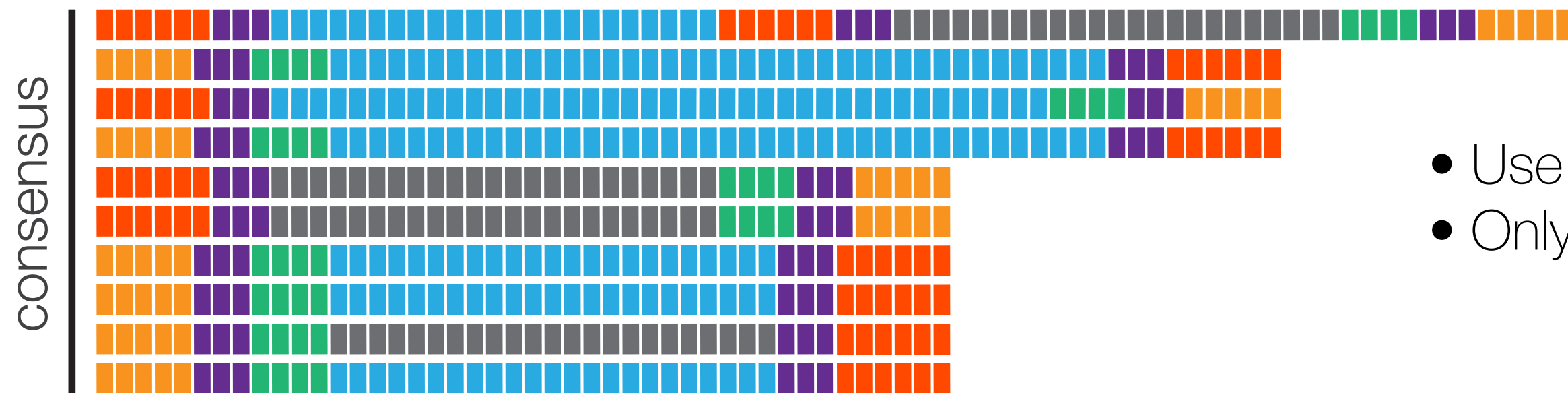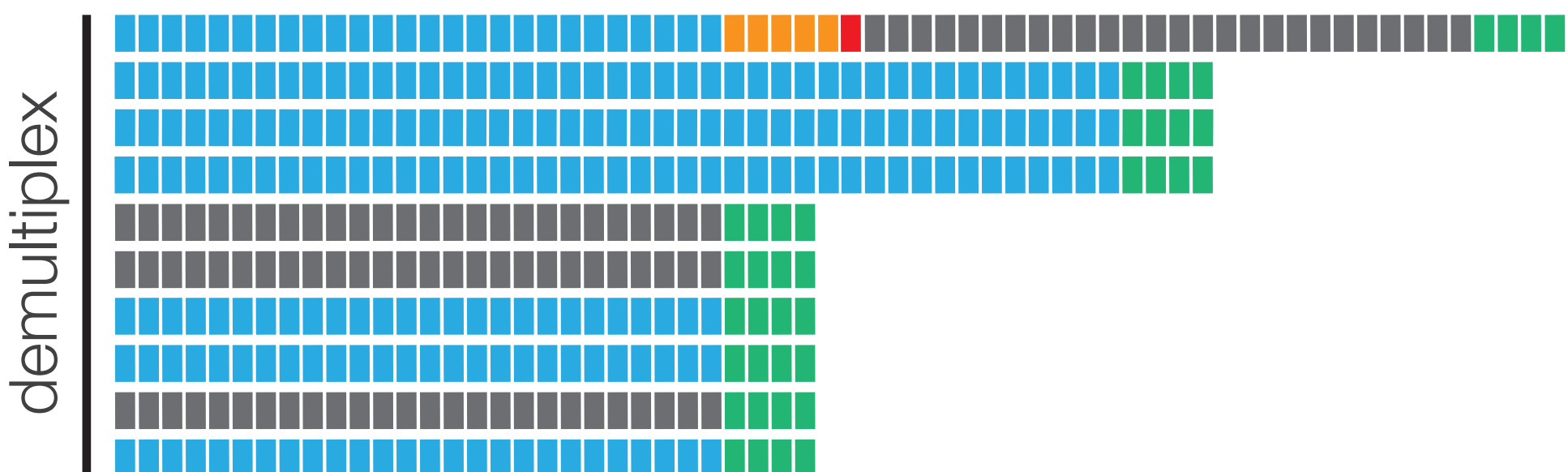Iso-Seq Clustering

