
All 204 genes modulated greater than 2-fold in asynchronously grown WT cells following IR.

Induced genes not present in the CESR

Gene Name	Annotation
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cell cycle control

<i>pyp3</i>	PROTEIN-TYROSINE PHOSPHATASE 3
<i>cdt2</i>	TARGET OF CDC10 TRANSCRIPTION FACTOR
<i>cdc18</i>	CELL DIVISION CONTROL PROTEIN 18; REPLICATION INITIATION
<i>wis2</i>	HEAT SHOCK-INDUCIBLE 40 KDA CYCLOPHILIN- LIKE PROTEIN

DNA repair

<i>rhp51: rad51</i>	DNA REPAIR PROTEIN RAD51 HOMOLOG; MEIOTIC RECOMBINATION PROTEIN
<i>dinB</i>	TRANSLESION DNA REPAIR POLYMERASE
<i>rhp54: rad54</i>	DNA REPAIR PROTEIN RHP54
<i>rad50</i>	DNA REPAIR PROTEIN, YEAST RAD50 HOMOLOG

signal transduction and transcriptional regulation

SPCC290.04	PUTATIVE TRANSCRIPTIONAL REGULATOR
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SPBPB2B2.06c	PUTATIVE 5' NUCLEOTIDASE FAMILY PROTEIN
SPBC21B10.13c	HOMEODOMAIN PROTEIN
SPAC869.02c	PROBABLE FLAVOHEMOPROTEIN

stress response

SPBC3B9.01	PROTEIN SIMILAR TO YEAST YBR101C INVOLVED IN RESISTANCE TO H ₂ O ₂
SPBC216.04c	PUTATIVE TRANSCRIPTIONAL REGULATOR
<i>swo1: hsp90</i>	HEAT SHOCK PROTEIN 90 HOMOLOG
<i>trr1: caf4</i>	THIOREDOXIN REDUCTASE
<i>stil</i>	ACTIVATOR OF HSP70 AND HSP90 CHAPERONES

transporters

SPBC1683.03c	MFS TRANSPORTER OF UNKNOWN SPECIFICITY
SPBC16A3.17c	MFS EFFLUX TRANSPORTER OF UNKNOWN SPECIFICITY
SPAC17C9.16c	MFS MULTIDRUG EFFLUX TRANSPORTER
<i>nic1</i>	NICOT HEAVY METAL ION TRANSPORTER
SPAC1399.01c	PUTATIVE PURINE PERMEASE

sulphur metabolism

SPCC1281.07c	PROTEIN WITH GLUTATHIONE S TRANSFERASE DOMAIN
SPCC191.09c	PUTATIVE GLUTATHIONE S-TRANSFERASE

nucleotide metabolism

SPAC1002.17c	PROBABLE URACIL PHOSPHORIBOSYLTRANSFERASE
SPCC965.14c	PUTATIVE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASE ZINC-BINDING PROTEIN

other metabolism

SPBC409.13	6, 7-DIMETHYL-8-RIBITYLLUMAZINE SYNTHASE; DMRL SYNTHASE FAMILY
SPCC24B10.20	HYPOTHETICAL SHORT CHAIN DEHYDROGENASE
SPAC26H5.09c	HYPOTHETICAL OXIDOREDUCTASE
SPCC576.02	PUTATIVE HYDANTOIN RACEMASE
SPAC977.14c	PUTATIVE OXIDOREDUCTASE
SPCC132.04c	NAD-SPECIFIC GLUTAMATE DEHYDROGENASE
SPCC4B3.06c	HYPOTHETICAL PROTEIN
SPBC1539.07c	PROBABLE FORMALDEHYDE DEHYDROGENASE
SPCC1223.09	URICASE

sequence orphans

SPAC17H9.18c	VERY HYPOTHETICAL PROTEIN
SPAPB1A10.05	HYPOTHETICAL PROTEIN
SPBC1289.06c	HYPOTHETICAL PROTEIN
SPCC338.08	HYPOTHETICAL PROTEIN

unknown function

SPCC18B5.02c	
SPBC1271.05c	ZINC FINGER ZF-AN1 PROTEIN
SPCC285.04	PUTATIVE TRANSTHYRETIN PRECURSOR
SPAC688.03c	CONSERVED HYPOTHETICAL PROTEIN
SPBP4H10.12	CONSERVED HYPOTHETICAL PROTEIN
SPAC5H10.05c	NADHDH_2 DOMAIN PROTEIN
SPBC17D11.03c	HYPOTHETICAL PROTEIN
SPCC663.07c	pseudogene
SPAC750.01	pseudogene
SPAC186.01	HYPOTHETICAL SERINE/THREONINE RICH PROTEIN
SPBC1685.12c	VERY HYPOTHETICAL PROTEIN
SPAC29B12.13	HYPOTHETICAL PROTEIN
SPAC630.04c	VERY HYPOTHETICAL PROTEIN

