Report

	SRR12574847_filtered	SRR12574848_filtered	SRR12574846_filtered
# contigs (>= 0 bp)	95	114	105
# contigs (>= 1000 bp)	54	62	60
# contigs (>= 5000 bp)	44	53	48
# contigs (>= 10000 bp)	43	49	46
# contigs (>= 25000 bp)	36	43	39
# contigs (>= 50000 bp)	29	33	30
Total length (>= 0 bp)	5091843	5193473	4971407
Total length (>= 1000 bp)	5079551	5177489	4957448
Total length (>= 5000 bp)	5056053	5159464	4929211
Total length (>= 10000 bp)	5049358	5130717	4914618
Total length (>= 25000 bp)	4933537	5016384	4798746
Total length (>= 50000 bp)	4651151	4663569	4442413
# contigs	59	66	65
Largest contig	563112	392848	351384
Total length	5082851	5180278	4960615
Reference length	5377795	5377795	5377795
GC (%)	64.18	64.18	64.15
Reference GC (%)	64.05	64.05	64.05
N50	163772	158034	179965
NG50	158784	157065	154056
N90	58679	52516	49597
NG90	39029	38081	19429
auN	222132.8	175811.1	179887.8
auNG	209950.0	169353.9	165933.1
L50	10	11	10
LG50	11	12	11
L90	28	33	31
LG90	34	38	41
# misassemblies	43	36	75
# misassembled contigs	22	14	30
Misassembled contigs length	3638146	2691280	4157226
# local misassemblies	10	10	50
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	1
# unaligned mis. contigs	0	3	2
# unaligned contigs	7 + 25 part	13 + 23 part	13 + 33 part
Unaligned length	464109	521706	504379
Genome fraction (%)	85.841	86.557	82.868
Duplication ratio	1.000	1.000	0.999
# N's per 100 kbp	5.63	0.00	1.96
# mismatches per 100 kbp	480.03	491.34	2154.21
# indels per 100 kbp	9.98	10.84	39.41
Largest alignment	481956	264685	197508
Total aligned length	4618294	4656674	4453607
NA50	87727	87797	64022
NGA50	83707	80674	59641
NA90	6695	-	-
NGA90	-	-	-
auNA	114523.0	90997.3	68397.4
auNGA	108242.0	87655.1	63091.5
LA50	19	20	25
LGA50	21	22	28
LA90	76	-	-
LGA90	-	-	-

