

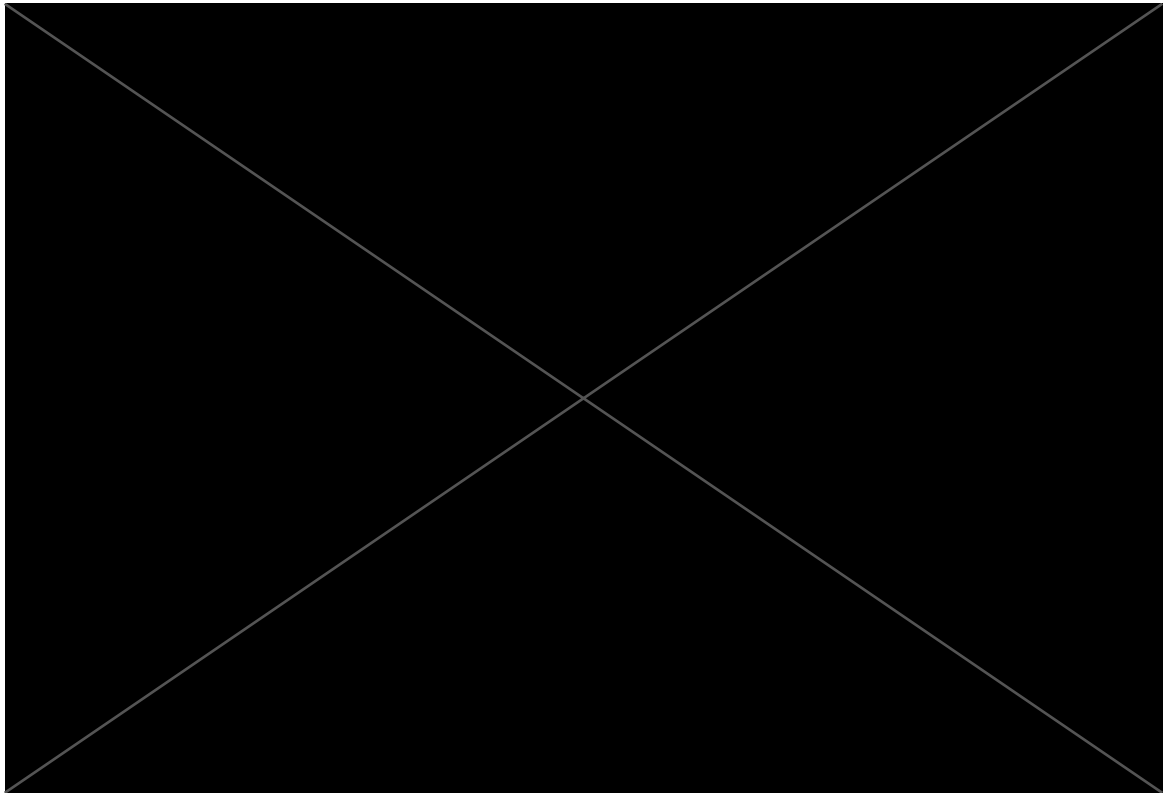
Kinnex-SingleCell-Release-PBMC-XXXXXXXXXX10x5p - Bio Sample 3

SUCCESSFUL

Copy

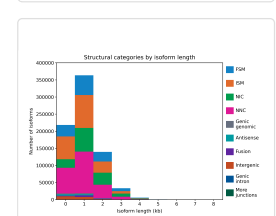
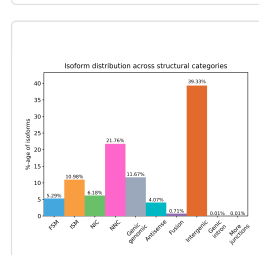
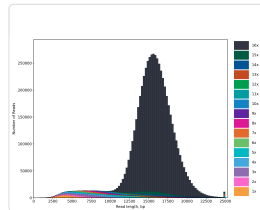
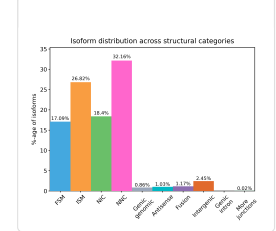
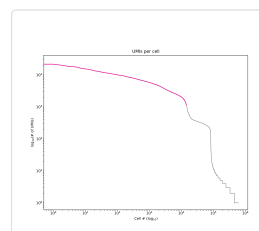
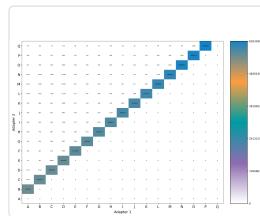
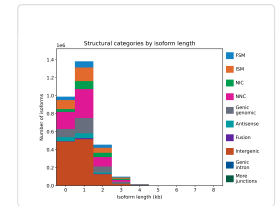
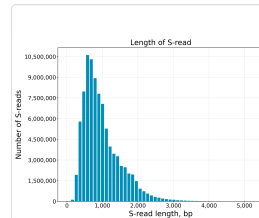
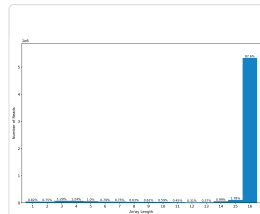
Delete

