Tools and Resources

Kevin MacPherson

8/24/18

S288C
Axial budding

VS.

W303
Bipolar budding

BUD4 is mutated in W303

ACE2, *CBK1*, and *BUD4* in Budding and Cell Separation

Warren P. Voth, Aileen E. Olsen, Mohammed Sbia,† Karen H. Freedman,‡ and David J. Stillman*

Department of Pathology, University of Utah Health Sciences Center, Salt Lake City, Utah 84132

Received 14 January 2005/Accepted 6 April 2005

Mutations in the RAM network genes, including *CBK1*, *MOB2*, *KIC1*, *HYM1*, and *TAO3*, cause defects in bud site selection, asymmetric apical growth, and mating projections. Additionally, these mutants show altered colony morphology, cell separation defects, and reduced *CTS1* expression, phenotypes also seen by mutating the Ace2 transcription factor. We show that an *ACE2* multicopy plasmid suppresses the latter three defects of RAM network mutations, demonstrating that Ace2 is downstream of the RAM network and suggesting that these phenotypes are caused by reduced expression of Ace2 target genes. We show that wild-type W303 strains have a *bud4* mutation and that combining *bud4* with either *ace2* or *cbk1* in haploids results in altered colony morphology. We describe a timed sedimentation assay that allows quantitation of cytokinesis defects and subtle changes in budding pattern and cell shape. Experiments examining budding patterns and sedimentation rates both show that Ace2 and Cbk1 have independent functions in addition to their common pathway in transcription of genes such as *CTS1*. *SWI5* encodes a transcription factor paralogous to *ACE2*. Additive effects are seen in *cbk1 swi5* strains, and we show that activation of some target genes, such as *EGT2*, requires either Swi5 or Ace2 with Cbk1. The relative roles and interactions of Ace2, Cbk1, and Bud4 in bud site selection, polarized growth, and cell separation are discussed.

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Variant Viewer

yeastgenome.org/variant-viewer

BUD4 / YJR092W Anillin-like protein

Location: Chromosome X 598735..603078

DNA Protein

Download Legend

SNP at Chromosome X 599034

1000 1500

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SEY6210		T	A	G	C	G	C	T	G	C	A	C	T	C
W303		T	A	G	C	G	C	T	G	C	A	C	T	C
JK9-3d		T	A	G	C	G	C	T	G	C	A	C	T	C
FL100		T	A	G	C	G	C	T	G	C	A	C	T	C
CEN.PK		T	A	G	C	G	C	T	G	C	A	C	T	C
D273-10B		T	A	G	C	G	C	T	G	C	A	C	T	C
Sigma1278b		T	A	G	C	G	C	T	G	C	A	C	T	C
RM11-1a		T	G	G	C	G	C	T	G	C	A	T	C	C
SK1		T	A	G	C	G	C	T	G	C	A	C	T	C
Y55		A	A	C	T	A	T	A	A	T	G	C	C	A

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1000 1500

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X2180-1A		T	A	G	C	G	C	T	G	C	A	C	T	C
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W303		T	A	G	C	G	C	T	G	C	A	C	T	C
JK9-3d		T	A	G	C	G	C	T	G	C	A	C	T	C
FL100		T	A	G	C	G	C	T	G	C	A	C	T	C
CEN.PK		T	A	G	C	G	C	T	G	C	A	C	T	C
D273-10B		T	A	G	C	G	C	T	G	C	A	C	T	C
Sigma1278b		T	A	G	C	G	C	T	G	C	A	C	T	C
RM11-1a		T	G	G	C	G	C	T	G	C	A	T	C	C
SK1		T	A	G	C	G	C	T	G	C	A	C	T	C
Y55		A	A	C	T	A	T	A	A	T	G	C	C	A

	1	87	143	202	243	300	429
S288C		T	A	G	C	G	C
X2180-1A		T	A	G	C	G	C
SEY6210		T	A	G	C	G	C
W303		T	A	G	C	G	C
JK9-3d		T	A	G	C	G	C
FL100		T	A	G	C	G	C
CEN.PK		T	A	G	C	G	C
D273-10B		T	A	G	C	G	C
Sigma1278b		T	A	G	C	G	C
RM11-1a		T	G	G	C	G	C
SK1		T	A	G	C	G	C
Y55		A	A	C	T	A	T

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1000 1500

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X2180-1A		T	A	G	C	G	C	T	G	C	A	C	T	C
SEY6210		T	A	G	C	G	C	T	G	C	A	C	T	C
W303		T	A	G	C	G	C	T	G	C	A	C	T	C
JK9-3d		T	A	G	C	G	C	T	G	C	A	C	T	C
FL100		T	A	G	C	G	C	T	G	C	A	C	T	C
CEN.PK		T	A	G	C	G	C	T	G	C	A	C	T	C
D273-10B		T	A	G	C	G	C	T	G	C	A	C	T	C
Sigma1278b		T	A	G	C	G	C	T	G	C	A	C	T	C
RM11-1a		T	G	G	C	G	C	T	G	C	A	T	C	C
SK1		T	A	G	C	G	C	T	G	C	A	C	T	C
Y55		A	A	C	T	A	T	A	A	T	G	C	C	A

Variant Viewer

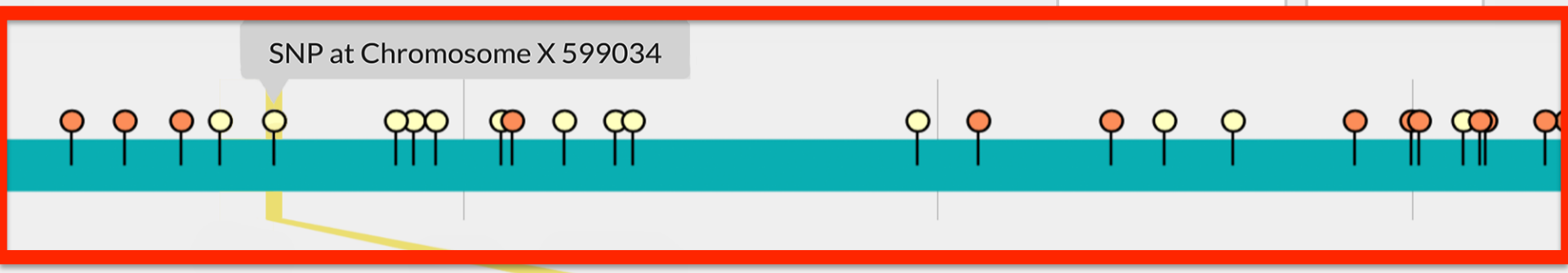
yeastgenome.org/variant-viewer

BUD4 / YJR092W Anillin-like protein

Location: Chromosome X 598735..603078

DNA Protein

Download Legend



	1	87	143	202	243	300	429	447	471	540	551	606	660	678
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X2180-1A		T	A	G	C	G	C	T	G	C	A	C	T	C
SEY6210		T	A	G	C	G	C	T	G	C	A	C	T	C
W303		T	A	G	C	G	C	T	G	C	A	C	T	C
JK9-3d		T	A	G	C	G	C	T	G	C	A	C	T	C
FL100		T	A	G	C	G	C	T	G	C	A	C	T	C
CEN.PK		T	A	G	C	G	C	T	G	C	A	C	T	C
D273-10B		T	A	G	C	G	C	T	G	C	A	C	T	C
Sigma1278b		T	A	G	C	G	C	T	G	C	A	C	T	C
RM11-1a		T	G	G	C	G	C	T	G	C	A	T	C	C
SK1		T	A	G	C	G	C	T	G	C	A	C	T	C
Y55		A	A	C	T	A	T	A	A	T	G	C	C	A

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SNP at Chromosome X 599034

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W303		T	A	G	C	G	C	T	G	C	A	C	T	C
JK9-3d		T	A	G	C	G	C	T	G	C	A	C	T	C
FL100		T	A	G	C	G	C	T	G	C	A	C	T	C
CEN.PK		T	A	G	C	G	C	T	G	C	A	C	T	C
D273-10B		T	A	G	C	G	C	T	G	C	A	C	T	C
Sigma1278b		T	A	G	C	G	C	T	G	C	A	C	T	C
RM11-1a		T	G	G	C	G	C	T	G	C	A	T	C	C
SK1		T	A	G	C	G	C	T	G	C	A	C	T	C
Y55		A	A	C	T	A	T	A	A	T	G	C	C	A

Variant Viewer

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BUD4 / YJR092W Anillin-like protein

Location: Chromosome X 598735..603078

DNA Protein

Download Legend

SNP at Chromosome X 599034

1000

- Insertion
- Deletion
- Synonymous SNP
- Nonsynonymous SNP
- Intron SNP
- Untranslatable SNP

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X2180-1A		T	A	G	C	G	C	T					C
SEY6210		T	A	G	C	G	C	T					C
W303		T	A	G	C	G	C	T					C
JK9-3d		T	A	G	C	G	C	T	G	C	A	C	T	C
FL100		T	A	G	C	G	C	T	G	C	A	C	T	C
CEN.PK		T	A	G	C	G	C	T	G	C	A	C	T	C
D273-10B		T	A	G	C	G	C	T	G	C	A	C	T	C
Sigma1278b		T	A	G	C	G	C	T	G	C	A	C	T	C
RM11-1a		T	G	G	C	G	C	T	G	C	A	T	C	C
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Y55		A	A	C	T	A	T	A	A	T	G	C	C	A

Variant Viewer

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BUD4 / YJR092W Anillin-like protein

DNA Protein

Location: Chromosome X 598735..603078

Download Legend

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SEY6210	P	S	I	L	GDITFNRGDLLSLSFDEELGQDFANFL		P	E	E	H H	I	E	Y
W303	P	S	I	L	----------		P	E	E	H H	I	E	Y
JK9-3d	P	S	I	L	GDITFNRGDLLSLSFDEELGQDFANFL		P	E	E	H H	I	E	Y
FL100	P	S	I	L	GDITFNRGDLLSLSFDEELGQDFANFL		P	E	E	H H	I	E	Y
CEN.PK	P	S	V	L	GDITFNRGDLLSLSFDEELGQDFANFL		L	E	K	H H	I	E	Y
D273-10B	P	S	V	L	GDITFNRGDLLSLSFDEELGQDFANFL		L	G	E	P R	V	K	Y
Sigma1278b	P	S	I	L	GDITFNRGDLLSLSFDEELGQDFANFL		P	E	E	H H	I	E	Y
RM11-1a	S	S	V	P	GDITFNRGDLLSLSFDEELGQDFANFL		P	E	E	H R	I	E	H
SK1	P	S	I	L	GDITFNRGDLLSLSFDEELGQDFANFL		P	E	E	H H	I	E	Y
Y55	P	Y	V	P	GDITFNRGDLLSSSFDEELGQDFANFL		P	E	E	H H	I	E	Y

Variant Viewer

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BUD4 / YJR092W Anillin-like protein

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DNA Protein

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	585	666	746	789	813	840	880	1009	1064	1231	1243	1275	1304
S288C	P	S	I	L	GDITFNRGDLLSLSFDEELGQDFANFL		P	E	E	H H	I	E	Y
X2180-1A	P	S	I	L	GDITFNRGDLLSLSFDEELGQDFANFL		P	E	E	H H	I	E	Y
SEY6210	P	S	I	L	GDITFNRGDLLSLSFDEELGQDFANFL		P	E	E	H H	I	E	Y
W303	P	S	I	L	----------		P	E	E	H H	I	E	Y
JK9-3d	P	S	I	L	GDITFNRGDLLSLSFDEELGQDFANFL		P	E	E	H H	I	E	Y
FL100	P	S	I	L	GDITFNRGDLLSLSFDEELGQDFANFL		P	E	E	H H	I	E	Y
CEN.PK	P	S	V	L	GDITFNRGDLLSLSFDEELGQDFANFL		L	E	K	H H	I	E	Y
D273-10B	P	S	V	L	GDITFNRGDLLSLSFDEELGQDFANFL		L	G	E	P R	V	K	Y
Sigma1278b	P	S	I	L	GDITFNRGDLLSLSFDEELGQDFANFL		P	E	E	H H	I	E	Y
RM11-1a	S	S	V	P	GDITFNRGDLLSLSFDEELGQDFANFL		P	E	E	H R	I	E	H
SK1	P	S	I	L	GDITFNRGDLLSLSFDEELGQDFANFL		P	E	E	H H	I	E	Y
Y55	P	Y	V	P	GDITFNRGDLLSSSFDEELGQDFANFL		P	E	E	H H	I	E	Y

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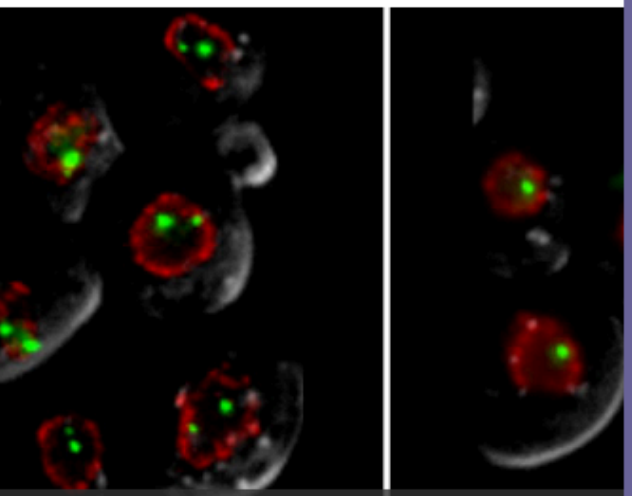
Align Strain Sequences
Synteny Viewer

About SGD

The *Saccharomyces* Genome Database (SGD) provid
integrated biological information for the budding yea
cerevisiae along with search and analysis tools to exp
enabling the discovery of functional relationships be
gene products in fungi and higher organisms.



nes (green) coalesce into foci after heat shock (nu
of S. Chowdhary and A. Kainth, Gross Lab, LSU Hea

ngs

cs Meeting
August 26, 2018 -
versity, Stanford, California

(Almost) All Hands on Deck for Calcineurin -
July 31, 2018
If there was a World Cup soccer championship
for cellular proteins, it's a pretty sure bet that

Tweets by @yeastgenome

SGD Project
@yeastgenome
Congrats to @YeastCourseCSH
plate race

Enter gene name, GO term, chromosome, or list of

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Strains

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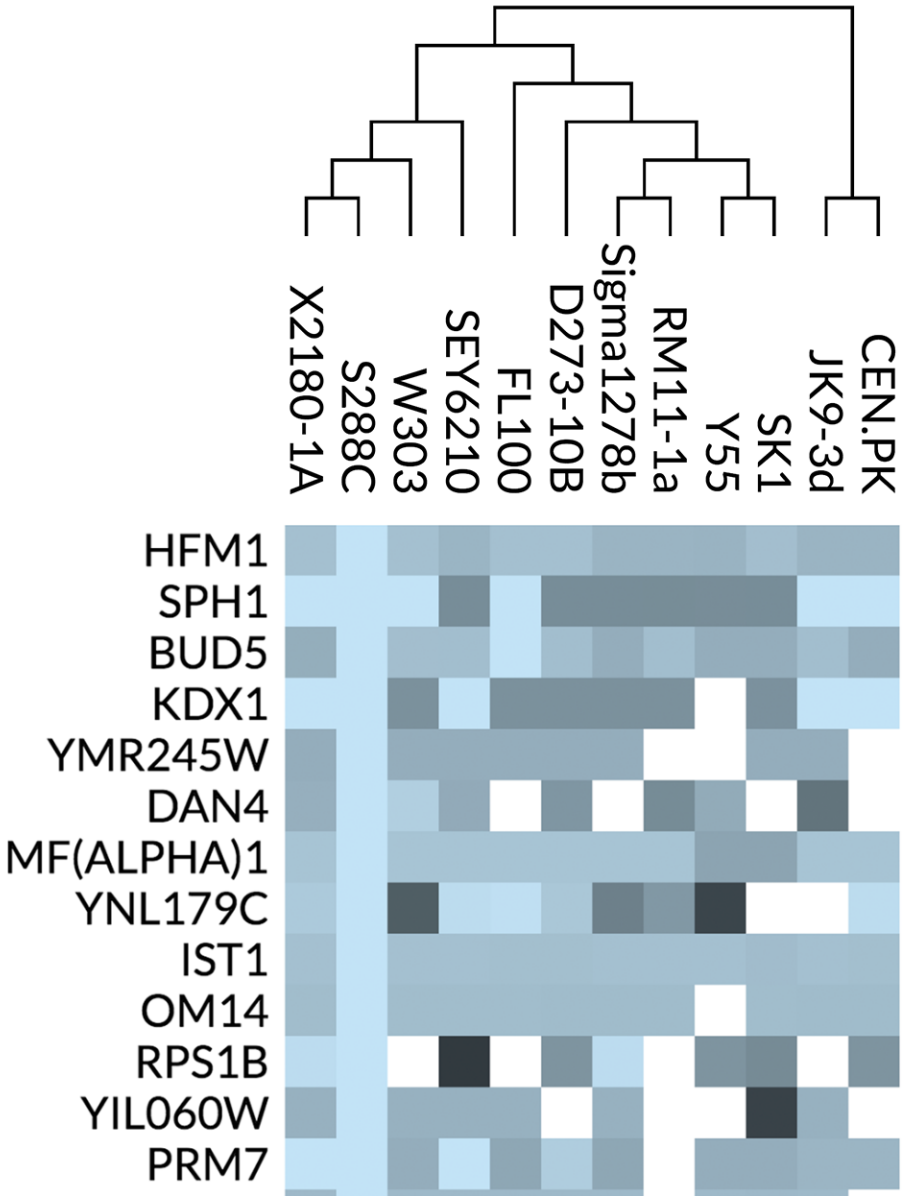
DNA

Protein



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Alignment Score

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Strains

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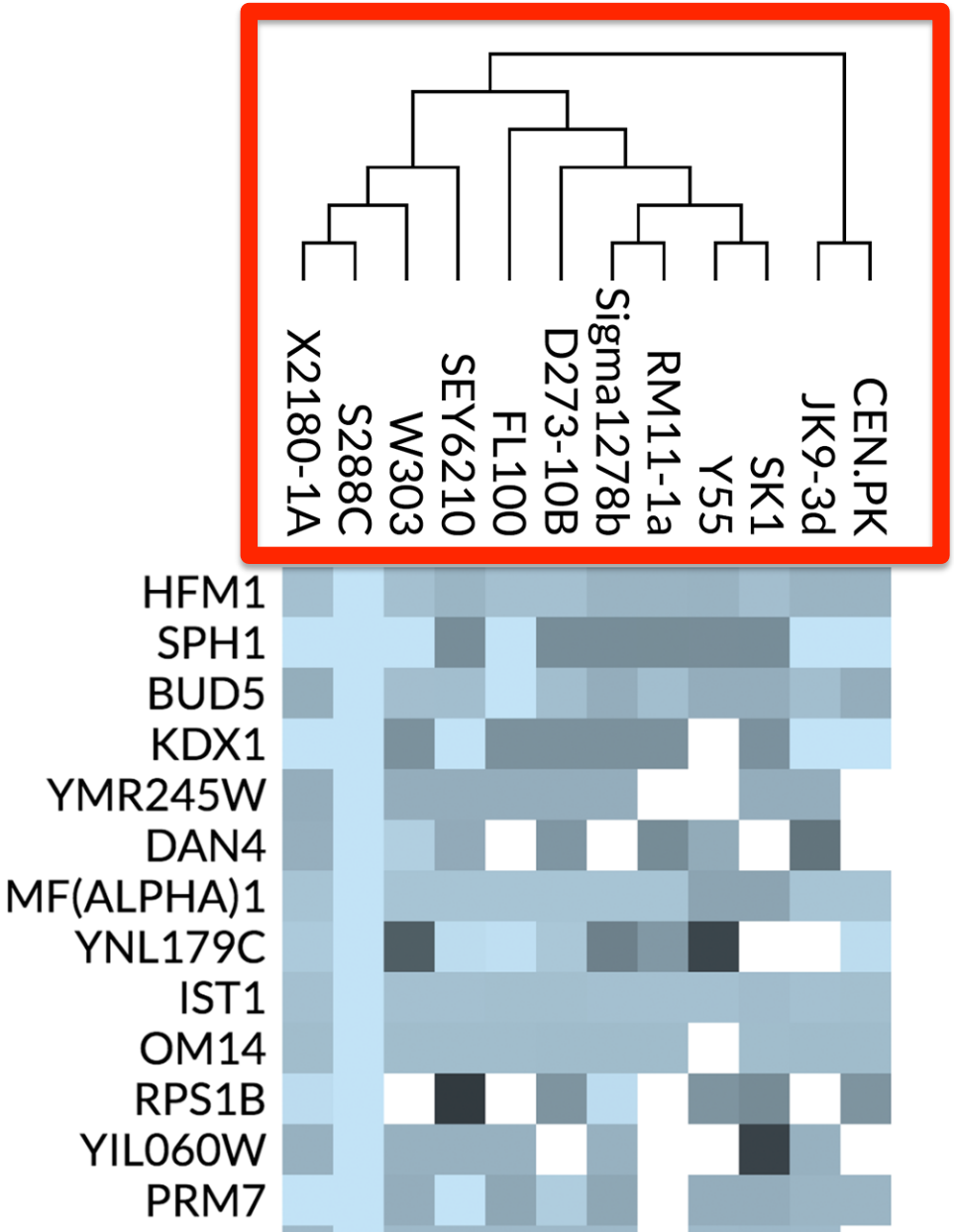
DNA

Protein



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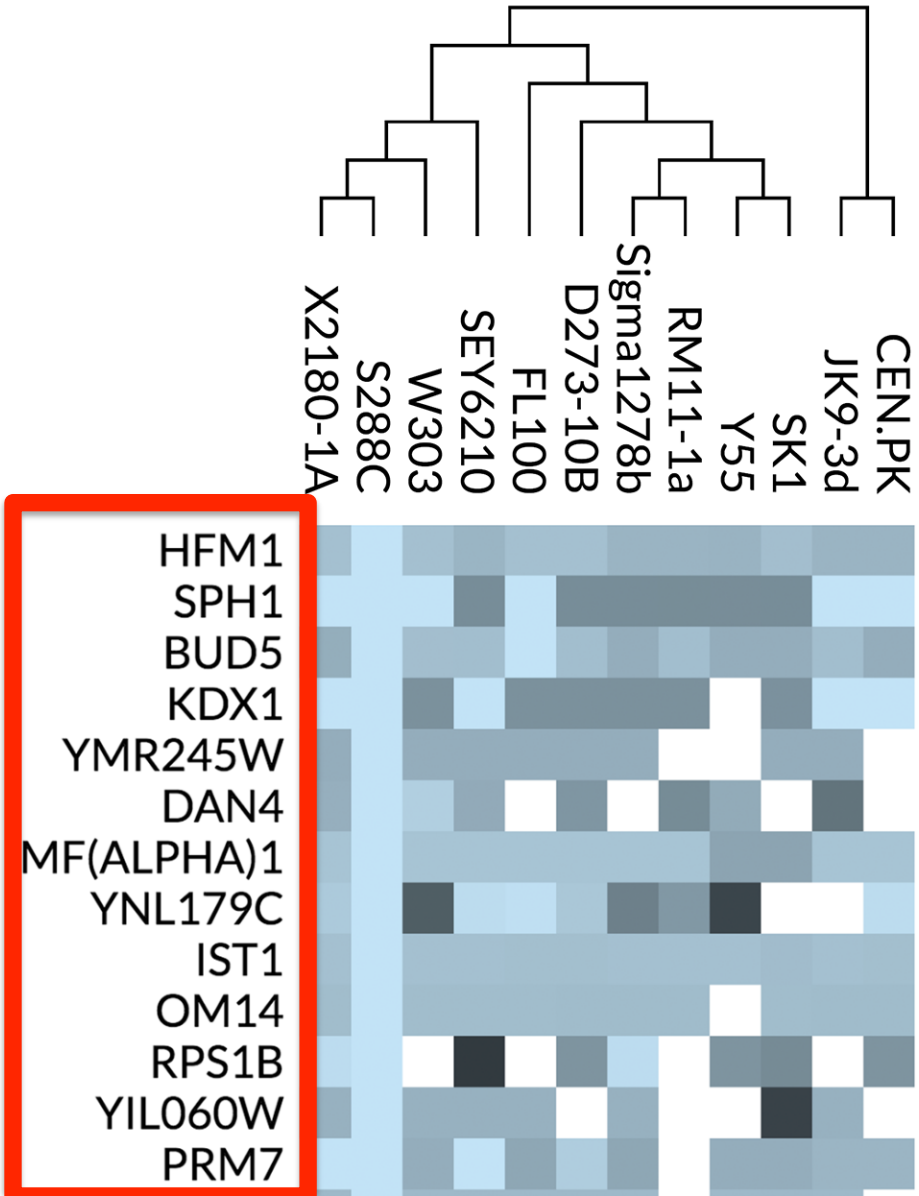

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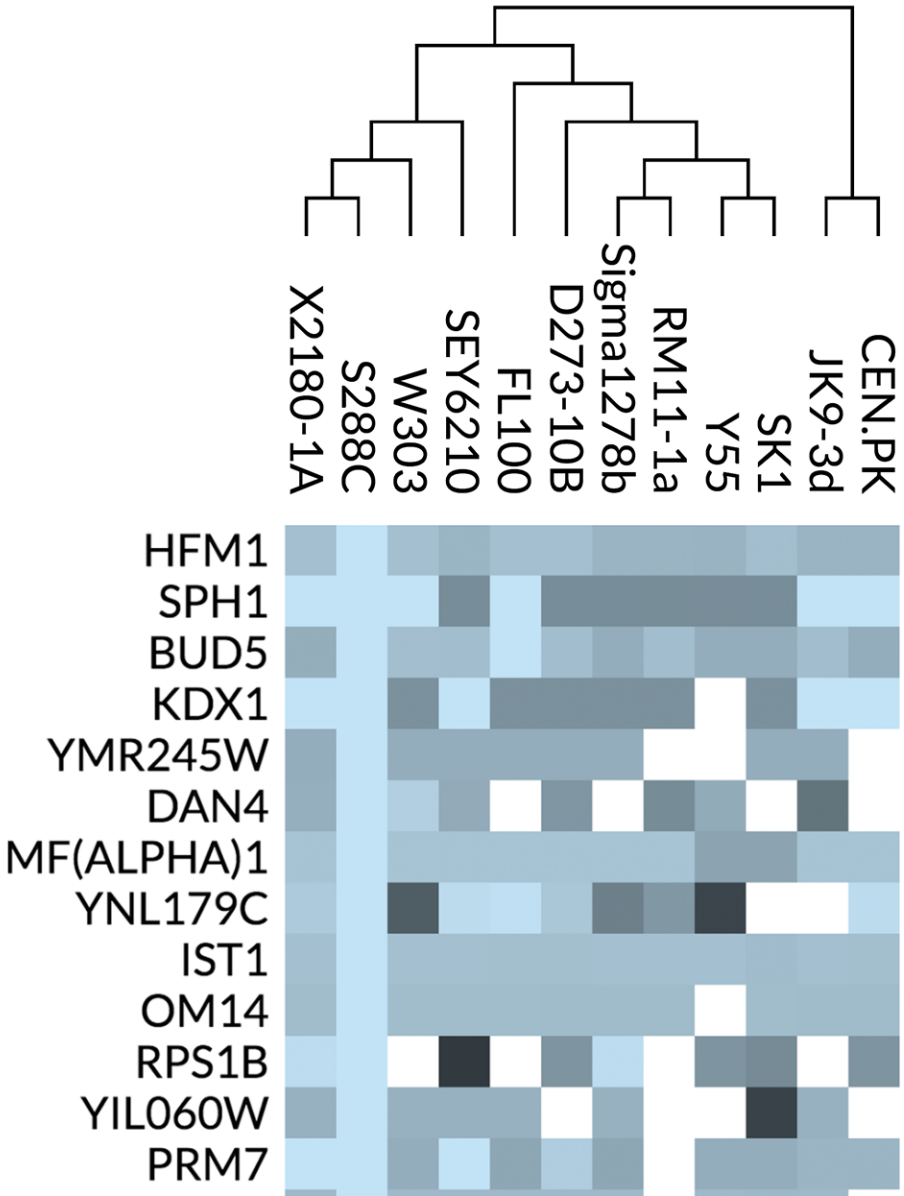
DNA

