Linkage and QTL mapping for Sus scrofa chromosome 5

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Citation Report

#	Article	IF	Citations
1	SNP detection and genetic mapping of porcine genes encoding enzymes in hepatic metabolic pathways and evaluation of linkage with carcass traits. Animal Genetics, 2005, 36, 050912025950003-???.	0.6	26
2	QTL mapping for teat number in an Iberian-by-Meishan pig intercross. Animal Genetics, 2005, 36, 050823030348002-???.	0.6	40
3	Chapter 20 Manipulation of the ecosystem of pigs through biotechnology. Biology of Growing Animals, 2006, , 585-596.	0.3	0
4	Results of a whole-genome quantitative trait locus scan for growth, carcass composition and meat quality in a porcine four-way cross. Animal Genetics, 2006, 37, 543-553.	0.6	54
5	Associations of MYF5 gene polymorphisms with meat quality traits in different domestic pig (Sus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.6	10
6	QTL for the heritable inverted teat defect in pigs. Mammalian Genome, 2008, 19, 127-138.	1.0	24
7	Association of MYF5 and MYOD1 Gene Polymorphisms and Meat Quality Traits in Large WhiteÂÃ—ÂMeishan F2 Pig Populations. Biochemical Genetics, 2008, 46, 720-732.	0.8	38
8	Mapping of the porcine FBN2, YWHAQ, CNN3, DCN, POSTN, SPARC, RBM39 and GNAS genes, expressed in foetal skeletal muscles. Animal Genetics, 2008, 39, 204-205.	0.6	7
9	Alternative splicing at exon 28 of the acetylâ€coenzyme A carboxylase Î± gene in adult pigs and embryos. Animal Genetics, 2008, 39, 205-206.	0.6	2
10	Analysis of mRNA expression of CNN3, DCN, FBN2, POSTN, SPARC and YWHAQ genes in porcine foetal and adult skeletal muscles. Czech Journal of Animal Science, 2008, 53, 181-186.	0.5	10
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12	Genome-wide QTL mapping for three traits related to teat number in a White Duroc Ã— Erhualian pig resource population. BMC Genetics, 2009, 10, 6.	2.7	37
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14	Analysis of the mouse highâ€growth region in pigs. Journal of Animal Breeding and Genetics, 2009, 126, 404-412.	0.8	10
15	Detecting QTL for feed intake traits and other performance traits in growing pigs in a PiÃ©trainâ€“Large White backcross. Animal, 2010, 4, 1308-1318.	1.3	17
16	Four loci differentially expressed in muscle tissue depending on water-holding capacity are associated with meat quality in commercial pig herds. Molecular Biology Reports, 2010, 37, 595-601.	1.0	22
17	Epistatic QTL pairs associated with meat quality and carcass composition traits in a porcine Duroc Ã— Pietrain population. Genetics Selection Evolution, 2010, 42, 39.	1.2	16
18	A single nucleotide polymorphism in suppressor of cytokine signalling-2 is associated with growth and feed conversion efficiency in pigs. Animal Genetics, 2011, 42, 219-221.	0.6	0

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19	Genes with expression levels correlating to drip loss prove association of their polymorphism with water holding capacity of pork. Molecular Biology Reports, 2012, 39, 97-107.	1.0	6
20	A genomeâ€wide linkage analysis for reproductive traits in F 2 L arge W hite Ã— M eishan cross gilts. Animal Genetics, 2014, 45, 191-197.	0.6	39
21	QTL analysis of body weight and carcass body length traits in an F₂intercross between Landrace and Korean native pigs. Animal Genetics, 2014, 45, 589-592.	0.6	19
22	High-resolution association mapping of number of teats in pigs reveals regions controlling vertebral development. BMC Genomics, 2014, 15, 542.	1.2	62
23	Antioxidant activities and protective effects of duck embryo peptides against H2 O2-induced oxidative damage in HepG2 cells. Poultry Science, 2019, 98, 7118-7128.	1.5	21
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25	Relations between the polymorphism in the coding and 5â€™-flanking regions of the porcine <i>MYOD1</i> and <i>MYF5</i> genes and productive traits in pigs. Journal of Animal and Feed Sciences, 2006, 15, 225-235.	0.4	5
26	Identification of loci affecting teat number by genome-wide association studies on three pig populations. Asian-Australasian Journal of Animal Sciences, 2017, 30, 1-7.	2.4	22
27	Mapping, Tissue Distribution and Polymorphism of Porcine Retinol Binding Protein Genes (RBP5 and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	2.4	4
28	Expression and Genetic Effects of GLI Pathogenesis-Related 1 Gene on Backfat Thickness in Pigs. Genes, 2022, 13, 1448.	1.0	0