

Animal Quantitative Trait Loci (QTL) Database (Animal QTLdb)

This database collects publicly available trait mapping data, including QTL (phenotype/expression, eQTL), candidate gene and association data (GWAS), and copy number variations (CNV) mapped to livestock animal genomes. It aims to facilitate locating and comparing discoveries within and between species



Cattle QTL

There are **191,181** currently released QTL data (including eQTL/SNP associations) curated from **731** publications. These data are lifted to **5** genome builds. The curated data represent **680** different base traits and **347** trait variants. (see [cattle data summary](#) for more details).



Chicken QTL

There are **15,581** currently released QTL data (including eQTL/SNP associations) curated from **211** publications. These data are lifted to **4** genome builds. The curated data represent **372** different traits and **161** trait variants. (see [chicken data summary](#) for more details).



Goat QTL

There are **1501** currently released QTL data (including eQTL/SNP associations) curated from **22** publications. These data are lifted to **2** genome builds. The curated data represent **26** different base traits and **94** trait variants. (see [goat data summary](#) for more details).



Horse QTL

There are **2,216** currently released QTL data (including eQTL/SNP associations) curated from **85** publications. These data are lifted to **2** genome builds. The curated data represent **65** different base traits and **1** trait variants. (see [horse data summary](#) for more details).



Pig QTL

There are **48,875** currently released QTL data (including eQTL/SNP associations) curated from **426** publications. These data are lifted to **3** genome builds. The curated data represent **673** different base traits and **768** trait variants. (see [pig data summary](#) for more details).



Rainbow Trout QTL

There are **2,201** currently released QTL data (including eQTL/SNP associations) curated from **12** publications. These data are lifted to **2** genome builds. The curated data represent **47** different base traits and **6** trait variants. (see [rainbow trout data summary](#) for more details).



Sheep QTL

There are **4,605** currently released QTL data (including eQTL/SNP associations) curated from **165** publications. These data are lifted to **4** genome builds. The curated data represent **272** different base traits and **213** trait variants. (see [sheep data summary](#) for more details).

Let us use the Animal QTLdb to identify QTL for milk associated traits, a similar exercise can be done for your traits of interest (e.g: reproduction, meat associated traits, etc.)

1. Start by selecting the 'Cattle QTL database'.

2. Navigate to the search and analysis and use the query box to enter traits of interest or browse their available datasets for a more accurate key word.

CattleQTLdb

general search search

This Cattle Quantitative Trait Locus (QTL) Database (**Cattle QTLdb**) contains cattle QTL and association data curated from published data. The database is designed to facilitate the process for users to compare, confirm, and locate the most plausible location for genes responsible for quantitative traits important to cattle production. We have been striving our best to curate all available data, and adding tools to the QTLdb for users to accomplish many data meta-analysis and comparison tasks.

The current release of the Cattle QTLdb contains **191,181** QTLs/associations from **731** publications. Those QTLs / associations represent **680** different base traits and **347** trait variants. (see **data summary** for more recent updates). The released data have also been submitted to the NCBI Gene, Ensembl, and UCSC databases, where the QTL information can be retrieved and analyzed using the respective tools on these sites. New tools and functions are continually added. Please see the **release history** or **FAQ** for new updates.

Information in the **Cattle QTLdb** can be accessed in the following ways:

1. Search and Analysis

Tools for search by chromosomes, traits, breeds, publications, candidate genes, etc. and tools for data analysis primed with search.

2. Traits view:

- By Cattle QTLdb trait hierarchies
- By Vertebrate Traits **NEW** (REF. VT ONTOLOGY)
- By Livestock Production Traits **NEW** (REF. LPT ONTOLOGY)
- By Clinical Measurements **NEW** (REF. CMO ONTOLOGY)

3. Maps view:


- Chromosome view (with added feature alignments)
- Alignments with other annotations in **JBrowse**.
- Alignments with other annotations in **JBrowse2**.


