Report

	final.contigs
# contigs (>= 1000 bp)	296
# contigs (>= 5000 bp)	219
# contigs (>= 10000 bp)	155
# contigs (>= 25000 bp)	61
# contigs (>= 50000 bp)	12
Total length (>= 1000 bp)	4667003
Total length (>= 5000 bp)	4435102
Total length (>= 10000 bp)	3954031
Total length (>= 25000 bp)	2444381
Total length (>= 50000 bp)	761705
# contigs	304
Largest contig	82743
Total length	4672341
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.79
N50	26975
NG50	26975
N75	13965
NG75	14207
L50	57
LG50	57
L75	117
LG75	116
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.956
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10.37
# indels per 100 kbp	0.00
Largest alignment	82743
NA50	26975
NGA50	26975
NA75	13965
NGA75	14207
LA50	57
LGA50	57
LA75	117
LGA75	116

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	0
# mismatches	481
# indels	0
# short indels	0
# long indels	0
Indels length	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).

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).















