Table S2. Additional target genes of Sfu1

ORF (Assembly6)	ORF (Assembly19)[a]	*Gene name*	Description	Fold changes[b]
				Δ*SFU1* (H-Fe) vs. Wt (H-Fe)
6.6384	19.1415/19.8991	*RBT2*	Repressed by TUP1 protein 2; ferrireductase-like	3.1
6.8497	19.7056	*DIP5*	Dicarboxylic amino acid permease	4.0
6.4008	19.8319/19.700	*SEO1*	Putative permease	6.3
6.1277	19.1926/19.9482	*SEF1*	Putative transcription factor; Zn2Cys6 cluster	2.0
6.5341	19.1579/19.9152		No good homologies	2.0
6.35	19.12751	*ACT2*	Similar to Mucor mucedo acyl-CoA thioester hydrolase	-3.6
6.590	19.4395	*AIP1*	Actin cortical patch	-2.7
6.115	19.84/19.7729	*CAN3*	N terminus of CAN1-like basic amino acid permease	-2.3
6.8814	19.6817/19.14109	*FCR1*	N term of fungal Zn(2)-Cys(6) binuclear cluster similar to FCR1	-3.4
6.5625	19.7965	*FCY2*	Purine-cytosine permease	-2.3
6.485	19.8714	*FDH1*	NAD-formate dehydrogenase	-6.5
6.3525	19.638/19/8252	*FDH1*	Possible formate dehydrogenase	-5.4
6.2663	19.1775	*FDH1*	Similar to formate dehydrogenases	-9.2
6.2662	19.1774	*FDH1*	Similar to formate dehydrogenases	-8.1
6.6483	19.3672/19.11156	*GAL10*	UDP glucose-4-epimerase	-5.4
6.6486	19.3675/19.11159	*GAl7*	Galactose-1-P uridylyl transferase	-4.2
6.204	19.5622	*GLC3*	Similar to Alpha-1,4-glucan branching enzyme	-2.1
6.1565	19.6249/19.13627	*HKA1*	C terminus of high affinity potassium transporter	-8.6
6.1494	19.2803/19.10321	*HEM13*	Coproporphyrinogen III oxidase	-2.3
6.42	19.2003	*HNM2*	Similar to N terminus of 6.6357, choline transporter	-2.0
6.2379	19.2020/19.9570	*HXT4*	Hexose transporter	-8.9
6.4407	19.11523	*ILV3*	Dihydroxyacid dehydratase	-2.5
6.8318	19.5329/19.12789		No good homologies	-2.2
6.214	19.9351		No good homologies	-2.0
6.4418	19.4052/19.11534		No good homologies	-3.5
6.8673	19.5437/19.12892	*RHR2*	DL-glycerol-3-phosphatase	-3.5
6.498	19.3467	*SEC27*	COP1 betasubunit; ER-to-Golgi trafficking	-2.2
6.3509	19.3962		Similar to hypothetical protein C33G8.2	-2.3
6.2549	19.802	*UGA99*	4-Aminobutyrate aminotransferase (GABA transaminase)	-2.1
6.8294	19.5305/19.12765		Weak similarity to Ca38F10.05	-2.3
6.3754	19.4907/19.12373		Similar to S. cerevisiae YCR061	-2.4
6.1218	19.1354/19.8934		Similar to S. cerevisiae YER067	-12.1
6.1848	19.11817		Similar to S. cerevisiae YPR009	-7.7
6.4409	19.11525		Similar to S. cerevisiae YPR115	-3.3
6.2584	19.4869/19.12333	*SFU1*	Similar to fungal siderophore regulator; fungal GATA-type factor	-15.7
6.4277	19.2608/19.10139	*ADH2*	Secondary alcohol dehydrogenase	-2.4
6.7574	19.6586/19.13939	*ECM13*	Cell wall structure, biosynthesis	-3.1
6.8766	19.7514	*PCK1*	PEP carboxykinase	-5.7
6.8394	19.7313	*SSU1*	Major facilitator superfamily protein	-3.9
6.7775	19.3038/19.10556	*TPS2*	Trehalose-6-phosphate phosphatase	-2.0
6.3941	19.5293/19.12751	*ACH2*	Non-yeast cytosolic long chain Acyl-CoA thioesterase	-2.6
6.4196	19.1198	*ADH1*	Alcohol dehydrogenase	-2.1
6.1310	19.2121/19.9669	*ALS*	Agglutinin-like protein	-3.3
6.3000	19.1097/19.8699	*ALS99*	Agglutinin-like protein	-3.4
6.3075	19.4556	*ALS99*	Agglutinin-like protein	-3.2
6.3074	19.4555	*ALS99*	Agglutinin-like protein	-3.0
6.3985	19.4774/19.12237	*AOX1*	Constitutive alternative oxidase	-3.0
6.3984	19.4773	*AOX2*	C terminus of inducible alternative oxidase 2	-12.6
6.7449	19.4036/19.11519	*APM1*	Medium subunit of clathrin-associated protein AP-1 complex	-2.2
6.4943	19.2849	*AQY1*	Aquaporin water channel protein	-5.1
6.1971	19.1945	*AUR1*	Phosphatidylinositol:ceramide phosphoinositol transferase	-2.0
6.8395	19.7314	*CDG1*	Similar to cysteine dioxygenases	-2.5
6.9126	19.5911/19.13332	*CMK1*	Calmodulin-dependent protein kinase1	-2.0
6.1328	19.2356	*CRZ99*	Similar to calcineurin-responsive transcription factor	-2.3
6.3067	19.3794/19.11274	*CSR1*	Candida suppressor of S. cerevisiae rok1, Zn finger protein	-2.1
6.1104	19.4777/19.12241	*DAK2*	Dihydroxyacetone kinase	-2.0
6.1685	19.4698	*DHP99*	Similar to hypothetical protein in Drosophila Mela	-3.2
6.8861	19.6770/19.14062	*ENT4*	Cytoskeletal adaptor	-2.5
6.4414	19.4048/19.11530	*FAD3*	Non-S. cerevisiae fatty acid desaturase	-2.8
6.6481	19.3670/19.11154	*GAL10*	Galactokinase	-2.5
6.8322	19.5333/19.12793	*GCN1*	Translational activator of GCN4	-2.5
6.3428	19.9738	*GDH2*	NAD-glutamate dehydrogenase	-2.1
6.8468	19.7085	*GLE1*	Contains nuclear-export-signal (NES)	-2.7
6.1595	19.986	*GLY1*	Threonine Aldolase: glycine metabolism	-2.2

