

Report

	combined.final.contigs
# contigs (≥ 1000 bp)	10
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 1000 bp)	19455
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	17
Largest contig	4182
Total length	23435
Reference length	1424092
GC (%)	46.08
Reference GC (%)	38.87
N50	1821
N75	1308
L50	5
L75	9
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 10 part
Unaligned length	13516
Genome fraction (%)	0.445
Duplication ratio	1.565
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2351.27
# indels per 100 kbp	315.61
Largest alignment	4113
Total aligned length	7592
NGA50	-

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

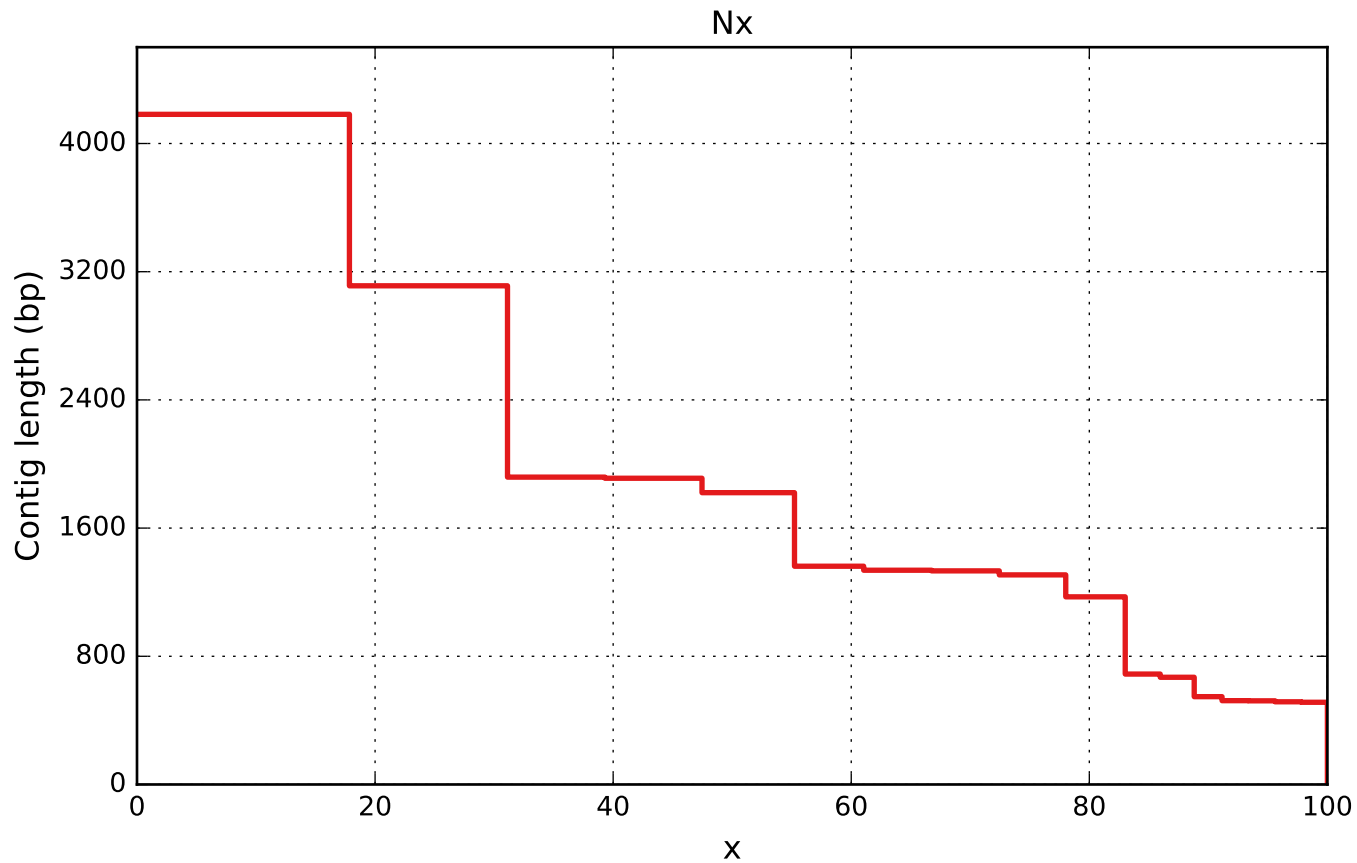
	combined.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	149
# indels	20
# indels (<= 5 bp)	19
# indels (> 5 bp)	1
Indels length	54

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).

