

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	14516
# contigs ( $\geq 1000$ bp)	3305
Total length ( $\geq 0$ bp)	10906907
Total length ( $\geq 1000$ bp)	4828390
# contigs	9297
Largest contig	4582
Total length	9059430
Reference length	11094646
GC (%)	50.38
Reference GC (%)	50.48
N50	1044
NG50	899
N75	742
NG75	579
L50	3013
LG50	4065
L75	5595
LG75	7925
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2463
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	81.736
Duplication ratio	1.059
# N's per 100 kbp	0.00
# mismatches per 100 kbp	146.81
# indels per 100 kbp	0.39
Largest alignment	4582
NA50	1044
NGA50	899
NA75	742
NGA75	579
LA50	3014
LGA50	4066
LA75	5596
LGA75	7926

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

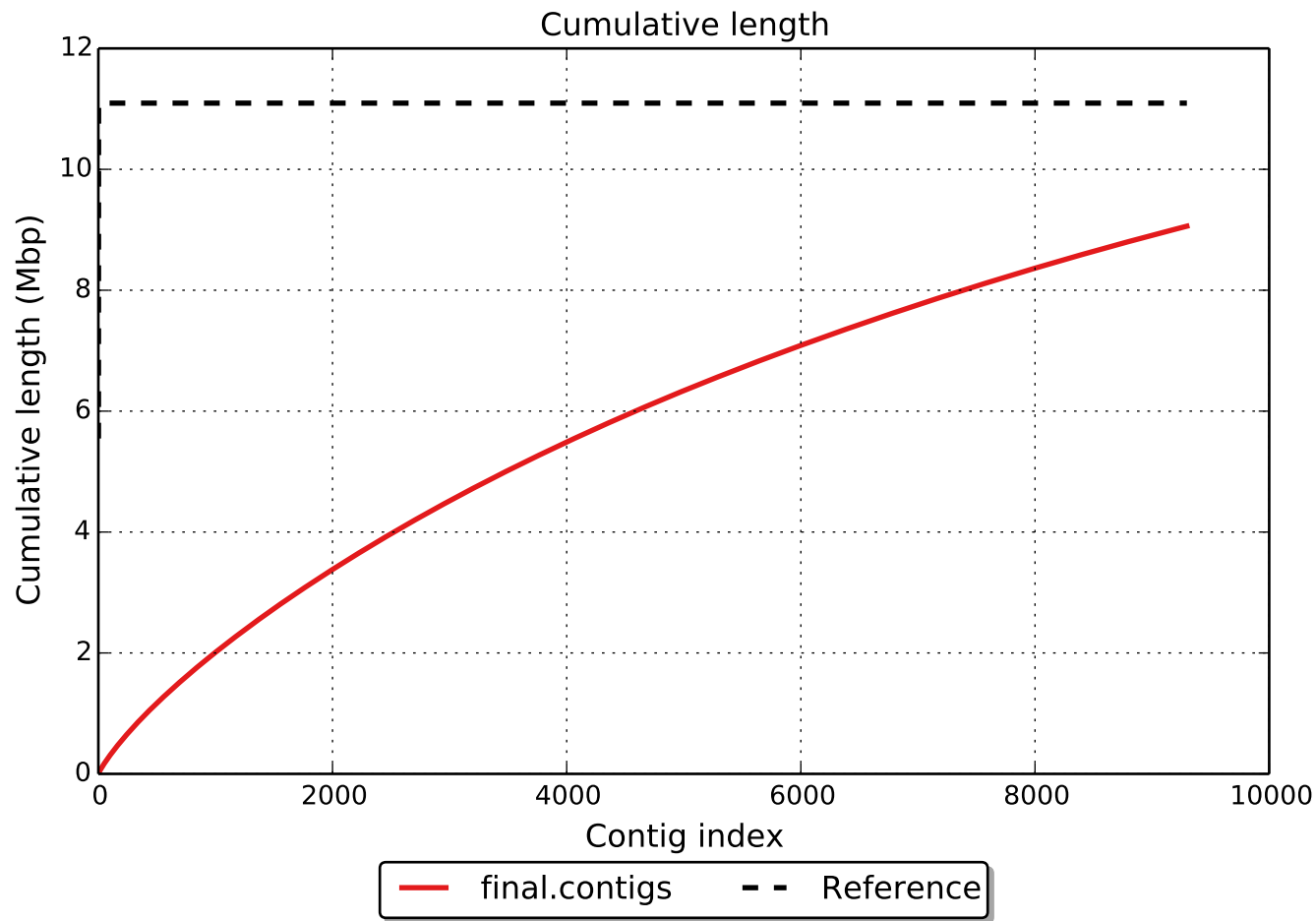
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	2463
# local misassemblies	1
# mismatches	13313
# indels	35
# short indels	35
# long indels	0
Indels length	36

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## Unaligned report

	final.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

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GC content

