

Identifying genes from QTL using RNA expression and the PhenoGen website

5th Webinar for Quantitative Genetics Tools for Mapping Trait Variation to Mechanisms, Therapeutics, and Interventions

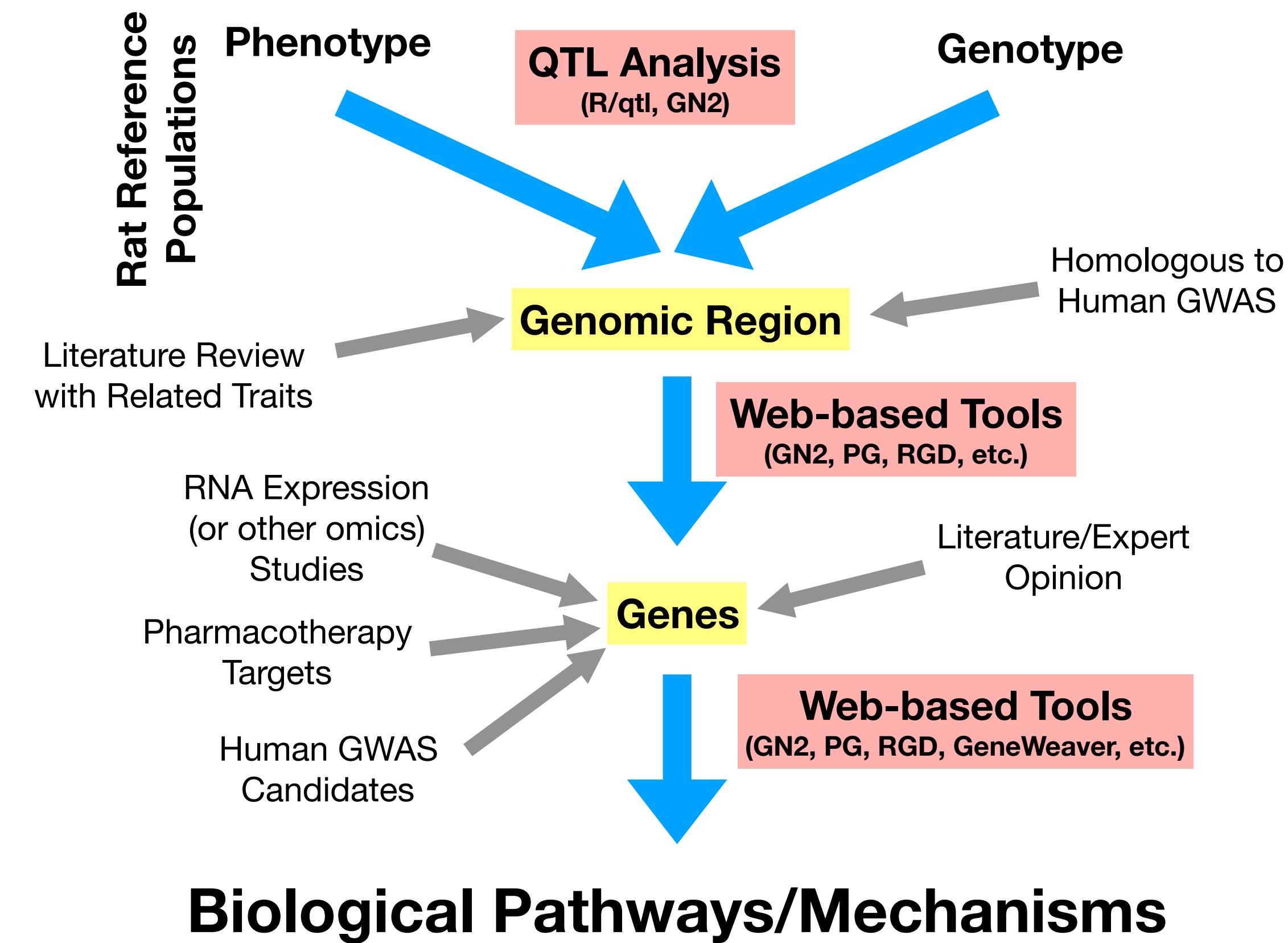
Laura Saba, PhD
University of Colorado Anschutz Medical Campus
NIDA Center of Excellence in Omics, Systems Genetics and the Addictome (P30 DA044223)
PhenoGen: The heritable transcriptome and alcoholism (R24 AA013162)

Quantitative Genetics Tools for Mapping Trait Variation to Mechanisms, Therapeutics, and Interventions Webinar Series

Forward Genetics in Model Organisms

Goal of the Series:

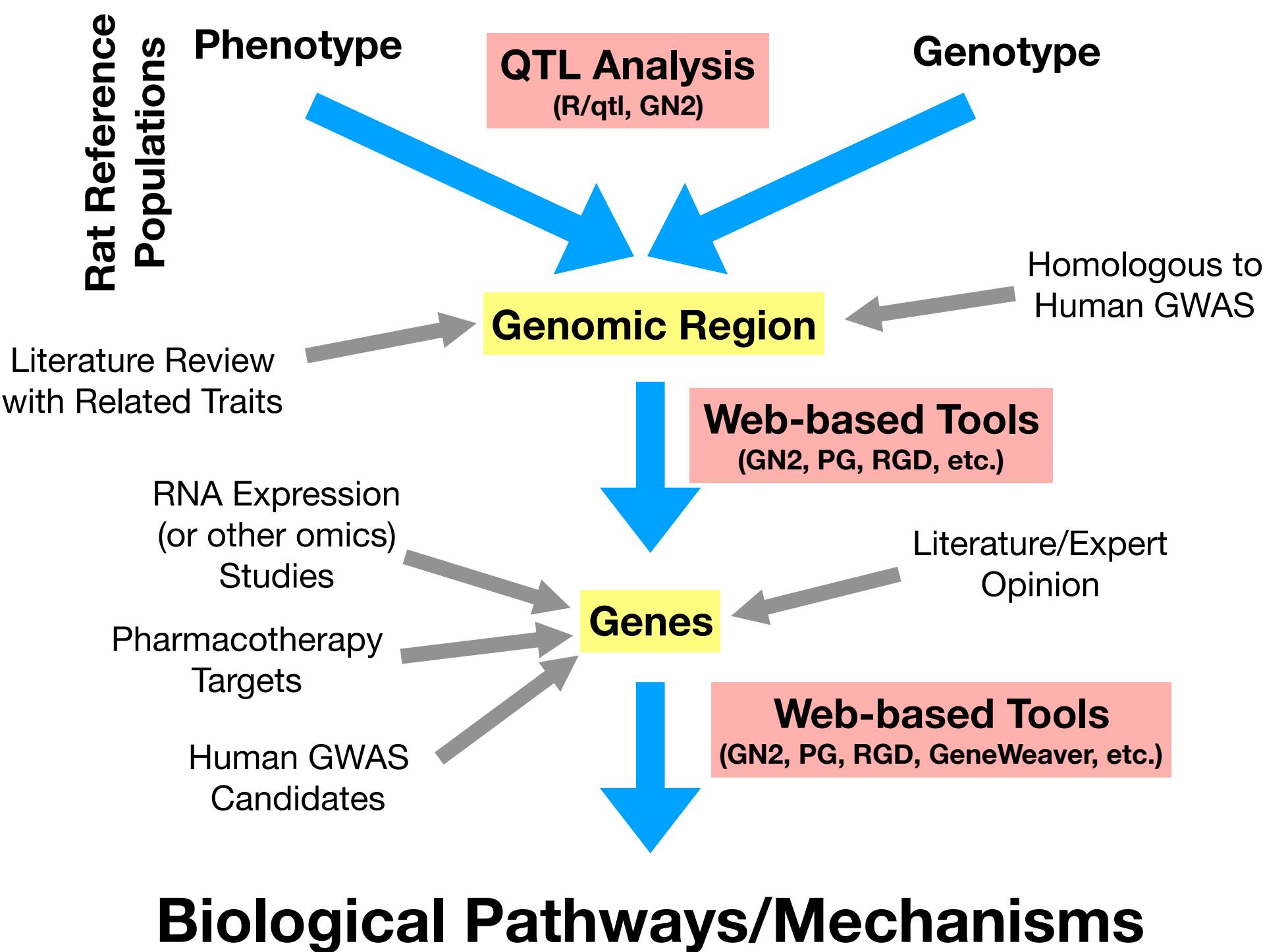
Transverse the path from trait variance to QTL to gene variant to molecular networks to mechanisms to therapeutic and interventions



Recap of Webinar Series

- **Introduction to Quantitative Trait Loci (QTL) Analysis** - Presented by Dr. Saunak Sen
- **Mapping Addiction and Behavioral Traits and Getting at Causal Gene Variants with GeneNetwork** - Presented by Dr. Rob Williams
- **Introduction to expression (e)QTL and their role in connecting QTL to genes and molecular networks** - Presented by Dr. Laura Saba
- **From Candidate Genes to Causal Variants—Strategies for and Examples of Identifying Genes and Sequence Variants in Rodent Populations** - Presented by Dr. Rob Williams

Forward Genetics in Model Organisms

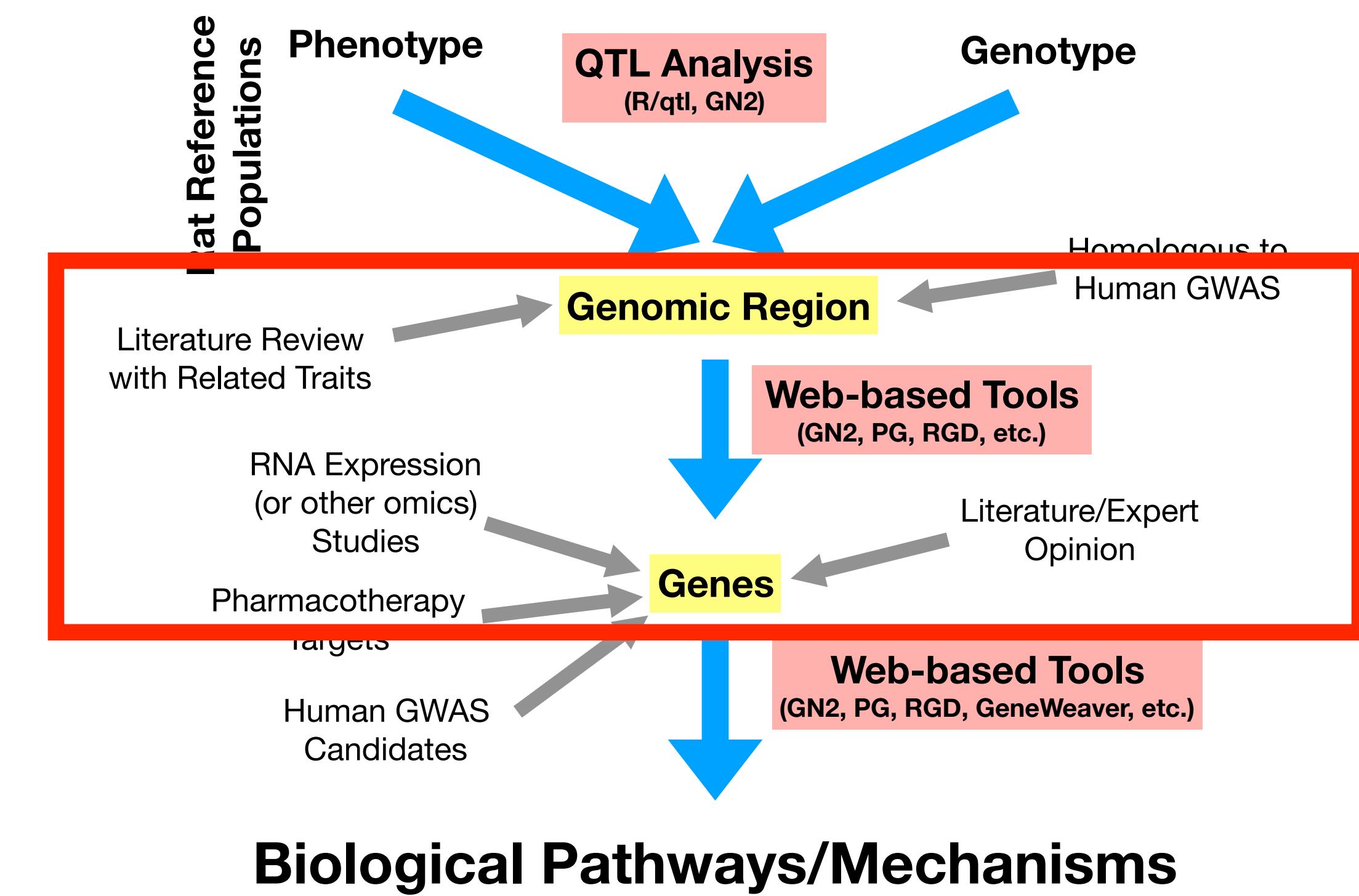


Outline

Demonstrate how to use the PhenoGen website to identify transcripts:

- Physically located within a QTL
- Physically located within a QTL and expressed in brain
- With a brain cis eQTL within the QTL
- With any brain eQTL within the QTL
- Within a co-expression network controlled from the same region as the QTL

Forward Genetics in Model Organisms



Introduction to the PhenoGen Website (<https://phenogen.org>)

Goal of the PhenoGen Project

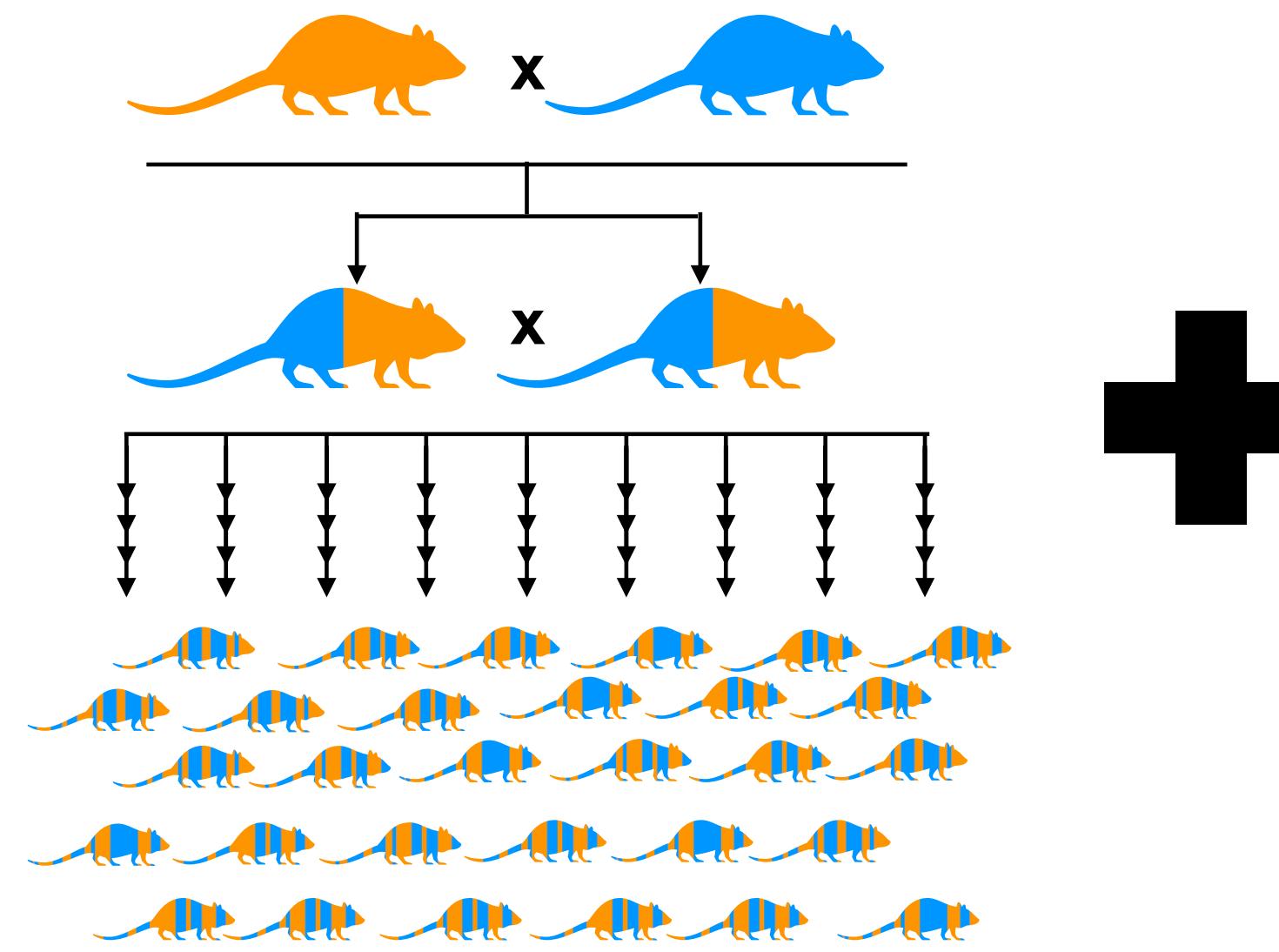
To build a resource that will provide data leading to a “systems genetic” understanding of complex disease-related traits

- The resource is based on a large panel of genetically-defined inbred rat strains and includes their genome sequences and global levels of gene expression in two organs (brain and liver).
- These data will be integrated to identify genetic and molecular regulators of gene expression and to describe the interactions among genes as a system of inter-dependent components that work together to predispose an individual to complex disease.

