

GEPHE SUMMARY

	Gephebase Gene	GepheID
Insulin-like growth factor 1 (IGF1) (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~Insulin-like+growth+factor+1+(IGF1)^#gephebase-summary-title)	GP00000501	
	Entry Status	Main curator
Published	Martin	

PHENOTYPIC CHANGE

	Trait Category		
Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Morphology^#gephebase-summary-title)			
	Trait		
Body size (https://www.gephebase.org/search-criteria?/and+Trait=~Body+size^#gephebase-summary-title)			
	Trait State in Taxon A		
Canis familiaris - Small breeds			
	Trait State in Taxon B		
Canis familiaris - Giant breeds			
	Ancestral State		
Data not curated			
	Taxonomic Status		
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Domesticated^#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Canis lupus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Canis+lupus^#gephebase-summary-title)		Canis lupus familiaris (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Canis+lupus+familiaris^#gephebase-summary-title)	
	Common Name		Common Name
gray wolf		dog	
	Synonyms		Synonyms
gray wolf; grey wolf; Canis lupus Linnaeus, 1758		Canis canis; Canis domesticus; Canis familiaris; dog; dogs; Canis familiaris Linnaeus, 1758; Canis lupus familiaris Linnaeus, 1758	
	Rank		Rank
species		subspecies	
	Lineage		Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria; Carnivora; Caniformia; Canidae; Canis		cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria; Carnivora; Caniformia; Canidae; Canis; Canis lupus	
	Parent		Parent
Canis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9611)		Canis lupus (gray wolf) - (Rank: species) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9612)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
9612 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9612)		9615 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9615)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		Yes	
			Taxon B Description
		Canis familiaris - Giant breeds	

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Mus musculus
Igf1		P05017 (http://www.uniprot.org/uniprot/P05017)
	Synonyms	GenebankID or UniProtKB
Igf-1; Igf-I; C730016P09Rik		AH117168 (https://www.ncbi.nlm.nih.gov/nucore/AH117168)
	String	
-		
	Sequence Similarities	
Belongs to the insulin family.		
	GO - Molecular Function	
GO:0008083 : growth factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008083)		
GO:0005496 : steroid binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005496)		
GO:0005179 : hormone activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005179)		
GO:0005158 : insulin receptor binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005158)		
GO:0005159 : insulin-like growth factor receptor binding		

(<https://www.ebi.ac.uk/QuickGO/term/GO:0005159>)
GO:0005178 : integrin binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0005178>)
GO:0043539 : protein serine/threonine kinase activator activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043539>)

GO - Biological Process

GO:0043066 : negative regulation of apoptotic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043066>)
GO:0007399 : nervous system development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007399>)
GO:0045944 : positive regulation of transcription by RNA polymerase II
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045944>)
GO:0006417 : regulation of translation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006417>)
GO:0030166 : proteoglycan biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030166>)
GO:0045893 : positive regulation of transcription, DNA-templated
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045893>)
GO:0010629 : negative regulation of gene expression
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010629>)
GO:1901215 : negative regulation of neuron death
(<https://www.ebi.ac.uk/QuickGO/term/GO:1901215>)
GO:0051246 : regulation of protein metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051246>)
GO:0008283 : cell proliferation (<https://www.ebi.ac.uk/QuickGO/term/GO:0008283>)
GO:0097192 : extrinsic apoptotic signaling pathway in absence of ligand
(<https://www.ebi.ac.uk/QuickGO/term/GO:0097192>)
GO:0008284 : positive regulation of cell proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0008284>)
GO:0050731 : positive regulation of peptidyl-tyrosine phosphorylation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0050731>)
GO:0051897 : positive regulation of protein kinase B signaling
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051897>)
GO:0046579 : positive regulation of Ras protein signal transduction
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046579>)
GO:0035264 : multicellular organism growth
(<https://www.ebi.ac.uk/QuickGO/term/GO:0035264>)
GO:0008285 : negative regulation of cell proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0008285>)
GO:2001237 : negative regulation of extrinsic apoptotic signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:2001237>)
GO:0010628 : positive regulation of gene expression
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010628>)
GO:0043568 : positive regulation of insulin-like growth factor receptor signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043568>)
GO:0043410 : positive regulation of MAPK cascade
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043410>)
GO:0060740 : prostate gland epithelium morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060740>)
GO:0060736 : prostate gland growth (<https://www.ebi.ac.uk/QuickGO/term/GO:0060736>)
GO:0030307 : positive regulation of cell growth
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030307>)
GO:0048468 : cell development (<https://www.ebi.ac.uk/QuickGO/term/GO:0048468>)
GO:0001649 : osteoblast differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001649>)
GO:0050679 : positive regulation of epithelial cell proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0050679>)
GO:0045669 : positive regulation of osteoblast differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045669>)
GO:0007623 : circadian rhythm (<https://www.ebi.ac.uk/QuickGO/term/GO:0007623>)
GO:0030324 : lung development (<https://www.ebi.ac.uk/QuickGO/term/GO:0030324>)
GO:0010468 : regulation of gene expression
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010468>)
GO:0030104 : water homeostasis (<https://www.ebi.ac.uk/QuickGO/term/GO:0030104>)
GO:0045840 : positive regulation of mitotic nuclear division
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045840>)
GO:0048009 : insulin-like growth factor receptor signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048009>)
GO:0001974 : blood vessel remodeling
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001974>)
GO:0010001 : glial cell differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010001>)
GO:0045471 : response to ethanol (<https://www.ebi.ac.uk/QuickGO/term/GO:0045471>)
GO:0048286 : lung alveolus development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048286>)
GO:0060463 : lung lobe morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060463>)
GO:0048661 : positive regulation of smooth muscle cell proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048661>)

