



COLLECTION

G3 10th Anniversary collection

The Genetics Society of America launched G3: Genes|Genomes|Genetics as an Open Access journal in the summer of 2011. Ten years and more than 3000 publications later, we are proud that our community believes in our mission and chooses to publish with us.

And that mission? Serving the field of genetics by publishing high-quality, useful, and robust papers without subjective decisions about impact.

In this special 10th anniversary collection, explore some of the most cited papers from G3's first decade—from Investigations and Mutant Screen Reports to Genome Reports and Software & Data Resources.

Also, be sure to check out Editor in Chief Brenda Andrews' s anniversary [editorial](#), as well as our special [celebratory store](#).

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- [Genome Reports](#)
- [Mutant Screen Reports](#)
- [Software and Data Resources](#)

HIGHEST CITED

INVESTIGATIONS

Canopy Temperature and Vegetation Indices from High-Throughput Phenotyping Improve Accuracy of Pedigree and Genomic Selection for Grain Yield in Wheat

Jessica Rutkoski et al.

G3 Genes|Genomes|Genetics, Volume 6, Issue 9, 1 September 2016, Pages 2799–2808,
<https://doi.org/10.1534/g3.116.032888>

		CT-GF	CT-VEG	GNDVI-GF	GNDVI-VEG	RNDVI-GF	RNDVI-VEG	GY	
Training Set									
Test set									*
Univariate prediction									
		Phenotypic data present		Phenotypic data absent		Phenotypic data present		Phenotypic data absent	
Training Set									
Test set									*
Multivariate prediction									
		Phenotypic data present		Phenotypic data absent		Phenotypic data present		Phenotypic data absent	
Training Set									
Test set									*

Genomic selection can be applied prior to phenotyping, enabling shorter breeding cycles and greater rates of genetic gain relative to phenotypic selection. Traits measured using high-throughput phenotyping based on proximal or remote sensing could be useful for improving pedigree and genomic

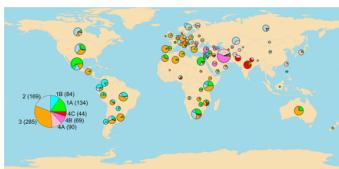
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INVESTIGATIONS

A Genome-Wide Association Study of Resistance to Stripe Rust (*Puccinia striiformis* f. sp. *tritici*) in a Worldwide Collection of Hexaploid Spring Wheat (*Triticum aestivum* L.)

Marco Maccaferri et al.

G3 Genes|Genomes|Genetics, Volume 5, Issue 3, 1 March 2015, Pages 449–465,
<https://doi.org/10.1534/g3.114.014563>



New races of *Puccinia striiformis* f. sp. *tritici* (Pst), the causal pathogen of wheat stripe rust, show high virulence to previously deployed resistance genes and are responsible for large yield losses worldwide. To identify new sources of resistance we performed a genome-wide association study

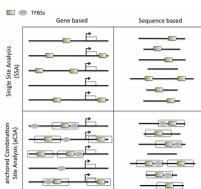
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INVESTIGATIONS

oPOSSUM-3: Advanced Analysis of Regulatory Motif Over-Representation Across Genes or ChIP-Seq Datasets

Andrew T Kwon et al.

G3 Genes|Genomes|Genetics, Volume 2, Issue 9, 1 September 2012, Pages 987–1002,
<https://doi.org/10.1534/g3.112.003202>



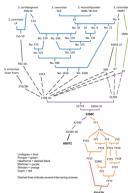
oPOSSUM-3 is a web-accessible software system for identification of over-represented transcription factor binding sites (TFBS) and TFBS families in either DNA sequences of co-expressed genes or sequences generated from high-throughput methods, such as ChIP-Seq. Validation of the system with known ...

INVESTIGATIONS

The Reference Genome Sequence of *Saccharomyces cerevisiae*: Then and Now

Stacia R Engel et al.

G3 Genes|Genomes|Genetics, Volume 4, Issue 3, 1 March 2014, Pages 389–398,
<https://doi.org/10.1534/g3.113.008995>



The genome of the budding yeast *Saccharomyces cerevisiae* was the first completely sequenced from a eukaryote. It was released in 1996 as the work of a worldwide effort of hundreds of researchers. In the time since, the yeast genome has been intensively studied by geneticists, molecular biologists, ...

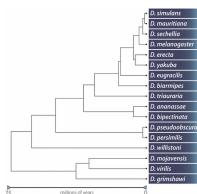
GENOME REPORT

Highly Contiguous Genome Assemblies of 15 *Drosophila* Species Generated Using Nanopore Sequencing

Danny E Miller et al.

G3 Genes|Genomes|Genetics, Volume 8, Issue 10, 1 October 2018, Pages 3131–3141,
<https://doi.org/10.1534/g3.118.200160>

The *Drosophila* genus is a unique group containing a wide range of species that occupy diverse ecosystems. In addition to the most widely studied species, *Drosophila melanogaster*, many other members in this genus also possess a well-developed set of genetic tools. Indeed, high-quality genomes exist ...