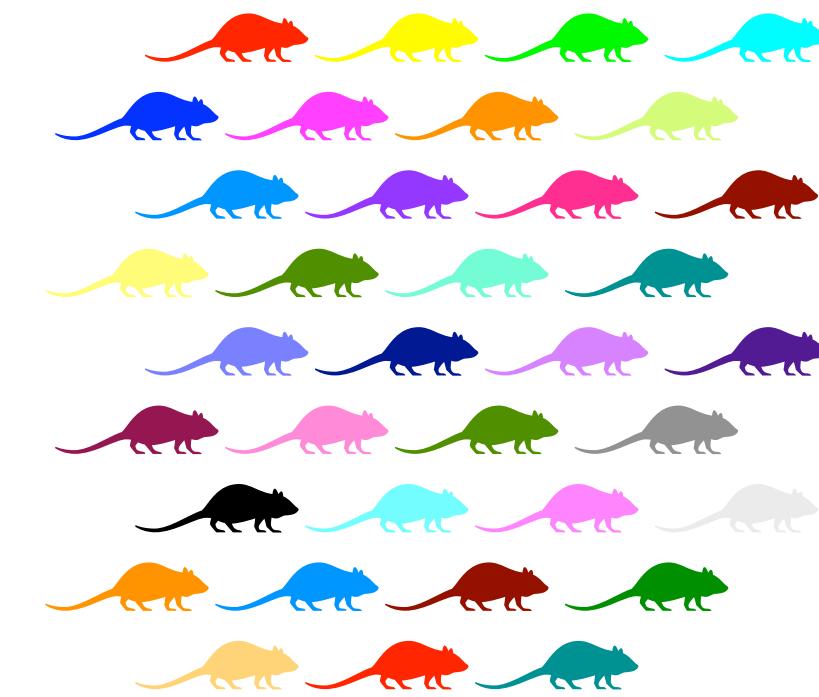
Hybrid Rat Diversity Panel

A Renewable Genetically Defined Population for Cumulative Biology

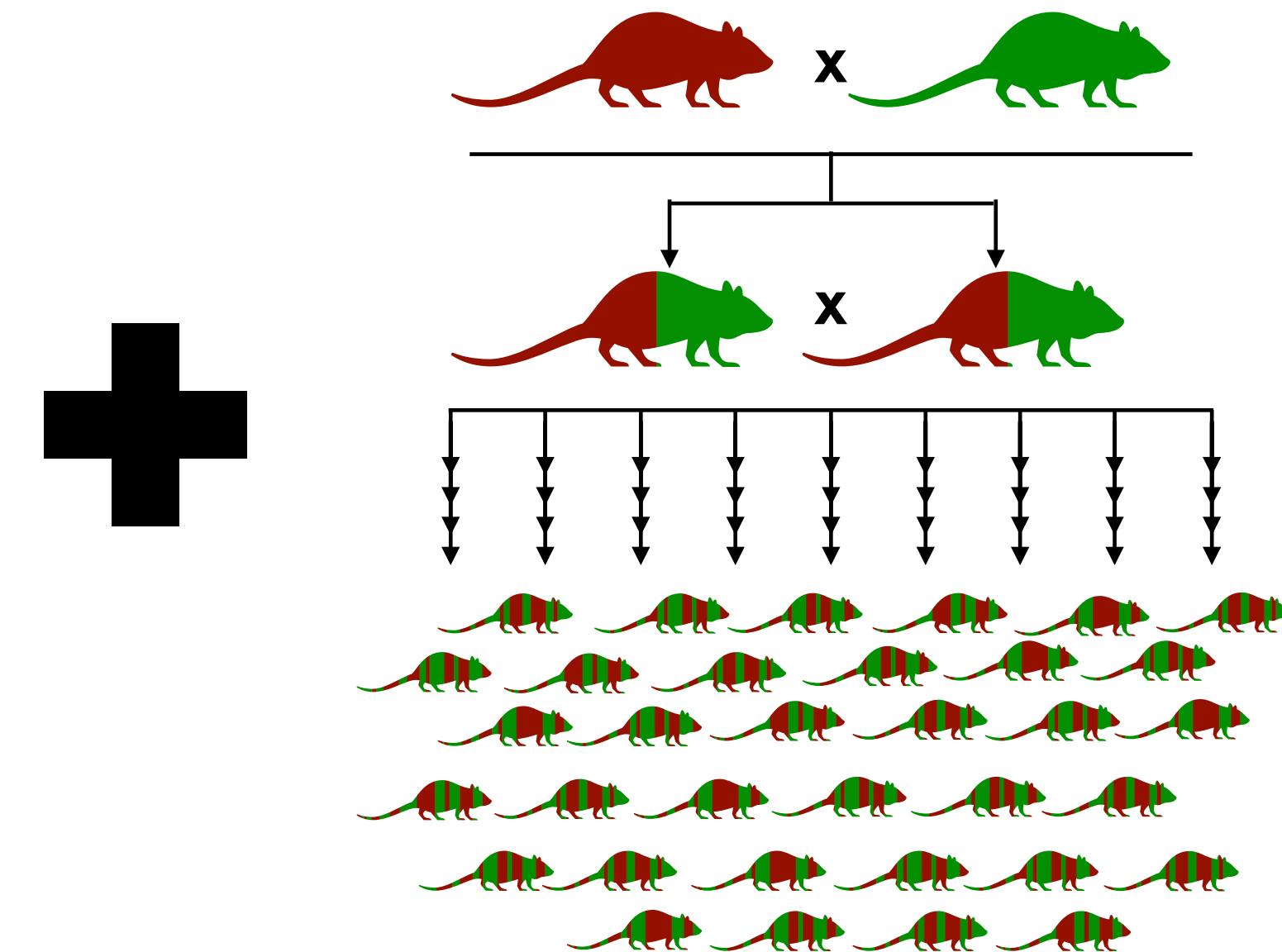
- Susceptibility/predisposition studies
- Mechanistic Biology Studies
- Systems/Network Biology Studies
- Toxicologic Analysis
- Pharmaco/toxicokinetics
- Proof of Concept Studies



**HXB/BXH Recombinant
Inbred Panel
(30 strains)**



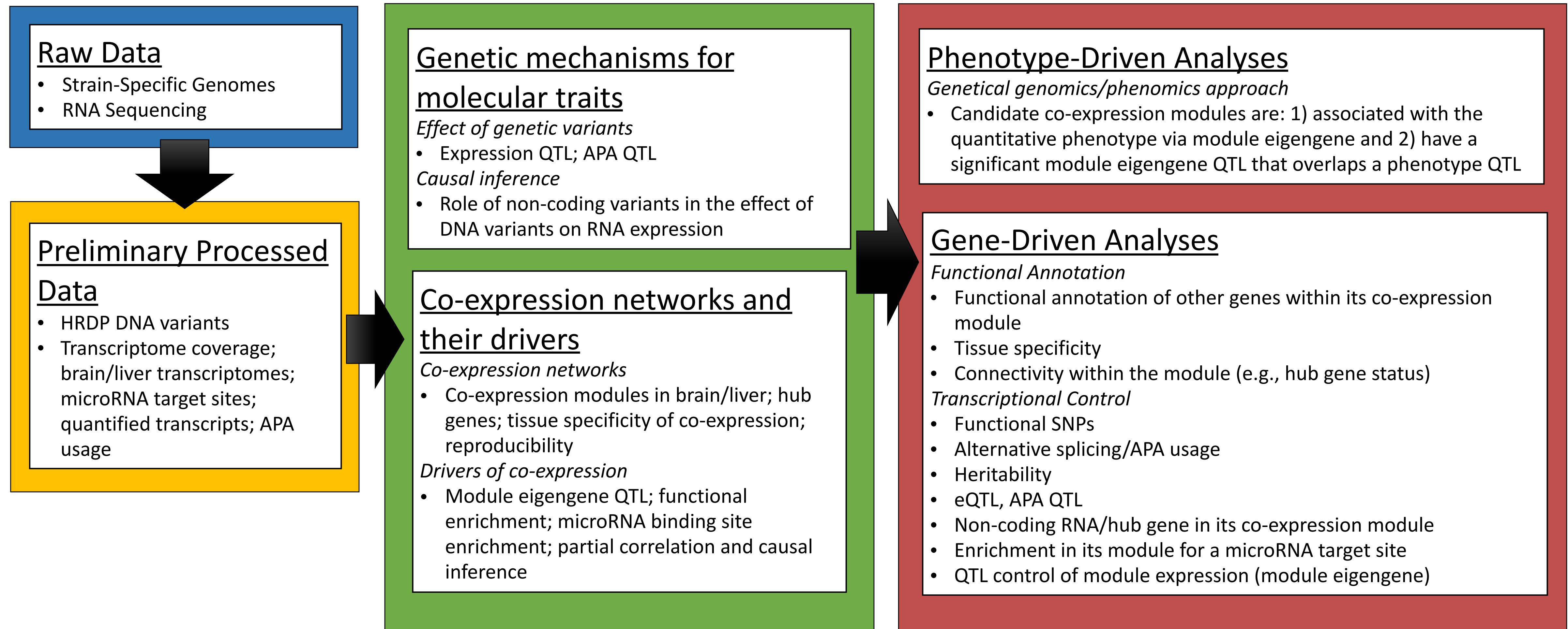
**Divergent Classic Inbred
Strains
(35 strains)**



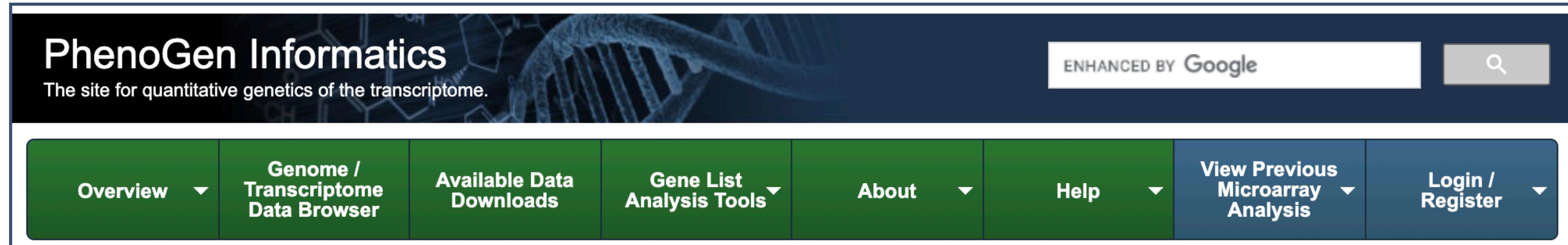
**FXLE/LEXF Recombinant
Inbred Panel
(34 strains)**

All strains being established at the Medical College of Wisconsin, Dr. Melinda Dwinell

Overview of transcriptomic and genomic information gathered and disseminated as part of the PhenoGen/HRDP Project



Features of PhenoGen

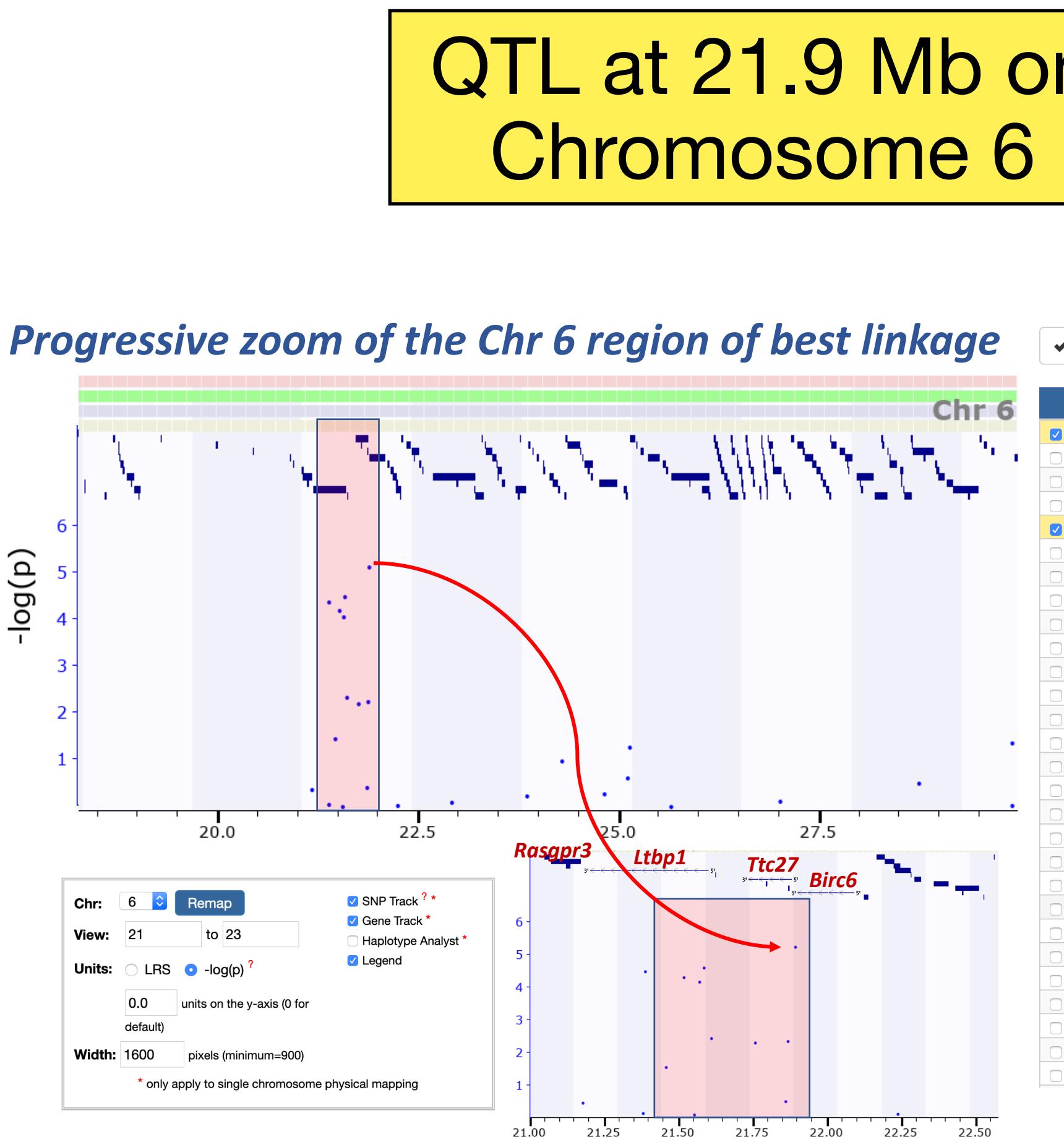


- Genome/Transcriptome Data Browser
 - Visualization tool at the genome level that includes information on small RNA, long non-coding RNA, protein coding RNA, and circular RNA
- Available Data Downloads
 - Includes processed RNA expression data from the HRDP using version control (new version released approximately yearly)
 - Data files from publications
 - Strain-specific genomes
 - Reconstructed brain and liver transcriptomes (based on short read RNA-Seq)
 - Updated brain and liver polyadenylated transcriptomes (based on single molecule RNA sequencing; coming soon)
- Gene List Analysis Tools
 - Annotation
 - eQTL
 - Co-expression networks
 - Multi-mir (identification of microRNA binding site)
 - Gene Ontology enrichment
 - Promotor analysis
 - Homologs

