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# Using the Iso-Seq Application on SMRT Link and BioConda

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 @Magdoll



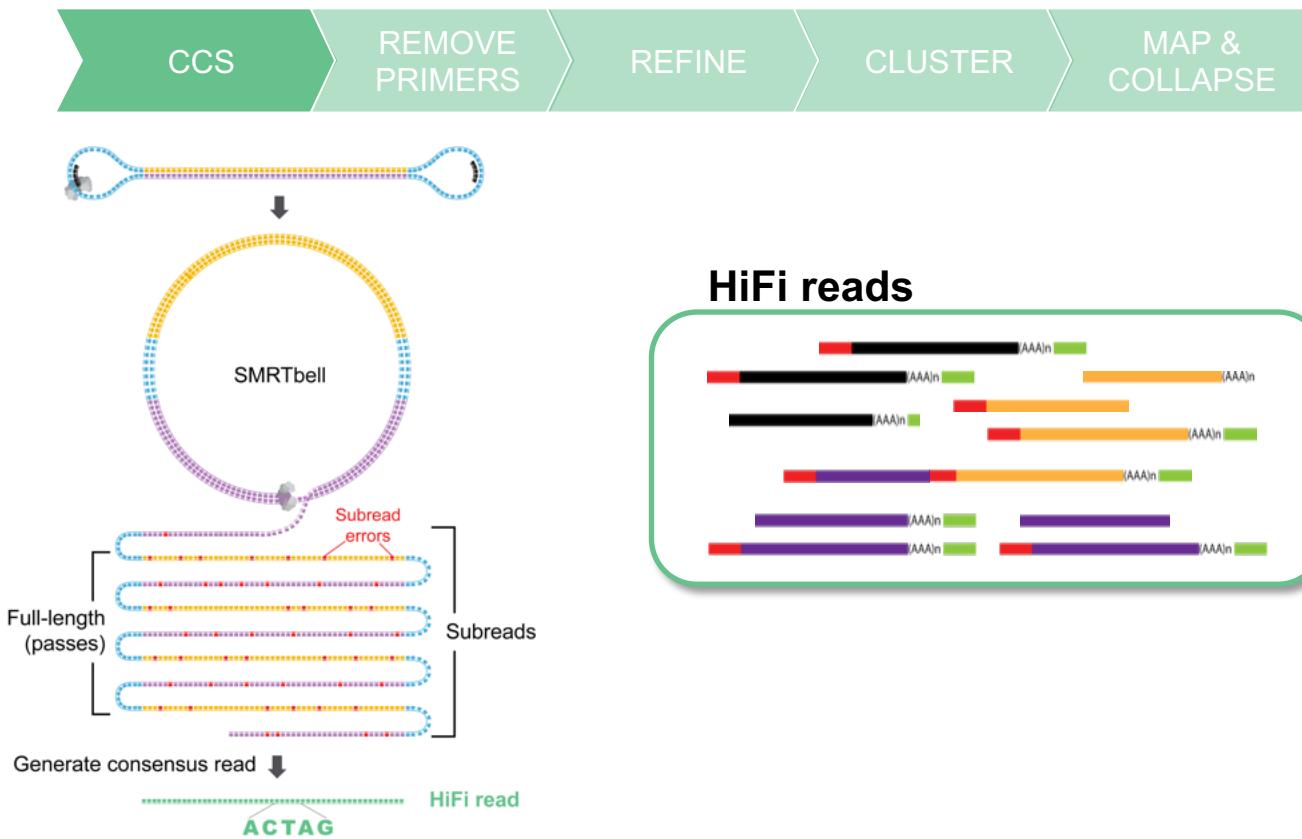
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# Why use Iso-Seq analysis?

# ISO-SEQ ANALYSIS MAIN FEATURES

- No reference genome required
- No transcriptome assembly required
- Recovers full-length (5' to 3') transcripts
- Yields highly accurate (>99%) transcripts

