

**Web Table A. Diploid homozygous deletion mutants that are sensitive to  $\gamma$ -irradiation: sensitivity to other agents, cell cycle responses and relatedness to human genes**

Yeast gene/ORF <sup>a</sup>	Human genes that code for proteins with shared homology to yeast proteins		$\gamma$ -ray <sup>d</sup>	Bleo <sup>e</sup>	MMS <sup>f</sup>	HU <sup>g</sup>	Camp <sup>h</sup>	UV <sup>i</sup>	G2/M cells (checkpoint) <sup>j</sup>	
	Gene <sup>b</sup>	<i>P</i> value <sup>c</sup> (log)							Unirradiated	Irradiated
Replication recombination repair										
<i>RAD1</i>	<i>ERCC4</i>	−111	SS	=	S	=	=	SSS	=	>>
<i>RAD10</i>	<i>ERCC1</i>	−12	S	=	=	=	=	SSS	=	=
<i>RAD6</i>	<i>UBE2B</i>	−61	SSS	SS	SSS	SS	=	SSS	=	>>
<i>RAD18</i>	<i>ZNF173</i>	−07	SSS	SS	SSS	SS	=	SSS	=	>>
<i>RAD50</i>	<i>RAD50</i> <i>CENPE</i> ** <i>TRP11</i> *	−156 −22 −20	SSS	SSS	SSS	SSS	SSS	SS	=	>>
<i>XRS2</i>	—	—	SSS	SSS	SSS	SSS	SSS	SS	=	>>
<i>RAD51</i>	<i>RAD51</i>	−130	SSS	SSS	SSS	SSS	SSS	SS	=	>>
<i>RAD52</i>	<i>RAD52</i>	−40	SSS	SSS	SSS	SSS	SS	SS	=	>>
<i>RAD55</i>	<i>RAD51L1</i>	−04	SSS	SSS	SSS	SS	SSS	SS	=	>>
<i>RAD57</i>	<i>RAD51L1</i>	−19	SSS	SSS	SSS	S	SSS	S	=	>>
<i>RAD27</i>	<i>FEN1</i>	−118	SS	=	SSS	=	=	S	=	=
<i>HPR1</i>	MGC5350 (i)	−04	SS	SS	SSS	SS	S	S	=	>>
<i>HPR5</i>	—	—	SSS	SS	SSS	SS	SSS	SS	=	>>
<i>APN1</i>	—	—	S	SS	SS	S	=	=	=	>>
<i>MUS81</i>	FLJ21012 (i)	−18	SS	S	SSS	S	SSS	S	=	>>
<i>MMS2</i>	<i>UBE2V2</i>	−36	S	=	SSS	=	=	SS	=	=
<i>SGS1</i>	<i>BLM</i>	−103	S	S	SSS	S	S	S	=	>>
<i>POL32</i>	—	—	SS	SS	SSS	SS	=	S	>>	>
<i>REM50</i>	—	—	S	S	SSS	SS	SSS	SS	=	>>
Checkpoint										
<i>RAD9</i>	<i>DSPP</i>	−11	SSS	=	=	=	=	=	<	<<
<i>RAD17</i>	—	—	SS	=	=	=	SS	S	<	<<
<i>MEC3</i>	—	—	SS	=	=	=	SS	S	<	<<
<i>SFP1</i>	—	—	SSS	SS	=	SS	S	S	<	<<
Nuclear pore complex										
<i>NUP84</i>	<i>NUP107</i> (i)	−16	SSS	SS	SSS	S	SSS	SS	>>	>
<i>NUP120</i>	—	—	SSS	SS	SSS	SS	SS	SS	=	=
<i>NUP133</i>	—	—	SSS	S	SSS	SS	SS	SS	=	=
<i>NUP170</i>	<i>NUP155</i>	−30	S	S	=	=	=	=	=	>>
<i>NUP188</i>	KIAA0169 (i)	−04	S	=	=	=	=	=	=	>>

