Report

# contigs (>= 0 bp)		lferriphilum_1contig
# contigs (>= 5000 bp)	# contigs (>= 0 bp)	1
# contigs (>= 10000 bp)	# contigs (>= 1000 bp)	1
# contigs (>= 25000 bp) 1 # contigs (>= 50000 bp) 2577733 Total length (>= 0 bp) 2577733 Total length (>= 1000 bp) 2577733 Total length (>= 5000 bp) 2577733 Total length (>= 5000 bp) 2577733 Total length (>= 5000 bp) 2577733 Total length (>= 25000 bp) 2577733 Total length (>= 50000 bp) 2577733 Total length (>= 50000 bp) 2577733 # contigs 1 Largest contig 2577733 Total length 2577733 Reference length 2610531 GC (%) 54.22 Reference GC (%) 54.14 N50 2577733 NG50 2577733 NG50 2577733 NG75 2577733 L50 2577733 L50 1 LG50 1 LG50 1 L75 1 LG75 1 # misassemblies 2 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 0 # unaligned mis. contigs 0 # unaligned length 0 Genome fraction (%) 97.566 Duplication ratio 1.012 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.12 # indels per 100 kbp 3.57 Total aligned length 2577692 NA50 1921378 NA75 644322 NGA75 644322 LA50 1 LG50 1 LA75 2	# contigs (>= 5000 bp)	1
# contigs (>= 50000 bp) 1 Total length (>= 0 bp) 2577733 Total length (>= 1000 bp) 2577733 Total length (>= 5000 bp) 2577733 Total length (>= 5000 bp) 2577733 Total length (>= 10000 bp) 2577733 Total length (>= 25000 bp) 2577733 Total length (>= 50000 bp) 2577733 Total length (>= 50000 bp) 2577733 # contigs 1 Largest contig 2577733 Reference length 2610531 GC (%) 54.22 Reference GC (%) 54.14 N50 2577733 NG50 2577733 NG50 2577733 NG75 2577733 L50 1 LG50 1 L75 1 LG75 1 # misassemblies 2 # misassembled contigs length 2577733 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 97.566 Duplication ratio 1.012 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.12 # indels per 100 kbp 0.12 # indels per 100 kbp 0.2577692 NA50 1921378 NG75 644322 NGA75 644322 NGA75 644322 NGA75 644322 LA50 1 LGA50 1 LA75 2	# contigs (>= 10000 bp)	1
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Total length (>= 50000 bp) 2577733 # contigs 1 Largest contig 2577733 Total length 2577733 Reference length 2610531 GC (%) 54.22 Reference GC (%) 54.14 N50 2577733 NG50 2577733 N75 2577733 L50 1 LG50 1 L75 1 # misassemblies 2 # misassembled contigs 1 Misassembled contigs length 2577733 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned length 0 Genome fraction (%) 97.566 Duplication ratio 1.012 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.12 # indels per 100 kbp 3.57 Largest alignment 1921378 NA50 1921378 NA50 1921378 NA75 644322 <t< td=""><td>Total length (>= 10000 bp)</td><td>2577733</td></t<>	Total length (>= 10000 bp)	2577733
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Largest contig 2577733 Total length 2577733 Reference length 2610531 GC (%) 54.22 Reference GC (%) 54.14 N50 2577733 NG50 2577733 NG75 2577733 L50 1 LG50 1 L75 1 LG75 1 # misassemblies 2 # misassembled contigs 1 Misassembled contigs 0 # unaligned mis. contigs 0 # unaligned mis. contigs 0 # unaligned length 0 Genome fraction (%) 97.566 Duplication ratio 1.012 # N's per 100 kbp 0.12 # indels per 100 kbp 3.57 Largest alignment 1921378 Total aligned length 2577692 NA50 1921378 NGA50 1921378 NGA75 644322 LA50 1 LGA50 1 <td>Total length (>= 50000 bp)</td> <td>2577733</td>	Total length (>= 50000 bp)	2577733
Total length 2577733 Reference length 2610531 GC (%) 54.22 Reference GC (%) 54.14 N50 2577733 NG50 2577733 NG50 2577733 NG75 2577733 L50 1 LG50 1 L75 1 LG75 1 # misassemblies 2 # misassembled contigs 1 Misassembled contigs 1 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned contigs 0 # unaligned length 0 Genome fraction (%) 97.566 Duplication ratio 1.012 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.57 Largest alignment 1921378 NGA50 1921378 NGA50 1921378 NGA75 644322 LA50 1 LG50 1	# contigs	1
