

Report

	durio_zibethinus
# contigs (>= 0 bp)	981
# contigs (>= 1000 bp)	981
# contigs (>= 5000 bp)	896
# contigs (>= 10000 bp)	590
# contigs (>= 25000 bp)	137
# contigs (>= 50000 bp)	64
Total length (>= 0 bp)	37518394
Total length (>= 1000 bp)	37518394
Total length (>= 5000 bp)	37254985
Total length (>= 10000 bp)	34954926
Total length (>= 25000 bp)	28007139
Total length (>= 50000 bp)	25740609
# contigs	981
Largest contig	1977600
Total length	37518394
Reference length	26551601
GC (%)	30.98
Reference GC (%)	30.98
N50	380517
NG50	546186
N75	24314
NG75	354321
L50	27
LG50	14
L75	143
LG75	30
# misassemblies	233
# misassembled contigs	132
Misassembled contigs length	22821315
# local misassemblies	274
# unaligned mis. contigs	19
# unaligned contigs	528 + 266 part
Unaligned length	7158836
Genome fraction (%)	97.284
Duplication ratio	1.175
# N's per 100 kbp	0.00
# mismatches per 100 kbp	304.51
# indels per 100 kbp	131.43
Largest alignment	1260843
Total aligned length	30344629
NA50	160039
NGA50	302694
NA75	12949
NGA75	129300
LA50	47
LGA50	23
LA75	287
LGA75	55

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

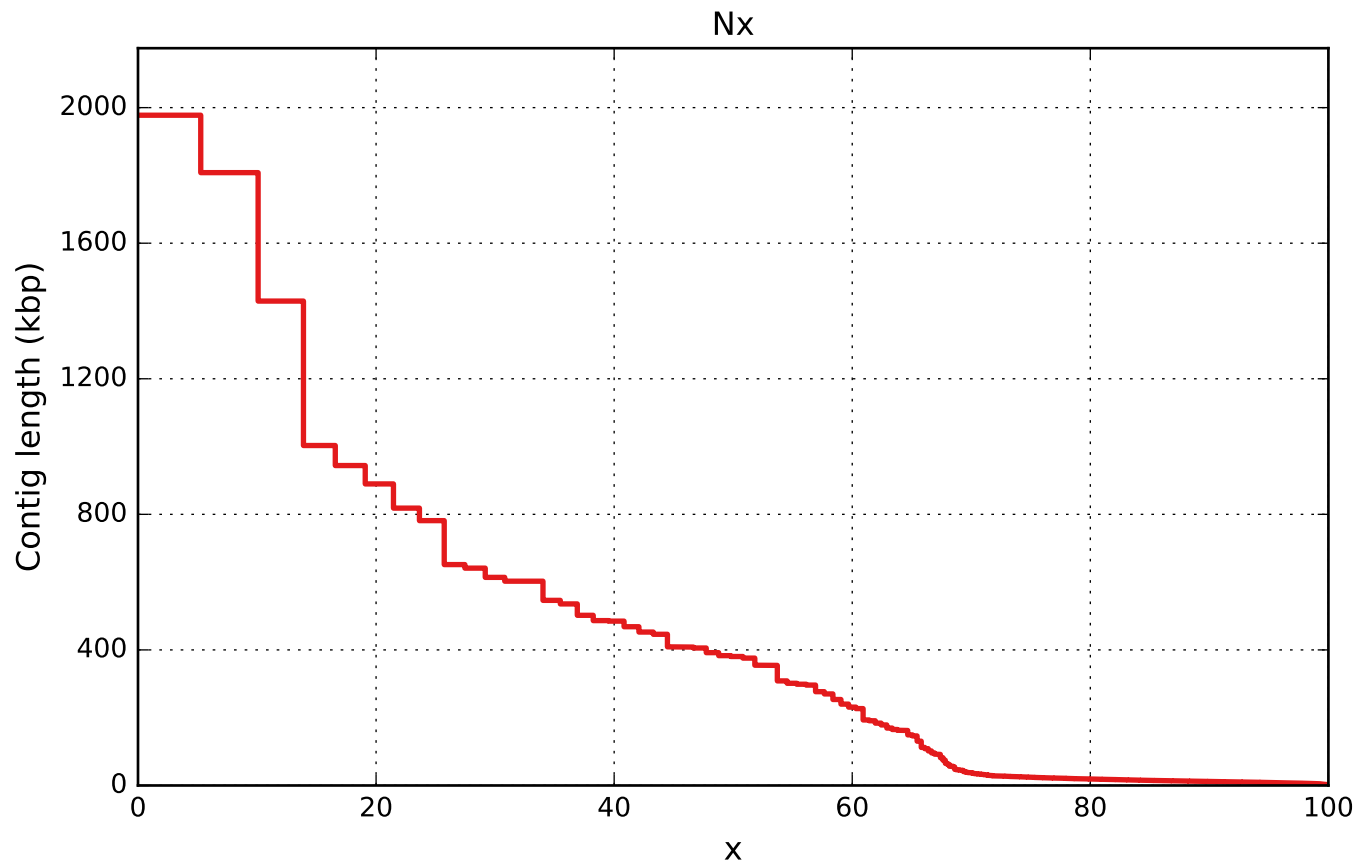
	durio_zibethinus
# misassemblies	233
# relocations	232
# translocations	0
# inversions	1
# misassembled contigs	132
Misassembled contigs length	22821315
# local misassemblies	274
# unaligned mis. contigs	19
# mismatches	78656
# indels	33949
# indels (≤ 5 bp)	31708
# indels (> 5 bp)	2241
Indels length	73207

