




# Iso-Seq Deduplication

transcript gene A   
transcript gene B   
optional polyA 

3' cDNA primer   
5' cDNA primer   
sample barcode 

UMI   
cell barcode 

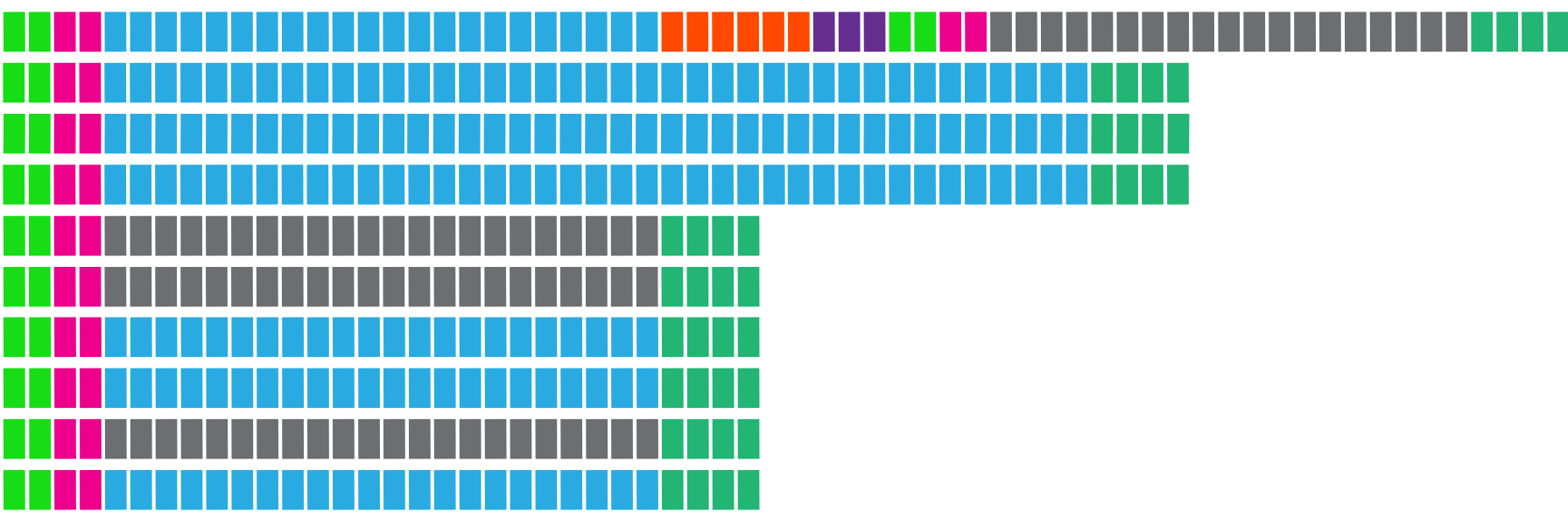
Version 2

consensus



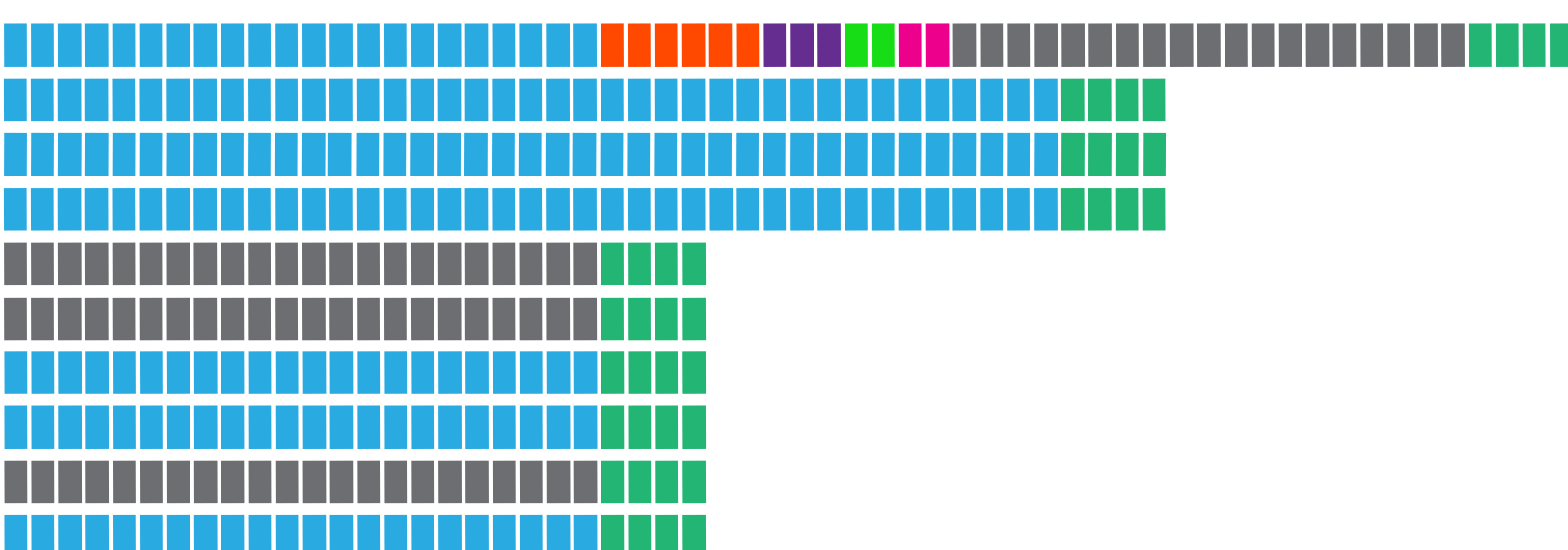
- Use **polished** CCS reads
- Only full-pass ZMWs

