4DN OMICS working group call on Mar 24, 2020

Attendees:

- Bing Ren
- Andy Schroeder @dcic
- Irene X. Fan, Riccardo Calandrelli, Sheng Zhong @oh
- Andrea @dcic
- Iddil Bekirov
- Ian Fingerman
- Judy Mietz
- Koray Kirli @dcic
- Luisa Mercado @dcic
- Erez Lieberman-Aiden
- Sarah @dcic
- Sean Hanlon
- Burak Alver
- 1. Review protocols that are in the pipeline for recommendation to the 4DN SC:
 - 1. PLAC-seq/HiChIP/in situ ChIA-PET,
 - iMARGI. Note: This iMARGI protocol (see also Wu et al., 2019) is approved by 4DN to analyze the cumulative characteristics of RNA-chromatin interactions. This approval does not include the application of iMARGI to the identification of a specific RNA to a specific genomic sequence, which remains in the investigative research domain of each individual lab.
 - 3. Methyl-HiC/HiCulfite (bulk)
 - 4. Single cell Methyl-HiC
 - 5. sci-Hi-C
 - i. https://data.4dnucleome.org/protocols/14a85428-382c-4487-b8cd-d4c49fd7cfea/
 - ii.
- 2. Planning for future meeting agendas. Please note that the current protocols recommended to 4DN and in various stages of discussion can be found here.
 - a. SPRITE
 - b. Micro-C
 - c. COLA
 - d. Updates from previously approved protocols, by users or inventors.
 - e.

Discussion:

1. iMARGI: presentation on the protocol was made, experimental parts were excellent, questions on data analysis aspect. Consensus is emerging on what exactly this method is designed to do.

Action item -

- 1. Reach out to Yijun's lab to discuss this on the next Omics WG call.
- 2. Erez and Sheng will discuss potential revision to iMARGI write up, for discussion in next session.
- 3. Erez and Bing will discuss Methyl-HiC/HiCulfite protocols.
- 4. Update correct combinatorial HiC protocol

References

Wu, W. et al. Mapping RNA-chromatin interactions by sequencing with iMARGI. *Nat Protoc* **14**, 3243-3272, doi:10.1038/s41596-019-0229-4 (2019).