Report

	final assetions
#time (1000 km)	final.contigs
# contigs (>= 1000 bp)	898
# contigs (>= 5000 bp)	334
# contigs (>= 10000 bp)	88
# contigs (>= 25000 bp)	4
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4516556
Total length (>= 5000 bp)	3021546
Total length (>= 10000 bp)	1285249
Total length (>= 25000 bp)	107033
Total length (>= 50000 bp)	0
# contigs	1051
Largest contig	27406
Total length	4630410
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	6702
NG50	6679
N75	3892
NG75	3875
L50	214
LG50	215
L75	438
LG75	440
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.820
Duplication ratio	1.020
# N's per 100 kbp	0.00
# mismatches per 100 kbp	22.57
# indels per 100 kbp	0.04
Largest alignment	27406
NA50	6702
NGA50	6679
NA75	3892
NGA75	3875
LA50	214
LGA50	214
LA75	438
LGA75	430
LGA75	L 440

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	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	1025
# indels	2
# short indels	2
# long indels	0
Indels length	2

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	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# 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).















