

PhenoGen Informatics

The site for quantitative genetics of the transcriptome

<http://phenogen.ucdenver.edu>

The PhenoGen Group

Led by Boris Tabakoff, Paula Hoffman, and Laura Saba

Anschutz Medical Campus

University of Colorado Denver

**Please use Firefox for optimal results and to follow along in the workshop

Acknowledgements

The PhenoGen Group:

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Collaborators:

Morton Printz, PhD; Michal Pravenec, PhD

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Outline

1. Introduction to PhenoGen Informatics and the Hybrid Rat Diversity Panel
2. Interactive demo of candidate gene approach
3. Downloadable data
4. Future directions with HRDP and PhenoGen

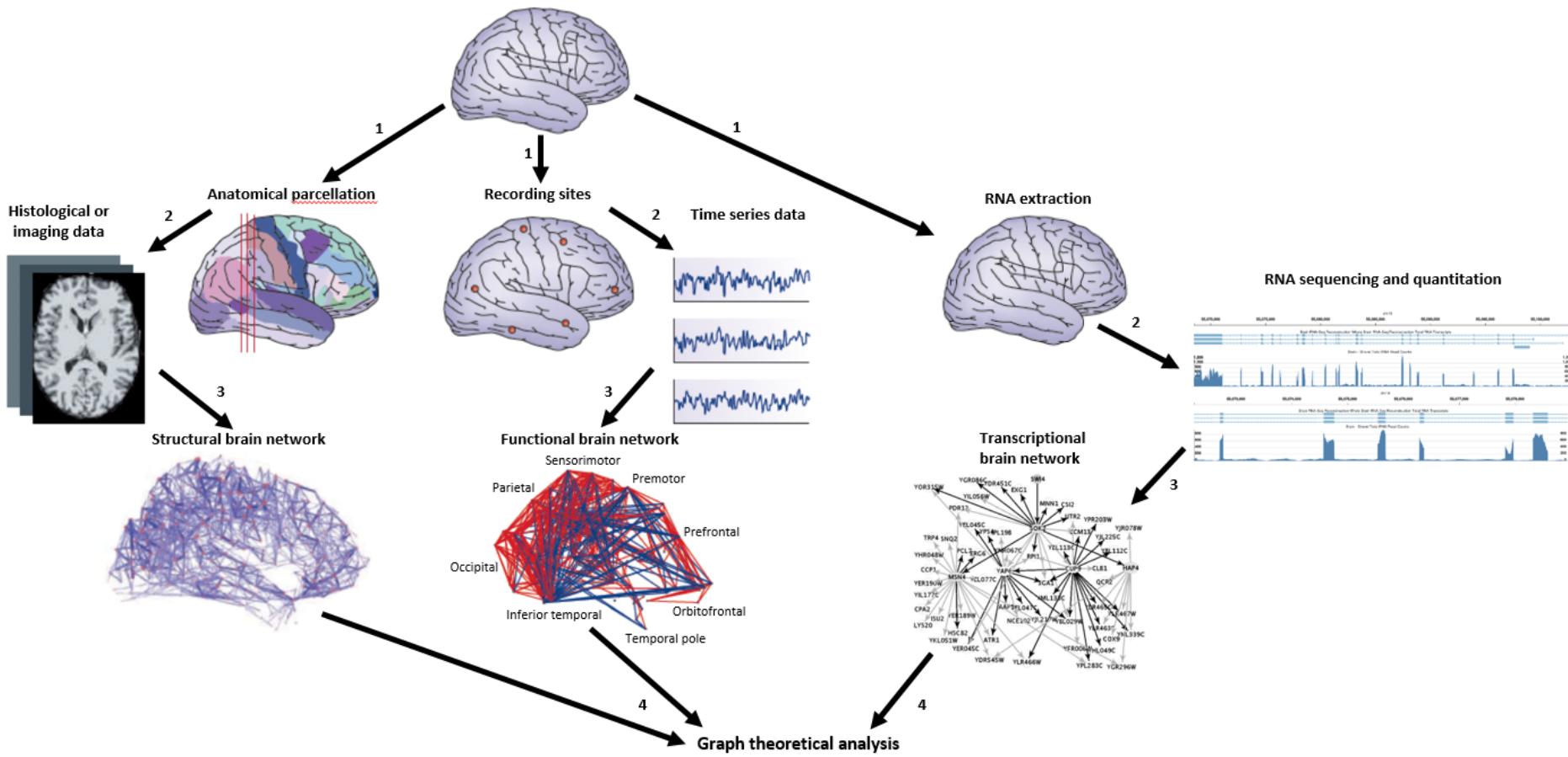
Goal for the PhenoGen Project

Transcriptional Connectome

To generate a new image of organs as networks of interacting elements (transcripts)

- Collect genome sequence and full transcriptome information for organs (brain, liver, heart).
 - We have completed exon array analysis for these three organs
 - RNA-Seq for brain and liver in 30 strains of the HXB/BXH panel and 10 classic inbred strains completed
 - RNA-Seq for heart of the RI progenitor strains completed

Brain Transcriptional Connectome



Why Networks?

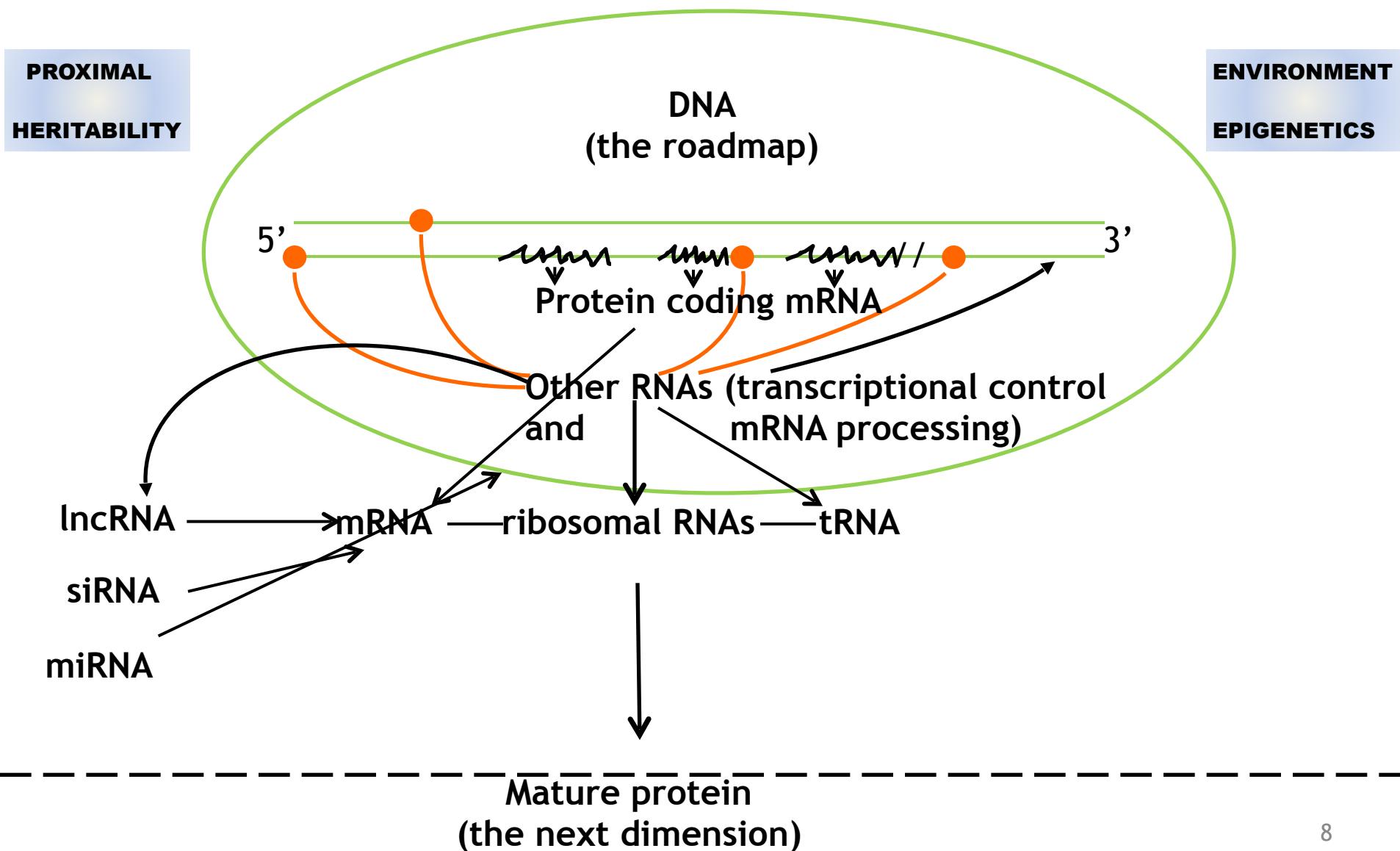
1. The brain is a complex hierarchical network spatio-temporally linked through structure and function.
2. Complex pathologic traits can be conceptualized as systems disorders of failed network regulation.
3. The brains structural and functional systems have features of complex networks that can be described through application of “graph theory” (small world topology).
4. The generation of a “Transcriptional Connectome” representing the Resting State transcriptional networks provides power for understanding predisposition to disease, etiology of organ or behavioral pathology and response to medications or toxins.

Why Study the RNA Dimension

Transcriptome links DNA and complex traits/diseases

- A. RNA is one of the first quantitative links between DNA sequence and phenotype (an endophenotype).
- B. Transcriptome information addresses part of the GWAS Gap: how does an identified DNA polymorphic locus contribute to disease?
- C. First step where DNA sequence and environment interact.
- D. Implementation of graph theory at the transcript level provides insight into genetic/environmental interactions that are the basis for susceptibility to complex diseases.

The RNA Dimension (the true intermediate phenotype)

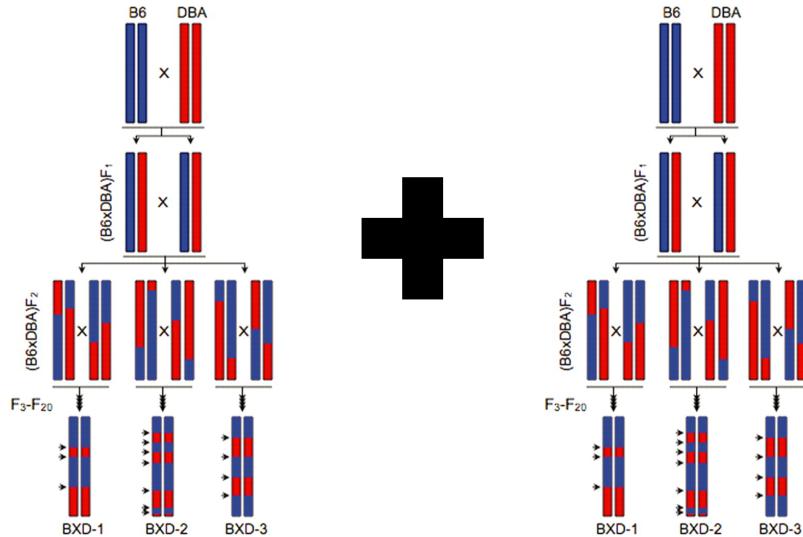


Co-expression as a measure of the “connectome”

- Theory - if the magnitude of RNA expression of two transcripts correlates over multiple “environments” (genomes), then the two transcripts are involved in similar biological processes
- Caveats when multiple environments are multiple genetic backgrounds (false positive correlations)
 - Linkage Disequilibrium
 - Cell-type mixing proportions

