UC DAVIS
VETERINARY MEDICINE

UNIVERSITY OF Nebraska
Lincoln®

GRAYSON-JOCKEY CLUB
RESEARCH FOUNDATION, INC.

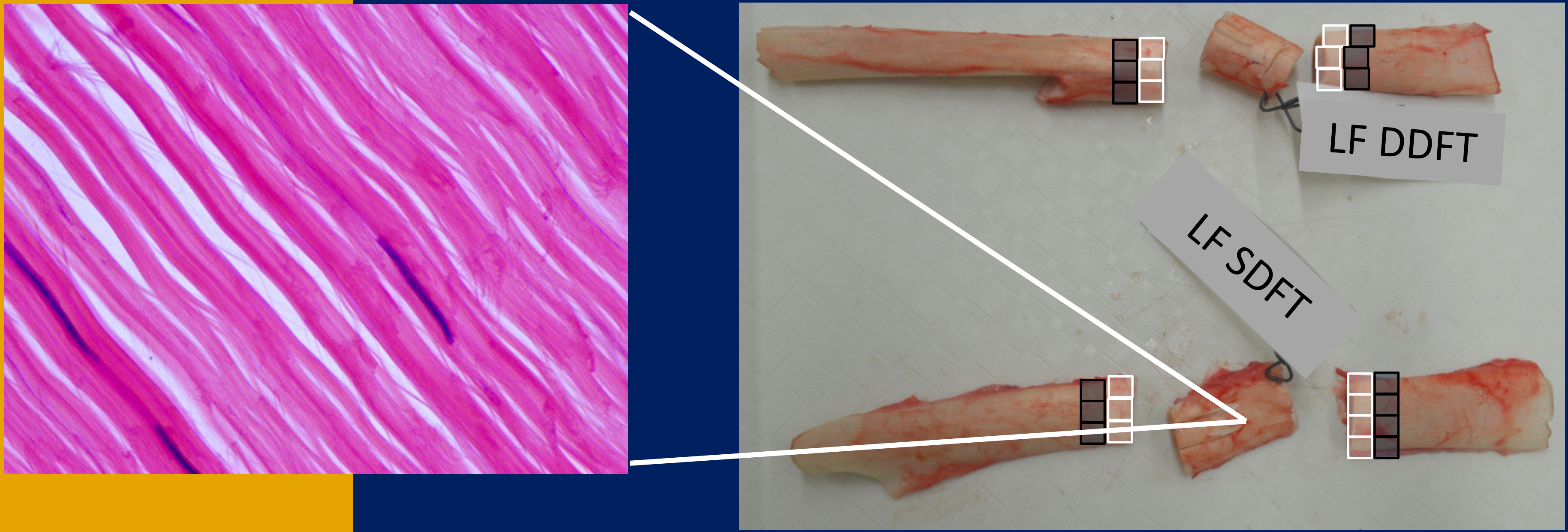
USDA

FAANG: An Update on Equine Studies

UCD/UNL Biobank

2 Healthy Thoroughbred mares (4-5 yr)

- Full clinical phenotyping
- >80 tissues, 4 fluid types and 9 microbiome sites collected



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FAANG: Equine Studies

- Whole-genome sequencing (20x): Complete
- 8 prioritized tissues
  - RNA-seq (mRNA and small RNA): Complete
  - ChIP-seq Underway
    - H3K4me1
    - H3K4me3
    - H3K27me3
    - H3K27ac
  - RRBS (National Research Institute, Poland; Underway)
- **Adopt a Tissue Initiative:** additional tissues supported by other laboratories
  - RNA-seq (mRNA and small RNA) Complete
  - Phase II Underway

Adopt-A-Tissue Collaborators

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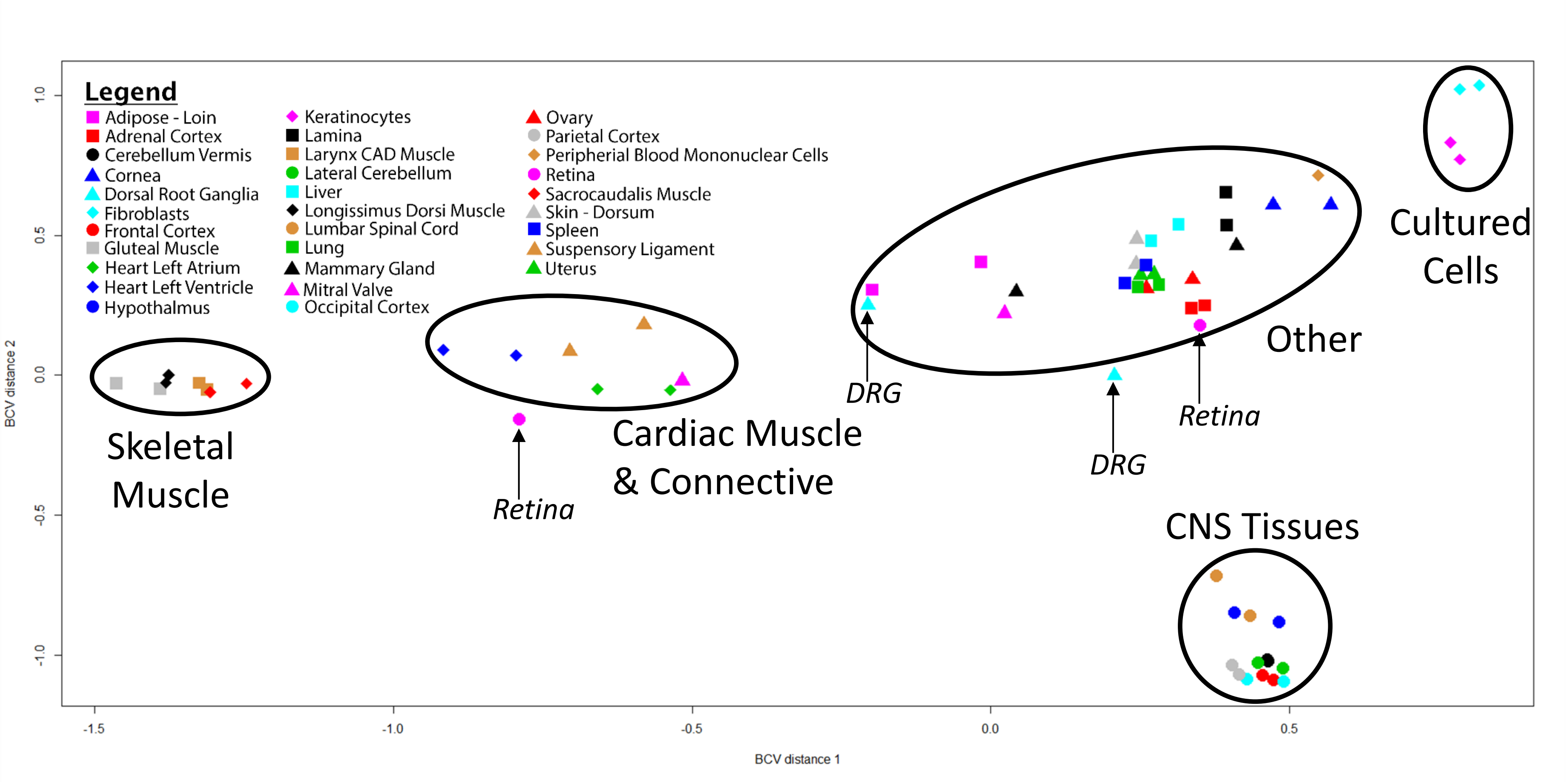
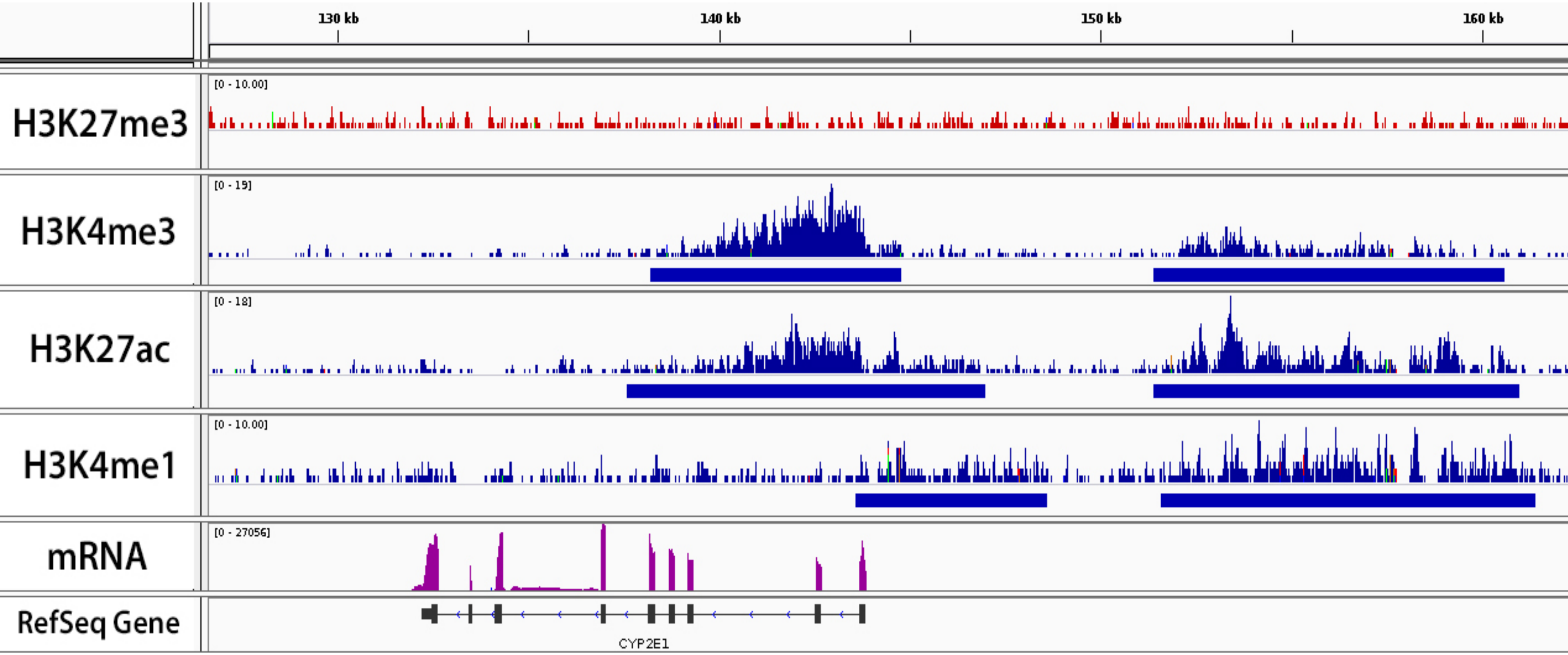
FAANG

mRNA Results – MDS Plot



Preliminary Results

diagenode
Innovating Epigenetics Solutions



CYP2E1 highly expressed in liver

Extension of biobank

Keratinocyte
cell culture

Fibroblast
cell culture

Centromere
Mapping

Methylation
Profile
(RRBS)

INSTYTUT ZOOTECHNIKI
PAŃSTWOWY INSTYTUT BADAWCZY
NATIONAL RESEARCH INSTITUTE
OF ANIMAL PRODUCTION

Biobank

Microbiome
Analysis

UNIVERSITY OF
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Karyotypes

Additional Equine FAANG Initiatives

UMN (McCue/Mickelson)

Tools to Link Phenotype to Genotype in the Horse
RNA-seq in Horse and Turkey Transcriptomics
Tools for Precision Medicine in the Horse

12 adult Quarter Horses or QH related breeds
mRNA, lncRNA and miRNA - 16 tissues

Cornell University (Antczak)

Expression Signatures of Equid Lymphocyte Subsets Defined By Single Cell Sequencing

Acknowledgements

- Collaborators around the globe
- Funding Sources

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NIFA

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Center for Equine Health

PAG 2018 POSTERS

340 Nicole Kingsley – *“Optimization of equine ChIP-Seq for the functional annotation of animal genomes”*

342 Erin Burns, *“Update on the equine FAANG initiative – how the community is using the biobank”*

343 Shauna Tietze, *“Refined phenotypes associated with the equine FAANG biobank: Microbiome Sequencing”*

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