

RHO2 (#gephebase-summary-title)	Gephebase Gene	GP00000986	GepheID
Published	Entry Status	Martin	Main curator

Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Physiology~#gephebase-summary-title)		Trait Category
Temperature tolerance / virulence (https://www.gephebase.org/search-criteria?/and+Trait=~Temperature tolerance / virulence~#gephebase-summary-title)		Trait
Saccharomyces cerevisiae - clinical strain		Trait State in Taxon A
Saccharomyces cerevisiae - laboratory strain		Trait State in Taxon B
Data not curated		Ancestral State
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Intraspecific~#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)	Latin Name
baker’s yeast	baker’s yeast	Common Name
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	Synonyms
species	species	Rank
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	Lineage
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)	Parent
4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	NCBI Taxonomy ID
Yes	Yes	is Taxon A an Intraspecies?
Saccharomyces cerevisiae - clinical strain	Saccharomyces cerevisiae - laboratory strain	Taxon A Description
		Taxon B Description

RHO2 YNL090W; N2237 4932.YNL090W (http://string-db.org/newstring.cgi/show_network_section.pl?identifier= 4932.YNL090W)	Generic Gene Name Synonyms String Sequence Similarities GO - Molecular Function GO:0019901 : protein kinase binding (https://www.ebi.ac.uk/QuickGO/term/GO:0019901) GO:0005525 : GTP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005525) GO:0003924 : GTPase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003924) GO - Biological Process	UniProtKB <i>Saccharomyces cerevisiae</i> (strain ATCC 204508 / S288c) P06781 (http://www.uniprot.org/uniprot/P06781) GenebankID or UniProtKB CAA95965 (https://www.ncbi.nlm.nih.gov/nuccore/CAA95965)
--	--	--

GO:0008360 : regulation of cell shape
(<https://www.ebi.ac.uk/QuickGO/term/GO:0008360>)
GO:0007015 : actin filament organization
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007015>)
GO:0007266 : Rho protein signal transduction
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007266>)
GO:0051017 : actin filament bundle assembly
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051017>)
GO:0030010 : establishment of cell polarity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030010>)
GO:0030950 : establishment or maintenance of actin cytoskeleton polarity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030950>)
GO:0031505 : fungal-type cell wall organization
(<https://www.ebi.ac.uk/QuickGO/term/GO:0031505>)
GO:0007017 : microtubule-based process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007017>)
GO:0032956 : regulation of actin cytoskeleton organization
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032956>)
GO:0030334 : regulation of cell migration
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030334>)
GO:0007264 : small GTPase mediated signal transduction
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007264>)

GO - Cellular Component

GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)
GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)
GO:0016020 : membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0016020>)
GO:0043231 : intracellular membrane-bounded organelle
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043231>)
GO:0005938 : cell cortex (<https://www.ebi.ac.uk/QuickGO/term/GO:0005938>)
GO:0032153 : cell division site (<https://www.ebi.ac.uk/QuickGO/term/GO:0032153>)

	Presumptive Null
Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Unknown~#gephebase-summary-title)	
	Molecular Type
Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=~Cis-regulatory~#gephebase-summary-title)	
	Aberration Type
Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=~Unknown~#gephebase-summary-title)	
	Molecular Details of the Mutation
3'UTR polymorphism	
	Experimental Evidence
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping~#gephebase-summary-title)	
	Main Reference
Dissecting the architecture of a quantitative trait locus in yeast. (2002) (https://pubmed.ncbi.nlm.nih.gov/11907579)	
	Authors
Steinmetz LM; Sinha H; Richards DR; Spiegelman JL; Oefner PJ; McCusker JH; Davis RW	
	Abstract
Most phenotypic diversity in natural populations is characterized by differences in degree rather than in kind. Identification of the actual genes underlying these quantitative traits has proved difficult. As a result, little is known about their genetic architecture. The failures are thought to be due to the different contributions of many underlying genes to the phenotype and the ability of different combinations of genes and environmental factors to produce similar phenotypes. This study combined genome-wide mapping and a new genetic technique named reciprocal-hemizygosity analysis to achieve the complete dissection of a quantitative trait locus (QTL) in <i>Saccharomyces cerevisiae</i> . A QTL architecture was uncovered that was more complex than expected. Functional linkages both in cis and in trans were found between three tightly linked quantitative trait genes that are neither necessary nor sufficient in isolation. This arrangement of alleles explains heterosis (hybrid vigour), the increased fitness of the heterozygote compared with homozygotes. It also demonstrates a deficiency in current approaches to QTL dissection with implications extending to traits in other organisms, including human genetic diseases.	
	Additional References
Complex genetic interactions in a quantitative trait locus. (2006) (https://pubmed.ncbi.nlm.nih.gov/16462944)	

RELATED GEPHE

	Related Genes
No matches found.	
	Related Haplotypes
No matches found.	

EXTERNAL LINKS

COMMENTS

