

CITATION REPORT

List of articles citing

Design of a high density SNP genotyping assay in the pig using SNPs identified and characterized by next generation sequencing technology

DOI: 10.1371/journal.pone.0006524
PLoS ONE, 2009, 4, e6524.

Source: <https://exaly.com/paper-pdf/45341735/citation-report.pdf>

Version: 2024-04-28

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

#	Paper	IF	Citations
533	SNP Analysis with Duplicated Fish Genomes: Differentiation of SNPs, Paralogous Sequence Variants, and Multisite Variants. 2010 , 133-150		2
532	SNP Discovery through De Novo Deep Sequencing Using the next Generation of DNA Sequencers. 2010 , 69-90		1
531	Origin and Genetic Diversity of Pig Breeds. 2010 ,		9
530	Transgenic pigs as models for translational biomedical research. 2010 , 88, 653-64		182
529	Utilization of next-generation sequencing platforms in plant genomics and genetic variant discovery. 2010 , 25, 553-570		105
528	Assignment of chromosomal locations for unassigned SNPs/scaffolds based on pair-wise linkage disequilibrium estimates. 2010 , 11, 171		12
527	Pig genome sequence--analysis and publication strategy. 2010 , 11, 438		116
526	Copy number variation in the porcine genome inferred from a 60 k SNP BeadChip. 2010 , 11, 593		86
525	Knobbed acrosome defect is associated with a region containing the genes STK17b and HECW2 on porcine chromosome 15. 2010 , 11, 699		17
524	A genome-wide association study on androstenone levels in pigs reveals a cluster of candidate genes on chromosome 6. 2010 , 11, 42		73
523	Massive parallel sequencing in animal genetics: wherefroms and wheretos. 2010 , 41, 561-9		37
522	Analysis of the non-recombining Y chromosome defines polymorphisms in domestic pig breeds: ancestral bases identified by comparative sequencing. 2010 , 41, 619-29		14
521	Genome-wide SNP detection in the great tit <i>Parus major</i> using high throughput sequencing. 2010 , 19 Suppl 1, 89-99		71
520	Polydactyl inheritance in the pig. 2010 , 101, 469-75		8
519	Advances in porcine genomics and proteomics--a toolbox for developing the pig as a model organism for molecular biomedical research. 2010 , 9, 208-19		118
518	Genetic control of host resistance to porcine reproductive and respiratory syndrome virus (PRRSV) infection. 2010 , 154, 161-9		52
517	The pig as a model animal for studying cognition and neurobehavioral disorders. 2011 , 7, 359-83		49

516	The distal end of porcine chromosome 6p is involved in the regulation of skatole levels in boars. 2011 , 12, 35		20
515	Genome wide SNP discovery, analysis and evaluation in mallard (<i>Anas platyrhynchos</i>). 2011 , 12, 150		55
514	Molecular Biology: Animal. 2011 , 792-797		
513	Evaluation of approaches for identifying population informative markers from high density SNP chips. 2011 , 12, 45		52
512	Whole-genome association analyses for lifetime reproductive traits in the pig. 2011 , 89, 988-95		63
511	Genome-wide footprints of pig domestication and selection revealed through massive parallel sequencing of pooled DNA. <i>PLoS ONE</i> , 2011 , 6, e14782	3-7	103
510	Extent of linkage disequilibrium and effective population size in Finnish Landrace and Finnish Yorkshire pig breeds. 2011 , 89, 609-14		84
509	Genomic Diversity in Pig (<i>Sus scrofa</i>) and its Comparison with Human and other Livestock. 2011 , 12, 138-46		25
508	Association of 5-hydroxytryptamine (serotonin) receptor 4 (5-HTR4) gene polymorphisms with asthma. 2011 , 16, 630-8		7
507	Genomic regions associated with ventro-cranial chronic pleuritis in pig. 2011 , 128, 314-8		3
506	Identification of high utility SNPs for population assignment and traceability purposes in the pig using high-throughput sequencing. 2011 , 42, 613-20		37
505	Genetic diversity in the European wild boar <i>Sus scrofa</i> : phylogeography, population structure and wild x domestic hybridization. 2011 , 41, 125-137		73
504	Genome-wide genetic marker discovery and genotyping using next-generation sequencing. 2011 , 12, 499-510		1723
503	A 6-bp deletion in the TYRP1 gene causes the brown colouration phenotype in Chinese indigenous pigs. 2011 , 106, 862-8		40
502	Partial short-read sequencing of a highly inbred Iberian pig and genomics inference thereof. 2011 , 107, 256-64		15
501	Whole-genome SNP association analysis of reproduction traits in the Finnish Landrace pig breed. <i>Genetics Selection Evolution</i> , 2011 , 43, 42	4-9	26
500	The receptor locus for <i>Escherichia coli</i> F4ab/F4ac in the pig maps distal to the MUC4-LMLN region. 2011 , 22, 122-9		29
499	Sequencing technologies and genome sequencing. 2011 , 52, 413-35		426

498	Identification, utilisation and mapping of novel transcriptome-based markers from blackcurrant (<i>Ribes nigrum</i>). 2011 , 11, 147	27
497	Using SNP array data to test for host genetic and breed effects on Porcine Reproductive and Respiratory Syndrome Viremia. 2011 , 5 Suppl 4, S28	2
496	A first generation integrated map of the rainbow trout genome. 2011 , 12, 180	47
495	The development and characterization of a 60K SNP chip for chicken. 2011 , 12, 274	147
494	Large scale genome-wide association and LDLA mapping study identifies QTLs for boar taint and related sex steroids. 2011 , 12, 362	37
493	Analysis of muscle and ovary transcriptome of <i>Sus scrofa</i> : assembly, annotation and marker discovery. 2011 , 18, 343-51	19
492	Multi-ethnic studies in complex traits. 2011 , 20, R206-13	51
491	The pig genome project has plenty to squeal about. 2011 , 134, 9-18	13
490	A single nucleotide polymorphism set for paternal identification to reduce the costs of trait recording in commercial pig breeding. 2011 , 89, 1661-8	12
489	Microsatellite mapping of quantitative trait loci affecting female reproductive tract characteristics in Meishan x Large White F(2) pigs. 2012 , 90, 37-44	11
488	A high density SNP array for the domestic horse and extant <i>Perissodactyla</i> : utility for association mapping, genetic diversity, and phylogeny studies. 2012 , 8, e1002451	156
487	Single nucleotide polymorphism association study for backfat and intramuscular fat content in the region between SW2098 and SW1881 on pig chromosome 6. 2012 , 90, 1081-7	7
486	Regions of homozygosity in the porcine genome: consequence of demography and the recombination landscape. 2012 , 8, e1003100	178
485	A common dataset for genomic analysis of livestock populations. 2012 , 2, 429-35	59
484	Strong signatures of selection in the domestic pig genome. 2012 , 109, 19529-36	367
483	New phenotypes for new breeding goals in pigs. 2012 , 6, 535-43	56
482	The pig: a model for human infectious diseases. 2012 , 20, 50-7	573
481	Genetic mapping of quantitative trait loci (QTL) for body-weight in Atlantic salmon (<i>Salmo salar</i>) using a 6.5 K SNP array. 2012 , 358-359, 61-70	50

480	An association and haplotype analysis of porcine maternal infanticide: a model for human puerperal psychosis?. 2012 , 159B, 908-27	7
479	Genome-wide linkage analysis of QTL for growth and body composition employing the PorcineSNP60 BeadChip. 2012 , 13, 41	24
478	A defect in dystrophin causes a novel porcine stress syndrome. 2012 , 13, 233	25
477	Estimation of linkage disequilibrium in four US pig breeds. 2012 , 13, 24	104
476	A genome-wide detection of copy number variations using SNP genotyping arrays in swine. 2012 , 13, 273	69
475	Genome-wide SNP discovery in walnut with an AGSNP pipeline updated for SNP discovery in allogamous organisms. 2012 , 13, 354	34
474	Whole genome SNP discovery and analysis of genetic diversity in Turkey (Meleagris gallopavo). 2012 , 13, 391	49
473	Genome-wide association study for T lymphocyte subpopulations in swine. 2012 , 13, 488	17
472	Development of a genetic tool for product regulation in the diverse British pig breed market. 2012 , 13, 580	25
471	A genome wide association study for backfat thickness in Italian Large White pigs highlights new regions affecting fat deposition including neuronal genes. 2012 , 13, 583	64
470	High-resolution autosomal radiation hybrid maps of the pig genome and their contribution to the genome sequence assembly. 2012 , 13, 585	14
469	A high density recombination map of the pig reveals a correlation between sex-specific recombination and GC content. 2012 , 13, 586	113
468	A comprehensive survey of copy number variation in 18 diverse pig populations and identification of candidate copy number variable genes associated with complex traits. 2012 , 13, 733	76
467	Novel approach for deriving genome wide SNP analysis data from archived blood spots. 2012 , 5, 503	9
466	Consistent divergence times and allele sharing measured from cross-species application of SNP chips developed for three domestic species. 2012 , 12, 1145-50	38
465	Porcine arthrogyrosis multiplex congenita (AMC): new diagnostic test and narrowed candidate region. 2012 , 26, 248-52	4
464	Identification of Nucleotide Variation in Genomes Using Next-Generation Sequencing. 2012 , 257-276	
463	Identification of genome-wide copy number variations among diverse pig breeds by array CGH. 2012 , 13, 725	38

