Report

# contigs (>= 1000 bp) 341 # contigs (>= 5000 bp) 174 # contigs (>= 10000 bp) 74 # contigs (>= 25000 bp) 6 # contigs (>= 50000 bp) 6 # contigs (>= 50000 bp) 00 Total length (>= 10000 bp) 1882513 Total length (>= 10000 bp) 1166646 Total length (>= 25000 bp) 173599 Total length (>= 50000 bp) 50 # contigs 465 Largest contig 35550 Total length 2436589 Reference length 4641652 GC (%) 50.85 Reference GC (%) 50.78 N50 9738 NG50 1614 N75 5427 L50 80 LG50 313 L75 164 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 0 0 + 0 part Unaligned length 0 Genome fraction (%) 52.134 Duplication ratio 1.007 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.007 # mismatches per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50 313 LA75 164		
# contigs (>= 5000 bp)		final.contigs
# contigs (>= 10000 bp)	# contigs (>= 1000 bp)	341
# contigs (>= 25000 bp) 6 # contigs (>= 50000 bp) 0 Total length (>= 1000 bp) 1882513 Total length (>= 10000 bp) 1166646 Total length (>= 25000 bp) 173599 Total length (>= 50000 bp) 0 # contigs 465 Largest contig 35550 Total length 2436589 Reference length 4641652 GC (%) 50.85 Reference GC (%) 50.78 N50 9738 NG50 1614 N75 5427 L50 80 LG50 313 L75 164 # misassemblies 1 # misassembled contigs 1 # misassembled contigs length 5468 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 52.134 Duplication ratio 1.007 # N's per 100 kbp 0.00 # mismatches per 100 kbp 428.79 # indels per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50 313		174
# contigs (>= 50000 bp) Total length (>= 1000 bp) Total length (>= 5000 bp) 1882513 Total length (>= 10000 bp) 1166646 Total length (>= 25000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) # contigs 465 Largest contig 35550 Total length 2436589 Reference length 4641652 GC (%) 50.78 Reference GC (%) N50 9738 NG50 1614 N75 L50 80 LG50 1313 L75 164 # misassemblies 1 # misassemblies 1 # misassembled contigs I Misassembled contigs I Misassembled contigs I Unaligned length Genome fraction (%) Genome fraction (%) Total length Find the service of the servic		74
Total length (>= 1000 bp) 2357750 Total length (>= 5000 bp) 1882513 Total length (>= 10000 bp) 1166646 Total length (>= 25000 bp) 173599 Total length (>= 50000 bp) 0 # contigs 465 Largest contig 35550 Total length 2436589 Reference length 4641652 GC (%) 50.85 Reference GC (%) 50.78 N50 9738 NG50 1614 N75 5427 L50 80 LG50 313 L75 164 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 5468 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 52.134 Duplication ratio 1.007 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 35550 NA50 <td># contigs (>= 25000 bp)</td> <td>6</td>	# contigs (>= 25000 bp)	6
Total length (>= 5000 bp) 1882513 Total length (>= 10000 bp) 1166646 Total length (>= 25000 bp) 173599 Total length (>= 50000 bp) 0 # contigs 465 Largest contig 35550 Total length 2436589 Reference length 4641652 GC (%) 50.85 Reference GC (%) 50.78 N50 9738 NG50 1614 N75 5427 L50 80 LG50 313 L75 164 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 5468 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 52.134 Duplication ratio 1.007 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614 <td># contigs (>= 50000 bp)</td> <td>0</td>	# contigs (>= 50000 bp)	0
Total length (>= 10000 bp) 1166646 Total length (>= 25000 bp) 173599 Total length (>= 50000 bp) 0 # contigs 465 Largest contig 35550 Total length 2436589 Reference length 4641652 GC (%) 50.85 Reference GC (%) 50.78 N50 9738 NG50 1614 N75 5427 L50 80 LG50 313 L75 164 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 5468 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 52.134 Duplication ratio 1.007 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614		2357750
Total length (>= 25000 bp) 173599 Total length (>= 50000 bp) 0 # contigs 465 Largest contig 35550 Total length 2436589 Reference length 4641652 GC (%) 50.85 Reference GC (%) 50.78 N50 9738 NG50 1614 N75 5427 L50 80 LG50 313 L75 164 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 5468 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 52.134 Duplication ratio 1.007 # N's per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50	Total length (>= 5000 bp)	1882513
Total length (>= 50000 bp) 0 # contigs 465 Largest contig 35550 Total length 2436589 Reference length 4641652 GC (%) 50.85 Reference GC (%) 50.78 N50 9738 NG50 1614 N75 5427 L50 80 LG50 313 L75 164 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 5468 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 52.134 Duplication ratio 1.007 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50 313	Total length (>= 10000 bp)	1166646
# contigs	Total length (>= 25000 bp)	173599
Largest contig 35550 Total length 2436589 Reference length 4641652 GC (%) 50.85 Reference GC (%) 50.78 N50 9738 NG50 1614 N75 5427 L50 80 LG50 313 L75 164 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 5468 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 52.134 Duplication ratio 1.007 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50 313	Total length (>= 50000 bp)	0
Total length 2436589 Reference length 4641652 GC (%) 50.85 Reference GC (%) 50.78 N50 9738 NG50 1614 N75 5427 L50 80 LG50 313 L75 164 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 5468 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 52.134 Duplication ratio 1.007 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50 313	# contigs	465
