

# Report

	contigs
# contigs ( $\geq 0$ bp)	319
# contigs ( $\geq 1000$ bp)	136
# contigs ( $\geq 5000$ bp)	104
# contigs ( $\geq 10000$ bp)	81
# contigs ( $\geq 25000$ bp)	53
# contigs ( $\geq 50000$ bp)	37
Total length ( $\geq 0$ bp)	4606247
Total length ( $\geq 1000$ bp)	4564721
Total length ( $\geq 5000$ bp)	4480098
Total length ( $\geq 10000$ bp)	4313499
Total length ( $\geq 25000$ bp)	3884378
Total length ( $\geq 50000$ bp)	3352307
# contigs	144
Largest contig	264572
Total length	4570595
Reference length	9283304
N50	76208
N75	43808
L50	20
L75	39
# misassemblies	5
# misassembled contigs	5
Misassembled contigs length	310368
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	49.202
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	539.71
# indels per 100 kbp	0.46
Largest alignment	264572
NA50	76208
NA75	41603
LA50	20
LA75	40

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

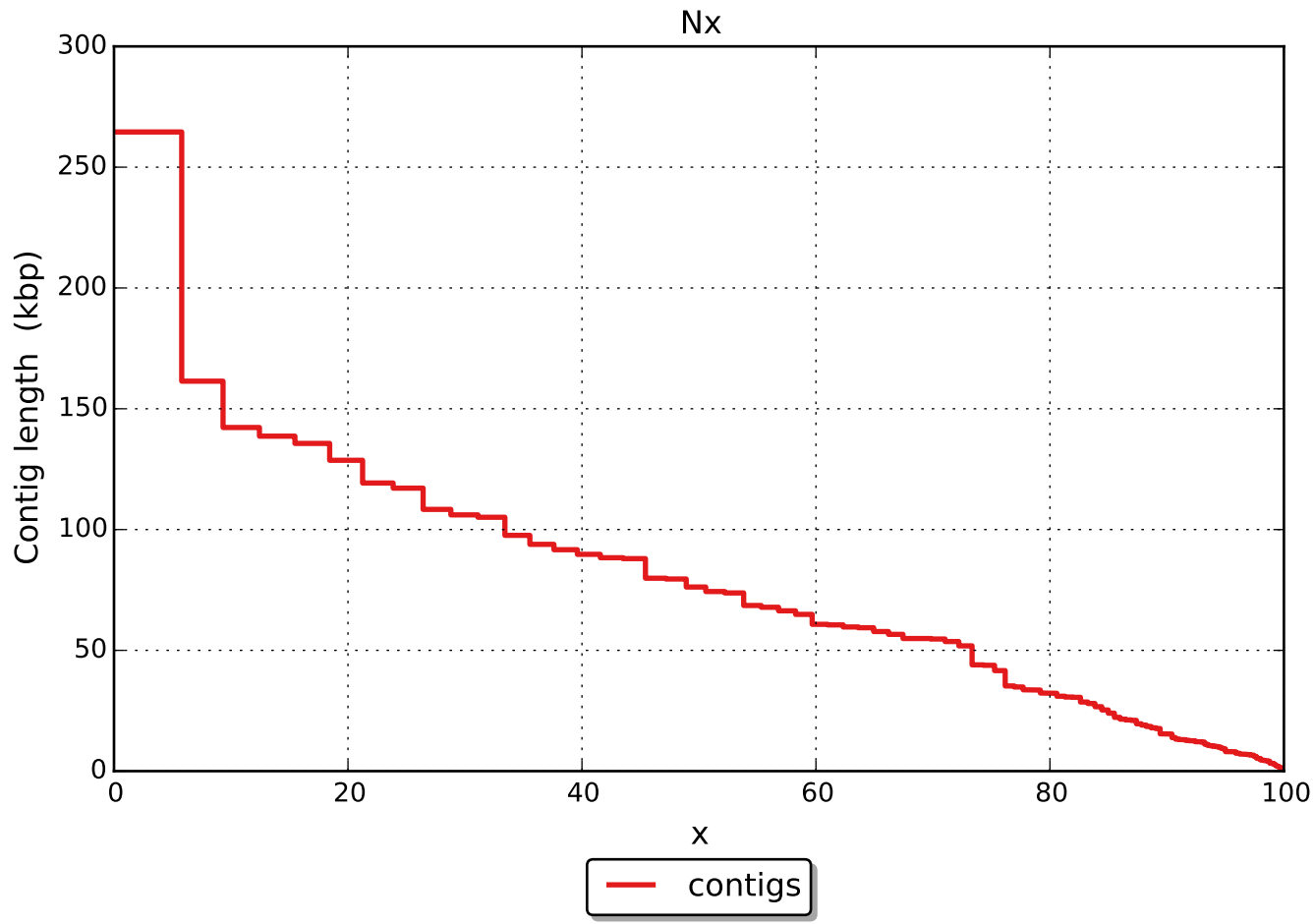
	contigs
# misassemblies	5
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	4
# possibly misassembled contigs	0
# misassembled contigs	5
Misassembled contigs length	310368
# local misassemblies	3
# mismatches	24652
# indels	21
# short indels	21
# long indels	0
Indels length	28

