Report

# contigs (>= 1000 bp) 108 # contigs (>= 5000 bp) 82 # contigs (>= 25000 bp) 82 # contigs (>= 25000 bp) 40 # contigs (>= 50000 bp) 40 # contigs (>= 50000 bp) 21 Total length (>= 1000 bp) 3521952 Total length (>= 10000 bp) 3428883 Total length (>= 10000 bp) 3229812 Total length (>= 25000 bp) 2532410 Total length (>= 50000 bp) 1861491 # contigs 182 Largest contig 186891 Total length 3541698 Reference length 4641652 GC (%) 50.88 Reference GC (%) 50.79 N50 52546 NG50 33321 N75 22200 NG75 2361 L50 20 LG50 33 L75 46 LG75 124 # misassemblies 1 # misassembled contigs 1 # misassembled contigs 1 Misassembled contigs 10 # local misassemblies 2 # unaligned length 0 Genome fraction (%) 75.323 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 34 LA50 20 LGA50 34 LA75 46 LGA75 125		scaffolds
# contigs (>= 10000 bp)	# contigs (>= 1000 bp)	
# contigs (>= 10000 bp)		108
# contigs (>= 25000 bp) 40 # contigs (>= 50000 bp) 21 Total length (>= 1000 bp) 3521952 Total length (>= 5000 bp) 3428883 Total length (>= 10000 bp) 3229812 Total length (>= 25000 bp) 2532410 Total length (>= 50000 bp) 1861491 # contigs 182 Largest contig 186891 Total length 3541698 Reference length 4641652 GC (%) 50.88 Reference GC (%) 50.79 N50 52546 NG50 33321 N75 22200 NG75 2361 L50 20 LG50 33 L75 46 LG75 124 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 75.323 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1009.55 # indels per 100 kbp 0.72 Largest alignment 186891 NA50 31609 NA75 22200 NGA75 22361 LA50 20 LGA50 34 LA50 20 LGA50 34		82
# contigs (>= 50000 bp) 21 Total length (>= 1000 bp) 3521952 Total length (>= 5000 bp) 3428883 Total length (>= 10000 bp) 3229812 Total length (>= 25000 bp) 2532410 Total length (>= 50000 bp) 1861491 # contigs 182 Largest contig 186891 Total length 3541698 Reference length 4641652 GC (%) 50.88 Reference GC (%) 50.79 N50 52546 NG50 33321 N75 22200 NG75 2361 L50 20 LG50 33 L75 46 LG75 124 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 75.323 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1009.55 # indels per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 34 LA75 46 LGA50 20 LGA50 34 LA75 46		40
Total length (>= 1000 bp) 3521952 Total length (>= 5000 bp) 3428883 Total length (>= 10000 bp) 3229812 Total length (>= 25000 bp) 2532410 Total length (>= 50000 bp) 1861491 # contigs 182 Largest contig 186891 Total length 3541698 Reference length 4641652 GC (%) 50.88 Reference GC (%) 50.79 N50 52546 NG50 33321 N75 22200 NG75 2361 L50 20 LG50 33 L75 46 LG75 124 # misassembled contigs 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 75.323 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1009.55 # indels per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 346 LA50 20 LGA50 34 LA75 466		21
Total length (>= 10000 bp) 3229812 Total length (>= 25000 bp) 2532410 Total length (>= 50000 bp) 1861491 # contigs 182 Largest contig 186891 Total length 3541698 Reference length 4641652 GC (%) 50.88 Reference GC (%) 50.79 N50 52546 NG50 33321 N75 22200 NG75 2361 L50 20 LG50 33 L75 46 LG75 124 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 75.323 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1009.55 # indels per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LG50 314 LA50 20 LG50 314 LA75 46		3521952
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Total length (>= 50000 bp) 1861491 # contigs 182 Largest contig 186891 Total length 3541698 Reference length 4641652 GC (%) 50.88 Reference GC (%) 50.79 N50 52546 NG50 33321 N75 22200 NG75 2361 L50 20 LG50 33 L75 46 LG75 124 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 75.323 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # mismatches per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LA50	Total length (>= 10000 bp)	3229812
# contigs 182 Largest contig 186891 Total length 3541698 Reference length 4641652 GC (%) 50.88 Reference GC (%) 50.79 N50 52546 NG50 33321 N75 22200 NG75 2361 L50 20 LG50 33 L75 46 LG75 124 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 1 # local misassemblies 2 # unaligned length 0 Genome fraction (%) 75.323 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1009.55 # indels per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34 LA50 20 LGA50 34	Total length (>= 25000 bp)	2532410
Largest contig 186891 Total length 3541698 Reference length 4641652 GC (%) 50.88 Reference GC (%) 50.79 N50 52546 NG50 33321 N75 22200 NG75 2361 L50 20 LG50 33 L75 46 LG75 124 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 75.323 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34 LA75 46	Total length (>= 50000 bp)	1861491
Total length 3541698 Reference length 4641652 GC (%) 50.88 Reference GC (%) 50.79 N50 52546 NG50 33321 N75 22200 NG75 2361 L50 20 LG50 33 L75 46 LG75 124 # misassemblies 1 # misassembled contigs 66116 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 75.323 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1009.55 # indels per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34	# contigs	182
Reference length 4641652 GC (%) 50.88 Reference GC (%) 50.79 N50 52546 NG50 33321 N75 22200 NG75 2361 L50 20 LG50 33 L75 46 LG75 124 # misassemblies 1 # local misassembled contigs 1 Misassembled contigs length 66116 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 75.323 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1009.55 # indels per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34 LA75 46	Largest contig	186891
GC (%) 50.88 Reference GC (%) 50.79 N50 52546 NG50 33321 N75 22200 NG75 2361 L50 20 LG50 33 L75 46 LG75 124 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 75.323 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1009.55 # indels per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34 LA75 46	Total length	3541698
