

# Introduction to FAANG - Goals and Opportunities (2)

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# Contents

*On goals and current activities:*

- the FAANG Data Coordination Centre

*On the objectives of funded projects in several countries*

- The three H2020 projects starting in 2019

# FAANG Data Coordination Centre

## Aims:

- Ensuring data is richly described, available and searchable.
- Ensuring data is consistently reported and presented.
- Support standardisation of protocols and analysis methods.
- Facilitating data openness, reusability and cross-project analysis.

**Build and maintain the data portal:**

<http://data.faang.org>

***Provide data coordination support:***

[faang-dcc@ebi.ac.uk](mailto:faang-dcc@ebi.ac.uk)

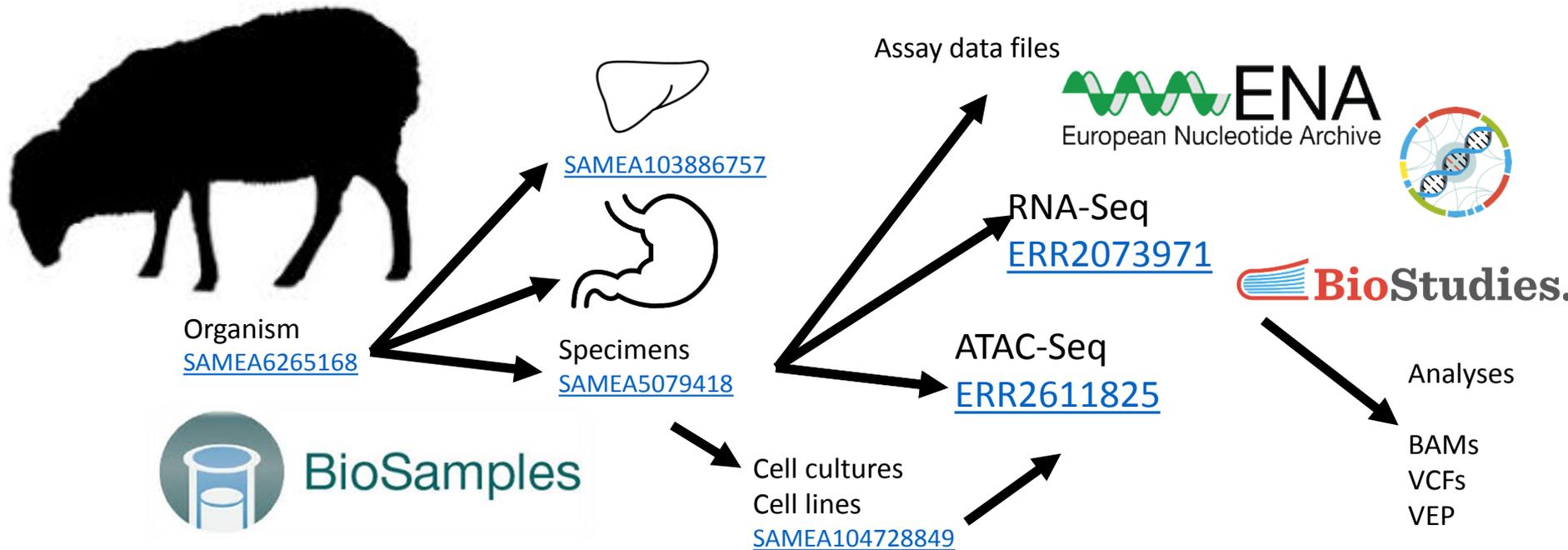
**P176 The FAANG Data Coordination Centre: Infrastructure to enable functional annotation of livestock genomes.**

A. Sokolov\*, J. Fan, G. Cochrane, D. Zerbinio, P. Harrison, and P. Flicek, *EMBL-EBI, Hinxton, UK.*

**Friday PM: FAANG: Hands on metadata validation and data submission training workshop**  
(COST Action CA15112 'FAANG-Europe')

# The FAANG data model

- Separately register animals, samples and experiments and analyses.



<http://phylopic.org/>

# FAANG Data portal: <http://data.faang.org/>

- **Single access point for all FAANG data.**
- Data held across different biological archives is indexed to allow **direct download.**
- Richly described FAANG data enables **powerful filters to narrow down to records of interest.**

The screenshot shows the FAANG website interface. At the top is a navigation menu with links: Home, Organisms, Specimens (selected), Datasets, Protocols, Files, Search, and Help. Below the menu is the heading "FAANG specimens" and a "Download data" button. To the left are filter panels for "Standard" (FAANG: 9374, Legacy (basic): 8389), "Sex" (female: 8045, male: 6745, not determined: 2953), and "Organism" (Bos taurus: 4954, Ovis aries: 3588). The main area is a table of specimens with columns: BioSample ID, Material, Organism part/Cell type, Sex, Organism, Breed, Standard, and Paper published.

