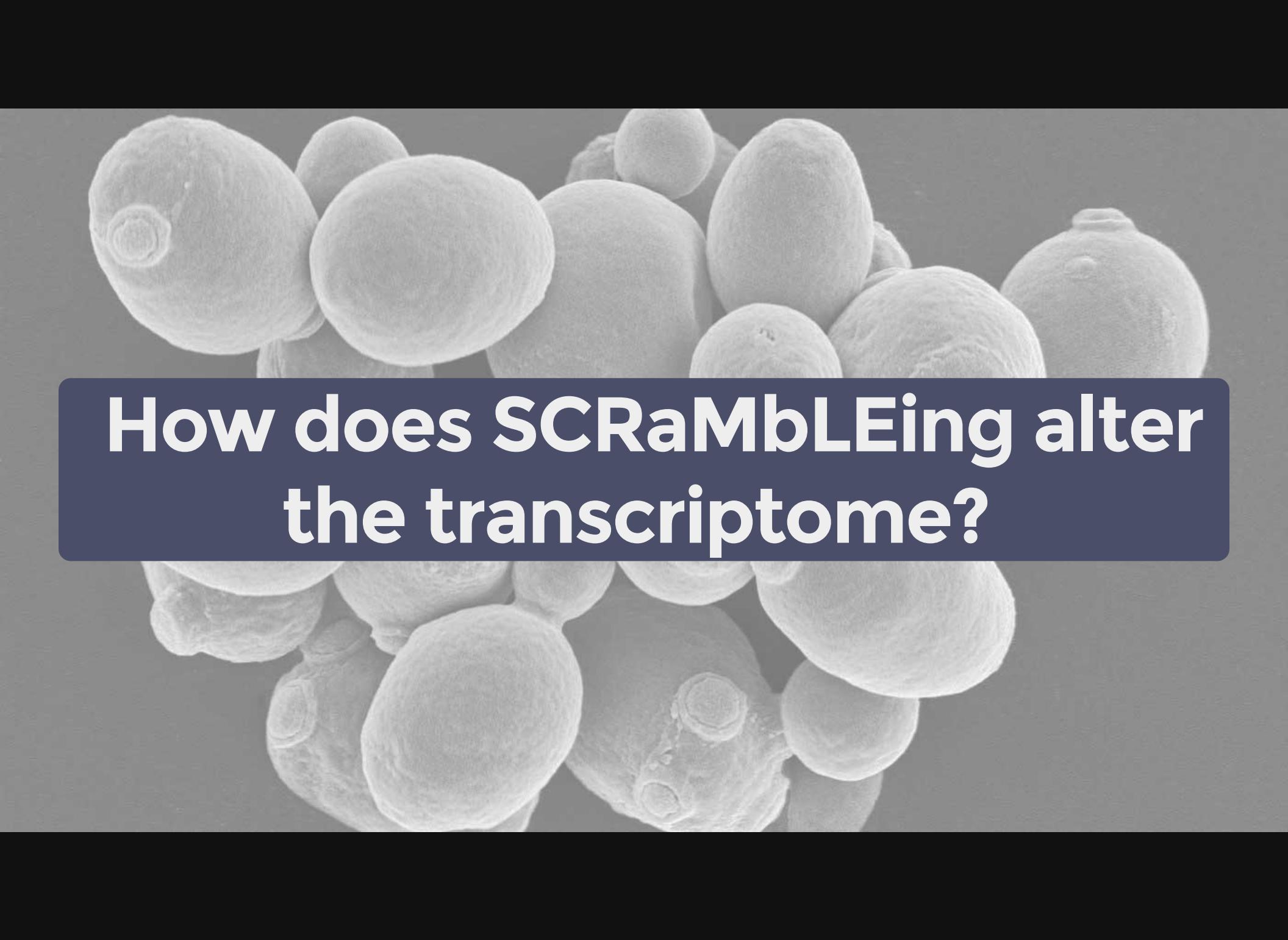


# **Genomic and Transcriptomic Characterization of SCRaMbLE strains**

Aaron Brooks /  @scalefreegan

Lars Steinmetz's Group | EMBL Heidelberg

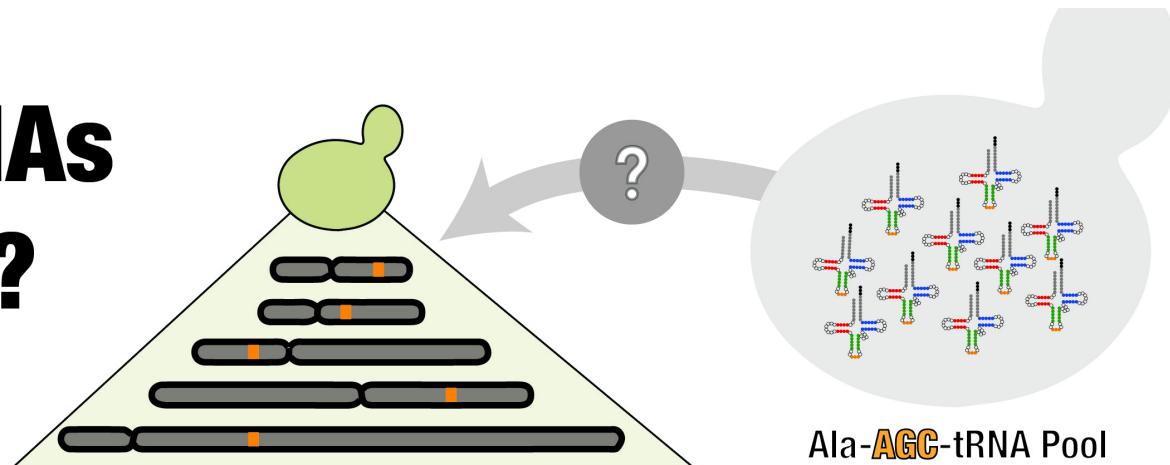


