Report

	contigs
# contigs (>= 0 bp)	4625
# contigs (>= 1000 bp)	1842
# contigs (>= 5000 bp)	27
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4956070
Total length (>= 1000 bp)	3547158
Total length (>= 5000 bp)	170490
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3132
Largest contig	9419
Total length	4485562
Reference length	4641652
GC (%)	50.77
Reference GC (%)	50.79
N50	1699
NG50	1649
N75	1090
NG75	1034
L50	845
LG50	891
L75	1667
LG75	1778
# misassemblies	11
# misassembled contigs	11
Misassembled contigs length	24569
# local misassemblies	5
# unaligned contigs	0 + 1 part
Unaligned length	10
Genome fraction (%)	92.278
Duplication ratio	1.047
# N's per 100 kbp	0.00
# mismatches per 100 kbp	383.31
# indels per 100 kbp	0.82
Largest alignment	9419
NA50	1693
NGA50	1641
NA75	1086
NGA75	1030
LA50	848
LGA50	894
LA75	1673
LGA75	1784

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).
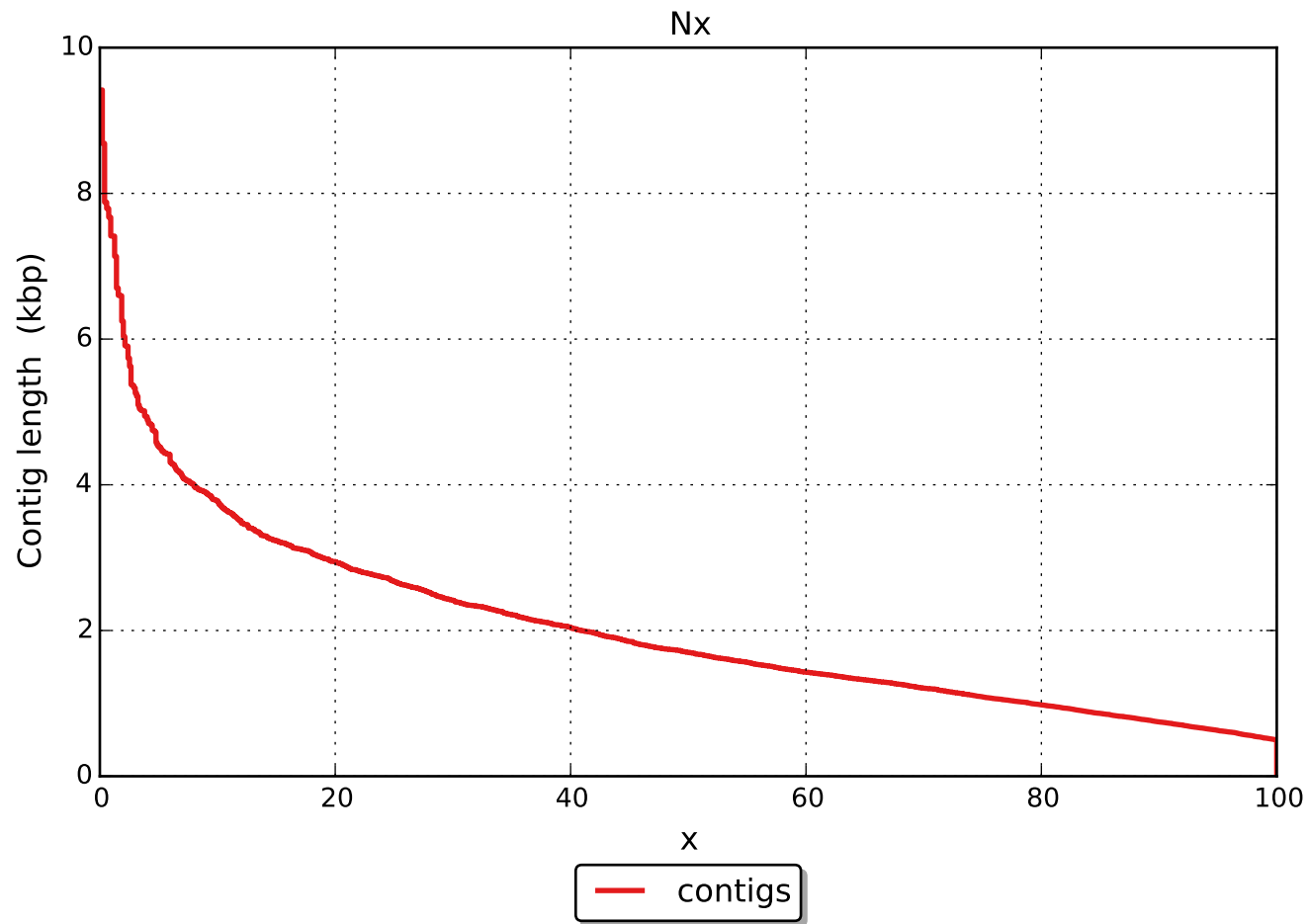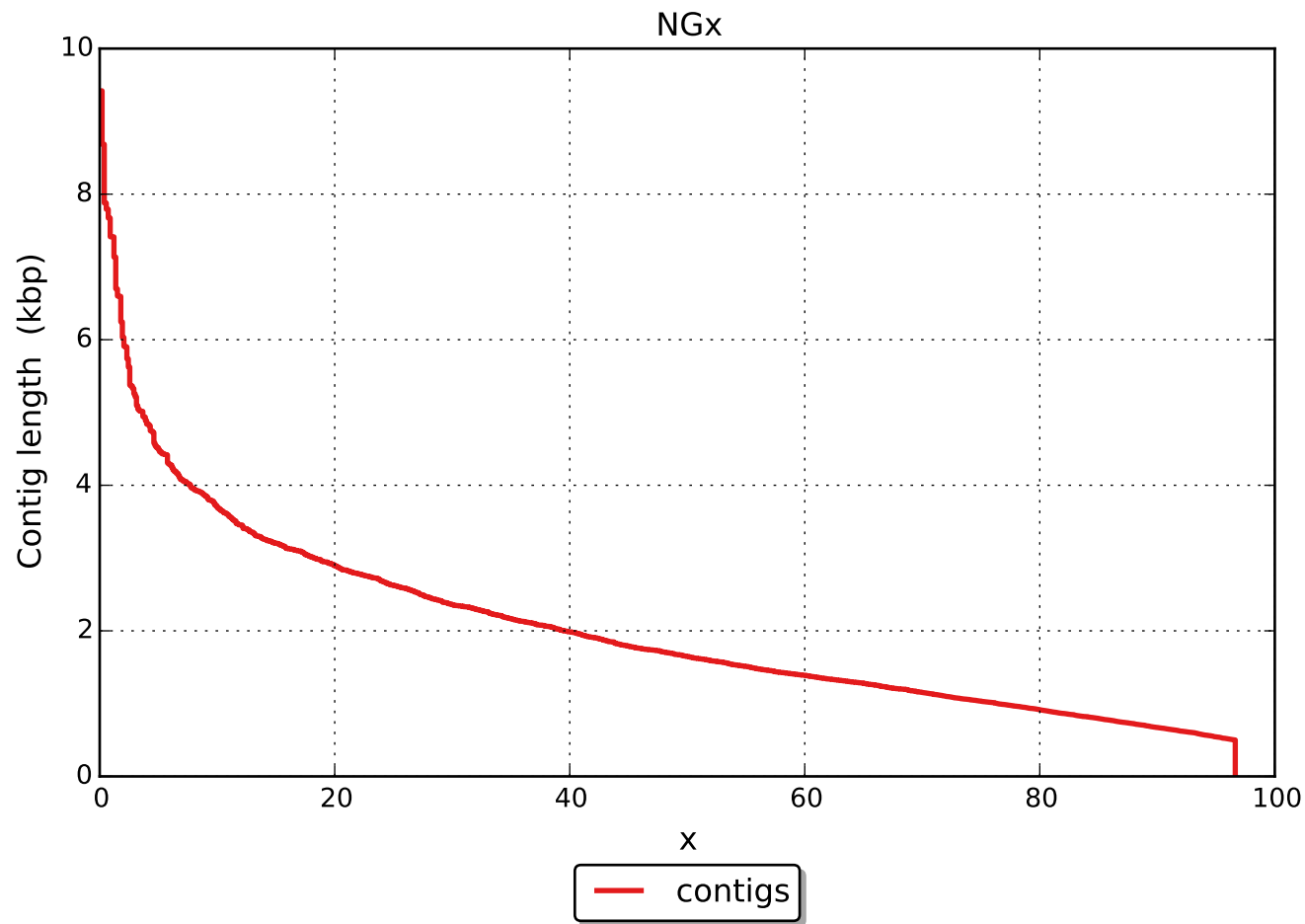
