Report

# contigs (>= 1000 bp)		scaffolds
# contigs (>= 5000 bp)	# contigs (>= 1000 bp)	
# contigs (>= 10000 bp)		156
# contigs (>= 25000 bp)		ļ
# contigs (>= 50000 bp) 26 Total length (>= 1000 bp) 4809905 Total length (>= 5000 bp) 4640116 Total length (>= 10000 bp) 4329702 Total length (>= 25000 bp) 3429026 Total length (>= 50000 bp) 3429026 Total length (>= 50000 bp) 2359457 # contigs 249 Largest contig 200996 Total length 4826572 Reference length 4641652 GC (%) 50.73 Reference GC (%) 50.78 N50 46002 NG50 50917 N75 20816 NG75 23959 L50 28 LG50 26 L75 66 LG75 60 # misassemblies 3 # misassembled contigs 2 Misassembled contigs 127194 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 86.799 Duplication ratio 1.198 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1098.19 NA50 41789 NGA50 47800 NA75 23565 LA50 28 LGA50 26 LA75 668		57
Total length (>= 1000 bp) 4809905 Total length (>= 5000 bp) 4640116 Total length (>= 10000 bp) 4329702 Total length (>= 25000 bp) 3429026 Total length (>= 50000 bp) 2359457 # contigs 249 Largest contig 200996 Total length 4826572 Reference length 4641652 GC (%) 50.73 Reference GC (%) 50.78 N50 46002 NG50 50917 N75 20816 NG75 23959 L50 28 LG50 26 L75 66 LG75 60 # misassemblies 3 # misassembled contigs 2 Misassembled contigs 127194 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 86.799 Duplication ratio 1.198 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1098.19 # indels per 100 kbp 0.52 Largest alignment 200996 NA50 47800 NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 66		26
Total length (>= 10000 bp)	Total length (>= 1000 bp)	4809905
Total length (>= 25000 bp) 3429026 Total length (>= 50000 bp) 2359457 # contigs 249 Largest contig 200996 Total length 4826572 Reference length 4641652 GC (%) 50.73 Reference GC (%) 50.78 N50 46002 NG50 50917 N75 20816 NG75 23959 L50 28 LG50 26 L75 66 LG75 60 # misassemblies 3 # local misassembled contigs 2 Misassembled contigs length 127194 # local misassemblies 4 # unaligned length 0 Genome fraction (%) 86.799 Duplication ratio 1.198 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.52 Largest alignment 200996 NA50 47800 NA75 20059 <td< td=""><td>Total length (>= 5000 bp)</td><td>4640116</td></td<>	Total length (>= 5000 bp)	4640116
Total length (>= 50000 bp) 2359457 # contigs 249 Largest contig 200996 Total length 4826572 Reference length 4641652 GC (%) 50.73 Reference GC (%) 50.78 N50 46002 NG50 50917 N75 20816 NG75 23959 L50 28 LG50 26 L75 66 LG75 60 # misassemblies 3 # local misassembled contigs 2 Misassembled contigs length 127194 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 86.799 Duplication ratio 1.198 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.52 Largest alignment 200996 NA50 47800 NA75 20059 NGA5	Total length (>= 10000 bp)	4329702
# contigs 249 Largest contig 200996 Total length 4826572 Reference length 4641652 GC (%) 50.73 Reference GC (%) 50.78 N50 46002 NG50 50917 N75 20816 NG75 23959 L50 28 LG50 26 L75 66 LG75 60 # misassemblies 3 # misassembled contigs 2 Misassembled contigs 127194 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 86.799 Duplication ratio 1.198 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1098.19 # indels per 100 kbp 0.52 Largest alignment 200996 NA50 47800 NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 68	Total length (>= 25000 bp)	3429026
Largest contig 200996 Total length 4826572 Reference length 4641652 GC (%) 50.73 Reference GC (%) 50.78 N50 46002 NG50 50917 N75 20816 NG75 23959 L50 28 LG50 26 L75 66 LG75 60 # misassemblies 3 # misassembled contigs 2 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 86.799 Duplication ratio 1.198 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.52 Largest alignment 200996 NA50 41789 NGA50 47800 NA75 20059 NGA50 47800 NA75 23565 LA50 28 LGA50 26 LA75	Total length (>= 50000 bp)	2359457
Total length 4826572 Reference length 4641652 GC (%) 50.73 Reference GC (%) 50.78 N50 46002 NG50 50917 N75 20816 NG75 23959 L50 28 LG50 26 L75 66 LG75 60 # misassemblies 3 # local misassembled contigs 2 Misassembled contigs length 127194 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 86.799 Duplication ratio 1.198 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.52 Largest alignment 200996 NA50 47800 NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 68 <td># contigs</td> <td>249</td>	# contigs	249
Reference length 4641652 GC (%) 50.73 Reference GC (%) 50.78 N50 46002 NG50 50917 N75 20816 NG75 23959 L50 28 LG50 26 L75 66 LG75 60 # misassemblies 3 # local misassembled contigs 2 Misassembled contigs length 127194 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 86.799 Duplication ratio 1.198 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.52 Largest alignment 200996 NA50 41789 NGA50 47800 NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 68	Largest contig	200996
GC (%) 50.73 Reference GC (%) 50.78 N50 46002 NG50 50917 N75 20816 NG75 23959 L50 28 LG50 26 L75 66 LG75 60 # misassemblies 3 # misassembled contigs 2 Misassembled contigs 127194 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 86.799 Duplication ratio 1.198 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.52 Largest alignment 200996 NA50 41789 NGA50 47800 NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 68	Total length	4826572
Reference GC (%) 50.78 N50 46002 NG50 50917 N75 20816 NG75 23959 L50 28 LG50 26 L75 66 LG75 60 # misassemblies 3 # misassembled contigs 2 Misassembled contigs length 127194 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 86.799 Duplication ratio 1.198 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1098.19 # indels per 100 kbp 0.52 Largest alignment 200996 NA50 41789 NGA50 47800 NA75 2059 NGA75 23565 LA50 28 LGA50 26 LA75 68	Reference length	4641652
N50 46002 NG50 50917 N75 20816 NG75 23959 L50 28 LG50 26 L75 66 LG75 60 # misassemblies 3 # misassembled contigs 2 Misassembled contigs length 127194 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 86.799 Duplication ratio 1.198 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1098.19 # indels per 100 kbp 0.52 Largest alignment 200996 NA50 47800 NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 68	GC (%)	50.73
