

KinnexRelease-UHRR2024-RevioSPRQ

SUCCESSFUL

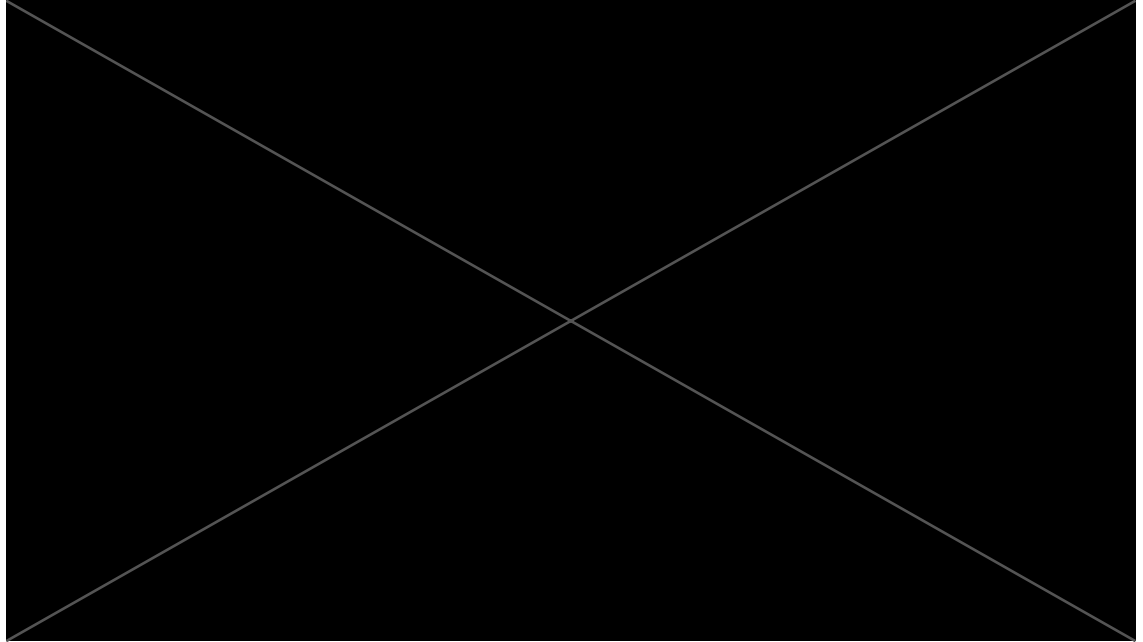
Copy Delete

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

Display All

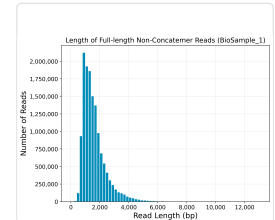
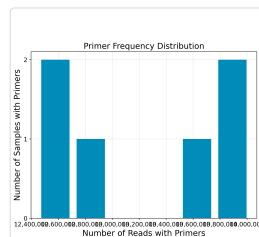
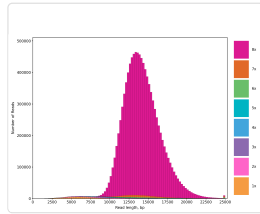
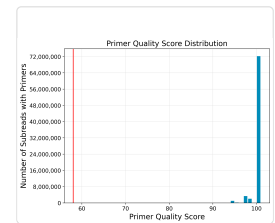
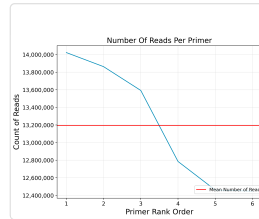
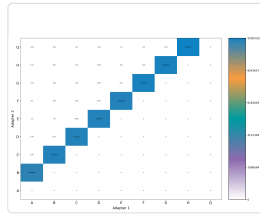
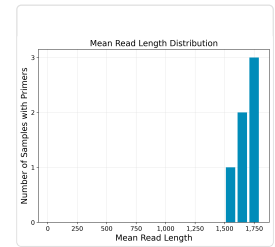
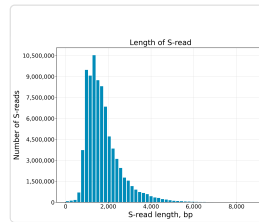
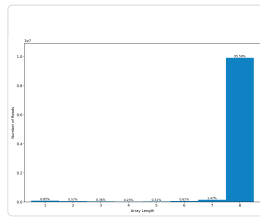
Status

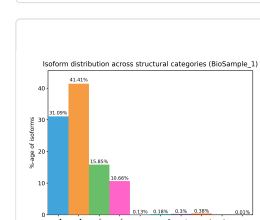
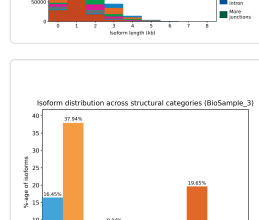
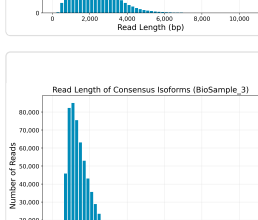
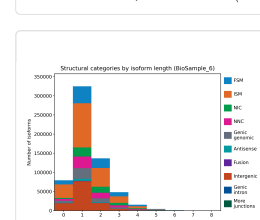
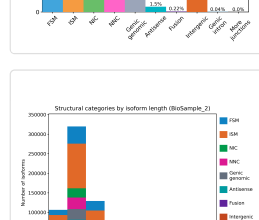
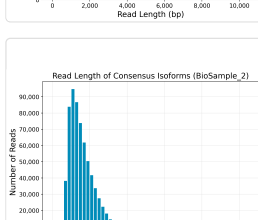
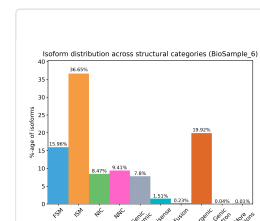
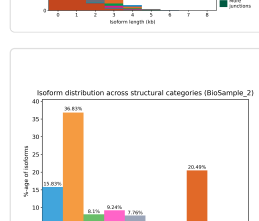
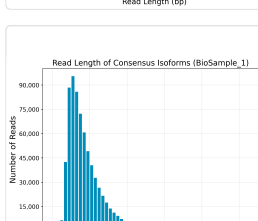
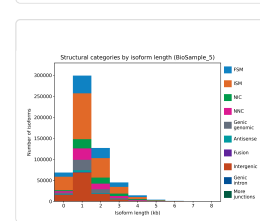
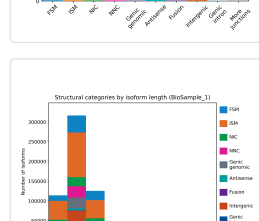
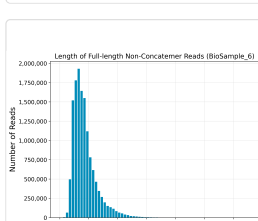
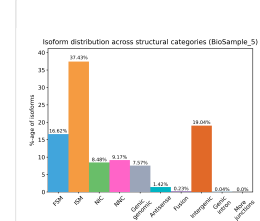
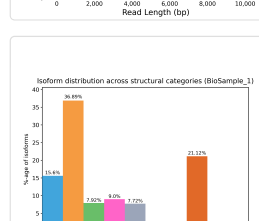
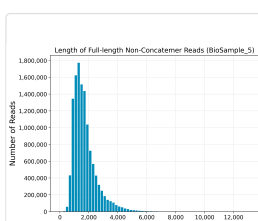
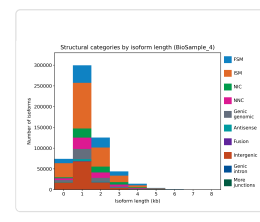
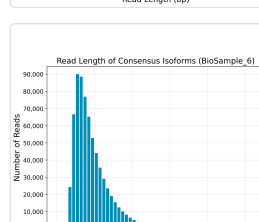
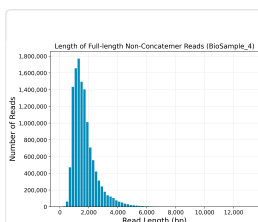
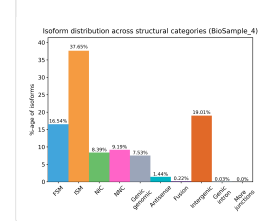
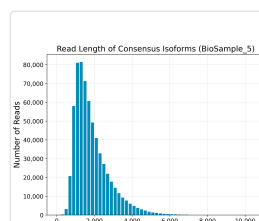
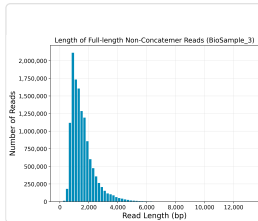
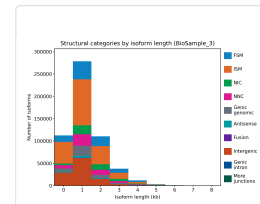
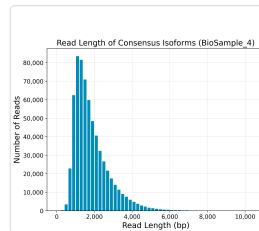
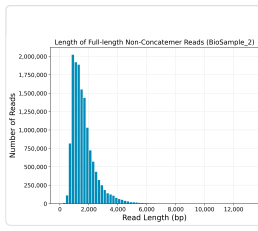
Analysis KinnexRelease-UHRR2024-RevioSPRQ

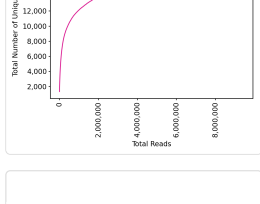
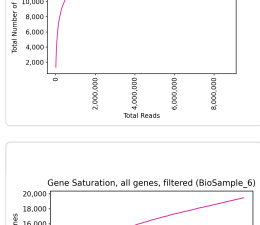
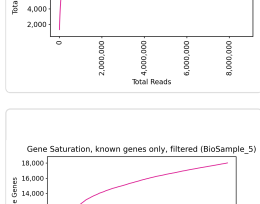
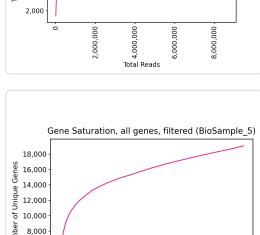
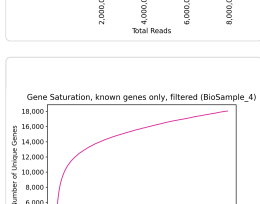
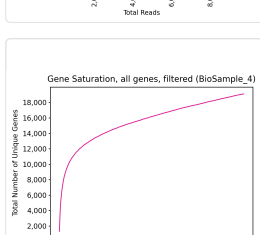
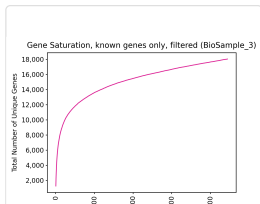
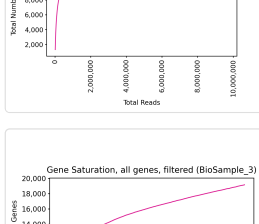
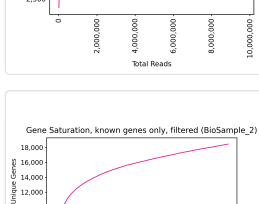
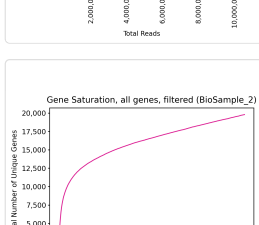
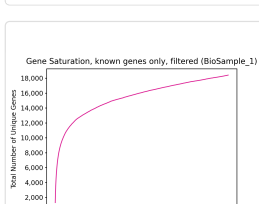
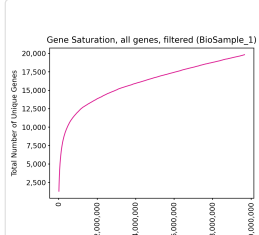
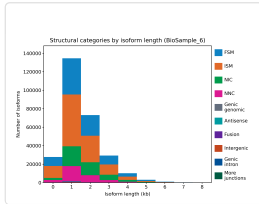
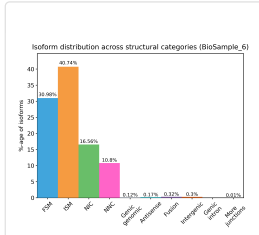
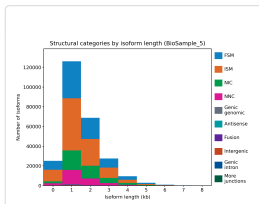
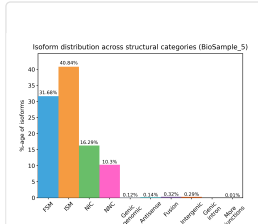
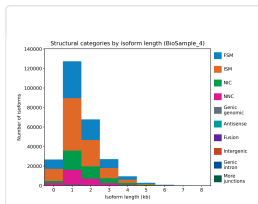
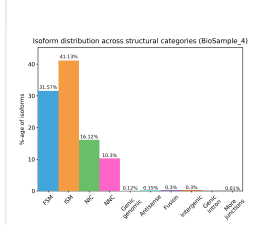
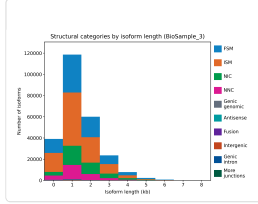
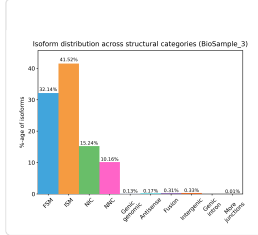
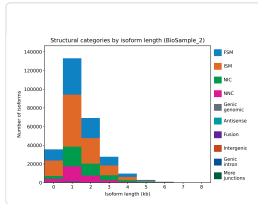
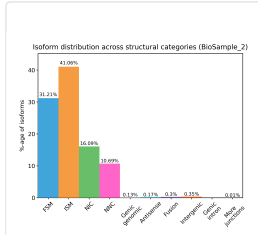
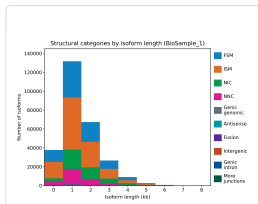


► Analysis Parameters

Thumbnails



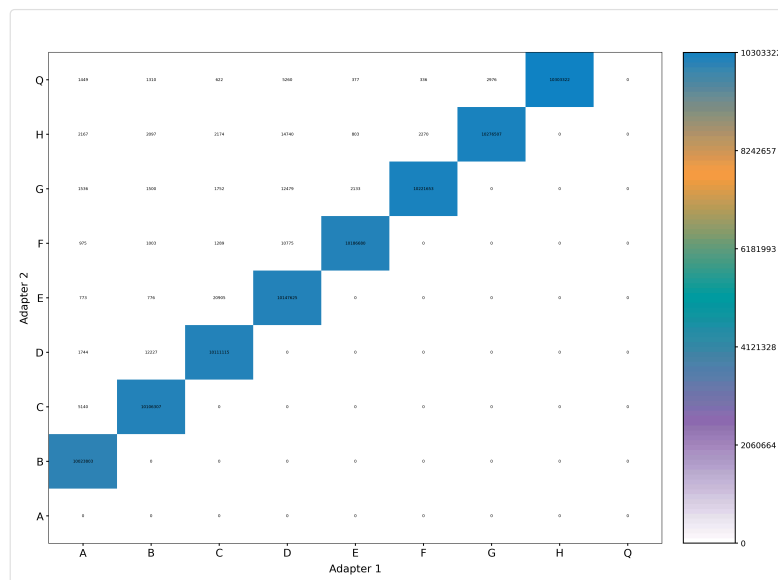
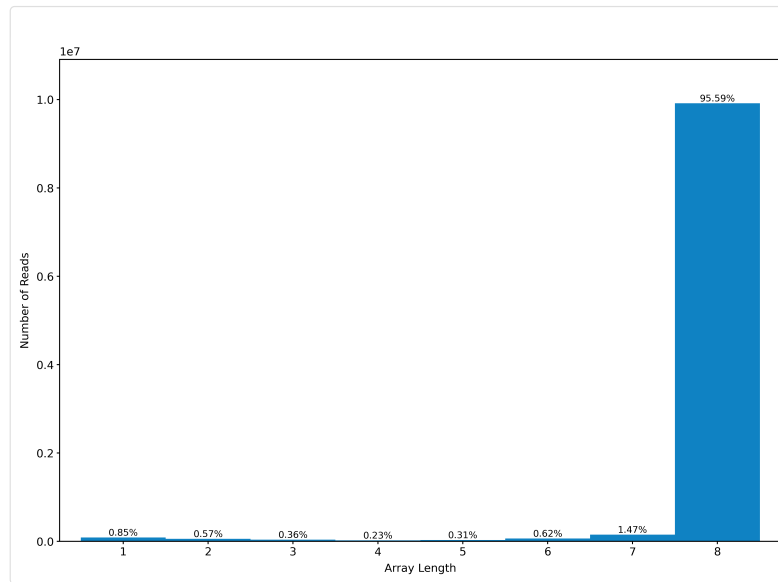




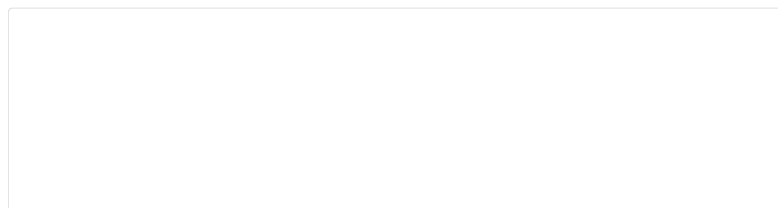
Read Segmentation

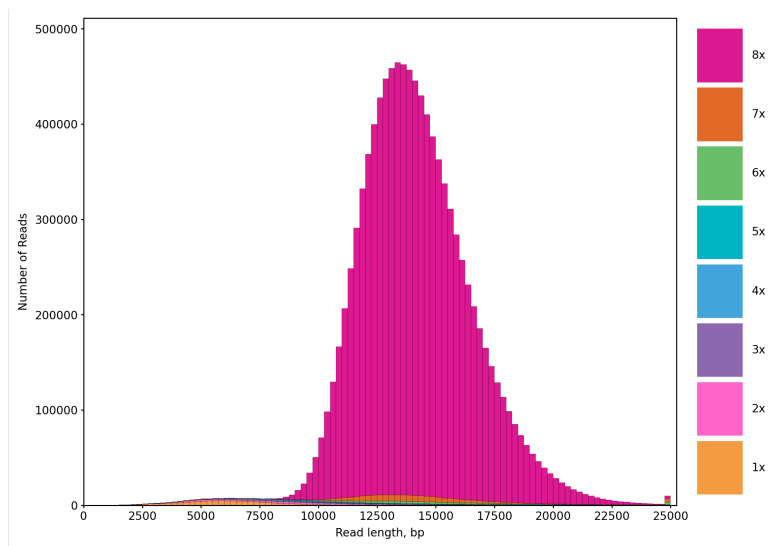
Value	Analysis Metric
10,448,251	Reads
81,377,012	Segmented reads (S-reads)
1,758	Mean length of S-reads
94.93 %	Percent of reads with full arrays
7.79	Mean array size (concatenation factor)

Segmentation Statistics

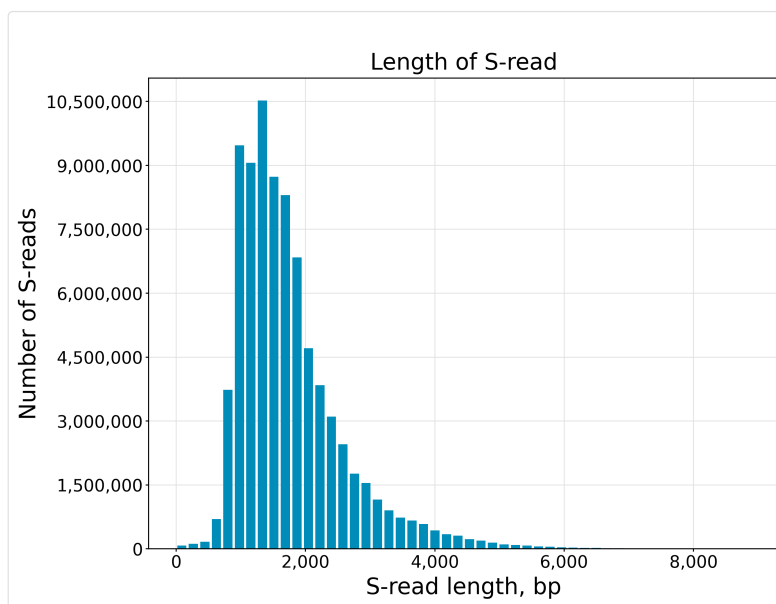


Length of Reads





S-read Length Distribution



Read Classification

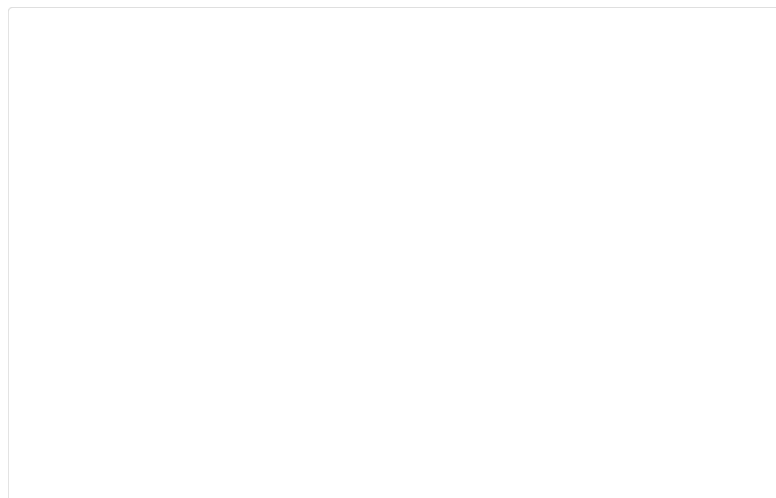
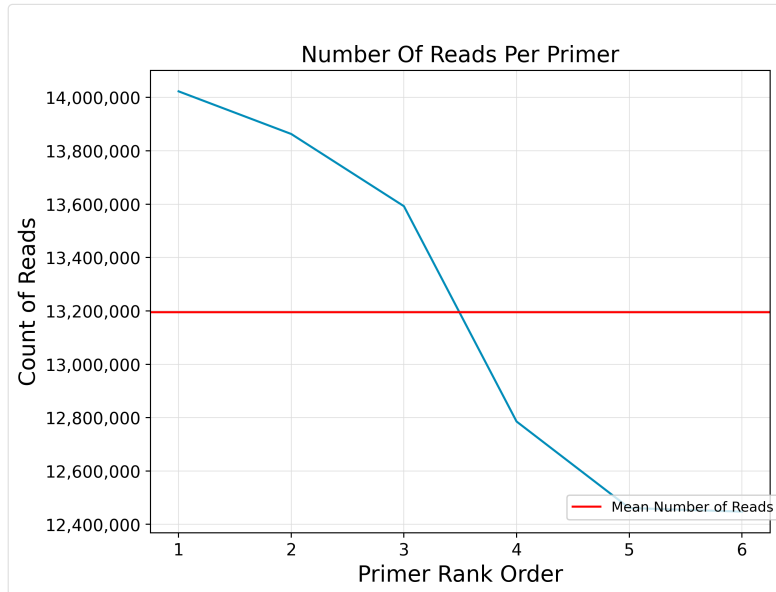
Value	Analysis Metric
81,377,012	Reads
79,172,198	Reads with 5' and 3' Primers
79,056,207	Non-Concatamer Reads with 5' and 3' Primers
78,994,987	Non-Concatamer Reads with 5' and 3' Primers and Poly-A Tail (FLNC Reads)
1,643	Mean Length of FLNC Reads
6	Unique Primers
13,195,366	Mean Reads per Primer
14,022,714	Max. Reads per Primer
12,447,639	Min. Reads per Primer
2,204,814	Reads without Primers