From QTL to Gene on PhenoGen

Phenotypic QTL for Nicotine Seeking

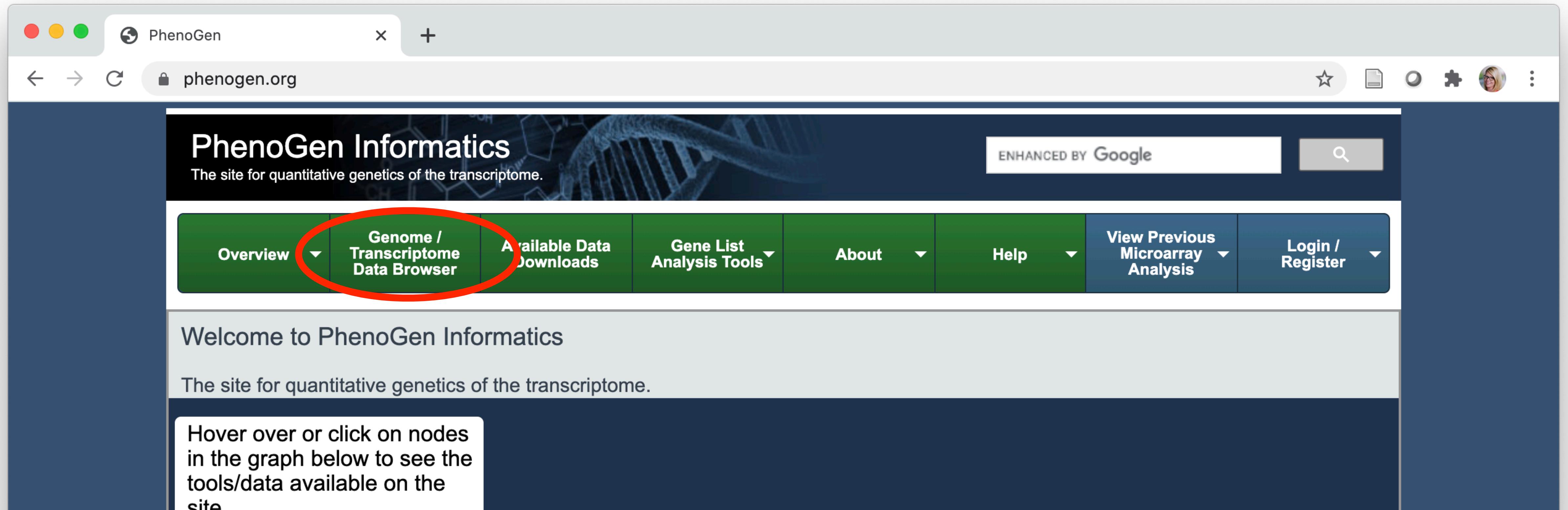
From webinar #2 by Dr. Williams



	Index	Record	Description	Mean	Authors	Year
	505	HSR_10505	Central nervous system, behavior: Ratio of licks on the active over inactive spout during a progressive ratio (PR) session tested after 10 fixed ratio sessions in male and female adolescents (41 to 51 days old) trained using a socially acquired nicotine intravenous self-administration procedure where licking was used as the operant response (Chen lab cohort, UTHSC) [ratio]	7.204	Wang T, Chitre A, Garcia Martines A, Han W, Polesskaya O, Solberg Woods L, et al.	2020

Slide 17. Zoomed to a small region of Chr 6 near markers with the highest linkage scores (LOD 5.19 at 21.9 Mb).

Navigating to the Genome Browser



Specify region of interest and view

The screenshot shows the PhenoGen Informatics website interface. At the top, there is a navigation bar with links for Overview, Genome / Transcriptome Data Browser, Available Data Downloads, Gene List Analysis Tools, About, Help, View Previous Microarray Analysis, and Login / Register. Below the navigation bar, there are two main input fields:

- 1. Specify a Gene or Region to get started:** This section contains a text input field for "Gene Identifier or Region" containing "chr6:20900000-22900000" and a dropdown for "Species" set to "Rattus norvegicus".
- 2. What data do you want to view?** This section contains a dropdown for "Initial View" set to "Genome/Transcriptome (Predefined)" and a "Create Custom View" button.

Two arrows point from callout boxes to these sections:

- An arrow points from a yellow callout box labeled "Enter QTL location using base pairs" to the "Gene Identifier or Region" input field.
- An arrow points from a yellow callout box labeled "Choose 'view' to start with" to the "Initial View" dropdown.

Enter QTL location using base pairs
For this demo, I chose 1 Mb on either side of peak, but could also use Bayesian Credible Interval or LOD drop interval

Choose 'view' to start with
View determines the tracks that are shown by default tracks can be customized later.

Limit to tracks of interest

The screenshot shows a genome browser interface for rat chromosome 6. At the top, there are search and filter fields for genes and regions. Below the search bar is a navigation menu with various links like 'Overview', 'Gene List Analysis Tools', and 'Help'. A large central area displays a genomic track viewer for chromosome 6, showing gene tracks and RNA-seq data. A red arrow points to the 'Select/Edit Views' button at the top right of the track viewer.

Click 'Select/Edit Views'

This screenshot shows the 'Select/Edit Views' dialog box. It lists various pre-defined genomic views for rat, including 'Genome (Predefined)', 'Transcriptome (Predefined)', and several RNA-seq and microarray datasets. A red arrow points to the 'View/Edit Track List' tab, which is highlighted. Another red circle highlights the 'X' icon next to a specific track entry (e.g., 'Liver Total-RNA Transcriptome (BN-Lx/SHR)') in the list, indicating it can be removed.

Click 'View/
Edit Track
List' tab

Click on the 'X'
to eliminate a
specific track

Click 'View/
Edit Track
List' tab

Click 'Apply
View' button to
finalize choices

This screenshot shows the 'Select/Edit Views' dialog box again, but now with fewer tracks listed. The 'View/Edit Track List' tab is still selected. A red arrow points to the 'Apply View' button at the bottom right of the dialog, which has been highlighted with a red circle.

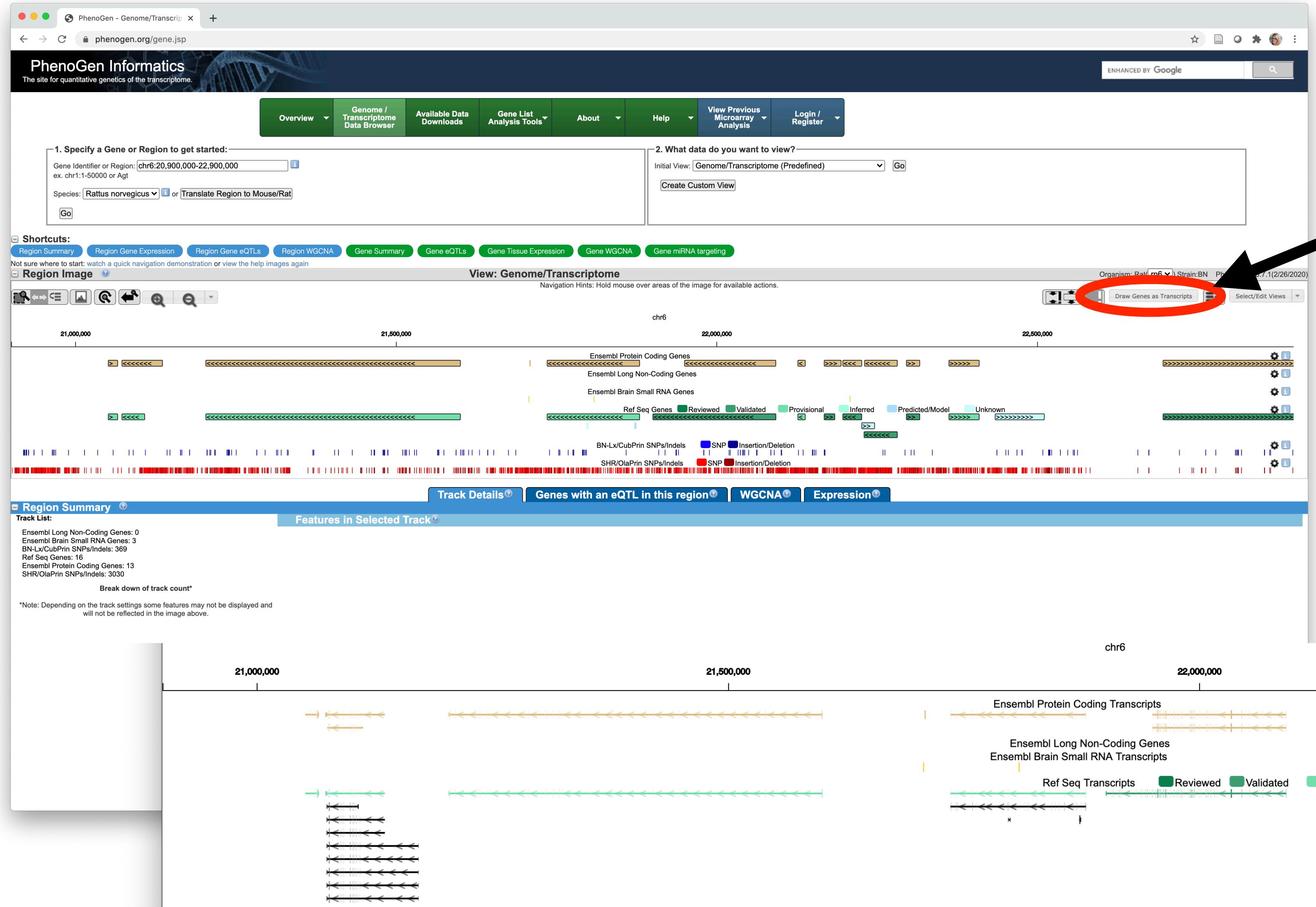
Apply View

Description of Tracks

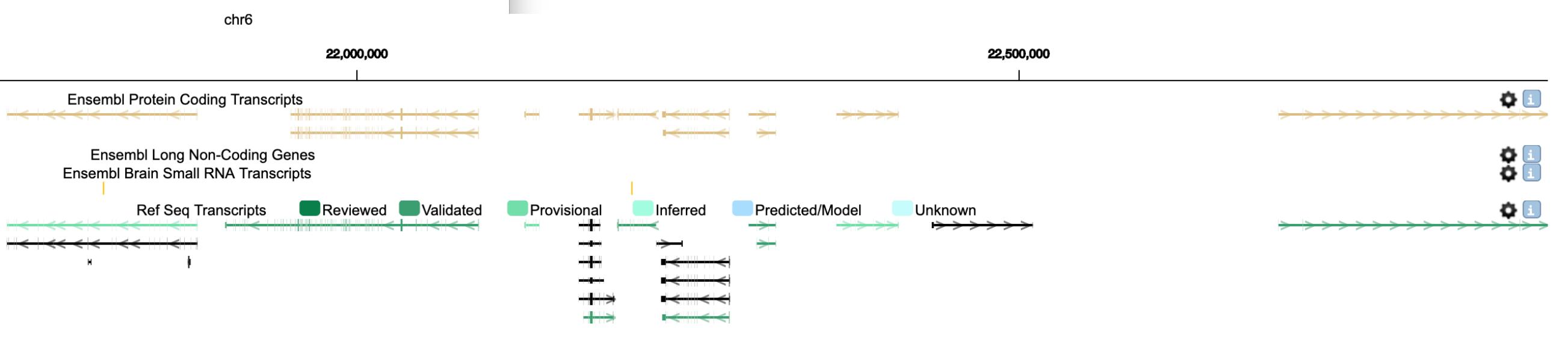
Order	Track Name	Organism	Edit
1	Reference Genomic Sequence		
2	Ensembl Protein Coding Genes		
3	Total RNA Transcriptome merged from Brain, Heart, Liver	Rat only	
4	Brain Total-RNA Transcriptome		
5	Liver Total-RNA Transcriptome (BN-Lx/SHR)	Rat only	
6	Heart Total-RNA Transcriptome	Rat only	
7	Ensembl Long Non-Coding Genes		
8	Ensembl Small RNA Genes		
9	Brain Transcriptome Small RNA	Rat only	
10	Liver Transcriptome Small RNA	Rat only	
11	Heart Transcriptome Small RNA	Rat only	
12	Ref Seq Genes		
13	BN-Lx SNPs small Insertion / Deletions	Rat only	

- **Ensembl tracks** - Ensembl gene are split up into protein-coding, long non-coding, and small RNA
- **Reconstructed Transcriptome tracks**
 - these tracks include transcripts that were reconstructed from short read RNA sequencing in brain, liver, and heart and include total RNA or small RNA
- **SNPs and Indel tracks** - these tracks include SNPs and Indels from the SHR and BN-Lx (progenitors of the HXB/BXH recombinant inbred panel)

