Report

# contigs (>= 1000 bp) 95 # contigs (>= 5000 bp) 70 # contigs (>= 10000 bp) 64 # contigs (>= 25000 bp) 51 # contigs (>= 25000 bp) 51 # contigs (>= 50000 bp) 34 Total length (>= 1000 bp) 4555837 Total length (>= 10000 bp) 4502124 Total length (>= 10000 bp) 4456744 Total length (>= 25000 bp) 4258489 Total length (>= 50000 bp) 3679265 # contigs 107 Largest contig 327154 Total length (>= 50000 bp) 3679265 # contigs 107 Largest contig 327154 Total length (>= 50000 bp) 3679265 # contigs 107 Largest contig 327154 Total length 4563292 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 112427 NG50 97783 N75 57924 NG75 56868 L50 14 LG50 15 L75 30 LG75 31 # misassemblies 1 # misassembled contigs 1 # misassembled contigs 1 Misassembled contigs 1 # unaligned contigs 1 # unaligned length 53 Genome fraction (%) 98.251 Duplication ratio 1.001 # N's per 100 kbp 9.89 Largest alignment 327154 NA50 112427 NGA50 97783 NA75 57924 NA50 112427 NGA50 97783 NA75 57924 NA50 112427 NGA50 97783 NA75 57924 NGA75 56868 LA50 114 LGA50 15 LA75 56868 LA50 15 LA75 56868 LA50 15 LA75 30 LGA75 31		
# contigs (>= 5000 bp)		final.contigs
# contigs (>= 10000 bp)	# contigs (>= 1000 bp)	95
# contigs (>= 25000 bp)	# contigs (>= 5000 bp)	70
# contigs (>= 50000 bp)	# contigs (>= 10000 bp)	64
Total length (>= 1000 bp) 4555837 Total length (>= 5000 bp) 4502124 Total length (>= 10000 bp) 4456744 Total length (>= 25000 bp) 4258489 Total length (>= 50000 bp) 3679265 # contigs 107 Largest contig 327154 Total length 4563292 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 112427 NG50 97783 N75 57924 NG75 56868 L50 14 LG50 15 L75 30 LG75 31 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 45889 # local misassemblies 11 Unaligned length 53 Genome fraction (%) 98.251 Duplication ratio 1.001 # mismatches per 100 kbp 9.89 Largest alignment	# contigs (>= 25000 bp)	51
Total length (>= 5000 bp) 4502124 Total length (>= 10000 bp) 4456744 Total length (>= 25000 bp) 4258489 Total length (>= 50000 bp) 3679265 # contigs 107 Largest contig 327154 Total length 4563292 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 112427 NG50 97783 N75 57924 NG75 56868 L50 14 LG50 15 L75 30 LG75 31 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 45889 # local misassemblies 11 # unaligned length 53 Genome fraction (%) 98.251 Duplication ratio 1.001 # N's per 100 kbp 9.89 Largest alignment 327154 NA50 97783 <	# contigs (>= 50000 bp)	34
Total length (>= 10000 bp) 4456744 Total length (>= 25000 bp) 3679265 # contigs 107 Largest contig 327154 Total length 4563292 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 112427 NG50 97783 N75 57924 NG75 56868 L50 14 LG50 15 L75 30 LG75 31 # misassemblies 1 # local misassemblies 1 # local misassemblies 11 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.251 Duplication ratio 1.001 # N's per 100 kbp 9.89 Largest alignment 327154 NA50 97783 NA75 57924 NGA50 97783 NA75 5686	Total length (>= 1000 bp)	4555837
Total length (>= 25000 bp) 3679265 # contigs 107 Largest contig 327154 Total length 4563292 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 112427 NG50 97783 N75 57924 NG75 56868 L50 14 LG50 15 L75 30 LG75 31 # misassemblies 1 # local misassembled contigs 1 # local misassemblies 11 # local misassemblies 11 # unaligned length 53 Genome fraction (%) 98.251 Duplication ratio 1.001 # N's per 100 kbp 9.89 Largest alignment 327154 NA50 112427 NGA50 97783 NA75 56868 LA50 14 LGA50 15	Total length (>= 5000 bp)	4502124
Total length (>= 50000 bp) 3679265 # contigs 107 Largest contig 327154 Total length 4563292 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 112427 NG50 97783 N75 57924 NG75 56868 L50 14 LG50 15 L75 30 LG75 31 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 # local misassemblies 11 # unaligned length 53 Genome fraction (%) 98.251 Duplication ratio 1.001 # N's per 100 kbp 9.89 Largest alignment 327154 NA50 112427 NGA50 97783 NA75 57924 NGA50 97783 NA75 56868 LA50 14 LA50 15	Total length (>= 10000 bp)	4456744
