

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	3543
# contigs ( $\geq 1000$ bp)	293
# contigs ( $\geq 5000$ bp)	0
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	2114137
Total length ( $\geq 1000$ bp)	380096
Total length ( $\geq 5000$ bp)	0
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	1907
Largest contig	3225
Total length	1461390
Reference length	4641652
N50	763
N75	607
L50	701
L75	1241
# misassemblies	8
# misassembled contigs	8
Misassembled contigs length	8370
# local misassemblies	0
# unaligned contigs	1 + 5 part
Unaligned length	899
Genome fraction (▼)	31.440
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	218.87
# indels per 100 kbp	10.35
Largest alignment	3225
NA50	761
NA75	606
LA50	702
LA75	1244

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).

## Misassemblies report

	final.contigs
# misassemblies	8
# relocations	8
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	8
Misassembled contigs length	8370
# local misassemblies	0
# mismatches	3194
# indels	151
# short indels	147
# long indels	4
Indels length	357

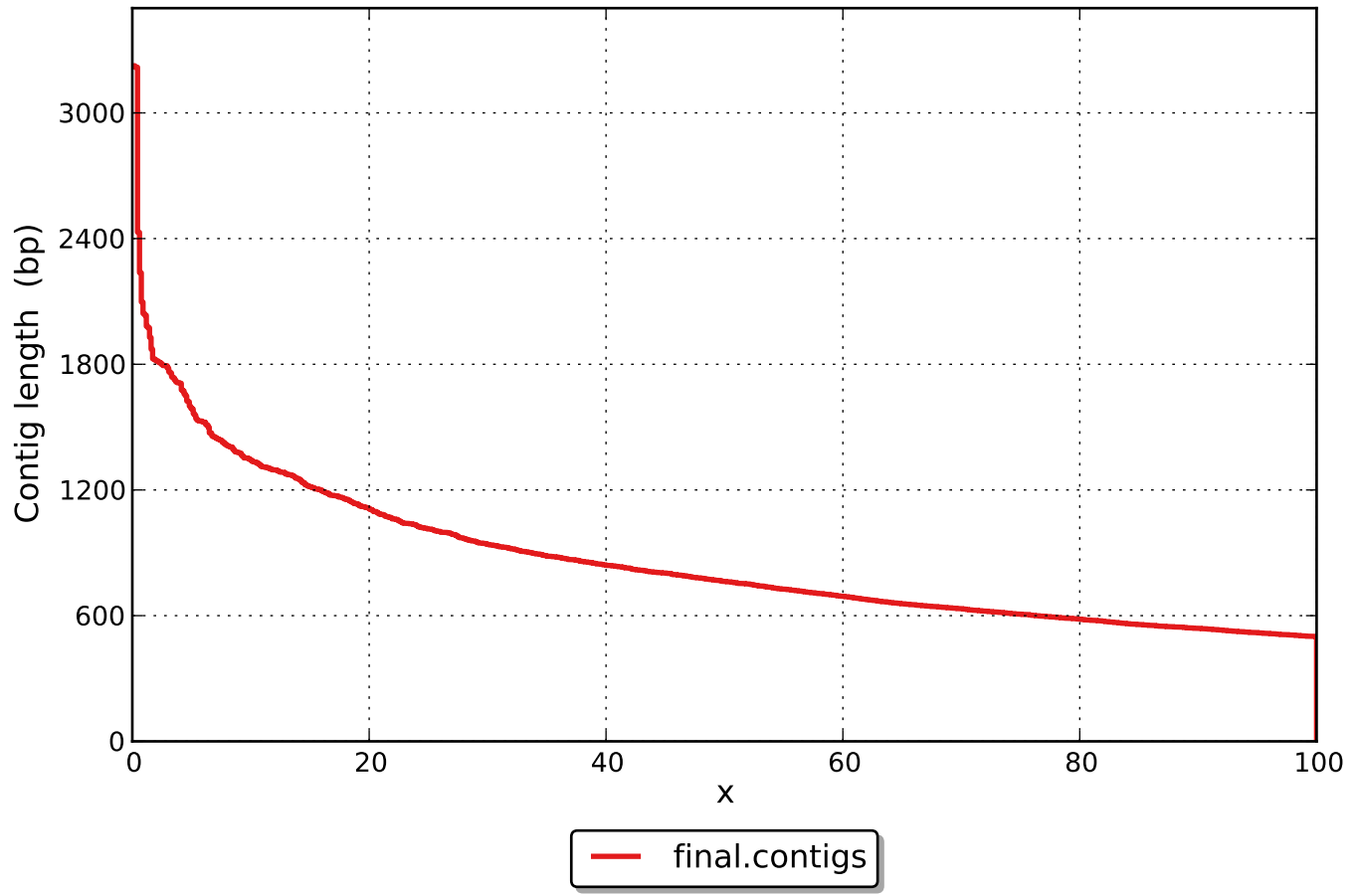
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

