

Gephebase Gene		GepheID
RME1 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~RME1~#gephebase-summary-title)	GP00000994	Main curator
Published	Entry Status	Martin

Physiology (#https://www.gephebase.org/search-criteria?/and+Trait+Category=~Physiology)		Trait Category	
Sporulation efficiency (#https://www.gephebase.org/search-criteria?/and+Trait=~Sporulation+efficiency)		Trait	
Saccharomyces cerevisiae - SK1 strain		Trait State in Taxon A	
Saccharomyces cerevisiae - S288c strain		Trait State in Taxon B	
Taxon A		Ancestral State	
Domesticated (#https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Domesticated)		Taxonomic Status	
Taxon A		Taxon B	
Saccharomyces cerevisiae (#https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Saccharomyces+cerevisiae)		Saccharomyces cerevisiae (#https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Saccharomyces+cerevisiae)	
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; Saccharomyces 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; Saccharomyces 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	
Taxon A Description		Taxon B Description	
Saccharomyces cerevisiae - SK1 strain		Saccharomyces cerevisiae - S288c strain	

UniProtKB	Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
RME1		P32338 (http://www.uniprot.org/uniprot/P32338)
CSP1; YGR044C	Synonyms	GenebankID or UniProtKB
	String	DQ116804 (https://www.ncbi.nlm.nih.gov/nuccore/DQ116804)
4932.YGR044C (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YGR044C)	Sequence Similarities	
-		
	GO - Molecular Function	
GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)		
GO:0000981 : DNA-binding transcription factor activity, RNA polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:0000981)		
GO:0000978 : RNA polymerase II proximal promoter sequence-specific DNA binding		

(https://www.ebi.ac.uk/QuickGO/term/GO:0000978)	GO - Biological Process	
GO:0045944 : positive regulation of transcription by RNA polymerase II (https://www.ebi.ac.uk/QuickGO/term/GO:0045944)		
GO:0000122 : negative regulation of transcription by RNA polymerase II (https://www.ebi.ac.uk/QuickGO/term/GO:0000122)		
GO:0051301 : cell division (https://www.ebi.ac.uk/QuickGO/term/GO:0051301)		
GO:0045835 : negative regulation of meiotic nuclear division (https://www.ebi.ac.uk/QuickGO/term/GO:0045835)		
GO:0051038 : negative regulation of transcription involved in meiotic cell cycle (https://www.ebi.ac.uk/QuickGO/term/GO:0051038)		
GO:0036095 : positive regulation of invasive growth in response to glucose limitation by positive regulation of transcription from RNA polymerase II promoter (https://www.ebi.ac.uk/QuickGO/term/GO:0036095)		
GO:0071931 : positive regulation of transcription involved in G1/S transition of mitotic cell cycle (https://www.ebi.ac.uk/QuickGO/term/GO:0071931)		
	GO - Cellular Component	
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)		Presumptive Null
No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No~#gephebase-summary-title)		Molecular Type
Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=~Cis-regulatory~#gephebase-summary-title)		Aberration Type
Deletion (https://www.gephebase.org/search-criteria?/and+Aberration Type=~Deletion~#gephebase-summary-title)		Deletion Size
1-9 bp		
		Molecular Details of the Mutation
single nucleotide deletion in promoter region		
		Experimental Evidence
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping~#gephebase-summary-title)		Main Reference
Quantitative trait loci mapped to single-nucleotide resolution in yeast. (2005) (https://pubmed.ncbi.nlm.nih.gov/16273108)		Authors
Deutschbauer AM; Davis RW		Abstract
Identifying the genetic variation underlying quantitative trait loci remains problematic. Consequently, our molecular understanding of genetically complex, quantitative traits is limited. To address this issue directly, we mapped three quantitative trait loci that control yeast sporulation efficiency to single-nucleotide resolution in a noncoding regulatory region (RME1) and to two missense mutations (TAO3 and MKT1). For each quantitative trait locus, the responsible polymorphism is rare among a diverse set of 13 yeast strains, suggestive of genetic heterogeneity in the control of yeast sporulation. Additionally, under optimal conditions, we reconstituted approximately 92% of the sporulation efficiency difference between the two genetically distinct parents by engineering three nucleotide changes in the appropriate yeast genome. Our results provide the highest resolution to date of the molecular basis of a quantitative trait, showing that the interaction of a few genetic variants can have a profound phenotypic effect.		
		Additional References

RELATED GEPHE

7 (IME1, RAS2, RME1 [possible pseudo-replicate of laboratory strain entry], RSF1, SWS2, TAO3, MKT1) (https://www.gephebase.org/search-criteria?/or+Taxon ID=~4932~/and+Trait=Sporulation efficiency/and+groupHaplotypes=true#gephebase-summary-title)	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS