GEPHE SUMMARY

Gephebase Gene
Kit ligand (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Kit ligand^#gephebase-summary-title)

GepheID
GP00001349

Entry Status
Published

Main curator
Prigent

PHENOTYPIC CHANGE

Trait Category
Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Morphology^#gephebase-summary-title)

Trait
Coloration (hair) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration (hair)^#gephebase-summary-title)

Trait State in Taxon A
Human-brown hair

Trait State in Taxon B
Human northern Europeans ; blond hair

Ancestral State
Taxon A

Taxonomic Status
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)

Taxon A

Latin Name
Homo sapiens (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Homo sapiens^#gephebase-summary-title)

Common Name
human

Synonyms
human; man; Homo sapiens Linnaeus, 1758; Home sapiens; Homo sampiens; Homo sapeins; Homo sapian; Homo sapians; Homo sapien; Homo sapience; Homo sapiense; Homo sapients; Homo sapines; Homo spaiens; Homo spiens; Humo sapiens

Rank
species

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

Parent
Homo () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9605)

NCBI Taxonomy ID
9606 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9606)

is Taxon A an Infraspecies?
No

Taxon B

Latin Name
Homo sapiens (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Homo sapiens^#gephebase-summary-title)

Common Name
human

Synonyms
human; man; Homo sapiens Linnaeus, 1758; Home sapiens; Homo sampiens; Homo sapeins; Homo sapian; Homo sapians; Homo sapien; Homo sapience; Homo sapiense; Homo sapients; Homo sapines; Homo spaiens; Homo spiens; Humo sapiens

Rank
species

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

Parent
Homo () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9605)

NCBI Taxonomy ID
9606 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9606)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
KITLG

Synonyms
SF; MGF; SCF; SLF; DCUA; FPH2; FPHH; KL-1; Kitl; SHEP7; DFNA69

String
9606.ENSP00000228280 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9606.ENSP00000228280)

Sequence Similarities
Belongs to the SCF family.

GO - Molecular Function
GO:0005125 : cytokine activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005125)
GO:0008083 : growth factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008083)
GO:0046934 : phosphatidylinositol-4,5-bisphosphate 3-kinase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0046934)

UniProtKB Homo sapiens
P21583 (http://www.uniprot.org/uniprot/P21583)

GenebankID or UniProtKB
()

GO:0005088 : Ras guanyl-nucleotide exchange factor activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0005088)
GO:0005173 : stem cell factor receptor binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0005173)

GO - Biological Process

GO:0007155 : cell adhesion (https://www.ebi.ac.uk/QuickGO/term/GO:0007155)
GO:0007165 : signal transduction (https://www.ebi.ac.uk/QuickGO/term/GO:0007165)
GO:0001755 : neural crest cell migration
(https://www.ebi.ac.uk/QuickGO/term/GO:0001755)
GO:0008283 : cell proliferation (https://www.ebi.ac.uk/QuickGO/term/GO:0008283)
GO:0035234 : ectopic germ cell programmed cell death
(https://www.ebi.ac.uk/QuickGO/term/GO:0035234)
GO:0035162 : embryonic hemopoiesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0035162)
GO:0097192 : extrinsic apoptotic signaling pathway in absence of ligand
(https://www.ebi.ac.uk/QuickGO/term/GO:0097192)
GO:0008584 : male gonad development
(https://www.ebi.ac.uk/QuickGO/term/GO:0008584)
GO:0000165 : MAPK cascade (https://www.ebi.ac.uk/QuickGO/term/GO:0000165)
GO:0033026 : negative regulation of mast cell apoptotic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0033026)
GO:0001541 : ovarian follicle development
(https://www.ebi.ac.uk/QuickGO/term/GO:0001541)
GO:0008284 : positive regulation of cell proliferation
(https://www.ebi.ac.uk/QuickGO/term/GO:0008284)
GO:1902035 : positive regulation of hematopoietic stem cell proliferation
(https://www.ebi.ac.uk/QuickGO/term/GO:1902035)
GO:0002687 : positive regulation of leukocyte migration
(https://www.ebi.ac.uk/QuickGO/term/GO:0002687)
GO:0043406 : positive regulation of MAP kinase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0043406)
GO:0070668 : positive regulation of mast cell proliferation
(https://www.ebi.ac.uk/QuickGO/term/GO:0070668)
GO:0045636 : positive regulation of melanocyte differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0045636)
GO:0002763 : positive regulation of myeloid leukocyte differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0002763)
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 - Cellular Component

GO:0016021 : integral component of membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0016021)
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:0005576 : extracellular region (https://www.ebi.ac.uk/QuickGO/term/GO:0005576)
GO:0005615 : extracellular space (https://www.ebi.ac.uk/QuickGO/term/GO:0005615)
GO:0005856 : cytoskeleton (https://www.ebi.ac.uk/QuickGO/term/GO:0005856)
GO:0030175 : filopodium (https://www.ebi.ac.uk/QuickGO/term/GO:0030175)
GO:0030027 : lamellipodium (https://www.ebi.ac.uk/QuickGO/term/GO:0030027)

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

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

Molecular Details of the Mutation

A>G SNP(rs12821256) 350kb upstream of transcription start

Experimental Evidence

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

Main Reference

A molecular basis for classic blond hair color in Europeans. (2014) (https://pubmed.ncbi.nlm.nih.gov/24880339)

Authors

Guenther CA; Tasic B; Luo L; Bedell MA; Kingsley DM

Abstract

Hair color differences are among the most obvious examples of phenotypic variation in humans. Although genome-wide association studies (GWAS) have implicated multiple loci in human pigment variation, the causative base-pair changes are still largely unknown. Here we dissect a regulatory region of the KITLG gene (encoding KIT ligand) that is significantly associated with common blond hair color in northern Europeans. Functional tests demonstrate that the region contains a regulatory enhancer that drives expression in developing hair follicles. This enhancer contains a common SNP (rs12821256) that alters a binding site for the lymphoid enhancer-binding factor 1 (LEF1) transcription factor, reducing LEF1 responsiveness and enhancer activity in cultured human keratinocytes. Mice carrying ancestral or derived variants of the human KITLG enhancer exhibit significant differences in hair pigmentation, confirming that altered regulation of an essential growth factor contributes to the classic blond hair phenotype found in northern Europeans.

Additional References

RELATED GEPHE

Related Genes

14 (Agouti (ASIP), EGFR, EIF2S2, GSS (glutathione synthetase), IRF4, MC1R, MFSD12, Oca2, OPRM1, SLC24A5 (NCKX5), SLC45A2=MATP, TPCN2, tyrosinase (TYR), tyrosinase-related protein 1 (TYRP1)) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^9606^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^Kit ligand^/and+Taxon ID=^9606^/or+Gene Gephebase=^Kit ligand^/and+Taxon ID=^9606^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

mutation alters a sequence that resembles a consensus LEF binding motif