

Report

	durian.contigs
# contigs (>= 0 bp)	655
# contigs (>= 1000 bp)	655
# contigs (>= 5000 bp)	634
# contigs (>= 10000 bp)	497
# contigs (>= 25000 bp)	157
# contigs (>= 50000 bp)	81
Total length (>= 0 bp)	31329483
Total length (>= 1000 bp)	31329483
Total length (>= 5000 bp)	31267062
Total length (>= 10000 bp)	30151981
Total length (>= 25000 bp)	24695069
Total length (>= 50000 bp)	22082948
# contigs	655
Largest contig	2182527
Total length	31329483
Reference length	23775123
GC (%)	31.03
Reference GC (%)	30.18
N50	286878
NG50	412262
N75	33649
NG75	162902
L50	26
LG50	15
L75	116
LG75	36
# misassemblies	165
# misassembled contigs	102
Misassembled contigs length	15039921
# local misassemblies	227
# unaligned mis. contigs	8
# unaligned contigs	283 + 189 part
Unaligned length	5699571
Genome fraction (%)	94.472
Duplication ratio	1.141
# N's per 100 kbp	0.00
# mismatches per 100 kbp	349.71
# indels per 100 kbp	204.36
Largest alignment	2007113
Total aligned length	25619065
NA50	125325
NGA50	265801
NA75	16174
NGA75	96952
LA50	46
LGA50	25
LA75	226
LGA75	65

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

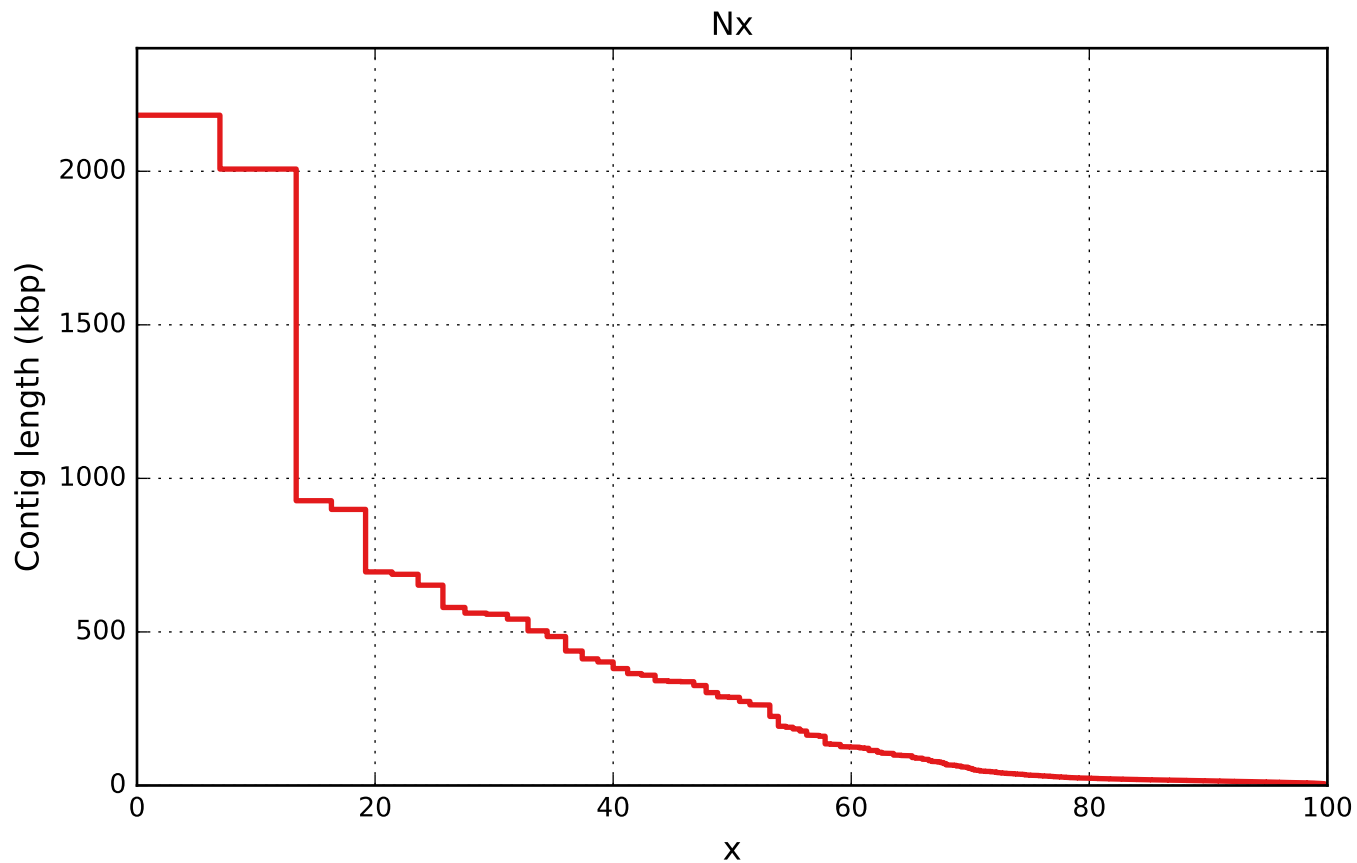
	durian.contigs
# misassemblies	165
# relocations	164
# translocations	0
# inversions	1
# misassembled contigs	102
Misassembled contigs length	15039921
# local misassemblies	227
# unaligned mis. contigs	8
# mismatches	78547
# indels	45900
# indels ( $\leq 5$ bp)	43990
# indels ( $> 5$ bp)	1910
Indels length	81352

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

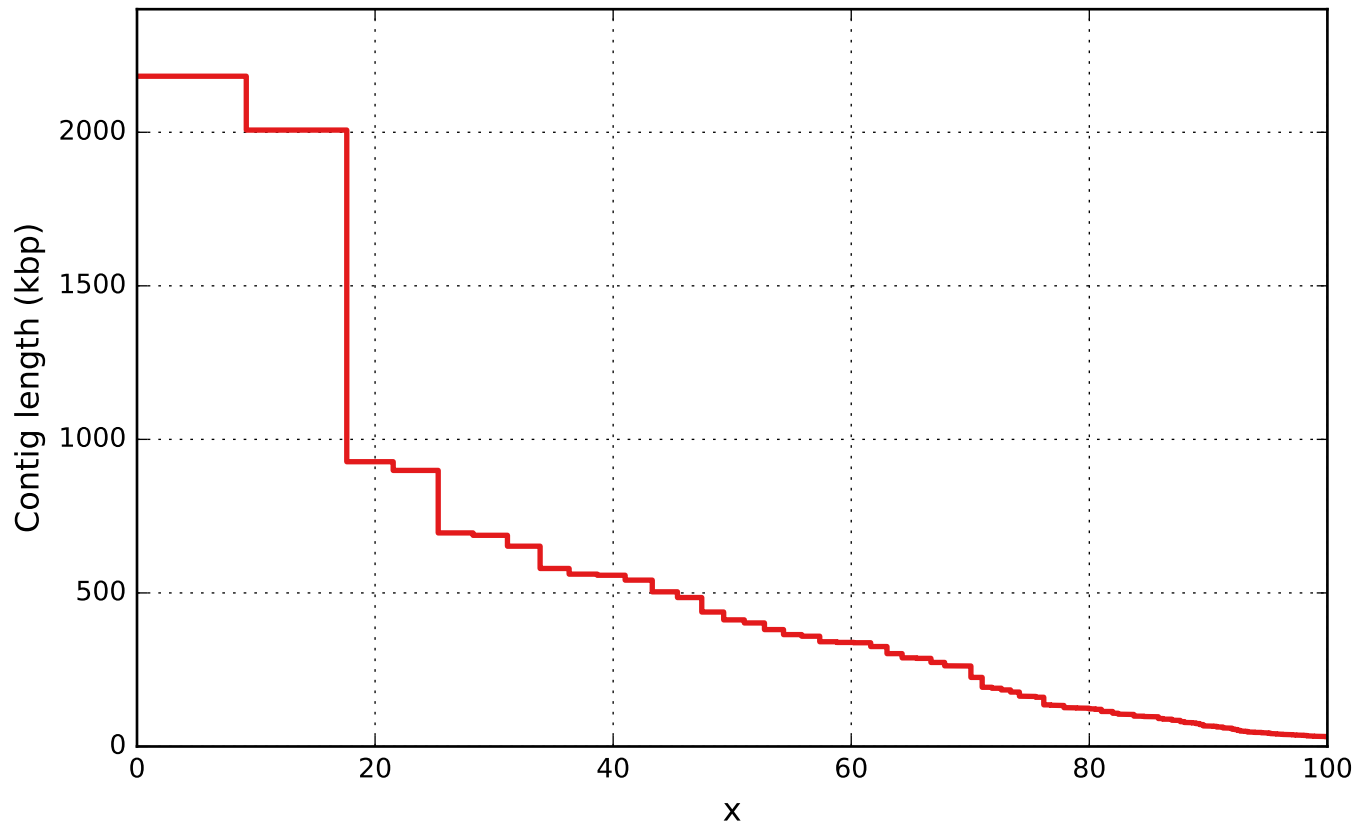
## Unaligned report

	durian.contigs
# fully unaligned contigs	283
Fully unaligned length	3830612
# partially unaligned contigs	189
Partially unaligned length	1868959
# N's	0