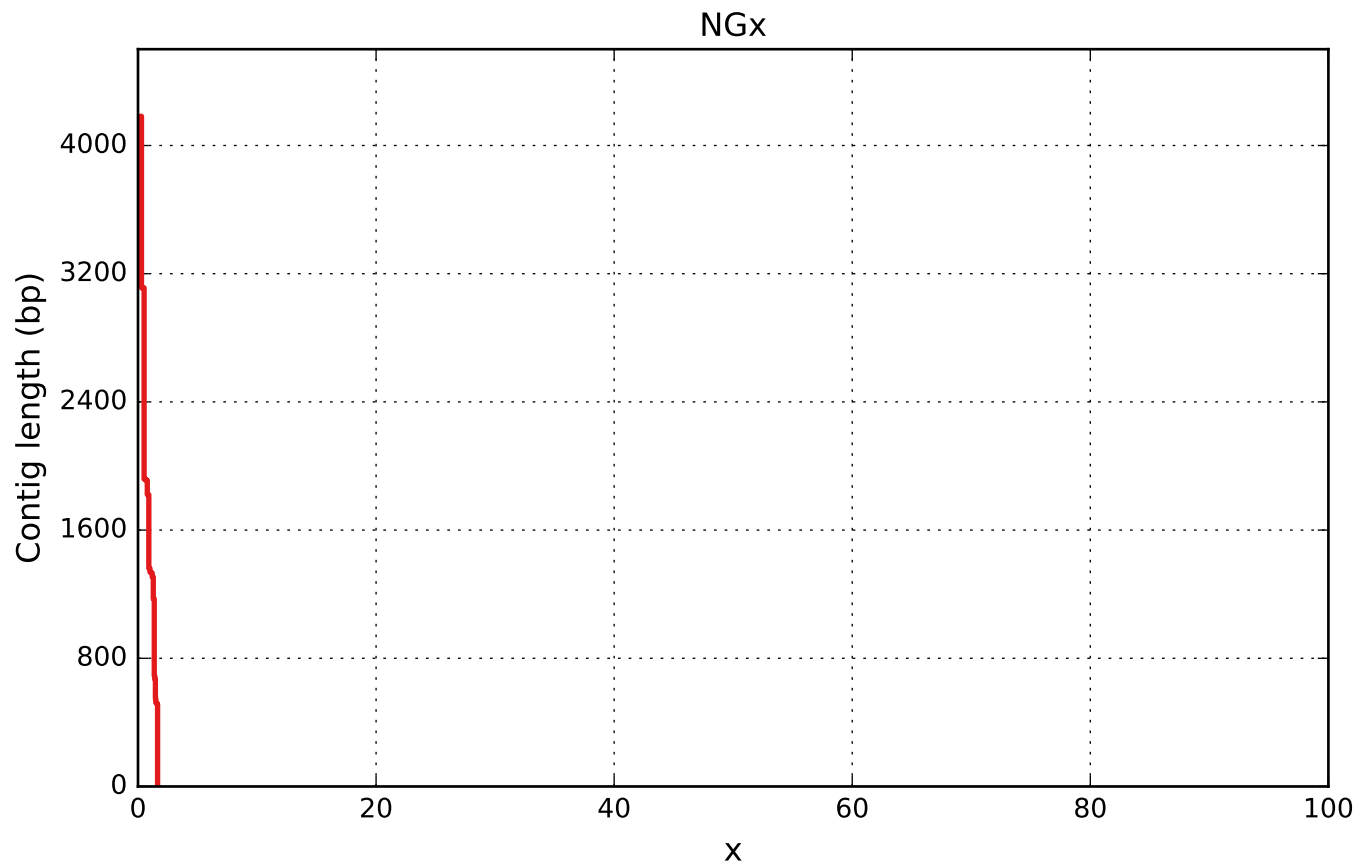
Unaligned report

	combined.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	10
Partially unaligned length	13516
# N's	0