Chromatin silencing telomeres										
<i>RSC1</i>	FLJ11064 (i)	-18	SSS	SSS	S	=	=	=	=	=
<i>ASF1</i>	DKFZP547E2110 (i)	-50	SS	SS	SSS	SS	SSS	SS	>>	>
<i>RSC2</i>	<i>PBI</i> (i)	-20	S	=	=	=	=	S	=	>>
<i>ARD1</i>	<i>ARD1</i> (i)	-41	SS	S	=	=	=	S	=	=
<i>NAT3</i>	<i>ARD1</i> (i)	-35	SSS	SS	SSS	=	=	=	=	=
<i>EST1</i>	—	—	S	S	=	=	=	=	>>	>
<i>SPT10</i>	—	—	SS	SSS	S	=	SS	S	=	=
<i>DHH1</i>	<i>DDX6*</i> <i>DDX10*</i>	-162 -49	SSS	SS	SS	SSS	=	=	=	>>
Mitotic chromosome transmission										
<i>CHL1</i>	<i>DDX11</i> <i>TNFRSF6B*</i>	-116 -24	SSS	SS	SS	=	S	S	=	=
<i>CTF4</i>	<i>AND-1</i> (i)	-23	SSS	SS	SSS	SS	SSS	S	>>	>
<i>CTF8</i>	—	—	SSS	SS	SSS	SS	SSS	SS	=	=
<i>ANC1</i>	<i>MLLT3*</i> <i>MLLT1*</i>	-10 -09	SSS	SS	SS	SS	=	=	>>	>
<i>PAT1</i>	—	—	S	SSS	S	SS	=	=	=	=
<i>SCP160</i>	<i>HDLBP</i>	-53	SS	SS	=	=	=	=	=	=
<i>BIK1</i>	<i>RSN</i> <i>CENPE**</i>	-18 -06	S	S	=	=	=	=	=	>>
Vacuolar/Golgi/endocytosis										
<i>VID21</i>	—	—	SSS	SS	SSS	=	SS	S	>>	>
<i>VID31</i>	<i>IVL</i> <i>CENP-E**</i>	-16 -04	SSS	SSS	SSS	SSS	SSS	S	>>	>
<i>GOS1</i>	<i>GOSR1</i>	-16	SSS	SS	SSS	SSS	=	S	=	>>
<i>VMA7</i>	<i>ATP6S14</i> (i)	-26	S	=	S	=	=	=	=	=
<i>VPH2-YKL118W</i>	—	—	S	S	S	SS	=	=	=	=
<i>RUD3</i>	<i>DOC1</i> (i) <i>CENPE**</i>	-12 -11	S/R	SS	=	=	=	=	ND	ND
<i>MNN11</i>	—	—	S	S	=	=	=	=	=	=
<i>CLC1</i>	<i>CLTA</i>	-05	SS	SSS	SS	SS	S	S	>>	>
Ubiquitin degradation pathway										
<i>GRR1</i>	MGC15482 (i)	-25	SSS	SS	SS	SS	SS	SS	=	>>
<i>UBR1</i>	KIAA0349 (i)	-22	S	=	=	=	=	=	=	=
<i>PRE9</i>	<i>PSMA4</i>	-70	S	=	=	=	=	=	=	=
<i>YNR068C</i>	—	—	SS	SSS	=	=	=	=	=	>>
<i>UBC13</i>	<i>UBE2N</i> <i>E2-EPF**(i)</i>	-60 -29	S	=	SSS	=	=	SS	=	=
<i>DOC1</i>	<i>APC10</i> (i)	-22	S	S	=	S	=	S	>>	>

