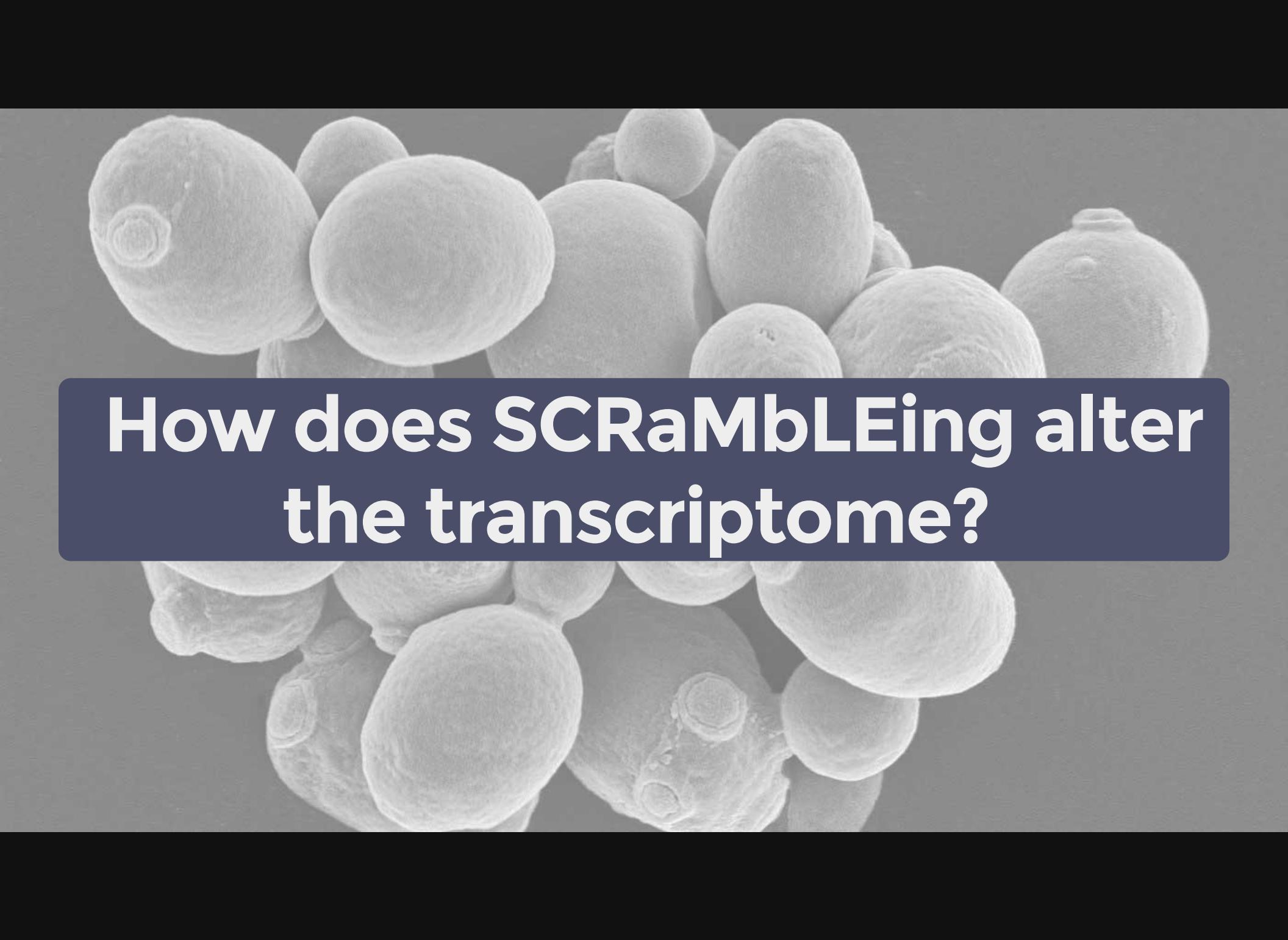


Genomic and Transcriptomic Characterization of SCRaMbLE strains

Aaron Brooks /  @scalefreegan

Lars Steinmetz's Group | EMBL Heidelberg

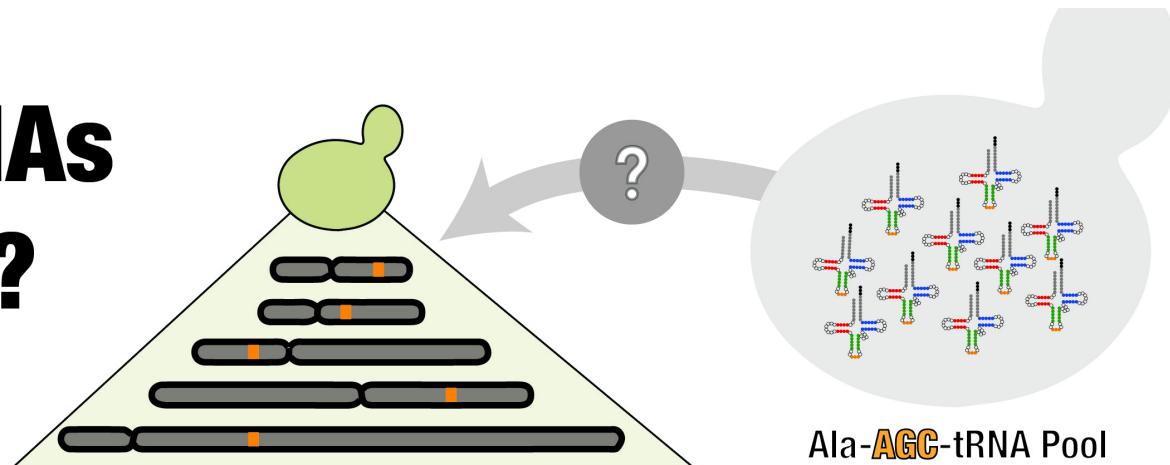


