

Report

	final.contigs
# contigs (≥ 0 bp)	5326
# contigs (≥ 1000 bp)	809
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	3611011
Total length (≥ 1000 bp)	1111056
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	5326
Largest contig	4425
Total length	3611011
Reference length	4641652
GC (%)	50.66
Reference GC (%)	50.79
N50	754
NG50	606
N75	511
NG75	334
L50	1614
LG50	2377
L75	3075
LG75	4912
# misassemblies	6
# misassembled contigs	6
Misassembled contigs length	12815
# local misassemblies	3
# unaligned contigs	2902 + 17 part
Unaligned length	1829198
Genome fraction (%)	38.002
Duplication ratio	1.010
# N's per 100 kbp	0.00
# mismatches per 100 kbp	606.26
# indels per 100 kbp	0.28
Largest alignment	3996
NGA50	-

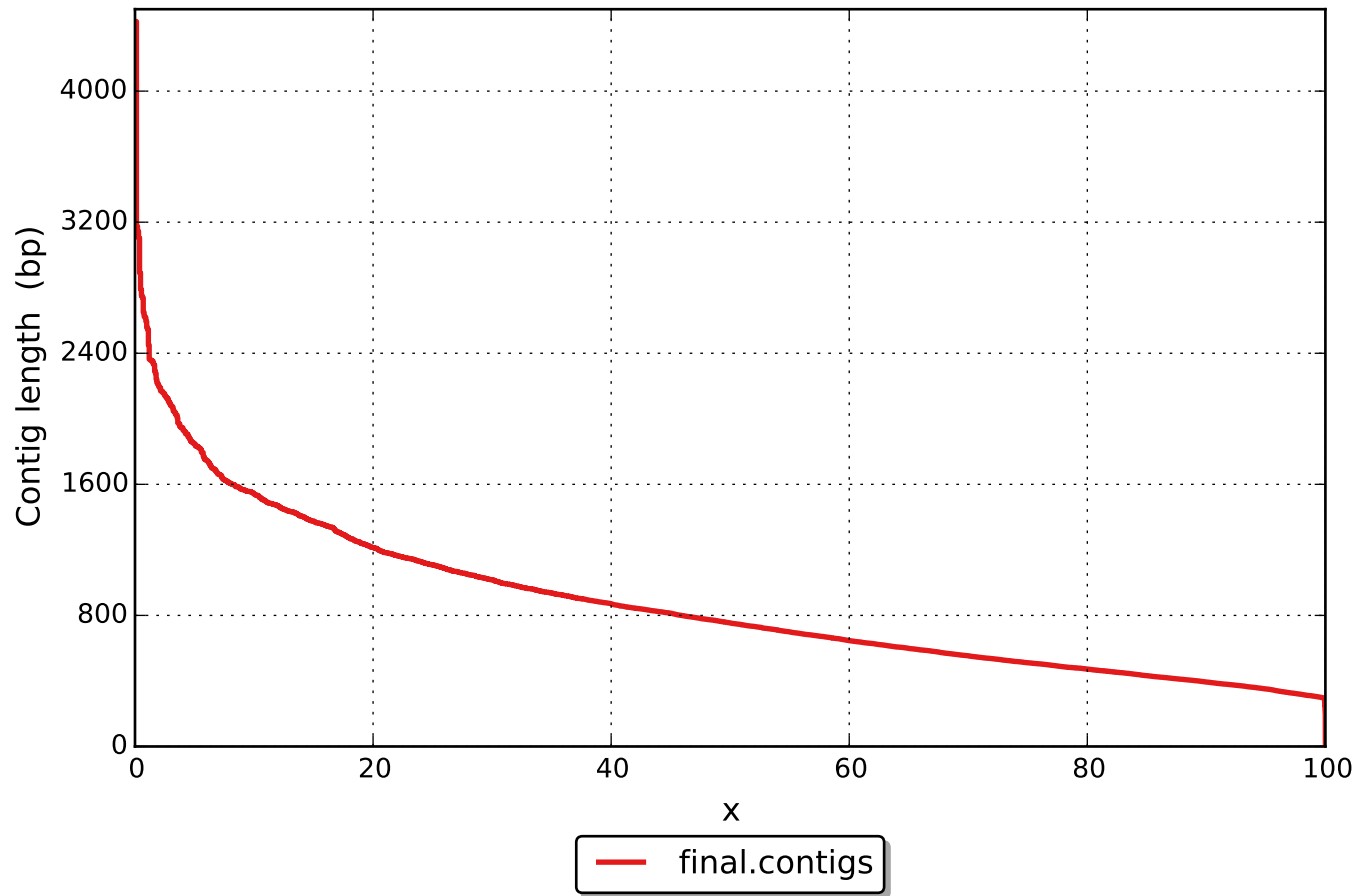
Misassemblies report

	final.contigs
# misassemblies	6
# relocations	6
# translocations	0
# inversions	0
# misassembled contigs	6
Misassembled contigs length	12815
# local misassemblies	3
# mismatches	10694
# indels	5
# short indels	5
# long indels	0
Indels length	5

