

Supplemental Table S1: Identification of Pka1-regulated proteins by quantitative proteomics in *C. neoformans*.

GO categories ^a	Gene number	Protein Identification	Fold change ^b		<i>p</i> -value ^c
			Pka1-repression ^c	Pka1-induction ^d	
Metabolic processes					
	CNAG_00057	Fructose-1,6-bisphosphatase I	0.347	-1.840	0.041
	CNAG_00084*	Glutamine-tRNA ligase	-0.333	-1.883	0.001
	CNAG_00094	NAD-dependent epimerase/dehydratase	-0.148	-1.796	0.026
	CNAG_00275*	Uncharacterized protein	0.279	-2.126	0.000
	CNAG_00311	3-hydroxyisobutyryl-CoA hydrolase	0.821	-0.768	0.004
	CNAG_00441	Inosine-5-monophosphate dehydrogenase	-0.209	1.088	0.023
	CNAG_00520	Uncharacterized protein	0.933	-1.839	0.031
	CNAG_00524	Acetyl-CoA acyltransferase 2	1.327	-1.302	0.016
	CNAG_00573	NADH dehydrogenase (Ubiquinone) 1 alpha subcomplex 6	1.367	-1.558	0.017
	CNAG_00827	Ribose 5-phosphate isomerase	1.173	-2.182	0.027
	CNAG_00866	Transketolase	1.367	-0.862	0.046
	CNAG_01137*	Aconitate hydratase, mitochondrial	0.956	-0.164	0.001
	CNAG_01657	Fumarate hydratase, mitochondrial	0.838	-2.059	0.019
	CNAG_02035	Triosephosphate isomerase	0.537	-0.712	0.033
	CNAG_02181	Dihydrokaempferol 4-reductase	-0.038	-1.429	0.031
	CNAG_02230	Phosphoketolase	1.841	-1.086	0.013
	CNAG_02326	V-type proton ATPase catalytic subunit A	0.973	-1.145	0.012
	CNAG_02445	Phosphoacetylglucosamine mutase	0.864	-0.926	0.043
	CNAG_02918*	Acetyl-CoA C-acetyltransferase	1.251	-1.135	0.000
	CNAG_03019	Long-chain acyl-CoA synthetase	1.069	-1.414	0.025
	CNAG_03040*	Transketolase	1.370	-1.378	0.000
	CNAG_03128*	Gamma-glutamyltransferase	0.832	-1.830	0.000
	CNAG_03225	Malate dehydrogenase	0.868	-0.995	0.027
	CNAG_03345*	DIS3-like exonuclease 2	0.305	-1.084	0.003
	CNAG_03596	2-oxoglutarate dehydrogenase E2 component	0.920	-0.789	0.049
	CNAG_04025*	Transaldolase	1.972	-2.181	0.000
	CNAG_04346	Dihydrodipicolinate synthase	0.728	-1.197	0.039
	CNAG_04485	Long-chain acyl-CoA synthetase	0.551	-1.577	0.024

GO categories ^a	Gene number	Protein Identification	Fold change ^b		<i>p</i> -value ^e
			Pka1-repression ^c	Pka1-induction ^d	
	CNAG_04531	Enoyl-CoA hydratase	0.485	-2.695	0.013
	CNAG_05077	Glycosyl hydrolase	0.771	-1.358	0.014
	CNAG_05097	ATP-dependent (S)-NAD(P)H-hydrate dehydratase	0.846	-1.730	0.046
	CNAG_05144	Carbonic anhydrase	0.663	-1.706	0.020
	CNAG_05179	Ubiquinol-cytochrome c reductase core subunit 2	0.551	-0.642	0.042
	CNAG_05260*	Glutamate decarboxylase	0.441	-0.895	0.003
	CNAG_05828	UDP-N-acetylglucosamine pyrophosphorylase	0.920	-1.253	0.042
	CNAG_05900	Glycine-tRNA ligase	1.036	-2.112	0.026
	CNAG_05907	Pyruvate carboxylase	0.211	-0.840	0.020
	CNAG_06316	Glycine cleavage system H protein	-0.931	0.182	0.008
	CNAG_07363	Isocitrate dehydrogenase, NAD-dependent	0.186	-0.923	0.021
	CNAG_07372	6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase	1.435	-2.549	0.006
	CNAG_07400	Aspartate-tRNA(Asn) ligase	0.771	-2.251	0.017
	CNAG_07547	Uncharacterized protein	0.954	-1.752	0.004
Catabolic processes					
	CNAG_01108*	Allantoicase	0.567	-1.869	0.003
	CNAG_01594	Glycine dehydrogenase	0.069	-1.200	0.032
	CNAG_02780*	Kynureninase BNA5	1.134	-2.248	0.004
	CNAG_03542	Arginase	0.701	-0.490	0.013
	CNAG_03674	Oxoglutarate dehydrogenase (Succinyl-transferring), E1 component	0.036	-1.563	0.028
	CNAG_04948	Tubulin beta	0.284	-1.932	0.016
Biosynthetic processes					
	CNAG_00393	1,4-alpha-glucan-branching enzyme	1.076	-2.472	0.031
	CNAG_00797	Acetyl-coenzyme A synthetase	0.126	-0.621	0.018
	CNAG_00834	Phosphatidylserine decarboxylase	1.256	-1.407	0.004
	CNAG_00992	Homocitrate synthase, mitochondrial	1.115	-0.991	0.043
	CNAG_01238*	Arginine biosynthesis bifunctional protein ArgJ, mitochondrial	0.966	-0.913	0.000
	CNAG_01539	Myo-inositol-1-phosphate synthase	0.244	-0.306	0.043
	CNAG_01623	tRNA pseudouridine(55) synthase	-0.559	-0.031	0.016