462	A genome-wide association study identifies two novel promising candidate genes affecting <i>Escherichia coli</i> F4ab/F4ac susceptibility in swine. <i>PLoS ONE</i> , 2012 , 7, e32127	3-7	27
461	Identification and association analysis of several hundred single nucleotide polymorphisms within candidate genes for back fat thickness in Italian Large White pigs using a selective genotyping approach. 2012 , 90, 2450-64		59
460	Genome-wide association study for intramuscular fatty acid composition in an Iberian Landrace cross. 2012 , 90, 2883-93		54
459	Chilling rate effects on pork loin tenderness in commercial processing plants. 2012 , 90, 2842-9		15
458	Genome-wide association study of swine farrowing traits. Part I: genetic and genomic parameter estimates. 2012 , 90, 3353-9		27
457	Uncontrolled admixture and loss of genetic diversity in a local Vietnamese pig breed. 2012 , 2, 962-75		13
456	Genome-wide association study of swine farrowing traits. Part II: Bayesian analysis of marker data. 2012 , 90, 3360-7		41
455	A whole-genome association study for pig reproductive traits. 2012 , 43, 18-26		112
454	Detection of a quantitative trait locus associated with resistance to <i>Ascaris suum</i> infection in pigs. 2012 , 42, 383-91		12
453	Development of a 44K SNP assay focussing on the analysis of a varroa-specific defence behaviour in honey bees (<i>Apis mellifera carnica</i>). 2012 , 12, 323-32		35
452	The design and cross-population application of a genome-wide SNP chip for the great tit <i>Parus major</i> . 2012 , 12, 753-70		46
451	Whole genome sequencing for quantifying germline mutation frequency in humans and model species: cautious optimism. 2012 , 750, 96-106		23
450	Recombination rates across porcine autosomes inferred from high-density linkage maps. 2012 , 43, 620-3		19
449	Molecular tools and analytical approaches for the characterization of farm animal genetic diversity. 2012 , 43, 483-502		82
448	Genome-wide association scan and phased haplotype construction for quantitative trait loci affecting boar taint in three pig breeds. 2012 , 13, 22		34
447	Genome-wide single nucleotide polymorphism analysis reveals recent genetic introgression from domestic pigs into Northwest European wild boar populations. 2013 , 22, 856-66		84
446	Modelling and visualizing fine-scale linkage disequilibrium structure. 2013 , 14, 179		3
445	Reintroductions and genetic introgression from domestic pigs have shaped the genetic population structure of Northwest European wild boar. 2013 , 14, 43		33

444	Genotype imputation accuracy in a F2 pig population using high density and low density SNP panels. 2013 , 14, 38		35
443	Evolutionary dynamics of copy number variation in pig genomes in the context of adaptation and domestication. 2013 , 14, 449		92
442	Genetic dissection of growth traits in a Chinese indigenous × commercial broiler chicken cross. 2013 , 14, 151		42
441	Genome-wide SNP validation and mantle tissue transcriptome analysis in the silver-lipped pearl oyster, <i>Pinctada maxima</i> . 2013 , 15, 647-58		25
440	Improved estimation of inbreeding and kinship in pigs using optimized SNP panels. 2013 , 14, 92		26
439	Genomic selection using low density marker panels with application to a sire line in pigs. <i>Genetics Selection Evolution</i> , 2013 , 45, 28	4.9	42
438	Genome-wide analysis of porcine backfat and intramuscular fat fatty acid composition using high-density genotyping and expression data. 2013 , 14, 845		38
437	Genome-wide and local pattern of linkage disequilibrium and persistence of phase for 3 Danish pig breeds. 2013 , 14, 115		33
436	Measuring inbreeding and inbreeding depression on pig growth from pedigree or SNP-derived metrics. 2013 , 130, 349-60		71
435	Applications of next-generation sequencing to phylogeography and phylogenetics. 2013 , 66, 526-38		426
434	Next-generation sequencing: the future of molecular genetics in poultry production and food safety. 2013 , 92, 562-72		51
433	Genetic diversity analysis of elite European maize (<i>Zea mays</i> L.) inbred lines using AFLP, SSR, and SNP markers reveals ascertainment bias for a subset of SNPs. 2013 , 126, 133-41		67
432	Genetic analysis of behavior traits in swine production. 2013 , 157, 28-37		24
431	Porcine colonization of the Americas: a 60k SNP story. 2013 , 110, 321-30		42
430	Genomic prediction in animals and plants: simulation of data, validation, reporting, and benchmarking. 2013 , 193, 347-65		251
429	Genome-wide prediction of age at puberty and reproductive longevity in sows. 2013 , 44, 387-97		29
428	Molecular advances in QTL discovery and application in pig breeding. 2013 , 29, 215-24		43
427	Switchgrass genomic diversity, ploidy, and evolution: novel insights from a network-based SNP discovery protocol. 2013 , 9, e1003215		481

426	Signatures of diversifying selection in European pig breeds. 2013 , 9, e1003453		131
425	Linkage disequilibrium and haplotype block structure in six commercial pig lines. 2013 , 91, 3493-501		44
424	Genome sequencing reveals fine scale diversification and reticulation history during speciation in <i>Sus</i> . 2013 , 14, R107		97
423	Farm-by-farm analysis of microsatellite, mtDNA and SNP genotype data reveals inbreeding and crossbreeding as threats to the survival of a native Spanish pig breed. 2013 , 44, 259-66		19
422	Livestock and the promise of genomics. 2013 , 56, 556-66		6
421	A genome-wide association study to detect genetic variation for postpartum dysgalactia syndrome in five commercial pig breeding lines. 2013 , 44, 502-8		8
420	Disentangling two QTL on porcine chromosome 12 for backfat fatty acid composition. 2013 , 24, 168-86		8
419	Breeding and Genetics Symposium: networks and pathways to guide genomic selection. 2013 , 91, 537-52		46
418	Methods of tagSNP selection and other variables affecting imputation accuracy in swine. 2013 , 14, 8		33
417	Conservation genomic analysis of domestic and wild pig populations from the Iberian Peninsula. 2013 , 14, 106		63
416	Opportunities for genome-wide selection for pig breeding in developing countries. 2013 , 91, 4617-27		4
415	Fine mapping and single nucleotide polymorphism effects estimation on pig chromosomes 1, 4, 7, 8, 17 and X. 2013 , 36, 511-9		7
414	Polymorphism in the ELOVL6 gene is associated with a major QTL effect on fatty acid composition in pigs. <i>PLoS ONE</i> , 2013 , 8, e53687	3-7	36
413	Genetic diversity, linkage disequilibrium and selection signatures in chinese and Western pigs revealed by genome-wide SNP markers. <i>PLoS ONE</i> , 2013 , 8, e56001	3-7	143
412	Genome-wide association analyses for fatty acid composition in porcine muscle and abdominal fat tissues. <i>PLoS ONE</i> , 2013 , 8, e65554	3-7	34
411	Evaluation of SNP Data from the Malus Infinium Array Identifies Challenges for Genetic Analysis of Complex Genomes of Polyploid Origin. <i>PLoS ONE</i> , 2013 , 8, e67407	3-7	15
410	Genotyping by genome reducing and sequencing for outbred animals. <i>PLoS ONE</i> , 2013 , 8, e67500	3-7	51
409	Genome-wide association study for cytokines and immunoglobulin G in swine. <i>PLoS ONE</i> , 2013 , 8, e74846.7		10

408	A genome-wide association study points out the causal implication of SOX9 in the sex-reversal phenotype in XX pigs. <i>PLoS ONE</i> , 2013 , 8, e79882	3.7	12
407	De novo sequencing, characterization, and comparison of inflorescence transcriptomes of <i>Cornus canadensis</i> and <i>C. florida</i> (Cornaceae). <i>PLoS ONE</i> , 2013 , 8, e82674	3.7	10
406	Genome-wide association of meat quality traits and tenderness in swine. 2013 , 91, 4043-50		44
405	Design and characterization of a 52K SNP chip for goats. <i>PLoS ONE</i> , 2014 , 9, e86227	3.7	121
404	A powerful tool for genome analysis in maize: development and evaluation of the high density 600 k SNP genotyping array. 2014 , 15, 823		168
403	Genome sequencing and analysis of Mangalica, a fatty local pig of Hungary. 2014 , 15, 761		30
402	Population history and genomic signatures for high-altitude adaptation in Tibetan pigs. 2014 , 15, 834		81
401	Genome-wide association study identifies QTLs for EBV of Backfat Thickness and average daily gain in Duroc pigs. 2014 , 50, 1308-1315		3
400	DNA Markers for Food Products Authentication. 2014 , 6, 579-596		46
399	A splice mutation in the PHKG1 gene causes high glycogen content and low meat quality in pig skeletal muscle. 2014 , 10, e1004710		56
398	Mixed model methods for genomic prediction and variance component estimation of additive and dominance effects using SNP markers. <i>PLoS ONE</i> , 2014 , 9, e87666	3.7	60
397	Development of the catfish 250K SNP array for genome-wide association studies. 2014 , 7, 135		74
396	Linkage disequilibrium patterns and persistence of phase in purebred and crossbred pig (<i>Sus scrofa</i>) populations. 2014 , 15, 126		25
395	A genomewide association study for average daily gain in Italian Large White pigs. 2014 , 92, 1385-94		47
394	A resource of single-nucleotide polymorphisms for rainbow trout generated by restriction-site associated DNA sequencing of doubled haploids. 2014 , 14, 588-96		41
393	Mutation discovery for Mendelian traits in non-laboratory animals: a review of achievements up to 2012. 2014 , 45, 157-70		26
392	Persistency of accuracy of genomic breeding values for different simulated pig breeding programs in developing countries. 2014 , 131, 367-78		12
391	A genome-wide association study reveals a novel candidate gene for sperm motility in pigs. 2014 , 151, 201-7		22

