Report

# contigs (>= 0 bp) 3817 # contigs (>= 1000 bp) 119 # contigs (>= 10000 bp) 0 # contigs (>= 10000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 1910447 Total length (>= 10000 bp) 147351 Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3817 Largest contig 2634 Total length 1910447 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 50.3 N75 397 L50 1368 L75 2439 # misassembles 4 # misassembled contigs 4 Misassembled contigs 4 Misassembled contigs 9 # unaligned contigs 13886 Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463 NGA50		final.contigs
# contigs (>= 5000 bp) 0 # contigs (>= 10000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 25000 bp) 0 Total length (>= 0 bp) 1910447 Total length (>= 1000 bp) 147351 Total length (>= 5000 bp) 0 Total length (>= 5000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3817 Largest contig 2634 Total length 1910447 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 503 N75 397 L50 1368 L75 2439 # misassembles 4 # misassembled contigs 4 Misassembled contigs 4 Misassembled contigs 7880 # local misassemblies 0 # unaligned contigs 13886 Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	# contigs (>= 0 bp)	3817
# contigs (>= 10000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 1910447 Total length (>= 1000 bp) 147351 Total length (>= 5000 bp) 0 Total length (>= 5000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 5000 bp) 0 Total length (>= 5000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3817 Largest contig 2634 Total length 1910447 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 503 N75 397 L50 1368 L75 2439 # misassemblies 4 # misassembled contigs 4 Misassembled contigs 4 Misassembled contigs 4 Misassembled contigs 2297 + 8 part Unaligned length 138866 Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	# contigs (>= 1000 bp)	119
# contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 1910447 Total length (>= 1000 bp) 147351 Total length (>= 5000 bp) 0 Total length (>= 5000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3817 Largest contig 2634 Total length 1910447 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 503 N75 397 L50 1368 L75 2439 # misassemblies 4 # misassembled contigs 4 Misassembled contigs 4 Misassembled contigs 4 Misassembled contigs 4 # local misassemblies 0 # unaligned length 138866 Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	# contigs (>= 5000 bp)	0
# contigs (>= 50000 bp) 0 Total length (>= 0 bp) 1910447 Total length (>= 1000 bp) 147351 Total length (>= 5000 bp) 0 Total length (>= 5000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3817 Largest contig 2634 Total length 1910447 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 503 N75 397 L50 1368 L75 2439 # misassembled contigs 4 # misassembled contigs 4 # misassembled contigs 4 # misassembled contigs 9 # unaligned contigs 19886 Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	# contigs (>= 10000 bp)	0
Total length (>= 0 bp) 1910447 Total length (>= 1000 bp) 147351 Total length (>= 5000 bp) 0 Total length (>= 5000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3817 Largest contig 2634 Total length 1910447 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 503 N75 397 L50 1368 L75 2439 # misassembled contigs 4 # misassembled contigs 4 # misassembled contigs 4 Misassembled contigs 9 # unaligned contigs 19880 # unaligned contigs 2297 + 8 part 19880 Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	# contigs (>= 25000 bp)	0
Total length (>= 1000 bp) 147351 Total length (>= 5000 bp) 0 Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3817 Largest contig 2634 Total length 1910447 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 503 N75 397 L50 1368 L75 2439 # misassemblies 4 # misassembled contigs 4 Misassembled contigs length 7880 # local misassemblies 0 # unaligned length 1138866 Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	# contigs (>= 50000 bp)	0
Total length (>= 5000 bp) 0 Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3817 Largest contig 2634 Total length 1910447 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 503 N75 397 L50 1368 L75 2439 # misassemblies 4 # misassembled contigs 4 Misassembled contigs length 7880 # local misassemblies 0 # unaligned contigs 2297 + 8 part Unaligned length 1138866 Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	Total length (>= 0 bp)	1910447
Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3817 Largest contig 2634 Total length 1910447 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 503 N75 397 L50 1368 L75 2439 # misassemblies 4 # misassembled contigs 4 Misassembled contigs length 7880 # local misassemblies 0 # unaligned length 1138866 Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	Total length (>= 1000 bp)	147351
Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3817 Largest contig 2634 Total length 1910447 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 503 N75 397 L50 1368 L75 2439 # misassemblies 4 # misassembled contigs 4 Misassembled contigs length 7880 # local misassemblies 0 # unaligned contigs 2297 + 8 part Unaligned length 1138866 Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	Total length (>= 5000 bp)	0