GO categories ^a	Gene number	Protein Identification	Fold change ^b		<i>p</i> -value ^e
			Pka1-repression ^c	Pka1-induction ^d	
	CNAG_01890	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase	0.411	-1.374	0.022
	CNAG_02460	Coproporphyrinogen III oxidase	0.759	-3.133	0.010
	CNAG_02763	Phenylalanine-tRNA ligase, beta subunit	0.681	-0.789	0.034
	CNAG_02825	Argininosuccinate lyase	0.549	-1.635	0.041
	CNAG_02976*	Riboflavin kinase	0.711	-0.337	0.002
	CNAG_03270	Adenylosuccinate lyase	0.693	-1.802	0.007
	CNAG_03738	Pantetheine-phosphate adenylyltransferase	0.530	-1.436	0.016
	CNAG_04195	O-methyltransferase	0.702	-1.943	0.005
	CNAG_04621	Glycogen(Starch) synthase	0.139	-0.570	0.023
	CNAG_04822	Deoxyhypusine synthase	0.921	-1.755	0.014
	CNAG_04835	Dihydrodipicolinate synthase	0.352	-1.799	0.034
	CNAG_04879	Glycogen debranching enzyme	0.453	-1.164	0.006
	CNAG_05122	Homoserine O-acetyltransferase	1.311	-1.553	0.026
	CNAG_05148	Beta-1,2-xylosyltransferase 1	-0.176	-2.938	0.021
	CNAG_06400	Plasma-membrane proton-efflux P-type ATPase	1.113	-1.253	0.010
	CNAG_06421	Acetolactate synthase, small subunit	0.344	-1.272	0.042
	CNAG_06432	Acetate kinase	0.622	-2.153	0.016
	CNAG_06489	Adenosine kinase	0.723	-1.512	0.014
	CNAG_06679	Anthranilate synthase component I	0.636	-1.048	0.016
	CNAG_06830	Histidinol dehydrogenase	0.424	-0.591	0.047
	CNAG_06849	Saccharopine dehydrogenase [NAD(+), L-lysine-forming]	0.090	-1.783	0.048
	CNAG_06908	Pyridoxal biosynthesis lyase pdxS	0.886	-0.818	0.014
	CNAG_07780	Geranylgeranyl diphosphate synthase, type III	0.495	-0.803	0.017
Cellular processes					
	CNAG_00072	Protein disulfide-isomerase	0.494	-1.012	0.034
	CNAG_00700*	Phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	0.363	-1.495	0.001
	CNAG_00935	DNA-binding protein	0.298	-0.629	0.025
	CNAG_01362	Cell cycle control protein cwf19	0.265	-2.094	0.027

