

Genome-Wide Survey of SNP Variation Uncovers the Ge

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Marcadores SNP: conceitos básicos, aplicações no manejo e no melhoramento animal e perspectivas para o futuro. Revista Brasileira De Zootecnia, 2009, 38, 64-71.	0.3	18
2	Development and Characterization of a High Density SNP Genotyping Assay for Cattle. PLoS ONE, 2009, 4, e5350.	1.1	813
3	A Validated Genome Wide Association Study to Breed Cattle Adapted to an Environment Altered by Climate Change. PLoS ONE, 2009, 4, e6676.	1.1	122
4	Bovine respiratory disease research (1983-2009). Animal Health Research Reviews, 2009, 10, 131-139.	1.4	127
5	Resolving the evolution of extant and extinct ruminants with high-throughput phylogenomics. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 18644-18649.	3.3	196
6	Lessons from the Bovine Genome: Implications for Human Nutrition and Research. Journal of Nutrition, 2009, 139, 1271-1272.	1.3	2
7	It's a Bull's Market. Science, 2009, 324, 478-479.	6.0	28
8	Divergent evolution in the cytoplasmic domains of PRLR and GHR genes in Artiodactyla. BMC Evolutionary Biology, 2009, 9, 172.	3.2	19
9	Genome wide signatures of positive selection: The comparison of independent samples and the identification of regions associated to traits. BMC Genomics, 2009, 10, 178.	1.2	85
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12	High-resolution haplotype block structure in the cattle genome. BMC Genetics, 2009, 10, 19.	2.7	141
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18	OPTIMIZATION METHODS FOR SELECTING FOUNDER INDIVIDUALS FOR CAPTIVE BREEDING OR REINTRODUCTION OF ENDANGERED SPECIES. , 2009, , 43-53.		13

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19	A comparison of five methods to predict genomic breeding values of dairy bulls from genome-wide SNP markers. <i>Genetics Selection Evolution</i> , 2009, 41, 56.	1.2	171
20	A catalogue of validated single nucleotide polymorphisms in bovine orthologs of mammalian imprinted genes and associations with beef production traits. <i>Animal</i> , 2010, 4, 1958-1970.	1.3	15
21	DNA footprints of livestock domestication and evolutionary history. <i>Advances in Animal Biosciences</i> , 2010, 1, 538-545.	1.0	0
22	Effect of SNP origin on analyses of genetic diversity in cattle. <i>Animal Production Science</i> , 2010, 50, 792.	0.6	15
23	Genetic diversity and structure in <i>Bos taurus</i> and <i>Bos indicus</i> populations analyzed by SNP markers. <i>Animal Science Journal</i> , 2010, 81, 281-289.	0.6	52
24	Genomic Characterization and Chromosomal Mapping of 5 River Buffalo Skeletal Muscle Differentiation Master Genes. <i>Cytogenetic and Genome Research</i> , 2010, 128, 221-227.	0.6	6
25	2009 Presidential Address: Beyond Darwin? Evolution, Coevolution, and the American Society of Human Genetics. <i>American Journal of Human Genetics</i> , 2010, 86, 311-315.	2.6	1
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29	Genome wide scan for quantitative trait loci affecting tick resistance in cattle (<i>Bos taurus</i> × <i>Bos</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	1.2	31
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34	Quantitative trait loci for variation in immune response to a Foot-and-Mouth Disease virus peptide. <i>BMC Genetics</i> , 2010, 11, 107.	2.7	33
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40	Genetic heterogeneity at the bovine <i>KIT</i> gene in cattle breeds carrying different putative alleles at the <i>spotting</i> locus. <i>Animal Genetics</i> , 2010, 41, 295-303.	0.6	73
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44	Polymorphisms in <i>POMC</i> are not associated with dry matter intake and average daily gain phenotypes in beef cattle. <i>Animal Genetics</i> , 2010, 41, 669-669.	0.6	3
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74	Detection and correction of false segmental duplications caused by genome mis-assembly. <i>Genome Biology</i> , 2010, 11, R28.	13.9	96
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110	Partial-genome evaluation of postweaning feed intake and efficiency of crossbred beef cattle ^{1,2} . <i>Journal of Animal Science</i> , 2011, 89, 1731-1741.	0.2	64
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123	Next generation sequencing of African and Indicine cattle to identify single nucleotide polymorphisms. <i>Animal Production Science</i> , 2012, 52, 133.	0.6	11
124	On the way to functional agro biodiversity: coat colour gene variability in goats. <i>Animal</i> , 2012, 6, 41-49.	1.3	13
125	NetView: A High-Definition Network-Visualization Approach to Detect Fine-Scale Population Structures from Genome-Wide Patterns of Variation. <i>PLoS ONE</i> , 2012, 7, e48375.	1.1	113
126	Genome-wide association mapping of milk production traits in Braunvieh cattle. <i>Journal of Dairy Science</i> , 2012, 95, 5357-5364.	1.4	29