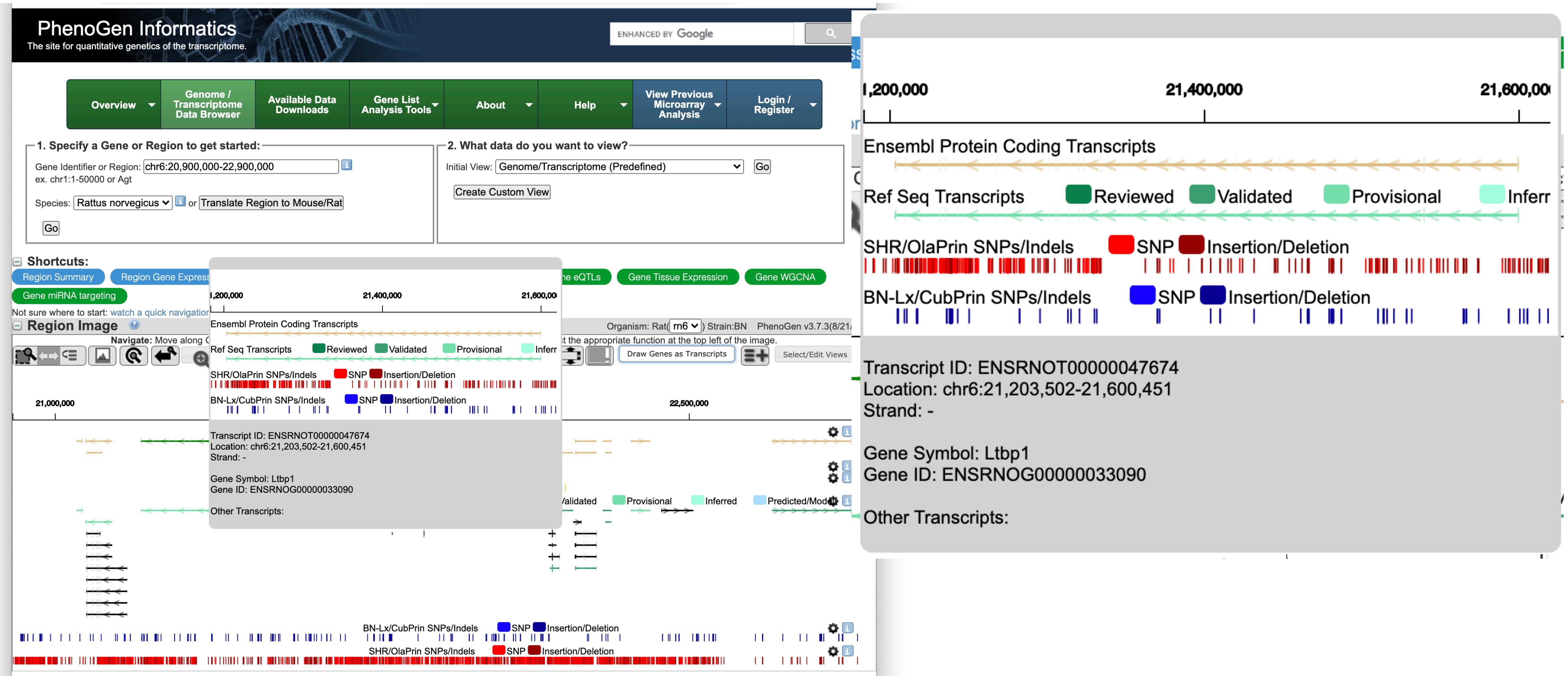
Gene view vs. transcript view



Click on 'Draw Genes as Transcripts' to toggle between the two different views



Scroll-over for gene details



Genes physically located in QTL

Region Summary

Region Summary ?

Track Details ? Genes with an eQTL in this region ? WGCNA ? Expression ?

Track List:

Ensembl Long Non-Coding Genes: 0
Ensembl Brain Small RNA Transcripts: 3
BN-Lx/CubPrin SNPs/Indels: 369
Ref Seq Transcripts: 34
Ensembl Protein Coding Transcripts: 17
SHR/OlaPrin SNPs/Indels: 3030

Break down of track count*

*Note: Depending on the track settings some features may not be displayed and will not be reflected in the image above.

Region Summary ?

Track List:

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Break down of track count*

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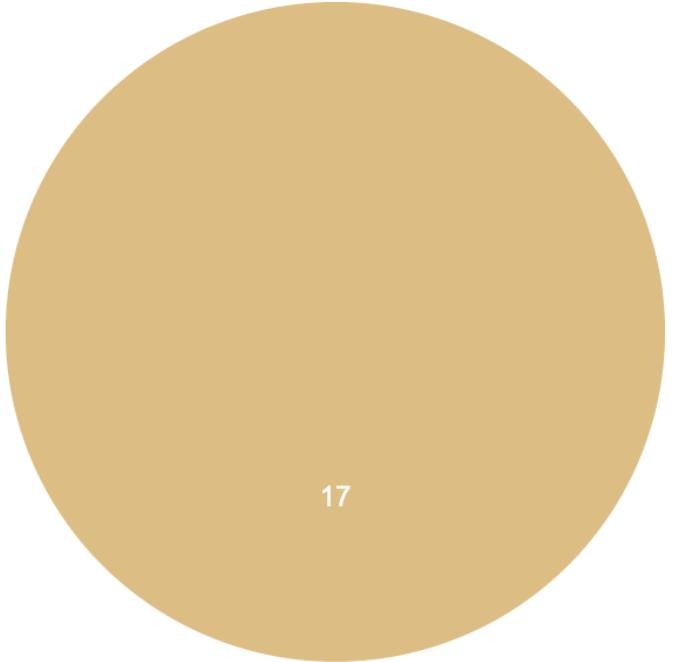
Ensembl Protein Coding Transcripts

Region Summary

Track List:

- Ensembl Long Non-Coding Genes: 0
- Ensembl Brain Small RNA Transcripts: 3
- BN-Lx/CubPrin SNPs/Indels: 369
- Ref Seq Transcripts: 34
- Ensembl Protein Coding Transcripts: 17
- SHR/OlaPrin SNPs/Indels: 3030

Break down of track count*



*Note: Depending on the track settings some features may not be displayed and will not be reflected in the image above.

Features in Selected Track

Filter List | **View Columns**

Export As: [Copy](#) [CSV](#) [Excel](#) [PDF](#)

Search:

Image ID (Transcript/Feature ID)	RNA-Seq Transcript Matches	Gene Symbol	Gene ID	Gene Description	Location	Strand	Exon SNPs / Indels	Transcript Information		Ensembl Transcriptome HRDP v5 Ribosome Depleted TotalRNA										
								# Transcripts	Ensembl	RNA-Seq	Whole Brain			Liver			eqTL	TPM	eqTL	TPM
											Median	Range	Heritability	cis	trans	Median				
ENSRNOT00000011630	PRN6.5T0068569 - 89.3% of Exons Match, 25 Perfect Exon Matches,	Alk	ENSRNOG0000008683	ALK receptor tyrosine kinase	chr6: 22,696,397-23,203,775	+		1	18	0.455	0.1-1.04	0.62	0.0	0.0-0.06	0.99	0.15-2.36				
ENSRNOT00000008687	PRN6.5T0201564 - 100.0% of Exons Match, 7 Perfect Exon Matches, 1 Fuzzy Exon Matches, 2 Extra Exons,	Memo1	ENSRNOG0000006340	mediator of cell motility 1	chr6: 22,362,484-22,409,579	+	BN-Lx: 0 / 1 SHR: 23 / 20	1	12	5.045	0.79-13.6	0.47	3.835	0.21-15.69	0.55	17.2	1.48-51.63			
ENSRNOT00000087805	PRN6.5T0201566 - 60.0% of Exons Match, 3 Perfect Exon Matches,	Dpy30	ENSRNOG0000027126	dpy 30 histone methyltransferase complex regulatory subunit	chr6: 22,296,128-22,316,894	+	BN-Lx: 0 / 2 SHR: 42 / 44	2	65	6.46	0.93-21.97	0.31	5.81	0.41-23.69	0.37					
ENSRNOT00000039375	PRN6.5T0068524 - Transcript Match: ENSRNOT00000039375 16 Perfect Exon Matches,	Spast	ENSRNOG0000027136	spastin	chr6: 22,230,928-22,281,886	-	SHR: 37 / 12	2	18	3.34	0.49-12.73	0.44	1.385	0.1-5.19	0.61	4.74	0.42-20.28			
ENSRNOT0000007919	PRN6.5T0068518 - Transcript Match: ENSRNOT0000007919 14 Perfect Exon Matches,	Slc30a6	ENSRNOG0000005856	solute carrier family 30 member 6	chr6: 22,197,040-22,226,421	-	SHR: 4 / 0	1	8	1.565	0.23-4.15	0.36	2.155	0.14-5.75	0.42	2.38	0.19-6.46			
ENSRNOT0000007655	PRN6.5T0068515 - Transcript Match: ENSRNOT0000007655 9 Perfect Exon Matches,	Nlrc4	ENSRNOG0000005810	NLR family, CARD domain containing 4	chr6: 22,167,919-22,194,250	+	BN-Lx: 0 / 2 SHR: 5 / 5	1	11	0.09	0.02-0.27	0.69	9.79E-5	chr6:21718219	0.39	0.01-1.24	0.69	0.14	0.02-0.45	
ENSRNOT0000007607	PRN6.5T0201553 - 83.3% of Exons Match, 5 Perfect	Yipf4	ENSRNOG0000005610	Yip1 domain family, member 4	chr6: 22,126,870-22,138,286	-	BN-Lx: 0 / 2 SHR: 1 / 1	1	16	5.97	0.82-21.76	0.38	7.0	0.41-42.84	0.46	7.2E-3	chr6:21240950	9.1	0.54-48.05	

Ensembl Protein Coding Transcripts

Transcript Information									
# Transcripts i									
Image ID (Transcript/Feature ID) i	RNA-Seq Transcript Matches i d	Gene Symbol i d	Gene ID d	Gene Description i d	Location d	Strand d	Exon SNPs / Indels i d	Ensembl d	RNA- Seq d
+ ENSRNOT00000011630 PRN6.5T0068569 PRN6.5T0068570 PRN6.5T0068575 PRN6.5T0068571	+ PRN6.5T0068569 - 89.3% of Trx:ENSRNOT00000011630 Exons Match, 25 Perfect Exon Matches, + PRN6.5T0201564 - 100.0% of Trx:ENSRNOT0000008687 Exons Match, 7 Perfect Exon Matches, 1 Fuzzy Exon Matches, 2 Extra Exons,	Alk	ENSRNOG0000008683 All Organisms: NCBI UniProt Rat: NCBI UniProt RGD	ALK receptor tyrosine kinase	chr6: 22,696,397- 23,203,775	+		1	18
+ ENSRNOT0000008687 PRN6.5T0201564 PRN6.5T0201568 PRN6.5T0201569 PRN6.5T0201570	Trx:ENSRNOT0000008687 Exons Match, 7 Perfect Exon Matches, 1 Fuzzy Exon Matches, 2 Extra Exons,	Memo1	ENSRNOG0000006340 All Organisms: NCBI UniProt Rat: NCBI UniProt RGD	mediator of cell motility 1	chr6: 22,362,484- 22,409,579	+	BN-Lx: 0 / 1 SHR: 23 / 20	1	12
+ ENSRNOT00000087805 ENSRNOT00000039132 PRN6.5T0201566 PRN6.5T0068532 PRN6.4T0069976	+ PRN6.5T0201566 - 60.0% of Trx:ENSRNOT00000087805 Exons Match, 3 Perfect Exon Matches,	Dpy30	ENSRNOG0000027126 All Organisms: NCBI UniProt Rat: NCBI UniProt RGD	dpy 30 histone methyltransferase complex regulatory subunit	chr6: 22,296,128- 22,316,894	+	BN-Lx: 0 / 2 SHR: 42 / 44	2	65
+ ENSRNOT00000039375 ENSRNOT00000079137 PRN6.5T0068524 PRN6.5T0201562 PRN6.5T0068525	+ PRN6.5T0068524 - Transcript Match: ENSRNOT00000039375 16 Perfect Exon Matches,	Spast	ENSRNOG0000027136 All Organisms: NCBI UniProt Rat: NCBI UniProt RGD	spastin	chr6: 22,230,928- 22,281,886	-	SHR: 37 / 12	2	18
+ ENSRNOT0000007919 PRN6.5T0068518 PRN6.4T0069955 PRN6.4T0294337 PRN6.5T0068517	+ PRN6.5T0068518 - Transcript Match: ENSRNOT0000007919 14 Perfect Exon Matches,	Slc30a6	ENSRNOG0000005856 All Organisms: NCBI UniProt Rat: NCBI UniProt RGD	solute carrier family 30 member 6	chr6: 22,197,040- 22,226,421	-	SHR: 4 / 0	1	8
+ ENSRNOT0000007655 PRN6.5T0068515 PRN6.5T0201558 PRN6.5T0201557 PRN6.5T0201559	+ PRN6.5T0068515 - Transcript Match: ENSRNOT0000007655 9 Perfect Exon Matches,	Nrcc4	ENSRNOG0000005810 All Organisms: NCBI UniProt Rat: NCBI UniProt RGD	NLR family, CARD domain containing 4	chr6: 22,167,919- 22,194,250	+	BN-Lx: 0 / 2 SHR: 5 / 5	1	11
+ ENSRNOT0000007607 PRN6.5T0201553 PRN6.5T0068512 PRN6.4T0294332	+ PRN6.5T0201553 - 83.3% of Trx:ENSRNOT0000007607 Exons Match, 5 Perfect	Yipf4	ENSRNOG0000005610 All Organisms: NCBI UniProt Rat: NCBI UniProt RGD	Yip1 domain family, member 4	chr6: 22,126,870- 22,138,286	-	BN-Lx: 0 / 2 SHR:	1	16

- **Image ID** - Ensembl transcript IDs and reconstruction transcript IDs associated with a gene
- **RNA-Seq Transcript Matches** - describes how a reconstructed transcript compares to the Ensembl transcript
- **Gene Symbol** - links out to Gene View in PhenoGen
- **Gene ID** - links to external databases
- **Exon SNPs/Indels** - reports number of SNPs and Indels for BN-Lx and SHR compared to reference genome
- **# Transcripts** - number of splice variants annotated in the Ensembl database and in the combined (brain, heart, and liver) reconstruction

Export gene table

Region Summary

Track List:

- Ensembl Long Non-Coding Genes: 0
- Ensembl Brain Small RNA Transcripts: 3
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- Ref Seq Transcripts: 34
- Ensembl Protein Coding Transcripts: 17
- SHR/OlaPrin SNPs/Indels: 3030

Break down of track count*

17

*Note: Depending on the track settings some features may not be displayed and will not be reflected in the image above.

