

UHRR_brain_kinnex_IDT_captured

SUCCESSFUL

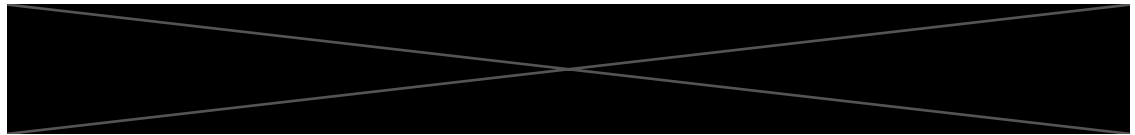


- ▼ Analysis Overview
- Status
- Thumbnails
- Display All
- Read Segmentation
- Read Classification
- Transcript Clustering
- Transcript Mapping and Classification
- Data

Display All

Status

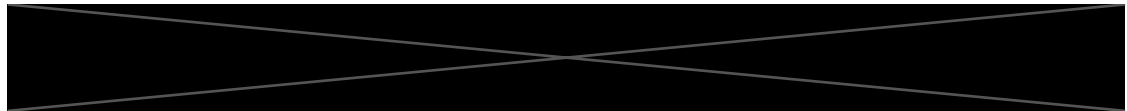
Analysis UHRR_brain_kinnex_IDT_captured
Analysis ID 8725
Status SUCCESSFUL: 131 tasks finished



Application Read Segmentation and Iso-Seq
SMRT Link Version 13.1.0.221970

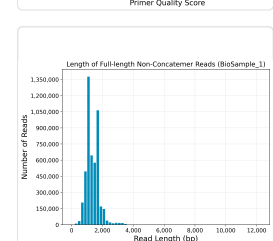
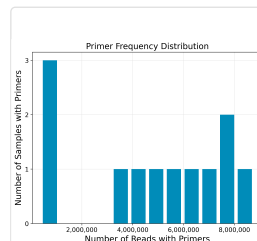
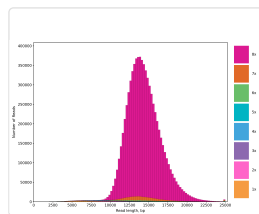
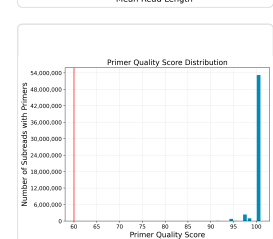
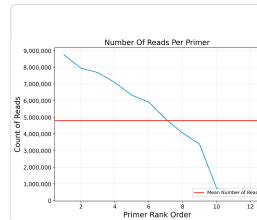
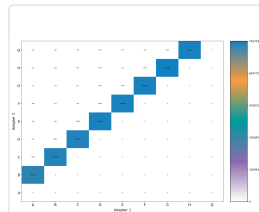
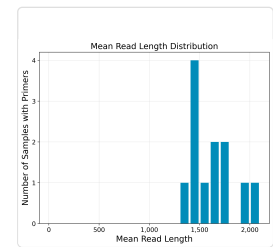
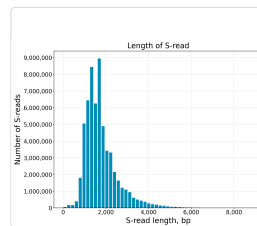
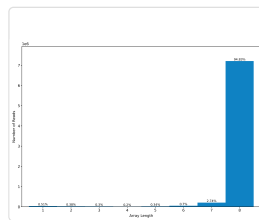
Inputs

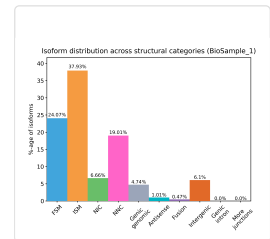
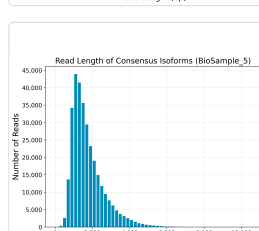
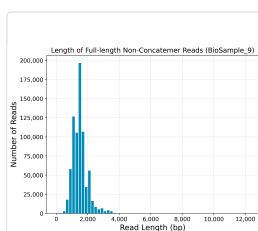
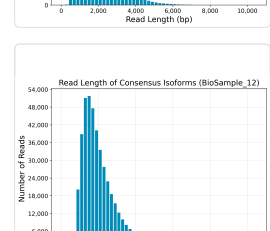
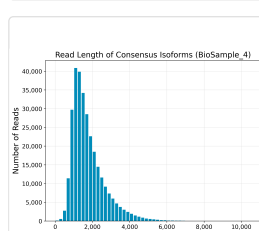
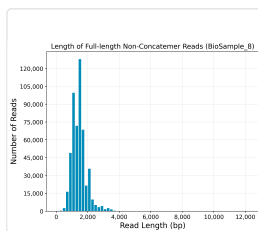
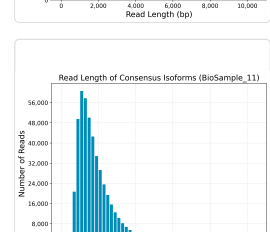
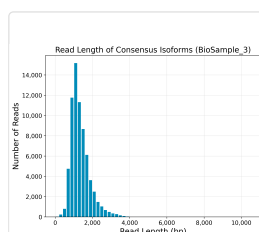
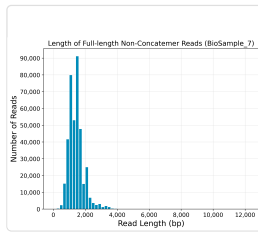
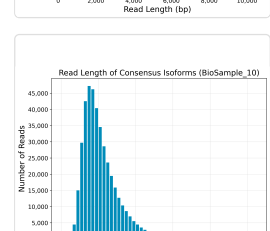
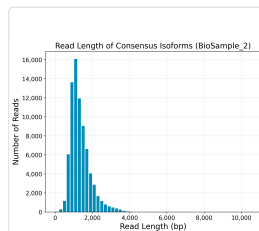
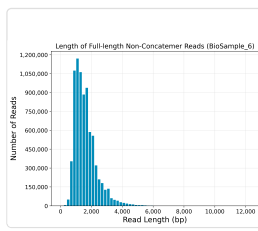
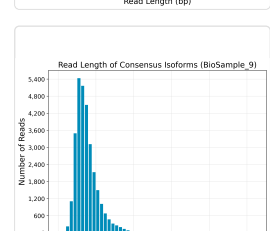
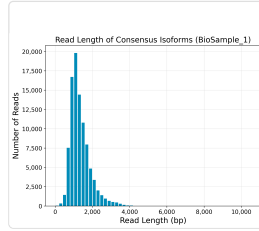
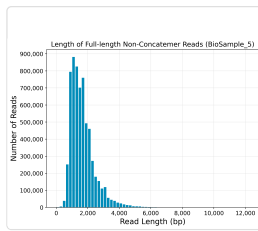
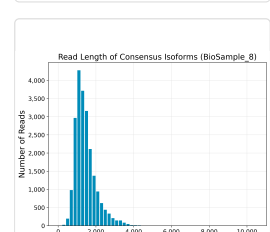
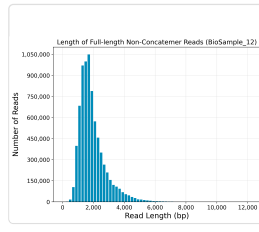
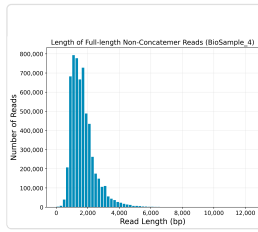
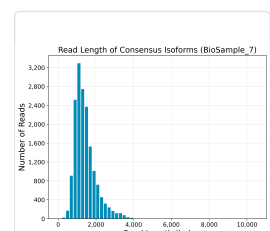
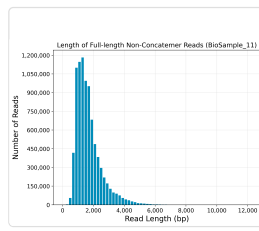
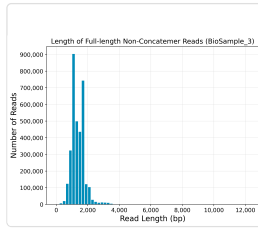
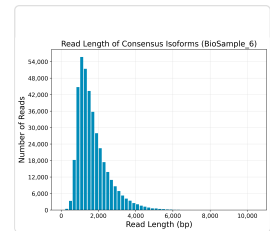
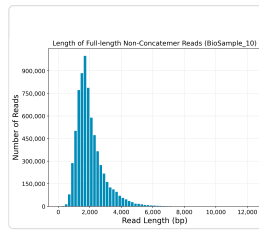
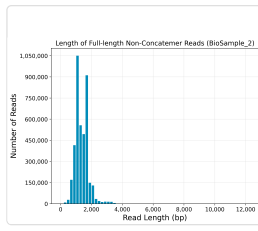
Data Type ↑	Name ↑	Import Com
BarcodeSet	Barcode Sets: Iso-Seq v2 Barcoded cDNA...	Yes
BarcodeSet	Barcode Sets: MAS-Seq Adapter v3 (MAS8)	Yes
ConsensusReadSet	HiFi Reads: 12plex_UHRR_Brain_Kinnex_ID...	Yes
ReferenceSet	References: Human Genome hg38, with Ge...	Yes

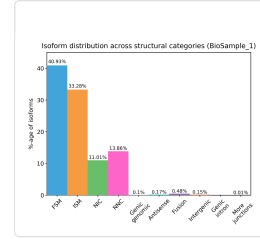
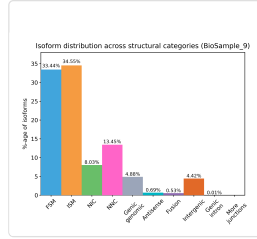
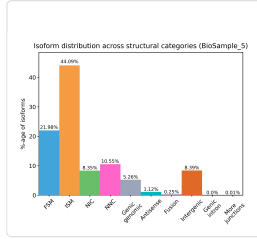
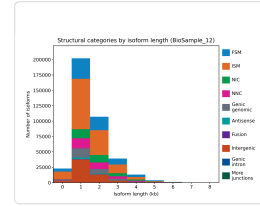
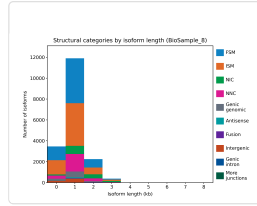
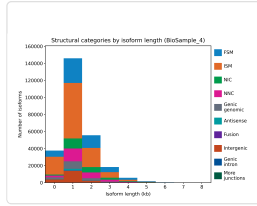
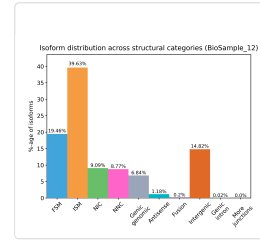
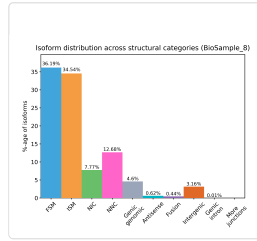
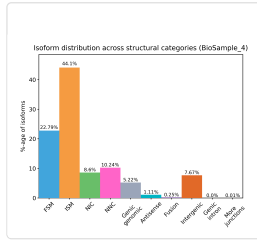
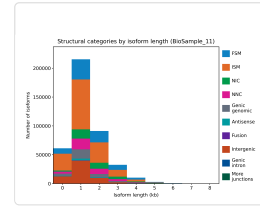
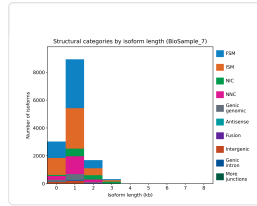
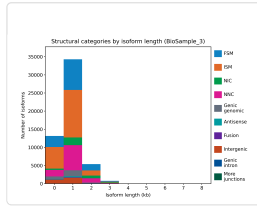
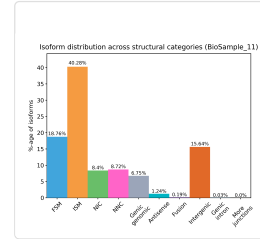
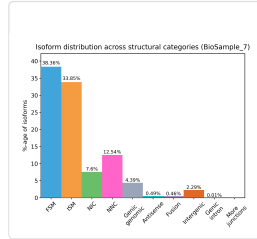
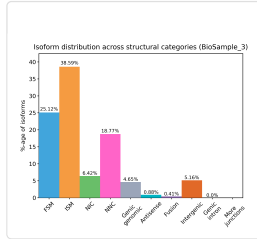
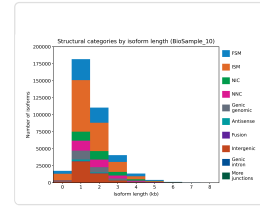
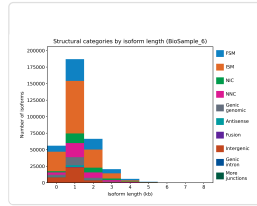
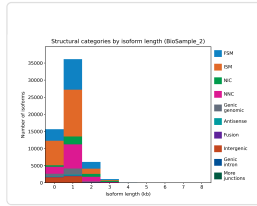
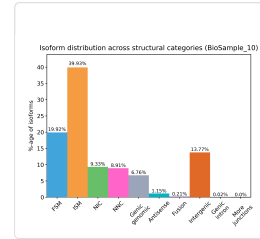
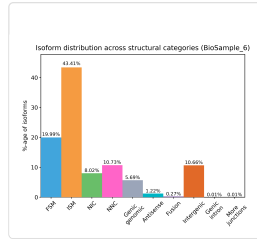
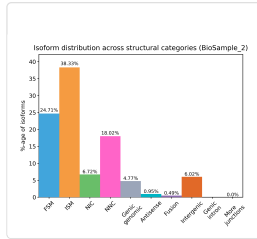
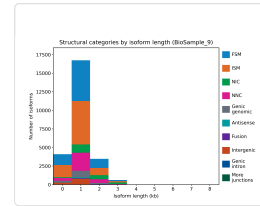
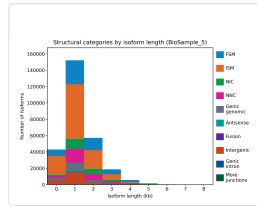
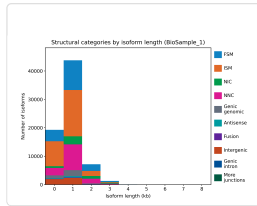


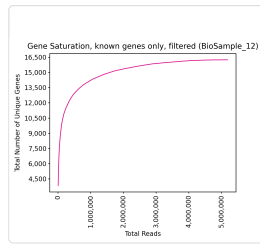
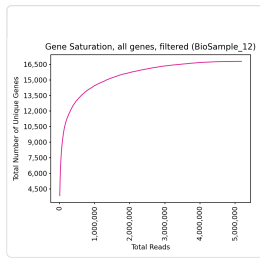
► Analysis Parameters

Thumbnails





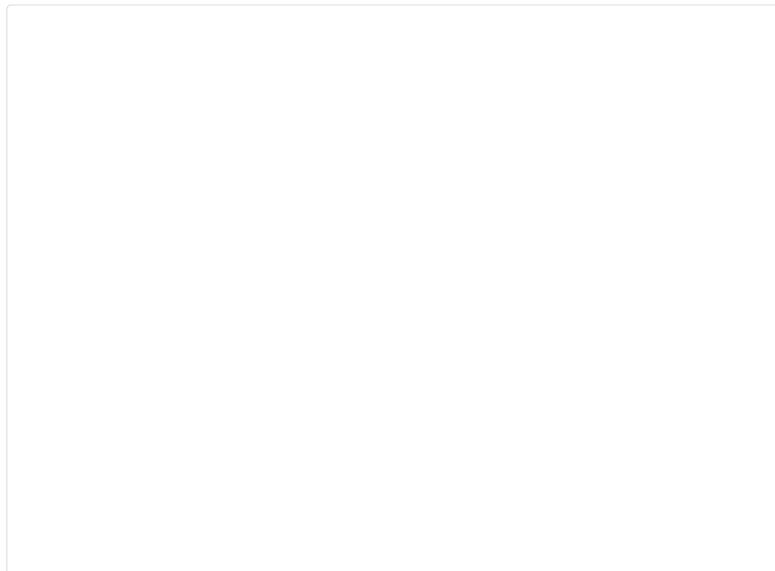
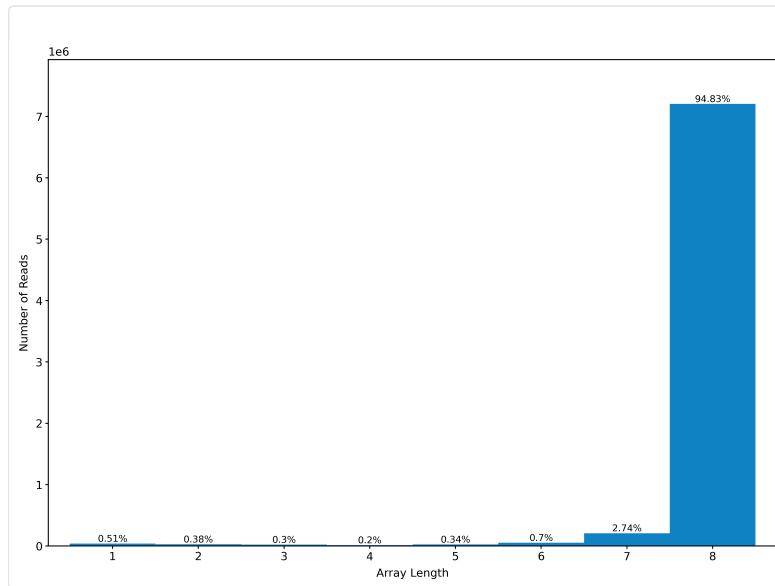


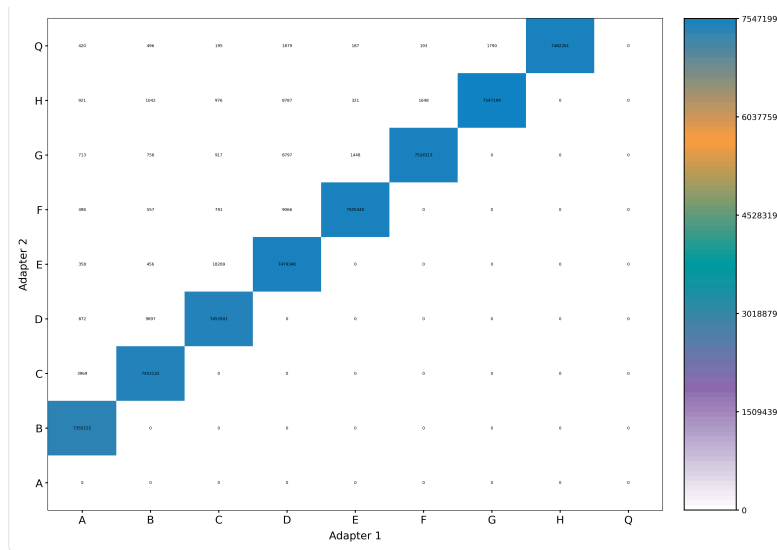


Read Segmentation

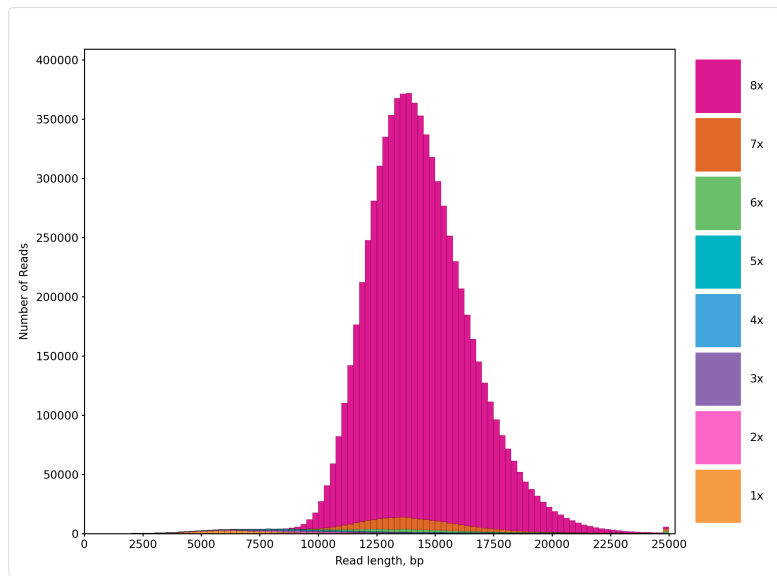
Value	Analysis Metric
7,621,916	Reads
59,799,238	Segmented reads (S-reads)
1,782	Mean length of S-reads
94.57 %	Percent of reads with full arrays
7.85	Mean array size (concatenation factor)

Segmentation Statistics

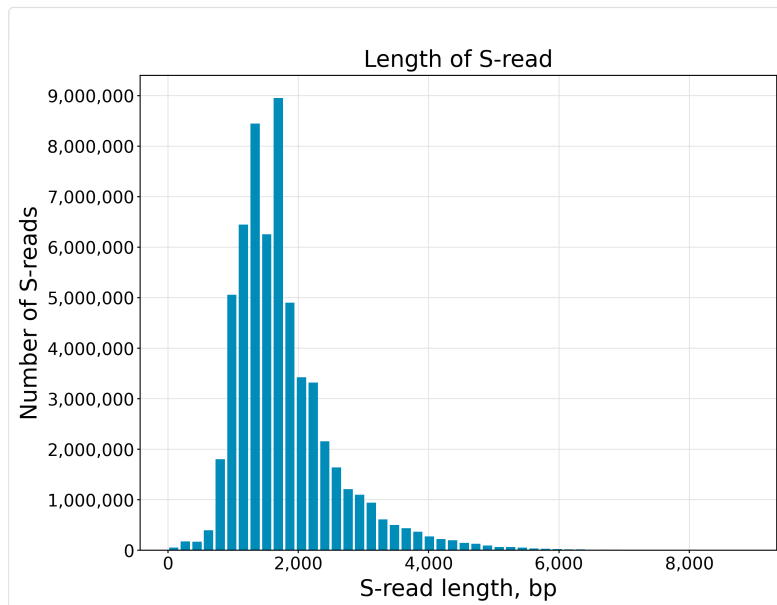




Length of Reads



S-read Length Distribution



Read Classification

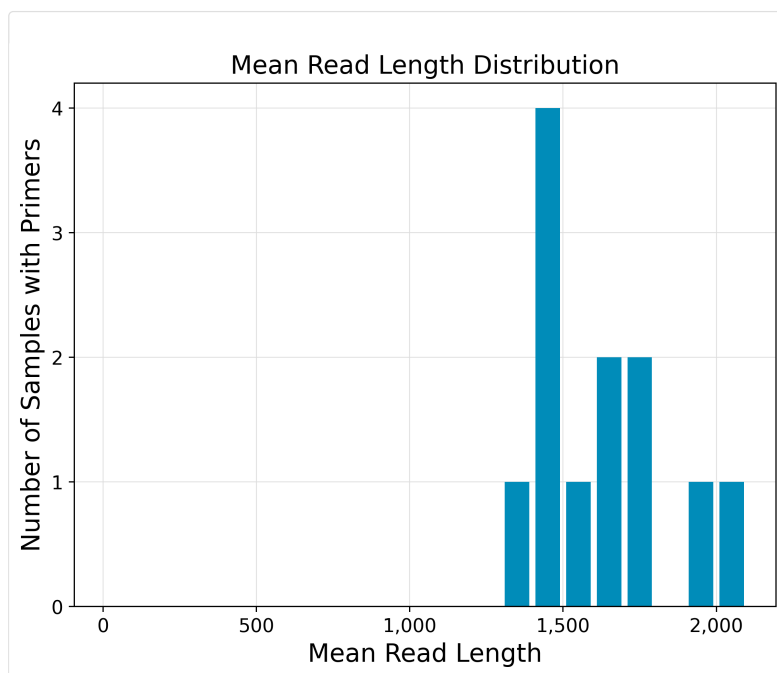
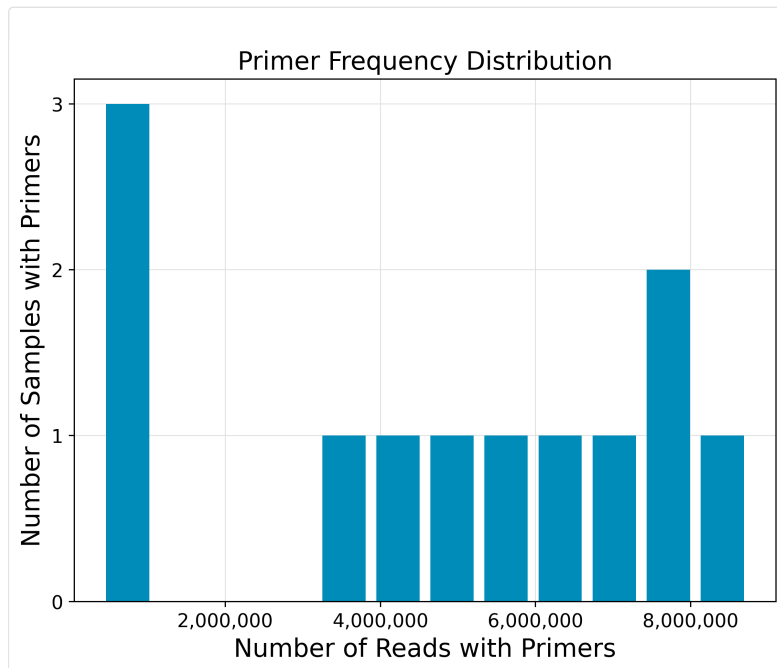
Value	Analysis Metric
59,799,238	Reads
57,734,211	Reads with 5' and 3' Primers
57,667,867	Non-Concatamer Reads with 5' and 3' Primers
57,517,651	Non-Concatamer Reads with 5' and 3' Primers and Poly-A Tail (FLNC Reads)
1,668	Mean Length of FLNC Reads
12	Unique Primers
4,811,184	Mean Reads per Primer
8,757,463	Max. Reads per Primer
393,810	Min. Reads per Primer
2,065,027	Reads without Primers
96.12%	Percent Bases in Reads with Primers
96.54%	Percent Reads with Primers

Primer Data

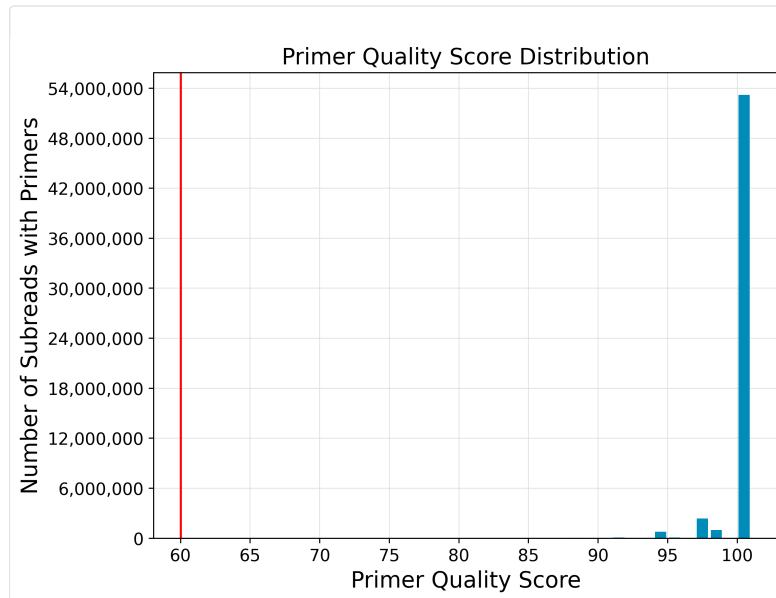
Bio Sample N...	Primer Name	CCS Reads	Mean Primer...	Reads with 5...	Non-Concat...
BioSample_1	IsoSeqX_bc0...	4,893,400	99.7	4,893,400	4,891,262
BioSample_2	IsoSeqX_bc0...	4,061,072	99.7	4,061,072	4,058,910
BioSample_3	IsoSeqX_bc0...	3,392,116	99.7	3,392,116	3,391,176
BioSample_4	IsoSeqX_bc0...	5,911,881	99.7	5,911,881	5,901,064
BioSample_5	IsoSeqX_bc0...	6,325,623	99.7	6,325,623	6,319,886
BioSample_6	IsoSeqX_bc0...	7,945,516	99.7	7,945,516	7,940,246
BioSample_7	IsoSeqX_bc07...	393,810	99.7	393,810	393,468
BioSample_8	IsoSeqX_bc0...	525,702	99.7	525,702	525,187
BioSample_9	IsoSeqX_bc0...	756,764	99.7	756,764	756,065
BioSample_10	IsoSeqX_bc10...	7,087,263	99.7	7,087,263	7,076,731
BioSample_11	IsoSeqX_bc11...	8,757,463	99.7	8,757,463	8,742,764
BioSample_12	IsoSeqX_bc12...	7,683,601	99.7	7,683,601	7,671,108
Bio Sample 1	No Primer	2,065,027	0.0	0	0

Primer Read Statistics

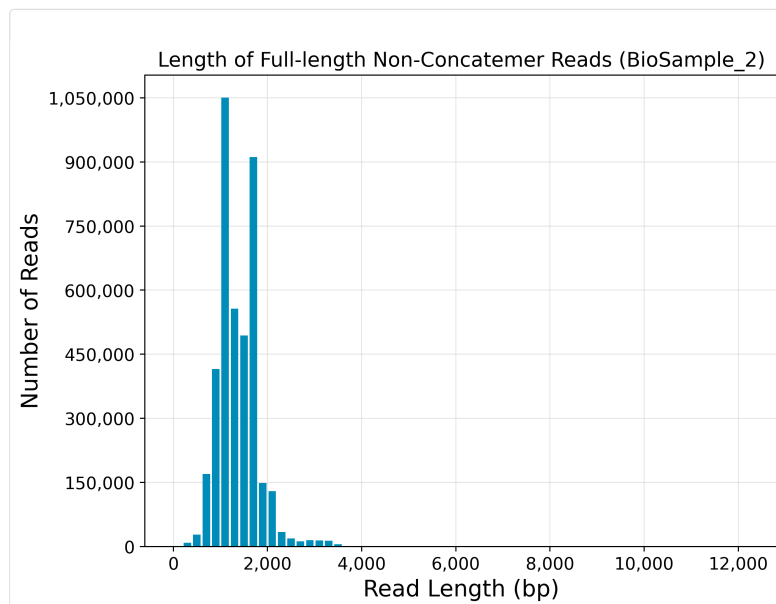
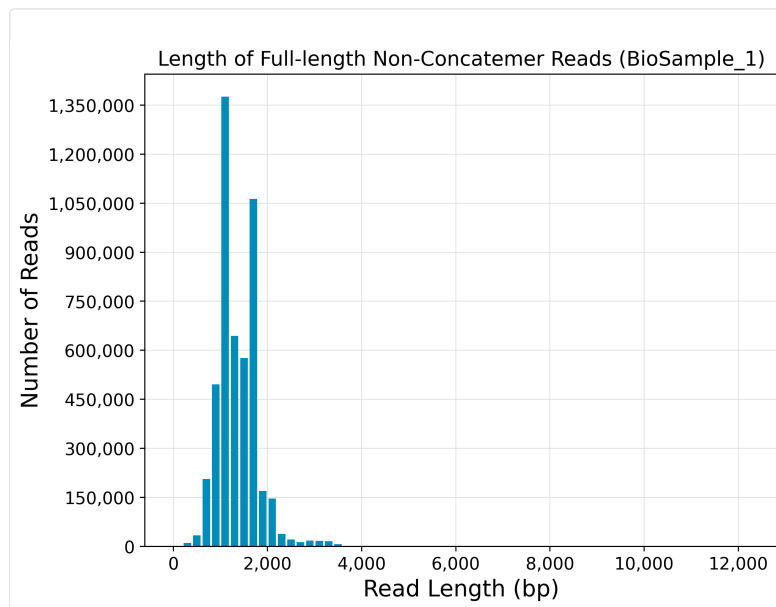
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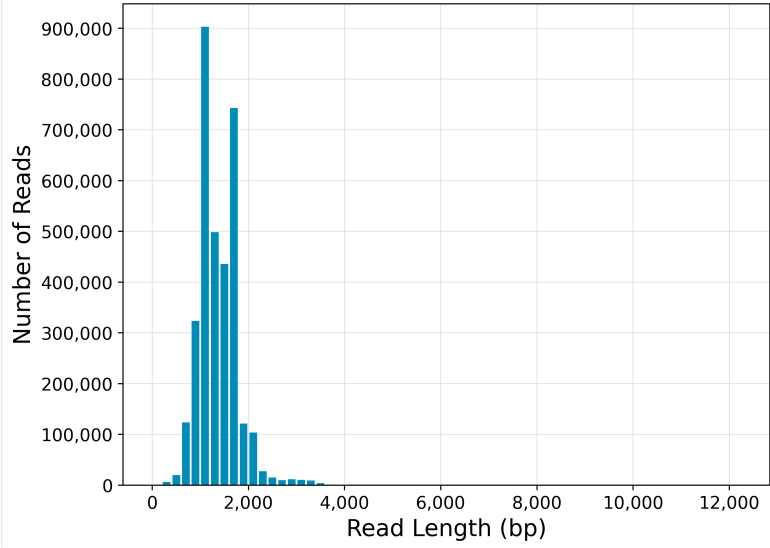
Primer Quality Scores



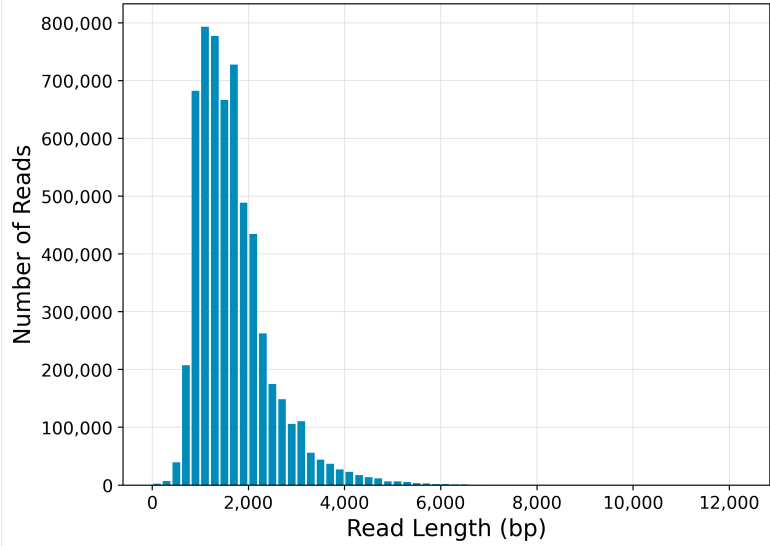
Length of Full-length Non-Concatemer Reads



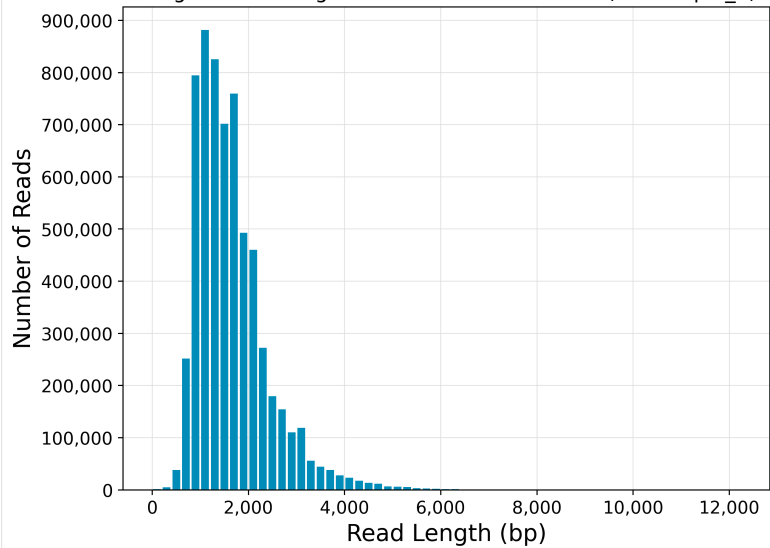
Length of Full-length Non-Concatemer Reads (BioSample_3)

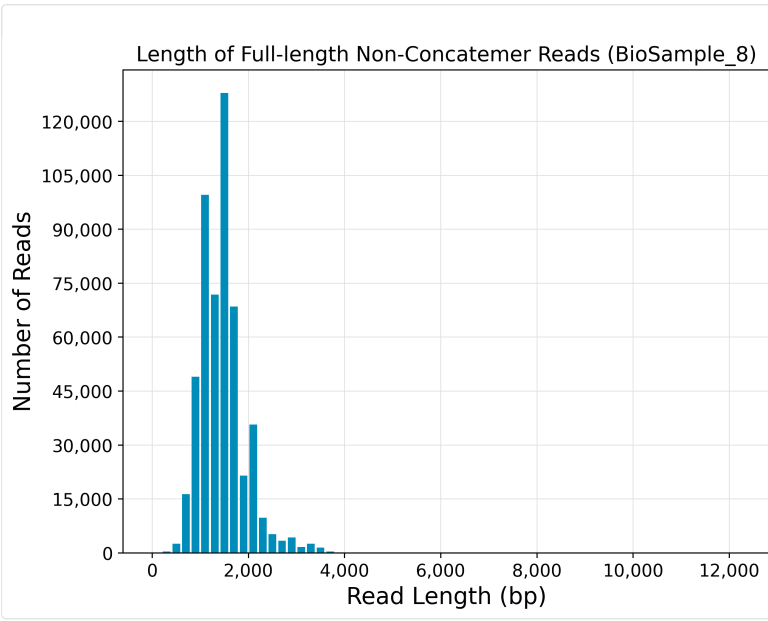
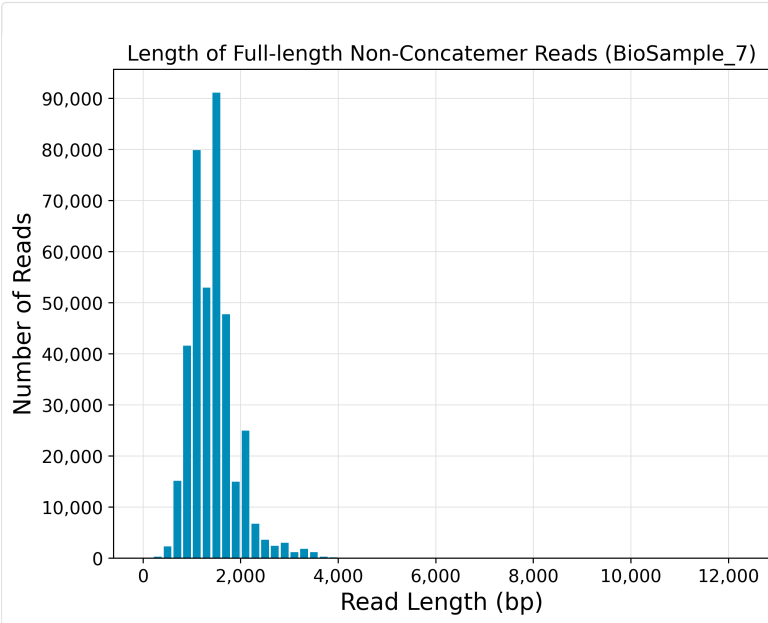
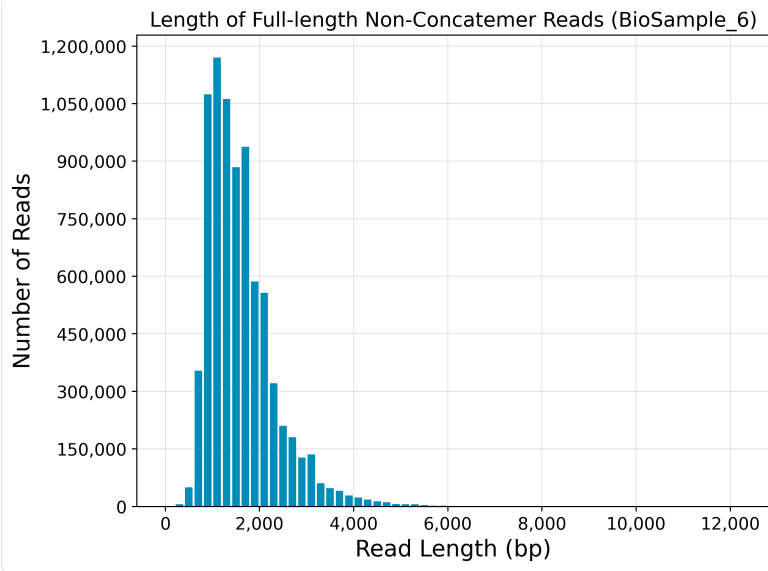


Length of Full-length Non-Concatemer Reads (BioSample_4)

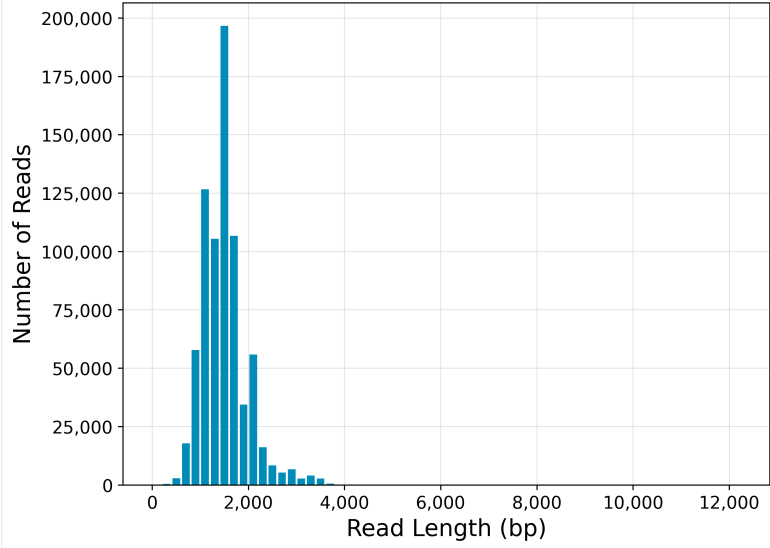


Length of Full-length Non-Concatemer Reads (BioSample_5)

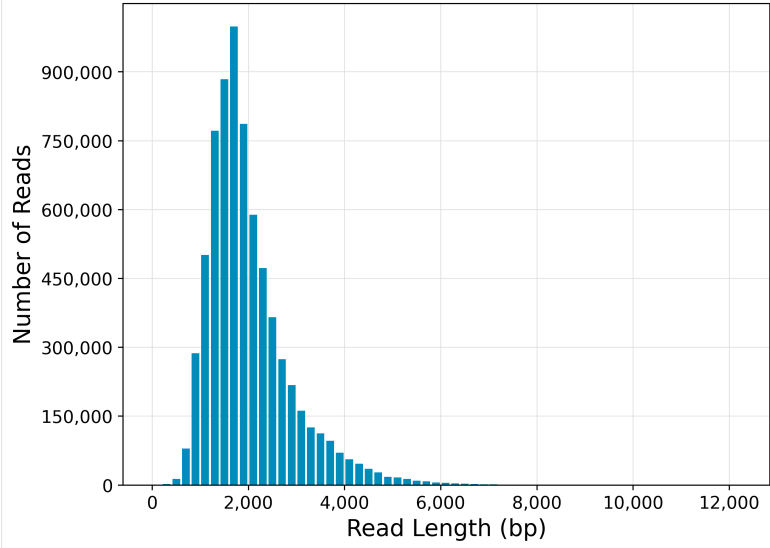




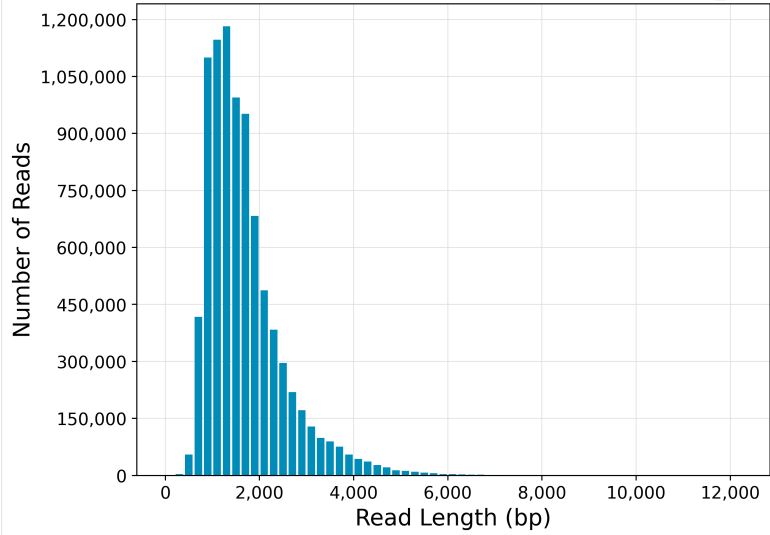
Length of Full-length Non-Concatemer Reads (BioSample_9)

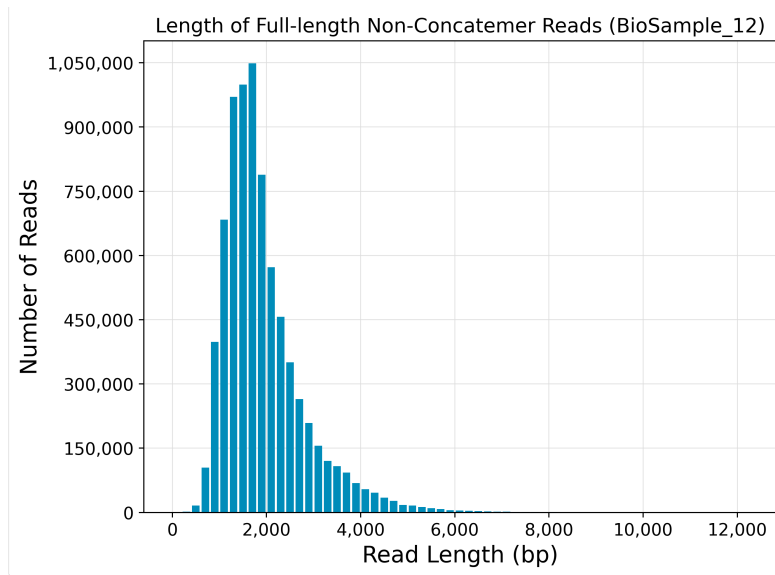


Length of Full-length Non-Concatemer Reads (BioSample_10)



Length of Full-length Non-Concatemer Reads (BioSample_11)

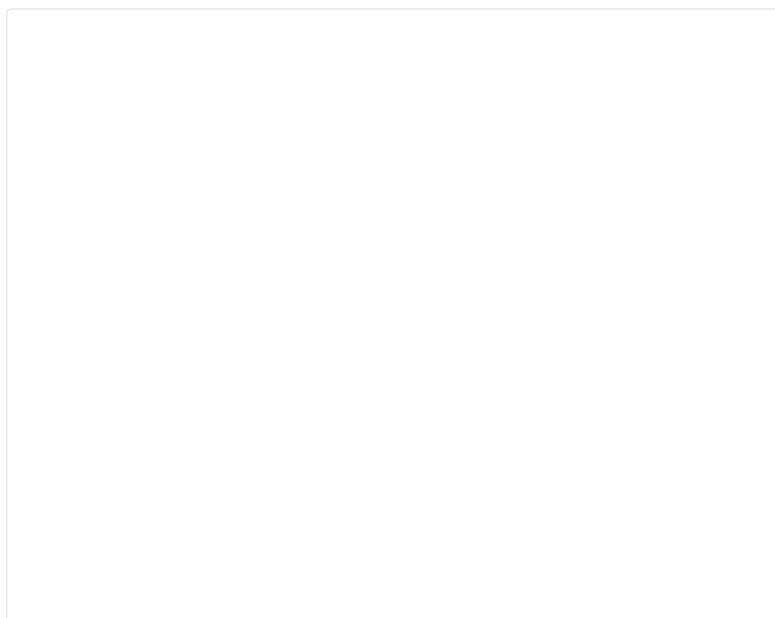




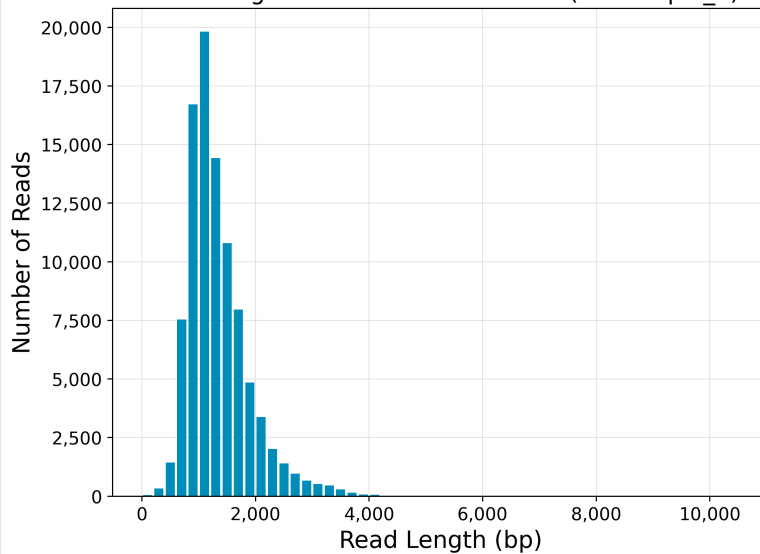
Summary Metrics

Sample Name ↓↑	Number of High-Quality Isoforms ↓↑
BioSample_1	93,909
BioSample_2	77,365
BioSample_3	69,509
BioSample_4	300,213
BioSample_5	316,156
BioSample_6	384,969
BioSample_7	16,808
BioSample_8	21,791
BioSample_9	29,943
BioSample_10	413,823
BioSample_11	470,867
BioSample_12	437,250

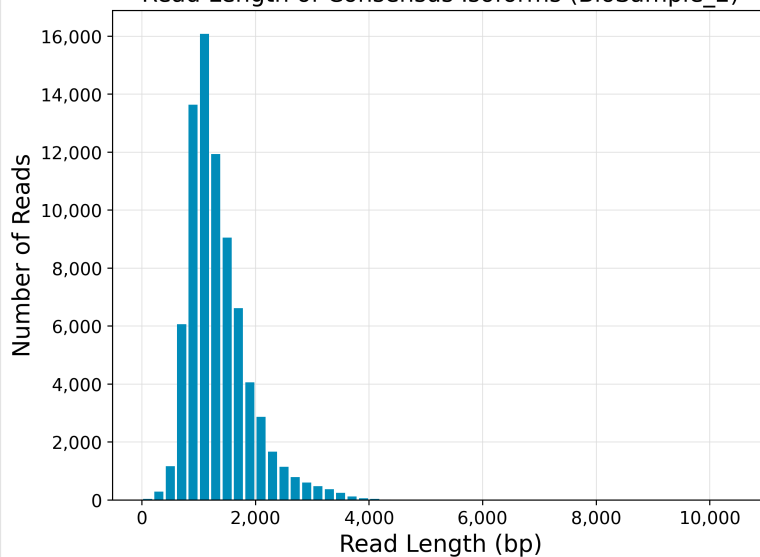
Length of Consensus Isoforms



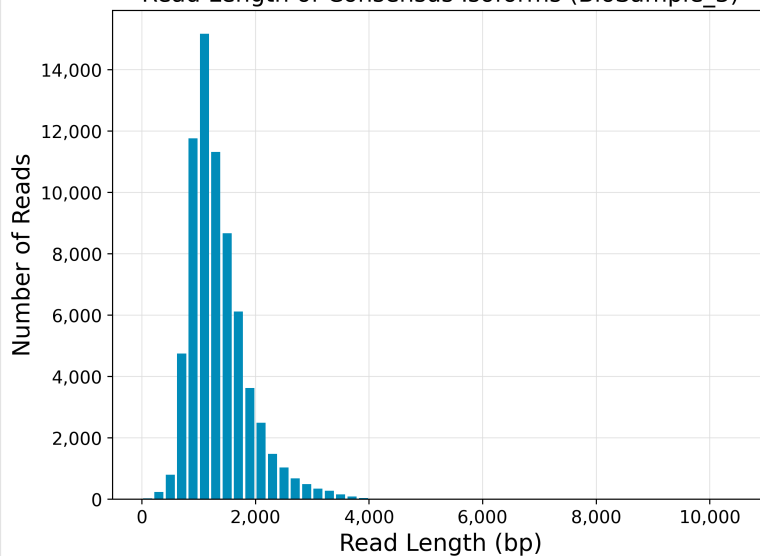
Read Length of Consensus Isoforms (BioSample_1)



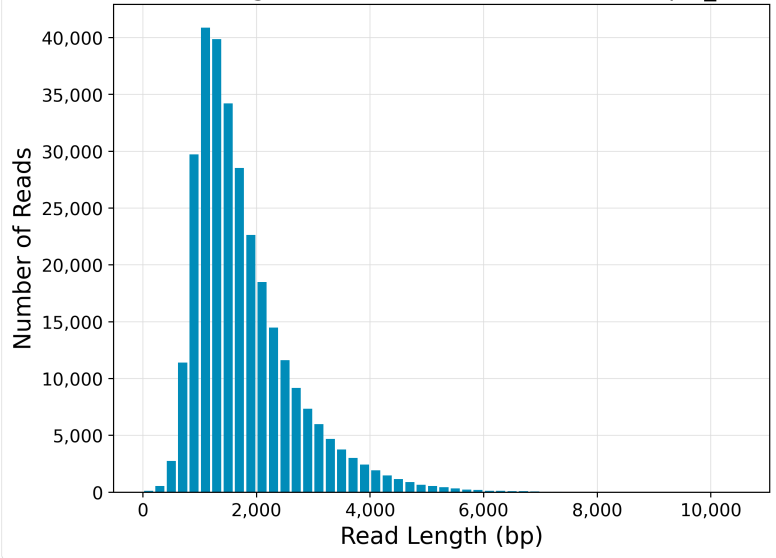
Read Length of Consensus Isoforms (BioSample_2)



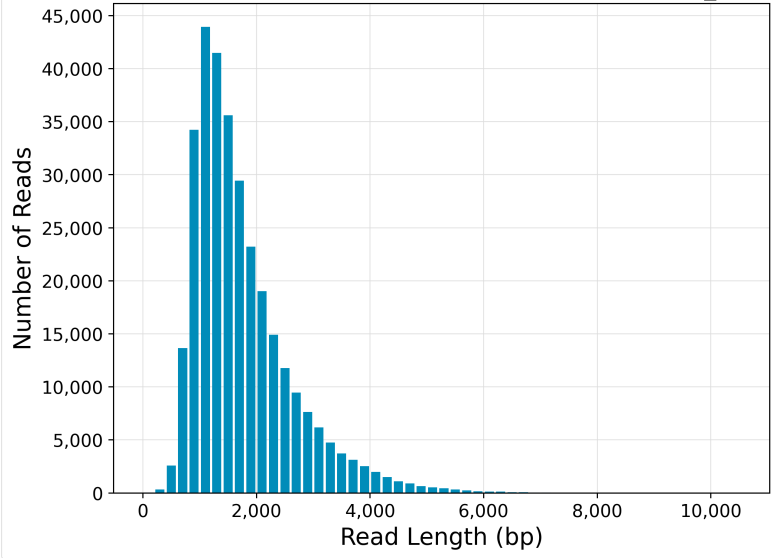
Read Length of Consensus Isoforms (BioSample_3)



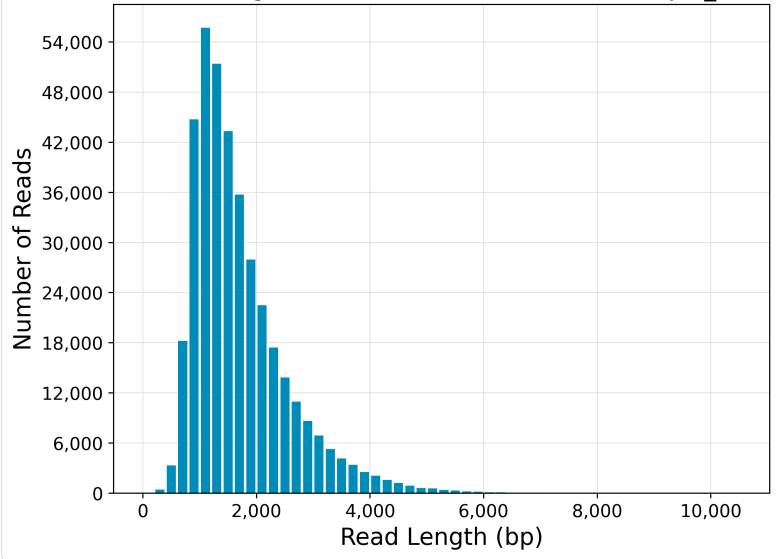
Read Length of Consensus Isoforms (BioSample_4)



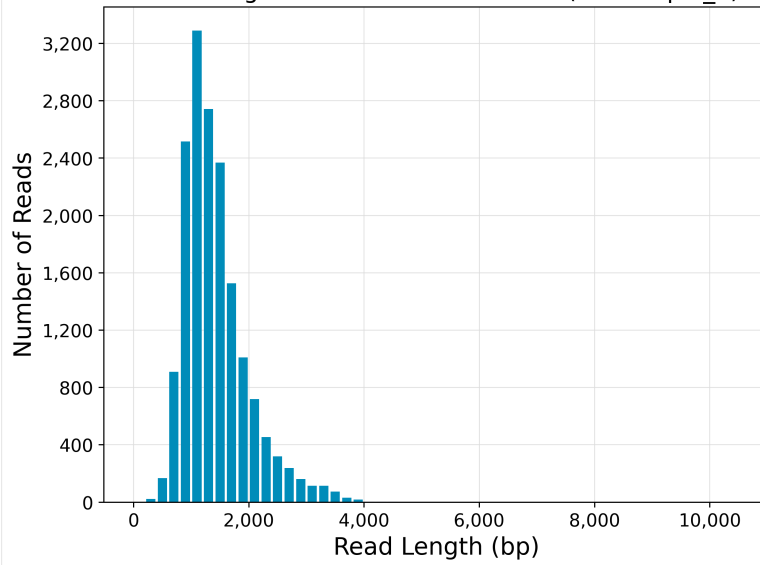
Read Length of Consensus Isoforms (BioSample_5)



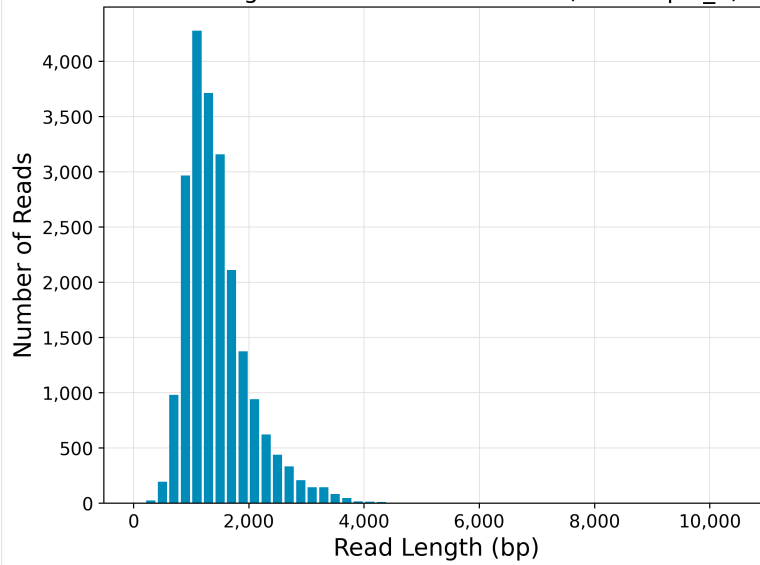
Read Length of Consensus Isoforms (BioSample_6)



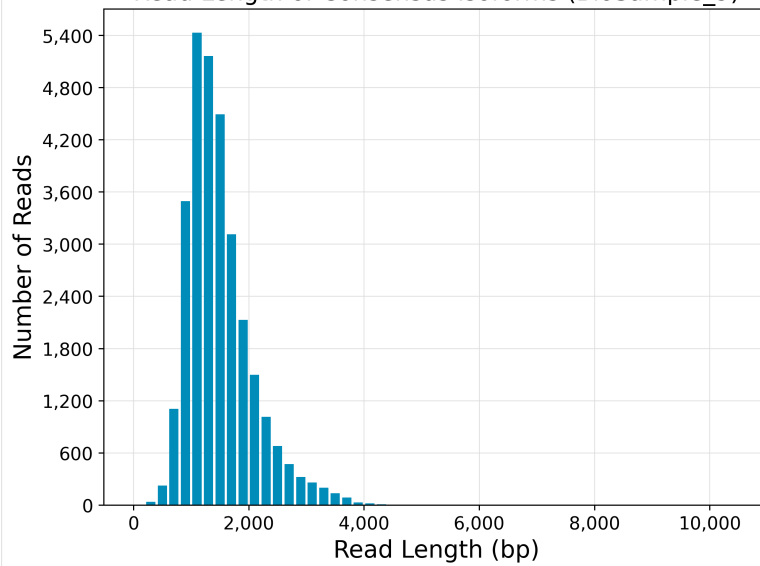
Read Length of Consensus Isoforms (BioSample_7)



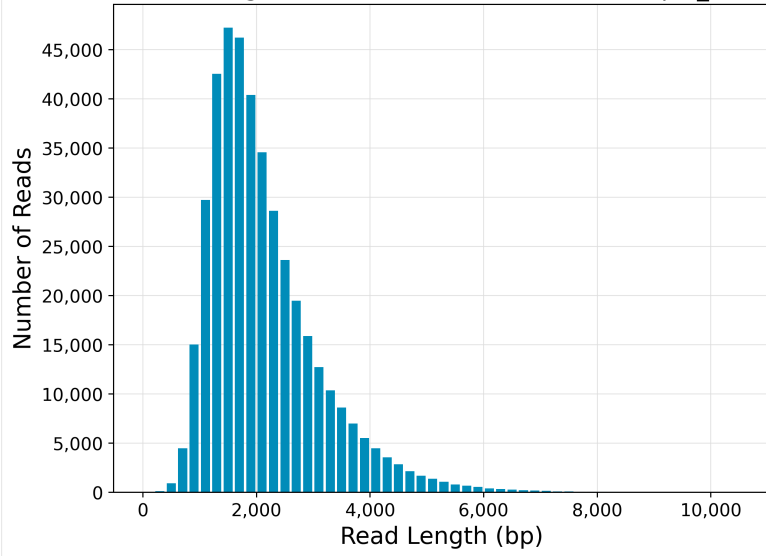
Read Length of Consensus Isoforms (BioSample_8)



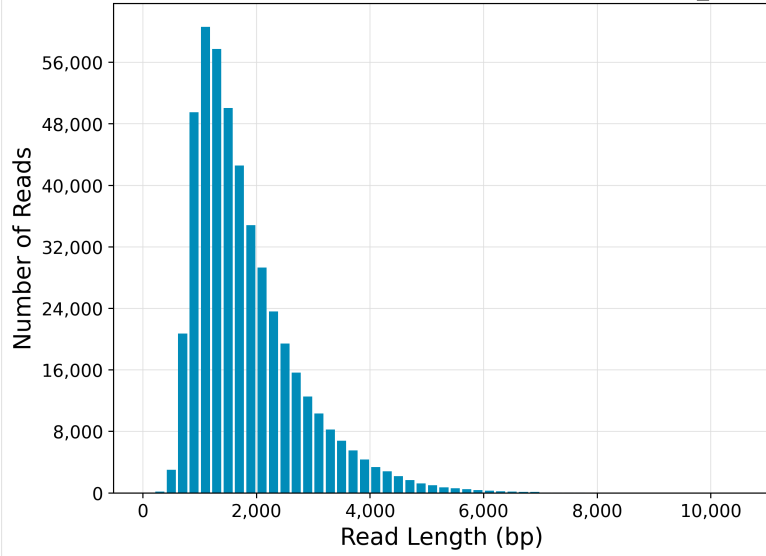
Read Length of Consensus Isoforms (BioSample_9)



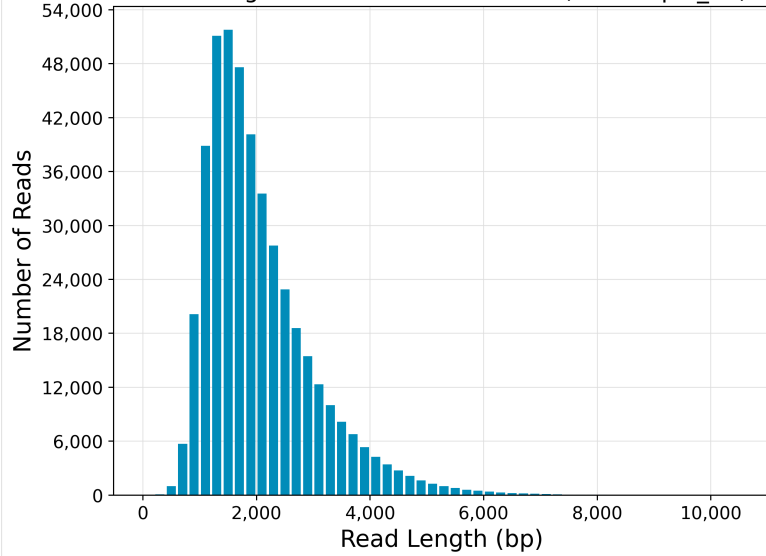
Read Length of Consensus Isoforms (BioSample_10)



Read Length of Consensus Isoforms (BioSample_11)



Read Length of Consensus Isoforms (BioSample_12)



Classification Summary Metrics

Sample N...	Genes	Genes, filt...	Known Ge...	Isoforms	Isoforms, ...	Known iso...
BioSample_1	16,876	9,139	9,036	46,557	24,755	14,769
BioSample_2	15,011	8,334	8,265	38,821	20,921	12,864
BioSample_3	13,729	7,951	7,895	35,438	19,492	12,111
BioSample_4	40,497	16,215	15,883	131,498	73,571	37,301
BioSample_5	43,921	16,495	16,120	139,099	75,978	38,012
BioSample_6	58,035	17,320	16,816	171,828	86,445	41,081
BioSample_7	5,140	3,958	3,950	9,780	6,824	4,996
BioSample_8	6,279	4,601	4,590	12,519	8,422	6,034
BioSample_9	8,178	5,626	5,605	17,157	11,026	7,545
BioSample...	72,258	16,619	16,077	195,081	89,807	40,550
BioSample...	87,747	17,507	16,801	220,672	95,287	43,566
BioSample...	79,605	16,775	16,237	207,251	92,098	41,442

Transcript Classification (BioSample_1)

Category	Count	CAGE Detected	CAGE Detected ...	polyA Motif Det...
FSM	17244	11483	66.59%	7952
ISM	27168	3598	13.24%	13257
NIC	4769	2858	59.92%	2033
NNC	13620	8313	61.03%	5281
Antisense	722	83	11.49%	226
Fusion	339	185	54.57%	176
More junctions	3	2	66.66%	0
Genic intron	1	0	0.00%	1
Genic genomic	3398	909	26.75%	1212
Intergenic	4366	48	1.09%	1376

Transcript Classification (BioSample_2)

Category	Count	CAGE Detected	CAGE Detected ...	polyA Motif Det...
FSM	14587	9681	66.36%	6705
ISM	22632	2962	13.08%	11006
NIC	3968	2293	57.78%	1693
NNC	10639	6413	60.27%	4206
Antisense	558	66	11.82%	159
Fusion	287	146	50.87%	155
More junctions	2	2	100.00%	1
Genic intron	0	0	0.00%	0
Genic genomic	2815	695	24.68%	973
Intergenic	3552	37	1.04%	1117

Transcript Classification (BioSample_3)

Category	Count	CAGE Detected	CAGE Detected ...	polyA Motif Det...
FSM	13472	9063	67.27%	6172
ISM	20690	2670	12.90%	10188
NIC	3442	2019	58.65%	1491
NNC	10062	6058	60.20%	4078
Antisense	472	75	15.88%	153
Fusion	222	129	58.10%	125
More junctions	0	0	0.00%	0
Genic intron	2	0	0.00%	0
Genic genomic	2493	605	24.26%	937
Intergenic	2765	32	1.15%	872

Transcript Classification (BioSample_4)

Category	Count	CAGE Detected	CAGE Detected ...	polyA Motif Det...
FSM	60504	36025	59.54%	27937
ISM	117054	11502	9.82%	61397
NIC	22836	16492	72.21%	10669
NNC	27192	16149	59.38%	12553
Antisense	2942	271	9.21%	971
Fusion	651	377	57.91%	304
More junctions	31	19	61.29%	15
Genic intron	7	1	14.28%	1
Genic genomic	13854	3814	27.52%	5017
Intergenic	20368	183	0.89%	6611

Transcript Classification (BioSample_5)

Category	Count	CAGE Detected	CAGE Detected ...	polyA Motif Det...
FSM	61326	36057	58.79%	28559
ISM	122978	11610	9.44%	65061
NIC	23290	16610	71.31%	10986
NNC	29422	17503	59.48%	13710
Antisense	3111	267	8.58%	1009
Fusion	709	411	57.96%	315
More junctions	29	17	58.62%	13
Genic intron	11	2	18.18%	1
Genic genomic	14661	3791	25.85%	5388
Intergenic	23412	185	0.79%	7619

Transcript Classification (BioSample_6)

Category	Count	CAGE Detected	CAGE Detected ...	polyA Motif Det...
FSM	67588	38293	56.65%	31446
ISM	146741	13096	8.92%	78167
NIC	27104	18776	69.27%	12782
NNC	36264	21037	58.01%	16887
Antisense	4139	305	7.36%	1383
Fusion	909	497	54.67%	408
More junctions	18	13	72.22%	9
Genic intron	21	1	4.76%	4
Genic genomic	19244	4377	22.74%	7055
Intergenic	36045	226	0.62%	11984

Transcript Classification (BioSample_7)

Category	Count	CAGE Detected	CAGE Detected ...	polyA Motif Det...
FSM	5367	4345	80.95%	2564
ISM	4736	937	19.78%	2419
NIC	1063	553	52.02%	469
NNC	1755	1101	62.73%	990
Antisense	69	9	13.04%	27
Fusion	65	48	73.84%	37
More junctions	0	0	0.00%	0
Genic intron	1	0	0.00%	0
Genic genomic	614	105	17.10%	239
Intergenic	321	6	1.86%	101

Transcript Classification (BioSample_8)

Category	Count	CAGE Detected	CAGE Detected ...	polyA Motif Det...
FSM	6523	5195	79.64%	3192
ISM	6227	1189	19.09%	3116
NIC	1400	708	50.57%	604
NNC	2285	1405	61.48%	1237
Antisense	111	14	12.61%	32
Fusion	80	61	76.25%	44
More junctions	0	0	0.00%	0
Genic intron	1	0	0.00%	1
Genic genomic	830	145	17.46%	347
Intergenic	569	6	1.05%	183

Transcript Classification (BioSample_9)

Category	Count	CAGE Detected	CAGE Detected ...	polyA Motif Det...
FSM	8351	6524	78.12%	3985
ISM	8628	1586	18.38%	4479
NIC	2005	1072	53.46%	898
NNC	3358	2041	60.78%	1754
Antisense	172	15	8.72%	57
Fusion	133	90	67.66%	63
More junctions	0	0	0.00%	0
Genic intron	2	0	0.00%	0
Genic genomic	1218	254	20.85%	482
Intergenic	1105	10	0.90%	346

Transcript Classification (BioSample_10)

Category	Count	CAGE Detected	CAGE Detected ...	polyA Motif Det...
FSM	73691	46542	63.15%	34739
ISM	147725	16438	11.12%	83020
NIC	34517	26131	75.70%	16250
NNC	32976	20779	63.01%	15456
Antisense	4257	249	5.84%	1354
Fusion	778	487	62.59%	355
More junctions	17	12	70.58%	10
Genic intron	70	0	0.00%	20
Genic genomic	24997	4948	19.79%	9479
Intergenic	50926	296	0.58%	17180

Transcript Classification (BioSample_11)

Category	Count	CAGE Detected	CAGE Detected ...	polyA Motif Det...
FSM	77887	47999	61.62%	36445
ISM	167249	19295	11.53%	91987
NIC	34863	26434	75.82%	16415
NNC	36191	23226	64.17%	16798
Antisense	5133	332	6.46%	1616
Fusion	803	500	62.26%	382
More junctions	10	9	90.00%	6
Genic intron	110	1	0.90%	28
Genic genomic	28009	5582	19.92%	10429
Intergenic	64941	393	0.60%	21407

Transcript Classification (BioSample_12)

Category	Count	CAGE Detected	CAGE Detected ...	polyA Motif Det...
FSM	75865	47474	62.57%	35716
ISM	154534	17461	11.29%	86200
NIC	35426	26773	75.57%	16645
NNC	34182	21696	63.47%	16092
Antisense	4596	264	5.74%	1406
Fusion	772	488	63.21%	356
More junctions	17	7	41.17%	7
Genic intron	87	0	0.00%	22
Genic genomic	26666	5191	19.46%	10000
Intergenic	57782	314	0.54%	19553

Transcript Classification, filtered (BioSample_1)

Category	Count	CAGE Detected	CAGE Detected,...	polyA Detected
FSM	15848	10594	66.84%	7952
ISM	12884	2112	16.39%	6742
NIC	4264	2544	59.66%	1963
NNC	5368	3253	60.59%	2360
Antisense	67	6	8.95%	38
Fusion	187	100	53.47%	104
More junctions	3	2	66.66%	0
Genic intron	0	0	0.00%	0
Genic genomic	38	19	50.00%	24
Intergenic	59	4	6.77%	43

Transcript Classification, filtered (BioSample_2)

Category	Count	CAGE Detected	CAGE Detected,...	polyA Detected
FSM	13397	8947	66.78%	6705
ISM	10763	1789	16.62%	5585
NIC	3535	2021	57.17%	1642
NNC	4242	2529	59.61%	1928
Antisense	58	2	3.44%	40
Fusion	156	76	48.71%	89
More junctions	1	1	100.00%	0
Genic intron	0	0	0.00%	0
Genic genomic	39	19	48.71%	15
Intergenic	26	1	3.84%	21

Transcript Classification, filtered (BioSample_3)

Category	Count	CAGE Detected	CAGE Detected,...	polyA Detected
FSM	12428	8378	67.41%	6172
ISM	10023	1601	15.97%	5263
NIC	3072	1788	58.20%	1439
NNC	4081	2439	59.76%	1876
Antisense	42	6	14.28%	27
Fusion	132	74	56.06%	74
More junctions	0	0	0.00%	0
Genic intron	0	0	0.00%	0
Genic genomic	29	15	51.72%	12
Intergenic	25	2	8.00%	19

Transcript Classification, filtered (BioSample_4)

Category	Count	CAGE Detected	CAGE Detected,...	polyA Detected
FSM	54428	32225	59.20%	27937
ISM	56583	6873	12.14%	31757
NIC	20651	14953	72.40%	10336
NNC	14536	8964	61.66%	7461
Antisense	215	32	14.88%	139
Fusion	498	293	58.83%	267
More junctions	25	18	72.00%	14
Genic intron	0	0	0.00%	0
Genic genomic	171	87	50.87%	70
Intergenic	174	21	12.06%	112

Transcript Classification, filtered (BioSample_5)

Category	Count	CAGE Detected	CAGE Detected,...	polyA Detected
FSM	55307	32331	58.45%	28559
ISM	59189	6939	11.72%	33377
NIC	21163	15113	71.41%	10670
NNC	15552	9496	61.05%	8045
Antisense	240	36	15.00%	148
Fusion	546	324	59.34%	278
More junctions	22	15	68.18%	11
Genic intron	0	0	0.00%	0
Genic genomic	233	107	45.92%	97
Intergenic	210	23	10.95%	131

Transcript Classification, filtered (BioSample_6)

Category	Count	CAGE Detected	CAGE Detected,...	polyA Detected
FSM	60805	34311	56.42%	31446
ISM	69674	7866	11.28%	39736
NIC	24636	17118	69.48%	12409
NNC	19132	11474	59.97%	9875
Antisense	307	49	15.96%	182
Fusion	700	393	56.14%	359
More junctions	17	13	76.47%	9
Genic intron	0	0	0.00%	0
Genic genomic	286	136	47.55%	117
Intergenic	286	21	7.34%	185

Transcript Classification, filtered (BioSample_7)

Category	Count	CAGE Detected	CAGE Detected,...	polyA Detected
FSM	5078	4126	81.25%	2564
ISM	2811	582	20.70%	1603
NIC	948	478	50.42%	458
NNC	814	482	59.21%	543
Antisense	3	2	66.66%	1
Fusion	47	37	78.72%	29
More junctions	0	0	0.00%	0
Genic intron	0	0	0.00%	0
Genic genomic	11	4	36.36%	6
Intergenic	5	1	20.00%	4

Transcript Classification, filtered (BioSample_8)

Category	Count	CAGE Detected	CAGE Detected,...	polyA Detected
FSM	6147	4920	80.03%	3192
ISM	3600	722	20.05%	2006
NIC	1215	599	49.30%	581
NNC	1084	622	57.38%	706
Antisense	4	0	0.00%	3
Fusion	62	50	80.64%	38
More junctions	0	0	0.00%	0
Genic intron	0	0	0.00%	0
Genic genomic	16	5	31.25%	11
Intergenic	7	0	0.00%	6

Transcript Classification, filtered (BioSample_9)

Category	Count	CAGE Detected	CAGE Detected,...	polyA Detected
FSM	7815	6121	78.32%	3985
ISM	4888	988	20.21%	2812
NIC	1784	943	52.85%	866
NNC	1565	904	57.76%	962
Antisense	8	3	37.50%	4
Fusion	92	63	68.47%	50
More junctions	0	0	0.00%	0
Genic intron	0	0	0.00%	0
Genic genomic	19	8	42.10%	9
Intergenic	13	0	0.00%	10

Transcript Classification, filtered (BioSample_10)

Category	Count	CAGE Detected	CAGE Detected,...	polyA Detected
FSM	65805	41387	62.89%	34739
ISM	79317	9690	12.21%	48631
NIC	30762	23279	75.67%	15811
NNC	17226	11773	68.34%	9032
Antisense	185	49	26.48%	119
Fusion	505	323	63.96%	273
More junctions	11	9	81.81%	8
Genic intron	0	0	0.00%	0
Genic genomic	161	86	53.41%	95
Intergenic	407	48	11.79%	321

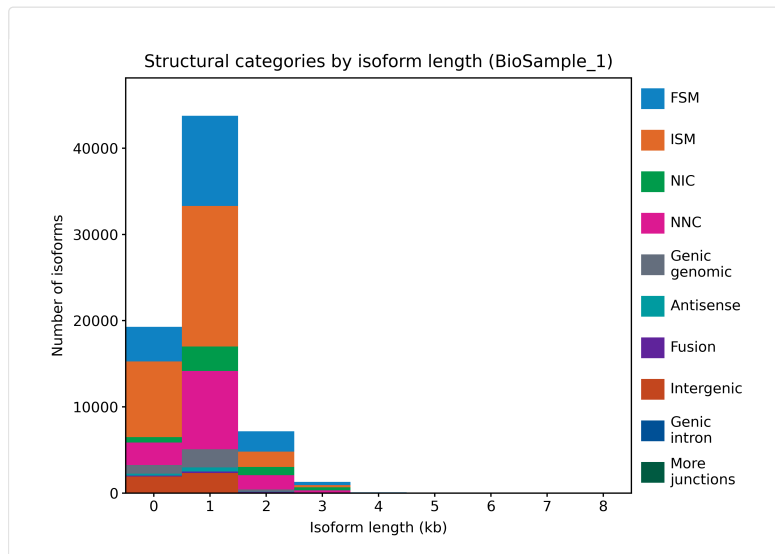
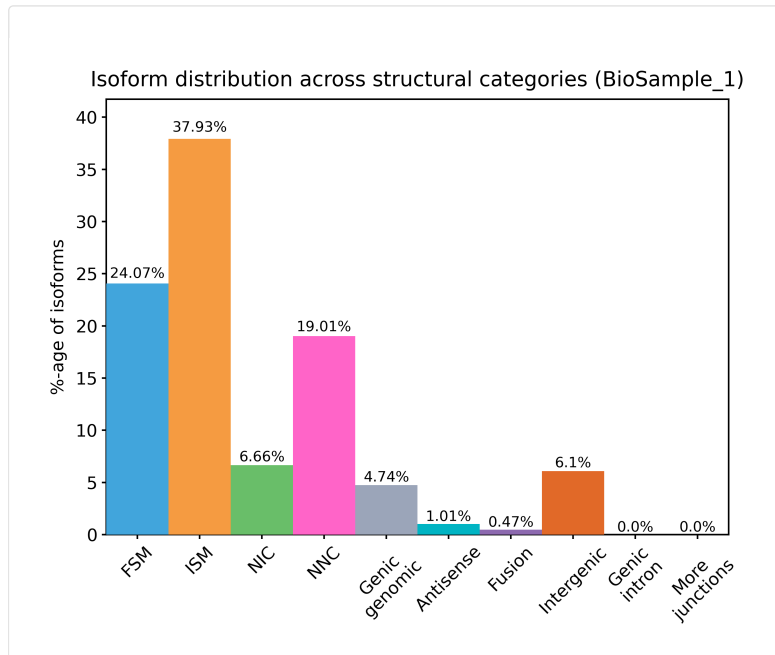
Transcript Classification, filtered (BioSample_11)

Category	Count	CAGE Detected	CAGE Detected,...	polyA Detected
FSM	69371	42503	61.26%	36445
ISM	85302	11304	13.25%	51406
NIC	31124	23565	75.71%	15961
NNC	19079	13146	68.90%	10060
Antisense	264	72	27.27%	170
Fusion	514	329	64.00%	272
More junctions	10	9	90.00%	6
Genic intron	0	0	0.00%	0
Genic genomic	220	107	48.63%	111
Intergenic	510	71	13.92%	379

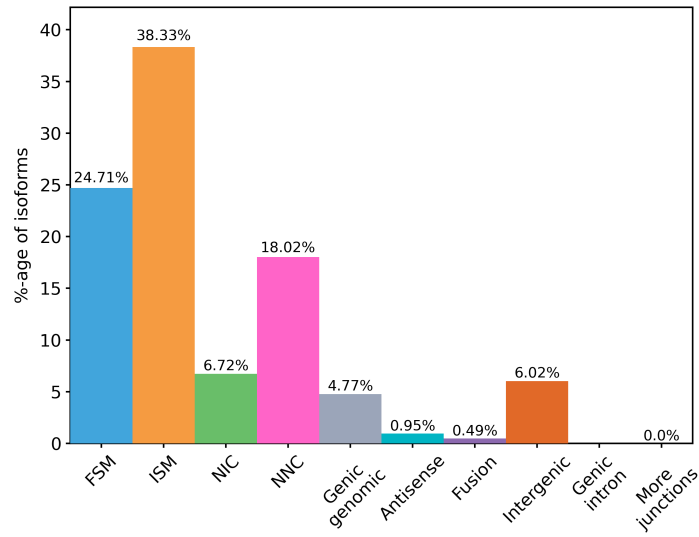
Transcript Classification, filtered (BioSample_12)

Category	Count	CAGE Detected	CAGE Detected,...	polyA Detected
FSM	67705	42065	62.12%	35716
ISM	81919	10247	12.50%	50068
NIC	31603	23882	75.56%	16173
NNC	17810	12232	68.68%	9481
Antisense	173	53	30.63%	108
Fusion	485	333	68.65%	260
More junctions	9	5	55.55%	7
Genic intron	0	0	0.00%	0
Genic genomic	171	95	55.55%	94
Intergenic	405	63	15.55%	319

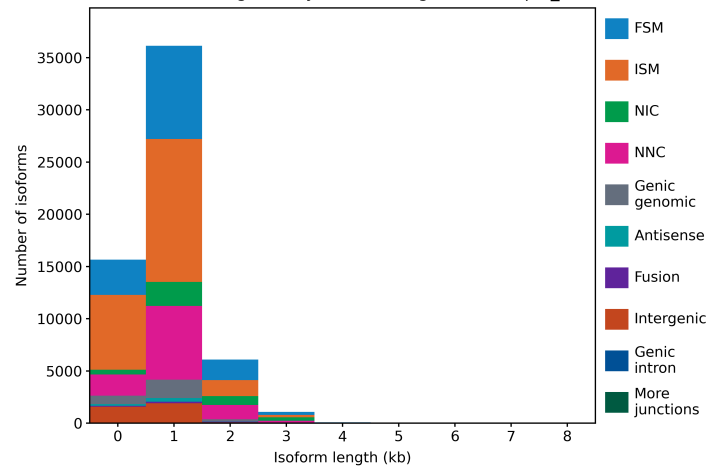
Transcript Classification Plots



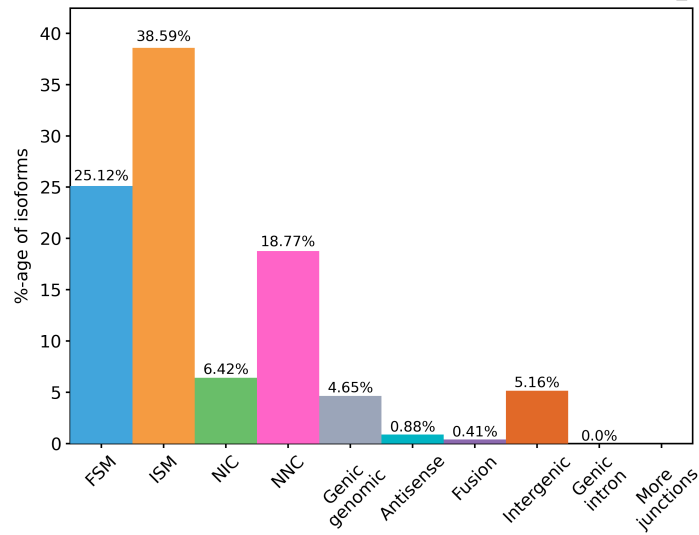
Isoform distribution across structural categories (BioSample_2)



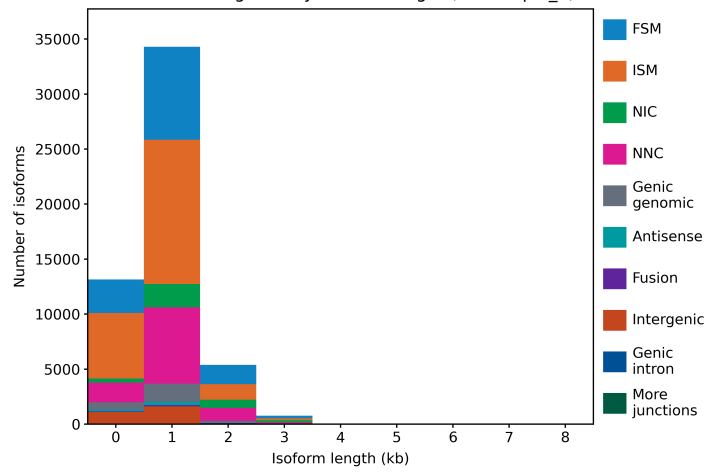
Structural categories by isoform length (BioSample_2)



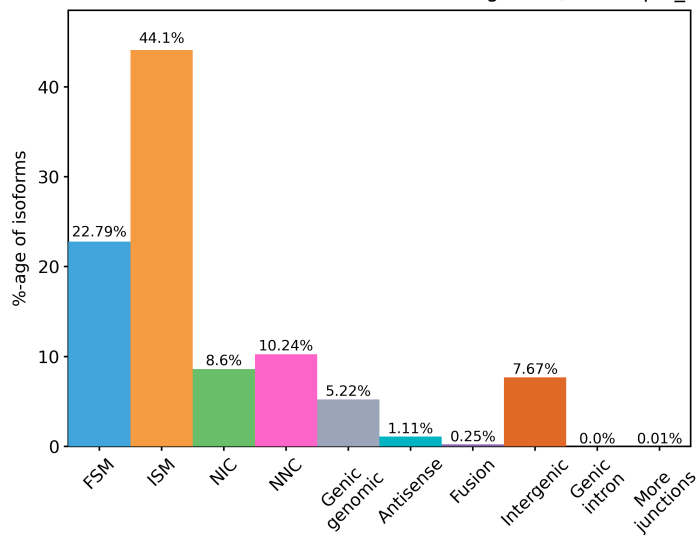
Isoform distribution across structural categories (BioSample_3)



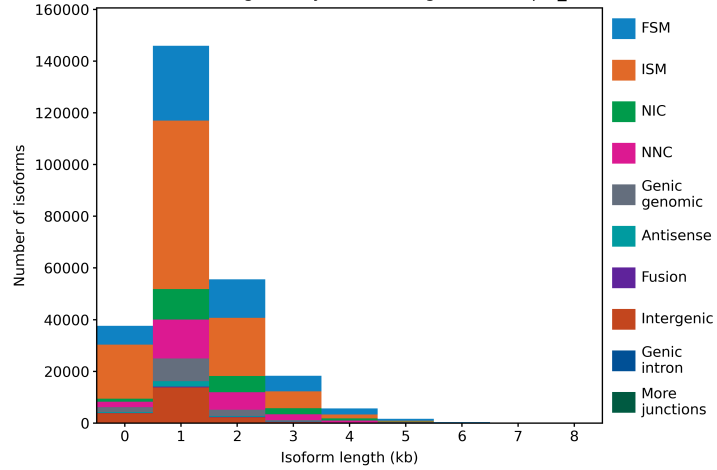
Structural categories by isoform length (BioSample_3)



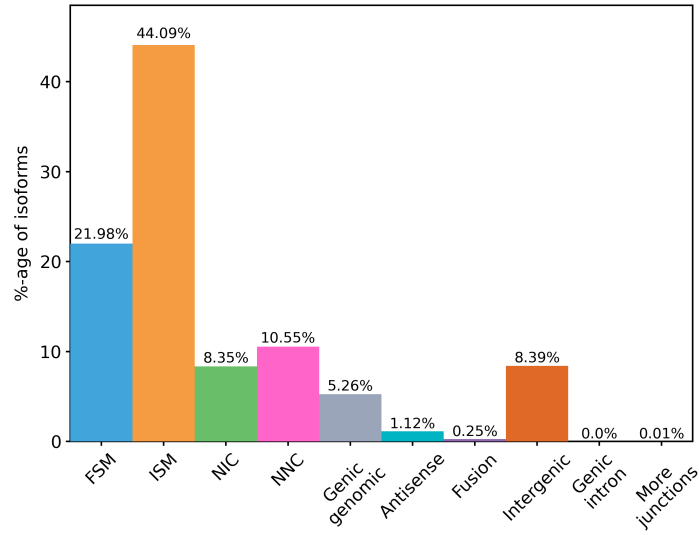
Isoform distribution across structural categories (BioSample_4)



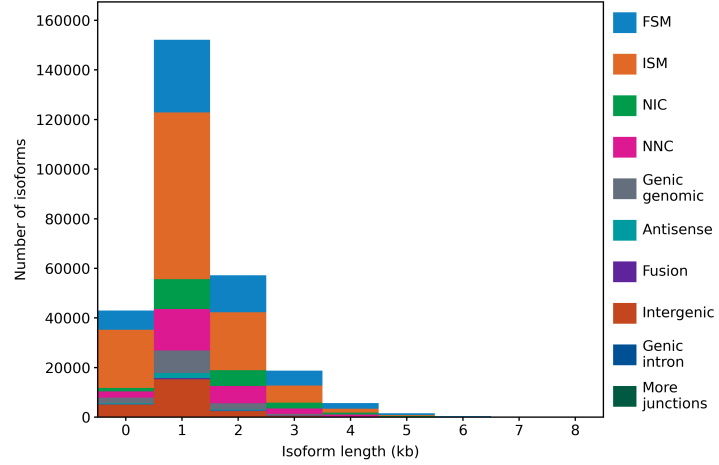
Structural categories by isoform length (BioSample_4)



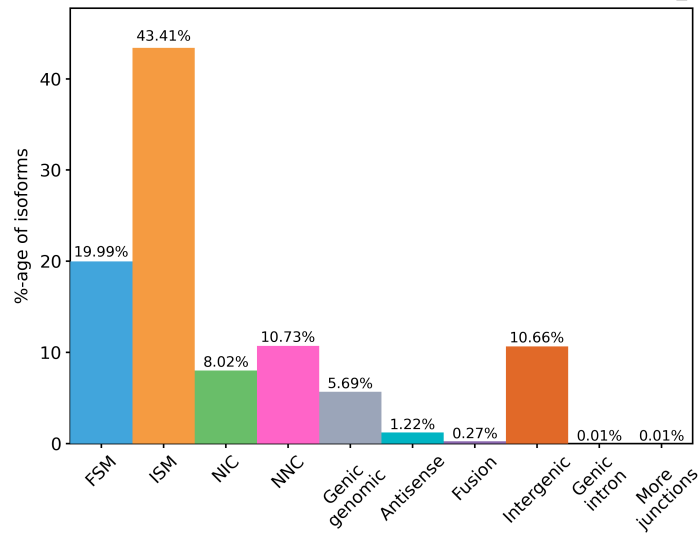
Isoform distribution across structural categories (BioSample_5)



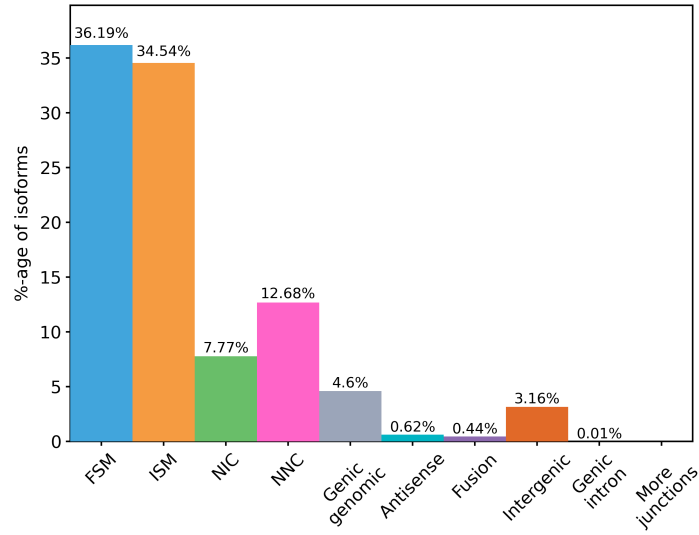
Structural categories by isoform length (BioSample_5)