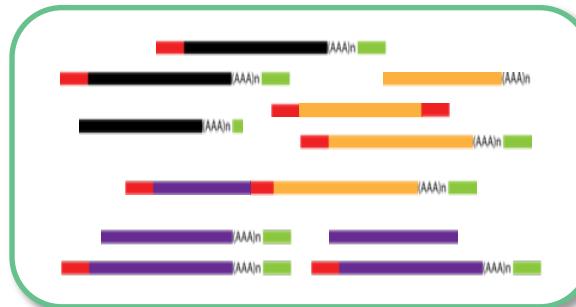
# HIFI READS FROM CCS



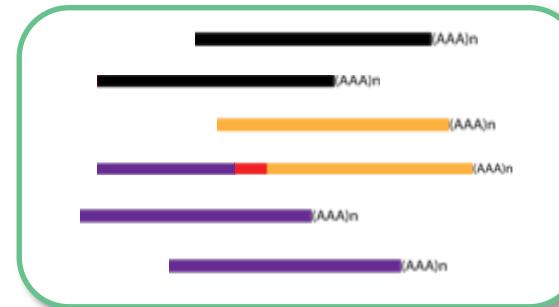
# FULL-LENGTH READS HAVE 5' AND 3' PRIMERS



HiFi reads



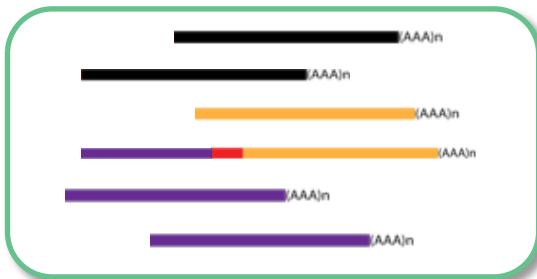
FL reads



# REMOVE CONCATEMERS AND POLY(A) TAILS



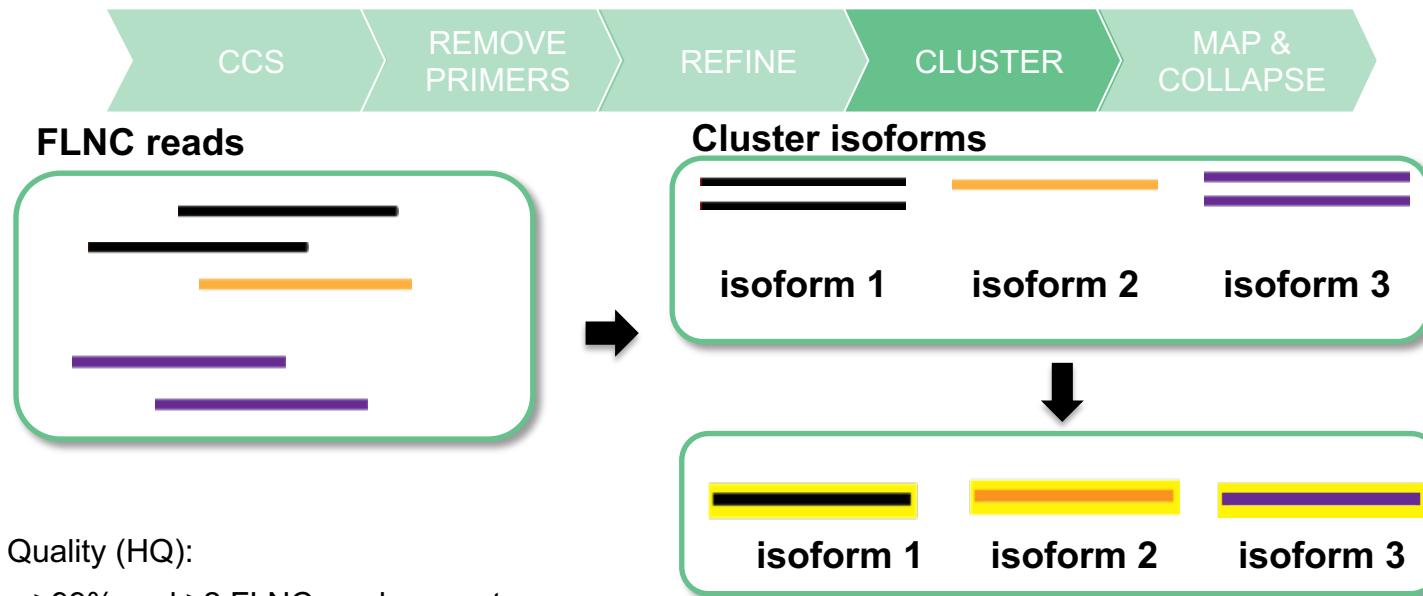
FL reads



FLNC reads



# CLUSTER TO GET ISOFORMS



- High Quality (HQ):  
accuracy  $\geq 99\%$  and  $\geq 2$  FLNC read support
- Low Quality (LQ):  
accuracy  $< 99\%$  and  $\geq 2$  FLNC read support

