Supplemental Table 2. Gene Expression Responses to Sampangine in C. albicans

ORF	Gene symbol	Sc Ortholog	Description	Fold Change
orf19.2048			Transcription is positively regulated by Sfu1p	16.5
orf19.7187	CaMAM33	MAM33	Mitochondrial acidic matrix protein (by homology)	7.9
orf19.822	IPF8762		unknown function	5.9
orf19.6898	IPF2234		unknown function	5.2
orf19.251	IPF17186	HSP31	unknown function	4.8
orf19.717	CaHSP60	HSP60	Heat Shock Protein 60 (HSP60)	4.4
orf19.3656	CaCOX15	COX15	cytochrome oxidase assembly factor (by homology)	4.4
orf19.5025	CaMET3	MET3	ATP sulfurylase	4.2
orf19.2262	IPF11105	ZTA1	probable quinone oxidoreductase	4.1
orf19.7325	CaSCO1	SCO1	Inner mitochondrial membrane protein (by homology)	3.9
orf19.2524	CaMGE1	MGE1	heat shock protein (by homology)	3.9
orf19.7203	CaMRP7	MRP7	Mitochondrial ribosomal protein YmL2 precursor (by homology)	3.8
orf19.828	IPF8752	MRPL24	similar to Saccharomyces cerevisiae Mrpl24p ribosomal protein of the large subunit, mitochondrial (by homology)	3.8
orf19.3797	CaMRPL11	MRPL11	Mitochondrial ribosomal protein (by komology)	3.7
orf19.863	CaMRPL35	MRPL35	Ribosomal protein of the large subunit, mitochondrial (by homology)	3.7
orf19.5161	CaMRPL49	MRPL49	ribosomal protein mitochondrial	3.5
orf19.6402	CaCYS3	CYS3	cystathionine gamma-lyase by homology	3.5
orf19.1662	CaMRP1.3f	MRP1	Mitochondrial ribosomal protein of the small subunit, 3-prime end (by homology)	3.5
orf19.2754	CaTIM13	TIM13	subunit of mitochondrial protein import machinery-like by homology	3.4
orf19.5673	CaOPT7		unknown function	3.4
orf19.4018	IPF3361	RSM7	putative mitochondrial ribosomal protein S7 (by homology)	3.4
orf19.5645	CaMET15	MET15	O-acetylhomoserine O-acetylserine sulphydrylase	3.3
orf19.3367		MRPL22	Predicted ORF in Assemblies 19 and 20	3.3

orf19.3297	IPF6223	RSM27	unknown function	3.3
orf19.4932	CaMEF1	MEF1	mitochondrial translation elongation factor G (by homology)	3.3
orf19.6047	CaTUF1	TUF1	Translation elongation factor TU (by homology)	3.2
orf19.7331	CaFCY24	FCY24	Putative purine-cytosine transport protein	3.2
orf19.7042	IPF3080		unknown function (by homology)	3.2
orf19.7019	CaYML6	YML6	Ribosomal protein, mitochondrial (by homology)	3.2
orf19.2275	IPF10301	MNP1	putative 60S ribosomal protein L7/L12 homolog, mitochondrial precursor	3.2
orf19.1896	CaSSC1	SSC1	Mitochondrial heat shock protein 70-related protein (by homology)	3.2
orf19.3559	IPF3184.exon2	MRPS35	unknown function, exon 2	3.2
orf19.7577	CaMSS51	MSS51	involved in maturation of COX1 and COB mRNA (by homology)	3.1
orf19.5759	CaSNQ2	SNQ2	multidrug resistance protein (by homology)	3.1
orf19.6565	CaOXA1	OXA1	Cytochrome oxidase biogenesis protein (by homology)	3.1
orf19.397	CaMRPL28	MRPL28	mitochondrial ribosomal protein of the large subunit (by homology)	3.1
orf19.6420	IPF1341	PGA13	Similarity to mucin proteins (by homology)	3.1
