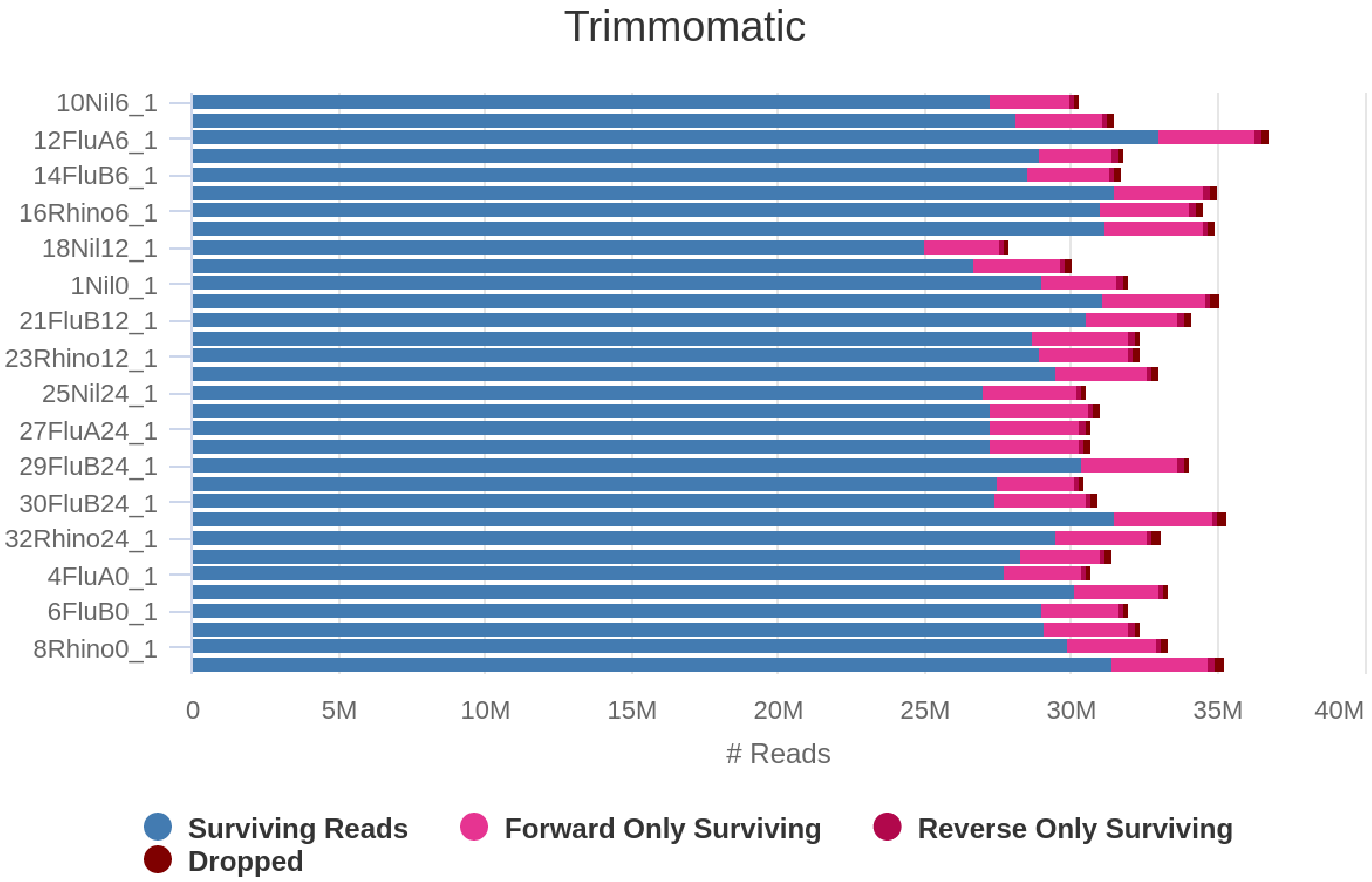
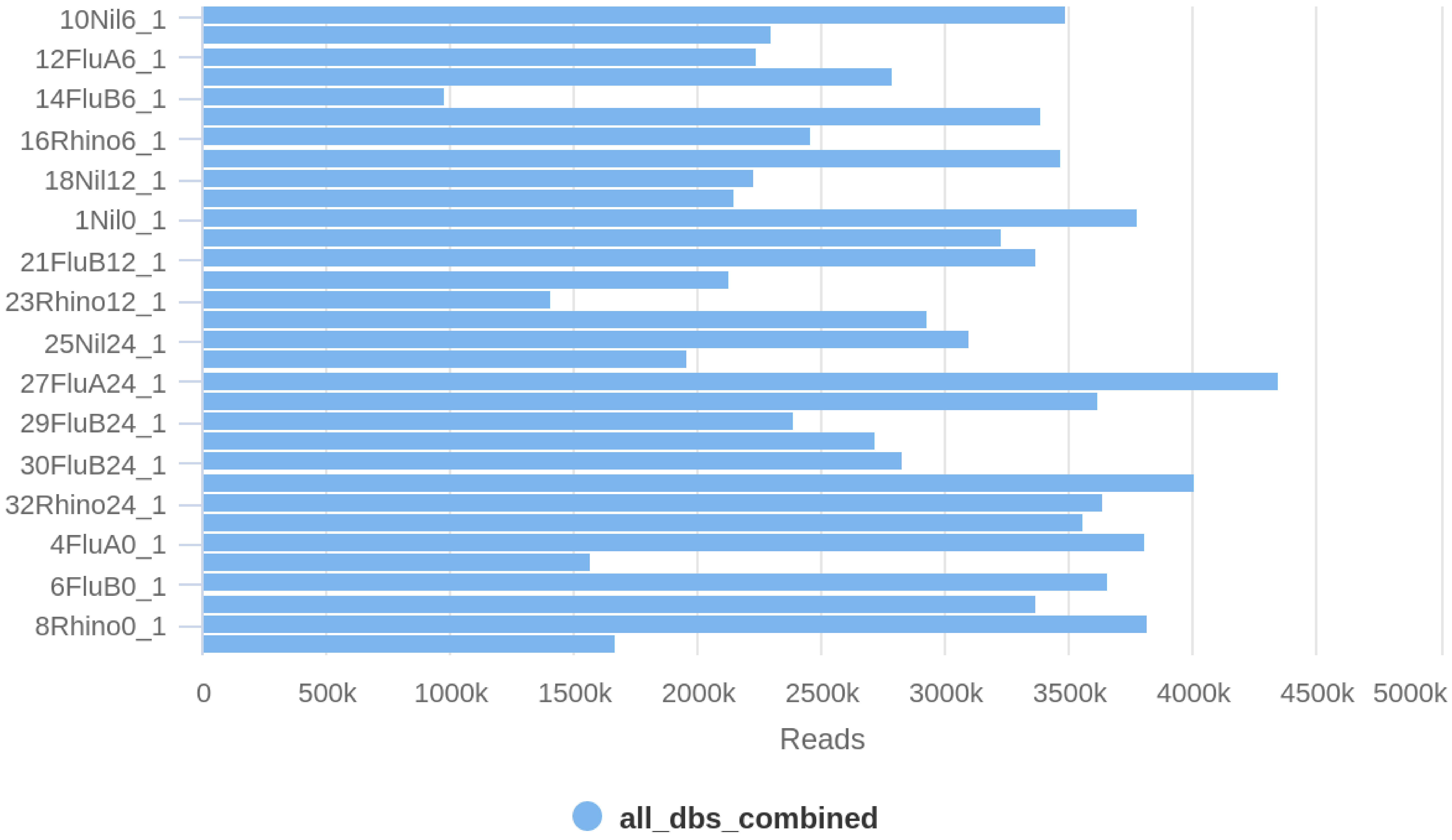
General Statistics

