

- ▼ Analysis Overview
  - Status
  - Thumbnails
  - Display All
- Read Segmentation
- Read Classification
- Transcript Clustering
- Transcript Mapping and Classification
- Data

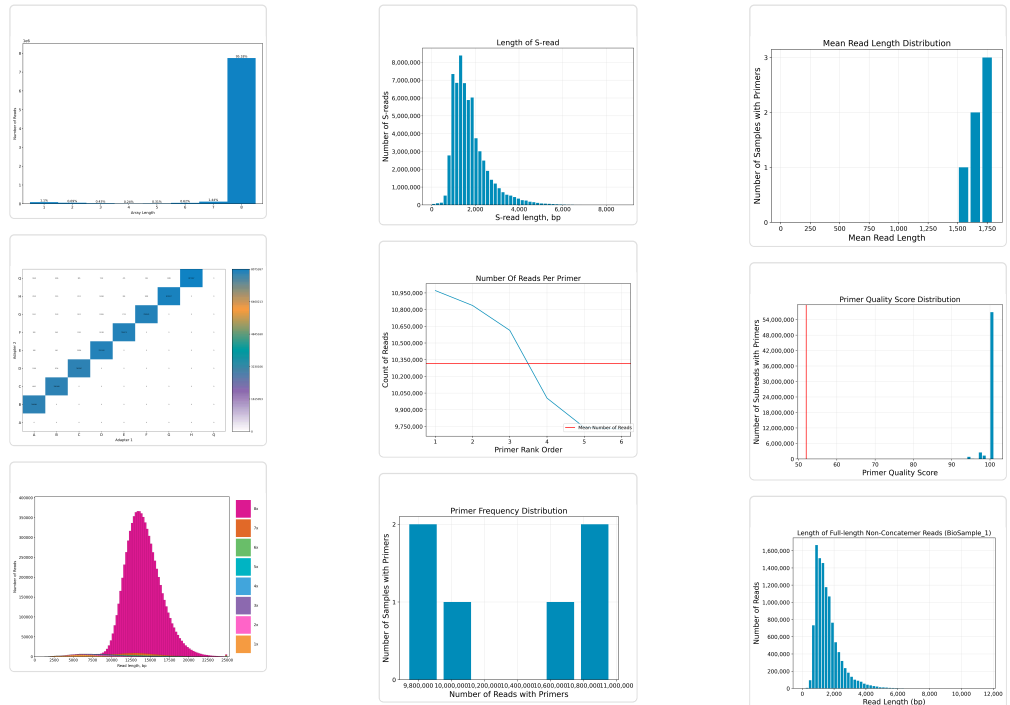
## Display All

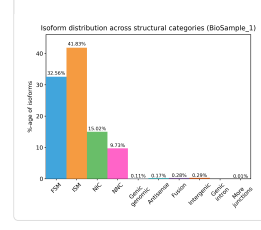
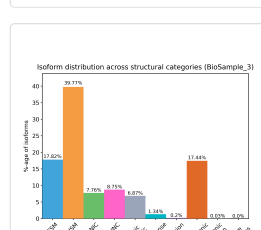
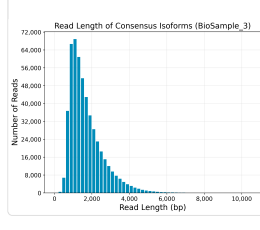
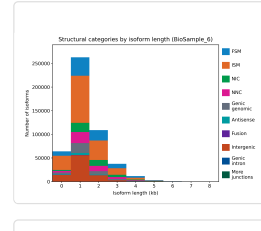
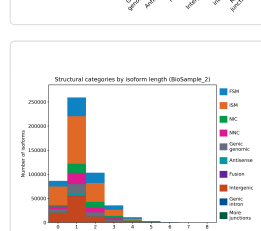
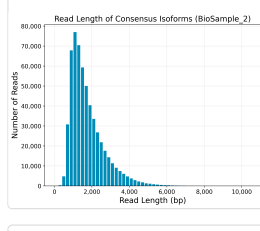
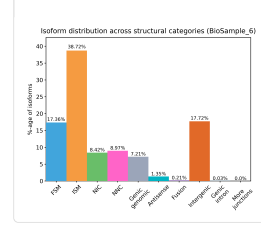
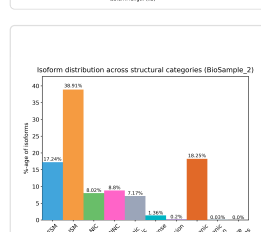
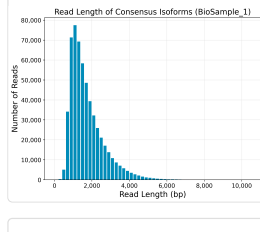
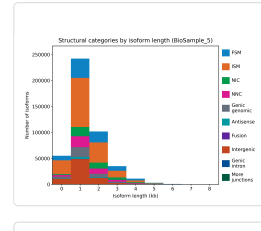
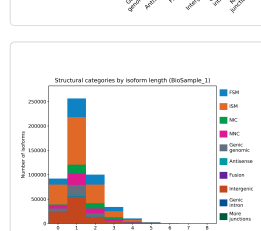
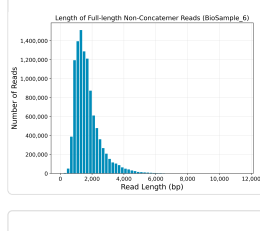
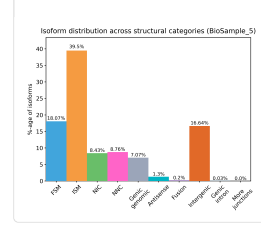
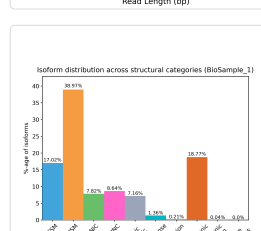
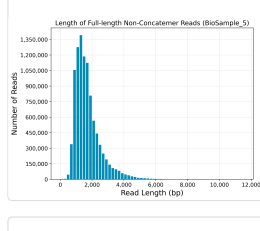
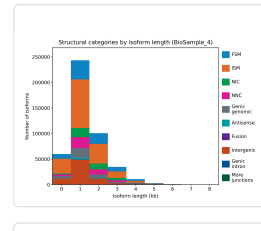
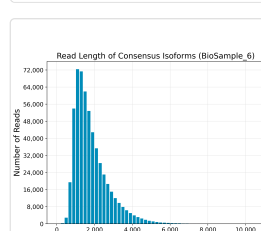
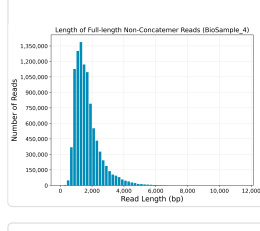
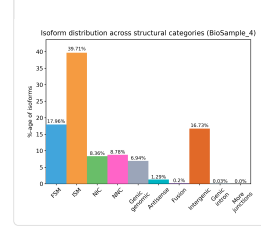
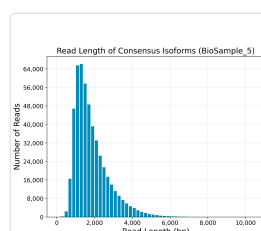
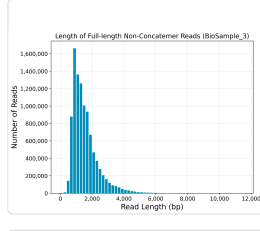
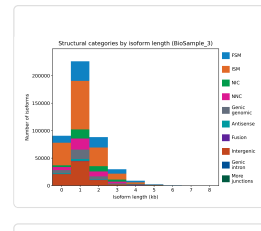
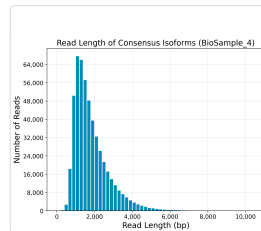
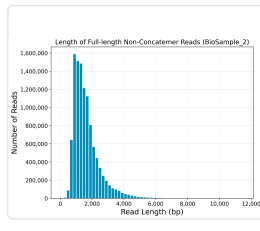
Status

Analysis KinnexRelease-UHRR2024-Revio-largeMem

## ► Analysis Parameters

### Thumbnails



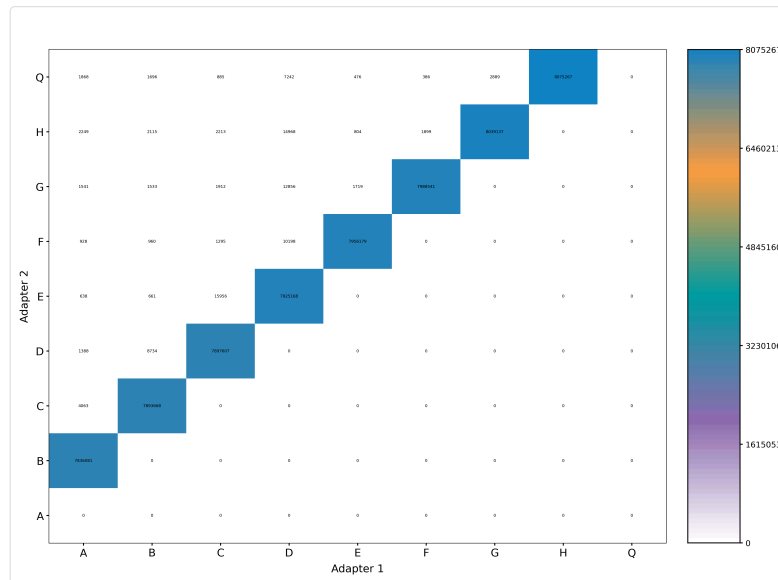
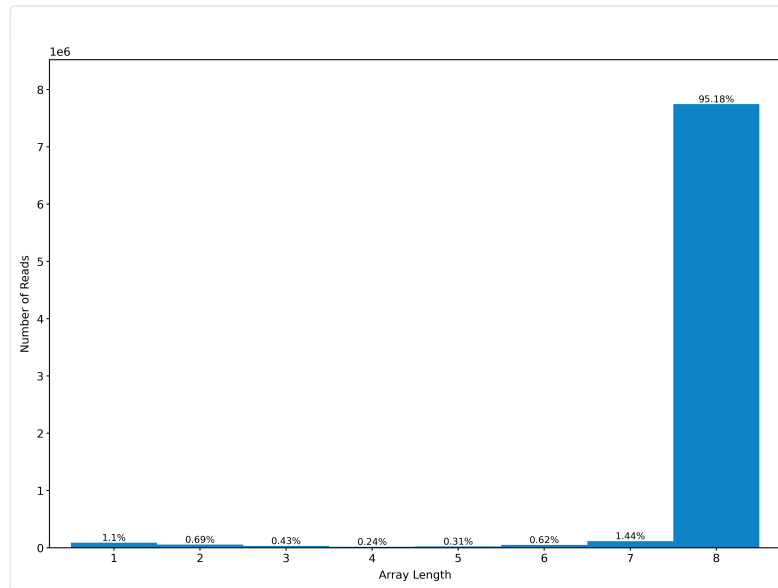




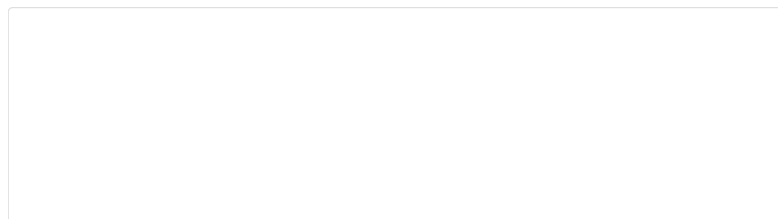
## Read Segmentation

Value	Analysis Metric
8,247,394	Reads
63,611,648	Segmented reads (S-reads)
1,753	Mean length of S-reads
93.94 %	Percent of reads with full arrays
7.71	Mean array size (concatenation factor)

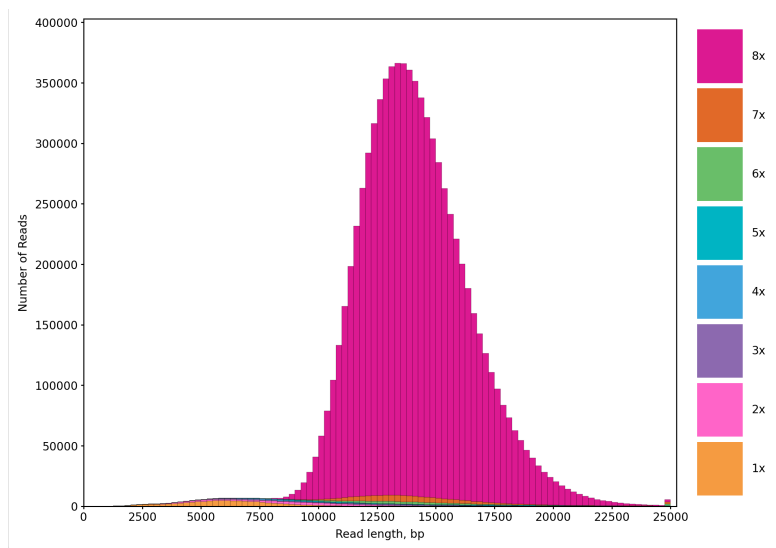
## Segmentation Statistics



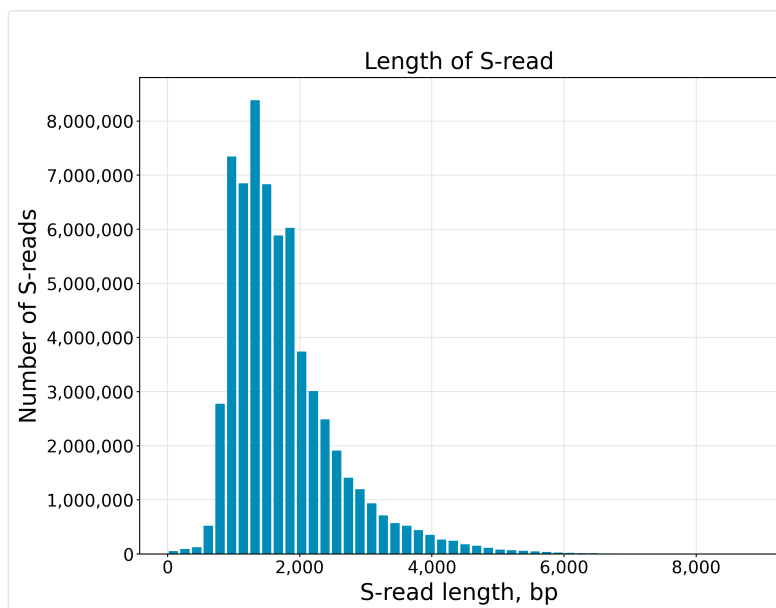
## Length of Reads







## S-read Length Distribution



## Read Classification

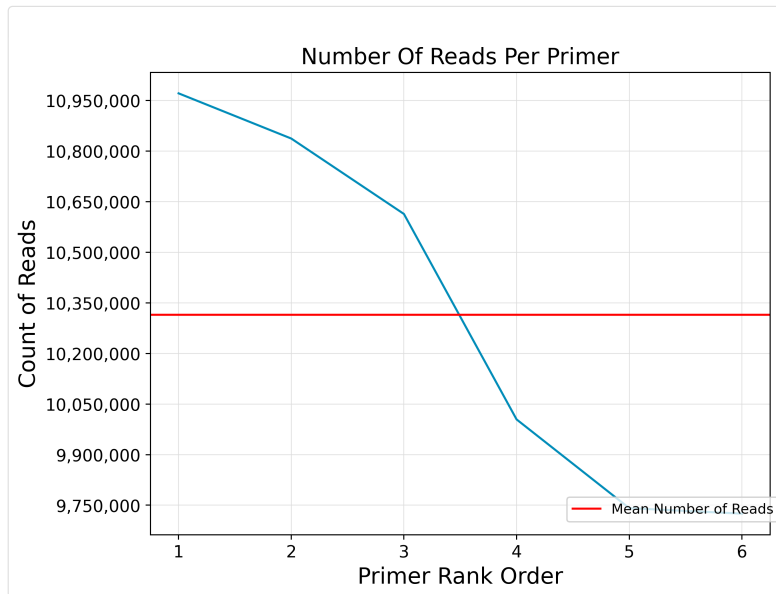
Value	Analysis Metric
63,611,648	Reads
61,892,704	Reads with 5' and 3' Primers
61,801,961	Non-Concatamer Reads with 5' and 3' Primers
61,750,312	Non-Concatamer Reads with 5' and 3' Primers and Poly-A Tail (FLNC Reads)
1,638	Mean Length of FLNC Reads
6	Unique Primers
10,315,450	Mean Reads per Primer
10,971,293	Max. Reads per Primer
9,724,898	Min. Reads per Primer
1,718,944	Reads without Primers

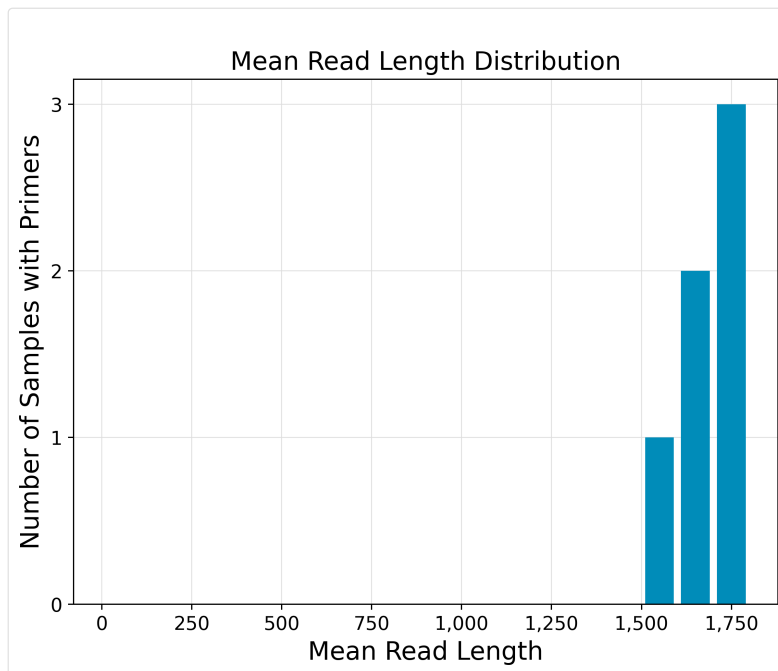
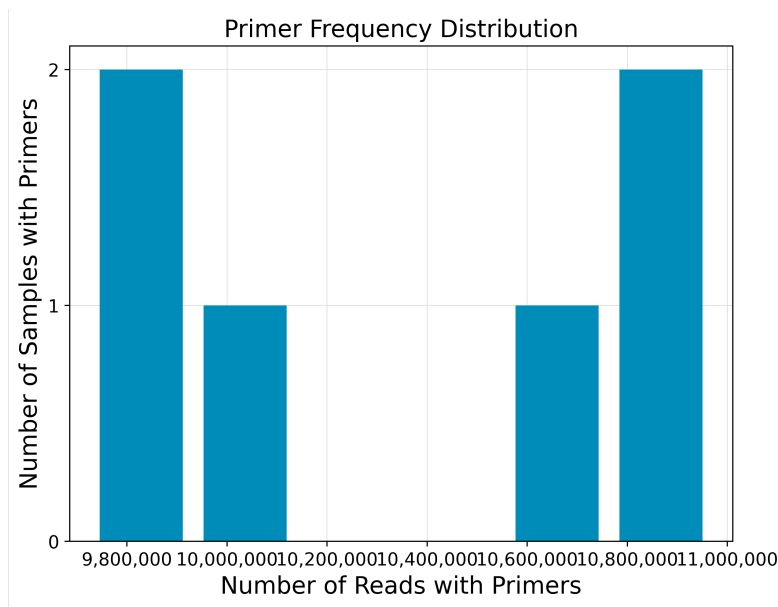
Value	Analysis Metric
96.86%	Percent Bases in Reads with Primers
97.29%	Percent Reads with Primers

## Primer Data

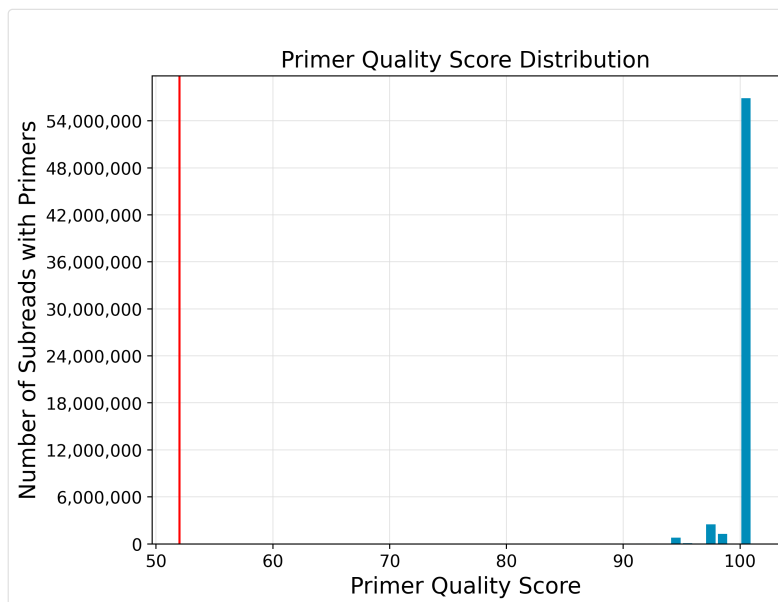
Bio Sample Name	Primer Name	CCS Reads	Mean Primer Quality	Reads with 5' and 3' Primers	Non-Concatamer Reads with 5' and 3' Primers
BioSample_1	IsoSeqX_bc0...	10,837,278	99.7	10,837,278	10,826,932
BioSample_2	IsoSeqX_bc0...	10,971,293	99.7	10,971,293	10,953,670
BioSample_3	IsoSeqX_bc0...	10,004,352	99.7	10,004,352	9,987,358
BioSample_4	IsoSeqX_bc0...	9,741,274	99.7	9,741,274	9,726,755
BioSample_5	IsoSeqX_bc0...	9,724,898	99.7	9,724,898	9,709,743
BioSample_6	IsoSeqX_bc0...	10,613,609	99.7	10,613,609	10,597,503
UNASSIGNED	No Primer	1,718,944	0.0	0	0

## Primer Read Statistics

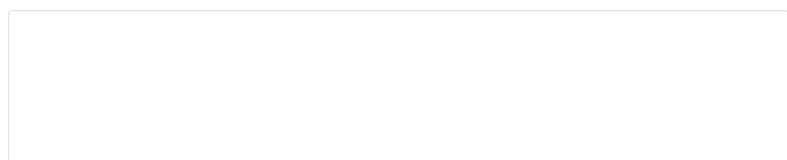
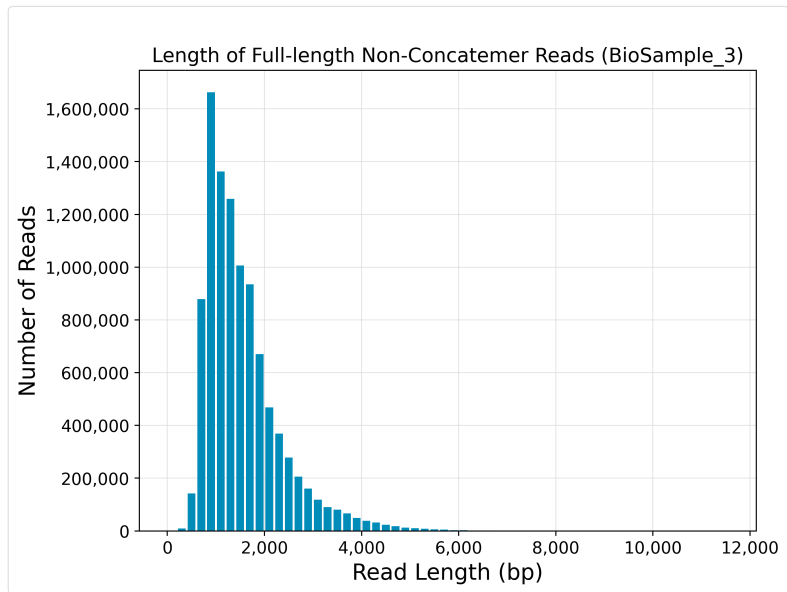
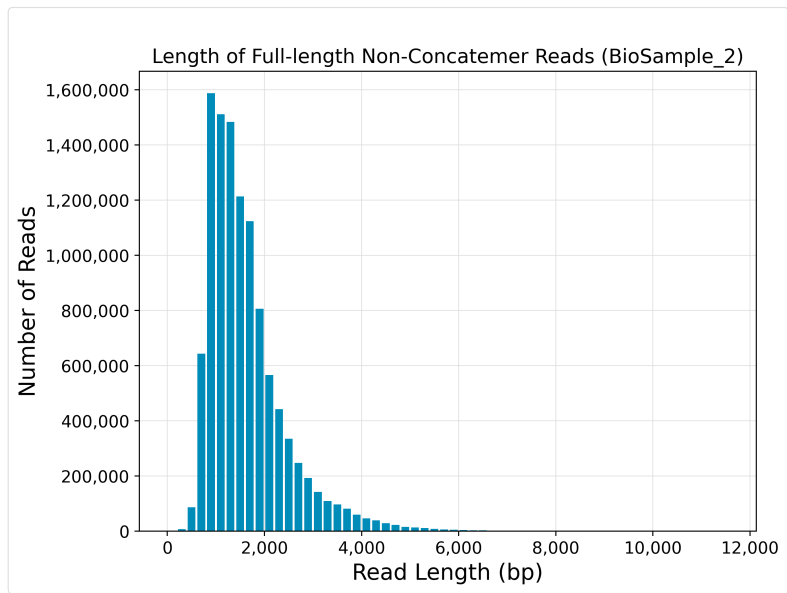
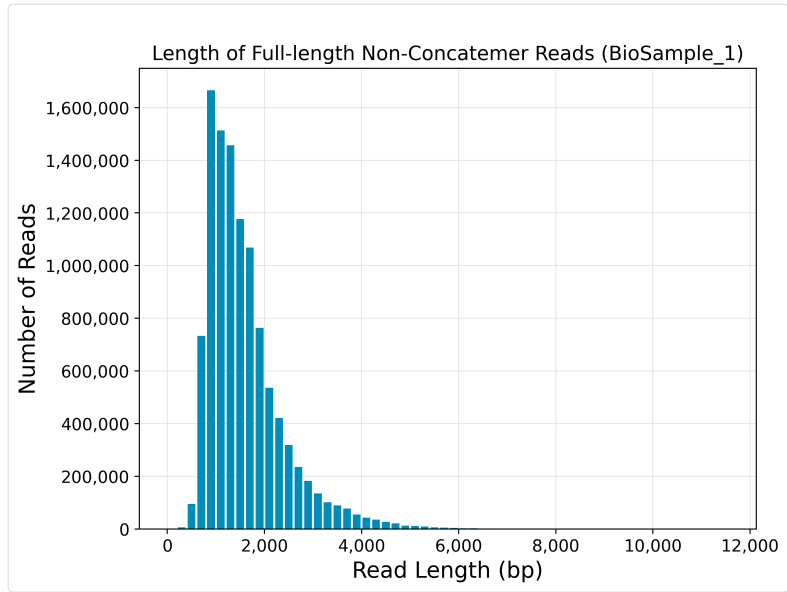




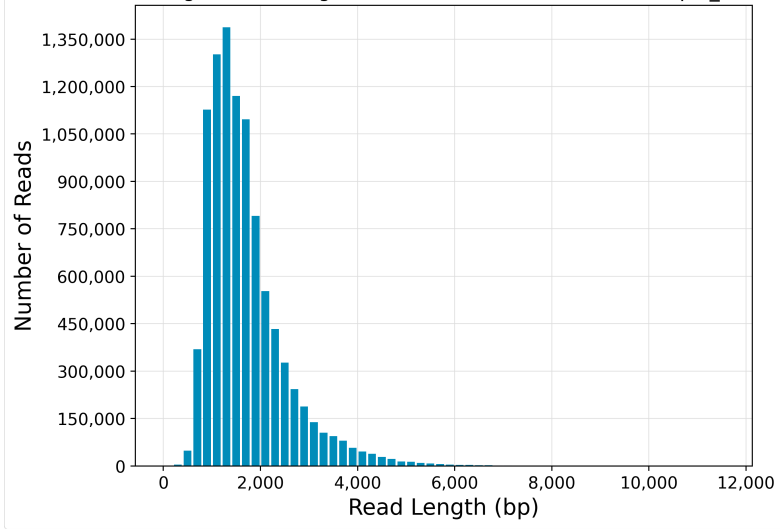
## Primer Quality Scores



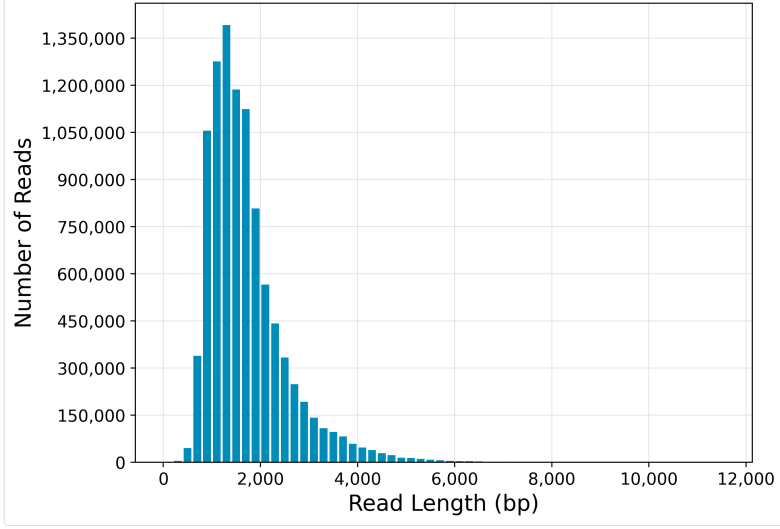
# Length of Full-length Non-Concatemer Reads