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Reference GC (%) 54.14 N50 2577733 NG50 2577733 N75 2577733 NG75 2577733 L50 1 LG50 1 L75 1 LG75 1 # misassemblies 2 # misassembled contigs 1 Misassembled contigs length 2577733 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned mis. contigs 0 # unaligned length 0 Genome fraction (%) 97.566 Duplication ratio 1.012 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.12 # indels per 100 kbp 3.57 Largest alignment 1921378 Total aligned length 2577692 NA50 1921378 NGA50 1921378 NA75 644322 NGA75 644322 LA50 1 LGA50 1 LA75 2	Reference length	2610531
Reference GC (%) 54.14 N50 2577733 NG50 2577733 N75 2577733 NG75 2577733 L50 1 LG50 1 L75 1 LG75 1 # misassemblies 2 # misassembled contigs 1 Misassembled contigs 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.566 Duplication ratio 1.012 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.12 # indels per 100 kbp 3.57 Largest alignment 1921378 Total aligned length 2577692 NA50 1921378 NGA50 1921378 NGA50 1921378 NGA75 644322 LA50 1 LA50 1 LA75 2		54.22
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N75 2577733 NG75 2577733 L50 1 LG50 1 L75 1 LG75 1 # misassemblies 2 # misassembled contigs 1 Misassembled contigs length 2577733 # local misassemblies 0 # unaligned mis. contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.566 Duplication ratio 1.012 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.12 # indels per 100 kbp 3.57 Largest alignment 1921378 Total aligned length 2577692 NA50 1921378 NGA50 1921378 NA75 644322 NGA75 644322 LA50 1 LA50 1 LA75 2	N50	2577733
NG75 2577733 L50 1 LG50 1 L75 1 LG75 1 # misassemblies 2 # misassembled contigs 1 Misassembled contigs length 2577733 # local misassemblies 0 # unaligned mis. contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.566 Duplication ratio 1.012 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.12 # indels per 100 kbp 3.57 Largest alignment 1921378 Total aligned length 2577692 NA50 1921378 NGA50 1921378 NA75 644322 NGA75 644322 LA50 1 LGA50 1 LA75 2	NG50	2577733
L50 1 LG50 1 L75 1 # misassemblies 2 # misassembled contigs 1 Misassembled contigs length 2577733 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.566 Duplication ratio 1.012 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.12 # indels per 100 kbp 3.57 Largest alignment 1921378 Total aligned length 2577692 NA50 1921378 NGA50 1921378 NA75 644322 NGA75 644322 LA50 1 LGA50 1 LA75 2	N75	2577733
LG50 1 L75 1 LG75 1 # misassemblies 2 # misassembled contigs 1 Misassembled contigs length 2577733 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.566 Duplication ratio 1.012 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.12 # indels per 100 kbp 3.57 Largest alignment 1921378 Total aligned length 2577692 NA50 1921378 NGA50 1921378 NA75 644322 NGA75 644322 LA50 1 LA50 1 LA75 2	NG75	2577733
L75 1 LG75 1 # misassemblies 2 # misassembled contigs 1 Misassembled contigs length 2577733 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.566 Duplication ratio 1.012 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.12 # indels per 100 kbp 3.57 Largest alignment 1921378 Total aligned length 2577692 NA50 1921378 NGA50 1921378 NA75 644322 NGA75 644322 LA50 1 LA50 1 LA50 1 LA75 2	L50	1
LG75 1 # misassemblies 2 # misassembled contigs 1 Misassembled contigs length 2577733 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.566 Duplication ratio 1.012 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.12 # indels per 100 kbp 3.57 Largest alignment 1921378 Total aligned length 2577692 NA50 1921378 NGA50 1921378 NA75 644322 NGA75 644322 LA50 1 LGA50 1 LA75 2	LG50	1
# misassemblies 2 # misassembled contigs 1 Misassembled contigs length 2577733 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned length 0 Genome fraction (%) 97.566 Duplication ratio 1.012 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.12 # indels per 100 kbp 3.57 Largest alignment 1921378 Total aligned length 2577692 NA50 1921378 NGA50 1921378 NA75 644322 NGA75 644322 LA50 1 LGA50 1 LA75 2	L75	1
# misassembled contigs 1 Misassembled contigs length 2577733 # local misassemblies 0 # unaligned mis. contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.566 Duplication ratio 1.012 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.57 Largest alignment 1921378 Total aligned length 2577692 NA50 1921378 NGA50 1921378 NA75 644322 NGA75 644322 LA50 1 LGA50 1 LA75 2	LG75	1
Misassembled contigs length 2577733 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.566 Duplication ratio 1.012 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.57 Largest alignment 1921378 Total aligned length 2577692 NA50 1921378 NGA50 1921378 NA75 644322 NGA75 644322 LA50 1 LGA50 1 LA75 2	# misassemblies	2
# local misassemblies 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.566 Duplication ratio 1.012 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.57 Largest alignment 1921378 Total aligned length 2577692 NA50 1921378 NGA50 1921378 NA75 644322 LA50 1 LGA50 1 LA75 2	# misassembled contigs	1
# unaligned mis. contigs # unaligned contigs 0 + 0 part Unaligned length Genome fraction (%) P7.566 Duplication ratio 1.012 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.57 Largest alignment Total aligned length NGA50 NA50 NGA50 NA75 NGA75 LA50 1 LA50 1 LGA50 1 LA75	Misassembled contigs length	2577733
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.566 Duplication ratio 1.012 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.57 Largest alignment 1921378 Total aligned length 2577692 NA50 1921378 NGA50 1921378 NA75 644322 NGA75 644322 LA50 1 LGA50 1 LA75 2	# local misassemblies	0
Unaligned length 0 Genome fraction (%) 97.566 Duplication ratio 1.012 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.12 # indels per 100 kbp 3.57 Largest alignment 1921378 Total aligned length 2577692 NA50 1921378 NGA50 1921378 NA75 644322 NGA75 644322 LA50 1 LGA50 1 LA75 2	# unaligned mis. contigs	0
Genome fraction (%) 97.566 Duplication ratio 1.012 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.12 # indels per 100 kbp 3.57 Largest alignment 1921378 Total aligned length 2577692 NA50 1921378 NGA50 1921378 NA75 644322 NGA75 644322 LA50 1 LGA50 1 LA75 2	# unaligned contigs	0 + 0 part
Duplication ratio 1.012 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.12 # indels per 100 kbp 3.57 Largest alignment 1921378 Total aligned length 2577692 NA50 1921378 NGA50 1921378 NA75 644322 NGA75 644322 LA50 1 LGA50 1 LA75 2	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 0.12 # indels per 100 kbp 3.57 Largest alignment 1921378 Total aligned length 2577692 NA50 1921378 NGA50 1921378 NA75 644322 NGA75 644322 LA50 1 LGA50 1 LA75 2	Genome fraction (%)	97.566
# mismatches per 100 kbp 0.12 # indels per 100 kbp 3.57 Largest alignment 1921378 Total aligned length 2577692 NA50 1921378 NGA50 1921378 NA75 644322 NGA75 644322 LA50 1 LGA50 1 LA75 2	Duplication ratio	1.012
# indels per 100 kbp 3.57 Largest alignment 1921378 Total aligned length 2577692 NA50 1921378 NGA50 1921378 NA75 644322 NGA75 644322 LA50 1 LGA50 1 LA75 2	# N's per 100 kbp	0.00
# indels per 100 kbp 3.57 Largest alignment 1921378 Total aligned length 2577692 NA50 1921378 NGA50 1921378 NA75 644322 NGA75 644322 LA50 1 LGA50 1 LA75 2	# mismatches per 100 kbp	0.12
Total aligned length 2577692 NA50 1921378 NGA50 1921378 NA75 644322 NGA75 644322 LA50 1 LGA50 1 LA75 2	# indels per 100 kbp	3.57
Total aligned length 2577692 NA50 1921378 NGA50 1921378 NA75 644322 NGA75 644322 LA50 1 LGA50 1 LA75 2	Largest alignment	1921378
NGA50 1921378 NA75 644322 NGA75 644322 LA50 1 LGA50 1 LA75 2	Total aligned length	2577692
NGA50 1921378 NA75 644322 NGA75 644322 LA50 1 LGA50 1 LA75 2	NA50	1921378
NGA75 644322 LA50 1 LGA50 1 LA75 2		1921378
LA50 1 LGA50 1 LA75 2	NA75	644322
LGA50 1 LA75 2	NGA75	644322
LA75 2	LA50	1
	LGA50	1
LGA75 2	LA75	2
	LGA75	2

