

参 考 文 献

- 奥·西费利. 叶绿体分子遗传学 [M]. 郝水等, 译. 长沙: 湖南科学技术出版社, 1987.
- 包满珠. 花卉学 [M]. 2 版. 北京: 中国农业出版社, 2012.
- 曹家树, 秦岭. 园艺植物种质资源学 [M]. 北京: 中国农业出版, 2005.
- 陈蕴, 吴开贤, 罗富成. 我国草坪草引种研究现状与进展 [J]. 草业科学, 2008, 10: 128-133.
- 段凌凤, 杨万能. 水稻表型组学研究概况和展望 [J]. 生命科学, 2016, 28 (10): 1129-1137.
- 段忠取, 朱军. 全基因组关联分析研究进展 [J]. 浙江大学学报 (农业与生命科学版), 2015, 41 (4): 385-393.
- 樊龙江, 王卫娣, 王斌, 等. 作物育种相关数据及大数据技术育种利用 [J]. 浙江大学学报 (农业与生命科学版), 2016, 42 (1): 30-39.
- 樊龙江, 吴三玲, 邱杰, 等. 生物信息学 [M]. 杭州: 浙江大学出版社, 2017.
- 方欣, 卢山, 于宗霞, 等. 青蒿素的生物合成研究 [J]. 科技导报, 2015, 33 (20): 31-35.
- 韩振海. 园艺作物种质资源学 [M]. 北京: 中国农业大学出版社, 2009.
- 雷彬彬, 李双双, 刘国政, 等. 高等植物线粒体基因组进化分析 [J]. 分子植物育种, 2012, 4: 490-500.
- 李付广, 袁有禄. 棉花分子育种学 [M]. 北京: 中国农业大学出版社, 2013.
- 李诗渊, 赵国屏, 王金. 合成生物学技术的研究进展——DNA 合成, 组装与基因组编辑 [J]. 生物工程学报, 2017, 33 (3): 343-360.
- 李双双, 薛龙飞, 苏爱国, 等. 高等植物线粒体基因组测序和序列分析 [J]. 中国农业大学学报, 2011, 16: 22-27.
- 李响. 利用单细胞测序技术剖析玉米遗传重组交换和单倍体诱导的机制 [D]. 武汉: 华中农业大学, 2017.
- 刘铁燕, 陈明生. 稻属植物的基因组进化 [J]. 生物多样性, 2014, 22 (1).
- 穆金虎, 陈玉泽, 冯慧, 等. 作物育种学领域新的革命: 高通量的表型组学时代 [J]. 植物科学学报, 2016, 34 (6): 962-971.
- 邵洁, 李建华, 王凯博, 等. 植物底盘: 天然产物合成生物学研究的新热点 [J]. 生物加工过程, 2017, 15 (5): 24-31.
- 唐萍, 彭程. 叶绿体基因组进化的速率和方式 [J]. 生物学通报, 2010, 45 (6): 8-10.
- 汪俏梅, 曹家树. 芥子油苷研究进展及其在蔬菜育种上的应用前景 [J]. 园艺学报, 2001, 28 (s1): 669-675.
- 王福军, 赵开军. 基因组编辑技术应用于作物遗传改良的进展与挑战 [J]. 中国农业科学, 2018, 51 (1): 1-16.
- 王森. 基于高通量测序的异源四倍体棉花超高密度 SNP 分子遗传图谱的构建及重要性状 QTL 定位 [D]. 南京: 南京农业大学, 2013.
- 王向峰, 才卓. 中国种业科技创新的智能时代——“玉米育种 4.0” [J]. 玉米科学, 2019, 27 (01): 1-9.
- 王营营, 黄璐, 樊龙江. 菰 (*Zizania latifolia*) 主要农艺性状及其驯化育种 [J]. 浙江大学学报 (农业与生命科学版), 2013, 39 (6): 629-635.
- 杨焕明. 基因组学 [M]. 北京: 科学出版社, 2016.

- 杨金水. 基因组学 [M]. 3 版. 北京: 高等教育出版社, 2013.
- 尤琪. 组学数据整合与功能模块化分析构建棉花全基因组注释体系 [D]. 北京: 中国农业大学, 2017.
- 张立新, 卢从明, 彭连伟, 等. 利用合成生物学原理提高光合作用效率的研究进展 [J]. 生物工程学报, 2017, 33 (3): 486-493.
- 张启发. 作物功能基因组学 [M]. 北京: 科学出版社, 2019.
- 张倩倩, 郑童, 予茜, 等. 生长素与植物根尖干细胞巢的维持 [J]. 植物学报, 2018, 53 (1): 126-138.
- 张先恩. 合成生物学专刊序言 [J]. 生物工程学报, 2017, 33 (3): 311-314.
- 张韵洁, 李德铎. 叶绿体系统发育基因组学的研究进展 [J]. 植物分类与资源学报, 2011, 33 (4): 365-375.
- 中国生物技术发展中心, 深圳华大基因研究院. 基因组学方法 [M]. 北京: 科学出版社, 2012.
- 钟广炎, 江东. 中国国家果树种质资源圃建设与研究回顾及展望 [J]. 中国农业科学, 2007, 40 (增刊 1): 342-347.
- 周想春, 邢永忠. 基因组编辑技术在植物基因功能鉴定及作物育种中的应用 [J]. 遗传, 2016, 38 (3): 227-242.
- 朱婷婷, 张磊, 陈万生, 等. 1342 个植物叶绿体基因组分析 [J]. 基因组学与应用生物学, 2017, 36 (10): 4323-4333.
- Brown TA. 基因组 3 [M]. 袁建刚等, 译. 北京: 科学出版社, 2009.
- 3, 000 Rice Genomes Project. The 3, 000 rice genomes project [J]. GigaScience, 2014, 3 (1): 2047-217X-3-7.
- Abe A, Kosugi S, Yoshida K, et al. Genome sequencing reveals agronomically important loci in rice using MutMap [J]. Nature Biotechnology, 2012, 30 (2): 174.
- Adams KL, Wendel JF. Polyploidy and genome evolution in plants [J]. Current Opinion in Plant Biology, 2005, 8 (2): 135-141.
- Adams MD, Kelley JM, Gocayne JD, et al. Complementary DNA sequencing: expressed sequence tags and human genome project [J]. Science, 1991, 252 (5013): 1651-1656.
- Adato A, Mandel T, Mintz-Oron S, et al. Fruit-surface flavonoid accumulation in tomato is controlled by a SIMYB12-regulated transcriptional network [J]. PLoS Genetics, 2009, 5 (12): e1000777.
- Adem M, Beyene D, Feyissa T. Recent achievements obtained by chloroplast transformation [J]. Plant Methods, 2017, 13 (1): 30.
- Akama S, Shimizu-Inatsugi R, Shimizu KK, et al. Genome-wide quantification of homeolog expression ratio revealed nonstochastic gene regulation in synthetic allopolyploid Arabidopsis [J]. Nucleic Acids Research, 2014, 42 (6): e46.
- Akpınar BA, Magni F, Yuce M, et al. The physical map of wheat chromosome 5DS revealed gene duplications and small rearrangements [J]. BMC Genomics, 2015, 16 (1): 453.
- Aldous EK, George B, Almahmoud ME, et al. *De novo* genome sequencing and comparative genomics of date palm (*Phoenix dactylifera*) [J]. Nature Biotechnology, 2011, 29 (6): 521-527.
- Allbed A, Kumar L. Soil salinity mapping and monitoring in arid and semi-arid regions using remote sensing technology: a review [J]. Advances in Remote Sensing, 2013, 2 (04): 373.
- Allen JO, Fauron CM, Minx P, et al. Comparisons among two fertile and three male-sterile mitochondrial genomes of maize [J]. Genetics, 2007, 177 (2): 1173-1192.
- Alverson AJ, Rice DW, Dickinson S, et al. Origins and recombination of the bacterial-sized multichromosomal mitochondrial genome of cucumber [J]. The Plant Cell, 2011, 23 (7): 2499-2513.

- An J, Lai J, Sajjanhar A, et al. miRPlant: an integrated tool for identification of plant miRNA from RNA sequencing data [J]. BMC Bioinformatics, 2014, 15 (1): 275.
- Anderson JE, Michno J, Kono TJY, et al. Genomic variation and DNA repair associated with soybean transgenesis: a comparison to cultivars and mutagenized plants [J]. BMC Biotechnology. 2016, 16 (1): 41.
- Anderson S, Bankier AT, Barrell BG, et al. Sequence and organization of the mitochondrial human genome [J]. Nature, 1981, 290 (5806): 457-465.
- Andersson SGE, Kurland CG. Origins of mitochondria and hydrogenosomes [J]. Current Opinion In Microbiology, 1999, 2 (5): 535-541.
- Andorf CM, Cannon EK, Portwood JL, et al. MaizeGDB update: new tools, data and interface for the maize model organism database [J]. Nucleic Acids Research, 2015, 44 (D1): D1195-D1201.
- Andrade-Sanchez P, Gore MA, Heun JT, et al. Development and evaluation of a field-based high-throughput phenotyping platform [J]. Functional Plant Biology, 2014, 41 (1): 68-79.
- Annaluru N, Muller H, Mitchell LA, et al. Total synthesis of a functional designer eukaryotic chromosome [J]. Science, 2014, 344 (6179): 55-58.
- Antipov D, Korobeynikov A, McLean JS, et al. HybridSPAdes: an algorithm for hybrid assembly of short and long reads [J]. Bioinformatics, 2015, 32 (7): 1009-1015.
- Applequist WL, Cronn R, Wendel JF. Comparative development of fiber in wild and cultivated cotton [J]. Evolution & Development, 2001, 3 (1): 3-17.
- Arabidopsis Genome Initiative. Analysis of the genome sequence of the flowering plant *Arabidopsis thaliana* [J]. Nature, 2000, 408 (6814): 796.
- Aranzana MJ, Kim S, Zhao K, et al. Genome-wide association mapping in Arabidopsis identifies previously known flowering time and pathogen resistance genes [J]. PLoS Genetics, 2005, 1 (5): e60.
- Arikait S, Xia R, Kakrana A, et al. An atlas of soybean small RNAs identifies phased siRNAs from hundreds of coding genes [J]. The Plant Cell, 2014, 26 (12): 4584.
- Arite T, Iwata H, Ohshima K, et al. DWARF10, an RMS1/MAX4/DAD1 ortholog, controls lateral bud outgrowth in rice [J]. The Plant Journal, 2007, 51 (6): 1019-1029.
- Arriola MB, Velmurugan N, Zhang Y, et al. Genome sequences of *Chlorella sorokiniana* UTEX 1602 and *Micractinium conductrix* SAG 241. 80: implications to maltose excretion by a green alga [J]. The Plant Journal, 2018, 93 (3): 566-586.
- Ashikari M, Sakakibara H, Lin S, et al. Cytokinin oxidase regulates rice grain production [J]. Science, 2005, 309 (5735): 741-745.
- Atwell S, Huang YS, Vilhjálmsson BJ, et al. Genome-wide association study of 107 phenotypes in *Arabidopsis thaliana* inbred lines [J]. Nature, 2010, 465 (7298): 627.
- Avni R, Nave M, Barad O, et al. Wild emmer genome architecture and diversity elucidate wheat evolution and domestication [J]. Science, 2017, 357 (6346): 93.
- Badouin H, Gouzy J, Grassa CJ, et al. The sunflower genome provides insights into oil metabolism, flowering and Asterid evolution [J]. Nature, 2017, 546 (7656): 148.
- Bai X, Huang Y, Hu Y, et al. Duplication of an upstream silencer of FZP increases grain yield in rice [J]. Nature Plants, 2017, 3 (11): 885.
- Baldi P, Brunak S, Bach F. Bioinformatics: the machine learning approach [M]. Massachusetts: MIT Press, 2001.
- Ballester AR, Molthoff J, de Vos R, et al. Biochemical and molecular analysis of pink tomatoes: deregulated

- expression of the gene encoding transcription factor SIMYB12 leads to pink tomato fruit color [J]. *Plant Physiology*, 2010, 152 (1): 71-84.
- Banaei-Moghaddam AM, Meier K, Karimi-Ashtiyani R, et al. Formation and expression of pseudogenes on the B chromosome of rye [J]. *The Plant Cell*, 2013, 25 (7): 2536-2544.
- Bancroft I, Morgan C, Fraser F, et al. Dissecting the genome of the polyploid crop oilseed rape by transcriptome sequencing [J]. *Nature Biotechnology*, 2011, 29 (8): 762.
- Banks JA, Nishiyama T, Hasebe M, et al. The *Selaginella* genome identifies genetic changes associated with the evolution of vascular plants [J]. *Science*, 2011, 332 (6032): 960.
- Bao Z, Eddy SR. Automated *de novo* identification of repeat sequence families in sequenced genomes [J]. *Genome Research*, 2002, 12 (8): 1269-1276.
- Bardou F, Ariel F, Simpson CG, et al. Long noncoding RNA modulates alternative splicing regulators in *Arabidopsis* [J]. *Developmental Cell*, 2014, 30 (2): 166-176.
- Bassel GW, Glaab E, Marquez J, et al. Functional network construction in *Arabidopsis* using rule-based machine learning on large-scale data sets [J]. *The Plant Cell*, 2011, 23 (9): 3101-3116.
- Baucom RS, Estill JC, Chaparro C, et al. Exceptional diversity, non-random distribution, and rapid evolution of retroelements in the B73 maize genome [J]. *PLoS Genetics*, 2009, 5 (11): e1000732.
- Baudelet PH, Ricochon G, Linder M, et al. A new insight into cell walls of Chlorophyta [J]. *Algal Research*, 2017, 25: 333-371.
- Bausher MG, Singh ND, Lee SB, et al. The complete chloroplast genome sequence of *Citrus sinensis* (L.) Osbeck var. 'Ridge Pineapple': organization and phylogenetic relationships to other angiosperms [J]. *BMC Plant Biology*, 2006, 6 (1): 21.
- Bayer PE, Hurgobin B, Golicz AA, et al. Assembly and comparison of two closely related *Brassica napus* genomes [J]. *Plant Biotechnology Journal*, 2017, 15 (12): 1602-1610.
- Bedbrook JR, Bogorad L. Endonuclease recognition sites mapped on *Zea mays* chloroplast DNA [J]. *Proceedings of the National Academy of Sciences*, 1976, 73 (12): 4309-4313.
- Begun DJ, Holloway AK, Stevens K, et al. Population genomics: Whole-genome analysis of polymorphism and divergence in *Drosophila simulans* [J]. *Plos Biology*, 2007, 5 (11): e310.
- Bellaïche Y, Mogila V, Perrimon N. I-SceI endonuclease, a new tool for studying DNA double-strand break repair mechanisms in *Drosophila* [J]. *Genetics*, 1999, 152 (3): 1037-1044.
- Belope T, Gronvold L, Kumar A, et al. Utilization of deletion ins to anchor and order sequences along the wheat 7Bchro- mosome [J]. *Theoretical and Applied Genetics*, 2014, 127 (9): 2029-2040.
- Benke A, Urbany C, Stich B. Genome-wide association mapping of iron homeostasis in the maize association population [J]. *BMC Genetics*, 2015, 16 (1): 1.
- Bennett MD, Leitch IJ, Price HJ, et al. Comparisons with *Caenorhabditis* (approximately 100 Mb) and *Drosophila* (approximately 175 Mb) using flow cytometry show genome size in *Arabidopsis* to be approximately 157 Mb and thus approximately 25% larger than the *Arabidopsis* genome initiative estimate of 125 Mb [J]. *Annals of Botany*, 2003, 91 (5): 547-557.
- Berardini TZ, Mundodi S, Reiser L, et al. Functional annotation of the *Arabidopsis* genome using controlled vocabularies [J]. *Plant Physiology*, 2004, 135 (2): 745.
- Bergthorsson U, Richardson AO, Young GJ, et al. Massive horizontal transfer of mitochondrial genes from diverse land plant donors to the basal angiosperm *Amborella* [J]. *Proceedings of the National Academy of*

- Sciences, 2004, 101 (51): 17747-17752.
- Berlin K, Koren S, Chin CS, et al. Assembling large genomes with single-molecule sequencing and locality-sensitive hashing [J]. *Nature Biotechnology*, 2015, 33 (6): 623-630.
- Berman JJ. Principles of big data: preparing, sharing, and analyzing complex information [M]. Waltham: Newnes, 2013.
- Bernardo R, Charcosset A. Usefulness of gene information in marker-assisted recurrent selection: a simulation appraisal [J]. *Crop Science*, 2006, 46 (2): 614-621.
- Bernardo R, Yu J. Prospects for genomewide selection for quantitative traits in maize [J]. *Crop Science*, 2007, 47 (3): 1082-1090.
- Bertioli DJ, Cannon SB, Froenicke L, et al. The genome sequences of *Arachis duranensis* and *Arachis ipaensis*, the diploid ancestors of cultivated peanut [J]. *Nature Genetics*, 2016, 48 (4): 438-446.
- Bevan MW, Uauy C, Wulff BBH, et al. Genomic innovation for crop improvement [J]. *Nature*, 2017, 543 (7645): 346.
- Bi X, Cheng YJ, Hu B, et al. Nonrandom domain organization of the Arabidopsis genome at the nuclear periphery [J]. *Genome Research*, 2017, 27 (7): 1162-1173.
- Bianconi E, Piovesan A, Facchin F, et al. An estimation of the number of cells in the human body [J]. *Annals of Human Biology*, 2013, 40 (6): 463-471.
- Bibikova M, Beumer K, Trautman JK, et al. Enhancing gene targeting with designed zinc finger nucleases [J]. *Science*, 2003, 300 (5620): 764-764.
- Black IVWC, Baer CF, Antolin MF, et al. Population genomics: genome-wide sampling of insect populations [J]. *Annual Review of Entomology*, 2001, 46 (1): 441-469.
- Blanc G, Agarkova I, Grimwood J, et al. The genome of the polar eukaryotic microalga *Coccomyxa subellipsoidea* reveals traits of cold adaptation [J]. *Genome Biology*, 2012, 13 (5): R39.
- Blanc G, Barakat A, Guyot R, et al. Extensive duplication and reshuffling in the Arabidopsis genome [J]. *The Plant Cell*, 2000, 12 (7): 1093-1101.
- Blanc G, Duncan G, Agarkova I, et al. The *Chlorella variabilis* NC64A genome reveals adaptation to photosymbiosis, coevolution with viruses, and cryptic sex [J]. *The Plant Cell*, 2010, 22 (9): 2943-2955.
- Blanc G, Wolfe K H. Widespread paleopolyploidy in model plant species inferred from age distributions of duplicate genes [J]. *The Plant Cell*, 2004, 16 (7): 1667-1678.
- Blanc-Mathieu R, Verhelst B, Derelle E, et al. An improved genome of the model marine alga *Ostreococcus tauri* unfolds by assessing Illumina *de novo* assemblies [J]. *BMC Genomics*, 2014, 15 (1): 1103.
- Boch J, Scholze H, Schornack S, et al. Breaking the code of DNA binding specificity of TAL-type III effectors [J]. *Science*, 2009, 326 (5959): 1509-1512.
- Boetzer M, Henkel CV, Jansen HJ, et al. Scaffolding pre-assembled contigs using SSPACE [J]. *Bioinformatics*, 2010, 27 (4): 578-579.
- Boetzer M, Pirovano W. SSPACE-LongRead: scaffolding bacterial draft genomes using long read sequence information [J]. *BMC Bioinformatics*, 2014, 15 (1): 211.
- Boetzer M, Pirovano W. Toward almost closed genomes with GapFiller [J]. *Genome Biology*, 2012, 13 (6): R56.
- Bogen C, Al-Dilaimi A, Albersmeier A, et al. Reconstruction of the lipid metabolism for the microalga *Monoraphidium neglectum* from its genome sequence reveals characteristics suitable for biofuel production [J]. *BMC Genomics*, 2013, 14 (1): 926.

- Bombarely A, Moser M, Amrad A, et al. Insight into the evolution of the Solanaceae from the parental genomes of *Petunia hybrida* [J]. *Nature Plants*, 2016, 2 (6): 16074.
- Bonen L. RNA splicing in plant mitochondria [M]//Plant mitochondria. New York: Springer, 2011: 131-155.
- Bonev B, Cavalli G. Organization and function of the 3D genome [J]. *Nature Reviews Genetics*, 2016, 17 (11): 661.
- Bonierbale MW, Plaisted RL, Tanksley SD. RFLP maps based on a common set of clones reveal modes of chromosomal evolution in potato and tomato [J]. *Genetics*, 1988, 120 (4): 1095-1103.
- Bordes A, Ertekin S, Weston J, et al. Fast kernel classifiers with online and active learning [J]. *Journal of Machine Learning Research*, 2005, 6 (Sep): 1579-1619.
- Borges L, Bruneau A, Cardoso D, et al. Towards a new classification system for legumes: progress report from the 6th International Legume Conference [J]. *South African Journal of Botany*, 2013, 89: 3-9.
- Borsani O, Zhu J, Verslues PE, et al. Endogenous siRNAs derived from a pair of natural cis-antisense transcripts regulate salt tolerance in *Arabidopsis* [J]. *Cell*, 2005, 123 (7): 1279-1291.
- Bowers JE, Chapman BA, Rong J, et al. Unraveling angiosperm genome evolution by phylogenetic analysis of chromosomal duplication events [J]. *Nature*, 2003, 422 (6930): 433.
- Bowman JL, Kohchi T, Yamato KT, et al. Insights into land plant evolution garnered from the *Marchantia polymorpha* genome [J]. *Cell*, 2017, 171 (2): 287-304. e15.
- Boynton JE, Gillham NW, Harris EH, et al. Chloroplast transformation in *Chlamydomonas* with high velocity microprojectiles [J]. *Science*, 1988, 240 (4858): 1534-1538.
- Bradbury LMT, Fitzgerald TL, Henry RJ, et al. The gene for fragrance in rice [J]. *Plant Biotechnology Journal*, 2005, 3 (3): 363-370.
- Bradbury PJ, Zhang Z, Kroon DE, et al. TASSEL: software for association mapping of complex traits in diverse samples [J]. *Bioinformatics*, 2007, 23 (19): 2633-2635.
- Brenchley R, Spannagl M, Pfeifer M, et al. Analysis of the bread wheat genome using whole-genome shotgun sequencing [J]. *Nature*, 2012, 491 (7426): 705.
- Briggs JA, Weinreb C, Wagner DE, et al. The dynamics of gene expression in vertebrate embryogenesis at single-cell resolution [J]. *Science*, 2018, 360 (6392): eaar5780.
- Briskine RV, Paape T, Shimizu - Inatsugi R, et al. Genome assembly and annotation of *Arabidopsis halleri*, a model for heavy metal hyperaccumulation and evolutionary ecology [J]. *Molecular Ecology Resources*, 2017, 17 (5): 1025-1036.
- Brown PJ, Upadhyayula N, Mahone GS, et al. Distinct genetic architectures for male and female inflorescence traits of maize [J]. *PLoS Genetics*, 2011, 7 (11): e1002383.
- Brown TA. *Genomes 4* [M]. New York: Garland Science, 2017.
- Browne DR, Jenkins J, Schmutz J, et al. Draft nuclear genome sequence of the liquid hydrocarbon-accumulating green microalga *Botryococcus braunii* race B (Showa) [J]. *Genome Announc.*, 2017, 5 (16): e00215-17.
- Bruneau A, Mercure M, Lewis GP, et al. Phylogenetic patterns and diversification in the caesalpinoid legumes [J]. *Botany*, 2008, 86 (7): 697-718.
- Buckler ES, Holland JB, Bradbury PJ, et al. The genetic architecture of maize flowering time [J]. *Science*, 2009, 325 (5941): 714-718.
- Bukowski R, Guo X, Lu Y, et al. Construction of the third-generation *Zea mays* haplotype map [J]. *Gigascience*, 2017, 7 (4): gix134.

- Burger G, Gray MW, Lang BF. Mitochondrial genomes: anything goes [J]. Trends in Genetics, 2003, 19 (12): 709-716.
- Burn JE, Bagnall DJ, Metzger JD, et al. DNA methylation, vernalization, and the initiation of flowering [J]. Proceedings of the National Academy of Sciences, 1993, 90 (1): 287-291.
- Burns JA, Paasch A, Narechania A, et al. Comparative genomics of a bacterivorous green alga reveals evolutionary causalities and consequences of phago-mixotrophic mode of nutrition [J]. Genome Biology and Evolution, 2015, 7 (11): 3047-3061.
- Burton JN, Adey A, Patwardhan RP, et al. Chromosome-scale scaffolding of *de novo* genome assemblies based on chromatin interactions [J]. Nature Biotechnology, 2013, 31 (12): 1119.
- Busoms S, Paaanen P, Marburger S, et al. Fluctuating selection on migrant adaptive sodium transporter alleles in coastal *Arabidopsis thaliana* [J]. Proceedings of the National Academy of Sciences, 2018, 115 (52): E12443-E12452.
- Buti M, Moretto M, Barghini E, et al. The genome sequence and transcriptome of *Potentilla micrantha* and their comparison to *Fragaria vesca* (the woodland strawberry) [J]. Gigascience, 2018, 7 (4): 1.
- Byrne SL, Nagy I, Pfeifer M, et al. A synteny - based draft genome sequence of the forage grass *Lolium perenne* [J]. The Plant Journal, 2015, 84 (4): 11.
- Cai C, Wang X, Liu B, et al. *Brassica rapa* genome 2.0: a reference upgrade through sequence re-assembly and gene re-annotation [J]. Molecular Plant, 2017, 10 (4): 649-651.
- Cai J, Liu X, Vanneste K, et al. The genome sequence of the orchid *Phalaenopsis equestris* [J]. Nature Genetics, 2015, 47 (2): 65-72.
- Caicedo AL, Williamson SH, Hernandez RD, et al. Genome-wide patterns of nucleotide polymorphism in domesticated rice [J]. PLoS Genetics, 2007, 3 (9): e163.
- Calus MPL, Veerkamp RF. Accuracy of breeding values when using and ignoring the polygenic effect in genomic breeding value estimation with a marker density of one SNP per cM [J]. Journal of Animal Breeding and Genetics, 2007, 124 (6): 362-368.
- Cao J, Schneeberger K, Ossowski S, et al. Whole-genome sequencing of multiple *Arabidopsis thaliana* populations [J]. Nature Genetics, 2011, 43 (10): 956.
- Cao K, Zheng Z, Wang L, et al. Comparative population genomics reveals the domestication history of the peach, *Prunus persica*, and human influences on perennial fruit crops [J]. Genome Biology, 2014, 15 (7): 415.
- Capecchi MR. The new mouse genetics: altering the genome by gene targeting [J]. Trends in Genetics, 1989, 5: 70-76.
- Carlsson J, Glimelius K. Cytoplasmic male-sterility and nuclear encoded fertility restoration [M]. Plant Mitochondria. New York: Springer, 2011: 469-491.
- Carreres BM, de Jaeger L, Springer J, et al. Draft genome sequence of the oleaginous green alga *Tetradasmus obliquus* UTEX 393 [J]. Genome Announc. , 2017, 5 (3): e01449-16.
- Casillas S, Barbadilla A. Molecular population genetics [J]. Genetics, 2017, 205 (3): 1003-1035.
- Cerda S, Weitzman SA. Influence of oxygen radical injury on DNA methylation [J]. Mutation Research/Reviews in Mutation Research, 1997, 386 (2): 141-152.
- Chalhoub B, Denoeud F, Liu S, et al. Early allopolyploid evolution in the post-Neolithic *Brassica napus* oilseed genome [J]. Science, 2014, 345 (6199): 950-953.
- Chandler VL, Brendel V. The maize genome sequencing project [J]. Plant Physiology, 2002, 130 (4): 1594-1597.

- Chang S, Wang Y, Lu J, et al. The mitochondrial genome of soybean reveals complex genome structures and gene evolution at intercellular and phylogenetic levels [J]. *PLoS One*, 2013, 8 (2): e56502.
- Chao S, Zhang W, Dubcovsky J, et al. Evaluation of genetic diversity and genome-wide linkage disequilibrium among US wheat (*Triticum aestivum* L.) germplasm representing different market classes [J]. *Crop Science*, 2007, 47 (3): 1018-1030.
- Chapman J, Mascher M, Bulu A, et al. A whole-genome shotgun approach for assembling and anchoring the hexaploid bread wheat genome [J]. *Genome Biology*, 2015, 16: 26.
- Chaw SM, Chun-Chieh Shih A, Wang D, et al. The mitochondrial genome of the gymnosperm *Cycas taitungensis* contains a novel family of short interspersed elements, Bpu sequences, and abundant RNA editing sites [J]. *Molecular Biology and Evolution*, 2008, 25 (3): 603-615.
- Che R, Tong H, Shi B, et al. Control of grain size and rice yield by GL2-mediated brassinosteroid responses [J]. *Nature Plants*, 2016, 2 (1): 15195.
- Chekanova JA, Gregory BD, Reverdatto SV, et al. Genome-wide high-resolution mapping of exosome substrates reveals hidden features in the Arabidopsis transcriptome [J]. *Cell*, 2007, 131 (7): 1340-1353.
- Chekanova JA. Long non-coding RNAs and their functions in plants [J]. *Current Opinion in Plant Biology*, 2015, 27: 207-216.
- Chen C, Begcy K, Liu K, et al. Heat stress yields a unique MADS box transcription factor in determining seed size and thermal sensitivity [J]. *Plant Physiology*, 2016a, 171 (1): 606-622.
- Chen C, Xing D, Tan L, et al. Single-cell whole-genome analyses by Linear Amplification via Transposon Insertion (LIANTI) [J]. *Science*, 2017a, 356 (6334): 189-194.
- Chen D, Neumann K, Friedel S, et al. Dissecting the phenotypic components of crop plant growth and drought responses based on high-throughput image analysis [J]. *The Plant Cell*, 2014a, 26 (12): 4636-4655.
- Chen G, Wang X, Hao J, et al. Genome-wide association implicates candidate genes conferring resistance to maize rough dwarf disease in maize [J]. *PloS One*, 2015, 10 (11): e0142001.
- Chen J, Huang Q, Gao D, et al. Whole-genome sequencing of *Oryza brachyantha* reveals mechanisms underlying *Oryza* genome evolution [J]. *Nature Communications*, 2013a, 4: 1595.
- Chen J, Shrestha R, Ding J, et al. Genome-wide association study and QTL mapping reveal genomic loci associated with Fusarium ear rot resistance in tropical maize germplasm [J]. *G3: Genes, Genomes, Genetics*, 2016b, 6 (12): 3803-3815.
- Chen L, Yu Y, Zhang X, et al. PcircRNA_finder: a software for circRNA prediction in plants [J]. *Bioinformatics*, 2016c, 32 (22): 3528-3529.
- Chen L, Zhang P, Fan Y, et al. Circular RNAs mediated by transposons are associated with transcriptomic and phenotypic variation in maize [J]. *New Phytologist*, 2018, 217 (3): 1292-1306.
- Chen S, Yang Y, Shi W, et al. Badh2, encoding betaine aldehyde dehydrogenase, inhibits the biosynthesis of 2-acetyl-1-pyrroline, a major component in rice fragrance [J]. *The Plant Cell*, 2008, 20 (7): 1850-1861.
- Chen W, Gao Y, Xie W, et al. Genome-wide association analyses provide genetic and biochemical insights into natural variation in rice metabolism. [J]. *Science Foundation in China*, 2014b, 46 (2): 714-721.
- Chen X, Sun S, Liu F, et al. A transcriptomic profile of topping responsive non-coding RNAs in tobacco roots (*Nicotiana tabacum*). *BMC Genomics*, 2019 20: 856.
- Chen ZJ. Genomic and epigenetic insights into the molecular bases of heterosis [J]. *Nature Reviews Genetics*, 2013b, 14 (7): 471.