**How does SCRaMBLEing alter  
the transcriptome?**

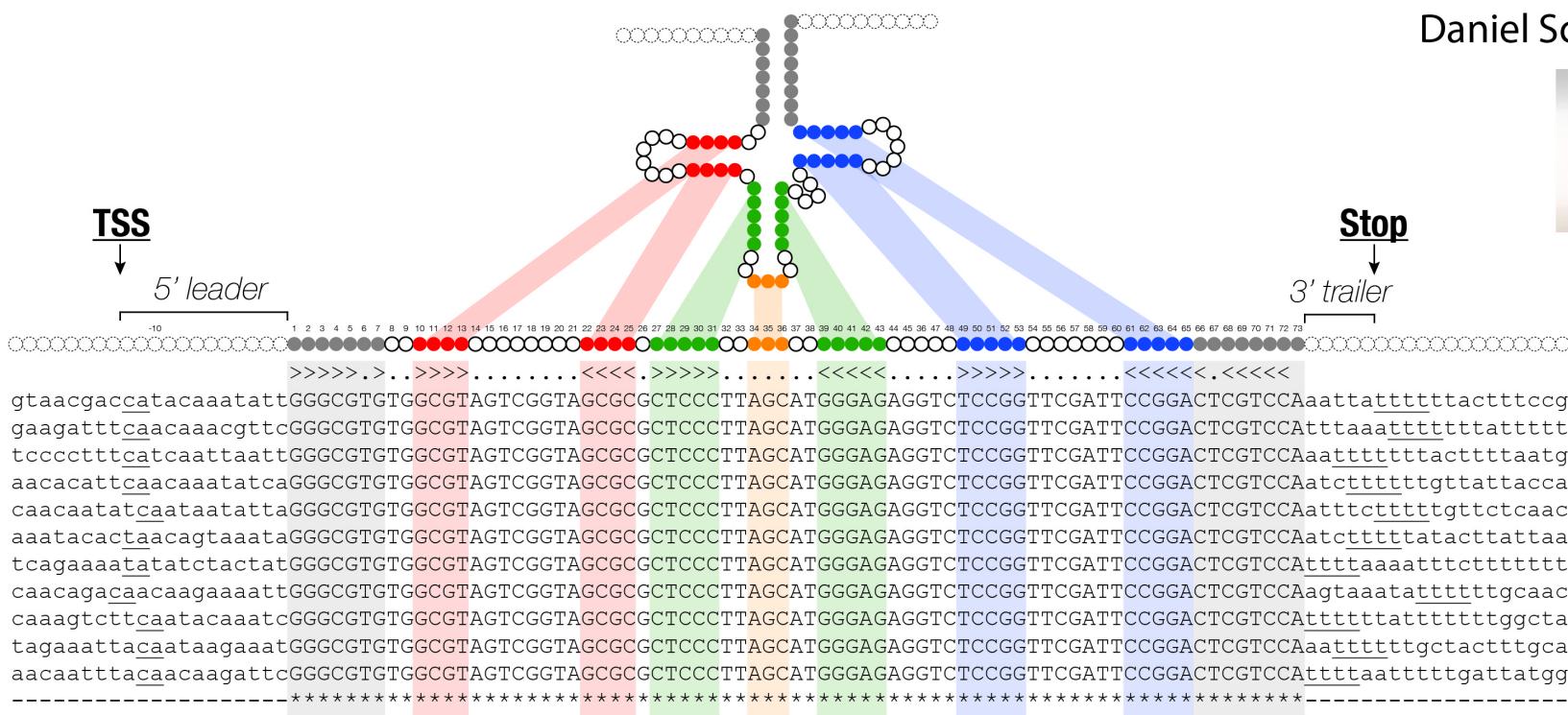
# Two snapshots

- Transcript isoform variation      synIXR SCRaMbLE
- tRNA genomic origins      tRNA neochromosome

# Where do tRNAs come from?



## Ala precursor tRNA

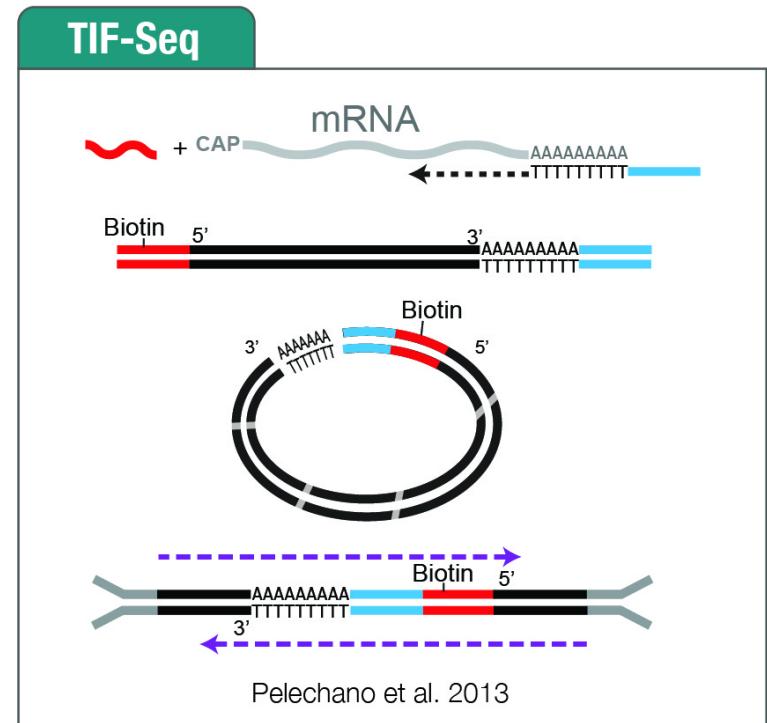
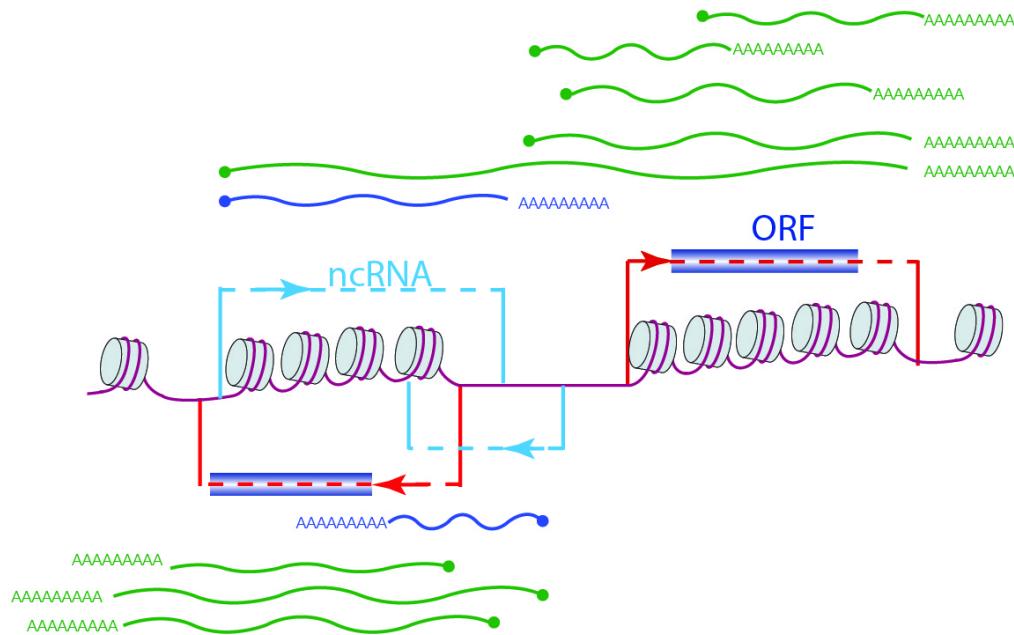


Daniel Schraivogel

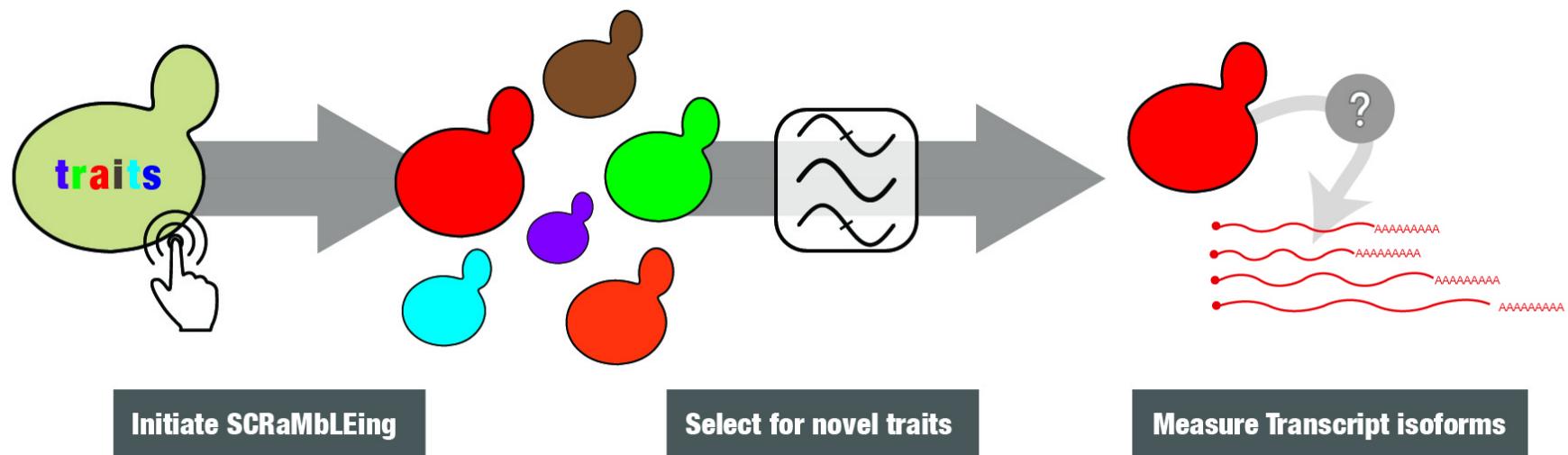


**Does SCRaMbLEing generate  
transcriptome diversity?**

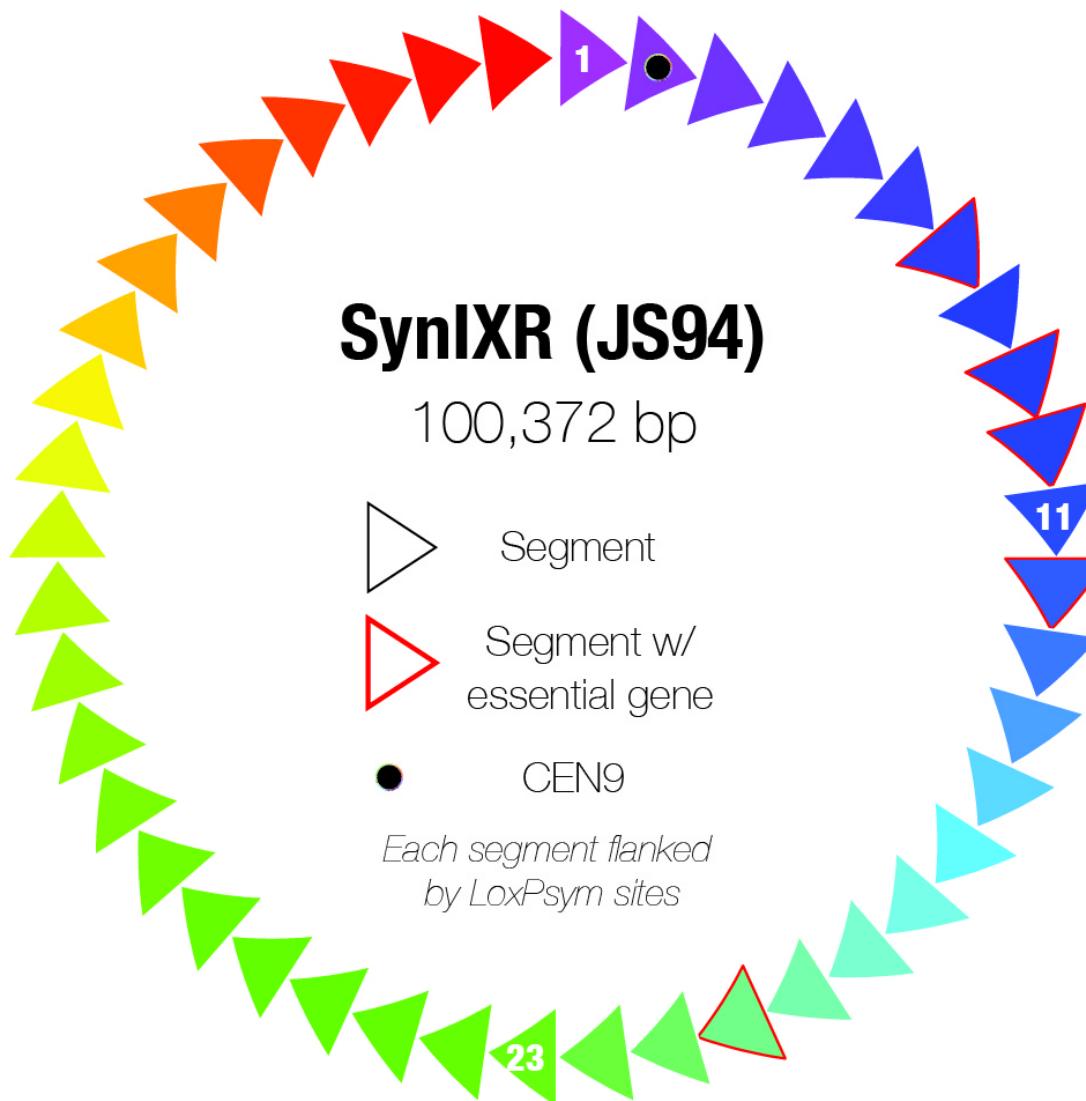
# Observation: pervasive transcription, genome-wide