NG50 50917 N75 20816 NG75 23959 L50 28 LG50 26 L75 66 LG75 60 # misassemblies 3 # misassembled contigs 2 Misassembled contigs length 127194 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 86.799 Duplication ratio 1.198 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1098.19 # indels per 100 kbp 0.52 Largest alignment 200996 NA50 41789 NGA50 47800 NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 68	Reference GC (%)	50.78
N75 20816 NG75 23959 L50 28 LG50 26 L75 66 LG75 60 # misassemblies 3 # misassembled contigs 2 Misassembled contigs length 127194 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 86.799 Duplication ratio 1.198 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1098.19 # indels per 100 kbp 0.52 Largest alignment 200996 NA50 41789 NGA50 47800 NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 68	N50	46002
NG75 23959 L50 28 LG50 26 L75 66 LG75 60 # misassemblies 3 # misassembled contigs 2 Misassembled contigs length 127194 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 86.799 Duplication ratio 1.198 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1098.19 # indels per 100 kbp 0.52 Largest alignment 200996 NA50 41789 NGA50 47800 NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 68	NG50	50917
L50 28 LG50 26 L75 66 LG75 60 # misassemblies 3 # misassembled contigs 2 Misassembled contigs length 127194 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 86.799 Duplication ratio 1.198 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1098.19 # indels per 100 kbp 0.52 Largest alignment 200996 NA50 41789 NGA50 47800 NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 68	N75	20816
LG50 26 L75 66 LG75 60 # misassemblies 3 # misassembled contigs 2 Misassembled contigs length 127194 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 86.799 Duplication ratio 1.198 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1098.19 # indels per 100 kbp 0.52 Largest alignment 200996 NA50 47800 NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 68	NG75	23959
L75 66 LG75 60 # misassemblies 3 # misassembled contigs 2 Misassembled contigs length 127194 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 86.799 Duplication ratio 1.198 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1098.19 # indels per 100 kbp 0.52 Largest alignment 200996 NA50 47800 NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 68	L50	28
LG75 60 # misassemblies 3 # misassembled contigs 2 Misassembled contigs length 127194 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 86.799 Duplication ratio 1.198 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1098.19 # indels per 100 kbp 0.52 Largest alignment 200996 NA50 41789 NGA50 47800 NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 68	LG50	26
# misassemblies 3 # misassembled contigs 2 Misassembled contigs length 127194 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 86.799 Duplication ratio 1.198 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1098.19 # indels per 100 kbp 0.52 Largest alignment 200996 NA50 41789 NGA50 47800 NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 68	L75	66
# misassembled contigs 2 Misassembled contigs length 127194 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 86.799 Duplication ratio 1.198 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1098.19 # indels per 100 kbp 0.52 Largest alignment 200996 NA50 41789 NGA50 47800 NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 68	LG75	60
Misassembled contigs length 127194 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 86.799 Duplication ratio 1.198 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1098.19 # indels per 100 kbp 0.52 Largest alignment 200996 NA50 41789 NGA50 47800 NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 68	# misassemblies	3
# local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 86.799 Duplication ratio 1.198 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1098.19 # indels per 100 kbp 0.52 Largest alignment 200996 NA50 41789 NGA50 47800 NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 68	# misassembled contigs	2
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 86.799 Duplication ratio 1.198 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1098.19 # indels per 100 kbp 200996 NA50 41789 NGA50 47800 NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 68	Misassembled contigs length	127194
Unaligned length 0 Genome fraction (%) 86.799 Duplication ratio 1.198 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1098.19 # indels per 100 kbp 0.52 Largest alignment 200996 NA50 41789 NGA50 47800 NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 68	# local misassemblies	4
Genome fraction (%) 86.799 Duplication ratio 1.198 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1098.19 # indels per 100 kbp 0.52 Largest alignment 200996 NA50 41789 NGA50 47800 NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 68		0 + 0 part
Duplication ratio 1.198 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1098.19 # indels per 100 kbp 0.52 Largest alignment 200996 NA50 41789 NGA50 47800 NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 68	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 1098.19 # indels per 100 kbp 0.52 Largest alignment 200996 NA50 41789 NGA50 47800 NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 68	Genome fraction (%)	86.799
# mismatches per 100 kbp 1098.19 # indels per 100 kbp 0.52 Largest alignment 200996 NA50 41789 NGA50 47800 NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 68		
# indels per 100 kbp 0.52 Largest alignment 200996 NA50 41789 NGA50 47800 NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 68		0.00
Largest alignment 200996 NA50 41789 NGA50 47800 NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 68	# mismatches per 100 kbp	
NA50 41789 NGA50 47800 NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 68	# indels per 100 kbp	0.52
NGA50 47800 NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 68	Largest alignment	200996
NA75 20059 NGA75 23565 LA50 28 LGA50 26 LA75 68		41789
NGA75 23565 LA50 28 LGA50 26 LA75 68		47800
LA50 28 LGA50 26 LA75 68		ļ
LGA50 26 LA75 68	NGA75	23565
LA75 68		28
		26
LGA75 61		
	LGA75	61