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

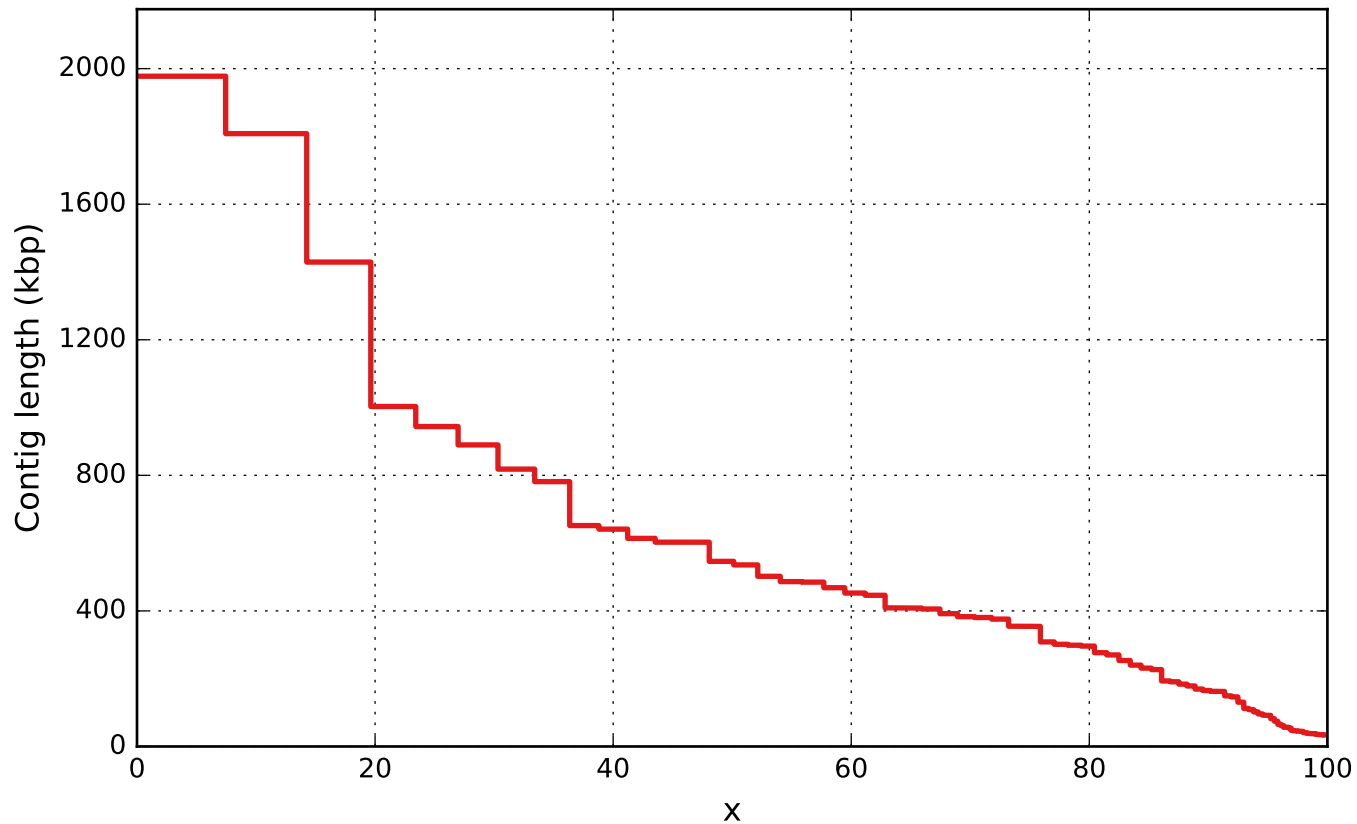
	durio_zibethinus
# fully unaligned contigs	528
Fully unaligned length	4932820
# partially unaligned contigs	266
Partially unaligned length	2226016
# N's	0

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).

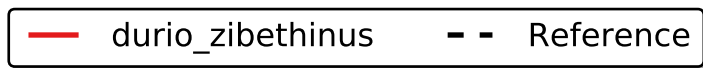
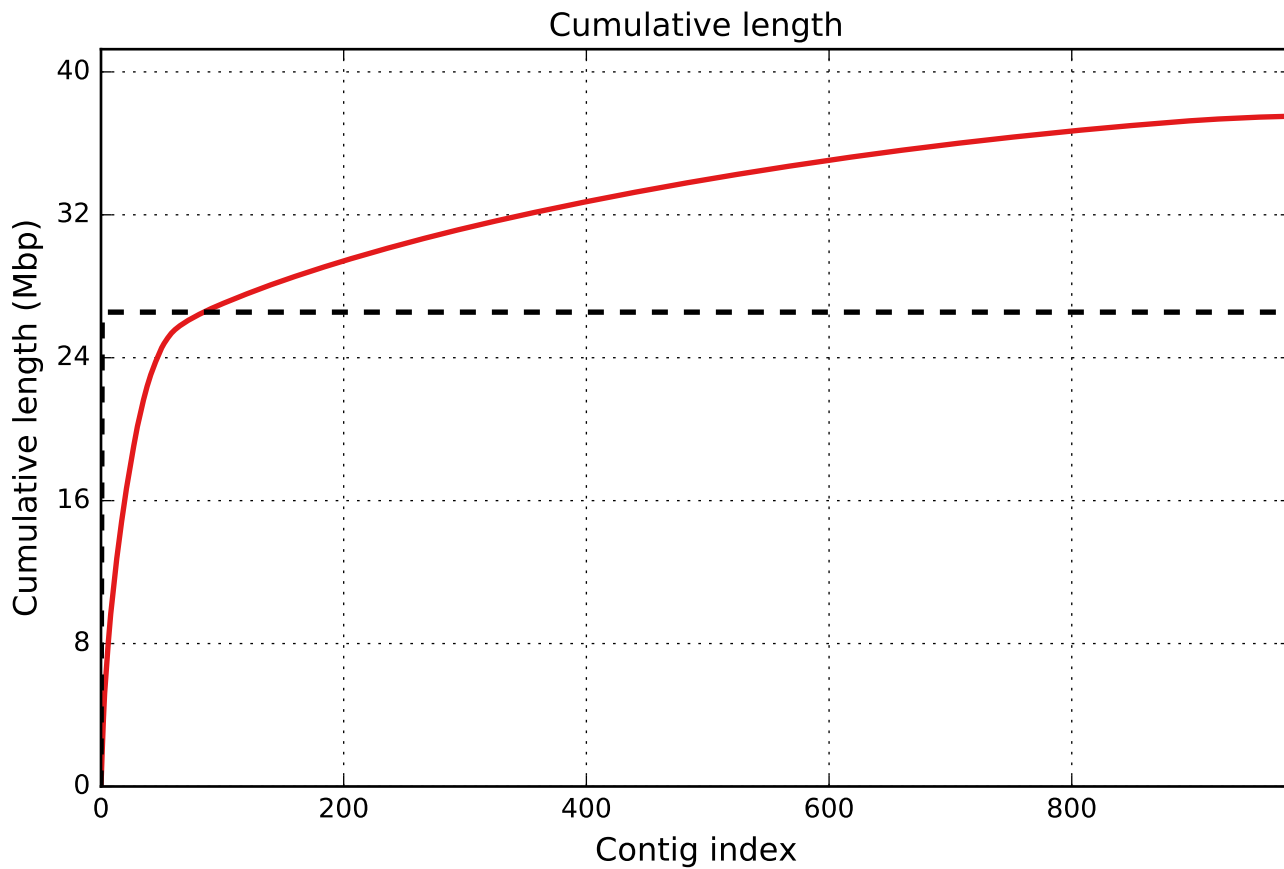


