




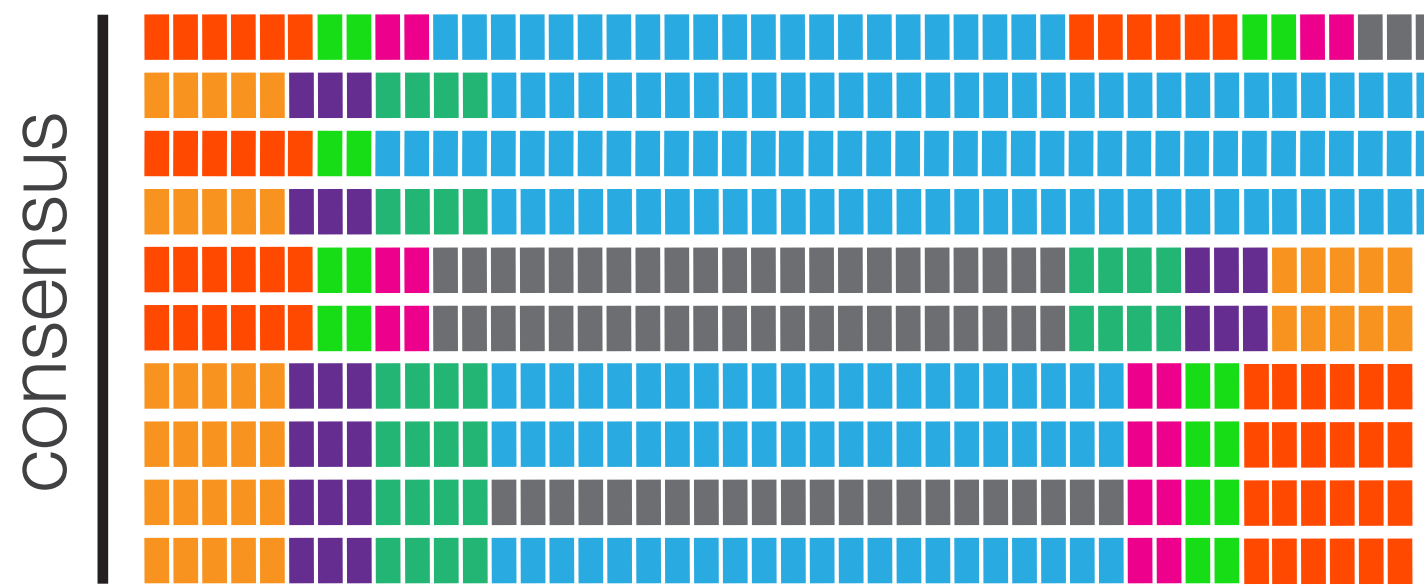
Iso-Seq Deduplication

transcript gene A 
transcript gene B 
optional polyA 

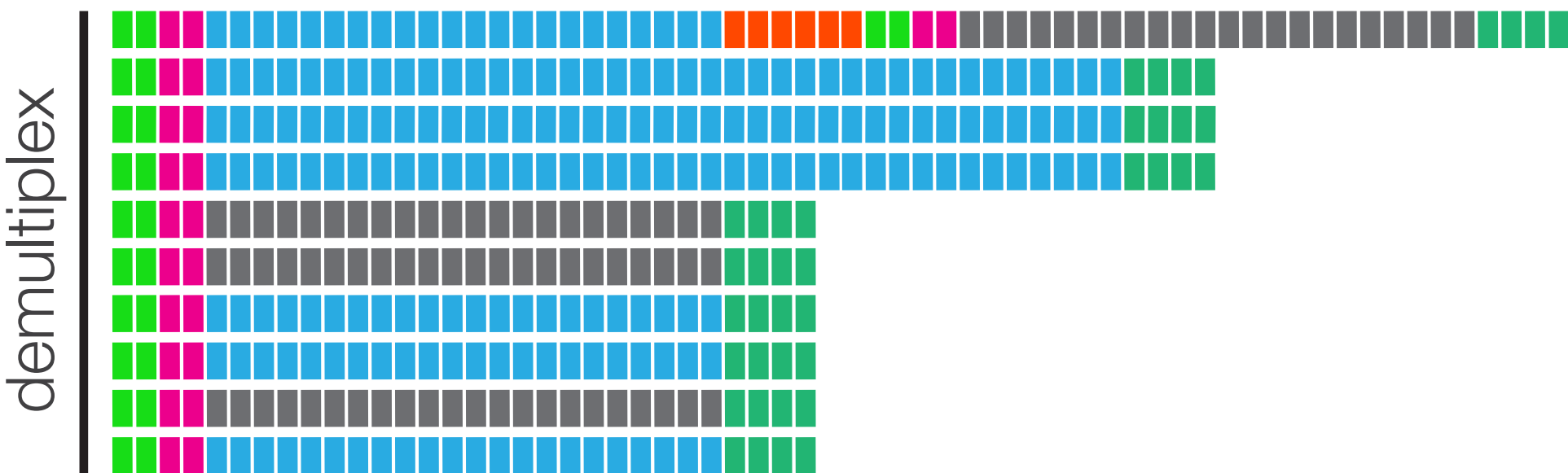
3' cDNA primer 
5' cDNA primer 
sample barcode 