# contigs 107 Largest contig 327154 Total length 4563292 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 112427 NG50 97783 N75 57924 NG75 56868 L50 14 LG50 15 L75 30 LG75 31 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 45889 # local misassemblies 11 # unaligned length 53 Genome fraction (%) 98.251 Duplication ratio 1.001 # N's per 100 kbp 9.89 Largest alignment 327154 NA50 112427 NGA50 97783 NA75 57924 NGA75 56868 LA50 14 LGA50 15 LA75 30	Total length (>= 25000 bp)	4258489
Largest contig 327154 Total length 4563292 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 112427 NG50 97783 N75 57924 NG75 56868 L50 14 LG50 15 L75 30 LG75 31 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 45889 # local misassemblies 11 # unaligned length 53 Genome fraction (%) 98.251 Duplication ratio 1.001 # N's per 100 kbp 9.00 # mismatches per 100 kbp 9.89 Largest alignment 327154 NA50 112427 NGA50 97783 NA75 57924 NGA50 97783 NA75 56868 LA50 14 LGA50 15 LA75 30	Total length (>= 50000 bp)	3679265
Total length 4563292 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 112427 NG50 97783 N75 57924 NG75 56868 L50 14 LG50 15 L75 30 LG75 31 # misassemblies 1 # local misassembled contigs 1 # local misassemblies 11 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.251 Duplication ratio 1.001 # N's per 100 kbp 9.00 # mismatches per 100 kbp 9.89 Largest alignment 327154 NA50 97783 NA75 57924 NGA50 97783 NA75 56868 LA50 14 LGA50 15 LA75 30	# contigs	107
Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 112427 NG50 97783 N75 57924 NG75 56868 L50 14 LG50 15 L75 30 LG75 31 # misassemblies 1 # local misassembled contigs 1 Misassembled contigs length 45889 # local misassemblies 11 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.251 Duplication ratio 1.001 # Ni's per 100 kbp 9.00 # mismatches per 100 kbp 9.89 Largest alignment 327154 NA50 112427 NGA50 97783 NA75 57924 NGA75 56868 LA50 14 LGA50 15 LA75 30	Largest contig	327154
GC (%) 50.79 Reference GC (%) 50.79 N50 112427 NG50 97783 N75 57924 NG75 56868 L50 14 LG50 15 L75 30 LG75 31 # misassemblies 1 # local misassembled contigs 1 # local misassemblies 11 # local misassemblies 11 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.251 Duplication ratio 1.001 # N's per 100 kbp 9.89 Largest alignment 327154 NA50 112427 NGA50 97783 NA75 57924 NGA75 56868 LA50 14 LGA50 15 LA75 30	Total length	4563292
Reference GC (%) 50.79 N50 112427 NG50 97783 N75 57924 NG75 56868 L50 14 LG50 15 L75 30 LG75 31 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 45889 # local misassemblies 11 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.251 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 9.89 Largest alignment 327154 NA50 112427 NGA50 97783 NA75 57924 NGA75 56868 LA50 14 LGA50 15 LA75 30	Reference length	4641652
N50 112427 NG50 97783 N75 57924 NG75 56868 L50 14 LG50 15 L75 30 LG75 31 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 45889 # local misassemblies 11 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.251 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.86 # indels per 100 kbp 9.89 Largest alignment 327154 NA50 112427 NGA50 97783 NA75 57924 NGA75 56868 LA50 14 LGA50 15 LA75 30	GC (%)	50.74
N50 112427 NG50 97783 N75 57924 NG75 56868 L50 14 LG50 15 L75 30 LG75 31 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 45889 # local misassemblies 11 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.251 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.86 # indels per 100 kbp 9.89 Largest alignment 327154 NA50 112427 NGA50 97783 NA75 57924 NGA75 56868 LA50 14 LGA50 15 LA75 30	Reference GC (%)	50.79
N75 57924 NG75 56868 L50 14 LG50 15 L75 30 LG75 31 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 45889 # local misassemblies 11 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.251 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.86 # indels per 100 kbp 9.89 Largest alignment 327154 NA50 112427 NGA50 97783 NA75 57924 NGA75 56868 LA50 14 LGA50 15 LA75 30	N50	112427
NG75 56868 L50 14 LG50 15 L75 30 LG75 31 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 45889 # local misassemblies 11 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.251 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.86 # indels per 100 kbp 9.89 Largest alignment 327154 NA50 112427 NGA50 97783 NA75 57924 NGA75 56868 LA50 14 LGA50 15 LA75 30	NG50	97783
L50 14 LG50 15 L75 30 LG75 31 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 45889 # local misassemblies 11 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.251 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.86 # indels per 100 kbp 9.89 Largest alignment 327154 NA50 112427 NGA50 97783 NA75 57924 NGA75 56868 LA50 14 LGA50 15 LA75 30	N75	57924
