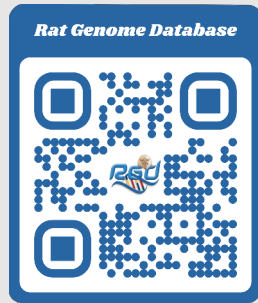


Navigating public resources for quantitative genetics, phenotypes and omics data for my research

Complex Trait Community – Rat Genomics Meeting October 2024

Mahima Vedi - Rat Genome Database



[Home](#)[Data](#)[Analysis & Visualization](#)[Diseases](#)[Phenotypes & Models](#)[Pathways](#)[Community](#)[Advanced Search \(OLGA\)](#)[OntoMate \(Literature Search\)](#)[JBrowse \(Genome Browser\)](#)[Synteny Browser \(VCMaP\)](#)[Variant Visualizer](#)[Multi-Ontology Enrichment \(MOET\)](#)[Gene-Ortholog Location Finder \(GOLF\)](#)[InterViewer \(Protein-Protein Interactions\)](#)[PhenoMiner \(Quatitative Phenotypes\)](#)[Gene Annotator](#)[OLGA \(Gene List Generator\)](#)[AllianceMine](#)[GViewer \(Genome Viewer\)](#)

RGD virtual office hours are available by appointment. [Contact us](#) to schedule a

[Other Species Portals](#)

Visualization

Variant Visualizer

| Variant | C | A | T | |
|-------------------|---|---|---|---|
| ACI/N (KNAW) | A | C | A | T |
| BBDP/WorN (ICL) | G | C | G | T |
| ACI/EurMcwi (ICL) | A | C | A | T |
| BN-Lx/Cub (ICL) | G | A | G | C |

VCMaP

Synteny Browser



OLGA

Gene List Generator

(hypertension INTERSECT synaptic signal)

764

Disease Portals



Phenotypes and Models





v1.0.3

Backbone

Backbone Species

Rat



Backbone Assembly

mRatBN7.2 (primary)



Load by:



Gene



Position



Flanking Genes

Gene Symbol

Mthfr (Chr5)

Chromosome: 5 (Length: 166,875,058 bp)

Gene Start: 158465248 bp

Gene Stop: 158484999 bp

Comparative Species

+ Add Species

Human



GRCh38 (primary)



Remove

Mouse



GRCm39 (primary)



Remove

Clear All

▶ Load VCMaP

Visibility

Species: ☒ Rat ☒ Human ☒ Mouse

☒ Overview Panel

☐ Mirrored Overview

Navigation

Search and Select Gene ⓘ

Search loaded genes...

Viewed Regions ⓘ

Select from history... ▼

Rat Chr5:158,346,742 - 158,603,505

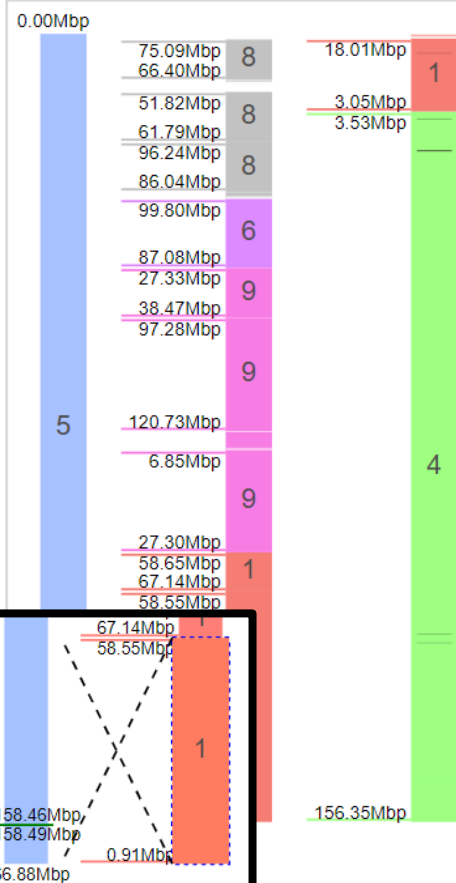
Zoom Out << < < <

649.92x

>> >> >> >> Zoom In

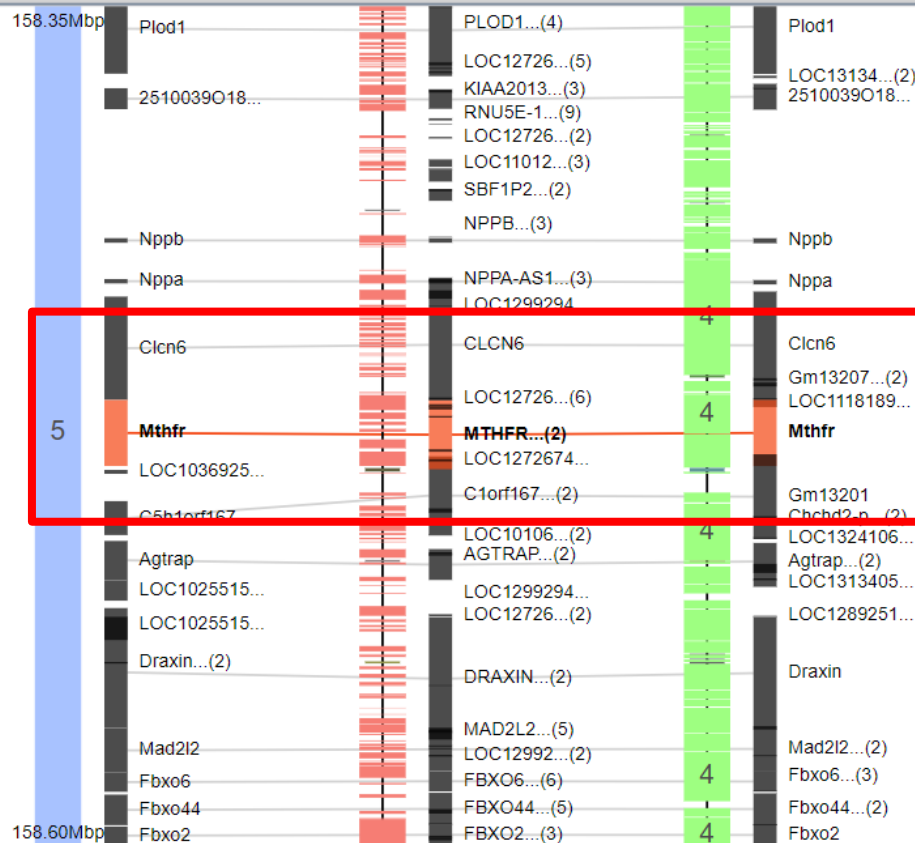
Overview

Rat mRatBN7.2 Human GRCh38 Mouse GRCh39



Detailed

Rat mRatBN7.2 Genes Human GRCh38 Genes Mouse GRCh39 Genes



Selected Data

3 Selected Genes

Mthfr (methylenetetrahydrofolate reductase)