All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
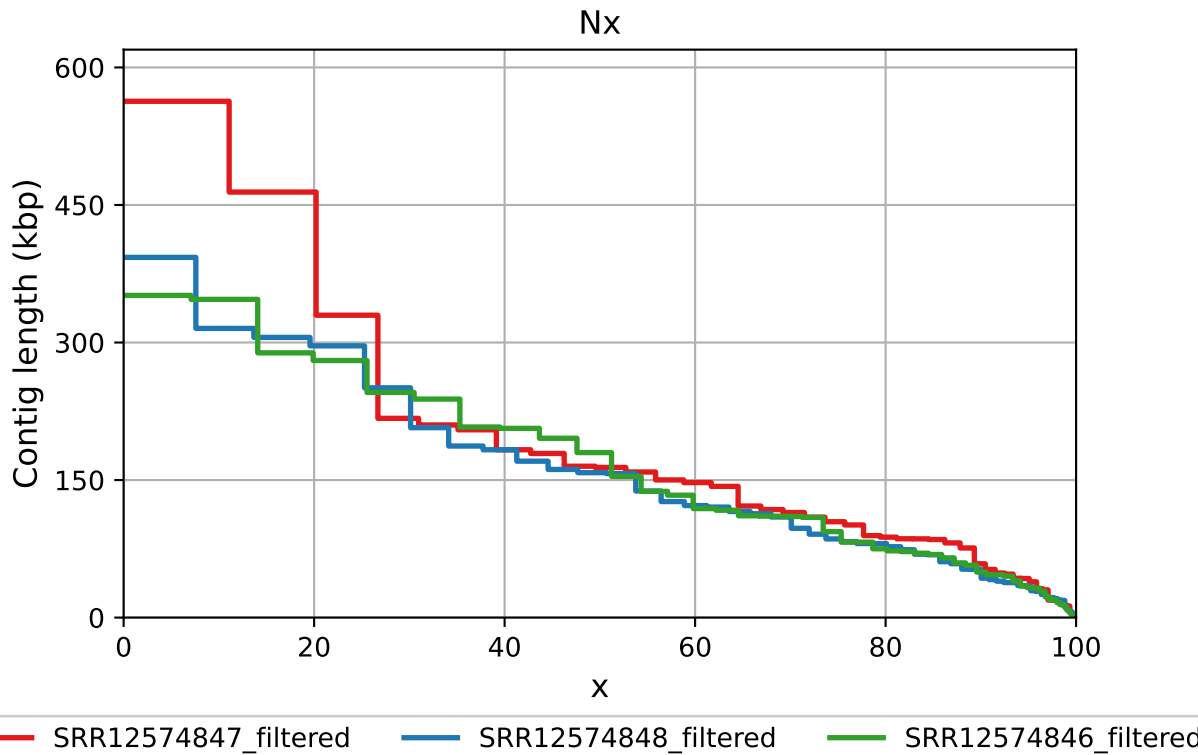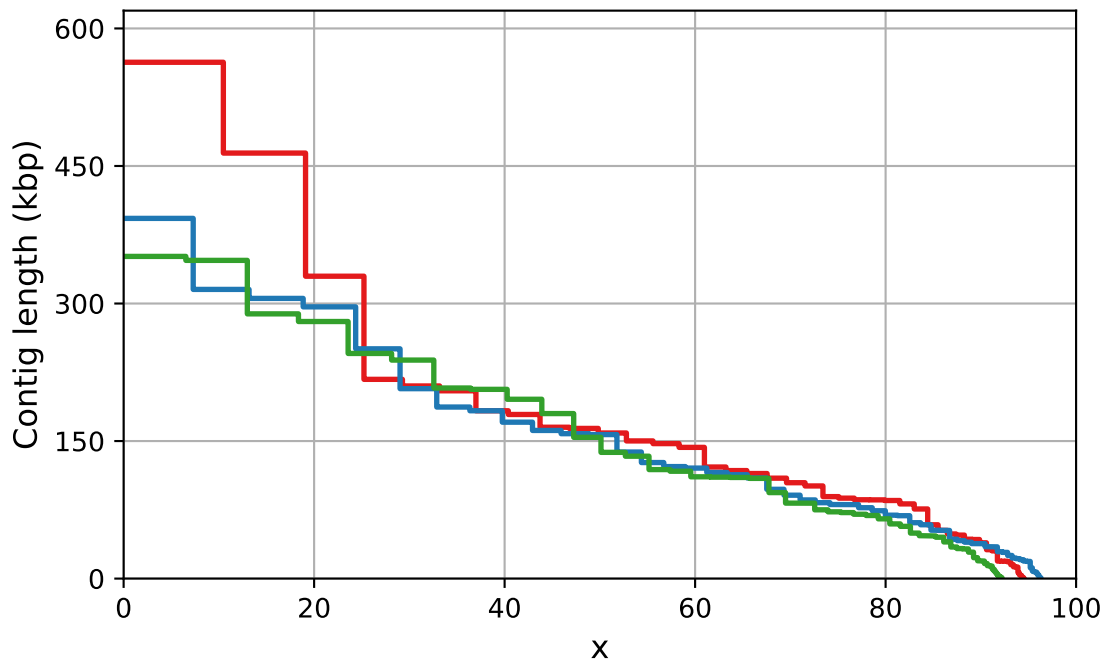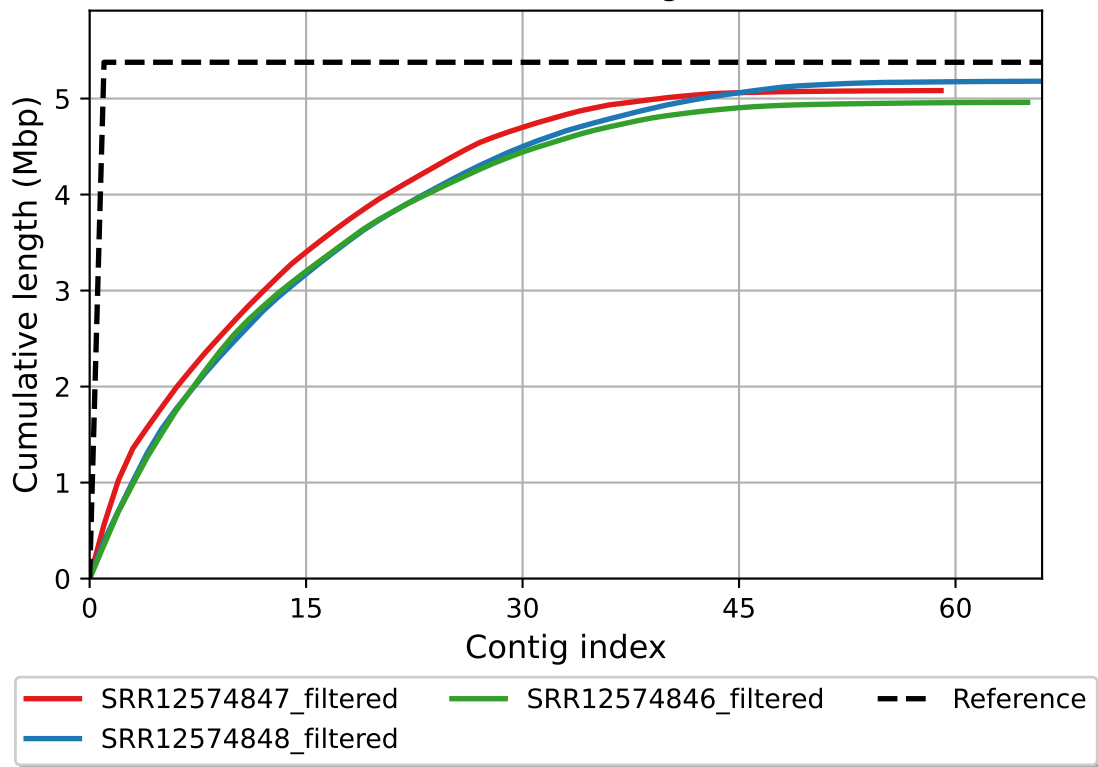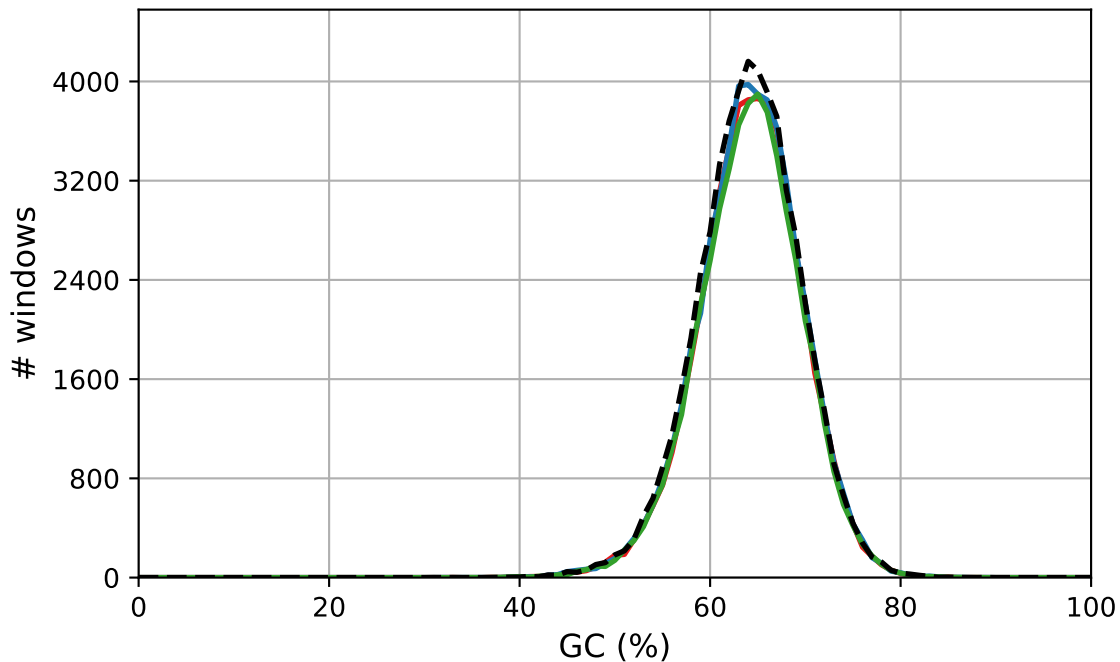
Misassemblies report