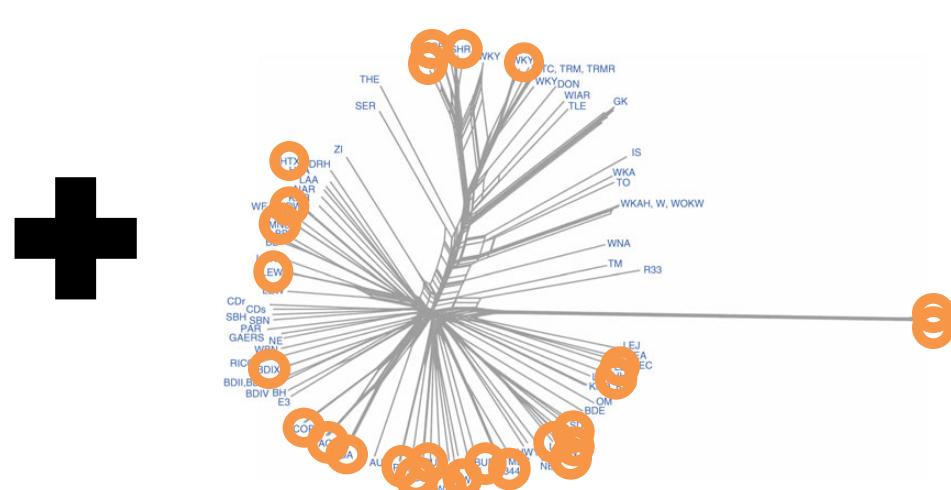
A Renewable Genetically Defined Population for Cumulative Biology

The Hybrid Rat Diversity Panel



30 HXB/BXH
Recombinant
Inbred Strains

32 LEXF/FXLE
Recombinant
Inbred Strains



34 Classic Inbred Strains

A Renewable Genetically Defined Population for Cumulative Biology

The Hybrid Rat Diversity Panel



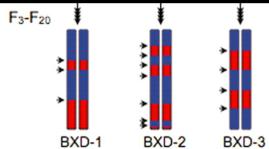
Power to detect loci that contribute 10-20% to genetic variance

Power to detect significant genetic correlations as small as 0.28

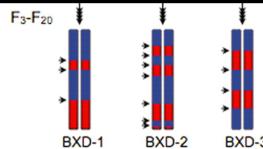
Power to perform high resolution mapping (median haplotype block size = 225 Kb)

Power to detect GXE effects through static genetic composition

Power to replicate and grow data



30 HXB/BXH
Recombinant
Inbred Strains



32 LEXF/FXLE
Recombinant
Inbred Strains



34 Classic Inbred Strains

CANDIDATE GENE EXAMPLE

Genome View

1. Click Genome/ Transcriptome Data Browser
2. Type in Rat/Mouse Official Gene Symbol into “Gene Identifier or Region” box
3. Select Rattus Norvegicus from “Species” box
4. Select Genome (Predefined) from “Initial View” box
5. Click “Go”

The site for quantitative genetics of the transcriptome.

PhenoGen Informatics

Overview Genome / Transcriptome Data Browser Available Data Downloads Gene List Analysis Tools Microarray Analysis Tools QTL Tools About Help Login/ Register

Welcome to PhenoGen Informatics

The site for quantitative genetics of the transcriptome.

Hover over or click on nodes in the graph below to see the tools/data available on the site.

Green no login required.
Blue sections require a login.
Pause

PhenoGen - Genome/Transcri > Gene: Ipcf1 (ENSRNOG0000...)

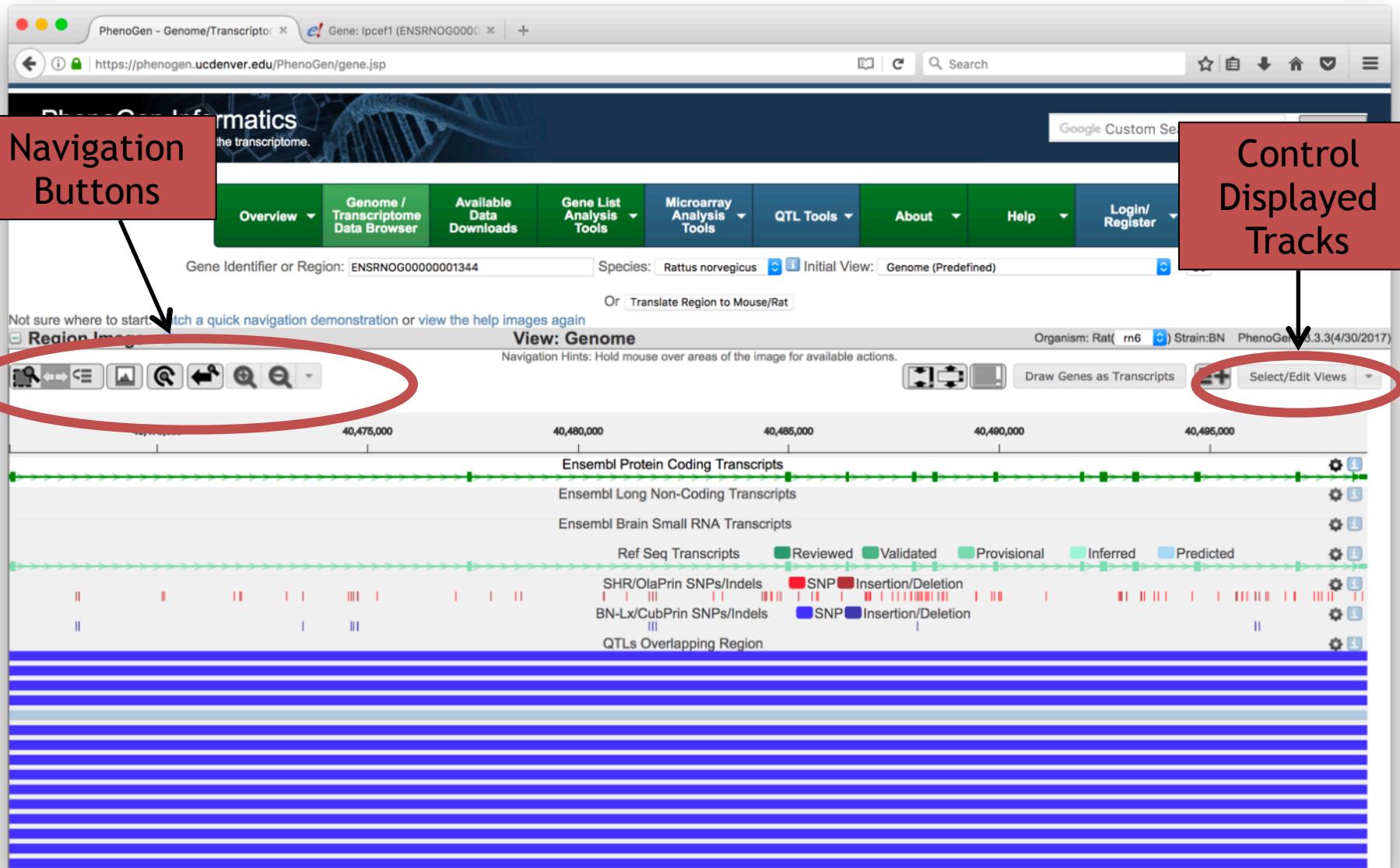
PhenoGen Informatics

1. Enter a gene identifier(e.g. gene symbol, probe set ID, Ensembl ID, etc.) in the gene field.
or
Enter a region such as
"chr1:1-50000" which would be Chromosome 1 @ bp 1-50,000.
"chr1:5000+2000" which would be Chromosome 1 @ bp 3,000-7,000.
"chr1:5000+2000" which would be Chromosome 1 @ bp 5,000-7,000.
or
Click on the Translate Region to Mouse/Rat to find regions on the Mouse/Rat genome that correspond to a region of interest in the Human/Mouse/Rat genome.

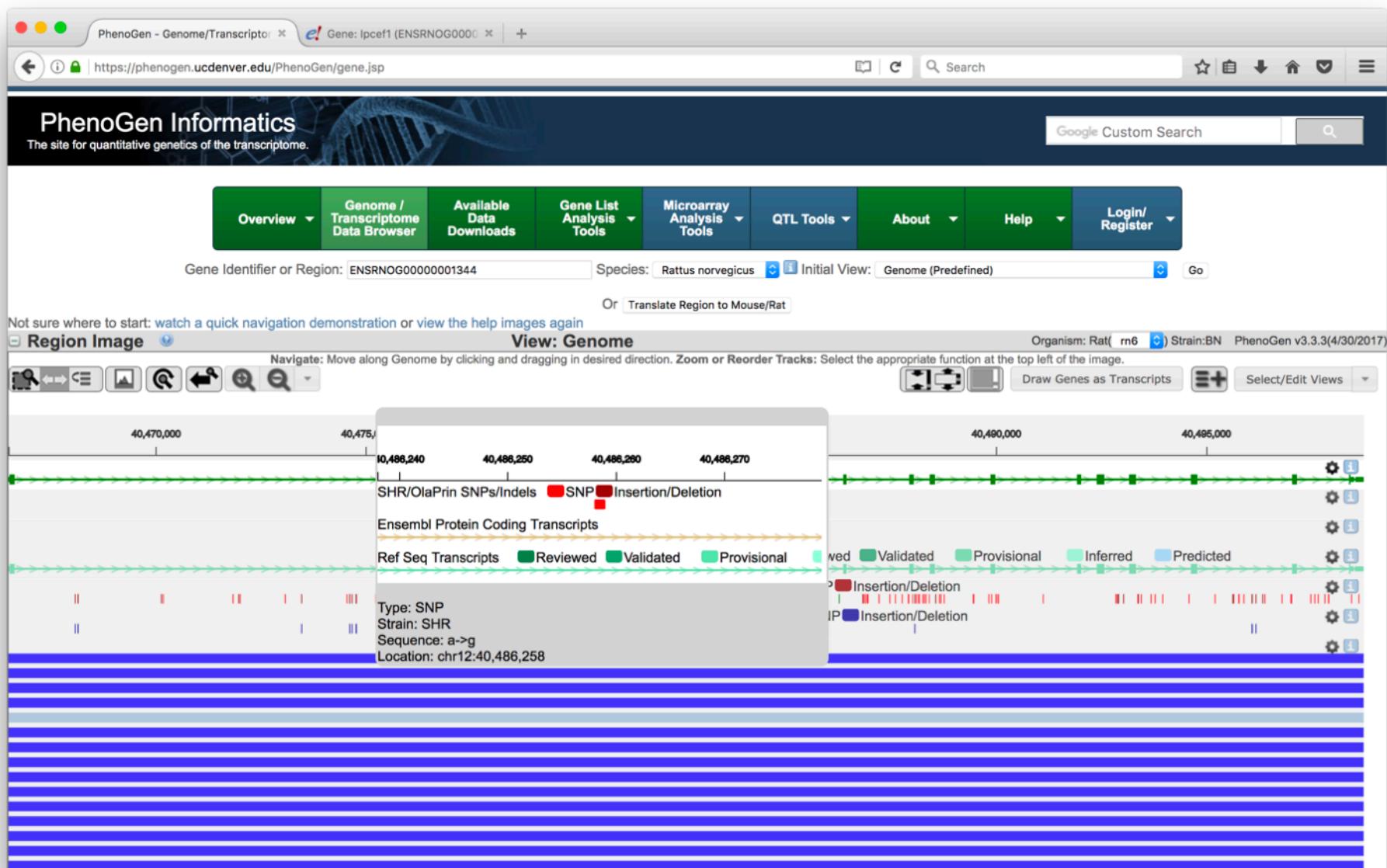
2. Choose a species.
3. Click Get Transcription Details.