4. Downloads:


- All data lifted to build ARS_UCD1.2 in .bed format
- All data lifted to build ARS_UCD1.2 in .gff format
- All data lifted to build ARS_UCD1.2 in .sam format
- All data lifted to build ARS_UCD2.0 in .bed format
- All data lifted to build ARS_UCD2.0 in .gff format
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- All data lifted to build Btau4.6 in .bed format
- All data lifted to build Btau4.6 in .gff format
- All data lifted to build Btau4.6 in .sam format
- All data lifted to build Btau5.0 in .bed format
- All data lifted to build Btau5.0 in .gff format
- All data lifted to build Btau5.0 in .sam format
- All data lifted to build UMD3.1 in .bed format
- All data lifted to build UMD3.1 in .gff format
- All data lifted to build UMD3.1 in .sam format
- All curated data in .tsv format


5. Data Summary:


Database statistics by chromosomes, traits, trait types, journals, publication years, etc.


**GMOD**
- Gbrowse
- Jbrowse

**QTL on Gbrowse**
- Jbrowse

**Frequently Asked Questions**

**Video Tutorials**

**New Data**
- Curation
- Batch load

**Data Downloads**

Grand search: Comprehensive search by traits, publications, genes, breeds, etc. go
mysql search tips

Targeted Queries

- Search by **QTL ID**
go
- Search by **publication**
author, title, etc. go
[search hint]
- Search by **breed**
Holstein go Use boolean ☒ AND ☐ OR ☐
- Find related data by **trait**
coat color go Use boolean ☒ AND ☐ OR ☐
(See results in a **trait-centric** view)
- Search by associated **gene**
IGF go
(See results in a **gene-centric** view)
- Search by **genome locations**
2:123-12137653 go

Data Analysis Tools

- View genome distribution data for a **trait**
Search for fat OR Browse traits
- "Chromosome Walker": Find neighboring QTL
Chr. 1 Start at 4500000 bp, view 5000000 bp, step 4200000 bp to the right ... go
- Whole genome **enrichment analysis** of QTL/associations
- By trait types go
- By traits / genome locations go **NEW**
(versn:beta)

Batch Query Tools

- Search QTL/association data with a list of **SNP rs IDs** **NEW**
One or more SNP "rs" numbers separated with space, comma, tab or line breaks. A SNP rs number must start with "rs"
go

Search our data alliances sites

where data are ingrated for mining with their tools:
→ Explore at **NCBI GeneDB**, or **Ensembl**, or **UCSC**.

NCBI Gene DB: fat go
Ensembl Phenotypes: fat go
UCSC Genome: fat go

Results pop out as a distribution summary, along with QTL dataset available in tabular format for download

Targeted Queries

Search by QTL ID

go

Search by publication

go

[search hint]

Search by breed

go

Use boolean ☒ AND ☐ OR ☒

Find related data by trait

go

Use boolean ☒ AND ☐ OR ☒

(See results in a trait-centric view)

Search by associated gene

go

(See results in a gene-centric view)

Search by genome locations

go

Data Analysis Tools

View genome distribution data for a trait

Search for

OR

Browse traits

"Chromosome Walker": Find neighboring QTL

Chr. Start at bp, view bp, step bp to the

go

Whole genome enrichment analysis of QTL/associations

By trait types

go

By traits / genome locations

go

NEW

(versn:beta)

Batch Query Tools

Search QTL/association data with a list of SNP rs IDs

NEW

One or more SNP "rs" numbers separated with space, comma, tab or line breaks. A SNP rs number must start with "rs"

go

QTL/Associations distribution analysis tool

Search for traits with a key word(s):

mysql search tips

☒ QTL

☐ Associations

☐ Both QTL and associations

go

Data distribution summary:

"fat" related QTL on

	Chr.	Number of QTL found
Fatness	1	27
Fatty acid content	1	20
Meat/fat color	1	5
Milk composition - fat	1	52
Fatness	2	60
Fatty acid content	2	35
Meat/fat color	2	4
Milk composition - fat	2	55
Sensory characteristics	2	1
Fatness	3	10
Fatty acid content	3	25
Meat/fat color	3	6
Milk composition - fat	3	35
Fatness	4	20

A bar diagram showing the distribution of "fat" related QTL/associations based on counts of reported data

Chromosomes

NEW

There are 6 trait types matched your search. You have new options to explore further with these links:

- Sensory characteristics
- Milk composition - fat
- Blood parameters
- Fatty acid content
- Meat/fat color
- Fatness