LG50 15 L75 30 LG75 31 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 45889 # local misassemblies 11 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.251 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.86 # indels per 100 kbp 9.89 Largest alignment 327154 NA50 112427 NGA50 97783 NA75 57924 NGA75 56868 LA50 14 LGA50 15 LA75 30	NG75	56868
L75 30 LG75 31 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 45889 # local misassemblies 11 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.251 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.86 # indels per 100 kbp 9.89 Largest alignment 327154 NA50 112427 NGA50 97783 NA75 57924 NGA75 56868 LA50 14 LGA50 15 LA75 30	L50	14
LG75 31 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 45889 # local misassemblies 11 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.251 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.86 # indels per 100 kbp 989 Largest alignment 327154 NA50 112427 NGA50 97783 NA75 57924 NGA75 56868 LA50 14 LGA50 15 LA75 30	LG50	15
# misassemblies 1 # misassembled contigs 1 Misassembled contigs length 45889 # local misassemblies 11 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.251 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.86 # indels per 100 kbp 9.89 Largest alignment 327154 NA50 112427 NGA50 97783 NA75 57924 NGA75 56868 LA50 14 LGA50 15 LA75 30	L75	30
# misassembled contigs	LG75	31
Misassembled contigs length 45889 # local misassemblies 11 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.251 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.86 # indels per 100 kbp 9.89 Largest alignment 327154 NA50 112427 NGA50 97783 NA75 57924 NGA75 56868 LA50 14 LGA50 15 LA75 30	# misassemblies	1
# local misassemblies 11 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.251 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.86 # indels per 100 kbp 9.89 Largest alignment 327154 NA50 112427 NGA50 97783 NA75 57924 NGA75 56868 LA50 14 LGA50 155 LA75 30	# misassembled contigs	1
# unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.251 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.86 # indels per 100 kbp 9.89 Largest alignment 327154 NA50 112427 NGA50 97783 NA75 57924 NGA75 56868 LA50 14 LGA50 15 LA75 30	Misassembled contigs length	45889
Unaligned length 53 Genome fraction (%) 98.251 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.86 # indels per 100 kbp 9.89 Largest alignment 327154 NA50 112427 NGA50 97783 NA75 57924 NGA75 56868 LA50 14 LGA50 15 LA75 30	# local misassemblies	11
Genome fraction (%) 98.251 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.86 # indels per 100 kbp 9.89 Largest alignment 327154 NA50 112427 NGA50 97783 NA75 57924 NGA75 56868 LA50 14 LGA50 15 LA75 30	# unaligned contigs	0 + 1 part
Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.86 # indels per 100 kbp 9.89 Largest alignment 327154 NA50 112427 NGA50 97783 NA75 57924 NGA75 56868 LA50 14 LGA50 15 LA75 30	Unaligned length	53
# N's per 100 kbp 0.00 # mismatches per 100 kbp 59.86 # indels per 100 kbp 9.89 Largest alignment 327154 NA50 112427 NGA50 97783 NA75 57924 NGA75 56868 LA50 14 LGA50 15 LA75 30	Genome fraction (%)	98.251
# mismatches per 100 kbp 59.86 # indels per 100 kbp 9.89 Largest alignment 327154 NA50 112427 NGA50 97783 NA75 57924 NGA75 56868 LA50 14 LGA50 15 LA75 30	Duplication ratio	1.001
# indels per 100 kbp 9.89 Largest alignment 327154 NA50 112427 NGA50 97783 NA75 57924 NGA75 56868 LA50 14 LGA50 15 LA75 30	# N's per 100 kbp	0.00
Largest alignment 327154 NA50 112427 NGA50 97783 NA75 57924 NGA75 56868 LA50 14 LGA50 15 LA75 30	# mismatches per 100 kbp	59.86
NA50 112427 NGA50 97783 NA75 57924 NGA75 56868 LA50 14 LGA50 15 LA75 30	# indels per 100 kbp	9.89
NGA50 97783 NA75 57924 NGA75 56868 LA50 14 LGA50 15 LA75 30	Largest alignment	327154
NA75 57924 NGA75 56868 LA50 14 LGA50 15 LA75 30	NA50	
NGA75 56868 LA50 14 LGA50 15 LA75 30	NGA50	97783
LA50 14 LGA50 15 LA75 30	NA75	57924
LGA50 15 LA75 30	NGA75	56868
LA75 30	LA50	14
	LGA50	15
LGA75 31		30
	LGA75	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).

Misassemblies report

	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	45889
# local misassemblies	11
# mismatches	2730
# indels	451
# short indels	450
# long indels	1
Indels length	712

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	53
# 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).















