

Table 1. Induced CESR genes

Gene Name	Annotation
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Carbohydrate metabolism

<i>ntp1</i>	neutral trehalase.
SPACUNK4.16C	putative alpha-trehalose-phosphate synthase.
<i>tps1</i>	alpha,alpha-trehalose-phosphate synthase.
SPAC22F8.05	putative alpha,alpha-trehalose-phosphate synthase.
SPAC4H3.03C	conserved protein (mainly bacterial), no apparent <i>S. cerevisiae</i> homolog
<i>zwf1</i>	glucose-6-phosphate 1-dehydrogenase; ntose phosphate pathway
SPAC3C7.13C	glucose-6-phosphate 1-dehydrogenase involved in pentose phosphate pathway
SPBC24C6.09C	ortholog of human transketolase in pentose phosphate pathway
SPACUNK4.17	glucose/fructose oxidoreductase
SPBC12C2.04	similar to <i>S. pombe</i> CUNK4.17 glucose/fructose oxidoreductase
SPAPB1A11.03	putative FMN dependent dehydrogenase
<i>exg3</i>	glucan 1,3-beta-glucosidase
<i>tms1</i>	putative sorbitol dehydrogenase
<i>gpd1</i>	NADH-dependent glycerol-3-phosphate dehydrogenase involved in glycerol phosphate shuttle of oxidative phosphorylation.
<i>gut2</i>	glycerol-3-phosphate dehydrogenase involved in glycerol phosphate shuttle of oxidative phosphorylation.
SPBC1773.06C	alcohol dehydrogenase
SPBC1289.14	adducin N terminal domain protein
SPAC513.02	similarity to phosphoglycerate mutases; involved in glycolytic pathway
SPBC20F10.10	similar to <i>S. cerevisiae</i> Pcl7p, utilization of alternative carbon sources
SPCC306.08C	malate dehydrogenase involved in citric acid cycle.
SPAC26F1.07	probable oxidoreductase.; aldo/keto family.
SPBC215.11C	putative oxidoreductase; aldo/keto family
SPAC19G12.09	putative aldose reductase; aldo/keto family; similar to <i>S. cerevisiae</i> Ydl124p
SPAC2F3.05C	aldo/keto reductase family oxidoreductase
SPAC22A12.17C	short chain dehydrogenase; possible sorbitol utilization
SPAC139.05	probable succinate semialdehyde dehydrogenase; similar to <i>S. cerevisiae</i> Uga2p.

Signaling and transcriptional regulation

<i>ptc4</i>	protein phosphatase 2c isoform
<i>pyp2</i>	protein-tyrosine phosphatase 2; inactivates Sty1p kinase in response to stress.
<i>ptc1</i>	protein phosphatase 2c
SPCC1322.08	putative serine/threonine protein kinase, similar to <i>S. cerevisiae</i> Rck2p, which is a substrate for Hog1p
SPAC1E11.03	serine/threonine protein kinase; similar to <i>S. cerevisiae</i> Yak1p
SPCC1020.10	putative serine/threonine protein kinase; similar to <i>S. cerevisiae</i> Npr1p
<i>cgs1</i>	regulatory subunit for cAMP-dependent protein kinase A, similar to <i>S. cerevisiae</i> Bcy1p
<i>pkal/tpk/git6</i>	CAMP-dependent protein kinase catalytic subunit, similar to <i>S. cerevisiae</i> Tpk1-3p
<i>pcr1/mts2</i>	b-zip transcription factor pcr1, similar to <i>S. pombe</i> Atf21p and Atf1p; roles in mating, meiosis and stress response

<i>mpr1/spy1</i>	stress response regulator phosphotransmitter, similar to <i>S. cerevisiae</i> Ypd1p, plays a role in regulation of the G(2)/M cell cycle progression.
<i>atf1</i>	transcription factor Atf1p
SPBC1105.14	putative Zinc-finger transcriptional activator, similar to <i>S. cerevisiae</i> Msn2p
SPAC1348.12	zinc finger protein
SPCC320.03	zinc-finger protein,
SPAC57A10.09C	nonhistone chromosomal protein 6b; similar to <i>S. cerevisiae</i> Nhp6bp, involved in DNA binding and bending in transcription of a number of genes
<i>git5</i>	G-protein beta subunit Git5p; involved in glucose response pathway.
SPCP31B10.06	C2-domain protein; synaptotagmin family (has PKC domain)

Lipid or fatty acid metabolism

SPAC4D7.02C	putative glycerophosphoryl diester phosphodiesterase
SPAPB24D3.08C	putative NADP dependent oxidoreductase
SPAC4H3.08	putative short chain dehydrogenase; similar to <i>S. cerevisiae</i> Fox2p involved peroxisomal fatty acid beta-oxidation pathway
SPAC521.03	putative short chain dehydrogenase; similar to <i>S. cerevisiae</i> Ymr226p
SPAC26F1.04C	containing Zinc-binding dehydrogenases domain; similar to <i>S. cerevisiae</i> Ybr026p
SPAC23D3.11	putative short chain dehydrogenase; similar to <i>S. cerevisiae</i> Ayr1p

