

### ***Repressed CESR genes***

Gene Name	Annotation
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#### **Transporters:**

SPBC36.03C	MSF drug efflux transporter of unknown specificity
SPCC584.13	APC amino acid transporter
SPBC8E4.01C	MFS inorganic phosphate transporter
SPCC330.07C	MFS efflux transporter of unknown specificity
SPBC1683.01	MFS inorganic phosphate transporter
SPAC23D3.12	MFS inorganic phosphate transporter
SPBC36.01C	MFS drug efflux transporter of unknown specificity
SPCC965.13	MFS amiloride efflux transporter; car1 homologue

#### **Ribosomal proteins and protein synthesis**

SPAC19A8.07C	U3 snoRNP component; required for pre-18S rRNA processing; similar to <i>S. cerevisiae</i> IMP4
rpl24-3 60S	ribosomal protein L24C (L30)
rpl7-3 60S	ribosomal protein L7
SPCC320.11C	putative protein involved in 60S ribosome subunit biogenesis
SPBC11G11.03	putative 60S acidic ribosomal protein
SPBC776.17	putative Protein involved in pre-rRNA processing and ribosome assembly; by similarity to yeast rrp7
SPBC800.06	Protein required for biogenesis of the 60S ribosomal subunit; possibly localized to the nucleolus; similar to <i>S. cerevisiae</i> BRX1
SPCC1183.07	putative rRNA biogenesis protein; rrp5 homolog; multiple S1 rna binding domain protein
SPAC1486.09	Protein that may associates with the 26S proteasome; by similarity to yeast nob1
SPAC18B11.06	putative U3 snoRNP component; required for pre-18S rRNA processing; similar to <i>S. cerevisiae</i> LCP5
SPBC29A3.16	putative regulator of ribosome synthesis by similarity to yeast rrs1
SPAC56F8.09	possibly involved in cleavage at site A2 in pre-rRNA; ribosomal RNA processing pathway; similar to <i>S. cerevisiae</i> RRP8
SPBC9B6.07	Protein involved in maturation of 25S rRNA; by similarity to yeast rrp1
kap123	putative importin beta-4 subunit; Karyopherin-beta involved in nuclear import of ribosomal proteins
SPCC18.12C	"tRNA synthetase class II (D K N), cytoplasmic"
gar1	pre-mrna processing protein Gar1p

#### **RNA helicases**

dbp2	DEAD/DEAH box helicase; putative pre-mRNA splicing factor; human p68-like protein; similar to <i>S. cerevisiae</i> DPB2; contains large 3' intron like <i>S. cerevisiae</i> DBP2
SPAC6G9.10C	DNA2/NAM family DEAD-box type RNA helicase; putative positive effector of tRNA-splicing endonuclease; required for intron cleavage of tRNAs; possibly involved in snRNA and snoRNA maturation; similar to <i>S. cer.</i> SEN1
SPAC1F7.02C	probable ATP-dependent RNA helicase
SPAC823.08C	putative ATP-dependent RNA helicase
SPCC1827.01C	hypothetical helicase
SPCC17D1.06	putative ATP-dependent RNA helicase

prh1	probable ATP-dependent RNA helicase, signalling and transcription factors
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### Putative transcription factors and general transcription

SPAC17H9.04C	RNA-binding / Ran zinc finger protein
SPAC6G10.12C	hypothetical zinc-finger protein; possibly involved in metallothionein expression
SPAC683.02C	hypothetical zinc-finger protein
SPBC215.06C	protein with a putative zinc finger domain, has similarity to mouse LYAR cell growth regulating nucleolar protein
tef5	elongation factor 1 beta
rpa49	DNA-directed RNA polymerase I 49 kd polypeptide
rpc34	DNA-directed RNA polymerase III subunit
SPBC23E6.09	tpr domain protein; putative general repressor of RNA polymerase II transcription that is brought to target promoters by sequence-specific DNA-binding proteins by similarity to yeast ssn6

