

## **Curriculum Vitae of Jun WANG**

Professor, PhD

Director of BGI

Distinguished Professor of State Key Laboratory for Quality Research in Chinese  
Medicines

Macau University of Science and Technology



Professor Wang obtained the Bachelor and PhD degrees from Peking University in 1997 and 2002, respectively. He is a Ph.D. supervisor, winner of National Science Fund for Distinguished Young Scholars, national 973 Plan chief scientist, director of BGI -Shenzhen, professor of University of Copenhagen and Aarhus University, visiting professor of Macau University of Science and Technology, Chinese University of Hong Kong and Sun Yat-sen University.

With interdisciplinary academic excellence in the fields of mathematical statistics, computer science and biology which he has been developing since joining the Human Genome Project in 1999, Prof. Wang has made successful achievements in many cutting-edge areas, such as the association of gut flora and complex diseases, human genetics research, single-cell cancer genome research, and the development of advanced bioinformatics tools. Accordingly, a number of pioneering and original scientific achievements with significant international influence have been yield. Up to June 2013, he has published 213 SCI papers (total SCI citation: 27151 times), among which he first/co-first or corresponding/co-corresponding authored 113; 85 were published in top-tier international scientific journals as *Nature* (and other Nature Publishing Group journals), *Science*, *The New England Journal of Medicine*, *Cell* (and other Cell Press journals).

journals) and he first/co-first or corresponding/co-corresponding authored 54 (total SCI citation: 21593 times) of them. Among the major scientific and technological contributions of Prof. Wang, 9 research achievements were awarded "the world's top ten scientific and technological progress" and "(one of) the top ten scientific and technological progress in China" by academicians of EE the Chinese Academy of Science and Chinese Academy of Engineering ; 6 were awarded "the world's top ten scientific and technological news" and "the top ten scientific and technological news in China" by Science and Technology Daily; 3 were awarded "the top ten research news of Basic Science in China" jointly by the Ministry of science & technology and the China Association for Science and Technology. Many related articles have been selected as "Research Highlights" by Nature China. His research was financially supported by Ministry of Science and Technology, National Natural Science Foundation of China, Guangdong Province and Shenzhen City Government.

Due to his outstanding contributions to the fields of genomics and bioinformatics, Prof. Wang as an individual has received more than 20 awards, such as "Zhou Guangzhao Award" by the Zhou Guangzhao Foundation in 2013, "You Bring Charm to the World Award" by Phoenix TV in 2013, "Scientific Chinese for 2012" by China Association for Science in 2013, "Nature's 10-Ten people who mattered this year" by Nature in 2012, "Youth Scientific Award in China" in 2011, "Guangdong Youth 'May Fourth' Medal" in 2011, "National Model Worker" in 2010, "the State Council Special Allowance" in 2008, "China's Top Ten Scientific and Technological Progress" in 2008, "Guangdong 'May Day' Labor Medal" in 2008, "National New Century BaiQianWan Talents" in 2006, "Royal Danish Foundation Award" in 2006, "the Chinese Academy of Sciences Outstanding Scientific and Technical Achievement Award" in 2003, "Outstanding Young People of the Central State Organs" in 2003, "Hong Kong QiuShi Foundation: Award for Excellent Scientific Team Achievements" in 2002, "the Major Chinese Academy of Sciences Major Innovation Award" in 2002.

**Education:**

July, 1997, B. Sc. (Peking University, Beijing, China)

July, 2002, D. Sc. (Peking University, Beijing, China)

**Professional Chronology:**

Mar.,1999-Apr.,2007	Researcher, Director of Bioinformatics, Director of Beijing Center, Beijing Genomics Research Center, as Beijing Genomics Institute, Chinese academy of sciences, Beijing, China
Aug., 2004- present	Visiting Professor, Institute of Human Genetics, University of Aarhus, Denmark
Sep., 2006-Sep., 2009	Ole Rømer Professor, Department of Human Genetics, Biochemistry and Molecular Biology, University of Southern Denmark, Denmark
Dec., 2008-Nov., 2011	Visiting Professor, Zhongshan School of Medicine, Sun Yat-sen University, Guangzhou, China
Dec., 2008-Dec., 2012	Executive Director/ Researcher, BGI, Shenzhen, China
Mar., 2009-present	Visiting Professor, School of Biomedical Sciences, The Chinese University of Hong Kong, Hong Kong, China
Oct., 2009-present	Ole Rømer Professor, Department of Biology, University of Copenhagen, Denmark
Jan., 2013-present	Director/ Researcher, BGI, Shenzhen, China
Jun., 2013-present	Distinguished Professor, Macau Institute for Applied Research in Medicine and Health, Macau University of Science and Technology, Macau, China

**Teaching Subjects:**

- 1) Bioinformatics Frontiers

**Research Fields:**

- 1) Bioinformatics

- 2) Genomics
- 3) Human Population Genetics
- 4) Chinese Herbs Modernization

**Awards:**

- 1) Nature's 10-Ten people who mattered this year, Nature , 2012
- 2) Zhou Guangzhao Award, Zhou Guangzhao Foundation, 2013
- 3) You Bring Charm to the World Award, Phoenix TV, 2013
- 4) Scientific Chinese for 2012, China Association for Science, 2013
- 5) Shenzhen Natural Science Prize for 2010, Shenzhen City, 2012
- 6) Shenzhen Technology Invention Prize for 2011, Shenzhen City, 2012
- 7) Youth Scientific Award in China, China Assosiation for Science and Technology, 2011
- 8) Guangdong Youth "May Fourth" Medal, Guangdong Provincial Government, 2011
- 9) National Model Worker, the State Council, 2010
- 10) Shenzhen Science and Technology Innovation Prize, Shenzhen City, 2009
- 11) the State Council Special Allowance, the State Council, 2008
- 12) Guangdong "May Day" Labor Medal, Guangdong Provincial Government, 2008
- 13) China's Top Ten Scientific and Technological Progress, Academicians of the Chinese Academy of Sciences and Chinese Academy of Engineering, 2008
- 14) Award for Science and Sino-Danish Collaboration, Denmark, 2007
- 15) National New Century BaiQianWan Talents, the China National Authorities, 2006
- 16) The Danish Research Council: Young Elite Scientist, Royal Danish Foundation Award, 2006
- 17) Chinese Academy of Sciences Outstanding Scientific and Technical Achievement Award, Chinese Academy of Sciences, 2003
- 18) Outstanding Young People of the Central State Organs, the China National

Authorities, 2003

- 19) Award for Excellent Scientific Team Achievements, Hong Kong QiuShi Foundation, 2002
- 20) the Major Chinese Academy of Sciences Major Innovation Award, Chinese Academy of Sciences, 2002

**Selected Publications:**

- 1) Y.-H. Huang, Y.-R. Li, D.-W. Burt, H.-L. Chen, Y. Zhang, W.-B. Qian, H. Kim, S.-Q. Gan, Y.-Q. Zhao, J.-W. Li, K. Yi, H.-P. Feng, P.-Y. Zhu, B. Li, Q.-Y. Liu, S. Fairley, K.-E. Magor, Z.-L. Du, X.-X. Hu, L. Goodman, H. Tafer, A. Vignal, T. Lee, K.-W. Kim, Z.-Y. Sheng, Y. An, S. Searle, J. Herrero, M.-A. M. Groenen, R.-P. M. A. Crooijmans, T. Faraut, Q.-L. Cai, R.-G. Webster, J.-R. Aldridge, W.-C. Warren, S. Bartschat, S. Kehr, M. Marz, P.-F. Stadler, J. Smith, R.-H. S. Kraus, Y.-F. Zhao, L.-M. Ren, J. Fei, M. Morisson, P. Kaiser, D.-K. Griffin, M. Rao, F. Pitel, **J. Wang**, N. Li. The duck genome and transcriptome provide insight into an avian influenza virus reservoir species. *Nature Genetic*. **45**, 776–783, 2013.
- 2) X.-J. Zhan, S.-K. Pan, J.Y. Wang, A. Dixon, J. He, M.-G. Muller, P.-X. Ni, L. Hu, Y. Liu, H.-L. Hou, Y.-P. Chen, J.-Q. Xia, Q. Luo, P.-W. Xu, Y. Chen, S.-G. Liao, C.-C. Cao, S.-K. Gao, Z.-B. Wang, Z. Yue, G.-Q. Li, Y. Yin, N.-C. Fox, **J. Wang**, M.-W. Bruford. Peregrine and saker falcon genome sequences provide insights into evolution of a predatory lifestyle. *Nature Genetics*, **45**, 563–566, 2013.
- 3) H.-Q. Ling, S.-C. Zhao, D.-C. Liu, J.-Y. Wang, H. Sun, C. Zhang, H.-J. Fan, D. Li, L.-L. Dong, Y. Tao, C. Gao, H.-L. Wu, Y.-W. Li, Y. Cui, X.-S. Guo, S.-S. Zheng, B. Wang, K. Yu, Q.-S. Liang, W.-L. Yang, X.-Y. Lou, J. Chen, M.-J. Feng, J.-B. Jian, X.-F. Zhang, G.-B. Luo, Y. Jiang, J.-J. Liu, Z.-B. Wang, Y.-H. Sha, B.-R. Zhang, H.-J. Wu, D.-Z. Tang, Q.-H. Shen, P.-Y. Xue, S.-H. Zou, X.-J. Wang, X. Liu, F.-M. Wang, Y.-P. Yang, X.-L. An, Z.-Y. Dong, K.-P. Zhang, X.-Q. Zhang, M.-C. Luo, J. Dvorak, Y.-P. Tong, J. Wang, H.-M. Yang, Z.-S. Li, D.-W. Wang, A.-M. Zhang, **J. Wang**. Draft genome of the wheat A-genome progenitor *Triticum urartu*. *Nature*, **496**, 87–90, 2013.
- 4) J.-Z. Jia, S.-C. Zhao, X.-Y. Kong, Y.-R. Li, G.-Y. Zhao, W.-M. He, R. Appels, M. Pfeifer, Y. Tao, X.-Y. Zhang, R.-L. Jing, C. Zhang, Y.-Z. Ma, L.-F. Gao, C. Gao, M.

- Spannagl, K.-F. X. Mayer, D. Li, S.-K. Pan, F.-Y. Zheng, Q. Hu, X.-C. Xia, J.-W. Li, Q.-S. Liang, J. Chen, T. Wicker, C.-Y. Gou, H.-H. Kuang, G.-Y. He, Y.-D. Luo, B. Keller, Q.-J. Xia, P. Lu, J.-Y. Wang, H.-F. Zou, R.-Z. Zhang, J.-Y. Xu, J.-L. Gao, C. Middleton, Z.-W. Quan, G.-M. Liu, J. Wang, International Wheat Genome Sequencing Consortium, H.-M. Yang, X. Liu, Z.-H. He, L. Mao, **J. Wang**. *Aegilops tauschii* draft genome sequence reveals a gene repertoire for wheat adaptation. *Nature*, **496**, 91–95, 2013.
- 5) J.-F. Chen, Q.-F. Huang, D.-Y. Gao, J.-Y. Wang, Y.-S. Lang, T.-Y. Liu, B. Li, Z.-T. Bai, J.-L. Goicoechea, C.-Z. Liang, C.-B. Chen, W.-L. Zhang, S.-H. Sun, Y. Liao, X.-M. Zhang, L. Yang, C.-L. Song, M.-J. Wang, J.-F. Shi, G. Liu, J.-J. Liu, H.-L. Zhou, W.-L. Zhou, Q.-L. Yu, N. An, Y. Chen, Q.-L. Cai, B. Wang, B.-H. Liu, J.-M. Min, Y. Huang, H.-L. Wu, Z.-Y. Li, Y. Zhang, Y. Yin, W.-Q. Song, J.-M. Jiang, S.-A. Jackson, R.-A. Wing, **J. Wang**, M.-S. Chen. Whole-genome sequencing of *Oryza brachyantha* reveals mechanisms underlying *Oryza* genome evolution. *Nature Communications*, **4**, 1595, 2013.
- 6) Y. Fan, Z.-Y. Huang, C.-C. Cao, C.-S. Chen, Y.-X. Chen, D.-D. Fan, J. He, H.-L. Hou, L. Hu, X.-T. Hu, X.-T. Jiang, R. Lai, Y.-S. Lang, B. Liang, S.-G. Liao, D. Mu, Y.-Y. Ma, Y.-Y. Niu, X.-Q. Sun, J.-Q. Xia, J. Xiao, Z.-Q. Xiong, L. Xu, L. Yang, Y. Zhang, W. Zhao, X.-D. Zhao, Y.-T. Zheng, J.-M. Zhou, Y.-B. Zhu, G.-J. Zhang, **J. Wang**, Y.-G. Yao. Genome of the Chinese tree shrew. *Nature Communications*, **4**, 1426, 2013.
- 7) M.-D. Shapiro, Z. Kronenberg, C. Li, E.-T. Domyan, H.-L. Pan, M. Campbell, H. Tan, C.-D. Huff, H.-F. Hu, A.-I. Vickrey, S.-C.A. Nielsen, S.-A. Stringham, H. Hu, E. Willerslev, M.-T.P. Gilbert, M. Yandell, G.-J. Zhang, **J. Wang**. Genomic Diversity and Evolution of the Head Crest in the Rock Pigeon. *Science*, **339**, 1063-1067, 2013.
- 8) R.-K. Varshney, C. Song, R.-K. Saxena, S. Azam, S. Yu, A.-G. Sharpe, S. Cannon, J. Baek, B.-D. Rosen, B. Tar'an, T. Millan, X.-D. Zhang, L.-D. Ramsay, A. Iwata, Y. Wang, W. Nelson, A.-D. Farmer, P.-M. Gaur, C. Soderlund, R.-V. Penmetsa, C.-Y. Xu, A.-K. Bharti, W.-M. He, P. Winter, S.-C. Zhao, J.-K. Hane, N. Carrasquilla-Garcia, J.-A. Condie, H.-D. Upadhyaya, M.-C. Luo, M. Thudi, C.-L.L. Gowda, N.-P. Singh, J. Lichtenzveig, K.-K. Gali, J. Rubio, N. Nadarajan, J. Dolezel,

- K.-C. Bansal, X. Xu, D. Edwards, G.-Y Zhang, G. Kahl, J. Gil, K.-B. Singh, S.-K. Datta, S.-A. Jackson, **J.Wang**, D.-R. Cook. Draft genome sequence of chickpea (*Cicer arietinum*) provides a resource for trait improvement. *Nature Biotechnology*, **31**, 240–246, 2013.
- 9) M.-S. You, Z. Yue, W.-Y. He, X.-H. Yang, G. Yang, M. Xie, D.-L. Zhan, S.-W. Baxter, L. Vasseur, G.-M. Gurr, C.-J. Douglas, J.-L. Bai, P. Wang, K. Cui, S.-G. Huang, X.-C. Li, Q. Zhou, Z.-Y Wu, Q.-L Chen, C.-H Liu, B. Wang, X.-J. Li, X.-F. Xu, C.-X. Lu, M. Hu, J.-W. Davey, S.-M. Smith, M.-S. Chen, X.-F. Xia, W.-Q. Tang, F.-S. Ke, D.-D. Zheng, Y.-L Hu, F.-Q. Song, Y.-C. You, X.-L. Ma, L. Peng, Y.-K. Zheng, Y. Liang, Y.-Q. Chen, L.-Y. Yu, Y.-N. Zhang, Y.-Y. Liu, G.-Q. Li, L. Fang, J.-X. Li, X. Zhou, Y.-D. Luo, C.-Y. Gou, J.-Y Wang, J. Wang, H.-M. Yang, **J. Wang**. A heterozygous moth genome provides insights into herbivory and detoxification. *Nature Genetics*, **45**, 220–225, 2013.
- 10) Q.-X. Zhang, W.-B. Chen, L.-D. Sun, F.-Y. Zhao, B.-Q. Huang, W.-R Yang, Y. Tao, J. Wang, Z.-Q. Yuan, G.-Y. Fan, Z. Xing, C.-L. Han, H.-T. Pan, X. Zhong, W.-F. Shi, X.-M. Liang, D.-L. Du, F.-M Sun, Z.-D. Xu, R.-J. Hao, T. Lv, Y.-M. Lv, Z.-Q. Zheng, M. Sun, L. Luo, M. Cai, Y.-K. Gao, J.-Y. Wang, Y. Yin, X. Xu, T.-R. Cheng, **J. Wang**. The genome of *Prunus mume*. *Nature Communications*, **3**, 1318, 2012.
- 11) Y. Dong, M. Xie, Y. Jiang, N.-Q. Xiao, X.-Y. Du, W.-G. Zhang, G. Tosser-Klopp, J.-H. Wang, S. Yang, J. Liang, W.-B. Chen, J. Chen, P. Zeng, Y. Hou, C. Bian, S.-K. Pan, Y.-X. Li, X. Liu, W.-L. Wang, B. Servin, B. Sayre, B. Zhu, D. Sweeney, Ri. Moore, W.-H. Nie, Y.-Y. Shen, R.-P. Zhao, G.-J. Zhang, J.-Q. Li, T. Faraut, J. Womack, Y.-P. Zhang, J. Kijas, N. Cockett, X. Xu, S.-H. Zhao, **J. Wang**, W. Wang. Sequencing and automated whole-genome optical mapping of the genome of a domestic goat (*Capra hircus*). *Nature Biotechnology*, **31**, 135–141, 2013.
- 12) J.-J. Michaelson, Y.-J. Shi, M. Gujra, H.-C. Zheng, D. Malhotra, X. Jin, M.-H. Jian, G.-M. Liu, D. Greer, A. Bhandari, W.-T. Wu, R. Corominas, Á. Peoples, A. Koren, A. Gore, S.-L. Kang, G.-N. Lin, J. Estabillo, T. Gadomski, B. Singh, K. Zhang, N. Akshoomoff, C. Corsello, S. McCarroll, L.-M. Iakoucheva, Y.-R. Li, **J. Wang**, J. Sebat. Whole-genome sequencing in autism identifies hot spots for de novo germline mutation. *Cell*, **151**, 1431-1442, 2012.
- 13) G.-J. Zhang, C. Cowled, Z.-L. Shi, Z.-Y. Huang, K.-A. Bishop-Lilly, X.-D. Fang,

- J.-W. Wynne, Z.-Q. Xiong, M.-L. Baker, W. Zhao, M. Tachedjian, Y.-B. Zhu, P. Zhou, X.-T. Jiang, J. Ng, L. Yang, L.-J. Wu, J. Xiao, Y. Feng, Y.-X. Chen, X.-Q. Sun, Y. Zhang, G.-A. Marsh, G. Cramer, C.-C. Broder, K.-G. Frey, L.-F Wang, **J. Wang**. Comparative analysis of bat genomes provides insight into the evolution of flight and immunity. *Science*, **339**, 456-460, 2012.
- 14) S.-G. Guo, J.-G. Zhang, H.-H. Sun, J. Salse, W. J. Lucas, H.-Y. Zhang, Y. Zheng, L.-Y. Mao, Y. Ren, Z.-W. Wang, J.-M. Min, X.-S. Guo, F. Murat, B.-K. Ham, Z.-L. Zhang, S. Gao, M.-Y. Huang, Y.-M. Xu, S.-L. Zhong, A. Bombarely, L. A. Mueller, H. Zhao, H.-J. He, Y. Zhang, Z.-H. Zhang, S.-W. Huang, T. Tan, E. Pang, K. Lin, Q. Hu, H.-H. Kuang, P.-X. Ni, B. Wang, J.-G. Liu, Q.-H. Kou, W.-J. Hou, X.-H. Zou, J. Jiang, G.-Y. Gong, K. Klee, H. Schoof, Y. Huang, X.-S. Hu, S.-S. Dong, D.-Q. Liang, J. Wang, K. Wu, Y. Xia, X. Zhao, Z.-Q. Zheng, M. Xing, X.-M. Liang, B.-Q. Huang, T. Lv, J.-Y. Wang, Y. Yin, H.-P. Yi, R.-Q. Li, M.-Z. Wu, A. Levi, X.-P. Zhang, J. J. Giovannoni, **J. Wang**, Y.-F. Li, Z.-J. Fei, Y. Xu. The draft genome of watermelon (*Citrullus lanatus*) and resequencing of 20 diverse accessions. *Nature Genetics*, **45**, 51-58, 2012.
- 15) J.-J. Qin, Y.-R. Li, Z.-M. Cai, S.-H. Li, J.-F. Zhu, F. Zhang, S.-S. Liang, W.-W. Zhang, Y.-L. Guan, D.-Q. Shen, Y.-Q. Peng, D.-Y. Zhang, Z.-Y. Jie, W.-X. Wu, Y.-W. Qin, W.-B. Xue, J.-H. Li, L.-C. Han, D.-H. Lu, P.-X. Wu, Y.-L. Dai, X.-J. Sun, Z.-S. Li, A.-F. Tang, S.-L. Zhong, X.-P. Li, W.-C. Chen, R. Xu, M.-B. Wang, Q. Feng, M.-H. Gong, J. Yu, Y.-Y. Zhang, M. Zhang, T. Hansen, G. Sanchez, J. Raes, G. Falony, S. Okuda, M. Almeida, E. LeChatelier, P. Renault, N. Pons, J.-M. Batto, Z.-X. Zhang, H. Chen, R.-F. Yang, W.-M. Zheng, S.-G. Li, H.-M. Yang, J. Wang, S. D. Ehrlich, R. Nielsen, O. Pedersen, K. Kristiansen, **J. Wang**. A metagenome-wide association study of gut microbiota in type 2 diabetes. *Nature*, **490**, 55-60, 2012.
- 16) G.-F. Zhang, X.-D. Fang, X.-M. Guo, L. Li, R.-B. Luo, F. Xu, P.-C. Yang, L.-L. Zhang, X.-T. Wang, H.-G. Qi, Z.-Q. Xiong, H.-Y. Que, Y.-L. Xie, P. W. H. Holland, J. Paps, Y.-B. Zhu, F.-C. Wu, Y.-X. Chen, J.-F. Wang, C.-F. Peng, J. Meng, L. Yang, J. Liu, B. Wen, N. Zhang, Z.-Y. Huang, Q.-H. Zhu, Y. Feng, A. Mount, D. Hedgecock, Z. Xu, Y.-J. Liu, T. D. Lošo, Y.-S. Du, X.-Q. Sun, S.-D. Zhang, B.-H. Liu, P.-Z. Cheng, X.-T. Jiang, J. Li, D.-D. Fan, W. Wang, W.-J. Fu, T. Wang, B. Wang, J.-B. Zhang, Z.-Y. Peng, Y.-X. Li, N. Li, J.-P. Wang, M.-S. Chen, Y. He, F.-J. Tan, X.-R.

- Song, Q.-M. Zheng, R.-L. Huang, H.-L. Yang, X.-D. Du, L. Chen, M. Yang, P. M. Gaffney, S. Wang, L.-H. Luo, Z.-C. She, Y. Ming, W. Huang, S. Zhang, B.-Y. Huang, Y. Zhang, T. Qu, P.-X. Ni, G.-Y. Miao, J.-Y. Wang, Q. Wang, C. E. W. Steinberg, H.-Y. Wang, N. Li, L.-M. Qian, G.-J. Zhang, Y.-R. Li, H.-M. Yang, X. Liu, J. Wang, Y. Yin, **J. Wang**. The oyster genome reveals stress adaptation and complexity of shell formation. *Nature*, **490**, 49-54, 2012.
- 17) S.-Q. Zhang, T. Jiang, M. Li, X. Zhang, Y.-Q. Ren, S.-C. Wei, L.-D. Sun, H. Cheng, Y. Li, X.-Y. Yin, Z.-M. Hu, Z.-Y. Wang, Y. Liu, B.-R. Guo, H.-Y. Tang, X.-F. Tang, Y.-T. Ding, J.-B. Wang, P. Li, B.-Y. Wu, W. Wang, X.-F. Yuan, J.-S. Hou, W.-W. Ha, W.-J. Wang, Y.-J. Zhai, J. Wang, F.-F. Qian, F.-S. Zhou, G. Chen, X.-B. Zuo, X.-D. Zheng, Y.-J. Sheng, J.-P. Gao, B. Liang, P. Li, J. Zhu, F.-L. Xiao, P.-G. Wang, Y. Cui, H. Li, S.-X. Liu, M. Gao, X. Fan, S.-K. Shen, M. Zeng, G.-Q. Sun, Y. Xu, J.-Chu Hu, T.-T. He, Y.-R. Li, H.-M. Yang, J. Wang, Z.-Y. Yu, H.-F. Zhang, X. Hu, K. Yang, J. Wang, S.-X. Zhao, Y.-W. Zhou, J.-J. Liu, W.-D. Du, L. Zhang, K. Xia, S. Yang, **J. Wang**, X.-J. Zhang. Exome sequencing identifies MVK mutations in disseminated superficial actinic porokeratosis. *Nature Genetics*, **44**, 1156-1160, 2012.
- 18) K.-B. Wang, Z.-W. Wang, F.-G. Li, W.-W. Ye, J.-Y. Wang, G.-L. Song, Z. Yue, L. Cong, H.-H. Shang, S.-L. Zhu, C.-S. Zou, Q. Li, Y.-L. Yuan, C.-R. Lu, H.-L. Wei, C.-Y. Gou, Z.-Q. Zheng, Y. Yin, X.-Y. Zhang, K. Liu, B. Wang, C. Song, N. Shi, R. J. Kohel, R. G. Percy, J. Z. Yu, Y.-X. Zhu, **J. Wang**, S.-X. Yu. The draft genome of a diploid cotton *Gossypium raimondii*. *Nature Genetics*, **44**, 1098-1103, 2012.
- 19) Q. Qiu, G.-J. Zhang, T. Ma, W.-B. Qian, J.-Y. Wang, Z.-Q. Ye, C.-C. Cao, Q.-J. Hu, J. Kim, D. M. Larkin, L. Auvil, B. Capitanu, J. Ma, H. A. Lewin, X.-J. Qian, Y.-S. Lang, R. Zhou, L.-Z. Wang, K. Wang, J.-Q. Xia, S.-G. Liao, S.-K. Pan, X. Lu, H.-L. Hou, Y. Wang, X.-T. Zang, Y. Yin, H. Ma, J. Zhang, Z.-F. Wang, Y.-M. Zhang, D.-W. Zhang, T. Yonezawa, M. Hasegawa, Y. Zhong, W.-B. Liu, Y. Zhang, Z.-Y. Huang, S.-X. Zhang, R.-J. Long, H.-M. Yang, J. Wang, J. A. Lenstra, D. N. Cooper, Y. Wu, **J. Wang**, P. Shi, J. Wang, J.-Q. Liu. The yak genome and adaptation to life at high altitude. *Nature Genetics*, **44**, 946-949, 2012.
- 20) W.-K. Sung, H.-C. Zheng, S.-Y. Li, R.-H. Chen, X. Liu, Y.-R. Li, N. P. Lee, W. H. Lee, P. N. Ariyaratne, C. Tennakoon, F. H. Mulawadi, K. F. Wong, A. M. Liu, R. T. Poon, S. T. Fan, K. L. Chan, Z.-L. Gong, Y.-J. Hu, Z. Lin, G. Wang, Q.-H. Zhang, T.

- D. Barber, W.-C. Chou, A. Aggarwal, K. Hao, W. Zhou, C.-S. Zhang, J. Hardwick, C. Buser, J.-C. Xu, Z.-Y. Kan, H.-Y. Dai, M. Mao, C. Reinhard, **J. Wang**, J.-M. Luk. Genome-wide survey of recurrent HBV integration in hepatocellular carcinoma. *Nature Genetics*, **44**, 765-769, 2012.
- 21) G.-Y. Zhang, X. Liu, Z.-W. Quan, S.-F. Cheng, X. Xu, S.-K. Pan, M. Xie, P. Zeng, Z. Yue, W.-L. Wang, Y. Tao, C. Bian, C.-L. Han, Q.-J. Xia, X.-H. Peng, R. Cao, X.-H. Yang, D.-L. Zhan, J.-C. Hu, Y.-X. Zhang, H.-N. Li, H. Li, N. Li, J.-Y. Wang, C. Wang, R.-Y. Wang, T. Guo, Y.-J. Cai, C.-Z. Liu, H.-T. Xiang, Q.-X. Shi, P. Huang, Q.-C. Chen, Y.-R. Li, **J. Wang**, Z.-H. Zhao, J. Wang. Genome sequence of foxtail millet (*Setaria italica*) provides insights into grass evolution and biofuel potential. *Nature Biotechnology*, **30**, 549-554, 2012.
- 22) X. Xu, Y. Hou, X.-Y. Yin, L. Bao, A.-F. Tang, L.-T Song, F.-Q. Li, S. Tsang, K. Wu, H.-J. Wu, W.-M. He, L. Zeng, M.-J. Xing, R.-H. Wu, H. Jiang, X. Liu, D.-D. Cao, G.-W. Guo, X.-D. Hu, Y.-T. Gui, Z.-S. Li, W.-Y. Xie, X.-J. Sun, M. Shi, Z.-M. Cai, B. Wang, M.-M. Zhong, J.-X. Li, Z.-H. Lu, N. Gu, X.-Q. Zhang, L. Goodman, L. Bolund, J. Wang, H.-M. Yang, K. Kristiansen, M. Dean, Y.-R. Li, **J. Wang**. Single-cell exome sequencing reveals single-nucleotide mutation characteristics of a kidney tumor. *Cell*, **148**, 886-895, 2012.
- 23) Y. Hou, L.-T. Song, P. Zhu, B. Zhang, Y. Tao, X. Xu, F.-Q. Li, K. Wu, J. Liang, D. Shao, H.-J. Wu, X.-F. Ye, C. Ye, R.-H. Wu, M. Jian, Y. Chen, W. Xie, R.-R. Zhang, L. Chen, X. Liu, X.-T. Yao, H.-C. Zheng, C. Yu, Q.-B. Li, Z.-L. Gong, M. Mao, X. Yang, L. Yang, J.-X. Li, W. Wang, Z.-H. Lu, N. Gu, G. Laurie, L. Bolund, K. Kristiansen, J. Wang, H.-M. Yang, Y.-R. Li, X.-Q. Zhang, **J. Wang**. Single-cell exome sequencing and monoclonal evolution of a JAK2-negative myeloproliferative neoplasm. *Cell*, **148**, 873-885, 2012.
- 24) Z.-Y. Peng, Y.-B. Cheng, B. C.-M. Tan, L. Kang, Z.-J. Tian, Y.-K. Zhu, W.-W. Zhang, Y. Liang, X.-D. Hu, X.-M. Tan, J. Guo, Z.-R. Dong, Y. Liang, L. Bao, **J. Wang**. Comprehensive analysis of RNA-Seq data reveals extensive RNA editing in a human transcriptome. *Nature Biotechnology*, **30**, 253-260, 2012.
- 25) N.-D. Young, A.-R. Jex, B. Li, S.-P. Liu, L.-F. Yang, Z.-J. Xiong, Y.-R. Li, C. Cantacessi, R. S. Hall, X. Xu, F.-Y. Chen, X. Wu, A. Zerlotini, G. Oliveira, A. Hofmann, G.-J. Zhang, X.-D. Fang, Y. Kang, B.-E. Campbell, A. Loukas, S.

- Ranganathan, D. Rollinson, G. Rinaldi, P.-J. Brindley, H.-M. Yang, **J. Wang**, J. Wang, R.-B. Gasser. Whole-genome sequence of *Schistosoma haematobium*. *Nature Genetics*, **44**, 221-225, 2012.
- 26) X. Xu, X. Liu, S. Ge, J. D. Jensen, F.-Y. Hu, X. Li, Y. Dong, R. N. Gutenkunst, L. Fang, L. Huang, J.-X. Li, W.-M. He, G.-J. Zhang, X.-M. Zheng, F.-M. Zhang, Y.-R. Li, C. Yu, K. Kristiansen, X.-Q. Zhang, J. Wang, M. Wright, S. McCouch, R. Nielsen, **J. Wang**, W. Wang. Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. *Nature Biotechnology*, **30**, 105-111, 2012.
- 27) G.-W. Guo, Y.-T. Gui, S.-J. Gao, A.-F. Tang, X.-D. Hu, Y. Huang, W.-L. Jia, Z.-S. Li, M.-H. He, L. Sun, P.-F. Song, X.-J. Sun, X.-K. Zhao, S.-M. Yang, C.-Z. Liang, S.-Q. Wan, F.-J. Zhou, C. Chen, J.-L. Zhu, X.-X. Li, M.-H. Jian, L. Zhou, R. Ye, P.-D. Huang, J. Chen, T. Jiang, X. Liu, Y. Wang, J. Zou, Z.-M. Jiang, R.-H. Wu, S. Wu, F. Fan, Z.-F. Zhang, L. Liu, R.-L. Yang, X.-W. Liu, H.-B. Wu, W.-H. Yin, X. Zhao, Y.-C. Liu, H.-H. Peng, B.-H. Jiang, Q.-X. Feng, C.-L. Li, J. Xie, J.-X. Lu, K. Kristiansen, Y.-R. Li, X.-Q. Zhang, S.-G. Li, J. Wang, H.-M. Yang, Z.-M. Cai , **J. Wang**. Frequent mutations of genes encoding ubiquitin-mediated proteolysis pathway components in clear cell renal cell carcinoma. *Nature Genetics*, **44**, 17-19, 2012.
- 28) A.-R. Jex, S.-P. Liu, B. Li, N.-D. Young, R.-S. Hall, Y.-R. Li, L.-F. Yang, N. Zeng, X. Xu, Z.-J. Xiong, F.-Y. Chen, X. Wu, G.-J. Zhang, X.-D. Fang, Y. Kang, G.-A. Anderson, T.-W. Harris, B.-E. Campbell, J. Vlaminck, T. Wang, C. Cantacessi, E.-M. Schwarz, S. Ranganathan, P. Geldhof, P. Nejsum, P.-W. Sternberg, H.-M. Yang, **J. Wang**, J. Wang, R.-B. Gasser. *Ascaris suum* draft genome. *Nature*, **479**, 529-533, 2011.
- 29) E.-B. Kim, X.-D. Fang, A.-A. Fushan, Z.-Y. Huang, A.-V. Lobanov, L.-J. Han, S.-M. Marino, X.-Q. Sun, A.- A. Turanov, P.-C. Yang, S.-H Yim, X. Zhao, M.-V. Kasaikina, N. Stoletzki, C.-F. Peng, P. Polak, Z.-Q. Xiong, A.-K, Y.-B. Zhu, Y.-X. Chen, G.-V. Kryukov, Q. Zhang, L. Peshkin, L. Yang, R.-T. Bronson, R. Buffenstein, B. Wang, C.-L. Han, Q.-Y. Li, L. Chen, W. Zhao, S.-R. Sunyaev, T.-J. Park, G.-J. Zhang, **J. Wang**, V.-N. Gladyshev. Genome sequencing reveals insights into physiology and longevity of the naked mole rat. *Nature*, **479**, 223-227, 2011.

- 30) M. Rasmussen, X.-S. Guo, Y. Wang, K. E. Lohmueller, S. Rasmussen, A. Albrechtsen, L. Skotte, S. Lindgreen, M. Metspalu, T. Jombart, T. Kivisild, W.-W. Zhai, A. Eriksson, A. Manica, L. Orlando, F. M. D. L. Vega, S. Tridico, E. Metspalu, K. Nielsen, M. C. Á vila-Arcos, J. V. M. Mayar, C. Muller, J. Dortch, M. T. P. Gilbert, O. Lund, A. Wesolowska, M. Karmin, L. A. Weinert, B. Wang, J. Li, S.-S. Tai, F. Xiao, T. Hanihara, G. v. Driem, A. R. Jha, F.-X. Ricaut, P. d. Knijff, A. B. Migliano, I. G. Romero, K. Kristiansen, D. M. Lambert, S. Brunak, P. Forster, B. Brinkmann, O. Nehlich, M. Bunce, M. Richards, R. Gupta, C. D. Bustamante, A. Krogh, R. A. Foley, M. M. Lahr, F. Balloux, T. S. Pontén, R. Villemans, R. Nielsen, **J. Wang**, E. Willerslev. An aboriginal Australian genome reveals separate human dispersals into Asia. *Science*, **334**, 94-98, 2011.
- 31) The Brassica rapa Genome Sequencing Project Consortium, X.-W. Wang, H.-Z. Wang, **J. Wang**, R.-F. Sun, J. Wu, S.-Y. Liu, Y.-Q. Bai, J.-H. Mun, I. Bancroft, F. Cheng, S.-W. Huang, X.-X Li, W. Hua, J.-Y. Wang, X.-Y. Wang, M. Freeling, J. C. Pires, A. H. Paterson, B. Chalhoub, B. Wang, A. Hayward, A.-G. Sharpe, B.-S. Park, B. Weisshaar, B.-H. Liu, B. Li, B. Liu, C.-B Tong, C. Song, C. Duran, C.-F. Peng, C.-Y. Geng, C. Koh, C.-Y. Lin, D. Edwards, D.-S. Mu, D. Shen, E. Soumpourou, F. Li, F. Fraser, G. Conant, G. Lassalle, G. J. King, G. Bonnema, H.-B. Tang, H.-P. Wang, H. Belcram, H.-L. Zhou, H. Hirakawa, H. Abe, H. Guo, H. Wang, H.-Z. Jin, I. A. P. Parkin, J. Batley, J.-S. Kim, J. Just, J.-W. Li, J.-H. Xu, J. Deng, J. A. Kim, J.-P. Li, J.-Y. Yu, J.-L. Meng, J.-P. Wang, J.-M. Min, J. Poulaing, J. Wang, K. Hatakeyama, K. Wu, L. Wang, L. Fang, M. Trick, M. G. Links, M. Zhao, M.-N. Jin, N. Ramchiary, N. Drou, P. J. Berkman, Q.-L. Cai, Q.-F. Huang, R.-Q. Li, S. Tabata, S.-F. Cheng, S. Zhang, S.-J. Zhang, S.-M. Huang, S. Sato, S.-L. Sun, S.-J. Kwon, S.-R. Choi, T.-H. Lee, W. Fan, X. Zhao, X. Tan, X. Xu, Y. Wang, Y. Qiu, Y. Yin, Y.-R. Li, Y.-C. Du, Y.-C. Liao, Y. Lim, Y. Narusaka, Y.-P. Wang, Z.-Y. Wang, Z.-Y. Li, Z.-W. Wang, Z.-Y. Xiong, Z.-H. Zhang. The genome of the mesopolyploid crop species *Brassica rapa*. *Nature Genetics*, **43**, 1035-1039, 2011.
- 32) Y.-T. Gui, G.-W. Guo, Y. Huang, X.-D. Hu, A.-F. Tang, S.-J. Gao, R.-H. Wu, C. Chen, X.-X. Li, L. Zhou, M.-H. He, Z.-S. Li, X.-J. Sun, W.-L. Jia, J.-N. Chen, S.-M. Yang, F.-J. Zhou, X.-K. Zhao, S.-Q. Wan, R. Ye, C.-Z. Liang, Z.-S. Liu, P.-D. Huang, C.-X. Liu, H. Jiang, Y. Wang, H.-C. Zheng, L. Sun, X.-W. Liu, Z.-M. Jiang, D.-F.

- Feng, J. Chen, S. Wu, J. Zou, Z.-F. Zhang, R.-L. Yang, J. Zhao, C.-J. Xu, W.-H. Yin, Z.-C. Guan, J.-X. Ye, H. Zhang, J.-X. Li, K. Kristiansen, M. L. Nickerson, D. Theodorescu, Y.-R. Li, X.-Q. Zhang, S.-G. Li, J. Wang, H.-M. Yang, **J. Wang**, Z.-M. Cai. Frequent mutations of chromatin remodeling genes in transitional cell carcinoma of the bladder. *Nature Genetics*, **43**, 875-878, 2011.
- 33) X. Xu, H. Nagarajan, N. E. Lewis, S.-K. Pan, Z.-M. Cai, X. Liu, W.-B. Chen, M. Xie, W.-L. Wang, S. Hammond, M. R. Andersen, N. Neff, B. Passarelli, W. Koh, H. C. Fan, J.-B. Wang, Y.-T. Gui, K. H. Lee, M. J. Betenbaugh, S. R. Quake, I. Famili, B. O. Palsson , **J. Wang**. The genomic sequence of the Chinese hamster ovary (CHO)-K1 cell line. *Nature Biotechnology*, **29**, 735-741, 2011.
- 34) Y.-R. Li, H.-C. Zheng, R.-B. Luo, H.-L. Wu, H.-M. Zhu, R.-Q. Li, H.-Z. Cao, B.-X. Wu, S.-J. Huang, H.-J. Shao, H.-Z. Ma, F. Zhang, S.-J. Feng, W. Zhang, H.-L. Du, G. Tian, J.-X. Li, X.-Q. Zhang, S.-G. Li, L. Bolund, K. Kristiansen, A. J. Smith, A. I. F. Blakemore, L. J. M. Coin, H.-M. Yang, J. Wang , **J. Wang**. Structural variation in two human genomes mapped at single-nucleotide resolution by whole genome *de novo* assembly. *Nature Biotechnology*, **29**, 723-730, 2011.
- 35) **J. Wang**. Genome-sequencing anniversary. Personal genomes: for one and for all. *Science*, **331**, 690, 2011.
- 36) H.-M. Lam, X. Xu, X. Liu, W.-B Chen, G.-H. Yang, F.-L. Wong, M.-W. Li, W.-M. He, N. Qin, B. Wang, J. Li, M. Jian, J. Wang, G.-H. Shao, **J. Wang**, Samuel S.-M. Sun , G.-Y. Zhang. Resequencing of 31 wild and cultivated soybean genomes identifies patterns of genetic diversity and selection. *Nature Genetics*, **42**, 1053-1059, 2010.
- 37) J.-S. Lai, R.-Q. Li, X. Xu, W.-W. Jin, M.-L. Xu, H.-N. Zhao, Z.-K. Xiang, W.-B. Song, K. Ying, M. Zhang, Y.-P. Jiao, P.-X. Ni, J.-G. Zhang, D. Li, X.-S. Guo, K.-X. Ye, M. Jian, B. Wang, H.-S. Zheng, H.-Q Liang, X.-Q. Zhang, S.-C. Wang, S.-J. Chen, J.-S. Li, Y. Fu, N. M. Springer, H.-M. Yang, J. Wang, J.-R. Dai, P. S. Schnable, **J. Wang**. Genome-wide patterns of genetic variation among elite maize inbred lines. *Nature Genetics*, **42**, 1027-1030, 2010.
- 38) Y.-R. Li, N. Vinckenbosch, G. Tian, E. H. Sanchez, T. Jiang, H. Jiang, A. Albrechtsen, G. Andersen, H.-Z. Cao, T. Korneliussen, N. Grarup, Y.-R. Guo, I. Hellman, X. Jin, Q.-B. Li, J.-T. Liu, X. Liu, T. Sparsø, M.-F. Tang, H.-L. Wu, R.-H.

