

# PATRICK S. SCHNABLE

C.F. Curtiss Distinguished Professor  
Iowa Corn Endowed Chair in Genetics  
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## EDUCATION

Cornell University, B.S., Agronomy, 1981  
Iowa State University, Ph.D., Plant Breeding and Cytogenetics, 1986

## PROFESSIONAL EXPERIENCE

1981-1986 Graduate Research Assistant, Laboratory of Peter Peterson, Iowa State University  
1986-1988 NIH Postdoctoral Fellow, Laboratory of Heinz Saedler, Max-Planck-Institut für Züchtungsforschung, Köln, Germany  
1988-1994 Assistant Professor, Iowa State University  
1994-1998 Associate Professor, Iowa State University  
1998-present Professor, Iowa State University  
1999-present Founding Member, Center for Bioinformatics and Biological Statistics  
1999-2003 Founding Director, Center for Plant Transformation & Gene Expression  
1999-2023 Founding Director, Center for Plant Genomics  
2002-2006 Associate Chair and Chair, Interdepartmental Genetics Graduate Program  
2005-2010 Associate Director, Plant Sciences Institute  
2007-2013 Director, Center for Carbon Capturing Crops  
2007-2013 Baker Professor of Agronomy  
2013-present Iowa Corn Promotion Board Endowed Chair in Genetics  
2013-present C.F. Curtiss Distinguished Professor  
2014-present Baker Scholar of Agricultural Entrepreneurship  
2014-present Director, Plant Sciences Institute  
2017-present Lead, Digital and Precision Ag Economic Development Platform  
2010-present Co-Founder and Managing Partner, Data2Bio LLC  
2014-present Co-Founder and Co-Managing Partner, Dryland Genetics Inc.  
2017-present Co-Founder and Managing Partner, EnGeniousAg LLC

## HONORS

- ISU Department of Agronomy Plant Breeding Research Award, 1985

- Max-Planck-Institute Postdoctoral Fellowship, 1986
- Iowa State Research Excellence Award, 1986
- Gamma Sigma Delta Honor Society, 1986
- National Institutes of Health Postdoctoral Fellowship, 1987-1988
- Raymond and Mary Baker Agronomic Excellence Award, 2000
- Iowa State University, College of Agriculture Research Team Award, 2005
- Best Paper Award, IEEE International Parallel and Distributed Processing Symposium, 2006
- Finalist, Computerworld Honors Program, 2007
- Changjang Scholar, China Agriculture University, 2009-2012
- Outstanding Achievement in Research Award, College of Agriculture and Life Sciences, Iowa State University, 2010
- Fellow, American Association for the Advancement of Science (AAAS), 2010

#### REVIEW PANELS, ADVISORY BOARDS and EDITORIAL POSTS

|              |   |
|--------------|---|
| 1990         | DOE, Energy Biosciences Panel   |
| 2001         | NSF Technical Review Team of Missouri MaizeDB   |
| 2001-2003    | Scientific Advisory Board, NSF-funded Potato Genome Project   |
| 2003         | Committee of Visitors, Training Cluster, NSF-DBI  |
| 2003-2004    | Grant Review Panel, NSF Small Business Innovation Research, Agricultural Biotechnology  |
| 2003-2007    | Scientific Advisory Board, NSF-funded Cell Wall Project   |
| 2003-2007    | Scientific Advisory Board, NSF-funded Wheat SNP Project   |
| 2003-2008    | Scientific Advisory Board, NSF-funded Maize Genomic Diversity Project   |
| 2005-2009    | Elected Member-at-Large of the AAAS Section Committee, Agriculture, Food and Renewable Resources Section                              |
| 2006         | Grant Review Panel, NSF SEI-BIO   |
| 2006-2011    | MaizeGDB Working Group  |
| 2007         | Invited to testify to National Research Council Committee: "The National Plant Genome Initiative: Achievements and Future Directions" |
| 2007         | Invited to testify to National Research Council Committee: "A Study of Technologies to Benefit Farmers in Africa and South Asia"      |
| 2008-2011    | Associate Editor, The Plant Genome  |
| 2008-Present | Editorial Board, PLoS Genetics<br>2008-2015, Associate Editor<br>2015-Present, Consulting Editor                                      |
| 2009         | Grant Review Panel, Agriculture and Agri-Food Canada  |
| 2009         | Grant Review Panel, NSF Bioinformatics  |
| 2009-2010    | NextGen Sequencing Working Group, NSF iPlant Consortium   |
| 2009-2010    | Steering Committee, "Functionality and the Corn Genome" workshop (NCGA)   |
| 2009-present | Organizer, Maize Genetics Workshop, Plant and Animal Genome Meeting   |
| 2009-2013    | External Advisory Board, French wheat chromosome 3B genome sequencing project   |