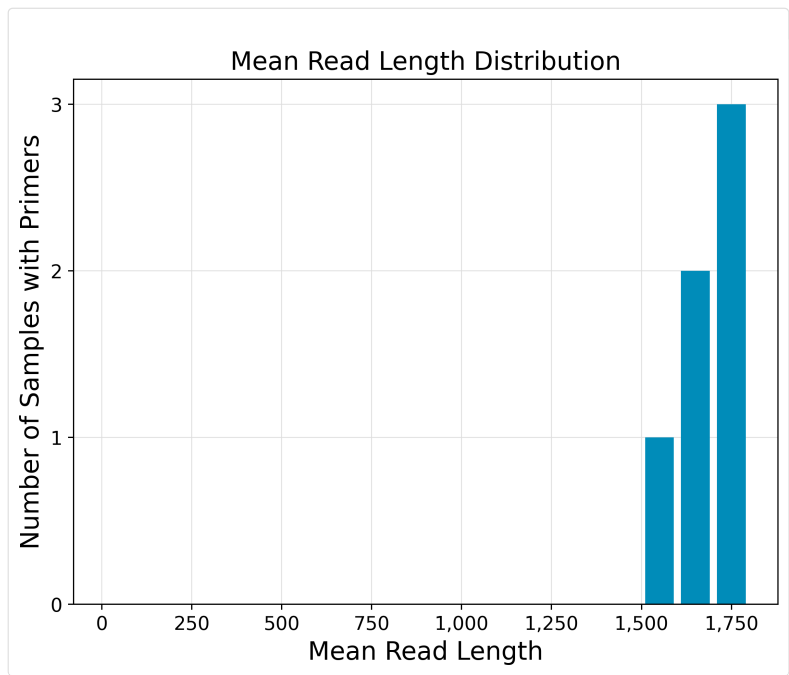
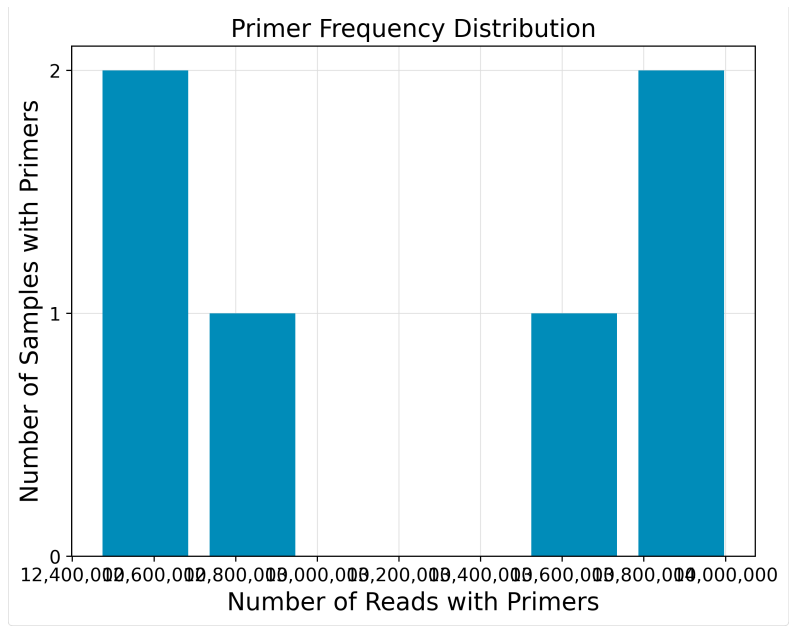
Value	Analysis Metric
96.86%	Percent Bases in Reads with Primers
97.29%	Percent Reads with Primers

Primer Data

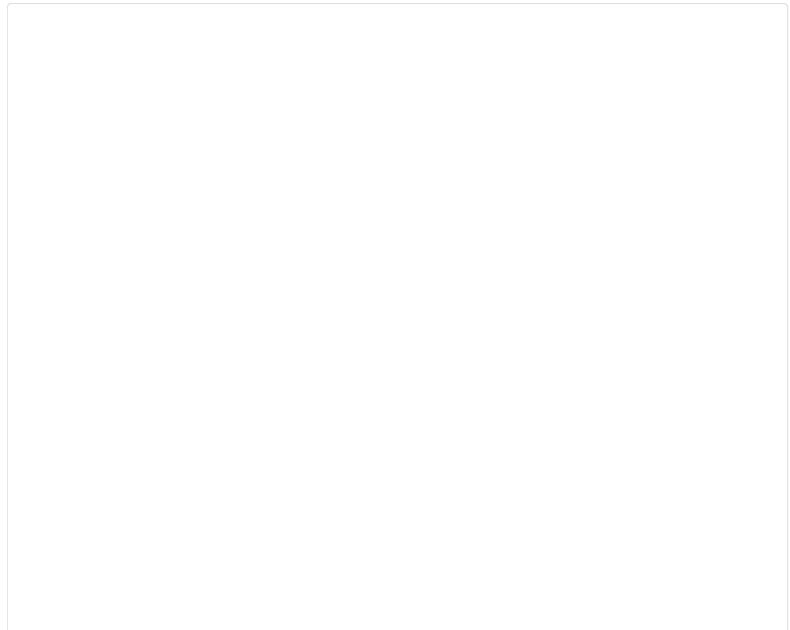
Bio Sample Name	Primer Name	CCS Reads	Mean Primer Quality	Reads with 5' and 3' Primers	Non-Concatamer Reads with 5' and 3' Primers
BioSample_1	IsoSeqX_bc0...	13,862,874	99.7	13,862,874	13,849,727
BioSample_2	IsoSeqX_bc0...	14,022,714	99.7	14,022,714	14,000,396
BioSample_3	IsoSeqX_bc0...	12,785,414	99.7	12,785,414	12,763,898
BioSample_4	IsoSeqX_bc0...	12,461,249	99.7	12,461,249	12,442,253
BioSample_5	IsoSeqX_bc0...	12,447,639	99.7	12,447,639	12,428,554
BioSample_6	IsoSeqX_bc0...	13,592,308	99.7	13,592,308	13,571,379
UNASSIGNED	No Primer	2,204,814	0.0	0	0

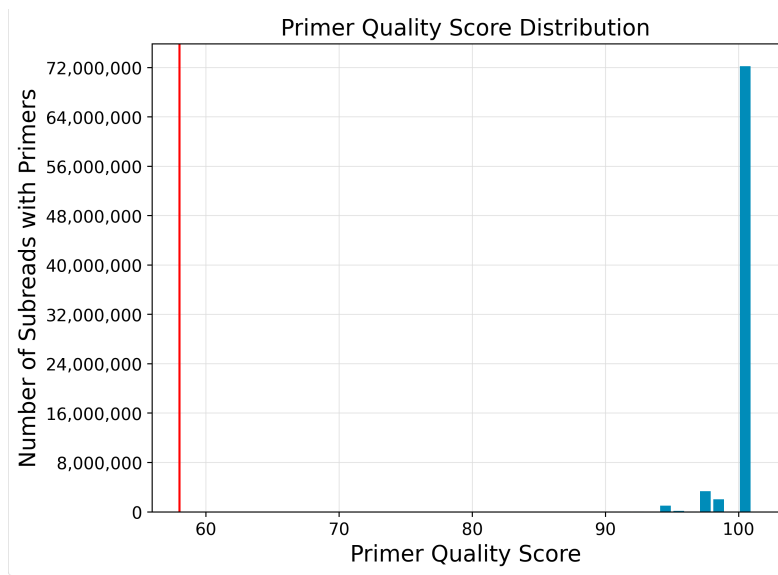
Primer Read Statistics



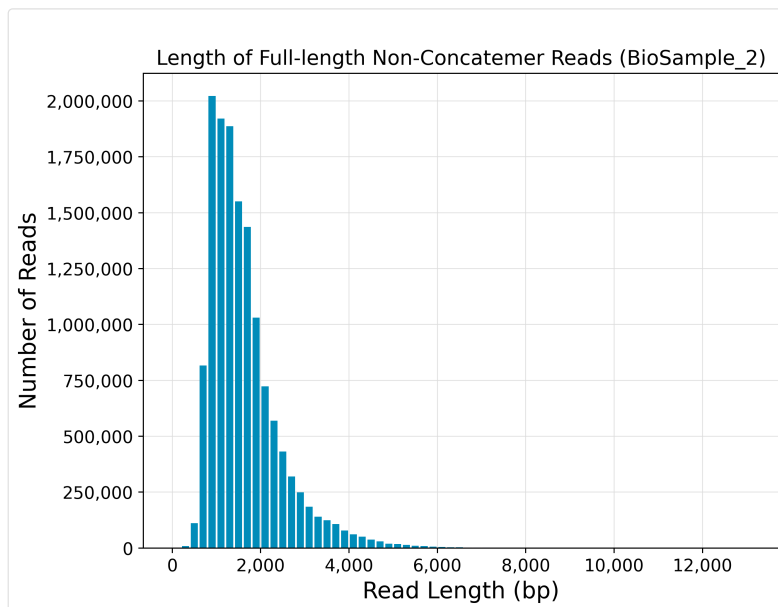
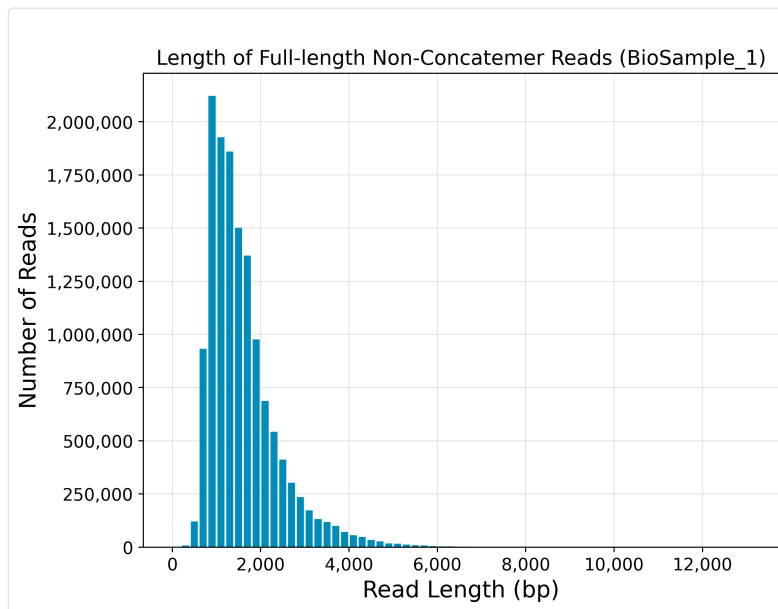


