

# Contributions of Equine FAANG to the Research Community

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**Jessica Petersen** – University of Nebraska  
*on Behalf of the Equine FAANG Consortium*

**Carrie Finno** – UC Davis

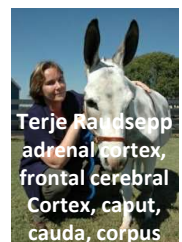
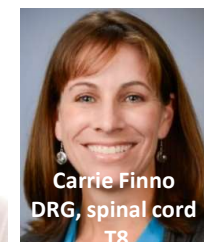
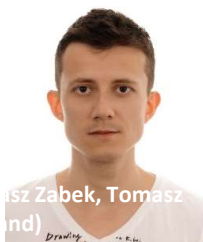
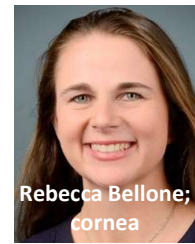
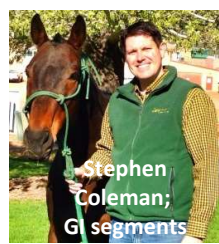
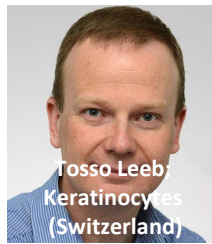
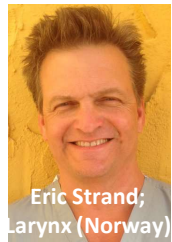
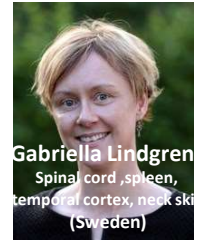
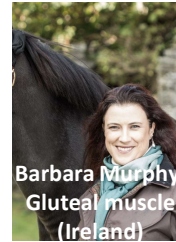
**Rebecca Bellone** – UC Davis

**Ted Kalbfleisch** – Univ of Kentucky

**Elena Giulotto** – Univ of Pavia

**Countless others** – list to follow





# (HUGE) Acknowledgement



Erin Hales (Burns)



Nicole Kingsley



Callum Donnelly



Sichong Peng



Alexa Barber



Anna Dahlgren



Eleonora Cappelletti



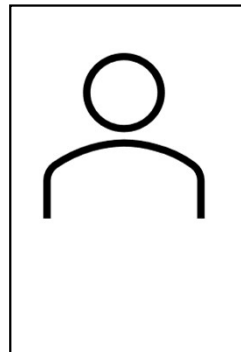
Francesca Piras



Wasma Abdelgadir



Reem Hijaz



Simone Vignati

2016



## 35th INTERNATIONAL SOCIETY FOR ANIMAL GENETICS CONFERENCE

7.23.16 – 7.27.2016 • Salt Lake City, Utah

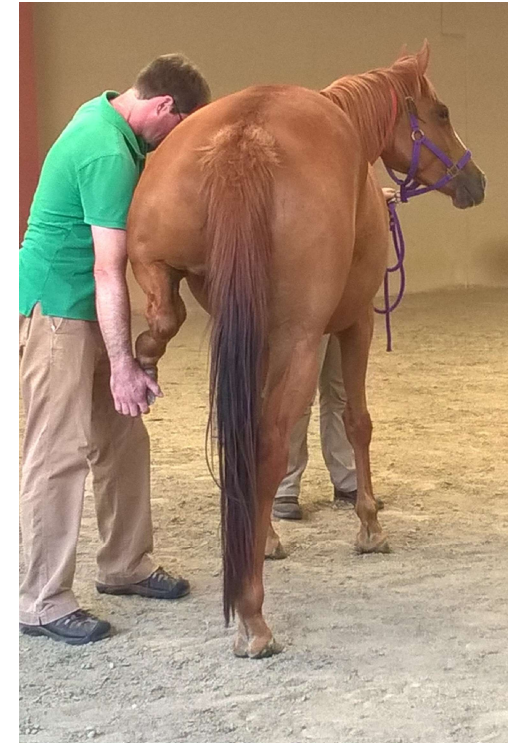
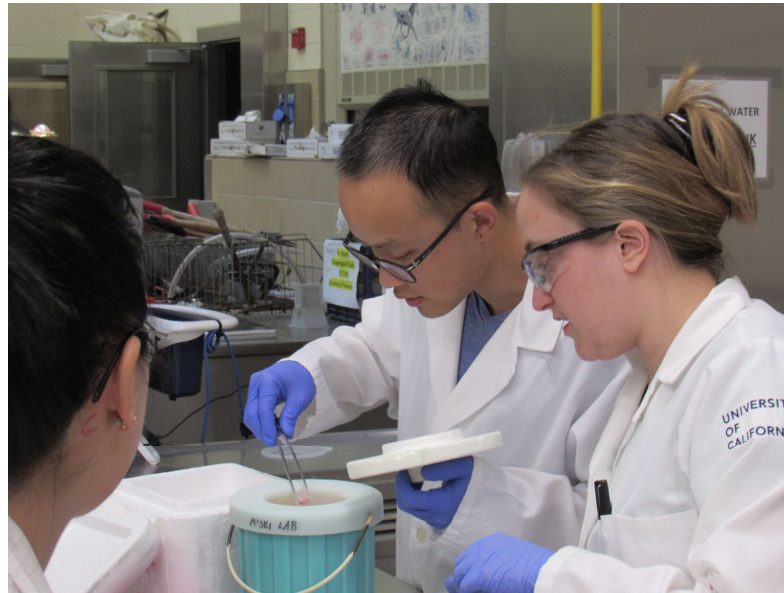
# Equine FAANG - Sample collection (mares)

2016

- Thoroughbreds
- 2 female adult
- 80-100 tissues/horse
- Fully phenotyped



Dr. Verena Affolter



2018



## Generation of an equine biobank to be used for Functional Annotation of Animal Genomes project

E. N. Burns<sup>\*</sup>, M. H. Bordbari<sup>\*</sup>, M. J. Mienaltowski<sup>†</sup>, V. K. Affolter<sup>‡</sup>, M. V. Barro<sup>\*</sup>, F. Gianino<sup>§</sup>, G. Gianino<sup>\*</sup>, E. Giulotto<sup>¶</sup>, T. S. Kalbfleisch<sup>\*\*</sup>, S. A. Katzman<sup>††</sup>, M. Lassaline<sup>††</sup>, T. Leeb<sup>‡‡</sup>, M. Mack<sup>§</sup>, E. J. Müller<sup>§§¶¶</sup>, J. N. MacLeod<sup>\*\*\*</sup>, B. Ming-Whitfield<sup>\*</sup>, C. R. Alanis<sup>\*</sup>, T. Raudsepp<sup>†††</sup>, E. Scott<sup>†</sup>, S. Vig<sup>§</sup>, H. Zhou<sup>†</sup>, J. L. Petersen<sup>‡‡‡</sup>, R. R. Bellone<sup>\*§</sup> and C. J. Finno<sup>\*</sup>



Erin Hales (Burns)