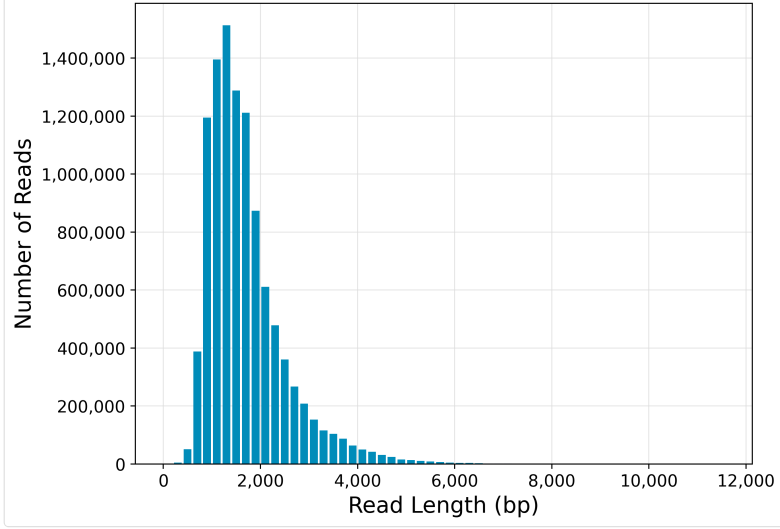
Length of Full-length Non-Concatemer Reads (BioSample\_4)



Length of Full-length Non-Concatemer Reads (BioSample\_5)



Length of Full-length Non-Concatemer Reads (BioSample\_6)



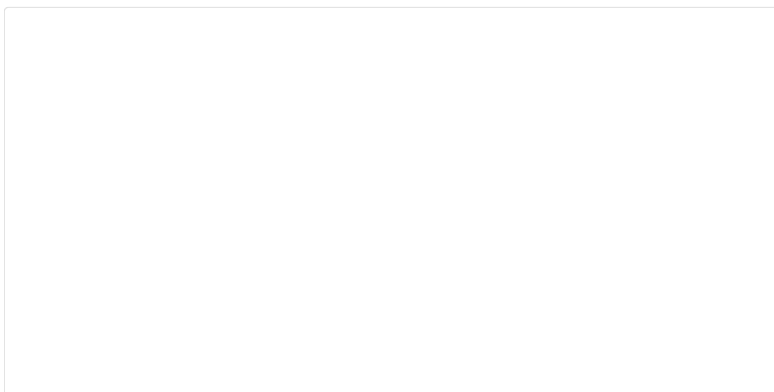
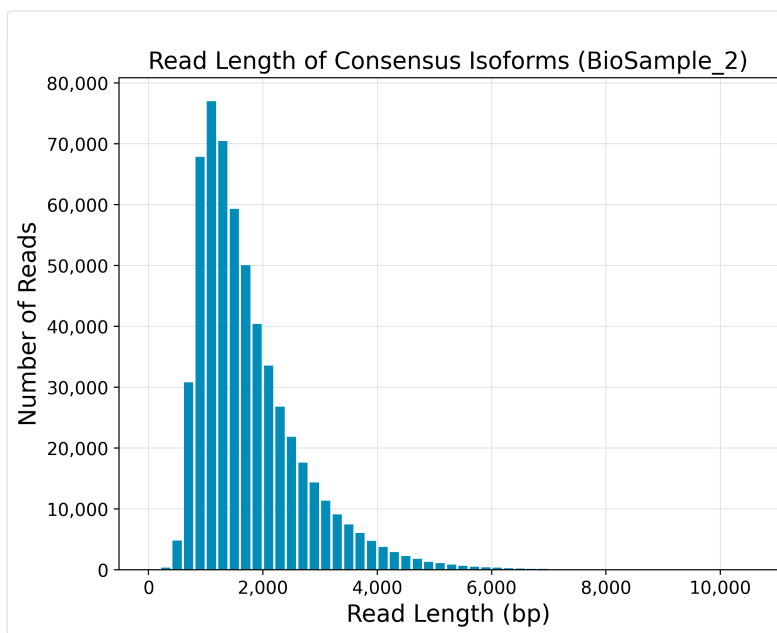
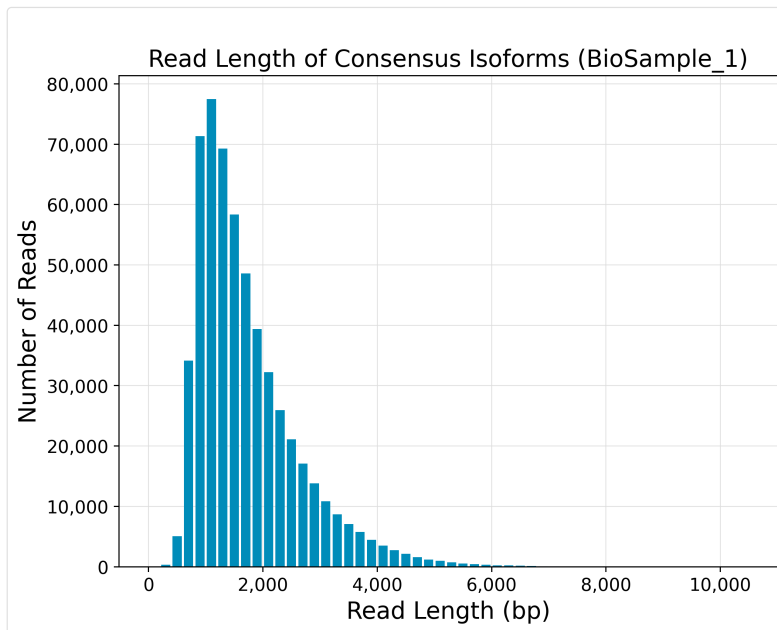
## Summary Metrics

Sample Name ⌵

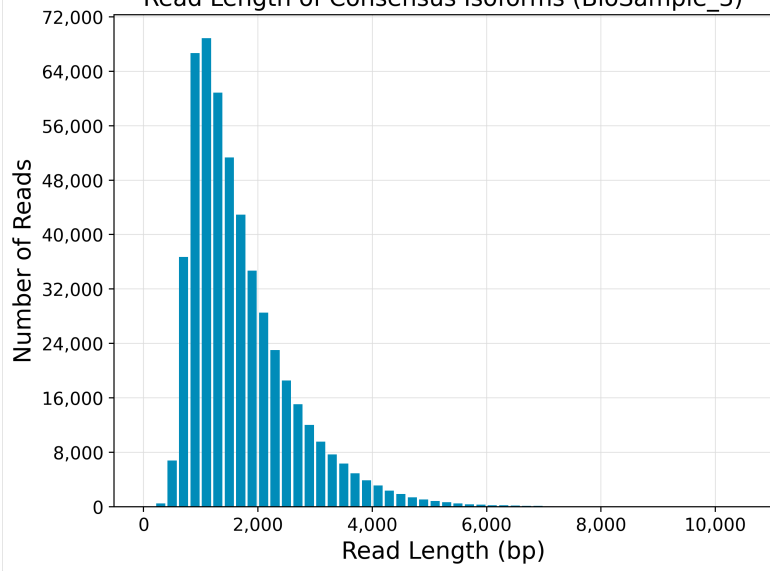
Number of High-Quality Isoforms ⌵


### Length of Consensus Isoforms

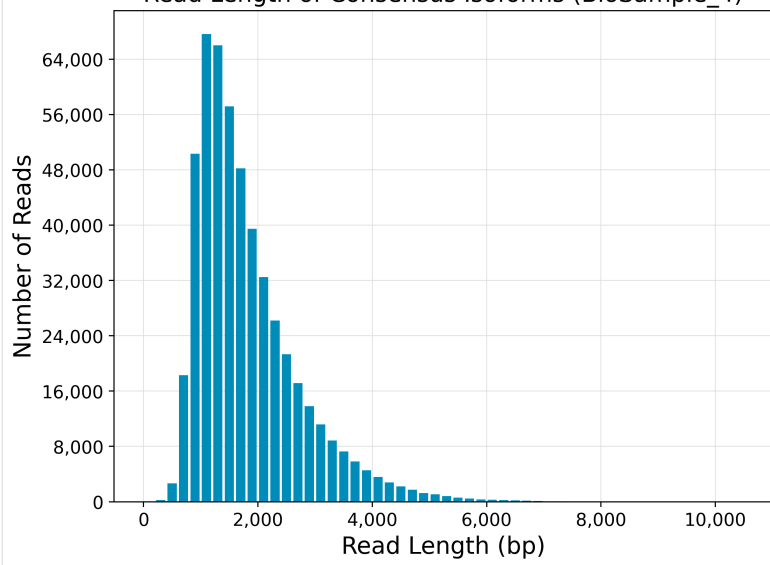
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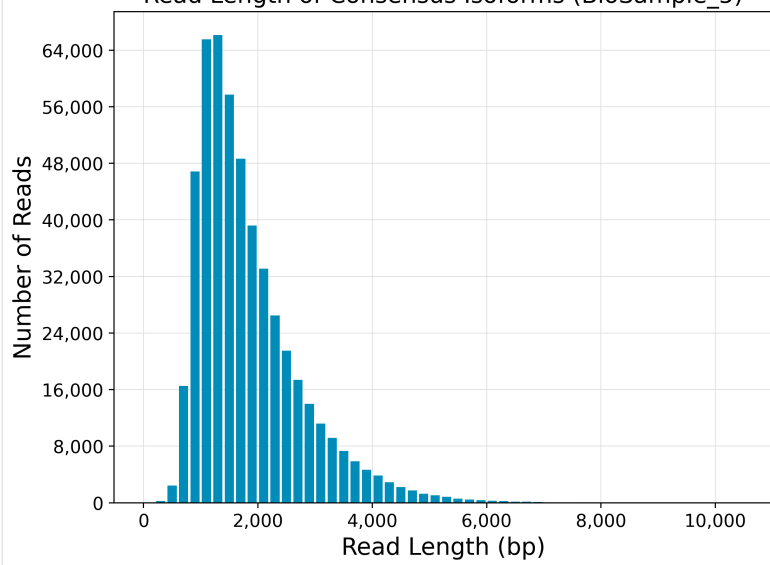
Read Length of Consensus Isoforms (BioSample\_3)