Features in Selected Track

Filter List

Export As: Copy CSV Excel

The Gene Table can be downloaded or copied

PRN6.5T0068569 - PRN6.5T0068569 - 89.3% of Trx:ENSRNOT00000011630 Exons Match, 25 Perfect Exon Matches, + PRN6.5T0201564 - 100.0% of Trx:ENSRNOT0000008687 Exons Match, 7 Perfect Exon Matches, 1 Fuzzy Exon Matches, 2 Extra Exons, + PRN6.5T0201566 - 60.0% of Trx:ENSRNOT00000087805 Exons Match, 3 Perfect Exon Matches, + ENSRNOT00000039132 PRN6.5T0201566 PRN6.5T0068532 PRN6.4T0069976 + ENSRNOT00000039375 Transcript Match: ENSRNOT00000039375 16 Perfect Exon Matches, + PRN6.5T0068524 - Transcript Match: ENSRNOT00000079137 PRN6.5T0068524 PRN6.5T0201562 PRN6.5T0068525 + ENSRNOT0000007919 PRN6.5T0068518 PRN6.4T0069955 PRN6.4T0294337 PRN6.5T0068517 + ENSRNOT0000007655 PRN6.5T0068515 PRN6.5T0201558 PRN6.5T0201557 PRN6.5T0201559 + ENSRNOT0000007607 PRN6.5T0201553 PRN6.5T0201549 PRN6.4T0294332

ALK receptor tyrosine kinase

mediator of cell motility 1

dpy 30 histone methyltransferase complex regulatory subunit

spastin

solute carrier family 30 member 6

NLR family, CARD domain containing 4

Yip1 domain family, member 4

chr6: 22,696,397-23,203,775

chr6: 22,362,484-22,409,579

chr6: 22,296,128-22,316,894

chr6: 22,230,928-22,281,886

chr6: 22,197,040-22,226,421

chr6: 22,167,919-22,194,250

chr6: 22,126,870-22,138,286

1 18 0.455 0.1-1.04 0.62

1 12 5.045 0.79-13.6 0.47

2 65 6.46 0.93-21.97 0.31

2 18 3.34 0.49-12.73 0.44

1 8 1.565 0.23-4.15 0.36

1 11 0.09 0.02-0.27 0.69 9.79E-5 chr6:21718219

1 16 5.97 0.82-21.76 0.38

0.0 0.0-0.06

3.835 0.21-15.69 0.55

5.81 0.41-23.69 0.37

1.385 0.1-5.19 0.61

2.155 0.14-5.75 0.42

0.39 0.01-1.24 0.69

7.0 0.41-42.84 0.46

Export As: Copy CSV Excel

Source Code (GitHub) | Legal Notices | Privacy Policy | Like | Follow

Genes Physically Located in Nicotine Seeking QTL (13 genes; 17 transcripts)

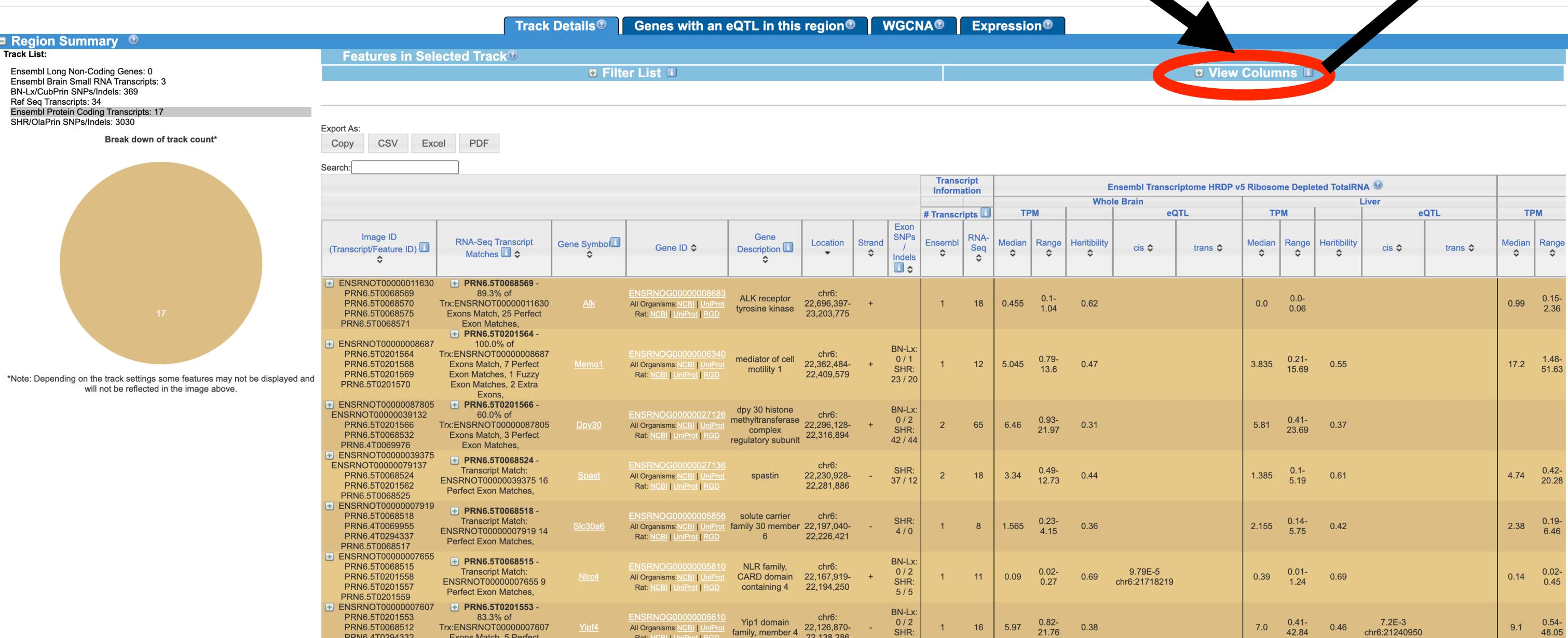
Gene Symbol	Gene Description
Alk	ALK receptor tyrosine kinase
Memo1	mediator of cell motility 1
Dpy30	dpy 30 histone methyltransferase complex regulatory
Spast	spastin
Slc30a6	solute carrier family 30 member 6
Nlrc4	NLR family, CARD domain containing 4
Yipf4	Yip1 domain family, member 4
Birc6	baculoviral IAP repeat containing 6
Ttc27	tetratricopeptide repeat domain 27
AABR07063197.1	
Ltbp1	latent transforming growth factor beta binding protein 1
Rasgrp3	RAS guanyl releasing protein 3
Fam98a	family with sequence similarity 98, member A

Genes physically located in QTL
and expressed in brain

Limit Results to Only Ensembl Transcriptome Quantitation

Click on ‘View Columns’ to limit to only Ensembl Results

Remove the
check mark from
‘Reconstruction
Transcriptome
Data’



Ensembl Transcriptome HRDP v5 Ribosome Depleted Total RNA

Ribosomal RNA-depleted Total RNA (>200 nt) from rat brain and liver

- Paired end reads; Illumina HiSeq/NovaSeq; approximately 60 million reads per sample
- 45 inbred strains; 3 males per strain
 - 30 HXB/BXH recombinant inbred strains
 - 15 classic inbred strains

Processed RNA-Seq data available for download from PhenoGen

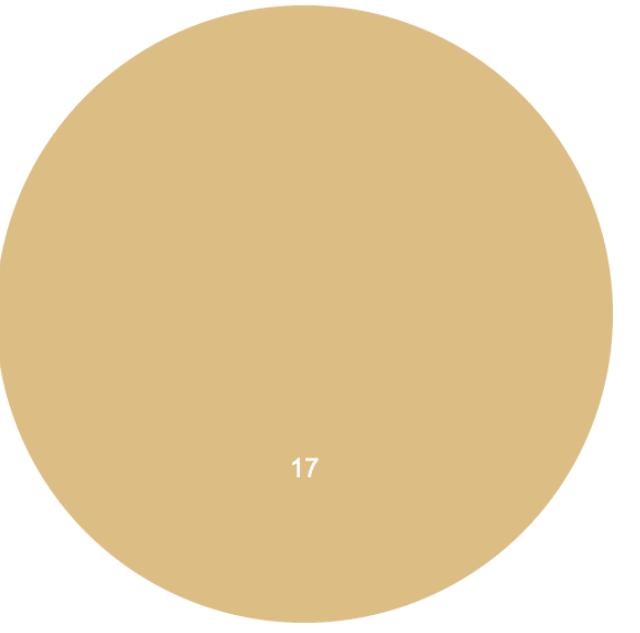
Track Details

Region Summary

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Break down of track count*



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Features in Selected Track

Filter List [View Columns](#)

Export As: [Copy](#) [CSV](#) [Excel](#) [PDF](#)

Search:

Image ID (Transcript/Feature ID)	RNA-Seq Transcript Matches	Gene Symbol	Gene ID	Gene Description	Location	Strand	Exon SNPs / Indels	Transcript Information		Ensembl Transcriptome HRDP v5 Ribosome Depleted TotalRNA											
								# Transcripts	TPM	Whole Brain			eQTL			TPM			Liver		
								Ensembl	RNA-Seq	Median	Range	Heritability	cis	trans	Median	Range	Heritability	cis	trans		
ENSNNOT00000011630	PRN6.5T0068569 - 89.3% of PRN6.5T0068569, PRN6.5T0068570, PRN6.5T0068575, PRN6.5T0068571	Alk	ENSRNOG0000008683	All Organisms:NCBI UniProt Rat: NCBI UniProt RGD	ALK receptor tyrosine kinase	chr6: 22,696,397-23,203,775	+	1	18	0.455	0.1-1.04	0.62	0.0	0.0-0.06							
ENSNNOT0000008687	PRN6.5T0201564, PRN6.5T0201568, PRN6.5T0201569, PRN6.5T0201570	Memo1	ENSRNOG0000006340	All Organisms:NCBI UniProt Rat: NCBI UniProt RGD	mediator of cell motility 1	chr6: 22,362,484-22,409,579	+	BN-Lx: 0 / 1 SHR: 23 / 20	1	12	5.045	0.79-13.6	0.47	3.835	0.21-15.69						
ENSNNOT00000087805	PRN6.5T0201566, PRN6.5T0068532, PRN6.4T0069976	Dpy30	ENSRNOG00000027126	All Organisms:NCBI UniProt Rat: NCBI UniProt RGD	dpy 30 histone methyltransferase complex regulatory subunit	chr6: 22,296,128-22,316,894	+	BN-Lx: 0 / 2 SHR: 42 / 44	2	65	6.46	0.93-21.97	0.31	5.81	0.41-23.69						
ENSNNOT00000039375	PRN6.5T0068524, PRN6.5T0201562, PRN6.5T0068525	Spast	ENSRNOG00000027136	All Organisms:NCBI UniProt Rat: NCBI UniProt RGD	spastin	chr6: 22,230,928-22,281,886	-	SHR: 37 / 12	2	18	3.34	0.49-12.73	0.44	1.385	0.1-5.19						
ENSNNOT0000007919	PRN6.5T0068518, PRN6.4T0069955, PRN6.4T0294337, PRN6.5T0068517	Slc30a6	ENSRNOG0000005856	All Organisms:NCBI UniProt Rat: NCBI UniProt RGD	solute carrier family 30 member 6	chr6: 22,197,040-22,226,421	-	SHR: 4 / 0	1	8	1.565	0.23-4.15	0.36	2.155	0.14-5.75						
ENSNNOT0000007655	PRN6.5T0068515, PRN6.5T0201558, PRN6.5T0201557, PRN6.5T0201559	Nlrc4	ENSRNOG0000005810	All Organisms:NCBI UniProt Rat: NCBI UniProt RGD	NLR family, CARD domain containing 4	chr6: 22,167,919-22,194,250	+	BN-Lx: 0 / 2 SHR: 5 / 5	1	11	0.09	0.02-0.27	0.69	9.79E-5	chr6:21718219						
ENSNNOT0000007607	PRN6.5T0201553, PRN6.5T0068512, PRN6.4T0294332, PRN6.4T0294333	Yipf4	ENSRNOG0000005610	All Organisms:NCBI UniProt Rat: NCBI UniProt RGD	Yip1 domain family, member 4	chr6: 22,126,870-22,138,286	-	BN-Lx: 0 / 2 SHR: 58 / 30	1	16	5.97	0.82-21.76	0.38	7.0	0.41-42.84						

TPM		
Median	Range	Heritability
0.455	0.1-1.04	0.62
5.045	0.79-13.6	0.47
6.46	0.93-21.97	0.31
3.34	0.49-12.73	0.44

Track Details - Transcriptome Information

- **TPM** - Transcripts per million transcripts
 - Accounts for difference in library sizes between samples and for differences in transcript lengths between transcripts
 - **Median** - is the median across all biological replicates and across all 45 strains
 - **Range** - the minimum and maximum across all biological replicates and across all 45 strains
- **Heritability** - proportion of total variance attributed to strain
 - A broad sense heritability was calculated using a one-way ANOVA

Filtering Track Details Table Based on Median TPM

Click on 'Filter List' to reduce table to only genes that are expressed in either liver or brain

Region Summary

Track List:
Ensembl Long Non-Coding Genes: 0
Ensembl Brain Small RNA Transcripts: 3
BN-LxCubPrin SNPs/Indels: 369
RefSeq Transcripts: 34
Ensembl Protein Coding Transcripts: 17
SHR/OlaPrin SNPs/Indels: 3030

Break down of track count*

Features in Selected Track

Filter List

Median TPM >=:

Heritability >=:

Has cis-eQTL:

Has trans-eQTL:

Export As: Copy CSV Excel PDF

Search:

Image ID (Transcript/Feature ID)	RNA-Seq Transcript Matches	Gene Symbol	Gene ID	Gene Description	Location	Strand	Exon SNPs/Indels	Transcript Information		Ensembl Transcriptome HRDP v5 Ribosome Depleted TotalRNA												
								# Transcripts	Ensembl	RNA-Seq	Whole Brain			eQTL			Liver			eQTL		
											TPM	Median	Range	Heritability	cis	trans	TPM	Median	Range	Heritability	cis	trans
ENSRNOT00000008687	PRN6.5T0201564 - PRN6.5T0201568 PRN6.5T0201569 PRN6.5T0201570	Memo1	ENSRNOG00000006340	mediator of cell motility 1	chr6: 22,362,484- 22,409,579	+	BN-Lx: All Organisms: NCB UniProt Rat: NCB UniProt RGD	1	12	5.045	0.79- 13.6	0.47	3.835	0.21- 15.69	0.55							
ENSRNOT000000087805	PRN6.5T0201566 - ENSRNOT00000039132 PRN6.5T0201566 PRN6.5T0068532 PRN6.4T0069976	Dpy30	ENSRNOG00000027126	dpy 30 histone methyltransferase complex regulatory subunit	chr6: 22,296,128- 22,316,894	+	BN-Lx: All Organisms: NCB UniProt Rat: NCB UniProt RGD	2	65	6.46	0.93- 21.97	0.31	5.81	0.41- 23.69	0.37							
ENSRNOT00000039375	PRN6.5T0068524 - ENSRNOT00000079137 PRN6.5T0068524 PRN6.5T0201562 PRN6.5T0068525	Spast	ENSRNOG00000027136	spastin	chr6: 22,230,928- 22,281,886	-	SHR: All Organisms: NCB UniProt Rat: NCB UniProt RGD	2	18	3.34	0.49- 12.73	0.44	1.385	0.1- 5.19	0.61							
ENSRNOT00000007919	PRN6.5T0068518 - ENSRNOT0000007919 14 Perfect Exon Matches,	Slc30a6	ENSRNOG00000005856	solute carrier family 30 member 6	chr6: 22,197,040- 22,226,421	-	SHR: All Organisms: NCB UniProt Rat: NCB UniProt RGD	1	8	1.565	0.23- 4.15	0.36	2.155	0.14- 5.75	0.42							
ENSRNOT00000007607	PRN6.5T0201553 - PRN6.5T0068512 PRN6.4T0294332 PRN6.4T0294333	Yipf4	ENSRNOG00000005610	Yip1 domain family, member 4	chr6: 22,126,870- 22,138,286	-	BN-Lx: All Organisms: NCB UniProt Rat: NCB UniProt RGD	1	16	5.97	0.82- 21.76	0.38	7.0	0.41- 42.84	0.46 7.2E-3 chr6:21240950							
ENSRNOT000000083128	PRN6.5T0201540 - ENSRNOT00000006830 PRN6.5T0201540 PRN6.5T0201541 PRN6.5T0201542	Birc6	ENSRNOG00000027191	baculoviral IAP repeat containing 6	chr6: 21,950,100- 22,092,346	-	BN-Lx: All Organisms: NCB UniProt Rat: NCB UniProt RGD	2	57	6.32	1.06- 23.07	0.55	7.445	0.33- 23.46	0.73 6.06E-9 chr15:104444382							
ENSRNOT00000006505	PRN6.5T0068485 - ENSRNOT00000006505 PRN6.4T0294308 PRN6.5T0068480 PRN6.5T0068481	Ttc27	ENSRNOG00000042932	tetratricopeptide repeat domain 27	chr6: 21,735,834- 21,880,003	-	SHR: All Organisms: NCB UniProt Rat: NCB UniProt RGD	1	15	2.72	0.35- 5.96	0.41	8.21E-7 chr5:116356396	1.85	0.07- 4.27	0.54						

*Note: Depending on the track settings some features may not be displayed and will not be reflected in the image above.