Gene Identifier or Region: Aldh2 Species: Rattus norvegicus Initial View: Genome (Predefined) Go

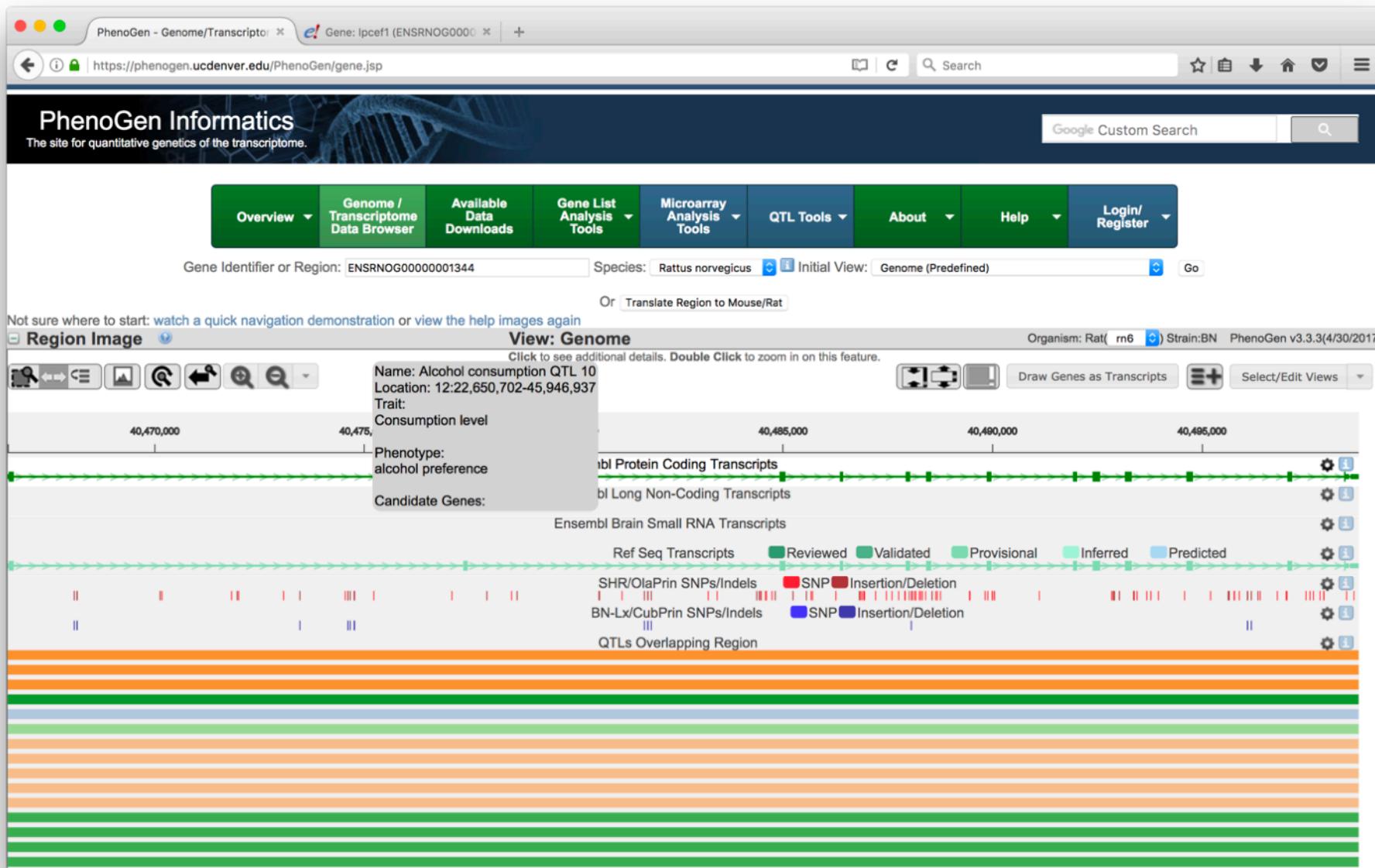
Or Translate Region to Mouse/Rat Demonstrations



Genetic Variants Between Parental Strains of RI Panel



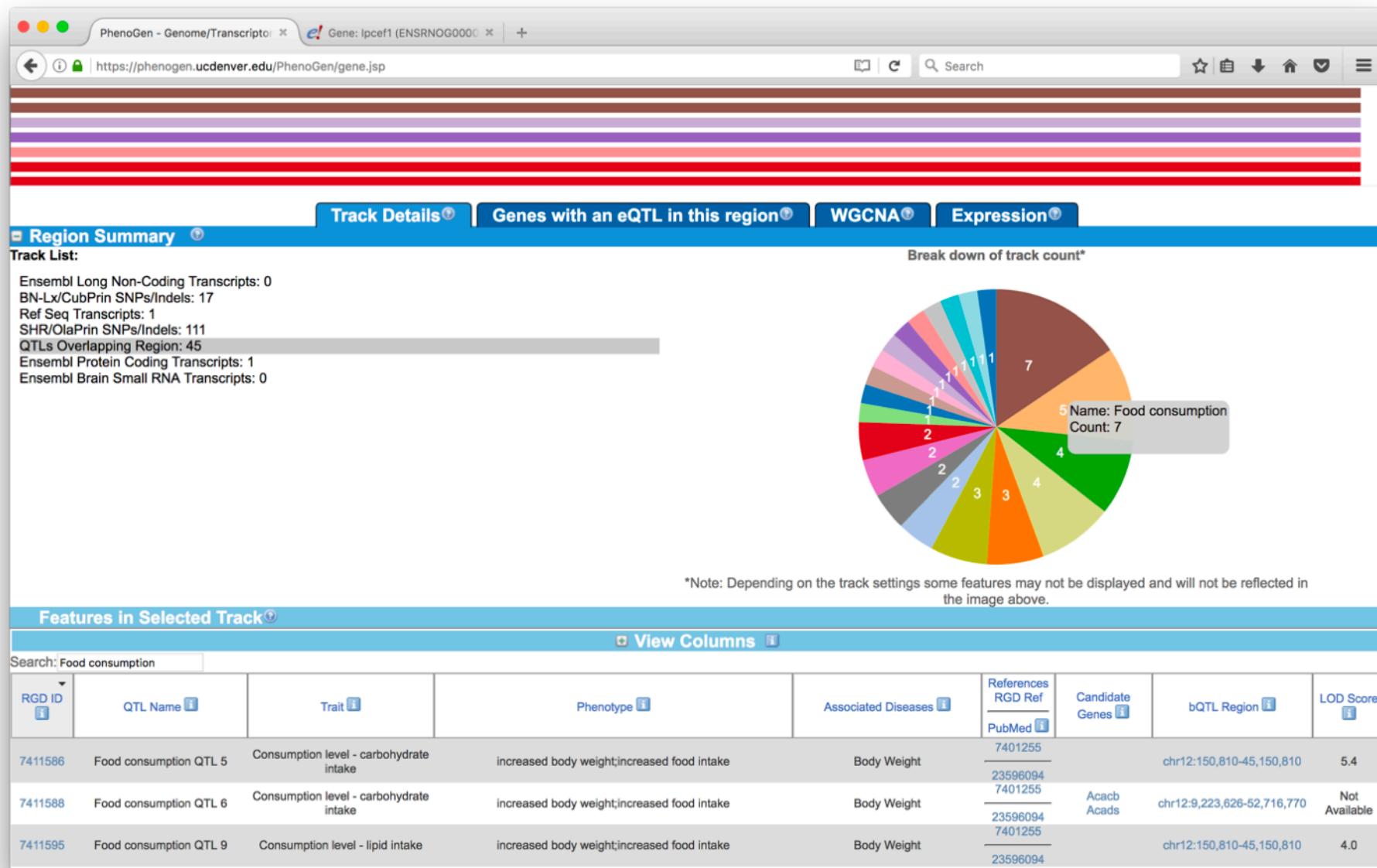
Published Behavioral/Physiologic QTL



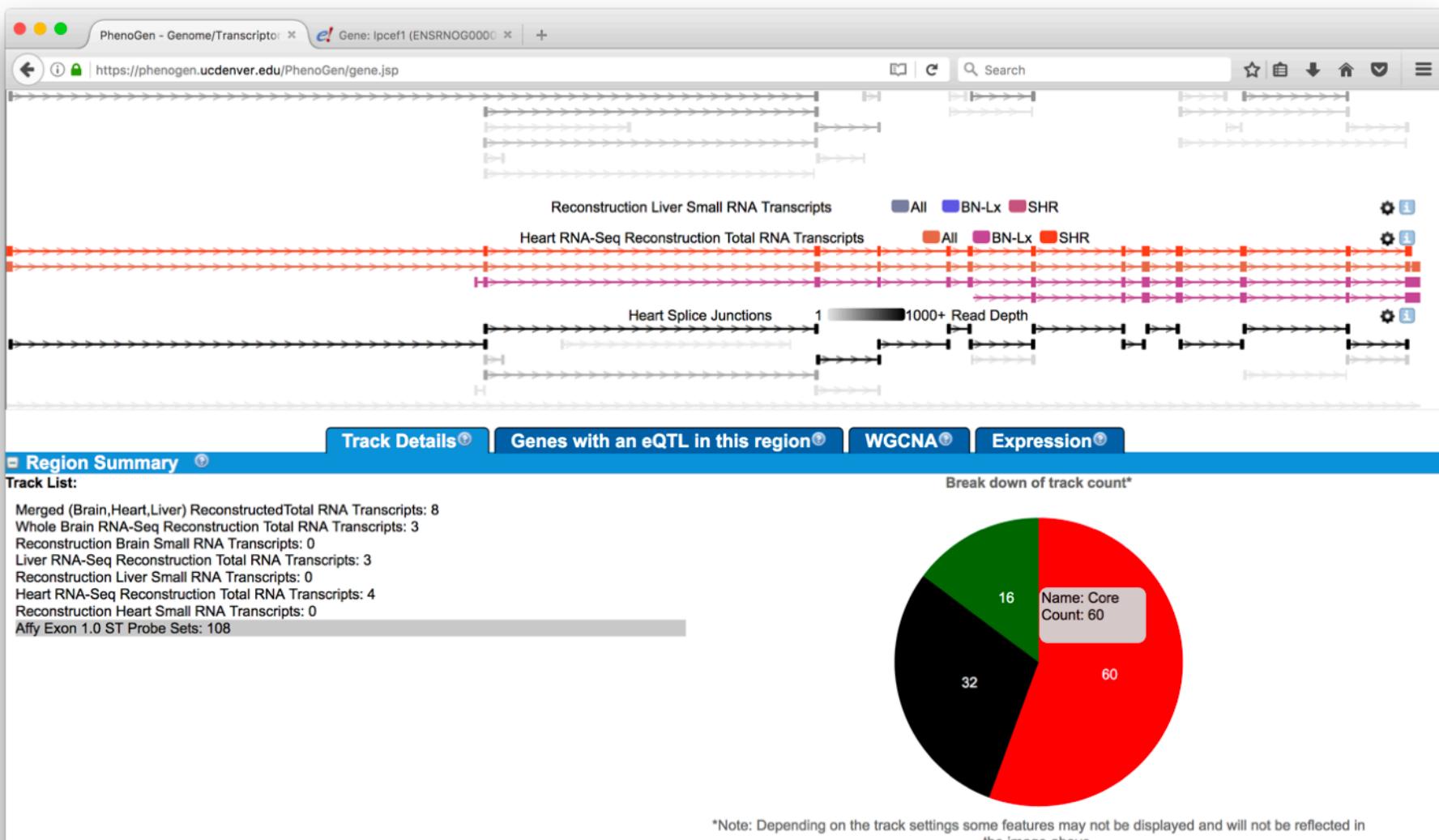
Get Region Summary



Region Summary



Alternate Region Summary Under Different View



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

Transcriptome View

PhenoGen - Genome/Transcrip... +

https://phenogen.ucdenver.edu/PhenoGen/gene.jsp

Search

PhenoGen Informatics
The site for quantitative genetics of the transcriptome.

Google Custom Search

Overview ▾ Genome / Transcriptome Data Browser Available Data Downloads Gene List Analysis Tools Microarray Analysis Tools QTL Tools ▾ About ▾ Help ▾ Login/ Register ▾

Gene Identifier or Region: ENSRNOG00000018191 Species: Rattus norvegicus Initial View: Transcriptome (Predefined) Go

Or Translate Region to Mouse/Rat

Not sure where to start: watch a quick navigation demonstration or view the help images again

Region Image

View: Genome

Navigation Hints: Hold mouse over areas of the image for available actions.

Organism: Rat(rn6) Strain:BN PhenoGen v3.3.3(4/30/2017)

43,500,000 43,550,000 43,600,000 43,650,000 43,700,000

Ensembl Protein Coding Transcripts

Sign in to see views/tracks not created on this computer.

