PRELIMINARY RESULTS ON THE DEVELOPMENT OF AN RNA-SEQ-BASED BIOMARKER PANEL TO DIFFERENTIATE GROWTH RATES IN *Sparus aurata*

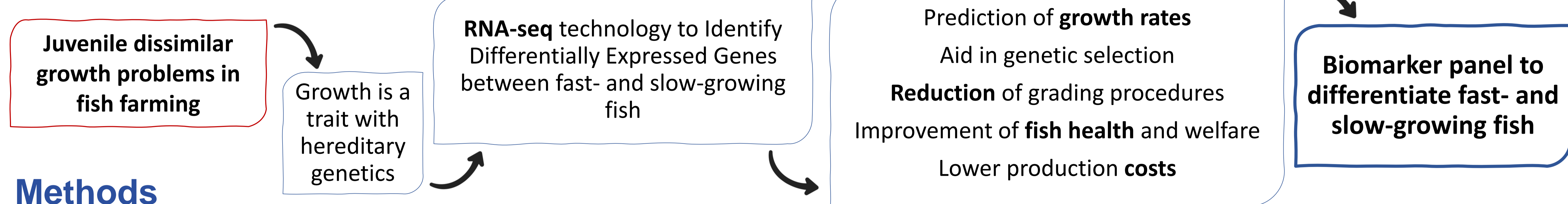Morgana Angelo[1], Iris A.L. Silva[1], Marisa Barata[2], Florbela Soares[1,2], Bárbara Requeijo[1], Pedro Pousão-Ferreira[1,2], Cátia Lourenço-Marques[1,2,*]
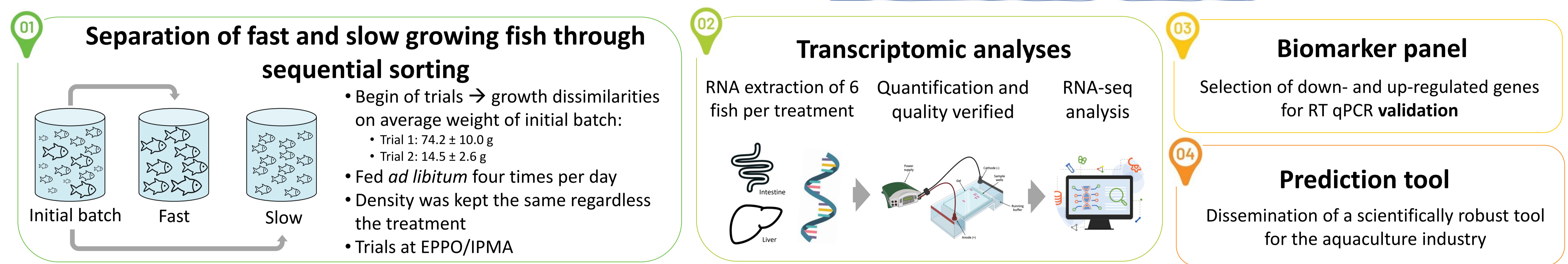
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Overview

Juvenile dissimilar growth problems in fish farming

Growth is a trait with hereditary genetics

RNA-seq technology to Identify Differentially Expressed Genes between fast- and slow-growing fish

Prediction of **growth rates**
Aid in genetic selection
Reduction of grading procedures
Improvement of **fish health** and welfare
Lower production **costs**

Biomarker panel to differentiate fast- and slow-growing fish

Methods

01 **Separation of fast and slow growing fish through sequential sorting**

Initial batch   Fast   Slow

- Begin of trials → growth dissimilarities on average weight of initial batch:
  - Trial 1: 74.2 ± 10.0 g
  - Trial 2: 14.5 ± 2.6 g
- Fed *ad libitum* four times per day
- Density was kept the same regardless the treatment
- Trials at EPPO/IPMA

02 **Transcriptomic analyses**

RNA extraction of 6 fish per treatment   Quantification and quality verified   RNA-seq analysis

03 **Biomarker panel**

Selection of down- and up-regulated genes for RT qPCR **validation**

04 **Prediction tool**

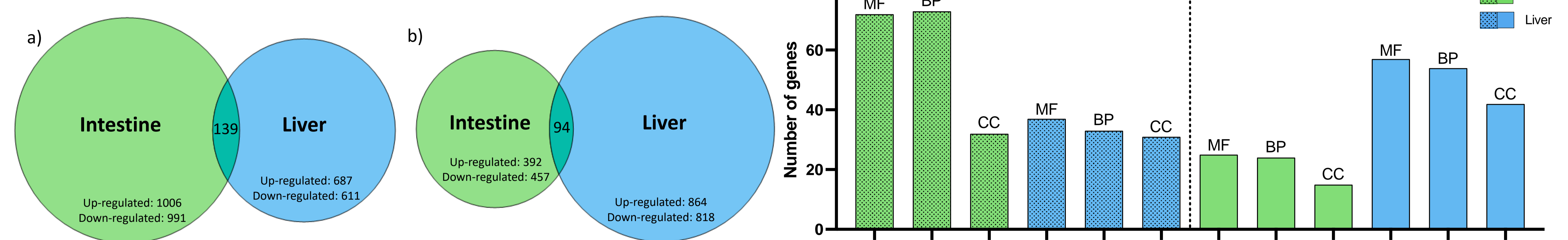Dissemination of a scientifically robust tool for the aquaculture industry