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

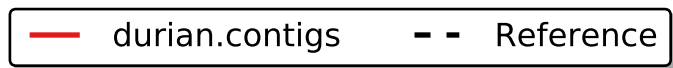
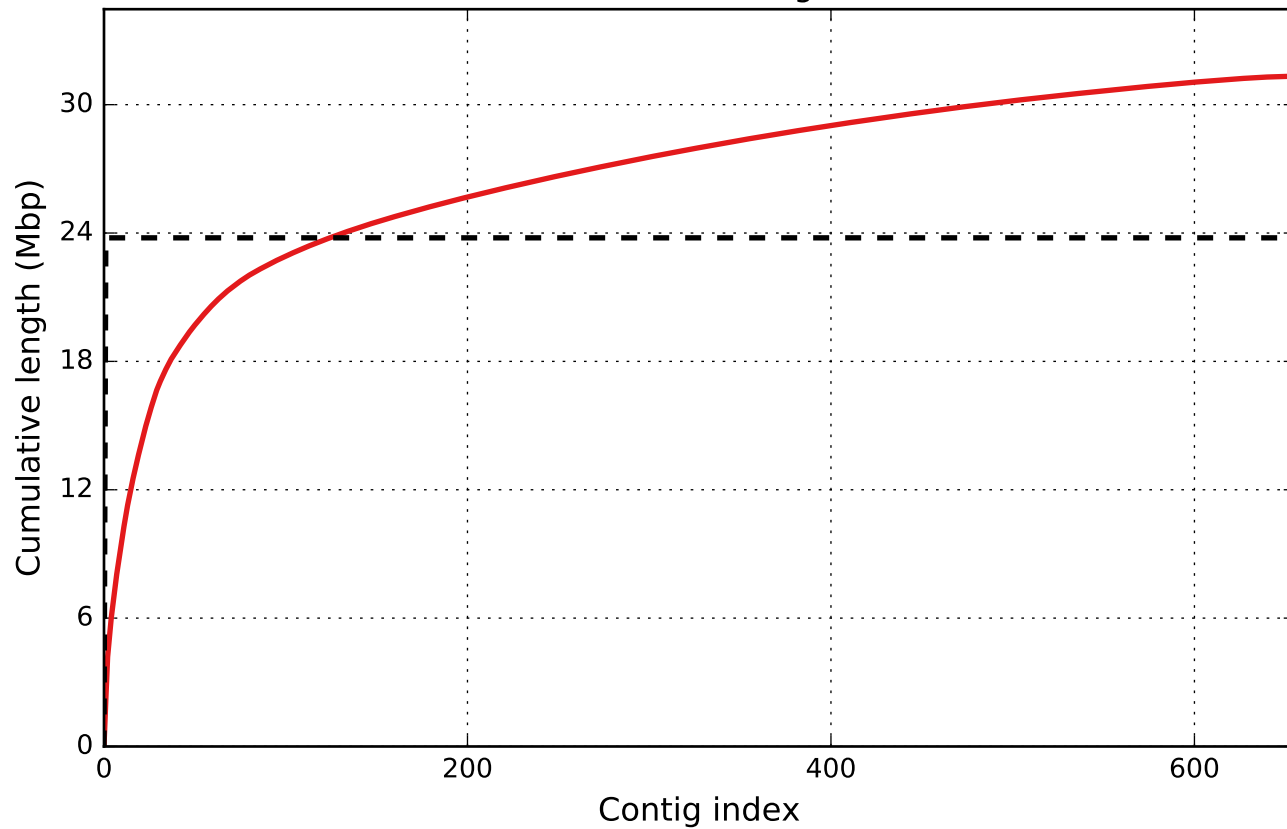