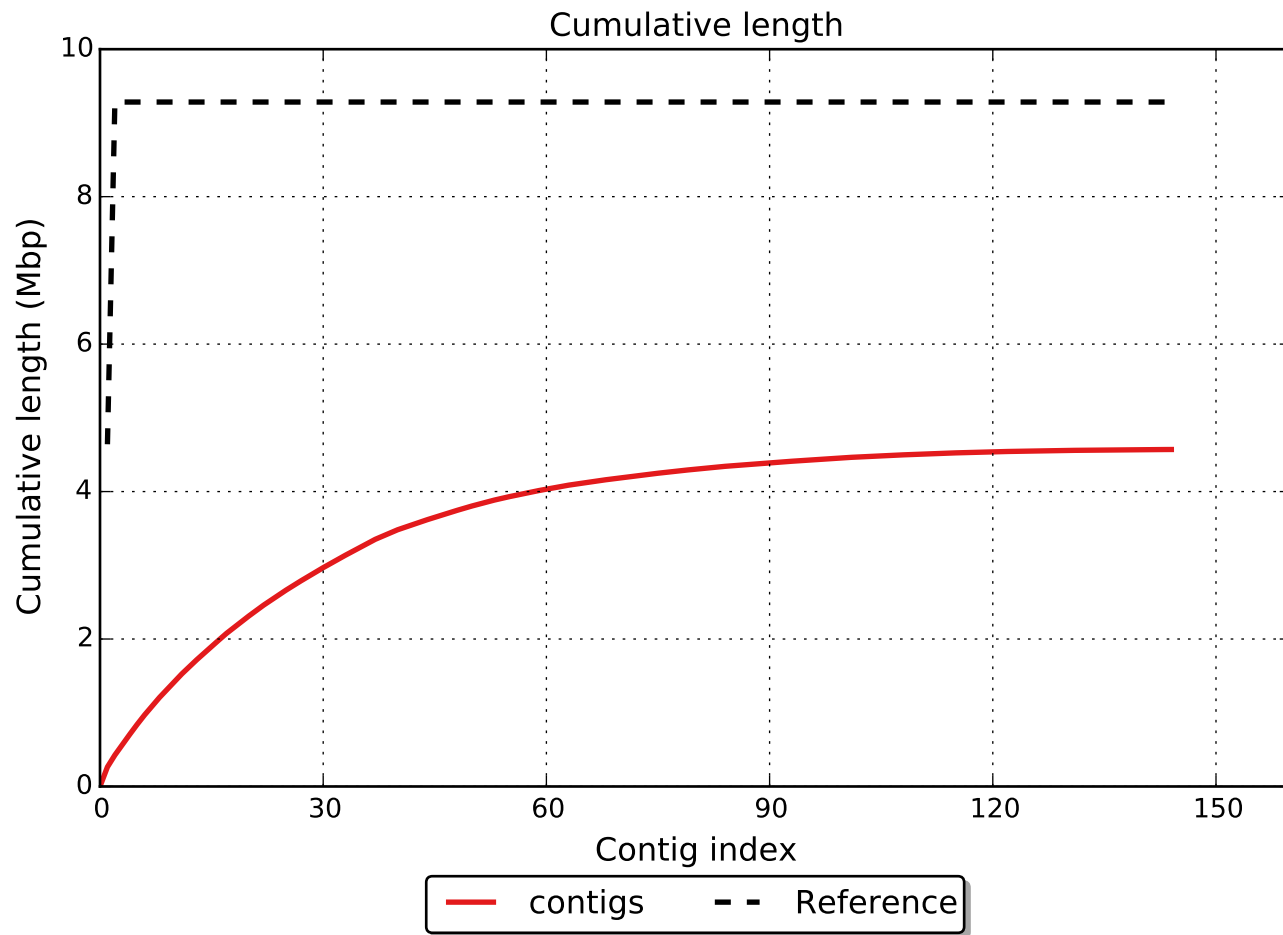
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