

GeneWeaver: A tool for Integrative Functional Genomics

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Integrative Functional Genomics

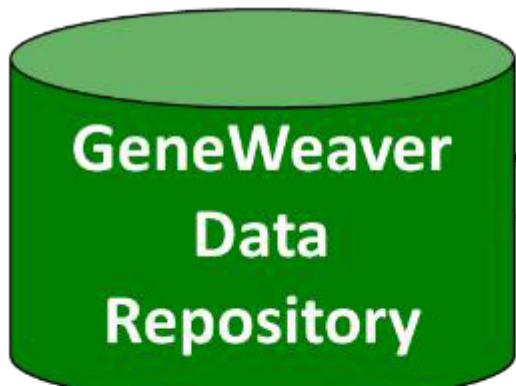
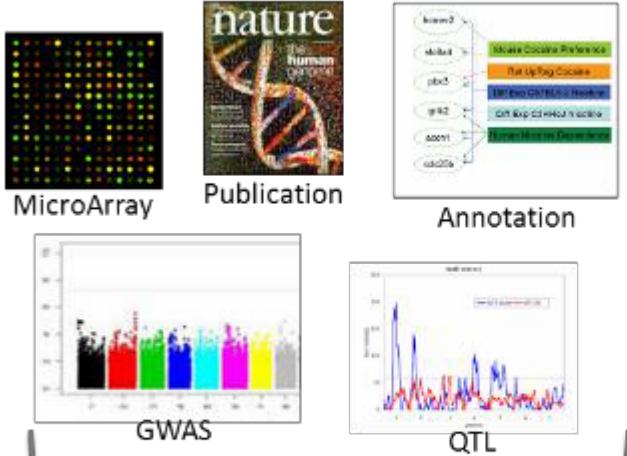
- “Biological Discovery Using Diverse High-Throughput Genomic Data”
- Goal: Integrate genetic and genomic investigation in human subjects and model organisms, to understand complex diseases.



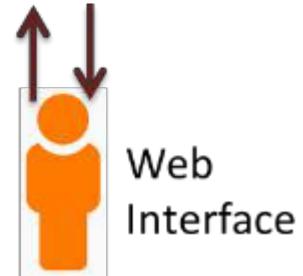
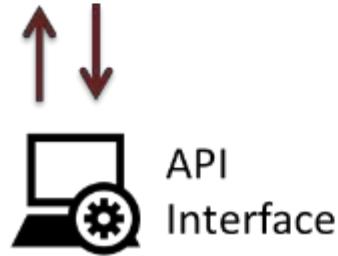
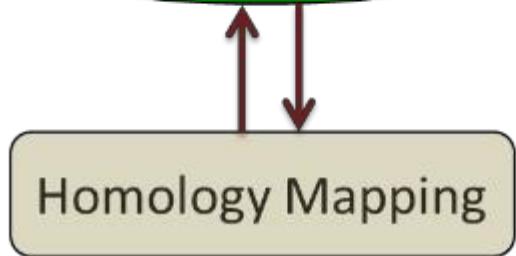
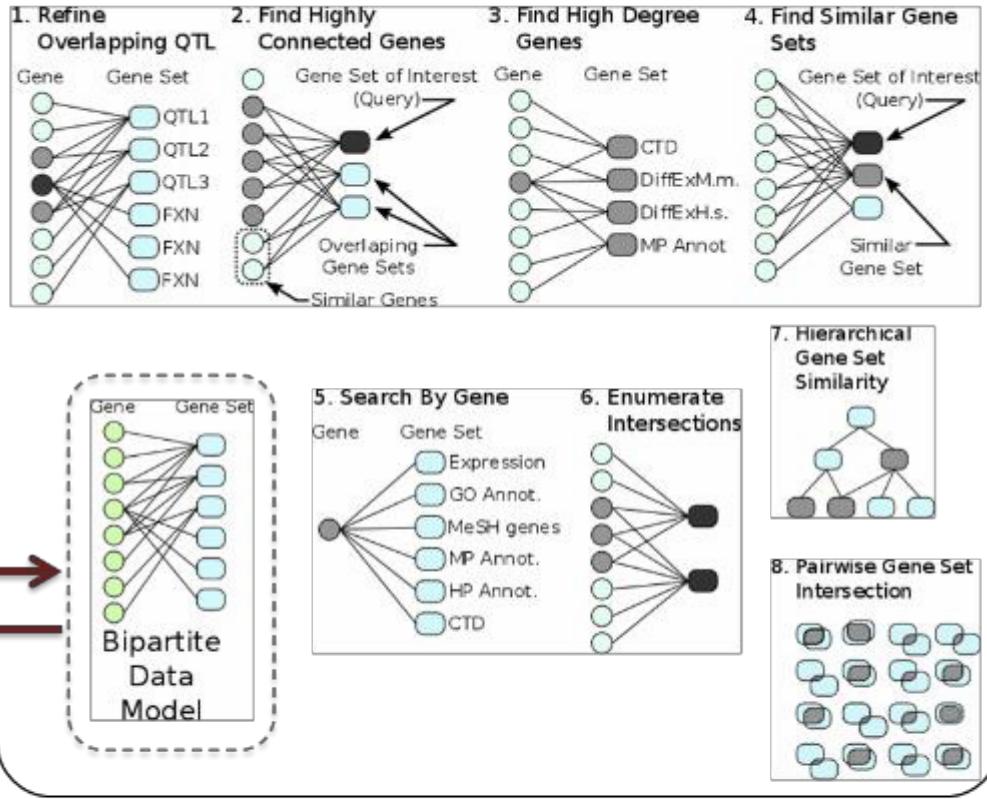
Integrative Functional Genomics

- 21st Century- Decreased costs of genome sequencing has brought the BigData boom, large data sets, with high diversity, numerous species, disease models, conditions.
- Aggregating and analyzing this data to answer questions related to the common and distinct molecular basis of disease.





Tools

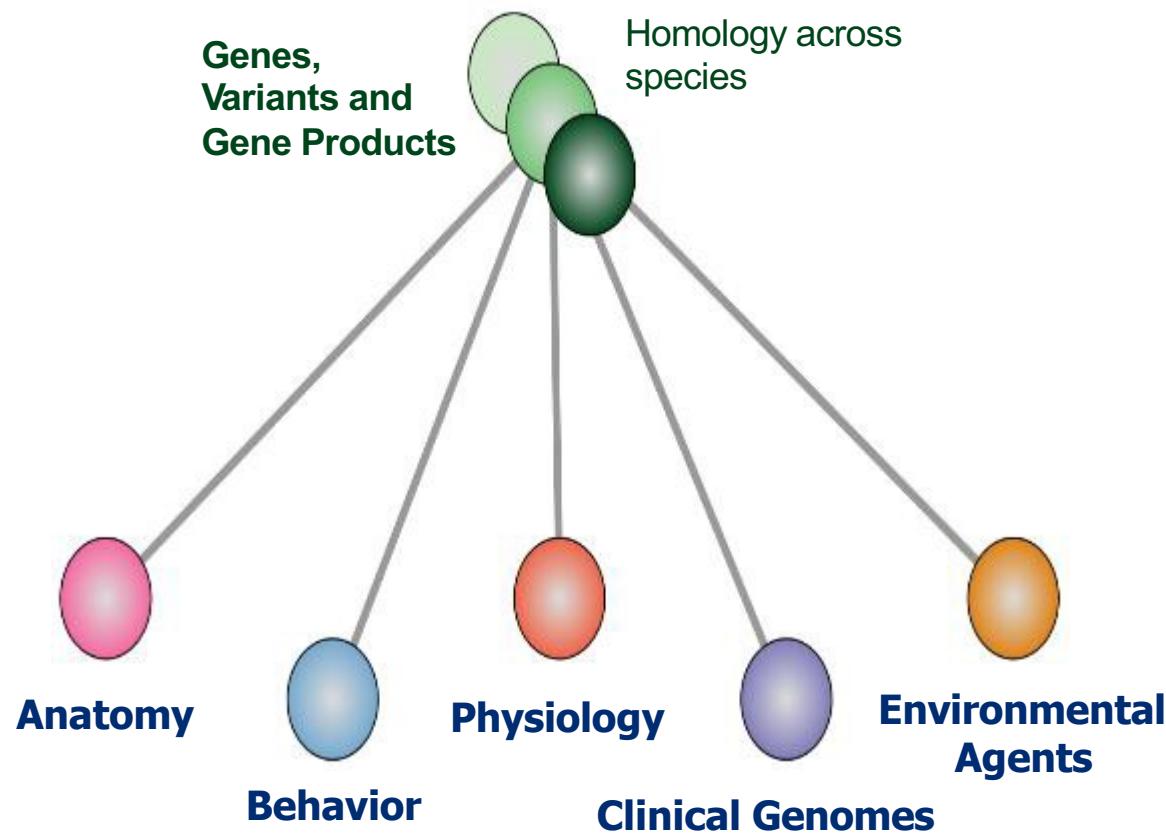


Baker EJ, Jay JJ, Bubier JA, Langston MA, Chesler EJ. Nucleic Acids Res. 2012

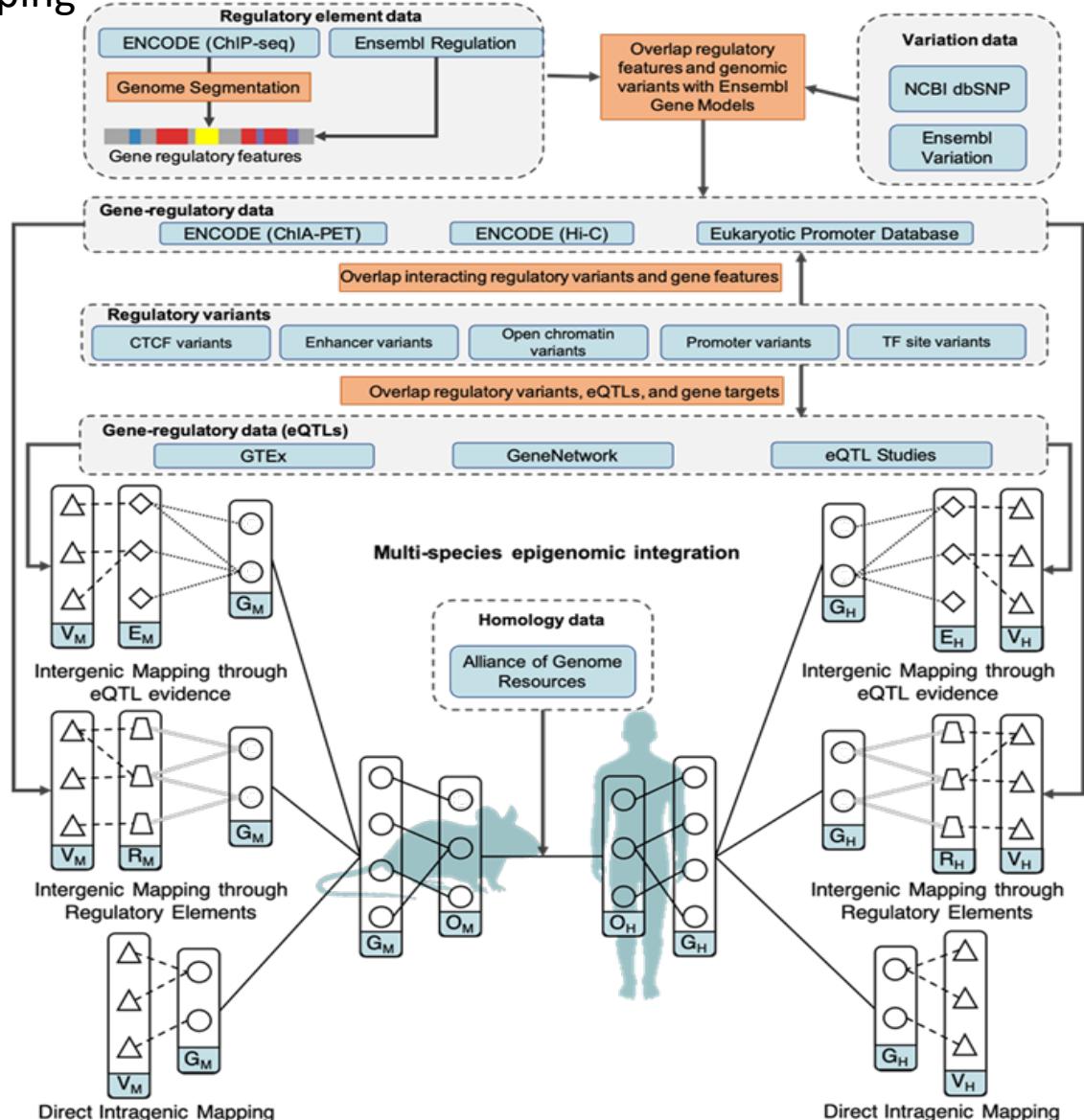


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ODE IDs are a reference to find the consilience among associations of biomolecular entities and related concepts



Regulatory Variant Based Mapping



geneweaver.org



A system for the integration and analysis of heterogeneous functional genomics data.

Search GeneSets like "mouse, Ap3m2, alcohol"

GeneSets

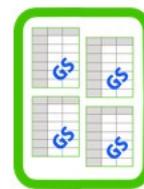
Genes

Abstracts

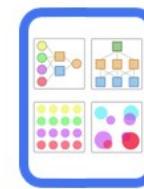
Annotations



Upload GeneSets



Manage Projects



Analyze and Discover GeneSet Relations



Help

Types of Functional Genomics Data

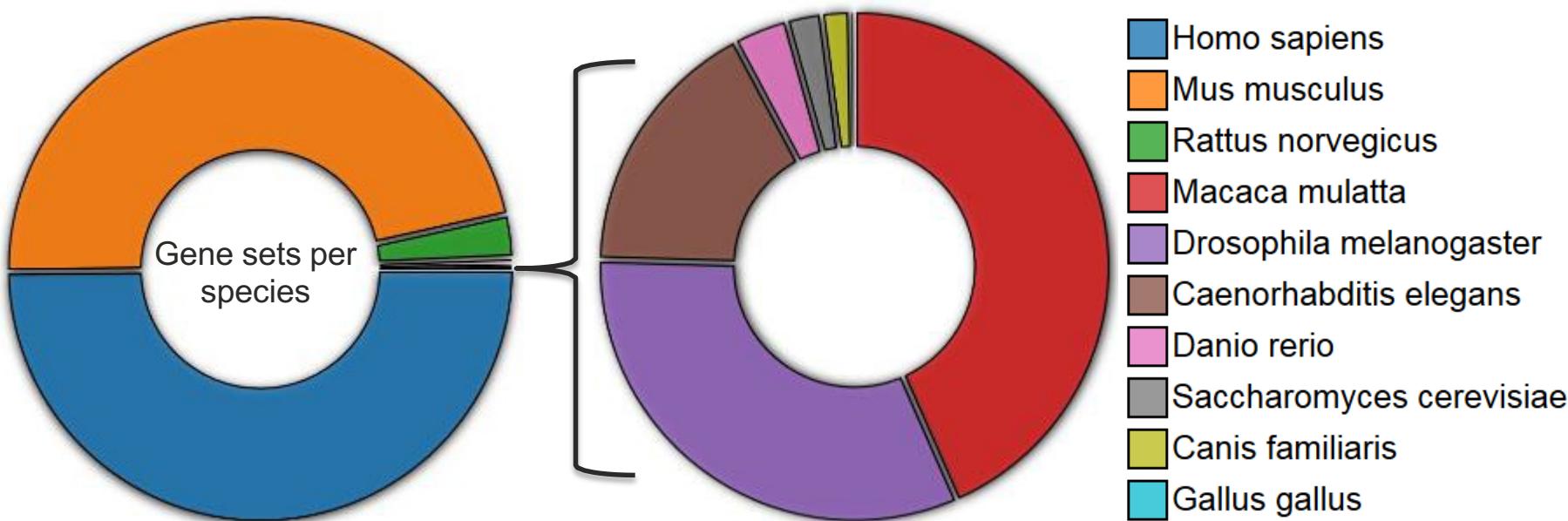
- Mapping Data
 - QTL Positional Candidates (Mouse and Rat)
 - GWAS Candidate
- Expression Data
 - DRG (Drug Regulated Genes)-From literature
 - ABA (Allen Brain Atlas)-Mouse
 - CTD (Comparative Toxicogenomics Database)-9 species