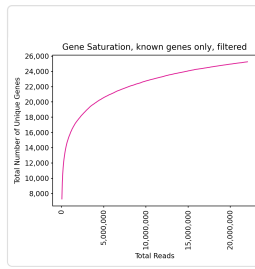
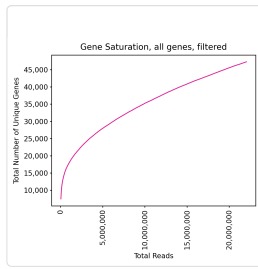
- Analysis Overview
 - Status
 - Thumbnails
 - Display All
- Read Segmentation
- Read Statistics
- Cell Statistics
- Transcript Statistics
- Data



Analysis Parameters

Thumbnails

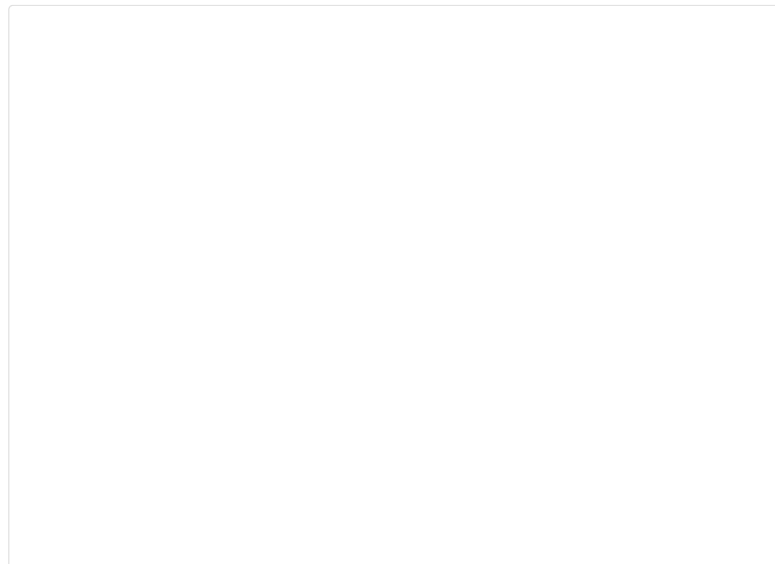
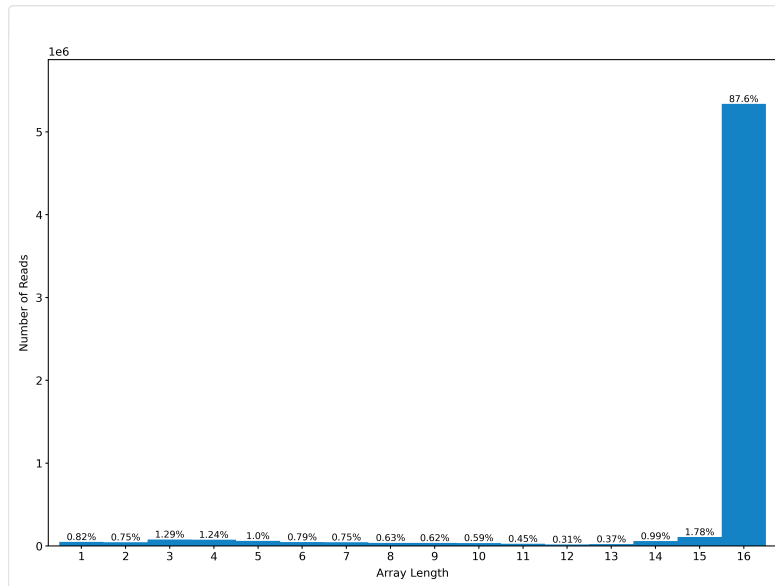


