Report

# contigs (>= 1000 bp)		final.contigs
# contigs (>= 5000 bp)	# contigs (>= 1000 bp)	
# contigs (>= 10000 bp)		278
# contigs (>= 25000 bp) 37 # contigs (>= 50000 bp) 3 Total length (>= 1000 bp) 4814459 Total length (>= 5000 bp) 4454823 Total length (>= 5000 bp) 4454823 Total length (>= 10000 bp) 3728761 Total length (>= 50000 bp) 1385398 Total length (>= 50000 bp) 199824 # contigs 453 Largest contig 74919 Total length 4846610 Reference length 4857432 GC (%) 52.20 Reference GC (%) 52.22 N50 18511 NG50 18511 N75 10564 NG75 10518 L50 86 L75 171 LG75 172 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned length 0 Genome fraction (%) 98.659 Duplication ratio 1.011 # N's per 100 kbp 0.00 # mismatches per 100 kbp 34.85 # indels per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NA75 10518 LA50 86 LGA50 86 LGA50 86 LGA50 86 LGA50 86 LGA50 86		
# contigs (>= 50000 bp)		37
Total length (>= 1000 bp)		3
Total length (>= 5000 bp) 4454823 Total length (>= 10000 bp) 3728761 Total length (>= 25000 bp) 1385398 Total length (>= 50000 bp) 199824 # contigs 453 Largest contig 74919 Total length 4846610 Reference length 4857432 GC (%) 52.20 Reference GC (%) 52.22 N50 18511 NG50 18511 N75 10564 NG75 10518 L50 86 L75 171 LG75 172 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # unaligned length 0 Genome fraction (%) 98.659 Duplication ratio 1.011 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NA75 10564 <		4814459
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Total length (>= 25000 bp) 1385398 Total length (>= 50000 bp) 199824 # contigs 453 Largest contig 74919 Total length 4846610 Reference length 4857432 GC (%) 52.20 Reference GC (%) 52.22 N50 18511 NG50 18511 N75 10564 NG75 10518 L50 86 L75 171 LG75 172 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned length 0 Genome fraction (%) 98.659 Duplication ratio 1.011 # N's per 100 kbp 0.00 # mismatches per 100 kbp 34.85 # indels per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NGA50 18511		3728761
# contigs 453 Largest contig 74919 Total length 4846610 Reference length 4857432 GC (%) 52.20 Reference GC (%) 52.22 N50 18511 NG50 18511 N75 10564 NG75 10518 L50 86 L75 171 LG75 171 LG75 172 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.659 Duplication ratio 1.011 # N's per 100 kbp 0.00 # mismatches per 100 kbp 34.85 # indels per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NGA50 18511 NGA50 18511 NGA75 10564 NGA75 10518 LA50 86 LGA50 86 LA75 171		1385398
# contigs 453 Largest contig 74919 Total length 4846610 Reference length 4857432 GC (%) 52.20 Reference GC (%) 52.22 N50 18511 NG50 18511 N75 10564 NG75 10518 L50 86 L75 171 LG75 171 LG75 172 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.659 Duplication ratio 1.011 # N's per 100 kbp 0.00 # mismatches per 100 kbp 34.85 # indels per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NGA50 18511 NGA50 18511 NGA75 10564 NGA75 10518 LA50 86 LGA50 86 LA75 171	Total length (>= 50000 bp)	199824
Total length 4846610 Reference length 4857432 GC (%) 52.20 Reference GC (%) 52.22 N50 18511 NG50 18511 N75 10564 NG75 10518 L50 86 LG50 86 L75 171 LG75 172 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Unaligned length 0 Genome fraction (%) 98.659 Duplication ratio 1.011 # N's per 100 kbp 0.00 # mismatches per 100 kbp 34.85 # indels per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NGA50 18511 NA75 10564 NGA75 10518 LA50 86 LA50 86 LA75 171		453
Reference length 4857432 GC (%) 52.20 Reference GC (%) 52.22 N50 18511 NG50 18511 N75 10564 NG75 10518 L50 86 LG50 86 L75 171 LG75 172 # misassemblies 0 # local misassembles 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.659 Duplication ratio 1.011 # N's per 100 kbp 0.00 # mismatches per 100 kbp 34.85 # indels per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NGA50 18511 NA75 10564 NGA75 10518 LA50 86 LA75 171	Largest contig	74919
GC (%) 52.20 Reference GC (%) 52.22 N50 18511 NG50 18511 N75 10564 NG75 10518 L50 86 LG50 86 L75 171 LG75 172 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.659 Duplication ratio 1.011 # N's per 100 kbp 0.00 # mismatches per 100 kbp 34.85 # indels per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NA75 10564 NGA75 10518 LA50 86 LA75 171	Total length	4846610
GC (%) 52.20 Reference GC (%) 52.22 N50 18511 NG50 18511 N75 10564 NG75 10518 L50 86 LG50 86 L75 171 LG75 172 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.659 Duplication ratio 1.011 # N's per 100 kbp 0.00 # mismatches per 100 kbp 34.85 # indels per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NA75 10564 NGA75 10518 LA50 86 LA75 171	Reference length	4857432
N50 18511 NG50 18511 N75 10564 NG75 10518 L50 86 LG50 86 L75 171 LG75 172 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.659 Duplication ratio 1.011 # N's per 100 kbp 0.00 # mismatches per 100 kbp 34.85 # indels per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NA75 10564 NGA75 10518 LA50 86 LGA50 86 LA75 171		52.20
NG50 18511 N75 10564 NG75 10518 L50 86 LG50 86 L75 171 LG75 172 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.659 Duplication ratio 1.011 # N's per 100 kbp 0.00 # mismatches per 100 kbp 34.85 # indels per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NA75 10564 NGA75 10518 LA50 86 LGA50 86 LA75 171		52.22
