

Development of a 63K SNP Array for Cotton and High-density Mapping of Intra- and Inter-specific Populations of *Gossypium* spp.

Amanda M. Hulse-Kemp^{1,2}, Jana Lemm³, Joerg Plieske³, Hamid Ashrafi⁴, Ramesh Buyyarapu⁵, David D. Fang⁶, James Frelichowski⁷, Marc Giband^{8,9}, Steve Hague¹, Lori L. Hinze⁷, Kelli J. Kochan¹⁰, Penny K. Riggs^{10,2}, Jodi A. Scheffler¹¹, Joshua A. Udall¹², Mauricio Ulloa¹³, Shirley S. Wang⁷, Qian-Hao Zhu¹⁴, Sumit K. Bag¹⁵, Archana Bhardwaj¹⁵, John J. Burke¹³, Robert L. Byers¹², Michel Claverie⁸, Michael A. Gore¹⁶, David B. Harker¹², Md S. Islam⁶, Johnie N. Jenkins¹⁷, Don C. Jones¹⁸, Jean-Marc Lacape⁸, Danny J. Llewellyn¹⁴, Richard G. Percy⁷, Alan E. Pepper^{19,2}, Jesse A. Poland²⁰, Krishan Mohan Rai¹⁵, Samir V. Sawant¹⁵, Sunil Kumar Singh¹⁵, Andrew Spriggs¹⁴, Jen M. Taylor¹⁴, Fei Wang¹, Scott M. Yourstone¹², Xiuting Zheng¹, Cindy T. Lawley²¹, Martin W. Ganai³, Allen Van Deynze⁴, Iain W. Wilson¹⁴, David M. Stelly^{1,2,22}

¹Department of Soil & Crop Sciences, Texas A&M University, College Station, Texas 77843, USA

²Interdisciplinary Degree Program in Genetics, Texas A&M University, College Station, Texas 77843, USA

³TraitGenetics GmbH, 06466 Gatersleben, Germany

⁴Department of Plant Sciences and Seed Biotechnology Center, University of California-Davis, Davis, California 95616, USA

⁵Dow AgroSciences, Trait Genetics & Technologies, Indianapolis, Indiana 46268, USA

⁶USDA-ARS-SRRC, Cotton Fiber Bioscience Research Unit, New Orleans, Louisiana 70124, USA

⁷USDA-ARS-SPARC, Crop Germplasm Research Unit, College Station, Texas 77845, USA

⁸CIRAD, UMR AGAP, Montpellier, F34398, France

⁹EMBRAPA, Algodão, Nucleo Cerrado, 75.375-000 Santo Antônio de Goias, GO, Brazil

¹⁰Department of Animal Science, Texas A&M University, College Station, Texas, 77843, USA

¹¹USDA-ARS, Jamie Whitten Delta States Research Center, Stoneville, Mississippi 38776, USA

¹²Brigham Young University, Plant and Wildlife Science Department, Provo, Utah 84602, USA

¹³USDA-ARS, PA, Plant Stress and Germplasm Development Research Unit, Lubbock, Texas 79415, USA

¹⁴CSIRO Agriculture Flagship, Black Mountain Laboratories, ACT 2601, Australia

¹⁵CSIR-National Botanical Research Institute, Plant Molecular Biology Division, Lucknow-226001, UP, India

¹⁶Plant Breeding and Genetics Section, School of Integrative Plant Science, Cornell University, Ithaca, New York, 14853, USA

¹⁷USDA-ARS, Genetics and Precision Agriculture Research, Mississippi State, Mississippi, 39762, USA

¹⁸Cotton Incorporated, Agricultural Research, Cary, North Carolina, 27513, USA

¹⁹Department of Biology, Texas A&M University, College Station, Texas, 77843, USA

²⁰Wheat Genetics Resource Center, Department of Plant Pathology and Department of Agronomy, Kansas State University, Manhattan, Kansas, 66506, USA