transcript gene A
transcript gene B
optional polyA

3' cDNA primer
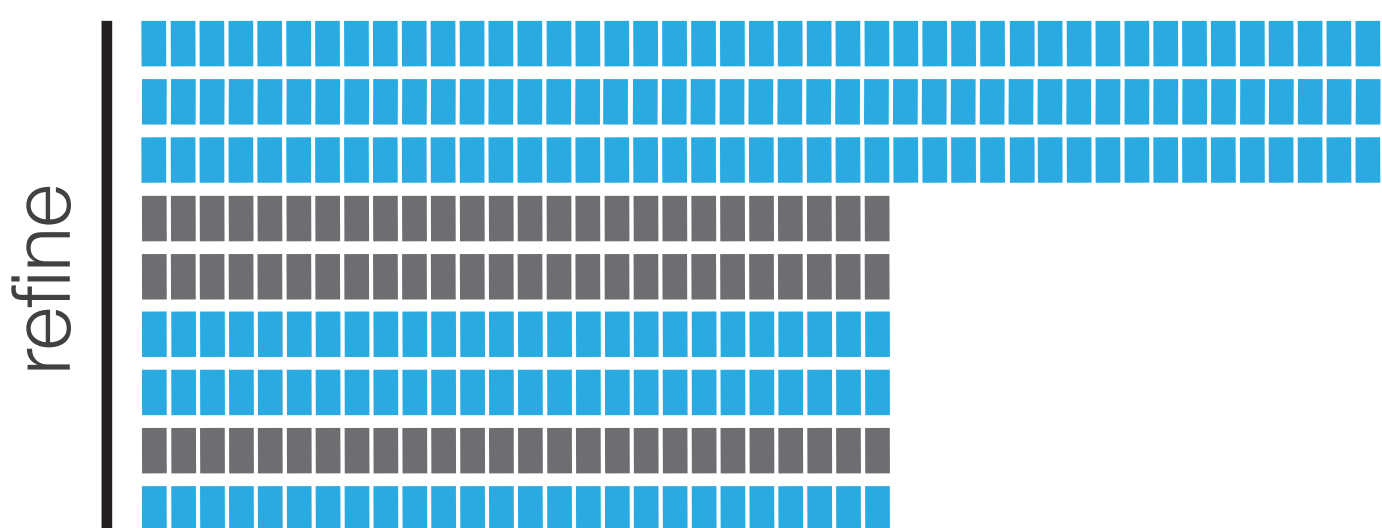5' cDNA primer
sample barcode