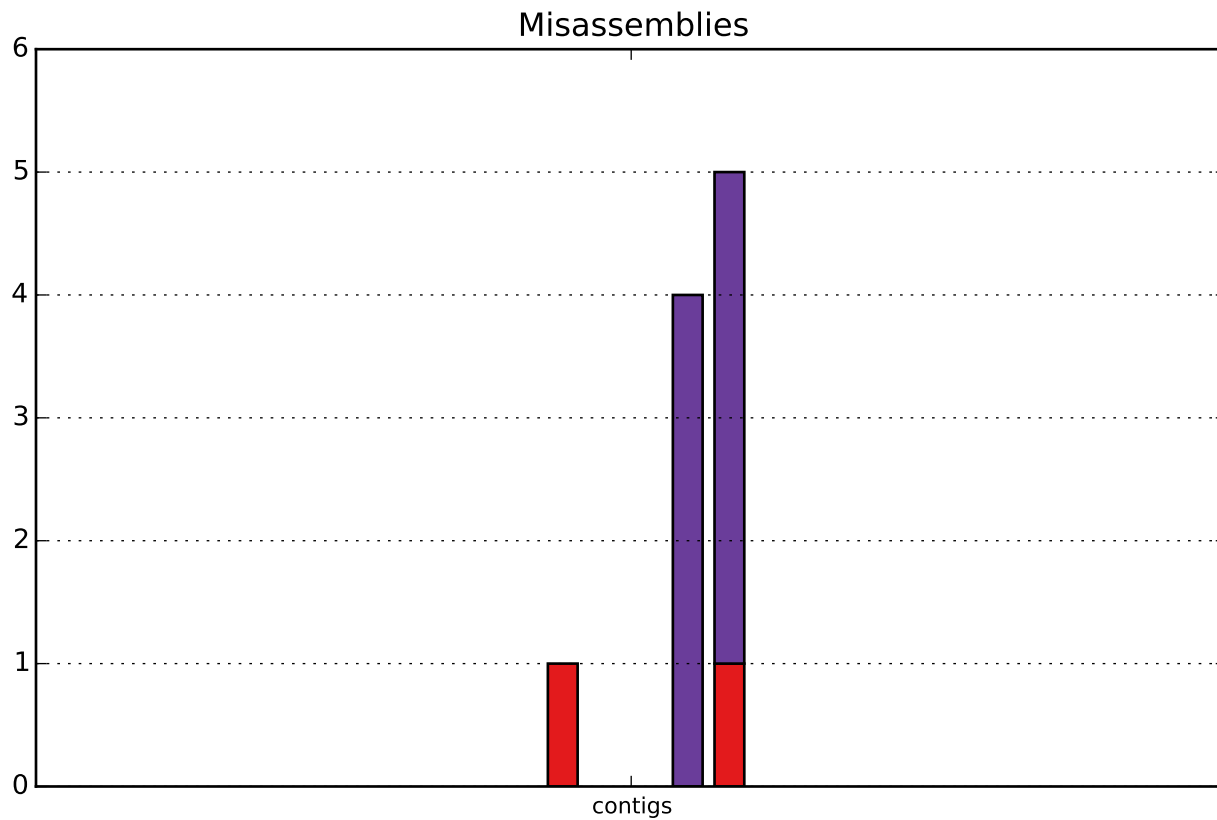
## Unaligned report