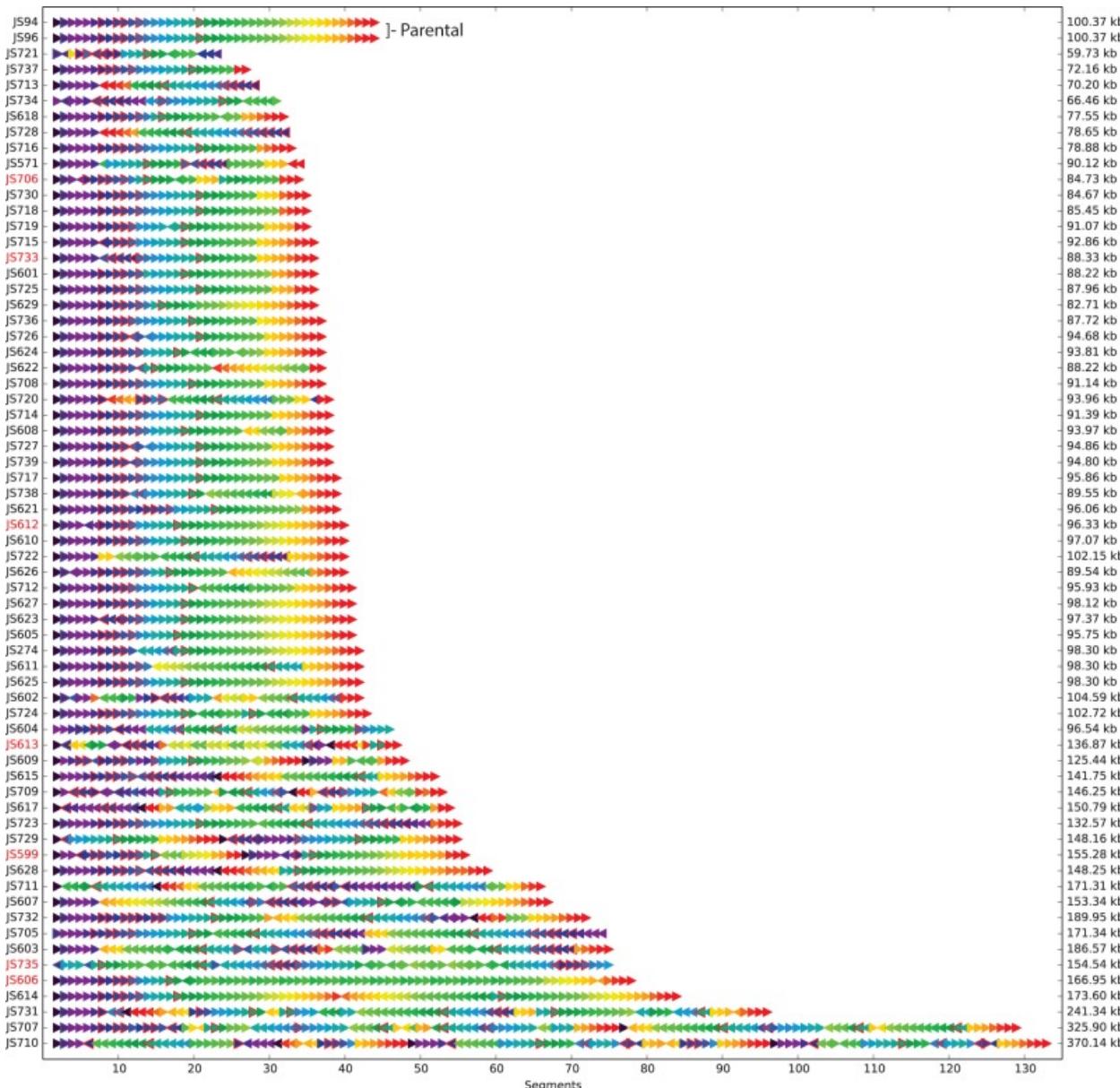
# Are transcript isoforms associated with SCRaMbLE phenotypes?