41 Citations

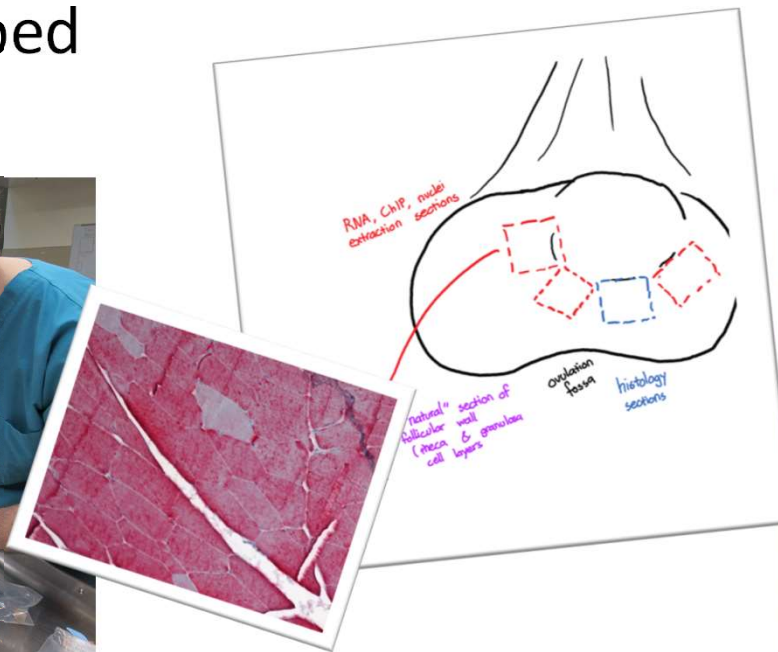
# Equine FAANG - Stallions

2020

- Thoroughbreds
- 2 male adult
- ~100 tissues/horse
- Fully phenotyped



United States Department of Agriculture  
National Institute of Food and Agriculture  
Award: 2019-67015-29340





2021

## Generation of a Biobank From Two Adult Thoroughbred Stallions for the Functional Annotation of Animal Genomes Initiative

*Callum G. Donnelly<sup>1</sup>, Rebecca R. Bellone<sup>1,2</sup>, Erin N. Hales<sup>3</sup>, Annee Nguyen<sup>1</sup>, Scott A. Katzman<sup>4</sup>, Ghislaine A. Dujovne<sup>1</sup>, Kelly E. Knickelbein<sup>4</sup>, Felipe Avila<sup>2</sup>, Ted S. Kalbfleisch<sup>5</sup>, Elena Giulotto<sup>6</sup>, Nicole B. Kingsley<sup>2</sup>, Jocelyn Tanaka<sup>2</sup>, Elizabeth Esdaile<sup>2</sup>, Sichong Peng<sup>1</sup>, Anna Dahlgren<sup>1</sup>, Anna Fuller<sup>7</sup>, Michael J. Mienaltowski<sup>8</sup>, Terje Raudsepp<sup>9</sup>, Verena K. Affolter<sup>10</sup>, Jessica L. Petersen<sup>7</sup> and Carrie J. Finno<sup>1\*</sup>*

OPEN ACCESS

*Edited by:*

10 Citations

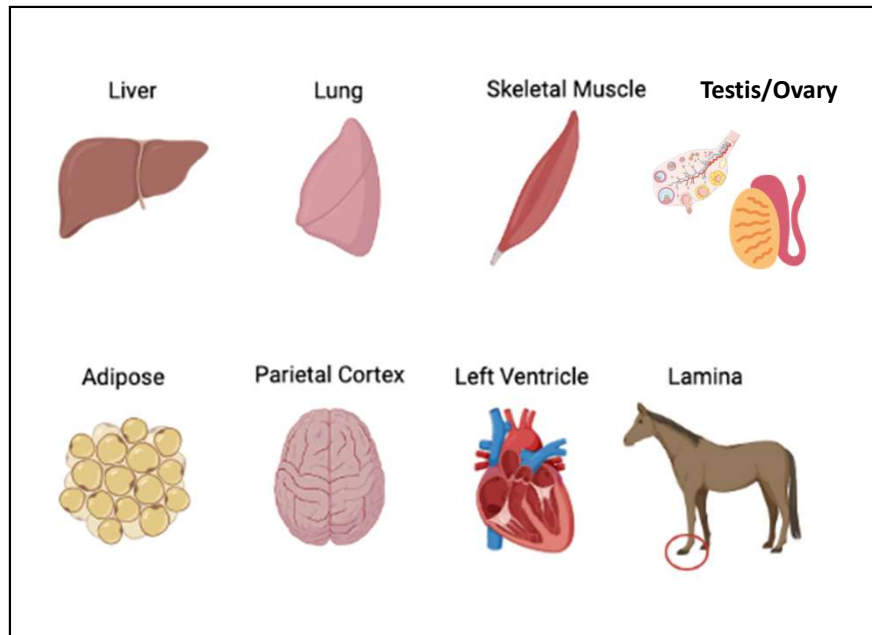


Callum Donnelly

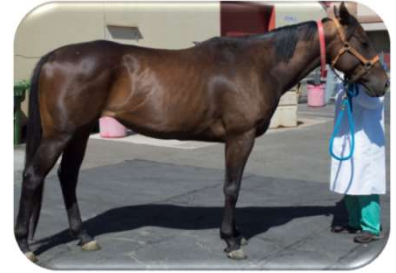


# Assays for Functional Annotation

- RNA-seq
- **Iso-seq**
- ChIP-seq
  - Histones
  - CTCF
- **ATAC-seq**
- RRBS



AH1  
5 yr mare



AH2  
4 yr mare



AH3  
3 yr stallion



AH4  
4 yr stallion









2020



Article

## Functionally Annotating Regulatory Elements in the Equine Genome Using Histone Mark ChIP-Seq

N. B. Kingsley <sup>1,2</sup> , Colin Kern <sup>3</sup>, Catherine Creppe <sup>4</sup>, Erin N. Hales <sup>2</sup> , Huaijun Zhou <sup>3</sup> ,  
T. S. Kalbfleisch <sup>5</sup>, James N. MacLeod <sup>5</sup>, Jessica L. Petersen <sup>6</sup> , Carrie J. Finno <sup>2</sup>  and  
Rebecca R. Bellone <sup>1,2,\*</sup> 



