

Genetic analysis of quantitative traits in medaka fish and humans

Ian Brettell

2022-05-25

Contents

1	About	5
1.1	Usage	5
1.2	Render book	5
1.3	Preview book	6
2	Genomic variations in the MIKK panel	7

Chapter 1

About

This is a *sample* book written in **Markdown**. You can use anything that Pandoc’s Markdown supports; for example, a math equation $a^2 + b^2 = c^2$.

1.1 Usage

Each **bookdown** chapter is an .Rmd file, and each .Rmd file can contain one (and only one) chapter. A chapter *must* start with a first-level heading: **# A good chapter**, and can contain one (and only one) first-level heading.

Use second-level and higher headings within chapters like: **## A short section** or **### An even shorter section**.

The **index.Rmd** file is required, and is also your first book chapter. It will be the homepage when you render the book.

1.2 Render book

You can render the HTML version of this example book without changing anything:

1. Find the **Build** pane in the RStudio IDE, and
2. Click on **Build Book**, then select your output format, or select “All formats” if you’d like to use multiple formats from the same book source files.

Or build the book from the R console:

```
bookdown::render_book()
```

To render this example to PDF as a `bookdown::pdf_book`, you'll need to install XeLaTeX. You are recommended to install TinyTeX (which includes XeLaTeX): <https://yihui.org/tinytex/>.

1.3 Preview book

As you work, you may start a local server to live preview this HTML book. This preview will update as you edit the book when you save individual .Rmd files. You can start the server in a work session by using the RStudio add-in “Preview book”, or from the R console:

```
bookdown::serve_book()
```

Chapter 2

Genomic variations in the MIKK panel

This project was carried out in collaboration with Felix Loosli's group at the Karlsruhe Institute of Technology (KIT), and Jochen Wittbrodt's group in the Centre for Organismal Studies (COS) at the University of Heidelberg.

This chapter will set out my contributions to the the following pair of papers published on bioRxiv, which have recently been accepted for publication in *Genome Biology*:

- Tomas Fitzgerald et al.¹
- Adrien Leger et al.²

Genomic variations and epigenetic landscape of the Medaka Inbred Kiyosu-Karlsruhe (MIKK) panel. 2021. bioRxiv: doi.org/10.1101/2021.05.17.444424.
*Joint-first author We substantially revised the manuscripts for both papers during the review process for *Genome Biology*, so my contributions extend further than what is contained in the bioRxiv versions, most noticeably with the inclusion of the nucleotide diversity analysis.

Fitzgerald, Tomas, Ian Brettell, Adrien Leger, Nadeshda Wolf, Natalja Kusminski, Jack Monahan, Carl Barton, et al. "The Medaka Inbred Kiyosu-Karlsruhe (MIKK) Panel." *Genome Biology* 23, no. 1 (February 21, 2022): 59. <https://doi.org/10.1186/s13059-022-02623-z>.

Leger, Adrien, Ian Brettell, Jack Monahan, Carl Barton, Nadeshda Wolf, Natalja Kusminski, Cathrin Herder, et al. "Genomic Variations and Epigenomic

¹"The Medaka Inbred Kiyosu-Karlsruhe (MIKK) Panel," *Genome Biology* 23, no. 1 (February 21, 2022): 59, <https://doi.org/10.1186/s13059-022-02623-z>.

²"Genomic Variations and Epigenomic Landscape of the Medaka Inbred Kiyosu-Karlsruhe (MIKK) Panel," *Genome Biology* 23, no. 1 (February 21, 2022): 58, <https://doi.org/10.1186/s13059-022-02602-4>.

Landscape of the Medaka Inbred Kiyosu-Karlsruhe (MIKK) Panel.” *Genome Biology* 23, no. 1 (February 21, 2022): 58. <https://doi.org/10.1186/s13059-022-02602-4>.