GEPHE SUMMARY

Gephebase Gene
Kit ligand

GephelD
GP00001349

Entry Status
Published

Main curator
Prigent

PHENOTYPIC CHANGE

Trait Category
Morphology

Trait
Coloration (hair)

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

Taxon A

Latin Name
Homo sapiens

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)

NCBI Taxonomy ID
9606

is Taxon A an Infraspecies?
No

Taxon B

Latin Name
Homo sapiens

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)

NCBI Taxonomy 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

Sequence Similarities
Belongs to the SCF family.

GO - Molecular Function
GO:0005125 : cytokine activity
GO:0008083 : growth factor activity
GO:0046934 : phosphatidylinositol-4,5-bisphosphate 3-kinase activity
GO:0005088 : Ras guanyl-nucleotide exchange factor activity
GO:0005173 : stem cell factor receptor binding

GO - Biological Process
GO:0007155 : cell adhesion

UniProtKB Homo sapiens
P21583

GenebankID or UniProtKB

GO:0007165 : signal transduction
GO:0001755 : neural crest cell migration
GO:0008283 : cell proliferation
GO:0035234 : ectopic germ cell programmed cell death
GO:0035162 : embryonic hemopoiesis
GO:0097192 : extrinsic apoptotic signaling pathway in absence of ligand
GO:0008584 : male gonad development
GO:0000165 : MAPK cascade
GO:0033026 : negative regulation of mast cell apoptotic process
GO:0001541 : ovarian follicle development
GO:0008284 : positive regulation of cell proliferation
GO:1902035 : positive regulation of hematopoietic stem cell proliferation
GO:0002687 : positive regulation of leukocyte migration
GO:0043406 : positive regulation of MAP kinase activity
GO:0070668 : positive regulation of mast cell proliferation
GO:0045636 : positive regulation of melanocyte differentiation
GO:0002763 : positive regulation of myeloid leukocyte differentiation
GO:0050731 : positive regulation of peptidyl-tyrosine phosphorylation
GO:0051897 : positive regulation of protein kinase B signaling
GO:0046579 : positive regulation of Ras protein signal transduction

GO - Cellular Component
GO:0016021 : integral component of membrane
GO:0005886 : plasma membrane
GO:0005737 : cytoplasm
GO:0005576 : extracellular region
GO:0005615 : extracellular space
GO:0005856 : cytoskeleton
GO:0030175 : filopodium
GO:0030027 : lamellipodium

Presumptive Null
No

Molecular Type
Cis-regulatory

Aberration Type
SNP

Molecular Details of the Mutation
A>G SNP(rs12821256) 350kb upstream of transcription start

Experimental Evidence
Association Mapping

Main Reference
A molecular basis for classic blond hair color in Europeans. (2014)

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), HERC2, IRF4, MC1R, Oca2, OPRM1, SLC24A5 (NCKX5), SLC45A2=MATP, TPCN2, tyrosinase (TYR), tyrosinase-related protein 1 (TYRP1))
Related Haplotypes
1

COMMENTS

mutation alters a sequence that resembles a consensus LEF binding motif