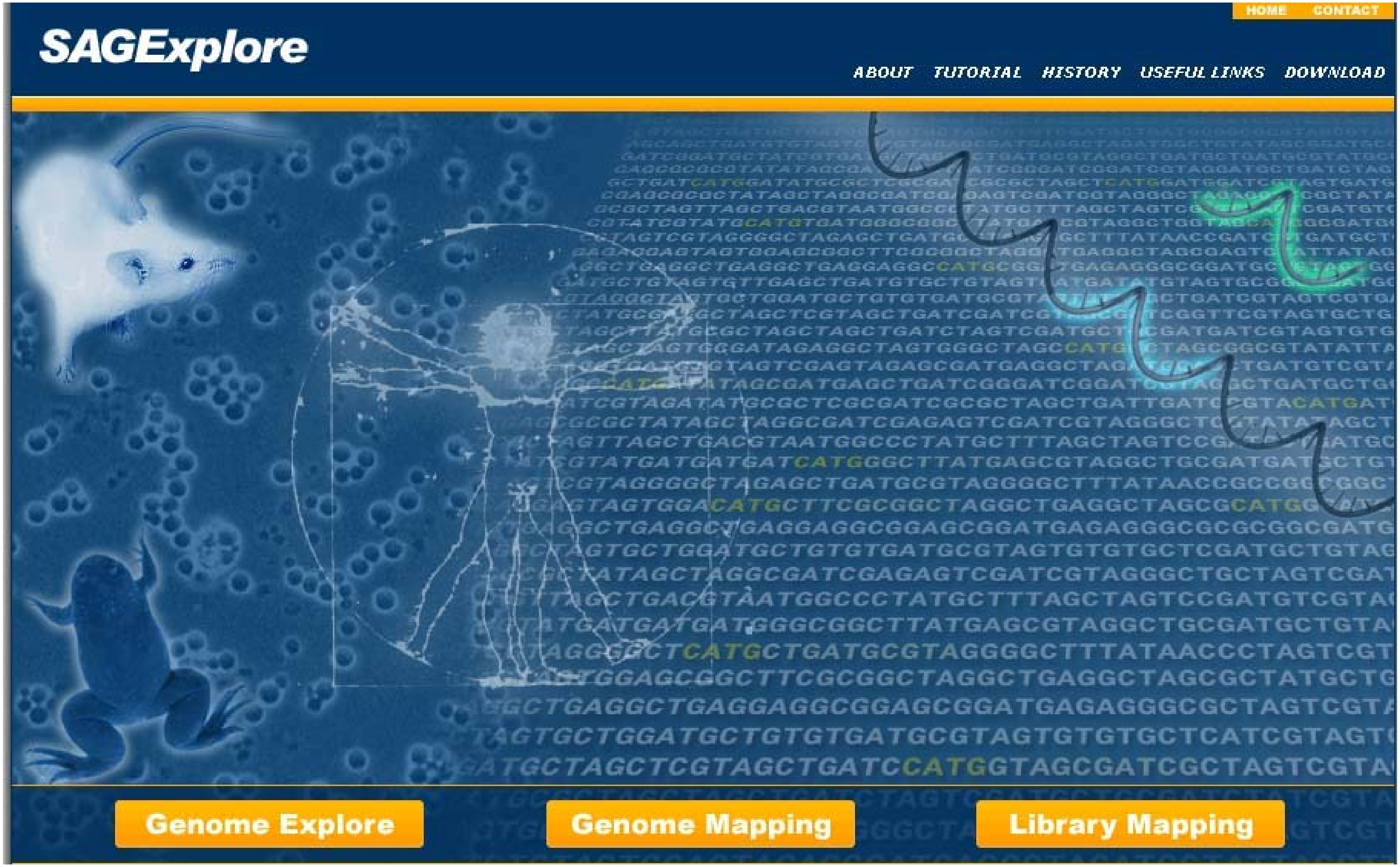
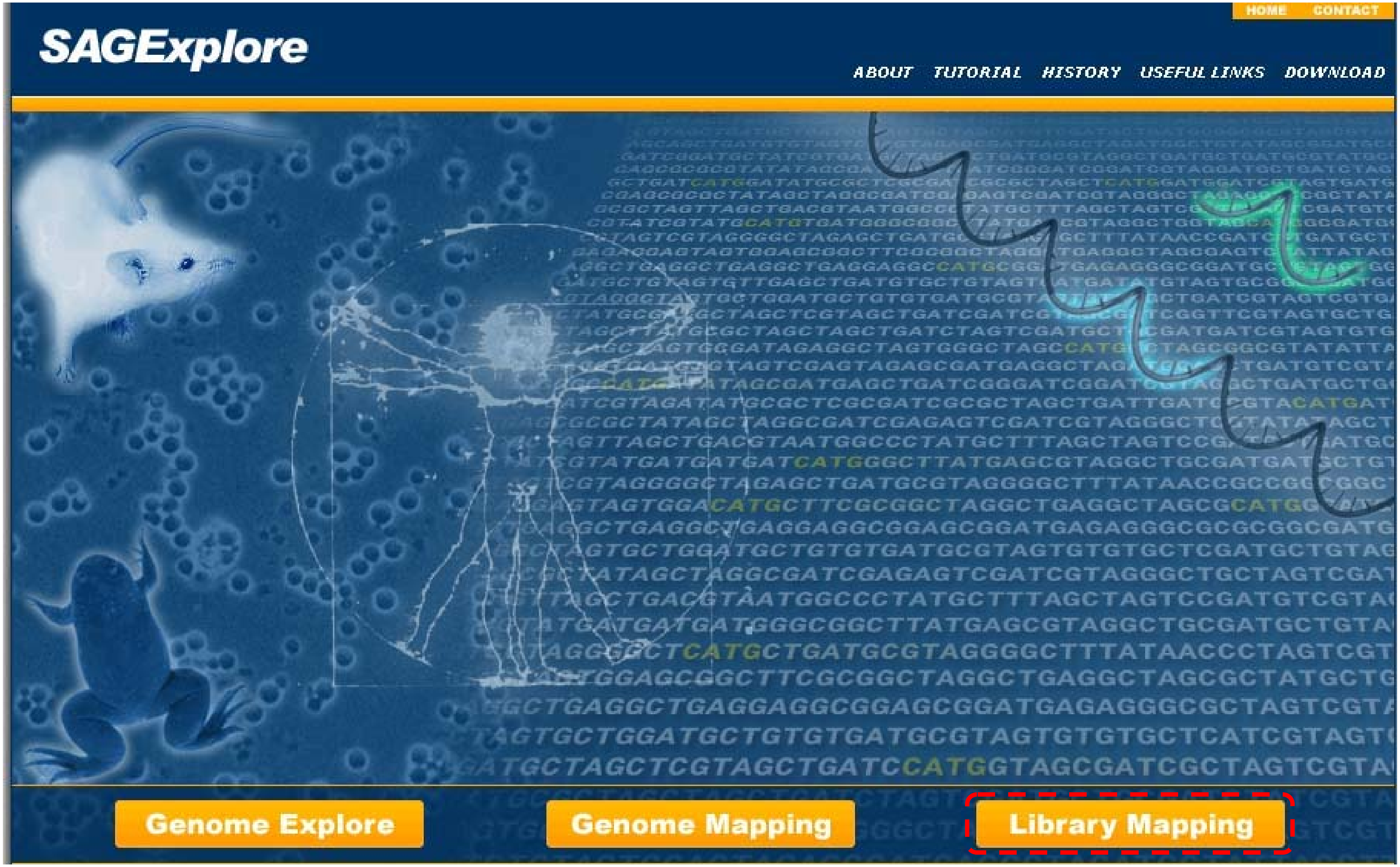
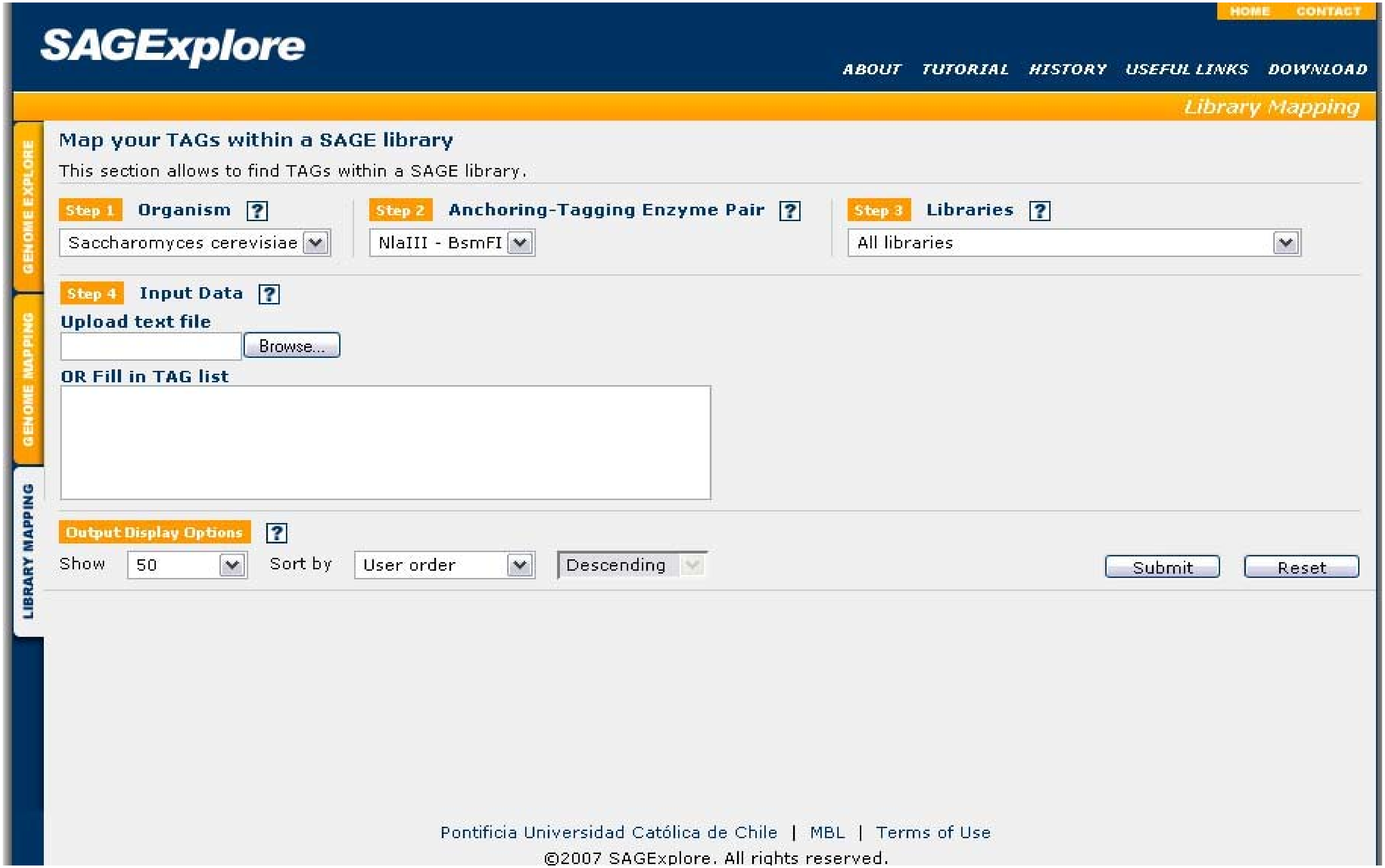


