Report

	conting
#	contigs
# contigs (>= 1000 bp)	66
# contigs (>= 5000 bp)	45
# contigs (>= 10000 bp)	42
# contigs (>= 25000 bp)	38
# contigs (>= 50000 bp)	26
Total length (>= 1000 bp)	4501866
Total length (>= 5000 bp)	4467294
Total length (>= 10000 bp)	4444769
Total length (>= 25000 bp)	4372570
Total length (>= 50000 bp)	3973108
# contigs	95
Largest contig	332301
Total length	4520641
Reference length	4641652
GC (%)	50.78
Reference GC (%)	50.79
N50	169489
NG50	169489
N75	95039
NG75	87458
L50	10
LG50	10
L75	19
LG75	20
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.365
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	522.44
# indels per 100 kbp	0.73
Largest alignment	332301
NA50	169489
NGA50	169489
NA75	95039
NGA75	87458
LA50	10
LGA50	10
LA75	19
LGA75	20

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	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	23611
# indels	33
# short indels	33
# long indels	0
Indels length	33

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).