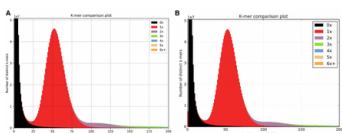


GENOME REPORTS

A Genome Assembly of the Barley ‘Transformation Reference’ Cultivar Golden Promise

Miriam Schreiber et al.

G3 Genes|Genomes|Genetics, Volume 10, Issue 6, 1 June 2020, Pages 1823–1827, <https://doi.org/10.1534/g3.119.401010>



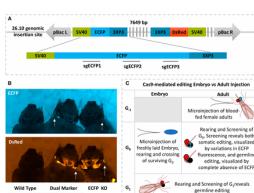
Barley (*Hordeum vulgare*) is one of the most important crops worldwide and is also considered a research model for the large-genome small grain temperate cereals. Despite genomic resources improving all the time, they are limited for the cv. Golden Promise, the most efficient genotype for genetic ...

INVESTIGATIONS

Cas9-Mediated Gene-Editing in the Malaria Mosquito *Anopheles stephensi* by ReMOT Control

Vanessa M Macias et al.

G3 Genes|Genomes|Genetics, Volume 10, Issue 4, 1 April 2020, Pages 1353–1360, <https://doi.org/10.1534/g3.120.401133>



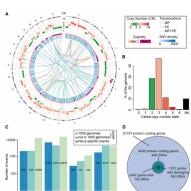
Innovative tools are essential for advancing malaria control and depend on an understanding of molecular mechanisms governing transmission of malaria parasites by *Anopheles* mosquitoes. CRISPR/Cas9-based gene disruption is a powerful method to uncover underlying biology of vector-pathogen ...

INVESTIGATIONS

The Genomic and Transcriptomic Landscape of a HeLa Cell Line

Jonathan J M Landry et al.

G3 Genes|Genomes|Genetics, Volume 3, Issue 8, 1 August 2013, Pages 1213–1224, <https://doi.org/10.1534/g3.113.005777>



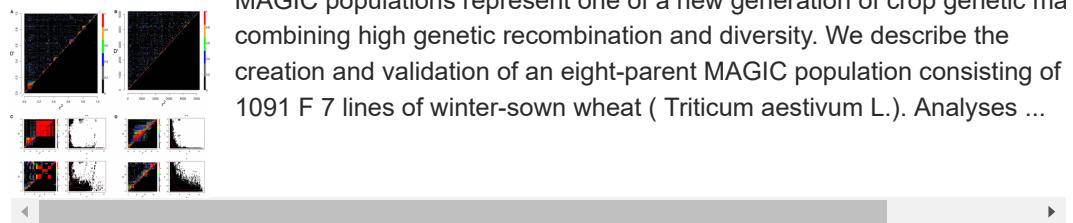
HeLa is the most widely used model cell line for studying human cellular and molecular biology. To date, no genomic reference for this cell line has been released, and experiments have relied on the human reference genome. Effective design and interpretation of molecular genetic studies performed ...

INVESTIGATIONS

An Eight-Parent Multiparent Advanced Generation Inter-Cross Population for Winter-Sown Wheat: Creation, Properties, and Validation

Ian J Mackay et al.

G3 Genes|Genomes|Genetics, Volume 4, Issue 9, 1 September 2014, Pages 1603–1610, <https://doi.org/10.1534/g3.114.012963>

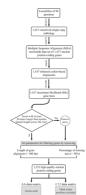


INVESTIGATIONS

Reconstructing the Backbone of the Saccharomycotina Yeast Phylogeny Using Genome-Scale Data

Xing-Xing Shen et al.

G3 Genes|Genomes|Genetics, Volume 6, Issue 12, 1 December 2016, Pages 3927–3939, <https://doi.org/10.1534/g3.116.034744>



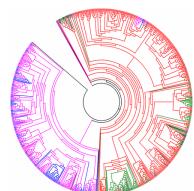
Understanding the phylogenetic relationships among the yeasts of the subphylum Saccharomycotina is a prerequisite for understanding the evolution of their metabolisms and ecological lifestyles. In the last two decades, the use of rDNA and multilocus data sets has greatly advanced our understanding ...

INVESTIGATIONS

Single and Multi-trait GWAS Identify Genetic Factors Associated with Production Traits in Common Bean Under Abiotic Stress Environments

Atena Oladzad et al.