Rat Chr5: 158,465,248 - 158,484,999

[View RGD Gene Report](#)

[View in RGD JBrowse](#)

MTHFR (methylenetetrahydrofolate reductase)

Human Chr1: 11,785,723 - 11,805,964

[View RGD Gene Report](#)

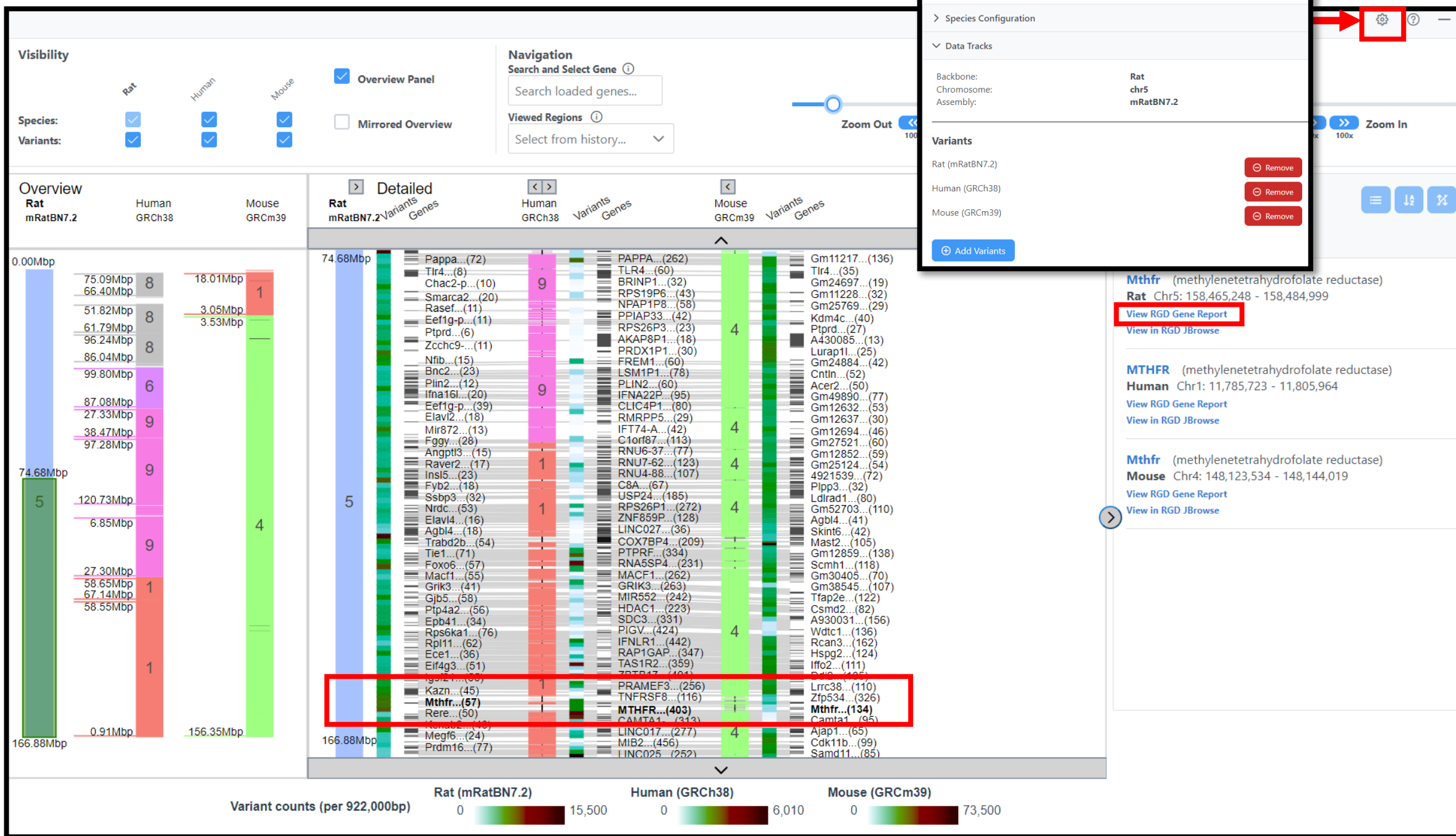
[View in RGD JBrowse](#)

Mthfr (methylenetetrahydrofolate reductase)

Mouse Chr4: 148,123,534 - 148,144,019

[View RGD Gene Report](#)

[View in RGD JBrowse](#)



Settings

> Species Configuration

▼ Data Tracks

Backbone: Rat
Chromosome: chr5
Assembly: mRatBN7.2

Variants


Rat (mRatBN7.2) [Remove]
Human (GRCh38) [Remove]
Mouse (GRCm39) [Remove]

[Add Variants]

Mthfr (methylenetetrahydrofolate reductase)
Rat Chr5: 158,465,248 - 158,484,999
[View RGD Gene Report](#)
[View in RGD JBrowse](#)

MTHFR (methylenetetrahydrofolate reductase)
Human Chr1: 11,785,723 - 11,805,964
[View RGD Gene Report](#)
[View in RGD JBrowse](#)

Mthfr (methylenetetrahydrofolate reductase)
Mouse Chr4: 148,123,534 - 148,144,019
[View RGD Gene Report](#)
[View in RGD JBrowse](#)



Gene: Mthfr (methylenetetrahydrofolate reductase) Rattus norvegicus

General

Symbol: Mthfr
Name: methylenetetrahydrofolate reductase
RGD ID: 1309952
Description: Enables NADP binding activity; interleukin-1; and response to vitamin B12 deficiency; cardiovascular disease; metabolic pathway; altered folate metabolism
Type: protein-coding
RefSeq Status: **VALIDATED**
Previously known as: 5,10-methylenetetrahydrofolate reductase

