

Comparing the *in vitro* RTgutGC (Rainbow trout) intestinal cell line to native gastrointestinal tissue

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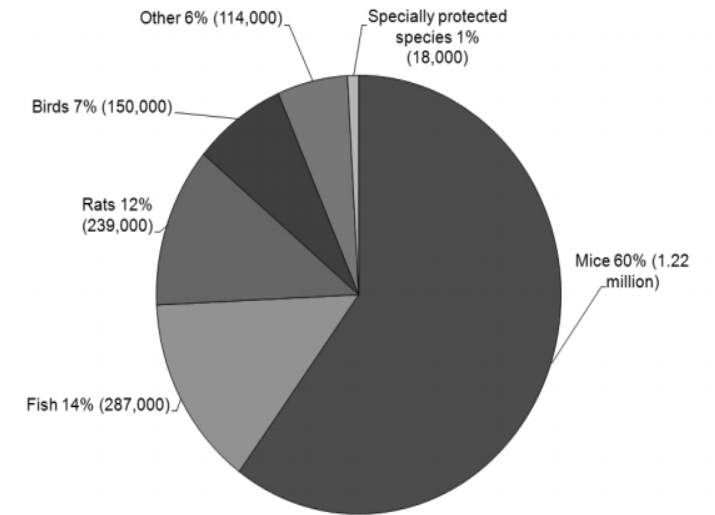
Animals in the laboratory (UK)

- Animals (Scientific Procedures) Act 1986 (ASPA)
- Governed by the Animals in Science Regulation Unit

“..regulate the use of animals in scientific research for the benefit of people, animals and the environment through the provision of impartial licensing procedures and evidence based advice, and by encouraging the development and use of the 3Rs (replacement, reduction and refinement)”

- 5 % decrease in live animal usage (2015 to 2016) ¹
 - 206,000 procedural decrease since 2015

Figure 2: Experimental procedures by species, 2016

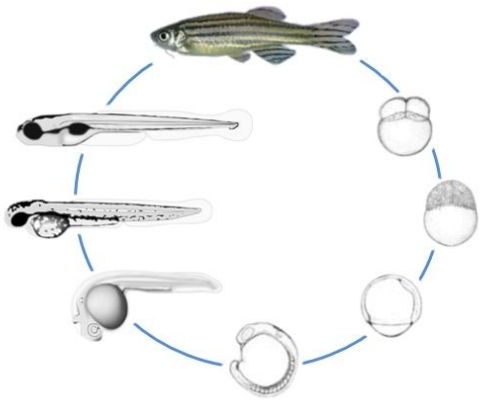


Importance of fish

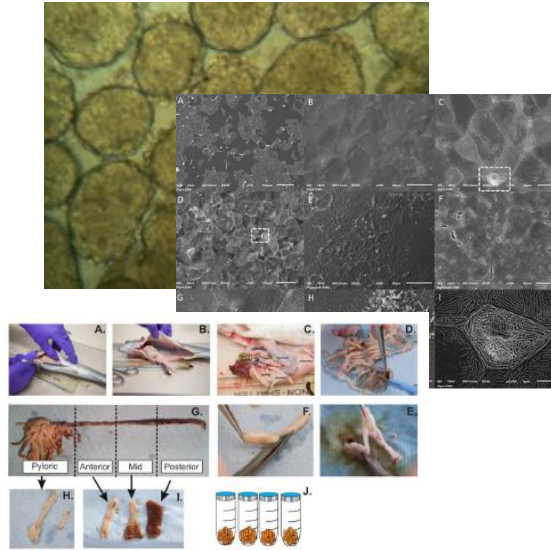
- As rodent research fell fish procedures increased
- Represent 14% of procedural animals
- Why used?
 - Chemicals produced by industry must be assessed under REACH legislation in Europe
 - UK (12,291 registrations of 5,674 substances) ¹
 - Germany (22,612 registrations of 10,313 substances) ¹
 - Austria (1169, registrations of 843 substance) ¹
 - Millions of fish could be used for bioaccumulation assessment along (pharmaceuticals)
 - Continued use of fish in research (physiology, disease, nutrition...)