Nicole Kingsley

36 Citations

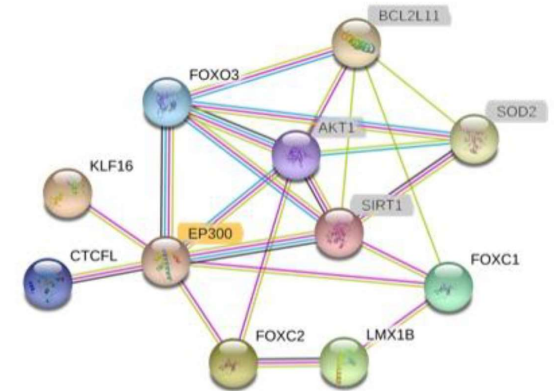
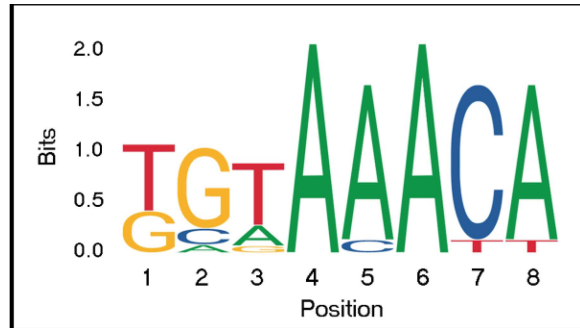
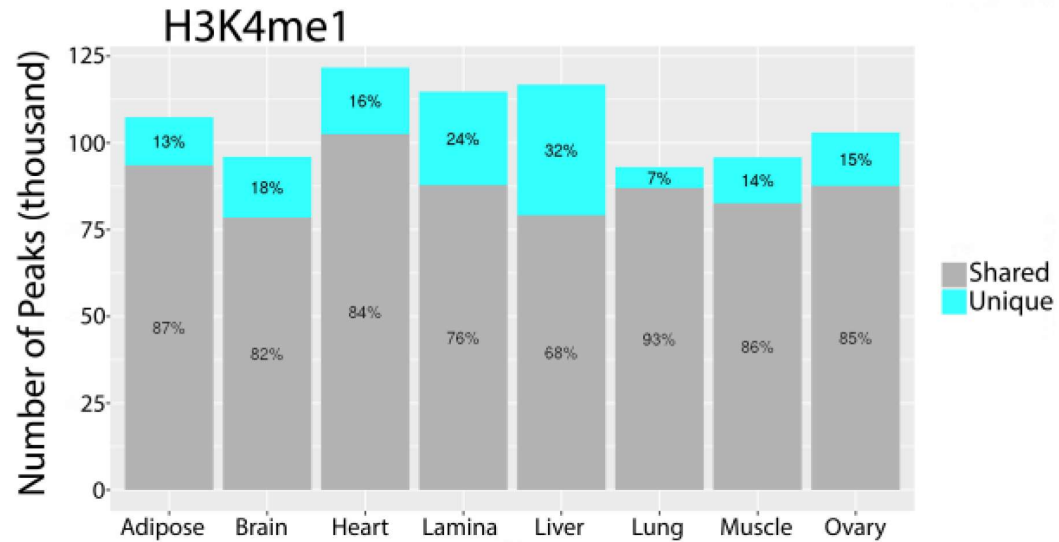
### EquCab3 – Annotation

Coding genes	20,955
Non-coding genes	9,014
Small non-coding genes	1,761
Long non-coding genes	7,244
Misc non-coding genes	9
Pseudogenes	402

### Results of ChIP-seq

Histone Mark	Avg # Peaks	% Genome Covered
H3K4me1	106,018	4.0
H3K4me3	27,924	1.6
H3K27ac	75,878	3.1
H3K27me3	8,368	3.7

# Histone Marks - Mares





2020

Article

## Comparison of Poly-A<sup>+</sup> Selection and rRNA Depletion in Detection of lncRNA in Two Equine Tissues Using RNA-seq

Anna R. Dahlgren<sup>1</sup>, Erica Y. Scott<sup>2</sup>, Tamer Mansour<sup>1</sup>, Erin N. Hales<sup>1</sup>, Pablo J. Ross<sup>2</sup>, Theodore S. Kalbfleisch<sup>3</sup>, James N. MacLeod<sup>3</sup>, Jessica L. Petersen<sup>4</sup>, Rebecca R. Bellone<sup>1,5</sup> and Carrie I. Finno<sup>1,\*</sup>

8 Citations



Anna Dahlgren



ORIGINAL RESEARCH  
published: 16 June 2021  
doi: 10.3389/fgene.2021.641788



## Successful ATAC-Seq From Snap-Frozen Equine Tissues

Sichong Peng<sup>1</sup>, Rebecca Bellone<sup>1,2</sup>, Jessica L. Petersen<sup>2</sup>, Theodore S. Kalbfleisch<sup>4</sup> and Carrie J. Finno<sup>1\*</sup>

9 Citations

2021



Sichong Peng



## “Adopt-a-Tissue” Initiative Advances Efforts to Identify Tissue-Specific Histone Marks in the Mare

*N. B. Kingsley<sup>1,2</sup>, Natasha A. Hamilton<sup>3</sup>, Gabriella Lindgren<sup>4,5</sup>, Ludovic Orlando<sup>6</sup>, Ernie Bailey<sup>7</sup>, Samantha Brooks<sup>8</sup>, Molly McCue<sup>9</sup>, T. S. Kalbfleisch<sup>7</sup>, James N. MacLeod<sup>7</sup>, Jessica L. Petersen<sup>10</sup>, Carrie J. Finno<sup>2</sup> and Rebecca R. Bellone<sup>1,2\*</sup>*

2021


11 Citations

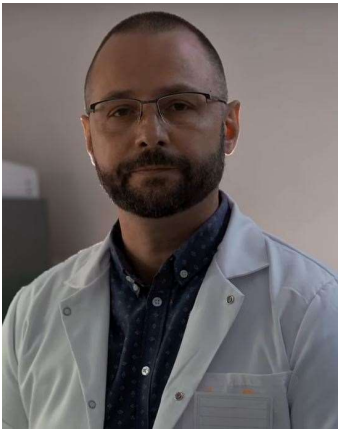


Nicole Kingsley



## Another lesson from unmapped reads: in-depth analysis of RNA-Seq reads from various horse tissues

Artur Gurgul<sup>1</sup>  · Tomasz Szmatola<sup>1</sup> · Ewa Ocloń<sup>1</sup> · Igor Jasielczuk<sup>1</sup> · Ewelina Semik-Gurgul<sup>2</sup> · Carrie J. Finno<sup>3</sup> · Jessica L. Petersen<sup>4</sup> · Rebecca Bellone<sup>3,5</sup> · Erin N. Hales<sup>3</sup> · Tomasz Ząbek<sup>2</sup> · Zbigniew Arent<sup>1</sup> · Małgorzata Kotula-Balak<sup>6</sup> · Monika Bugno-Poniewierska<sup>7</sup>



Artur Gurgul

2 Citations

2022

RESEARCH ARTICLE

# Functional annotation of the animal genomes: An integrated annotation resource for the horse

Sichong Peng<sup>1</sup>, Anna R. Dahlgren<sup>1</sup>, Callum G. Donnelly<sup>1</sup>, Erin N. Hales<sup>1</sup>, Jessica L. Petersen<sup>2</sup>, Rebecca R. Bellone<sup>1,3</sup>, Ted Kalbfleisch<sup>4</sup>, Carrie J. Finno<sup>1\*</sup>