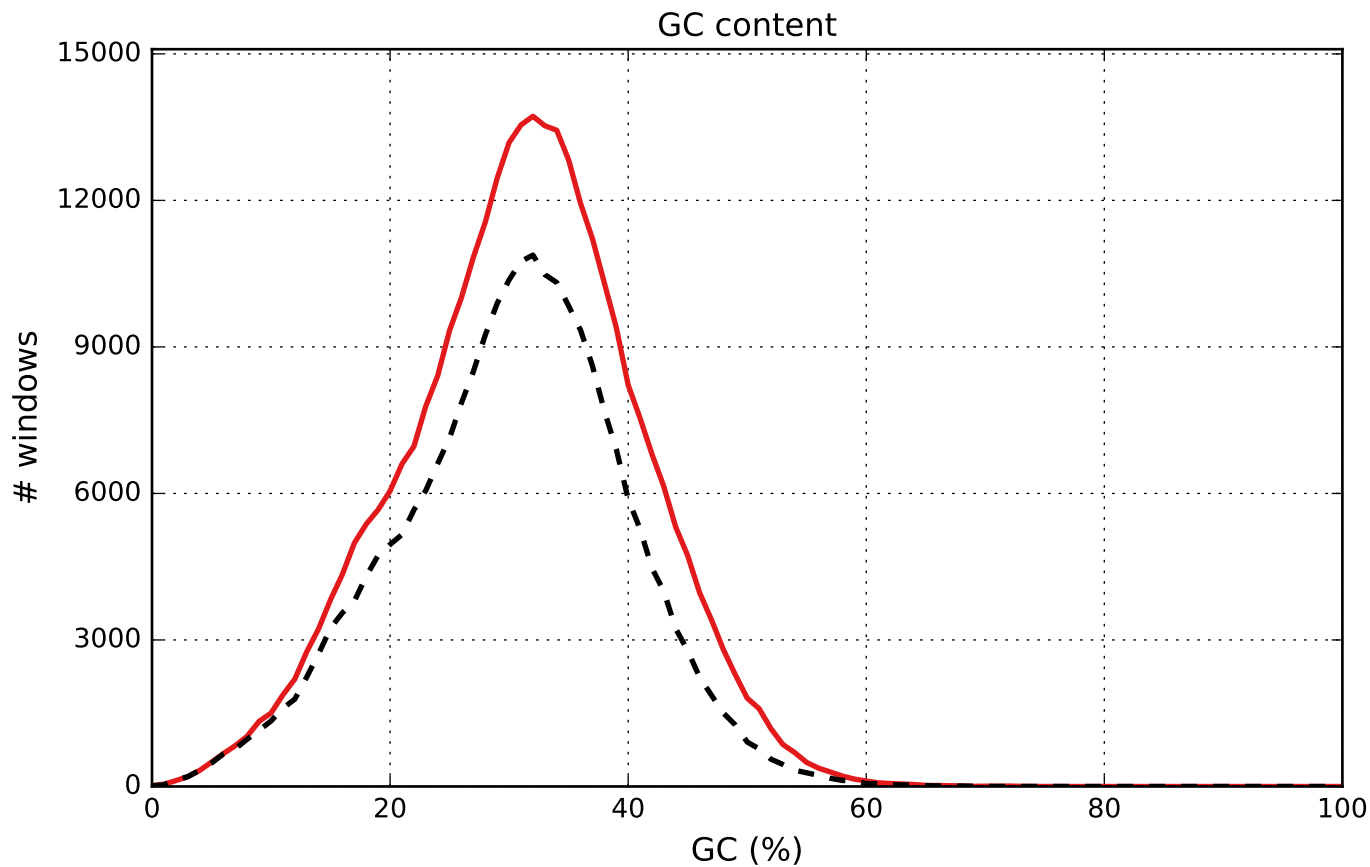
NGx



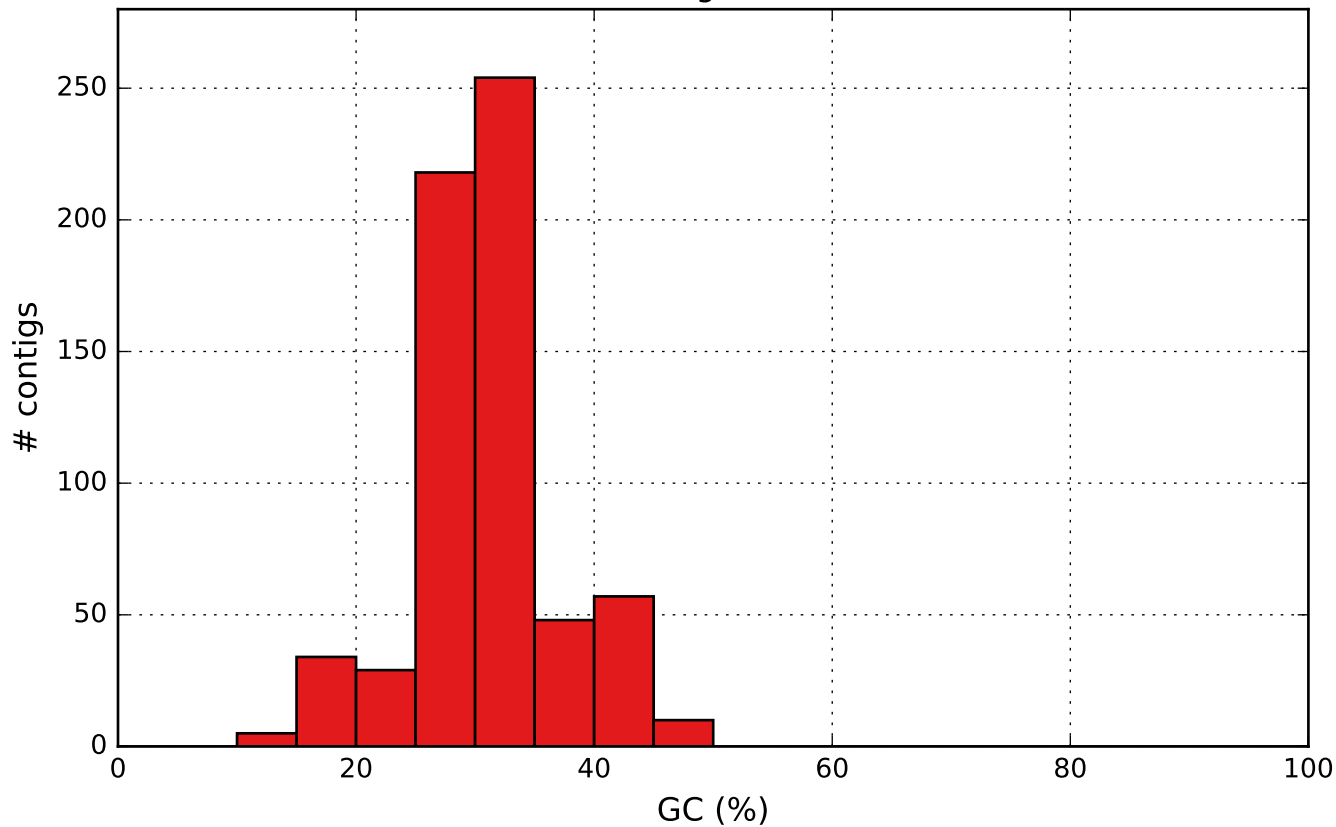
— durian.contigs


Cumulative length