SAGExplore web server tutorial for Module III: Library Mapping



III.- Library Mapping Module:

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



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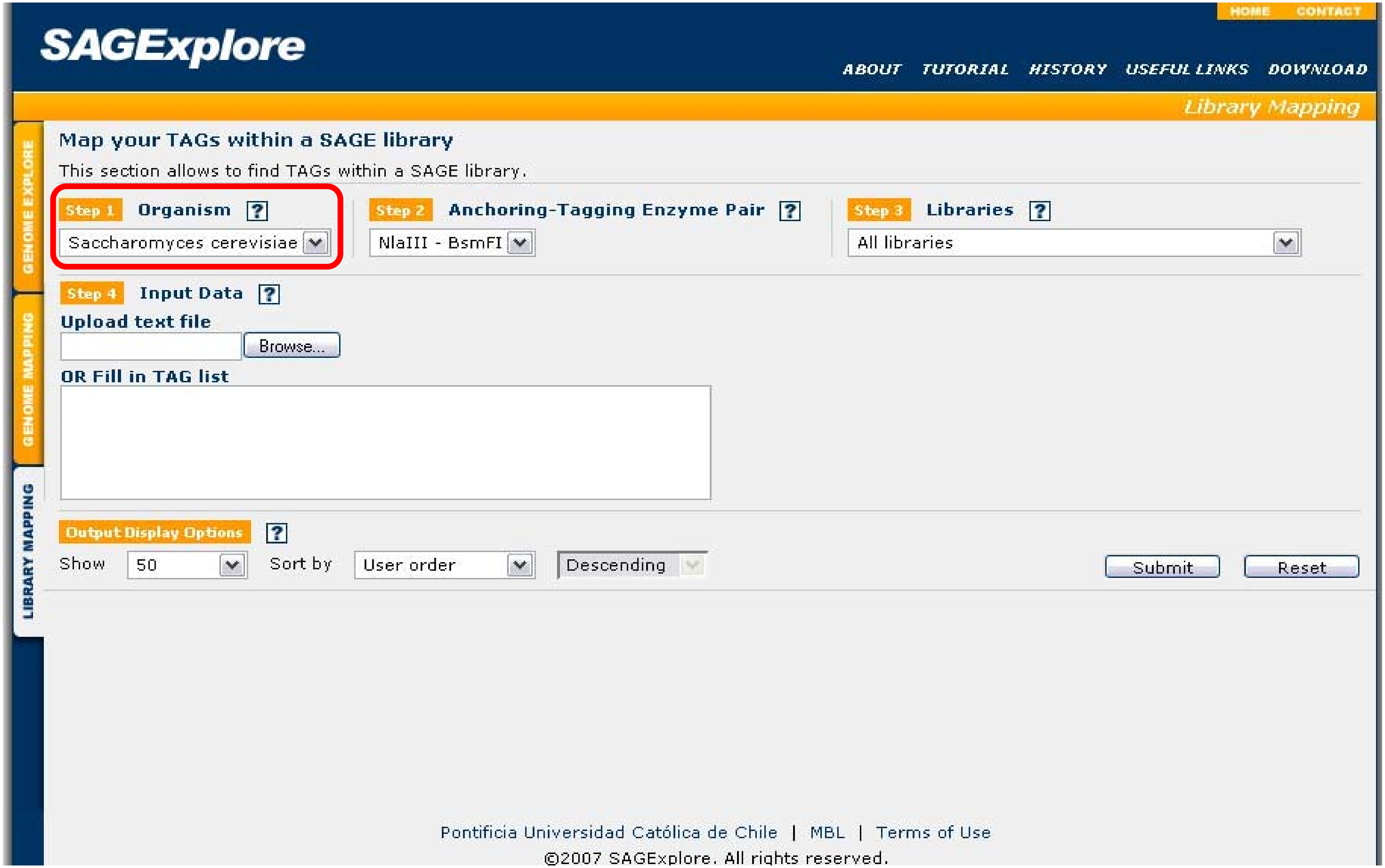
III.- Library Mapping Module Form: The user must follow four sequential steps in this form. Online help with the relevant details is provided for each step.



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

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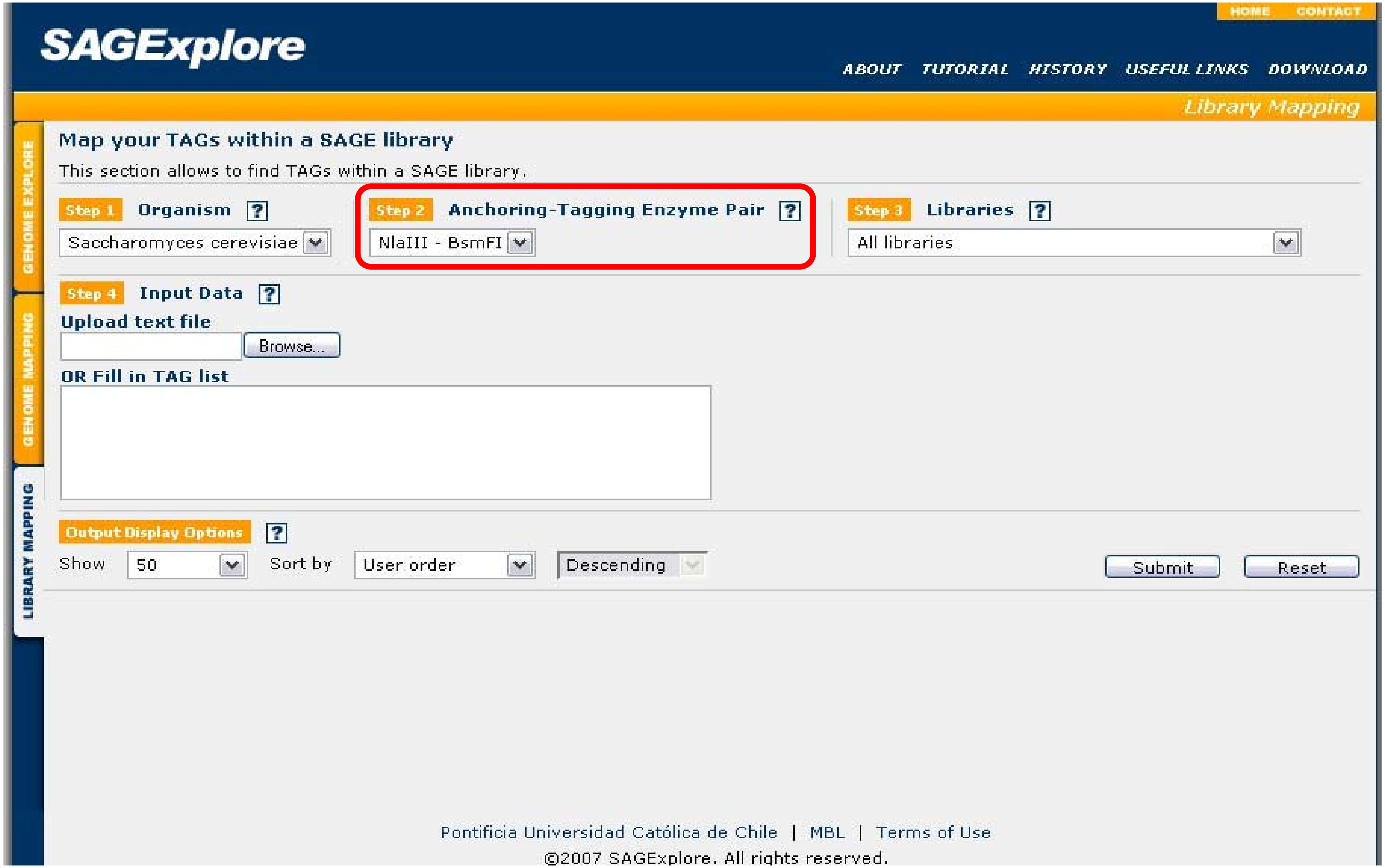
Step 1: The user must select the organism of interest. Currently, only *Saccharomyces cerevisiae* is available. In the near future, other organisms will be added.



