Report

	contigs
# contigs (>= 0 bp)	729
# contigs (>= 1000 bp)	609
# contigs (>= 5000 bp)	317
# contigs (>= 10000 bp)	156
# contigs (>= 25000 bp)	15
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4532714
Total length (>= 1000 bp)	4483857
Total length (>= 5000 bp)	3697021
Total length (>= 10000 bp)	2535307
Total length (>= 25000 bp)	420372
Total length (>= 50000 bp)	0
# contigs	648
Largest contig	41412
Total length	4512204
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	11536
NG50	10950
N75	6478
NG75	5921
L50	130
LG50	136
L75	262
LG75	278
# misassemblies	14
# misassembled contigs	14
Misassembled contigs length	215181
# local misassemblies	18
# unaligned contigs	0 + 2 part
Unaligned length	129
Genome fraction (%)	96.984
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	225.45
# indels per 100 kbp	1.87
Largest alignment	32784
NA50	10950
NGA50	10638
NA75	6295
NGA75	5723
LA50	133
LGA50	139
LA75	269
LGA75	285

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

	contigs
# misassemblies	14
# relocations	14
# translocations	0
# inversions	0
# misassembled contigs	14
Misassembled contigs length	215181
# local misassemblies	18
# mismatches	10149
# indels	84
# short indels	78
# long indels	6
Indels length	203

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).
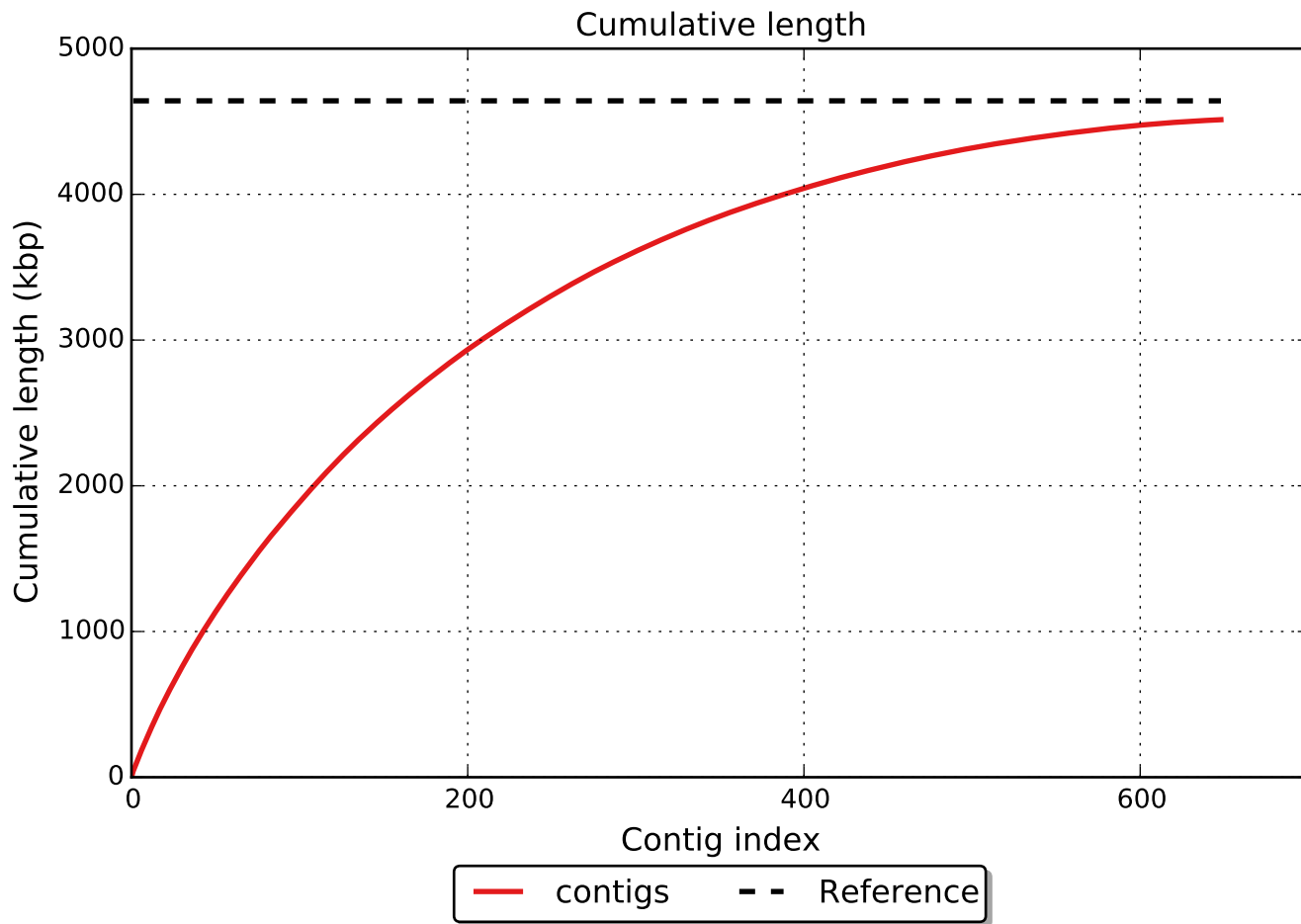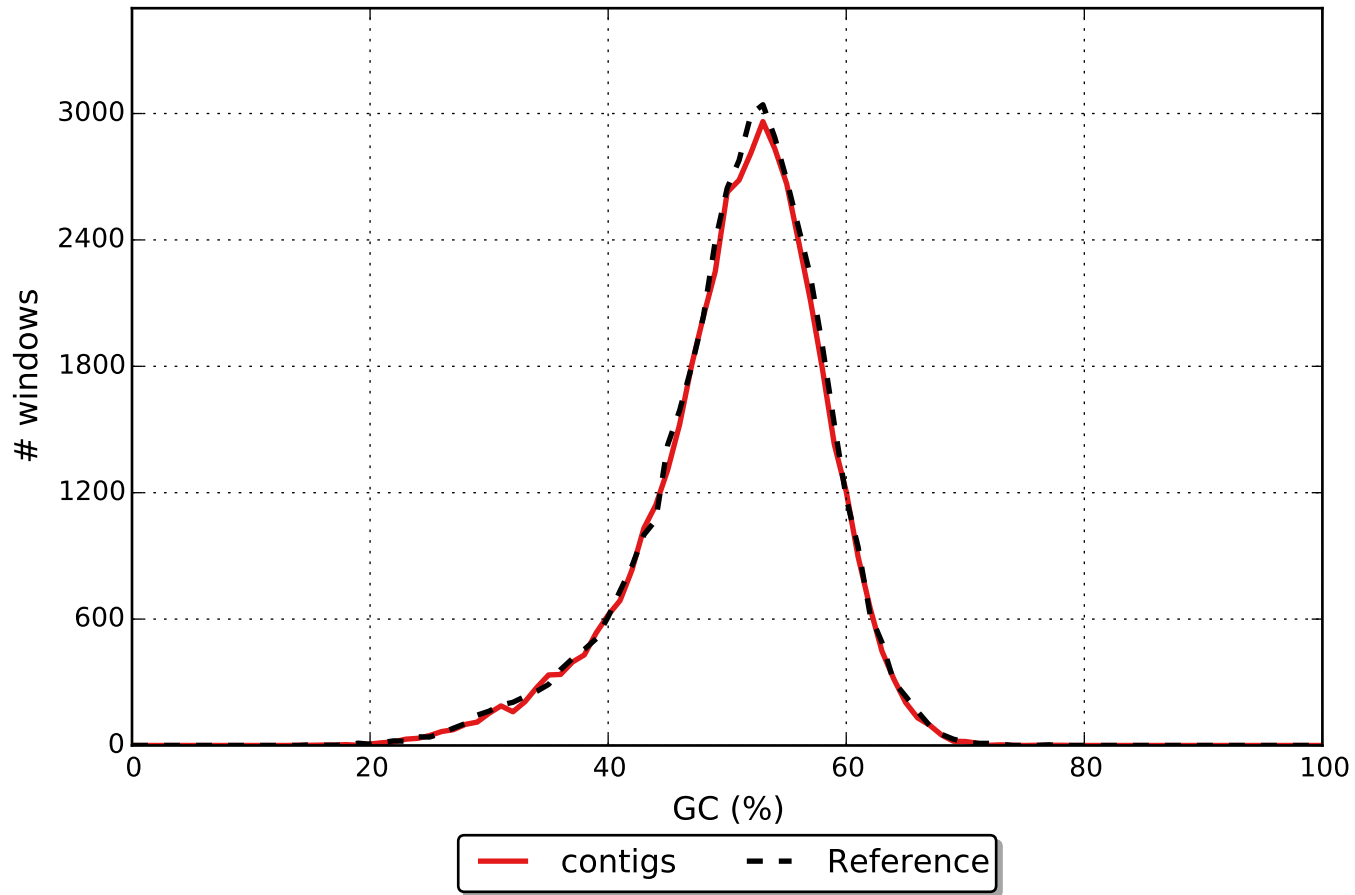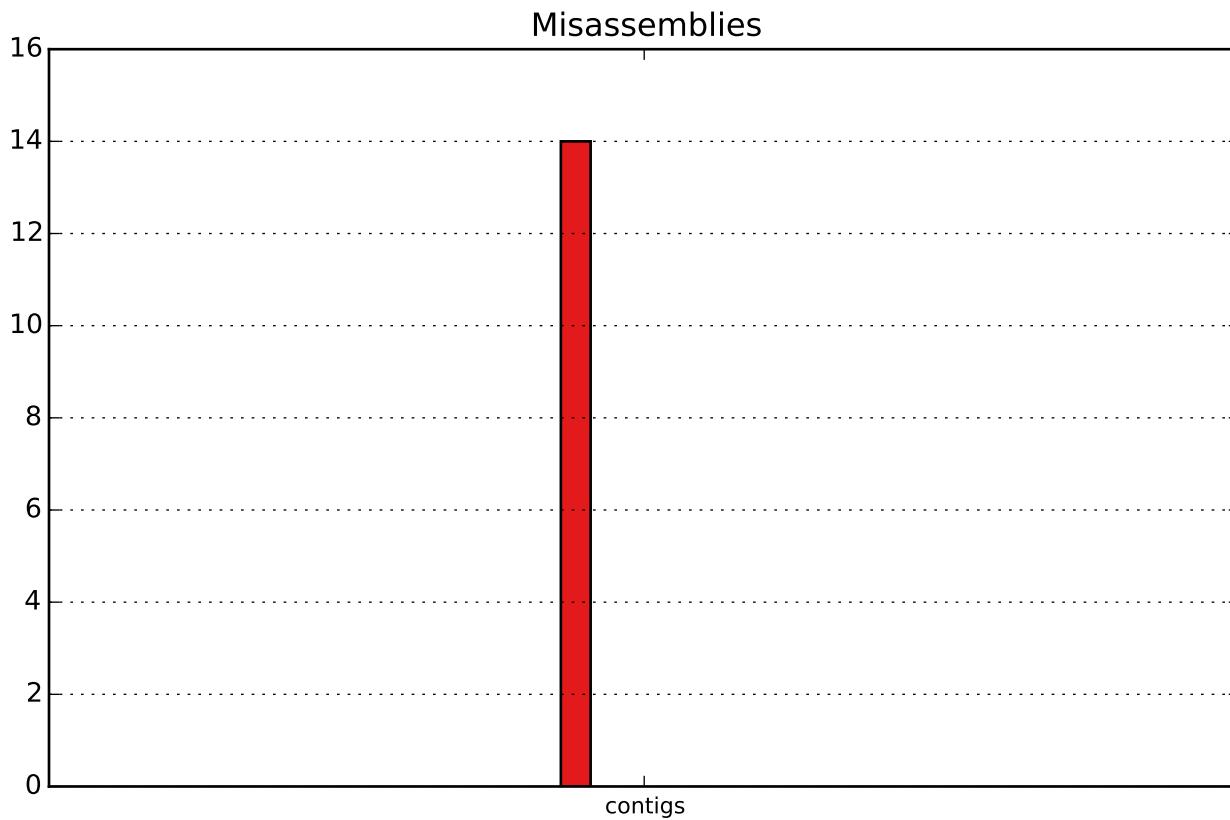
Unaligned report

