

GEPHE SUMMARY

Gephebase Gene
PRDM9

Entry Status
Published

GepheID
GP00001640

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

Latin Name
Bos taurus

Common Name
cattle

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

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; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos

Parent
Bos (oxen, cattle) - (Rank: genus)

NCBI Taxonomy ID
9913

is Taxon A an Intraspecies?
Yes

Taxon A Description
Bulls from the Netherlands and New-Zealand

Taxon B

Latin Name
Bos taurus

Common Name
cattle

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

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; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos

Parent
Bos (oxen, cattle) - (Rank: genus)

NCBI Taxonomy ID
9913

is Taxon B an Intraspecies?
Yes

Taxon B Description
Bulls from the Netherlands and New-Zealand

GENOTYPIC CHANGE

Generic Gene Name
PRDM9

Synonyms
ZNF596

String
-

Sequence Similarities
-

GO - Molecular Function
GO:0046872 : metal ion binding
GO:0003676 : nucleic acid binding

GO - Biological Process
GO:0006355 : regulation of transcription, DNA-templated

GO - Cellular Component
-

UniProtKB *Bos taurus*
A6QNW2

GenebankID or UniProtKB

Presumptive Null

No

Molecular Type

Coding

Aberration Type

Deletion

Deletion Size

1-9 bp

Molecular Details of the Mutation

variation in the C-terminal tandem array of Cys2His2 zinc-finger domains: 22 domains > 20 domains decreasing 6-fold Genome wide hot window usage in Crossing Over

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, REC114, REC8, RNF212, SMC3)

Related Haplotypes

2

EXTERNAL LINKS

COMMENTS