Report

	contigs
# contigs (>= 1000 bp)	64
# contigs (>= 5000 bp)	45
# contigs (>= 3000 bp) # contigs (>= 10000 bp)	43
# contigs (>= 25000 bp)	38
# contigs (>= 50000 bp)	26
Total length (>= 1000 bp)	4499762
Total length (>= 5000 bp)	4467294
Total length (>= 10000 bp)	4444769
Total length (>= 25000 bp)	4372570
Total length (>= 50000 bp)	3973108
# contigs	93
Largest contig	332301
Total length	4518537
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 (%)	97.321
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	521.48
# 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
LOA/3	

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	23557
# indels	33
# short indels	33
# long indels	0
Indels length	33

All statistics are based on contigs of size \geq 500 bp, unless otherwise noted (e.g., "# contigs (\geq 0 bp)" and "Total length (\geq 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).