<b>Transcription/RNA metabolism</b>										
<i>BUR2</i>	—	—	SSS	SSS	SSS	SSS	SS	SSS	=	>>
<i>CDC40</i>	<i>PRP17</i> <i>CDC20(P55cdc)**</i>	-76 -07	SS	SS	SSS	SSS	=	SS	>>	>
<i>LOC1</i>	—	—	SS	=	S	S	S	S	=	=
<i>RPB9</i>	<i>POLR2I</i>	-25	SS	SS	SS	SS	S	S	=	>>
<i>RTF1</i>	KIAA0252 (i)	-22	SS	=	=	=	=	S	=	=
<i>MRT4</i>	LOC51154 (i)	-43	SS	=	=	S	=	=	<	<<
<i>RAI1</i>	DOM3Z	-11	S	=	=	S	=	=	<	<<
<i>CCR4</i>	KIAA1194 (i) <i>CCRN4L</i>	-71 -23	S	=	=	SSS	SS	S	=	=
<i>REF2</i>	—	—	S	SS	S	S	=	=	=	>>
<i>GRF10</i>	<i>PITX2</i>	-09	S	SS	=	=	=	=	=	>>
<i>CKB1</i>	<i>CSNK2B</i>	-45	S	S	=	=	=	=	=	=
<i>HF11</i>	—	—	SS	SS	SS	SSS	S	S	>>	>
<b>Cytokinesis cytoskeleton spindle</b>										
<i>BEM1</i>	<i>SH3D5</i> <i>ARGBP2</i> (i) <i>YES</i> <i>FYN</i>	-09 -08 -06 -04	SSS	SSS	SS	SS	S	SS	=	>>
<i>AKR1</i>	FLJ10852 (i) <i>TP53BP2</i> <i>BCL3*</i> <i>BARD1</i>	-43 -06 -06 -05	SS	SSS	S	SS	SS	=	=	>>
<i>BFR1</i>	<i>EEA1</i> <i>CENPE**</i> <i>DOC1</i> (i) <i>TRIP11*</i>	-14 -12 -11 -05	SS	SS	=	=	=	=	=	=
<i>RVS161</i>	<i>BIN3</i> <i>AMPH</i> <i>BIN2</i>	-20 -17 -13	SS	SSS	SS	SSS	S	S	=	>>
<i>RVS167</i>	<i>BIN1</i> <i>AMPH</i> <i>AIP1</i> <i>EEN*</i> <i>BIN2</i>	-12 -09 -08 -08 -07	SS	SSS	SS	SS	SS	S	=	>>
<i>HOF1</i>	<i>GAS7*</i>	-11	S	SSS	SS	=	=	=	=	>>
<i>PFD1</i>	<i>PFDN1</i>	-05	S	=	=	=	=	=	=	=
<i>CNM67</i>	<i>CENPF</i> <i>DOC1</i> (i) <i>CENPE**</i>	-10 -09 -04	S	S	SS	SS	S	=	>>	>
<i>SAC6</i>	<i>LCPI*</i>	-119	SS	SS	=	S	=	S	=	>>

<b>Mitochondrial</b>										
<i>RSM7</i>	<i>RPS5</i>	-04	S	=	=	=	=	=	=	>>
<i>MRPL31</i>	—	—	S	S	=	=	=	=	=	=
<i>YMR293C</i>	FLJ10989 (i)	-60	S	S	=	=	=	S	=	>>
<i>ADK1</i>	<i>AK2</i>	-70	S	SSS	S	S	=	S	=	=
<i>LIP5</i>	<i>LIP1</i> (i)	-81	S	=	S	=	=	S	>>	>
<i>MCT1</i>	—	—	S	S	S	=	=	S	=	>>
<i>IMG2</i>	<i>C11orf4(NOF1**)</i>	-05	S	S	=	=	=	=	=	=
<i>FIL1</i>	—	—	S	S	=	=	=	=	=	>>
<i>TOM37</i>	<i>MTX1</i>	-05	SS	SS	=	=	=	=	=	=
<b>Cell wall heat shock</b>										
<i>SSE1</i>	HSP105B (i) <i>ORP150</i> (i)	-139 -62	SS	S	=	=	=	=	=	>>
<i>HSP150</i>	—	—	S	=	=	=	=	=	=	=
<i>CIS3</i>	—	—	S	=	=	=	=	=	=	=
<i>PDR13</i>	<i>HSPA8</i>	-57	S	SSS	=	=	=	=	=	=
<i>BCK1</i>	<i>MAP3K3</i> <i>JAK2*</i> <i>MAP3K7(C-TAK1**)</i> <i>PLK**</i> (i) <i>WEE1**</i>	-52 -23 -23 -22 -12	S	S	S	=	=	=	<	<<
<i>LHS1</i>	<i>ORP150</i> (i)	-56	S	S	=	=	=	=	>>	>
<i>CWH36</i>	—	—	S	S	=	SS	S	=	=	=
<i>CAX4</i>	—	—	S	SS	S	S	S	S	>>	>
<i>SMI1</i>	—	—	S	S	=	=	=	=	=	=
<b>Translation/ribosomal</b>										
<i>FUN12</i>	<i>IF2</i> (i)	-169	SSS	SS	SSS	SS	S	S	=	=
<i>RSA1</i>	—	—	S	=	=	S	=	=	=	=
<i>SRO9</i>	FLJ10378 (i)	-10	S/R	=	=	=	=	SS	ND	ND
<b>Pseudohyphal growth</b>										
<i>DIA4</i>	FLJ20450 (i)	-58	SS	SS	S	=	=	S	=	>>
<i>YEL033W</i>	—	—	S	=	=	=	=	=	=	=
<b>Meiotic</b>										
<i>UME6</i>	—	—	SS	S	S	SS	SS	=	=	>>
<i>IDS2</i>	—	—	S	=	=	=	=	=	=	=
<b>Karyogamy</b>										
<i>JEM1</i>	<i>DNAJA3</i>	-14	SS	SS	S	=	=	=	=	=
<i>ZUO1</i>	<i>ZRF1</i> <i>DNAJC7</i>	-60 -07	S	SSS	=	=	=	=	=	=
<b>Sterol metabolism</b>										
<i>ERG28</i>	<i>C14orf1</i>	-15	S/R	SSS	S	=	SS	=	ND	ND
<i>ERG3</i>	<i>SC5DL</i>	-73	S/R	SS	SSS	SS	=	=	ND	ND
<i>GUP1</i>	<i>KIAA1173</i> (i)	-13	S/R	SS	=	=	=	=	ND	ND
<i>ARV1</i>	<i>ARV1</i> (i)	-10	S/R	S	S	SS	=	=	=	=