Data Download

A	B	C	D	E	F	G	H	I	J
QTL	FA-C20:0	QTL:135836	Chr.15: 64.41 cM (64.35-64.47)	cChr.15:47401521-47490641 bp	Breed:Simment	Fatty acid content: Arachidic acid co	PT:meat fatty acid C20:0 content		
QTL	FA-C20:0	QTL:135833	Chr.12: 18.19 cM (18.14-18.25)	cChr.12:13808617-13899093 bp	Breed:Simment	Fatty acid content: Arachidic acid co	PT:meat fatty acid C20:0 content		
QTL	FA-C20:0	QTL:135830	Chr.4: 102.99 cM (102.95-103.04)	cChr.4:107500383-107596828 bp	Breed:Simment	Fatty acid content: Arachidic acid co	PT:meat fatty acid C20:0 content		
QTL	FA-C20:0	QTL:135837	Chr.23: 16.62 cM (16.56-16.67)	cChr.23:11405225-11477969 bp	Breed:Simment	Fatty acid content: Arachidic acid co	PT:meat fatty acid C20:0 content		
QTL	FA-C20:0	QTL:135834	Chr.12: 93.54 cM (93.54-93.54)	cChr.12:71221794-71224710 bp	Breed:Simment	Fatty acid content: Arachidic acid co	PT:meat fatty acid C20:0 content		
QTL	FA-C20:0	QTL:135831	Chr.6: 26.67 cM (26.61-26.72)	cChr.6:24101030-24196486 bp	Breed:Simment	Fatty acid content: Arachidic acid co	PT:meat fatty acid C20:0 content		
QTL	FA-C20:0	QTL:135835	Chr.14: 47.73 cM (47.66-47.79)	cChr.14:35502126-35599284 bp	Breed:Simment	Fatty acid content: Arachidic acid co	PT:meat fatty acid C20:0 content		

3. Use the QTL /Association analysis tool and download the data, select the candidate genes, from the list for further studies, you can search for them in bulk or select one at a time, for convenience, we shall select the first one.

QTL/Associations distribution analysis tool

Search for traits with a key word(s):
fat
mysql search tips

☐ QTL

☒ Associations

☐ Both QTL and associations

go

Data distribution summary:

"fat" related Associations on

Chr.

Number of Associations found


Fatness	1	191
Fatty acid content	1	4
Meat/fat color	1	2
Milk composition - fat	1	306
Milk composition - protein	1	2
Fatness	2	161
Fatty acid content	2	3
Meat/fat color	2	15
Milk composition - fat	2	359

A bar diagram showing the distribution of "fat" related QTL/associations based on counts of reported data

- NEW
- There are 11 trait types matched your search. You have new options to explore further with these links:
- Sensory characteristics
 - Milk composition - fat
 - Milk composition - protein
 - Growth
 - Milk composition - other
 - Milk processing trait
 - Blood parameters
 - Fatty acid content
 - Meat/fat color
 - Chemistry
 - Fatness

