

PMR1 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~PMR1~#gephebase-summary-title)	Gephebase Gene	GP00000914	GepheID
Published	Entry Status	Martin	Main curator

Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Physiology^#gephebase-summary-title)		Trait Category
Metal tolerance (manganese) (https://www.gephebase.org/search-criteria?/and+Trait=~Metal tolerance (manganese)^#gephebase-summary-title)		Trait
Saccharomyces cerevisiae - wild strains		Trait State in Taxon A
Saccharomyces cerevisiae - BY and other laboratory strains (Mn2+ sensitive)		Trait State in Taxon B
Taxon A		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=4930)		Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930)
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)
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
Yes		Yes
Taxon A Description		Taxon B Description
Saccharomyces cerevisiae - wild strains		Saccharomyces cerevisiae - BY and other laboratory strains (Mn2+ sensitive)

PMR1	Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
	Synonyms	P13586 (http://www.uniprot.org/uniprot/P13586)
BSD1; LDB1; SSC1; SCC1; YGL167C; G1666		GenebankID or UniProtKB
	String	NP_011348 (https://www.ncbi.nlm.nih.gov/nucore/NP_011348)
4932.YGL167C (http://string-db.org/newstring_cgj/show_network_section.pl?identifier=4932.YGL167C)	Sequence Similarities	
Belongs to the cation transport ATPase (P-type) (TC 3.A.3) family.		
GO - Molecular Function		
GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)		
GO:0005388 : calcium-transporting ATPase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005388)		
GO:0005509 : calcium ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005509)		

GO:0008553 : proton-exporting ATPase activity, phosphorylative mechanism
(<https://www.ebi.ac.uk/QuickGO/term/GO:0008553>)
GO:0015410 : manganese-transporting ATPase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0015410>)

GO - Biological Process

GO:0006874 : cellular calcium ion homeostasis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006874>)
GO:0070588 : calcium ion transmembrane transport
(<https://www.ebi.ac.uk/QuickGO/term/GO:0070588>)
GO:0006828 : manganese ion transport
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006828>)
GO:0006816 : calcium ion transport (<https://www.ebi.ac.uk/QuickGO/term/GO:0006816>)
GO:0030026 : cellular manganese ion homeostasis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030026>)
GO:0016236 : macroautophagy (<https://www.ebi.ac.uk/QuickGO/term/GO:0016236>)

GO - Cellular Component

GO:0016021 : integral component of membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)
GO:0000139 : Golgi membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0000139>)
GO:0005794 : Golgi apparatus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005794>)

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

Leu548Phe

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

CRISPR-directed mitotic recombination enables genetic mapping without crosses. (2016) (<https://pubmed.ncbi.nlm.nih.gov/27230379>)

Authors

Sadhu MJ; Bloom JS; Day L; Kruglyak L

Abstract

Linkage and association studies have mapped thousands of genomic regions that contribute to phenotypic variation, but narrowing these regions to the underlying causal genes and variants has proven much more challenging. Resolution of genetic mapping is limited by the recombination rate. We developed a method that uses CRISPR (clustered, regularly interspaced, short palindromic repeats) to build mapping panels with targeted recombination events. We tested the method by generating a panel with recombination events spaced along a yeast chromosome arm, mapping trait variation, and then targeting a high density of recombination events to the region of interest. Using this approach, we fine-mapped manganese sensitivity to a single polymorphism in the transporter Pmr1. Targeting recombination events to regions of interest allows us to rapidly and systematically identify causal variants underlying trait differences.

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Additional References

RELATED GEPHE

Related Genes

5 (MAM3, metallothionein CUP1, Plasma membrane ATPase 1, Vacuolar transporter chaperone 1, Vacuolar transporter chaperone 4) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=~4932~/and+Trait=Metal tolerance/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