Protein



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Alignment Score

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Strains

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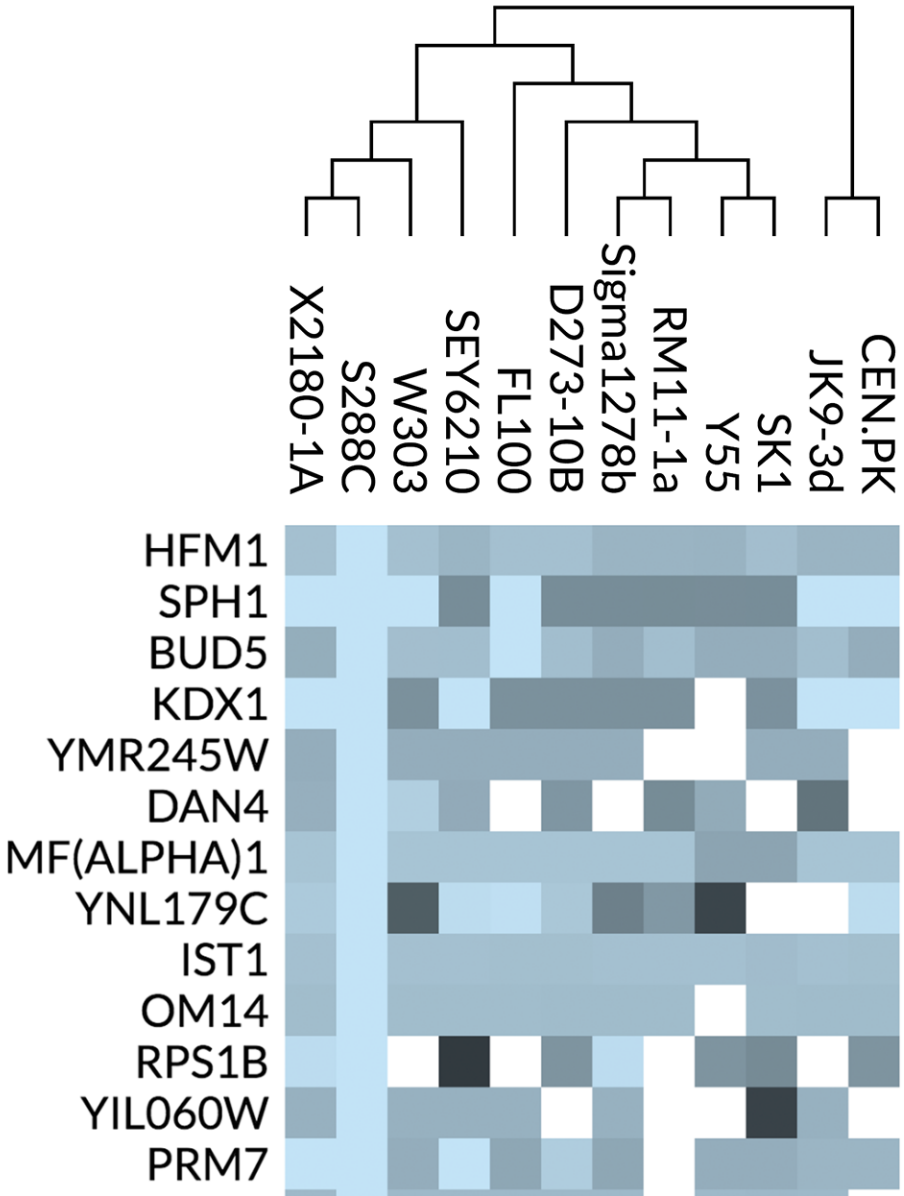
DNA

Protein



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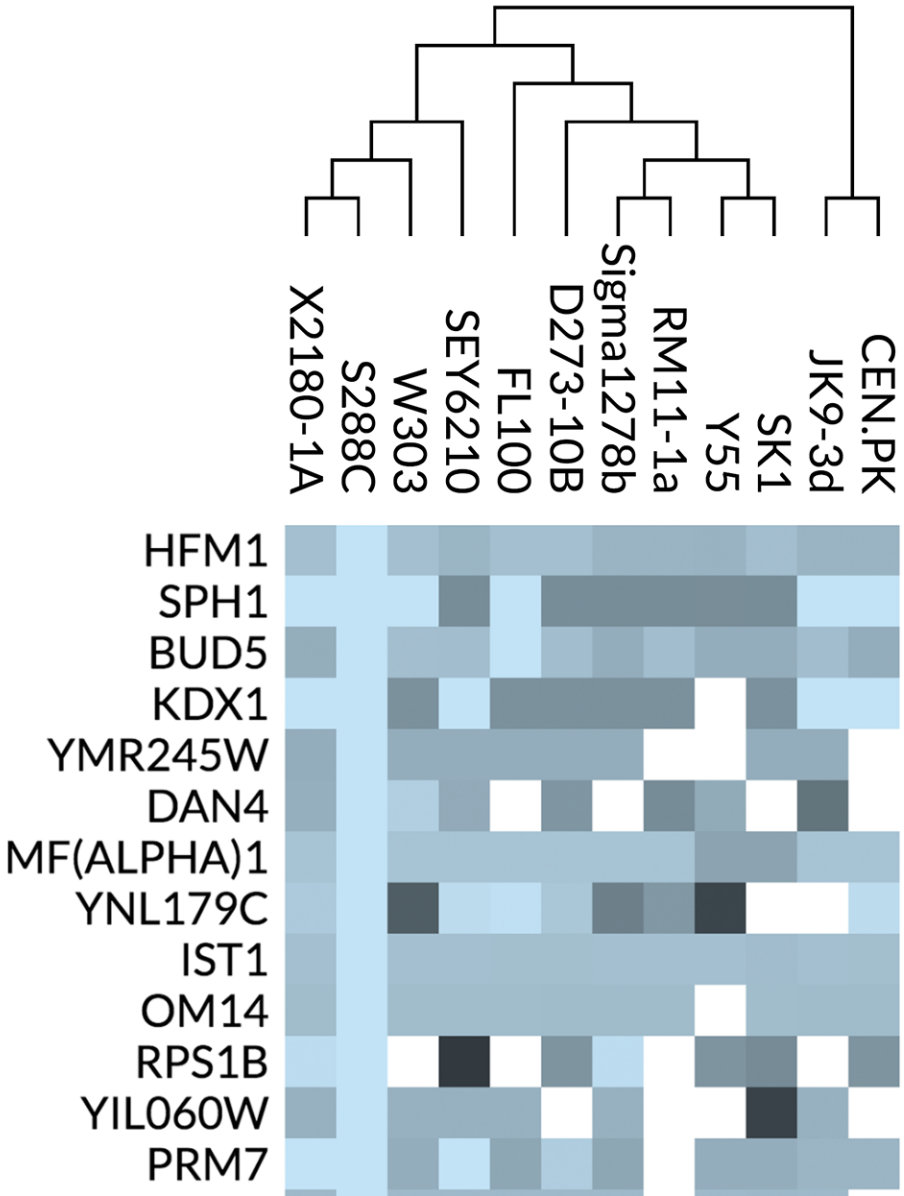
Filter

Strains

Settings

DNA

Protein



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Alignment Score

1.00 0.00

N/A

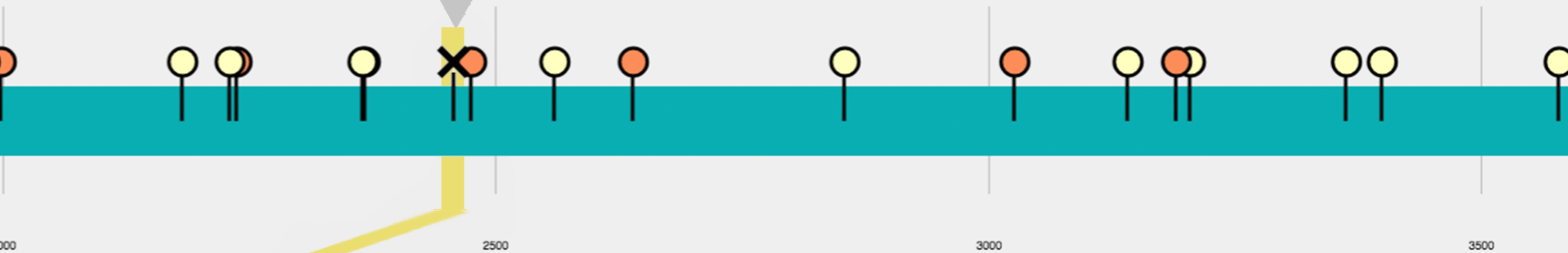
BUD4 / YJR092W Anillin-like protein

DNA Protein

Location: Chromos

Download Legend

Deletion at Chromosome X 601191



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X2180-1A	G	T	G	C	C	A	C	G	G	C	A	A
SEY6210	G	T	G	C	C	A	C	G	G	C	A	A
W303	-	T	G	C	C	A	C	G	G	C	A	A
JK9-3d	G	T	G	C	C	A	C	G	G	C	A	A
FL100	G	T	G	C	C	A	C	G	G	C	A	A
CEN.PK	G	T	G	T	C	A	T	A	A	C	A	A
D273-10B	G	T	G	T	C	G	C	G	G	T	G	G
Sigma1278b	G	T	G	C	C	A	C	G	G	C	A	A
RM11-1a	G	T	G	C	T	A	C	G	G	C	A	A
SK1	G	T	A	C	C	A	C	G	G	C	A	A
Y55	G	C	G	C	C	A	C	G	G	C	A	A

/ YJR092W Anillin-like protein

Chromos

Deletion at Chromosome X 601191

2500 3000

2457 2474 2559 2639 2853 3026 3141 3190 3204

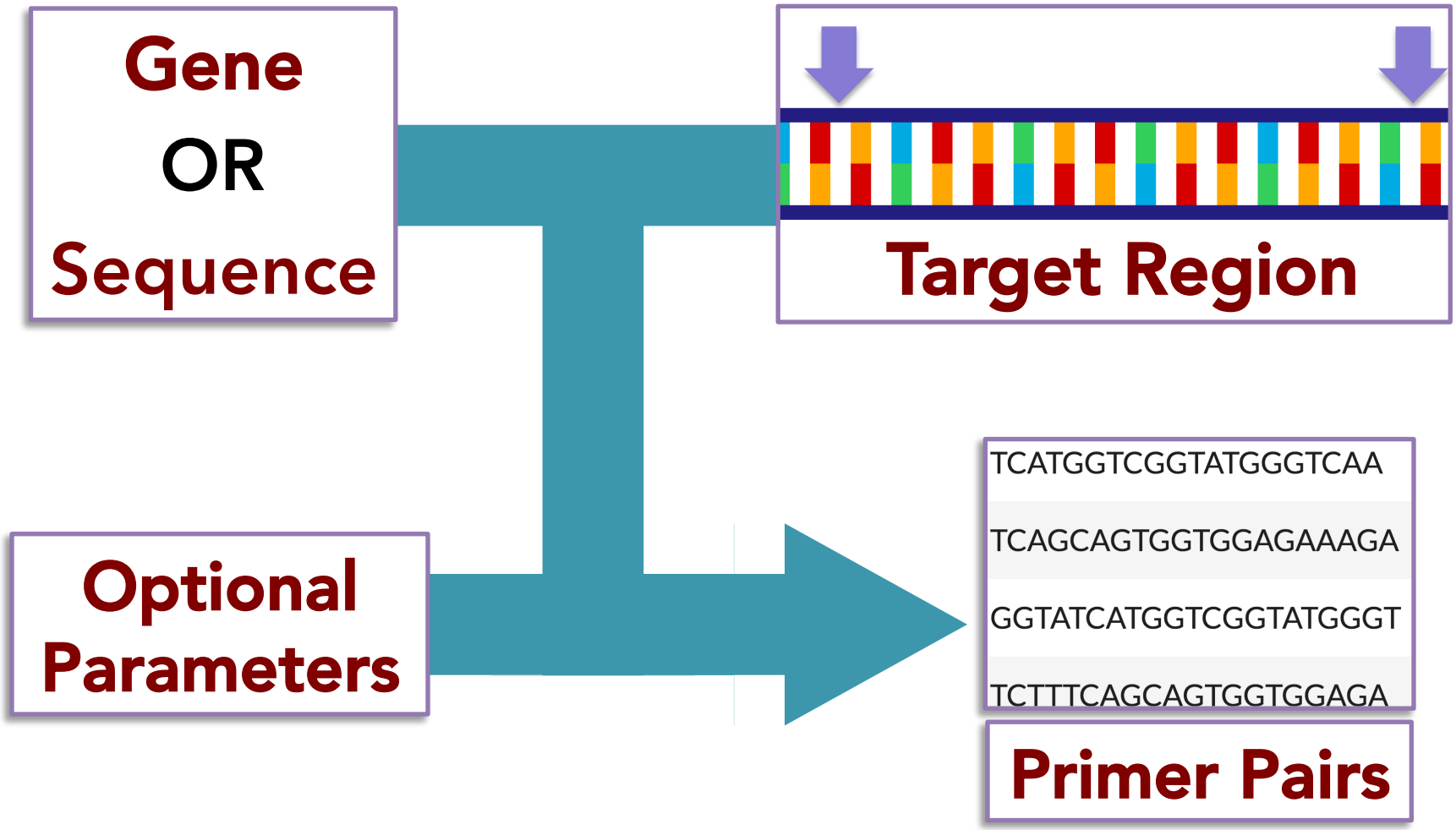
G T G C C A C G G

	2457	2474	2559	2639
S288C	G	T	G	C
X2180-1A	G	T	G	C
SEY6210	G	T	G	C
W303	-	T	G	C
JK9-3d	G	T	G	C
FL100	G	T	G	C
CEN.PK	G	T	G	T

SGD moved to cloud!