1	Association	FA-C20:	QTL:16092	Chr.4: 78 cM (42.1	Chr.4:42705800-45	Breed:Simment	Fatty acid content: Arachidic ac	PT:meat fatty acid C20:0 content	Candidate gene: 280836 (NCBIgene)
2	Association	FA-C20:	QTL:16102	Chr.4: 91.41 cM (5	Chr.4:92451163-92	Breed:Simment	Fatty acid content: Arachidic ac	PT:meat fatty acid C20:0 content	Candidate gene: 280836 (NCBIgene)
3	Association	FA-C20:	QTL:20601	Chr.14: 47.4 cM (;	Chr.14:17733693-1	Breed:Hanwoo	Fatty acid content: Arachidonic	PT:meat fatty acid cis-5,8,11,14-C20:4 cont	Candidate gene: 281759 (NCBIgene)
4	Association	FA-C20:	QTL:16404	Chr.7: 106.55 cM	Chr.7:88444385-88	Breed:Hanwoo	Fatty acid content: Arachidonic	PT:meat fatty acid cis-5,8,11,14-C20:4 content	
5	Association	AI	QTL:71090	Chr.19: 115.92 cM	Chr.19:50791462-5	Breed:Fleckvieh	Fatty acid content: Atherogenic	PT:meat fatty acid content	Associated gene: 281152 (NCBIgene)
6	Association	AI	QTL:71098	Chr.19: 115.92 cM	Chr.19:50793355-5	Breed:Fleckvieh	Fatty acid content: Atherogenic	PT:meat fatty acid content	Associated gene: 281152 (NCBIgene)
7	Association	AI	QTL:71101	Chr.19: 115.92 cM	Chr.19:50791462-5	Breed:Fleckvieh	Fatty acid content: Atherogenic	PT:meat fatty acid content	Associated gene: 281152 (NCBIgene)
8	Association	AI	QTL:71108	Chr.19: 115.92 cM	Chr.19:50793355-5	Breed:Fleckvieh	Fatty acid content: Atherogenic	PT:meat fatty acid content	Associated gene: 281152 (NCBIgene)
9	Association	BCARO	QTL:20654	Chr.15: 25 cM (14	Chr.15:10848754-1	Breed:Jersey, Li	Chemistry: beta-carotene conc	VT:adipose beta-carotene amount	Candidate gene: 514135 (NCBIgene)
10	Association	BCARO	QTL:20657	Chr.15: 25 cM (14	Chr.15:10848754-1	Breed:Jersey, Li	Chemistry: beta-carotene conc	VT:adipose beta-carotene amount	Candidate gene: 514135 (NCBIgene)
11	Association	BCARO	QTL:20662	Chr.15: 25 cM (14	Chr.15:10848754-11003736	bp	Chemistry: beta-carotene conc	VT:adipose beta-carotene amount	Candidate gene: 514135 (NCBIgene)
12	Association	BCARO	QTL:20663	Chr.14: 25.4 cM (1	Chr.14:7066512-72	Breed:Jersey, Li	Chemistry: beta-carotene conc	VT:adipose beta-carotene amount	Candidate gene: 526726 (NCBIgene)
13	Association	BCARO	QTL:20665	Chr.14: 25.4 cM (1	Chr.14:7066512-7225131	bp	Chemistry: beta-carotene conc	VT:adipose beta-carotene amount	Candidate gene: 526726 (NCBIgene)
14	Association	BCARO	QTL:11397	Chr.15: 22.9 cM (;	Chr.15:11422188-1	Breed:Jersey, Li	Chemistry: beta-carotene conc	VT:adipose beta-carotene amount	Candidate gene: 514135 (NCBIgene)
15	Association	BNEFA	QTL:11537	Chr.14: 0.5 cM (2.	Chr.14:1966885-21	Breed:Holstein	Blood parameters: Blood non-	VT:blood free fatty acid amount CMO:blood	Candidate gene: 282609 (NCBIgene)
16	Association	BNEFA	QTL:11540	Chr.14: 0.5 cM (2.	Chr.14:1966885-21	Breed:Holstein	Blood parameters: Blood non-	VT:blood free fatty acid amount CMO:blood	Candidate gene: 282609 (NCBIgene)
17	Association	C14IND	QTL:16082	Chr.4: 91.41 cM (5	Chr.4:92451006-92	Breed:Simment	Fatty acid content: C14 index	PT:meat fatty acid content	Candidate gene: 280836 (NCBIgene)
18	Association	C14IND	QTL:16096	Chr.4: 78 cM (42.1	Chr.4:42705800-45	Breed:Simment	Fatty acid content: C14 index	PT:meat fatty acid content	Candidate gene: 280836 (NCBIgene)
19	Association	C14IND	QTL:16103	Chr.4: 91.41 cM (5	Chr.4:92451163-92	Breed:Simment	Fatty acid content: C14 index	PT:meat fatty acid content	Candidate gene: 280836 (NCBIgene)
20	Association	C14IND	QTL:18896	Chr.19: 79.8 cM (1	Chr.19:49960796-5	Breed:Hanwoo	Fatty acid content: C14 index	PT:meat fatty acid content	Candidate gene: 281152 (NCBIgene)

4. Use the NCBI gene database and enter the gene id in the search box, the results are shown below.



National Library of Medicine
National Center for Biotechnology Information

Gene

Gene

280836[uid]

×


Search

Create RSS Save search Advanced

Full Report ▾

Send to: ▾

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 Showing Current items.

