

The regulatory GENome of SWine and CHicken:  
functional annotation during development

## Aims and Outcomes of H2020 GENE-SWitCH\*

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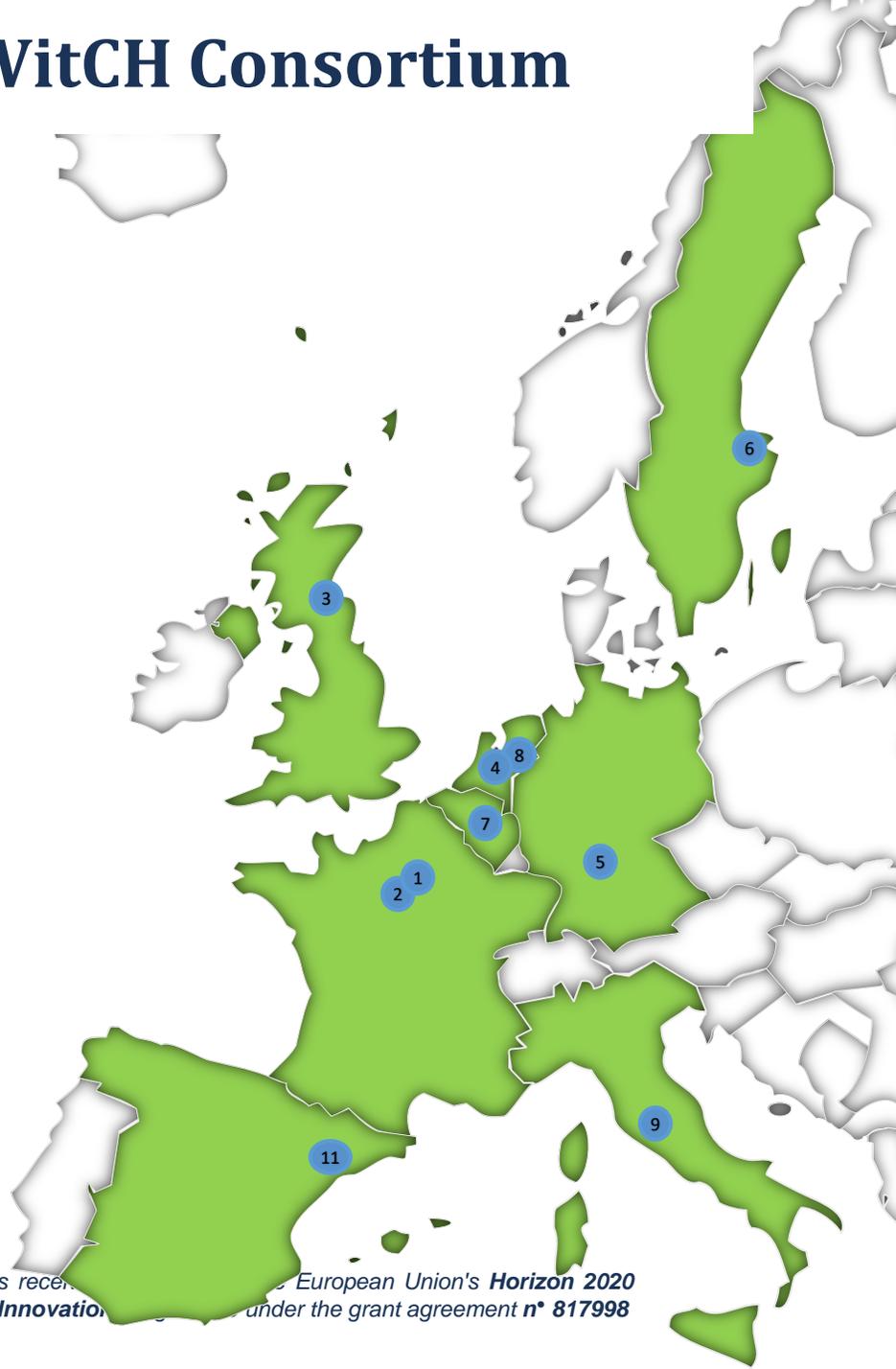
PAG31, Functional Annotation of Animal Genomes workshop, January 16, 2024



This project has received funding from the European Union's **Horizon 2020**  
**Research and Innovation** Programme under the grant agreement n° 817998