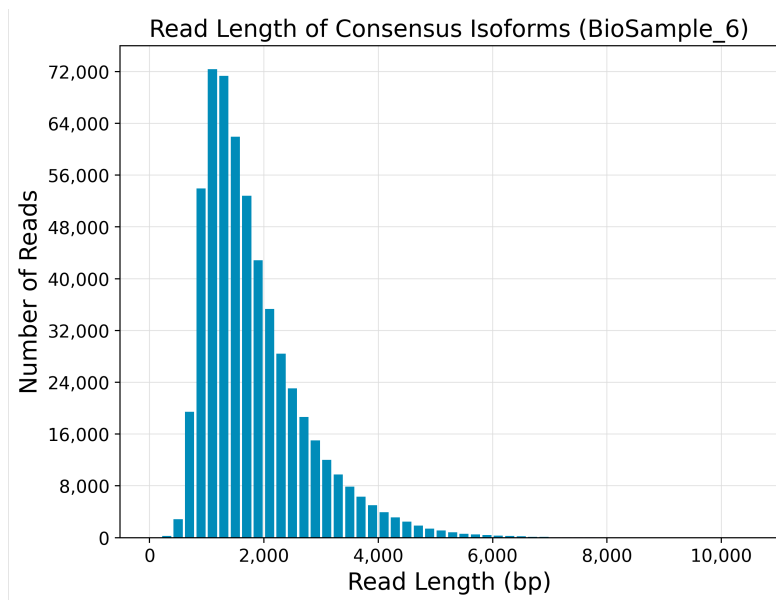


Read Length of Consensus Isoforms (BioSample\_4)



Read Length of Consensus Isoforms (BioSample\_5)





## Classification Summary Metrics

Sample Name	Genes	Genes, filtered	Known Genes, filtered	Isoforms	Isoforms, filtered	Known isoforms, filtered
BioSample_1	117,695	18,407	17,446	273,104	106,190	46,640
BioSample_2	115,810	18,513	17,576	273,656	107,319	46,798
BioSample_3	101,625	17,858	17,087	242,574	97,866	45,188
BioSample_4	99,422	17,824	17,099	244,342	101,472	45,052
BioSample_5	98,165	17,627	16,910	242,387	100,588	44,497
BioSample_6	111,094	18,286	17,382	268,729	108,345	46,297

## Transcript Classification (BioSample\_1)

Category	Count	CAGE Detected	CAGE Detected (%)	polyA Motif Detected
FSM	84627	49637	58.65%	39985
ISM	193712	20882	10.77%	107435
NIC	38893	28781	74.00%	18301
NNC	42948	26045	60.64%	20242
Antisense	6777	407	6.00%	2209
Fusion	1021	604	59.15%	509
More junctions	21	14	66.66%	8
Genic intron	184	0	0.00%	47
Genic genomic	35585	5829	16.38%	13340
Intergenic	93328	405	0.43%	31115

## Transcript Classification (BioSample\_2)



Category	Count	CAGE Detected	CAGE Detected (%)	polyA Motif Detected
FSM	86197	51444	59.68%	40521
ISM	194599	21476	11.03%	107299
NIC	40111	29985	74.75%	18853
NNC	44026	27122	61.60%	20601
Antisense	6820	402	5.89%	2154
Fusion	1015	631	62.16%	486
More junctions	18	11	61.11%	6
Genic intron	170	0	0.00%	36
Genic genomic	35858	6260	17.45%	13432
Intergenic	91251	484	0.53%	30331

### Transcript Classification (BioSample\_3)

Category	Count	CAGE Detected	CAGE Detected (%)	polyA Motif Detected
FSM	79738	48251	60.51%	37220
ISM	177941	20533	11.53%	97286
NIC	34733	26203	75.44%	16287
NNC	39156	24493	62.55%	18247
Antisense	5998	384	6.40%	1778
Fusion	913	529	57.94%	426
More junctions	16	9	56.25%	7
Genic intron	120	0	0.00%	29
Genic genomic	30759	5778	18.78%	11450
Intergenic	78046	429	0.54%	25560

### Transcript Classification (BioSample\_4)

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Category	Count	CAGE Detected	CAGE Detected (%)	polyA Motif Detected
FSM	81520	49037	60.15%	38572
ISM	180218	19743	10.95%	100245
NIC	37944	28263	74.48%	17972
NNC	39837	24525	61.56%	18741
Antisense	5841	339	5.80%	1872
Fusion	905	540	59.66%	438
More junctions	18	10	55.55%	11
Genic intron	155	2	1.29%	39
Genic genomic	31519	5601	17.77%	11880
Intergenic	75915	358	0.47%	25387

### Transcript Classification (BioSample\_5)

Category	Count	CAGE Detected	CAGE Detected (%)	polyA Motif Detected
FSM	81241	49447	60.86%	38408
ISM	177593	19784	11.14%	99157
NIC	37916	28510	75.19%	18003
NNC	39404	24552	62.30%	18764
Antisense	5842	329	5.63%	1834
Fusion	889	537	60.40%	434
More junctions	17	11	64.70%	6
Genic intron	128	0	0.00%	31
Genic genomic	31786	5703	17.94%	12183
Intergenic	74836	373	0.49%	25195

### Transcript Classification (BioSample\_6)

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Category	Count	CAGE Detected	CAGE Detected (%)	polyA Motif Detected
FSM	85100	50885	59.79%	40006
ISM	189778	20791	10.95%	105426
NIC	41270	30786	74.59%	19528
NNC	43937	27143	61.77%	20731
Antisense	6611	375	5.67%	2061
Fusion	1049	658	62.72%	504
More junctions	21	10	47.61%	10
Genic intron	133	1	0.75%	29
Genic genomic	35322	6049	17.12%	13298
Intergenic	86847	438	0.50%	29224

### Transcript Classification, filtered (BioSample\_1)

Category	Count	CAGE Detected	CAGE Detected, (%)	polyA Detected
FSM	75699	44140	58.30%	39985
ISM	97262	12239	12.58%	59240
NIC	34930	25798	73.85%	17857
NNC	22632	14970	66.14%	12117
Antisense	397	97	24.43%	254
Fusion	645	410	63.56%	369
More junctions	16	12	75.00%	7
Genic intron	0	0	0.00%	0
Genic genomic	258	127	49.22%	134
Intergenic	672	70	10.41%	516

### Transcript Classification, filtered (BioSample\_2)

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Category	Count	CAGE Detected	CAGE Detected, (%)	polyA Detected
FSM	76873	45638	59.36%	40521
ISM	97528	12685	13.00%	59020
NIC	35915	26802	74.62%	18383
NNC	22651	15237	67.26%	11991
Antisense	334	96	28.74%	211
Fusion	640	424	66.25%	361
More junctions	16	10	62.50%	6
Genic intron	0	0	0.00%	0
Genic genomic	283	145	51.23%	150
Intergenic	682	109	15.98%	491

### Transcript Classification, filtered (BioSample\_3)

Category	Count	CAGE Detected	CAGE Detected, (%)	polyA Detected
FSM	71046	42757	60.18%	37220
ISM	88982	11991	13.47%	53588
NIC	31028	23420	75.48%	15866
NNC	19978	13487	67.50%	10552
Antisense	318	85	26.72%	184
Fusion	577	359	62.21%	307
More junctions	8	5	62.50%	6
Genic intron	0	0	0.00%	0
Genic genomic	237	119	50.21%	115
Intergenic	532	77	14.47%	392

### Transcript Classification, filtered (BioSample\_4)

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Category	Count	CAGE Detected	CAGE Detected, (%)	polyA Detected
FSM	72904	43580	59.77%	38572
ISM	92191	11721	12.71%	56039
NIC	34022	25321	74.42%	17492
NNC	20771	13918	67.00%	10902
Antisense	274	70	25.54%	186
Fusion	579	369	63.73%	323
More junctions	13	8	61.53%	11
Genic intron	0	0	0.00%	0
Genic genomic	245	128	52.24%	118
Intergenic	516	62	12.01%	384

### Transcript Classification, filtered (BioSample\_5)

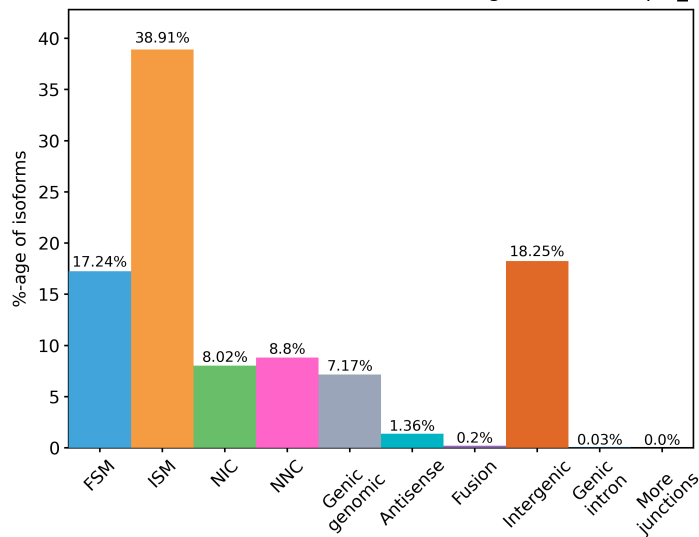
Category	Count	CAGE Detected	CAGE Detected, (%)	polyA Detected
FSM	72791	44048	60.51%	38408
ISM	90703	11699	12.89%	55443
NIC	34003	25554	75.15%	17520
NNC	20515	13980	68.14%	10946
Antisense	270	78	28.88%	162
Fusion	574	361	62.89%	331
More junctions	8	6	75.00%	5
Genic intron	0	0	0.00%	0
Genic genomic	211	115	54.50%	111
Intergenic	510	67	13.13%	381