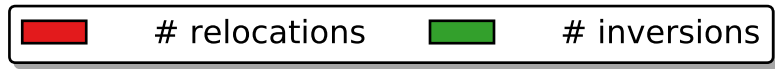
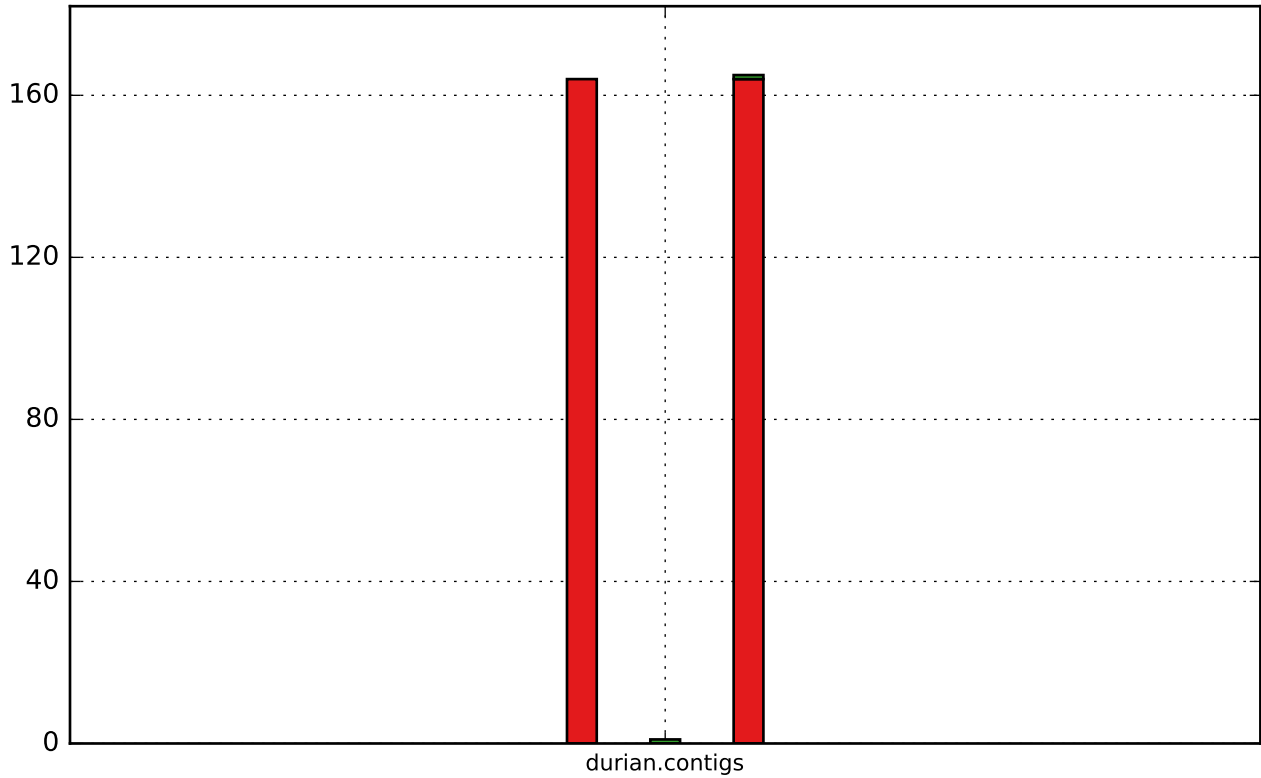
durian.contigs GC content