demultiplex



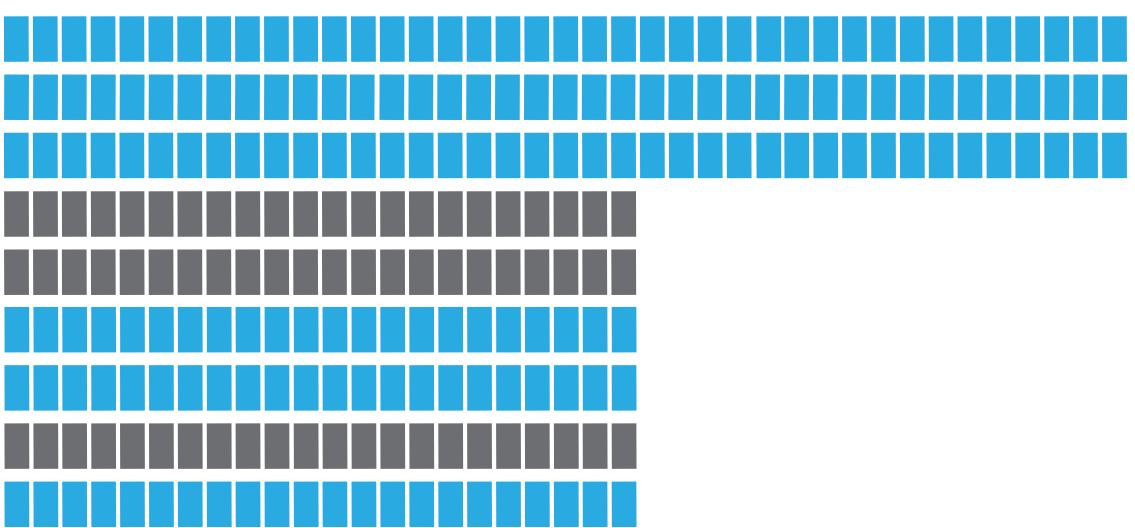
- Barcoded and unbarcoded cDNA primer removal
- Orientation
- Unwanted primer combination removal

tag



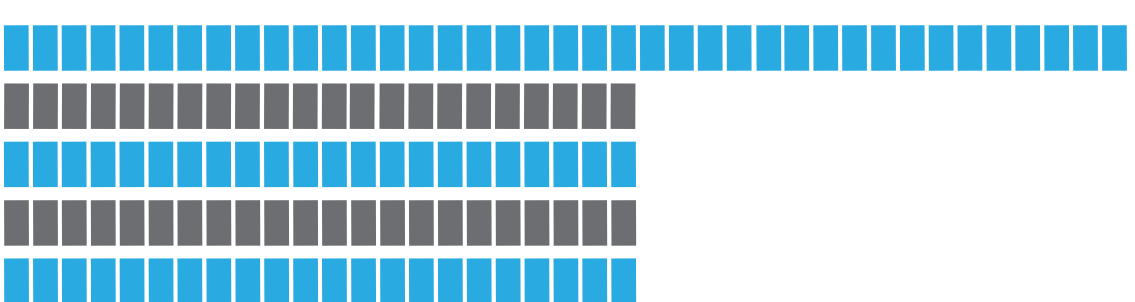
- Clip UMIs and cell barcodes
- Tag read metadata with those information

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