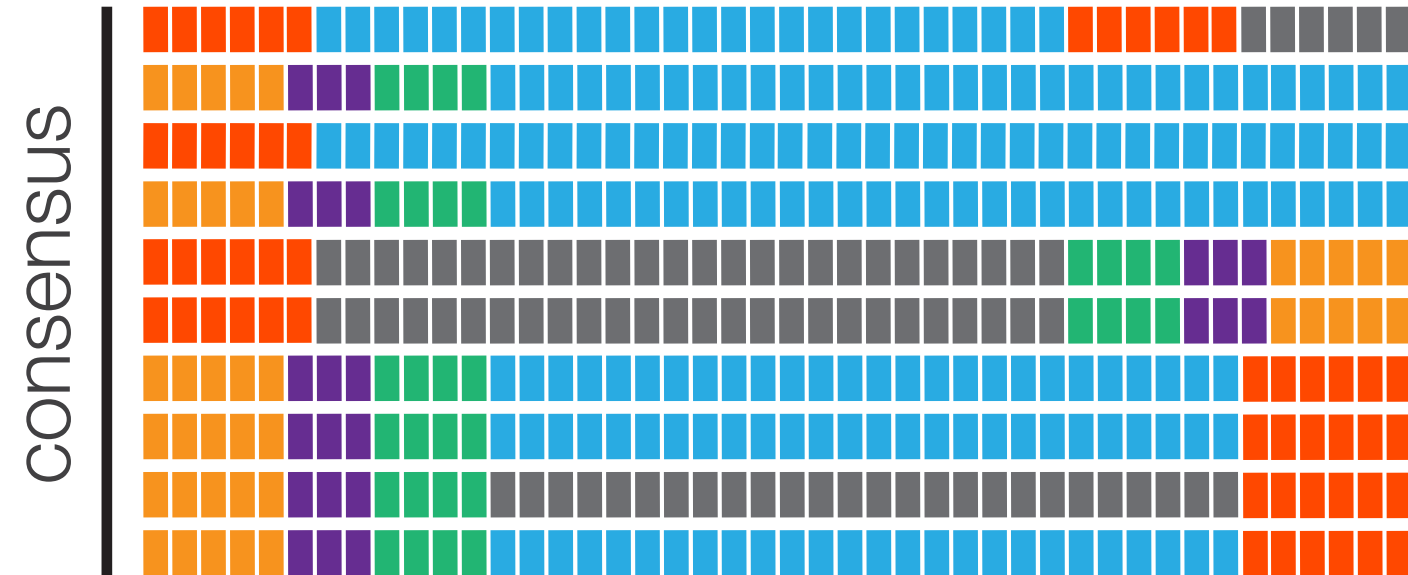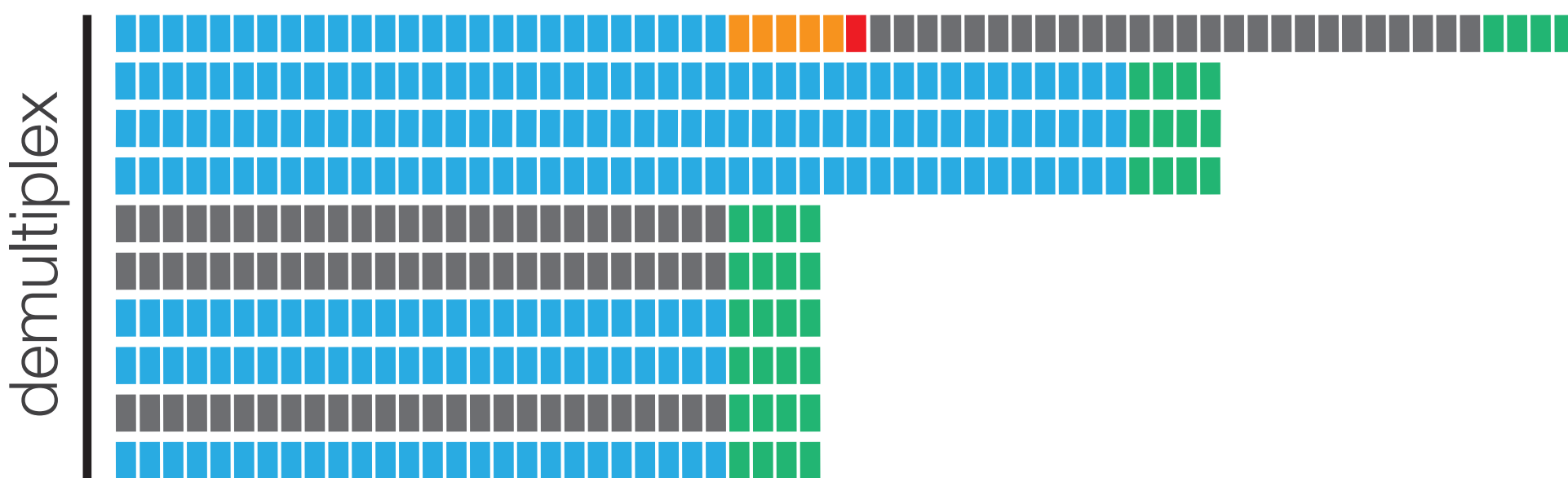# Iso-Seq Clustering