¹<https://echa.europa.eu/registration-statistics-infograph#>

Alternative approaches to live fish



Early-life stage



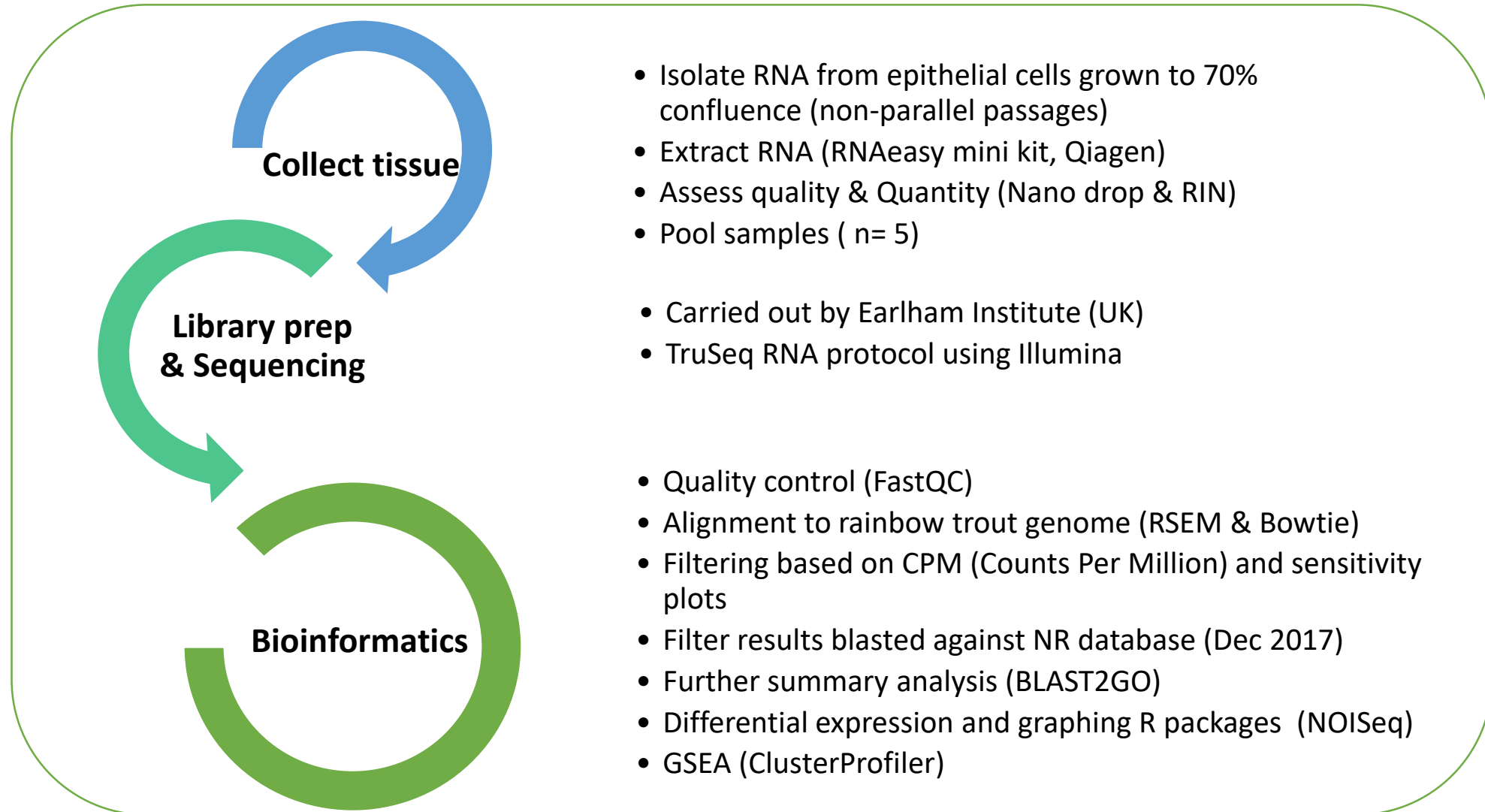
Ex-vivo (primary cells)



In vitro

- **Numerous studies use the RTgutGC as a toxicology model**
 - However, minimum knowledge of how much model deviates from origin tissue
- **Aim is to characterize the transcriptome of the RTgutGC cell line**
 - Identify large number of genes/targets
 - Mechanism of action
 - Eventually identify potential mode of action of compound based on physiological and transcriptome similarity to origin tissue using replacement mode

