Report

	spades_ctg	mulksg_ctg
# contigs (>= 0 bp)	1751	1869
# contigs (>= 1000 bp)	133	131
# contigs (>= 5000 bp)	87	88
# contigs (>= 10000 bp)	73	72
# contigs (>= 25000 bp)	52	52
# contigs (>= 50000 bp)	31	31
Total length (>= 0 bp)	6172031	6201368
Total length (>= 1000 bp)	5659814	5645794
Total length (>= 5000 bp)	5559213	5550058
Total length (>= 10000 bp)	5455791	5434370
Total length (>= 25000 bp)	5095328	5097662
Total length (>= 50000 bp)	4327522	4328168
# contigs	219	232
Largest contig	605742	605742
Total length	5716869	5713200
Reference length	5224283	5224283
GC (%)	35.24	35.24
Reference GC (%)	35.58	35.58
N50	112026	112026
NG50	136462	136462
N75	51092	51166
NG75	68074	68074
L50	12	12
LG50	10	10
L75	31	31
LG75	25	25
# misassemblies	3	3
# misassembled contigs	3	3
Misassembled contigs length	4422	4403
# local misassemblies	3	3
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	42	42
# unaligned contigs	143 + 70 part	156 + 70 part
Unaligned length	5448768	5444625
Genome fraction (%)	5.060	5.059
Duplication ratio	1.014	1.016
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	3809.53	3814.40
# indels per 100 kbp	21.94	22.32
Largest alignment	30865	30865
Total aligned length	267683	268157
NGA50	-	-