# MAP AND COLLAPSE ISOFORMS

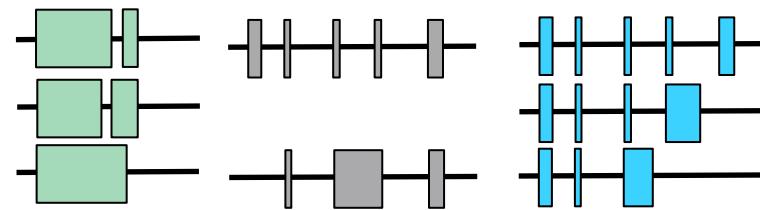


High-Quality, Full-Length Polished Isoforms



Map to Reference Genome  
Minimap2 (pbmm2)

Gene A      Gene B      Gene C



## BENEFITS OF ISO-SEQ ANALYSIS APPLICATION

- High-quality transcripts
- Full-Length Non-concatemer reads
- Mapped & collapsed isoforms
- Removes artifacts
- Removes poly(A) tails



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# Iso-Seq Analysis Using pbBioConda

# INSTRUCTIONS TUTORIAL

Follow the instructions tutorial for installing all the software needed.

- If you do not have an HPC server to install pbbioconda, you should have already:
  - Create an AWS account
  - Create an AWS Linux Instance to run Iso-Seq 3 Analysis Pipeline
  - Connect to your AWS Instance
  
- Upgrades and Install Software

# DOWNLOAD THE DATA

[https://downloads.pacbcloud.com/public/dataset/ISMB\\_workshop/](https://downloads.pacbcloud.com/public/dataset/ISMB_workshop/)

## Index of /public/dataset/ISMB\_workshop/isoseq3

<u>Name</u>	<u>Last modified</u>	<u>Size</u>	<u>Description</u>
 <a href="#">Parent Directory</a>		-	
 <a href="#">results/</a>	2020-09-23 07:31	-	
 <a href="#">alz.ccs.bam</a>	2020-06-15 11:52	84M	
 <a href="#">isoseq_primers.fasta</a>	2020-09-23 07:03	62	
 <a href="#">run.sh</a>	2020-09-23 07:23	430	

Example:

```
$ wget -nv https://downloads.pacbcloud.com/public/dataset/ISMB_workshop/isoseq3/alz.ccs.bam
```

## SPECIFY ISO-SEQ PRIMERS

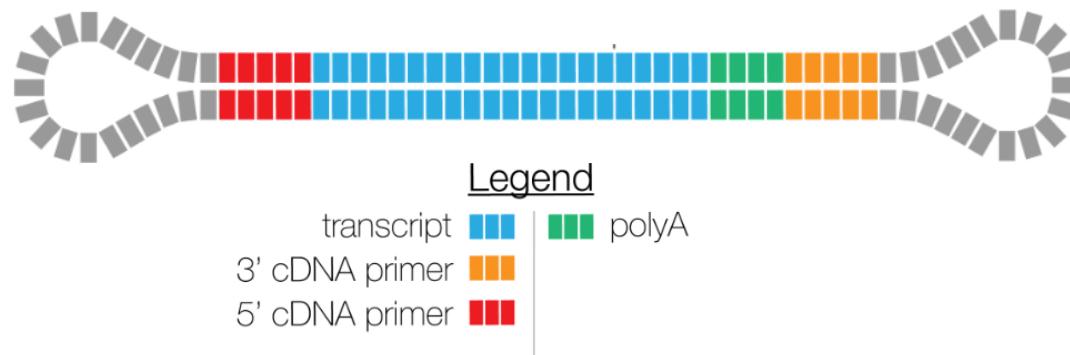
```
$ more primers.fasta
```

```
>5p
```

```
GCAATGAAGTCGCAGGGTTGGG
```

```
>3p
```

```
GTACTCTGCGTTGATAACCACTGCTT
```



## INPUT CCS BAM FILE

```
$ samtools view -h alz.ccs.bam
```

```
m141008_060349_42194_c100704972550000001823137703241586_s1_p0/63/ccs4*0255
**00CCCGGGGATCCTCTAGAATGC~~~~~RG:Z:83ba013f np:i:35
rq:f:f:0.999682 sn:B:f,11.3175,6.64119,11.6261,14.5199 zm:i:63
```

# REFERENCE GENOME

```
$ grep '>' hg38.fa # to list the headers per chromosome
```

```
>chr1 AC:CM000663.2 gi:568336023 LN:248956422 rl:Chromosome M5:6aef897c3d6ff0c78a  
ff06ac189178dd AS:GRCh38  
>chr2 AC:CM000664.2 gi:568336022 LN:242193529 rl:Chromosome M5:f98db672eb0993dcfd  
abafe2a882905c AS:GRCh38  
>chr3 AC:CM000665.2 gi:568336021 LN:198295559 rl:Chromosome M5:76635a41ea913a405d  
ed820447d067b0 AS:GRCh38  
>chr4 AC:CM000666.2 gi:568336020 LN:190214555 rl:Chromosome M5:3210fecf1eb92d5489  
da4346b3fddc6e AS:GRCh38  
>chr5 AC:CM000667.2 gi:568336019 LN:181538259 rl:Chromosome M5:a811b3dc9fe66af729  
dc0dddf7fa4f13 AS:GRCh38 hm:47309185-49591369  
...
```

# SOFTWARE INSTALLATION CHECK

Access to your conda environment

```
$ source activate <name of your environment>
```

Check your installation

```
$ isoseq3 --version
```

```
isoseq3 3.4.x
```

```
$ lima --version
```

```
lima 1.11.0
```

```
$ pbmm2 --version
```

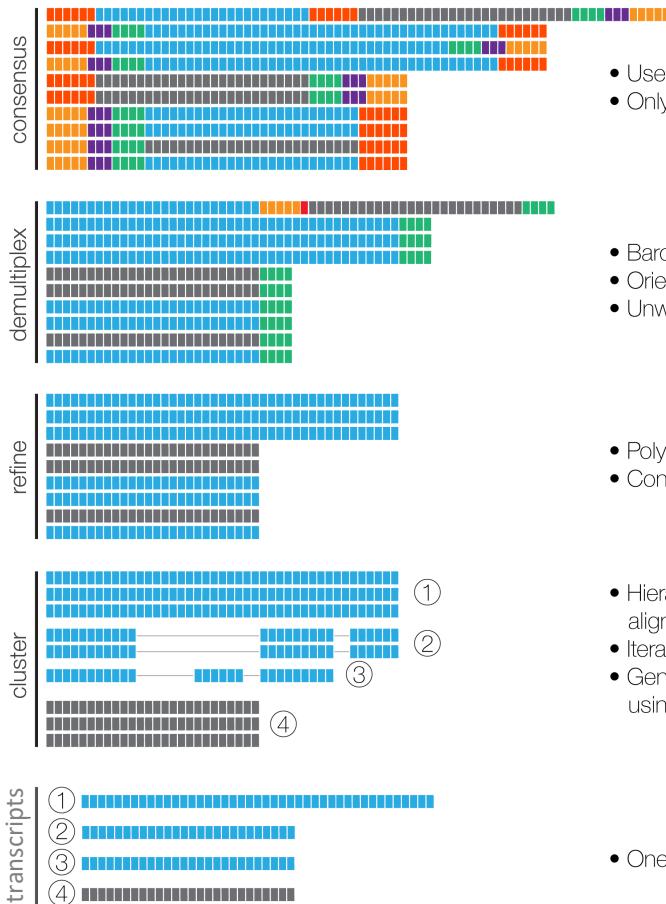
```
pbmm2 1.3.0
```



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# ISO-SEQ WORKFLOW

# ISO-SEQ WORKFLOW



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

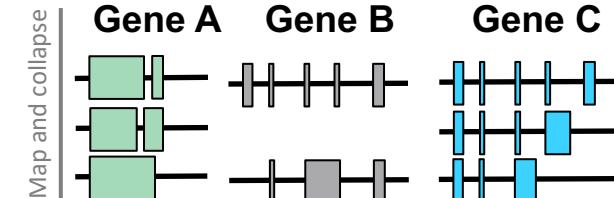
- Barcoded and unbarcoded cDNA primer removal
- Orientation
- Unwanted primer combination removal