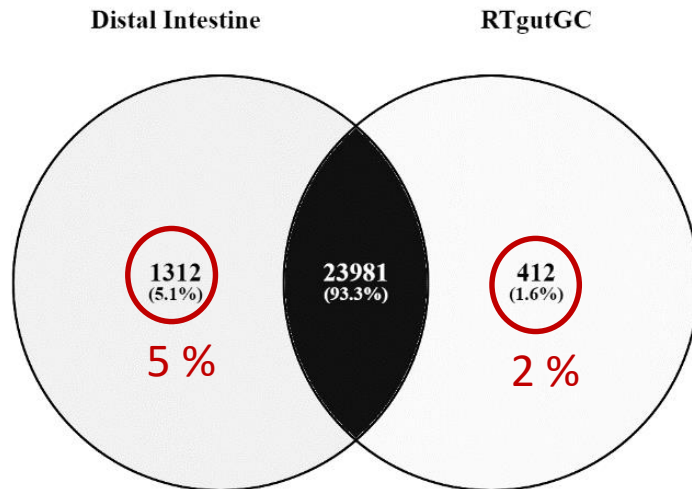
Experimental design and analysis



Results:

Alignment

- 79,245 transcripts following alignment (REFSEQ)
- Filter based on CPM > 5
- RPKM normalisation
- 25,705 transcripts



Differentially expressed genes (DEG)

DEG in the cell line compared to the tissue

- **Unmodified data**
 - 17855 DEG
 - 8454 (**up**) + 9401 (**down**)
- **Removal of duplicated Gene ID's**
 - 12,014 DEG
 - 5709 (**up**) + 6305 (**down**)

Top 10 DEG

Up-regulated

- 1 Ferritin, middle subunit-like
- 2 Heat shock cognate protein 70a
- 3 Ferritin H-2
- 4 Ferritin H-1
- 5 Elongation factor EF1-alpha
- 6 Ferritin H-3
- 7 Simple type II keratin K8b (S2)
- 8 Glutathione S-transferase P-like
- 9 Lipoprotein lipase-like
- 1 Neuroblast differentiation-associated protein
0 (AHNAK-like)

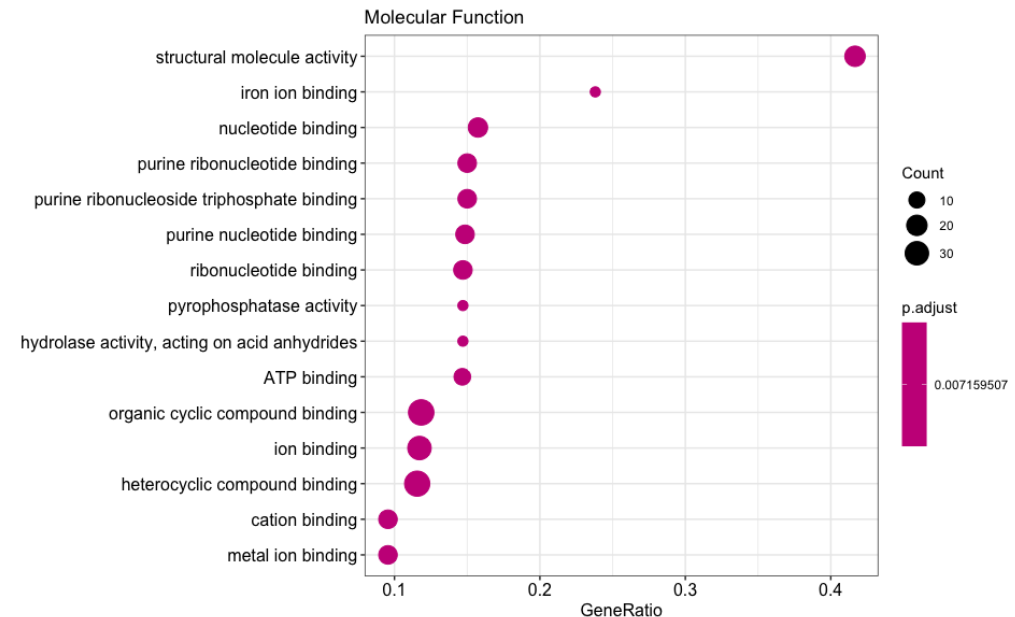
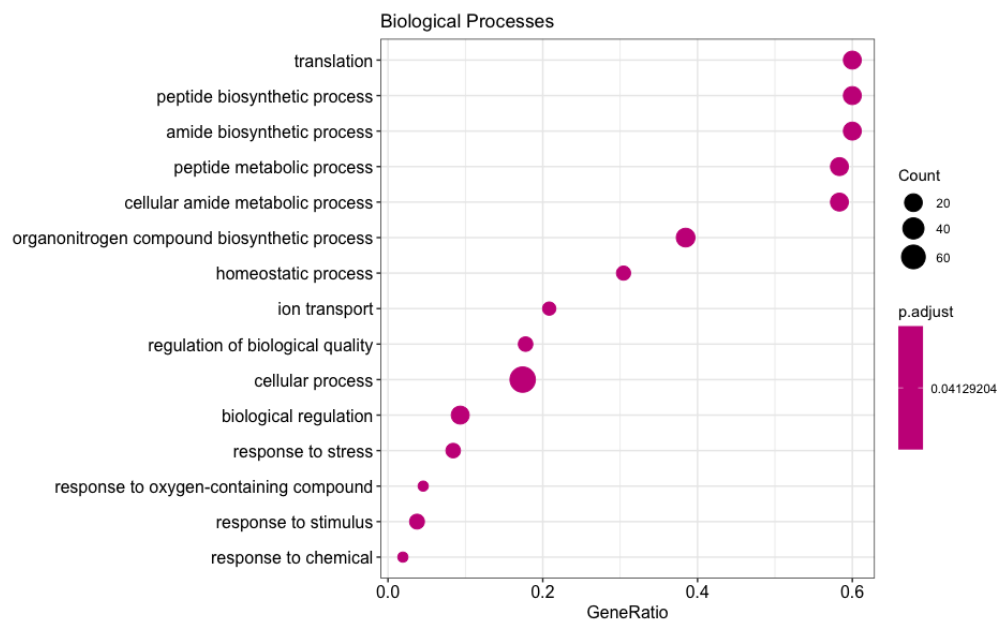
Down-regulated