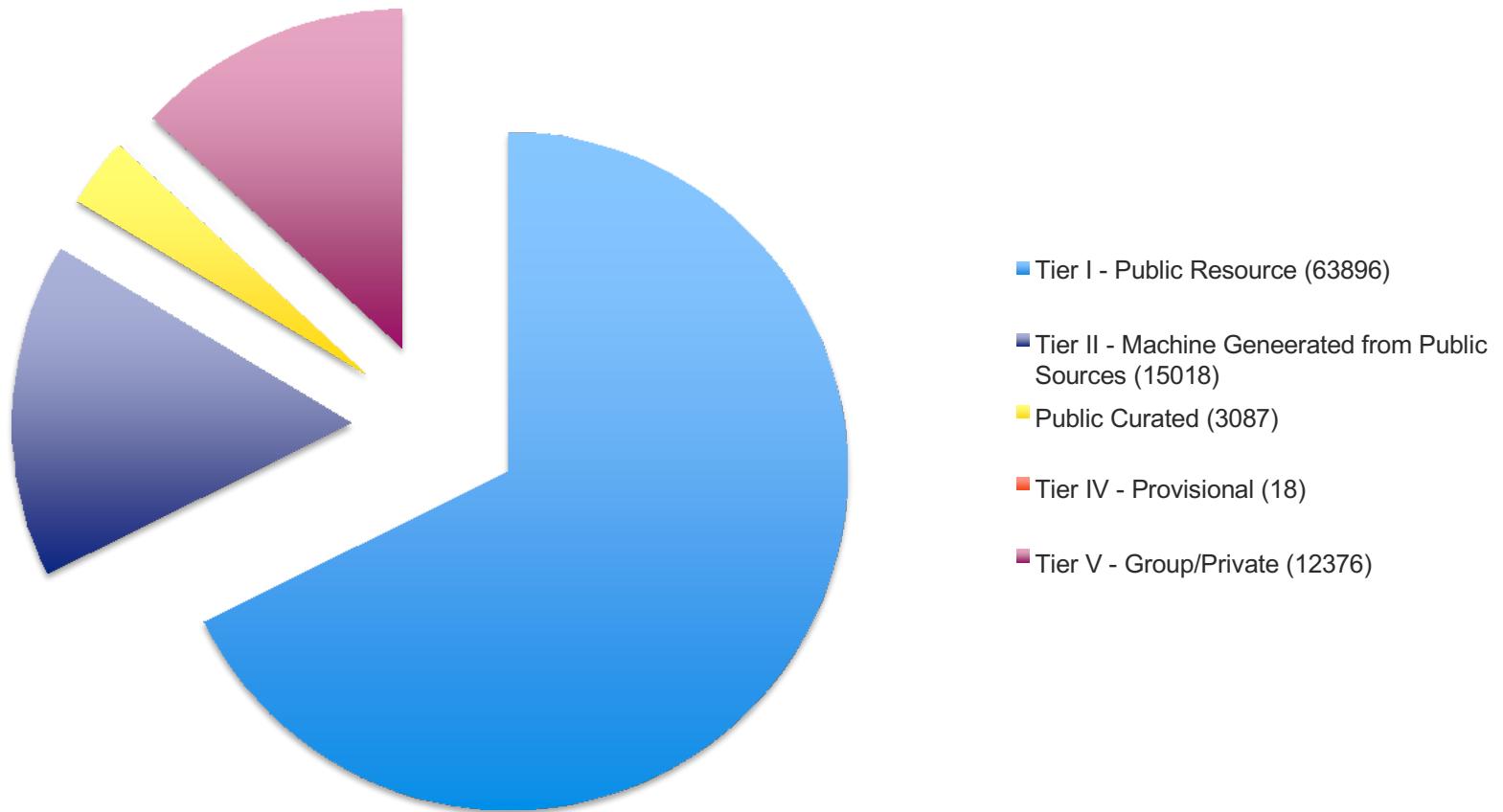
Types of Functional Genomics Data

- Functional Annotations
 - GO (Gene Ontology Annotations) Human and Mouse
 - MP (Mammalian Phenotype Ontology) Mouse
 - HP (Human Phenotype Ontology)
 - OMIM (Online Mendelian Inheritance in Man)
 - MeSH (Medical Subject Headings)
- Pathway Data
 - KEGG (Kyoto Encyclopedia of Genes and Genomes)
 - MSigDB (Molecular Signatures Database)
 - PC (Pathway Commons)

Supported Species



Data Tiers



Baker EJ, Bubier JA, Reynolds T, Langston MA, Chesler EJ. Nucleic Acids Res. 2012



Anatomy of a GeneSet

Tier III GS14890 · Downregulated genes in five combined brain regions (Amygdala, Hippocampus, Nucleus Accumbens, Pre Frontal Cortex and Ventral Tegmental Area) in C57BL/6J mice

DESCRIPTION: This gene set comprises 25 genes that are downregulated within each of five brain regions (amygdala (Amyg), hippocampus (HP), nucleus accumbens (NA), prefrontal cortex (PFC) and ventral tegmental area (VTA)) when chronic nicotine treatment is administered to C57BL/6J mice only. Background: Studies involving use of chronic nicotine treatment identify unique nicotine addiction genes and the biological processes they mediate in C3H/HeJ and C57BL/6J mice. Results are obtained using gene expression profiling via cDNA microarrays and gene ontology.

LABEL: DwnReg Nicotine C57BL/6J

DATE ADDED: 2009-01-20

DATE UPDATED: 2017-05-01

SPECIES: *Mus musculus*

AUTHORS: Wang J, Gutala R, Hwang YY, Kim JM, Konu

TITLE: *Strain- and region-specific gene expression treatment.*

JOURNAL: *Genes, brain, and behavior* Feb 2008, Vol

ABSTRACT: A pathway-focused complementary DNA gene expression profiles in the amygdala ventral tegmental area of C3H/HeJ and C57BL/6J mice (1% saccharin for 2 weeks). A balanced expression identification of 3.5-22.1% and 4.1-14.3%

- [Export Genes](#)
- [Export OmicsSoft](#)
- [Similar GeneSets](#)
- [Request Curation](#)
- [Add Geneset to Project](#)
- [Share Geneset w/ Group\(s\)](#)

Annotation Information

Mesh Terms Adult Mouse Anatomy Mammalian Phenotype Gene Ontology

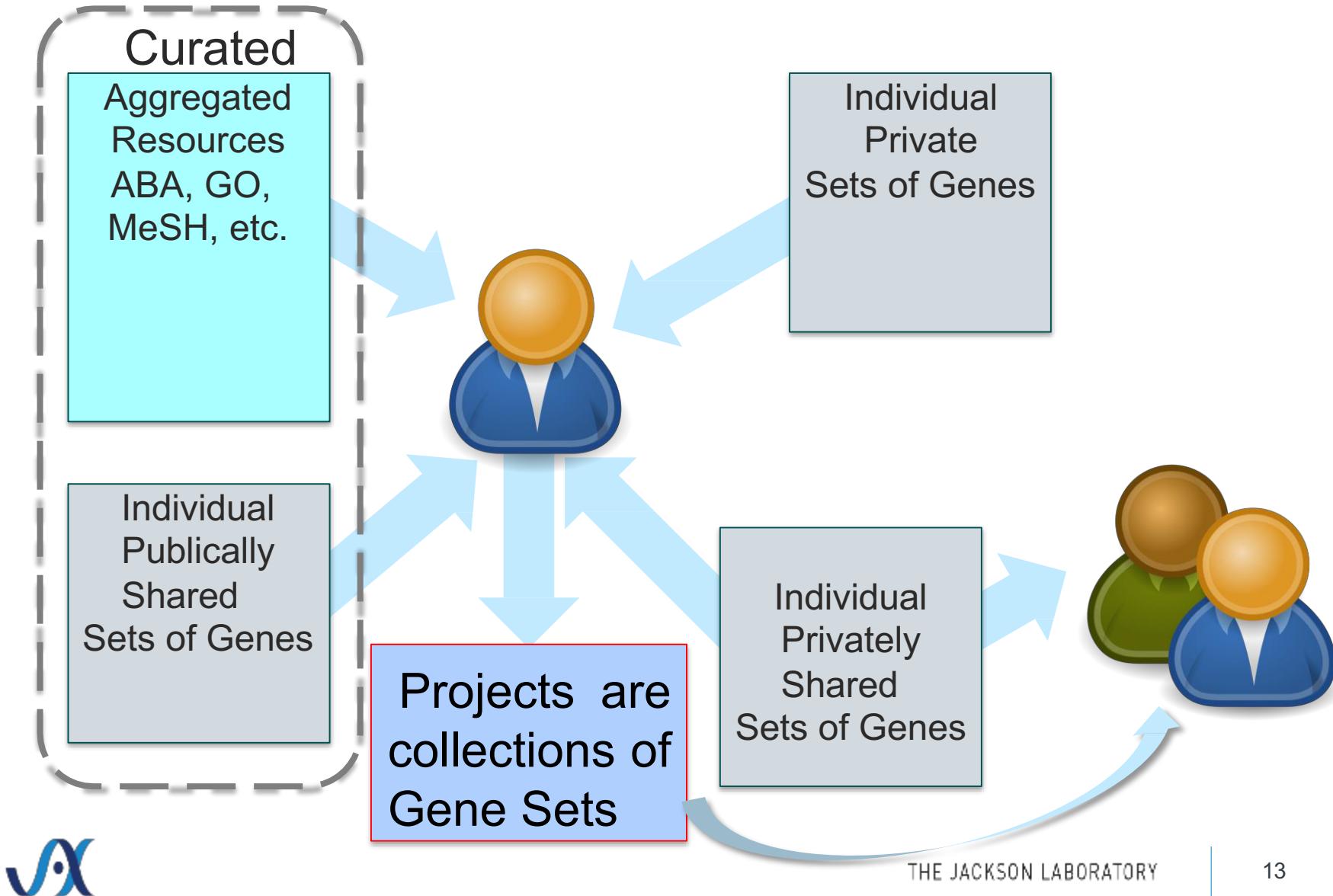
Brain (D001921) Mice, Inbred C3H (D008809) Drinking (D004328) Animals (D000818) Species Specificity (D013045)
DNA (D004247) Principal Component Analysis (D026341) Polymerase Chain Reaction (D016133) Mice (D051379)
Gene Expression Profiling (D020860) Research Report (D058028) Biological Processes (D055894) Behavior, Animal (D001522)
Water (D014867) Therapeutics (D013812) Neurons (D009474) Reverse Transcriptase Polymerase Chain Reaction (D020133)

Gene List - 22 Genes

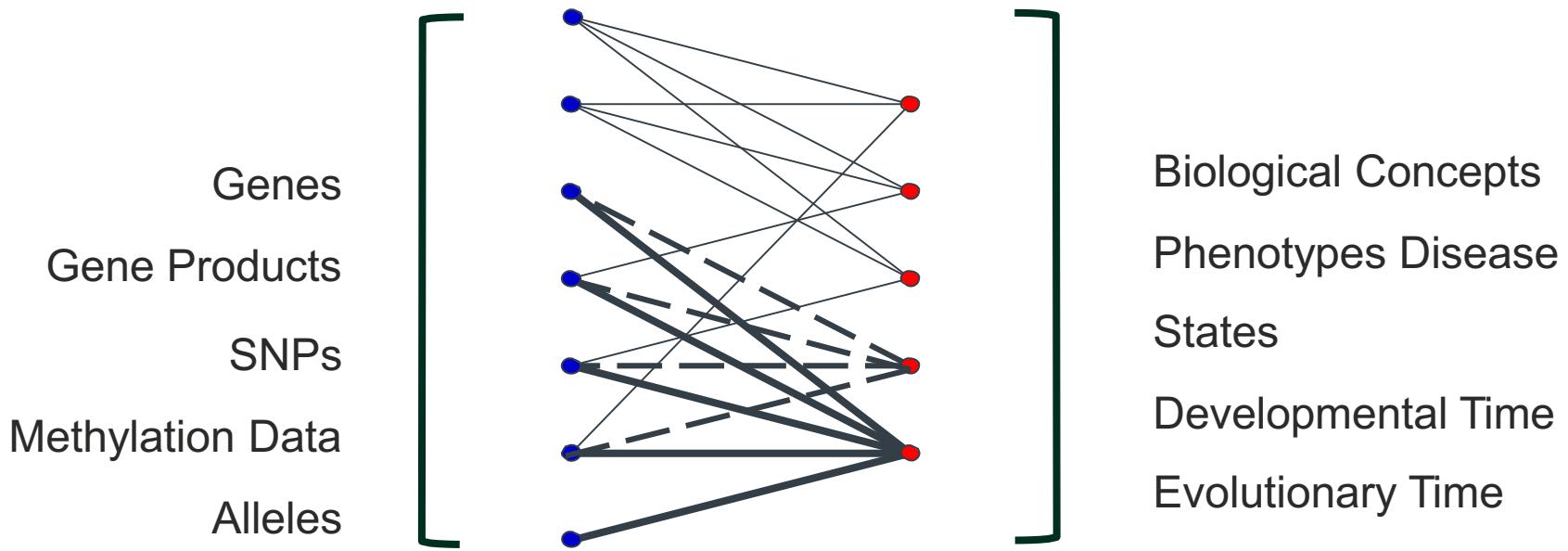
DEFAULT	GENE SYMBOL	HOMOLOGY	SCORE	PRIORITY	LINKOUTS	EMPHASIS	Add Genes to GeneSet	Sequence Analysis (D020411)	Polymerases (D012321)	Saccharin (D012439)	7)	6624)	dition (IMP:0002555)	gment (GO:0048513)	ase activity (GO:0043739)	
Chrna2	Chrna2		1.0000													
Chrb2	Chrb2		1.0000													
Gabt1	Slc6a1		1.0000													
Gria2	Gria2		1.0000													
Grik2	Grik2		1.0000													
Slc6a4	Slc6a4		1.0000													