LEP leptin [*Bos taurus* (cattle)]

Gene ID: 280836, updated on 5-Mar-2024

Summary

Official Symbol

LEP provided by [VGNC](#)

Official Full Name

leptin provided by [VGNC](#)

Primary source

[VGNC:VGNC:30842](#)

See related

[BGD:BT11292](#)

Gene type

protein coding

RefSeq status

PROVISIONAL

Organism

[Bos taurus](#)

Lineage

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Artiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos

Download Datasets

Table of contents

Summary

Genomic context

Genomic regions, transcripts, and products

Bibliography

Pathways from PubChem

General gene information

Markers, Homology, Gene Ontology

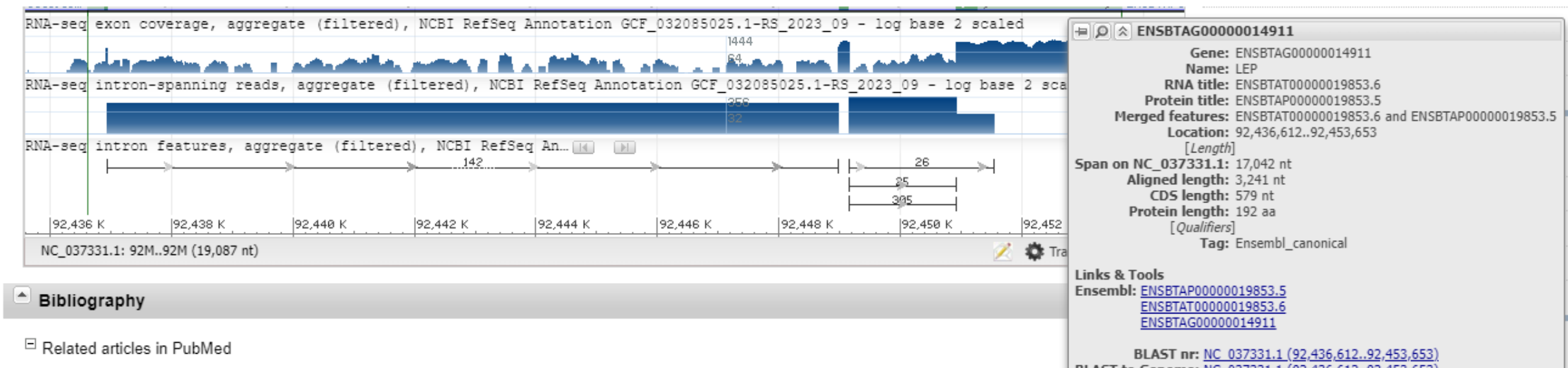
General protein information

NCBI Reference Sequences (RefSeq)