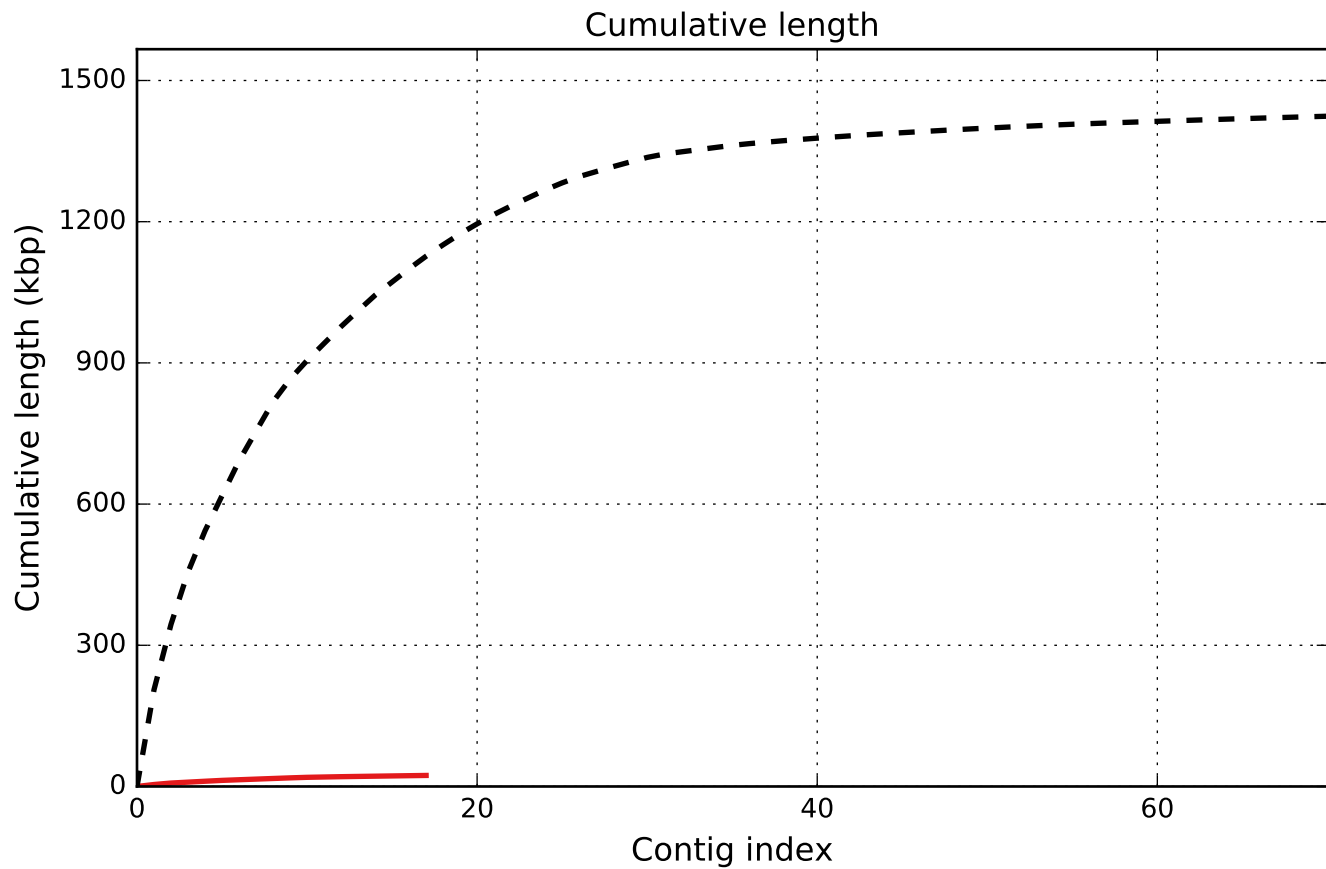
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



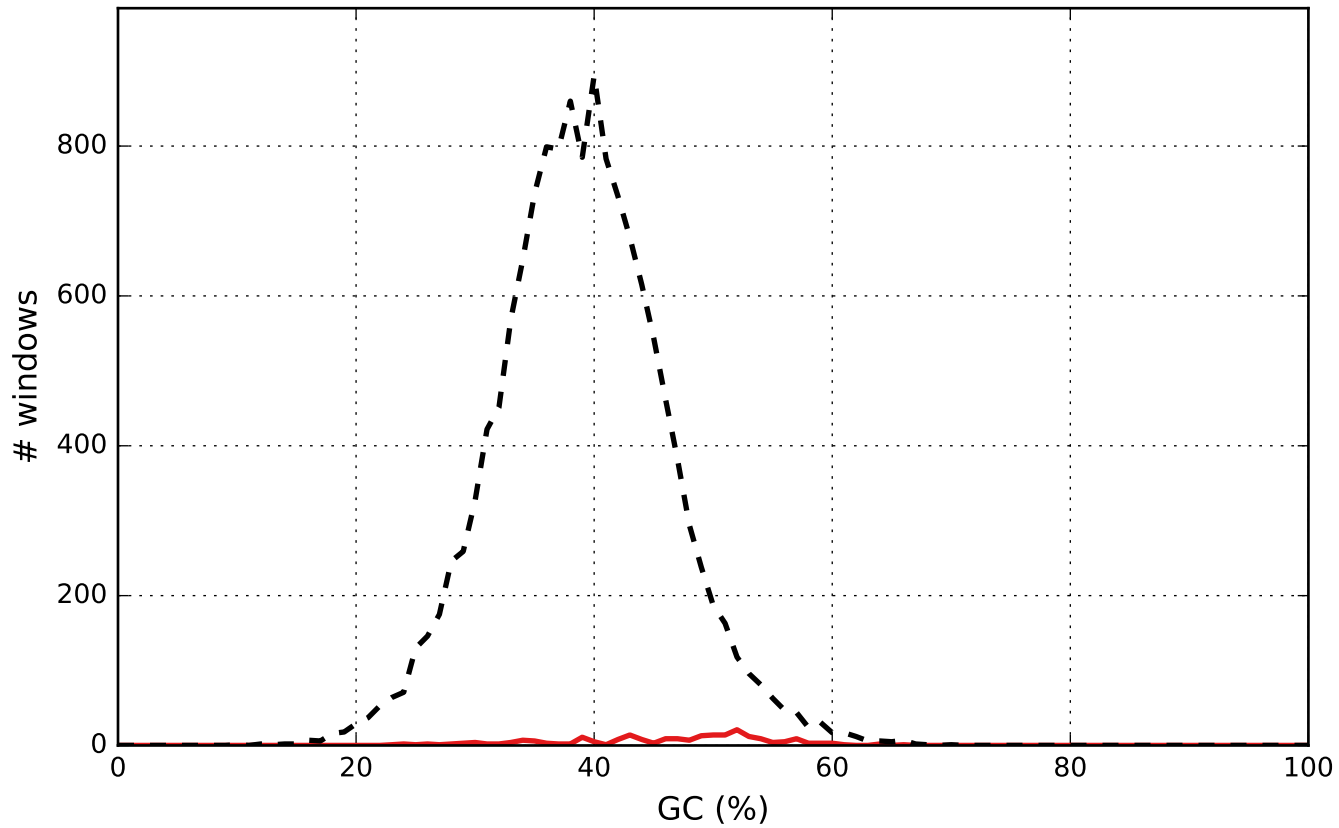
— combined.final.contigs



— combined.final.contigs