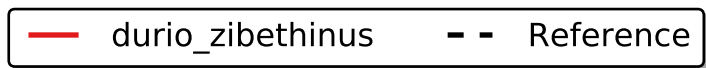
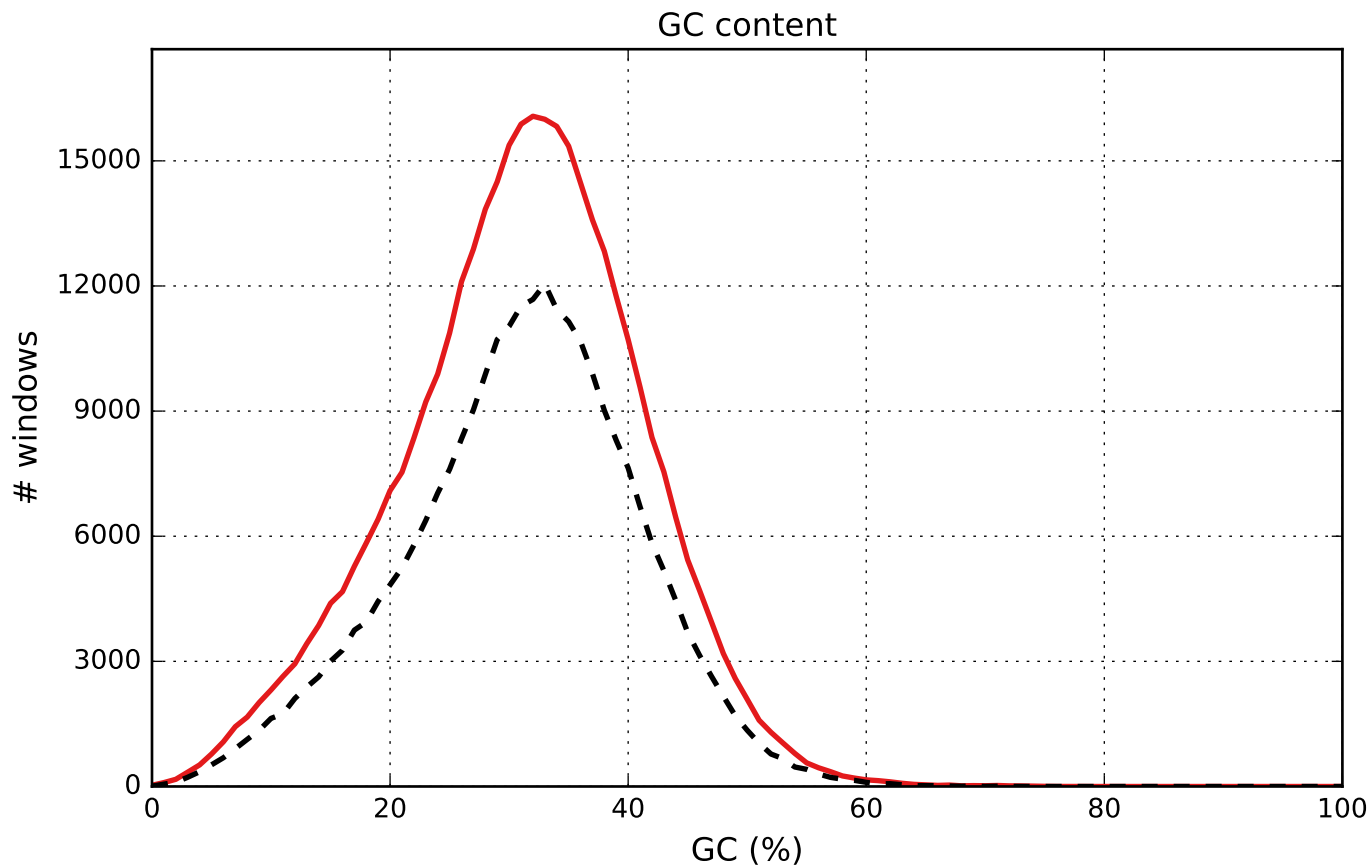
— durio_zibethinus

