GEPHE SUMMARY

Gephebase Gene
REC8 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^REC8^#gephebase-summary-title)

GepheID
GP00001638

Entry Status
Published

Main curator
Prigent

PHENOTYPIC CHANGE

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

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

Trait State in Taxon A
Sperm Crossing-over Rate 1

Trait State in Taxon B
Sperm Crossing-over Rate 2

Ancestral State
Unknown

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

Taxon A

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

Common Name
cattle

Synonyms
Bos bovis; Bos primigenius taurus; cattle; bovine; cow; dairy cow; domestic cattle; domestic cow; Bos taurus Linnaeus, 1758; Bos Tauurus

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; Laurasiatheria; Artiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos

Parent
Bos (oxen, cattle) - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9903)

NCBI Taxonomy ID
9913 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9913)

is Taxon A an Infraspecies?
Yes

Taxon A Description
Bulls from the Netherlands and New-Zealand

Taxon B

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

Common Name
cattle

Synonyms
Bos bovis; Bos primigenius taurus; cattle; bovine; cow; dairy cow; domestic cattle; domestic cow; Bos taurus Linnaeus, 1758; Bos Tauurus

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; Laurasiatheria; Artiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos

Parent
Bos (oxen, cattle) - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9903)

NCBI Taxonomy ID
9913 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9913)

is Taxon B an Infraspecies?
Yes

Taxon B Description
Bulls from the Netherlands and New-Zealand

GENOTYPIC CHANGE

Generic Gene Name
REC8

Synonyms
-

String
9913.ENSBTAP00000003504 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9913.ENSBTAP00000003504)

Sequence Similarities
-

GO - Molecular Function
GO:0003682 : chromatin binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003682)

GO - Biological Process
GO:0072520 : seminiferous tubule development (https://www.ebi.ac.uk/QuickGO/term/GO:0072520)

UniProtKB Bos taurus
E1BL69 (http://www.uniprot.org/uniprot/E1BL69)

GenebankID or UniProtKB
()

GO:0051321 : meiotic cell cycle (https://www.ebi.ac.uk/QuickGO/term/GO:0051321)
GO:0007286 : spermatid development
(https://www.ebi.ac.uk/QuickGO/term/GO:0007286)
GO:0000724 : double-strand break repair via homologous recombination
(https://www.ebi.ac.uk/QuickGO/term/GO:0000724)
GO:0006302 : double-strand break repair
(https://www.ebi.ac.uk/QuickGO/term/GO:0006302)
GO:0001556 : oocyte maturation (https://www.ebi.ac.uk/QuickGO/term/GO:0001556)
GO:0007062 : sister chromatid cohesion
(https://www.ebi.ac.uk/QuickGO/term/GO:0007062)
GO:0009566 : fertilization (https://www.ebi.ac.uk/QuickGO/term/GO:0009566)
GO:0007141 : male meiosis I (https://www.ebi.ac.uk/QuickGO/term/GO:0007141)
GO:0007130 : synaptonemal complex assembly
(https://www.ebi.ac.uk/QuickGO/term/GO:0007130)

GO - Cellular Component

GO:0000778 : condensed nuclear chromosome kinetochore
(https://www.ebi.ac.uk/QuickGO/term/GO:0000778)
GO:0000800 : lateral element (https://www.ebi.ac.uk/QuickGO/term/GO:0000800)
GO:0001673 : male germ cell nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0001673)
GO:0030893 : meiotic cohesin complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0030893)
GO:0034991 : nuclear meiotic cohesin complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0034991)

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 in intron 12 with reduction in Genome-wide recombination rate

Experimental Evidence

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

Main Reference

Genetic variants in REC8, RNF212, and PRDM9 influence male recombination in cattle. (2012) (https://pubmed.ncbi.nlm.nih.gov/22844258)

Authors

Sandor C; Li W; Coppieters W; Druet T; Charlier C; Georges M

Abstract

We use >250,000 cross-over events identified in >10,000 bovine sperm cells to perform an extensive characterization of meiotic recombination in male cattle. We map Quantitative Trait Loci (QTL) influencing genome-wide recombination rate, genome-wide hotspot usage, and locus-specific recombination rate. We fine-map three QTL and present strong evidence that genetic variants in REC8 and RNF212 influence genome-wide recombination rate, while genetic variants in PRDM9 influence genome-wide hotspot usage.

Additional References

RELATED GEPHE

Related Genes

11 (CEP55, CPLX1, FMN1, GCLM, MSH4, NEK9, PABPN1, PRDM9, REC114, RNF212, SMC3) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^9913^/and+Trait=Recombination rate/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS