

▼ Analysis Overview

Status

Thumbnails

Display All

► Read Segmentation

► Read Classification

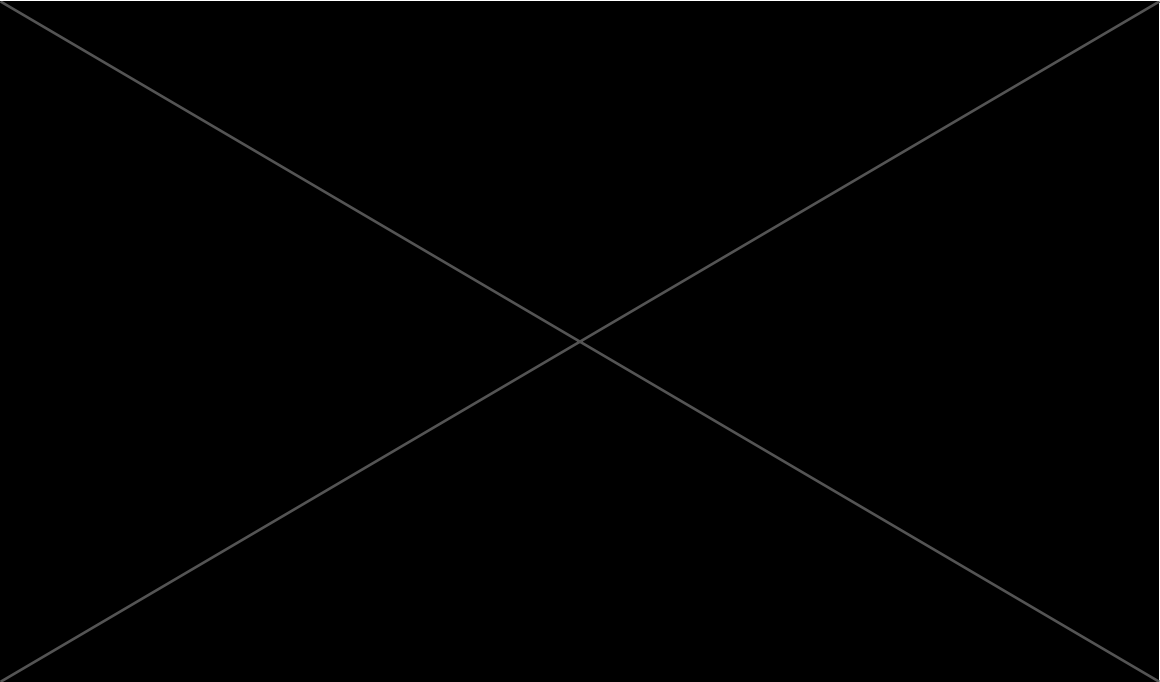
► Transcript Clustering

► Transcript Mapping and Classification

► Data

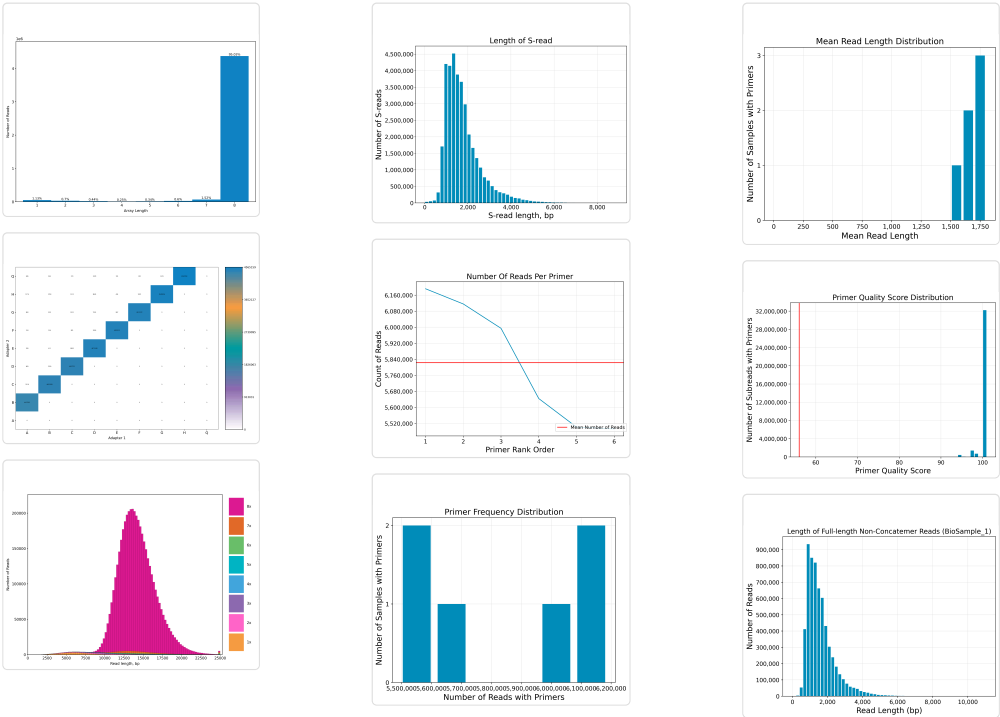
Display All

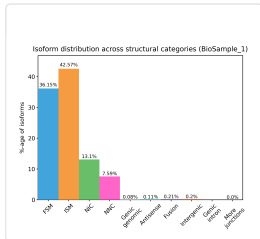
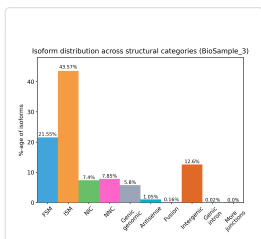
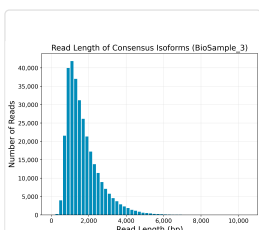
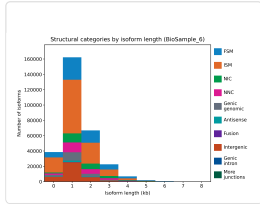
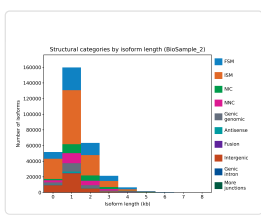
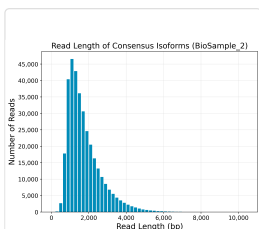
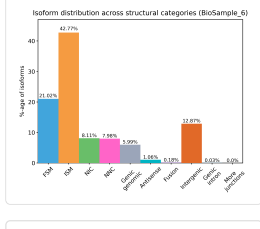
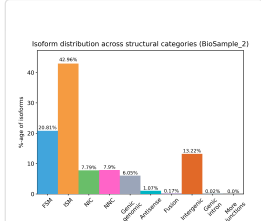
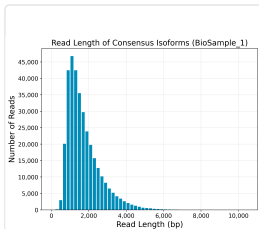
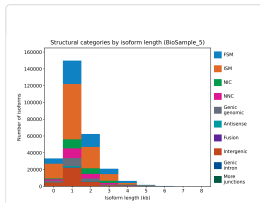
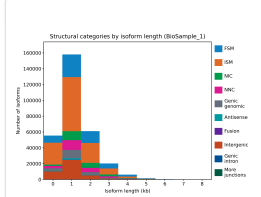
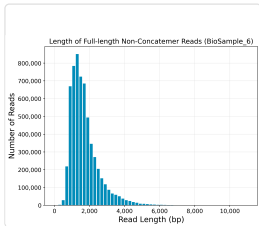
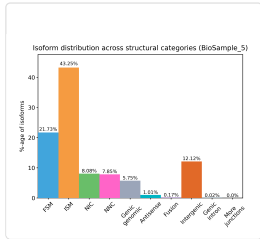
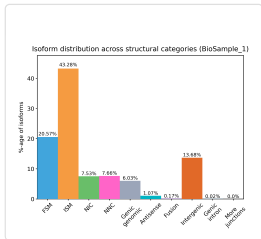
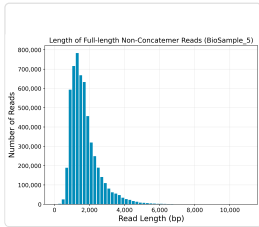
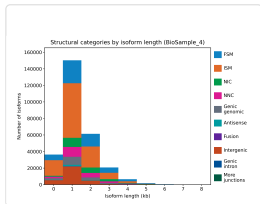
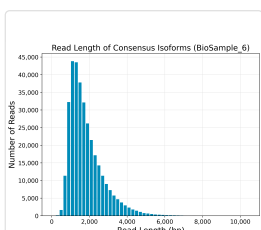
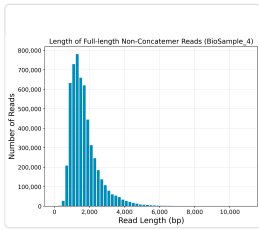
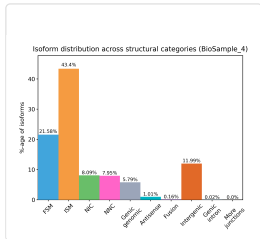
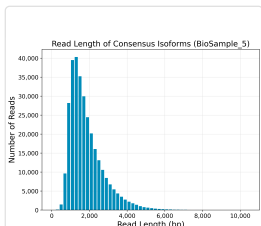
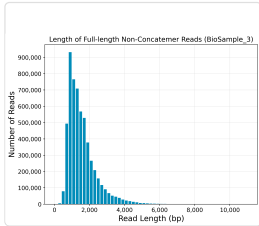
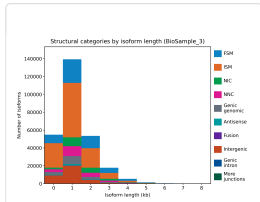
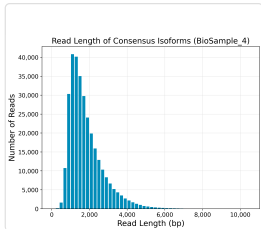
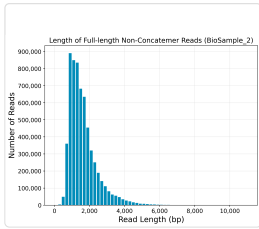
Status

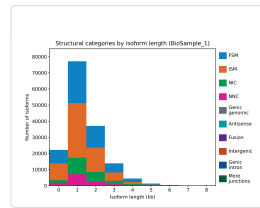


► Analysis Parameters

Thumbnails



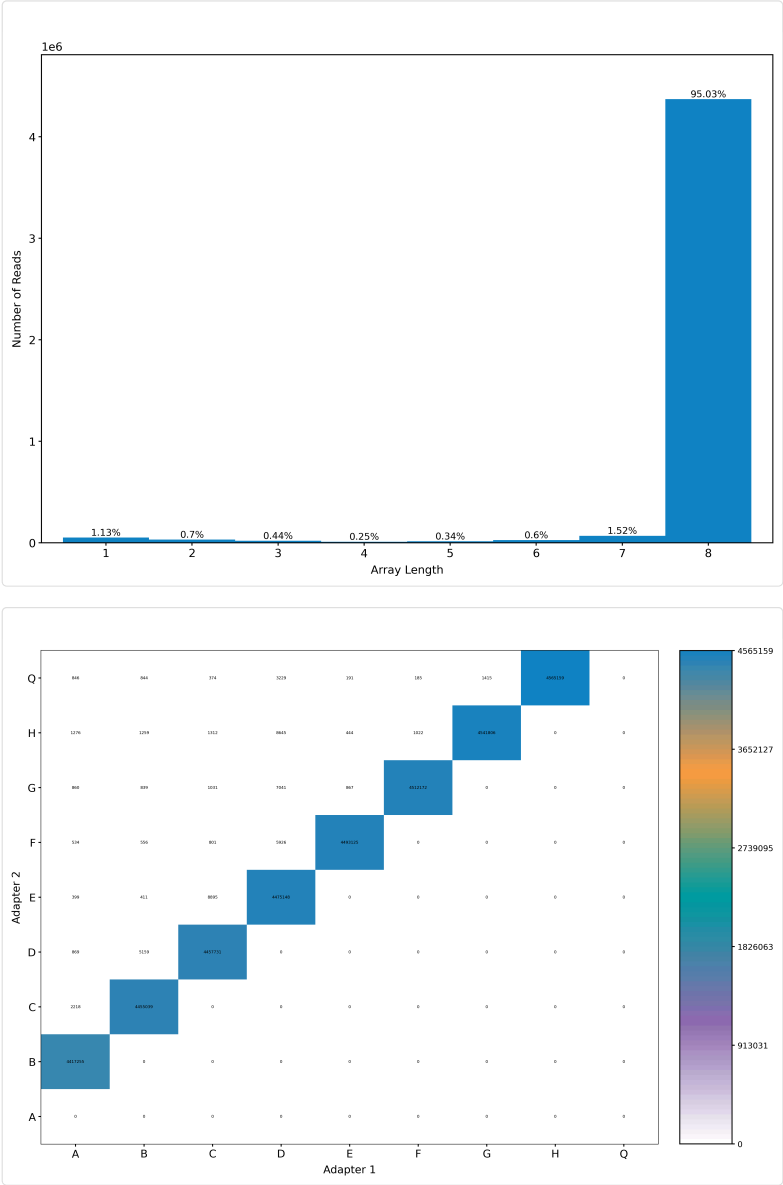




Read Segmentation

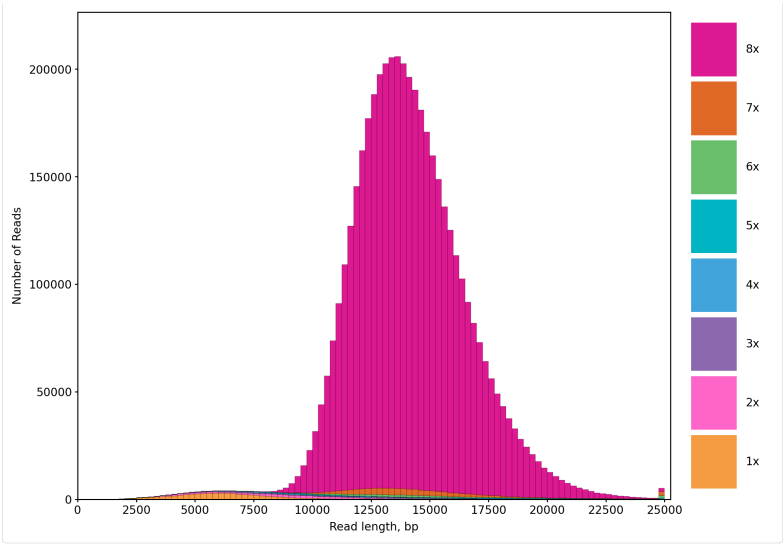
Value	Analysis Metric
4,642,616	Reads
35,917,435	Segmented reads (S-reads)
1,759	Mean length of S-reads
94.14 %	Percent of reads with full arrays
7.74	Mean array size (concatenation factor)

Segmentation Statistics

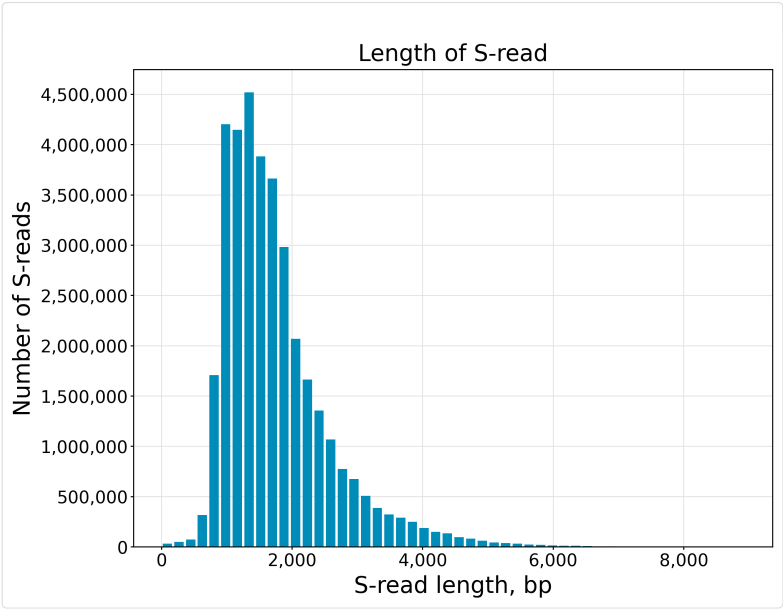


Length of Reads





S-read Length Distribution



Read Classification

Value	Analysis Metric
35,917,435	Reads
34,940,590	Reads with 5' and 3' Primers
34,889,371	Non-Concatamer Reads with 5' and 3' Primers
34,856,077	Non-Concatamer Reads with 5' and 3' Primers and Poly-A Tail (FLNC Reads)
1,644	Mean Length of FLNC Reads
6	Unique Primers
5,823,431	Mean Reads per Primer
6,191,609	Max. Reads per Primer
5,492,791	Min. Reads per Primer
976,845	Reads without Primers

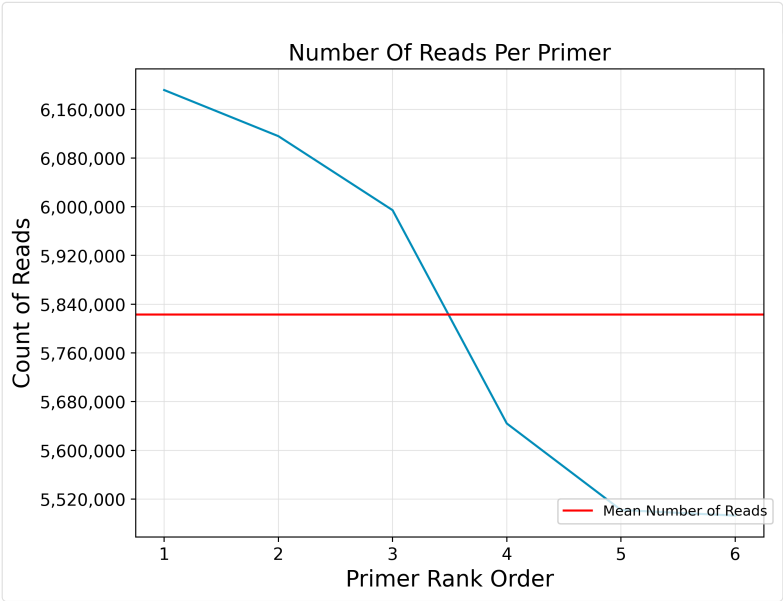
Value	Analysis Metric
96.83%	Percent Bases in Reads with Primers
97.28%	Percent Reads with Primers

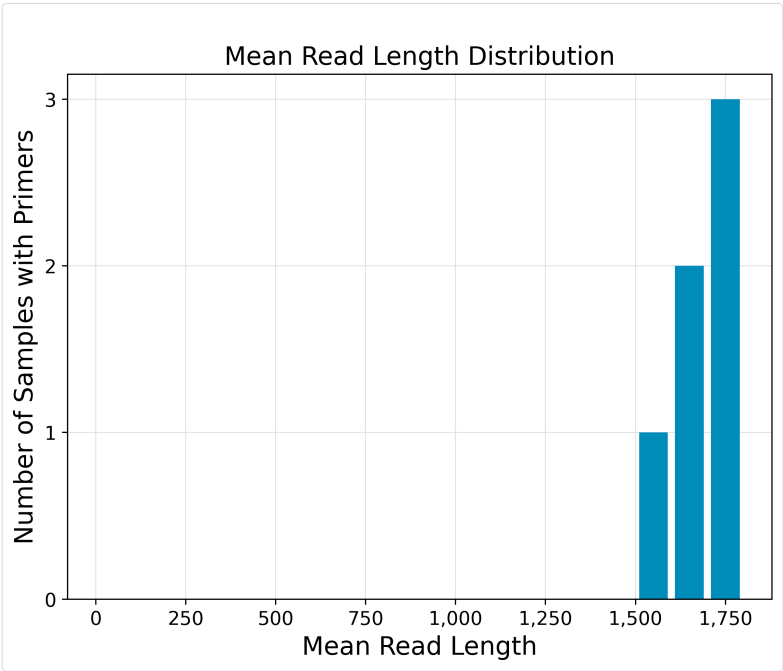
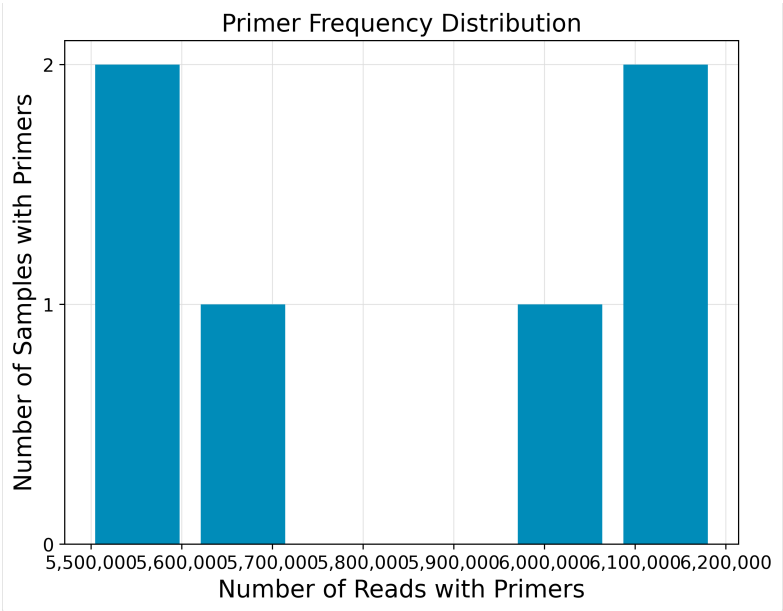
Primer Data

Search ...

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...	6,115,867	99.7	6,115,867	6,110,007
BioSample_2	IsoSeqX_bc0...	6,191,609	99.7	6,191,609	6,181,747
BioSample_3	IsoSeqX_bc0...	5,644,070	99.7	5,644,070	5,634,586
BioSample_4	IsoSeqX_bc0...	5,501,929	99.7	5,501,929	5,493,617
BioSample_5	IsoSeqX_bc0...	5,492,791	99.7	5,492,791	5,484,323
BioSample_6	IsoSeqX_bc0...	5,994,324	99.7	5,994,324	5,985,091
UNASSIGNED	No Primer	976,845	0.0	0	0

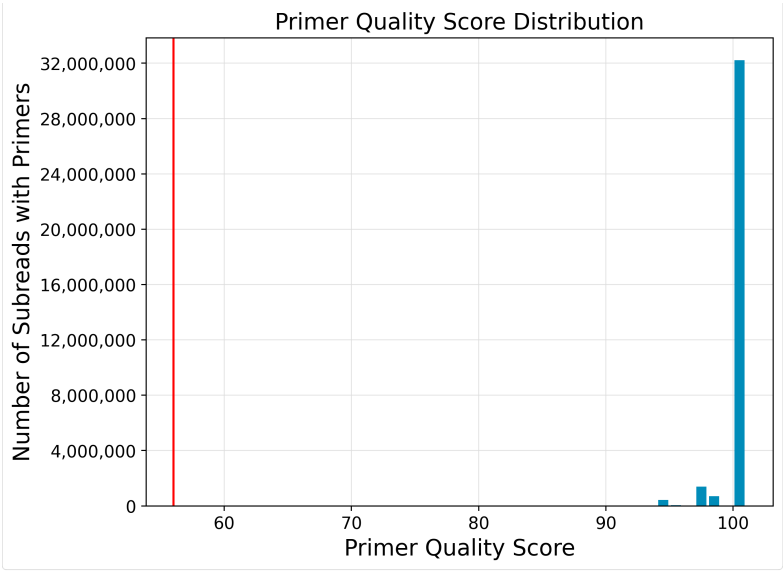
Primer Read Statistics



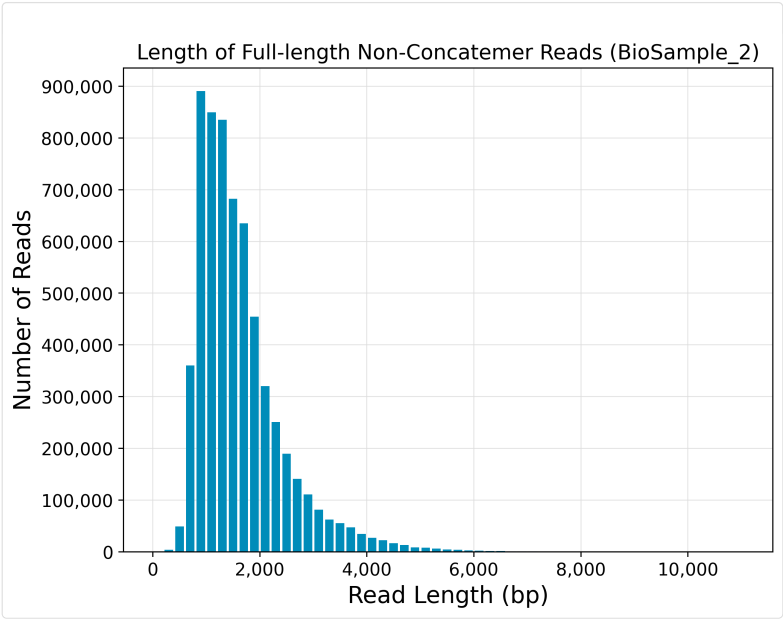
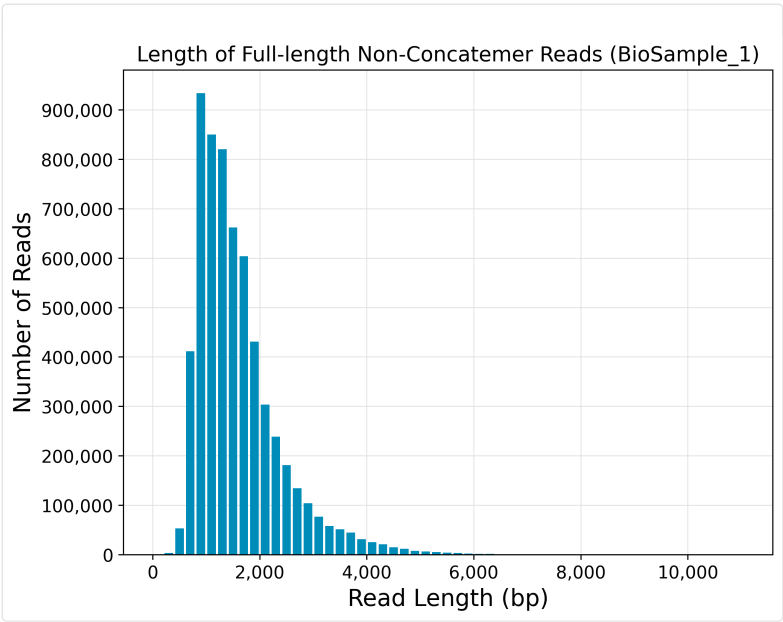


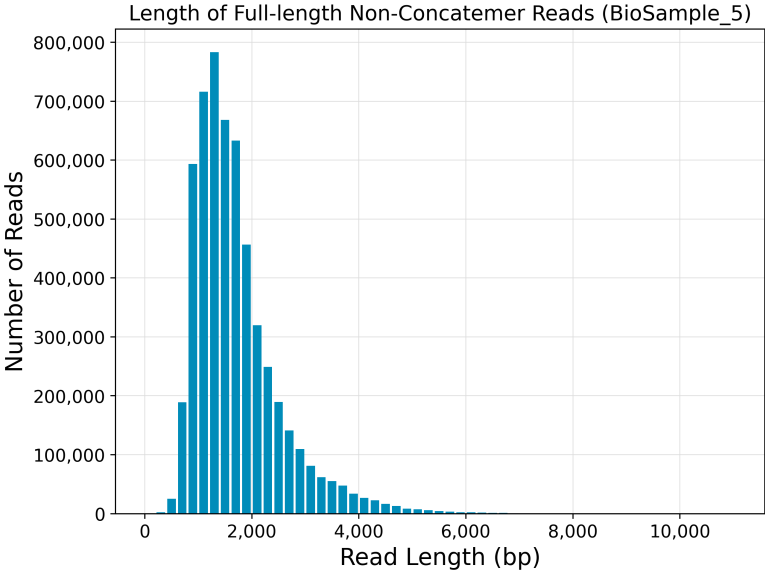
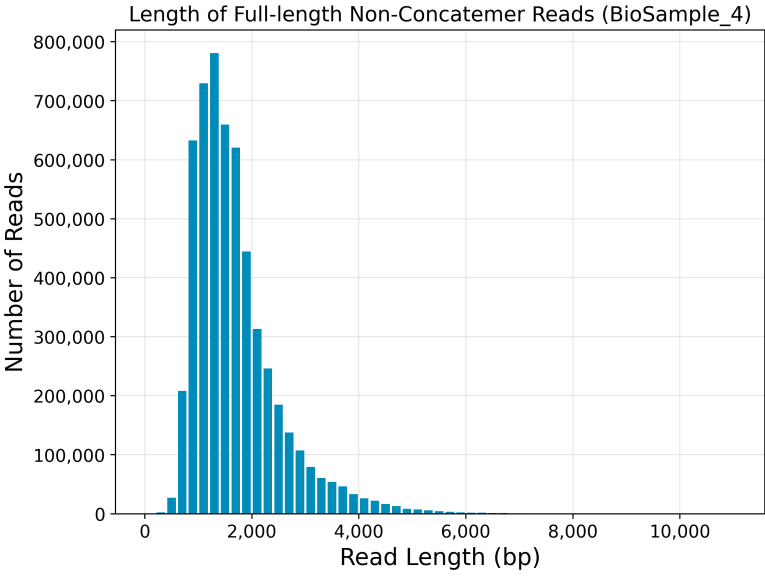
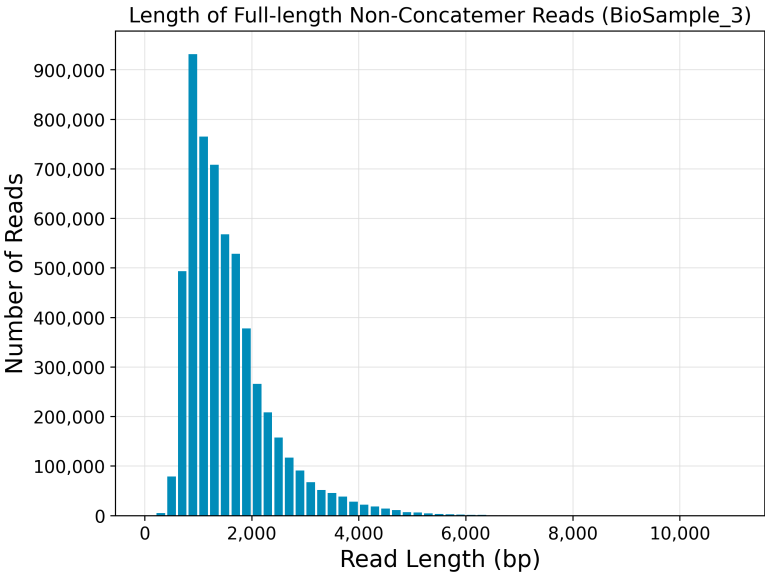
Primer Quality Scores

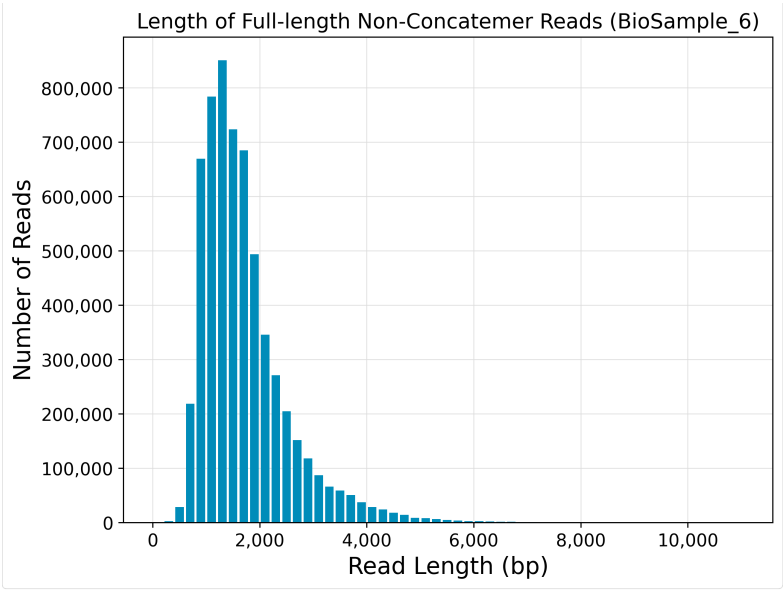




Length of Full-length Non-Concatemer Reads





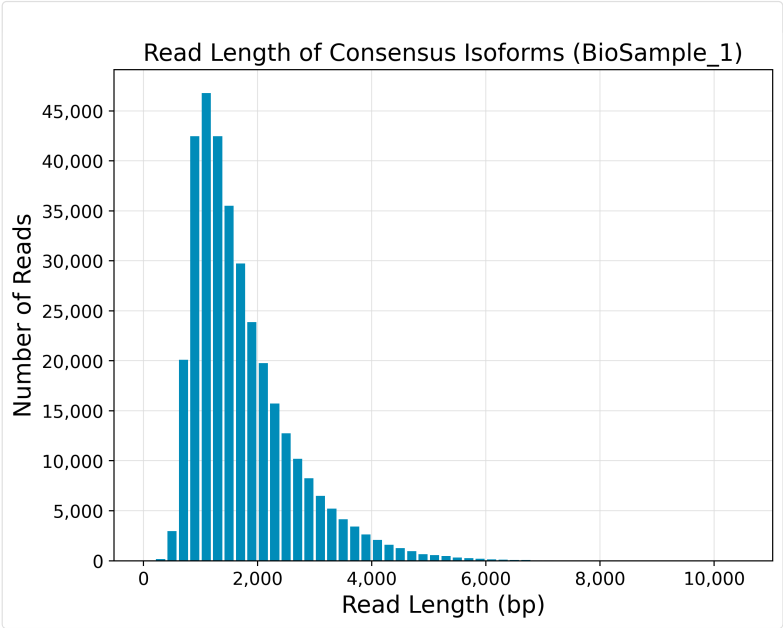


Summary Metrics

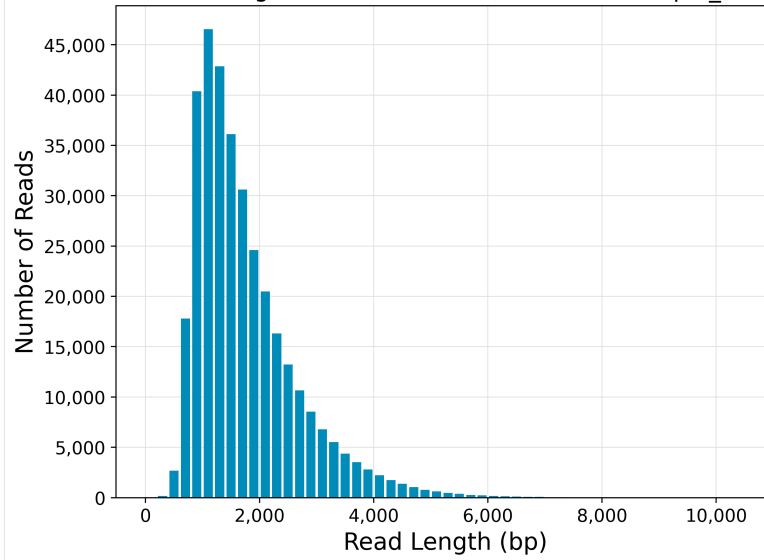
Search ...

Sample Name ⬆	Number of High-Quality Isoforms ⬆
BioSample_1	341,643
BioSample_2	343,992
BioSample_3	308,750
BioSample_4	312,177
BioSample_5	309,854
BioSample_6	336,893

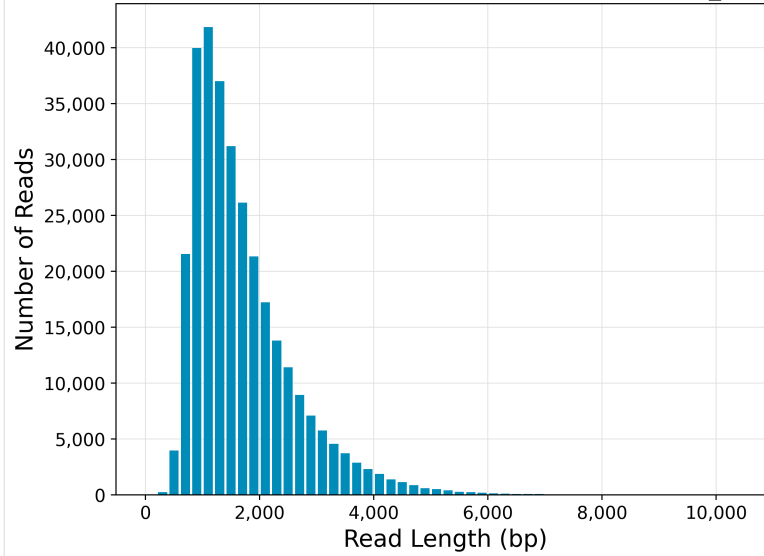
Length of Consensus Isoforms



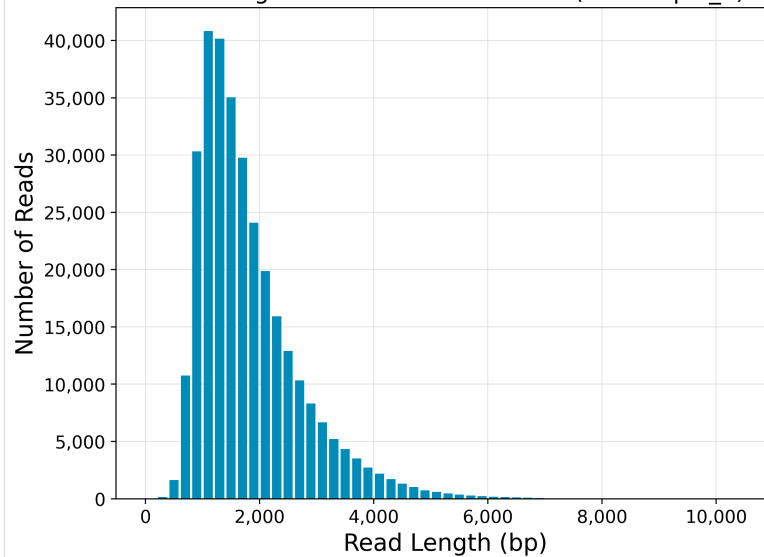
Read Length of Consensus Isoforms (BioSample_2)

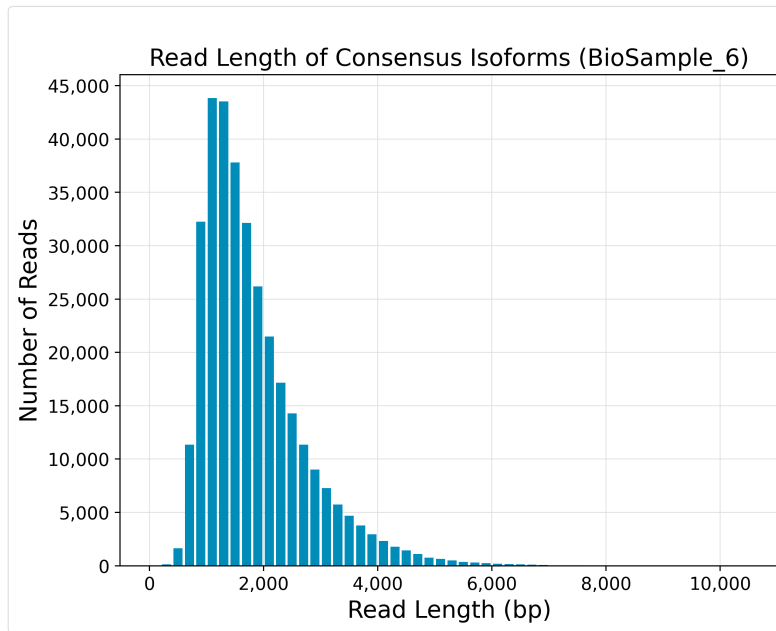


Read Length of Consensus Isoforms (BioSample_3)



Read Length of Consensus Isoforms (BioSample_4)





							Search ...
Sample Name	Genes	Genes, filtered	Known Genes, filtered	Isoforms	Isoforms, filtered	Known isoforms, filtered	
BioSample_1	61,504	15,893	15,447	154,545	71,835	38,528	
BioSample_2	60,675	15,927	15,514	155,795	73,375	38,772	
BioSample_3	53,912	15,484	15,124	138,742	66,838	37,331	
BioSample_4	52,821	15,575	15,234	140,380	69,317	37,111	
BioSample_5	52,827	15,471	15,124	139,294	68,686	36,797	
BioSample_6	58,705	15,884	15,447	153,102	73,486	38,335	

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

FSM	62412	39377	63.09%	29719
ISM	131272	14276	10.87%	73747
NIC	22829	17576	76.98%	10855
NNC	23227	14415	62.06%	11157
Antisense	3240	254	7.83%	1034
Fusion	504	320	63.49%	249
More junctions	7	5	71.42%	4
Genic intron	66	4	6.06%	12
Genic genomic	18296	3917	21.40%	6915
Intergenic	41489	269	0.64%	13733

Transcript Classification (BioSample_2)

Search ...

Category ⬆ ⬆	Count ⬆ ⬆	CAGE Detected ⬆ ⬆	CAGE Detected (%) ⬆ ⬆	polyA Motif Detected ⬆ ⬆
FSM	63557	40538	63.78%	29998
ISM	131193	14750	11.24%	73284
NIC	23791	18414	77.39%	11305
NNC	24132	15264	63.25%	11487
Antisense	3283	244	7.43%	1011
Fusion	520	315	60.57%	264
More junctions	13	8	61.53%	7
Genic intron	70	0	0.00%	19
Genic genomic	18479	4104	22.20%	7008
Intergenic	40379	260	0.64%	13116

Transcript Classification (BioSample_3)

Search ...

Category ⬆ ⬆	Count ⬆ ⬆	CAGE Detected ⬆ ⬆	CAGE Detected (%) ⬆ ⬆	polyA Motif Detected ⬆ ⬆
FSM	58815	38100	64.77%	27734
ISM	118884	13987	11.76%	65913
NIC	20190	15752	78.01%	9403
NNC	21423	13670	63.80%	10002
Antisense	2864	257	8.97%	833
Fusion	431	275	63.80%	201
More junctions	9	5	55.55%	4
Genic intron	61	0	0.00%	12
Genic genomic	15817	3741	23.65%	5998
Intergenic	34368	260	0.75%	11218

Transcript Classification (BioSample_4)

Category ↕	Count ↕	CAGE Detected ↕	CAGE Detected (%) ↕	polyA Motif Detected ↕
FSM	59959	38719	64.57%	28514
ISM	120598	13454	11.15%	68015
NIC	22487	17467	77.67%	10670
NNC	22095	13950	63.13%	10605
Antisense	2793	214	7.66%	880
Fusion	453	278	61.36%	219
More junctions	13	8	61.53%	6
Genic intron	54	0	0.00%	12
Genic genomic	16085	3695	22.97%	6185
Intergenic	33321	225	0.67%	11016

Transcript Classification (BioSample_5)

Category ↕	Count ↕	CAGE Detected ↕	CAGE Detected (%) ↕	polyA Motif Detected ↕
FSM	59937	38928	64.94%	28582
ISM	119302	13286	11.13%	67328
NIC	22300	17402	78.03%	10687
NNC	21650	13788	63.68%	10365
Antisense	2790	208	7.45%	867
Fusion	477	300	62.89%	235
More junctions	12	10	83.33%	5
Genic intron	68	2	2.94%	10
Genic genomic	15864	3578	22.55%	6122
Intergenic	33427	256	0.76%	11232

Transcript Classification (BioSample_6)

Category ↕	Count ↕	CAGE Detected ↕	CAGE Detected (%) ↕	polyA Motif Detected ↕
FSM	63055	40293	63.90%	29946
ISM	128310	14220	11.08%	72413
NIC	24324	18778	77.19%	11545
NNC	23947	15059	62.88%	11487
Antisense	3188	232	7.27%	1032
Fusion	527	337	63.94%	256
More junctions	13	8	61.53%	8
Genic intron	82	1	1.21%	27

Genic genomic	17981	3947	21.95%	6974
Intergenic	38605	249	0.64%	12836

Transcript Classification, filtered (BioSample_1)

Category ⬆ ⬆	Count ⬆ ⬆	CAGE Detected ⬆ ⬆	CAGE Detected, (%) ⬆ ⬆	polyA Detected ⬆ ⬆
FSM	56554	35464	62.70%	29719
ISM	66602	8437	12.66%	40482
NIC	20495	15752	76.85%	10474
NNC	11868	8095	68.20%	6351
Antisense	179	53	29.60%	107
Fusion	322	224	69.56%	173
More junctions	6	5	83.33%	4
Genic intron	0	0	0.00%	0
Genic genomic	130	75	57.69%	61
Intergenic	307	44	14.33%	224

Transcript Classification, filtered (BioSample_2)

Category ⬆ ⬆	Count ⬆ ⬆	CAGE Detected ⬆ ⬆	CAGE Detected, (%) ⬆ ⬆	polyA Detected ⬆ ⬆
FSM	57217	36307	63.45%	29998
ISM	66783	8810	13.19%	40407
NIC	21424	16554	77.26%	10955
NNC	12253	8469	69.11%	6464
Antisense	168	51	30.35%	99
Fusion	320	203	63.43%	173
More junctions	10	7	70.00%	5
Genic intron	0	0	0.00%	0
Genic genomic	149	87	58.38%	65
Intergenic	279	44	15.77%	190

Transcript Classification, filtered (BioSample_3)

Category ⬆ ⬆	Count ⬆ ⬆	CAGE Detected ⬆ ⬆	CAGE Detected, (%) ⬆ ⬆	polyA Detected ⬆ ⬆
FSM	52953	34074	64.34%	27734
ISM	60187	8196	13.61%	36167
NIC	17979	14035	78.06%	9096
NNC	10731	7423	69.17%	5613
Antisense	139	47	33.81%	85

Fusion	277	190	68.59%	134
More junctions	9	5	55.55%	4
Genic intron	0	0	0.00%	0
Genic genomic	124	80	64.51%	60
Intergenic	248	38	15.32%	172

Transcript Classification, filtered (BioSample_4)

Search ...

Category ↕	Count ↕	CAGE Detected ↕	CAGE Detected, (%) ↕	polyA Detected ↕
FSM	54226	34829	64.22%	28514
ISM	62168	8011	12.88%	37833
NIC	20203	15675	77.58%	10290
NNC	11230	7742	68.94%	6005
Antisense	150	54	36.00%	92
Fusion	286	182	63.63%	155
More junctions	9	6	66.66%	5
Genic intron	0	0	0.00%	0
Genic genomic	105	66	62.85%	49
Intergenic	223	43	19.28%	154

Transcript Classification, filtered (BioSample_5)

Search ...

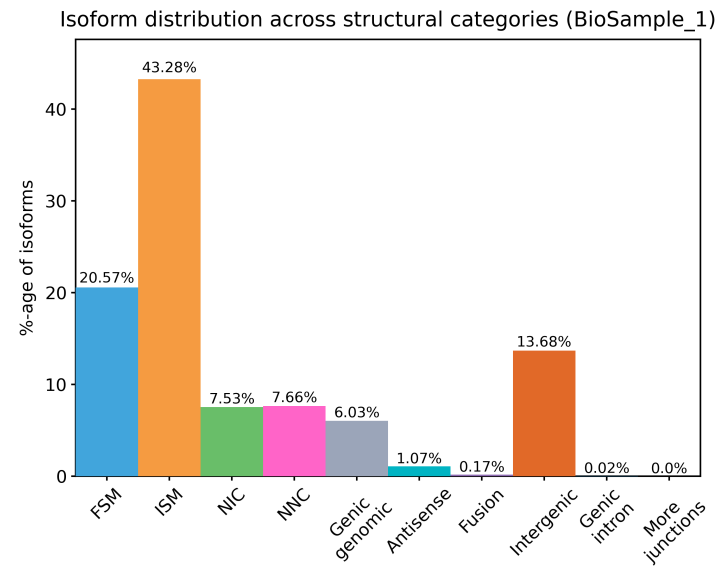
Category ↕	Count ↕	CAGE Detected ↕	CAGE Detected, (%) ↕	polyA Detected ↕
FSM	54237	35030	64.58%	28582
ISM	61820	7929	12.82%	37706
NIC	20075	15660	78.00%	10322
NNC	11013	7709	69.99%	5875
Antisense	140	42	30.00%	86
Fusion	298	197	66.10%	165
More junctions	9	8	88.88%	4
Genic intron	0	0	0.00%	0
Genic genomic	112	63	56.25%	52
Intergenic	242	44	18.18%	173

Transcript Classification, filtered (BioSample_6)

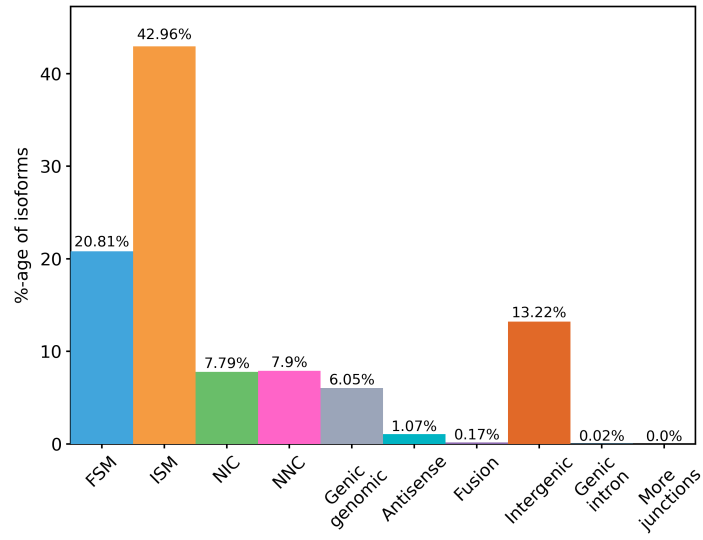
Search ...

Category ↕	Count ↕	CAGE Detected ↕	CAGE Detected, (%) ↕	polyA Detected ↕
FSM	56978	36194	63.52%	29946
ISM	66144	8455	12.78%	40345
NIC	21859	16871	77.18%	11178

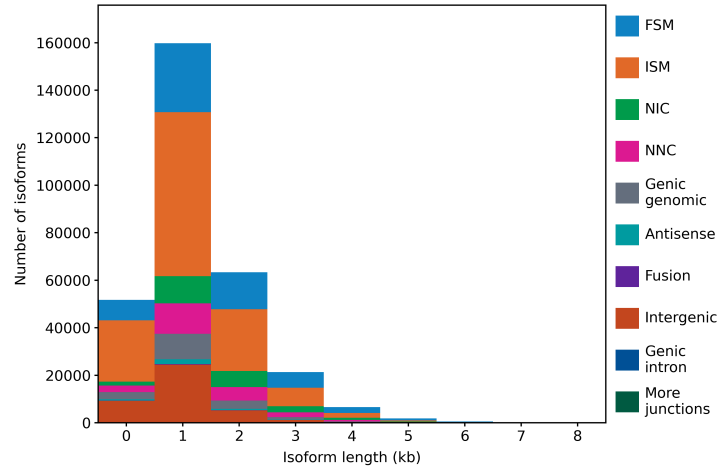
Category	2005	2007	Ratio	1975
NNC	12353	8476	68.61%	6585
Antisense	156	45	28.84%	98
Fusion	334	216	64.67%	179
More junctions	10	7	70.00%	7
Genic intron	0	0	0.00%	0
Genic genomic	129	79	61.24%	68
Intergenic	310	50	16.12%	231



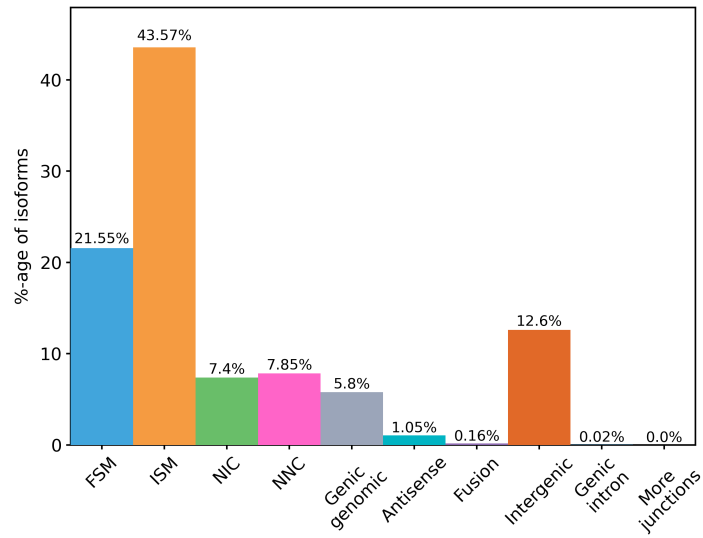
Isoform distribution across structural categories (BioSample_2)



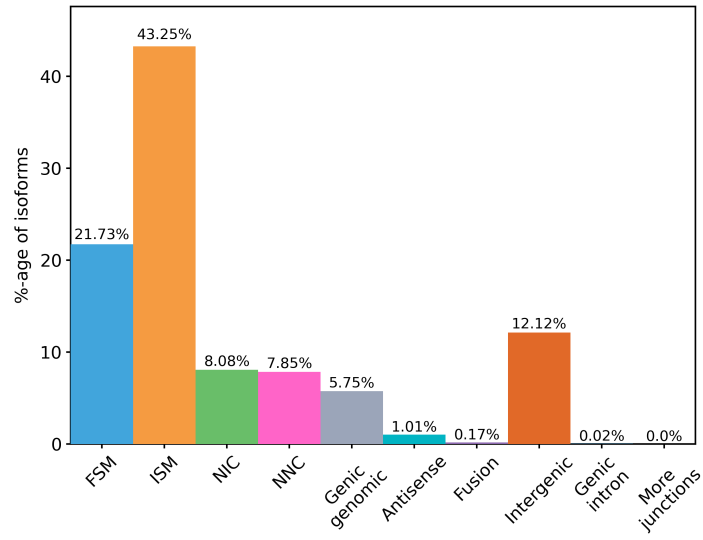
Structural categories by isoform length (BioSample_2)



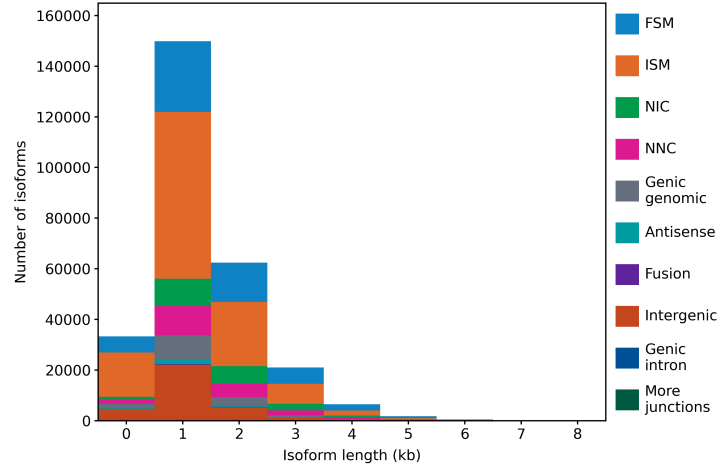
Isoform distribution across structural categories (BioSample_3)



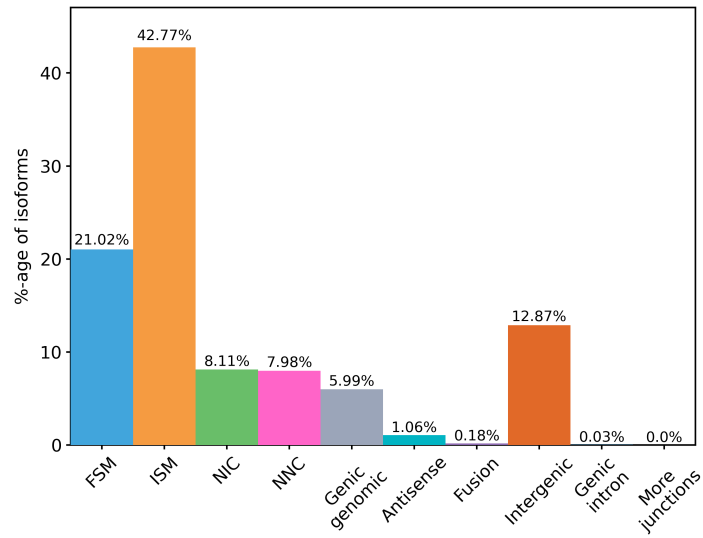
Isoform distribution across structural categories (BioSample_5)

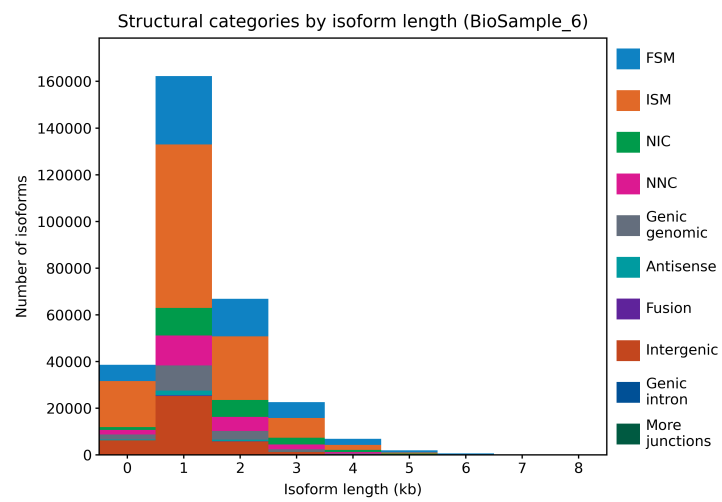


Structural categories by isoform length (BioSample_5)

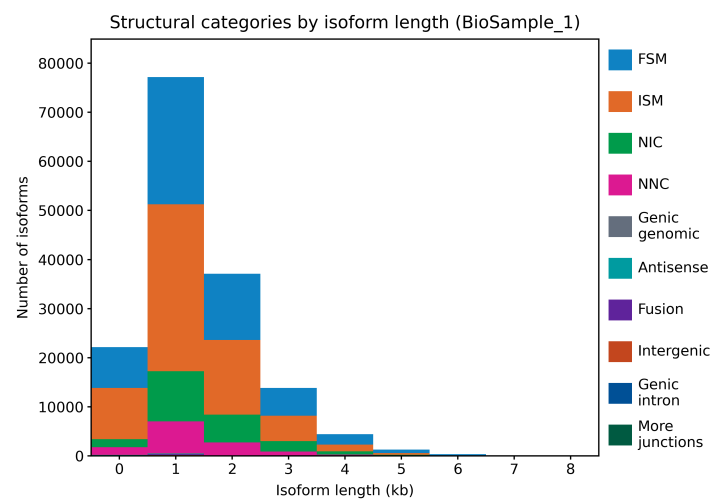
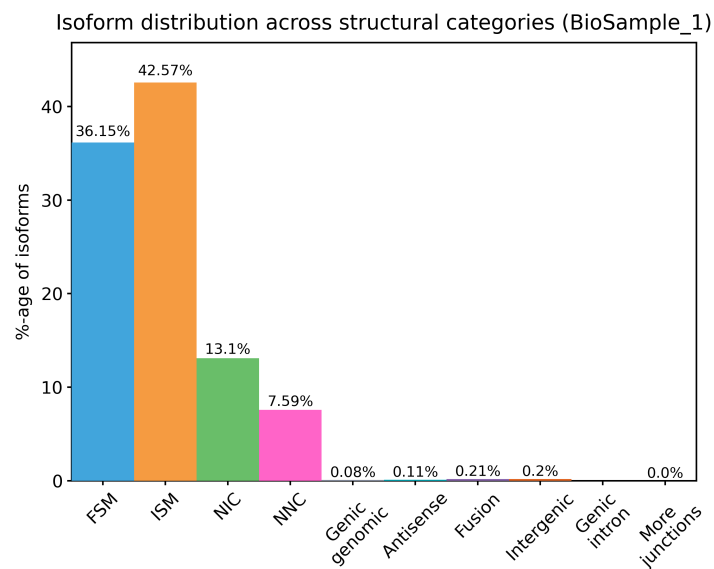


Isoform distribution across structural categories (BioSample_6)

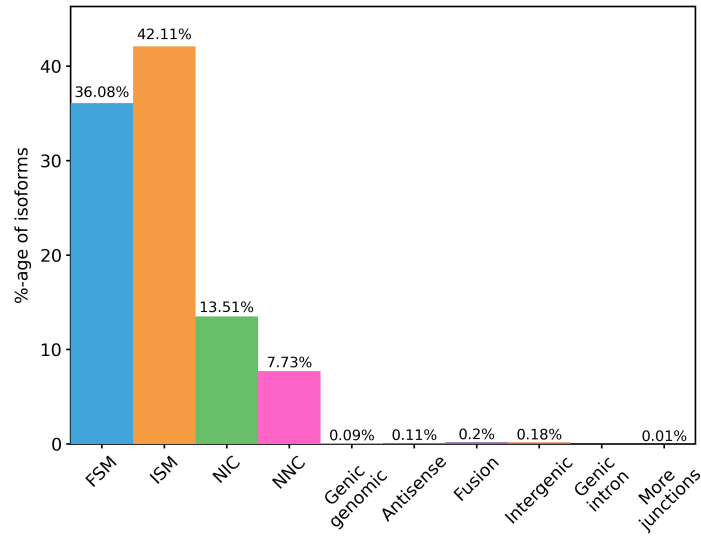




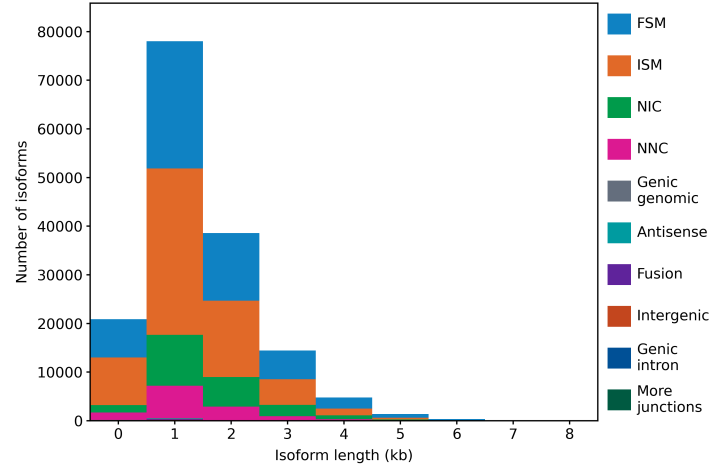
Transcript Classification Plots, filtered