- Wu, C. Yu, H.-C. Zheng, A. Astrup, L. Bolund, J. Holmkvist, T. Jørgensen, K. Kristiansen, O. Schmitz, T. W. Schwartz, X.-Q. Zhang, R.-Q. Li, H.-M. Yang, J. Wang, T. Hansen, O. Pedersen, R. Nielsen , **J. Wang**. Resequencing of 200 human exomes identifies an excess of low-frequency non-synonymous coding variants. *Nature Genetics*, **42**, 969-972, 2010.
- 39) R. Bonasio, G.-J. Zhang, C.-Y. Ye, N. S. Mutti, X.-D. Fang, N. Qin, G. Donahue, P.-C. Yang, Q.-Y. Li, C. Li, P. Zhang, Z.-Y. Huang, S. L. Berger, D. Reinberg, **J. Wang**, J. Liebig. Genomic comparison of the ants *Camponotus floridanus* and *Harpegnathos saltator*. *Science*, **329**, 1068-1071, 2010.
- 40) X. Yi, Y. Liang, E. H. Sanchez, X. Jin, Z. X. P. Cuo, J. E. Pool, X. Xu, H. Jiang, N. Vinckenbosch, T. S. Korneliussen, H.-C. Zheng, T. Liu, W.-M. He, K. Li, R.-B. Luo, X.-F. Nie, H.-L. Wu, M.-R. Zhao, H.-Z. Cao, J. Zou, Y. Shan, S.-Z. Li, Q. Yang, Asan, P.-X. Ni, G. Tian, J.-M. Xu, X. Liu, T. Jiang, R.-H. Wu, G.-Y. Zhou, M.-F. Tang, J.-J. Qin, T. Wang, S.-J. Feng, G.-H. Li, Huasang, J.-B. Luosang, W. Wang, F. Chen, Y.-D. Wang, X.-G. Zheng, Z. Li, Z. Bianba, G. Yang, X.-P. Wang, S.-H. Tang, G.-Y. Gao, Y. Chen, Z. Luo, L. Gusang, Z. Cao, Q.-H. Zhang, W.-H. Ouyang, X.-L. Ren, H.-Q. Liang, H.-S. Zheng, Y.-B. Huang, J.-X. Li, L. Bolund, K. Kristiansen, Y.-R. Li, Y. Zhang, X.-Q. Zhang, R.-Q. Li, S.-G. Li, H.-M. Yang, R. Nielsen, **J. Wang**, J. Wang. Sequencing of 50 human exomes reveals adaptation to high altitude. *Science*, **329**, 75-78, 2010.
- 41) H. Xiang, J.-D. Zhu, Q. Chen, F.-Y. Dai, X. Li, M.-W. Li, H.-Y. Zhang, G.-J. Zhang, D. Li, Y. Dong, L. Zhao, Y. Lin, D.-J. Cheng, J. Yu, J.-F. Sun, X.-Y. Zhou, K.-L. Ma, Y.-H. He, Y.-X. Zhao, S.-C. Guo, M.-Z. Ye, G.-W. Guo, Y.-R. Li, R.-Q. Li, X.-Q. Zhang, L.-J. Ma, K. Kristiansen, Q.-H. Guo, J.-H. Jiang, S. Beck, Q.-Y. Xia, W. Wang, **J. Wang**. Single base-resolution methylome of the silkworm reveals a sparse epigenomic map. *Nature Biotechnology*, **28**, 516-520, 2010.
- 42) J.-J. Qin, R.-Q. Li, J. Raes, M. Arumugam, K.-S. Burgdorf, C. Manichanh, T. Nielsen, N. Pons, F. Levenez, T. Yamada, D. R. Mende, J.-H. Li, J.-M. Xu, S.-C. Li, D.-F. Li, J.-J. Cao, B. Wang, H.-Q. Liang, H.-S. Zheng, Y.-L. Xie, J.-L. Tap, P. Lepage, M. Bertalan, J.-M. Batto, T. Hansen, D. L. Paslier, A. Linneberg, H. B. Nielsen, E. Pelletier, P. Renault, T. S. Ponten, K. Turner, H.-M. Zhu, C. Yu, S.-T. Li, M. Jian, Y. Zhou, Y.-R. Li, X.-Q. Zhang, S.-G. Li, N. Qin, H.-M. Yang, J. Wang, S.

- Brunak, J. Doré, F. Guarner, K. Kristiansen, O. Pedersen, J. Parkhill, J. Weissenbach, MetaHIT Consortium, P. Bork, S. D. Ehrlich , **J. Wang**. A human gut microbial gene catalogue established by metagenomic sequencing. *Nature*, **464**, 59-65, 2010.
- 43) M. Rasmussen, Y.-R. Li, S. Lindgreen, J. S. Pedersen, A. Albrechtsen, I. Moltke, M. Metspalu, E. Metspalu, T. Kivisild, R. Gupta, M. Bertalan, K. Nielsen, M. T. P. Gilbert, Y. Wang, M. Raghavan, P. F. Campos, H. M. Kamp, A. S. Wilson, A. Gledhill, S. Tridico, M. Bunce, E. D. Lorenzen, J. Binladen, X.-S. Guo, J. Zhao, X.-Q. Zhang, H. Zhang, Z. Li, M.-F. Chen, L. Orlando, K. Kristiansen, M. Bak, N. Tommerup, C. Bendixen, T. L. Pierre, B. Grønnow, M. Meldgaard, C. Andreasen, S. A. Fedorova, L. P. Osipova, T. F. G. Higham, C. B. Ramsey, T. v. O. Hansen, F. C. Nielsen, M. H. Crawford, S. Brunak, T. S. Pontén, R. Villemans, R. Nielsen, A. Krogh, **J. Wang**, E. Willerslev. Ancient human genome sequence of an extinct Palaeo-Eskimo. *Nature*, **463**, 757-762, 2010.
- 44) R.-Q. Li, W. Fan, G. Tian, H.-M. Zhu, L. He, J. Cai, Q.-F. Huang, Q.-L. Cai, B. Li, Y.-Q. Bai, Z.-H. Zhang, Y.-P. Zhang, W. Wang, J. Li, F.-W. Wei, H. Li, M. Jian, J.-W. Li, Z.-L. Zhang, R. Nielsen, D.-W. Li, W.-J. Gu, Z.-T. Yang, Z.-L. Xuan, O. A. Ryder, F. C.-C. Leung, Y. Zhou, J.-J Cao, X. Sun, Y.-G. Fu, X.-D. Fang, X.-S. Guo, B. Wang, R. Hou, F.-J. Shen, B. Mu, P.-X. Ni, R.-M. Lin, W.-B. Qian, G.-D. Wang, C. Yu, W.-H. Nie, J.-H. Wang, Z.-G. Wu, H.-Q. Liang, J.-M Min, Q. Wu, S.-F. Cheng, J. Ruan, M.-W. Wang, Z.-B. Shi, M. Wen, B.-H. Liu, X.-L. Ren, H.-S. Zheng, D. Dong, K. Cook, G. Shan, H. Zhang, C. Kosiol, X.-Y. Xie, Z.-H. Lu, H.-C. Zheng, Y.-R. Li, C. C. Steiner, T. T.-Y. Lam, S.-Y. Lin, Q.-H. Zhang, G.-Q. Li, J. Tian, T.-M. Gong, H.-D. Liu, D.-J. Zhang, L. Fang, C. Ye, J.-B. Zhang, W.-B. Hu, A.-L. Xu, Y.-Y. Ren, G.-J. Zhang, M. W. Bruford, Q.-B. Li, L.-J. Ma, Y.-R. Guo, N. An, Y.-J. Hu, Y. Zheng, Y.-Y. Shi, Z.-Q. Li, Q. Liu, Y.-L. Chen, J. Zhao, N. Qu, S.-C. Zhao, F. Tian, X.-L. Wang, H.-Y. Wang, L.-Z. Xu, X. Liu, T. Vinar, Y.-J Wang, T.-W. Lam, S.-M. Yiu, S.-P. Liu, H.-M. Zhang, D.-S. Li, Y. Huang, X. Wang, G.-H. Yang, Z. Jiang, J.-Y. Wang, N. Qin, L. Li, J.-X. Li, L. Bolund, K. Kristiansen, G. K.-S. Wong, M. Olson, X.-Q. Zhang, S.-G. Li, H.-M. Yang, J. Wang, **J. Wang**. The sequence and de novo assembly of the giant panda genome. *Nature*, **463**, 311-317, 2010.
- 45) R.-Q. Li, Y.-R. Li, H.-C. Zheng, R.-B. Luo, H.-M. Zhu, Q.-B. Li, W.-B. Qian, Y.-Y. Ren, G. Tian, J.-X. Li, G.-Y. Zhou, X. Zhu, H.-L. Wu, J.-J. Qin, X. Jin, D.-F. Li,

- H.-Z. Cao, X.-D. Hu, H. Blanche, H. Cann, X.-Q. Zhang, S.-G. Li, L. Bolund, K. Kristiansen, H.-M. Yang, **J. Wang**, J. Wan. Building the sequence map of the human pan-genome. *Nature Biotechnology*, **28**, 57-63, 2010.
- 46) S.-W. Huang, R.-Q. Li, Z.-H. Zhang, L. Li, X.-F. Gu, W. Fan, W. J. Lucas, X.-W. Wang, B.-Y. Xie, P.-X. Ni, Y.-Y. Ren, H.-M. Zhu, J. Li, K. Lin, W.-W. Jin, Z.-J. Fei, G.-C. Li, J. Staub, A. Kilian, E.-A.G.van.der. Vossen, Y. Wu, J. Guo, J. He, Z.-Q. Jia, Y. Ren, G. Tian, Y. Lu, J. Ruan, W.-B. Qian, M.-W Wang, Q.-F. Huang, B. Li, Z.-L. Xuan, J.-J. Cao, A. san, Z.-G. Wu, J.-B. Zhang, Q.-L. Cai, Y.-Q. Bai, B.-W. Zhao, Y.-H. Han, Y. Li, X.-F Li, S.-H. Wang, Q.-X. Shi, S.-Q. Liu, W.- K. Cho, J.-Y. Kim, Y. Xu, K. Heller-Uszynska, H. Miao, Z.-C. Cheng, S.-P Zhang, J. Wu, Y.-H. Yang, H.-X. Kang, M. Li, H.-Q. Liang, X.-L. Ren, Z.-B. Shi, M. Wen, M. Jian, H.-L. Yang, G.-J. Zhang, Z.-T. Yang, R. Chen, S.-F. Liu, J.-W. Li, L.-J. Ma, H. Liu, Y. Zhou, J. Zhao, X.-D. Fang, G.-Q. Li, L. Fang, Y.-R. Li, D.-Y. Liu, H.-K. Zheng, Y. Zhang, N. Qin, Z. Li, G.-H. Yang, S. Yang, L. Bolund, K. Kristiansen, H.-C. Zheng, S.-C. Li, X.-Q. Zhang, H.-M. Yang, J. Wang, R.-F. Su, B.-X. Zhang, S.-Z. Jiang, **J. Wang**, Y.-C. Du , S.-G. Li. The genome of the cucumber, *Cucumis sativus* L.. *Nature Genetics*, **41**, 1275-1281, 2009.
- 47) Q.-Y. Xia, Y.-R. Guo, Z. Zhang, D. Li, Z.-L. Xuan, Z. Li, F.-Y. Dai, Y.-R. Li, D.-J. Cheng, R.-Q. Li, T.-C. Cheng, T. Jiang, C. Becquet, X. Xu, C. Liu, X.-F Zha, W. Fan, Y. Lin, Y.-H Shen, L. Jiang, J. Jensen, I. Hellmann, S. Tang, P. Zhao, H.-F Xu, C. Yu, G.-J. Zhang, J. Li, J.-J. Cao, S.-P. Liu, N.-J He, Y. Zhou, H. Liu, J. Zhao, C. Ye, Z.-H Du, G.-Q. Pan, A.-C. Zhao, H.-J. Shao, W. Zeng, P. Wu, C.-F Li, M,-H Pan, J,-J Li, X.-Y Yin, D.-W. Li, J. Wang, H.-S. Zheng, W. Wang, X.-Q. Zhang, S.-G. Li, H.-M. Yang, Ch. Lu, R. Nielsen, Z.-Y. Zhou, J. Wang, Z.-H. Xiang, **J. Wang**. Complete resequencing of 40 genomes reveals domestication events and genes in silkworm (*Bombyx*). *Science*, **326**, 433-436, 2009.
- 48) Y.-R. Li , **J. Wang**. Faster human genome sequencing. *Nature Biotechnology*, **27**, 820-821, 2009.
- 49) **J. Wang**, W. Wang, R.-Q. Li, Y.-R. Li, G. Tian, L. Goodman, W. Fan, J.-Q. Zhang, J. Li, J.-B. Zhang, Y.-R. Guo, B.-X. Feng, H. Li, Y. Lu, X.-D. Fang, H.-Q. Liang, Z.-L. Du, D. Li, Y.-Q. Zhao, Y.-J. Hu, Z.-Z. Yang, H.-C. Zheng, I. Hellmann, M. Inouye, J. Pool, X. Yi, J. Zhao, J.-J. Duan, Y. Zhou, J.-J. Qin, L.-J. Ma, G.-Q. Li, Z.-T. Yang,

- G.-J. Zhang, B. Yang, C. Yu, F. Liang, W.-J. Li, S.-C. Li, D.-W. Li, P.-X. Ni, J. Ruan, Q.-B. Li, H.-M. Zhu, D.-Y. Liu, Z.-K. Lu, N. Li, G.-W. Guo, J.-G. Zhang, J. Ye, L. Fang, Q. Hao, Q. Chen, Y. Liang, Y.-Y. Su, A. San, C. Ping, S. Yang, F. Chen, L. Li, K. Zhou, H.-K. Zheng, Y.-Y. Ren, L. Yang, Y. Gao, G.-H. Yang, Z. Li, X.-L. Feng, K. Kristiansen, G. K.-S. Wong, R. Nielsen, R. Durbin, L. Bolund, X.-Q. Zhang, S.-G. Li, H.-M. Yang , J. Wang. The diploid genome sequence of an Asian individual. *Nature*, **456**, 60-65, 2008.
- 50) H. Rohde, J.-J. Qin, Y.-J. Cui, D.-F. Li, N.-J. Loman, M. Hentschke, W.-T. Chen, F. Pu, Y.-Q. Peng, J.-H. Li, F. Xi, S.-H. Li, Y. Li, Z.-X. Zhang, X.-W. Yang, M.-R. Zhao, P. Wang, Y.-L. Guan, Z. Cen, X.-N. Zhao, M.-T. Christner, R. Kobbe, S. Loos, J. Oh, L. Yang, A. Danchin, G.-F. Gao, Y.-J. Song, Y.-R. Li, H.-M. Yang, J. Wang, J.-G. Xu, M.-J. Pallen, **J. Wang**, M. Aepfelbacher, R.-F. Yang and the E. coli O104:H4 Genome Analysis Crowd-Sourcing Consortium. Open-source genomic analysis of Shiga-toxin-producing E. coli O104:H4. *The New England Journal of Medicine*, **365**, 718-724, 2011.
- 51) Biology analysis group, Q.-Y. Xia, Z.-Y. Zhou, C. Lu, D.-J. Cheng, F.-Y. Dai, B. Li, P. Zhao, X.-f. Zha, T.-C. Cheng, C.-L. Chai, G.-Q. Pan, J.-S. Xu, C. Liu, Y. Lin, J.-F. Qian, Y. Hou, Z.-L. Wu, G.-R. Li, M.-H. Pan, C.-F. Li, Y.-H. Shen, X.-Q. Lan, L.-W. Yuan, T. Li, H.-F. Xu, G.-W. Yang, Y.-J. Wan, Y. Zhu, M.-D. Yu, W.-D. Shen, D.-Y. Wu, Z.-H. Xiang, Genome analysis group, J. Yu, **J. Wang**, R.-Q. Li, J.-P. Shi, H. Li, G.-Y. Li, J.-N. Su, X.-L. Wang, G.-Q. Li, Z.-J. Zhang, Q.-F. Wu, J. Li, Q.-P. Zhang, N. Wei, J.-Z. Xu, H.-B. Sun, L. Dong, D.-Y. Liu, S.-L. Zhao, X.-L. Zhao, Q.-S. Meng, F.-D. Lan, X.-G. Huang, Y.-Z. Li, L. Fang, C.-F. Li, D.-W. Li, Y.-Q. Sun, Z.-P. Zhang, Z. Yang, Y.-Q. Huang, Y. Xi, Q.-H. Qi, D.-D. He, H.-Y. Huang, X.-W. Zhang, Z.-Q. Wang, W.-J. Li, Y.-Z. Cao, Y.-P. Yu, H. Yu, J.-H. Li, J.-H. Ye, H. Chen, Y. Zhou, B. Liu, J. Wang, J. Ye, H. Ji, S.-T. Li, P.-X. Ni, J.-G. Zhang, Y. Zhang, H.-K. Zheng, B.-Y. Mao, W. Wang, C. Ye, S.-G. Li, J. Wang, G. K.-S. Wong, H.-M. Yang. A draft sequence for the genome of the domesticated silkworm (*Bombyx mori*). *Science*, **306**, 1937-1940, 2004.
- 52) **J. Wang**, J.-G. Zhang, H.-K. Zheng, J. Li, D.-Y. Liu, H. Li, R. Samudrala, J. Yu , G. K.-S. Wong. Mouse transcriptome: neural evolution of 'non-coding' complementary DNAs. *Nature*, **431**, 1 p following 757, 2004.

