

# John P. Didion, PhD

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## Education

Doctor of Philosophy, Bioinformatics, University of North Carolina, Chapel Hill, NC, 2008-2014.

Bachelor of Science, Computer Science, Northwestern University, Evanston, IL, 2001.

## Positions Held

2014-Present	<b>Collins Group, National Human Genome Research Institute</b> <i>Postdoctoral Fellow</i> Investigating the role of epigenetics in common complex disease, especially type 2 diabetes.	Bethesda, MD
2009-2014	<b>Pardo-Manuel de Villena Laboratory, Univ. of North Carolina</b> <i>Research Assistant</i> Characterized the genetic determinants of two meiotic drive systems in the mouse. First, conducted a GWAS of wild mice to identify genes associated with the accumulation of Robertsonian translocations. Second, mapped a novel meiotic drive locus, <i>R2d2</i> , and multiple modifier loci responsible for extreme TRD in the Collaborative Cross. Also developed CLASP, a software tool for validation of cell lines used in research.	Chapel Hill, NC
2007-2008	<b>Aebersold Laboratory, Institute for Systems Biology</b> <i>Computational Biology Software Engineer</i> Developed informatics software to support proteomics research. Created TIQAM, a workflow management system for MRM (Multiple Reaction Monitoring) experiments.	Seattle, WA
2004-2007	<b>Muze, Inc.</b> <i>Software Development Engineer</i>	Seattle, WA
2003-2004	<b>Encyclopaedia Britannica, Online Services</b> <i>Software Developer</i>	Chicago, IL
2001-2003	<b>ThoughtWorks, LLC</b> <i>Software Developer/Consultant</i>	Chicago, IL

## Publications

9. **Didion JP**, et al. High-throughput SNP profiling of mouse cell lines identifies their strain origin and reveals cross-contamination and widespread aneuploidy. *BMC Genomics* 2014, in press.
8. Calaway JD, Lenarcic AB, **Didion JP**, Wang JR, Searle JB, McMillan L, Valdar W, Pardo-Manuel de Villena F. Genetic architecture of skewed X inactivation in the laboratory mouse. *PLoS Genetics* 2013, e1003853.
7. **Didion JP** and Pardo-Manuel de Villena F. Deconstructing *Mus gemischus*: advances in understanding ancestry, structure and variation in the genome of the laboratory mouse. *Mammalian Genome*

2013 24:1-2.  
Cover article

6. **Didion JP\***, Yang H\*, et al. Discovery of novel variants in genotyping arrays improves genotype retention and reduces ascertainment bias. *BMC Genomics* 2012, 13:34.  
\* Co-first author
5. Collaborative Cross Consortium. The genome architecture of the Collaborative Cross mouse genetic reference population. *Genetics* 2012, 190:389-401.  
Cover article
4. Yang H, Wang J, **Didion JP**, et al. Subspecific Origin and Haplotype Diversity in the Laboratory Mouse. *Nature Genetics* 2011, 43:648-655.
3. Aylor D, ...11 others..., **Didion JP**, et al. Genetic Analysis of Complex Traits in the Emerging Collaborative Cross. *Genome Research* 2011, 21:1213-1222.
2. Eisener-Dorman A\*, **Didion JP\***, Santos C\*, Calaway JD\*. The 23rd International Mammalian Genome Conference meeting report. *Mammalian Genome* 2010, 21:217-223.  
\* Co-first author
1. Lange V, Malmstrom JA, **Didion JP**, et al. Targeted Quantitative Analysis of *Streptococcus pyogenes* Virulence Factors by Multiple Reaction Monitoring. *Molecular & Cellular Proteomics* 2008, 7:1489-1500.

### *Submitted and In Prep*

**Didion JP**, et al. A multi-megabase copy number gain causes maternal transmission ratio distortion on mouse Chromosome 2. Under review.

**Didion JP**, et al. Genetic loci associated with preferential segregation of Robertsonian translocations identified by genome-wide association study of wild mice. In prep.

Crowley JJ, ...13 others..., **Didion JP**, et al. Pervasive allelic imbalance revealed by allele-specific gene expression in highly divergent mouse crosses. Under review.

Calabrese JM, Starmer J, Yee D, Fedoriw AM, Smith K, Safi A, **Didion JP**, et al. Defining principles of gene and regulatory element imprinting in mouse trophoblast stem cells. Under review.

Chandler RL, Damrauer JS, Raab J, **Didion JP**, et al. Concurrent ARID1A loss and PIK3CA activation leads to aggressive ovarian tumorigenesis in the mouse. Under review.

### Honors and Awards

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| 2009-2010 | <b>Bioinformatics and Computational Biology Training Grant (GM067553-04)</b><br>Institution-awarded fellowship |
| 2009/9    | <b>International Mammalian Genome Society Fellowship</b><br>Travel grant                                       |

## Invited Presentations

2012/2	<b>High-throughput mammalian genetics</b> University of North Carolina
2011/1	<b>High-throughput epigenetics: a methylation assay for the mouse</b> Center for Genome Dynamics (Bar Harbor, ME)

## Other Presentations, Meetings and Posters

2013/9	<b>27th Intl. Mammalian Genome Conference (Salamanca, Spain)</b> <i>Verne Chapman Young Scientist Award</i>	oral presentation
2013/5	<b>12th Annual Meeting of the Complex Traits Community (Madison, WI)</b> <i>Chicago Prize for Best Graduate Student Presentation</i>	oral presentation
2012/9	<b>16th EBM Conference (Marseille, France)</b>	oral presentation, poster
2012/9	<b>UNC Genetics Department Retreat (Myrtle Beach, SC)</b>	oral presentation
2011/9	<b>UNC Genetics Department Retreat (Myrtle Beach, SC)</b>	poster
2011/6	<b>Genetics Society of America Mouse Genetics (Washington D.C.)</b>	poster
2011/6	<b>National Centers for Systems Biology Annual Meeting (Duke University)</b>	poster
2010/10	<b>23rd Intl. Mammalian Genome Conference (Heraklion, Greece)</b> <i>Genome Research Award for Outstanding Poster</i>	oral presentation, poster
2010/9	<b>UNC Genetics Department Retreat (Myrtle Beach, SC)</b>	poster
2010/5	<b>9th Annual Meeting of the Complex Traits Community (Chicago, IL)</b>	oral presentation
2009/9	<b>22nd Intl. Mammalian Genome Conference (San Diego, CA)</b>	oral presentation, poster
2009/9	<b>UNC Genetics Department Retreat (Asheville, NC)</b>	poster

## Teaching

2013-14	<b>Undergraduate senior research project</b> Mentor
2013	<b>Genetic Analysis 2</b> Teaching Assistant

## Professional Memberships and Service

2013-2015	<b>Secretariat, International Mammalian Genome Society</b> Honorary Member
2013/9	<b>Abstract Review Committee, UNC Genetics Department Retreat</b>

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