

Report

	final.contigs
# contigs (>= 1000 bp)	292
# contigs (>= 5000 bp)	228
# contigs (>= 10000 bp)	161
# contigs (>= 25000 bp)	56
# contigs (>= 50000 bp)	15
Total length (>= 1000 bp)	4875925
Total length (>= 5000 bp)	4670566
Total length (>= 10000 bp)	4158702
Total length (>= 25000 bp)	2453183
Total length (>= 50000 bp)	1113377
# contigs	300
Largest contig	119580
Total length	4881850
Reference length	4857432
GC (℥)	52.23
Reference GC (℥)	52.23
N50	25298
NG50	25298
N75	14195
NG75	14241
L50	56
LG50	56
L75	120
LG75	119
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	99.979
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	119580
NA50	25298
NGA50	25298
NA75	14195
NGA75	14241
LA50	56
LGA50	56
LA75	120
LGA75	119

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

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	0
# indels	0
# short indels	0
# long indels	0
Indels length	0

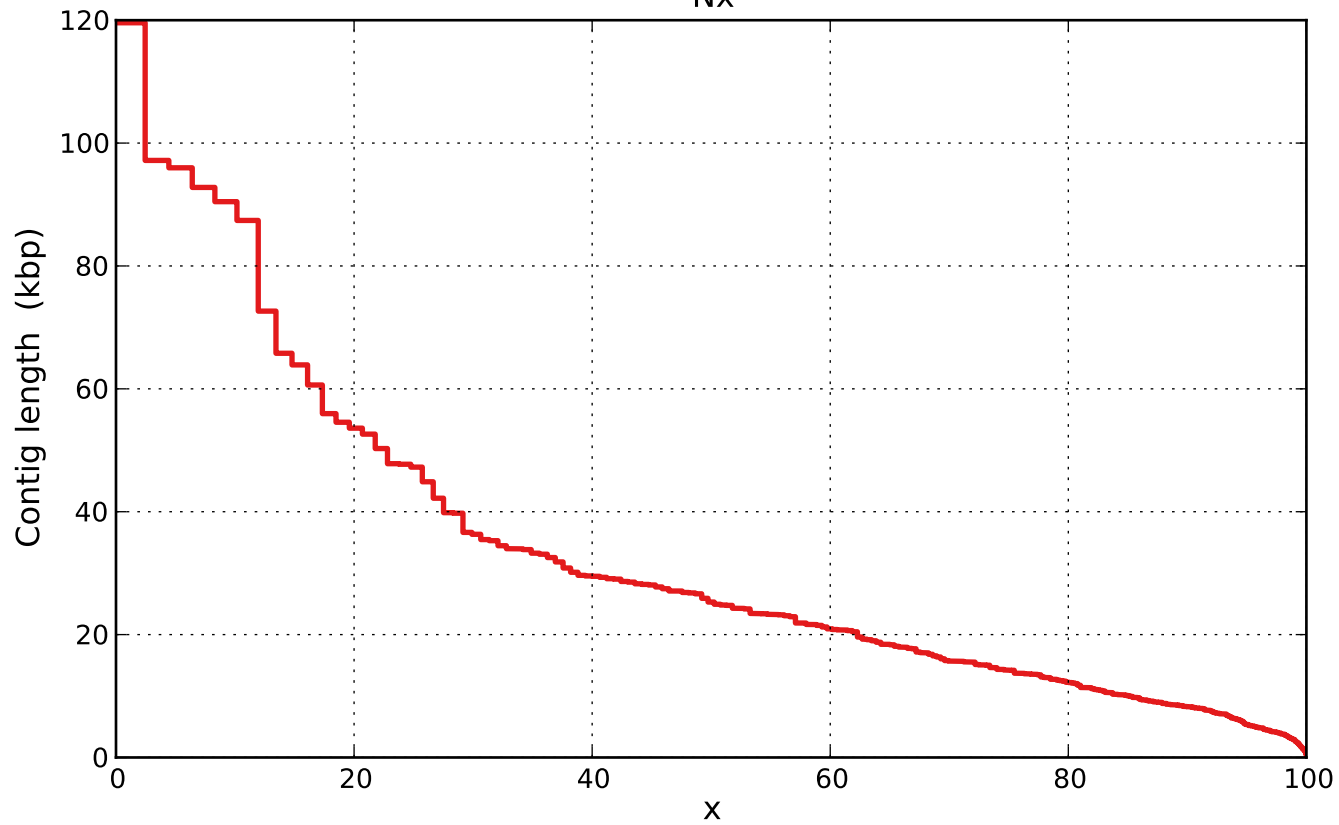
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

