

Table S3.SRR1-dependent Oxidative Stress Responsive Genes

orf19 Designation	Gene Name	Molecular Function	Fold Changes (treated vs. untreated)			
			SRR1/SRR1		?srr1/?srr1	
			Exp 1	Exp2	Exp 1	Exp 2
orf19.113	<i>CIP1</i>	Unknown	217.4	444.2	44.2	112.0
orf19.3121	<i>GST1</i>	transcription corepressor activity	153.9	449.2	58.9	43.8
orf19.1763	<i>IFR1</i>	Unknown	59.0	218.8	27.2	41.8
orf19.3122	<i>ARR3</i>	arsenite transmembrane transporter activity	44.8	78.9	18.5	20.2
orf19.720	<i>GST3</i>	transcription corepressor activity	43.7	72.6	4.4	15.5
orf19.3150	<i>GRE2</i>	oxidoreductase activity	42.5	63.3	8.4	10.9
orf19.4474		Unknown	35.5	57.8	9.9	29.0
orf19.3234		NADPH dehydrogenase activity	34.6	61.5	15.5	20.1
orf19.3131	<i>OYE32</i>	NADPH dehydrogenase activity	25.3	39.2	8.6	8.1
orf19.4970		Unknown	23.8	89.2	5.0	5.7
orf19.87	<i>GPX1</i>	glutathione peroxidase activity	20.4	6.3	2.6	1.7
orf19.2244		Unknown	18.4	22.6	5.7	7.9
orf19.7320	<i>LIP7</i>	lipase activity	18.4	7.4	2.2	2.3
orf19.6999		Unknown	18.3	118.9	4.9	3.3
orf19.3309		Unknown	17.6	18.4	5.8	5.5
orf19.2262		AU-rich element binding, NADPH:quinone reductase activity	16.9	21.8	7.4	10.4
orf19.6595	<i>RTA4</i>	phospholipid-translocating ATPase activity	15.7	39.8	2.4	3.3
orf19.2933		ubiquitin-specific protease activity	15.4	21.2	5.7	7.7
orf19.7469	<i>ARG1</i>	argininosuccinate synthase activity	14.7	23.1	3.0	3.2
orf19.6997		Unknown	14.3	22.2	4.0	3.8
orf19.2515		Unknown	13.7	25.0	3.3	3.7
orf19.1126		Unknown	13.0	15.3	1.5	3.4
orf19.6781		transcription factor activity	12.7	26.5	4.3	6.3
orf19.5498	<i>EFH1</i>	transcription factor activity	12.7	23.4	1.6	0.7
orf19.6947	<i>GTT11</i>	glutathione transferase activity	11.9	14.5	4.6	5.8
orf19.5877	<i>ATF1</i>	alcohol O-acetyltransferase activity	11.4	13.8	4.9	6.0
orf19.847	<i>YIM1</i>	endopeptidase activity	11.2	15.2	4.4	4.8
orf19.3021		Unknown	11.0	26.9	2.9	3.0
orf19.1406		Unknown	10.6	15.4	5.1	7.7
orf19.2346		Unknown	10.2	11.6	4.5	5.3
orf19.3588		Unknown	10.1	10.1	3.2	4.5
orf19.5094	<i>BUL1</i>	Unknown	9.8	17.7	2.9	3.3
orf19.3282	<i>BMT3</i>	Unknown	9.8	12.6	2.8	2.9
orf19.1149	<i>MRF1</i>	DNA binding	9.6	12.4	2.7	2.6
orf19.2480.1	<i>AUT7</i>	Unknown	9.3	17.6	3.6	5.1
orf19.896	<i>CHK1</i>	two-component sensor activity, osmosensor activity	9.0	16.0	1.9	3.7
orf19.6311		Unknown	9.0	25.8	1.0	3.8
orf19.7531		Unknown	8.9	9.4	3.6	3.8
orf19.2769		endopeptidase inhibitor activity	8.5	10.1	1.7	2.2
orf19.6139	<i>FRE7</i>	ferric-chelate reductase activity	8.3	15.7	3.4	2.6
orf19.419		Unknown	8.2	22.6	4.2	4.2
orf19.4307		Unknown	8.1	11.4	3.0	5.8
orf19.7442		Unknown	7.8	5.7	1.5	1.1
orf19.4411	<i>HOS1</i>	histone deacetylase activity	7.8	8.3	2.9	3.0
orf19.1504		Unknown	7.6	7.4	2.1	3.2
orf19.6196		Unknown	7.6	10.6	3.5	4.2
