Report

# contigs (>= 1000 bp) 6 # contigs (>= 5000 bp) 0 # contigs (>= 10000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 10000 bp) 11152 Total length (>= 10000 bp) 0 Total length (>= 5000 bp) 0 Total length (>= 50000 bp) 0 # contigs 79 Largest contig 3640 Total length (>= 50000 bp) 0 # contigs 79 Largest contig 3640 Total length 55228 Reference length 4641652 GC (%) 50.90 Reference GC (%) 50.79 N50 618 N75 555 L50 29 L75 555 L50 29 L75 53 # misassemblies 2 # misassembles 2 # misassembled contigs 2 # misassembled contigs 0 # unaligned contigs length 2438 # local misassemblies 0 # unaligned length 42 Genome fraction (%) 1.189 Duplication ratio 1.000 # N's per 100 kbp 308.11 # indels per 100 kbp 9.06 Largest alignment 3640 NA50 616 NGA50 NA75 552 LA50 30 LA75 554		
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Reference length 4641652 GC (%) 50.90 Reference GC (%) 50.79 N50 618 N75 555 L50 29 L75 53 # misassemblies 2 # misassembled contigs 2 Misassembled contigs length 2438 # local misassemblies 0 # unaligned contigs 0 + 1 part Unaligned length 42 Genome fraction (%) 1.189 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 308.11 # indels per 100 kbp 9.06 Largest alignment 3640 NA50 616 NGA50 - NA75 552 LA50 30		3640
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N50 618 N75 555 L50 29 L75 53 # misassemblies 2 # misassembled contigs 2 Misassembled contigs length 2438 # local misassemblies 0 # unaligned contigs 0 + 1 part Unaligned length 42 Genome fraction (%) 1.189 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 308.11 # indels per 100 kbp 9.06 Largest alignment 3640 NA50 616 NGA50 - NA75 552 LA50 30	GC (%)	50.90
N75 555 L50 29 L75 53 # misassemblies 2 # misassembled contigs 2 Misassembled contigs length 2438 # local misassemblies 0 # unaligned contigs 0 + 1 part Unaligned length 42 Genome fraction (%) 1.189 Duplication ratio 1.000 # N's per 100 kbp 308.11 # indels per 100 kbp 9.06 Largest alignment 3640 NA50 616 NGA50 - NA75 552 LA50 30	Reference GC (%)	50.79
L50 29 L75 53 # misassemblies 2 # misassembled contigs 2 Misassembled contigs length 2438 # local misassemblies 0 # unaligned contigs 0 + 1 part Unaligned length 42 Genome fraction (%) 1.189 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 308.11 # indels per 100 kbp 9.06 Largest alignment 3640 NA50 616 NGA50 - NA75 552 LA50 30	N50	618
L75 53 # misassemblies 2 # misassembled contigs 2 Misassembled contigs length 2438 # local misassemblies 0 # unaligned contigs 0 + 1 part Unaligned length 42 Genome fraction (%) 1.189 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 308.11 # indels per 100 kbp 9.06 Largest alignment 3640 NA50 616 NGA50 - NA75 552 LA50 30	N75	555
# misassemblies 2 # misassembled contigs 2 Misassembled contigs length 2438 # local misassemblies 0 # unaligned contigs 0 + 1 part Unaligned length 42 Genome fraction (%) 1.189 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 308.11 # indels per 100 kbp 9.06 Largest alignment 3640 NA50 616 NGA50 - NA75 552 LA50 30	L50	29
# misassembled contigs 2 Misassembled contigs length 2438 # local misassemblies 0 # unaligned contigs 0 + 1 part Unaligned length 42 Genome fraction (%) 1.189 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 308.11 # indels per 100 kbp 9.06 Largest alignment 3640 NA50 616 NGA50 - NA75 552 LA50 30	L75	53
Misassembled contigs length 2438 # local misassemblies 0 # unaligned contigs 0 + 1 part Unaligned length 42 Genome fraction (%) 1.189 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 308.11 # indels per 100 kbp 9.06 Largest alignment 3640 NA50 616 NGA50 - NA75 552 LA50 30		2
# local misassemblies 0 # unaligned contigs 0 + 1 part Unaligned length 42 Genome fraction (%) 1.189 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 308.11 # indels per 100 kbp 9.06 Largest alignment 3640 NA50 616 NGA50 - NA75 552 LA50 30)	2
# unaligned contigs 0 + 1 part Unaligned length 42 Genome fraction (%) 1.189 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 308.11 # indels per 100 kbp 9.06 Largest alignment 3640 NA50 616 NGA50 - NA75 552 LA50 30	Misassembled contigs length	2438
Unaligned length 42 Genome fraction (%) 1.189 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 308.11 # indels per 100 kbp 9.06 Largest alignment 3640 NA50 616 NGA50 - NA75 552 LA50 30	# local misassemblies	•
Genome fraction (%) 1.189 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 308.11 # indels per 100 kbp 9.06 Largest alignment 3640 NA50 616 NGA50 - NA75 552 LA50 30)	0 + 1 part
Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 308.11 # indels per 100 kbp 9.06 Largest alignment 3640 NA50 616 NGA50 - NA75 552 LA50 30	Unaligned length	42
# N's per 100 kbp 0.00 # mismatches per 100 kbp 308.11 # indels per 100 kbp 9.06 Largest alignment 3640 NA50 616 NGA50 - NA75 552 LA50 30	Genome fraction (%)	1.189
# mismatches per 100 kbp 308.11 # indels per 100 kbp 9.06 Largest alignment 3640 NA50 616 NGA50 NA75 552 LA50 308.11	Duplication ratio	1.000
# indels per 100 kbp 9.06 Largest alignment 3640 NA50 616 NGA50 - NA75 552 LA50 30		0.00
Largest alignment 3640 NA50 616 NGA50 - NA75 552 LA50 30	,	308.11
NA50 616 NGA50 - NA75 552 LA50 30	,	9.06
NGA50 - NA75 552 LA50 30	Largest alignment	3640
NA75 552 LA50 30	NA50	616
LA50 30	NGA50	-
	NA75	552
LA75 54	LA50	30
	LA75	54