G3 Genes|Genomes|Genetics, Volume 9, Issue 6, 1 June 2019, Pages 1881–1892, <https://doi.org/10.1534/g3.119.400072>



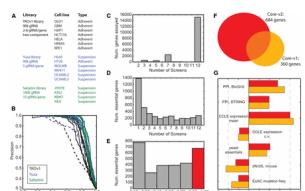
The genetic improvement of economically important production traits of dry bean (*Phaseolus vulgaris* L.), for geographic regions where production is threatened by drought and high temperature stress, is challenging because of the complex genetic nature of these traits. Large scale SNP data sets for ...

INVESTIGATIONS

Evaluation and Design of Genome-Wide CRISPR/SpCas9 Knockout Screens

Traver Hart et al.

G3 Genes|Genomes|Genetics, Volume 7, Issue 8, 1 August 2017, Pages 2719–2727, <https://doi.org/10.1534/g3.117.041277>



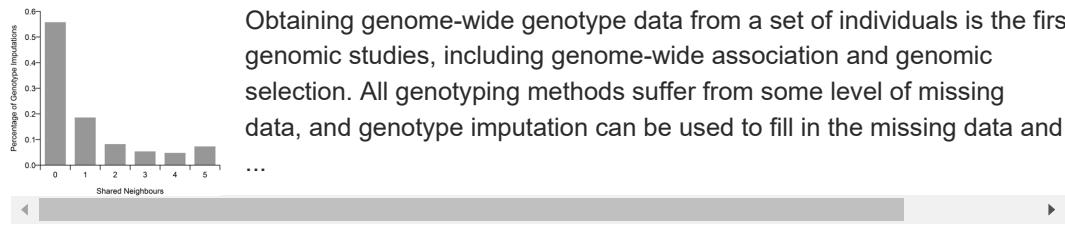
The adaptation of CRISPR/SpCas9 technology to mammalian cell lines is transforming the study of human functional genomics. Pooled libraries of CRISPR guide RNAs (gRNAs) targeting human protein-coding genes and encoded in viral vectors have been used to systematically create gene knockouts in a ...

INVESTIGATIONS

LinkImpute: Fast and Accurate Genotype Imputation for Nonmodel Organisms

Daniel Money et al.

G3 Genes|Genomes|Genetics, Volume 5, Issue 11, 1 November 2015, Pages 2383–2390, <https://doi.org/10.1534/g3.115.021667>



Obtaining genome-wide genotype data from a set of individuals is the first step in many genomic studies, including genome-wide association and genomic selection. All genotyping methods suffer from some level of missing data, and genotype imputation can be used to fill in the missing data and

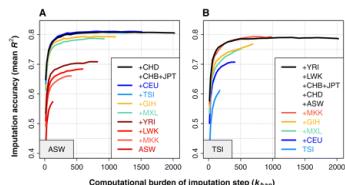
INVESTIGATION

Genotype Imputation with Thousands of Genomes

Bryan Howie et al.

G3 Genes|Genomes|Genetics, Volume 1, Issue 6, 1 November 2011, Pages 457–470,

<https://doi.org/10.1534/g3.111.001198>



Genotype imputation is a statistical technique that is often used to increase the power and resolution of genetic association studies. Imputation methods work by using haplotype patterns in a reference panel to predict unobserved genotypes in a study dataset, and a number of approaches have been ...

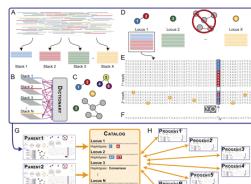
INVESTIGATION

Stacks: Building and Genotyping Loci De Novo From Short-Read Sequences

Julian M Catchen et al.

G3 Genes|Genomes|Genetics, Volume 1, Issue 3, 1 August 2011, Pages 171–182,

<https://doi.org/10.1534/g3.111.000240>



Advances in sequencing technology provide special opportunities for genotyping individuals with speed and thrift, but the lack of software to automate the calling of tens of thousands of genotypes over hundreds of individuals has hindered progress. Stacks is a software system that uses short-read ...

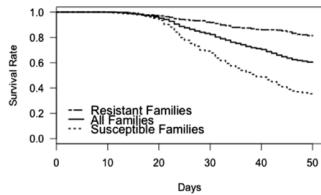
GENOMIC SELECTION

Genomic Predictions and Genome-Wide Association Study of Resistance Against *Piscirickettsia salmonis* in Coho Salmon (*Oncorhynchus kisutch*) Using ddRAD Sequencing

Agustín Barría et al.

G3 Genes|Genomes|Genetics, Volume 8, Issue 4, 1 April 2018, Pages 1183–1194,

<https://doi.org/10.1534/g3.118.200053>



Piscirickettsia salmonis is one of the main infectious diseases affecting coho salmon (*Oncorhynchus kisutch*) farming, and current treatments have been ineffective for the control of this disease. Genetic improvement for *P. salmonis* resistance has been proposed as a feasible alternative for the ...

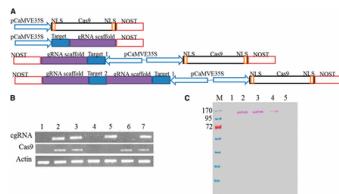
INVESTIGATIONS

RNA-Guided Genome Editing for Target Gene Mutations in Wheat

Santosh Kumar Upadhyay et al.

