Report

# contigs (>= 0 bp) 4321 # contigs (>= 1000 bp) 27 # contigs (>= 5000 bp) 0 # contigs (>= 10000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 1948663 Total length (>= 1000 bp) 0 Total length (>= 1000 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 4321 Largest contig 1965 Total length 1948663 Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.76 Reference GC (%) 50.79 N50 450 N75 374 L50 1684 L75 2876 # misassembles 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # unaligned contigs length 0 # unaligned length 1938660 Genome fraction (%) 0.215 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337 NGA50		final.contigs
# contigs (>= 5000 bp) 0 # contigs (>= 10000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 25000 bp) 0 Total length (>= 0 bp) 1948663 Total length (>= 1000 bp) 0 Total length (>= 5000 bp) 0 Total length (>= 5000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 5000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 4321 Largest contig 1965 Total length 1948663 Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.79 N50 450 N75 374 L50 1684 L75 2876 # misassembles 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # unaligned contigs 1938660 Genome fraction (%) 0.215 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	# contigs (>= 0 bp)	4321
# contigs (>= 10000 bp)	# contigs (>= 1000 bp)	27
# contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 1948663 Total length (>= 1000 bp) 33234 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 4321 Largest contig 1965 Total length 1948663 Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.79 N50 450 N75 374 L50 1684 L75 2876 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 1938660 # unaligned contigs 4299 + 4 part 1938660 Genome fraction (%) 0.215 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	# contigs (>= 5000 bp)	0
# contigs (>= 50000 bp) 0 Total length (>= 0 bp) 1948663 Total length (>= 1000 bp) 33234 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 # contigs 4321 Largest contig 1965 Total length 1948663 Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.79 N50 450 N75 374 L50 1684 L75 2876 # misassembled contigs 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 1938660 Genome fraction (%) 0.215 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	# contigs (>= 10000 bp)	0
Total length (>= 0 bp) 1948663 Total length (>= 1000 bp) 33234 Total length (>= 5000 bp) 0 Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 4321 Largest contig 1965 Total length 1948663 Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.79 N50 450 N75 374 L50 1684 L75 2876 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 4299 + 4 part Unaligned length 1938660 Genome fraction (%) 0.215 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 <td># contigs (>= 25000 bp)</td> <td>0</td>	# contigs (>= 25000 bp)	0
Total length (>= 1000 bp) 33234 Total length (>= 5000 bp) 0 Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 4321 Largest contig 1965 Total length 1948663 Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.79 N50 450 N75 374 L50 1684 L75 2876 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # unaligned contigs 4299 + 4 part Unaligned length 1938660 Genome fraction (%) 0.215 Duplication ratio 1.001 # N's per 100 kbp 0.00 # indels per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	# 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 4321 Largest contig 1965 Total length 1948663 Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.79 N50 450 N75 374 L50 1684 L75 2876 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 4299 + 4 part Unaligned length 1938660 Genome fraction (%) 0.215 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	Total length (>= 0 bp)	1948663
Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 4321 Largest contig 1965 Total length 1948663 Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.79 N50 450 N75 374 L50 1684 L75 2876 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned length 1938660 Genome fraction (%) 0.215 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	Total length (>= 1000 bp)	33234
Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 4321 Largest contig 1965 Total length 1948663 Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.79 N50 450 N75 374 L50 1684 L75 2876 # misassemblies 0 # incal misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 4299 + 4 part Unaligned length 1938660 Genome fraction (%) 0.215 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	Total length (>= 5000 bp)	0
Total length (>= 50000 bp) 0 # contigs 4321 Largest contig 1965 Total length 1948663 Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.79 N50 450 N75 374 L50 1684 L75 2876 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned rontigs 4299 + 4 part Unaligned length 1938660 Genome fraction (%) 0.215 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	Total length (>= 10000 bp)	0
# contigs 4321 Largest contig 1965 Total length 1948663 Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.79 N50 450 N75 374 L50 1684 L75 2876 # misassembles 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 4299 + 4 part Unaligned length 1938660 Genome fraction (%) 0.215 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	Total length (>= 25000 bp)	0
Largest contig 1965 Total length 1948663 Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.79 N50 450 N75 374 L50 1684 L75 2876 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 4299 + 4 part Unaligned length 1938660 Genome fraction (%) 0.215 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	Total length (>= 50000 bp)	0
Total length 1948663 Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.79 N50 450 N75 374 L50 1684 L75 2876 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 4299 + 4 part Unaligned length 1938660 Genome fraction (%) 0.215 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	# contigs	4321
Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.79 N50 450 N75 374 L50 1684 L75 2876 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 4299 + 4 part Unaligned length 1938660 Genome fraction (%) 0.215 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	Largest contig	1965
GC (%) 50.76 Reference GC (%) 50.79 N50 450 N75 374 L50 1684 L75 2876 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 4299 + 4 part Unaligned length 1938660 Genome fraction (%) 0.215 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	Total length	1948663
Reference GC (%) 50.79 N50 450 N75 374 L50 1684 L75 2876 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 4299 + 4 part Unaligned length 1938660 Genome fraction (%) 0.215 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	Reference length	4641652
N50 450 N75 374 L50 1684 L75 2876 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 4299 + 4 part Unaligned length 1938660 Genome fraction (%) 0.215 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	GC (%)	50.76
N75 374 L50 1684 L75 2876 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 4299 + 4 part Unaligned length 1938660 Genome fraction (%) 0.215 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	Reference GC (%)	50.79
L50 1684 L75 2876 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 4299 + 4 part Unaligned length 1938660 Genome fraction (%) 0.215 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	N50	450
L75 2876 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 4299 + 4 part Unaligned length 1938660 Genome fraction (%) 0.215 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	N75	374
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 4299 + 4 part Unaligned length 1938660 Genome fraction (%) 0.215 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	L50	1684
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 4299 + 4 part Unaligned length 1938660 Genome fraction (%) 0.215 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	L75	2876
Misassembled contigs length # local misassemblies 0 # unaligned contigs 4299 + 4 part Unaligned length 1938660 Genome fraction (%) Duplication ratio # N's per 100 kbp mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	# misassemblies	0
# local misassemblies 0 # unaligned contigs 4299 + 4 part Unaligned length 1938660 Genome fraction (%) 0.215 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	# misassembled contigs	0
# unaligned contigs 4299 + 4 part Unaligned length 1938660 Genome fraction (%) 0.215 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	Misassembled contigs length	0
Unaligned length 1938660 Genome fraction (%) 0.215 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	# local misassemblies	0
Genome fraction (%) 0.215 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	# unaligned contigs	4299 + 4 part
Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	Unaligned length	1938660
# N's per 100 kbp 0.00 # mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	Genome fraction (%)	0.215
# mismatches per 100 kbp 710.28 # indels per 100 kbp 0.00 Largest alignment 1337	Duplication ratio	1.001
# indels per 100 kbp 0.00 Largest alignment 1337	# N's per 100 kbp	0.00
Largest alignment 1337	# mismatches per 100 kbp	710.28
	# indels per 100 kbp	0.00
NGA50 -	Largest alignment	1337
	NGA50	-

Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	71
# indels	0
# short indels	0
# long indels	0
Indels length	0

Unaligned report

	final.contigs
# fully unaligned contigs	4299
Fully unaligned length	1937351
# partially unaligned contigs	4
# with misassembly	1
# both parts are significant	4
Partially unaligned length	1309
# N's	0