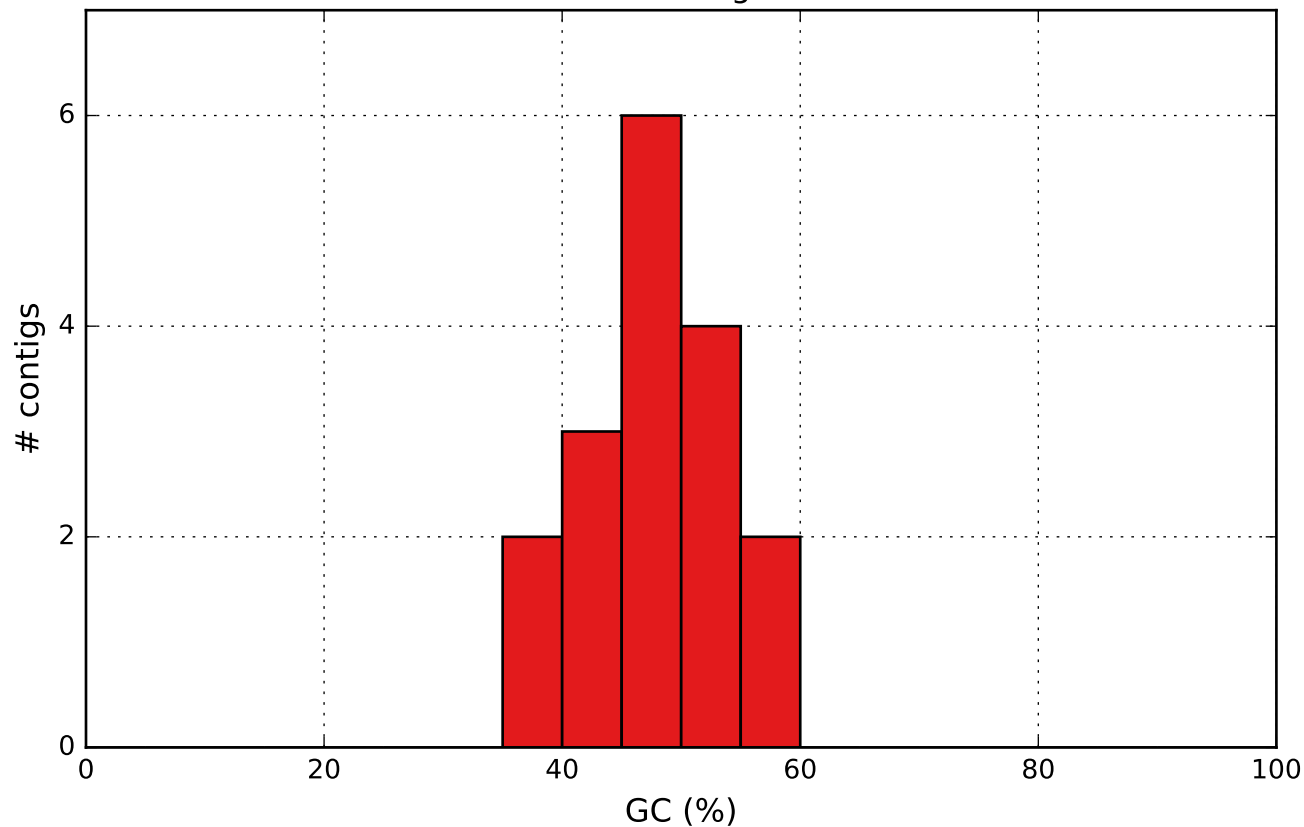



GC content

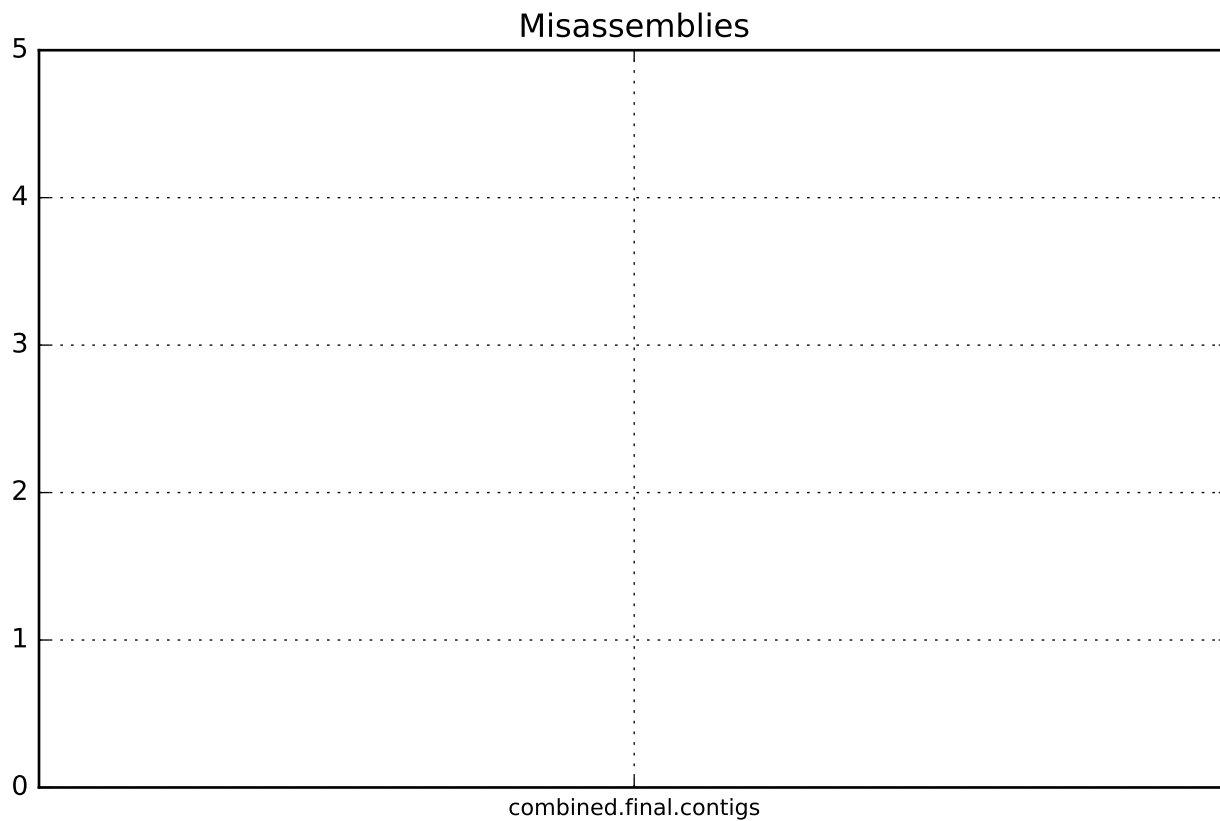