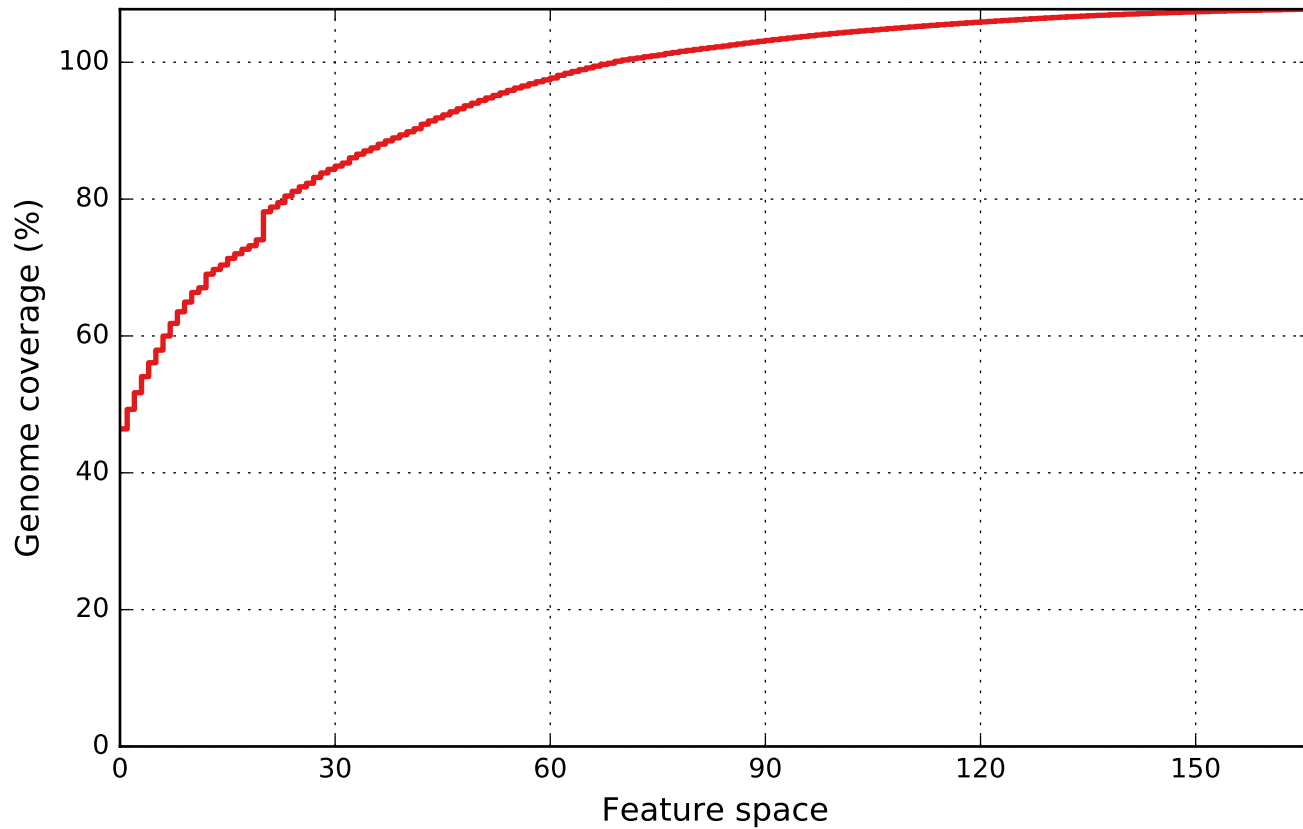
 durian.contigs



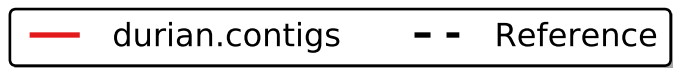
