

GEPHE SUMMARY

	Gephebase Gene		GepheID
Prx1 = Mhox = Prrx1 (<a #gephebase-summary-title"="" +prx1+"mhox="+Prrx1+" href="https://www.gephebase.org/search-criteria?/and+GeneGephebase=">https://www.gephebase.org/search-criteria?/and+GeneGephebase="+Prx1+"Mhox="+Prrx1+"#gephebase-summary-title)	GP00000934		
	Entry Status	Martin	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Morphology (<a +morphology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+TraitCategory=">https://www.gephebase.org/search-criteria?/and+TraitCategory="+Morphology+"#gephebase-summary-title)		Trait	
Limb length (<a +limb="" href="https://www.gephebase.org/search-criteria?/and+Trait=" length+"#gephebase-summary-title"="">https://www.gephebase.org/search-criteria?/and+Trait="+Limb length+"#gephebase-summary-title)			
	Trait State in Taxon A		
Mus musculus		Trait State in Taxon B	
Carollia perspicillata			
	Ancestral State		
Data not curated		Taxonomic Status	
Intergeneric or Higher (<a +intergeneric="" higher+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=" or="">https://www.gephebase.org/search-criteria?/and+TaxonomicStatus="+Intergeneric or Higher+"#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Mus musculus (<a +mus="" href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=" musculus+"#gephebase-summary-title"="">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="+Mus musculus+"#gephebase-summary-title)		Carollia perspicillata (<a +carollia="" href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=" perspicillata+"#gephebase-summary-title"="">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="+Carollia perspicillata+"#gephebase-summary-title)	
	Common Name		Common Name
house mouse		Seba’s short-tailed bat	
	Synonyms		Synonyms
house mouse; mouse; Mus musculus Linnaeus, 1758; mice C57BL/6xCBA/CaJ hybrid		Seba’s short-tailed bat; Carollia perspicillata (Linnaeus, 1758)	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus		cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria; Chiroptera; Microchiroptera; Phyllostomidae; Carollinae; Carollia	
	Parent		Parent
Mus () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 862507)		Carollia () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 40232)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
10090 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 10090)		40233 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 40233)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Mus musculus
Prrx1		P63013 (http://www.uniprot.org/uniprot/P63013)	
	Synonyms		GenebankID or UniProtKB
K-2; Pmx; Pmx1; Prx1; mHox; AA755424; AI385634; AI843499; A230024N07Rik		ABD59349 (https://www.ncbi.nlm.nih.gov/nuccore/ABD59349)	
	String		
10090.ENSMUSP000000027878 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=10090.ENSMUSP000000027878)			
	Sequence Similarities		
Belongs to the paired homeobox family.			
	GO - Molecular Function		
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)			
GO:0000978 : RNA polymerase II proximal promoter sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000978)			
GO:0001078 : proximal promoter DNA-binding transcription repressor activity, RNA polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:0001078)			
GO:0003713 : transcription coactivator activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003713)			

GO:0071837 : HMG box domain binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0071837>)

GO - Biological Process

GO:0045944 : positive regulation of transcription by RNA polymerase II
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045944>)
GO:0030326 : embryonic limb morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030326>)
GO:0048704 : embryonic skeletal system morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048704>)
GO:0000122 : negative regulation of transcription by RNA polymerase II
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000122>)
GO:0060021 : roof of mouth development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060021>)
GO:0048844 : artery morphogenesis (<https://www.ebi.ac.uk/QuickGO/term/GO:0048844>)
GO:0051216 : cartilage development (<https://www.ebi.ac.uk/QuickGO/term/GO:0051216>)
GO:0048664 : neuron fate determination
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048664>)
GO:0048701 : embryonic cranial skeleton morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048701>)
GO:0042472 : inner ear morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042472>)
GO:0002053 : positive regulation of mesenchymal cell proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0002053>)
GO:0045880 : positive regulation of smoothened signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045880>)
GO:0042474 : middle ear morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042474>)
GO:0097150 : neuronal stem cell population maintenance
(<https://www.ebi.ac.uk/QuickGO/term/GO:0097150>)
GO:0070570 : regulation of neuron projection regeneration
(<https://www.ebi.ac.uk/QuickGO/term/GO:0070570>)

GO - Cellular Component

GO:0005829 : cytosol (<https://www.ebi.ac.uk/QuickGO/term/GO:0005829>)
GO:0005654 : nucleoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005654>)
GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)

	Presumptive Null
Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Unknown~#gephebase-summary-title)	
Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=~Cis-regulatory~#gephebase-summary-title)	Molecular Type
	Aberration Type
Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=~Unknown~#gephebase-summary-title)	
	Molecular Details of the Mutation
Not identified	
	Experimental Evidence
Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Candidate Gene~#gephebase-summary-title)	
	Main Reference
Regulatory divergence modifies limb length between mammals. (2008) (https://pubmed.ncbi.nlm.nih.gov/18198333)	
	Authors
Cretekos CJ; Wang Y; Green ED; Martin JF; Rasweiler JJ; Behringer RR	
	Abstract
Natural selection acts on variation within populations, resulting in modified organ morphology, physiology, and ultimately the formation of new species. Although variation in orthologous proteins can contribute to these modifications, differences in DNA sequences regulating gene expression may be a primary source of variation. We replaced a limb-specific transcriptional enhancer of the mouse Prx1 locus with the orthologous sequence from a bat. Prx1 expression directed by the bat enhancer results in elevated transcript levels in developing forelimb bones and forelimbs that are significantly longer than controls because of endochondral bone formation alterations. Surprisingly, deletion of the mouse Prx1 limb enhancer results in normal forelimb length and Prx1 expression, revealing regulatory redundancy. These findings suggest that mutations accumulating in pre-existing noncoding regulatory sequences within a population are a source of variation for the evolution of morphological differences between species and that cis-regulatory redundancy may facilitate accumulation of such mutations.	
	Additional References

RELATED GEPHE

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

EXTERNAL LINKS

COMMENTS

