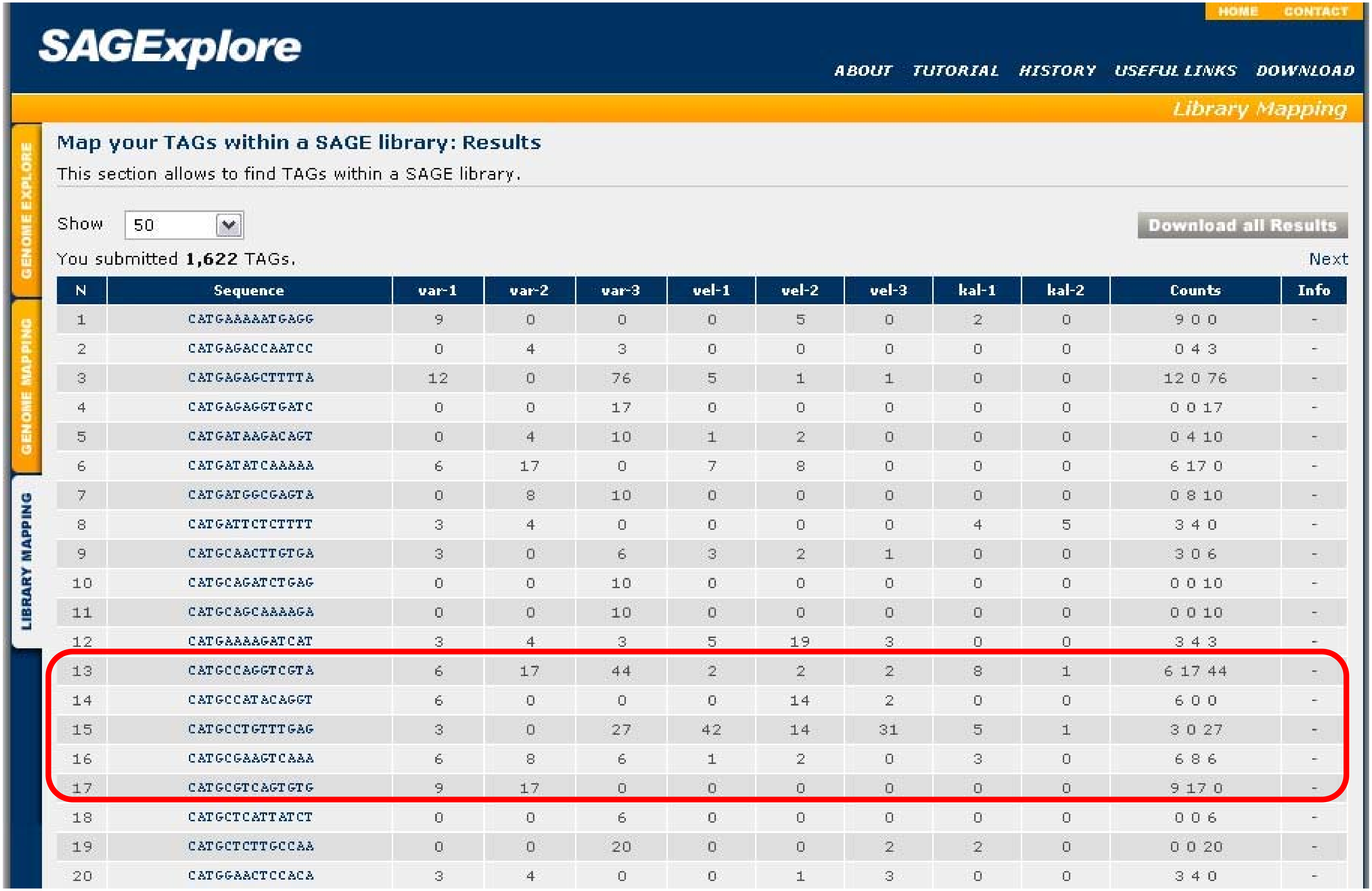
This section allows to find TAGs within a SAGE library.

Show: 50

You submitted **1,622** TAGs.

N	Sequence	var-1	var-2	var-3	vel-1	vel-2	vel-3	kal-1	kal-2	Counts	Info
1	CATGAAAAATGAGG	9	0	0	0	5	0	2	0	9 0 0	-
2	CATGAGACCAATCC	0	4	3	0	0	0	0	0	0 4 3	-
3	CATGAGAGCTTTTA	12	0	76	5	1	1	0	0	12 0 76	-
4	CATGAGAGGTGATC	0	0	17	0	0	0	0	0	0 0 17	-
5	CATGATAAGACAGT	0	4	10	1	2	0	0	0	0 4 10	-
6	CATGATATCAAAAA	6	17	0	7	8	0	0	0	6 17 0	-
7	CATGATGGCGAGTA	0	8	10	0	0	0	0	0	0 8 10	-
8	CATGATTCTCTTTT	3	4	0	0	0	0	4	5	3 4 0	-
9	CATGCAACTTGTGA	3	0	6	3	2	1	0	0	3 0 6	-
10	CATGCAGATCTGAG	0	0	10	0	0	0	0	0	0 0 10	-
11	CATGCAGCAAAAGA	0	0	10	0	0	0	0	0	0 0 10	-
12	CATGAAAAGATCAT	3	4	3	5	19	3	0	0	3 4 3	-
13	CATGCCAGGTCGTA	6	17	44	2	2	2	8	1	6 17 44	-
14	CATGCCATACAGGT	6	0	0	0	14	2	0	0	6 0 0	-
15	CATGCCTGTTTGAG	3	0	27	42	14	31	5	1	3 0 27	-
16	CATGCGAAGTCAAA	6	8	6	1	2	0	3	0	6 8 6	-
17	CATGCGTCAGTGTG	9	17	0	0	0	0	0	0	9 17 0	-
18	CATGCTCATTATCT	0	0	6	0	0	0	0	0	0 0 6	-
19	CATGCTCTTGCCAA	0	0	20	0	0	2	2	0	0 0 20	-
20	CATGGAACTCCACA	3	4	0	0	1	3	0	0	3 4 0	-

Query Results: A custom label for each tag is displayed here, if it was provided by the user.



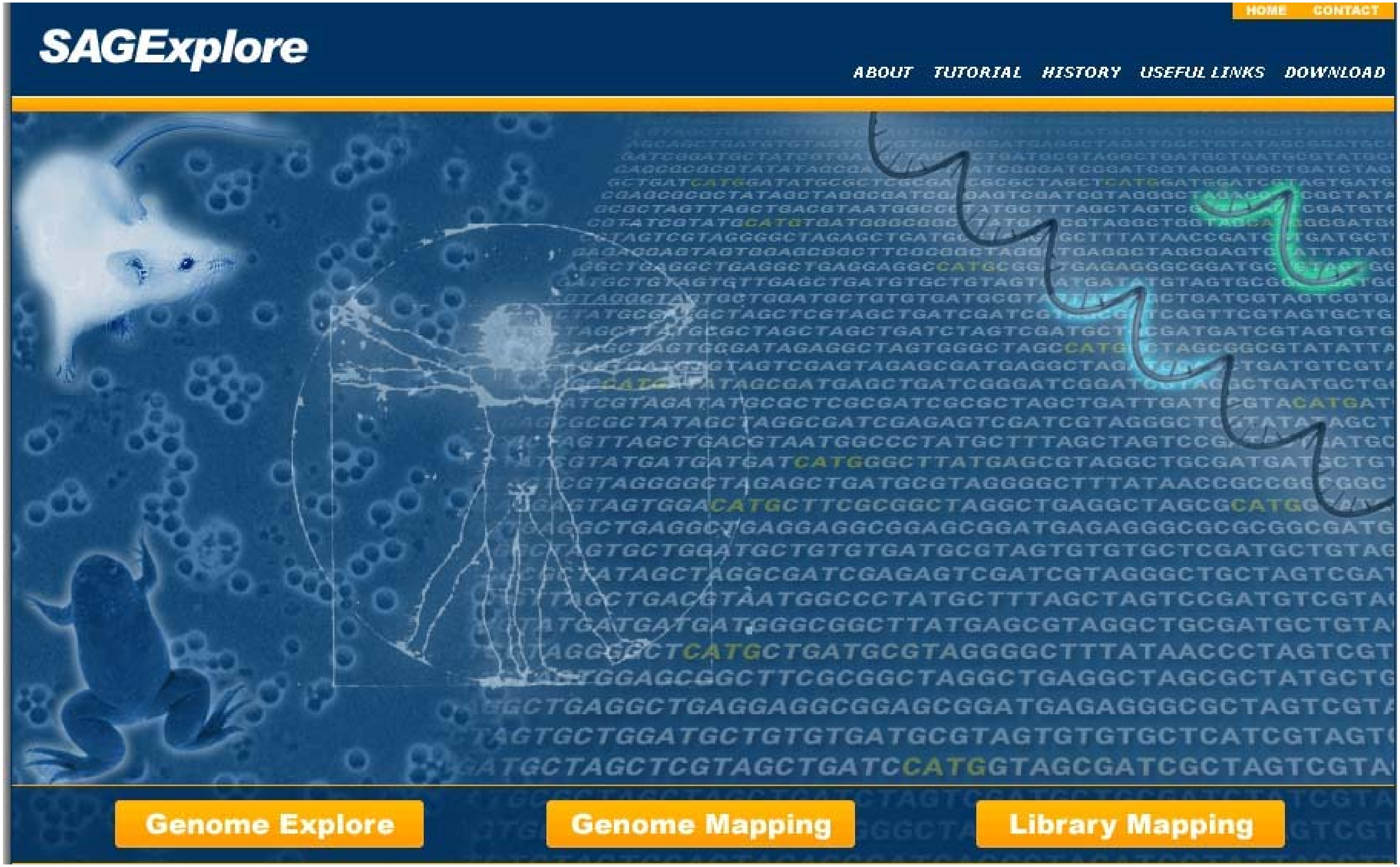
Map your TAGs within a SAGE library: Results