|              |   |
|--------------|---|
| 2010-2012    | International Scientific Advisory Board, 10th International Congress on Plant Molecular Biology 2012, Jeju, Korea   |
| 2011         | Co-organizer, Banbury Conference (CSHL): “Genotype to Phenotype: Deriving Biological Knowledge from Large Genomic Datasets”, 16-19 October 2011, Cold Spring Harbor, NY |
| 2011         | Organizer “Genomics to Agronomics” Session, American Seed Trade Association, Chicago IL 8 December 2011   |
| 2011-2012    | Organizing Committee, International Conference of Heterosis Utilization in Crops, 21-24 August 2012, Xian, China  |
| 2011-2016    | Scientific Advisory Board, NSF-funded <i>Amborella</i> Genome Project   |
| 2013-2018    | International Advisory Board, Centre for Biotechnological and Agricultural Research, Olomouc, Czech Republic  |
| 2013-2016    | Scientific Advisory Council, GeneSeek   |
| 2013-2014    | National Plant Science Council  |
| 2013-2017    | Scientific Advisory Board, NSF-funded <i>Aegilops tauschii</i> Genome Sequencing Project  |
| 2013-present | Co-lead, Maize Genomes to Fields Initiative   |
| 2014-2023    | Member, Scientific Advisory Board, Hi-Fidelity Genetics, Durham, NC   |
| 2014-2019    | Member, Scientific Advisory Board, US-based crop breeding company   |
| 2014-2014    | Member, CAST Board of Representatives (ASPB representative)   |
| 2015         | Scientific Committee, EUCARPIA Maize and Sorghum conference, "Genomics and Phenomics for Model-Based Maize and Sorghum Breeding"  |
| 2016-present | Member, Scientific Advisory Board, CTC (a Brazilian sugarcane breeding company)   |
| 2017         | Organizing Committee, Nebraska EPSCoR “Predictive Crop Design: Genome-to-Phenome”   |
| 2017-present | Member, Scientific Advisory Board, Kemin Industries, Des Moines, IA   |
| 2021-present | Member, Agronomy Department Advisory Council  |
| 2021-present | Member, Agronomy Department Baker Council   |

## PROFESSIONAL AFFILIATIONS

- American Association for the Advancement of Science
  - “Golden Goose Award” Nominating Committee (ASPB Representative)
- American Society of Plant Biologists
  - Executive Committee, 2012-2016
  - Science Policy Committee, 2008-2016
    - Chair, 2012-2016
  - Pioneer Hi-Bred International Graduate Student Prize Committee, 2009-2013
- Genetics Society of America
  - Public Policy Committee, 2013-2016
- Maize Genetics Cooperative
  - Steering Committee, 1993-1996; 2002-2004
  - Maize Genetics Executive Committee

- Member, 2000-2004, 2006-2012, 2014-2018
- Chair, 2003-2004, 2007-2009

PUBLICATIONS (refereed; invited author):

<https://orcid.org/0000-0001-9169-5204>

Schnable has an h-index of 87 (as calculated by Google Scholar, <http://scholar.google.com/citations?user=UW4mNTW0nOkC&hl=en>, on 1/2024) with a total of over 29,000 citations and over 10,000 since 2019. Reflecting his interest in computational approaches to biology he has an Erdős number of 3.

