SGD Variant Viewer

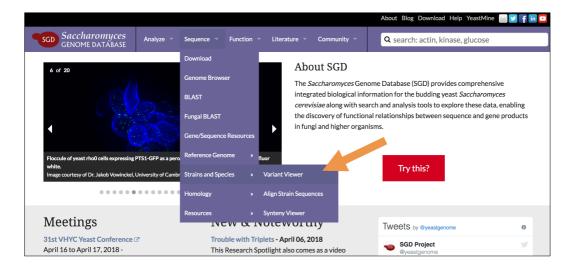
SGD's Variant Viewer (https://yeastgenome.org/variant-viewer) is an open-source web application that compares nucleotide and amino acid sequence differences between 12 common *S. cerevisiae* laboratory strains. For a given open reading frame, Variant Viewer breaks down the position and nature of any 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.

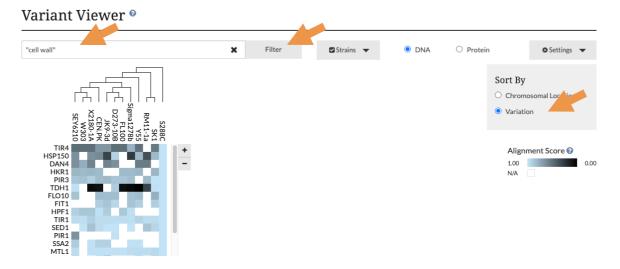
In this exercise, we will use Variant Viewer to find out what genetic differences between Sigma1278b and S288C explain why they differ in their ability to form pseudohyphae.

S288C vs. Sigma1278b: Cell Wall

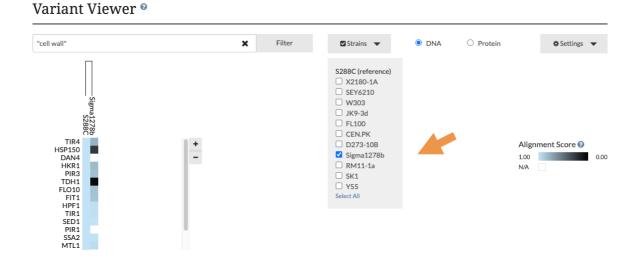
• Open the SGD home page (www.yeastgenome.org), open the Sequence tab on top of the page, then select Strains and Species followed by Variant Viewer from the pull-down menus. Or just type in the URL: yeastgenome.org/variant-viewer



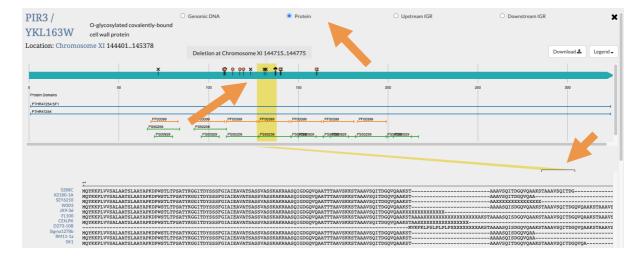
• The **Filter** box accepts one or more genes, as well as Gene Ontology (GO) terms. Because we are interested in genes involved in cell wall development, search for the GO term "**cell wall**," sort by variation in the settings pull-down, and then click Filter.



- 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.
 - O 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.



• 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.



- Now that we have identified that a deleted section of protein in a cell wall protein of Sigma1278b, we have a clue as to why this strain behaves differently from S288C. To examine PIR3 more closely, click the name to go to the locus summary page. From the PIR3 Locus Summary page, you can see in the Description that this protein is known to vary between strains.
- In the list of references below, you'll find papers referring to the role of this cell wall protein (and its relations) in heat shock, response to toxins, and cell wall integrity. The differences in this protein between strains might contribute to variations in behavior, such as differences in pseudohyphal growth for Sigma1278b relative to S288C

References 1 9

1. Toh-e A, et al. (1993) Three yeast genes, PIR1, Pland PIR3, containing internal tandem repeats, are related to each other, and PIR1 and PIR2 are required for tolerance to heat shock. Yeast 9(5):481-94 PMID:8322511 SGD Paper DOI full text PubMed

2. Yun DJ, et al. (1997) Stress proteins on the yeast cell surface determine resistance to osmotin, a plant antifungal protein. Proc Natl Acad Sci U S A 94(13):7082-7 PMID:9192695 SGD Paper DOI full text PMC full text PubMed

3. Doolin MT, et al. (2001) Overlapping and distinct roles of the duplicated yeast transcription factors Ace2p and Swi5p. Mol Microbiol 40(2):422-32 PMID:11309124 SGD Paper DOI full text PubMed

4. Porter SE, et al. (2002) The yeast pafl-rNA polymerase II complex is required for full expression of a subset of cell cycle-regulated genes. Eukaryot Cell 1(5):830-42 PMID:12455700 SGD Paper DOI full text PMC full text PubMed

5. Jung US and Levin DE (1999) Genome-wide analysis of gene expression regulated by the yeast cell wall integrity signalling pathway.

Variant Viewer: Sequence Tab

Mol Microbiol 34(5):1049-57 PMID: 10594829 SGD Paper DOI full text PubMed

• Variant Viewer is also embedded in the Sequence tab of every gene page, with the data for the gene already pre-loaded from the results of the Variant Viewer search. This allows you to look at the variant information for a gene without starting from the tool's entry page.