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).
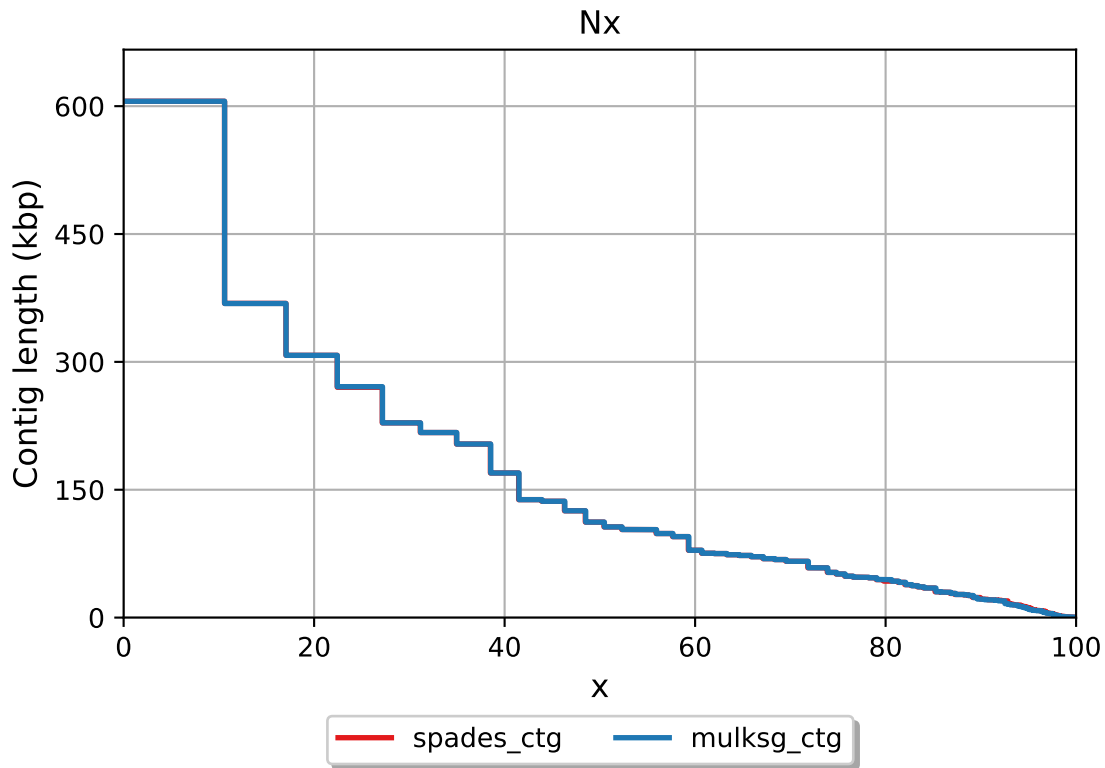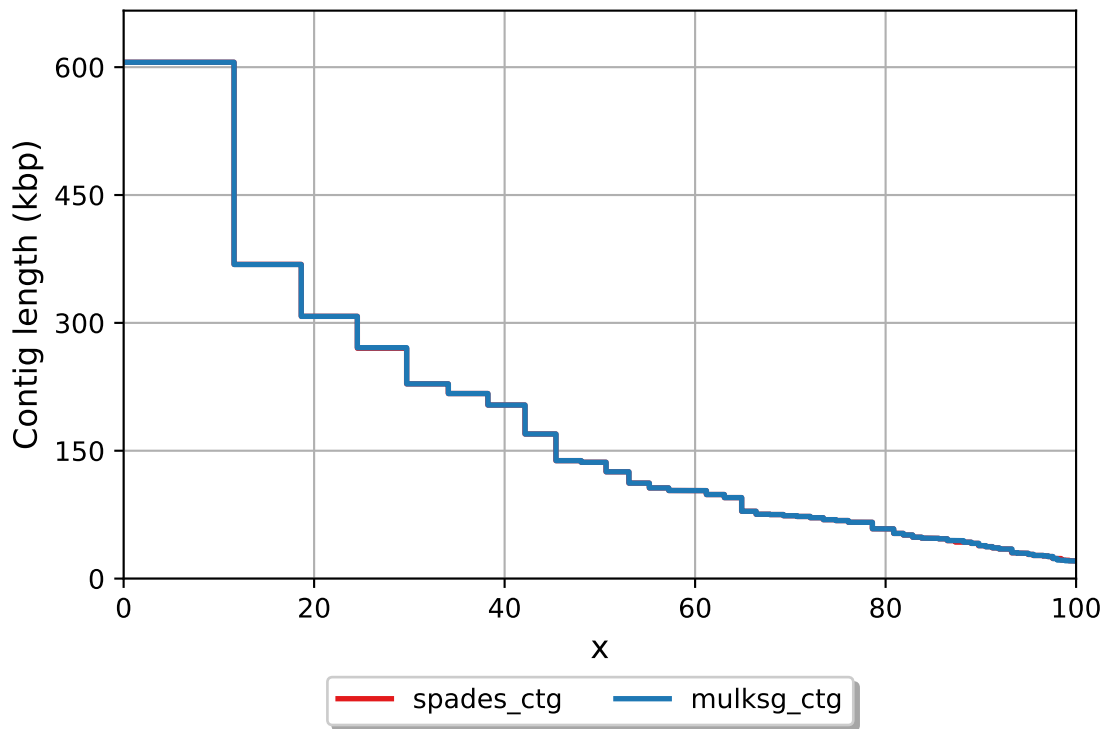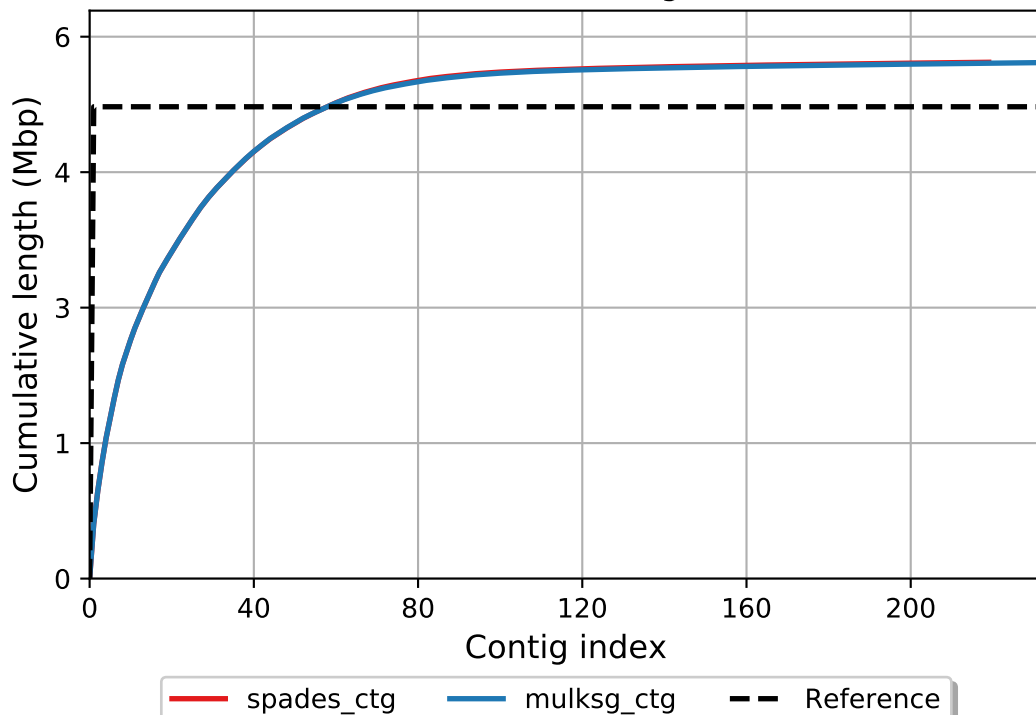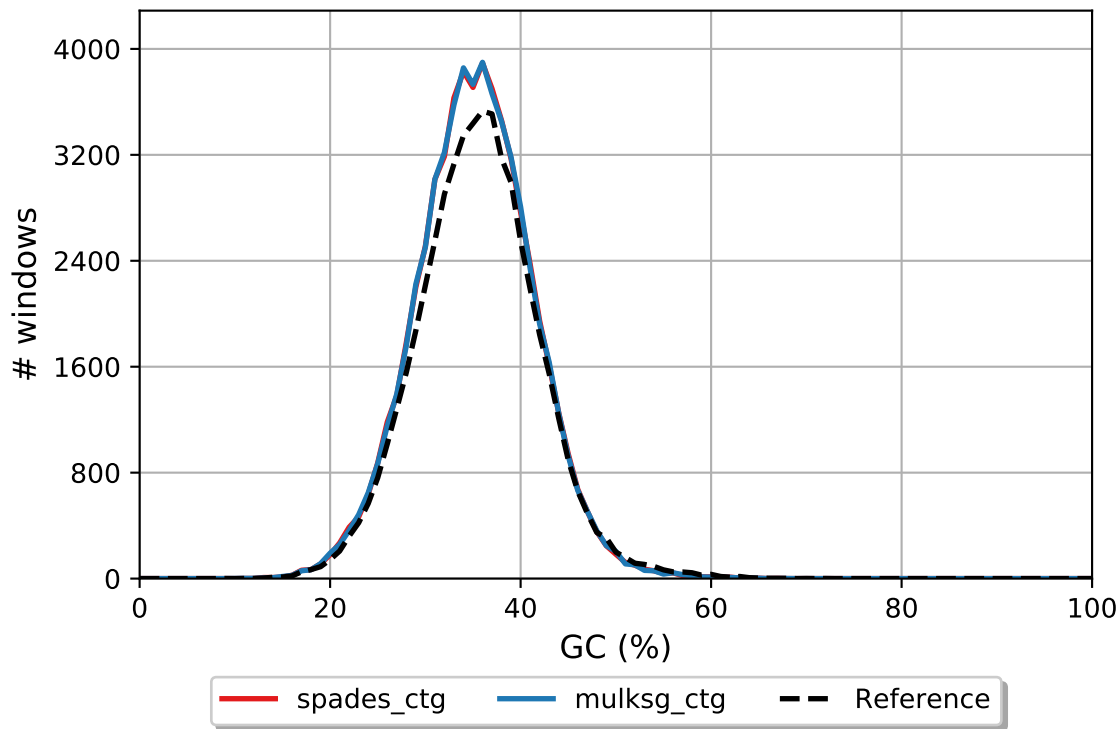
Misassemblies report