Click on a view to select it and view preview/details.

View types: All Views

Select a view below (click apply to display the view and return to the browser):

Transcriptome (Predefined) (9 tracks)

Transcriptome (Predefined) (12 tracks) **(highlighted)**

Liver RNA-Seq (Predefined) (7 tracks) (Rat Only)

Brain RNA-Seq (Predefined) (8 tracks)

Liver Microarray/RNA-Seq (Predefined) (9 tracks) (Rat Only)

Brain Microarray/RNA-Seq (Predefined) (8 tracks)

Heart RNA-Seq (Predefined) (7 tracks) (Rat Only)

Apply View

Description/Preview View/Edit Track List

Provides general Transcriptome Data including RNA-Seq transcriptomes, Affymetrix probesets, and RNA-Seq read count depth tracks.

Preview

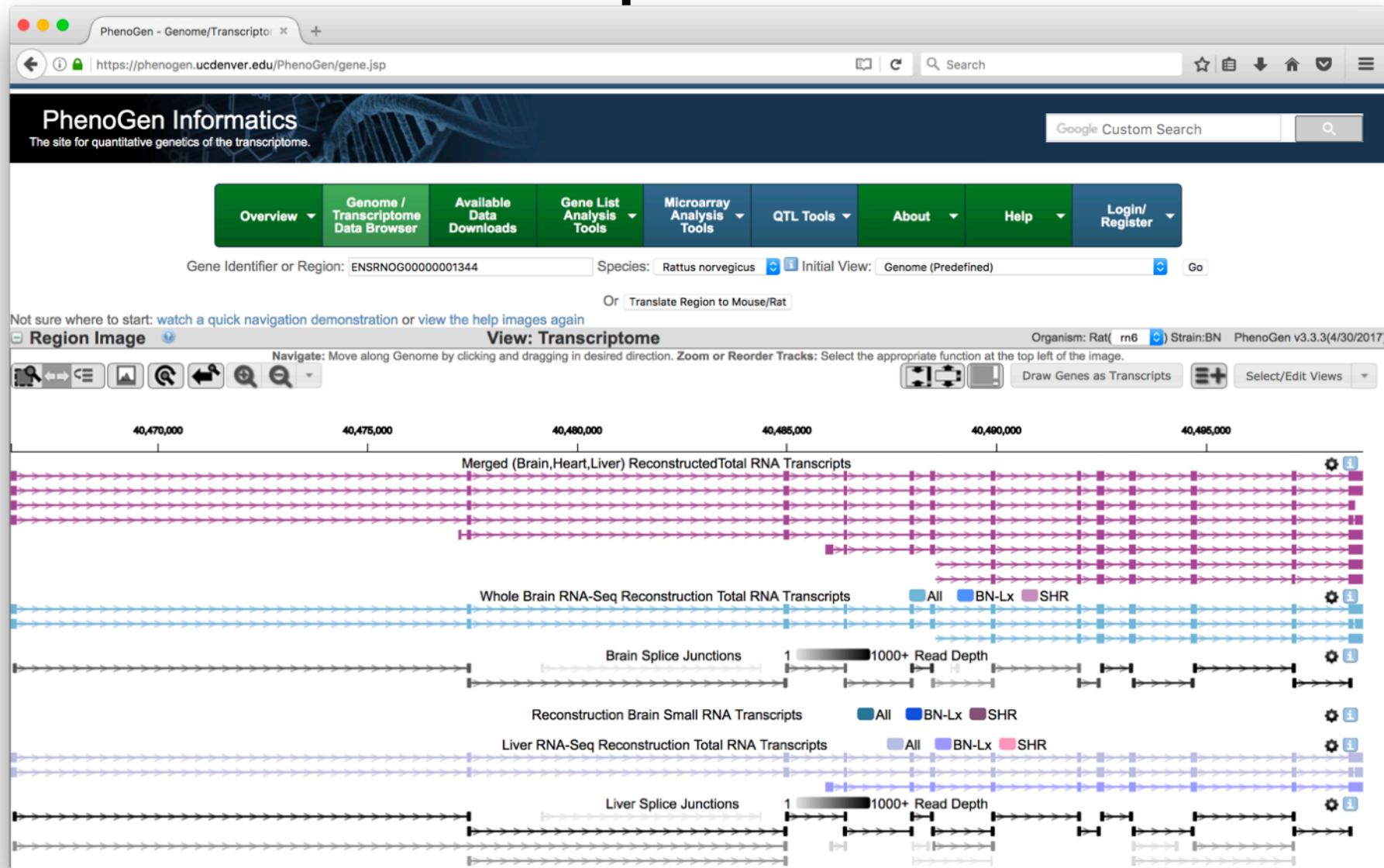
43,500,000 43,600,000 43,700,000

Merged (Brain,Heart,Liver) ReconstructedTotal RNA Genes

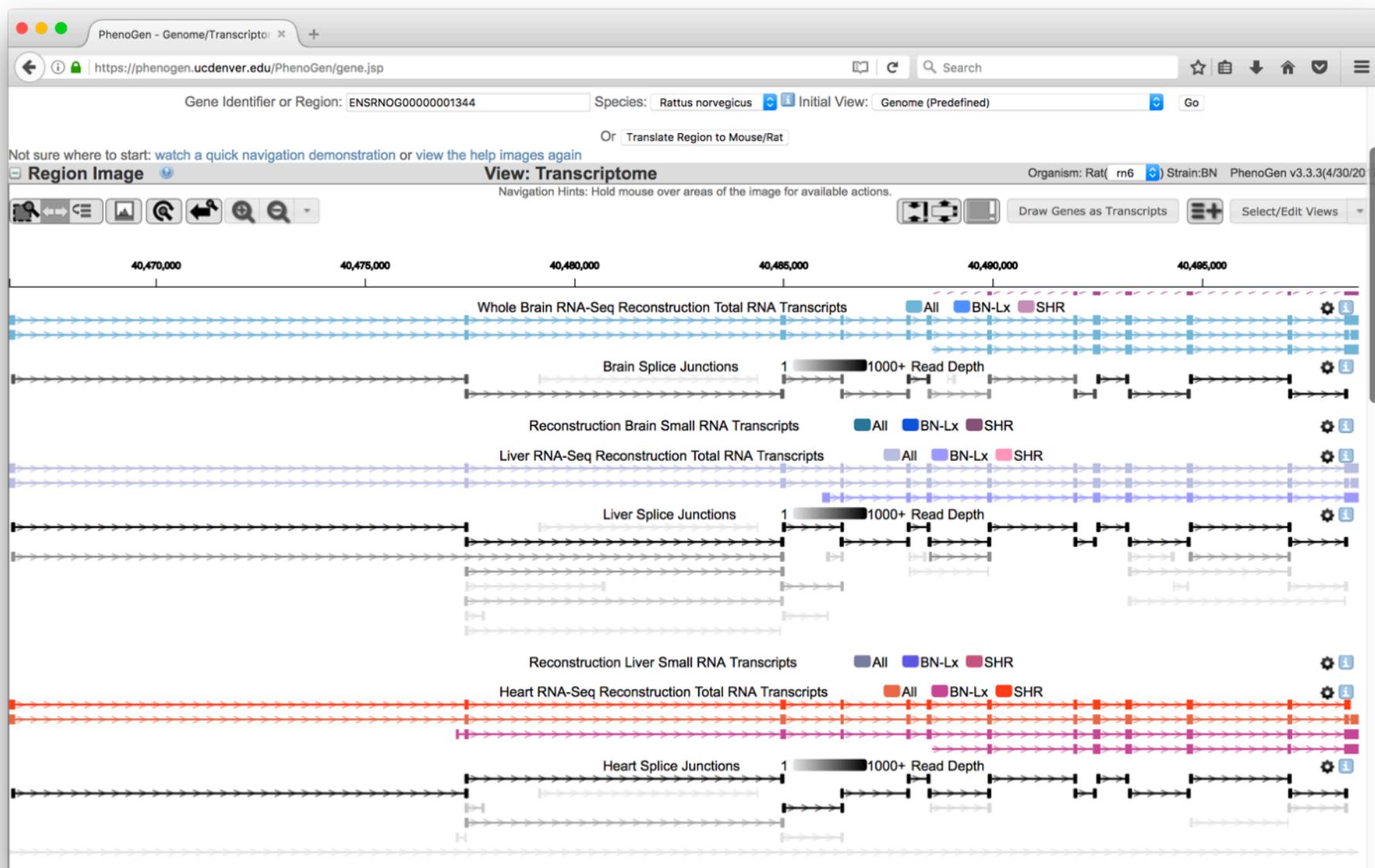
Whole Brain RNA-Seq Reconstruction Total RNA Genes

1. Click “Select/Edit Views” box.
2. Select “Transcriptome (Predefined) (6 tracks)” in Select a view below box
3. Click “Apply View” button

Transcriptome View



Aldh2 - In Brain, Heart, and Liver Reconstruction

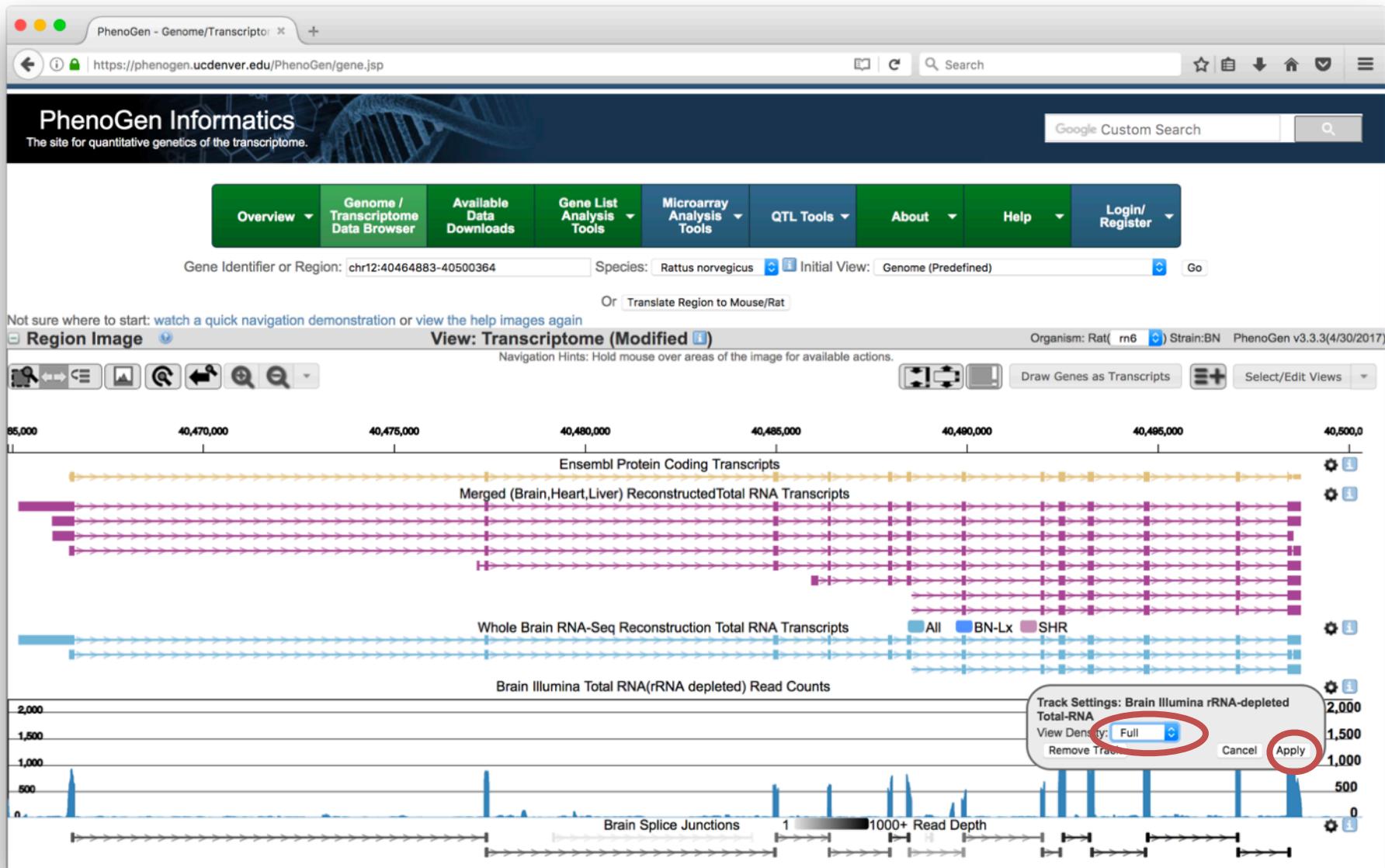


Add RNA-Seq Counts

1. Click on “Select/Edit Views”
2. Click on “View/Edit Track List” Tab
3. Click on plus icon
4. Select row with track to be added.
5. Click “Add Track”. This can be repeated for different tracks.
6. Click “Apply View” when all desired tracks have been added.