UMI 
cell barcode 

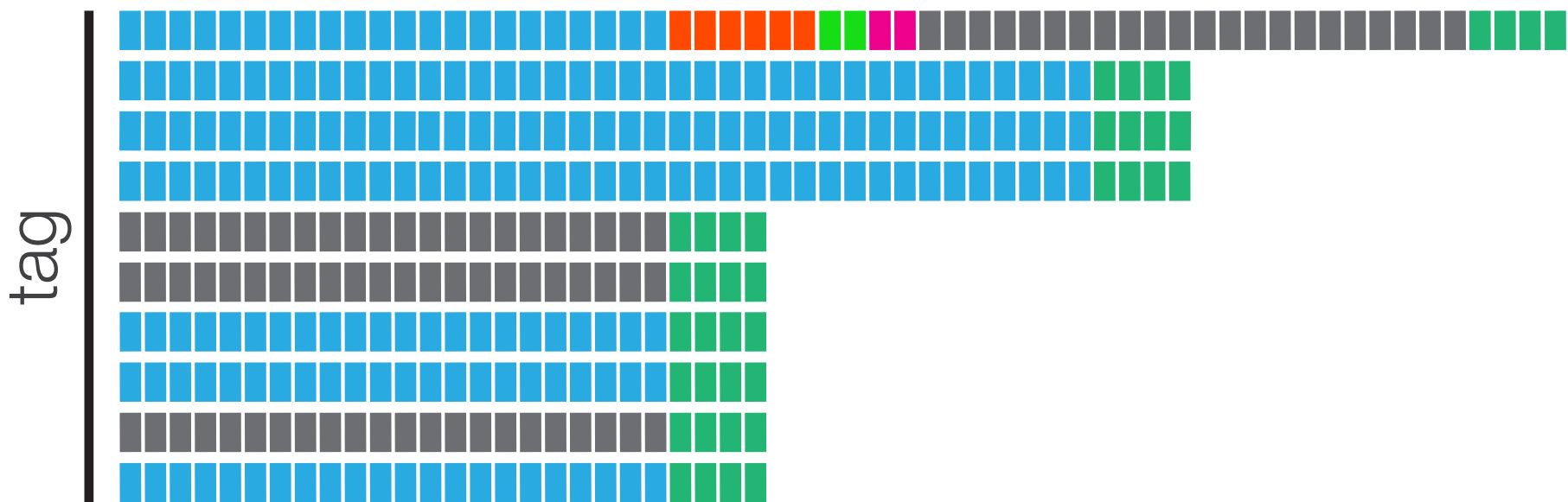
Version 1, Dr. Amin Töpfer



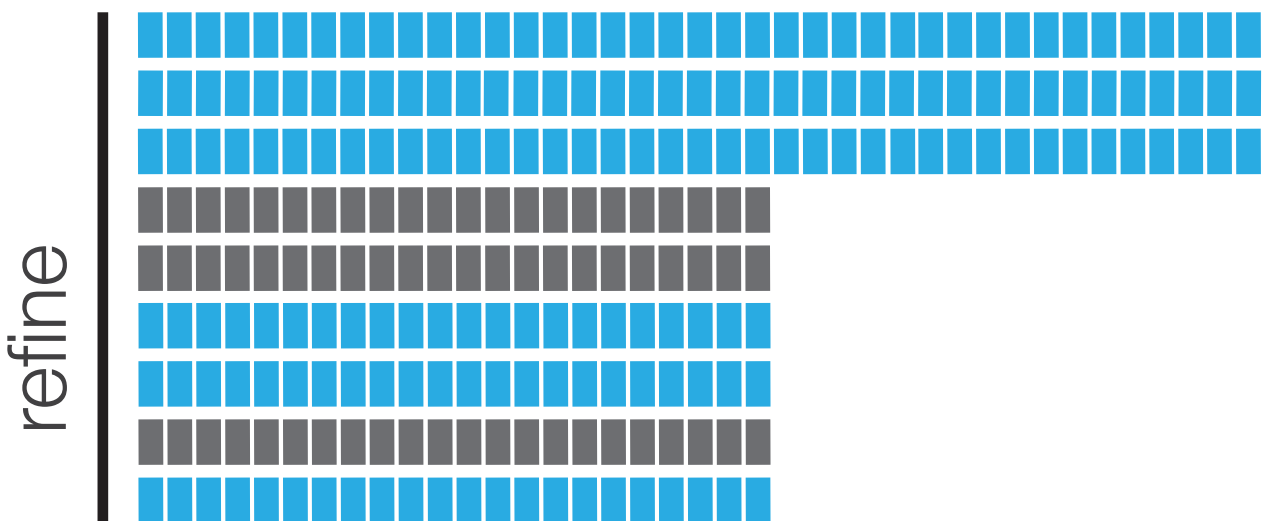
- Use **polished** CCS reads
- Only full-pass ZMWs



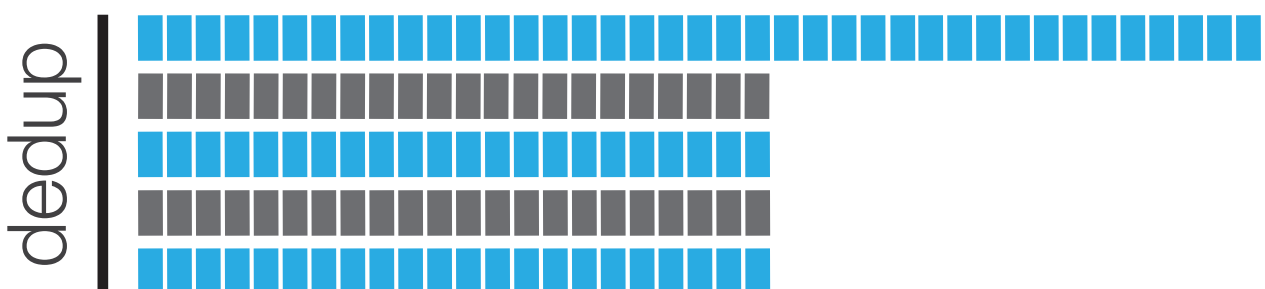
- Barcoded and unbarcoded cDNA primer removal
- Orientation
- Unwanted primer combination removal



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



- PolyA tail trimming
- Concatemer removal



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