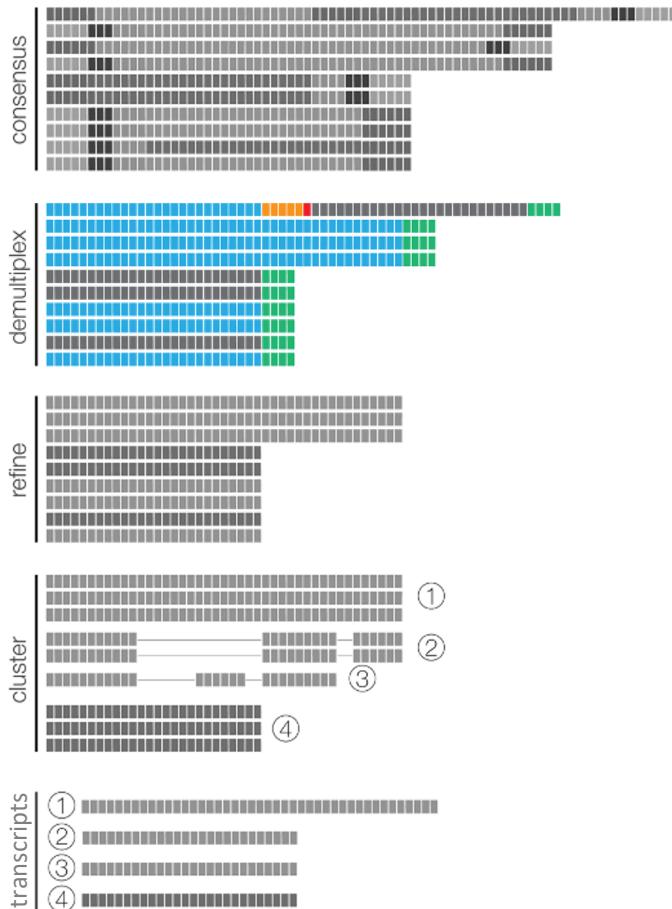
- PolyA tail trimming
- Concatemer removal

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

- One consensus per read cluster

- Align to reference genome
- Remove redundancy





## PRIMER REMOVAL & DEMULTIPLEXING

Command line:

```
lima --isoseq --dump-clips --peek-guess -j 24\  
alz.ccs.bam isoseq_primers.fasta alz.demult.bam
```

Input files:

alz.ccs.bam #HiFi reads  
isoseq\_primers.fasta #Iso-Seq primers

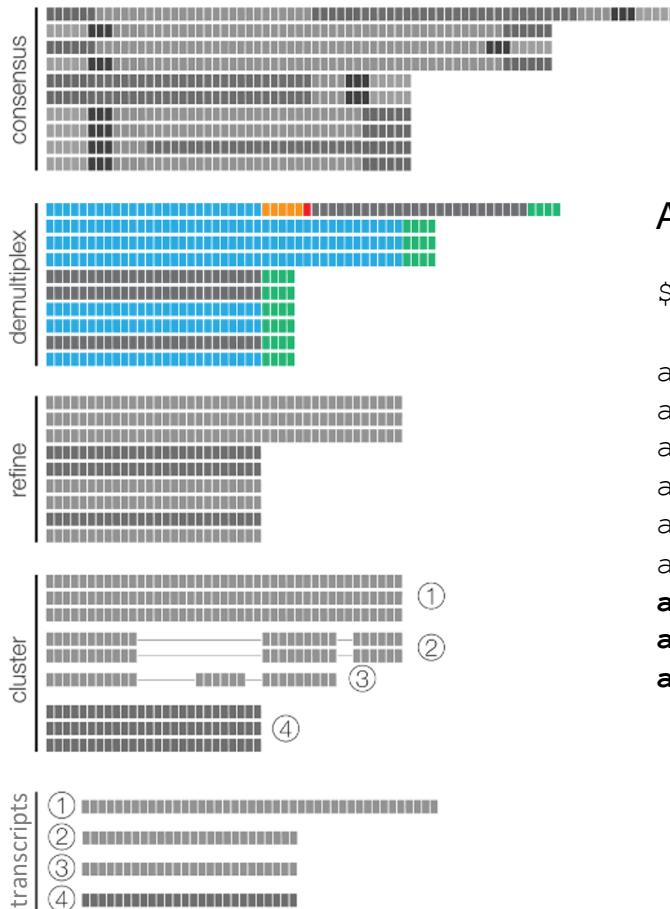
Output files:

alz.demult.bam

Options:

- isoseq #specialized isoseq option for lima
- dump-clips # show the clipped primers
- peek-guess # remove spurious false positive signal
- j 24 # Number of threads to use