The screenshot shows the PhenoGen Informatics web application. At the top, there is a navigation bar with links for Overview, Genome / Transcriptome Data Browser, Available Data Downloads, Gene List Tools, Microarray Analysis Tools, QTL Tools, About, Help, and Login/Register. Below the navigation bar, the URL is https://phenogen.ucdenver.edu/PhenoGen/gene.jsp. The main content area displays a "Region Image" with various genomic tools and a "View: Transcriptome" section. A red box labeled "1." highlights the "Select/Edit Views" button in the top right corner of the main window. The "View: Transcriptome" section has a red box labeled "2." highlighting the "View/Edit Track List" tab. On the left, a modal window titled "Select a Track to add to Transcriptome" is open. It contains a list of available tracks, with one track highlighted in blue. A red box labeled "4." points to this highlighted track. To the right of the modal, another smaller window titled "Select/Edit Views" is also open, with a red box labeled "5." pointing to the "Add Track" button. Finally, a red box labeled "6." points to the "Apply View" button at the bottom right of the "Select/Edit Views" window.

Expand RNA-Seq Read Counts



Selected Feature Summary

To get the Selected Feature Summary, click on the transcript in the Transcriptome View

PhenoGen - Genome/Transcriptor

https://phenogen.ucdenver.edu/PhenoGen/gene.jsp

Gene Details | Gene eQTLs | Expression Data | miRNA Targeting Gene(multiMiR) | WGCNA

Selected Feature Summary

Gene Symbol: Aldh2
Location: chr12: 40,466,495-40,498,752
Strand: +
Description: aldehyde dehydrogenase 2 family (mitochondrial)
Links: ENSRNOG00000001344
All Organisms:NCBI | UniProt
Rat: NCBI | UniProt | RGD

Exonic Variants:
Common: 0 (SNPs) / 0 (Insertions/Deletions)
BN-Lx/CubPrin: 0 (SNPs) / 0 (Insertions/Deletions)
SHR/OlaPrin: 2 (SNPs) / 0 (Insertions/Deletions)
SHR/NCrIPrin: 0 (SNPs) / 0 (Insertions/Deletions)
F344: 0 (SNPs) / 0 (Insertions/Deletions)

Transcripts:
ENSRNOT00000001816
PRN6T0162338 - 100.0% of Trx:ENSRNOT00000001816 Exons Match, 11 Perfect Exon Matches, 3' Extended, 5' Extended, 5' Extended, -1 Extra Exons,
PRN6T0080327 - Transcript Match: ENSRNOT00000001816 14 Perfect Exon Matches,
PRN6T0162339 - 78.6% of Trx:ENSRNOT00000001816 Exons Match, 9 Perfect Exon Matches, 5' Extended, 5' Extended,
PRN6T0262547 - 92.9% of Trx:ENSRNOT00000001816 Exons Match, 11 Perfect Exon Matches, 3' Extended, 5' Extended,
PRN6T0080327 - Transcript Match: ENSRNOT00000001816 14 Perfect Exon Matches,
PRN6T0262548 - 92.9% of Trx:ENSRNOT00000001816 Exons Match, 10 Perfect Exon Matches, 1 Fuzzy Exon Matches, 5' Extended, 5' Extended,
PRN6T0262549 - 50.0% of Trx:ENSRNOT00000001816 Exons Match, 4 Perfect Exon Matches, 1 Fuzzy Exon Matches, 5' Extended, 5' Extended,
PRN6T0080326 - 100.0% of Trx:ENSRNOT00000001816 Exons Match, 11 Perfect Exon Matches, 3' Extended, 5' Extended, 5' Extended, -1 Extra Exons,
PRN6T0080327 - Transcript Match: ENSRNOT00000001816 14 Perfect Exon Matches,
PRN6T0080328 - 57.1% of Trx:ENSRNOT00000001816 Exons Match, 5 Perfect Exon Matches, 1 Fuzzy Exon Matches, 5' Extended, 5' Extended,
PRN6T0080326 - 100.0% of Trx:ENSRNOT00000001816 Exons Match, 11 Perfect Exon Matches, 3' Extended, 5' Extended, 5' Extended, -1 Extra Exons,
PRN6T0162338 - 100.0% of Trx:ENSRNOT00000001816 Exons Match, 11 Perfect Exon Matches, 3' Extended, 5' Extended, 5' Extended, -1 Extra Exons,
PRN6T0262547 - 92.9% of Trx:ENSRNOT00000001816 Exons Match, 11 Perfect Exon Matches, 3' Extended, 5' Extended,
PRN6T0080327 - Transcript Match: ENSRNOT00000001816 14 Perfect Exon Matches,
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PRN6T0162339 - 78.6% of Trx:ENSRNOT00000001816 Exons Match, 9 Perfect Exon Matches, 5' Extended, 5' Extended,
PRN6T0080328 - 57.1% of Trx:ENSRNOT00000001816 Exons Match, 5 Perfect Exon Matches, 1 Fuzzy Exon Matches, 5' Extended, 5' Extended,
PRN6T0262549 - 50.0% of Trx:ENSRNOT00000001816 Exons Match, 4 Perfect Exon Matches, 1 Fuzzy Exon Matches, 5' Extended, 5' Extended,

Affy Probe Set Data: Overlapping Probe Set Count:24

Probe sets detected above background*:

Tissue	Number of probe sets detected above background* in more than 1% of samples (out of 24 probe sets for this gene)	Avg % of samples DABG*	Range
Brain	12	61 %	5.56 - 100 %
Heart	15	91 %	18.1 - 100 %
Liver	16	97 %	50.94 - 100 %
Brown	15	87 %	1.04 - 100

Probe Set Heritability:

Tissue	Number of probe sets with a heritability greater than 0.33 (out of 24 probe sets for this gene)	Avg Herit	Range
Brain	11	0.49	0.35 - 0.82
Heart	16	0.66	0.34 - 0.92
Liver	19	0.52	0.37 - 0.92
Brown	15	0.62	0.4 - 0.9

Gene eQTL

PhenoGen - Genome/Transcriptor <https://phenogen.ucdenver.edu/PhenoGen/gene.jsp>

Gene Details [Gene eQTLs](#) [Expression Data](#) [miRNA Targeting Gene\(multiMiR\)](#) [WGCNA](#)

Selected Feature Summary

eQTL Image Options

Data Source: [RNA-Seq](#) P-value Threshold for Highlighting: 0.01

Tissues: Include at least one tissue. Excluded Included Chromosomes: (chr12 must be included) Excluded Included

Brain Liver

Chr 1 Chr 2 Chr 3 Chr 4 Chr 5 Chr 6

Click to run Circos

Circos: an Information Aesthetic for Comparative Genomics.

RNA-Seq Based Gene Level eQTLs

Inside of border below, the mouse wheel zooms. Outside of the border, the mouse wheel scrolls. Download Circos image: [Download](#)

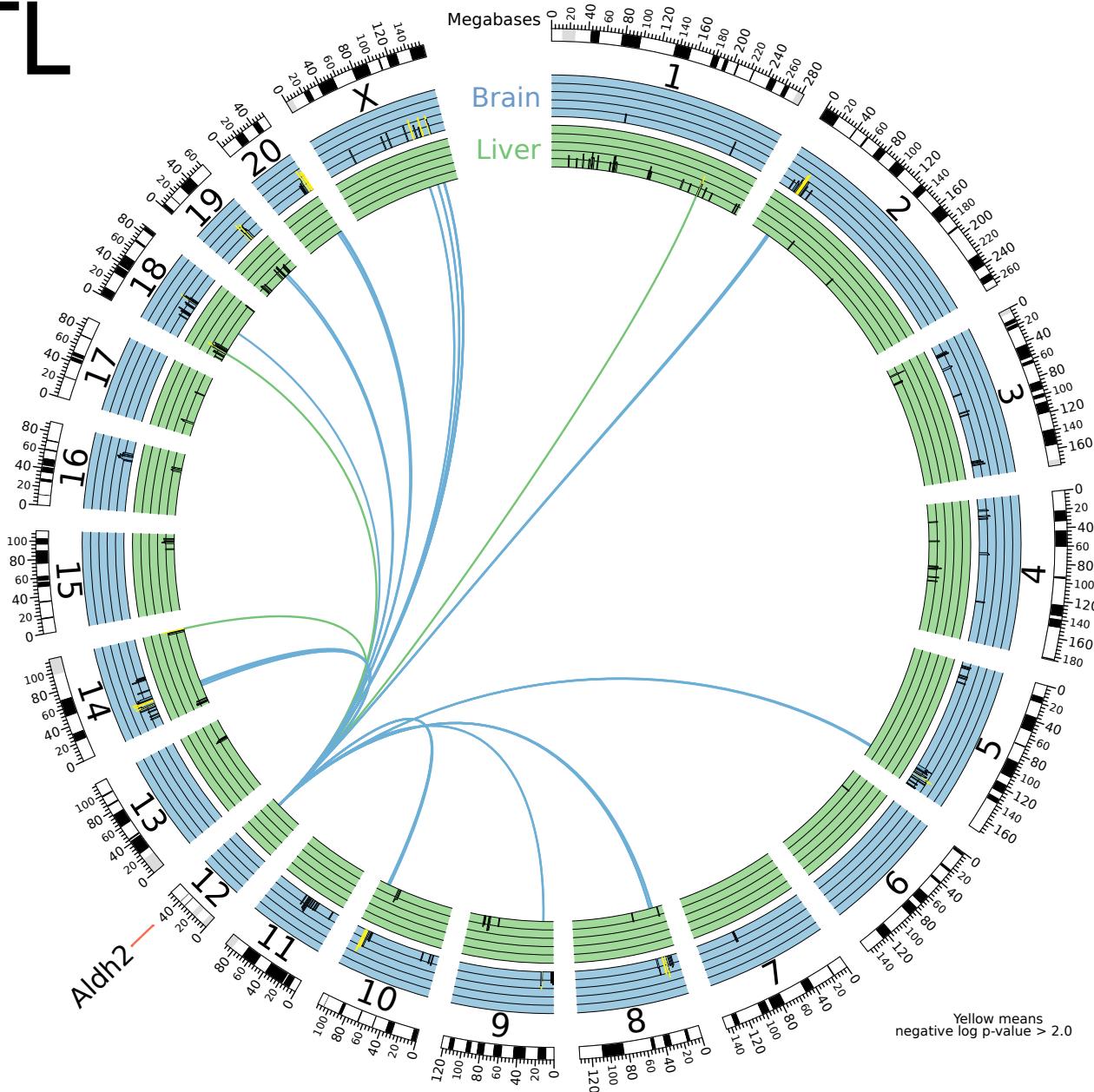
Megabases 0 20 40 60 80 100 120 140 160 180 200 220 240 260 280 300 320 340 360