- 53) **J. Wang**, S.-T. Li, Y. Zhang, H.-K. Zheng, Z. Xu, J. Ye, J. Yu, G. Wong. Vertebrate gene predictions and the problem of large genes. *Nature Review Genetics*, **4**, 741-749, 2003.
- 54) J. Yu, S.-N. Hu, **J. Wang**, G. K.-S. Wong, S.-G. Li, B. Liu, Y.-J. Deng, L. Dai, Y. Zhou, X.-Q. Zhang, M.-L. Cao, J. Liu, J.-D. Sun, J.-B. Tang, Y.-J. Chen, X.-B. Huang, W. Lin, C. Ye, W. Tong, L.-J. Cong, J.-N. Geng, Y.-J. Han, L. Li, W. Li, G.-Q. Hu, X.-G. Huang, W.-J. Li, J. Li, Z.-W. Liu, L. Li, J.-P. Liu, Q.-H. Qi, J.-S. Liu, L. Li, T. Li, X.-G. Wang, H. Lu, T.-T. Wu, M. Zhu, P.-X. Ni, H. Han, W. Dong, X.-Y. Ren, X.-L. Feng, P. Cui, X.-R. Li, H. Wang, X. Xu, W.-X. Zhai, Z. Xu, J.-S. Zhang, S.-J. He, J.-G. Zhang, J.-C. Xu, K.-L. Zhang, X.-W. Zheng, J.-H. Dong, W.-Y. Zeng, L. Tao, J. Ye, J. Tan, X.-D. Ren, X.-W. Chen, J. He, D.-F. Liu, W. Tian, C.-G. Tian, H.-A. Xia, Q.-Y. Bao, G. Li, H. Gao, T. Cao, J. Wang, W.-M. Zhao, P. Li, W. Chen, X.-D. Wang, Y. Zhang, J.-F. Hu, J. Wang, S. Liu, J. Yang, G.-Y. Zhang, Y.-Q. Xiong, Z.-J. Li, L. Mao, C.-S. Zhou, Z. Zhu, R.-S. Chen, B.-L. Hao, W.-M. Zheng, S.-Y. Chen, W. Guo, G.-J. Li, S.-Q. Liu, M. Tao, J. Wang, L.-H. Zhu, L.-P. Yuan, and H.-M. Yang. A draft sequence of the rice genome (*Oryza sativa* L. ssp. *indica*). *Science*, **296**, 79-92, 2002.
- 55) R.-L. Ge, Q.-L. Cai, Y.-Y. Shen, A. San, L. Ma, Y. Zhang, X. Yi, Y. Chen, L.-F. Yang, Y. Huang, R.-J He, Y.-Y. Hui, M.-R. Hao, Y. Li, B. Wang, X.-H. Ou, J.-H. Xu, Y.-F. Zhang, K. Wu, C.-Y Geng, W.-P. Zhou, T.-C. Zhou, D.-M. Irwin, Y.-Z. Yang, L. Ying, H.-H. Bao, J. Kim, D.-M. Larkin, J. Ma, H.-A. Lewin, J.-C. Xing, Roy.-N. Platt II, D.-A. Ray, L. Auvil, B. Capitanu, X.-F Zhang, G.-J. Zhang, R.-W. Murphy, **J. Wang**, Y.-P. Zhang, J. Wang. Draft genome sequence of the Tibetan antelope. *Nature Communications*, **4**, 1858, 2013.
- 56) Z. Wang, J.-P. Anaya, A. Zadissa, W.-Q. Li, Y. Niimura, Z.-Y. Huang, C.-Y. Li, S. White, Z.-Q. Xiong, D.-M. Fang, B. Wang, Y. Ming, Y. Chen, Y. Zheng, S. Kuraku, M. Pignatelli, J. Herrero, K. Beal, M. Nozawa, Q.-Y. Li, J. Wang, H.-Y. Zhang, L.-L. Yu, S. Shigenobu, J.-Y. Wang, J.-N Liu, P. Flieck, S. Searle, **J. Wang**, S. Kuratani, Y. Yin, B. Aken, G.-J. Zhang, N. Irie. The draft genomes of soft-shell turtle and green sea turtle yield insights into the development and evolution of the turtle-specific body plan. *Nature Genetics*, **45**, 701–706, 2013.
- 57) M. Blaser, P. Bork, C. Fraser, R. Knight, **J. Wang**. The microbiome explored: recent

- insights and future challenges. *Nature Reviews Microbiology* 11, 213-217 (2013).
- 58) R. Pisko, Z.-Y. Peng, **J. Wang**, J.-B. Li. Lack of evidence for existence of noncanonical RNA editing. *Nature Biotechnology*, **31**, 19–20, 2013.
- 59) S.-C. Zhao, P.-P. Zheng, S.-S. Dong, X.-J Zhan, Q. Wu, X.-S. Guo, Y.-B. Hu, W.-M. He, S.-M. Zhang, W. Fan, L.-F. Zhu, D. Li, X.-M Zhang, Q. Chen, H.-M. Zhang, Z.-H. Zhang, X.-L. Jin, J.-G. Zhang, H.-M. Yang, J. Wang, **J. Wang**, F.-W. Wei. Whole-genome sequencing of giant pandas provides insights into demographic history and local adaptation. *Nature Genetics*, **45**, 67-71, 2012.
- 60) **J. Wang**, as one of the Principal Investigators (Production and Analysis Group) and Steering Committee member in The 1000 Genomes Project Consortium. The 1000 Genomes Project Consortium, *et al.* An integrated map of genetic variation from 1,092 human genomes. *Nature*, **491**, 56-65, 2012.
- 61) **J. Wang**, as one of the Principal Investigators (Production and Analysis Group) and Steering Committee member in The 1000 Genomes Project Consortium. The 1000 Genomes Project Consortium. A map of human genome variation from population-scale sequencing. *Nature*, **467**, 1061-1073, 2010.
- 62) **J. Wang** as one of first authors in the International Chicken Polymorphism Map Consortium. International Chicken Polymorphism Map Consortium. A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. *Nature*, **432**, 717-722, 2004.
- 63) M.-B. Hufford, X. Xu, J.-V. Heerwaarden, T. Pyhäjärvi, J.-M. Chia, R.-A. Cartwright, R.-J. Elshire, J.-C. Glaubitz, K.-E. Guill, S.-M. Kaepller, J.-S. Lai, P.-L. Morrell, L.-M. Shannon, C. Song, N.-M. Springer, R.-A.S. Wagner, P. Tiffin, **J. Wang**, G.-Y. Zhang, J. Doebley, M.-D. McMullen, D. Ware, E.-S. Buckler, S. Yang, R.-I. Jeffrey. Comparative population genomics of maize domestication and improvement. *Nature Genetics*, **44**, 808-811, 2012.
- 64) J.-M. Chia, C. Song, P. J. Bradbury, D. Costich, N. de Leon, J. Doebley, R. J. Elshire, B. Gaut, L. Geller, J. C. Glaubitz, M. Gore, K. E. Guill, J. Holland, M. B. Hufford, J.-S. Lai, M. Li, X. Liu, Y.-L. Lu, R. McCombie, R. Nelson, J. Poland, B. M. Prasanna, T. Pyhäjärvi, T.-Z. Rong, R. S. Sekhon, Q. Sun, M. I. Tenaillon, F. Tian, **J. Wang**, X. Xu, Z.-W. Zhang, S. M. Kaepller, R.-I. Jeffrey, M. D. McMullen, E. S. Buckler, G.-Y. Zhang, Y.-B. Xu , D. Ware. Maize HapMap2 identifies extant

variation from a genome in flux. *Nature Genetics*, **44**, 803-807, 2012.

- 65) M.-R. Nelson, D. Wegmann, M.-G. Ehm, D. Kessner, P.-St. Jean, C. Verzilli, J.-D. Shen, Z.-Z. Tang, S.-A. Bacanu, D. Fraser, L.-L. Warren, J. Aponte, M. Zawistowski, X. Liu, H. Zhang, Y. Zhang, J. Li, Y. Li, L. Li, P. Woollard, S. Topp, M. D. Hall, K. Nangle, **J. Wang**, G. Abecasis, L.-R. Cardon, S. Zöllner, J.-C. Whittaker, S.-L. Chissoe1, J. Novembre, V. Mooser. An abundance of rare functional variants in 202 drug target genes sequenced in 14,002 people. *Science*, **337**, 100-104, 2012.
- 66) D.-G. MacArthur, S. Balasubramanian, A. Frankish, N. Huang, J. Morris, K. Walter, L. Jostins, L. Habegger, J.-K. Pickrell, S.-B. Montgomery, C.-A. Albers, Z.-D. Zhang, D.-F. Conrad, G. Lunter, H.-C. Zheng, Q. Ayub, Mark. A. DePristo, E. Banks, M. Hu, R.-E. Handsaker, J.-A. Rosenfeld, M. Fromer, M. Jin, X.-M. J. Mu, E. Khurana, K. Ye, M. Kay, G.-I. Saunders, M.-M. Suner, T. Hunt, I.-H.A. Barnes, C. Amid, R. C.-S. Denise, A.-H. Bignell, C. Snow, B. Yngvadottir, S. Bumpstead, D.-N. Cooper, Y.-L Xue, I.-G. Romero, 1000 Genomes Project Consortium, **J. Wang**, Y.-R. Li, R.-A. Gibbs, S.-A. McCarroll, E.-T. Dermitzakis, J.-K. Pritchard, J.-C. Barrett, J. Harrow, M.-E. Hurles, M.-B. Gerstein, T.-S. Chris. A systematic survey of loss-of-function variants in human protein-coding genes. *Science*, **335**, 823-828, 2012.
- 67) M.-A.M. Groenen, A.-L. Archibald, H. Uenishi, C.-K. Tuggle, Y. Takeuchi, M.-F. Rothschild, R.-G. Claire, C. Park, D. Milan, H. JanMegens, S.-T. Li, D. Larkin, H. Kim, L.-A.F. Frantz, M. Caccamo, H. Ahn, B. L. Aken, A. Anselmo, C. Anthon, L. Auvil, B. Badaoui, C. W. Beattie, C. Bendixen, D. Berman, F. Blecha, J. Blomberg, L. Bolund, M. Bosse, S. Botti, B.-J. Zhan, M. Bystrom, B. Capitanu, C.-S. Denise, P. Chardon, C. Chen, R. Cheng, S.-H. Choi, W. Chow, R. C. Clark, C. Clee, R. P. M.-A. Crooijmans, H.-D. Dawson, P. Dehais, F. De. Sapiro, BertDibbits, N. Drou, Z.-Q. Du, K. Eversole, J.-o. Fadista, S. Fairley, T. Faraut, G.-J. Faulkner, K.-E. Fowler, M. Fredholm, E. Fritz, J. G. R. Gilbert, E. Giuffra, J. Gorodkin, D.-K. Griffin, J.-L. Harrow, A. Hayward, K. Howe, Z.-L. Hu, S.-J. Humphray, T. Hunt, H. Hornshøj, J.-T. Jeon, P. Jern, M. Jones, J. Jurka, H. Kanamori, R. Kapetanovic, J. Kim, J.-H. Kim, K.-W. Kim, T.-H. Kim, G. Larson, K. Lee, K.-T. Lee, R. Leggett, H. A. Lewin, Y.-R. Li, W.-S. Liu, J.-E. Loveland, Y. Lu, J.-K. Lunney, J. Ma, O. Madsen, K. Mann, L. Matthews, S. McLaren, T. Morozumi, M. P. Murtaugh, J. Narayan, D.-T. Nguyen,

- P.-X. Ni, S.-J. Oh, S. Onteru, F. Panitz, E.-W. Park, H.-S. Park, G. Pascal, Y. Paudel, P.-E. Miguel, R.-G. Ricardo, J. M. Reecy, R.-Z. Sandra, G. A. Rohrer, L. Rund, Y.-M. Sang, K. Schachtschneider, J. G. Schraiber, J. Schwartz, L. Scobie, C. Scott, S. Searle, B. Servin, B. R. Southey, G. Sperber, P. Stadler, J. V. Sweedler, H. Tafer, B. Thomsen, R. Wali, J. Wang, **J. Wang**, S. White, X. Xu, M. Yerle, G.-J. Zhang, J.-G. Zhang, J. Zhang, S.-H. Zhao, J. Rogers, C. Churcher, L. B. Schook. Analyses of pig genomes provide insight into porcine demography and evolution. *Nature*, **491**, 393-398, 2012.
- 68) **J. Wang**, as one of the authors in the The Tomato Genome Consortium. The Tomato Genome Consortium. The tomato genome sequence provides insights into fleshy fruit evolution. *Nature*, **485**, 635-641, 2012.
- 69) M.-Z. Li, H.-L. Wu, Z.-G. Luo, Y.-D. Xia, J.-Q. Guan, T. Wang, Y.-R. Gu, L. Chen, K. Zhang, J.-D. Ma, Y.-K. Liu, Z.-J. Zhong, J. Nie, S.-L. Zhou, Z.-P. Mu, X.-Y. Wang, J.-J. Qu, L. Jing, H.-Y. Wang, S.-J. Huang, N. Yi, Z. Wang, D.-X. Xi, J. Wang, G.-L. Yin, L. Wang, N. Li, Z. Jiang, Q.-L. Lang, H.-S. Xiao, A. Jiang, L. Zhu, Y.-Z. Jiang, G.-Q. Tang, M.-M. Mai, S.-R. Shuai, N. Li, K. Li, J.-Y. Wang, X.-Q. Zhang, Y.-R. Li, H.-S. Chen, X.-L. Gao, G. S. Plastow, S. Beck, H.-M. Yang, J. Wang, **J. Wang**, X.-W. Li, R.-Q. Li. An atlas of DNA methylomes in porcine adipose and muscle tissues. *Nature Communications*, **3**, 850, 2012.
- 70) R.-K. Varshney, W.-B. Chen, Y.-P. Li, A.-K. Bharti, R.-K. Saxena, J.-A. Schlueter, M. T. A. Donoghue, S. Azam, G.-Y. Fan, A.-M. Whaley, A.-D. Farmer, J. Sheridan, A. Iwata, R. Tuteja, R.-V. Penmetsa, W. Wu, H.-D. Upadhyaya, S.-P. Yang, T. Shah, K. B. Saxena, T. Michael, W.-R. McCombie, B. Yang, G.-Y. Zhang, H.-M. Yang, **J. Wang**, C. Spillane, D. R. Cook, G. D. May, X. Xu, S. A. Jackson. Draft genome sequence of pigeonpea (*Cajanus cajan*), an orphan legume crop of resource-poor farmers. *Nature Biotechnology*, **30**, 83-89, 2011.
- 71) G.-M. Yan, G.-J. Zhang, X.-D. Fang, Y.-F. Zhang, C. Li, F. Ling, D.-N. Cooper, Q.-Y. Li, Y. Li, A.-J. Gool, H.-L. Du, J.-S. Chen, R.-H. Chen, P. Zhang, Z.-Y. Huang, J.-R. Thompson, Y.-H. Meng, Y.-Q. Bai, J.-F. Wang, M. Zhuo, T. Wang, Y. Huang, L.-Q. Wei, J.-W. Li, Z.-W. Wang, H.-F. Hu, P.-C. Yang, L. Le, P.-D. Stenson, B. Li, X.-M. Liu, E.-V. Ball, N. An, Q.-F. Huang, Y. Zhang, W. Fan, X.-Q. Zhang, Y.-R. Li, W. Wang, M.-G. Katze, B. Su, R. Nielsen, H.-M. Yang, **J. Wang**, X.-N. Wang, J. Wang.

Genome sequencing and comparison of two nonhuman primate animal models, the cynomolgus and Chinese rhesus macaques. *Nature Biotechnology*, **29**, 1019-1023, 2011.

- 72) **J. Wang**, as one of the Principal Investigators in The Potato Genome Sequencing Consortium. The Potato Genome Sequencing Consortium. Genome sequence and analysis of the tuber crop potato. *Nature*, **475**, 189-195, 2011.
- 73) **J. Wang**, as one of the Principal Investigators (Production and Analysis Group) and Steering Committee member in The 1000 Genomes Project Consortium. D.-F. Conrad, J. E. M. Keebler, M.-A. DePristo, S.-J. Lindsay, Y.-J. Zhang, F. Casals, Y. Idaghdour, C.-L. Hartl, C. Torroja, K.-V. Garimella, M. Zilversmit, R. Cartwright, G.-A. Rouleau, M. Daly, E.-A. Stone, M.-E. Hurles , P. Awadalla for the 1000 Genomes Project. Variation in genome-wide mutation rates within and between human families. *Nature Genetics*, **43**, 712-714, 2011.
- 74) **J. Wang**, as one of the Principal Investigators (Production and Analysis Group) and Steering Committee member in The 1000 Genomes Project Consortium. Ryan.-D. Hernandez, J.-L. Kelley, E. Elyashiv, S.-C. Melton1, A. Auton, G. McVean, 1000 Genomes Project, G. Sella, Molly Przeworski. Classic selective sweeps were rare in recent human evolution. *Science*, **331**, 920-924, 2011.
- 75) R.-E. Mills, K. Walter, C. Stewart, R.-E. Handsaker, K. Chen, C. Alkan, A. Abyzov, S.-C. Yoon, K. Ye, R.-K. Cheetham, A. Chinwalla, D.-F. Conrad, Y.-T. Fu, F. Grubert, I. Hajirasouliha, F. Hormozdiari, L.-M. Iakoucheva, Z. Iqbal, S. Kang, J.-M. Kidd, M.-K. Konkel, J. Korn, E. Khurana, D. Kural, H.-Y. K. Lam, J. Leng, R.-Q. Li, Y.-R. Li, C.-Y. Lin, R.-B. Luo, X.-J. Mu, J. Nemesh, H.-E. Peckham, T. Rausch, A. Scally, X.-H. Shi, M.-P. Stromberg, A.-M. Stütz, A.-E. Urban, J.-A. Walker, J.-T. Wu, Y.-J. Zhang, Z.-D. Zhang, M.-A. Batzer, L. Ding, G.-T. Marth, G. McVean, J. Sebat, M. Snyder, **J. Wang**, K. Ye, E.-E. Eichler, M.-B. Gerstein, M.-E. Hurles, C. Lee, S.-A. McCarroll, J.-O. Korbel , 1000 Genomes Project. Mapping copy number variation by population-scale genome sequencing. *Nature*, **470**, 59-65, 2011.
- 76) M. Arumugam, J. Raes, E. Pelletier, D.-L. Paslier, T. Yamada, D.-R. Mende, G.-R. Fernandes, J. Tap, T. Bruls, J.-M. Batto, M. Bertalan, N. Borruel, F. Casellas, L. Fernandez, L. Gautier, T. Hansen, M. Hattori, T. Hayashi, M. Kleerebezem, K. Kurokawa, M. Leclerc, F. Levenez, C. Manichanh, H.-B. Nielsen, T. Nielsen, N.

- Pons, J. Poulain, J.-J. Qin, S.-P. Thomas, S. Tims, D. Torrents, E. Ugarte, E.-G. Zoetendal, **J. Wang**, F. Guarner, O. Pedersen, M. Willem, S. Brunak, J. Doré, MetaHIT Consortium (additional members), J. Weissenbach, S.-D. Ehrlich , P. Bork. Enterotypes of the human gut microbiome. *Nature*, **473**, 174-180, 2011.
- 77) **J. Wang**, as one of the Principal Investigators (Production and Analysis Group) and Steering Committee member in The 1000 Genomes Project Consortium. Peter.-H. Sudman, J.-O. Kitzman, F. Antonacci1, C. Alkan, M. Malig, A. Tselenko, N. Sampas, L. Bruhn, J. Shendure, 1000 Genomes Project, E.-E. Eichler. Diversity of human copy number variation and multicopy genes. *Science*, **330**, 641-646, 2010.
- 78) E. Heard, S. Tishkoff, John.-A. Todd, M. Vidal, G.-P. Wagner, **J. Wang**, D. Weigel, R. Young. Ten years of genetics and genomics: what have we achieved and where are we heading? *Nature Reviews Genetics*, **11**, 723-733, 2010.
- 79) **J. Wang**, as one of The Schistosoma japonicum Genome Sequencing and Functional Analysis Consortium. The Schistosoma japonicum Genome Sequencing and Functional Analysis Consortium. The *Schistosoma japonicum* genome reveals features of host–parasite interplay. *Nature*, **460**, 345-351, 2009.
- 80) **J. Wang** as one of the authors in Drosophila 12 Genomes Consortium. Drosophila 12 Genomes Consortium. Evolution of genes and genomes on the Drosophila phylogeny. *Nature*, **450**, 203-218, 2007.
- 81) L. Li, X.-F. Wang, V. Stolc, X.-Y. Li, D.-F. Zhang, N. Su, W. Tongprasit, S.-G. Li, Z.-K. Cheng, **J. Wang**, X.-W. Deng. Genome wide transcription analyses in rice using tiling microarrays. *Nature Genetics*, **38**, 124-129, 2006.
- 82) D.-M. Muzny, S.-E. Scherer, R. Kaul, J. Wang, J. Yu, R. Sudbrak, C.-J. Buhay, R. Chen, A. Cree, Y. Ding, D.-R. Shannon, R. Gill, P. Gunaratne, R.-A. Harris, A.-C. Hawes, J. Hernandez, A.-V. Hodgson, J. Hume, A. Jackson, Z.-M. Khan, K.-S. Christie, L.-R. Lewis, R.-J. Lozado, M.-L. Metzker, A. Milosavljevic, G.-R. Miner, M.-B. Morgan, L.-V. Nazareth, G. Scott, E. Sodergren, X.-Z. Song, D. Steffen, S.-R. Wei, D.-A. Wheeler, M.-W. Wright, K.-C. Worley, Y. Yuan, Z.-D. Zhang, C.-Q. Adams, M.-A. Lari, M. Ayele, M.-J. Brown, G. Chen, Z.-J. Chen, J. Clendenning, K.-P. Blankenburg, R.-S. Chen, Z. Chen, C. Davis, O. Delgado, H.-H. Dinh, W. Dong, H. Draper, S. Ernst, G. Fu, M.-L. Garay, D.-K. Garcia, W. Gillett, J. Gu, B. Hao, E. Haugen, P. Havlak, X. He, S. Hennig, S.-N. Hu, W. Huang, L.-R. Jackson,

L.-S. Jacob, S.-H. Kelly, M. Kube, R. Levy, Z.-W. Li, B. Liu, J. Liu, W. Liu, J. Lu, M. Maheshwari, B.-V. Nguyen, G.-O. Okwuonu, A. Palmeiri, S. Pasternak, L.-M. Perez, K.-A. Phelps, F.-J. H. Plopper, B.-Q. Qiang, C. Raymond, R. Rodriguez, C. Saenphimmachak, J. Santibanez, H. Shen, Y. Shen, S. Subramanian, P.-E. Tabor, D. Verduzco, L. Waldron, J. Wang, **J. Wang**, Q.-Y. Wang, G.-A. Williams, G. K.-S. Wong, Z.-J. Yao, J.-K. Zhang, X.-Q. Zhang, G.-P. Zhao, J.-L. Zhou, Y. Zhou, further contributors, D. Nelson, H. Lehrach, R. Reinhardt, S.-L. Naylor, H.-M. Yang, Ma. Olson, G. Weinstock and R.-A. Gibbs. The DNA sequence, annotation and analysis of human chromosome 3. *Nature*, **440**, 1194-1198, 2006.