# PRIMER REMOVAL & DEMULTIPLEXING

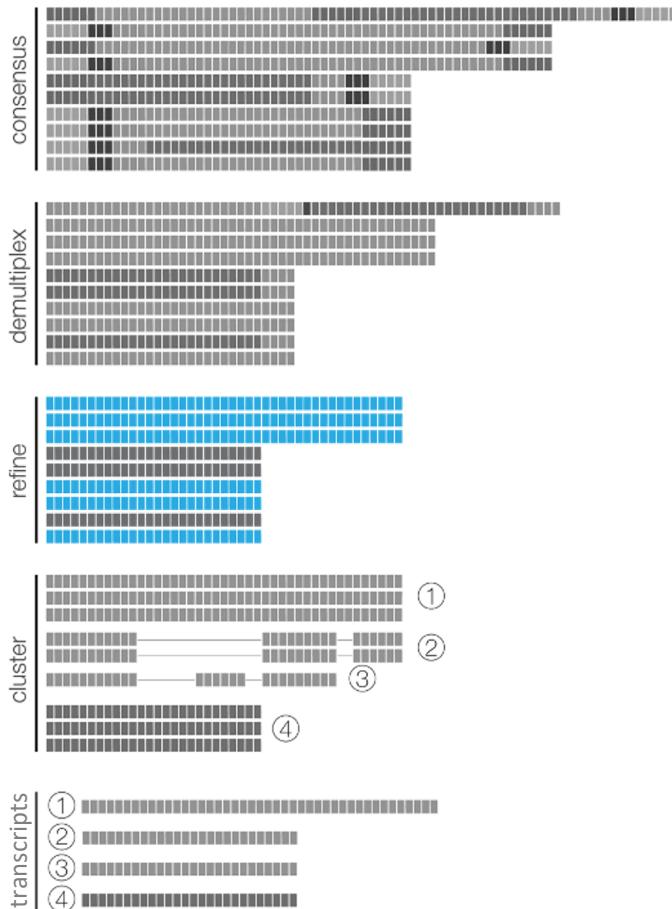


After completion, you will see the following files:

```
$ ls -ltrh
```

```
alz.demult.json
alz.demult.lima.clips
alz.demult.lima.counts
alz.demult.lima.guess
alz.demult.lima.report
alz.demult.lima.summary
alz.demult.5p--3p.bam
alz.demult.5p--3p.bam.pbi
alz.demult.5p--3p.subreadset.xml
```

#lima reports



## TRIMMING POLY(A) TAILS AND CONCATEMER REMOVAL

Command line:

```
isoseq3 refine --require-polya\  
alz.demult.5p--3p.bam\ isoseq_primers.fasta  
alz.flnc.bam
```

Input files:

alz.demult.5p--3p.bam  
isoseq\_primers.fasta

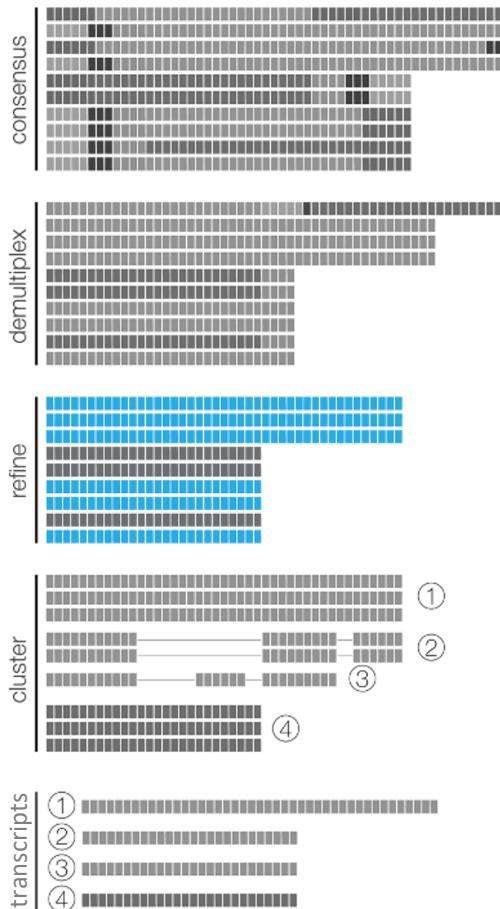
Output files:

alz.flnc.bam

Options:

--require-polya #if your transcripts have a polyA tail

# TRIMMING POLY(A) TAILS AND CONCATEMER REMOVAL

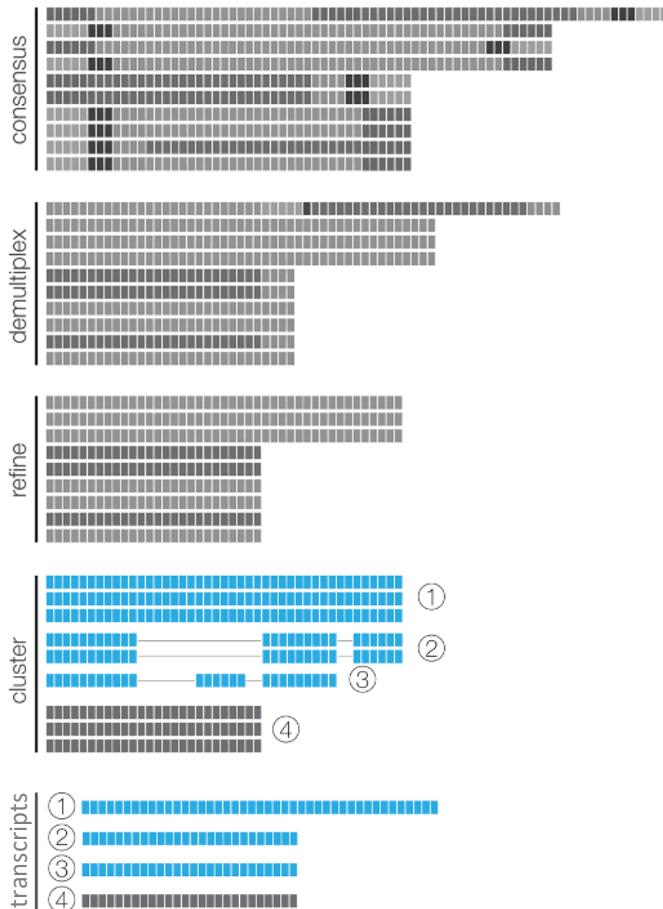


After completion, you will see the following files:

```
$ ls -ltrh
```

```
alz.flnc.bam
alz.flnc.bam.pbi
alz.flnc.consensusreadset.xml
alz.flnc.filter_summary.json
alz.flnc.report.csv
```

#isoseq3 refine reports



## ISOFORMS

Command line:

```
isoseq3 cluster alz.flnc.bam alz.polished.bam \  
--verbose --use-qvs
```

Input files:

alz.flnc.bam

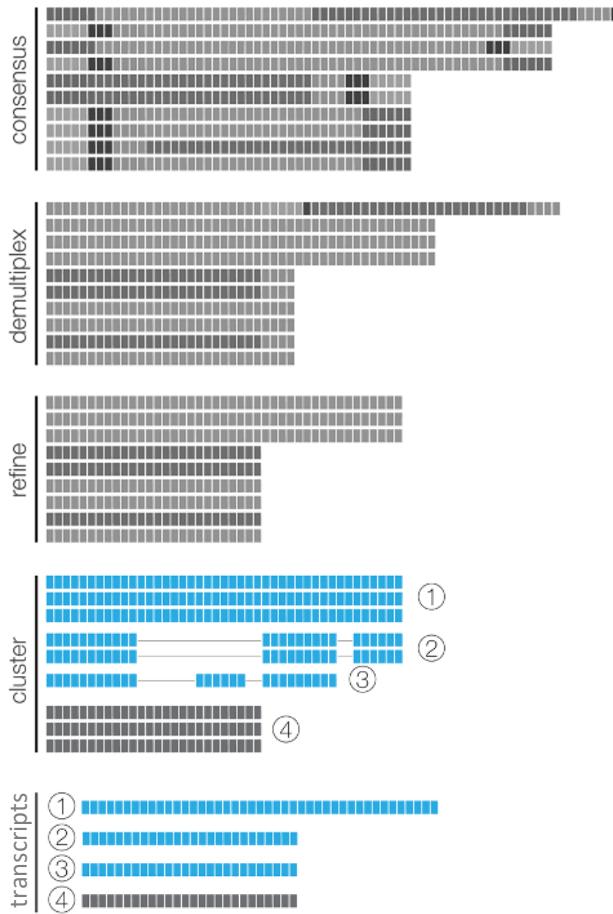
Output files:

alz.flnc.bam

Options:

```
--verbose #if your transcripts have a polyA tail  
--use-qvs #Use CCS QVs, sets --poa-cov 100
```

# ISOFORMS



After completion, you will see the following files:

```
$ ls -ltrh
```

```
alz.polished.bam  
alz.polished.bam.pbi  
alz.polished.transcriptset.xml  
alz.polished.cluster  
alz.polished.cluster_report.csv  
alz.polished.hq.bam  
alz.polished.hq.bam.pbi  
alz.polished.hq.fasta.gz  
alz.polished.lq.bam  
alz.polished.lq.bam.pbi  
alz.polished.lq.fasta.gz
```

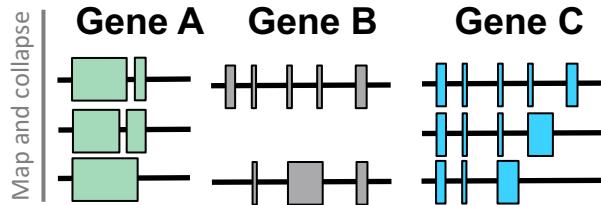
Because the ccs input is Polished, the isoseq3 cluster output is already polished!

