

[Genome Explore](#)

[Genome Mapping](#)

[Library Mapping](#)

SAGExplore web server tutorial for Module II: Genome Mapping

The banner features a blue background with a faint DNA sequence. On the left, there is a glowing mouse and a glowing frog. In the center, a glowing human figure is shown with a network of lines connecting to various points on the DNA sequence. On the right, a glowing green 'M' is visible. At the bottom, there are three orange buttons: 'Genome Explore', 'Genome Mapping' (which is highlighted with a red dashed border), and 'Library Mapping'.

II.- Genome Mapping Module:

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

Map your TAGs within a Genome

This section allows to find TAGs within a Genome.

Step 1 Organism [?](#)
 Step 2 Anchoring-Tagging Enzyme Pair [?](#)
 Step 3 Odds ratio for confidence class assignments [?](#)

Saccharomyces cerevisiae ▼
 NlaIII - BsmFI ▼
 5 ▼

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

| TAG Class | | Genomic Type | | TAG Confidence | TAG Location | | Internal Poly-A next? |
|--------------------------------|--------------------------------------|--|--|---|---|--|---|
| <input type="radio"/> Platinum | <input type="radio"/> Copper | <input checked="" type="checkbox"/> Known Protein | <input checked="" type="checkbox"/> smRNA | <input checked="" type="checkbox"/> High | <input checked="" type="checkbox"/> ORF | <input checked="" type="checkbox"/> Exon | <input checked="" type="checkbox"/> Yes |
| <input type="radio"/> Gold | <input type="radio"/> Iron | <input checked="" type="checkbox"/> Hypothetical Protein | <input checked="" type="checkbox"/> tRNA | <input checked="" type="checkbox"/> Low | <input checked="" type="checkbox"/> 3'UTR | <input checked="" type="checkbox"/> Intron | <input checked="" type="checkbox"/> No |
| <input type="radio"/> Silver | <input type="radio"/> Silicon | <input checked="" type="checkbox"/> rRNA | <input checked="" type="checkbox"/> Intergenic A | <input checked="" type="checkbox"/> Undefined | <input checked="" type="checkbox"/> 5'UTR | | |
| <input type="radio"/> Aluminum | <input checked="" type="radio"/> All | <input checked="" type="checkbox"/> snoRNA | <input checked="" type="checkbox"/> Intergenic B | | | | |
| | | <input checked="" type="checkbox"/> snRNA | <input checked="" type="checkbox"/> Intergenic C | | | | |

Step 5 Input Data [?](#)

Upload text file

OR Fill in TAG list

Output Display Options [?](#)

Show ▼
 Sort by ▼
 ▼

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.

Map your TAGs within a Genome

This section allows to find TAGs within a Genome.

Step 1 Organism ?
Step 2 Anchoring-Tagging Enzyme Pair ?
Step 3 Odds ratio for confidence class assignments ?

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

| TAG Class | | Genomic Type | | TAG Confidence | TAG Location | | Internal Poly-A next ? |
|--------------------------------|--------------------------------------|--|--|---|---|--|---|
| <input type="radio"/> Platinum | <input type="radio"/> Copper | <input checked="" type="checkbox"/> Known Protein | <input checked="" type="checkbox"/> smRNA | <input checked="" type="checkbox"/> High | <input checked="" type="checkbox"/> ORF | <input checked="" type="checkbox"/> Exon | <input checked="" type="checkbox"/> Yes |
| <input type="radio"/> Gold | <input type="radio"/> Iron | <input checked="" type="checkbox"/> Hypothetical Protein | <input checked="" type="checkbox"/> tRNA | <input checked="" type="checkbox"/> Low | <input checked="" type="checkbox"/> 3'UTR | <input checked="" type="checkbox"/> Intron | <input checked="" type="checkbox"/> No |
| <input type="radio"/> Silver | <input type="radio"/> Silicon | <input checked="" type="checkbox"/> rRNA | <input checked="" type="checkbox"/> Intergenic A | <input checked="" type="checkbox"/> Undefined | <input checked="" type="checkbox"/> 5'UTR | | |
| <input type="radio"/> Aluminum | <input checked="" type="radio"/> All | <input checked="" type="checkbox"/> snoRNA | <input checked="" type="checkbox"/> Intergenic B | | | | |
| | | <input checked="" type="checkbox"/> snRNA | <input checked="" type="checkbox"/> Intergenic C | | | | |

Step 5 Input Data ?

Upload text file

OR Fill in TAG list

Output Display Options ?

Show Sort by

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 [?](#) **Step 2 Anchoring-Tagging Enzyme Pair** [?](#) **Step 3 Odds ratio for confidence class assignments** [?](#)

Saccharomyces cerevisiae 5

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

| TAG Class | | Genomic Type | | TAG Confidence | TAG Location | | Internal Poly-A next? |
|--------------------------------|--------------------------------------|--|--|---|---|--|---|
| <input type="radio"/> Platinum | <input type="radio"/> Copper | <input checked="" type="checkbox"/> Known Protein | <input checked="" type="checkbox"/> smRNA | <input checked="" type="checkbox"/> High | <input checked="" type="checkbox"/> ORF | <input checked="" type="checkbox"/> Exon | <input checked="" type="checkbox"/> Yes |
| <input type="radio"/> Gold | <input type="radio"/> Iron | <input checked="" type="checkbox"/> Hypothetical Protein | <input checked="" type="checkbox"/> tRNA | <input checked="" type="checkbox"/> Low | <input checked="" type="checkbox"/> 3'UTR | <input checked="" type="checkbox"/> Intron | <input checked="" type="checkbox"/> No |
| <input type="radio"/> Silver | <input type="radio"/> Silicon | <input checked="" type="checkbox"/> rRNA | <input checked="" type="checkbox"/> Intergenic A | <input checked="" type="checkbox"/> Undefined | <input checked="" type="checkbox"/> 5'UTR | | |
| <input type="radio"/> Aluminum | <input checked="" type="radio"/> All | <input checked="" type="checkbox"/> snoRNA | <input checked="" type="checkbox"/> Intergenic B | | | | |
| | | <input checked="" type="checkbox"/> snRNA | <input checked="" type="checkbox"/> Intergenic C | | | | |

Step 5 Input Data [?](#)

Upload text file

OR Fill in TAG list

Output Display Options [?](#)

Show Sort by

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
Step 2 Anchoring-Tagging Enzyme Pair
Step 3 Odds ratio for confidence class assignments

Step 4 TAG categories and genomic mapping contexts to display:

| TAG Class | | Genomic Type | | TAG Confidence | TAG Location | | Internal Poly-A next ? |
|--------------------------------|--------------------------------------|--|--|---|---|--|---|
| <input type="radio"/> Platinum | <input type="radio"/> Copper | <input checked="" type="checkbox"/> Known Protein | <input checked="" type="checkbox"/> smRNA | <input checked="" type="checkbox"/> High | <input checked="" type="checkbox"/> ORF | <input checked="" type="checkbox"/> Exon | <input checked="" type="checkbox"/> Yes |
| <input type="radio"/> Gold | <input type="radio"/> Iron | <input checked="" type="checkbox"/> Hypothetical Protein | <input checked="" type="checkbox"/> tRNA | <input checked="" type="checkbox"/> Low | <input checked="" type="checkbox"/> 3'UTR | <input checked="" type="checkbox"/> Intron | <input checked="" type="checkbox"/> No |
| <input type="radio"/> Silver | <input type="radio"/> Silicon | <input checked="" type="checkbox"/> rRNA | <input checked="" type="checkbox"/> Intergenic A | <input checked="" type="checkbox"/> Undefined | <input checked="" type="checkbox"/> 5'UTR | | |
| <input type="radio"/> Aluminum | <input checked="" type="radio"/> All | <input checked="" type="checkbox"/> snoRNA | <input checked="" type="checkbox"/> Intergenic B | | | | |
| | | <input checked="" type="checkbox"/> snRNA | <input checked="" type="checkbox"/> Intergenic C | | | | |

Step 5 Input Data

Upload text file

OR Fill in TAG list

Output Display Options

Show Sort by

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 [?](#) **Step 2 Anchoring-Tagging Enzyme Pair** [?](#) **Step 3 Odds ratio for confidence class assignments** [?](#)
 Saccharomyces cerevisiae NlaIII - BsmFI 5