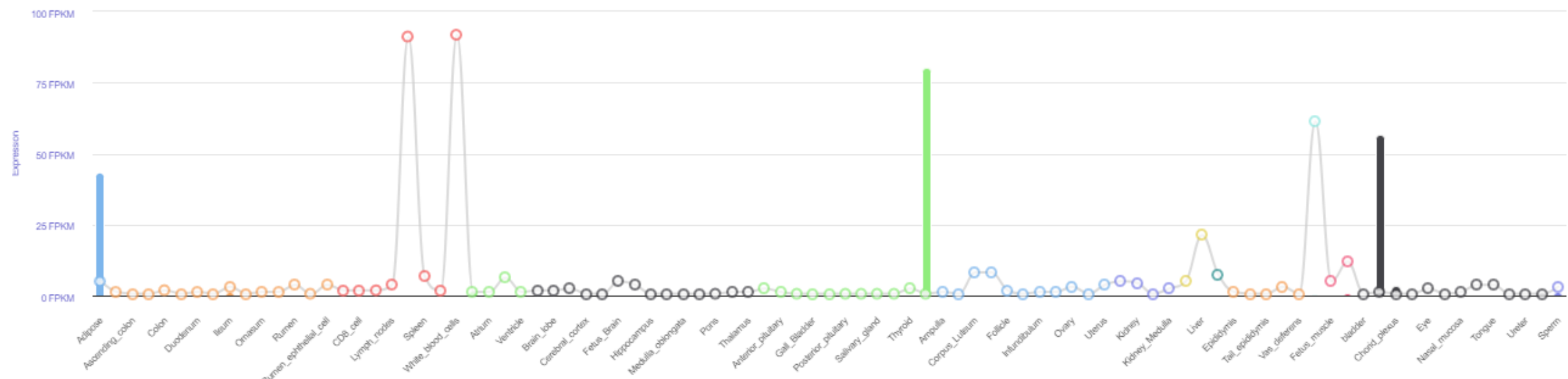
Related sequences

Additional links

5. Navigate to the gene features, and long hold on the gene, copy the gene id(ENSBTAG000000000.....)



6. Use the Animal genome Atlas and you will find the cattle tissue specific gene expression distribution

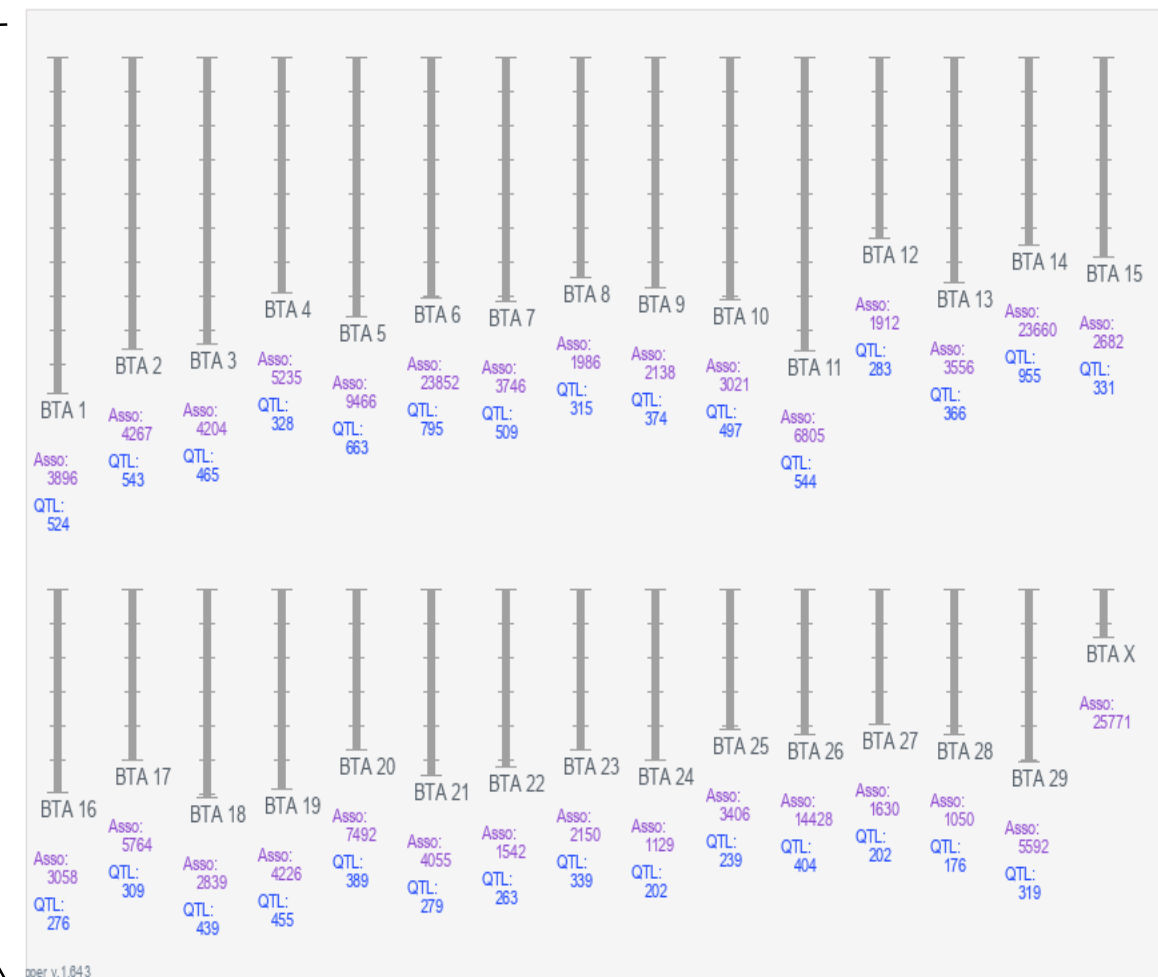
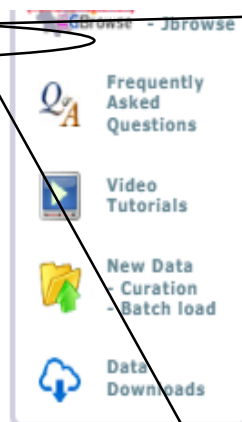


Now, return back to Animal QTLdb, as we map the QTL on the chromosomes, and try to identify the associated SNPs on these chromosomes and the associated genes.