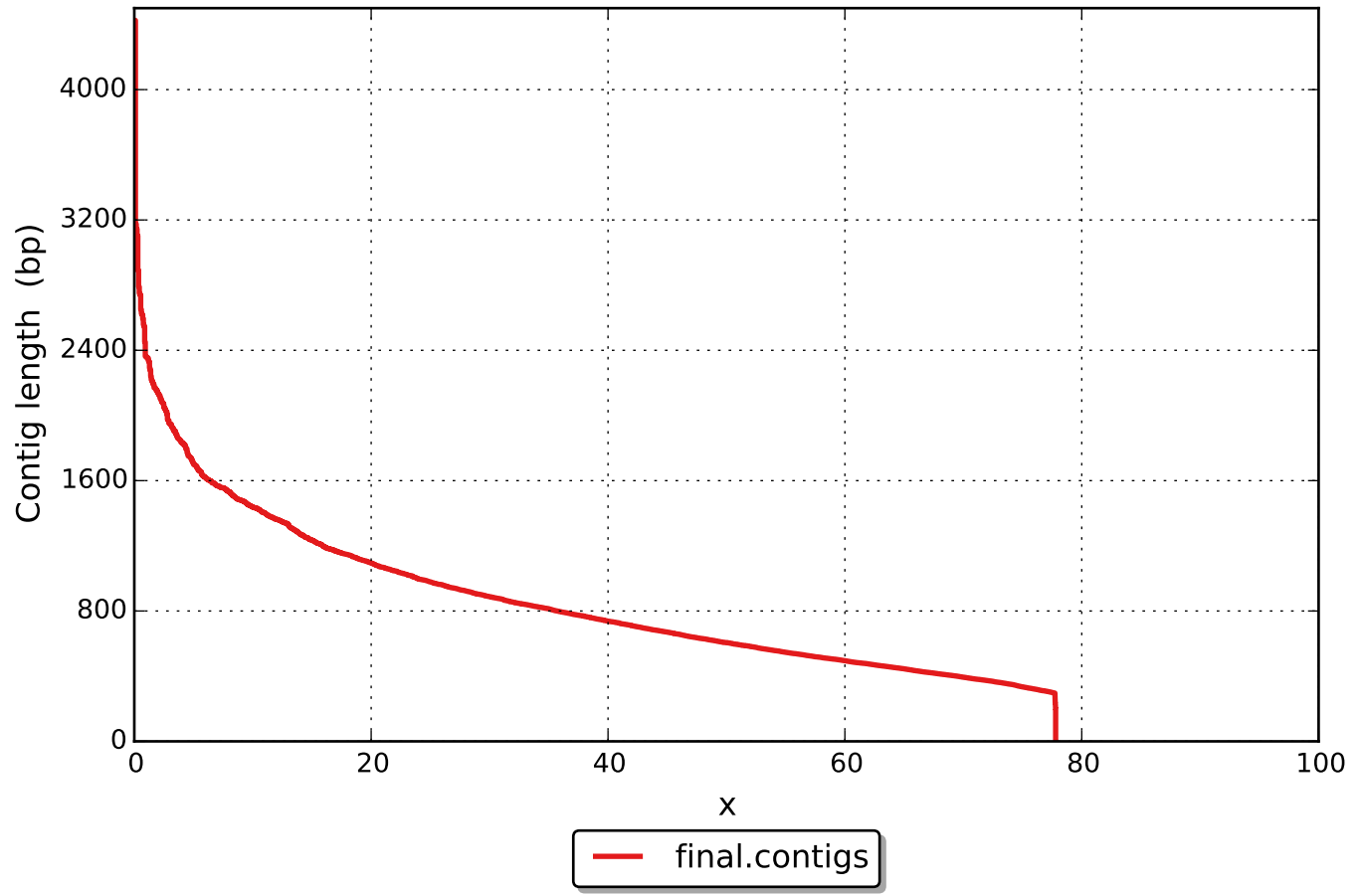
Unaligned report

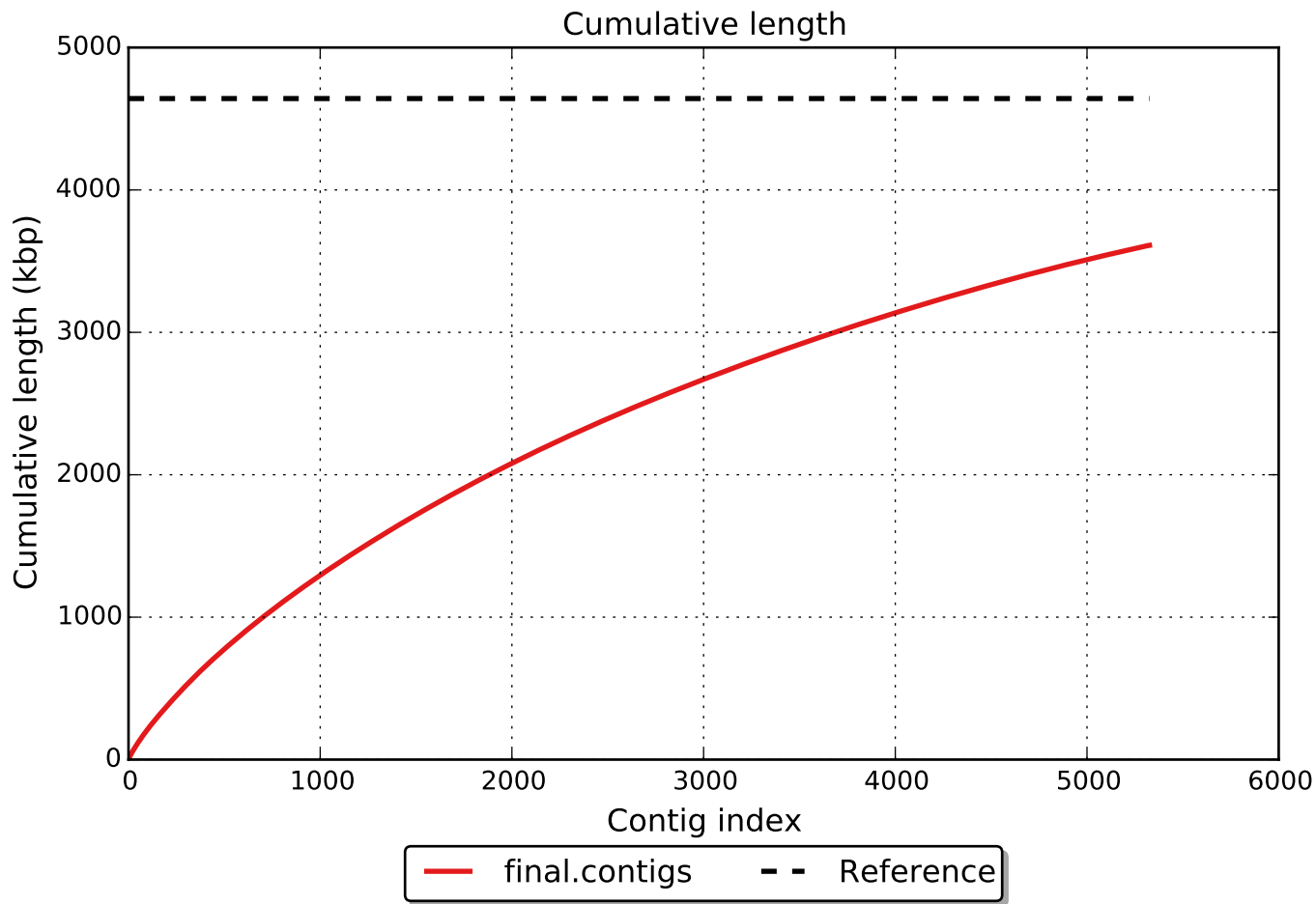
	final.contigs
# fully unaligned contigs	2902
Fully unaligned length	1823645
# partially unaligned contigs	17
# with misassembly	1
# both parts are significant	17
Partially unaligned length	5553
# N's	0

