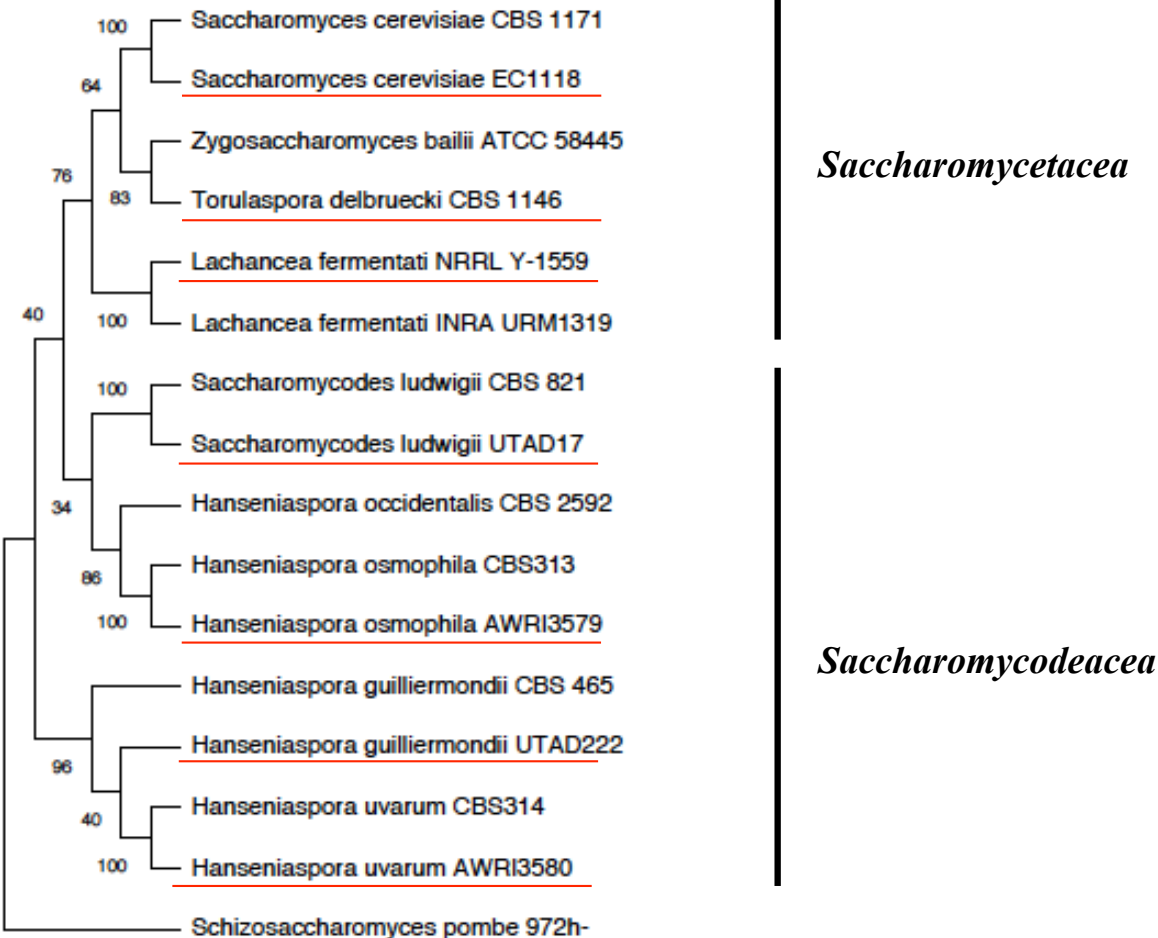
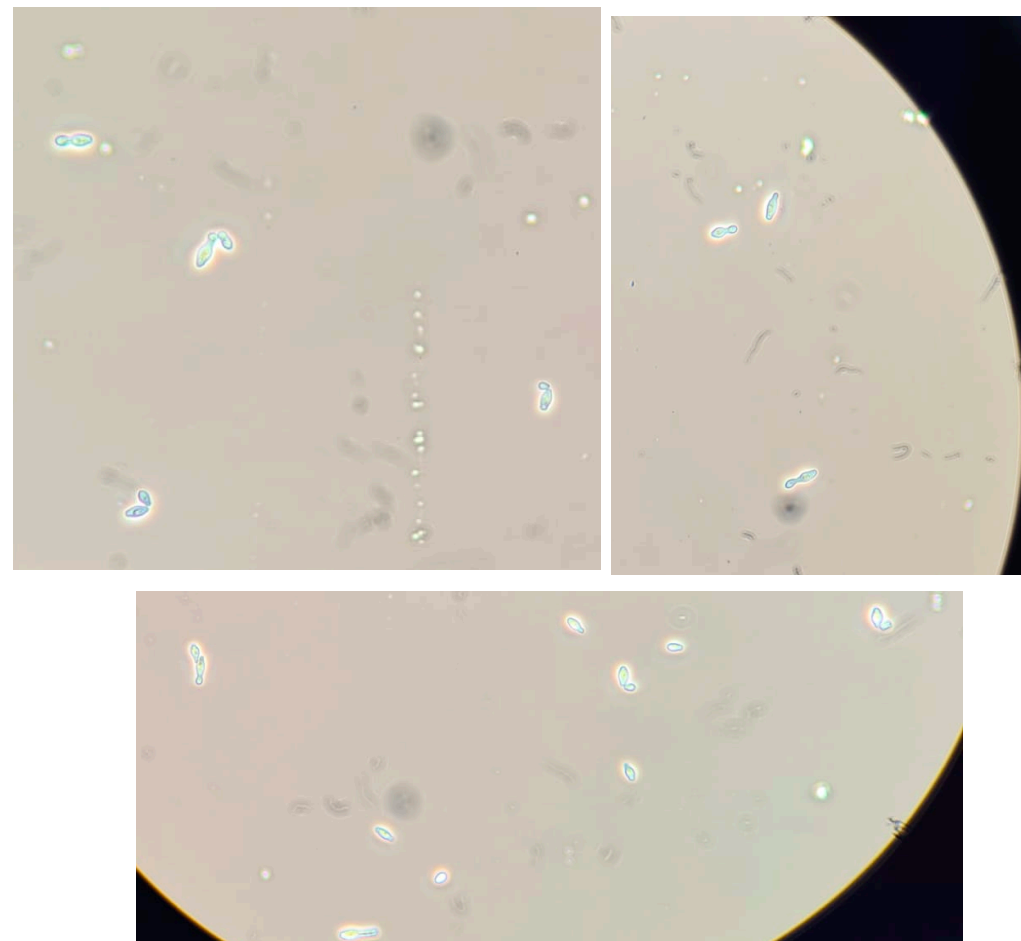
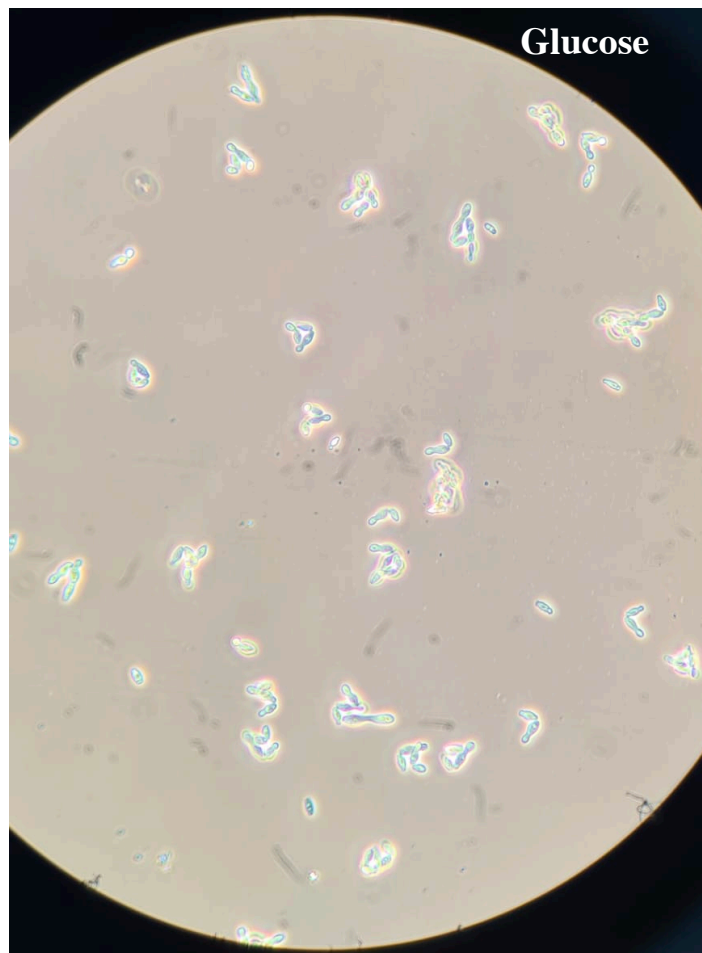


**Figure S1** – Dendrogram of the alignment obtained for the Internal transcribed spacer (ITS) of different yeast strains belonging to the *Saccharomycodeacea* and *Saccharomycetacea* families, including the strains that were used for the comparative proteomic analysis described in Fig.3 (underlined in red). The ITS sequences of the strains were retrieved directly from the NCBI database or in some cases from available genomic sequences.