#isoseq3 cluster reports

#high quality isoforms ( $\geq 0.99$ )

#low quality isoforms ( $< 0.99$ )

# MAP



Command line:

```
pbmm2 align hg38.fa alz.polished.hq.bam  
alz.aligned.bam  
-j 24 --preset ISOSEQ -sort --log-level INFO
```

Input files:

alz.polished.hq.bam  
hg38.fa

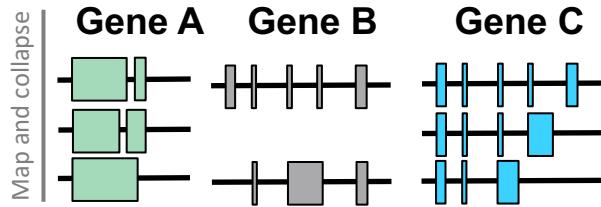
Output files:

alz.aligned.bam

Options:

- j 24 #Number of threads to use
- preset ISOSEQ #select the alignment mode
- sort #Generate sorted BAM file
- log-level INFO #show progress

# MAP

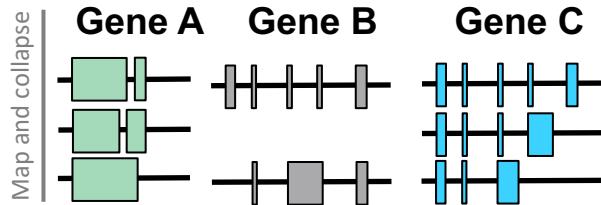


After completion, you will see the following files:

```
$ ls -ltrh
```

```
alz_aligned.bam  
alz_aligned.bam.bai
```

# COLLAPSE



Command line:

```
isoseq3 collapse alz.aligned.bam alz.collapsed.gff
```

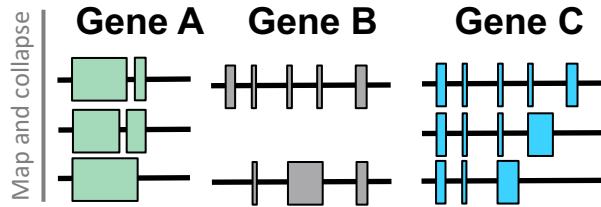
Input files:

alz.aligned.bam

Output files:

alz.collapsed.gff

# COLLAPSE



After completion, you will see the following files:

```
$ ls -ltrh
```

```
alz.collapsed.report.json  
alz.collapsed.abundance.txt  
alz.collapsed.read_stat.txt  
alz.collapsed.group.txt  
alz.collapsed.gff  
alz.collapsed.fasta
```

#report, stats and list ]

# PUBLICLY AVAILABLE ISO-SEQ DATA SETS

[https://github.com/PacificBiosciences/IsoSeq\\_SA3nUP/wiki/Iso-Seq-in-house-datasets](https://github.com/PacificBiosciences/IsoSeq_SA3nUP/wiki/Iso-Seq-in-house-datasets)

## Iso Seq in house datasets

Elizabeth Tseng edited this page on Oct 8, 2019 · 12 revisions

Last Updated: 10/07/2019

Below are datasets that have been run in-house at PacBio.

### Alzheimer Brain (released Oct 2019)

- [Download Link](#)

Library prep Iso-Seq® Express Template Preparation for Sequel® and Sequel® II Systems

Sequencing Sequel II System with Sequel II Binding Kit 1.0 and Sequel II Sequencing Kit 1.0

Run time: 24 hrs pre-extension, 4 movie time. Sequenced on 1 SMRT Cell 8M.

# ISO-SEQ ANALYSIS TERMINOLOGY

NAME	ABBR	EXPLANATION
<b>Full-Length Reads</b>	FL Reads	CCS reads with 5' and 3' cDNA primers removed
<b>Full-Length, Non-Concatemer Reads</b>	FLNC Reads	CCS reads with 5' and 3' cDNA primers, polyA tail, and concatemers removed
<b>High-Quality Isoforms</b>	HQ Isoforms	Polished transcript sequences with predicted accuracy $\geq 99\%$ & $\geq 2$ FLNC
<b>Low-Quality Isoforms</b>	LQ Isoforms	Polished transcript sequences with predicted accuracy $< 99\%$ & $\geq 2$ FLNC



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