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

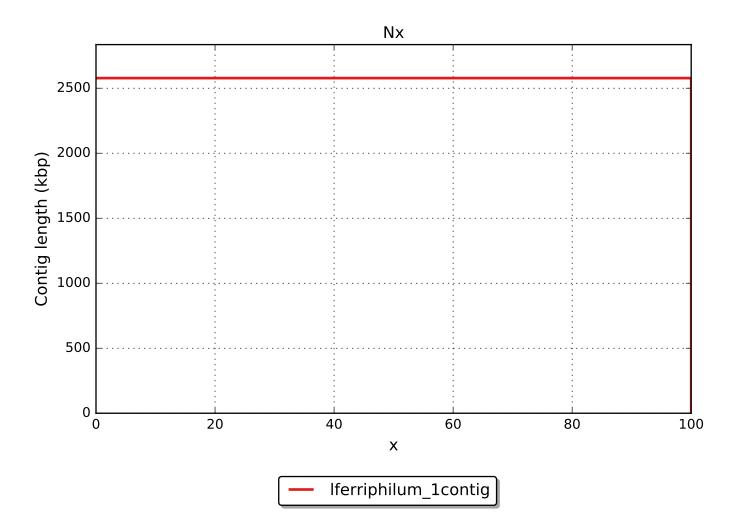
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# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	2577733
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	3
# indels	91
# indels (<= 5 bp)	91
# indels (> 5 bp)	0
Indels length	93

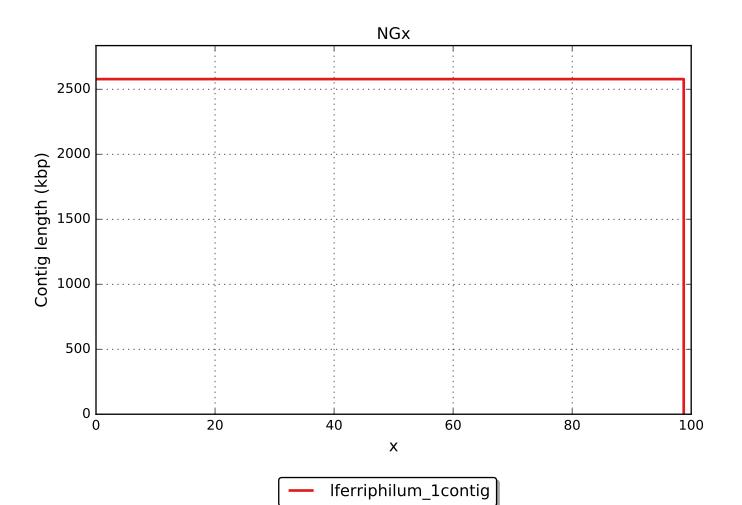
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