NGx

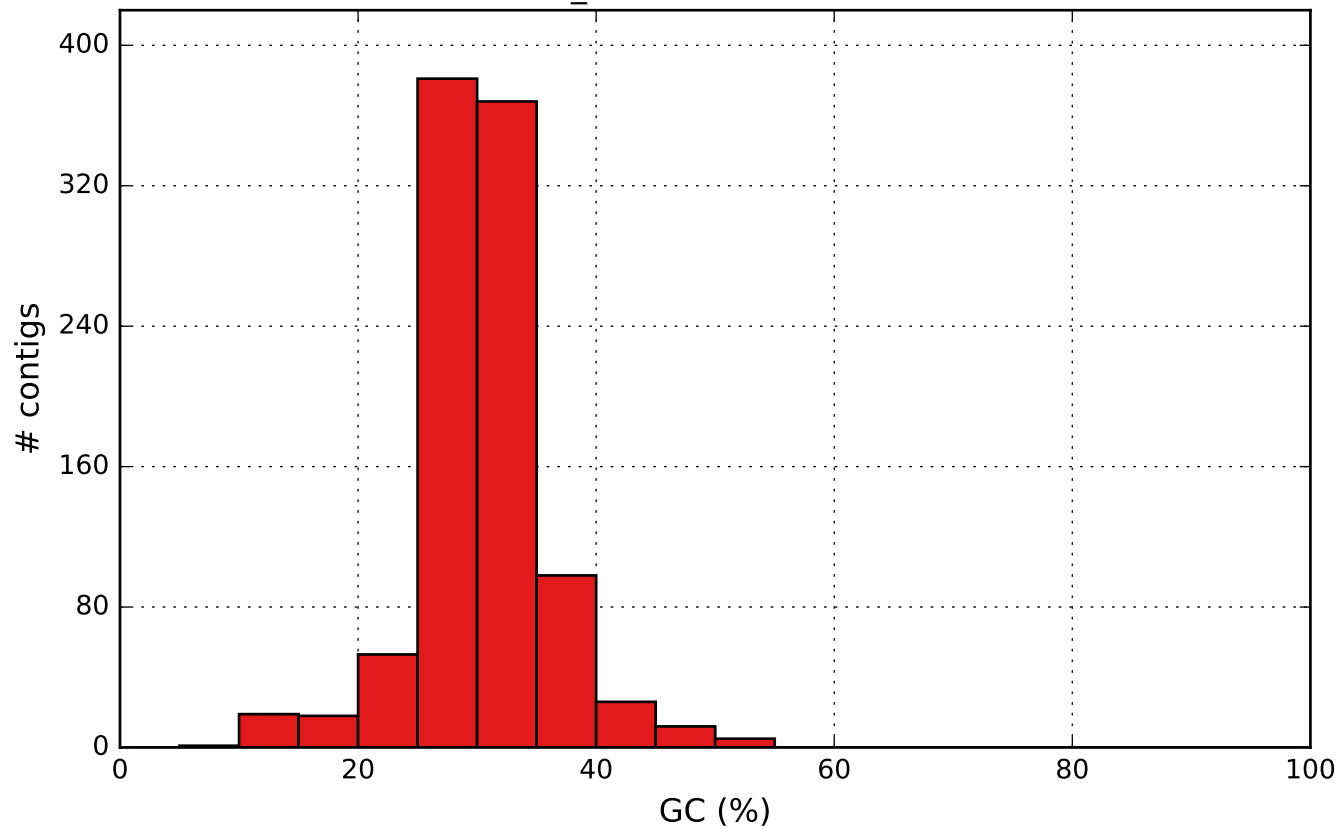



— durio_zibethinus



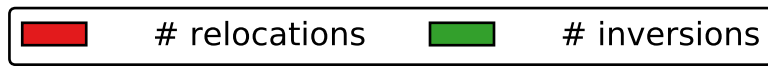
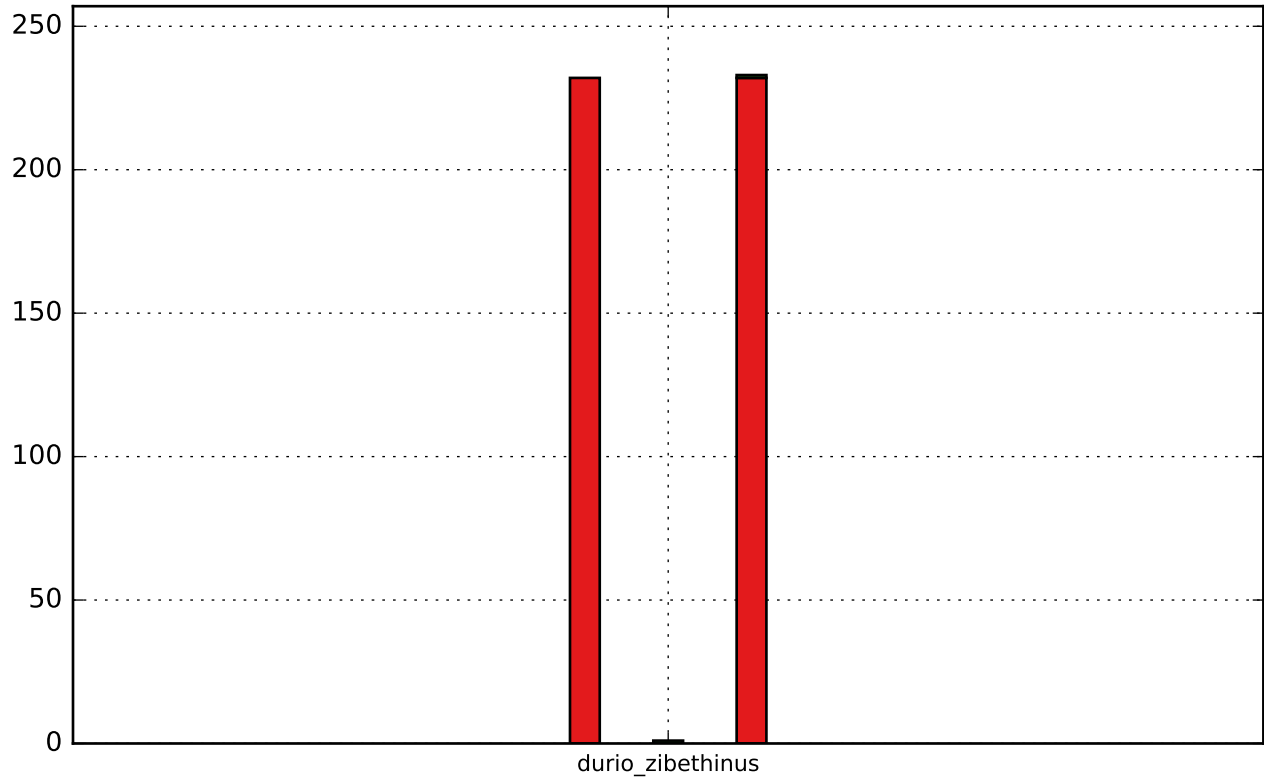