**How does SCRaMBLEing alter
the transcriptome?**

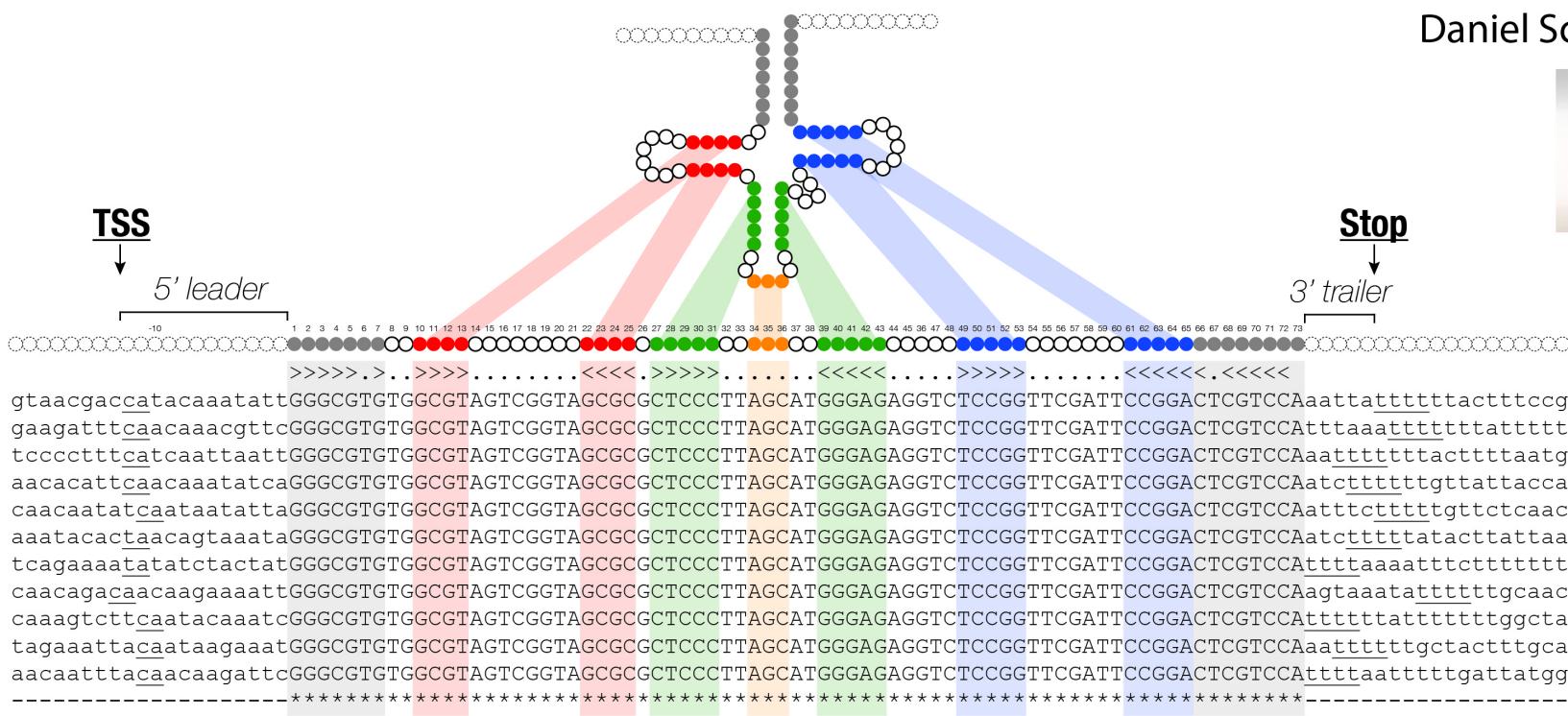
Two snapshots

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

Where do tRNAs come from?