G3 Genes|Genomes|Genetics, Volume 3, Issue 12, 1 December 2013, Pages 2233–2238,

<https://doi.org/10.1534/g3.113.008847>



The clustered, regularly interspaced, short palindromic repeats-associated protein (Cas) system has been used as an efficient tool for genome editing. We report the application of CRISPR-Cas-mediated genome editing to wheat (*Triticum aestivum*), the most important food crop ...

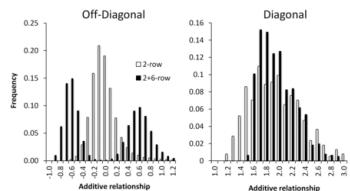
GENOMIC SELECTION

Shrinkage Estimation of the Realized Relationship Matrix

Jeffrey B Endelman, Jean-Luc Jannink

G3 Genes|Genomes|Genetics, Volume 2, Issue 11, 1 November 2012, Pages 1405–1413,

<https://doi.org/10.1534/g3.112.004259>



The additive relationship matrix plays an important role in mixed model prediction of breeding values. For genotype matrix X (loci in columns), the product XX' is widely used as a realized relationship matrix, but the scaling of this matrix is ambiguous. Our first objective was to derive a proper ...

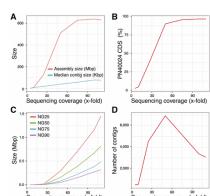
GENOME REPORTS

Diploid Genome Assembly of the Wine Grape Carménère

Andrea Minio et al.

G3 Genes|Genomes|Genetics, Volume 9, Issue 5, 1 May 2019, Pages 1331–1337,

<https://doi.org/10.1534/g3.119.400030>



In this genome report, we describe the sequencing and annotation of the genome of the wine grape Carménère (clone 02, VCR-702). Long considered extinct, this old French wine grape variety is now cultivated mostly in Chile where it was imported in the 1850s just before the European phylloxera ...

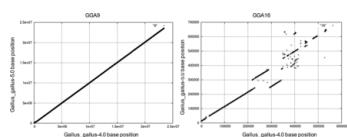
INVESTIGATIONS

A New Chicken Genome Assembly Provides Insight into Avian Genome Structure

Wesley C Warren et al.

G3 Genes|Genomes|Genetics, Volume 7, Issue 1, 1 January 2017, Pages 109–117,

<https://doi.org/10.1534/g3.116.035923>



The importance of the *Gallus gallus* (chicken) as a model organism and agricultural animal merits a continuation of sequence assembly improvement efforts. We present a new version of the chicken genome assembly (*Gallus_gallus-5.0*;

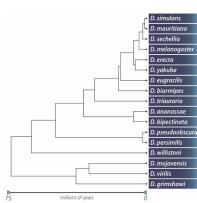
GCA_000002315.3), built from combined long single molecule sequencing ...

GENOME REPORTS

GENOME REPORT

Highly Contiguous Genome Assemblies of 15 Drosophila Species Generated Using Nanopore Sequencing

Danny E Miller et al.



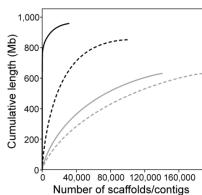
The *Drosophila* genus is a unique group containing a wide range of species that occupy diverse ecosystems. In addition to the most widely studied species, *Drosophila melanogaster*, many other members in this genus also possess a well-developed set of genetic tools. Indeed, high-quality genomes exist ...

GENOME REPORT

Highly Continuous Genome Assembly of Eurasian Perch (*Perca fluviatilis*) Using Linked-Read Sequencing

Mikhail Yu Ozerov et al.

G3 Genes|Genomes|Genetics, Volume 8, Issue 12, 1 December 2018, Pages 3737–3743,
<https://doi.org/10.1534/g3.118.200768>



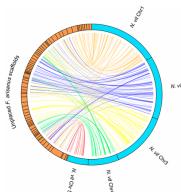
The Eurasian perch (*Perca fluviatilis*) is the most common fish of the Percidae family and is widely distributed across Eurasia. Perch is a popular target for professional and recreational fisheries, and a promising freshwater aquaculture species in Europe. However, despite its high ecological, ...

GENOME REPORTS

Whole Genome Sequencing of the Braconid Parasitoid Wasp *Fopius arisanus*, an Important Biocontrol Agent of Pest Teprtid Fruit Flies

Scott M Geib et al.

G3 Genes|Genomes|Genetics, Volume 7, Issue 8, 1 August 2017, Pages 2407–2411,
<https://doi.org/10.1534/g3.117.040741>



The braconid wasp *Fopius arisanus* (Sonan) is an important biological control agent of tropical and subtropical pest fruit flies, including two important global pests, the Mediterranean fruit fly (*Ceratitis capitata*), and the oriental fruit fly (*Bactrocera dorsalis*). The goal of this study was ...