- **Schnable PS**, PA Peterson (1986) Distribution of genetically active *Cy* elements among diverse maize lines. **Maydica (McClintock issue)** 31:59-81.
- **Schnable PS**, PA Peterson (1988) The *Mutator*-related *Cy* transposable element of *Zea mays* L. behaves as a near-Mendelian factor. **Genetics** 120(2):587-596.
- **Schnable PS**, PA Peterson (1989) Genetic evidence of a relationship between two maize transposable element systems: *Cy* and *Mutator*. **Mol Gen Genet** 215(2):317-321.
- **Schnable PS**, PA Peterson, H Saedler (1989) The *bz-rcy* allele of the *Cy* transposable element system of *Zea mays* contains a *Mu*-like element insertion. **Mol Gen Genet** 217:459-463.
- Menssen A, S Höhmann, W Martin, **PS Schnable**, PA Peterson, H Saedler, A Gierl (1990) The *En/Spm* transposable element of *Zea mays* contains splice sites at the termini generating a novel intron from a *dSpm* element in the *A2* gene. **EMBO J** 9(10):3051-3057.
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- **Schnable PS**, RP Wise (1994) Recovery of heritable, transposon-induced, mutant alleles of the *rf2* nuclear restorer of T-cytoplasm maize. **Genetics** 136(3):1171-1185.
- Wen T-J, **PS Schnable** (1994) Analyses of mutants of three genes that influence root hair development in *Zea mays* (*Gramineae*) suggest that root hairs are dispensable. **Am J Bot** 81:833-842.
- Civardi L, Y Xia, KJ Edwards, **PS Schnable**, BJ Nikolau (1994) The relationship between genetic and physical distances of the cloned *a1-sh2* interval of the *Zea mays* L. genome. **Proc Natl Acad Sci** 91(17):8268-8272.
- Wise RP, **PS Schnable** (1994) Mapping complementary genes in maize: Positioning the *rf1* and *rf2* nuclear-fertility restorer loci of Texas (T) cytoplasm relative to RFLP and visible markers. **Theoretical & Applied Genetics**, 88: 785-795.
- **Schnable PS**, PS Stinard, T-J Wen, S Heinen, D Weber, L Zhang, JD Hansen, BJ Nikolau (1994) The genetics of cuticular wax biosynthesis. **Maydica (Robertson issue)**, 39:279-287.

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- Han C-D, RJ Derby, **PS Schnable**, RA Martienssen (1995) Characterization of the plastids affected by class II albino mutations of maize at the morphological and transcript levels. **Maydica (Coe issue)** 40:13-22.
- Kasemsuwan T, JL Jane, **PS Schnable**, P Stinard, D Robertson (1995) Characterization of the dominant mutant amylose-extender (*Ael-5180*) maize starch. **Cereal Chem** , 72:457-464.
- Xu XJ, A-P Hsia, L Zhang, BJ Nikolau, **PS Schnable** (1995) Meiotic recombination break points resolve at high rates at the 5' end of a maize coding sequence. **Plant Cell**, 7(12):2151-2161.
- Hsia A-P, **PS Schnable** (1996) DNA sequence analyses support the role of interrupted gap repair in the origin of internal deletions of the maize transposon, *MuDR*. **Genetics**, 142(2):603-618.
- Cui X, RP Wise, **PS Schnable** (1996) The *rf2* nuclear restorer gene of male-sterile T-cytoplasm maize. **Science**, 272(5266):1334-1336. (*A commentary on this manuscript solicited by journal editors and written by Charles S. Levings III was provided in 272: 1279-1280*)
- Wise RP, CL Dill, **PS Schnable** (1996) *Mutator*-induced mutations of the *rf1* nuclear fertility restorer of T-cytoplasm maize alter the accumulation of T-*urf13* mitochondrial transcripts. **Genetics**, 143(3):1383-1394.
- Xia YJ, BJ Nikolau, **PS Schnable** (1996) Cloning and characterization of *CER2*, an *Arabidopsis* gene that affects cuticular wax accumulation. **Plant Cell**, 8(8): 1291-1304.
- Hansen JD, J Pyee, Y Xia, T-J Wen, DS Robertson, PE Kolattukudy, BJ Nikolau, **PS Schnable** (1997) The *glossy1* locus of maize and an epidermis-specific cDNA from *Kleinhia odora* define a class of receptor-like proteins required for the normal accumulation of cuticular waxes. **Plant Physiology**, 113(4):1091-1100.
- Xu X, C Dietrich, M Delledonne, Y Xia, TJ Wen, DS Robertson, BJ Nikolau, **PS Schnable** (1997) Sequence analysis of the cloned *glossy8* gene of maize suggests that it may code for a beta-ketoacyl reductase required for the biosynthesis of cuticular waxes. **Plant Physiology**, 115(2):501-510.
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- **Schnable PS**, RP Wise (1998) The molecular basis of cytoplasmic male sterility and fertility restoration. **Trends in Plant Science**, 3(5):175-180.
- **Schnable PS**, A-P Hsia, BJ Nikolau (1998) Genetic recombination in plants. **Current Opinion in Plant Biology**, 1(2):123-129.