Ala precursor tRNA

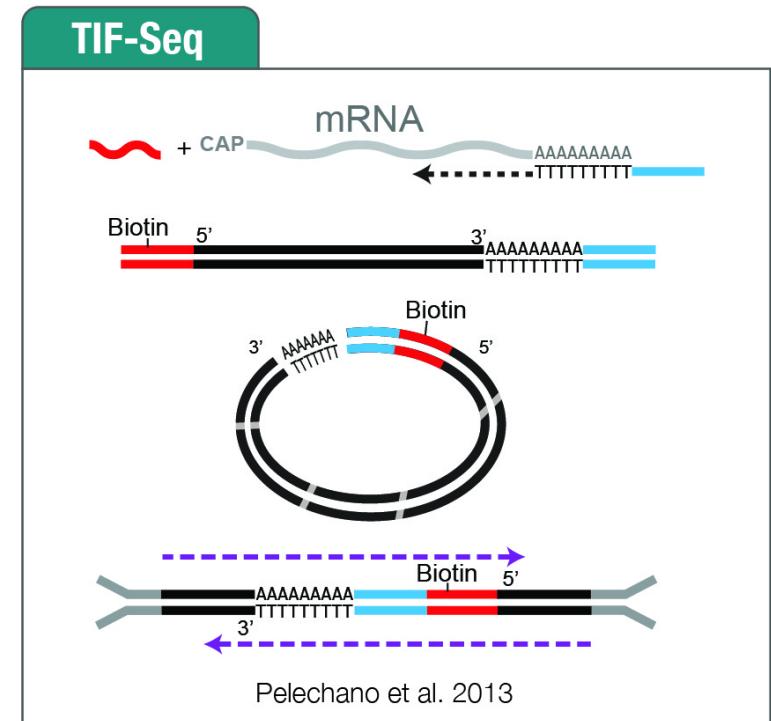
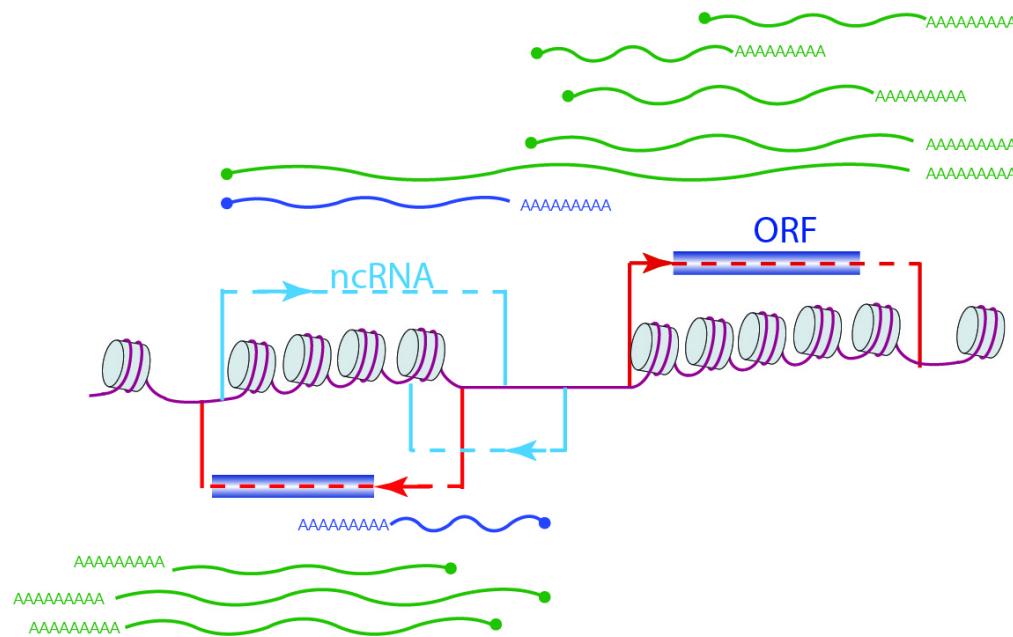