**(\* ) Jun 2019 - Dec. 2023**

# GENE-SWitCH Consortium



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3.  THE UNIVERSITY of EDINBURGH
4.  WAGENINGEN UNIVERSITY & RESEARCH
5.  EMBL-EBI
6.  UPPSALA UNIVERSITET
7.  diagenode  
Innovating Epigenetic Solutions
8.  EFFAB  
European Forum of Farm Animal Breeders
9.  EAAP
10.  HENDRIX GENETICS
11.  IRTA

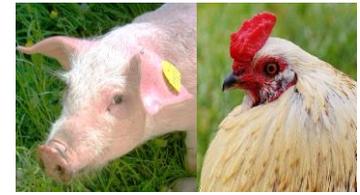
Collaboration with 3 breeding companies/ associations (Aviagen, Hypor B.V. and IFIP)



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# The global aim



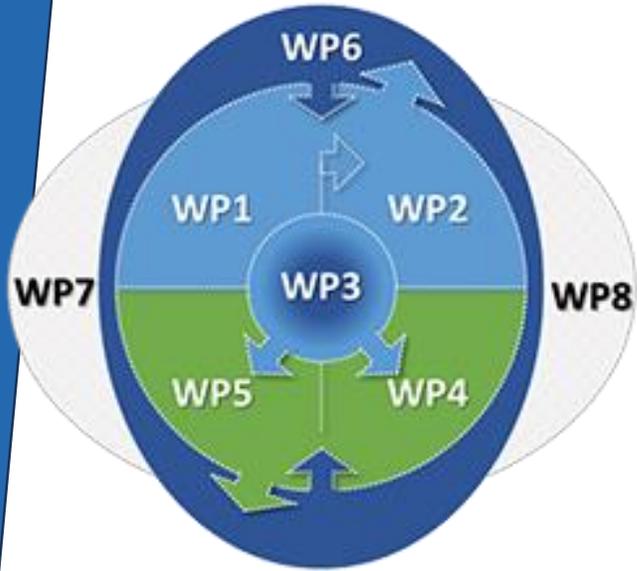
- To deliver underpinning knowledge on the pig and chicken genomes and
- to enable its translation to the pig and poultry sectors

## The underlying questions:

Can we identify and characterize the role of functional genomic elements – *and in particular those that are active/poised/repressed during development* – in the determination of the phenotypes of the adult animal?

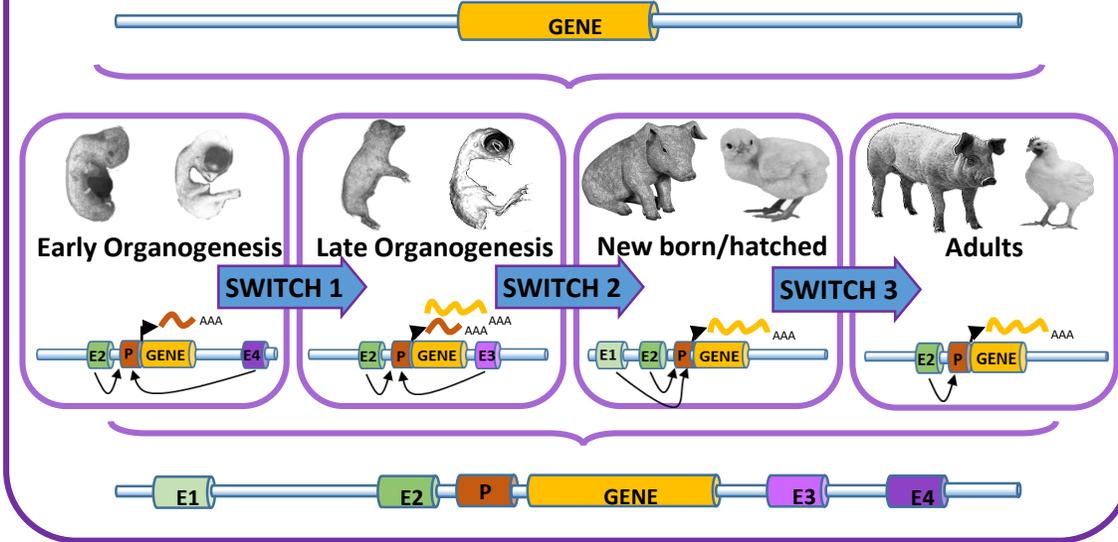
What's the relative impact of their genetic variation on main production traits?