- Chen ZJ. Molecular mechanisms of polyploidy and hybrid vigor [J]. *Trends in Plant Science*, 2010, 15 (2): 57-71.
- Chen Z, Zhao N, Li S, et al. Plant mitochondrial genome evolution and cytoplasmic male sterility [J]. *Critical Reviews in Plant Sciences*, 2017, 36 (1): 55-69.
- Cheng F, Liang J, Cai C, et al. Genome sequencing supports a multi-vertex model for Brassiceae species [J]. *Current Opinion in Plant Biology*, 2017b, 36: 79-87.
- Cheng F, Mandáková T, Wu J, et al. Deciphering the diploid ancestral genome of the mesohexaploid *Brassica rapa* [J]. *The Plant Cell*, 2013, 25 (5): 1541-1554.
- Cheng F, Sun R, Hou X, et al. Subgenome parallel selection is associated with morphotype diversification and convergent crop domestication in *Brassica rapa* and *Brassica oleracea* [J]. *Nature Genetics*, 2016, 48 (10): 1218.
- Cheng F, Wu J, Fang L, et al. Biased gene fractionation and dominant gene expression among the subgenomes of *Brassica rapa* [J]. *PloS One*, 2012, 7 (5): e36442.
- Cheng S, Bergh EVD, Zeng P, et al. The *Tarenaya hassleriana* genome provides insight into reproductive trait and genome evolution of crucifers [J]. *Plant Cell*, 2013, 25 (8): 2813-2830.
- Cheng S, Yi X, Cheng J, et al. Genetic analysis of Fusarium head blight resistance in CIMMYT bread wheat line C615 using traditional and conditional QTL mapping [J]. *Frontiers in Plant Science*, 2018, 9: 573.
- Chi KR. Singled out for sequencing [J]. *Nature Methods*, 2014, 11 (1): 13-17.
- Chia JM, Song C, Bradbury PJ, et al. Maize HapMap2 identifies extant variation from a genome in flux [J]. *Nature Genetics*, 2012, 44 (7): 803.
- Chin CS, Peluso P, Sedlazeck FJ, et al. Phased diploid genome assembly with single-molecule real-time sequencing [J]. *Nature Methods*, 2016, 13 (12): 1050.
- Ching ADA, Caldwell KS, Jung M, et al. SNP frequency, haplotype structure and linkage disequilibrium in elite maize inbred lines [J]. *BMC Genetics*, 2002, 3 (1): 19.
- Chodavarapu RK, Feng S, Ding B, et al. Transcriptome and methylome interactions in rice hybrids [J]. *Proceedings of the National Academy of Sciences*, 2012, 109 (30): 12040-12045.
- Chor B, Horn D, Goldman N, et al. Genomic DNA k-mer spectra: models and modalities [J]. *Genome Biology*, 2009, 10 (10): R108.
- Choulet F, Alberti A, Theil S, et al. Structural and functional partitioning of bread wheat chromosome 3B [J]. *Science*, 2014, 345 (6194): 1249721.
- Christin PA, Edwards EJ, Besnard G, et al. Adaptive evolution of C4 photosynthesis through recurrent lateral gene transfer [J]. *Current Biology*, 2012, 22 (5): 445-449.
- Chu Q, Shen E, Ye CY, et al. Emerging roles of plant circular RNAs [J]. *Journal of Plant Cell Development*, 2018, 1 (1): 1.
- Chu Q, Zhang X, Zhu X, et al. PlantcircBase: a database for plant circular RNAs [J]. *Molecular Plant*, 2017, 10 (8): 1126-1128.
- Chu QJ, Bai PP, Zhu XT, et al. Characteristics of plant circular RNAs [J]. *Briefings in Bioinformatics*, 2018, bby111.
- Chuang CF, Meyerowitz EM. Specific and heritable genetic interference by double-stranded RNA in *Arabidopsis thaliana* [J]. *Proceedings of the National Academy of Sciences*, 2000, 97 (9): 4985-4990.
- Chung WH, Jeong N, Kim J, et al. Population structure and domestication revealed by high-depth resequencing of Korean cultivated and wild soybean genomes [J]. *DNA Research*, 2014, 21 (2): 153-167.

- Clark RM, Schweikert G, Toomajian C, et al. Common sequence polymorphisms shaping genetic diversity in *Arabidopsis thaliana* [J]. *Science*, 2007, 317 (5836): 338-342.
- Clark RT, MacCurdy RB, Jung JK, et al. Three-dimensional root phenotyping with a novel imaging and software platform [J]. *Plant Physiology*, 2011, 156 (2): 455-465.
- Clavijo BJ, Venturini L, Schudoma C, et al. An improved assembly and annotation of the allohexaploid wheat genome identifies complete families of agronomic genes and provides genomic evidence for chromosomal translocations [J]. *Genome Research*, 2017, 27 (5): 885-896.
- Clegg MT, Gaut BS, Learn GH, et al. Rates and patterns of chloroplast DNA evolution [J]. *Proceedings of the National Academy of Sciences*, 1994, 91 (15): 6795-6801.
- Clifton SW, Minx P, Fauron CMR, et al. Sequence and comparative analysis of the maize NB mitochondrial genome [J]. *Plant Physiology*, 2004, 136 (3): 3486-3503.
- Coart E, van Glabeke S, De Loose M, et al. Chloroplast diversity in the genus *Malus*: new insights into the relationship between the European wild apple (*Malus sylvestris* (L.) Mill.) and the domesticated apple (*Malus domestica* Borkh.) [J]. *Molecular Ecology*, 2006, 15 (8): 2171-2182.
- Cohen SP, Liu H, Argueso CT, et al. RNA-Seq analysis reveals insight into enhanced rice Xa7-mediated bacterial blight resistance at high temperature [J]. *PloS One*, 2017, 12 (11): e0187625.
- Colbert T, Till BJ, Tompa R, et al. High-throughput screening for induced point mutations [J]. *Plant Physiology*, 2001, 126 (2): 480-484.
- Collins F. Has the revolution arrived? [J]. *Nature*, 2010, 464 (7289): 674.
- Cong L, Ran FA, Cox D, et al. Multiplex genome engineering using CRISPR/Cas systems [J]. *Science*, 2013, 339 (6121): 819-823.
- Conn VM, Hugouvieux V, Nayak A, et al. A circRNA from SEPALLATA3 regulates splicing of its cognate mRNA through R-loop formation [J]. *Nature Plants*, 2017, 3 (5): 17053.
- Cook JP, McMullen MD, Holland JB, et al. Genetic architecture of maize kernel composition in the nested association mapping and inbred association panels [J]. *Plant Physiology*, 2012, 158 (2): 824-834.
- Copetti D, Búrquez A, Bustamante E, et al. Extensive gene tree discordance and hemiplasy shaped the genomes of North American columnar cacti [J]. *Proceedings of the National Academy of Sciences*, 2017, 114 (45): 12003-12008.
- Cornille A, Gladieux P, Smulders MJM, et al. New insight into the history of domesticated apple: secondary contribution of the European wild apple to the genome of cultivated varieties [J]. *Plos Genetics*, 2012, 8 (5): e1002703.
- Cortijo S, Wardenaar R, Colomé-Tatché M, et al. Mapping the epigenetic basis of complex traits [J]. *Science*, 2014, 343 (6175): 1145-1148.
- Cosner ME, Raubeson LA, Jansen RK. Chloroplast DNA rearrangements in Campanulaceae: phylogenetic utility of highly rearranged genomes [J]. *BMC Evolutionary Biology*, 2004, 4 (1): 27.
- Covshoff S, Szecowka M, Hughes TE, et al. C4 photosynthesis in the rice paddy: insights from the noxious weed *Echinochloa glabrescens* [J]. *Plant Physiology*, 2016, 170 (1): 57-73.
- Cronn R, Liston A, Parks M, et al. Multiplex sequencing of plant chloroplast genomes using Solexa sequencing-by-synthesis technology [J]. *Nucleic Acids Research*, 2008, 36 (19): e122.
- Cronn RC, Small RL, Haselkorn T, et al. Rapid diversification of the cotton genus (*Gossypium*: *Malvaceae*) revealed by analysis of sixteen nuclear and chloroplast genes [J]. *American Journal of Botany*, 2002, 89 (4): 579-590.

707-725.

- Crossa J, Pérez-Rodríguez P, Cuevas J, et al. Genomic selection in plant breeding: methods, models, and perspectives [J]. *Trends in Plant Science*, 2017, 22 (11): 961-975.
- Crouse HV. The controlling element in sex chromosome behavior in *Sciara* [J]. *Genetics*, 1960, 45 (10): 1429.
- Cruz F, Julca I, Gómez-Garrido J, et al. Genome sequence of the olive tree, *Olea europaea* [J]. *Gigascience*, 2016, 5 (1): 29.
- Cubry P, Tranchant-Dubreuil C, Thuillet AC, et al. The rise and fall of African rice cultivation revealed by analysis of 246 new genomes [J]. *Current Biology*, 2018, 28 (14): 2274-2282. e6.
- Cui P, Liu H, Lin Q, et al. A complete mitochondrial genome of wheat (*Triticum aestivum* cv. *Chinese Yumai*), and fast evolving mitochondrial genes in higher plants [J]. *Journal of Genetics*, 2009, 88 (3): 299-307.
- Cui Y, Song BK, Li LF, et al. Little white lies: pericarp color provides insights into the origins and evolution of Southeast Asian weedy rice [J]. *G3: Genes, Genomes, Genetics*, 2016a, 6 (12): 4105-4114.
- Cui Z, Luo J, Qi C, et al. Genome-wide association study (GWAS) reveals the genetic architecture of four husk traits in maize [J]. *BMC Genomics*, 2016b, 17 (1): 946.
- Cupp JD, Nielsen BL. Minireview: DNA replication in plant mitochondria [J]. *Mitochondrion*, 2014, 19: 231-237.
- D'hont A, Denoeud F, Aury JM, et al. The banana (*Musa acuminata*) genome and the evolution of monocotyledonous plants [J]. *Nature*, 2012, 488 (7410): 213-217.
- Daccord N, Celton JM, Linsmith G, et al. High-quality de novo assembly of the apple genome and methylome dynamics of early fruit development [J]. *Nature Genetics*, 2017, 49 (7): 1099.
- Dai L, Wu L, Dong Q, et al. Genome-wide association study of field grain drying rate after physiological maturity based on a resequencing approach in elite maize germplasm [J]. *Euphytica*, 2017, 213 (8): 182.
- Dai X, Hu Q, Cai Q, et al. The willow genome and divergent evolution from poplar after the common genome duplication [J]. *Cell Research*, 2014, 24 (10): 1274-1277.
- Daniell H, Lin CS, Yu M, et al. Chloroplast genomes: diversity, evolution, and applications in genetic engineering [J]. *Genome Biology*, 2016, 17 (1): 134.
- Davies JOJ, Oudelaar AM, Higgs DR, et al. How best to identify chromosomal interactions: a comparison of approaches [J]. *Nature Methods*, 2017, 14 (2): 125.
- de Felippes FF, Marchais A, Sarazin A, et al. A single miR390 targeting event is sufficient for triggering TAS3-tasiRNA biogenesis in *Arabidopsis* [J]. *Nucleic Acids Research*, 2017, 45 (9): 5539-5554.
- de Vega JJ, Ayling S, Hegarty M, et al. Red clover (*Trifolium pratense* L.) draft genome provides a platform for trait improvement [J]. *Scientific Reports*, 2015, 5 (1): 17394.
- de Chiara TM, Robertson EJ, Efstratiadis A. Parental imprinting of the mouse insulin-like growth factor II gene [J]. *Cell*, 1991, 64 (4): 849-859.
- Dekker J, Rippe K, Dekker M, et al. Capturing chromosome conformation [J]. *Science*, 2002, 295 (5558): 1306-1311.
- Dell'Acqua M, Gatti DM, Pea G, et al. Genetic properties of the MAGIC maize population: a new platform for high definition QTL mapping in *Zea mays* [J]. *Genome Biology*, 2015, 16 (1): 167.
- Deng S, Wu X, Wu Y, et al. Characterization and precise mapping of a QTL increasing spike number with pleiotropic effects in wheat [J]. *Theoretical and Applied Genetics*, 2011, 122 (2): 281-289.
- Deng X, Song X, Wei L, et al. Epigenetic regulation and epigenomic landscape in rice [J]. *National Science Review*, 2016, 3 (3): 309-327.

- Denoeud F, Carreteropaulet L, Dereeper A, et al. The coffee genome provides insight into the convergent evolution of caffeine biosynthesis [J]. *Science*, 2014, 345 (6201): 1181-1184.
- Derelle E, Ferraz C, Rombauts S, et al. Genome analysis of the smallest free-living eukaryote *Ostreococcus tauri* unveils many unique features [J]. *Proceedings of the National Academy of Sciences*, 2006, 103 (31): 11647-11652.
- Deschamps S, Zhang Y, Llaca V, et al. A chromosome-scale assembly of the sorghum genome using nanopore sequencing and optical mapping [J]. *Nature Communications*, 2018, 9 (1): 4844.
- Dhaubhadel S, Gijzen M, Moy P, et al. Transcriptome analysis reveals a critical role of CHS7 and CHS8 genes for isoflavonoid synthesis in soybean seeds [J]. *Plant Physiology*, 2007, 143 (1): 326.
- Diao X, Freeling M, Lisch D. Horizontal transfer of a plant transposon [J]. *PLoS Biology*, 2005, 4 (1): e5.
- Dierckxsens N, Mardulyn P, Smits G. NOVOPlasty: *de novo* assembly of organelle genomes from whole genome data [J]. *Nucleic Acids Research*, 2016, 45 (4): e18.
- Ding J, Ali F, Chen G, et al. Genome-wide association mapping reveals novel sources of resistance to northern corn leaf blight in maize [J]. *BMC Plant Biology*, 2015, 15 (1): 206.
- Ding Z, Wang C, Chen S, et al. Diversity and selective sweep in the OsAMT1;1 genomic region of rice [J]. *BMC Evolutionary Biology*, 2011, 11 (1): 61.
- Dohm JC, Minoche AE, Holtgräwe D, et al. The genome of the recently domesticated crop plant sugar beet (*Beta vulgaris*) [J]. *Nature*, 2014, 505 (7484): 546.
- Dolezel J, Bartos J, Voglmayr H, et al. Nuclear DNA content and genome size of trout and human [J]. *Cytometry. Part A: the journal of the International Society for Analytical Cytology*, 2003, 51 (2): 127-128; author reply 129.
- Doležel J, Greilhuber J, Suda J. Estimation of nuclear DNA content in plants using flow cytometry [J]. *Nature Protocols*, 2007, 2 (9): 2233.
- Dong AX, Xin HB, Li ZJ, et al. High quality assembly of the reference genome for scarlet sage, *Salvia splendens*, an economically important ornamental plant. [J]. *Gigascience*, 2018a, 7 (7).
- Dong P, Tu X, Chu PY, et al. 3D chromatin architecture of large plant genomes determined by local A/B compartments [J]. *Molecular Plant*, 2017, 10 (12): 1497-1509.
- Dong X, Chen J, Li T, et al. Parent-of-origin-dependent nucleosome organization correlates with genomic imprinting in maize [J]. *Genome Research*, 2018b, 28 (7): 1020-1028.
- Dong Y, Yang X, Liu J, et al. Pod shattering resistance associated with domestication is mediated by a NAC gene in soybean [J]. *Nature Communications*, 2014, 5: 3352.
- Dostie J, Richmond TA, Arnaout RA, et al. Chromosome Conformation Capture Carbon Copy (5C): a massively parallel solution for mapping interactions between genomic elements [J]. *Genome Research*, 2006, 16 (10): 1299-1309.
- Doyle EL, Booher NJ, Standage DS, et al. TAL Effector-Nucleotide Targeter (TALE-NT) 2.0: tools for TAL effector design and target prediction [J]. *Nucleic Acids Research*, 2012, 40 (W1): W117-W122.
- Drouin G, Daoud H, Xia J. Relative rates of synonymous substitutions in the mitochondrial, chloroplast and nuclear genomes of seed plants [J]. *Molecular Phylogenetics and Evolution*, 2008, 49 (3): 827-831.
- Du H, Yu Y, Ma Y, et al. Sequencing and de novo assembly of a near complete indica rice genome [J]. *Nature Communications*, 2017, 8: 15324.
- Du X, Huang G, He S, et al. Resequencing of 243 diploid cotton accessions based on an updated A genome

- identifies the genetic basis of key agronomic traits [J]. *Nature Genetics*, 2018, 50 (6): 796.
- Duan N, Bai Y, Sun H, et al. Genome re-sequencing reveals the history of apple and supports a two-stage model for fruit enlargement [J]. *Nature Communications*, 2017, 8 (1): 249.
- Duan P, Ni S, Wang J, et al. Regulation of OsGRF4 by OsmiR396 controls grain size and yield in rice [J]. *Nature Plants*, 2016, 2 (1): 15203.
- Duan Z, Andronescu M, Schutz K, et al. A three-dimensional model of the yeast genome [J]. *Nature*, 2010, 465 (7296): 363.
- Dudchenko O, Batra SS, Omer AD, et al. De novo assembly of the *Aedes aegypti* genome using Hi-C yields chromosome-length scaffolds [J]. *Science*, 2017, 356 (6333): 92-95.
- Dufay M, Touzet P, Maurice S, et al. Modelling the maintenance of male-fertile cytoplasm in a gynodioecious population [J]. *Heredity*, 2007, 99 (3): 349.
- Dufourmantel N, Dubald M, Matringe M, et al. Generation and characterization of soybean and marker - free tobacco plastid transformants over - expressing a bacterial 4 - hydroxyphenylpyruvate dioxygenase which provides strong herbicide tolerance [J]. *Plant Biotechnology Journal*, 2007, 5 (1): 118-133.
- Dunn JJ, Studier FW, Gottesman M. Complete nucleotide sequence of bacteriophage T7 DNA and the locations of T7 genetic elements [J]. *Journal of Molecular Biology*, 1983, 166 (4): 477-535.
- Durai S, Mani M, Kandavelou K, et al. Zinc finger nucleases: custom-designed molecular scissors for genome engineering of plant and mammalian cells [J]. *Nucleic Acids Research*, 2005, 33 (18): 5978-5990.
- Durvasula A, Fulgione A, Gutaker RM, et al. African genomes illuminate the early history and transition to selfing in *Arabidopsis thaliana* [J]. *Proceedings of the National Academy of Sciences*, 2017, 114 (20): 5213-5218.
- Efroni I, Mello A, Nawy T, et al. Root regeneration triggers an embryo-like sequence guided by hormonal interactions [J]. *Cell*, 2016, 165 (7): 1721-1733.
- Eichten SR, Briskine R, Song J, et al. Epigenetic and genetic influences on DNA methylation variation in maize populations [J]. *The Plant Cell*, 2013, 25 (8): 2783-2797.
- Eklblom R, Wolf JBW. A field guide to whole - genome sequencing, assembly and annotation [J]. *Evolutionary Applications*, 2014, 7 (9): 1026-1042.
- El Baidouri M, Kim KD, Abernathy B, et al. Genic C-Methylation in soybean Is associated with gene paralogs relocated to transposable element-rich pericentromeres [J]. *Molecular Plant*, 2018, 11 (3): 485-495.
- Elowitz MB, Leibler S. A synthetic oscillatory network of transcriptional regulators [J]. *Nature*, 2000, 403 (6767): 335.
- English AC, Richards S, Han Y, et al. Mind the gap: upgrading genomes with Pacific Biosciences RS long-read sequencing technology [J]. *PloS One*, 2012, 7 (11): e47768.
- Evans LM, Slavov GT, Rodgersmelnick E, et al. Population genomics of *Populus trichocarpa* identifies signatures of selection and adaptive trait associations [J]. *Nature Genetics*, 2014, 46 (10): 1089-1096.
- Fabre J, Dauzat M, Nègre V, et al. PHENOPSIS DB: an information system for *Arabidopsis thaliana* phenotypic data in an environmental context [J]. *BMC Plant Biology*, 2011, 11 (1): 77.
- Fan J, Bai P, Ning Y, et al. The monocot-specific receptor-like kinase SDS2 controls cell death and immunity in rice [J]. *Cell Host & Microbe*, 2018, 23 (4): 498-510. e5.
- Fan J, Ning K, Zeng X, et al. Genomic foundation of starch-to-lipid switch in oleaginous *Chlorella* spp [J]. *Plant Physiology*, 2015, 169 (4): 2444-2461.
- Fan Y, Yang J, Mathioni SM, et al. PMS1T, producing phased small-interfering RNAs, regulates photoperiod-

- sensitive male sterility in rice [J]. *Proceedings of the National Academy of Sciences*, 2016, 113 (52): 15144-15149.
- Fang C , Li W , Li G , et al. Cloning of Ln gene through combined approach of map-based cloning and association study in soybean [J]. *Journal of Genetics and Genomics*, 2013, 40 (2): 93-96.
- Fang C, Ma Y, Wu S, et al. Genome-wide association studies dissect the genetic networks underlying agronomical traits in soybean [J]. *Genome Biology*, 2017a, 18 (1): 161.
- Fang H, Huangfu L, Chen R, et al. Ancestor of land plants acquired the DNA-3-methyladenine glycosylase (MAG) gene from bacteria through horizontal gene transfer [J]. *Scientific Reports*, 2017b, 7 (1): 9324.
- Fang L, Gong H, Hu Y, et al. Genomic insights into divergence and dual domestication of cultivated allotetraploid cottons [J]. *Genome Biology*, 2017c, 18 (1): 33.
- Fang L, Guan X, Zhang T. Asymmetric evolution and domestication in allotetraploid cotton (*Gossypium hirsutum* L.) [J]. *The Crop Journal*, 2017d, 5 (2): 159-165.
- Fang L, Wang Q, Hu Y, et al. Genomic analyses in cotton identify signatures of selection and loci associated with fiber quality and yield traits [J]. *Nature Genetics*, 2017e, 49 (7): 1089.
- Farfan IDB, Gerald N, Murray SC, et al. Genome wide association study for drought, aflatoxin resistance, and important agronomic traits of maize hybrids in the sub-tropics [J]. *PLoS One*, 2015, 10 (2): e0117737.
- Farrell JA, Wang Y, Riesenfeld SJ, et al. Single-cell reconstruction of developmental trajectories during zebrafish embryogenesis [J]. *Science*, 2018, 360 (6392): eaar3131.
- Fatokun C, Girma G, Abberton M, et al. Genetic diversity and population structure of a mini-core subset from the world cowpea (*Vigna unguiculata* (L.) Walp.) germplasm collection [J]. *Scientific Reports*, 2018, 8 (1): 16035.
- Featherston J, Arakaki Y, Hanschen ER, et al. The 4-celled *Tetrabaena socialis* nuclear genome reveals the essential components for genetic control of cell number at the origin of multicellularity in the volvocine lineage [J]. *Molecular Biology and Evolution*, 2017, 35 (4): 855-870.
- Fei Q, Xia R, Meyers BC. Phased, secondary, small interfering RNAs in posttranscriptional regulatory networks [J]. *The Plant Cell*, 2013, 25 (7): 2400-2415.
- Feng Q, Zhang Y, Hao P, et al. Sequence and analysis of rice chromosome 4 [J]. *Nature*, 2002, 420 (6913): 316.
- Feng S, Cokus SJ, Zhang X, et al. Conservation and divergence of methylation patterning in plants and animals [J]. *Proceedings of the National Academy of Sciences*, 2010, 107 (19): 8689-8694.
- Feng Z, Zhang B, Ding W, et al. Efficient genome editing in plants using a CRISPR/Cas system [J]. *Cell Research*, 2013, 23 (10): 1229.
- Ferguson-Smith AC. Genomic imprinting: the emergence of an epigenetic paradigm [J]. *Nature Reviews Genetics*, 2011, 12 (8): 565.
- Filichkin SA, Priest HD, Givan SA, et al. Genome-wide mapping of alternative splicing in *Arabidopsis thaliana* [J]. *Genome Research*, 2010, 20 (1): 45-58.
- Fiorani F, Schurr U. Future scenarios for plant phenotyping [J]. *Annual Review of Plant Biology*, 2013, 64: 267-291.
- Fleischmann RD, Adams MD, White O, et al. Whole-genome random sequencing and assembly of

- Haemophilus influenzae Rd [J]. *Science*, 1995, 269 (5223): 496-512.
- Fletcher RS, Mullen JL, Heiliger A, et al. QTL analysis of root morphology, flowering time, and yield reveals trade-offs in response to drought in *Brassica napus* [J]. *Journal of Experimental Botany*, 2015, 66 (1): 245-256.
- Flint-Garcia SA. Genetics and consequences of crop domestication [J]. *Journal of Agricultural and Food Chemistry*, 2013, 61 (35): 8267-8276.
- Foflonker F, Price DC, Qiu H, et al. Genome of the halotolerant green alga *Picochlorum* sp. reveals strategies for thriving under fluctuating environmental conditions [J]. *Environmental Microbiology*, 2015, 17 (2): 412-426.
- Forcato M, Nicoletti C, Pal K, et al. Comparison of computational methods for Hi-C data analysis [J]. *Nature Methods*, 2017, 14 (7): 679.
- Fournier-Level A, Korte A, Cooper MD, et al. A map of local adaptation in *Arabidopsis thaliana* [J]. *Science*, 2011, 334 (6052): 86-89.
- Franco-Zorrilla JM, Valli A, Todesco M, et al. Target mimicry provides a new mechanism for regulation of microRNA activity [J]. *Nature Genetics*, 2007, 39 (8): 1033.
- Fransz P, de Jong H. From nucleosome to chromosome: a dynamic organization of genetic information [J]. *The Plant Journal*, 2011, 66 (1): 4-17.
- Frerigmann H, Gigolashvili T. MYB34, MYB51, and MYB122 distinctly regulate indolic glucosinolate biosynthesis in *Arabidopsis thaliana* [J]. *Molecular Plant*, 2014, 7 (5): 814-828.
- Fricke W, Pritchard J, Leigh RA, et al. Cells of the upper and lower epidermis of barley (*Hordeum vulgare* L.) leaves exhibit distinct patterns of vacuolar solutes [J]. *Plant Physiology*, 1994, 104 (4): 1201-1208.
- Fu J, Cheng Y, Linghu J, et al. RNA sequencing reveals the complex regulatory network in the maize kernel [J]. *Nature Communications*, 2013a, 4: 2832.
- Fu Y, Foden JA, Khayter C, et al. High-frequency off-target mutagenesis induced by CRISPR-Cas nucleases in human cells [J]. *Nature Biotechnology*, 2013b, 31 (9): 822.
- Fu Y, Li L, Hao S, et al. Draft genome sequence of the Tibetan medicinal herb *Rhodiola crenulata* [J]. *Gigascience*, 2017, 6 (6): 1-5.
- Fuentes P, Zhou F, Erban A, et al. A new synthetic biology approach allows transfer of an entire metabolic pathway from a medicinal plant to a biomass crop [J]. *Elife*, 2016, 5: e13664.
- Furbank RT, Tester M. Phenomics-technologies to relieve the phenotyping bottleneck [J]. *Trends in Plant Science*, 2011, 16 (12): 635-644.
- Galanie S, Thodey K, Trenchard IJ, et al. Complete biosynthesis of opioids in yeast [J]. *Science*, 2015, 349 (6252): 1095-1100.
- Gale MD, Devos KM. Comparative genetics in the grasses [J]. *Proceedings of the National Academy of Sciences*, 1998, 95 (5): 1971-1974.
- Gallusci P, Dai Z, Génard M, et al. Epigenetics for plant improvement: current knowledge and modeling avenues [J]. *Trends in Plant Science*, 2017, 22 (7): 610-623.
- Gan X, Hay A, Kwantes M, et al. The Cardamine hirsuta genome offers insight into the evolution of morphological diversity [J]. *Nature Plants*, 2016, 2 (11): 16167.

- Gan X, Stegle O, Behr J, et al. Multiple reference genomes and transcriptomes for *Arabidopsis thaliana* [J]. Nature, 2011, 477 (7365): 419.
- Gao C, Wang Y, Shen Y, et al. Oil accumulation mechanisms of the oleaginous microalga *Chlorella protothecoides* revealed through its genome, transcriptomes, and proteomes [J]. BMC Genomics, 2014a, 15 (1): 582.
- Gao F, Wang K, Liu Y, et al. Blocking miR396 increases rice yield by shaping inflorescence architecture [J]. Nature Plants, 2016, 2 (1): 15196.
- Gao F, Wang X, Li X, et al. Long-read sequencing and *de novo* genome assembly of *Ammopiptanthus nanus*, a desert shrub [J]. Gigascience, 2018a, 7 (7): giy074.
- Gao S, Fang J, Xu F, et al. CYTOKININ OXIDASE/DEHYDROGENASE4 integrates cytokinin and auxin signaling to control rice crown root formation [J]. Plant Physiology, 2014b, 165 (3): 1035-1046.
- Gao Y, Wang H, Liu C, et al. *De novo* genome assembly of the red silk cotton tree (*Bombax ceiba*). [J]. Gigascience, 2018b, 7 (5): giy051.
- Gao ZY, Zhao SC, He WM, et al. Dissecting yield-associated loci in super hybrid rice by resequencing recombinant inbred lines and improving parental genome sequences [J]. Proceedings of the National Academy of Sciences, 2013, 110 (35): 14492-14497.
- Garcia-Mas J, Benjak A, Sanseverino W, et al. The genome of melon (*Cucumis melo* L.) [J]. Proceedings of the National Academy of Sciences, 2012, 109 (29): 11872-11877.
- Gardner TS, Cantor CR, Collins JJ. Construction of a genetic toggle switch in *Escherichia coli* [J]. Nature, 2000, 403 (6767): 339.
- Garris AJ, Tai TH, Coburn J, et al. Genetic structure and diversity in *Oryza sativa* L [J]. Genetics, 2005, 169 (3): 1631-1638.
- Garsmeur O, Schnable JC, Almeida A, et al. Two evolutionarily distinct classes of paleopolyploidy [J]. Molecular Biology and Evolution, 2014, 31 (2): 448-454.
- Garvin T, Aboukhalil R, Kendall J, et al. Interactive analysis and assessment of single-cell copy-number variations [J]. Nature Methods, 2015, 12 (11): 1058.
- Gates M, Tschudi G. The synthesis of morphine [J]. Journal of the American Chemical Society, 1952, 74 (4): 1109-1110.
- Gaut BS, d' Ennequin MLT, Peek AS, et al. Maize as a model for the evolution of plant nuclear genomes [J]. Proceedings of the National Academy of Sciences, 2000, 97 (13): 7008-7015.
- Gaut BS, Doebley JF. DNA sequence evidence for the segmental allotetraploid origin of maize [J]. Proceedings of the National Academy of Sciences, 1997, 94 (13): 6809-6814.
- Gaut BS. Evolutionary dynamics of grass genomes [J]. New Phytologist, 2002, 154 (1): 15-28.
- Gaut BS. Molecular clocks and nucleotide substitution rates in higher plants [M]. Evolutionary Biology. Boston: Springer, 1998: 93-120.
- Gawad C, Koh W, Quake SR. Single-cell genome sequencing: current state of the science [J]. Nature Reviews Genetics, 2016, 17 (3): 175.
- Gepts P. The contribution of genetic and genomic approaches to plant domestication studies [J]. Current Opinion in Plant Biology, 2014, 18: 51-59.