Daniel Schraivogel

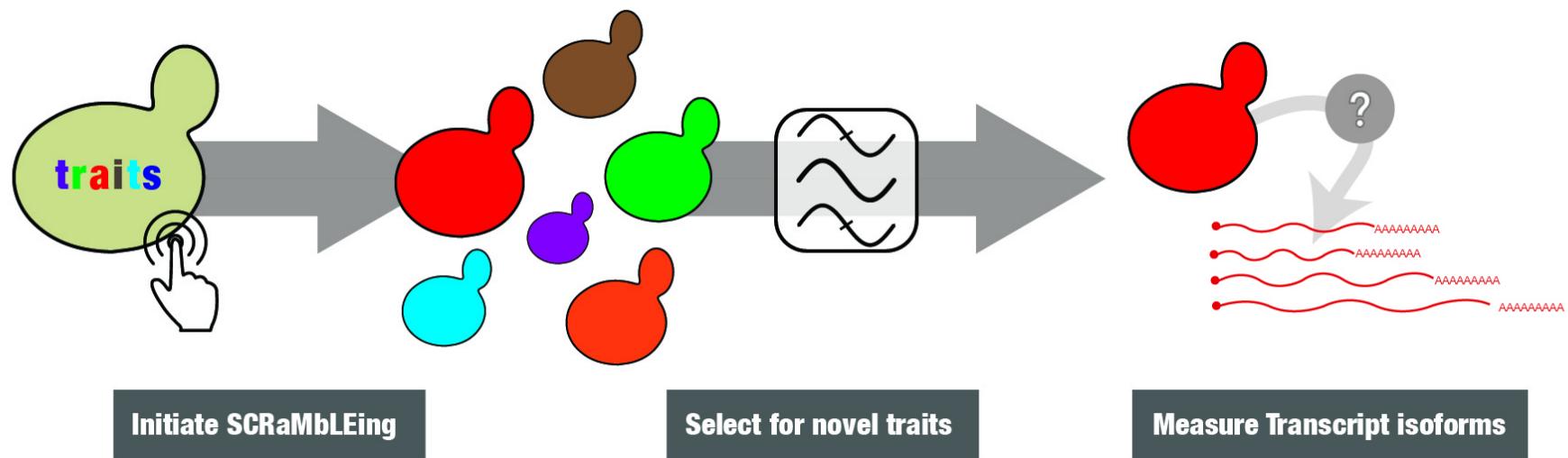


Does SCRaMbLEing generate transcriptome diversity?

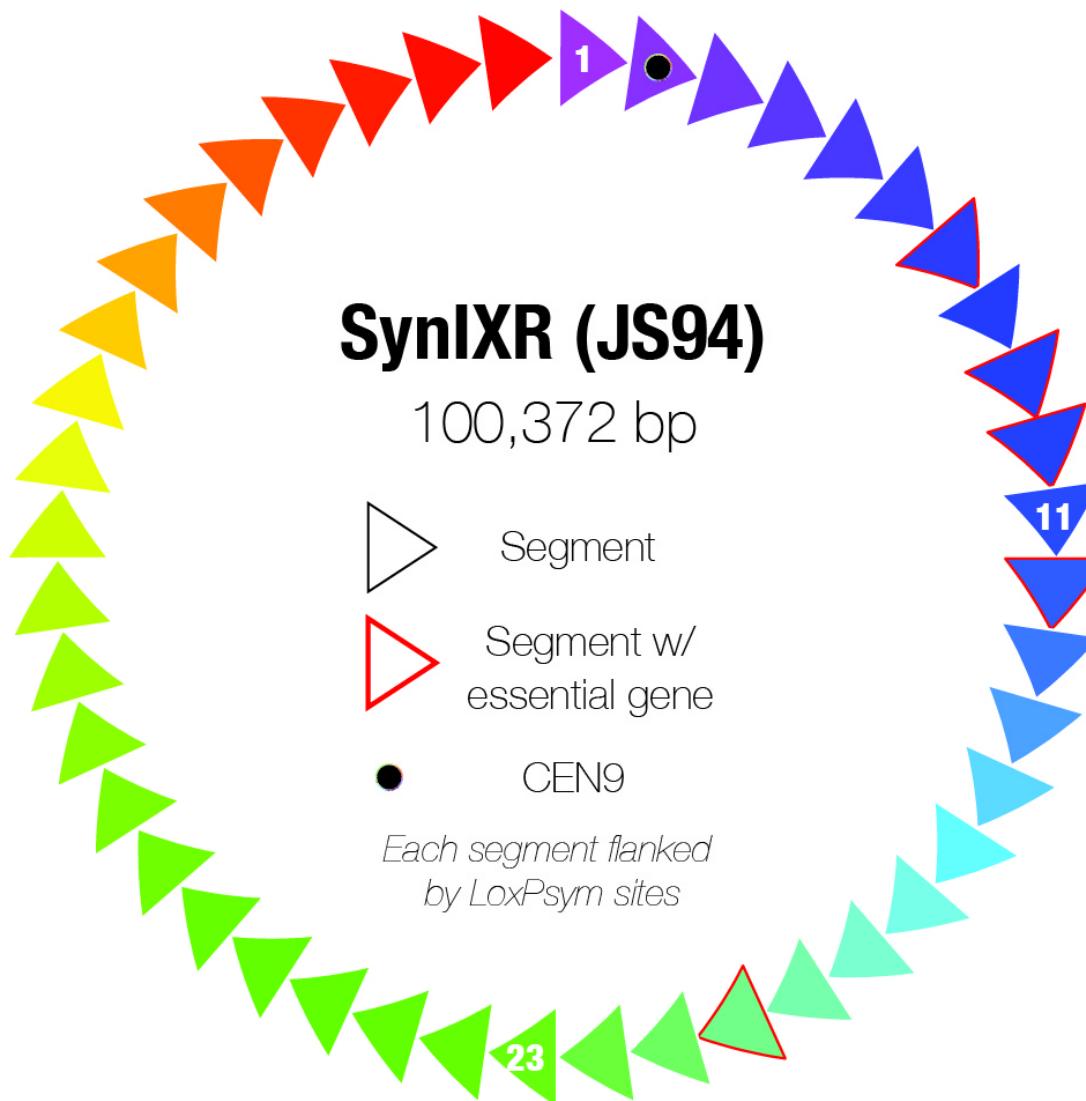
Observation: pervasive transcription, genome-wide



