## Report

[	uniq-contigs-contigs
# contigs (>= 0 bp)	6
# contigs (>= 1000 bp)	2
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	541715
Total length (>= 1000 bp)	539375
Total length (>= 5000 bp)	539375
Total length (>= 10000 bp)	539375
Total length (>= 25000 bp)	539375
Total length (>= 50000 bp)	539375
# contigs	6
Largest contig	400663
Total length	541715
Reference length	599940
GC (%)	51.08
Reference GC (%)	51.01
N50	400663
NG50	400663
N75	138712
NG75	138712
L50	1
LG50	1
L75	2
LG75	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	89.997
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	400663
Total aligned length	541715
NA50	400663
NGA50	400663
NA75	138712
NGA75	138712
LA50	1
LGA50	1
LA75	2
LGA75	2

All statistics are based on contigs of size >=400 bp, unless otherwise noted (e.g., "# contigs (>=0 bp)" and "Total length (>=0 bp)" include all contigs).

## Misassemblies report

	uniq-contigs-contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	0
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

All statistics are based on contigs of size >= 400 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

## Unaligned report

	uniq-contigs-contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

All statistics are based on contigs of size >= 400 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).



