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127	Validation of single nucleotide polymorphisms associated with milk production traits in dairy cattle. <i>Journal of Dairy Science</i> , 2012, 95, 864-875.	1.4	40
128	Improving accuracy of genomic predictions within and between dairy cattle breeds with imputed high-density single nucleotide polymorphism panels. <i>Journal of Dairy Science</i> , 2012, 95, 4114-4129.	1.4	516
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132	Understanding and predicting complex traits: knowledge from cattle. <i>Human Molecular Genetics</i> , 2012, 21, R45-R51.	1.4	64
133	Adaptive evolution of Toll-like receptor 5 in domesticated mammals. <i>BMC Evolutionary Biology</i> , 2012, 12, 122.	3.2	38
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138	Combining evidence of selection with association analysis increases power to detect regions influencing complex traits in dairy cattle. <i>BMC Genomics</i> , 2012, 13, 48.	1.2	31
139	Analysis of genetic diversity in Brown Swiss, Jersey and Holstein populations using genome-wide single nucleotide polymorphism markers. <i>BMC Research Notes</i> , 2012, 5, 161.	0.6	17
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146	Beef cattle breeding in Australia with genomics: opportunities and needs. <i>Animal Production Science</i> , 2012, 52, 100.	0.6	21
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154	Bayesian genome-wide association analysis of growth and yearling ultrasound measures of carcass traits in Brangus heifers1. <i>Journal of Animal Science</i> , 2012, 90, 3398-3409.	0.2	86
155	Modern Taurine Cattle Descended from Small Number of Near-Eastern Founders. <i>Molecular Biology and Evolution</i> , 2012, 29, 2101-2104.	3.5	131
156	Optimization of a SNP assay for genotyping <i>Theobroma cacao</i> under field conditions. <i>Molecular Breeding</i> , 2012, 30, 33-52.	1.0	22
157	Genetic variations of <i>ANGPTL6</i> gene and their associations with growth traits and slaughter traits in Qinchuan cattle. <i>Molecular Biology Reports</i> , 2012, 39, 9223-9232.	1.0	6
158	The <i>RIPK2</i> gene: a positional candidate for tick burden supported by genetic associations in cattle and immunological response of knockout mouse. <i>Immunogenetics</i> , 2012, 64, 379-388.	1.2	9
159	Exclusion of <i>COL2A1</i> in canine Legg-Perthes disease. <i>Animal Genetics</i> , 2012, 43, 112-113.	0.6	4
160	Evaluation of polymorphisms within the genes <i>GHSR</i> and <i>SLC2A2</i> that are within a region on bovine chromosome 1 (BTA1) previously associated with feed intake and weight gain. <i>Animal Genetics</i> , 2012, 43, 112-112.	0.6	1
161	Whole-genome analysis for backfat thickness in a tropically adapted, composite cattle breed from Brazil. <i>Animal Genetics</i> , 2012, 43, 518-524.	0.6	3
162	SNP-based association mapping of the polled gene in divergent cattle breeds. <i>Animal Genetics</i> , 2012, 43, 595-598.	0.6	26
163	Genetic markers on BTA14 predictive for residual feed intake in beef steers and their effects on carcass and meat quality traits. <i>Animal Genetics</i> , 2012, 43, 599-603.	0.6	10
164	Molecular tools and analytical approaches for the characterization of farm animal genetic diversity. <i>Animal Genetics</i> , 2012, 43, 483-502.	0.6	104
165	Investigation of the genetic architecture of a bone carcass weight QTL on BTA6. <i>Animal Genetics</i> , 2012, 43, 654-661.	0.6	9

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167	Non-replication of genome-wide based associations of efficient food conversion in dairy cows. <i>Animal Genetics</i> , 2012, 43, 781-784.	0.6	6
168	Variation in the <i>XKR4</i> gene was significantly associated with subcutaneous rump fat thickness in indicine and composite cattle. <i>Animal Genetics</i> , 2012, 43, 785-789.	0.6	46
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