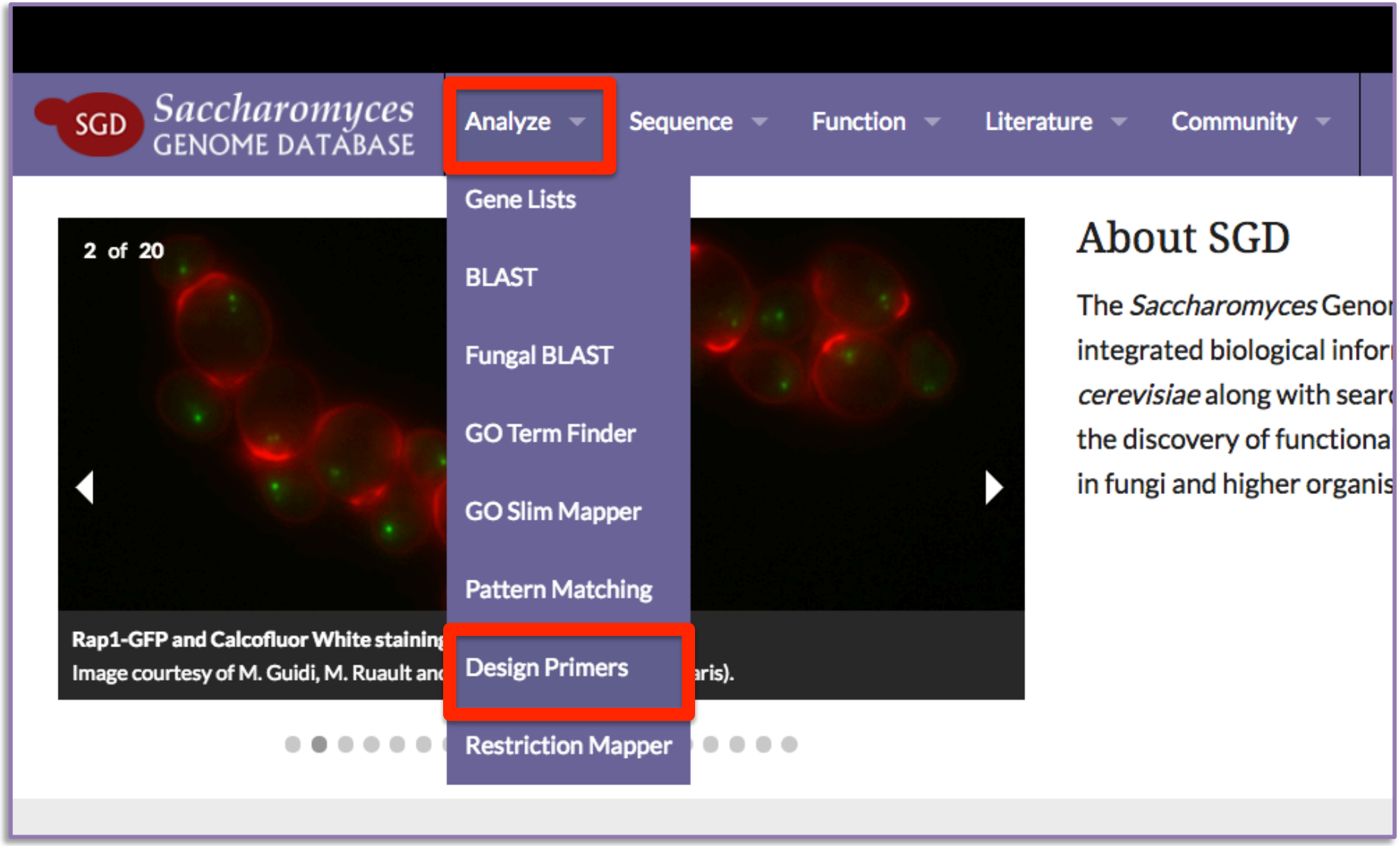
Primer Design

yeastgenome.org/primer3



Primer Design

yeastgenome.org/primer3



Primer Design: Uses Primer3-py package

Sequences of primer sets available to the community

Design your own primers:

Please input gene name OR sequence

Locus: Enter a standard gene name or systematic ORF name (i.e. ACT1, YKR054C)

OR

Enter the DNA Sequence (NOTE: Paste in DNA sequence only; all headers, comments, numbers and spaces should be removed)

Target Region

(NOTE: primers will be chosen from the flanking regions just **outside** of this defined region)

Start: bp from DNA sequence start OR gene START codon, where neg # = upstream:

500

End: bp from DNA sequence start OR from gene START codon:

900

Maximum product size in bp, cannot be less than target size (Optional):

Force Start position of primers

Forces the 3' endpoints of the left and right primers to Target Start and End respectively:

- (•) NO
- ( ) YES

Primer Design: Uses Primer3-py package

Sequences of primer sets available to the community

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900

Maximum product size in bp, cannot be less than target size (Optional):

Force Start position of primers

Forces the 3' endpoints of the left and right primers to Target Start and End respectively:

- (•) NO
- ( ) YES

Primer Length

Minimum primer length: 18

Optimum primer length: 20

Maximum primer length: 23

Primer Composition

Minimum percent GC: 30

Optimum percent GC: 50

Maximum percent GC: 70

Melting Temperature

Minimum Tm: 57

Optimum Tm: 59

Maximum Tm: 62

Primer Annealing

Max Self Complementarity: 8

Max 3' Self Complementarity: 3

Max Pair Complementarity: 8

Max 3' Pair Complementarity: 3

Pick Primers OR Reset to Defaults

Start: bp from DNA sequence start OR gene START codon, where neg # = upstream:

500

End: bp from DNA sequence start OR from gene START codon:

900

Maximum product size in bp, cannot be less than target size (Optional):

Force Start position of primers

Forces the 3' endpoints of the left and right primers to Target Start and End respectively:

- (•) NO
- ( ) YES

Primer Length

Minimum primer length: 18

Optimum primer length: 20

Maximum primer length: 23

Primer Composition

Minimum percent GC: 30

Optimum percent GC: 50

Maximum percent GC: 70

Melting Temperature

Minimum Tm: 57

Optimum Tm: 59

Maximum Tm: 62

Primer Annealing

Max Self Complementarity: 8

Max 3' Self Complementarity: 3

Max Pair Complementarity: 8

Max 3' Pair Complementarity: 3

Pick Primers OR Reset to Defaults

Start: bp from DNA sequence start OR gene START codon, where neg # = upstream:

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End: bp from DNA sequence start OR from gene START codon:

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Forces the 3' endpoints of the left and right primers to Target Start and End respectively:

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Primer Length

Minimum primer length: 18

Optimum primer length: 20

Maximum primer length: 23

Primer Composition

Minimum percent GC: 30

Optimum percent GC: 50

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Melting Temperature

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Max Self Complementarity: 8

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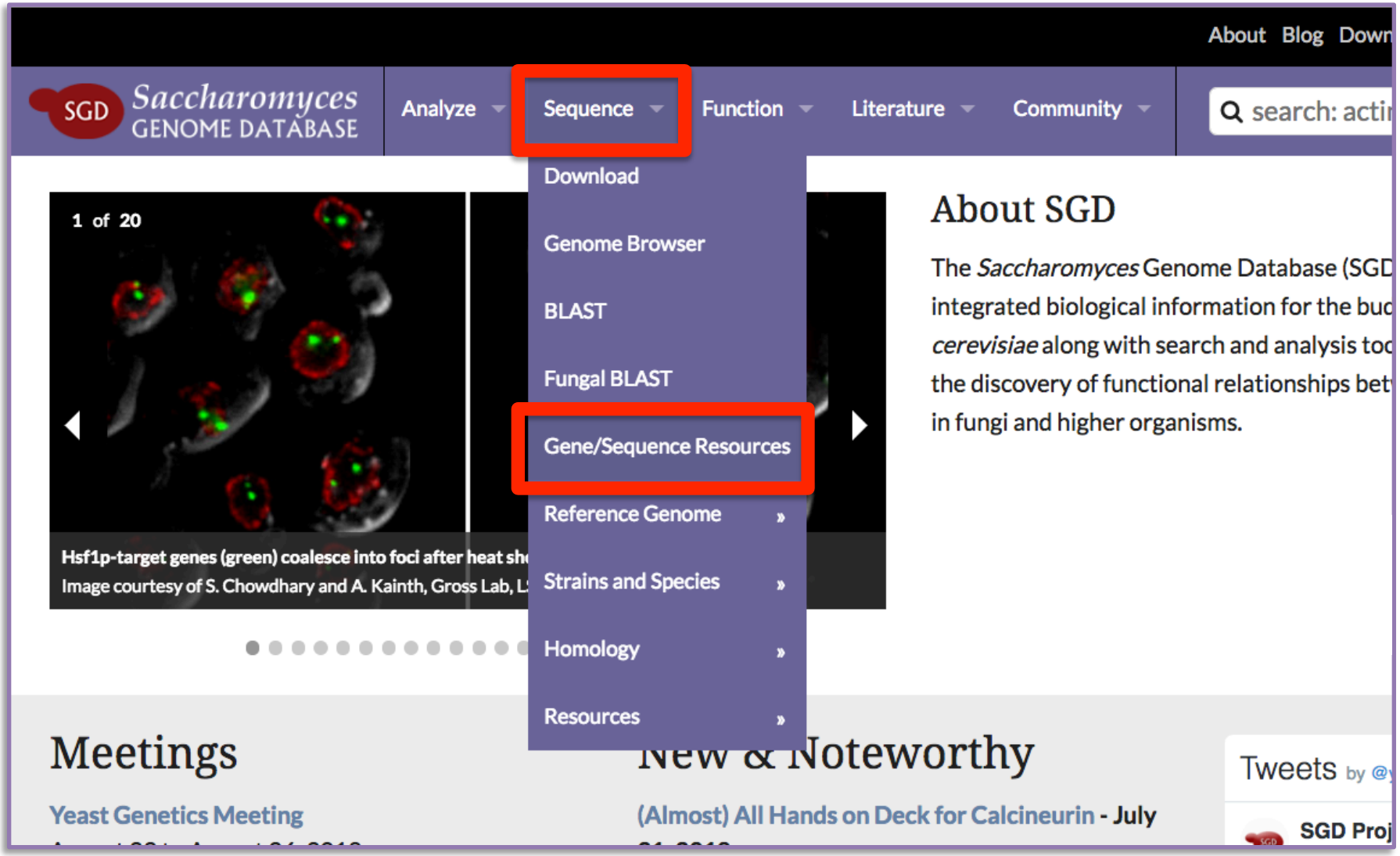
Pick Primers OR Reset to Defaults

Gene/Sequence Resources

yeastgenome.org/seqTools



Gene/Sequence Resources

The Gene/Sequence Resources tool allows retrieval of a list of options for accessing biological information, table/map displays, and sequence analysis tools for **1. a list of named genes or sequences. 2. a specified chromosomal region**, **or** **3. a raw DNA or protein sequence.**

1. Search a list of genes

Enter a list of names:

[space-separated standard gene names (and/or ORF and/or SGDID). Example: SIR2 YHR023W SGD:S000000001. The maximum gene number for this search is 50. It will take first 50 genes if more than 50 are provided.]

If available, add flanking basepairs

Upstream:

Downstream:

☐ Use the reverse complement

Pick one or more strains:

(Select or unselect multiple strains by pressing the Control (PC) or Command (Mac) key while clicking.)

- S. cerevisiae Reference Strain S288C
- S. cerevisiae Strain CEN.PK2-1Ca_JRIV01000000
- S. cerevisiae Strain D273-10B_JRIY00000000
- S. cerevisiae Strain FL100_JRIT00000000
- S. cerevisiae Strain JK9-3d_JRIZ00000000
- S. cerevisiae Strain RM11-1A_JRIP00000000
- S. cerevisiae Strain SEY6210_JRIW00000000
- S. cerevisiae Strain Sigma1278b-10560-6B_JRIQ00000000
- S. cerevisiae Strain W303_JRIU00000000
- S. cerevisiae Strain X2180-1A_JRIX00000000
- S. cerevisiae Strain Y55_JRIF00000000

Submit Form | Reset Form

OR 2. Search a specified chromosomal region of S288C genome

Pick a chromosome:

-- choose a chromosome --

Then enter coordinates (optional)

Note: Enter coordinates in ascending order for the Watson strand and descending order for the Crick strand.