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- Liu F, X Cui, HT Horner, H Weiner, **PS Schnable** (2001) Mitochondrial aldehyde dehydrogenase activity is required for male fertility in maize. **Plant Cell**, 13(5):1063-1078. (*Cover image*)
- Bennetzen, JL, VL Chandler, **PS Schnable** (2001) National Science Foundation-Sponsored Workshop Report. Maize Genome Sequencing Project. **Plant Physiology**, 127:1572-1578.
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- Xu X, Dietrich CR, Lessire R, Nikolau BJ, **PS Schnable** (2002) The endoplasmic reticulum-associated maize GL8 protein is a component of the acyl-Coenzyme A elongase involved in the production of cuticular waxes. **Plant Physiology**, 128(3): 924-934.
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- Skibbe D, F Liu, TJ Wen, MD Yandea-Nelson, X Cui, J Cao, CR Simmons, **PS Schnable** (2002) Characterization of the aldehyde dehydrogenase gene families of *Zea mays* and *Arabidopsis*. **Plant Molecular Biology**, 48(5):751-764.
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- Cui X, AP Hsia, F Liu, DA Ashlock, RP Wise, **PS Schnable** (2003) Alternative transcription initiation sites and polyadenylation sites are recruited during *Mu* suppression at the *rf2a* locus of maize. **Genetics**, 163(2):685-698.

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- **Schnable, PS**, F Hochholdinger, M Nakazono (2004) Global expression profiling applied to plant development. **Current Opinion in Plant Biology**, 7(1):50-56.
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- da Costa é Silva O, R Lorbiecke, P Garg, L Müller, M Waßmann, P Lauert, M Scanlon, AP Hsia, **PS Schnable**, K Krupinska, U Wienand (2004) The *Etched1* gene of *Zea mays* (L.) encodes a zinc ribbon protein that belongs to the transcriptionally active chromosome (TAC) of plastids and is similar to the transcription factor TFIIS. **Plant Journal**, 38(6): 923-939.
- Kirch HH, D Bartels, Y Wei, **PS Schnable**, AJ Wood (2004) The ALDH gene superfamily of *Arabidopsis*. **Trends in Plant Science**, 9(8):371-377.
- Chou HH, AP Hsia, DL Mooney, **PS Schnable** (2004) PICKY: oligo microarray design for large genomes. **Bioinformatics**, 20(17):2893-2902. (Epub 2004 Jun 4)
- Fu Y, AP Hsia, L Guo, **PS Schnable** (2004) Types and frequencies of sequencing errors in methyl-filtered and high C<sub>0</sub>t maize genome survey sequences. **Plant Physiology**, 135(4):2040-2045. (Epub: 2004 Aug 6)
- Hochholdinger F, L Guo, **PS Schnable** (2004) Lateral roots affect the proteome of the primary root of maize (*Zea mays* L.). **Plant Mol Biology**, 56(3):397-412. (*Selected as an Editors' Choice by MaizeGDB, 2/05*).
- Yandea-Nelson MD, Q Zhou, H Yao, X Xu, BJ Nikolau, **PS Schnable** (2005) *MuDR* transposase increases the frequency of meiotic crossovers in the vicinity of a *Mu* insertion in the maize *al* gene. **Genetics**, 169(2):917-929. (Epub: 2004 Oct 16)
- Hsia AP, TJ Wen, HD Chen, Z Liu, MD Yandea-Nelson, Y Wei, L Guo, **PS Schnable** (2005) Temperature Gradient Capillary Electrophoresis (TGCE) – A tool for the high throughput discovery and mapping of SNPs and IDPs. **Theoretical Applied Genetics**, 111(2): 218-225. (Epub: 2005 May 24)
- Yao H, L Guo, Y Fu, LA Borsuk, TJ Wen, DS Skibbe, X Cui, BE Scheffler, J Cao, SJ Emrich, DA Ashlock, **PS Schnable** (2005) Evaluation of five *ab initio* gene prediction programs for the discovery of maize genes. **Plant Mol Biology**, 57(3):445-460.
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Fulmer, **PS Schnable** (2005) Using the biological taxonomy to access biological literature with PathBinderH. **Bioinformatics**, 21(10):2560-2562. (Epub: 2005 Mar 15)