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

| TAG Class | | Genomic Type | | TAG Confidence | TAG Location | | Internal Poly-A next ? |
|--------------------------------|--------------------------------------|--|--|---|---|--|---|
| <input type="radio"/> Platinum | <input type="radio"/> Copper | <input checked="" type="checkbox"/> Known Protein | <input checked="" type="checkbox"/> smRNA | <input checked="" type="checkbox"/> High | <input checked="" type="checkbox"/> ORF | <input checked="" type="checkbox"/> Exon | <input checked="" type="checkbox"/> Yes |
| <input type="radio"/> Gold | <input type="radio"/> Iron | <input checked="" type="checkbox"/> Hypothetical Protein | <input checked="" type="checkbox"/> tRNA | <input checked="" type="checkbox"/> Low | <input checked="" type="checkbox"/> 3'UTR | <input checked="" type="checkbox"/> Intron | <input checked="" type="checkbox"/> No |
| <input type="radio"/> Silver | <input type="radio"/> Silicon | <input checked="" type="checkbox"/> rRNA | <input checked="" type="checkbox"/> Intergenic A | <input checked="" type="checkbox"/> Undefined | <input checked="" type="checkbox"/> 5'UTR | | |
| <input type="radio"/> Aluminum | <input checked="" type="radio"/> All | <input checked="" type="checkbox"/> snoRNA | <input checked="" type="checkbox"/> Intergenic B | | | | |
| | | <input checked="" type="checkbox"/> snRNA | <input checked="" type="checkbox"/> Intergenic C | | | | |

Step 5 Input Data [?](#)

Upload text file

OR Fill in TAG list

Output Display Options [?](#)

Show Sort by

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 [?](#) **Step 2 Anchoring-Tagging Enzyme Pair** [?](#) **Step 3 Odds ratio for confidence class assignments** [?](#)

Saccharomyces cerevisiae 5

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

| TAG Class | | Genomic Type | | TAG Confidence | TAG Location | | Internal Poly-A next? |
|--------------------------------|--------------------------------------|--|--|---|---|--|---|
| <input type="radio"/> Platinum | <input type="radio"/> Copper | <input checked="" type="checkbox"/> Known Protein | <input checked="" type="checkbox"/> smRNA | <input checked="" type="checkbox"/> High | <input checked="" type="checkbox"/> ORF | <input checked="" type="checkbox"/> Exon | <input checked="" type="checkbox"/> Yes |
| <input type="radio"/> Gold | <input type="radio"/> Iron | <input checked="" type="checkbox"/> Hypothetical Protein | <input checked="" type="checkbox"/> tRNA | <input checked="" type="checkbox"/> Low | <input checked="" type="checkbox"/> 3'UTR | <input checked="" type="checkbox"/> Intron | <input checked="" type="checkbox"/> No |
| <input type="radio"/> Silver | <input type="radio"/> Silicon | <input checked="" type="checkbox"/> rRNA | <input checked="" type="checkbox"/> Intergenic A | <input checked="" type="checkbox"/> Undefined | <input checked="" type="checkbox"/> 5'UTR | | |
| <input type="radio"/> Aluminum | <input checked="" type="radio"/> All | <input checked="" type="checkbox"/> snoRNA | <input checked="" type="checkbox"/> Intergenic B | | | | |
| | | <input checked="" type="checkbox"/> snRNA | <input checked="" type="checkbox"/> Intergenic C | | | | |

Step 5 Input Data [?](#)

Upload text file

OR Fill in TAG list

Output Display Options [?](#)

Show Sort by

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 text area. The input format is explained in the help link for this step. Full tag sequences must be provided (ie. including the CATG).

Map your TAGs within a Genome

This section allows to find TAGs within a Genome.

Step 1 Organism [?](#) **Step 2 Anchoring-Tagging Enzyme Pair** [?](#) **Step 3 Odds ratio for confidence class assignments** [?](#)
 Saccharomyces cerevisiae 5

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

| TAG Class | | Genomic Type | | TAG Confidence | TAG Location | | Internal Poly-A next? |
|--------------------------------|--------------------------------------|--|--|---|---|--|---|
| <input type="radio"/> Platinum | <input type="radio"/> Copper | <input checked="" type="checkbox"/> Known Protein | <input checked="" type="checkbox"/> smRNA | <input checked="" type="checkbox"/> High | <input checked="" type="checkbox"/> ORF | <input checked="" type="checkbox"/> Exon | <input checked="" type="checkbox"/> Yes |
| <input type="radio"/> Gold | <input type="radio"/> Iron | <input checked="" type="checkbox"/> Hypothetical Protein | <input checked="" type="checkbox"/> tRNA | <input checked="" type="checkbox"/> Low | <input checked="" type="checkbox"/> 3'UTR | <input checked="" type="checkbox"/> Intron | <input checked="" type="checkbox"/> No |
| <input type="radio"/> Silver | <input type="radio"/> Silicon | <input checked="" type="checkbox"/> rRNA | <input checked="" type="checkbox"/> Intergenic A | <input checked="" type="checkbox"/> Undefined | <input checked="" type="checkbox"/> 5'UTR | | |
| <input type="radio"/> Aluminum | <input checked="" type="radio"/> All | <input checked="" type="checkbox"/> snoRNA | <input checked="" type="checkbox"/> Intergenic B | | | | |
| | | <input checked="" type="checkbox"/> snRNA | <input checked="" type="checkbox"/> Intergenic C | | | | |

Step 5 Input Data [?](#)

Upload text file

OR Fill in TAG list

Output Display Options [?](#)

Show Sort by

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 [?](#) **Step 2 Anchoring-Tagging Enzyme Pair** [?](#) **Step 3 Odds ratio for confidence class assignments** [?](#)
 Saccharomyces cerevisiae NlaIII - BsmFI 5

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

| TAG Class | | Genomic Type | | TAG Confidence | TAG Location | | Internal Poly-A next ? |
|--------------------------------|--------------------------------------|--|--|---|---|--|---|
| <input type="radio"/> Platinum | <input type="radio"/> Copper | <input checked="" type="checkbox"/> Known Protein | <input checked="" type="checkbox"/> smRNA | <input checked="" type="checkbox"/> High | <input checked="" type="checkbox"/> ORF | <input checked="" type="checkbox"/> Exon | <input checked="" type="checkbox"/> Yes |
| <input type="radio"/> Gold | <input type="radio"/> Iron | <input checked="" type="checkbox"/> Hypothetical Protein | <input checked="" type="checkbox"/> tRNA | <input checked="" type="checkbox"/> Low | <input checked="" type="checkbox"/> 3'UTR | <input checked="" type="checkbox"/> Intron | <input checked="" type="checkbox"/> No |
| <input type="radio"/> Silver | <input type="radio"/> Silicon | <input checked="" type="checkbox"/> rRNA | <input checked="" type="checkbox"/> Intergenic A | <input checked="" type="checkbox"/> Undefined | <input checked="" type="checkbox"/> 5'UTR | | |
| <input type="radio"/> Aluminum | <input checked="" type="radio"/> All | <input checked="" type="checkbox"/> snoRNA | <input checked="" type="checkbox"/> Intergenic B | | | | |
| | | <input checked="" type="checkbox"/> snRNA | <input checked="" type="checkbox"/> Intergenic C | | | | |

Step 5 Input Data [?](#)

Upload text file

OR Fill in TAG list

Output Display Options [?](#)

Show Sort by

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

[Download all Results](#) [Expression Map](#)

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

[Next](#)

| 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 | | | | | 3 4 0 | - |
| 2 | Un | CATGACACCACCAG | 3 | 1.000 | Fe | Int | int,opORF | 0 | 1 | 140213 | + | N.A. | YAL005C | | | | | 3 0 10 | - |
| 3 | Un | CATGGAGGAGATT | 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 | CATGTAAAAA | 2 | 1.000 | Fe | Int | int | 0 | 2 | 622839 | + | N.A. | --- | | | | | 6 4 0 | - |
| 14 | Un | CATGGCGTTGAGG | 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 | CATGCTCTCTCGTT | 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 | CATGATATCAAAA | 2 | 0.375 | Al | ORF | ORFv | 7 | 4 | 179499 | + | MSH5 | YDL154W | | | | | 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

[Download all Results](#)
[Expression Map](#)

