Supplemental Table 1. Gene Expression Responses to Sampangine in S. cerevisiae

ORF	Gene symbol	Description	Fold Change
YJR150C	DAN1	cell wall mannoprotein|induced during anaerobic growth	67.5
YLR460C		Hypothetical ORF	37.0
YCR102C		Putative protein of unknown function; involved in copper metabolism; similar to C.carbonum toxD gene	17.6
YKL086W	SRX1	ATP-dependent cysteine sulfinic acid reductase	15.1
YOL101C	IZH4	Membrane protein involved in zinc metabolism, member of the four-protein IZH family, expression induced by fatty acids and altered zinc levels; deletion reduces sensitivity to excess zinc; possible role in sterol metabolism	14.4
YOR237W	HES1	similar to human oxysterol binding protein	11.4
YER011W	TIR1	Cold-shock induced protein of the Srp1p/Tip1p family of serine-alanine-rich proteins. Encodes a stress-response cell wall mannoprotein and this gene is downregulated at acidic pH.	9.9
YAR068W		putative membrane protein	9.7
YNL134C		Putative protein of unknown function with similarity to dehydrogenases from other model organisms; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus	9.3
YFL057C	AAD4	aryl-alcohol dehydrogenase (putative)	6.7
YJR047C	ANB1	translation initiation factor eIF-5A, anaerobically expressed form	6.2
YHR211W	FLO5	Lectin-like protein involved in flocculation, cell wall protein that binds to mannose chains on the surface of other cells, confers floc-forming ability that is chymotrypsin resistant but heat labile; similar to Flo1p	6.2
YOL151W	GRE2	NADPH-dependent methylglyoxal reductase (D-lactaldehyde dehydrogenase); stress induced (osmotic, ionic, oxidative, heat shock and heavy metals); regulated by the HOG pathway	6.0
YOR011W	AUS1	ATP-binding cassette (ABC) family	5.6
YDR044W	HEM13	coproporphyrinogen III oxidase	5.6
YML058w-a	HUG1	Protein involved in the Mec1p-mediated checkpoint pathway that responds to DNA damage or replication arrest, transcription is induced by DNA damage	5.2
YBR244W	GPX2	Phospholipid hydroperoxide glutathione peroxidase induced by glucose starvation that protects cells from phospholipid hydroperoxides and nonphospholipid peroxides during oxidative stress	5.1
YOL161C	PAU20	Hypothetical protein	5.0
YNR073C		Hypothetical ORF	4.8
YOR153W	PDR5	multidrug resistance transporter	4.7
YIL176C	PAU14	Hypothetical protein	4.7
YAR066W		putative membrane protein	4.6

YFL056C	AAD6	aryl-alcohol dehydrogenase (putative)	4.6
YLL064C	PAU18	Hypothetical protein	4.4
YLL060C	GTT2	glutathione transferase	4.3
YJL223C	PAU1	Part of 23-member seripauperin multigene family encoded mainly in subtelomeric regions, active during alcoholic fermentation, regulated by anaerobiosis, negatively regulated by oxygen, repressed by heme	4.3
YDR046C	BAP3	valine transporter	4.2
YHR048W	YHK8	Putative protein of unknown function, has similarity to multidrug resistance proteins; expression of gene is up-regulated in cells exhibiting reduced susceptibility to azoles	4.0
YNR075W	COS10	Protein of unknown function, member of a family of conserved, often subtelomerically-encoded proteins	4.0
YKR066C	CCP1	cytochrome c peroxidase	3.9
YJR149W		Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	3.9
YDR275W	BSC2	Transcript encoded by this ORF shows a high level of stop codon bypass	3.8
YLR297W		Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the vacuole; YLR297W is not an essential gene	3.7
YLL025W	DAN2	Hypothetical ORF /// putative cell wall protein	3.7
YML131W		Putative protein of unknown function with similarity to oxidoreductases; mRNA expression is increased in a HOG1 and SKO1-dependent manner after osmotic shock; GFP-fusion protein localizes to the cytoplasm	3.6
YJL213W		Protein of unknown function that may interact with ribosomes; periodically expressed during the yeast metabolic cycle; phosphorylated in vitro by the mitotic exit network (MEN) kinase complex, Dbf2p/Mob1p	3.6
YBR085W	AAC3	ADP/ATP translocator	3.5
YBL075C	SSA3	heat shock protein of HSP70 family	3.5
YLR413W		Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery	3.5
YNR076W	PAU6	Part of 23-member seripauperin multigene family encoded mainly in subtelomeric regions, active during alcoholic fermentation, regulated by anaerobiosis, negatively regulated by oxygen, repressed by heme	3.5
YLR461W	PAU4	Part of 23-member seripauperin multigene family encoded mainly in subtelomeric regions, active during alcoholic fermentation, regulated by anaerobiosis, negatively regulated by oxygen, repressed by heme	3.4
YJR156C	THI12	Protein involved in synthesis of the thiamine precursor hydroxymethylpyrimidine (HMP); member of a subtelomeric gene family including THI5, THI11, THI12, and THI13	3.2
YPR009W	SUT2	Involved in sterol uptake; homologous to SUT1	3.2
YGR035C		Protein of unknown function, potential Cdc28p substrate; transcription is activated by paralogous transcription factors Yrm1p and Yrr1p along with genes involved in multidrug resistance	3.2