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- Fu Y\*, SJ Emrich\*, L Guo, T-J Wen, S Aluru, DA Ashlock, **PS Schnable** (2005) Quality assessment of maize assembled genomic islands (MAGIs) and large-scale experimental verification of predicted genes. **Proceedings National Academy Science**, 102(34):12282-12287. (Epub: 2005 Aug 15)
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- Skibbe DS, **PS Schnable** (2005) Male sterility in maize. **Maydica**, 50:367-376.
- Kresovich S and 35 additional authors including **PS Schnable** (2005) Toward sequencing the sorghum genome: a US National Science Foundation-sponsored workshop report. **Plant Physiology**, 138:1898-1902.
- Yao H, **PS Schnable** (2005) *Cis*-effects on meiotic recombination across distinct *a1-sh2* intervals in a common *Zea* genetic background. **Genetics**, 170(4):1929-1944. (Epub: 2005 Jun 3)
- Hochholdinger F, K Woll, L Guo, **PS Schnable** (2005) The accumulation of abundant soluble proteins changes early in the development of the primary roots of maize (*Zea mays* L.). **Proteomics**, 5(18):4885-4893. (*Cover image*)
- Maher PM, H-H Chou, E Hahn, T-J Wen, **PS Schnable** (2006) GRAMA: genetic mapping analysis of temperature gradient capillary electrophoresis data. **Theoretical Applied Genetics**, 113(1):156-162. (Epub: 2006 Apr 20)
- Swanson-Wagner RA\*, Y Jia\*, R DeCook, LA Borsuk, D Nettleton, **PS Schnable** (2006). All possible modes of gene action are observed in a global comparison of gene expression in a maize F<sub>1</sub> hybrid and its inbred parents. **Proceedings National Academy Science**, 103(18): 6805-6810. (Epub: 2006 Apr 25; "*recommended*" by the Faculty of 1000 Biology; identified by Thomson Reuters Scientific's Essential Science Indicators as the most highly cited paper in the research front map "On Applying Genome-Wide Selection"; podcast solicited by ScienceWatch.com: <http://www.in-cites.com/media/podcasts/PatSchnable.mp3>)
- Skibbe DS, X Wang, X Zhao, LA Borsuk, D Nettleton, **PS Schnable** (2006) Scanning microarrays at multiple intensities enhances discovery of differentially expressed genes. **Bioinformatics**, 22(15):1863-1870. (Epub: 2006 May 26)