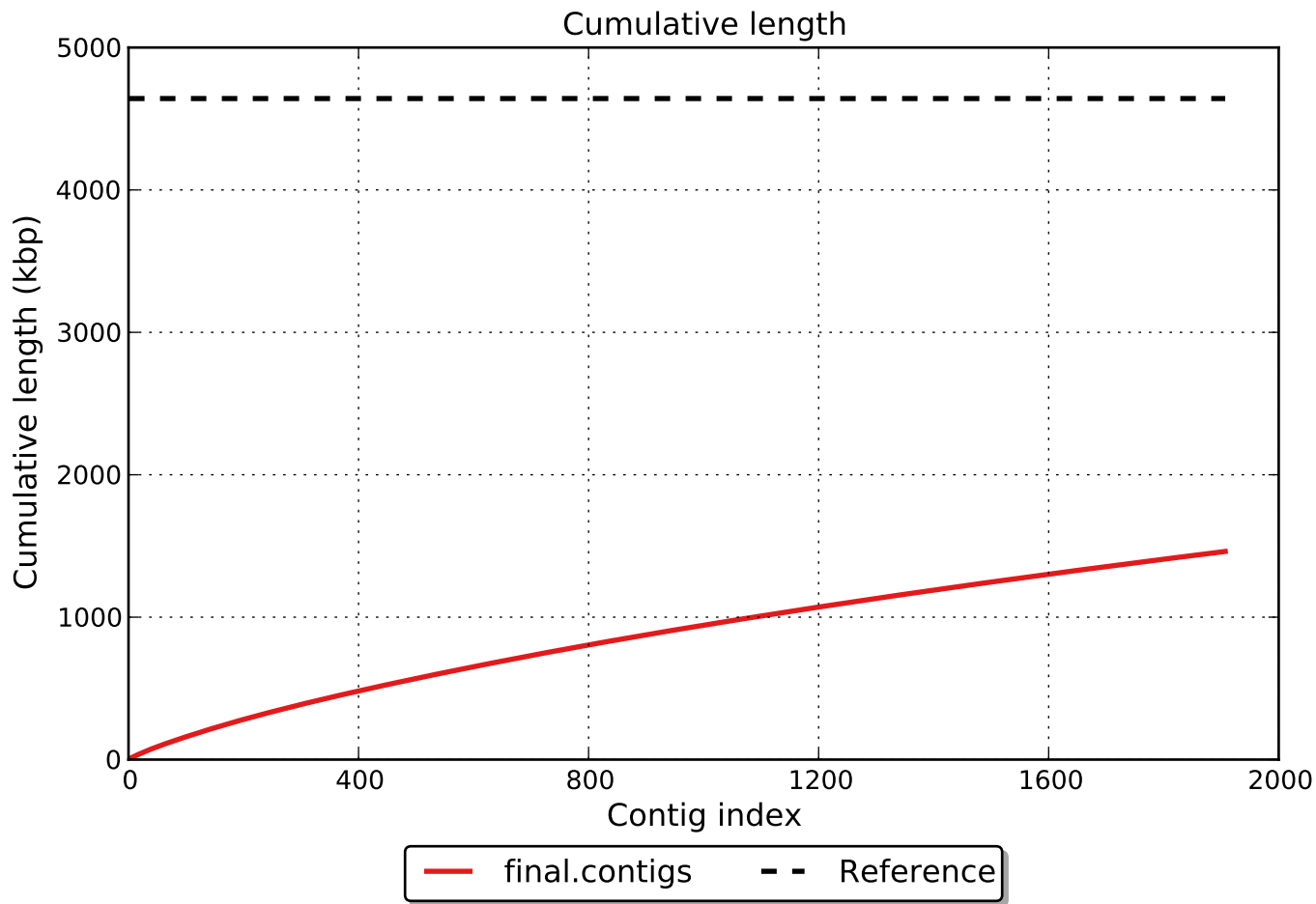
## Unaligned report

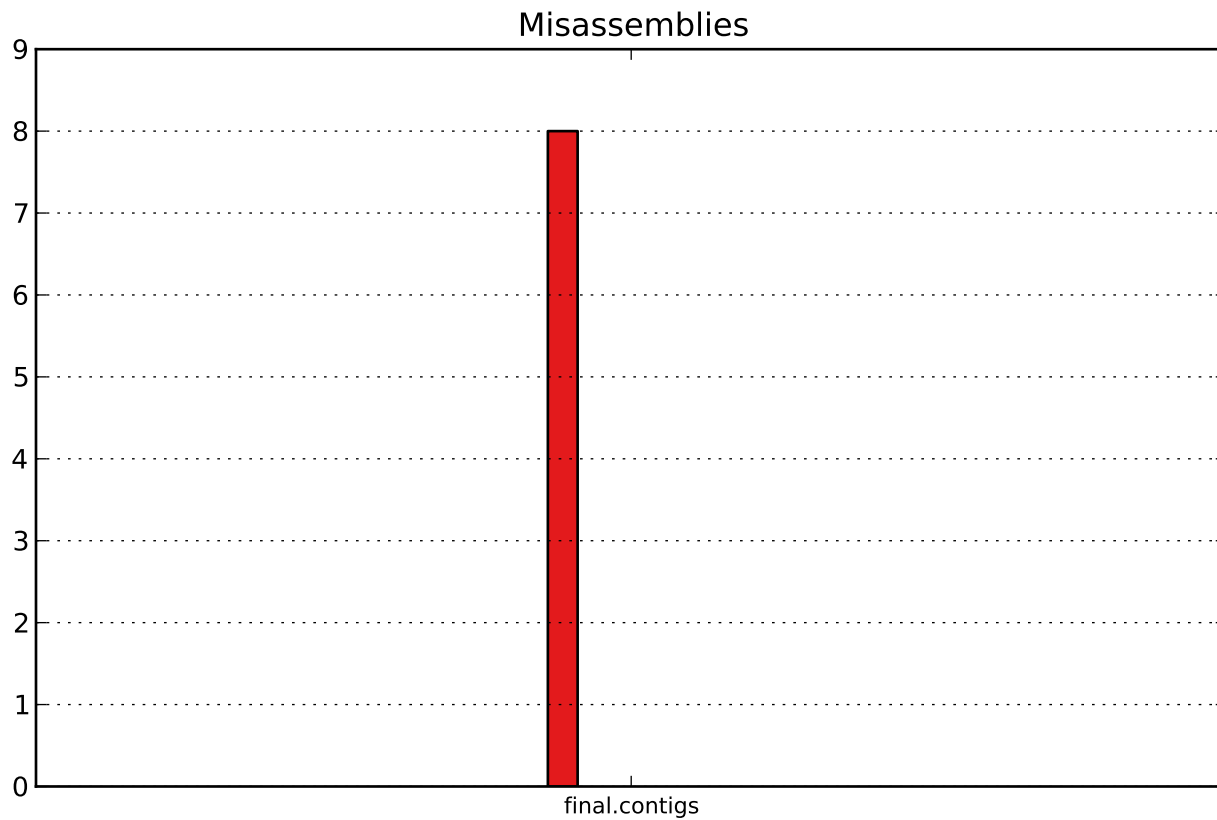
	final.contigs
# fully unaligned contigs	1
Fully unaligned length	626
# partially unaligned contigs	5
# with misassembly	0
# both parts are significant	0
Partially unaligned length	273
# N's	0