View Cattle QTL by Chromosomes

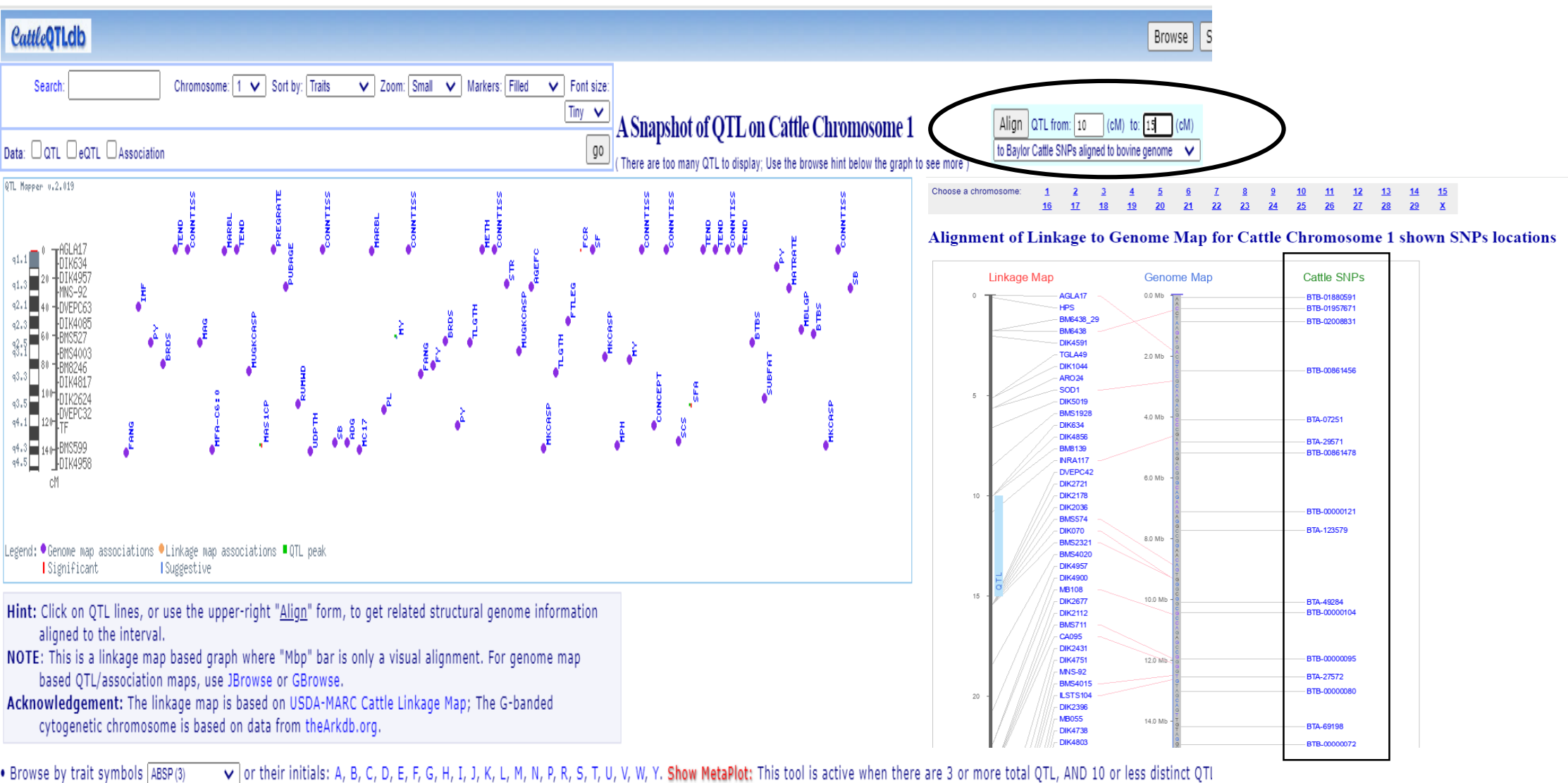
(Click on a chromosome to start. Or go to [Cattle QTL Mapviewer at NCBI](#))