# What are the final sequences of SCRaMbLED genomes?



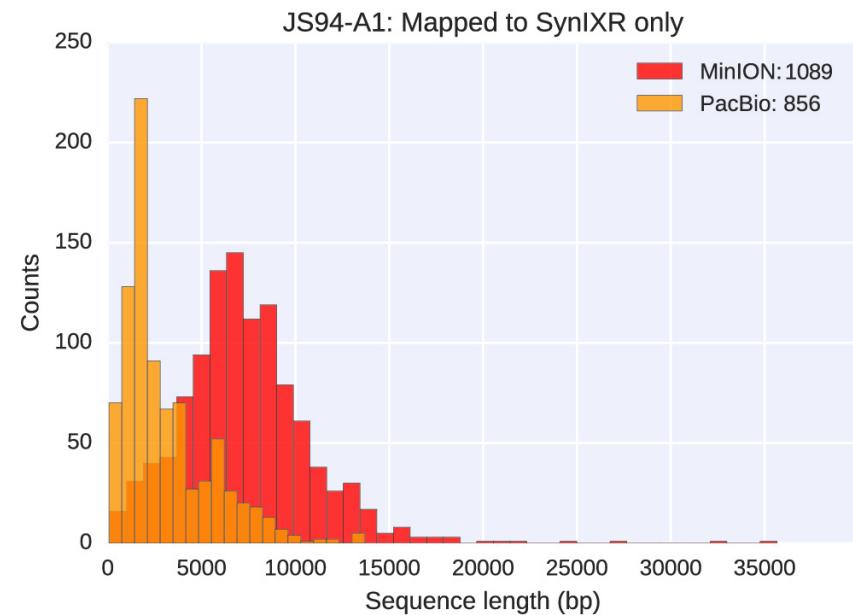
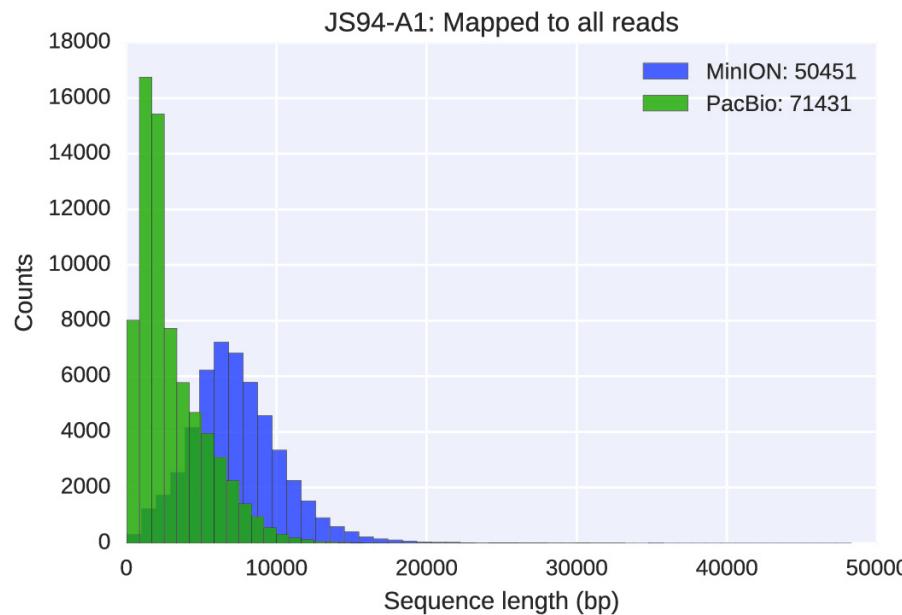
# Short reads cannot always reassemble SCRaMbLED genomes



