## Report

	anonymous_gsa
# contigs (>= 0 bp)	7675
# contigs (>= 1000 bp)	1170
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4105759
Total length (>= 1000 bp)	1806613
Total length (>= 5000 bp)	5071
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2809
Largest contig	5071
Total length	2989729
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.79
N50	1156
NG50	769
N75	797
L50	880
LG50	1762
L75	1662
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	56
Genome fraction (%)	64.291
Duplication ratio	1.002
# N's per 100 kbp	1.87
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	5071
NA50	1156
NGA50	769
NA75	797
LA50	880
LGA50	1762
LA75	1662

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

	anonymous_gsa
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	0
# indels	0
# short indels	0
# long indels	0
Indels length	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).

## Unaligned report

	anonymous_gsa
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	56
# N's	56

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).