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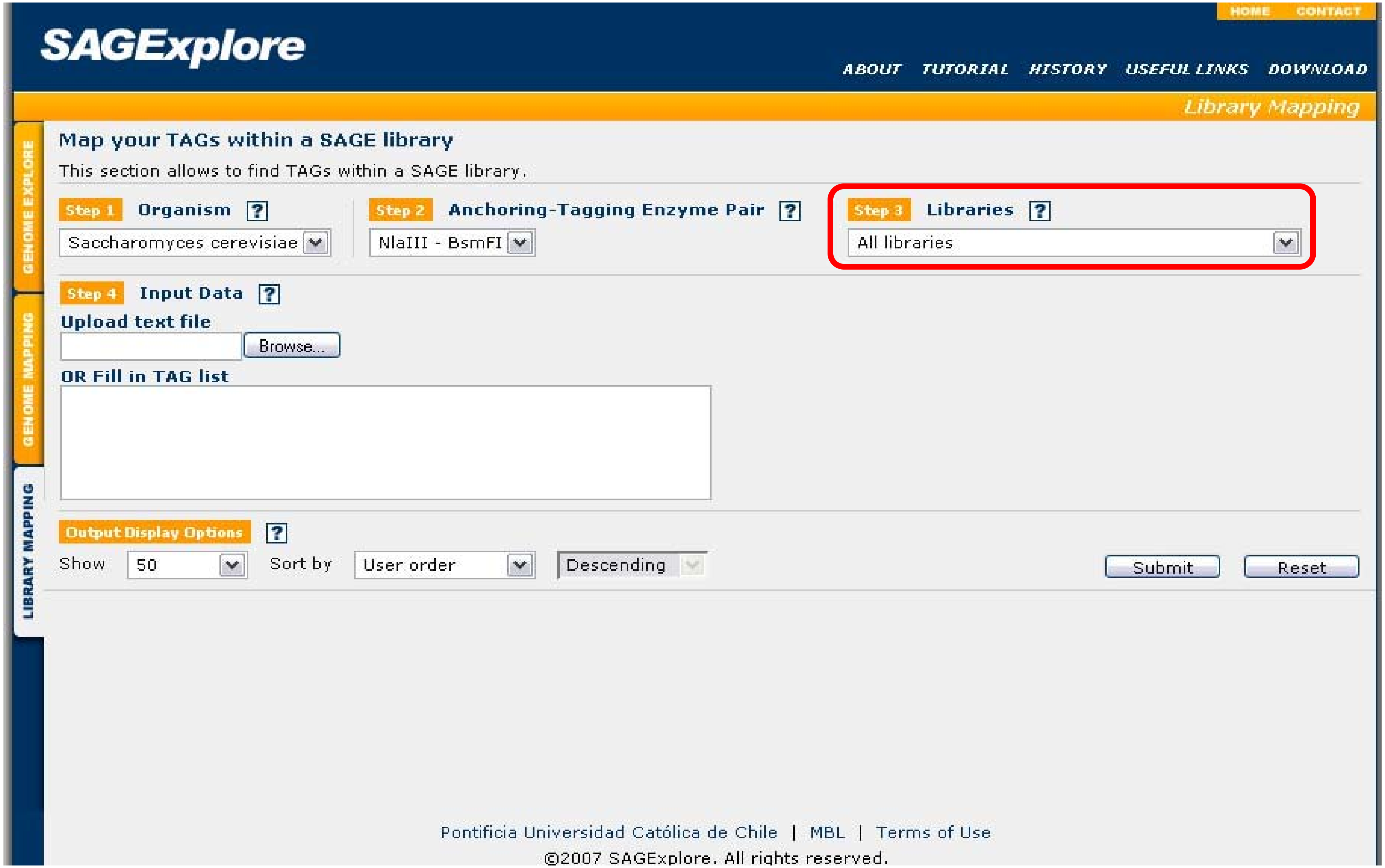
Step 2: The user must select the anchoring-tagging enzyme pair used in SAGE. Currently, only the pair NlaIII-BsmFI is available. In the near future, other enzyme pairs such as the one used in Long-SAGE will be added.



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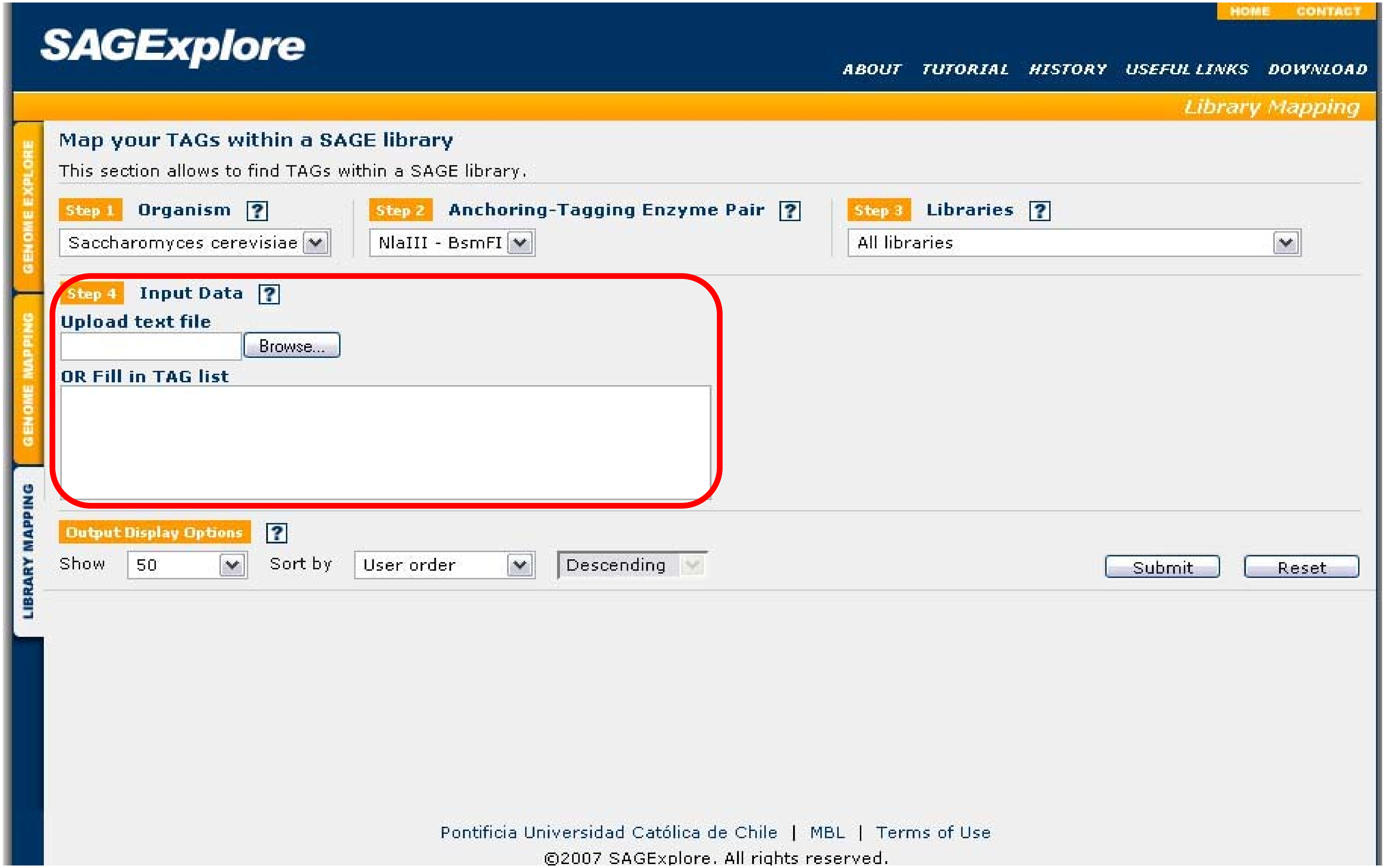
Step 3: The user must select an experimental library of SAGE tags. By default, all libraries will be selected. In the case of Saccharomyces cerevisiae, eight independent libraries have been reported and are included in the server.