Total length (>= 50000 bp) 0 # contigs 3817 Largest contig 2634 Total length 1910447 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 503 N75 397 L50 1368 L75 2439 # misassemblies 4 # misassembled contigs 4 Misassembled contigs length 7880 # local misassemblies 0 # unaligned contigs 2297 + 8 part Unaligned length 1138866 Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	Total length (>= 10000 bp)	0
# contigs 3817 Largest contig 2634 Total length 1910447 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 50.3 N75 397 L50 1368 L75 2439 # misassembles 4 # misassembled contigs 4 Misassembled contigs 4 Misassembled contigs 4 Unaligned contigs 2297 + 8 part Unaligned length 1138866 Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	Total length (>= 25000 bp)	0
Largest contig 2634 Total length 1910447 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 503 N75 397 L50 1368 L75 2439 # misassemblies 4 # misassembled contigs 4 Misassembled contigs length 7880 # local misassemblies 0 # unaligned contigs 2297 + 8 part Unaligned length 1138866 Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	Total length (>= 50000 bp)	0
Total length 1910447 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 50.3 N75 397 L50 1368 L75 2439 # misassemblies 4 # misassembled contigs 4 Misassembled contigs length 7880 # local misassemblies 0 # unaligned contigs 2297 + 8 part Unaligned length 1138866 Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	# contigs	3817
Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 503 N75 397 L50 1368 L75 2439 # misassemblies 4 # misassembled contigs 4 Misassembled contigs length 7880 # local misassemblies 0 # unaligned contigs 2297 + 8 part Unaligned length 1138866 Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	Largest contig	2634
GC (%) 50.78 Reference GC (%) 50.79 N50 503 N75 397 L50 1368 L75 2439 # misassemblies 4 # misassembled contigs 4 Misassembled contigs 4 Misassembled contigs 1980 # local misassemblies 0 # unaligned contigs 2297 + 8 part 138866 Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	Total length	1910447
Reference GC (%) 50.79 N50 503 N75 397 L50 1368 L75 2439 # misassemblies 4 # misassembled contigs 4 Misassembled contigs length 7880 # local misassemblies 0 # unaligned contigs 2297 + 8 part Unaligned length 1138866 Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	Reference length	4641652
N50 503 N75 397 L50 1368 L75 2439 # misassemblies 4 # misassembled contigs 4 Misassembled contigs length 7880 # local misassemblies 0 # unaligned contigs 2297 + 8 part Unaligned length 1138866 Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	GC (%)	50.78
N75 397 L50 1368 L75 2439 # misassemblies 4 # misassembled contigs 4 Misassembled contigs length 7880 # local misassemblies 0 # unaligned contigs 2297 + 8 part Unaligned length 1138866 Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	Reference GC (%)	50.79
L50 1368 L75 2439 # misassemblies 4 # misassembled contigs 4 Misassembled contigs length 7880 # local misassemblies 0 # unaligned contigs 2297 + 8 part Unaligned length 1138866 Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	N50	503
L75 2439 # misassemblies 4 # misassembled contigs 4 Misassembled contigs length 7880 # local misassemblies 0 # unaligned contigs 2297 + 8 part Unaligned length 1138866 Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	N75	397
# misassemblies 4 # misassembled contigs 4 Misassembled contigs length 7880 # local misassemblies 0 # unaligned contigs 2297 + 8 part Unaligned length 1138866 Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	L50	1368
# misassembled contigs 4 Misassembled contigs length 7880 # local misassemblies 0 # unaligned contigs 2297 + 8 part Unaligned length 1138866 Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	L75	2439
Misassembled contigs length 7880 # local misassemblies 0 # unaligned contigs 2297 + 8 part Unaligned length 1138866 Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	# misassemblies	4
# local misassemblies 0 # unaligned contigs 2297 + 8 part Unaligned length 1138866 Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	# misassembled contigs	4
# unaligned contigs 2297 + 8 part Unaligned length 1138866 Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	Misassembled contigs length	7880
Unaligned length 1138866 Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	# local misassemblies	0
Genome fraction (%) 16.557 Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	# unaligned contigs	2297 + 8 part
Duplication ratio 1.004 # N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	Unaligned length	1138866
# N's per 100 kbp 0.00 # mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	Genome fraction (%)	16.557
# mismatches per 100 kbp 610.01 # indels per 100 kbp 0.91 Largest alignment 2463	Duplication ratio	1.004
# indels per 100 kbp 0.91 Largest alignment 2463	# N's per 100 kbp	0.00
Largest alignment 2463	# mismatches per 100 kbp	610.01
	# indels per 100 kbp	0.91
NGA50 -	Largest alignment	2463
	NGA50	-

Misassemblies report

	final.contigs
# misassemblies	4
# relocations	4
# translocations	0
# inversions	0
# misassembled contigs	4
Misassembled contigs length	7880
# local misassemblies	0
# mismatches	4688
# indels	7
# short indels	7
# long indels	0
Indels length	7

Unaligned report

	final.contigs
# fully unaligned contigs	2297
Fully unaligned length	1136254
# partially unaligned contigs	8
# with misassembly	0
# both parts are significant	8
Partially unaligned length	2612
# N's	0

