Nx

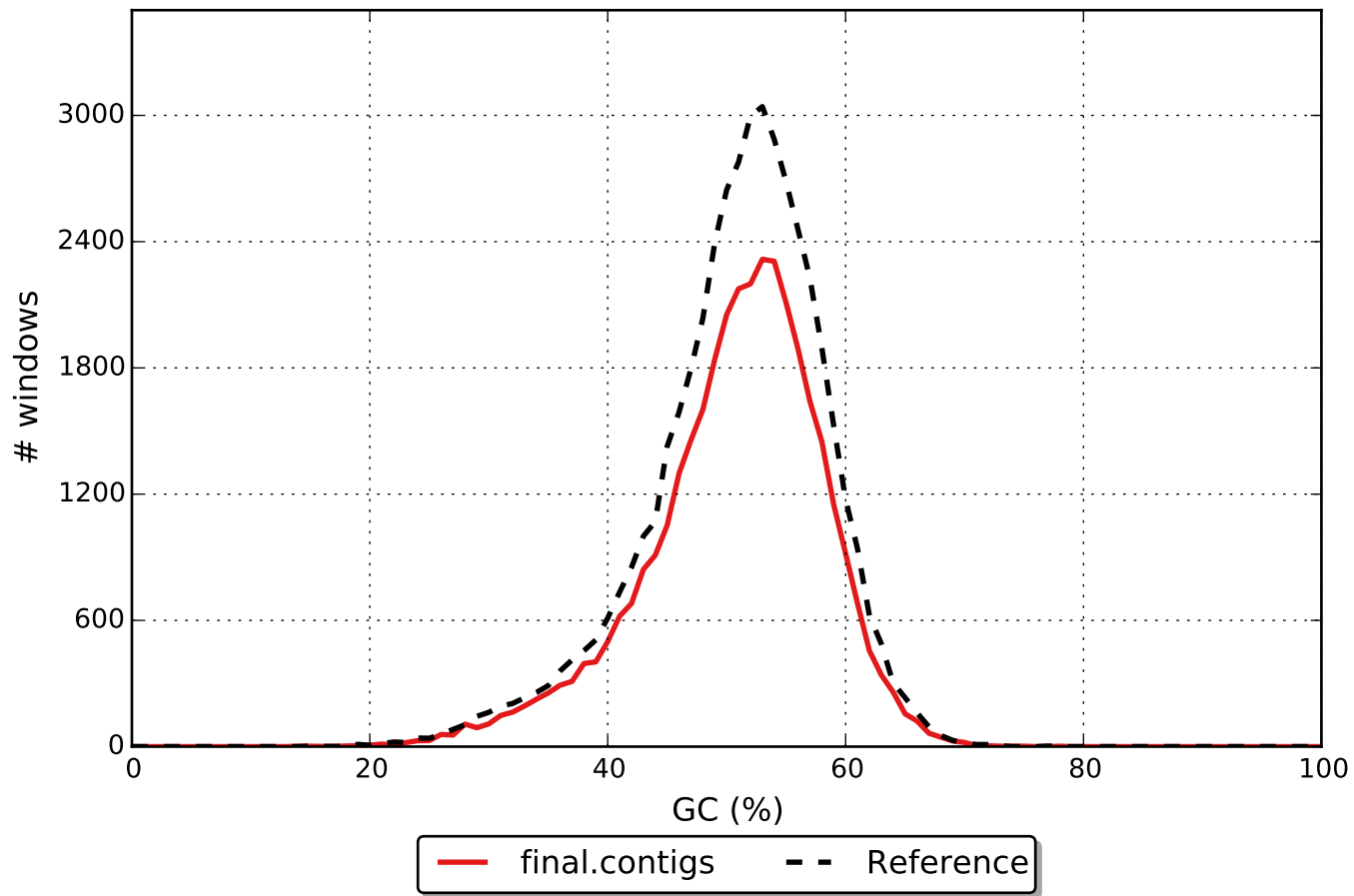