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

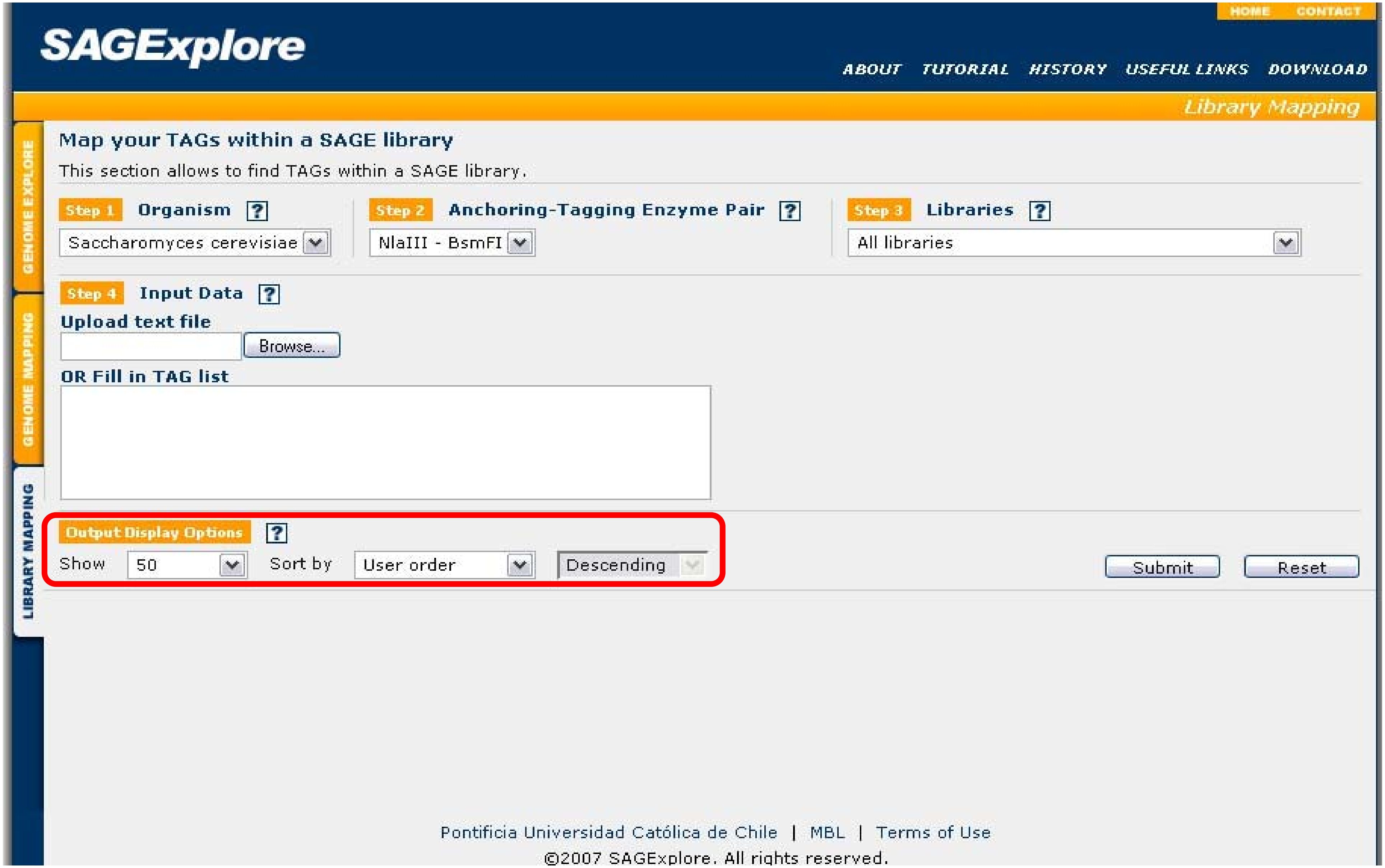
Output Display Options

Show: 50

Sort by: User order

Descending

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 sequences must be provided (ie. including the CATG sequence 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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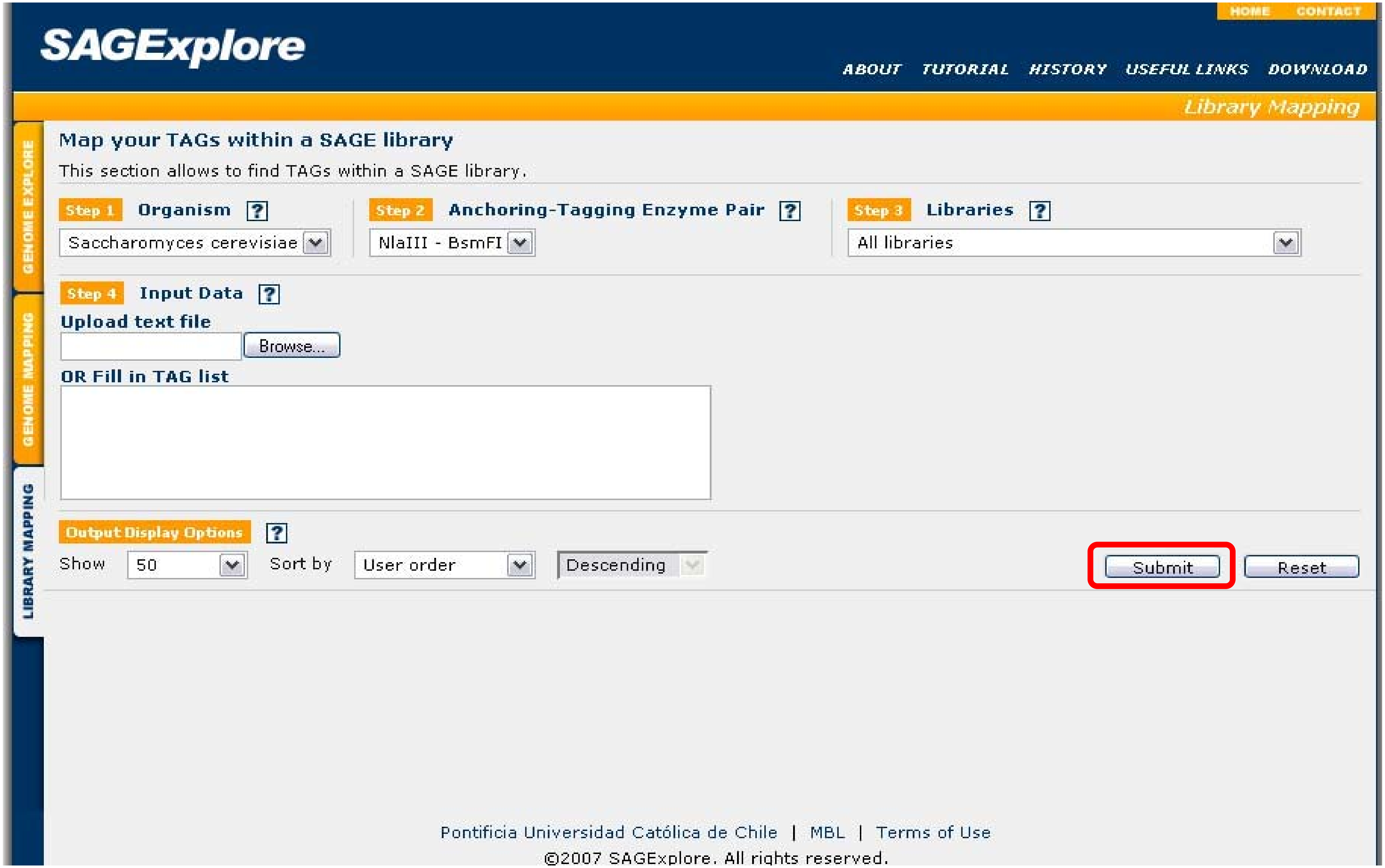
Pre-submit: Before submitting the query, the user can choose the number of rows to display per page and also how to sort the results.



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

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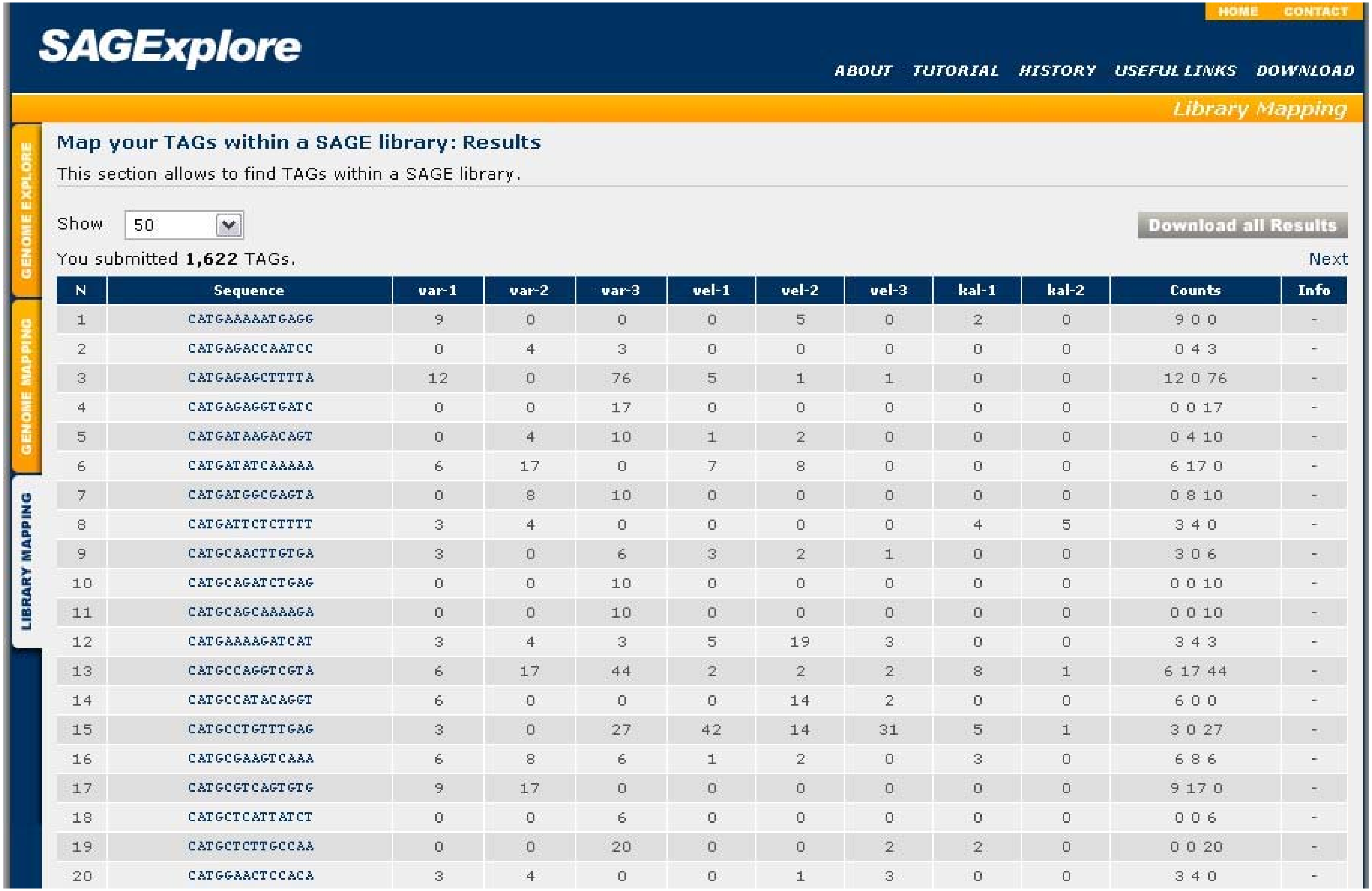
Submit: The user is ready to submit the query to the server.



Map your TAGs within a SAGE library: Results

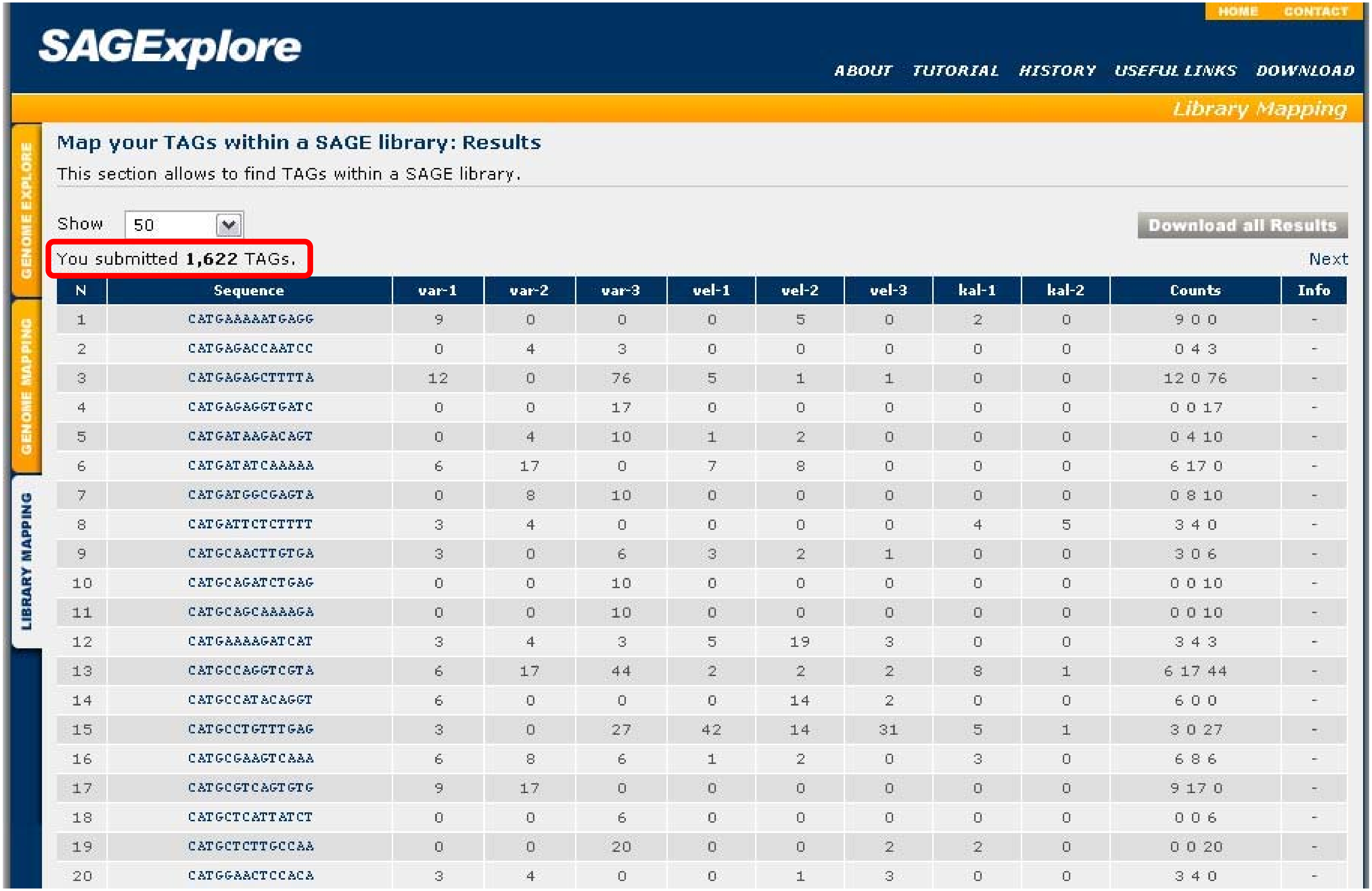
This section allows to find TAGs within a SAGE library.