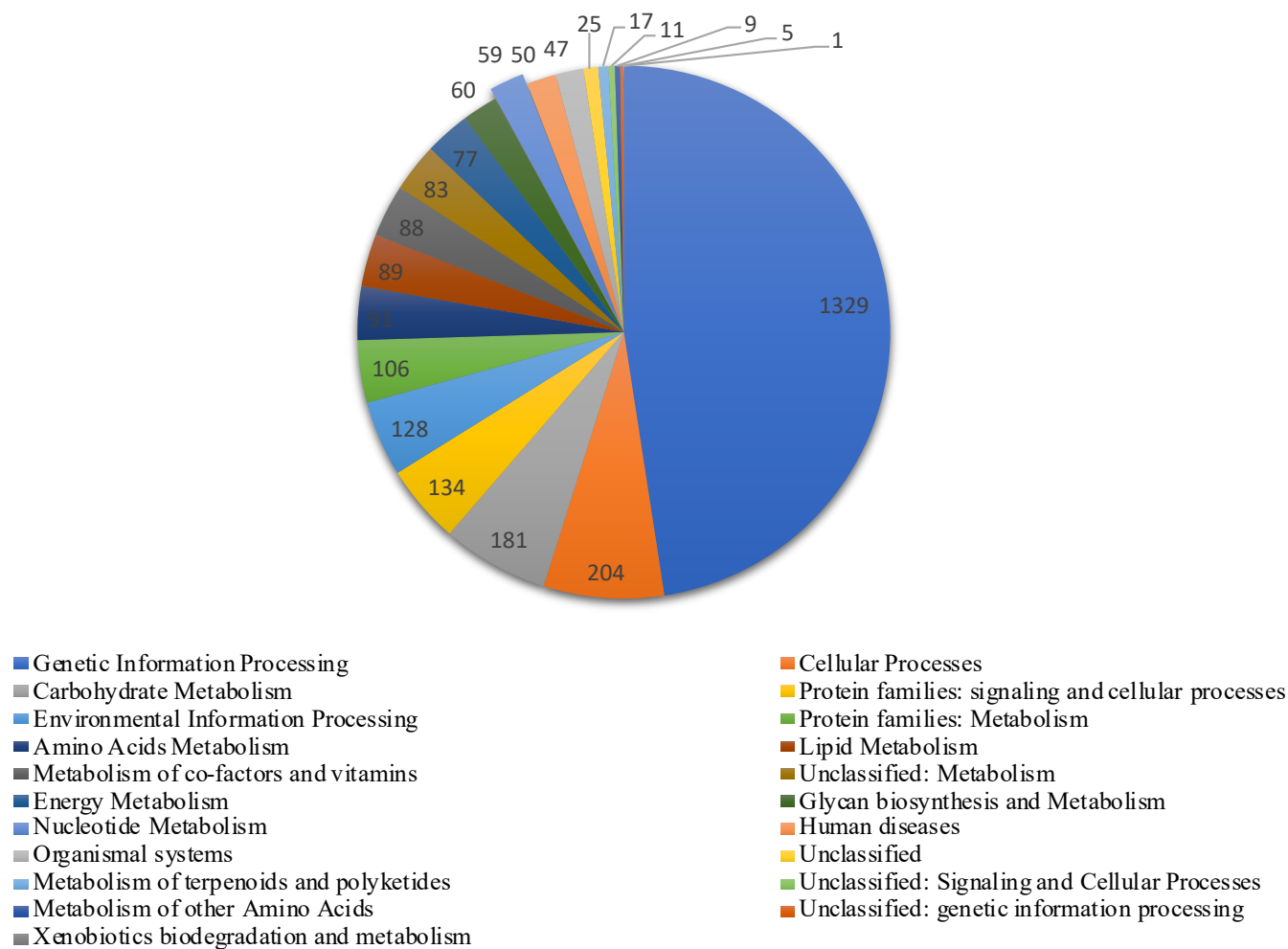


**Figure S2** – Optic microscopy photographs of *S. ludwigii* UTAD17 during growth in minimal medium supplemented with glucose (2%) or GlcNAc (2%) as the sole carbon sources. Both images were obtained with a 40x objective after 6h of cultivation, at 30°C and with 250 rpm, in the selected growth media. The images demonstrate the absence of filamentous growth.