Sharing data among users and groups with graded access and exposure

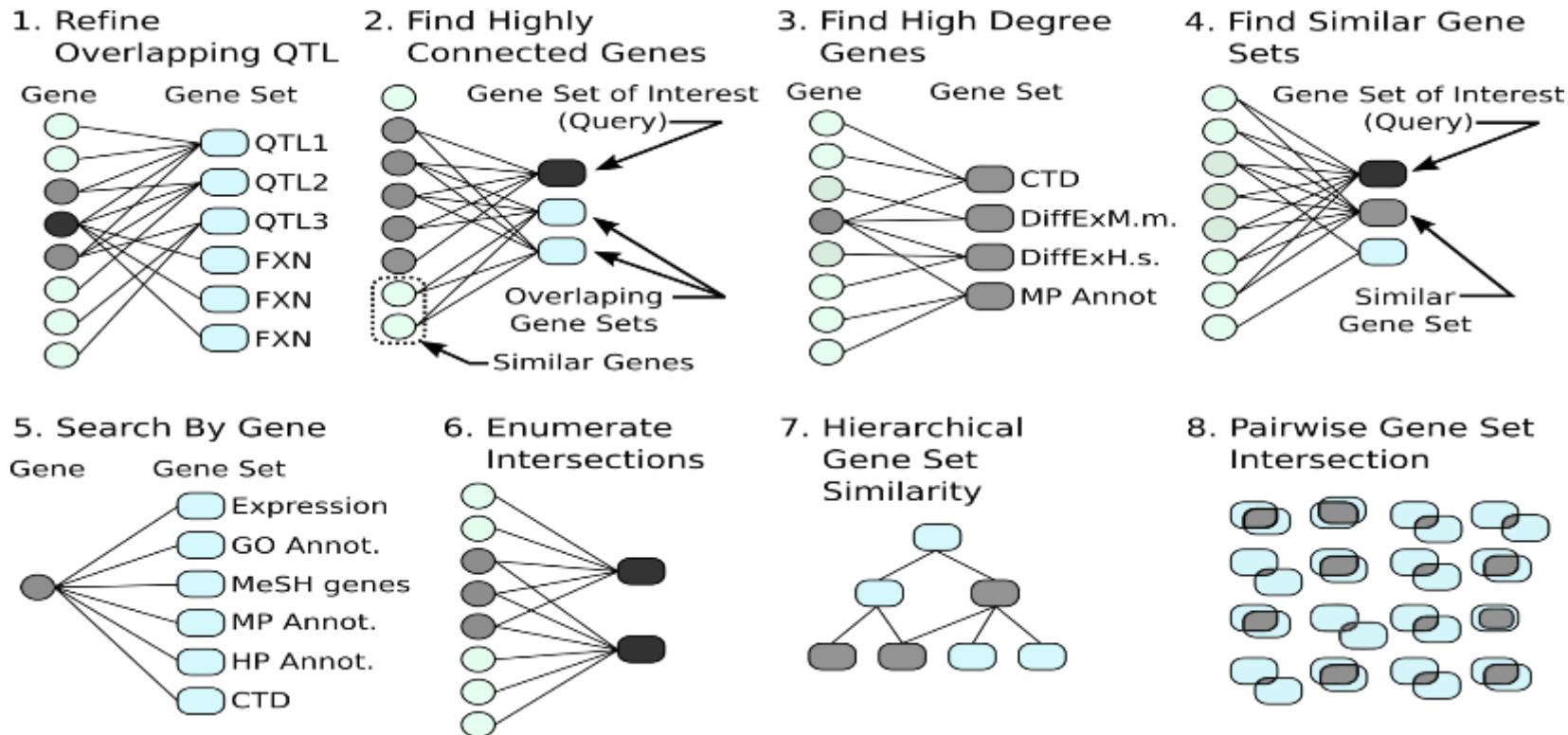


Generalized Bipartite Model

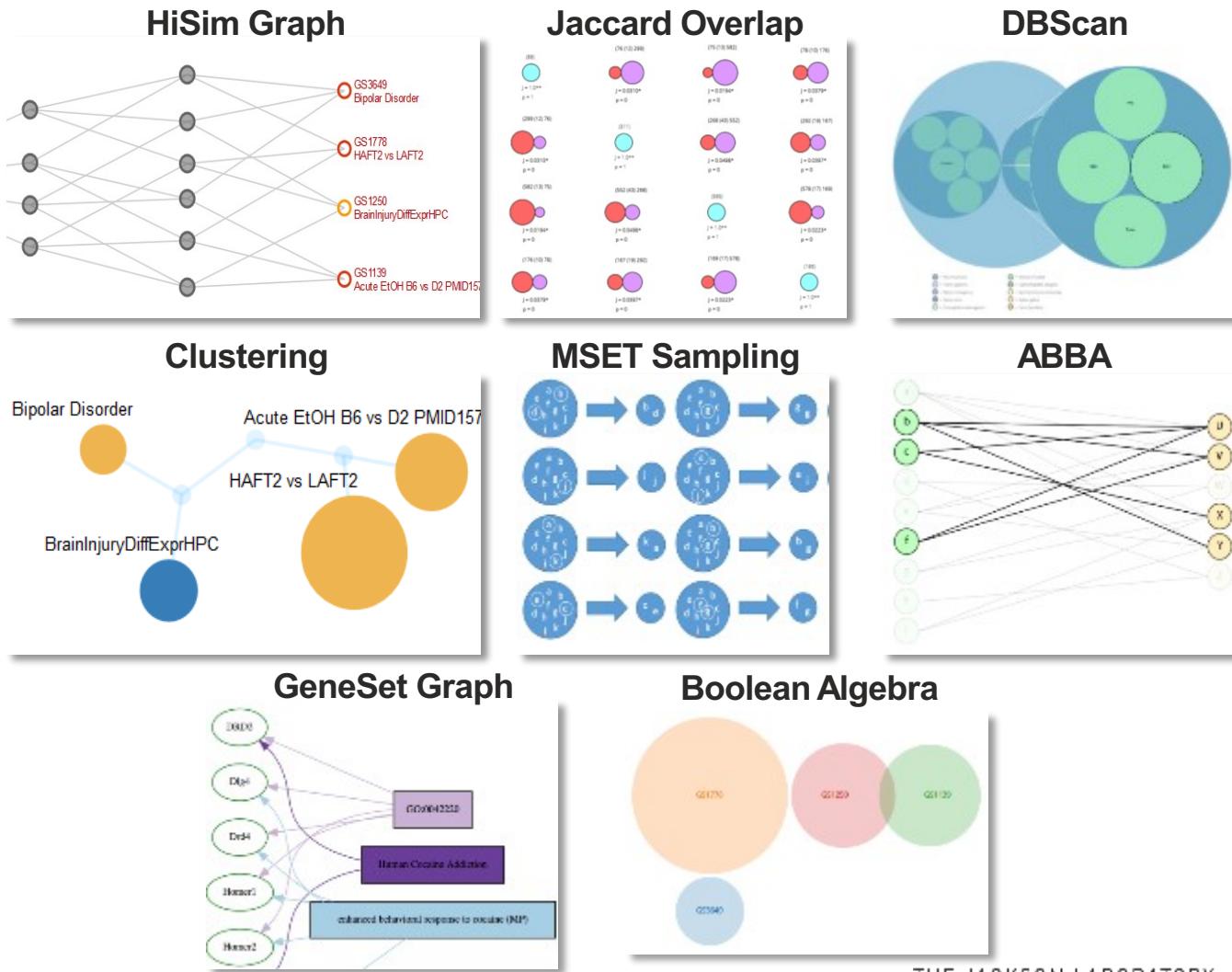


Baker EJ, Jay JJ, Philip VM, Zhang Y, Li Z, Kirova R, Langston MA, Chesler EJ. Ontological Discovery Environment: a system for integrating gene-phenotype associations. *Genomics*. 2009 Dec;94(6):377-87.

Integrative Functional Genomics Strategies



Tools for Integrative Functional Genomics



GW2 has a fully enabled API interface

- GeneWeaver functions are powered by WebServices
 - Data egress and bulk data submission
 - Enables reproducible database queries and tool execution
 - Retrieves data as JSON or images of tool results
 - Individual security key enabled
 - Documentation is included in public release
-
- <https://geneweaver.org/help/#api>



Summary of some of the tools

- **GeneSet Clustering** uses hierarchical clustering to organize GeneSets by their similarity to each other.
- **Boolean Algebra** performs set operations on GeneSets
- **ABBA** allows you to query the entire GeneWeaver database for genes with similar relationships to genes from a list of interest.
- **DBSCAN** performs a gene-centric clustering based on selected GeneSets.
- **MSET** returns gene enrichment based on selected GeneSets
- **Combine** exports GeneSets as a gene by GeneSet matrix.

 [HiSim Graph](#)◀
Biclique-based analysis used to generate hierarchical maps of gene set intersections.

 [GeneSet Graph](#)◀
Visualize the Gene-GeneSet graph.

 [Jaccard Similarity](#)◀
Calculate Jaccard Coefficients for all pairwise combinations of GeneSets.

 [GeneSet Clustering](#)◀
Use Jaccard Distance to cluster GeneSets. More □

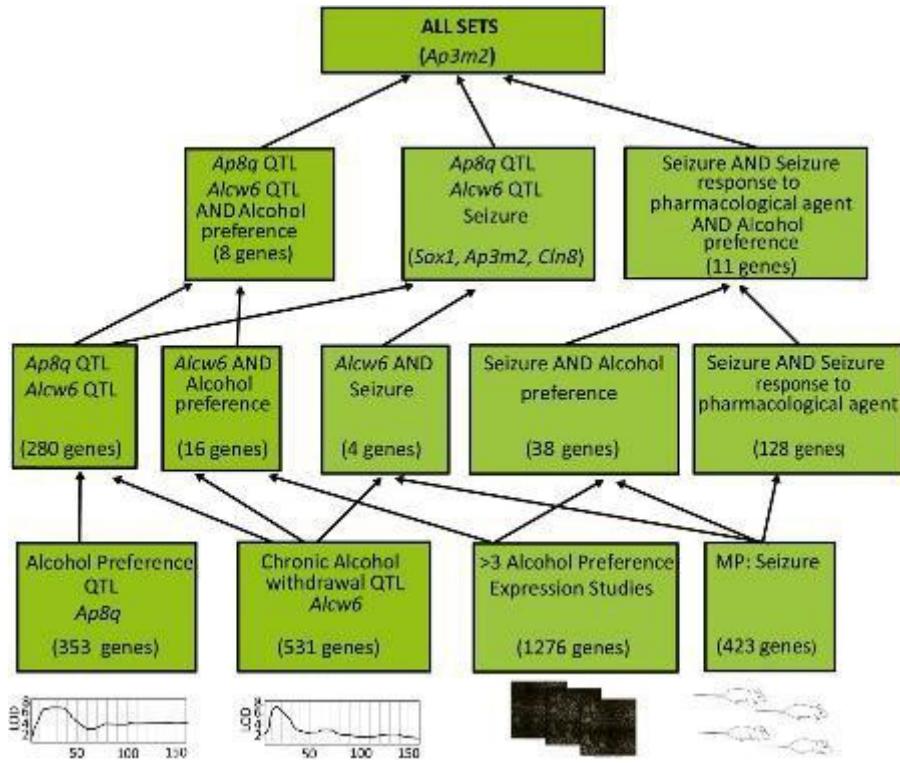
 [MSET](#)◀ Enrichment test for all GeneSets selected.

 [ABBA Gene Search](#)◀
Find genes most closely associated with your gene(s) of interest.

 [Boolean Algebra](#)◀
Use advanced set logic to integrate multiple GeneSets. More □

 [DBSCAN Gene Clustering](#)◀
Density-based clustering algorithm for genes.

Finding models for related facets of alcohol use disorder



GS75568: Differential in the nucleus accumbens of iP rats between the ethanol and saccharin groups: PMID:[18405950](#)



GS137407: Differential expression basolateral amygdala alcoholic and control: PMID:[22302827](#)



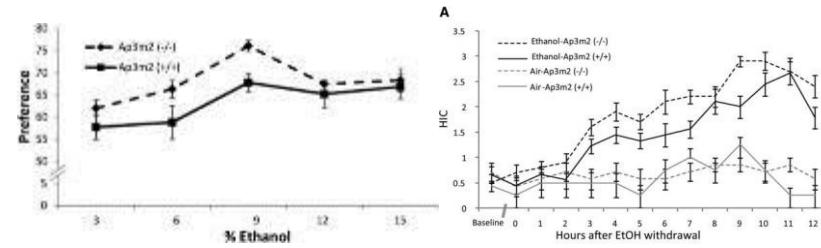
GS137413: Differential expression central nucleus of amygdala alcoholic and control PMID:[22302827](#)



GS246373: Differential expression hippocampus of alcoholic and control PMID:[26041984](#)



GS3647: Meta-analysis of 6 isogenic and three selected lines with elevated voluntary consumption of ethanol. PMID:[16618939](#)

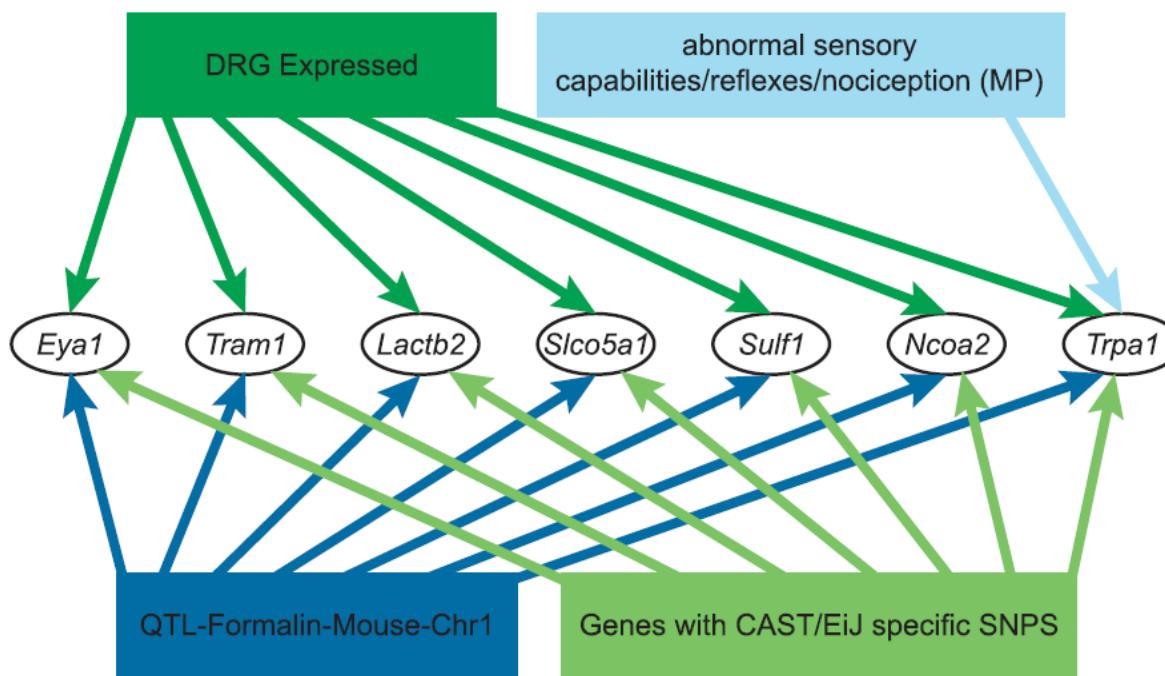


Bubier et al Genetics 2014



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Trpa1 is the highest-ranking candidate gene in the *Nociq4* Diversity outbred QTL meeting both genetic and functional criteria.

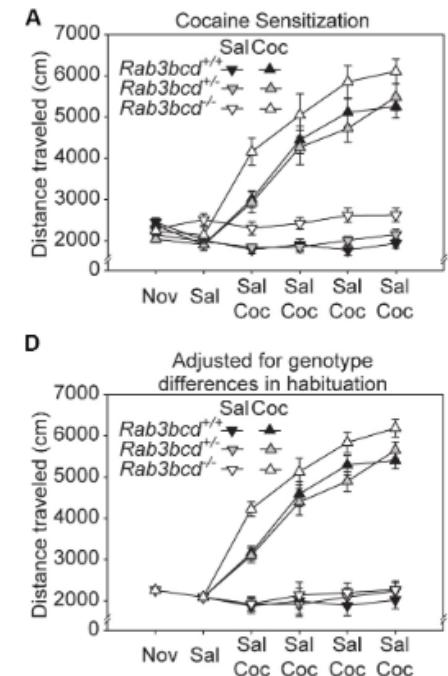
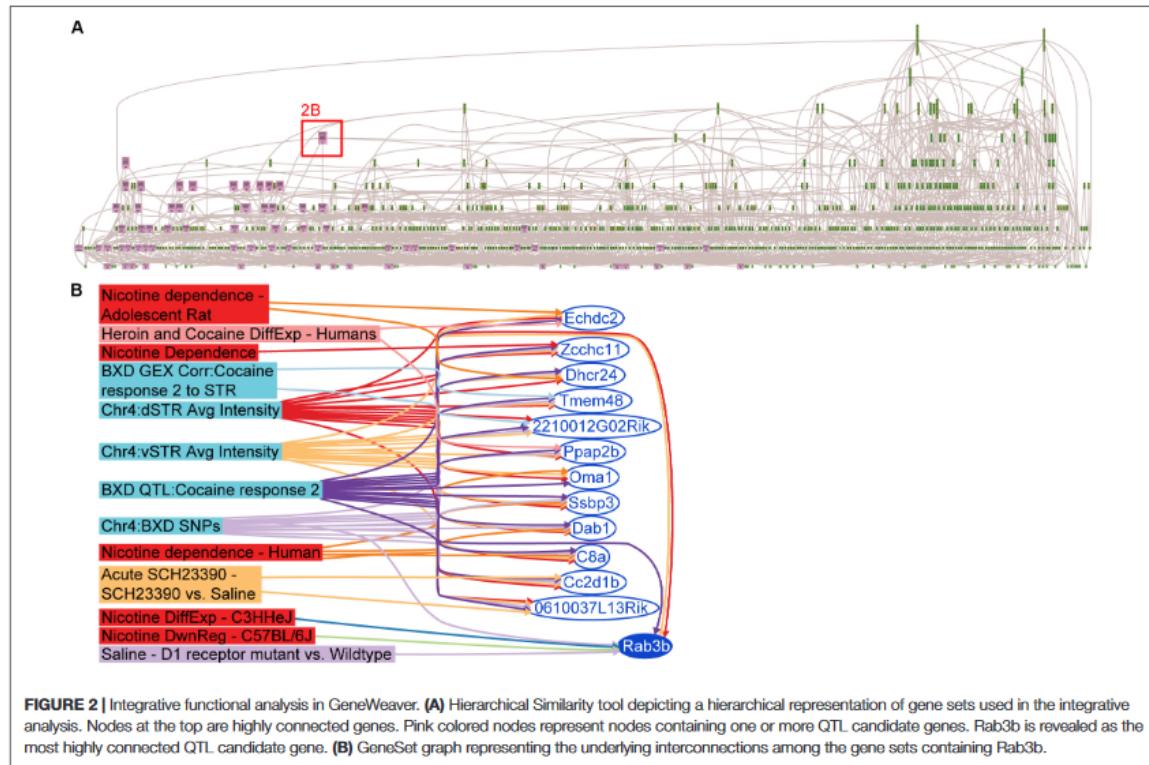