YDL020C	RPN4	Transcription factor that stimulates expression of proteasome genes; Rpn4p levels are in turn regulated by the 26S proteasome in a negative feedback control mechanism; RPN4 is transcriptionally regulated by various stress responses	3.2
YPR071W		Hypothetical ORF	3.1
YKL071W		Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	3.1
YJR124C		Hypothetical ORF	3.1
YAL062W	GDH3	NADP-linked glutamate dehydrogenase	3.0
YDR533C	HSP31	Possible chaperone and cysteine protease with similarity to E. coli Hsp31 and S. cerevisiae Hsp32p, Hsp33p, and Sno4p; member of the DJ-1/ThiJ/PfpI superfamily, which includes human DJ-1 involved in Parkinson's disease; exists as a dimer	3.0
YBR284W		Putative protein of unknown function; YBR284W is not an essential gene; null mutant exhibits decreased resistance to rapamycin and wortmannin	3.0
YOR009W	TIR4	cell wall mannoprotein	3.0
YBR092C	PHO3	acid phosphatase	3.0
YOR226C	ISU2	Iron-sulfur cluster nifU-like protein	3.0
YGL075C	MPS2	Essential membrane protein localized at the nuclear envelope and spindle pole body (SPB), required for insertion of the newly duplicated SPB into the nuclear envelope; potentially phosphorylated by Cdc28p	2.9
YOL002C	IZH2	Membrane protein involved in zinc metabolism, member of the four-protein IZH family, direct target of the Zap1p transcription factor, expression induced by zinc deficiency and fatty acids, deletion increases sensitivity to elevated zinc	2.9
YPL257W		Hypothetical ORF	2.9
YGR177C	ATF2	alcohol acetyltransferase	2.9
YDR472W	TRS31	targeting complex (TRAPP) component involved in ER to Golgi membrane traffic	2.9
YCR104W	PAU3	Part of 23-member seripauperin multigene family encoded mainly in subtelomeric regions, active during alcoholic fermentation, regulated by anaerobiosis, negatively regulated by oxygen, repressed by heme	2.9
YGL039W		Oxidoreductase, catalyzes NADPH-dependent reduction of the bicyclic diketone bicyclo[2.2.2]octane-2,6-dione (BCO2,6D) to the chiral ketoalcohol (1R,4S,6S)-6-hydroxybicyclo[2.2.2]octane-2-one (BCO2one6ol)	2.9
YGR213C	RTA1	involved in 7-aminocholesterol resistance	2.8
YLR099C	ICT1	Protein of unknown function, null mutation leads to an increase in sensitivity to Calcofluor white; expression of the gene is induced in the presence of isooctane	2.8
YGL209W	MIG2	contains zinc fingers very similar to zinc fingers in Mig1p	2.8
YKL125W	RRN3	DNA independent RNA polymerase I transcription factor	2.8