GO:0060527 : prostate epithelial cord arborization involved in prostate glandular acinus morphogenesis (<https://www.ebi.ac.uk/QuickGO/term/GO:0060527>)

GO:1990314 : cellular response to insulin-like growth factor stimulus (<https://www.ebi.ac.uk/QuickGO/term/GO:1990314>)

GO:1905564 : positive regulation of vascular endothelial cell proliferation (<https://www.ebi.ac.uk/QuickGO/term/GO:1905564>)

GO:0007613 : memory (<https://www.ebi.ac.uk/QuickGO/term/GO:0007613>)

GO:0046326 : positive regulation of glucose import (<https://www.ebi.ac.uk/QuickGO/term/GO:0046326>)

GO:0000187 : activation of MAPK activity (<https://www.ebi.ac.uk/QuickGO/term/GO:0000187>)

GO:0042531 : positive regulation of tyrosine phosphorylation of STAT protein (<https://www.ebi.ac.uk/QuickGO/term/GO:0042531>)

GO:0009408 : response to heat (<https://www.ebi.ac.uk/QuickGO/term/GO:0009408>)

GO:0030335 : positive regulation of cell migration (<https://www.ebi.ac.uk/QuickGO/term/GO:0030335>)

GO:2000679 : positive regulation of transcription regulatory region DNA binding (<https://www.ebi.ac.uk/QuickGO/term/GO:2000679>)

GO:0014068 : positive regulation of phosphatidylinositol 3-kinase signaling (<https://www.ebi.ac.uk/QuickGO/term/GO:0014068>)

GO:0042127 : regulation of cell proliferation (<https://www.ebi.ac.uk/QuickGO/term/GO:0042127>)

GO:0032148 : activation of protein kinase B activity (<https://www.ebi.ac.uk/QuickGO/term/GO:0032148>)

GO:0035630 : bone mineralization involved in bone maturation (<https://www.ebi.ac.uk/QuickGO/term/GO:0035630>)

GO:0048754 : branching morphogenesis of an epithelial tube (<https://www.ebi.ac.uk/QuickGO/term/GO:0048754>)

GO:0001775 : cell activation (<https://www.ebi.ac.uk/QuickGO/term/GO:0001775>)

GO:1904646 : cellular response to amyloid-beta (<https://www.ebi.ac.uk/QuickGO/term/GO:1904646>)

GO:0071333 : cellular response to glucose stimulus (<https://www.ebi.ac.uk/QuickGO/term/GO:0071333>)

GO:0050650 : chondroitin sulfate proteoglycan biosynthetic process (<https://www.ebi.ac.uk/QuickGO/term/GO:0050650>)

GO:0050974 : detection of mechanical stimulus involved in sensory perception (<https://www.ebi.ac.uk/QuickGO/term/GO:0050974>)

GO:0070371 : ERK1 and ERK2 cascade (<https://www.ebi.ac.uk/QuickGO/term/GO:0070371>)

