浙江省科学技术奖公示信息表（单位提名）

提名奖项：（科学技术进步奖）

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| 成果名称 | 猪遗传资源鉴别、评价与保护 |
| 提名等级 | 浙江省科学技术进步奖一等奖 |
| 提名书相关内容 | 一、项目相关授权专利1. 潘玉春、岳阳、王起山、张哲、徐忠、孙浩、刘登英、赵伟、马裴裴，2021：小梅山猪及生肉制品的SNP标记组合和鉴定方法，ZL201711008654.9
2. 潘玉春、王起山、岳阳，2020：中梅山猪及生肉制品的SNP标记组合和鉴定方法，ZL201910463209.4
3. 潘玉春、王起山、岳阳，2020：沙乌头猪及生肉制品的SNP标记组合和鉴定方法，ZL201910462657.2
4. 潘玉春、王起山、岳阳，2020：枫泾猪及生肉制品的SNP标记组合和鉴定方法，ZL201910462663.8
5. 王起山、潘玉春、岳阳，2020：太湖流域地方品种猪各个品种及生肉制品的SNP标记组合和鉴定方法，ZL201910462661.9。
6. 王起山、潘玉春、岳阳，2020：嘉兴黑猪及生肉制品的SNP标记组合和鉴定方法，ZL201910462678.4。
7. 王起山、潘玉春、岳阳，2020：浦东白猪及生肉制品的SNP标记组合和鉴定方法，ZL201910463234.2。
8. 王起山、潘玉春、岳阳，2020：二花脸猪及生肉制品的SNP标记组合和鉴定方法，ZL201910462660.4。
9. 潘玉春、陈强、杨玉梅、王起山、张向喆、马育芳、陈振亮、廖荣荣、涂盈盈、颉孝贤、王振、贺鹏飞、张哲，2014：基于基因组简化与二代测序DNA文库构建方法及试剂盒，ZL20121358999.8。
10. 潘玉春、吴潇、高运臻、谭桂芳、王起山，2010：猪肉质性状相关基因TRIM63的分离核酸序列，ZL201010553991.8。
11. 潘玉春、吴潇、高运臻、谭桂芳、王起山，2009：猪总产仔数性状相关基因MMP3的分离核酸序列，ZL 200910045962.8。
12. 潘玉春、吴潇、高运臻、谭桂芳、王起山，2009：猪肉质性状相关基因TRIM54的分离核酸序列，ZL200910045959.6。
13. 潘玉春、吴潇、高运臻、谭桂芳、王起山，2009：猪肉质性状相关基因TRIM63的分离核酸序列，ZL 200910045960.9。

二、项目相关软件著作权1. 王振、张振洋、赵伟、张哲、王起山、潘玉春，2023：猪遗传资源数字保种库平台V1.0，2023SR1273434。
2. 王擎宇、张振洋、叶晓微、谷家民、王振、张哲、王起山、潘玉春，2024：基于单倍体型参考集的猪缺失基因型填补软件(简称 PHARP) V2.0，2024，2024SR2093270。
3. 张振洋、张哲、韩贺、潘玉春、王起山、王振，2023：针对自动喂料记录仪的表型组挖掘系统V1.0，2023SR1630595。
4. 苗健、张哲、张振洋、陈子韬、王振、王起山、潘玉春，2022：iPIGs-基于机器学习的猪品种鉴别平台（简称：iPIGs）V1.0，2022SR1405248。
5. 王振、张振洋、潘玉春、王起山、张哲、赵伟、曹彩云、孙嘉宝，2022：基于单倍体型参考集的猪缺失基因型填补软件(简称：PHARP) V1.0，2022SR0625448。
6. 潘玉春、杨玉梅、王起山、张向喆、陈强、王振、贺鹏飞，2012：远交群体高通量富集测序缺失基因型填补系统软件（BLUPig），2012SR083631。
7. 徐玲瑶、王振、余鹏飞、谢沁沁、江金芸、刘爽、曹彩云、谷家民、张振洋、赵伟、庄亿铮、张哲、王起山、潘玉春，2024：PHiSA-猪海马体单细胞图谱在线平台（简称：PHiSA）V1.0，2024SR2245984。
8. 余鹏飞、王振、谢沁沁、刘爽、赵伟、张振洋、张哲、王起山、潘玉春，2024：金华猪肠道单细胞图谱在线平台V1.0，2024SR1628827。

三、项目相关论文1. Zhao Q, Liu H, Zhang Q, Qadri QR, Pan Y, Su G, Li P, Huang R. Optimal Combination of Different Selection and Mating Strategies on Exploiting Genetic Diversity and Genetic Gain in Small Pig Conservation Populations. J Anim Breed Genet. 2024 Dec 18. doi: 10.1111/jbg.12917. Epub ahead of print. PMID: 39692266.