Primer Quality Scores

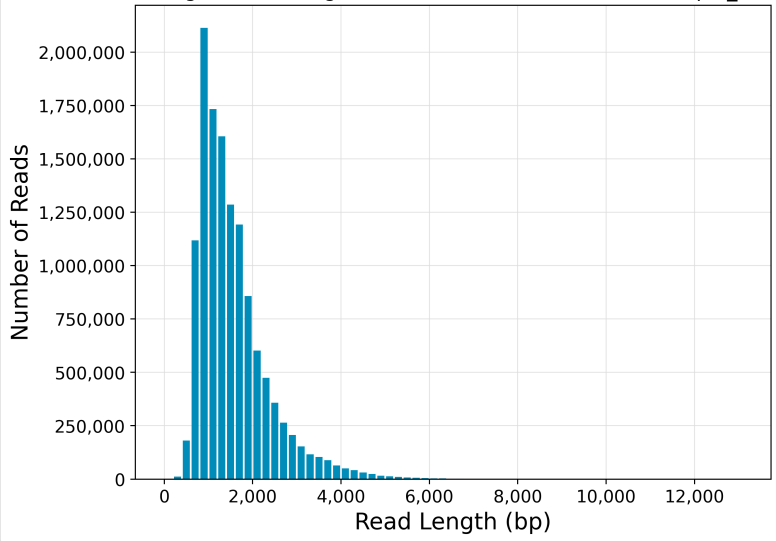




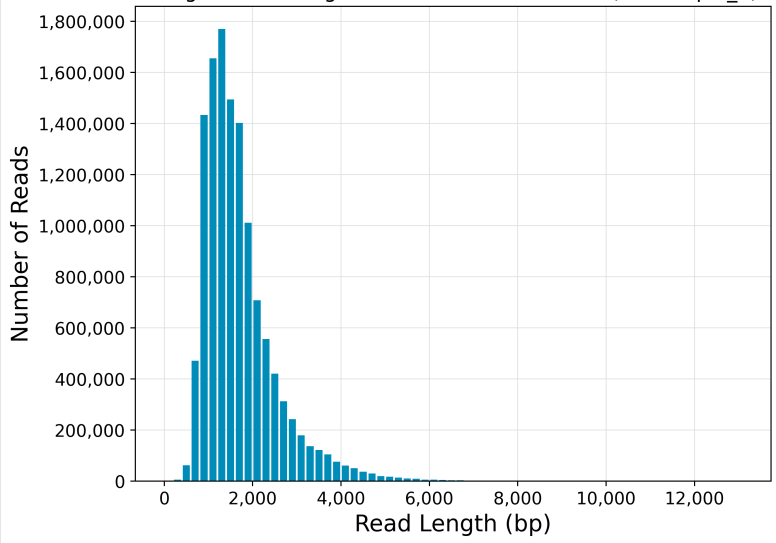
Length of Full-length Non-Concatemer Reads



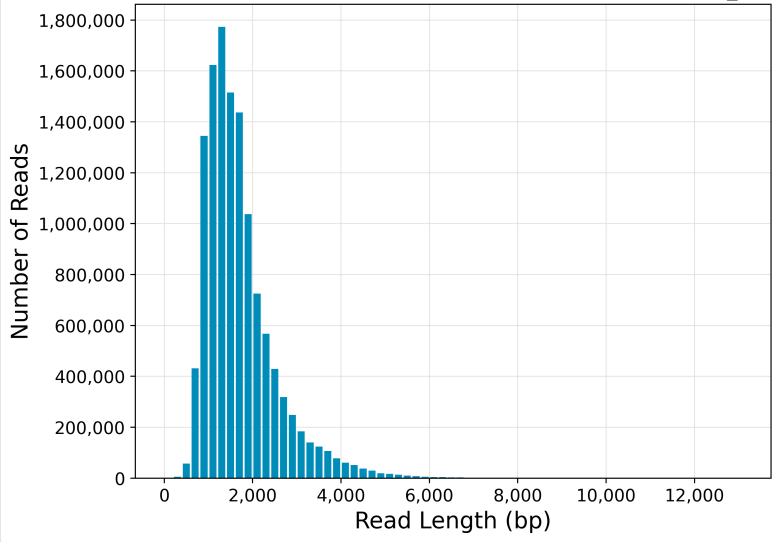
Length of Full-length Non-Concatemer Reads (BioSample_3)

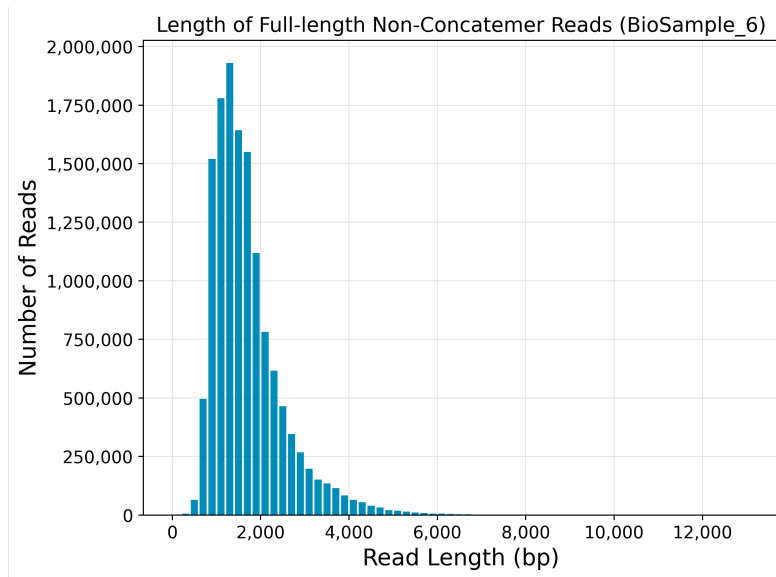


Length of Full-length Non-Concatemer Reads (BioSample_4)



Length of Full-length Non-Concatemer Reads (BioSample_5)

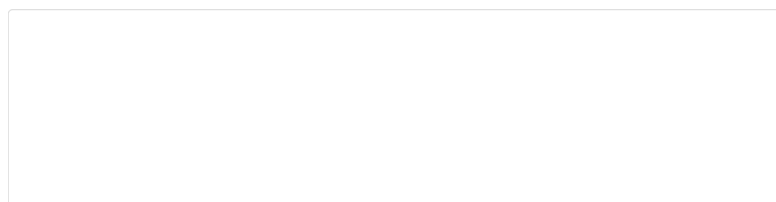
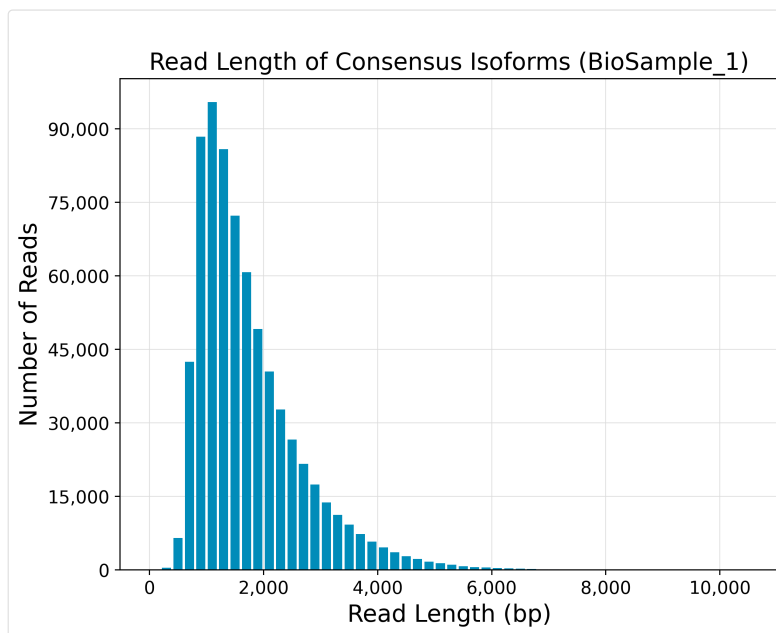




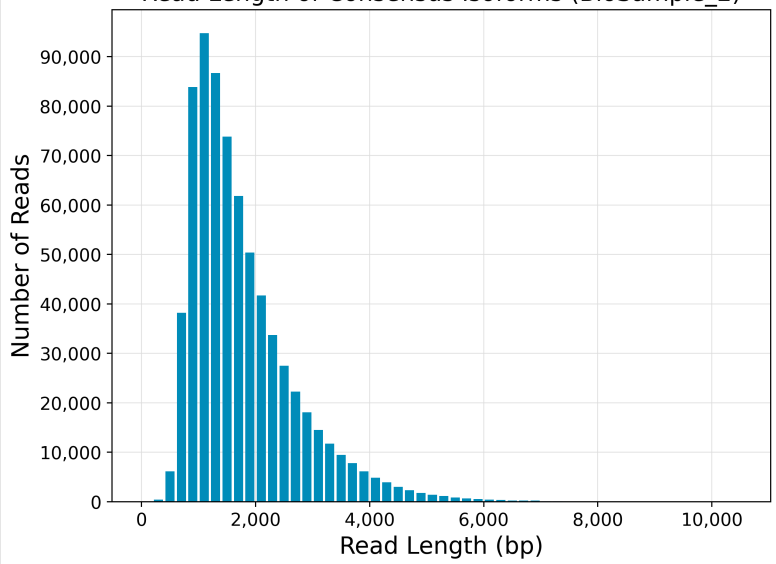
Summary Metrics

Sample Name <small>⬆</small>	Number of High-Quality Isoforms <small>⬆</small>
BioSample_1	707,469
BioSample_2	710,849
BioSample_3	638,096
BioSample_4	641,808
BioSample_5	637,722
BioSample_6	696,210

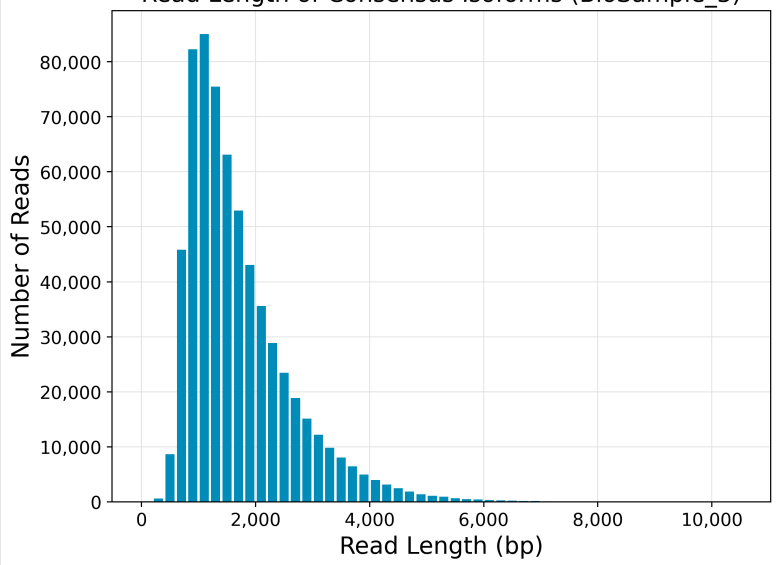
Length of Consensus Isoforms



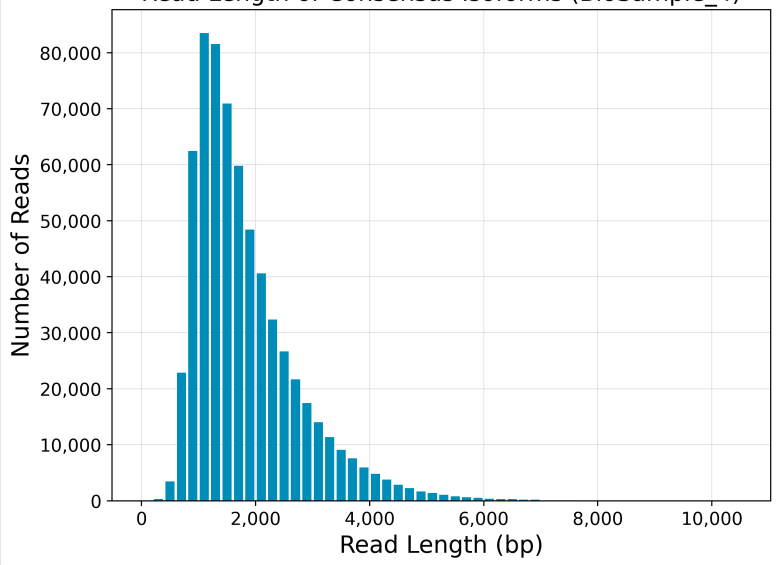
Read Length of Consensus Isoforms (BioSample_2)

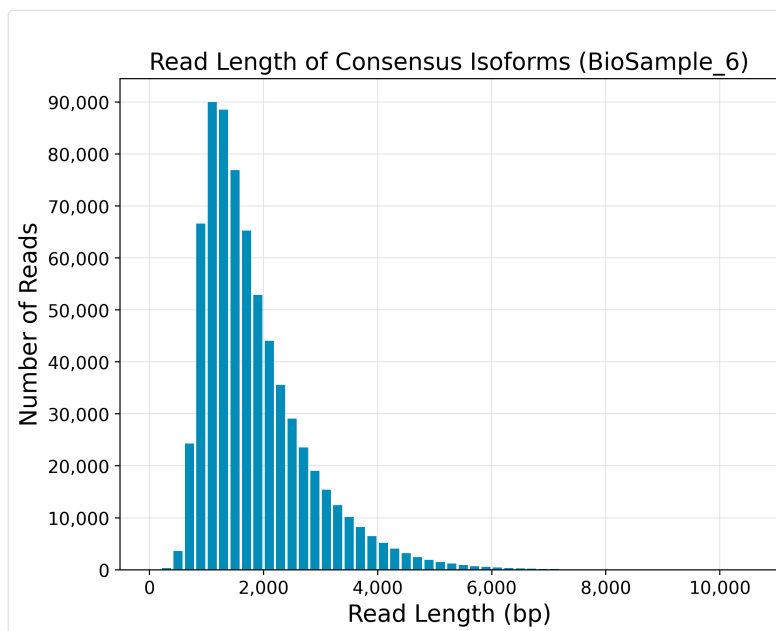
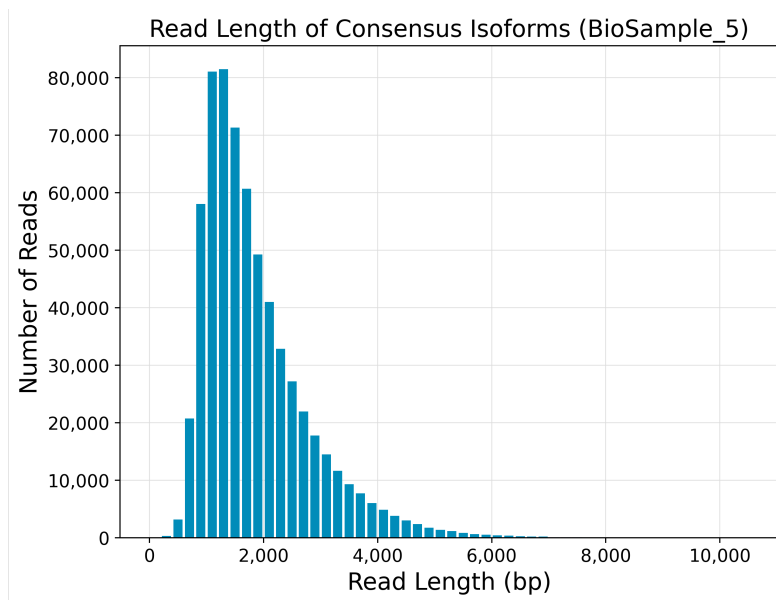


Read Length of Consensus Isoforms (BioSample_3)



Read Length of Consensus Isoforms (BioSample_4)





Classification Summary Metrics

Sample Name	Genes	Genes, filtered	Known Genes, filtered	Isoforms	Isoforms, filtered	Known isoforms, filtered
BioSample_1	157,400	19,823	18,412	352,654	126,373	50,410
BioSample_2	154,163	19,781	18,454	353,247	128,306	50,790
BioSample_3	134,938	19,163	18,042	310,716	115,523	49,017
BioSample_4	132,732	19,107	18,038	314,579	120,458	48,695
BioSample_5	132,242	19,060	18,019	313,552	120,242	48,396
BioSample_6	148,315	19,443	18,260	347,465	129,051	50,013

Transcript Classification (BioSample_1)

Category	Count	CAGE Detected	CAGE Detected (%)	polyA Motif Detected

FSM	96568	55005	56.95%	45466
ISM	228278	24612	10.78%	125329
NIC	49007	35273	71.97%	23183
NNC	55699	33382	59.93%	25999
Antisense	9282	511	5.50%	2985
Fusion	1280	744	58.12%	641
More junctions	23	15	65.21%	12
Genic intron	241	2	0.82%	63
Genic genomic	47784	7129	14.91%	17794
Intergenic	130712	543	0.41%	43502

Transcript Classification (BioSample_2)

Category	Count	CAGE Detected	CAGE Detected (%)	polyA Motif Detected
FSM	98406	56714	57.63%	46152
ISM	228940	25318	11.05%	125311
NIC	50323	36711	72.95%	23612
NNC	57428	34980	60.91%	26822
Antisense	9310	520	5.58%	2948
Fusion	1355	812	59.92%	670
More junctions	29	16	55.17%	15
Genic intron	245	0	0.00%	53
Genic genomic	48211	7533	15.62%	18022
Intergenic	127376	565	0.44%	42567

Transcript Classification (BioSample_3)

Category	Count	CAGE Detected	CAGE Detected (%)	polyA Motif Detected
FSM	91448	53490	58.49%	42428
ISM	210891	24150	11.45%	114503
NIC	43307	32104	74.13%	20197
NNC	50240	31003	61.70%	23076
Antisense	8223	503	6.11%	2586
Fusion	1157	678	58.59%	586
More junctions	21	15	71.42%	8
Genic intron	204	1	0.49%	58
Genic genomic	41135	6919	16.82%	15082
Intergenic	109211	564	0.51%	35922

Transcript Classification (BioSample_4)

Category	Count	CAGE Detected	CAGE Detected (%)	polyA Motif Detected
FSM	93215	54493	58.45%	43914
ISM	212166	23175	10.92%	117139
NIC	47308	34807	73.57%	22358
NNC	51789	31609	61.03%	24356
Antisense	8091	413	5.10%	2536
Fusion	1227	734	59.82%	613
More junctions	28	13	46.42%	17
Genic intron	176	0	0.00%	36
Genic genomic	42458	6825	16.07%	15993
Intergenic	107109	503	0.46%	35806

Transcript Classification (BioSample_5)

Category	Count	CAGE Detected	CAGE Detected (%)	polyA Motif Detected
FSM	93118	54693	58.73%	43693
ISM	209692	23145	11.03%	116367
NIC	47539	34928	73.47%	22636
NNC	51350	31419	61.18%	24231
Antisense	7978	423	5.30%	2569
Fusion	1278	762	59.62%	625
More junctions	23	15	65.21%	11
Genic intron	210	1	0.47%	58
Genic genomic	42417	6737	15.88%	16094
Intergenic	106675	504	0.47%	36252

Transcript Classification (BioSample_6)

Category	Count	CAGE Detected	CAGE Detected (%)	polyA Motif Detected
FSM	97528	56384	57.81%	45903
ISM	223895	24536	10.95%	123397
NIC	51778	37743	72.89%	24554
NNC	57519	34986	60.82%	27133
Antisense	9200	487	5.29%	2962
Fusion	1412	840	59.49%	682
More junctions	35	20	57.14%	16
Genic intron	221	1	0.45%	61

Genic genomic	47679	7307	15.32%	18081
Intergenic	121684	571	0.46%	40806

Transcript Classification, filtered (BioSample_1)

Category	Count	CAGE Detected	CAGE Detected, (%)	polyA Detected
FSM	85882	48753	56.76%	45466
ISM	114372	14449	12.63%	69250
NIC	43777	31457	71.85%	22654
NNC	29434	19273	65.47%	15674
Antisense	504	115	22.81%	310
Fusion	842	517	61.40%	480
More junctions	17	13	76.47%	10
Genic intron	0	0	0.00%	0
Genic genomic	350	175	50.00%	182
Intergenic	1039	104	10.00%	795

Transcript Classification, filtered (BioSample_2)

Category	Count	CAGE Detected	CAGE Detected, (%)	polyA Detected
FSM	87218	50027	57.35%	46152
ISM	114742	14775	12.87%	69589
NIC	44956	32687	72.70%	23070
NNC	29868	19728	66.05%	16035
Antisense	475	119	25.05%	288
Fusion	844	520	61.61%	493
More junctions	21	13	61.90%	11
Genic intron	0	0	0.00%	0
Genic genomic	365	185	50.68%	186
Intergenic	987	108	10.94%	756

Transcript Classification, filtered (BioSample_3)

Category	Count	CAGE Detected	CAGE Detected, (%)	polyA Detected
FSM	81176	47225	58.17%	42428
ISM	104871	14069	13.41%	63001
NIC	38490	28452	73.92%	19711
NNC	25658	17049	66.44%	13548
Antisense	421	119	28.26%	249

Fusion	778	481	61.82%	441
More junctions	15	13	86.66%	8
Genic intron	0	0	0.00%	0
Genic genomic	320	156	48.75%	165
Intergenic	824	87	10.55%	628

Transcript Classification, filtered (BioSample_4)

Category	Count	CAGE Detected	CAGE Detected, (%)	polyA Detected
FSM	82985	48290	58.19%	43914
ISM	108121	13594	12.57%	65708
NIC	42383	31110	73.40%	21807
NNC	27073	17941	66.26%	14492
Antisense	407	99	24.32%	232
Fusion	791	492	62.19%	447
More junctions	19	11	57.89%	13
Genic intron	0	0	0.00%	0
Genic genomic	306	167	54.57%	156
Intergenic	784	100	12.75%	587

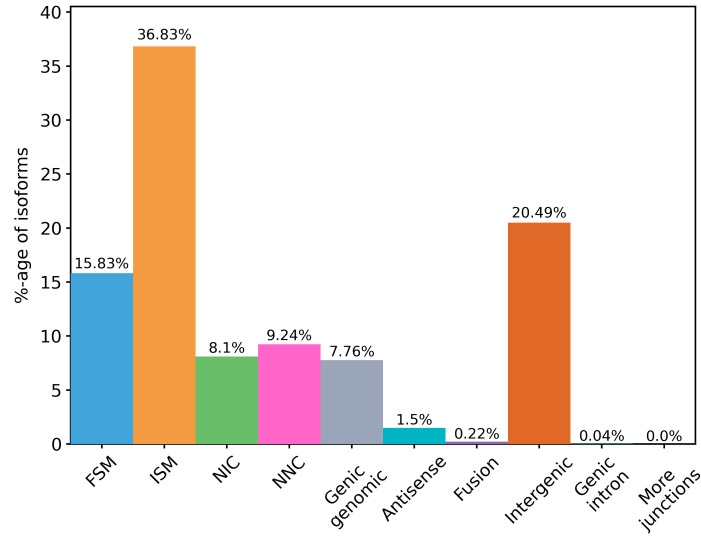
Transcript Classification, filtered (BioSample_5)