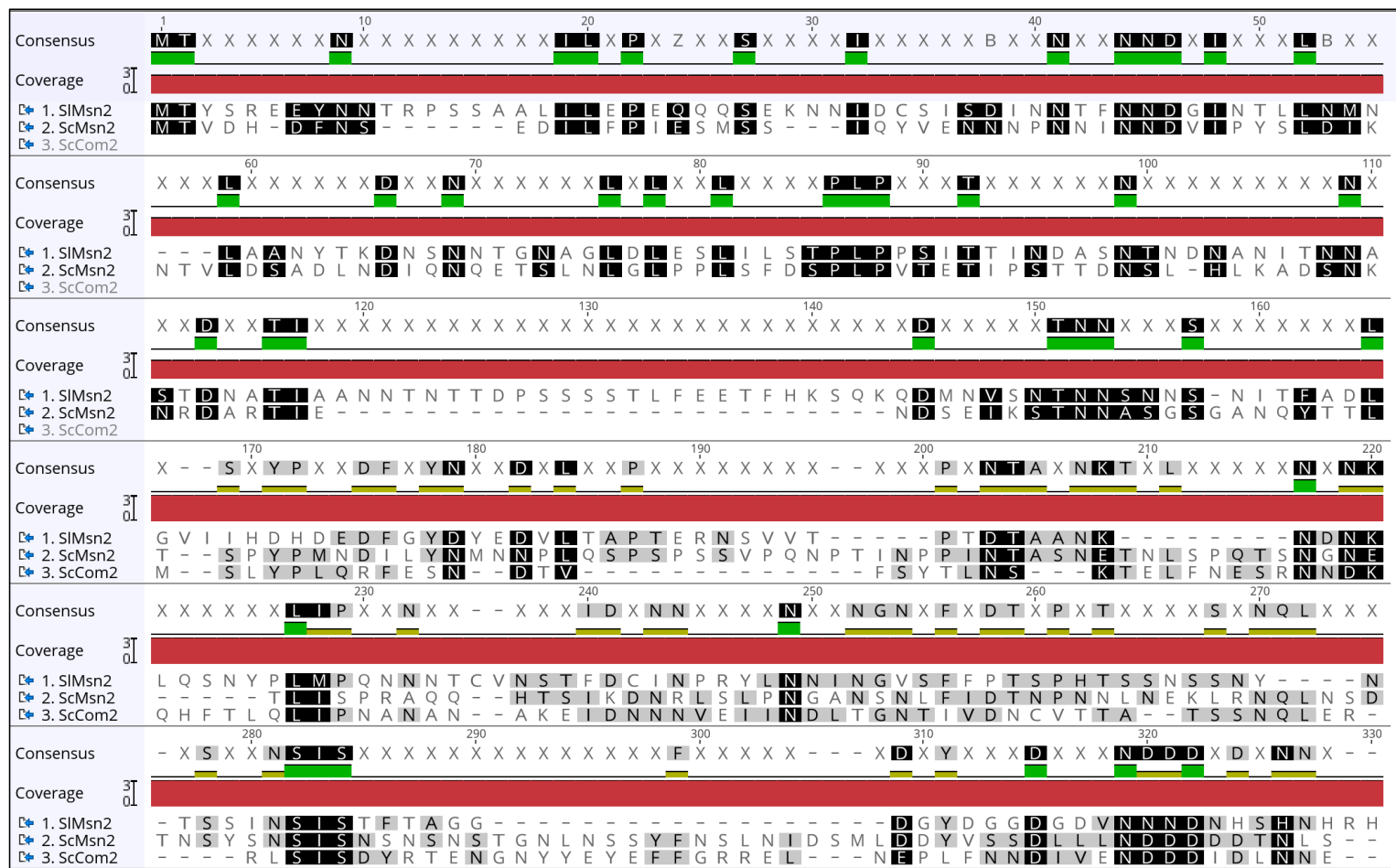
**GlcNAc**



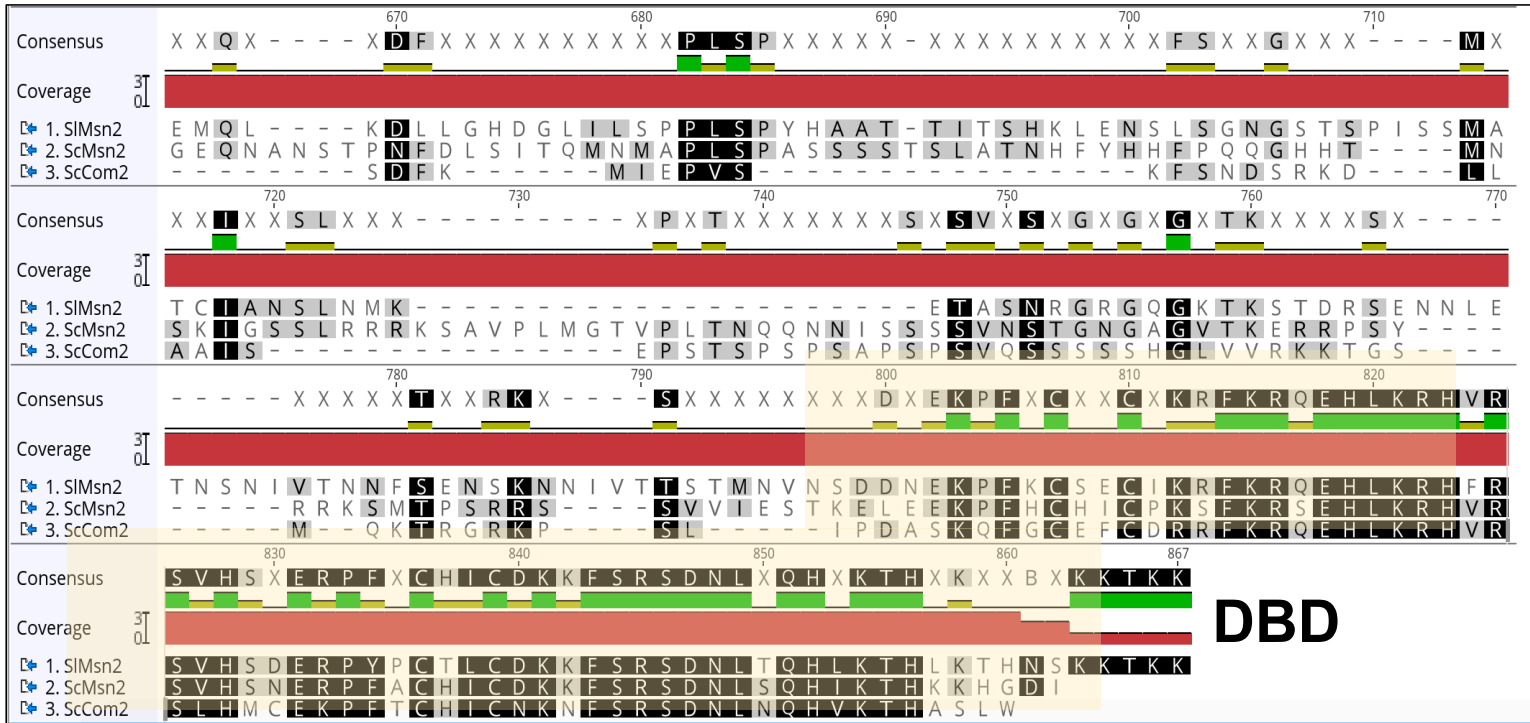
**Figure S3** – Functional analysis of *S. ludwigii* UTAD17 as indicated by the metabolic reconstruction tool BLASTkoala. The number of *S. ludwigii* UTAD17 genes clustered in each of the functional categories is indicated inside the pie chart.



**Figure S4 – Comparison of the amino acid sequence of the transcription factors ScCom2, ScMsn2 and SIMsn2 (ORF *SCLUD3.g330*).** Using the available amino acid sequences for the different proteins a multiBLASTP analysis was undertaken using “Geneious Multiple Sequence Alignment ClustalW”. Conserved residues are indicated in black boxes, being clear the highest degree of similarity at the C-terminal domain of the proteins which are known to harbor the DNA-binding domain of ScMsn2.







**Figure S5 – Amino acid sequence alignment of the sulfite efflux pumps *Ssu1* of *S. cerevisiae* and the four predicted orthologues in *S. ludwigii* UTAD17.** This alignment was performed with “Geneious Multiple Sequence Alignment ClustalW” using the amino acid sequences ScSsu1, SCLUD1.g608, SCLUD1.g612, SCLUD1.g608b, SCLUD1.g612b. The red arrow indicates the premature STOP codon found in the predicted sequences of two of the *S. ludwigii* UTAD17 orthologues.