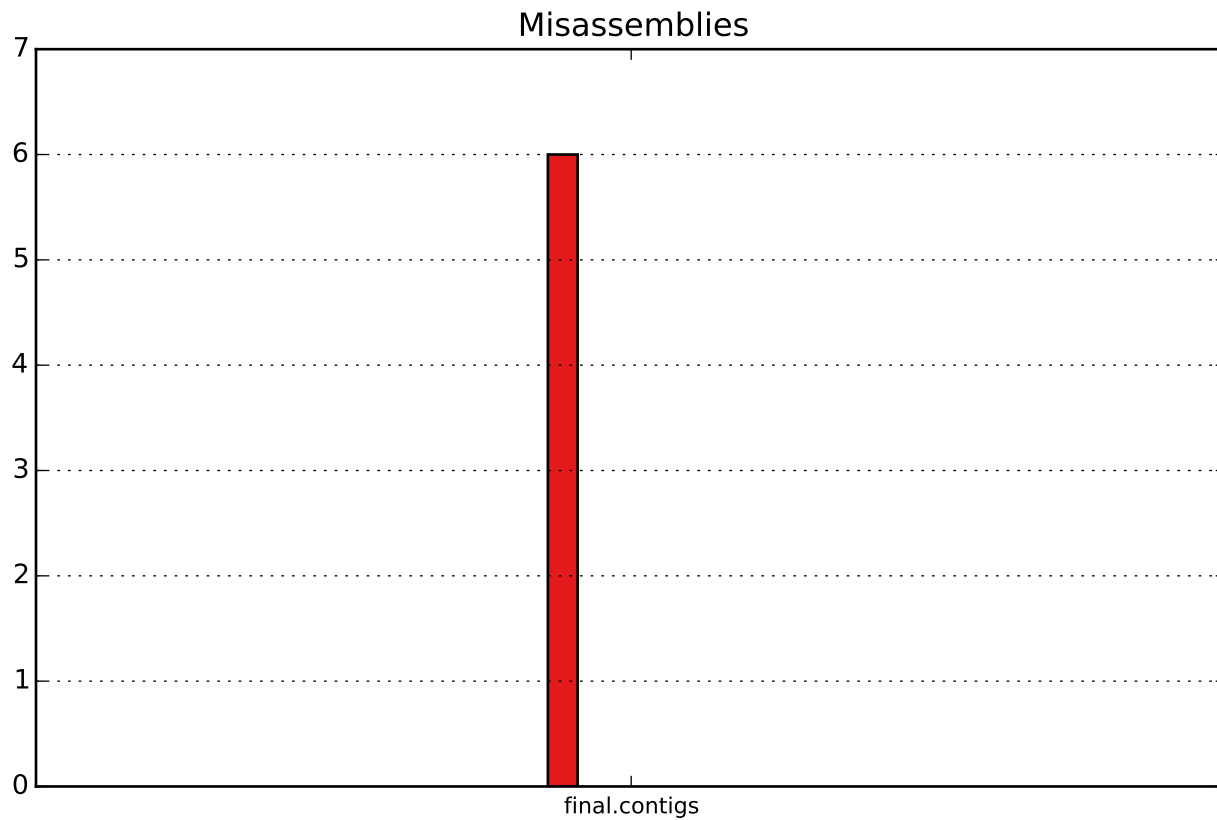
NGx



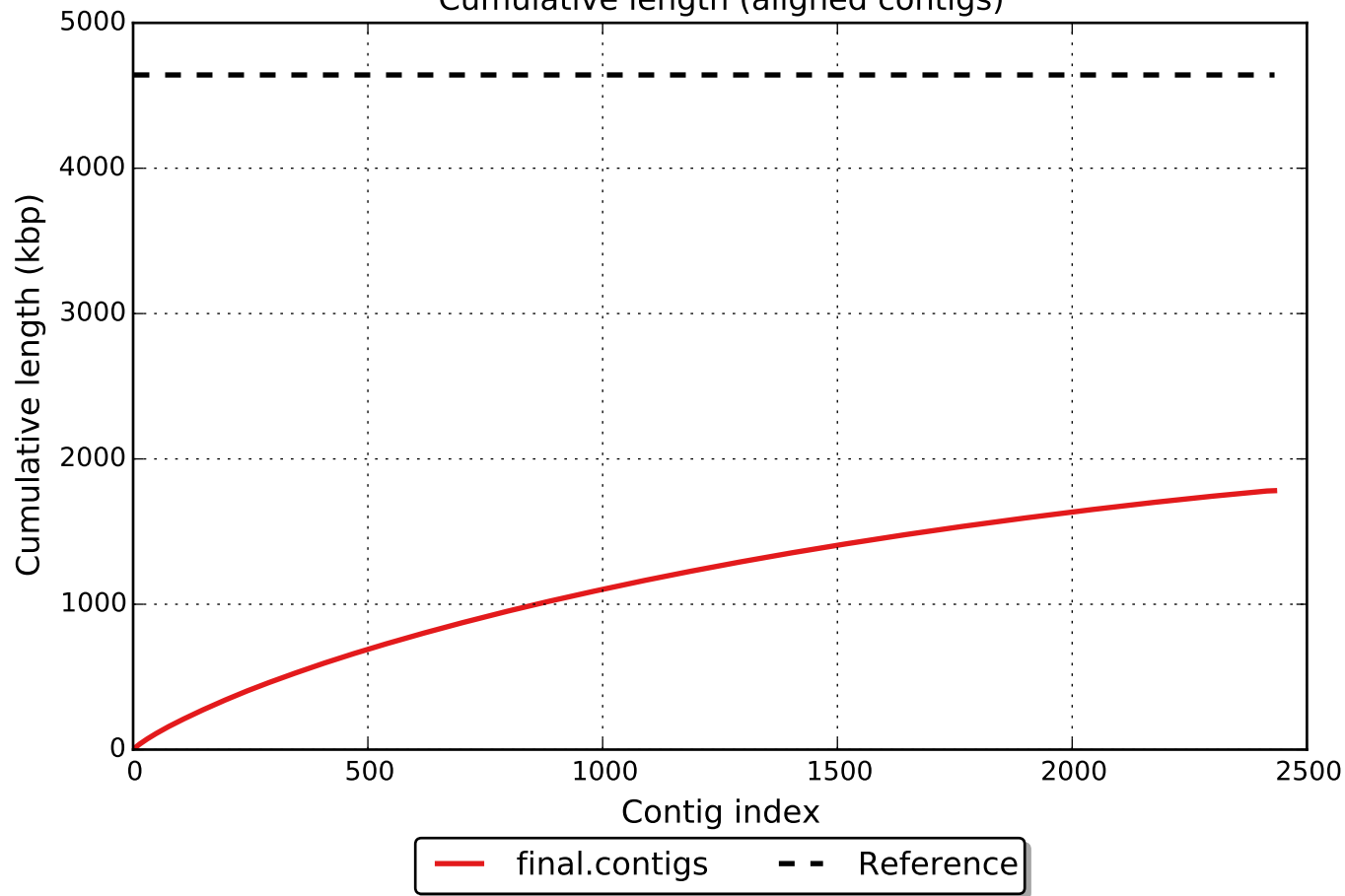