orf19.803		4-aminobutyrate transaminase activity	7.5	16.3	3.1	2.8
orf19.7393		NADH kinase activity	7.4	6.9	2.4	2.5
orf19.6605		Unknown	7.3	12.8	3.1	5.7
orf19.1277		Unknown	7.2	16.8	2.3	2.2
orf19.1359		Unknown	7.2	7.1	3.5	3.5
orf19.6306		aldehyde dehydrogenase (NAD) activity	7.0	12.1	3.0	2.7
orf19.5610	<i>ARG3</i>	ornithine carbamoyltransferase activity	6.9	8.1	0.7	1.0
orf19.6148		structural constituent of cytoskeleton	6.9	9.0	1.9	2.9
orf19.782		Unknown	6.9	16.1	2.0	3.5
orf19.771	<i>LPG20</i>	aryl-alcohol dehydrogenase activity	6.8	5.7	2.0	1.9
orf19.2812		Unknown	6.7	5.4	0.6	0.9
orf19.6508		protein transporter activity	6.7	17.4	1.9	3.6
orf19.2210		Unknown	6.6	2.9	1.1	1.5
orf19.3771	<i>ARG8</i>	N2-acetyl-L-ornithine:2-oxoglutarate 5-aminotransferase activity	6.6	7.7	0.7	0.6
orf19.2693	<i>GST2</i>	transcription corepressor activity	6.4	8.4	2.8	3.3
orf19.7381	<i>ZCF37</i>	transcription factor activity	6.4	6.1	2.2	2.1
orf19.2028	<i>MXR1</i>	peptide-methionine-(S)-S-oxide reductase activity	6.3	16.2	2.5	5.8
orf19.2784		Unknown	6.2	2.6	0.5	1.2
orf19.822		Unknown	6.1	41.0	3.1	4.5
orf19.6758		aldo-keto reductase activity	6.0	8.1	1.1	1.8
orf19.6706	<i>GYP7</i>	Rab GTPase activator activity	6.0	6.1	1.6	2.1
orf19.5809		arylformamidase activity, kynurenine-oxoglutarate transaminase activity	5.9	7.5	2.7	2.7
orf19.916		Unknown	5.9	8.9	2.0	2.9
orf19.7043		Unknown	5.9	4.1	0.6	1.4
orf19.6844	<i>ICL1</i>	isocitrate lyase activity	5.8	25.2	3.0	9.1
orf19.7585	<i>INO1</i>	inositol-3-phosphate synthase activity	5.8	8.2	1.1	0.8
orf19.1789.1	<i>LYS1</i>	saccharopine dehydrogenase (NAD+, L-lysine-forming) activity	5.8	6.8	1.1	1.4
orf19.337		Unknown	5.7	8.1	2.2	3.5
orf19.4072	<i>IFF6</i>	Unknown	5.7	3.4	2.6	1.7
orf19.5924	<i>ZCF31</i>	Unknown	5.7	4.8	2.0	1.9
orf19.2982		kinase activator activity	5.7	12.9	2.8	3.1
orf19.3818	<i>GOA1</i>	Unknown	5.6	5.2	1.2	1.3
orf19.103	<i>KAR5</i>	Unknown	5.5	25.9	0.9	1.4
orf19.5614		ribonuclease H activity	5.5	8.0	2.2	2.5
orf19.5662	<i>PEP7</i>	phosphatidylinositol 3-phosphate binding	5.5	5.0	2.6	2.2
orf19.6606		Unknown	5.4	5.9	1.9	2.4
orf19.3507	<i>MCR1</i>	cytochrome-b5 reductase activity	5.3	5.1	1.8	1.8
orf19.4795		Unknown	5.3	8.1	0.7	0.8
orf19.94		Unknown	5.2	6.5	0.6	0.5
orf19.4658		Unknown	5.2	7.3	2.4	2.7
orf19.376		Unknown	5.2	3.6	1.6	1.8
orf19.5876		Unknown	5.1	11.2	2.3	3.5
orf19.5250		Unknown	5.1	6.0	2.0	2.7
orf19.6287	<i>AAT21</i>	L-aspartate:2-oxoglutarate aminotransferase activity	5.1	5.6	2.2	2.3
orf19.6757	<i>GCY1</i>	aldehyde reductase activity	5.1	7.0	2.0	3.3
orf19.5587		Unknown	5.1	4.9	1.6	1.2
orf19.4368		Unknown	5.0	6.0	2.4	2.6
orf19.1297		Unknown	5.0	2.8	0.9	0.9
orf19.27		Unknown	5.0	3.0	0.7	0.7
orf19.716		Unknown	5.0	6.8	1.4	1.3

			Fold Changes (treated vs. untreated)			
orf19 Designation	Gene Name	Molecular Function	SRR1/SRR1		Asrr1/Asrr1	