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

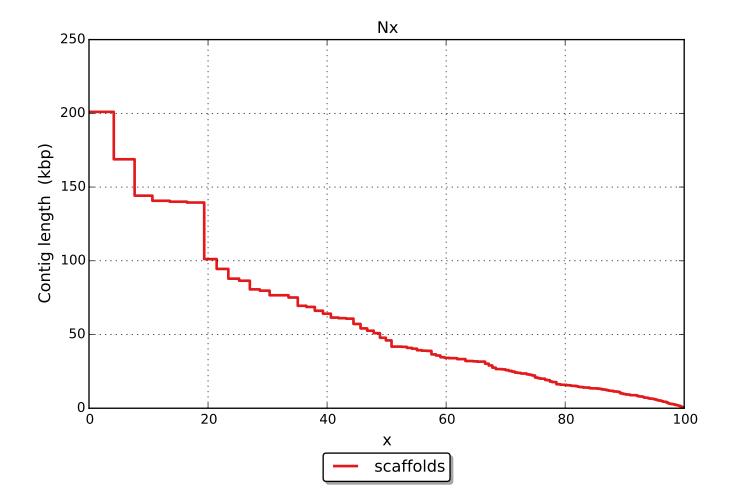
	scaffolds
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	127194
# local misassemblies	4
# mismatches	44245
# indels	21
# short indels	21
# long indels	0
Indels length	21

