Report

	final.contigs
# contigs (>= 1000 bp)	339
# contigs (>= 5000 bp)	244
# contigs (>= 10000 bp)	156
# contigs (>= 25000 bp)	60
# contigs (>= 50000 bp)	6
Total length (>= 1000 bp)	4661955
Total length (>= 5000 bp)	4384441
Total length (>= 10000 bp)	3732404
Total length (>= 25000 bp)	2257347
Total length (>= 50000 bp)	391967
# contigs	356
Largest contig	81775
Total length	4674811
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.79
N50	21936
NG50	23578
N75	11700
NG75	12028
L50	64
LG50	63
L75	136
LG75	133
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.951
Duplication ratio	1.008
# N's per 100 kbp	0.00
# mismatches per 100 kbp	9.85
# indels per 100 kbp	0.00
Largest alignment	81775
NA50	21936
NGA50	23576
NA75	11700
NGA75	12028
LA50	64
LGA50	63
LA75	136
LGA75	133
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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	457
# 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).