— combined.final.contigs - - Reference

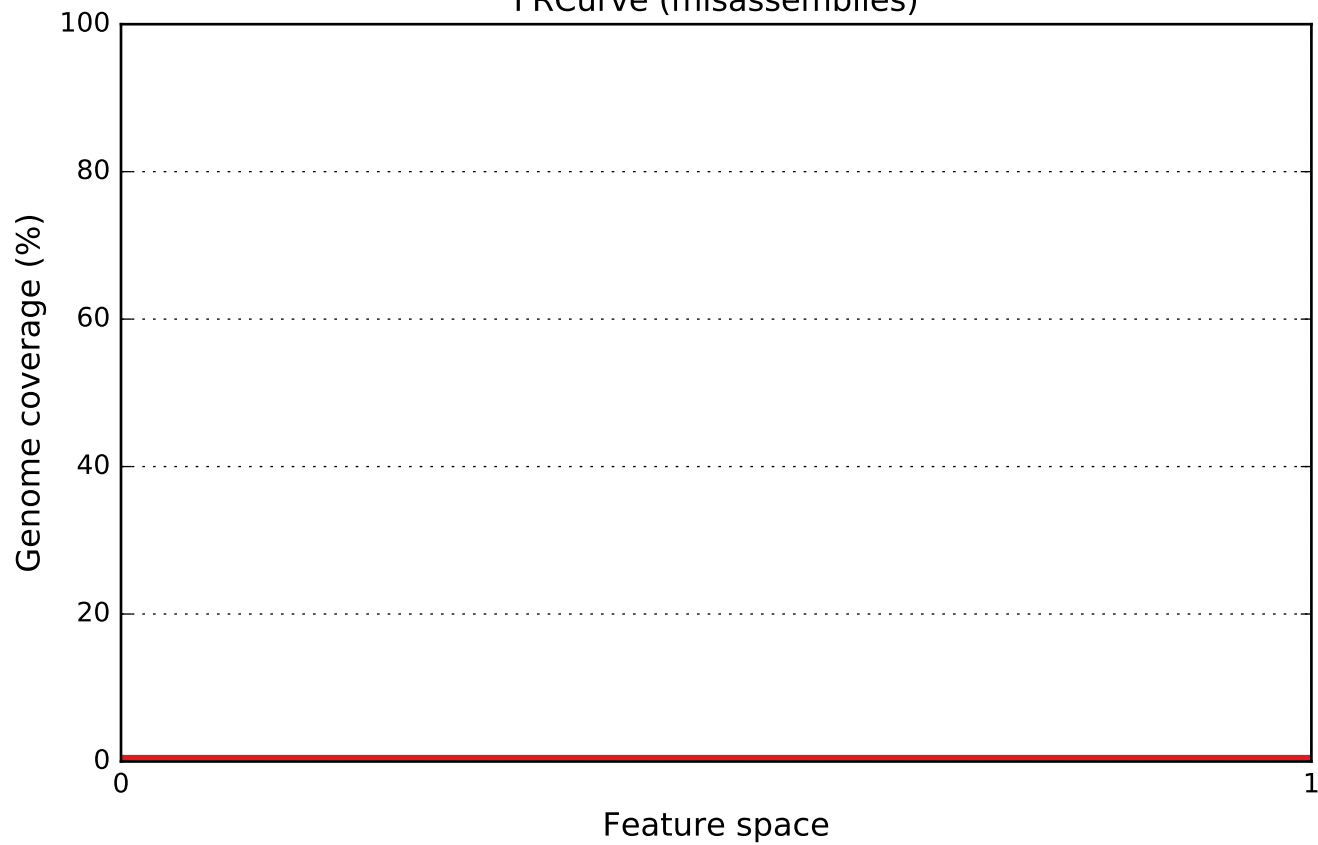
combined.final.contigs GC content



