

Report

	spades_ctg	mulksq_ctg
# contigs (>= 0 bp)	188	196
# contigs (>= 1000 bp)	49	49
# contigs (>= 5000 bp)	39	39
# contigs (>= 10000 bp)	37	37
# contigs (>= 25000 bp)	31	31
# contigs (>= 50000 bp)	25	25
Total length (>= 0 bp)	5386534	5390352
Total length (>= 1000 bp)	5358271	5358271
Total length (>= 5000 bp)	5336305	5336305
Total length (>= 10000 bp)	5322587	5322587
Total length (>= 25000 bp)	5223188	5223188
Total length (>= 50000 bp)	4994795	4994795
# contigs	55	58
Largest contig	676503	676503
Total length	5362226	5364139
Reference length	5224283	5224283
GC (%)	35.33	35.33
Reference GC (%)	35.58	35.58
N50	270560	270560
NG50	270560	270560
N75	135536	135536
NG75	136515	136515
L50	7	7
LG50	7	7
L75	14	14
LG75	13	13
# misassemblies	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	3	3
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# unaligned contigs	0 + 5 part	3 + 5 part
Unaligned length	196944	198857
Genome fraction (%)	98.813	98.813
Duplication ratio	1.001	1.001
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	1.63	1.69
# indels per 100 kbp	2.03	2.03
Largest alignment	676503	676503
Total aligned length	5165075	5165075
NA50	270560	270560
NGA50	270560	270560
NA75	135536	135536
NGA75	136515	136515
LA50	7	7
LGA50	7	7
LA75	14	14
LGA75	13	13

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

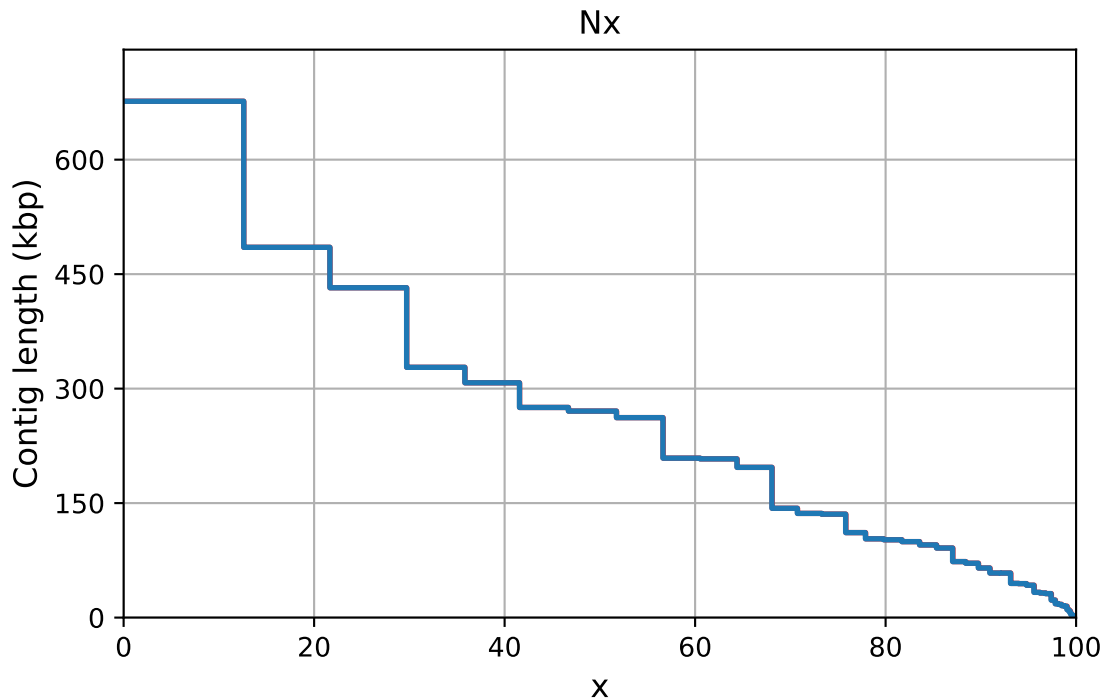
	spades_ctg	mulksq_ctg
# misassemblies	0	0
# contig misassemblies	0	0
# c. relocations	0	0
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	3	3
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# mismatches	84	87
# indels	105	105
# indels (<= 5 bp)	95	95
# indels (> 5 bp)	10	10
Indels length	534	534

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

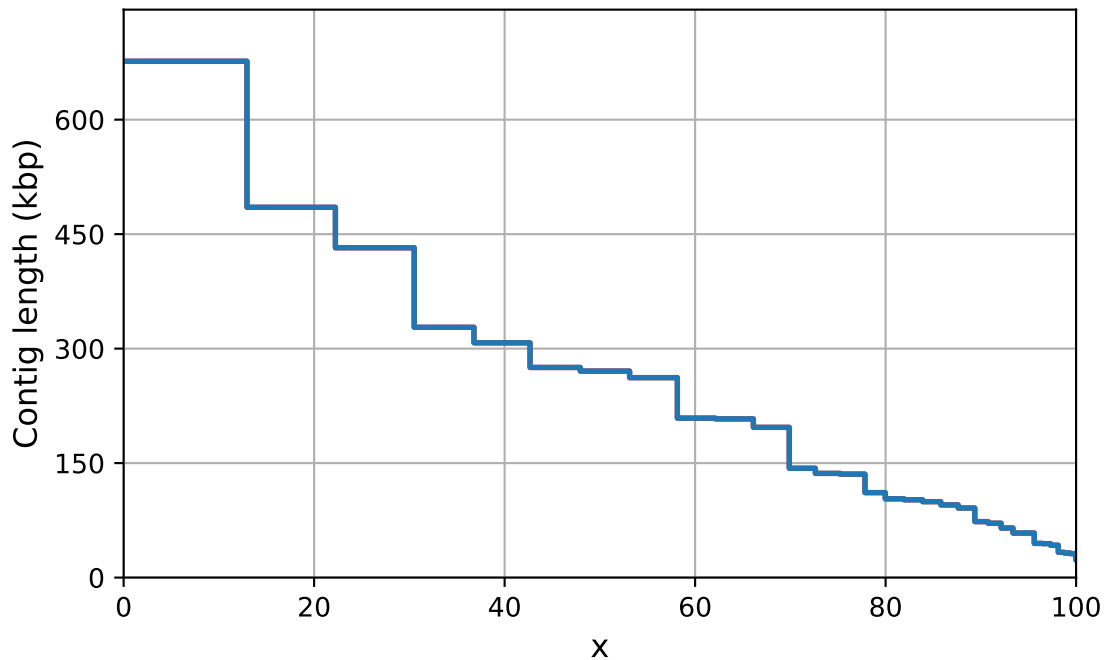
	spades_ctg	mulksg_ctg
# fully unaligned contigs	0	3
Fully unaligned length	0	1913
# partially unaligned contigs	5	5
Partially unaligned length	196944	196944
# N's	0	0

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).



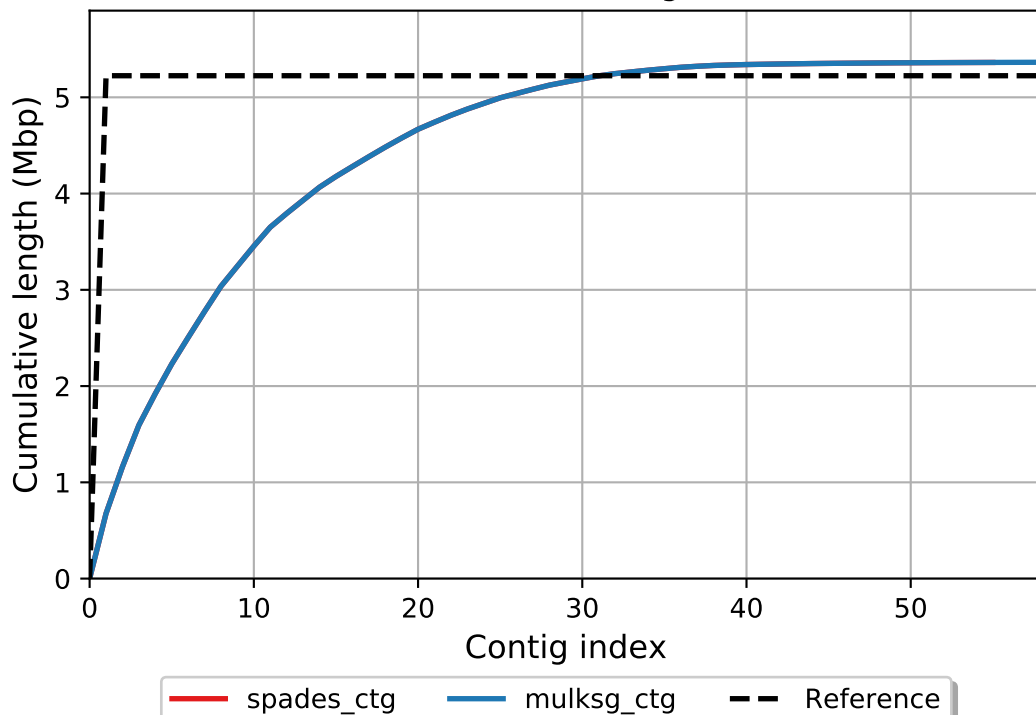
spades_ctg mulksg_ctg

NGx

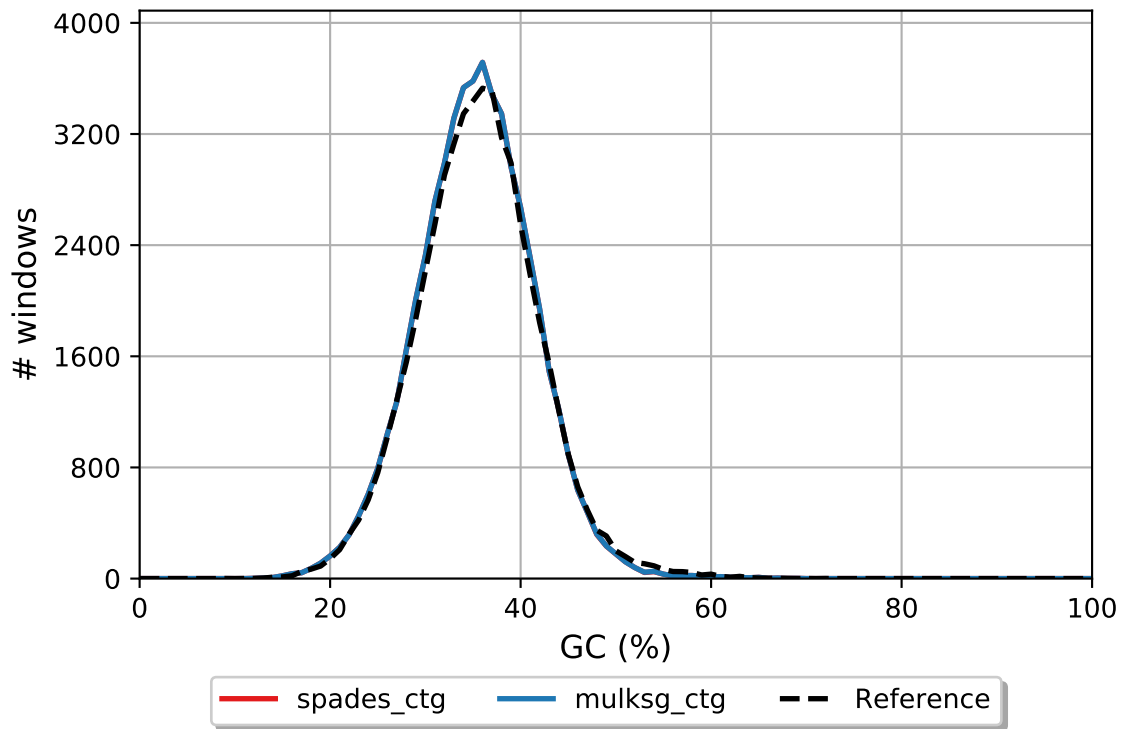


spades_ctg mulksg_ctg

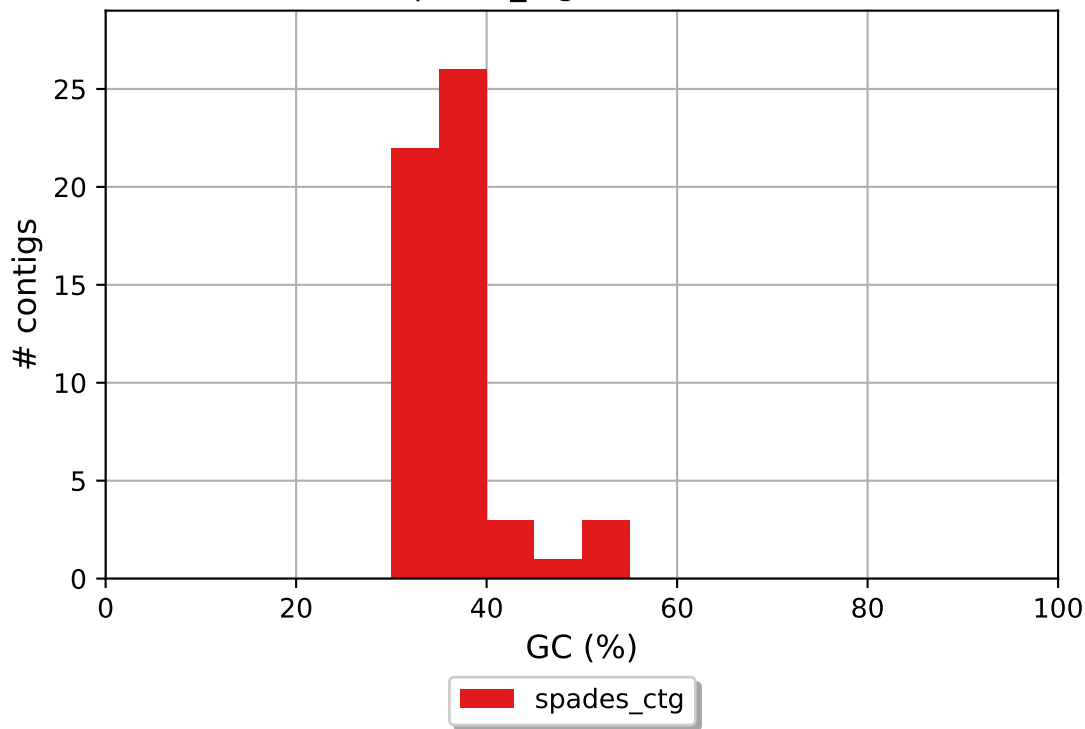
Cumulative length



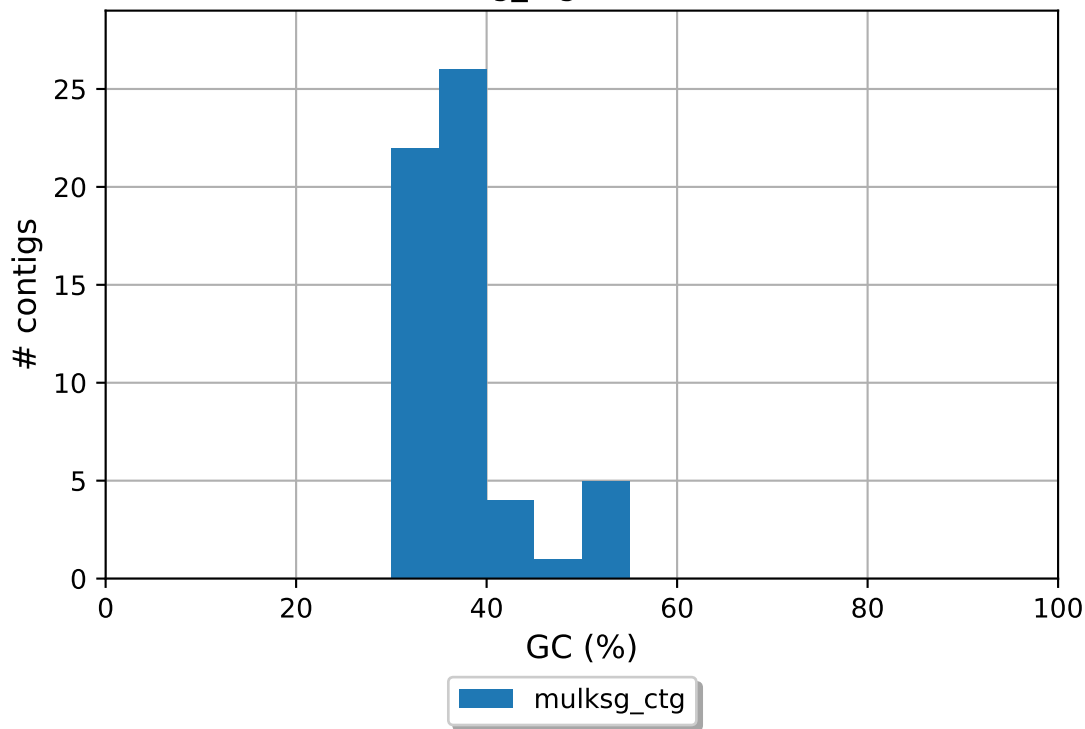
GC content



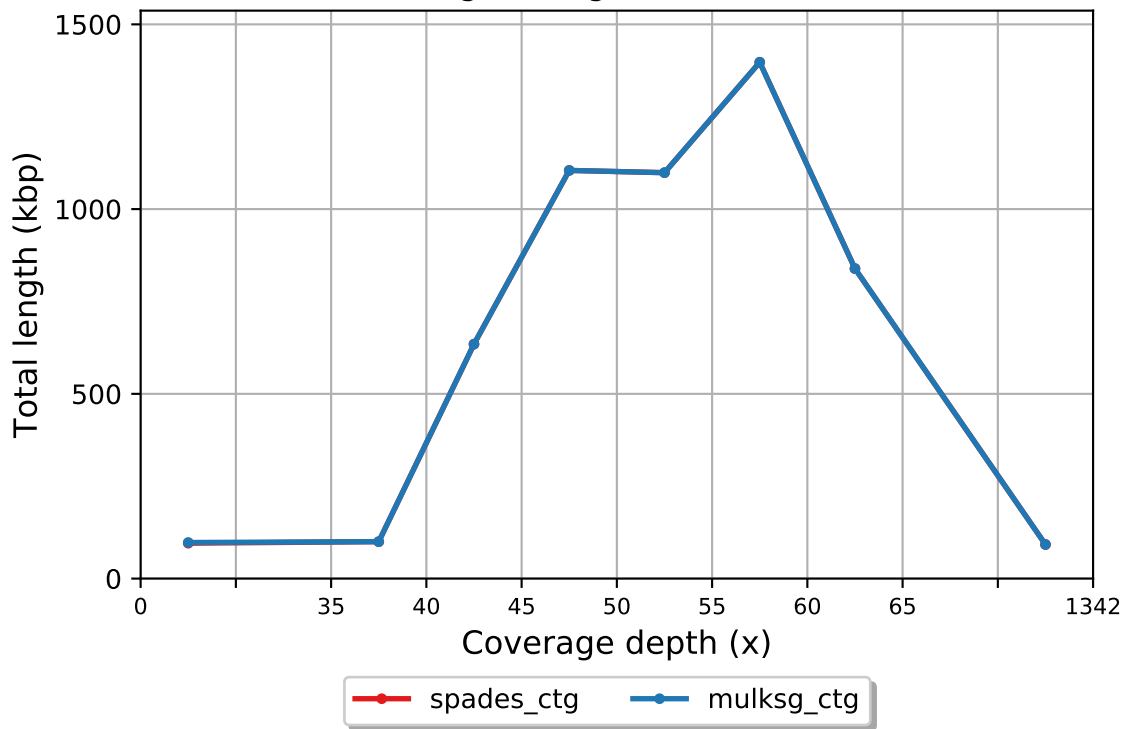
spades_ctg GC content



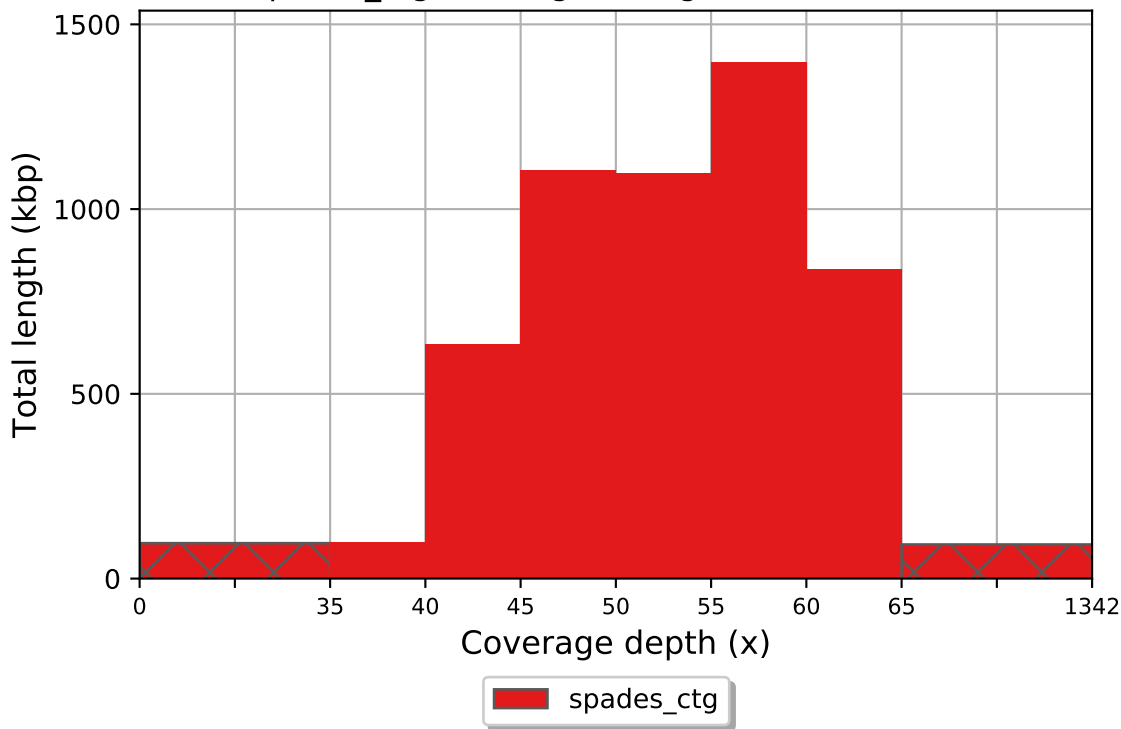
mulksg_ctg GC content



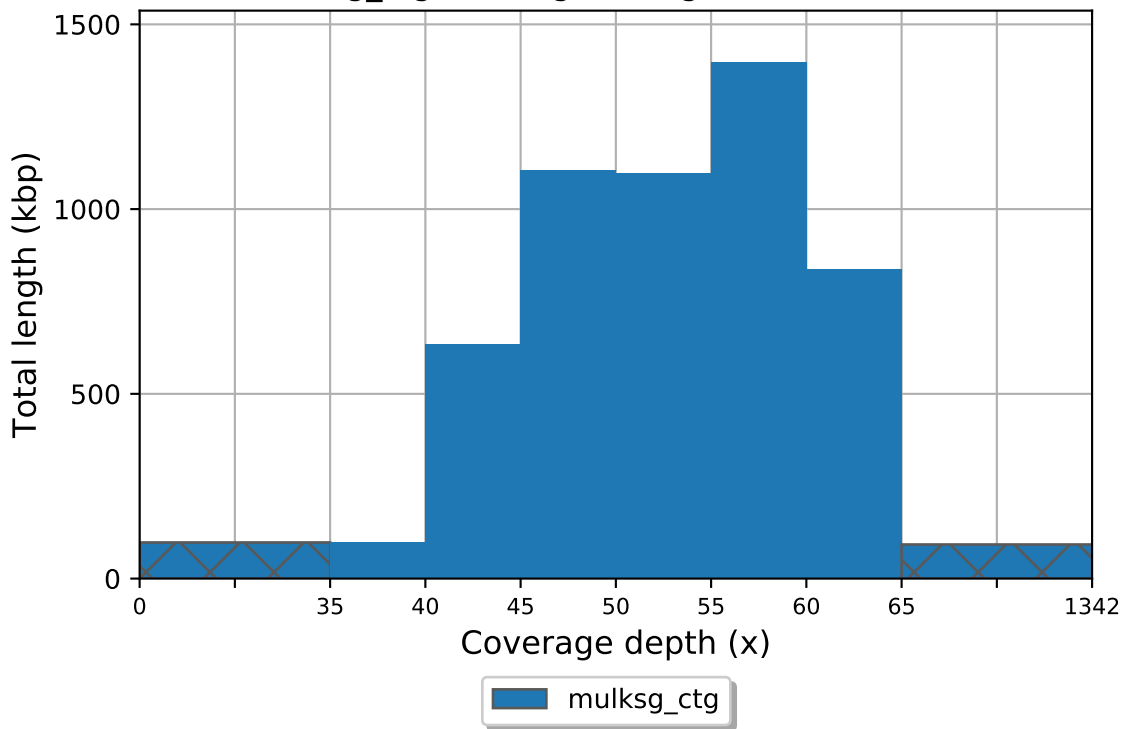
Coverage histogram (bin size: 5x)



spades_ctg coverage histogram (bin size: 5x)



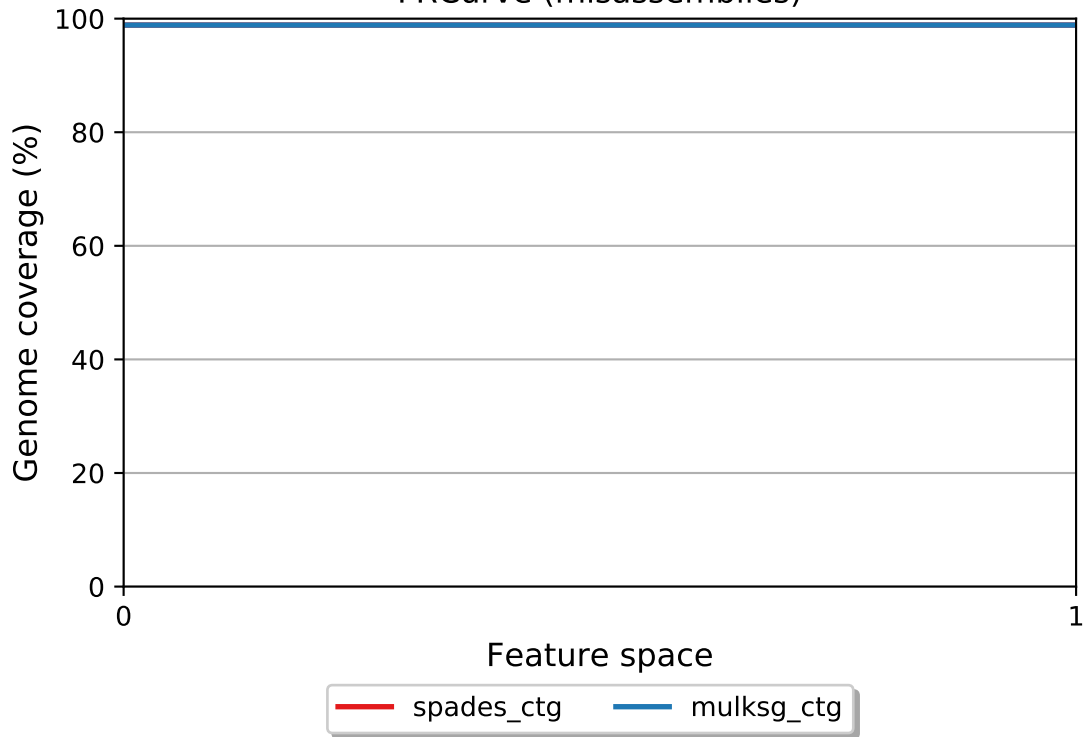
mulksg_ctg coverage histogram (bin size: 5x)