Results

Fig 1. Venn diagram of number of differentially expressed genes (DGEs) in each analyzed tissue for fast versus slow-growing comparison in *Sparus aurata* in a) Trial 1 and b) Trial 2.

a)
Intestine — Up-regulated: 1006, Down-regulated: 991
139
Liver — Up-regulated: 687, Down-regulated: 611

b)
Intestine — Up-regulated: 392, Down-regulated: 457
94
Liver — Up-regulated: 864, Down-regulated: 818

Figure 3. Individual final body weigh distribution of slow- and fast-growing *Sparus aurata* in each trial.
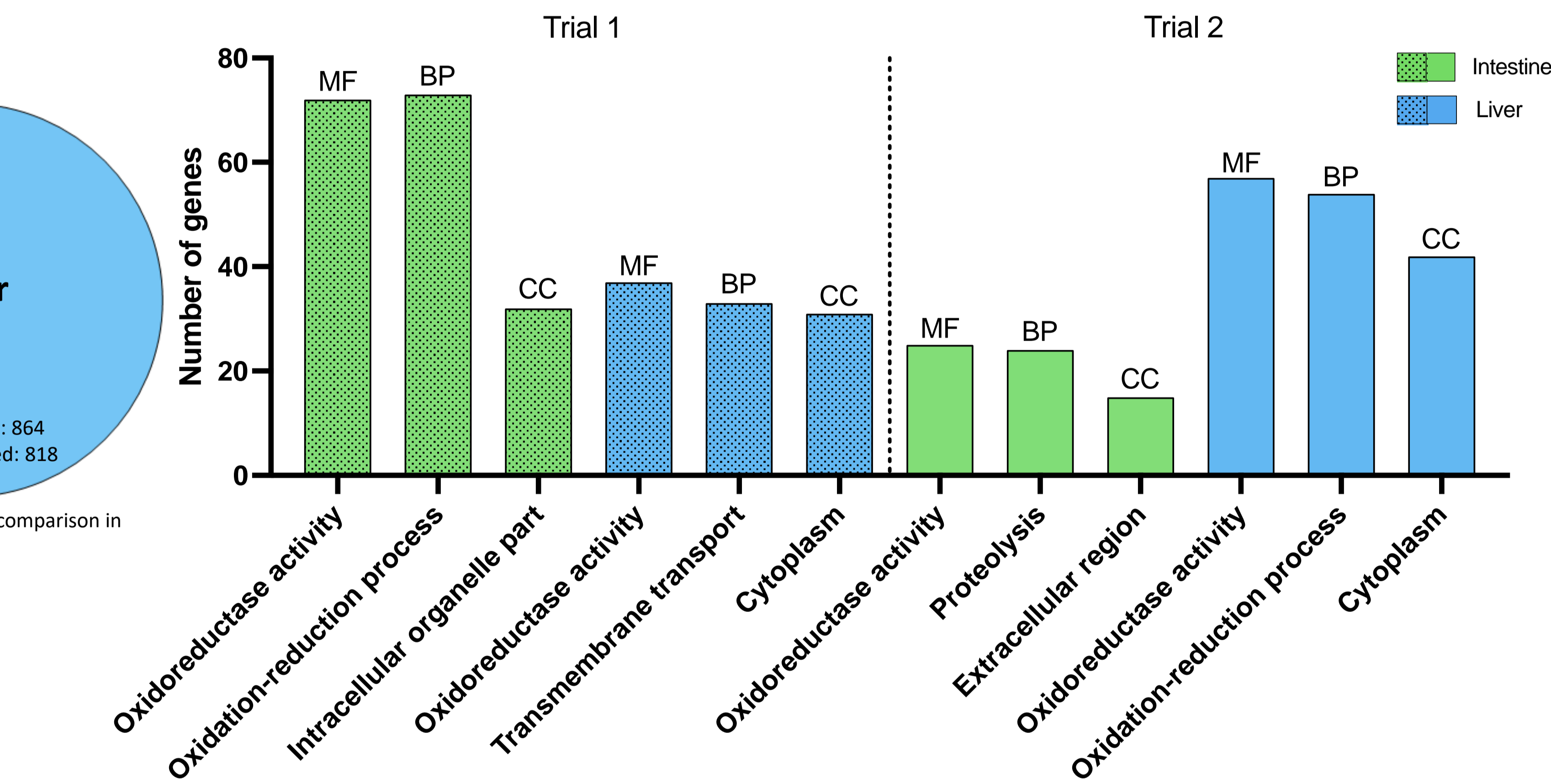