<b>Others</b>										
<i>HTL1</i>	—	—	SSS	SS	SS	SS	=	S	=	>>
<i>ADO1</i>	<i>ADK</i>	−61	SS	S	=	=	=	=	=	=
<i>SHE1</i>	—	—	S	SS	=	=	=	=	=	=
<i>PFK2</i>	<i>PFKP</i>	−175	S	=	=	S	=	S	=	=
<i>GND1</i>	<i>PGD</i>	−127	S	S	=	=	=	=	>>	>
<b>Unknown ORFs</b>										
YBL006C	—	—	S	=	S	=	=	=	=	>>
YCL016C ( <i>DCC1</i> )	MGC5528 (i)	−10	SSS	SS	SSS	SS	SS	S	>>	>
YDR014W	—	—	SSS	S	S	=	=	=	=	=
YDR149C- 5' <i>NUM1</i>	—	—	S/R	SS	=	=	=	=	ND	ND
YDR433W- 3' <i>NPL3</i>	—	—	SS	S	SSS	S	S	S	=	>>
YDL115C	—	—	SS	SSS	=	=	=	S	=	=
YDL151C ( <i>FYV3</i> )- 5' <i>RPC53</i>	—	—	SS	SS	=	S	S	S	=	=
YEL072W	—	—	SS	S	=	=	=	S	=	=
YGR165W	—	—	S	=	S	=	=	=	=	>>
YHR081W	<i>CID</i> (i)	−05	S	=	=	=	=	=	=	=
YJL188C ( <i>BUD19</i> )- 3' <i>RPL39</i>	—	—	SS	=	S	S	SS	SS	=	=
YJL193W	—	—	S	=	=	=	=	=	>>	>
YLR235C- 3' <i>TOP3</i>	—	—	SS	SS	SSS	SSS	SSS	SS	>>	>
YLR320W ( <i>MMS22</i> )	—	—	SS	SS	SSS	SS	SSS	S	>>	>
YLR322W- 5' <i>SFH1</i>	—	—	SS	SS	=	=	=	S	=	=
YLR435W- 5'YLR434C	LOC90121 (i)	−13	SS	SS	=	S	S	=	=	=
YML010C-B- 3' <i>SPT5</i>	—	—	SS	=	=	=	=	=	=	=
YML010W-A- 3' <i>SPT5</i>	—	—	S	=	=	=	=	=	=	=
YML013C-A- 3'YML013W	—	—	S	SS	=	=	=	=	=	=
YML014W	KIAA1456 (i)	−14	S	S	=	=	=	=	=	>>
YOR258W	FLJ20157 (i)	−13	S/R	SS	=	=	=	=	ND	ND
YPL055C	—	—	S	=	=	=	=	=	=	=
YPL066W	—	—	S	=	S	=	=	=	<	<<
YPL071C	—	—	S	=	=	=	=	=	=	=
<b>Totals, n=138</b>										
SSS			31	23	35	13	15	5	—	—
SS			39	46	14	31	16	20	—	—
S			60	31	26	19	17	43	—	—
= (or S/R)			8	38	63	75	90	70	—	—

