Examples of FAANG associated projects

- WUR-pigENCODE: Martien Groenen

- Canada and FAANG: Graham Plastow

- Strategy to identify regulatory mutations affecting complex traits: Amanda Chamberlain

- Equine FAANG: Carrie Finno

WU FAANG pilot projects

Martien Groenen, Richard Crooijmans, Hendrik-Jan Megens, Ole Madsen

Expression and methylation analyses in pig

- **RNAseq and miRNA data**
  - Improve gene annotation (mRNA)
  - lncRNA
  - miRNA

- **RRBS data**
  - CpG

Co-expression, correlations

- **Samples: 3 boars (Large white, Duroc, Pietrain)**
  - liver, spleen, testis, brain (frontal lobe), muscle (all)
  - olfactory bulb, lung and lymph node from (LW only)

lncRNAs and miRNAs

lncRNAs (Ole Madsen)

- FEELnc (provided by Thomas Derrien, University of Rennes, France)
  - Number of mRNA : 30585
  - Number of lncRNA : 35046
  - Number of lncRNA without interaction with coding gene: **19832**

MiRNAs (Anoop Arya)

- miRDeep2

  - Predicted a total of **1071** precursors.
    - Of these 689 are putative predicted precursors and382 are known precursors

ChIP-seq

- ## Histone marks

  - H3K27ac   active enhancers and promoters
  - H3K4me3   promoter active genes
  - H3K27me3   silenced genes (active during developmental stages)
  - H3K4me1   active enhancers

- ## Samples

  - Cell lines (pig intestine, liver)
  - Tissues (start with pig intestine and liver)
  - FR-AgENCODE tissues

- ## In collaboration with the Molecular Biology Group of the Radboud University, Nijmegen (Henk Stunnenberg)

ChIPseq

- Porcine small intestinal epithelial cell line (IPEC-J2)
  - established from normal intestinal epithelium cells isolated from the jejunum of a neonatal, unsuckled pig
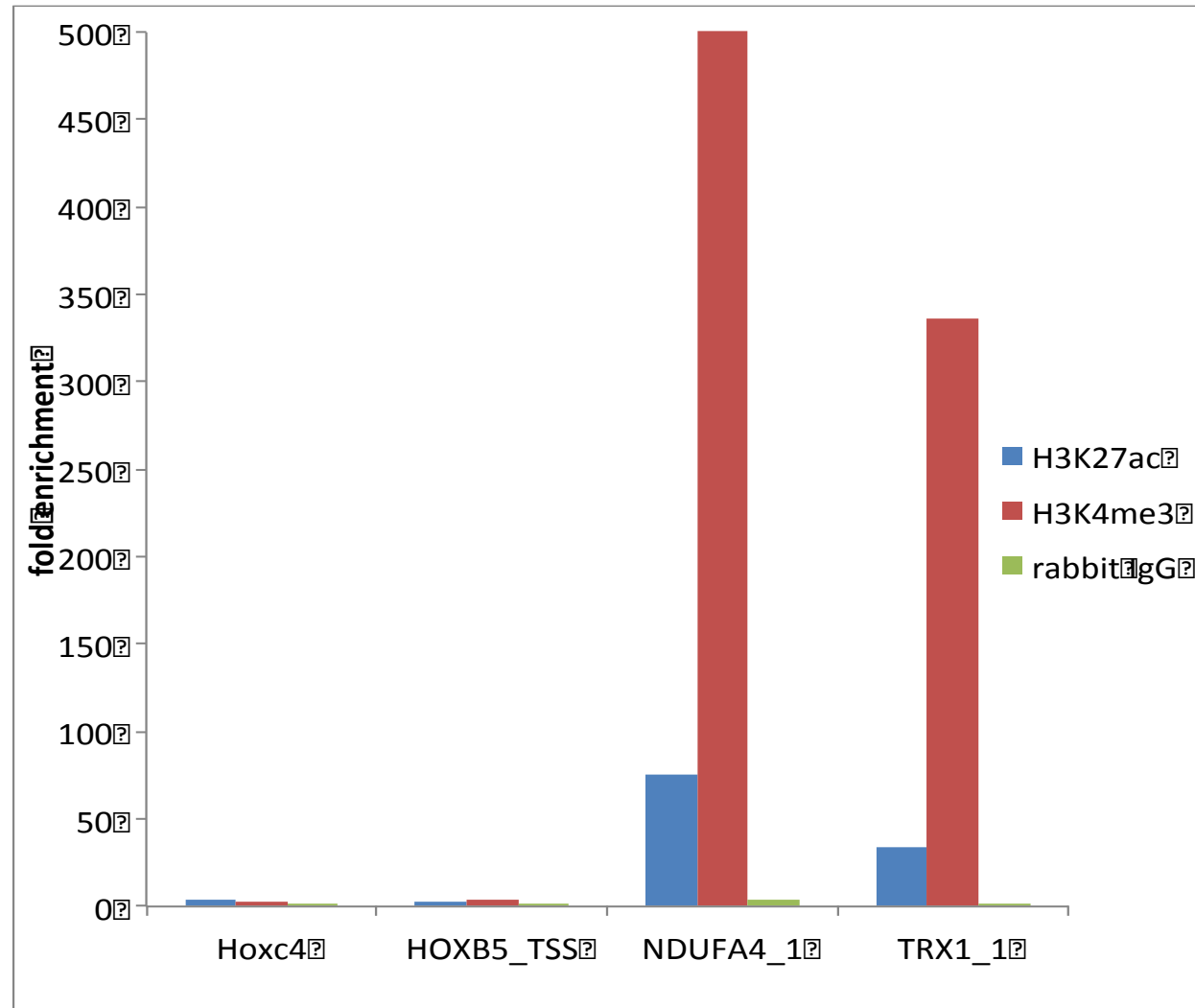
- Liver cell line

- WGS (30x)
- RNAseq
- RRBS

- Histone marks
  - H3K27ac
  - H3K4me3
  - H3K27me3
  - H3K4me1

- Controls (qPCR)
  - HOXC4
  - HOXB5
  - NDUFA4*
  - TRX1*

expressed (above 100 fpkm) in all our RNA-seq data

ChIPseq

Canada and FAANG

PAG

January 11th 2016
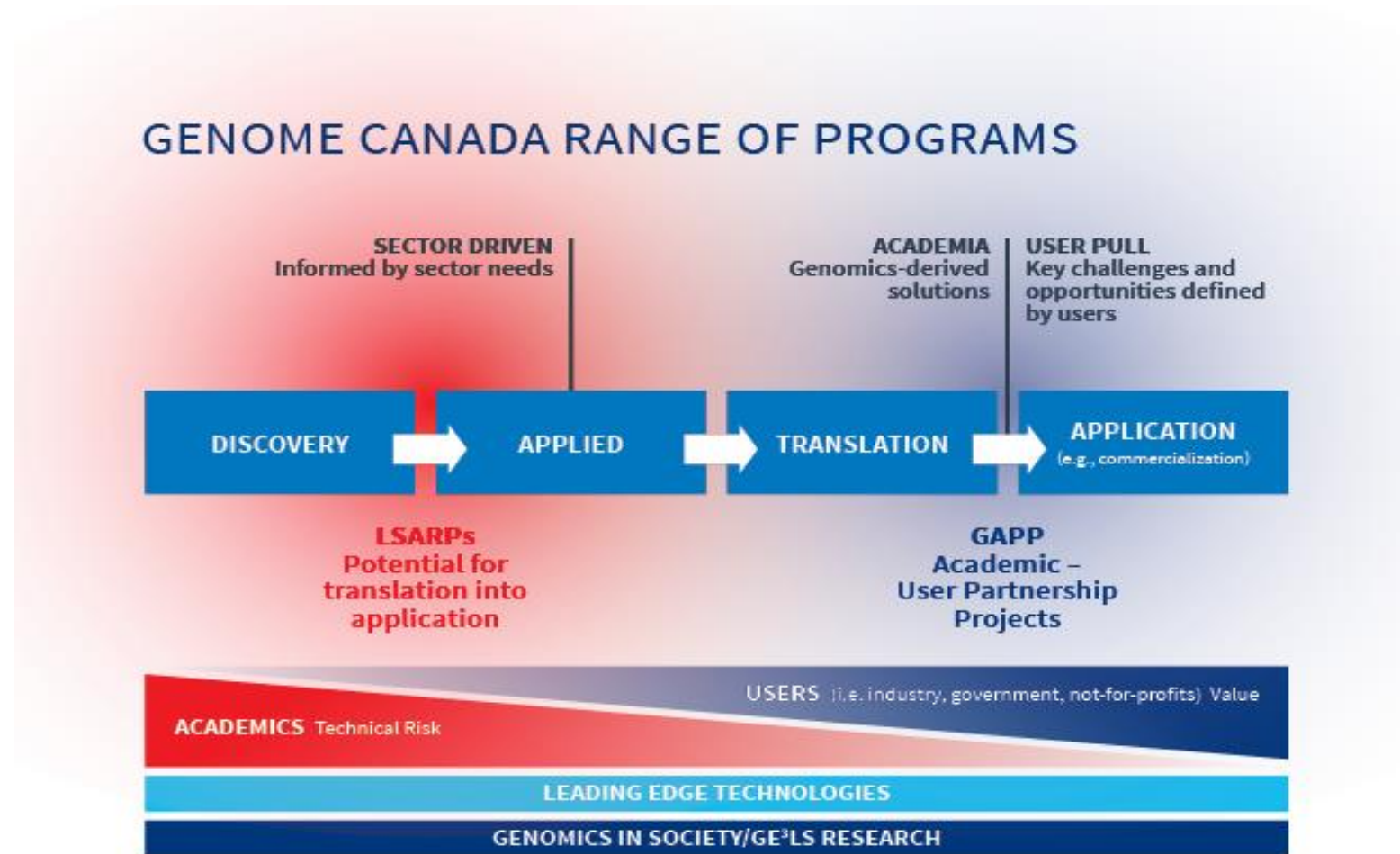
Leading Canada's genomics enterprise

Genome Canada Collaboration Opportunities and Funding for Livestock Genomics, D Bailey W158 10th January

Programs that take discoveries from lab to society

Application of Genomics to Improve Disease Resilience and Sustainability in Pork Production

Project Leader: Michael Dyck (U of Alberta)

Genome Centres: Genome Alberta and Genome Prairie

Project Budget: $9,801,714

Project Partners:

- ALGP2
- PigGen Canada
- ALMA
- Genome Alberta - PEDV
- Swine Innovation Pork
- Saskatchewan Ministry Agriculture and Food
- INRA
- National Pork Board
- Alltech Inc.
- OGI

Pigs

- Application of genomics to improve disease resilience and sustainability in pork production

- 2016 - 2019

- Industry collaboration with Large White * Landrace F1 barrows in a "natural challenge" – samples from sick/healthy pigs. (samples can potentially be collected from female litter mates)

- Collection of tissues from LW*LR fetuses (PRRSV challenge plus controls – several time points d84-98 of pregnancy)

Increasing Feed Efficiency and Reducing Methane emissions through Genomics: A New Promising Goal for the Canadian Dairy Industry

Project Leader: Filippo Miglior (U of Guelph)

Genome Centres: Genome Alberta and Ontario Genomics

Project Budget: $10,306,910

Project Partners:

- Canadian Dairy Network
- Dairy Producers
- GrowSafe System
- Ontario Ministry of Research and Innovation
- Australia DEDJTR
- UK Scottish Research College
- USDA Beltsville Research Herd
- Qualitas, Switzerland

Dairy Cattle

- **W146 Increasing Feed Efficiency and Reducing Methane Emissions Using Genomics: An International Approach**
- *Date: Saturday, January 9, 2016, Time: 2:30 PM*
- *[Christine F. Baes](#) , Centre for the Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada*

- Extremes of feed efficiency and methane emission
- Core tissues
- Core assays

Reverse Vaccinology Approach for the Prevention of Mycobacterial Disease in Cattle

Project Leaders: Andy Potter (VIDO), Robert Hancock (UBC)

Genome Centres: Genome Prairie and Genome BC

Project Budget: $ 7,358,606

Project Partners:

- University of Saskatchewan

- Genome BC

- AFBI (Agri-Food and Biosciences Institute)

Additional Support

- Federal, provincial and industry support for livestock genomics efforts
- Co-funding and international collaboration are key success factors

Development and Deployment of MBVs/gEPDs for Feed Efficiency and Carcass Traits that Perform in Commercial Beef Cattle

Project Leader: John Basarab (U of Alberta), Donagh Berry (Teagasc), John Crowley (U of Alberta)

Genome Centre: Genome Alberta

Project Budget: $4,473,035

Project Partners:

- Genome Alberta
- ALMA
- BIO
- Beefbooster Inc.
- CCHMS
- ICBF
- USDA-ARS

Existing plan

- Collection of FAANG tissues from animals of "high and low" feed efficiency based on EBVs (and GEBVs) includes methane emission

- Potential to expand to carcass and quality traits

- Crossbred steers (defined breed type) and primarily slaughter age

- Project focus on variant identification

New supporting application to Alberta Livestock and Meet Agency

- LoI due 11th January 2016
- *Outline plan*
- Select extreme animals on ebv (or breed Hi/Hi and Lo/Lo) for feed efficiency and methane yield.
- Run a time series at say 4 key points (pre-weaning, first test, puberty, and adult). Last 3 will have own phenotype.
- Collect core FAANG tissues (inc. rumen) from 2 heifers and 2 steers at each time point – 16 samples per trait.
- Angus or Crossbred population (with breed proportions)
- RNAseq and analysis/bioinformatics in Canada, core samples banked and sent (with staff) to expert labs running FAANG core assays (e.g. ChIP-seq assays. DNase-seq or ATAC-seq and Hi-C).

Ontario Ministry of Agriculture

- PI: **Angela Canovas (**P0518 P580)
- Canadian and international partners
Stephen Miller (AgResearch, NZ), Juan Medrano (UC Davis), Sinead Waters (Teagasc, Ire)
- Focus feed efficiency (and meat quality)
- Cattle

  Angus x Simental (UoG Research herd)
  Adult (n=14 animals)

  Holstein (UoG Research herd)
  Adult (n=14 animals)
- Pig
Duroc
Adult, male (n=14 animals)

- Muscle, Adipose, Liver, Gut, Brain

Agriculture and AgriFood Canada

- PI: **Eveline M. Ibeagha-Awemu**

- Dairy and Swine Research and Development Centre, Sherbrooke, Qubec

- Holstein, >2nd lactation (6 cows)
Duodenum, Ileum, Rumen, Colon, Milk fat, Adipose tissue, Skeletal muscle, Liver, Lung, Heart, Kidney, Spleen

- W020 MicroRNAs are Master Regulators of the Bovine Lactation Curve
Date: Tuesday, January 12, 2016 Time: 1:50 PM

- P0087 Long Non-Coding RNA (lncRNA) Is Abundantly Expressed in the Gastro Intestinal Tract of Calves

Collaborators

- University of Alberta: Michael Dyck, Leluo Guan, Paul Stothard, John Basarab (AAF)

- University of Saskatchewan: John Harding

- University of Guelph: Angela Canovas, Christine Baes, Filippo Miglior (CDN)

- Agriculture and Agri-Food Canada: Carolyn Fitzsimmons (UofA), ChangXi Li (UofA), Eveline Ibeagha-Awemu

- Roslin Institute: Alan Archibald, Mick Watson

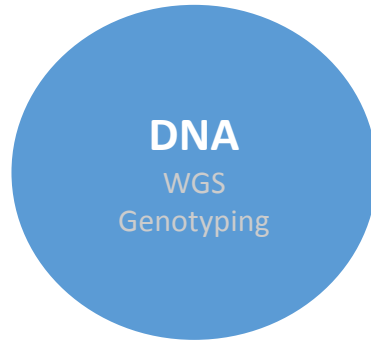- FAANG ASA – Elisabetta Giuffra, Huaijun Zhou

GenomeCanada   **and FAANG**
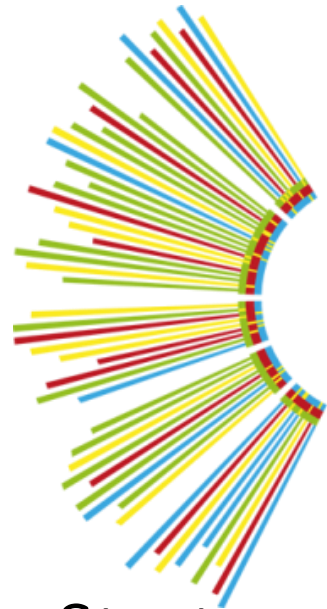
Strategy to identify regulatory mutations affecting complex traits

Amanda Chamberlain, Mike Goddard, Majid Khansefid, Min Wang, Iona Macleod, Ben Hayes

What assays are we using?

DNA
WGS
Genotyping

RNA
RNAseq
Small RNAseq

Chromatin
ChIPseq
ATACseq

39 million variants – 1000 bulls
Ref populations genotyped
GWAS
genomic selection

Gene Atlas Tissue Bank
Experimental populations
eQTL
ASE
Non coding RNA
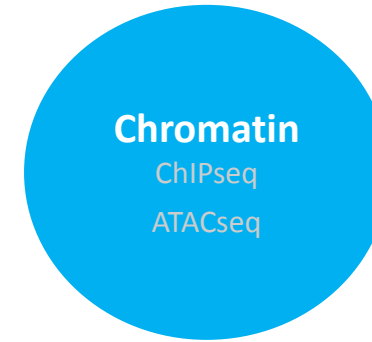
Gene Atlas Tissue Bank
Experimental populations
Public Data
Enhancers
Promoters
TF binding sites

Our strategy for identifying regulatory variants
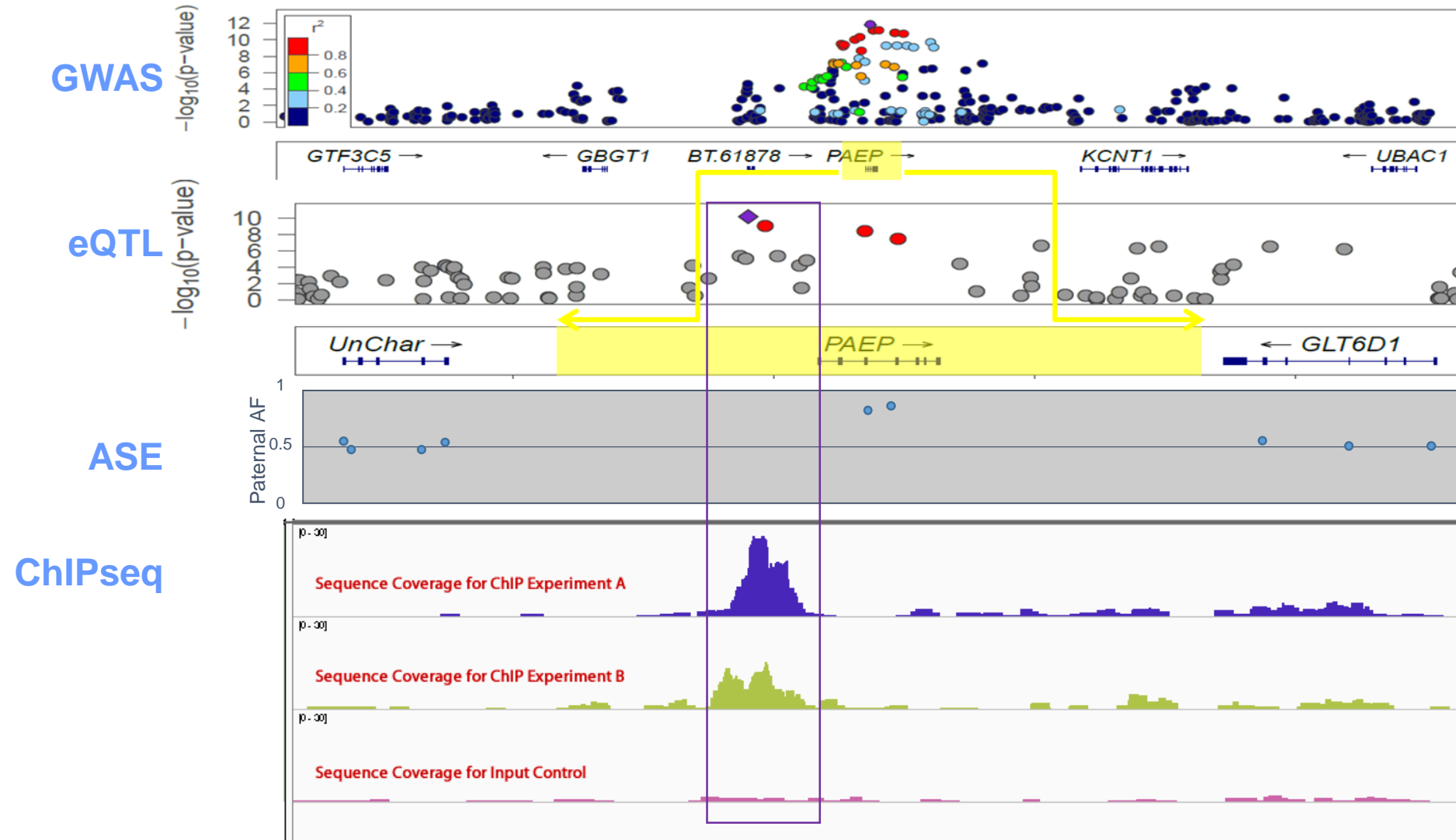
Summary

- Strategy involves using QTL, eQTL, ASE, non-coding RNA, ChIPseq marks, public data to identify regulatory variants and use in genomic prediction.

- Contribution to FAANG:
  - 39 tissues from 2 cows and their foetus'
  - RNAseq
  - ChIPseq (H3K4me1, H3K4me3, H3K27ac, H3K27me3, CTCF)
  - Bioproject PRJNA251439, FAANG tag

- Other data currently available:
  - 1 cow, 18 tissues non-stranded RNAseq, 2 tissues stranded RNAseq, Bioproject PRJNA251439, SRA SRP042639
  - 3 cows, milk and white blood cells stranded RNAseq, Bioproject PRJNA305942, SRA SRP067373

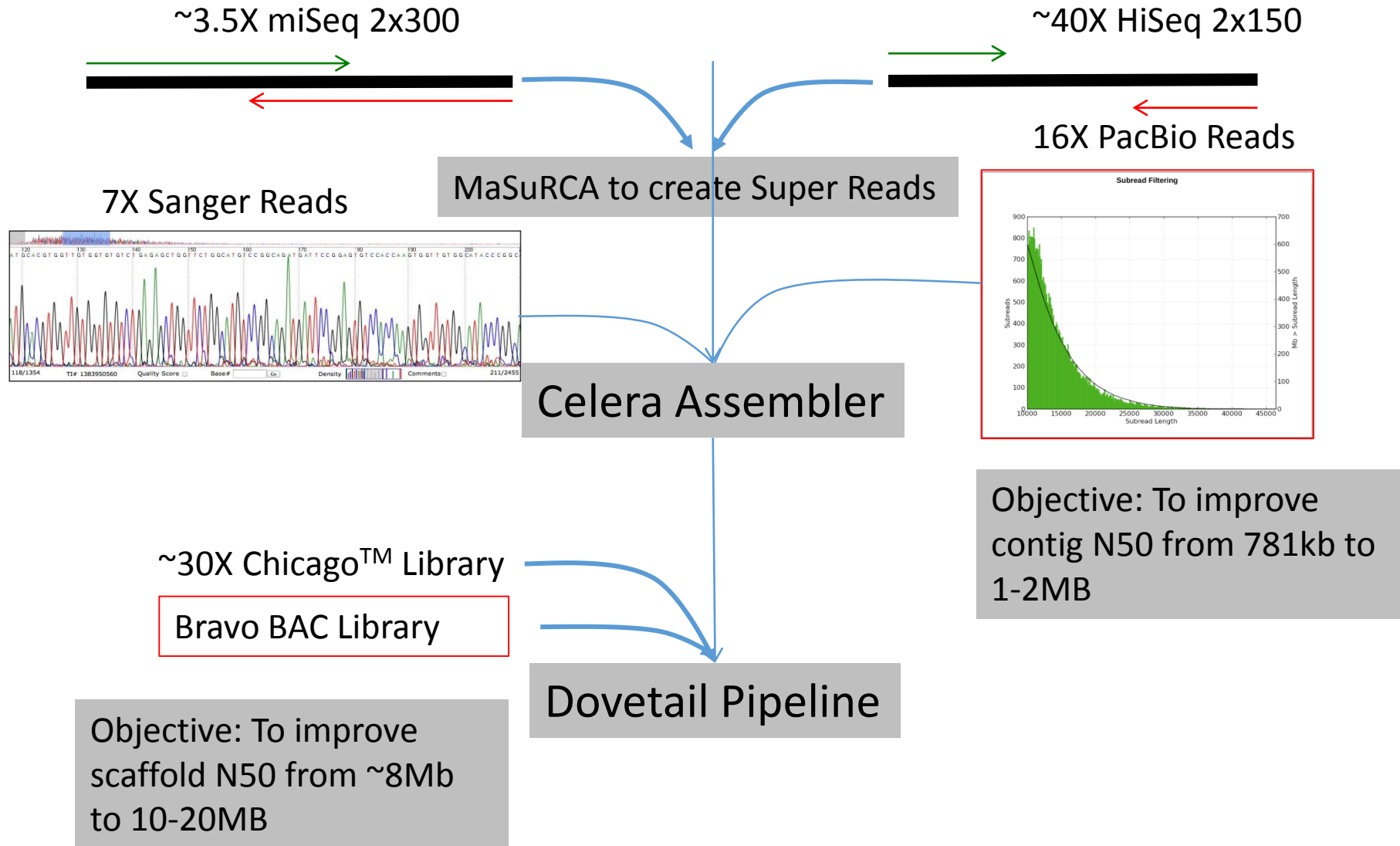# FAANG Associated Projects Update: Equine

Carrie Finno

A Community Effort to Functionally Annotate the Equine Genome and Facilitate Genome to Phenome Analyses

Equine Genome

- 2007 Equine Genome-6.8X Coverage

    -EquCab2.0 (Wade *et al.*, 2009)

- Towards EquCab3.0
    - Kalbfleisch, MacLeod, Orlando *et al*. W293)
   - -Morris Animal Foundation D15EQ-019

Structural Annotation

- RNA-seq

  1) Gene structure ~69K transcripts from pool of 43 tissues (Thoroughbred)

  - Hestand *et al.*, 2015 PLoS One 10(6):e0124375

  2) Eight tissue-specific transcription profiles (multiple breeds): embryo (ICM and TE), cerebellum, brainstem, spinal cord, retina, skeletal muscle, and skin.

  - Mansour *et al.* (P0563)

  - Publically available resource- UCSC track hubs

  - Tissue Specificity

  - Improve annotation: Extension of UTRs & Identification of novel transcripts including ncRNA

  - Correcting potential errors

Equine Functional Annotation: Proposed

- Samples: 2 Adult Thoroughbred horses (female and male)

- 50 tissues to be collected

- 8 prioritized tissues for assays: Skeletal muscle, liver, ovary/testis, cerebral cortex, spleen, heart, lung, and laminae

- Assays: WGS, RNA-Seq, microRNA-Seq, ChIP-seq (H3K4me3, H3K4me1, H3K27me3, H3K27ac, CTCF) and DNase-Seq

- Funding:
  - USDA Species Coordinator funds for sample collection
  - Submitted grant pending (Finno, Petersen, Bellone)
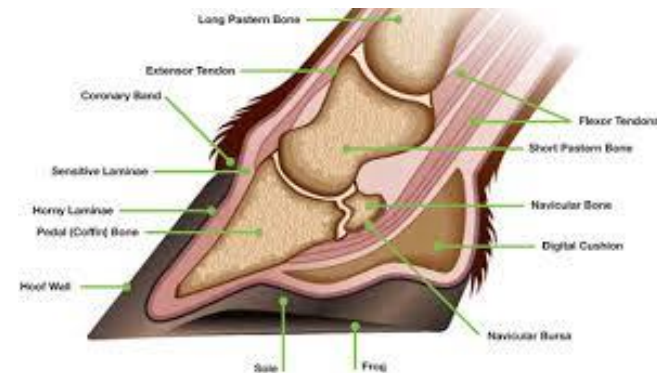
James MacLeod
University of Kentucky

Ernest Bailey
University of Kentucky

Jessica Petersen
University of Nebraska

Carrie Finno
University of California-Davis

Ted Kalbfleisch
University of Louisville

Samantha Brooks
University of Florida

Michael Mienaltowski
University of California-Davis

Molly McCue
University of Minnesota

Stephen Coleman
Colorado State University

Rebecca Bellone
University of California-Davis

Jim Mickelson
University of Minnesota

Ottmar Distl
University Veterinary
Medicine, Hannover