Induced genes present in the CESR

Gene Name	Annotation
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cell cycle control

<i>ptc1</i>	PROTEIN PHOSPHATASE 2C HOMOLOG 1
SPAC1E11.03	PROTEIN KINASE; YEAST YAK1 HOMOLOG

DNA repair

<i>eme1</i>	INVOLVED IN NUCLEOTIDE-EXCISION REPAIR
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signaling and transcriptional regulation

SPCP31B10.06	C2-DOMAIN PROTEIN; SYNAPTOTAGMIN FAMILY
<i>srk1</i>	SERINE/THREONINE-PROTEIN KINASE.
SPCC320.03	HYPOTHETICAL ZINC-FINGER PROTEIN
<i>pka1: tpk: git6</i>	CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT
SPBC660.05	HYPOTHETICAL GLYCINE RICH PROTEIN
<i>cgs1</i>	CAMP-DEPENDENT PROTEIN KINASE REGULATORY CHAIN
SPBC660.06	HYPOTHETICAL GLYCINE RICH PROTEIN

protein folding and protein degradation

<i>isp6</i>	SEXUAL DIFFERENTIATION PROCESS PUTATIVE SUBTILASE-TYPE PROTEINASE ISP6
<i>psi</i>	PSI PROTEIN
SPBC4F6.17c	YEAST CHAPERONIN HSP78 HOMOLOG
SPBC16D10.08c	PUTATIVE CHAPERONIN; HEAT SHOCK PROTEIN
<i>hsp16</i>	HEAT SHOCK PROTEIN 16
SPBC1711.12	PUTATIVE DIPEPTIDYL PEPTIDASE
SPCC1442.07c	PUTATIVE ZN-PROTEASE

stress response

<i>grx1</i>	THIOLTRANSFERASE
<i>cta1</i>	CATALASE
<i>obr1</i>	BREFELDIN A RESISTANCE PROTEIN
<i>rds1</i>	STRESS RESPONSE PROTEIN RDS1P

ish1 NUCLEAR ENVELOPE PROTEIN
SPBC2A9.02 PUTATIVE DYHYDROFLAVANOL-4-REDUCTASE

transporters

SPCC965.06 PUTATIVE POTASSIUM CHANNEL SUBUNIT
SPBC36.02c MFS DRUG EFFLUX TRANSPORTER OF UNKNOWN
SPECIFICITY
SPCC569.05c MFS DRUG EFFLUX TRANSPORTER OF UNKNOWN
SPECIFICITY
SPCC757.11c CONSERVED MEMBRANE PROTEIN; POSSIBLE
TRANSPORTER
bfr1: hba2 MFS BREFELDIN A EFFLUX TRANSPORTER
SPAC11D3.05 MFS DRUG EFFLUX TRANSPORTER OF UNKNOWN
SPECIFICITY
SPBC609.04 MFS MULTIDRUG EFFLUX TRANSPORTER

carbohydrate metabolism

tms1 PUTATIVE SORBITOL DEHYDROGENASE
SPBC215.11c PUTATIVE OXIDOREDUCTASE
SPBC1773.06c ALCOHOL DEHYDROGENASE
SPAC513.02 PROTEIN WITH SIMILARITY TO
PHOSPHOGLYCERATE MUTASES
SPBC12C2.04 CONSERVED HYPOTHETICAL PROTEIN
SPAC2F3.05c ALDO/KETO REDUCTASE FAMILY
OXIDOREDUCTASE

<i>zwf1</i>	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE
SPACUNK4.17	PUTATIVE SUGAR OXIDOREDUCTASE; POSSIBLE SORBITOL UTILISATION
<i>ntp1</i>	NEUTRAL TREHALASE
<i>tps1</i>	ALPHA, ALPHA-TREHALOSE-PHOSPHATE SYNTHASE
SPAC26F1.07	PROBABLE OXIDOREDUCTASE
<i>exg3</i>	GLUCAN 1, 3-BETA-GLUCOSIDASE
SPAC22A12.17c	SHORT CHAIN DEHYDROGENASE
<i>gpd1</i>	GLYCEROL-3-PHOSPHATE DEHYDROGENASE
<i>gut2</i>	GLYCEROL-3-PHOSPHATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
SPAC19G12.09	PUTATIVE ALDOSE REDUCTASE
SPBC24C6.09c	HYPOTHETICAL PROTEIN WITH LOW SIMILARITY TO TRANSKETOLASE
SPAC22F8.05	PUTATIVE ALPHA, ALPHA-TREHALOSE- PHOSPHATE SYNTHASE
SPACUNK4.16c	PUTATIVE ALPHA-TREHALOSE-PHOSPHATE SYNTHASE

lipid or fatty acid metabolism

SPAC1F7.12	OXIDOREDUCTASE SIMILAR TO PYRIDOXAL REDUCTASE
SPAC23D3.11	PUTATIVE SHORT CHAIN DEHYDROGENASE
<i>plr</i>	PYRIDOXAL REDUCTASE