- 83) **J. Wang**, as one of the authors in the International Chicken Genome Sequencing Consortium. International Chicken Genome Sequencing Consortium. Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. *Nature*, **432**, 695-716, 2004.
- 84) **J. Wang**, as one of the authors in the International Human Genome Sequencing Consortium. International Human Genome Sequencing Consortium. Finishing the euchromatic sequence of the human genome. *Nature*, **431**, 931-945, 2004.
- 85) **J. Wang**, as one of the authors in the International Human Genome Sequencing Consortium. International Human Genome Sequencing Consortium. Initial sequencing and analysis of the human genome. *Nature*, **409**, 860-921, 2001.

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**简介：**王俊研究员于 1997 年毕业于北京大学，同年就读于同校，2002 年获博士学位。博士生导师，国家杰出青年基金获得者，973 首席科学家，现任深圳华大基因研究院院长，丹麦哥本哈根大学、奥胡斯大学教授，澳门科技大学、香港中文大学、中山大学客座教授。

自 1999 年参与人类基因组计划以来，王俊研究员以其数理统计学、计算机科学和生物学等交叉学科的知识积累，在肠道菌群与复杂疾病的关系、人类基因组学研究、单细胞肿瘤基因组研究、生物信息学工具开发等领域开展了大量开拓性的工作，产生了一批具有重大国际影响力的原创性研究成果。截止 2013 年 6 月发表 SCI 学术论文 213 篇，其中一作或通讯作者 113 篇，SCI 总引高达 27151 次；在国际顶尖杂志 Nature 及其子刊、Science、Cell 及 the New England Journal of Medicine 上共发表论文 85 篇，其中一作或通讯作者 54 篇，总引 21593，单篇最高总引 1505 次。主要科技成就中有九项科研成果入选中科院主办两院院士评选的“世界十大科技进展”和“中国十大科技进展”；六项入选由科技日报主持评选的“国际十大科技新闻”和“国内十大国际新闻”；三项入选由科技部和中国科协组织评选

的“中国基础科学研究十大新闻”，相关论文多次被 Nature China 评为亮点文章。他的研究得到了国家科技部、国家自然基金委、广东省及深圳市政府的大力资助。基于在基因组学和生物信息学领域的卓越贡献，王俊研究员获得了 20 余项奖励，诸如：2013 年荣获[周光召基金会：周光召科技奖、凤凰卫视：影响世界华人大奖、中国科协：科学中国人 2012 年度人物]，2012 年荣获[《自然》杂志：2012 全球科学界年度十大人物]，2011 年荣获[中国青年科技奖、广东省“五四”青年奖章]，2010 年荣获[全国劳动模范]，2008 年荣获[国务院特殊津贴、广东省“五一”劳动奖章、中国十大科技进展]，2006 年荣获[新世纪百千万人才工程国家级人选、丹麦皇家基金会奖]，2003 年荣获[中国科学院杰出科技成就奖，中央国家机关优秀青年]，2002 年[香港求是科技基金求是杰出科技成就奖、中国科学院重大创新贡献奖]等。

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1997 年 7 月，北京大学理学学士学位

2002 年 7 月，北京大学理学博士学位

#### 工作经历：

1999 年 3 月-2007 年 4 月，北京华大基因研究中心暨中国科学院北京基因组研究所研究员、生物信息室主任、北京中心主任

2004 年 8 月-今，丹麦奥胡斯大学人类遗传学研究所客座教授

2006 年 9 月-2009 年 9 月，南丹麦大学人类遗传学生物及分子生物学系 Ole Rømer 教授

2008 年 12 月-2011 年 11 月，中山大学中山医学院兼职教授

2008 年 12 月-2012 年 12 月，深圳华大基因研究院执行院长、研究员

2009 年 3 月-今，香港中文大学生物医学学院客座教授

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2013 年 1 月-今，深圳华大基因研究院院长、研究员

2013 年 6 月-今，澳门科技大学中药质量研究国家重点实验室特聘教授

**授课科目：**生物信息学前沿

**研究领域：**生物信息学、基因组学、人类群体遗传学、中药现代化

**获奖：**

《自然》杂志：2012 全球科学界年度十大人物（2012 年），周光召基金会：周光召科技奖（2013 年），凤凰卫视：影响世界华人大奖（2013 年），科学中国人 2012 年度人物（2013 年），2010 年度深圳市自然科学奖（2012 年），2011 年度深圳市技术发明奖（2012 年），中国青年科技奖（2011 年），广东省“五四”青年奖章（2011 年），全国劳动模范（2010 年），2008 年度深圳市科技创新奖（2009 年），国务院特殊津贴（2008 年），广东省“五一”劳动奖章（2008 年），中国十大科技进展（2008 年），中丹合作科学奖（2007 年），新世纪百千万人才工程国家级人选（2006 年），丹麦皇家基金会奖（2006 年），中国科学院杰出科技成就奖（2003 年），中央国家机关优秀青年（2003 年），香港求是科技基金求是杰出科技成就奖（2002 年），中国科学院重大创新贡献奖（2002 年）。

## 研究論文：

- 1) Y.-H. Huang, Y.-R. Li, D.-W. Burt, H.-L. Chen, Y. Zhang, W.-B. Qian, H. Kim, S.-Q. Gan, Y.-Q. Zhao, J.-W. Li, K. Yi, H.-P. Feng, P.-Y. Zhu, B. Li, Q.-Y. Liu, S. Fairley, K.-E. Magor, Z.-L. Du, X.-X. Hu, L. Goodman, H. Tafer, A. Vignal, T. Lee, K.-W. Kim, Z.-Y. Sheng, Y. An, S. Searle, J. Herrero, M.-A. M. Groenen, R.-P. M. A. Crooijmans, T. Faraut, Q.-L. Cai, R.-G. Webster, J.-R. Aldridge, W.-C. Warren, S. Bartschat, S. Kehr, M. Marz, P.-F. Stadler, J. Smith, R.-H. S. Kraus, Y.-F. Zhao, L.-M. Ren, J. Fei, M. Morisson, P. Kaiser, D.-K. Griffin, M. Rao, F. Pitel, **J. Wang**, N. Li. The duck genome and transcriptome provide insight into an avian influenza virus reservoir species. *Nature Genetic*. **45**, 776–783, 2013.
- 2) X.-J. Zhan, S.-K. Pan, J.Y. Wang, A. Dixon, J. He, M.-G. Muller, P.-X. Ni, L. Hu, Y. Liu, H.-L. Hou, Y.-P. Chen, J.-Q. Xia, Q. Luo, P.-W. Xu, Y. Chen, S.-G. Liao, C.-C. Cao, S.-K. Gao, Z.-B. Wang, Z. Yue, G.-Q. Li, Y. Yin, N.-C. Fox, **J. Wang**, M.-W. Bruford. Peregrine and saker falcon genome sequences provide insights into evolution of a predatory lifestyle. *Nature Genetics*, **45**, 563–566, 2013.
- 3) H.-Q. Ling, S.-C. Zhao, D.-C. Liu, J.-Y. Wang, H. Sun, C. Zhang, H.-J. Fan, D. Li, L.-L. Dong, Y. Tao, C. Gao, H.-L. Wu, Y.-W. Li, Y. Cui, X.-S. Guo, S.-S. Zheng, B. Wang, K. Yu, Q.-S. Liang, W.-L. Yang, X.-Y. Lou, J. Chen, M.-J. Feng, J.-B. Jian, X.-F. Zhang, G.-B. Luo, Y. Jiang, J.-J. Liu, Z.-B. Wang, Y.-H. Sha, B.-R. Zhang, H.-J. Wu, D.-Z. Tang, Q.-H. Shen, P.-Y. Xue, S.-H. Zou, X.-J. Wang, X. Liu, F.-M. Wang, Y.-P. Yang, X.-L. An, Z.-Y. Dong, K.-P. Zhang, X.-Q. Zhang, M.-C. Luo, J. Dvorak, Y.-P. Tong, J. Wang, H.-M. Yang, Z.-S. Li, D.-W. Wang, A.-M. Zhang, **J. Wang**. Draft genome of the wheat A-genome progenitor *Triticum urartu*. *Nature*, **496**, 87–90, 2013.
- 4) J.-Z. Jia, S.-C. Zhao, X.-Y. Kong, Y.-R. Li, G.-Y. Zhao, W.-M. He, R. Appels, M. Pfeifer, Y. Tao, X.-Y. Zhang, R.-L. Jing, C. Zhang, Y.-Z. Ma, L.-F. Gao, C. Gao, M. Spannagl, K.-F. X. Mayer, D. Li, S.-K. Pan, F.-Y. Zheng, Q. Hu, X.-C. Xia, J.-W. Li, Q.-S. Liang, J. Chen, T. Wicker, C.-Y. Gou, H.-H. Kuang, G.-Y. He, Y.-D. Luo, B. Keller, Q.-J. Xia, P. Lu, J.-Y. Wang, H.-F. Zou, R.-Z. Zhang, J.-Y. Xu, J.-L. Gao, C. Middleton, Z.-W. Quan, G.-M. Liu, J. Wang, International Wheat Genome

Sequencing Consortium, H.-M. Yang, X. Liu, Z.-H. He, L. Mao, **J. Wang**. *Aegilops tauschii* draft genome sequence reveals a gene repertoire for wheat adaptation. *Nature*, **496**, 91–95, 2013.

- 5) J.-F. Chen, Q.-F. Huang, D.-Y. Gao, J.-Y. Wang, Y.-S. Lang, T.-Y. Liu, B. Li, Z.-T. Bai, J.-L. Goicoechea, C.-Z. Liang, C.-B. Chen, W.-L. Zhang, S.-H. Sun, Y. Liao, X.-M. Zhang, L. Yang, C.-L. Song, M.-J. Wang, J.-F. Shi, G. Liu, J.-J. Liu, H.-L. Zhou, W.-L. Zhou, Q.-L. Yu, N. An, Y. Chen, Q.-L. Cai, B. Wang, B.-H. Liu, J.-M. Min, Y. Huang, H.-L. Wu, Z.-Y. Li, Y. Zhang, Y. Yin, W.-Q. Song, J.-M. Jiang, S.-A. Jackson, R.-A. Wing, **J. Wang**, M.-S. Chen. Whole-genome sequencing of *Oryza brachyantha* reveals mechanisms underlying *Oryza* genome evolution. *Nature Communications*, **4**, 1595, 2013.
- 6) Y. Fan, Z.-Y. Huang, C.-C. Cao, C.-S. Chen, Y.-X. Chen, D.-D. Fan, J. He, H.-L. Hou, L. Hu, X.-T. Hu, X.-T. Jiang, R. Lai, Y.-S. Lang, B. Liang, S.-G. Liao, D. Mu, Y.-Y. Ma, Y.-Y. Niu, X.-Q. Sun, J.-Q. Xia, J. Xiao, Z.-Q. Xiong, L. Xu, L. Yang, Y. Zhang, W. Zhao, X.-D. Zhao, Y.-T. Zheng, J.-M. Zhou, Y.-B. Zhu, G.-J. Zhang, **J. Wang**, Y.-G. Yao. Genome of the Chinese tree shrew. *Nature Communications*, **4**, 1426, 2013.
- 7) M.-D. Shapiro, Z. Kronenberg, C. Li, E.-T. Domjan, H.-L. Pan, M. Campbell, H. Tan, C.-D. Huff, H.-F. Hu, A.-I. Vickrey, S.-C.A. Nielsen, S.-A. Stringham, H. Hu, E. Willerslev, M.-T.P. Gilbert, M. Yandell, G.-J. Zhang, **J. Wang**. Genomic Diversity and Evolution of the Head Crest in the Rock Pigeon. *Science*, **339** , 1063-1067, 2013.
- 8) R.-K. Varshney, C. Song, R.-K. Saxena, S. Azam, S. Yu, A.-G. Sharpe, S. Cannon, J. Baek, B.-D. Rosen, B. Tar'an, T. Millan, X.-D. Zhang, L.-D. Ramsay, A. Iwata, Y. Wang, W. Nelson, A.-D. Farmer, P.-M. Gaur, C. Soderlund, R.-V. Penmetsa, C.-Y. Xu, A.-K. Bharti, W.-M. He, P. Winter, S.-C. Zhao, J.-K. Hane, N. Carrasquilla-Garcia, J.-A. Condie, H.-D. Upadhyaya, M.-C. Luo, M. Thudi, C.-L.L. Gowda, N.-P. Singh, J. Lichtenzveig, K.-K. Gali, J. Rubio, N. Nadarajan, J. Dolezel, K.-C. Bansal, X. Xu, D. Edwards, G.-Y Zhang, G. Kahl, J. Gil, K.-B. Singh, S.-K. Datta, S.-A. Jackson, **J.Wang**, D.-R. Cook. Draft genome sequence of chickpea (*Cicer arietinum*) provides a resource for trait improvement. *Nature Biotechnology*, **31**, 240–246, 2013.

- 9) M.-S. You, Z. Yue, W.-Y. He, X.-H. Yang, G. Yang, M. Xie, D.-L. Zhan, S.-W. Baxter, L. Vasseur, G.-M. Gurr, C.-J. Douglas, J.-L. Bai, P. Wang, K. Cui, S.-G. Huang, X.-C. Li, Q. Zhou, Z.-Y Wu, Q.-L Chen, C.-H Liu, B. Wang, X.-J. Li, X.-F. Xu, C.-X. Lu, M. Hu, J.-W. Davey, S.-M. Smith, M.-S. Chen, X.-F. Xia, W.-Q. Tang, F.-S. Ke, D.-D. Zheng, Y.-L Hu, F.-Q. Song, Y.-C. You, X.-L. Ma, L. Peng, Y.-K. Zheng, Y. Liang, Y.-Q. Chen, L.-Y. Yu, Y.-N. Zhang, Y.-Y. Liu, G.-Q. Li, L. Fang, J.-X. Li, X. Zhou, Y.-D. Luo, C.-Y. Gou, J.-Y Wang, J. Wang, H.-M. Yang, **J. Wang**. A heterozygous moth genome provides insights into herbivory and detoxification. *Nature Genetics*, **45**, 220–225, 2013.
- 10) Q.-X. Zhang, W.-B. Chen, L.-D. Sun, F.-Y. Zhao, B.-Q. Huang, W.-R Yang, Y. Tao, J. Wang, Z.-Q. Yuan, G.-Y. Fan, Z. Xing, C.-L. Han, H.-T. Pan, X. Zhong, W.-F. Shi, X.-M. Liang, D.-L. Du, F.-M Sun, Z.-D. Xu, R.-J. Hao, T. Lv, Y.-M. Lv, Z.-Q. Zheng, M. Sun, L. Luo, M. Cai, Y.-K. Gao, J.-Y. Wang, Y. Yin, X. Xu, T.-R. Cheng, **J. Wang**. The genome of *Prunus mume*. *Nature Communications*, **3**, 1318, 2012.
- 11) Y. Dong, M. Xie, Y. Jiang, N.-Q. Xiao, X.-Y. Du, W.-G. Zhang, G. Tosser-Klopp, J.-H. Wang, S. Yang, J. Liang, W.-B. Chen, J. Chen, P. Zeng, Y. Hou, C. Bian, S.-K. Pan, Y.-X. Li, X. Liu, W.-L. Wang, B. Servin, B. Sayre, B. Zhu, D. Sweeney, Ri. Moore, W.-H. Nie, Y.-Y. Shen, R.-P. Zhao, G.-J. Zhang, J.-Q. Li, T. Faraut, J. Womack, Y.-P. Zhang, J. Kijas, N. Cockett, X. Xu, S.-H. Zhao, **J. Wang**, W. Wang. Sequencing and automated whole-genome optical mapping of the genome of a domestic goat (*Capra hircus*). *Nature Biotechnology*, **31**, 135–141, 2013.
- 12) J.-J. Michaelson, Y.-J. Shi, M. Gujra, H.-C. Zheng, D. Malhotra, X. Jin, M.-H. Jian, G.-M. Liu, D. Greer, A. Bhandari, W.-T. Wu, R. Corominas, Á. Peoples, A. Koren, A. Gore, S.-L. Kang, G.-N. Lin, J. Estabillo, T. Gadomski, B. Singh, K. Zhang, N. Akshoomoff, C. Corsello, S. McCarroll, L.-M. Iakoucheva, Y.-R. Li, **J. Wang**, J. Sebat. Whole-genome sequencing in autism identifies hot spots for de novo germline mutation. *Cell*, **151**, 1431-1442, 2012.
- 13) G.-J. Zhang, C. Cowled, Z.-L. Shi, Z.-Y. Huang, K.-A. Bishop-Lilly, X.-D. Fang, J.-W. Wynne, Z.-Q. Xiong, M.-L. Baker, W. Zhao, M. Tachedjian, Y.-B. Zhu, P. Zhou, X.-T. Jiang, J. Ng, L. Yang, L.-J. Wu, J. Xiao, Y. Feng, Y.-X. Chen, X.-Q. Sun, Y. Zhang, G.-A. Marsh, G. Crameri, C.-C. Broder, K.-G. Frey, L.-F Wang, **J. Wang**. Comparative analysis of bat genomes provides insight into the evolution of flight

and immunity. *Science*, **339**, 456-460, 2012.

- 14) S.-G. Guo, J.-G. Zhang, H.-H. Sun, J. Salse, W. J. Lucas, H.-Y. Zhang, Y. Zheng, L.-Y. Mao, Y. Ren, Z.-W. Wang, J.-M. Min, X.-S. Guo, F. Murat, B.-K. Ham, Z.-L. Zhang, S. Gao, M.-Y. Huang, Y.-M. Xu, S.-L. Zhong, A. Bombarely, L. A. Mueller, H. Zhao, H.-J. He, Y. Zhang, Z.-H. Zhang, S.-W. Huang, T. Tan, E. Pang, K. Lin, Q. Hu, H.-H. Kuang, P.-X. Ni, B. Wang, J.-G. Liu, Q.-H. Kou, W.-J. Hou, X.-H. Zou, J. Jiang, G.-Y. Gong, K. Klee, H. Schoof, Y. Huang, X.-S. Hu, S.-S. Dong, D.-Q. Liang, J. Wang, K. Wu, Y. Xia, X. Zhao, Z.-Q. Zheng, M. Xing, X.-M. Liang, B.-Q. Huang, T. Lv, J.-Y. Wang, Y. Yin, H.-P. Yi, R.-Q. Li, M.-Z. Wu, A. Levi, X.-P. Zhang, J. J. Giovannoni, **J. Wang**, Y.-F. Li, Z.-J. Fei, Y. Xu. The draft genome of watermelon (*Citrullus lanatus*) and resequencing of 20 diverse accessions. *Nature Genetics*, **45**, 51-58, 2012.
- 15) J.-J. Qin, Y.-R. Li, Z.-M. Cai, S.-H. Li, J.-F. Zhu, F. Zhang, S.-S. Liang, W.-W. Zhang, Y.-L. Guan, D.-Q. Shen, Y.-Q. Peng, D.-Y. Zhang, Z.-Y. Jie, W.-X. Wu, Y.-W. Qin, W.-B. Xue, J.-H. Li, L.-C. Han, D.-H. Lu, P.-X. Wu, Y.-L. Dai, X.-J. Sun, Z.-S. Li, A.-F. Tang, S.-L. Zhong, X.-P. Li, W.-C. Chen, R. Xu, M.-B. Wang, Q. Feng, M.-H. Gong, J. Yu, Y.-Y. Zhang, M. Zhang, T. Hansen, G. Sanchez, J. Raes, G. Falony, S. Okuda, M. Almeida, E. LeChatelier, P. Renault, N. Pons, J.-M. Batto, Z.-X. Zhang, H. Chen, R.-F. Yang, W.-M. Zheng, S.-G. Li, H.-M. Yang, J. Wang, S. D. Ehrlich, R. Nielsen, O. Pedersen, K. Kristiansen, **J. Wang**. A metagenome-wide association study of gut microbiota in type 2 diabetes. *Nature*, **490**, 55-60, 2012.
- 16) G.-F. Zhang, X.-D. Fang, X.-M. Guo, L. Li, R.-B. Luo, F. Xu, P.-C. Yang, L.-L. Zhang, X.-T. Wang, H.-G. Qi, Z.-Q. Xiong, H.-Y. Que, Y.-L. Xie, P. W. H. Holland, J. Paps, Y.-B. Zhu, F.-C. Wu, Y.-X. Chen, J.-F. Wang, C.-F. Peng, J. Meng, L. Yang, J. Liu, B. Wen, N. Zhang, Z.-Y. Huang, Q.-H. Zhu, Y. Feng, A. Mount, D. Hedgecock, Z. Xu, Y.-J. Liu, T. D. Lošo, Y.-S. Du, X.-Q. Sun, S.-D. Zhang, B.-H. Liu, P.-Z. Cheng, X.-T. Jiang, J. Li, D.-D. Fan, W. Wang, W.-J. Fu, T. Wang, B. Wang, J.-B. Zhang, Z.-Y. Peng, Y.-X. Li, N. Li, J.-P. Wang, M.-S. Chen, Y. He, F.-J. Tan, X.-R. Song, Q.-M. Zheng, R.-L. Huang, H.-L. Yang, X.-D. Du, L. Chen, M. Yang, P. M. Gaffney, S. Wang, L.-H. Luo, Z.-C. She, Y. Ming, W. Huang, S. Zhang, B.-Y. Huang, Y. Zhang, T. Qu, P.-X. Ni, G.-Y. Miao, J.-Y. Wang, Q. Wang, C. E. W. Steinberg, H.-Y. Wang, N. Li, L.-M. Qian, G.-J. Zhang, Y.-R. Li, H.-M. Yang, X. Liu, J.