<sup>a</sup> ORFs with reserved gene name are in parentheses. Deletions that result in partial overlapping deletions of genes or ORFs on the complementary DNA strand are indicated below by the designation 5' or 3' to indicate which end of the gene or ORF has overlapping sequences. One ORF, YLR320W, has been designated **MMS22** based on the extreme hypersensitivity of haploids of either mating type (data not shown) and diploids to MMS or HU following deletion. Haploid deletions of *MMS22* were also moderately sensitive to  $\gamma$ -irradiation and had slight sensitivity to UV. Lethality of the null mutation following treatment with each individual DNA damaging agent suggests that *MMS22* may have a role in DNA repair. Functional designations were assigned based on descriptions in the YPD database (see [www.proteome.com](http://www.proteome.com)). Several of the genes (such as *ANCI* and *PAT1*) have multiple functions. Human proteins that have been implicated in cancer are in bold.

<sup>b</sup> Homology to human gene sequences was determined by BLASTP analysis against the human genome database as of October 3, 2001 (see [www.ncbi.nlm.nih.gov/BLAST/](http://www.ncbi.nlm.nih.gov/BLAST/)) using yeast protein sequences obtained from the SGD database (<http://genome-www.stanford.edu/Saccharomyces/>). To filter out spurious matches to human sequences of low complexity, human protein sequences were subjected to a second BLASTP analysis against the yeast protein database that removes low complexity segments using SEG algorithm filtering (see SGD BLAST analysis). Those sequence matches that retained a *P* value  $<10^{-4}$  following this second, more rigorous analysis were judged to be significant as described by Altschul *et al.*<sup>48</sup>.

\* Yeast proteins with homology to oncogenes identified at chromosomal breakpoint sites (the Atlas of Genetics and Cytogenetics in Oncology and Haematology at <http://www.infobiogen.fr/services/chromcancer>) were identified using BLAST analysis against the known and predicted yeast protein sequence database at SGD.

\*\* Human genes found to be significantly induced or repressed following  $\gamma$ -irradiation<sup>49</sup>.

(i) Interim Gene symbol assigned by the Locus Link database (see [www.ncbi.nlm.nih.gov/LocusLink/index](http://www.ncbi.nlm.nih.gov/LocusLink/index)). All other human gene designations have been recognized by the HUGO nomenclature committee (see [www.gdb.org/](http://www.gdb.org/)).

<sup>c</sup> Human proteins that have regions of homology (BLAST *P* value  $<10^{-4}$ ) are listed. Those without known homologues are denoted "—".

<sup>d</sup> The  $\gamma$ -ray dose is 80 Krads. Levels of radiation sensitivity as determined by ability of cells to give rise to colonies after dilution replica plating and irradiation (see Fig. 1); SS, moderate sensitivity; S, detectable sensitivity; =, wildtype levels of radiation toleration; S/R, slow recovery following irradiation, but no apparent loss in survival. Survival fractions following  $\gamma$ -irradiation ranged from 0.5% to 29% for the newly identified  $\gamma$ -ray sensitive deletion strains. Wild type (Rad<sup>+</sup>) survival was 47%.

<sup>e</sup> 4  $\mu$ g/ml bleomycin (sensitivity defined as above).

<sup>f</sup> 2 mM methyl methanesulfonate (sensitivity defined as above).

<sup>g</sup> 100 mM hydroxyurea (sensitivity defined as above).

<sup>h</sup> 10  $\mu$ g/ml camptothecin in 25 mM HEPES buffer, pH 7.2 (sensitivity defined as above).

<sup>i</sup> 60 J/m<sup>2</sup> ultraviolet light (sensitivity defined as above).

<sup>j</sup> The % of large budded cells (corresponding to G2/M) determined in logarithmically growing cultures (unirradiated) or at 3 hrs post-irradiation (6 Krads) incubation in growth medium. Levels comparable to wild type are denoted as '=' for 15–20% G2/M cells unirradiated and 30–40% irradiated; cells are considered checkpoint deficient (< ; <<) if the G2/M cells are <15% for unirradiated cells and <30% for irradiated cells. Enhanced  $\gamma$ -ray arrest (>) is indicated if the % G2/M cells is comparable to wildtype (=) for unirradiated cells but > 45% for the irradiated cells. Cells were considered as exhibiting high levels of spontaneous (i.e., constitutive arrest) if the unirradiated cultures had >35–40% large-budded cells. ND, not determined.