

# GEPHE SUMMARY

EGLN1 ( <a href="https://www.gephebase.org/search-criteria?/and+Gene">https://www.gephebase.org/search-criteria?/and+Gene</a> Gephebase=^EGLN1^#gephebase-summary-title)	Gephebase Gene	GP00000262	GephelD
Published	Entry Status	Martin	Main curator

## PHENOTYPIC CHANGE

Trait Category			
Physiology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait">https://www.gephebase.org/search-criteria?/and+Trait</a> Category=^Physiology^#gephebase-summary-title)	Trait		
Hypoxia response ( <a href="https://www.gephebase.org/search-criteria?/and+Trait=^Hypoxia">https://www.gephebase.org/search-criteria?/and+Trait=^Hypoxia</a> response^#gephebase-summary-title)	Trait State in Taxon A		
Homo sapiens - lowlands	Trait State in Taxon B		
Homo sapiens - Andean highlands	Ancestral State		
Data not curated	Taxonomic Status		
Intraspecific ( <a href="https://www.gephebase.org/search-criteria?/and+Taxonomic">https://www.gephebase.org/search-criteria?/and+Taxonomic</a> Status=^Intraspecific^#gephebase-summary-title)			
Taxon A	Latin Name	Taxon B	Latin Name
Homo sapiens ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Homo+sapiens^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Homo+sapiens^#gephebase-summary-title</a> )		Homo sapiens ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Homo+sapiens^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Homo+sapiens^#gephebase-summary-title</a> )	
human	Common Name	human	Common Name
human; man; Homo sapiens Linnaeus, 1758; Home sapiens; Homo sampaies; Homo sapien; Homo sapians; Homo sapien; Homo sapience; Homo sapiense; Homo sapients; Homo sapines; Homo spaiens; Homo spiens; Homo sapiens	Synonyms	human; man; Homo sapiens Linnaeus, 1758; Home sapiens; Homo sampaies; Homo sapien; Homo sapians; Homo sapien; Homo sapience; Homo sapiense; Homo sapients; Homo sapines; Homo spaiens; Homo spiens; Homo sapiens	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Euarchontoglires; Primates; Haplorrhini; Simiiformes; Catarrhini; Hominoidea; Hominidae; Homininae; Homo	Lineage	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Euarchontoglires; Primates; Haplorrhini; Simiiformes; Catarrhini; Hominoidea; Hominidae; Homininae; Homo	Lineage
Homo () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9605">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9605</a> )	Parent	Homo () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9605">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9605</a> )	Parent
9606 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9606">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9606</a> )	NCBI Taxonomy ID	9606 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9606">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9606</a> )	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

## GENOTYPIC CHANGE

EGLN1	Generic Gene Name	UniProtKB Homo sapiens
HPH2; PHD2; SM20; ECYT3; HALAH; HPH-2; HIFPH2; ZMYND6; C1orf12; HIF-PH2; PNAS-118; PNAS-137	Synonyms	GenebankID or UniProtKB
9606.ENSPO0000355601 ( <a href="http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9606.ENSPO0000355601">http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9606.ENSPO0000355601</a> )	String	AF277176 ( <a href="https://www.ncbi.nlm.nih.gov/nuccore/AF277176">https://www.ncbi.nlm.nih.gov/nuccore/AF277176</a> )
-	Sequence Similarities	
GO:0016706 : oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0016706">https://www.ebi.ac.uk/QuickGO/term/GO:0016706</a> )	GO - Molecular Function	

GO:0019899 : enzyme binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0019899>)  
GO:0008198 : ferrous iron binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0008198>)  
GO:0031418 : L-ascorbic acid binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0031418>)  
GO:0031545 : peptidyl-proline 4-dioxygenase activity  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0031545>)  
GO:0031543 : peptidyl-proline dioxygenase activity  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0031543>)

