### Project Description

**Project title** | Verifying the candidate genes of GWAS with RNA-seq data  
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**Main subject area** | Animal Genomics  
**Supervisor and Position** | Zexi Cai, Researcher  
**E-mail** |  
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**Co-Supervisor(s), Position(s)** | Goutam Sahana, Senior researcher  
**E-mail** |  
**Project start** | To be decided in agreement with the supervisor.  
**Physical location of project and students work** | Center for Quantitative Genetics and Genomics, AU Foulum, DK-8830 Tjele  

**Project description**

**Project goal and background**  
With the advance of next-generation sequencing and variants imputation. We have dozens of traits that have been tested with the whole-genome sequencing level of imputed variants. However, the underlined genetic determinates still reminded being verified. Nowadays, more and more RNA-seq dataset are publicly available, which give us the opportunity to utilize these dataset to exam the significant hits we obtained from genome-wide association study (GWAS).

**Specific research topic(s)**  
1. Differential expression genes (DEG) analysis  
2. Integrate DEG result with GWAS hits.  
3. The shared genetics determinates between highly correlation traits

**Methods**  
DEG analysis, post-GWAS, genetic correlation analysis, usage of public dataset

**Additional information**  
30-45-60 ECTS thesis as appropriate. The MSc student is invited to co-author a scientific publication.