SLAUGHTER QUALITY OF ATLANTIC SALMON (*SALMO SALAR*) USING COMPUTERIZED TOMOGRAPHY

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Motivation

- Current slaughter quality evaluation:
  - ✓Costly, time consuming and laborious
  - ✓Based on relatives
  - ✓Measurement error

Reliable genetic evaluation of slaughter quality in Atlantic salmon using individual CT-phenotypes of breeding candidates.

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Data: manual dissection and CT data

Manual dissection N=3044

- Harvest weight, gutted weight, fillet weight, body length
- Fat precentage with NIR
- Pigmentation, wounds, gaping, melanin spots, fillet deformity

- Alternative methods for measuring fat and pigmentation assessed

CT scanning, dead fish N=2012

- Virtual cuts

- Phenotypes from CT scans created using 3D image analysis of the different x-ray absorption properties of different tissues

CT scanning, live fish N=1425

- Feasibility

- Similar phenotypes as in dead fish scanning

- Additionally: proportion cuts

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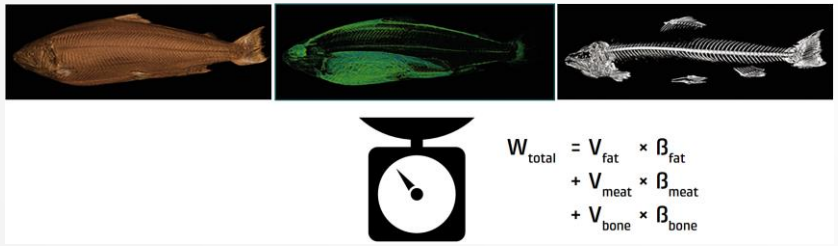
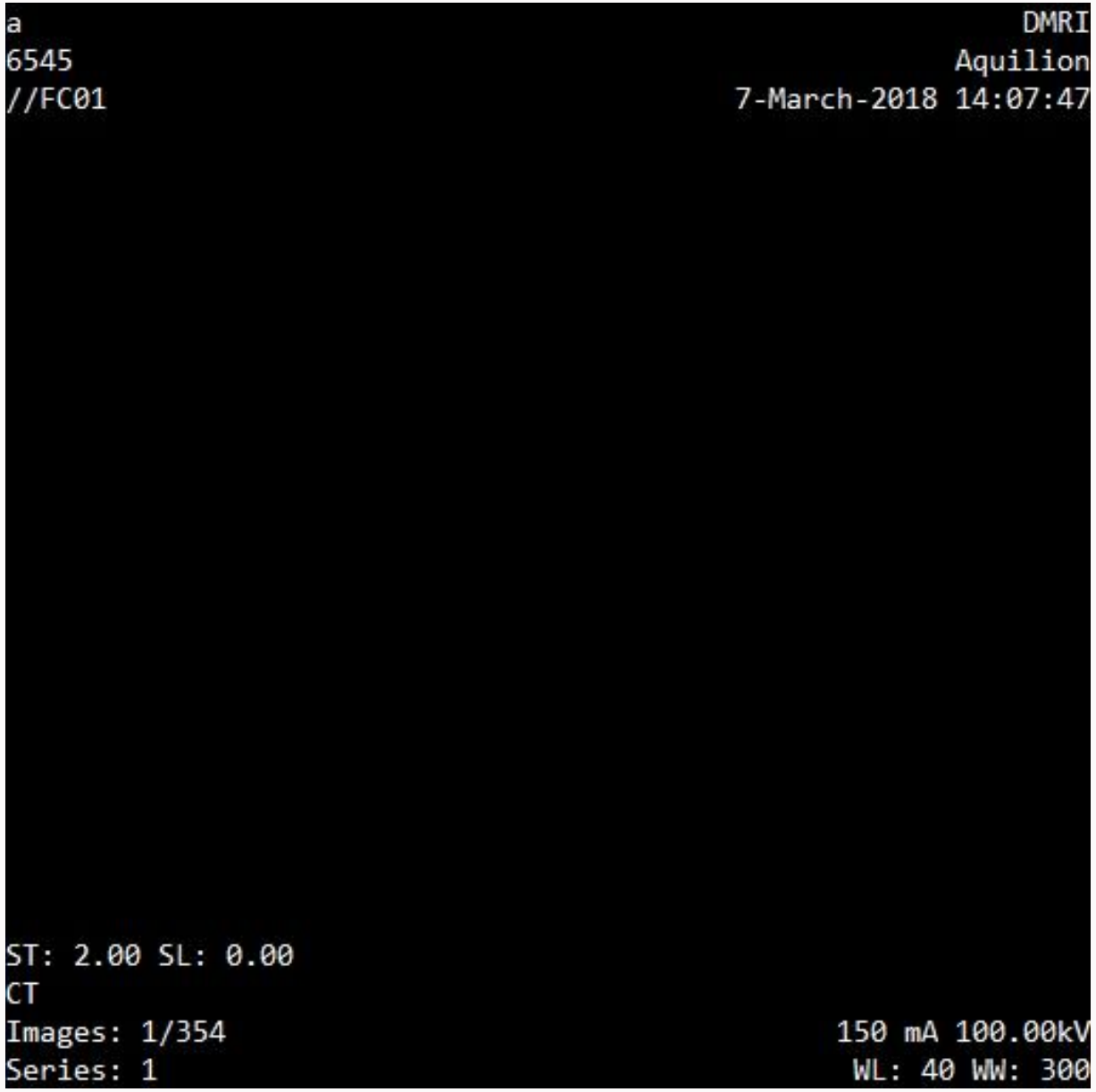
CT scanning

