

GEPHE SUMMARY

Gephebase Gene
REC8

Entry Status
Published

GepheID
GP00001638

Main curator
Prigent

PHENOTYPIC CHANGE

Trait Category
Physiology

Trait
Recombination rate (male)

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

	Taxon A	Taxon B
Latin Name	<i>Bos taurus</i>	<i>Bos taurus</i>
Common Name	cattle	cattle
Synonyms	Bos bovis; Bos primigenius taurus; cattle; bovine; cow; dairy cow; domestic cattle; domestic cow; Bos taurus Linnaeus, 1758; Bos Taurus	Bos bovis; Bos primigenius taurus; cattle; bovine; cow; dairy cow; domestic cattle; domestic cow; Bos taurus Linnaeus, 1758; Bos Taurus
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; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos
Parent	Bos (oxen, cattle) - (Rank: genus)	Bos (oxen, cattle) - (Rank: genus)
NCBI Taxonomy ID	9913	9913
is Taxon A an Intraspecies?	Yes	Yes
Taxon A Description	Bulls from the Netherlands and New-Zealand	Bulls from the Netherlands and New-Zealand

GENOTYPIC CHANGE

Generic Gene Name
REC8

Synonyms
-

String
9913.ENSBTAP00000003504

Sequence Similarities
-

GO - Molecular Function
GO:0003682 : chromatin binding

GO - Biological Process
GO:0072520 : seminiferous tubule development
GO:0051321 : meiotic cell cycle
GO:0007286 : spermatid development
GO:0000724 : double-strand break repair via homologous recombination
GO:0006302 : double-strand break repair

UniProtKB *Bos taurus*
E1BL69

GenebankID or UniProtKB

GO:0001556 : oocyte maturation
GO:0007062 : sister chromatid cohesion
GO:0009566 : fertilization
GO:0007141 : male meiosis I
GO:0007130 : synaptonemal complex assembly

GO - Cellular Component

GO:0000778 : condensed nuclear chromosome kinetochore
GO:0000800 : lateral element
GO:0001673 : male germ cell nucleus
GO:0030893 : meiotic cohesin complex
GO:0034991 : nuclear meiotic cohesin complex

Presumptive Null

No

Molecular Type

Cis-regulatory

Aberration Type

SNP

Molecular Details of the Mutation

A>G in intron 12 with reduction in Genome-wide recombination rate

Experimental Evidence

Linkage Mapping

Main Reference

Genetic variants in REC8, RNF212, and PRDM9 influence male recombination in cattle. (2012)

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)

Related Haplotypes

No matches found.

COMMENTS