			Exp 1	Exp2	Exp 1	Exp 2
orf19.4543	UGA2	succinate-semialdehyde dehydrogenase [NAD(P)+] activity	5.0	5.1	2.2	2.1
orf19.3605		Unknown	5.0	5.4	1.4	1.5
orf19.697		Unknown	5.0	4.6	1.8	2.0
orf19.6793		Unknown	4.9	9.9	2.4	2.2
orf19.7204		Unknown	4.9	8.9	1.5	2.9
orf19.1392		chaperone binding, protein disulfide isomerase activity	4.9	3.2	1.9	1.5
orf19.2738	SUL2	sulfate transmembrane transporter activity	4.8	5.8	1.5	1.3
orf19.3508		Unknown	4.8	5.7	0.7	0.7
orf19.3123.2		cytidine deaminase activity	4.8	6.3	2.0	2.5
orf19.6126	KGD2	dihydropyrimidinase activity	4.8	5.5	2.5	2.1
orf19.5387	VPS8	Unknown	4.8	5.0	2.2	1.4
orf19.5169		amidase activity	4.6	4.6	1.8	1.5
orf19.4145	ZCF20	specific RNA polymerase II transcription factor activity	4.6	6.2	2.3	2.6
orf19.7187	MAM33	Unknown	4.6	5.2	1.7	2.0
orf19.2921		alpha-tubulin binding, chaperone binding	4.5	3.7	2.0	1.8
orf19.1255	ZCF5	transcription factor activity	4.5	4.5	2.3	2.1
orf19.183	HIS3	imidazoleglycerol-phosphate dehydratase activity	4.5	6.5	1.5	3.0
orf19.4119	SPO72	Unknown	4.5	5.4	2.2	2.0
orf19.6048		dolichyl-phosphate-mannose-protein mannosyltransferase activity	4.5	5.0	2.2	1.7
orf19.6724	FUM12	fumarate hydratase activity	4.5	5.9	1.3	1.0
orf19.4800	RIM20	Unknown	4.5	4.1	2.2	2.1
orf19.5784		Unknown	4.4	4.0	1.8	2.0
orf19.1767		ubiquitin-specific protease activity	4.4	5.8	2.2	2.8
orf19.1266		Unknown	4.4	2.9	1.0	0.9
orf19.7210		Unknown	4.4	5.3	2.1	2.3
orf19.5059	GCS1	glutamate-cysteine ligase activity	4.4	7.3	2.2	3.3
orf19.6385	ACO1	aconitate hydratase activity, DNA binding	4.4	4.4	1.9	1.8
orf19.3435		Unknown	4.3	17.8	0.8	0.7
orf19.897		protein binding	4.3	6.5	2.2	3.2
orf19.2870		Unknown	4.3	6.4	1.2	2.0
orf19.864		protein binding	4.3	2.5	1.5	1.1
orf19.7032		Unknown	4.2	5.5	1.2	1.6
orf19.6168		structural constituent of cytoskeleton	4.2	2.8	2.1	1.4
orf19.3425		Unknown	4.2	4.2	1.5	1.0
orf19.5634	FRP1	ferric-chelate reductase activity	4.2	3.7	1.3	0.9
orf19.2461	PRN4	Unknown	4.2	7.3	2.1	2.7
orf19.2517		drug transporter activity	4.2	2.5	1.3	0.8
orf19.6725	FUM12	fumarate hydratase activity	4.2	2.7	1.3	1.3
orf19.6464		Unknown	4.1	6.3	1.8	2.7
orf19.1325	ECM38	protein-glutamine gamma-glutamyltransferase activity	4.1	2.1	1.2	0.3
orf19.4527	HGT1	glucose transmembrane transporter activity	4.1	8.1	2.0	2.6
orf19.2646	ZCF13	specific RNA polymerase II transcription factor activity	4.1	4.2	1.5	2.1
orf19.5158		Unknown	4.1	5.4	1.8	2.3
orf19.3659		Unknown	4.1	6.8	2.0	2.5
orf19.4056	GAT2	transcription factor activity	4.1	6.3	1.8	2.2
orf19.740	HAP41	transcription activator activity	4.0	7.6	1.9	2.2
orf19.1375	LEU42	2-isopropylmalate synthase activity	4.0	7.7	1.9	1.7
orf19.2770		Unknown	4.0	4.3	1.0	1.1
orf19.2952	EXG2	glucan 1,3-beta-glucosidase activity	4.0	3.6	1.3	1.4