BioSample ID ↓	Material ↑↓	Organism part/Cell type ↑↓	Sex ↑↓	Organism ↑↓	Breed ↑↓	Standard	Paper published
<a href="#">SAMEA104728909</a>	specimen from organism	esophagus	female	Equus caballus	Thoroughbred	FAANG	⊗
<a href="#">SAMEA104728908</a>	specimen from organism	sesamoid bone	female	Equus caballus	Thoroughbred	FAANG	⊗
<a href="#">SAMEA104728907</a>	specimen from organism	lower back skin	female	Equus caballus	Thoroughbred	FAANG	⊗
<a href="#">SAMEA104728906</a>	specimen from organism	synovial fluid	female	Equus caballus	Thoroughbred	FAANG	⊗
<a href="#">SAMEA104728905</a>	specimen from organism	yellow bone marrow	female	Equus caballus	Thoroughbred	FAANG	⊗
<a href="#">SAMEA104728904</a>	specimen from organism	suspensory ligament	female	Equus caballus	Thoroughbred	FAANG	⊗
<a href="#">SAMEA104728903</a>	specimen from organism	frontal cortex	female	Equus caballus	Thoroughbred	FAANG	⊗

# What makes the FAANG collection special

## Comparison to legacy datasets highlights the importance of:

- Rich, consistent and validated metadata data descriptions.
- Standardised core assays from contributing projects.
- Mandatory sampling and experiment protocols connected to each dataset available with the data for download.
- FAANG working groups moving towards standardised analysis pipelines and protocols.

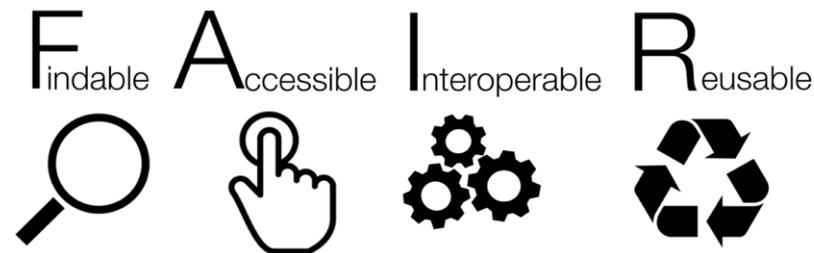


Photo: CODATA

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# Horizon 2020 Societal Challenge 2 SFS-30-2018-2019-2020: Agri-Aqua Labs

Scope A. [2018]: Understanding the genome of farmed animals, its expression and translation into traits

- Target one or more farmed animal **species (both terrestrial and aquatic)** (...) **address correlations** between normal and abnormal situations (...) May target different physiological and developmental stages and different breeds.
- Use **FAANG standards/core assays** – Data should be submitted to relevant European biological data archives to ensure they are available to the community (EMBL-EBI).
- Proposals should include a task to **cluster with other projects financed under this topic**. Accent on **International cooperation and Open Science**

**Budget: 18 million euros (3 projects, 6M € each).**



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## **BovReg**

Identification of functionally active genomic regions relevant to phenotypic diversity and plasticity in cattle

## **AQUA-FAANG**

Advancing European Aquaculture by Genome Functional Annotation

## **GENE-SWitCH**

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



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# BovReg, AQUA-FAANG, GENE-SWitCH

## *Common features:*

- Main focus on functional annotation of these genomes
- Using improved annotations: all include tasks of scope-oriented research ('post-FAANG')
- Consistent efforts in dissemination, training and networking activities.



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# BovReg

September 2019 – August 2023

Coordinator: **Christa Kühn**

Leibniz-Institut für Nutztierbiologie (FBN)

[Kuehn@Fbn-Dummerstorf.De](mailto:Kuehn@Fbn-Dummerstorf.De)



## BovReg features:

- Annotation of the *Bos taurus* genome
- Key traits: robustness (fertility)  
health (mastitis)  
biological efficiency (production – feed efficiency)

**Today: Domestic Animal Sequencing and Annotation – Auditorium 2**

**17:00 OP124 BovReg: An international consortium for functional annotation of the bovine genome.**

C. Kühn et al.



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# BovReg Objectives

To generate and validate functional genome data and standardized analysis technologies based on all **FAANG core assays**, providing a **catalogue of functionally active genomic features** relevant to phenotypic diversity and plasticity in cattle

## Specifically:

- ▶ Establish **new laboratory and bioinformatics tools**
- ▶ **Annotate functionally active genomic regions** for tissues that are highly relevant for the BovReg target traits, five ontogenetic stages, both gender and six new cell lines from dairy and beef breeds
- ▶ **Map functional parameters** (ranging from transcriptome to intermediate phenome to phenotype) to newly annotated genomic features
- ▶ Develop **prototype models for integrating biological knowledge** on regulatory variation in genomic selection
- ▶ Provide **targeted training, dissemination and communication** activities as well as assess **social perception**



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# BovReg Consortium

- 20 (19) partners
- 13 countries & 2 international organisations

- Belgium (2)
- Denmark
- Finland
- France (2)
- Germany (2)
- Netherlands (2)
- Poland
- Portugal
- Spain
- Switzerland
- United Kingdom (2)
- Canada (Australia)
- EAAP
- EMBL-ERI