Misassemblies report

	contigs
# misassemblies	11
# relocations	11
# translocations	0
# inversions	0
# misassembled contigs	11
Misassembled contigs length	24569
# local misassemblies	5
# mismatches	16418
# indels	35
# short indels	32
# long indels	3
Indels length	198

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
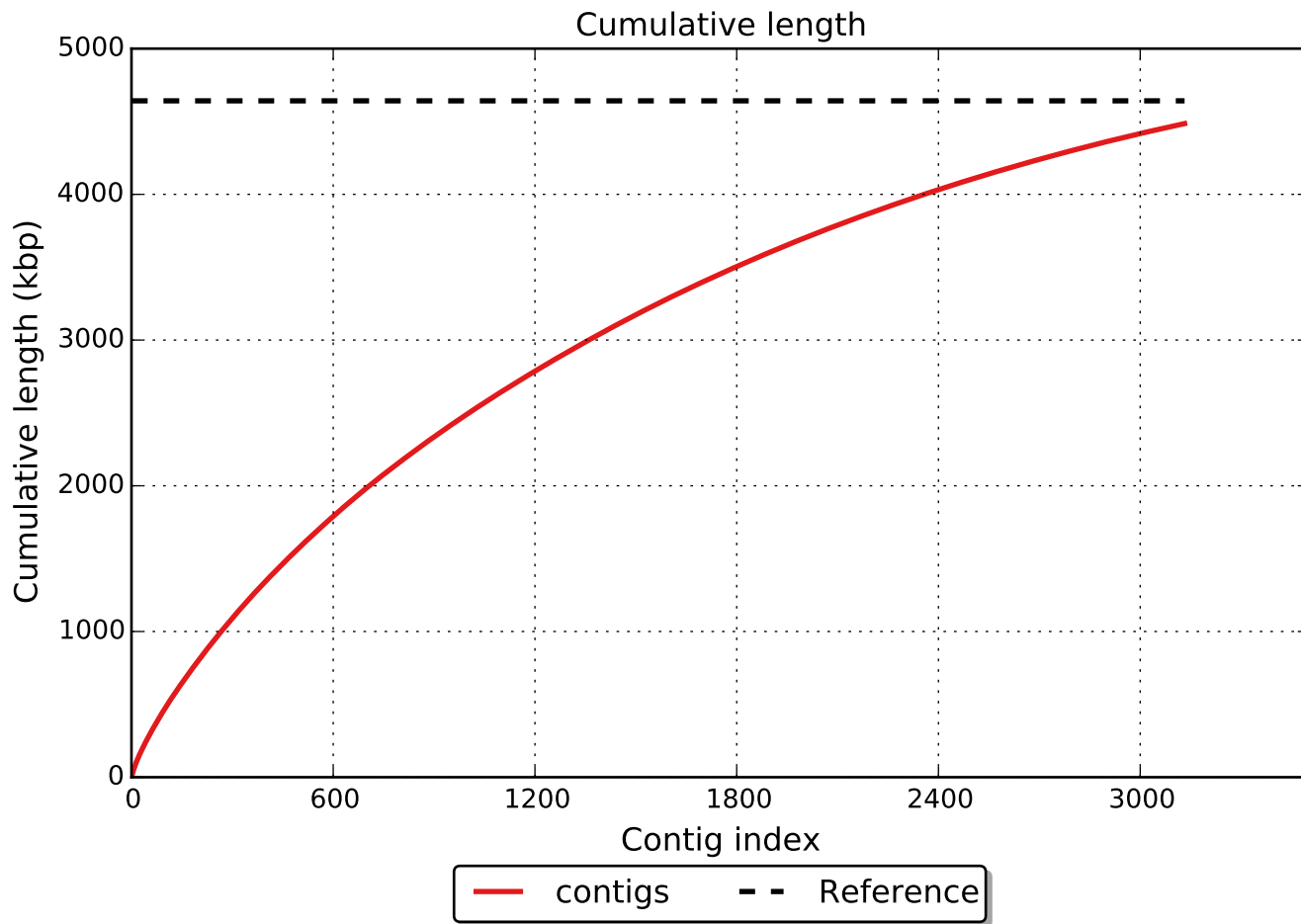
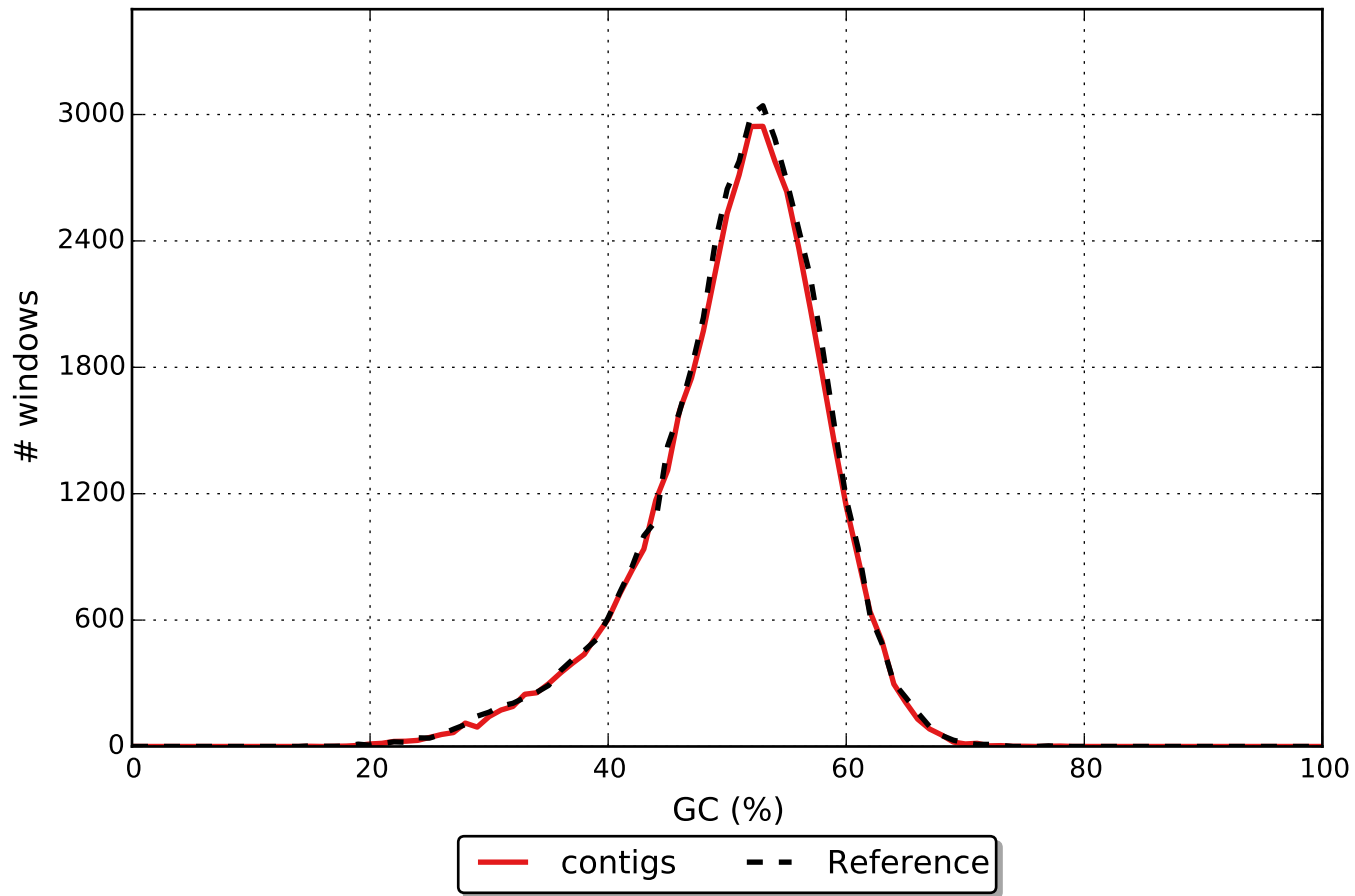|	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	10
# N's	0

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
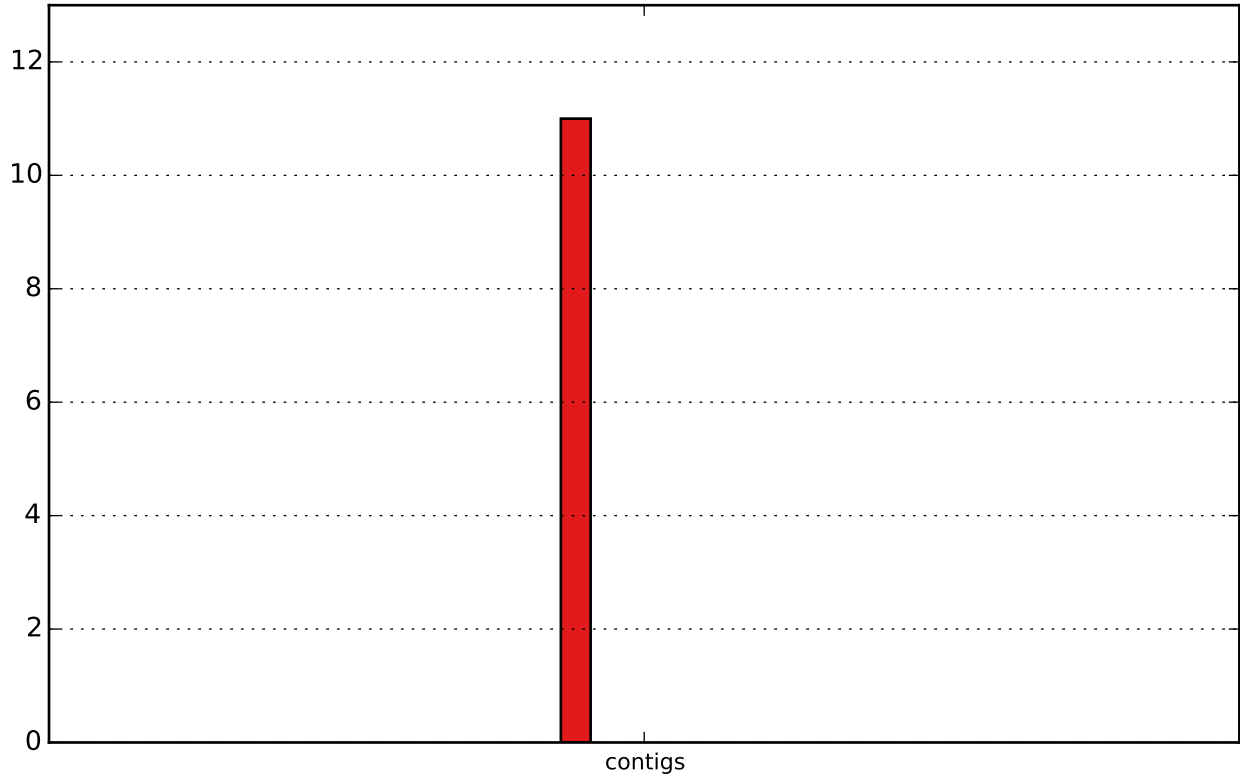
Misassemblies

Cumulative length (aligned contigs)