	spades_ctg	mulksg_ctg
# misassemblies	3	3
# contig misassemblies	3	3
# c. relocations	3	3
# 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	3	3
Misassembled contigs length	4422	4403
# local misassemblies	3	3
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	42	42
# mismatches	10070	10081
# indels	58	59
# indels (<= 5 bp)	56	57
# indels (> 5 bp)	2	2
Indels length	102	105

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	143	156
Fully unaligned length	655437	651484
# partially unaligned contigs	70	70
Partially unaligned length	4793331	4793141
# 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).
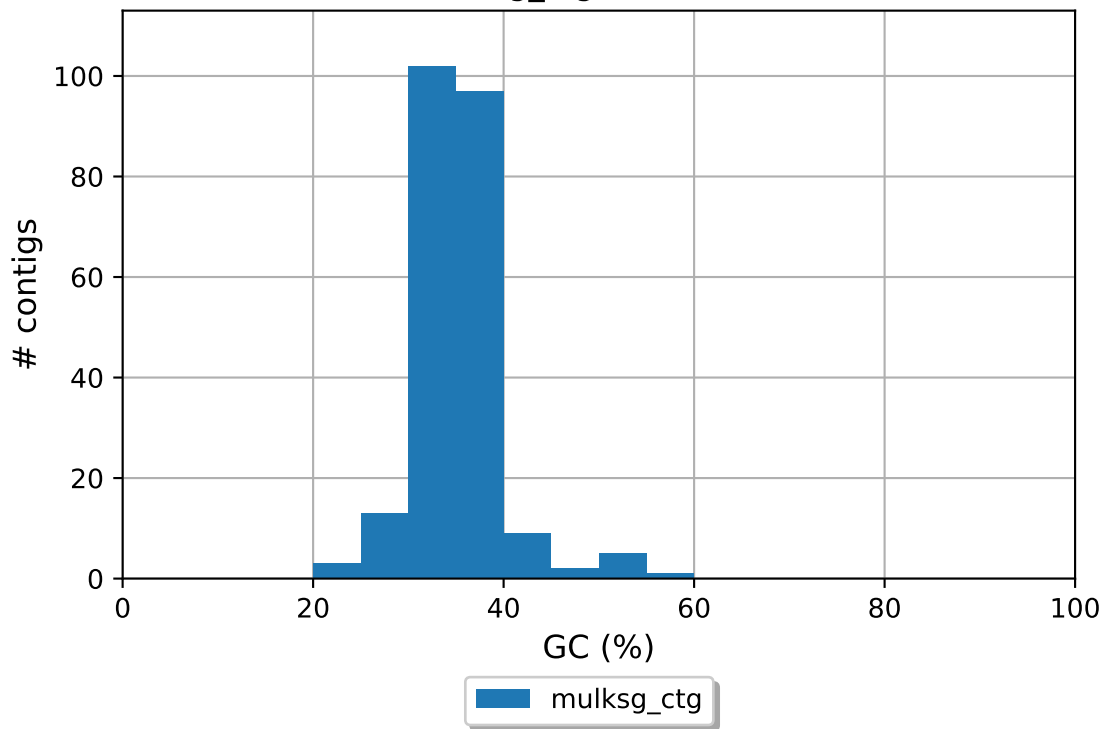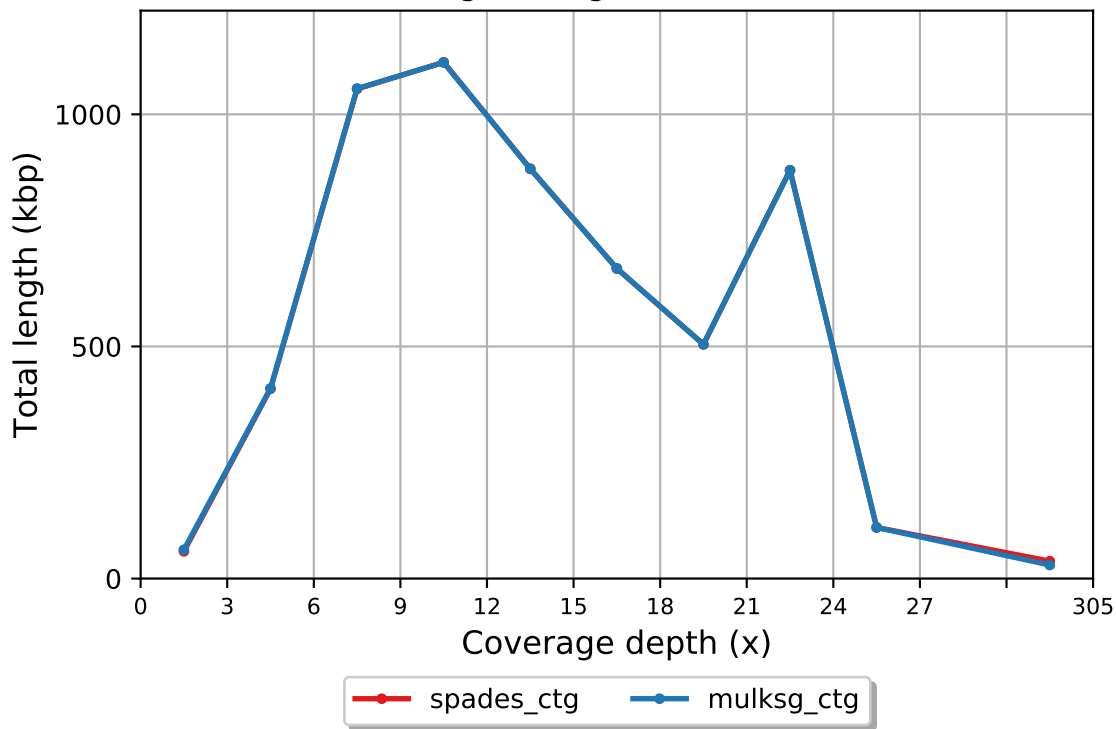
Nx