	SRR12574847_filtered	SRR12574848_filtered	SRR12574846_filtered
# misassemblies	43	36	75
# contig misassemblies	43	36	75
# c. relocations	43	36	75
# c. translocations	0	0	0
# c. inversions	0	0	0
# scaffold misassemblies	0	0	0
# s. relocations	0	0	0
# s. translocations	0	0	0
# s. inversions	0	0	0
# misassembled contigs	22	14	30
Misassembled contigs length	3638146	2691280	4157226
# local misassemblies	10	10	50
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	1
# unaligned mis. contigs	0	3	2
# mismatches	22169	22880	95940
# indels	461	505	1755
# indels (<= 5 bp)	362	402	1450
# indels (> 5 bp)	99	103	305
Indels length	3727	2946	10937

All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

	SRR12574847_filtered	SRR12574848_filtered	SRR12574846_filtered
# fully unaligned contigs	7	13	13
Fully unaligned length	49674	143070	96972
# partially unaligned contigs	25	23	33
Partially unaligned length	414435	378636	407407
# N's	286	0	97

All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

| Contig length (kbp) | x |

- SRR12574847_filtered
- SRR12574848_filtered
- SRR12574846_filtered

NGx

Cumulative length

GC content

SRR12574847_filtered GC content
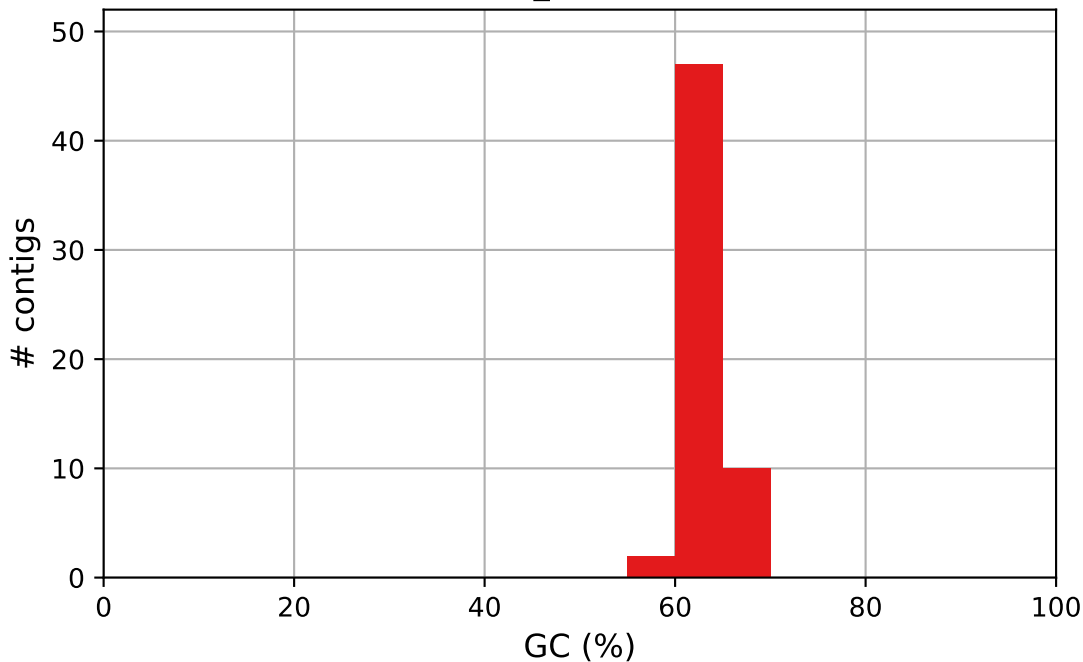
SRR12574848_filtered GC content
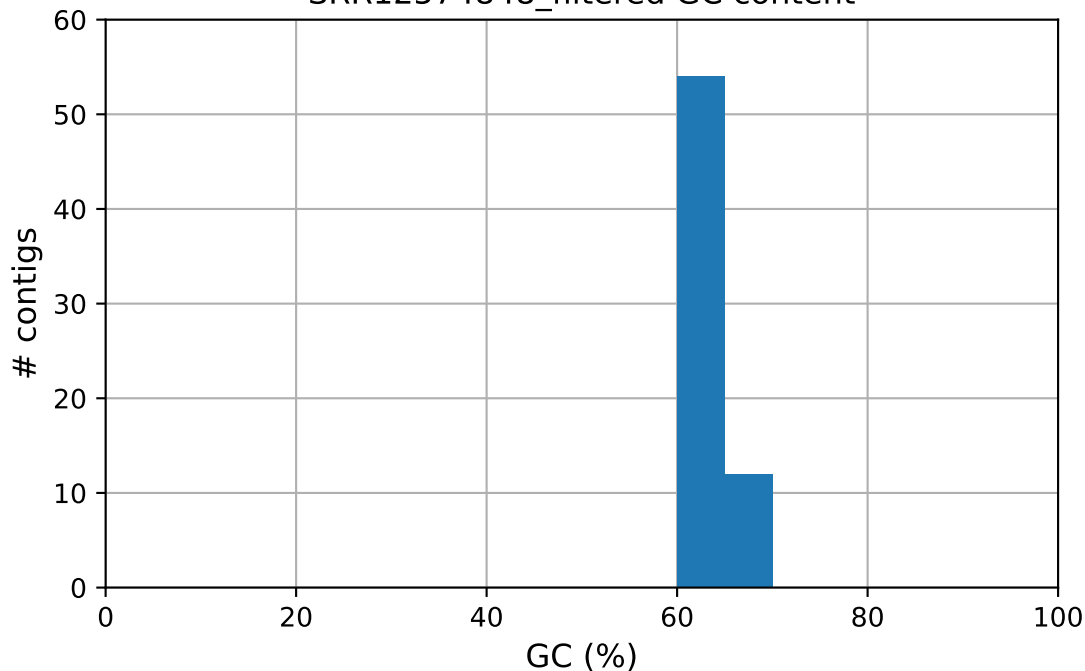
SRR12574846_filtered GC content