#### GO - Biological Process

GO:0045944 : positive regulation of transcription by RNA polymerase II  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045944>)  
GO:1901214 : regulation of neuron death  
(<https://www.ebi.ac.uk/QuickGO/term/GO:1901214>)  
GO:0006879 : cellular iron ion homeostasis  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006879>)  
GO:0055008 : cardiac muscle tissue morphogenesis  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0055008>)  
GO:0060347 : heart trabecula formation  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060347>)  
GO:0060711 : labyrinthine layer development  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060711>)  
GO:0051344 : negative regulation of cyclic-nucleotide phosphodiesterase activity  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051344>)  
GO:0043433 : negative regulation of DNA-binding transcription factor activity  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043433>)  
GO:0032364 : oxygen homeostasis (<https://www.ebi.ac.uk/QuickGO/term/GO:0032364>)  
GO:0018401 : peptidyl-proline hydroxylation to 4-hydroxy-L-proline  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0018401>)  
GO:0045765 : regulation of angiogenesis  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045765>)  
GO:0099175 : regulation of postsynapse organization  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0099175>)  
GO:0099576 : regulation of protein catabolic process at postsynapse, modulating synaptic transmission (<https://www.ebi.ac.uk/QuickGO/term/GO:0099576>)  
GO:0061418 : regulation of transcription from RNA polymerase II promoter in response to hypoxia (<https://www.ebi.ac.uk/QuickGO/term/GO:0061418>)  
GO:0001666 : response to hypoxia (<https://www.ebi.ac.uk/QuickGO/term/GO:0001666>)  
GO:0071731 : response to nitric oxide (<https://www.ebi.ac.uk/QuickGO/term/GO:0071731>)  
GO:0060412 : ventricular septum morphogenesis  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060412>)

#### GO - Cellular Component

GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)  
GO:0005829 : cytosol (<https://www.ebi.ac.uk/QuickGO/term/GO:0005829>)  
GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)  
GO:0098978 : glutamatergic synapse  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0098978>)  
GO:0014069 : postsynaptic density (<https://www.ebi.ac.uk/QuickGO/term/GO:0014069>)

Presumptive Null

Unknown (<https://www.gephebase.org/search-criteria?/and+Presumptive+Null=^Unknown^#gephebase-summary-title>)

Molecular Type

Unknown (<https://www.gephebase.org/search-criteria?/and+Molecular+Type=^Unknown^#gephebase-summary-title>)

Aberration Type

Unknown (<https://www.gephebase.org/search-criteria?/and+Aberration+Type=^Unknown^#gephebase-summary-title>)

Molecular Details of the Mutation

unknown

Experimental Evidence

Association Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=^Association+Mapping^#gephebase-summary-title>)

Main Reference

Identifying signatures of natural selection in Tibetan and Andean populations using dense genome scan data. (2010) (<https://pubmed.ncbi.nlm.nih.gov/20838600>)

Authors

Bigham A; Bauchet M; Pinto D; Mao X; Akey JM; Mei R; Scherer SW; Julian CG; Wilson MJ; LÃ³pez HerrÃ©ez D; Brutsaert T; Parra EJ; Moore LG; Shrimer MD

Abstract

High-altitude hypoxia (reduced inspired oxygen tension due to decreased barometric pressure) exerts severe physiological stress on the human body. Two high-altitude regions where humans have lived for millennia are the Andean Altiplano and the Tibetan Plateau. Populations living in these regions exhibit unique circulatory, respiratory, and hematological adaptations to life at high altitude. Although these responses have been well characterized physiologically, their underlying genetic basis remains unknown. We performed a genome scan to identify genes showing evidence of adaptation to hypoxia. We looked across each chromosome to identify genomic regions with previously unknown function with respect to altitude phenotypes. In addition, groups of genes functioning in oxygen metabolism and sensing were examined to test the hypothesis that particular pathways have been involved in genetic adaptation to altitude. Applying four population genetic statistics commonly used for detecting signatures of natural selection, we identified selection-nominated candidate genes and gene regions in these two populations (Andeans and Tibetans) separately. The Tibetan and Andean patterns of genetic adaptation are largely distinct from one another, with both populations showing evidence of positive natural selection in different genes or gene regions. Interestingly, one gene previously known to be important in cellular oxygen sensing, EGLN1 (also known as PHD2), shows evidence of positive selection in both Tibetans and Andeans. However, the pattern of variation for this gene differs between the two populations. Our results indicate that several key HIF-regulatory and targeted genes are responsible for adaptation to high altitude in Andeans and Tibetans, and several different chromosomal regions are implicated in the putative response to selection. These data suggest a genetic role in high-altitude adaption and provide a basis for future genotype/phenotype association studies necessary to confirm the role of selection-nominated candidate genes and gene regions in adaptation to altitude.

Additional References

Related Genes

4 (BHLHE41, EPAS1, PPAR-alpha, hemoglobin; HBA and HBB) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=%9606%/and+Trait=Hypoxia response/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

1 (<https://www.gephebase.org/search-criteria?/or+Gene Gephebase=%EGLN1%/and+Taxon ID=%9606%/or+Gene Gephebase=%EGLN1%/and+Taxon ID=%9606%#gephebase-summary-title>)

## EXTERNAL LINKS

## COMMENTS