durio_zibethinus GC content

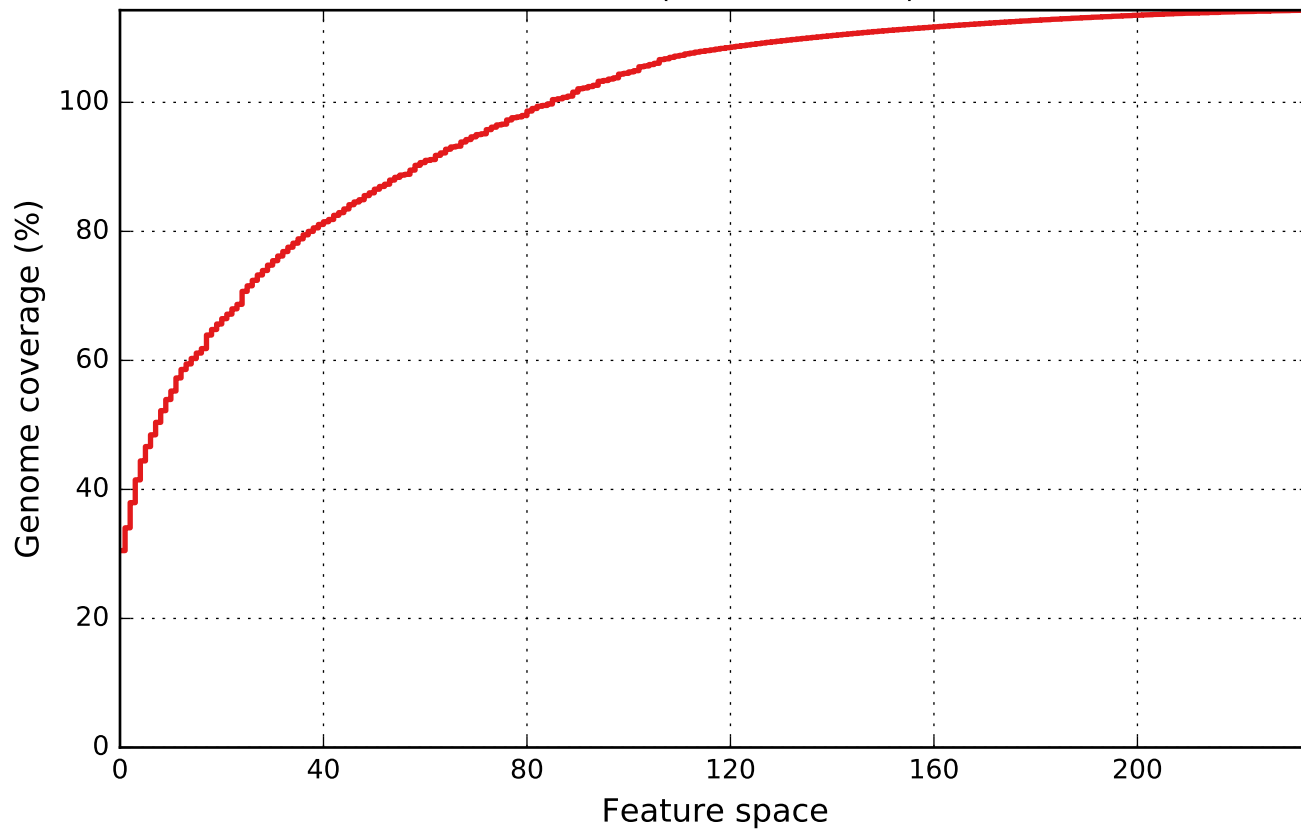


 durio_zibethinus

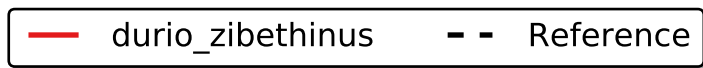