transcript gene A

transcript gene B

optional polyA

3' cDNA primer

5' cDNA primer

sample barcode

Version 8, Dr. Armin Töpfer
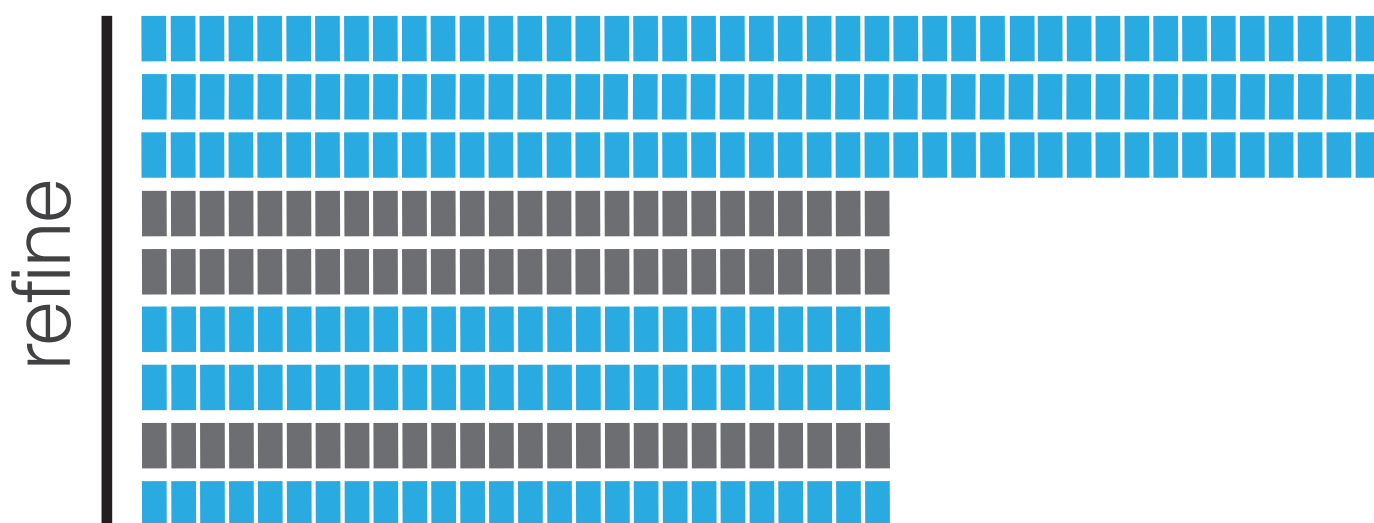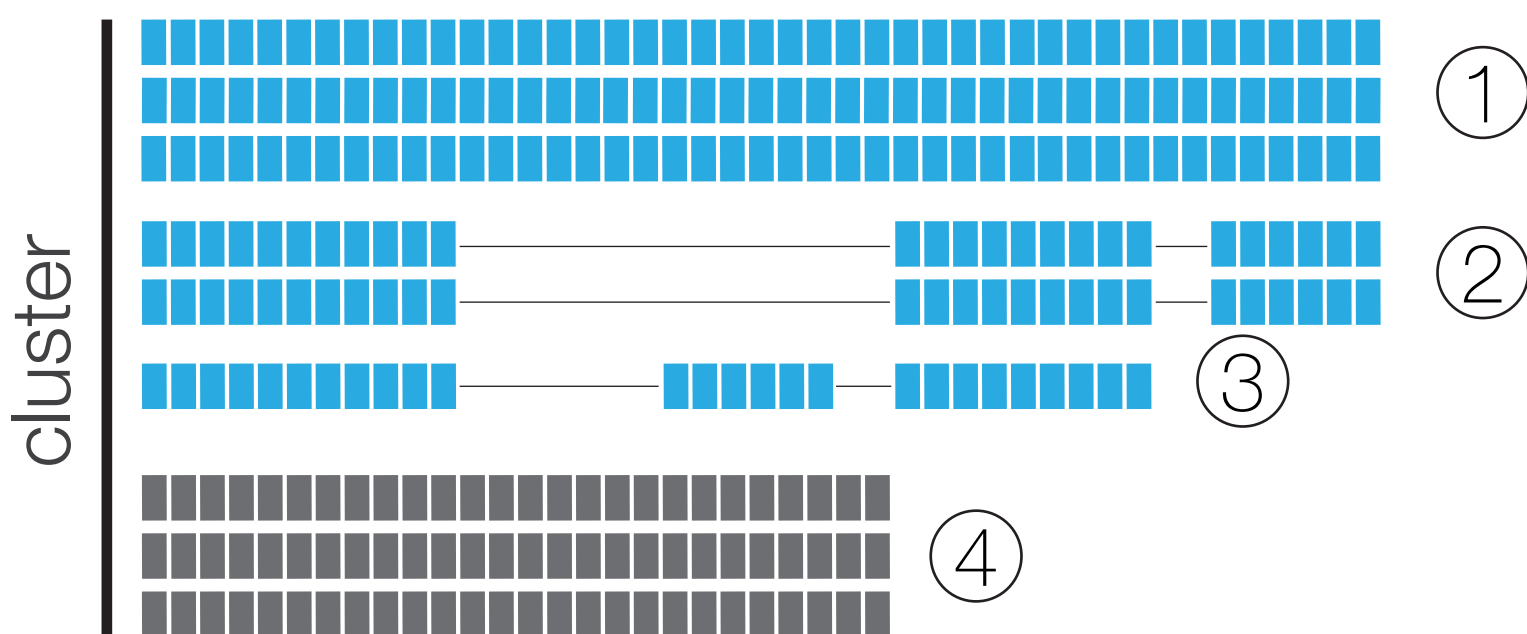
consensus