4 Citations



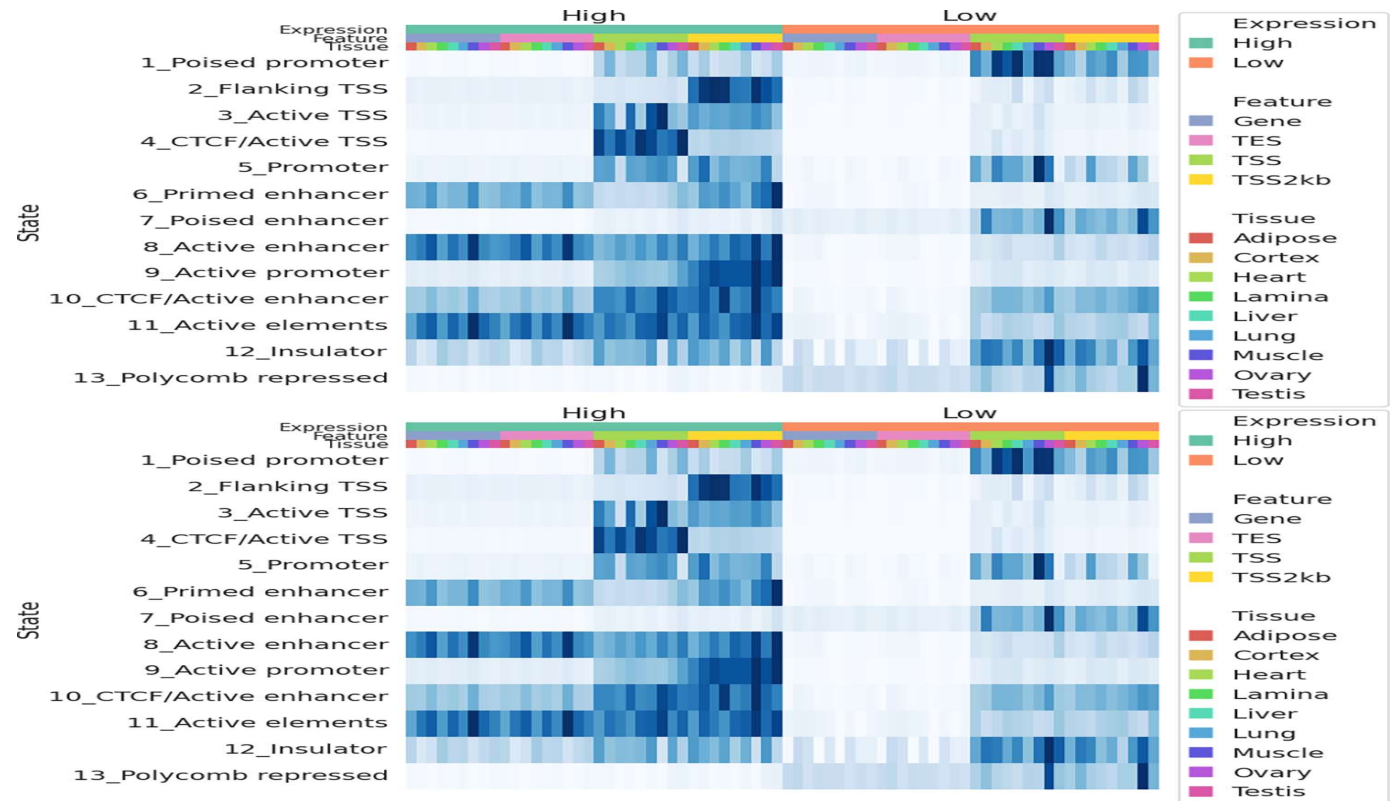
Sichong Peng



Alexa Barber

# ATAC-Seq

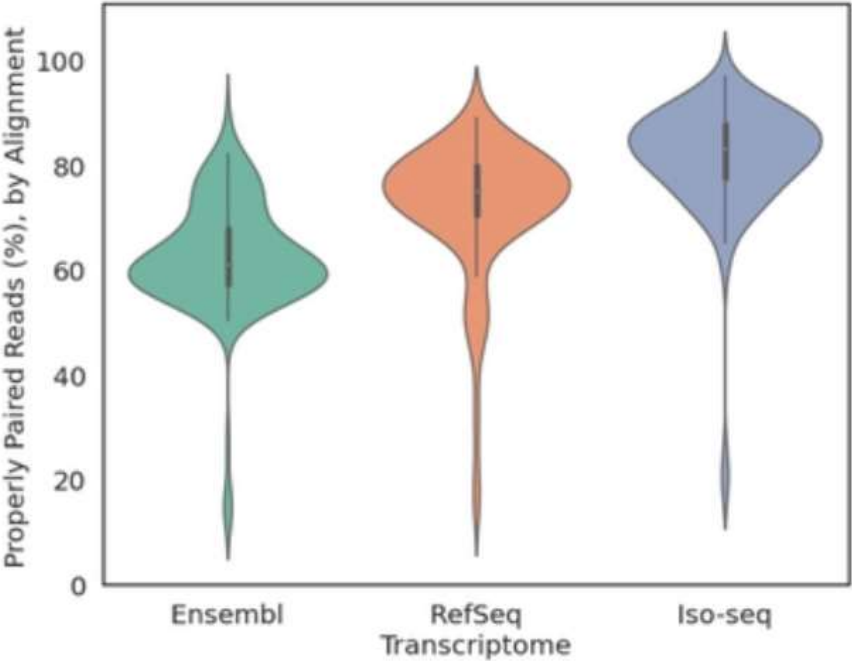
Tissue	Peak Count	Tissue-Specific
Adipose	77,655	22,884
Heart	89,386	19,730
Liver	95,048	31,460
Ovary	66,726	16,588
Testis	78,164	31,880





# Iso-Seq Transcriptome

Notable improvement in mapping



	<b>Ensembl</b>	<b>RefSeq</b>	<b>FAANG</b>
Genes	29,969	33,146	36,239
Transcripts	59,087	77,102	153,492
Isoform / Gene	2.0	2.3	4.2
Coding genes	20,955	21,129	26,631

2023

# communications biology








ARTICLE



<https://doi.org/10.1038/s42003-023-05335-7>

OPEN

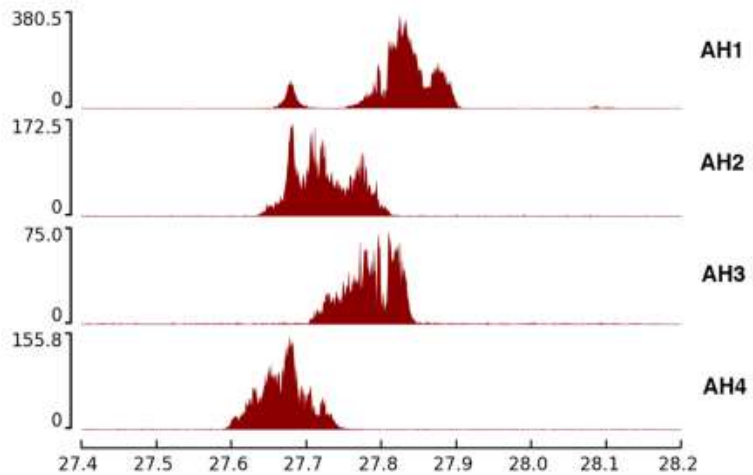
## The localization of centromere protein A is conserved among tissues

Eleonora Cappelletti <sup>1,6</sup>, Francesca M. Piras <sup>1,6</sup>, Lorenzo Sola<sup>1</sup>, Marco Santagostino <sup>1</sup>,  
Jessica L. Petersen <sup>2</sup>, Rebecca R. Bellone<sup>3,4</sup>, Carrie J. Finno <sup>3</sup>, Sichong Peng<sup>3</sup>, Ted S. Kalbfleisch <sup>5</sup>,  
Ernest Bailey<sup>5</sup>, Solomon G. Nergadze<sup>1</sup> & Elena Giulotto <sup>1</sup>✉