2. Zhao, Q., H. Liu, Q. R. Qadri, Q. Wang, Y. Pan and G. Su (2021). "Long-term impact of conventional and optimal contribution conservation methods on genetic diversity and genetic gain in local pig breeds." Heredity (Edinb) 127(6): 546-553.
3. Zhao, Q. B., E. Lopez-Cortegano, F. O. Oyelami, Z. Zhang, P. P. Ma, Q. S. Wang and Y. C. Pan (2021). "Conservation Priorities Analysis of Chinese Indigenous Pig Breeds in the Taihu Lake Region." Front Genet 12: 558873.
4. Zhao, Q. B., F. O. Oyelami, Q. R. Qadri, H. Sun, Z. Xu, Q. S. Wang and Y. C. Pan (2021). "Identifying the unique characteristics of the Chinese indigenous pig breeds in the Yangtze River Delta region for precise conservation." BMC Genomics 22(1): 151.
5. Zhao, Q. B., H. Sun, Z. Zhang, Z. Xu, B. S. Olasege, P. P. Ma, X. Z. Zhang, Q. S. Wang and Y. C. Pan (2019). "Exploring the Structure of Haplotype Blocks and Genetic Diversity in Chinese Indigenous Pig Populations for Conservation Purpose." Evol Bioinform Online 15: 1176934318825082.
6. Miao, J., Chen, Z., Zhang, Z. et al. A web tool for the global identification of pig breeds. Genet Sel Evol 55, 18 (2023). https://doi.org/10.1186/s12711-023-00788-0
7. Wang, Z., Zhang, Z., Chen, Z. et al. PHARP: a pig haplotype reference panel for genotype imputation. Sci Rep 12, 12645 (2022). https://doi.org/10.1038/s41598-022-15851-x
8. Xiao, Q., Z. Zhang, H. Sun, Q. Wang and Y. Pan, 2017： Pudong White pig: a unique genetic resource disclosed by sequencing data. Animal 11(7): 1117-1124.
9. Xiao, Q., Z. Zhang, H. Sun, H. Yang, M. Xue, X. Liu, W. Zhang, Y. Zhen, M. Zhu, Q. Wang and Y. Pan, 2017： Genetic variation and genetic structure of five Chinese indigenous pig populations in Jiangsu Province revealed by sequencing data. Animal Genetics 48(5): 596-599.
10. Z. Wang, Q.Chen, R. Liao, Z. Zhang, X. Zhang, X. Liu, M. Zhu, W. Zhang, M. Xue, H.Yang, Y. Zheng, Q. Wang and Y. Pan, 2016: Genome-wide genetic variation discovery in Chinese Taihu pig breeds using next generation sequencing. Animal Genetics, DOI: 10.1111/age.12465.
11. Z. Wang, Q. Chen, Y. Yang, R. Liao, J. Zhao, Z. Zhang, Z. Chen, X. Zhang, M. Xue, H. Yang, Y. Zheng, Q. Wang and Y. Pan, 2015: Genetic diversity and population structure of six Chinese indigenous pig breeds in the Taihu Lake region revealed by sequencing data. Animal Genetics, 09/2015; 46(6).
12. Yumei Yang, Qishan Wang, Qiang Chen, Rongrong Liao, Xiangzhe Zhang, Hongjie Yang, Youmin Zheng, Zhiwu Zhang, Yuchun Pan, 2014: A New Genotype Imputation Method with Tolerance to High Missing Rate and Rare Variants. PloS ONE, 9(6): e101025.
13. Qiang Chen, Yufang Ma, Yumei Yang, Zhenliang Chen, Rongrong Liao, Xiaoxian Xie, Zhen Wang, Pengfei He, Yingying Tu, Xiangzhe Zhang, Changsuo Yang, Hongjie Yang, Fuqing Yu, Youmin Zheng, Zhiwu Zhang, Qishan Wang\*, Yuchun Pan\*, 2013: Genotyping by Genome Reducing and Sequencing for Outbred Animals. PloS ONE, 8(7): e67500.
