

**Online workshop on
Molecular data analysis through
Bioinformatics tools**

**Linkage mapping, QTL analysis and Genome wide
association mapping (GWAS)**



Sujan Mamidi
Sr. Scientist (Computational Biology)
HudsonAlpha Institute for Biotechnology
Huntsville, AL





Sujan Mamidi

HudsonAlpha Institute for Biotechnology
Verified email at hudsonalpha.org - [Homepage](#)

Genomics Statistical Genetics Population and Quantitative... Bioinformatics

FOLLOW

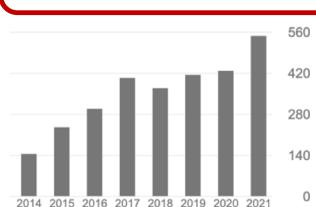
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TITLE	CITED BY	YEAR
A reference genome for common bean and genome-wide analysis of dual domestications J Schmutz, PE McClean, S Mamidi, GA Wu, SB Cannon, J Grimwood, ... Nature genetics 46 (7), 707-713	981	2014
Genome-Wide Association Study Reveals Novel Quantitative Trait Loci Associated with Resistance to Multiple Leaf Spot Diseases of Spring Wheat G Suraj, M Sujan, B Michael, X Mai, BG Gina, BA Tika Plos One 9 (9), e108179	141	2014
Genome-Wide Association Analysis Identifies Candidate Genes Associated with Iron Deficiency Chlorosis in Soybean S Mamidi, S Chikara, RJ Goos, DL Hyten, D Annam, SM Moghaddam, ... The Plant Genome 4 (3), 154-164	136	2011
Synteny mapping between common bean and soybean reveals extensive blocks of shared	125	2010

Summary

- 17+ years of research
- 5+ years teaching
- ~ 51 Research Articles
- 1 book chapter
- 15+ supervisions
- 30+ collaborations
- 10+ workshops
- 70+ posters/presentations

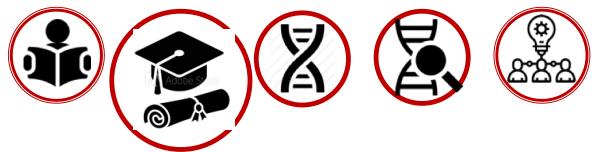
EDUCATION



- **BSc (Agriculture)**

ANGRAU, Bapatla, AP, India

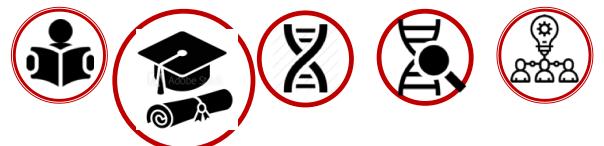




Ph.D (Genomics and Bioinformatics)

North Dakota State University, Fargo, US





- Located in Fargo, North Dakota
- Temperatures in winter < 0 C (-18F), Cold days feels like -40C
- About 50 inches of snow in winter



Theor Appl Genet (2010) 121:1103–1116
DOI 10.1007/s00122-010-1375-9

ORIGINAL PAPER

Linkage Map

Syntenic relationships among legumes revealed
using a gene-based genetic linkage map of common bean
(*Phaseolus vulgaris* L.)

Melody McConnell · Sujan Mamidi · Rian Lee ·
Shireen Chikara · Monica Rossi · Roberto Papa ·
Phillip McClean

McClean et al. BMC Genomics 2010, 11:184
<http://www.biomedcentral.com/1471-2164/11/184>

Synteny/Comparative Genomics

RESEARCH ARTICLE

Open Access



Synteny mapping between common bean and soybean reveals extensive blocks of shared loci

Phillip E McClean^{1,2*}, Sujan Mamidi¹, Melody McConnell¹, Shireen Chikara¹, Rian Lee^{1,2}

Genome-Wide Association Analysis Identifies Candidate Genes Associated with Iron Deficiency Chlorosis in Soybean **Association Mapping**

Sujan Mamidi, Shireen Chikara, R. Jay Goos, David L. Hyten, Deepa Annam, Samira Mafi Moghaddam, Rian K. Lee, Perry B. Cregan, and Phillip E. McClean*

CSIRO PUBLISHING

Functional Plant Biology, 2011, 38, 953–967
<http://dx.doi.org/10.1071/FP11124>

RESEARCH FR

Heredity

Population Genomics/ Demography

Investigation of the domestication of common bean (*Phaseolus vulgaris*) using multilocus sequence data

Sujan Mamidi^{A,D,E}, Monica Rossi^B, Deepa Annam^C, Samira Moghaddam^{A,D},
Rian Lee^{A,D}, Roberto Papa^B and Phillip McClean^{A,D}

Heredity (2013) 110, 267–276
© 2013 Macmillan Publishers Limited. All rights reserved 0018-067W/13
www.nature.com/hdy

ORIGINAL ARTICLE

Demographic factors shaped diversity in the two gene pools of wild common bean *Phaseolus vulgaris* L.