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

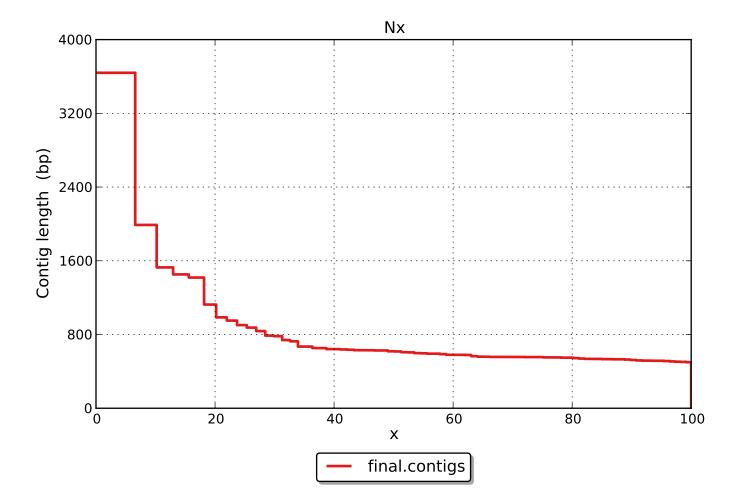
	final.contigs
# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	2438
# local misassemblies	0
# mismatches	170
# indels	5
# short indels	5
# long indels	0
Indels length	5

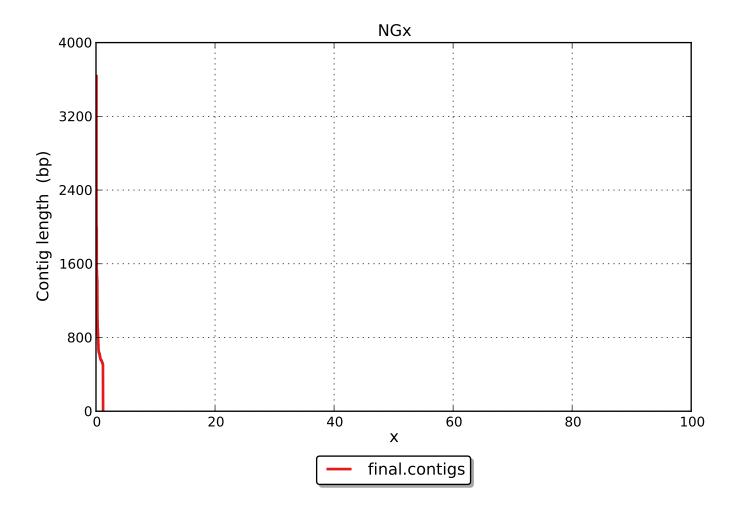
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