☐ Use the reverse complement

Gene/Sequence Resources

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Pick one or more strains:

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- S. cerevisiae Reference Strain S288C
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- S. cerevisiae Strain RM11-1A_JRIP00000000
- S. cerevisiae Strain SEY6210_JRIW00000000
- S. cerevisiae Strain Sigma1278b-10560-6B_JRIQ00000000
- S. cerevisiae Strain W303_JRIU00000000
- S. cerevisiae Strain X2180-1A_JRIX00000000
- S. cerevisiae Strain Y55_JRIF00000000

Submit Form | Reset Form

OR 2. Search a specified chromosomal region of S288C genome

Pick a chromosome:

-- choose a chromosome --

Then enter coordinates (optional)

Note: Enter coordinates in ascending order for the Watson strand and descending order for the Crick strand.

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Upstream:

Downstream:

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- S. cerevisiae Reference Strain S288C
- S. cerevisiae Strain CEN.PK2-1Ca_JRIV01000000
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- S. cerevisiae Strain W303_JRIU00000000
- S. cerevisiae Strain X2180-1A_JRIX00000000
- S. cerevisiae Strain Y55_JRIF00000000

Submit Form | Reset Form

OR 2. Search a specified chromosomal region of S288C genome

Pick a chromosome:

-- choose a chromosome --

Then enter coordinates (optional)

Note: Enter coordinates in ascending order for the Watson strand and descending order for the Crick strand.

☐ Use the reverse complement

Upstream:

Downstream:

Use the reverse complement

S. cerevisiae Strain Sigma1278b-10560-6B_JRIQ00000000
S. cerevisiae Strain W303_JRIU00000000
S. cerevisiae Strain X2180-1A_JRIX00000000
S. cerevisiae Strain Y55_JRIF00000000

Submit Form | Reset Form

OR 2. Search a specified chromosomal region of S288C genome

Pick a chromosome:

-- choose a chromosome --

Then enter coordinates (optional)

to

The entire chromosome sequence will be displayed if no coordinates are entered.

Note: Enter coordinates in ascending order for the Watson strand and descending order for the Crick strand.

Use the reverse complement

Submit Form | Reset Form

OR 3. Analyze a raw DNA or Protein sequence

Type or Paste a:

DNA

Sequence:

The sequence **MUST** be provided in RAW format, no comments (numbers are okay).

Use the reverse complement (for DNA sequence only)

Submit Form | Reset Form

Upstream:

Downstream:

Use the reverse complement

S. cerevisiae Strain Sigma1278b-10560-6B_JRIQ00000000
S. cerevisiae Strain W303_JRIU00000000
S. cerevisiae Strain X2180-1A_JRIX00000000
S. cerevisiae Strain Y55_JRIF00000000

Submit Form | Reset Form

OR 2. Search a specified chromosomal region of S288C genome

Pick a chromosome:

-- choose a chromosome --

Then enter coordinates (optional)

to

The entire chromosome sequence will be displayed if no coordinates are entered.

Note: Enter coordinates in ascending order for the Watson strand and descending order for the Crick strand.

Use the reverse complement

Submit Form | Reset Form

OR 3. Analyze a raw DNA or Protein sequence

Type or Paste a:

DNA

Sequence:

The sequence **MUST** be provided in RAW format, no comments (numbers are okay).

Use the reverse complement (for DNA sequence only)

Submit Form | Reset Form

Gene/Sequence Resources

The currently displayed gene(s)/sequence(s) are RAD51/YER095W, RAD52/YML032C, RAD50/YNL250W

Download All Sequences: Genomic DNA (.fsa) | Genomic DNA (.gcg) | Coding DNA (.fsa) | Coding DNA (.gcg) | Protein (.fsa) | Protein (.gcg)

Gene Name	RAD51/YER095W	RAD52/YML032C	RAD50/YNL250W
Locus and Homolog Details	SGD | Alliance	SGD | Alliance	SGD | Alliance
Genome Display (S288C)	JBrowse	JBrowse	JBrowse
Alignment/Variation	Variant Viewer Strain Alignment Fungal Alignment	Variant Viewer Strain Alignment Fungal Alignment	Variant Viewer Strain Alignment Fungal Alignment
Sequence Downloads			
* DNA of Region	Fasta | GCG	Fasta | GCG	Fasta | GCG
* Coding Sequence of Selected ORF	Fasta | GCG	Fasta | GCG	Fasta | GCG
* Protein Translation of Selected ORF	Fasta | GCG	Fasta | GCG	Fasta | GCG
Sequence Analysis	S288C BLAST Fungal BLAST Design Primers Genome Restriction Map Restriction Fragments 6 Frame Translation	S288C BLAST Fungal BLAST Design Primers Genome Restriction Map Restriction Fragments 6 Frame Translation	S288C BLAST Fungal BLAST Design Primers Genome Restriction Map Restriction Fragments 6 Frame Translation

Gene/Sequence Resources

The currently displayed gene(s)/sequence(s) are RAD51/YER095W, RAD52/YML032C, RAD50/YNL250W

Download All Sequences: Genomic DNA (.fsa) | Genomic DNA (.gcg) | Coding DNA (.fsa) | Coding DNA (.gcg) | Protein (.fsa) | Protein (.gcg)

Gene Name	RAD51/YER095W	RAD52/YML032C	RAD50/YNL250W
Locus and Homolog Details	SGD | Alliance	SGD | Alliance	SGD | Alliance
Genome Display (S288C)	JBrowse	JBrowse	JBrowse
Alignment/Variation	Variant Viewer Strain Alignment Fungal Alignment	Variant Viewer Strain Alignment Fungal Alignment	Variant Viewer Strain Alignment Fungal Alignment
Sequence Downloads			
* DNA of Region	Fasta | GCG	Fasta | GCG	Fasta | GCG
* Coding Sequence of Selected ORF	Fasta | GCG	Fasta | GCG	Fasta | GCG
* Protein Translation of Selected ORF	Fasta | GCG	Fasta | GCG	Fasta | GCG
	S288C	S288C	S288C
Sequence Analysis	BLAST Fungal BLAST Design Primers Genome Restriction Map Restriction Fragments 6 Frame Translation	BLAST Fungal BLAST Design Primers Genome Restriction Map Restriction Fragments 6 Frame Translation	BLAST Fungal BLAST Design Primers Genome Restriction Map Restriction Fragments 6 Frame Translation

Gene/Sequence Resources

The currently displayed gene(s)/sequence(s) are RAD51/YER095W, RAD52/YML032C, RAD50/YNL250W

Download All Sequences: Genomic DNA (.fsa) | Genomic DNA (.gcg) | Coding DNA (.fsa) | Coding DNA (.gcg) | Protein (.fsa) | Protein (.gcg)

Gene Name	RAD51/YER095W	RAD52/YML032C	RAD50/YNL250W
Locus and Homolog Details	SGD | Alliance	SGD | Alliance	SGD | Alliance
Genome Display (S288C)	JBrowse	JBrowse	JBrowse
Alignment/Variation	Variant Viewer Strain Alignment Fungal Alignment	Variant Viewer Strain Alignment Fungal Alignment	Variant Viewer Strain Alignment Fungal Alignment
Sequence Downloads			
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Gene/Sequence Resources

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Gene Name	RAD51/YER095W	RAD52/YML032C	RAD50/YNL250W
Locus and Homolog Details	SGD | Alliance	SGD | Alliance	SGD | Alliance
Genome Display (S288C)	JBrowse	JBrowse	JBrowse
Alignment/Variation	Variant Viewer Strain Alignment Fungal Alignment	Variant Viewer Strain Alignment Fungal Alignment	Variant Viewer Strain Alignment Fungal Alignment
Sequence Downloads			
* DNA of Region	Fasta | GCG	Fasta | GCG	Fasta | GCG
* Coding Sequence of Selected ORF	Fasta | GCG	Fasta | GCG	Fasta | GCG
* Protein Translation of Selected ORF	Fasta | GCG	Fasta | GCG	Fasta | GCG
	S288C	S288C	S288C
Sequence Analysis	BLAST Fungal BLAST Design Primers Genome Restriction Map Restriction Fragments 6 Frame Translation	BLAST Fungal BLAST Design Primers Genome Restriction Map Restriction Fragments 6 Frame Translation	BLAST Fungal BLAST Design Primers Genome Restriction Map Restriction Fragments 6 Frame Translation

Sequence Downloads

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* Protein Translation of Selected ORF	Fasta | GCG

S288C

Sequence Analysis

BLAST
Fungal BLAST
Design Primers
Genome Restriction Map
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6 Frame Translation

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CEN.PK
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FL100
JK9-3d
RM11-1a
✓ S288C
SEY6210
Sigma1278b
W303
X2180-1A
Y55

Sequence Analysis

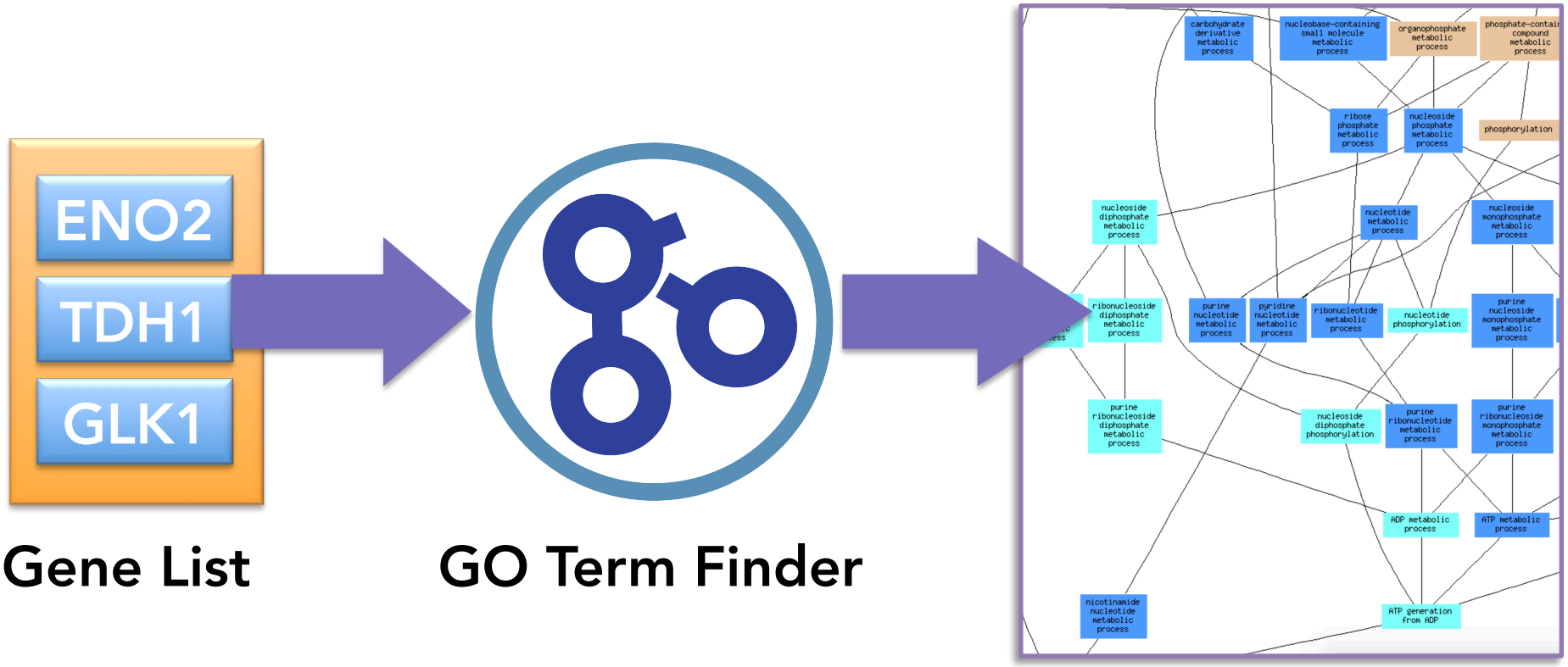
Genome Restriction Map

Restriction Fragments

6 Frame Translation

GO Term Finder

yeastgenome.org/goTermFinder



Gene List

GO Term Finder

Associated Functions

GO Term Finder

yeastgenome.org/goTermFinder

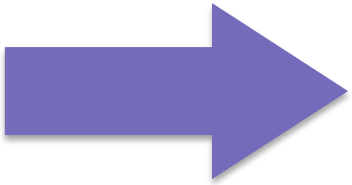
Gene Ontology (GO)