Coverage histogram (bin size: 1x)

Legend:
- SRR12574847_filtered
- SRR12574848_filtered
- SRR12574846_filtered
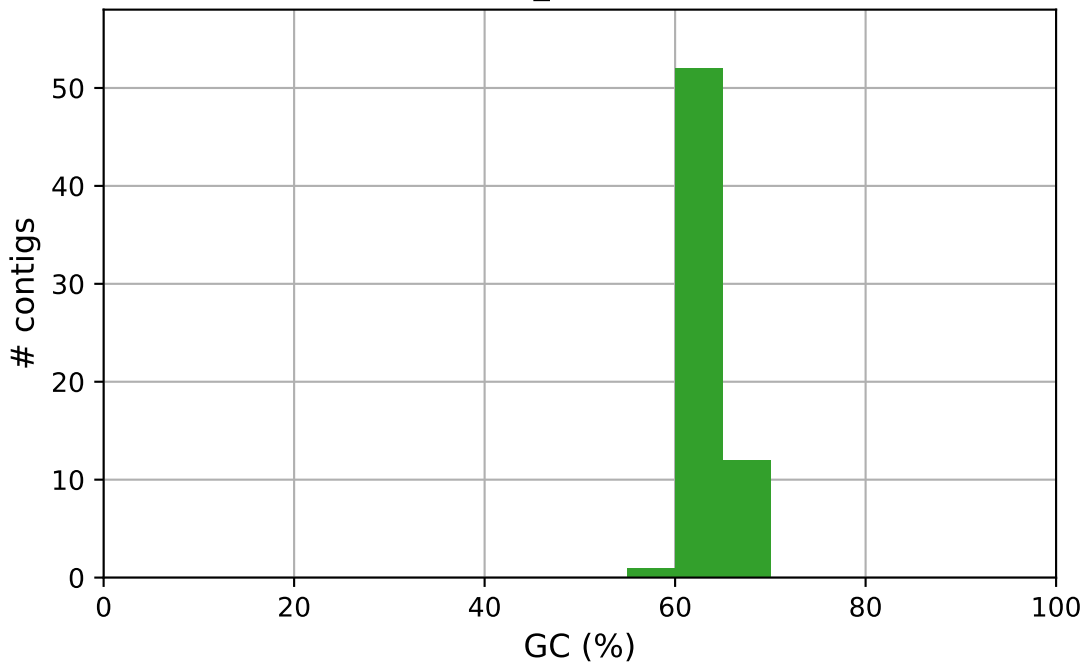