

	Gephebase Gene	GepheID
RAD5 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^RAD5^#gephebase-summary-title)	GP00000950	Main curator
Published	Entry Status	Martin

Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Physiology^#gephebase-summary-title)		Trait Category	
Xenobiotic resistance (https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic+resistance^#gephebase-summary-title)		Trait	
Saccharomyces cerevisiae - S288c strain		Trait State in Taxon A	
Saccharomyces cerevisiae - RM strain		Trait State in Taxon B	
Data not curated		Ancestral State	
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Domesticated^#gephebase-summary-title)		Taxonomic Status	
Taxon A		Taxon B	
Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Saccharomyces+cerevisiae^#gephebase-summary-title)		Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Saccharomyces+cerevisiae^#gephebase-summary-title)	
baker's yeast		baker's yeast	
Saccharomyces capensis; Saccharomyces italicus; Saccharomyces oviformis; Saccharomyces uvarum var. melibiosus; baker's yeast; S. cerevisiae; brewer's yeast; ATCC 18824; ATCC:18824; CBS 1171; CBS:1171; NRRL Y-12632; NRRL:Y:12632; Saccaromyces cerevisiae; Saccharomyce cerevisiae; Saccharomyes cerevisiae; Sccharomyces cerevisiae		Saccharomyces capensis; Saccharomyces italicus; Saccharomyces oviformis; Saccharomyces uvarum var. melibiosus; baker's yeast; S. cerevisiae; brewer's yeast; ATCC 18824; ATCC:18824; CBS 1171; CBS:1171; NRRL Y-12632; NRRL:Y:12632; Saccaromyces cerevisiae; Saccharomyce cerevisiae; Saccharomyes cerevisiae; Sccharomyces cerevisiae	
species		species	
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces		cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	
Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)		Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	
NCBI Taxonomy ID 4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)		NCBI Taxonomy ID 4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
Yes		Yes	
Saccharomyces cerevisiae - S288c strain		Saccharomyces cerevisiae - RM strain	

Generic Gene Name	UniProtKB <i>Saccharomyces cerevisiae</i> (strain ATCC 204508 / S288c)
RA D5	P32849 (http://www.uniprot.org/uniprot/P32849)
Synonyms	GenebankID or UniProtKB
REV2; SNM2; YLR032W	M96644 (https://www.ncbi.nlm.nih.gov/nuccore/M96644)
String	
4932.YLR032W (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YLR032W)	
Sequence Similarities	
Belongs to the SNF2/RAD54 helicase family.	
GO - Molecular Function	
GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)	
GO:0008270 : zinc ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0008270)	
GO:0000403 : Y-form DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000403)	

GO:0008094 : DNA-dependent ATPase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0008094>)
GO:0000400 : four-way junction DNA binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000400>)
GO:0009378 : four-way junction helicase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009378>)

GO - Biological Process

GO:0000209 : protein polyubiquitination
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000209>)
GO:0006302 : double-strand break repair
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006302>)
GO:0042275 : error-free postreplication DNA repair
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042275>)
GO:0070987 : error-free translesion synthesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0070987>)
GO:0042276 : error-prone translesion synthesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042276>)
GO:0010994 : free ubiquitin chain polymerization
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010994>)
GO:0006301 : postreplication repair (<https://www.ebi.ac.uk/QuickGO/term/GO:0006301>)

GO - Cellular Component

GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)
GO:0000790 : nuclear chromatin (<https://www.ebi.ac.uk/QuickGO/term/GO:0000790>)
GO:0000781 : chromosome, telomeric region
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000781>)

Presumptive Null

No (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No~#gephebase-summary-title>)

Molecular Type

Coding (<https://www.gephebase.org/search-criteria?/and+Molecular Type=~Coding~#gephebase-summary-title>)

Aberration Type

SNP (<https://www.gephebase.org/search-criteria?/and+Aberration Type=~SNP~#gephebase-summary-title>)

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

I791S

Experimental Evidence

Linkage Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping~#gephebase-summary-title>)

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference

Identification and dissection of a complex DNA repair sensitivity phenotype in Baker’s yeast. (2008) (<https://pubmed.ncbi.nlm.nih.gov/18617998>)

Authors

Demogines A; Smith E; Kruglyak L; Alani E

Abstract

Complex traits typically involve the contribution of multiple gene variants. In this study, we took advantage of a high-density genotyping analysis of the BY (S288c) and RM strains of *Saccharomyces cerevisiae* and of 123 derived spore progeny to identify the genetic loci that underlie a complex DNA repair sensitivity phenotype. This was accomplished by screening hybrid yeast progeny for sensitivity to a variety of DNA damaging agents. Both the BY and RM strains are resistant to the ultraviolet light-mimetic agent 4-nitroquinoline 1-oxide (4-NQO); however, hybrid progeny from a BYxRM cross displayed varying sensitivities to the drug. We mapped a major quantitative trait locus (QTL), RAD5, and identified the exact polymorphism within this locus responsible for 4-NQO sensitivity. By using a backcrossing strategy along with array-assisted bulk segregant analysis, we identified one other locus, MKT1, and a QTL on Chromosome VII that also link to the hybrid 4-NQO-sensitive phenotype but confer more minor effects. This work suggests an additive model for sensitivity to 4-NQO and provides a strategy for mapping both major and minor QTL that confer background-specific phenotypes. It also provides tools for understanding the effect of genetic background on sensitivity to genotoxic agents.

Additional References

Dissection of genetically complex traits with extremely large pools of yeast segregants. (2010) (<https://pubmed.ncbi.nlm.nih.gov/20393561>)

RELATED GEPHE

Related Genes

15 (APJ1, ERG3, ERG5, ERG6, ERG7, LEU2, PHO84, SWS2, TSA2, CIS1, FRM2, GPX2, RTA1, cytochrome b, MKT1) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=~4932~/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