Reference length 4641652 GC (%) 50.85 Reference GC (%) 50.78 N50 9738 NG50 1614 N75 5427 L50 80 LG50 313 L75 164 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 5468 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 52.134 Duplication ratio 1.007 # N's per 100 kbp 0.00 # mismatches per 100 kbp 428.79 # indels per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50 313	Largest contig	35550
GC (%) 50.85 Reference GC (%) 50.78 N50 9738 NG50 1614 N75 5427 L50 80 LG50 313 L75 164 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 5468 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 52.134 Duplication ratio 1.007 # N's per 100 kbp 0.00 # mismatches per 100 kbp 428.79 # indels per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50 313	Total length	2436589
Reference GC (%) 50.78 N50 9738 NG50 1614 N75 5427 L50 80 LG50 313 L75 164 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 5468 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 52.134 Duplication ratio 1.007 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50 313	Reference length	4641652
N50 9738 NG50 1614 N75 5427 L50 80 LG50 313 L75 164 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 5468 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 52.134 Duplication ratio 1.007 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50 313	GC (%)	50.85
NG50 1614 N75 5427 L50 80 LG50 313 L75 164 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 5468 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 52.134 Duplication ratio 1.007 # N's per 100 kbp 0.00 # mismatches per 100 kbp 428.79 # indels per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50 313	Reference GC (%)	50.78
N75 5427 L50 80 LG50 313 L75 164 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 5468 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 52.134 Duplication ratio 1.007 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50 313	N50	9738
L50 80 LG50 313 L75 164 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 5468 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 52.134 Duplication ratio 1.007 # N's per 100 kbp 0.00 # mismatches per 100 kbp 428.79 # indels per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50 313	NG50	1614
LG50 313 L75 164 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 5468 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 52.134 Duplication ratio 1.007 # N's per 100 kbp 0.00 # mismatches per 100 kbp 428.79 # indels per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50 313	N75	5427
L75 164 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 5468 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 52.134 Duplication ratio 1.007 # N's per 100 kbp 0.00 # mismatches per 100 kbp 428.79 # indels per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50 313	L50	80
# misassemblies 1 # misassembled contigs 1 Misassembled contigs length 5468 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 52.134 Duplication ratio 1.007 # N's per 100 kbp 0.00 # mismatches per 100 kbp 428.79 # indels per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50 313	LG50	313
# misassembled contigs 1 Misassembled contigs length 5468 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 52.134 Duplication ratio 1.007 # N's per 100 kbp 0.00 # mismatches per 100 kbp 428.79 # indels per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50 313	L75	164
Misassembled contigs length 5468 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 52.134 Duplication ratio 1.007 # N's per 100 kbp 0.00 # mismatches per 100 kbp 428.79 # indels per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50 313	# misassemblies	1
# local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 52.134 Duplication ratio 1.007 # N's per 100 kbp 0.00 # mismatches per 100 kbp 428.79 # indels per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50 313		1
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 52.134 Duplication ratio 1.007 # N's per 100 kbp 0.00 # mismatches per 100 kbp 428.79 # indels per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50 313	Misassembled contigs length	5468
Unaligned length 0 Genome fraction (%) 52.134 Duplication ratio 1.007 # N's per 100 kbp 0.00 # mismatches per 100 kbp 428.79 # indels per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50 313	# local misassemblies	0
Genome fraction (%) 52.134 Duplication ratio 1.007 # N's per 100 kbp 0.00 # mismatches per 100 kbp 428.79 # indels per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50 313		0 + 0 part
Duplication ratio 1.007 # N's per 100 kbp 0.00 # mismatches per 100 kbp 428.79 # indels per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50 313	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 428.79 # indels per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50 313	Genome fraction (%)	52.134
# mismatches per 100 kbp 428.79 # indels per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50 313	Duplication ratio	1.007
# indels per 100 kbp 0.00 Largest alignment 35550 NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50 313	# N's per 100 kbp	0.00
Largest alignment 35550 NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50 313	# mismatches per 100 kbp	428.79
NA50 9738 NGA50 1614 NA75 5385 LA50 80 LGA50 313	# indels per 100 kbp	0.00
NGA50 1614 NA75 5385 LA50 80 LGA50 313	Largest alignment	35550
NA75 5385 LA50 80 LGA50 313	NA50	9738
LA50 80 LGA50 313	NGA50	1614
LGA50 313		5385
	LA50	80
LA75 164		313
	LA75	164

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	0
# translocations	0
# inversions	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	5468
# local misassemblies	0
# mismatches	10376
# 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).

















