Report

	final anakina
	final.contigs
# contigs (>= 0 bp)	19079
# contigs (>= 1000 bp)	1825
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	10223444
Total length (>= 1000 bp)	2641490
Total length (>= 5000 bp)	11201
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	5856
Largest contig	6045
Total length	5441810
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	981
NG50	1074
N75	702
NG75	817
L50	1906
LG50	1516
L75	3547
LG75	
	2756
# misassemblies	12
# misassembled contigs	12
Misassembled contigs length	13727
# local misassemblies	5
# unaligned contigs	166 + 83 part
Unaligned length	99658
Genome fraction (%)	93.377
Duplication ratio	1.233
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1230.00
# indels per 100 kbp	1.73
Largest alignment	6045
NA50	978
NGA50	1071
NA75	700
NGA75	813
LA50	1910
LGA50	1519
LA75	3557
LGA75	2763

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	12
# relocations	6
# translocations	0
# inversions	6
# misassembled contigs	12
Misassembled contigs length	13727
# local misassemblies	5
# mismatches	53311
# indels	75
# short indels	74
# long indels	1
Indels length	82

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	166
Fully unaligned length	90650
# partially unaligned contigs	83
# with misassembly	0
# both parts are significant	0
Partially unaligned length	9008
# N's	0

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