390	A genome-wide linkage analysis for reproductive traits in F2 Large White × Meishan cross gilts. 2014 , 45, 191-7	31
389	Genome-wide association analysis for growth, muscularity and meat quality in PiErain pigs. 2014 , 45, 350-6	13
388	Single-nucleotide polymorphism discovery in <i>Leptographium longiclavatum</i> , a mountain pine beetle-associated symbiotic fungus, using whole-genome resequencing. 2014 , 14, 401-10	13
387	Identifying genetic loci controlling neonatal passive transfer of immunity using a hybrid genotyping strategy. 2014 , 45, 340-9	4
386	New insight into the SSC8 genetic determination of fatty acid composition in pigs. <i>Genetics Selection Evolution</i> , 2014 , 46, 28	4-9 13
385	An SNP-based second-generation genetic map of <i>Daphnia magna</i> and its application to QTL analysis of phenotypic traits. 2014 , 15, 1033	39
384	A whole genomic scan to detect selection signatures between Berkshire and Korean native pig breeds. 2014 , 56, 23	10
383	Recombination of the porcine X chromosome: a high density linkage map. 2014 , 15, 148	11
382	Investigations on the pattern of linkage disequilibrium and selection signatures in the genomes of German PiErain pigs. 2014 , 131, 473-82	9
381	Accuracy of estimation of genomic breeding values in pigs using low-density genotypes and imputation. 2014 , 4, 623-31	32
380	Identification of QTL affecting resistance/susceptibility to acute <i>Actinobacillus pleuropneumoniae</i> infection in swine. 2014 , 25, 180-91	15
379	On the relationship between an Asian haplotype on chromosome 6 that reduces androstenone levels in boars and the differential expression of <i>SULT2A1</i> in the testis. 2014 , 15, 4	6
378	Development and validation of a high density SNP genotyping array for Atlantic salmon (<i>Salmo salar</i>). 2014 , 15, 90	153
377	A genome-wide scan for signatures of selection in Chinese indigenous and commercial pig breeds. 2014 , 15, 7	48
376	Are evaluations on young genotyped animals benefiting from the past generations?. 2014 , 97, 3930-42	37
375	Applied animal genomics: results from the field. 2014 , 2, 105-39	81
374	Copy number variants in a highly inbred Iberian porcine strain. 2014 , 45, 357-66	17
373	Genomewide association and identification of candidate genes for ovulation rate in swine. 2014 , 92, 3792-803	24

372	Mining the pig genome to investigate the domestication process. 2014 , 113, 471-84		18
371	Rapid screening for phenotype-genotype associations by linear transformations of genomic evaluations. 2014 , 15, 246		33
370	Detection of genome-wide copy number variations in two chicken lines divergently selected for abdominal fat content. 2014 , 15, 517		28
369	High-resolution association mapping of number of teats in pigs reveals regions controlling vertebral development. 2014 , 15, 542		41
368	Whole-genome sequence analysis reveals differences in population management and selection of European low-input pig breeds. 2014 , 15, 601		33
367	The porcine innate immune system: an update. 2014 , 45, 321-43		151
366	A genome-wide association study of production traits in a commercial population of Large White pigs: evidence of haplotypes affecting meat quality. <i>Genetics Selection Evolution</i> , 2014 , 46, 12	4-9	60
365	From SNP co-association to RNA co-expression: novel insights into gene networks for intramuscular fatty acid composition in porcine. 2014 , 15, 232		31
364	Development and evaluation of the first high-throughput SNP array for common carp (<i>Cyprinus carpio</i>). 2014 , 15, 307		79
363	Analysis of the genetics of boar taint reveals both single SNPs and regional effects. 2014 , 15, 424		20
362	Untangling the hybrid nature of modern pig genomes: a mosaic derived from biogeographically distinct and highly divergent <i>Sus scrofa</i> populations. 2014 , 23, 4089-102		32
361	Genomic analysis reveals selection for Asian genes in European pigs following human-mediated introgression. 2014 , 5, 4392		97
360	A high-density SNP genotyping array for rice biology and molecular breeding. 2014 , 7, 541-53		168
359	Genomic information in pig breeding: Science meets industry needs. 2014 , 166, 94-100		23
358	Associations between single nucleotide polymorphisms in 33 candidate genes and meat quality traits in commercial pigs. 2014 , 45, 508-16		16
357	Asian low-androstenone haplotype on pig chromosome 6 does not unfavorably affect production and reproduction traits. 2014 , 45, 874-7		1
356	Using haplotypes for the prediction of allelic identity to fine-map QTL: characterization and properties. <i>Genetics Selection Evolution</i> , 2014 , 46, 45	4-9	3
355	Efficiency of different selection strategies against boar taint in pigs. 2014 , 8, 11-9		12

354	Genomic selection in a pig population including information from slaughtered full sibs of boars within a sib-testing program. 2015 , 9, 750-9		4
353	Genomic inbreeding coefficients based on the distribution of the length of runs of homozygosity in a closed line of Iberian pigs. <i>Genetics Selection Evolution</i> , 2015 , 47, 81	4.9	26
352	Software solutions for the livestock genomics SNP array revolution. 2015 , 46, 343-53		16
351	Efficiency of genomic prediction for boar taint reduction in Danish Landrace pigs. 2015 , 46, 607-16		6
350	Implementing meta-analysis from genome-wide association studies for pork quality traits. 2015 , 93, 5607-17		12
349	Imputation of genotypes in Danish purebred and two-way crossbred pigs using low-density panels. <i>Genetics Selection Evolution</i> , 2015 , 47, 54	4.9	9
348	A study of vertebra number in pigs confirms the association of vertnin and reveals additional QTL. 2015 , 16, 129		28
347	Genome-wide association study reveals a locus for nasal carriage of <i>Staphylococcus aureus</i> in Danish crossbred pigs. 2015 , 11, 290		8
346	Accuracy of Predicted Genomic Breeding Values in Purebred and Crossbred Pigs. 2015 , 5, 1575-83		29
345	Estimation of Additive, Dominance, and Imprinting Genetic Variance Using Genomic Data. 2015 , 5, 2629-37		24
344	Comparison of iterated single-step and Bayesian regressions on genomic evaluations for age at 100 kg in swine. 2015 , 93, 4675-83		
343	Genomewide association analysis for average birth interval and stillbirth in swine. 2015 , 93, 529-40		10
342	Relationships among and variation within rare breeds of swine. 2015 , 93, 3810-3		9
341	Accuracy of genomic prediction using deregressed breeding values estimated from purebred and crossbred offspring phenotypes in pigs. 2015 , 93, 3313-21		9
340	Genome Wide Association Analysis Reveals New Production Trait Genes in a Male Duroc Population. <i>PLoS ONE</i> , 2015 , 10, e0139207	3.7	28
339	Exome Capture with Heterologous Enrichment in Pig (<i>Sus scrofa</i>). <i>PLoS ONE</i> , 2015 , 10, e0139328	3.7	1
338	Reduced Representation Libraries from DNA Pools Analysed with Next Generation Semiconductor Based-Sequencing to Identify SNPs in Extreme and Divergent Pigs for Back Fat Thickness. 2015 , 2015, 950737		11
337	Accuracy of genome-enabled prediction exploring purebred and crossbred pig populations. 2015 , 93, 4684-91		6

336	Genome-wide association analyses for boar taint components and testicular traits revealed regions having pleiotropic effects. 2015 , 16, 36		16
335	Porcine models of muscular dystrophy. 2015 , 56, 116-26		25
334	Genome-wide association analyses for meat quality traits in Chinese Erhualian pigs and a Western Duroc ((Landrace Yorkshire) commercial population. <i>Genetics Selection Evolution</i> , 2015 , 47, 44	4.9	41
333	Copy number variations in high and low fertility breeding boars. 2015 , 16, 280		18
332	Using genome-wide measures of coancestry to maintain diversity and fitness in endangered and domestic pig populations. 2015 , 25, 970-81		53
331	Susceptibility loci for umbilical hernia in swine detected by genome-wide association. 2015 , 51, 1000-1006		2
330	Artificial selection on introduced Asian haplotypes shaped the genetic architecture in European commercial pigs. 2015 , 282, 20152019		18
329	Quality control of genotypes using heritability estimates of gene content at the marker. 2015 , 199, 675-81		19
328	A flexible multi-species genome-wide 60K SNP chip developed from pooled resequencing of 240 Eucalyptus tree genomes across 12 species. 2015 , 206, 1527-40		88
327	The development and characterization of a 57K single nucleotide polymorphism array for rainbow trout. 2015 , 15, 662-72		131
326	Development, validation and genetic analysis of a large soybean SNP genotyping array. 2015 , 81, 625-36		97
325	A systems genetics study of swine illustrates mechanisms underlying human phenotypic traits. 2015 , 16, 88		10
324	Single nucleotide polymorphism analysis of Korean native chickens using next generation sequencing data. 2015 , 42, 471-7		9
323	Genome-wide association analysis reveals genetic loci and candidate genes for meat quality traits in Chinese Laiwu pigs. 2015 , 26, 181-90		35
322	Genetic mapping in grapevine using SNP microarray intensity values. 2015 , 35, 1		14
321	Single-copy gene based 50 K SNP chip for genetic studies and molecular breeding in rice. <i>Scientific Reports</i> , 2015 , 5, 11600	4.9	88
320	TRES: Identification of Discriminatory and Informative SNPs from Population Genomic Data. 2015 , 106, 672-6		17
319	A genome-wide association study in large white and landrace pig populations for number piglets born alive. <i>PLoS ONE</i> , 2015 , 10, e0117468	3.7	25

318	The chimerical genome of Isla del Coco feral pigs (Costa Rica), an isolated population since 1793 but with remarkable levels of diversity. 2015 , 24, 2364-78		11
317	Genomic selection for boar taint compounds and carcass traits in a commercial pig population. 2015 , 174, 10-17		23
316	Genomic Selection, a New Era for Pork Quality Improvement. 2015 , 3, 27-37		5
315	Genome-wide association study using deregressed breeding values for cryptorchidism and scrotal/inguinal hernia in two pig lines. <i>Genetics Selection Evolution</i> , 2015 , 47, 18	4.9	21
314	Maximizing crossbred performance through purebred genomic selection. <i>Genetics Selection Evolution</i> , 2015 , 47, 16	4.9	22
313	A hidden Markov approach for ascertaining cSNP genotypes from RNA sequence data in the presence of allelic imbalance by exploiting linkage disequilibrium. 2015 , 16, 61		1
312	A genome-wide scan for signatures of directional selection in domesticated pigs. 2015 , 16, 130		47
311	Not All SCID Pigs Are Created Equally: Two Independent Mutations in the Artemis Gene Cause SCID in Pigs. 2015 , 195, 3171-9		32
310	A meta analysis of genome-wide association studies for limb bone lengths in four pig populations. 2015 , 16, 95		19
309	A single-nucleotide polymorphism-based approach for rapid and cost-effective genetic wolf monitoring in Europe based on noninvasively collected samples. 2015 , 15, 295-305		67
308	Bayesian GWAS and network analysis revealed new candidate genes for number of teats in pigs. 2015 , 56, 123-32		26
307	Design of a 9K illumina BeadChip for polar bears (<i>Ursus maritimus</i>) from RAD and transcriptome sequencing. 2015 , 15, 587-600		34
306	Sexual dimorphism in livestock species selected for economically important traits. 2016 , 94, 3684-3692		16
305	Genetic Diversity Analysis of South and East Asian Duck Populations Using Highly Polymorphic Microsatellite Markers. 2016 , 29, 471-8		9
304	Evaluation of Genome-Enabled Selection for Bacterial Cold Water Disease Resistance Using Progeny Performance Data in Rainbow Trout: Insights on Genotyping Methods and Genomic Prediction Models. 2016 , 7, 96		68
303	Efficient genomic prediction based on whole-genome sequence data using split-and-merge Bayesian variable selection. <i>Genetics Selection Evolution</i> , 2016 , 48, 49	4.9	27
302	Genomics in the common carp. 2016 , 247-274		1
301	Effect of candidate gene polymorphisms on reproductive traits in a Large White pig population. 2016 , 87, 1455-1463		4

300	Genome-wide association study reveals regions associated with gestation length in two pig populations. 2016 , 47, 223-6		6
299	Analysis of the porcine APOA2 gene expression in liver, polymorphism identification and association with fatty acid composition traits. 2016 , 47, 552-9		15
298	Genomewide single nucleotide polymorphism discovery in Atlantic salmon (<i>Salmo salar</i>): validation in wild and farmed American and European populations. 2016 , 16, 1002-11		79
297	Twenty years of artificial directional selection have shaped the genome of the Italian Large White pig breed. 2016 , 47, 181-91		16
296	Accuracy of genomic prediction of purebreds for cross bred performance in pigs. 2016 , 133, 443-451		13
295	A comparison of methods to estimate genomic relationships using pedigree and markers in livestock populations. 2016 , 133, 452-462		9
294	Genome-wide patterns of copy number variation in the Chinese yak genome. 2016 , 17, 379		32
293	Expression-based GWAS identifies variants, gene interactions and key regulators affecting intramuscular fatty acid content and composition in porcine meat. <i>Scientific Reports</i> , 2016 , 6, 31803	4-9	38
292	Application of single-step genomic evaluation for crossbred performance in pig. 2016 , 94, 936-48		33
291	Genomic selection in pigs: state of the art and perspectives. 2016 , 15, 211-232		33
290	After genome-wide association studies: Gene networks elucidating candidate genes divergences for number of teats across two pig populations. 2016 , 94, 1446-58		8
289	Genomewide association analysis of sow lactation performance traits in lines of Yorkshire pigs divergently selected for residual feed intake during grow-finish phase. 2016 , 94, 2317-31		4
288	Genetic parameters and trends for production and reproduction traits of a Landrace herd in China. 2016 , 15, 1069-1075		8
287	Genome-wide mapping of copy number variations in commercial hybrid pigs using a high-density SNP genotyping array. 2016 , 52, 85-92		3
286	Conservation priorities of Iberoamerican pig breeds and their ancestors based on microsatellite information. 2016 , 117, 14-24		9
285	Revealing new candidate genes for reproductive traits in pigs: combining Bayesian GWAS and functional pathways. <i>Genetics Selection Evolution</i> , 2016 , 48, 9	4-9	37
284	The role of mitochondrial DNA copy number, variants, and haplotypes in farm animal developmental outcome. 2016 , 56 Suppl, S133-46		8
283	Genome-wide single nucleotide polymorphism (SNP) identification and characterization in a non-model organism, the African buffalo (<i>Syncerus caffer</i>), using next generation sequencing. 2016 , 81, 595-603		8

282	Meta-analysis of genome-wide association from genomic prediction models. 2016 , 47, 36-48		21
281	Ensemble Feature Selection using Rank Aggregation Methods for Population Genomic Data. 2016 ,		0
280	Genome-wide association studies for fatty acid metabolic traits in five divergent pig populations. <i>Scientific Reports</i> , 2016 , 6, 24718	4.9	21
279	Genomewide association studies for hematological traits and T lymphocyte subpopulations in a Duroc \times Erhualian F resource population. 2016 , 94, 5028-5041		7
278	Assigning breed origin to alleles in crossbred animals. <i>Genetics Selection Evolution</i> , 2016 , 48, 61	4.9	26
277	Genomic evaluation by including dominance effects and inbreeding depression for purebred and crossbred performance with an application in pigs. <i>Genetics Selection Evolution</i> , 2016 , 48, 92	4.9	42
276	Refining genomewide association for growth and fat deposition traits in an F pig population. 2016 , 94, 1387-97		6
275	Crossbreed evaluations in single-step genomic best linear unbiased predictor using adjusted realized relationship matrices. 2016 , 94, 909-19		27
274	Genome-wide study on intramuscular fat in Italian Large White pig breed using the PorcineSNP60 BeadChip. 2016 , 133, 277-82		23
273	Population structure and genome characterization of local pig breeds in Russia, Belorussia, Kazakhstan and Ukraine. <i>Genetics Selection Evolution</i> , 2016 , 48, 16	4.9	25
272	Comparison of host genetic factors influencing pig response to infection with two North American isolates of porcine reproductive and respiratory syndrome virus. <i>Genetics Selection Evolution</i> , 2016 , 48, 43	4.9	28
271	Genetic architecture of fatty acid composition in the longissimus dorsi muscle revealed by genome-wide association studies on diverse pig populations. <i>Genetics Selection Evolution</i> , 2016 , 48, 5	4.9	34
270	Transcriptome analysis and molecular marker discovery in <i>Solanum incanum</i> and <i>S. aethiopicum</i> , two close relatives of the common eggplant (<i>Solanum melongena</i>) with interest for breeding. 2016 , 17, 300		44
269	Genetic diversity analysis of two commercial breeds of pigs using genomic and pedigree data. <i>Genetics Selection Evolution</i> , 2016 , 48, 24	4.9	42
268	Development and use of molecular markers: past and present. 2016 , 36, 290-302		120
267	Genome-wide association and identification of candidate genes for age at puberty in swine. 2016 , 17, 50		27
266	Diversity analysis and genomic prediction of <i>Sclerotinia</i> resistance in sunflower using a new 25 K SNP genotyping array. 2016 , 129, 317-29		15
265	Genomic diversity and differentiation of a managed island wild boar population. 2016 , 116, 60-7		28