GO Term Finder

yeastgenome.org/goTermFinder

Gene

GLK1



Function

glucokinase activity

Process

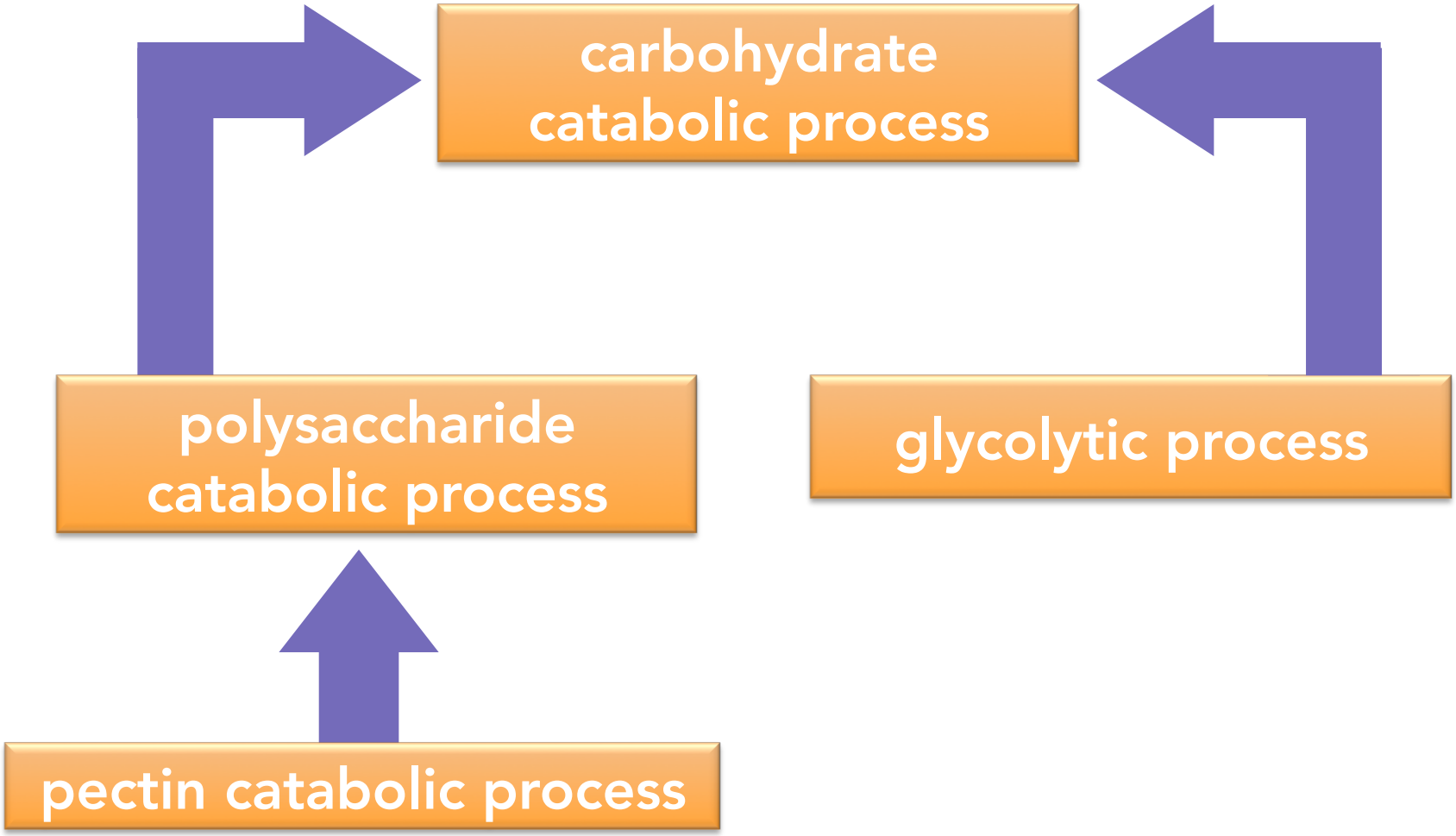
glycolytic process

Component

cytosol

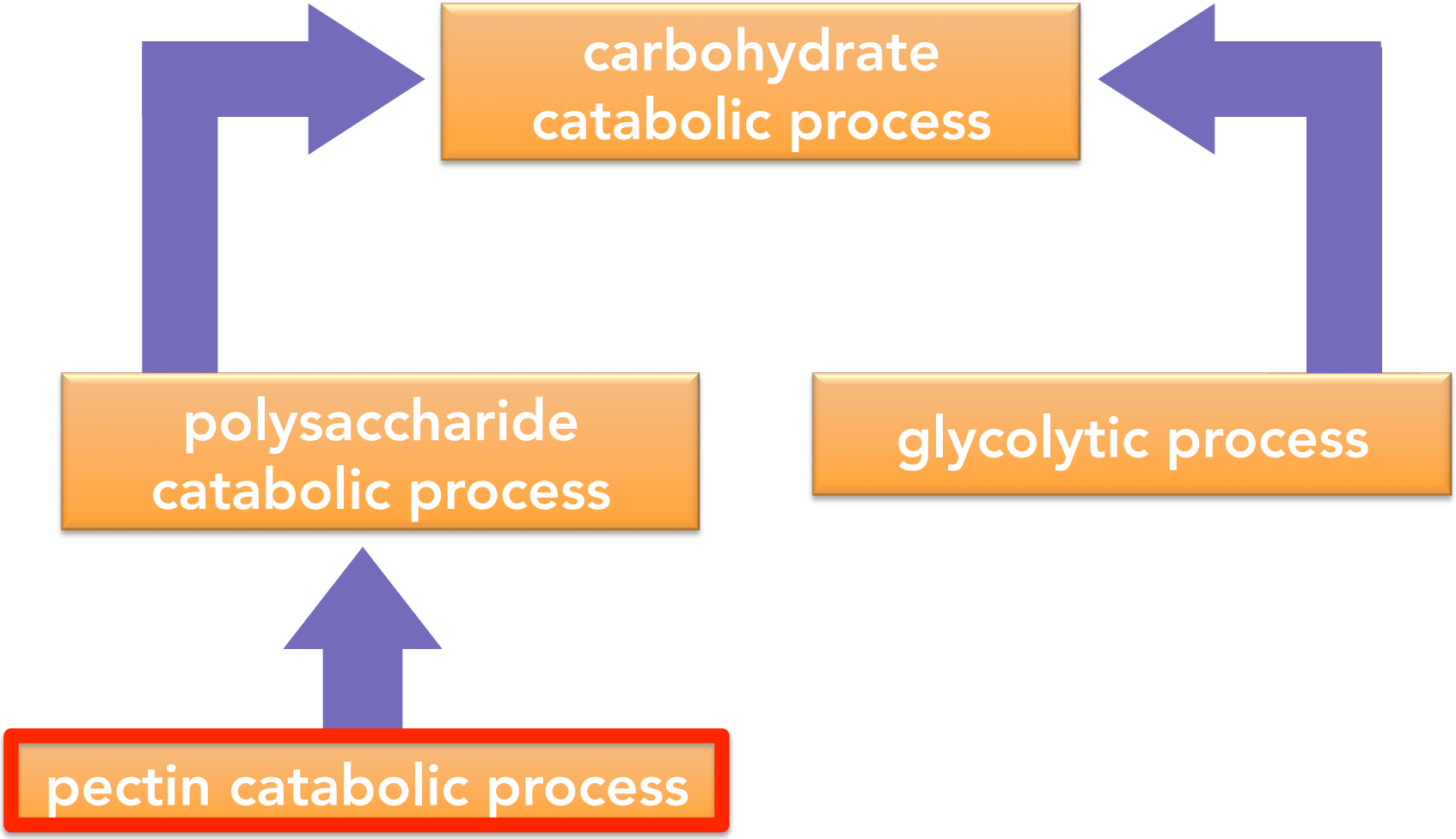
GO Term Finder

yeastgenome.org/goTermFinder



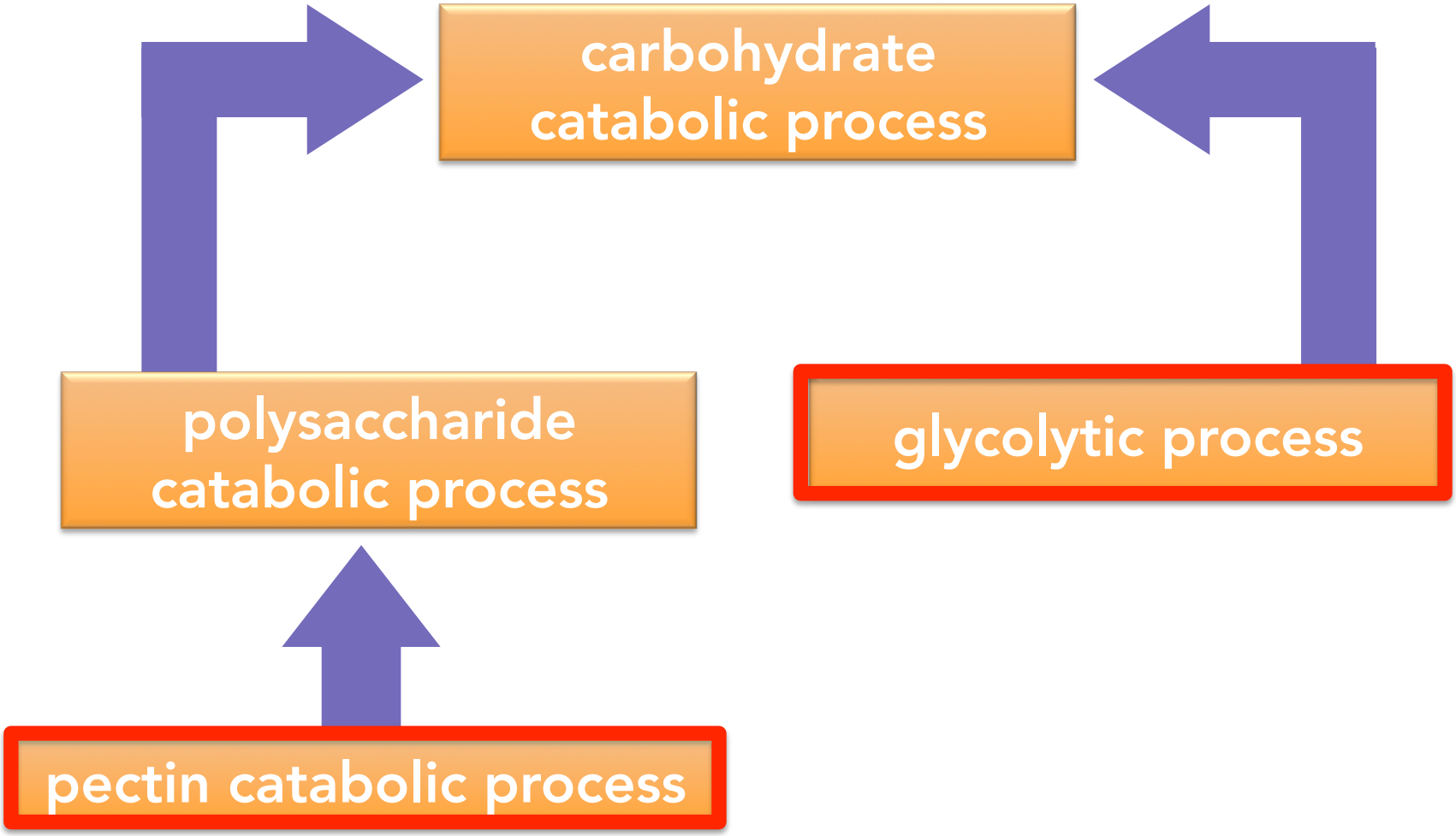
GO Term Finder

yeastgenome.org/goTermFinder



GO Term Finder

yeastgenome.org/goTermFinder



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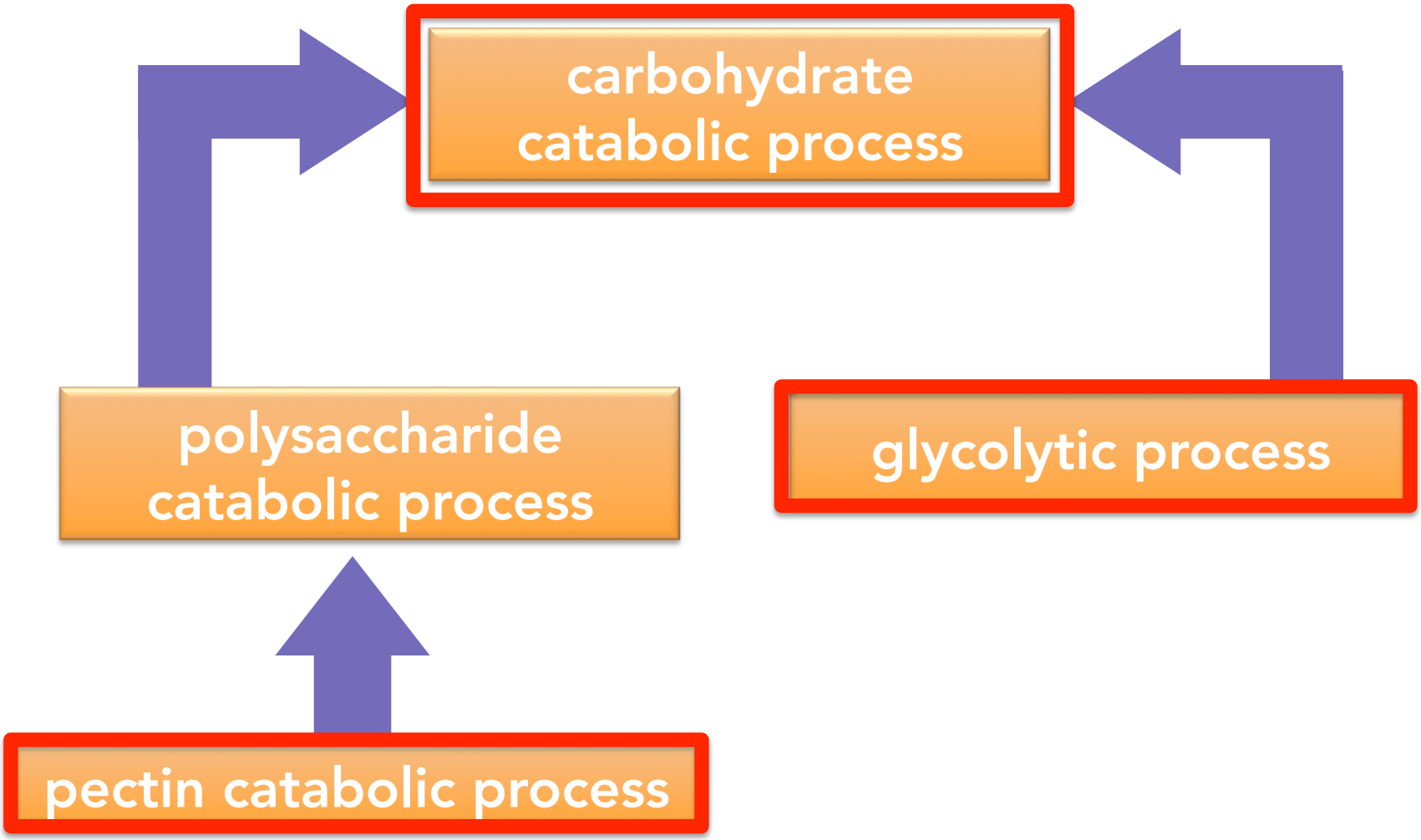