GENOME REPORTS

Comparative Genomics of Two Sequential *Candida glabrata* Clinical Isolates

Luis Vale-Silva et al.

G3 Genes|Genomes|Genetics, Volume 7, Issue 8, 1 August 2017, Pages 2413–2426,
<https://doi.org/10.1534/g3.117.042887>

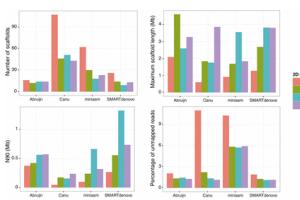


Candida glabrata is an important fungal pathogen which develops rapid antifungal resistance in treated patients. It is known that azole treatments lead to antifungal resistance in this fungal species and that multidrug efflux transporters are involved in this process. Specific mutations in the ...

GENOME REPORT

High-Quality de Novo Genome Assembly of the *Dekkera bruxellensis* Yeast Using Nanopore MinION Sequencing

Téo Fournier et al.



Genetic variation in natural populations represents the raw material for phenotypic diversity. Species-wide characterization of genetic variants is crucial to have a deeper insight into the genotype-phenotype relationship. With the advent of new sequencing strategies and more recently the release ...

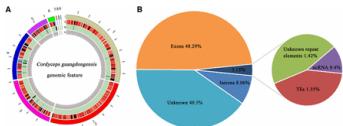
GENOME REPORTS

Whole Genome Sequence of an Edible and Potential Medicinal Fungus, *Cordyceps guangdongensis*

Chenghua Zhang et al.

G3 Genes|Genomes|Genetics, Volume 8, Issue 6, 1 June 2018, Pages 1863–1870,

<https://doi.org/10.1534/g3.118.200287>



Cordyceps guangdongensis is an edible fungus which was approved as a novel food by the Chinese Ministry of Public Health in 2013. It also has a broad prospect of application in pharmaceutical industries, with many medicinal activities. In this study, the whole genome of *C. guangdongensis* GD15, a ...

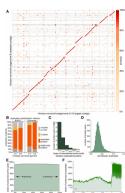
GENOME REPORT

Insight into the Recent Genome Duplication of the Halophilic Yeast *Hortaea werneckii*: Combining an Improved Genome with Gene Expression and Chromatin Structure

Sunita Sinha et al.

G3 Genes|Genomes|Genetics, Volume 7, Issue 7, 1 July 2017, Pages 2015–2022,

<https://doi.org/10.1534/g3.117.040691>



Extremophilic organisms demonstrate the flexibility and adaptability of basic biological processes by highlighting how cell physiology adapts to environmental extremes. Few eukaryotic extremophiles have been well studied and only a small number are amenable to laboratory cultivation and ...

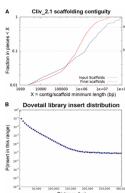
GENOME REPORTS

Improved Genome Assembly and Annotation for the Rock Pigeon (*Columba livia*)

Carson Holt et al.

G3 Genes|Genomes|Genetics, Volume 8, Issue 5, 1 May 2018, Pages 1391–1398,

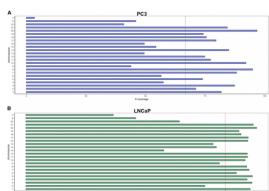
<https://doi.org/10.1534/g3.117.300443>



The domestic rock pigeon (*Columba livia*) is among the most widely distributed and phenotypically diverse avian species. *C. livia* is broadly studied in ecology, genetics, physiology, behavior, and evolutionary biology, and has recently emerged as a model for understanding the molecular basis of ...

GENOME REPORT

Whole-Genome Sequence of the Metastatic PC3 and LNCaP Human Prostate Cancer Cell Lines



The bone metastasis-derived PC3 and the lymph node metastasis-derived LNCaP prostate cancer cell lines are widely studied, having been described in thousands of publications over the last four decades. Here, we report short-read whole-genome sequencing (WGS) and de novo assembly of PC3 (ATCC ...

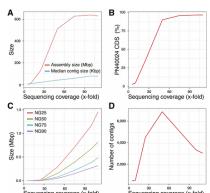
GENOME REPORTS

Diploid Genome Assembly of the Wine Grape Carménère

Andrea Minio et al.

G3 Genes|Genomes|Genetics, Volume 9, Issue 5, 1 May 2019, Pages 1331–1337,

<https://doi.org/10.1534/g3.119.400030>



In this genome report, we describe the sequencing and annotation of the genome of the wine grape Carménère (clone 02, VCR-702). Long considered extinct, this old French wine grape variety is now cultivated mostly in Chile where it was imported in the 1850s just before the European phylloxera ...