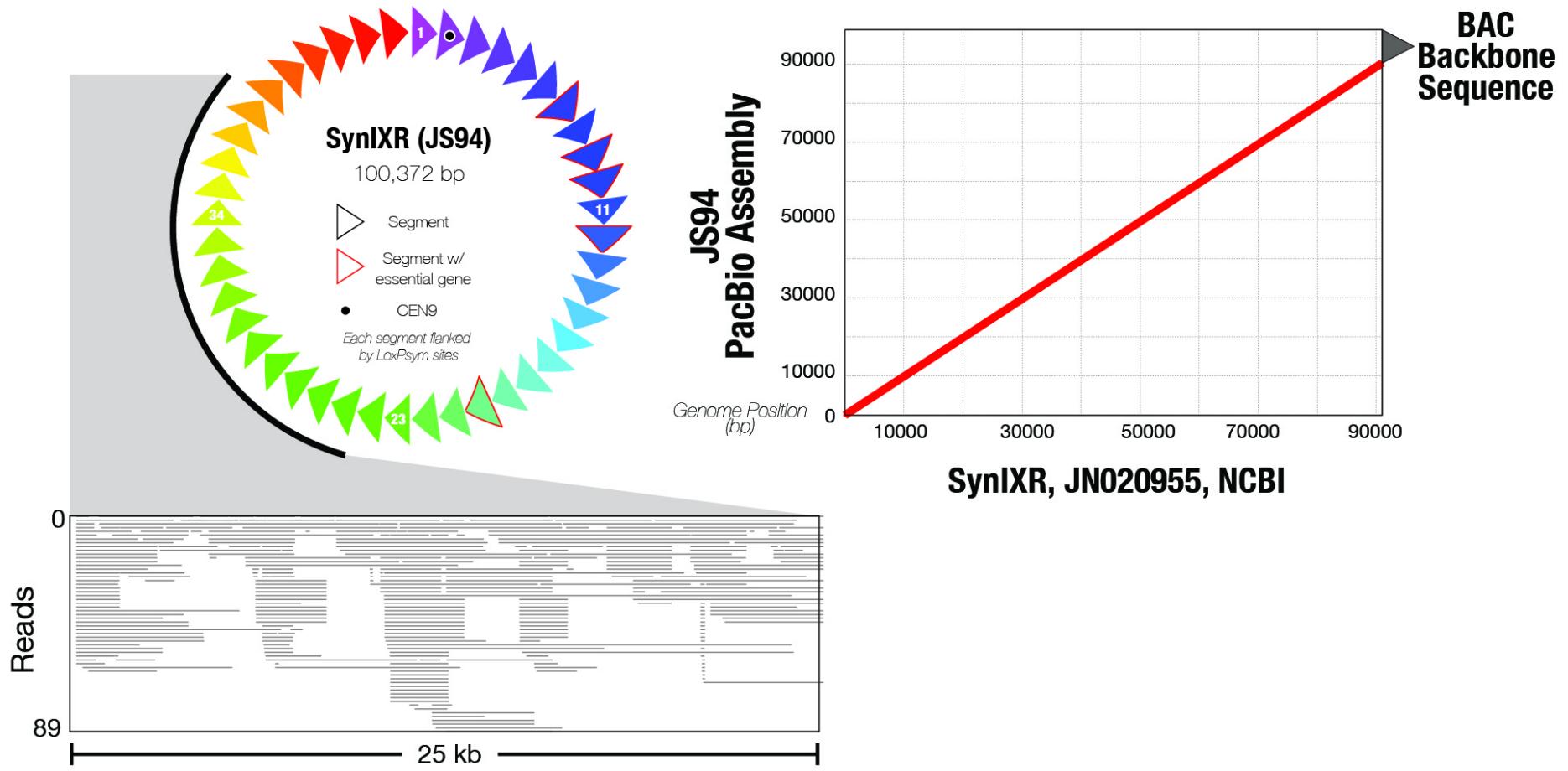
Shen et al 2016



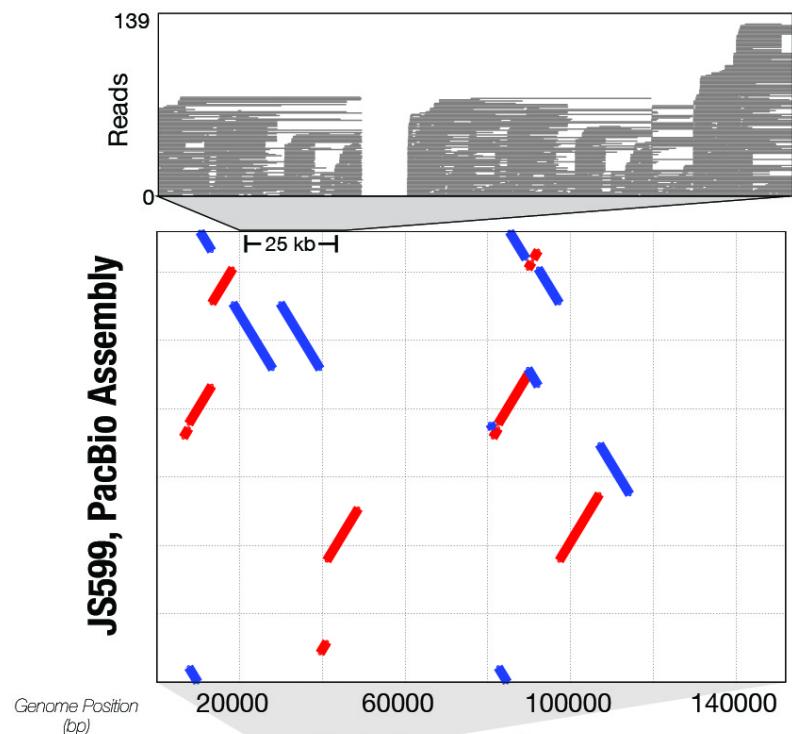
Short-read sequencing was able to determine unique sequence reconstructions for 39 out of the 64 synIXR SCRaMbLE strains. We have since been aiming to provide unique reconstructions for the remaining 25 strains for which short-read technologies were insufficient.