NGx

Cumulative length

GC content

spades_ctg GC content
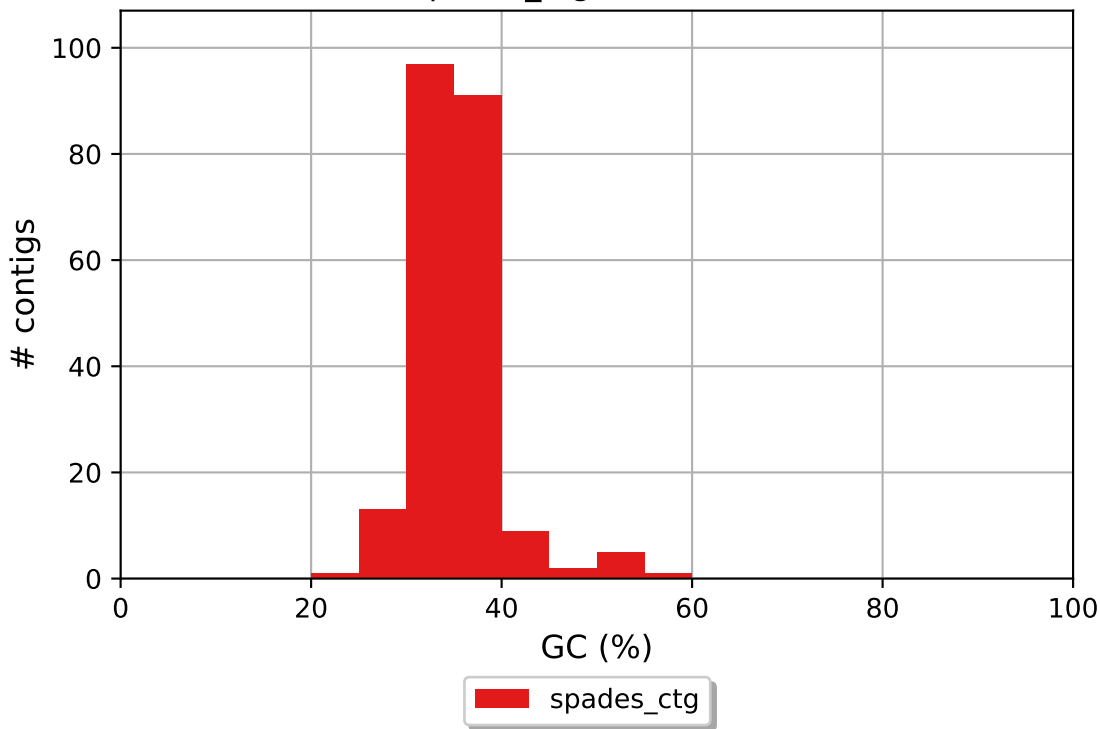
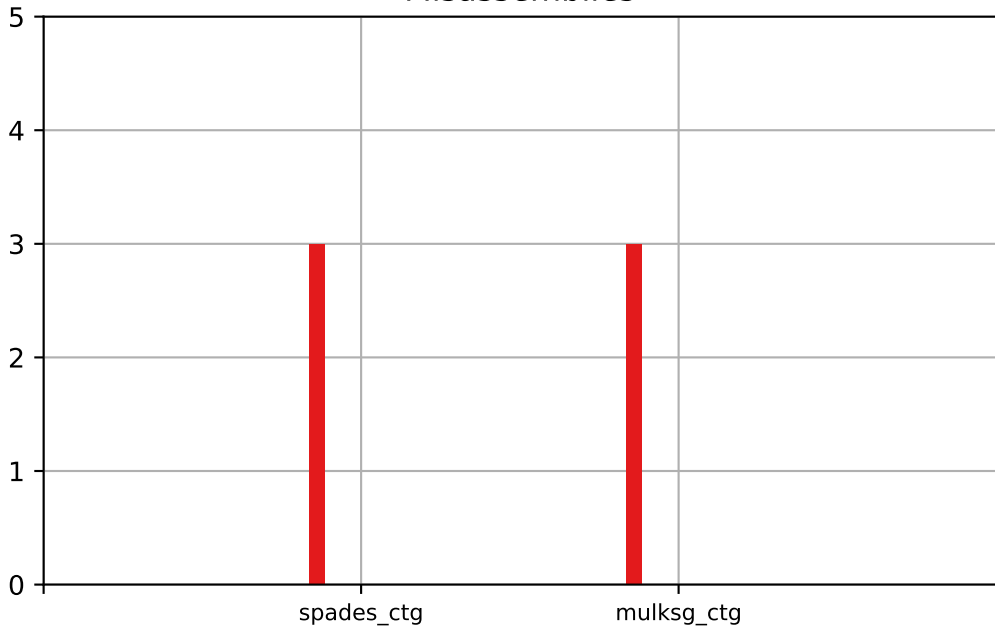mulksg_ctg GC content

Coverage histogram (bin size: 3x)