²¹Illumina Inc., 499 Illinois Street, San Francisco, California, 94158, USA

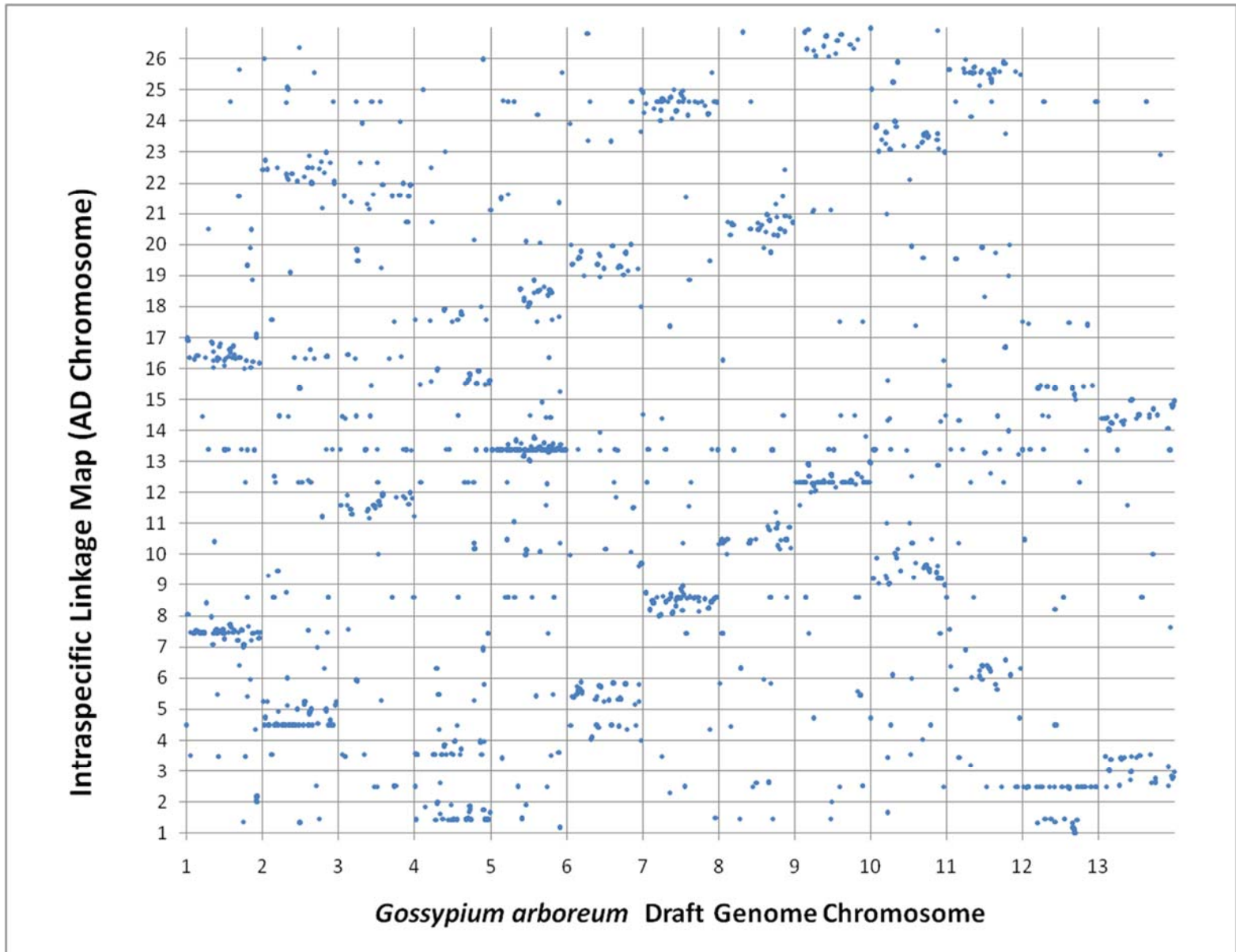
²²Corresponding Author, email: stelly@tamu.edu

Cotton sequences utilized for array construction are available at: <http://www.cottongen.org>

Corresponding author: David M. Stelly, Texas A&M University, 370 Olsen Blvd., 2474 TAMU, College Station, TX 77843-2474. 979-845-2745 (Phone). 979-845-0456 (Fax). stelly@tamu.edu.