YGL261C	PAU11	Putative protein of unknown function; mRNA expression appears to be regulated by SUT1 and UPC2	2.7
YDR453C	TSA2	thioredoxin-peroxidase (TPx); reduces H2O2 and alkyl hydroperoxides with the use of hydrogens provided by thioredoxin, thioredoxin reductase, and NADPH	2.7
YDR213W	UPC2	zinc finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type	2.7
YKL051W	SFK1	Suppressor of PI Four Kinase	2.7
YCR087C-A	LUG1	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the nucleolus	2.7
YOR377W	ATF1	alcohol acetyltransferase	2.7
YMR325W	PAU19	Hypothetical protein	2.6
YDR542W	PAU10	Hypothetical protein	2.6
YER188c-a		Putative protein of unknown function	2.6
YKL224C	PAU16	Putative protein of unknown function	2.6
YER064C		Non-essential nuclear protein; null mutation has global effects on transcription	2.6
YAR020C	PAU7	Part of 23-member seripauperin multigene family encoded mainly in subtelomeric regions, active during alcoholic fermentation, regulated by anaerobiosis, negatively regulated by oxygen, repressed by heme	2.6
YDR256C	CTA1	catalase A	2.6
YBL064C	PRX1	Mitochondrial peroxiredoxin (1-Cys Prx) with thioredoxin peroxidase activity, has a role in reduction of hydroperoxides; induced during respiratory growth and under conditions of oxidative stress	2.6
YKR050W	TRK2	low affinity potassium transport|membrane protein	2.5
YJR151C	DAN4	cell wall mannoprotein	2.5
YIL011W	TIR3	cell wall mannoprotein	2.5
YOR262W		Cytoplasmic protein of unknown function; essential gene with similarity to YLR243W; contains an ATP/GTP binding site motif	2.5
YKL106W	AAT1	aspartate aminotransferase	2.5
YGL259W	YPS5	GPI-anchored aspartic protease	2.5
YJR116W		Putative protein of unknown function	2.5
YAR069C		Identified by gene-trapping, microarray-based expression analysis, and genome-wide homology searching	2.5
YBR301W	DAN3	Cell wall mannoprotein with similarity to Tir1p, Tir2p, Tir3p, and Tir4p; expressed under anaerobic conditions, completely repressed during aerobic growth	2.5
YPL189W	GUP2	active glycerol transporter (putative)	2.5
YIL066C	RNR3	ribonucleotide reductase, large (R1) subunit	2.5
YDR240C	SNU56	U1 snRNP protein	2.5

YJL082W	IML2	Protein of unknown function, green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus	2.5
YNR071C		Hypothetical ORF	2.4
YLL056C		Protein of unknown function, transcription is activated by paralogous transcription factors Yrm1p and Yrr1p along with genes involved in multidrug resistance	2.4
YGR131W		Hypothetical ORF	2.4
YKL047W		Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	2.4
YGR294W	PAU12	Hypothetical protein	2.4
YCR020C	PET18	Protein required for respiratory growth and stability of the mitochondrial genome	2.4
YOR028C	CIN5	bZIP (basic-leucine zipper) protein|can activate transcription from a promoter containing a Yap recognition site	2.4
YKL162C-A		Similar to PIR1, PIR2 and PIR3 proteins	2.4
YPR134W	MSS18	Protein involved in splicing intron a15beta of COX1	2.4
YFL050C	ALR2	Probable Mg(2+) transporter; overexpression confers increased tolerance to Al(3+) and Ga(3+) ions	2.4
YLR437C		Putative protein of unknown function; epitope tagged protein localizes to the cytoplasm	2.4
YOR106W	VAM3	syntaxin family	2.3
YDL024C	DIA3	Protein of unknown function, involved in invasive and pseudohyphal growth	2.3
YJL116C	NCA3	With NCA2, regulates proper expression of subunits 6 (Atp6p) and 8 (Atp8p) of the Fo-F1 ATP synthase	2.3
YGL162W	SUT1	Involved in sterol uptake	2.3
YNL024C		Putative protein of unknown function with seven beta-strand methyltransferase motif; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	2.3
YDR032C	PST2	Protoplasts-SecreTed protein; the gene product was detected among the proteins secreted by regenerating protoplasts	2.3
YOR162C	YRR1	transcription factor	2.3
YLR077W		The authentic, non-tagged protein was localized to the mitochondria	2.3
YJR056C		Hypothetical ORF	2.3
YKR052C	MRS4	carrier protein	2.2
YLL011W	SOF1	U3 snoRNP protein	2.2
YGR281W	YOR1	ABC transporter	2.2
YOR175C		Member of the MBOAT family of putative membrane-bound O-acyltransferases	2.2
YAL059W	ECM1	Protein of unknown function, localized in the nucleoplasm and the nucleolus, genetically interacts with MTR2 in 60S ribosomal protein subunit export	2.2