Brain Liver

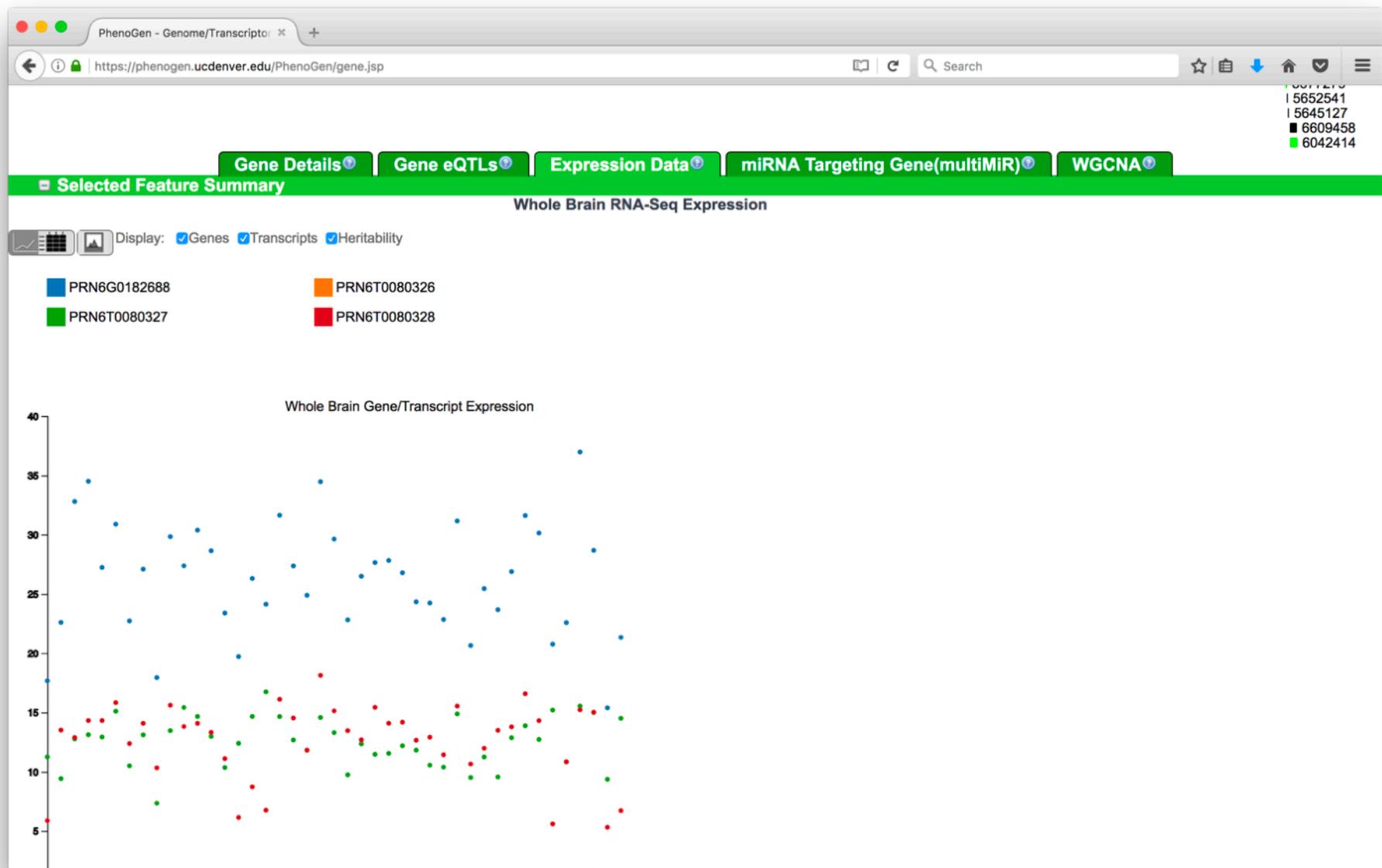
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X

?

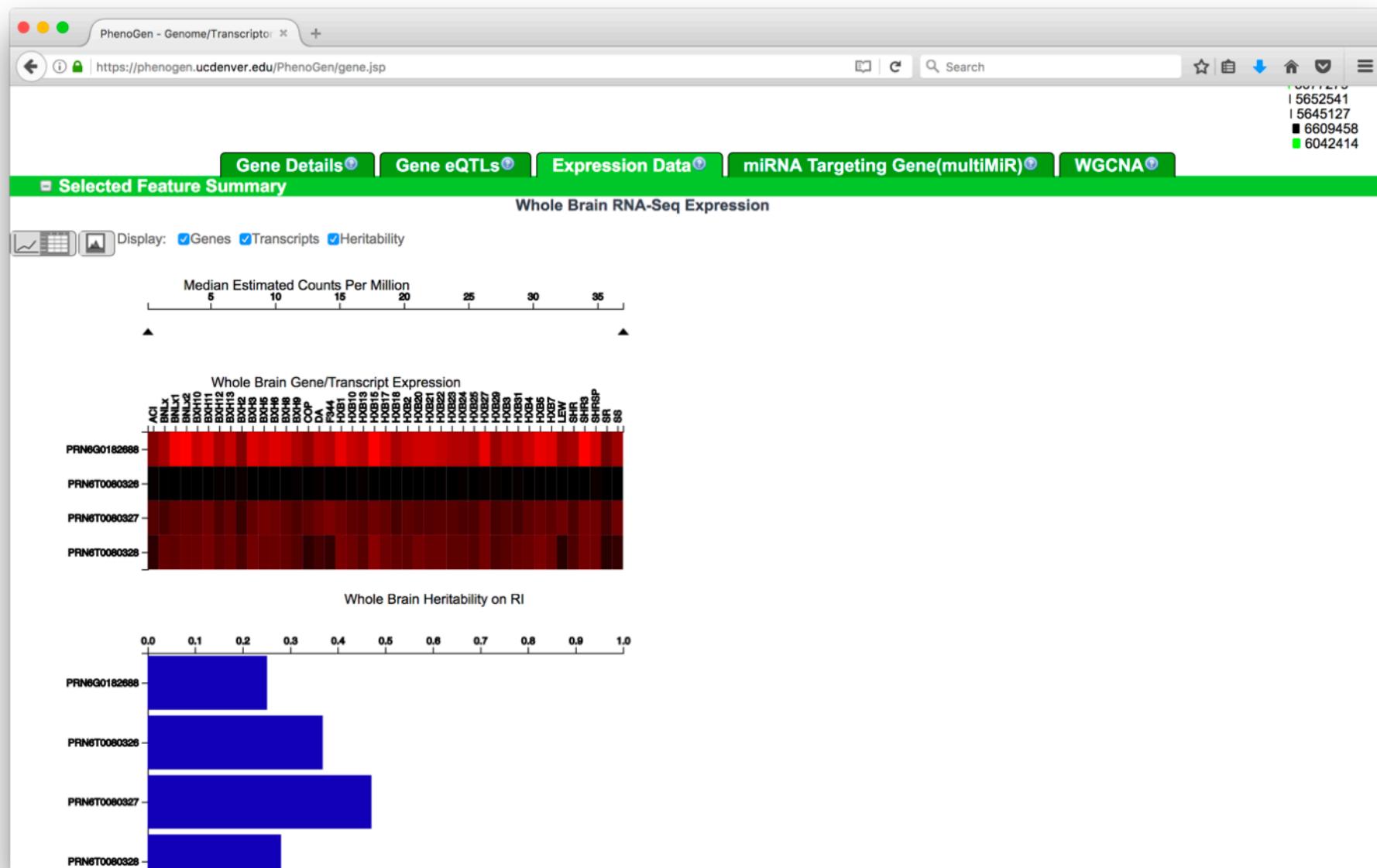
Gene eQTL



Expression Data



Expression Data - Alternative View



MicroRNA Target Binding Sites

The screenshot shows a web browser window for the Phenogen platform. The URL is https://phenogen.ucdenver.edu/PhenoGen/gene.jsp. The interface includes a navigation bar with tabs for Gene Details, Gene eQTLs, Expression Data, miRNA Targeting Gene(multiMiR), and WGCNA. A green header bar displays "Selected Feature Summary" and "multiMiR Options". Below this, validation settings like "Validation Level: All" and "Predicted Cutoff Type: Top percentage of miRNA targets" are shown. The main content area is titled "Target Information" and lists "Gene Symbol: P2rx4", "Gene Entrez ID: 29659", and "Gene Ensembl ID: ENSRNOG00000001300". The "multiMiR Results" section contains a search bar and a table comparing target prediction across various databases. The table has columns for mature miRNA accession, mature miRNA ID, and validation status (Validated or Predicted) across platforms like miRecords, miRTarBase, TarBase, DIANA-microT-CDS, EIMMo, MicroCosm, miRanda, miRDB, PicTar, PITA, and TargetScan. It also includes summary statistics for total validated, predicted, and all entries.

Mature miRNA Accession (click for miRBase)	Mature miRNA ID (click to view details)	Validated			Predicted								Total		
		miRecords	miRTarBase	TarBase	DIANA-microT-CDS	EIMMo	MicroCosm	miRanda	miRDB	PicTar	PITA	TargetScan	Total Validated	Total Predicted	Total All
MIMAT0000825	mo-miR-106b-5p	-	-	-	-	X	-	-	X	-	-	0	2	2	
MIMAT0000602	mo-miR-20a-5p	-	-	-	-	X	-	-	-	-	-	0	1	1	
MIMAT0000608	mo-miR-351-5p	-	-	-	-	X	-	-	-	-	-	0	1	1	
MIMAT0000786	mo-miR-17-5p	-	-	-	-	X	-	-	-	-	-	0	1	1	
MIMAT0000817	mo-miR-93-5p	-	-	-	-	X	-	-	-	-	-	0	1	1	
MIMAT0000829	mo-miR-125a-5p	-	-	-	-	X	-	-	-	-	-	0	1	1	
MIMAT0000830	mo-miR-125b-5p	-	-	-	-	X	-	-	-	-	-	0	1	1	
MIMAT0000839	mo-miR-133a-3p	-	-	-	-	X	-	-	-	-	-	0	1	1	
MIMAT0000895	mo-miR-291a-3p	-	-	-	-	X	-	-	-	-	-	0	1	1	
MIMAT0003126	mo-miR-133b-3p	-	-	-	-	X	-	-	-	-	-	0	1	1	
MIMAT0003211	mo-miR-20b-5p	-	-	-	-	X	-	-	-	-	-	0	1	1	
MIMAT0005323	mo-miR-532-3p	-	-	-	-	-	X	-	-	-	-	0	1	1	
MIMAT0017822	mo-miR-291b	-	-	-	-	-	X	-	-	-	-	0	1	1	

Showing 1 to 13 of 13 entries

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WEIGHTED GENE CO-EXPRESSION NETWORK ANALYSIS (WGCNA)

Weighted Gene Co-Expression Network Analysis

Why Not Just Use Correlation?

1. Simple correlation does not give connectivity.
2. How are we measuring co-expression?
 - Scale-Free Network
 - Network has few highly connected genes rather than each gene have similar connectivity
 - **Biologically motivated**, fewer highly connected genes means that a system is more robust to failure of any one gene
3. How do we get a **robust** measure of connectivity for identifying modules?
 - Topological Overlap Measure
 - Includes a measure of how many “friends” two genes have in common
 - Protects against spurious correlations among genes

Summary of Expression Pattern Within Co-Expression Module

- Eigengene
 - First Principal Component
 - Maximize the amount of variance in expression captured by a single value per strain/sample
- Hub Gene
 - Most ‘connected’ gene within a module
 - May have biological implications

WGCNA

The screenshot shows a web browser window for the PhenoGen - Genome/TranscripTOR application at <https://phenogen.ucdenver.edu/PhenoGen/gene.jsp>. The main navigation bar includes tabs for Gene Details, Gene eQTLs, Expression Data, miRNA Targeting Gene(multiMiR), and WGCNA. The WGCNA tab is currently active, indicated by a green background and white text. Below the tabs, a green header bar displays "Selected Feature Summary". The central content area shows a visualization with a red dot labeled "1" and the word "coral". On the left, there are several small icons. In the center, there are dropdown menus for "Data Source: RNA-Seq" and "Tissue: Liver". On the right, there is a "Views:" section with a radio button selected for "Module". Other options include "Eigengene eQTL", "Gene Ontology", "miRNA Targets", and "Meta Module (nearest neighbors)". At the bottom of the page, there is a footer with copyright information, links to Source Code (GitHub), Legal Notices, Privacy Policy, and social media follow buttons for Facebook, Google+, and Twitter.