Antioxidants

<i>trx2</i>	thioredoxin II
<i>zym1</i>	zinc metallothionein
<i>ctal</i>	catalase
<i>gpx1</i>	glutathione peroxidase
<i>grx1</i>	thioltransferase
SPCC576.03C	thioredoxin peroxidase
SPAC688.04C	glutathione-S-transferase 3
<i>pmp20</i>	peroxisomal membrane protein Pmp20p, similar to <i>S. cerevisiae</i> Ahp1p, an antioxidant induced by peroxide

DNA repair

SPBC23G7.11	DNA-3-methyladenine glycosidase; putative base excision repair-DNA repair
<i>cmb1</i>	HMG box mismatch binding protein; likely to be involved in DNA repair.

Transporters

SPBC3H7.02	SulP sulfate transporter
SPCC965.06	putative potassium channel subunit

Protein folding and protein degradation

<i>hsp16</i>	heat shock protein 16
<i>hsp9</i>	heat shock protein 9
<i>Psi1</i>	heat-shock protein
SPAC2C4.15C	ubiquitin regulatory domain (UBX) protein, similar to <i>S. cerevisiae</i> Ydr330p
SPCC4G3.03	hypothetical protein similar to <i>S. cerevisiae</i> YLR149C, putative apoptotic protease activating factor
SPCC338.12	sequence orphan
<i>isp6</i>	sexual differentiation process protein; putative subtilase-type proteinase

Others

SPAC513.07	putative cinnamoyl-coa reductase, involved in vitamin/cofactor metabolism
<i>plr</i>	pyridoxal reductase, Aldo/keto reductase family domain. Similar to <i>S. cerevisiae</i> Ypr127p pyridoxal reductase catalyzes the NADPH-dependent reduction of pyridoxal to form pyridoxine (vitamin B6)
<i>rds1</i>	stress response protein
SPBC2A9.02	putative dyhydroflavanol-4-reductase; similar to <i>S. cerevisiae</i> Yll056p, involved in cell stress.
<i>mvp1</i>	putative vacuolar protein sorting protein
SPAC26F1.14C	putative flavoprotein; similar to human mitochondrial apoptosis-inducing factor; involved in cell death.
SPBC16A3.02C	putative quinone oxidoreductase; zinc binding oxidoreductase
SPBC23G7.10C	putative NADH-dependent flavin oxidoreductase
SPAC2E1P3.01	putative dehydrogenase by similarity
SPBC1773.17C	putative glycerate- and formate-dehydrogenase
<i>vip1</i>	protein with RNA recognition motif
SPAC19B12.08	putative protein that mediates attachment of autophagosomes to microtubules, by similarity to <i>S. cerevisiae</i> Aut2p
SPBC725.10	similar to peripheral-type benzodiazepine receptor
SPBC106.02C	ParBc-like nuclease domain; similar to <i>S. cerevisiae</i> YKL086W
SPAC22E12.03C	THIJ/PFPI family protein; putative thiamine biosynthesis enzyme
SPCC1183.11	mechano-sensitive ion channel domain
SPBC30D10.14	putative hydrolase; similar to <i>S. cerevisiae</i> Yal049p, which plays crucial role in chlorocatechol degradation
SPAC23D3.05C	alcohol dehydrogenase, pseudogene
SPAC25H1.02	JOR domain, possibly chromatin associated
SPAC977.13C	putative hydrolase, pseudogene

52 Genes with unknown function

SPAC167.06C	SPAC2C4.17C	SPCC1235.01	SPBP4H10.10
SPAC23H3.15C	SPAC869.09	SPAC23C11.06C	SPCC736.15
SPBC119.03	SPCC191.01	SPBC11C11.06C	SPAC11D3.01C
SPAC11D3.13	SPAC9E9.04	SPCC61.03	SPCC16A11.15C
SPBC23G7.06C	SPACUNK4.15	SPBC1271.08C	SPCC1494.03
SPCC576.04	SPCC757.03C	SPBC660.05	SPBC660.06
SPAC3C7.05C	SPAC27D7.10C	SPAC31A2.12	SPBC21H7.06C
SPAC27D7.11C	SPAC607.08C	SPBC725.03	SPCC417.05C
SPAC57A7.05	SPBC1105.13C	SPCC338.18	SPAC22G7.11C
SPAC11E3.14	SPAC16A10.01	SPBC21C3.19	SPBC365.12C
SPAC27D7.09C	SPAC22H12.01C	SPBC56F2.06	SPBC428.10
SPCC63.14	SPCC1393.12	SPAC637.03	SPAC15E1.02C
SPBC1539.04	SPBC20F10.03	SPBC16E9.16C	SPAC5H10.02C