# Three specific interconnected aims



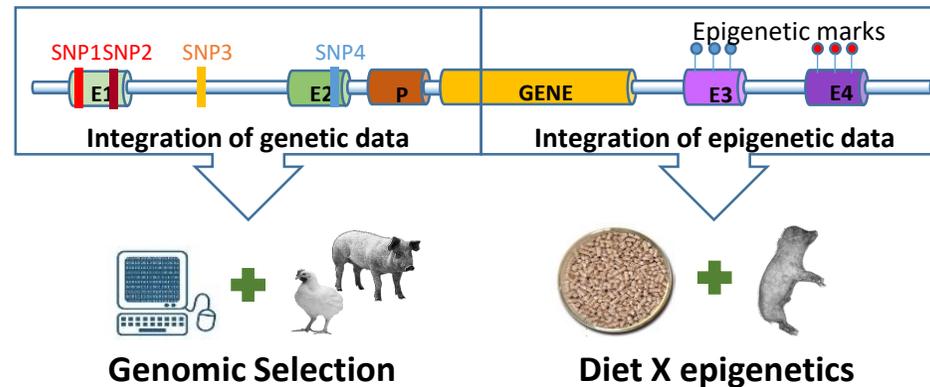
WP7 (Project management and consortium coordination)  
 WP8 (Ethics requirements)

## A. Functional annotations across tissues and developmental stages



WP1, WP2

## B. Using functional annotations for precision animal breeding



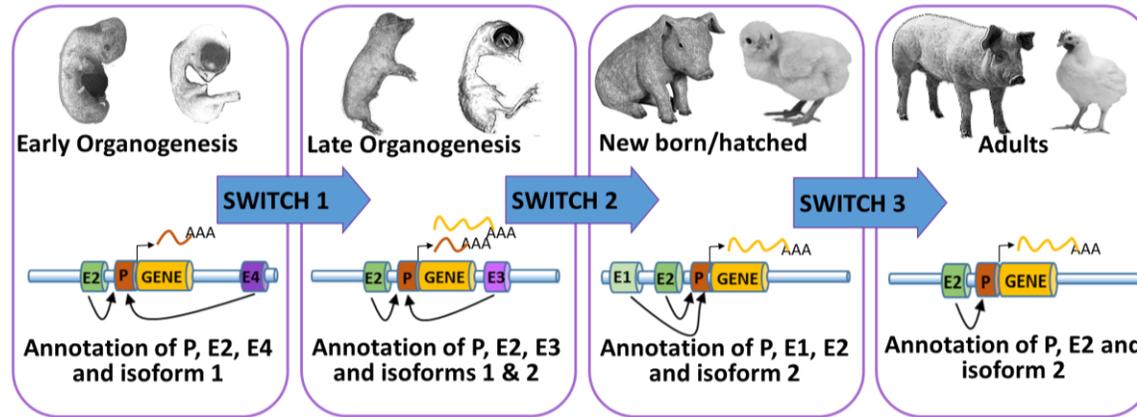
WP4, WP5



C. Standardization of data and processes,  
 dissemination and outreach

WP3, WP6

# Aim A - Functional annotations across tissues and developmental stages



- Identify the functional elements of chicken and pig genomes in 7 tissues across 3 developmental stages.
  - Characterize their tissue specificity and temporal dynamics (“switches”)
  - Characterize their patterns of conservation and variation (mammals vs. birds).
- Deliver high-quality, richly annotated genome annotation maps open to the community.



EMBL-EBI

INRAE

Inserm

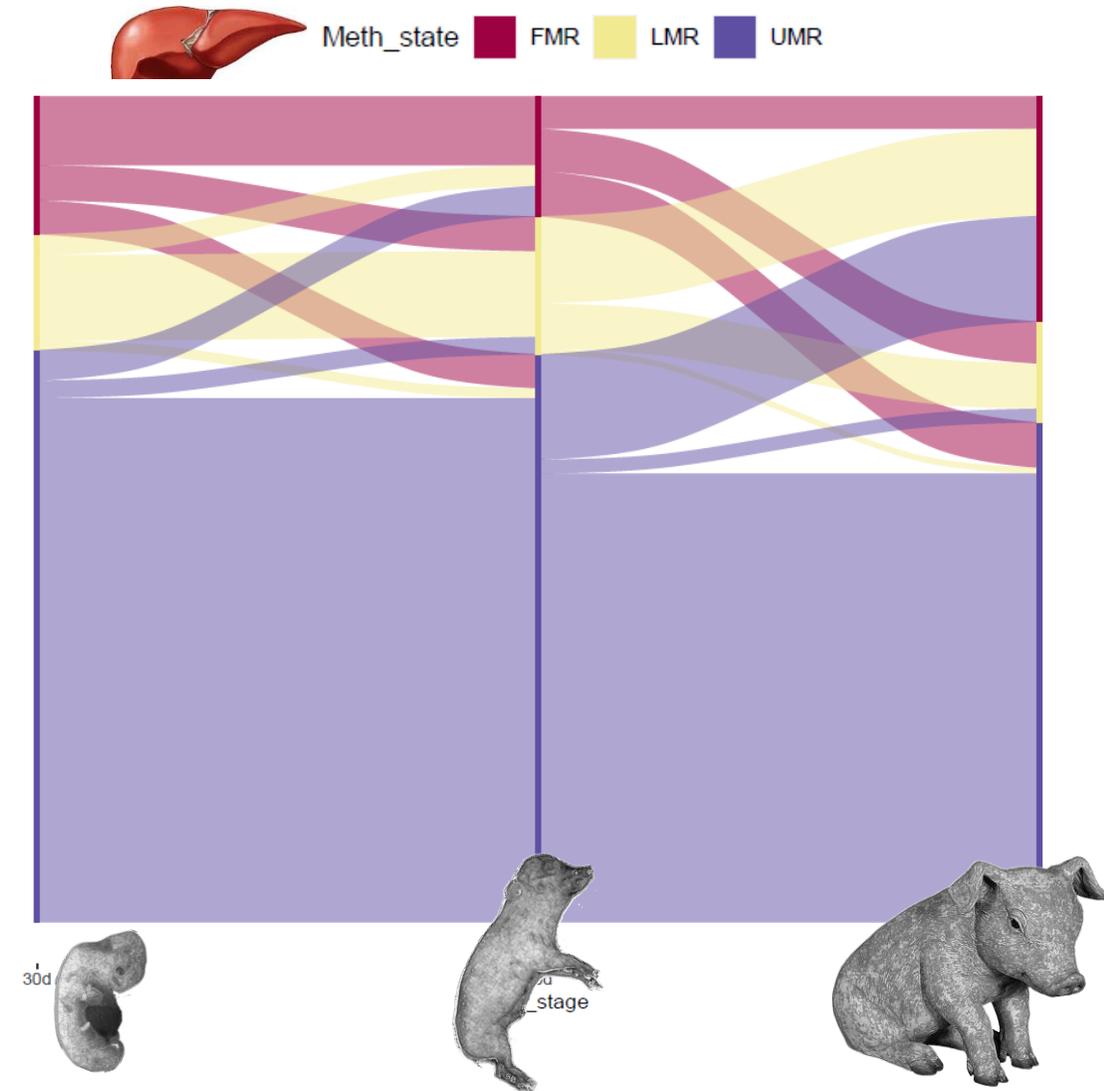
WAGENINGEN  
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diagenode

# Aim A - Dynamics of functional sequences and comparative analyses

Assay	Number of libraries		Raw reads number per library (mean)		Accession Number	
	SSC	GGA	SSC	GGA	SSC	GGA
<b>ATAC-seq</b>	84	84	100M	105M	PRJEB44468	PRJEB45945
<b>ChIP-seq</b>	IgG	78	77	48M	58M	local server
	CTCF	82	78	51M	52M	local server
	H3K4me1	80	76	95M	115M	local server
	H3K4me3	83	76	50M	57M	local server
	H3K27me3	83	81	103M	126M	local server
	H3K27Ac	84	77	53M	61M	local server
<b>RNA-seq</b>	mRNA-seq	84	84	150M		PRJEB41970 PRJEB42025
	smallRNA-seq	84	84	65M		PRJEB42001 PRJEB42041
	Iso-seq	21	21	3.5M		PRJEB50963 PRJEB48060
<b>DNA methylation</b>	RRBS	63	63	59M	55M	PRJEB41822 PRJEB41829
	WGBS	21	21	36X*	31X*	PRJEB42772 PRJEB42775
<b>Capture Hi-C</b>	12	12	180M	200M	PRJEB44486	local server

All raw data on <https://data.faaang.org/GENE-SWitCH> and ENA under the terms of the Fort Lauderdale agreement and Toronto Statement.



