

Serial translocation by means of circular intermediates cattle

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Ancestral haplotype-based association mapping with generalized linear mixed models accounting for stratification. <i>Bioinformatics</i> , 2012, 28, 2467-2473.	4.1	46
2	Mechanisms of Gene Duplication and Translocation and Progress towards Understanding Their Relative Contributions to Animal Genome Evolution. <i>International Journal of Evolutionary Biology</i> , 2012, 2012, 1-10.	1.0	29
3	Copy number variation in the cattle genome. <i>Functional and Integrative Genomics</i> , 2012, 12, 609-624.	3.5	60
5	Detection of copy number variants in the horse genome and examination of their association with recurrent laryngeal neuropathy. <i>Animal Genetics</i> , 2013, 44, 206-208.	1.7	34
6	Molecular consequences of animal breeding. <i>Current Opinion in Genetics and Development</i> , 2013, 23, 295-301.	3.3	46
7	Models and Algorithms for Genome Evolution. <i>Computational Biology</i> , 2013, , .	0.2	7
8	Sorting genomes with rearrangements and segmental duplications through trajectory graphs. <i>BMC Bioinformatics</i> , 2013, 14, S9.	2.6	13
9	Genetics of Pigmentation in Dogs and Cats. <i>Annual Review of Animal Biosciences</i> , 2013, 1, 125-156.	7.4	65
10	At the cutting-edge of grape and wine biotechnology. <i>Trends in Genetics</i> , 2013, 29, 263-271.	6.7	40
11	Molecular genetics of coat colour variations in White Galloway and White Park cattle. <i>Animal Genetics</i> , 2013, 44, 450-453.	1.7	45
12	Comparative genomics: a revolutionary tool for wine yeast strain development. <i>Current Opinion in Biotechnology</i> , 2013, 24, 192-199.	6.6	35
13	Use of Ancestral Haplotypes in Genome-Wide Association Studies. <i>Methods in Molecular Biology</i> , 2013, 1019, 347-380.	0.9	2
14	Genome-Wide Association Studies and Genomic Prediction. <i>Methods in Molecular Biology</i> , 2013, , .	0.9	53
15	Ectopic KIT Copy Number Variation Underlies Impaired Migration of Primordial Germ Cells Associated with Gonadal Hypoplasia in Cattle (<i>Bos taurus</i>). <i>PLoS ONE</i> , 2013, 8, e75659.	2.5	29
16	A Genome Scan Conducted in a Multigenerational Pedigree with Convergent Strabismus Supports a Complex Genetic Determinism. <i>PLoS ONE</i> , 2013, 8, e83574.	2.5	2
18	Pseudoautosomal Region 1 Length Polymorphism in the Human Population. <i>PLoS Genetics</i> , 2014, 10, e1004578.	3.5	24
19	Mutation discovery for Mendelian traits in non-laboratory animals: a review of achievements up to 2012. <i>Animal Genetics</i> , 2014, 45, 157-170.	1.7	33
20	Genes on B chromosomes of vertebrates. <i>Molecular Cytogenetics</i> , 2014, 7, 99.	0.9	40

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21	Efficiency of haplotype-based methods to fine-map QTLs and embryonic lethal variants affecting fertility: Illustration with a deletion segregating in Nordic Red cattle. <i>Livestock Science</i> , 2014, 166, 167-175.	1.6	1
22	Identification of a major locus interacting with MC1R and modifying black coat color in an F2 Nellore-Angus population. <i>Genetics Selection Evolution</i> , 2014, 46, 4.	3.0	29
23	The genetics of brown coat color and white spotting in domestic yaks (<i>Bos grunniens</i>). <i>Animal Genetics</i> , 2014, 45, 652-659.	1.7	34
24	The challenges and importance of structural variation detection in livestock. <i>Frontiers in Genetics</i> , 2014, 5, 37.	2.3	104
25	Cytogenetics and chromosome maps. , 0, , 103-129.		2
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27	Genome-Wide Study of Structural Variants in Bovine Holstein, MontbÃ©liarde and Normande Dairy Breeds. <i>PLoS ONE</i> , 2015, 10, e0135931.	2.5	52
28	Adaptive potential of genomic structural variation in human and mammalian evolution. <i>Briefings in Functional Genomics</i> , 2015, 14, 358-368.	2.7	20
29	RAPTR-SV: a hybrid method for the detection of structural variants. <i>Bioinformatics</i> , 2015, 31, 2084-2090.	4.1	18
30	The Effect of a Coat Colour-Associated Genes Polymorphism on Animal Health â€” A Review. <i>Annals of Animal Science</i> , 2015, 15, 3-17.	1.6	11
31	Genomic Insights into the <i>Saccharomyces sensu stricto</i> Complex. <i>Genetics</i> , 2015, 199, 281-291.	2.9	115
32	Genomic data as the "hitchhiker's guide" to cattle adaptation: tracking the milestones of past selection in the bovine genome. <i>Frontiers in Genetics</i> , 2015, 6, 36.	2.3	23
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40	Genome-wide identification of copy number variation using high-density single-nucleotide polymorphism array in Japanese Black cattle. <i>BMC Genetics</i> , 2016, 17, 26.	2.7	39
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43	Chromosome Aberrations and Fertility Disorders in Domestic Animals. <i>Annual Review of Animal Biosciences</i> , 2016, 4, 15-43.	7.4	65
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58	A complex structural variant at the <i>KIT</i> locus in cattle with the Pinzgauer spotting pattern. <i>Animal Genetics</i> , 2019, 50, 423-429.	1.7	12
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