GO Term Finder

yeastgenome.org/goTermFinder

APPLIED AND ENVIRONMENTAL MICROBIOLOGY, Sept. 2008, p. 5759–5768 Vol. 74, No. 18
0099-2240/08/$08.00+0 doi:10.1128/AEM.01030-08

Physiological and Transcriptional Responses to High Concentrations of Lactic Acid in Anaerobic Chemostat Cultures of *Saccharomyces cerevisiae*[▽]

Derek A. Abbott,[1,2] Erwin Suir,[1,2] Antonius J. A. van Maris,[1,2]* and Jack T. Pronk[1,2]

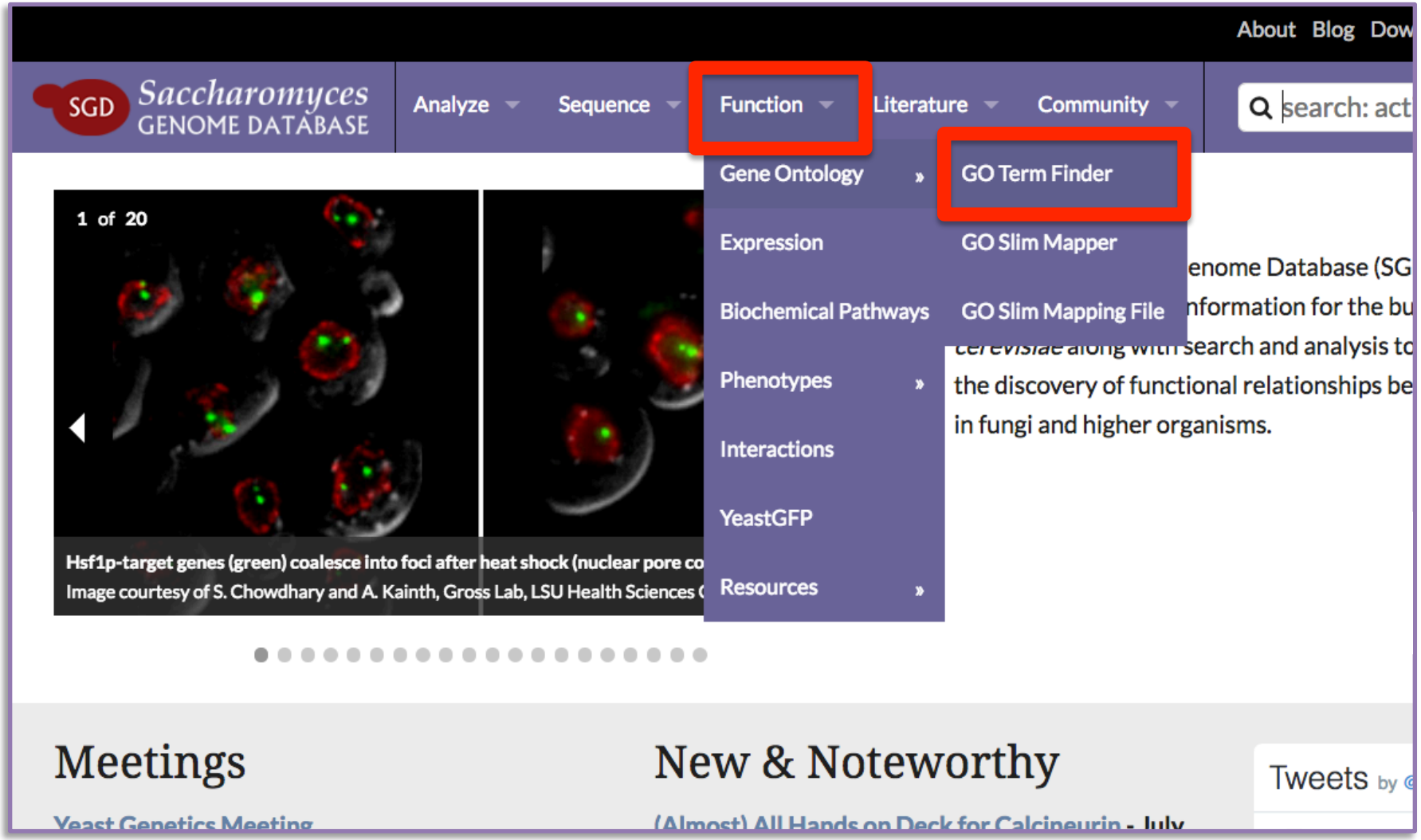
Department of Biotechnology, Delft University of Technology, Julianalaan 67, 2628 BC Delft, The Netherlands,[1] and Kluyver Centre for Genomics of Industrial Fermentation, Julianalaan 67, 2628 BC Delft, The Netherlands[2]

Received 8 May 2008/Accepted 22 July 2008

How does the cell respond to lactic acid stress?

GO Term Finder

yeastgenome.org/goTermFinder



Gene Ontology Term Finder

The GO Term Finder (Version 0.86) searches for significant shared GO terms, or parents of those GO terms, used to describe the genes in your list to help you discover what the genes may have in common. To map annotations of a group of genes to more general terms and/or to bin them in broad categories, use the GO Slim Mapper.

Default Settings: 1. All genes/features that have GO annotations in the database, 2. All annotations in the database (manually curated, high-throughput, and computational annotations), and 3. Hits with p-value < 0.01 will be displayed on the results page.

Submit Form | Reset Form

Step 1. Query Set (Your Input)

Enter Gene/ORF names (separated by a return or a space):

Note: If you have a big gene list (>100), save it as a file and upload it below.

OR Upload a file of Gene/ORF names (.txt or .tab format):

Choose File No file chosen

Step 2. Choose Ontology

Pick an ontology aspect:

- Process
- Function
- Component

Search using default settings or use Step 3, Step 4, and/or Step 5 below to customize your options.

Step 3. Specify your background set of genes

Use default background set (all features in the database that have GO annotations)**OR Enter Gene/ORF names** (separated by a return or a space):

Note: If you have a big background list (>100), save it as a file and upload it below.

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Choose File No file chosen

Step 4. Optional Input

Pick evidence codes to exclude for calculation:

HDA HGI HMP IBA IC IEA IDA IEP IGI
IKR IMP IMR IPI IRD ISA ISM ISO ISS
NAS ND TAS

Pick a p-value below (default is 0.01):

0.01

Calculate false discovery rate (FDR)?

FDR

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Calculate false discovery rate (FDR)?

FDR

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IKR IMP IMR IPI IRD ISA ISM ISO ISS
NAS ND TAS

Pick a p-value below (default is 0.01):

0.01

Calculate false discovery rate (FDR)?

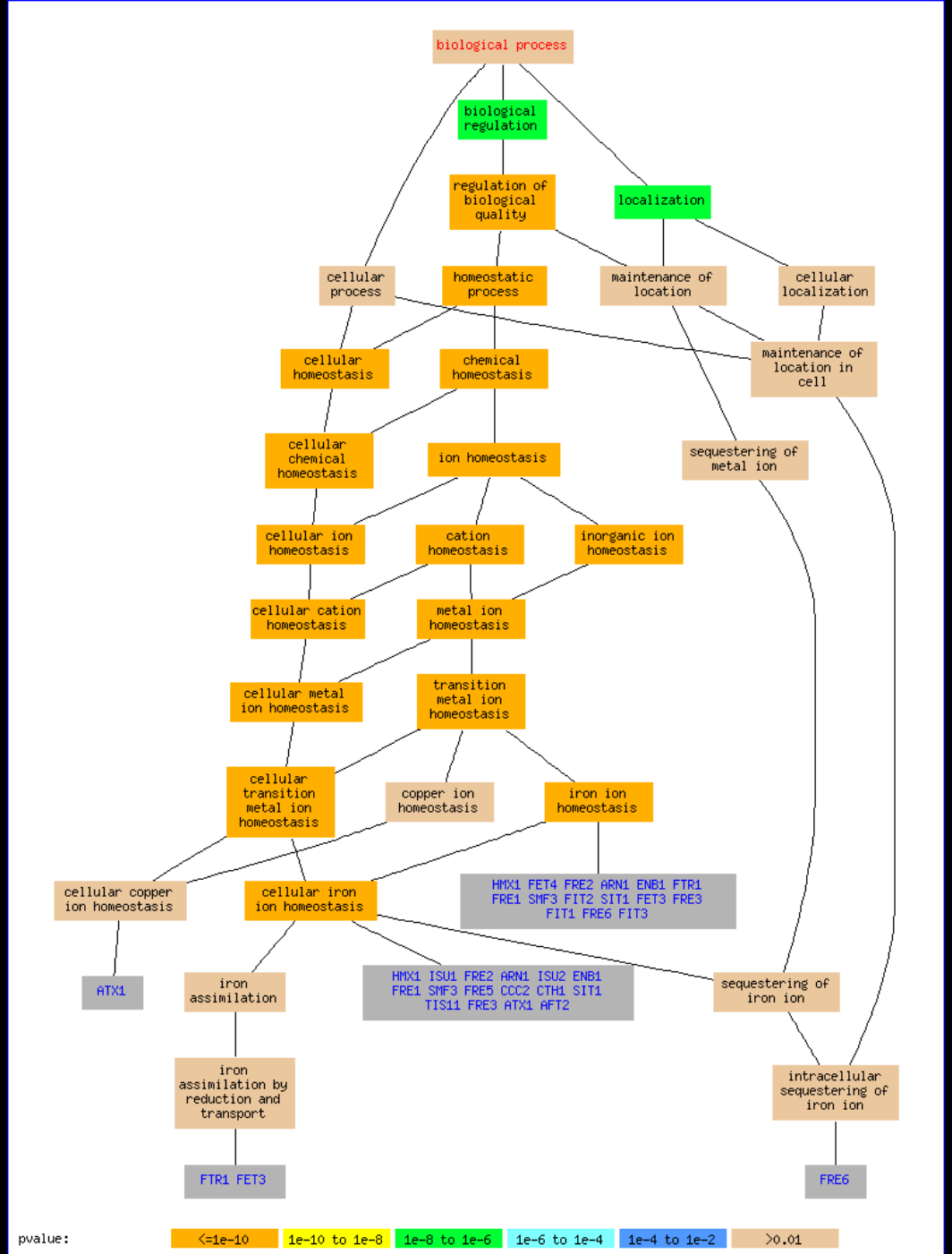
FDR

Submit Form | Reset Form

Gene Ontology term	Cluster frequency	Genome frequency	Corrected P-value	FDR	False Positives	Genes annotated to the term
ion transport	37 of 180 genes, 20.6%	398 of 7166 genes, 5.6%	1.58e-09	0.00%	0.00	YPR128C, YPR156C, YOR316C, YHL040C, YJR160C, YOR383C, YGR243W, YDR534C, YDR536W, YLL052C, YOR161C, YNL231C, YGL071W, YIL121W, YPR149W, YOR382W, YDR270W, YLR034C, YDR033W, YEL065W, YMR077C, YGL255W, YCL008C, YMR058W, YOL158C, YOR348C, YGR065C, YMR011W, YHR092C, YOR381W, YHR094C, YJL214W, YJR158W, YKL220C, YER145C, YGR138C, YNL259C
iron ion homeostasis	15 of 180 genes, 8.3%	59 of 7166 genes, 0.8%	7.43e-09	0.00%	0.00	YLR205C, YKL220C, YOR383C, YEL065W, YOL158C, YNL259C, YMR058W, YDR534C, YER145C, YLR034C, YLR136C, YDR270W, YOR382W, YOR381W, YHL040C
transition metal ion homeostasis	16 of 180 genes, 8.9%	89 of 7166 genes, 1.2%	4.03e-07	0.00%	0.00	YOR383C, YEL065W, YOL158C, YMR058W, YDR534C, YDR270W, YOR382W, YLR034C, YHL040C, YOR316C, YLR205C, YKL220C, YER145C, YNL259C, YLR136C, YOR381W
transition metal ion transport	12 of 180 genes, 6.7%	48 of 7166 genes, 0.7%	1.21e-06	0.00%	0.00	YDR270W, YLR034C, YOR381W, YOR316C, YGL255W, YIL121W, YGL071W, YKL220C, YER145C, YNL259C, YOL158C, YMR058W
cellular iron ion homeostasis	12 of 180 genes, 6.7%	48 of 7166 genes, 0.7%	1.21e-06	0.00%	0.00	YOR381W, YHL040C, YDR270W, YLR136C, YLR034C, YER145C, YMR058W, YOL158C, YNL259C, YEL065W, YKL220C, YLR205C
iron chelate transport	7 of 180 genes, 3.9%	11 of 7166 genes, 0.2%	1.49e-06	0.00%	0.00	YDR534C, YOL158C, YHL040C, YOR381W, YEL065W, YOR382W, YOR383C
siderophore transport	7 of 180 genes, 3.9%	11 of 7166 genes, 0.2%	1.49e-06	0.00%	0.00	YOL158C, YDR534C, YOR381W, YHL040C, YOR383C, YEL065W, YOR382W
cation transport	23 of 180 genes, 12.8%	223 of 7166 genes, 3.1%	5.52e-06	0.00%	0.00	YDR270W, YLR034C, YPR156C, YOR316C, YJR160C, YGL255W, YMR058W, YOL158C, YDR536W, YOR348C, YOR161C, YMR011W, YHR092C, YOR381W, YHR094C, YJL214W, YJR158W, YKL220C, YGL071W, YIL121W, YER145C, YNL259C, YGR138C
metal ion homeostasis	16 of 180 genes, 8.9%	114 of 7166 genes, 1.6%	1.70e-05	0.00%	0.00	YLR136C, YOR381W, YKL220C, YLR205C, YER145C, YNL259C, YOR382W, YDR270W, YLR034C, YOR316C, YHL040C, YEL065W, YOR383C, YDR534C, YMR058W, YOL158C
homeostatic	28 of 180 genes,	345 of 7166	2.39e-05	0.00%	0.00	YIL040W, YOR381W, YBR014C, YLR136C, YGL253W, YLL052C, YHR031C, YNL259C, YFR003C, YER145C, YLR109W, YKL220C, YLR205C, YCL061C, YDL059C, YOR316C,