Recla et al *Pain* 2019

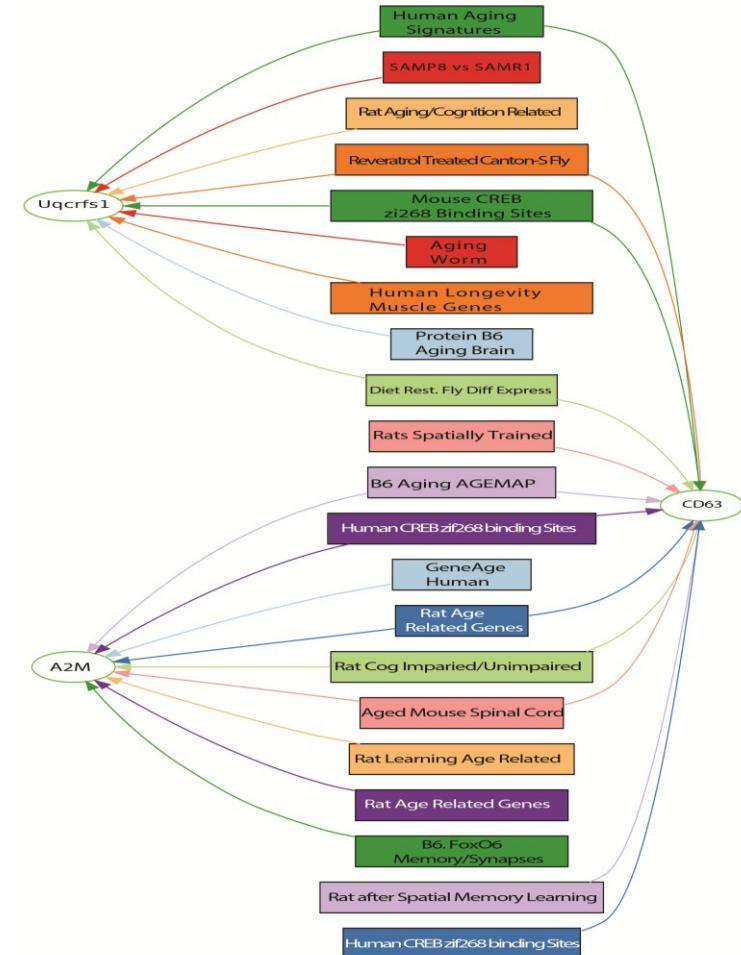
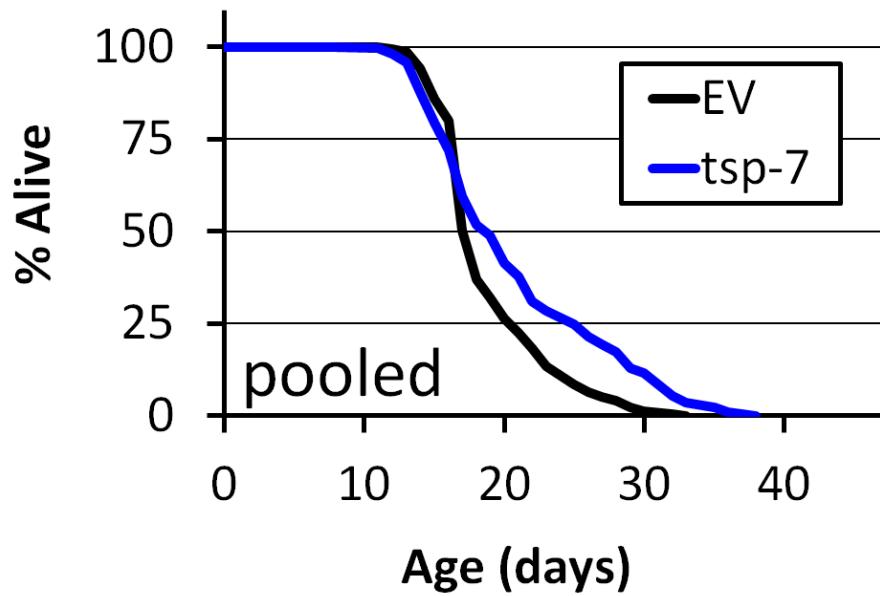


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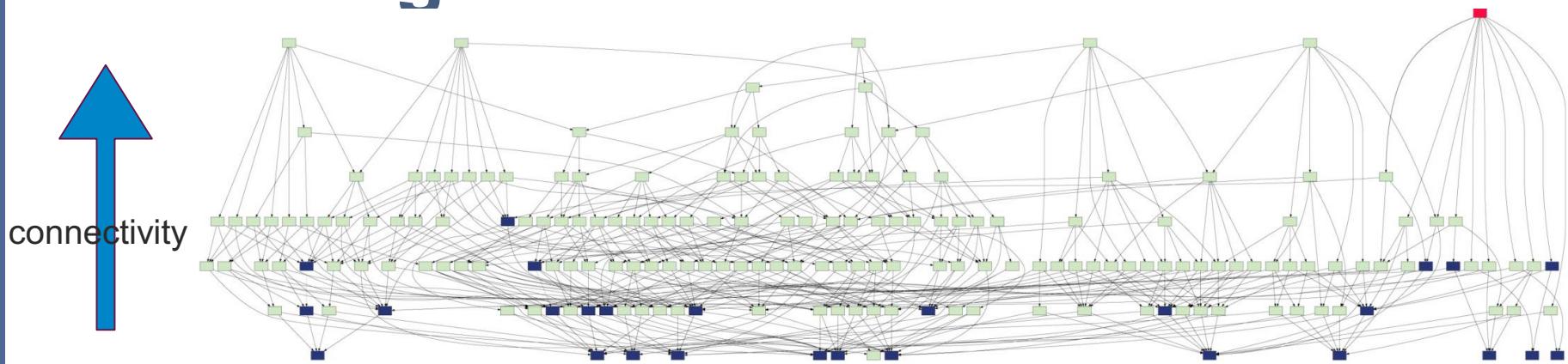
Role for *Rab3b* in Habituation and Cocaine Induced Locomotor Activation



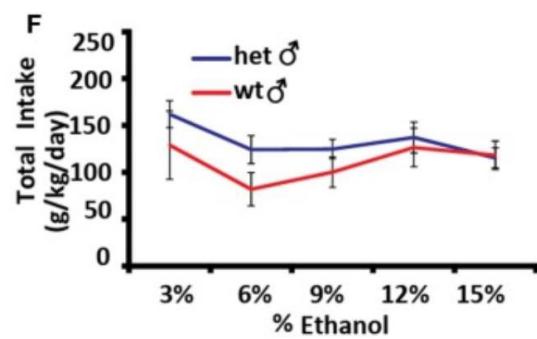
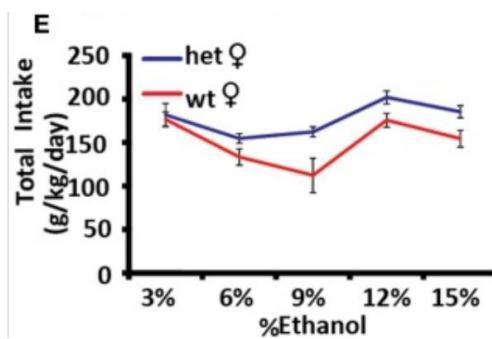
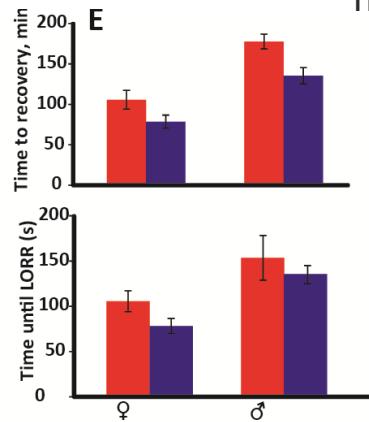
Aggregated Expression data across species suggest a role for CD63 in aging



Hierarchical similarity graph of experimentally derived alcohol related genes sets



The most frequently represented genomic results in alcohol preference studies are not currently associated with alcoholism.



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GW2

Introduction to web-based analysis with GeneWeaver2

geneweaver.org

This is a guided tour of beta.geneweaver.org designed to highlight the use of major tools. Steps and explanations are given to generate the results shown. Additional tools, features, usage hints and approaches are marked “Tip”.

GeneWeaver is a web-based gene-centered database with integrated tools. It can combine diverse data sets from multiple species and experiment types, and allows simple and powerful data sharing publicly or across collaborative groups.

Point your browser to: geneweaver.org

<https://geneweaver.org/help/>

The screenshot shows the GeneWeaver homepage with a green header bar. On the left is the GeneWeaver logo, and on the right are links for "Manage GeneSets", "Curation", "Analyze GeneSets", and "Welcome guest!". Below the header is the main content area featuring the GeneWeaver logo and a brief description: "A system for the integration and analysis of heterogeneous functional genomics data. You can [sign in](#), [create an account](#), or continue to use GeneWeaver anonymously." A search bar with placeholder text "Search GeneSets like 'mouse, Ap3m2, alcohol'" is followed by a "Search" button and zoom controls. Below the search bar are four filter checkboxes: "GeneSets" (checked), "Genes" (checked), "Abstracts" (checked), and "Annotations" (checked). The main area contains four large, colorful icons with labels: "Upload GeneSets" (orange square with a green arrow pointing up and a blue "GS" icon), "Manage Projects" (green square with a grid of blue "GS" icons), "Analyze and Discover GeneSet Relations" (blue square with various colored data visualization icons), and "Help" (pink square with a large white question mark).

Many of the GeneWeaver tools can be used by guest users, however, for this tutorial we will create an account. If you already have an account, **log into your existing account and proceed to the next slide.**

Hover over the “Welcome Guest!” link at the top of the page and click “Create Account”.

The screenshot shows the GeneWeaver homepage with a green header bar. In the top right corner, there is a dropdown menu labeled "Welcome Guest!". The menu contains three items: "Sign In", "Forgot Password", and "Create Account". Below the header, the GeneWeaver logo is displayed, followed by a brief description: "A system for the integration and analysis of heterogeneous functional genomics data. You can sign in, create an account, or continue to use GeneWeaver anonymously." A search bar is present with placeholder text "Search GeneSets like 'mouse, Ap3m2, alcohol'". Below the search bar are four checkboxes: "GeneSets" (checked), "Genes" (checked), "Abstracts" (checked), and "Annotations" (checked). A "Search" button is located to the right of the search bar.

On the account creation page, fill in the required fields (first and last names, e-mail, and password) and click "Sign Up".

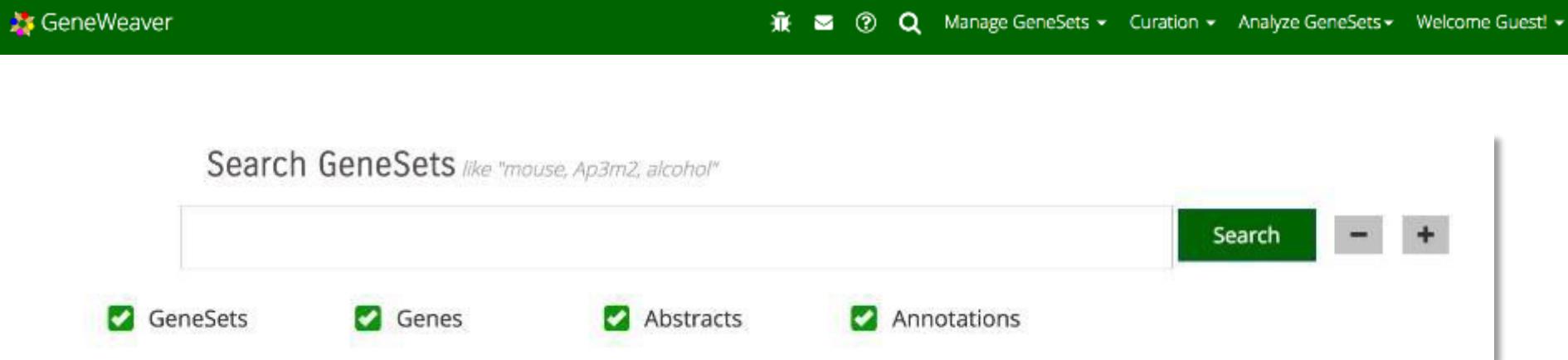
NOTE: If you perform analysis without a user account, all results and projects will be lost at the conclusion of a session.



Data in GeneWeaver is organized into sets of genes, or GeneSets. These sets contain some simple metadata, such as a name, description, and publication info, along with the set of genes. All of this information can be searched to find a set of interest.

Searching GeneWeaver for data sets is possible through the **Search Bar** found on the front page or via the **Search** icon found in the menu.

Click on the search icon to view the search page.



A screenshot of the GeneWeaver web interface. At the top, there is a dark green header bar with the "GeneWeaver" logo on the left and various navigation links like "Manage GeneSets", "Curation", "Analyze GeneSets", and "Welcome Guest!" on the right. Below the header is a search bar with the placeholder text "Search GeneSets like 'mouse, Ap3m2, alcohol'". To the right of the search bar is a green "Search" button and two small gray buttons with minus and plus signs. Below the search bar are four filter checkboxes: "GeneSets" (checked), "Genes" (checked), "Abstracts" (checked), and "Annotations" (checked). The main content area below these filters is currently empty.

Search for “**Nicotine hippocampus**” to find all the public GeneSets relating to Nicotine studies in the Hippocampus that have already been upload to GeneWeaver.

Tip: From the search results page you can click on the plus sign to show a little more detail about the set, such as species and publication info. You can also click on the GeneSet name to see the full details and the list of genes included in the set on a separate page.

The screenshot shows the GeneWeaver search interface. At the top, there are tabs for General, Tiers, Species, and Attributions. Below these are global filters for 'Include Provisional' (9) and 'Include Deprosoted' (0). A slider indicates 'Geneset Size: 1 to 294'. The search bar contains 'Nicotine hippocampus' with a 'Search' button and +/- zoom controls. Below the search bar are checkboxes for GeneSets, Genes, Abstracts, and Annotations. Buttons for 'Share Selected w/ Group' and 'Add Selected to Project' are also present. The main area displays 'RETURNING 16 RESULTS: PAGE 1 OF 1' with a page number '1'. A table lists three results:

	TIER	SPECIES	SIZE	ATTR.	GENESET
	Tier III	Mm	294		GS14888: Differentially expressed genes modulated by nicotine in five combined brain regions (Amygdala, Hippocampus, Nucleus Accumbens, Pre Frontal Cortex and Ventral Tegmental Area) for C3H/HeJ mice
	Tier III	Mm	192		GS14889: Differentially expressed genes modulated by nicotine in five combined brain regions (Amygdala, Hippocampus, Nucleus Accumbens, Pre Frontal Cortex and Ventral Tegmental Area) in C57BL/6J mice
	Tier III	Mm	22		GS14890: Downregulated genes in five combined brain regions (Amygdala, Hippocampus, Nucleus Accumbens, Pre Frontal Cortex and Ventral Tegmental Area) in C57BL/6J mice

On the left side, there are sections for Tiers (No Tier, I: Resources, II: Pro-Curated, III: Curated, IV: Provisional, V: Private), Species (Mus musculus, Homo sapiens), and Attributions.

Tip: You can restrict your search to specific species, collaboration groups, or curation level (Tiers I – Tiers V). You can also narrow the search scope by searching only the GeneSets, the Genes, the Abstracts or the Ontologies.

Tip: Creating powerful queries with Boolean search is also possible using “AND”, “OR”, “NOT” and parentheses to craft a precise query.

The screenshot displays a search interface with four main filter panels, each with tabs for General, Tiers, Species, and Attributions. The Tiers tab is selected for all panels.

- GLOBAL FILTERS:**
 - Include **Provisional** (9)
 - Include **Deprecated** (0)A horizontal slider indicates a Geneset Size from 1 to 294.
- FILTER BY TIER:**
 - I: Resources** (15)
 - Homo sapiens** (15)
 - DRG** (15)
 - III: Curated** (10)
 - Mus musculus** (9)
 - No Attribution** (9)
 - Rattus norvegicus** (1)
 - No Attribution** (1)
 - FILTER BY SPECIES:**
 - Mus musculus** (9)
 - III: Curated** (9)
 - No Attribution** (9)
 - Homo sapiens** (15)
 - I: Resources** (15)
 - DRG** (15)
 - Rattus norvegicus** (1)
 - III: Curated** (1)
 - No Attribution** (1)
 - FILTER BY ATTRIBUTIONS:**
 - No Attribution** (10)
 - III: Curated** (10)
 - Mus musculus** (9)
 - Rattus norvegicus** (1)
 - DRG** (15)
 - I: Resources** (15)
 - Homo sapiens** (15)

From the GeneSet details page, you can read more about the set, including a link to the provided publication in PubMed, if available, and ontology annotation information. On the second half of the page, you will find a list of the genes in the GeneSet, along with a set of linkouts to other sites, and the score associated with the gene (type of score value depends on the source), and homology assertions.

Tip # GS14890 · Downregulated genes in five combined brain regions (Amygdala, Hippocampus, Nucleus Accumbens, Pre Frontal Cortex and Ventral Tegmental Area) in C57BL/6J mice

DESCRIPTION: This gene set comprises 25 genes that are downregulated within each of five brain regions (amygdala (Amyg), Hippocampus (HPl), nucleus accumbens (NAc), prefrontal cortex (PFC) and ventral tegmental area (VTA)) when chronic nicotine treatment is administered to C57BL/6 mice only. Background: Studies involving use of chronic nicotine treatment identify unique nicotine addiction genes and the biological processes they mediate in C3H/HeJ and C57BL/6 mice. Results are obtained using gene expression profiling via cDNA microarrays and gene ontology.

LABEL: DownReg Nicotine C57BL/6J

DATE ADDED: 2009-01-20

DATE UPDATED: 2017-05-01

SPECIES: *Mus musculus*

AUTHORS: Wang J, Gutals R, Hwang YY, Kim JM, Konu O, Ma Z, Li MD

TITLE: Strain- and region-specific gene expression profiles in mouse brain in response to chronic nicotine treatment.

JOURNAL: *Genes, brain, and behavior* Feb 2008; Vol 7, pp. 78-87

ABSTRACT: A pathway-focused complementary DNA microarray and gene ontology analysis were used to investigate gene expression profiles in the amygdala, Hippocampus, nucleus accumbens, prefrontal cortex (PFC) and ventral tegmental area of C3H/HeJ and C57BL/6 mice receiving nicotine in drinking water (100 μg/ml in 2% saccharin for 2 weeks). A balanced experimental design and rigorous statistical analysis have led to the identification of 3.5–22.1% and 4.1–14.3% of the 639 sequence-verified genes as significantly modulated in the aforementioned brain regions of the C3H/HeJ and C57BL/6J strains, respectively. Comparisons of differential expression among brain tissues showed that only a small number of genes were altered in the differential response to nicotine in the different brain regions. Exploratory analysis showed that the differential response to nicotine was primarily observed in the hippocampus, i.e. cell

Annotation Information

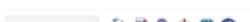
Mesh Terms: Adult Mammal Anatomy, Mammalian Phenotype, Gene Ontology

- Brain (3301121) | Nervous, Inbred C57 (3303081) | Drinking (3304301) | Animals (3300013) | Reelin, Receptivity (3315828)
- DNA (3291011) | Principal Component Analysis (3293211) | Polymerase Chain Reaction (3291121) | Mice (3301276)
- Gene Expression Profiling (3290909) | Research Report (3290932) | Biological Process (3295094) | Behavior, Animal (3291522)
- Micro (3291487) | Thiomicrospira (3291312) | Micros (3291474) | Reverse Transcriptase Polymerase Chain Reaction (3291535)
- Amygdala (3290818) | Prefrontal Cortex (3291387) | Thalamus (3291830) | Nodulus, Accessory (3290812)
- cRNA-Directed DNA Polymerases (3291214) | Nervous, Segregated Area (3291527) | Oligonucleotide Array Sequence Analysis (3290411)
- Mice, Inbred C57BL (3290816) | Cells (3291277) | Transcription, Genomic (3291415) | DNA-Directed RNA Polymerases (3291321)
- Actin, Cytoskeletal (3290316) | DNA Complementary (3291807) | Identifiers (3291810) | Axoneme (3291338)
- Cell (Physiology) (3291271) | Cell Cycle (3290512) | Cell Division (3291241) | Research Design (3291270)
- Genomic Transmission (3290423) | Modine (3290502) | Organogenesis (3290360) | Hippocampus (3290426)
- Amygdala (3290817) | Nerve (32903217) | Intra (3290818) | Hippocampus (3290818) | adrenergic (MP_3028590)
- cell (3290818) | Exacerbation of nervous disorders (3290818) | Inflammation (3290818) | Organ development (3290818) | gene expression (3290467)
- response to alcohol (GO_0023649) | cell cycle (GO_3081946) | G1/S arrest-specific crack-DNA glycosylase activity (GO_0021261)

-  Export Genes
-  Export OmicsSoft
-  Similar GeneSets
-  Request Curation
-  Add Geneset to Project
-  Share Geneset w/ Group(s)

Tip: Using the “Gene Symbol” drop-down box, you can change the type of identifier used in the list. From this page you can also export the displayed genes to a tab-separated file for use in other software.

Gene List - 22 Genes

DEFAULT	GENE SYMBOL	HOMOLOGY	SCORE	PRIORITY	LINKOUTS	EMPHASIS
Chrm2	Chrm2		1.0000			OFF
Chrb2	Chrb2		1.0000			OFF
Gabt1	Slc6a1		1.0000			OFF
Gria2	Gria2		1.0000			OFF
Grik2	Grik2		1.0000			OFF
Slo6a4	Slo6a4		1.0000			OFF
Itgb7	Itgb7		1.0000			OFF
Wnt4	Wnt4		1.0000			OFF
Apoebc1	Apoebc1		1.0000			OFF
Rps2ka1	Rps2ka1		1.0000			OFF
Psmc5	Psmc5		1.0000			OFF
Rab4b	Rab4b		1.0000			OFF

 Go back to search results now

On the search results page, you can use the checkboxes and drop-down menu to add GeneSets to a new project. Projects allow you to run tools and analyze sets of GeneSets.

Click on the checkboxes next to the following nicotine GeneSets: GS14890, GS14891, GS14892, GS14893.

Use the orange button to “**Add Selected to Project**”, which adds the GeneSets to a new project.

In the pop-up window, **click “Create New Project”, supply an informative name for the new project, and click the “Submit” button.**

You should now see your new project in the pop-up window.

Select the name of your project, then click “Submit”.

New Project Name

New Project Name:

nicotine expression

Comments:

Add Selected GeneSets to Project(s)

The following GeneSet(s) will be added:

GS14890, GS14891, GS14892, GS14893

Select which projects to add to (hold shift to select more than one):

alcohol epigenetic and transcriptomic sets
epigenetic and paraclique alcoholism
nicotine expression
test-project

When a new Project is created, it will be available from the “**Analyze GeneSets**” page, where you can see the Project, its GeneSets, and the analysis tools available. Projects can be wholly or piecewise selected for analysis. The Analysis tools, listed on the left, provide a graphical depiction of the tools’ results to aid with selection.

Navigate to the “Analyze GeneSets” page by clicking the link in the menu.

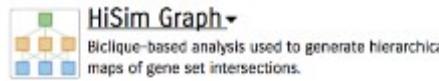
Tip: GeneSets can be easily removed from a project by clicking the “trash” icon on the right side. Projects can be removed, shared, or marked as important from the ‘Manage Projects’ page.

Tip: Most of the analysis tools have options to tweak their output. These options are available by clicking the plus sign next to the tool.

Analysis Tools

Projects

 HiSim Graph  Biclique-based analysis used to generate hierarchical maps of gene set intersections. Help 	 GeneSet Graph  Visualize the Gene-GeneSet graph. Help 	 Jaccard Similarity  Calculate Jaccard Coefficients for all pairwise combinations of GeneSets. Help 	 GeneSet Clustering  Use Jaccard Distance to cluster GeneSets. Help 	 MSET  Enrichment test for all GeneSets selected. Help 	 ABBA Gene Search  Find genes most closely associated with your gene(s) of interest. Help 																																																								
<table border="1"><tbody><tr><td></td><td> alcohol epigenetic and transcriptomic sets</td><td></td><td></td><td></td></tr><tr><td></td><td> epigenetic and paraclique alcoholism</td><td></td><td></td><td></td></tr><tr><td></td><td> nicotine expression</td><td></td><td></td><td></td></tr><tr><td></td><td> test-project</td><td></td><td></td><td></td></tr><tr><td><input type="checkbox"/></td><td>Tier III</td><td>Mm.</td><td colspan="3">GS14890: Downregulated genes in five combined brain regions</td></tr><tr><td><input type="checkbox"/></td><td>Tier II</td><td>Mm.</td><td colspan="3">22 (Amygdala, Hippocampus, Nucleus Accumbens, Pre Frontal Cortex and Ventral Tegmental Area) in C57BL/6J mice</td></tr><tr><td><input type="checkbox"/></td><td>Tier II</td><td>Mm.</td><td colspan="3">GS14891: Upregulated genes in five combined brain regions</td></tr><tr><td><input type="checkbox"/></td><td>Tier II</td><td>Mm.</td><td colspan="3">54 (Amygdala, Hippocampus, Nucleus Accumbens, Pre Frontal Cortex and Ventral Tegmental Area) in C57BL/6J mice</td></tr><tr><td><input type="checkbox"/></td><td>Tier III</td><td>Mm.</td><td colspan="3">GS14892: Downregulated genes in five brain regions (Amygdala, Hippocampus, Nucleus Accumbens, Pre Frontal Cortex and Ventral Tegmental Area) in C3H/HeJ mice</td></tr><tr><td><input type="checkbox"/></td><td>Tier II</td><td>Mm.</td><td colspan="3">GS14893: Upregulated genes in three brain regions, Nucleus Accumbens, Pre Frontal Cortex, and Ventral Tegmental Area, in C3H/HeJ mice</td></tr></tbody></table>							 alcohol epigenetic and transcriptomic sets					 epigenetic and paraclique alcoholism					 nicotine expression					 test-project				<input type="checkbox"/>	Tier III	Mm.	GS14890: Downregulated genes in five combined brain regions			<input type="checkbox"/>	Tier II	Mm.	22 (Amygdala, Hippocampus, Nucleus Accumbens, Pre Frontal Cortex and Ventral Tegmental Area) in C57BL/6J mice			<input type="checkbox"/>	Tier II	Mm.	GS14891: Upregulated genes in five combined brain regions			<input type="checkbox"/>	Tier II	Mm.	54 (Amygdala, Hippocampus, Nucleus Accumbens, Pre Frontal Cortex and Ventral Tegmental Area) in C57BL/6J mice			<input type="checkbox"/>	Tier III	Mm.	GS14892: Downregulated genes in five brain regions (Amygdala, Hippocampus, Nucleus Accumbens, Pre Frontal Cortex and Ventral Tegmental Area) in C3H/HeJ mice			<input type="checkbox"/>	Tier II	Mm.	GS14893: Upregulated genes in three brain regions, Nucleus Accumbens, Pre Frontal Cortex, and Ventral Tegmental Area, in C3H/HeJ mice		
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DisableBootstrap:

NodeCutoff:

Homology: Included

Excluded

GenesInNode:

UseFDR:

HideUnEmphasized:

p-Value:

MinOverlap:

MinGenes:

PermutationTimeLimit:

MaxInNode:

Permutations:

MaxLevel:

Run

To run an analysis tool, simply select Projects and/or GeneSets and then click the button on the left representing the tool you wish to run.

Tip: Click the name of the analysis tool to expand the list of available options.

Tip: Projects are very useful for organizing similar studies. For example, by keeping experimental nicotine data in one project, and morphine data in another project, you can simply select both projects at once to run a comparative analysis, while keeping the collections distinct. Select your nicotine project and then run the “HiSim Graph” tool. You will be shown a status page while the tool is running (or waiting to run) which keeps you informed of the progress of the analysis.

Tip: The ‘Results’ page also keeps track of previous and on-going tool runs.

The screenshot shows a results interface for a project named "test-project". The interface includes a sidebar with a green checkmark icon and a minus sign, and a main content area with a table-like structure. The table lists five entries, each with a blue checkmark icon, a red "Tier III" button, an orange "Mm." button, a numerical ID, and a detailed description of the gene set. The descriptions mention specific brain regions and mouse strains (C57BL/6J or C3H/HeJ). Each entry has a small folder, trash, and plus sign icon to its right.

			test-project
<input checked="" type="checkbox"/>	Tier III	Mm.	GS14890: Downregulated genes in five combined brain regions (Amygdala, Hippocampus, Nucleus Accumbens, Pre Frontal Cortex and Ventral Tegmental Area) in C57BL/6 mice 22
<input checked="" type="checkbox"/>	Tier III	Mm.	GS14891: Upregulated genes in five combined brain regions (Amygdala, Hippocampus, Nucleus Accumbens, Pre Frontal Cortex and Ventral Tegmental Area) in C57BL/6 mice 54
<input checked="" type="checkbox"/>	Tier III	Mm.	GS14892: Downregulated genes in five brain regions (Amygdala, Hippocampus, Nucleus Accumbens, Pre Frontal Cortex and Ventral Tegmental Area) in C3H/HeJ mice 14
<input checked="" type="checkbox"/>	Tier III	Mm.	GS14893: Upregulated genes in three brain regions, Nucleus Accumbens, Pre Frontal Cortex, and Ventral Tegmental Area, in C3H/HeJ mice 75

HiSim Graph
Biclique-based analysis used to generate hierarchical maps of gene set intersections.

DisableBootstrap:

NodeCutoff:

Homology: Included Excluded

GenesInNode:

UseFDR:

HideUnEmphasized:

p-Value:

MinOverlap:

MinGenes:

PermutationTimeLimit:

MaxInNode:

Permutations:

MaxLevel:

Run

Expand your nicotine project and view its contents by clicking the plus (+) icon next to its name.

Select your nicotine project and then run the “HiSim Graph” tool. You will be shown a status page while the tool is running (or waiting to run) which keeps you informed of the progress of the analysis.

Tip: The ‘Results’ page also keeps track of previous and on-going tool runs.

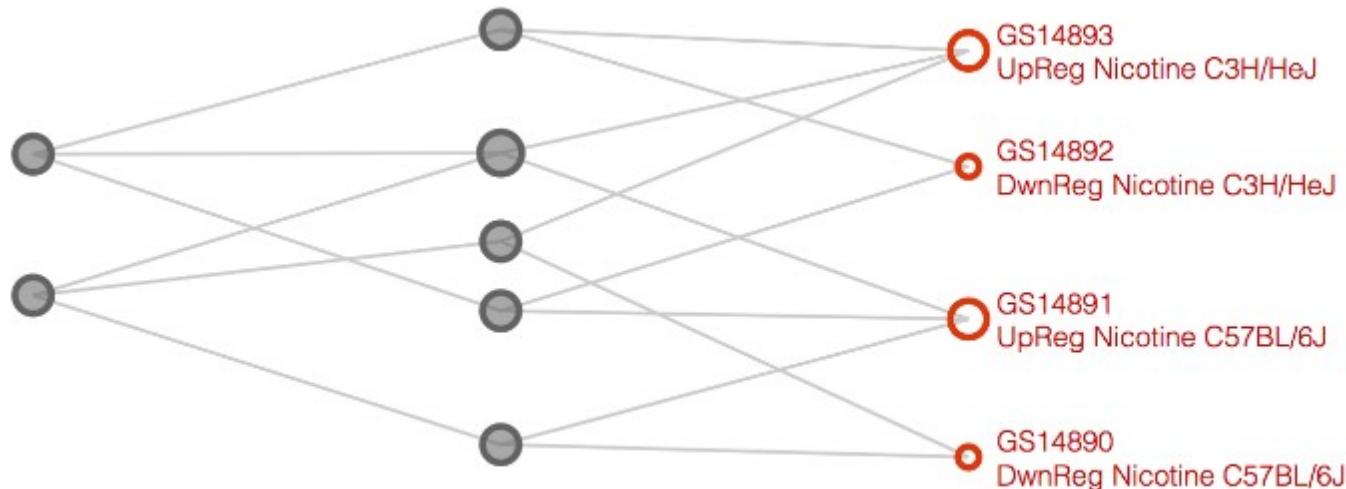


<input checked="" type="checkbox"/>	-	test-project
<input checked="" type="checkbox"/>	Tier III	Mm.
22	GS14890: Downregulated genes in five combined brain regions (Amygdala, Hippocampus, Nucleus Accumbens, Pre Frontal Cortex and Ventral Tegmental Area) in C57BL/6 mice	  
<input checked="" type="checkbox"/>	Tier III	Mm.
54	GS14891: Upregulated genes in five combined brain regions (Amygdala, Hippocampus, Nucleus Accumbens, Pre Frontal Cortex and Ventral Tegmental Area) in C57BL/6 mice	  
<input checked="" type="checkbox"/>	Tier III	Mm.
14	GS14892: Downregulated genes in five brain regions (Amygdala, Hippocampus, Nucleus Accumbens, Pre Frontal Cortex and Ventral Tegmental Area) in C3H/HeJ mice	  
<input checked="" type="checkbox"/>	Tier III	Mm.
75	GS14893: Upregulated genes in three brain regions, Nucleus Accumbens, Pre Frontal Cortex, and Ventral Tegmental Area, in C3H/HeJ mice	  

The HiSim Graph tool organizes multi-set intersections into a hierarchical directed acyclic graph (DAG). This organization infers an ontological relationship directly from the empirical data present in the original input sets. Genes in nodes at the top of the graph play a role in multiple phenotypes.