	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	129
# N's	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).
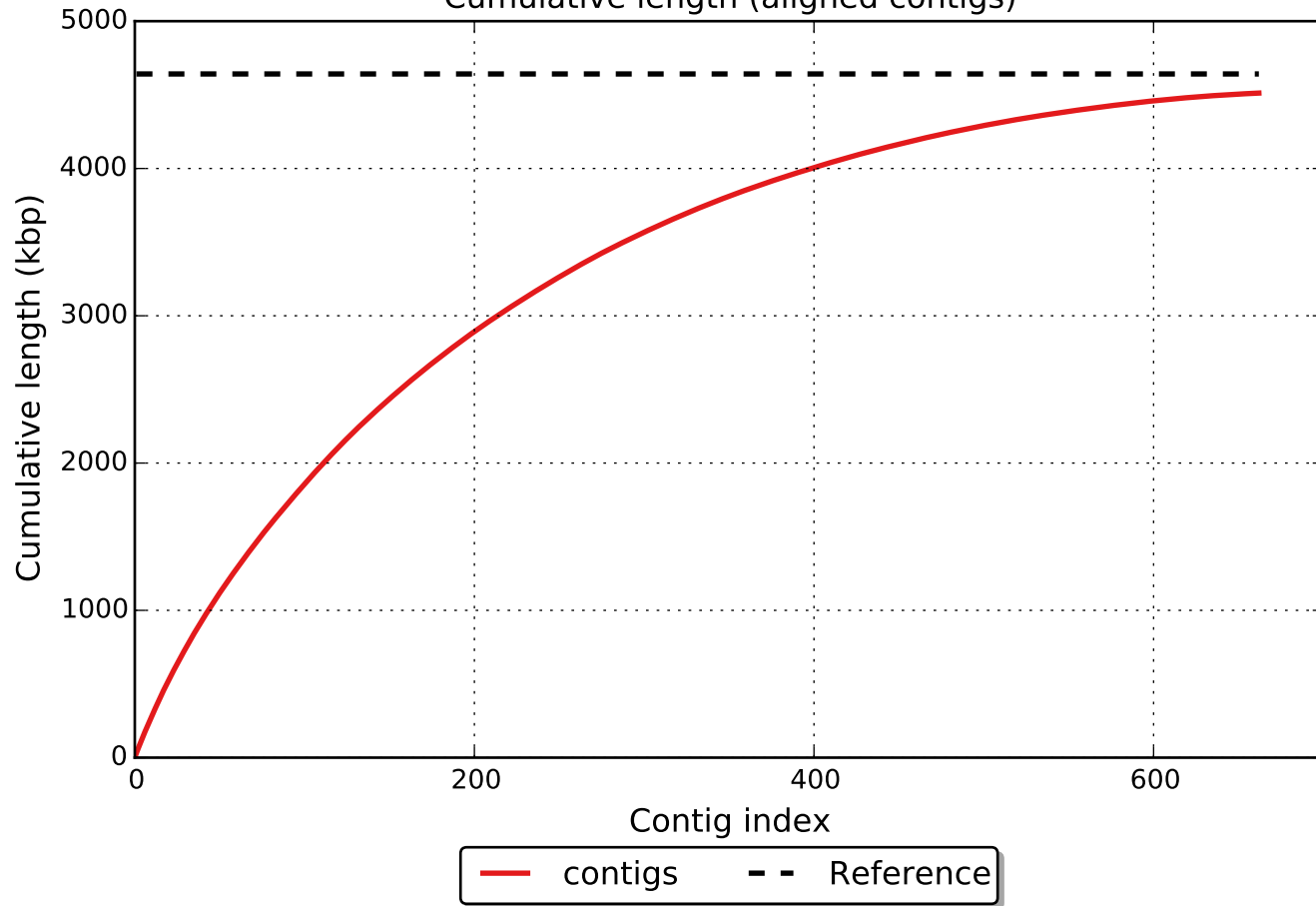