Sample Name	% Dropped	% rRNA	% Dups	% GC	M Seqs	% Aligned	M Aligned	M Reads Mapped	% Assigned	M Assigned
10Nil6_1	0.7%	6.4%	56.8%	50%	25.4	93.2%	23.3	47.4	90.6%	21.5
11FluA6_1	0.7%	4.1%	57.2%	49%	26.9	92.9%	24.6	50	91.0%	22.8
12FluA6_1	0.7%	3.4%	60.3%	49%	31.9	93.2%	29.2	59.5	91.0%	27
13FluB6_1	0.6%	4.8%	61.8%	48%	27.5	84.2%	22.8	46.3	91.1%	21.1
14FluB6_1	0.7%	1.7%	61.8%	48%	28	83.1%	22.9	46.6	91.1%	21.2
15Rhino6_1	0.7%	5.4%	59.7%	49%	29.8	93.5%	27.4	55.7	90.8%	25.3
16Rhino6_1	0.8%	4.0%	58.9%	49%	29.8	93.5%	27.4	55.7	90.9%	25.3
17Nil12_1	0.7%	5.6%	59.5%	49%	29.4	93.9%	27.1	55.2	91.2%	25.2
18Nil12_1	0.8%	4.5%	56.3%	49%	23.9	94.1%	22.1	44.9	91.1%	20.5
19FluA12_1	0.8%	4.0%	57.3%	49%	25.6	91.6%	23.1	46.9	91.1%	21.4
1Nil0_1	0.7%	6.5%	57.6%	50%	27.1	94.1%	25	51	90.6%	23.1
20FluA12_1	0.8%	5.2%	59.9%	49%	29.5	91.5%	26.5	53.9	91.3%	24.6
21FluB12_1	0.7%	5.5%	71.3%	46%	28.8	55.9%	15.8	32.2	90.5%	14.6
22FluB12_1	0.7%	3.7%	71.7%	46%	27.6	54.2%	14.7	29.9	90.3%	13.5
23Rhino12_1	0.7%	2.4%	57.9%	49%	28.2	92.2%	25.5	51.9	91.0%	23.6
24Rhino12_1	0.7%	5.0%	58.3%	49%	28	92.3%	25.4	51.7	91.1%	23.5
25Nil24_1	0.7%	5.7%	56.8%	49%	25.5	93.3%	23.4	47.5	90.4%	21.5
26Nil24_1	0.8%	3.6%	57.8%	49%	26.3	93.3%	24.1	49	90.5%	22.2
27FluA24_1	0.7%	8.0%	57.2%	49%	25.1	88.8%	21.9	44.5	90.0%	20
28FluA24_1	0.7%	6.6%	57.0%	49%	25.4	89.3%	22.4	45.4	90.1%	20.5
29FluB24_1	0.6%	3.9%	75.2%	44%	29.1	40.9%	11.7	23.8	85.8%	10.2
2Nil0_1	0.6%	4.9%	57.4%	49%	26.1	94.2%	24.1	49.1	90.6%	22.2
30FluB24_1	0.7%	5.2%	76.1%	44%	26	37.7%	9.6	19.6	86.7%	8.5
31Rhino24_1	0.7%	6.4%	58.2%	49%	29.5	93.0%	27	54.8	91.1%	25
32Rhino24_1	1.0%	6.2%	58.2%	49%	27.6	93.0%	25.3	51.4	91.2%	23.4
3FluA0_1	0.6%	6.3%	57.8%	49%	26.5	94.0%	24.5	49.8	90.6%	22.5
4FluA0_1	0.6%	6.9%	57.0%	49%	25.8	94.0%	23.8	48.5	90.6%	22
5FluB0_1	0.6%	2.6%	59.2%	49%	29.3	94.1%	27.1	55.1	90.7%	25
6FluB0_1	0.6%	6.3%	57.7%	49%	27.1	94.3%	25.1	51.1	90.7%	23.2
7Rhino0_1	0.7%	5.8%	57.4%	49%	27.4	93.8%	25.2	51.4	90.4%	23.2
8Rhino0_1	0.7%	6.4%	58.5%	49%	27.9	93.5%	25.7	52.2	90.5%	23.6
9Nil6_1	1.1%	2.7%	60.4%	49%	30.6	93.1%	28	57	90.8%	25.9


Trimmomatic
10Nil6_1
12FluA6_1
14FluB6_1
16Rhino6_1
18Nil12_1
1Nil0_1
21FluB12_1
23Rhino12_1
25Nil24_1
27FluA24_1
29FluB24_1
30FluB24_1
32Rhino24_1
4FluA0_1
6FluB0_1
8Rhino0_1
0
5M
10M
15M
20M
25M
30M
35M
40M
Reads
Surviving Reads
Forward Only Surviving
Reverse Only Surviving
Dropped

Created with MultiQC

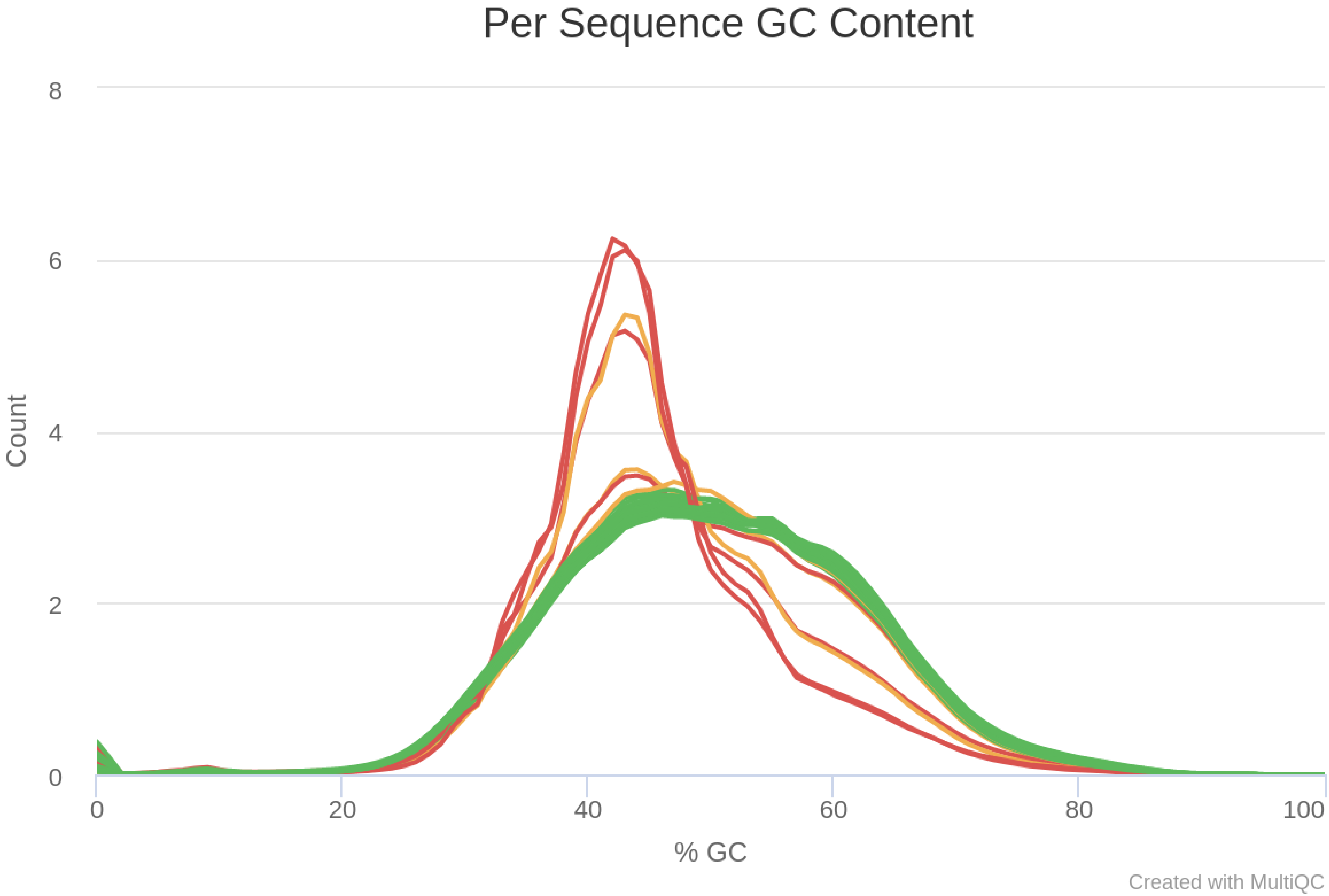
SortMeRNA hits

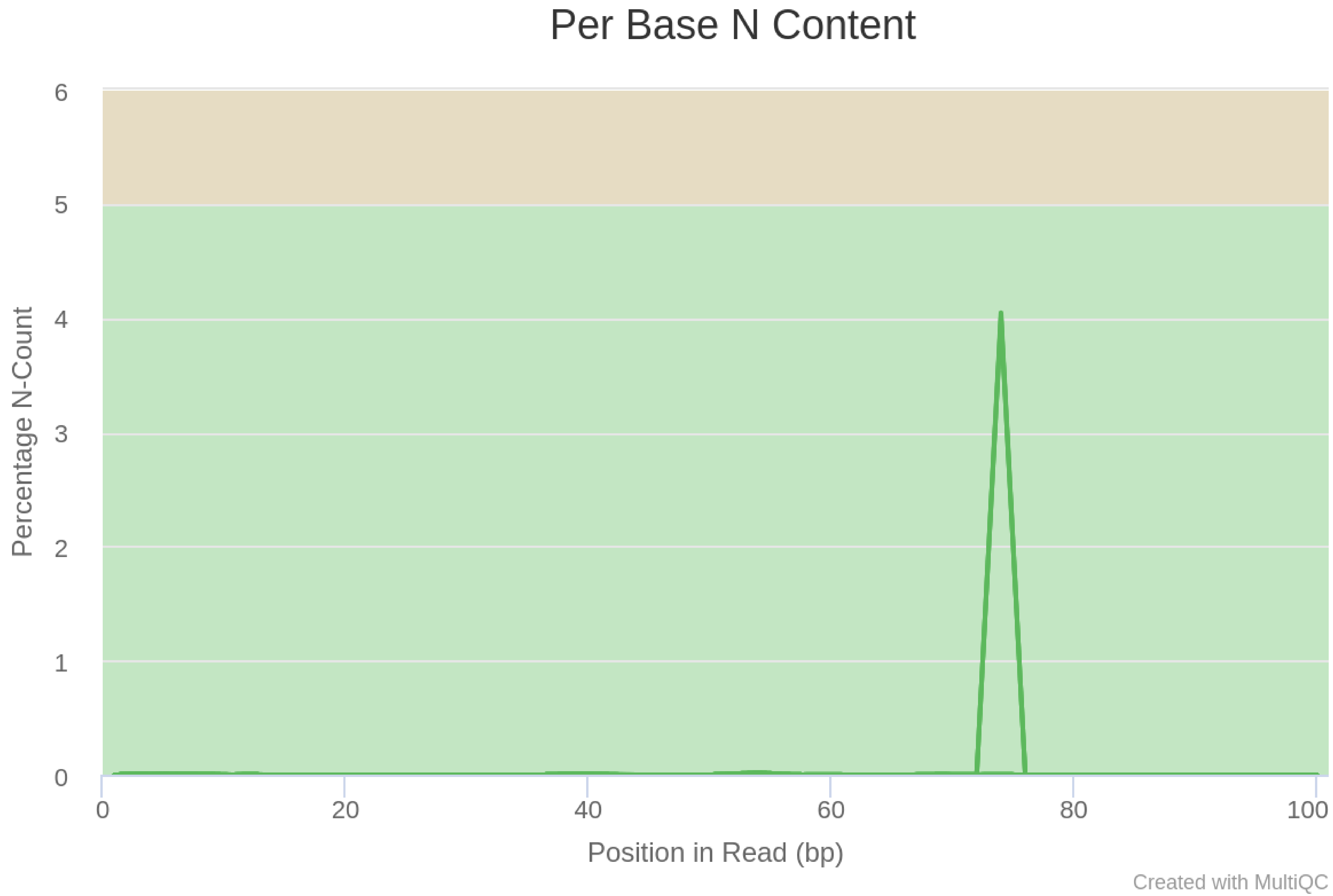


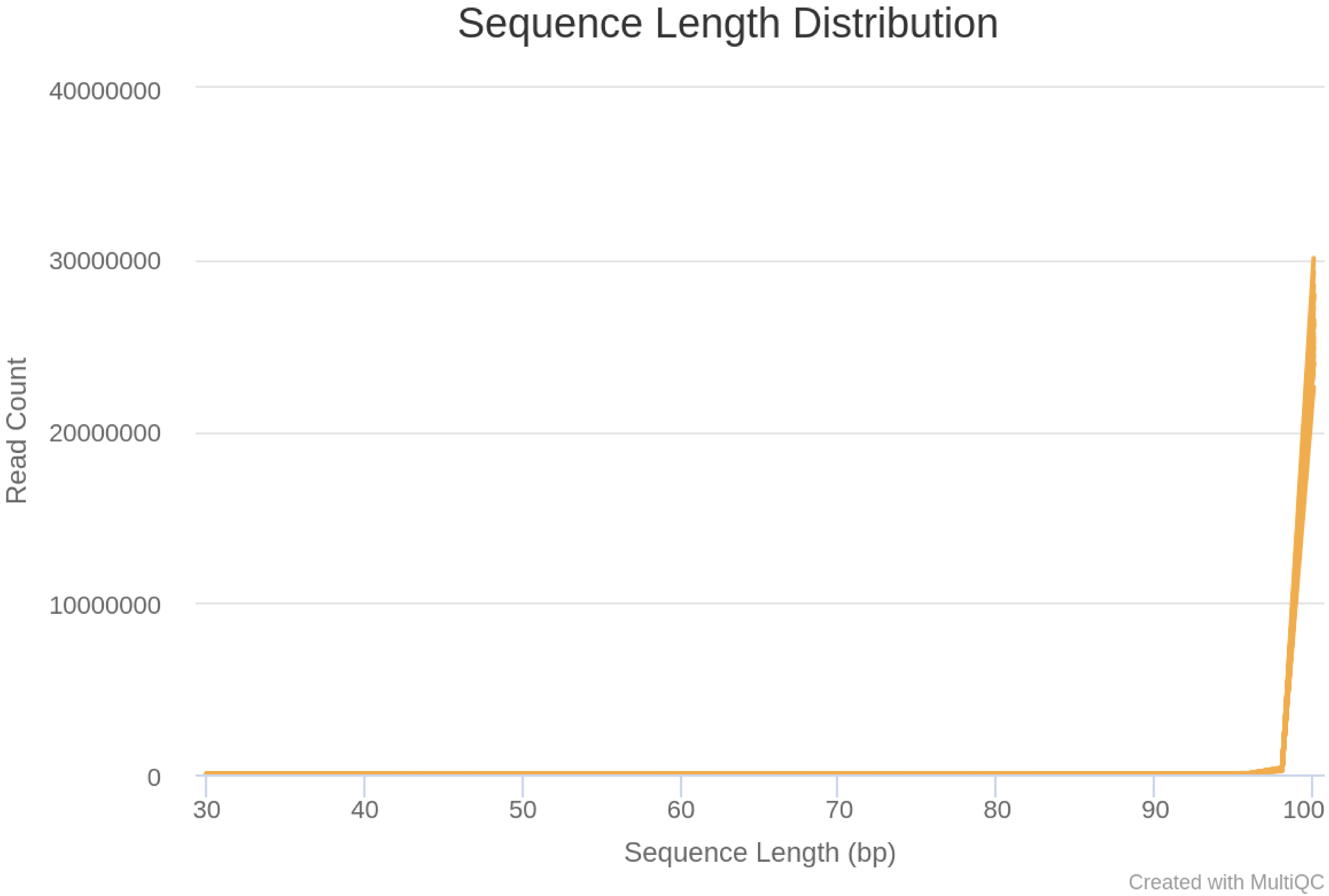
Created with MultiQC

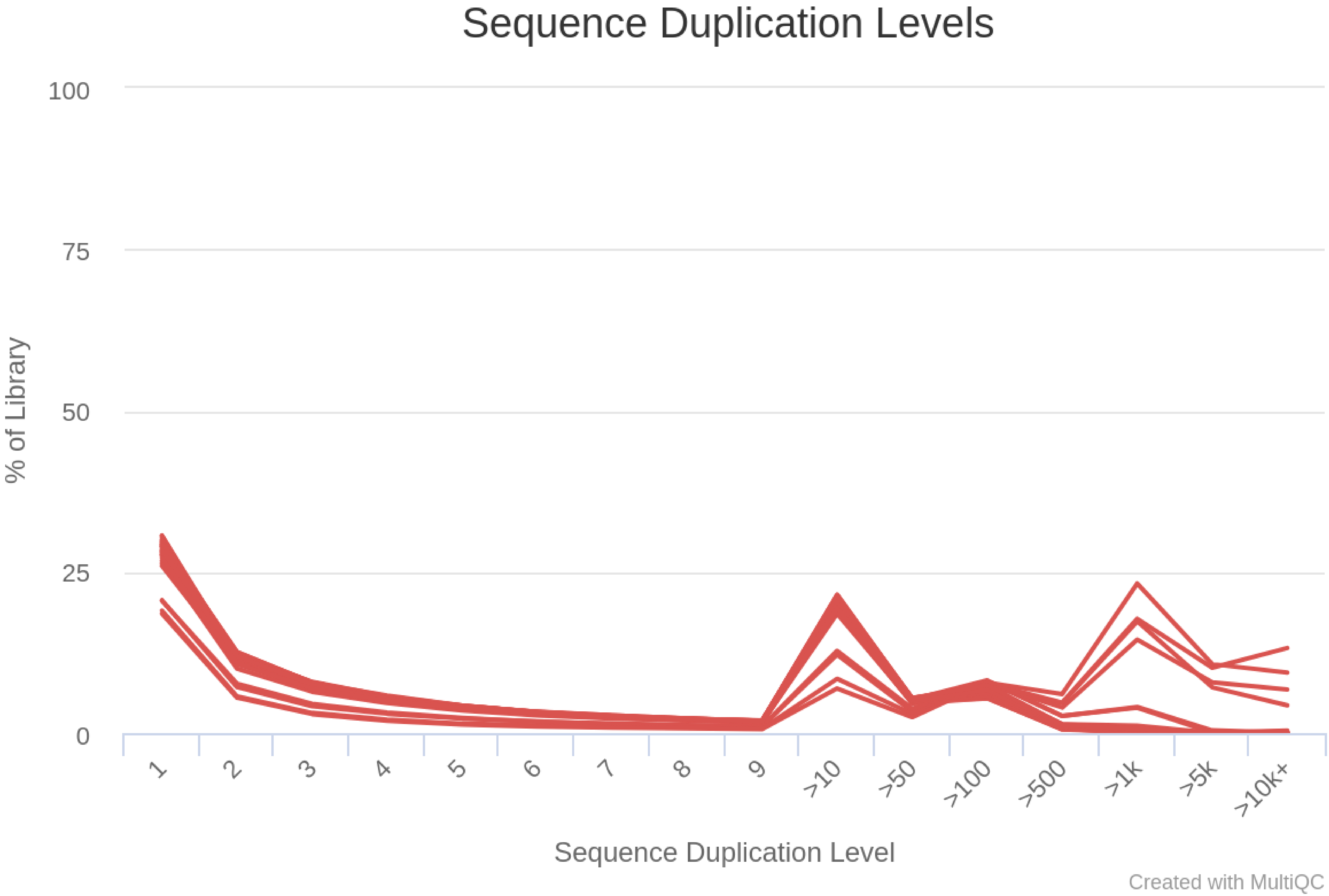

Mean Quality Scores
40
30
20
10
0
Phred Score
20
40
60
80
100
Position (bp)
Created with MultiQC

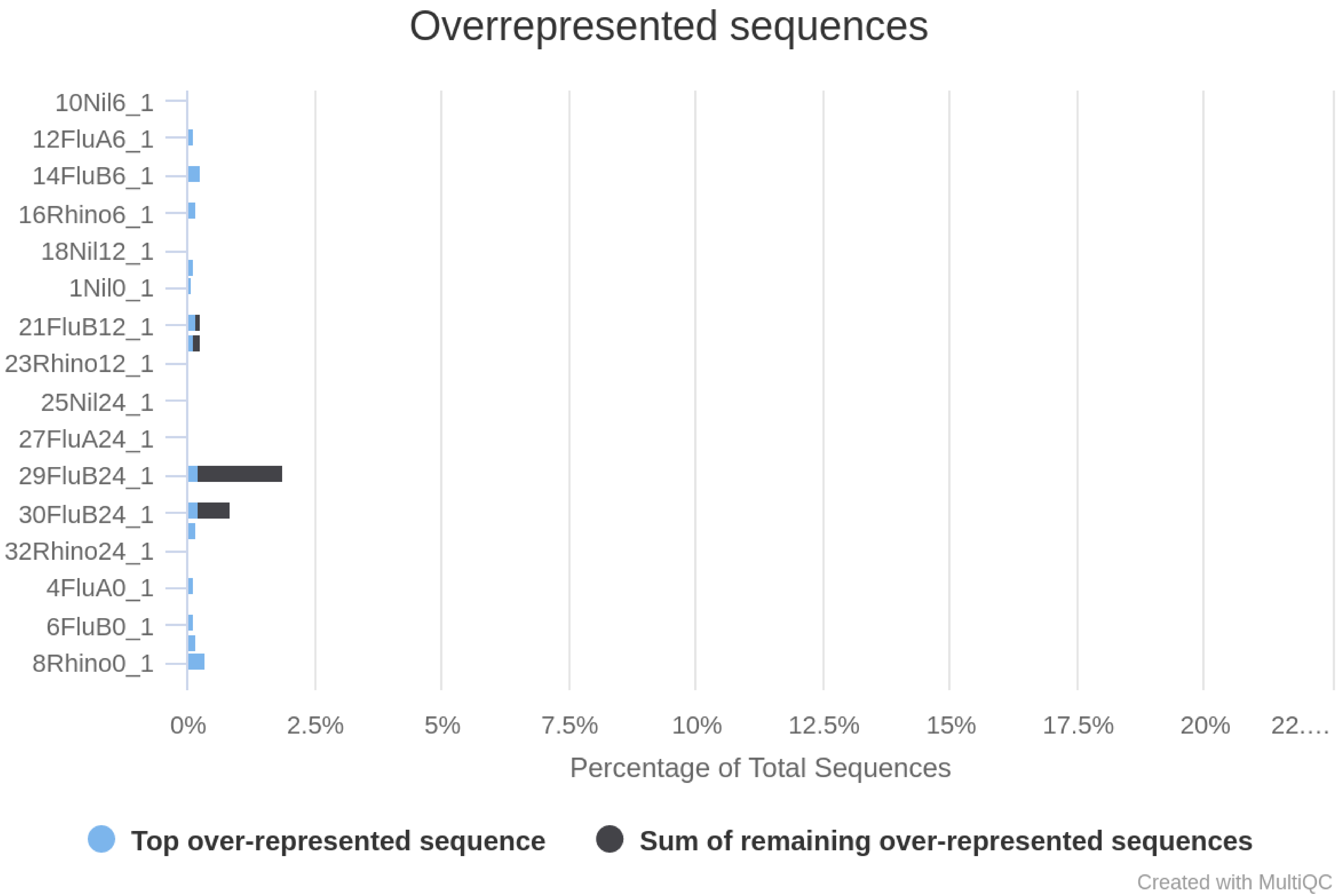

Per Sequence Quality Scores
Count
30000000
25000000
20000000
15000000
10000000
5000000
0
0
5
10
15
20
25
30
35
Mean Sequence Quality (Phred Score)
Created with MultiQC


Per Sequence GC Content
Count
8
6
4
2
0
0
20
40
60
80
100
% GC
Created with MultiQC

