



## **Redefining the future of cattle breeding**

Led by FBN, scientists from the EU, Switzerland, international organizations, Canada and Australia are launching a large-scale research project to identify functions in the cow genome that are relevant to the diversity and plasticity of phenotypes in cattle (Full Title: Identification of functionally active genomic features relevant to phenotypic diversity and plasticity in cattle; in short BovReg). Twenty leading laboratories from all over the world joined forces for this four-year project, with researchers from various disciplines, to form a global interdisciplinary team.

The EU funded project is coordinated by Professor Dr. Christa Kühn, Director of the Institute of Genome Biology, FBN Dummerstorf near Rostock in Germany. The total value of funding for the project amounts to 6 million euro and it will run for four years as part of the EU H2020 Research & Innovation Program. The official start (kick-off) with scientists from 13 partner countries and two international organizations in attendance, took place on 23 and 24 September 2019 at the coordinator's premises.

The aim is to gain detailed knowledge on cattle pheno-and genotypes with respect to robustness, health and biological efficiency. The knowledge developed within BovReg should also be particularly applicable to small cattle breeds of regional relevance and distribution, and thus contribute to the conservation of biological diversity in farmed animals.

In addition to experts in cattle research, numerous scientists form BovReg's unique consortium combining expertise in bioinformatics, molecular genetics, quantitative genetics, animal breeding, reproduction physiology, and, as special feature, ethical and social sciences. International data-sharing standards will be extended or newly developed based on genetic analyses and new bioinformatic methods established during the project. Outcomes will be integrated into the worldwide molecular-biology competence network called "Functional Annotation of Animal Genomes (FAANG/[animalgenome.org](http://animalgenome.org))" and made available to the wider scientific community. In parallel to the ENCODE initiative ([encodeproject.org](http://encodeproject.org)), which is dedicated to characterize the function of the human genome, FAANG is working on the identification of functional regulators within animal genomes.