YGR168C		Putative protein of unknown function	2.2
YJL035C	TAD2	tRNA-specific adenosine deaminase subunit	2.2
YFR012W		Hypothetical ORF	2.1
YLR247C	IRC20	Putative helicase; localized to mitochondria and the nucleus; YLR247C is not an essential gene; null mutant displays increased levels of spontaneous Rad52 foci	2.1
YJR097W	JJJ3	Protein that may function as a cochaperone, as suggested by the presence of a DnaJ-like domain	2.1
YBR119W	MUD1	U1 snRNP A protein	2.1
YAR029W		Member of DUP240 gene family but contains no transmembrane domains; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern	2.1
YKR086W	PRP16	ATP-binding protein (putative)	2.1
YKL219W	COS9	Protein of unknown function, member of a family of conserved, often subtelomerically-encoded proteins	2.0
YML043C	RRN11	rDNA transcription factor component	2.0
YLR108C		Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the nucleus	2.0
YCR048W	ARE1	acyl-CoA cholesterol acyltransferase (sterol-ester synthetase)	2.0
YDL137W	ARF2	ADP-ribosylation factor 2	-2.0
YER170W	ADK2	adenylate kinase|mitochondrial GTP:AMP phosphotransferase	-2.0
YMR210W		Putative acyltransferase with similarity to Eeb1p and Eht1p, has a minor role in medium-chain fatty acid ethyl ester biosynthesis; may be involved in lipid metabolism and detoxification	-2.0
YMR002W	MIC17	Mitochondrial intermembrane space cysteine motif protein; MIC17 is not an essential gene	-2.0
YER175C	TMT1	Trans-aconitate Methyltransferase 1	-2.1
YJL167W	ERG20	farnesyl diphosphate synthetase (FPP synthetase)	-2.1
YIL155C	GUT2	glycerol-3-phosphate dehydrogenase	-2.1
YLR214W	FRE1	cupric reductase|ferric reductase	-2.2
YML120C	NDI1	NADH dehydrogenase (ubiquinone)	-2.2
YER024W	YAT2	carnitine acetyltransferase	-2.2
YER141W	COX15	cytochrome oxidase assembly factor	-2.2
YKL151C		Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	-2.2
YBR230C	OM14	Integral mitochondrial outer membrane protein; abundance is decreased in cells grown in glucose relative to other carbon sources; appears to contain 3 alpha-helical transmembrane segments; ORF encodes a 97-basepair intron	-2.3

YJR025C	BNA1	3-hydroxyanthranilic acid dioxygenase	-2.3
YPL081W	RPS9A	ribosomal protein S9A (S13) (rp21) (YS11)	-2.3
YBR050C	REG2	Glc7p regulatory subunit	-2.3
YOL083W		Hypothetical ORF	-2.3
YHR216W	IMD2	IMP dehydrogenase homolog	-2.3
YGR032W	GSC2	1,3-beta-D-glucan synthase catalytic component	-2.3
YHR051W	COX6	cytochrome c oxidase subunit	-2.3
YOL158C	ENB1	enterobactin transporter	-2.4
YKL150W	MCR1	NADH-cytochrome b5 reductase	-2.4
YIL111W	COX5B	cytochrome c oxidase chain Vb	-2.4
YHR092C	HXT4	high affinity glucose transporter	-2.5
YLR038C	COX12	cytochrome c oxidase subunit VIb	-2.5
YOR375C	GDH1	NADP-specific glutamate dehydrogenase	-2.5
YOR215C		Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	-2.5
YDL130W-A	STF1	ATPase stabilizing factor	-2.6
YNR060W	FRE4	Ferric reductase, reduces a specific subset of siderophore-bound iron prior to uptake by transporters; expression induced by low iron levels	-2.6
YBR294W	SUL1	sulfate uptake is mediated by specific sulfate transporters SUL1 and SUL2, which control the concentration of endogenous activated sulfate intermediates.	-2.6
YOR185C	GSP2	GTP-binding protein|Gsp1p homolog	-2.6
YER044C	ERG28	Endoplasmic reticulum membrane protein, may facilitate protein-protein interactions between the Erg26p dehydrogenase and the Erg27p 3-ketoreductase and/or tether these enzymes to the ER	-2.6
YDR529C	QCR7	ubiquinol cytochrome C oxidoreductase subunit 7 (14 kDa)	-2.6
YOR384W	FRE5	Putative ferric reductase with similarity to Fre2p; expression induced by low iron levels	-2.7
YDL110C	TMA17	Protein of unknown function that associates with ribosomes	-2.8
YDL174C	DLD1	D-lactate ferricytochrome c oxidoreductase	-2.8
YGR183C	QCR9	ubiquinol cytochrome c oxidoreductase complex 7.3 kDa subunit 9	-2.8
YMR015C	ERG5	cytochrome P450|involved in C-22 denaturation of the ergosterol side-chain	-2.8
YDR516C	EMI2	Non-essential protein of unknown function required for transcriptional induction of the early meiotic-specific transcription factor IME1, also required for sporulation	-2.9