spades_ctg coverage histogram (bin size: 3x)
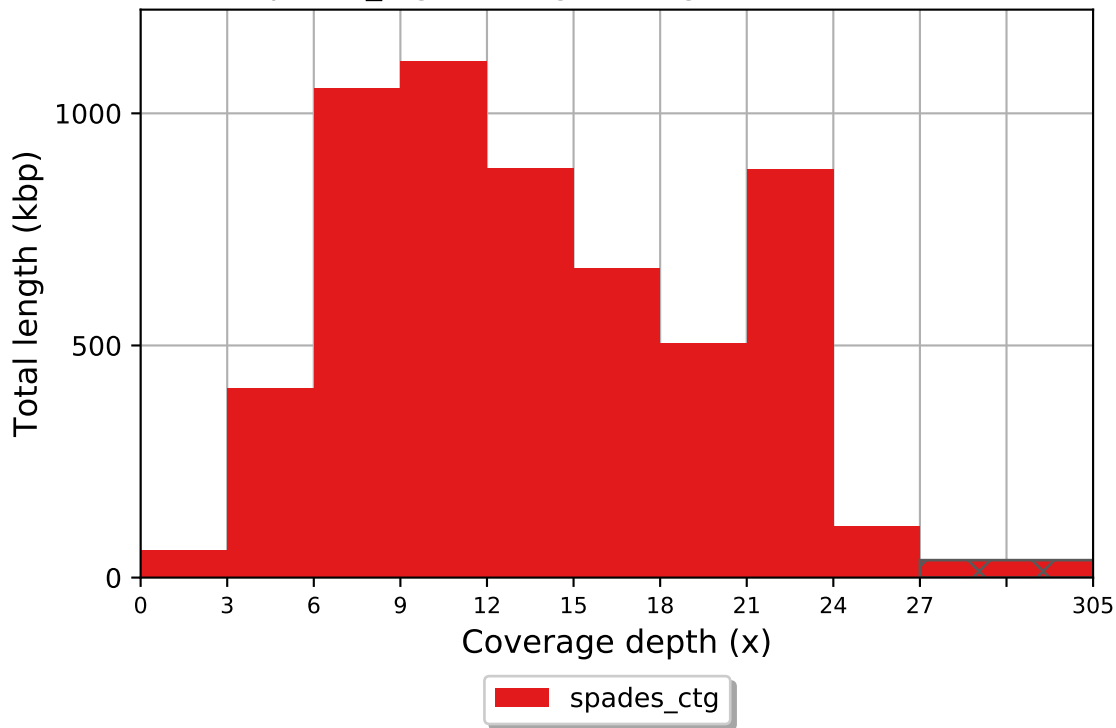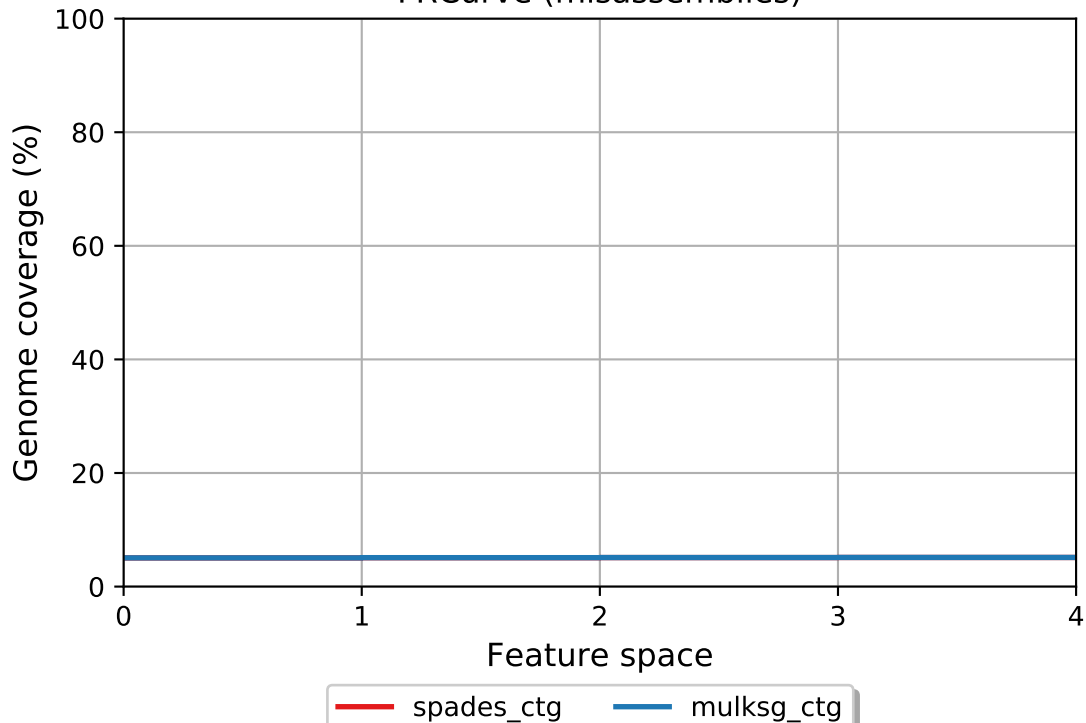
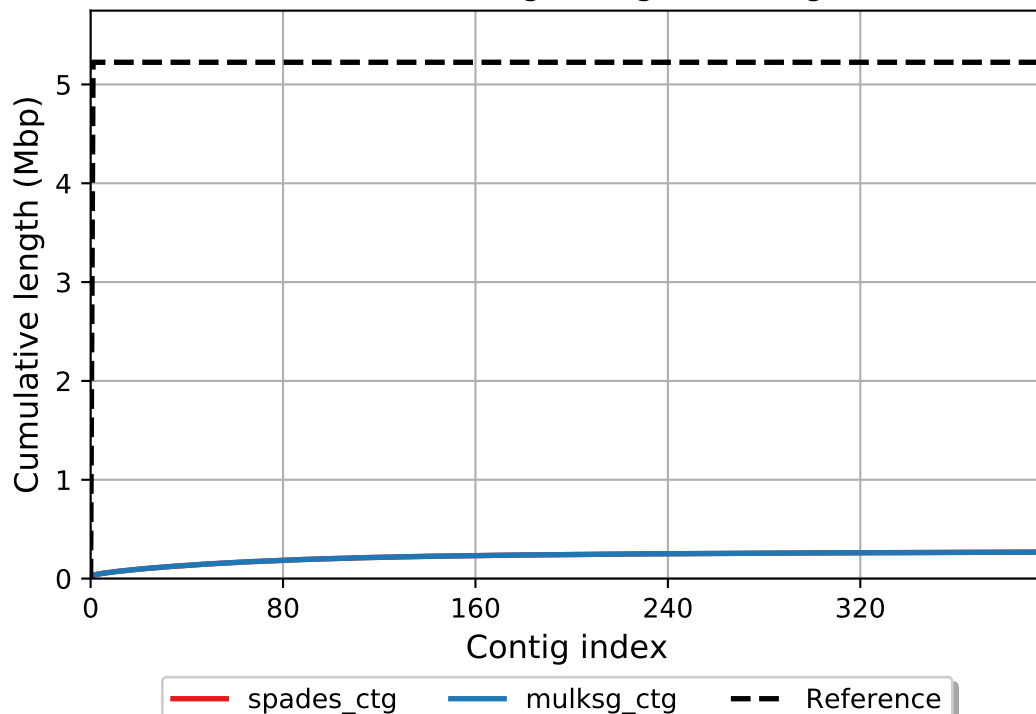mulksg_ctg coverage histogram (bin size: 3x)
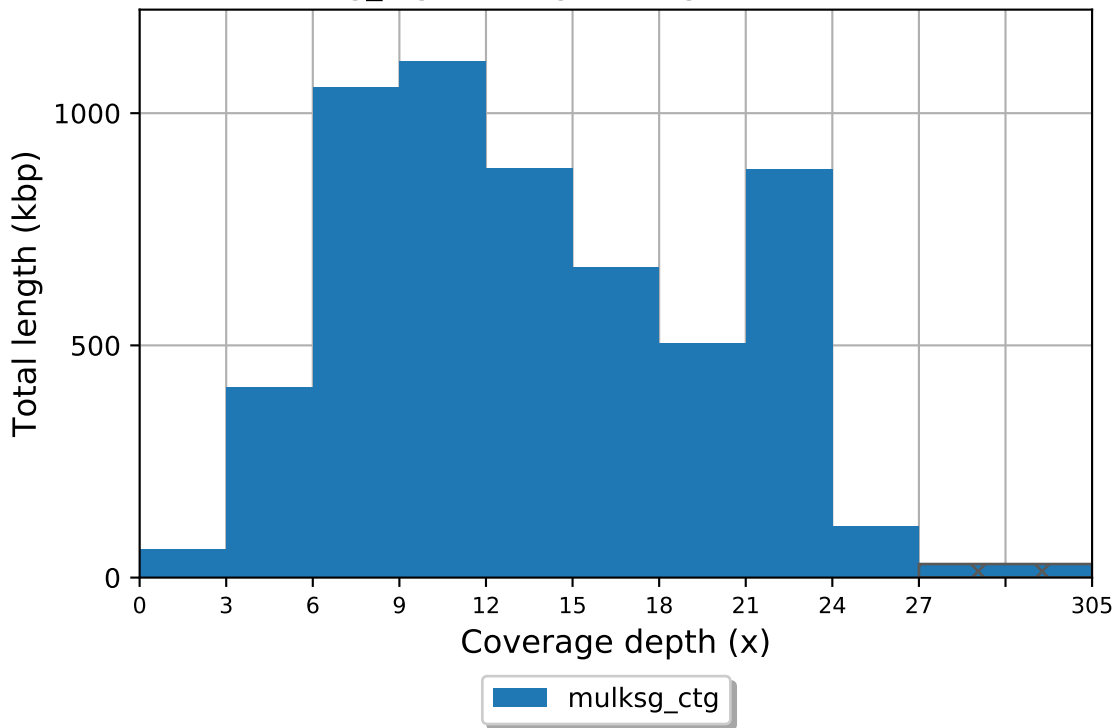
Misassemblies

