GEPHE SUMMARY

Gephebase Gene
LPAR1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^LPAR1^#gephebase-summary-title)
Entry Status
Published

GepheID
GP00001612
Main curator
Prigent

PHENOTYPIC CHANGE

Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)
Trait
Hematopoiesis (blood monocyte count) (https://www.gephebase.org/search-criteria?/and+Trait=^Hematopoiesis (blood monocyte count)^#gephebase-summary-title)
Trait State in Taxon A
Human - Estonia Biobank
Trait State in Taxon B
Human - Estonia Biobank
Ancestral State
Unknown
Taxonomic Status
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)

	Taxon A	Taxon B
Latin Name	Homo sapiens (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Homo sapiens^#gephebase-summary-title)	Homo sapiens (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Homo sapiens^#gephebase-summary-title)
Common Name	human	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	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	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	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)	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)	9606 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9606)
is Taxon A an Infraspecies? / is Taxon B an Infraspecies?	Yes	Yes
Taxon A Description / Taxon B Description	Human - Estonia Biobank	Human - Estonia Biobank

GENOTYPIC CHANGE

Generic Gene Name
LPAR1
Synonyms
EDG2; LPA1; VZG1; GPR26; edg-2; vzg-1; Gpcr26; Mrec1.3; rec.1.3
String
9606.ENSP00000351755 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 9606.ENSP00000351755)
Sequence Similarities
Belongs to the G-protein coupled receptor 1 family.
GO - Molecular Function
GO:0030165 : PDZ domain binding (https://www.ebi.ac.uk/QuickGO/term/GO:0030165)
GO:0004930 : G protein-coupled receptor activity

UniProtKB Homo sapiens
Q92633 (http://www.uniprot.org/uniprot/Q92633)
GenebankID or UniProtKB
()

(https://www.ebi.ac.uk/QuickGO/term/GO:0004930)
GO:0001965 : G-protein alpha-subunit binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0001965)
GO:0035727 : lysophosphatidic acid binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0035727)
GO:0070915 : lysophosphatidic acid receptor activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0070915)

GO - Biological Process

GO:0007186 : G protein-coupled receptor signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0007186)
GO:0010977 : negative regulation of neuron projection development
(https://www.ebi.ac.uk/QuickGO/term/GO:0010977)
GO:0060999 : positive regulation of dendritic spine development
(https://www.ebi.ac.uk/QuickGO/term/GO:0060999)
GO:0043410 : positive regulation of MAPK cascade
(https://www.ebi.ac.uk/QuickGO/term/GO:0043410)
GO:0008360 : regulation of cell shape
(https://www.ebi.ac.uk/QuickGO/term/GO:0008360)
GO:0007204 : positive regulation of cytosolic calcium ion concentration
(https://www.ebi.ac.uk/QuickGO/term/GO:0007204)
GO:0060326 : cell chemotaxis (https://www.ebi.ac.uk/QuickGO/term/GO:0060326)
GO:0043123 : positive regulation of I-kappaB kinase/NF-kappaB signaling
(https://www.ebi.ac.uk/QuickGO/term/GO:0043123)
GO:0043065 : positive regulation of apoptotic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0043065)
GO:0021549 : cerebellum development
(https://www.ebi.ac.uk/QuickGO/term/GO:0021549)
GO:0000187 : activation of MAPK activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0000187)
GO:0007193 : adenylate cyclase-inhibiting G protein-coupled receptor signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0007193)
GO:0042552 : myelination (https://www.ebi.ac.uk/QuickGO/term/GO:0042552)
GO:0051482 : positive regulation of cytosolic calcium ion concentration involved in
phospholipase C-activating G protein-coupled signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0051482)
GO:0035025 : positive regulation of Rho protein signal transduction
(https://www.ebi.ac.uk/QuickGO/term/GO:0035025)
GO:0043951 : negative regulation of cAMP-mediated signaling
(https://www.ebi.ac.uk/QuickGO/term/GO:0043951)
GO:0014003 : oligodendrocyte development
(https://www.ebi.ac.uk/QuickGO/term/GO:0014003)
GO:0007202 : activation of phospholipase C activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0007202)
GO:0032060 : bleb assembly (https://www.ebi.ac.uk/QuickGO/term/GO:0032060)
GO:1904566 : cellular response to 1-oleoyl-sn-glycerol 3-phosphate
(https://www.ebi.ac.uk/QuickGO/term/GO:1904566)
GO:0071453 : cellular response to oxygen levels
(https://www.ebi.ac.uk/QuickGO/term/GO:0071453)
GO:0022038 : corpus callosum development
(https://www.ebi.ac.uk/QuickGO/term/GO:0022038)
GO:0021554 : optic nerve development
(https://www.ebi.ac.uk/QuickGO/term/GO:0021554)
GO:0071673 : positive regulation of smooth muscle cell chemotaxis
(https://www.ebi.ac.uk/QuickGO/term/GO:0071673)
GO:0051496 : positive regulation of stress fiber assembly
(https://www.ebi.ac.uk/QuickGO/term/GO:0051496)