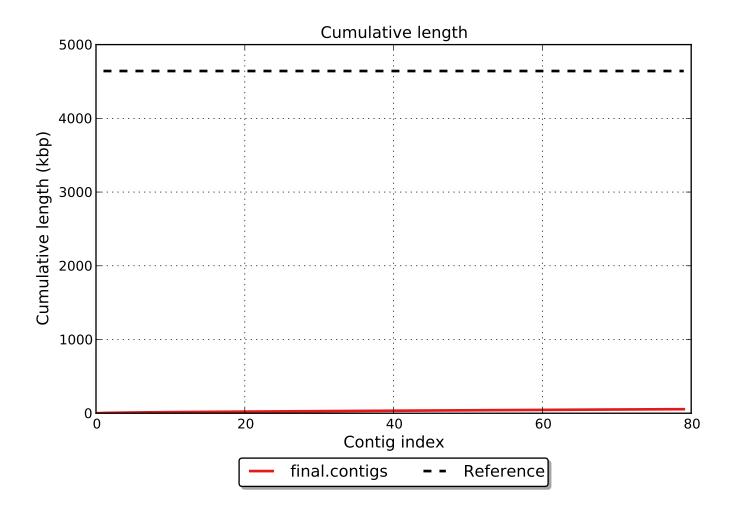
Unaligned report

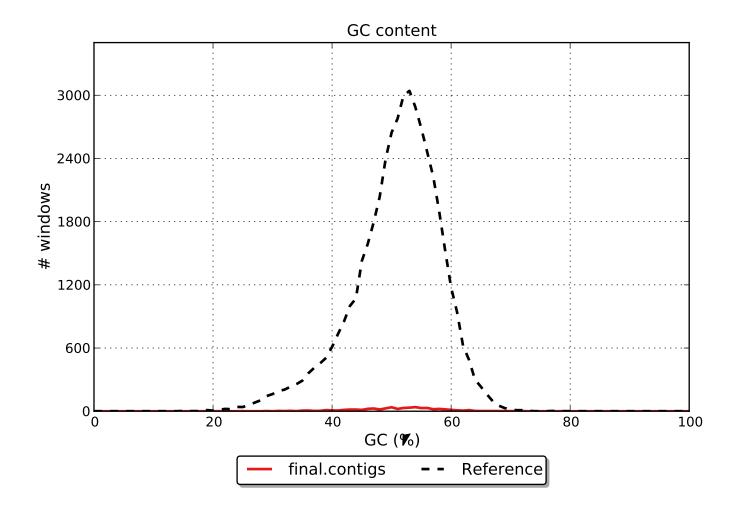
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	42
# N's	0

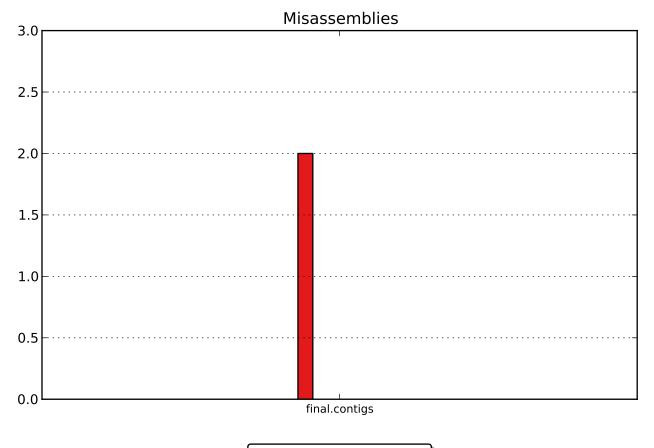
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).











relocations