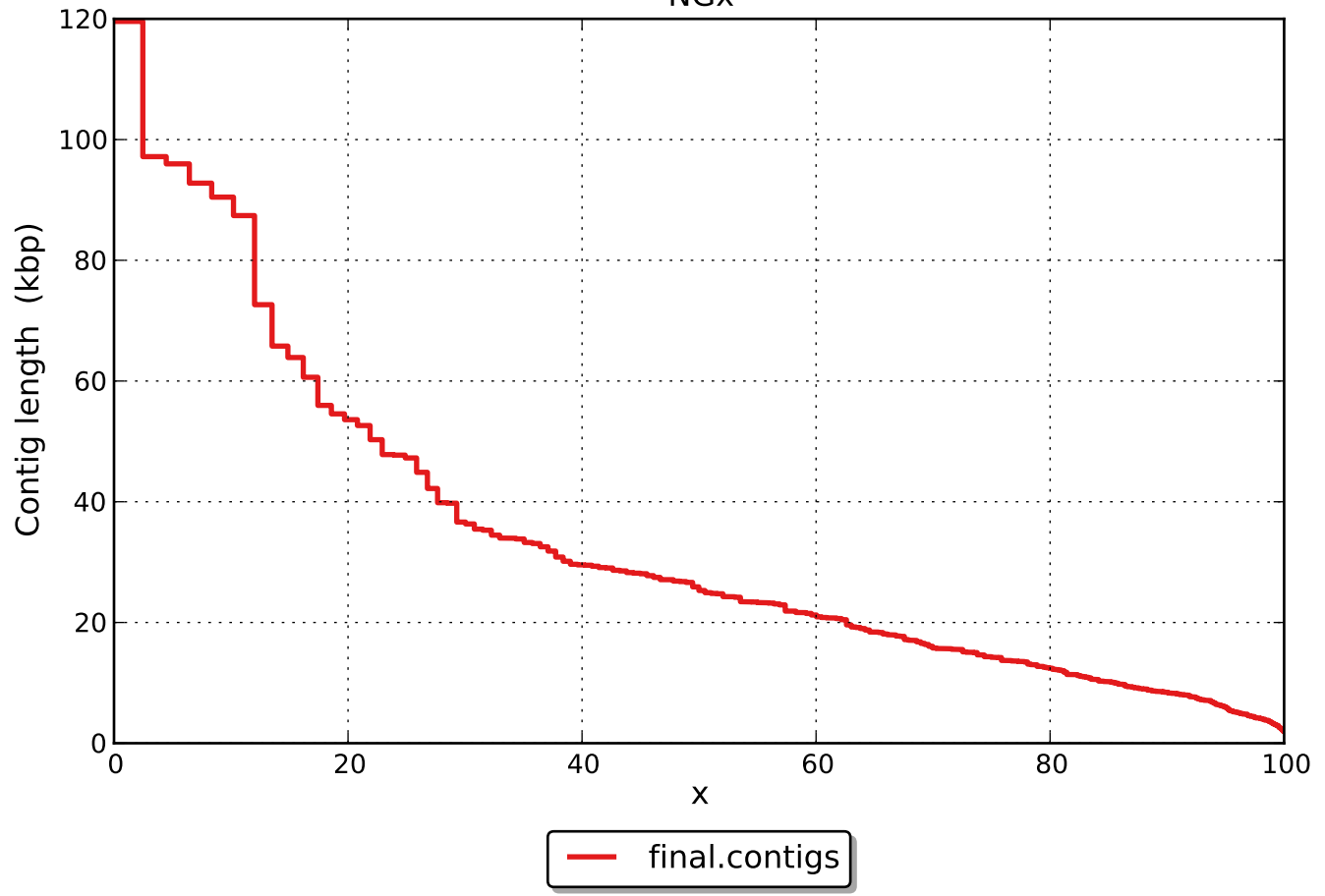
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