Array IDs

Assembly: mRatBN7.2
View all Variants in Variant Visualizer

☐ Exon ☐ Intron ☒ All

Summary

Mthfr has 281 RGD Records - Rattus norvegicus

Annotation

- RGD Manual Disease
- Imported Disease - ClinVar
- Imported Disease - CTD
- Imported Disease - MGI
- Imported Disease - OMIM
- Gene-Chemical Interaction
- Gene Ontology
- Molecular Pathway
- Phenotype
- Mammalian Phenotype

References

- References - curated
- PubMed References

Genomics

- Comparative Map Data
- Variants**
- Damaging Variants
- miRNA Target Status
- QTLs in Region (mRatBN7.2)
- Genetic Models

Expression

- RNA-SEQ Expression

Sequence

- Nucleotide Sequences
- Reference Sequences

Variant Visualizer

Home Edit Strains Edit Gene List Assembly mRatBN7.2

Select samples to compare

Select Sequence Group (Optional)

☒ Classic Inbred Strains ☐ FXLE/LEFX Recombinant Inbred Panel ☐ HXB/BXH Recombinant Inbred Panel

Select Samples

| | | |
|--|--|--|
| <input checked="" type="checkbox"/> ACI/EurMcwi (2019) | <input checked="" type="checkbox"/> F344/StmMcwi (2019) | <input type="checkbox"/> HXB18/lpc |
| <input checked="" type="checkbox"/> ACI/EurMcwi (2019NG) | <input checked="" type="checkbox"/> FHH/EurMcwi (2019) | <input type="checkbox"/> HXB20/lpcv |
| <input checked="" type="checkbox"/> ACI/N (2020) | <input checked="" type="checkbox"/> FHH/EurMcwi (2019NG) | <input type="checkbox"/> HXB20/lpc |
| <input checked="" type="checkbox"/> BDIX/NemOdaMcwi (2022) | <input type="checkbox"/> FXLE12/Stm (2019NG) | <input type="checkbox"/> HXB23/lpc |
| <input checked="" type="checkbox"/> BN-Lx/CubMcwi (2019) | <input type="checkbox"/> FXLE12/StmMcwi (2021) | <input type="checkbox"/> HXB31/lpc |
| <input checked="" type="checkbox"/> BN-Lx/CubMcwi (2019NG) | <input type="checkbox"/> FXLE12/StmMcwi (2023) | <input type="checkbox"/> HXB4/lpcv |
| <input checked="" type="checkbox"/> BN/Crl (2021) | <input type="checkbox"/> FXLE13/Stm (2019NG) | <input checked="" type="checkbox"/> LE/Stm (2019) |
| <input checked="" type="checkbox"/> BN/HsdMcwi (2019) | <input type="checkbox"/> FXLE13/StmMcwi (2023) | <input checked="" type="checkbox"/> LEW/Crl (2019) |
| <input checked="" type="checkbox"/> BN/NHsdMcwi (2019NG) | <input type="checkbox"/> FXLE14/Stm (2019NG) | <input checked="" type="checkbox"/> LEW/Crl (2019NG) |
| <input checked="" type="checkbox"/> BN/NHsdMcwi (2020) | <input type="checkbox"/> FXLE14/StmMcwi (2023) | <input type="checkbox"/> LEXF10A/StmMc |
| <input checked="" type="checkbox"/> BN/NHsdMcwi (2021) | <input type="checkbox"/> FXLE15/Stm (2019NG) | <input type="checkbox"/> LEXF10B/StmMc |
| <input checked="" type="checkbox"/> BN/NHsdMcwi (2022) | <input type="checkbox"/> FXLE15/StmMcwi (2021) | <input type="checkbox"/> LEXF10C/Stm (20 |
| <input checked="" type="checkbox"/> BN/NHsdMcwi (2023) | <input type="checkbox"/> FXLE15/StmMcwi (2023) | <input type="checkbox"/> LEXF10C/StmMc |
| <input checked="" type="checkbox"/> BN/Rij (2021) | <input type="checkbox"/> FXLE16/Stm (2020) | <input type="checkbox"/> LEXF11/Stm (202 |
| <input checked="" type="checkbox"/> BN/SsN (2020) | <input type="checkbox"/> FXLE17/Stm (2019NG) | <input type="checkbox"/> LEXF1A/Stm (20 |
| <input checked="" type="checkbox"/> BUF/MnaMcwi (2022) | <input type="checkbox"/> FXLE17/StmMcwi (2023) | <input type="checkbox"/> LEXF1C/Stm (20 |
| <input checked="" type="checkbox"/> BUF/N (2020) | <input type="checkbox"/> FXLE18/Stm (2020) | <input type="checkbox"/> LEXF1C/StmMcw |
| <input type="checkbox"/> BXH2/CubMcwi (2020) | <input type="checkbox"/> FXLE19/StmMcwi (2022) | <input type="checkbox"/> LEXF2A/Stm (20 |
| <input type="checkbox"/> BXH2/CubMcwi (2023) | <input type="checkbox"/> FXLE20/Stm (2020NG) | <input type="checkbox"/> LEXF2A/StmMcw |
| <input type="checkbox"/> BXH2/CubMcwi (2023) | <input type="checkbox"/> FXLE20/StmMcwi (2023) | <input type="checkbox"/> LEXF2B/Stm (20 |

Full-screen view

General

Strain: SS-Mthfr^{em1}Mcwi

Symbol: SS-Mthfr^{em1}Mcwi
Strain: SS-Mthfr^{em1}
Substrain: Mcwi
RGD ID: 5131965
Citation ID: RRID:RGD_5131965
Ontology ID: RS:0002594
Alleles: Mthfr^{em1}Mcwi
Also Known As: SS-Mthfr^{em1}Mcwi; SS-Mthfr^{em1}Mcwi
Type: mutant
Available Source: Not Available
Origination: PhysGen Knockouts
Description: This strain was produced by injecting ZFNs targeting the sequence CCCCAGCCCCGATCtgaggCGACGAGCAOTGGCA into SS/JrHsdMcwi (2019NG) embryos.
Last Known Status: Cryopreserved Sperm (as of 2017-01-26)

| Rat Assembly | Chr | Position (strand) | Source | JBrowse |
|--------------|-----|---------------------------|---------------------|-----------|
| mRatBN7.2 | 5 | 158,467,728 - 158,467,755 | RGD_MAPPER_PIPELINE | mRatBN7.2 |
| Rnor_6.0 | 5 | 164,844,642 - 164,844,360 | RGD_MAPPER_PIPELINE | Rnor6.0 |
| Rnor_5.0 | 5 | 168,502,556 - 168,522,350 | RGD_MAPPER_PIPELINE | Rnor5.0 |
| RGSC_v3.4 | 5 | 165,112,850 - 165,126,885 | RGD_MAPPER_PIPELINE | RGSC3.4 |

