## Report

	contigs
# contigs (>= 0 bp)	2530
# contigs (>= 1000 bp)	1513
# contigs (>= 5000 bp)	126
# contigs (>= 10000 bp)	6
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4420927
Total length (>= 1000 bp)	3847662
Total length (>= 5000 bp)	814849
Total length (>= 10000 bp)	64940
Total length (>= 25000 bp)	0 13 10
Total length (>= 50000 bp)	0
# contigs	2086
	11817
Largest contig	4269178
Total length	
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	2702
NG50	2510
N75	1583
NG75	1334
L50	496
LG50	568
L75	1007
LG75	1199
# misassemblies	7
# misassembled contigs	6
Misassembled contigs length	22773
# local misassemblies	12
# unaligned contigs	0 + 4 part
Unaligned length	883
Genome fraction (%)	91.770
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	6.53
# indels per 100 kbp	0.45
Largest alignment	11817
NA50	2694
NGA50	2506
NA75	1581
NGA75	1333
LA50	499
LGA50	571
LA75	1012
LGA75	1203
LGA/J	1203

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	7
# relocations	7
# translocations	0
# inversions	0
# misassembled contigs	6
Misassembled contigs length	22773
# local misassemblies	12
# mismatches	278
# indels	19
# short indels	18
# long indels	1
Indels length	111

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	4
# with misassembly	0
# both parts are significant	1
Partially unaligned length	883
# 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).

