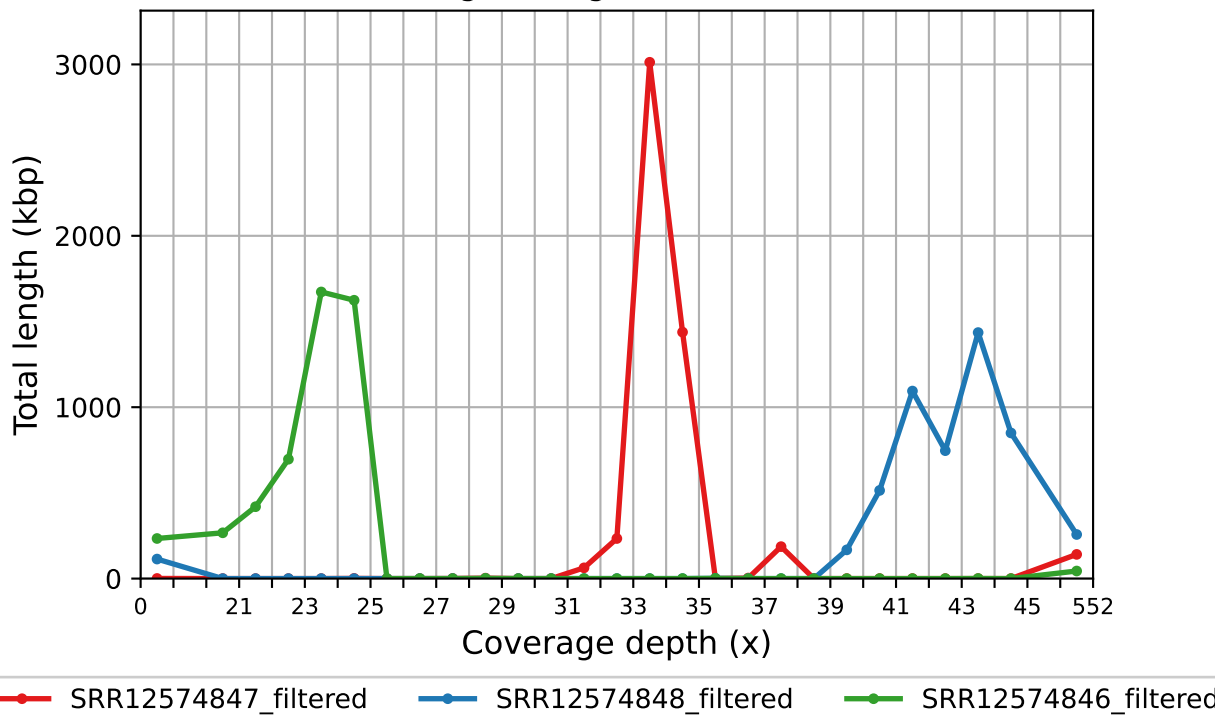
SRR12574847_filtered coverage histogram (bin size: 1x)
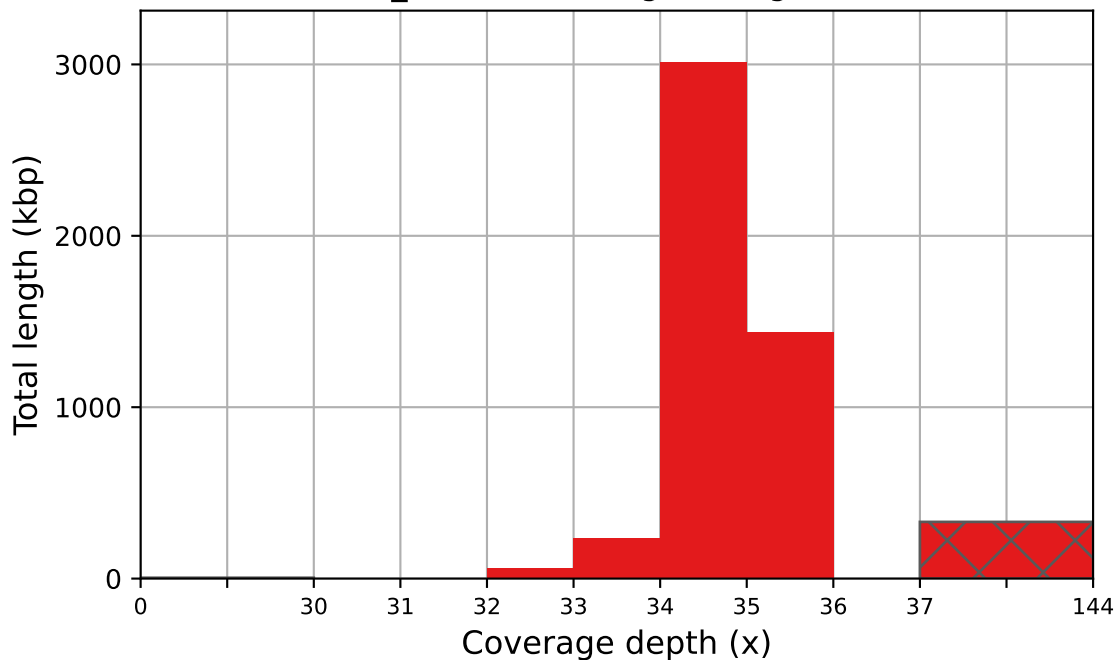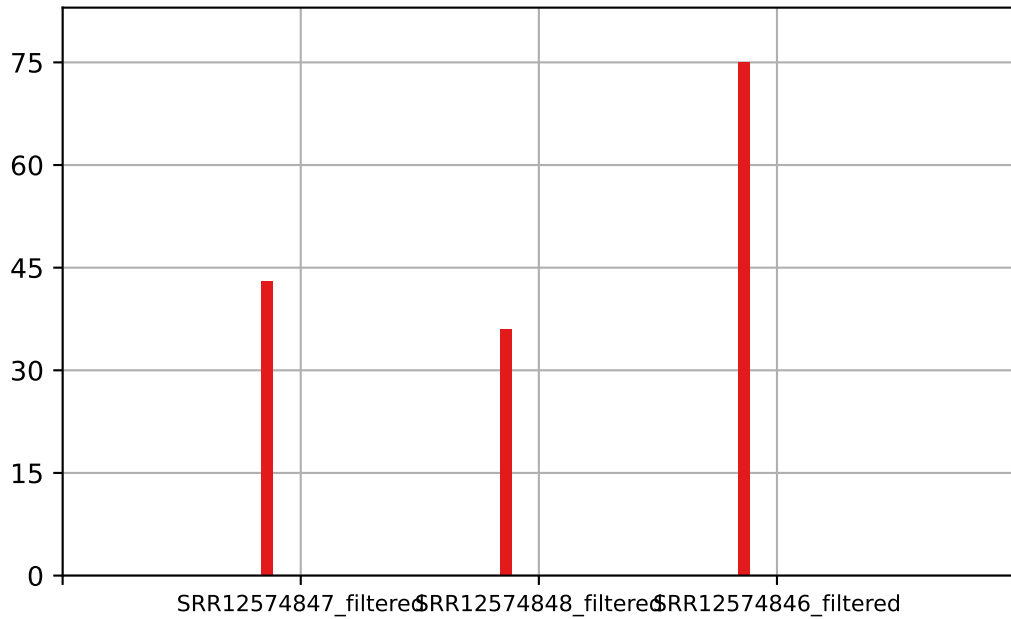