



A European infrastructure for farmed animal genotype to phenotype research

Deliverable 7.4 List of Services that can be provided to RIA projects

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1. Introduction

The EuroFAANG research infrastructure (RI) project aims to enable genotype to phenotype (G2P) research in farmed animals on a pan-European level by providing researchers with access to key services and resources including FAIR access to data and metadata via the FAANG data portal, *in vitro* cellular models, biobanking facilities, genome editing tools, and training/expertise on a range of G2P topics.

The key aim of Task 7.3 is to explore synergies with Research and Innovation Action (RIA) projects, engaging with those projects to assess their research goals and needs that could be met by a RI, as well as the results and outputs of these projects that could be incorporated into a RI service portfolio.

EuroFAANG RI organised a dedicated session at EAAP, August 2023, where coordinators of RIA projects were invited to present their objectives and/or results, depending on their state of progress. Since September 2024, the EuroFAANG RI consortium has been working with partners of past or ongoing INFRAIA projects on animal phenotyping in order to identify expectations of the user community as well as services that the RI could offer them (Task 7.2).

Recently, the EuroFAANG RI has collaborated with the consortia of three INFRAIA projects for animal phenotyping (AQUAEXCEL, PIGWEB, SmartCow) in order to propose a new RI on farm animal genomics and phenomics, named GenoPHEnix. This proposal was submitted to the ESFRI roadmap in April 2025 as described in the D7.3 report. GenoPHEnix would provide services to an enlarged user community as compared to the initial target of EuroFAANG.

Deliverable 7.4 aims to list the services that could be provided to RIA projects, both now and in the future, by a EuroFAANG RI, possibly in the frame of a larger RI consortium, GenoPHEnix.

2. Methods

We first targeted the six projects that make up the EuroFAANG 'umbrella' platform; that is, three Horizon Europe projects that formed the foundation of the EuroFAANG platform (AQUA-FAANG, BovReg, GENE-SWitCH; all now completed), and three active Horizon Europe projects (RUMIGEN, GEroNIMO, HoloRuminant). If the EuroFAANG RI was actively providing services today, the partners in these projects would collectively represent the core user community of the infrastructure, so their feedback on the services a RI should offer is highly relevant and valuable. We arranged an online workshop with the coordinators of the six projects (September 2024) to discuss synergies with their research activities. Since then, we have continued discussions with individual projects in order to define how a RI for G2P research in farmed animals could serve their specific needs. A detailed overview of the feedback provided by each project is available in Annex 1.

We also plan to contact leaders of projects being prepared for the next Horizon Europe call, informing them about the services that EuroFAANG can offer. As a result, the leaders of these projects may consider highlighting relevant EuroFAANG services in their workplan.

Furthermore, a user survey was launched by EFFAB as part of foundational GenoPHEnix activities. The results of this survey can be used to identify which services proposed by EuroFAANG are likely to be most requested by the scientific community.

In the below sections, we first list the EuroFAANG services that are already planned for a future active RI (i.e. those that were included in the GenoPHEnix proposal and would be available to users during the implementation phase of the RI; part 3). Since this is a large number of services, we have simplified the list by including the main categories. The full list of all services is included in Annex 2.

We have then summarised feedback from the six EuroFAANG platform projects regarding the resources and services that they think are important for their own research activities (part 4). This information is presented in the context of the wider feedback we received on GenoPHEnix services from all potential users of the RI (part 4.2).

3. <u>EuroFAANG services included in the GenoPHEnix service</u> catalogue

The EuroFAANG services included in the GenoPHEnix proposal can be broadly divided into four categories:

- 1. Laboratory Services (16 service categories)
- 2. Data and associated services (5 service categories)
- 3. Biobanking (3 service categories)
- 4. Education and training services (8 service categories)

If EuroFAANG was an active RI today, these services would be on offer to the research community (or, in some cases, under development at certain partner institutions to be offered at a later date). As such, this represents a comprehensive list of services that could be offered to RIA projects, in line with the aim of Deliverable 7.4.

Below we have listed all 32 service categories. This provides a shorter and more digestible overview of the services that EuroFAANG plans to provide, whilst a full list of all individual services is provided in Annex 2.

Laboratory Services

- 1. Advanced Analytical Services for Cellular Models
- 2. Biochemistry, structural analysis
- 3. Biosample analysis
- 4. Biosample collection and analysis preparation
- 5. Cell and organoid laboratory

- 6. Custom Cell-Based In-vitro Research Models
- 7. Detailed molecular characterisation of organoids and/or tissue
- 8. Development of organoids
- 9. G2P Genetic analyses
- 10. Genome analysis and assembly
- 11. Genome editing
- 12. Genomics
- 13. Histology
- 14. Microscopy and image analysis
- 15. Molecular biology
- 16. Spectrometry

Data and Associated Services

- 17. Advanced Analytical Services for Cellular Models
- 18. Breeding applications using G2P data
- 19. Data Services
- 20. G2P Genetic analyses
- 21. Genome analysis and assembly

Biobanking Services

- 22. Biobanking
- 23. Genomics
- 24. Sample Management

Training Services

- 25. Biobanking
- 26. Biosample collection and analysis preparation
- 27. Breeding applications using G2P data
- 28. Communication
- 29. Metadata and data standards
- 30. Detailed molecular characterization of organoids and/or tissue
- 31. Ethics
- 32. Genome editing

4. Feedback on the need for RI services from the G2P research community

4.1 Feedback from EuroFAANG project coordinators

We have had ongoing correspondence with the six EuroFAANG platform projects to assess synergies with these projects, including the services these projects (and future research efforts by their partners) would find useful. A summary of relevant feedback is provided below:

• All projects highlighted the importance of organised and accessible data, metadata, and protocols. Collectively the projects have generated a range of standardised protocols,

data and metadata that will be available to the community, and the continued management, storage and accessibility of these resources is of great importance (i.e. consistent with FAIR data principles). A more flexible and user-friendly FAANG data portal (e.g. improved data submission solutions and data visualization, harmonised ontologies with other communities) should also be a focus.

- Several projects have identified access to coherent phenotyping data as a bottleneck to
 research efforts. Since industry generates large amounts of phenotyping data, the
 importance of improved cross-sector resource/data sharing was also stressed. Data
 encryption strategies provided via a RI can streamline data sharing across sectors (see
 EuroFAANG Deliverable 6.2).
- Generation of functional annotation data and expansion of the FAANG data portal to incorporate other 'emerging' farmed animal species would be of benefit, e.g. marine invertebrates and insect species.
- CRISPR screens for high throughput identification of genes and gene regulators impacting (for example) disease resistance is of interest. This is highly technically challenging for non-mammalian species and would benefit from the combined resources available via an RI.
- Tackling traits linked to the challenges of climate change and new production environments is a key future goal. This will need development of/access to various tools including e.g. relevant phenotyping tools (*in vitro* and *in vivo*).
- Moving from 'bulk tissue' (as has been the focus in EuroFAANG projects) to 'single cell' approaches will help to more precisely understand the biology underlying key traits.
- Organoid models adapted to phenotypes of interest offer a promising alternative to in vivo experimentation, and would be a highly valuable resource if made available through a RI.
- In general, the development of a centralized, organized 'one-stop shop' for priority cell lines and other *in vitro* models (e.g. organoids) would be of great benefit to future research endeavours.
- The development of cost-effective, high-throughput genotyping and epigenotyping tools
 is a key priority. Such tools would represent a significant advancement for fundamental
 research and applied breeding programs. Currently, most animal selection programs rely
 on SNP genotyping arrays, which, while effective, do not capture epigenetic variation.
- A major opportunity for advancing animal genetics lies in the application of artificial
 intelligence to existing genomic and phenotypic datasets. Large volumes of high-quality
 data have already been generated, but the full potential of these datasets often remains
 underexploited due to limitations in traditional analytical approaches. Al and machine
 learning methods offer powerful tools to uncover complex patterns, model non-linear
 relationships, and integrate heterogeneous data types (e.g., genomics, epigenomics,
 phenotypes, environmental variables).
- Epi-genome editing can align with genome editing in in vitro models, but has specific
 challenges. An epi-genetic hub of genome editing efforts within the RI would be
 beneficial.

4.2 GenoPHEnix survey results

The survey was sent to potential users of the research infrastructure (i.e. the farmed animal G2P research community) in order to gauge the level of interest from different stakeholder groups. This included assessing which services are of most interest to potential users. The survey was completed by a total of 106 different institutions/units, which collectively covered over 6000 researchers, engineers and technicians from different sectors (higher education organisations, public research institutes, private companies).

Survey respondents were asked to select five services that their unit/institute would most need access to. As shown in Figure 1 below, the most popular service category was data services, followed by biobanking and genome editing. Other popular service categories from the EuroFAANG list provided above included G2P genetic analyses, breeding applications, genome analysis and biosample analysis. Note that Figure 1 also features services not provided by EuroFAANG that would be proposed as part of the extended consortium of GenoPHEnix.

These results reflect a broad current interest in improved data access/sharing and defining relevant metadata, as well as accessing relevant samples via biobanks and, in general, a widespread shared aim of defining the link between genomes and observable traits.

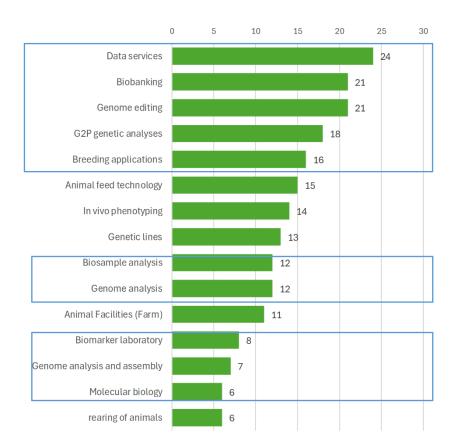


Figure 1: Most popular GenoPHEnix services according to the 'potential user survey' distributed as part of the ESFRI roadmap proposal 2025. Survey respondents were asked to choose the RI services their unit/institution would most need access to. Note, services proposed by EuroFAANG are shown within blue frames, while other services are proposed by GenoPHEnix partners who were not part of the EuroFAANG RI project.

In the same survey, respondents were also asked to reflect on the type/nature of access and resources provided by GenoPHEnix that most align with their research needs. As shown in Figure 2, data provision proved the most popular resource (selected by 66 respondents). This answer was particularly popular with industry (selected by 17 companies). Training opportunities and experimental and laboratory facilities were also popular answers, reflecting a broad interest in the service categories offered by GenoPHEnix.

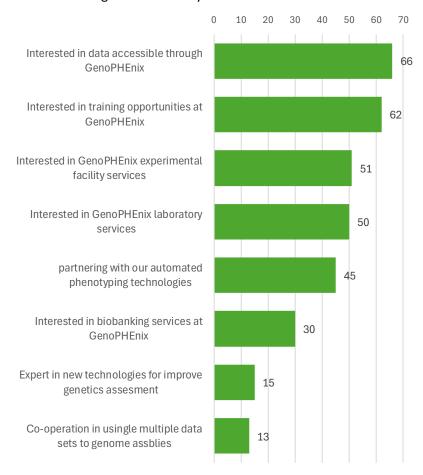


Figure 2: Nature of possible collaborations between RI users and GenoPHEnix, according to our survey. Survey respondents were asked to select the type of access/resource made available by GenoPHEnix that most aligns with their current research needs.

5. Conclusions

Preparation of the GenoPHEnix proposal (submitted for inclusion in the ESFRI roadmap, April 2025) has supported the curation of a list of services that can be provided to RIA projects. In this report, we have listed the GenoPHEnix services that are pertinent to EuroFAANG and its potential user groups, which collectively constitutes 32 service categories across four different service themes (laboratory services, data and associated services, biobanking services, and education and training services).

In addition to listing the EuroFAANG services that could be provided to RIA projects, we have assessed the current interest in different services/service categories from key potential user groups. This has been achieved via a GenoPHEnix user survey and also through ongoing discussions with the coordinators of six EuroFAANG platform H2020 projects. These activities have revealed a strong interest/need for a range of services that can be made available via a farmed

animal G2P RI, in particular those related to data access and analysis tools, biobanking facilities, *in vitro* models for G2P research, and genome editing.

We plan to continue discussions with potential users of EuroFAANG services, including the coordinators/partners of the six EuroFAANG platform projects. In particular it will be key to engage with the three active projects as they draw to a close over the coming 18 months, and discuss how a RI can support prolonged impact of project results and outputs, as well as serve future research goals connected to these projects. We plan to attend the final conferences of these projects to discuss ongoing synergies between their partners and EuroFAANG/GenoPHEnix.

Before the conclusion of the EuroFAANG concept development phase, we also plan to engage with leaders of project proposals currently being developed for submission for the next Horizon Europe call, such that they might consider highlighting relevant GenoPHEnix services in their workplan.

Collectively these ongoing discussions will help to continually shape the EuroFAANG service catalogue, identifying any gap that exists (including those that might appear in the future as new technological advancements arise), and ensuring the RI can serve the farmed animal G2P research community as comprehensively and effectively as possible.

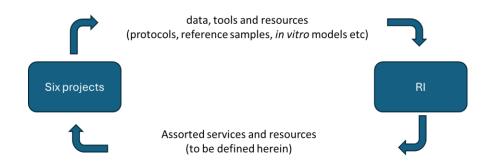
6. Annex 1 – Overview of feedback from RIA project coordinators

Synergies with six EuroFAANG platform RIA projects

Introduction

Reciprocal synergies exist between the EuroFAANG Research Infrastructure (RI) and the six projects that currently constitute the EuroFAANG platform. Reciprocal synergies are defined as follows:

- 1. Data, tools and resources (protocols, reference samples, *in vitro* models etc) arising from the six EuroFAANG projects that can be **integrated into a platform of RI services**, supporting the long-term impact of these projects.
- 2. Participants of these six projects are likely future RI users. What services/resources would they want access to, and how would this benefit future research activities? Feedback on these questions will help to compile the 'list of services that can be proposed to RIA projects' (Deliverable 7.4)



For your project, please provide feedback related to reciprocal synergies with EuroFAANG and its services/resources, as described above. Below we have outlined three synergy themes, each with a range of sub-questions for your consideration. You do not need to answer all questions, but appreciate if you can provide as much feedback as possible relevant to your project.

For context, the main five service categories as set out in EuroFAANG reporting were as follows:

- 1. Access to **protocols and data**, including genomic and phenotyping data, and sample metadata
- 2. Access to **biobanks** of reference samples, including organoids and genome-edited cell lines
- 3. Access to *in vitro* methods and tools to bridge G2P knowledge gaps
- 4. Access to world-leading **expertise** in G2P research for livestock
- 5. Access to **training** to build the next generation of researchers in farmed animal G2P

Questions for projects

<u>Theme 1: Services, tools, resources produced in your project that could be included in a G2P infrastructure</u>

- Which outputs/tools/resources do you foresee could be included in a RI service portfolio to broaden their access and longevity? These can fall within the five key categories shown above, or be in addition to these categories.

Examples include: make project data available to be used in larger studies. Make your samples available for further analyses, to add new data to existing datasets? Make your protocols available (and promoted to relevant audiences). Contribute to a network of experts to design new tools/resources. Disseminate your know-how in training sessions organized by EuroFAANG?

Who are the potential users of such RI services (academia or industry, or both; members of the project, or non-project partners)

Theme 2: Services, tools, resources that could have served your project, or serve your ongoing and future research activities

- Were there any major bottlenecks in the project that restricted progress, could certain services/resources have helped if readily available?
- If a continuation of your H2020 project was funded (i.e. version 2.0), what would the major approaches and goals be? Do you believe that a RI could help you reach your goals? Can you describe scenario(s) showing how?
- Will other current/future projects generate new data/protocols that you would wish to share using the FAANG data portal? Would you wish for support from a centralized person to assist with data formatting and uploading?

Theme 3: Other activities to support long-term impact of project

- How do you monitor that the data, protocols, resources produced in your project are valued and utilized by the community? Do you think these have been sufficiently valued so far? Are relevant people outside of your project aware of the resources? Could your projects impact be maintained and developed further via EuroFAANG?
- Is there anything you would have done differently during your H2020 project to secure long term innovation and impact of the project results, if you'd known the EuroFAANG infrastructure would be available as a platform for this?
- What was the role of industry in the project? Is there interest from industry in uptake of project results?
- Considering your project's potential to impact on breeding practices and livestock performance, how do/would you link your molecular data or *in vitro* results (for example at the cellular level) to *in vivo* phenotypes?

AQUA-FAANG (2019-2023)

Main aim: generate genome-wide functional annotation maps for the six most important fish species within European aquaculture, and exploit their contribution to variation in sustainability traits, focusing on improved disease resistance.

1. Services and resources that could be integrated into a G2P research infrastructure

AQUA-FAANG partners developed tailored functional annotation protocols describing how to generate RNA, ATAC and ChIP (3-4 marks) sequencing libraries for six aquaculture species, across multiple different tissues from males and females at different stages of sexual maturation, during embryonic development, and in head kidney primary immune cells; today all are available via the FAANG data portal. These working protocols are a springboard for researchers wanting to generate functional annotation data in fish species and it is desirable to increase their visibility and interoperability for the purpose

of optimization. More work is therefore needed to engage relevant stakeholders, particularly from industry, and also to encourage continued upload of relevant data via FAANG data portal/updating of protocols. An important function of a research infrastructure should be updating protocols and engaging with those who e.g. want to apply these protocols to new species, tissues and cells. An RI could also offer a service for testing protocols, or at least ensuring that there is a certain standard to them.

- Besides functional annotation protocols, other valuable protocols were developed in AQUA-FAANG, e.g. to establish clonal gene edited lines for investigating immune/antiviral responses and promoting viral replication. Such gene-edited cell lines could also be valuable tools for an infrastructure if available (INRAE).
- Various loss of function Chinook salmon embryo (CHSE) cell lines were produced for studying immune responses, and could be included in EuroFAANG biobanks. These KO cell lines provide a new opportunity to test directly the importance of targeted genes for the innate antiviral response in salmonids.
- All six species were used to develop primary cell cultures of head kidney cells. Although they were not edited, these were tested for immune response *in vitro*, and could be made available via the RI.
- Breeding companies already using genomic data (e.g. SNPs) for animal selection, would benefit from efforts that combine information about functional genomics with QTL data to select SNPs for the arrays / panels they use when calculating breeding values. There is evidence to say that intelligent SNP selection using functional data may improve genetic gain which is an important message to communicate to industry. A research infrastructure should be prepared to support a company wishing to explore this approach for precision breeding, including all activity from sample processing for variant detection and functional annotation, to SNP array design and genotyping.
- AQUA-FAANG was a substantial undertaking involving international collaboration, and project participants have developed competence over a range of activities from animal sampling to bioinformatic data processing. There is no doubt that many other farmed species would benefit from the types of data this project generated, including other finfish species, plus emerging farmed species such as insects and marine invertebrates. We believe that the lessons learnt from AQUA-FAANG can contribute expertise and resources to provide a 'one stop shop' for diverse animal breeding programs and can include a provision for training sessions.
- A range of project videos and webinars, including results and reflections from academic and industry partners

2. Services and tools that could have served the project or could serve future projects

- Future/current projects expansion of FAANG data portal to e.g. shellfish and insects is of great interest, as is expansion of FAANG data portal for phenotyping data. Including more species diversity would trigger an evaluation of current metadata terms and the likely introduction of new, rich terms capturing essential sample/assay information.
- The project has expanded and more precisely defined putative targets for genome editing to improve key traits for the six aquaculture species, but more work is needed to know how to best modify the genes to get the desired phenotype. An RI with expertise in genome editing for farmed animals could support this.

- CRISPR screens for high throughput identification of genes and gene regulators impacting (for example) disease resistance is also of interest. This is also highly technically challenging for non-mammalian species and would benefit from the combined resources available via an RI.
- Access to curated industry data (genotype, phenotype, etc) would be of great benefit to
 various future efforts in both the applied and research arenas. For several wellestablished species, industry possesses vast datasets covering multiple generations and
 experiments. Academic access to data of this scale and continuity can facilitate genomic
 based identification of trait associated variants, and allows RI investigators to re-use and
 review valuable data using the newest bioinformatic pipelines and latest supporting
 foundational data (e.g. updated reference genomes).
- Genomic analyses in AQUA-FAANG all involved use of 'bulk' tissue single cell genomic
 analyses are of great interest for future studies and would help refine the understanding
 of biology driving key traits by associating functional annotation data with gene
 expression or epigenomic features such as chromatin openness, at the individual cell
 level.
- Additional work is needed to understand genetic variation in aquaculture species, for example by capturing the evolutionary conservation of SNP positions across taxa, and using this in genomic prediction. Further, aquaculture genetics, as in other farm animals, is focused on SNP data, but this is only one type of marker, and structural variants, which are often causal genetic variants, should be comprehensively captured and overlapped with functional annotations in future projects using pangenomic approaches.
- Tackling traits linked to the challenges of climate change and new production environments is a key future goal in aquaculture. This will need development of/access to various tools including e.g. relevant phenotyping tools (*in vitro* and *in vivo*)

3. Other activities to support long-term impact of the project

- Future projects could benefit from increased industry involvement, potentially codesigning experiments with industry. Efforts to support the industry-academia interface in aquaculture are important, and EuroFAANG could play an active role. It requires sustained effort and correspondence across the interface to arrange workshops and identify opportunities for funding etc.
- Building an aquaculture 'hub' in EuroFAANG to continue interaction between the various
 partners and to connect future projects that are using AQUA-FAANG data (and generating
 their own relevant datasets), or otherwise continuing efforts towards overarching AQUAFAANG goals (advancing aquaculture through genomics/functional annotation).

GENE-SWitCH (2019-2023)

Main aim: To deliver underpinning knowledge on the pig and chicken genomes and to enable its translation to the pig and poultry sectors.

1. Services and tools that could be part of a G2P research infrastructure

• A broad range of FAIR resources: detailed protocols describing sample preparation and library productions; stored raw sequencing data, primary analysis outputs and metadata clearly describing the samples and experimental procedures; ready-to-use pipelines used

- for primary analysis. Collectively, these resources enable others to easily reperform experiments without the need for extensive optimization, and/or reuse the produced data without missing information or the need to write new analysis pipelines.
- A repository of tissue samples for pig and chicken, including stomach, cerebral cortex, large intestine, spleen, gonads, heart, cerebellum, skin, lungs. A part of these samples is still available and on request.
- Commercial kit for nuclei preparation and ATAC-Seq libraries' production from frozen tissues (ATAC-seq package for tissue | Diagenode C01080006)
- The first Ensembl regulatory builds for pig and chicken.
- Project videos and webinars addressed to different stakeholder types.
- Innovative genomics selection models that include the use of functional annotations, tested in commercial populations for traits pertaining to health, reproductions and efficiency – can improve genomic prediction (accuracy) in pig and poultry sectors if utilized appropriately by animal breeding companies.
- Functional and evolutionary trait heritability (FAETH) scores for each variant in pigs for use in genomic selection. This was—tested in commercial herds and provides a relevant reference for other farmed species.
- Data documenting the impact of maternal diets on the epigenome of pig fetuses and offspring. The results of this study provide a basis for further (epigenetic) studies in the context of better farm animal management (e.g., using more sustainable feed)

2. Services and tools that could have served the project or could serve future projects

- GENE-SWitCH submitted all the annotation datasets to the FAANG Data Portal as soon as
 they were produced and quality checked. While together with the other H2020 projects
 we contributed considerably to its development, the FAANG Data Portal should become
 more user-friendly and allocate several additional features in the near future (indeed,
 presently this is in progress in in collaboration with Elixir).
- More than allocating dedicated personnel for submissions to the Portal, I believe in training activities for using an improved Portal.
- I think that any project should open-share data and metadata. Hopefully, this will become straightforward asap solutions will be available to share private companies' data.
- Availability of *in vitro* cell models completed with metadata standards would provide an important support to validate the prediction of targeted molecular functions.
- If a v.2 project:
 - a. If the RI was operational, we could dedicate sufficient time to fully exploit the annotation datasets for gaining insights into comparative genomics aspects of pig and chicken development.
 - b. Access to single-cell omics of these species to provide a reference for deconvoluting tissue bulk data and better interpret biology, and in general access to new analysis pipelines based on latest technologies. We would surely also generate single-cell omics datasets).

3. Other activities to support long-term impact of the project

- We have disseminated data and results globally and quite efficiently, but quantifying the use of data, protocols and resources outside of previous project collaborators and their networks (e.g. nf-core) is difficult. For the future, it would be nice if these information on consultation and use became visible in the Portal.
- We have actively co-built EuroFAANG, also in view to ensure a long-term impact of our project.
- Industry (breeding, biotech) was actively involved, as main Partners and third linked partners. They co-created the results and are capitalizing on them in their R&D activities.
- A big part of project's results concern the improvement and test of genomic selection models that include the information on functional annotations. We did not use cell models as this could only follow to the research we made.

BovReg (2019-2024)

Main aim: 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

1. Services and tools that could be part of a G2P research infrastructure

- Access to data: all functional annotation data released by end of 2024 (including protocols and metadata). Also, metaGWAS analysis data (to project members and associated industry partners)
- Structural and functional characterization of popular bovine cell lines
- Supplementation of commercial genotyping chip with polymorphic mobile genomic element insertion sites.

2. Services and tools that could have served the project or could serve future projects

- Access to phenotyping data (coherent phenotypes across countries/partners/experiments). Data sharing agreements with industry.
- Centralized, organized one-stop shop for available cell lines including metadata current info is highly scattered
- A more flexible and user-friendly FAANG data portal, especially if want broad usership (i.e., outside of the experts with the EuroFAANG projects). This can include improved data submission solutions and data visualization, harmonized ontologies with other communities.
- The potential for the knowledge gained through BovReg (insight into regulatory regions)
 to improve genomic evaluation models has not been fully realized, and this should be
 further explored in future projects. The adoption of these models is not fully transparent
 in the bovine community.
- Structural and functional characterization of priority cell lines and organoids is needed.
- From 'bulk tissue' functional annotation towards single cell
- Need to explore the effect of epigenetic modulation of phenotypes
- Artificial intelligence approaches in G2P research

3. Other activities to support long-term impact of the project

- Upload of relevant data beyond the BovReg project depends on resources for data generation and upload within new projects. Can RI play a role in supporting this?
- FAANG data portal is treasure trove for protocols, including from BovReg, but how the
 extent to which these are taken up and utilized by the community is difficult to measure.
 Can RI support optimal awareness and utilization of protocols? Data use/value is easier
 to track via citations.
- If we had known the EuroFAANG RI project would be available as a platform to support long term impact of BovReg beyond the funding, we would have more actively tried to create follow-up projects that align directly with project aims this is something the active EuroFAANG projects should consider.
- Impact of project/results on industry is unclear integration of mobile genetic elements (MGEs) on genoptyping chip and low coverage sequencing technology for phenotyping has been adopted by industry, but uptask of new functional data in genomic prediction models is not clear at this stage.

GEroNIMO

Main aim: Provide chicken and pig breeders with new knowledge and tools to promote innovative genome- and epigenome-enabled selection methods for traits related to production, efficiency, productive longevity, fertility, resilience and welfare.

1. Services and tools that could be part of a G2P research infrastructure

- Project data will remain available for use in future, larger-scale studies. This includes phenotypes related to Efficient Livestock Production traits, as well as genotypes, epigenotypes, and transcriptomic data. While phenotypic data from private companies are not currently intended for public release, all molecular data generated within GEroNIMO will be accessible via the FAANG data portal. These include nearly 10,000 epigenotypes (from various tissues), genotypes, and over 2,000 RNA-seq datasets across three species: pig, chicken, and quail. The data were generated at different developmental stages or ages, and under diverse environmental conditions.
- Bioinformatic pipelines for DNA methylation analysis—including implementation in the *nf-core/methylseq* framework—will be made available to the community. In parallel, GEroNIMO is developing improved genetic models and analytical tools, such as transmissibility model analyses and the construction of various relationship matrices based on epigenetic information. These models aim to integrate epigenetic data to enhance predictive accuracy. In the future, a research infrastructure could offer a full range of services—from sample processing to analyses of genotyping and epigenotyping data—tailored to the needs of breeding companies interested in adopting these innovative approaches.
- GEroNIMO is a major initiative founded on international collaboration, through which
 participants have developed extensive expertise across a wide range of activities, from
 animal sampling to precise phenotyping, bioinformatic data analysis or improved genetic
 modelling. GEroNIMO partners can thus make valuable contributions to the EuroFAANG
 Research Infrastructure, in expert support and training.

2. Services and tools that could serve the project or could serve future projects

- One of the key priorities for future research and innovation should be the development of cost-effective, high-throughput genotyping and epigenotyping tools. Such a tool would represent a significant advancement for fundamental research and applied breeding programs. Currently, most animal selection programs rely on SNP genotyping arrays, which, while effective, do not capture epigenetic variation. GEroNIMO is studying this increasingly recognised layer of biological regulation that influences traits of economic and health importance, in monogastrics, in the context of the need for improved adaptation to environmental changes. An integrated genotyping/epigenotyping platform would give breeders a more complete picture of the genome and its regulatory landscape, potentially enabling more precise selection and quicker genetic progress. In the long term, this tool could replace existing genotyping arrays, offering enhanced functionality at a comparable or reduced cost. Ensuring that such technologies are accessible and scalable should be a central objective of future initiatives in this field. This has the potential to transform breeding strategies and improve the sustainability and efficiency of monogastric livestock production.
- A major opportunity for advancing animal genetics lies in the application of artificial intelligence (AI) to existing genomic and phenotypic datasets. Large volumes of high-quality data have already been generated through previous and ongoing research, including GEroNIMO. However, the full potential of these datasets often remains underexploited due to limitations in traditional analytical approaches. AI and machine learning methods offer powerful tools to uncover complex patterns, model non-linear relationships, and integrate heterogeneous data types (e.g., genomics, epigenomics, phenotypes, environmental variables). By applying AI to these existing resources, we can enhance trait prediction accuracy, identify novel genetic and epigenetic markers, and accelerate genetic improvement.
- Organoid models adapted to phenotypes of interest offer a promising alternative to in vivo experimentation, which may be impractical or ethically challenging in livestock species. These in vitro systems provide a controlled and reproducible environment to functionally assess the impact of genetic and epigenetic variants on key phenotypic variability. As such, organoids represent a valuable tool to bridge the gap between genomic data and phenotypic expression.
- Private partners are engaged and interested in the potential to include non-genetic parameters—such as functional information or epigenetic marks—into genetic evaluation models. They also recognize the value of breeding strategies that preserve genetic diversity, ensuring long-term resilience and adaptability. Strengthening collaboration with the private sector is crucial, not only to promote sustainable breeding practices, but also to enable research access to large-scale, high-quality field data that only professionals can provide—thereby greatly enhancing the relevance and impact of scientific studies.

3. Other activities to support long-term impact of the project

Continued upload of data to the FAANG data portal and ongoing communications support
are essential to ensure EuroFAANG projects' lasting visibility and utility. This continuous
data sharing fosters transparency, reproducibility, and enables further meta-analyses and
comparative studies.

• In parallel, sustained communication efforts are crucial to disseminate results, maintain engagement with stakeholders, and promote uptake of project outputs, facilitating knowledge transfer beyond GEroNIMO consortium. Notably, private sector partners (breeders) have been involved from the beginning, highlighting the potential to include non-genetic parameters in genetic models, and the need to preserve genetic diversity. Continued interaction with them to support uptake of project results is needed.

RUMIGEN

Main aim: improving ruminant breeding through genetic, genomic (including genome editing) and epigenomic approaches

1. Services and tools that could be part of a G2P research infrastructure

- WGS and epigenetic data to improve bovine genome assemblies and annotation will be made available for further exploitations.
- Improved genetic models for genomic selection and conservation of genetic diversity for local breeds will be made available.
- Genome edited sheep and goat animals have been produced by Rumigen: their tissues and cells could be biobanked and made available to the research community.
- EpiChip (Illumina 40K) cost-effective tool to epigenotype cows will be commercially available for scientific community around September 2025.

2. Services and tools that could serve the project or could serve future projects

- European epigenetic observatory gather together the people working together on epigenetics, and better understand the impact of different environments across EU on different performance traits, identifying biomarkers etc.
- Epi-genome editing can align with genome editing in *in vitro* models, but has specific challenges; could have epi-genetic hub of genome editing efforts in the RI.

3. Other activities to support long-term impact of the project

- Private sector partners (breeders) might be interested in the potential to include epigenetic parameters in genetic models and in using breeding practices to preserve genetic diversity. Continued interaction with them in the future will ensure optimal impact of the carried researches.
- Animal models (GE and/or introgressed) developed in Rumigen could be commercially developed by the breeders, taking into account potential evolution of the EU legislation on GE animals.

HoloRuminant

Main aim: Elucidate the role of ruminant-associated microbiomes and their interplay with the host animal in early life and throughout fundamental life events

1. Services and tools that could be part of a G2P research infrastructure

• Database (HoloR) and repository (HoloR-tools): includes all bioinformatic pipelines and large scale international and standardised data generated in the project:

The project includes the development and maintenance of HoloR, a comprehensive database that stores standardized, large-scale, international datasets generated throughout the study. Accompanying this is HoloR-tools, a curated repository that hosts all bioinformatic pipelines and analytical tools used in the project. Together, these resources ensure reproducibility, facilitate data sharing, and support collaborative research efforts in microbiome and host genomics.

 High-Quality Metagenome-Assembled Genomes (HQ-MAGs) from ruminants Microbiomes:

The project generates and catalogues high-quality MAGs mainly from the prokaryotic members of the ruminant microbiome. These genomic resources significantly enhance existing reference databases, enabling a more comprehensive understanding of the taxonomic and functional diversity within ruminant ecosystems. This, in turn, provides critical insights into host-microbiome interactions and their role in animal health and productivity

- Microbial signatures associated with host key performance indicators (KPIs).
 Distinct microbial profiles associated with essential host KPIs, such as feed efficiency, methane emissions, growth rate, or disease resistance, are identified. These microbial signatures can inform the development of novel microbiome-targeted interventions, including next-generation probiotics and microbiome-modulatory strategies that integrate nutritional and breeding approaches for enhanced animal performance.
- Host genetic variants linked to KPIs and microbial signatures.
 The project will identify specific host genetic variants that are linked with both animal performance traits and microbiome composition. These genetic markers can be integrated into commercial genotyping arrays (SNP chips), enabling their routine application in livestock breeding programs. This integration supports the selection of animals with desirable genetic and microbial traits, contributing to more sustainable and efficient breeding strategies.

2. Services and tools that could serve the project or could serve future projects

- Updated reference gene catalogue of the rumen microbiome
- Novel probiotics with a beneficial impact on animal health, sustainability and productivity
- Cost-effective custom SNPs array with beneficial impact on microbial and host performance.
- Novel statistical models for genomic prediction integrating microbiome and host-genomic information.
- Novel computational tools to explore associations between microbiomes and hostperformance.

3. Other activities to support long-term impact of the project

- Contribute to the FAANG data portal.
- Future projects could benefit from a curated and standardized hologenomics databases including phenotype, microbial and genomics information.

7. Annex 2 - Full list of Services

Laboratory Services

Type of service	Service leader	Service name	Species	Access type	Protocol readiness
Advanced Analytical Services for	Forschungsinstitut für Nutztierbiologie	Advanced Analytical Services for Cellular Models - laser capture	All	Physical access	Established
Cellular Models		Advanced Analytical Services for Cellular Models - cell counting	All	Physical access	
		Advanced Analytical Services for Cellular Models - flow cytometry (and sorting) -	All	Physical access	Established
		Advanced Analytical Services for Cellular Models - Live cell imaging - cell culture	All	Physical access	Established/Developmental
		Advanced Analytical Services for Cellular Models - Bioenergetics (Seahorse, ATP, LDH) -	All	Physical access	Established/Developmental
		Advanced Analytical Services for Cellular Models - Real-Time Cell Analysis (xCELLigence)	All	Physical access	Established/Developmental
		Advanced Analytical Services for Cellular Models - genomics	All	Physical access	
		Advanced Analytical Services for Cellular Models - epigenetics	All	Physical access	Established
		Advanced Analytical Services for Cellular Models - transcriptomics -	All	Physical access	Established/Developmental
		Advanced Analytical Services for Cellular Models - metabolomics	All	Physical access	Established
		Advanced Analytical Services for Cellular Models - single cell transcriptomics	All	Physical access	Established/Developmental
		Advanced Analytical Services for Cellular Models - Targeted multiplex qPCR/gene profiling (BioMark)	All	Physical access	Established/Developmental
		Advanced Analytical Services for Cellular Models - Immuncytochemical analysis	All	Physical access	Established
	Luonnonvarakeskus	Cell laboratory service	Dairy	Wide virtual access	Developmental
	Norges miljø- og biovitenskapelige universitet	Advanced Analytical Services for Cellular Models, Single-target and genome- screening gene-editing in cultured cells with transfection/transduction	All	Hybrid access	Established
		Advanced Analytical Services for Cellular Models; CRISPR gene-editing in vivo, early stage salmon and zebrafish	All	Hybrid access	Established
		Advanced Analytical Services for Cellular Models; Development of CRISPR Screening library (GeCKO), all annotated species	All	Remote access	
Biochemistry, structural analysis	Institut national de recherche pour l'agriculture,	Laboratory analyses, aquaculture species - biochemical analyses	Fish	Hybrid access	Established
,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	l'alimentation et l'environnement	Laboratory analyses, aquaculture species -structural and chemical analysis	Fish	Hybrid access	Established
	Wageningen University	Aquaculture; lab analysis of proximate composition of fish, feed, faeces and sludge)	Fish	Hybrid access	Established
	Ελληνικό Κέντρο Θαλάσσιων Ερευνών	Laboratory analyses, aquaculture species - biochemical analyses	Fish	Hybrid access	Established
Biology	Jihoceska Univerzita v Ceskych Budejovicich	Analyses of the effect xenobiotics on physiology of aquatic organisms	Fish	Hybrid access	established
o,	, ,	Analyses of the histopathological changes in tissues of aquatic organisms (fish, crayfish, amphibians and bivalve molluscs)	Fish	Hybrid access	established
		Flow cytometry, cell composition, hematology and imuno enzymes (lysozyme, protein normalisation, alkaline phosphatase)	Fish	Hybrid access	established
		High-speed fluorescent microscopy and patch-clamp technique to study sperm physiology and signaling.	Fish	Hybrid access	developmental
		Detailed evaluation and recording of spermatozoa motility, including flagellar motion (training available).	Fish	Hybrid access	Established
		Evaluation and analysis of other sperm quality parameters, including metabolomic profiling, osmotic resistance, oxidative phosphorylation, and	Fish	Hybrid access	Established
	Ελληνικό Κέντρο Θαλάσσιων Ερευνών	oxidative stress. Laboratory facilities, aquaculture species - bioassays	Fish	Hybrid access	Established
	Listification control	Laboratory analyses, aquaculture species - marine biology	Fish	Hybrid access	Established
		, , , , , , , , , , , , , , , , , , , ,		1	

Type of service	Service leader	Service name	Species	Access type	Protocol readiness
osample analysis	Consejo Superior de Investigaciones Científicas	Advanced Analytical Services - aquaculture species - biochemical &	Fish	Physical access	Established
		ecotoxicological analyses			
		Advanced Analytical Services - aquaculture species - immunological analysis	Fish	Physical access	Established
	Luonnonvarakeskus	Laboratory of nutrition - chemical analysis	All	Hybrid access	Established
		Chemical and physical analysis of pellets	All	Hybrid access	Established
		Measurement for meat ja egg quality	Poultry	Remote access	Established
	Norges miljø- og biovitenskapelige universitet	Biosample analysis, Nanopore sequencing (Promethion), DNA, RNA, Amplicons, Pore-C	All	Hybrid access	Established/Developmental
		Biosample analysis, Single-cell RNAseq, multiome, dscHi-C-multiome (10X chromium)	All	Hybrid access	Established
		Biosample analysis, High-throughpout genotyping (Affymetrix)	All	Remote access	Established
		Biosample analysis, Functional Genomic assays (ATAC-Seq, ChIP-seq)	All	Hybrid access	Established
	Wageningen Research	air quality lab	Dairy	Hybrid access	Established
	. 9 - 9 - 11 - 11 - 11 - 11 - 11 - 11 -	environmental service laboratory	Dairy	Hybrid access	Established
iosample collection and analysis	Consejo Superior de Investigaciones Científicas	Biosample collection and analysis preparation - aquaculture species - blood	Fish	Physical access	Established
preparation		sampling Biosample collection and analysis preparation - aquaculture species - tissue sampling	Fish	Physical access	Established
		Biosample collection and analysis preparation - aquaculture species - histological analysis	Fish	Physical access	Established
		Biosample collection and analysis preparation - aquaculture species - biochemical analysis	Fish	Physical access	Established
		Biosample collection and analysis preparation - aquaculture species -	Fish	Physical access	Established
		immunological analysis Biosample collection and analysis preparation - aquaculture species - multi-omics	Fish	Physical access	Established
	Forschungsinstitut für Nutztierbiologie	Biosample collection and analysis preparation - Animal husbandry	All	Physical access	Established
		Biosample collection and analysis preparation - Animal husbandry - Quarantine for customer provided animals	All	Physical access	
		Biosample collection and analysis preparation - Animal testing - Routine	All	Physical access	
		Biosample collection and analysis preparation - Animal testing - Specific treatments and phenotypes	All	Physical access	
		Biosample collection and analysis preparation - Tissue sampling	All	Physical access	Established/Developmental
		Biosample collection and analysis preparation - Blood sampling	All	Physical access	Established
		Biosample collection and analysis preparation - Animal testing applications & experimental design	All	Physical access	
		Biosample collection and analysis preparation - Histological analysis	All	Physical access	Established/Developmental
		Biosample collection and analysis preparation - Biochemical analysis	All	Physical access	Established
		Biosample collection and analysis preparation - Gene expression analysis	All	Physical access	Established
		Biosample collection and analysis preparation - Physical meat analysis	All	Physical access	Established
		Biosample collection and analysis preparation - Chondro- and Osteogenesis (clearing and staining technique)	All	Physical access	Established/Developmental
		Biosample collection and analysis preparation - Morphometric analysis	All	Physical access	Established
		Biosample collection and analysis preparation - Lipididomics	All	Physical access	Established

Type of service	Service leader	Service name	Species	Access type	Protocol readiness
Cell and organoid laboratory	Aarhus Universitet	Cell and orgonoid laboratory	All	Hybrid access	Developmental
	Institut national de recherche pour l'agriculture,	laser microdissection	All	Hybrid access	Established
	l'alimentation et l'environnement	Cell counting	All	Hybrid access	Established
		Cell sorting	All	Hybrid access	Established
		production of organoids (1 month)	All	Hybrid access	Established
		organoids image analysis	mammals	Hybrid access	Established
	Jihoceska Univerzita v Ceskych Budejovicich	Analysis of hormonal activities of pure substances and environmental samples in	Fish	Hybrid access	established
		vitro			
	University of Edinburgh	Biobanking; Development of organoids; Cell lines; iPSCs; cell lines;	Pig, Chicken,	Remote access	established
			Cow		
	Wageningen University	Experimental assays using organoids and cell lines;	All	Hybrid access	Established
		Cripr/Cas assays organoids,	All	Hybrid access	Developmental
		Crisp/Cas assays cell lines / primary cells,	All	Hybrid access	Developmental
		Detailed molecular characterization of organoids and/or tissue; Isolation of single	All	Hybrid access	Established
		cells/nuclei using Singulator (S2 genomics)		•	
		detailed molecular characterization of organoids and/or tissue;single cell/nuclei	All	Hybrid access	Established
		RNA-seq using 10x genomics system;		,	
		detailed molecular characterization of organoids and/or tissue; single cells/nuclei	All	Hybrid access	Established
		ATAC-seq using 10x genomics system,		,	
stom Cell-Based In-vitro Research	Consejo Superior de Investigaciones Científicas	Custom Cell-Based In-vitro Research - aquaculture species - cell lines	Fish	Physical access	Established
odels	,,	Custom Cell-Based In-vitro Research - aquaculture species - cell counting & flow	Fish	Physical access	Established
vioueis		cytometry		,	
		Custom Cell-Based In-vitro Research - aquaculture species - antimicrobial testing	Fish	Physical access	Established
		custom cen suscum na o nescuron aquacunare species anamicrosiantesting		ysicai access	Establishea
		Custom Cell-Based In-vitro Research - aquaculture species - ecotoxicology testing	Fish	Physical access	Established
		custom cen susca in the research adjudentare species economicology testing		T Trystear decess	Established
	Forschungsinstitut für Nutztierbiologie	Custom Cell-Based In-vitro Research Models - Primary cell culture	All	Physical access	Established
	3 ,	Custom Cell-Based In-vitro Research Models - Primary cell culture - Tissue sample	All	Physical access	Developmental
		- Stem cells - A.Baerii & A.Gueldenstaettii/Hybrid Strugeon		•	•
		Custom Cell-Based In-vitro Research Models - Primary cell culture - Tissue sample	All	Physical access	Developmental
		- Stem cells		,	
		Custom Cell-Based In-vitro Research Models - blood cells - trunk blood	All	Physical access	Established
		Custom Cell-Based In-vitro Research Models - stem cells -	All	Physical access	Established
		Custom Cell-Based In-vitro Research Models - stem cells	All	Physical access	Experimental
		Custom Cell-Based In-vitro Research Models - stem cells	All	Physical access	Developmental
		Custom Cell-Based In-vitro Research Models - cell lines - tissue sample - stem	All	Physical access	Developmental
		cells	All	i ilysical access	Developmental
		Custom Cell-Based In-vitro Research Models - cell lines - tissue sample - stem	All	Physical access	Developmental
		cells	All	Filysical access	Developmental
		Custom Cell-Based In-vitro Research Models - cell lines - other well-known-	All	Dhysical access	Established/Developmental
		standard cell models	All	Physical access	Lstabiisrieu/Developmentai
			All	Dhysical access	Douglopment-1
	Manager at the standard line and the standard line and the standard line at the standard line	Custom Cell-Based In-vitro Research Models - cell lines - cell models		Physical access	Developmental
	Norges miljø- og biovitenskapelige universitet	Cell-Based In-vitro Research Models, from salmonids (ASK, ASSF, SHK, CHSE,	All	Hybrid access	Established
		CSFL), Cow (BT, MDBK) and Pig (PK15, IPEGJ2)	A.II		
		Cell-Based In-vitro Research Models, stable cell-line development from salmonids	All	Hybrid access	
		and livestock.			
	Wageningen University	Laboratory analyses, aquaculture species - bacterial expression	Fish	Hybrid access	Established

Type of service	Service leader	Service name	Species	Access type	Protocol readiness
Detailed molecular characterisation of organoids and/or tissue	Jihoceska Univerzita v Ceskych Budejovicich	Phenotyping of fish tissues using DNA, RNA and protein detection and analysis	Fish	Hybrid access	Established
	University of Edinburgh	Detailed molecular characterization of organoids and/or tissue; Isolation of single	all	Remote access	established
		cells/nuclei using OctoMACS dissociator;			
evelopment of organoids	Institut national de recherche pour l'agriculture, l'alimentation et l'environnement	Production of stem cells	All	Hybrid access	Established
	Wageningen University	Development of Organoids for well established tissues-species;	All	Hybrid access	Established
		Development of Organoids for new tissues-species;	All	Hybrid access	Developmental
2P Genetic analyses	Aarhus Universitet	Multiomics and Systems Biology for Deep Phenotyping laboratory	All	Hybrid access	Developmental
enome analysis and assembly	Norges miljø- og biovitenskapelige universitet	Genome analyses and assembly; De novo genome assembly, pan genomic	All	Remote access	Established
		assemblies, variant (SNP/SV) detection, functional annotation			
	Wageningen University	Genome analysis and assembly, on site de novo genome assembly,	All	Physical access	Established
		Genome analysis and assembly, remote de novo genome assembly,	All	Remote access	Established
		Genome analysis and assembly; On site T2T de novo genome assembly;	All	Physical access	Developmental
		Genome analysis and assembly; Remote T2T de novo genome assembly;	All	Remote access	Developmental
		Genome analysis and assembly; SNP and SV detection;	All	Physical access	Established
		Genome analysis and assembly; Training of SNP and SV detection;	All	Physical access	Established
		Genome analysis and assembly; Development and use of CADD scores;	All	Physical access	Established/Developmental
		Genome analysis and assembly; Genome methylation analysis;	All	Physical access	Established
		Genome analysis and assembly; Genome methylation analysis; DNA or available data;	All	Physical access	Established
		Genome analysis and assembly, Identification of deleterious variants;	All	Physical access	Established
	Ελληνικό Κέντρο Θαλάσσιων Ερευνών	Laboratory analyses, aquaculture species - sequencing	Fish	Hybrid access	Established
Genome editing	Jihoceska Univerzita v Ceskych Budejovicich	Reverse genetics using CRISPR/Cas9 to study gene function in zebrafish, common	Fish	Hybrid access	established
	University of Edinburgh	carp and sterlet sturgeon Genome Editing; Catalogues of single RNAs	Pig, Chicken,	Remote access	established
	University of Edinburgh	denome Editing, Catalogues of Single KNAS	Cow	Remote access	established
		Genome editing; CRISPR lentivirus library	Pig, Chicken,	Remote access	established
		denome earling, exist went will as its ary	Cow	Nemote decess	established
		Genome editing; Flow sorting for screen	Pig, Chicken,	Remote access	established
		denotific editing, flow softing for screen	Cow	Nemote access	established
		Genome Editing; Genome editing in vitro ;	all	Remote access	Established
		Genome editing; Amplicon sequencing	Pig, Chicken,	Remote access	established
			Cow		
enomics	Consejo Superior de Investigaciones Científicas	Advanced Analytical Services - aquaculture species - genomics analysis	Fish	Physical access	Established
	Institut national de recherche pour l'agriculture,	transcriptomics (qPCR)	All	Hybrid access	Established
	l'alimentation et l'environnement	single-cell transcriptomics	All	Hybrid access	Established
		Miseq 16S sequencing	all	Remote access	Established
		organoids gene expression analysis	mammals	Hybrid access	Established
	Luonnonvarakeskus	Genomics laboratory service	All	Hybrid access	Established
		Genomics laboratory service	Fish	Hybrid access	Established
	University of Edinburgh	Detailed molecular characterization of organoids and/or tissue; single cell/nuclei	all	Remote access	established
		RNA-seq using Parse BioSciences system;			
		Detailed molecular characterization of organoids and/or tissue; single cell/nuclei	all	Remote access	established
		RNA-seq using 10x genomics system;			
		Detailed molecular characterization of organoids and/or tissue; single cell/nuclei	all	Remote access	established
		ATAC-seq using 10x genomics system;			
		Genome editing; CRISPR screen data analysis	Pig, Chicken, Cow	Remote access	established
		Genome analyses and assembly; CAGE-Seq library preparation	all	Remote access	established
		Genome analyses and assembly; Illumina sequencing NextSeq 2000	all	Remote access	established

Type of service	Service leader	Service name	Species	Access type	Protocol readiness
Histology	Institut national de recherche pour l'agriculture,	Histology staining	All	Hybrid access	Established
	l'alimentation et l'environnement	immunocytochemical analysis	all	Remote access	Established
		histological slide digitization	all	Hybrid access	Established
		organoids immunocharacterization	mammals	Hybrid access	Established
Microscopy and image analysis	Institut national de recherche pour l'agriculture,	Laboratory analyses, aquaculture species - light microscopy	Fish	Hybrid access	Established
	l'alimentation et l'environnement	Laboratory analyses, aquaculture species - microscopy and bio-imaging	Fish	Hybrid access	Established
	Wageningen Research	Laboratory analyses, aquaculture species - bio-imaging	fish	Hybrid access	Established
	Wageningen University	Laboratory analyses, aquaculture species - electron microscopy	Fish	Hybrid access	Established
Molecular biology	Consejo Superior de Investigaciones Científicas	Advanced Analytical Services - aquaculture species - transcriptomics analysis	Fish	Physical access	Established
		Advanced Analytical Services - aquaculture species - epigenetics analysis	Fish	Physical access	Established
		Advanced Analytical Services - aquaculture species - proteomics analysis	Fish	Physical access	Established
		Advanced Analytical Services - aquaculture species - metabolomics analysis	Fish	Physical access	Established
		Advanced Analytical Services - aquaculture species - metagenomics analysis	Fish	Physical access	Established
		Advanced Analytical Services - aquaculture species - targeted PCR arrays	Fish	Physical access	Established
	Jihoceska Univerzita v Ceskych Budejovicich	Analysis of mRNA expression of different genes in tissues of fish and amphibians	Fish	Hybrid access	established
		Gene expresion analysis (RNA isolation, quality check, primer design)	Fish	Hybrid access	established
		Microbiome analysis in fish and aquaculture systems	Fish	Hybrid access	established
	Luonnonvarakeskus	Microbiome analysis in ruminants and monogastrics using NGS sequencing	Dairy	Hybrid access	Established
	Wageningen University	Aquaculture; lab analysis of immune responses (real-time PCR, ELISA of antibody	Fish	Hybrid access	Established
		or cytokine production, flow cytometric analysis of changes in leukocyte cell)			
		Laboratory analyses, aquaculture species - flow cytometry	Fish	Hybrid access	Established
	Ελληνικό Κέντρο Θαλάσσιων Ερευνών	Laboratory analyses, aquaculture species - identification, molecular typing and phylogenetic analysis	Fish	Hybrid access	Established
		Laboratory analyses, aquaculture species - molecular biology and -omics	Fish	Hybrid access	Established
Spectrometry	Wageningen University	Laboratory analyses, aquaculture species - absorbance and fluorescence spectrometry	Fish	Hybrid access	Established

Data and associated services

pe of service	Service leader	Service name	Species	Access type	Protocol readiness
eeding applications using G2P d	lata Aarhus Universitet	Genomics and metagenomics	All	Hybrid access	Established
		Single cell gene expression analysis; FarmGTEx	All	Hybrid access	Established
	Jihoceska Univerzita v Ceskych Budejovicich	Managing and designing a long-term sustainable breeding program in common	Fish	Hybrid access	established
	, ,	carp under pond aquaculture and experience in managing fish genetic resources		,	
	Luonnonvarakeskus	Breeding applications using G2P data; Breeding value estimation (linear mixed models, deep learning);	All	Remote access	Established
	Norges miljø- og biovitenskapelige universitet	Breeding applications using G2P data; Breeding value calculation, pedigree and genotype analysis, simulated breeding, breed delimination	All	Remote access	Established
	Wageningen University	Breeding applications using G2P data; Breeding value estimation (linear mixed models, asreml, MiXBlup);	All	Hybrid access	Established
		Breeding applications using G2P data; Genomic prediction (linear mixed models, bayesian models, single-step);	All	Hybrid access	Established
		Breeding applications using G2P data; Genotype imputation (Beagle, Flmpute, FindHap, STITCH, GLIMPSE, HBimpute);	All	Hybrid access	Established
		Breeding applications using G2P data; Identifying duplicate genotypes,	All	Hybrid access	Established
		Breeding applications using G2P data;Breed and (sub)population identification delimination(Structure, PCA, Haplotype analysis);	All	Hybrid access	Established
		Breeding applications using G2P data; Compare breeding strategies for population management using simulations;	All	Hybrid access	Established
		Breeding applications using G2P data; Identify parents for next generation and candidates for conservation	All	Hybrid access	Established
		Breeding applications using G2P data; Simulating breeding program scenarios	All	Hybrid access	Established
		Breeding applications using G2P data; Optimization of breeding program design	All	Hybrid access	Established
a services	Aarhus Universitet	Comuter vision and Database for Large scale real-time phenotyping	All	Hybrid access	Established
	Consejo Superior de Investigaciones Científicas	Advanced Analytical Services - aquaculture species - multi-omics - data integration & processing	Fish	Physical access	Established
	European Bioinformatics Institute	Data repositories; European Nucleotide Archive - Submission of raw nucelotide data and analysis files	All	Wide virtual access	Established
		Data repositories; Expression Atlas	All	Wide virtual access	Established
		Data repositories; BioSamples - metadata for biological samples	All	Wide virtual access	Established
		Ensembl Genome Browser	All	Wide virtual access	Established
		Data repositories; Metabolights	All	Wide virtual access	Established
		Other databases suitable for phenotyping information; BioStudies	All	Wide virtual access	Established
		Other databases suitable for phenotyping information; BioImage Archive	All	Wide virtual access	Established
		Data portal; FAANG Data Portal - brokered data portal to manage and collate data from FAANG projects, this will be expanded for GenoPHEnix to include	All	Wide virtual access	Established
		brokering of phenotype information			
	to the transfer of the second	Data and compute	All	Wide virtual access	Established
	Institut national de recherche pour l'agriculture, l'alimentation et l'environnement	Data services, aquaculture species - advanced imaging technologies	Fish	Hybrid access	Established
		Data services, aquaculture species, image processing	Fish	Hybrid access	Established
	Jihoceska Univerzita v Ceskych Budejovicich	Application of CFD models for air flow in the breeding hall	Fish	Hybrid access	established
		Assisting in the collection of quantitative data and DNA samples from fish for estimates of genetic parameters as part of or prior to the implementation of a	Fish	Physical access	established
		breeding program Statistical analysis of quantitative data and estimation of genetic parameters of performance traits in fish (heritability, genetic correlations, breeding values)	Fish	Hybrid access	Established
	Luonnonvarakeskus	Bioinformatics	All	Remote access	Established

Type of service	Service leader	Service name	Species	Access type	Protocol readiness
Data services	Wageningen Research	Data services, aquaculture species - advanced imaging technologies	Fish	Hybrid access	Established
		Data services, aquaculture species, image processing	Fish	Hybrid access	Established
	Ελληνικό Κέντρο Θαλάσσιων Ερευνών	Bioinformatics	Fish	Hybrid access	Established
G2P Genetic analyses	Luonnonvarakeskus	G2P Genetic analyses; estimation of genetic parameters;	All	Remote access	Established
		G2P Genetic analyses; identification of associated genomic regions;	All	Remote access	Established
	Norges miljø- og biovitenskapelige universitet	G2P Genetic analyses; Identification of associated genomic regions; GWAS, models, simulate genotype and phenotype data, comparative genomics, ge relatedness		Remote access	Established

Biobanking services

Type of service	Service leader	Service name	Species	Access type	Protocol readiness
Biobanking	Institut national de recherche pour l'agriculture,	Biobanking Sample distribution	All	Remote access	Established
	l'alimentation et l'environnement				
	Jihoceska Univerzita v Ceskych Budejovicich	Development and testing of short-term sperm storage methods and	Fish	Hybrid access	Established
		cryopreservation protocols for cryobanking and practical applications.			
	Luonnonvarakeskus	Biobanking: Tissue samples and biobank of strains of salmonids in multiple	All	Hybrid access	Established
		species			
		Biobanking: Frosen semen and embryos, tissue samples from live biobanks of	cattle, small	Remote access	Established
		livestock	ruminants,		
			poultry		
	University of Edinburgh	Biobanking; Isolation and preservation of primary cells	Pig, Chicken,	Remote access	established
			Cow		
	Wageningen Research	cryo preservation for livestock, aquatic	all	Physical access	Established
		biobanking for livestock, aquatic species	all	Physical access	Established
	Wageningen University	Biobanking; biobanking of biological specimen;	All	Remote access	Established
		Biobanking; distribution of biosamples;	All	Remote access	Established
Genomics	Institut national de recherche pour l'agriculture,	DNA extraction from blood	All	Remote access	Established
	l'alimentation et l'environnement	quality control of nucleic acids	All	Remote access	Established
		quantification of DNA	All	Remote access	Established
		DNA extraction from feces	mammals, birds	Remote access	Established
		DNA extraction from semen	all	Remote access	Established
		RNA extraction from blood	mammals	Remote access	Established
		RNA extraction from tissue	mammals, birds	Remote access	Established
Sample management	Institut national de recherche pour l'agriculture,	sample collection : blood or solid tissue	All	Remote access	Established
	l'alimentation et l'environnement	storage of DNA, blood, tissues	All	Remote access	Established
		sample entry into collection : blood or tissue	all	Remote access	Established
		sample entry into collection : semen	pig, chicken	Remote access	Established
		storage of semen	pig, chicken	Remote access	Established
		cell storage	all	Remote access	Established
		distribution of DNA aliquots	all	Remote access	Established
	University of Edinburgh	Biobanking; Germplasm cryopreservation	all	Remote access	established

Education and training services

	Service leader	Service name	Species	Access type	Protocol readiness
Biobanking	Institut national de recherche pour l'agriculture,	G2P in a dish: biobanking in vitro models	All	Physical access	Established
	l'alimentation et l'environnement	Quality management of biobanks (ISO 9001)	All	Remote access	Established
Biosample collection and analysis	Jihoceska Univerzita v Ceskych Budejovicich	Course of sampling and biochemical analyses	Fish	Hybrid access	developmental
preparation		Training on fish feed and fish flesh analysis	Fish	Hybrid access	Developmental
Breeding applications using G2P data	Jihoceska Univerzita v Ceskych Budejovicich	Show of a long-term sustainable selection program in common carp under pond aquaculture and experience in managing fish genetic resources	Fish	Hybrid access	Established
C	To be defined	A helf des Osteres Communication Constitution	All	Dhysical access	Established
Communication	To be defined Aarhus Universitet	A half-day Outreach Communications Capacity Development training	All	Physical access	Established
Data		Validation and use of sensor outputs		Remote access	
	Institut national de recherche pour l'agriculture,	Who needs experimental research if we have Big Data?	All	Wide virtual access	Established
	l'alimentation et l'environnement	Utilization of ontologies	All	Remote access	Established
		Integration and analysis of omic and non-omic data for genome and phenome research	All	Remote access	Established
	Jihoceska Univerzita v Ceskych Budejovicich	Experimental data mangement: from generating protocols to sharing data	All	Remote access	Established
	Wageningen University	A 2-day FAIR–data workshop	All	Remote access	Established
	To be defined	Harmonizing standards for FAIR genome and phenome research : from cell to population	All	Remote access	Developmental
		A half-day workshop on data sharing	All	Remote access	Developmental
		Developing standards for phenotypic and environmental data for science and industrial applications	All	Remote access	Developmental
		Encryption of Industry phenotype	All	Remote access	Developmental
Detailed molecular characterisation of organoids and/or tissue	Jihoceska Univerzita v Ceskych Budejovicich	Training on in situ hybridization and immunohistochemistry	Fish	Physical access	Established
Ethics	Institut national de recherche pour l'agriculture,	Ethics in experiments on animals	All	Physical access	Established/Developmenta
	l'alimentation et l'environnement	G2P in a dish: in vitro vs in vivo G2P research and the links to industry	All	Remote access	Established
		G2P in a dish: In vitro G2P "3Rs" research in domesticated species"	All	Hybrid access	Established
Genome editing	Jihoceska Univerzita v Ceskych Budejovicich	Training on genetic engineering and embryo mictoinjection	Fish	Physical access	Established
In vivo phenotyping of animal	Jihoceska Univerzita v Ceskych Budejovicich	Application of machine vision to improve animal welfare	Cow/pig/poultry	Hybrid access	developmental
behavior		Training - new sensors and AI data procesing in fish welfare monitoring	Fish	Remote access	developmental
In vivo phenotyping of nutritional	Forschungsinstitut für Nutztierbiologie	Respiration chamber and methane emission	Dairy and Beef	Physical access	Established
efficiency and emissions through gold	Institut de Recerca i Tecnologia Agroalimentàries	Feed efficiency in dairy cattle	Dairy	Remote access	Established
standard methods	Institut national de recherche pour l'agriculture, l'alimentation et l'environnement	Gold standard methods to assess key phenotypes in ruminant nutrition	Dairy and Beef	Physical access	Established
	Scotland's Rural College	Feed efficiency of beef cattle and measurement techniques	Beef	Remote access	Established
	•	Ruminant methane emissions and measurement techniques	Dairy and Beef	Remote access	Established
	Jihoceska Univerzita v Ceskych Budejovicich	Training on fish digestibility, fish feed formulation and manufacture	Fish	Hybrid access	developmental
In vivo phenotyping of nutritional	Institut national de recherche pour l'agriculture,	Biomarkers assisted-predictions of feed efficiency and their main determinants in		Remote access	Established
efficiency and emissions through	l'alimentation et l'environnement	cattle	*		
proxies	Scotland's Rural College	Microbiome proxies for methane emissions and feed efficiency	Dairy and Beef	Remote access	Established
	· · · · · · · · · · · · · · · · · · ·	Proxies for methane emissions and feed efficiency, other than microbiome	Dairy and Beef	Remote access	Established

Type of service	Service leader	Service name	Species	Access type	Protocol readiness
In vivo phenotyping of production performances	Consejo Superior de Investigaciones Científicas	Animal facilities - aquaculture species - formation and training of technicians on bluefin tuna rearing	Fish	Hybrid access	Established
	Forschungsinstitut für Nutztierbiologie	Metabolic and nutritional investigations using stable isotope tracer	pig	Physical access	Established
	Institut national de recherche pour l'agriculture,	Fish nutrition and feeding	Fish	Remote access	Established
	l'alimentation et l'environnement	Progress in nutritional concepts, methods and technologies to feed pigs: Animal		Physical access	Established
		nutrition and feeding: from issues to research questions and methods to answer	6	,	
		them.			
	Jihoceska Univerzita v Ceskych Budejovicich	Optimization of fish husbandry, optimization of culture conditions during various ontogenic stages	Fish	Physical access	established
	Sveriges lantbruksuniversitet	Basic management and standard traits in pig research facilities	Pig	Physical access	Established
	Jihoceska Univerzita v Ceskych Budejovicich	Training on integrated aquaculture methods - aquaponics, biofloc, anaerobic digestion, aerobic digestion, hydroponics and water/sludge analysis	Fish	Hybrid access	developmental
		Technology for weight estimation and detection of dead broilers in the breeding hall	Poultry	Hybrid access	Developmental
		Training on intensive culture of warmwater fish species	Fish	Hybrid access	Developmental
Laboratory techniques	Institut national de recherche pour l'agriculture,	G2P in a dish: light sheet imaging	All	Physical access	Established
	l'alimentation et l'environnement	G2P in a dish: analysis of single cell data: theory, research examples and practice	All	Physical access	Established
		G2P in a dish: Genome editing in fish cell lines: investigating genes involved	All	Physical access	Established
		G2P in a dish: culture, transfection and imaging of fish cell lines	All	Physical access	Established
		G2P in a dish: culture, transfection and imaging of pig organoids	All	Physical access	Established
		G2P in a dish: From Pluripotent Stem cells to organoids in domestic animals,	All	Remote access	Established