

# HOLOGENOMIC ANALYSIS REVEALS COMBINED INFLUENCE OF HOST GENETICS AND GUT MICROBIOME ON FEED EFFICIENCY IN ATLANTIC SALMON *Salmo salar*

July Ariñez<sup>1\*</sup>, Gareth Difford<sup>1</sup>, Hanne Dvergedal<sup>1,2</sup>, Gunnar Klemetsdal<sup>1</sup>

<sup>1</sup>Department of Animal and Aquacultural Sciences, Faculty of Biosciences, Norwegian University of Life Sciences, Ås, Norway

<sup>2</sup>AquaGen AS, Trondheim, Norway

july.arines@nmbu.no

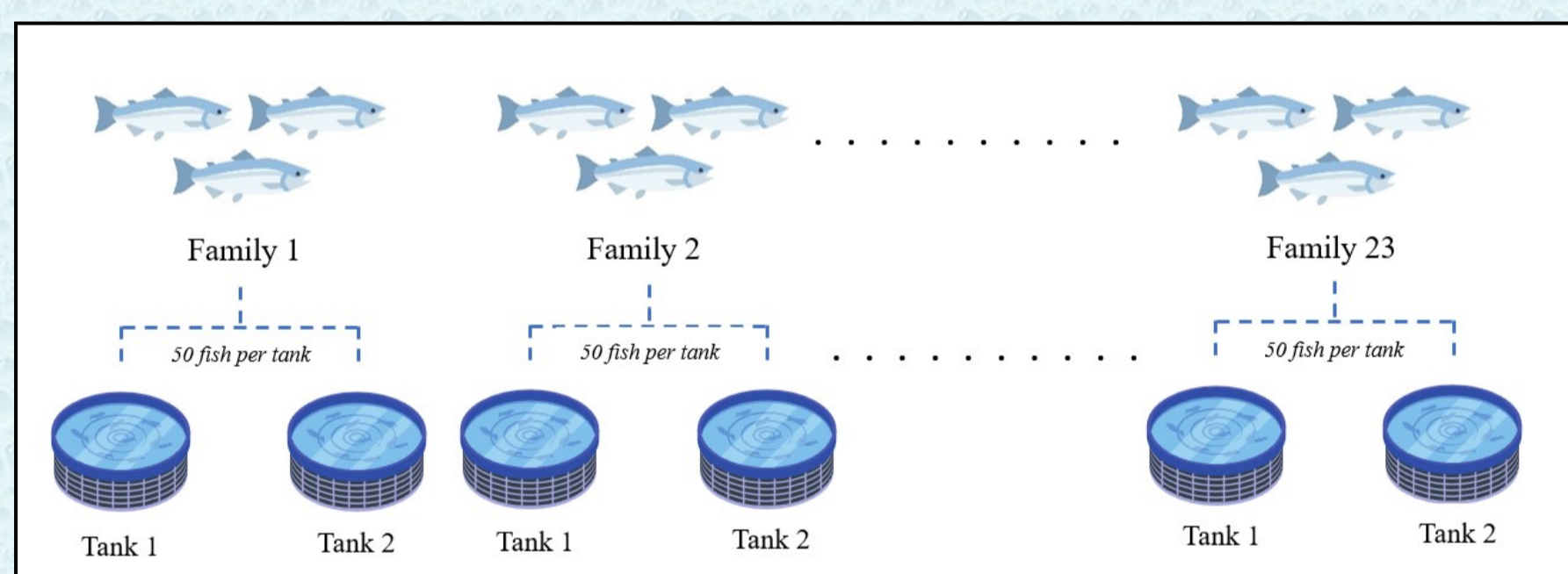
## INTRODUCTION

- Increasing the feed efficiency (FE) of farmed fish contributes to the long-term sustainability of aquaculture.
- As fish are kept communally in rearing facilities, measuring FE on an individual basis is very challenging.
- The use of stable isotopes for the individual measurement of FE in Atlantic salmon has been successfully done<sup>[1]</sup>.
- The gut microbiome participates in feed digestion and nutrient metabolism thus their influence on FE merits investigation.
- The holo-omic framework can be used to dissect the contribution of host genetics and gut microbiome on a trait<sup>[2]</sup>. However, this has not yet been adopted for analysing FE in any aquaculture species.