### Others

mei2	mei2 regulatory protein
SPAC13G7.13C	putative protein required for sporulation and formation of meiotic spindle; by similarity to yeast rim4; has two RNA recognition motif (RRM) domains
isp4	sexual differentiation process protein isp4
mis3	strong similarity to yeast cell division and spore germination protein Krr1p
SPAC1B9.03C	similarity to yeast mating protein SSF1
SPBC16C6.12C	protein possibly involved in cell morphogenesis, cytoskeletal regulation; establishment of cell polarity; by similarity to yeast LAS1
SPBP23A10.11C	serine-rich protein; putative cell wall; possible septation and/or ageing, by similarity
SPBC106.14C	possibly required for actin cytoskeletal organisation by similarity to yeast sda1
psu1	cell wall synthesis protein psu1
SPCC24B10.11C	hypothetical protein; predicted coiled-coil region; sequence orphan
SPAC1142.04	possible nuclear pore complex by similarity to yeast YOR206W; putative coiled-coil regions
SPCC297.04C	SET domain protein
SPBC1734.01C	hypothetical protein; similar to <i>S. cerevisiae</i> YDR365C which is null lethal
SPBC16E9.10C	AAA ATPase
SPAPB1A10.14	hypothetical protein; sequence orphan
SPBC839.07	rhodanase domain protein
SPBPB7E8.01	hypothetical protein; sequence orphan; predicted N-term signal sequence
SPAC926.08C	hypothetical protein; similar to <i>S. cerevisiae</i> YKR081C; contains Pfam-B_20446
SPBC776.08C	hypothetical protein; similar to <i>S. cerevisiae</i> YGR090W
SPAC14C4.09	putative Glucanase; by similarity to <i>Penicillium purpurogenum</i> mutanase; subcellular localization of GFP fusion: membrane
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lps1	pseudouridylate synthase
SPAC890.05	conserved hypothetical protein with G-patch domain
SPBC3B8.05	possibly involved in dipthamide synthesis; similar to <i>S. cerevisiae</i> YIL103W; and human OVCA1 (candidate tumour supressor)
mfm2	M-factor precursor 2
SPBC887.17	putative uracil permease

eng1	endo-1,3-beta-glucanase
SPAC23H4.15	hypothetical protein; similar to <i>S. cerevisiae</i> YDL060W- which is null lethal; contains Pfam-B_1475 and Pfam-B_6211
nrd1	negative regulator of differentiation 1 Nrd1p
SPBC83.15	conserved hypothetical protein; similar to <i>S. cerevisiae</i> YGL111W
SPAC8F11.04	hypothetical protein; similar to <i>S. cerevisiae</i> YKR060W
SPCC1223.14	chorismate synthase
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SPAC19B12.01	similar to <i>S. cerevisiae</i> YNL313C Protein of unknown function, YNL313C has tetratricopeptide (TPR) repeats
SPBC947.04	hypothetical serine/threonine rich repeat protein
SPAC23A1.03	putative adenine phosphoribosyltransferase (APRT); similar to <i>S. cerevisiae</i> APT1; member of the phosphoribosyl transferases family
ade8	adenylosuccinate lyase
ade9	C-1-tetrahydrofolate synthase, mitochondrial precursor includes; methylenetetrahydrofolate dehydrogenase; methylenetetrahydrofolate cyclohydrolase; formyltetrahydrofolate synthetase
SPAC10F6.03C	probable CTP synthase
SPBC8D2.10C	putative arginine n-methyltransferase
SPAC30C2.02	hypothetical protein; similar to <i>S. cerevisiae</i> YJR070C
sou1	sorbitol utilization protein sou1; short chain dehydrogenase
ura3	dihydroorotate dehydrogenase precursor
SPAC222.06	putative Nuclear protein with HMG-like acidic region, required for propagation of M1 double-stranded RNA; by similarity to yeast mak16
fkbp39	peptidyl prolyl cis-trans isomerase
SPBC19F5.05C	pescadillo-like hypothetical protein; yeast homolog YGR103W purifies as part of nuclear pore complex
SPBC1778.01C	zuotin like protein; putative zdna binding; dnaj domain containing protein
SPBC1711.07	WD repeat protein; possible nuclear pore complex associated
SPBC29A3.06	WD repeat protein
SPBC14F5.06	putative RNase L inhibitor
SPBC4F6.14	RNA binding ribonucleoprotein
SPBC1198.02	adenosine deaminase
abp2	ars binding protein 2
SPBC23E6.05	conserved hypothetical protein
SPAC20G8.09C	hypothetical protein; similar to <i>S. cerevisiae</i> YNL132W/KRE33, which is essential and induced by glucose repression; highly conserved
SPAC23C4.17	putative Methyltransferase that methylates cytidine to 5-methyl-cytidine (m5C) at several positions in different tRNAs; by similarity to yeast ncl1
gln1	glutamine synthetase
SPBC32H8.05	hypothetical protein; similar to <i>S. cerevisiae</i> YBL028C
SPBP8B7.20C	putative nucleolar protein; NOL1/NOP2/sun family
SPBC25B2.09C	arginyl-trna synthetase, putative cytoplasmic
SPCP1E11.11	conserved hypothetical protein; pumilio-like
SPBC8D2.18C	putative adenosylhomocysteinase
SPAC6G9.02C	RNA binding protein
SPBC21C3.08C	ornithine aminotransferase (EC 2.6.1.13)
pho4	thiamine-repressible acid phosphatase precursor
SPBC16D10.01C	homolog of yeast tc1; Protein that interacts with protein phosphatase 2C
SPCC613.08	putative cdk inhibitor by similarity to human tok1