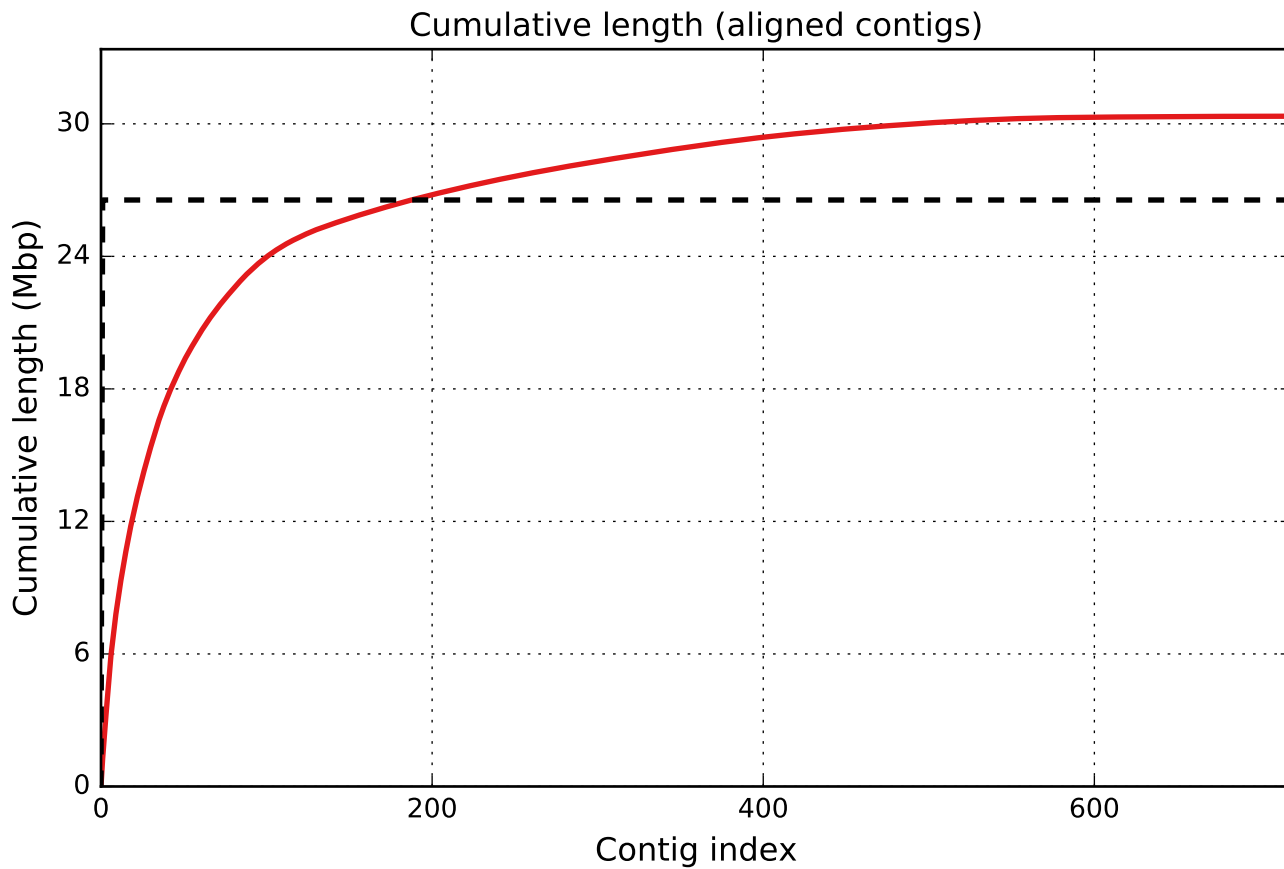
Misassemblies



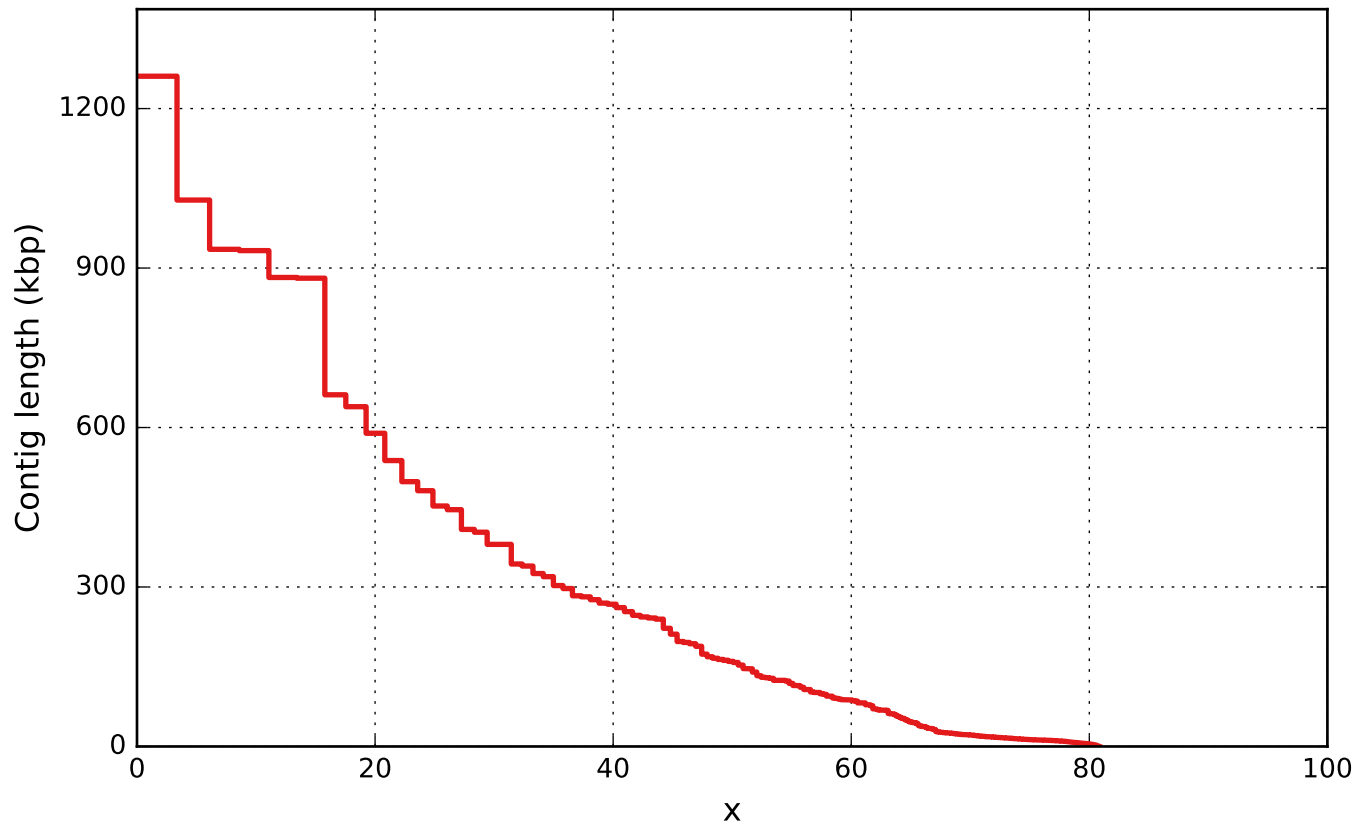
FRCurve (misassemblies)



