

## **Supplementary Data for Garcia-Sanchez *et al.***

Transcript profiling data for *C. albicans* CAI8 versus CAI4 is presented  
Using SAM, the False Discovery Rate was set at 10%

wild type 1 = CAI4

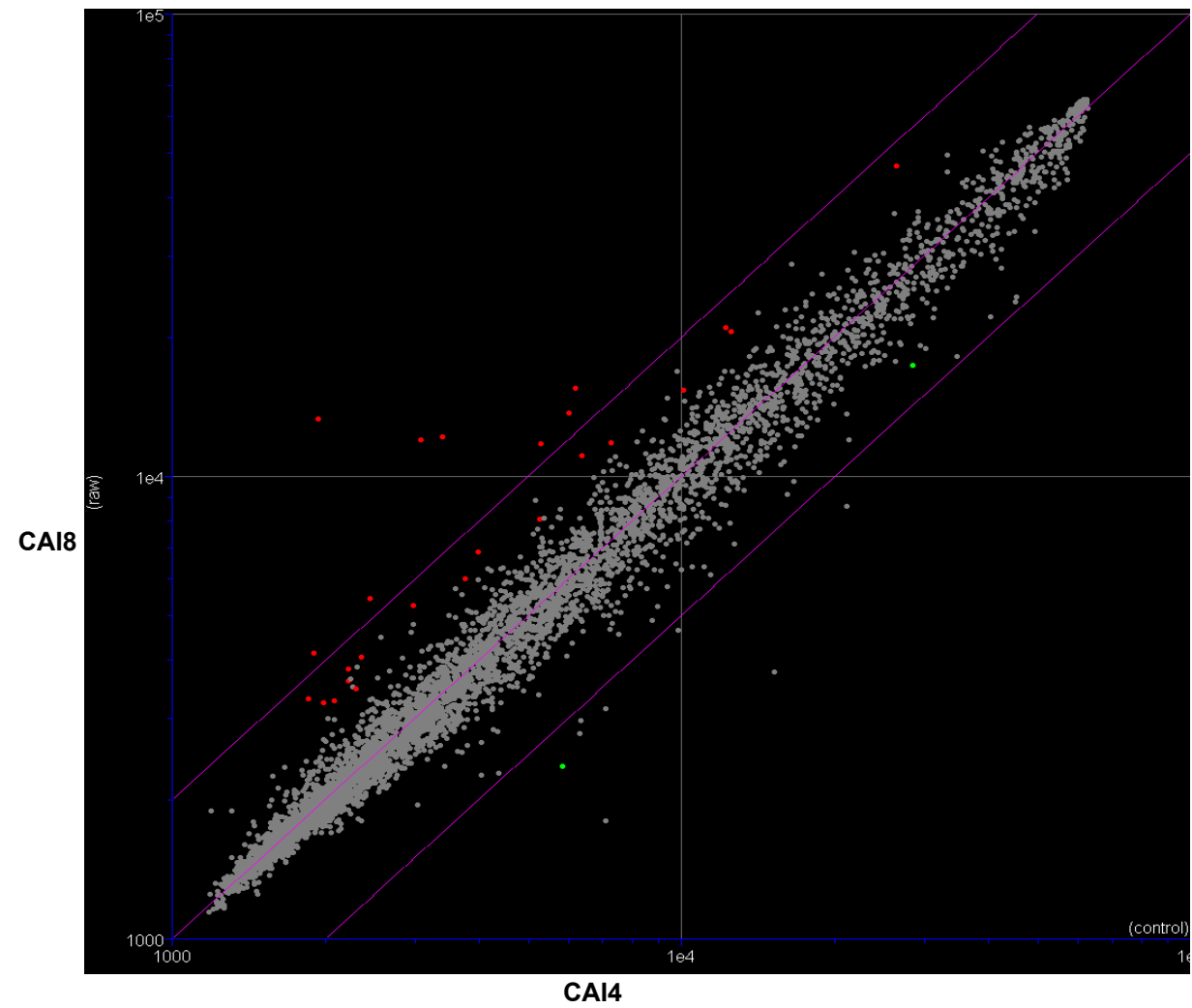
wild type 2 = CAI8

All were analysed in YPD at 30C in mid-exponential growth phase

Lists of regulated genes are presented

The full dataset is available at [http://www.pasteur.fr/recherche/unites/Galar\\_Fungail/](http://www.pasteur.fr/recherche/unites/Galar_Fungail/)

# Transcript profiling of CAI8 versus CAI4



The fold-regulation of genes that were regulated in CAI8 compared with CAI4 are shown

The fold-regulation of these genes in wrinkly *ssn6* (*ssn6* wk) and smooth *ssn6* cells (*ssn6* sm) are also shown.