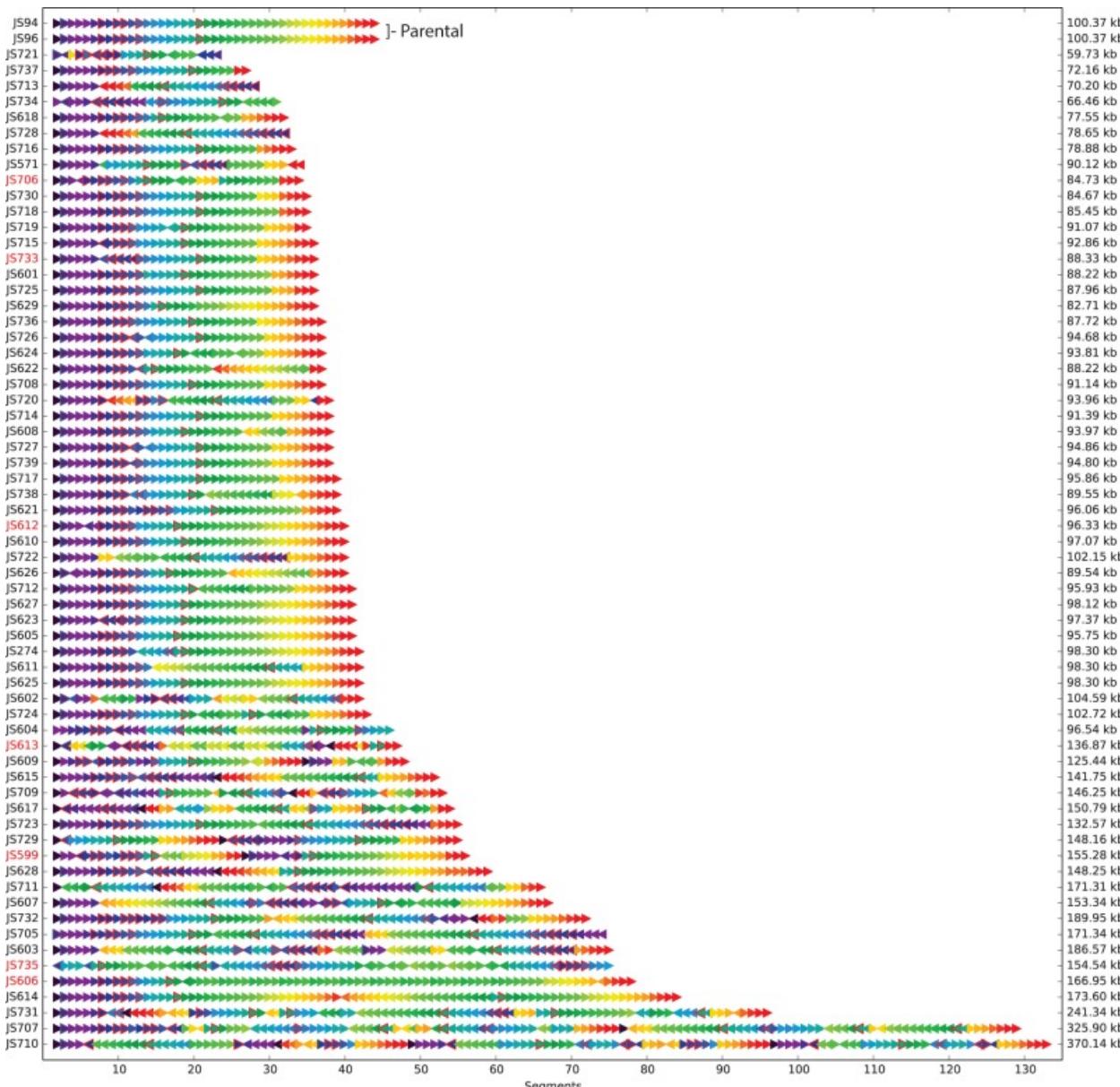
Are transcript isoforms associated with SCRaMbLE phenotypes?