2 Citations



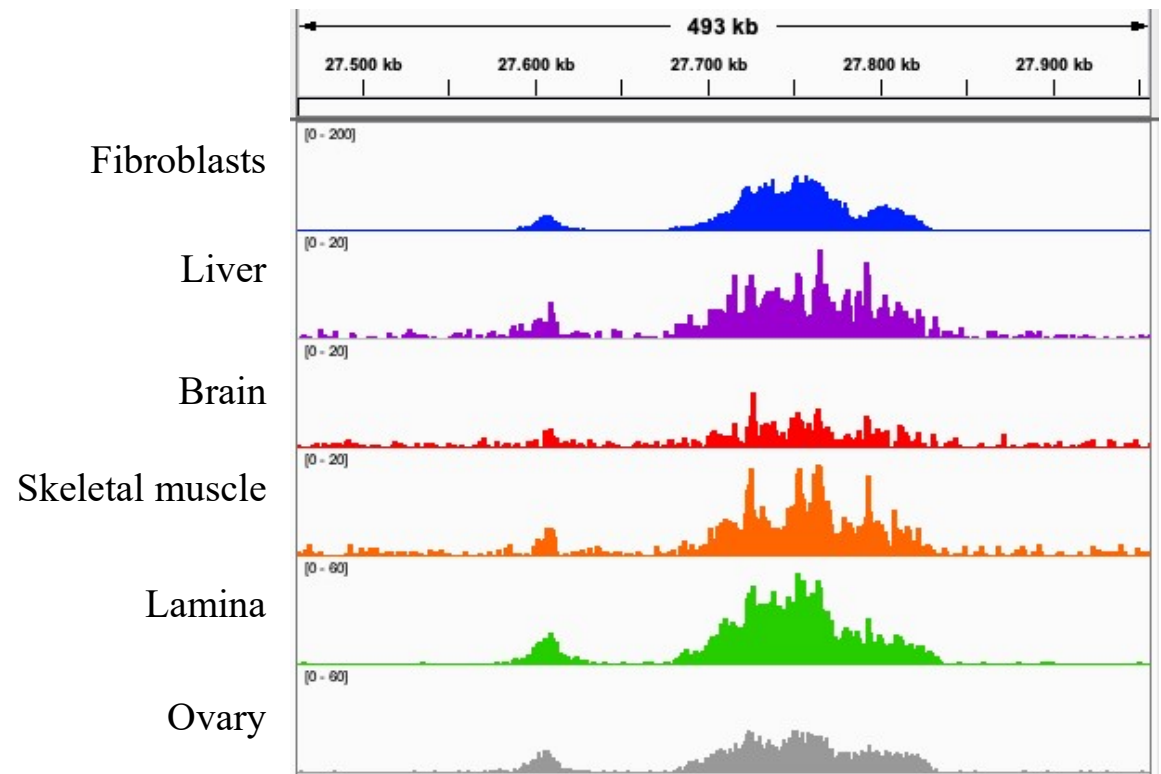
Eleonora Cappelletti



ECA11 centromere positions  
vary among horses

Positions do not vary by tissue

ECA\_UCD\_AH1





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## A Comprehensive Allele Specific Expression Resource for the Equine Transcriptome

Harrison D. Heath, Sichong Peng, Tomasz Szmatoła, Rebecca R. Bellone, Theodore Kalbfleisch, Jessica L. Petersen,  
 Carrie J. Finno

doi: <https://doi.org/10.1101/2023.12.31.573798>



Harrison Heath

**RRBS**

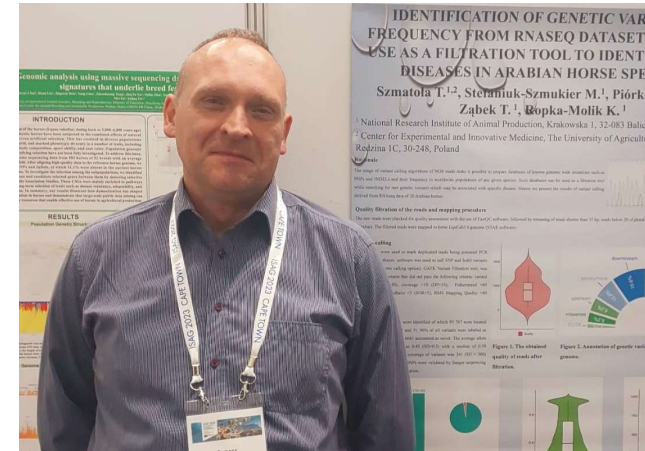


Jakub Cieslak



Jonah Cullen

**miRNA**



Tomasz Zabek

STANDARD ARTICLE

Journal of Veterinary Internal Medicine **ACVIM**  
American College of  
Veterinary Internal Medicine

## Investigation of high gamma-glutamyltransferase syndrome in California Thoroughbred racehorses

Sichong Peng<sup>1</sup> | K. Gary Magdesian<sup>2</sup> | Joseph Dowd<sup>3</sup> | Jeffrey Blea<sup>4</sup> |  
Ryan Carpenter<sup>5</sup> | Wayne Ho<sup>6</sup> | Carrie J. Finno<sup>1</sup>

**PLOS GENETICS**

RESEARCH ARTICLE

## A nonsense variant in Rap Guanine Nucleotide Exchange Factor 5 (*RAPGEF5*) is associated with equine familial isolated hypoparathyroidism in Thoroughbred foals

Victor N. Rivas<sup>1</sup>, K. Gary Magdesian<sup>2</sup>, Sophia Fagan<sup>3</sup>, Nathan M. Slovis<sup>4</sup>, Daniela Luethy<sup>5</sup>, Laura H. Javscas<sup>6</sup>, Brian G. Caserto<sup>7</sup>, Andrew D. Miller<sup>8</sup>, Anna R. Dahlgren<sup>1</sup>, Janel Peterson<sup>1</sup>, Erin N. Hales<sup>1</sup>, Sichong Peng<sup>1</sup>, Katherine D. Watson<sup>9</sup>, Mustafa K. Khokha<sup>3</sup>, Carrie J. Finno<sup>1\*</sup>

Hisey et al. *BMC Genomics* (2020) 21:848  
<https://doi.org/10.1186/s12864-020-07265-8>

BMC Genomics

RESEARCH ARTICLE

Open Access

## Whole genome sequencing identified a 16 kilobase deletion on ECA13 associated with distichiasis in Friesian horses

E. A. Hisey<sup>1</sup>, H. Hermans<sup>2</sup>, Z. T. Lounsberry<sup>1</sup>, F. Avila<sup>1</sup>, R. A. Grahn<sup>1</sup>, K. E. Knickelbein<sup>1,3</sup>, S. A. Duward-Akhurst<sup>4</sup>, M. E. McCue<sup>4</sup>, T.S. Kalbfleisch<sup>5</sup>, M. E. Lassaline<sup>6</sup>, W. Back<sup>2,7</sup> and R. R. Bellone<sup>1,8\*</sup>