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			Pka1-repression ^c	Pka1-induction ^d	
	CNAG_01846	Flavoprotein	1.040	-0.915	0.020
	CNAG_04851	Transitional endoplasmic reticulum ATPase	0.547	-1.275	0.026
Transcription					
	CNAG_00409	Uncharacterized protein	1.234	-1.083	0.037
	CNAG_02022*	DNA-directed RNA polymerase II subunit RPB3	0.107	-4.335	0.002
	CNAG_02428	GC-rich sequence DNA-binding factor	0.778	-0.777	0.021
	CNAG_04284	Uncharacterized protein	0.687	-0.948	0.027
	CNAG_04765	Actin-related protein 2/3 complex subunit 3	0.511	-1.048	0.026
	CNAG_05221	Histone H2A	1.324	-2.370	0.028
	CNAG_05437	Nascent polypeptide-associated complex subunit beta	0.775	-1.356	0.013
	CNAG_07464	Transcription factor	1.076	-1.569	0.040
Proteolysis and Protein folding					
	CNAG_01881	Molecular chaperone GrpE	1.557	-2.879	0.005
	CNAG_01899	Prefoldin alpha subunit	1.574	-2.132	0.031
	CNAG_03627	Peptidyl-prolyl cis-trans isomerase	0.648	-1.725	0.049
	CNAG_06106	Chaperone regulator	-0.603	0.152	0.006
	CNAG_06602*	Cysteine-type peptidase	1.580	-2.278	0.001
Oxidation-reduction					
	CNAG_01027	Succinate-semialdehyde dehydrogenase (NADP)	0.739	-0.944	0.020
	CNAG_01097	Short-chain dehydrogenase/reductase SDR	1.601	-0.884	0.041
	CNAG_01102	Oxidoreductase	1.273	-0.546	0.006
	CNAG_01540	Dehydrogenase	-0.068	-2.413	0.033
	CNAG_01558	Chlorophyll synthesis pathway protein BchC	0.891	-2.288	0.016
	CNAG_02000	Short-chain dehydrogenase	0.674	-1.069	0.036
	CNAG_02794	Dihydroorotate dehydrogenase (Fumarate)	0.387	-2.131	0.038
	CNAG_03011	Glycerate-and formate-dehydrogenase	0.473	-1.665	0.011
	CNAG_03663	L-lactate dehydrogenase	0.916	-1.423	0.041
	CNAG_03701	Pentafunctional AROM polypeptide	0.339	-0.425	0.012
	CNAG_03948	NAD(P)H:quinone oxidoreductase, type IV	0.992	-3.089	0.012

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			Pka1-repression ^c	Pka1-induction ^d	
	CNAG_04955	Oxidoreductase	1.619	-2.046	0.012
	CNAG_05256	Catalase	0.926	-0.418	0.022
	CNAG_05258	Glucose-methanol-choline oxidoreductase	1.226	-0.246	0.005
	CNAG_06074*	Cytoplasmic protein, variant	0.822	-1.348	0.003
	CNAG_07316	Hydroxyacid-oxoacid transhydrogenase	0.295	-0.622	0.049
Transport					
	CNAG_01204	ATP synthase F1, delta subunit	1.113	-0.902	0.006
	CNAG_01274	Coatomer subunit gamma	0.397	-0.964	0.013
	CNAG_01586	F-type H-transporting ATPase subunit B	1.005	-3.091	0.012
	CNAG_01870	Electron transfer flavoprotein beta subunit	0.483	-1.140	0.005
	CNAG_02434	Copper chaperone	0.302	-1.288	0.006
	CNAG_02833	NADH dehydrogenase (Ubiquinone) 1 beta subcomplex 7	-0.713	-3.012	0.032
	CNAG_03153	Sec14 cytosolic factor, variant	0.432	-1.575	0.030
	CNAG_03418	Exportin-1	0.393	-0.799	0.040
	CNAG_03722	RAN protein binding protein	0.741	-1.301	0.032
	CNAG_03861	Cytochrome c oxidase subunit 5a	1.153	-2.326	0.024
	CNAG_04209	Voltage-gated potassium channel protein beta-2 subunit	0.592	-1.466	0.026
	CNAG_04362	ATP-dependent RNA helicase DBP5	0.333	-1.194	0.046
	CNAG_04684	Protein transporter SEC23	0.952	-2.173	0.021
	CNAG_04985	Nascent polypeptide-associated complex subunit alpha	0.772	-1.780	0.021
	CNAG_05132	Cytochrome c oxidase subunit 5b	0.813	-1.885	0.010
	CNAG_05615	Syntaxin 1B/2/3	0.487	-0.673	0.020
	CNAG_05882	Class E vacuolar protein-sorting machinery protein HSE1, variant	0.926	-1.154	0.026
	CNAG_05884	Importin beta-4 subunit	1.118	-1.269	0.044
	CNAG_06101	ADP,ATP carrier protein	1.055	-1.747	0.009
	CNAG_06806	Electron transfer flavoprotein alpha subunit	1.259	-2.187	0.027
	CNAG_07322	Uncharacterized protein	0.770	-0.548	0.028
	CNAG_07487*	F-type H-transporting ATPase subunit D	0.973	-0.699	0.002
	CNAG_07862	Fumarate reductase	0.595	-1.667	0.007