GO:0031017 : exocrine pancreas development (<https://www.ebi.ac.uk/QuickGO/term/GO:0031017>)

GO:0048839 : inner ear development (<https://www.ebi.ac.uk/QuickGO/term/GO:0048839>)

GO:0060426 : lung vasculature development (<https://www.ebi.ac.uk/QuickGO/term/GO:0060426>)

GO:0030879 : mammary gland development (<https://www.ebi.ac.uk/QuickGO/term/GO:0030879>)

GO:0014896 : muscle hypertrophy (<https://www.ebi.ac.uk/QuickGO/term/GO:0014896>)

GO:0045445 : myoblast differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0045445>)

GO:0051450 : myoblast proliferation (<https://www.ebi.ac.uk/QuickGO/term/GO:0051450>)

GO:0014904 : myotube cell development (<https://www.ebi.ac.uk/QuickGO/term/GO:0014904>)

GO:0060766 : negative regulation of androgen receptor signaling pathway (<https://www.ebi.ac.uk/QuickGO/term/GO:0060766>)

GO:1904193 : negative regulation of cholangiocyte apoptotic process (<https://www.ebi.ac.uk/QuickGO/term/GO:1904193>)

GO:0043154 : negative regulation of cysteine-type endopeptidase activity involved in apoptotic process (<https://www.ebi.ac.uk/QuickGO/term/GO:0043154>)

GO:0070373 : negative regulation of ERK1 and ERK2 cascade (<https://www.ebi.ac.uk/QuickGO/term/GO:0070373>)

GO:0002683 : negative regulation of immune system process (<https://www.ebi.ac.uk/QuickGO/term/GO:0002683>)

GO:0010656 : negative regulation of muscle cell apoptotic process (<https://www.ebi.ac.uk/QuickGO/term/GO:0010656>)

GO:1900142 : negative regulation of oligodendrocyte apoptotic process (<https://www.ebi.ac.uk/QuickGO/term/GO:1900142>)

GO:0060283 : negative regulation of oocyte development (<https://www.ebi.ac.uk/QuickGO/term/GO:0060283>)

GO:0050732 : negative regulation of peptidyl-tyrosine phosphorylation (<https://www.ebi.ac.uk/QuickGO/term/GO:0050732>)

GO:0090201 : negative regulation of release of cytochrome c from mitochondria (<https://www.ebi.ac.uk/QuickGO/term/GO:0090201>)

GO:0034392 : negative regulation of smooth muscle cell apoptotic process (<https://www.ebi.ac.uk/QuickGO/term/GO:0034392>)

GO:1905460 : negative regulation of vascular associated smooth muscle cell apoptotic process (<https://www.ebi.ac.uk/QuickGO/term/GO:1905460>)

GO:0014065 : phosphatidylinositol 3-kinase signaling

(<https://www.ebi.ac.uk/QuickGO/term/GO:0014065>)
GO:0048015 : phosphatidylinositol-mediated signaling
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048015>)
GO:0042104 : positive regulation of activated T cell proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042104>)
GO:0043536 : positive regulation of blood vessel endothelial cell migration
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043536>)
GO:0070886 : positive regulation of calcineurin-NFAT signaling cascade
(<https://www.ebi.ac.uk/QuickGO/term/GO:0070886>)
GO:0010613 : positive regulation of cardiac muscle hypertrophy
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010613>)
GO:0061051 : positive regulation of cell growth involved in cardiac muscle cell development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0061051>)
GO:0021940 : positive regulation of cerebellar granule cell precursor proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0021940>)
GO:0043388 : positive regulation of DNA binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043388>)
GO:0045600 : positive regulation of fat cell differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045600>)
GO:0048146 : positive regulation of fibroblast proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048146>)
GO:0060252 : positive regulation of glial cell proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060252>)
GO:0045725 : positive regulation of glycogen biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045725>)
GO:0045821 : positive regulation of glycolytic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045821>)
GO:0010560 : positive regulation of glycoprotein biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010560>)
GO:2000288 : positive regulation of myoblast proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:2000288>)
GO:0033160 : positive regulation of protein import into nucleus, translocation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0033160>)
GO:0050714 : positive regulation of protein secretion
(<https://www.ebi.ac.uk/QuickGO/term/GO:0050714>)
GO:0071902 : positive regulation of protein serine/threonine kinase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0071902>)
GO:0014911 : positive regulation of smooth muscle cell migration
(<https://www.ebi.ac.uk/QuickGO/term/GO:0014911>)
GO:0090031 : positive regulation of steroid hormone biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0090031>)
GO:1904075 : positive regulation of trophectodermal cell proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:1904075>)
GO:1904707 : positive regulation of vascular smooth muscle cell proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:1904707>)
GO:0060741 : prostate gland stromal morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060741>)
GO:0043491 : protein kinase B signaling
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043491>)
GO:0050821 : protein stabilization (<https://www.ebi.ac.uk/QuickGO/term/GO:0050821>)
GO:0051924 : regulation of calcium ion transport
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051924>)
GO:0032878 : regulation of establishment or maintenance of cell polarity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032878>)
GO:0045428 : regulation of nitric oxide biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045428>)
GO:0001932 : regulation of protein phosphorylation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001932>)
GO:0007608 : sensory perception of smell
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007608>)
GO:0014834 : skeletal muscle satellite cell maintenance involved in skeletal muscle
regeneration (<https://www.ebi.ac.uk/QuickGO/term/GO:0014834>)
GO:0060509 : type I pneumocyte differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060509>)
GO:0060510 : type II pneumocyte differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060510>)

