

HMGA2 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~HMGA2*#gephebase-summary-title)	Gephebase Gene	GP00000484	GepheID
Published	Entry Status	Martin	Main curator

Taxon A		Taxon B	
Morphology (https://www.gephebase.org/search-criteria?/and+Trait=^Morphology^#gephebase-summary-title)	Trait Category	Canis lupus (https://www.gephebase.org/search-criteria?/and+Trait=^Body size^#gephebase-summary-title)	Trait
Canis familiaris - various breeds	Trait State in Taxon A	Canis familiaris - various breeds	Trait State in Taxon B
Taxon A	Ancestral State	Taxon A	Ancestral State
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated^#gephebase-summary-title)	Taxonomic Status	Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated^#gephebase-summary-title)	Taxonomic Status
Canis lupus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Canis lupus^#gephebase-summary-title)	Latin Name	Canis lupus familiaris (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Canis lupus familiaris^#gephebase-summary-title)	Latin Name
gray wolf	Common Name	dog	Common Name
gray wolf; grey wolf; Canis lupus Linnaeus, 1758	Synonyms	Canis canis; Canis domesticus; Canis familiaris; dog; dogs; Canis familiaris Linnaeus, 1758; Canis lupus familiaris Linnaeus, 1758	Synonyms
species	Rank	subspecies	Rank
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	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; Canis lupus	Lineage
Canis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9611)	Parent	Canis lupus (gray wolf) - (Rank: species) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9612)	Parent
9612 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9612)	NCBI Taxonomy ID	9615 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9615)	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

HMGA2	Generic Gene Name	P52926 (http://www.uniprot.org/uniprot/P52926)	UniProtKB Homo sapiens
BABL; LIPO; HMGIC; HMGI-C; STQTL9	Synonyms	AGV01257 (https://www.ncbi.nlm.nih.gov/nuccore/AGV01257)	GenebankID or UniProtKB
9606.ENSPO0000384026 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSPO0000384026)	String		
	Sequence Similarities		
Belongs to the HMGA family.			
	GO - Molecular Function		
GO:0008134 : transcription factor binding (https://www.ebi.ac.uk/QuickGO/term/GO:0008134)			
GO:0044212 : transcription regulatory region DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0044212)			
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)			
GO:0000981 : DNA-binding transcription factor activity, RNA polymerase II-specific			

(<https://www.ebi.ac.uk/QuickGO/term/GO:0000981>)
GO:0001077 : proximal promoter DNA-binding transcription activator activity, RNA polymerase II-specific (<https://www.ebi.ac.uk/QuickGO/term/GO:0001077>)
GO:0000978 : RNA polymerase II proximal promoter sequence-specific DNA binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0000978>)
GO:0003680 : AT DNA binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0003680>)
GO:0001078 : proximal promoter DNA-binding transcription repressor activity, RNA polymerase II-specific (<https://www.ebi.ac.uk/QuickGO/term/GO:0001078>)
GO:0003712 : transcription coregulator activity (<https://www.ebi.ac.uk/QuickGO/term/GO:0003712>)
GO:0051575 : 5'-deoxyribose-5-phosphate lyase activity (<https://www.ebi.ac.uk/QuickGO/term/GO:0051575>)
GO:0070742 : C2H2 zinc finger domain binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0070742>)
GO:0035497 : cAMP response element binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0035497>)
GO:0008301 : DNA binding, bending (<https://www.ebi.ac.uk/QuickGO/term/GO:0008301>)
GO:0003906 : DNA-(apurinic or apyrimidinic site) endonuclease activity (<https://www.ebi.ac.uk/QuickGO/term/GO:0003906>)
GO:0004677 : DNA-dependent protein kinase activity (<https://www.ebi.ac.uk/QuickGO/term/GO:0004677>)
GO:0035501 : MH1 domain binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0035501>)
GO:0035500 : MH2 domain binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0035500>)
GO:0031492 : nucleosomal DNA binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0031492>)
GO:0046332 : SMAD binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0046332>)