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: Typical output of the Library Mapping Form.



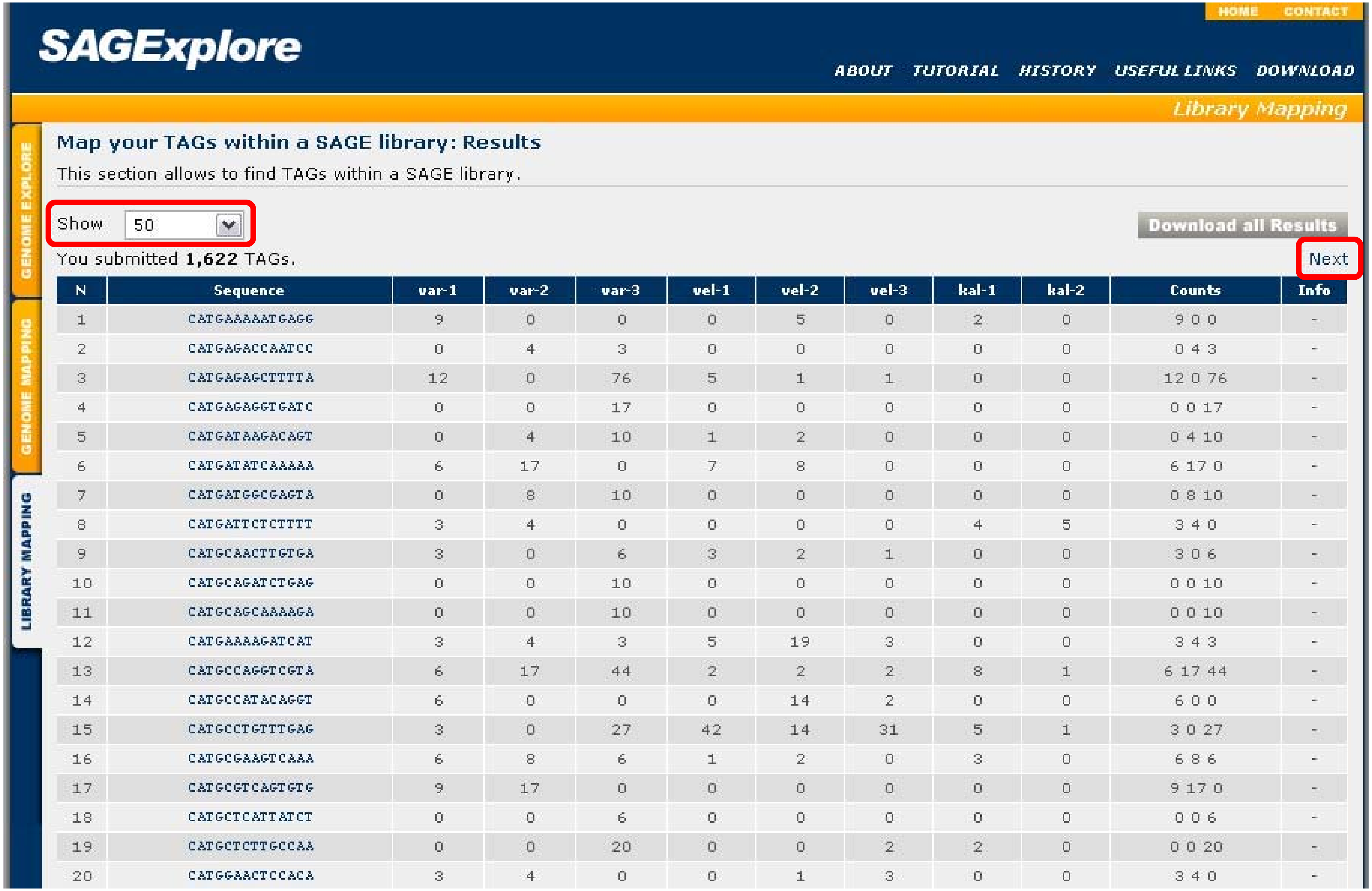
Map your TAGs within a SAGE library: Results

This section allows to find TAGs within a SAGE library.

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.



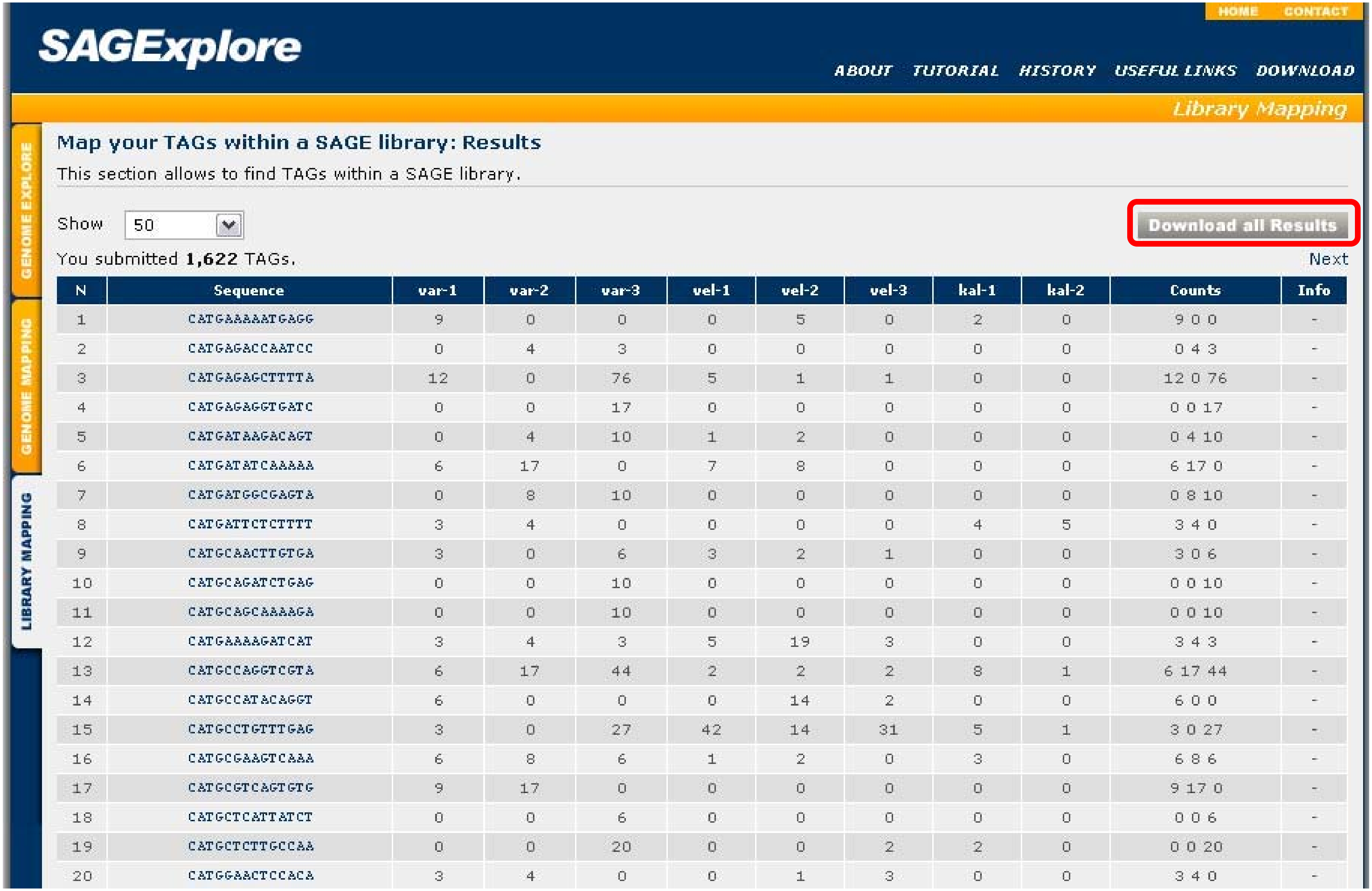
Map your TAGs within a SAGE library: Results

