

GEPHE SUMMARY

<p>TMPRSS6 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~TMPRSS6^#gephebase-summary-title)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>Entry Status</p>	<p>GP00001618</p> <p>Prigent</p>	<p>GepheID</p> <p>Main curator</p>
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PHENOTYPIC CHANGE

<p>Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Physiology^#gephebase-summary-title)</p> <p>Hematopoiesis (mean blood corpuscular hemoglobin) (https://www.gephebase.org/search-criteria?/and+Trait=~Hematopoiesis+(mean+blood+corpuscular+hemoglobin)^#gephebase-summary-title)</p> <p>Human - Estonia Biobank</p> <p>Human - Estonia Biobank</p> <p>Unknown</p> <p>Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Intraspecific^#gephebase-summary-title)</p>	<p>Trait Category</p> <p>Trait</p> <p>Trait State in Taxon A</p> <p>Trait State in Taxon B</p> <p>Ancestral State</p> <p>Taxonomic Status</p>	<p>Taxon A</p> <p>Latin Name</p> <p>Homo sapiens (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Homo+sapiens^#gephebase-summary-title)</p> <p>Common Name</p> <p>human</p> <p>Synonyms</p> <p>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</p> <p>Rank</p> <p>species</p> <p>Lineage</p> <p>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</p> <p>Parent</p> <p>Homo () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9605)</p> <p>NCBI Taxonomy ID</p> <p>9606 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9606)</p> <p>is Taxon A an Intraspecies?</p> <p>Yes</p> <p>Taxon A Description</p> <p>Human - Estonia Biobank</p>	<p>Taxon B</p> <p>Latin Name</p> <p>Homo sapiens (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Homo+sapiens^#gephebase-summary-title)</p> <p>Common Name</p> <p>human</p> <p>Synonyms</p> <p>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</p> <p>Rank</p> <p>species</p> <p>Lineage</p> <p>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</p> <p>Parent</p> <p>Homo () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9605)</p> <p>NCBI Taxonomy ID</p> <p>9606 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9606)</p> <p>is Taxon B an Intraspecies?</p> <p>Yes</p> <p>Taxon B Description</p> <p>Human - Estonia Biobank</p>
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GENOTYPIC CHANGE

<p>TMPRSS6</p> <p>IRIDA; UNQ354/PRO618</p> <p>9606.ENSPO0000334962 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSPO0000334962)</p> <p>Belongs to the peptidase S1 family.</p> <p>GO:0004222 : metalloendopeptidase activity</p>	<p>Generic Gene Name</p> <p>Synonyms</p> <p>String</p> <p>Sequence Similarities</p> <p>GO - Molecular Function</p>	<p>Q8IU80 (http://www.uniprot.org/uniprot/Q8IU80)</p> <p>()</p>	<p>UniProtKB Homo sapiens</p> <p>GenebankID or UniProtKB</p>
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(<https://www.ebi.ac.uk/QuickGO/term/GO:0004222>)
 GO:0004252 : serine-type endopeptidase activity
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0004252>)

GO - Biological Process

GO:0045944 : positive regulation of transcription by RNA polymerase II
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0045944>)
 GO:0030198 : extracellular matrix organization
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0030198>)
 GO:0006508 : proteolysis (<https://www.ebi.ac.uk/QuickGO/term/GO:0006508>)
 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:0006879 : cellular iron ion homeostasis
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0006879>)
 GO:0001525 : angiogenesis (<https://www.ebi.ac.uk/QuickGO/term/GO:0001525>)
 GO:0055072 : iron ion homeostasis (<https://www.ebi.ac.uk/QuickGO/term/GO:0055072>)
 GO:0035556 : intracellular signal transduction
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0035556>)
 GO:0030574 : collagen catabolic process
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0030574>)
 GO:0022617 : extracellular matrix disassembly
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0022617>)
 GO:0042730 : fibrinolysis (<https://www.ebi.ac.uk/QuickGO/term/GO:0042730>)
 GO:0033619 : membrane protein proteolysis
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0033619>)
 GO:0030514 : negative regulation of BMP signaling pathway
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0030514>)
 GO:0097264 : self proteolysis (<https://www.ebi.ac.uk/QuickGO/term/GO:0097264>)

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:0005615 : extracellular space (<https://www.ebi.ac.uk/QuickGO/term/GO:0005615>)

Presumptive Null

No (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title>)

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

T>C at the associated SNP. Another SNP variant in strong LD p.V736A previously reported to influence iron homeostasis

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

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; PÄrrn K; Fischer K; Milani L; MÄrqi 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, LPAR1, PIK3CG, PSMD13,

No matches found.

EXTERNAL LINKS

COMMENTS