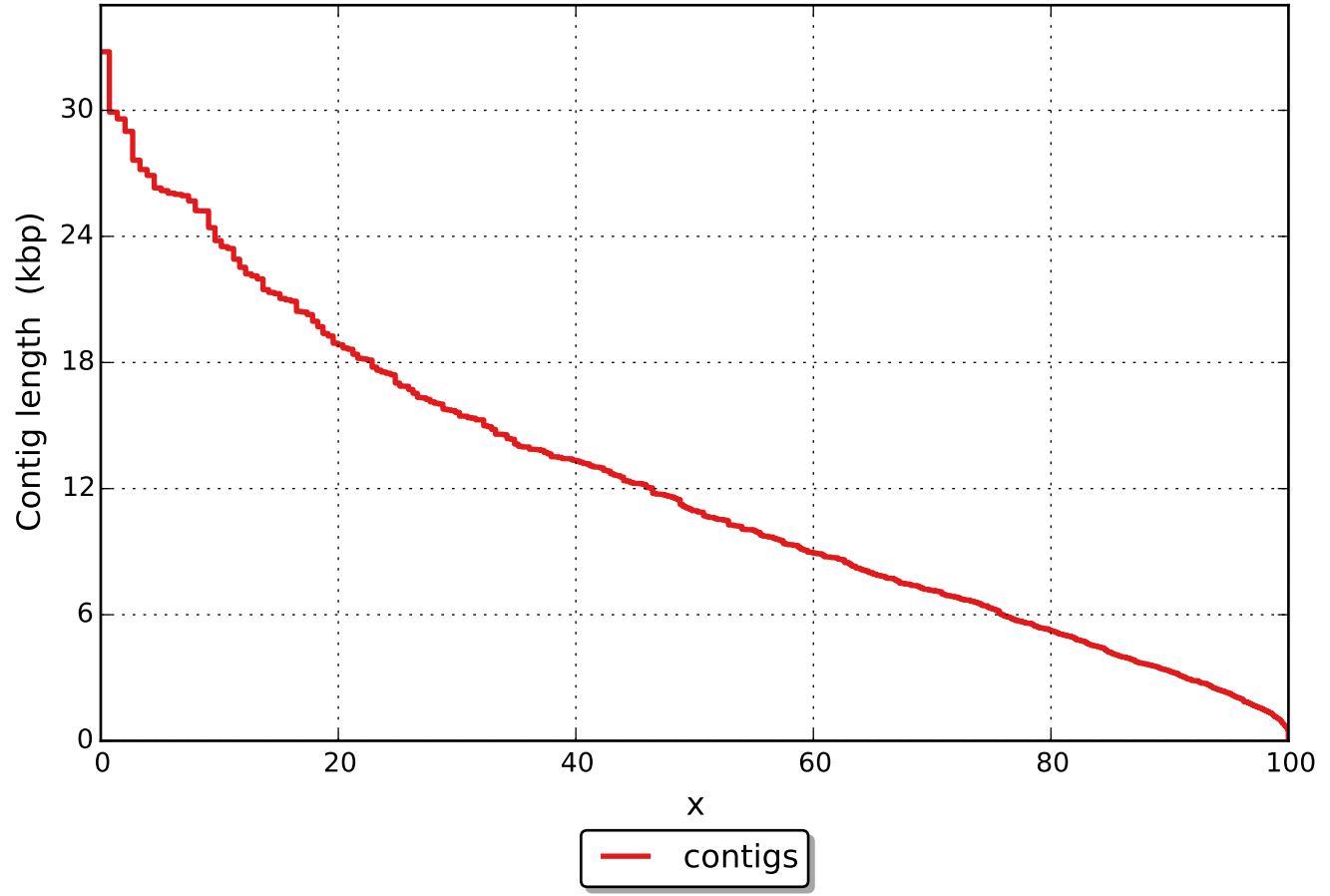
Cumulative length

Misassemblies
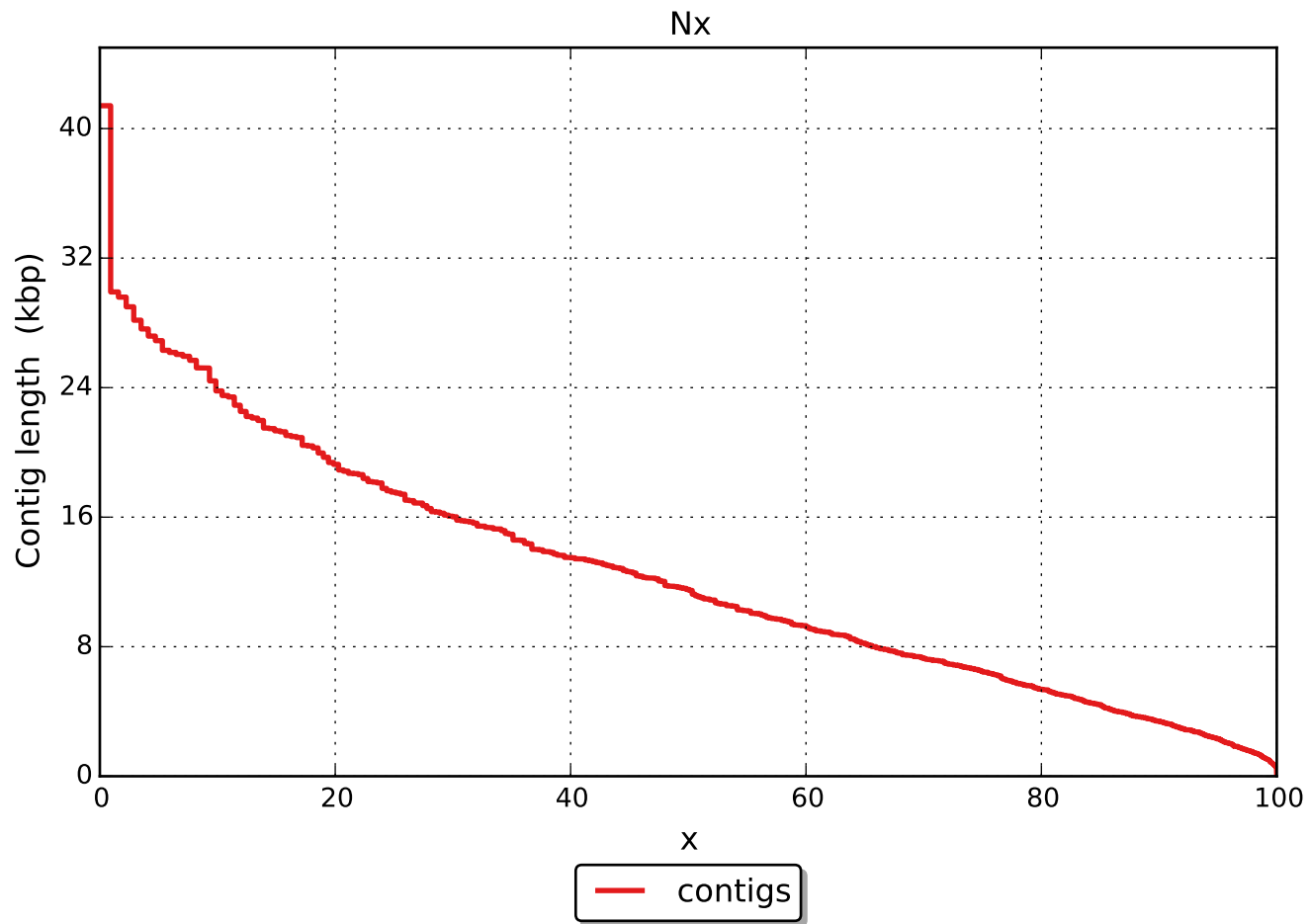