Report

# contigs (>= 1000 bp) 351 # contigs (>= 5000 bp) 237 # contigs (>= 10000 bp) 154 # contigs (>= 25000 bp) 53 # contigs (>= 25000 bp) 53 # contigs (>= 50000 bp) 65 Total length (>= 10000 bp) 4558643 Total length (>= 10000 bp) 4232041 Total length (>= 10000 bp) 3637276 Total length (>= 25000 bp) 1963920 Total length (>= 25000 bp) 379345 # contigs 380 Largest contig 94038 Total length (>= 50000 bp) 379345 # contigs 380 Largest contig 94038 Total length (>= 50000 bp) 379345 # contigs 380 Largest contig 94038 Total length 4581351 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 22582 NG50 21954 N75 12278 NG75 11457 L50 67 LG50 68 L75 136 LG75 140 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 1 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 98.147 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 94038 NA50 22582 NGA50 11457 LGA50 67 LGA50 68 LA75 11457 LAG50 67 LGA50 67 LGA50 67 LGA55 136		
# contigs (>= 5000 bp)		final.contigs
# contigs (>= 10000 bp)		351
# contigs (>= 25000 bp)	# contigs (>= 5000 bp)	237
# contigs (>= 50000 bp)		
Total length (>= 1000 bp)	# contigs (>= 25000 bp)	53
Total length (>= 5000 bp) 4232041 Total length (>= 10000 bp) 3637276 Total length (>= 25000 bp) 1963920 Total length (>= 50000 bp) 379345 # contigs 380 Largest contig 94038 Total length 4581351 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 22582 NG50 21954 N75 12278 NG75 11457 L50 67 LG50 68 L75 136 LG75 140 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 98.147 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 9		6
Total length (>= 10000 bp) 3637276 Total length (>= 25000 bp) 1963920 Total length (>= 50000 bp) 379345 # contigs 380 Largest contig 94038 Total length 4581351 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 22582 NG50 21954 N75 12278 NG75 11457 L50 67 LG50 68 L75 136 LG75 140 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 98.147 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 94038 NA50 22582	1	4558643
Total length (>= 25000 bp) 1963920 Total length (>= 50000 bp) 379345 # contigs 380 Largest contig 94038 Total length 4581351 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 22582 NG50 21954 N75 12278 NG75 11457 L50 67 LG50 68 L75 136 LG75 140 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 98.147 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.40 # indels per 100 kbp 0.00 Largest alignment 94038 NA50 22582	1	4232041
# contigs 380 Largest contig 94038 Total length (>= 50000 bp) 379345 # contigs 380 Largest contig 94038 Total length 4581351 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 22582 NG50 21954 N75 12278 NG75 11457 L50 67 LG50 68 L75 136 LG75 140 # misassemblies 1 # misassembled contigs 1 # misassembled contigs 1 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.147 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.40 # indels per 100 kbp 0.00 Largest alignment 94038 NA50 22582 NGA75 11457 LGA50 68 LA75 136 LGA50 68 LA75 136		3637276
# contigs 380 Largest contig 94038 Total length 4581351 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 22582 NG50 21954 N75 12278 NG75 11457 L50 67 LG50 68 L75 136 LG75 140 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.147 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.40 # indels per 100 kbp 0.40 Largest alignment 94038 NA50 22582 NGA50 21954 NA75 12278 NGA75 11457 LA5		1963920
Largest contig 94038 Total length 4581351 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 22582 NG50 21954 N75 12278 NG75 11457 L50 67 LG50 68 L75 136 LG75 140 # misassemblies 1 # local misassembled contigs 1 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.147 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.40 # indels per 100 kbp 0.00 Largest alignment 94038 NA50 22582 NGA50 21954 NA75 12278 NGA75 11457 LA50 67 LGA50 68	Total length (>= 50000 bp)	379345
Total length 4581351 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 22582 NG50 21954 N75 12278 NG75 11457 L50 67 LG50 68 L75 136 LG75 140 # misassemblies 1 # local misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.147 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.40 # indels per 100 kbp 0.00 Largest alignment 94038 NA50 22582 NGA50 21954 NA75 12278 NGA75 11457 LA50 67 </td <td># contigs</td> <td>380</td>	# contigs	380
Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 22582 NG50 21954 N75 12278 NG75 11457 L50 67 LG50 68 L75 136 LG75 140 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.147 Duplication ratio 1.006 # mismatches per 100 kbp 0.00 # mismatches per 100 kbp 0.40 # indels per 100 kbp 0.00 Largest alignment 94038 NA50 22582 NGA50 21954 NA75 12278 NGA75 11457 LA50 67 LGA50 68 LA75 136		94038
GC (%) 50.74 Reference GC (%) 50.79 N50 22582 NG50 21954 N75 12278 NG75 11457 L50 67 LG50 68 L75 136 LG75 140 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.147 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.40 # indels per 100 kbp 0.00 Largest alignment 94038 NA50 22582 NGA50 21954 NA75 12278 NGA75 11457 LA50 67 LGA50 68 LA75 136	Total length	4581351
Reference GC (%) 50.79 N50 22582 NG50 21954 N75 12278 NG75 11457 L50 67 LG50 68 L75 136 LG75 140 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.147 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.40 # indels per 100 kbp 0.00 Largest alignment 94038 NA50 22582 NGA50 21954 NA75 12278 NGA75 11457 LA50 67 LGA50 68 LA75 136	Reference length	4641652
N50 22582 NG50 21954 N75 12278 NG75 11457 L50 67 LG50 68 L75 136 LG75 140 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.147 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.40 # indels per 100 kbp 0.00 Largest alignment 94038 NA50 22582 NGA50 21954 NA75 12278 NGA75 11457 LA50 67 LGA50 68 LA75 136		50.74
NG50 21954 N75 12278 NG75 11457 L50 67 LG50 68 L75 136 LG75 140 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.147 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.40 # indels per 100 kbp 0.00 Largest alignment 94038 NA50 22582 NGA50 21954 NA75 12278 NGA75 11457 LA50 67 LGA50 68 LA75 136	Reference GC (%)	50.79
N75 12278 NG75 11457 L50 67 L650 68 L75 136 LG75 140 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.147 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.40 # indels per 100 kbp 0.00 Largest alignment 94038 NA50 22582 NGA50 21954 NA75 12278 NGA75 11457 LA50 67 LGA50 68 LA75 136	N50	22582
NG75 11457 L50 67 LG50 68 L75 136 LG75 140 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.147 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.40 # indels per 100 kbp 0.00 Largest alignment 94038 NA50 22582 NGA50 21954 NA75 12278 NGA75 11457 LA50 67 LGA50 68 LA75 136	NG50	21954
L50 67 LG50 68 L75 136 LG75 140 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.147 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.40 # indels per 100 kbp 0.00 Largest alignment 94038 NA50 22582 NGA50 21954 NA75 12278 NGA75 11457 LA50 67 LGA50 68 LA75 136	N75	12278
LG50 68 L75 136 LG75 140 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.147 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.40 # indels per 100 kbp 0.00 Largest alignment 94038 NA50 22582 NGA50 21954 NA75 12278 NGA75 11457 LA50 67 LGA50 68 LA75 136	NG75	11457
L75 136 LG75 140 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.147 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.40 # indels per 100 kbp 0.00 Largest alignment 94038 NA50 22582 NGA50 21954 NA75 12278 NGA75 11457 LA50 67 LGA50 68 LA75 136	L50	67
LG75 140 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.147 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.40 # indels per 100 kbp 0.00 Largest alignment 94038 NA50 22582 NGA50 21954 NA75 12278 NGA75 11457 LA50 67 LGA50 68 LA75 136		
# misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.147 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.40 # indels per 100 kbp 0.00 Largest alignment 94038 NA50 22582 NGA50 21954 NA75 12278 NGA75 11457 LA50 67 LGA50 68 LA75 136	L75	136
# misassembled contigs	LG75	140
Misassembled contigs length 15109 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.147 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.40 # indels per 100 kbp 0.00 Largest alignment 94038 NA50 22582 NGA50 21954 NA75 12278 NGA75 11457 LA50 67 LGA50 68 LA75 136		1
# local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.147 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.40 # indels per 100 kbp 0.00 Largest alignment 94038 NA50 22582 NGA50 21954 NA75 12278 NGA75 11457 LA50 67 LGA50 68 LA75 136	Į.	1
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.147 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.40 # indels per 100 kbp 0.00 Largest alignment 94038 NA50 22582 NGA50 21954 NA75 12278 NGA75 11457 LA50 67 LGA50 68 LA75 136	Misassembled contigs length	15109
Unaligned length 0 Genome fraction (%) 98.147 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.40 # indels per 100 kbp 0.00 Largest alignment 94038 NA50 22582 NGA50 21954 NA75 12278 NGA75 11457 LA50 67 LGA50 68 LA75 136	# local misassemblies	0
Genome fraction (%) 98.147 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.40 # indels per 100 kbp 0.00 Largest alignment 94038 NA50 22582 NGA50 21954 NA75 12278 NGA75 11457 LA50 67 LGA50 68 LA75 136	# unaligned contigs	0 + 0 part
Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.40 # indels per 100 kbp 0.00 Largest alignment 94038 NA50 22582 NGA50 21954 NA75 12278 NGA75 11457 LA50 67 LGA50 68 LA75 136		0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 0.40 # indels per 100 kbp 0.00 Largest alignment 94038 NA50 22582 NGA50 21954 NA75 12278 NGA75 11457 LA50 67 LGA50 68 LA75 136	Genome fraction (%)	98.147
# mismatches per 100 kbp 0.40 # indels per 100 kbp 0.00 Largest alignment 94038 NA50 22582 NGA50 21954 NA75 12278 NGA75 11457 LA50 67 LGA50 68 LA75 136	Duplication ratio	1.006
# indels per 100 kbp 0.00 Largest alignment 94038 NA50 22582 NGA50 21954 NA75 12278 NGA75 11457 LA50 67 LGA50 68 LA75 136	# N's per 100 kbp	0.00
Largest alignment 94038 NA50 22582 NGA50 21954 NA75 12278 NGA75 11457 LA50 67 LGA50 68 LA75 136		0.40
NA50 22582 NGA50 21954 NA75 12278 NGA75 11457 LA50 67 LGA50 68 LA75 136		0.00
NGA50 21954 NA75 12278 NGA75 11457 LA50 67 LGA50 68 LA75 136	Largest alignment	94038
NA75 12278 NGA75 11457 LA50 67 LGA50 68 LA75 136	NA50	22582
NGA75 11457 LA50 67 LGA50 68 LA75 136	NGA50	21954
LA50 67 LGA50 68 LA75 136	NA75	12278
LGA50 68 LA75 136	NGA75	11457
LA75 136	LA50	67
	LGA50	68
LCA75		136
LGA75 140	LGA75	140

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	15109
# local misassemblies	0
# mismatches	18
# indels	0
# short indels	0
# long indels	0
Indels length	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).

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).