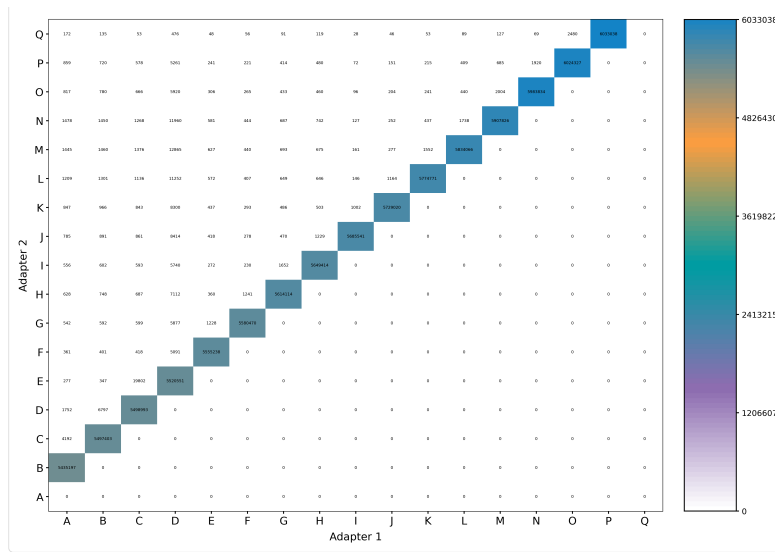


Read Segmentation

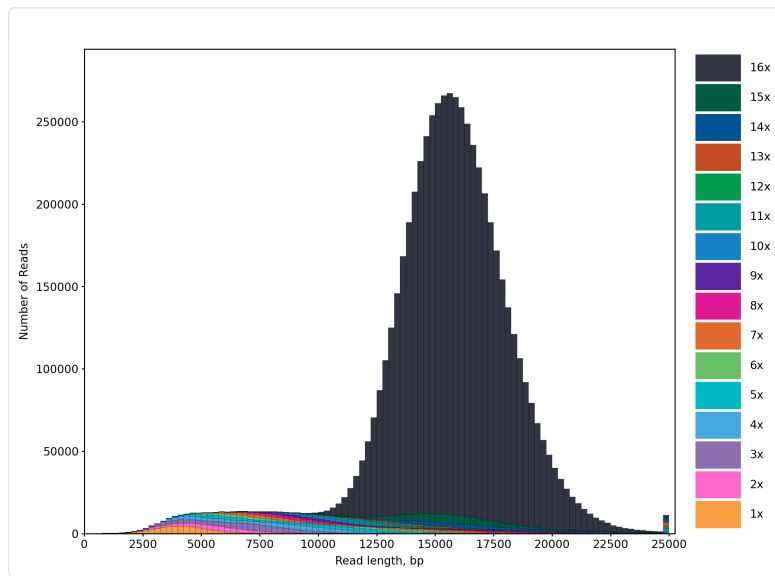
Value	Analysis Metric
6,104,086	Reads
91,323,803	Segmented reads (S-reads)
980	Mean length of S-reads
87.46 %	Percent of reads with full arrays
14.96	Mean array size (concatenation factor)