Hover over the leftmost node in the map to examine the genes it contains more closely.

Right click on a node to either view the GeneSet details or examine genes at the intersection of those sets.



Many features of the HiSim Graph can be modified by clicking on ‘Tool options’ or ‘Visualization Options’.

Tool Options ▾

DisableBootstrap: NodeCutoff: Homology: Included Excluded

GenesInNode: UseFDR: HideUnEmphasized:

p-Value: MinOverlap: MinGenes:

PermutationTimeLimit: MaxInNode: Permutations:

MaxLevel:

Re-Run Tool

Visualization Options ▾

Highlight Genes, GeneSets, or Species:

Download as... ▾

The GeneSet Intersection List shows all the sets in consideration, and a matrix of the genes associated with them. When a single species-specific gene is shown, a green circle is visible, but when multi-species data are compared, homology clusters are indicated with brown circles. In the example below, you could read it as “genes with homology to Kcnk1 are found in all 4 mouse and rat GeneSets.”

Tip: Linkouts for more information are also available (as with the geneset details page).

Tip: This page can also be exported to a TSV or CSV file (readable by Excel) for other uses by clicking the “Download as...” button.

Gene Intersection Table

Download as... ▾

- = Exact same gene in all sets
- = Homologous gene cluster

Gene Symbol

Abl1

Acn1

Gspt1

Adra1b

Cdc25c

Grik2

Links

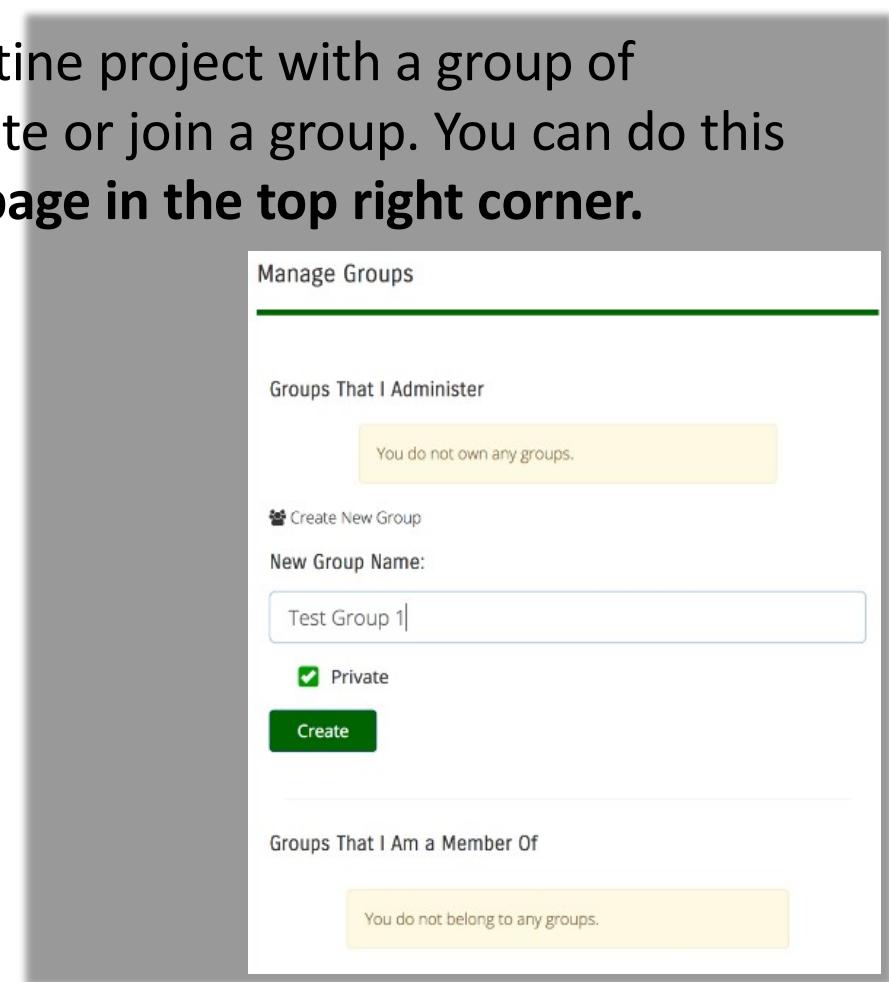


Let's say we want to share our Nicotine project with a group of collaborators. First, we need to create or join a group. You can do this by **clicking the “Account Settings” page in the top right corner.**

Click “Create New Group”, type a group name in the “New Group Name” box, then click the “Create” button.

Tip: For other group functions, click on the icons.

Tip: Explore this page for other useful functions.



We're also going to join a public group so we can analyze GeneSets that have been shared with us.

Click the “Join Public Group” button and search the list of public groups for “GeneWeaver Tutorial”.

Select the group and click “Submit”.

Manage Groups

Groups That I Administer

CheslerLab	Public	None	
------------	--------	------	--

Create New Group

Groups That I Am a Member Of

2015TswallowRNaseq	Public	None	
--------------------	--------	------	--

Join Public Group

Join Public Groups

Select which public groups you would like to join.

Select which projects to join:

- jaxTestGroup
- jaxTestGroup
- jaxTestGroup
- jaxTestGroup
- GeneWeaver Stress

Let's go to the “Manage Projects” page.

Hover your mouse over the “Manage GeneSets” link in the menu, then click the “Manage Projects” link.

Shared Projects provide a useful way to share analyses with collaboration groups. Any project you have can be shared by clicking the ‘share’ icon, then selecting the group from the pop-up window.

The screenshot shows the OmicsSoft interface. On the left, under 'Projects', there is a table with columns: PROJECT NAME, SIZE, and DATE. A row shows a project named 'test project' with size '8'. To the right of the table is a vertical 'Actions' menu with buttons for Delete Projects, Remove GeneSets, New Project, Combine GeneSets, and Export OmicsSoft. A blue arrow points from the 'share' icon in the 'test project' row to a 'Share Projects with Groups' dialog box. This dialog has a green header and a white body. It contains the text 'Select Groups to add to test project.' and a checkbox labeled 'Test Group 1'. At the bottom are 'Close' and 'Update Groups' buttons.

Projects

PROJECT NAME	SIZE	DATE
+ test project	8	

Actions

- Delete Projects
- Remove GeneSets
- New Project
- Combine GeneSets
- Export OmicsSoft

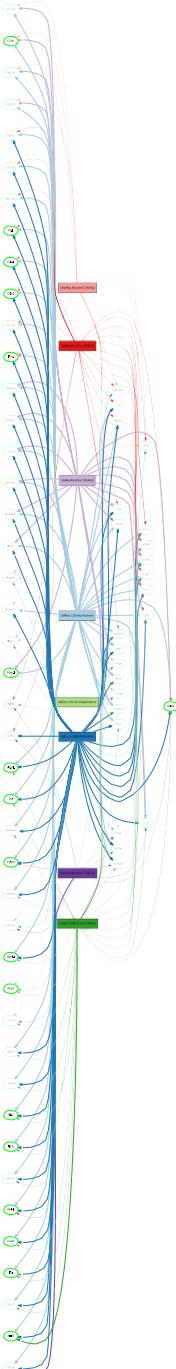
Share Projects with Groups

Select Groups to add to **test project**.

Test Group 1

Close **Update Groups**

Share your project with the group you created. Click the “share” icon, select your group name, then click the “Update Groups” button.



Let's browse the genes in the “Nicotine Hippocampus” project.

Navigate back to the “Analyze GeneSets” page.

At the bottom of the page you should see projects that have been shared with you.

Shared Projects

GeneWeaver Tutorial

+ Nicotine Hippocampus (Shared by timothy_reynolds@baylor.edu)

Select it and run the “**GeneSet Graph**” tool. This tool simply draws a node for every gene, and one for every GeneSet, and connects them with a line if they are associated. To aid comprehension, genes are arranged by connectedness (degree) from left to right (lower-higher).

You'll notice that the resulting image is very tall and hard to read (and this was only 8 GeneSets!). This is an example of when it is good to change tool options. Options can be changed from the “**Analyze GeneSets**” page, or from the results page by clicking “**Tool Options.**” (shown below)

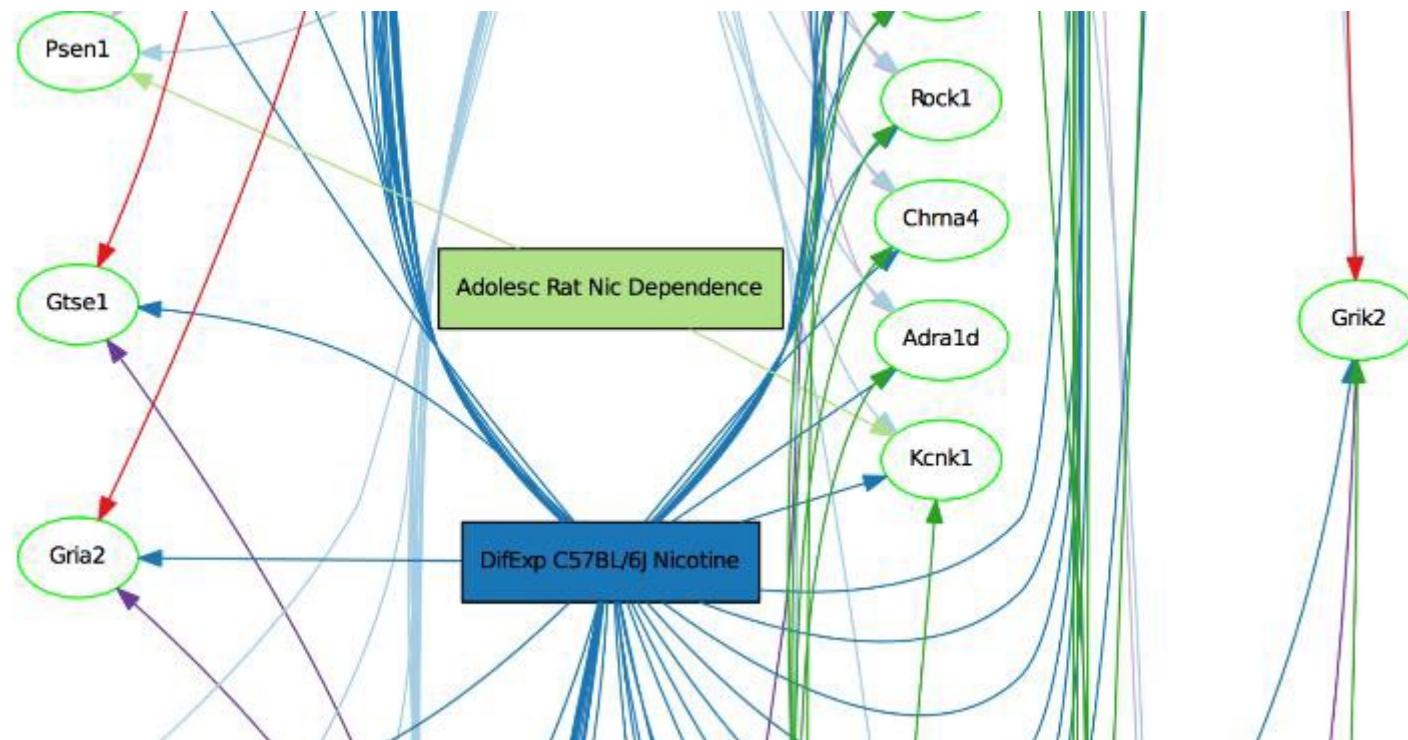
The image at left has a MinDegree of 2, let's increase that to 3 and then rerun the tool.

Tool Options ▾

Homology:	<input checked="" type="radio"/> Included	MinDegree:	Auto	SupressDisconnected:	<input type="radio"/> Off
	<input type="radio"/> Excluded				<input checked="" type="radio"/> On
Re-Run Tool					

That's better. From this result, we can see that Grik2 is connected to 6 GeneSets and might warrant further study. Some of the 5-way genes might be interesting as well.

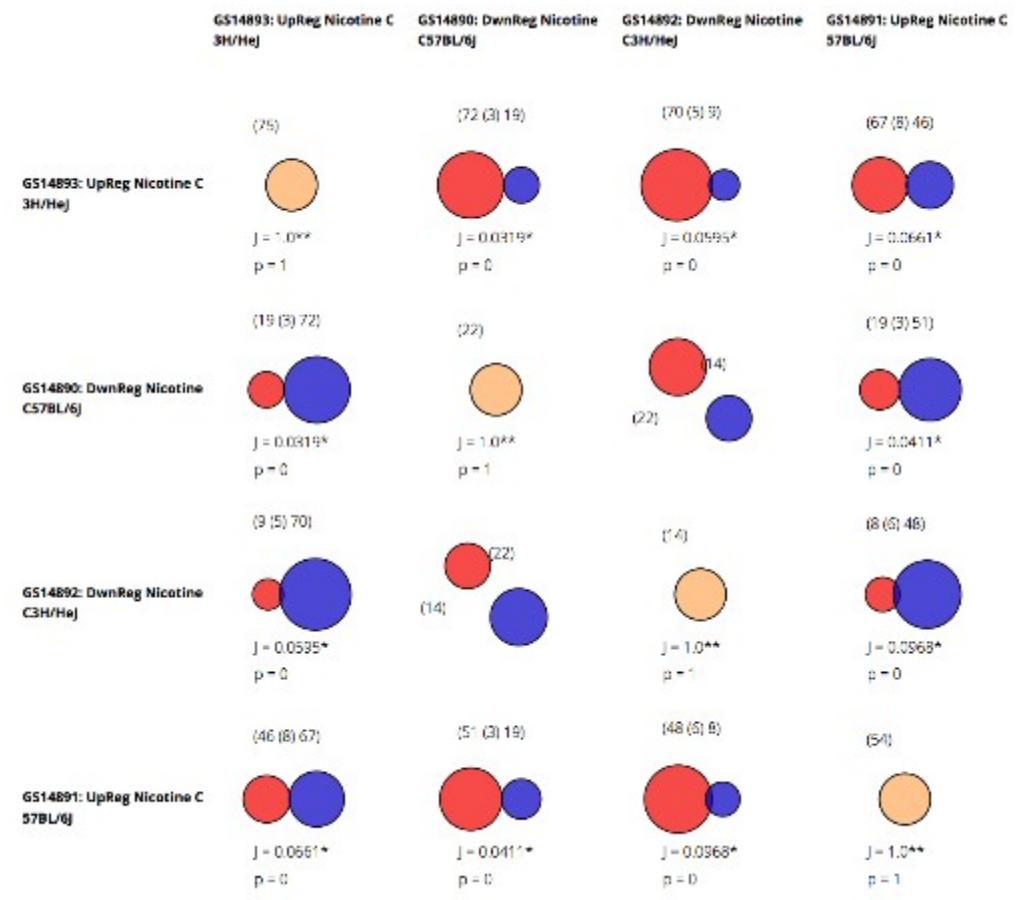
Tip: You can click on any gene in this image to search GeneWeaver for other GeneSets that contain that gene.



Let's try out one more tool before we move on. **Navigate back to the "Analyze GeneSets page" and using the same project, run the "Jaccard Similarity" tool.**

The Jaccard Similarity results give a large-scale, pairwise view of GeneSet overlaps. The Jaccard similarity coefficient is a positive match score for the similarity of set-set composition. Using this tool, you can quickly see when sets are highly overlapping or completely disjoint, and refine projects with more informative GeneSets.

Tip: Click on any intersection to bring up the GeneSet Intersection page discussed earlier in this tutorial.



Uploading your own data to GeneWeaver is fast and easy! Let's get started by going to: “Manage GeneSets” -> “Upload GeneSet”. This brings us to the upload page, where we need to provide a little bit of information:

GeneSet MetaContent

Please enter some descriptive info about this GeneSet, please confirm that your GeneSet MetaContent meets the guidelines outlined in our [Curation Standards](#) to ensure rapid acceptance by our curation team, or, in the case of private data, maximum integration into available GeneWeaver datasets.

GeneSet Name *:

GeneSet Figure Label *:

Score Type *:

GeneSet Description *:

Access Permissions

Access Restrictions ⓘ *: Private

Group(s): TimTest
GeneWeaver Stress

Reference Information

If this experiment has been published and listed in PubMed, just enter the PubMed ID below to automatically fill in the publication info, otherwise you may manually enter publication information. Providing this will allow others to discover and use your data more quickly, provide a means to link here directly from PubMed, and streamline our curation efforts.

PubMed ID:

Manual Entry [v](#)

Name – Shown in GeneSet Lists and Projects. Short but descriptive is best.

Label – Used to label nodes in results. Less than 24 characters recommended.