orf19.5741	ALS1	protein binding, cell adhesion molecule binding	4.0	15.4	1.6	1.5
orf19.7184		Unknown	4.0	4.5	1.7	2.2
orf19.7053	GAC1	protein phosphatase type 1 regulator activity	4.0	5.6	0.9	0.6
orf19.5846		general RNA polymerase II transcription factor activity	4.0	3.4	1.5	1.4
orf19.5426		triglyceride lipase activity	3.9	3.0	1.9	1.5
orf19.6704		Unknown	3.9	4.3	1.1	1.6
orf19.7436.1	ECM15	Unknown	3.9	3.9	1.2	1.3
orf19.589		GTPase activity, GTP binding	3.9	5.4	2.0	2.4
orf19.4135	PRC2	Unknown	3.9	3.7	1.1	0.8
orf19.4655	OPT6	oligopeptide transporter activity	3.9	2.8	1.1	1.0
orf19.1990	SNX4	phosphatidylinositol 3-phosphate binding	3.9	5.2	1.7	1.6
orf19.5974	ATG9	Unknown	3.8	5.1	1.1	1.4
orf19.4324		Unknown	3.8	4.2	0.8	1.5
orf19.6522		anion:cation symporter activity	3.8	4.9	1.7	2.0
orf19.5867	WSC1	Unknown	3.8	3.2	1.0	1.4
orf19.7158		anion:cation symporter activity	3.8	5.0	1.7	1.8
orf19.5813		Unknown	3.8	7.4	1.5	3.7
orf19.2344	ASR1	Unknown	3.8	6.1	0.6	0.5
orf19.6993	GAP2	polyamine transmembrane transporter activity	3.8	5.2	1.4	1.3
orf19.5961		Unknown	3.8	6.2	1.9	2.4
orf19.6305		threonine aldolase activity	3.8	4.0	1.5	1.6
orf19.3439		Unknown	3.7	8.1	1.3	2.4
orf19.3851		Unknown	3.7	2.5	1.2	0.6
orf19.1296		RNA splicing factor activity, transesterification mechanism	3.7	2.1	0.3	0.9
orf19.6058	GLO1	lactoylglutathione lyase activity	3.7	4.8	1.9	2.1
orf19.1159		homoserine O-acetyltransferase activity	3.7	3.4	1.4	1.0
orf19.670.2		Unknown	3.7	6.5	0.9	1.2
orf19.4979	KNS1	protein serine/threonine kinase activity	3.7	7.9	0.8	1.3
orf19.931		Unknown	3.7	4.5	1.8	1.5
orf19.996		adenylate cyclase activity	3.7	3.5	0.8	0.5
orf19.6788		Unknown	3.6	73.3	1.6	1.9
orf19.541		Unknown	3.6	4.2	1.3	1.5
orf19.4864		serine hydrolase activity	3.6	3.8	0.8	1.1
orf19.3369	MOH1	Unknown	3.6	21.8	1.8	2.5
orf19.4177	HIS5	histidinol-phosphate transaminase activity	3.5	3.6	1.4	1.4
orf19.7521	REP1	Unknown	3.5	2.5	1.2	1.0
orf19.4114	FAA2-1	long-chain-fatty-acid-CoA ligase activity	3.5	3.6	1.8	1.1
orf19.6680	FGR27	transcription factor activity	3.5	3.0	1.6	1.3
orf19.1339	CPY1	carboxypeptidase activity	3.5	2.6	1.6	1.3
orf19.6043		D-lactate dehydrogenase (cytochrome) activity	3.4	3.4	1.4	1.2
orf19.6493		Unknown	3.4	12.0	0.8	3.5
orf19.2047		Unknown	3.4	3.1	0.9	0.9
orf19.1529		Unknown	3.4	4.1	1.0	0.7
orf19.4816		Unknown	3.4	3.3	1.3	1.3
orf19.6941		diacylglycerol O-acyltransferase activity	3.4	3.7	1.0	0.8
orf19.7365		Unknown	3.4	3.0	1.0	0.9
orf19.4859		Rab guanyl-nucleotide exchange factor activity	3.3	7.3	1.7	1.5

orf19 Designation	Gene Name	Molecular Function	Fold Changes (treated vs. untreated)			
			SRR1/SRR1		Δsrr1/Δsrr1	
			Exp 1	Exp2	Exp 1	Exp 2
orf19.2623		transcription factor activity	3.3	3.2	1.3	1.6
orf19.3644		Unknown	3.3	5.1	1.6	2.3
orf19.1365		Unknown	3.3	3.2	1.2	1.1