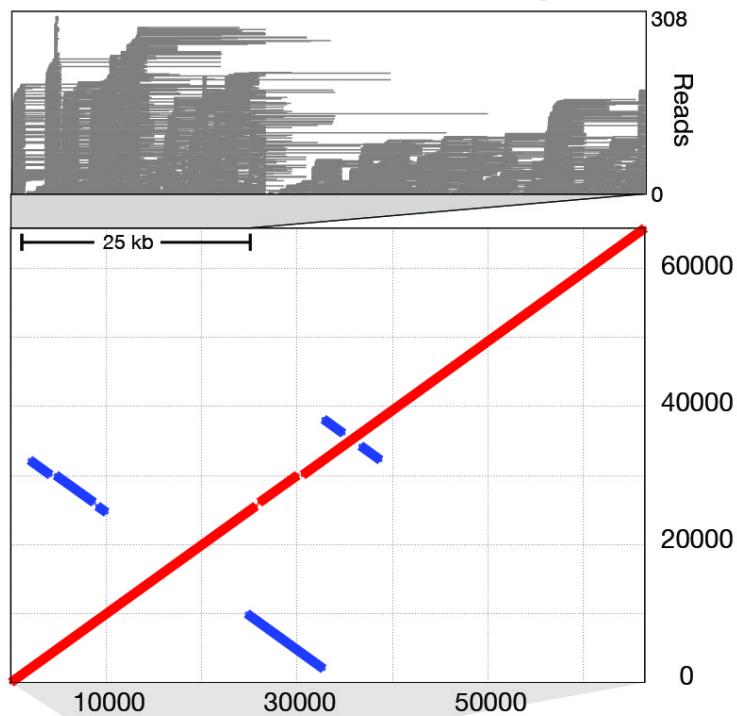
Technology	Samples/Run	Reads/Sample	Avg Read Length	Max Read Length
MinION	1	50,451	7,504	60,845
PacBio	2	166,746	3,842	38,975
PacBio	6	57,090	3,954	37,727



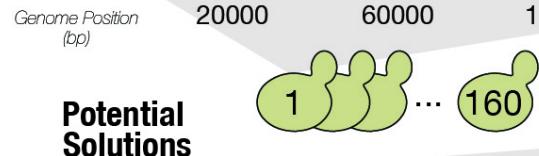
**JS599\_1 Short Read Assembly**



**JS734\_1 Short Read Assembly**

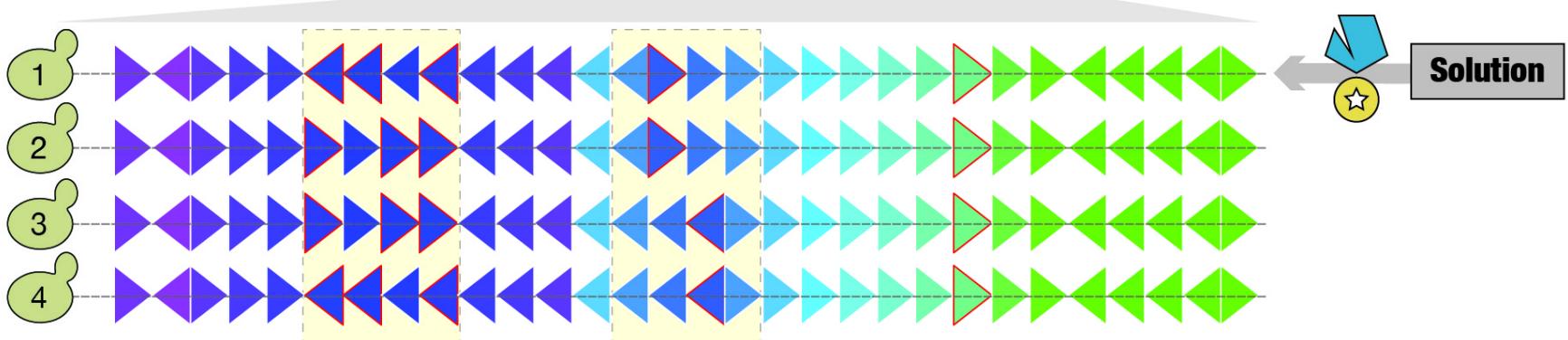


**JS599, PacBio Assembly**



**Potential Solutions**

**JS734**





# Acknowledgements: Steinmetz Lab



Sc2.0 Travel Fellowship Committee  
Thank you!

Grace Wilsey Foundation



**Lars Steinmetz group:** Raeka Aiyar, Chiara Baccin, Francesca Briganti, Aaron Brooks, Sandra Clauder-Münster, Gozde Durmus, Lin Gen, Bianca Hennig, Saiful Islam, Petra Jakob, \*Andreas Johansson\*, Allan Jones, Will Mueller, Mariona Nadal Ribelles, Michelle Nguyen, Ragini Phansalkar, Kevin Roy, Daniel Schraivogel, Michael Sikora, Han Sun, Chelsea Szu-Tu Lars Veltén, Sibylle Vonesch, Wu Wei, Felix Wertek, Jingyan Wu, Chenchen Zhu

Roy Walker, Patrick Cai, University of Edinburgh

Jonathon Blake and Vladimir Benes, EMBL Genomics Core Facility

Lisa Sadzewicz and Luke Tallon, University of Maryland