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


[Next](#)

| 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 | | | | | 3 4 0 | - |
| 2 | Un | CATGACACCACCAG | 3 | 1.000 | Fe | Int | int,opORF | 0 | 1 | 140213 | + | N.A. | YAL005C | | | | | 3 0 10 | - |
| 3 | Un | CATGGAGGAGATT | 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 | CATGCACCTCAACT | 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 | CATGGAAAATCCGGT | 2 | 0.807 | Si | Int | int,opORF | 0 | 2 | 576616 | + | N.A. | YBR170C | | | | | 3 0 3 | - |
| 13 | Un | CATGTAAAAA | 2 | 1.000 | Fe | Int | int | 0 | 2 | 622839 | + | N.A. | --- | | | | | 6 4 0 | - |
| 14 | Un | CATGGCGTTGAGG | 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 | CATGCACCTCAACT | 20 | 1.000 | Fe | Int | int | 0 | 3 | 90077 | + | N.A. | --- | | | | | 12 8 3 | - |
| 18 | Un | CATGCTCTCTCGTT | 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 | CATGATATCAAAA | 2 | 0.375 | Al | ORF | ORFv | 7 | 4 | 179499 | + | MSH5 | YDL154W | | | | | 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 

[Download all Results](#)
[Expression Map](#)

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

[Next](#)

| 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 | | | | | 3 4 0 | - |
| 2 | Un | CATGACACCACCAG | 3 | 1.000 | Fe | Int | int,opORF | 0 | 1 | 140213 | + | N.A. | YAL005C | | | | | 3 0 10 | - |
| 3 | Un | CATGGAGGAGATT | 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 | CATGCACCTCAACT | 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 | CATGGAAAATCCGGT | 2 | 0.807 | Si | Int | int,opORF | 0 | 2 | 576616 | + | N.A. | YBR170C | | | | | 3 0 3 | - |
| 13 | Un | CATGTAAAAA | 2 | 1.000 | Fe | Int | int | 0 | 2 | 622839 | + | N.A. | --- | | | | | 6 4 0 | - |
| 14 | Un | CATGGCGTTGAGG | 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 | CATGCACCTCAACT | 20 | 1.000 | Fe | Int | int | 0 | 3 | 90077 | + | N.A. | --- | | | | | 12 8 3 | - |
| 18 | Un | CATGCTCTCTCGTT | 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 | CATGATATCAAAA | 2 | 0.375 | Al | ORF | ORFv | 7 | 4 | 179499 | + | MSH5 | YDL154W | | | | | 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

[Download all Results](#)

[Expression Map](#)

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

[Next](#)

| 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 | | | | | 3 4 0 | - |
| 2 | Un | CATGACACCACCAG | 3 | 1.000 | Fe | Int | int,opORF | 0 | 1 | 140213 | + | N.A. | YAL005C | | | | | 3 0 10 | - |
| 3 | Un | CATGGAGGAGATT | 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 | CATGCACCTTCAACT | 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 | CATGGAAAATCCGGT | 2 | 0.807 | Si | Int | int,opORF | 0 | 2 | 576616 | + | N.A. | YBR170C | | | | | 3 0 3 | - |
| 13 | Un | CATGTAAAAA | 2 | 1.000 | Fe | Int | int | 0 | 2 | 622839 | + | N.A. | --- | | | | | 6 4 0 | - |
| 14 | Un | CATGGCGTTGAGG | 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 | CATGCACCTTCAACT | 20 | 1.000 | Fe | Int | int | 0 | 3 | 90077 | + | N.A. | --- | | | | | 12 8 3 | - |
| 18 | Un | CATGCTCTCTCGTT | 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 | CATGATATCAAAA | 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.

Show

[Download all Results](#) [Expression Map](#)

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

[Next](#)

| N | TC | Seq | Freq | Odds | Cl | LocD | LocT | TrPos | Ch | Ini | Str | StdName | SysName | GC | TD | DS | BI | Cn | Info |
|----|----|----------------|------|-------|----|------|-----------|-------|----|--------|-----|---------|----------|----|----|----|----|-----------|------|
| 1 | Un | CATGGTACACAAAG | 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 | CATGGAGGAGATT | 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 | CATGCACCTCAACT | 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 | CATGTAAAAA | 2 | 1.000 | Fe | Int | int | 0 | 2 | 622839 | + | N.A. | --- | | | | | 6 4 0 | - |
| 14 | Un | CATGGCGTTGAGG | 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 | CATGCACCTCAACT | 20 | 1.000 | Fe | Int | int | 0 | 3 | 90077 | + | N.A. | --- | | | | | 12 8 3 | - |
| 18 | Un | CATGCTCTCTCGTT | 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 | CATGATATCAAAA | 2 | 0.375 | Al | ORF | ORFv | 7 | 4 | 179499 | + | MSH5 | YDL154W | | | | | 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

This section allows to find TAGs within a Genome.

Show

[Download all Results](#) [Expression Map](#)

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

[Next](#)

| 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 | | | | | 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 | CATGCACCTCAACT | 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 | CATGTAAAAA | 2 | 1.000 | Fe | Int | int | 0 | 2 | 622839 | + | N.A. | --- | | | | | 6 4 0 | - |
| 14 | Un | CATGGCGTTGAGG | 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 | CATGCACCTCAACT | 20 | 1.000 | Fe | Int | int | 0 | 3 | 90077 | + | N.A. | --- | | | | | 12 8 3 | - |
| 18 | Un | CATGCTCTCTCGTT | 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 | CATGATATCAAAA | 2 | 0.375 | Al | ORF | ORFv | 7 | 4 | 179499 | + | MSH5 | YDL154W | | | | | 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.

Show

[Download all Results](#) [Expression Map](#)

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

[Next](#)

| 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 | | | | | 3 4 0 | - |
| 2 | Un | CATGACACCACCAG | 3 | 1.000 | Fe | Int | int,opORF | 0 | 1 | 140213 | + | N.A. | YAL005C | | | | | 3 0 10 | - |
| 3 | Un | CATGGAGGAGATT | 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 | CATGCACCTCAACT | 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 | CATGGAATCCGGT | 2 | 0.807 | Si | Int | int,opORF | 0 | 2 | 576616 | + | N.A. | YBR170C | | | | | 3 0 3 | - |
| 13 | Un | CATGTAAAAA | 2 | 1.000 | Fe | Int | int | 0 | 2 | 622839 | + | N.A. | --- | | | | | 6 4 0 | - |
| 14 | Un | CATGGCGTTGAGG | 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 | CATGCACCTCAACT | 20 | 1.000 | Fe | Int | int | 0 | 3 | 90077 | + | N.A. | --- | | | | | 12 8 3 | - |
| 18 | Un | CATGCTCTCTCGTT | 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 | CATGATATCAAAA | 2 | 0.375 | Al | ORF | ORFv | 7 | 4 | 179499 | + | MSH5 | YDL154W | | | | | 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

This section allows to find TAGs within a Genome.

Show

[Download all Results](#) [Expression Map](#)

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

[Next](#)

| 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 | | | | | 3 4 0 | - |
| 2 | Un | CATGACACCACCAG | 3 | 1.000 | Fe | Int | int,opORF | 0 | 1 | 140213 | + | N.A. | YAL005C | | | | | 3 0 10 | - |
| 3 | Un | CATGGAGGAGATT | 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 | CATGCACCTCAACT | 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 | CATGGAAAATCCGGT | 2 | 0.807 | Si | Int | int,opORF | 0 | 2 | 576616 | + | N.A. | YBR170C | | | | | 3 0 3 | - |
| 13 | Un | CATGTAAAAA | 2 | 1.000 | Fe | Int | int | 0 | 2 | 622839 | + | N.A. | --- | | | | | 6 4 0 | - |
| 14 | Un | CATGGCGTTGAGG | 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 | CATGCACCTCAACT | 20 | 1.000 | Fe | Int | int | 0 | 3 | 90077 | + | N.A. | --- | | | | | 12 8 3 | - |
| 18 | Un | CATGCTCTCTCGTT | 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 | CATGATATCAAAA | 2 | 0.375 | Al | ORF | ORFv | 7 | 4 | 179499 | + | MSH5 | YDL154W | | | | | 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.



