

SGD Variant Viewer

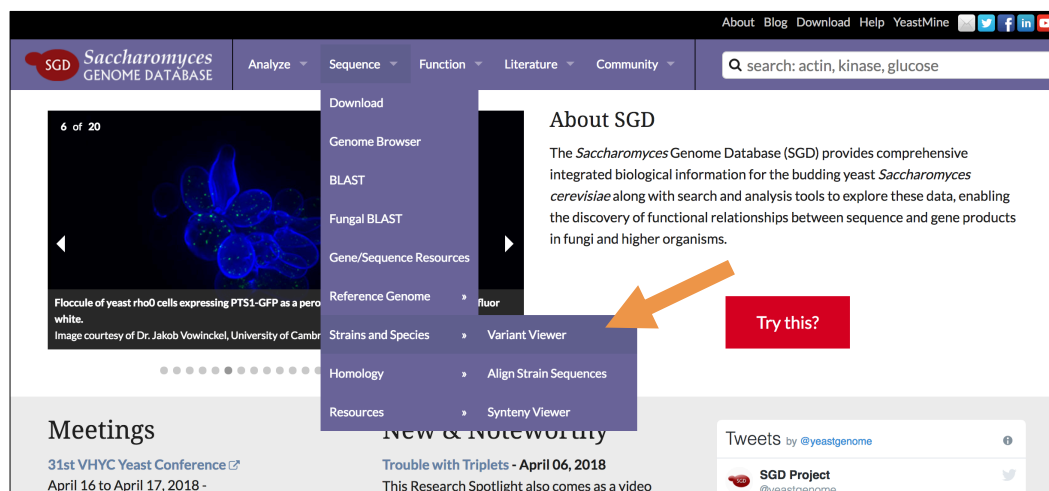
SGD's Variant Viewer (<https://yeastgenome.org/variant-viewer>) is an open-source web application that compares nucleotide and amino acid sequence differences between 12 common *S. cerevisiae* laboratory strains. For a given open reading frame, Variant Viewer breaks down the position and nature of any strain-specific sequence differences relative to the reference strain S288C. When used at a multi-gene level, it also provides a matrix of alignment scores that enables quick identification of genes with higher or lower variation.

Variant Viewer can be used to probe the genetic differences between *S. cerevisiae* strains that give rise to their unique phenotypes. For example, while haploid S288C cells exhibit an axial budding pattern, diploid cells exhibit a bipolar budding pattern. On the other hand, strain W303 shows bipolar bud site selection in both haploid and diploid cells.

In this exercise, we will use Variant Viewer to find out what genetic differences between Sigma1278b and S288C explain why they differ in their ability to form pseudohyphae.