GO - Biological Process

GO:0007275 : multicellular organism development (<https://www.ebi.ac.uk/QuickGO/term/GO:0007275>)
GO:0009615 : response to virus (<https://www.ebi.ac.uk/QuickGO/term/GO:0009615>)
GO:0043066 : negative regulation of apoptotic process (<https://www.ebi.ac.uk/QuickGO/term/GO:0043066>)
GO:0045944 : positive regulation of transcription by RNA polymerase II (<https://www.ebi.ac.uk/QuickGO/term/GO:0045944>)
GO:0006355 : regulation of transcription, DNA-templated (<https://www.ebi.ac.uk/QuickGO/term/GO:0006355>)
GO:0000122 : negative regulation of transcription by RNA polymerase II (<https://www.ebi.ac.uk/QuickGO/term/GO:0000122>)
GO:0045892 : negative regulation of transcription, DNA-templated (<https://www.ebi.ac.uk/QuickGO/term/GO:0045892>)
GO:0045893 : positive regulation of transcription, DNA-templated (<https://www.ebi.ac.uk/QuickGO/term/GO:0045893>)
GO:0051301 : cell division (<https://www.ebi.ac.uk/QuickGO/term/GO:0051301>)
GO:0010628 : positive regulation of gene expression (<https://www.ebi.ac.uk/QuickGO/term/GO:0010628>)
GO:2000774 : positive regulation of cellular senescence (<https://www.ebi.ac.uk/QuickGO/term/GO:2000774>)
GO:0035986 : senescence-associated heterochromatin focus assembly (<https://www.ebi.ac.uk/QuickGO/term/GO:0035986>)
GO:0006325 : chromatin organization (<https://www.ebi.ac.uk/QuickGO/term/GO:0006325>)
GO:0048863 : stem cell differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0048863>)
GO:0001837 : epithelial to mesenchymal transition (<https://www.ebi.ac.uk/QuickGO/term/GO:0001837>)
GO:0048762 : mesenchymal cell differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0048762>)
GO:0048333 : mesodermal cell differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0048333>)
GO:2000648 : positive regulation of stem cell proliferation (<https://www.ebi.ac.uk/QuickGO/term/GO:2000648>)
GO:0043065 : positive regulation of apoptotic process (<https://www.ebi.ac.uk/QuickGO/term/GO:0043065>)
GO:0002062 : chondrocyte differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0002062>)
GO:0045444 : fat cell differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0045444>)
GO:0040008 : regulation of growth (<https://www.ebi.ac.uk/QuickGO/term/GO:0040008>)
GO:0006284 : base-excision repair (<https://www.ebi.ac.uk/QuickGO/term/GO:0006284>)
GO:0035988 : chondrocyte proliferation (<https://www.ebi.ac.uk/QuickGO/term/GO:0035988>)
GO:0031052 : chromosome breakage (<https://www.ebi.ac.uk/QuickGO/term/GO:0031052>)
GO:0030261 : chromosome condensation (<https://www.ebi.ac.uk/QuickGO/term/GO:0030261>)
GO:0042769 : DNA damage response, detection of DNA damage (<https://www.ebi.ac.uk/QuickGO/term/GO:0042769>)
GO:0035987 : endodermal cell differentiation