 combined.final.contigs

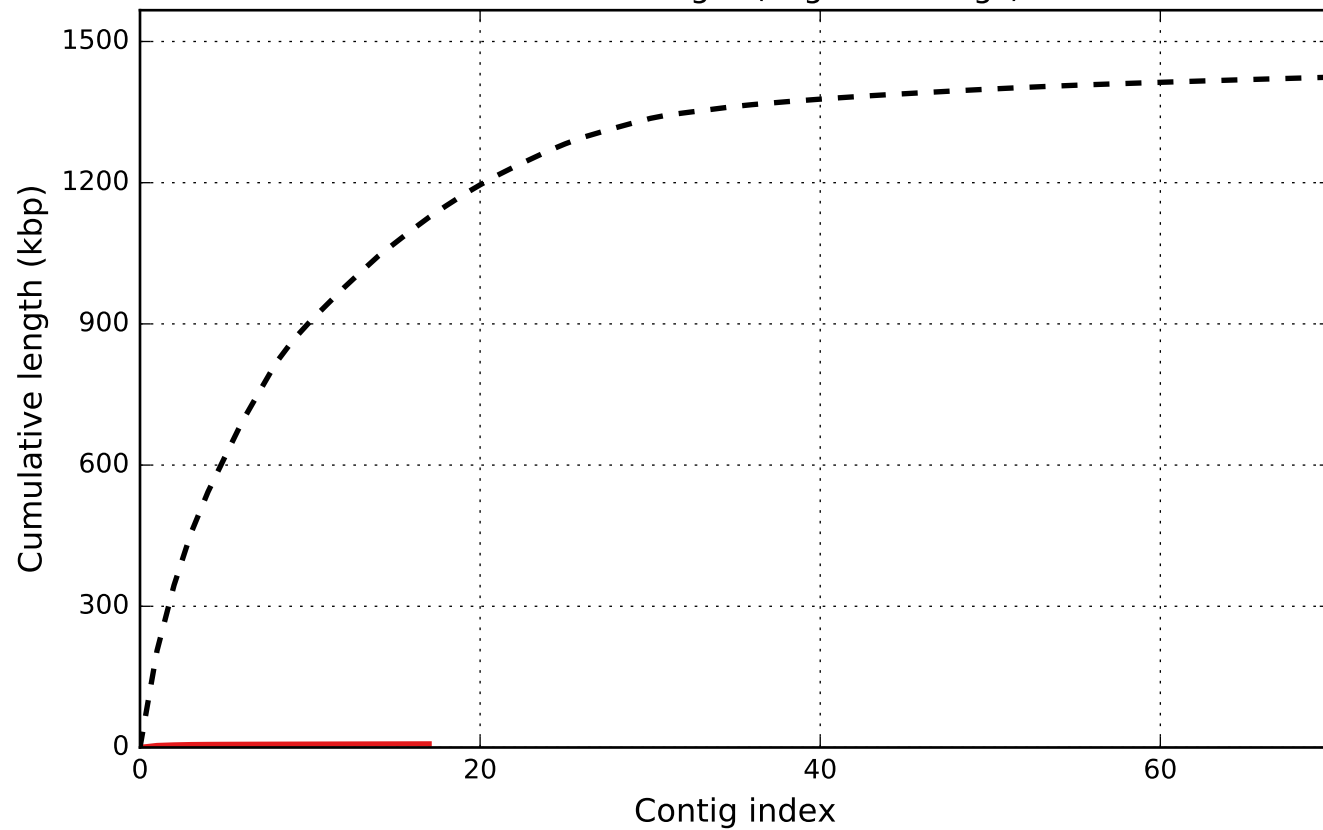


FRCurve (misassemblies)