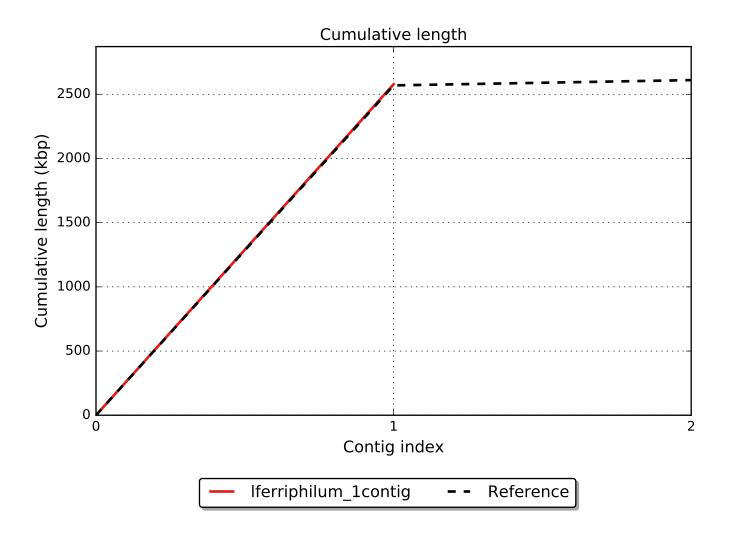
Unaligned report

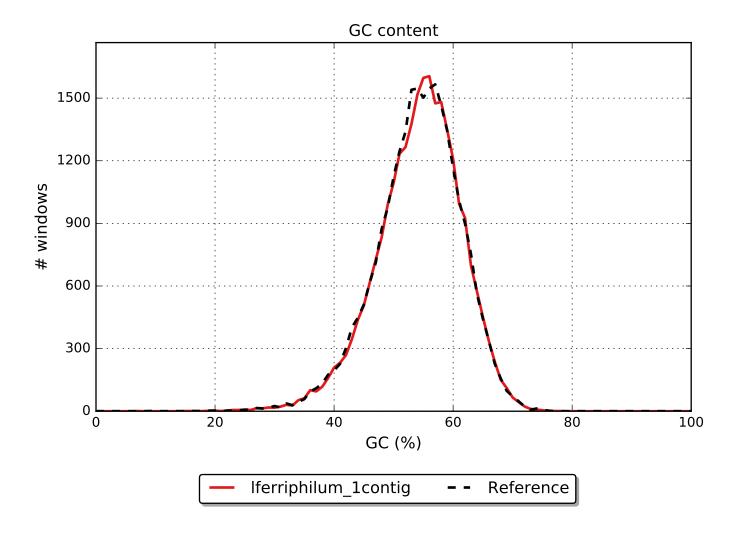
	lferriphilum_1contig
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

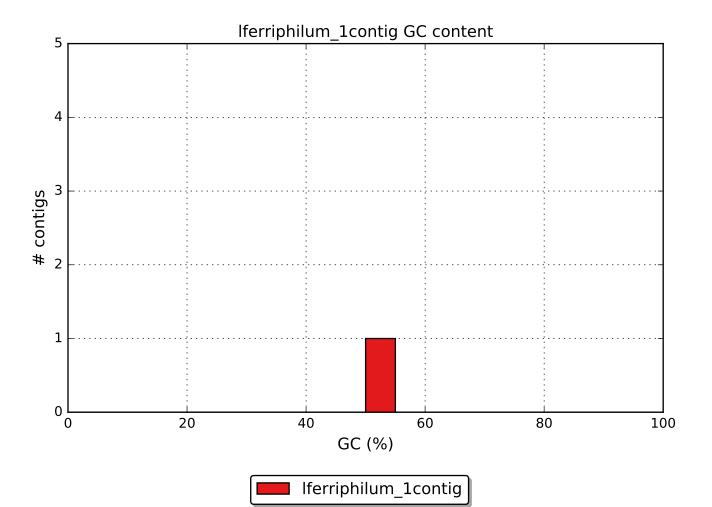
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