S Mamidi^{1,2}, M Rossi³, SM Moghaddam^{1,2}, D Annam⁴, R Lee^{1,2}, R Papa^{3,5} and PE McClean^{1,2}



- **Research Scientist**

North Dakota State University, Fargo, US



Black beans



Navy beans



Light Red Kidney beans



Dark Red Kidney beans



Cranberry beans



Great Northern beans



Pinto beans



Yellow eye beans



Small Red beans



White Kidney beans



Pink beans



Soldier beans



Soybean

Common Bean

Variant Discovery

ORIGINAL RESEARCH ARTICLE
published: 13 May 2014
doi: 10.3389/fpls.2014.00466

Developing market class specific InDel markers from next generation sequence data in *Phaseolus vulgaris* L.

Samira Mafi Moghadam^{1,2}, Qijian Song², Sujan Mamidi^{1,2}, Jeremy Schmutz⁴, Rian Lee², Perry Cregan¹, Juan M. Osorno² and Phillip E. McClean^{1,*}

¹ Department of Plant Sciences, North Dakota State University, Fargo, ND, USA

² Department of Plant Sciences, North Dakota State University, Fargo, ND, USA

³ Soybean Genetics and Improvement Laboratory, United States Department of Agriculture, Agricultural Research Service, Beltsville, MD, USA

⁴ HudsonAlpha Institute, Huntsville, AL, USA

Introgression; QTL analysis

Sequence-Based Introgression Mapping
Identifies Candidate White Mold Tolerance Genes
in Common Bean

Sujan Mamidi, Phillip N. Miklas, Jennifer Trapp, Erin Felicetti, Jane Grimwood,
Jeremy Schmutz, Rian Lee, and Phillip E. McClean*

nature
genetics

OPEN

Whole Genome; Pop Genomics

A reference genome for common bean and genome-wide
analysis of dual domestications

Jeremy Schmutz^{1,2,17}, Phillip E McClean^{3,17}, Sujan Mamidi³, G Albert Wu¹, Steven B Cannon⁴, Jane Grimwood², Jerry Jenkins², Shengqiang Shu¹, Qijian Song⁵, Carolina Chavarro⁶, Miryada Torres-Torres⁶, Valerie Geffroy^{7,8}, Samira Mafi Moghadam³, Dongying Gao⁹, Brian Abernathy⁹, Kerrie Barry¹, Matthew Blair⁹, Mark A Brick¹⁰, Mansi Chovatia¹, Paul Gepts¹¹, David M Goodstein¹, Michael Gonzales⁹, Uffe Hellsten¹, David I Hyten^{5,16}, Gaofeng Jia⁵, James D Kelly¹², Dave Kudrna¹³, Rian Lee³, Manon M S Richard⁷, Phillip N Miklas¹⁴, Juan M Osorno³, Josiane Rodrigues^{5,16}, Vincent Thareau⁷, Carlos A Urrea¹⁵, Mei Wang¹, Yeisoo Yu¹³, Ming Zhang¹, Rod A Wing¹³, Perry B Cregan⁵, Daniel S Rokhsar¹ & Scott A Jackson⁶

Mol Breeding (2016) 36:6
DOI 10.1007/s11032-015-0431-1

Methodology



Optimization of genotyping by sequencing (GBS) data
in common bean (*Phaseolus vulgaris* L.)