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- Yandeau-Nelson MD, BJ Nikolau, **PS Schnable** (2006) Effects of *trans*-acting genetic modifiers on the rates and distribution of meiotic recombination across the *al-sh2* interval of maize. **Genetics**, 174:101-112. (Epub: 2006 Jul 2; “recommended” by the *Faculty of 1000 Biology*)
- Fu Y, TJ Wen, YI Ronin, HD Chen, L Guo, DI Mester, Y Yang, M Lee, AB Korol, DA Ashlock, **PS Schnable** (2006) Genetic dissection of intermated recombinant inbred lines using a new genetic map of maize. **Genetics**, 174(3): 1671-1683. (Epub 2006 Sep 1)
- Ohtsu K, H Takahashi, **PS Schnable**, M Nakazono (2007) Cell type-specific gene expression profiling in plants by using a combination of laser microdissection and high-throughput technologies. **Plant & Cell Physiology**, 48(1):3-7. (Epub: 2006 Dec 5)
- Emrich SJ\*, WB Barbazuk\*, L Li, **PS Schnable** (2007) Gene discovery and annotation using LCM-454 transcriptome sequencing. **Genome Research**, 17(1): 69-73. (Epub: 2006 Nov 9)
- Emrich SJ\*, L Li\*, TJ Wen, MD Yandeau-Nelson, Y Fu, L Guo, HH Chou, S Aluru, DA Ashlock, **PS Schnable** (2007) Nearly identical paralogs: implications for maize (*Zea mays* L.) genome evolution. **Genetics**, 175(1):429-439. (Epub: 2006 Nov 16) (*Featured in Science (315:302) as in Editor’s Choice: Highlights of the recent literature; selected as an Editors’ Choice by MaizeGDB, 12/06*).
- Travers SE, MD Smith, J Bai, SH Hulbert, JE Leach, **PS Schnable**, AK Knapp, GA Milliken, PA Fay, A Saleh, KA Garrett (2007) Ecological genomics: making the leap from model systems in the lab to native populations in the field. **Front Ecol Environ**, 5(1):19-24.
- Li J, AP Hsia, **PS Schnable** (2007) Recent advances in plant recombination. **Current Opinion in Plant Science**, 10(2):131-135. (Epub: 8 Feb 2007)
- Buckner B, J Beck, KF Browning, AE Fritz, LD Grantham, E Hoxha, ZN Kamvar, AN Lough, O Nikolova, **PS Schnable**, MJ Scanlon, and D Janick-Buckner (2007) Involving undergraduates in the annotation and analysis of global gene expression studies: creation of a maize shoot apical meristem expression database. **Genetics**, 176(2):741-747.
- Kalyanaraman A, SJ Emrich, **PS Schnable**, S. Aluru (2007) Assembling genomes on large-scale parallel computers. **Journal of Parallel and Distributed Computing**, Vol. 67:1240-1255. (*Special issue devoted to IPDPS best papers*)
- Zhang X, S Madi, LA Borsuk, DS Nettleton, RJ Elshire, B Buckner, D Janick-Buckner, J Beck, M Timmermans, **PS Schnable**, MJ Scanlon (2007) Laser microdissection of narrow sheath mutant maize uncovers novel gene expression in the shoot apical meristem. **PLoS Genetics**, 3(6):1040-1052. (*Selected an Editors’ Choice by MaizeGDB, 7/07*).
- Li J, LC Harper, I Golubovskaya, CR Wang, DF Weber, RB Meeley, J McElverd, B Bowen, WZ Cande, **PS Schnable** (2007) Functional analysis of maize RAD51 in meiosis and double-strand break repair. **Genetics**, 176(3): 1469–1482. (*Selected by journal*)

*editors as an “Issue Highlight”; selected as an Editors’ Choice by MaizeGDB, 8/07).*

- Barbazuk WB, SJ Emrich, HD Chen, L Li, **PS Schnable** (2007) SNP discovery via 454 transcriptome sequencing. **Plant J**, 51(5): 910-918. (*Cited in Wikipedia: <http://en.wikipedia.org/wiki/RNA-Seq>*)
- Ohtsu K, M Smith, SJ Emrich, LA Borsuk, R Zhou, T Chen, X Zhang, M Timmermans, J Beck, B Buckner, D Janick-Buckner, D Nettleton, MJ Scanlon, **PS Schnable** (2007) Global gene expression analysis of the shoot apical meristem of maize (*Zea mays* L.). **Plant J**, 52(3):391-404. (*“Recommended” by the Faculty of 1000 Biology; selected as an Editors’ Choice by MaizeGDB, 10/07).*
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- 10,704,091 Genotyping by next-generation sequencing (issued 7 July 2020)
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