- Three salmon scanned at a time
- Toshiba Aquilion 16
- 2 mm slice thickness





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Genetic parameters

Variable	h2	c2
Manual slaughter		
MHWT	0.26 (0.07)	0.05 (0.03)
MGWT	0.29 (0.08)	0.04 (0.03)
MFWT	0.28 (0.08)	0.06 (0.03)
MFAT (%)	0.33 (0.08)	0.04 (0.03)
CT scanning		
FWT_CT	0.22 (0.08)	0.04 (0.03)
FFAT_CT (g)	0.35 (0.10)	0.03 (0.03)
FFAT_CT (%)	0.48 (0.06)	-
INTFAT_CT	0.21 (0.04)	0.07 (0.04)

Variable	h2	c2
Live fish CT		
FWT_CT	0.31 (0.09)	0.07 (0.03)
FFAT_CT (g)	0.35 (0.09)	0.06 (0.03)
FFAT_CT (%)	0.34 (0.08)	0.02 (0.03)
INTFAT_CT	0.35 (0.08)	0.04 (0.03)
Live fish CT: proportions		
LOINMEAT	0.24 (0.10)	0.10 (0.04)
LOINFAT (g)	0.42 (0.10)	0.04 (0.04)
LOINFAT (%)	0.47 (0.08)	-
NQC_MEAT	0.25 (0.10)	0.07 (0.04)