DOI: 10.1534/g3.115.018416

A



B

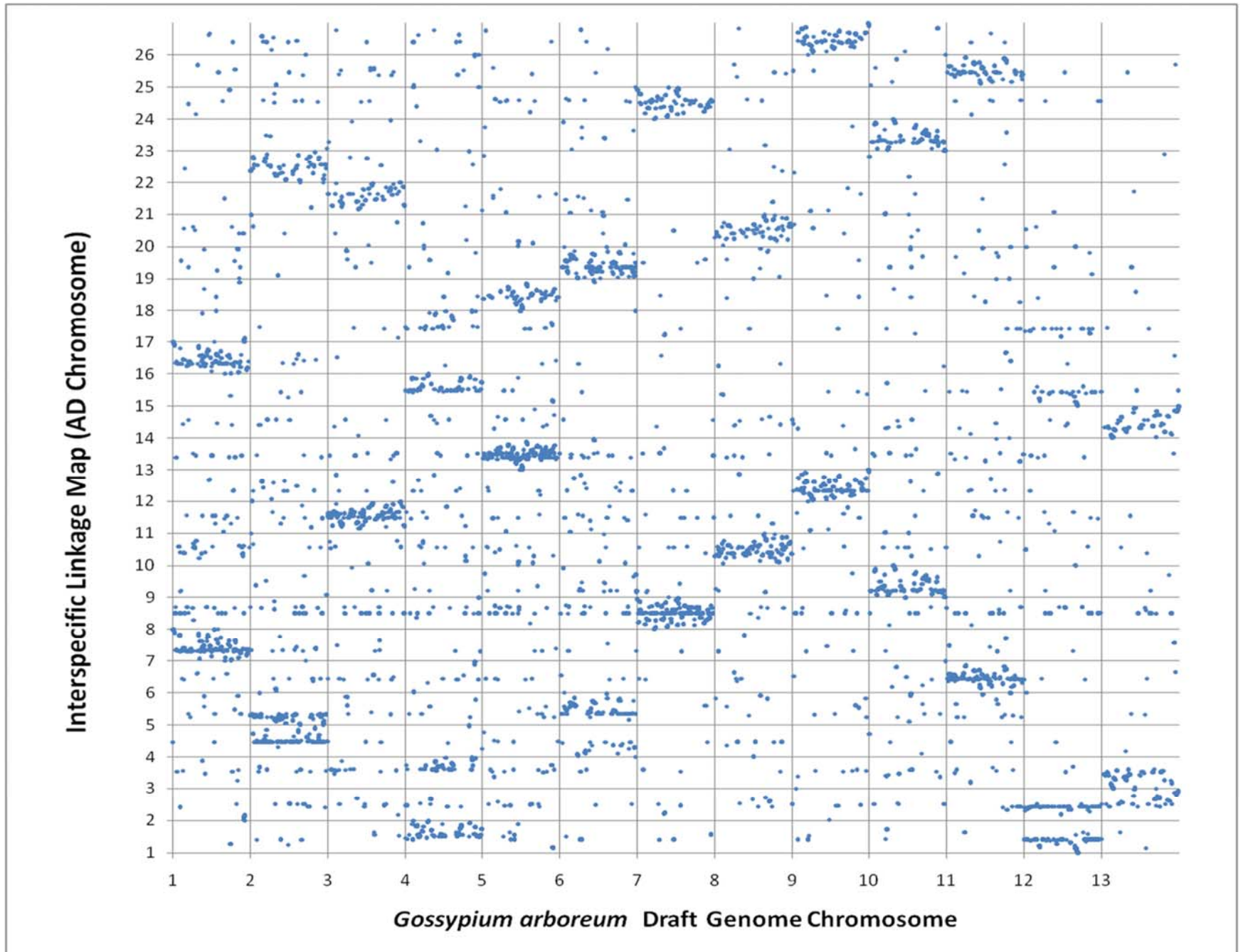


Figure S1 Dot plot of the syntenic positions of SNP markers in the allotetraploid linkage maps versus the BGI *G. arboreum* draft genome. The 26 allotetraploid chromosomes are shown on the y-axis and the 13 chromosomes of *G. arboreum* are shown on the x-axis. A.) Intra-specific linkage map displaying positions of 3,863 mapped SNP in *G. hirsutum* with alignments to *G. arboreum*. B.) Inter-specific linkage map (*G. hirsutum* genetic standard line Texas Marker -1 by *G. barbadense* line 3-79) displaying positions of 11,344 mapped SNP with alignments to *G. arboreum*.

Tables S1-S2

Available for download at www.g3journal.org/lookup/suppl/doi:10.1534/g3.115.018416/-/DC1

Table S1 Excel spreadsheet listing all 70K markers and their descriptions on the CottonSNP63K.

Table S2 Excel spreadsheet showing results of assay design of discovery group sets using Illumina's Assay Design Tool.