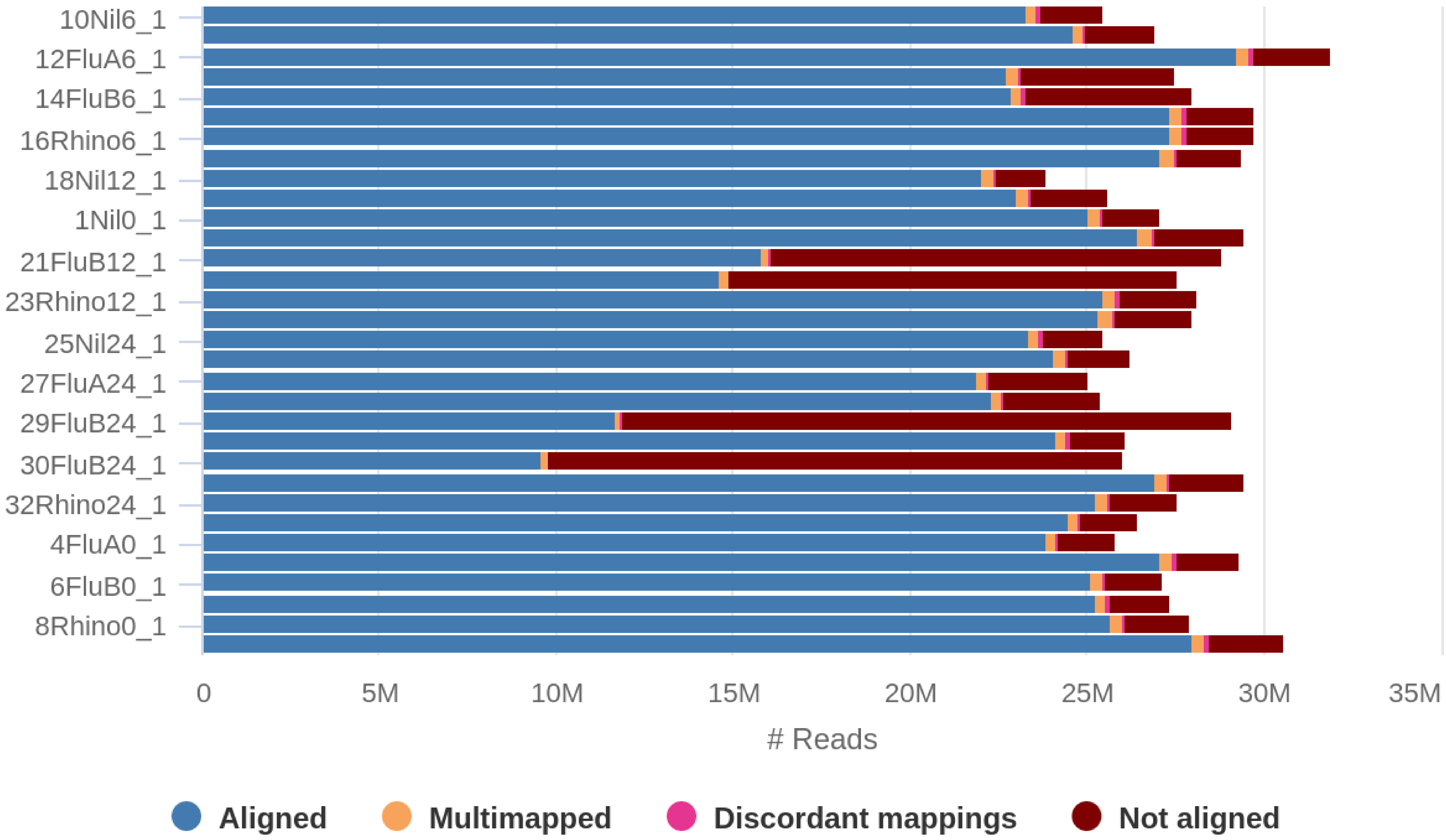

Per Base N Content
Percentage N-Count
6
5
4
3
2
1
0
0
20
40
60
80
100
Position in Read (bp)
Created with MultiQC


Sequence Length Distribution
Read Count
40000000
30000000
20000000
10000000
0
30
40
50
60
70
80
90
100
Sequence Length (bp)
Created with MultiQC