GO categories ^a	Gene number	Protein Identification	Fold change ^b		<i>p</i> -value ^e
			Pka1-repression ^c	Pka1-induction ^d	
Phosphorylation/Dephosphorylation					
	CNAG_03706*	Serine/threonine-protein phosphatase	-0.209	0.778	0.002
	CNAG_03864	Uncharacterized protein	0.594	-0.760	0.020
	CNAG_07740	Uncharacterized protein	0.676	-1.394	0.039
Unknown/Unclassified					
	CNAG_00162	Alternative oxidase, mitochondrial	2.148	-1.597	0.030
	CNAG_00315	HHE domain-containing protein	1.523	-0.217	0.050
	CNAG_00469	Endoplasmic reticulum protein	-0.569	1.216	0.044
	CNAG_00978	NADH dehydrogenase (Ubiquinone) 1 alpha subcomplex 9	1.125	-1.748	0.034
	CNAG_00990*	F-type H-transporting ATPase subunit H	1.268	-2.387	0.001
	CNAG_01191	Nuclear pore complex protein Nup62	1.261	-1.725	0.019
	CNAG_01241	Enzyme regulator	0.397	-1.439	0.040
	CNAG_01432	Ribosome assembly protein 4, variant	1.162	-0.933	0.023
	CNAG_01653*	Cytokine inducing-glycoprotein	-4.515	3.130	0.002
	CNAG_01744	Phosphatase	0.934	-1.785	0.011
	CNAG_02722	Aldose reductase	0.689	-1.067	0.039
	CNAG_02752	Short-chain dehydrogenase	0.712	-0.571	0.032
	CNAG_02943*	Cytoplasmic protein, variant	1.241	-1.851	0.003
	CNAG_03267	Splicing factor 3B subunit 2	1.653	-1.766	0.032
	CNAG_03319	Phospholipid binding protein	0.667	-0.946	0.008
	CNAG_03396	NAD diphosphatase	0.919	-1.811	0.006
	CNAG_03771	DNA binding protein Ncp1, variant	0.494	-1.850	0.005
	CNAG_03813*	Replication factor A3	0.654	-1.014	0.000
	CNAG_03993	RP/EB family microtubule-associated protein	1.455	-2.622	0.014
	CNAG_04151	Oxysterol-binding protein	0.272	-1.820	0.010
	CNAG_04203	Uncharacterized protein	0.449	-1.600	0.026
	CNAG_04566*	Beta-flanking protein	1.262	-1.426	0.000
	CNAG_05030	Zinc finger protein 830	1.529	-3.428	0.004
	CNAG_05100*	ENTH domain-containing protein c	0.367	-1.879	0.003

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			Pka1-repression ^c	Pka1-induction ^d	
	CNAG_05311	Arsenite-resistant protein ASR2	0.579	-1.254	0.029
	CNAG_05434	NADH dehydrogenase (Ubiquinone) 1 alpha subcomplex 2	1.796	-1.473	0.005
	CNAG_05465	Guanine nucleotide-binding protein subunit beta-like protein	0.153	-0.941	0.023
	CNAG_05745	Cytoplasmic protein	0.855	-0.745	0.043
	CNAG_05848	Splicing factor U2AF 65 kDa subunit	2.413	-1.784	0.019
	CNAG_06631*	Myosin heavy chain	1.402	-1.664	0.003
	CNAG_06646	Protein YOP1	0.744	-1.957	0.014
	CNAG_07446	Mitochondrial protein	0.961	-1.197	0.027
	CNAG_07925	Nucleoprotein TPR	0.921	-1.622	0.005
Hypothetical					
	CNAG_00012	Uncharacterized protein	0.531	-1.942	0.015
	CNAG_00286	Uncharacterized protein	0.946	-0.712	0.027
	CNAG_00465	Uncharacterized protein	1.705	-2.745	0.033
	CNAG_00577	Uncharacterized protein	0.947	-2.372	0.021
	CNAG_00626	Uncharacterized protein	1.847	-2.929	0.006
	CNAG_00858	Uncharacterized protein	1.419	0.092	0.029
	CNAG_00995	Uncharacterized protein	2.104	-1.866	0.026
	CNAG_01052	Uncharacterized protein	0.497	-2.396	0.013
	CNAG_01089	Uncharacterized protein	0.982	-2.625	0.046
	CNAG_01222	Uncharacterized protein	1.067	-2.116	0.009
	CNAG_01317	Uncharacterized protein	0.439	-2.061	0.021
	CNAG_01375	Uncharacterized protein	1.482	-0.618	0.022
	CNAG_01644	Uncharacterized protein	1.480	-1.871	0.045
	CNAG_01743	Uncharacterized protein	0.898	-0.957	0.011
	CNAG_01811	Uncharacterized protein	0.596	-0.546	0.018
	CNAG_01892	Uncharacterized protein	2.176	-3.841	0.014
	CNAG_02118	Uncharacterized protein	0.580	-1.284	0.013
	CNAG_02129	Uncharacterized protein	1.445	-0.730	0.012
	CNAG_02263*	Uncharacterized protein	0.466	-1.928	0.001