Segmentation Statistics

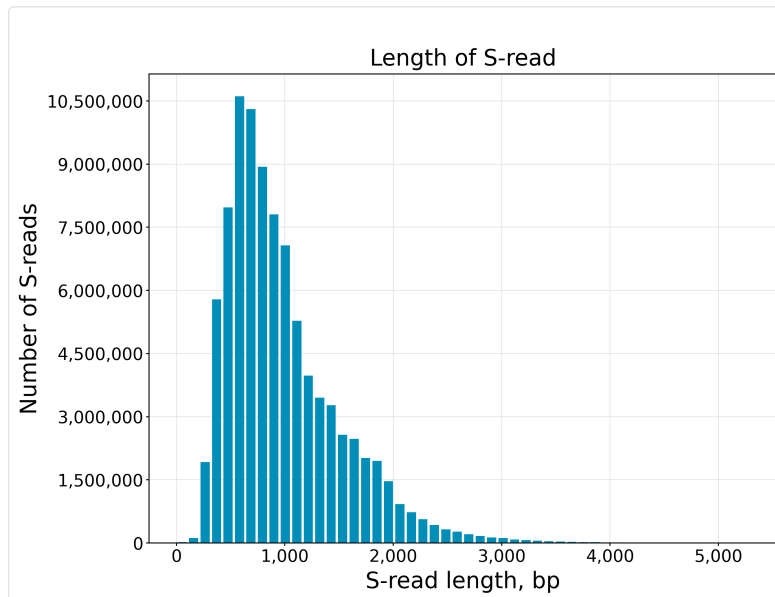




Length of Reads



S-read Length Distribution



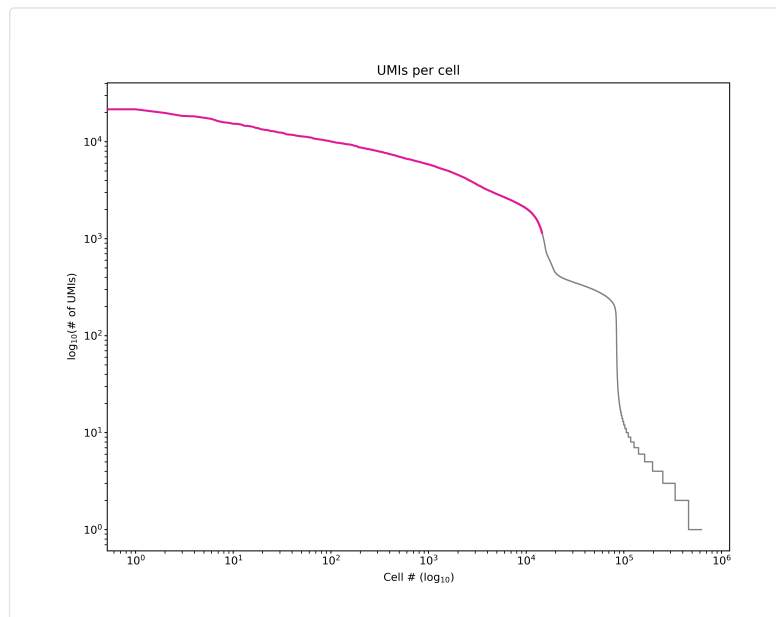
Read Statistics

Value	Analysis Metric
91,323,803	Reads
SEGMENT	Read Type
90,598,328	Reads with 5' and 3' Primers with extracted UMIs and Barcodes
89,790,396	Non-Concatamer Reads with 5' and 3' Primers and Poly-A Tail (FLNC reads)
85,414,801	FLNC Reads with Valid Barcodes
88,711,954	FLNC Reads with Valid Barcodes, corrected
44,323,585	Reads after Barcode Correction and UMI Deduplication

Cell Statistics

Value	Analysis Metric
13,984	Estimated Number of Cells
64.57%	Reads in Cells
4,146	Mean Reads per Cell
2,498	Median UMIs per Cell

Barcode Rank Plot



Transcript Statistics

Value	Analysis Metric
46,891,707	FLNC Reads Mapped Confidently to Genome
29,306,513	FLNC Reads Mapped Confidently to Transcriptome

Value	Analysis Metric
1,211,163	Total Unique Genes
47,269	Total Unique Genes, filtered
32,767	Total Unique Genes, known genes only
25,243	Total Unique Genes, filtered, known genes only
2,554,446	Total Unique Transcripts
505,275	Total Unique Transcripts, filtered
88,761	Total Unique Transcripts, known transcripts only
78,022	Total Unique Transcripts, filtered, known transcripts only

Transcript Summary

Value ↑	Analysis Metric ↑
1,170	Median Genes per Cell
917	Median Genes per Cell, known genes only
1,314	Median Transcripts per Cell
714	Median Transcripts per Cell, known transcripts only
1,211,163	Total Unique Genes
32,767	Total Unique Genes, known genes only
2,554,446	Total Unique Transcripts
88,761	Total Unique Transcripts, known transcripts only