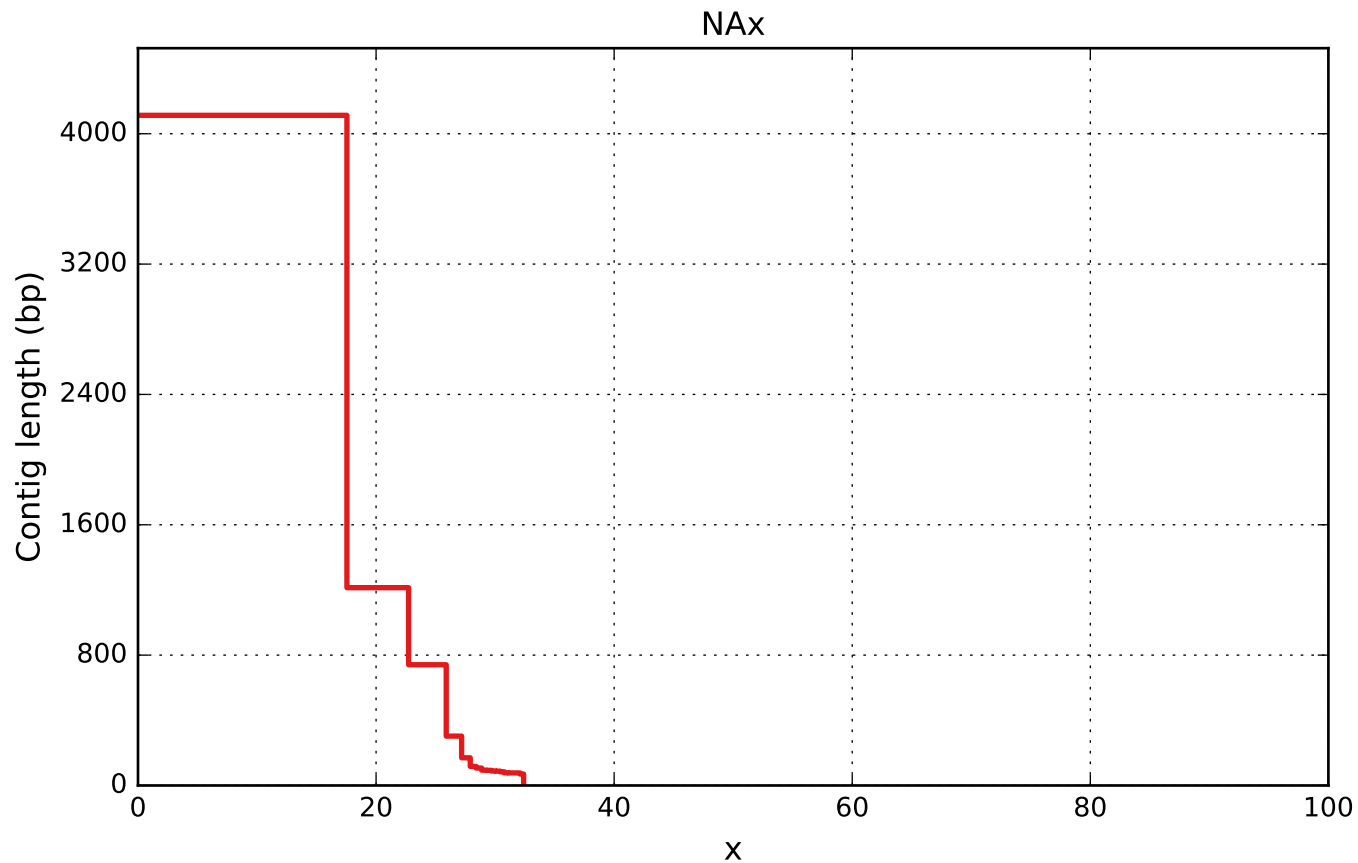


— combined.final.contigs

Cumulative length (aligned contigs)

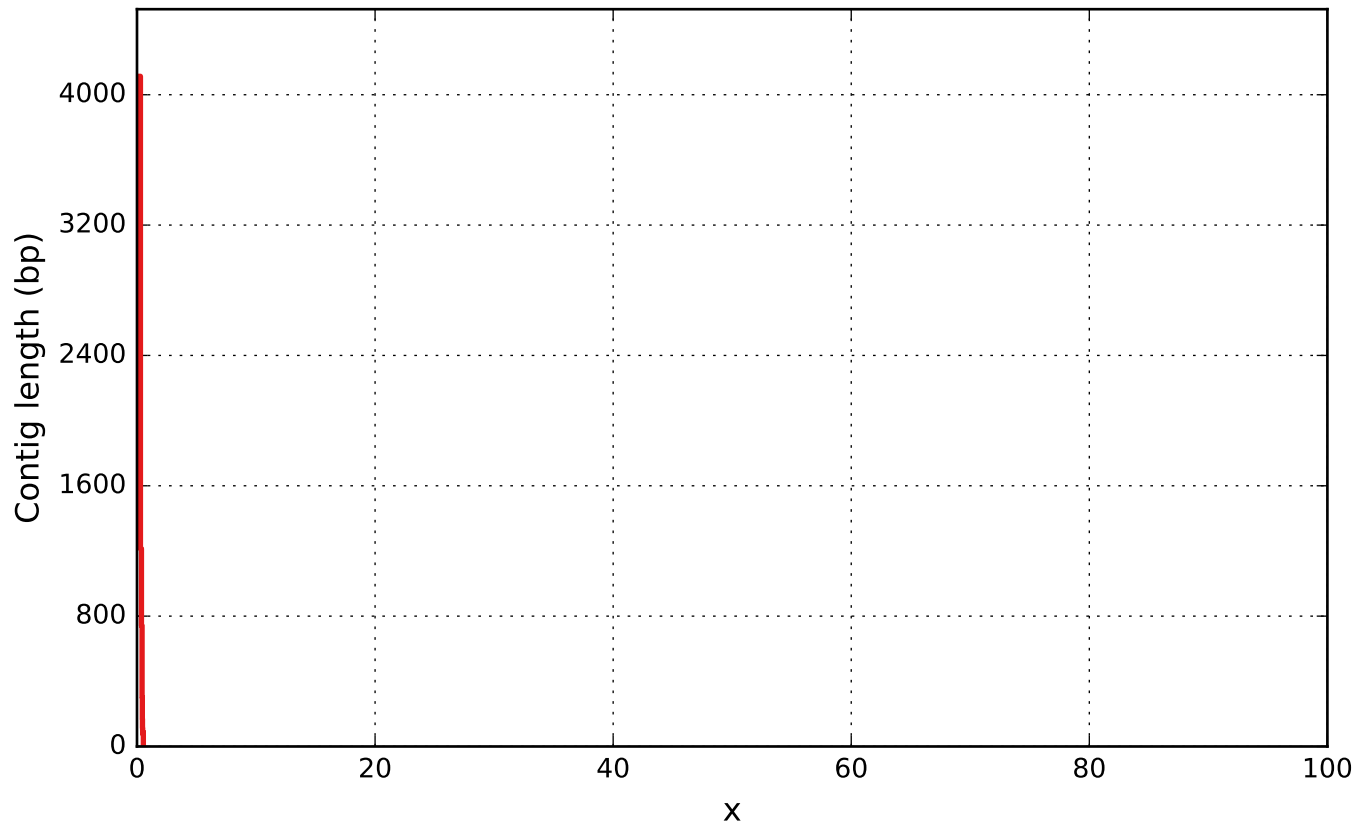


— combined.final.contigs - - Reference



— combined.final.contigs

NGAx



— combined.final.contigs