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:0005615 : extracellular space (<https://www.ebi.ac.uk/QuickGO/term/GO:0005615>)
GO:0043025 : neuronal cell body (<https://www.ebi.ac.uk/QuickGO/term/GO:0043025>)
GO:0035867 : α 5 β 3 integrin-IGF-1-IGF1R complex
(<https://www.ebi.ac.uk/QuickGO/term/GO:0035867>)
GO:0070382 : exocytic vesicle (<https://www.ebi.ac.uk/QuickGO/term/GO:0070382>)
GO:0042567 : insulin-like growth factor ternary complex
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042567>)
GO:0005614 : interstitial matrix (<https://www.ebi.ac.uk/QuickGO/term/GO:0005614>)
GO:0031091 : platelet alpha granule (<https://www.ebi.ac.uk/QuickGO/term/GO:0031091>)

Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Unknown~#gephebase-summary-title)	Presumptive Null
Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=~Cis-regulatory~#gephebase-summary-title)	Molecular Type
Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=~Unknown~#gephebase-summary-title)	Aberration Type
Not identified / several haplotypes	Molecular Details of the Mutation
Association Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Association Mapping~#gephebase-summary-title)	Experimental Evidence
A single IGF1 allele is a major determinant of small size in dogs. (2007) (https://pubmed.ncbi.nlm.nih.gov/17412960)	Main Reference
Sutter NB; Bustamante CD; Chase K; Gray MM; Zhao K; Zhu L; Padhukasahasram B; Karlins E; Davis S; Jones PG; Quignon P; Johnson GS; Parker HG; Fretwell N; Mosher DS; Lawler DF; Satyaraj E; Nordborg M; Lark KG; Wayne RK; Ostrander EA	Authors
The domestic dog exhibits greater diversity in body size than any other terrestrial vertebrate. We used a strategy that exploits the breed structure of dogs to investigate the genetic basis of size. First, through a genome-wide scan, we identified a major quantitative trait locus (QTL) on chromosome 15 influencing size variation within a single breed. Second, we examined genetic variation in the 15-megabase interval surrounding the QTL in small and giant breeds and found marked evidence for a selective sweep spanning a single gene (IGF1), encoding insulin-like growth factor 1. A single IGF1 single-nucleotide polymorphism haplotype is common to all small breeds and nearly absent from giant breeds, suggesting that the same causal sequence variant is a major contributor to body size in all small dogs.	Abstract
Derived variants at six genes explain nearly half of size reduction in dog breeds. (2013) (https://pubmed.ncbi.nlm.nih.gov/24026177)	Additional References

RELATED GEPHE

5 (growth hormone receptor (GHR), HMGA2, Insulin-like growth factor receptor 1 (IGF1R), SMAD family member 2 (SMAD2), stanniocalcin 2 (STC2)) (https://www.gephebase.org/search-criteria?/or+Taxon ID=~9612~/and+Trait=Body size/or+Taxon ID=~9615~/and+Trait=Body size/and+groupHaplotypes=true#gephebase-summary-title)	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS