
*All 118 genes modulated greater than 2-fold after IR in G2 synchronised cells
(repressed genes are underlined)*

INDUCED GENES

cell cycle

<i>cdc22</i>	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CHAIN
<i>smc3</i>	PUTATIVE COHESIN, COILED-COIL PROTEIN OF THE SMC FAMILY INVOLVED IN SISTER CHROMATID COHESION; SMC1 DIMERIZATION PARTNER
<i>cdc18*</i>	CELL DIVISION CONTROL PROTEIN 18; REPLICATION INITIATION
<i>cdt2*</i>	TARGET OF CDC10 TRANSCRIPTION FACTOR
<i>rep2</i>	TRANSCRIPTIONAL ACTIVATOR, ZINC FINGER
<i>ssb1: rpa1: rad11</i>	REPLICATION FACTOR-A PROTEIN 1
<i>cig2: cyc17</i>	G2/MITOTIC-SPECIFIC CYCLIN CIG2/CYC17
<i>cdt1</i>	CELL DIVISION CYCLE PROTEIN CDT1; REPLICATION FACTOR
<i>poll: swi7: pola</i>	DNA POLYMERASE ALPHA
<i>slp1</i>	WD-DOMAIN PROTEIN; CDC20/P55CDC/FIZZY HOMOLOG
<i>cdc15*</i>	PHOSPHOPROTEIN
<i>etd1*</i>	ETD1 PROTEIN
<i>eng1*</i>	ENDO-1, 3-BETA-GLUCANASE

<i>mrc1</i>	HYPOTHETICAL COILED-COIL PROTEIN
<i>cut6</i>	ACETYL-COA CARBOXYLASE; CUT6 HOMOLOGUE
<i>spd1</i> *	S-PHASE DELAYING PROTEIN 1

DNA repair

<i>rhp54: rad54</i> *	DNA REPAIR PROTEIN RHP54
<i>dinB</i> *	PUTATIVE TRANSLESION DNA REPAIR POLYMERASE
<i>rad21</i>	DOUBLE-STRAND-BREAK REPAIR PROTEIN RAD21
<i>rhp51: rad51</i> *	DNA REPAIR PROTEIN RAD51 HOMOLOG; MEIOTIC RECOMBINATION PROTEIN

signaling and transcriptional control

SPCC290.04*	PUTATIVE TRANSCRIPTIONAL REGULATOR; ZINC FINGER
SPBC21B10.13c*	HOMEODOMAIN PROTEIN
SPAC869.02c*	PROBABLE FLAVOHEMOPROTEIN
SPAC6F12.06	RHO GDP DISSOCIATION INHIBITOR
SPBC19G7.04	CONSERVED HYPOTHETICAL PROTEIN; POSSIBLE TRANSCRIPTIONAL REGULATOR
SPAC11D3.01c	PROTEIN WITH SIMILARITY TO NEUROSPORA CONIDIATION SPECIFIC PROTEIN

stress response

<i>pmp20</i>	PEROXISOMAL MEMBRANE PROTEIN PMP20P,
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	AHPC-TSA FA MILY PROTEIN
<i>ctal*</i>	CATALASE
<i>trr1: caf4*</i>	THIOREDOXIN REDUCTASE
<i>rds1*</i>	STRESS RESPONSE PROTEIN RDS1P
<i>obr1*</i>	BREFELDIN A RESISTANCE PROTEIN

carbohydrate metabolism

SPBC215.11c*	PUTATIVE OXIDOREDUCTASE; ALDO-KETO FAMILY
SPBC1773.06c*	ALCOHOL DEHYDROGENASE
SPCC188.01c	PUTATIVE ALPHA-AMYLASE PRECURSOR
<i>zwf1*</i>	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE
<i>exg1*</i>	EXO-BETA-1, 3-GLUCANASE
SPBC646.06c	PUTATIVE GLUCANASE; BY SIMILARITY TO PENICILLIUM PURPuroGENUM MUTANASE

sulphur metabolism

SPCC191.09c*	PUTATIVE GLUTATHIONE S-TRANSFERASE
<i>gst2*</i>	GLUTATHIONE S-TRANSFERASE
SPCC1281.07c*	PROTEIN WITH GLUTATHIONE S TRANSFERASE DOMAIN

nucleotide metabolism

SPAC1002.17c*	PROBABLE URACIL PHOSPHORIBOSYLTRANSFERASE
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SPBC1683.06c*	PUTATIVE INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE
SPCC965.14c*	PUTATIVE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASE ZINC-BINDING PROTEIN
SPAC644.05c*	DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE
SPBC106.02c*	PARBC-LIK NUCLEASE DOMAIN; SIMILAR TO YKL086W

fatty acid and lipid metabolism

SPCC1450.16c	HYPOTHETICAL PROTEIN; SIMILAR TO YEAST YKR089C
SPCC1281.06c	ACYL-COA DESATURASE 1
SPBC646.07c	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE SIMILAR TO RAT SYNAPTIC GLYCOPROTEIN SC2
SPBC18H10.02	PUTATIVE LONG-CHAIN-FATTY-ACID--COA LIGASE
<i>plr</i> *	PYRIDOXAL REDUCTASE
SPAC1F7.12*	OXIDOREDUCTASE SIMILAR TO PYRIDOXAL REDUCTASE
SPAC19B12.02c*	PROTEIN SIMILAR TO YEAST GAS1 GLYCOPHOSPHOLIPID-ANCHORED SURFACE GLYCOPROTEIN
SPAC1687.16c	C-5 STEROL DESATURASE
SPAC589.09	PUTATIVE PHOSPHATIDYLINOSITOL