Stephan Schröder · Sujan Mamidi ·
Rian Lee · Michael R. McKain ·
Phillip E. McClean · Juan M. Osorno

Association Mapping

OPEN ACCESS Freely available online

PLOS ONE



Genome-Wide Association Studies Identifies Seven Major
Regions Responsible for Iron Deficiency Chlorosis in
Soybean (*Glycine max*)

Sujan Mamidi^{1,2}, Rian K. Lee^{1,2}, Jay R. Goos³, Phillip E. McClean^{1,2*}



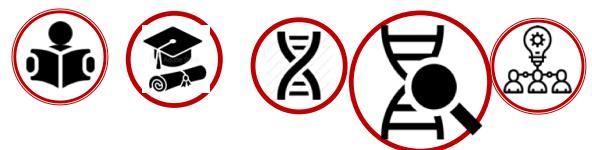
Sr. Scientist (Computational Biology)
HudsonAlpha Institute for Biotechnology,
Huntsville, US





HudsonAlpha is a **nonprofit research** institute dedicated to:

1. Research
2. Education
3. Knowledge Sharing- Bioentrepreneurs
4. Bioinformatics & Sequencing
5. Genomics Medicine



First clinic to offer genomic medicine

Mission:

- By using the power of genomics, solve cases of **undiagnosed disease** and provide answers to families and physicians.
- Give patients the best clinical care and a **positive medical experience**.

<https://www.al.com/news/2019/11/now-4-years-old-alabama-genomic-medicine-clinic-is-changing-lives.html>



- Screened about **400 patients**.
 - Two-thirds were adults, and one third were children.

Some of the more common symptoms seen include, but aren't limited to:

- Unexplained developmental delay or intellectual disability
- Neurological (seizures, epilepsy, poor muscle tone, neuropathy, myopathy, etc)
- Immune deficiency
- Other unexplained physical symptoms
- Unexplained heart abnormalities or disease

HudsonAlpha's connections to Human Genome

- Myers led a team at the Stanford Human Genome Center, CA
- Contributed > 10 percent of the data.
- Jane Grimwood, and Jeremy Schmutz Assembled 320 Mbp of human chromosomes **5, 16 and 19.**



articles

Initial sequencing and analysis of the human genome

International Human Genome Sequencing Consortium*

*A partial list of authors appears on the opposite page. Affiliations are listed at the end of the paper.

The human genome holds an extraordinary trove of information about human development, physiology, medicine and evolution. Here we report the results of an international collaboration to produce and make freely available a draft sequence of the human genome. We also present an initial analysis of the data, describing some of the insights that can be gleaned from the sequence.

The rediscovery of Mendel's laws of heredity in the opening weeks of the 20th century^{1–3} sparked a scientific quest to understand the nature and content of genetic information that has propelled biology for the last hundred years. The scientific progress made falls naturally into four main phases, corresponding roughly to the four quarters of the century. The first established the cellular basis of heredity: the chromosomes. The second defined the molecular basis of heredity: the DNA double helix. The third unlocked the informational basis of heredity, with the discovery of the biological mechanism by which cells read the information contained in genes and with

coordinate regulation of the genes in the clusters.

- There appear to be about 30,000–40,000 protein-coding genes in the human genome—only about twice as many as in worm or fly. However, the genes are more complex, with more alternative splicing generating a larger number of protein products.
- The full set of proteins (the 'proteome') encoded by the human genome is more complex than those of invertebrates. This is due in part to the presence of vertebrate-specific protein domains and motifs (an estimated 7% of the total), but more to the fact that vertebrates appear to have arranged pre-existing components into a



Richard Myers

President and Science director,
HudsonAlpha Institute for
Biotechnology

Previous: Stanford Human Genome
Center, Stanford University School of
Medicine



Jeremy Schmutz Computational Genomics

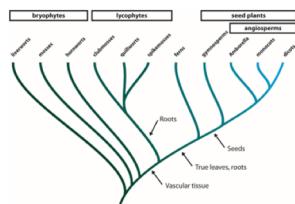
- **Plant Program Leader,**
Department of Energy,
Joint Genome Institute,
Walnut Creek, Calif.
- **Faculty Investigator,**
HudsonAlpha Institute
for Biotechnology.



Jane Grimwood

- Experimental Genomics
- **Faculty Investigator,**
HudsonAlpha Institute
for Biotechnology
 - **Adjunct Faculty,**
Department of Biology,
University of Alabama
in Huntsville

