




Iso-Seq Deduplication

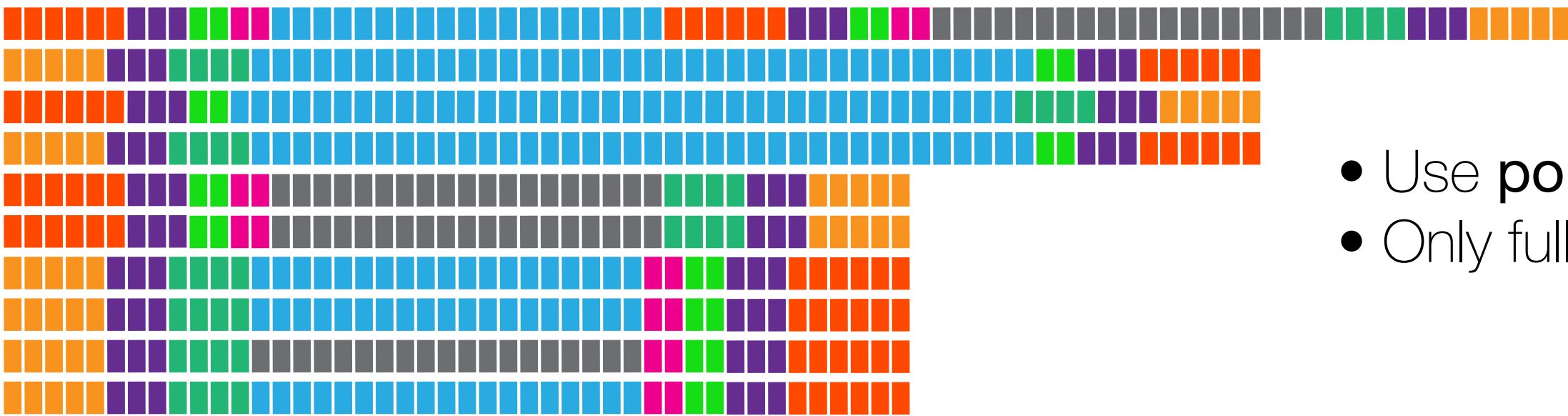
transcript gene A 
transcript gene B 
optional polyA 