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

demultiplex

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

refine

- PolyA tail trimming
- Concatemer removal

cluster

①
②
③
④

- Hierarchical, n*log(n) clustering, alignment of shorter to longer sequences
- Iterative cluster merging
- Generate consensus for each read cluster using QV guided PoA

fasta output

①
②
③
④
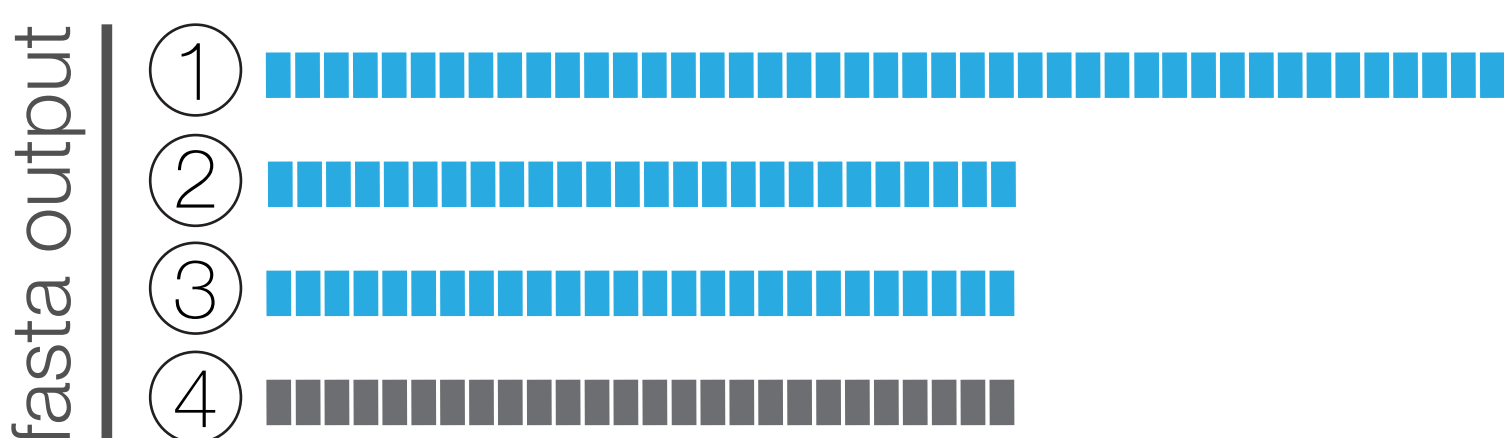
- Fasta output is split into HQ and LQ reads
- One consensus per read cluster