MUTANT SCREEN REPORTS

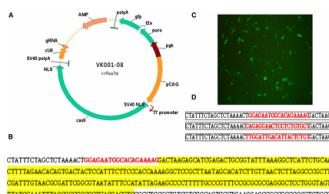
MUTANT SCREEN REPORT

Site-Directed Genome Knockout in Chicken Cell Line and Embryos Can Use CRISPR/Cas Gene Editing Technology

Qisheng Zuo et al.

G3 Genes|Genomes|Genetics, Volume 6, Issue 6, 1 June 2016, Pages 1787–1792,

<https://doi.org/10.1534/g3.116.028803>



The present study established an efficient genome editing approach for the construction of stable transgenic cell lines of the domestic chicken (*Gallus gallus domesticus*). Our objectives were to facilitate the breeding of high-yield, high-quality chicken strains, and to investigate gene function ...

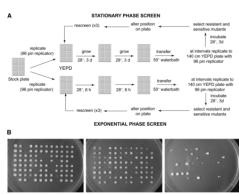
MUTANT SCREEN REPORTS

Saccharomyces cerevisiae Genes Involved in Survival of Heat Shock

Stefanie Jarolim et al.

G3 Genes|Genomes|Genetics, Volume 3, Issue 12, 1 December 2013, Pages 2321–2333,

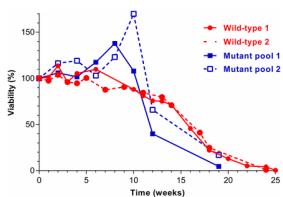
<https://doi.org/10.1534/g3.113.007971>



The heat-shock response in cells, involving increased transcription of a specific set of genes in response to a sudden increase in temperature, is a highly conserved biological response occurring in all organisms. Despite considerable attention to the processes activated during heat shock, less is ...

MUTANT SCREEN REPORT

Parallel Profiling of Fission Yeast Deletion Mutants for Proliferation and for Lifespan During Long-Term Quiescence



Genetic factors underlying aging are remarkably conserved from yeast to human. The fission yeast *Schizosaccharomyces pombe* is an emerging genetic model to analyze cellular aging. Chronological lifespan (CLS) has been studied in stationary-phase yeast cells depleted for glucose, which only survive ...

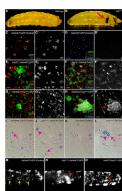
MUTANT SCREEN REPORT

A Genetic Screen Reveals an Unexpected Role for Yorkie Signaling in JAK/STAT–Dependent Hematopoietic Malignancies in *Drosophila melanogaster*

Abigail M Anderson et al.

G3 Genes|Genomes|Genetics, Volume 7, Issue 8, 1 August 2017, Pages 2427–2438,

<https://doi.org/10.1534/g3.117.044172>



A gain-of-function mutation in the tyrosine kinase JAK2 (JAK2 V617F) causes human myeloproliferative neoplasms (MPNs). These patients present with high numbers of myeloid lineage cells and have numerous complications. Since current MPN therapies are not curative, there is a need to find new ...

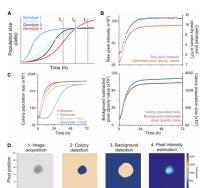
MUTANT SCREEN REPORT ORIGINAL ARTICLE

Scan–o–matic: High–Resolution Microbial Phenomics at a Massive Scale

Martin Zackrisson et al.

G3 Genes|Genomes|Genetics, Volume 6, Issue 9, 1 September 2016, Pages 3003–3014,

<https://doi.org/10.1534/g3.116.032342>



The capacity to map traits over large cohorts of individuals—phenomics—lags far behind the explosive development in genomics. For microbes, the estimation of growth is the key phenotype because of its link to fitness. We introduce an automated microbial phenomics framework that delivers accurate, ...

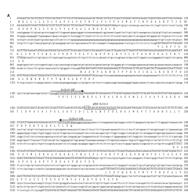
MUTANT SCREEN REPORT

CRISPR/Cas9–Mediated Genome Editing and Mutagenesis of EcChi4 in *Exopalaemon carinicauda*

Tianshu Gui et al.

G3 Genes|Genomes|Genetics, Volume 6, Issue 11, 1 November 2016, Pages 3757–3764,

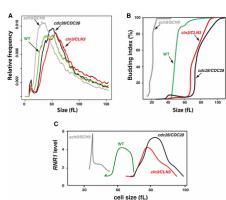
<https://doi.org/10.1534/g3.116.034082>



The development of the type II clustered regularly interspaced short palindromic repeats (CRISPR) system has resulted in the revolution of genetic engineering, and this technology has been applied in the genome editing of various species. However, there are no reports about target-specific genome ...

MUTANT SCREEN REPORTS

Genome–Wide Screen for Haploinsufficient Cell Size Genes in the Opportunistic Yeast *Candida albicans*



One of the most critical but still poorly understood aspects of eukaryotic cell proliferation is the basis for commitment to cell division in late G1 phase, called Start in yeast and the Restriction Point in metazoans. In all species, a critical cell size threshold coordinates cell growth with cell ...