### Transcript Classification, filtered (BioSample\_6)

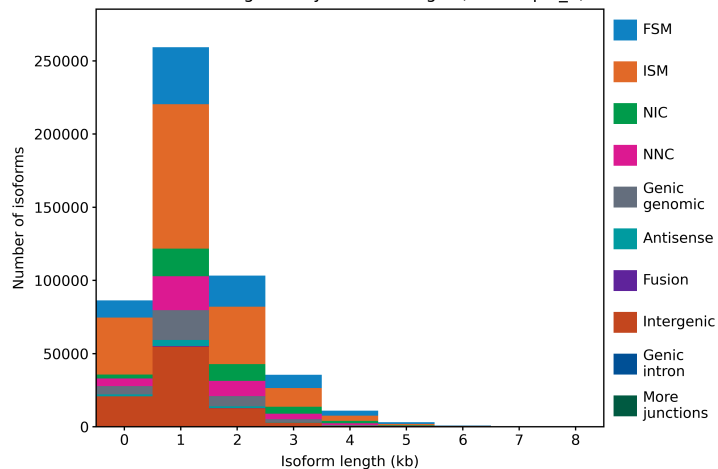
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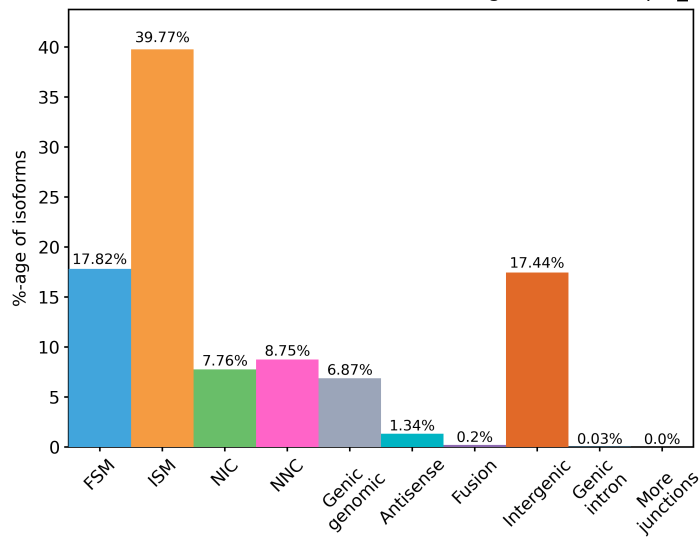
Isoform distribution across structural categories (BioSample\_2)



Structural categories by isoform length (BioSample\_2)



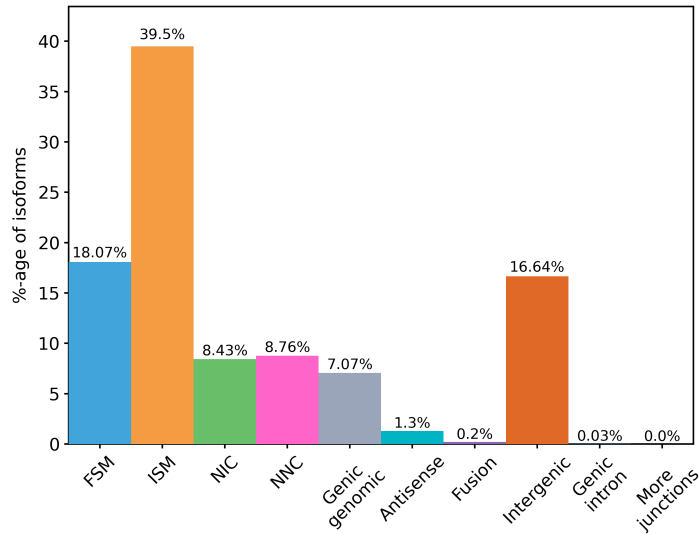
Isoform distribution across structural categories (BioSample\_3)



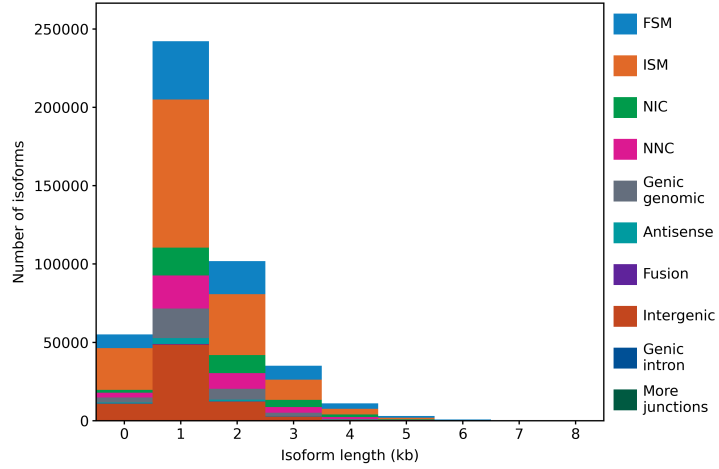




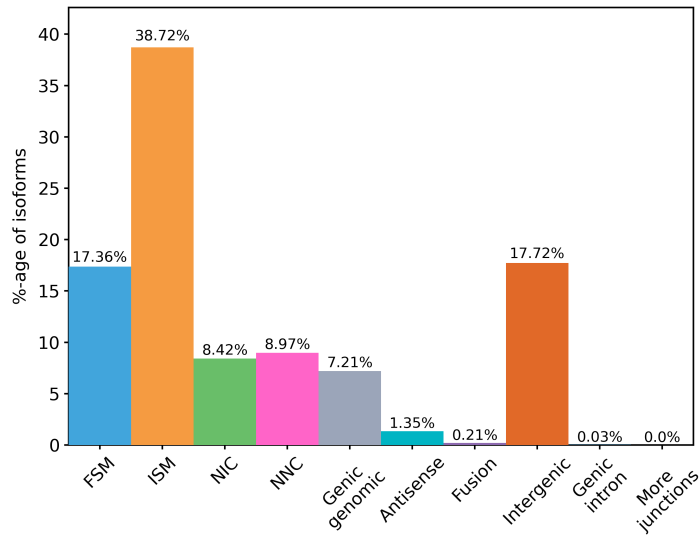
Isoform distribution across structural categories (BioSample\_5)



Structural categories by isoform length (BioSample\_5)

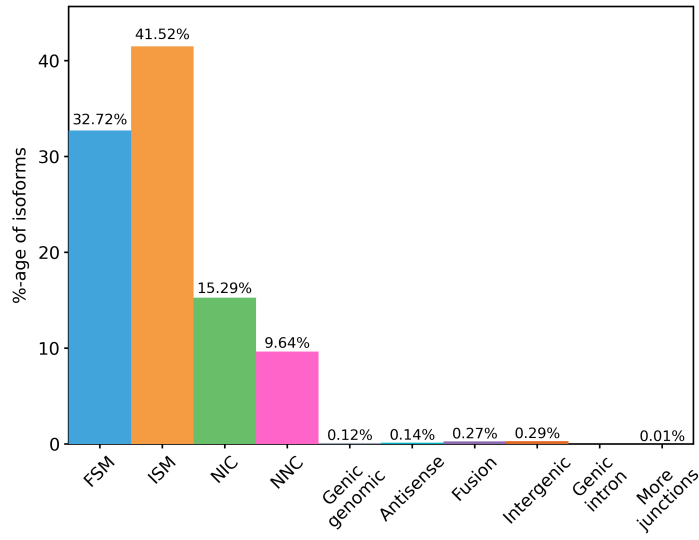


Isoform distribution across structural categories (BioSample\_6)

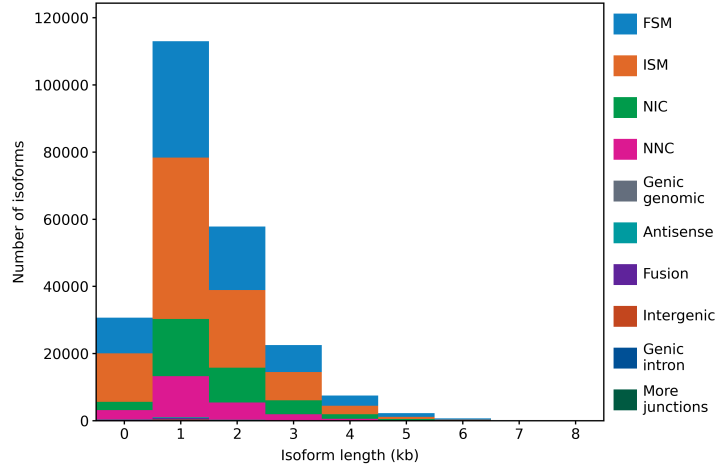




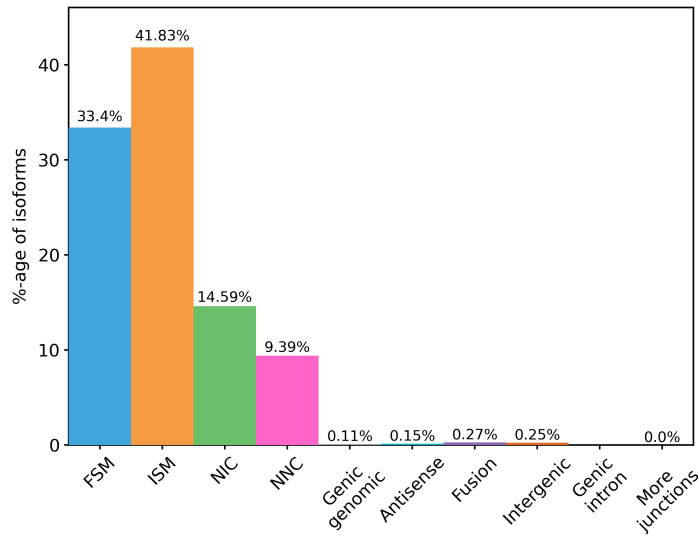
Isoform distribution across structural categories (BioSample\_2)



Structural categories by isoform length (BioSample\_2)