PhenoGen - Genome/TranscripTOR

Gene Details Gene eQTLs Expression Data miRNA Targeting Gene(multiMiR) WGCNA

Selected Feature Summary

Data Source: RNA-Seq Tissue: Liver

Views:

- Module
- Eigengene eQTL
- Gene Ontology
- miRNA Targets
- Meta Module (nearest neighbors)

Navigation Hints: Hold mouse over areas of the image for available actions.

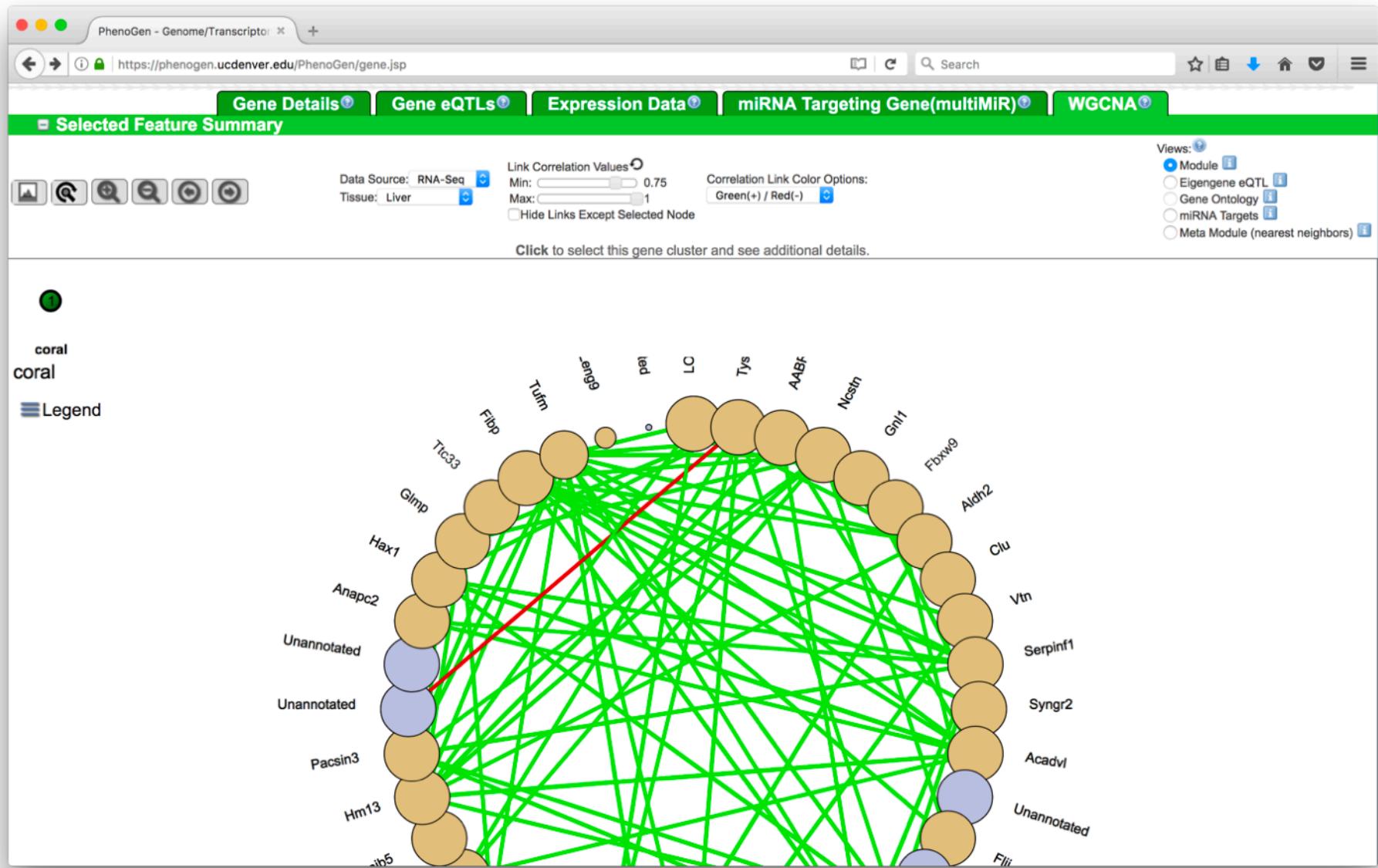
1

coral

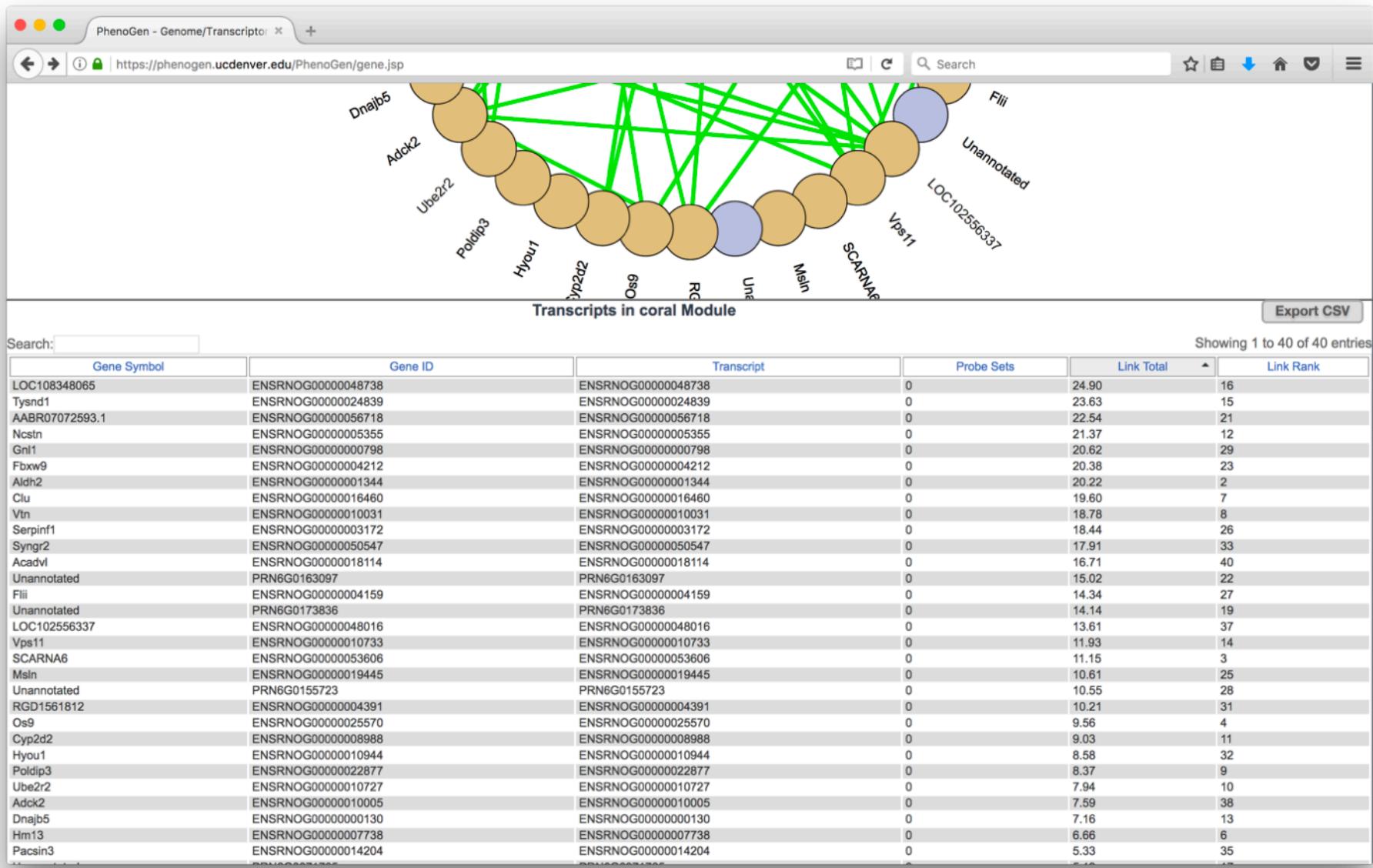
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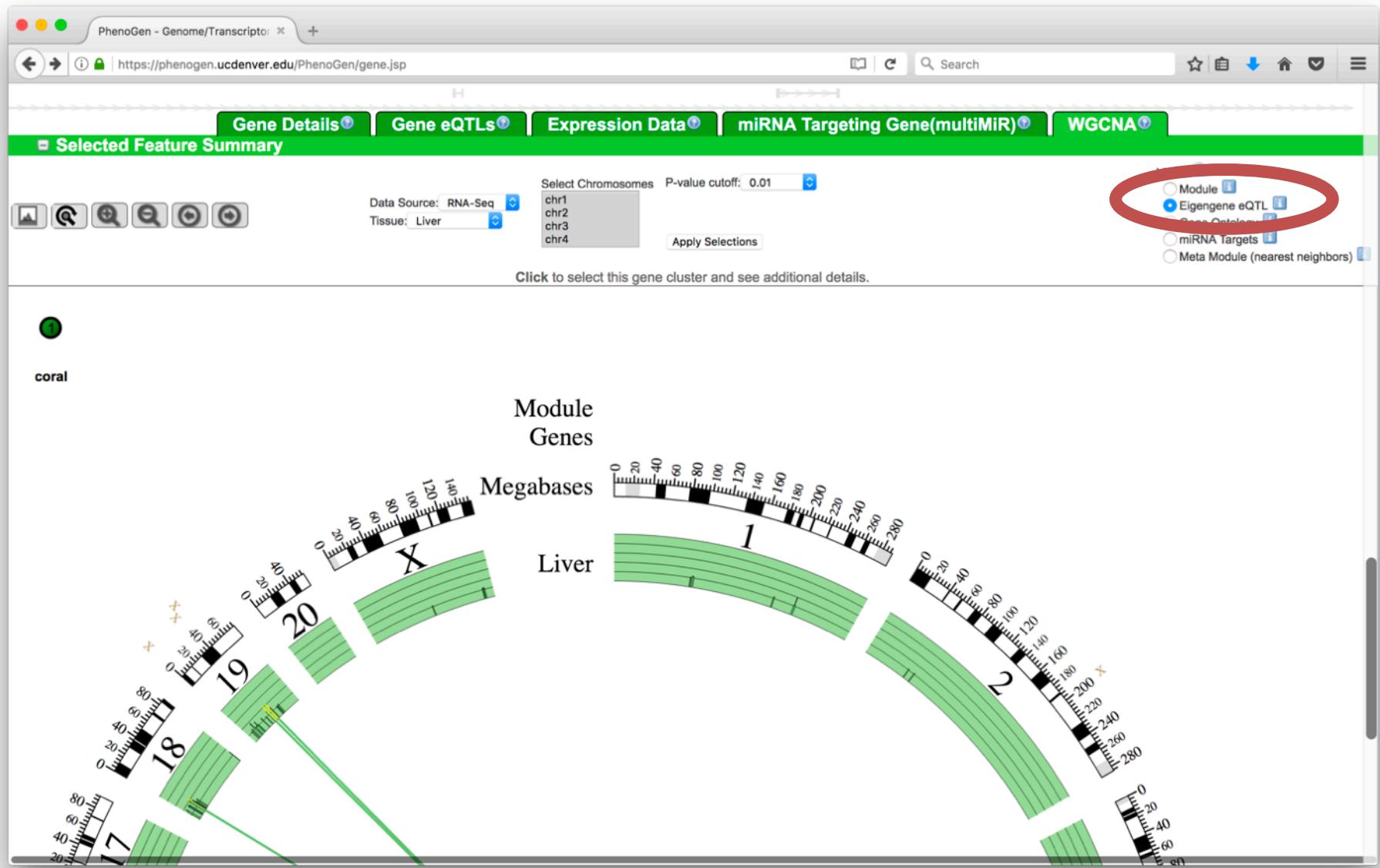
Coral Module