orf19.1107		Unknown	3.3	8.3	1.5	1.7
orf19.4898		Unknown	3.3	3.8	1.2	1.4
orf19.3794	CSR1	DNA binding, specific RNA polymerase II transcription factor activity	3.3	4.1	1.0	1.7
orf19.4253		Ras GTPase activator activity	3.3	2.7	1.1	1.1
orf19.629	IFD7	Unknown	3.3	7.2	1.1	2.5
orf19.1785		Unknown	3.3	4.3	1.3	1.7
orf19.5003		GTPase regulator activity, protein binding	3.3	3.4	1.4	1.7
orf19.313	DAL4	allantoin uptake transmembrane transporter activity	3.3	3.7	1.4	1.0
orf19.2836		Unknown	3.2	5.4	0.8	1.2
orf19.4905		Unknown	3.2	2.7	1.6	1.2
orf19.448		Unknown	3.2	4.0	1.2	1.8
orf19.2361		histone acetyltransferase activity, sequence-specific DNA binding	3.2	4.1	1.1	1.7
orf19.5730		Unknown	3.2	4.0	1.5	1.5
orf19.2172	ARA1	D-arabinose 1-dehydrogenase [NAD(P)+] activity	3.2	2.7	1.1	1.1
orf19.6678		Unknown	3.2	2.9	0.6	0.6
orf19.6443		dodecenoyl-CoA delta-isomerase activity	3.1	2.6	1.2	0.9
orf19.6049		protein kinase activator activity	3.1	3.0	1.4	0.7
orf19.6690		Unknown	3.1	3.8	1.3	1.5
orf19.2248	ARE2	sterol O-acyltransferase activity	3.1	3.3	1.4	1.3
orf19.3607		Unknown	3.1	4.7	1.0	1.5
orf19.4317	GRE3	aldehyde reductase activity, glucose 1-dehydrogenase (NADP+) activity	3.1	4.3	1.2	2.0
orf19.7448	LYS9	saccharopine dehydrogenase (NADP+, L-glutamate-forming) activity	3.1	3.6	1.0	1.0
orf19.6805		Unknown	3.1	4.4	1.6	2.1
orf19.3633		Unknown	3.1	5.4	0.8	1.2
orf19.7596		Unknown	3.1	2.6	0.8	0.5
orf19.5248	MSO1	Unknown	3.0	3.1	0.8	1.0
orf19.277	TH16	hydroxyethylthiazole kinase activity, thiamin-phosphate diphosphorylase activity	3.0	2.7	0.9	1.0
orf19.5851	STE13	aminopeptidase activity	3.0	5.9	1.2	1.0
orf19.5718		Unknown	3.0	5.3	1.4	2.3
orf19.4894		Unknown	3.0	4.2	1.2	1.1
orf19.3372		Unknown	3.0	3.0	1.4	1.1
orf19.7434	GLG2	glycogenin glucosyltransferase activity	3.0	2.7	1.0	1.0
orf19.147	YAK1	protein Kinase activity	3.0	3.6	1.4	0.9
orf19.1721	NCE103	carbonate dehydratase activity	3.0	4.6	1.1	1.8
orf19.7156	FAA2-3	long-chain-fatty-acid-CoA ligase activity	3.0	4.5	1.2	0.8
orf19.5056		enzyme activator activity	3.0	4.3	0.9	1.3
orf19.5025	MET3	sulfate adenyltransferase (ATP) activity	3.0	6.5	0.6	0.8
orf19.851		Unknown	3.0	3.8	1.4	1.6
orf19.6850		transcription factor activity, ubiquitin-protein ligase activity	3.0	3.3	1.5	1.4
orf19.3007.2		Unknown	3.0	3.1	1.4	1.5
orf19.3060		dolichyl-diphosphooligosaccharide-protein glycotransferase activity	2.9	2.9	1.1	1.3
orf19.7504		Unknown	2.9	5.7	0.9	1.7
orf19.5599	MDL2	ATP binding, ATPase activity, coupled to transmembrane movement	2.9	2.6	1.2	1.1
orf19.1974	TFS1	lipid binding, peptidase inhibitor activity	2.9	2.9	0.8	1.0
orf19.6675		Unknown	2.9	3.7	1.4	1.1
orf19.6950		Unknown	2.9	20.4	1.3	2.5
orf19.6353		Unknown	2.9	2.4	1.2	0.9
orf19.5620		Unknown	2.9	3.5	1.2	1.3
orf19.4507		Unknown	2.9	2.9	0.9	0.7
orf19.2789		Unknown	2.9	3.4	1.4	1.3