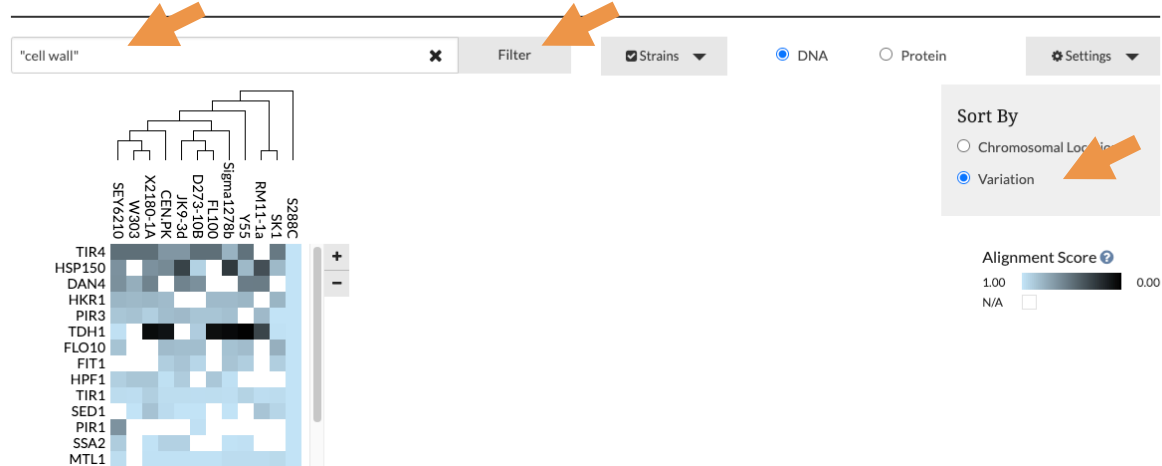
S288C vs. Sigma1278b: Cell Wall

- Open the SGD home page (www.yeastgenome.org), open the Sequence tab on top of the page, then select Strains and Species followed by Variant Viewer from the pull-down menus. Or just type in the URL: yeastgenome.org/variant-viewer



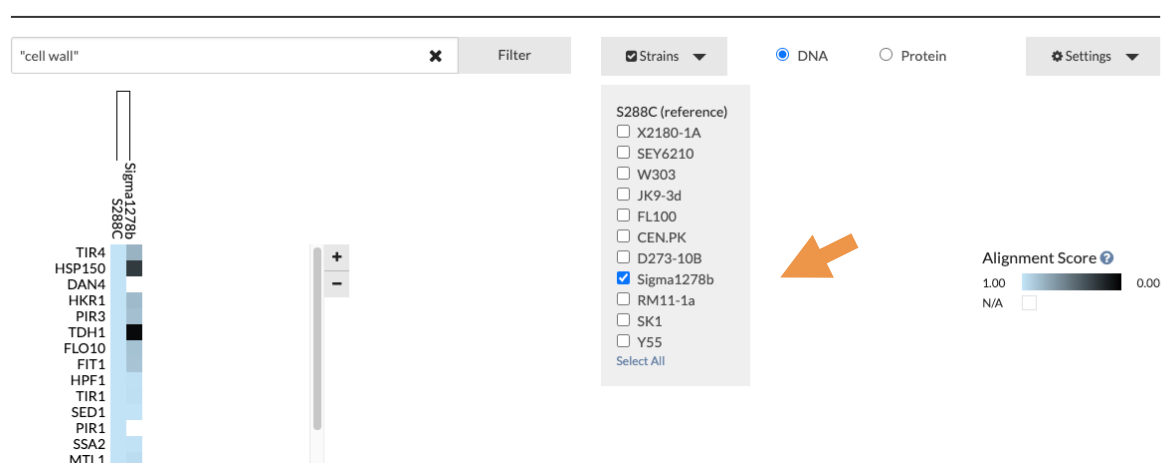
- The **Filter** box accepts one or more genes, as well as Gene Ontology (GO) terms. Because we are interested in genes involved in cell wall development, search for the GO term “**cell wall**,” sort by variation in the settings pull-down, and then click Filter.

Variant Viewer



- The **matrix**, shown on the left, will have changed to only include the genes that localize to cell walls.
 - This matrix enables you to visualize high-level differences in multiple genes relative to strain S288C. Each square in the matrix corresponds to one of the twelve strains in Variant Viewer, shown at the top, and to an open reading frame, shown on the left.
 - The color of each square indicates how similar the sequence is relative to strain S288C. As indicated on the Alignment Score figure on the right, lighter shades of blue indicate high sequence similarity whereas darker shades indicate more dissimilarity. Note that if the square is white, it means a comparison could not be made.
- Next, we will want to make the matrix display only info for the strains we are interested in (S288C and Sigma1287b). Open the **Strains** pull-down menu, press Deselect All, then re-select Sigma1287b.

Variant Viewer



- Click on **PIR3** (O-glycosylated covalently bound cell wall protein) and in the sequence window select **Protein**. Scroll with your mouse along the green bar of sequence to see what the changes between strains are due to. Find the deletion beginning at Chr X1144715 and compare the protein sequences below.

BUD4 / YJR092W

Sequence Overview

Reference Strain: S288C

Alternative Reference Strains

Variants

Other Strains

History

Resources

Variants

☐ Genomic DNA ☒ Protein ☐ Upstream IGR ☐ Downstream IGR

Location: [Chromosome X 598735..603078](#)

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