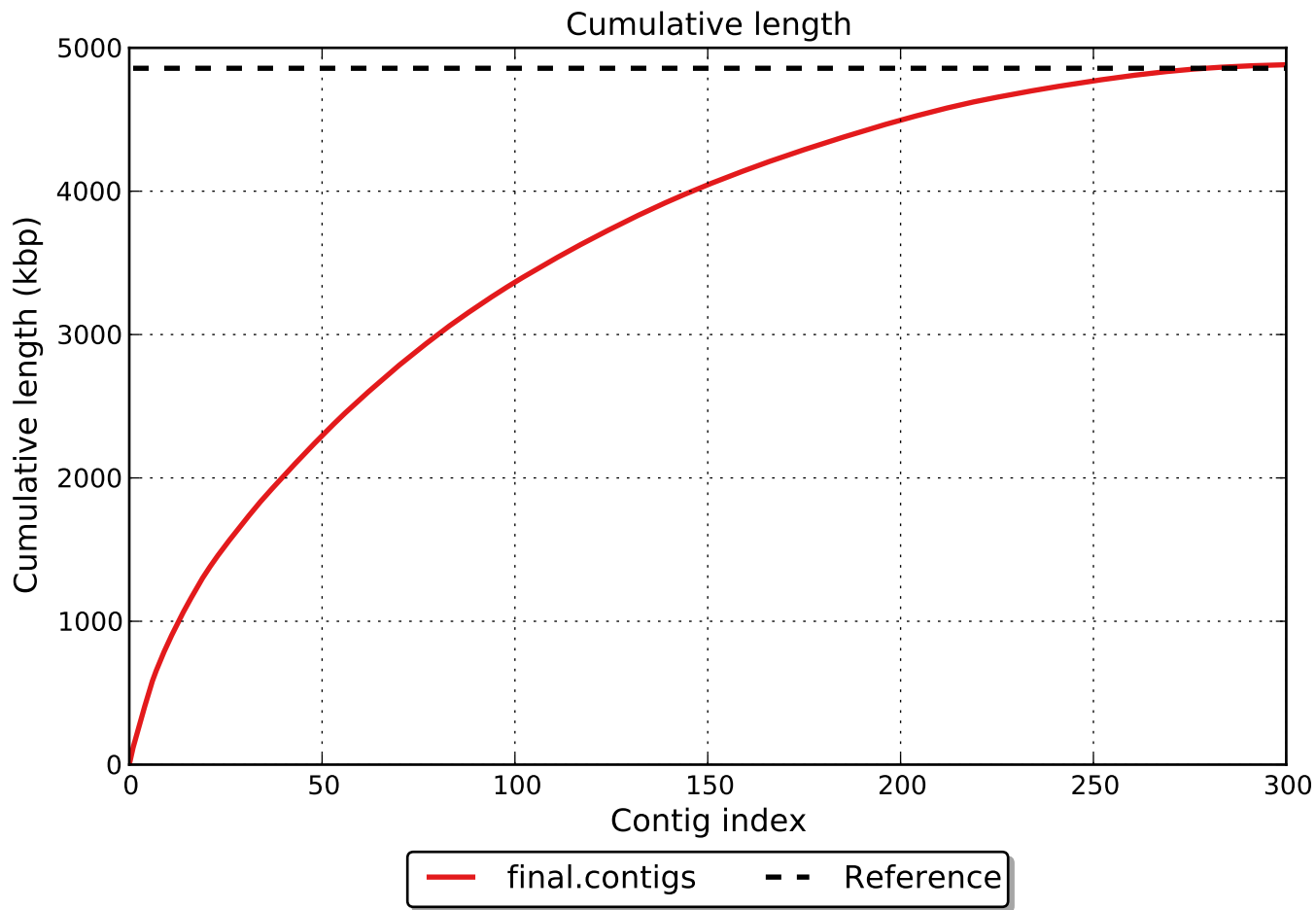
Nx



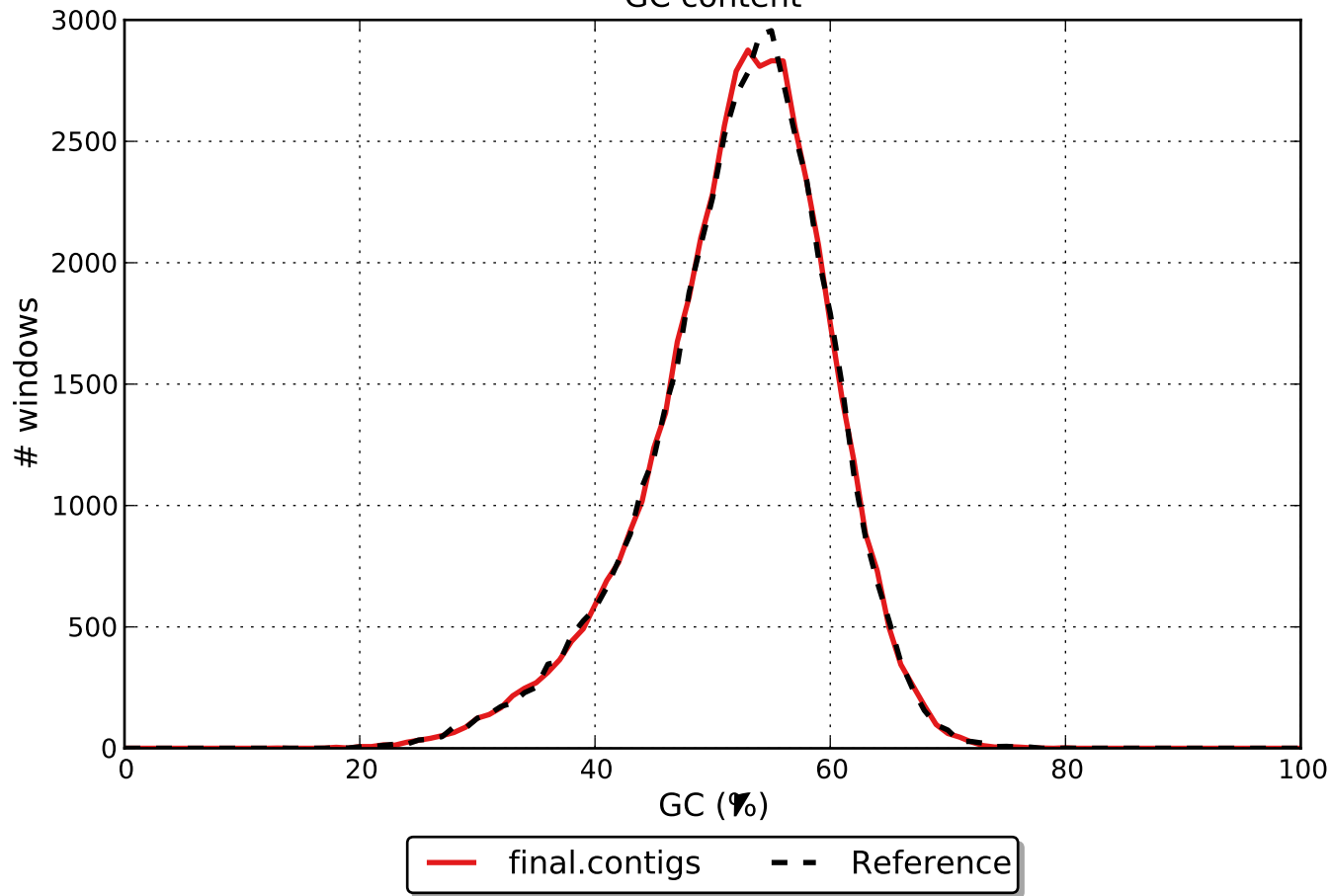