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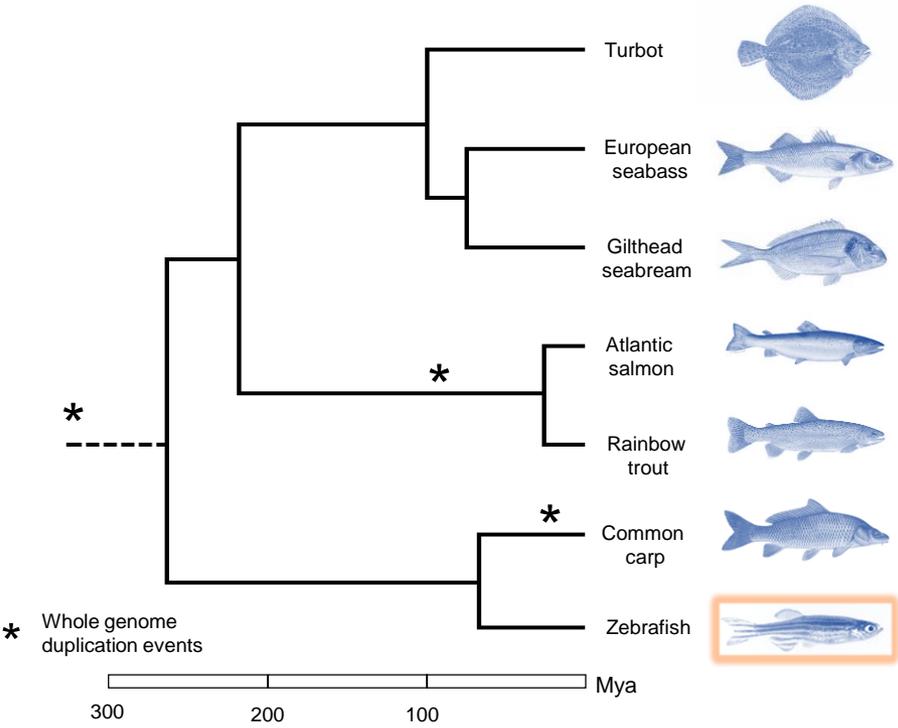


**FAANG**  
Functional Annotation of Animal Genomes

# AQUA-FAANG

May 2019 – April 2023

Coordinator: **Sigbjørn Lien**  
Norwegian Univ. Life Sciences (NMBU)  
[sigbjorn.lien@nmbu.no](mailto:sigbjorn.lien@nmbu.no)

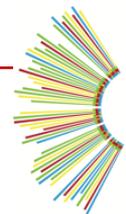


## Overall objective

To generate genome-wide functional annotation maps for the six commercially most important fish species within European aquaculture *and* exploit their contribution to variation in traits of commercial relevance, focusing on improved resistance to disease.



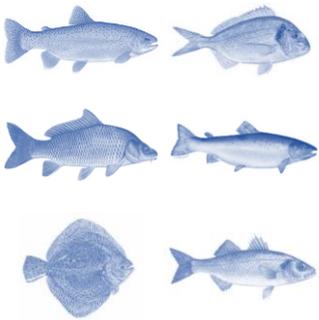
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# Overall concept of AQUA-FAANG

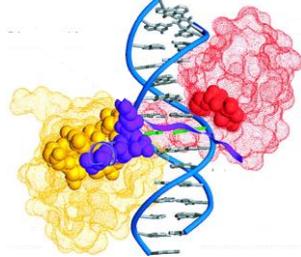
Six main farmed fish in Europe:



Reference genomes including gene annotation

## AQUA-FAANG:

Step-improvement in functional annotation of genome regulation and expression



Overall objective

*Scientific*  *Commercial*

1) Standardize protocols - share data and expertise

2) Annotation of healthy and immune active states

3) Predict disease resistance and other traits

4) Enhance functional annotation by a comparative understanding

5) Engage stakeholders and ensure results are converted to practice

Specific objectives

*European Aquaculture:*

- **SUSTAINABLE**
- **COMPETITIVE**
- **PROFITABLE**

# AQUA-FAANG: Standardized cross-species functional annotation maps

## 'BodyMaps' (WP1)

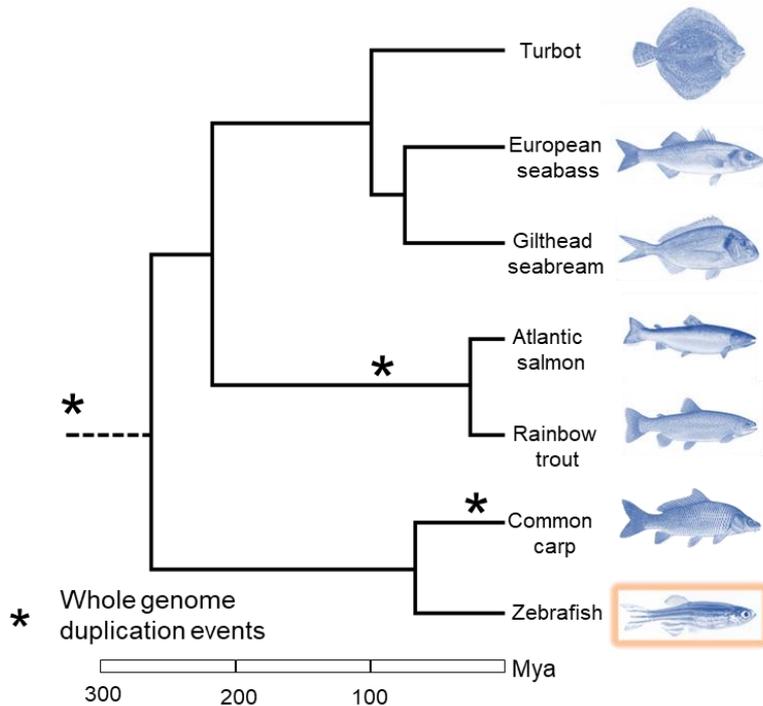
- N=4, Juveniles (unsexed)
- N=6 (50/50 male/female)
- Eight tissues

## 'DevMaps' (WP1)

- Five embryonic stages: blastula to post segmentation
- Matched to DANIO-CODE efforts

## 'ImmunoMaps' (WP3)

- Standardized stimulations using viral and bacterial PAMPs/mimics; *in vivo* and *in vitro*

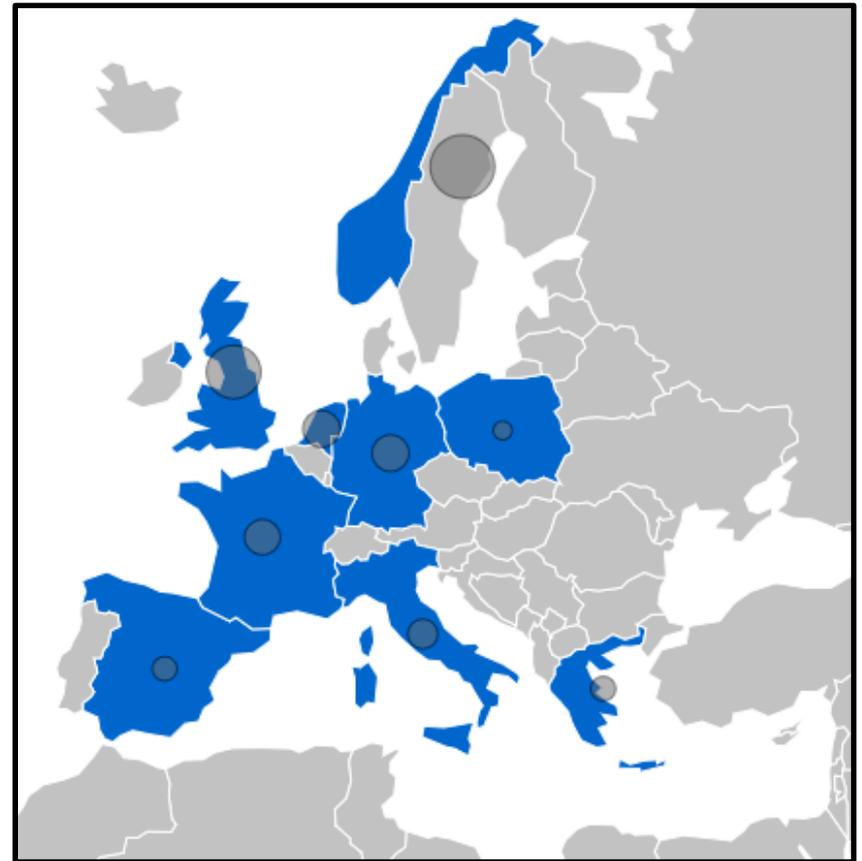


# AQUA-FAANG Consortium

Participant organization name	
1	Norwegian University of Life Sciences
2	The University of Edinburgh
3	European Molecular Biology Laboratory
4	Wageningen University
5	Institut National de la Recherche Agronomique
6	European Forum of Farm Animal Breeders
7	The University Court of the University of Aberdeen
8	Universita Degli Studi di Padova
9	Hellenic Centre for Marine Research
10	Universidad de Santiago de Compostela
11	Polska Akademia Nauk
12	Universitat de Barcelona
13	University of Birmingham
14	Imperial College of Science Technology and Medicine
15	Xelect Limited
16	Aqua Gen AS
17	Valle Cà Zuliani SocietaAgricola.R.L.
18	Panittica Italia Societa Agricola SRL
19	Ovapiscis S.A.
20	Stolt Sea Farm S.A.
21	Aquicultura Balear SA
22	Geneaqua SL
23	Syndicat Des Selectionneurs Avicoles et Aquacoles Francais
24	Nirefs Ichthiokalliergeies Anonymi Etairia

Academia

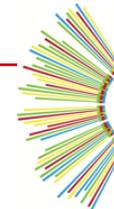
Industry / SMEs



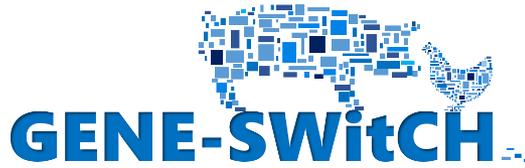
Eight European Countries



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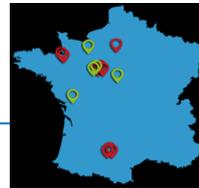
Coordinator: **Elisabetta Giuffra**  
INRA, Div. Animal Genetics  
[elisabetta.giuffra@inra.fr](mailto:elisabetta.giuffra@inra.fr)



July 2019 – June 2023

## Overall objective

GENE-SWitCH aims to deliver new underpinning knowledge on the functional genomes of two main monogastric farm species (pig and chicken) and to enable immediate translation to the pig and poultry sectors.



**The INRA group:**

**GABI Unit (Jouy-en-Josas):** Elisabetta Giuffra, Hervé Acloque, Andrea Rau; Mayrone Langellaz (technician) and Fanny Mollandin (PhD student); a postdoc will be hired in 2020.

**GenPhySE Unit (Toulouse):** Sylvain Foissac, Sarah Djebali, Hélène Gilbert; *an engineer will be hired in 2019;*

**GetPlaGe:** Jérôme Lluch

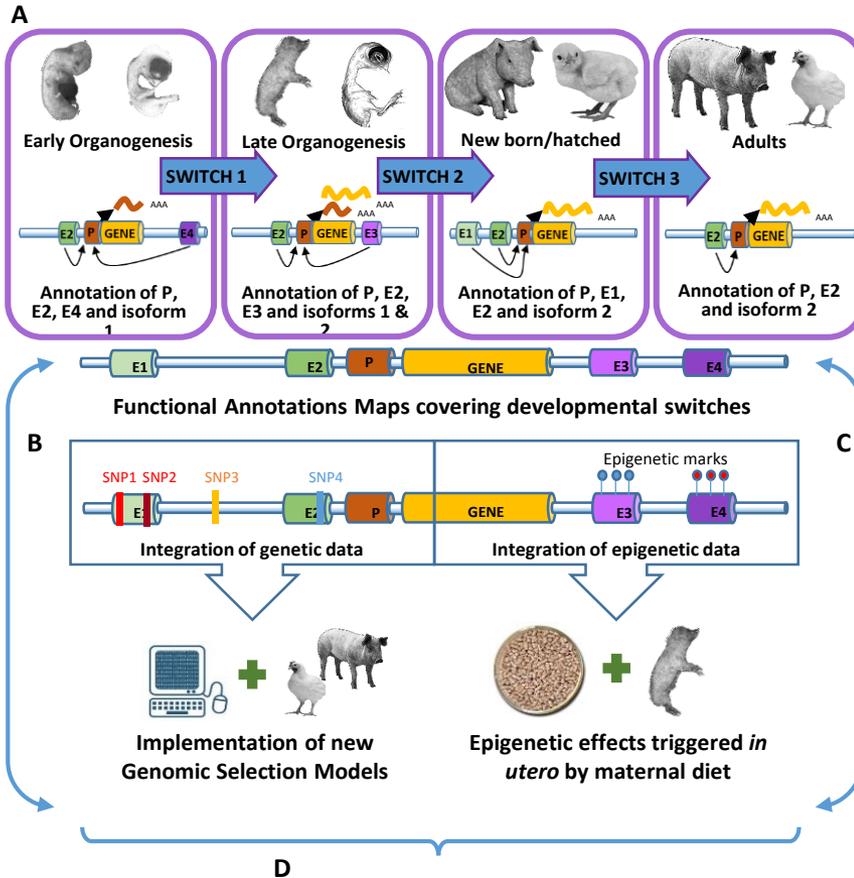


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# Concept



Focus on the regulatory dynamics (“switches”) of the genome during development from foetus/embryo to adult stages

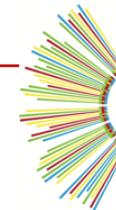
Synergistic with current FAANG efforts (i.e. US projects)



Towards more sustainable pig and poultry production systems

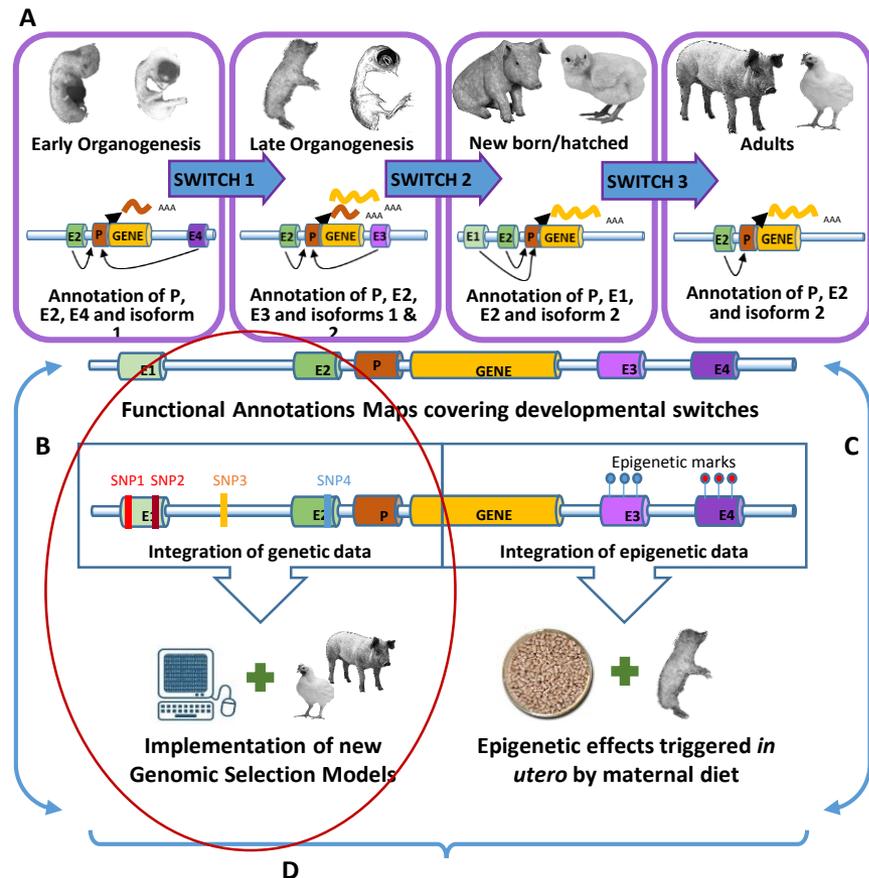


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# Concept



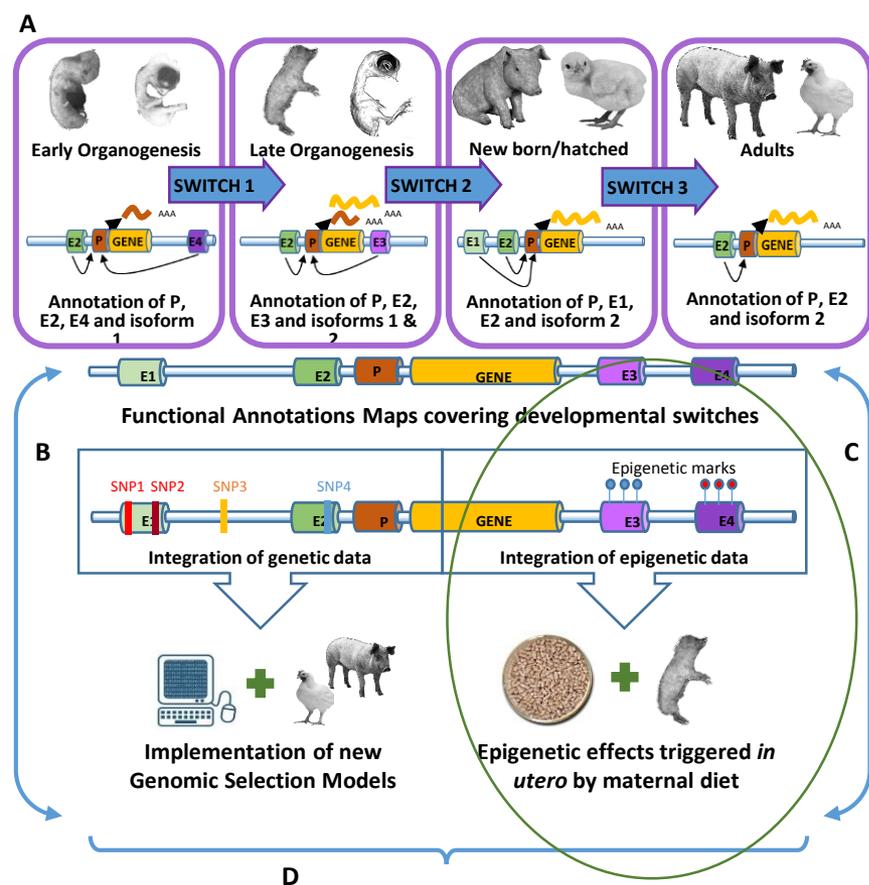
To empirically investigate the potential benefit of using functional annotation in genomic prediction:

- New genomic prediction models using information of functional annotation will be developed.
- Species-specific approaches in pigs and chickens to shed light on the relationship between genetic variation and end-trait phenotypes, and epistatic interactions.
- Validations in commercial populations of both species (phenotyped for growth rate).



Towards more sustainable pig and poultry production systems

# Concept



**Diet – one of the greatest environmental determinants – may influence fetal development but also exert a long-lasting impact on the offspring's growth and health into adulthood.**

- will examine the impact of differences in fibre contents in maternal diet on the epigenome of developing pig foetuses and weaned piglets



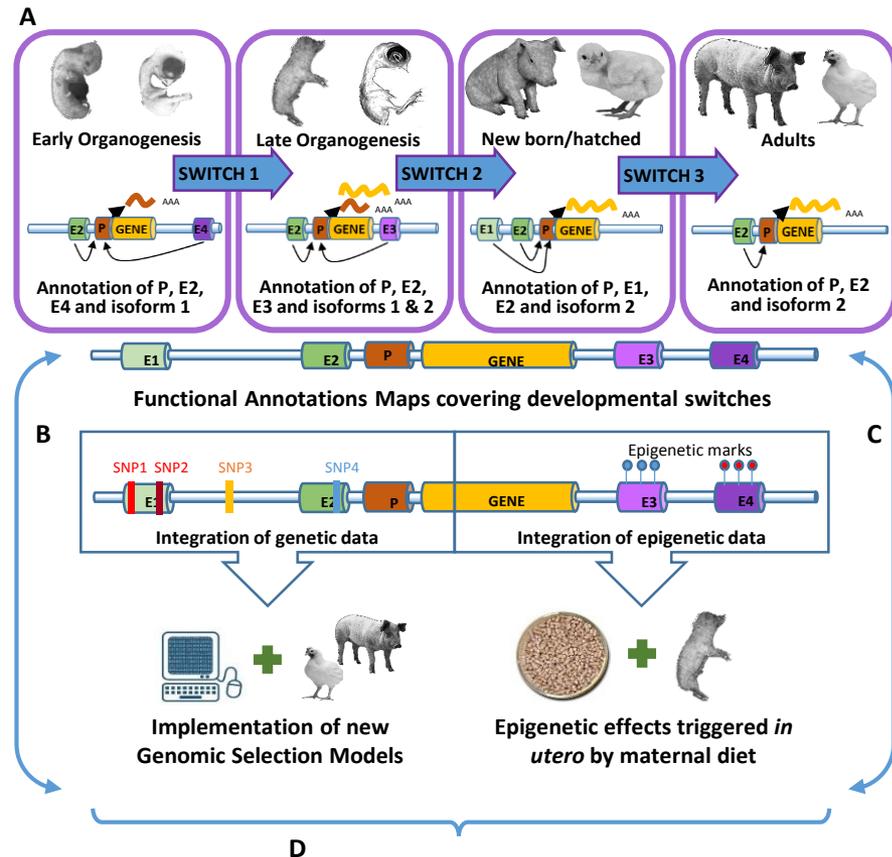
Towards more sustainable pig and poultry production systems