Version 9

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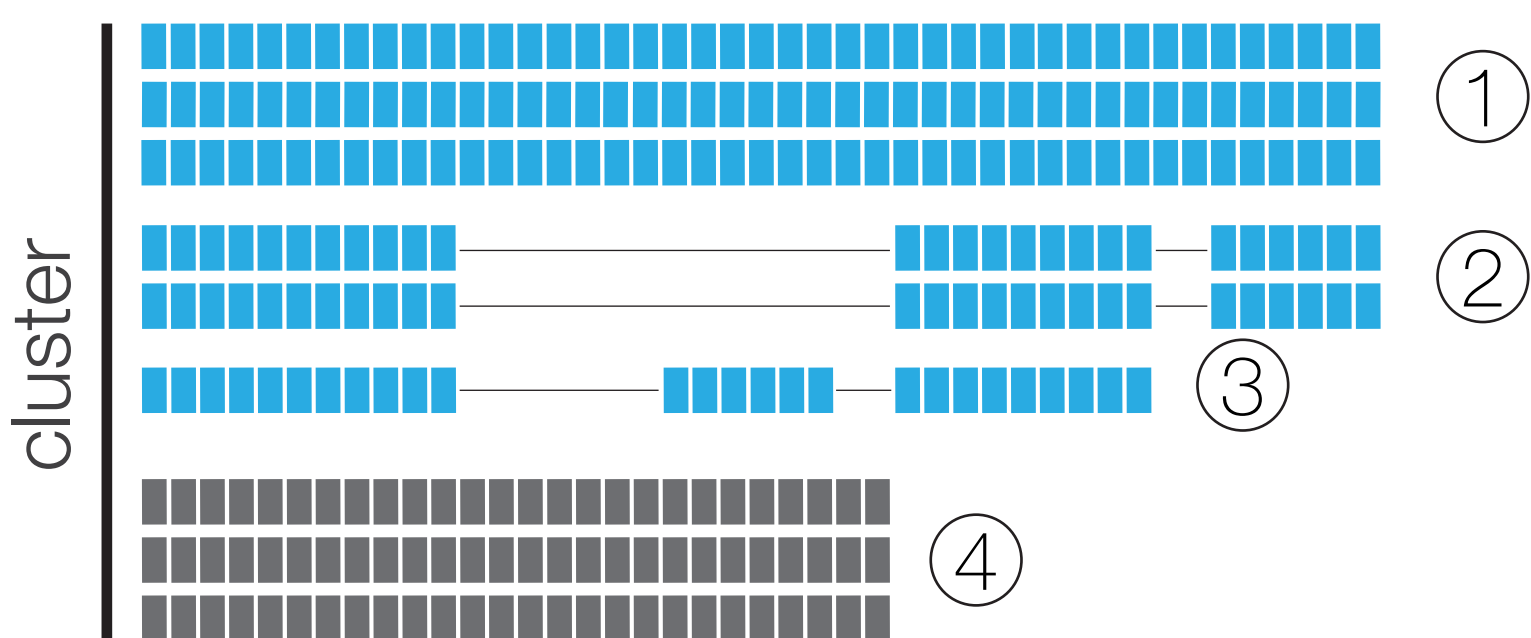- Use **polished** CCS reads
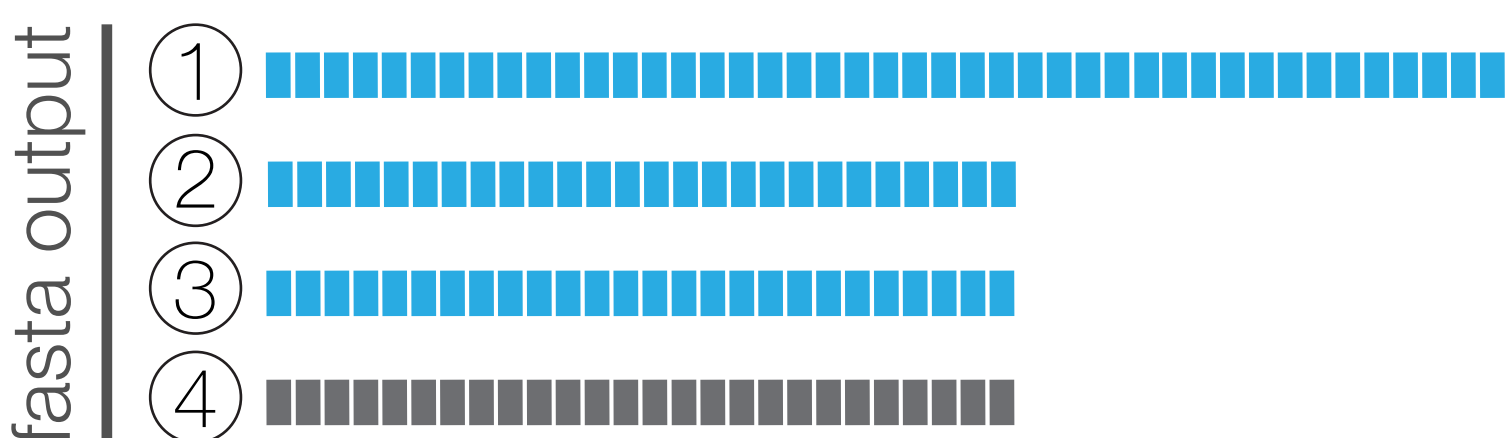- Only full-pass ZMWs

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

refine
- PolyA tail trimming
- Concatemer removal

cluster
- 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
- Fasta output is split into HQ and LQ reads
- One consensus per read cluster