METABOLISM

transport

SPCC794.03	APC AMINO ACID TRANSPORTER
SPAC1B3.16c	MFS TRANSPORTER OF UNKNOWN SPECIFICITY
<i>fip1</i> *	IRON PERMEASE
SPAC1F8.03c*	MFS EFFLUX TRANSPORTER OF UNKNOWN SPECIFICITY
SPCC965.06*	PUTATIVE POTASSIUM CHANNEL SUBUNIT
<i>frp1</i> *	FERRIC REDUCTASE TRANSMEMBRANE COMPONENT
SPCC1840.12	SIMILARITY TO OLIGOPEPTIDE TRANSPORTER (OPT) FAMILY; ISP4-LIKE
<u>SPAC1142.05*</u>	POSSIBLE COPPER TRANSPORTER

others

SPBC23G7.10c*	PUTATIVE NADH-DEPENDENT FLAVIN OXIDOREDUCTASE
<i>ppr1</i> *	PUTATIVE TRANSCRIPTIONAL REGULATORY PROTEIN
SPCC663.06c*	PUTATIVE SHORT CHAIN DEHYDROGENASE PROTEIN
SPCC663.08c*	PUTATIVE SHORT CHAIN DEHYDROGENASE
SPACUNK4.10	PUTATIVE 2-HYDROXYACID DEHYDROGENASE
SPAC513.06c*	PROBABLE DIMERIC DIHYDRODIOL

	DEHYDROGENASE
SPCC576.02*	PUTATIVE HYDANTOIN RACEMASE
SPBC119.03	PUTATIVE CATECHOL O-METHYLTRANSFERASE
SPCC1223.09*	URICASE
SPCC24B10.20*	HYPOTHETICAL SHORT CHAIN DEHYDROGENASE
SPBC409.13*	6, 7-DIMETHYL-8-RIBITYLLUMAZINE SYNTHASE; DMRL SYNTHASE FAMILY
SPAC5H10.10	PUTATIVE NADPH DEHYDROGENASE
SPBP8B7.05c	CARBONIC ANHYDRASE
SPBC2A9.02*	PUTATIVE DYHYDROFLAVANOL-4-REDUCTASE
SPCC1773.03c	AMINOTRANSFERASE
<u>SPCC1322.14c</u>	PUTATIVE POLYPHOSPHATE SYNTHETASE; BY SIMILARITY TO YEAST VTC4
SPAC26H5.09c*	HYPOTHETICAL OXIDOREDUCTASE
SPBC1271.07c*	ACETYLTRANSFERASE
SPCC285.01c	QUINONE OXIDOREDUCTASE
SPCC4B3.18	CONSERVED HYPOTHETICAL PROTEIN
SPCC4B3.02c	PUTATIVE MEMBRANE PROTEIN REQUIRED FOR ER TO GOLGI TRANSPORT; BY SIMILARITY TO YEAST GOT1
<u>pmt2</u>	PMT2 METHYLTRANSFERASE
<i>klp8</i> *	KINESIN-LIKE PROTEIN
SPAC513.07*	PUTATIVE CINNAMOYL-COA REDUCTASE
<i>hsp16</i> *	HEAT SHOCK PROTEIN 16

sequence orphans

SPAC17H9.18c*	VERY HYPOTHETICAL PROTEIN
SPCC338.08*	HYPOTHETICAL PROTEIN
SPBC8E4.02c	HYPOTHETICAL PROTEIN
SPAC140.03	HYPOTHETICAL PROTEIN
SPBC1271.08c*	VERY HYPOTHETICAL PROTEIN
SPCC191.03c	VERY HYPOTHETICAL PROTEIN
SPBC27.05*	VERY HYPOTHETICAL PROTEIN
SPCC320.02c*	ASPARAGINE-RICH PROTEIN
SPAC15E1.02c	HYPOTHETICAL PROTEIN
SPAC15A10.09c*	HYPOTHETICAL PROTEIN
SPAC27D7.12c	PUTATIVE PEROXIREDOXIN

unknown

SPAC27D7.11c*	HYPOTHETICAL PROTEIN
SPBC17D11.03c*	HYPOTHETICAL PROTEIN
SPAC1002.18	HYPOTHETICAL PROTEIN, CONSERVED IN OTHER YEASTS (GAILLARDIN ET AL)
SPAC3G6.05	CONSERVED HYPOTHETICAL PROTEIN
SPAP14E8.02	HYPOTHETICAL SERINE-RICH PROTEIN; SIMILAR TO S. CEREVISIAE TOS4
SPAC1786.01c	HYPOTHETICAL PROTEIN
SPBP4H10.12*	CONSERVED HYPOTHETICAL PROTEIN; SIMILAR TO YEAST YBR137W
SPAP8A3.02c	HYPOTHETICAL PROTEIN
SPAC30D11.11	HYPOTHETICAL PROTEIN; SIMILAR TO YEAST

	YLR023C; PUTATIVE TRANSMEMBRANE:
SPAC2E1P3.05c	PUTATIVE CELLULOSE BINDING BETA GLUCOSIDASE
SPAC227.14	SIMILARITY TO URIDINE KINASE
SPCC1906.02c	HYPOTHETICAL PROTEIN
SPAC27D7.09c*	HYPOTHETICAL PROTEIN
SPCC18B5.02c*	
SPAC29B12.13*	HYPOTHETICAL PROTEIN
SPCC285.04*	PUTATIVE TRANSTHYRETIN PRECURSOR
SPBC4F6.12*	LIM DOMAIN PROTEIN; LEUPAXIN LIKE
SPAC17A2.02c	HYPOTHETICAL PROTEIN
SPCC977.01	HYPOTHETICAL PROTEIN (PARTIAL)
SPAC4H3.04c	HYPOTHETICAL PROTEIN

genes marked * also modulated greater than 2-fold in asynchronous WT cells after IR.