

Additional File 8: Differentially-expressed genes in wild type yeast after 1 h treatment with 100 μ M BPS. The genes were differentially expressed in at least two out of three independent experiments at a p-value of less than 0.1. Expression data for each experiment (#1, 2 and 3) are given in logarithmic scale with base of two. Localization of gene products and their functions are from the *Saccharomyces* Genome Database (<http://www.yeastgenome.org>) and MIPS-Comprehensive Yeast Genome Database (<http://mips.gsf.de/proj/yeast/CYGD/db/index.html>).

UP REGULATED GENES (n = 100)

Gene ID	Gene Name	#1	#2	#3	Localization	Function
<i>Carbohydrate metabolism (4)</i>						
YAL038W	CDC19	1.03	0.59	0.88	cytosol	pyruvate kinase
YBR110W	ALG1		0.36	0.3	membrane	beta-1,4-mannosyltransferase
YCL040W	GLK1	0.69	0.44	0.33	cytosol	glucokinase
YGR254W	ENO1	0.74		0.86	Cytoplasm	Enolase
<i>Iron metabolism (17)</i>						
YDR270W	CCC2		0.51	0.75	Golgi	copper-transporting P-type ATPase
YDR534C	FIT1		1.5	1.41	Cell wall	Cell wall protein involved in iron uptake
YEL065W	SIT1	1.4	1.43	1.18	Endosome	Siderophore Iron Transport
YFL041W	FET5		0.62	0.51	vacuole	multicopper oxidase
YGL071W	AFT1	0.66	0.37		Nucleus; cytoplasm	iron responsive transcription activator
YKL220C	FRE2	0.69	0.8	1.07	Plasma membrane	Ferric reductase
YKR052C	MRS4		0.48	0.51	mitochondria	mitochondrial carrier protein
YLR136C	TIS11	0.92	1.62	1.59	Unknown	Zinc finger containing protein
YLR205C	HMX1		0.96	0.82	membrane	Homology to heme oxygenases
YLR214W	FRE1	1.72	0.61	0.46	Plasma membrane	Ferric (and cupric) reductase
YMR058W	FET3	0.97	0.64	0.68	Plasma membrane	multicopper oxidase
YMR319C	FET4	0.5	0.54	0.46	Plasma membrane	low-affinity iron transporter
YOL158C	ARN4	0.77	1.6	1.31	Endosome	Siderophore transporter
YOR381W	FRE3		1.36	0.99	plasma membrane	Ferric reductase activity
YOR382W	FIT2	1.08	2.65	2.66	Cell wall	Cell wall protein involved in iron transport

Gene ID	Gene Name	#1	#2	#3	Localization	Function
<i>Iron metabolism (cont'd)</i>						
YOR383C	FIT3	1.07	2.61	2.38	Cell wall	Cell wall protein involved in iron transport
YOR384W	FRE5		1.27	1.27	Unknown	Ferric reductase activity
<i>Lipid metabolism (2)</i>						
YGL055W	OLE1	0.62	0.45		ER	delta-9-fatty acid desaturase
YJR073C	OPI3	0.63	0.3		ER	phosphatidylcholine biosynthesis
<i>Metal homeostasis (4)</i>						
YGL255W	ZRT1	1.61	0.9	0.88	Plasma membrane	High-affinity zinc transport protein
YHR175W	CTR2		0.54	0.44	vacuole	Putative low-affinity copper transport protein
YKL175W	ZRT3	0.56	0.47		vacuole	Zinc transporter
YLR034C	SMF3		0.47	0.44	vacuole	Metal transporter (iron)
<i>Nucleotide metabolism (15)</i>						
YBL002W	HTB2		0.53	0.85	Nucleus	Histone H2B
YBL005W-A	YBL005W-A	1.17	0.62	0.94	nucleus	TyA Gag protein
YBL034C	STU1	0.67	0.92	0.97	cytoskeleton	Spindle formation
YBL101W-A	YBL101W-A		0.48	0.52	nucleus	TyA Gag protein
YBR012W-A	YBR012W-A	1.23		0.92	nucleus	TyA Gag protein
YDR118W	APC4		0.29	0.48	Nucleus	anaphase promoting complex (APC) subunit
YDR263C	DIN7		0.31	0.44	mitochondria	DNA damage inducible gene
YDR423C	CAD1		0.38	0.42	Nucleus	basic leucine zipper transcription factor responsive to cadimium
YEL042W	GDA1		0.51	0.53	Golgi apparatus	guanosine diphosphatase
YHL027W	RIM101	0.71	0.96	0.61	Nucleus	transcriptional activator required for entry into meiosis
YIL126W	STH1		0.25	0.43	Nucleus	helicase related protein
YJR105W	ADO1		0.43	0.62	Unknown	adenosine kinase
YKL043W	PHD1		0.41	0.49	Nucleus	putative TF
YML039W	YML039W		0.32	0.31	nucleus	TyB Gag-Pol protein
YMR287C	MSU1		0.3	0.41	mitochondria	Protein essential for mitochondrial biogenesis; exonuclease component
<i>Others (9)</i>						
YAL012W	CYS3	0.53	0.3		Unknown	cystathionine gamma-lyase
YDL234C	GYP7		0.44	0.46	Unknown	GTPase activating protein (GAP)
YDR264C	AKR1	0.92	0.77	0.5	membrane	ankyrin repeat-containing protein
YER024W	YAT2	1.02	1.28	1.21	Unknown	carnitine acetyltransferase
YLR109W	AHP1	0.91	0.77	0.47	Cytoplasm	thioredoxin peroxidase
YML121W	GTR1	1.03		0.94	Cytoplasm	putative small GTPase
YNL192W	CHS1	0.54	0.37		Plasma membrane	Chitin synthase 1

Gene ID	Gene Name	#1	#2	#3	Localization	Function
<i>Others (cont'd)</i>						
YOL016C	CMK2		0.46	0.72	Unknown	calmodulin-dependent protein kinase
YPL171C	OYE3		0.44	0.44	Cytoplasm	NADPH dehydrogenase
<i>Protein metabolism (5)</i>						
YBR118W	TEF2	0.84	0.6	0.83	Ribosome	translation elongation factor
YGL123W	RPS2		0.55	0.77	Cytoplasm	ribosomal protein
YJL138C	TIF2	0.56		0.81	Cytoplasm	translation initiation activity
YLR121C	YPS3		0.31	0.3	Plasma membrane	GPI-anchored aspartic protease
YPL154C	PEP4		0.44	0.44	Vacuole	vacuolar proteinase A
<i>Stress (2)</i>						
YDR171W	HSP42	0.55	0.51	0.52	Cytoplasm	Heat shock protein
YGL073W	HSF1	1.9	2.33	2.32	Nucleus	Heat shock transcription factor
<i>Transporters (6)</i>						
YEL063C	CAN1		0.77	0.81	Plasma membrane	arginine permease
YGL006W	PMC1		0.31	0.35	Vacuole	Calcium ion transporter
YGR138C	TPO2		0.42	0.43	vacuolar membrane; plasma membrane	Polyamine transporter
YHL035C	YHL035C		0.85	0.81	membrane	ABC transporter
YJL094C	KHA1		0.38	0.42	membrane	putative H ⁺ /K ⁺ antiporter
YNL003C	PET8		0.32	0.34	mitochondria	Member of family of mitochondrial carrier proteins
<i>Functionally unknown genes (36)</i>						
YAL061W	YAL061W		0.37	0.39	Unknown	Unknown
YAL065C	YAL065C		0.28	0.34	Unknown	Unknown
YAR068W	YAR068W		0.37	0.44	Unknown	Unknown
YBL111C	YBL111C	0.53	0.24		Unknown	Unknown
YBR005W	YBR005W		0.35	0.4	Unknown	Unknown
YBR047W	YBR047W		0.52	0.59	Unknown	Unknown
YCR007C	YCR007C	0.58		0.35	Unknown	Unknown
YDL048C	STP4		0.32	0.36	Unknown	Involved in pre-tRNA splicing and in uptake of branched-chain amino acids
YDL124W	YDL124W		0.57	0.54	Unknown	Unknown
YDR033W	MRH1	0.94	0.52		Plasma membrane	Unknown
YDR271C	YDR271C		0.8	0.84	Unknown	Unknown
YEL076C-A	YEL076C-A		0.32	0.35	Unknown	Unknown
YEL076W-C	YEL076W-C		0.3	0.38	Unknown	Unknown

Gene ID	Gene Name	#1	#2	#3	Localization	Function
<i>Functionally unknown genes (cont'd)</i>						
YER053C	YER053C		0.27	0.36	vacuole	homology to mitochondrial phosphate transporter, but not itself
YFL010C	WWM1	0.52	0.34		Cytoplasm	Unknown
YFR024C	YFR024C		0.53	0.43	Unknown	Unknown
YFR024C-A	LSB3		0.41	0.42	Unknown	Unknown
YGR053C	YGR053C		0.47	0.38	Unknown	Unknown
YHR214W-A	YHR214W-A		0.42	0.51	Unknown	Unknown
YIL028W	YIL028W		0.58	0.38	Unknown	Unknown
YIL146C	ECM37		0.48	0.56	Unknown	Unknown
YJL078C	PRY3		0.33	0.36	Cell wall	Unknown
YKL153W	YKL153W		0.55	0.68	Unknown	Unknown
YLR126C	YLR126C		0.48	0.59	Unknown	Unknown
YLR194C	YLR194C		0.68	0.49	Unknown	Unknown
YLR280C	YLR280C		0.46	0.46	Unknown	Unknown
YLR297W	YLR297W		0.37	0.33	Unknown	Unknown
YLR327C	YLR327C		0.36	0.46	Unknown	Unknown
YLR443W	ECM7		0.64	0.91	membrane	Cell wall maintenance
YMR084W	YMR084W		0.93	0.5	Unknown	Unknown
YMR251W	YMR251W		1.51	1.28	Unknown	Unknown
YNL143C	YNL143C	0.74		0.34	Unknown	Unknown
YOL098C	YOL098C		0.57	0.82	Unknown	Unknown
YOR247W	SRL1	0.55	0.54		Unknown	Unknown
YOR291W	YOR291W	0.76	0.6	0.91	membrane	Unknown
YPR157W	YPR157W		0.51	0.35	Unknown	Unknown

DOWN REGULATED GENES (n = 42)

Gene ID	Gene Name	#1	#2	#3	Localization	Function
<i>Energy metabolism (5)</i>						
YDR178W	SDH4	-0.5	-0.32	-0.44	mitochondria	succinate dehydrogenase membrane anchor subunit
YKL087C	CYT2		-0.29	-0.34	mitochondria	cytochrome c1 heme lyase
YLR304C	ACO1		-0.77	-0.86	mitochondria	aconitase
YNL111C	CYB5		-0.29	-0.39	microsome	cytochrome b5
YPR191W	QCR2	-0.83		-0.33	mitochondria	ubiquinol cytochrome-c reductase core protein 2
<i>Nucleotide metabolism (5)</i>						
YGR092W	DBF2	-0.68		-0.3	Unknown	involved in nuclear division
YKL109W	HAP4	-0.68	-0.29	-0.39		Transcriptional activator involved in carbohydrate metabolism
YLR398C	SKI2		-0.51	-0.61	Nucleus cytoplasm	helicase (putative)
YML061C	PIF1	-0.53		-0.4	Nucleus; mitochondria	DNA helicase
YPL001W	HAT1	-0.53	-0.44		cytoplasm; nucleus	histone acetyltransferase
<i>Others (6)</i>						
YBR093C	PHO5		-0.33	-0.43	Cell wall; periplasmic space	Acid phosphatase
YGL032C	AGA2	-0.62	-0.39	-0.44	Cell wall	a-agglutinin adhesion subunit
YGR174C	CBP4	-0.74	-0.33	-0.4	Mitochondria	Essential for the expression and activity of ubiquinol-cytochrome c reductase
YHR096C	HXT5		-0.41	-0.42	Plasma membrane	Hexose transporter
YLL009C	COX17	-0.49		-0.95	Cytosol; mitochondria	Intracellular copper transport
YMR015C	ERG5		-0.3	-0.41	ER	Cytochrome P450-involved in C-22 denaturation of the ergosterol side-chain
<i>Protein metabolism (5)</i>						
YDL184C	RPL41A	-0.55		-0.44	Cytoplasm	Ribosomal protein L41A
YGL009C	LEU1		-1.64	-0.74	Cytosol	Leucine biosynthesis

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<i>Protein metabolism (cont'd)</i>						
YGR084C	MRP13		-1.41	-0.37	Mitochondria	Mitochondrial ribosomal protein
YIL018W	RPL2B	-0.71		-0.55	Cytosol	Ribosomal protein L2B
YLR325C	RPL38	-0.66		-0.37	Cytosol	Ribosomal protein L38
<i>Stress (2)</i>						
YER174C	GRX4		-0.58	-0.7	Unknown	Glutaredoxin
YKR066C	CCP1		-0.89	-0.97	Mitochondria	Cytochrome c peroxidase
<i>Functionally unknown genes (19)</i>						
YBL044W	YBL044W		-0.31	-0.75	Unknown	Unknown
YDL162C	YDL162C	-1.5	-0.29		Unknown	Unknown
YDR154C	YDR154C	-0.55		-0.37	Unknown	Unknown
YDR494W	RSM28		-0.28	-0.33	Mitochondria	Mitochondrial ribosomal protein
YER156C	YER156C		-0.36	-0.47	Unknown	Unknown
YFL012W	YFL012W	-0.86		-0.65	Unknown	Unknown
YGR226C	YGR226C		-0.54	-0.79	Unknown	Unknown
YGR270W	YTA7		-1.34	-1.73	Unknown	ATPase activity
YJL200C	YJL200C		-0.4	-0.35	Unknown	Homology to aconitase
YKL208W	CBT1	-0.63	-0.43		Unknown	Unknown
YNL109W	YNL109W	-0.83		-0.51	Unknown	Unknown
YNL120C	YNL120C	-0.64	-0.34		Unknown	Unknown
YNL122C	YNL122C	-0.62		-0.3	Unknown	Unknown
YNL303W	YNL303W	-0.47		-0.42	Unknown	Unknown
YNR025C	YNR025C		-0.26	-0.39	Unknown	Unknown
YOL109W	YOL109W	-0.63		-0.36	Unknown	Unknown
YOR338W	YOR338W		-0.32	-0.3	Unknown	Unknown
YPL170W	DAP1		-0.28	-0.35	Membrane	Unknown
YPL182C	YPL182C		-0.25	-0.33	Unknown	Unknown