- Wang, Y. Yin, **J. Wang**. The oyster genome reveals stress adaptation and complexity of shell formation. *Nature*, **490**, 49-54, 2012.
- 17) S.-Q. Zhang, T. Jiang, M. Li, X. Zhang, Y.-Q. Ren, S.-C. Wei, L.-D. Sun, H. Cheng, Y. Li, X.-Y. Yin, Z.-M. Hu, Z.-Y. Wang, Y. Liu, B.-R. Guo, H.-Y. Tang, X.-F. Tang, Y.-T. Ding, J.-B. Wang, P. Li, B.-Y. Wu, W. Wang, X.-F. Yuan, J.-S. Hou, W.-W. Ha, W.-J. Wang, Y.-J. Zhai, J. Wang, F.-F. Qian, F.-S. Zhou, G. Chen, X.-B. Zuo, X.-D. Zheng, Y.-J. Sheng, J.-P. Gao, B. Liang, P. Li, J. Zhu, F.-L. Xiao, P.-G. Wang, Y. Cui, H. Li, S.-X. Liu, M. Gao, X. Fan, S.-K. Shen, M. Zeng, G.-Q. Sun, Y. Xu, J.-Chu Hu, T.-T. He, Y.-R. Li, H.-M. Yang, J. Wang, Z.-Y. Yu, H.-F. Zhang, X. Hu, K. Yang, J. Wang, S.-X. Zhao, Y.-W. Zhou, J.-J. Liu, W.-D. Du, L. Zhang, K. Xia, S. Yang, **J. Wang**, X.-J. Zhang. Exome sequencing identifies MVK mutations in disseminated superficial actinic porokeratosis. *Nature Genetics*, **44**, 1156-1160, 2012.
- 18) K.-B. Wang, Z.-W. Wang, F.-G. Li, W.-W. Ye, J.-Y. Wang, G.-L. Song, Z. Yue, L. Cong, H.-H. Shang, S.-L. Zhu, C.-S. Zou, Q. Li, Y.-L. Yuan, C.-R. Lu, H.-L. Wei, C.-Y. Gou, Z.-Q. Zheng, Y. Yin, X.-Y. Zhang, K. Liu, B. Wang, C. Song, N. Shi, R. J. Kohel, R. G. Percy, J. Z. Yu, Y.-X. Zhu, **J. Wang**, S.-X. Yu. The draft genome of a diploid cotton *Gossypium raimondii*. *Nature Genetics*, **44**, 1098-1103, 2012.
- 19) Q. Qiu, G.-J. Zhang, T. Ma, W.-B. Qian, J.-Y. Wang, Z.-Q. Ye, C.-C. Cao, Q.-J. Hu, J. Kim, D. M. Larkin, L. Auvil, B. Capitanu, J. Ma, H. A. Lewin, X.-J. Qian, Y.-S. Lang, R. Zhou, L.-Z. Wang, K. Wang, J.-Q. Xia, S.-G. Liao, S.-K. Pan, X. Lu, H.-L. Hou, Y. Wang, X.-T. Zang, Y. Yin, H. Ma, J. Zhang, Z.-F. Wang, Y.-M. Zhang, D.-W. Zhang, T. Yonezawa, M. Hasegawa, Y. Zhong, W.-B. Liu, Y. Zhang, Z.-Y. Huang, S.-X. Zhang, R.-J. Long, H.-M. Yang, J. Wang, J. A. Lenstra, D. N. Cooper, Y. Wu, **J. Wang**, P. Shi, J. Wang, J.-Q. Liu. The yak genome and adaptation to life at high altitude. *Nature Genetics*, **44**, 946-949, 2012.
- 20) W.-K. Sung, H.-C. Zheng, S.-Y. Li, R.-H. Chen, X. Liu, Y.-R. Li, N. P. Lee, W. H. Lee, P. N. Ariyaratne, C. Tennakoon, F. H. Mulawadi, K. F. Wong, A. M. Liu, R. T. Poon, S. T. Fan, K. L. Chan, Z.-L. Gong, Y.-J. Hu, Z. Lin, G. Wang, Q.-H. Zhang, T. D. Barber, W.-C. Chou, A. Aggarwal, K. Hao, W. Zhou, C.-S. Zhang, J. Hardwick, C. Buser, J.-C. Xu, Z.-Y. Kan, H.-Y. Dai, M. Mao, C. Reinhard, **J. Wang**, J.-M. Luk. Genome-wide survey of recurrent HBV integration in hepatocellular carcinoma. *Nature Genetics*, **44**, 765-769, 2012.

- 21) G.-Y. Zhang, X. Liu, Z.-W. Quan, S.-F. Cheng, X. Xu, S.-K. Pan, M. Xie, P. Zeng, Z. Yue, W.-L. Wang, Y. Tao, C. Bian, C.-L. Han, Q.-J. Xia, X.-H. Peng, R. Cao, X.-H. Yang, D.-L. Zhan, J.-C. Hu, Y.-X. Zhang, H.-N. Li, H. Li, N. Li, J.-Y. Wang, C. Wang, R.-Y. Wang, T. Guo, Y.-J. Cai, C.-Z. Liu, H.-T. Xiang, Q.-X. Shi, P. Huang, Q.-C. Chen, Y.-R. Li, **J. Wang**, Z.-H. Zhao, J. Wang. Genome sequence of foxtail millet (*Setaria italica*) provides insights into grass evolution and biofuel potential. *Nature Biotechnology*, **30**, 549-554, 2012.
- 22) X. Xu, Y. Hou, X.-Y. Yin, L. Bao, A.-F. Tang, L.-T Song, F.-Q. Li, S. Tsang, K. Wu, H.-J. Wu, W.-M. He, L. Zeng, M.-J. Xing, R.-H. Wu, H. Jiang, X. Liu, D.-D. Cao, G.-W. Guo, X.-D. Hu, Y.-T. Gui, Z.-S. Li, W.-Y. Xie, X.-J. Sun, M. Shi, Z.-M. Cai, B. Wang, M.-M. Zhong, J.-X. Li, Z.-H. Lu, N. Gu, X.-Q. Zhang, L. Goodman, L. Bolund, J. Wang, H.-M. Yang, K. Kristiansen, M. Dean, Y.-R. Li, **J. Wang**. Single-cell exome sequencing reveals single-nucleotide mutation characteristics of a kidney tumor. *Cell*, **148**, 886-895, 2012.
- 23) Y. Hou, L.-T. Song, P. Zhu, B. Zhang, Y. Tao, X. Xu, F.-Q. Li, K. Wu, J. Liang, D. Shao, H.-J. Wu, X.-F. Ye, C. Ye, R.-H. Wu, M. Jian, Y. Chen, W. Xie, R.-R. Zhang, L. Chen, X. Liu, X.-T. Yao, H.-C. Zheng, C. Yu, Q.-B. Li, Z.-L. Gong, M. Mao, X. Yang, L. Yang, J.-X. Li, W. Wang, Z.-H. Lu, N. Gu, G. Laurie, L. Bolund, K. Kristiansen, J. Wang, H.-M. Yang, Y.-R. Li, X.-Q. Zhang, **J. Wang**. Single-cell exome sequencing and monoclonal evolution of a JAK2-negative myeloproliferative neoplasm. *Cell*, **148**, 873-885, 2012.
- 24) Z.-Y. Peng, Y.-B. Cheng, B. C.-M. Tan, L. Kang, Z.-J. Tian, Y.-K. Zhu, W.-W. Zhang, Y. Liang, X.-D. Hu, X.-M. Tan, J. Guo, Z.-R. Dong, Y. Liang, L. Bao, **J. Wang**. Comprehensive analysis of RNA-Seq data reveals extensive RNA editing in a human transcriptome. *Nature Biotechnology*, **30**, 253-260, 2012.
- 25) N.-D. Young, A.-R. Jex, B. Li, S.-P. Liu, L.-F. Yang, Z.-J. Xiong, Y.-R. Li, C. Cantacessi, R. S. Hall, X. Xu, F.-Y. Chen, X. Wu, A. Zerlotini, G. Oliveira, A. Hofmann, G.-J. Zhang, X.-D. Fang, Y. Kang, B.-E. Campbell, A. Loukas, S. Ranganathan, D. Rollinson, G. Rinaldi, P.-J. Brindley, H.-M. Yang, **J. Wang**, J. Wang, R.-B. Gasser. Whole-genome sequence of *Schistosoma haematobium*. *Nature Genetics*, **44**, 221-225, 2012.
- 26) X. Xu, X. Liu, S. Ge, J. D. Jensen, F.-Y. Hu, X. Li, Y. Dong, R. N. Gutenkunst, L.

- Fang, L. Huang, J.-X. Li, W.-M. He, G.-J. Zhang, X.-M. Zheng, F.-M. Zhang, Y.-R. Li, C. Yu, K. Kristiansen, X.-Q. Zhang, J. Wang, M. Wright, S. McCouch, R. Nielsen, **J. Wang**, W. Wang. Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. *Nature Biotechnology*, **30**, 105-111, 2012.
- 27) G.-W. Guo, Y.-T. Gui, S.-J. Gao, A.-F. Tang, X.-D. Hu, Y. Huang, W.-L. Jia, Z.-S. Li, M.-H. He, L. Sun, P.-F. Song, X.-J. Sun, X.-K. Zhao, S.-M. Yang, C.-Z. Liang, S.-Q. Wan, F.-J. Zhou, C. Chen, J.-L. Zhu, X.-X. Li, M.-H. Jian, L. Zhou, R. Ye, P.-D. Huang, J. Chen, T. Jiang, X. Liu, Y. Wang, J. Zou, Z.-M. Jiang, R.-H. Wu, S. Wu, F. Fan, Z.-F. Zhang, L. Liu, R.-L. Yang, X.-W. Liu, H.-B. Wu, W.-H. Yin, X. Zhao, Y.-C. Liu, H.-H. Peng, B.-H. Jiang, Q.-X. Feng, C.-L. Li, J. Xie, J.-X. Lu, K. Kristiansen, Y.-R. Li, X.-Q. Zhang, S.-G. Li, J. Wang, H.-M. Yang, Z.-M. Cai , **J. Wang**. Frequent mutations of genes encoding ubiquitin-mediated proteolysis pathway components in clear cell renal cell carcinoma. *Nature Genetics*, **44**, 17-19, 2012.
- 28) A.-R. Jex, S.-P. Liu, B. Li, N.-D. Young, R.-S. Hall, Y.-R. Li, L.-F. Yang, N. Zeng, X. Xu, Z.-J. Xiong, F.-Y. Chen, X. Wu, G.-J. Zhang, X.-D. Fang, Y. Kang, G.-A. Anderson, T.-W. Harris, B.-E. Campbell, J. Vlaminck, T. Wang, C. Cantacessi, E.-M. Schwarz, S. Ranganathan, P. Geldhof, P. Nejsum, P.-W. Sternberg, H.-M. Yang, **J. Wang**, J. Wang, R.-B. Gasser. *Ascaris suum* draft genome. *Nature*, **479**, 529-533, 2011.
- 29) E.-B. Kim, X.-D. Fang, A.-A. Fushan, Z.-Y. Huang, A.-V. Lobanov, L.-J. Han, S.-M. Marino, X.-Q. Sun, A.- A. Turanov, P.-C. Yang, S.-H Yim, X. Zhao, M.-V. Kasaikina, N. Stoletzki, C.-F. Peng, P. Polak, Z.-Q. Xiong, A.-K, Y.-B. Zhu, Y.-X. Chen, G.-V. Kryukov, Q. Zhang, L. Peshkin, L. Yang, R.-T. Bronson, R. Buffenstein, B. Wang, C.-L. Han, Q.-Y. Li, L. Chen, W. Zhao, S.-R. Sunyaev, T.-J. Park, G.-J. Zhang, **J. Wang**, V.-N. Gladyshev. Genome sequencing reveals insights into physiology and longevity of the naked mole rat. *Nature*, **479**, 223-227, 2011.
- 30) M. Rasmussen, X.-S. Guo, Y. Wang, K. E. Lohmueller, S. Rasmussen, A. Albrechtsen, L. Skotte, S. Lindgreen, M. Metspalu, T. Jombart, T. Kivisild, W.-W. Zhai, A. Eriksson, A. Manica, L. Orlando, F. M. D. L. Vega, S. Tridico, E. Metspalu, K. Nielsen, M. C. Á vila-Arcos, J. V. M. Mayar, C. Muller, J. Dortch, M. T. P. Gilbert,

O. Lund, A. Wesolowska, M. Karmin, L. A. Weinert, B. Wang, J. Li, S.-S. Tai, F. Xiao, T. Hanihara, G. v. Driem, A. R. Jha, F.-X. Ricaut, P. d. Knijff, A. B. Migliano, I. G. Romero, K. Kristiansen, D. M. Lambert, S. Brunak, P. Forster, B. Brinkmann, O. Nehlich, M. Bunce, M. Richards, R. Gupta, C. D. Bustamante, A. Krogh, R. A. Foley, M. M. Lahr, F. Balloux, T. S. Pontén, R. Villemans, R. Nielsen, **J. Wang**, E. Willerslev. An aboriginal Australian genome reveals separate human dispersals into Asia. *Science*, **334**, 94-98, 2011.

- 31) The Brassica rapa Genome Sequencing Project Consortium, X.-W. Wang, H.-Z. Wang, **J. Wang**, R.-F. Sun, J. Wu, S.-Y. Liu, Y.-Q. Bai, J.-H. Mun, I. Bancroft, F. Cheng, S.-W. Huang, X.-X Li, W. Hua, J.-Y. Wang, X.-Y. Wang, M. Freeling, J. C. Pires, A. H. Paterson, B. Chalhoub, B. Wang, A. Hayward, A.-G. Sharpe, B.-S. Park, B. Weisshaar, B.-H. Liu, B. Li, B. Liu, C.-B Tong, C. Song, C. Duran, C.-F. Peng, C.-Y. Geng, C. Koh, C.-Y. Lin, D. Edwards, D.-S. Mu, D. Shen, E. Soumpourou, F. Li, F. Fraser, G. Conant, G. Lassalle, G. J. King, G. Bonnema, H.-B. Tang, H.-P. Wang, H. Belcram, H.-L. Zhou, H. Hirakawa, H. Abe, H. Guo, H. Wang, H.-Z. Jin, I. A. P. Parkin, J. Batley, J.-S. Kim, J. Just, J.-W. Li, J.-H. Xu, J. Deng, J. A. Kim, J.-P. Li, J.-Y. Yu, J.-L. Meng, J.-P. Wang, J.-M. Min, J. Poulaing, J. Wang, K. Hatakeyama, K. Wu, L. Wang, L. Fang, M. Trick, M. G. Links, M. Zhao, M.-N. Jin, N. Ramchiary, N. Drou, P. J. Berkman, Q.-L. Cai, Q.-F. Huang, R.-Q. Li, S. Tabata, S.-F. Cheng, S. Zhang, S.-J. Zhang, S.-M. Huang, S. Sato, S.-L. Sun, S.-J. Kwon, S.-R. Choi, T.-H. Lee, W. Fan, X. Zhao, X. Tan, X. Xu, Y. Wang, Y. Qiu, Y. Yin, Y.-R. Li, Y.-C. Du, Y.-C. Liao, Y. Lim, Y. Narusaka, Y.-P. Wang, Z.-Y. Wang, Z.-Y. Li, Z.-W. Wang, Z.-Y. Xiong, Z.-H. Zhang. The genome of the mesopolyploid crop species *Brassica rapa*. *Nature Genetics*, **43**, 1035-1039, 2011.
- 32) Y.-T. Gui, G.-W. Guo, Y. Huang, X.-D. Hu, A.-F. Tang, S.-J. Gao, R.-H. Wu, C. Chen, X.-X. Li, L. Zhou, M.-H. He, Z.-S. Li, X.-J. Sun, W.-L. Jia, J.-N. Chen, S.-M. Yang, F.-J. Zhou, X.-K. Zhao, S.-Q. Wan, R. Ye, C.-Z. Liang, Z.-S. Liu, P.-D. Huang, C.-X. Liu, H. Jiang, Y. Wang, H.-C. Zheng, L. Sun, X.-W. Liu, Z.-M. Jiang, D.-F. Feng, J. Chen, S. Wu, J. Zou, Z.-F. Zhang, R.-L. Yang, J. Zhao, C.-J. Xu, W.-H. Yin, Z.-C. Guan, J.-X. Ye, H. Zhang, J.-X. Li, K. Kristiansen, M. L. Nickerson, D. Theodorescu, Y.-R. Li, X.-Q. Zhang, S.-G. Li, J. Wang, H.-M. Yang, **J. Wang**, Z.-M. Cai. Frequent mutations of chromatin remodeling genes in transitional cell

carcinoma of the bladder. *Nature Genetics*, **43**, 875-878, 2011.

- 33) X. Xu, H. Nagarajan, N. E. Lewis, S.-K. Pan, Z.-M. Cai, X. Liu, W.-B. Chen, M. Xie, W.-L. Wang, S. Hammond, M. R. Andersen, N. Neff, B. Passarelli, W. Koh, H. C. Fan, J.-B. Wang, Y.-T. Gui, K. H. Lee, M. J. Betenbaugh, S. R. Quake, I. Famili, B. O. Palsson , **J. Wang**. The genomic sequence of the Chinese hamster ovary (CHO)-K1 cell line. *Nature Biotechnology*, **29**, 735-741, 2011.
- 34) Y.-R. Li, H.-C. Zheng, R.-B. Luo, H.-L. Wu, H.-M. Zhu, R.-Q. Li, H.-Z. Cao, B.-X. Wu, S.-J. Huang, H.-J. Shao, H.-Z. Ma, F. Zhang, S.-J. Feng, W. Zhang, H.-L. Du, G. Tian, J.-X. Li, X.-Q. Zhang, S.-G. Li, L. Bolund, K. Kristiansen, A. J. Smith, A. I. F. Blakemore, L. J. M. Coin, H.-M. Yang, J. Wang , **J. Wang**. Structural variation in two human genomes mapped at single-nucleotide resolution by whole genome *de novo* assembly. *Nature Biotechnology*, **29**, 723-730, 2011.
- 35) **J. Wang**. Genome-sequencing anniversary. Personal genomes: for one and for all. *Science*, **331**, 690, 2011.
- 36) H.-M. Lam, X. Xu, X. Liu, W.-B Chen, G.-H. Yang, F.-L. Wong, M.-W. Li, W.-M. He, N. Qin, B. Wang, J. Li, M. Jian, J. Wang, G.-H. Shao, **J. Wang**, Samuel S.-M. Sun , G.-Y. Zhang. Resequencing of 31 wild and cultivated soybean genomes identifies patterns of genetic diversity and selection. *Nature Genetics*, **42**, 1053-1059, 2010.
- 37) J.-S. Lai, R.-Q. Li, X. Xu, W.-W. Jin, M.-L. Xu, H.-N. Zhao, Z.-K. Xiang, W.-B. Song, K. Ying, M. Zhang, Y.-P. Jiao, P.-X. Ni, J.-G. Zhang, D. Li, X.-S. Guo, K.-X. Ye, M. Jian, B. Wang, H.-S. Zheng, H.-Q Liang, X.-Q. Zhang, S.-C. Wang, S.-J. Chen, J.-S. Li, Y. Fu, N. M. Springer, H.-M. Yang, J. Wang, J.-R. Dai, P. S. Schnable, **J. Wang**. Genome-wide patterns of genetic variation among elite maize inbred lines. *Nature Genetics*, **42**, 1027-1030, 2010.
- 38) Y.-R. Li, N. Vinckenbosch, G. Tian, E. H. Sanchez, T. Jiang, H. Jiang, A. Albrechtsen, G. Andersen, H.-Z. Cao, T. Korneliussen, N. Grarup, Y.-R. Guo, I. Hellman, X. Jin, Q.-B. Li, J.-T. Liu, X. Liu, T. Sparsø, M.-F. Tang, H.-L. Wu, R.-H. Wu, C. Yu, H.-C. Zheng, A. Astrup, L. Bolund, J. Holmkvist, T. Jørgensen, K. Kristiansen, O. Schmitz, T. W. Schwartz, X.-Q. Zhang, R.-Q. Li, H.-M. Yang, J. Wang, T. Hansen, O. Pedersen, R. Nielsen , **J. Wang**. Resequencing of 200 human exomes identifies an excess of low-frequency non-synonymous coding variants.

