## Report

	contigs
# contigs (>= 1000 bp)	21
# contigs (>= 5000 bp)	19
# contigs (>= 10000 bp)	19
# contigs (>= 25000 bp)	17
# contigs (>= 50000 bp)	16
Total length (>= 1000 bp)	4770955
Total length (>= 5000 bp)	4770933
Total length (>= 10000 bp)	4764662
Total length (>= 25000 bp)	4704002
Total length (>= 50000 bp)	4710910
	<b>-</b>
# contigs	663403
Largest contig	663492
Total length	4771781
Reference length	4641652
GC (%)	50.71
Reference GC (%)	50.79
N50	422118
NG50	422118
N75	227737
NG75	321943
L50	5
LG50	5
L75	9
LG75	8
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	162886
Genome fraction (%)	99.219
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	207.10
# indels per 100 kbp	0.59
Largest alignment	663492
NA50	362589
NGA50	378035
NA75	227737
NGA75	227737
LA50	6
LGA50	5
LA75	9
LGA75	9

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	1
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	9538
# indels	27
# short indels	26
# long indels	1
Indels length	38

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	1
# with misassembly	0
# both parts are significant	1
Partially unaligned length	162886
# 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).