orf19.4841	SHY1	unfolded protein binding	2.9	2.3	1.3	1.0
orf19.1949	VPS1	GTPase activity	2.9	5.2	1.2	1.6
orf19.156	FGR51	Unknown	2.8	3.8	1.3	1.4
orf19.7472	IFF4	Unknown	2.8	13.3	0.9	0.8
orf19.1608		Unknown	2.8	6.0	0.7	0.8
orf19.7567		Unknown	2.8	6.2	1.2	1.6
orf19.2613	ECM4	glutathione transferase activity	2.8	3.4	0.6	0.8
orf19.7629		Unknown	2.8	3.3	1.4	1.0
orf19.3932		Unknown	2.8	5.7	1.0	1.2
orf19.4262		mRNA binding	2.8	3.3	1.0	1.0
orf19.7324	TH13	Unknown	2.8	2.4	0.8	0.8
orf19.3910		Unknown	2.8	2.9	0.6	0.5
orf19.5940	ZCF32	transcription factor activity	2.8	2.6	0.8	0.6
orf19.4722		transcription coactivator activity	2.8	2.3	1.2	1.2
orf19.2838		Unknown	2.8	2.8	0.6	0.3
orf19.6322	ARD	L-arabinitol 2-dehydrogenase activity	2.8	4.9	1.3	2.2
orf19.2031	VPS24	protein binding	2.8	6.9	0.8	1.2
orf19.1180		2-aminoacidipate transaminase activity	2.8	3.0	1.0	1.1
orf19.7281	PDK2	Unknown	2.8	2.4	0.5	0.5
orf19.7078		Unknown	2.7	3.2	0.7	0.8
orf19.3901		Unknown	2.7	3.7	1.4	1.6
orf19.860	BMT8	Unknown	2.7	3.1	0.8	0.6
orf19.5843		Unknown	2.7	3.9	0.1	1.7
orf19.3293		oxidoreductase activity	2.7	3.1	1.4	1.0
orf19.4907		Unknown	2.7	2.6	1.0	0.9
orf19.1976		Unknown	2.7	6.3	1.3	2.1
orf19.6141	HGT16	glucose transmembrane transporter activity	2.7	2.6	0.7	0.4
orf19.2768	AMS1	alpha-mannosidase activity	2.7	5.1	0.6	0.8
orf19.6888		Unknown	2.7	4.9	1.1	1.5
orf19.3859		ketoreductase activity	2.7	2.3	1.3	1.0
orf19.6830		Unknown	2.7	3.6	0.8	1.3
orf19.5204		Unknown	2.7	2.6	0.9	1.1
orf19.91		Unknown	2.6	4.8	1.2	1.6
orf19.4903		N-acetylglucosaminylphosphatidylinositol deacetylase activity	2.6	2.6	0.4	0.5
orf19.2666		importin-alpha export receptor activity	2.6	5.1	1.3	1.5
orf19.7497		Unknown	2.6	2.3	1.3	1.0
orf19.1461		Unknown	2.6	3.4	1.2	1.3
orf19.3878		Unknown	2.6	4.1	1.3	1.2
orf19.3093	MSH2	ATP binding, ATPase activity, DNA binding	2.6	3.1	0.8	0.7
orf19.6296		protein binding	2.6	3.1	0.8	1.4
orf19.1019		Unknown	2.6	4.2	1.2	1.5
orf19.2030		Unknown	2.6	5.7	1.0	1.9
orf19.7060		Unknown	2.6	3.1	1.3	1.3

orf19 Designation	Gene Name	Molecular Function	Fold Changes (treated vs. untreated)			
			SRR1/SRR1		Δsrr1/Δsrr1	
			Exp 1	Exp2	Exp 1	Exp 2
orf19.732		2,4-dienoyl-CoA reductase (NADPH) activity	2.6	5.2	0.9	1.8
orf19.5295		Unknown	2.5	3.0	0.5	0.5
orf19.4883		Unknown	2.5	4.3	0.6	0.6
orf19.3201	<i>MTLA1</i>	DNA binding, transcription factor activity	2.5	3.6	1.1	1.7
orf19.1760	<i>RAS1</i>	GTPase activity, GTP binding	2.5	2.4	1.2	1.0
orf19.1777		ubiquitin-specific protease activity	2.5	2.7	1.1	0.9
orf19.3846	<i>LYS4</i>	homoaconitate hydratase activity	2.5	2.9	1.2	1.3
orf19.2446		Unknown	2.5	2.7	0.7	0.8
orf19.862		Unknown	2.5	2.1	0.7	0.9
orf19.4772	<i>SSU81</i>	osmosensor activity	2.5	2.2	1.2	0.9
orf19.5142	<i>DFR1</i>	dihydrofolate reductase activity, drug binding	2.5	3.7	1.1	1.8