*Nature Genetics*, **42**, 969-972, 2010.

- 39) R. Bonasio, G.-J. Zhang, C.-Y. Ye, N. S. Mutti, X.-D. Fang, N. Qin, G. Donahue, P.-C. Yang, Q.-Y. Li, C. Li, P. Zhang, Z.-Y. Huang, S. L. Berger, D. Reinberg, **J. Wang**, J. Liebig. Genomic comparison of the ants *Camponotus floridanus* and *Harpegnathos saltator*. *Science*, **329**, 1068-1071, 2010.
- 40) X. Yi, Y. Liang, E. H. Sanchez, X. Jin, Z. X. P. Cuo, J. E. Pool, X. Xu, H. Jiang, N. Vinckenbosch, T. S. Korneliussen, H.-C. Zheng, T. Liu, W.-M. He, K. Li, R.-B. Luo, X.-F. Nie, H.-L. Wu, M.-R. Zhao, H.-Z. Cao, J. Zou, Y. Shan, S.-Z. Li, Q. Yang, Asan, P.-X. Ni, G. Tian, J.-M. Xu, X. Liu, T. Jiang, R.-H. Wu, G.-Y. Zhou, M.-F. Tang, J.-J. Qin, T. Wang, S.-J. Feng, G.-H. Li, Huasang, J.-B. Luosang, W. Wang, F. Chen, Y.-D. Wang, X.-G. Zheng, Z. Li, Z. Bianba, G. Yang, X.-P. Wang, S.-H. Tang, G.-Y. Gao, Y. Chen, Z. Luo, L. Gusang, Z. Cao, Q.-H. Zhang, W.-H. Ouyang, X.-L. Ren, H.-Q. Liang, H.-S. Zheng, Y.-B. Huang, J.-X. Li, L. Bolund, K. Kristiansen, Y.-R. Li, Y. Zhang, X.-Q. Zhang, R.-Q. Li, S.-G. Li, H.-M. Yang, R. Nielsen, **J. Wang**, J. Wang. Sequencing of 50 human exomes reveals adaptation to high altitude. *Science*, **329**, 75-78, 2010.
- 41) H. Xiang, J.-D. Zhu, Q. Chen, F.-Y. Dai, X. Li, M.-W. Li, H.-Y. Zhang, G.-J. Zhang, D. Li, Y. Dong, L. Zhao, Y. Lin, D.-J. Cheng, J. Yu, J.-F. Sun, X.-Y. Zhou, K.-L. Ma, Y.-H. He, Y.-X. Zhao, S.-C. Guo, M.-Z. Ye, G.-W. Guo, Y.-R. Li, R.-Q. Li, X.-Q. Zhang, L.-J. Ma, K. Kristiansen, Q.-H. Guo, J.-H. Jiang, S. Beck, Q.-Y. Xia, W. Wang, **J. Wang**. Single base-resolution methylome of the silkworm reveals a sparse epigenomic map. *Nature Biotechnology*, **28**, 516-520, 2010.
- 42) J.-J. Qin, R.-Q. Li, J. Raes, M. Arumugam, K.-S. Burgdorf, C. Manichanh, T. Nielsen, N. Pons, F. Levenez, T. Yamada, D. R. Mende, J.-H. Li, J.-M. Xu, S.-C. Li, D.-F. Li, J.-J. Cao, B. Wang, H.-Q. Liang, H.-S. Zheng, Y.-L. Xie, J.-L. Tap, P. Lepage, M. Bertalan, J.-M. Batto, T. Hansen, D. L. Paslier, A. Linneberg, H. B. Nielsen, E. Pelletier, P. Renault, T. S. Ponten, K. Turner, H.-M. Zhu, C. Yu, S.-T. Li, M. Jian, Y. Zhou, Y.-R. Li, X.-Q. Zhang, S.-G. Li, N. Qin, H.-M. Yang, J. Wang, S. Brunak, J. Doré, F. Guarner, K. Kristiansen, O. Pedersen, J. Parkhill, J. Weissenbach, MetaHIT Consortium, P. Bork, S. D. Ehrlich, **J. Wang**. A human gut microbial gene catalogue established by metagenomic sequencing. *Nature*, **464**, 59-65, 2010.
- 43) M. Rasmussen, Y.-R. Li, S. Lindgreen, J. S. Pedersen, A. Albrechtsen, I. Moltke, M.

- Metspalu, E. Metspalu, T. Kivisild, R. Gupta, M. Bertalan, K. Nielsen, M. T. P. Gilbert, Y. Wang, M. Raghavan, P. F. Campos, H. M. Kamp, A. S. Wilson, A. Gledhill, S. Tridico, M. Bunce, E. D. Lorenzen, J. Binladen, X.-S. Guo, J. Zhao, X.-Q. Zhang, H. Zhang, Z. Li, M.-F. Chen, L. Orlando, K. Kristiansen, M. Bak, N. Tommerup, C. Bendixen, T. L. Pierre, B. Grønnow, M. Meldgaard, C. Andreasen, S. A. Fedorova, L. P. Osipova, T. F. G. Higham, C. B. Ramsey, T. v. O. Hansen, F. C. Nielsen, M. H. Crawford, S. Brunak, T. S. Pontén, R. Villemans, R. Nielsen, A. Krogh, **J. Wang**, E. Willerslev. Ancient human genome sequence of an extinct Palaeo-Eskimo. *Nature*, **463**, 757-762, 2010.
- 44) R.-Q. Li, W. Fan, G. Tian, H.-M. Zhu, L. He, J. Cai, Q.-F. Huang, Q.-L. Cai, B. Li, Y.-Q. Bai, Z.-H. Zhang, Y.-P. Zhang, W. Wang, J. Li, F.-W. Wei, H. Li, M. Jian, J.-W. Li, Z.-L. Zhang, R. Nielsen, D.-W. Li, W.-J. Gu, Z.-T. Yang, Z.-L. Xuan, O. A. Ryder, F. C.-C. Leung, Y. Zhou, J.-J Cao, X. Sun, Y.-G. Fu, X.-D. Fang, X.-S. Guo, B. Wang, R. Hou, F.-J. Shen, B. Mu, P.-X. Ni, R.-M. Lin, W.-B. Qian, G.-D. Wang, C. Yu, W.-H. Nie, J.-H. Wang, Z.-G. Wu, H.-Q. Liang, J.-M Min, Q. Wu, S.-F. Cheng, J. Ruan, M.-W. Wang, Z.-B. Shi, M. Wen, B.-H. Liu, X.-L. Ren, H.-S. Zheng, D. Dong, K. Cook, G. Shan, H. Zhang, C. Kosiol, X.-Y. Xie, Z.-H. Lu, H.-C. Zheng, Y.-R. Li, C. C. Steiner, T. T.-Y. Lam, S.-Y. Lin, Q.-H. Zhang, G.-Q. Li, J. Tian, T.-M. Gong, H.-D. Liu, D.-J. Zhang, L. Fang, C. Ye, J.-B. Zhang, W.-B. Hu, A.-L. Xu, Y.-Y. Ren, G.-J. Zhang, M. W. Bruford, Q.-B. Li, L.-J. Ma, Y.-R. Guo, N. An, Y.-J. Hu, Y. Zheng, Y.-Y. Shi, Z.-Q. Li, Q. Liu, Y.-L. Chen, J. Zhao, N. Qu, S.-C. Zhao, F. Tian, X.-L. Wang, H.-Y. Wang, L.-Z. Xu, X. Liu, T. Vinar, Y.-J Wang, T.-W. Lam, S.-M. Yiu, S.-P. Liu, H.-M. Zhang, D.-S. Li, Y. Huang, X. Wang, G.-H. Yang, Z. Jiang, J.-Y. Wang, N. Qin, L. Li, J.-X. Li, L. Bolund, K. Kristiansen, G. K.-S. Wong, M. Olson, X.-Q. Zhang, S.-G. Li, H.-M. Yang, J. Wang, **J. Wang**. The sequence and de novo assembly of the giant panda genome. *Nature*, **463**, 311-317, 2010.
- 45) R.-Q. Li, Y.-R. Li, H.-C. Zheng, R.-B. Luo, H.-M. Zhu, Q.-B. Li, W.-B. Qian, Y.-Y. Ren, G. Tian, J.-X. Li, G.-Y. Zhou, X. Zhu, H.-L. Wu, J.-J. Qin, X. Jin, D.-F. Li, H.-Z. Cao, X.-D. Hu, H. Blanche, H. Cann, X.-Q. Zhang, S.-G. Li, L. Bolund, K. Kristiansen, H.-M. Yang, **J. Wang**, J. Wan. Building the sequence map of the human pan-genome. *Nature Biotechnology*, **28**, 57-63, 2010.
- 46) S.-W. Huang, R.-Q. Li, Z.-H. Zhang, L. Li, X.-F. Gu, W. Fan, W. J. Lucas, X.-W.

- Wang, B.-Y. Xie, P.-X. Ni, Y.-Y. Ren, H.-M. Zhu, J. Li, K. Lin, W.-W. Jin, Z.-J. Fei, G.-C. Li, J. Staub, A. Kilian, E.-A.G.van.der. Vossen, Y. Wu, J. Guo, J. He, Z.-Q. Jia, Y. Ren, G. Tian, Y. Lu, J. Ruan, W.-B. Qian, M.-W Wang, Q.-F. Huang, B. Li, Z.-L. Xuan, J.-J. Cao, A. san, Z.-G. Wu, J.-B. Zhang, Q.-L. Cai, Y.-Q. Bai, B.-W. Zhao, Y.-H. Han, Y. Li, X.-F Li, S.-H. Wang, Q.-X. Shi, S.-Q. Liu, W.- K. Cho, J.-Y. Kim, Y. Xu, K. Heller-Uszynska, H. Miao, Z.-C. Cheng, S.-P Zhang, J. Wu, Y.-H. Yang, H.-X. Kang, M. Li, H.-Q. Liang, X.-L. Ren, Z.-B. Shi, M. Wen, M. Jian, H.-L. Yang, G.-J. Zhang, Z.-T. Yang, R. Chen, S.-F. Liu, J.-W. Li, L.-J. Ma, H. Liu, Y. Zhou, J. Zhao, X.-D. Fang, G.-Q. Li, L. Fang, Y.-R. Li, D.-Y. Liu, H.-K. Zheng, Y. Zhang, N. Qin, Z. Li, G.-H. Yang, S. Yang, L. Bolund, K. Kristiansen, H.-C. Zheng, S.-C. Li, X.-Q. Zhang, H.-M. Yang, J. Wang, R.-F. Su, B.-X. Zhang, S.-Z. Jiang, **J. Wang**, Y.-C. Du , S.-G. Li. The genome of the cucumber, *Cucumis sativus* L.. *Nature Genetics*, **41**, 1275-1281, 2009.
- 47) Q.-Y. Xia, Y.-R. Guo, Z. Zhang, D. Li, Z.-L. Xuan, Z. Li, F.-Y. Dai, Y.-R. Li, D.-J. Cheng, R.-Q. Li, T.-C. Cheng, T. Jiang, C. Becquet, X. Xu, C. Liu, X.-F Zha, W. Fan, Y. Lin, Y.-H Shen, L. Jiang, J. Jensen, I. Hellmann, S. Tang, P. Zhao, H.-F Xu, C. Yu, G.-J. Zhang, J. Li, J.-J. Cao, S.-P. Liu, N.-J He, Y. Zhou, H. Liu, J. Zhao, C. Ye, Z.-H Du, G.-Q. Pan, A.-C. Zhao, H.-J. Shao, W. Zeng, P. Wu, C.-F Li, M.-H Pan, J.-J Li, X.-Y Yin, D.-W. Li, J. Wang, H.-S. Zheng, W. Wang, X.-Q. Zhang, S.-G. Li, H.-M. Yang, Ch. Lu, R. Nielsen, Z.-Y. Zhou, J. Wang, Z.-H. Xiang, **J. Wang**. Complete resequencing of 40 genomes reveals domestication events and genes in silkworm (*Bombyx*). *Science*, **326**, 433-436, 2009.
- 48) Y.-R. Li , **J. Wang**. Faster human genome sequencing. *Nature Biotechnology*, **27**, 820-821, 2009.
- 49) **J. Wang**, W. Wang, R.-Q. Li, Y.-R. Li, G. Tian, L. Goodman, W. Fan, J.-Q. Zhang, J. Li, J.-B. Zhang, Y.-R. Guo, B.-X. Feng, H. Li, Y. Lu, X.-D. Fang, H.-Q. Liang, Z.-L. Du, D. Li, Y.-Q. Zhao, Y.-J. Hu, Z.-Z. Yang, H.-C. Zheng, I. Hellmann, M. Inouye, J. Pool, X. Yi, J. Zhao, J.-J. Duan, Y. Zhou, J.-J. Qin, L.-J. Ma, G.-Q. Li, Z.-T. Yang, G.-J. Zhang, B. Yang, C. Yu, F. Liang, W.-J. Li, S.-C. Li, D.-W. Li, P.-X. Ni, J. Ruan, Q.-B. Li, H.-M. Zhu, D.-Y. Liu, Z.-K. Lu, N. Li, G.-W. Guo, J.-G. Zhang, J. Ye, L. Fang, Q. Hao, Q. Chen, Y. Liang, Y.-Y. Su, A. San, C. Ping, S. Yang, F. Chen, L. Li, K. Zhou, H.-K. Zheng, Y.-Y. Ren, L. Yang, Y. Gao, G.-H. Yang, Z. Li, X.-L. Feng, K.

- Kristiansen, G. K.-S. Wong, R. Nielsen, R. Durbin, L. Bolund, X.-Q. Zhang, S.-G. Li, H.-M. Yang , J. Wang. The diploid genome sequence of an Asian individual. *Nature*, **456**, 60-65, 2008.
- 50) H. Rohde, J.-J. Qin, Y.-J. Cui, D.-F. Li, N.-J. Loman, M. Hentschke, W.-T. Chen, F. Pu, Y.-Q. Peng, J.-H. Li, F. Xi, S.-H. Li, Y. Li, Z.-X. Zhang, X.-W. Yang, M.-R. Zhao, P. Wang, Y.-L. Guan, Z. Cen, X.-N. Zhao, M.-T. Christner, R. Kobbe, S. Loos, J. Oh, L. Yang, A. Danchin, G.-F. Gao, Y.-J. Song, Y.-R. Li, H.-M. Yang, J. Wang, J.-G. Xu, M.-J. Pallen, **J. Wang**, M. Aepfelbacher, R.-F. Yang and the E. coli O104:H4 Genome Analysis Crowd-Sourcing Consortium. Open-source genomic analysis of Shiga-toxin-producing E. coli O104:H4. *The New England Journal of Medicine*, **365**, 718-724, 2011.
- 51) Biology analysis group, Q.-Y. Xia, Z.-Y. Zhou, C. Lu, D.-J. Cheng, F.-Y. Dai, B. Li, P. Zhao, X.-f. Zha, T.-C. Cheng, C.-L. Chai, G.-Q. Pan, J.-S. Xu, C. Liu, Y. Lin, J.-F. Qian, Y. Hou, Z.-L. Wu, G.-R. Li, M.-H. Pan, C.-F. Li, Y.-H. Shen, X.-Q. Lan, L.-W. Yuan, T. Li, H.-F. Xu, G.-W. Yang, Y.-J. Wan, Y. Zhu, M.-D. Yu, W.-D. Shen, D.-Y. Wu, Z.-H. Xiang, Genome analysis group, J. Yu, **J. Wang**, R.-Q. Li, J.-P. Shi, H. Li, G.-Y. Li, J.-N. Su, X.-L. Wang, G.-Q. Li, Z.-J. Zhang, Q.-F. Wu, J. Li, Q.-P. Zhang, N. Wei, J.-Z. Xu, H.-B. Sun, L. Dong, D.-Y. Liu, S.-L. Zhao, X.-L. Zhao, Q.-S. Meng, F.-D. Lan, X.-G. Huang, Y.-Z. Li, L. Fang, C.-F. Li, D.-W. Li, Y.-Q. Sun, Z.-P. Zhang, Z. Yang, Y.-Q. Huang, Y. Xi, Q.-H. Qi, D.-D. He, H.-Y. Huang, X.-W. Zhang, Z.-Q. Wang, W.-J. Li, Y.-Z. Cao, Y.-P. Yu, H. Yu, J.-H. Li, J.-H. Ye, H. Chen, Y. Zhou, B. Liu, J. Wang, J. Ye, H. Ji, S.-T. Li, P.-X. Ni, J.-G. Zhang, Y. Zhang, H.-K. Zheng, B.-Y. Mao, W. Wang, C. Ye, S.-G. Li, J. Wang, G. K.-S. Wong, H.-M. Yang. A draft sequence for the genome of the domesticated silkworm (*Bombyx mori*). *Science*, **306**, 1937-1940, 2004.
- 52) **J. Wang**, J.-G. Zhang, H.-K. Zheng, J. Li, D.-Y. Liu, H. Li, R. Samudrala, J. Yu , G. K.-S. Wong. Mouse transcriptome: neural evolution of 'non-coding' complementary DNAs. *Nature*, **431**, 1 p following 757, 2004.
- 53) **J. Wang**, S.-T. Li, Y. Zhang, H.-K. Zheng, Z. Xu, J. Ye, J. Yu, G. Wong. Vertebrate gene predictions and the problem of large genes. *Nature Review Genetics*, **4**, 741-749, 2003.
- 54) J. Yu, S.-N. Hu, **J. Wang**, G. K.-S. Wong, S.-G. Li, B. Liu, Y.-J. Deng, L. Dai, Y.

- Zhou, X.-Q. Zhang, M.-L. Cao, J. Liu, J.-D. Sun, J.-B. Tang, Y.-J. Chen, X.-B. Huang, W. Lin, C. Ye, W. Tong, L.-J. Cong, J.-N. Geng, Y.-J. Han, L. Li, W. Li, G.-Q. Hu, X.-G. Huang, W.-J. Li, J. Li, Z.-W. Liu, L. Li, J.-P. Liu, Q.-H. Qi, J.-S. Liu, L. Li, T. Li, X.-G. Wang, H. Lu, T.-T. Wu, M. Zhu, P.-X. Ni, H. Han, W. Dong, X.-Y. Ren, X.-L. Feng, P. Cui, X.-R. Li, H. Wang, X. Xu, W.-X. Zhai, Z. Xu, J.-S. Zhang, S.-J. He, J.-G. Zhang, J.-C. Xu, K.-L. Zhang, X.-W. Zheng, J.-H. Dong, W.-Y. Zeng, L. Tao, J. Ye, J. Tan, X.-D. Ren, X.-W. Chen, J. He, D.-F. Liu, W. Tian, C.-G. Tian, H.-A. Xia, Q.-Y. Bao, G. Li, H. Gao, T. Cao, J. Wang, W.-M. Zhao, P. Li, W. Chen, X.-D. Wang, Y. Zhang, J.-F. Hu, J. Wang, S. Liu, J. Yang, G.-Y. Zhang, Y.-Q. Xiong, Z.-J. Li, L. Mao, C.-S. Zhou, Z. Zhu, R.-S. Chen, B.-L. Hao, W.-M. Zheng, S.-Y. Chen, W. Guo, G.-J. Li, S.-Q. Liu, M. Tao, J. Wang, L.-H. Zhu, L.-P. Yuan, and H.-M. Yang. A draft sequence of the rice genome (*Oryza sativa* L. ssp. *indica*). *Science*, **296**, 79-92, 2002.
- 55) R.-L. Ge, Q.-L. Cai, Y.-Y. Shen, A. San, L. Ma, Y. Zhang, X. Yi, Y. Chen, L.-F. Yang, Y. Huang, R.-J He, Y.-Y. Hui, M.-R. Hao, Y. Li, B. Wang, X.-H. Ou, J.-H. Xu, Y.-F. Zhang, K. Wu, C.-Y Geng, W.-P. Zhou, T.-C. Zhou, D.-M. Irwin, Y.-Z. Yang, L. Ying, H.-H. Bao, J. Kim, D.-M. Larkin, J. Ma, H.-A. Lewin, J.-C. Xing, Roy.-N. Platt II, D.-A. Ray, L. Auvil, B. Capitanu, X.-F Zhang, G.-J. Zhang, R.-W. Murphy, **J. Wang**, Y.-P. Zhang, J. Wang. Draft genome sequence of the Tibetan antelope. *Nature Communications*, **4**, 1858, 2013.
- 56) Z. Wang, J.-P. Anaya, A. Zadissa, W.-Q. Li, Y. Niimura, Z.-Y. Huang, C.-Y. Li, S. White, Z.-Q. Xiong, D.-M. Fang, B. Wang, Y. Ming, Y. Chen, Y. Zheng, S. Kuraku, M. Pignatelli, J. Herrero, K. Beal, M. Nozawa, Q.-Y. Li, J. Wang, H.-Y. Zhang, L.-L. Yu, S. Shigenobu, J.-Y. Wang, J.-N Liu, P. Flieck, S. Searle, **J. Wang**, S. Kuratani, Y. Yin, B. Aken, G.-J. Zhang, N. Irie. The draft genomes of soft-shell turtle and green sea turtle yield insights into the development and evolution of the turtle-specific body plan. *Nature Genetics*, **45**, 701–706, 2013.
- 57) M. Blaser, P. Bork, C. Fraser, R. Knight, **J. Wang**. The microbiome explored: recent insights and future challenges. *Nature Reviews Microbiology* 11, 213-217 (2013).
- 58) R. Pisko, Z.-Y. Peng, **J. Wang**, J.-B. Li. Lack of evidence for existence of noncanonical RNA editing. *Nature Biotechnology*, **31**, 19–20, 2013.
- 59) S.-C. Zhao, P.-P. Zheng, S.-S. Dong, X.-J Zhan, Q. Wu, X.-S. Guo, Y.-B. Hu, W.-M.

