

PROJECT DESCRIPTION – Master’s Thesis at the Center for  
Quantitative genetics and Genomic (<https://qgg.au.dk/>)

Project title	Verifying the candidate genes of GWAS with RNA-seq data
Main subject area	Animal Genomics
Supervisor and Position E-mail	Zexi Cai, Researcher
Co-Supervisor(s), Position(s) E-mail	Goutam Sahana, Senior researcher
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
<b><i>Project description</i></b>	
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.