N75 10564 NG75 10518 L50 86 LG50 86 L75 171 LG75 172 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.659 Duplication ratio 1.011 # N's per 100 kbp 0.00 # mismatches per 100 kbp 34.85 # indels per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NGA50 18511 NA75 10564 NGA75 10518 LA50 86 LGA50 86 LA75 171	N50	18511
NG75 10518 L50 86 LG50 86 L75 171 LG75 172 # misassemblies 0 Misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.659 Duplication ratio 1.011 # N's per 100 kbp 0.00 # mismatches per 100 kbp 34.85 # indels per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NGA50 18511 NA75 10564 NGA75 10518 LA50 86 LA75 171	NG50	18511
L50 86 LG50 86 L75 171 LG75 172 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.659 Duplication ratio 1.011 # N's per 100 kbp 0.00 # mismatches per 100 kbp 34.85 # indels per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NGA50 18511 NA75 10564 NGA75 10518 LA50 86 LGA50 86 LA75 171	N75	10564
LG50 86 L75 171 LG75 172 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.659 Duplication ratio 1.011 # N's per 100 kbp 0.00 # mismatches per 100 kbp 34.85 # indels per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NGA50 18511 NA75 10564 NGA75 10518 LA50 86 LGA50 86 LA75 171	NG75	10518
L75 171 LG75 172 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.659 Duplication ratio 1.011 # N's per 100 kbp 0.00 # mismatches per 100 kbp 34.85 # indels per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NA75 10564 NGA75 10518 LA50 86 LGA50 86 LA75 171	L50	86
LG75 172 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.659 Duplication ratio 1.011 # N's per 100 kbp 0.00 # mismatches per 100 kbp 34.85 # indels per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NA75 10564 NGA75 10518 LA50 86 LGA50 86 LA75 171	LG50	86
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.659 Duplication ratio 1.011 # N's per 100 kbp 0.00 # mismatches per 100 kbp 34.85 # indels per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NGA50 18511 NA75 10564 NGA75 10518 LA50 86 LGA50 86 LA75 171	L75	171
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.659 Duplication ratio 1.011 # N's per 100 kbp 0.00 # mismatches per 100 kbp 34.85 # indels per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NGA50 18511 NA75 10564 NGA75 10518 LA50 86 LGA50 86 LA75 171	LG75	172
Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.659 Duplication ratio 1.011 # N's per 100 kbp 0.00 # mismatches per 100 kbp 34.85 # indels per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NGA50 18511 NA75 10564 NGA75 10518 LA50 86 LGA50 86 LA75 171	# misassemblies	0
# local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.659 Duplication ratio 1.011 # N's per 100 kbp 0.00 # mismatches per 100 kbp 34.85 # indels per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NGA50 18511 NA75 10564 NGA75 10518 LA50 86 LGA50 86 LA75 171	# misassembled contigs	0
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.659 Duplication ratio 1.011 # N's per 100 kbp 0.00 # mismatches per 100 kbp 34.85 # indels per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NGA50 18511 NA75 10564 NGA75 10518 LA50 86 LGA50 86 LA75 171	Misassembled contigs length	0
Unaligned length 0 Genome fraction (%) 98.659 Duplication ratio 1.011 # N's per 100 kbp 0.00 # mismatches per 100 kbp 34.85 # indels per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NGA50 18511 NA75 10564 NGA75 10518 LA50 86 LGA50 86 LA75 171	# local misassemblies	1
Genome fraction (%) 98.659 Duplication ratio 1.011 # N's per 100 kbp 0.00 # mismatches per 100 kbp 34.85 # indels per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NGA50 18511 NA75 10564 NGA75 10518 LA50 86 LGA50 86 LA75 171		0 + 0 part
Duplication ratio 1.011 # N's per 100 kbp 0.00 # mismatches per 100 kbp 34.85 # indels per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NGA50 18511 NA75 10564 NGA75 10518 LA50 86 LGA50 86 LA75 171	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 34.85 # indels per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NGA50 18511 NA75 10564 NGA75 10518 LA50 86 LGA50 86 LA75 171		
# mismatches per 100 kbp 34.85 # indels per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NGA50 18511 NA75 10564 NGA75 10518 LA50 86 LGA50 86 LA75 171	•	1.011
# indels per 100 kbp 0.02 Largest alignment 74919 NA50 18511 NGA50 18511 NA75 10564 NGA75 10518 LA50 86 LGA50 86 LA75 171		0.00
Largest alignment 74919 NA50 18511 NGA50 18511 NA75 10564 NGA75 10518 LA50 86 LGA50 86 LA75 171	# mismatches per 100 kbp	34.85
NA50 18511 NGA50 18511 NA75 10564 NGA75 10518 LA50 86 LGA50 86 LA75 171	# indels per 100 kbp	0.02
NGA50 18511 NA75 10564 NGA75 10518 LA50 86 LGA50 86 LA75 171	Largest alignment	74919
NA75 10564 NGA75 10518 LA50 86 LGA50 86 LA75 171	NA50	18511
NGA75 10518 LA50 86 LGA50 86 LA75 171	NGA50	18511
LA50 86 LGA50 86 LA75 171	NA75	10564
LGA50 86 LA75 171	NGA75	10518
LA75 171	LA50	86
	LGA50	86
LGA75 172	LA75	171
	LGA75	172

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	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	1670
# indels	1
# short indels	1
# long indels	0
Indels length	1

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	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).















