

## Report

	final.contigs
# contigs (>= 0 bp)	2131
# contigs (>= 1000 bp)	1571
Total length (>= 0 bp)	5180453
Total length (>= 1000 bp)	4770568
# contigs	2131
Largest contig	16656
Total length	5180453
Reference length	5547323
GC (%)	50.27
Reference GC (%)	50.48
N50	3482
NG50	3285
N75	1969
NG75	1673
L50	467
LG50	521
L75	953
LG75	1105
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	6200
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	90.584
Duplication ratio	1.031
# N's per 100 kbp	0.00
# mismatches per 100 kbp	39.70
# indels per 100 kbp	0.30
Largest alignment	16656
NA50	3482
NGA50	3285
NA75	1967
NGA75	1669
LA50	467
LGA50	521
LA75	954
LGA75	1106

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

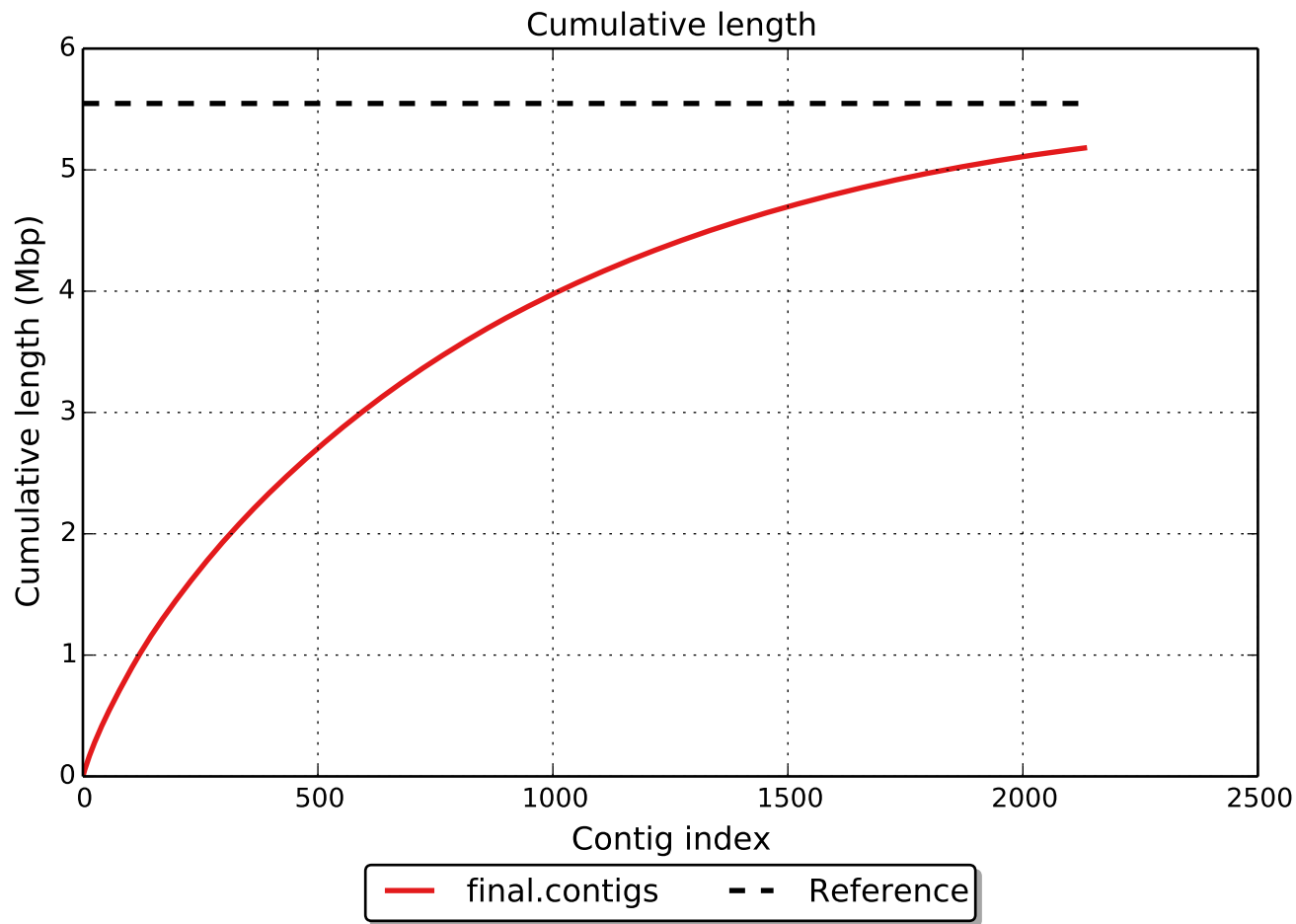
	final.contigs
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	6200
# local misassemblies	4
# mismatches	1995
# indels	15
# short indels	12
# long indels	3
Indels length	57

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	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).



GC content