SPAC4D7.02c PUTATIVE GLYCEROPHOSPHORYL DIESTER
PHOSPHODIESTERASES

SPAC4H3.08 PUTATIVE SHORT CHAIN DEHYDROGENASE

suphur metabolism

gst2 GLUTATHIONE S-TRANSFERASE

SPCC576.03c THIOREDOXIN PEROXIDASE;

trx2 THIOREDOXIN II

gpx1 GLUTATHIONE PEROXIDASE

nucleotide metabolism

SPAC1F8.04c PUTATIVE CHLOROXYDROLASE/DEAMINASE

SPBC106.02c PARBC-LIK NUCLEASE DOMAIN

SPBC1683.06c PUTATIVE INOSINE-URIDINE PREFERRING
NUCLEOSIDE HYDROLASE

others

SPCC663.06c PUTATIVE SHORT CHAIN DEHYDROGENASE
PROTEIN

SPAC513.06c PROBABLE DIMERIC DIHYDRODIOL
DEHYDROGENASE

SPAC139.05 PROBABLE SUCCINATE SEMIALDEHYDE
DEHYDROGENASE

SPBC1271.07c ACETYLTRANSFERASE

SPCC663.08c PUTATIVE SHORT CHAIN DEHYDROGENASE

SPAC23D3.05c	ALCOHOL DEHYDROGENASE PSEUDOGENE
<i>slt1</i>	SLT1 PROTEIN
SPAC513.07	PUTATIVE CINNAMOYL-COA REDUCTASE
SPBC30D10.14	PUTATIVE HYDROLASE
<i>meu8</i>	PUTATIVE BETAINE ALDEHYDE DEHYDROGENASE; MEIOTIC EXPRESSION UPREGULATED
SPAC26F1.14c	PUTATIVE FLAVOPROTEIN
SPBC16A3.02c	PUTATIVE QUINONE OXIDOREDUCTASE; ZINC BINDING OXIDOREDUCTASE
SPAC23C11.06c	HYPOTHETICAL PROTEIN LOW SIMILARITY TO YEAST YNL115C
SPCC8E4.10c	ALDOLASE AND ADDUCIN N TERMINAL DOMAIN PROTEIN
SPAC2E1P3.01	PUTATIVE DEHYDROGENASE BY SIMILARITY
SPBC725.10	SIMILAR TO PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR
SPBC23G7.10c	PUTATIVE NADH-DEPENDENT FLAVIN OXIDOREDUCTASE

sequence orphans

SPAC22H12.01c	HYPOTHETICAL PROTEIN
SPBC1271.08c	VERY HYPOTHETICAL PROTEIN
SPBC11C11.06c	HYPOTHETICAL PROTEIN
SPCC191.01	HYPOTHETICAL PROTEIN

SPBC1347.11	HYPOTHETICAL PROTEIN
SPCC320.02c	ASPARAGINE-RICH PROTEIN
SPBC428.10	SERINE/LYSINE RICH HYPOTHETICAL PROTEIN
SPAC25H1.01c	HYPOTHETICAL SERINE-RICH PROTEIN
SPBC56F2.06	HYPOTHETICAL PROTEIN
SPAC32A11.02c	HYPOTHETICAL COILED-COIL PROTEIN
SPBC1105.13c	VERY HYPOTHETICAL PROTEIN

unknown

SPAC27D7.09c	HYPOTHETICAL PROTEIN
SPAC27D7.10c	HYPOTHETICAL PROTEIN
SPBC21H7.06c	HYPOTHETICAL PROTEIN
SPBC21C3.19	HYPOTHETICAL PROTEIN; SIMILAR TO YHR087W
SPAC57A7.05	HYPOTHETICAL PROTEIN; LEUCINE-SERINE RICH
SPBC1677.01c	HYPOTHETICAL PROTEIN
SPBC725.03	HYPOTHETICAL PROTEIN
SPCC16E9.16c	pseudogene
SPAC23G3.03	PUTATIVE PEPTIDE MONOOXYGENASE
SPAC11D3.13	CONSERVED HYPOTHETICAL PROTEIN
SPAC4H3.03c	HYPOTHETICAL PROTEIN
SPAC607.08c	CONSERVED HYPOTHETICAL PROTEIN; SIMILAR TO YFL034W
SPCC736.15	HYPOTHETICAL PROTEIN
SPAC27D7.11c	HYPOTHETICAL PROTEIN;
SPBC1539.04	HYPOTHETICAL PROTEIN