orf19.7512		catalytic activity, oxygen binding	2.5	2.8	0.9	0.6
orf19.3814		Unknown	2.5	3.2	1.0	0.9
orf19.2724		Unknown	2.4	3.7	0.9	1.7
orf19.5006.1		SNAP receptor activity	2.4	6.7	1.2	2.2
orf19.816	<i>DCK2</i>	Unknown	2.4	2.9	0.9	0.9
orf19.1449		Unknown	2.4	2.1	0.7	0.6
orf19.4733	<i>YMC2</i>	transporter activity	2.4	2.2	0.9	0.6
orf19.7379	<i>FAA2</i>	long-chain-fatty-acid-CoA ligase activity	2.4	5.0	1.1	0.9
orf19.6068	<i>SVF1</i>	Unknown	2.4	2.4	0.9	0.9
orf19.3865	<i>RFX1</i>	sequence-specific DNA binding, transcription activator activity	2.4	5.0	1.2	1.3
orf19.3221		contributes to carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity	2.4	2.2	0.6	0.7
orf19.1765		Unknown	2.4	2.1	0.7	0.9
orf19.1933		Unknown	2.4	2.5	1.1	0.8
orf19.2846		Unknown	2.4	2.2	0.3	0.9
orf19.1037		Unknown	2.4	3.0	0.8	0.4
orf19.2451	<i>PGA45</i>	Unknown	2.4	2.8	1.1	1.3
orf19.4980	<i>HSP70</i>	peptide binding, unfolded protein binding	2.3	3.7	1.1	1.5
orf19.5053		acetyltransferase activity, chromatin binding	2.3	2.9	1.0	1.0
orf19.4577		signal transducer activity	2.3	3.5	0.9	1.1
orf19.6910	<i>PSF1</i>	Unknown	2.3	2.4	0.9	0.8
orf19.3869		Unknown	2.3	2.3	0.3	0.3
orf19.2828		alpha-tubulin binding, chaperone binding, microtubule binding	2.3	2.3	0.6	1.0
orf19.317		purine-nucleoside phosphorylase activity	2.3	2.3	0.8	1.0
orf19.4097		Unknown	2.3	2.4	0.8	0.8
orf19.4183	<i>MUC1</i>	Unknown	2.3	2.3	0.9	1.1
orf19.479		Unknown	2.3	2.1	0.9	0.9
orf19.7566		amino acid transmembrane transporter activity	2.3	3.8	1.1	1.1
orf19.3226		Unknown	2.3	2.7	0.7	0.9
orf19.3405	<i>ZCF18</i>	transcription factor activity	2.3	2.7	0.9	1.3
orf19.2970	<i>LYS2</i>	L-aminoadipate-semialdehyde dehydrogenase activity	2.3	2.6	1.0	0.7
orf19.5553		methionine-R-sulfoxide reductase activity	2.3	2.3	1.0	1.2
orf19.5125		Unknown	2.3	3.8	1.0	0.7
orf19.5963		Unknown	2.2	2.3	0.9	1.0
orf19.3019		enzyme activator activity	2.2	4.6	0.9	0.9
orf19.192		Unknown	2.2	2.1	0.4	0.7
orf19.3879		Unknown	2.2	2.7	0.8	0.8
orf19.3612	<i>PST2</i>	2-hydroxy-1,4-benzoquinone reductase activity	2.2	2.0	0.6	0.7
orf19.1307		Unknown	2.2	2.2	0.9	0.8
orf19.554	<i>DIT2</i>	oxidoreductase activity, oxygen binding	2.2	2.9	0.8	1.1
orf19.2075	<i>DFG5</i>	Unknown	2.2	2.5	0.8	0.8
orf19.2791		myosin I binding	2.2	2.6	0.9	0.9
orf19.6848	<i>VPS16</i>	contributes to phosphoinositide binding	2.2	2.1	0.9	0.8
orf19.5194.1		Unknown	2.2	2.7	1.0	1.0
orf19.1814		1-phosphatidylinositol 4-kinase activity	2.2	2.0	0.9	0.9
orf19.1377	<i>IPK2</i>	phosphoinositide 3-kinase activity, protein binding	2.2	3.3	0.8	0.8
orf19.1462	<i>SMP2</i>	phosphatidate phosphatase activity	2.1	2.2	1.0	0.9
orf19.3285		Unknown	2.1	2.0	0.7	0.9
orf19.4209		ubiquitin activating enzyme activity	2.1	2.7	1.1	1.2
orf19.5797	<i>PI-PLC</i>	phosphoinositide phospholipase C activity	2.1	2.3	0.5	0.6