3. Maps view:
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 - Alignments with other annotations in [JBrowse](#).
 - Alignments with other annotations in [JBrowse2](#).
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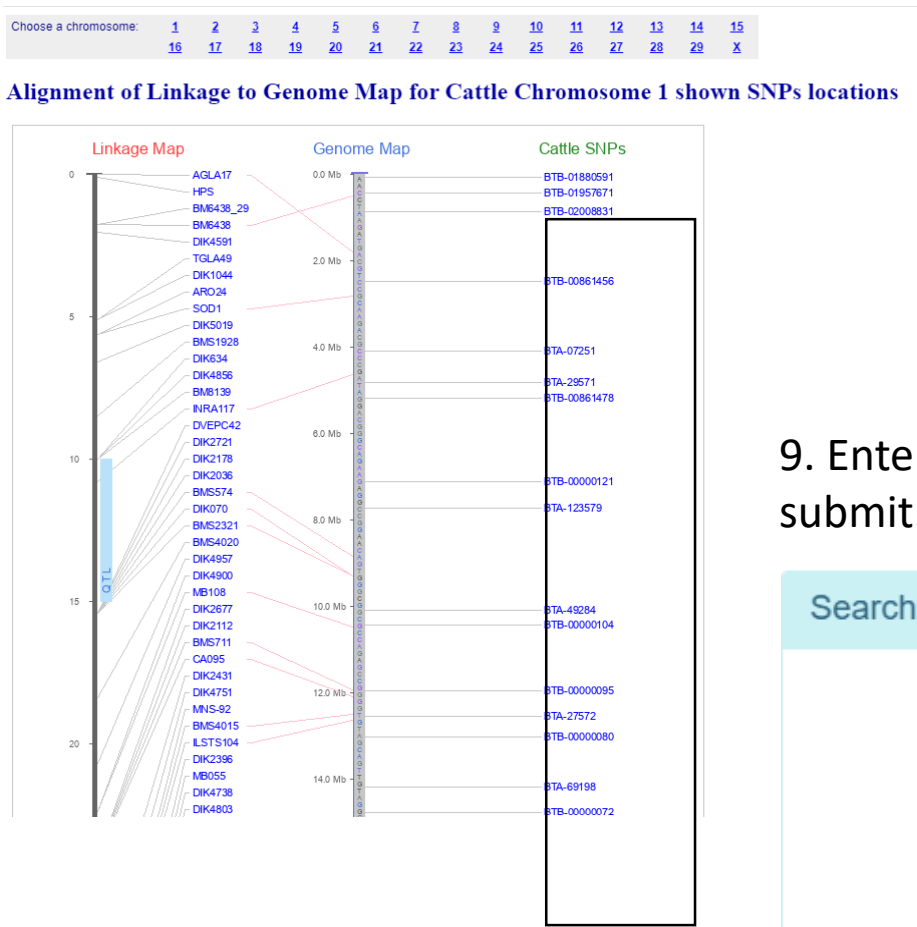


Acknowledgement: The Chromosome drawn is mainly based on USDA-MARC Cattle Linkage Map

7. You can visualize the QTL map at a higher resolution by zooming into the chromosome structure, aligning the linkage map to the SNP locations of the chromosome and identifying the reported SNPs.



8. The identified SNPs can be annotated on the Animal SNP Atlas, a comprehensive database for livestock SNP analysis.





ATC**C**ATG
ATC**G**ATG
ATC**T**ATG

Animal-SNPAtlas

A comprehensive SNP resource for multiple animals



ATC**C**ATG
ATC**G**TTG
ATC**G**G**T**G



HomeSNPImputationLinkage DisequilibriumVisualizationDownloadHelp

Species select (Cattle)

9. Enter the relevant SNP information in the query box and select the MAF, and submit.

Search SNPs of cattle

Region

e.g., "Chr1:139146-217226"

MAF

e.g., ">0.05"

Submit