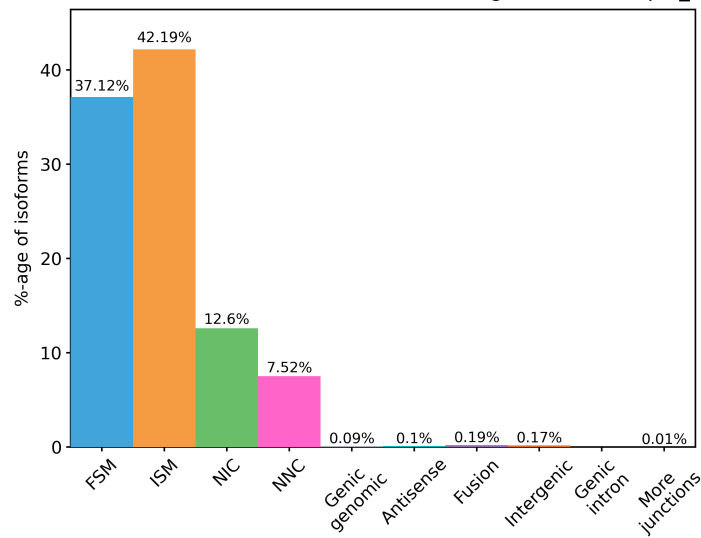
Isoform distribution across structural categories (BioSample_2)



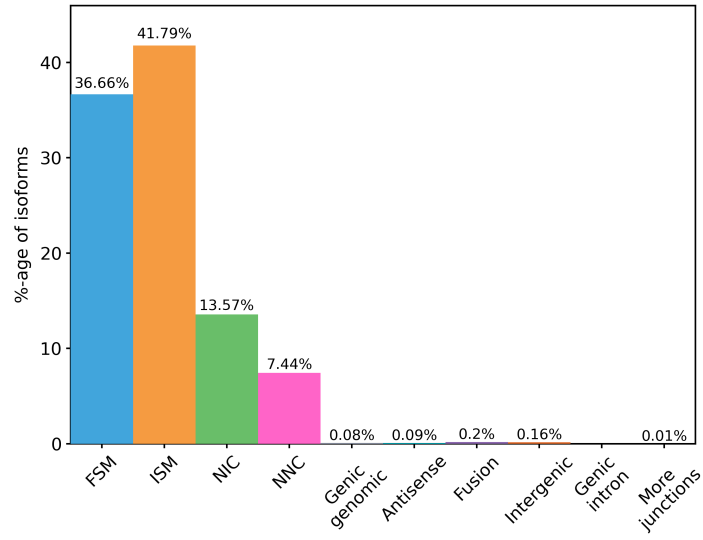
Structural categories by isoform length (BioSample_2)



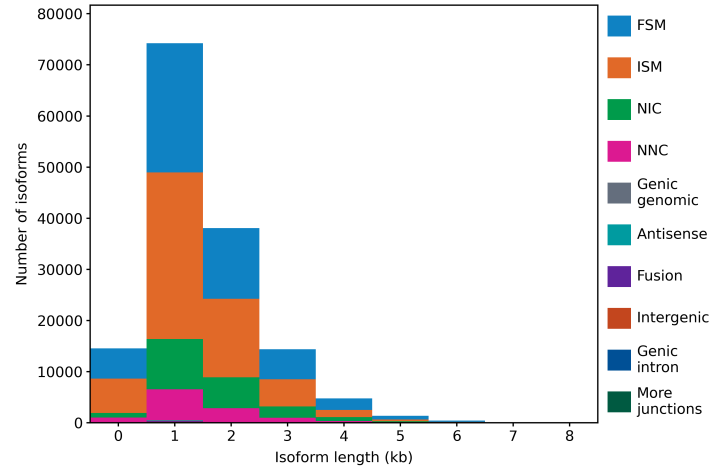
Isoform distribution across structural categories (BioSample_3)



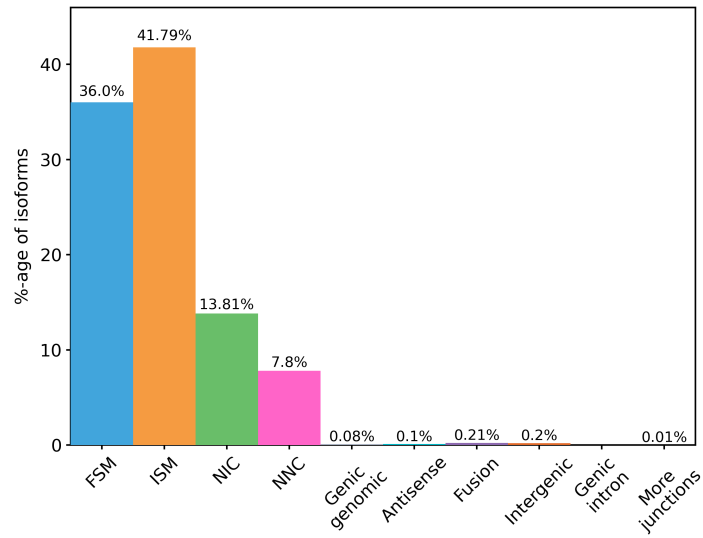
Isoform distribution across structural categories (BioSample_5)

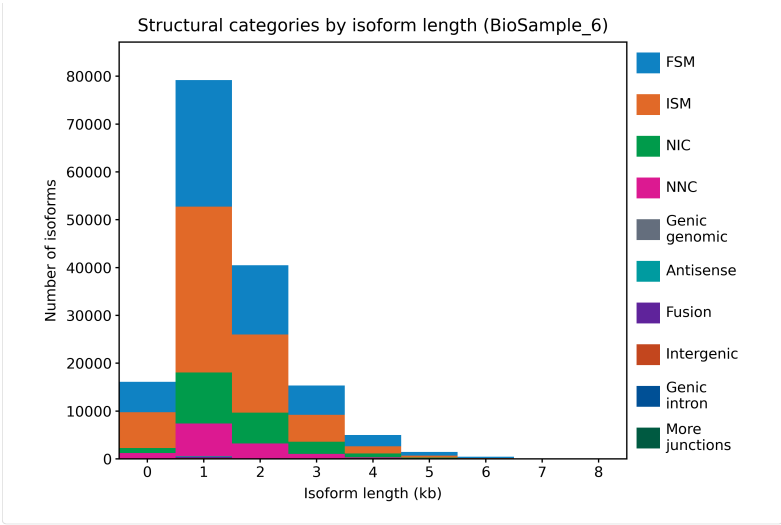


Structural categories by isoform length (BioSample_5)

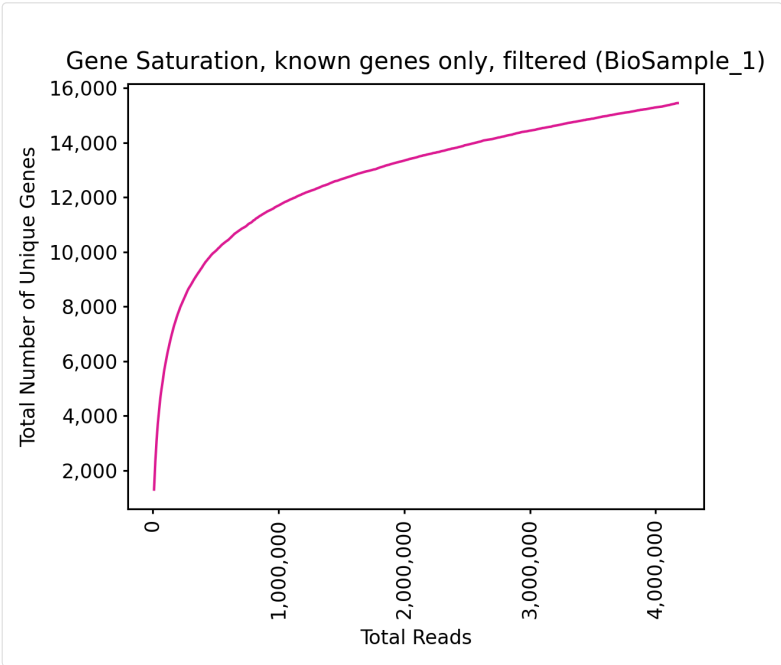


Isoform distribution across structural categories (BioSample_6)