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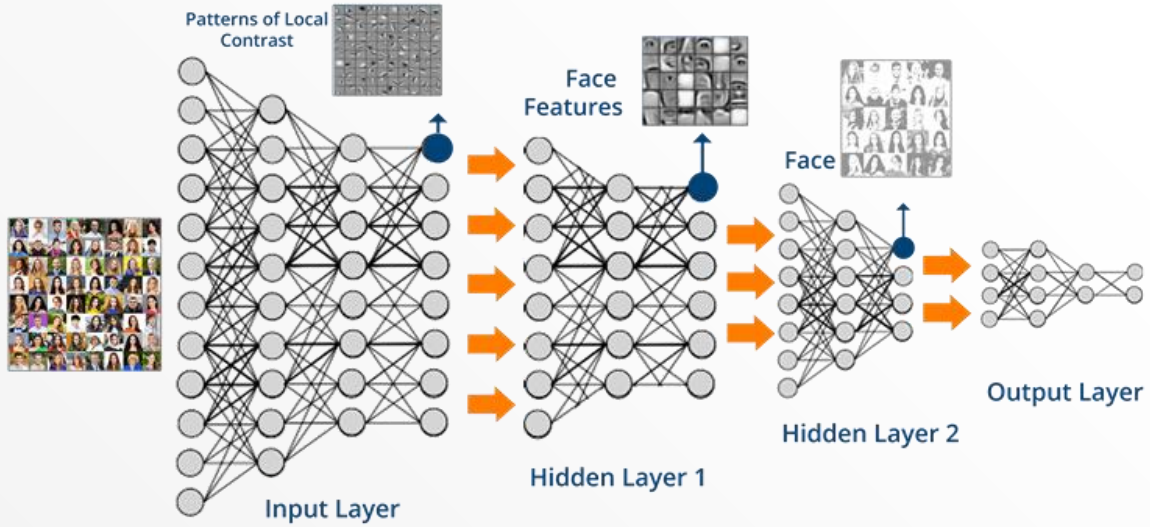
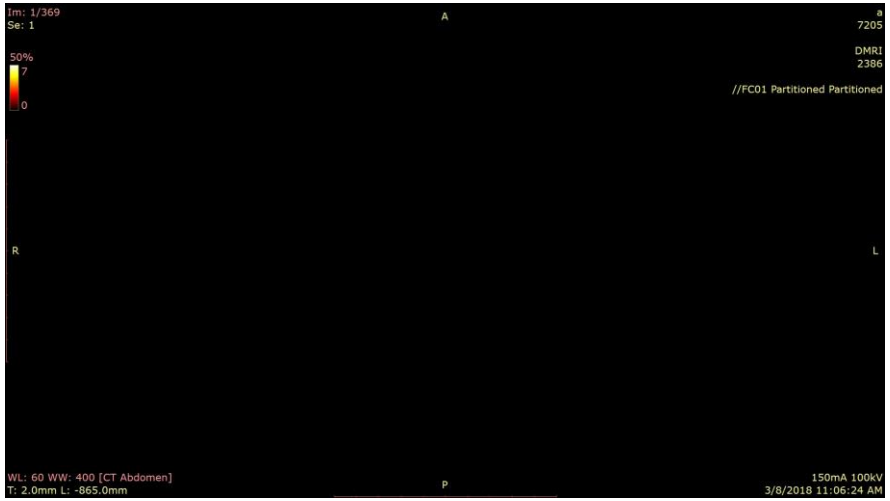
Variable	MHWT (g)	MFWT (g)	FAT (%)	FWT_CT	FFAT_CT (g)	FFAT_CT (%)	INTFAT_CT
MHWT (g)		0.89 (0.02)	0.35 (0.09)	-	0.92 (0.02)	0.61 (0.07)	0.69 (0.06)
MFWT (g)	0.90 (0.00)		0.65 (0.06)	1.0 (0.00)	0.95 (0.01)	0.68 (0.06)	0.72 (0.05)
FAT (%)	0.37 (0.02)	0.43 (0.02)		0.64 (0.08)	0.85 (0.04)	0.91 (0.03)	0.21 (0.12)
FWT_CT	-	0.94 (0.00)	0.52 (0.02)		0.90 (0.02)	0.56 (0.08)	0.56 (0.08)
FFAT_CT (g)	0.91 (0.00)	0.88 (0.01)	0.65 (0.02)	0.92 (0.02)		0.87 (0.03)	0.39 (0.10)
FFAT_CT (%)	0.57 (0.02)	0.57 (0.02)	0.67 (0.02)	0.55 (0.02)	0.82 (0.01)		0.11 (0.11)
INTFAT_CT	0.80 (0.01)	0.75 (0.01)	0.39 (0.03)	0.77 (0.01)	0.66 (0.02)	0.35 (0.03)	

Other results:

- Melanin spots
- The Q-point NIR system
- SORS





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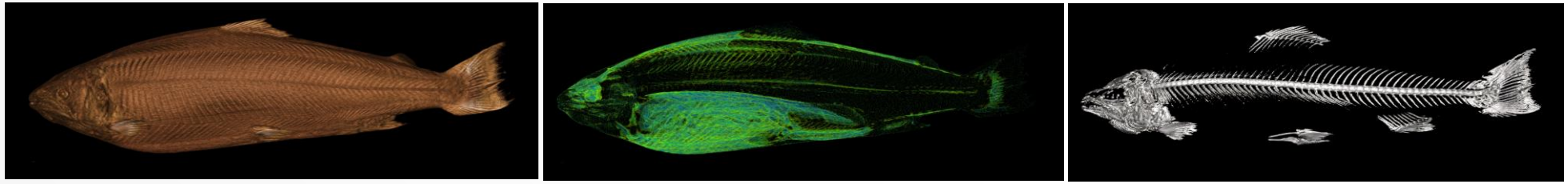
Conclusions

CT scanning and derived virtual cuts reliably describe the slaughter quality of the fish relative to carcass composition and fat content