14. Caiyun Cao, Jian Miao, Qinqin Xie, Jiabao Sun, Hong Cheng, Zhenyang Zhang, Fen Wu, Shuang Liu, Xiaowei Ye, Huanfa Gong, Zhe Zhang, Qishan Wang, Yuchun Pan, Zhen Wang, A near telomere-to-telomere genome assembly of the Jinhua pig: enabling more accurate genetic research, GigaScience, Volume 14, 2025, giaf048, https://doi.org/10.1093/gigascience/giaf048
15. Fu W, Xie Q, Yu P, Liu S, Xu L, Ye X, Zhao W, Wang Q, Pan Y, Zhang Z, Wang Z. Corrigendum: Pig jejunal single-cell RNA landscapes revealing breed-specific immunology differentiation at various domestication stages. Front Immunol. 2025 Mar 13;16:1588642. doi: 10.3389/fimmu.2025.1588642. Erratum for: A Corrigendum on Pig jejunal single-cell RNA landscapes revealing breed-specific immunology differentiation at various domestication stages By Fu W, Xie Q, Yu P, Liu S, Xu L, Ye X, Zhao W, Wang Q, Pan Y, Zhang Z and Wang Z (2025) Front. Immunol. 16:1530214. doi: 10.3389/fimmu.2025.1530214. PMID: 40151617; PMCID: PMC11947721.
16. Wang, Z., Pan, D., Xie, X., Zhong, Z., Wang, F., & Xiao, Q. (2025). Genome-wide detection of runs of homozygosity in Ding'an pigs revealed candidate genes relating to meat quality traits. BMC Genomics, 26(1), 316.
17. Liu C, Chen Z, Zhang Z, Wang Z, Guo X, Pan Y, Wang Q. Unveiling the Genetic Mechanism of Meat Color in Pigs through GWAS, Multi-Tissue, and Single-Cell Transcriptome Signatures Exploration. Int J Mol Sci. 2024 Mar 26;25(7):3682. doi: 10.3390/ijms25073682. PMID: 38612491; PMCID: PMC11012088.
18. Miao J, Wei X, Cao C, Sun J, Xu Y, Zhang Z, Wang Q, Pan Y, Wang Z. Pig pangenome graph reveals functional features of non-reference sequences. J Anim Sci Biotechnol. 2024 Feb 22;15(1):32. doi: 10.1186/s40104-023-00984-4. PMID: 38389084; PMCID: PMC10882747.
19. Lai X, Liu S, Miao J, Shen R, Wang Z, Zhang Z, Gong H, Li M, Pan Y, Wang Q. Eubacterium siraeum suppresses fat deposition via decreasing the tyrosine-mediated PI3K/AKT signaling pathway in high-fat diet-induced obesity. Microbiome. 2024 Oct 30;12(1):223. doi: 10.1186/s40168-024-01944-4. PMID: 39478562; PMCID: PMC11526712.
20. S.Q. Liu, Y.J. Xu, Z.T. Chen, H. Li, Z. Zhang, Q.S. Wang, Y.C. Pan,Genome-wide detection of runs of homozygosity and heterozygosity in Tunchang pigs,animal,Volume 18, Issue 8,2024
21. Wang, Z., Zhong, Z., Xie, X., Wang, F., Pan, D., Wang, Q., Pan, Y., Xiao, Q., & Tan, Z. (2024). Detection of Runs of Homozygosity and Identification of Candidate Genes in the Whole Genome of Tunchang Pigs. Animals, 14(2), 201.
22. Xie Q, Zhang Z, Chen Z, Sun J, Li M, Wang Q, Pan Y. Integration of Selection Signatures and Protein Interactions Reveals NR6A1, PAPPA2, and PIK3C2B as the Promising Candidate Genes Underlying the Characteristics of Licha Black Pig. Biology (Basel). 2023 Mar 25;12(4):500. doi: 10.3390/biology12040500. PMID: 37106701; PMCID: PMC10135650.
23. Lai X, Zhang Z, Zhang Z, Liu S, Bai C, Chen Z, Qadri QR, Fang Y, Wang Z, Pan Y, Wang Q. Integrated microbiome-metabolome-genome axis data of Laiwu and Lulai pigs. Sci Data. 2023 May 13;10(1):280. doi: 10.1038/s41597-023-02191-2. PMID: 37179393; PMCID: PMC10183000.
24. Liu S, Lai X, Xie Q, Wang Z, Pan Y, Wang Q, Zhang Z. Holo-omics analysis reveals the influence of gut microbiota on obesity indicators in Jinhua pigs. BMC Microbiol. 2023 Nov 3;23(1):322. doi: 10.1186/s12866-023-03011-8. PMID: 37923989; PMCID: PMC10623862.