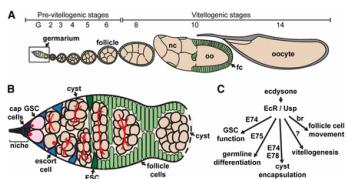
MUTANT SCREEN REPORTS

A Genetic Mosaic Screen Reveals Ecdysone-Responsive Genes Regulating Drosophila Oogenesis

Elizabeth T Ables et al.

G3 Genes|Genomes|Genetics, Volume 6, Issue 8, 1 August 2016, Pages 2629–2642,

<https://doi.org/10.1534/g3.116.028951>



Multiple aspects of Drosophila oogenesis, including germline stem cell activity, germ cell differentiation, and follicle survival, are regulated by the steroid hormone ecdysone. While the transcriptional targets of ecdysone signaling during development have been studied extensively, targets in the ...

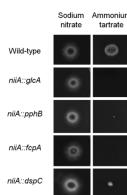
MUTANT SCREEN REPORT

Systematic Global Analysis of Genes Encoding Protein Phosphatases in Aspergillus fumigatus

Lizziane K Winkelströter et al.

G3 Genes|Genomes|Genetics, Volume 5, Issue 7, 1 July 2015, Pages 1525–1539,

<https://doi.org/10.1534/g3.115.016766>



Aspergillus fumigatus is a fungal pathogen that causes several invasive and noninvasive diseases named aspergillosis. This disease is generally regarded as multifactorial, considering that several pathogenicity determinants are present during the establishment of this illness. It is necessary to ...

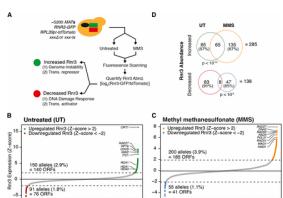
MUTANT SCREEN REPORTS

Leveraging DNA Damage Response Signaling to Identify Yeast Genes Controlling Genome Stability

Jason A Hendry et al.

G3 Genes|Genomes|Genetics, Volume 5, Issue 5, 1 May 2015, Pages 997–1006,

<https://doi.org/10.1534/g3.115.016576>



Oncogenesis frequently is accompanied by rampant genome instability, which fuels genetic heterogeneity and resistance to targeted cancer therapy. We have developed an approach that allows precise, quantitative measurement of genome instability in high-throughput format in the *Saccharomyces* ...

SOFTWARE AND DATA RESOURCES

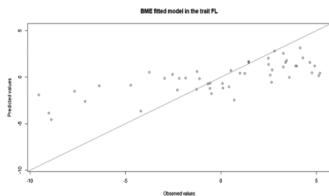
SOFTWARE AND DATA RESOURCES

An R Package for Bayesian Analysis of Multi-environment and Multi-trait Multi-environment Data for Genome-Based Prediction

Osval A Montesinos-López et al.

G3 Genes|Genomes|Genetics, Volume 9, Issue 5, 1 May 2019, Pages 1355–1369,

<https://doi.org/10.1534/g3.119.400126>



Evidence that genomic selection (GS) is a technology that is revolutionizing plant breeding continues to grow. However, it is very well documented that its success strongly depends on statistical models, which are used by GS to perform predictions of candidate genotypes that were not phenotyped.

...

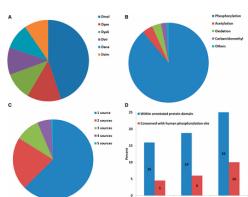
SOFTWARE AND DATA RESOURCES

iProteinDB: An Integrative Database of Drosophila Post-translational Modifications

Yanhui Hu et al.

G3 Genes|Genomes|Genetics, Volume 9, Issue 1, 1 January 2019, Pages 1–11,

<https://doi.org/10.1534/g3.118.200637>



Post-translational modification (PTM) serves as a regulatory mechanism for protein function, influencing their stability, interactions, activity and localization, and is critical in many signaling pathways. The best characterized PTM is phosphorylation, whereby a phosphate is added to an acceptor ...

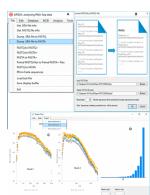
SOFTWARE AND DATA RESOURCES

ARSDA: A New Approach for Storing, Transmitting and Analyzing Transcriptomic Data

Xuhua Xia

G3 Genes|Genomes|Genetics, Volume 7, Issue 12, 1 December 2017, Pages 3839–3848,

<https://doi.org/10.1534/g3.117.300271>



Two major stumbling blocks exist in high-throughput sequencing (HTS) data analysis. The first is the sheer file size, typically in gigabytes when uncompressed, causing problems in storage, transmission, and analysis. However, these files do not need to be so large, and can be reduced without loss ...