GO - Cellular Component

GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)
GO:0005887 : integral component of plasma membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0005887)
GO:0043025 : neuronal cell body (https://www.ebi.ac.uk/QuickGO/term/GO:0043025)
GO:0005768 : endosome (https://www.ebi.ac.uk/QuickGO/term/GO:0005768)
GO:0043197 : dendritic spine (https://www.ebi.ac.uk/QuickGO/term/GO:0043197)
GO:0009986 : cell surface (https://www.ebi.ac.uk/QuickGO/term/GO:0009986)
GO:0043198 : dendritic shaft (https://www.ebi.ac.uk/QuickGO/term/GO:0043198)

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 at the associated SNP. 2 variants located in an uncharacterized long noncoding RNA

Experimental Evidence

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

Main Reference

Comprehensive population-based genome sequencing provides insight into hematopoietic regulatory mechanisms. (2017) (https://pubmed.ncbi.nlm.nih.gov/28031487)

Authors

Guo MH; Nandakumar SK; Ulirsch JC; Zekavat SM; Buenrostro JD; Natarajan P; Salem RM; Chiarle R; Mitt M; Kals M; PÃ¤rn K; Fischer K; Milani L; MÃ¤gi R; Palta P; Gabriel SB; Metspalu A; Lander ES; Kathiresan S; Hirschhorn JN; Esko T; Sankaran VG

Abstract

Genetic variants affecting hematopoiesis can influence commonly measured blood cell traits. To identify factors that affect hematopoiesis, we performed association studies for blood cell traits in the population-based Estonian Biobank using high-coverage whole-genome sequencing (WGS) in 2,284 samples and SNP genotyping in an additional 14,904 samples. Using up to 7,134 samples with available phenotype data, our analyses identified 17 associations across 14 blood cell traits. Integration of WGS-based fine-mapping and complementary epigenomic datasets provided evidence for causal mechanisms at several loci, including at a previously undiscovered basophil count-associated locus near the master hematopoietic transcription factor CEBPA The fine-mapped variant at this basophil count association near CEBPA overlapped an enhancer active in common myeloid progenitors and influenced its activity. In situ perturbation of this enhancer by CRISPR/Cas9 mutagenesis in hematopoietic stem and progenitor cells demonstrated that it is necessary for and specifically regulates CEBPA expression during basophil differentiation. We additionally identified basophil count-associated variation at another more pleiotropic myeloid enhancer near GATA2, highlighting regulatory mechanisms for ordered expression of master hematopoietic regulators during lineage specification. Our study illustrates how population-based genetic studies can provide key insights into poorly understood cell differentiation processes of considerable physiologic relevance.

Additional References

RELATED GEPHE

Related Genes

12 (ARHGEF3, BAK1, CCAAT-enhancer-binding protein alpha (CEBPA), F2RL2, GATA-binding protein 2 (GATA2), HBS1L-MYB, JAK2, JMJD1C, PIK3CG, PSMD13, TMPRSS6, WDR66) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^9606^/and+Trait=Hematopoiesis/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS