



# An Overview of the Sheep and Buffalo Gene Expression Atlas Projects

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Plant and Animal Genomes Conference

FAANG Session

12<sup>th</sup> January 2018



THE UNIVERSITY *of* EDINBURGH

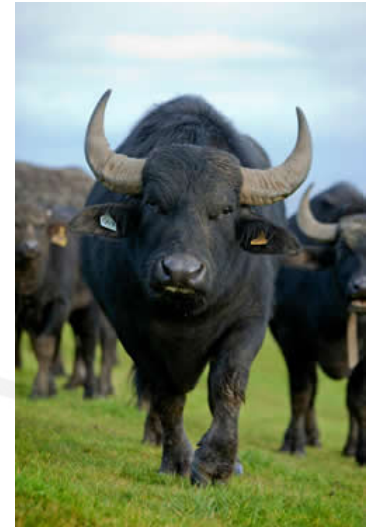


# The Sheep and Water Buffalo Gene Expression Atlas Projects



The Sheep and Buffalo Gene Expression Atlas Projects had 3 key objectives:

1. Analyse gene expression data across tissues and cell types in sheep and water buffalo to provide insight into gene, cell and tissue function.
2. Improve annotation of the current versions of the sheep and water buffalo genomes and increase the resources available for ruminant genetics and genomics.
3. Increase our understanding of the transcriptomic control of complex traits in ruminants.



# Tissue Collection and Atlas Design

## Buffalo Gene Expression Atlas

Eighty tissues and cell types were collected per animal from eight adult buffalo (4 male, 4 female)

- Mediterranean, Pandharpuri, Bhadawari breeds
- Animals were between 6 months (Mediterranean) and 4-5 years (Indian)



Mediterranean



Pandharpuri



Bhadawari

## Sheep Gene Expression Atlas

120 tissues were collected from each of 3 adult male and 3 adult female Texel x Scottish Blackface sheep (~2 years of age)

80 tissues were collected from each of 3 TxBF lambs at birth, 3 at one and 3 at 8 weeks of age

Fetal and maternal tissues were collected from days 23, 35 and 100 of gestation



# Sequencing and Data Analysis



Illumina TruSeq libraries (125bp paired-end) were prepared by Edinburgh Genomics and run on the HiSeq v2500. In total: 429 libraries for sheep and 220 for water buffalo.

All FASTQ files were deposited in the Short Read Archive with associated FAANG metadata.

To analyse the data we used two approaches:

HiSat2-StringTie pipeline with either Oar v3.1 or UMD\_CASPUR\_WB\_2.0 as the reference (conventional alignment based, novel transcript detection and validation of existing gene models).

Kallisto two-pass approach (high speed, alignment-free, using Oar v3.1 cDNAs as the reference transcriptome).

Gene expression was estimated as TPM (transcripts per million) by Kallisto and visualised in the network cluster analysis software Miru, Kajeka Ltd.

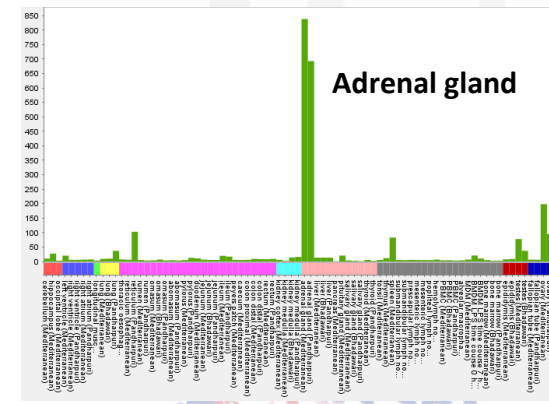
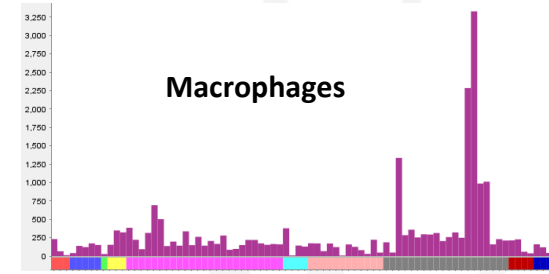
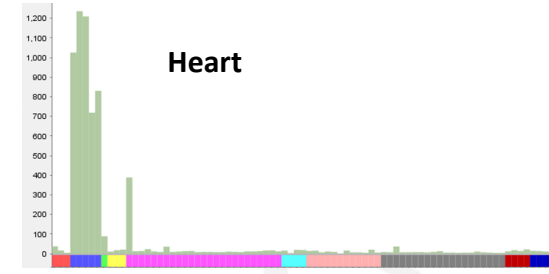
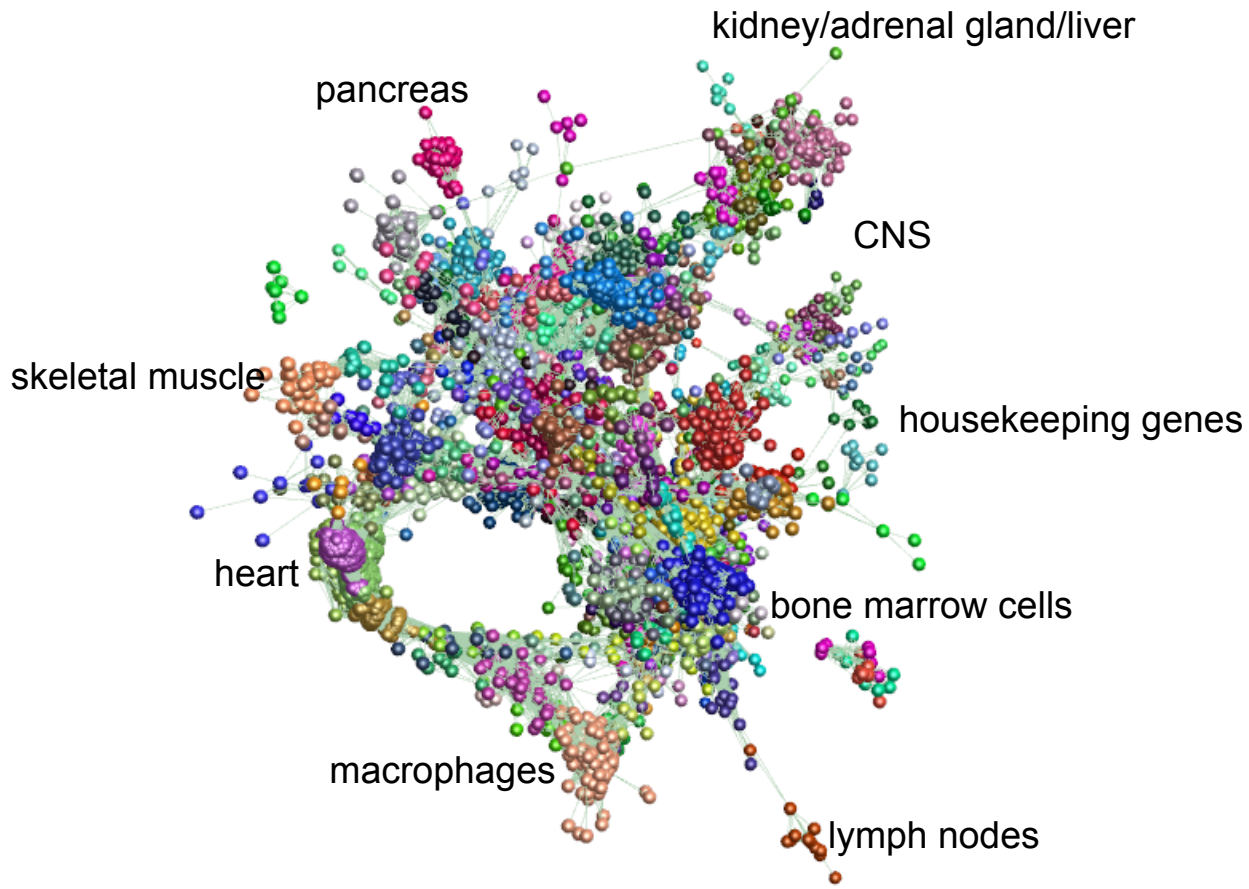




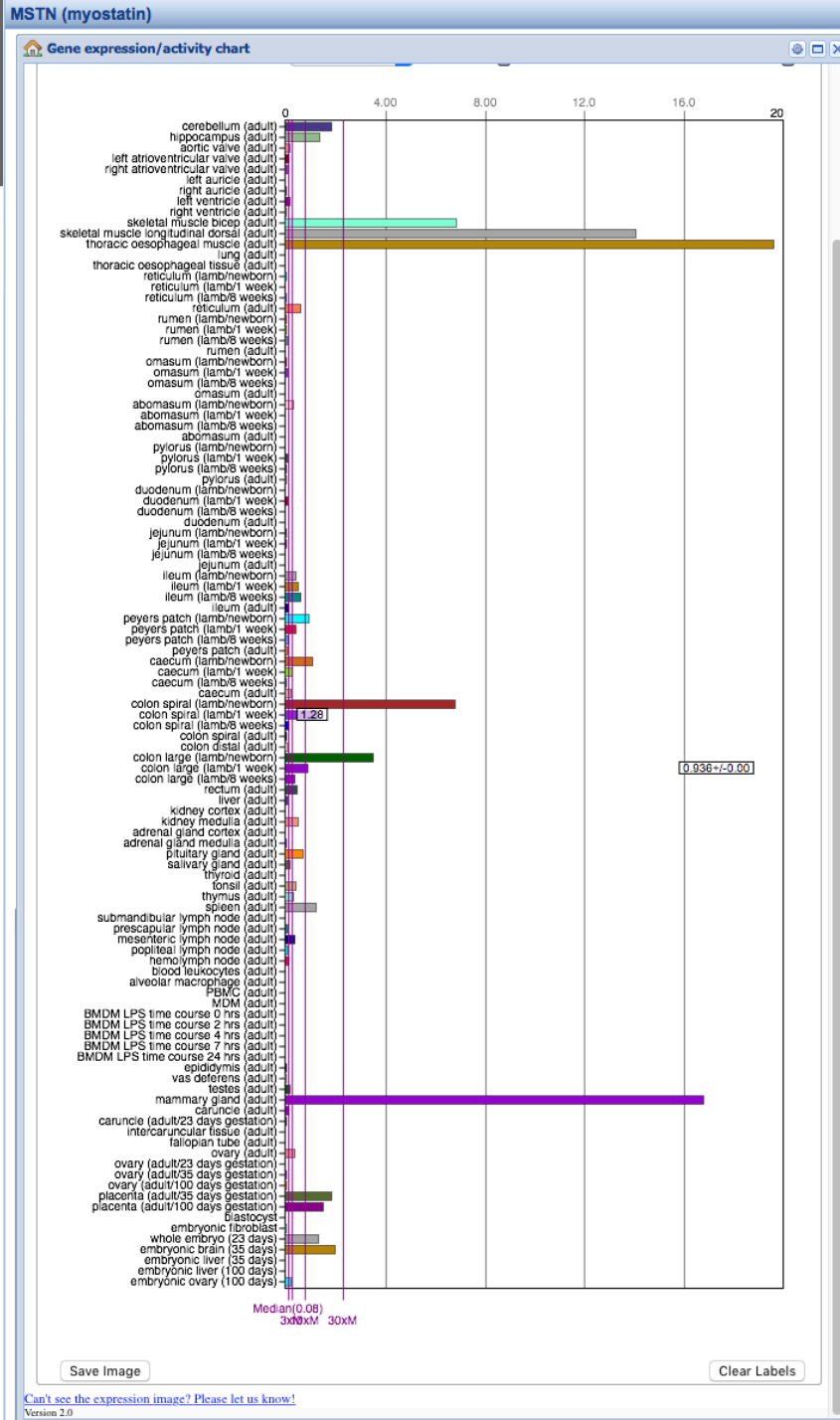
# Visualizing the gene expression atlas datasets



Miru 見る



Gene-to-gene network graph of the water buffalo atlas dataset using a pairwise Pearson correlation  $r > 0.8$



Gene Identifiers	
Symbol:	MSTN
Description:	myostatin
Accessions:	443449 (NCBI Gene) ENSOARG00000016285 (Ensembl) O18830 (UniProt)
Aliases:	GDF-8, GDF8
Genome Location:	chr2:118144443-118149433 (oviAri3)
Function:	
Interpro:	Transforming growth factor-beta, N-terminal (IPR001111) Transforming growth factor-beta, C-terminal (IPR001839) Cystine-knot cytokine (IPR029034)
Transcripts:	NM_001009428.2 ENSOART00000017734
Proteins:	NP_001009428.1 ENSOARP00000017487
Reporters:	



# Gene Expression Profiles Across Tissues in Sheep



<http://biogps.org/sheepatlas/>



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RESEARCH ARTICLE

## A high resolution atlas of gene expression in the domestic sheep (*Ovis aries*)

Emily L. Clark , Stephen J. Bush , Mary E. B. McCulloch, Iseabail L. Farquhar, Rachel Young, Lucas Lefevre, Clare Pridans, Hiu G. Tsang, Chunlei Wu, Cyrus Afrasiabi, Mick Watson, C. Bruce Whitelaw, Tom C. Freeman, [ ... ], David A. Hume [ [view all](#) ]

Version 2 Published: September 15, 2017 • <https://doi.org/10.1371/journal.pgen.1006997>

Can't see the expression image? Please let us know!  
Version 2.0

# Acknowledgements



## Roslin

David Hume  
Kim Summers  
Rachel Young  
Lucas Lefevre  
Stephen Bush  
Prasun Dutta  
Zofia Lisowski  
Charity Muriuki  
Iseabail Farquhar  
Lindsey Waddell  
Kristin Sauter  
Clare Pridans  
Gemma Davis  
Anna Raper  
Ailsa Carlisle  
Fiona Houston  
Tim Regan  
Mark Barnett  
Sara Clohisey  
Alan Archibald  
Steve Bishop  
Mick Watson  
Bruce Whitelaw



## Dryden Farm

Tim King  
Peter Tennant  
Adrian Ritchie  
Alison Mackenzie



## Edinburgh Genomics

Karim Gharbi  
Richard Talbot  
Helen Gunter



## BioGPS

Andrew Su  
Chunlei Wu  
Cyrus Afrasiabi



## CCMB

Satish Kumar  
Akshay Joshi  
Herojeet Singh  
M. Manikandan



## BAIF - Uruli Kanchan

Suresh Gokhale  
RJ Santosh  
Velu Dhanikachalam



## INRA Jouy-en-Josas

Dominique Rocha  
Gabriel Guillocheau



## PTP Lodi

Daniela Iamartino  
Nadia Fiandese  
Sara Botti

## University of Adelaide

John Williams



## FAANG-DCC



Tom Freeman