FRCurve (misassemblies)
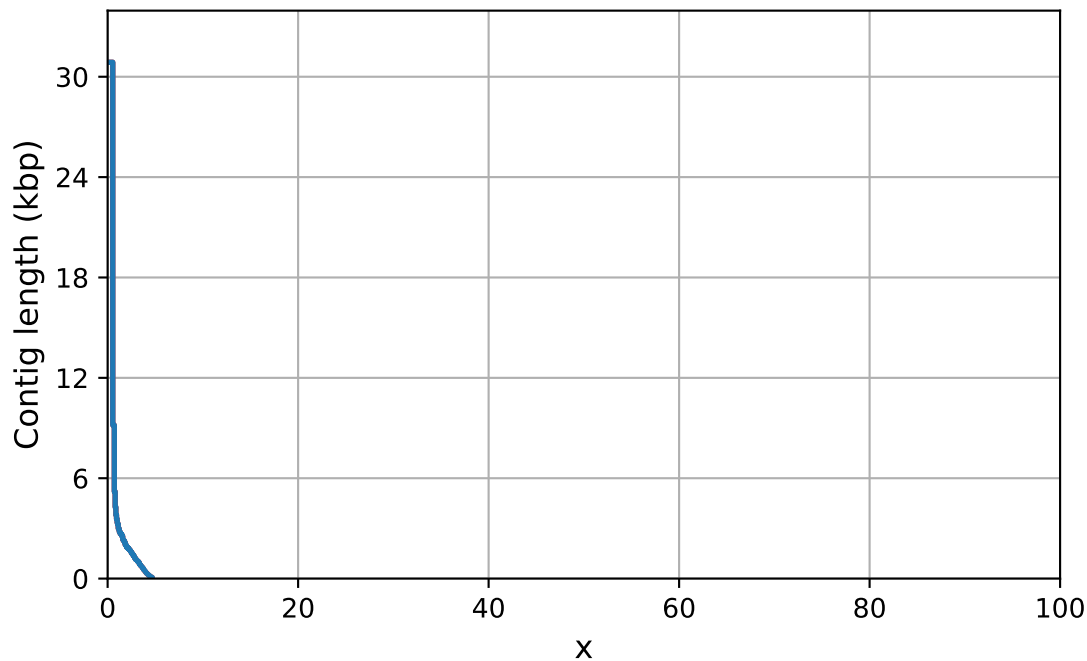
Cumulative length (aligned contigs)