What are the final sequences of SCRaMbLED genomes?



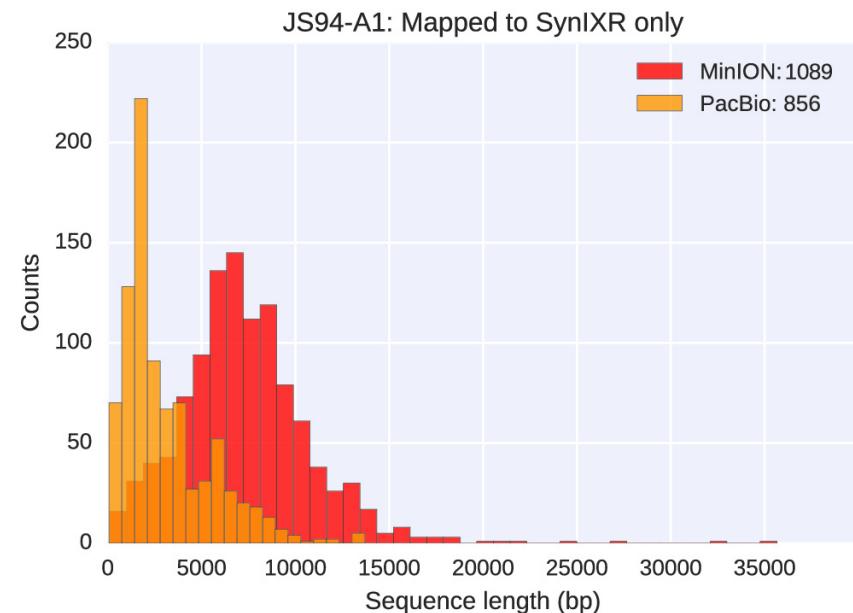
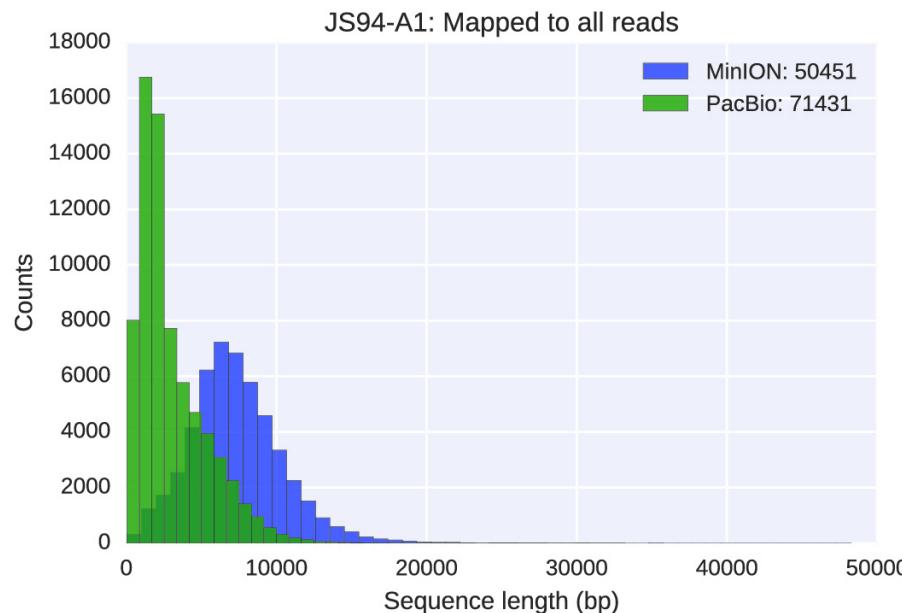
Short reads cannot always reassemble SCRaMbLED genomes



