Figure S1 – Dendogram 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.

- Genetic Information Processing
- Carbohydrate Metabolism
- Environmental Information Processing
- Amino Acids Metabolism
- Metabolism of co-factors and vitamins
- Energy Metabolism
- Nucleotide Metabolism
- Organismal systems
- Metabolism of terpenoids and polyketides
- Metabolism of other Amino Acids
- Xenobiotics biodegradation and metabolism

- Cellular Processes
- Protein families: signaling and cellular processes
- Protein families: Metabolism
- Lipid Metabolism
- Unclassified: Metabolism
- Glycan biosynthesis and Metabolism
- Human diseases
- Unclassified
- Unclassified: Signaling and Cellular Processes
- Unclassified: genetic information processing

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.g608b, 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.

		1	10	20	30		40	50	60		70		80		90		100		110
Consensus		MXXXXXKX	××××××××××××××××××××××××××××××××××××××	SLXDXFXF	PFWFVTVMGT	GISSX	LHXFPYP,	AXWLRICS	YIMFALCC				(VYXKR	XXXXX	YFXXF	FXXX	PXNLF	WGTYXM	
Coverage	5T																		
1. SSU1_YEAST			VANWVL			GISSN	LYSFPYP	ARWLRICS	Y I MEALAC	LIFIA	QALQ			K S F R		FRNM		WGTYPM	
3 SCLUD1.g608		MANTGRIKK		SLIDEFA	FWFVTVMGT	GISSS		AKWLRICS	Y MFALCC		OTAVE		/ I YVKR		YVOR	EVS I	PINNL F	WGTYAM	GFCTIIN
4. SCLUD1.g608b		MMK-SHKN	SMMTFT	SLVDNEN SLVDNEN	YWFVTVMGT YWFVTVMGT	GSSSCM	T H D F P F P T H D F P F P	GL <mark>WLRICS'</mark> GLWLRICS'	YVMFGLCA YVMFGLCA		QTALV		VY FKR	TRMPQ TRMPO	I F Y G	F I K S	PTNLY	WGTYSM	GMCSMIN GMCSMIN
Consensus			13 		140	150 X 191 X	160 X AWG		170	180		190	D	200		210		220	23
Consensus									~	~~~									
Coverage	5T																		
1. SSU1_YEAST 2. SCLUD1.g608		FLGALSKA Ymytlasn	NTTKSP EASHSY	TN <mark>ARNLM</mark> K OSKNL	FVYVLWWYD AVYVLWWVD	LANCLV	IAWGISF ⊤AW∀ITF	LIWHDYYPI CWKYT	LEGIGNYP	SYNIK Hod	MASENM	K S V L L L O S F L L L	D PL	VVVAS VVVSS	S⊂G⊤F SSG©F	TMS E TMS E	I I FHA	FNRN I Q FNRN I Q	LITLVIC
3. SCLUD1.g612		YMYILASN	EASHSY	KQSKNL	AVYVLWWVD	VTISLG	TAWVITE	CWKYT		HQDI	LSKNL	QSFLLL	P	VVVSS	S S G C F	TMSE	ETQH	FNRNIQ	LLTLVIT
4. SCLUD1.g608b		YIFLMLKS	5 TNTTNY	ERSNTFIN		MISTM		L HWKENNKI	V	[PVVS	VVICS		TMSD		FNRNVQ	TTTLVMM
5. SCLUDT.go120		HIFLMLNS.	240	250	260		270	280	290	[300	IPMITI	310	VVICS	320	TWISD	330	FINKINVQ	340
Consensus		ALXWLEAI	XXVFXVX	AVYFWNLY	(INGIPDMXX			QGSYGVQL	×DNI×KY	XXKYY	кв∎ххт	R-XXX	(XX AV X	XXFKI	×ġ×n×		xsigu	FFTXYS	V×ST×SY
Coverage	50																		
1. SSU1_YEAST										AGKYY				WCFKI				FFTVIS	
3. SCLUD1.g612		ALLWLHAT	LVFLVL	SVYFWNL	/INGIPDIMK	-VFTCF			SDNILKY	IKKYH/	A NT GDE	R-EYLS	SV LAV G	YSFKV	FGLUL	ALL	MSCGI	FFTFYS	FASIASY
4. SCLUD1.g608b			MVFTVT	AVYFWNLY	VNGMPDMV S	NTSTCF	TCVGPMG	QGSYGIQL	C S D V V R Y	MELHY		<u>_</u>	M-AI	SFFKT	TGGTT	GTW	ISCGL	FFVIYS	VSSMFLF
5. SCLUD1.g612b		AMCWLQA 350	36	AVYEWNLY 0	370	380	ICVGPMG 390	QGSYGIQL)	400	MELEY 410		420	M -AI	430	GG	440	SCGL	450 450	461 461
Consensus		YNKXXN	×××	XXXRXXX	HKGWWAMTF	PXGTMA	LSTKEXW	VQYXXXXP	ÅFRVLS	VIYXG			TLXX	XXKXX	XXXXX	(xxxx)	×××∎s	GXXXXX	xxxxxx
Coverage	5								-										
1. SSU1 YEAST	01	YNKKENEN	E T G	KVKRVMT	HKGEWGMTE	PMGTMS	GNEELY	νογνρ	YAFRVIG	TIYGG			TLHE	SKKML	HAARK	SSLF		GTEKTT	VSPYNS
2. SCLUD1.g608		YNTIPUFN	SNLNT S A	NEN rimh	HKGWWAMTF	PLGTMA	LSTKE	QYDRIAP	GAFRVLS	VIYSG	CVIST	FCLLO		VYQWI	KDYNY	TTKI	NNRKIS	GNNEEQ	DQEVGIL
3. SCLUD1.g612			SNLNI S A		HKGWWAMIF				IGAFRVLS IDAEDMIS						K D Y N Y M D K K D		ITIGH	GNNEEQ M	DQEVGIL
5. SCLUD1.g612b		MOKTED			QKSWWAMPF	PTGTMA	LSTKETW	VQYGAFID	RAFRMIS	VFFAM		MTCLIC	TCNHY	I F K Q P I	MRK K D	YD N	ITICH	M	
Consensus		XXXXXXEG		4/8 RLA															
Coverage	5I																		
1. SSU1_YEAST				RLA															
3. SCLUD1.g612			NFSF*																
4. SCLUD1.g608b			•																
5. SCLUD 1.g612D			ς ι																