## Report

Г	final.contigs
# contigs (>= 0 bp)	1855
# contigs (>= 1000 bp)	1172
# contigs (>= 5000 bp)	657
# contigs (>= 10000 bp)	313
# contigs (>= 25000 bp)	35
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	9481088
Total length (>= 1000 bp)	9209664
Total length (>= 5000 bp)	7805100
Total length (>= 10000 bp)	5335038
Total length (>= 25000 bp)	1077390
Total length (>= 50000 bp)	51384
# contigs	1287
Largest contig	51384
Total length	9296959
Reference length	9283304
N50	11772
N75	6689
L50	250
L75	514
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	29999
# local misassemblies	2
# unaligned contigs	0 + 1 part
Unaligned length	138
Genome fraction (%)	98.827
Duplication ratio	1.013
# N's per 100 kbp	0.00
# mismatches per 100 kbp	18.77
# indels per 100 kbp	0.04
Largest alignment	51384
NA50	11772
NA75	6689
LA50	250
LA75	514
	-

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

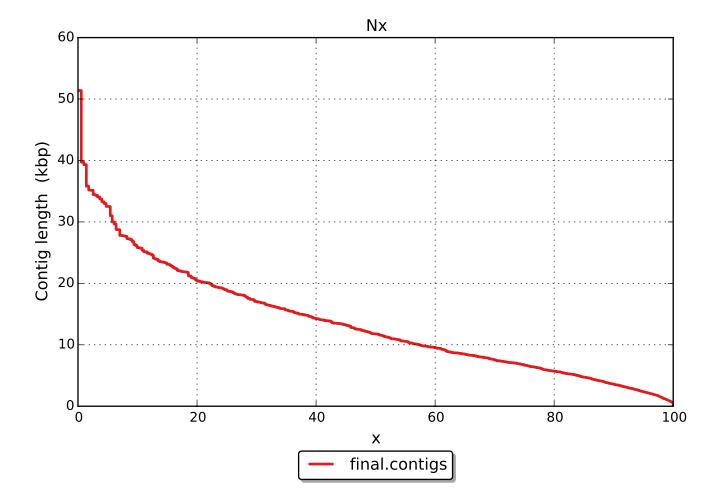
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	29999
# local misassemblies	2
# mismatches	1722
# indels	4
# short indels	4
# long indels	0
Indels length	4

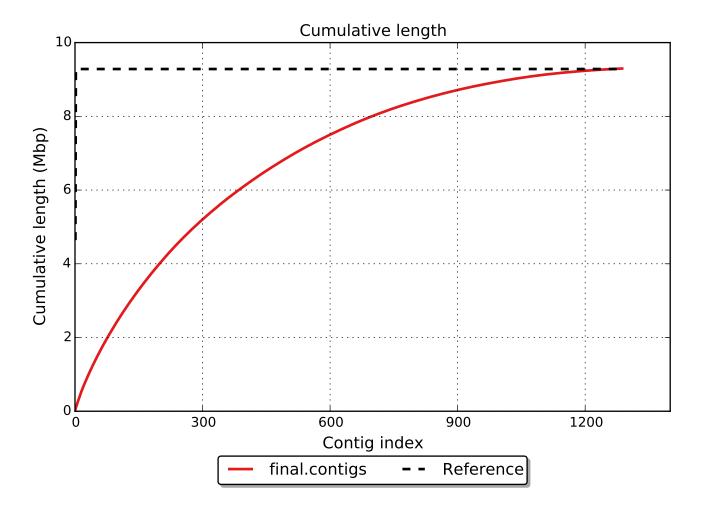
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

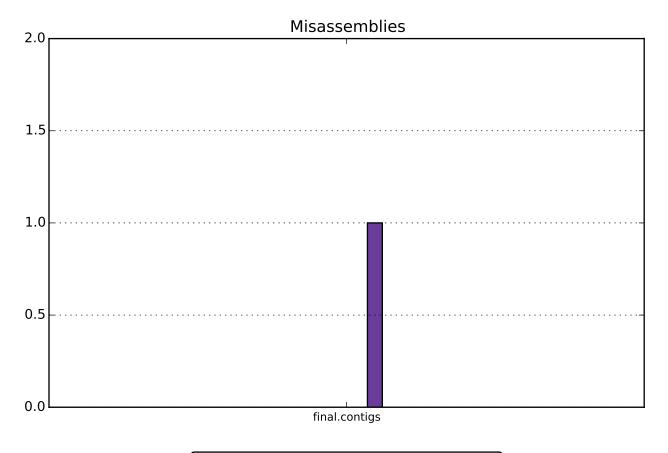
## Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	138
# 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).







# interspecies translocations

