Report

	final.contigs
# contigs (>= 0 bp)	55818
# contigs (>= 1000 bp)	0
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	16992122
Total length (>= 1000 bp)	0
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	55818
Largest contig	778
Total length	16992122
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	311
NG50	394
N75	261
NG75	368
L50	23273
LG50	5245
L75	37910
LG75	8296
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	32517 + 77 part
Unaligned length	11016589
Genome fraction (%)	75.400
Duplication ratio	1.707
# N's per 100 kbp	0.00
# mismatches per 100 kbp	745.59
# indels per 100 kbp	0.00
Largest alignment	642
NGA50	260
NGA75	245
LGA50	7792
LGA75	12395

Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	26094
# indels	0
# short indels	0
# long indels	0
Indels length	0

Unaligned report

	final.contigs
# fully unaligned contigs	32517
Fully unaligned length	11001745
# partially unaligned contigs	77
# with misassembly	0
# both parts are significant	77
Partially unaligned length	14844
# N's	0















