Report

Report	
	contigs
# contigs (>= 0 bp)	135
# contigs (>= 1000 bp)	74
# contigs (>= 5000 bp)	55
# contigs (>= 10000 bp)	51
# contigs (>= 25000 bp)	43
# contigs (>= 50000 bp)	29
Total length (>= 0 bp)	4574837
Total length (>= 1000 bp)	4556264
Total length (>= 5000 bp)	4517738
Total length (>= 10000 bp)	4488470
Total length (>= 25000 bp)	4369226
Total length (>= 50000 bp)	3866888
# contigs	86
Largest contig	327173
Total length	4564581
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	133050
NG50	132608
N75	78649
NG75	67374
L50	11
LG50	12
L75	22
LG75	23
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	7
# local misassemblies	· ·
# unaligned contigs	0 + 0 part
Unaligned length	00.206
Genome fraction (%)	98.306 1.000
Duplication ratio # N's per 100 kbp	0.00
# mismatches per 100 kbp	1.78
# indels per 100 kbp	0.20
Largest alignment	327173
NA50	133050
NGA50	132608
NA75	78649
NGA75	67374
LA50	11
LGA50	12
LA75	22
LGA75	23
LUA/J	

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
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	7
# mismatches	81
# indels	9
# short indels	8
# long indels	1
Indels length	96

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).