25. Wu F, Chen Z, Zhang Z, Wang Z, Zhang Z, Wang Q, Pan Y. The Role of SOCS3 in Regulating Meat Quality in Jinhua Pigs. Int J Mol Sci. 2023 Jun 24;24(13):10593. doi: 10.3390/ijms241310593. PMID: 37445769; PMCID: PMC10341949.
26. Wang, F., Zha, Z., He, Y., Li, J., Zhong, Z., Xiao, Q., & Tan, Z. (2023). Genome-Wide Re-Sequencing Data Reveals the Population Structure and Selection Signatures of Tunchang Pigs in China. Animals, 13(11), 1835.
27. Zhong, Z., Wang, Z., Xie, X., Tian, S., Wang, F., Wang, Q., Ni, S., Pan, Y., & Xiao, Q. (2023). Evaluation of the Genetic Diversity, Population Structure and Selection Signatures of Three Native Chinese Pig Populations. Animals, 13(12), 2010.
28. Zhong, Z. Q., Li, R., Wang, Z., Tian, S. S., Xie, X. F., Wang, Z. Y., Na, W., Wang, Q. S., Pan, Y. C., & Xiao, Q. (2023). Genome-wide scans for selection signatures in indigenous pigs revealed candidate genes relating to heat tolerance. Animal, 17(7), 100882.
29. Chen Z, Ye X, Zhang Z, Zhao Q, Xiang Y, Xu N, Wang Q, Pan Y, Guo X, Wang Z. Genetic diversity and selection signatures of four indigenous pig breeds from eastern China. Anim Genet. 2022 Aug;53(4):506-509. doi: 10.1111/age.13208. Epub 2022 Apr 30. PMID: 35489815.
30. Chen Z, Zhang Z, Wang Z, Zhang Z, Wang Q, Pan Y. Heterozygosity and homozygosity regions affect reproductive success and the loss of reproduction: A case study with litter traits in pigs. Comput Struct Biotechnol J. 2022 Jul 26;20:4060-4071. doi: 10.1016/j.csbj.2022.07.039. PMID: 35983229; PMCID: PMC9364102.
31. Cao R, Feng J, Xu Y, Fang Y, Zhao W, Zhang Z, Zhang Z, Li M, Wang Q, Pan Y. Genomic Signatures Reveal Breeding Effects of Lulai Pigs. Genes (Basel). 2022 Oct 28;13(11):1969. doi: 10.3390/genes13111969. PMID: 36360207; PMCID: PMC9689693.
32. Chen, Z., Y. Li, Z. Zhang, W. Zhao, Z. Zhang, Y. Xiang, Q. Wang, Y. Pan, X. Guo and Z. Wang (2021). "Genome-wide epistatic interactions of litter size at birth in Chinese indigenous pigs." Anim Genet 52(5): 739-743.
33. Fang, Y. F., X. Y. Hao, Z. Xu, H. Sun, Q. B. Zhao, R. Cao, Z. Zhang, P. P. Ma, Y. X. Sun, Z. M. Qi, Q. K. Wei, Q. S. Wang and Y. C. Pan (2021). "Genome-Wide Detection of Runs of Homozygosity in Laiwu Pigs Revealed by Sequencing Data." Frontiers in Genetics 12.
34. Guo, L., H. Sun, Q. Zhao, Z. Xu, Z. Zhang, D. Liu, Q. R. Qadri, P. Ma, Q. Wang and Y. Pan (2021). "Positive selection signatures in Anqing six-end-white pig population based on reduced-representation genome sequencing data." Animal Genetics 52(2): 143-154.
35. Oyelami, F. O., Q. Zhao, Z. Xu, Z. Zhang, H. Sun, Z. Zhang, P. Ma, Q. Wang and Y. Pan (2020). "Haplotype Block Analysis Reveals Candidate Genes and QTLs for Meat Quality and Disease Resistance in Chinese Jiangquhai Pig Breed." Front Genet 11: 752.
36. Wu, F., H. Sun, S. Lu, X. Gou, D. Yan, Z. Xu, Z. Zhang, Q. R. Qadri, Z. Zhang, Z. Wang, Q. Chen, M. Li, X. Wang, X. Dong, Q. Wang and Y. Pan (2020). "Genetic Diversity and Selection Signatures Within Diannan Small-Ear Pigs Revealed by Next-Generation Sequencing." Front Genet 11: 733.