Category	Count	CAGE Detected	CAGE Detected, (%)	polyA Detected
FSM	82818	48439	58.48%	43693
ISM	106787	13562	12.70%	65273
NIC	42598	31222	73.29%	22072
NNC	26940	18027	66.91%	14311
Antisense	379	101	26.64%	221
Fusion	838	521	62.17%	474
More junctions	20	15	75.00%	11
Genic intron	0	0	0.00%	0
Genic genomic	310	156	50.32%	149
Intergenic	761	93	12.22%	576

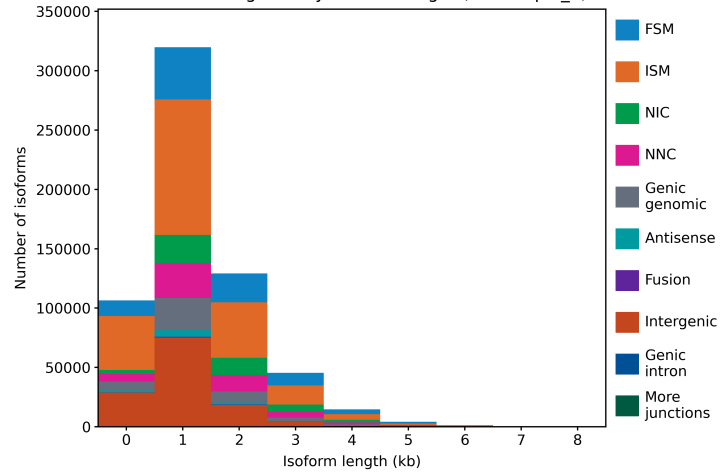
Transcript Classification, filtered (BioSample_6)

Category	Count	CAGE Detected	CAGE Detected, (%)	polyA Detected
FSM	86591	49878	57.60%	45903
ISM	113847	14397	12.64%	69238
NIC	46275	33681	72.78%	23952

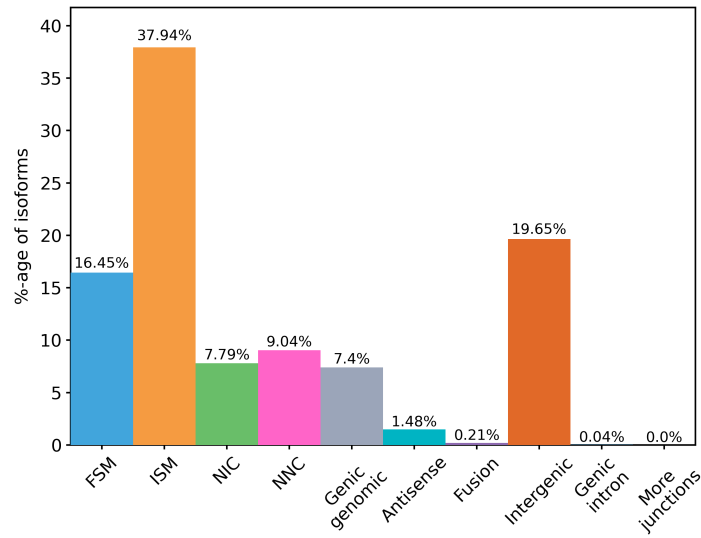
Isoform distribution across structural categories (BioSample_2)



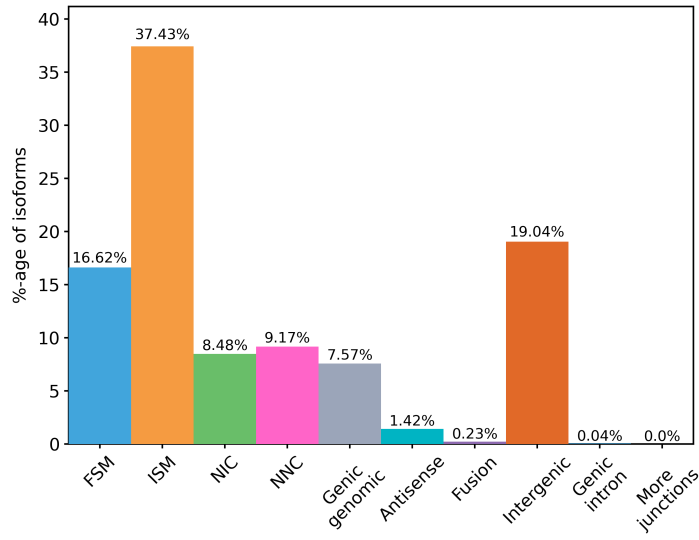
Structural categories by isoform length (BioSample_2)



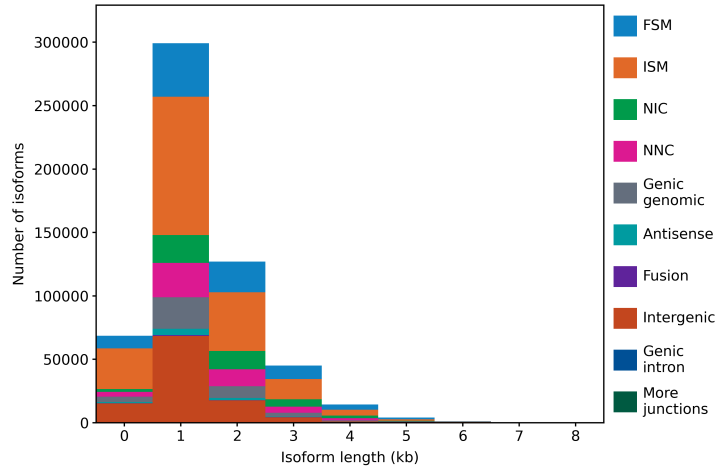
Isoform distribution across structural categories (BioSample_3)



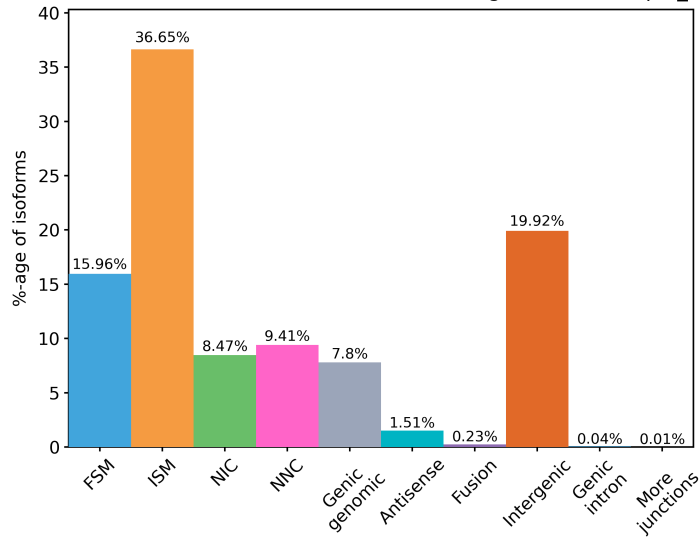
Isoform distribution across structural categories (BioSample_5)



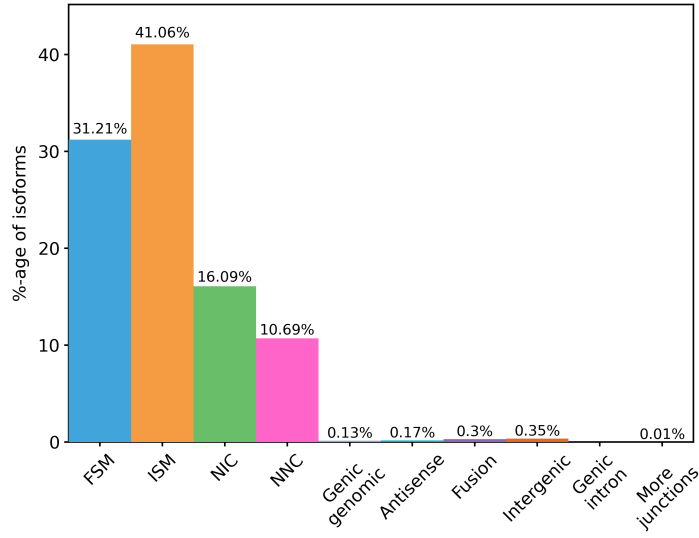
Structural categories by isoform length (BioSample_5)



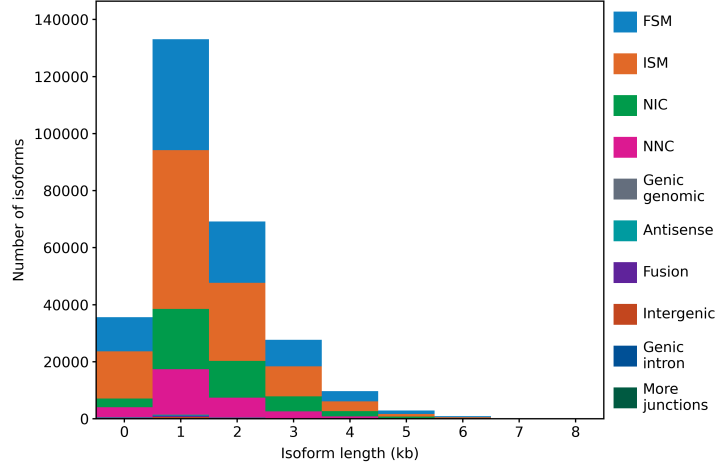
Isoform distribution across structural categories (BioSample_6)



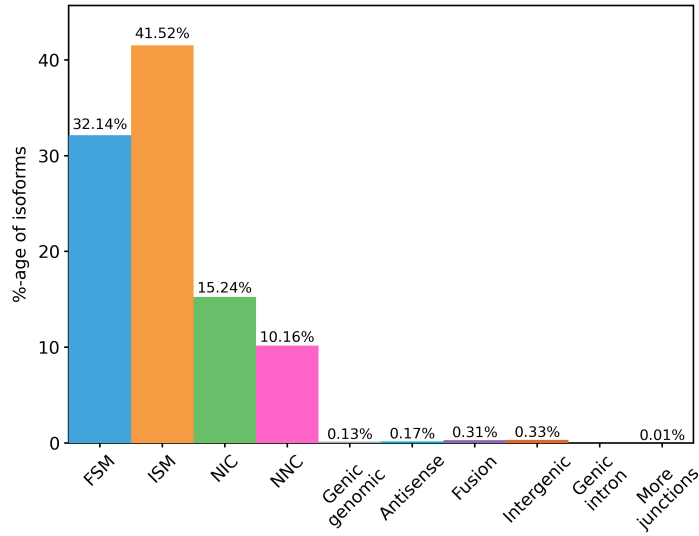
Isoform distribution across structural categories (BioSample_2)