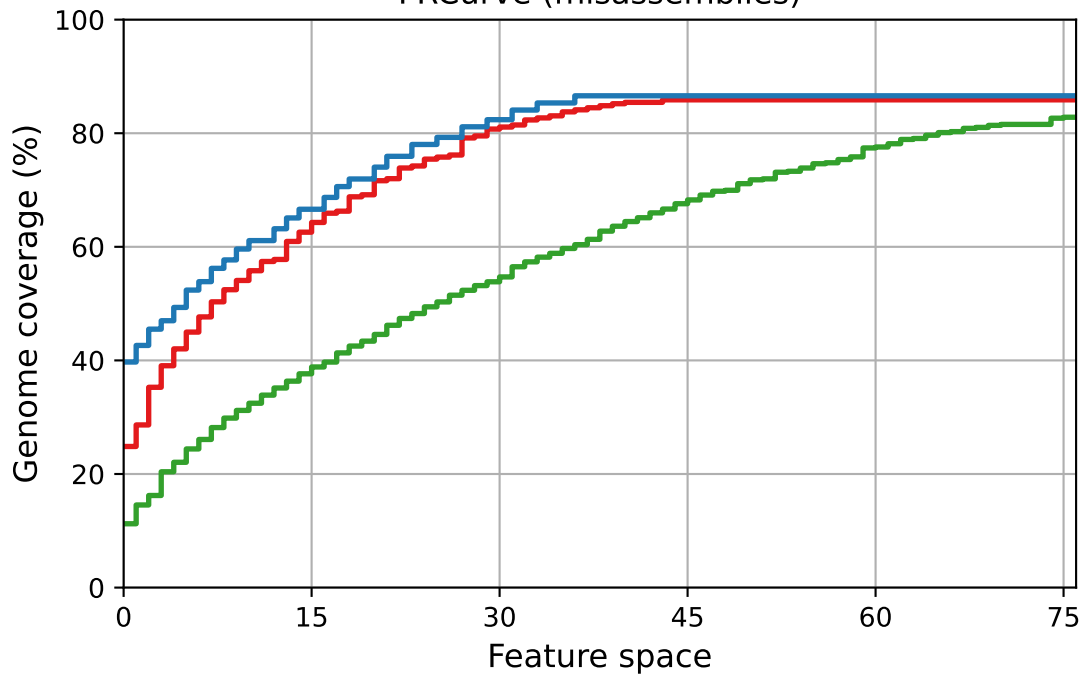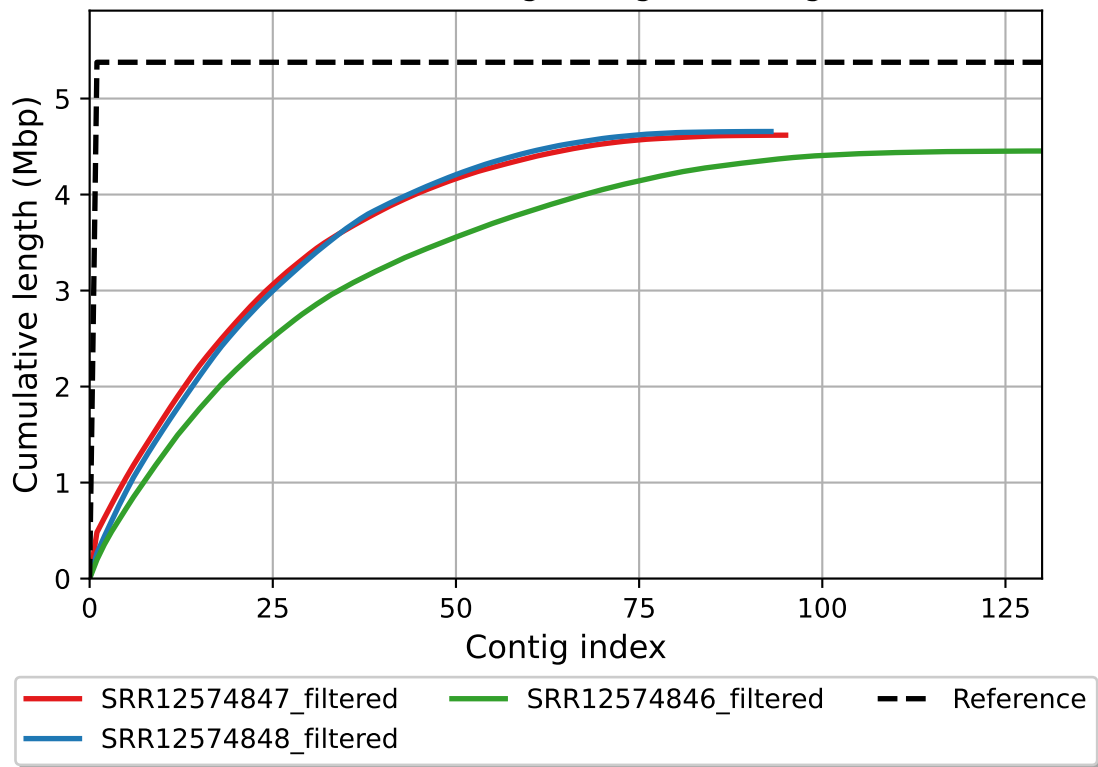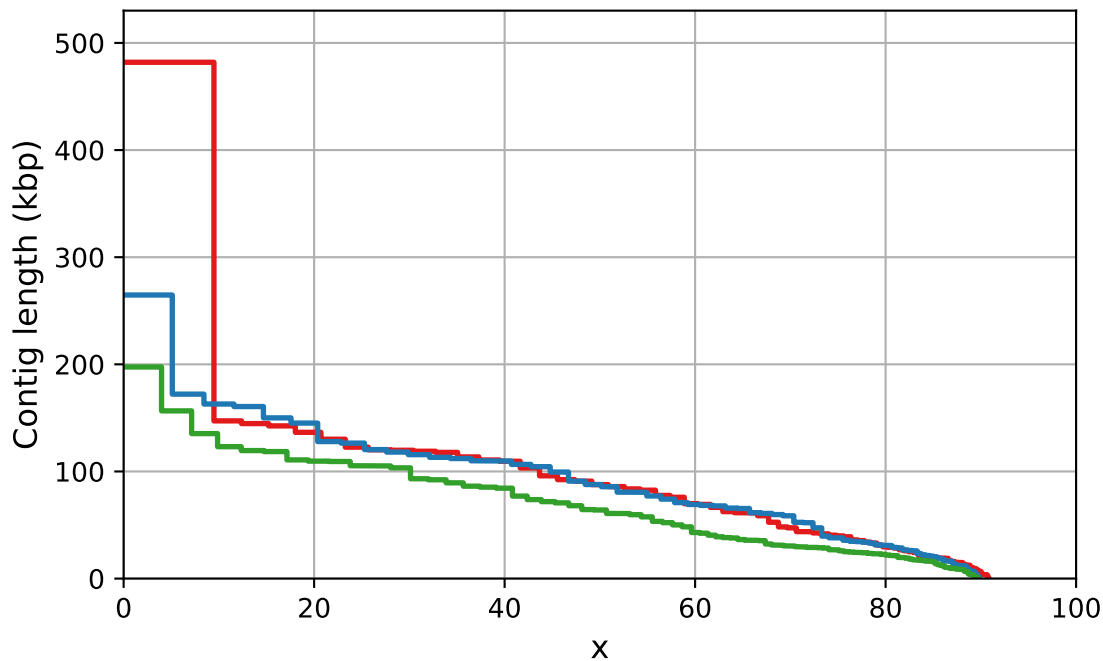
SRR12574848_filtered coverage histogram (bin size: 1x)