Transcript Summary, filtered

Value ↑	Analysis Metric ↑
697	Median Genes per Cell
689	Median Genes per Cell, known genes only
771	Median Transcripts per Cell
623	Median Transcripts per Cell, known transcripts only
47,269	Total Unique Genes
25,243	Total Unique Genes, known genes only
505,275	Total Unique Transcripts
78,022	Total Unique Transcripts, known transcripts only

Transcript Classification

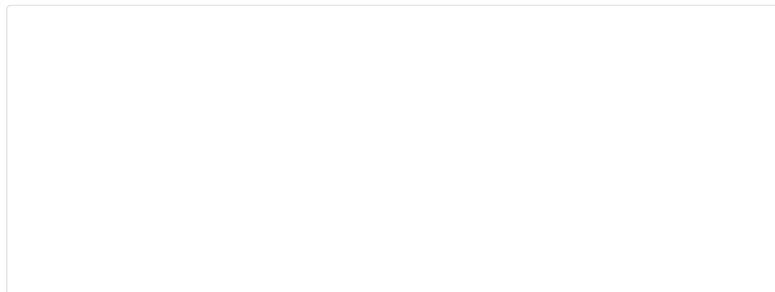
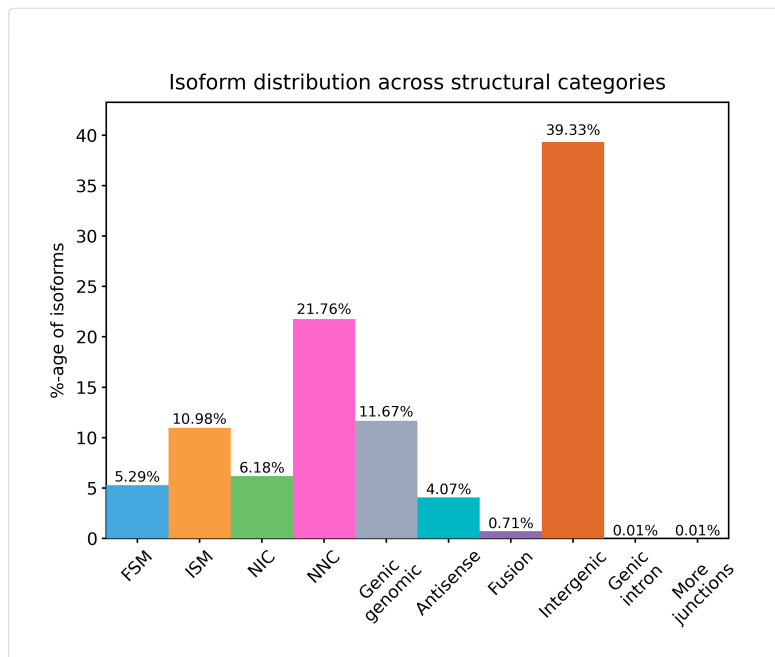
Category ↑	Count ↑	CAGE Detected ↑	CAGE Detected ... ↑	polyA Motif Det... ↑
FSM	155693	98617	63.34%	49487
ISM	323299	161223	49.86%	90471
NIC	181954	133623	73.43%	60642

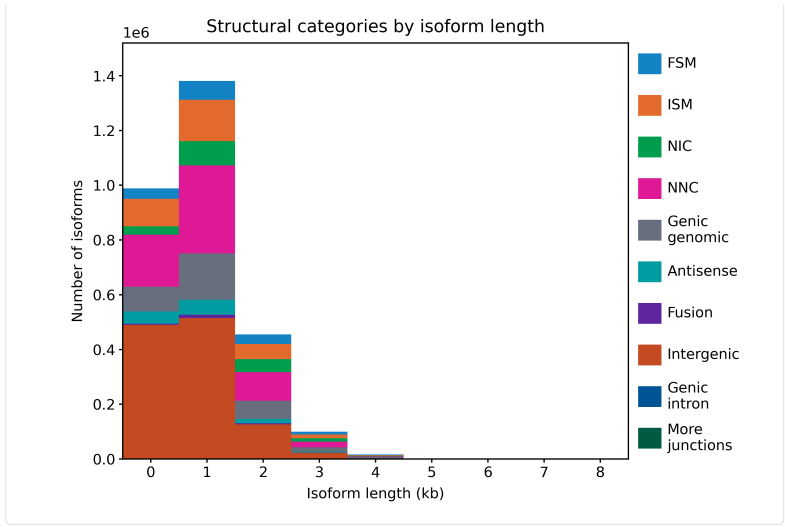
NNC	640769	440094	68.68%	250338
Antisense	119708	5204	4.34%	36293
Fusion	20949	12814	61.16%	9137
More junctions	212	123	58.01%	88
Genic intron	353	1	0.28%	117
Genic genomic	343584	81694	23.77%	103384
Intergenic	1158156	8592	0.74%	389904