37. Sun, H., Z. Zhang, B. S. Olasege, Z. Xu, Q. Zhao, P. Ma, Q. Wang and Y. Pan (2019). "Application of partial least squares in exploring the genome selection signatures between populations." Heredity (Edinb) 122(3): 288-293.
38. Xu, Z., H. Sun, Z. Zhang, C. Y. Zhang, Q. B. Zhao, Q. Xiao, B. S. Olasege, P. P. Ma, X. Z. Zhang, Q. S. Wang and Y. C. Pan (2019). "Selection signature reveals genes associated with susceptibility loci affecting respiratory disease due to pleiotropic and hitchhiking effect in Chinese indigenous pigs." Asian-Australas J Anim Sci.
39. Xu, Z., H. Sun, Z. Zhang, Q. Zhao, B. S. Olasege, Q. Li, Y. Yue, P. Ma, X. Zhang, Q. Wang and Y. Pan (2019). "Assessment of Autozygosity Derived From Runs of Homozygosity in Jinhua Pigs Disclosed by Sequencing Data." Front Genet 10: 274.
40. Sun H., Wang Z., Zhang Z., Xiao Q., Mawed S., Xu Z., Zhang X., Yang H., Zhu M., Xue M., Liu X., Zhang W., Zhen Y., Wang QS., Pan YC, 2018：Genomic signatures reveal selection of characteristics within and between Meishan pig populations. Anim Genet (in press).
41. Z. Zhang, Z. Wang, Y. Yang, J. Zhao, Q. Chen, R. Liao, Z. Chen, X. Zhang, M. Xue, H. Yang, Y. Zheng, Q. Wang and Y. Pan, 2015: Identification of pleiotropic genes and gene sets underlying growth and immunity traits: a case study on Meishan pigs. Animal, 1-8, DOI: 10.1017/S1751731115002761.
42. 贺鹏飞，王起山，薛明，张哲，陈强，王振，杨红杰，潘玉春, 2014：中国地方猪品种登记网络平台的构建。上海交通大学学报（农业科学版）， 32:5, 89-94。
43. 程洪,张振洋,白炯堂,许贝贝,王振,潘玉春.“冻精+鲜精”混精对母猪繁殖性能的影响[J].中国畜禽种业,2024,20(2):83-88
44. 肖倩，张哲，孙浩，王振，赵静，廖荣荣，张向喆，沈大德，储野根，王起山，潘玉春，2016：浦东白猪及其杂种猪胴体与肉质性能分析。畜牧与兽医，2016,48(2): 49-53。
45. 肖倩，张哲，孙浩，王振，赵静，廖荣荣，张向喆，沈大德，储野根，王起山，潘玉春，2016：浦东白猪杂交试验报告——繁殖性能与育肥性能。畜牧与兽医，2016,48(5): 70-72。
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| 主要完成单位 | 1.单位名称：浙江大学2.单位名称：上海交通大学3.单位名称：海南大学4.单位名称：浙江青莲食品有限公司 |
| 提名单位 | 浙江大学 |
| 提名意见 | 项目针对我国地方品种资源，聚焦种猪遗传资源的鉴别、评价与保护三大核心问题，开展了一系列技术创新：一是建立了猪遗传资源精准分子鉴别体系，开发了品种鉴别平台iDIGS，推动了我国猪遗传资源的精准鉴别，借以重新发现了北港猪和龙游乌猪。二是对江、浙、沪、鲁、皖、滇、琼等省份的40余个地方猪种的分子种质特性，进行了系统评价，揭示了其独特的遗传特性，挖掘了与耐热应激、优质肉质、繁殖能力、抗病性等相关的基因，为其后续开展精准育种的开发利用提供了关键性的基础数据，推动了遗传资源的高效利用。三是突破传统基于系谱的常规保种方法，创新性提出基于基因组信息，建立一套新的高效的保种理论与技术体系。在此基础上开发了“地方猪品种数字保种库”，为遗传资源的长期保护、监督提供参照标准；同时开发了“地方猪遗传资源登记网络平台”，配合全国畜牧总站开展了地方品种登记。以上工作，对我国地方猪遗传资源的保护与高效利用奠定了极为重要的基础，是对遗传资源开发利用的国家战略重大需求，具有极大的社会公益性。项目共发表论文45篇（SCI论文40篇），获发明专利13项、软件著作权8项，经济与社会效益显著，仅2021~2023年取得直接经济效益8.85亿元、间接经济效益10.25亿元。我单位认真审阅了该成果推荐书及附件材料，确认全部材料真实有效，相关栏目内容符合填写要求，按规定进行了公示且无异议，建议申报浙江省科技进步奖。 |