Score Type – Denotes the types of score used with the gene list (e.g. p-value, fold change, etc.)

Description – Used to describe the experiment and selection criteria for the set. Should probably be similar to the Table caption for published results.

Access Restrictions – Describes who can access this set, Everyone (Public), just you (Private), or groups of collaborators (Group).

Species - Select the species that the genes map to

Input File – You can either upload a plain text file, or copy and past a list by using the “copy/paste genes” button.

Differentially Expressed Genes and Coexpression Networks

Genome Biol. 2014 Apr 22;15(4):R65. doi: 10.1186/gb-2014-15-4-r65.

Chronic cocaine-regulated epigenomic changes in mouse nucleus accumbens.

Feng J, Wilkinson M, Liu X, Purushothaman I, Ferguson D, Vialou V, Maze I, Shao N, Kennedy P, Koo J, Dias C, Laitman B, Stockman V, LaPlant Q, Cahill ME, Nestler EJ, Shen L.

Erratum in

Erratum to: Chronic cocaine-regulated epigenomic changes in mouse nucleus accumbens. [Genome Biol. 2015]

Abstract

BACKGROUND: Increasing evidence supports a role for altered gene expression in mediating the lasting effects of cocaine on the brain, and recent work has demonstrated the involvement of chromatin modifications in these alterations. However, all such studies to date have been restricted by their reliance on microarray technologies that have intrinsic limitations.

RESULTS: We use next generation sequencing methods, RNA-seq and ChIP-seq for RNA polymerase II and several histone methylation marks, to obtain a more complete view of cocaine-induced changes in gene expression and associated adaptations in numerous modes of chromatin regulation in the mouse nucleus accumbens, a key brain reward region. We demonstrate an unexpectedly large number of pre-mRNA splicing alterations in response to repeated cocaine treatment. In addition, we identify combinations of chromatin changes, or signatures, that correlate with cocaine-dependent regulation of gene expression, including those involving pre-mRNA alternative splicing. Through bioinformatic prediction and biological validation, we identify one particular splicing factor, A2BP1(Rbfox1/Fox-1), which is enriched at genes that display certain chromatin signatures and contributes to drug-induced behavioral abnormalities. Together, this delineation of the cocaine-induced epigenome in the nucleus accumbens reveals several novel modes of regulation by which cocaine alters the brain.

CONCLUSIONS: We establish combinatorial chromatin and transcriptional profiles in mouse nucleus accumbens after repeated cocaine treatment. These results serve as an important resource for the field and provide a template for the analysis of other systems to reveal new transcriptional and epigenetic mechanisms of neuronal regulation.

PMID: 24758366 PMCID: [PMC4073058](#) DOI: [10.1186/gb-2014-15-4-r65](https://doi.org/10.1186/gb-2014-15-4-r65)



We'll go through these steps using an existing publication, but feel free to use your own.

Feng et al. Chronic cocaine-regulated epigenomic changes in mouse nucleus accumbens. *Genome Biology*. 2014 15:R65.

(PMID 24758366)

Data from Table S1

Differential RNA-seq lists. Differential gene lists from repeated and acute cocaine RNA-seq experiments; differential splicing lists from repeated cocaine RNA-seq experiments. Cuffdiff was used to perform differential analysis for various transcriptomic events.

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4073058/bin/gb-2014-15-4-r65-S3.xlsx>

READY TO USE FILE

<http://www.geneweaver.org/docs/DiffChronic.xlsx>

Gene Information

Species *: Rattus norvegicus

Gene Identifiers *: Gene Symbol

Gene List ⓘ [Switch to File Upload](#)

Grb10	1.868
Nr4a3	1.754
Mmd	1.736
Rundr1	1.714
Impact	1.68
Cleu2	1.664
Eifb	1.652
Xrg4	1.641
Cred2	1.577
Egr1	1.574
Atppav1b2	1.571
Dmrt1	1.561
Ockn1b	1.516
Dusp6	1.542
Hmgcr1	1.529
LOC360586	1.52

[Download Gene List](#)

First, fill out the GeneSet metacontent. Use the default access settings.

GeneSet MetaContent - GS225469

Please complete the descriptive information about this GeneSet. Follow the guidelines outlined in our [Curation Standards](#) to facilitate acceptance of your public data submission by GeneWeaver Curators. Following these guidelines for private data will assist you and your team in interpreting results and taking advantage of text and ontology analysis tools.

GeneSet Name *: Chronic cocaine mouse RNASeq Nucleus Accumbens (NAc)

GeneSet Figure Label *: Chronic cocaine mouse RNASeq NAC

Score Type *: P-Value ▾

GeneSet Description *:
Differential expression by RNASeq NAc in response to repeated cocaine doses, q-values uploaded. C57BL/6 mice

[Manual Entry](#) ▾

Gene Information

Species *:

Mus musculus ▾

Gene Identifiers *:

Gene Symbol ▾

Gene List ⓘ

Switch to File Upload		
3110035E14Rik	1.14E-05	
1500015O10Rik	0.0765495	
Dis3l2	4.04E-08	
Gin1	0.00505883	
Cntnap5b	0.0016447	
Wdr12	0.000286549	
Ipcef1	1.28E-08	
Ctgf	4.52E-10	
Pln	5.01E-05	
Ggt1	1.63E-06	
Oprm1	0.00601829	
Nt5dc1	0.00395658	
Gm9766	0.0119274	
Gm623	0.0001195	

Add the publication ID (**24758366**).
Select “Mus musculus” as the species
and “Gene Symbol” as the gene identifier
type.

Copy and paste the gene list from

The DiffChronic.xlsx file

Click the “Review GeneSet” button.

NOTE: You will be taken to a second page where you can verify genes associated with this data upload.

Click the “GeneSet Details” button to view your GeneSet.

SPECIES:	Mus musculus 			
IDENTIFIER:	symbol 			
GENE LIST:	YOUR IDENTIFIER	GENEWEAVER ID	VALUE	
	Cck	300	6.54E-9	 
	Fgf1	756	0.00141564	 
	Ctgf	773	4.52E-10	 
	Ggt1	905	0.00000163	 
	Hba-a1	1149	4.33E-10	 
	Hba-a2	1150	0.0000466	 
	Hbb-b1	1154	0.0000160	 
	Hbb-b2	1155	0.000546616	 
	Oprm1	1989	0.00601829	 
	Prkcd	2105	0.00513453	 
	Pln	2129	0.0000501	 
	Ttr	2819	0	 

 Add Gene

 Save Updates

 Cancel Edit

Warning: Please Note: Edits to this page (other than Species and Identifier) will not persist to your GeneSet unless you click 'Save Updates'. Also, if you click 'Cancel Edit', any changes on this page will be reverted. 

When upload completes, you will be taken to your new GeneSet details page. From here, you can add it to Projects and do further analysis.

Tier III GS225469 · Chronic cocaine mouse RNASeq Nucleus Accumbens (NAc)

DESCRIPTION: Differential expression by RNASeq NAc in response to repeated cocaine doses, q-values uploaded.
C57BL/6 mice

LABEL: Chronic cocaine mouse RNASeq NAc

SCORE TYPE: P-Value

DATE ADDED: None

DATE UPDATED: 2018-02-01

SPECIES: [Mus musculus](#)

AUTHORS: Feng J, Wilkinson M, Liu X, Purushothaman I, Ferguson D, Vialou V, Maze I, Shao N, Kennedy P, Koo J, Dias C, Laitman B, Stockman V, LaPlant Q, Cahill ME, Nestler EJ, Shen L

TITLE: [Chronic cocaine-regulated gene expression in the mouse nucleus accumbens](#)

JOURNAL: [Genome biology](#) Apr 2014, 15(4):100

ABSTRACT: Increasing evidence supports the role of chronic cocaine in neuroadaptations in the brain, and recent work has shown that cocaine-induced changes in chromatin regulation in the nucleus accumbens are dependent on the brain-derived neurotrophic factor (BDNF) signaling pathway. However, all such technologies that have been used to study cocaine-induced changes in chromatin regulation in the nucleus accumbens have been limited to the analysis of a small number of genes. Here, we used ChIP-seq for RNA polymerase II and histone H3K4me3 to analyze the genome-wide distribution of these epigenetic marks in the nucleus accumbens of mice chronically treated with cocaine. We identified a large number of genes that show cocaine-induced changes in chromatin regulation in the nucleus accumbens. In addition, we identify combinatorial regulation of gene expression by multiple transcription factors, including cAMP response element-binding protein (CREB), nuclear factor kappa-light-chain-enhancer of activated B cells (NF- κ B), and p53, which are known to regulate gene expression in the nucleus accumbens. Our results provide a comprehensive analysis of the genome-wide distribution of epigenetic marks in the nucleus accumbens of mice chronically treated with cocaine, and identify a large number of genes that show cocaine-induced changes in chromatin regulation in the nucleus accumbens.

[Export Data](#)
 [Similar GeneSets](#)
 [Request Curation](#)
 [Add Geneset to Project](#)
 [Share Geneset w/ Group\(s\)](#)
 [Set Threshold](#)

[Add Genes to GeneSet](#)

Filter Gene Symbol:

25

Showing 1 to 25 of 90 entries

1 2 3 4 Next

UPLOADED AS	GENE SYMBOL	HOMOLOGY	SCORE	PRIORITY	LINKOUTS	EMPHASIS
1500015O10Rik	1500015O10Rik		0.077	0		<input type="checkbox"/> OFF
3110035E14Rik	3110035E14Rik		0.0	0		<input type="checkbox"/> OFF
4732471D19Rik	4732471D19Rik		0.0	0		<input type="checkbox"/> OFF
6430573F11Rik	6430573F11Rik		0.02	0		<input type="checkbox"/> OFF
Abi3bp	Abi3bp		0.016	0		<input type="checkbox"/> OFF

General Tiers Species
Attributions

GLOBAL FILTERS Include **Provisional** (83) Include **Deprecated** (145)

Geneset Size: 1 to 4708

TIERS No Tier (0) I: Resources (234) II: Pro-Curated (0) III: Curated (17) IV: Provisional (0) V: Private (23)**SPECIES** Mus musculus (128) Homo sapiens (75) Rattus norvegicus (70) Macaca mulatta (1)**ATTRIBUTION****Search GeneSets** like "mouse, Ap3m2, alcohol"

"Cocaine Addiction" OR "Chronic Cocaine"

Search

-

+

 GeneSets Genes Abstracts Annotations

Share Selected w/ Group

Add Selected to Project

RETURNING 46 RESULTS: PAGE 1 OF 2

1 2

	TIER	SPECIES	SIZE	ATTR.	GENESET
<input type="checkbox"/>	Tier III	Hs	38		G51256: Gene Expression in Human Hippocampus from Cocaine Addicts
<input type="checkbox"/>	Tier III	Hs	25		G5135214: Gene Expression in Postmortem Hippocampus from Alcoholics and Cocaine Addicts
<input type="checkbox"/>	Tier III	Rn	25		G5135215: Postmortem Hippocampus from Alcoholics and Cocaine Addicts and Alcohol preferring (P) and Non-preferring (NP) Rats
<input type="checkbox"/>	Tier I	Rn	84	DRG	G587486: Table 1: Genes that were identified as being differentially regulated in the rat striatum following cocaine self-administration. (Whole Table) [DRG]
<input type="checkbox"/>	Tier I	Rn	26	DRG	G587487: Table 2: Circadian genes and genes regulated by/associated with the circadian system that were identified as being differentially regulated in the rat striatum following cocaine self-administration. (Whole Table) [DRG]
<input type="checkbox"/>	Tier III	Hs	19		G5136985: Genes with significant differential expression (FDR < 0.2) observed in chronic cocaine-addicted individuals



In Group=GeneWeaver Tutorial

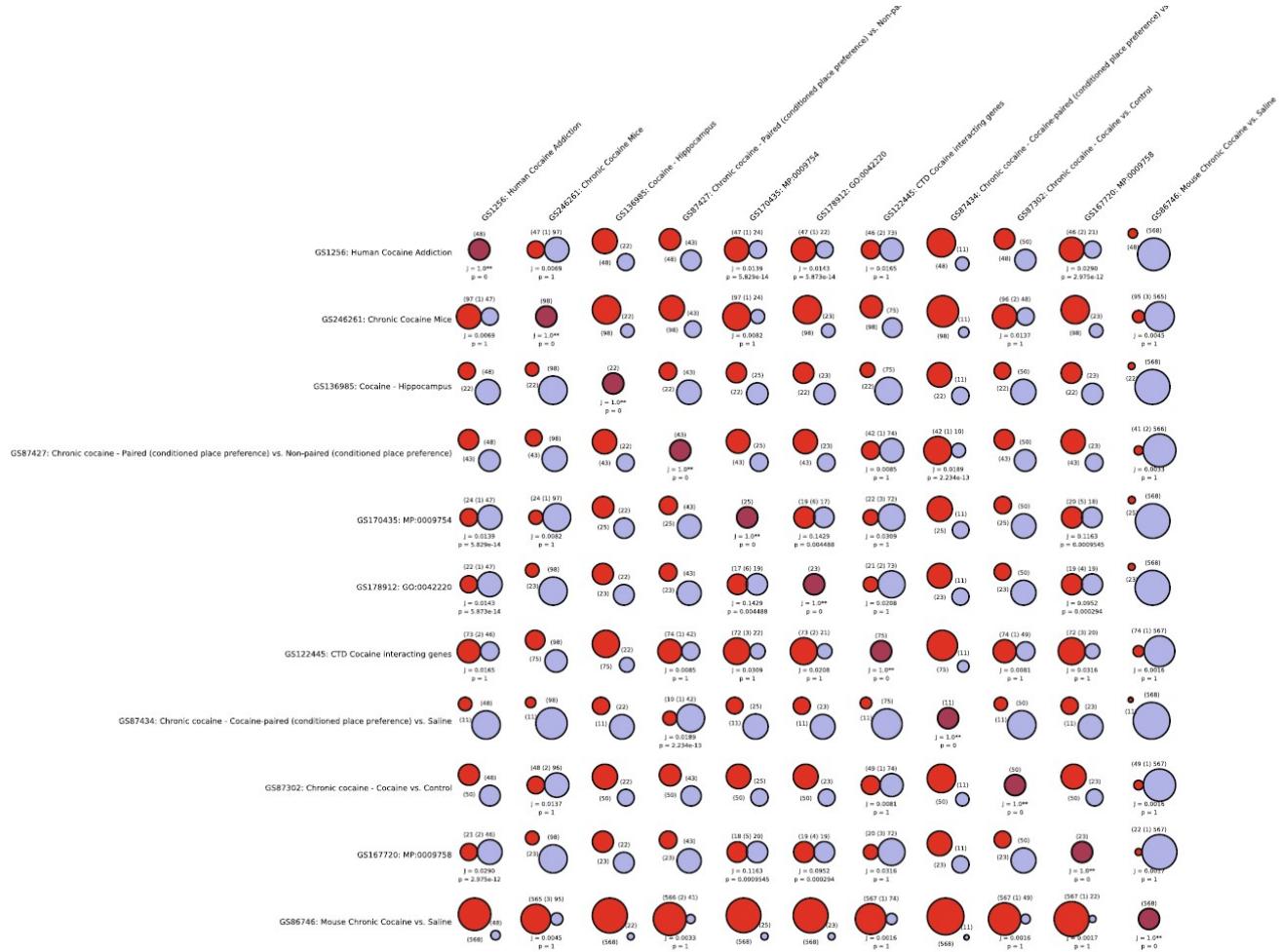
Chronic Cocaine Demo

Selected gene sets retrieved from the GeneWeaver database related to chronic cocaine addiction in mouse, rat, and human

GeneSet ID	Description	Number of genes in set	Species	Reference
GS170435	Enhanced behavioral response to cocaine	25	Mouse	MP:0009754
GS87427	Genes significantly changed after cocaine CPP treatment in the hippocampus	43	Rat	17640290
GS178912	Response to cocaine	23	Mouse	GO:0042220
GS136985	Genes with significant differential expression (FDR<0.2) observed in chronic cocaine-addicted individuals	22	Human	21464311
GS86746	List of cocaine-treated WT vs. Saline-treated WT significantly regulated genes	571	Mouse	17988634
GS1256	Gene expression in human hippocampus from cocaine addicts	48	Human	18000554
GS87302	Transcripts differentially expressed in the majority of cocaine users	50	Human	15009677