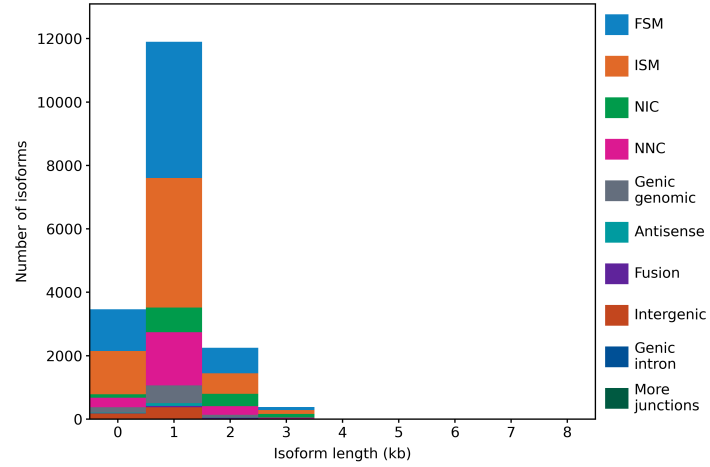
Isoform distribution across structural categories (BioSample_6)



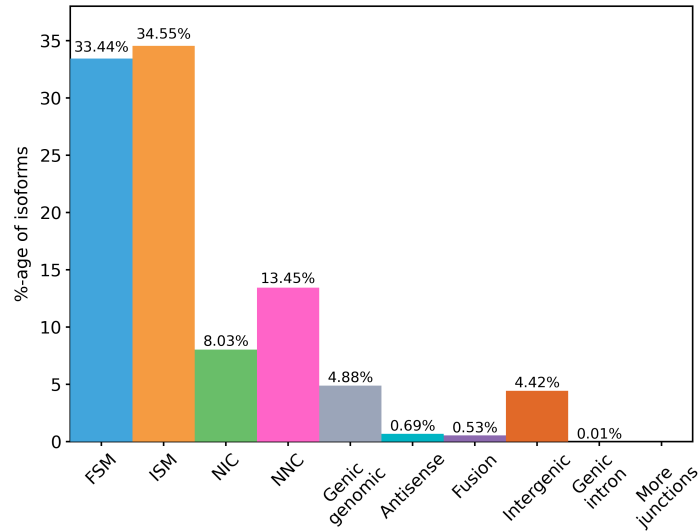
Isoform distribution across structural categories (BioSample_8)



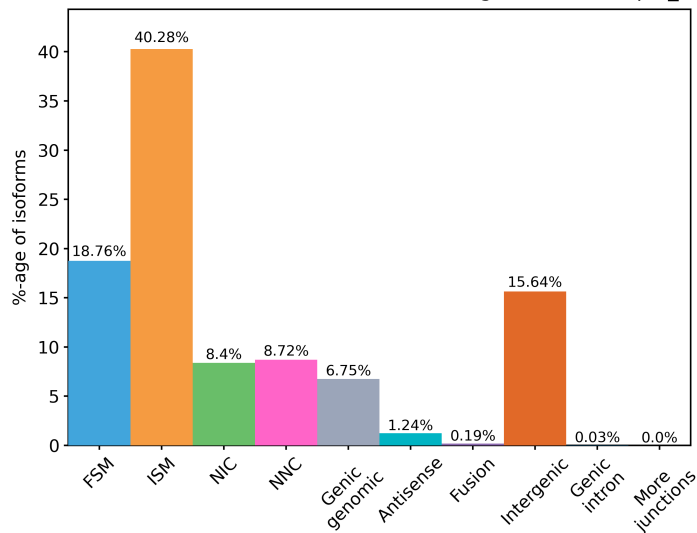
Structural categories by isoform length (BioSample_8)



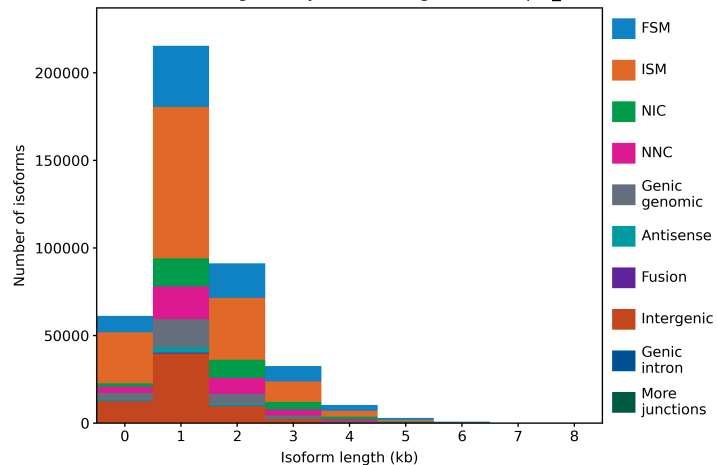
Isoform distribution across structural categories (BioSample_9)



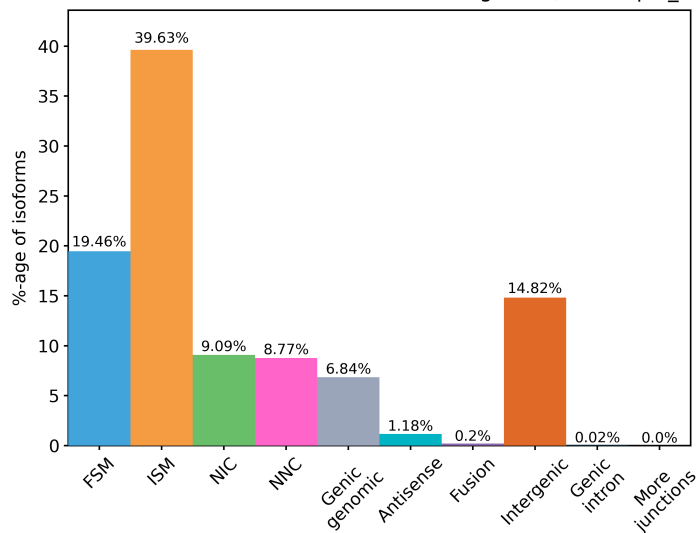
Isoform distribution across structural categories (BioSample_11)



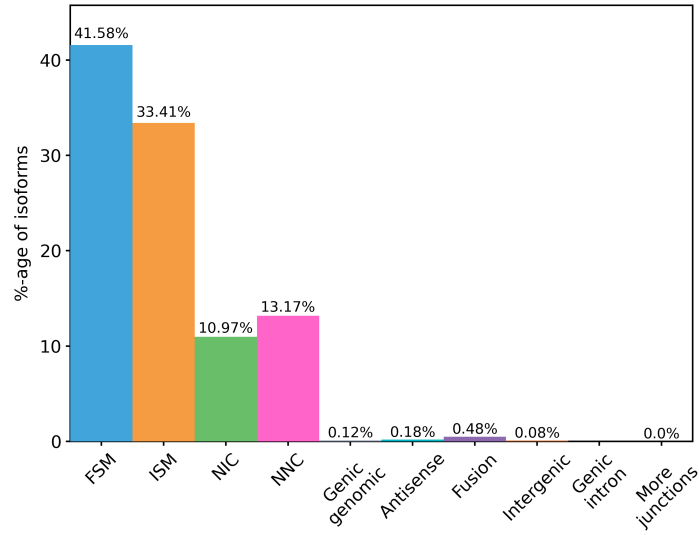
Structural categories by isoform length (BioSample_11)



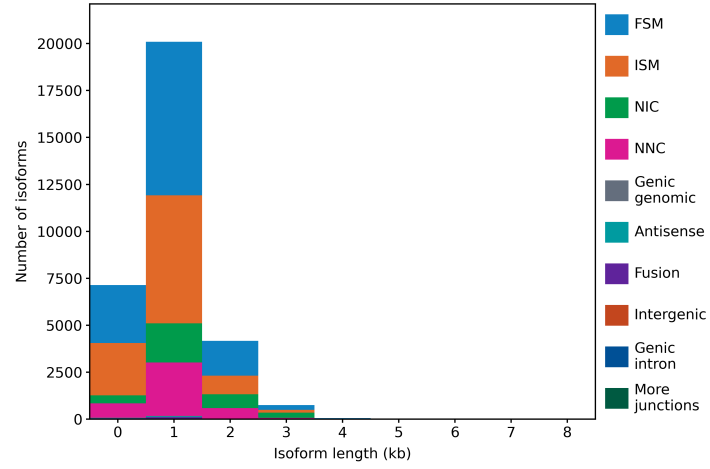
Isoform distribution across structural categories (BioSample_12)



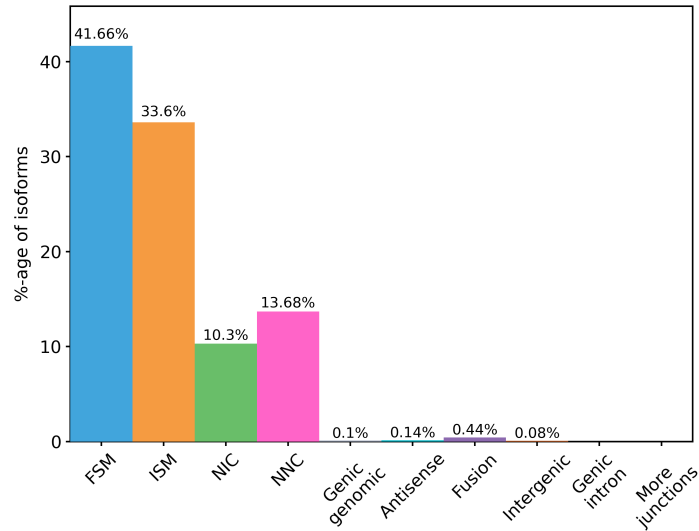
Isoform distribution across structural categories (BioSample_2)



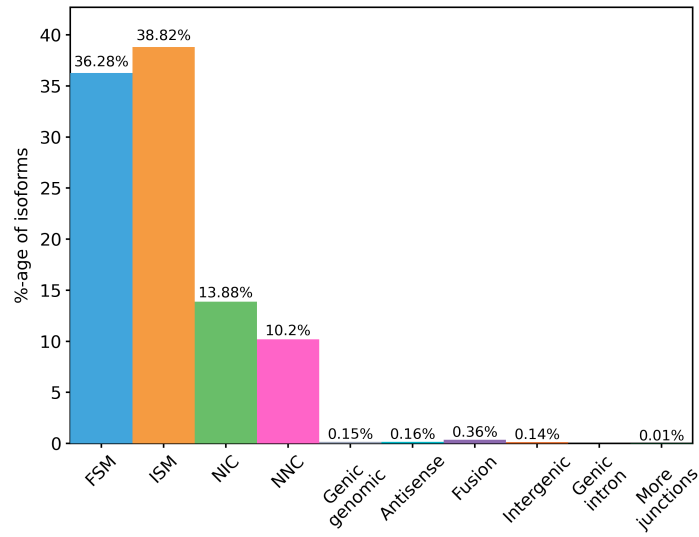
Structural categories by isoform length (BioSample_2)



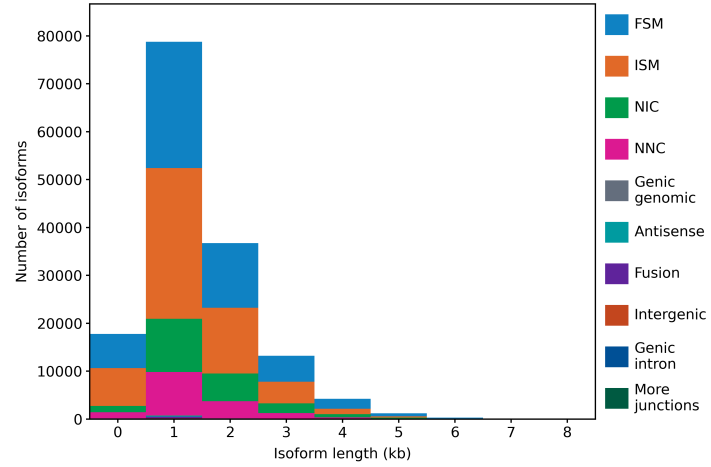
Isoform distribution across structural categories (BioSample_3)



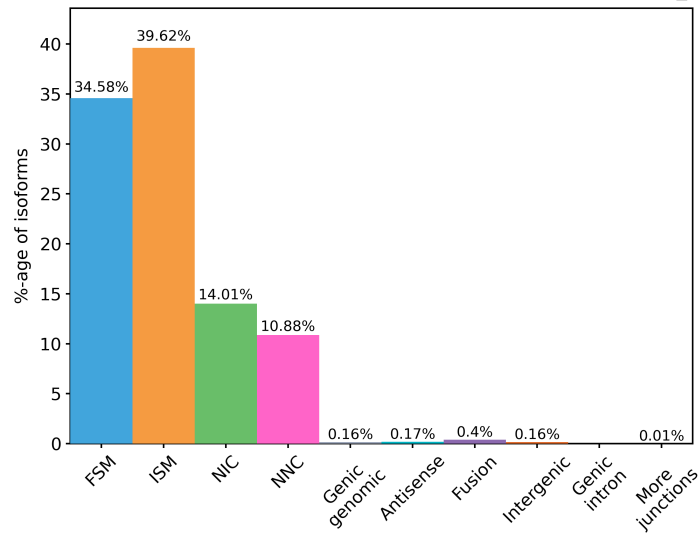
Isoform distribution across structural categories (BioSample_5)



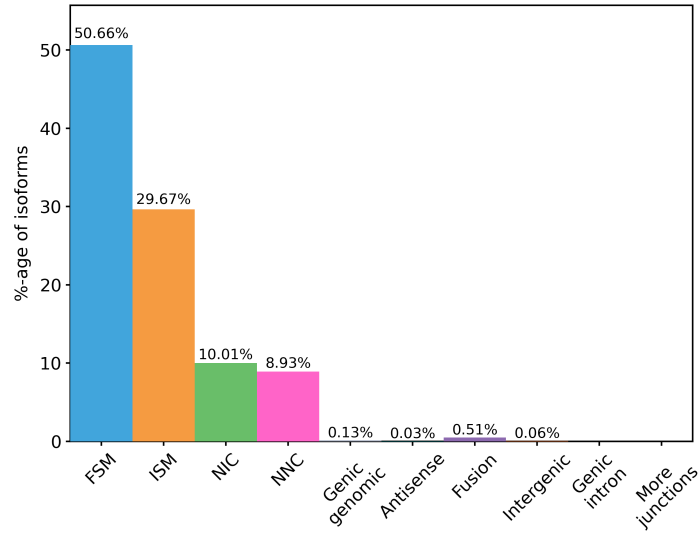
Structural categories by isoform length (BioSample_5)



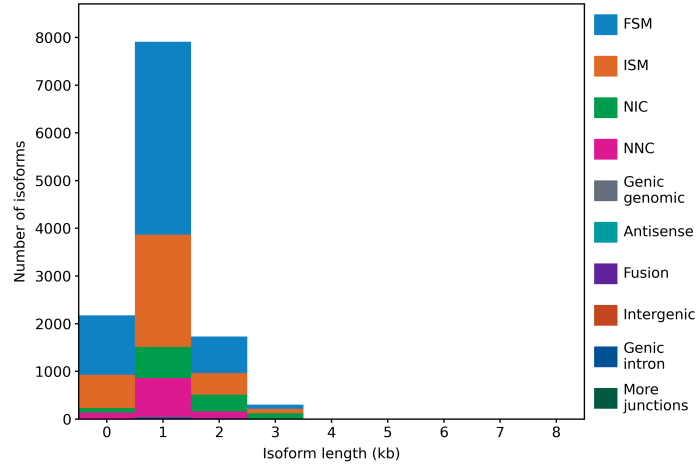
Isoform distribution across structural categories (BioSample_6)



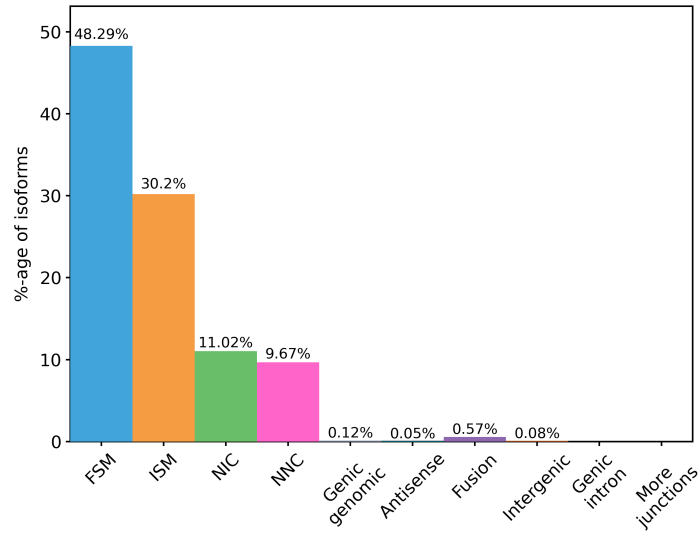
Isoform distribution across structural categories (BioSample_8)



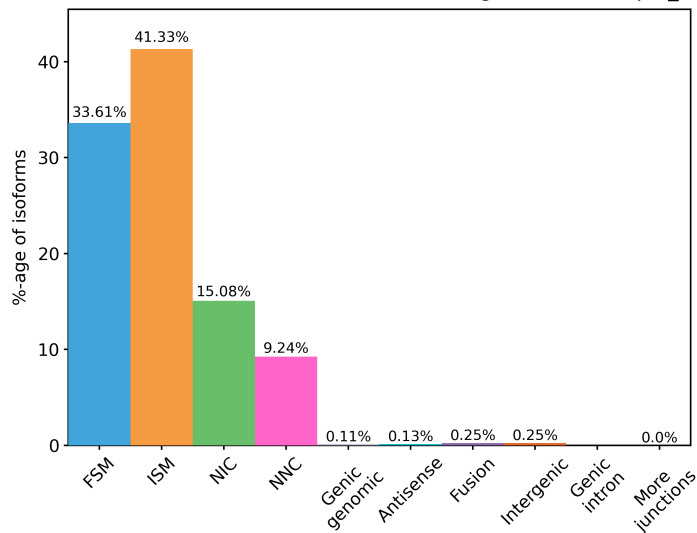
Structural categories by isoform length (BioSample_8)



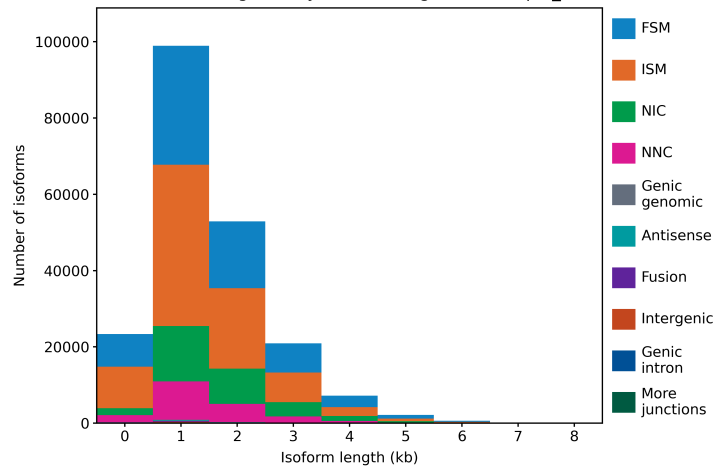
Isoform distribution across structural categories (BioSample_9)