- 1 Cathepsin L1-like
- 2 Uncharacterized LOC110528711
- 3 Fatty acid binding protein 2
- 4 Apolipoprotein B-100-like
- 5 Actin, cytoplasmic 1
- 6 Uncharacterized LOC110494266
- 7 UPF0183 protein C16orf70 homolog
- 8 Cadherin related family member 2
- 9 Galectin-2-like
- 10 Mannan-binding lectin H2

Gene set enrichment analysis (GSEA)

“Method to identify classes of genes or proteins that are over-represented in a large set of genes or proteins”

- GSEA performed on full list of transcripts of the RTgutGC (Following removal of 0 count sequences)
 - 46,023 transcripts
 - Limited to top 15 biological processes and molecular function



GO-Annotations

Molecular function

- 1 Organic cyclic compound binding
- 2 Heterocyclic compound binding
- 3 Ion binding
- 4 Protein binding
- 5 Hydrolase activity
- 6 Small molecular binding
- 7 Carbohydrate derivative binding
- 8 Transferase activity
- 9 Catalytic activity (acting on protein)
- 10 DNA binding transcription factor activity

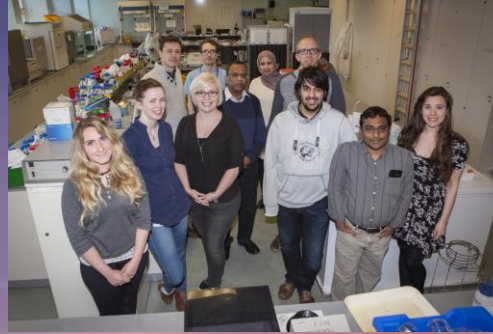
Biological Processes

- 1 Organic substance metabolic process
- 2 Primary metabolic process
- 3 Cellular metabolic process
- 4 Nitrogen compound metabolic process
- 5 Biosynthesis process
- 6 Regulation of biological process
- 7 Regulation of cellular process
- 8 Response to chemical
- 9 Cellular response to stimulus
- 10 Response to stress

Conclusions

- By describing and mining the gene profile of the only fish intestinal cell line, this study has:
 - For the first time, established comparability to native tissue
 - Facilitated informed experimental design in toxicology using this cell line
 - Aided in identification of functional and pathway annotation (*Ongoing*)
 - Aided in genomic studies in aquatic cell lines
 - Provided code for analysis so can be replicated in the future (*Ongoing*)
 - Developed a genetic toolkit which others can help shape 3Rs research using aquatic cell lines

Project team and staff at
University of Plymouth



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**RESEARCH
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