264	SNP Identification from Next-Generation Sequencing Datasets. 2017 , 288-307		
263	Minimum sample sizes for population genomics: an empirical study from an Amazonian plant species. 2017 , 17, 1136-1147		113
262	Deciphering the regulation of porcine genes influencing growth, fatness and yield-related traits through genetical genomics. 2017 , 28, 130-142		4
261	SNP Array Development, Genotyping, Data Analysis, and Applications. 2017 , 308-337		2
260	A set of 20 multiplexed single nucleotide polymorphism (SNP) markers specifically selected for the identification of the wild boar (<i>Sus scrofa scrofa</i>) and the domestic pig (<i>Sus scrofa domesticus</i>). 2017 , 9, 671-675		5
259	Integration of liver gene co-expression networks and eGWAs analyses highlighted candidate regulators implicated in lipid metabolism in pigs. <i>Scientific Reports</i> , 2017 , 7, 46539	4.9	18
258	Exploring the genetics of feed efficiency and feeding behaviour traits in a pig line highly selected for performance characteristics. 2017 , 292, 1001-1011		31
257	Host Genome Influence on Gut Microbial Composition and Microbial Prediction of Complex Traits in Pigs. 2017 , 206, 1637-1644		69
256	Development of a Medium Density Combined-Species SNP Array for Pacific and European Oysters (and). 2017 , 7, 2209-2218		40
255	Gene networks for total number born in pigs across divergent environments. 2017 , 28, 426-435		2
254	Host genetics of response to porcine reproductive and respiratory syndrome in nursery pigs. 2017 , 209, 107-113		13
253	Bayesian analysis of pig growth curves combining pedigree and genomic information. 2017 , 201, 34-40		4
252	Status and future perspectives of single nucleotide polymorphisms (SNPs) markers in farmed fishes: Way ahead using next generation sequencing. 2017 , 6, 81-86		9
251	FIFS: A data mining method for informative marker selection in high dimensional population genomic data. 2017 , 90, 146-154		8
250	Zika Virus Causes Persistent Infection in Porcine Conceptuses and may Impair Health in Offspring. 2017 , 25, 73-86		29
249	Development and validation of a novel SNP panel for the genetic characterization of Italian chicken breeds by next-generation sequencing discovery and array genotyping. 2017 , 96, 3858-3866		4
248	A genome-wide association study identifies genomic loci associated with backfat thickness, carcass weight, and body weight in two commercial pig populations. 2017 , 58, 499-508		21
247	Genome-wide Target Enrichment-aided Chip Design: a 66 K SNP Chip for Cashmere Goat. <i>Scientific Reports</i> , 2017 , 7, 8621	4.9	5

246	Genome-wide genetic structure and differentially selected regions among Landrace, Erhualian, and Meishan pigs using specific-locus amplified fragment sequencing. <i>Scientific Reports</i> , 2017 , 7, 10063	4.9	6
245	A comparative integrated gene-based linkage and locus ordering by linkage disequilibrium map for the Pacific white shrimp, <i>Litopenaeus vannamei</i> . <i>Scientific Reports</i> , 2017 , 7, 10360	4.9	25
244	A survey of single nucleotide polymorphisms identified from whole-genome sequencing and their functional effect in the porcine genome. 2017 , 48, 404-411		7
243	Genomic evaluation using SNP- and haplotype-based genomic relationship matrices in a closed line of Duroc pigs. 2017 , 88, 1465-1474		7
242	Association of genetic variants and expression levels of porcine FABP4 and FABP5 genes. 2017 , 48, 660-668		4
241	Imputation-Based Whole-Genome Sequence Association Study Rediscovered the Missing QTL for Lumbar Number in Sutai Pigs. <i>Scientific Reports</i> , 2017 , 7, 615	4.9	28
240	Efficiency of SNP and SSR-based analysis of genetic diversity, population structure, and relationships among cowpea (<i>Vigna unguiculata</i> (L.) Walp.) germplasm from East Africa and IITA inbred lines. 2017 , 20, 107-128		7
239	Genetic analysis of teat number in pigs reveals some developmental pathways independent of vertebra number and several loci which only affect a specific side. <i>Genetics Selection Evolution</i> , 2017 , 49, 4	4.9	13
238	Genome-wide detection of genetic markers associated with growth and fatness in four pig populations using four approaches. <i>Genetics Selection Evolution</i> , 2017 , 49, 21	4.9	29
237	Use of multi-trait and random regression models to identify genetic variation in tolerance to porcine reproductive and respiratory syndrome virus. <i>Genetics Selection Evolution</i> , 2017 , 49, 37	4.9	14
236	Genetic diversity, extent of linkage disequilibrium and persistence of gametic phase in Canadian pigs. 2017 , 18, 6		25
235	Origin and phylogenetic status of the local Ashanti Dwarf pig (ADP) of Ghana based on genetic analysis. 2017 , 18, 193		7
234	Genome-wide association study confirm major QTL for backfat fatty acid composition on SSC14 in Duroc pigs. 2017 , 18, 369		21
233	Identification of new single nucleotide polymorphisms affecting total number born and candidate genes related to ovulation rate in Chinese Erhualian pigs. 2017 , 48, 48-54		17
232	Distinguishing migration events of different timing for wild boar in the Balkans. 2017 , 44, 259-270		6
231	Estimates of the actual relationship between half-sibs in a pig population. 2017 , 134, 109-118		3
230	Assessment of genetic differentiation and genetic assignment of commercial rainbow trout strains using a SNP panel. 2017 , 468, 120-125		3
229	Genome-wide association studies identify susceptibility loci affecting respiratory disease in Chinese Erhualian pigs under natural conditions. 2017 , 48, 30-37		16

228	Novel harmful recessive haplotypes for reproductive traits in pigs. 2017 , 134, 129-135		11
227	Gene engineering in swine for agriculture. 2017 , 16, 2792-2804		2
226	Genome-wide SNP data unveils the globalization of domesticated pigs. <i>Genetics Selection Evolution</i> , 2017 , 49, 71	4-9	63
225	Deciphering the genetic regulation of peripheral blood transcriptome in pigs through expression genome-wide association study and allele-specific expression analysis. 2017 , 18, 967		15
224	The role of genomics in pig improvement. 2017 , 57, 2360		2
223	Similar Genetic Architecture with Shared and Unique Quantitative Trait Loci for Bacterial Cold Water Disease Resistance in Two Rainbow Trout Breeding Populations. 2017 , 8, 156		40
222	Construction and evaluation of a high-density SNP array for the Pacific oyster (<i>Crassostrea gigas</i>). <i>PLoS ONE</i> , 2017 , 12, e0174007	3-7	35
221	Use of haplotypes to identify regions harbouring lethal recessive variants in pigs. <i>Genetics Selection Evolution</i> , 2017 , 49, 57	4-9	5
220	Regularized quantile regression for SNP marker estimation of pig growth curves. 2017 , 8, 59		4
219	Genome-wide association study in an F2 Duroc x Pietrain resource population for economically important meat quality and carcass traits. 2017 , 95, 545-558		18
218	Genomewide association of piglet responses to infection with one of two porcine reproductive and respiratory syndrome virus isolates. 2017 , 95, 16-38		20
217	A genome-wide association study of reproductive traits in a Yorkshire pig population. 2018 , 209, 67-72		6
216	Molecular population structure for feral swine in the United States. 2018 , 82, 821-832		10
215	Utility of pooled sequencing for association mapping in nonmodel organisms. 2018 , 18, 825-837		29
214	Expression analysis of candidate genes for fatty acid composition in adipose tissue and identification of regulatory regions. <i>Scientific Reports</i> , 2018 , 8, 2045	4-9	41
213	Population Genomics of Animal Domestication and Breed Development. 2018 , 709-753		2
212	Genome-wide associations identify novel candidate loci associated with genetic susceptibility to tuberculosis in wild boar. <i>Scientific Reports</i> , 2018 , 8, 1980	4-9	11
211	Genomic prediction of piglet response to infection with one of two porcine reproductive and respiratory syndrome virus isolates. <i>Genetics Selection Evolution</i> , 2018 , 50, 3	4-9	6

210	Power and precision of QTL mapping in simulated multiple porcine F2 crosses using whole-genome sequence information. 2018 , 19, 22		4
209	A whole-genome association study for litter size and litter weight traits in pigs. 2018 , 211, 87-97		9
208	Genome-wide association studies, meta-analyses and derived gene network for meat quality and carcass traits in pigs. 2018 , 58, 1100		9
207	Combined GWAS and LDLA approaches to improve genome-wide quantitative trait loci detection affecting carcass and meat quality traits in pig. 2018 , 135, 148-158		7
206	Genotyping-by-sequencing through transcriptomics: implementation in a range of crop species with varying reproductive habits and ploidy levels. 2018 , 16, 877-889		22
205	Automatic delineation of brain regions on MRI and PET images from the pig. 2018 , 294, 51-58		14
204	Porcine Y-chromosome variation is consistent with the occurrence of paternal gene flow from non-Asian to Asian populations. 2018 , 120, 63-76		9
203	Genome-wide association study reveals genetic loci and candidate genes for average daily gain in Duroc pigs. 2018 , 31, 480-488		9
202	Genome-wide detection of selective signatures in a Duroc pig population. 2018 , 17, 2528-2535		9
201	Hotspots of recent hybridization between pigs and wild boars in Europe. <i>Scientific Reports</i> , 2018 , 8, 17372-9		25
200	Genome-wide association studies and meta-analysis uncovers new candidate genes for growth and carcass traits in pigs. <i>PLoS ONE</i> , 2018 , 13, e0205576	3-7	7
199	Required properties for markers used to calculate unbiased estimates of the genetic correlation between populations. <i>Genetics Selection Evolution</i> , 2018 , 50, 65	4-9	8
198	Livestock 2.0 - genome editing for fitter, healthier, and more productive farmed animals. 2018 , 19, 204		65
197	Harnessing longitudinal information to identify genetic variation in tolerance of pigs to Porcine Reproductive and Respiratory Syndrome virus infection. <i>Genetics Selection Evolution</i> , 2018 , 50, 50	4-9	9
196	Extent of third-order linkage disequilibrium in a composite line of Iberian pigs. 2018 , 19, 60		1
195	The genetic connectedness calculated from genomic information and its effect on the accuracy of genomic prediction. <i>PLoS ONE</i> , 2018 , 13, e0201400	3-7	2
194	Genomic data reveals large similarities among Canadian and French maternal pig lines. 2018 , 98, 809-817		1
193	Linkage disequilibrium pattern and genome-wide association mapping for meat traits in multiple porcine F crosses. 2018 , 49, 403-412		4

192	Genetic diversity, population structure and phylogenetic relationships of three indigenous pig breeds from Jiangxi Province, China, in a worldwide panel of pigs. 2018 , 49, 275-283		8
191	Applications and efficiencies of the first cat 63K DNA array. <i>Scientific Reports</i> , 2018 , 8, 7024	4.9	26
190	Discovery of SNPs for individual identification by reduced representation sequencing of moose (<i>Alces alces</i>). <i>PLoS ONE</i> , 2018 , 13, e0197364	3.7	8
189	Using genome wide association studies to identify common QTL regions in three different genetic backgrounds based on Iberian pig breed. <i>PLoS ONE</i> , 2018 , 13, e0190184	3.7	8
188	Genetic relationships of antibody response, viremia level, and weight gain in pigs experimentally infected with porcine reproductive and respiratory syndrome virus1. 2018 , 96, 3565-3581		9
187	Deleterious alleles in the context of domestication, inbreeding, and selection. 2019 , 12, 6-17		36
186	A Genomics Perspective on Pig Domestication. 2019 ,		3
185	Market Drivers and Discovering Technologies in Meat Species Identification. 2019 , 12, 2416-2429		10
184	Genome Sequencing Technologies in Livestock Health System. 2019 , 339-348		
183	Next-Generation Sequencing Vis-Vis Veterinary Health Management. 2019 , 463-470		
182	Genetic Diversity of Indigenous Pigs from South China Area Revealed by SNP Array. <i>Animals</i> , 2019 , 9,	3.1	11
181	Improving accuracy of direct and maternal genetic effects in genomic evaluations using pooled boar semen: a simulation study1. 2019 , 97, 3237-3245		1
180	A functional regulatory variant of MYH3 influences muscle fiber-type composition and intramuscular fat content in pigs. 2019 , 15, e1008279		30
179	Genetics without genes? The centrality of genetic markers in livestock genetics and genomics. 2019 , 41, 50		3
178	Landscape of Loci and Candidate Genes for Muscle Fatty Acid Composition in Pigs Revealed by Multiple Population Association Analysis. 2019 , 10, 1067		2
177	Review: innovation through research in the North American pork industry. 2019 , 13, 2951-2966		2
176	Rediscover and Refine QTLs for Pig Scrotal Hernia by Increasing a Specially Designed F Population and Using Whole-Genome Sequence Imputation Technology. 2019 , 10, 890		2
175	Genomic diversity, linkage disequilibrium and selection signatures in European local pig breeds assessed with a high density SNP chip. <i>Scientific Reports</i> , 2019 , 9, 13546	4.9	46

174	Performance of whole genome prediction for growth traits in a crossbred chicken population. 2019 , 98, 1968-1975	4
173	An exonic splicing enhancer mutation in causes aberrant alternative splicing and severe congenital hypothyroidism in Bama pigs. 2019 , 12,	4
172	A new chicken 55K SNP genotyping array. 2019 , 20, 410	13
171	Genome-Wide Association Study Reveals Candidate Genes for Growth Relevant Traits in Pigs. 2019 , 10, 302	19
170	Genome-Wide Signatures of Selection Detection in Three South China Indigenous Pigs. 2019 , 10,	9
169	Genome-Wide SNP Discovery in Indigenous Cattle Breeds of South Africa. 2019 , 10, 273	10
168	Balancing selection at a premature stop mutation in the myostatin gene underlies a recessive leg weakness syndrome in pigs. 2019 , 15, e1007759	10
167	Assessing <i>Sus scrofa</i> diversity among continental United States, and Pacific islands populations using molecular markers from a gene banks collection. <i>Scientific Reports</i> , 2019 , 9, 3173	4-9 2
166	Genetics and Health. 2019 , 42-49	
165	GWAS for Meat and Carcass Traits Using Imputed Sequence Level Genotypes in Pooled F2-Designs in Pigs. 2019 , 9, 2823-2834	13
164	Accuracy of genomic predictions using different imputation error rates in aquaculture breeding programs: A simulation study. 2019 , 503, 225-230	11
163	Combining genome-wide association analyses and gene interaction networks to reveal new genes associated with carcass traits, meat quality and fatty acid profiles in pigs. 2019 , 220, 180-189	6
162	Genetic correlation of fatty acid composition with growth, carcass, fat deposition and meat quality traits based on GWAS data in six pig populations. 2019 , 150, 47-55	31
161	SNPs associated with body weight and backfat thickness in two pig breeds identified by a genome-wide association study. 2019 , 111, 1583-1589	7
160	Strategies for within-litter selection of piglets using ultra-low density SNP panels. 2019 , 220, 173-179	1
159	Genetic control of longissimus dorsi muscle gene expression variation and joint analysis with phenotypic quantitative trait loci in pigs. 2019 , 20, 3	16
158	Identification of factors associated with virus level in tonsils of pigs experimentally infected with porcine reproductive and respiratory syndrome virus. 2019 , 97, 536-547	3
157	Selecting the hologenome to breed for an improved feed efficiency in pigs-A novel selection index. 2020 , 137, 14-22	15

156	Assessment of relationships between pigs based on pedigree and genomic information. 2020 , 14, 697-705		2
155	Runs of homozygosity islands in Italian cosmopolitan and autochthonous pig breeds identify selection signatures in the porcine genome. 2020 , 240, 104219		12
154	Loci Associated With Antibody Response in Feral Swine () Infected With. <i>Frontiers in Veterinary Science</i> , 2020 , 7, 554674	3.1	3
153	Optimizing genomic reference populations to improve crossbred performance. <i>Genetics Selection Evolution</i> , 2020 , 52, 65	4.9	3
152	Single-step genome-wide association study for social genetic effects and direct genetic effects on growth in Landrace pigs. <i>Scientific Reports</i> , 2020 , 10, 14958	4.9	7
151	Identification of strong candidate genes for backfat and intramuscular fatty acid composition in three crosses based on the Iberian pig. <i>Scientific Reports</i> , 2020 , 10, 13962	4.9	11
150	Genome Wide Assessment of Genetic Variation and Population Distinctiveness of the Pig Family in South Africa. 2020 , 11, 344		7
149	An improved pig reference genome sequence to enable pig genetics and genomics research. 2020 , 9,		60
148	Genetic Diversity and Ancestral Study for Korean Native Pigs Using 60K SNP Chip. <i>Animals</i> , 2020 , 10,	3.1	2
147	Genome-Wide Analysis Reveals Human-Mediated Introgression from Western Pigs to Indigenous Chinese Breeds. 2020 , 11,		6
146	Genetic improvement of livestock, from conventional breeding to biotechnological approaches. 2020 , 393-405		2
145	Development of a low-density panel for genomic selection of pigs in Russia. 2020 , 4, 264-274		1
144	Whole genome resequencing of the Iranian native dogs and wolves to unravel variome during dog domestication. 2020 , 21, 207		1
143	Introgression of Eastern Chinese and Southern Chinese haplotypes contributes to the improvement of fertility and immunity in European modern pigs. 2020 , 9,		12
142	Mixed ancestry from wild and domestic lineages contributes to the rapid expansion of invasive feral swine. 2020 , 29, 1103-1119		10
141	Matching STR and SNP genotyping to discriminate between wild boar, domestic pigs and their recent hybrids for forensic purposes. <i>Scientific Reports</i> , 2020 , 10, 3188	4.9	12
140	Modern genetic and genomic improvement of the pig. 2020 , 249-262		2
139	Inference of Breed Structure in Farm Animals: Empirical Comparison between SNP and Microsatellite Performance. 2020 , 11,		8