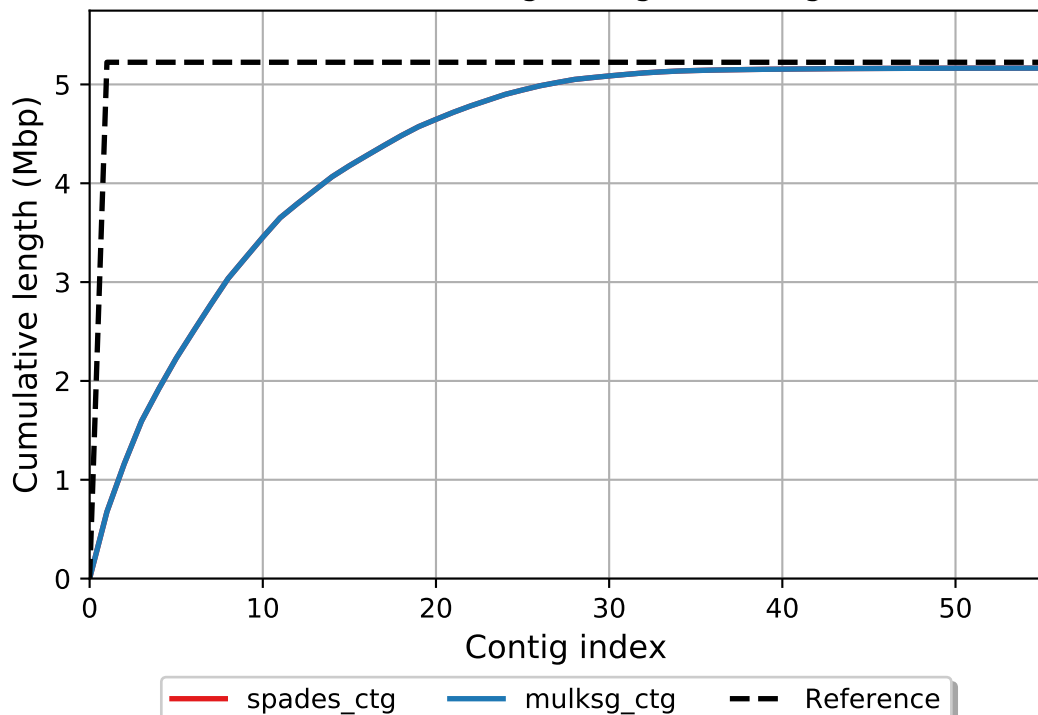
Misassemblies



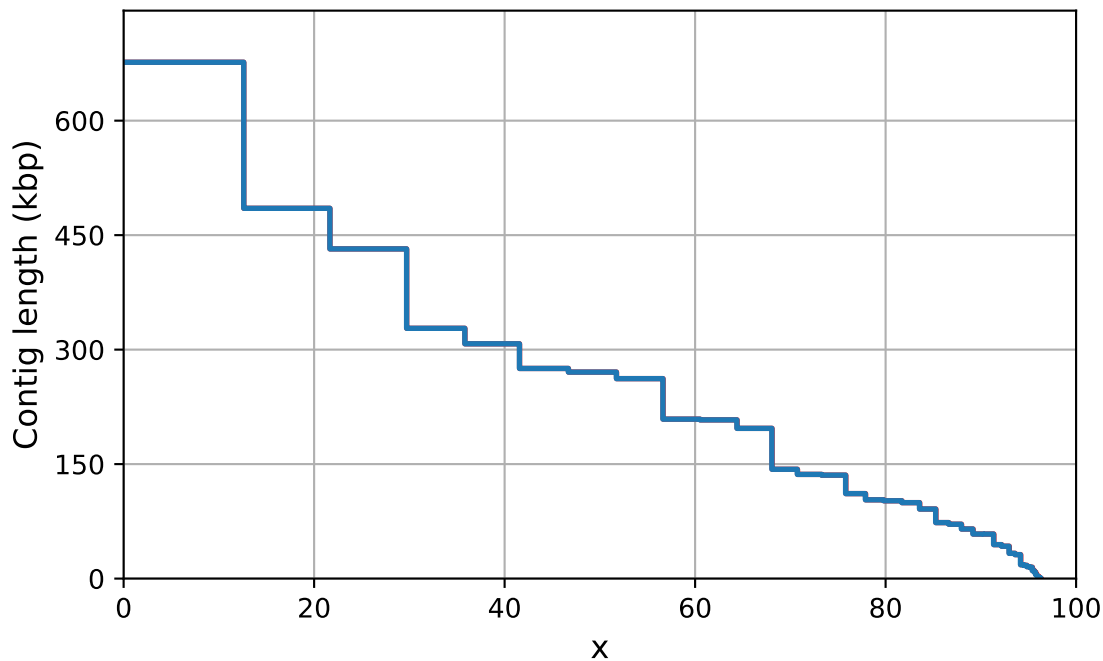
FRCurve (misassemblies)