SPAC21E11.04	PUTATIVE TRANSCRIPTIONAL REGULATORY PROTEIN
SPAC6G10.03c	HYPOTHETICAL PROTEIN
SPCC576.04	PUTATIVE RECEPTOR-ASSOCIATED PROTEIN
SPAC26F1.04c	PUTATIVE MITOCHONDRIAL RESPIRATORY FUNCTION PROTEIN

repressed genes.

cell cycle control

<i>cdc15</i>	PHOSPHOPROTEIN
<i>eng1</i>	ENDO-1, 3-BETA-GLUCANASE
SPBC3E7.12c	VERY PUTATIVE CHITIN SYNTHASE REGULATORY FACTOR
SPBC83.18c	HYPOTHETICAL PROTEIN WITH C2 DOMAIN
<i>etd1</i>	ETD1 PROTEIN
<i>spd1</i>	S-PHASE DELAYING PROTEIN 1
SPAC6G10.12c	HYPOTHETICAL ZINC-FINGER PROTEIN
<i>mip1</i>	DNA POLYMERASE GAMMA, MITOCHONDRIAL

cell metabolism

SPAC19B12.02c	PROTEIN SIMILAR TO YEAST GAS1 GLYCOPHOSPHOLIPID-ANCHORED SURFACE GLYCOPROTEIN
SPCC644.05c	DEOXYURIDINE 5'-TRIPHOSPHATE

	NUCLEOTIDOHYDROLASE
SPBC359.02	PUTATIVE ALANINE RACEMASE
<i>h4.2: hhf2</i>	HISTONE H4
<i>sou1</i>	SORBITOL UTILIZATION PROTEIN SOU1; SHORT CHAIN DEHYDROGENASE
SPAPB1A10.14	HYPOTHETICAL PROTEIN
<i>exg1</i>	EXO-BETA-1, 3-GLUCANASE
SPCC1739.06c	UROPORPHYRIN METHYLTRANSFERASE
<i>rpc17</i>	RNA POLYMERASE III SUBUNIT

transporters

SPAC1F8.03c	MFS EFFLUX TRANSPORTER OF UNKNOWN SPECIFICITY
SPAC869.05c	SULP SULFATE TRANSPORTER
<i>frp1</i>	FERRIC REDUCTASE TRANSMEMBRANE COMPONENT
SPBC4F6.09	MFS EFFLUX TRANSPORTER OF UNKNOWN SPECIFICITY
SPAC1142.05	POSSIBLE COPPER TRANSPORTER
<i>fip1</i>	IRON PERMEASE

sequence orphans

SPBC27.05	VERY HYPOTHETICAL PROTEIN
SPAC343.20	VERY HYPOTHETICAL PROTEIN
SPBC2A9.07c	HYPOTHETICAL PROTEIN

SPBC1709.12	HYPOTHETICAL PROTEIN
SPAPJ760.03c	HYPOTHETICAL THREONINE-RICH PROTEIN
SPAC29B12.08	HYPOTHETICAL SER/PRO-RICH PROTEIN
SPAC15A10.09c	HYPOTHETICAL PROTEIN
<hr/>	
others	
<hr/>	
<i>rds1</i>	STRESS RESPONSE PROTEIN RDS1P
<i>sap1</i>	U2 SNRNP COMPONENT
<i>bet1</i>	PUTATIVE ER-GOLGI SNARE
SPAC3F10.15c	VERY HYPOTHETICAL PROTEIN
SPBC30B4.05	PUTATIVE KARYOPHERIN-BETA INVOLVED IN THE NUCLEAR EXPORT OF KARYOPHERIN-ALPHA
<i>klp8</i>	KINESIN-LIKE PROTEIN
SPAC11E3.13c	PUTATIVE GLYCOLIPID ANCHORED SURFACE PROTEIN; POSSIBLE INVOLVEMENT IN CELL WALL MAINTENANCE
SPAC23H4.19	PUTATIVE CELL WALL BIOGENESIS PROTEIN
SPBC27.04	COILED-COIL PROTEIN SIMILAR TO YEAST RAD50 INVOLVED IN RECOMBINATIONAL DNA REPAIR
SPAPYUG7.03c	HYPOTHETICAL PROTEIN
SPAC19G12.16c	HYPOTHETICAL SERINE-THREONINE RICH
<i>dbp2</i>	HUMAN P68-LIKE PROTEIN; PUTATIVE SPLICEOSOME COMPONENT
<i>rpc34</i>	DNA-DIRECTED RNA POLYMERASE III SUBUNIT

unknown

SPCC18.01c

HYPOTHETICAL SERINE RICH PROTEIN

SPBC4F6.12

LIM DOMAIN PROTEIN; LEUPAXIN LIKE