138	Conservation Genomic Analysis of the Croatian Indigenous Black Slavonian and Turopolje Pig Breeds. 2020 , 11, 261			10
137	Development of a 64 SNV panel for breed authentication in Iberian pigs and their derived meat products. 2020 , 167, 108152			8
136	Applying an association weight matrix in weighted genomic prediction of boar taint compounds. 2021 , 138, 442-453			0
135	Genomics for Food Security With Efficient and Sustainable Livestock Production. 2021 , 229-244			0
134	Development of a 76k Alpaca () Single Nucleotide Polymorphisms (SNPs) Microarray. 2021 , 12,			1
133	The long-term effects of genomic selection: Response to selection, additive genetic variance and genetic architecture.			1
132	Integrated Genome-Wide Analysis of MicroRNA Expression Quantitative Trait Loci in Pig Longissimus Dorsi Muscle. 2021 , 12, 644091			1
131	Characterization of a haplotype-reference panel for genotyping by low-pass sequencing in Swiss Large White pigs.			
130	How array design creates SNP ascertainment bias. <i>PLoS ONE</i> , 2021 , 16, e0245178	3.7		11
129	Characterization of a haplotype-reference panel for genotyping by low-pass sequencing in Swiss Large White pigs. 2021 , 22, 290			3
128	Classical, Molecular, and Genomic Cytogenetics of the Pig, a Clinical Perspective. <i>Animals</i> , 2021 , 11,	3.1		3
127	Discrimination of single-point mutations in unamplified genomic DNA via Cas9 immobilized on a graphene field-effect transistor. 2021 , 5, 713-725			16
126	Genome-wide detection of CNV regions and their potential association with growth and fatness traits in Duroc pigs. 2021 , 22, 332			5
125	Single-Step Genome Wide Association Study Identifies QTL Signals for Untrimmed and Trimmed Thigh Weight in Italian Crossbred Pigs for Dry-Cured Ham Production. <i>Animals</i> , 2021 , 11,	3.1		0
124	Design and evaluation of a custom 50K Infinium SNP array for egg-type chickens. 2021 , 100, 101044			0
123	A further look at quantitative trait loci for growth and fatness traits in a White Duroc × Erhualian F intercross population. 2021 , 1-12			0
122	A further survey of the quantitative trait loci affecting swine body size and carcass traits in five related pig populations. 2021 , 52, 621-632			2
121	Canine Genetics and Genomics.			

120	Genetic relationship between purebred and synthetic pigs for growth performance using single step method. 2021 , 34, 967-974	0
119	Comparison of three statistical approaches for feature selection for fine-scale genetic population assignment in four pig breeds. 2021 , 53, 395	2
118	High-density single nucleotide polymorphism chip-based conservation genetic analysis of indigenous pig breeds from Shandong Province, China. 2021 , 34, 1123-1133	0
117	Breed identification of meat using machine learning and breed tag SNPs. 2021 , 125, 107971	1
116	Development and testing of a combined species SNP array for the European seabass (<i>Dicentrarchus labrax</i>) and gilthead seabream (<i>Sparus aurata</i>). 2021 , 113, 2096-2107	10
115	An imputed whole-genome sequence-based GWAS approach pinpoints causal mutations for complex traits in a specific swine population. 2021 , 1	0
114	Genomic selection in salmonids: new discoveries and future perspectives. 2021 , 29, 2259-2289	5
113	Associations of natural variation in the CD163 and other candidate genes on host response of nursery pigs to porcine reproductive and respiratory syndrome virus infection. 2021 , 99,	0
112	Development and validation of a 1 K sika deer (<i>Cervus nippon</i>) SNP Chip. 2021 , 22, 35	1
111	Assessment of Mosaicism and Detection of Cryptic Alleles in CRISPR/Cas9-Engineered Neurofibromatosis Type 1 and Mutant Porcine Models Reveals Overlooked Challenges in Precision Modeling of Human Diseases. 2021 , 12, 721045	1
110	An Efficient Score Test Integrated with Empirical Bayes for Genome-Wide Association Studies. 2021 , 12, 742752	0
109	Vector space algebra for scaling and centering relationship matrices under non-Hardy-Weinberg equilibrium conditions. <i>Genetics Selection Evolution</i> , 2021 , 53, 7	4.9 0
108	Incorporation of genetic technologies associated with applied reproductive technologies to enhance world food production. 2014 , 752, 77-96	2
107	Next-generation sequencing in veterinary medicine: how can the massive amount of information arising from high-throughput technologies improve diagnosis, control, and management of infectious diseases?. 2015 , 1247, 415-36	21
106	Genome-wide Association Studies Reveal Similar Genetic Architecture with Shared and Unique QTL for Bacterial Cold Water Disease Resistance in Two Rainbow Trout Breeding Populations.	1
105	Development and validation of a combined species SNP array for the European seabass (<i>Dicentrarchus labrax</i>) and gilthead seabream (<i>Sparus aurata</i>).	2
104	Required marker properties for unbiased estimates of the genetic correlation between populations.	1
103	An improved pig reference genome sequence to enable pig genetics and genomics research.	15

102	How Array Design affects SNP Ascertainment Bias.		2
101	Genome-wide association study identifies Loci for body composition and structural soundness traits in pigs. <i>PLoS ONE</i> , 2011, 6, e14726	3.7	149
100	A large maize (<i>Zea mays</i> L.) SNP genotyping array: development and germplasm genotyping, and genetic mapping to compare with the B73 reference genome. <i>PLoS ONE</i> , 2011, 6, e28334	3.7	422
99	SNP discovery and development of a high-density genotyping array for sunflower. <i>PLoS ONE</i> , 2012, 7, e29814	3.7	91
98	The imprinted gene DIO3 is a candidate gene for litter size in pigs. <i>PLoS ONE</i> , 2012, 7, e31825	3.7	28
97	Development and evaluation of a 9K SNP array for peach by internationally coordinated SNP detection and validation in breeding germplasm. <i>PLoS ONE</i> , 2012, 7, e35668	3.7	164
96	Sequence-based genotyping for marker discovery and co-dominant scoring in germplasm and populations. <i>PLoS ONE</i> , 2012, 7, e37565	3.7	103
95	Susceptibility towards enterotoxigenic <i>Escherichia coli</i> F4ac diarrhea is governed by the MUC13 gene in pigs. <i>PLoS ONE</i> , 2012, 7, e44573	3.7	37
94	Prediction of altered 3'-UTR miRNA-binding sites from RNA-Seq data: the swine leukocyte antigen complex (SLA) as a model region. <i>PLoS ONE</i> , 2012, 7, e48607	3.7	14
93	Development and evaluation of SoySNP50K, a high-density genotyping array for soybean. <i>PLoS ONE</i> , 2013, 8, e54985	3.7	344
92	A high throughput genotyping approach reveals distinctive autosomal genetic signatures for European and Near Eastern wild boar. <i>PLoS ONE</i> , 2013, 8, e55891	3.7	22
91	A genome-wide association study to detect QTL for commercially important traits in Swiss Large White boars. <i>PLoS ONE</i> , 2013, 8, e55951	3.7	29
90	Identification of genome-wide copy number variations among diverse pig breeds using SNP genotyping arrays. <i>PLoS ONE</i> , 2013, 8, e68683	3.7	26
89	Genome-wide SNP and STR discovery in the Japanese crested ibis and genetic diversity among founders of the Japanese population. <i>PLoS ONE</i> , 2013, 8, e72781	3.7	6
88	Enhancing genome-wide copy number variation identification by high density array CGH using diverse resources of pig breeds. <i>PLoS ONE</i> , 2014, 9, e87571	3.7	21
87	A genome-wide association study reveals dominance effects on number of teats in pigs. <i>PLoS ONE</i> , 2014, 9, e105867	3.7	36
86	A co-association network analysis of the genetic determination of pig conformation, growth and fatness. <i>PLoS ONE</i> , 2014, 9, e114862	3.7	23
85	Genome-Wide Copy Number Variations Using SNP Genotyping in a Mixed Breed Swine Population. <i>PLoS ONE</i> , 2015, 10, e0133529	3.7	10