	CAI8 vs CAI4	<i>ssn6</i> wk	<i>ssn6</i> sm			
<b>up 1.5 10FDR</b>						
CA6139	0.4	1.0	0.4	ADE2	phosphoribosylaminoimidazole carboxylase	YOR128c
CA4878	0.6	1.1	1.8	OXA1	Cytochrome oxidase biogenesis protein (by homology)	YER154w
<b>down 0.667 10FDR</b>						
CA1216	6.7	1.0	1.7	EBP1	NADPH dehydrogenase	YHR179w
CA4030	6.5	1.2	1.4	EBP4	NADPH dehydrogenase (by homology)	YHR179w
CA4391	4.2	1.0	0.9	ARR3	involved in arsenite transport (by homology)	YPR201w
CA3564	3.5	1.2	0.8	IPF7817	putative NADH-dependent flavin oxidoreductase (by homolog	YPL171c
CA2016	2.5	1.0	1.9	IPF3415	similar to <i>Saccharomyces cerevisiae</i> Yim1p mitochondrial inn	YMR152w
CA1181	2.3	1.3	1.6	UGA12.5f	4-aminobutyrate aminotransferase (GABA transaminase), 5- $\alpha$	YGR019w
CA1333	2.2	1.0	1.0	MRF1	mitochondrial respiratory function protein (by homology)	YBR026c
CA0671	2.2	1.1	1.3	GRP4	putative reductase (by homology)	YOL151w
CA3821	2.2	1.0	1.1	IPF6990	unknown function	YGL114w
CA2836	2.1	1.1	1.2	ARG5,6	acetylglutamate kinase and acetylglutamyl-phosphate reductase	YER069w
CA1180	2.0	0.9	1.2	UGA12.3f	4-aminobutyrate aminotransferase (GABA transaminase), 3- $\alpha$	YGR019w
CA1964	2.0	1.3	1.6	IFR2	unknown function	YNL134c
2262.1	2.0	1.0	0.8			
CA6037	1.9	0.9	1.0	ERC4	ethionine resistance protein (by homology)	YDR338c
CA4426	1.8	1.0	1.1	AMD21	amidase (by homology)	YDR242w
CA3886	1.8	1.5	1.3	IPF12963	ubiquitin-mediated protein degradation (by homology)	YMR275c
CA1693	1.8	1.1	1.0	IPF17054	unknown function	no match (e-value > 0.05)
CA3461	1.7	28.4	2.2	CFL2	ferric reductase (by homology)	YNR060w
CA2310	1.7	1.5	1.0	LEU42	2-isopropylmalalate synthase (by homology)	YNL104c
CA3033	1.7	1.0	1.0	IPF13202	unknown function	YMR068w
CA2975	1.7	1.0	1.3	ARO9	aromatic amino acid aminotransferase II (by homology)	YHR137w
CA2520	1.7	1.5	3.3	IPF20104	alcohol dehydrogenase (by homology)	YMR318c
CA0874	1.7	0.8	1.0	CPA1	Arginine-specific carbamoylphosphate synthase, small chain	YOR303w
CA3367	1.7	0.8	0.8	IPF4667	unknown Function	YDR380w

CA1099	1.6	1.1	0.9	IPF12312	unknown function	no match (e-value > 0.05)
CA3771	1.6	2.0	1.2	SOU1	Sorbitol utilization protein Sou1p [ <i>Candida albicans</i> ]	YNL202w
CA0877	1.6	0.8	0.9	CNH1	Na <sup>+</sup> /H <sup>+</sup> antiporter	YLR138w
CA0184	1.6	0.7	0.8	IPF19142	unknown function	YGR237c
CA4658	1.6	1.0	1.0	IPF3092	unknown function	no match (e-value > 0.05)
CA5535	1.6	1.2	1.3	IPF2839	unknown function	no match (e-value > 0.05)
CA4441	1.6	1.0	1.0	IPF2268.3f	unknown function, 3-prime end	no match (e-value > 0.05)
CA2731	1.5	1.0	0.8	URIC	uricase (urate oxidase) (by homology)	no match (e-value > 0.05)
CA2489	1.5	1.7	1.2	IPF7217	unknown function	YGR097w
CA3260	1.5	1.0	1.5	IPF7968	unknown function	YNL229c