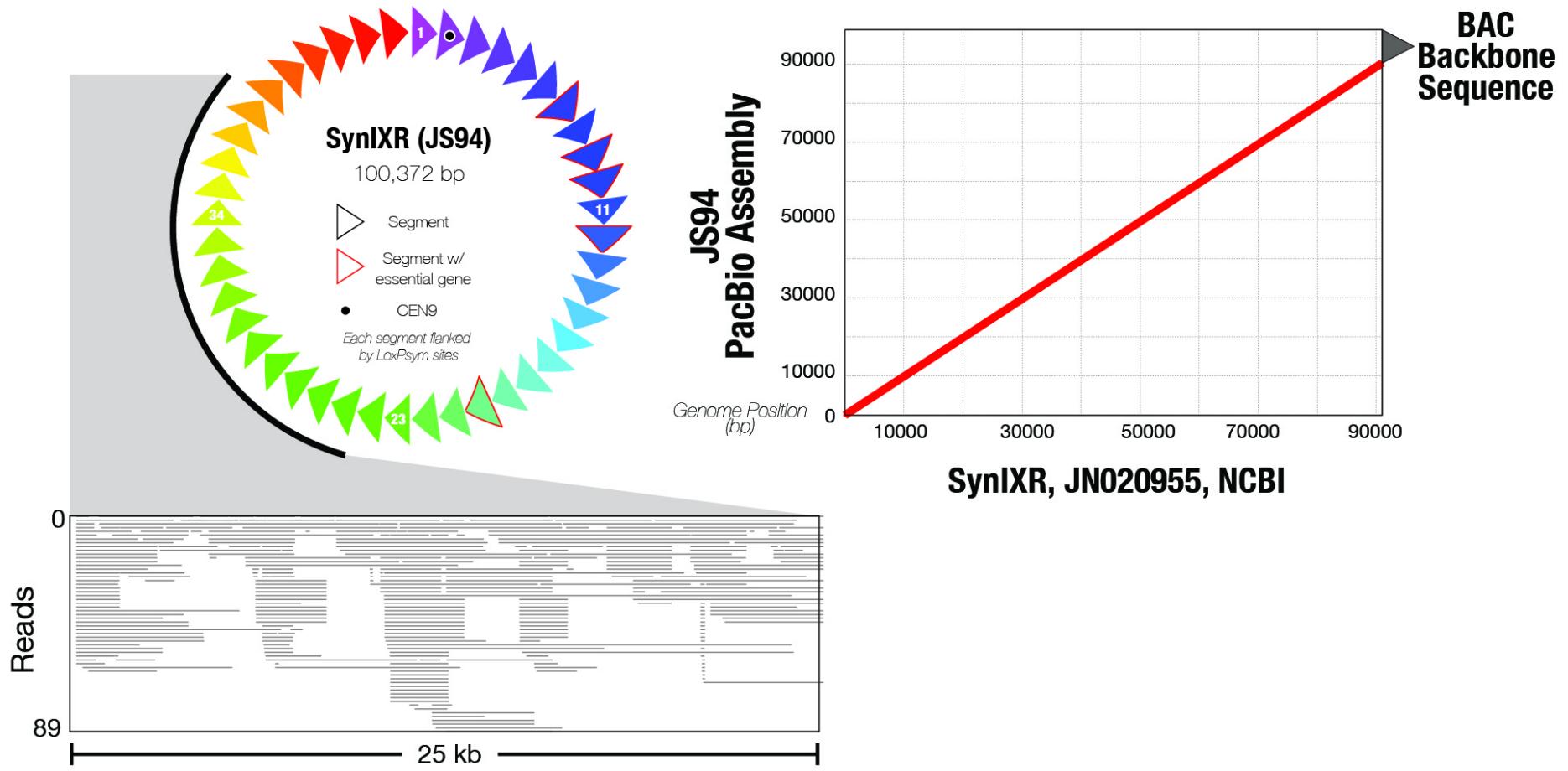
Shen et al 2016



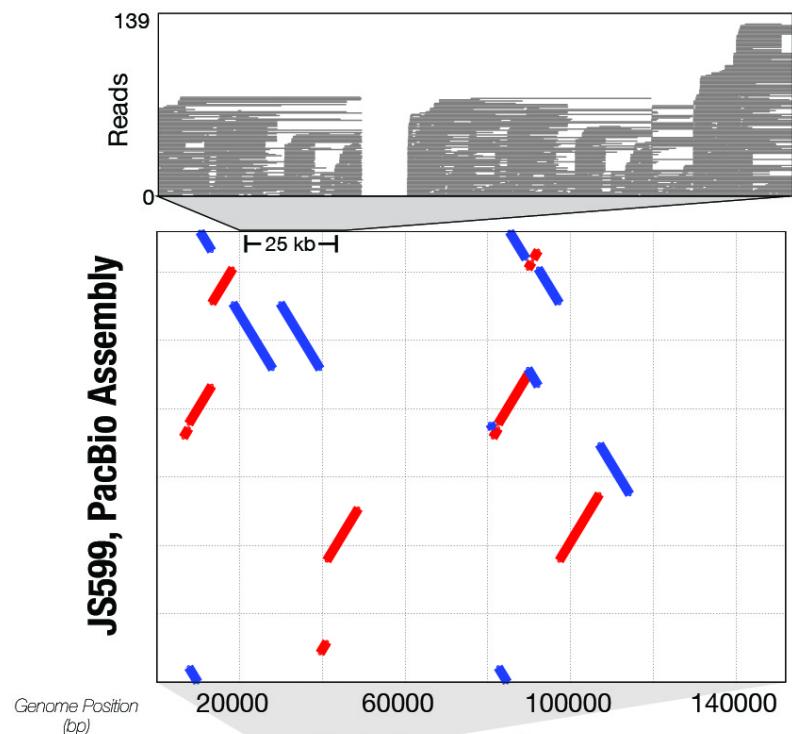
Short-read sequencing was able to determine unique sequence reconstructions for 39 out of the 64 synIXR SCRaMbLE strains. We have since been aiming to provide unique reconstructions for the remaining 25 strains for which short-read technologies were insufficient.