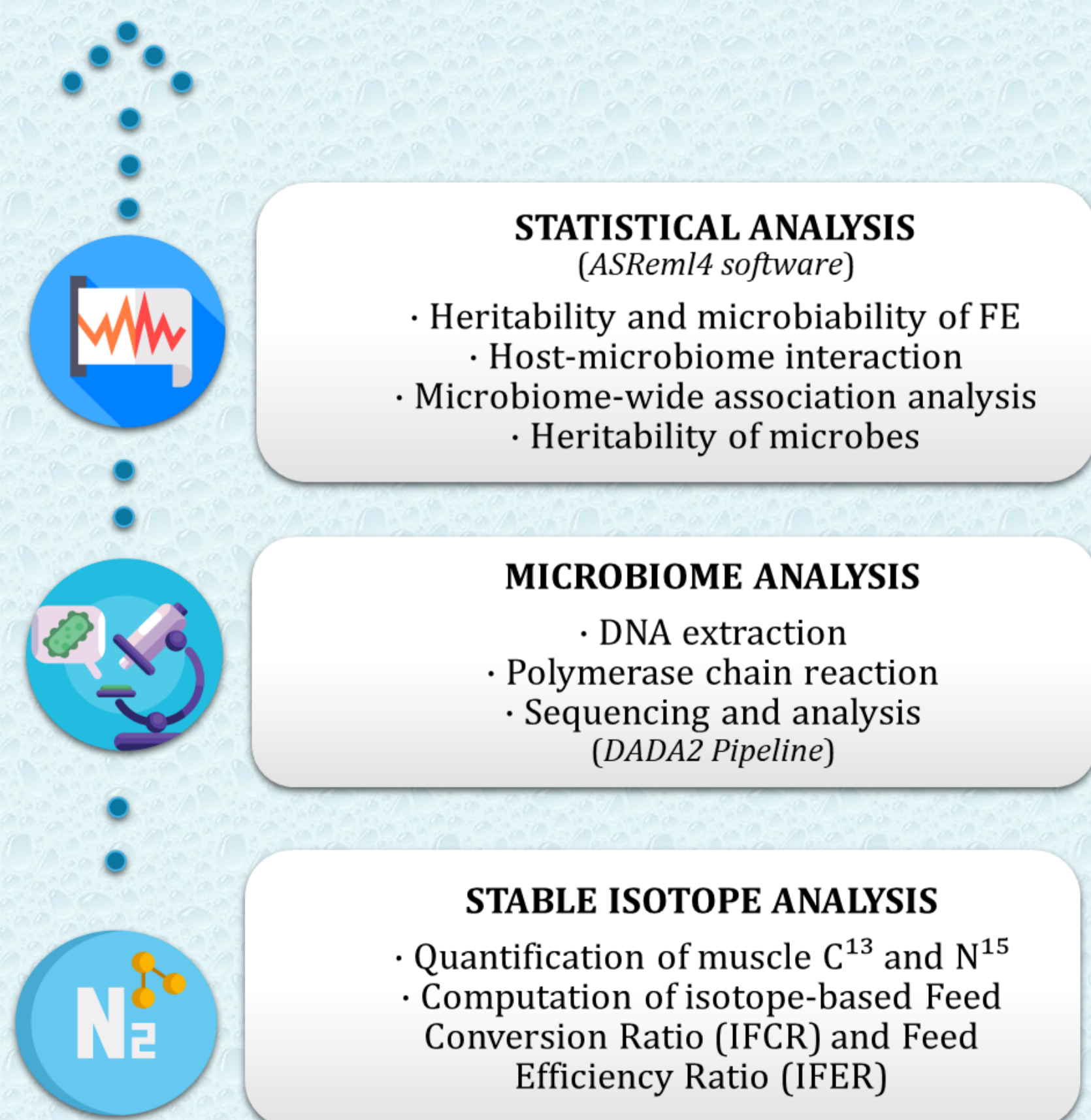
## OBJECTIVES

- Determine the heritability, microbiability and host-microbiome interaction effects on growth and FE in Atlantic salmon.
- Identify and estimate the heritability of most influential microbes.