# Ancient segmentally duplicated *LCORL* retrocopies in equids

Kevin Batcher<sup>1</sup>, Scarlett Varney<sup>1</sup>, Terje Raudsepp<sup>2</sup>, Matthew Jevit<sup>2</sup>, Peter Dickinson<sup>3</sup>, Vidhya Jagannathan<sup>4</sup>, Tosso Leeb<sup>4</sup>, Danika Bannasch<sup>1\*</sup>



Article  
**Comparative Transcriptome Profiling Analysis Uncovers Novel Heterosis-Related Candidate Genes Associated with Muscular Endurance in Mules**

Shan Gao<sup>†</sup>, Hojjat Asadollahpour Nanaei<sup>†</sup>, Bin Wei, Yu Wang, Xihong Wang, Zongjun Li, Xuelei Dai, Zhichao Wang, Yu Jiang and Junjie Shao<sup>\*</sup>

## Integrative genomics analysis highlights functionally relevant genes for equine behaviour

Amy R. Holtby<sup>1,2</sup> | Thomas J. Hall<sup>2</sup> | Beatrice A. McGivney<sup>1</sup> | Haige Han<sup>3</sup> | Keith J. Murphy<sup>3,4</sup> | David E. MacHugh<sup>1,5</sup> | Lisa M. Katz<sup>6</sup> | Emmeline W. Hill<sup>1,2</sup>

## REPRODUCTION RESEARCH

## New insights in equine steroidogenesis: an in-depth look at steroid signaling in the placenta

S C Loux<sup>1</sup>, A J Conley<sup>2</sup>, K E Scoggin<sup>1</sup>, H El-Sheikh Ali<sup>1,3</sup>, P Dini<sup>1,4</sup> and B A Ball<sup>1</sup>



# Prediction of histone post-translational modification patterns based on nascent transcription data

Zhong Wang<sup>1,2,8</sup>, Alexandra G. Chivu<sup>1,3,8</sup>, Lauren A. Choate<sup>1</sup>, Edward J. Rice<sup>1</sup>, Donald C. Miller<sup>1</sup>, Tinyi Chu<sup>1</sup>, Shao-Pei Chou<sup>1</sup>, Nicole B. Kingsley<sup>4</sup>, Jessica L. Petersen<sup>5</sup>, Carrie J. Finno<sup>6</sup>, Rebecca R. Bellone<sup>4</sup>, Douglas F. Antczak<sup>1</sup>, John T. Lis<sup>3</sup> and Charles G. Danko<sup>1,7</sup> ✉

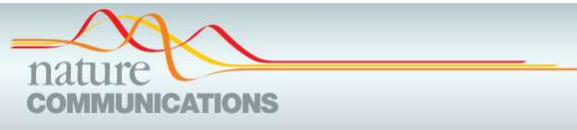
Science

## RESEARCH ARTICLE

EVOLUTIONARY BIOLOGY

# DNA methylation networks underlying mammalian traits

Amin Haghani<sup>1,2,\*†</sup>, Caesar Z. Li<sup>3,4†</sup>, Todd R. Robeck<sup>5</sup>, Joshua Zhang<sup>1</sup>, Ake T. Lu<sup>1,2</sup>, Julia A. Victoria A. Acosta-Rodriguez<sup>7</sup>, Danielle M. Adams<sup>8</sup>, Abdulaziz N. Alacaili<sup>9</sup>, Javier Almunia<sup>1</sup>



ARTICLE

<https://doi.org/10.1038/s41467-021-27754-y>

OPEN

# DNA methylation aging and transcriptomic studies in horses

Steve Horvath<sup>1,2,10,11✉</sup>, Amin Haghani<sup>1,10</sup>, Sichong Peng<sup>3</sup>, Erin N. Hales<sup>3</sup>, Joseph A. Zoller<sup>2</sup>, Ken Raj<sup>4</sup>, Brenda Larison<sup>5,6</sup>, Todd R. Robeck<sup>7</sup>, Jessica L. Petersen<sup>8</sup>, Rebecca R. Bellone<sup>3,9</sup> & Carrie J. Finno<sup>3,11✉</sup>

nature aging



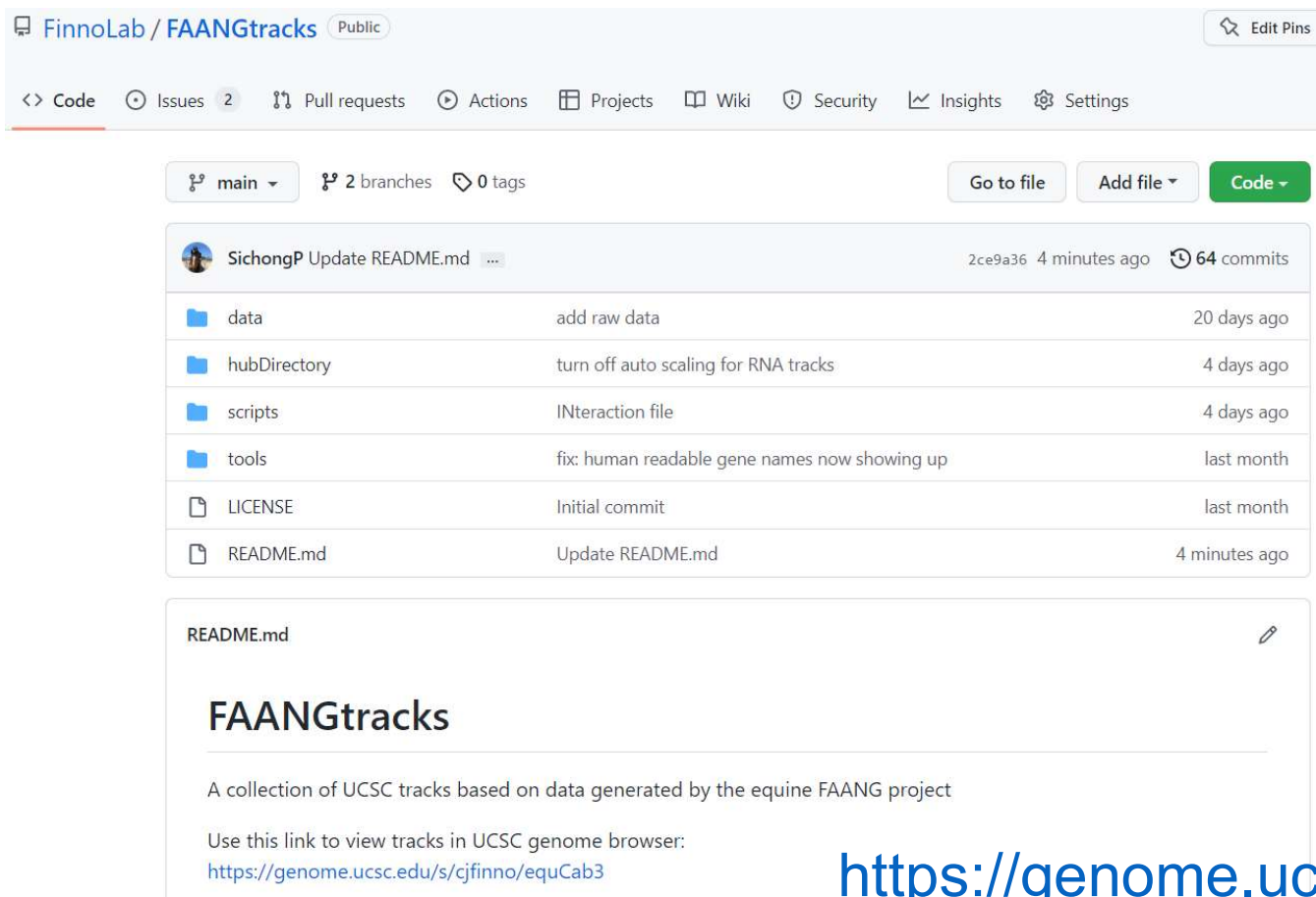
Resource

<https://doi.org/10.1038/s43587-023-00462-6>

# Universal DNA methylation age across mammalian tissues

# Simplifying Data Accessibility

- UCSC track hub



FinnoLab / FAANGtracks Public Edit Pins

<> Code Issues 2 Pull requests Actions Projects Wiki Security Insights Settings

main 2 branches 0 tags Go to file Add file Code

File	Commit Message	Time
data	add raw data	20 days ago
hubDirectory	turn off auto scaling for RNA tracks	4 days ago
scripts	INteraction file	4 days ago
tools	fix: human readable gene names now showing up	last month
LICENSE	Initial commit	last month
README.md	Update README.md	4 minutes ago

README.md

## FAANGtracks

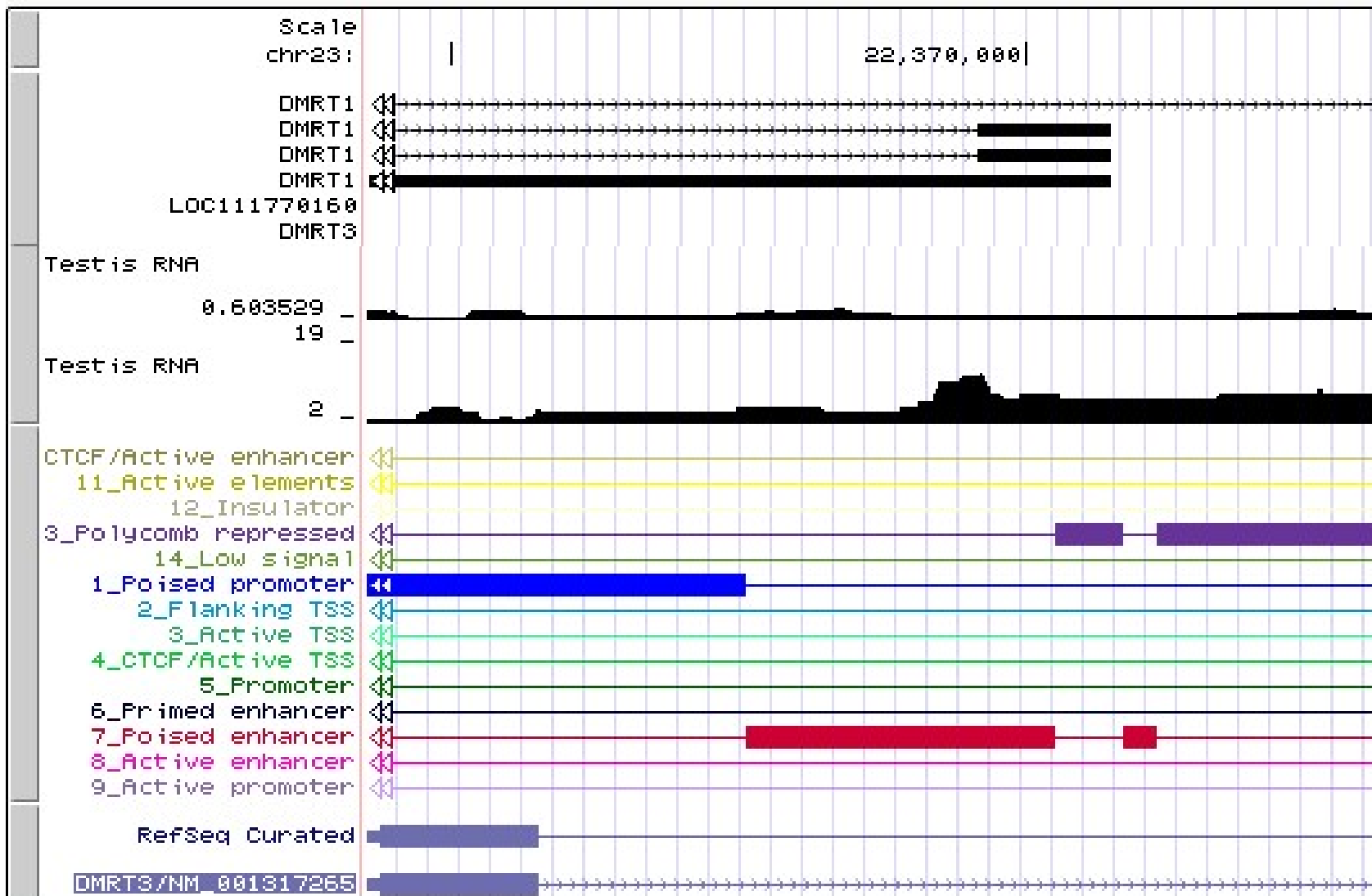
A collection of UCSC tracks based on data generated by the equine FAANG project

Use this link to view tracks in UCSC genome browser:  
<https://genome.ucsc.edu/s/cjfinno/equCab3>

<https://genome.ucsc.edu/s/cjfinno/equCab3>



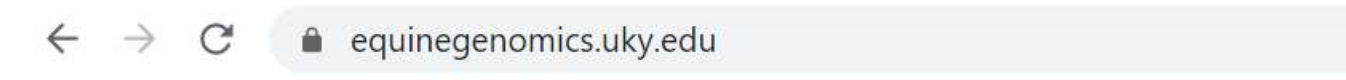
# DMRT1 Testis



# Simplifying Data Usage

- Equine Data Portal

<https://equinegenomics.uky.edu/>



## Equine FAANG Data and Resources

Video explaining and demonstrating the use of this web resource:

[YouTube video](#)

Resource Description	URL
Whole Genome Shotgun Sequence Data	<a href="#">faangHorses_WGS</a>
RNA-Seq Data	<a href="#">faangHorses_RNASeq</a>
ChIP-Seq Data	<a href="#">faangHorses_ChIP-Seq</a>
EquCab3 Genome Resources	<a href="#">genomeResources</a>
Genome files for the Integrative Genomics Viewer (IGV)	<a href="#">IGV.genomeFiles</a>

# equinegenomics.uky.edu

IGV

File Genomes View Tracks Regions Tools Help

ensembl.Ec\_build-3.0.wMSY.fs All

Go

Load from URL

File URL:

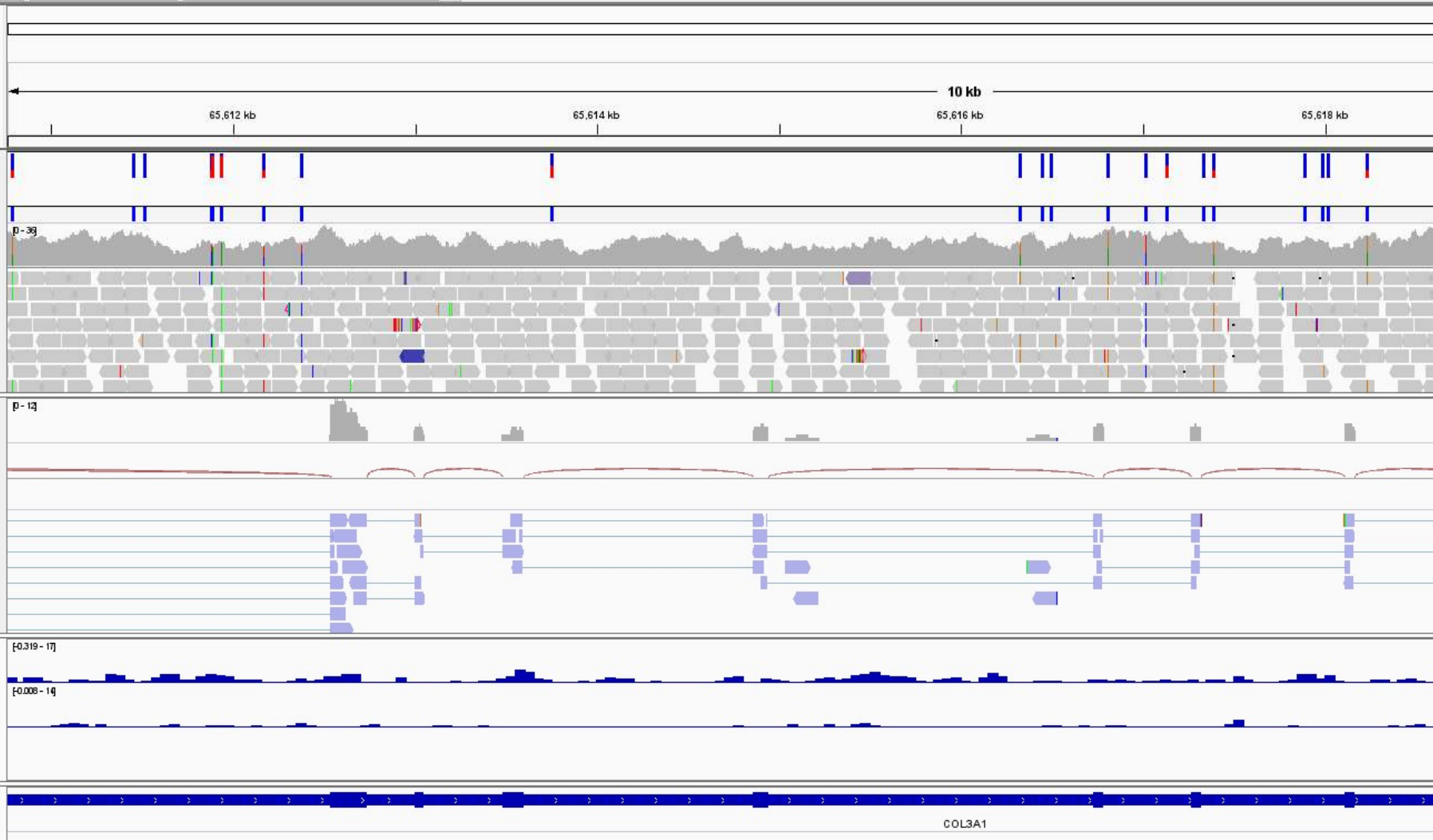
Specify url to an index file. **Required for BAM and indexed files**

Index URL:

https://equinegenomics.uky.edu/ x +

equinegenomics.uky.edu/faangHorses\_RNASeq.htm

Animal	Tissue	Data Type	Bam URL	Bam Index
AH1	AdiposeLoin	RNA-Seq	<a href="#">bamFile</a>	<a href="#">bamIndex</a>
AH1	AdrenalCortex	RNA-Seq	<a href="#">bamFile</a>	<a href="#">bamIndex</a>
AH1	Cecum	RNA-Seq	<a href="#">bamFile</a>	<a href="#">bamIndex</a>
AH1	CecumVermis	RNA-Seq	<a href="#">bamFile</a>	<a href="#">bamIndex</a>
AH1	Cornea	RNA-Seq	<a href="#">bamFile</a>	<a href="#">bamIndex</a>
AH1	DDFT	RNA-Seq	<a href="#">bamFile</a>	<a href="#">bamIndex</a>
AH1	DRG	RNA-Seq	<a href="#">bamFile</a>	<a href="#">bamIndex</a>
AH1	Duodenum	RNA-Seq	<a href="#">bamFile</a>	<a href="#">bamIndex</a>
AH1	Fibroblasts	RNA-Seq	<a href="#">bamFile</a>	<a href="#">bamIndex</a>
AH1	ForelimbFetlock	RNA-Seq	<a href="#">bamFile</a>	<a href="#">bamIndex</a>
AH1	FrontalCortex	RNA-Seq	<a href="#">bamFile</a>	<a href="#">bamIndex</a>
AH1	GlutealMuscle	RNA-Seq	<a href="#">bamFile</a>	<a href="#">bamIndex</a>
AH1	Hypothalamus	RNA-Seq	<a href="#">bamFile</a>	<a href="#">bamIndex</a>
AH1	Ileum	RNA-Seq	<a href="#">bamFile</a>	<a href="#">bamIndex</a>
AH1	Jejunum	RNA-Seq	<a href="#">bamFile</a>	<a href="#">bamIndex</a>
AH1	Keratinocytes	RNA-Seq	<a href="#">bamFile</a>	<a href="#">bamIndex</a>
AH1	KidneyCortex	RNA-Seq	<a href="#">bamFile</a>	<a href="#">bamIndex</a>
AH1	KidneyMedulla	RNA-Seq	<a href="#">bamFile</a>	<a href="#">bamIndex</a>
AH1	Lamina	RNA-Seq	<a href="#">bamFile</a>	<a href="#">bamIndex</a>
AH1	Larynx	RNA-Seq	<a href="#">bamFile</a>	<a href="#">bamIndex</a>



SNPs

WGS

RNA-seq

CHIP-seq

COL3A1



# Equine FAANG = A Win for the Horse

## Utility for:

- Equine Geneticists
- Genomics researcher across species
- Other equine/animal scientists
  - Nutrition
  - Reproduction
  - Health & Physiology
  - Performance



# Where are we going?

- Additional data analyses using existing data
- Additional data collection using existing samples
  
- Equine Pangenome and Pantranscriptomes
- Equine Variant Database
  
- (need) Additional developmental stages
  
- Continuing to improve means to access and use data

# Acknowledgements

- Equine Community Tissue “Adopters”



United States Department of Agriculture  
National Institute of Food and Agriculture  
Award: 2019-67015-29340