CT scanning can be performed on live fish



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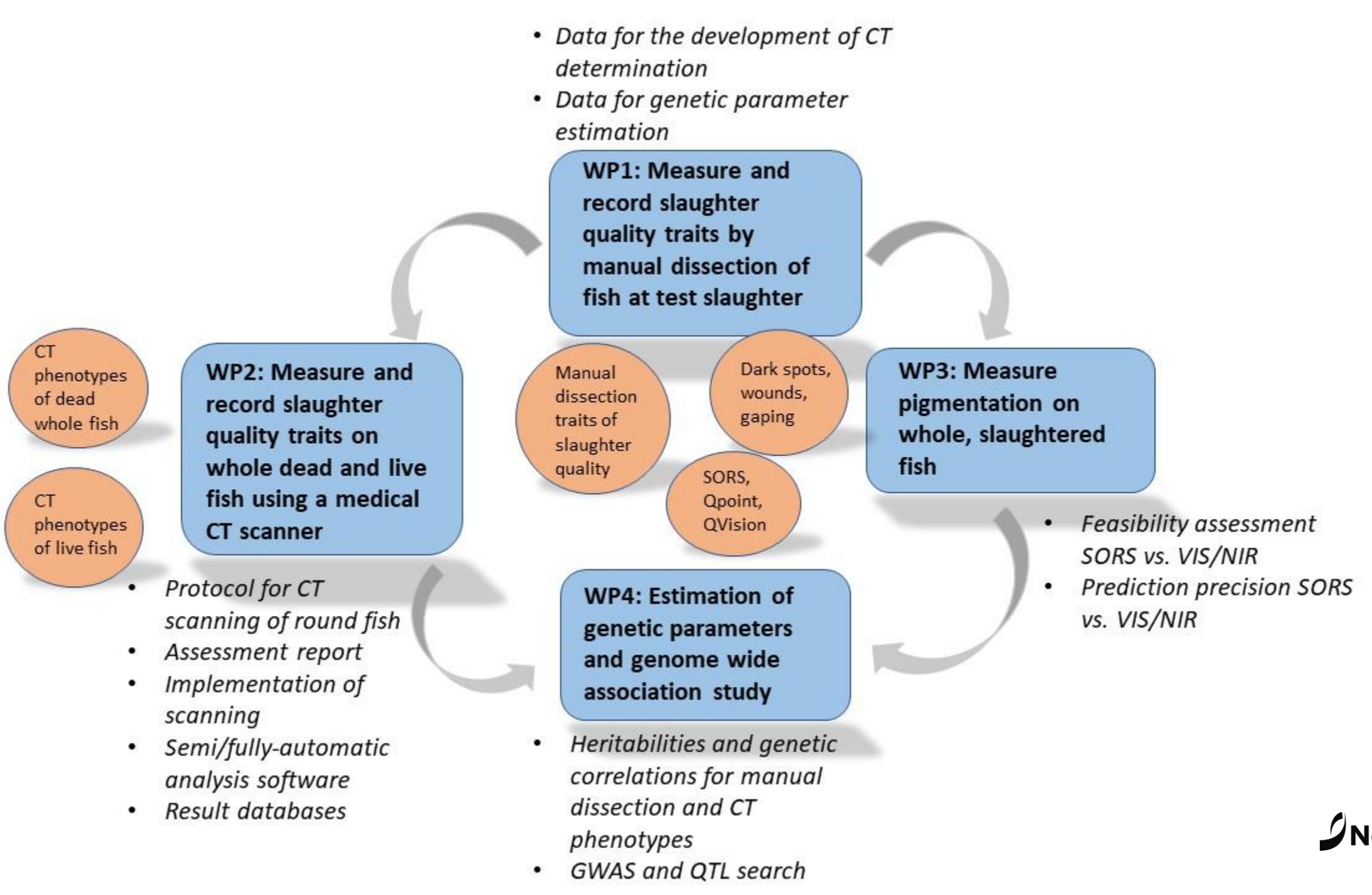
• Data for the development of CT determination
• Data for genetic parameter estimation
WP1: Measure and record slaughter quality traits by manual dissection of fish at test slaughter
Manual dissection traits of slaughter quality
Dark spots, wounds, gaping
SORS, Qpoint, QVision
WP2: Measure and record slaughter quality traits on whole dead and live fish using a medical CT scanner
CT phenotypes of dead whole fish
CT phenotypes of live fish
WP3: Measure pigmentation on whole, slaughtered fish
• Feasibility assessment SORS vs. VIS/NIR
• Prediction precision SORS vs. VIS/NIR
• Protocol for CT scanning of round fish
• Assessment report
• Implementation of scanning
• Semi/fully-automatic analysis software
• Result databases
WP4: Estimation of genetic parameters and genome wide association study
• Heritabilities and genetic correlations for manual dissection and CT phenotypes
• GWAS and QTL search

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