Report

Report	
	contigs
# contigs (>= 0 bp)	658
# contigs (>= 1000 bp)	549
# contigs (>= 5000 bp)	315
# contigs (>= 10000 bp)	156
# contigs (>= 25000 bp)	23
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4568599
Total length (>= 1000 bp)	4524473
Total length (>= 5000 bp)	3888483
Total length (>= 10000 bp)	2739753
Total length (>= 25000 bp)	753541
Total length (>= 50000 bp)	0
# contigs	586
Largest contig	42373
Total length	4552541
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	12409
NG50	12041
N75	7109
NG75	6847
L50	114
LG50	118
L75	237
LG75	247
# misassemblies	9
# misassembled contigs	9
Misassembled contigs length	138206
# local misassemblies	6
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.785
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	179.67
# indels per 100 kbp	0.37
Largest alignment	42373
NA50	12041
NGA50	11653
NA75	7089
NGA75	6844
LA50	116
LGA50	120
LA75	239
LGA75	249

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	9
# relocations	9
# translocations	0
# inversions	0
# misassembled contigs	9
Misassembled contigs length	138206
# local misassemblies	6
# mismatches	8155
# indels	17
# short indels	14
# long indels	3
Indels length	184

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).