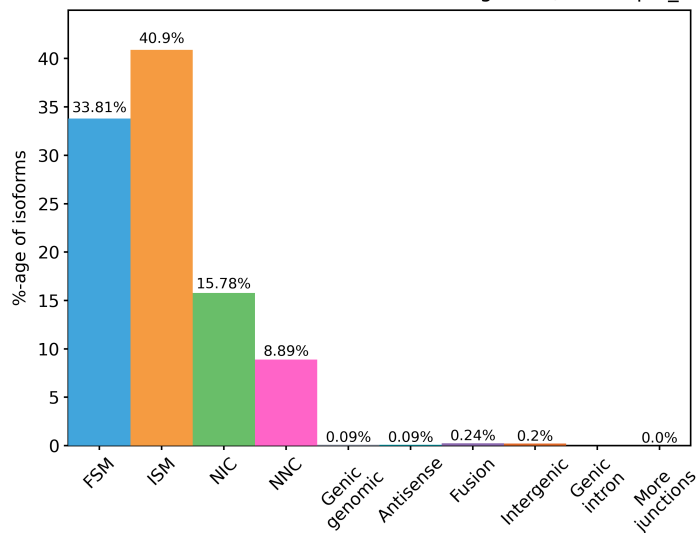
Isoform distribution across structural categories (BioSample_11)

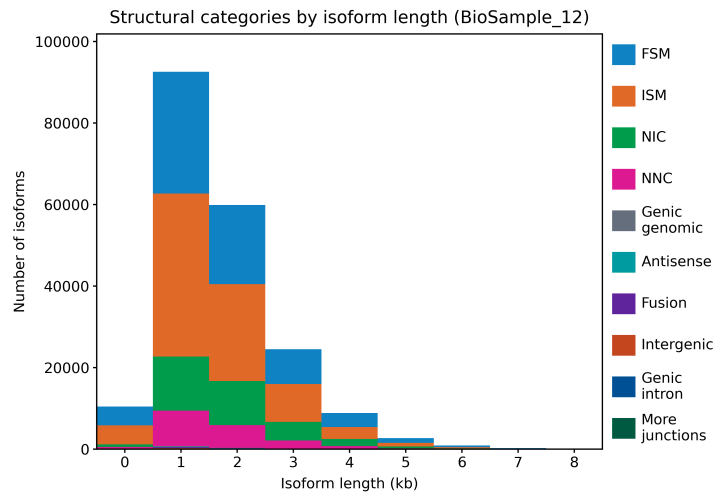


Structural categories by isoform length (BioSample_11)

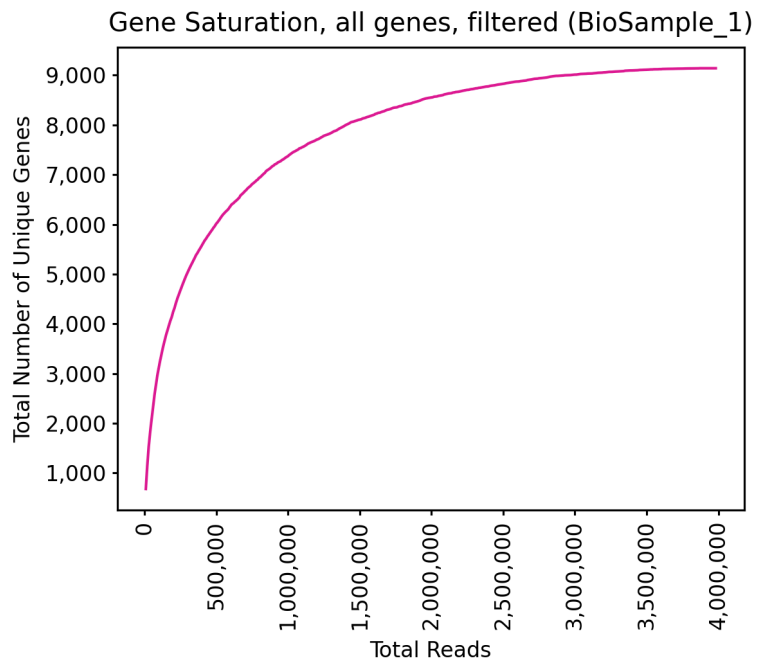


Isoform distribution across structural categories (BioSample_12)

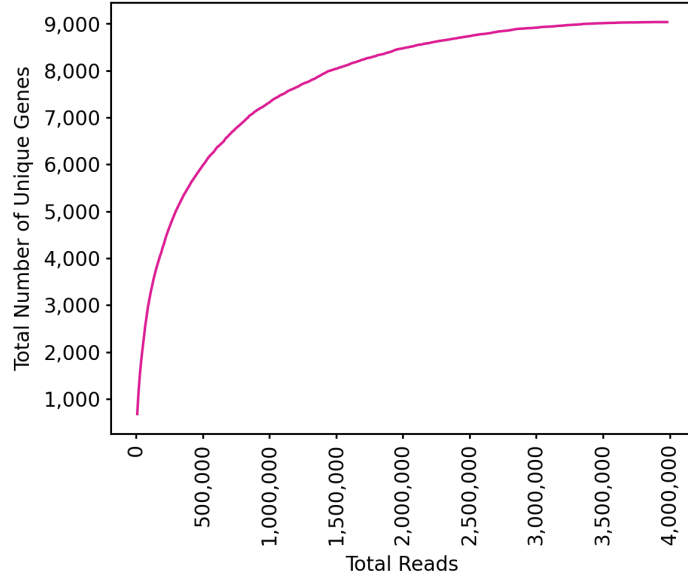




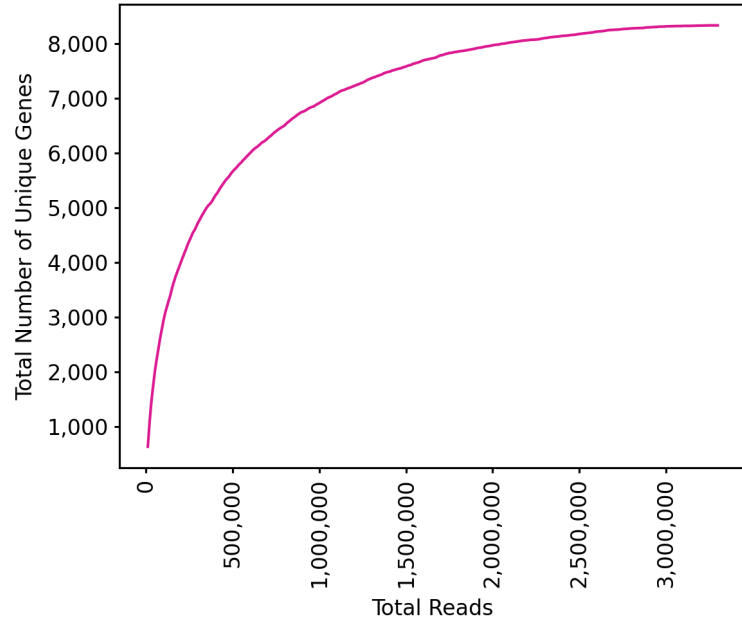
Gene Saturation



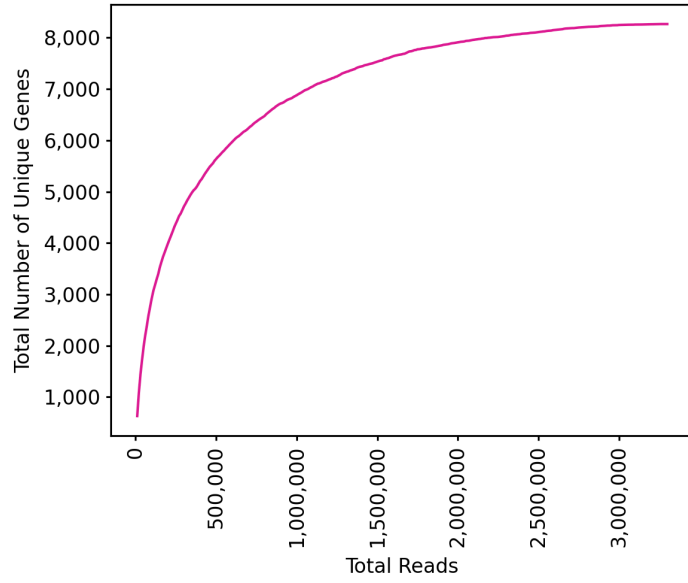
Gene Saturation, known genes only, filtered (BioSample_1)



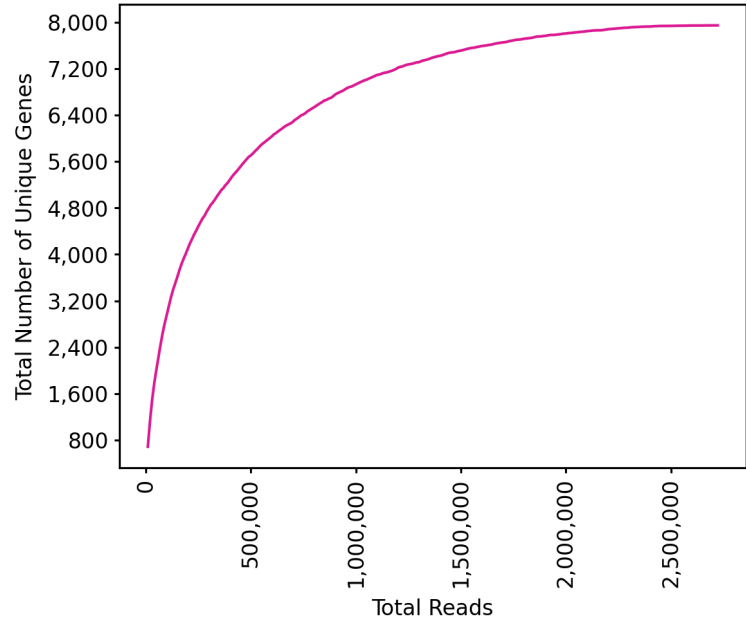
Gene Saturation, all genes, filtered (BioSample_2)



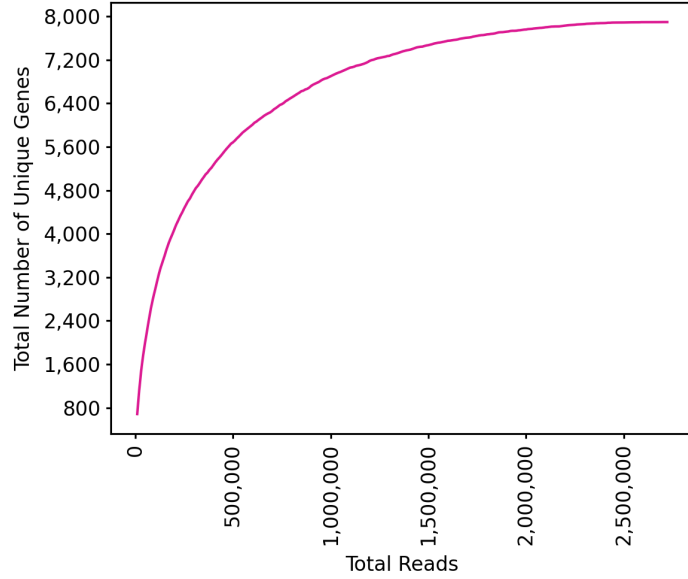
Gene Saturation, known genes only, filtered (BioSample_2)



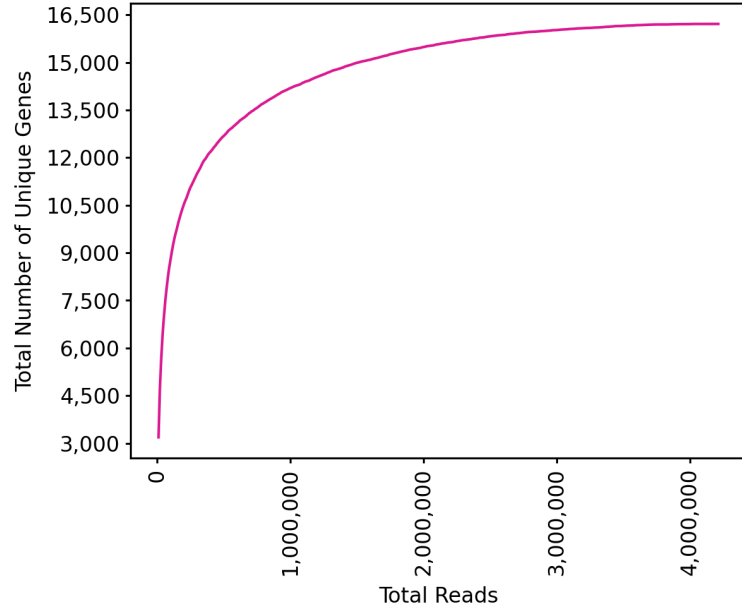
Gene Saturation, all genes, filtered (BioSample_3)



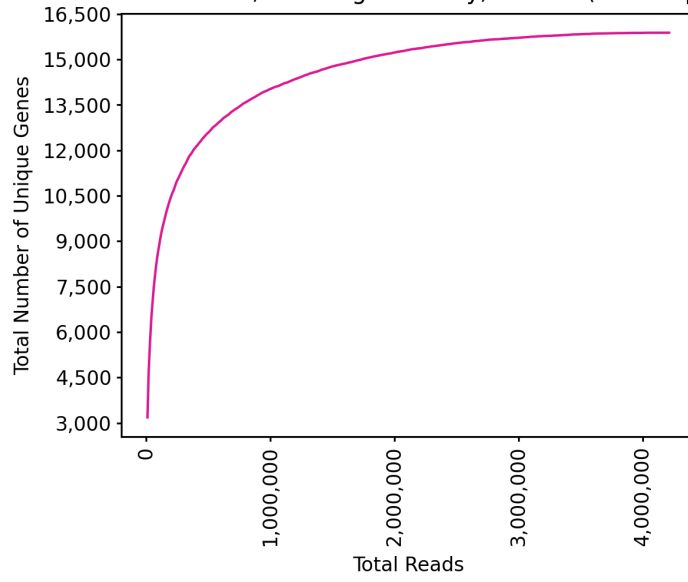
Gene Saturation, known genes only, filtered (BioSample_3)



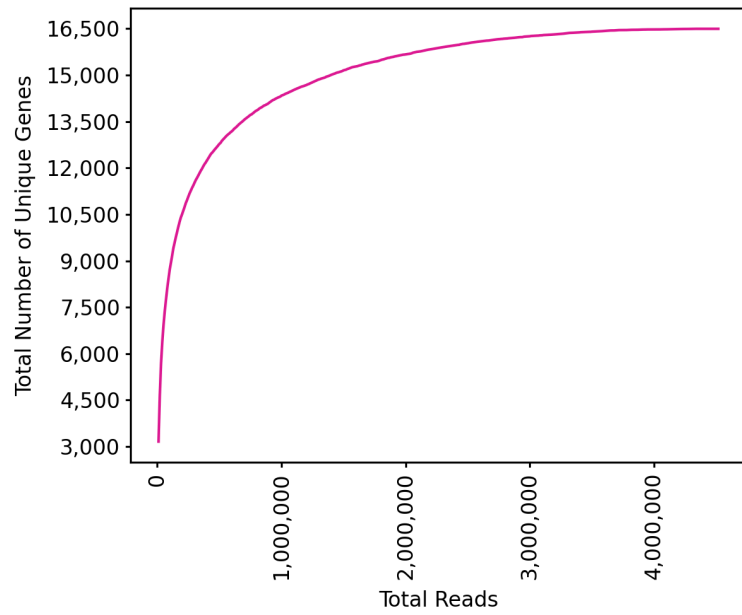
Gene Saturation, all genes, filtered (BioSample_4)



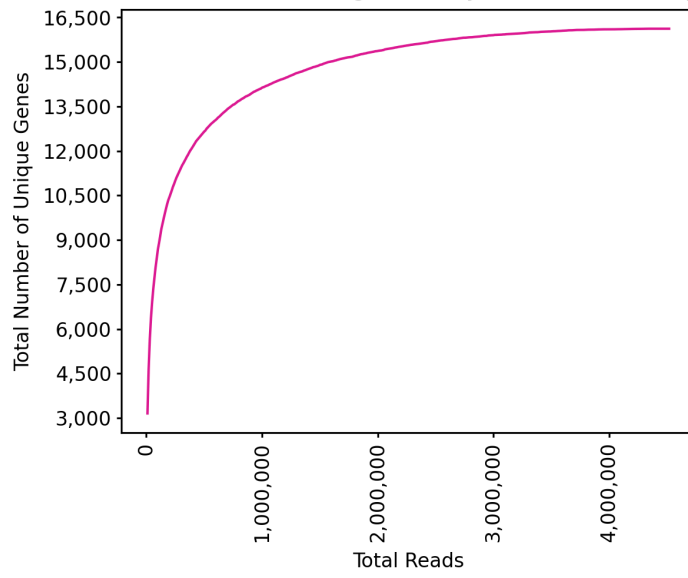
Gene Saturation, known genes only, filtered (BioSample_4)



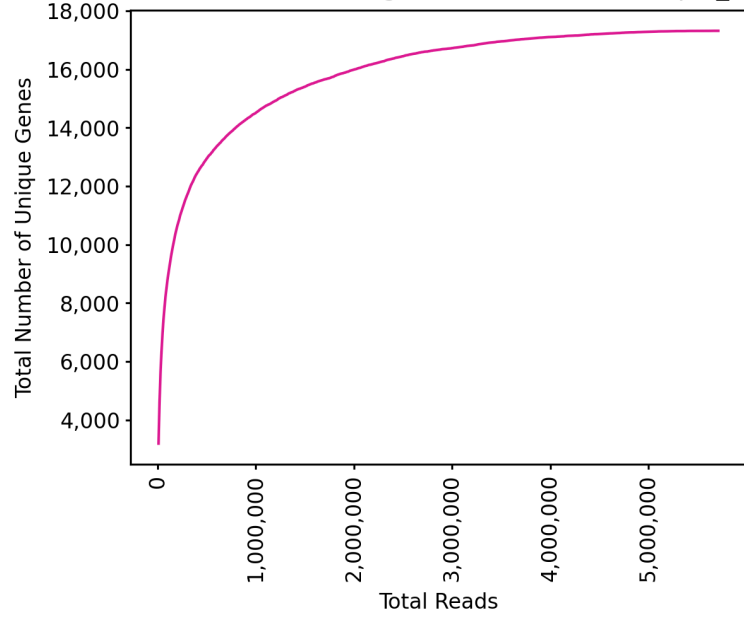
Gene Saturation, all genes, filtered (BioSample_5)