Transcript Classification, filtered

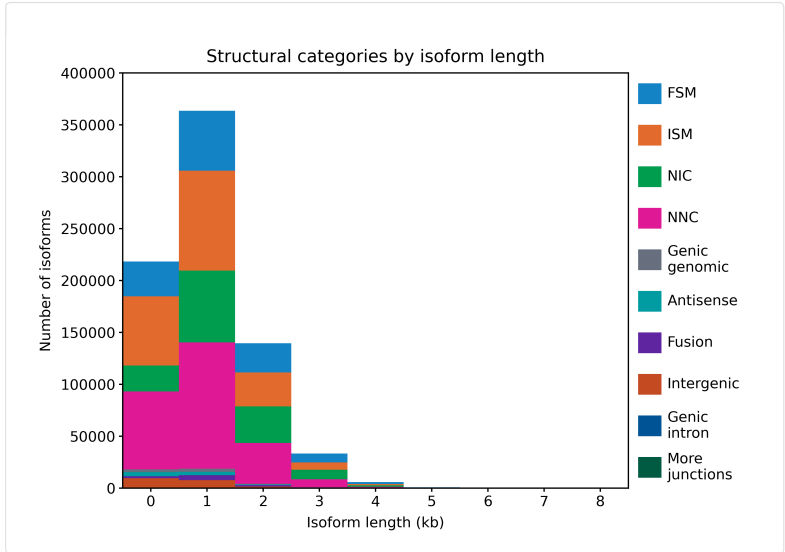
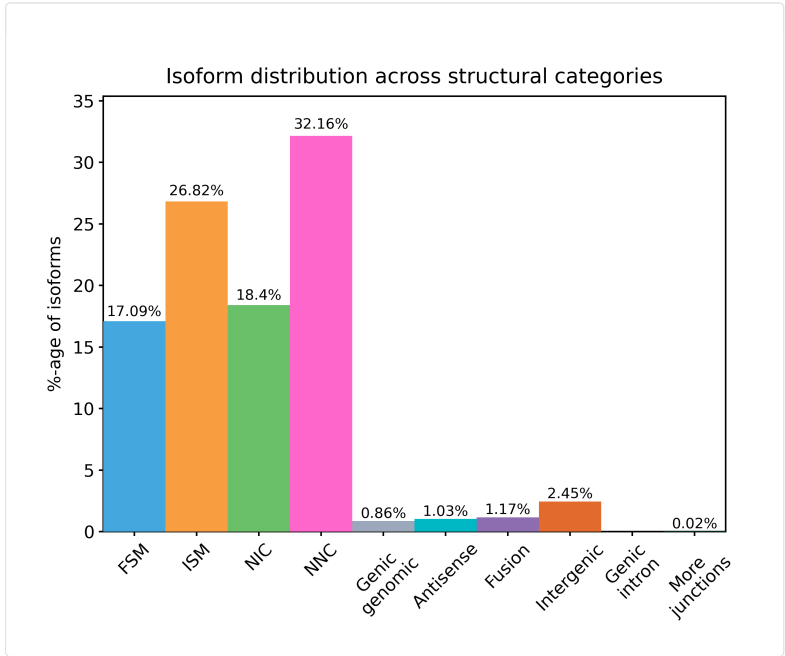
Category ↓↑	Count ↓↑	CAGE Detected ↓↑	CAGE Detected,... ↓↑	polyA Detected ↓↑	p
FSM	130235	84371	64.78%	49487	
ISM	204345	118042	57.76%	72306	
NIC	140207	102969	73.44%	59922	
NNC	245010	170435	69.56%	117603	
Antisense	7814	1146	14.66%	4415	
Fusion	8902	5564	62.50%	4716	
More junctions	123	77	62.60%	70	
Genic intron	0	0	0.00%	0	
Genic genomic	6554	3696	56.39%	2920	
Intergenic	18643	1190	6.38%	11074	