84	Genome-Wide Analysis in Swine Associates Corneal Graft Rejection with Donor-Recipient Mismatches in Three Novel Histocompatibility Regions and One Locus Homologous to the Mouse H-3 Locus. <i>PLoS ONE</i> , 2016 , 11, e0152155	3.7	8
83	STR Profiling for Discrimination between Wild and Domestic Swine Specimens and between Main Breeds of Domestic Pigs Reared in Belarus. <i>PLoS ONE</i> , 2016 , 11, e0166563	3.7	7
82	Comparative genome-wide methylation analysis of longissimus dorsi muscles between Japanese black (Wagyu) and Chinese Red Steppes cattle. <i>PLoS ONE</i> , 2017 , 12, e0182492	3.7	21
81	Genome-wide association analysis reveals genetic loci and candidate genes for feeding behavior and eating efficiency in Duroc boars. <i>PLoS ONE</i> , 2017 , 12, e0183244	3.7	20
80	Systems genomics study reveals expression quantitative trait loci, regulator genes and pathways associated with boar taint in pigs. <i>PLoS ONE</i> , 2018 , 13, e0192673	3.7	9
79	Genome-wide association study of the backfat thickness trait in two pig populations. 2014 , 1, 91		4
78	A genome-wide association study of five meat quality traits in Yorkshire pigs. 2014 , 1, 137		10
77	Genome-wide association analysis reveals genetic loci and candidate genes associated with intramuscular fat in Duroc pigs. 2017 , 4, 335		2
76	New susceptibility loci for cutaneous melanoma risk and progression revealed using a porcine model. 2018 , 9, 27682-27697		8
75	The development and application of genomic selection as a new breeding paradigm. 2012 , 2, 10-15		58
74	Analysing the recolonisation of a highly fragmented landscape by wild boar using a landscape genetic approach. 2019 , 2019,		3
73	Engineering Gene Control Circuits with Allosteric Ribozymes in Human Cells as a Medicine of the Future. 2012 , 71-92		6
72	Identification of loci affecting teat number by genome-wide association studies on three pig populations. 2017 , 30, 1-7		10
71	Extent of linkage disequilibrium and effective population size of the Landrace population in Korea. 2018 , 31, 1078-1087		2
70	Application of single-step genomic evaluation using social genetic effect model for growth in pig. 2019 , 32, 1836-1843		2
69	Genetic Structure of and Evidence for Admixture between Western and Korean Native Pig Breeds Revealed by Single Nucleotide Polymorphisms. 2014 , 27, 1263-9		6
68	Transcription factor organic cation transporter 1 (OCT-1) affects the expression of porcine Klotho (KL) gene. 2016 , 4, e2186		1
67	Genome-wide single nucleotide polymorphism array and whole-genome sequencing reveal the inbreeding progression of Banna minipig inbred line. 2021 ,		1

- 66 Genome-wide associations for immune traits in two maternal pig lines. **2021**, 22, 717 1
- 65 Population genomic, olfactory, dietary, and gut microbiota analyses demonstrate the unique evolutionary trajectory of feral pigs. **2021**, 2 2
- 64 Generation of pig primary fibroblast cells harboring defective *MC4R* genes by *N*-ethyl-*N*-nitrosourea mutagenesis: A gene-driven, nontransgenic approach to pig improvement. **2013**, 03, 139-147
- 63 Variance of Inbreeding Values Calculated from Marker Genotypes in a Simple Experimental Family. **2014**, 51, 143-151
- 62 Genomics of Food Animals. **2014**, 433-453
- 61 Development of an Economic-trait Genetic Marker by Applying Next-generation Sequencing Technologies in a Whole Genome. **2014**, 24, 1258-1267 1
- 60 Examination of the Number of Loci Necessary for Inbreeding Evaluation with DNA Markers. **2015**, 52, 161-169
- 59 Origin and phylogenetic status of the local Ashanti Dwarf pig (ADP) of Ghana based on evidence from mtDNA analysis, *MC1R*, and Y-chromosome haplotypes.
- 58 Omics and bioinformatics approaches to target boar taint.
- 57 Genetic Improvement of Local Goats. **2017**, 111-134
- 56 Integration of Omics Approaches for Low-Phosphorus Tolerance in Maize. **2017**, 235-262
- 55 Analysis of genetic characteristics of pig breeds using information on single nucleotide polymorphisms. **2019**, 32, 485-493 2
- 54 Chromosomal Abnormalities in Swine and Their Impact on Production and Profitability. **2019**, 508-518
- 53 Analysis of *HEPH* Gene Polymorphism on the X Chromosome for Identification of Wild Boar and Domestic Pig. **2020**, 56, 1099-1108 0
- 52 Whole genome resequencing of the Iranian native dogs and wolves to unravel variome during dog domestication.
- 51 Whole genome resequencing of the Iranian native dogs and wolves to unravel variome during dog domestication.
- 50 Engineering Gene Control Circuits with Allosteric Ribozymes in Human Cells as a Medicine of the Future. 860-883
- 49 Genome-Wide Association Studies/SNP Chips. **2022**, 365-392

48 FMixFN: A Fast Big Data-Oriented Genomic Selection Model Based on an Iterative Conditional Expectation algorithm. **2021**, 12, 721600 0

47 Pig Breeding for Increased Sustainability. **2022**, 1-41

46 Weighted genome-wide association study reveals new candidate genes related to boar taint compounds 1. **2022**, 257, 104845

45 Resilience to Historical Human Manipulations in the Genomic Variation of Italian Wild Boar Populations. **2022**, 10, 1

44 Quantitative Evaluation of Nonlinear Methods for Population Structure Visualization & Inference.

43 The long-term effects of genomic selection: 1. Response to selection, additive genetic variance, and genetic architecture.. *Genetics Selection Evolution*, **2022**, 54, 19 4.9 1

42 Introgressive hybridisation between domestic pigs (*Sus scrofa domesticus*) and endemic Corsican wild boars (*S. s. meridionalis*): effects of human-mediated interventions.. **2022**,

41 Molecular Marker Techniques and Recent Advancements. **2022**, 1-21

40 Genome wide copy number variations using Porcine 60K SNP Beadchip in Landlly pigs.. **2022**, 1-9 0

39 Design and performance of a bovine 200 k SNP chip developed for endangered German Black Pied cattle (DSN).. **2021**, 22, 905 1

38 Genomic consequences of a century of inbreeding and isolation in the Danish wild boar population.

37 DataSheet_1.docx. **2019**,

36 Data_Sheet_1.docx. **2019**,

35 Data_Sheet_1.PDF. **2020**,

34 Table_1.XLSX. **2020**,

33 Table_2.XLSX. **2020**,

32 Table_3.XLSX. **2020**,

31 Table_4.XLSX. **2020**,

30	Table_5.XLSX. 2020,		
29	DataSheet_1.pdf. 2019,		
28	DataSheet_2.docx. 2019,		
27	Data_Sheet_1.DOCX. 2020,		
26	Data_Sheet_2.PDF. 2020,		
25	Table_1.DOCX. 2020,		
24	Table_2.DOCX. 2020,		
23	Table_3.XLSX. 2020,		
22	Data_Sheet_1.docx. 2020,		
21	Admixture and breed traceability in European indigenous pig breeds and wild boar using genome-wide SNP data.. <i>Scientific Reports</i> , 2022, 12, 7346	4.9	1
20	A 20-SNP Panel as a Tool for Genetic Authentication and Traceability of Pig Breeds. <i>Animals</i> , 2022, 12, 1335	3.1	0
19	Genome-Wide Association Studies, Runs of Homozygosity Analysis, and Copy Number Variation Detection to Identify Reproduction-Related Genes in Bama Xiang Pigs. <i>Frontiers in Veterinary Science</i> , 9,	3.1	0
18	Nucleotide resolution genetic mapping in pigs by publicly accessible whole genome imputation.		0
17	Genomic tools reveal complex social organization of an invasive large mammal (<i>Sus scrofa</i>). <i>Biological Invasions</i> ,	2.7	
16	Functional genomics of reproduction in pigs: Are we there yet?. <i>Molecular Reproduction and Development</i> ,	2.6	
15	Estimation of dam line composition of 3-way crossbred animals using genomic information. <i>Genetics Selection Evolution</i> , 2022, 54,	4.9	0
14	Quantitative evaluation of nonlinear methods for population structure visualization and inference.		
13	Progress and opportunities through use of genomics in animal production. 2022,		0

- 12 Factors influencing pregnancy, litter size, and reproductive parameters of invasive wild pigs. ○
- 11 Expression and Genetic Effects of GLI Pathogenesis-Related 1 Gene on Backfat Thickness in Pigs. **2022**, 13, 1448 ○
- 10 The Role of the Environment in Shaping the Genomic Variation in an Insular Wild Boar Population. **2022**, 14, 774 ○
- 9 Design and validation of a 63K genome-wide SNP-genotyping platform for caribou/reindeer (*Rangifer tarandus*). **2022**, 23, ○
- 8 Pig Breeding for Increased Sustainability. **2023**, 139-179 ○
- 7 Failing the four-gamete test enables exact phasing: the CornersAlgorithm. **2022**, 54, ○
- 6 Genome Editing and Protein Energy Malnutrition. **2023**, 215-232 ○
- 5 Evaluation of six machine learning classification algorithms in pig breed identification using SNPs array data. ○
- 4 Mitochondrial DNA Deficiency and Supplementation in *Sus scrofa* Oocytes Influence Transcriptome Profiles in Oocytes and Blastocysts. **2023**, 24, 3783 1
- 3 Conservation prioritisation through genomic reconstruction of demographic histories applied to two endangered suids in the Malay Archipelago. ○
- 2 Improving and Going Beyond Reference Genomes. **2023**, 255-326 ○
- 1 Genomics in animal breeding from the perspectives of matrices and molecules. **2023**, 160, ○