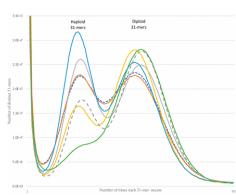
SOFTWARE AND DATA RESOURCES

Genomic Variation Among and Within Six Juglans Species

Kristian A Stevens et al.

G3 Genes|Genomes|Genetics, Volume 8, Issue 7, 1 July 2018, Pages 2153–2165,

<https://doi.org/10.1534/g3.118.200030>



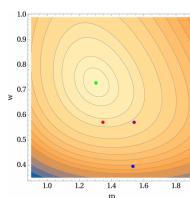
Genomic analysis in Juglans (walnuts) is expected to transform the breeding and agricultural production of both nuts and lumber. To that end, we report here the determination of reference sequences for six additional relatives of Juglans regia : Juglans sigillata (also from section Dioscaryon), ...

SOFTWARE AND DATA RESOURCES

rSalvador: An R Package for the Fluctuation Experiment

Qi Zheng

G3 *Genes|Genomes|Genetics*, Volume 7, Issue 12, 1 December 2017, Pages 3849–3856,
<https://doi.org/10.1534/g3.117.300120>



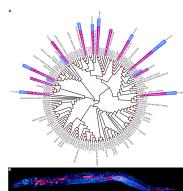
The past few years have seen a surge of novel applications of the Luria-Delbrück fluctuation assay protocol in bacterial research. Appropriate analysis of fluctuation assay data often requires computational methods that are unavailable in the popular web tool FALCOR. This paper introduces an R ...

SOFTWARE AND DATA RESOURCES

CeMbio – The *Caenorhabditis elegans* Microbiome Resource

Philipp Dirksen et al.

G3 *Genes|Genomes|Genetics*, Volume 10, Issue 9, 1 September 2020, Pages 3025–3039,
<https://doi.org/10.1534/g3.120.401309>



The study of microbiomes by sequencing has revealed a plethora of correlations between microbial community composition and various life-history characteristics of the corresponding host species. However, inferring causation from correlation is often hampered by the sheer compositional complexity ...

SOFTWARE AND DATA RESOURCES

Meta-analysis of Diets Used in Drosophila Microbiome Research and Introduction of the Drosophila Dietary Composition Calculator (DDCC)

Danielle N A Lesperance, Nichole A Broderick

G3 *Genes|Genomes|Genetics*, Volume 10, Issue 7, 1 July 2020, Pages 2207–2211,
<https://doi.org/10.1534/g3.120.401235>



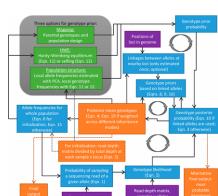
Nutrition is a major factor influencing many aspects of *Drosophila melanogaster* physiology. However, a wide range of diets, many of which are termed “standard” in the literature, are utilized for *D. melanogaster* research, leading to inconsistencies in reporting of nutrition-dependent phenotypes ...

SOFTWARE AND DATA RESOURCES

polyRAD: Genotype Calling with Uncertainty from Sequencing Data in Polyploids and Diploids

Lindsay V Clark et al.

G3 *Genes|Genomes|Genetics*, Volume 9, Issue 3, 1 March 2019, Pages 663–673,
<https://doi.org/10.1534/g3.118.200913>

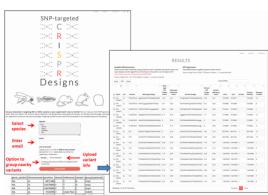


Low or uneven read depth is a common limitation of genotyping-by-sequencing (GBS) and restriction site-associated DNA sequencing (RAD-seq), resulting in high missing data rates, heterozygotes miscalled as homozygotes, and uncertainty of allele copy number in heterozygous polyploids. Bayesian ...

SOFTWARE AND DATA RESOURCES

SNP–CRISPR: A Web Tool for SNP–Specific Genome Editing

Chiao-Lin Chen et al.



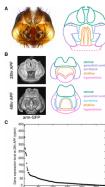
CRISPR-Cas9 is a powerful genome editing technology in which a single guide RNA (sgRNA) confers target site specificity to achieve Cas9-mediated genome editing. Numerous sgRNA design tools have been developed based on reference genomes for humans and model organisms. However, existing resources are ...

SOFTWARE AND DATA RESOURCES

An Atlas of Transcription Factors Expressed in Male Pupal Terminalia of *Drosophila melanogaster*

Ben J Vincent et al.

G3 Genes|Genomes|Genetics, Volume 9, Issue 12, 1 December 2019, Pages 3961–3972,
<https://doi.org/10.1534/g3.119.400788>



During development, transcription factors and signaling molecules govern gene regulatory networks to direct the formation of unique morphologies. As changes in gene regulatory networks are often implicated in morphological evolution, mapping transcription factor landscapes is important, especially ...