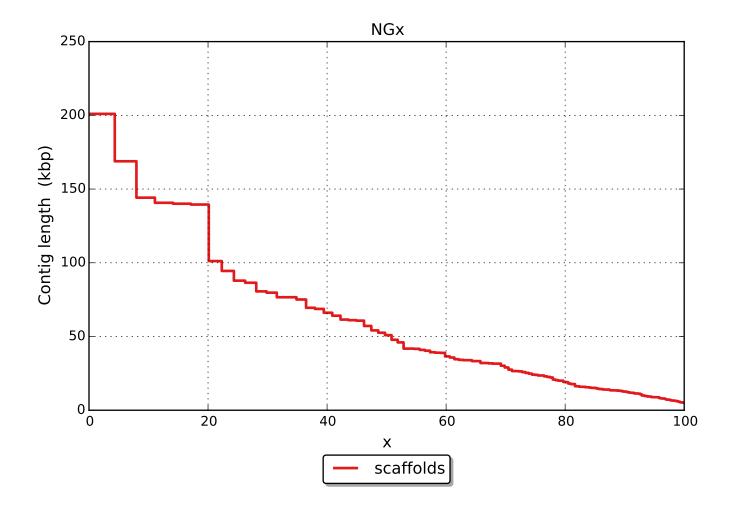
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

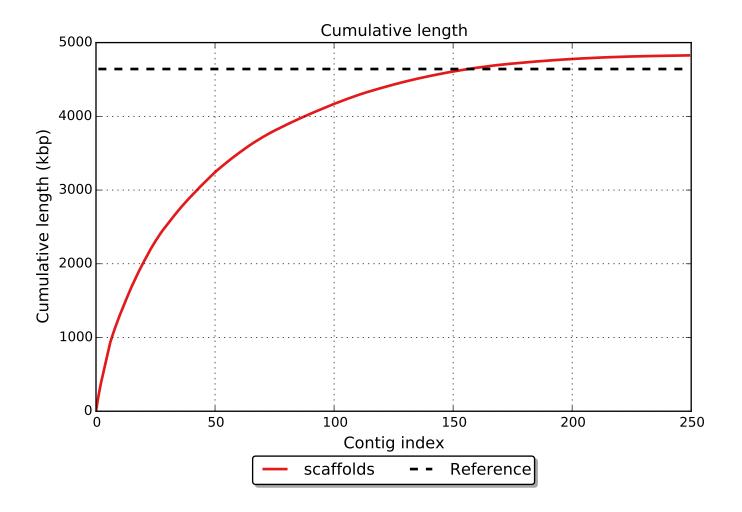
Unaligned report

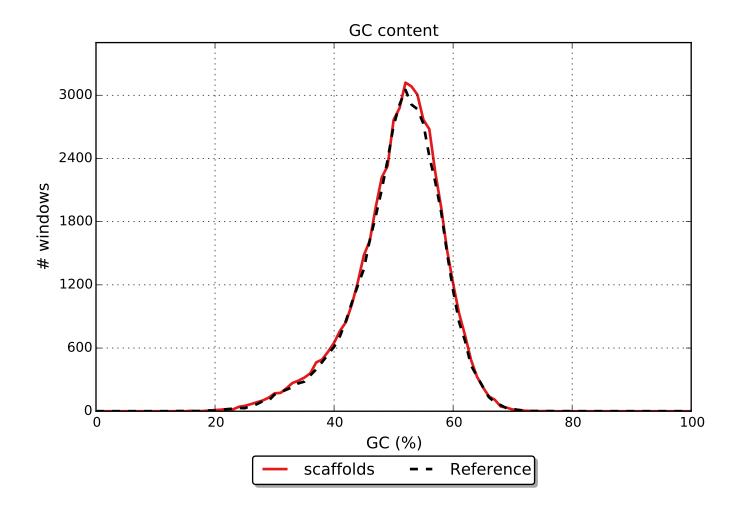
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

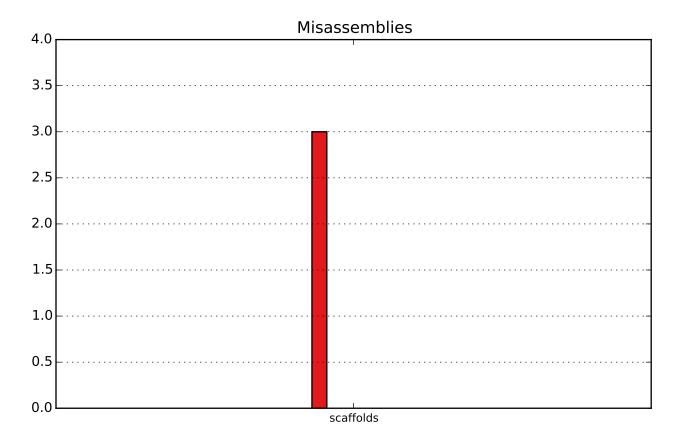
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).











relocations