orf19.4739	CaMSS116	MSS116	RNA helicase of the DEAD box family (by homology)	3.1
orf19.6183	IPF3445	TIM8	Unknown function	3.1
orf19.3205	CaMRPL36	MRPL36	ribosomal protein YmL36 precursor, mitochondrial (by homology)	3.0
orf19.7012	CaLPA4	LPA4	Similar to ribosomal protein S16, mitochondrial (by homology)	3.0
orf19.585	CaMRPL17	MRPL17	ribosomal protein of the large subunit (YmL30), mitochondrial (by homology)	3.0
orf19.755	CaMRPL37	MRPL37	Mitochondrial ribosomal protein YmL37 (by homology)	3.0
orf19.4190	IPF7999	TIM14	unknown function	2.9
orf19.7485	CaMRPL9	MRPL9	Mitochondrial ribosomal protein of the large subunit (by homology)	2.9
orf19.1485	CaMRPL31	MRPL31	Mitochondrial ribosomal protein	2.9
orf19.6136	IPF12778	MRPL4	ribosomal protein, mitochondrial (by homology)	2.9
orf19.10252	CaSUL1	SUL1	High-affinity sulfate transport protein (by homology)	2.8

orf19.3480	IPF17681	RSM23	similar to Saccharomyces cerevisiae Rsm23p involved in mitochondrial function (by homology)	2.8
orf19.688	IPF9582	MRPS18	similar to Saccharomyces cerevisiae Mrps18p ribosomal protein of the small subunit, mitochondrial (by homology)	2.8
orf19.1300	IPF13552	OMS1	putative methyltransferase (by homology)	2.8
orf19.7386	IPF3331	MBA1	unknown function	2.8
orf19.125	CaEBP1	EBP1	NADPH dehydrogenase	2.8
orf19.3106	CaMET16	MET16	3 -phosphoadenylylsulfate reductase (by homology)	2.8
orf19.2337	CaALP1	ALP1	amino-acid permease (by homology)	2.8
orf19.5064	CaMRPL3	MRPL3	ribosomal protein of the large subunit, mitochondrial (by homology)	2.8
orf19.3532	CaMRPL10.3	MRPL10	ribosomal protein, 3-prime end (by homology)	2.7
orf19.7514	CaPCK1	PCK1	phosphoenolpyruvate carboxykinase	2.7
orf19.484	CaMRPL40	MRPL40	Putative mitochondrial ribosomal protein (by homology)	2.7
orf19.8604	CaMRPS5	MRPS5	Probable ribosomal protein S5, mitochondrial (by homology)	2.7
orf19.3064	CaMRPL27	MRPL27	ribosomal protein (by homology)	2.7
orf19.6853	IPF8454		unknown function	2.7
orf19.549	IPF4276	MRPL32	similar to Saccharomyces cerevisiae Mrpl32p putative mitochondrial ribosomal protein (by homology)	2.7
orf19.2520	CaMRPS28	MRPS28	ribosomal protein (by homology)	2.7
orf19.2214	CaMRPL7	MRPL7	Ribosomal protein of the large subunit, mitochondrial (by homology)	2.7
orf19.5747	CaMRP4	MRP4	Ribosomal protein of the small subunit mitochondrial (by homology)	2.7
orf19.989		MRPS5	Predicted ORF in Assemblies 19 and 20	2.7
orf19.1159	IPF7616		putative homoserine O-acetyltransferase (by homology)	2.7
orf19.685	CaYHM1	GGC1	Putative mitochondrial carrier protein; fungal-specific	2.7
orf19.4947	IPF18761	YPR098C	unknown function	2.7
orf19.6406	IPF1308	SWS2	Similarity to ribosomal protein S13 (by homology)	2.7
orf19.5811	CaMET1	MET1	siroheme synthase (by homology)	2.7

orf19.7050	IPF447	NOP15	unknown function	2.6
orf19.2039	CaMSF1	MSF1	phenylalanine--tRNA ligase	2.6