Quick Search:

[Site Map](#) | [Full Search](#) | [Help](#) | [Contact SGD](#) | [Home](#)

[Community Info](#)

[Submit Data](#)

[BLAST](#)

[Primers](#)

[PatMatch](#)

[Gene/Seq Resources](#)

[Advanced Search](#)

[Virtual Library](#)

SSB1/YDL229W Summary

[Help](#)

Summary

Locus History

Literature

Gene Ontology

Phenotype

Interactions

Expression

Protein

[Alternative single page format](#)

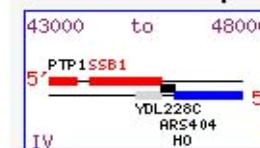
SSB1 BASIC INFORMATION [[View References](#)]

| | |
|-----------------------|--|
| Standard Name | <i>SSB1</i> (see Nomenclature conflict Note) |
| Systematic Name | YDL229W |
| Alias | <i>YG101</i> 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 | <ul style="list-style-type: none"> ATPase activity (IDA) unfolded protein binding (IDA, ISS, TAS) |
| Biological Process | <ul style="list-style-type: none"> cotranslational protein folding (IDA) protein biosynthesis (IMP, IPI, TAS) |

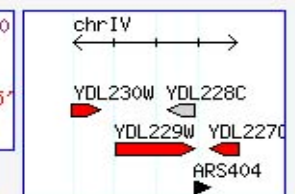
SSB1 RESOURCES

Click on map for expanded view

SGD ORF map



GBrowse



Literature

Literature Guide

Retrieve Sequences

Genomic DNA

SGD Query: An example of the results obtained when querying 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.

Show

[Download all Results](#) [Expression Map](#)

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

[Next](#)

| 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 | | | | | 3 4 0 | - |
| 2 | Un | CATGACACCACCAG | 3 | 1.000 | Fe | Int | int,opORF | 0 | 1 | 140213 | + | N.A. | YAL005C | | | | | 3 0 10 | - |
| 3 | Un | CATGGAGGAGATT | 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 | CATGGAAAATCCGGT | 2 | 0.807 | Si | Int | int,opORF | 0 | 2 | 576616 | + | N.A. | YBR170C | | | | | 3 0 3 | - |
| 13 | Un | CATGTAAAAA | 2 | 1.000 | Fe | Int | int | 0 | 2 | 622839 | + | N.A. | --- | | | | | 6 4 0 | - |
| 14 | Un | CATGGCGTTGAGG | 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 | CATGCTCTCTCGTT | 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 | CATGATATCAAAA | 2 | 0.375 | Al | ORF | ORFv | 7 | 4 | 179499 | + | MSH5 | YDL154W | | | | | 6 17 0 | - |

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

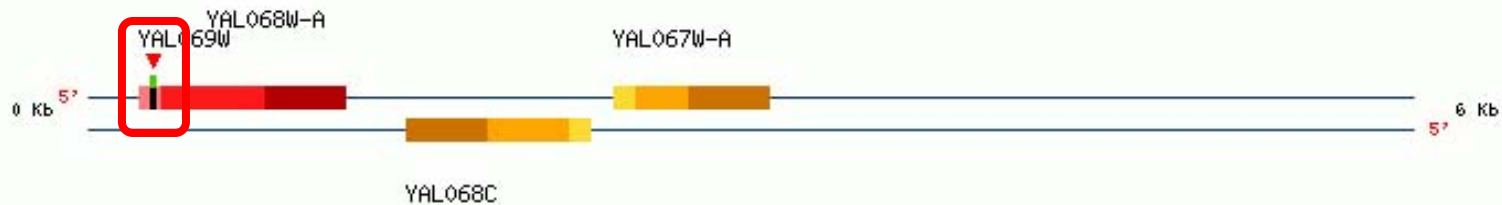
Genomic Context

Organism: *Sacharomyces cerevisiae*

Fragment Displayed: 1 - 6,000



100 Kb Chromosome: 1 Length: 230,208 bp



Keys:

Chromosome:

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

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.

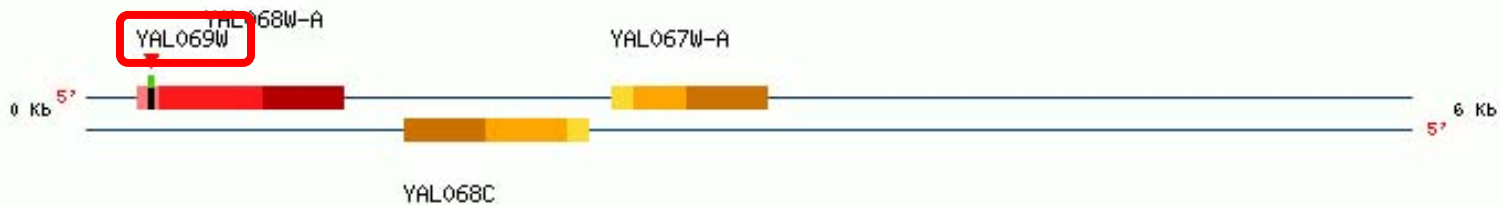
Genomic Context

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
- 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.

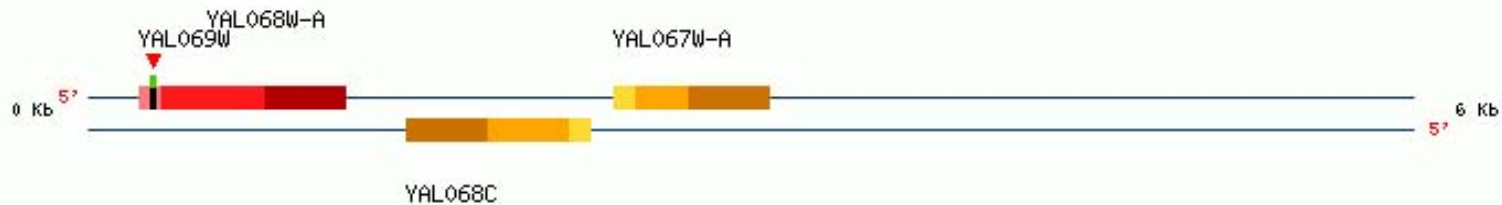
Genomic Context

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
- 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.

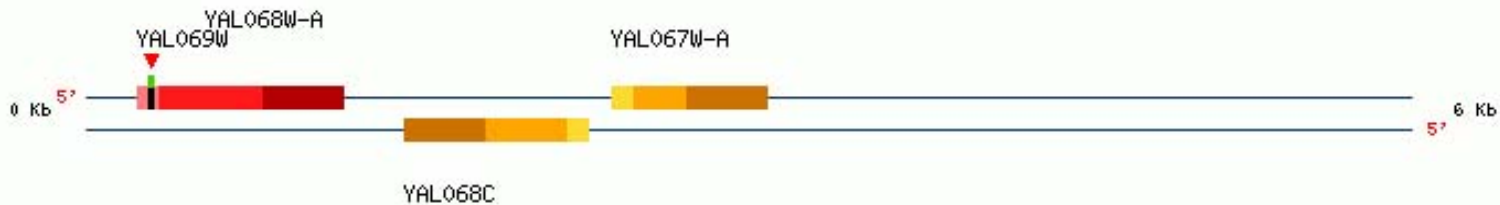
Genomic Context

Organism: *Sacharomyces cerevisiae*

Fragment Displayed: 1 - 6,000



100 Kb Chromosome: 1 Length: 230,208 bp



Keys:

Chromosome:

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

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.

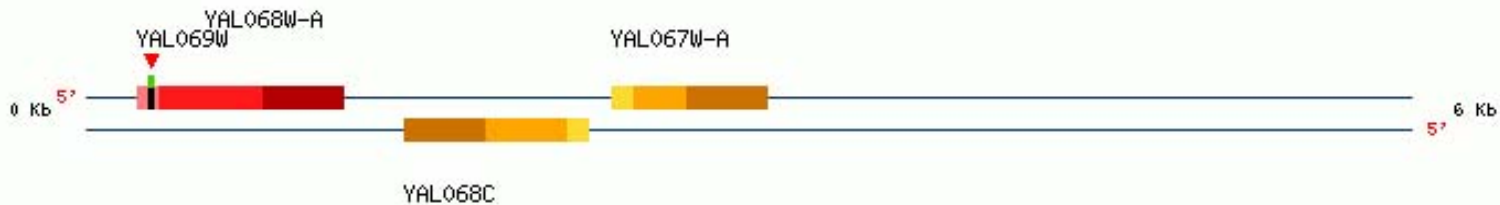
Genomic Context

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.