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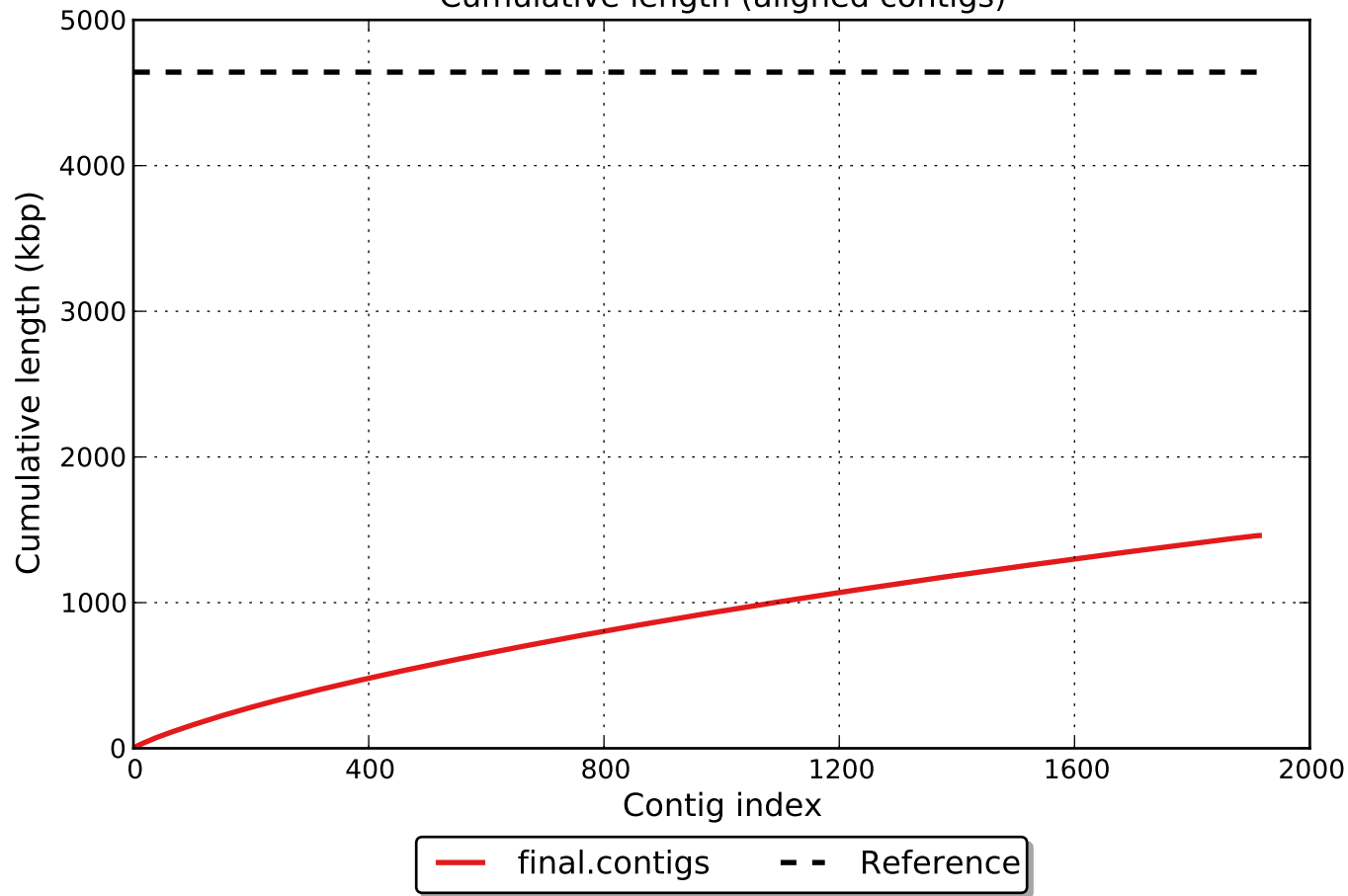
Nx







Cumulative length (aligned contigs)



NAx