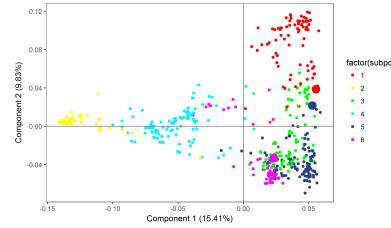
Genomics for discovery science



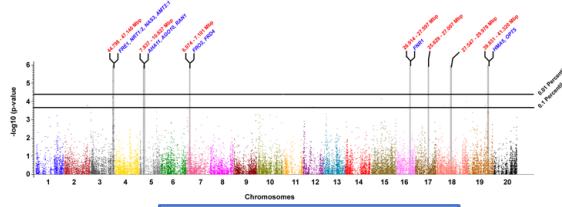
Comparative Genomics



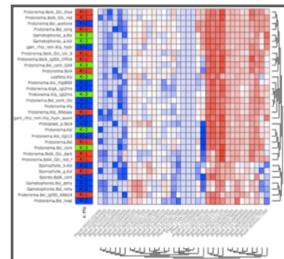
Reference Genome



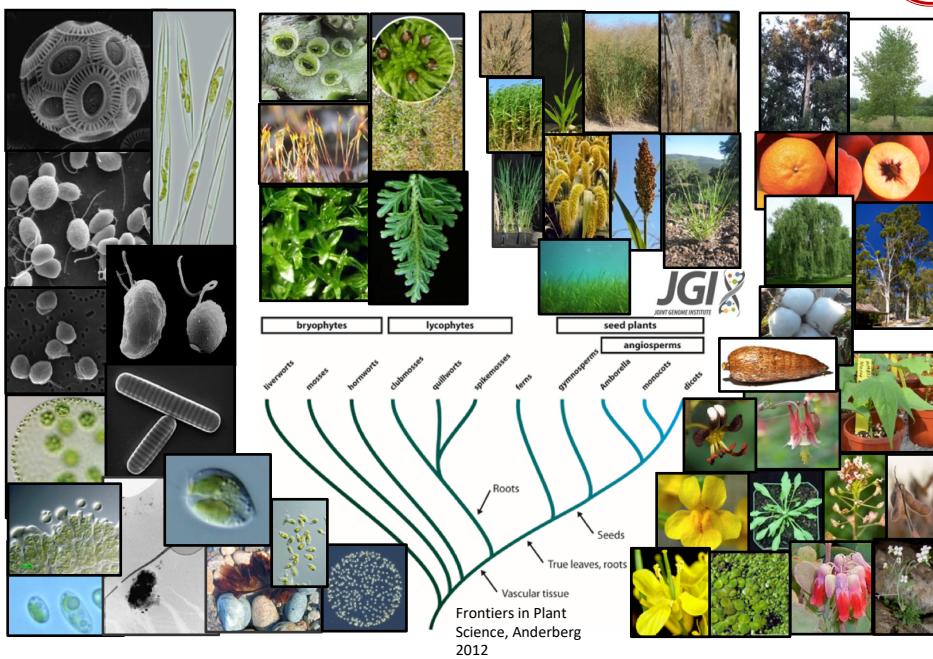
Population Diversity & Genomics



Quantitative Genomics



Transcriptomics and Functional Assays



- More than 150 plants sequenced
- Represents > 50% of plant genomes sequenced



Insights into Land Plant Evolution Garnered from the *Marchantia polymorpha* Genome



A reference genome for common bean and genome-wide analysis of dual domestications



The *Selaginella* Genome Identifies Genetic Changes Associated with the Evolution of Vascular Plants



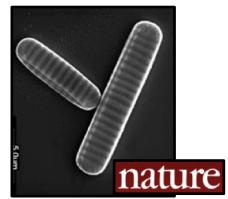
The high-quality draft genome of peach (*Prunus persica*) identifies unique patterns of genetic diversity, domestication and genome evolution



Sequencing of diverse mandarin, pummelo and orange genomes reveals complex history of admixture during citrus domestication



The genome of *Eucalyptus grandis*



Evolutionary genomics of the cold-adapted diatom *Fragilaropsis cylindrus*



Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs



The *Capsella rubella* genome and the genomic consequences of rapid mating system evolution



Repeated polyploidization of *Gossypium* genomes and the evolution of spinnable cotton fibres



Reference genome sequence of the model plant *Setaria*



The genome of the seagrass *Zostera marina* reveals angiosperm adaptation to the sea



THOMSON REUTERS

HIGHLY CITED RESEARCHERS

>100 Plant Genome Projects

>50 Science, Nature & Cell Papers

My Work

- Variant discovery
- Population genomics
 - Climatic Adaptation
 - Demography
 - Adaptation
- Epi genomics
- Pan genomics
- Functional Genomics