17

Filter List

Median TPM >= : 1

Heritability >=:

Has cis-eQTL:

Has trans-eQTL:

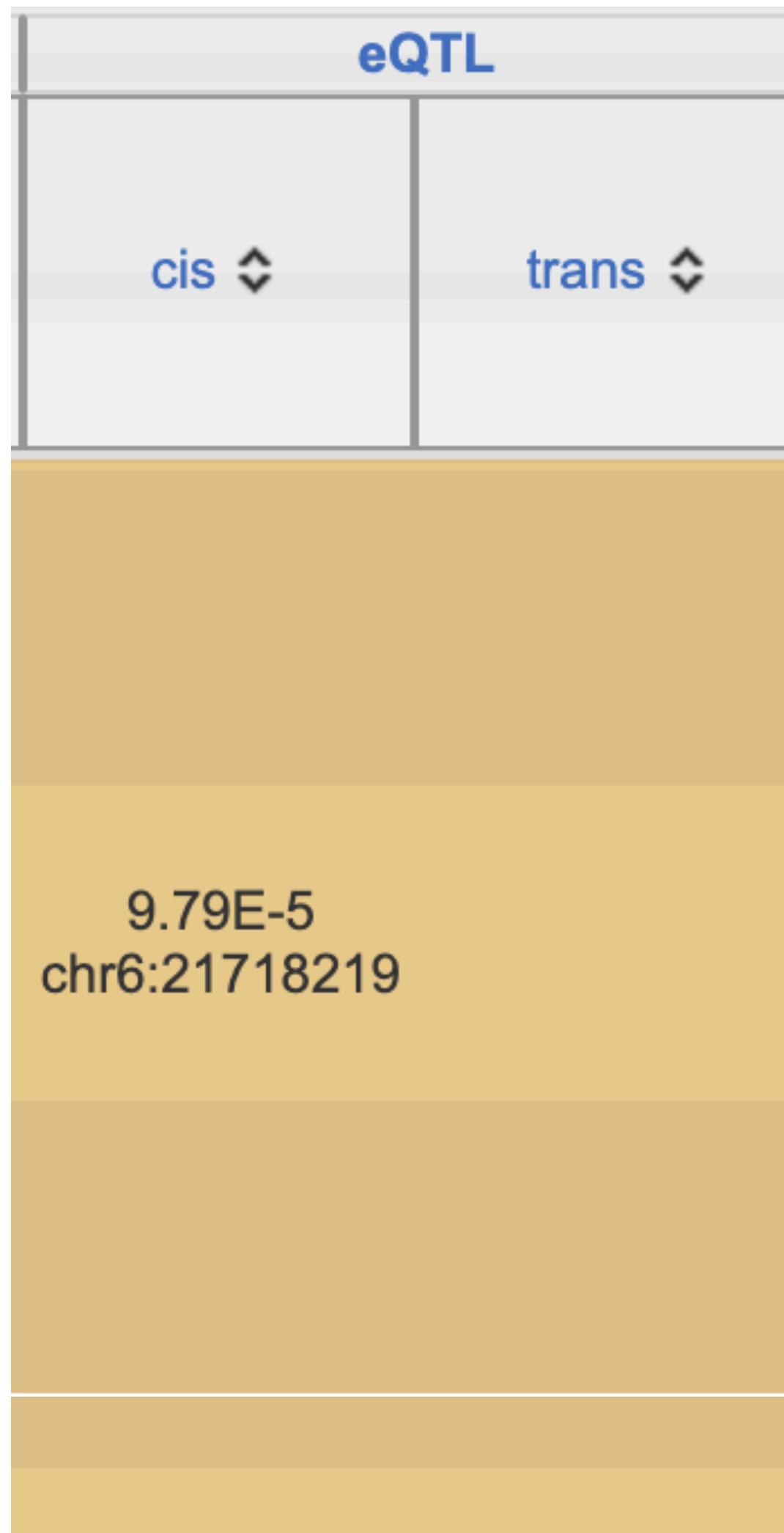
Enter a TPM threshold to filter the table by

Genes physically located in the QTL and expressed in brain/liver (10 genes)

Gene Symbol	Brain Expression TPM - Median	Brain Expression TPM - Range	Liver Expression TPM - Median	Liver Expression TPM - Range
Memo1	5.0	0.79-13.6	3.8	0.21-15.69
Dpy30	6.5	0.93-21.97	5.8	0.41-23.69
Spast	3.3	0.49-12.73	1.4	0.1-5.19
Slc30a6	1.6	0.23-4.15	2.2	0.14-5.75
Yipf4	6.0	0.82-21.76	7.0	0.41-42.84
Birc6	6.3	1.06-23.07	7.5	0.33-23.46
Ttc27	2.7	0.35-5.96	1.9	0.07-4.27
Ltbp1	0.3	0.05-0.68	1.0	0.04-2.25
Rasgrp3	2.4	0.56-8.8	1.8	0.1-6.18
Fam98a	2.6	0.44-8.77	2.0	0.06-6.95

**Genes with a *cis*-eQTL in brain
within phenotypic QTL**

cis-eQTL in brain and liver of HRDP



- 41 HRDP strains
 - 2 strains excluded due to lack of genotype data
 - 2 strains eliminated because another closely related strain was included among the 15 classic inbred strains
- GEMMA with LOCO used for mapping
 - GEMMA - accounts for population structure using a mixed linear regression
 - LOCO (Leave-One-Chromosome-Out) - calculates the kinship matrix for GEMMA using all chromosomes except the chromosome being tested.
- Cis eQTL p-values are adjusted for multiple testing using a Bonferroni correction when multiple SNPs are within 1 Mb of the transcript start or stop site
- Cis eQTL are reported if its adjusted p-value is less than 0.01.

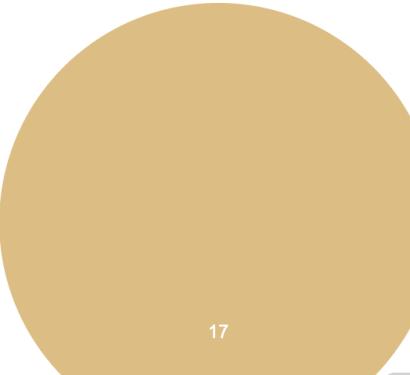
Filter based on cis-eQTL Status

Click on ‘Filter List’ to reduce table to only genes with a cis-eQTL in either liver or brain

Region Summary

Track List:
Ensembl Long Non-Coding Genes: 0
Ensembl Brain Small RNA Transcripts: 3
BN-Lx/CubPrin SNPs/Indels: 369
Ref Seq Transcripts: 34
Ensembl Protein Coding Transcripts: 17
SHR/OlaPrin SNPs/Indels: 3030

Break down of track count*



Name: null
Count: 17

*Note: Depending on the track settings some features may not be displayed and will not be reflected in the image above.

Track Dev Genes with an eQTL in this region WGCNA Expression

Features in Selected Track

Filter List

Median TPM >= :

Heritability >= :

Has cis-eQTL:

Has trans-eQTL:

View Columns

RNA-Seq Transcript Matches Ensembl Transcriptome Data
Gene ID Description Location and Strand
Reconstruction Transcriptome Data All Array Data

Transcript Information

# Transcripts	Ensembl Transcriptome HRDP v5 Ribosome Depleted TotalRNA										
	Whole Brain			Liver							
Ensembl	RNA-Seq	TPM	Median	Range	Heritability	TPM	Median	Range	Heritability	cis	trans
1	11	0.09	0.02-0.27	0.69	9.79E-5	chr6:21718219	0.39	0.01-1.24	0.69		
1	16	5.97	0.82-21.76	0.38			7.0	0.41-42.84	0.46	7.2E-3	chr6:21240950
2	39	2.44	0.56-8.8	0.59	1.21E-4	chr6:21718219	1.835	0.1-6.18	0.63		

Export As: Copy CSV Excel PDF
Search:

Note: The screenshot shows a 'Filter List' button highlighted with a red circle, and arrows point from this button to both the 'Has cis-eQTL' checkbox in the top right and the 'Has trans-eQTL' checkbox in the bottom right of the 'Filter List' interface.

Filter List

Median TPM >= :

Heritability >= :

Has cis-eQTL:

Has trans-eQTL:

Click on ‘Has cis-eQTL’

Genes with a **cis** eQTL within the QTL for Nicotine Seeking (3 genes)

Gene Symbol	Brain Expression TPM - Median	Brain Expression TPM - Range	Brain Expression Heritability	Brain Expression cis-eQTL Adjusted P-value	Brain Expression cis-eQTL Location	Liver Expression TPM - Median	Liver Expression TPM - Range	Liver Expression Heritability	Liver Expression cis-eQTL Adjusted P-value	Liver Expression cis-eQTL Location
Nlrc4	0.1	0.02-0.27	0.69	0.00010	chr6: 21,718,219	0.4	0.01-1.24	0.69		
Yipf4	6.0	0.82-21.76	0.38			7.0	0.41-42.84	0.46	0.007	chr6: 21,240,950
Rasgrp3	2.4	0.56-8.8	0.59	0.00012	chr6: 21,718,219	1.8	0.1-6.18	0.63		

From Rob's Presentation

Relevant biology—links from GeneWiki

GeneWiki Entries

GeneWiki enables you to enrich the annotation of genes and transcripts. Please submit or edit a GeneWiki note (500 characters max) related to a gene, its transcripts, or proteins. When possible include PubMed identifiers or web resource links (URL addresses). Please ensure that the additions will have widespread use. For additional information, check the GeneWiki [help document](#).

GeneWiki for Rasgrp3: [New GeneWiki Entry](#)

GeneNetwork:
There is no GeneWiki entry for this gene.

GeneRIF from NCBI:

- Expressed in developing blood vessels, Rasgrp3 contributes to the incidence of cardiovascular defects found in embryos from diabetic mothers. ([Mus musculus](#)) [PubMed](#)
- RasGRP1, but not RasGRP3, is required for thymocyte positive selection and invariant natural killer T cell selection. ([Mus musculus](#)) [PubMed](#)
- RasGRP3 limits inflammatory response by activating Rap1 on low-intensity pathogen infection, setting a threshold for preventing excessive inflammatory response. ([Mus musculus](#)) [PubMed](#)
- RasGRP1/3-deficient progenitors show impaired migration toward the CCR9 ligand, CCL25, suggesting that RasGRP1 and RasGRP3 may regulate progenitor entry into the thymus through a CCR9-dependent mechanism. ([Mus musculus](#)) [PubMed](#)
- These results indicate that RasGRP3 is implicated in phorbol ester-induced, PKC-independent exocytosis. ([Rattus norvegicus](#)) [PubMed](#)
- Together these data demonstrate a novel mechanism in which the balance between stability and plasticity in dendritic spines depends on binding of drebrin to actin filaments in a manner that is regulated by Ras. ([Rattus norvegicus](#)) [PubMed](#)
- Observational study and genome-wide association study of gene-disease association. ([HuGE Navigator](#)) ([Homo sapiens](#)) [PubMed](#)

> [Eur J Neurosci](#). 2008 Jun;27(11):2847-59. doi: 10.1111/j.1460-9568.2008.06269.x.

Interactions Between Drebrin and Ras Regulate Dendritic Spine Plasticity

Virginie Biou ¹, Heike Brinkhaus, Robert C Malenka, Andrew Matus

Affiliations + expand

PMID: 18588530 DOI: [10.1111/j.1460-9568.2008.06269.x](#)

Abstract

Dendritic spines are major sites of morphological plasticity in the CNS, but the molecular mechanisms that regulate their dynamics remain poorly understood. Here we show that the association of drebrin with actin filaments plays a major role in regulating dendritic spine stability and plasticity. Overexpressing drebrin or the internal actin-binding site of drebrin in rat hippocampal neurons destabilized mature dendritic spines so that they lost synaptic contacts and came to resemble immature dendritic filopodia. Drebrin-induced spine destabilization was dependent on Ras activation: expression of constitutively active Ras destabilized spine morphology whereas drebrin-induced spine destabilization was rescued by co-expressing dominant negative Ras. Conversely, RNAi-mediated drebrin knockdown prevented Ras-induced destabilization and promoted spine maturation in developing neurons. Together these data demonstrate a novel mechanism in which the balance between stability and plasticity in dendritic spines depends on binding of drebrin to actin filaments in a manner that is regulated by Ras.

Similar articles

[Drebrin A regulates dendritic spine plasticity and synaptic function in mature cultured hippocampal neurons.](#)

Slide 23. Left. Rasgrp3 GeneWiki page. RIF link to a paper on CNS plasticity.

**Genes with any eQTL in brain
within phenotypic QTL**

Genes with an eQTL in this region

Track Details 

Genes with an eQTL in this region 

WGCNA 

Expression 

Genes with an eQTL overlapping this region(HRDP v5 RNA-Seq ensembl Data(Cis and Trans eQTLs)) 

Filter eQTLs

This region did not contain a QTL for any gene given the current parameters. You can change the filtering parameters by clicking the filter button or expand the region in the browser.

Genes with an eQTL in this region

Track Details ⓘ Genes with an eQTL in this region ⓘ WGCNA ⓘ Expression ⓘ

Genes with an eQTL overlapping this region(HRDP v5 RNA-Seq ensembl Data(Cis and Trans eQTLs)) ⓘ

Filter eQTLs

This region did not contain a QTL for any gene given the current parameters. You can change the filtering parameters by clicking the filter button or expand the region in the browser.