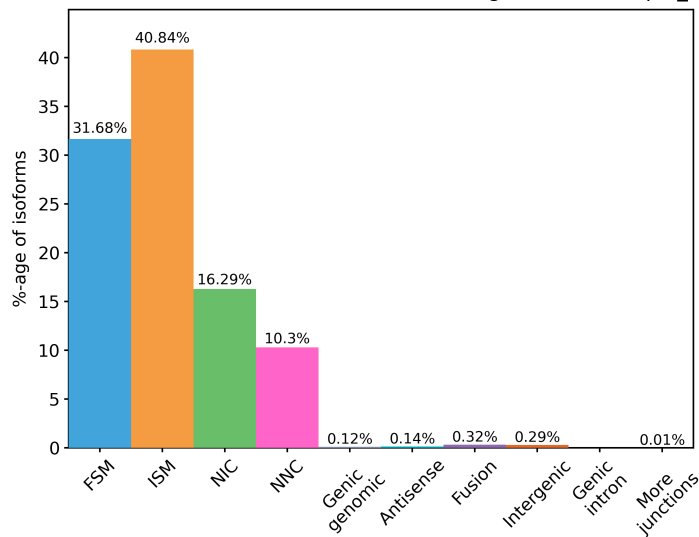
Structural categories by isoform length (BioSample_2)



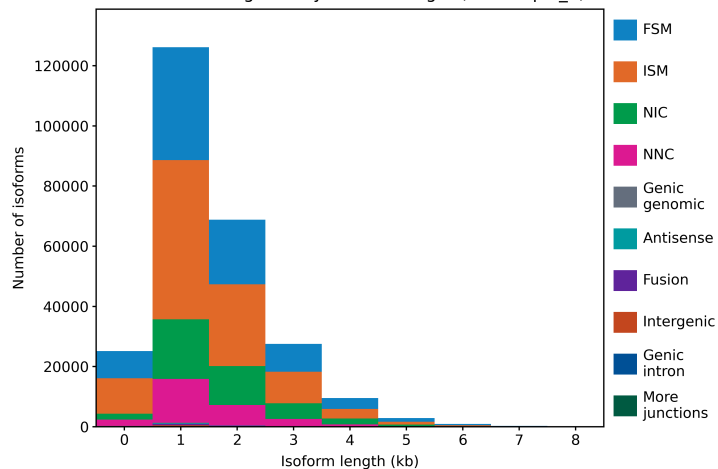
Isoform distribution across structural categories (BioSample_3)



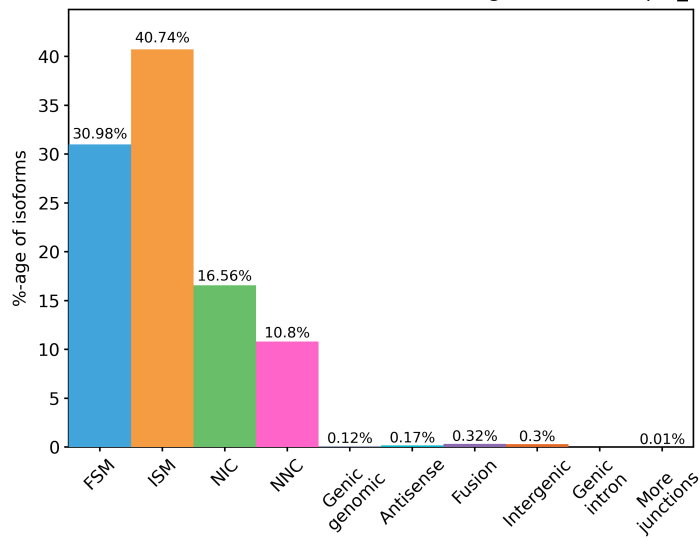
Isoform distribution across structural categories (BioSample_5)

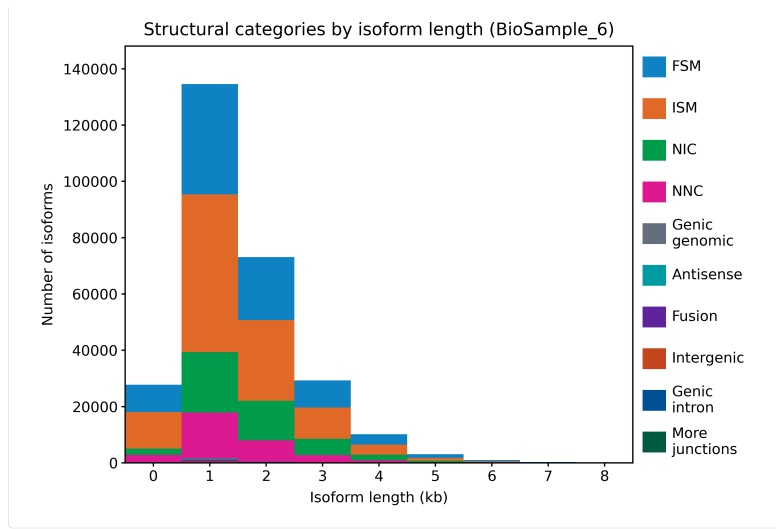


Structural categories by isoform length (BioSample_5)

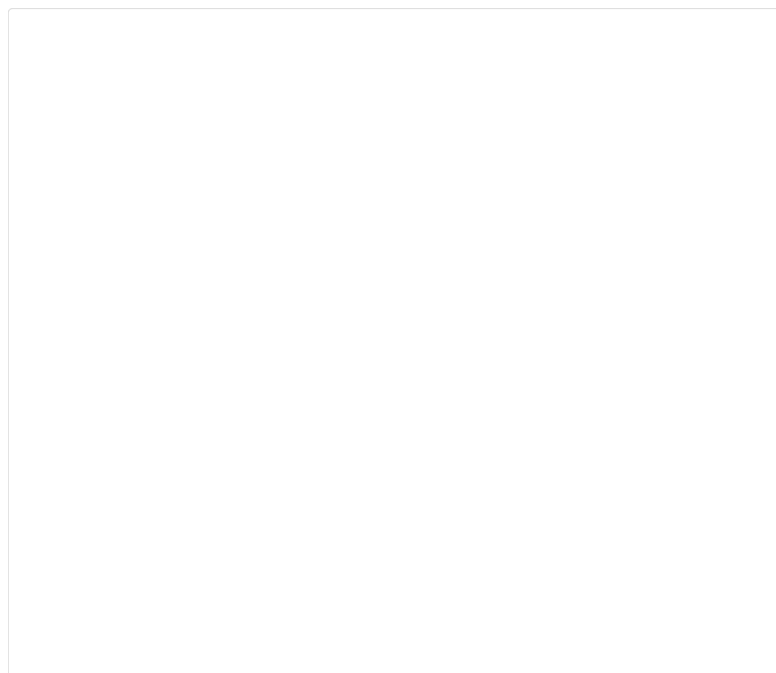
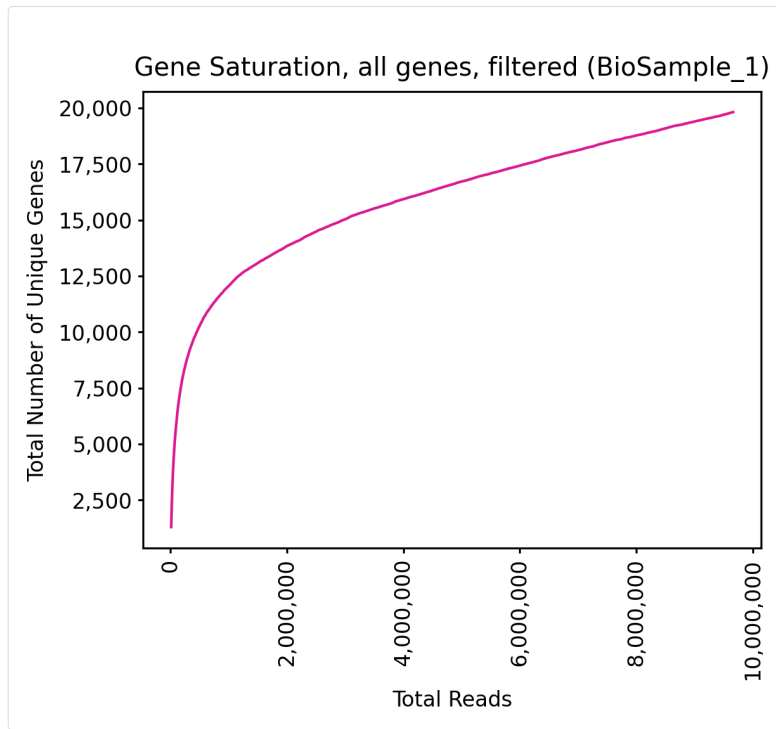


Isoform distribution across structural categories (BioSample_6)

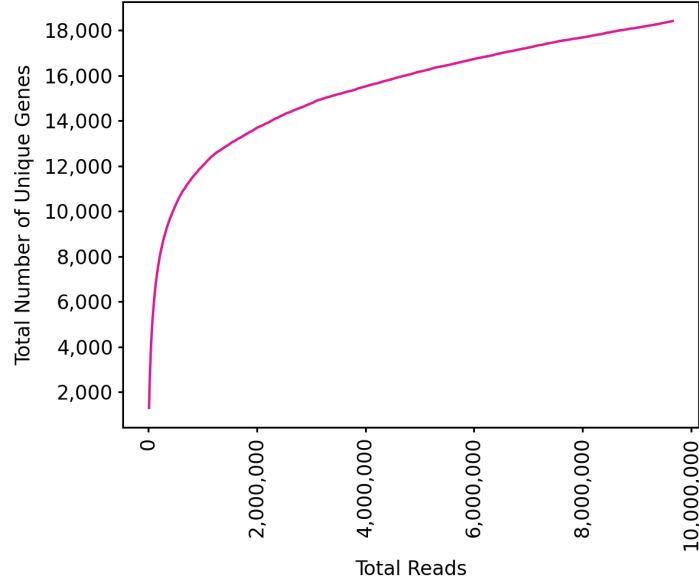




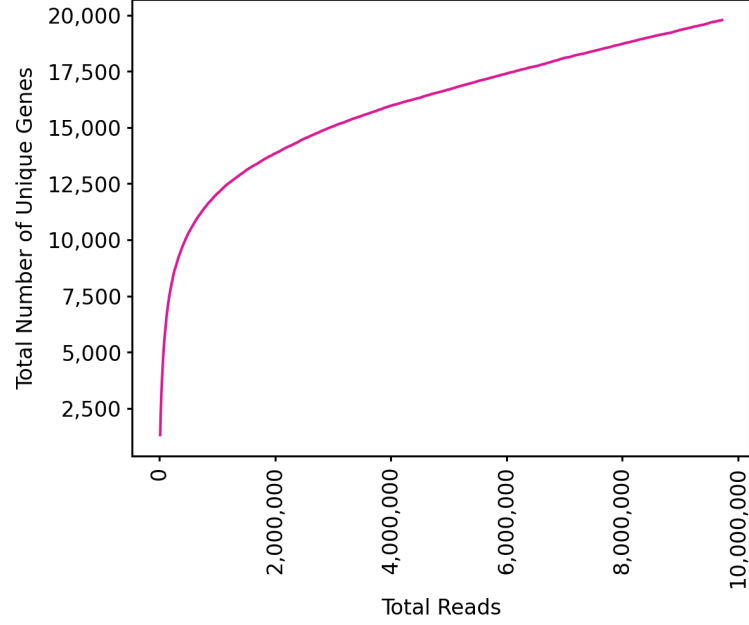
Gene Saturation



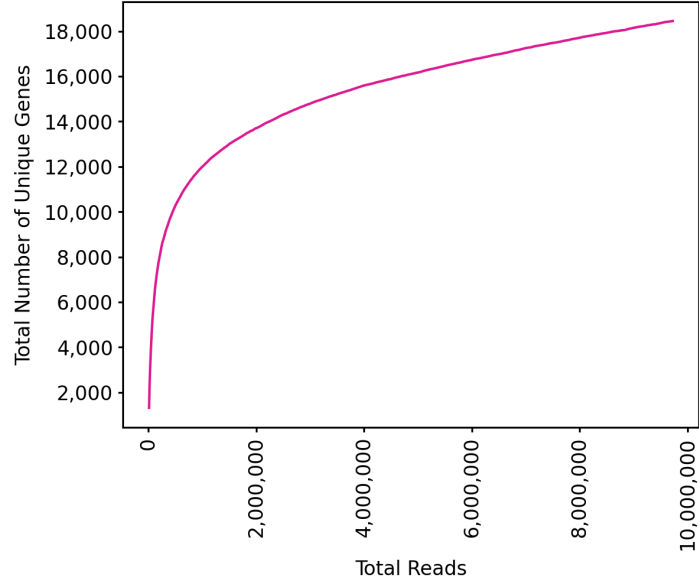
Gene Saturation, known genes only, filtered (BioSample_1)