orf19.7310	IPF5981	MSC1	similar to Saccharomyces cerevisiae Gin3p (by homology)	2.6
orf19.3696	CaTOM22	TOM22	mitochondrial outer membrane import receptor complex subunit (by homology)	2.6
orf19.5201	IPF7585	RSM18	unknown function	2.6
orf19.5444	CaTIM44	TIM44	mitochondrial inner membrane import receptor	2.6
orf19.5282	IPF4696		unknown Function	2.6
orf19.6208	CaMEF2	MEF2	translation elongation factor (by homology)	2.6
orf19.336	IPF1537	YAH1	putative adrenodoxin and ferrodoxin (by homolgy)	2.6
orf19.1416	CaCOX11	COX11	cytochrome-c oxidase assembly protein by homology to S. cerevisiae	2.5
orf19.7603	IPF660	YMR244C-A	unknown function	2.5
orf19.51	IPF11177	CLU1	similar to Saccharomyces cerevisiae Clu1p translation initiation factor eIF3 (p135 subunit) (by homology)	2.5
orf19.1162	IPF13081		unknown function	2.5
orf19.6129	CaMRPL8	MRPL8	mitochondrial 60s ribosomal subunit (by homology)	2.5
orf19.4176	IPF6175	MRPS17	unknown function	2.5
orf19.4056	IPF7666	GAT2	unknown function	2.5
orf19.3167	IPF3174	COX10	Farnesyl transferase (by homology)	2.5
orf19.5515	CaCBP3	CBP3	involved in cytochrome-c reductase assembly (by homology)	2.4
orf19.4273	IPF16549		Unknown function	2.4
orf19.2533	CaPRS	YER087W	prolyl-tRNA synthetase, 3-prime end	2.4
orf19.498	CaNAM9	NAM9	mitochondrial ribosomal protein	2.4
orf19.6696	CaTIM9	TIM9	Mitochondrial inner membrane translocase (by homology)	2.4
orf19.4309	CaGRP2	GRP2	Reductase (by homology)	2.4
orf19.2639	IPF6970		unknown function	2.4
orf19.6503	IPF3928		unknown function	2.4

orf19.7665	IPF4935	COX16	unknown function	2.4
orf19.2803	CaHEM13	HEM13	by homology S. cerev.: coproporphyrinogen III oxidase	2.3
orf19.5610	IPF13176.3	ARG3	ornithine carbamoyltransferase, 3-prime end (by homology)	2.3
orf19.1545	IPF6505	MRPS8	unknown function	2.3
orf19.6515	CaHSP90	HSP90	heat shock protein	2.3
orf19.5279	IPF4703	MRPL51	unknown Function	2.3
orf19.439	IPF5933	MHR1	similar to Saccharomyces cerevisiae Mhr1p involved in mitochondrial homologous DNA recombination (by homology)	2.3
orf19.4099	CaECM17	ECM17	Putative sulfite reductase (by homology)	2.3
orf19.6524	CaTOM40	TOM40	mitochondrial import receptor chain TOM40 (by homology)	2.3
orf19.1151	IPF11713		unknown function	2.3
orf19.4980	CaSSA4	SSA4	cahsp70 mRNA for heat shock	2.3
orf19.9512	CaCYC3	CYC3	cytochrome C heme lyase	2.3
orf19.12536	IPF12312		unknown function	2.3
orf19.4536	CaCYS4	CYS4	cystathionine beta-synthase (by homology)	2.3
orf19.3026	CaMAS1	MAS1	Mitochondrial processing protease (by homology)	2.2
orf19.3577	CaCOQ5	COQ5	C-methyltransferase (by homology)	2.2
orf19.5420	CaRML2	RML2	Ribosomal L2 protein, mitochondrial (by homology)	2.2
orf19.1149	CaMRF1	MRF1	mitochondrial respiratory function protein (by homology)	2.2
orf19.5288	CaIFE2	IFE2	Unknown function	2.2
orf19.1967	CaIMG1	IMG1	Ribosomal protein, mitochondrial (by homology)	2.2