↓

Filter Settings

Data Source: RNA-Seq ⓘ Transcriptome Data: Ensembl ⓘ

eQTL P-Value Cut-off: 0.000001 ⓘ Genome Wide eQTLs: Genome Wide ⓘ

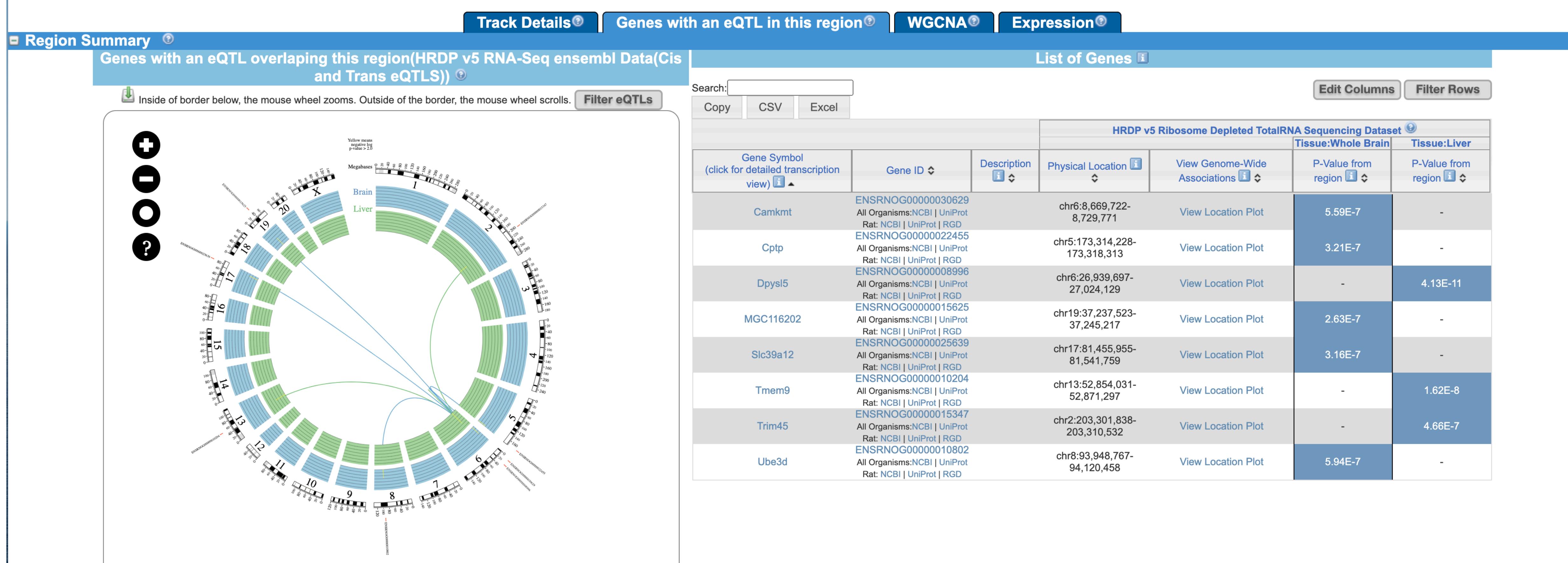
Tissues: Include at least one tissue. ⓘ

Chromosomes: (chr6 must be included) ⓘ

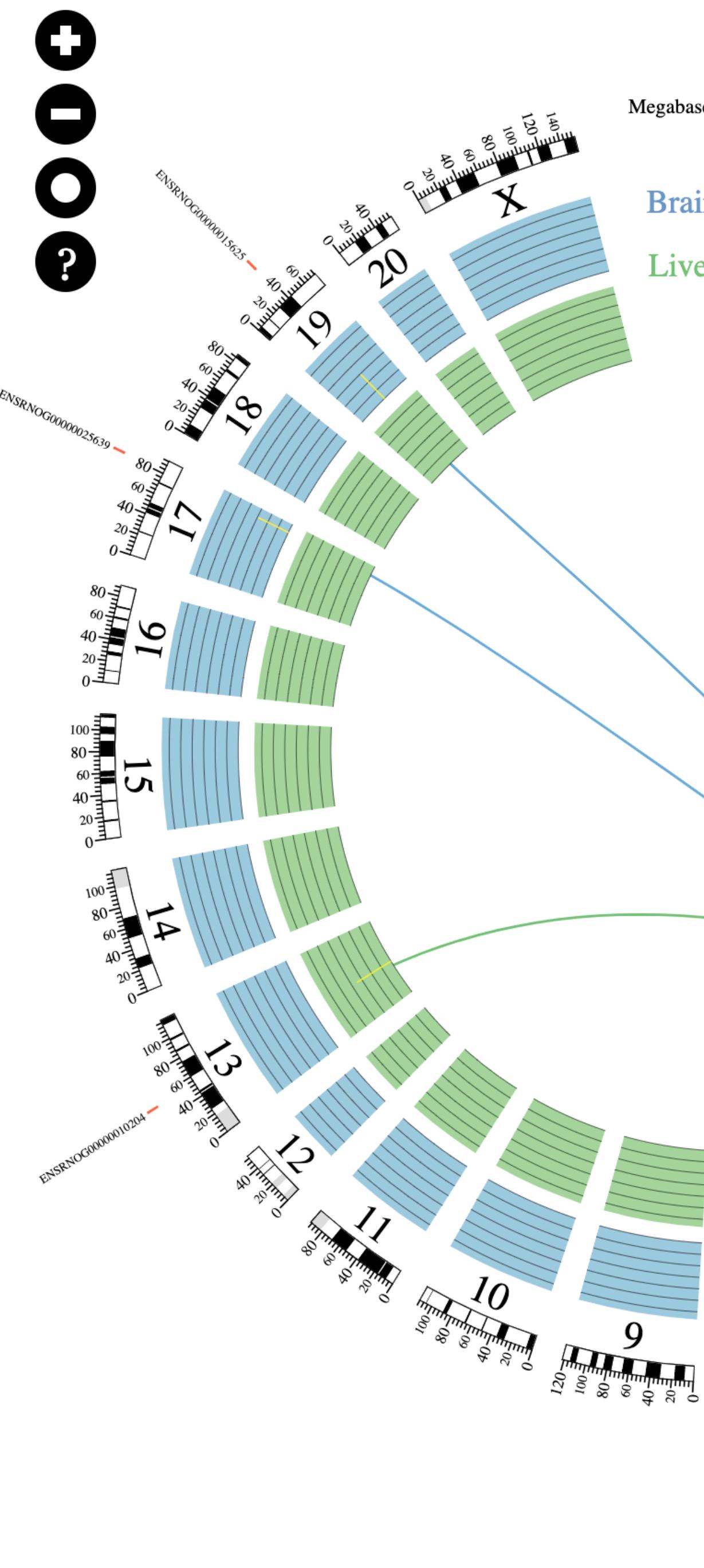
Excluded	Included	Excluded	Included
>	Brain Liver	>	Chr 1 Chr 2 Chr 3 Chr 4 Chr 5 Chr 6
»		»	
<		<	
«		«	

Run Filter

Extended QTL Region - For demo purposes

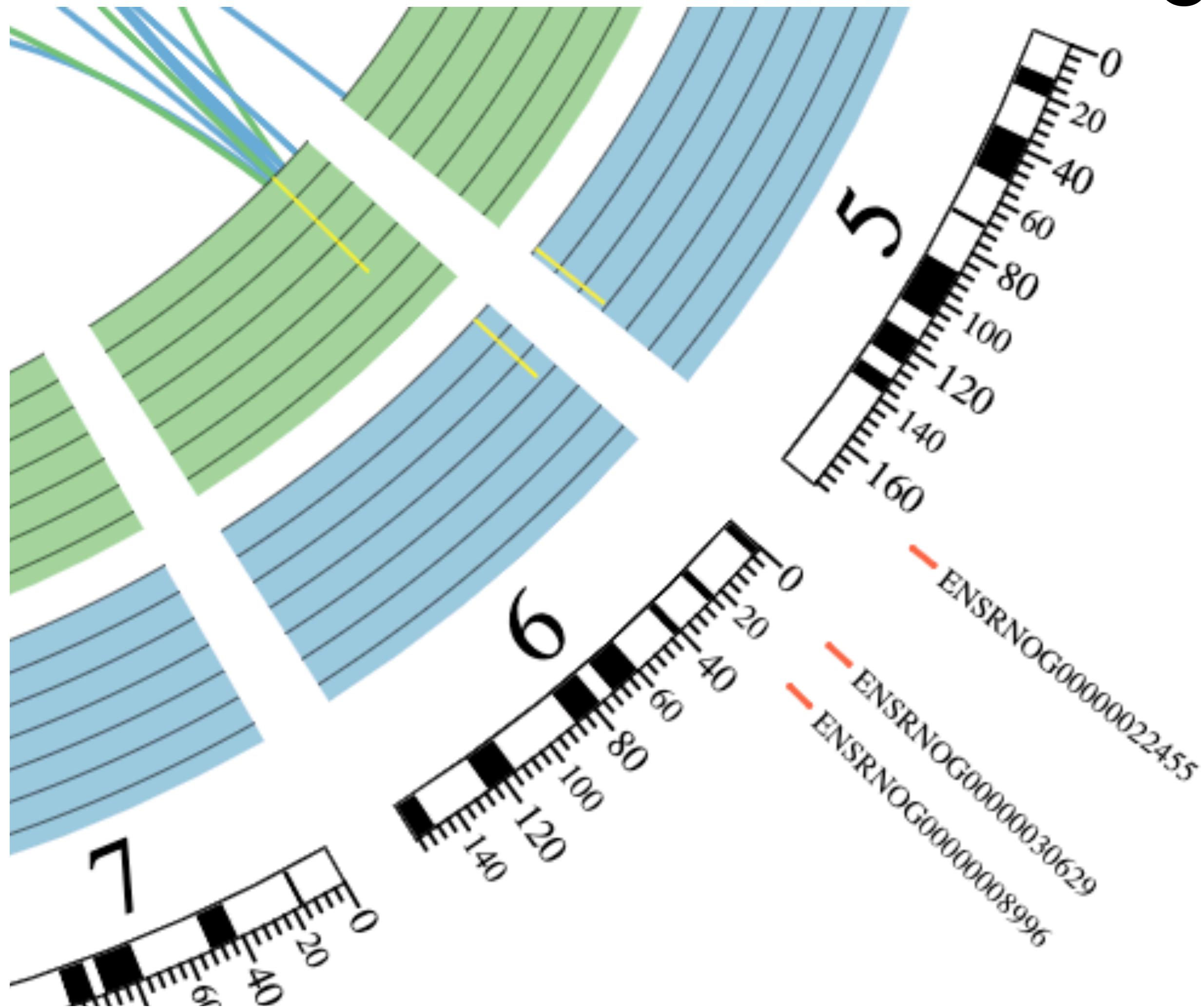


Circos Plot For Visualizing eQTL



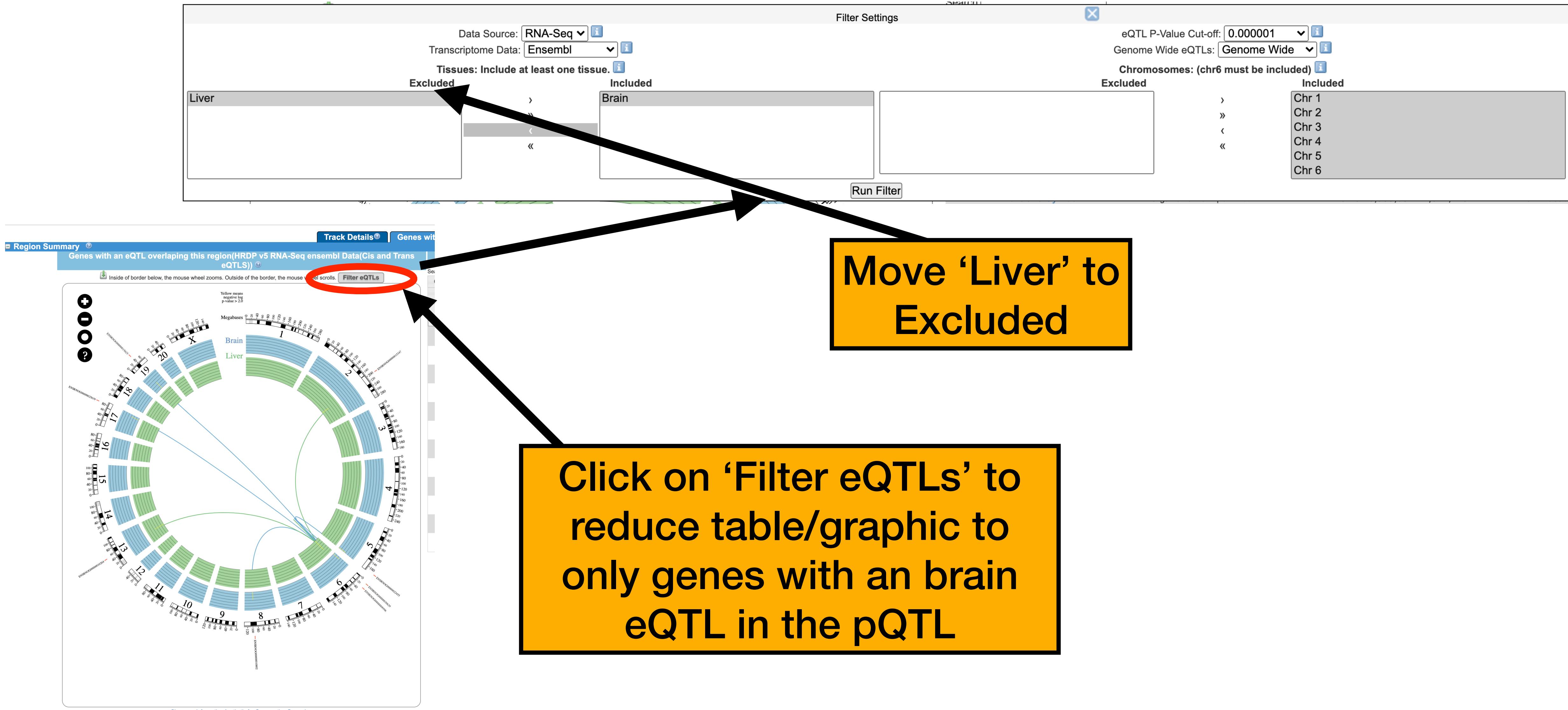
- **Different colored bands** - eQTL in different tissues
- **Yellow peaks within colored bands** - location marks the physical location of the gene; height is related to log base 10 p-value of the eQTL within the chosen region
- **Lines through center of circle** - connect physical location of genes with location of eQTL
- **Gene IDs along outside of circle** - physical location of Ensembl genes with an eQTL in the region

Circos Plot For Visualizing eQTL

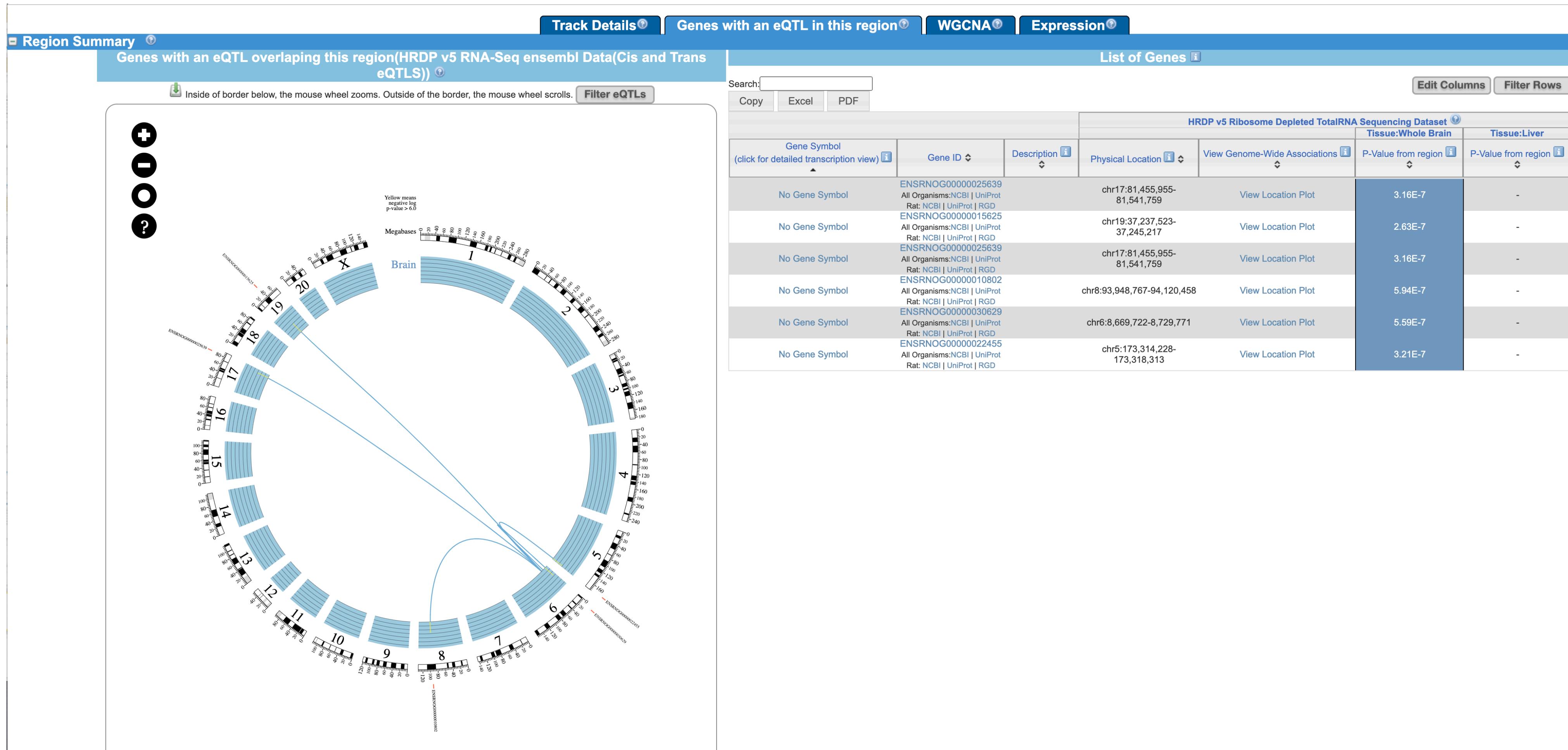


- **Different colored bands** - eQTL in different tissues
- **Yellow peaks within colored bands** - location marks the physical location of the gene; height is related to log base 10 p-value of the eQTL within the chosen region
- **Lines through center of circle** - connect physical location of genes with location of eQTL
- **Gene IDs along outside of circle** - physical location of Ensembl genes with an eQTL in the region