Coral Module Table



Eigengene eQTL

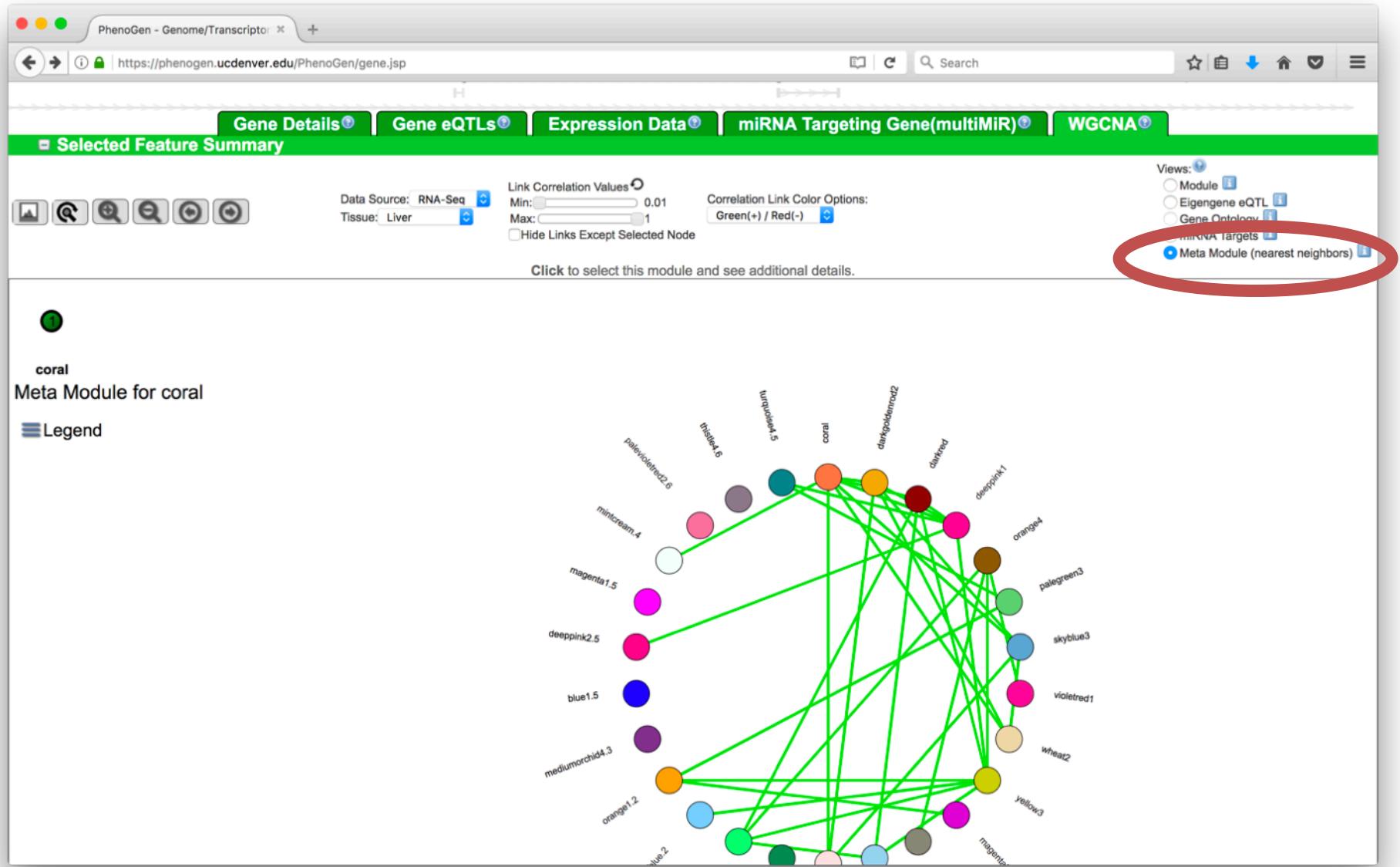


Circos

Eigengene eQTL



Meta-Modules



DOWNLOADS

Downloadable Files

- Microarray Expression Data
 - Raw
 - Processed
 - eQTL/heritability
- Genotype Data
- RNA-Seq Data
 - Raw
 - Processed
- Code
 - Github

Downloads

PhenoGen - Download Resources <https://phenogen.ucdenver.edu/PhenoGen/web/sysbio/resources.jsp>

PhenoGen Informatics
The site for quantitative genetics of the transcriptome.

Google Custom Search

Available Data Downloads

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.

Microarray RNA/DNA Sequencing Genomic Marker Publications Human Genotyping

Expression Data Files

Organism	Dataset	Tissue	Array	Expression Values	eQTL	Heritability	Masks
Mouse	Public BXD RI Mice	Whole Brain	Affymetrix GeneChip Mouse Genome 430 2.0 [Mouse430_2]				
Mouse	Public ILSXISS RI Mice	Whole Brain	Affymetrix GeneChip Mouse Exon 1.0 ST Array				
Mouse	Public Inbred Mice	Whole Brain	Affymetrix GeneChip Mouse Genome 430 2.0 [Mouse430_2]				
Rat	Public HXB/BXH RI Rats	Whole Brain	GE Healthcare CodeLink Rat Whole Genome Bioarray				
Rat	Public HXB/BXH RI Rats (Brain, Exon Arrays)	Whole Brain	Affymetrix GeneChip Rat Exon 1.0 ST Array				
Rat	Public HXB/BXH RI Rats (Heart, Exon Arrays)	Heart	Affymetrix GeneChip Rat Exon 1.0 ST Array				
Rat	Public HXB/BXH RI Rats (Liver, Exon Arrays)	Liver	Affymetrix GeneChip Rat Exon 1.0 ST Array				
Rat	Public HXB/BXH RI Rats (Brown Adipose, Exon Arrays)	Brown Adipose	Affymetrix GeneChip Rat Exon 1.0 ST Array				

*The mask files are the same for all of these datasets.

Sequencing Downloads

PhenoGen - Download Resources

https://phenogen.ucdenver.edu/PhenoGen/web/sysbio/resources.jsp

Microarray RNA/DNA Sequencing Genomic Marker Publications Human Genotyping

RNA Sequencing BED/BAM Data Files

Organism	Strain	Tissue	Seq. Tech.	RNA Type	Read Type	Genome Versions	.BED/.BAM Files
Rat	BN-Lx/CubPrin	Brain	Illumina HiSeq2000	polyA+ (>200 nt) selected	100 bp paired-end	Rn6, Rn5	
Rat	SHR/OlaIpcvPrin	Brain	Illumina HiSeq2000	polyA+ (>200 nt) selected	100 bp paired-end	Rn6, Rn5	
Rat	BN-Lx/CubPrin	Brain	Illumina HiSeq2000	total RNA (>200 nt) after ribosomal RNA depletion	100 bp paired-end	Rn6, Rn5	
Rat	SHR/OlaIpcvPrin	Brain	Illumina HiSeq2000	total RNA (>200 nt) after ribosomal RNA depletion	100 bp paired-end	Rn6, Rn5	
Rat	BN-Lx/CubPrin	Brain	Illumina HiSeq2000	small RNA (<200 nt) selected	50 bp single-end	Rn5	
Rat	SHR/OlaIpcvPrin	Brain	Illumina HiSeq2000	small RNA (<200 nt) selected	50 bp single-end	Rn5	
Rat	BN-Lx/CubPrin	Brain	Helicos	total RNA (>200 nt) after ribosomal RNA depletion	~33 bp single-end	Rn5	
Rat	SHR/OlaIpcvPrin	Brain	Helicos	total RNA (>200 nt) after ribosomal RNA depletion	~33 bp single-end	Rn5	
Rat	BN-Lx/CubPrin	Heart	Illumina HiSeq2000	total RNA (>200 nt) after ribosomal RNA depletion	stranded 100 bp paired-end	Rn6	
Rat	SHR/OlaIpcvPrin	Heart	Illumina HiSeq2000	total RNA (>200 nt) after ribosomal RNA depletion	stranded 100 bp paired-end	Rn6	
Rat	BN-Lx/CubPrin	Liver	Illumina HiSeq2000	total RNA (>200 nt) after ribosomal RNA depletion	stranded 100 bp paired-end	Rn6	
Rat	SHR/OlaIpcvPrin	Liver	Illumina HiSeq2000	total RNA (>200 nt) after ribosomal RNA depletion	stranded 100 bp paired-end	Rn6	

Strain-specific Rat Genomes

Organism	Strain	Seq. Tech.	Genome Version	.fasta Files
Rat	BN-Lx/CubPrin	Illumina HiSeq2000	Rn6, Rn5	
Rat	SHR/OlaIpcvPrin	Illumina HiSeq2000	Rn6, Rn5	
Rat	SHR/NCrIPrin	Illumina HiSeq2000	Rn5	
Rat	presumptive F344*	Illumina HiSeq2000	Rn5	

Links to Reference Rat Genome(Strain BN): [FTP NCBI-Rn6](#) [FTP Ensembl-Rn5](#) [FTP Ensembl-Rn6](#)

RNA-Seq Transcriptome Reconstruction

Organism	Strains	Tissue	Assembled by	.gtf Files
Rat	BN-Lx/CubPrin, SHR/OlaIpcvPrin	Whole Brain	Cufflinks	
Rat	BN-Lx/CubPrin, SHR/OlaIpcvPrin	Heart	Cufflinks	
Rat	BN-Lx/CubPrin, SHR/OlaIpcvPrin	Liver	Cufflinks	

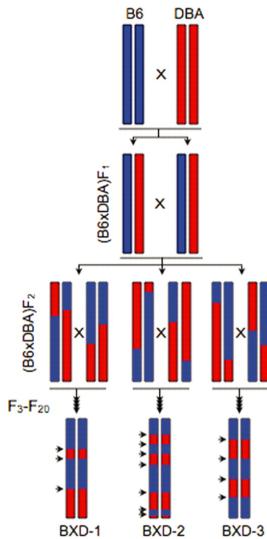
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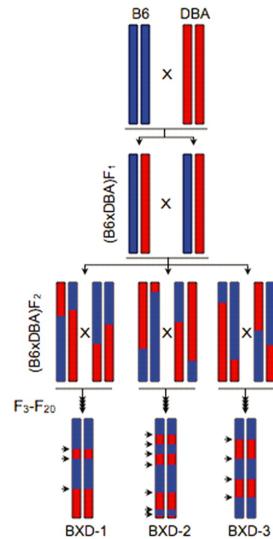
FUTURE DIRECTIONS

Data to Add

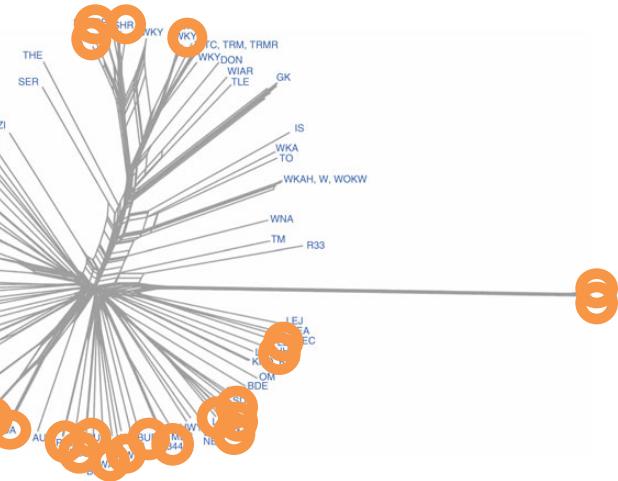
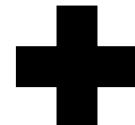
The Hybrid Rat Diversity Panel



30 HXB/BXH
Recombinant
Inbred Strains



32 LEXF/FXLE
Recombinant
Inbred Strains



34 Classic Inbred Strains

Brain, Liver, and Heart
(total RNA and small RNA)

Updated Analyses

- Protein-coding potential of novel transcripts
- Alternative Polyadenylation
- Network techniques for integrating protein-coding and non-coding
- Bayesian networks