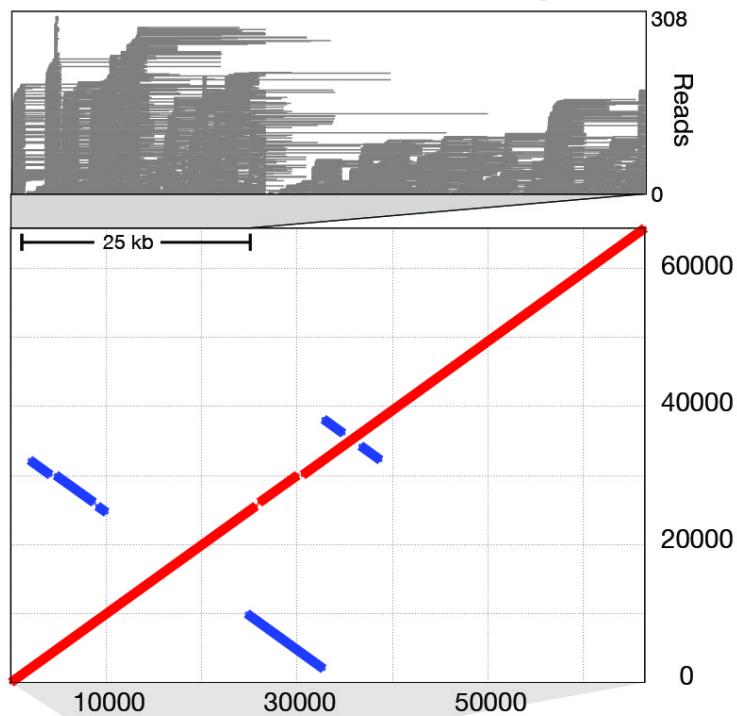
Technology	Samples/Run	Reads/Sample	Avg Read Length	Max Read Length
MinION	1	50,451	7,504	60,845
PacBio	2	166,746	3,842	38,975
PacBio	6	57,090	3,954	37,727



JS599_1 Short Read Assembly



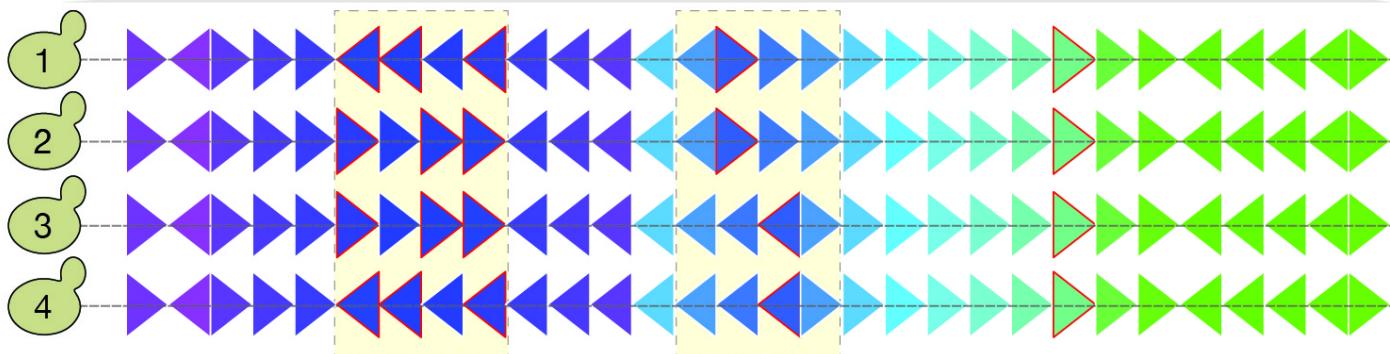
JS734_1 Short Read Assembly



Potential
Solutions



JS734



Solution



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