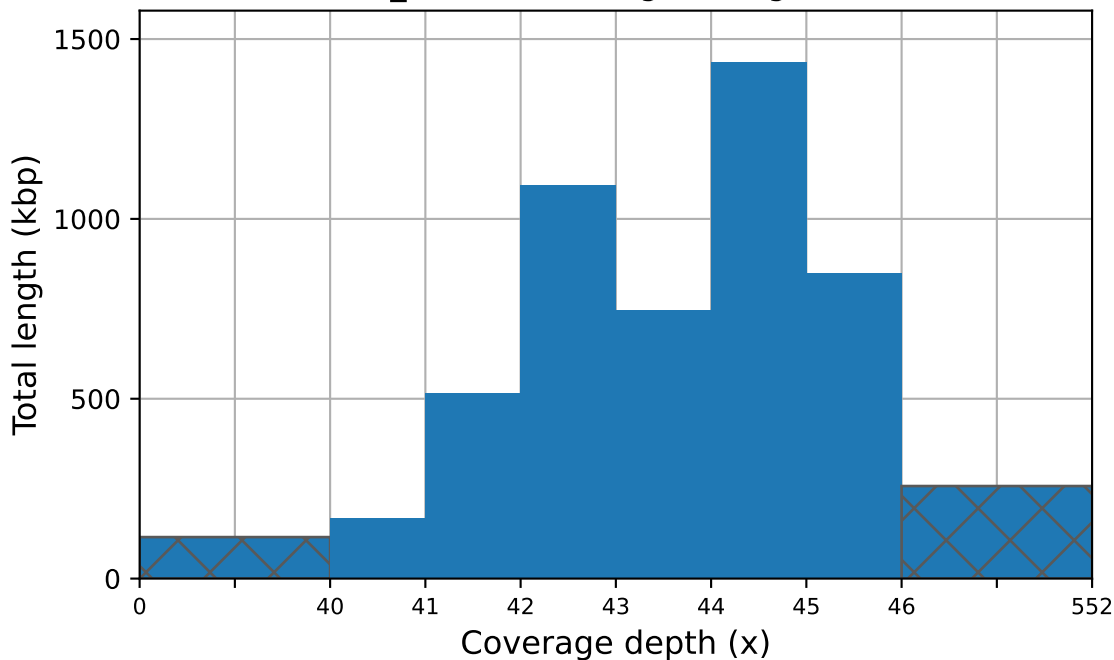
SRR12574846_filtered coverage histogram (bin size: 1x)
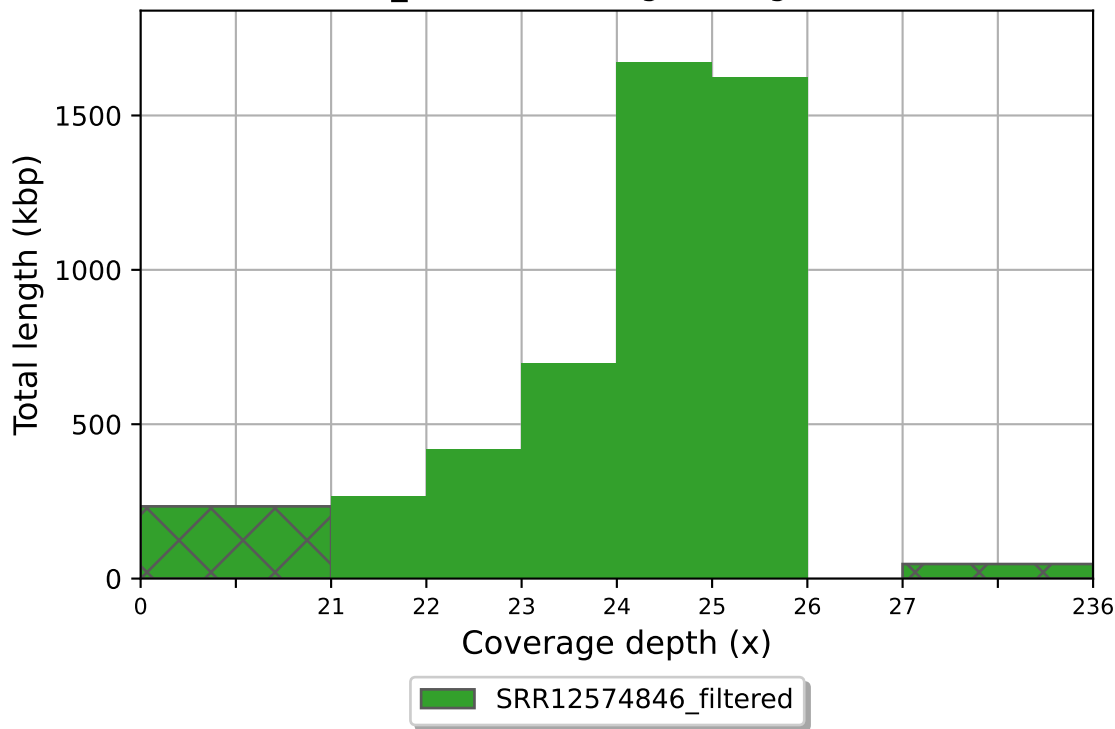
Misassemblies

