Report

	contigs
# contigs (>= 1000 bp)	134
# contigs (>= 5000 bp)	90
# contigs (>= 10000 bp)	67
# contigs (>= 25000 bp)	43
# contigs (>= 50000 bp)	28
Total length (>= 1000 bp)	4068577
Total length (>= 5000 bp)	3939360
Total length (>= 10000 bp)	3785460
Total length (>= 25000 bp)	3377443
Total length (>= 50000 bp)	2858021
# contigs	162
Largest contig	347033
Total length	4086891
Reference length	4641652
GC (%)	50.65
Reference GC (%)	50.78
N50	71087
NG50	64224
N75	36733
NG75	23006
L50	15
LG50	19
L75	33
LG75	48
# misassemblies	5
# misassembled contigs	2
Misassembled contigs length	139104
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	85.520
Duplication ratio	1.030
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1033.02
# indels per 100 kbp	0.65
Largest alignment	347033
NA50	68318
NGA50	63041
NA75	34689
NGA75	21304
LA50	15
LGA50	19
LA75	34
LGA75	50

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

	contigs
# misassemblies	5
# relocations	5
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	139104
# local misassemblies	2
# mismatches	41006
# indels	26
# short indels	26
# long indels	0
Indels length	27

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

	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).

