ion transport	37 of 180 genes, 20.6%	398 of 7166 genes, 5.6%	1.58e-09	0.00%	0.00	YPR128C, Y YDR536W, YDR270W, YMR058W, YHR094C, Y
iron ion homeostasis	15 of 180 genes, 8.3%	59 of 7166 genes, 0.8%	7.43e-09	0.00%	0.00	YLR205C, Y YER145C, Y
transition metal ion homeostasis	16 of 180 genes, 8.9%	89 of 7166 genes, 1.2%	4.03e-07	0.00%	0.00	YOR383C, Y YLR034C, Y YOR381W
transition metal ion transport	12 of 180 genes, 6.7%	48 of 7166 genes, 0.7%	1.21e-06	0.00%	0.00	YDR270W, YER145C, Y
cellular iron ion homeostasis	12 of 180 genes, 6.7%	48 of 7166 genes, 0.7%	1.21e-06	0.00%	0.00	YOR381W, YNL259C, Y
iron chelate transport	7 of 180 genes, 3.9%	11 of 7166 genes, 0.2%	1.49e-06	0.00%	0.00	YDR534C, Y

ion transport	37 of 180 genes, 20.6%	398 of 7166 genes, 5.6%	1.58e-09	0.00%	0.00	YPR128C, Y YDR536W, YDR270W, YMR058W, YHR094C, Y
iron ion homeostasis	15 of 180 genes, 8.3%	59 of 7166 genes, 0.8%	7.43e-09	0.00%	0.00	YLR205C, Y YER145C, Y
transition metal ion homeostasis	16 of 180 genes, 8.9%	89 of 7166 genes, 1.2%	4.03e-07	0.00%	0.00	YOR383C, Y YLR034C, Y YOR381W
transition metal ion transport	12 of 180 genes, 6.7%	48 of 7166 genes, 0.7%	1.21e-06	0.00%	0.00	YDR270W, YER145C, Y
cellular iron ion homeostasis	12 of 180 genes, 6.7%	48 of 7166 genes, 0.7%	1.21e-06	0.00%	0.00	YOR381W, YNL259C, Y
iron chelate transport	7 of 180 genes, 3.9%	11 of 7166 genes, 0.2%	1.49e-06	0.00%	0.00	YDR534C, Y


biological process
biological regulation
regulation of biological quality
localization
cellular process
homeostatic process
maintenance of location
cellular localization
cellular homeostasis
chemical homeostasis
maintenance of location in cell
cellular chemical homeostasis
ion homeostasis
sequestering of metal ion
cellular ion homeostasis
cation homeostasis
inorganic ion homeostasis
cellular cation homeostasis
metal ion homeostasis
cellular metal ion homeostasis
transition metal ion homeostasis
cellular transition metal ion homeostasis
copper ion homeostasis
iron ion homeostasis
cellular copper ion homeostasis
cellular iron ion homeostasis
HMX1 FET4 FRE2 ARN1 ENB1 FTR1 FRE1 SMF3 FIT2 SIT1 FET3 FRE3 FIT1 FRE6 FIT3
ATX1
iron assimilation
HMX1 ISU1 FRE2 ARN1 ISU2 ENB1 FRE1 SMF3 FRE5 CCC2 CTH1 SIT1 TIS11 FRE3 ATX1 AFT2
sequestering of iron ion
iron assimilation by reduction and transport
intracellular sequestering of iron ion
FTR1 FET3
FRE6
pvalue:
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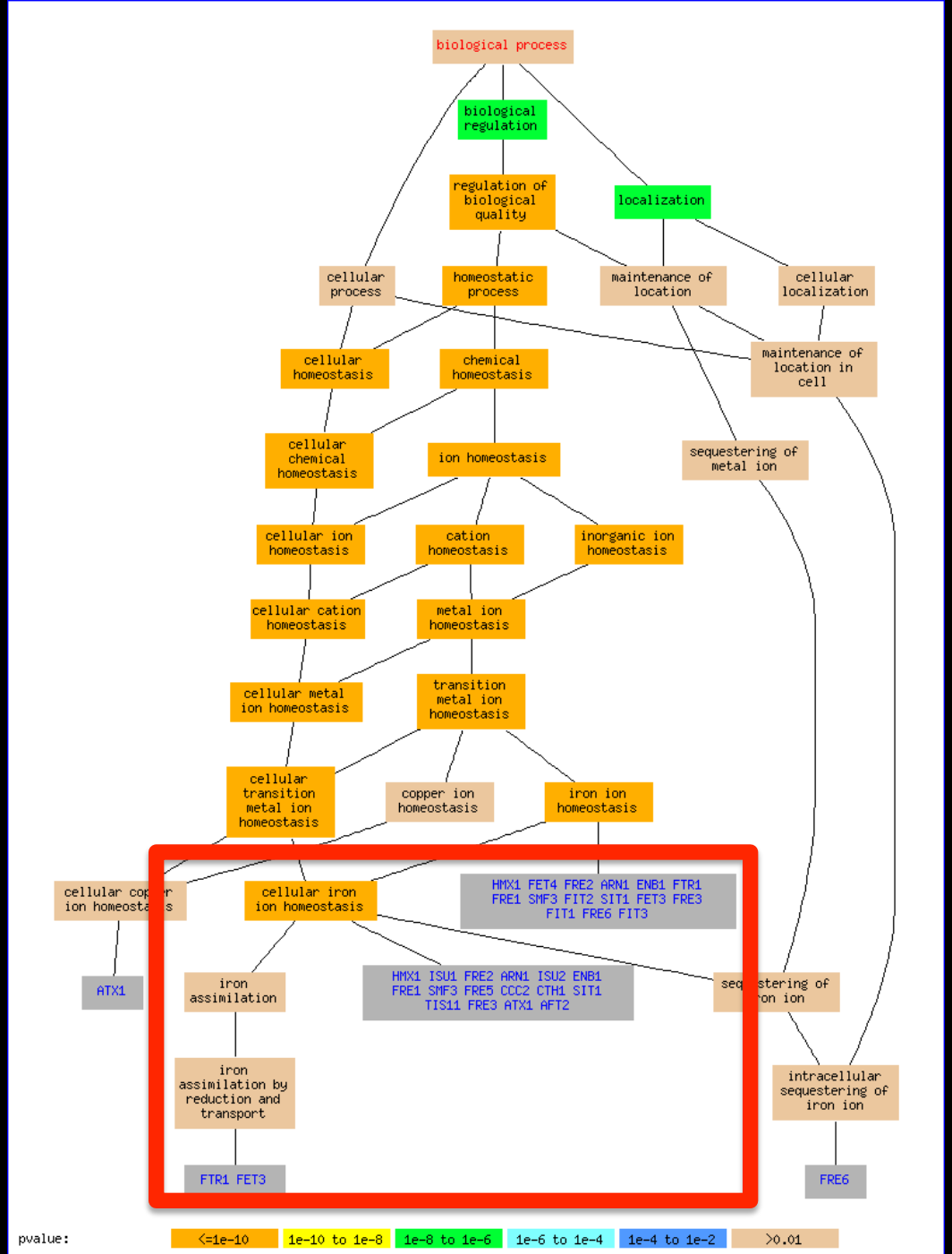
1e-10 to 1e-8
1e-8 to 1e-6
1e-6 to 1e-4
1e-4 to 1e-2
>0.01


biological process
biological regulation
regulation of biological quality
localization
cellular process
homeostatic process
maintenance of location
cellular localization
cellular homeostasis
chemical homeostasis
maintenance of location in cell
cellular chemical homeostasis
ion homeostasis
sequestering of metal ion
cellular ion homeostasis
cation homeostasis
inorganic ion homeostasis
cellular cation homeostasis
metal ion homeostasis
cellular metal ion homeostasis
transition metal ion homeostasis
cellular transition metal ion homeostasis
copper ion homeostasis
iron ion homeostasis
cellular copper ion homeostasis
cellular iron ion homeostasis
HMX1 FET4 FRE2 ARN1 ENB1 FTR1 FRE1 SMF3 FIT2 SIT1 FET3 FRE3 FIT1 FRE6 FIT3
ATX1
iron assimilation
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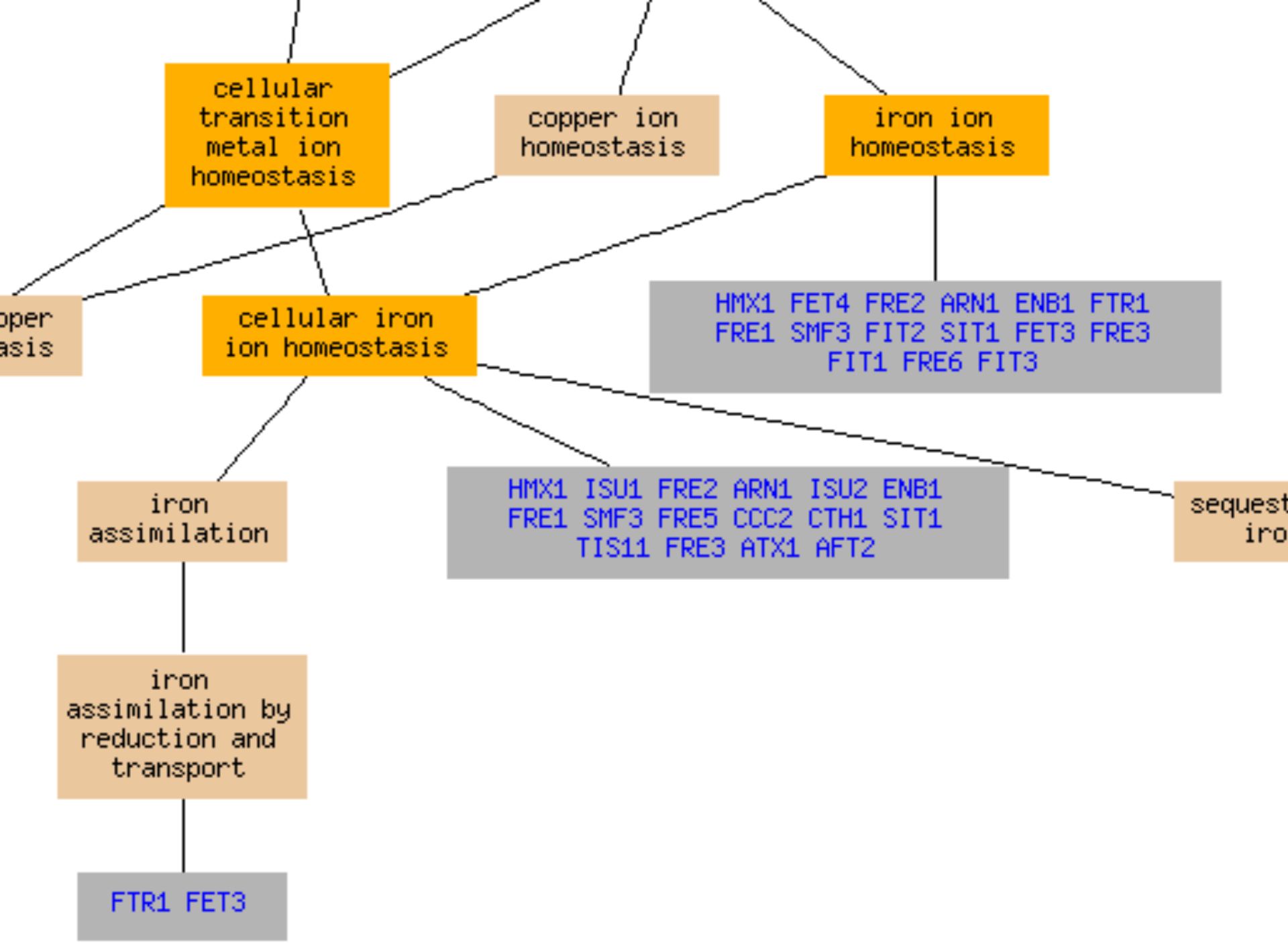
sequestering of iron ion
iron assimilation by reduction and transport
intracellular sequestering of iron ion
FTR1 FET3
FRE6
pvalue:
<=1e-10
1e-10 to 1e-8
1e-8 to 1e-6
1e-6 to 1e-4
1e-4 to 1e-2
>0.01


cellular transition metal ion homeostasis
copper ion homeostasis
iron ion homeostasis
oper asis
cellular iron ion homeostasis
HMX1 FET4 FRE2 ARN1 ENB1 FTR1 FRE1 SMF3 FIT2 SIT1 FET3 FRE3 FIT1 FRE6 FIT3
iron assimilation
HMX1 ISU1 FRE2 ARN1 ISU2 ENB1 FRE1 SMF3 FRE5 CCC2 CTH1 SIT1 TIS11 FRE3 ATX1 AFT2
sequest iro
iron assimilation by reduction and transport
FTR1 FET3

Thank you!

SGD Website

yeastgenome.org

Questions/Comments

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