Limit to Brain eQTL only



Genes with a brain eQTL in this region



Genes with a brain eQTL in this region

Gene name	Gene description	Physical Location	P-Value from region
Ube3d	ubiquitin protein ligase E3D	chr8: 93,948,767-94,120,458	5.94E-07
MGC116202	RIKEN cDNA 4931428F04 gene	chr19: 37,237,523-37,245,217	2.63E-07
Cptp	ceramide-1-phosphate transfer protein	chr5: 173,314,228-173,318,313	3.21E-07
Slc39a12	solute carrier family 39 member 12	chr17: 81,455,955-81,541,759	3.16E-07
Camkmt	calmodulin-lysine N-methyltransferase	chr6: 8,669,722-8,729,771	5.59E-07

Relationships with nicotine and other neurological phenotypes

RESEARCH ARTICLE



Role of zinc transporter ZIP12 in susceptibility-weighted brain magnetic resonance imaging (MRI) phenotypes and mitochondrial function

Morgan D. Strong¹ | Matthew D. Hart¹ | Tony Z. Tang¹ | Babajide A. Ojo¹ | Lei Wu¹ | Mariah R. Nacke¹ | Workneh T. Agidew¹ | Hong J. Hwang² | Peter R. Hoyt² | Ahmed Bettaieb³ | Stephen L. Clarke¹ | Brenda J. Smith¹ | Barbara J. Stoecker¹ | Edralin A. Lucas¹ | Dingbo Lin¹ | Winyoo Chowanadisai¹

¹Department of Nutritional Sciences, Oklahoma State University, Stillwater, OK, USA

²Department of Biochemistry and Molecular Biology, Oklahoma State University, Stillwater, OK, USA

³Department of Nutrition, University of Tennessee, Knoxville, TN, USA

Correspondence

Winyoo Chowanadisai, Department of Nutritional Sciences, Oklahoma State University-Stillwater, 301 Human Sciences, Stillwater, OK 74078, USA.
Email: winyoo.chowanadisai@okstate.edu

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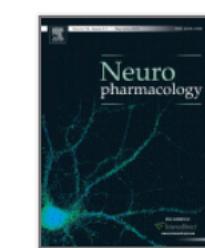
Abstract

Brain zinc dysregulation is linked to many neurological disorders. However, the mechanisms regulating brain zinc homeostasis are poorly understood. We performed secondary analyses of brain MRI GWAS and exome sequencing data from adults in the UK Biobank. Coding ZIP12 polymorphisms in zinc transporter ZIP12 (*SLC39A12*) were associated with altered brain susceptibility weighted MRI (swMRI). Conditional and joint association analyses revealed independent GWAS signals in linkage disequilibrium with 2 missense ZIP12 polymorphisms, rs10764176 and rs72778328, with reduced zinc transport activity. ZIP12 rare coding variants predicted to be deleterious were associated with similar impacts on brain swMRI. In Neuro-2a cells, ZIP12 deficiency by short hairpin RNA (shRNA) depletion or CRISPR/Cas9 genome editing resulted in impaired mitochondrial function, increased superoxide presence, and detectable protein carbonylation. Inhibition of Complexes I and IV of the electron transport chain reduced neurite outgrowth in ZIP12 deficient cells. Transcriptional coactivator PGC-1α, mitochondrial superoxide dismutase (SOD2), and chemical antioxidants α-tocopherol, MitoTEMPO, and MitoQ restored neurite extension impaired by ZIP12 deficiency. Mutant forms of α-synuclein and tau linked to familial Parkinson's disease and frontotemporal dementia, respectively, reduced neurite outgrowth in cells deficient in ZIP12. Zinc and ZIP12 may confer resilience against neurological diseases or premature aging of the brain.

harmacology

volume 50, issues 5–6, May–June 2009, Pages 1035–1040

ELSEVIER



Neuronal nicotinic acetylcholine receptors are modulated by zinc

Meta-analysis of genome-wide association studies of anxiety disorders

T Otowa, K Hek, [...] J M Hettema

Molecular Psychiatry 21, 1391–1399(2016) | Cite this article

1376 Accesses | 100 Citations | 21 Altmetric | Metrics

An Erratum to this article was published on 09 February 2016

Abstract

Anxiety disorders (ADs), namely generalized AD, panic disorder and phobias, are common, etiologically complex conditions with a partially genetic basis. Despite differing on diagnostic definitions based on clinical presentation, ADs likely represent various expressions of an underlying common diathesis of abnormal regulation of basic threat-response systems. We conducted genome-wide association analyses in nine samples of European ancestry from seven large, independent studies. To identify genetic variants contributing to genetic susceptibility shared across interview-generated DSM-based ADs, we applied two phenotypic approaches: (1) comparisons between categorical AD cases and supernormal controls, and (2) quantitative phenotypic factor scores (FS) derived from a multivariate analysis combining information across the clinical phenotypes. We used logistic and linear regression, respectively, to analyze the association between these phenotypes and genome-wide single nucleotide polymorphisms. Meta-analysis for each phenotype combined results across the nine samples for over 18 000 unrelated individuals. Each meta-analysis identified a different genome-wide significant region, with the following markers showing the strongest association: for case-control contrasts, rs1709393 located in an uncharacterized non-coding RNA locus on chromosomal band 3q12.3 ($P=1.65 \times 10^{-8}$); for FS, rs1067327 within *CAMKMT* encoding the calmodulin-lysine N-methyltransferase on chromosomal band 2p21 ($P=2.86 \times 10^{-9}$). Independent replication and further exploration of these findings are needed to more fully understand the role of these variants in risk and expression of ADs.

Conclusions

- The goal of the PhenoGen Project is to build a resource that will provide data leading to a “systems genetic” understanding of complex disease-related traits
- Deep and broad RNA expression information has been capture from brain and liver tissues of the Hybrid Rat Diversity Panel
- These data can be used to identify candidate genes from a phenotypic QTL by culling the genes that are physically located in the region based on RNA expression and specifically, eQTL in brain.
- Alternative candidate genes can also be identified via *trans* eQTL
- PhenoGen has many more tools that were not presented today but are useful for exploring the rat brain transcriptome

Data Availability

PhenoGen

Select the download icon() to download data from any of the datasets below. For some data types multiple options may be available. For these types, a window displays that allows you to choose specific files.

RNA-Seq

DNA-Seq

Microarray

Genomic Marker

Publications

RNA-Seq Transcriptome Reconstruction*[i]*

Organism	Strains	Tissue	Assembled by	.gtf Files
Rat	HRDP v5	Whole Brain	Stringtie	
Rat	HRDP v5	Liver	Stringtie	
Rat	HRDP v5	Heart	Stringtie	
Rat	HRDP v5	Merged	Stringtie	
Rat	BN-Lx/CubPrin, SHR/OlaLpcvPrin	Whole Brain	Cufflinks	
Rat	BN-Lx/CubPrin, SHR/OlaLpcvPrin	Heart	Cufflinks	
Rat	BN-Lx/CubPrin, SHR/OlaLpcvPrin	Liver	Cufflinks	
Rat	BN-Lx/CubPrin, SHR/OlaLpcvPrin	Whole Brain	Cufflinks	

Transcriptome Quantitation(Gene/Transcript, Ensembl/Reconstruction)*[i]*

Organism	Strains	Tissue	.csv Files
Rat	HRDP v5	Whole Brain	
Rat	HRDP v5	Liver	

Data Availability

GeneNetwork

The screenshot shows the GeneNetwork search interface. At the top, there is a navigation bar with links for GeneNetwork, Intro, Help, Tools, Collections (0), Source Code, and Sign in. Below the navigation bar is a search bar with dropdown menus for "Genes / Molecules" and "Search All".

Select and search

Species: Rat (rn6)

Group: Hybrid Rat Diversity Panel (Includes HXB/BXH)

Type: Brain mRNA

Dataset: PhenoGen Brain RNA Ensembl rlog (v5 Feb20)

Get Any: [Text input field]

Enter terms, genes, ID numbers in the **Search** field.
Use * or ? wildcards (Cyp*a?, synap*).
Use quotes for terms such as "tyrosine kinase".

Combined: [Text input field]

Buttons: Search, Make Default

Affiliates

- GeneNetwork 1 at UTHSC
- Genome Browser at UTHSC
- Systems Genetics at EPFL
- Bayesian Network Web Server at UTHSC
- GeneWeaver
- PhenoGen at University of Colorado
- WebGestalt at Baylor

News

- Our new preprint on homomorphic genome encryption is on bioRxiv
Private Genomes and Public SNPs: Homomorphic encryption of genotypes and phenotypes for shared quantitative genetics
[https://www.biorxiv.org/content/10.1101/2020.04.02.201865v1 ...](https://www.biorxiv.org/content/10.1101/2020.04.02.201865v1)
- Posted on Apr 5, 2020
- #ELIXIRvsCOVID19: #LS_RI @ELIXIREurope + several nodes participated in the week-long #biohackathon #covid_19_bh20 led by @pjotrprins

Acknowledgements

- Saba Lab:
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 - NIDA Core “Center of Excellence” in Omics, Systems Genetics and the Addictome (NIDA - P30DA044223; MPIs - Williams, Saba)
 - The heritable transcriptome and alcoholism (NIAAA - R24AA013162; MPIs - Tabakoff, Hoffman, Saba)

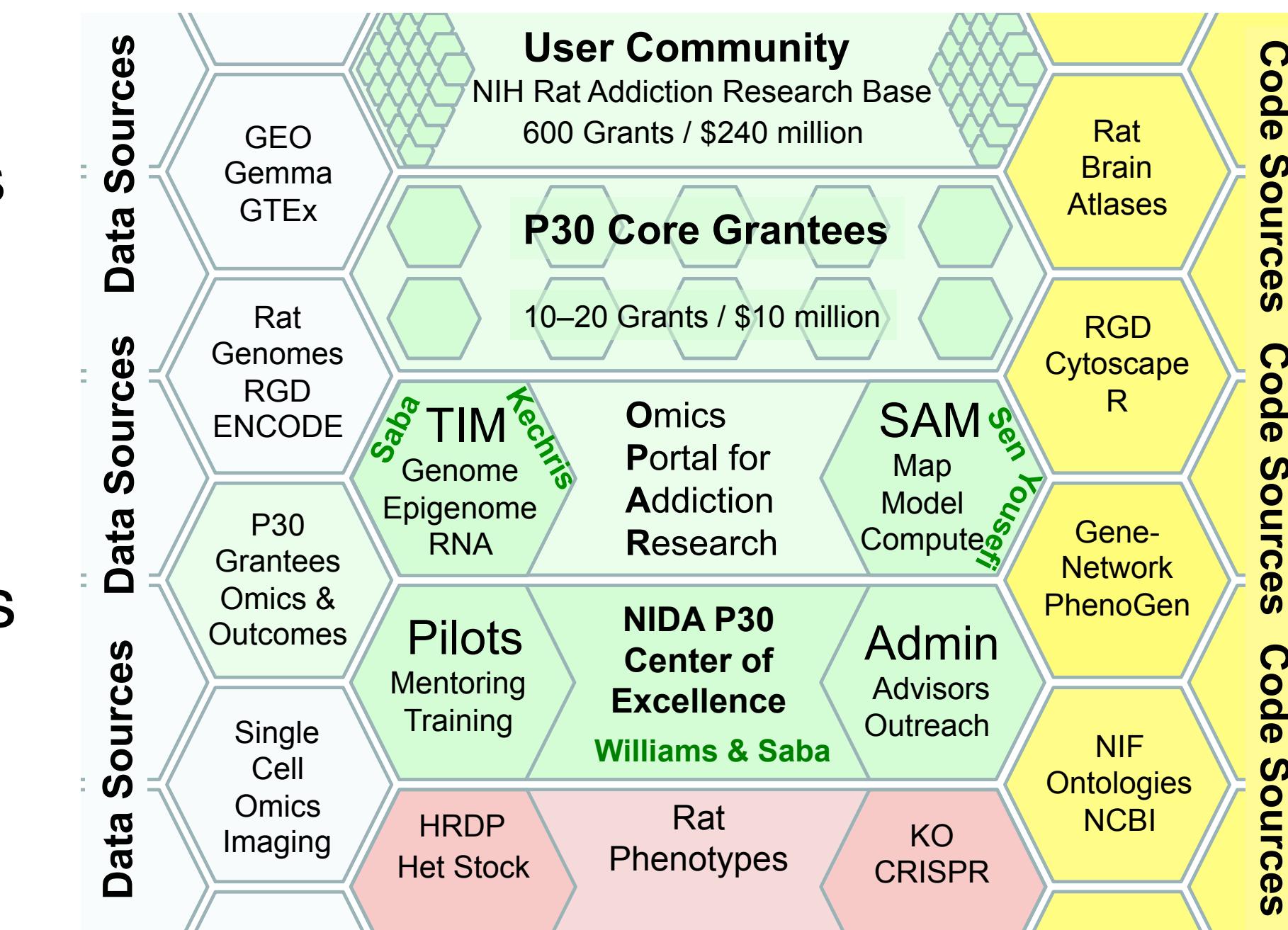


NIDA Core Center of Excellence in Omics,

System Genetics, and the Addictome

Co-Directors: Rob Williams (UTHSC) and Laura Saba (CU-AMC)

The **purpose** of the NIDA P30 Core Center of Excellence in Omics, Systems Genetics, and the Addictome is to empower and train researchers supported by NIH, NIDA, NIAAA, and other federal and state institutions to use more quantitative and testable ways to analyze genetic, epigenetic, and the environmental factors that influence drug abuse risk and treatment.



Our Approach:

- Omics Portal for Addiction Research (OPAR)
- Study design and RNA-Seq analysis services
- Training in Systems Genetics, RNA-Seq, and OPAR usage
- Funding for pilot grants

OSGA Webinar Schedule

Webinars are from 11:00am MST to 12:30pm MST on the second and fourth Fridays of the month. The first hour is demonstration/lecture and the last half hour is dedicated to questions/answers and general discussion of the topic.

Date	Topic	Speaker
August 28, 2020	Tools for QTL to gene: PhenoGen	Laura Saba
September 11, 2020	Sex as a biological covariate in genetic studies	Saunak Sen
September 25, 2020	Introduction to WGCNA	Laura Saba
October 9, 2020	Advanced topics in QTL analysis	Sen and friends