- Ghurye J, Pop M, Koren S, et al. Scaffolding of long read assemblies using long range contact information [J]. *BMC Genomics*, 2017, 18 (1): 527.
- Gibor A, Izawa M. The DNA content of the chloroplasts of acetabularia [J]. *Proceedings of the National Academy of Sciences*, 1963, 50 (6): 1164.
- Gibson DG, Glass JI, Lartigue C, et al. Creation of a bacterial cell controlled by a chemically synthesized genome [J]. *Science*, 2010, 329 (5987): 52-56.
- Gill RA, Ali B, Cui P, et al. Comparative transcriptome profiling of two *Brassica napus* cultivars under chromium toxicity and its alleviation by reduced glutathione [J]. *BMC Genomics*, 2016, 17 (1): 885.
- Giovannoni JJ, Wing RA, Ganai MW, et al. Isolation of molecular markers from specific chromosomal intervals using DNA pools from existing mapping populations [J]. *Nucleic Acids Research*, 1991, 19 (23): 6553-6568.
- Girard IJ, Tong C, Becker MG, et al. RNA sequencing of *Brassica napus* reveals cellular redox control of Sclerotinia infection [J]. *Journal of Experimental Botany*, 2017, 68 (18): 5079-5091.
- Go DE, Stottmann RW. The impact of CRISPR/Cas9-based genomic engineering on biomedical research and medicine [J]. *Current Molecular Medicine*, 2016, 16 (4): 343-352.
- Goff SA, Ricke D, Lan TH, et al. A draft sequence of the rice genome (*Oryza sativa* L. ssp. *japonica*) [J]. *Science*, 2002, 296 (5565): 92-100.
- Golicz AA, Batley J, Edwards D. Towards plant pangenomics [J]. *Plant Biotechnology Journal*, 2016, 14 (4): 1099-1105.
- Golicz AA, Singh MB, Bhalla PL. The long intergenic noncoding RNA (lincRNA) landscape of the soybean genome [J]. *Plant Physiology*, 2018, 176 (3): 2133-2147.
- Gong Q, Yang Z, Chen E, et al. A phi-class glutathione S-transferase gene for Verticillium wilt resistance in *Gossypium arboreum* identified in a genome-wide association study [J]. *Plant and Cell Physiology*, 2017, 59 (2): 275-289.
- Goodstein DM, Shu S, Howson R, et al. Phytozome: a comparative platform for green plant genomics [J]. *Nucleic Acids Research*, 2011, 40 (D1): D1178-D1186.
- Goodwin S, McPherson JD, McCombie WR. Coming of age: ten years of next-generation sequencing technologies [J]. *Nature Reviews Genetics*, 2016, 17 (6): 333.
- Gordon SP, Contreras-Moreira B, Woods DP, et al. Extensive gene content variation in the Brachypodium distachyon pan-genome correlates with population structure [J]. *Nature Communications*, 2017, 8 (1): 2184.
- Gore MA, Chia JM, Elshire RJ, et al. A first-generation haplotype map of maize [J]. *Science*, 2009, 326 (5956): 1115-1117.
- Goremykin V, Hirsch-Ernst KI, Wölfl S, et al. The chloroplast genome of the “basal” angiosperm *Calycanthus fertilis*-structural and phylogenetic analyses [J]. *Plant Systematics and Evolution*, 2003, 242 (1-4): 119-135.
- Goremykin VV, Holland B, Hirsch-Ernst KI, et al. Analysis of *Acorus calamus* chloroplast genome and its phylogenetic implications [J]. *Molecular Biology and Evolution*, 2005, 22 (9): 1813-1822.
- Gowda M, Das B, Makumbi D, et al. Genome-wide association and genomic prediction of resistance to maize lethal necrosis disease in tropical maize germplasm [J]. *Theoretical and Applied Genetics*, 2015, 128 (10): 1813-1822.

1957-1968.

- Greaves IK, Groszmann M, Ying H, et al. Trans chromosomal methylation in *Arabidopsis hybrids* [J]. Proceedings of the National Academy of Sciences, 2012, 109 (9): 3570-3575.
- Gregoriadis G. The carrier potential of liposomes in biology and medicine [J]. New England Journal of Medicine, 1976, 295 (13): 704-710.
- Gregory TR. Synergy between sequence and size in large-scale genomics [J]. Nature Reviews Genetics, 2005, 6 (9): 699.
- Griesmann M, Chang Y, Liu X, et al. Phylogenomics reveals multiple losses of nitrogen-fixing root nodule symbiosis [J]. Science, 2018, 361 (6398): t1743.
- Griffith M, Walker JR, Spies NC, et al. Informatics for RNA sequencing: a web resource for analysis on the cloud [J]. PLoS Computational Biology, 2015, 11 (8): e1004393.
- Grob S, Schmid MW, Grossniklaus U. Hi-C analysis in Arabidopsis identifies the KNOT, a structure with similarities to the flamenco locus of Drosophila [J]. Molecular Cell, 2014, 55 (5): 678-693.
- Grønlund JT, Eyres A, Kumar S, et al. Cell specific analysis of Arabidopsis leaves using fluorescence activated cell sorting [J]. Journal of Visualized Experiments, 2012 (68): e4214.
- Groszmann M, Greaves IK, Albertyn ZI, et al. Changes in 24-nt siRNA levels in Arabidopsis hybrids suggest an epigenetic contribution to hybrid vigor [J]. Proceedings of the National Academy of Sciences, 2011, 108 (6): 2617-2622.
- Groszmann M, Greaves IK, Fujimoto R, et al. The role of epigenetics in hybrid vigour [J]. Trends in Genetics, 2013, 29 (12): 684-690.
- Grover CE, Kim HR, Wing RA, et al. Incongruent patterns of local and global genome size evolution in cotton [J]. Genome Research, 2004, 14 (8): 1474-1482.
- Gualberto JM, Newton KJ. Plant mitochondrial genomes: dynamics and mechanisms of mutation [J]. Annual Review of Plant Biology, 2017, 68: 225-252.
- Guan R, Qu Y, Guo Y, et al. Salinity tolerance in soybean is modulated by natural variation in GmSALT3 [J]. The Plant Journal, 2014, 80 (6): 937-950.
- Guan R, Zhao Y, Zhang H, et al. Draft genome of the living fossil Ginkgo biloba [J]. Gigascience, 2016, 5 (1): 49.
- Guan Y, Qu H. A rapid method for isolating single cells from apple flesh [J]. Horticultural Plant Journal, 2017 (02): 4-9.
- Gui S, Peng J, Wang X, et al. Improving *Nelumbo nucifera* genome assemblies using high-resolution genetic maps and BioNano genome mapping reveals ancient chromosome rearrangements [J]. The Plant Journal, 2018, 94 (4): 721-734.
- Gulcher J, Stefánsson K. Population genomics: laying the groundwork for genetic disease modeling and targeting [J]. Clinical Chemistry and Laboratory Medicine, 1998, 36 (8): 523-527.
- Guo H, Zhu P, Wu X, et al. Single-cell methylome landscapes of mouse embryonic stem cells and early embryos analyzed using reduced representation bisulfite sequencing [J]. Genome Research, 2013a, 23 (12): 2126-2135.
- Guo L, Qiu J, Han Z, et al. A host plant genome (*Zizania latifolia*) after a century - long endophyte infection

- [J]. *The Plant Journal*, 2015, 83 (4): 600-609.
- Guo L, Qiu J, Li LF, et al. Genomic clues for crop-weed interactions and evolution [J]. *Trends in Plant Science*, 2018, 23 (12): 1102-1115.
- Guo L, Qiu J, Ye C, et al. *Echinochloa crus-galli* genome analysis provides insight into its adaptation and invasiveness as a weed [J]. *Nature Communications*, 2017, 8 (1): 1031.
- Guo M, Rupe MA, Zinselmeier C, et al. Allelic variation of gene expression in maize hybrids [J]. *The Plant Cell*, 2004, 16 (7): 1707-1716.
- Guo S, Xu Y, Liu H, et al. The interaction between OsMADS57 and OsTB1 modulates rice tillering via DWARF14 [J]. *Nature Communications*, 2013b, 4: 1566.
- Guo S, Zhang J, Sun H, et al. The draft genome of watermelon (*Citrullus lanatus*) and resequencing of 20 diverse accessions [J]. *Nature Genetics*, 2013c, 45 (1): 51.
- Guo X, Bao J, Fan L. Evidence of selectively driven codon usage in rice: implications for GC content evolution of Gramineae genes [J]. *FEBS Letters*, 2007, 581 (5): 1015-1021.
- Guo X, Gui Y, Wang Y, et al. Selection and mutation on microRNA target sequences during rice evolution [J]. *BMC Genomics*, 2008a, 9 (1): 454.
- Guo X, Ruan S, Hu W, et al. Chloroplast DNA insertions into the nuclear genome of rice: the genes, sites and ages of insertion involved [J]. *Functional & Integrative Genomics*, 2008b, 8 (2): 101-108.
- Guo X, Xu G, Zhang Y, et al. Incongruent evolution of chromosomal size in rice [J]. *Genetics & Molecular Research*, 2006, 5 (2): 373-389.
- Gupta A, Christensen RG, Rayla AL, et al. An optimized two-finger archive for ZFN-mediated gene targeting [J]. *Nature Methods*, 2012, 9 (6): 588.
- Gupta V, Estrada AD, Blakley I, et al. RNA-Seq analysis and annotation of a draft blueberry genome assembly identifies candidate genes involved in fruit ripening, biosynthesis of bioactive compounds, and stage-specific alternative splicing [J]. *Gigascience*, 2015, 4 (1): 5.
- Guyot R, Keller B. Ancestral genome duplication in rice [J]. *Genome*, 2004, 47 (3): 610-614.
- Hakeem K, Malik A, Vardar-Sukan F, et al. Erratum to: *Plant Bioinformatics: Decoding the Phyta* [M]. *Plant Bioinformatics*. New York: Springer, 2017.
- Hamblin MT, Fernandez MGS, Casa AM, et al. Equilibrium processes cannot explain high levels of short-and medium-range linkage disequilibrium in the domesticated grass *Sorghum bicolor* [J]. *Genetics*, 2005, 171 (3): 1247-1256.
- Han R, Jian C, Lv J, et al. Identification and characterization of microRNAs in the flag leaf and developing seed of wheat (*Triticum aestivum* L.) [J]. *BMC Genomics*, 2014, 15 (1): 289.
- Han X, Wang R, Zhou Y, et al. Mapping the mouse cell atlas by microwell-seq [J]. *Cell*, 2018, 172 (5): 1091-1107. e17.
- Hancock AM, Brachi B, Faure N, et al. Adaptation to climate across the *Arabidopsis thaliana* genome [J]. *Science*, 2011, 334 (6052): 83-86.
- Handa H. Linear plasmids in plant mitochondria: peaceful coexistences or malicious invasions? [J]. *Mitochondrion*, 2008, 8 (1): 15-25.
- Handa H. The complete nucleotide sequence and RNA editing content of the mitochondrial genome of

- rapeseed (*Brassica napus* L.): comparative analysis of the mitochondrial genomes of rapeseed and *Arabidopsis thaliana* [J]. *Nucleic Acids Research*, 2003, 31 (20): 5907-5916.
- Hane JK, Ming Y, Kamphuis LG, et al. A comprehensive draft genome sequence for lupin (*Lupinus angustifolius*), an emerging health food: insights into plant-microbe interactions and legume evolution [J]. *Plant Biotechnology Journal*, 2017, 15 (3): 318-330.
- Hanschen ER, Marriage TN, Ferris PJ, et al. The *Gonium pectorale* genome demonstrates co-option of cell cycle regulation during the evolution of multicellularity [J]. *Nature Communications*, 2016, 7: 11370.
- Hansey CN, Vaillancourt B, Sekhon RS, et al. Maize (*Zea mays* L.) genome diversity as revealed by RNA-sequencing [J]. *PLoS One*, 2012, 7 (3): e33071.
- Hao DC, Chen SL, Xiao PG. Molecular evolution and positive Darwinian selection of the chloroplast maturase matK [J]. *Journal of Plant Research*, 2010, 123 (2): 241-247.
- Hao Z, Li X, Xie C, et al. Identification of functional genetic variations underlying drought tolerance in maize using SNP markers [J]. *Journal of Integrative Plant Biology*, 2011, 53 (8): 641-652.
- Hardigan MA, Laimbeer FPE, Newton L, et al. Genome diversity of tuber-bearing *Solanum* uncovers complex evolutionary history and targets of domestication in the cultivated potato [J]. *Proceedings of the National Academy of Sciences*, 2017, 114 (46): E9999-E10008.
- Harland JR, de Wet MJM. Toward a rational classification of cultivated plants [J]. *Taxon*, 1971: 509-517.
- Harloff HJ, Lemcke S, Mittasch J, et al. A mutation screening platform for rapeseed (*Brassica napus* L.) and the detection of sinapine biosynthesis mutants [J]. *Theoretical and Applied Genetics*, 2012, 124 (5): 957-969.
- Harper AL, Trick M, Higgins J, et al. Associative transcriptomics of traits in the polyploid crop species *Brassica napus* [J]. *Nature Biotechnology*, 2012, 30 (8): 798.
- Hatzig SV, Frisch M, Breuer F, et al. Genome-wide association mapping unravels the genetic control of seed germination and vigor in *Brassica napus* [J]. *Frontiers in Plant Science*, 2015, 6: 221.
- Hayes BJ. QTL mapping, MAS, and genomic selection [J]. A short-course organized by Animal breeding & Genetics. Department of Animal Science, 2007, 1 (1): 3-4.
- He G, Chen B, Wang X, et al. Conservation and divergence of transcriptomic and epigenomic variation in maize hybrids [J]. *Genome Biology*, 2013a, 14 (6): R57.
- He G, Zhu X, Elling AA, et al. Global epigenetic and transcriptional trends among two rice subspecies and their reciprocal hybrids [J]. *The Plant Cell*, 2010, 22 (1): 17-33.
- He N, Zhang C, Qi X, et al. Draft genome sequence of the mulberry tree *Morus notabilis* [J]. *Nature Communications*, 2013b, 4 (9): 2445.
- He Y, Fu Y, Hu D, et al. QTL mapping of seed glucosinolate content responsible for environment in *Brassica napus* [J]. *Frontiers in Plant Science*, 2018, 9: 891.
- He Z, Wang L, Harper AL, et al. Extensive homoeologous genome exchanges in allopolyploid crops revealed by mRNA seq - based visualization [J]. *Plant Biotechnology Journal*, 2017, 15 (5): 594-604.
- He Z, Zhai W, Wen H, et al. Two evolutionary histories in the genome of rice: the roles of domestication genes [J]. *PLoS Genetics*, 2011, 7 (6): e1002100.
- Heffner EL, Sorrells ME, Jannink JL. Genomic selection for crop improvement [J]. *Crop Science*, 2009, 49

(1): 1-12.

- Helguera M, Rivarola M, Clavijo B, et al. New insights into the wheat chromosome 4D structure and virtual gene order, revealed by survey pyrosequencing [J]. *Plant Science*, 2015, 233: 200-212.
- Hellsten U, Wright KM, Jenkins J, et al. Fine-scale variation in meiotic recombination in *Mimulus* inferred from population shotgun sequencing [J]. *Proceedings of the National Academy of Sciences*, 2013, 110 (48): 19478-19482.
- Heo JB, Sung S. Vernalization-mediated epigenetic silencing by a long intronic noncoding RNA [J]. *Science*, 2011, 331 (6013): 76-79.
- Hibrand Saint-Oyant L, Ruttink T, Hamama L, et al. A high-quality genome sequence of *Rosa chinensis* to elucidate ornamental traits [J]. *Nature Plants*, 2018: 1-12.
- Hidalgo O, Pellicer J, Christenhusz M, et al. Is there an upper limit to genome size? [J]. *Trends in Plant Science*, 2017, 22 (7): 567-573.
- Hill JT, Demarest BL, Bisgrove BW, et al. MMAPPR: mutation mapping analysis pipeline for pooled RNA-seq [J]. *Genome Research*, 2013, 23 (4): 687-697.
- Hinton GE, Osindero S, Teh YW. A fast learning algorithm for deep belief nets [J]. *Neural Computation*, 2006, 18 (7): 1527-1554.
- Hirakawa H, Kaur P, Shirasawa K, et al. Draft genome sequence of subterranean clover, a reference for genus *Trifolium* [J]. *Scientific Reports*, 2016, 6 (1).
- Hirakawa H, Shirasawa K, Kosugi S, et al. Editor's choice: Dissection of the octoploid strawberry genome by deep sequencing of the genomes of *Fragaria* species [J]. *DNA Research*, 2014a, 21 (2): 169-181.
- Hirakawa H, Shirasawa K, Miyatake K, et al. Draft genome sequence of eggplant (*Solanum melongena* L.): the representative solanum species indigenous to the old world [J]. *DNA Research*, 2014b, 21 (6): 649-660.
- Hiratsuka J, Shimada H, Whittier R, et al. The complete sequence of the rice (*Oryza sativa*) chloroplast genome: intermolecular recombination between distinct tRNA genes accounts for a major plastid DNA inversion during the evolution of the cereals [J]. *Molecular and General Genetics MGG*, 1989, 217 (2-3): 185-194.
- Hirooka S, Hirose Y, Kanesaki Y, et al. Acidophilic green algal genome provides insights into adaptation to an acidic environment [J]. *Proceedings of the National Academy of Sciences*, 2017, 114 (39): E8304-E8313.
- Hirsch CN, Hirsch CD, Brohammer AB, et al. Draft assembly of elite inbred line PH207 provides insights into genomic and transcriptome diversity in maize [J]. *The Plant Cell*, 2016, 28 (11): 2700-2714.
- Hirschhorn JN, Daly MJ. Genome-wide association studies for common diseases and complex traits [J]. *Nature Reviews Genetics*, 2005, 6 (2): 95.
- Hobom B. Gene surgery: on the threshold of synthetic biology [J]. *Medizinische Klinik*, 1980, 75 (24): 834.
- Hoecker N, Keller B, Piepho HP, et al. Manifestation of heterosis during early maize (*Zea mays* L.) root development [J]. *Theoretical and Applied Genetics*, 2006, 112 (3): 421-429.
- Höfte H, Desprez T, Amselem J, et al. An inventory of 1152 expressed sequence tags obtained by partial sequencing of cDNAs from *Arabidopsis thaliana* [J]. *The Plant Journal*, 1993, 4 (6): 1051-1061.
- Horn F, Habekuß A, Stich B. Genes involved in barley yellow dwarf virus resistance of maize [J]. *Theoretical and Applied Genetics*, 2014, 127 (12): 2575-2584.

- Horton MW, Hancock AM, Huang YS, et al. Genome-wide patterns of genetic variation in worldwide *Arabidopsis thaliana* accessions from the RegMap panel [J]. *Nature Genetics*, 2012, 44 (2): 212.
- Hoshino A, Jayakumar V, Nitasaka E, et al. Genome sequence and analysis of the Japanese morning glory *Ipomoea nil* [J]. *Nature Communications*, 2016, 7: 13295.
- Hou Y, Song L, Zhu P, et al. Single-cell exome sequencing and monoclonal evolution of a JAK2-negative myeloproliferative neoplasm [J]. *Cell*, 2012, 148 (5): 873-885.
- Houben A. B chromosomes—a matter of chromosome drive [J]. *Frontiers in Plant Science*, 2017, 8: 210.
- Howell PM, Sharpe AG, Lydiat DJ. Homoeologous loci control the accumulation of seed glucosinolates in oilseed rape (*Brassica napus*) [J]. *Genome*, 2003, 46 (3): 454-460.
- Hsu PD, Lander ES, Zhang F. Development and applications of CRISPR-Cas9 for genome engineering [J]. *Cell*, 2014, 157 (6): 1262-1278.
- Hu TT, Pattyn P, Bakker EG, et al. The *Arabidopsis lyrata* genome sequence and the basis of rapid genome size change [J]. *Nature Genetics*, 2011, 43 (5): 476.
- Hu Y, Chen J, Fang L, et al. *Gossypium barbadense* and *Gossypium hirsutum* genomes provide insights into the origin and evolution of allotetraploid cotton [J]. *Nature Genetics*, 2019, 51 (4): 739.
- Huang CY, Ayliffe MA, Timmis JN. Direct measurement of the transfer rate of chloroplast DNA into the nucleus [J]. *Nature*, 2003, 422 (6927): 72.
- Huang H, Shi C, Liu Y, et al. Thirteen *Camellia* chloroplast genome sequences determined by high-throughput sequencing: genome structure and phylogenetic relationships [J]. *BMC Evolutionary Biology*, 2014, 14 (1): 151.
- Huang J, Zhang C, Zhao X, et al. The Jujube genome provides insights into genome evolution and the domestication of sweetness/acidity taste in fruit trees [J]. *Plos Genetics*, 2016a, 12 (12): e1006433.
- Huang J, Zhang J, Li W, et al. Genome - wide association analysis of ten chilling tolerance indices at the germination and seedling stages in maize [J]. *Journal of Integrative Plant Biology*, 2013a, 55 (8): 735-744.
- Huang L, Dong H, Zhou D, et al. Systematic identification of long non - coding RNA s during pollen development and fertilization in *Brassica rapa* [J]. *The Plant Journal*, 2018a, 96 (1): 203-222.
- Huang L, Yang M, Li L, et al. Whole genome re-sequencing reveals evolutionary patterns of sacred lotus (*Nelumbo nucifera*) [J]. *Journal of Integrative Plant Biology*, 2018b, 60 (1): 2-15.
- Huang S, Deng L, Guan M, et al. Identification of genome-wide single nucleotide polymorphisms in allopolyploid crop *Brassica napus* [J]. *BMC Genomics*, 2013b, 14 (1): 717.
- Huang S, Ding J, Deng D, et al. Draft genome of the Kiwifruit *Actinidia chinensis* [J]. *Nature Communications*, 2013c, 4: 2640.
- Huang S, Li R, Zhang Z, et al. The genome of the cucumber, *Cucumis sativus* L [J]. *Nature Genetics*, 2009a, 41 (12): 1275.
- Huang W, Du Y, Zhao X, et al. B chromosome contains active genes and impacts the transcription of A chromosomes in maize (*Zea mays* L.) [J]. *BMC Plant Biology*, 2016b, 16 (1): 88.
- Huang X, Feng Q, Qian Q, et al. High-throughput genotyping by whole-genome resequencing [J]. *Genome Research*, 2009b, 19 (6): 1068-1076.
- Huang X, Kurata N, Wei X, et al. A map of rice genome variation reveals the origin of cultivated rice [J].

- Nature, 2012a, 490 (7421): 497-501.
- Huang X, Wei X, Sang T, et al. Genome-wide association studies of 14 agronomic traits in rice landraces [J]. Nature Genetics, 2010, 42 (11): 961.
- Huang X, Yang S, Gong J, et al. Genomic analysis of hybrid rice varieties reveals numerous superior alleles that contribute to heterosis [J]. Nature Communications, 2015, 6: 6258.
- Huang X, Yang S, Gong J, et al. Genomic architecture of heterosis for yield traits in rice [J]. Nature, 2016c, 537 (7622): 629.
- Huang X, Zhao Y, Wei X, et al. Genome-wide association study of flowering time and grain yield traits in a worldwide collection of rice germplasm [J]. Nature Genetics, 2012b, 44 (1): 32.
- Hufford MB, Lubinsky P, Pyhäjärvi T, et al. The genomic signature of crop-wild introgression in maize [J]. PLoS Genetics, 2013, 9 (5): e1003477.
- Hufford MB, Xu X, van Heerwaarden J, et al. Comparative population genomics of maize domestication and improvement [J]. Nature Genetics, 2012, 44 (7): 808.
- Hughes JR, Roberts N, McGowan S, et al. Analysis of hundreds of cis-regulatory landscapes at high resolution in a single, high-throughput experiment [J]. Nature Genetics, 2014, 46 (2): 205.
- Hung HY, Shannon LM, Tian F, et al. ZmCCT and the genetic basis of day-length adaptation underlying the postdomestication spread of maize [J]. Proceedings of the National Academy of Sciences, 2012, 109 (28): E1913-E1921.
- Huot JL, Enkler L, Megel C, et al. Idiosyncrasies in decoding mitochondrial genomes [J]. Biochimie, 2014, 100: 95-106.
- Hurgobin B, Edwards D. SNP discovery using a pangenome: has the single reference approach become obsolete? [J]. Biology, 2017, 6 (1): 21.
- Hutchison CA, Chuang RY, Noskov VN, et al. Design and synthesis of a minimal bacterial genome [J]. Science, 2016, 351 (6280): aad6253.
- Ibarra-Laclette E, Lyons E, Hernández-Guzmán G, et al. Architecture and evolution of a minute plant genome [J]. Nature, 2013, 498 (7452): 94.
- Ilic K, SanMiguel PJ, Bennetzen JL. A complex history of rearrangement in an orthologous region of the maize, sorghum, and rice genomes [J]. Proceedings of the National Academy of Sciences, 2003, 100 (21): 12265-12270.
- Inamura K. Major tumor suppressor and oncogenic non-coding RNAs: clinical relevance in lung cancer [J]. Cells, 2017, 6 (2): 12.
- Institute KDNAR, European Union Chromosome 3 Arabidopsis Genome Sequencing Consortium. Sequence and analysis of chromosome 3 of the plant *Arabidopsis thaliana* [J]. Nature, 2000, 408 (6814): 820.
- International RGSP. The map-based sequence of the rice genome [J]. Nature, 2005, 436 (7052): 793.
- International Wheat Genome Sequencing Consortium. A chromosome-based draft sequence of the hexaploid bread wheat (*Triticum aestivum*) genome [J]. Science, 2014, 345 (6194): 1251788.
- International Wheat Genome Sequencing Consortium. Shifting the limits in wheat research and breeding using a fully annotated reference genome [J]. Science, 2018, 361 (6403): eaar7191.
- Iorizzo M, Ellison S, Senalik D, et al. A high-quality carrot genome assembly provides new insights into

- carotenoid accumulation and asterid genome evolution [J]. *Nature Genetics*, 2016, 48 (6): 657.
- Iorizzo M, Senalik D, Szklarczyk M, et al. *De novo* assembly of the carrot mitochondrial genome using next generation sequencing of whole genomic DNA provides first evidence of DNA transfer into an angiosperm plastid genome [J]. *BMC Plant Biology*, 2012, 12 (1): 61.
- Ishikawa R, Ohnishi T, Kinoshita Y, et al. Rice interspecies hybrids show precocious or delayed developmental transitions in the endosperm without change to the rate of syncytial nuclear division [J]. *The Plant Journal*, 2011, 65 (5): 798-806.
- Jaillon O, Aury JM, Noel B, et al. The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla [J]. *Nature*, 2007, 449 (7161): 463.
- Jansen RK, Cai Z, Raubeson LA, et al. Analysis of 81 genes from 64 plastid genomes resolves relationships in angiosperms and identifies genome-scale evolutionary patterns [J]. *Proceedings of the National Academy of Sciences*, 2007, 104 (49): 19369-19374.
- Janska H, Sarria R, Woloszynska M, et al. Stoichiometric shifts in the common bean mitochondrial genome leading to male sterility and spontaneous reversion to fertility [J]. *The Plant Cell*, 1998, 10 (7): 1163-1180.
- Jarvis DE, Ho YS, Lightfoot DJ, et al. The genome of *Chenopodium quinoa* [J]. *Nature*, 2017, 542 (7641): 307.
- Jena KK, Khush GS. Introgression of genes from *Oryza officinalis* Well ex Watt to cultivated rice, *O. sativa* L [J]. *Theoretical and Applied Genetics*, 1990, 80 (6): 737-745.
- Jeong DH, Park S, Zhai J, et al. Massive analysis of rice small RNAs: mechanistic implications of regulated microRNAs and variants for differential target RNA cleavage [J]. *The Plant Cell*, 2011, 23 (12): 4185-4207.
- Jeong N, Suh SJ, Kim MH, et al. Ln is a key regulator of leaflet shape and number of seeds per pod in soybean [J]. *The Plant Cell*, 2012, 24 (12): 4807-4818.
- Jeong YM, Kim N, Ahn BO, et al. Elucidating the triplicated ancestral genome structure of radish based on chromosome-level comparison with the Brassica genomes [J]. *Theoretical and Applied Genetics*, 2016, 129 (7): 1357-1372.
- Jia HM, Jia HJ, Cai QL, et al. The red bayberry genome and genetic basis of sex determination [J]. *Plant biotechnology journal*, 2019, 17 (2): 397-409.
- Jia J, Zhao S, Kong X, et al. *Aegilops tauschii* draft genome sequence reveals a gene repertoire for wheat adaptation [J]. *Nature*, 2013, 496 (7443): 91.
- Jia X, Zhang X, Qu J, et al. Optimization conditions of wheat mesophyll protoplast isolation [J]. *Agricultural Science*, 2016, 7: 850-858.
- Jiang W, Liu Y, Xia E, et al. Prevalent role of gene features in determining evolutionary fates of whole-genome duplication duplicated genes in flowering plants [J]. *Plant Physiology*, 2013, 161 (4): 1844-1861.
- Jiao Y, Peluso P, Shi J, et al. Improved maize reference genome with single-molecule technologies [J]. *Nature*, 2017, 546 (7659): 524.
- Jiao Y, Tausta SL, Gandotra N, et al. A transcriptome atlas of rice cell types uncovers cellular, functional and developmental hierarchies [J]. *Nature Genetics*, 2009, 41 (2): 258.
- Jiao Y, Wang Y, Xue D, et al. Regulation of OsSPL14 by OsmiR156 defines ideal plant architecture in rice [J]. *Nature Genetics*, 2010, 42 (6): 541.

- Jiao Y, Zhao H, Ren L, et al. Genome-wide genetic changes during modern breeding of maize [J]. *Nature Genetics*, 2012, 44 (7): 812.
- Jin J, Hua L, Zhu Z, et al. GAD1 encodes a secreted peptide that regulates grain number, grain length, and awn development in rice domestication [J]. *The Plant Cell*, 2016a, 28 (10): 2453-2463.
- Jin J, Huang W, Gao JP, et al. Genetic control of rice plant architecture under domestication [J]. *Nature Genetics*, 2008, 40 (11): 1365.
- Jin J, Tian F, Yang DC, et al. PlantTFDB 4.0: toward a central hub for transcription factors and regulatory interactions in plants [J]. *Nucleic Acids Research*, 2016b, 45: D1040–D1045.
- Jinek M, Chylinski K, Fonfara I, et al. A programmable dual-RNA-guided DNA endonuclease in adaptive bacterial immunity [J]. *Science*, 2012, 337 (6096): 816-821.
- Johnston JS, Pepper AE, Hall AE, et al. Evolution of genome size in Brassicaceae [J]. *Annals of Botany*, 2005, 95 (1): 229-235.
- Joly-Lopez Z, Bureau TE. Diversity and evolution of transposable elements in *Arabidopsis* [J]. *Chromosome Research*, 2014, 22 (2): 203-216.
- Kajitani R, Toshimoto K, Noguchi H, et al. Efficient *de novo* assembly of highly heterozygous genomes from whole-genome shotgun short reads [J]. *Genome Research*, 2014, 24 (8): 1384-1395.
- Kalisky T, Blainey P, Quake SR. Genomic analysis at the single-cell level [J]. *Annual Review of Genetics*, 2011, 45: 431-445.
- Kalvari I, Argasinska J, Quinones-Olvera N, et al. Rfam 13. 0: shifting to a genome-centric resource for non-coding RNA families [J]. *Nucleic Acids Research*, 2017, 46 (D1): D335-D342.
- Kang YJ, Kim SK, Kim MY, et al. Genome sequence of mungbean and insights into evolution within *Vigna* species [J]. *Nature Communications*, 2014, 5 (1): 5443.
- Kang YJ, Satyawan D, Shim S, et al. Draft genome sequence of adzuki bean, *Vigna angularis* [J]. *Scientific Reports*. 2015, 5: 8069.
- Kapralov MV, Filatov DA. Widespread positive selection in the photosynthetic Rubisco enzyme [J]. *BMC Evolutionary Biology*, 2007, 7 (1): 73.
- Karpagam R, Jawaharraj K, Ashokkumar B, et al. Unraveling the lipid and pigment biosynthesis in *Coelastrella* sp. M-60: Genomics-enabled transcript profiling [J]. *Algal Research*, 2018, 29: 277-289.
- Kasianov AS, Klepikova AV, Kulakovskiy IV, et al. High - quality genome assembly of *Capsella bursa - pastoris* reveals asymmetry of regulatory elements at early stages of polyploid genome evolution [J]. *The Plant Journal*, 2017, 91 (2): 278-291.
- Kastberger G, Stachl R. Infrared imaging technology and biological applications [J]. *Behavior Research Methods, Instruments, & Computers*, 2003, 35 (3): 429-439.
- Katiyar-Agarwal S, Morgan R, Dahlbeck D, et al. A pathogen-inducible endogenous siRNA in plant immunity [J]. *Proceedings of the National Academy of Sciences*, 2006, 103 (47): 18002-18007.
- Kato-Noguchi H. Barnyard grass-induced rice allelopathy and momilactone B [J]. *Journal of Plant Physiology*, 2011, 168 (10): 1016-1020.
- Kawahara Y, de la Bastide M, Hamilton JP, et al. Improvement of the *Oryza sativa* Nipponbare reference genome using next generation sequence and optical map data [J]. *Rice*, 2013, 6 (1): 4.

- Kawakatsu T, Huang SC, Jupe F, et al. Epigenomic diversity in a global collection of *Arabidopsis thaliana* accessions [J]. *Cell*, 2016, 166 (2): 492-505.
- Kay S, Hahn S, Marois E, et al. A bacterial effector acts as a plant transcription factor and induces a cell size regulator [J]. *Science*, 2007, 318 (5850): 648-651.
- Kelchtermans P, Bittremieux W, de Grave K, et al. Machine learning applications in proteomics research: How the past can boost the future [J]. *Proteomics*, 2014, 14 (4-5): 353-366.
- Kelliher T, Starr D, Su X, et al. One-step genome editing of elite crop germplasm during haploid induction [J]. *Nature Biotechnology*, 2019, 37 (3): 287.
- Kellner F, Kim J, Clavijo BJ, et al. Genome-guided investigation of plant natural product biosynthesis [J]. *Plant Journal*, 2015, 82 (4): 680-692.
- Kellogg EA. The evolutionary history of *Ehrhartoideae*, *Oryzeae*, and *Oryza* [J]. *Rice*, 2009, 2 (1): 1-14.
- Kelly K. Out of control: The rise of neo-biological civilization [M]. Reading, Massachusetts: Addison-Wesley, 1994.
- Kermicle JL. Dependence of the R-mottled aleurone phenotype in maize on mode of sexual transmission [J]. *Genetics*, 1970, 66 (1): 69.
- Khraiwesh B, Zhu JK, Zhu J. Role of miRNAs and siRNAs in biotic and abiotic stress responses of plants [J]. *Biochimica et Biophysica Acta (BBA)-Gene Regulatory Mechanisms*, 2012, 1819 (2): 137-148.
- Khush GS. Origin, dispersal, cultivation and variation of rice [J]. *Plant Molecular Biology*, 1997, 35 (1-2): 25-34.
- Kikuchi S, Satoh K, Nagata T, et al. Collection, mapping, and annotation of over 28, 000 cDNA clones from japonica rice [J]. *Science*, 2003, 301 (5631): 376-379.
- Kilby NJ, Leyser HMO, Furner IJ. Promoter methylation and progressive transgene inactivation in *Arabidopsis* [J]. *Plant Molecular Biology*, 1992, 20 (1): 103-112.
- Kim DM, Lee HS, Kwon SJ, et al. High-density mapping of quantitative trait loci for grain-weight and spikelet number in rice [J]. *Rice*, 2014a, 7 (1): 14.
- Kim G, LeBlanc ML, Wafula EK, et al. Genomic-scale exchange of mRNA between a parasitic plant and its hosts [J]. *Science*, 2014b, 345 (6198): 808-811.
- Kim MY, Lee S, van K, et al. Whole-genome sequencing and intensive analysis of the undomesticated soybean (*Glycine soja* Sieb. and Zucc.) genome [J]. *Proceedings of the National Academy of Sciences*. 2010, 107 (51): 22032-22037.
- Kim N, Jeong YM, Jeong S, et al. Identification of candidate domestication regions in the radish genome based on high-depth resequencing analysis of 17 genotypes [J]. *Theoretical and Applied Genetics*, 2016, 129 (9): 1797-1814.
- Kim S, Park J, Yeom SI, et al. New reference genome sequences of hot pepper reveal the massive evolution of plant disease-resistance genes by retroduplication [J]. *Genome Biology*, 2017a, 18 (1): 210.
- Kim S, Park M, Yeom SI, et al. Genome sequence of the hot pepper provides insights into the evolution of pungency in *Capsicum* species [J]. *Nature Genetics*, 2014c, 46 (3): 270-8.
- Kim S, Plagnol V, Hu TT, et al. Recombination and linkage disequilibrium in *Arabidopsis thaliana* [J]. *Nature Genetics*, 2007, 39 (9): 1151.
- Kim YM, Kim S, Koo N, et al. Genome analysis of *Hibiscus syriacus* provides insights of polyploidization

- and indeterminate flowering in woody plants [J]. *DNA Research An International Journal for Rapid Publication of Reports on Genes & Genomes*, 2017b, 24 (1): 71-80.
- Kinoshita T, Yadegari R, Harada JJ, et al. Imprinting of the MEDEA polycomb gene in the *Arabidopsis* endosperm [J]. *The Plant Cell*, 1999, 11 (10): 1945-1952.
- Kishimoto N, Higo H, Abe K, et al. Identification of the duplicated segments in rice chromosomes 1 and 5 by linkage analysis of cDNA markers of known functions [J]. *Theoretical and Applied Genetics*, 1994, 88 (6-7): 722-726.
- Kitashiba H, Li F, Hirakawa H, et al. Draft sequences of the radish (*Raphanus sativus* L.) genome [J]. *DNA Research*, 2014, 21 (5): 481-490.
- Klein AM, Mazutis L, Akartuna I, et al. Droplet barcoding for single-cell transcriptomics applied to embryonic stem cells [J]. *Cell*, 2015, 161 (5): 1187-1201.
- Knoop V, Brennicke A. Molecular biology of the plant mitochondrion [J]. *Critical Reviews in Plant Sciences*, 2002, 21 (2): 111-126.
- Knoop V, Unseld M, Marienfeld J, et al. Copia-, gypsy-and LINE-like retrotransposon fragments in the mitochondrial genome of *Arabidopsis thaliana* [J]. *Genetics*, 1996, 142 (2): 579-585.
- Kobayashi F, Wu J, Kanamori H, et al. A high-resolution physical map integrating an anchored chromosome with the BAC physical maps of wheat chromosome 6B [J]. *BMC Genomics*, 2015, 16: 595.
- Kobayashi M, Nagasaki H, Garcia V, et al. Genome-wide analysis of intraspecific DNA polymorphism in ‘Micro-Tom’ , a model cultivar of tomato (*Solanum lycopersicum*) [J]. *Plant and Cell Physiology*, 2014, 55 (2): 445-454.
- Koch MA, Wernisch M, Schmickl R. *Arabidopsis thaliana*’s wild relatives: an updated overview on systematics, taxonomy and evolution [J]. *Taxon*, 2008, 57 (3): 933-933.
- Koike-Yusa H, Li Y, Tan E P, et al. Genome-wide recessive genetic screening in mammalian cells with a lentiviral CRISPR-guide RNA library [J]. *Nature Biotechnology*, 2014, 32 (3): 267.
- Koller BH, Smithies O. Inactivating the beta 2-microglobulin locus in mouse embryonic stem cells by homologous recombination [J]. *Proceedings of the National Academy of Sciences*, 1989, 86 (22): 8932-8935.
- Kong D, Qu L, Zhang X, et al. Optimization of EMS Mutagenesis Condition and Screening of Mutants in *Gossypium arboreum* L [J]. *Cotton Science*, 2017, 29: 336-344.
- Kong F, Nan H, Cao D, et al. A new dominant gene E9 conditions early flowering and maturity in soybean [J]. *Crop Science*, 2014, 54 (6): 2529-2535.
- Körbes AP, Machado RD, Guzman F, et al. Identifying conserved and novel microRNAs in developing seeds of *Brassica napus* using deep sequencing [J]. *PloS One*, 2012, 7 (11): e50663.
- Koren S, Walenz BP, Berlin K, et al. Canu: scalable and accurate long-read assembly via adaptive k-mer weighting and repeat separation [J]. *Genome Research*, 2017, 27 (5): 722-736.
- Kozomara A, Griffiths-Jones S. miRBase: annotating high confidence microRNAs using deep sequencing data [J]. *Nucleic Acids Research*, 2013, 42 (D1): D68-D73.
- Kreitman M. Nucleotide polymorphism at the alcohol dehydrogenase locus of *Drosophila melanogaster* [J]. *Nature*, 1983, 304 (5925): 412.

- Kremnev D, Strand Å. Plastid encoded RNA polymerase activity and expression of photosynthesis genes required for embryo and seed development in Arabidopsis [J]. *Frontiers in Plant Science*, 2014, 5: 385.
- Kreps JA, Wu Y, Chang HS, et al. Transcriptome changes for Arabidopsis in response to salt, osmotic, and cold stress [J]. *Plant Physiology*, 2002, 130 (4): 2129-2141.
- Kromdijk J, Głowacka K, Leonelli L, et al. Improving photosynthesis and crop productivity by accelerating recovery from photoprotection [J]. *Science*, 2016, 354 (6314): 857-861.
- Kronbak R, Ingvarsdén CR, Madsen CK, et al. A novel approach to the generation of seamless constructs for plant transformation [J]. *Plant Methods*, 2014, 10 (1): 10.
- Ku HM, Vision T, Liu J, et al. Comparing sequenced segments of the tomato and Arabidopsis genomes: large-scale duplication followed by selective gene loss creates a network of synteny [J]. *Proceedings of the National Academy of Sciences*, 2000, 97 (16): 9121-9126.
- Kubaláková M, Vrána J, Číhalíková J, et al. Flow karyotyping and chromosome sorting in bread wheat (*Triticum aestivum* L.) [J]. *Theoretical and Applied Genetics*, 2002, 104 (8): 1362-1372.
- Kubo T, Newton KJ. Angiosperm mitochondrial genomes and mutations [J]. *Mitochondrion*, 2008, 8 (1): 5-14.
- Kubo T, Nishizawa S, Sugawara A, et al. The complete nucleotide sequence of the mitochondrial genome of sugar beet (*Beta vulgaris* L.) reveals a novel gene for tRNACys (GCA) [J]. *Nucleic Acids Research*, 2000, 28 (13): 2571-2576.
- Kühn K, Gualberto JM. Recombination in the stability, repair and evolution of the mitochondrial genome [M]. *Advances in Botanical Research*. Massachusetts: Academic Press, 2012, 63: 215-252.
- Kumar S, Dhingra A, Daniell H. Plastid-expressed betaine aldehyde dehydrogenase gene in carrot cultured cells, roots, and leaves confers enhanced salt tolerance [J]. *Plant Physiology*, 2004, 136 (1): 2843-2854.
- Kump KL, Bradbury PJ, Wissner RJ, et al. Genome-wide association study of quantitative resistance to southern leaf blight in the maize nested association mapping population [J]. *Nature Genetics*, 2011, 43 (2): 163.
- Kurakawa T, Ueda N, Maekawa M, et al. Direct control of shoot meristem activity by a cytokinin-activating enzyme [J]. *Nature*, 2007, 445 (7128): 652.
- Kyndt T, Quispe D, Zhai H, et al. The genome of cultivated sweet potato contains *Agrobacterium* T-DNAs with expressed genes: an example of a naturally transgenic food crop [J]. *Proceedings of the National Academy of Sciences*, 2015, 112 (18): 5844-5849.
- Lai J, Li R, Xu X, et al. Genome-wide patterns of genetic variation among elite maize inbred lines [J]. *Nature Genetics*, 2010, 42 (11): 1027.
- Lai X, Schnable JC, Liao Z, et al. Genome-wide characterization of non-reference transposable element insertion polymorphisms reveals genetic diversity in tropical and temperate maize [J]. *BMC Genomics*, 2017, 18 (1): 702.
- Lam H, Xu X, Liu X, et al. Resequencing of 31 wild and cultivated soybean genomes identifies patterns of genetic diversity and selection [J]. *Nature Genetics*, 2010, 42 (12): 1053-1059.
- Lan Y, Su N, Shen Y, et al. Identification of novel MiRNAs and MiRNA expression profiling during grain development in indica rice [J]. *BMC Genomics*, 2012, 13 (1): 264.

- Lander ES, Botstein D. Mapping mendelian factors underlying quantitative traits using RFLP linkage maps [J]. *Genetics*, 1989, 121 (1): 185-199.
- Lander ES, Waterman MS. Genomic mapping by fingerprinting random clones: a mathematical analysis [J]. *Genomics*, 1988, 2 (3): 231-239.
- Lang D, Ullrich KK, Murat F, et al. The *Physcomitrella patens* chromosome - scale assembly reveals moss genome structure and evolution [J]. *The Plant Journal*, 2018, 93 (3): 515-533.
- Lang Z, Gong Z. Small RNA biogenesis: novel roles of an RNase III enzyme [J]. *Nature Plants*, 2016, 2 (3): 16021.
- Lang Z, Wang Y, Tang K, et al. Critical roles of DNA demethylation in the activation of ripening-induced genes and inhibition of ripening-repressed genes in tomato fruit [J]. *Proceedings of the National Academy of Sciences*, 2017, 114 (22): E4511-E4519.
- Lauss K, Wardenaar R, Oka R, et al. Parental DNA methylation states are associated with heterosis in epigenetic hybrids [J]. *Plant Physiology*, 2018, 176 (2): 1627-1645.
- Law JA, Du J, Hale CJ, et al. Polymerase IV occupancy at RNA-directed DNA methylation sites requires SHH1 [J]. *Nature*, 2013, 498 (7454): 385.
- Law JA, Jacobsen SE. Establishing, maintaining and modifying DNA methylation patterns in plants and animals [J]. *Nature Reviews Genetics*, 2010, 11 (3): 204.
- Law SR, Narsai R, Whelan J. Mitochondrial biogenesis in plants during seed germination [J]. *Mitochondrion*, 2014, 19: 214-221.
- Lee MC W, Lopez-Diaz FJ, Khan SY, et al. Single-cell analyses of transcriptional heterogeneity during drug tolerance transition in cancer cells by RNA sequencing [J]. *Proceedings of the National Academy of Sciences*, 2014, 111 (44): E4726-E4735.
- Lee SB, Kaitanis C, Jansen RK, et al. The complete chloroplast genome sequence of *Gossypium hirsutum*: organization and phylogenetic relationships to other angiosperms [J]. *BMC Genomics*, 2006, 7 (1): 61.
- Lee TH, Tang H, Wang X, et al. PGDD: a database of gene and genome duplication in plants [J]. *Nucleic Acids Research*, 2012, 41 (D1): D1152-D1158.
- Leiboff S, Li X, Hu HC, et al. Genetic control of morphometric diversity in the maize shoot apical meristem [J]. *Nature Communications*, 2015, 6 (1): 8974.
- Leister D. How can the light reactions of photosynthesis be improved in plants? [J]. *Frontiers in Plant Science*, 2012, 3: 199.
- Leliaert F, Smith DR, Moreau H, et al. Phylogeny and molecular evolution of the green algae [J]. *Critical Reviews in Plant Sciences*, 2012, 31 (1): 1-46.
- Lemieux C, Otis C, Turmel M. A clade uniting the green algae *Mesostigma viride* and *Chlorokybus atrophycus* represents the deepest branch of the Streptophyta in chloroplast genome-based phylogenies [J]. *BMC Biology*, 2007, 5 (1): 2.
- Lesne A, Riposo J, Roger P, et al. 3D genome reconstruction from chromosomal contacts [J]. *Nature Methods*, 2014, 11 (11): 1141.
- Leung K, Zahn H, Leaver T, et al. A programmable droplet-based microfluidic device applied to multiparameter analysis of single microbes and microbial communities [J]. *Proceedings of the National*

- Academy of Sciences, 2012, 109 (20): 7665-7670.
- Li C, Huang L, Xu C, et al. Altered levels of histone deacetylase OsHDT1 affect differential gene expression patterns in hybrid rice [J]. PLoS One, 2011, 6 (7): e21789.
- Li F, Chen B, Xu KUN, et al. Genome-wide association study dissects the genetic architecture of seed weight and seed quality in rapeseed (*Brassica napus* L.) [J]. DNA research, 2014a, 21 (4): 355-367.
- Li F, Fan G, Lu C, et al. Genome sequence of cultivated Upland cotton (*Gossypium hirsutum* TM-1) provides insights into genome evolution [J]. Nature Biotechnology, 2015a, 33 (5): 524.
- Li F, Fan G, Wang K, et al. Genome sequence of the cultivated cotton *Gossypium arboreum* [J]. Nature Genetics, 2014b, 3 (6): 567-572.
- Li G. A new model calling procedure for Illumina BeadArray data [J]. BMC Genetics, 2016a, 17 (1): 90.
- Li H, Peng Z, Yang X, et al. Genome-wide association study dissects the genetic architecture of oil biosynthesis in maize kernels [J]. Nature Genetics, 2013a, 45 (1): 43.
- Li J, Meng X, Zong Y, et al. Gene replacements and insertions in rice by intron targeting using CRISPR-Cas9 [J]. Nature Plants, 2016b, 2 (10): 16139.
- Li JY, Wang J, Zeigler RS. The 3000 rice genome project: new opportunities and challenges for future rice research [J]. Giga Science, 2014g, 3 (1): 8.
- Li K, Wang H, Hu X, et al. Genome-wide association study reveals the genetic basis of stalk cell wall components in maize [J]. PLoS One, 2016c, 11 (8): e0158906.
- Li L, Eichten SR, Shimizu R, et al. Genome-wide discovery and characterization of maize long non-coding RNAs [J]. Genome Biology, 2014c, 15 (2): R40.
- Li L, Wang B, Liu Y, et al. The complete mitochondrial genome sequence of the hornwort megaceros *aenigmaticus* shows a mixed mode of conservative yet dynamic evolution in early land plant mitochondrial genomes [J]. Journal of Molecular Evolution, 2009, 68 (6): 665-678.
- Li LF, Li YL, Jia Y, et al. Signatures of adaptation in the weedy rice genome [J]. Nature Genetics, 2017a, 49 (5): 811.
- Li Q, Eichten SR, Hermanson PJ, et al. Genetic perturbation of the maize methylome [J]. The Plant Cell, 2014d, 26 (12): 4602-4616.
- Li Q, Lu X, Song Q, et al. Selection for a Zinc-finger protein contributes to seed oil increase during soybean domestication [J]. Plant Physiology, 2017b, 173 (4): 2208.
- Li Q, Yang X, Xu S, et al. Genome-wide association studies identified three independent polymorphisms associated with α -tocopherol content in maize kernels [J]. PLoS One, 2012, 7 (5): e36807.
- Li WV, Li JJ. An accurate and robust imputation method scImpute for single-cell RNA-seq data [J]. Nature Communications, 2018, 9 (1): 997.
- Li X, Kahveci T, Settles AM. A novel genome-scale repeat finder geared towards transposons [J]. Bioinformatics, 2007, 24 (4): 468-476.
- Li X, Kui L, Zhang J, et al. Improved hybrid de novo genome assembly of domesticated apple (*Malus × domestica*) [J]. Gigascience, 2016d, 5 (1): 35.
- Li X, Li L, Yan J. Dissecting meiotic recombination based on tetrad analysis by single-microspore sequencing in maize [J]. Nature Communications, 2015b, 6: 6648.

- Li X, Meng D, Chen S, et al. Single nucleus sequencing reveals spermatid chromosome fragmentation as a possible cause of maize haploid induction [J]. *Nature Communications*, 2017c, 8 (1): 991.
- Li X, Wang X, He K, et al. High-resolution mapping of epigenetic modifications of the rice genome uncovers interplay between DNA methylation, histone methylation, and gene expression [J]. *The Plant Cell*, 2008, 20 (2): 259-276.
- Li X, Waterman MS. Estimating the repeat structure and length of DNA sequences using ℓ -tuples [J]. *Genome Research*, 2003, 13 (8): 1916-1922.
- Li X, Zhou Z, Ding J, et al. Combined linkage and association mapping reveals QTL and candidate genes for plant and ear height in maize [J]. *Frontiers in Plant Science*, 2016e, 7: 833.
- Li Y, Li C, Bradbury P J, et al. Identification of genetic variants associated with maize flowering time using an extremely large multi - genetic background population [J]. *The Plant Journal*, 2016f, 86 (5): 391-402.
- Li Y, Wang J. Faster human genome sequencing [J]. *Nature Biotechnology*, 2009, 27 (9): 820.
- Li Y, Xiao J, Chen L, et al. Rice functional genomics research: past decade and future [J]. *Molecular Plant*, 2018, 11 (3): 359-380.
- Li Y, Zhao S, Ma J, et al. Molecular footprints of domestication and improvement in soybean revealed by whole genome re-sequencing [J]. *BMC Genomics*, 2013b, 14 (1): 579.
- Li Y, Zhou G, Ma J, et al. *De novo* assembly of soybean wild relatives for pan-genome analysis of diversity and agronomic traits [J]. *Nature Biotechnology*, 2014e, 32 (10): 1045-1052.
- Liang C, Wang Y, Zhu Y, et al. OsNAP connects abscisic acid and leaf senescence by fine-tuning abscisic acid biosynthesis and directly targeting senescence-associated genes in rice [J]. *Proceedings of the National Academy of Sciences*, 2014, 111 (27): 10013-10018.
- Libault M, Farmer A, Brechenmacher L, et al. Complete transcriptome of the soybean root hair cell, a single-cell model, and its alteration in response to *Bradyrhizobium japonicum* infection [J]. *Plant Physiology*, 2010, 152 (2): 541-552.
- Lieberman-Aiden E, van Berkum NL, Williams L, et al. Comprehensive mapping of long-range interactions reveals folding principles of the human genome [J]. *Science*, 2009, 326 (5950): 289-293.
- Lin D, Hong P, Zhang S, et al. Digestion-ligation-only Hi-C is an efficient and cost-effective method for chromosome conformation capture [J]. *Nature Genetics*, 2018, 50: 754-763.
- Lin T, Zhu G, Zhang J, et al. Genomic analyses provide insights into the history of tomato breeding [J]. *Nature Genetics*, 2014, 46 (11): 1220.
- Lin X, Kaul S, Rounsley S, et al. Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana* [J]. *Nature*, 1999, 402 (6763): 761-768.
- Lin Y, Min J, Lai R, et al. Genome-wide sequencing of longan (*Dimocarpus longan* Lour.) provides insights into molecular basis of its polyphenol-rich characteristics [J]. *Gigascience*, 2017, 6 (5): 1-14.
- Ling HQ, Ma B, Shi X, et al. Genome sequence of the progenitor of wheat A subgenome *Triticum urartu* [J]. *Nature*, 2018, 557 (7705): 424.
- Ling HQ, Zhao S, Liu D, et al. Draft genome of the wheat A-genome progenitor *Triticum urartu* [J]. *Nature*, 2013, 496 (7443): 87.
- Lipka AE, Gore MA, Magallanes-Lundback M, et al. Genome-wide association study and pathway-level

- analysis of tocochromanol levels in maize grain [J]. *G3: Genes, Genomes, Genetics*, 2013, 3 (8): 1287-1299.
- Lippert C, Sabatini R, Maher MC, et al. Identification of individuals by trait prediction using whole-genome sequencing data [J]. *Proceedings of the National Academy of Sciences*, 2017, 114 (38): 10166-10171.
- Lister R, O'Malley RC, Tonti-Filippini J, et al. Highly integrated single-base resolution maps of the epigenome in *Arabidopsis* [J]. *Cell*, 2008, 133 (3): 523-536.
- Liu B, Shi Y, Yuan J, et al. Estimation of genomic characteristics by analyzing k-mer frequency in *de novo* genome projects [J]. *Quantitative Biology*, 2013, 35 (s 1-3): 62-67.
- Liu B, Watanabe S, Uchiyama T, et al. The soybean stem growth habit gene *Dt1* is an ortholog of *Arabidopsis* *TERMINAL FLOWER1* [J]. *Plant Physiology*, 2010, 153 (1): 198.
- Liu C, Cheng YJ, Wang JW, et al. Prominent topologically associated domains differentiate global chromatin packing in rice from *Arabidopsis* [J]. *Nature Plants*, 2017a, 3 (9): 742.
- Liu C, Wang C, Wang G, et al. Genome-wide analysis of chromatin packing in *Arabidopsis thaliana* at single-gene resolution [J]. *Genome Research*, 2016a, 26 (8): 1057-1068.
- Liu C, Weigel D. Chromatin in 3D: progress and prospects for plants [J]. *Genome Biology*, 2015, 16 (1): 170.
- Liu H, Wang F, Xiao Y, et al. MODEM: multi-omics data envelopment and mining in maize [J]. *Database*, 2016b, 2016: baw117.
- Liu H, Shi J, Sun C, et al. Gene duplication confers enhanced expression of 27-kDa γ -zein for endosperm modification in quality protein maize [J]. *Proceedings of the National Academy of Sciences*, 2016c, 113 (18): 4964-4969.
- Liu J, Li G, Chang Z, et al. BinPacker: packing-based de novo transcriptome assembly from RNA-seq data [J]. *PLoS Computational Biology*, 2016e, 12 (2): e1004772.
- Liu J, Luo W, Qin N, et al. A 55 K SNP array-based genetic map and its utilization in QTL mapping for productive tiller number in common wheat [J]. *Theoretical and Applied Genetics*, 2018a, 131 (11): 2439-2450.
- Liu J, Wang W, Mei D, et al. Characterizing variation of branch angle and genome-wide association mapping in rapeseed (*Brassica napus* L.) [J]. *Frontiers in Plant Science*, 2016d, 7: 21.
- Liu LZ, Li JN. QTL Mapping of oleic acid, linolenic acid and erucic acid content in *Brassica napus* by using the high density SNP genetic map [J]. *Scientia Agricultura Sinica*, 2014, 47 (1): 24-32.
- Liu L, Du Y, Huo D, et al. Genetic architecture of maize kernel row number and whole genome prediction [J]. *Theoretical and Applied Genetics*, 2015a, 128 (11): 2243-2254.
- Liu MJ, Zhao J, Cai QL, et al. The complex jujube genome provides insights into fruit tree biology [J]. *Nature Communications*, 2014a, 5 (1): 5315.
- Liu Q, Chang S, Hartman GL, et al. Assembly and annotation of a draft genome sequence for *Glycine latifolia*, a perennial wild relative of soybean [J]. *The Plant Journal*, 2018b, 95 (1): 71-85.
- Liu Q, Zhou Y, Morrell PL, et al. Deleterious variants in Asian rice and the potential cost of domestication [J]. *Molecular Biology and Evolution*, 2017b, 34 (4): 908-924.
- Liu R, How-Kit A, Stammitt L, et al. A DEMETER-like DNA demethylase governs tomato fruit ripening [J]. *Proceedings of the National Academy of Sciences*, 2015b, 112 (34): 10804-10809.

- Liu S, Kandoth PK, Warren SD, et al. A soybean cyst nematode resistance gene points to a new mechanism of plant resistance to pathogens [J]. *Nature*, 2012, 492 (7428): 256.
- Liu S, Liu Y, Yang X, et al. The *Brassica oleracea* genome reveals the asymmetrical evolution of polyploid genomes [J]. *Nature Communications*, 2014b, 5: 3930.
- Liu S, Wang X, Wang H, et al. Genome-wide analysis of ZmDREB genes and their association with natural variation in drought tolerance at seedling stage of *Zea mays* L [J]. *PLoS Genetics*, 2013, 9 (9): e1003790.
- Liu T, Li Y, Duan W, et al. Cold acclimation alters DNA methylation patterns and confers tolerance to heat and increases growth rate in *Brassica rapa* [J]. *Journal of experimental botany*, 2017c, 68 (5): 1213-1224.
- Liu W, Stewart Jr CN. Plant synthetic biology [J]. *Trends in Plant Science*, 2015, 20 (5): 309-317.
- Liu X, Cheng J, Zhang G, et al. Engineering yeast for the production of breviscapine by genomic analysis and synthetic biology approaches [J]. *Nature Communications*, 2018c, 9 (1): 448.
- Liu X, Zhao B, Zheng H J, et al. *Gossypium barbadense* genome sequence provides insight into the evolution of extra-long staple fiber and specialized metabolites [J]. *Scientific Reports*, 2015c, 5: 14139.
- Liu Y, Li Q, Lu X, et al. Soybean GmMYB73 promotes lipid accumulation in transgenic plants [J]. *BMC Plant Biology*, 2014c, 14 (1): 73.
- Liu Y, Li X, Zhao J, et al. Direct evidence that suspensor cells have embryogenic potential that is suppressed by the embryo proper during normal embryogenesis [J]. *Proceedings of the National Academy of Sciences*, 2015d, 112 (40): 12432-12437.
- Lo S, Muñoz-Amatriaín M, Boukar O, et al. Identification of QTL controlling domestication-related traits in cowpea (*Vigna unguiculata* L. Walp) [J]. *Scientific Reports*, 2018, 8 (1): 6261.
- Loman NJ, Quick J, Simpson JT. A complete bacterial genome assembled de novo using only nanopore sequencing data [J]. *Nature Methods*, 2015, 12 (8): 733.
- Londo JP, Chiang YC, Hung KH, et al. Phylogeography of Asian wild rice, *Oryza rufipogon*, reveals multiple independent domestications of cultivated rice, *Oryza sativa* [J]. *Proceedings of the National Academy of Sciences*, 2006, 103 (25): 9578-9583.
- Long Q, Rabanal F, Meng D, et al. Massive genomic variation and strong selection in *Arabidopsis thaliana* lines from Sweden [J]. *Nature Genetics*, 2013, 45: 884-890.
- Long Y, Xia W, Li R, et al. Epigenetic QTL mapping in *Brassica napus* [J]. *Genetics*, 2011, 189 (3): 1093-1102.
- Lonsdale DM, Hodge TP, Fauron CMR. The physical map and organisation of the mitochondrial genome from the fertile cytoplasm of maize [J]. *Nucleic Acids Research*, 1984, 12 (24): 9249-9261.
- López-Flores I, Garrido-Ramos MA. The repetitive DNA content of eukaryotic genomes [M]. *Repetitive DNA*. Basel: Karger Publishers, 2012, 7: 1-28.
- Louwens M, Splinter E, van Driel R, et al. Studying physical chromatin interactions in plants using Chromosome Conformation Capture (3C) [J]. *Nature Protocols*, 2009, 4 (8): 1216.
- Lu F, Ammiraju JSS, Sanyal A, et al. Comparative sequence analysis of MONOCULM1-orthologous regions in 14 *Oryza* genomes [J]. *Proceedings of the National Academy of Sciences*, 2009, 106 (6): 2071-2076.
- Lu F, Romay MC, Glaubitz JC, et al. High-resolution genetic mapping of maize pan-genome sequence anchors [J]. *Nature Communications*, 2015, 6 (1): 6914.

- Lu G, Harper AL, Trick M, et al. Associative transcriptomics study dissects the genetic architecture of seed glucosinolate content in *Brassica napus* [J]. DNA Research, 2014, 21 (6): 613-625.
- Lu J, Tang T, Tang H, et al. The accumulation of deleterious mutations in rice genomes: a hypothesis on the cost of domestication [J]. Trends in Genetics, 2006, 22 (3): 126-131.
- Lu K, Wei L, Li X, et al. Whole-genome resequencing reveals *Brassica napus* origin and genetic loci involved in its improvement [J]. Nature Communications, 2019, 10 (1): 1154.
- Lu Q, Niu X, Zhang M, et al. Genome-wide association study of seed dormancy and the genomic consequences of improvement footprints in rice (*Oryza sativa* L.) [J]. Frontiers in Plant Science, 2018, 8: 2213.
- Lu S, Zhao X, Hu Y, et al. Natural variation at the soybean J locus improves adaptation to the tropics and enhances yield [J]. Nature Genetics, 2017, 49 (5): 773.
- Lu S, Zong C, Fan W, et al. Probing meiotic recombination and aneuploidy of single sperm cells by whole-genome sequencing [J]. Science, 2012, 338 (6114): 1627-1630.
- Lu T, Cui L, Zhou Y, et al. Transcriptome-wide investigation of circular RNAs in rice [J]. Rna, 2015, 21 (12): 2076-2087.
- Lu T, Lu G, Fan D, et al. Function annotation of the rice transcriptome at single-nucleotide resolution by RNA-seq [J]. Genome Research, 2010, 20 (9): 1238-1249.
- Lucas SJ, Akpnr BA, Kantar M, et al. Physical mapping in-tegrated with syntenic analysis to characterize the gene space of the long arm of wheat chromosome 1A [J]. PLoS One, 2013, 8 (4): e59542.
- Luedi PP, Dietrich FS, Weidman JR, et al. Computational and experimental identification of novel human imprinted genes [J]. Genome Research, 2007, 17 (12): 1723-1730.
- Luikart G, England PR, Tallmon D, et al. The power and promise of population genomics: from genotyping to genome typing [J]. Nature Reviews Genetics, 2003, 4 (12): 981.
- Luo MC, Gu YQ, Puiu D, et al. Genome sequence of the progenitor of the wheat D genome *Aegilops tauschii* [J]. Nature, 2017a, 551 (7681): 498.
- Luo MC, Gu YQ, You FM, et al. A 4-gigabase physical map unlocks the structure and evolution of the complex ge-nome of *Aegilops tauschi*, the wheat D-genome progenitor [J]. Proceedings of the National Academy of Sciences, 2013, 110 (19): 7940-7945.
- Luo R, Liu B, Xie Y, et al. SOAPdenovo2: an empirically improved memory-efficient short-read *de novo* assembler [J]. Gigascience, 2012, 1 (1): 18.
- Luo Z, Wang M, Long Y, et al. Incorporating pleiotropic quantitative trait loci in dissection of complex traits: seed yield in rapeseed as an example [J]. Theoretical and Applied Genetics, 2017b, 130 (8): 1569-1585.
- Ma B, Li T, Xiang Z, et al. MnTEdb, a collective resource for mulberry transposable elements [J]. Database, 2015 (a), 2015: bav004-bav004.
- Ma C, Zhang HH, Wang X. Machine learning for big data analytics in plants [J]. Trends in Plant Science, 2014, 19 (12): 798-808.
- Ma J, Bennetzen JL. Rapid recent growth and divergence of rice nuclear genomes [J]. Proceedings of the National Academy of Sciences, 2004, 101: 12404-12410.
- Ma L, Xin H, Qu L, et al. Transcription profile analysis reveals that zygotic division results in uneven

- distribution of specific transcripts in apical/basal cells of tobacco [J]. PLoS One, 2011, 6 (1): e15971.
- Ma L, Zhu F, Li Z, et al. TALEN-based mutagenesis of lipoxygenase LOX3 enhances the storage tolerance of rice (*Oryza sativa*) seeds [J]. PLoS One, 2015b, 10 (12): e0143877.
- Ma PF, Zhang YX, Guo ZH, et al. Evidence for horizontal transfer of mitochondrial DNA to the plastid genome in a bamboo genus [J]. Scientific Reports, 2015c, 5: 11608.
- Ma T, Wang J, Zhou G, et al. Genomic insights into salt adaptation in a desert poplar [J]. Nature Communications, 2013, 4: 2797.
- Ma Y, Liu L, Zhu C, et al. Molecular analysis of rice plants harboring a multi-functional T-DNA tagging system [J]. Journal of Genetics and Genomics, 2009, 36 (5): 267-276.
- Ma Y, Min L, Wang M, et al. Disrupted genome methylation in response to high temperature has distinct effects on microspore abortion and anther indehiscence [J]. The Plant Cell, 2018a, 30 (7): 1387-1403.
- Ma Z, He S, Wang X, et al. Resequencing a core collection of upland cotton identifies genomic variation and loci influencing fiber quality and yield [J]. Nature Genetics, 2018b, 50 (6): 803.
- Macas J, Meszaros T, Nouzova M. PlantSat: a specialized database for plant satellite repeats [J]. Bioinformatics, 2002, 18 (1): 28-35.
- Macas J, Neumann P, Novák P, et al. Global sequence characterization of rice centromeric satellite based on oligomer frequency analysis in large-scale sequencing data [J]. Bioinformatics, 2010, 26 (17): 2101-2108.
- Magwene PM, Willis JH, Kelly JK. The statistics of bulk segregant analysis using next generation sequencing [J]. PLoS Computational Biology, 2011, 7 (11): e1002255.
- Mahesh HB, Subba P, Advani J, et al. Multi-omics driven assembly and annotation of the sandalwood (*Santalum album*) genome [J]. Plant Physiology, 2018, 176 (4): 1764-2017.
- Mahmood S, Li Z, Yue X, et al. Development of INDELs markers in oilseed rape (*Brassica napus* L.) using re-sequencing data [J]. Molecular Breeding, 2016, 36 (6): 79.
- Mahner M, Kary M. What exactly are genomes, genotypes and phenotypes? And what about phenomes? [J]. Journal of Theoretical Biology, 1997, 186 (1): 55-63.
- Mahuku G, Chen J, Shrestha R, et al. Combined linkage and association mapping identifies a major QTL (qRtsc8-1), conferring tar spot complex resistance in maize [J]. Theoretical and Applied Genetics, 2016, 129 (6): 1217-1229.
- Maier RM, Neckermann K, Igloi GL, et al. Complete sequence of the maize chloroplast genome: gene content, hotspots of divergence and fine tuning of genetic information by transcript editing [J]. Journal of Molecular Biology, 1995, 251 (5): 614-628.
- Malmberg MM, Pembleton LW, Baillie RC, et al. Genotyping - by - sequencing through transcriptomics: implementation in a range of crop species with varying reproductive habits and ploidy levels [J]. Plant Biotechnology Journal, 2018, 16 (4): 877-889.
- Mammadov J, Rice JR, Chen W, et al. Genetic loci associated with gray leaf spot in maize: U. S. Patent Application 14/561, 496 [P]. 2015-6-18.
- Mao H, Sun S, Yao J, et al. Linking differential domain functions of the GS3 protein to natural variation of grain size in rice [J]. Proceedings of the National Academy of Sciences, 2010, 107 (45): 19579-19584.
- Mao H, Wang H, Liu S, et al. A transposable element in a NAC gene is associated with drought tolerance in

- maize seedlings [J]. *Nature Communications*, 2015, 6: 8326.
- Mao LF, Chen MH, Chu QJ, et al. RiceRelativesGD: a database of rice relatives for rice breeding [J]. *Database*, 2019, baz110.
- Marçais G, Kingsford C. A fast, lock-free approach for efficient parallel counting of occurrences of *K*-mers [J]. *Bioinformatics*, 2011, 27 (6): 764-770.
- Marchal C, Zhang J, Zhang P, et al. BED-domain-containing immune receptors confer diverse resistance spectra to yellow rust [J]. *Nature Plants*, 2018, 4 (9): 662.
- Marcussen T, Sandve SR, Heier L, et al. Ancient hybridizations among the ancestral genomes of bread wheat [J]. *Science*, 2014, 345 (6194): 1250092.
- Marí-Ordóñez A, Marchais A, Etcheverry M, et al. Reconstructing *de novo* silencing of an active plant retrotransposon [J]. *Nature Genetics*, 2013, 45 (9): 1029.
- Martin VJJ, Pitera DJ, Withers ST, et al. Engineering a mevalonate pathway in *Escherichia coli* for production of terpenoids [J]. *Nature biotechnology*, 2003, 21 (7): 796.
- Martin W, Rujan T, Richly E, et al. Evolutionary analysis of Arabidopsis, cyanobacterial, and chloroplast genomes reveals plastid phylogeny and thousands of cyanobacterial genes in the nucleus [J]. *Proceedings of the National Academy of Sciences*, 2002, 99 (19): 12246-12251.
- Martínez García PJ, Crepeau MW, Puiu D, et al. The walnut (*Juglans regia*) genome sequence reveals diversity in genes coding for the biosynthesis of non - structural polyphenols [J]. *Plant Journal*, 2016, 87 (5): 507-532.
- Marx V. Biology: The big challenges of big data [J]. *Nature*, 2013, 498: 255-260.
- Mascher M, Gundlach H, Himmelbach A, et al. A chromosome conformation capture ordered sequence of the barley genome [J]. *Nature*, 2017, 544 (7651): 427.
- Mason AS, Zhang J, Tollenaere R, et al. High - throughput genotyping for species identification and diversity assessment in germplasm collections [J]. *Molecular Ecology Resources*, 2015, 15 (5): 1091-1101.
- Mason AS, Higgins EE, Snowdon RJ, et al. A user guide to the Brassica60K Illumina Infinium™ SNP genotyping array [J]. *Theoretical and Applied Genetics*, 2017, 130 (4): 621-633.
- Mateo-Bonmatí E, Casanova-Sáez R, Candela H, et al. Rapid identification of angulata leaf mutations using next-generation sequencing [J]. *Planta*, 2014, 240 (5): 1113-1122.
- Matera JT, Monroe J, Smelser W, et al. Unique changes in mitochondrial genomes associated with reversions of S-type cytoplasmic male sterility in maize [J]. *PLoS One*, 2011, 6 (8): e23405.
- Mather KA, Caicedo AL, Polato NR, et al. The extent of linkage disequilibrium in rice (*Oryza sativa* L.) [J]. *Genetics*, 2007, 177 (4): 2223-2232.
- Matsuo T, Heller M, Petti L, et al. Persistence of the entire Epstein-Barr virus genome integrated into human lymphocyte DNA [J]. *Science*, 1984, 226 (4680): 1322-1325.
- Mayer KFX, Rogers J, Doležel J, et al. A chromosome-based draft sequence of the hexaploid bread wheat (*Triticum aestivum*) genome [J]. *Science*, 2014, 345 (6194): 1251788.
- Mayer K, Schüller C, Wambutt R, et al. Sequence and analysis of chromosome 4 of the plant *Arabidopsis thaliana* [J]. *Nature*, 1999, 402 (6763): 769-777.
- McKusick VA, Ruddle FH. A new discipline, a new name, a new journal [J]. *Genomics*, 1987, 1 (1): 1-2.

- McMullen MD, Kresovich S, Villeda HS, et al. Genetic properties of the maize nested association mapping population [J]. *Science*, 2009, 325 (5941): 737-740.
- Mehrotra S, Goyal V. Repetitive sequences in plant nuclear DNA: types, distribution, evolution and function [J]. *Genomics, Proteomics & Bioinformatics*, 2014, 12 (4): 164-171.
- Melkozernov AN, Barber J, Blankenship RE. Light harvesting in photosystem I supercomplexes [J]. *Biochemistry*, 2006, 45 (2): 331-345.
- Melters DP, Bradnam KR, Young HA, et al. Comparative analysis of tandem repeats from hundreds of species reveals unique insights into centromere evolution [J]. *Genome Biology*, 2013, 14 (1): R10.
- Meng F, Liu H, Wang K, et al. Development-associated microRNAs in grains of wheat (*Triticum aestivum* L.) [J]. *BMC Plant Biology*, 2013, 13 (1): 140.
- Merchant SS, Prochnik SE, Vallon O, et al. The *Chlamydomonas* genome reveals the evolution of key animal and plant functions [J]. *Science*, 2007, 318 (5848): 245-250.
- Mercy G, Mozziconacci J, Scolari VF, et al. 3D organization of synthetic and scrambled chromosomes [J]. *Science*, 2017, 355 (6329): eaaf4597.
- Meuwissen THE, Hayes BJ, Goddard ME. Prediction of total genetic value using genome-wide dense marker maps [J]. *Genetics*, 2001, 157 (4): 1819-29.
- Meyer RS, Purugganan MD. Evolution of crop species: genetics of domestication and diversification [J]. *Nature Reviews Genetics*, 2013, 14 (12): 840.
- Miah G, Rafii M, Ismail M, et al. A review of microsatellite markers and their applications in rice breeding programs to improve blast disease resistance [J]. *International Journal of Molecular Sciences*, 2013, 14 (11): 22499-22528.
- Mian MAR, Bailey MA, Tamulonis JP, et al. Molecular markers associated with seed weight in two soybean populations [J]. *Theoretical and Applied Genetics*, 1996, 93 (7): 1011-1016.
- Michael TP, VanBuren R. Progress, challenges and the future of crop genomes [J]. *Current Opinion in Plant Biology*, 2015, 24: 71-81.
- Michelmore RW, Paran I, Kesseli RV. Identification of markers linked to disease-resistance genes by bulked segregant analysis: a rapid method to detect markers in specific genomic regions by using segregating populations [J]. *Proceedings of the national academy of sciences*, 1991, 88 (21): 9828-9832.
- Ming R, Vanburen R, Liu Y, et al. Genome of the long-living sacred lotus (*Nelumbo nucifera* Gaertn.) [J]. *Genome Biology*, 2013, 14 (5): R41.
- Ming R, Vanburen R, Wai CM, et al. The pineapple genome and the evolution of CAM photosynthesis [J]. *Nature Genetics*, 2015, 47 (12): 1435-1442.
- Mishra B, Gupta DK, Pfenninger M, et al. A reference genome of the European Beech (*Fagus sylvatica* L.) [J]. *Gigascience*, 2018, 7 (6): 511.
- Mitchell LA, Wang A, Stracquadanio G, et al. Synthesis, debugging, and effects of synthetic chromosome consolidation: synVI and beyond [J]. *Science*, 2017, 355 (6329): eaaf4831.
- Mitsui Y, Shimomura M, Komatsu K, et al. The radish genome and comprehensive gene expression profile of tuberous root formation and development [J]. *Scientific Reports*, 2015, 5: 10835.
- Miura K, Ashikari M, Matsuoka M. The role of QTLs in the breeding of high-yielding rice [J]. *Trends in Plant*

- Science, 2011, 16 (6): 319-326.
- Miura K, Ikeda M, Matsubara A, et al. OsSPL14 promotes panicle branching and higher grain productivity in rice [J]. Nature Genetics, 2010, 42 (6): 545.
- Miyamoto K, Fujita M, Shenton MR, et al. Evolutionary trajectory of phytoalexin biosynthetic gene clusters in rice [J]. The Plant Journal, 2016, 87 (3): 293-304.
- Mjolsness E, de Coste D. Machine learning for science: state of the art and future prospects [J]. Science, 2001, 293 (5537): 2051-2055.
- Moghe GD, Hufnagel DE, Tang H, et al. Consequences of whole-genome triplication as revealed by comparative genomic analyses of the wild radish *Raphanus raphanistrum* and three other Brassicaceae species [J]. The Plant Cell, 2014, 26 (5): 1925-1937.
- Moissiard G, Cokus SJ, Cary J, et al. MORC family ATPases required for heterochromatin condensation and gene silencing [J]. Science, 2012, 336 (6087): 1448-1451.
- Monat C, Pera B, Ndjondjop MN, et al. *De novo* assemblies of three *Oryza glaberrima* accessions provide first insights about pan-genome of african rices [J]. Genome Biology & Evolution, 2017, 9 (1): evw253.
- Monnahan P, Kolář F, Baduel P, et al. Pervasive population genomic consequences of genome duplication in *Arabidopsis arenosa* [J]. Nature Ecology & Evolution, 2019, 3 (3): 457.
- Montenegro JD, Golicz AA, Bayer PE, et al. The pangenome of hexaploid bread wheat [J]. The Plant Journal, 2017, 90 (5): 1007-1013.
- Moore MJ, Dhingra A, Soltis PS, et al. Rapid and accurate pyrosequencing of angiosperm plastid genomes [J]. BMC Plant Biology, 2006, 6 (1): 17.
- Morales I, Alvaro JE, Urrestarazu M. Contribution of thermal imaging to fertigation in soilless culture [J]. Journal of Thermal Analysis and Calorimetry, 2014, 116 (2): 1033-1039.
- Moreau H, Verhelst B, Couloux A, et al. Gene functionalities and genome structure in *Bathycoccus prasinus* reflect cellular specializations at the base of the green lineage [J]. Genome Biology, 2012, 13 (8): R74.
- Moreau L, Charcosset A, Gallais A. Use of trial clustering to study QTL $\times$ environment effects for grain yield and related traits in maize [J]. Theoretical and Applied Genetics, 2004, 110 (1): 92-105.
- Mori K, Shirasawa K, Nogata H, et al. Identification of RAN1 orthologue associated with sex determination through whole genome sequencing analysis in fig (*Ficus carica* L.) [J]. Scientific Reports, 2017, 7: 41124.
- Morris GP, Ramu P, Deshpande SP, et al. Population genomic and genome-wide association studies of agroclimatic traits in sorghum [J]. Proceedings of the National Academy of Sciences, 2013, 110 (2): 453-458.
- Moscou MJ, Bogdanove AJ. A simple cipher governs DNA recognition by TAL effectors [J]. Science, 2009, 326 (5959): 1501-1501.
- Motamayor JC, Mockaitis K, Schmutz J, et al. The genome sequence of the most widely cultivated cacao type and its use to identify candidate genes regulating pod color [J]. Genome Biology, 2013, 14 (6): r53.
- Moyers BT, Morrell PL, McKay JK. Genetic costs of domestication and improvement [J]. Journal of Heredity, 2017, 109 (2): 103-116.
- Müller M, Lane N, Allen CA, et al. Origin of mitochondria and hydrogenosomes [J]. Current Opinion in Microbiology, 1999, 2 (5): 535-541.

- Multani DS, Jena KK, Brar DS, et al. Development of monosomic alien addition lines and introgression of genes from *Oryza australiensis* Domin. to cultivated rice *O. sativa* L [J]. Theoretical and Applied Genetics, 1994, 88 (1): 102-109.
- Mun JH, Chung H, Chung WH, et al. Construction of a reference genetic map of *Raphanus sativus* based on genotyping by whole-genome resequencing [J]. Theoretical and Applied Genetics, 2015, 128 (2): 259-272.
- Muñoz-Amatriáin M, Mirebrahim H, Xu P, et al. Genome resources for climate-resilient cowpea, an essential crop for food security [J]. The Plant Journal, 2017, 89 (5): 1042-1054.
- Myburg AA, Grattapaglia D, Tuskan GA, et al. The genome of *Eucalyptus grandis* [J]. Nature, 2014, 510 (7505): 356-362.
- Nagamura Y, Inoue T, Antonio BA, et al. Conservation of duplicated segments between rice chromosome 11 and 12 [J]. Japanese Journal of Breeding, 1995, 45 (3): 373-376.
- Nagel KA, Putz A, Gilmer F, et al., 2012. Growscreen-Rhizo is a novel phenotyping robot enabling simultaneous measurements of root and shoot growth for plants grown in soil-filled rhizotrons. Funct Plant Biol, 39: 1335-1337.
- Nakamura N, Hirakawa H, Sato S, et al. Genome structure of *Rosa multiflora*, a wild ancestor of cultivated roses [J]. DNA Research, 2017, 25 (2): 113-121.
- Nakao Y, Kanamori T, Itoh T, et al. Genome sequence of the lager brewing yeast, an interspecies hybrid [J]. DNA Research, 2009, 16 (2): 115-129.
- Napoli C, Lemieux C, Jorgensen R. Introduction of a chimeric chalcone synthase gene into petunia results in reversible co-suppression of homologous genes in trans [J]. The Plant Cell, 1990, 2 (4): 279-289.
- Narsai R, Secco D, Schultz MD, et al. Dynamic and rapid changes in the transcriptome and epigenome during germination and in developing rice (*Oryza sativa*) coleoptiles under anoxia and re - oxygenation [J]. The Plant Journal, 2017, 89 (4): 805-824.
- Navin N, Kendall J, Troge J, et al. Tumour evolution inferred by single-cell sequencing [J]. Nature, 2011, 472 (7341): 90.
- Neale DB, Wegrzyn JL, Stevens KA, et al. Decoding the massive genome of loblolly pine using haploid DNA and novel assembly strategies [J]. Genome Biology, 2014, 15 (3): R59.
- Nemhauser JL, Torii KU. Plant synthetic biology for molecular engineering of signalling and development [J]. Nature Plants, 2016, 2 (3): 16010.
- Ngu M, Massel K, Bonen L. Group II introns in wheat mitochondria have degenerate structural features and varied splicing pathways [J]. The International Journal of Biochemistry & Cell biology, 2017, 91: 156-167.
- Ni F, Qi J, Hao Q, et al. Wheat *Ms2* encodes for an orphan protein that confers male sterility in grass species [J]. Nature Communications, 2017, 8: 15121.
- Ni X, Zhuo M, Su Z, et al. Reproducible copy number variation patterns among single circulating tumor cells of lung cancer patients [J]. Proceedings of the National Academy of Sciences, 2013, 110 (52): 21083-21088.
- Ni Z, Kim ED, Ha M, et al. Altered circadian rhythms regulate growth vigour in hybrids and allopolyploids [J]. Nature, 2009, 457 (7227): 327.
- Nielsen R. Population genetic analysis of ascertained SNP data [J]. Human Genomics, 2004, 1 (3): 218.

- Nirmal RC, Furtado A, Wrigley C, et al. Influence of gene expression on hardness in wheat [J]. PLOS One, 2016, 11 (10): e0164746.
- Nishiyama T, Sakayama H, de Vries J, et al. The Chara genome: secondary complexity and implications for plant terrestrialization [J]. Cell, 2018, 174 (2): 448-464. e24.
- Niu Y, Shen B, Cui Y, et al. Generation of gene-modified cynomolgus monkey via *Cas9*/RNA-mediated gene targeting in one-cell embryos [J]. Cell, 2014, 156 (4): 836-843.
- Nordborg M, Borevitz JO, Bergelson J, et al. The extent of linkage disequilibrium in *Arabidopsis thaliana* [J]. Nature Genetics, 2002, 30 (2): 190.
- Nordborg M, Hu TT, Ishino Y, et al. The pattern of polymorphism in *Arabidopsis thaliana* [J]. PLoS Biology, 2005, 3 (7): e196.
- Notsu Y, Masood S, Nishikawa T, et al. The complete sequence of the rice (*Oryza sativa* L.) mitochondrial genome: frequent DNA sequence acquisition and loss during the evolution of flowering plants [J]. Molecular Genetics and Genomics, 2002, 268 (4): 434-445.
- Novák P, Ávila Robledillo L, Koblížková A, et al. TAREAN: a computational tool for identification and characterization of satellite DNA from unassembled short reads [J]. Nucleic Acids Research, 2017, 45 (12): e111.
- Novikova PY, Hohmann N, Nizhynska V, et al. Sequencing of the genus *Arabidopsis* identifies a complex history of nonbifurcating speciation and abundant trans-specific polymorphism [J]. Nature Genetics, 2016, 48 (9): 1077.
- Nowak MD, Russo G, Schlapbach R, et al. The draft genome of *Primula veris* yields insights into the molecular basis of heterostyly [J]. Genome Biology, 2015, 16 (1): 12.
- Nystedt B, Street NR, Wetterbom A, et al. The Norway spruce genome sequence and conifer genome evolution [J]. Nature, 2013, 497 (7451): 579-584.
- Oda K, Yamato K, Ohta E, et al. Gene organization deduced from the complete sequence of liverwort *Marchantia polymorpha* mitochondrial DNA: a primitive form of plant mitochondrial genome [J]. Journal of Molecular Biology, 1992, 223 (1): 1-7.
- Odintsova MS, Yurina NP. Chloroplast genomics of land plants and algae [M]//Biotechnological applications of photosynthetic proteins: biochips, biosensors and biodevices. Boston: Springer, 2006: 57-72.
- Ogihara Y, Isono K, Kojima T, et al. Structural features of a wheat plastome as revealed by complete sequencing of chloroplast DNA [J]. Molecular Genetics and Genomics, 2002, 266 (5): 740-746.
- Ohyama K, Fukuzawa H, Kohchi T, et al. Chloroplast gene organization deduced from complete sequence of liverwort *Marchantia polymorpha* chloroplast DNA [J]. Nature, 1986, 322 (6079): 572.
- Ohyama K, Takemura M, Oda K, et al. Gene content, organization and molecular evolution of plant organellar genomes and sex chromosomes—insights from the case of the liverwort *Marchantia polymorpha* [J]. Proceedings of the Japan Academy, Series B, 2009, 85 (3): 108-124.
- Okada K, Mao LF, Chen MH, et al. Green conservation of the biosynthetic gene cluster for momilactones, 2019, under review
- Olsen KM, Wendel JF, A bountiful harvest: genomic insights into crop domestication phenotypes [J]. Annual Review of Plant Biology, 2013, 64 (1): 47-70.

- Olukolu BA, Negeri A, Dhawan R, et al. A connected set of genes associated with programmed cell death implicated in controlling the hypersensitive response in maize [J]. *Genetics*, 2013, 193 (2): 609-620.
- Olukolu BA, Wang GF, Vontimitta V, et al. A genome-wide association study of the maize hypersensitive defense response identifies genes that cluster in related pathways [J]. *PLoS Genetics*, 2014, 10 (8): e1004562.
- Ossowski S, Schneeberger K, Clark RM, et al. Sequencing of natural strains of *Arabidopsis thaliana* with short reads [J]. *Genome Research*, 2008, 18 (12): 2024-2033.
- Ota S, Oshima K, Yamazaki T, et al. Highly efficient lipid production in the green alga *Parachlorella kessleri*: draft genome and transcriptome endorsed by whole-cell 3D ultrastructure [J]. *Biotechnology for Biofuels*, 2016, 9 (1): 13.
- Ou L, Li D, Lv J, et al. Pan-genome of cultivated pepper (*Capsicum*) and its use in gene presence-absence variation analyses [J]. *The New Phytologist*, 2018, 220 (2): 360.
- Owens BF, Lipka AE, Magallanes-Lundback M, et al. A foundation for provitamin A biofortification of maize: genome-wide association and genomic prediction models of carotenoid levels [J]. *Genetics*, 2014, 198 (4): 1699-1716.
- Pace J, Gardner C, Romay C, et al. Genome-wide association analysis of seedling root development in maize (*Zea mays* L.) [J]. *BMC Genomics*, 2015, 16 (1): 47.
- Paddon CJ, Westfall PJ, Pitera DJ, et al. High-level semi-synthetic production of the potent antimalarial artemisinin [J]. *Nature*, 2013, 496 (7446): 528.
- Palenik B, Grimwood J, Aerts A, et al. The tiny eukaryote *Ostreococcus* provides genomic insights into the paradox of plankton speciation [J]. *Proceedings of the National Academy of Sciences*, 2007, 104 (18): 7705-7710.
- Pan Q, Shai O, Lee LJ, et al. Deep surveying of alternative splicing complexity in the human transcriptome by high-throughput sequencing [J]. *Nature Genetics*, 2008, 40 (12): 1413.
- Pandey MK, Khan AW, Singh VK, et al. QTL - seq approach identified genomic regions and diagnostic markers for rust and late leaf spot resistance in groundnut (*Arachis hypogaea* L.) [J]. *Plant Biotechnology Journal*, 2017, 15 (8): 927-941.
- Paproki A, Sirault X, Berry S, et al. A novel mesh processing based technique for 3D plant analysis [J]. *BMC Plant Biology*, 2012, 12 (1): 63.
- Parry MAJ, Madgwick PJ, Bayon C, et al. Mutation discovery for crop improvement [J]. *Journal of Experimental Botany*, 2009, 60 (10): 2817-2825.
- Paszkowski J, Baur M, Bogucki A, et al. Gene targeting in plants [J]. *The EMBO Journal*, 1988, 7 (13): 4021-4026.
- Patel RK, Jain M. NGS QC Toolkit: a toolkit for quality control of next generation sequencing data [J]. *PLoS One*, 2012, 7 (2): e30619.
- Paterson AH, Bowers JE, Burow MD, et al. Comparative genomics of plant chromosomes [J]. *The Plant Cell*, 2000, 12 (9): 1523-1539.
- Paterson AH, Bowers JE, Chapman BA. Ancient polyploidization predating divergence of the cereals, and its consequences for comparative genomics [J]. *Proceedings of the National Academy of Sciences*, 2004, 101

- (26): 9903-9908.
- Paterson AH, Bowers JE, Peterson DG, et al. Structure and evolution of cereal genomes [J]. *Current Opinion in Genetics & Development*, 2003, 13 (6): 644-650.
- Paterson AH, Lander ES, Hewitt JD, et al. Resolution of quantitative traits into Mendelian factors by using a complete linkage map of restriction fragment length polymorphisms [J]. *Nature*, 1988, 335 (6192): 721.
- Paterson AH, Li ZK. Paleo-green revolution for rice [J]. *Proceedings of the National Academy of Sciences*, 2011, 108 (27): 10931-10932.
- Paterson AH, Wendel JF, Gundlach H, et al. Repeated polyploidization of *Gossypium* genomes and the evolution of spinnable cotton fibres [J]. *Nature*, 2012, 492 (7429): 423.
- Paulsen J, Liyakat Ali TM, Collas P. Computational 3D genome modeling using Chrom3D [J]. *Nature Protocols*, 2018, 13 (5): 1137-1152.
- Paux E, Sourdile P, Salse J, et al. A physical map of the 1-gigabase bread wheat chromosome 3B [J]. *Science*, 2008, 322 (5898): 101-104.
- Pear JR, Kawagoe Y, Schreckengost WE, et al. Higher plants contain homologs of the bacterial *celA* genes encoding the catalytic subunit of cellulose synthase [J]. *Proceedings of the National Academy of Sciences*, 1996, 93 (22): 12637-12642.
- Peiffer JA, Flint-Garcia SA, de Leon N, et al. The genetic architecture of maize stalk strength [J]. *Plos One*, 2013, 8 (6): e67066.
- Peiffer JA, Romay MC, Gore MA, et al. The genetic architecture of maize height [J]. *Genetics*, 2014, 196 (4): 1337-1356.
- Peng B, Kong H, Li Y, et al. OsAAP6 functions as an important regulator of grain protein content and nutritional quality in rice [J]. *Nature Communications*, 2014, 5 (1): 4847.
- Peng J, Richards DE, Hartley NM, et al. 'Green revolution' genes encode mutant gibberellin response modulators [J]. *Nature*, 1999, 400 (6741): 256.
- Peng Z, Lu Y, Li L, et al. The draft genome of the fast-growing non-timber forest species moso bamboo (*Phyllostachys heterocycla*) [J]. *Nature Genetics*, 2013, 45 (4): 456-461.
- Pennisi E. Single-cell sequencing tackles basic and biomedical questions [J]. *Science*, 2012, 336 (6084): 976-977.
- Pereira HS, Delgado M, Viegas W, et al. Rye (*Secale cereale*) supernumerary (B) chromosomes associated with heat tolerance during early stages of male sporogenesis [J]. *Annals of Botany*, 2016, 119 (3): 325-337.
- Pérez-Rodríguez P, Riano-Pachon DM, Corrêa L GG, et al. PlnTFDB: updated content and new features of the plant transcription factor database [J]. *Nucleic Acids Research*, 2009, 38 (suppl_1): D822-D827.
- Perry AS, Wolfe KH. Nucleotide substitution rates in legume chloroplast DNA depend on the presence of the inverted repeat [J]. *Journal of Molecular Evolution*, 2002, 55 (5): 501-508.
- Perry JA, Wang TL, Welham TJ, et al. A TILLING reverse genetics tool and a web-accessible collection of mutants of the legume *Lotus japonicus* [J]. *Plant Physiology*, 2003, 131 (3): 866-871.
- Pfeifer M, Kugler KG, Sandve SR, et al. Genome interplay in the grain transcriptome of hexaploid bread wheat [J]. *Science*, 2014, 345 (6194): 1250091.
- Philippe R, Paux E, Bertin I, et al. A high density physical map of chromosome 1BL supports evolutionary

- studies, map-based cloning and sequencing in wheat [J]. *Genome Biology*, 2013, 14 (6): R64 .
- Picelli S, Faridani OR, Björklund ÅK, et al. Full-length RNA-seq from single cells using Smart-seq2 [J]. *Nature Protocols*, 2014, 9 (1): 171.
- Ping J, Liu Y, Sun L, et al. *Dt2* is a Gain-of-Function MADS-Domain Factor Gene That Specifies Semideterminacy in Soybean [J]. *The Plant Cell*, 2014, 26 (7): 2831.
- Pires ND, Grossniklaus U. Different yet similar: evolution of imprinting in flowering plants and mammals [J]. *F1000 Prime Reports*, 2014, 6: 63.
- Plass C, Smiraglia DJ. Genome-Wide Analysis of DNA Methylation Changes in Human Malignancies [M]. *DNA Methylation: Development, Genetic Disease and Cancer*. Berlin: Springer, 2006, 310: 179-198.
- Poland JA, Bradbury PJ, Buckler ES, et al. Genome-wide nested association mapping of quantitative resistance to northern leaf blight in maize [J]. *Proceedings of the National Academy of Sciences*, 2011, 108 (17): 6893-6898.
- Pombert JF, Blouin NA, Lane C, et al. A lack of parasitic reduction in the obligate parasitic green alga *Helicosporidium* [J]. *PLoS Genetics*, 2014, 10 (5): e1004355.
- Poplin R, Chang PC, Alexander D, et al. A universal SNP and small-indel variant caller using deep neural networks [J]. *Nature Biotechnology*, 2018, 36 (10): 983.
- Potato Genome Sequencing Consortium. Genome sequence and analysis of the tuber crop potato [J]. *Nature*, 2011, 475 (7355): 189.
- Preuten T, Cincu E, Fuchs J, et al. Fewer genes than organelles: extremely low and variable gene copy numbers in mitochondria of somatic plant cells [J]. *The Plant Journal*, 2010, 64 (6): 948-959.
- Price AL, Jones NC, Pevzner PA. *De novo* identification of repeat families in large genomes [J]. *Bioinformatics*, 2005a, 21 (suppl_1): i351-i358.
- Price AL, Patterson NJ, Plenge RM, et al. Principal components analysis corrects for stratification in genome-wide association studies [J]. *Nature Genetics*, 2006, 38 (8): 904.
- Price HJ, Dillon SL, Hodnett G, et al. Genome evolution in the genus *Sorghum* (Poaceae) [J]. *Annals of Botany*, 2005b, 95 (1): 219-227.
- Pritchard JK, Stephens M, Donnelly P. Inference of population structure using multilocus genotype data [J]. *Genetics*, 2000, 155 (2): 945-959.
- Prochnik SE, Umen J, Nedelcu AM, et al. Genomic analysis of organismal complexity in the multicellular green alga *Volvox carteri* [J]. *Science*, 2010, 329 (5988): 223-226.
- Project AG. The Amborella genome and the evolution of flowering plants [J]. *Science*, 2013, 342 (6165): 1467.
- Pryszcz LP, Gabaldón T. Redundans: an assembly pipeline for highly heterozygous genomes [J]. *Nucleic Acids Research*, 2016, 44 (12): e113.
- Pucker B, Holtgräwe D, Sörensen TR, et al. A *de Novo* genome sequence assembly of the *Arabidopsis thaliana* accession niederzenn-1 displays presence/absence variation and strong synteny [J]. *Plos One*, 2016, 11 (10): e0164321.
- Purugganan MD, Fuller DQ. The nature of selection during plant domestication [J]. *Nature*, 2009, 457 (7231): 843.