Cumulative length (aligned contigs)

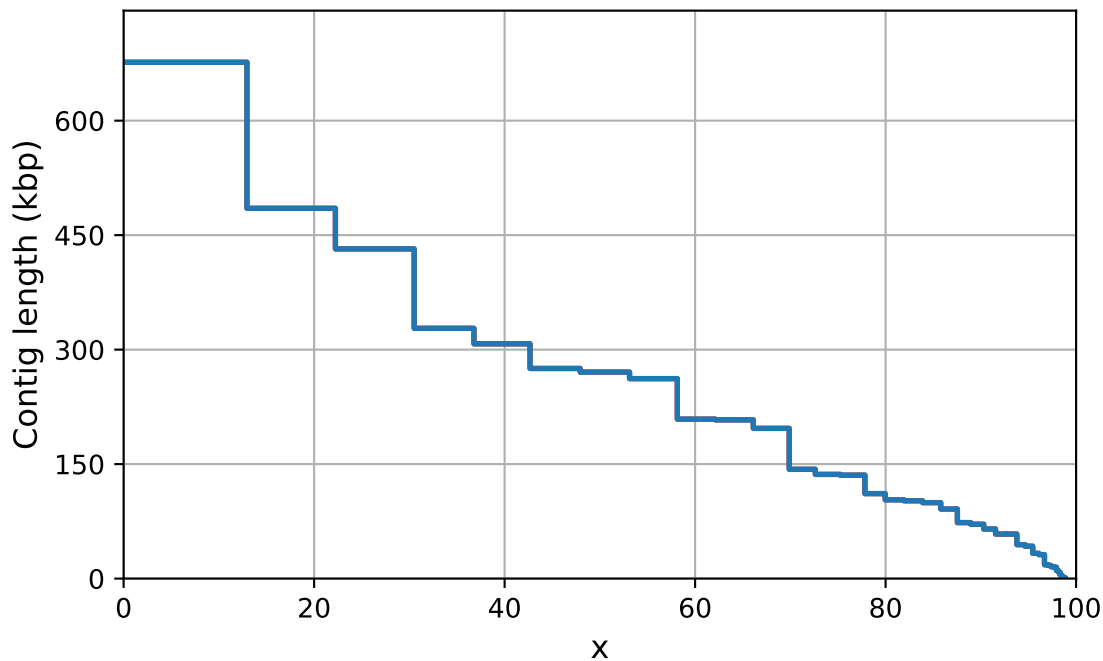


NAx



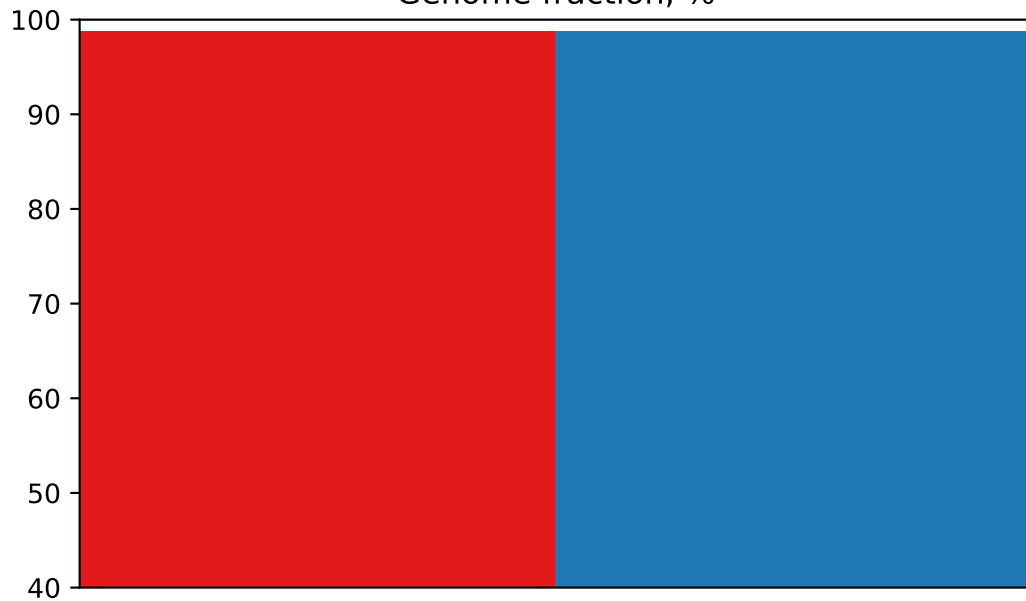
spades_ctg mulksg_ctg

NGAx



spades_ctg mulksg_ctg

Genome fraction, %



spades_ctg



mulksg_ctg