3' cDNA primer 
5' cDNA primer 
sample barcode 

UMI 
cell barcode 

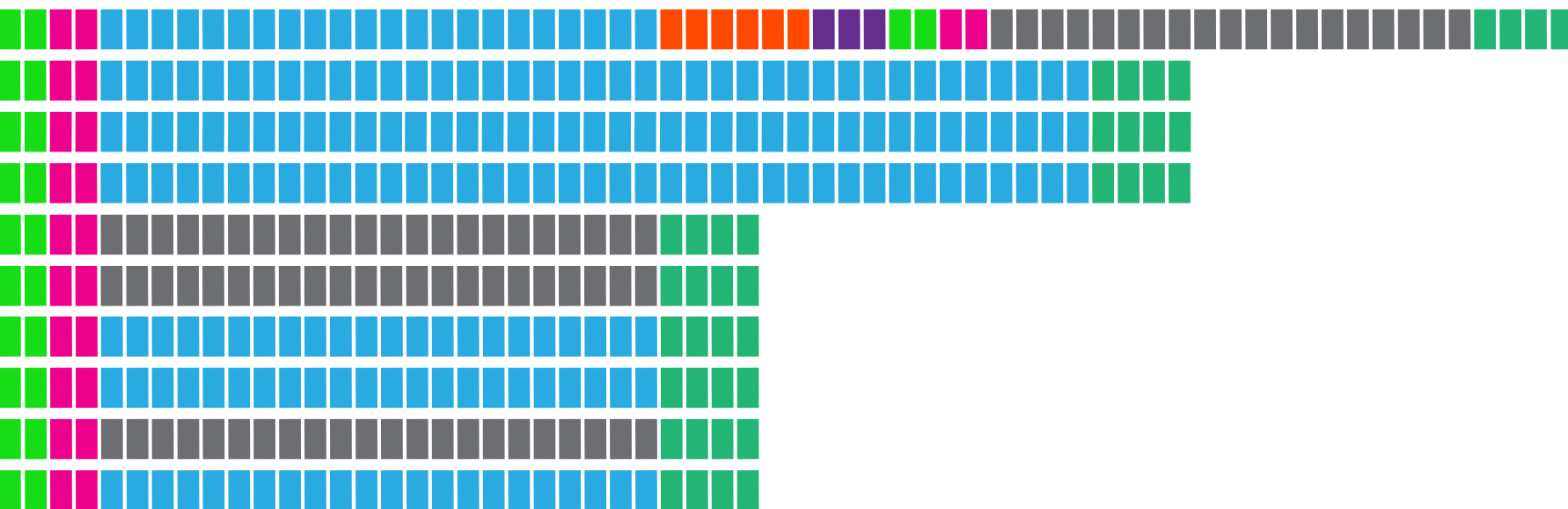
Version 2, Dr. Amin Töpfer

consensus



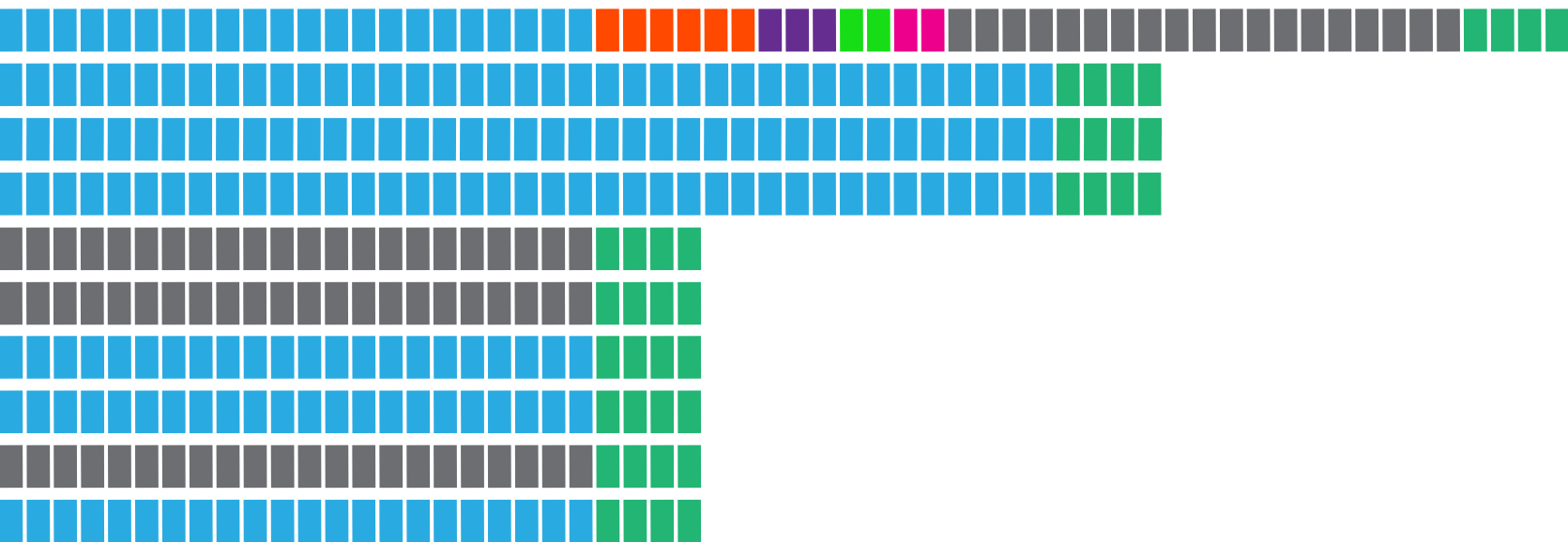
- Use **polished** CCS reads
- Only full-pass ZMWs

demultiplex



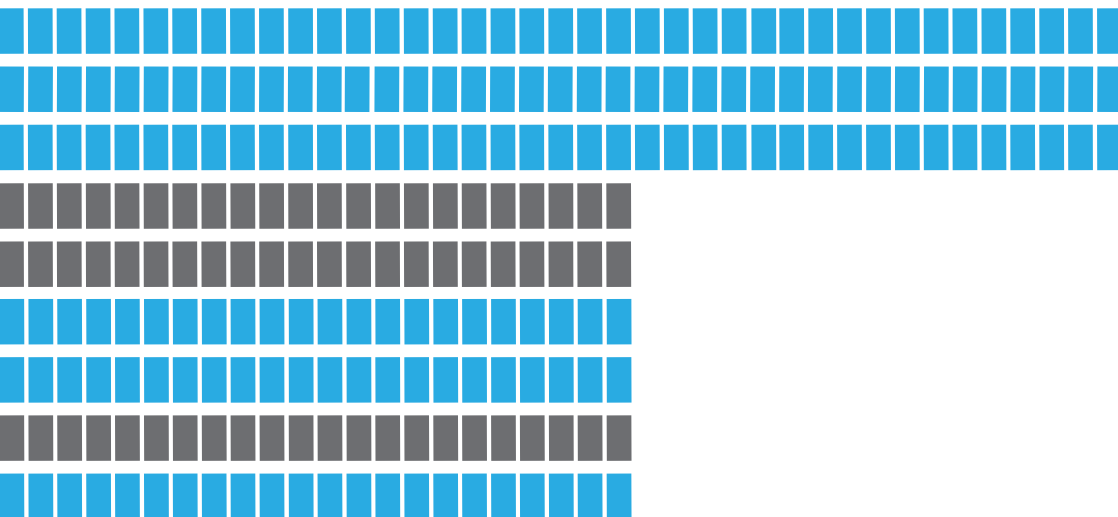
- Barcoded and unbarcoded cDNA primer removal
- Orientation
- Unwanted primer combination removal

tag



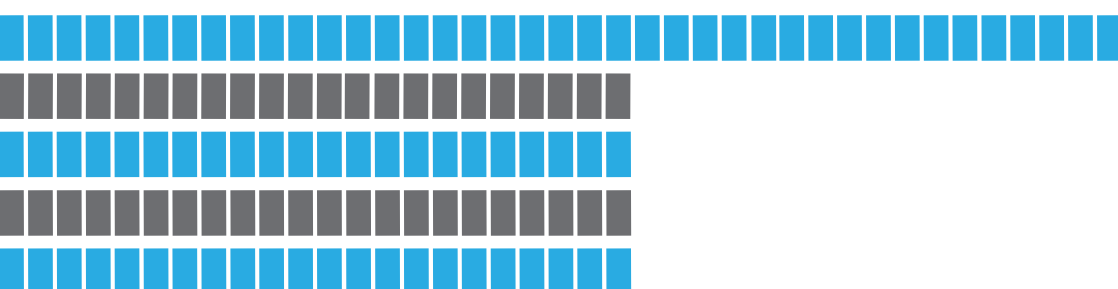
- Clip UMIs and cell barcodes
- Tag read metadata with those information

refine



- PolyA tail trimming
- Concatemer removal

dedup



- PCR deduplication, by clustering via barcode and UMI
- Generate cluster consensus using QV guided PoA
- Fasta output is split into HQ and LQ reads