Table S2. Continued

ORF (Assembly6)	ORF (Assembly19)[a]	*Gene name*	Description	Fold changes[b]
				Δ*SFU1* (H-Fe) vs. Wt (H-Fe)
6.1756	19.12173	*INT2*	Putative integrase from a polyprotein	-2.5
6.1340	19.1609	*KRI1*	KRRI-Interacting protein 1	-2.0
6.6106	19.3419/19.10923	*MAE1*	Mitochondrial malic enzyme	-3.9
6.8100	19.72		No good homologies	-3.5
6.8200	19.951/19.8566		No good homologies	-2.8
6.6457	19.3448		No good homologies	-2.6
6.1116	19.574		No good homologies	-2.4
6.2792	19.10952		No good homologies	-2.3
6.7146	19.6882/19.14171	*OSM1*	Hypertonic growth	-2.5
6.2574	19.10871	*PHM3*	Putative polyphosphate synthetase	-2.5
6.6500	19.431/19.8061		Potential fungal Zn(2)-Cys(6) binuclear cluster domain	-2.2
6.183	19.508	*QDR1*	N terminus of quinidine MFS-multidrug transporter	-9.8
6.7063	19.8138	*QDR1*	Similar to quinidine multidrug transporter	-13.7
6.8673	19.5437/19.12892	*PHR2*	DL-glycerol-3-phosphatase	-3.3
6.7052	19.1868/19.9424	*RNR2*	Small subunit of ribonucleotide reductase	-2.1
6.8803	19.6828/19.14120	*RRP1*	Maturation of rRNAs	-2.0
6.5977	19.2038/19.9586	*SDS22*	Positive regulator of type I protein phosphatase	-2.9
6.7197	19.3302/19.10812		Similar to dentin sialophosphoprotein precursor	-2.1
6.7258	19.4445/19.11925		Similar to putative disease resistance protein	-2.2
6.4795	19.2685/19.10200		Similar to glycoprotein gp2	-2.0
6.6713	19.822/19.8442		Similar to heat shock protease protein Hsp5	-8.3
6.4785	19.13071		Similar to histidine kinase A	-4.4
6.4410	19.4044/19.11526		Similar to putative protein	-2.6
6.8462	19.7091		Similar to unknown	-2.7
6.6769	19.666		Similar to S. cerevisiae YHR131c	-4.9
6.7442	19.4029/19.11512	*SQT1*	Ribosomal assembly	-2.7
6.6480-1	19.3669/19.11153	*STK99*	Serine/threonine protein kinase	-4.1
6.6480-2	19.3669/19.11153	*STK99*	Serine/threonine protein kinase	-3.5
6.3947	19.909/19.8527	*STP4*	tRNA splicing, uptake of branched-chain amino acids	-2.3
6.6485	19.3674/19.11158	*TGD99*	dTDP glucose-6-dehydratase	-2.1
6.6049	19.4941/19.12407	*TYE7*	Transcription factor; glycolytic gene expression	-2.4
6.3827	19.5288	*YAL060*	Zn-containing alcohol dehydrogenase	-2.4
6.5310	19.3712/19.11197	*YCR079*	Protein phosphatase of the PP2C family	-2.5
6.4411	19.4044/19.11526		Similar to S. cerevisiae YDR206	-2.0
6.5962	19.5136/19.12601		Similar to S. cerevisiae YGR017w	-2.4
6.4290	19.3544/19.11028		Putative NAD-dependent oxidoreductase	-2.0
6.653	19.9259		Similar to S. cerevisiae YNR018w	-3.9
6.2819	19.409/19.8039		Similar to S. cerevisiae YNR018w	-3.5
6.7448	19.4035/19.11518		Similar to GPI anchored surface protein GAS1	-2.4
6.4409	19.11525		Similar to S. cerevisiae YPR115	-2.5

[a] Identical or the most closely matched sequences in the assembly 19 of *C. albicans* genome project.

[b] Fold changes are derived from the average of four individual comparisons as described in experimental procedures. The positive and negative (shaded) values represent the transcripts having a higher expression level in the Δ*SFU1* mutant and the wildtype strain, respectively.