Genomic Context

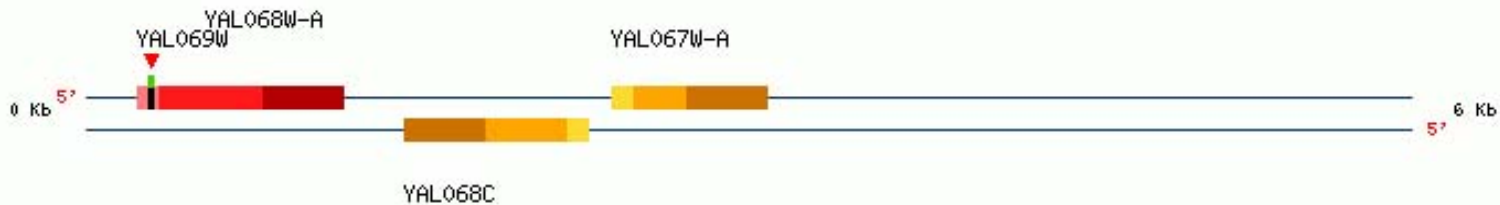
Organism: *Sacharomyces cerevisiae*

Fragment Displayed: 1 - 6,000



100 Kb

Chromosome: 1 Length: 230,208 bp



Keys:

Chromosome:

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

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

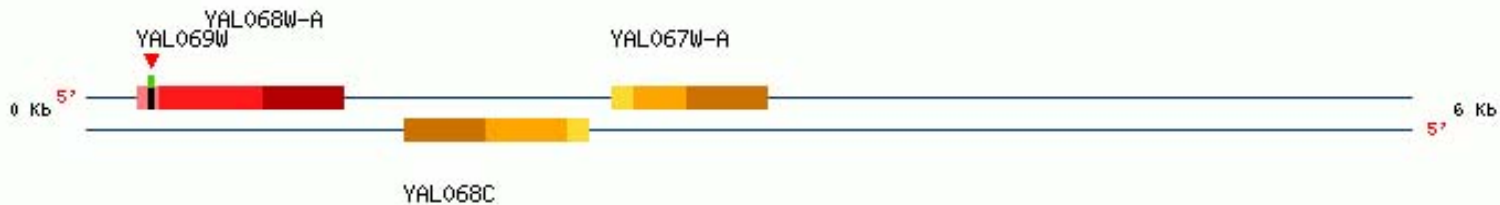
Organism: *Sacharomyces cerevisiae*

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.

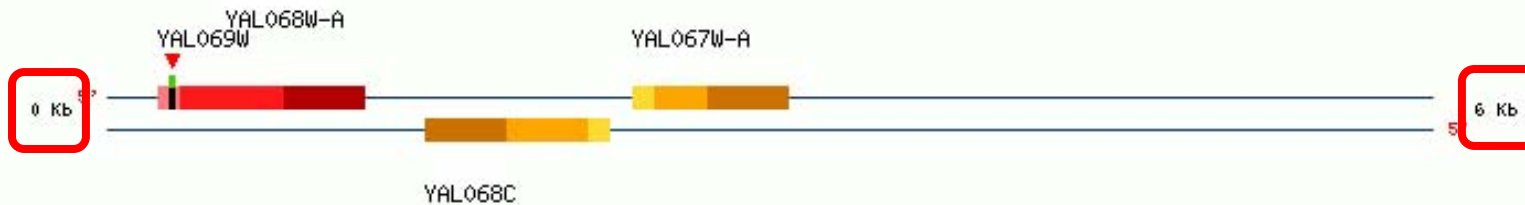
Genomic Context

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.

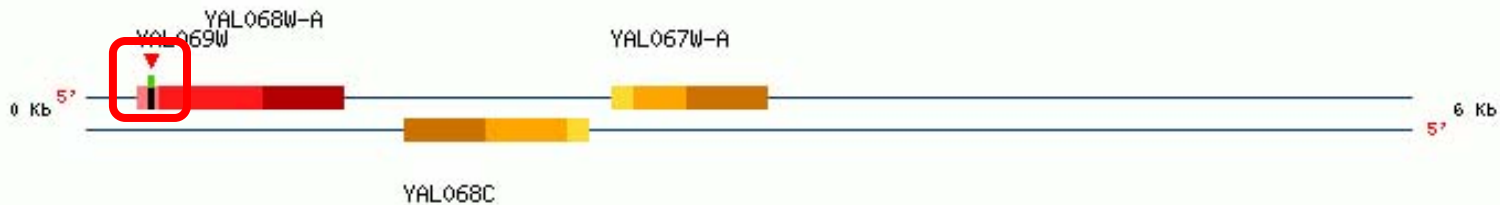
Genomic Context

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

[Download all Results](#) [Expression Map](#)

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

[Next](#)

| 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 | | | | | 3 4 0 | - |
| 2 | Un | CATGACACCACCAG | 3 | 1.000 | Fe | Int | int,opORF | 0 | 1 | 140213 | + | N.A. | YAL005C | | | | | 3 0 10 | - |
| 3 | Un | CATGGAGGAGATT | 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 | CATGCACCTTCAACT | 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 | CATGGAATCCGGT | 2 | 0.807 | Si | Int | int,opORF | 0 | 2 | 576616 | + | N.A. | YBR170C | | | | | 3 0 3 | - |
| 13 | Un | CATGTAAAAA | 2 | 1.000 | Fe | Int | int | 0 | 2 | 622839 | + | N.A. | --- | | | | | 6 4 0 | - |
| 14 | Un | CATGGCGTTGAGG | 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 | CATGCACCTTCAACT | 20 | 1.000 | Fe | Int | int | 0 | 3 | 90077 | + | N.A. | --- | | | | | 12 8 3 | - |
| 18 | Un | CATGCTTCTCGTT | 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 | CATGATATCAAAA | 2 | 0.375 | Al | ORF | ORFv | 7 | 4 | 179499 | + | MSH5 | YDL154W | | | | | 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

[Download all Results](#)
[Expression Map](#)

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

Next

| 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 | | | | | 3 4 0 | - |
| 2 | Un | CATGACACCACCAG | 3 | 1.000 | Fe | Int | int,opORF | 0 | 1 | 140213 | + | N.A. | YAL005C | | | | | 3 0 10 | - |
| 3 | Un | CATGGAGGAGATT | 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 | CATGCACCTCAACT | 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 | CATGTAAAAA | 2 | 1.000 | Fe | Int | int | 0 | 2 | 622839 | + | N.A. | --- | | | | | 6 4 0 | - |
| 14 | Un | CATGGCGTTGAGG | 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 | CATGCACCTCAACT | 20 | 1.000 | Fe | Int | int | 0 | 3 | 90077 | + | N.A. | --- | | | | | 12 8 3 | - |
| 18 | Un | CATGCTCTCTCGTT | 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 | CATGATATCAAAA | 2 | 0.375 | Al | ORF | ORFv | 7 | 4 | 179499 | + | MSH5 | YDL154W | | | | | 6 17 0 | - |