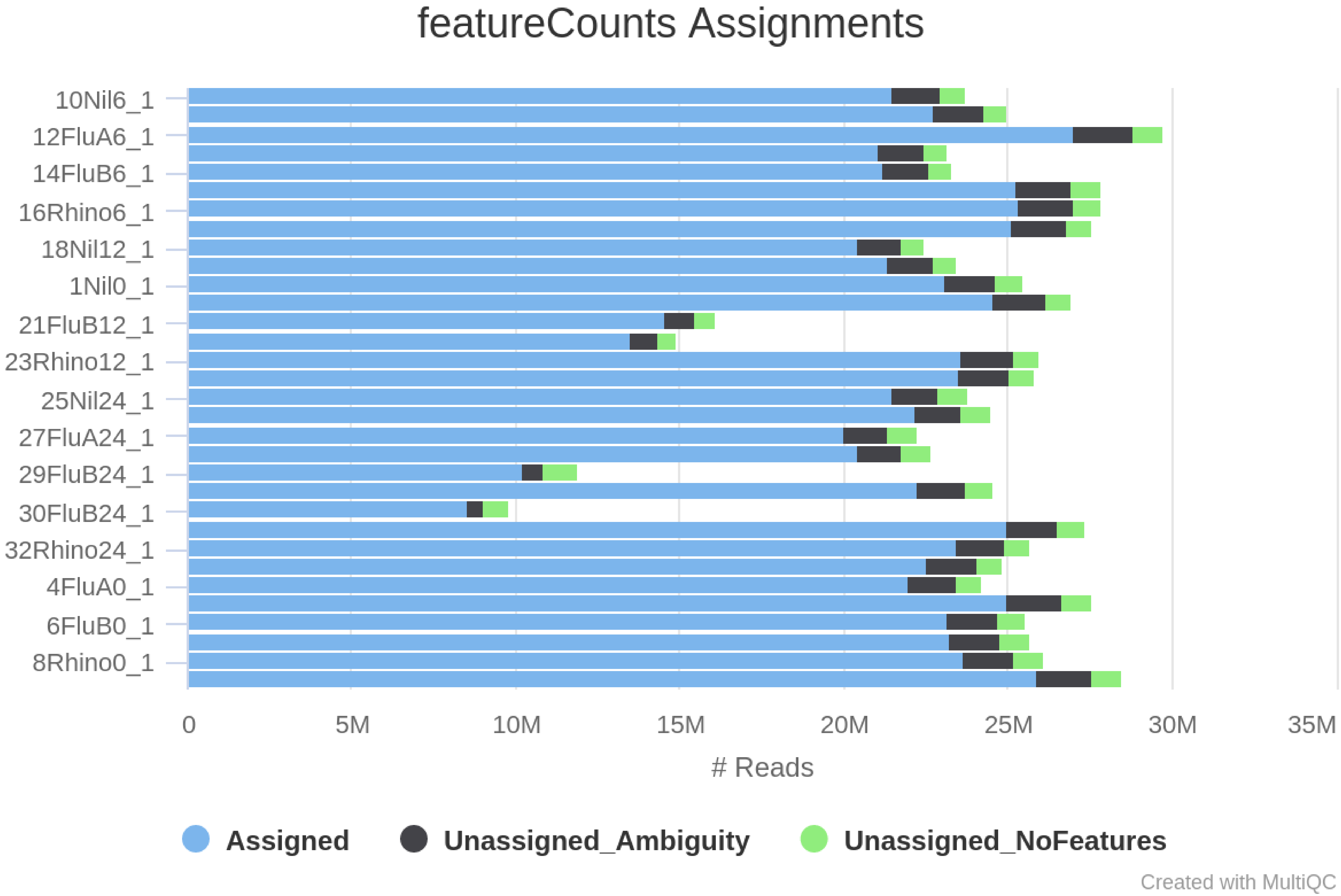

Sequence Duplication Levels
100
75
50
25
0
% of Library
1
2
3
4
5
6
7
8
9
>10
>50
>100
>500
>1k
>5k
>10k+
Sequence Duplication Level
Created with MultiQC


Overrepresented sequences
10Nil6_1
12FluA6_1
14FluB6_1
16Rhino6_1
18Nil12_1
1Nil0_1
21FluB12_1
23Rhino12_1
25Nil24_1
27FluA24_1
29FluB24_1
30FluB24_1
32Rhino24_1
4FluA0_1
6FluB0_1
8Rhino0_1
0%
2.5%
5%
7.5%
10%
12.5%
15%
17.5%
20%
22.…
Percentage of Total Sequences
Top over-represented sequence
Sum of remaining over-represented sequences
Created with MultiQC

Tophat Alignment Scores



Created with MultiQC


featureCounts Assignments
10Nil6_1
12FluA6_1
14FluB6_1
16Rhino6_1
18Nil12_1
1Nil0_1
21FluB12_1
23Rhino12_1
25Nil24_1
27FluA24_1
29FluB24_1
30FluB24_1
32Rhino24_1
4FluA0_1
6FluB0_1
8Rhino0_1
0
5M
10M
15M
20M
25M
30M
35M
Reads
Assigned
Unassigned_Ambiguity
Unassigned_NoFeatures
Created with MultiQC