Reference GC (%) 50.79 N50 52546 NG50 33321 N75 22200 NG75 2361 L50 20 LG50 33 L75 46 LG75 124 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 75.323 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1009.55 # indels per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34 LA75 46	Reference length	4641652
N50 52546 NG50 33321 N75 22200 NG75 2361 L50 20 LG50 33 L75 46 LG75 124 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 66116 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 75.323 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1009.55 # indels per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34 LA75 46	GC (%)	50.88
NG50 33321 N75 22200 NG75 2361 L50 20 LG50 33 L75 46 LG75 124 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 66116 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 75.323 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1009.55 # indels per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34 LA75 46	Reference GC (%)	50.79
N75 22200 NG75 2361 L50 20 LG50 33 L75 46 LG75 124 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 66116 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 75.323 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1009.55 # indels per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34 LA75 46	N50	52546
NG75 2361 L50 20 LG50 33 L75 46 LG75 124 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 66116 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 75.323 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1009.55 # indels per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34 LA75 46	NG50	33321
L50 20 LG50 33 L75 46 LG75 124 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 66116 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 75.323 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1009.55 # indels per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34 LA75 46	N75	22200
LG50 33 L75 46 LG75 124 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 66116 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 75.323 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1009.55 # indels per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34 LA75 46	NG75	2361
L75 46 LG75 124 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 66116 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 75.323 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1009.55 # indels per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34 LA75 46	L50	20
LG75 124 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 66116 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 75.323 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1009.55 # indels per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34 LA75 46	LG50	33
# misassemblies 1 # misassembled contigs 1 Misassembled contigs length 66116 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 75.323 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1009.55 # indels per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34	L75	46
# misassembled contigs 1 Misassembled contigs length 66116 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 75.323 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1009.55 # indels per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34 LA75 46	LG75	124
Misassembled contigs length 66116 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 75.323 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1009.55 # indels per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34 LA75 46	# misassemblies	1
# local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 75.323 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1009.55 # indels per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34 LA75 46	# misassembled contigs	1
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 75.323 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1009.55 # indels per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34 LA75 46	Misassembled contigs length	66116
Unaligned length 0 Genome fraction (%) 75.323 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1009.55 # indels per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34 LA75 46	# local misassemblies	2
Genome fraction (%) 75.323 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1009.55 # indels per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34 LA75 46		0 + 0 part
Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1009.55 # indels per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34 LA75 46	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 1009.55 # indels per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34 LA75 46		75.323
# mismatches per 100 kbp 1009.55 # indels per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34 LA75 46		1.013
# indels per 100 kbp 0.72 Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34 LA75 46	# N's per 100 kbp	0.00
Largest alignment 186891 NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34 LA75 46	# mismatches per 100 kbp	1009.55
NA50 51199 NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34 LA75 46	# indels per 100 kbp	
NGA50 31609 NA75 22200 NGA75 2361 LA50 20 LGA50 34 LA75 46	Largest alignment	186891
NA75 22200 NGA75 2361 LA50 20 LGA50 34 LA75 46		51199
NGA75 2361 LA50 20 LGA50 34 LA75 46		31609
LA50 20 LGA50 34 LA75 46		
LGA50 34 LA75 46	NGA75	2361
LA75 46		
LGA75 125		-
	LGA75	125

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	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	66116
# local misassemblies	2
# mismatches	35296
# indels	25
# short indels	25
# long indels	0
Indels length	31

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).















