Report

	Einal accessor
	final.contigs
# contigs (>= 1000 bp)	669
# contigs (>= 5000 bp)	326
# contigs (>= 10000 bp)	136
# contigs (>= 25000 bp)	7
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4376118
Total length (>= 5000 bp)	3401284
Total length (>= 10000 bp)	2071625
Total length (>= 25000 bp)	198815
Total length (>= 50000 bp)	0
# contigs	815
Largest contig	35550
Total length	4471328
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	9275
NG50	8865
N75	5183
NG75	4787
L50	154
LG50	163
L75	317
LG75	343
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	5468
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	94.827
Duplication ratio	1.016
# N's per 100 kbp	0.00
# mismatches per 100 kbp	530.06
# indels per 100 kbp	0.00
Largest alignment	35550
NA50	9275
NGA50	8865
NA75	5183
NGA75	4787
LA50	154
LGA50	163
LA75	317
LGA75	343
LGATS	J+3

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

	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	5468
# local misassemblies	0
# mismatches	23331
# 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

	final.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).

