Switchgrass



Setaria



Poplar



Panicum



Pecan



Zostera



Wheatgrass



Sorghum



Beans



Spagnum



ARTICLE

<https://doi.org/10.1038/s41467-019-10769-x>

OPEN

The genomic landscape of molecular responses to natural drought stress in *Panicum hallii*

John T. Lovell^{1,2}, Jerry Jenkins³, David B. Lowry³, Sujan Mamidi¹, Avinash Sreedasyam¹, Xiaoyu Weng², Kerrie Barry⁴, Jason Bonnette², Brandon Campetelli², Chris Daum⁴, Sean P. Gordon^{1,4,8}, Billie A. Gould⁵, Alibina Khasanova², Anna Lipzen⁴, Alice MacQueen¹, Juan Diego Palacio-Mejia¹, Christopher Plotz¹, Eugene V. Shakirov^{2,5}, Shengqiang Shu^{1,4}, Yuko Yoshinaga⁴, Matt Zane⁴, Dave Kudrna⁶, Jason D. Talag⁶, Daniel Rokhsar⁷, Jane Grimwood¹, Jeremy Schmutz^{1,4} & Thomas E. Juenger²

Hofmeister et al. *Genome Biology* (2020) 21:259
<https://doi.org/10.1186/s13059-020-02162-5>

Genome Biology

RESEARCH

Open Access



A genome assembly and the somatic genetic and epigenetic mutation rate in a wild long-lived perennial *Populus trichocarpa*

Brigitte T. Hofmeister¹, Johanna Denkena², Maria Colomé-Tatché^{2,3,4}, Yadollah Shahriary⁵, Rashmi Hazarika^{5,6}, Jane Grimwood^{7,8}, Sujan Mamidi⁷, Jerry Jenkins⁷, Paul P. Grabowski⁷, Avinash Sreedasyam⁷, Shengqiang Shu⁸, Kerrie Barry⁹, Kathleen Lail⁹, Catherine Adam⁹, Anna Lipzen⁴, Rotem Sorek¹⁰, Dave Kudrna¹⁰, Jayson Talag¹⁰, Rod Wing¹⁰, David W. Hall¹¹, Daniel Jacobsen¹², Gerald A. Tuskan¹², Jeremy Schmutz^{7,8}, Frank Johannes^{5,6*} and Robert J. Schmitz^{6,11*}

Genome sequences of wild and landrace tepary bean provide insight into evolution and domestication under heat stress **Nature Communications**

Samira MafiMoghadam^{1,2}, Atena Oladzad³, Chushin Koh^{4,5}, Larissa Ramsay⁴, John P. Hart⁶, Sujan Mamidi⁷, Genevieve Hoopes¹, Avinash Sreedasyam⁷, Andrew Wiersma^{1,2}, Dongyan Zhao¹, Jane Grimwood^{7,8}, John P. Hamilton¹, Jerry Jenkins^{7,8}, Brieanne Vaillancourt¹, Joshua C. Wood¹, Daniel Rokhsar⁸, Jeremy Schmutz^{7,8}, Sateesh Kagale⁹, Timothy Porch⁶, Kirstin E. Bett⁴, C. Robin Buell^{1,2,10}, and Phillip E. McClean³

nature
biotechnology

RESOURCE

<https://doi.org/10.1038/s41587-020-0681-2>

OPEN

A genome resource for green millet *Setaria viridis* enables discovery of agronomically valuable loci

Sujan Mamidi^{1,11}, Adam Healey^{1,11}, Pu Huang^{2,6,11}, Jane Grimwood¹, Jerry Jenkins¹, Kerrie Barry³, Avinash Sreedasyam¹, Shengqiang Shu^{1,3}, John T. Lovell¹, Maximilian Feldman^{1,7}, Jinxia Wu^{1,4}, Yuning Yu¹, Cindy Chen¹, Jenifer Johnson¹, Hitoshi Sakakibara^{5,8}, Takatoshi Kiba^{1,5,8}, Tetsuya Sakurai^{1,5,9}, Rachel Tavares^{2,10}, Dmitri A. Nusinow², Ivan Baxter², Jeremy Schmutz^{1,13}, Thomas P. Brutnell^{2,4} and Elizabeth A. Kellogg^{1,2,10}

