Hi-C Workshop

Date: 20th of May 2025
Location: Universitat de les Illes Balears, Edifici Antoni Maria Alcover i Sureda, Classroom 6
Time: 9:30 – 18:00

9:30 – 10:00. Welcome and Introduction

- Workshop goals and format
- Participant introductions (background and expertise)
- Setting expectations: open discussion format

10:00 – 11:00. The basics of Hi-C

- Principles of chromatin conformation capture and applications.
- Key differences: Hi-C vs PoreC and others

11:30 –11:45. Coffee break

11:15 – 13:00. Sample preparation and crosslinking optimization

- Overview of the protocol. Standard Input and Low input
- Key factors for successful fixation and crosslinking in laboratory
- Key differences with different tissues and challenging samples
- Discussion: What has worked best for different sample types?
- Ultra Low Input.
- Open troubleshooting discussion: Participants present real issues they've encountered

13:00 – 14:00. Lunch break

14:00 – 15:00. QC, Optimization and troubleshooting road map

- QC after crosslinking – is it necessary?
- Step-by-step troubleshooting strategy.
- Open discussion

15:00 – 15:30. Library preparation. How we work at Sanger Institute

- Fragmentation strategies: restriction enzyme vs. tagmentation
- Adapter ligation, PCR amplification, and indexing

15:30 – 16:00. Basic introduction in the interpretation of the Heatmap

16:00 - 16:30. Talk by Arima representative

16:40 – 17:10. Talk by OmniC representative

17:10 - 18:00. Wrap-up and next steps

- Key takeaways
- Areas needing further research or optimization
- Group discussion on solutions and alternative approaches
- Sharing optimized protocols and practical tips

HMW WORKSHOP

Date: 21st of May 2025
Location: Universitat de les Illes Balears, Edifici Antoni Maria Alcover i Sureda, Classroom 6
Time: 9:30 – 17:00

9:30 – 10:00. Welcome and Introduction

- Overview of the workshop's goals
- Participant introductions (brief background and expertise)
- Setting expectations: open discussion format
- Participant input: Introduce the topics that they are more interested in

10:00 – 10:45. The Fundamentals of HMW DNA extraction

- Importance of HMW DNA for long-read sequencing
- Key considerations: yield, integrity, purity
- Overview of the different types of extraction approaches (pros and cons of each)

11:00 – 11:15. Coffee break

11:15 – 11:45. Storage and Handling

- How to minimize damage and shearing of the samples.
- Handling and storage best practices
- Common contaminants and removal strategies?

11:45 – 13:00. Sample types and extraction methods

- Different sample types: blood, tissue, cells, environmental samples
- How do we disrupt/grind complex tissues?
- Comparing extraction methods (e.g., phenol-chloroform, column-based, bead-based)

- Group discussion: What has worked? What hasn't? Go case by case (every species and tissue type)

13:00 – 14:00. Lunch break

14:30 – 15:00. QC and library preparation

- Assessing HMW DNA quality (e.g., Nanodrop, Qubit, Femto, Agarose gels, TapeStation)
- Library prep considerations for Oxford Nanopore and PacBio
- Group discussion: Best QC practices for library preparation and lessons learned

15:00 – 16:30. Problem-solving session: case studies and live troubleshooting

- Participants present real problems they've encountered
- Open floor for suggestions and solutions
- Sharing alternative protocols and strategies

16:30 – 17:00. Wrap-up and next steps

- Key takeaways from the discussion.
- Areas needing further research or collaboration.
- Potential follow-ups (shared protocol repository, future meetings, minutes, tips….).