Position

158,467,728 158,467,755 164,844,642 164,844,360 168,502,556 168,522,350 165,112,850 165,126,885

Mutant Strains

| | |
|--------------------------------|--------------------------------|
| SS-Mthfr ^{em1} Mcwi/+ | SS-Mthfr ^{em1} Mcwi/+ |
|--------------------------------|--------------------------------|

Genome

Location ☐ Intergenic ☐ Genic ☐ Near Splice Site
☐ Intron ☐ 3 Prime UTR ☐ 5 Prime UTR
Variant Type ☐ SNV ☐ Insertion ☐ Deletion
Limit to ☐ Coding Exon ☐ Frameshift ☐ Premature Stop ☐ Readthrough

Protein

Amino Acid Change ☐ Synonymous ☐ Non-Synonymous
Polyphen Prediction ☒ Probably Damaging ☒ Possibly Damaging ☐ Benign

Call Statistics

Depth of Coverage Minimum Reads 1 Maximum Reads
Total Alleles Read ☐ 1 ☐ 2 ☐ 3 ☐ 4
Zygosity ☐ Heterozygous ☐ Homozygous ☐ Possibly Homozygous ☐ Exclude Low Read Percentage
2 alleles called between 15% and 85% of reads
Variant read in 100% of reads
Variants read in 85% to 99% of reads
Variant read in less than 15% of reads

Chromosome 5

Start Position 158,465,248 Stop Position 158,484,999 Update

Genes (+) Mthfr
Genes (-) --
mRatBN7.2 C

158,477,420

| | |
|--------------------------|---|
| SHR/OlaIpcvMcwi (2019NG) | - |
| SHRSP/A3NCrl (2019) | G |
| SHRSP/A3NCrl (2019NG) | G |
| SR/JrHsd (2020) | - |
| SS/HsdMcwiCrl (2021) | - |
| SS/JrHsd (2021) | - |
| SS/JrHsdMcwi (2019) | - |
| SS/JrHsdMcwi (2019NG) | - |
| WAG/RijCrl (2020) | - |
| WKY/N (2020) | G |
| WKY/NCrl (2019) | G |



Gene: MTHFR (methylenetetrahydrofolate reductase) Homo sapiens

Summary

Annotation

- RGD Manual Disease
- Imported Disease - ClinVar
- Imported Disease - CTD
- Imported Disease - MGI
- Imported Disease - OMIM
- Gene-Chemical Interaction
- Gene Ontology
- Molecular Pathway
- Phenotype
- Manual Human Phenotype -
- Imported Human Phenotype -
- Imported Human Phenotype -

References

- References - curated
- PubMed References

Genomics

- Comparative Map Data
- Variants**
- Clinical Variants
- miRNA Target Status
- QTLs in Region (GRCh38)
- Markers in Region

Expression

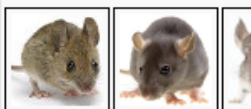
- BNA-SEQ Expression

General

Array IDs

Symbol: MTHFR
Name: methylenetetrahydrofolate reductase
RGD ID: 733483
HGNC Page: [HGNC:7436](#)
Description: Enables flavin adenine dinucleotide-dependent methylenetetrahydrofolate interconversions (multiple); and liver disease
Type: protein-coding
RefSeq Status: [REVIEWED](#)
Previously known as: 5,10-methylenetetrahydrofolate reductase

RGD Orthologs



Alliance Orthologs



More Info

[more info ...](#)


Allele / Splice: [See ClinVar data](#)
Latest Assembly: GRCh38 - Human Genome
Position:

| Human Assembly | Chr | Position (strand) |
|------------------------|-----|-----------------------------|
| GRCh38 | 1 | 11,785,723 - 11,805,964 (-) |
| GRCh38.p14 Ensembl | 1 | 11,785,723 - 11,806,455 (-) |
| GRCh37 | 1 | 11,845,780 - 11,866,021 (-) |
| Build 36 | 1 | 11,768,374 - 11,788,702 (-) |
| Build 34 | 1 | 11,780,944 - 11,800,248 |
| Celera | 1 | 10,959,433 - 10,979,782 (-) |
| Cytogenetic Map | 1 | p36.22 |
| HuRef | 1 | 11,000,872 - 11,021,217 (-) |
| CHM1_1 | 1 | 11,833,709 - 11,854,054 (-) |
| T2T-CHM13v2.0 | 1 | 11,329,802 - 11,350,048 (-) |

JBrowse:

[View Region in Genome Browser \(JBrowse\)](#)

| | | |
|-----------|--------------|------------|
| 1,775,000 | | 11,787,500 |
| | XM_005263463 | |
| | XM_011541496 | |
| | XM_017881388 | |



Home ▾ Data ▾ Analysis & Visualization ▾ Diseases ▾ Phenotypes & Models ▾ Pathways ▾ Community ▾

Advanced Search (OLGA)