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

SAGExplore

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

```
>scer|chr:4|+|229806-230618  
TTGAATCTGTAAGCCCCTTCGTGATATTTCAAGGTTAAATTACGAATTGCAGTTTTCAGTT  
AATCTTGGACTAACAAAGAAATCAAACAACCTAAGAAGAAAATGTCTGACTCTATTATTTTC  
CTTTGCTGCTTTCATCCTAGCTGATGCTGGTTTTGGAAATCACCTCTGACAACCTTATTGAC  
TATCACCAAGGCCGCTGGTGCTAATGTCGACAAACGTATGTACAAAAAATGC AACCTAAAAC  
GACTTTGTGTGACTACGAAGAGAAAGATTAGACAACAATCGTCCCGAGAAATGCGCAATT  
TTGAATAATGGGGGACAGAAAAAATTCATGTAACGTTTTCCCTCTAACATGATGAGATACT  
AGGGGGCAATACATGTAGAAATATTTCTCCATTAACGTATTTAACGGAAAGCACAAAGTCA  
GGATCGAATTACTTCTTCAAGGATCTCATTTTACTAACAAACTCAACGAATAACGACTCT  
TCCTATGGAGCTTGTTATATGTATCATTGAATTAGGTCTGGGCTGATGTTTACGCTAAGG  
CTTTGGAAGGTAAGGACTTGAAAGGAAATCCTATCTGGTTTTCCATAACGCTGGCCCTGTTG  
CTGGTGCTGGTGCTGCTTCTGGCGCTGCCGCTGCTGGTGGTGACGCTGCTGCTGAAGAAG  
AAAAAGAAAGAAAGCTGCTGAAGAATCTGACGACGACCATGGGTTTTCGGTTTTATTCGACT  
AAACATACAAGGAAAGTCATTTTTTTCTGCAACGTTTTTTTTACCCTTTATGTATATATATT  
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 downstream 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
```

```
TTGAAATCTGTAAGCCCCCTTCGGTATATTTCAAGGTTAAATTACGAATTGCAGTTTTCAGTT  
AATCTTGGACTAACAAAGAAATCAAACAACCTAAGAAGAAAATGCTCTGACTCTATTATTTTC  
CTTTGCTGCTTTCATCCTAGCTGATGCTGGTTTTGGAAATCACCTCTGACAACCTTATTGAC  
TATCACCAAGGCCGCTGGTGCTAATGTCGACAAACGTATGTACAAAAAATGC AACCTAAAAC  
GACTTTGTGTGACTACGAAGAGAAAGATTAGACAACAATCGTCCCGAGAAATGCGCAATT  
TTGAATAATGGGGGACAGAAAAAATTCATGTAACGTTTTCCCTCTAACATGATGAGATACT  
AGGGGGCAATACATGTAGAAATATTTCTCCATTAACGTATTTAACGGAAAGCACAAAGTCA  
GGATCGAATTACTTCTTCAAGGATCTCATTTTACTAACAAACTCAACGAATAACGACTCT  
TCCTATGGAGCTTGTTATATGTATCATTGAATTAGGTCTGGGCTGATGTTTACGCTAAGG  
CTTTGGAAGGTAAGGACTTGAAAGGAAATCCTATCTGGTTTTCCATAACGCTGGCCCTGTTG  
CTGGTGCTGGTGCTGCTTCTGGCGCTGCCGCTGCTGGTGGTGACGCTGCTGCTGAAGAAG  
AAAAAGAAAGAAAGCTGCTGAAGAATCTGACGACGACCATGGGTTTCGGTTTATTTCGACT  
AAACATACAAGGAAAGTCATTTTTTTCTGCAACGTTTTTTTTACCCTTTATGTATATATATT  
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

[Download all Results](#) [Expression Map](#)

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

[Next](#)

| 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 | | | | | 3 4 0 | - |
| 2 | Un | CATGACACCACCAG | 3 | 1.000 | Fe | Int | int,opORF | 0 | 1 | 140213 | + | N.A. | YAL005C | | | | | 3 0 10 | - |
| 3 | Un | CATGGAGGAGATT | 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 | CATGCACCTCAACT | 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 | CATGGAATCCGGT | 2 | 0.807 | Si | Int | int,opORF | 0 | 2 | 576616 | + | N.A. | YBR170C | | | | | 3 0 3 | - |
| 13 | Un | CATGTAAAAA | 2 | 1.000 | Fe | Int | int | 0 | 2 | 622839 | + | N.A. | --- | | | | | 6 4 0 | - |
| 14 | Un | CATGGCGTTGAGG | 2 | 1.000 | Al | UTR3 | ORFdu | 1 | 2 | 635140 | + | N.A. | YBR206W | | | | | 6 0 0 | - |
| 15 | Un | CATGCTCTGTTCT | 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 | CATGCACCTCAACT | 20 | 1.000 | Fe | Int | int | 0 | 3 | 90077 | + | N.A. | --- | | | | | 12 8 3 | - |
| 18 | Un | CATGCTCTCTCGTT | 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 | CATGATATCAAAA | 2 | 0.375 | Al | ORF | ORFv | 7 | 4 | 179499 | + | MSH5 | YDL154W | | | | | 6 17 0 | - |

Query Results: A query to the BLAST server at the NCBI is launched with the previously 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](#)