— final.contigs

NGx





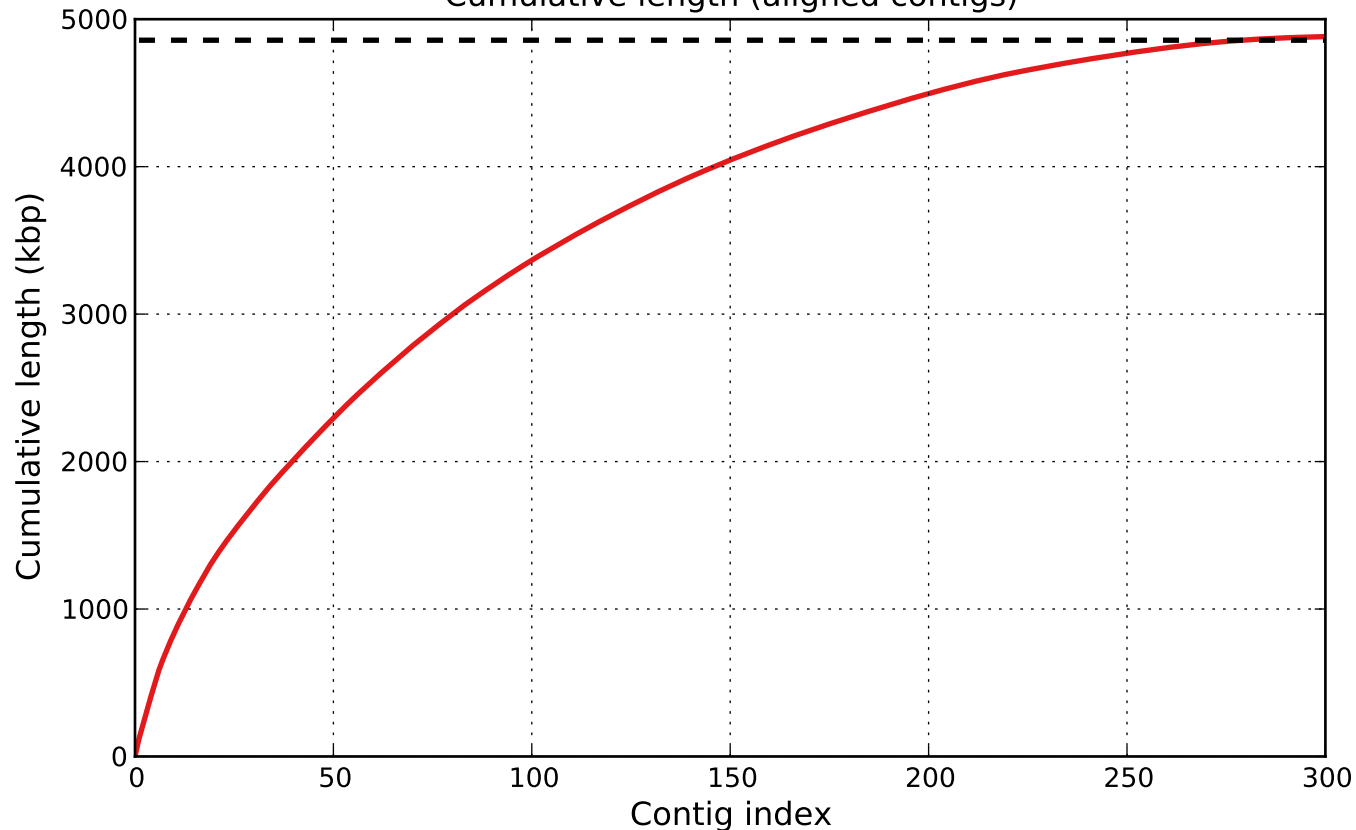
GC content