orf19.4022	CaSDH42	SDH42	succinate dehydrogenase membrane anchor subunit for sdh2p (by homology)	2.2
orf19.9664		NAT2	Predicted ORF in Assemblies 19 and 20	2.2
orf19.946	CaMET14	MET14	Adenylylsulfate kinase (by homology)	2.2
orf19.7306	IPF5987	YPR127W	unknown function	2.2

orf19.240	IPF10510	PAM17	unknown function	2.2
orf19.3795	CaAGP3	AGP3	amino acid-permease (by homology)	2.2
orf19.3350	IPF4814	MRP20	similar to Saccharomyces cerevisiae Mrp20p ribosomal protein of the large subunit, mitochondrial (by homology)	2.2
orf19.2244	IPF12897	YJR096W	putative oxidoreductase (by homology)	2.2
orf19.1352	CaTIM22	TIM22	Mitochondrial import inner membrane translocase subunit (by homology)	2.2
orf19.6041	CaRPO41	RPO41	Mitochondrial DNA-directed RNA polymerase (by homology)	2.2
orf19.2382	CaISM1	ISM1	isoleucyl-tRNA synthetase (by homology)	2.2
orf19.1862	IPF4065	YHR087W	unknown function	2.2
orf19.1528	CaMTF1	MTF1	RNA polymerase specific factor, mitochondrial (by homology)	2.2
orf19.6656	IPF2277	DUR3	unknown function	2.2
orf19.6062	IPF1415	YPL098C	unknown function	2.1
orf19.6672	CaMDJ1	MDJ1	Heat shock protein - chaperone (by homology)	2.1
orf19.5167	CaIFM1	IFM1	translation initiation factor 2 by homology	2.1
orf19.1617		YDR282C	Protein similar to S. cerevisiae Ydr282cp; transposon mutation affects filamentous growth	2.1
orf19.1201	IPF7165	DIA4	similar to Saccharomyces cerevisiae Dia4p seryl-tRNA synthetase (by homology)	2.1
orf19.5684	CaMRPL38	MRPL38	ribosomal protein of the large subunit(L14), mitochondrial, by homology	2.1
orf19.1483	IPF4406	YKL137W	unknown function	2.1
orf19.3301	IPF19802	MET30	similar to Saccharomyces cerevisiae Met30p involved in regulation of sulfur assimilation genes and cell cycle progression (by homology)	2.1
orf19.12214	IPF16405	RSM25	similar to saccharomyces cerevisiae Rsm25p protein of the small subunit of the mitochondrial ribosome (by homology)	2.1
orf19.2737	IPF9167	YDR109C	unknown function	2.1
orf19.5230	CaMRPS9	MRPS9	ribosomal protein S9 small subunit precursor	2.1
orf19.458	CaBCS1	BCS1	mitochondrial protein of the CDC48/PAS1/SEC18 (AAA) family of ATPases (by homology)	2.1
orf19.392	CaCBP4	CBP4	Ubiquinol--cytochrome-c reductase assembly factor (by homology)	2.1
orf19.62	IPF19484	TMA108	putative zinc amino peptidase (by homology)	2.1

orf19.5443	IPF4191	BNA4	unknown function	2.1
orf19.5698	IPF5446	MRPL1	putative ribosomal protein (by homology)	2.1
orf19.4076	CaMET10	MET10	Sulfite reductase flavin-binding subunit (by homology)	2.1
orf19.760	IPF3903		unknown function	2.1
orf19.150	IPF16036	TIM17	similar to Saccharomyces cerevisiae Tim17p mitochondrial inner membrane import translocase subunit (by homology)	2.1
orf19.2020	CaHXT61	HXT61	sugar transporter	2.1
orf19.4023	IPF3366	MRP2	Mitochondrial ribosomal protein (by homology)	2.0
orf19.1956	IPF14757		unknown function	2.0