Home Edit Sequences Edit Gene List Sequence Annotation Assembly GRCh38

Chromosome 1 Start Position 11,785,723 Stop Position 11,805,964

| Conservation | 1.0 | 1.0 | 0.001 | 1.0 | 0.011 | 0.008 | 1.0 | 0.041 | 1.0 | 0.325 | 0.001 | 0 | 0.001 | 0 | 0 | 1.0 | 1.0 | 0 | 0.997 | 0.979 | 0 | 1.0 | 0 | 0 | 1.0 | 1.0 | 0.008 | 1.0 | 0.998 | | |
|---------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----|---|
| Genes (+) | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | | | |
| Genes (-) | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | C | G | C | G | A | G | C | G | C | G | C | G | C | G | C | C | A | A | C | G | C | G | T | C | A | A | A | G | A | T | T |
| | 11,794,036 | 11,794,045 | 11,794,054 | 11,794,066 | 11,794,069 | 11,794,072 | 11,794,075 | 11,794,081 | 11,794,090 | 11,794,093 | 11,794,094 | 11,794,100 | 11,794,338 | 11,794,342 | 11,794,349 | 11,794,356 | 11,794,357 | 11,794,361 | 11,794,371 | 11,794,372 | 11,794,376 | 11,794,385 | 11,794,389 | 11,794,395 | 11,794,400 | 11,794,401 | 11,794,415 | 11,794,417 | 11,794,419 | | |
| ClinVar GRCh38 | CTT | GAA | CTT | GAA | GAA | CTT | GCA | GCG | GCG | GAA | CTT | CTA | AGG | AGG | CTT | CTA | AGG | AGG | CTT | GAA | TAT | ATG | ATG | ATG | GAA | GAA | AGG | ATC | ATG | CTA | |
| GWAS Catalog GRCh38 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | |

Variant Details

rs1801131

| | | | |
|-----------------------|----------------------------|------------------------------------|--|
| Source: | ClinVar GRCh38 | Variant Type: | snv |
| Assembly: | GRCh38 | Related Variants: | n/a |
| Position: | Chromosome: 1 - 11,794,419 | Conservation: | 0.968 (High sequence conservation) |
| Reference Nucleotide: | T | Clinical Significance: | likely pathogenic[risk factor]benign[likely benign]conflicting interpretations of pathogenicity[drug response]uncertain significance[no classifications from unflagged records]other[not provided] |
| Variant Nucleotide: | G | Condition: | Gastrointestinal stromal tumor [RCV000144922]Homocystinuria due to methylene tetrahydrofolate reductase deficiency [RCV001197542]MTHFR THERMOLABILE POLYMORPHISM [RCV000003698]MTHFR-related disorder [RCV003974792]Neural tube defects, folate-sensitive [RCV000350590]Schizophrenia, susceptibility to [RCV000003699]not provided [RCV000153515]not specified [RCV000430863] |
| Location: | GENIC | VID: | 8596141 |
| | | Go to Variant Page | |

Transcripts

| | |
|------------------------|------------------------|
| Gene Symbol: | MTHFR |
| Accession: | XM_005263463 |
| Location: | EXON |
| Amino Acid Prediction: | E to A (nonsynonymous) |