FRCurve (misassemblies)

SRR12574847_filtered
SRR12574848_filtered
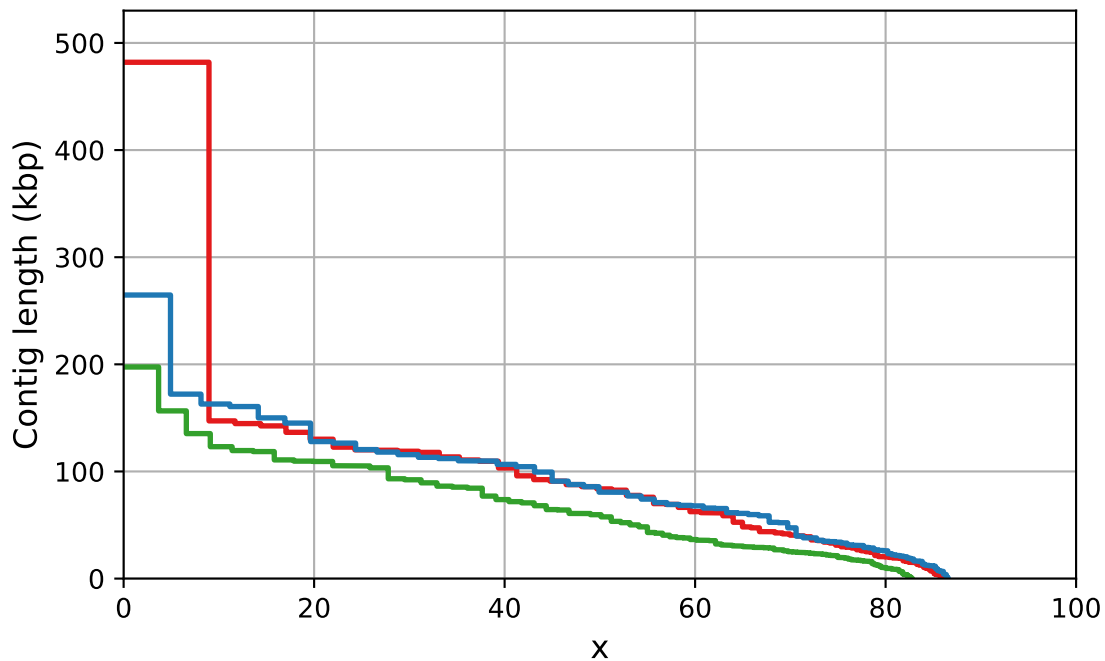SRR12574846_filtered

Cumulative length (aligned contigs)

NAx

SRR12574847_filtered   SRR12574848_filtered   SRR12574846_filtered

NGAx

Genome fraction, %

SRR12574847_filtered　　SRR12574848_filtered　　SRR12574846_filtered