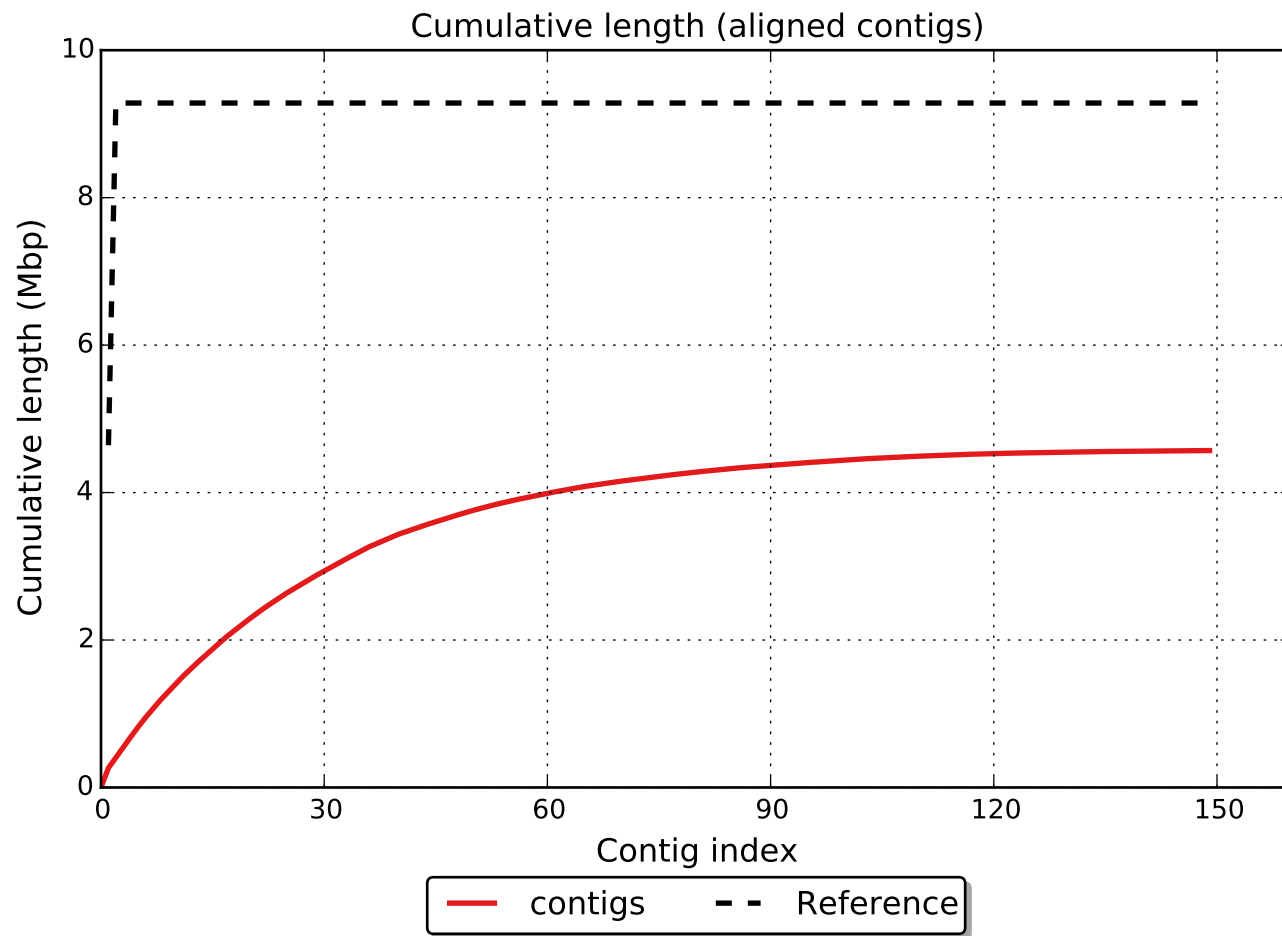
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).









NAx