GC content

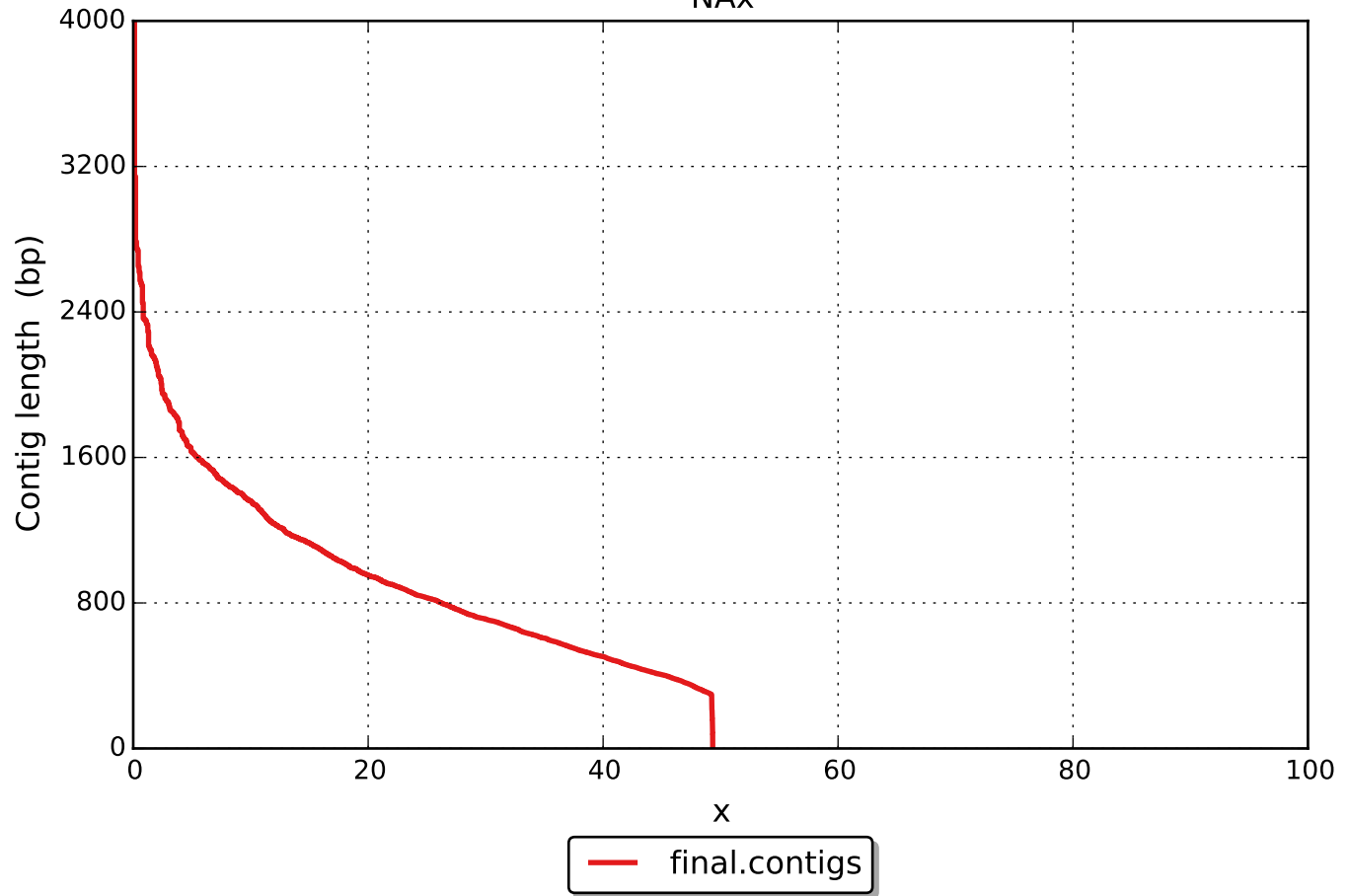




Cumulative length (aligned contigs)



NAx



NGAx