# Concept

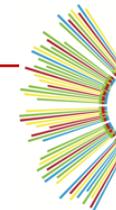


**Dissemination, training and networking activities are integral to the project**

- Data coordination, curation, validation, archiving, dissemination and publication through the European biological data archives and the FAANG Data Portal ([data.faang.org](http://data.faang.org)).
- Ensure that new knowledge and models are transferred to the breeding industry and other stakeholders.

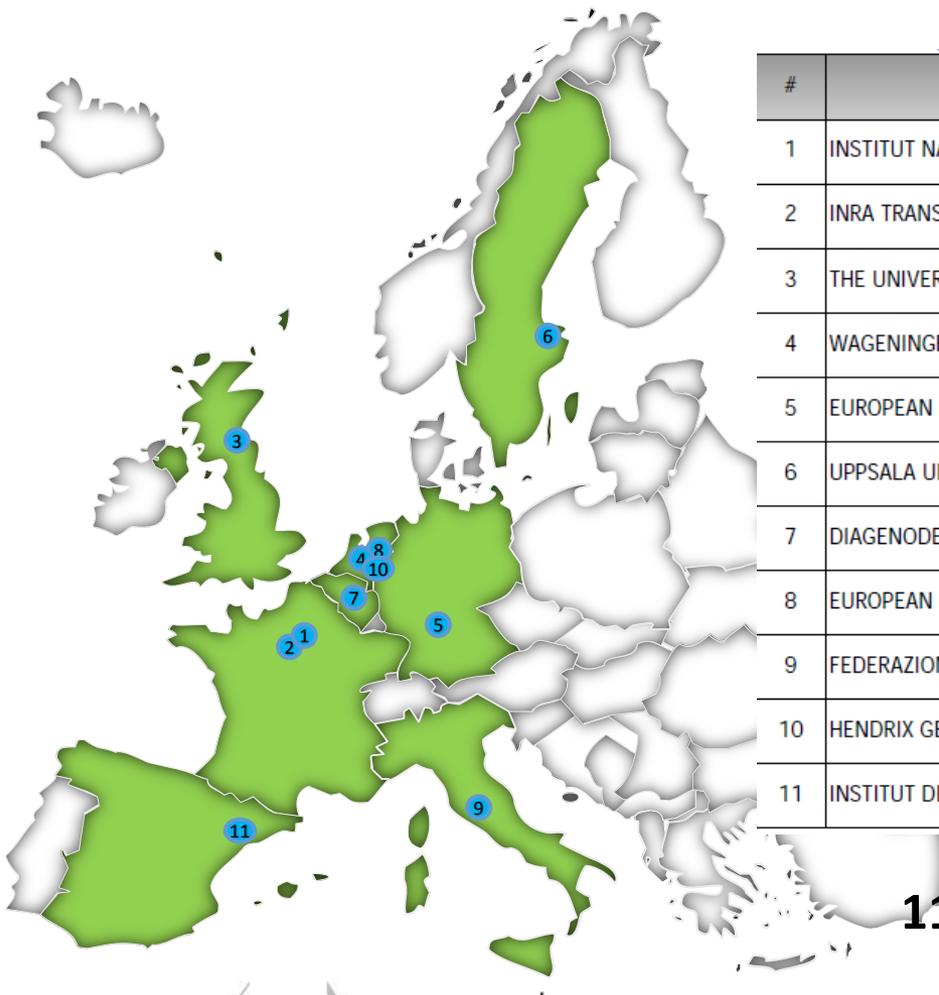


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# Consortium

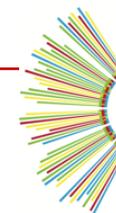


#	Participant Legal Name	Country
1	INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE	FR
2	INRA TRANSFERT S.A.	FR
3	THE UNIVERSITY OF EDINBURGH	United Kingdom
4	WAGENINGEN UNIVERSITY	Netherlands
5	EUROPEAN MOLECULAR BIOLOGY LABORATORY	Germany
6	UPPSALA UNIVERSITET	Sweden
7	DIAGENODE	Belgium
8	EUROPEAN FORUM OF FARM ANIMAL BREEDERS	Netherlands
9	FEDERAZIONE EUROPEA DI ZOOTECNICA	Italy
10	HENDRIX GENETICS B.V.	Netherlands
11	INSTITUT DE RECERCA I TECNOLOGIA AGROALIMENTARIES	Spain

**11 Partners from 8 countries**

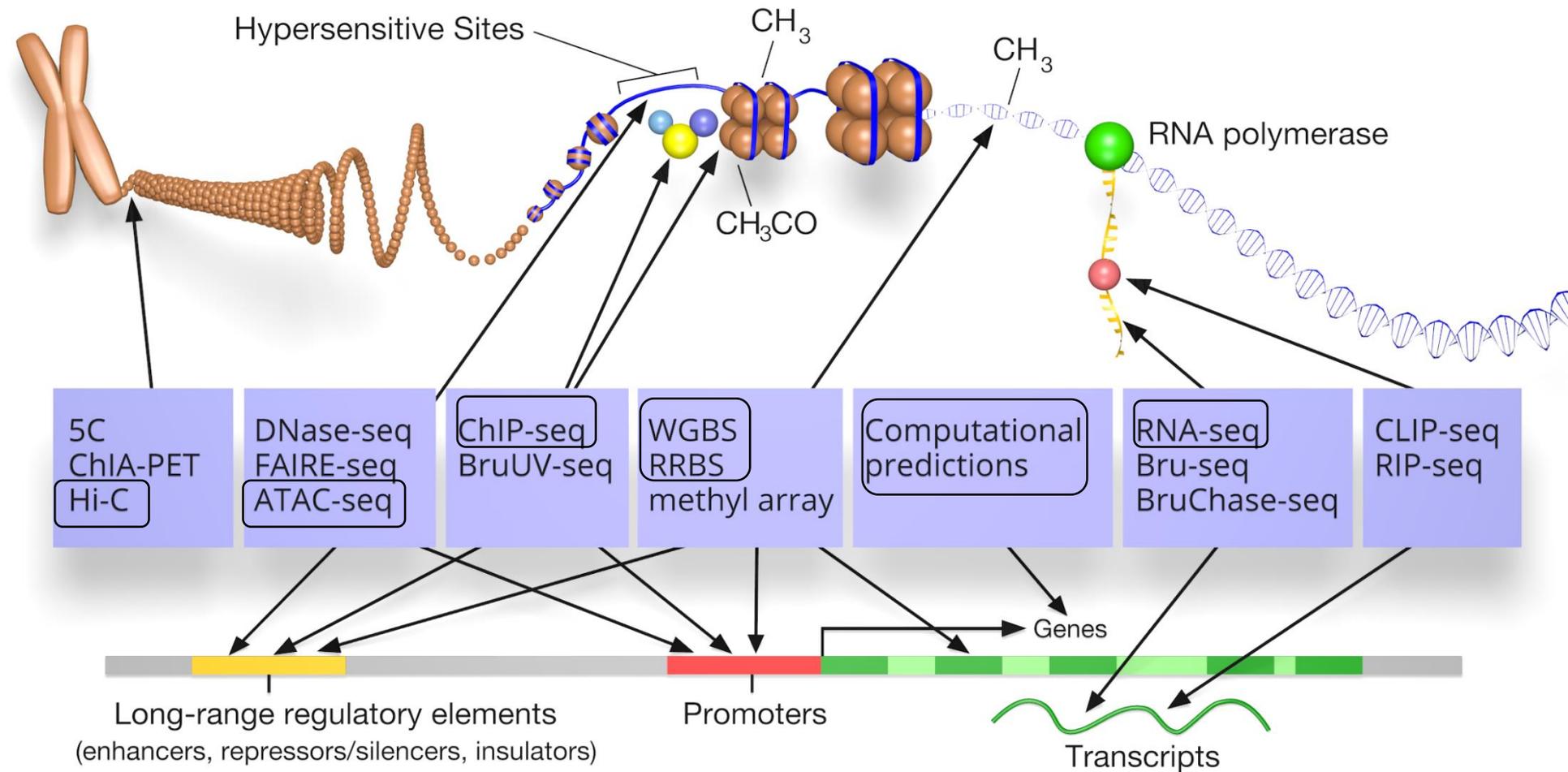


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# H2020 FAANG projects - Assays-by-sequence



By Forrest Tanaka, Data Coordinating Center, ENCODE project (<https://www.encodeproject.org/>), modified.

# Clustering of the three H2020 projects (a specific EC requirement)

## The Clustering Plan (in progress) will:

- **Empower the European component of FAANG (EU FAANG Node)**
  - Mutual participation of Coordinators and key Partners in some projects' events (e.g. kick off meetings) and dedicated meetings
  - Exchange and coordinate for implementing some of the activities related to Dissemination, Training and Networking
  - Training workshops in bioinformatics will be co-organized by all projects.
- **Pave a basis for further developments in comparative genomics (fish, birds, mammals)**



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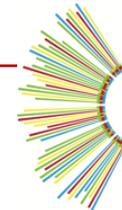
# Conclusions and Outlook

- > \$40 Million for FAANG world-wide and more to come
  - ~\$7.5M from USDA-NIFA-AFRI – including \$6 M in three major resource projects started in 2018
  - ~\$21M from EC H2020 in three new resource projects- starting in mid-2019
  - ~\$5M from Australia
  - ~\$7M from Canada
- Next five-ten years will see an explosion in functional data in the cattle, pig, chicken, sheep, horse, and fish genomes

***Realizing a Predictive Biology- increase usefulness to society and industry***



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# *Introduction to FAANG - Goals and Opportunities*

## Thanks for your attention!



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<https://www.faang.org/>

<http://faang-europe.org>

<http://data.faang.org>; [faang-dcc@ebi.ac.uk](mailto:faang-dcc@ebi.ac.uk) (Peter Harrison: [peter@ebi.ac.uk](mailto:peter@ebi.ac.uk))

<https://twitter.com/FAANGEurope>

<https://twitter.com/faangomics>