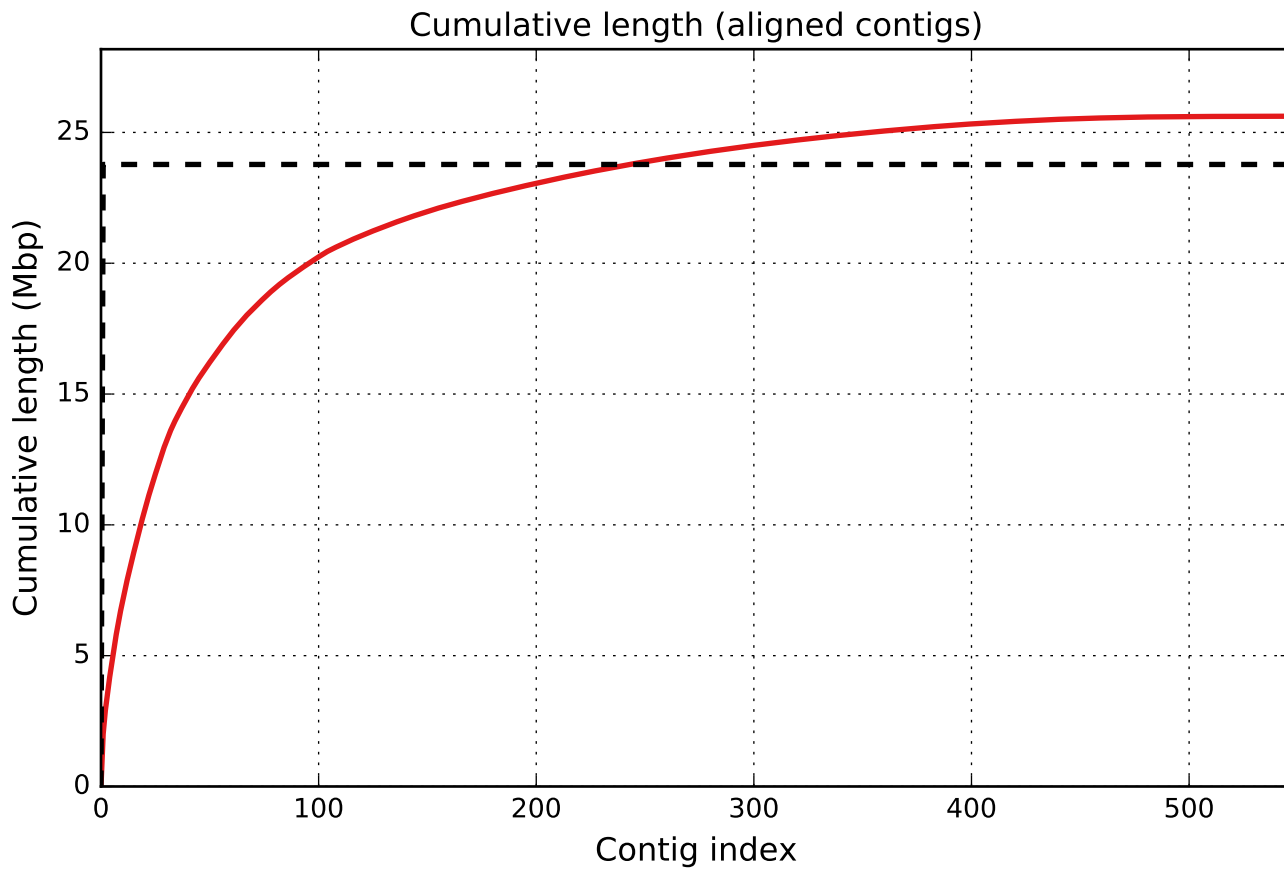
# Misassemblies



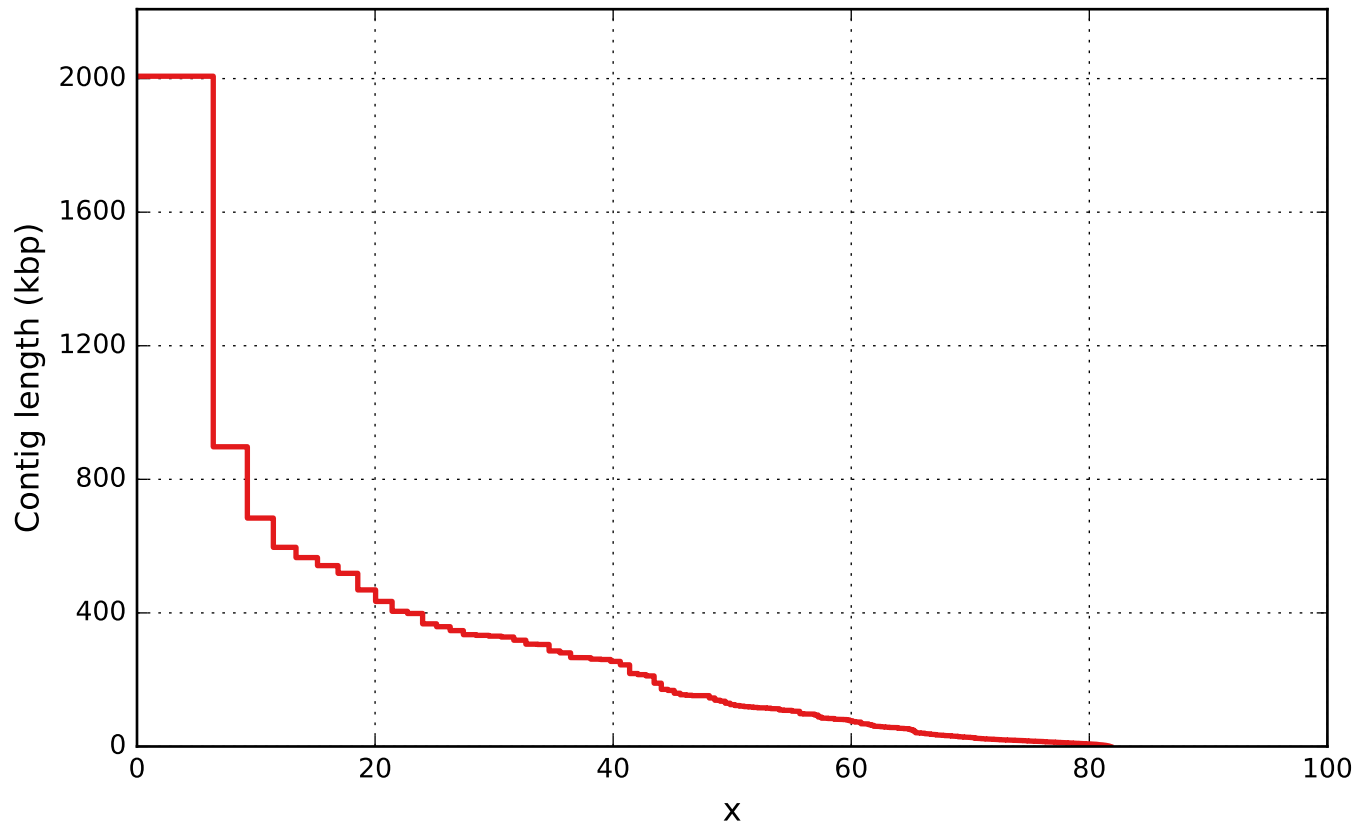
FRCurve (misassemblies)