Transcript Classification Plots





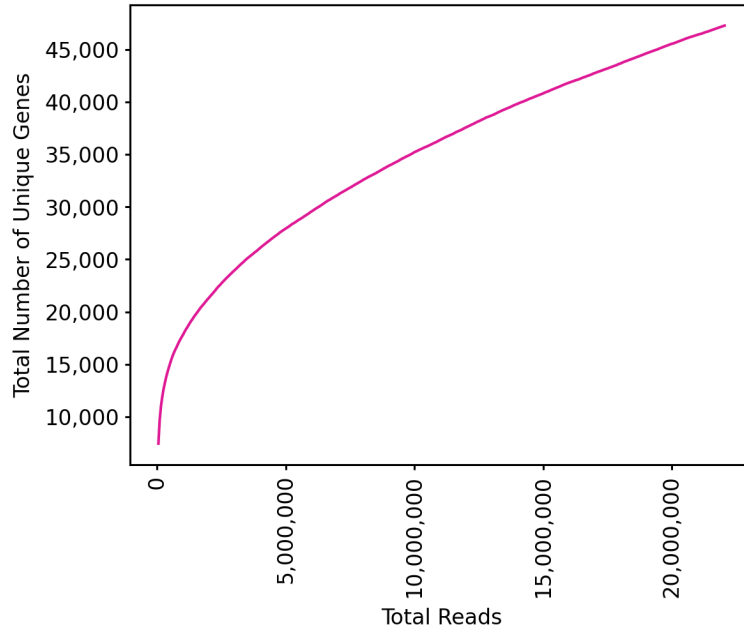
Transcript Classification Plots, filtered



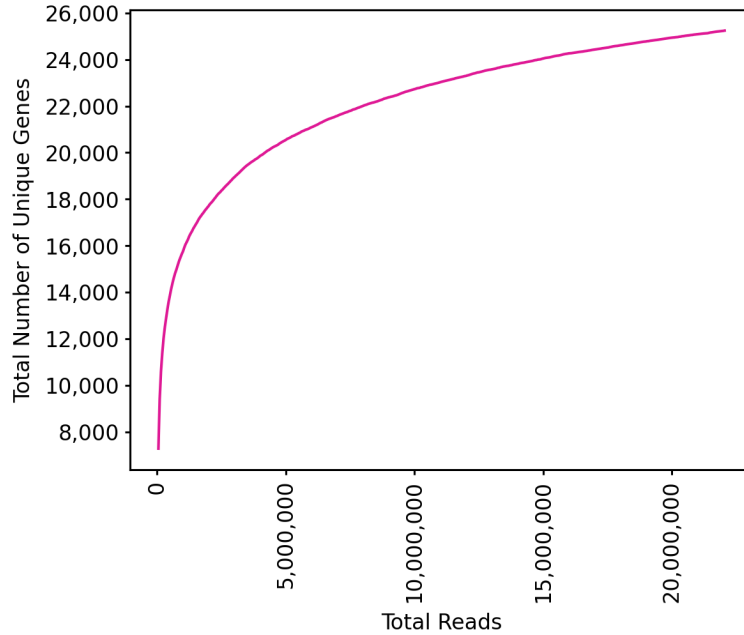
Gene Saturation



Gene Saturation, all genes, filtered









Gene Saturation, known genes only, filtered



File Downloads

Edit Output File Name Prefix

Example:analysis-Bio Sample 3-110677

File ↕	Size ↕	Type ↕
5pPBMC-Cell7 (Bio Sample 3) Segmented Reads	21 KB	ConsensusRead
 Report read segmentation	3 KB	JsonReport
 Deduplicated reads after cell barcode correction, unmapped, BAM	13 GB	bam
 Single-cell isoform and gene matrix, tar-gzipped	1 GB	tgz
 Segmented Reads, passing, unaligned	57 GB	bam
 Non-passing reads, unaligned	4 GB	bam
 Unique mapped transcripts, GFF	1 GB	gff