(<https://www.ebi.ac.uk/QuickGO/term/GO:0035987>)
GO:0031507 : heterochromatin assembly
(<https://www.ebi.ac.uk/QuickGO/term/GO:0031507>)
GO:0035978 : histone H2A-S139 phosphorylation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0035978>)
GO:0003131 : mesodermal-endodermal cell signaling
(<https://www.ebi.ac.uk/QuickGO/term/GO:0003131>)
GO:0007095 : mitotic G2 DNA damage checkpoint
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007095>)
GO:0043922 : negative regulation by host of viral transcription
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043922>)
GO:2000773 : negative regulation of cellular senescence
(<https://www.ebi.ac.uk/QuickGO/term/GO:2000773>)
GO:0043392 : negative regulation of DNA binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043392>)
GO:2001033 : negative regulation of double-strand break repair via nonhomologous end joining (<https://www.ebi.ac.uk/QuickGO/term/GO:2001033>)
GO:0045869 : negative regulation of single stranded viral RNA replication via double stranded DNA intermediate (<https://www.ebi.ac.uk/QuickGO/term/GO:0045869>)
GO:0090402 : oncogene-induced cell senescence
(<https://www.ebi.ac.uk/QuickGO/term/GO:0090402>)
GO:0045766 : positive regulation of angiogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045766>)
GO:0071158 : positive regulation of cell cycle arrest
(<https://www.ebi.ac.uk/QuickGO/term/GO:0071158>)
GO:0071864 : positive regulation of cell proliferation in bone marrow
(<https://www.ebi.ac.uk/QuickGO/term/GO:0071864>)
GO:2000685 : positive regulation of cellular response to X-ray
(<https://www.ebi.ac.uk/QuickGO/term/GO:2000685>)
GO:2001022 : positive regulation of response to DNA damage stimulus
(<https://www.ebi.ac.uk/QuickGO/term/GO:2001022>)
GO:2000679 : positive regulation of transcription regulatory region DNA binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:2000679>)
GO:0010564 : regulation of cell cycle process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010564>)
GO:2001038 : regulation of cellular response to drug
(<https://www.ebi.ac.uk/QuickGO/term/GO:2001038>)
GO:2000036 : regulation of stem cell population maintenance
(<https://www.ebi.ac.uk/QuickGO/term/GO:2000036>)

GO - Cellular Component

GO:0005654 : nucleoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005654>)
GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)
GO:0035985 : senescence-associated heterochromatin focus
(<https://www.ebi.ac.uk/QuickGO/term/GO:0035985>)
GO:0000228 : nuclear chromosome (<https://www.ebi.ac.uk/QuickGO/term/GO:0000228>)
GO:0032993 : protein-DNA complex
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032993>)
GO:0071141 : SMAD protein complex (<https://www.ebi.ac.uk/QuickGO/term/GO:0071141>)

Presumptive Null

Unknown ([https://www.gephebase.org/search-criteria?/and+Presumptive Null="+Unknown"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive Null=))

Molecular Type

Unknown ([https://www.gephebase.org/search-criteria?/and+Molecular Type="+Unknown"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular Type=))

Aberration Type

Unknown ([https://www.gephebase.org/search-criteria?/and+Aberration Type="+Unknown"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration Type=))

Molecular Details of the Mutation

unknown

Experimental Evidence

Association Mapping ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence="+Association Mapping"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental Evidence=))

Main Reference

Tracking footprints of artificial selection in the dog genome. (2010) (<https://pubmed.ncbi.nlm.nih.gov/20080661>)

Authors

Akey JM; Ruhe AL; Akey DT; Wong AK; Connelly CF; Madeoy J; Nicholas TJ; Neff MW

Abstract

The size, shape, and behavior of the modern domesticated dog has been sculpted by artificial selection for at least 14,000 years. The genetic substrates of selective breeding, however, remain largely unknown. Here, we describe a genome-wide scan for selection in 275 dogs from 10 phenotypically diverse breeds that were genotyped for over 21,000 autosomal SNPs. We identified 155 genomic regions that possess strong signatures of recent selection and contain candidate genes for phenotypes that vary most conspicuously among breeds, including size, coat color and texture, behavior, skeletal morphology, and physiology. In addition, we demonstrate a significant association between HAS2 and skin wrinkling in the Shar-Pei, and provide evidence that regulatory evolution has played a prominent role in the phenotypic diversification of modern dog breeds. Our results provide a first-generation map of selection in the dog, illustrate how such maps can rapidly inform the genetic basis of canine phenotypic variation, and provide a framework for delineating the mechanistic basis of how artificial selection promotes rapid and pronounced phenotypic evolution.

Additional References

Linked genetic variants on chromosome 10 control ear morphology and body mass among dog breeds. (2015) (<https://pubmed.ncbi.nlm.nih.gov/26100605>)

5 (growth hormone receptor (GHR), Insulin-like growth factor 1 (IGF1), 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 Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS