



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





BovReg features

- EU H2020 – funded consortium as contribution to global FAANG with focus on biology-informed breeding

- **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

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

- Time line September 2019 – August 2023





BovReg Consortium

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



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



BovReg Implementation



Establish laboratory and bioinformatics tools

Comprehensive genome annotation

Integrated data analysis for biological informed breeding

Open data distribution

Outreach and social impact

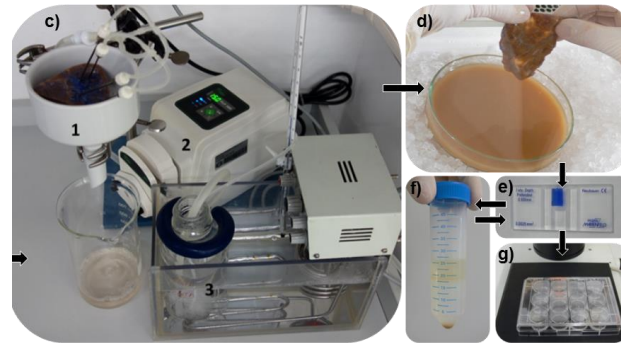
Activities within EU and global FAANG



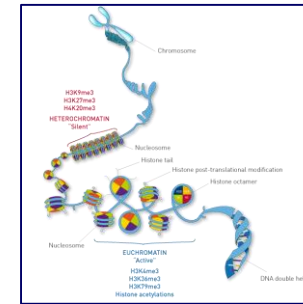


Establish laboratory and bioinformatics tools

► Development of Laboratory Tools and Resources for Bovine (WP1)

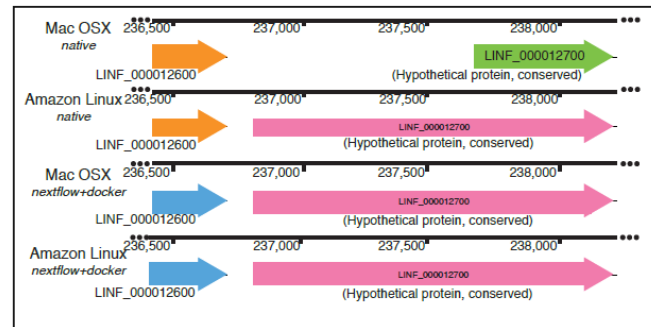


M. Schmicke, Halle

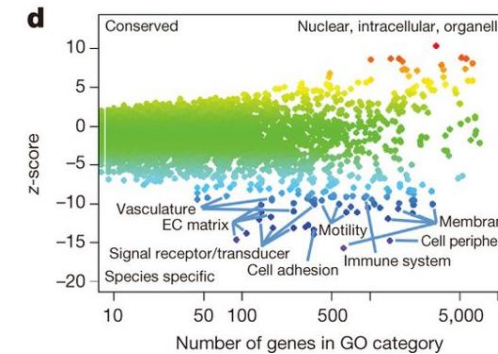


Diagenode

► Tools, Data and Pipelines for Bioinformatic Analyses within and beyond Bovine (WP3)



diTommaso et al., 2017



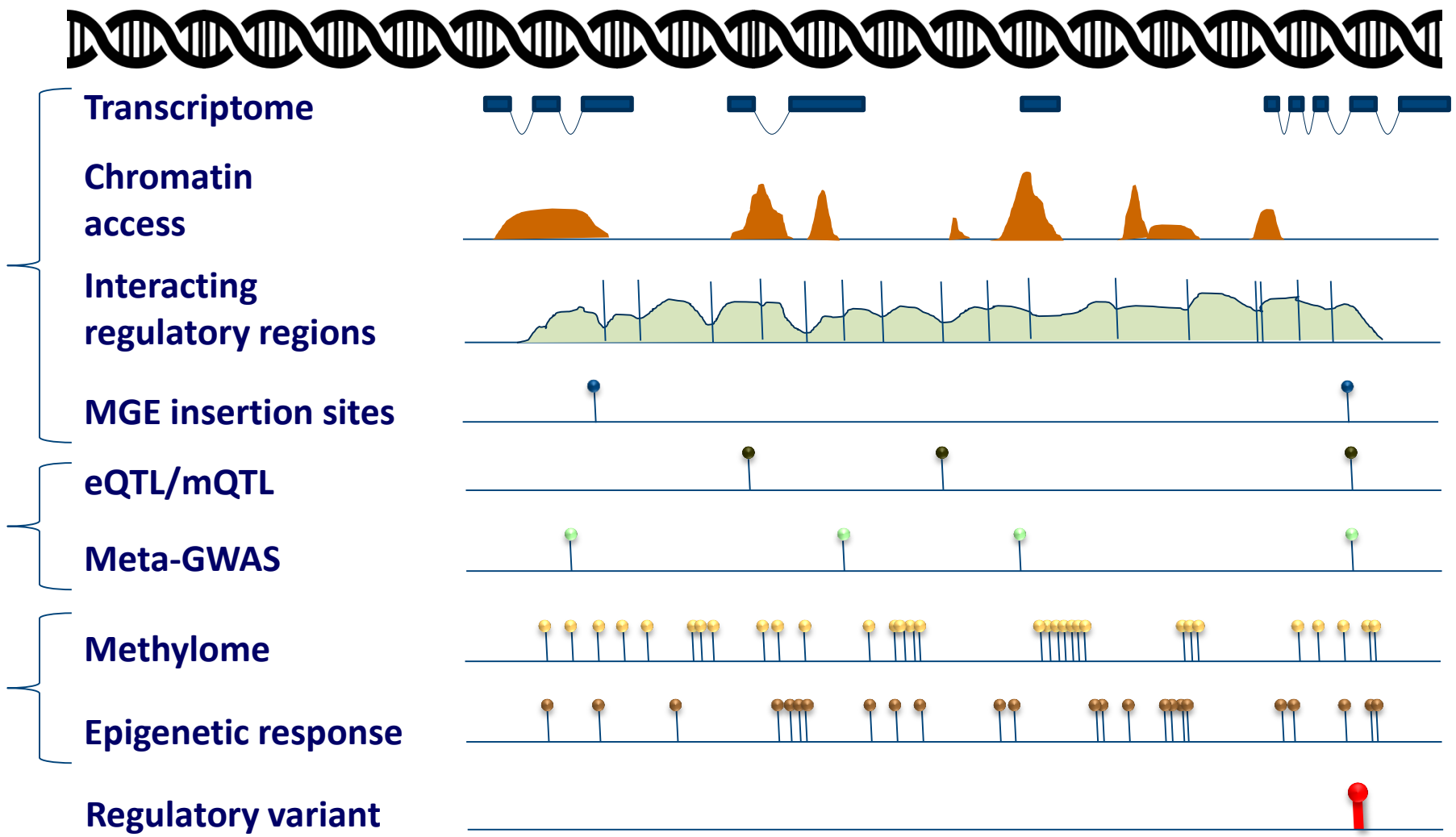
Yue et al. 2014



Comprehensive genome annotation



► Functional and structural genome annotation map (WP2, 4, 5, 6)



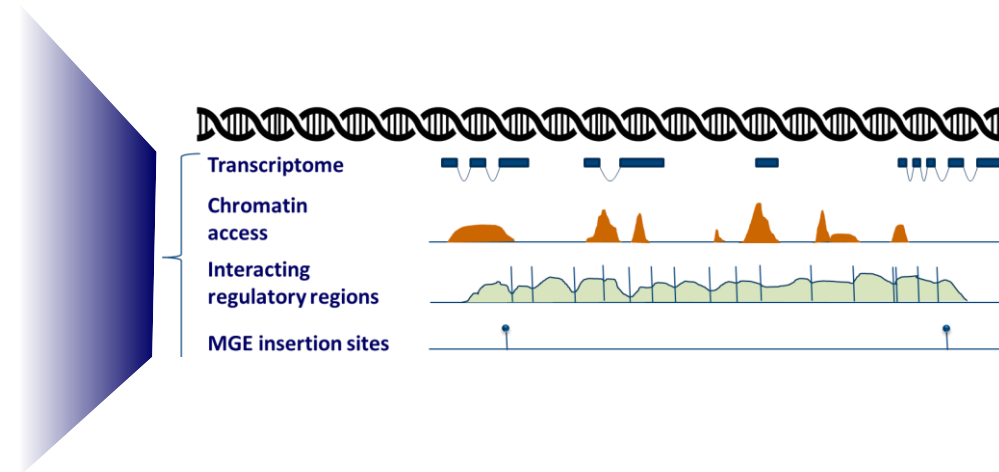


Comprehensive genome annotation

▶ WP2: Functional and structural genomics annotation (C. Charlier, GIGA)

Animals from both sexes, different ontogenetic stages, different environments, ~24 FAANG mostly Tier1 tissues

- Transcriptome analysis (global RNA, mRNA, ncRNA, CAGE)
- Analysis of regulatory regions (ATAC, ChIP)
- Interactions of regulatory regions (ChIRP, Hi-C)
- Full map of genomic sites polymorphic for the presence / absence of mobile genetic elements
- Establish the full map of functionally active elements



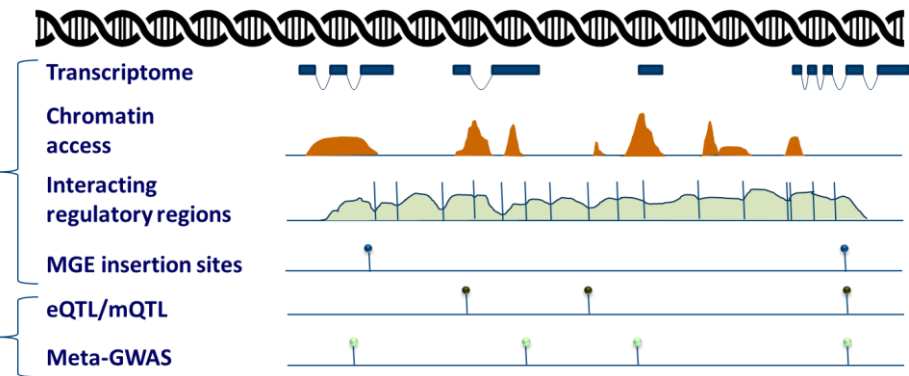
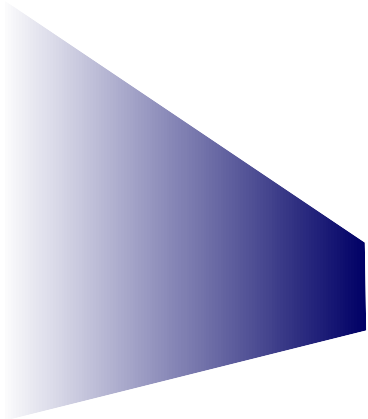


Comprehensive genome annotation



▶ WP4: Integrative genotype-phenotype data analysis (H. Pausch, ETH)

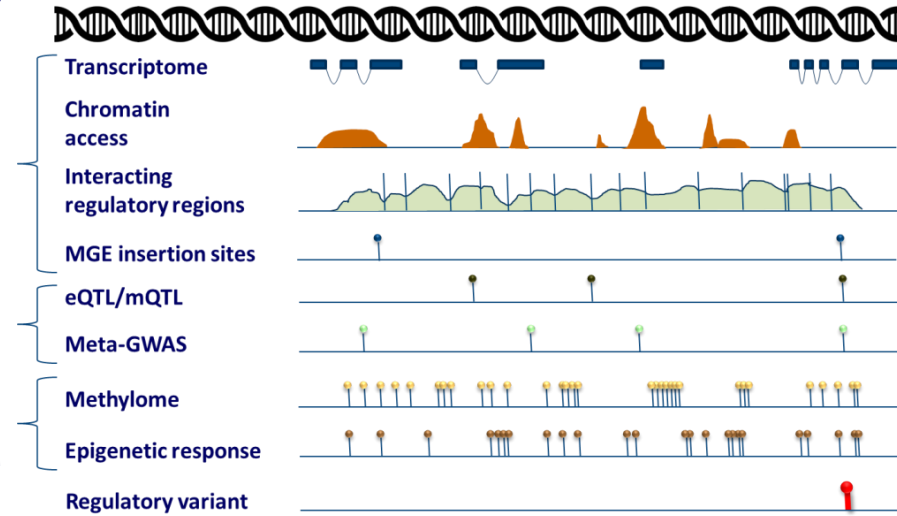
- Association testing between whole-genome sequence variants and BovReg key traits
- Effects of integration sites of mobile genomic elements
- eQTL and mQTL studies
- Integrating Omics data in GWAS



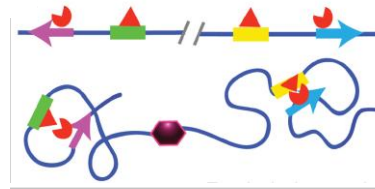
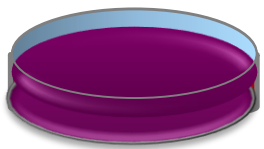
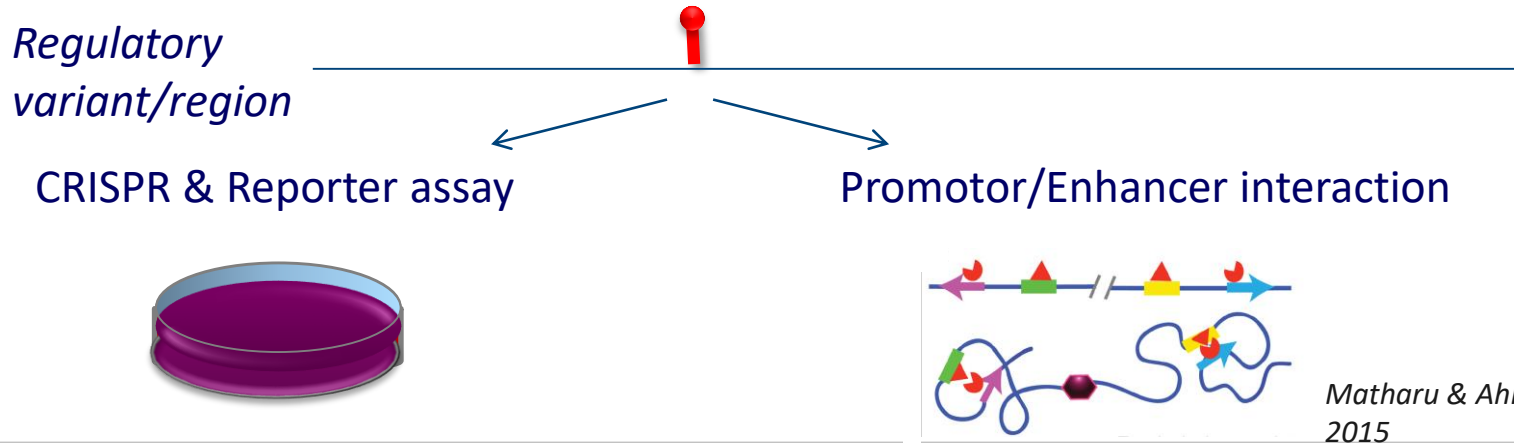


Comprehensive genome annotation

▶ WP5: Modelling epigenetic inter/transgenerational effects (*J. Vanselow, FBN*)



▶ WP 6: Functional validation of regulatory variants (*WP6, H. Taniguchi, PAS*)

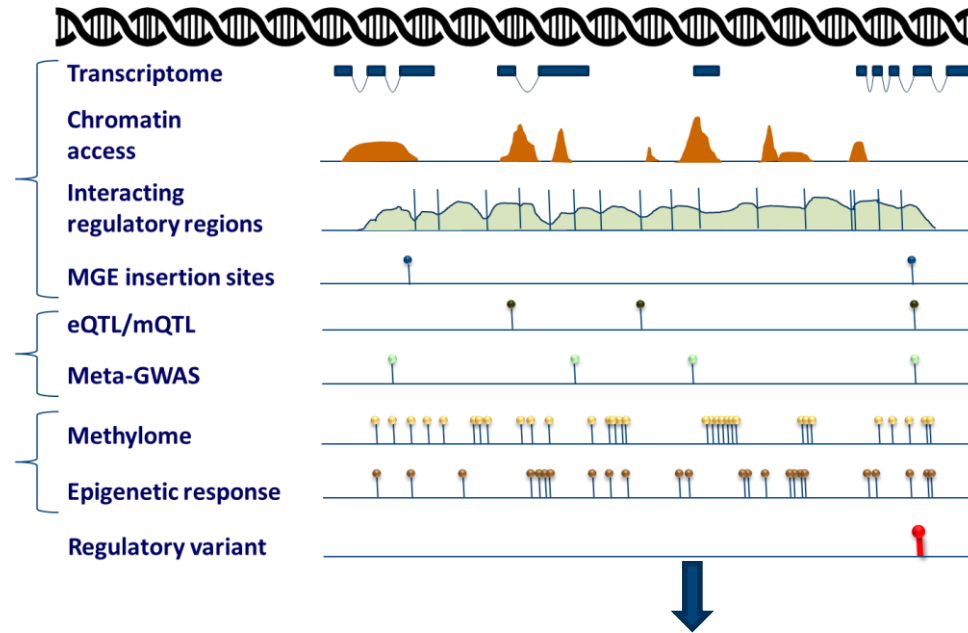




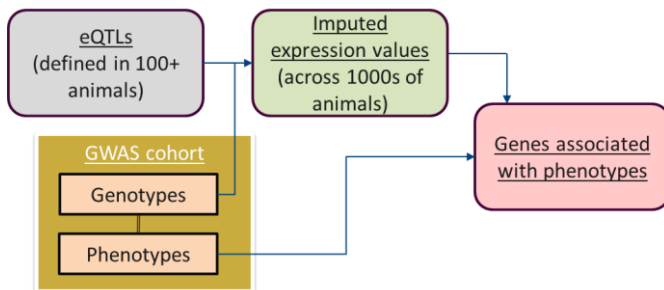
Integrated data analysis for biological informed breeding



Fully annotated genome



▶ Integrating Omics data in GWAS



▶ WP7: Biology-driven genomic prediction models (M. Lund, AU)

$$y = 1\mu + g_f + g_R + e; \quad \text{Fang et al., 2018}$$

- Models for biology driven genomic selection
- Validating biology-driven genomic selection within and across small breeds





Open data distribution


▶ WP10: Link to FAANG-DCC at EMBL-EBI (D. Zerbino, EMBL-EBI)

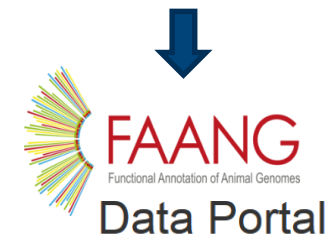
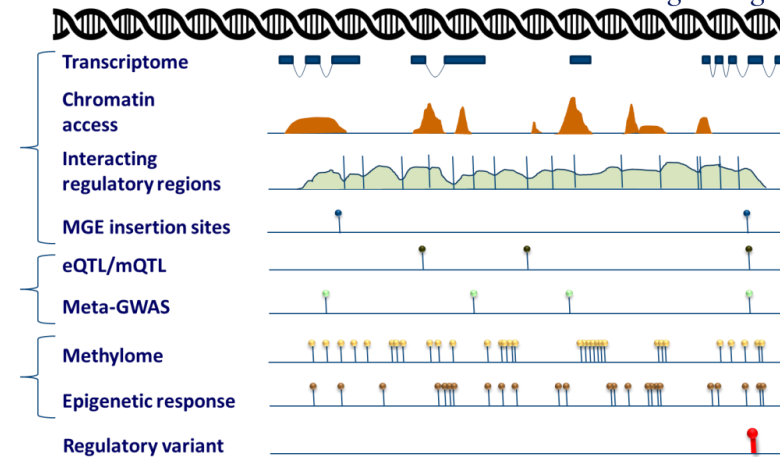
- Assay data distribution
- Metadata distribution
- Distribution of methods



FAANG-DCC EMBL-EBI 

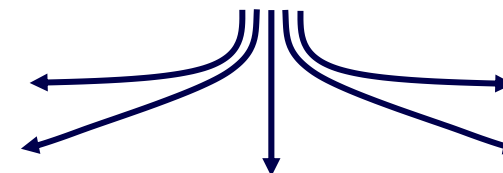
ENA  ENA
European Nucleotide Archive

Biosamples 



FAANG is the Functional Annotation of ANimal Genomes project. We are working to understand the genotype to phenotype link in domesticated animals.

This data portal will help find and browse FAANG's data. Let us know what you think at faang-dcc@ebi.ac.uk.

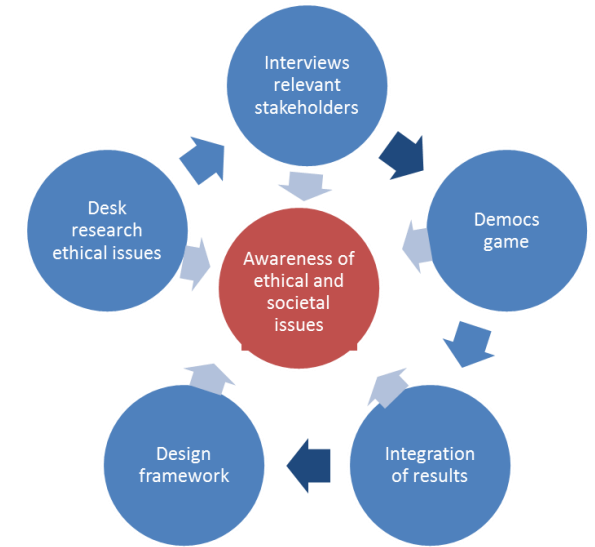


► WP8: Ethics and societal issues (*F. Meijboom, UU*)

- Mapping of societal context of livestock genomics: an ethical analysis
- Public engagement and social perception of new breeding technologies
- Synthesizing the analysis into framework(s) for stakeholder organizations

► WP 9: Training, communication and dissemination (*J. Vilkki, LUKE*)

- Coordination with other proposals of the call topic, FAANG-Europe (CA15112) and global FAANG
- Wet-lab, bioinformatics and statistical modelling training courses
- Communication about the project and its activities
- Dissemination and Demonstration

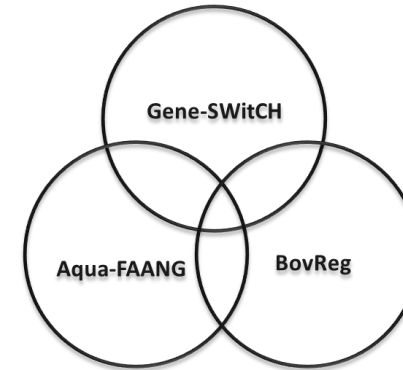




Activities within EU and global FAANG



- Clustering with other EU funded FAANG projects: European FAANG node
- Joint meetings associated with international conferences
- Comparative work: providing plug-ins to other EU H2020 and FAANG projects
- Workshops on newly developed wet-lab, bioinformatics and genomic prediction methods
- Participation in global FAANG working groups
- Member of Steering committee in global FAANG
- Link to EU-COST action FAANG
- Link to Ovine FAANG
- Link to NIFA FAANG project





BovReg kick-off meeting in Dummerstorf

Sep 23/24 2019



BovReg



@BovReg

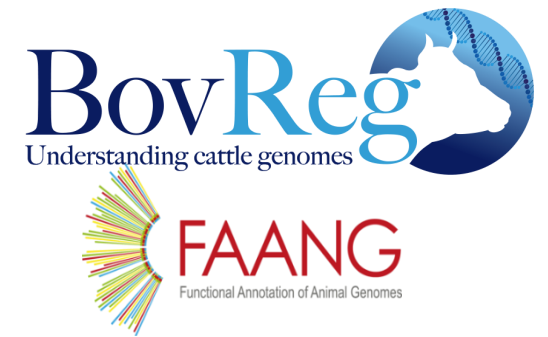
www.bovreg.eu (coming soon)



LEIBNIZ INSTITUTE
FOR FARM ANIMAL BIOLOGY

Christa Kühn, Coordinator EU H2020 BovReg
PAG meeting, FAANG workshop, San Diego, Jan 10th, 2020





Thank you for your attention

**Hiring postdocs with expertise in molecular biology/
cell culture: great opportunity to join the FBN team**

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