Misassemblies

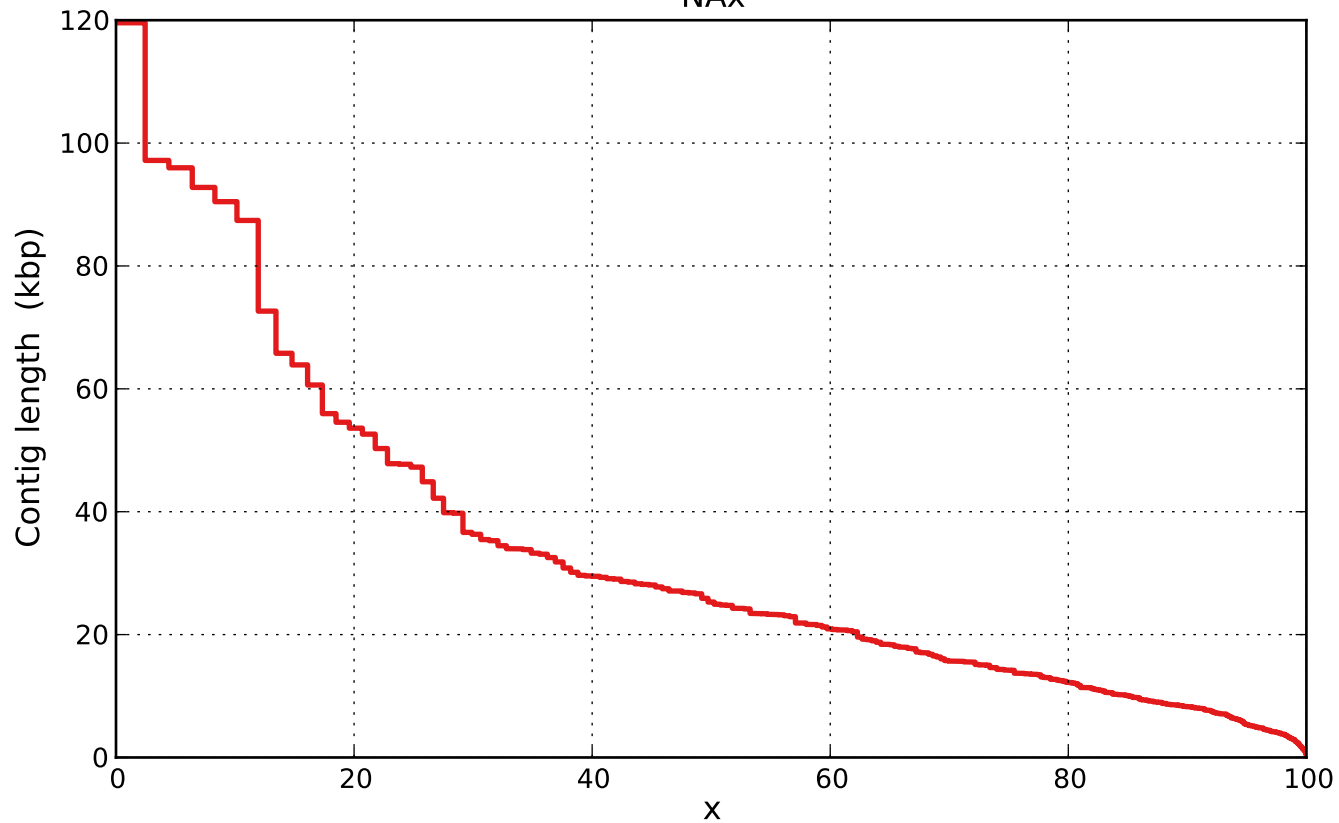


Cumulative length (aligned contigs)



— final.contigs - - Reference

NAx



— final.contigs

NGAx