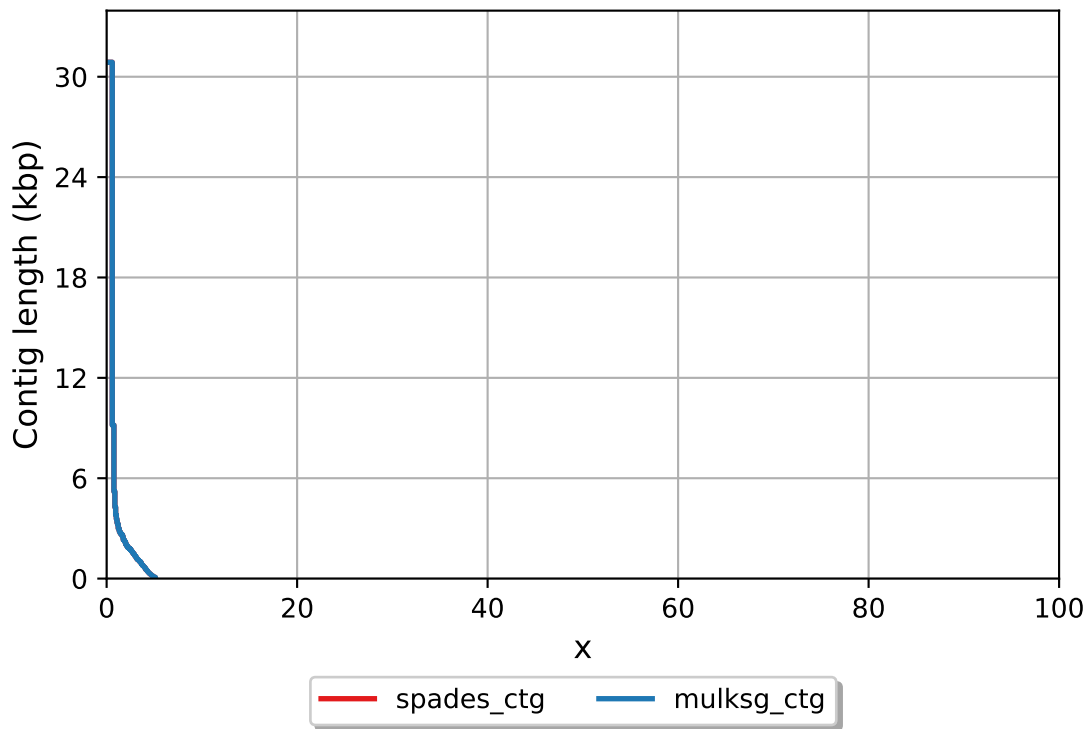NAx

Contig length (kbp) vs x

spades_ctg   mulksg_ctg

NGAx

Genome fraction, %

spades_ctg   mulksg_ctg