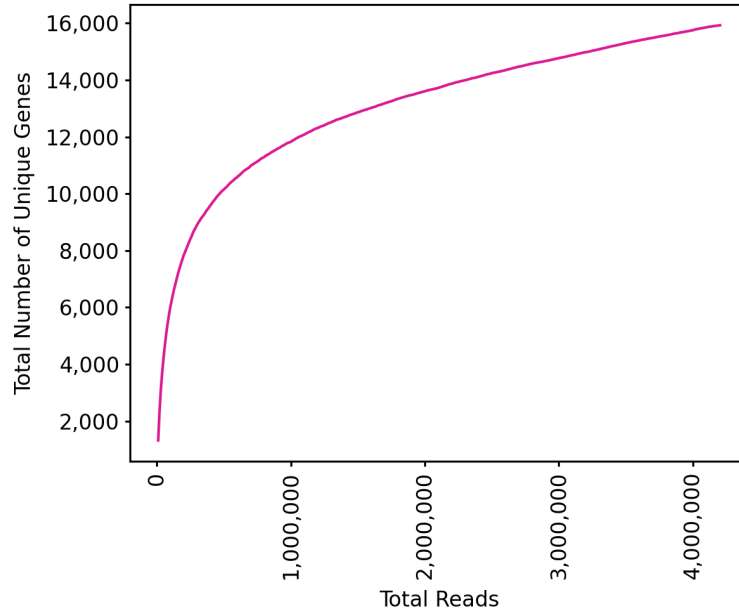




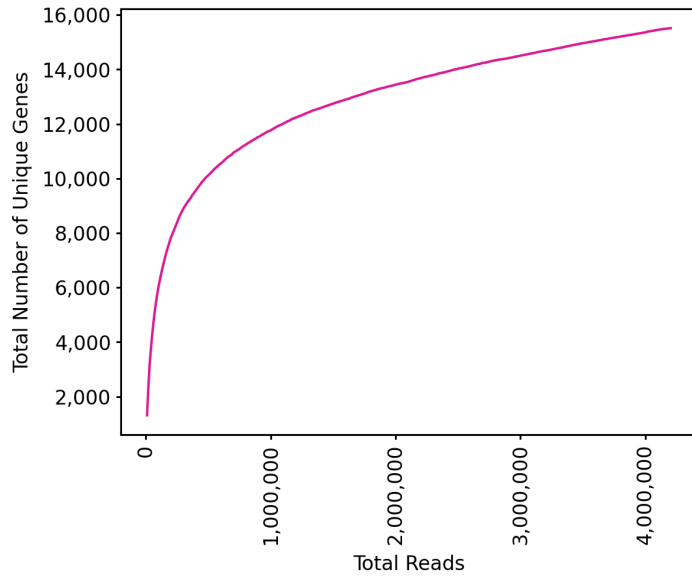
Gene Saturation



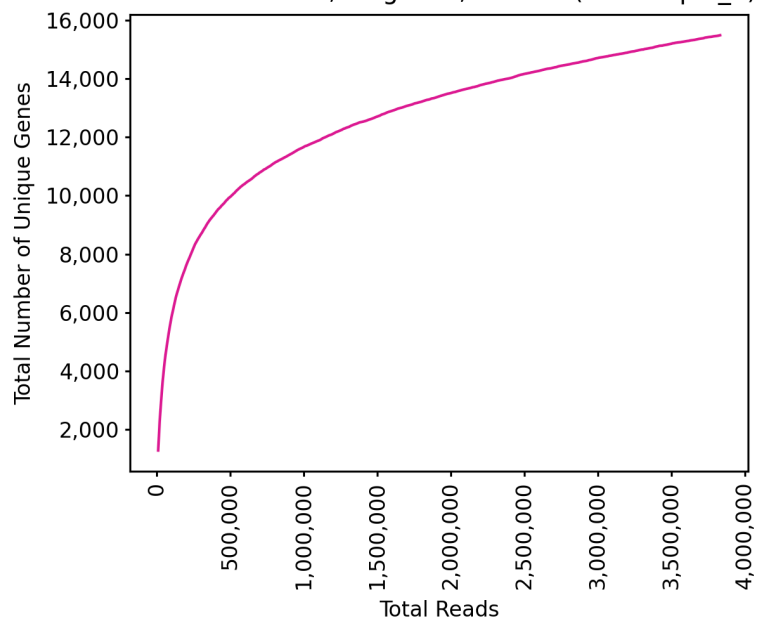
Gene Saturation, all genes, filtered (BioSample_2)



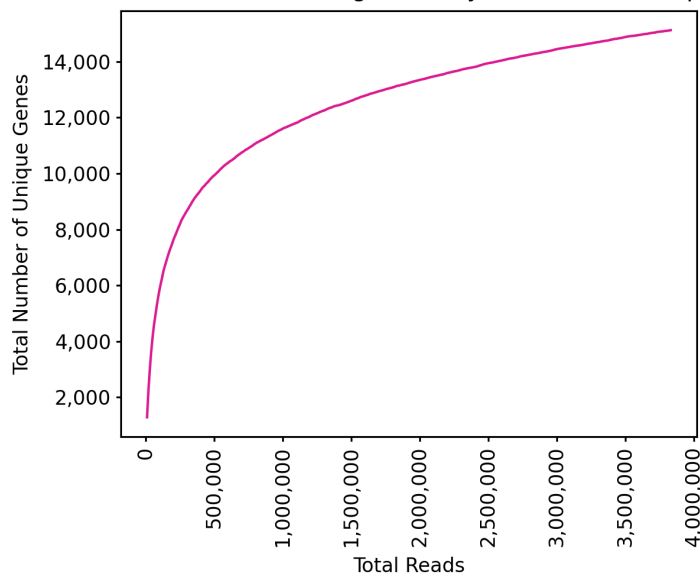
Gene Saturation, known genes only, filtered (BioSample_2)



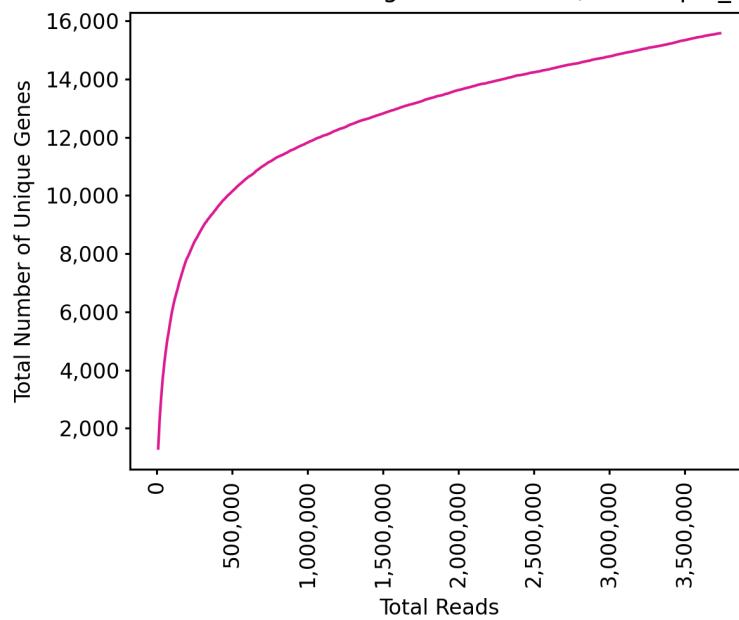
Gene Saturation, all genes, filtered (BioSample_3)



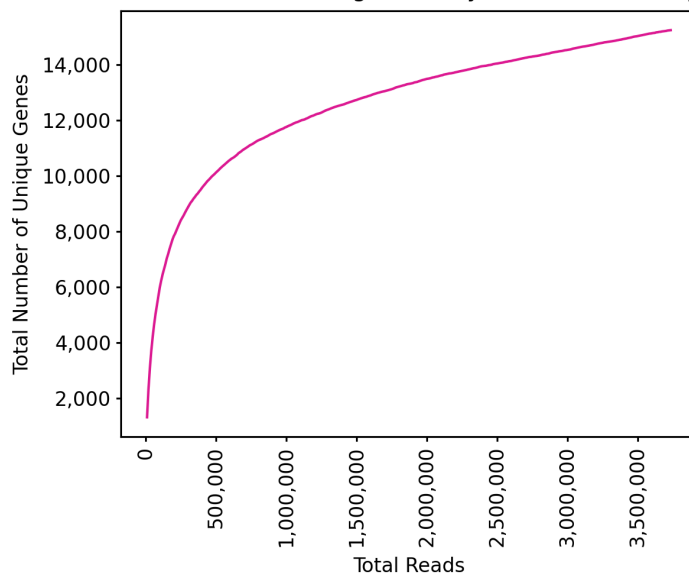
Gene Saturation, known genes only, filtered (BioSample_3)



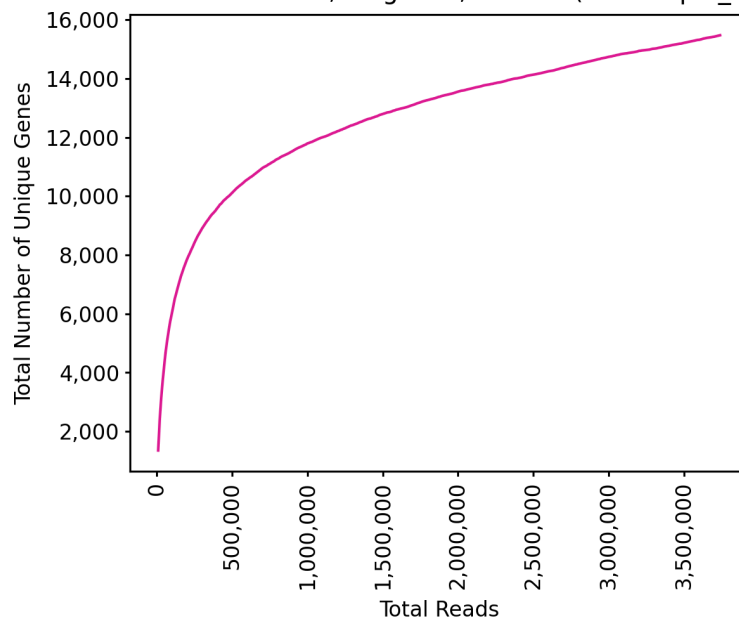
Gene Saturation, all genes, filtered (BioSample_4)



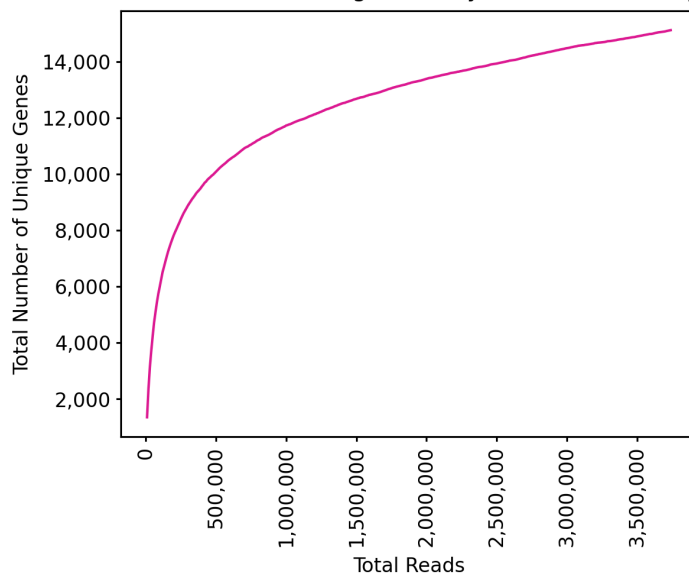
Gene Saturation, known genes only, filtered (BioSample_4)



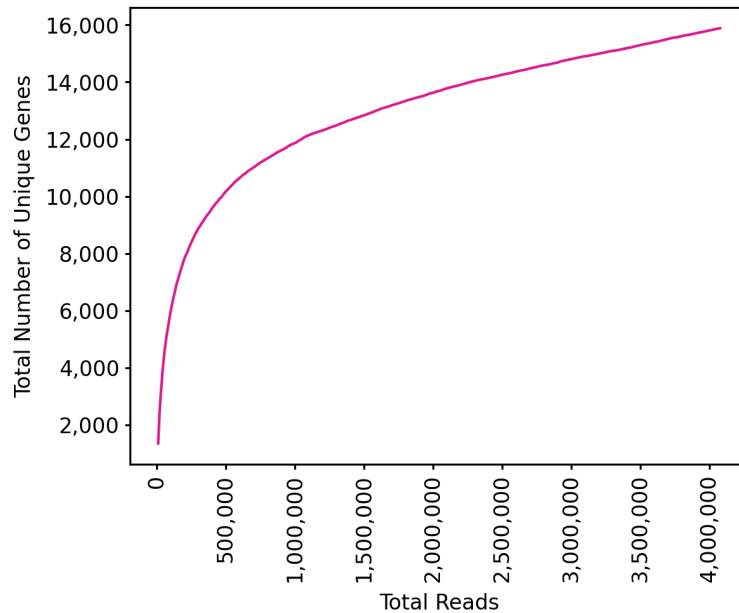
Gene Saturation, all genes, filtered (BioSample_5)



Gene Saturation, known genes only, filtered (BioSample_5)



Gene Saturation, all genes, filtered (BioSample_6)



Gene Saturation, known genes only, filtered (BioSample_6)