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

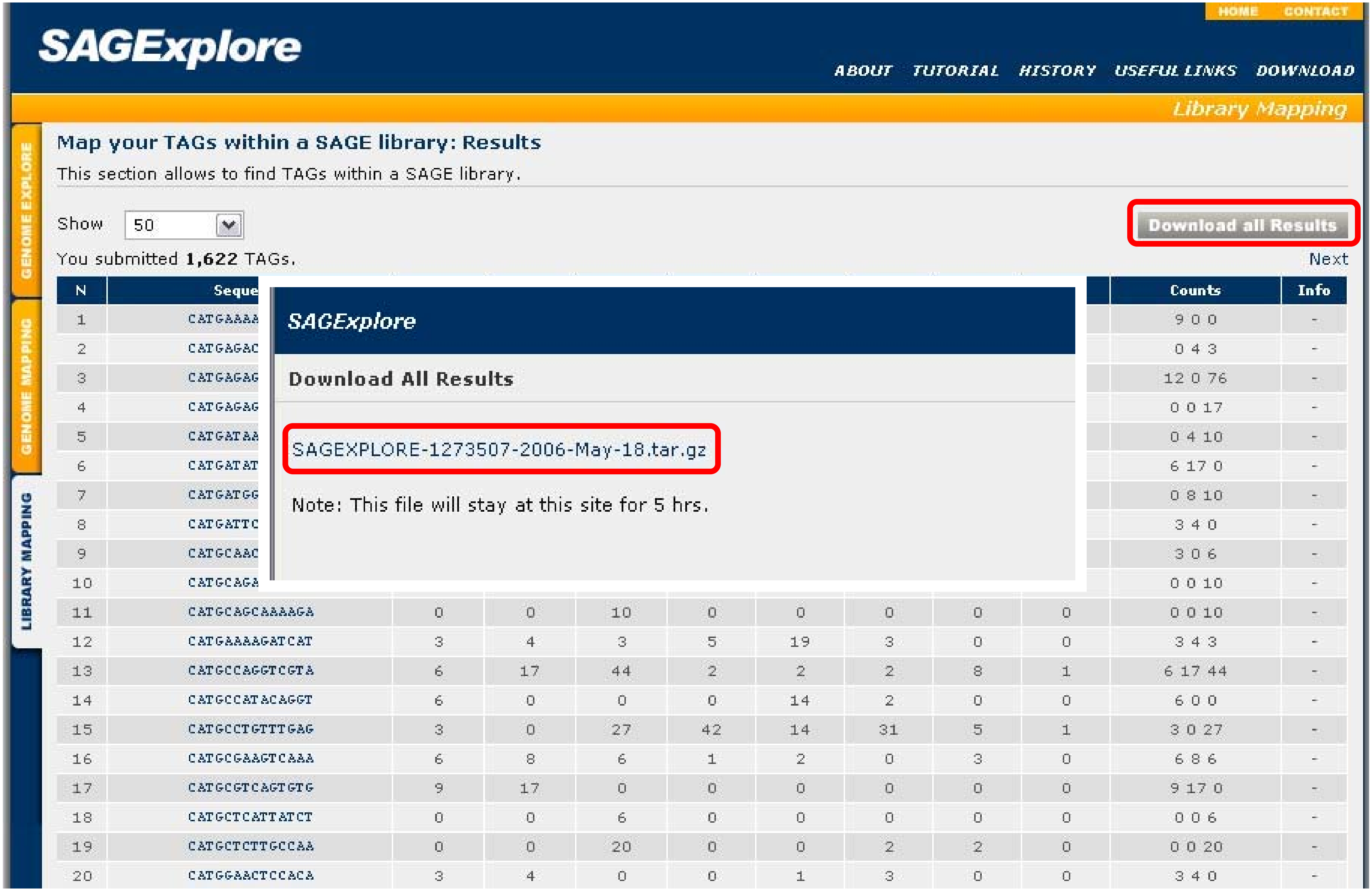
This section allows to find TAGs within a SAGE library.

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 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

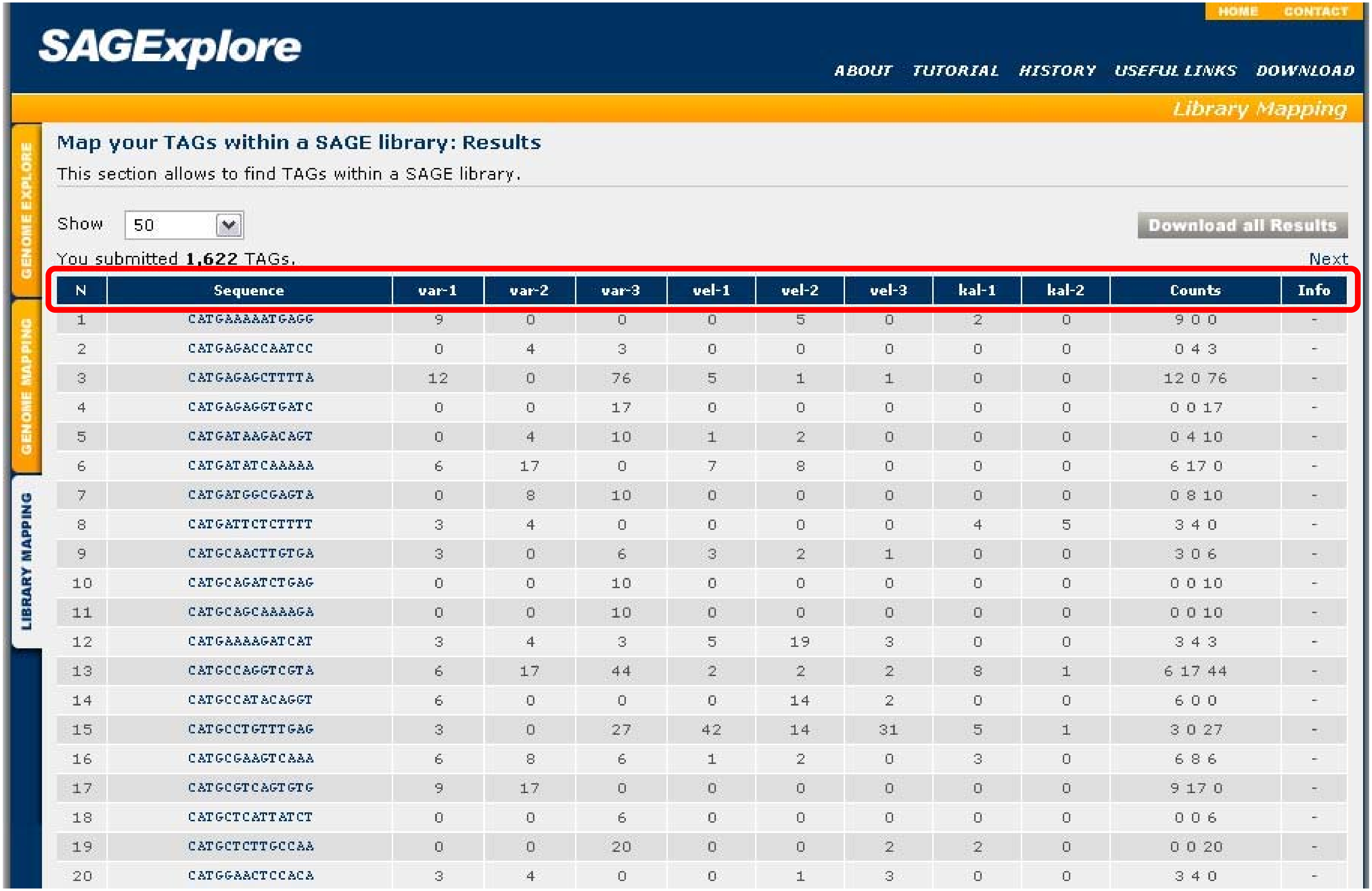
Download All Results

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.



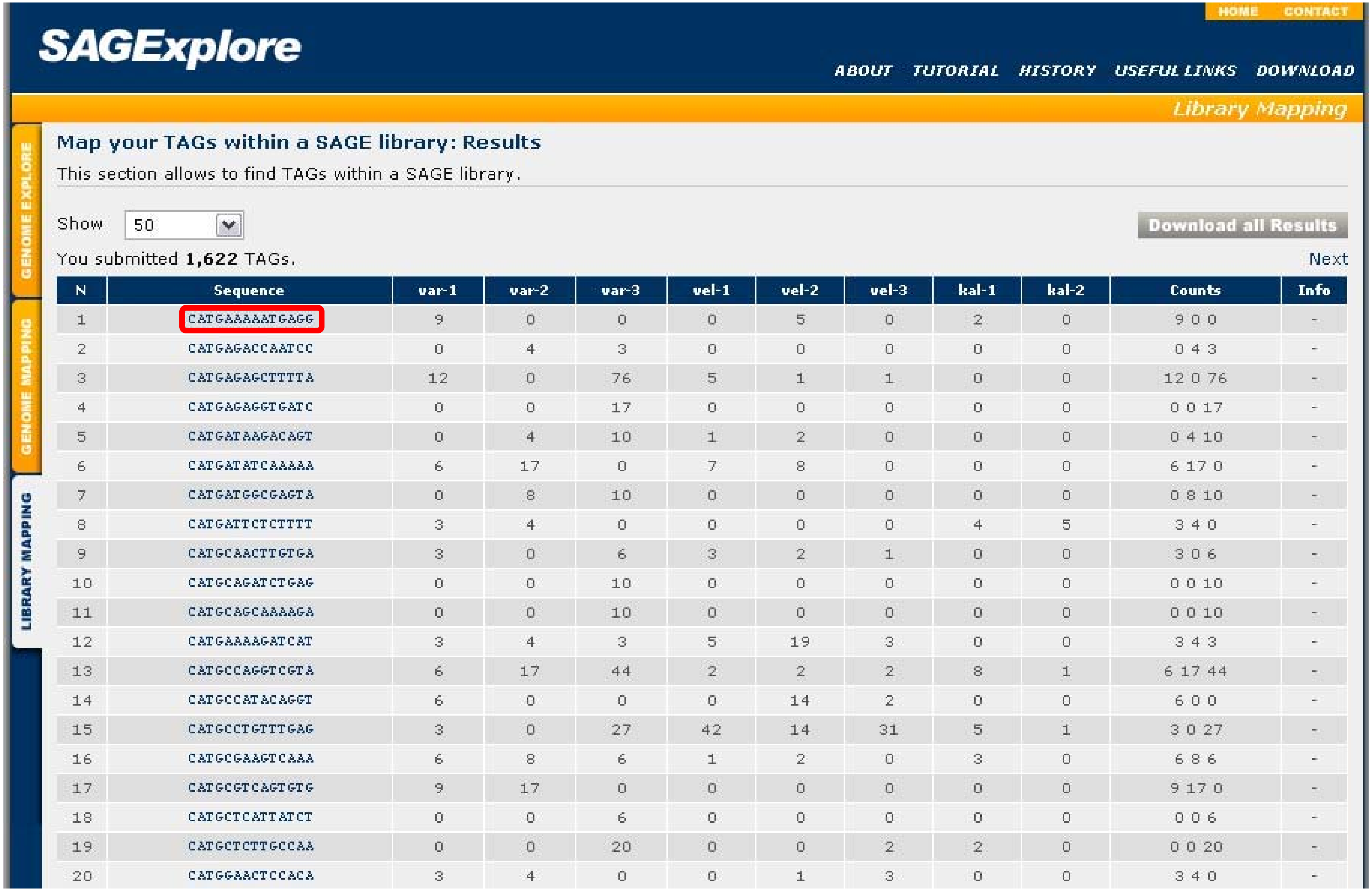
Map your TAGs within a SAGE library: Results

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.