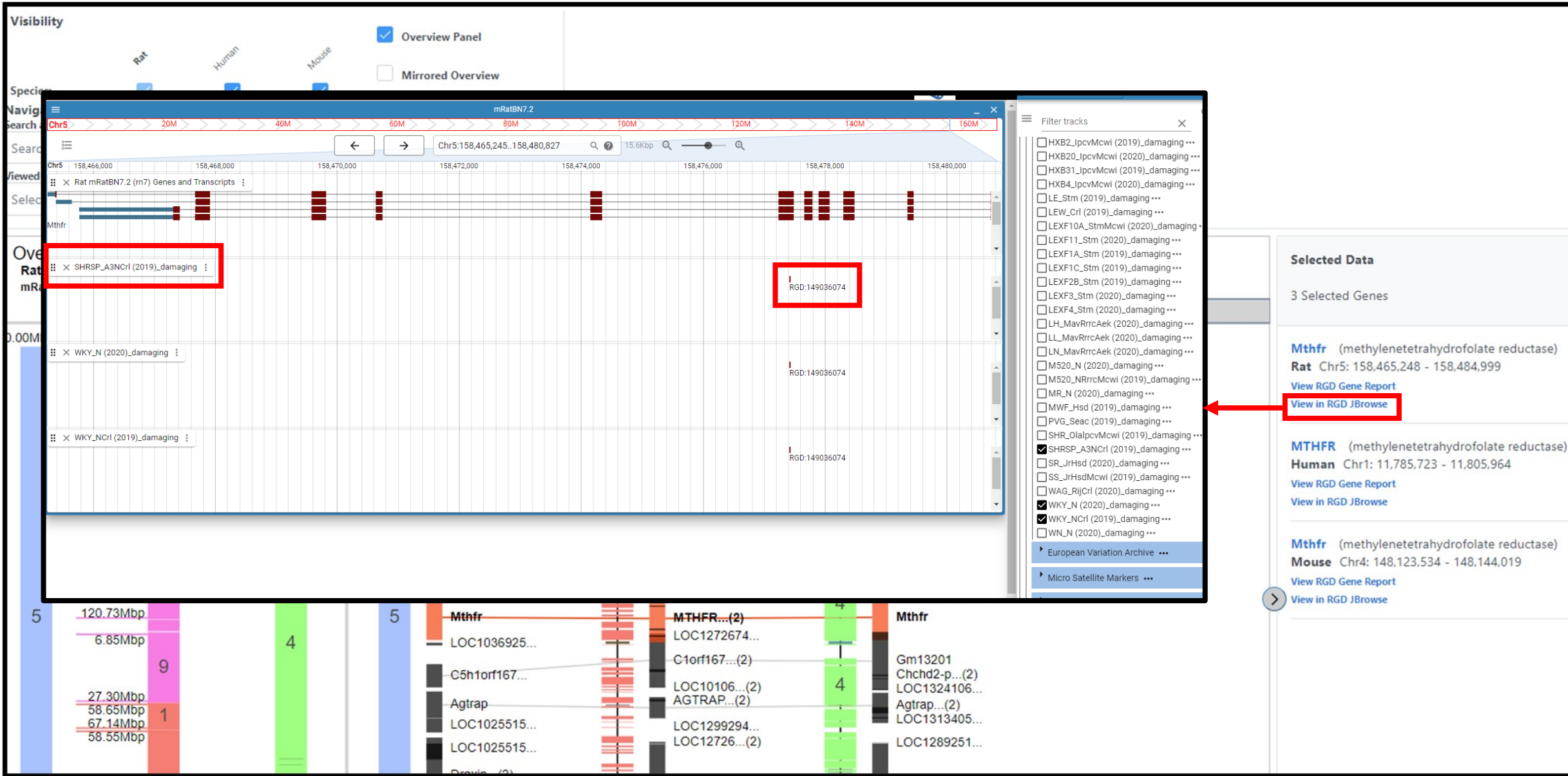
Variant Details

rs1801131

| | | | |
|-----------------------|----------------------------|------------------------------------|--|
| Source: | GWAS Catalog GRCh38 | Variant Type: | snv |
| Assembly: | GRCh38 | Related Variants: | n/a |
| Position: | Chromosome: 1 - 11,794,419 | Conservation: | 0.968 (High sequence conservation) |
| Reference Nucleotide: | T | Clinical Significance: | likely pathogenic[risk factor]benign[likely benign]conflicting interpretations of pathogenicity[drug response]uncertain significance[no classifications from unflagged records]other[not provided] |
| Variant Nucleotide: | G | Condition: | Gastrointestinal stromal tumor [RCV000144922]Homocystinuria due to methylene tetrahydrofolate reductase deficiency [RCV001197542]MTHFR THERMOLABILE POLYMORPHISM [RCV000003698]MTHFR-related disorder [RCV003974792]Neural tube defects, folate-sensitive [RCV000350590]Schizophrenia, susceptibility to [RCV000003699]not provided [RCV000153515]not specified [RCV000430863] |
| Location: | GENIC | VID: | 8596141 |
| | | Go to Variant Page | |

Transcripts

| | |
|------------------------|------------------------|
| Gene Symbol: | MTHFR |
| Accession: | XM_005263463 |
| Location: | EXON |
| Amino Acid Prediction: | E to A (nonsynonymous) |



Visibility

Species: ☒ Rat ☒ Human ☒ Mouse

☒ Overview Panel

☐ Mirrored Overview

Navigation

Search and Select Gene ⓘ

Search loaded genes...

Viewed Region

Select from

Overview

Rat

mRatBN7.2

0.00Mbp

5

6.85Mbp

27.30Mbp

58.65Mbp

67.14Mbp

58.55Mbp

9

1

4

LOC1036925...

C5h1orf167...

Agtrap

LOC1025515...

LOC1025515...

LOC1036925...

C1orf167...(2)

LOC10106...(2)

AGTRAP...(2)

LOC1299294...

LOC12726...(2)

Gm13201

Chchd2-p...(2)

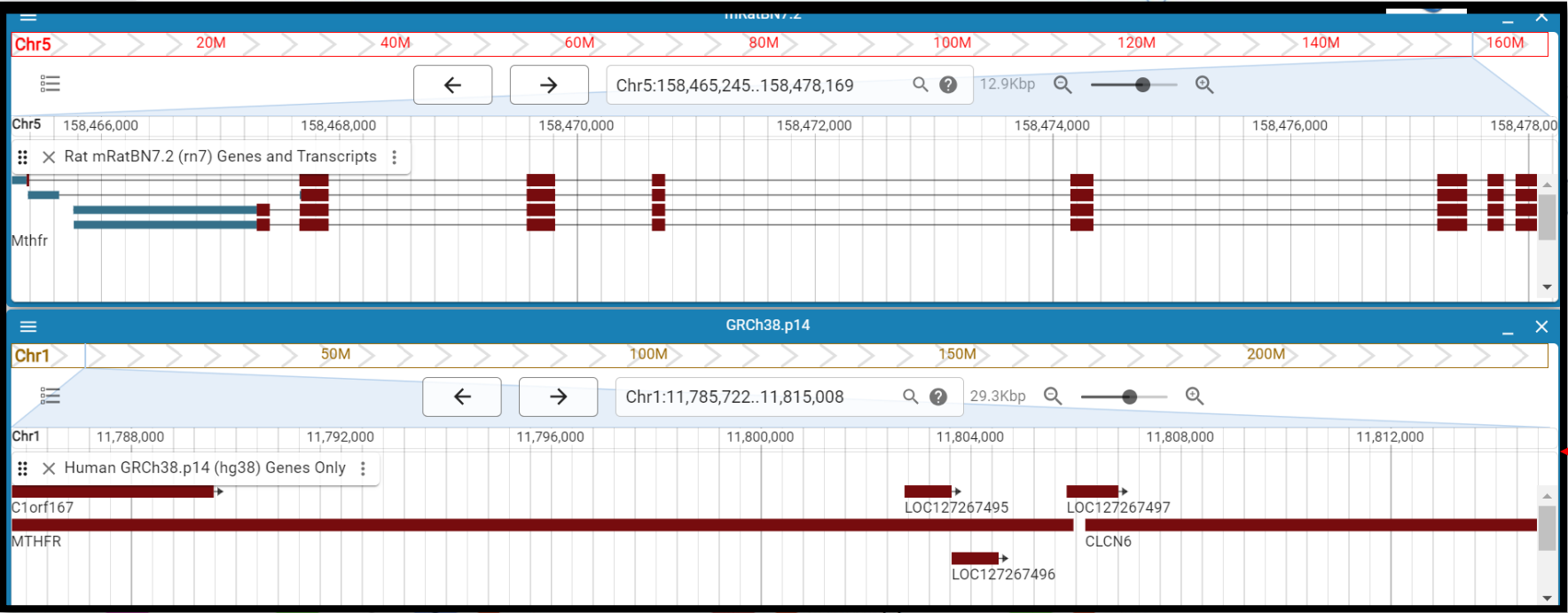
LOC1324106...

Agtrap...(2)

LOC1313405...

LOC1289251...

Rat Chr5:158,346,742 - 158,603,505



Selected Data

3 Selected Genes

Mthfr (methylenetetrahydrofolate reductase)
Rat Chr5: 158,465,248 - 158,484,999

[View RGD Gene Report](#)

[View in RGD JBrowse](#)

MTHFR (methylenetetrahydrofolate reductase)
Human Chr1: 11,785,723 - 11,805,964

[View RGD Gene Report](#)

[View in RGD JBrowse](#)

Mthfr (methylenetetrahydrofolate reductase)
Mouse Chr4: 148,123,534 - 148,144,019

[View RGD Gene Report](#)

[View in RGD JBrowse](#)

[Home](#)[Data](#)[Analysis & Visualization](#)[Diseases](#)[Phenotypes & Models](#)[Pathways](#)[Community](#)[Advanced Search \(OLGA\)](#)

RGD virtual office hours are available by appointment. [Contact us](#) to schedule a time.