YJL088W	ARG3	ornithine carbamoyltransferase	-2.9
YGL089C	MF(ALPHA)2	alpha mating factor	-2.9
YNL111C	CYB5	cytochrome b5	-3.0
YKR039W	GAP1	general amino acid permease	-3.0
YEL039C	CYC7	iso-2-cytochrome c	-3.0
YNL015W	PBI2	proteinase inhibitor I2B (PBI2)	-3.1
YEL024W	RIP1	Rieske iron-sulfur protein of the mitochondrial cytochrome bc1 complex	-3.1
YPR124W	CTR1	copper transport protein	-3.1
YLR126C		Putative protein of unknown function with similarity to glutamine amidotransferase proteins; has Aft1p-binding motif in the promoter; may be involved in copper and iron homeostasis; YLR126C is not an essential protein	-3.3
YDR461W	MFA1	a-factor mating pheromone precursor	-3.3
YHL040C	ARN1	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores	-3.3
YPL198W	RPL7B	ribosomal protein L7B (L6B) (rp11) (YL8)	-3.4
YGL191W	COX13	cytochrome c oxidase subunit VIa|may specifically interact with ATP	-3.4
YPR191W	QCR2	40 kDa ubiquinol cytochrome-c reductase core protein 2	-3.4
YGR087C	PDC6	pyruvate decarboxylase isozyme	-3.6
YEL065W	SIT1	ferrioxamine B permease	-3.6
YGR234W	YHB1	Nitric oxide oxidoreductase, flavohemoglobin involved in nitric oxide detoxification; plays a role in the oxidative and nitrosative stress responses	-3.7
YHL028W	WSC4	contains novel cysteine motif|integral membrane protein (putative)|similar to SLG1 (WSC1), WSC2 and WSC3	-3.8
YNL237W	YTP1	Probable type-III integral membrane protein of unknown function, has regions of similarity to mitochondrial electron transport proteins	-3.8
YKR046C	PET10	Protein of unknown function that co-purifies with lipid particles; expression pattern suggests a role in respiratory growth; computational analysis of large-scale protein-protein interaction data suggests a role in ATP/ADP exchange	-4.0
YNL052W	COX5A	cytochrome c oxidase chain Va	-4.4
YMR251W	GTO3	Putative cytosolic Omega class glutathione transferase	-4.5
YDR270W	CCC2	copper-transporting P-type ATPase with similarity to human Menkes and Wilsons genes	-5.0
YHR001W-A	QCR10	ubiqunol-cytochrome c oxidoreductase complex 8.5 kDa subunit	-5.2

YOR383C	FIT3	Cell wall protein involved in iron transport	-5.2
YMR145C	NDE1	Mitochondrial external NADH dehydrogenase, catalyzes the oxidation of cytosolic NADH; Nde1p and Nde2p are involved in providing the cytosolic NADH to the mitochondrial respiratory chain	-5.2
YLR367W	RPS22B	ribosomal protein S22B (S24B) (rp50) (YS22)	-5.6
YNL142W	MEP2	ammonia transport protein	-5.8
YLR205C	HMX1	ER localized, heme-binding peroxidase involved in the degradation of heme; does not exhibit heme oxygenase activity despite similarity to heme oxygenases; expression regulated by AFT1	-5.8
YER145C	FTR1	iron permease	-6.0
YLR136C	TIS11	Zinc finger containing homolog of mammalian TIS11, glucose repressible gene	-8.6
YHL047C	ARN2	triacetylfusarinine C transporter	-9.0
YMR058W	FET3	multicopper oxidase	-11.0
YGL187C	COX4	cytochrome c oxidase subunit IV	-13.2
YJR048W	CYC1	iso-1-cytochrome c	-13.3
YOR382W	FIT2	Cell wall protein involved in iron transport	-14.3