orf19.2908		Unknown	2.1	2.2	0.9	0.9
orf19.925		Unknown	2.1	2.1	0.9	0.8
orf19.4392	<i>DEM1</i>	Unknown	2.1	2.6	0.8	0.9
orf19.1877		Unknown	2.1	2.0	0.9	1.0
orf19.3764	<i>GSG1</i>	Unknown	2.1	2.0	0.7	1.0
orf19.4415		Unknown	2.1	3.0	0.7	1.0
orf19.6525		Unknown	2.1	2.9	1.0	1.0
orf19.1444		cytoskeletal adaptor activity	2.1	2.4	1.0	1.0
orf19.1793		phosphoinositide binding	2.1	4.1	1.0	2.0
orf19.6024		Unknown	2.1	3.8	0.9	1.0
orf19.1586	<i>FGR22</i>	phosphoinositide phospholipase C activity	2.1	2.4	0.6	0.6
orf19.5626		Unknown	2.1	3.0	1.0	1.0
orf19.3366	<i>CSH3</i>	unfolded protein binding	2.1	2.7	1.0	1.3
orf19.1711	<i>END3</i>	cytoskeletal adaptor activity, protein binding	2.1	2.4	0.5	0.7
orf19.3982		maltase activity	2.1	2.6	0.6	0.8
orf19.7483	<i>CRM1</i>	nuclear export signal receptor activity, protein transmembrane transporter activity	2.1	3.0	1.0	1.0
orf19.3660		Unknown	2.1	3.1	1.0	1.1
orf19.5224		protein kinase activity	2.1	3.4	0.6	0.5
orf19.3986	<i>PPR1</i>	transcription factor activity	2.1	12.8	1.0	1.1
orf19.2910	<i>PGA43</i>	Unknown	2.1	2.5	1.0	1.0
orf19.4088		hydroxyacylglutathione hydrolase activity	2.1	2.3	0.8	1.0
orf19.4630	<i>CPA1</i>	contributes to carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity	2.1	3.7	0.6	0.8
orf19.1344		Unknown	2.1	6.7	0.5	0.7
orf19.5552		Unknown	2.0	2.3	1.0	0.6
orf19.5029	<i>MODF</i>	ATP binding	2.0	2.3	0.4	0.5
orf19.6637		Unknown	2.0	2.4	1.0	1.0
orf19.4551	<i>CTN1</i>	carnitine O-acetyltransferase activity	2.0	4.1	0.8	0.9
orf19.6877	<i>PNG2</i>	Unknown	2.0	3.6	1.0	0.9
orf19.1360		Unknown	2.0	3.8	0.5	1.0
orf19.5544	<i>SAC6</i>	actin filament binding, protein binding	2.0	3.2	0.9	0.9
orf19.537		Unknown	2.0	4.7	0.7	1.0
orf19.4416	<i>VPS13</i>	Unknown	2.0	2.1	0.9	0.9
orf19.7550	<i>IFA14</i>	Unknown	2.0	2.3	0.5	0.9
orf19.638	<i>FDH1</i>	formate dehydrogenase activity	2.0	2.3	0.4	0.8
orf19.7627		Unknown	2.0	2.0	1.0	0.8
orf19.3762		peptide-acetyl-CoA secondary active transmembrane transporter activity	2.0	3.4	0.8	0.4

orf19 Designation	Gene Name	Molecular Function
orf19.868	ADAEC	Unknown
orf19.4807		inorganic diphosphatase activity
orf19.4076	MET10	sulfite reductase (NADPH) activity
orf19.4015	CAG1	GTPase activity, guanyl nucleotide binding
orf19.4530.1		Unknown
orf19.5423	EST3	contributes to telomerase activity
orf19.23	RTA3	phospholipid-translocating ATPase activity
orf19.2306		oxidoreductase activity
orf19.1762	OCA1	protein tyrosine phosphatase activity
orf19.529		Unknown
orf19.4086		Unknown

Fold Changes (treated vs. untreated)			
SRR1/SRR1		Δsrr1/Δsrr1	
Exp 1	Exp2	Exp 1	Exp 2
2.0	2.6	0.9	0.7
2.0	2.8	0.7	1.0
2.0	2.0	0.7	0.5
2.0	2.2	0.9	0.8
2.0	2.1	0.8	0.7
2.0	2.7	0.6	0.8
2.0	3.0	0.5	0.4
2.0	3.4	0.4	0.5
2.0	2.1	0.9	1.0
2.0	2.0	0.7	0.8
2.0	2.2	0.9	1.1