Other Species Portals

[OntoMate \(Literature Search\)](#)[JBrowse \(Genome Browser\)](#)[Synteny Browser \(VCMaP\)](#)[Variant Visualizer](#)[Multi-Ontology Enrichment \(MOET\)](#)[Gene-Ortholog Location Finder \(GOLF\)](#)[InterViewer \(Protein-Protein Interactions\)](#)[PhenoMiner \(Quatitative Phenotypes\)](#)[Gene Annotator](#)[OLGA \(Gene List Generator\)](#)[AllianceMine](#)[GViewer \(Genome Viewer\)](#)

Ontology & Annotation Ontomate (Literature) QTL Orthologs Genomic Region All...

Visualization

Variant Visualizer

| | C | A | T |
|-------------------|---|---|---|
| ACI/N (KNAW) | A | C | A |
| BBDP/WorN (ICL) | G | C | G |
| ACI/EurMcwi (ICL) | A | C | A |
| BN-Lx/Cub (ICL) | G | A | G |

VCMap
Synteny Browser



OLGA
Gene List Generator

(hypertension INTERSECT synaptic signal)

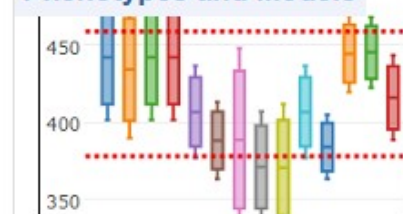
764

| | | |
|---|---|---|
| <input checked="" type="checkbox"/> Abet | <input checked="" type="checkbox"/> Intersect | <input checked="" type="checkbox"/> AAB |
| <input checked="" type="checkbox"/> Abca3 | | <input checked="" type="checkbox"/> AAB |
| <input checked="" type="checkbox"/> Abcc1 | | <input checked="" type="checkbox"/> AAB |
| <input checked="" type="checkbox"/> Abcc2 | | <input checked="" type="checkbox"/> AAB |

Disease Portals



Phenotypes and Models



PhenoMiner Database

Select a Category Tab in the lower right panel, then select values from categories of interest and select **"Generate Report"** to build report

☒ Rat Phenominer ☐ Chinchilla Phenominer

Clear

Vertebrate Traits

Filter based trait.

Rat Strains

Search for data related to one or more rat strains.

Clinical Measurements

Query by clinical measurement.

Measurement Methods

Filter results by Measurement method.

Experimental Conditions

Filter based condition.

Click on 'Generate Report' to view the results.

Generate Report

Vertebrate Trait Selection

pressure

select blood albumin amount(1394)
select venous blood pressure trait(2)
select arterial blood pressure trait(4956)
select pulmonary arterial blood pressure trait(4)
select heart left ventricular blood pressure trait(2109)
select heart right ventricular blood pressure trait(4)

Start Here

Vertebrate Traits Strains Clinical Measurements Measurement Methods Experimental Conditions

organ system trait(47878)
alimentary system trait(1174)
circulatory system trait(21809)
circulatory system morphology trait(4371)
circulatory system physiology trait(17438)
cardiovascular system physiology trait(17438)
blood physiology trait(9773)
hemodynamics trait(9346)
blood flow trait(2271)
blood pressure trait(7075)
arterial blood pressure trait(4960)
arterial blood pressure trait(495)
pulmonary arterial blood pressure trait(4)
heart blood pressure trait(2113)
venous blood pressure trait(2)

KCI/Kyo(2)
KFRS mutants(7)
KHR mutants(3)
LEC/Hok(2)
NAR/Slc(1)
OP/Jtt(1)
PCK-Pkhd1pck/CrljCrl(16)
SD mutants(56)
SHR mutants(12)
SHRSP mutant(2)
SS mutants(628)
SS Heterozygous mutants(54)
SS/JrHsdMcwi Heterozygous (ZFN) mutants(54)
SS-Chr 5BN-Cyp4a2em1Mcwi-/(4)
SS-Ets1em1Mcwi-/(4)
SS-Mstnem3Mcwi-/(4)
SS-Mthfrem1Mcwi-/(7)
SS-Nox4em2Mcwi-/(4)
SS-Renem1Mcwi-/(6)
SS-Sh2h3em1Mcwi-/(4)

47878 records under organ system trait VT including all its subcategories.
628 records under SS mutant strains with the selected VT

Entering a term in the search box filters the list below to show only matching terms. Additionally, choices made in one ontology will restrict the available options in others. For instance, selecting a VT will narrow down the strains to only those with relevant measurement data.

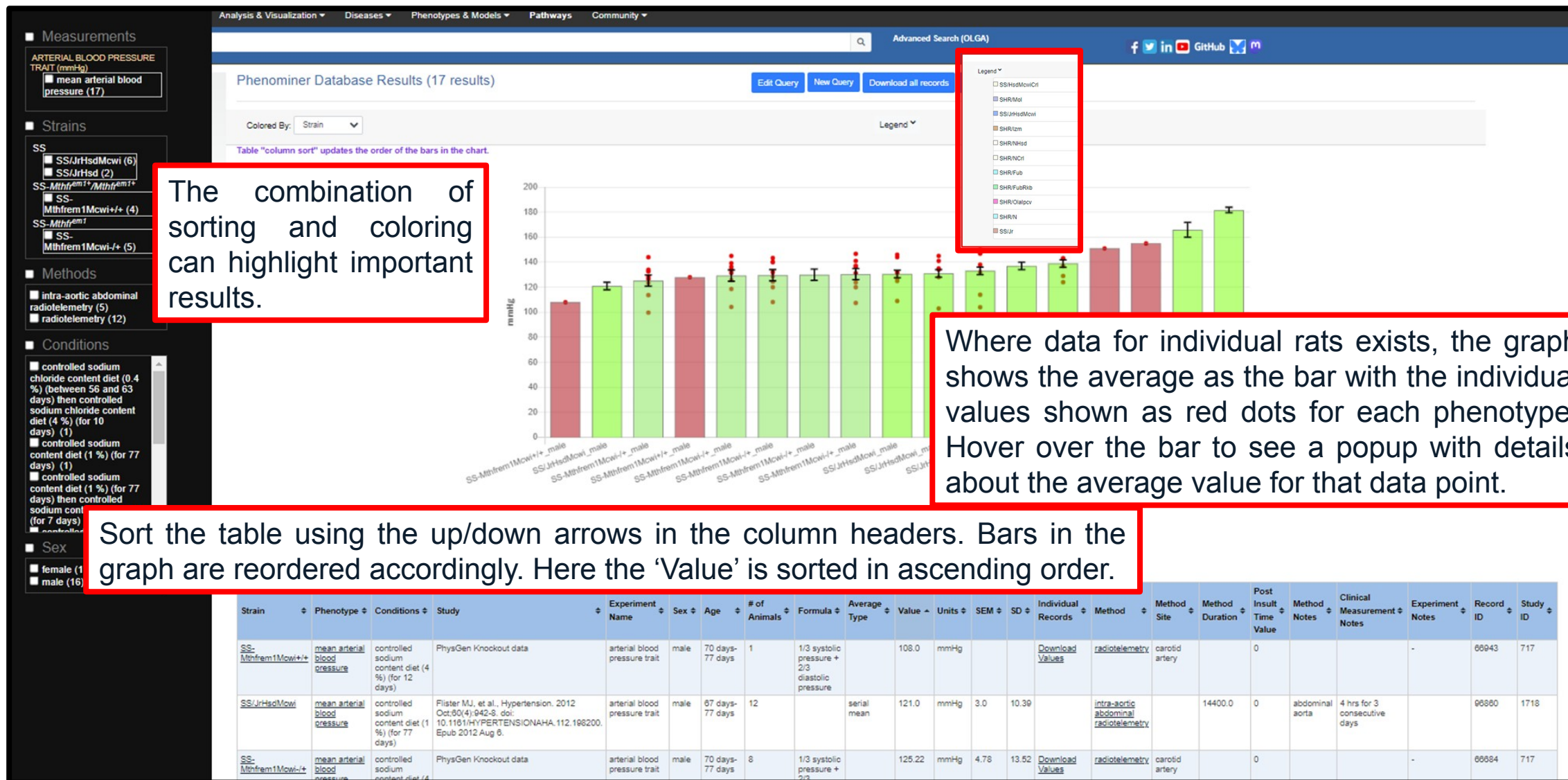
Data from the query can be downloaded. 'Download all records' is displayed on the pages for both unfiltered and filtered queries.