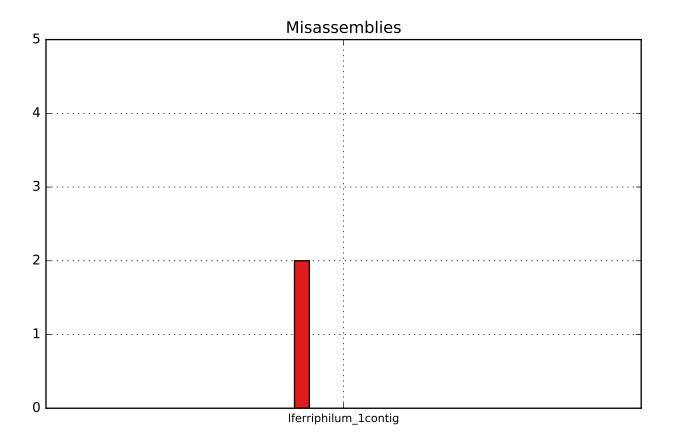




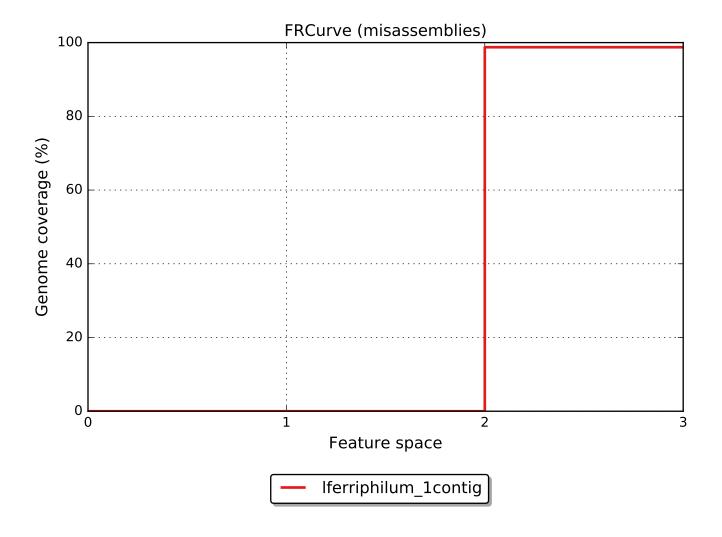


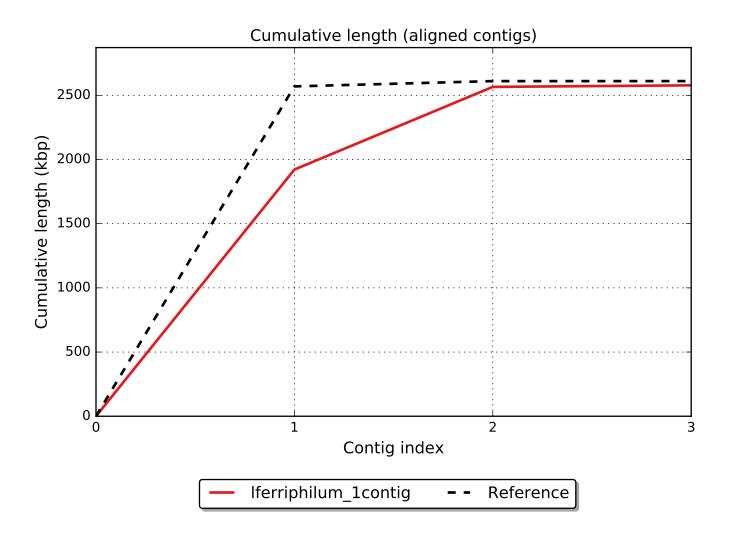


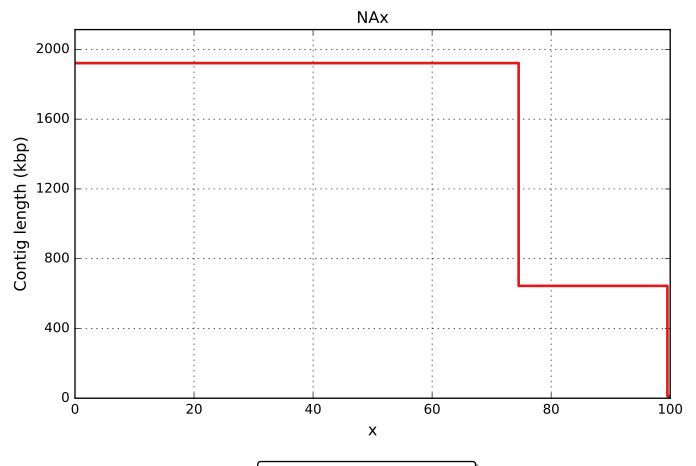




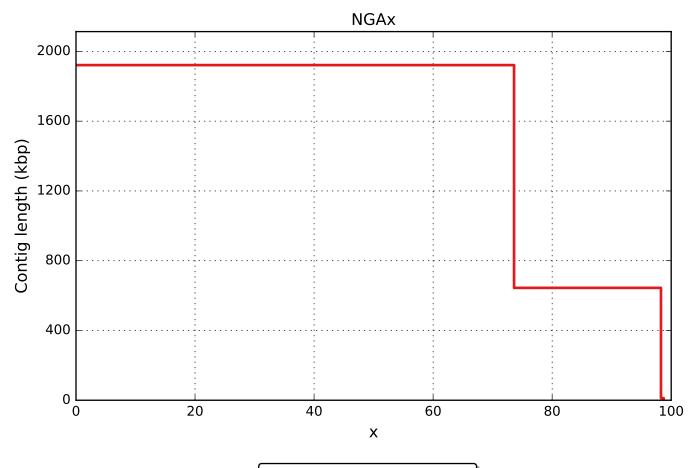








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