Nature

Article

Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass

<https://doi.org/10.1038/s41586-020-03127-1>

Received: 1 July 2020

John T. Lovell^{1,38,12}, Alice H. MacQueen^{2,38}, Sujan Mamidi^{1,38}, Jason Bonnette^{2,38},Jerry Jenkins^{1,38}, Joseph D. Napier², Avinash Sreedasyam¹, Adam Healey¹, Adam Session^{3,4},Shengqiang Shu¹, Kerrie Barry³, Stacy Bonos⁵, LoriBeth Boston¹, Christopher Daum³,

WORKSHOP REQUIREMENTS

Linkage map

- **Carthagene**

<https://miat.inrae.fr/CarthaGene/CarthaGene-releases.html>. (or)

<http://carlit.toulouse.inra.fr/cgi-bin/CG>

Instructions: <https://miat.inrae.fr/CarthaGene/install-1.2.html>

Prerequisites:

- ActiveTcl 8.4 <https://miat.inrae.fr/CarthaGene/tclpack/ActiveTcl8.4.19.4.292682-win32-ix86-threaded.exe>

CITATION: S. de Givry, M. Bouchez, P. Chabrier, D. Milan, et T. Schiex (2005).

CARTHAGENE: multipopulation integrated genetic and radiated hybrid mapping.
Bioinformatics, 21(8): 1703-1704 .

A screenshot of a web browser window with a red border. The address bar shows the URL: miat.inrae.fr/CarthaGene/CarthaGene-releases.html. Below the address bar is a navigation bar with icons for back, forward, and refresh. The main content area displays a heading "Microsoft Windows" and a sub-heading "Microsoft Windows 1.3.beta (23/01/2013 15:15)". A table below lists a single file entry:

Filename	Date	Size	D/L	Archive	Type
carthagene-1.3.beta-Windows.exe	23/01/2013 15:15	2,25 MB	1,164	i386	Other

QTL MAPPING

- **Qgene:** <http://www.qgene.org/qgene/download.php>

Manual:

http://www.qgene.org/qgene/current/docs/manual/Main_window.html

Prerequisites:

- Java JDK - <https://www.oracle.com/java/technologies/javase-downloads.html>

CITATION: Joehanes R, Nelson JC. (2008). QGene 4.0, an extensible Java QTL-analysis platform. Bioinformatics 24: 2788-2789.

← → ⌂ qgene.org/qgene/Download_QGene_all.php ☆ ⚑ EN G ↻ S Update :

_apps Learn CS program... Python Learn to Type | Fr... R » Other Bookmarks Reading List

QGene

Software for QTL data exploration

QGENE

- News
- History
- Download
- User manual
- Javadoc
- FAQ
- Contact us

Download QGene

QGene download links

[QGene 4.4.0](#)

The updated manual for 4.4.0 is still being prepared.

Javadoc for 4.4.0 is not ready yet. Sorry.

J. C. Nelson (jcn(at)ksu(dot)edu) and R. Joehanes
October 23, 2016

Association mapping

- **TASSEL** - <https://www.maizegenetics.net/tassel>

Manual:

<https://bitbucket.org/tasseladmin/tassel-5-source/wiki/UserManual>

Prerequisites:

- Java - <https://www.oracle.com/java/technologies/javase-downloads.html>

CITATION: Bradbury PJ, Zhang Z, Kroon DE, Casstevens TM, Ramdoss Y, Buckler ES. (2007) [TASSEL: Software for association mapping of complex traits in diverse samples](#). *Bioinformatics* **23**:2633-2635.

← → C maizegenetics.net/tassel ☆ 🔒 EN G 🖌 S Update

Apps Learn CS program... Python Learn to Type | Fr... R » Other Bookmarks Reading List

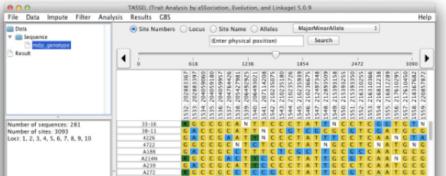


TASSEL 5.0

TASSEL Version 5.0 ([Getting Started!](#))
(Build: October 27, 2021 [Requires: Java 1.8](#))

[Tassel 5 Mac OS](#)
[Tassel 5 Windows 64 Bit](#)
[Tassel 5 Windows 32 Bit](#)
[Tassel 5 UNIX](#)

Alignment Viewer



Other Software

- **Textpad** - <https://www.textpad.com/download/index.html#downloads8>
- Microsoft Excel or WPS office (<https://www.wps.com/index.html>)

Slides and Data

- https://github.com/sujanmamidi/QuantGenomics_Tirupati