— durian.contigs

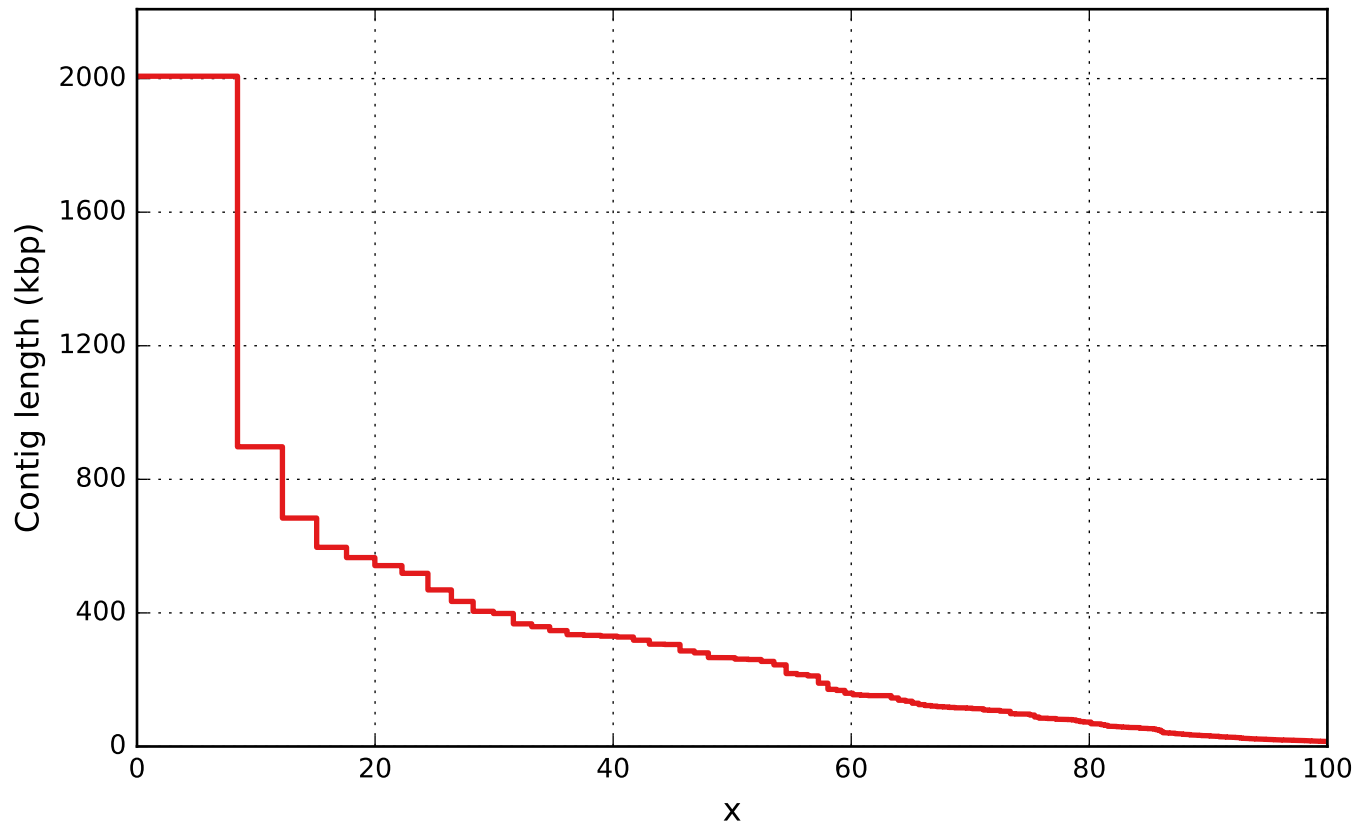


NAx



— durian.contigs

# NGAx



— durian.contigs