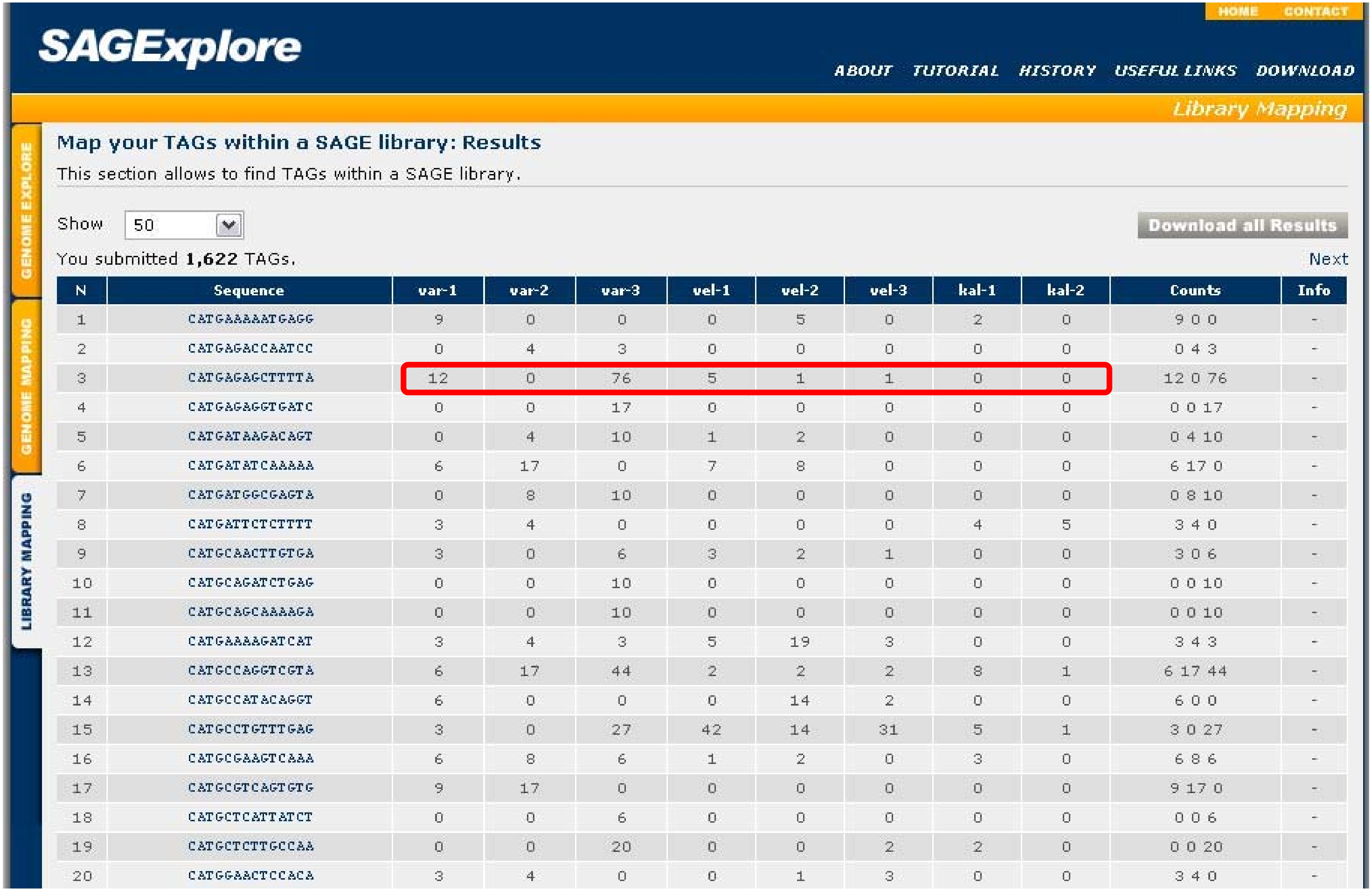
Map your TAGs within a SAGE library: Results

This section allows to find TAGs within a SAGE library.

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.



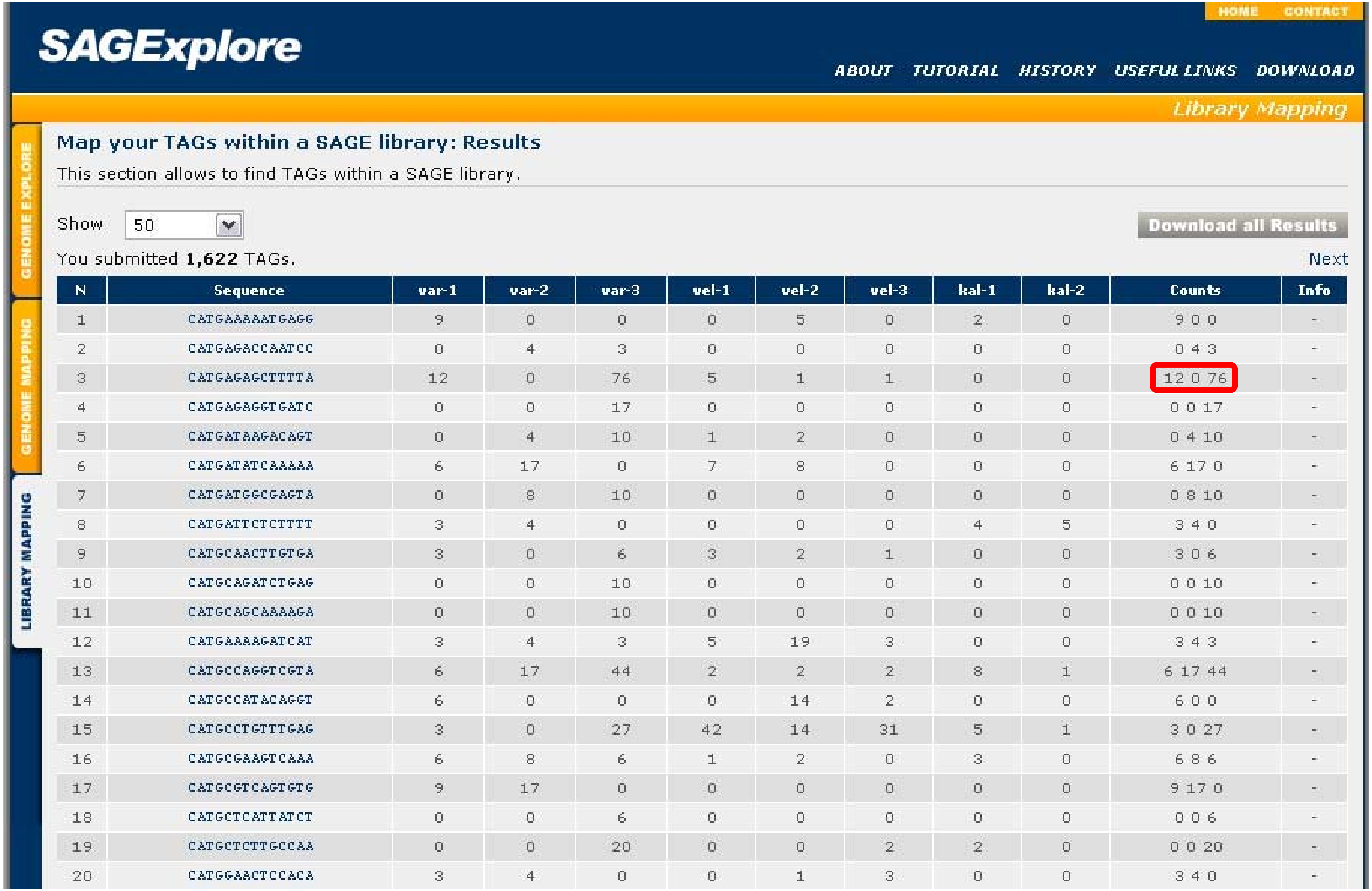
Map your TAGs within a SAGE library: Results

This section allows to find TAGs within a SAGE library.