- He, S.-M. Zhang, W. Fan, L.-F. Zhu, D. Li, X.-M Zhang, Q. Chen, H.-M. Zhang, Z.-H. Zhang, X.-L. Jin, J.-G. Zhang, H.-M. Yang, J. Wang, **J. Wang**, F.-W. Wei. Whole-genome sequencing of giant pandas provides insights into demographic history and local adaptation. *Nature Genetics*, **45**, 67-71, 2012.
- 60) **J. Wang**, as one of the Principal Investigators (Production and Analysis Group) and Steering Committee member in The 1000 Genomes Project Consortium. The 1000 Genomes Project Consortium, *et al.* An integrated map of genetic variation from 1,092 human genomes. *Nature*, **491**, 56-65, 2012.
- 61) **J. Wang**, as one of the Principal Investigators (Production and Analysis Group) and Steering Committee member in The 1000 Genomes Project Consortium. The 1000 Genomes Project Consortium. A map of human genome variation from population-scale sequencing. *Nature*, **467**, 1061-1073, 2010.
- 62) **J. Wang** as one of first authors in the International Chicken Polymorphism Map Consortium. International Chicken Polymorphism Map Consortium. A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. *Nature*, **432**, 717-722, 2004.
- 63) M.-B. Hufford, X. Xu, J.-V. Heerwaarden, T. Pyhäjärvi, J.-M. Chia, R.-A. Cartwright, R.-J. Elshire, J.-C. Glaubitz, K.-E. Guill, S.-M. Kaepller, J.-S. Lai, P.-L. Morrell, L.-M. Shannon, C. Song, N.-M. Springer, R.-A.S. Wagner, P. Tiffin, **J. Wang**, G.-Y. Zhang, J. Doebley, M.-D. McMullen, D. Ware, E.-S. Buckler, S. Yang, R.-I. Jeffrey. Comparative population genomics of maize domestication and improvement. *Nature Genetics*, **44**, 808-811, 2012.
- 64) J.-M. Chia, C. Song, P. J. Bradbury, D. Costich, N. de Leon, J. Doebley, R. J. Elshire, B. Gaut, L. Geller, J. C. Glaubitz, M. Gore, K. E. Guill, J. Holland, M. B. Hufford, J.-S. Lai, M. Li, X. Liu, Y.-L. Lu, R. McCombie, R. Nelson, J. Poland, B. M. Prasanna, T. Pyhäjärvi, T.-Z. Rong, R. S. Sekhon, Q. Sun, M. I. Tenaillon, F. Tian, **J. Wang**, X. Xu, Z.-W. Zhang, S. M. Kaepller, R.-I. Jeffrey, M. D. McMullen, E. S. Buckler, G.-Y. Zhang, Y.-B. Xu , D. Ware. Maize HapMap2 identifies extant variation from a genome in flux. *Nature Genetics*, **44**, 803-807, 2012.
- 65) M.-R. Nelson, D. Wegmann, M.-G. Ehm, D. Kessner, P.-St. Jean, C. Verzilli, J.-D. Shen, Z.-Z. Tang, S.-A. Bacanu, D. Fraser, L.-L. Warren, J. Aponte, M. Zawistowski, X. Liu, H. Zhang, Y. Zhang, J. Li, Y. Li, L. Li, P. Woppard, S. Topp, M. D. Hall, K.

- Nangle, **J. Wang**, G. Abecasis, L.-R. Cardon, S. Zöllner, J.-C. Whittaker, S.-L. Chissoe1, J. Novembre, V. Mooser. An abundance of rare functional variants in 202 drug target genes sequenced in 14,002 people. *Science*, **337**, 100-104, 2012.
- 66) D.-G. MacArthur, S. Balasubramanian, A. Frankish, N. Huang, J. Morris, K. Walter, L. Jostins, L. Habegger, J.-K. Pickrell, S.-B. Montgomery, C.-A. Albers, Z.-D. Zhang, D.-F. Conrad, G. Lunter, H.-C. Zheng, Q. Ayub, Mark. A. DePristo, E. Banks, M. Hu, R.-E. Handsaker, J.-A. Rosenfeld, M. Fromer, M. Jin, X.-M. J. Mu, E. Khurana, K. Ye, M. Kay, G.-I. Saunders, M.-M. Suner, T. Hunt, I.-H.A. Barnes, C. Amid, R. C.-S. Denise, A.-H. Bignell, C. Snow, B. Yngvadottir, S. Bumpstead, D.-N. Cooper, Y.-L Xue, I.-G. Romero, 1000 Genomes Project Consortium, **J. Wang**, Y.-R. Li, R.-A. Gibbs, S.-A. McCarroll, E.-T. Dermitzakis, J.-K. Pritchard, J.-C. Barrett, J. Harrow, M.-E. Hurles, M.-B. Gerstein, T.-S. Chris. A systematic survey of loss-of-function variants in human protein-coding genes. *Science*, **335**, 823-828, 2012.
- 67) M.-A.M. Groenen, A.-L. Archibald, H. Uenishi, C.-K. Tuggle, Y. Takeuchi, M.-F. Rothschild, R.-G. Claire, C. Park, D. Milan, H. JanMegens, S.-T. Li, D. Larkin, H. Kim, L.-A.F. Frantz, M. Caccamo, H. Ahn, B. L. Aken, A. Anselmo, C. Anthon, L. Auvil, B. Badaoui, C. W. Beattie, C. Bendixen, D. Berman, F. Blecha, J. Blomberg, L. Bolund, M. Bosse, S. Botti, B.-J. Zhan, M. Bystrom, B. Capitanu, C.-S. Denise, P. Chardon, C. Chen, R. Cheng, S.-H. Choi, W. Chow, R. C. Clark, C. Clee, R. P. M.-A. Crooijmans, H.-D. Dawson, P. Dehais, F. De. Sapiro, BertDibbits, N. Drou, Z.-Q. Du, K. Eversole, J.-o. Fadista, S. Fairley, T. Faraut, G.-J. Faulkner, K.-E. Fowler, M. Fredholm, E. Fritz, J. G. R. Gilbert, E. Giuffra, J. Gorodkin, D.-K. Griffin, J.-L. Harrow, A. Hayward, K. Howe, Z.-L. Hu, S.-J. Humphray, T. Hunt, H. Hornshøj, J.-T. Jeon, P. Jern, M. Jones, J. Jurka, H. Kanamori, R. Kapetanovic, J. Kim, J.-H. Kim, K.-W. Kim, T.-H. Kim, G. Larson, K. Lee, K.-T. Lee, R. Leggett, H. A. Lewin, Y.-R. Li, W.-S. Liu, J.-E. Loveland, Y. Lu, J.-K. Lunney, J. Ma, O. Madsen, K. Mann, L. Matthews, S. McLaren, T. Morozumi, M. P. Murtaugh, J. Narayan, D.-T. Nguyen, P.-X. Ni, S.-J. Oh, S. Onteru, F. Panitz, E.-W. Park, H.-S. Park, G. Pascal, Y. Paudel, P.-E. Miguel, R.-G. Ricardo, J. M. Reecy, R.-Z. Sandra, G. A. Rohrer, L. Rund, Y.-M. Sang, K. Schachtschneider, J. G. Schraiber, J. Schwartz, L. Scobie, C. Scott, S. Searle, B. Servin, B. R. Southey, G. Sperber, P. Stadler, J. V. Sweedler, H. Tafer, B.

- Thomsen, R. Wali, J. Wang, **J. Wang**, S. White, X. Xu, M. Yerle, G.-J. Zhang, J.-G. Zhang, J. Zhang, S.-H. Zhao, J. Rogers, C. Churcher, L. B. Schook. Analyses of pig genomes provide insight into porcine demography and evolution. *Nature*, **491**, 393-398, 2012.
- 68) **J. Wang**, as one of the authors in The Tomato Genome Consortium. The Tomato Genome Consortium. The tomato genome sequence provides insights into fleshy fruit evolution. *Nature*, **485**, 635-641, 2012.
- 69) M.-Z. Li, H.-L. Wu, Z.-G. Luo, Y.-D. Xia, J.-Q. Guan, T. Wang, Y.-R. Gu, L. Chen, K. Zhang, J.-D. Ma, Y.-K. Liu, Z.-J. Zhong, J. Nie, S.-L. Zhou, Z.-P. Mu, X.-Y. Wang, J.-J. Qu, L. Jing, H.-Y. Wang, S.-J. Huang, N. Yi, Z. Wang, D.-X. Xi, J. Wang, G.-L. Yin, L. Wang, N. Li, Z. Jiang, Q.-L. Lang, H.-S. Xiao, A. Jiang, L. Zhu, Y.-Z. Jiang, G.-Q. Tang, M.-M. Mai, S.-R. Shuai, N. Li, K. Li, J.-Y. Wang, X.-Q. Zhang, Y.-R. Li, H.-S. Chen, X.-L. Gao, G. S. Plastow, S. Beck, H.-M. Yang, J. Wang, **J. Wang**, X.-W. Li, R.-Q. Li. An atlas of DNA methylomes in porcine adipose and muscle tissues. *Nature Communications*, **3**, 850, 2012.
- 70) R.-K. Varshney, W.-B. Chen, Y.-P. Li, A.-K. Bharti, R.-K. Saxena, J.-A. Schlueter, M. T. A. Donoghue, S. Azam, G.-Y. Fan, A.-M. Whaley, A.-D. Farmer, J. Sheridan, A. Iwata, R. Tuteja, R.-V. Penmetsa, W. Wu, H.-D. Upadhyaya, S.-P. Yang, T. Shah, K. B. Saxena, T. Michael, W.-R. McCombie, B. Yang, G.-Y. Zhang, H.-M. Yang, **J. Wang**, C. Spillane, D. R. Cook, G. D. May, X. Xu, S. A. Jackson. Draft genome sequence of pigeonpea (*Cajanus cajan*), an orphan legume crop of resource-poor farmers. *Nature Biotechnology*, **30**, 83-89, 2011.
- 71) G.-M. Yan, G.-J. Zhang, X.-D. Fang, Y.-F. Zhang, C. Li, F. Ling, D.-N. Cooper, Q.-Y. Li, Y. Li, A.-J. Gool, H.-L. Du, J.-S. Chen, R.-H. Chen, P. Zhang, Z.-Y. Huang, J.-R. Thompson, Y.-H. Meng, Y.-Q. Bai, J.-F. Wang, M. Zhuo, T. Wang, Y. Huang, L.-Q. Wei, J.-W. Li, Z.-W. Wang, H.-F. Hu, P.-C. Yang, L. Le, P.-D. Stenson, B. Li, X.-M. Liu, E.-V. Ball, N. An, Q.-F. Huang, Y. Zhang, W. Fan, X.-Q. Zhang, Y.-R. Li, W. Wang, M.-G. Katze, B. Su, R. Nielsen, H.-M. Yang, **J. Wang**, X.-N. Wang, J. Wang. Genome sequencing and comparison of two nonhuman primate animal models, the cynomolgus and Chinese rhesus macaques. *Nature Biotechnology*, **29**, 1019-1023, 2011.
- 72) **J. Wang**, as one of the Principal Investigators in The Patato Genome Sequencing

Consortium. The Potato Genome Sequencing Consortium. Genome sequence and analysis of the tuber crop potato. *Nature*, **475**, 189-195, 2011.

- 73) **J. Wang**, as one of the Principal Investigators (Production and Analysis Group) and Steering Committee member in The 1000 Genomes Project Consortium. D.-F. Conrad, J. E. M. Keebler, M.-A. DePristo, S.-J. Lindsay, Y.-J. Zhang, F. Casals, Y. Idaghdour, C.-L. Hartl, C. Torroja, K.-V. Garimella, M. Zilversmit, R. Cartwright, G.-A. Rouleau, M. Daly, E.-A. Stone, M.-E. Hurles , P. Awadalla for the 1000 Genomes Project. Variation in genome-wide mutation rates within and between human families. *Nature Genetics*, **43**, 712-714, 2011.
- 74) **J. Wang**, as one of the Principal Investigators (Production and Analysis Group) and Steering Committee member in The 1000 Genomes Project Consortium. Ryan.-D. Hernandez, J.-L. Kelley, E. Elyashiv, S.-C. Melton1, A. Auton, G. McVean, 1000 Genomes Project, G. Sella, Molly Przeworski. Classic selective sweeps were rare in recent human evolution. *Science*, **331**, 920-924, 2011.
- 75) R.-E. Mills, K. Walter, C. Stewart, R.-E. Handsaker, K. Chen, C. Alkan, A. Abyzov, S.-C. Yoon, K. Ye, R.-K. Cheetham, A. Chinwalla, D.-F. Conrad, Y.-T. Fu, F. Grubert, I. Hajirasouliha, F. Hormozdiari, L.-M. Iakoucheva, Z. Iqbal, S. Kang, J.-M. Kidd, M.-K. Konkel, J. Korn, E. Khurana, D. Kural, H.-Y. K. Lam, J. Leng, R.-Q. Li, Y.-R. Li, C.-Y. Lin, R.-B. Luo, X.-J. Mu, J. Nemesh, H.-E. Peckham, T. Rausch, A. Scally, X.-H. Shi, M.-P. Stromberg, A.-M. Stütz, A.-E. Urban, J.-A. Walker, J.-T. Wu, Y.-J. Zhang, Z.-D. Zhang, M.-A. Batzer, L. Ding, G.-T. Marth, G. McVean, J. Sebat, M. Snyder, **J. Wang**, K. Ye, E.-E. Eichler, M.-B. Gerstein, M.-E. Hurles, C. Lee, S.-A. McCarroll, J.-O. Korbel , 1000 Genomes Project. Mapping copy number variation by population-scale genome sequencing. *Nature*, **470**, 59-65, 2011.
- 76) M. Arumugam, J. Raes, E. Pelletier, D.-L. Paslier, T. Yamada, D.-R. Mende, G.-R. Fernandes, J. Tap, T. Bruls, J.-M. Batto, M. Bertalan, N. Borruel, F. Casellas, L. Fernandez, L. Gautier, T. Hansen, M. Hattori, T. Hayashi, M. Kleerebezem, K. Kurokawa, M. Leclerc, F. Levenez, C. Manichanh, H.-B. Nielsen, T. Nielsen, N. Pons, J. Poulain, J.-J. Qin, S.-P. Thomas, S. Tims, D. Torrents, E. Ugarte, E.-G. Zoetendal, **J. Wang**, F. Guarner, O. Pedersen, M. Willem, S. Brunak, J. Doré, MetaHIT Consortium (additional members), J. Weissenbach, S.-D. Ehrlich , P. Bork. Enterotypes of the human gut microbiome. *Nature*, **473**, 174-180, 2011.

- 77) **J. Wang**, as one of the Principal Investigators (Production and Analysis Group) and Steering Committee member in The 1000 Genomes Project Consortium. Peter.-H. Sudman, J.-O. Kitzman, F. Antonacci1, C. Alkan, M. Malig, A. Tselenko, N. Sampas, L. Bruhn, J. Shendure, 1000 Genomes Project, E.-E. Eichler. Diversity of human copy number variation and multicopy genes. *Science*, **330**, 641-646, 2010.
- 78) E. Heard, S. Tishkoff, John.-A. Todd, M. Vidal, G.-P. Wagner, **J. Wang**, D. Weigel, R. Young. Ten years of genetics and genomics: what have we achieved and where are we heading? *Nature Reviews Genetics*, **11**, 723-733, 2010.
- 79) **J. Wang**, as one of The Schistosoma japonicum Genome Sequencing and Functional Analysis Consortium. The Schistosoma japonicum Genome Sequencing and Functional Analysis Consortium. The *Schistosoma japonicum* genome reveals features of host-parasite interplay. *Nature*, **460**, 345-351, 2009.
- 80) **J. Wang** as one of the authors in Drosophila 12 Genomes Consortium. Drosophila 12 Genomes Consortium. Evolution of genes and genomes on the Drosophila phylogeny. *Nature*, **450**, 203-218, 2007.
- 81) L. Li, X.-F. Wang, V. Stolc, X.-Y. Li, D.-F. Zhang, N. Su, W. Tongprasit, S.-G. Li, Z.-K. Cheng, **J. Wang**, X.-W. Deng. Genome wide transcription analyses in rice using tiling microarrays. *Nature Genetics*, **38**, 124-129, 2006.
- 82) D.-M. Muzny, S.-E. Scherer, R. Kaul, J. Wang, J. Yu, R. Sudbrak, C.-J. Buhay, R. Chen, A. Cree, Y. Ding, D.-R. Shannon, R. Gill, P. Gunaratne, R.-A. Harris, A.-C. Hawes, J. Hernandez, A.-V. Hodgson, J. Hume, A. Jackson, Z.-M. Khan, K.-S. Christie, L.-R. Lewis, R.-J. Lozado, M.-L. Metzker, A. Milosavljevic, G.-R. Miner, M.-B. Morgan, L.-V. Nazareth, G. Scott, E. Sodergren, X.-Z. Song, D. Steffen, S.-R. Wei, D.-A. Wheeler, M.-W. Wright, K.-C. Worley, Y. Yuan, Z.-D. Zhang, C.-Q. Adams, M.-A. Lari, M. Ayele, M.-J. Brown, G. Chen, Z.-J. Chen, J. Clendenning, K.-P. Blankenburg, R.-S. Chen, Z. Chen, C. Davis, O. Delgado, H.-H. Dinh, W. Dong, H. Draper, S. Ernst, G. Fu, M.-L. Garay, D.-K. Garcia, W. Gillett, J. Gu, B. Hao, E. Haugen, P. Havlak, X. He, S. Hennig, S.-N. Hu, W. Huang, L.-R. Jackson, L.-S. Jacob, S.-H. Kelly, M. Kube, R. Levy, Z.-W. Li, B. Liu, J. Liu, W. Liu, J. Lu, M. Maheshwari, B.-V. Nguyen, G.-O. Okwuonu, A. Palmeiri, S. Pasternak, L.-M. Perez, K.-A. Phelps, F.-J. H. Plopper, B.-Q. Qiang, C. Raymond, R. Rodriguez, C. Saenphimmachak, J. Santibanez, H. Shen, Y. Shen, S. Subramanian, P.-E. Tabor, D.

Verduzco, L. Waldron, J. Wang, **J. Wang**, Q.-Y. Wang, G.-A. Williams, G. K.-S. Wong, Z.-J. Yao, J.-K. Zhang, X.-Q. Zhang, G.-P. Zhao, J.-L. Zhou, Y. Zhou, further contributors, D. Nelson, H. Lehrach, R. Reinhardt, S.-L. Naylor, H.-M. Yang, Ma. Olson, G. Weinstock and R.-A. Gibbs. The DNA sequence, annotation and analysis of human chromosome 3. *Nature*, **440**, 1194-1198, 2006.

- 83) **J. Wang**, as one of the authors in the International Chicken Genome Sequencing Consortium. International Chicken Genome Sequencing Consortium. Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. *Nature*, **432**, 695-716, 2004.
- 84) **J. Wang**, as one of the authors in the International Human Genome Sequencing Consortium. International Human Genome Sequencing Consortium. Finishing the euchromatic sequence of the human genome. *Nature*, **431**, 931-945, 2004.
- 85) **J. Wang**, as one of the authors in the International Human Genome Sequencing Consortium. International Human Genome Sequencing Consortium. Initial sequencing and analysis of the human genome. *Nature*, **409**, 860-921, 2001.