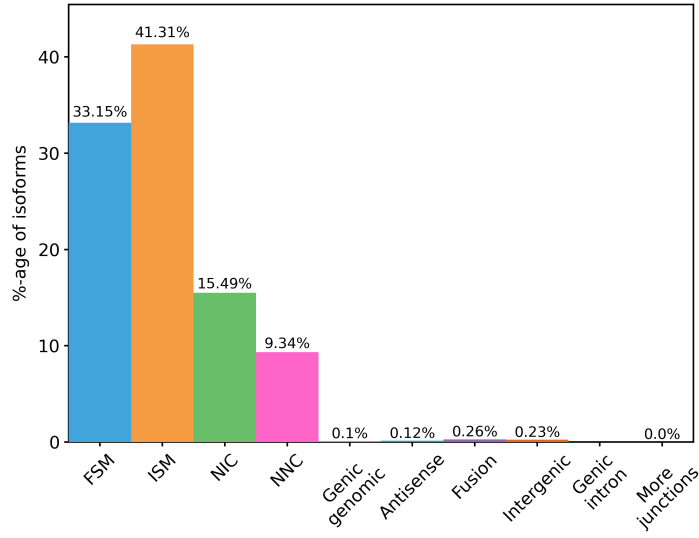


Isoform distribution across structural categories (BioSample\_3)

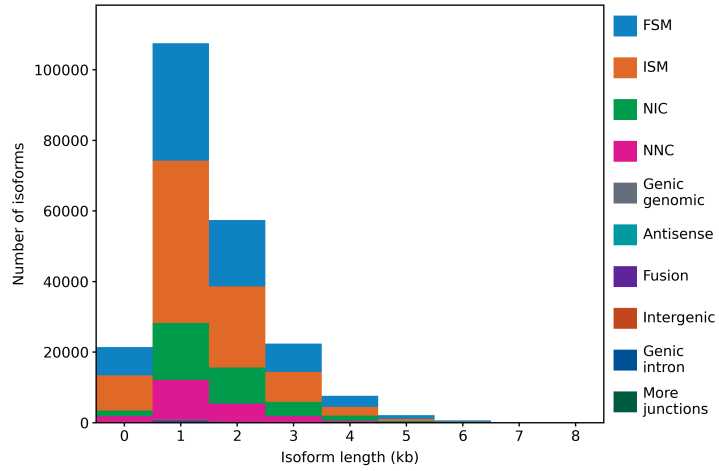




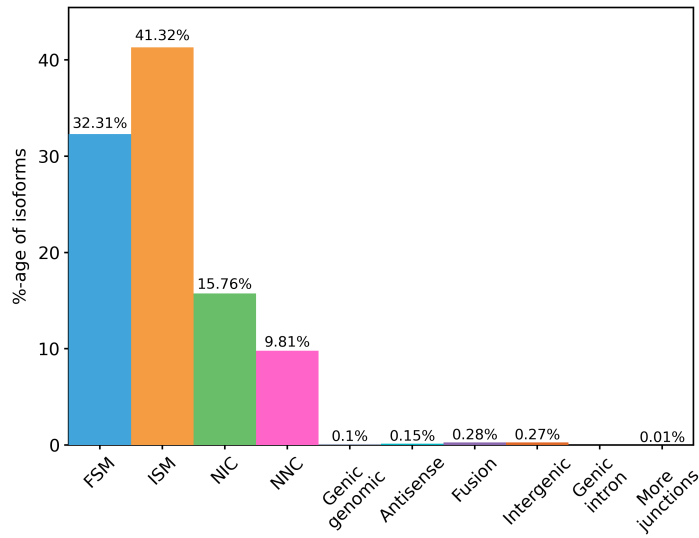
Isoform distribution across structural categories (BioSample\_5)

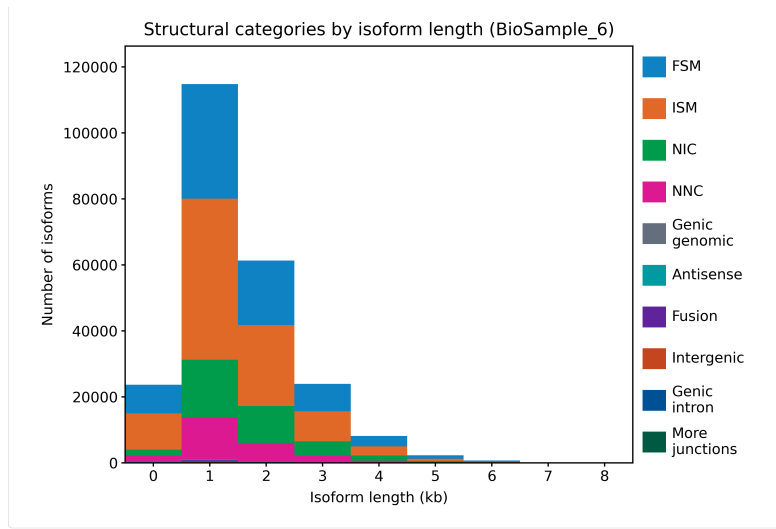


Structural categories by isoform length (BioSample\_5)

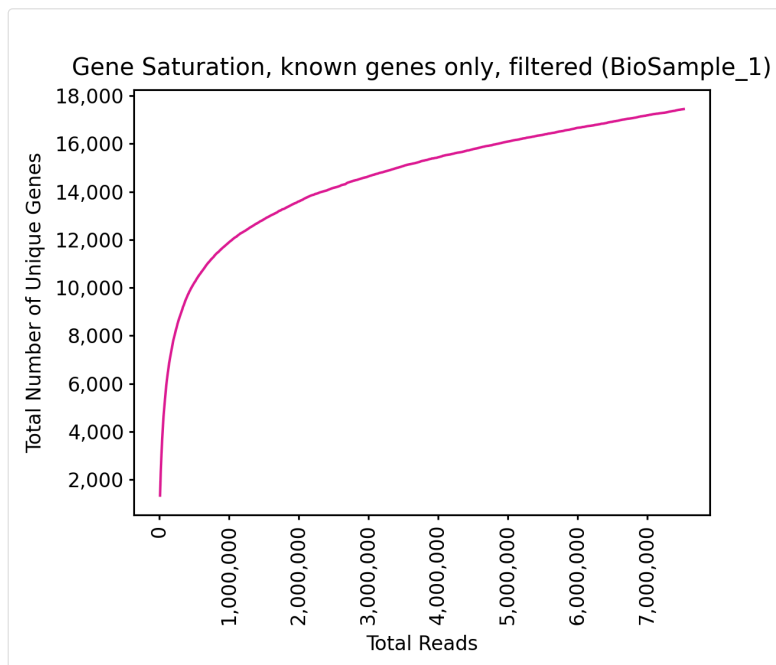


Isoform distribution across structural categories (BioSample\_6)

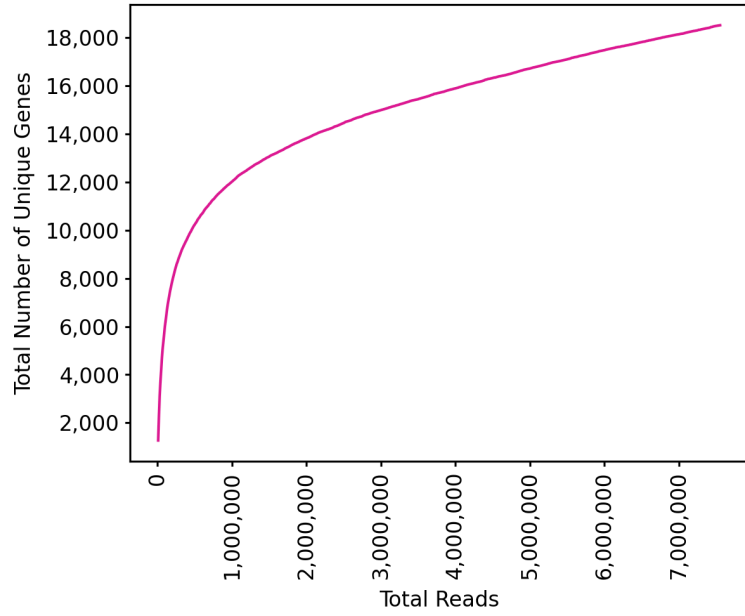




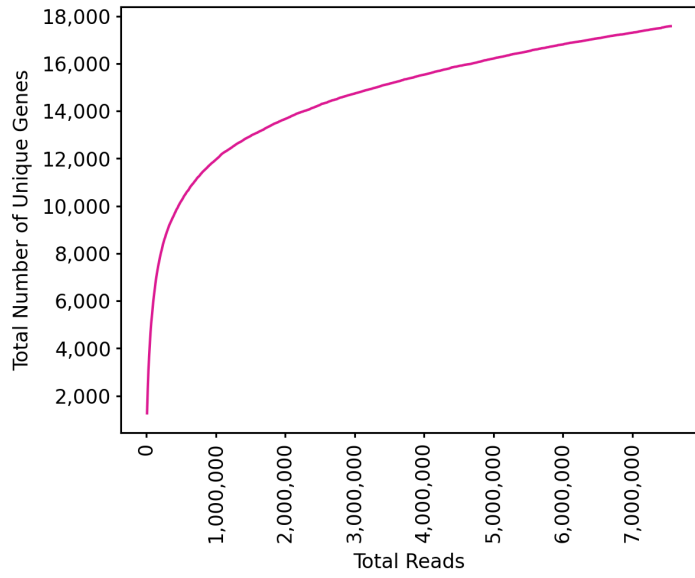
## Gene Saturation



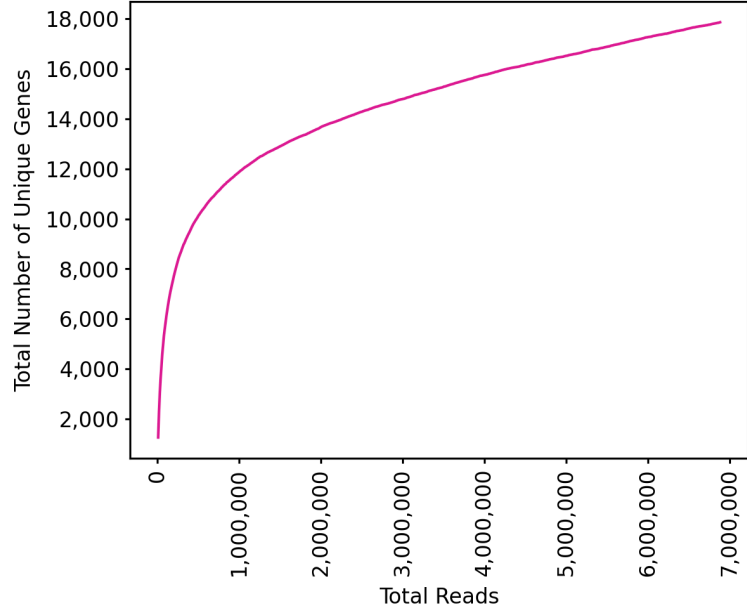
Gene Saturation, all genes, filtered (BioSample\_2)