```

TCACCAGTGTTAGGGTCAAGAACTGCATCAATACCGAAGAAGGGGAATGAGGCAGA
ACCCGGTTTCATTGGTGTAAACACCACCAGCCAGCGGGGTGACCAGATGCGAACCAATT
CTGTTTGCCAGTAGGTGTCTACAATGGGGATTTTCAATTTTACCTATTTTTCAGAGTAC
CACTCCCAAATTCAGCAGCAATTGGCTCACCGACCGAACCCAAAGCAACGCAAAGATTT
TAAGGAATGATTTTCGATGTAGGAATCACCAGCTCTTTTCAACAAACGCAAAGCAGTTG
  
```

[Choose a translation](#)

 TRANSLATED query - PROTEIN database **[blastx]**
[Set subsequence](#)

 From: To:
[Choose database](#)

nr

[Genetic codes](#)

Standard (1)

Now:

 or

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

This section allows to find TAGs within a Genome.

Show

[Download all Results](#) [Expression Map](#)

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

[Next](#)

| 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 | | | | | 3 4 0 | - |
| 2 | Un | CATGACACCACCAG | 3 | 1.000 | Fe | Int | int,opORF | 0 | 1 | 140213 | + | N.A. | YAL005C | | | | | 3 0 10 | - |
| 3 | Un | CATGGAGGAGATT | 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 | CATGCACCTTCAACT | 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 | CATGTAAAAA | 2 | 1.000 | Fe | Int | int | 0 | 2 | 622839 | + | N.A. | --- | | | | | 6 4 0 | - |
| 14 | Un | CATGGCGTTGAGG | 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 | CATGCACCTTCAACT | 20 | 1.000 | Fe | Int | int | 0 | 3 | 90077 | + | N.A. | --- | | | | | 12 8 3 | - |
| 18 | Un | CATGCTCTCTCGTT | 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 | CATGATATCAAAA | 2 | 0.375 | Al | ORF | ORFv | 7 | 4 | 179499 | + | MSH5 | YDL154W | | | | | 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.

Show

[Download all Results](#) [Expression Map](#)

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

[Next](#)

| 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 | | | | | 3 4 0 | - |
| 2 | Un | CATGACACCACCAG | 3 | 1.000 | Fe | Int | int,opORF | 0 | 1 | 140213 | + | N.A. | YAL005C | | | | | 3 0 10 | - |
| 3 | Un | CATGGAGGAGATT | 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 | CATGCACCTCAACT | 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 | CATGTAAAAA | 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 | CATGCACCTCAACT | 20 | 1.000 | Fe | Int | int | 0 | 3 | 90077 | + | N.A. | --- | | | | | 12 8 3 | - |
| 18 | Un | CATGCTCTCTCGTT | 2 | 1.000 | Al | ORF | ORFv | 1 | 4 | 45892 | + | SSB1 | YDL229W | | | | | 6 12 0 | - |
| 19 | Un | CATGTACATCATC | 2 | 1.000 | Al | UTR3 | ORFv | 1 | 4 | 99277 | + | MRPL11 | YDL202W | | | | | 6 17 0 | - |
| 20 | Un | CATGATATCAAAA | 2 | 0.375 | Al | ORF | ORFv | 7 | 4 | 179499 | + | MSH5 | YDL154W | | | | | 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).

Map your TAGs within a Genome: Results

This section allows to find TAGs within a Genome.

Show

[Download all Results](#)
[Expression Map](#)

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

[Next](#)

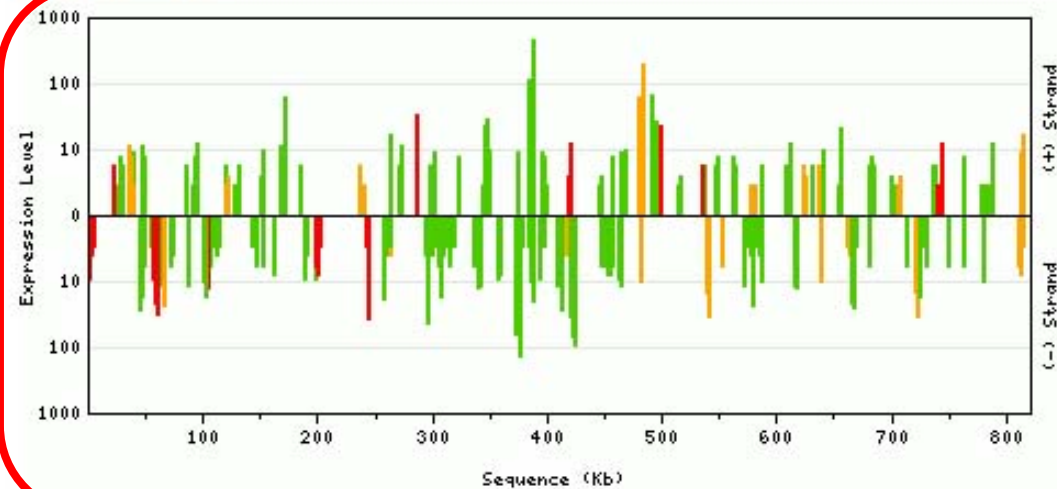
| N | TC | Seq | Freq | Odds | Cl | LocD | LocT | TrPos | Ch | Ini | Str | StdName | SysName | GC | TD | DS | BI | Cn | Info |
|----|----|-----------------|------|-------|----|------|-----------|-------|----|--------|-----|---------|----------|----|----|----|----|-----------|------|
| 1 | Un | CATGGTCAACAAAG | 2 | 0.807 | Si | Int | int,opORF | 0 | 1 | 43989 | + | N.A. | YAL054C | | | | | 3 4 0 | - |
| 2 | Un | CATGACACCACCAG | 3 | 1.000 | Fe | Int | int,opORF | 0 | 1 | 140213 | + | N.A. | YAL005C | | | | | 3 0 10 | - |
| 3 | Un | CATGGAGGAGATT | 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 | CATGCACCTTCAACT | 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 | CATGGAATCCGGT | 2 | 0.807 | Si | Int | int,opORF | 0 | 2 | 576616 | + | N.A. | YBR170C | | | | | 3 0 3 | - |