This section allows to find TAGs within a SAGE library.

You submitted **1,622** TAGs.

N	Sequence	var-1	var-2	var-3	vel-1	vel-2	vel-3	kal-1	kal-2	Counts	Info
1	CATGAAAAATGAGG	9	0	0	0	5	0	2	0	9 0 0	-
2	CATGAGACCAATCC	0	4	3	0	0	0	0	0	0 4 3	-
3	CATGAGAGCTTTTA	12	0	76	5	1	1	0	0	12 0 76	-
4	CATGAGAGGTGATC	0	0	17	0	0	0	0	0	0 0 17	-
5	CATGATAAGACAGT	0	4	10	1	2	0	0	0	0 4 10	-
6	CATGATATCAAAAA	6	17	0	7	8	0	0	0	6 17 0	-
7	CATGATGGCGAGTA	0	8	10	0	0	0	0	0	0 8 10	-
8	CATGATTCTCTTTT	3	4	0	0	0	0	4	5	3 4 0	-
9	CATGCAACTTGTGA	3	0	6	3	2	1	0	0	3 0 6	-
10	CATGCAGATCTGAG	0	0	10	0	0	0	0	0	0 0 10	-
11	CATGCAGCAAAAGA	0	0	10	0	0	0	0	0	0 0 10	-
12	CATGAAAAGATCAT	3	4	3	5	19	3	0	0	3 4 3	-
13	CATGCCAGGTCGTA	6	17	44	2	2	2	8	1	6 17 44	-
14	CATGCCATACAGGT	6	0	0	0	14	2	0	0	6 0 0	-
15	CATGCCTGTTTGAG	3	0	27	42	14	31	5	1	3 0 27	-
16	CATGCGAAGTCAAA	6	8	6	1	2	0	3	0	6 8 6	-
17	CATGCGTCAGTGTG	9	17	0	0	0	0	0	0	9 17 0	-
18	CATGCTCATTATCT	0	0	6	0	0	0	0	0	0 0 6	-
19	CATGCTCTTGCCAA	0	0	20	0	0	2	2	0	0 0 20	-
20	CATGGAACTCCACA	3	4	0	0	1	3	0	0	3 4 0	-

Query Results: The tags that did not match any known tag in the libraries are highlighted in red. These tags could represent unknown genes.



This is the end of the SAGExplore web server tutorial
Any comments or inquiries, please contact us