orf19.2259	IPF16143		unknown function	2.0
orf19.6752	IPF3492	RSM10	unknown function	2.0
orf19.445	IPF5924		unknown function	2.0
orf19.1977	CaURA4	URA4	dihydrooratase (by homology)	2.0
orf19.1857	IPF4684		unknown Function	-2.0
orf19.3731	CaERG25	ERG25	C-4 sterol methyl oxidase	-2.0
orf19.797	CaBAT21	BAT21	branched-chain amino acid transaminase (by homology)	-2.0
orf19.5293	IPF11879		unknown function	-2.0
orf19.1108	CaHAM1	HAM1	Controls 6-N-hydroxylaminopurine sensitivity and mutagenesis (by homology)	-2.1
orf19.3591	CaAPE3	APE3	aminopeptidase (by homology)	-2.1
orf19.2179	CaSIT1	SIT1	Ferrioxamine B permease by homology	-2.1
orf19.6899	IPF2232		unknown function	-2.1
orf19.5294	CaPDB1	PDB1	pyruvate dehydrogenase (by homology)	-2.1
orf19.6985	CaTEA1	TEA1	Putative transcription factor with zinc cluster DNA-binding motif; has similarity to S. cerevisiae Tea1p	-2.1
orf19.276	IPF10124		Alcohol acetyltransferase (by homology)	-2.2
orf19.4853	IPF7732	HCM1	similar to Saccharomyces cerevisiae Hcm1p transcription factor with fork head domain (by homology)	-2.2

orf19.907	CaFEN12		Predicted ORF from Assemblies 19 and 20; amphotericin B, caspofungin repressed	-2.3
orf19.3142	IPF3259		unknown function	-2.3
orf19.6586	IPF1617		unknown function	-2.3
orf19.3249	CaLAG1	LAG1	longevity-assurance protein (by homology)	-2.3
orf19.6570	IPF1651		purine nucleoside permease (by homology)	-2.3
orf19.1168	CaZCF3		Predicted zinc-finger protein of unknown function	-2.4
orf19.1631	CaERG6	ERG6	sterol transmethylase	-2.5
orf19.781	CaDUR31	DUR31	Urea transport protein (by homology)	-2.5
orf19.4802	CaFTH1	FTH1	iron transporter	-2.5
orf19.4966	IPF16755	AGC1	unknown function	-2.5
orf19.5660	CaPEX10.3	PEX10	peroxisomal assembly protein, 3-prime end (by homology)	-2.5
orf19.6993	CaGAP2	GAP2	general amino acid permease (by homology)	-2.6
orf19.7585	CaINO1	INO1	myo-inositol-1-phosphate synthase	-2.6
orf19.6073	CaHMX1	HMX1	Heme oxygenase; acts in utilization of hemin iron; gene transcriptionally activated by heat, low iron, or hemin; negatively regulated by Efg1p; expression greater in low iron; upregulated by Rim101p at pH 8	-2.9
orf19.3121	IPF12303		glutathione-S-transferase (by homology)	-2.9
orf19.4556	CaALS12.3f	ALS12	agglutinin-like protein, 3-prime end	-3.1
orf19.2602	CaOPT1	OPT1	oligopeptide transporter	-3.2
orf19.2591	CaBIO3	BIO3	DAPA aminotransferase (by homology)	-3.4
orf19.2593	CaBIO2	BIO2	biotin synthetase (by homology)	-3.5
orf19.5672	CaMEP2	MEP2	high affinity low capacity ammonia (by homology)	-3.7
orf19.2397	IPF14040		probable transporter (by homology)	-4.2
orf19.5636	CaRBT5	RBT5	GPI-anchored cell wall protein; has CRoW motif, not required for filamentous growth; expression is regulated by Rfg1p, Rim101p; repressed by Sfu1p, Hog1p, Tup1p; induced by serum, iron, alkaline pH, ketoconazole, or ciclopirox olamine	-4.5