- Putnam NH, O'Connell BL, Stites JC, et al. Chromosome-scale shotgun assembly using an *in vitro* method for long-range linkage [J]. *Genome Research*, 2016, 26 (3): 342-350.
- Qi J, Liu X, Shen D, et al. A genomic variation map provides insights into the genetic basis of cucumber domestication and diversity [J]. *Nature Genetics*, 2013, 45 (12): 1510.
- Qi X, Li MW, Xie M, et al. Identification of a novel salt tolerance gene in wild soybean by whole-genome sequencing [J]. *Nature Communications*, 2014, 5: 4340.
- Qian L, Qian W, Snowdon RJ. Haplotype hitchhiking promotes trait coselection in *Brassica napus* [J]. *Plant Biotechnology Journal*, 2016, 14 (7): 1578-1588.
- Qin C, Yu C, Shen Y, et al. Whole-genome sequencing of cultivated and wild peppers provides insights into *Capsicum* domestication and specialization [J]. *Proceedings of the National Academy of Sciences*, 2014, 111 (14): 5135-5140.
- Qin G, Xu C, Ming R, et al. The pomegranate (*Punica granatum* L.) genome and the genomics of punicalagin biosynthesis [J]. *Plant Journal*, 2017, 91 (6): 1108.
- Qiu D, Morgan C, Shi J, et al. A comparative linkage map of oilseed rape and its use for QTL analysis of seed oil and erucic acid content [J]. *Theoretical and Applied Genetics*, 2006, 114 (1): 67-80.
- Qiu J, Zhou Y, Mao L, et al. Genomic variation associated with local adaptation of weedy rice during domestication [J]. *Nature Communications*, 2017, 8: 15323.
- Qiu J, Zhu J, Fu F, et al. Genome re-sequencing suggested a weedy rice origin from domesticated indica-japonica hybridization: a case study from southern China [J]. *Planta*, 2014, 240 (6): 1353-1363.
- Qu CM, Li SM, Duan XJ, et al. Identification of candidate genes for seed glucosinolate content using association mapping in *Brassica napus* L. [J]. *Genes*, 2015, 6 (4): 1215-1229.
- Qu C, Jia L, Fu F, et al. Genome-wide association mapping and Identification of candidate genes for fatty acid composition in *Brassica napus* L. using SNP markers [J]. *BMC Genomics*, 2017, 18 (1): 232.
- Raissig MT, Baroux C, Grossniklaus U. Regulation and flexibility of genomic imprinting during seed development [J]. *The Plant Cell*, 2011, 23 (1): 16-26.
- Ramírez-González RH, Borrill P, Lang D, et al. The transcriptional landscape of polyploid wheat [J]. *Science*, 2018, 361 (6403): eaar6089.
- Ramos AM, Usié A, Barbosa P, et al. The draft genome sequence of cork oak [J]. *Inorganic Chemistry*, 2018, 5: 180069.
- Ran FA, Hsu PD, Lin CY, et al. Double nicking by RNA-guided *CRISPR Cas9* for enhanced genome editing specificity [J]. *Cell*, 2013, 154 (6): 1380-1389.
- Rao SSP, Huntley MH, Durand NC, et al. A 3D map of the human genome at kilobase resolution reveals principles of chromatin looping [J]. *Cell*, 2014, 159 (7): 1665-1680.
- Ratnayake G, Bain AL, Fletcher N, et al. RNA interference to enhance radiation therapy: Targeting the DNA damage response [J]. *Cancer Letters*, 2018, 439: 14-23.
- Raven JA, Allen JF. Genomics and chloroplast evolution: what did cyanobacteria do for plants? [J]. *Genome Biology*, 2003, 4 (3): 209.
- Raymond O, Gouzy J, Just J, et al. The *Rosa* genome provides new insights into the domestication of modern roses [J]. *Nature Genetics*, 2018, 50 (6): 772-777.

- Raza A, Minowada J, Barcos M, et al. Nobel prizes and restriction enzymes [J]. *Gene*, 1978, 4 (3): 181-182.
- Reagon M, Thurber CS, Olsen KM, et al. The long and the short of it: SD1 polymorphism and the evolution of growth trait divergence in US weedy rice [J]. *Molecular Ecology*, 2011, 20 (18): 3743-3756.
- Regulski M, Lu Z, Kendall J, et al. The maize methylome influences mRNA splice sites and reveals widespread paramutation-like switches guided by small RNA [J]. *Genome Research*, 2013, 23 (10): 1651-1662.
- Reinhart BJ, Weinstein EG, Rhoades MW, et al. MicroRNAs in plants [J]. *Genes & Development*, 2002, 16 (13): 1616-1626.
- Remington DL, Thornsberry JM, Matsuoka Y, et al. Structure of linkage disequilibrium and phenotypic associations in the maize genome [J]. *Proceedings of the National Academy of Sciences*, 2001a, 98 (20): 11479-11484.
- Remington DL, Ungerer MC, Purugganan MD. Map-based cloning of quantitative trait loci: progress and prospects [J]. *Genetics Research*, 2001b, 78 (3): 213-218.
- Rensing SA, Lang D, Zimmer AD, et al. The *Physcomitrella* genome reveals evolutionary insights into the conquest of land by plants [J]. *Science*, 2008, 319 (5859): 64-69.
- Reuter JA, Spacek DV, Snyder MP. High-throughput sequencing technologies [J]. *Molecular Cell*, 2015, 58 (4): 586-597.
- Reuzeau C, Frankard V, Hatzfeld Y, et al. Traitmill™: a functional genomics platform for the phenotypic analysis of cereals [J]. *Plant Genetic Resources*, 2006, 4 (1): 20-24.
- Revilla P, Rodríguez VM, Ordás A, et al. Association mapping for cold tolerance in two large maize inbred panels [J]. *BMC Plant Biology*, 2016, 16 (1): 127.
- Reyes-Chin-Wo S, Wang Z, Yang X, et al. Genome assembly with *in vitro* proximity ligation data and whole-genome triplication in lettuce [J]. *Nature Communications*, 2017, 8: 14953.
- Rhoades MW, Reinhart BJ, Lim LP, et al. Prediction of plant microRNA targets [J]. *Cell*, 2002, 110 (4): 513-520.
- Rice Chromosome 10 Sequencing Consortium. In-depth view of structure, activity, and evolution of rice chromosome 10 [J]. *Science*, 2003, 300 (5625): 1566-1569.
- Richardson SM, Mitchell LA, Stracquandano G, et al. Design of a synthetic yeast genome [J]. *Science*, 2017, 355 (6329): 1040-1044.
- Rieber L, Mahony S. miniMDS: 3D structural inference from high-resolution Hi-C data [J]. *Bioinformatics*, 2017, 33 (14): i261-i266.
- Riedelsheimer C, Brotman Y, Méret M, et al. The maize leaf lipidome shows multilevel genetic control and high predictive value for agronomic traits [J]. *Scientific Reports*, 2013, 3: 2479.
- Riedelsheimer C, Czedik-Eysenberg A, Grieder C, et al. Genomic and metabolic prediction of complex heterotic traits in hybrid maize [J]. *Nature Genetics*, 2012a, 44 (2): 217.
- Riedelsheimer C, Lisec J, Czedik-Eysenberg A, et al. Genome-wide association mapping of leaf metabolic profiles for dissecting complex traits in maize [J]. *Proceedings of the National Academy of Sciences*, 2012b, 109 (23): 8872-8877.
- Ris H, Plaut W. Ultrastructure of DNA-containing areas in the chloroplast of *Chlamydomonas* [J]. *The Journal*

- of Cell Biology, 1962, 13 (3): 383-391.
- Risch N, Merikangas K. The future of genetic studies of complex human diseases [J]. Science, 1996, 273 (5281): 1516-1517.
- Ro DK, Paradise EM, Ouellet M, et al. Production of the antimalarial drug precursor artemisinic acid in engineered yeast [J]. Nature, 2006, 440 (7086): 940.
- Roberts L. Timeline: A History of the Human Genome Project [J]. Science, 2001, 291 (5507): 1195-1200.
- Rodrigues JA, Zilberman D. Evolution and function of genomic imprinting in plants [J]. Genes & Development, 2015, 29 (24): 2517-2531.
- Romay MC, Millard MJ, Glaubitz JC, et al. Comprehensive genotyping of the USA national maize inbred seed bank [J]. Genome Biology, 2013, 14 (6): R55.
- Ross-Ibarra J, Morrell PL, Gaut BS. Plant domestication, a unique opportunity to identify the genetic basis of adaptation [J]. Proceedings of the National Academy of Sciences, 2007, 104 (suppl 1): 8641-8648.
- Roth MS, Cokus SJ, Gallaher SD, et al. Chromosome-level genome assembly and transcriptome of the green alga *Chromochloris zofingiensis* illuminates astaxanthin production [J]. Proceedings of the National Academy of Sciences, 2017, 114 (21): E4296-E4305.
- Rounsley SD, Glodek A, Sutton G, et al. The construction of Arabidopsis expressed sequence tag assemblies (a new resource to facilitate gene identification) [J]. Plant Physiology, 1996, 112 (3): 1177-1183.
- Rousseau M, Fraser J, Ferraiuolo MA, et al. Three-dimensional modeling of chromatin structure from interaction frequency data using Markov Chain Monte Carlo sampling [J]. BMC Bioinformatics, 2011, 12 (1): 414.
- Ruangrak E, Su X, Huang Z, et al. Fine mapping of a major QTL controlling early flowering in tomato using QTL-seq [J]. Canadian Journal of Plant Science, 2018, 98 (3): 672-682.
- Ruban A, Schmutzer T, Scholz U, et al. How next-generation sequencing has aided our understanding of the sequence composition and origin of B chromosomes [J]. Genes, 2017, 8 (11): 294.
- Rushton PJ, Somssich IE, Ringler P, et al. WRKY transcription factors [J]. Trends in Plant Science, 2010, 15 (5): 247-258.
- Sager R, Ishida MR. Chloroplast DNA in *Chlamydomonas* [J]. Proceedings of the National Academy of Sciences, 1963, 50 (4): 725.
- Sahebi M, Hanafi MM, van Wijnen AJ, et al. Contribution of transposable elements in the plants' genome [J]. Gene, 2018, 665: 155-166.
- Sakai H, Ikawa H, Tanaka T, et al. Distinct evolutionary patterns of *Oryza glaberrima* deciphered by genome sequencing and comparative analysis [J]. Plant Journal, 2011, 66 (5): 796.
- Sakai H, Kanamori H, Araikichise Y, et al. Construction of pseudomolecule sequences of the aus rice cultivar kasalath for comparative genomics of Asian cultivated rice [J]. DNA Research, 2014, 21 (4): 1131-1142.
- Sakai H, Lee SS, Tanaka T, et al. Rice Annotation Project Database (RAP-DB): an integrative and interactive database for rice genomics [J]. Plant and Cell Physiology, 2013, 54 (2): e6.
- Sakamoto T, Shibayama M, Kimura A, et al. Assessment of digital camera-derived vegetation indices in quantitative monitoring of seasonal rice growth [J]. ISPRS Journal of Photogrammetry and Remote Sensing, 2011, 66 (6): 872-882.

- Salmela L, Rivals E. LoRDEC: accurate and efficient long read error correction [J]. *Bioinformatics*, 2014, 30 (24): 3506-3514.
- Salojärvi J, Smolander OP, Nieminen K, et al. Genome sequencing and population genomic analyses provide insights into the adaptive landscape of silver birch [J]. *Nature Genetics*, 2017, 49 (6): 904.
- Salzman J, Chen RE, Olsen MN, et al. Cell-type specific features of circular RNA expression [J]. *PLoS Genetics*, 2013, 9 (9): e1003777.
- Samayoa LF, Malvar RA, McMullen MD, et al. Identification of QTL for resistance to Mediterranean corn borer in a maize tropical line to improve temperate germplasm [J]. *BMC Plant biology*, 2015, 15 (1): 265.
- Sander JD, Cade L, Khayter C, et al. Targeted gene disruption in somatic zebrafish cells using engineered TALENs [J]. *Nature Biotechnology*, 2011, 29 (8): 697.
- Sanger F, Air GM, Barrell BG, et al. Nucleotide sequence of bacteriophage $\phi X174$ DNA [J]. *Nature*, 1977a, 265 (5596): 687.
- Sanger F, Brownlee GG, Barrell BG. A two-dimensional fractionation procedure for radioactive nucleotides [J]. *Journal of Molecular Biology*, 1965, 13 (2): 373-IN4.
- Sanger F, Coulson AR, Hong GF, et al. Nucleotide sequence of bacteriophage λ DNA [J]. *Journal of Molecular Biology*, 1982, 162 (4): 729-773.
- Sanger F, Nicklen S, Coulson AR. DNA sequencing with chain-terminating inhibitors [J]. *Proceedings of the National Academy of Sciences*, 1977b, 74 (12): 5463-5467.
- Sanger F. The Croonian Lecture, 1975 Nucleotide sequences in DNA [J]. *Proceedings of the Royal Society of London. Series B. Biological Sciences*, 1975, 191 (1104): 317-333.
- Sanjana NE, Cong L, Zhou Y, et al. A transcription activator-like effector toolbox for genome engineering [J]. *Nature Protocols*, 2012, 7 (1): 171.
- Sasaki T, Matsumoto T, Yamamoto K, et al. The genome sequence and structure of rice chromosome 1 [J]. *Nature*, 2002, 420 (6913): 312.
- Sasaki T, Naumann U, Forai P, et al. Unusual case of apparent hypermutation in *Arabidopsis thaliana* [J]. *Genetics*, 2012, 192 (4): 1271-1280.
- Saski C, Lee S, Daniell H, et al. Complete chloroplast genome sequence of *Glycine max* and comparative analyses with other *Legume* genomes [J]. *Plant Molecular Biology*, 2005, 59 (2): 309-322.
- Sato S, Hirakawa H, Isobe S, et al. Sequence analysis of the genome of an oil-bearing tree, *Jatropha curcas* L. [J]. *DNA Research*, 2010, 18 (1): 65-76.
- Sato S, Nakamura Y, Kaneko T, et al. Complete structure of the chloroplast genome of *Arabidopsis thaliana* [J]. *DNA Research*, 1999, 6 (5): 283-290.
- Sato S, Nakamura Y, Kaneko T, et al. Genome structure of the *Legume*, *Lotus japonicus* [J]. *DNA Research*. 2008, 15 (4): 227-239.
- Satoh K, Ooe K, Nagayama H, et al. *Prototheca cutis* sp. nov. , a newly discovered pathogen of protothecosis isolated from inflamed human skin [J]. *International Journal of Systematic and Evolutionary Microbiology*, 2010, 60 (5): 1236-1240.
- Schatz MC, Maron LG, Stein JC, et al. Whole genome *de novo* assemblies of three divergent strains of rice, *Oryza sativa*, document novel gene space of aus and indica [J]. *Genome Biology*, 2014, 15 (11): 506.

- Scheben A, Edwards D. Genome editors take on crops [J]. *Science*, 2017, 355 (6330): 1122-1123.
- Schena M, Shalon D, Davis RW, et al. Quantitative monitoring of gene expression patterns with a complementary DNA Microarray [J]. *Science*, 1995, 270 (5235): 467-470.
- Schiessl S, Iniguez-Luy F, Qian W, et al. Diverse regulatory factors associate with flowering time and yield responses in winter-type *Brassica napus* [J]. *BMC Genomics*, 2015, 16 (1): 737.
- Schmid KJ, Sørensen TR, Stracke R, et al. Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in *Arabidopsis thaliana* [J]. *Genome Research*, 2003, 13 (6a): 1250-1257.
- Schmitz RJ, Schultz MD, Urich MA, et al. Patterns of population epigenomic diversity [J]. *Nature*, 2013, 495 (7440): 193.
- Schmutz J, Cannon SB, Schlueter J, et al. Genome sequence of the palaeopolyploid soybean [J]. *Nature*, 2010, 465 (7294): 120.
- Schmutz J, Mcclean PE, Mamidi S, et al. A reference genome for common bean and genome-wide analysis of dual domestications [J]. *Nature Genetics*, 2014, 46 (7): 707-713.
- Schmutzer T, Samans B, Dyrszka E, et al. Species-wide genome sequence and nucleotide polymorphisms from the model allopolyploid plant *Brassica napus* [J]. *Scientific Data*, 2015, 2: 150072.
- Schnable PS, Ware D, Fulton RS, et al. The B73 maize genome: complexity, diversity, and dynamics [J]. *Science*, 2009, 326 (5956): 1112-1115.
- Schneeberger K, Ossowski S, Ott F, et al. Reference-guided assembly of four diverse *Arabidopsis thaliana* genomes [J]. *Proceedings of the National Academy of Sciences*, 2011, 108 (25): 10249-10254.
- Schranz ME, Lysak MA, Mitchell-Olds T. The ABC's of comparative genomics in the *Brassicaceae*: building blocks of crucifer genomes [J]. *Trends in Plant Science*, 2006, 11 (11): 535-542.
- Schuler ML, Mantegazza O, Weber APM. Engineering C4 photosynthesis into C3 chassis in the synthetic biology age [J]. *The Plant Journal*, 2016, 87 (1): 51-65.
- Schultze M, Kondorosi A. Regulation of symbiotic root nodule development [J]. *Annual review of Genetics*, 1998, 32 (1): 33-57.
- Secco D, Wang C, Shou H, et al. Stress induced gene expression drives transient DNA methylation changes at adjacent repetitive elements [J]. *Elife*, 2015, 4: e09343.
- Sekhon RS, Briskine R, Hirsch CN, et al. Maize gene atlas developed by RNA sequencing and comparative evaluation of transcriptomes based on RNA sequencing and microarrays [J]. *PLoS One*, 2013, 8 (4): e61005.
- Seki M, Shinozaki K. Functional genomics using RIKEN *Arabidopsis thaliana* full-length cDNAs [J]. *Journal of Plant Research*, 2009, 122 (4): 355-366.
- Serres-Giardi L, Belkhir K, David J, et al. Patterns and evolution of nucleotide landscapes in seed plants [J]. *The Plant Cell*, 2012, 24 (4): 1379-1397.
- Severin AJ, Cannon SB, Graham MM, et al. Changes in twelve homoeologous genomic regions in soybean following three rounds of polyploidy [J]. *The Plant Cell*, 2011, 23 (9): 3129.
- Severin AJ, Woody JL, Bolon Y, et al. RNA-Seq Atlas of *Glycine max*: A guide to the soybean transcriptome [J]. *BMC Plant Biology*, 2010, 10 (1): 160.

- Shahid S, Kim G, Johnson NR, et al. MicroRNAs from the parasitic plant *Cuscuta campestris* target host messenger RNAs [J]. *Nature*, 2018, 553 (7686): 82.
- Shahmuradov IA, Akbarova YY, Solovyev VV, et al. Abundance of plastid DNA insertions in nuclear genomes of rice and *Arabidopsis* [J]. *Plant Molecular Biology*, 2003, 52 (5): 923-934.
- Shalem O, Sanjana NE, Hartenian E, et al. Genome-scale CRISPR-Cas9 knockout screening in human cells [J]. *Science*, 2014, 343 (6166): 84-87.
- Shan B, Marko R, Zhenming G, et al. Genetically engineered cerebral organoids model brain tumor formation [J]. *Nature Methods*, 2018, 15 (8): 631-639.
- Shan Q, Zhang Y, Chen K, et al. Creation of fragrant rice by targeted knockout of the *Os-BADH2* gene using TALEN technology [J]. *Plant Biotechnology Journal*, 2015, 13 (6): 791-800.
- Shan X, Ray DA, Bunge JA, et al. A bacterial artificial chromosome library for the Australian saltwater crocodile (*Crocodylus porosus*) and its utilization in gene isolation and genome characterization [C]. *BMC genomics*, BioMed Central, 2009, 10 (2): S9.
- Shang Y, Ma Y, Zhou Y, et al. Biosynthesis, regulation, and domestication of bitterness in cucumber [J]. *Science*, 2014, 346 (6213): 1084-1088.
- Shao M, Bai G, Rife TW, et al. QTL mapping of pre-harvest sprouting resistance in a white wheat cultivar Danby [J]. *Theoretical and Applied Genetics*, 2018, 131 (8): 1683-1697.
- Shapiro E, Biezuner T, Linnarsson S. Single-cell sequencing-based technologies will revolutionize whole-organism science [J]. *Nature Reviews Genetics*, 2013, 14 (9): 618.
- Shen D, Suhrkamp I, Wang Y, et al. Identification and characterization of micro RNA s in oilseed rape (*Brassica napus*) responsive to infection with the pathogenic fungus *Verticillium longisporum* using Brassica AA (*Brassica rapa*) and CC (*Brassica oleracea*) as reference genomes [J]. *New Phytologist*, 2014a, 204 (3): 577-594.
- Shen D, Wang S, Chen H, et al. Molecular phylogeny of miR390-guided trans-acting siRNA genes (TAS3) in the grass family [J]. *Plant Systematics and Evolution*, 2009, 283 (1-2): 125.
- Shen E, Zhu X, Hua S, et al. Genome-wide identification of oil biosynthesis-related long non-coding RNAs in allopolyploid *Brassica napus* [J]. *BMC Genomics*, 2018a, 19 (1): 745.
- Shen E, Zou J, Hubertus Behrens F, et al. Identification, evolution, and expression partitioning of miRNAs in allopolyploid *Brassica napus* [J]. *Journal of Experimental Botany*, 2015, 66 (22): 7241-7253.
- Shen Y, Liu J, Geng H, et al. *De novo* assembly of a Chinese soybean genome [J]. *Science China Life Sciences*, 2018b, 61 (8): 871-884.
- Shen Y, Sun S, Hua S, et al. Analysis of transcriptional and epigenetic changes in hybrid vigor of allopolyploid *Brassica napus* uncovers key roles for small RNAs [J]. *The Plant Journal*, 2017a, 91 (5): 874-893.
- Shen Y, Wang Y, Chen T, et al. Deep functional analysis of synII, a 770-kilobase synthetic yeast chromosome [J]. *Science*, 2017b, 355 (6329): eaaf4791.
- Shen Y, Zhang J, Liu Y, et al. DNA methylation footprints during soybean domestication and improvement [J]. *Genome Biology*, 2018c, 19 (1): 128.
- Shen Y, Zhou Z, Wang Z, et al. Global dissection of alternative splicing in paleopolyploid soybean [J]. *The Plant Cell*, 2014b, 26 (3): 996.

- Shen YT, Liu J, Geng HY, et al. *De novo* assembly of a Chinese soybean genome [J]. *Science China Life Science*, 2018d, 61 (8): 871-884.
- Shi C, Wang S, Xia EH, et al. Full transcription of the chloroplast genome in photosynthetic eukaryotes [J]. *Scientific Reports*, 2016, 6: 30135.
- Shimura K, Okada A, Okada K, et al. Identification of a biosynthetic gene cluster in rice for momilactones [J]. *Journal of Biological Chemistry*, 2007, 282 (47): 34013-34018.
- Shinozaki K, Ohme M, Tanaka M, et al. The complete nucleotide sequence of the tobacco chloroplast genome: its gene organization and expression [J]. *The EMBO Journal*, 1986, 5 (9): 2043-2049.
- Shirasawa K, Isuzugawa K, Ikenaga M, et al. The genome sequence of sweet cherry (*Prunus avium*) for use in genomics-assisted breeding [J]. *DNA Research*, 2017, 24 (5): 499-508.
- Shomura A, Izawa T, Ebana K, et al. Deletion in a gene associated with grain size increased yields during rice domestication [J]. *Nature Genetics*, 2008, 40 (8): 1023.
- Shukla VK, Doyon Y, Miller JC, et al. Precise genome modification in the crop species *Zea mays* using zinc-finger nucleases [J]. *Nature*, 2009, 459 (7245): 437.
- Si L, Chen J, Huang X, et al. *OsSPL13* controls grain size in cultivated rice [J]. *Nature Genetics*, 2016, 48 (4): 447.
- Siddiqui ZS, Cho JI, Park SH, et al. Phenotyping of rice in salt stress environment using high-throughput infrared imaging [J]. *Acta Botanica Croatica*, 2014, 73 (1): 312-321.
- Silva-Junior DB, Grattapaglia D, Novaes E, et al. Genome assembly of the Pink Ipê (*Handroanthus impetiginosus*, Bignoniaceae), a highly-valued ecologically keystone Neotropical timber forest tree [J]. *Gigascience*, 2017, 7 (1): gix125.
- Simillion C, Vandepoele K, van Montagu MCE, et al. The hidden duplication past of *Arabidopsis thaliana* [J]. *Proceedings of the National Academy of Sciences*, 2002, 99 (21): 13627-13632.
- Simonis M, Klous P, Splinter E, et al. Nuclear organization of active and inactive chromatin domains uncovered by chromosome conformation capture-on-chip (4C) [J]. *Nature Genetics*, 2006, 38 (11): 1348.
- Simpson JT, Workman RE, Zuzarte PC, et al. Detecting DNA cytosine methylation using nanopore sequencing [J]. *Nature Methods*, 2017, 14 (4): 407.
- Singh R, Ong-Abdullah M, Low ET, et al. Oil palm genome sequence reveals divergence of interfertile species in Old and New worlds [J]. *Nature*, 2013, 500 (7462): 335-339.
- Slade AJ, Fuerstenberg SI, Loeffler D, et al. A reverse genetic, nontransgenic approach to wheat crop improvement by TILLING [J]. *Nature Biotechnology*, 2005, 23 (1): 75.
- Sloan DB, Alverson AJ, Chuckalovcak JP, et al. Rapid evolution of enormous, multichromosomal genomes in flowering plant mitochondria with exceptionally high mutation rates [J]. *PLoS Biology*, 2012, 10 (1): e1001241.
- Sloan DB. One ring to rule them all? Genome sequencing provides new insights into the 'master circle' model of plant mitochondrial DNA structure [J]. *New Phytologist*, 2013, 200 (4): 978-985.
- Smallwood SA, Lee HJ, Angermueller C, et al. Single-cell genome-wide bisulfite sequencing for assessing epigenetic heterogeneity [J]. *Nature Methods*, 2014, 11 (8): 817.
- Smith DR. Does cell size impact chloroplast genome size? [J]. *Frontiers in Plant Science*, 2017, 8: 2116.

- Smith D, Lee RW. The mitochondrial and plastid genomes of *Volvox carteri*: bloated molecules rich in repetitive DNA [J]. BMC Genomics, 2009, 10 (1): 1.
- Sollars ES, Harper AL, Kelly LJ, et al. Genome sequence and genetic diversity of European ash trees [J]. Nature, 2016, 541 (7636): 212-216.
- Song BK, Chuah TS, Tam SM, et al. Malaysian weedy rice shows its true stripes: wild *Oryza* and elite rice cultivars shape agricultural weed evolution in Southeast Asia [J]. Molecular Ecology, 2014, 23 (20): 5003-5017.
- Song Q, Hyten DL, Jia G, et al. Development and evaluation of SoySNP50K, a high-density genotyping array for soybean [J]. Plos One, 2013, 8 (1): e54985.
- Song Q, Zhang T, Stelly DM, et al. Epigenomic and functional analyses reveal roles of epialleles in the loss of photoperiod sensitivity during domestication of allotetraploid cottons [J]. Genome Biology, 2017, 18 (1): 99.
- Song R, Llaca V, Messing J. Mosaic organization of orthologous sequences in grass genomes [J]. Genome Research, 2002, 12 (10): 1549-1555.
- Song XJ, Huang W, Shi M, et al. A QTL for rice grain width and weight encodes a previously unknown RING-type E3 ubiquitin ligase [J]. Nature Genetics, 2007, 39 (5): 623.
- Sotelo-Silveira M, Montes RAC, Sotelo-Silveira JR, et al. Entering the next dimension: Plant genomes in 3D [J]. Trends in Plant Science, 2018, 23 (7): 598-612.
- Soucy SM, Huang J, Gogarten JP. Horizontal gene transfer: building the web of life [J]. Nature Reviews Genetics, 2015, 16 (8): 472.
- South PF, Cavanagh AP, Liu HW, et al. Synthetic glycolate metabolism pathways stimulate crop growth and productivity in the field [J]. Science, 2019, 363 (6422): eaat9077.
- Springer NM, Anderson SN, Andorf CM, et al. The maize W22 genome provides a foundation for functional genomics and transposon biology [J]. Nature Genetics, 2018, 50 (9): 1282.
- Springer NM, Ying K, Fu Y, et al. Maize inbreds exhibit high levels of copy number variation (CNV) and presence/absence variation (PAV) in genome content [J]. PLoS Genetics, 2009, 5 (11): e1000734.
- Staňková H, Hastie AR, Chan S, et al. BioNano genome mapping of individual chromosomes supports physical mapping and sequence assembly in complex plant genomes [J]. Plant Biotechnology Journal, 2016, 14 (7): 1523-1531.
- Stern DB, Goldschmidt-Clermont M, Hanson MR. Chloroplast RNA metabolism [J]. Annual Review of Plant Biology, 2010, 61: 125-155.
- Stern DB, Lonsdale DM. Mitochondrial and chloroplast genomes of maize have a 12-kilobase DNA sequence in common [J]. Nature, 1982, 299 (5885): 698.
- Stevens KA, Wegrzyn J, Zimin A, et al. Sequence of the Sugar Pine Megagenome [J]. Genetics, 2016, 204 (4).
- Stevens KA, Woeste K, Chakraborty S, et al. Genomic variation among and within six juglans species [J]. G3 (Bethesda, Md.), 2018, 8 (7): g3-g200030.
- Straub SCK, Cronn RC, Edwards C, et al. Horizontal transfer of DNA from the mitochondrial to the plastid genome and its subsequent evolution in milkweeds (*Apocynaceae*) [J]. Genome Biology and Evolution, 2013, 5 (10): 1872-1885.

- Strigens A, Freitag NM, Gilbert X, et al. Association mapping for chilling tolerance in elite flint and dent maize inbred lines evaluated in growth chamber and field experiments [J]. *Plant, Cell & Environment*, 2013, 36 (10): 1871-1887.
- Stroud H, Greenberg MVC, Feng S, et al. Comprehensive analysis of silencing mutants reveals complex regulation of the *Arabidopsis* methylome [J]. *Cell*, 2013, 152 (1-2): 352-364.
- Su J, Li L, Zhang C, et al. Genome-wide association study identified genetic variations and candidate genes for plant architecture component traits in Chinese upland cotton [J]. *Theoretical and Applied Genetics*, 2018, 131 (6): 1299-1314.
- Subramanian S, Fu Y, Sunkar R, et al. Novel and nodulation-regulated microRNAs in soybean roots [J]. *BMC Genomics*, 2008, 9 (1): 160.
- Sun F, Fan G, Hu Q, et al. The high - quality genome of *Brassica napus* cultivar ‘ZS 11’ reveals the introgression history in semi - winter morphotype [J]. *The Plant Journal*, 2017a, 92 (3): 452-468.
- Sun H, Wu S, Zhang G, et al. Karyotype stability and unbiased fractionation in the paleo-allotetraploid *Cucurbita* genomes [J]. *Molecular Plant*, 2017b, 10 (10): 1293-1306.
- Sun J, Ma D, Tang L, et al. Population genomic analysis and *de novo* assembly reveal the origin of weedy rice as an evolutionary game [J]. *Molecular Plant*, 2019, 12 (5): 632-647.
- Sun J, Qian Q, Ma DR, et al. Introgression and selection shaping the genome and adaptive loci of weedy rice in northern China [J]. *New Phytologist*, 2013, 197 (1): 290-299.
- Sun L, Miao Z, Cai C, et al. GmHs1-1, encoding a calcineurin-like protein, controls hard-seededness in soybean [J]. *Nature Genetics*, 2015, 47 (8): 939.
- Sun S, Zhou Y, Chen J, et al. Extensive intraspecific gene order and gene structural variations between Mo17 and other maize genomes [J]. *Nature Genetics*, 2018, 50 (9): 1289.
- Sun Z, Wang X, Liu Z, et al. Genome - wide association study discovered genetic variation and candidate genes of fibre quality traits in *Gossypium hirsutum* L. [J]. *Plant Biotechnology Journal*, 2017c, 15 (8): 982-996.
- Sunkar R, Li YF, Jagadeeswaran G. Functions of microRNAs in plant stress responses [J]. *Trends in Plant Science*, 2012, 17 (4): 196-203.
- Sunkar R, Zhou X, Zheng Y, et al. Identification of novel and candidate miRNAs in rice by high throughput sequencing [J]. *BMC Plant Biology*, 2008, 8 (1): 25.
- Suwarno WB, Pixley KV, Palacios-Rojas N, et al. Genome-wide association analysis reveals new targets for carotenoid biofortification in maize [J]. *Theoretical and Applied Genetics*, 2015, 128 (5): 851-864.
- Svab Z, Hajdukiewicz P, Maliga P. Stable transformation of plastids in higher plants [J]. *Proceedings of the National Academy of Sciences*, 1990, 87 (21): 8526-8530.
- Svitashev S, Schwartz C, Lenderts B, et al. Genome editing in maize directed by CRISPR-Cas9 ribonucleoprotein complexes [J]. *Nature Communications*, 2016, 7: 13274.
- Swift H, The Constancy of Desoxyribose Nucleic Acid in Plant Nuclei [J]. *Proceedings of the National Academy of Sciences*, 1950, 36 (11): 643-654.
- Tabuchi H, Zhang Y, Hattori S, et al. LAX PANICLE2 of rice encodes a novel nuclear protein and regulates the formation of axillary meristems [J]. *The Plant Cell*, 2011, 23 (9): 3276-3287.

- Tajima F. DNA polymorphism in a subdivided population: the expected number of segregating sites in the two-subpopulation model [J]. *Genetics*, 1989, 123 (1): 229-240.
- Takagi H, Abe A, Yoshida K, et al. QTL - seq: rapid mapping of quantitative trait loci in rice by whole genome resequencing of DNA from two bulked populations [J]. *The Plant Journal*, 2013, 74 (1): 174-183.
- Tan L, Li X, Liu F, et al. Control of a key transition from prostrate to erect growth in rice domestication [J]. *Nature Genetics*, 2008, 40 (11): 1360.
- Tanaka H, Hirakawa H, Kosugi S, et al. Sequencing and comparative analyses of the genomes of zoysiagrasses [J]. *DNA Research*, 2016, 23 (2): dsw006.
- Tang F, Barbacioru C, Wang Y, et al. mRNA-Seq whole-transcriptome analysis of a single cell [J]. *Nature Methods*, 2009, 6 (5): 377.
- Tang H, Bowers JE, Wang X, et al. Synteny and collinearity in plant genomes [J]. *Science*, 2008, 320 (5875): 486-488.
- Tang H, Zhang X, Miao C, et al. ALLMAPS: robust scaffold ordering based on multiple maps [J]. *Genome Biology*, 2015a, 16 (1): 3.
- Tang H, Zheng X, Li C, et al. Multi-step formation, evolution, and functionalization of new cytoplasmic male sterility genes in the plant mitochondrial genomes [J]. *Cell Research*, 2017a, 27 (1): 130.
- Tang JD, Perkins A, Williams WP, et al. Using genome-wide associations to identify metabolic pathways involved in maize aflatoxin accumulation resistance [J]. *BMC Genomics*, 2015b, 16 (1): 673.
- Tang J, Chu C. MicroRNAs in crop improvement: Fine-tuners for complex traits [J]. *Nature Plants*, 2017b, 3 (7): 17077.
- Tarca AL, Carey VJ, Chen X, et al. Machine learning and its applications to biology [J]. *PLoS Computational Biology*, 2007, 3 (6): e116.
- Teh BT, Lim K, Yong CH, et al. The draft genome of tropical fruit durian (*Durio zibethinus*) [J]. *Nature Genetics*, 2017, 49 (11): 1633-1641.
- Tenaillon MI, Sawkins MC, Long AD, et al. Patterns of DNA sequence polymorphism along chromosome 1 of maize (*Zea mays* ssp. *mays* L.) [J]. *Proceedings of the National Academy of Sciences*, 2001, 98 (16): 9161-9166.
- Terasawa K, Odahara M, Kabeya Y, et al. The mitochondrial genome of the moss *Physcomitrella patens* sheds new light on mitochondrial evolution in land plants [J]. *Molecular Biology and Evolution*, 2006, 24 (3): 699-709.
- Tettelin H, Massignani V, Cieslewicz MJ, et al. Genome analysis of multiple pathogenic isolates of *Streptococcus agalactiae*: implications for the microbial “pan-genome” [J]. *Proceedings of the National Academy of Sciences*, 2005, 102 (39): 13950-13955.
- Tettelin H, Riley D, Cattuto C, et al. Comparative genomics: the bacterial pan-genome [J]. *Current Opinion in Microbiology*, 2008, 11 (5): 472-477.
- The 1001 Genomes Consortium. 1, 135 Genomes Reveal the global pattern of polymorphism in *Arabidopsis thaliana* [J]. *Cell*, 2016 166 (2): 481-491.
- Theologis A, Ecker JR, Palm CJ, et al. Sequence and analysis of chromosome 1 of the plant *Arabidopsis thaliana* [J]. *Nature*, 2000, 408 (6814): 816.

- Thirunavukkarasu N, Hossain F, Arora K, et al. Functional mechanisms of drought tolerance in subtropical maize (*Zea mays* L.) identified using genome-wide association mapping [J]. BMC Genomics, 2014, 15 (1): 1182.
- Tian F, Bradbury PJ, Brown PJ, et al. Genome-wide association study of leaf architecture in the maize nested association mapping population [J]. Nature Genetics, 2011, 43 (2): 159.
- Tian X, Zheng J, Hu S, et al. The rice mitochondrial genomes and their variations [J]. Plant Physiology, 2006, 140 (2): 401-410.
- Tian Z, Wang X, Lee R, et al. Artificial selection for determinate growth habit in soybean [J]. Proceedings of the National Academy of Sciences, 2010, 107 (19): 8563.
- Tieman D, Zhu G, Resende MFR, et al. A chemical genetic roadmap to improved tomato flavor [J]. Science, 2017, 355 (6323): 391-394.
- Till BJ, Reynolds SH, Weil C, et al. Discovery of induced point mutations in maize genes by TILLING [J]. BMC Plant Biology, 2004, 4 (1): 12.
- Timmermans MCP, Brutnell TP, Becraft PW. The 46th annual maize genetics conference. unlocking the secrets of the maize genome [J]. Plant Physiology, 2004, 136 (1): 2633-2640.
- Tomato Genome Consortium. The tomato genome sequence provides insights into fleshy fruit evolution [J]. Nature, 2012, 485 (7400): 635.
- Townsend JA, Wright DA, Winfrey RJ, et al. High-frequency modification of plant genes using engineered zinc-finger nucleases [J]. Nature, 2009, 459 (7245): 442.
- Trick M, Long Y, Meng J, et al. Single nucleotide polymorphism (SNP) discovery in the polyploid *Brassica napus* using Solexa transcriptome sequencing [J]. Plant Biotechnology Journal, 2009, 7 (4): 334-346.
- Trieu T, Cheng J. Large-scale reconstruction of 3D structures of human chromosomes from chromosomal contact data [J]. Nucleic Acids Research, 2014, 42 (7): e52.
- Troyer AF. Adaptedness and heterosis in corn and mule hybrids [J]. Crop Science, 2006, 46 (2): 528-543.
- Tsuruta H, Paddon CJ, Eng D, et al. High-level production of amorph-4, 11-diene, a precursor of the antimalarial agent artemisinin, in *Escherichia coli* [J]. PLoS One, 2009, 4 (2): e4489.
- Tucker EJ, Baumann U, Kouidri A, et al. Molecular identification of the wheat male fertility gene *Ms1* and its prospects for hybrid breeding [J]. Nature Communications, 2017, 8 (1): 869.
- Tulpan D, Leger S. The plant Orthology browser: an Orthology and gene-order visualizer for plant comparative genomics [J]. The Plant Genome, 2017, 10 (1).
- Turumtay H, Sandall C, Turumtay EA. Plant Metabolomics and Strategies [M]. Plant Omics: Trends and Applications. Springer, Cham, 2016: 399-406.
- Tuskan GA, Difazio S, Jansson S, et al. The Genome of Black Cottonwood, *Populus trichocarpa* (Torr. & Gray) [J]. Science, 2006, 313 (5793): 1596-1604.
- Udvardi MK, Kakar K, Wandrey M, et al. Legume transcription factors: global regulators of plant development and response to the environment [J]. Plant Physiology, 2007, 144 (2): 538-549.
- Unseld M, Marienfeld JR, Brandt P, et al. The mitochondrial genome of *Arabidopsis thaliana* contains 57 genes in 366,924 nucleotides [J]. Nature Genetics, 1997, 15 (1): 57.
- Unterseer S, Seidel MA, Bauer E, et al. European Flint reference sequences complement the maize pan-

- genome [J]. *BioRxiv*, 2017: 103747.
- Urasaki N, Takagi H, Natsume S, et al. Draft genome sequence of bitter melon (*Momordica charantia*), a vegetable and medicinal plant in tropical and subtropical regions [J]. *DNA Research*, 2016, 24 (1): 51-58.
- van de Peer Y, Mizrahi E, Marchal K. The evolutionary significance of polyploidy [J]. *Nature Reviews Genetics*, 2017, 18 (7): 411.
- van Dijk ADJ. Species-Specific Genome Sequence Databases: A Practical Review [M]//*Plant Genomics Databases*. New York: Humana Press, 2017: 173-181.
- van Inghelandt D, Melchinger AE, Martinant JP, et al. Genome-wide association mapping of flowering time and northern corn leaf blight (*Setosphaeria turcica*) resistance in a vast commercial maize germplasm set [J]. *BMC Plant Biology*, 2012, 12 (1): 56.
- Vanburen R, Bryant D, Bushakra JM, et al. The genome of black raspberry (*Rubus occidentalis*) [J]. *Plant Journal*, 2016, 87 (6): 535-547.
- Vanneste K, Baele G, Maere S, et al. Analysis of 41 plant genomes supports a wave of successful genome duplications in association with the Cretaceous–Paleogene boundary [J]. *Genome Research*, 2014, 24 (8): 1334-1347.
- Varshney RK, Chen W, Li Y, et al. Draft genome sequence of pigeonpea (*Cajanus cajan*), an orphan legume crop of resource-poor farmers [J]. *Nature Biotechnology*, 2012, 30 (1): 83-89.
- Varshney RK, Song C, Saxena RK, et al. Draft genome sequence of chickpea (*Cicer arietinum*) provides a resource for trait improvement [J]. *Nature Biotechnology*, 2013, 31 (3): 240-246.
- Vega JJD, Ayling S, Hegarty M, et al. Red clover (*Trifolium pratense* L.) draft genome provides a platform for trait improvement [J]. *Scientific Reports*, 2015, 5: 17394.
- Velasco R, Zharkikh A, Affourtit J, et al. The genome of the domesticated apple (*Malus × domestica* Borkh.) [J]. *Nature Genetics*, 2010, 42 (10): 833.
- Verde I, Abbott AG, Scalabrin S, et al. The high-quality draft genome of peach (*Prunus persica*) identifies unique patterns of genetic diversity, domestication and genome evolution [J]. *Nature Genetics*, 2013, 45 (5): 487-494.
- Vicient CM, Suoniemi A, Ananthawat-Jónsson K, et al. Retrotransposon BARE-1 and its role in genome evolution in the genus *Hordeum* [J]. *The Plant Cell*, 1999, 11 (9): 1769-1784.
- Vielle-Calzada JP, de la Vega OM, Hernández-Guzmán G, et al. The Palomero genome suggests metal effects on domestication [J]. *Science*, 2009, 326 (5956): 1078-1078.
- Vielle-Calzada JP, Thomas J, Spillane C, et al. Maintenance of genomic imprinting at the *Arabidopsis medea* locus requires zygotic DDM1 activity [J]. *Genes & Development*, 1999, 13 (22): 2971-2982.
- Vining KJ, Johnson SR, Ahkami A, et al. Draft genome sequence of *Mentha longifolia* and development of resources for mint cultivar improvement [J]. *Molecular Plant*, 2017, 10 (2): 323-339.
- Vision TJ, Brown DG, Tanksley SD. The origins of genomic duplications in *Arabidopsis* [J]. *Science*, 2000, 290 (5499): 2114-2117.
- Vitti JJ, Grossman SR, Sabeti PC. Detecting natural selection in genomic data [J]. *Annual Review of Genetics*, 2013, 47: 97-120.
- Vlasova A, Capella-Gutiérrez S, Rendón-Anaya M, et al. Genome and transcriptome analysis of the

- Mesoamerican common bean and the role of gene duplications in establishing tissue and temporal specialization of genes [J]. *Genome Biology*, 2016, 17 (1): 32.
- Vogel H, Badapanda C, Knorr E, et al. RNA - sequencing analysis reveals abundant developmental stage - specific and immunity - related genes in the pollen beetle *Meligethes aeneus* [J]. *Insect Molecular Biology*, 2014, 23 (1): 98-112.
- Vrána J, Kubaláková M, Simková H, et al. Flow sorting of mitotic chromosomes in common wheat (*Triticum aestivum* L.) [J]. *Genetics*, 2000, 156 (4): 2033-2041.
- Vurtture GW, Sedlazeck FJ, Nattestad M, et al. GenomeScope: Fast reference-free genome profiling from short reads [J]. *Bioinformatics*, 2017, 33 (14): 2202-2204.
- Wagner DE, Weinreb C, Collins ZM, et al. Single-cell mapping of gene expression landscapes and lineage in the zebrafish embryo [J]. *Science*, 2018, 360 (6392): 981-987.
- Wakasugi T, Nagai T, Kapoor M, et al. Complete nucleotide sequence of the chloroplast genome from the green alga *Chlorella vulgaris*: the existence of genes possibly involved in chloroplast division [J]. *Proceedings of the National Academy of Sciences*, 1997, 94 (11): 5967-5972.
- Wakasugi T, Tsudzuki T, Sugiura M. The genomics of land plant chloroplasts: gene content and alteration of genomic information by RNA editing [J]. *Photosynthesis Research*, 2001, 70 (1): 107-118.
- Walker BJ, Abeel T, Shea T, et al. Pilon: an integrated tool for comprehensive microbial variant detection and genome assembly improvement [J]. *PloS One*, 2014, 9 (11): e112963.
- Wallace JG, Rodgers-Melnick E, Buckler ES. On the road to Breeding 4. 0: unraveling the good, the bad, and the boring of crop quantitative genomics [J]. *Annual Review of Genetics*, 2018, 52: 421-444.
- Wambugu PW, Brozynska M, Furtado A, et al. Relationships of wild and domesticated rices (*Oryza* AA genome species) based upon whole chloroplast genome sequences [J]. *Scientific Reports*, 2015, 5: 13957.
- Wan Q, Guan X, Yang N, et al. Small interfering RNAs from bidirectional transcripts of GhMML3_A12 regulate cotton fiber development [J]. *New Phytologist*, 2016, 210 (4): 1298-1310.
- Wang BB, Brendel V. Genomewide comparative analysis of alternative splicing in plants [J]. *Proceedings of the National Academy of Sciences*, 2006a, 103 (18): 7175-7180.
- Wang B, Tseng E, Regulski M, et al. Unveiling the complexity of the maize transcriptome by single-molecule long-read sequencing [J]. *Nature Communications*, 2016a, 7: 11708.
- Wang B, Wu Z, Li Z, et al. Dissection of the genetic architecture of three seed - quality traits and consequences for breeding in *Brassica napus* [J]. *Plant Biotechnology Journal*, 2018a, 16 (7): 1336-1348.
- Wang B, Xue J, Li L, et al. The complete mitochondrial genome sequence of the liverwort *Pleurozia purpurea* reveals extremely conservative mitochondrial genome evolution in liverworts [J]. *Current Genetics*, 2009a, 55 (6): 601-609.
- Wang B, Zhu L, Zhao B, et al. Development of a Haploid-Inducer Mediated Genome Editing (IMGE) System for Accelerating Maize Breeding [J]. *Molecular Plant*, 2019a, 12 (4): 597-602.
- Wang C, Liu Q, Shen Y, et al. Clonal seeds from hybrid rice by simultaneous genome engineering of meiosis and fertilization genes [J]. *Nature Biotechnology*, 2019b, 37 (3): 283.
- Wang D, Liang G, Wang B, et al. Systematic microRNAome profiling reveals the roles of microRNAs in milk protein metabolism and quality: insights on low-quality forage utilization [J]. *Scientific Reports*, 2016b, 6:

21194.

- Wang D, Rousseau-Gueutin M, Timmis JN. Plastid sequences contribute to some plant mitochondrial genes [J]. *Molecular Biology and Evolution*, 2012a, 29 (7): 1707-1711.
- Wang D, Wu YW, Shih ACC, et al. Transfer of chloroplast genomic DNA to mitochondrial genome occurred at least 300 mya [J]. *Molecular Biology and Evolution*, 2007a, 24 (9): 2040-2048.
- Wang E, Wang J, Zhu X, et al. Control of rice grain-filling and yield by a gene with a potential signature of domestication [J]. *Nature Genetics*, 2008, 40 (11): 1370.
- Wang HLV, Chekanova JA. Long Noncoding RNAs in Plants [M]. *Long Non Coding RNA Biology*, Singapore: Springer, 2017: 133-154.
- Wang H, Chua NH, Wang XJ. Prediction of trans-antisense transcripts in *Arabidopsis thaliana* [J]. *Genome Biology*, 2006b, 7 (10): R92.
- Wang H, Chung PJ, Liu J, et al. Genome-wide identification of long noncoding natural antisense transcripts and their responses to light in *Arabidopsis* [J]. *Genome Research*, 2014a, 24 (3): 444-453.
- Wang H, Wu J, Sun S, et al. Glucosinolate biosynthetic genes in *Brassica rapa* [J]. *Gene*, 2011a, 487 (2): 135-142.
- Wang H, Xu X, Vieira FG, et al. The power of inbreeding: NGS-based GWAS of rice reveals convergent evolution during rice domestication [J]. *Molecular Plant*, 2016c, 9 (7): 975-985.
- Wang J, Fan HC, Behr B, et al. Genome-wide single-cell analysis of recombination activity and de novo mutation rates in human sperm [J]. *Cell*, 2012b, 150 (2): 402-412.
- Wang J, Meng X, Dobrovolskaya OB, et al. Non-coding RNAs and their roles in stress response in plants [J]. *Genomics, Proteomics & Bioinformatics*, 2017a, 15 (5): 301-312.
- Wang K, Gao F, Ji Y, et al. ORFH 79 impairs mitochondrial function via interaction with a subunit of electron transport chain complex- III in H-onglian cytoplasmic male sterile rice [J]. *New Phytologist*, 2013a, 198 (2): 408-418.
- Wang K, Wang Z, Li F, et al. The draft genome of a diploid cotton *Gossypium raimondii* [J]. *Nature Genetics*, 2012c, 44 (10): 1098.
- Wang L, Beissinger TM, Lorant A, et al. The interplay of demography and selection during maize domestication and expansion [J]. *Genome Biology*, 2017b, 18 (1): 215.
- Wang L, He F, Huang Y, et al. Genome of wild mandarin and domestication history of mandarin [J]. *Molecular Plant*, 2018b, 11 (8): 1024-1037.
- Wang L, Sun S, Jin J, et al. Coordinated regulation of vegetative and reproductive branching in rice [J]. *Proceedings of the National Academy of Sciences*, 2015a, 112 (50): 15504-15509.
- Wang L, Zhang Q. Boosting rice yield by fine-tuning SPL gene expression [J]. *Trends in Plant Science*, 2017c, 22 (8): 643-646.
- Wang M, Li W, Fang C, et al. Parallel selection on a dormancy gene during domestication of crops from multiple families [J]. *Nature Genetics*, 2018c, 50 (10): 1435.
- Wang M, Tu L, Lin M, et al. Asymmetric subgenome selection and *cis*-regulatory divergence during cotton domestication [J]. *Nature Genetics*, 2017d, 49 (4): 579.
- Wang M, Tu L, Yuan D, et al. Reference genome sequences of two cultivated allotetraploid cottons,

- Gossypium hirsutum* and *Gossypium barbadense* [J]. *Nature Genetics*, 2019c, 51 (2): 224.
- Wang M, Wang P, Lin M, et al. Evolutionary dynamics of 3D genome architecture following polyploidization in cotton [J]. *Nature Plants*, 2018d, 4 (2): 90.
- Wang M, Wang Q, Zhang B. Response of miRNAs and their targets to salt and drought stresses in cotton (*Gossypium hirsutum* L.) [J]. *Gene*, 2013b, 530 (1): 26-32.
- Wang M, Yu Y, Haberer G, et al. The genome sequence of African rice (*Oryza glaberrima*) and evidence for independent domestication [J]. *Nature Genetics*, 2014b, 46 (9): 982.
- Wang M, Yuan D, Tu L, et al. Long noncoding RNAs and their proposed functions in fibre development of cotton (*Gossypium* spp.) [J]. *New Phytologist*, 2015f, 207 (4): 1181-1197.
- Wang N, Thomson M, Bodles WJ, et al. Genome sequence of dwarf birch (*Betula nana*) and cross-species RAD markers [J]. *Molecular Ecology*, 2013c, 22 (11): 3098-3111.
- Wang S, Chen J, Zhang W, et al. Sequence-based ultra-dense genetic and physical maps reveal structural variations of allopolyploid cotton genomes [J]. *Genome Biology*, 2015b, 16 (1): 108.
- Wang S, Li S, Liu Q, et al. The OsSPL16-GW7 regulatory module determines grain shape and simultaneously improves rice yield and grain quality [J]. *Nature Genetics*, 2015c, 47 (8): 949.
- Wang S, Liu K, Zhang Q. Segmental duplications are common in rice genome [J]. *Acta Botanica Sinica*, 2000, 42 (11): 1150-1155.
- Wang S, Lv J, Zhang L, et al. MethyLRAD: a simple and scalable method for genome-wide DNA methylation profiling using methylation-dependent restriction enzymes [J]. *Open biology*, 2015d, 5 (11): 150130.
- Wang S, Wang JW, Yu N, et al. Control of plant trichome development by a cotton fiber MYB gene [J]. *The Plant Cell*, 2004, 16 (9): 2323-2334.
- Wang S, Wu K, Yuan Q, et al. Control of grain size, shape and quality by *OsSPL16* in rice [J]. *Nature Genetics*, 2012d, 44 (8): 950.
- Wang S, Zhu QH, Guo X, et al. Molecular evolution and selection of a gene encoding two tandem microRNAs in rice [J]. *FEBS Letters*, 2007b, 581 (24): 4789-4793.
- Wang T, Wei JJ, Sabatini DM, et al. Genetic screens in human cells using the *CRISPR-Cas9* system [J]. *Science*, 2014c, 343 (6166): 80-84.
- Wang W, Feng B, Xiao J, et al. Cassava genome from a wild ancestor to cultivated varieties [J]. *Nature Communications*, 2014d, 5 (5): 5110.
- Wang W, Mauleon R, Hu Z, et al. Genomic variation in 3, 010 diverse accessions of Asian cultivated rice [J]. *Nature*, 2018e, 557 (7703): 43.
- Wang W, Zhou X, Xiong H, et al. Papain-like and legumain-like proteases in rice: genome-wide identification, comprehensive gene feature characterization and expression analysis [J]. *BMC Plant Biology*, 2018f, 18 (1): 87.
- Wang XC, Chen H, Yang D, et al. Diversity of mitochondrial plastid DNAs (MTPTs) in seed plants [J]. *Mitochondrial DNA Part A*, 2018g, 29 (4): 635-642.
- Wang XJ, Gaasterland T, Chua NH. Genome-wide prediction and identification of *cis*-natural antisense transcripts in *Arabidopsis thaliana* [J]. *Genome Biology*, 2005a, 6 (4): R30.
- Wang X, Jin D, Wang Z, et al. Telomere - centric genome repatterning determines recurring chromosome

- number reductions during the evolution of eukaryotes [J]. *New Phytologist*, 2015e, 205 (1): 378-389.
- Wang X, Shi X, Hao B, et al. Duplication and DNA segmental loss in the rice genome: implications for diploidization [J]. *New Phytologist*, 2005b, 165 (3): 937-946.
- Wang X, Shi X, Li Z, et al. Statistical inference of chromosomal homology based on gene colinearity and applications to *Arabidopsis* and rice [J]. *BMC Bioinformatics*, 2006c, 7 (1): 447.
- Wang X, Tang H, Bowers JE, et al. Comparative inference of illegitimate recombination between rice and sorghum duplicated genes produced by polyploidization [J]. *Genome Research*, 2009b, 19 (6): 1026-1032.
- Wang X, Tang H, Paterson AH. Seventy million years of concerted evolution of a homoeologous chromosome pair, in parallel, in major *Poaceae* lineages [J]. *The Plant Cell*, 2011b, 23 (1): 27-37.
- Wang X, Wang H, Liu S, et al. Genetic variation in *ZmVPP1* contributes to drought tolerance in maize seedlings [J]. *Nature Genetics*, 2016d, 48 (10): 1233.
- Wang X, Wang H, Wang J, et al. The genome of the mesopolyploid crop species *Brassica rapa* [J]. *Nature Genetics*, 2011c, 43 (10): 1035.
- Wang X, Wang J, Jin D, et al. Genome alignment spanning major *Poaceae* lineages reveals heterogeneous evolutionary rates and alters inferred dates for key evolutionary events [J]. *Molecular Plant*, 2015f, 8 (6): 885-898.
- Wang X, Xu Y, Zhang S, et al. Genomic analyses of primitive, wild and cultivated *Citrus* provide insights into asexual reproduction [J]. *Nature Genetics*, 2017e, 49 (5): 765-772.
- Wang Y, Cao L, Zhang Y, et al. Map-based cloning and characterization of BPH29, a B3 domain-containing recessive gene conferring brown planthopper resistance in rice [J]. *Journal of experimental botany*, 2015g, 66 (19): 6035-6045.
- Wang Y, Cheng X, Shan Q, et al. Simultaneous editing of three homoeoalleles in hexaploid bread wheat confers heritable resistance to powdery mildew [J]. *Nature Biotechnology*, 2014e, 32 (9): 947.
- Wang Y, Chu P, Yang Q, et al. Complete mitochondrial genome of *Eruca sativa* Mill (Garden rocket) [J]. *PloS One*, 2014f, 9 (8): e105748.
- Wang Y, Fan G, Liu Y, et al. The sacred lotus genome provides insights into the evolution of flowering plants [J]. *Plant Journal*, 2013d, 76 (4): 557-567.
- Wang Y, Li P, Cao X, et al. Identification and expression analysis of miRNAs from nitrogen-fixing soybean nodules [J]. *Biochemical and Biophysical Research Communications*, 2009c, 378 (4): 799-803.
- Wang Y, Navin NE. Advances and applications of single-cell sequencing technologies [J]. *Molecular Cell*, 2015h, 58 (4): 598-609.
- Wang Y, Shen D, Bo S, et al. Sequence variation and selection of small RNAs in domesticated rice [J]. *BMC Evolutionary Biology*, 2010, 10 (1): 119.
- Wang ZY, Zheng FQ, Shen GZ, et al. The amylose content in rice endosperm is related to the post-transcriptional regulation of the waxy gene [J]. *The Plant Journal*, 1995, 7 (4): 613-622.
- Wang Z, Li J, Chen S, et al. *Poaceae*-specific *MS1* encodes a phospholipid-binding protein for male fertility in bread wheat [J]. *Proceedings of the National Academy of Sciences*, 2017f, 114 (47): 12614-12619.
- Warburton ML, Tang JD, Windham GL, et al. Genome-wide association mapping of *Aspergillus flavus* and aflatoxin accumulation resistance in maize [J]. *Crop Science*, 2015, 55 (5): 1857-1867.