Jaccard Overlap Tool



GeneSet Graph Tool

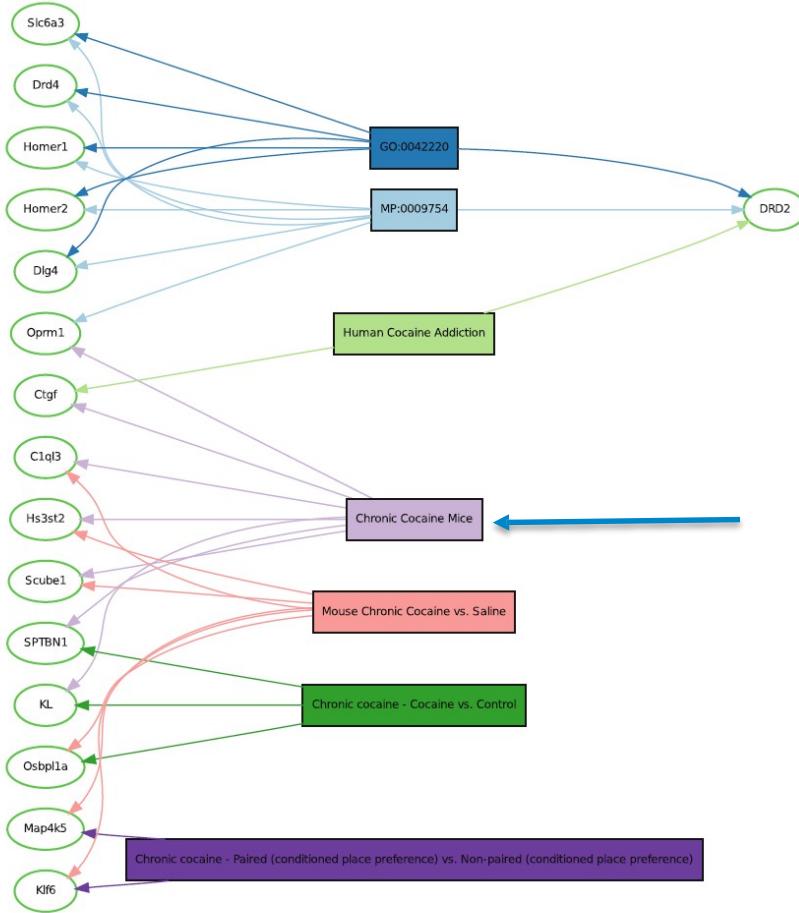


Fig. 16 GeneSet graph of the differentially expressed genes from chronic cocaine exposure in mice

Bubier, et al, 2017 Methods Mol Biol 1488:131-152

- ◆ This tutorial was intended to provide an introduction to practical approaches to the tools in GeneWeaver.
- ◆ There are many tools and approaches that can be combined to create particular workflows to address a variety of genetics questions. Additional tutorials and documentation can be found on the website.
- ◆ If you have any suggestions, comments, or questions please use the “Feedback” link located on every page.

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Primary data sources and identifiers

Table 1.1 Primary data sources and identifiers

Database	Institution	Example identifiers	Reference
Entrez Gene	NCBI	4852, 109648, 24604, 30281	Maglott, Ostell, Pruitt, and Tatusova (2007)
Ensembl Gene	EMBL	ENSG00000122585, ENSMUSG00000029819, ENSRNOG00000009768, ENSDARG00000036222	Flicek et al. (2012)
HGNC	HGNC	HGNC:7955	Seal, Gordon, Lush, Wright, and Bruford (2011)
MGI	JAX	MGI:97374	Blake, Bult, Kadin, Richardson, and Eppig (2011)
RGD	RGD	RGD:3197	Twigger, Shimoyama, Bromberg, Kwitek, and Jacob (2007)
ZFIN	ZNC	ZDB-GENE-980526-438	Bradford et al. (2011)

Some of the major primary data sources in biology and example identifiers contained within them.



Table 12 Primary gene symbols

OffidaJ symbol	Species	Other aliases
<i>NPY</i>	Human	<i>PYY4</i>
<i>Npy</i>	Mouse	<i>0710005A05Rik</i>
<i>Npy</i>	Rat	<i>NPY02, RATNPY, RATNPY02</i>
<i>Npt</i>	Zebrafish	<i>Si:dkey-22m8.5</i>
<i>Vtilb</i>	Mouse	<i>AU015348, GESJO, MVtilb, SNARE, Vti1-rp1</i>
<i>Gosr2</i>	Mouse	<i>RP23-272P17.5, 2310032N09Rik, C76855, Gs27, SNARE, m(mbrin</i>
<i>Napa</i>	Mouse	<i>1500039N14Rik, AW209_189, RA81, SNAPA, SNARE, a-SNAP, hyh</i>
<i>Napb</i>	Mouse	<i>RP23-377E1.3, Brp14, E161, I47, SNARE, b-SNAP</i>
<i>Napg</i>	Mouse	<i>2400003004Rik, SNARE</i>

(iene symhn1 3nd ali a s for tle Eerie *NPY* and its homolu and pnx..luct in variou s-speci or rnu§e genes- with the ali§ *SNARc* in NC.BI.



Integrative Functional Genomics: The quest for consilience



“...the evidence in favour of our induction is of a much higher and more forcible character when it enables us to explain and determine cases of a kind different from those which were contemplated in the formation of our hypothesis...

No accident could give rise to such extraordinary coincidence.”

-W. Whewell, 1847

Identification of GeneSets most similar to MeSH Alcoholism Term

GeneWeaver.org
A system for the integration of functional genomics experiments.

Welcome Guest! To ensure future access to your data, please [Register](#) — or [Login](#)

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GeneSets Similar to GS128735
Gene Set #128735 - Alcoholism MeSH associations in PubMed

Description: Genes associated to MeSH term 'Alcoholism' or a descendant in PubMed's curated annotations. METHOD: NCBI's gene2pubmed and e-utilities were used to associate MeSH PubMed annotations to Enzr Gene IDs. To control for outlier associations, curated annotations must have at least 2 occurrences to be retained. Retained annotations were then pushed to ancestor terms to ensure a complete tree. All data fetched 28 Feb 2012.

[« Back to GeneSet details](#)

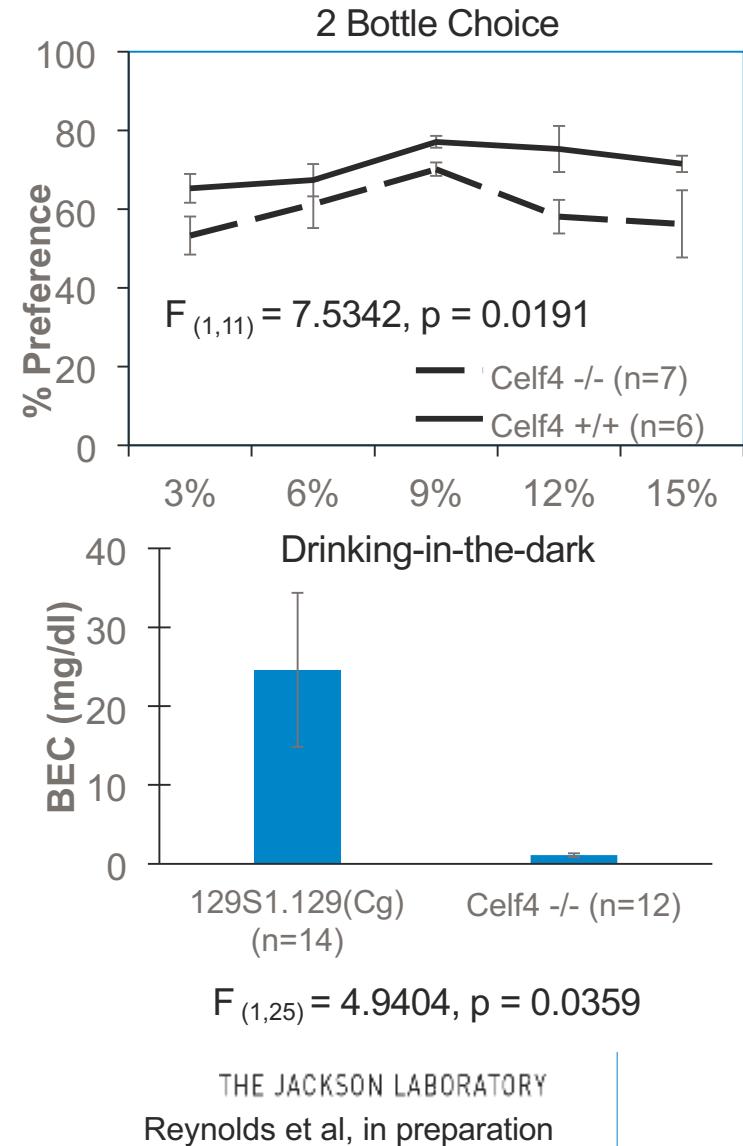
Similar GeneSets:

			Gene Similarity (Jaccard)		
<input type="checkbox"/>	+ Tier III	Human	14 Genes	GS216653: Protein Biomarkers of Alcohol Abuse	0.044444
<input type="checkbox"/>	+ Tier V	Mouse	151 Genes	GS137124: 142 enriched CELF4	0.041353
<input type="checkbox"/>	+ Tier I	Human	GO	4 Genes GS199997: GO:0004024 alcohol dehydrogenase activity, zinc-dependent	0.031496

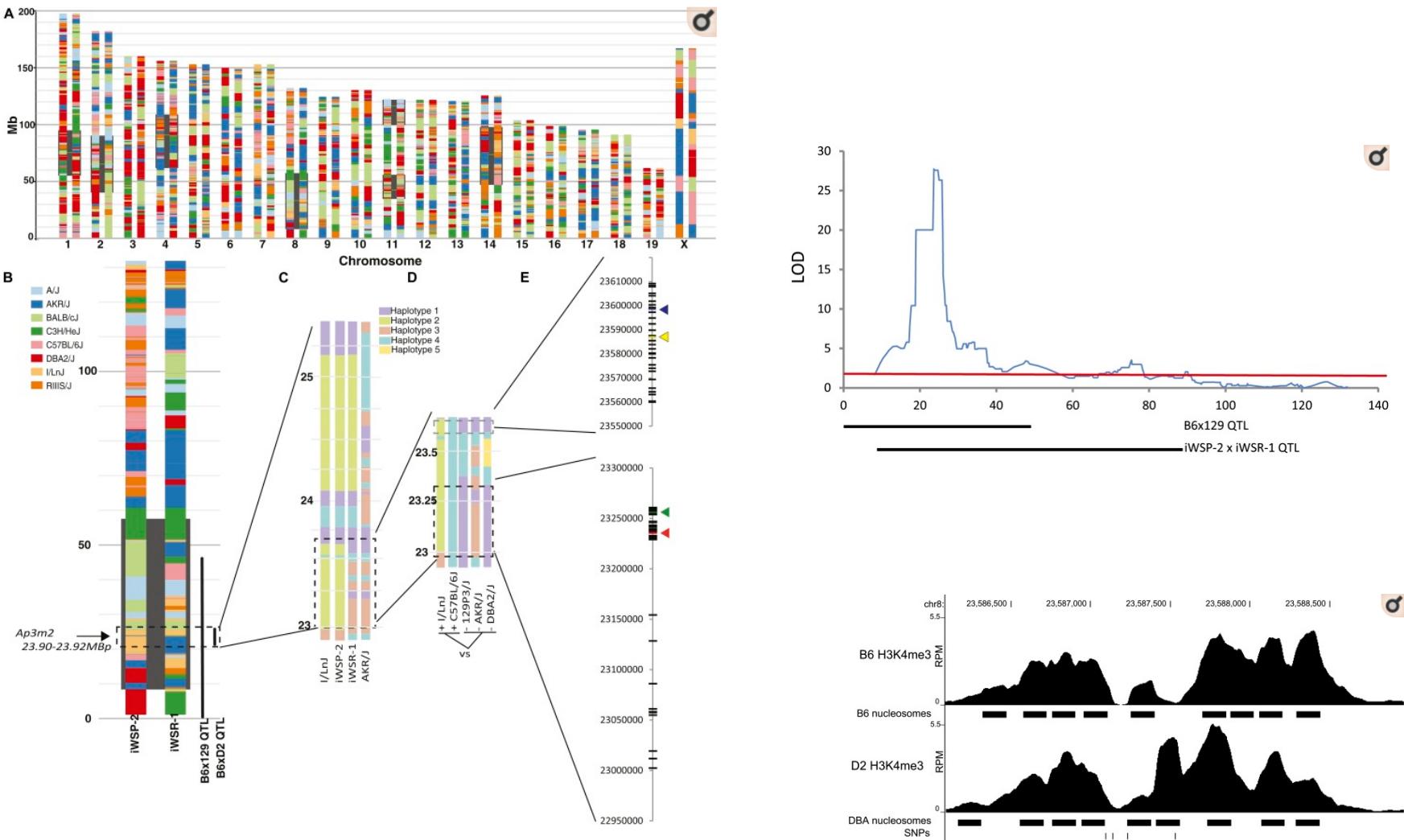
11

GS128735
116 Genes
Associated to MeSH term alcoholism

GS137124
142 Genes
Enriched in Celf4 -/- mice



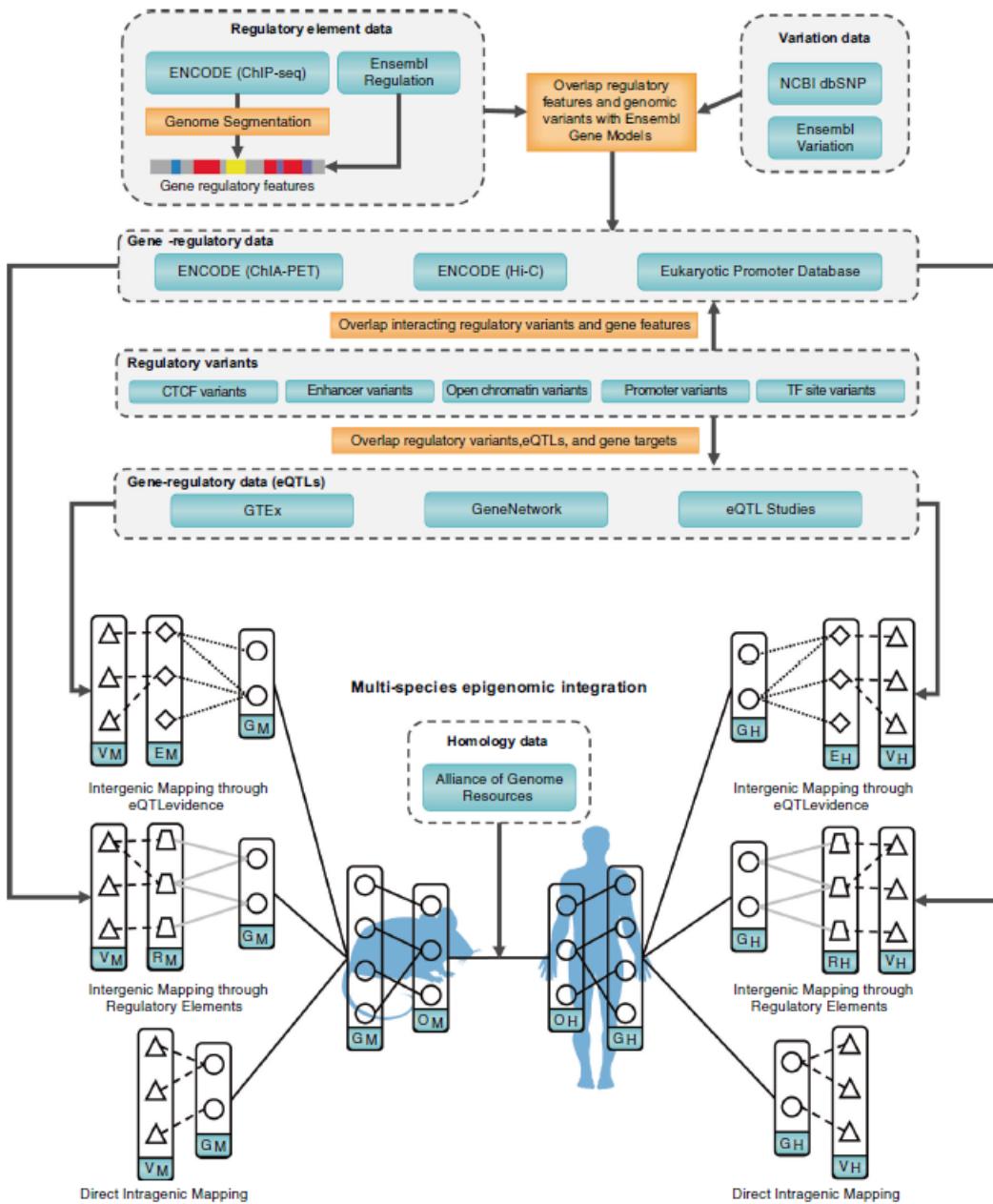
Genetic Variation in *Ap3m2* regulation



Bubier et al Genetics 2014

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Reynolds, NPP 2020



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