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			Pka1-repression ^c	Pka1-induction ^d	
	CNAG_02335*	Uncharacterized protein	0.679	-0.873	0.002
	CNAG_02400	Uncharacterized protein	1.079	-1.962	0.040
	CNAG_02842	Uncharacterized protein	0.062	-3.276	0.036
	CNAG_02843*	Uncharacterized protein	1.367	-1.208	0.003
	CNAG_02994	Uncharacterized protein	1.617	-1.235	0.005
	CNAG_03007	Uncharacterized protein	0.646	-1.311	0.012
	CNAG_03038	Uncharacterized protein	1.415	-0.994	0.005
	CNAG_03058	Uncharacterized protein	2.433	-1.737	0.009
	CNAG_03566*	Uncharacterized protein	2.316	-3.156	0.003
	CNAG_03677	Uncharacterized protein	0.898	-0.749	0.048
	CNAG_03688	Uncharacterized protein	3.035	-2.828	0.015
	CNAG_03705	Uncharacterized protein	1.662	-1.976	0.005
	CNAG_03841	Uncharacterized protein	0.742	-0.599	0.035
	CNAG_03873	Uncharacterized protein	1.346	-1.254	0.015
	CNAG_03961	Uncharacterized protein	2.081	-1.565	0.036
	CNAG_04163*	Uncharacterized protein	2.231	-0.887	0.003
	CNAG_04212	Uncharacterized protein	0.885	-1.310	0.043
	CNAG_04475*	Uncharacterized protein	0.818	-1.460	0.002
	CNAG_04680	Uncharacterized protein	0.294	-1.241	0.038
	CNAG_04954	Uncharacterized protein	0.523	-0.556	0.021
	CNAG_04962	Uncharacterized protein	0.540	-1.805	0.013
	CNAG_05001	Uncharacterized protein	1.117	-1.137	0.028
	CNAG_05131	Uncharacterized protein	0.899	-0.675	0.011
	CNAG_05312	Uncharacterized protein	-1.776	2.047	0.006
	CNAG_05570	Uncharacterized protein	1.495	-1.769	0.031
	CNAG_06109	Uncharacterized protein	1.860	-0.667	0.013
	CNAG_06113	Uncharacterized protein	0.148	-0.996	0.038
	CNAG_06328	Uncharacterized protein	0.149	-1.168	0.005
	CNAG_06475*	Uncharacterized protein	2.683	-1.270	0.003

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			Pka1-repression ^c	Pka1-induction ^d	
	CNAG_06577	Uncharacterized protein	2.056	-0.096	0.014
	CNAG_06765	Uncharacterized protein	0.566	-2.285	0.008
	CNAG_07382*	Uncharacterized protein	1.186	-1.713	0.002
	CNAG_07665	Uncharacterized protein	1.504	-1.703	0.041

^aGO term classification based on biological processes.

^b $P_{GAL7::PKA1/WT}$ normalized log₂ average fold change for three replicates under the respective glucose (repression) or galactose (induction) conditions.

^cPka1-repressed conditions (glucose-containing medium).

^dPka1-induced conditions (galactose-containing medium).

^eStatistical analysis performed between Pka1-repression and Pka1-induction values using Student's *t*-test (*p*-value < 0.05).

*Significant proteins after multiple hypothesis testing (FDR < 0.05).