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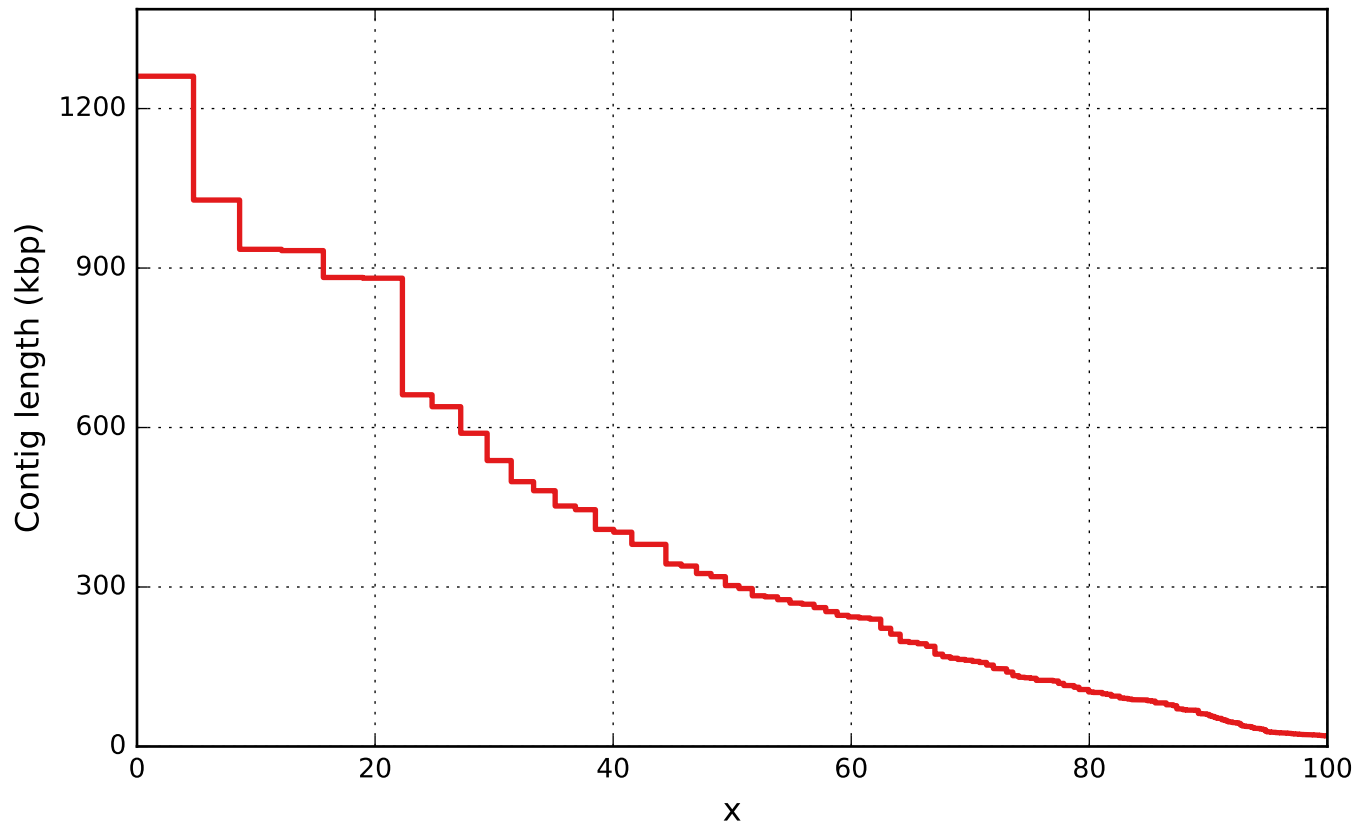


NAx



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NGAx



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