EuroFAANG newsletter

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EDITORIAL

By Geena Cartick and Joe Robertson

After three years, the **EuroFAANG Research Infrastructure (RI)** Concept Development Project has come to end, reflecting an important milestone in the establishment of a consolidated international platform for farmed animal genotype to phenotype (G2P) research across Europe.
Over the course of the project, EuroFAANG has demonstrated the value of bringing together diverse scientific communities, infrastructures, and stakeholders around a shared vision for advancing animal science.

The final project meeting took place in Hinxton, UK in November 2025, including presentations, discussions, and social activities for informal networking amongst participants. The meeting gathered stakeholders from a range of research backgrounds and disciplines, including those involved in other European infrastructure initiatives. The discussions highlighted not only scientific progress, but also the importance of interoperability, standardisation, and collaboration across disciplines and infrastructures.

A recurring theme throughout the meeting was the need to connect innovation with responsibility. EuroFAANG activities on genome editing, phenotyping, and data integration have underlined that scientific advances must be accompanied by careful consideration of animal welfare, societal expectations, data governance, and regulatory frameworks. The establishment of forums for structured dialogue—such as the genome editing think-tank and the growing links with ELIXIR and other infrastructures—has been a key achievement in this regard.

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Importantly, the project has also laid strong foundations for what comes next. The submission of the **GenoPHEnix** proposal to the 2026 ESFRI Roadmap update, developed jointly with complementary phenotyping initiatives, represents a major step toward a more integrated European research infrastructure for farmed animal science. In parallel, the approval of the **ELIXIR Domestic Animals Genome and Phenome Community** reflects growing recognition of the importance of domestic animal genomics and phenomics and provides a concrete pathway to continue developing data standards, workflows, and services beyond the lifetime of EuroFAANG.

With the project funding period now complete, work is underway toward the final reporting and review meeting. The EuroFAANG RI legacy lies not only in reports and deliverables, but in the **networks, shared understanding, and collaborative momentum** it has created. In particular, the establishment of lasting networks—most notably through the European genome editing think-tank—has provided a trusted platform for continued dialogue and collaboration across science, industry, and policy communities.

Many challenges remain, but the project has clearly demonstrated what is possible when communities work together across species, sectors, and disciplines. We would like to sincerely thank all partners, stakeholders, and contributors for their commitment and engagement over the past three years. Many important goals have been achieved, and numerous future opportunities created. We look forward to continuing this journey together as the vision for a European farmed animal genotype-to-phenotype research infrastructure moves into its next phase.

EuroFAANG
Research Infrastructure

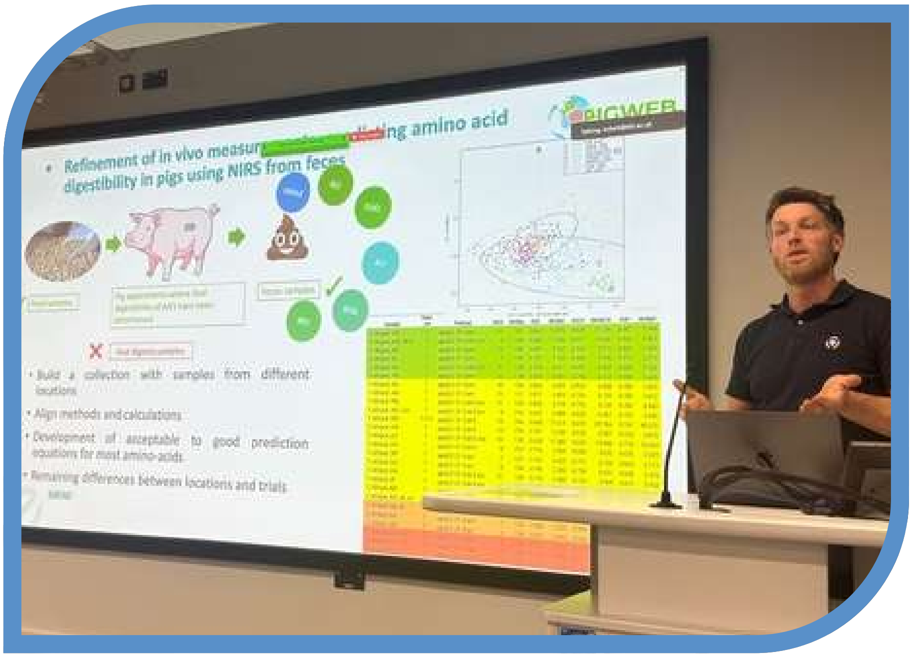
EUROFAANG FINAL CONFERENCE

By Emily Clark

The final conference of EuroFAANG RI took place on the 18-20 November 2025, exploring how collaboration and innovation can drive the future of animal science in Europe and beyond. The conference took place at EMBL-EBI in Hinxton, near Cambridge, UK, in the new Thornton Building. It ran in hybrid mode and 36 people attended in person with an average of 22 online each day.

All partners in the EuroFAANG RI project were represented by two people at least in person and other attendees included academics and industry stakeholders as well as invited speakers. Invited speakers were chosen to bridge gaps in the current concept development, expansion to GenoPHEnix and expansion to cover new areas not currently represented such as the animal health.

It took place over two half days and one full day. The programme was designed to facilitate discussion and also provide opportunity to discuss other infrastructures including EMBRC, VetBioNet and ELIXIR.



The first day focused on work package updates as well as several talks from invited speakers, several of which are summarised below.

Harnessing Marine Biobank and Biodiversity Data and Resources

Arnaud Laroquette presented on data management challenges in marine biobanks, highlighting two key challenges: connecting metadata to biological resources and linking research outcomes to original organisms. He described the European Marine Biology Resource Centre (EMBRC) as a centralized approach to managing marine data across 10 countries. Juan Pablo Narvaez-Gomez (EMBL-EBI) then demonstrated the Biodiversity Portal, which centralizes access to reference genomes and environmental data, allowing researchers to explore genomic features across different environments and geographic locations through interactive dashboards.

Machine Learning in Genetic Research

The first keynote speaker Natalie Twine (CSIRO) presented her research on using machine learning methods, particularly Random Forest and VariantSpark, for genetic association studies and epistasis screening. She demonstrated the scalability and effectiveness of these methods in identifying novel genetic interactions in diseases like Alzheimer's and coronary artery disease. She also shared recent work applying these methodologies to cattle breeding, showing improved accuracy for highly heritable traits. She highlighted the potential of these non-linear models to capture more genetic variance and work well for niche breeds. The discussion touched on the challenges of interpreting results from machine learning approaches and the need for new methods to control false positive rates.

The second day focused on expanding the infrastructure to include different perspectives.

Phenotyping Tools for Cattle Breeding – An industry perspective

Lars Peter Sørenson, from VikingGenetics, presented on "Practical Phenotyping Tools and Data Management" in the context of the cattle breeding industry. He highlighted the importance of phenotypes in breeding and the need for collaboration with research partners to develop new phenotyping tools.

Peter discussed the challenges faced by the industry, including increasing competition, climate and animal welfare concerns, and the need for high-quality data. He also touched on the use of new technologies like fresh semen and in vitro production, as well as the potential of speed breeding. Peter emphasized the importance of standardized protocols, cross-country data sharing, and robust data governance structures to improve data quality and reliability in breeding programs.

Facilities for Animal Breeding and Trait Development at INRAE

Development and implementation of new traits in animal breeding were discussed by two speakers from INRAE, focusing on feed efficiency and welfare traits. Rene Baumont (INRAE) presented on the use of a camera-based system to measure feed intake in dairy cows, highlighting its potential for commercial use despite high costs. The discussion touched on the challenges of defining and measuring welfare traits, as well as the need for better data quality and standardization across facilities. Etienne Labussiere (INRAE) then presented on the national research infrastructure in France, LIPH4SAS, which provides phenotyping services for farm animals across different species and environments. The contribution ended with a discussion on the potential for genomic selection in pigs based on digestive ability, noting that further work is needed to develop and implement these new traits.

Advancing Genome Editing and Biobanking Technologies

Challenges and opportunities in data management for animal science were also discussed highlighting the need for proper data organization and access, particularly in the context of genetic and phenotypic data. She emphasized the importance of developing ontologies and standards to make data meaningful and accessible, while also touching on the potential of federated learning as a solution for data privacy and sharing. Mike McGrew (U. Edinburgh) presented on the use of cellular platforms and sterile surrogates in poultry breeding, showcasing their potential for conserving genetic diversity and improving disease resistance.

Salmon Genetic Modification Research

Anna Wargelius concluded the session with a presentation on genome editing in Atlantic salmon, focusing on applications in aquaculture and the challenges of working with long life cycles in fish.

The discussion focused on genetic research in salmon, particularly regarding phenotyping methods and genetic modification techniques. Anna described her work with CRISPR and other methods to create genetically modified salmon, including sterile varieties and those with altered resistance to sea lice. She explained their approach to studying immune system responses and developing models for controlling fish reproduction.

New archives to consider – the Bioimage Archive

Matthew Hartley from EMBL-EBI presented on the BioImage Archive, explaining its role as a raw data resource for imaging data in biosciences. He highlighted the archive's capabilities in supporting reproducibility, data reuse, and metadata standards, particularly for microscopy and other imaging domains. Matthew also discussed the growing trend of mandatory data publication in journals, which could lead to increased use of the archive for imaging data.

Nextflow: building an nf-core community for farmed animals

Cédric Notredame (CRG) presented an overview of Nextflow, a programming language that addresses reproducibility issues in computational biology through the nf-core community. He highlighted its advantages over other workflow managers, including implicit parallelism and ease of use. Cedric discussed the growth of the Nextflow community, which has developed over 120 pipelines and hosts a Slack channel with 12,000 members. He emphasized the importance of community collaboration and governance in maintaining and improving these pipelines. Cédric also introduced the Nextflow Foundation, which aims to support pipeline development and maintenance. The talk concluded with a discussion on the bioinformatics skills required to use Nextflow, with Cédric noting that while coding knowledge is necessary, tools like ChatGPT can assist in generating code.

T2T Genome Assembly for Ruminants

Ted Kalbfleisch (University of Kentucky) presented on T2T (telomere-to-telomere) genome assembly. He explains that while complete genomes are not yet a fully solved problem, there is a lot of potential for discovery in the genomics space. He also highlighted that T2T assemblies provide superior resolution of haplotypes, structural variants, and repeat sequences compared to previous methods. The project aims to generate T2T assemblies for multiple ruminant species, with initial focus on 8 animals including cattle, sheep, and deer. The work is being done without any federal funding, and the team is actively seeking participation from researchers interested in contributing to the project.

Advancements in Comparative Genomics

The meeting covered several topics in genomics and comparative biology. Dan Macqueen (U. Edinburgh) discussed the AQUA-FAANG project, which studied genome regulation in farmed fish, and introduced a new project called WGDIP focusing on the process of genome rediploidization. He highlighted the challenges and opportunities in comparative genomics, emphasizing the need for standardized methods and better annotation for non-model species. The discussion also touched on the use of machine learning to predict bull fertility based on epigenome data, presented by Alexandre Asset (INRAE). The conversation ended with a reflection on the barriers and potential of comparative genomics, emphasizing the importance of continued investment in this field.

CRISPR Screens for Livestock Pathogens

Finn Grey from the Roslin Institute presented on high-throughput CRISPR screens for livestock pathogens. He discussed genome-wide screens to identify host factors critical for virus replication in various animal species, including pigs, chickens, and cats. Finn's team identified several genes that could be targeted for genetic editing to make animals resistant to specific viruses. They are also developing new screening methods, such as the TRIP-C approach, which allows for in vivo screens in chickens. Finn emphasized the potential of these screens to advance animal health and agriculture, and he welcomed collaborations with other researchers interested in using their screening libraries.

Advances in the animal health space

John O'Grady (UCD) presented his research on developing a machine learning classifier using peripheral blood RNA-seq data to distinguish between Mycobacterium bovis-infected cattle and controls, achieving promising results with an area under the receiver operating characteristic curve above 0.9. Sascha Trapp (INRAE) discussed the VetBioNet, a European research infrastructure project that provided access to high containment facilities and analytical platforms, and its successor project Isidore focusing on human infectious diseases. The conversation ended with a discussion on the role of animal health in a consolidated research infrastructure vision, highlighting the importance of functional annotation, emerging technologies, and data integration for improving livestock health traits.

Perspectives from the European Commission

The final day involved a discussion on the next steps and presentations from two project officers from the European Commission, Mihaela Constantin and Ángela Lahuerta-Marín; a summary of the progress of the GenoPHEnix ESFRI proposal; and an overview of the EU-LI-PHE COST Action for animal phenotyping from the University of Bologna, Italy.

To summarise, the final conference was a great success, with productive discussions that positively brought participants together, marking the conclusion of the project and setting off on the next phase with GenoPHEnix.

WHAT'S NEXT? THE FUTURE OF EUROFAANG RI

The EuroFAANG RI Concept Development Project has demonstrated what is possible in terms of a consolidated infrastructure for G2P research for farmed animals in Europe. Demonstrating the value of working together to deliver a unified vision for what needs to be achieved and how we can get there. We must now capialise on that powerful foundation to reach the next step. The EuroFAANG RI project consortia has joined with consortia for farmed animal phenotyping RI's PigWeb SmartCow and AquaExcel to submit the **GenoPHEnix** research infrastructure proposal to the 2026 update of the ESFRI Road Map. GenoPHEnix widens the EuroFAANG concept to include building access and capacity for farmed animal phenotyping and includes 14 partners from across Europe. The outcome of the GenoPHEnix proposal should be known towards the end of 2026 when we will share more news then.

Several research proposals and proposals for national infrastructures for animal and aquaculture science have also used the EuroFAANG RI project as a foundation and capitalised on the momentum provided by bringing the community together.

In addition, the *in vitro* models hub and components of the genome editing think-tank will continue with an idea for task force within the global FAANG initiative presented by Elisabetta Giuffra (INRAE - WP4) at the PAG 33 conference in San Diego in January. The Task Force would focus on sequence to consequence assays such as genome wide CRISPR screens and the importance of developing suitable *in vitro* systems for these.

We are also really happy about the news that the ELIXIR Domestic Animals Genome and Phenome Focus Group was approved to become an ELIXIR community in December 2025 providing a route to continue to develop the data infrastructure for farmed animal science in Europe further exploring as a community FAIR data sharing, workflow development and working within ELIXIR's life science strategy for biodiviersty, food security and pathogens. This is an exciting outcome of the EuroFAANG RI project recognising the gap within the ELIXIR Communities and importance of domestic animal data science in Europe.

EuroFAANG

UPCOMING EVENTS - 2026

Final EuroFAANG RI Gene Editing Think Tank Webinar

REGISTER NOW!

EuroFAANG

EuroFAANG RI Think Tank

Final Webinar

Wednesday, 21 January, 2026

15:00 – 17:00

Zoom room

Topic:

Gene Editing in Farmed Animals – Science, Applications and Responsible Innovation

The EuroFAANG RI Gene Editing Think Tank has played a key role in connecting scientific, societal, and regulatory perspectives on gene editing in farmed animals. With major EuroFAANG-linked projects—GERONIMO, RUMIGEN, and Gene-Switch—now delivering significant findings, and with growing interest at EU level in precision breeding and New Genomic Techniques (NGTs), this is an ideal moment to organise a final, consolidated webinar.

This event will synthesise the most relevant scientific advances, explore practical applications in livestock breeding, and provide space to discuss responsible innovation, societal expectations, and future pathways. It will also highlight the role of EuroFAANG RI in supporting harmonised pipelines, data resources, and collaboration for future research in Europe.

The webinar will explore:

- Scientific Advances in Gene Editing for Farmed Animals
- Practical applications of integrating gene editing into breeding and production systems
- Societal and ethical considerations about responsible innovation

Discover the full agenda and register on our website:

Think tank final webinar

EuroFAANG

UPCOMING EVENTS - 2026

RUMIGEN and GEroNIMO Joint final event

Funded by the European Union

BREEDING THE FUTURE

GENOMICS, EPIGENOMICS & SOCIETAL ACCEPTABILITY FOR SUSTAINABILITY IN LIVESTOCK

SAVE THE DATE

GEroNIMO and RUMIGEN Joint Final Event

Wednesday, 15 April, 2026
Brussels, Belgium

The joint event will take place at the University Foundation (Rue D'Egmont 11, 1000 Brussels) on the 15th of April 2026.

SAVE THE DATE and Join us to discuss livestock, selection and breeding strategies, epigenetics, new genomics and epigenomics technologies with a societal perspective.

Register now

The EuroFAANG RI project has received funding from European Union’s Horizon Europe research and innovation program under Grant Agreement No 101094718.