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The complete genome sequence of the budding yeast *Saccharomyces cerevisiae*, and its annotation, is maintained by the *Saccharomyces* Genome Database (SGD; www.yeastgenome.org), as a public resource for researchers. Until recently, the genome sequence displayed at SGD has been derived solely from the S288C strain background. We have now incorporated 11 additional *S. cerevisiae* genomes into SGD, as well as providing their annotation. We have also developed a new Variant Viewer to further support the community's analysis of these new data. Variant Viewer allows visualization and comparison of sequences from multiple strains. Users can quickly scan the entire genome, or a subset of genes, for overviews of both slight and significant sequence differences. SGD's Variant Viewer also includes a more detailed comparison of sequence differences between strains that highlights insertions, deletions, and SNPs that is available for both viewing and download. The Variant Viewer offers yet another way to explore the genomic sequence data available at SGD, as part of our continuing mission to educate students, enable bench researchers and facilitate scientific discovery. This work is supported by a grant from the NHGRI (U41 HG001315).

Enter lists of comma-separated loci or GO terms to display subsets of loci for comparison

This dendrogram shows similarity between strain sequences across the displayed set of genes

The dendrogram is redrawn as the displayed set of loci changes

Clicking on a locus will bring up a second display for the individual locus view

Locus Info: Names, description, physical chromosomal location

SNPs, insertions, and deletions are displayed in the locus view at positions where at least one of the strains deviates from the S288C sequence

Sequence is displayed for each strain with the specific nucleotides at each position displayed

www.yeastgenome.org/variant-viewer

SGD

Analyze

Sequence

Function

Literature

Community

Variant Viewer

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

Filter

Strains

DNA

Protein

Settings

Sort By

Chromosomal Location

Variation

Sort displayed loci by either variation or chromosomal location

Alignment Score

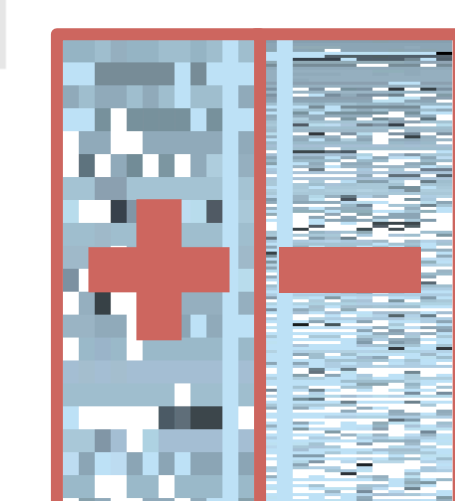
1.00

N/A

Alignment Scores represent the similarity of each gene in each strain relative to the S288C reference genome. A score of 1 indicates that the sequence of that gene in that strain is identical to that of S288C. A score of 0 indicates no similarity. Darker colors indicate more differences than lighter colors. A white square (N/A) indicates that no sequence data are available for that gene in that strain.

Turn on/off the display of certain strains

Compress the display to view more loci within your browser window



Visualize and compare sequence data across 12 different strains:

S288C	JK9-3d	SK1
CEN.PK	RM11-1a	W303
D273-10B	SEY6210	X2180-1A
FL100	Sigma1278b	Y55

CBF2 / YGR140W

Essential kinetochore protein

Location: Chromosome VII 767429..770299

SNP at Chromosome VII 768616

Download image of the annotated view

Download

Legend

Insertion
Deletion
Synonymous SNP
Nonsynonymous SNP
Intron SNP
Untranslatable SNP

	1	34	270	651	673	737	786	822	882	906	925	999	1029	1068	1099	1110	1124	1155	1188	1251	1311		
	ATGAGATCATCGATTTGTTTCTACTAAATG	A	T	A	G	T	C	C	A	T	C	A	A	C	T	G	T	T	G	A	T	A	C
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