- Washburn JD, Mejia-Guerra MK, Ramstein G, et al. Evolutionarily informed deep learning methods for predicting relative transcript abundance from DNA sequence [J]. *Proceedings of the National Academy of Sciences*, 2019, 116 (12): 5542-5549.
- Weber APM, Weber KL, Carr K, et al. Sampling the *Arabidopsis* transcriptome with massively parallel pyrosequencing [J]. *Plant physiology*, 2007, 144 (1): 32-42.
- Weeks DP, Spalding MH, Yang B. Use of designer nucleases for targeted gene and genome editing in plants [J]. *Plant Biotechnology Journal*, 2016, 14 (2): 483-495.
- Wei C, Yang H, Wang S, et al. Draft genome sequence of *Camellia sinensis* var. *sinensis* provides insights into the evolution of the tea genome and tea quality [J]. *Proceedings of the National Academy of Sciences*, 2018, 115 (18): 201719622.
- Wei D, Mei J, Fu Y, et al. Quantitative trait loci analyses for resistance to *Sclerotinia sclerotiorum* and flowering time in *Brassica napus* [J]. *Molecular Breeding*, 2014, 34 (4): 1797-1804.
- Wei L, Jian H, Lu K, et al. Genome - wide association analysis and differential expression analysis of resistance to *Sclerotinia* stem rot in *Brassica napus* [J]. *Plant Biotechnology Journal*, 2016, 14 (6): 1368-1380.
- Weigel D, Nordborg M. Population genomics for understanding adaptation in wild plant species [J]. *Annual Review of Genetics*, 2015, 49: 315-338.
- Wen W, Li D, Li X, et al. Metabolome-based genome-wide association study of maize kernel leads to novel biochemical insights [J]. *Nature Communications*, 2014, 5: 3438.
- Wendel JF, Grover CE. Taxonomy and evolution of the cotton genus, *Gossypium* [J]. *Cotton*, 2015 (agronmonogr57): 25-44.
- Wendel JF, Jackson SA, Meyers BC, et al. Evolution of plant genome architecture [J]. *Genome Biology*, 2016, 17 (1): 37.
- Wendel JF. Genome evolution in polyploids [M]. *Plant molecular evolution*, Dordrecht: Springer, 2000: 225-249.
- Wendel JF. The wondrous cycles of polyploidy in plants [J]. *American Journal of Botany*, 2015, 102 (11): 1753-1756.
- Weng J, Gu S, Wan X, et al. Isolation and initial characterization of GW5, a major QTL associated with rice grain width and weight [J]. *Cell Research*, 2008, 18 (12): 1199.
- Weng J, Xie C, Hao Z, et al. Genome-wide association study identifies candidate genes that affect plant height in Chinese elite maize (*Zea mays* L.) inbred lines [J]. *PLoS One*, 2011, 6 (12): e29229.
- Werner JE, Endo TR, Gill BS. Toward a cytogenetically based physical map of the wheat genome [J]. *Proceedings of the National Academy of Sciences*, 1992, 89 (23): 11307-11311.
- Wing RA, Purugganan MD, Zhang Q. The rice genome revolution: from an ancient grain to Green Super Rice [J]. *Nature Reviews Genetics*, 2018: 1.
- Woese CR, Kandler O, Wheelis ML. Towards a natural system of organisms: proposal for the domains Archaea, Bacteria, and Eucarya [J]. *Proceedings of the National Academy of Sciences*, 1990, 87 (12): 4576-4579.
- Wojciechowski MF, Lavin M, Sanderson MJ. A phylogeny of legumes (Leguminosae) based on analyses of

- the plastid matK gene resolves many well-supported subclades within the family [J]. *American Journal of Botany*, 2004, 91 (11): 1846-1862.
- Wolfe KH, Li WH, Sharp PM. Rates of nucleotide substitution vary greatly among plant mitochondrial, chloroplast, and nuclear DNAs [J]. *Proceedings of the National Academy of Sciences*, 1987, 84 (24): 9054-9058.
- Wolfe KH, Li WH. Molecular evolution meets the genomics revolution [J]. *Nature Genetics*, 2003, 33 (3s): 255.
- Wolfe KH, Shields DC. Molecular evidence for an ancient duplication of the entire yeast genome [J]. *Nature*, 1997, 387 (6634): 708.
- Worden AZ, Lee JH, Mock T, et al. Green evolution and dynamic adaptations revealed by genomes of the marine picoeukaryotes *Micromonas* [J]. *Science*, 2009, 324 (5924): 268-272.
- Wu D, Liang Z, Yan T, et al. Whole-genome resequencing of a worldwide collection of rapeseed accessions reveals the genetic basis of ecotype divergence [J]. *Molecular Plant*, 2019, 12 (1): 30-43.
- Wu GA, Prochnik S, Jenkins J, et al. Sequencing of diverse mandarin, pummelo and orange genomes reveals complex history of admixture during *Citrus* domestication [J]. *Nature Biotechnology*, 2014, 32 (7): 656.
- Wu GA, Terol J, Ibanez V, et al. Genomics of the origin and evolution of *Citrus* [J]. *Nature*, 2018, 554 (7692): 311.
- Wu J, Wang Y, Xu J, et al. Diversification and independent domestication of Asian and European pears [J]. *Genome Biology*, 2018, 19 (1): 77.
- Wu J, Wang Z, Shi Z, et al. The genome of the pear (*Pyrus bretschneideri* Rehd.) [J]. *Genome Research*, 2013, 23 (2): 396-408.
- Wu Q, Han TS, Chen X, et al. Long-term balancing selection contributes to adaptation in *Arabidopsis* and its relatives [J]. *Genome Biology*, 2017a, 18 (1): 217.
- Wu W, Yang YL, He WM, et al. Whole genome sequencing of a banana wild relative *Musa itinerans* provides insights into lineage-specific diversification of the *Musa* genus [J]. *Scientific Reports*, 2016a, 6: 31586.
- Wu X, Li Y, Shi Y, et al. Joint - linkage mapping and GWAS reveal extensive genetic loci that regulate male inflorescence size in maize [J]. *Plant Biotechnology Journal*, 2016b, 14 (7): 1551-1562.
- Wu Y, Li BZ, Zhao M, et al. Bug mapping and fitness testing of chemically synthesized chromosome X [J]. *Science*, 2017b, 355 (6329): eaaf4706.
- Wu Z, Cuthbert JM, Taylor DR, et al. The massive mitochondrial genome of the angiosperm *Silene noctiflora* is evolving by gain or loss of entire chromosomes [J]. *Proceedings of the National Academy of Sciences*, 2015, 112 (33): 10185-10191.
- Wu Z, Yang Y, Huang G, et al. Cotton functional genomics reveals global insight into genome evolution and fiber development [J]. *Journal of Genetics and Genomics*, 2017c, 44 (11): 511-518.
- Wuyun T, Wang L, Liu H, et al. The hardy rubber tree genome provides insights into the evolution of polyisoprene biosynthesis [J]. *Molecular Plant*, 2018, 11 (3): 429-442.
- Xia C, Zhang L, Zou C, et al. A TRIM insertion in the promoter of *Ms2* causes male sterility in wheat [J]. *Nature Communications*, 2017, 8: 15407.
- Xia EH, Zhang HB, Sheng J, et al. The tea tree genome provides insights into tea flavor and independent

- evolution of caffeine biosynthesis [J]. *Molecular Plant*, 2017, 10 (6): 866-877.
- Xia HB, Xia H, Ellstrand NC, et al. Rapid evolutionary divergence and ecotypic diversification of germination behavior in weedy rice populations [J]. *New Phytologist*, 2011, 191 (4): 1119-1127.
- Xia Z, Watanabe S, Yamada T, et al. Positional cloning and characterization reveal the molecular basis for soybean maturity locus E1 that regulates photoperiodic flowering [J]. *Proceedings of the National Academy of Sciences*, 2012, 109 (32): E2155.
- Xiao Y, Liu H, Wu L, et al. Genome-wide association studies in maize: praise and stargaze [J]. *Molecular Plant*, 2017a, 10 (3): 359-374.
- Xiao Y, Tong H, Yang X, et al. Genome - wide dissection of the maize ear genetic architecture using multiple populations [J]. *New Phytologist*, 2016, 210 (3): 1095-1106.
- Xiao Y, Xu P, Fan H, et al. The genome draft of coconut (*Cocos nucifera*) [J]. *Gigascience*, 2017b, 6 (11): 1-11.
- Xie K, Minkenberg B, Yang Y. Boosting *CRISPR/Cas9* multiplex editing capability with the endogenous tRNA-processing system [J]. *Proceedings of the National Academy of Sciences*, 2015, 112 (11): 3570-3575.
- Xie M, Chung C, Li M, et al. A reference-grade wild soybean genome [J]. *Nature Communications*, 2019, 10 (1): 1216.
- Xie ZX, Li BZ, Mitchell LA, et al. “Perfect” designer chromosome V and behavior of a ring derivative [J]. *Science*, 2017, 355 (6329): eaaf4704.
- Xin M, Wang Y, Yao Y, et al. Diverse set of microRNAs is responsive to powdery mildew infection and heat stress in wheat (*Triticum aestivum* L.) [J]. *BMC Plant Biology*, 2010, 10 (1): 123.
- Xiong Y, Liu T, Tian C, et al. Transcription factors in rice: a genome-wide comparative analysis between monocots and eudicots [J]. *Plant Molecular Biology*, 2005, 59 (1): 191-203.
- Xiong Z, Pires JC. Karyotype and identification of all homoeologous chromosomes of allopolyploid *Brassica napus* and its diploid progenitors [J]. *Genetics*, 2011, 187 (1): 37-49.
- Xu C, Jiao C, Sun H, et al. Draft genome of spinach and transcriptome diversity of 120 *Spinacia* accessions [J]. *Nature Communications*, 2017a, 8: 15275.
- Xu HM, Kong XD, Chen F, et al. Transcriptome analysis of *Brassica napus* pod using RNA-Seq and identification of lipid-related candidate genes [J]. *BMC Genomics*, 2015a, 16 (1): 858.
- Xu J, Yuan Y, Xu Y, et al. Identification of candidate genes for drought tolerance by whole-genome resequencing in maize [J]. *BMC Plant Biology*, 2014a, 14 (1): 83.
- Xu L, Hu K, Zhang Z, et al. Genome-wide association study reveals the genetic architecture of flowering time in rapeseed (*Brassica napus* L.) [J]. *DNA Research*, 2016, 23 (1): 43-52.
- Xu MY, Dong Y, Zhang QX, et al. Identification of miRNAs and their targets from *Brassica napus* by high-throughput sequencing and degradome analysis [J]. *BMC Genomics*, 2012a, 13 (1): 421.
- Xu Q, Chen LL, Ruan X, et al. The draft genome of sweet orange (*Citrus sinensis*) [J]. *Nature Genetics*, 2013, 45 (1): 59-92.
- Xu R, Wang Y, Zheng H, et al. Salt-induced transcription factor MYB74 is regulated by the RNA-directed DNA methylation pathway in *Arabidopsis* [J]. *Journal of Experimental Botany*, 2015b, 66 (19): 5997-6008.

- Xu S, He Z, Zhang Z, et al. The origin, diversification and adaptation of a major mangroveclade (Rhizophoraceae) revealed by whole-genome sequencing [J]. *National Science Review*, 2017b, 5: 721-734.
- Xu S, Zhu D, Zhang Q. Predicting hybrid performance in rice using genomic best linear unbiased prediction [J]. *Proceedings of the National Academy of Sciences*, 2014b, 111 (34): 12456-12461.
- Xu S. Estimating polygenic effects using markers of the entire genome [J]. *Genetics*, 2003, 163 (2): 789-801.
- Xu X, Hou Y, Yin X, et al. Single-cell exome sequencing reveals single-nucleotide mutation characteristics of a kidney tumor [J]. *Cell*, 2012b, 148 (5): 886-895.
- Xu X, Liu X, Ge S, et al. Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes [J]. *Nature Biotechnology*, 2012c, 30 (1): 105-111.
- Xu X, Zeng L, Tao Y, et al. Pinpointing genes underlying the quantitative trait loci for root-knot nematode resistance in palaeopolyploid soybean by whole genome resequencing [J]. *Proceedings of the National Academy of Sciences*, 2013, 110 (33): 13469-13474.
- Xu Y, Li P, Zou C, et al. Enhancing genetic gain in the era of molecular breeding [J]. *Journal of Experimental Botany*, 2017c, 68 (11): 2641-2666.
- Xu Y, Zhou X. Applications of single-cell sequencing for multiomics [M]//*Computational Systems Biology*. New York: Humana Press, 2018: 327-374.
- Xu Z, Wang H. LTR_FINDER: an efficient tool for the prediction of full-length LTR retrotransposons [J]. *Nucleic Acids Research*, 2007, 35 (suppl_2): W265-W268.
- Xue JY, Liu Y, Li L, et al. The complete mitochondrial genome sequence of the hornwort *Phaeoceros laevis*: retention of many ancient pseudogenes and conservative evolution of mitochondrial genomes in hornworts [J]. *Current Genetics*, 2010, 56 (1): 53-61.
- Xue S, Bradbury PJ, Casstevens T, et al. Genetic architecture of domestication-related traits in maize [J]. *Genetics*, 2016, 204 (1): 99-113.
- Xue Y, Warburton ML, Sawkins M, et al. Genome-wide association analysis for nine agronomic traits in maize under well-watered and water-stressed conditions [J]. *Theoretical and Applied Genetics*, 2013, 126 (10): 2587-2596.
- Yadav CB, Pandey G, Muthamilarasan M, et al. Epigenetics and Epigenomics of Plants [M]// *Plant Genetics and Molecular Biology*. Springer, Cham, 2018: 237-261.
- Yadav SP. The wholeness in suffix -omics, -omes, and the word om [J]. *Journal of Biomolecular Techniques* JBT, 2007, 18 (5): 277.
- Yagi M, Kosugi S, Hirakawa H, et al. Sequence analysis of the genome of carnation (*Dianthus caryophyllus* L.) [J]. *DNA Research*, 2013, 21 (3): 231-241.
- Yang C, Tang D, Zhang L, et al. Identification of QTL for ear row number and two-ranked versus many-ranked ear in maize across four environments [J]. *Euphytica*, 2015a, 206 (1): 33-47.
- Yang G, Liu Z, Gao L, et al. Genomic imprinting was evolutionarily conserved during wheat polyploidization [J]. *The Plant Cell*, 2018, 30 (1): 37-47.
- Yang J, Ferreira T, Morris AP, et al. Conditional and joint multiple-SNP analysis of GWAS summary statistics identifies additional variants influencing complex traits [J]. *Nature Genetics*, 2012, 44 (4): 369.
- Yang J, Liu D, Wang X, et al. The genome sequence of allopolyploid *Brassica juncea* and analysis of

- differential homoeolog gene expression influencing selection [J]. *Nature Genetics*, 2016, 48 (10): 1225.
- Yang K, Tian Z, Chen C, et al. Genome sequencing of adzuki bean (*Vigna angularis*) provides insight into high starch and low fat accumulation and domestication [J]. *Proceedings of the National Academy of Sciences*, 2015b, 112 (43): 13213-13218.
- Yang N, Lu Y, Yang X, et al. Genome wide association studies using a new nonparametric model reveal the genetic architecture of 17 agronomic traits in an enlarged maize association panel [J]. *PLoS Genetics*, 2014a, 10 (9): e1004573.
- Yang N, Xu XW, Wang RR, et al. Contributions of *Zea mays* subspecies *mexicana* haplotypes to modern maize [J]. *Nature Communications*, 2017a, 8 (1): 1874.
- Yang Q, Li Z, Li W, et al. CACTA-like transposable element in ZmCCT attenuated photoperiod sensitivity and accelerated the postdomestication spread of maize [J]. *Proceedings of the National Academy of Sciences*, 2013, 110 (42): 16969-16974.
- Yang W, Guo Z, Huang C, et al. Combining high-throughput phenotyping and genome-wide association studies to reveal natural genetic variation in rice [J]. *Nature Communications*, 2014b, 5: 5087.
- Yang W, Wang K, Zhang J, et al. The draft genome sequence of a desert tree *Populus pruinosa* [J]. *Gigascience*, 2017b, 6 (9): 1.
- Yang X, Hu R, Yin H, et al. The *Kalanchoë* genome provides insights into convergent evolution and building blocks of crassulacean acid metabolism [J]. *Nature Communications*, 2017c, 8 (1): 1899.
- Yao Y, Guo G, Ni Z, et al. Cloning and characterization of microRNAs from wheat (*Triticum aestivum* L.) [J]. *Genome biology*, 2007, 8 (6): R96.
- Yasodha R, Vasudeva R, Balakrishnan S, et al. Draft genome of a high value tropical timber tree, Teak (*Tectona grandis* L. f): insights into SSR diversity, phylogeny and conservation [J]. *DNA Research*, 2018, 25 (4): 409-419.
- Ye CY, Chen L, Liu C, et al. Widespread noncoding circular RNAs in plants [J]. *New Phytologist*, 2015, 208 (1): 88-95.
- Ye CY, Li T, Yin H, et al. Evolutionary analyses of non - family genes in plants [J]. *The Plant Journal*, 2013, 73 (5): 788-797.
- Ye CY, Lin Z, Li G, et al. *Echinochloa* chloroplast genomes: insights into the evolution and taxonomic identification of two weedy species [J]. *PLoS One*, 2014, 9 (11): e113657.
- Ye CY, Tang W, Wu D, et al. Genomic evidence of human selection on Vavilovian mimicry [J]. *Nature Ecology & Evolution*, 2019, 3 (10): 1-9.
- Ye CY, Zhang X, Chu Q, et al. Full-length sequence assembly reveals circular RNAs with diverse non-GT/AG splicing signals in rice [J]. *RNA Biology*, 2017, 14 (8): 1055-1063.
- Yong-Villalobos L, González-Morales SI, Wrobel K, et al. Methylome analysis reveals an important role for epigenetic changes in the regulation of the *Arabidopsis* response to phosphate starvation [J]. *Proceedings of the National Academy of Sciences*, 2015, 112 (52): E7293-E7302.
- Yoshida K, Noguchi K. Interaction between Chloroplasts and Mitochondria: Activity, Function, and Regulation of the Mitochondrial Respiratory System during Photosynthesis [M]. *Plant Mitochondria*, New York: Springer, 2011: 383-409.

- Yoshida S, Maruyama S, Nozaki H, et al. Horizontal gene transfer by the parasitic plant *Striga hermonthica* [J]. *Science*, 2010, 328 (5982): 1128.
- Young ND, Debellé F, Oldroyd GED, et al. The Medicago genome provides insight into the evolution of rhizobial symbioses [J]. *Nature*, 2011, 480 (7378): 520-524.
- Yu A, Lepère G, Jay F, et al. Dynamics and biological relevance of DNA demethylation in *Arabidopsis* antibacterial defense [J]. *Proceedings of the National Academy of Sciences*, 2013, 110 (6): 2389-2394.
- Yu J, Dossa K, Wang L, et al. PMDBase: a database for studying microsatellite DNA and marker development in plants [J]. *Nucleic Acids Research*, 2016, 45 (D1): D1046-D1053.
- Yu J, Golicz AA, Lu K, et al. Insight into the evolution and functional characteristics of the pan - genome assembly from sesame landraces and modern cultivars [J]. *Plant Biotechnology Journal*, 2018, 17 (5): 881-892.
- Yu J, Hu S, Wang J, et al. A draft sequence of the rice genome (*Oryza sativa* L. ssp. *indica*) [J]. *Science*, 2002, 296 (5565): 79-92.
- Yu J, Pressoir G, Briggs WH, et al. A unified mixed-model method for association mapping that accounts for multiple levels of relatedness [J]. *Nature Genetics*, 2006, 38 (2): 203.
- Yu J, Wang J, Wei L, et al. The Genomes of *Oryza sativa*: A history of duplications [J]. *Plos Biology*, 2005, 3 (2): 266-281.
- Yu SB, Li JX, Xu CG, et al. Importance of epistasis as the genetic basis of heterosis in an elite rice hybrid [J]. *Proceedings of the National Academy of Sciences*, 1997, 94 (17): 9226-9231.
- Yu X, Wang H, Zhong W, et al. QTL mapping of leafy heads by genome resequencing in the RIL population of *Brassica rapa* [J]. *PLoS One*, 2013b, 8 (10): e76059.
- Yuan D, Tang Z, Wang M, et al. The genome sequence of Sea-Island cotton (*Gossypium barbadense*) provides insights into the allopolyploidization and development of superior spinnable fibres [J]. *Scientific Reports*, 2015, 5: 17662.
- Yuan J, Li J, Yang Y, et al. Stress - responsive regulation of long non - coding RNA polyadenylation in *Oryza sativa* [J]. *The Plant Journal*, 2018, 93 (5): 814-827.
- Yuan Q, Hill J, Hsiao J, et al. Genome sequencing of a 239-kb region of rice chromosome 10L reveals a high frequency of gene duplication and a large chloroplast DNA insertion [J]. *Molecular Genetics and Genomics*, 2002, 267 (6): 713-720.
- Yue J, Hu X, Sun H, et al. Widespread impact of horizontal gene transfer on plant colonization of land [J]. *Nature Communications*, 2012, 3: 1152.
- Yurina NP, Odintsova MS. Mitochondrial genome structure of photosynthetic eukaryotes [J]. *Biochemistry (Moscow)*, 2016, 81 (2): 101-113.
- Zapata L, Ding J, Willing EM, et al. Chromosome-level assembly of *Arabidopsis thaliana* Ler reveals the extent of translocation and inversion polymorphisms [J]. *Proceedings of the National Academy of Sciences*, 2016, 113 (28): E4052.
- Zemach A, Kim MY, Hsieh PH, et al. The *Arabidopsis* nucleosome remodeler DDM1 allows DNA methyltransferases to access H1-containing heterochromatin [J]. *Cell*, 2013, 153 (1): 193-205.
- Zhai J, Jeong D, de Paoli E, et al. MicroRNAs as master regulators of the plant NB-LRR defense gene family

- via the production of phased, trans-acting siRNAs [J]. *Genes & Development*, 2011, 25 (23): 2540-2553.
- Zhang B, Pan X, Stellwag EJ. Identification of soybean microRNAs and their targets [J]. *Planta*, 2008, 229 (1): 161-182.
- Zhang GQ, Liu KW, Li Z, et al. The *Apostasia* genome and the evolution of orchids [J]. *Nature*, 2017a, 549 (7672): 379.
- Zhang G, Cheng Z, Zhang X, et al. Double repression of soluble starch synthase genes *SSIIa* and *SSIIIa* in rice (*Oryza sativa* L.) uncovers interactive effects on the physicochemical properties of starch [J]. *Genome*, 2011a, 54 (6): 448-459.
- Zhang G, Guo G, Hu X, et al. Deep RNA sequencing at single base-pair resolution reveals high complexity of the rice transcriptome [J]. *Genome Research*, 2010, 20 (5): 646-654.
- Zhang G, Liu X, Quan Z, et al. Genome sequence of foxtail millet (*Setaria italica*) provides insights into grass evolution and biofuel potential [J]. *Nature biotechnology*, 2012a, 30 (6): 549.
- Zhang H, Lang Z, Zhu JK. Dynamics and function of DNA methylation in plants [J]. *Nature Reviews Molecular Cell Biology*, 2018a, 19 (8): 489.
- Zhang H, Wang X, Pan Q, et al. QTG-Seq accelerates QTL fine mapping through QTL partitioning and whole-genome sequencing of bulked segregant samples [J]. *Molecular Plant*, 2019, 12 (3): 426-437.
- Zhang J, Chen LL, Sun S, et al. Building two indica rice reference genomes with PacBio long-read and Illumina paired-end sequencing data [J]. *Scientific Data*, 2016a, 3: 160076.
- Zhang J, Chen LL, Xing F, et al. Extensive sequence divergence between the reference genomes of two elite indica rice varieties Zhenshan 97 and Minghui 63 [J]. *Proceedings of the National Academy of Sciences*, 2016b, 113 (35): E5163-E5171.
- Zhang J, Liu Y, Xia EH, et al. Autotetraploid rice methylome analysis reveals methylation variation of transposable elements and their effects on gene expression [J]. *Proceedings of the National Academy of Sciences*, 2015a, 112 (50): E7022-E7029.
- Zhang J, Luo W, Zhao Y, et al. Comparative metabolomic analysis reveals a reactive oxygen species - dominated dynamic model underlying chilling environment adaptation and tolerance in rice [J]. *New Phytologist*, 2016c, 211 (4): 1295-1310.
- Zhang J, Mason AS, Wu J, et al. Identification of putative candidate genes for water stress tolerance in canola (*Brassica napus*) [J]. *Frontiers in Plant Science*, 2015b, 6: 1058.
- Zhang J, Wang H, Liu Z, et al. A naturally occurring variation in the *BrMAM-3* gene is associated with aliphatic glucosinolate accumulation in *Brassica rapa* leaves [J]. *Horticulture Research*, 2018b, 5 (1): 69.
- Zhang K, Martiny AC, Reppas NB, et al. Sequencing genomes from single cells by polymerase cloning [J]. *Nature Biotechnology*, 2006, 24 (6): 680.
- Zhang L, Pond SK, Gaut BS. A survey of the molecular evolutionary dynamics of twenty-five multigene families from four grass taxa [J]. *Journal of Molecular Evolution*, 2001, 52 (2): 144-156.
- Zhang L, Ren Y, Yang T, et al. Rapid evolution of protein diversity by de novo origination in *Oryza* [J]. *Nature Evolution & Ecology*, 2019a, 3 (4): 679.
- Zhang L, Wang M, Li N, et al. Long non-coding RNAs involve in resistance to *Verticillium dahliae*, a fungal disease in cotton [J]. *Plant Biotechnology Journal*, 2018c, 16 (6): 1172-1185.

- Zhang L, Xu P, Cai Y, The draft genome assembly of *Rhododendron delavayi* Franch. var. *delavayi* [J]. *Gigascience*, 2017b, 6 (10): 1-11.
- Zhang L, Yu H, Ma B, et al. A natural tandem array alleviates epigenetic repression of IPA1 and leads to superior yielding rice [J]. *Nature Communications*, 2017c, 8: 14789.
- Zhang N, Si H, Wang D. Techniques on isolation of single cells in potato [J]. *Chinese Potato Journal*, 2004, 18 (4;NUMB 78): 193-197.
- Zhang QJ, Zhu T, Xia EH, et al. Rapid diversification of five *Oryza* AA genomes associated with rice adaptation [J]. *Proceedings of the National Academy of Sciences*, 2014a, 70 (44): 4954-4962.
- Zhang Q, Chen W, Sun L, et al. The genome of *Prunus mume* [J]. *Nature Communications*, 2012b, 3 (4): 1318.
- Zhang Q, Liang Z, Cui X, et al. N6-methyladenine DNA methylation in japonica and indica Rice genomes and its association with gene expression, plant development, and stress responses [J]. *Molecular Plant*, 2018d, 11 (12): 1492-1508.
- Zhang Q, Zhang H, Sun L, et al. The genetic architecture of floral traits in the woody plant *Prunus mume* [J]. *Nature Communications*, 2018e, 9 (1): 1702.
- Zhang T, Hu Y, Jiang W, et al. Sequencing of allotetraploid cotton (*Gossypium hirsutum* L. acc. TM-1) provides a resource for fiber improvement [J]. *Nature Biotechnology*, 2015c, 33 (5): 531.
- Zhang TQ, Xu ZG, Shang GD, et al. A single-cell RNA sequencing profiles the developmental landscape of Arabidopsis root [J]. *Molecular Plant*, 2019b, 12 (5): 648-660.
- Zhang W, Zhao G, Luo Z, et al. Engineering the ribosomal DNA in a megabase synthetic chromosome [J]. *Science*, 2017d, 355 (6329): eaaf3981.
- Zhang X, Jiang H, Wang H, et al. Transcriptome analysis of rice seedling roots in response to potassium deficiency [J]. *Scientific Reports*, 2017e, 7 (1): 5523.
- Zhang X, Pérez-Rodríguez P, Semagn K, et al. Genomic prediction in biparental tropical maize populations in water-stressed and well-watered environments using low-density and GBS SNPs [J]. *Heredity*, 2015d, 114 (3): 291.
- Zhang X, Warburton ML, Setter T, et al. Genome-wide association studies of drought-related metabolic changes in maize using an enlarged SNP panel [J]. *Theoretical and Applied Genetics*, 2016d, 129 (8): 1449-1463.
- Zhang YC, Liao JY, Li ZY, et al. Genome-wide screening and functional analysis identify a large number of long noncoding RNAs involved in the sexual reproduction of rice [J]. *Genome Biology*, 2014b, 15 (12): 512.
- Zhang YC, Yu Y, Wang CY, et al. Overexpression of microRNA OsmiR397 improves rice yield by increasing grain size and promoting panicle branching [J]. *Nature Biotechnology*, 2013, 31 (9): 848.
- Zhang YJ, Ma PF, Li DZ. High-throughput sequencing of six bamboo chloroplast genomes: phylogenetic implications for temperate woody bamboos (*Poaceae: Bambusoideae*) [J]. *PloS One*, 2011b, 6 (5): e20596.
- Zhang Y, Ptacin JL, Fischer EC, et al. A semi-synthetic organism that stores and retrieves increased genetic information [J]. *Nature*, 2017f, 551 (7682): 644.
- Zhang Y, XU G, Guo X, et al. Two ancient rounds of polyploidy in rice genome [J]. *Journal of Zhejiang*

- University. Science. B, 2005, 6 (2): 87-90.
- Zhang Y, Zhang S, Hui L, et al. Genome and comparative transcriptomics of African wild rice *Oryza longistaminata*, provide insights into molecular mechanism of rhizomatousness and self-incompatibility [J]. Molecular Plant, 2015e, 8 (11): 1683-1686.
- Zhang Z, Belcram H, Gornicki P, et al. Duplication and partitioning in evolution and function of homoeologous Q loci governing domestication characters in polyploid wheat [J]. Proceedings of the National Academy of Sciences, 2011c, 108 (46): 18737-18742.
- Zhang Z, Mao L, Chen H, et al. Genome-wide mapping of structural variations reveals a copy number variant that determines reproductive morphology in cucumber [J]. The Plant Cell, 2015, 27 (6): 1595-1604.
- Zhao C, Takeshima R, Zhu J, et al. A recessive allele for delayed flowering at the soybean maturity locus E9 is a leaky allele of *FT2a*, a FLOWERING LOCUS T ortholog [J]. BMC Plant Biology, 2016, 16 (1): 20.
- Zhao D, Hamilton JP, Pham GM, et al. *De novo* genome assembly of *Camptotheca acuminata*, a natural source of the anti-cancer compound camptothecin [J]. Gigascience, 2017a, 6 (9): 1-7.
- Zhao G, Zou C, Li K, et al. The *Aegilops tauschii* genome reveals multiple impacts of transposons [J]. Nature Plants, 2017b, 3 (12): 946.
- Zhao Q, Feng Q, Lu H, et al. Pan-genome analysis highlights the extent of genomic variation in cultivated and wild rice [J]. Nature Genetics, 2018a, 50 (2): 278.
- Zhao T, Tao X, Feng S, et al. LncRNAs in polyploid cotton interspecific hybrids are derived from transposon neofunctionalization [J]. Genome Biology, 2018b, 19 (1): 195.
- Zhao T, Wang L, Li S, et al. Characterization of conserved circular RNA in polyploid *Gossypium* species and their ancestors [J]. FEBS Letters, 2017c, 591 (21): 3660-3669.
- Zhao W, Cheng Y, Zhang C, et al. Genome-wide identification and characterization of circular RNAs by high throughput sequencing in soybean [J]. Scientific Reports, 2017d, 7 (1): 5636.
- Zhao W, Zou W, Chen JJ. Topic modeling for cluster analysis of large biological and medical datasets [C]. BMC bioinformatics, BioMed Central, 2014, 15 (11): S11.
- Zhao YT, Wang M, Fu SX, et al. Small RNA profiling in two *Brassica napus* cultivars identifies microRNAs with oil production-and development-correlated expression and new small RNA classes [J]. Plant Physiology, 2012, 158 (2): 813-823.
- Zhong S, Zhang S, Fan X, et al. A single-cell RNA-seq survey of the developmental landscape of the human prefrontal cortex [J]. Nature, 2018, 555 (7697): 524.
- Zhou P, Silverstein KAT, Ramaraj T, et al. Exploring structural variation and gene family architecture with *de novo* assemblies of 15 Medicago genomes [J]. BMC Genomics, 2017, 18 (1): 261.
- Zhou Q, Zhang G, Zhang Y, et al. On the origin of new genes in *Drosophila* [J]. Genome research, 2008, 18 (9): 1446-1455.
- Zhou ZS, Song JB, Yang ZM. Genome-wide identification of *Brassica napus* microRNAs and their targets in response to cadmium [J]. Journal of Experimental Botany, 2012, 63 (12): 4597-4613.
- Zhou Z, Jiang Y, Wang Z, et al. Resequencing 302 wild and cultivated accessions identifies genes related to domestication and improvement in soybean [J]. Nature Biotechnology, 2015, 33 (4): 408-414.
- Zhu G, Wang S, Huang Z, et al. Rewiring of the fruit metabolome in tomato breeding [J]. Cell, 2018, 172 (1-2): 249-261. e12.
- Zhu QH, Spriggs A, Matthew L, et al. A diverse set of microRNAs and microRNA-like small RNAs in developing

- rice grains [J]. *Genome Research*, 2008, 18 (9): 1456-1465.
- Zhu Q, Ge S. Phylogenetic relationships among A - genome species of the genus *Oryza* revealed by intron sequences of four nuclear genes [J]. *New Phytologist*, 2005, 167 (1): 249-265.
- Zhu Q, Zheng X, Luo J, et al. Multilocus analysis of nucleotide variation of *Oryza sativa* and its wild relatives: severe bottleneck during domestication of rice [J]. *Molecular Biology and Evolution*, 2007, 24 (3): 875-888.
- Zhu W, Hu B, Becker C, et al. Altered chromatin compaction and histone methylation drive non-additive gene expression in an interspecific *Arabidopsis* hybrid [J]. *Genome Biology*, 2017, 18 (1): 157.
- Zhu Z, Tan L, Fu Y, et al. Genetic control of inflorescence architecture during rice domestication [J]. *Nature Communications*, 2013, 4: 2200.
- Zila CT, Ogut F, Romay MC, et al. Genome-wide association study of Fusarium ear rot disease in the USA maize inbred line collection [J]. *BMC Plant Biology*, 2014, 14 (1): 372.
- Zila CT, Samayoa LF, Santiago R, et al. A genome-wide association study reveals genes associated with Fusarium ear rot resistance in a maize core diversity panel [J]. *G3: Genes, Genomes, Genetics*, 2013, 3 (11): 2095-2104.
- Zimin AV, Puiu D, Hall R, et al. The first near-complete assembly of the hexaploid bread wheat genome, *Triticum aestivum* [J]. *Gigascience*, 2017, 6 (11): 1-7.
- Zimmer AD, Lang D, Buchta K, et al. Reannotation and extended community resources for the genome of the non-seed plant *Physcomitrella patens* provide insights into the evolution of plant gene structures and functions [J]. *BMC Genomics*, 2013, 14 (1): 498.
- Zong C, Lu S, Chapman AR, et al. Genome-wide detection of single-nucleotide and copy-number variations of a single human cell [J]. *Science*, 2012, 338 (6114): 1622-1626.
- Zou C, Zhang Y, Ouyang Z. HSA: Integrating multi-track Hi-C data for genome-scale reconstruction of 3D chromatin structure [J]. *Genome Biology*, 2016, 17 (1): 40.
- Zou J, Mao L, Qiu J, et al. Genome-wide selection footprints and deleterious variations in young Asian allotetraploid rapeseed [J]. *Plant Biotechnology Journal*, 2019, 17 (10): 1998-2010.
- Zou S, Wang H, Li Y, et al. The NB - LRR gene *Pm60* confers powdery mildew resistance in wheat [J]. *New Phytologist*, 2018, 218 (1): 298-309.
- Zou XH, Zhang FM, Zhang JG, et al. Analysis of 142 genes resolves the rapid diversification of the rice genus [J]. *Genome Biology*, 2008, 9 (3): R49.
- Zou YP, Hou XH, Wu Q, et al. Adaptation of *Arabidopsis thaliana* to the Yangtze River basin [J]. *Genome Biology*, 2017, 18 (1): 239-239.
- Zu Y, Tong X, Wang Z, et al. TALEN-mediated precise genome modification by homologous recombination in zebrafish [J]. *Nature Methods*, 2013, 10 (4): 329-333.