## METHODOLOGY

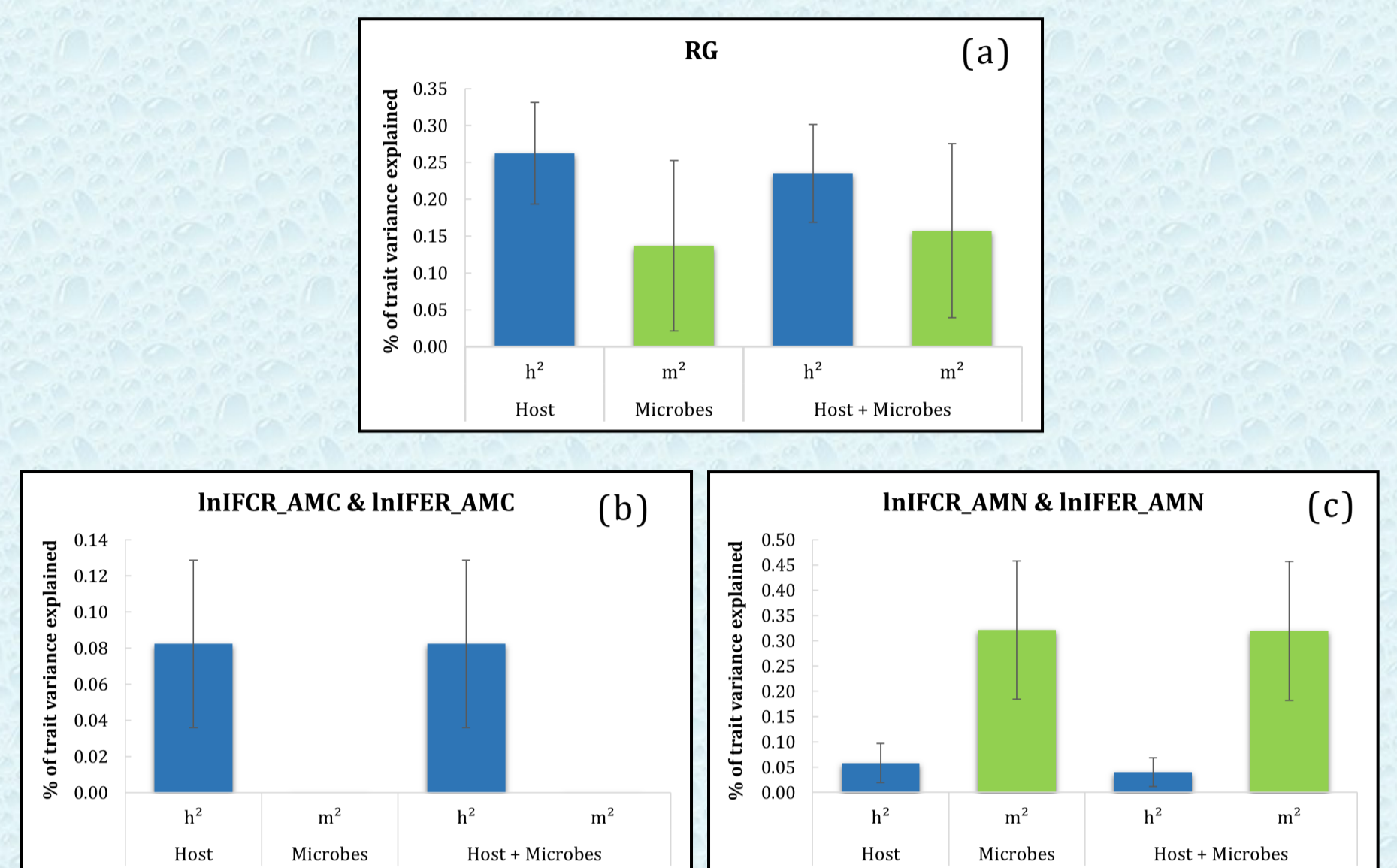


**Figure 1.** Design of the experiment with 23 full-sib families assigned to 46 tanks.

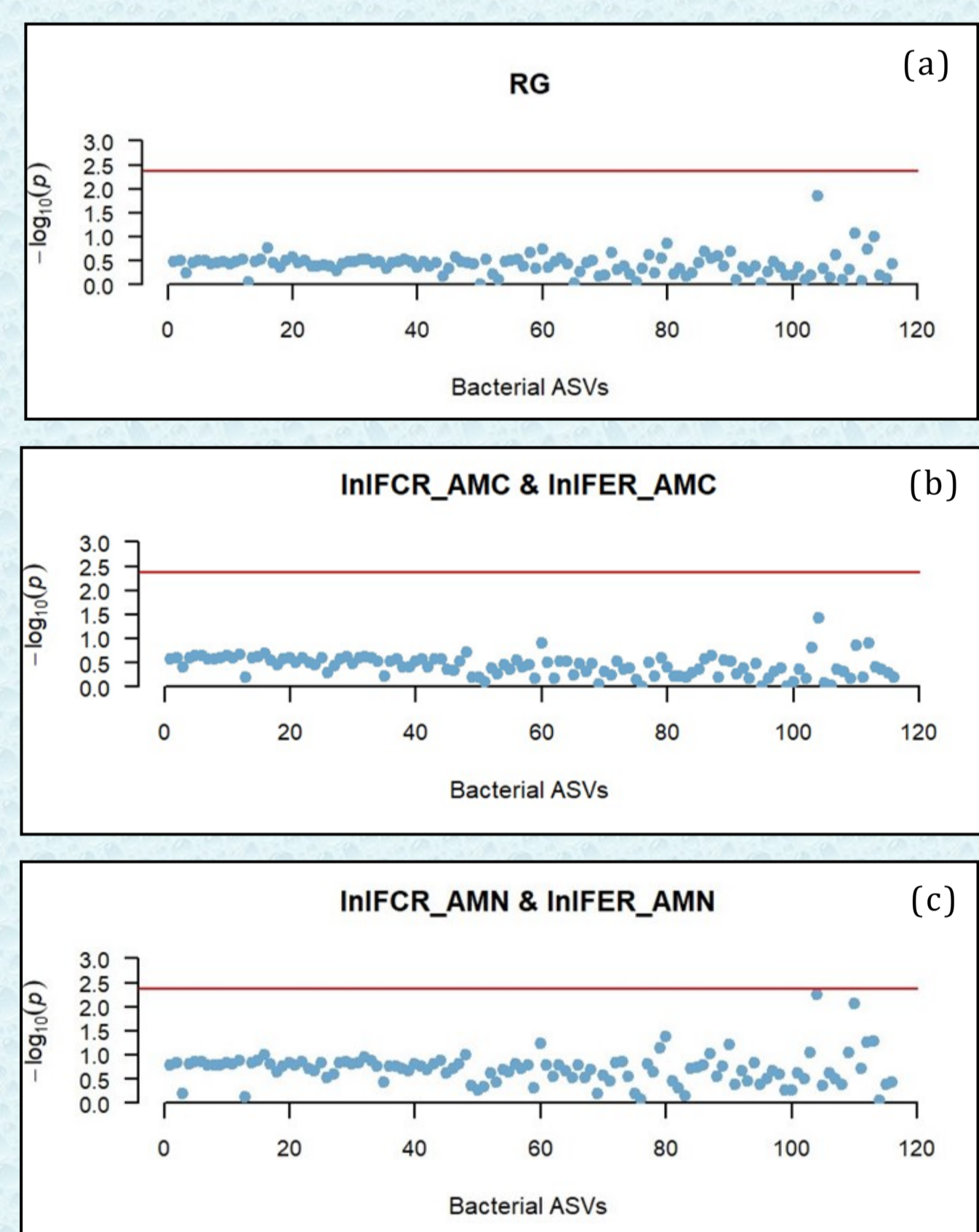


**Figure 2.** Process flow of data analysis.

## RESULTS



**Figure 3.** Heritability and microbiability estimates for (a) relative weight gain (RG), (b) AMC-based FE indicator traits and (c) AMN-based FE indicator traits based on host genetic ( $h^2$ ), microbial ( $m^2$ ) and host-microbiome interaction ( $h^2 + m^2$ ) effects.



**Figure 4.** Manhattan plots of microbiome-wide association analysis for (a) RG, (b) AMC-based FE indicator traits and (c) AMN-based FE indicator traits. Red line represents significance threshold at 5% computed as  $-\log_{10}(0.05/12)$ .

**Table 1.** Heritability ( $h^2$ ) estimates of ASVs linked to growth and FE.

Trait	$\sigma^2_a$	$\sigma^2_e$	$h^2$
ASV171 ( <i>Lactobacillus</i> )	1.99 ± 1.41	5.71 ± 2.39	0.26 ± 0.09*
ASV146 ( <i>Jeotgalibaca</i> )	0.83 ± 0.91	7.13 ± 2.67	0.10 ± 0.10
ASV185 ( <i>Hypomicrobium</i> )	1.72 <sup>a</sup> ± 0.00	6.39 ± 2.53	0.27 <sup>a</sup> ± 0.10

\*significant estimates at 0.05 level of significance, <sup>a</sup>variance and heritability estimates were multiplied with 10<sup>7</sup>

## KEY CONCLUSIONS

- Both growth and FE are affected by host genetics and gut microbiome and their influence to the trait are largely independent.
- *Jeotgalibaca* and *Lactobacillus* may be further investigated for improving FE in Atlantic salmon.

## REFERENCES

- Dvergedal, H. et al. (2019). Selection for feed efficiency in Atlantic salmon using individual indicator traits based on stable isotope profiling. *Genetics Selection Evolution*, 51, 13.
- Limborg, M. T. et al. (2018). Applied hologenomics: feasibility and potential in aquaculture. *Trends in Biotechnology*, 36(3), 252–264.

## ACKNOWLEDGEMENTS