Select the parameter to color the bars with the dropdown legend. Here the graph is colored by 'Strain'.

The result from 'Generate Report' consists of a graph, a list of filters, and a table of results. If measurements that use more than one unit have been selected, the graph is hidden until the user filters the measurement selection to a single unit.

The filters, graph and table are all interconnected. Applying filters on the left removes data from the table and graph.

| Strain | Phenotype | Conditions | Study | Experiment Name | Sex | Age | # of Animals | Formula | Average Type | Value | Units | SEM | SD | Individual Records | Method | Method Site | Method Duration | Post Insult Time Value | Method Notes | Clinical Measurement Notes | Experiment Notes | Record ID | Study ID |
|---|------------------------------|---|--|-------------------------------|------|-----------------|--------------|--|--------------|--------|-------|------|-------|---------------------------------|---------------------------------------|----------------|-----------------|------------------------|-----------------|------------------------------|------------------|-----------|----------|
| SS-Mthfr ^{fl} Mow ^{+/+} | mean arterial blood pressure | controlled sodium chloride content diet (0.4 %) (between 56 and 63 days) then controlled sodium chloride content diet (4 %) (for 10 days) (1) | PhysGen Knockout data | arterial blood pressure trait | male | 70 days-77 days | 1 | 1/3 systolic pressure + 2/3 diastolic pressure | | 108.0 | mmHg | | | Download Values | radiotelemetry | carotid artery | | 0 | | | - | 66943 | 717 |
| SS/JrHsdMow | mean arterial blood pressure | controlled sodium content diet (1 %) (for 77 days) (1) | Flister MJ, et al., Hypertension. 2012 Oct;60(4):942-8. doi: 10.1161/HYPERTENSION.112.198200. Epub 2012 Aug 6. | arterial blood pressure trait | male | 67 days-77 days | 12 | | serial mean | 121.0 | mmHg | 3.0 | 10.39 | | intra-aortic abdominal radiotelemetry | | 14400.0 | 0 | abdominal aorta | 4 hrs for 3 consecutive days | | 96860 | 1718 |
| SS-Mthfr ^{fl} Mow ^{+/+} | mean arterial blood pressure | controlled sodium content diet (1 %) (for 77 days) then controlled sodium content diet (8 %) (for 7 days) (1) | PhysGen Knockout data | arterial blood pressure trait | male | 70 days-77 days | 8 | 1/3 systolic pressure + 2/3 | | 125.22 | mmHg | 4.78 | 13.52 | Download Values | radiotelemetry | carotid artery | | 0 | | | - | 66684 | 717 |



Under controlled sodium content diet, mean arterial blood pressure differs between different SS strain types, influenced by the genetics, experimental conditions, age, etc. as shown in this graph.

The RGD Team:

Principal Investigator:
Anne Kwitek, PhD

Co-Investigator:
Mindy Dwinell, PhD

Curation Team:
Jennifer Smith, MSc
Stan Laulederkind, PhD
Tom Hayman, PhD
Shur-Jen Wang, PhD
Monika Tutaj, PhD
Mary Kaldunski, MSc
Mahima Vedi, PhD
Wendy Demos, MSc

Development Team:
Jeff De Pons, BSc
Marek Tutaj, MSc
Jyothi Thota, MSc
Logan Lamers, BA
Adam Gibson, BSc
Akhilanand Kundurthi, MSc
Varun Reddy Gollapally, MSc

Systems Administrator:
Kent C Brodie, MSMI

Database Administrator:
Stacy Zacher, MSc

Thank you!

<https://rgd.mcw.edu>



We gratefully acknowledge our funders:

RGD is funded by the National Heart, Lung, and Blood Institute (NHLBI; R01HL064541), and the National Human Genome Research Institute (NHGRI) as part of the Alliance of Genome Resources (U24HG010859).

Many thanks to our collaborators:

Dr. Melinda Dwinell and colleagues in The Hybrid Rat Diversity Program (*grant 5R24OD024617 from the NIH Office of the Director*),

Dr. Mingyu Liang, Dr. Aron Geurts, Dr. Pengyuan Liu and colleagues for generous provision of epigenomics data

(*grant 2P01HL082798 from the National Heart, Lung, and Blood Institute*),

Dr. Peter Doris for the strain-specific *de novo* assembly data,
the members of the International Rat Omics Consortium (IROC),

And to the researchers who contribute data and who faithfully use our website and data!



GLOBAL
CORE
BIODATA
RESOURCE