| 13 | Un | CATGTAAAAA | 2 | 1.000 | Fe | Int | int | 0 | 2 | 622839 | + | N.A. | --- | | | | | 6 4 0 | - |
| 14 | Un | CATGGCGTTGAGG | 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 | CATGCACCTTCAACT | 20 | 1.000 | Fe | Int | int | 0 | 3 | 90077 | + | N.A. | --- | | | | | 12 8 3 | - |
| 18 | Un | CATGCTCTCTCGTT | 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 | CATGATATCAAAA | 2 | 0.375 | Al | ORF | ORFv | 7 | 4 | 179499 | + | MSH5 | YDL154W | | | | | 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

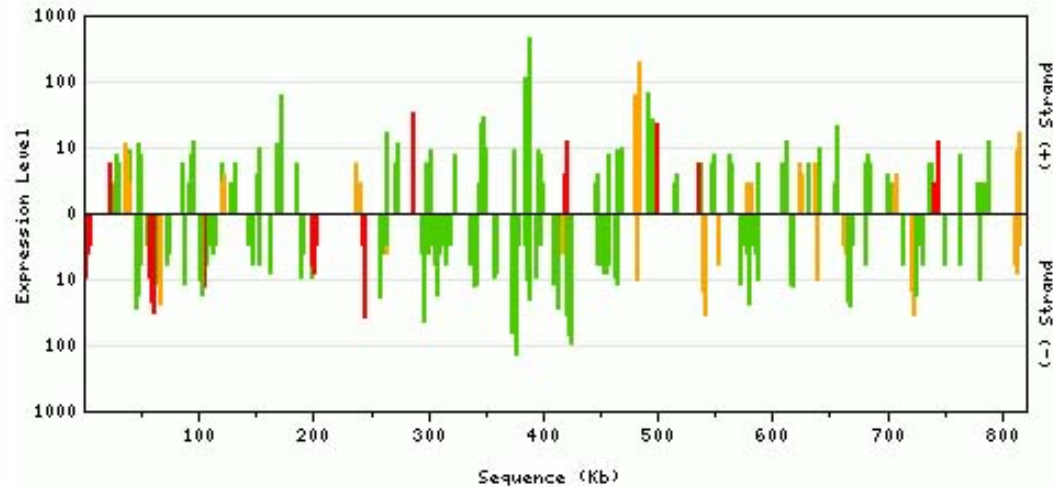
Expression Map: An expression map with the counts of all the mapped tags onto the genome is displayed. This is useful to detect transcriptionally active regions in a chromosome.

Expression Map

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

Organism: *Sacharomyces cerevisiae*

Chromosome: 2



Keys:

Color:

TAG of High Confidence TAG of Undefined Confidence TAG of Low Confidence

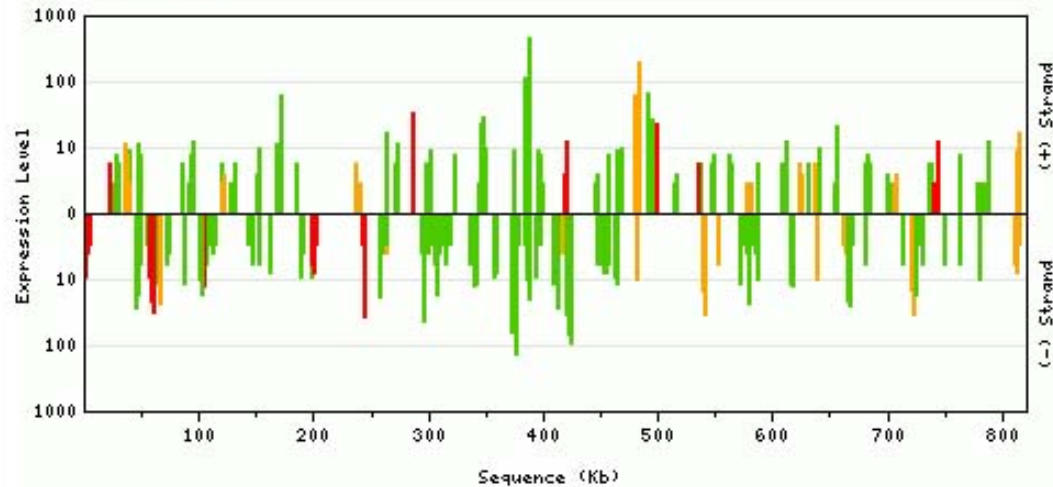
Expression Map: The user can select a single experimental condition or to display all of them simultaneously (as it is the case in this example). The 'show' button on the right must be clicked to make effective any change of parameters.

Expression Map

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

Organism: *Sacharomyces cerevisiae*

Chromosome: 2



Keys:

Color:

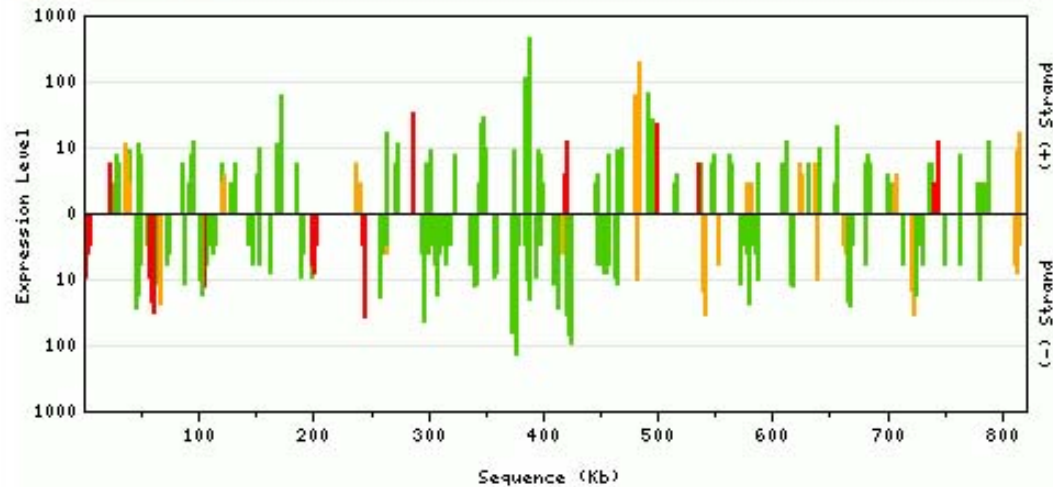
█ TAG of High Confidence █ TAG of Undefined Confidence █ TAG of Low Confidence

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.

Expression Map

Experimental Condition: Expression Level: to (range: 0-1000)Y-Axis Scale: Organism: *Sacharomyces cerevisiae*

Chromosome: 2



Keys:

Color:

 TAG of High Confidence TAG of Undefined Confidence TAG of Low Confidence

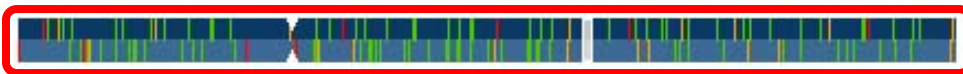
Expression Map: The user can select two types of scale for the Y axis of the graph: linear or logarithmic. The 'show' button on the right must be clicked to make effective any change of parameters.

Expression Map

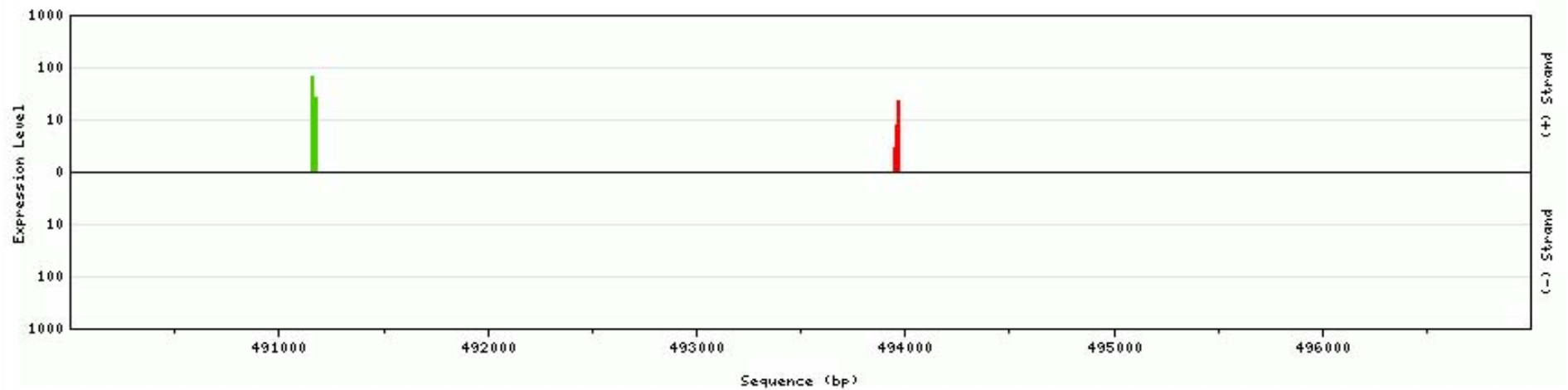
Experimental Condition: Expression Level: to (range: 0-1000) Y-Axis Scale:

Organism: *Sacharomyces cerevisiae*

Fragment Displayed: 490,001 - 497,000



100 Kb Chromosome: 2 Length: 813,178 bp



Keys:

Chromosome:

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

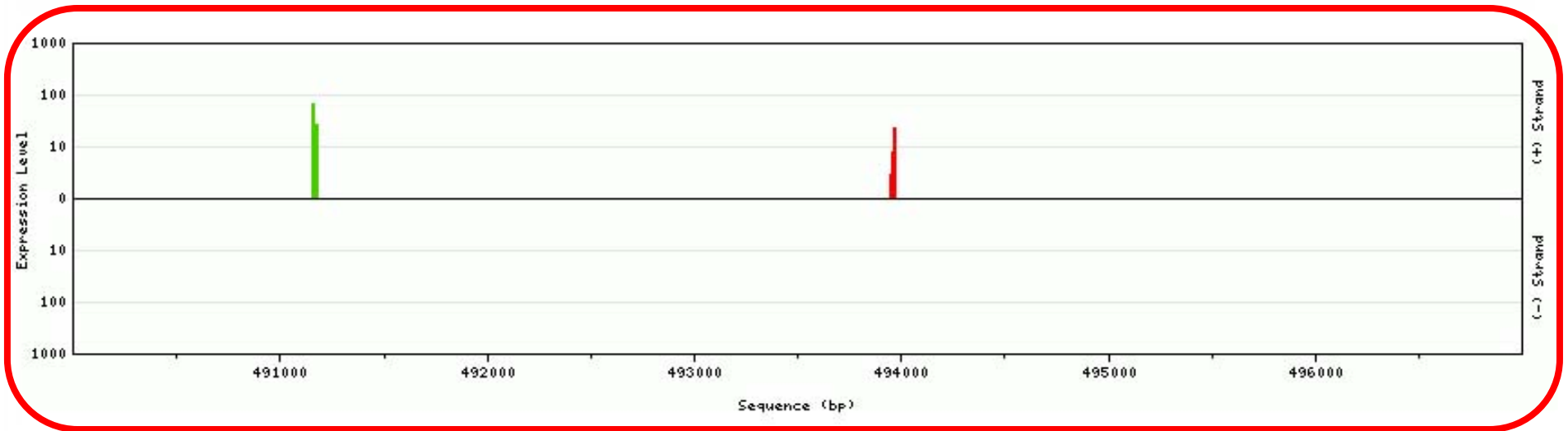
Expression Map: The tags mapped are graphically shown in the chromosome.

Expression Map

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

Organism: *Sacharomyces cerevisiae*

Fragment Displayed: 490,001 - 497,000



Keys:

Chromosome:

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

Expression Map

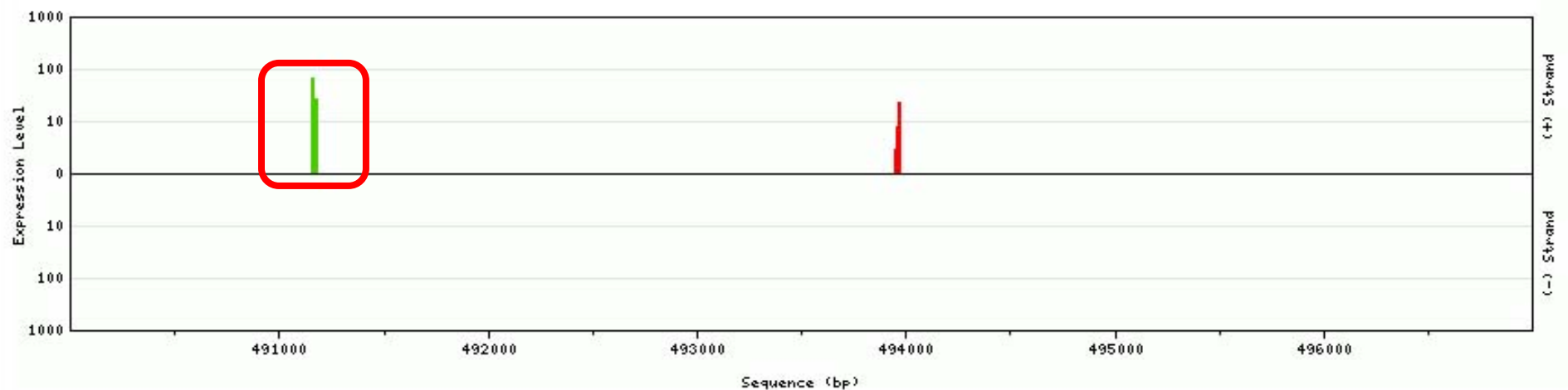
Experimental Condition: Expression Level: to (range: 0-1000) Y-Axis Scale:

Organism: *Sacharomyces 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 |
| | | TAG of Low 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.

The image displays the SAGExplore web server interface. The background is a dark blue grid of DNA sequence characters (A, T, C, G). On the left, there is a glowing white mouse and a glowing blue frog. In the center, a circular genome map is shown with a white outline and a blue interior. On the right, a green DNA sequence is highlighted. At the bottom, there are three orange buttons: "Genome Explore", "Genome Mapping", and "Library Mapping".

***This is the end of the SAGExplore web server tutorial for
Module II: Genome Mapping
Any comments or inquiries, please contact us***