Figure 2. Key biological processes (BP), molecular functions (MF) and cellular components (CC) in each analyzed tissue for fast versus slow-growing comparison.
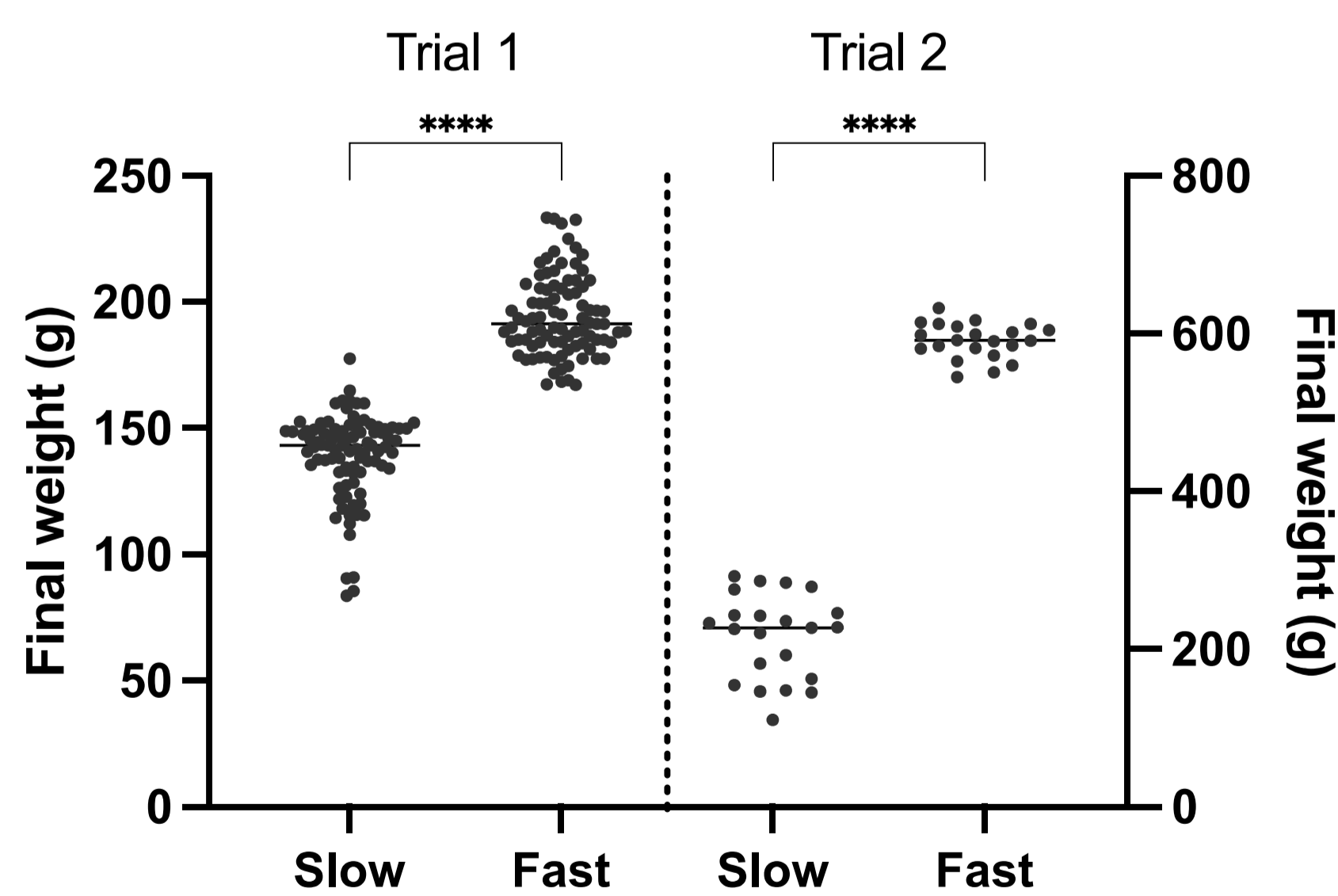
- Cluster analysis revealed that some groups of DGEs are **tissue-specific** (e.g. *ceacam5*, only expressed in the intestine), or **size specific** (e.g. *erbb3* only expressed in fast-growing fish – liver –, and *h4*, only expressed in slow-growing fish – intestine).

Conclusion

The preliminary results from the trials and RNA-seq analysis demonstrate the feasibility of this approach, showing clear distinctions in **gene expression profiles between fast and slow-growing fish**.

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