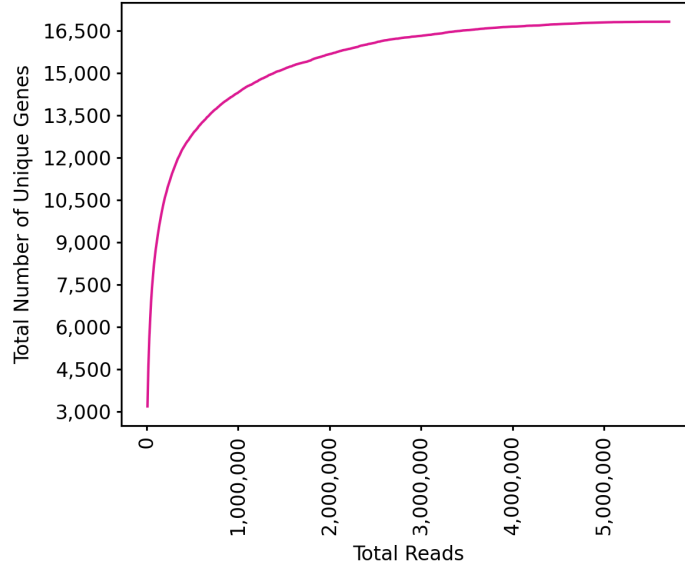
Gene Saturation, known genes only, filtered (BioSample_5)



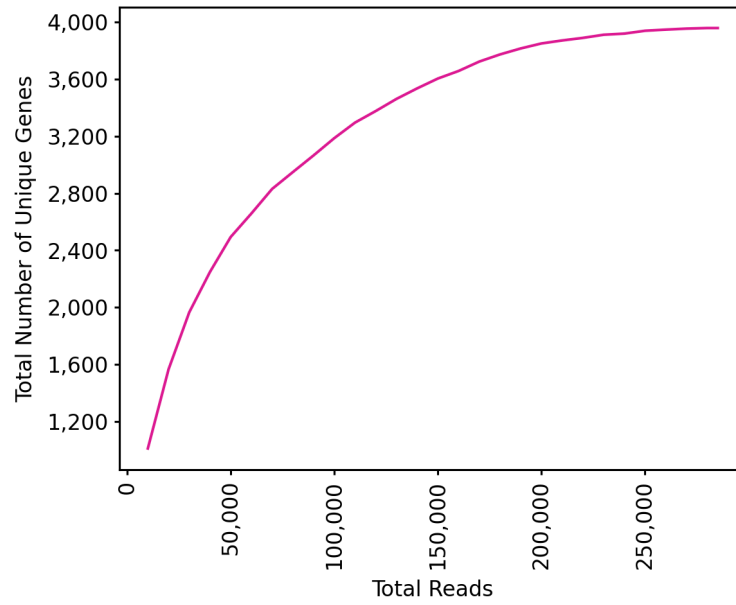
Gene Saturation, all genes, filtered (BioSample_6)



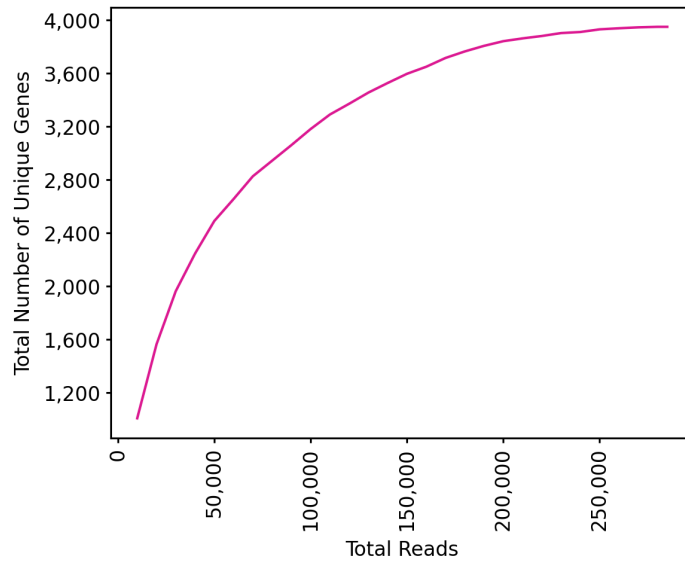
Gene Saturation, known genes only, filtered (BioSample_6)



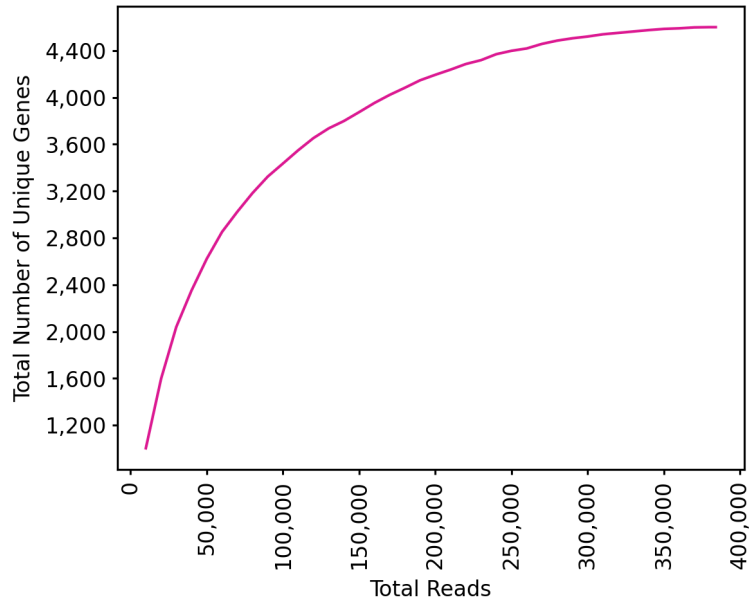
Gene Saturation, all genes, filtered (BioSample_7)



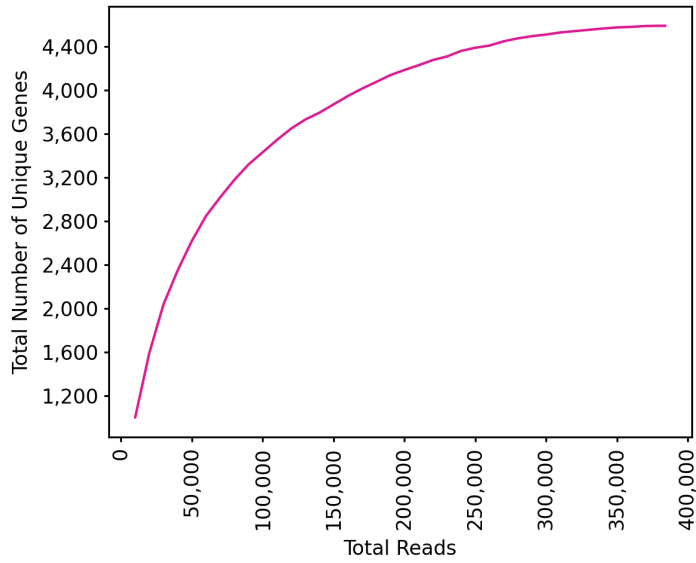
Gene Saturation, known genes only, filtered (BioSample_7)



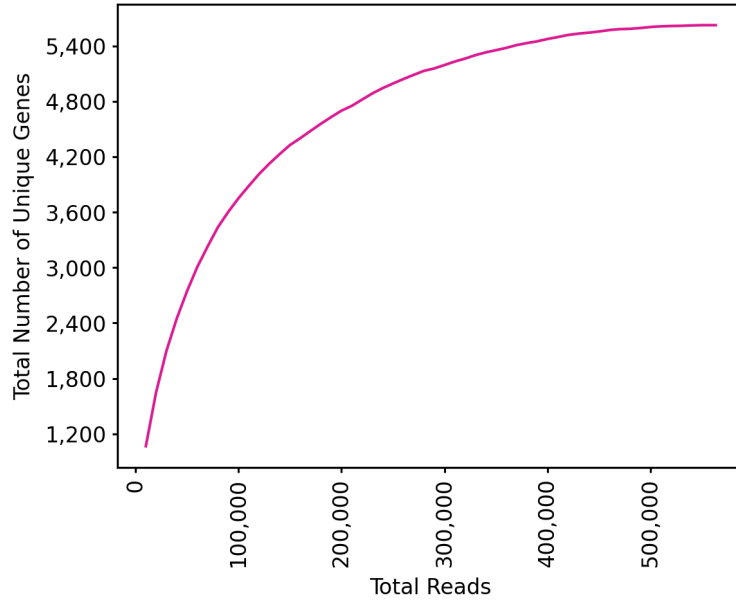
Gene Saturation, all genes, filtered (BioSample_8)



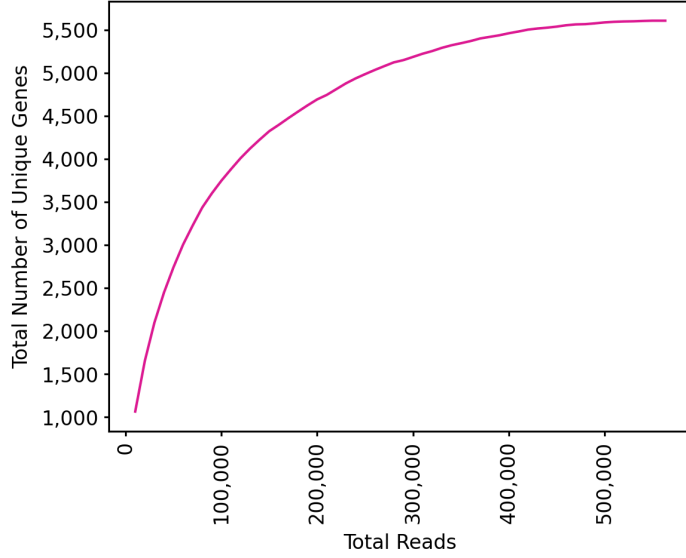
Gene Saturation, known genes only, filtered (BioSample_8)



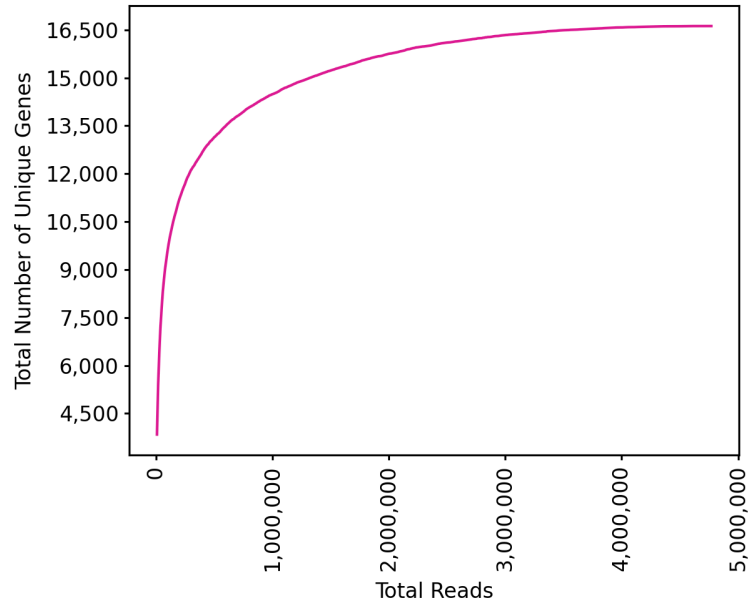
Gene Saturation, all genes, filtered (BioSample_9)



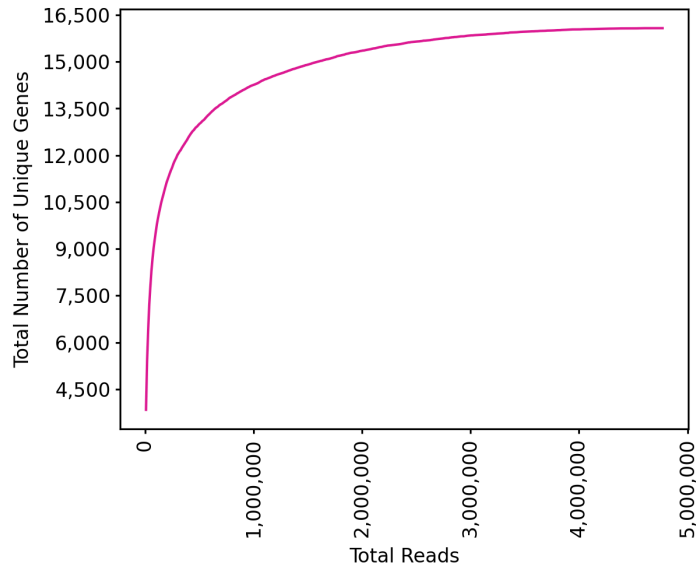
Gene Saturation, known genes only, filtered (BioSample_9)



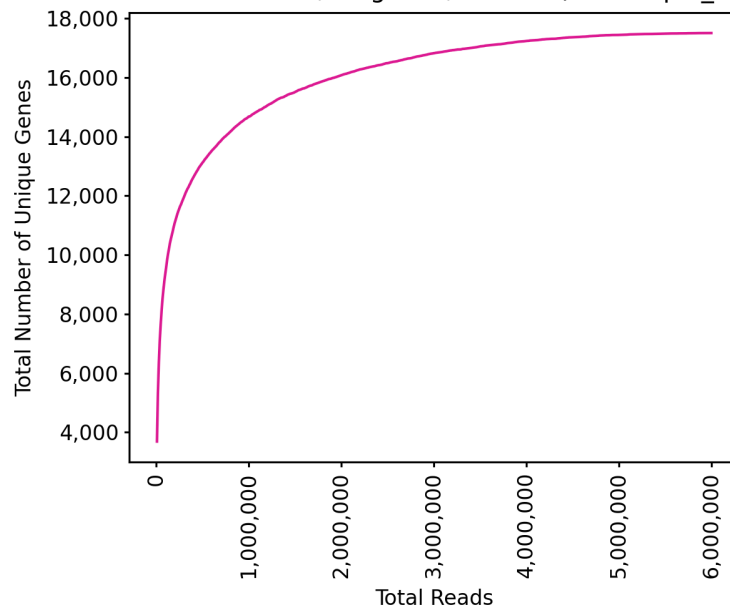
Gene Saturation, all genes, filtered (BioSample_10)



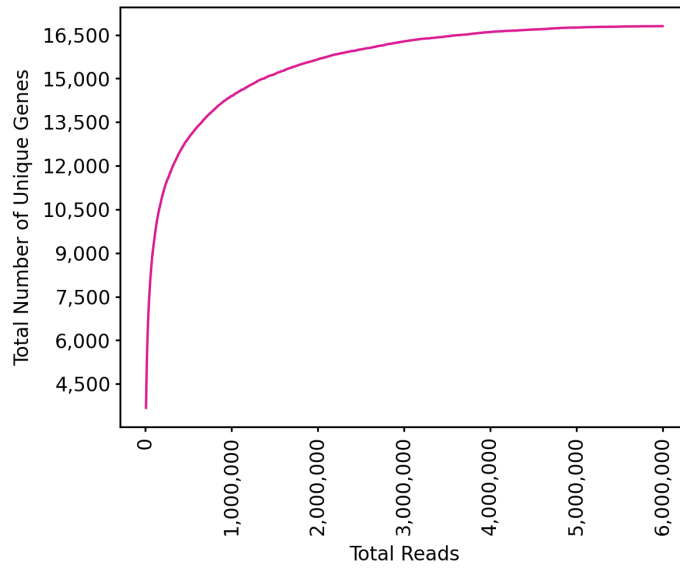
Gene Saturation, known genes only, filtered (BioSample_10)



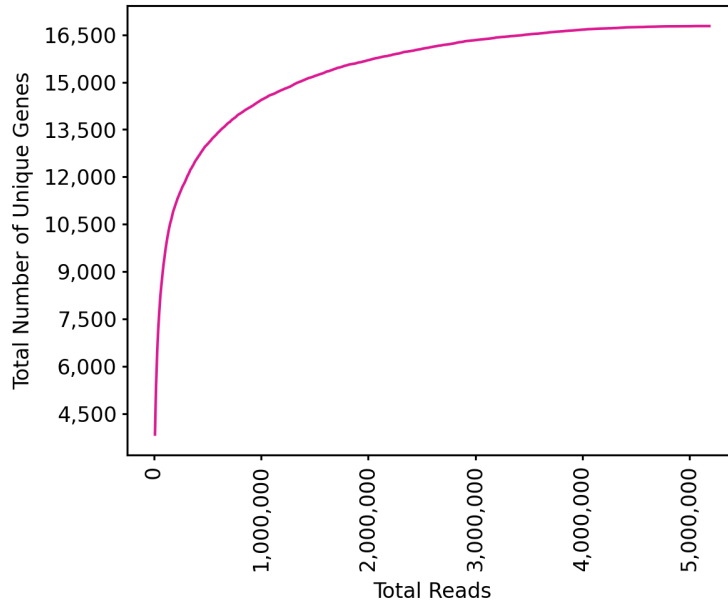
Gene Saturation, all genes, filtered (BioSample_11)



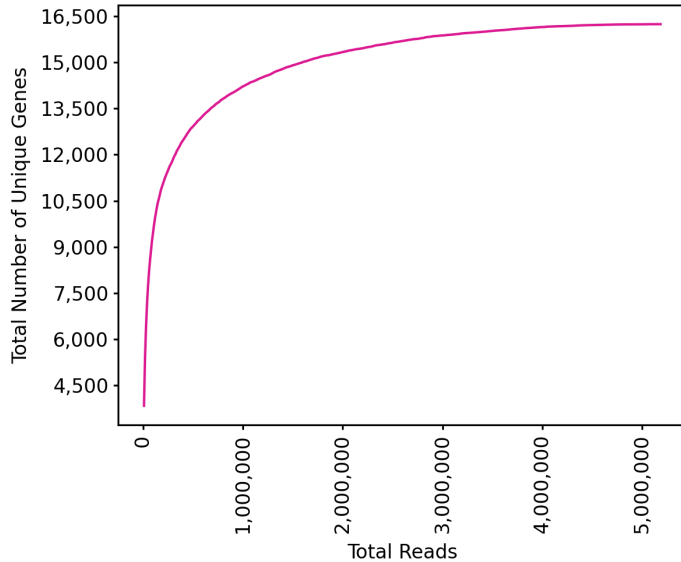
Gene Saturation, known genes only, filtered (BioSample_11)



Gene Saturation, all genes, filtered (BioSample_12)



Gene Saturation, known genes only, filtered (BioSample_12)



File Downloads

Edit Output File Name Prefix

Example:analysis-Bio Sample 1-8725

File ↓	Size ↓	Type ↓
12plex_UHRR_Brain_Kinnex_IDTcaptured-Cell1 (all samples)_Segmente...	21 KB	ConsensusRea
Report read_segmentation	3 KB	JsonReport
Full-Length Non-Concatemer Report (BioSample_12).	657 MB	csv
Full-Length Non-Concatemer Reads (BioSample_12).	9 GB	bam
Full-Length Non-Concatemer Report (BioSample_11).	748 MB	csv
Full-Length Non-Concatemer Reads (BioSample_11).	9 GB	bam
Full-Length Non-Concatemer Report (BioSample_10).	606 MB	csv
Full-Length Non-Concatemer Reads (BioSample_10).	8 GB	bam
Full-Length Non-Concatemer Report (BioSample_9).	64 MB	csv