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

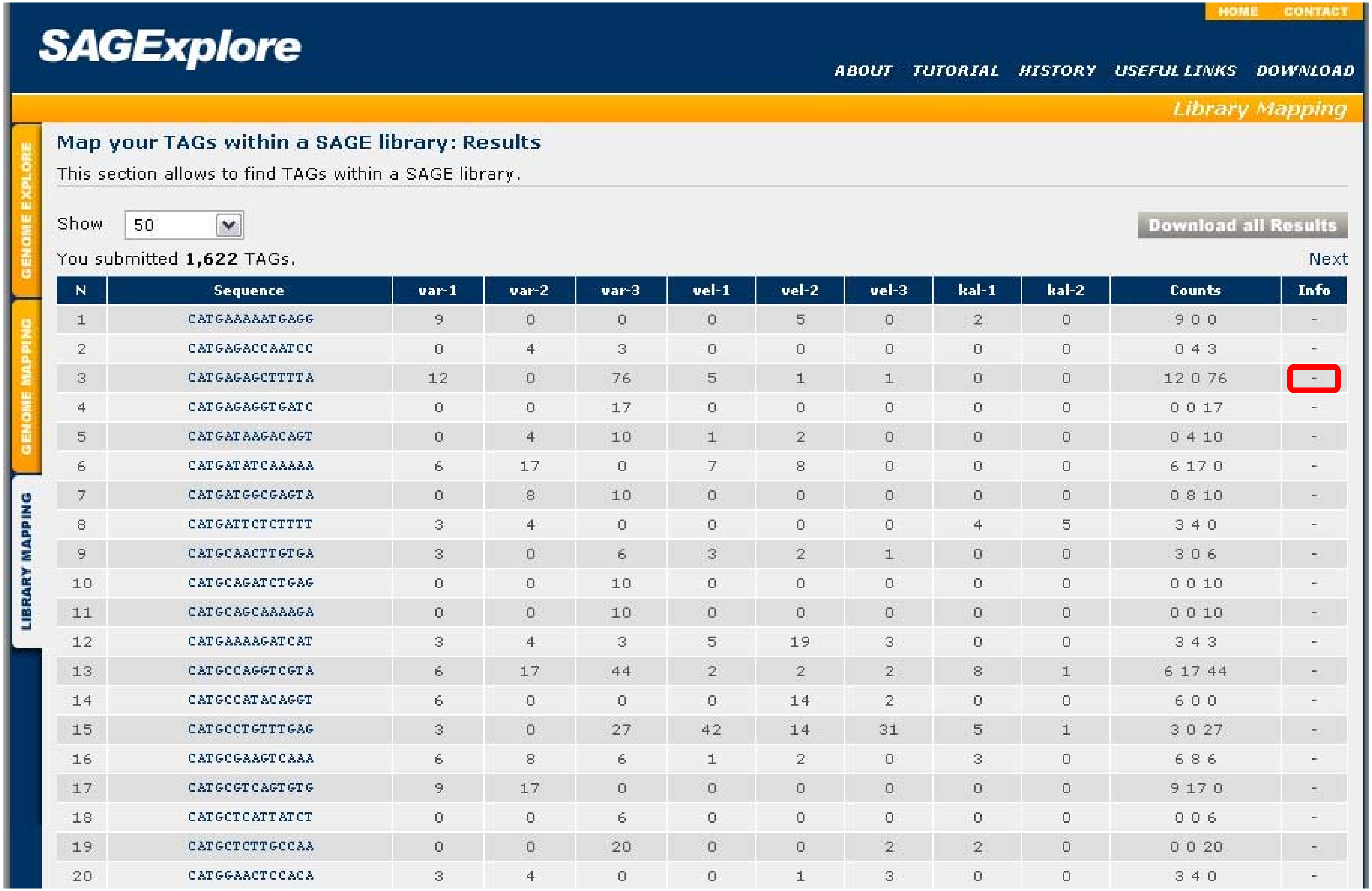
This section allows to find TAGs within a SAGE library.

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

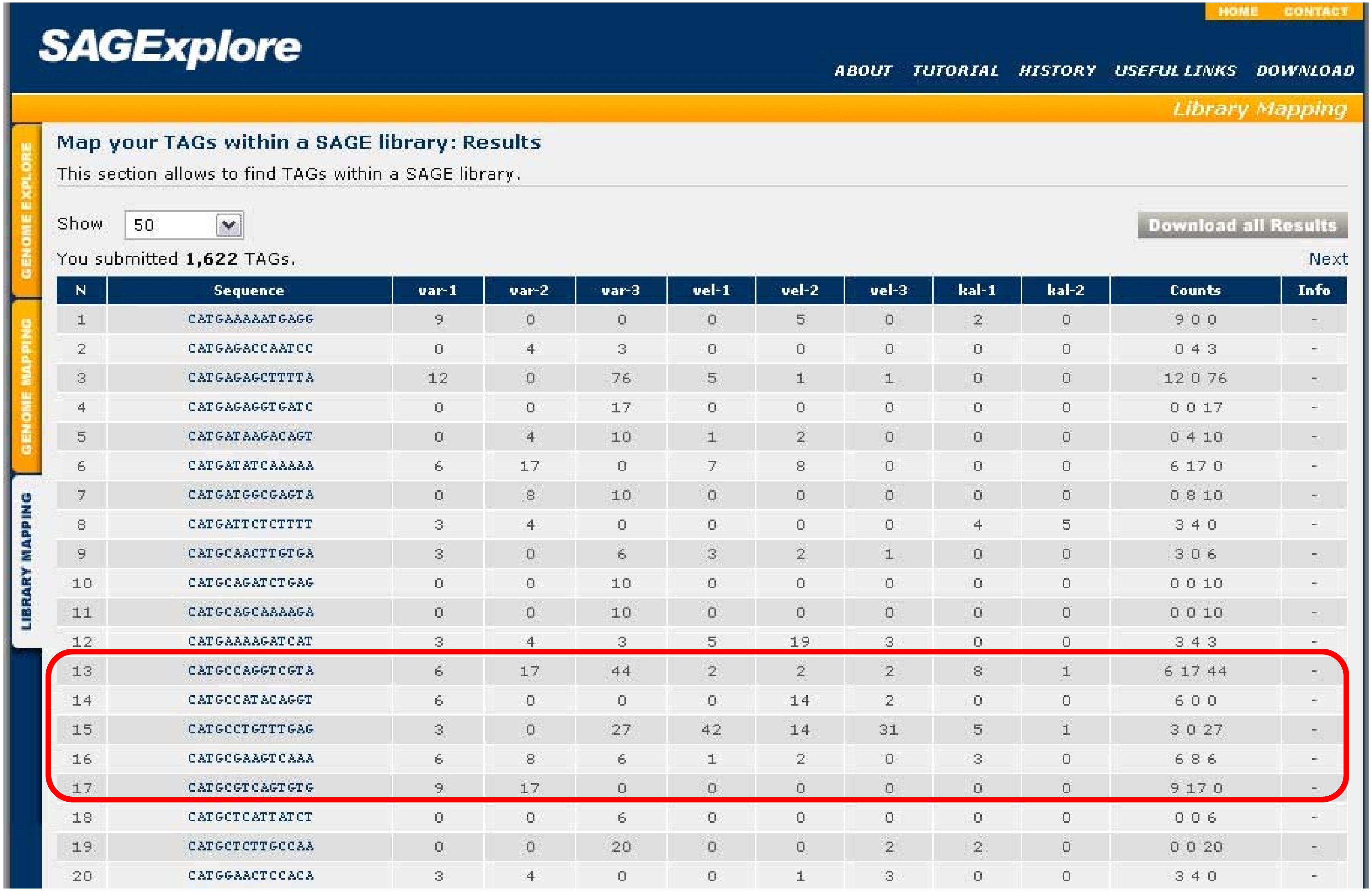
This section allows to find TAGs within a SAGE library.

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

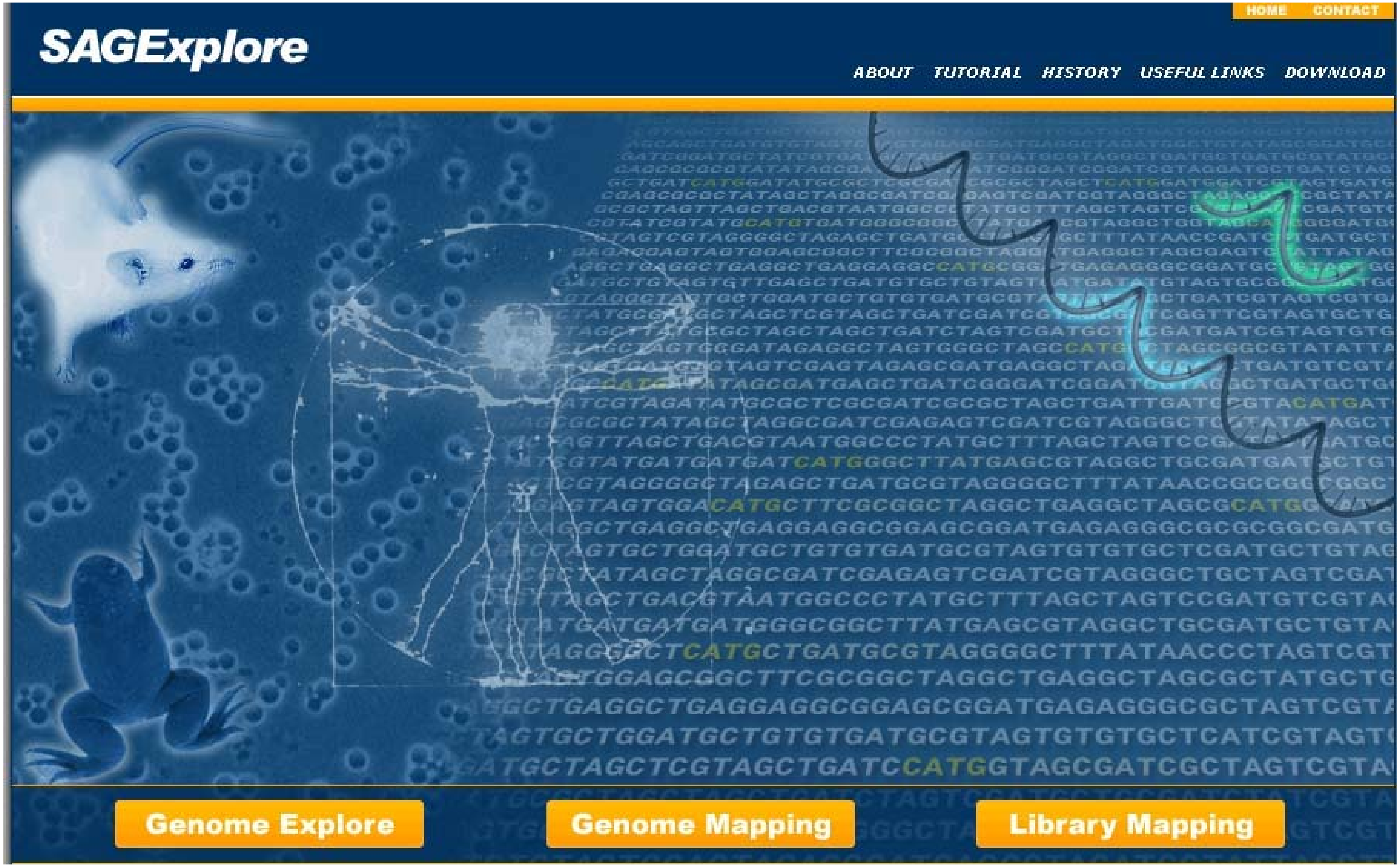
This section allows to find TAGs within a SAGE library.

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 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 for Module III: Library Mapping

Any comments or inquiries, please contact us