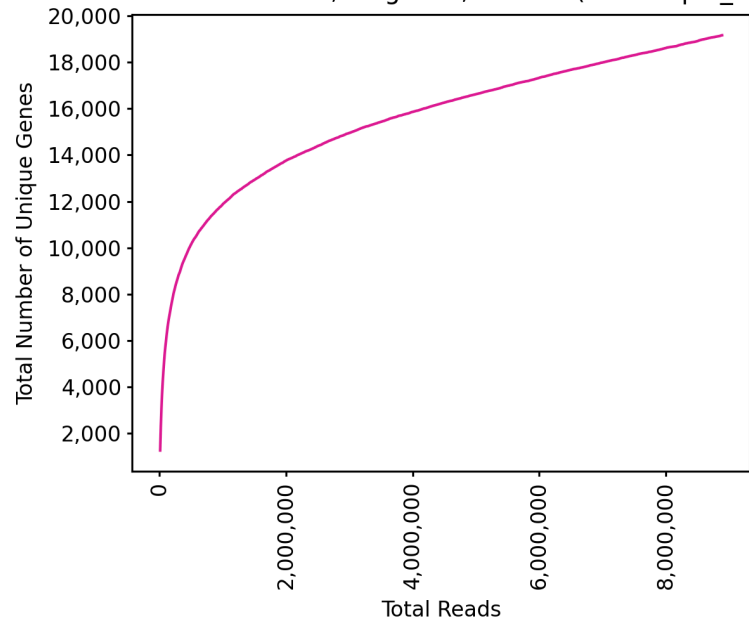
Gene Saturation, all genes, filtered (BioSample_2)



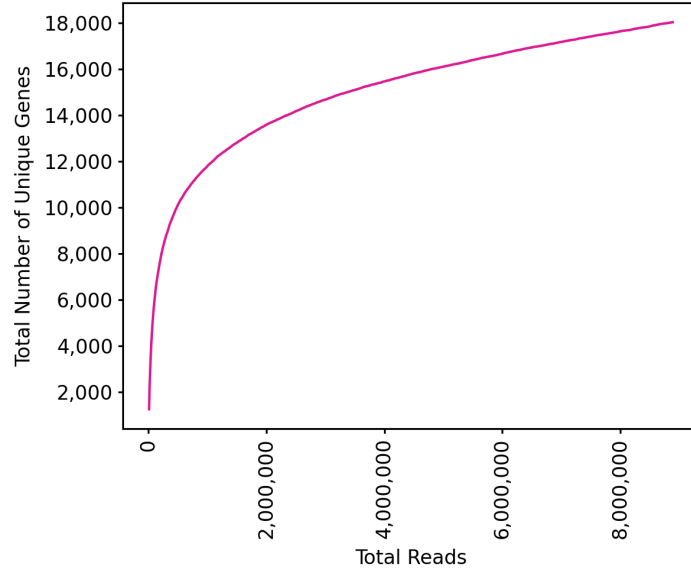
Gene Saturation, known genes only, filtered (BioSample_2)



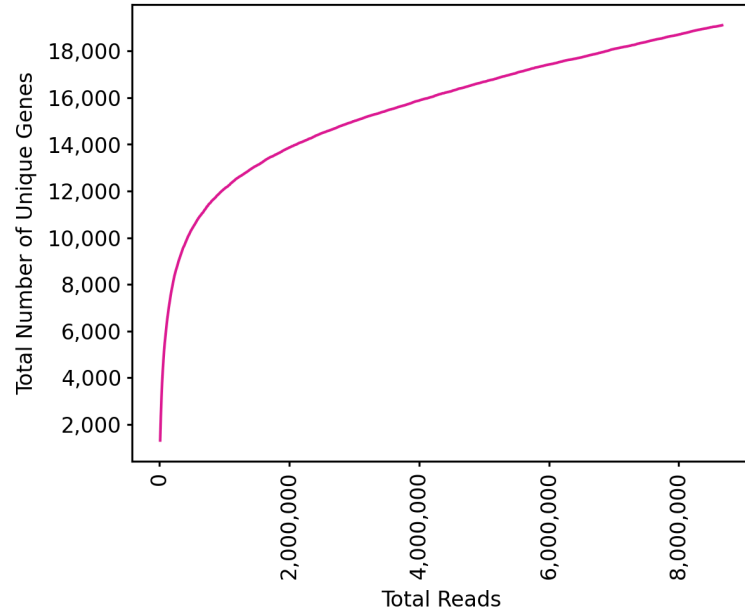
Gene Saturation, all genes, filtered (BioSample_3)



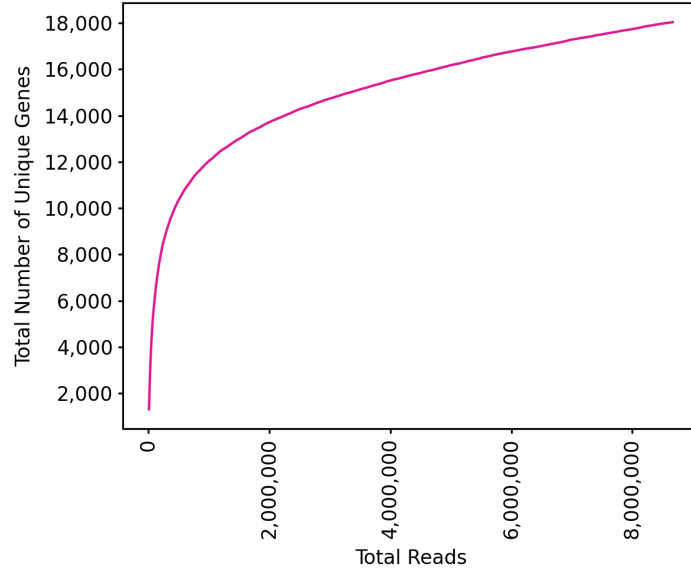
Gene Saturation, known genes only, filtered (BioSample_3)



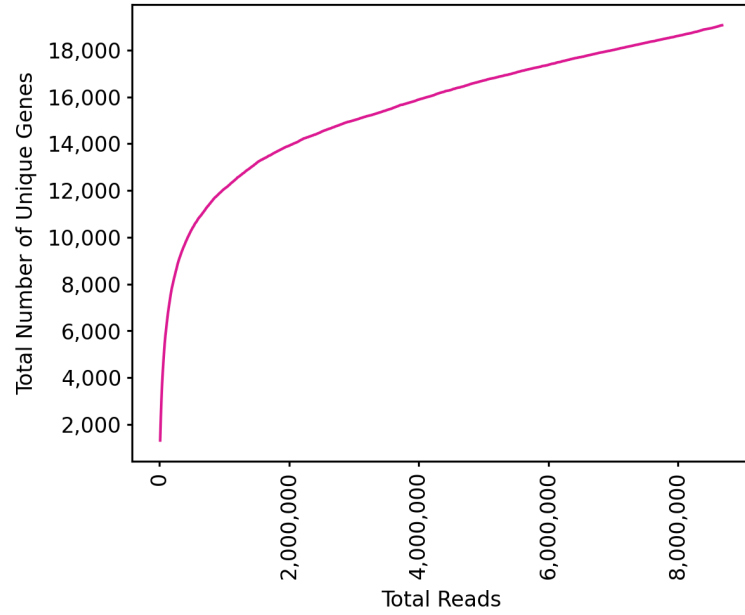
Gene Saturation, all genes, filtered (BioSample_4)



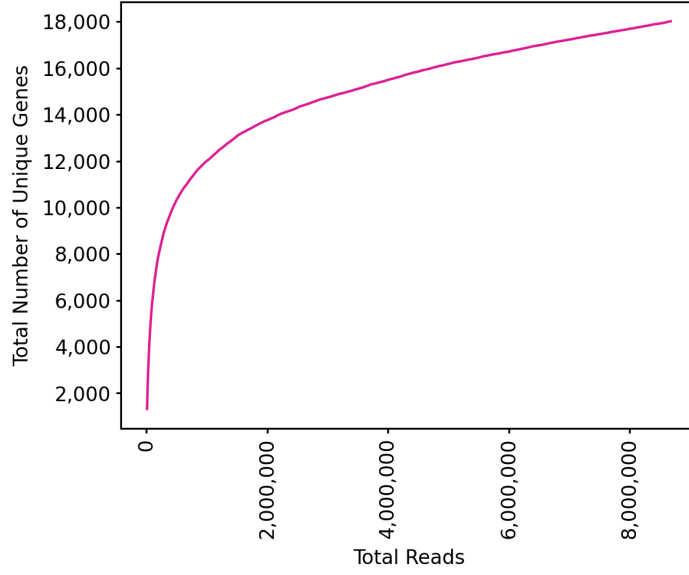
Gene Saturation, known genes only, filtered (BioSample_4)



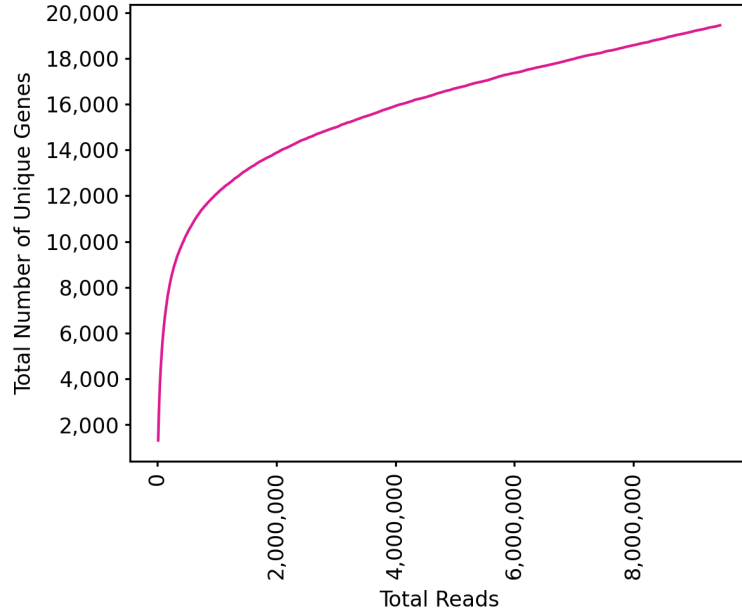
Gene Saturation, all genes, filtered (BioSample_5)



Gene Saturation, known genes only, filtered (BioSample_5)



Gene Saturation, all genes, filtered (BioSample_6)



Gene Saturation, known genes only, filtered (BioSample_6)