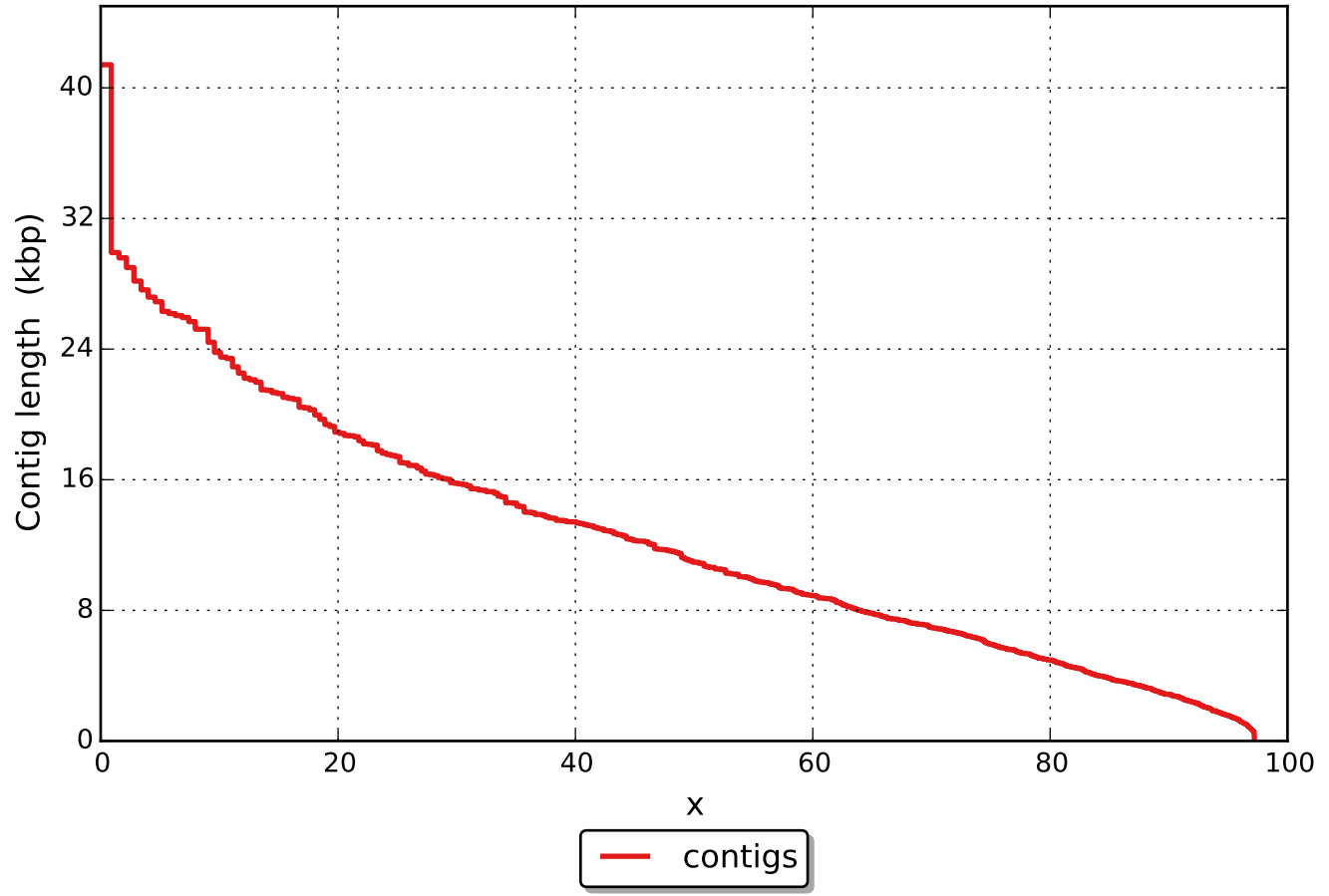
Cumulative length (aligned contigs)