Ex. of methylation 'switches' (PhD thesis by J. De Vos) – *papers in prep.*

# Aim A - Extensions and refinement of nf-core community pipelines and new developments

## **TAGADA: a scalable pipeline to improve genome annotations with RNA-seq data**

Cyril Kurylo, Cervin Guyomar, Sylvain Foissac , Sarah Djebali [Author Notes](#)

*NAR Genomics and Bioinformatics*, Volume 5, Issue 4, December 2023, lqad089,  
<https://doi.org/10.1093/nargab/lqad089>

## **nf-core/iseq: simple gene and isoform annotation with PacBio Iso-Seq long-read sequencing**

Sébastien Guizard , Katarzyna Miedzinska, Jacqueline Smith, Jonathan Smith, Richard I Kuo, Megan Davey, Alan Archibald, Mick Watson

*Bioinformatics*, Volume 39, Issue 5, May 2023, btad150,  
<https://doi.org/10.1093/bioinformatics/btad150>

## **GSM pipeline (bisulfite sequencing data) from extension of nf-core methyl-seq pipeline (De Vos et al. in prep.)**

**Github links for all assays' pipelines available on <https://data.fang.org/GENE-SWitCH>**

# Aim A- A first Ensembl Regulatory Build for pig and chicken (jungle fowl, a broiler and a white leghorn) genomes

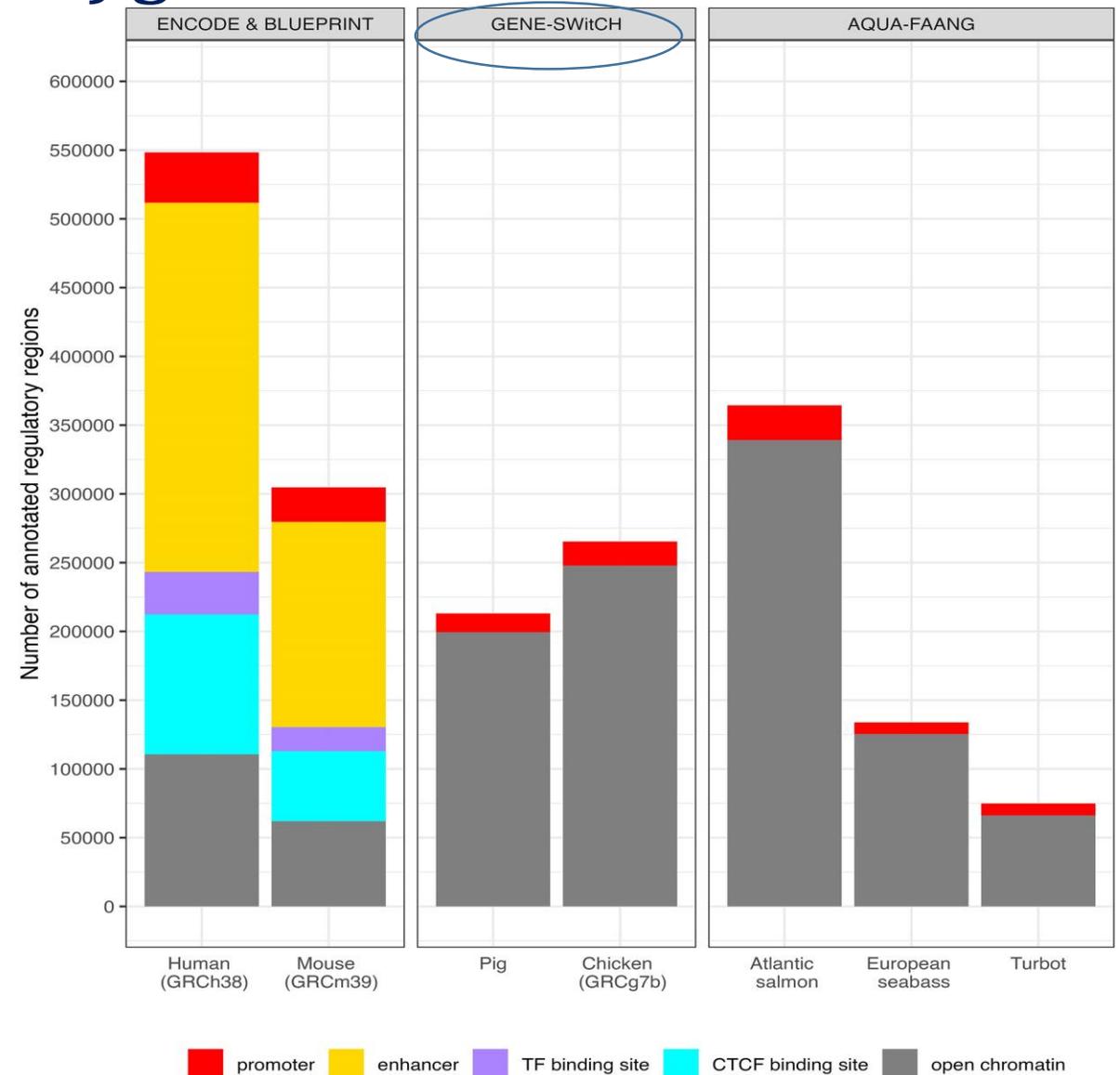


## Ensembl 2024

Peter W Harrison , M Ridwan Amode, Olanrewaju Austine-Orimoloye, Andrey G Azov, Matthieu Barba, If Barnes, Arne Becker, Ruth Bennett, Andrew Berry, Jyothish Bhai ...  
[Show more](#)

*Nucleic Acids Research*, Volume 52, Issue D1, 5 January 2024, Pages D891–D899,  
<https://doi.org/10.1093/nar/gkad1049>

Ensembl Release 111 (Jan 2024) relabeled some annotated regions as enhancers based on their overlap with relevant histone ChIP-seq peaks



# Aim B. Using functional annotation for precision animal breeding

*Two different approaches:*



Can functional annotations enhance the prediction accuracy of breeding values in commercial populations?



Provide a basis for future studies focused on better farm management (e.g. using lower-quality, more sustainable feed)

Presented at Cattle/Swine workshop, Sat. 14 Jan

# WP4: Improving predictive models for genomic selection



## Aim:

- Extend genomic prediction models to exploit new annotation maps of pig and chicken generated in GENE-SWitCH.

## Achieved by:

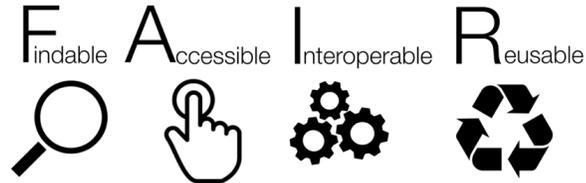
- Developing new genomic prediction models.
- Generating fine-mapped QTL and eQTL.
- Validating the models in large scale commercial data.

Next talk by Derek Bikhart



UPPSALA  
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# Aim C - Standardization of data and processes (WP3), dissemination and outreach (WP6)



- **Coordination, standardisation, validation, curation and archiving of GENE-SWitCH data**
- **Clustering activities with the other H2020 projects = start of EuroFAANG**
- **Enabling use of produced knowledge to improve the effectiveness of genomic selection in the pig and poultry sectors**
- **Implement training and capacity building activities for both academics and industry stakeholders**



## **Aim C - Some testimonials from stakeholders**

*(from: Stakeholder panel at GENE-SWitCH 4<sup>th</sup> AM, Rome, June 2023)28*

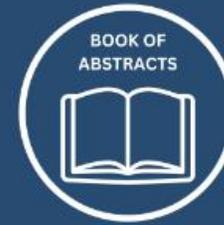
*"The GENE-SWitCH project represents a critical milestone in advancing animal breeding through functional annotation and genomics" **(FAO)***

*"The outcomes of this project have the potential to impact food security significantly."  
**(FAO)***

*"We can use the functional annotation data from GENE-SWitCH to reduce environmental load and mortality as well as increase animal health and welfare."  
**(attending breeding companies)***

*"The task of establishing a connection between genotype and phenotype poses a significant challenge. Fortunately, functional annotation is a valuable tool in guiding breeding companies towards addressing this issue." **(attending breeding companies)***

All about GENE-SWitCH is here: <https://www.gene-switch.eu/>



Hybrid event,  
6-8 Nov. 2023

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# A “final” big thanks to all participants and FAANG/EuroFAANG collaborators



**Final conference, Brussels 6-8 Nov. 2023**



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[www.gene-switch.eu](http://www.gene-switch.eu)