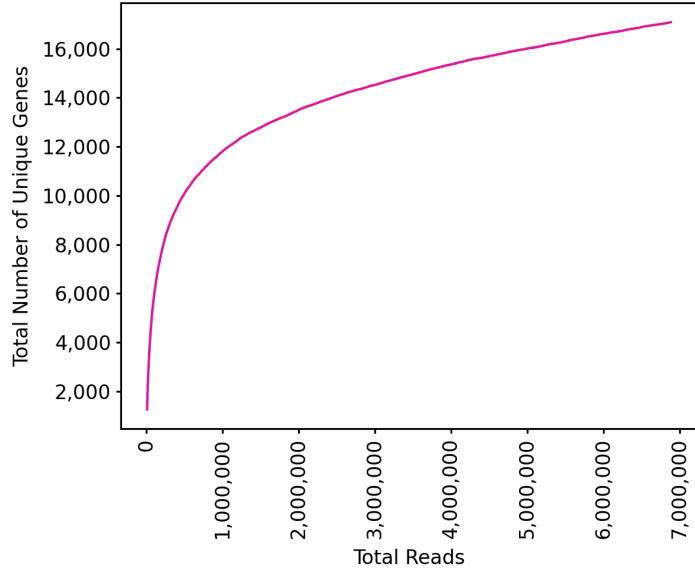
Gene Saturation, known genes only, filtered (BioSample\_2)



Gene Saturation, all genes, filtered (BioSample\_3)

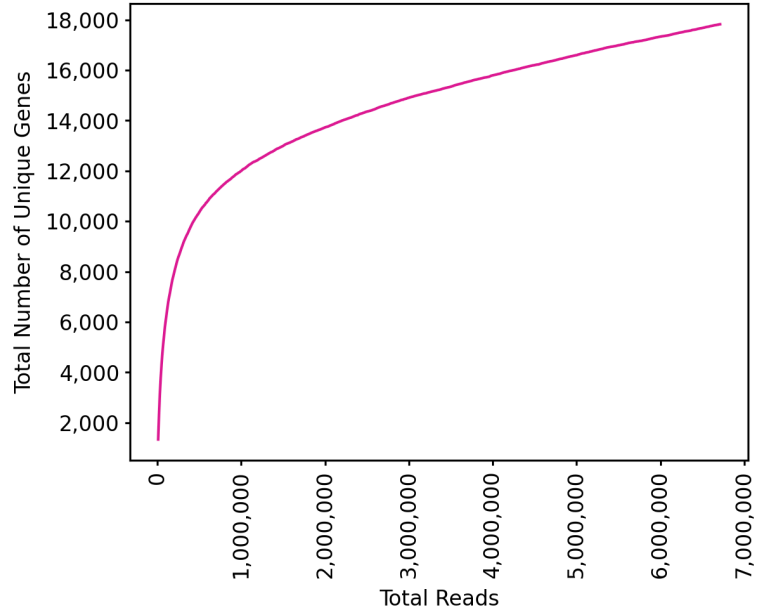


Gene Saturation, known genes only, filtered (BioSample\_3)

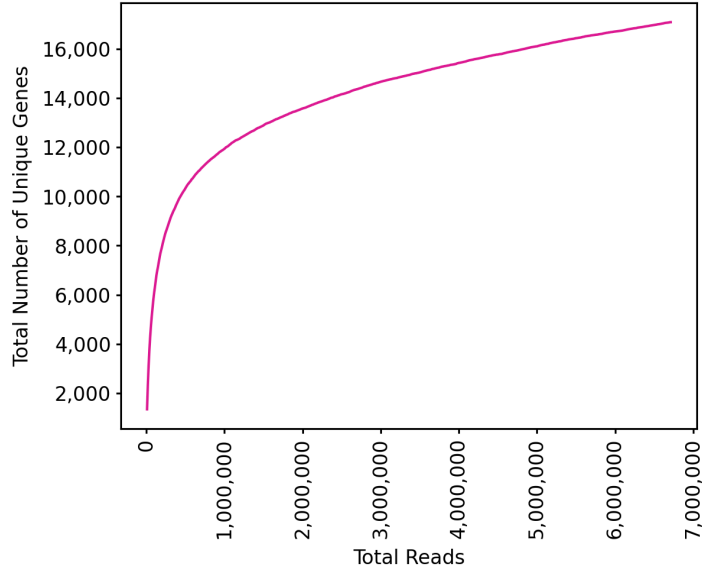




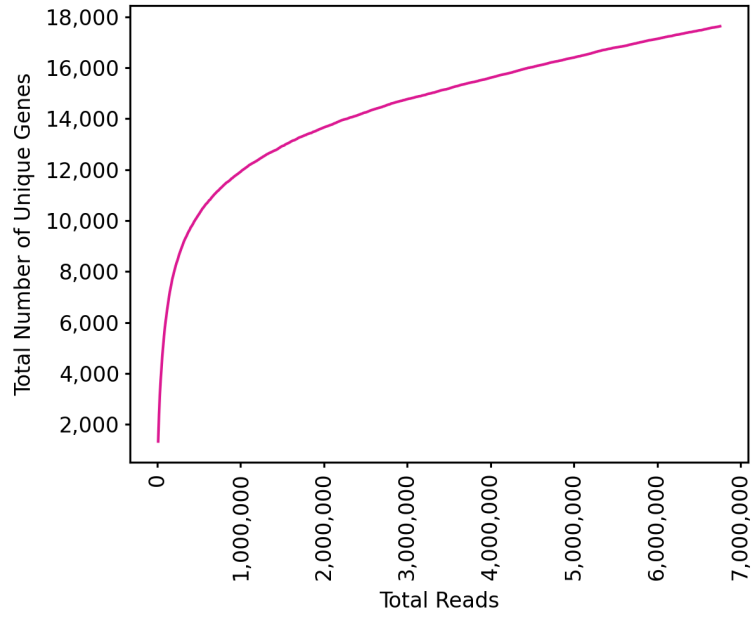
Gene Saturation, all genes, filtered (BioSample\_4)



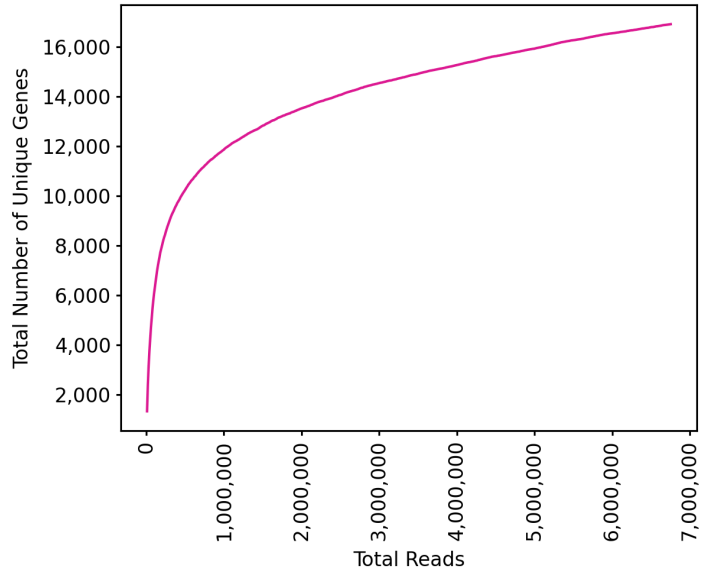
Gene Saturation, known genes only, filtered (BioSample\_4)



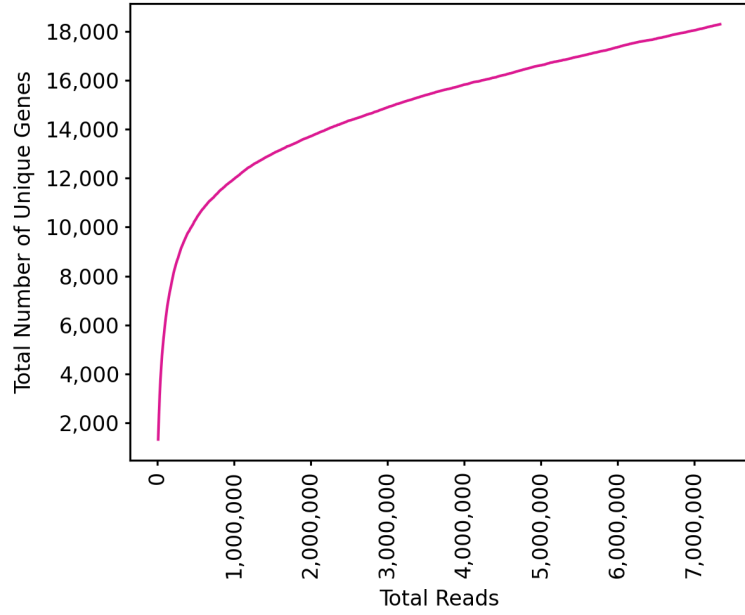
Gene Saturation, all genes, filtered (BioSample\_5)



Gene Saturation, known genes only, filtered (BioSample\_5)



Gene Saturation, all genes, filtered (BioSample\_6)



Gene Saturation, known genes only, filtered (BioSample\_6)

