Report

# contigs (>= 0 bp)		
# contigs (>= 1000 bp)		final.contigs
# contigs (>= 5000 bp) 33 # contigs (>= 10000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 7141500 Total length (>= 1000 bp) 3630565 Total length (>= 5000 bp) 215889 Total length (>= 10000 bp) 31260 Total length (>= 25000 bp) 0 Total length (>= 5000 bp) 0 Total length (>= 5000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 5038 Largest contig 11097 Total length 5832055 Reference length 9714864 N50 1379 N75 765 L50 1190 L75 2664 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 # unaligned length 0 Genome fraction (%) 85.433 Duplication ratio 1.065 # N's per 100 kbp 0.00 # mismatches per 100 kbp 545.06 # indels per 100 kbp 0.05 Largest alignment 11097 NA50 1379 NA75 765		8615
# contigs (>= 10000 bp) # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) Total length (>= 1000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 10000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp) # contigs Largest contig Total length S832055 Reference length N50 N75 Reference length N50 N75 Total L50 L75 2664 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned length 0 Genome fraction (%) Genome fraction (%) S5433 Duplication ratio 1.065 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1379 NA50 NA50 NA75 Total length 0 Total length 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		1807
# contigs (>= 25000 bp) # contigs (>= 50000 bp) Total length (>= 0 bp) Total length (>= 1000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 10000 bp) Total length (>= 10000 bp) Total length (>= 25000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp) # contigs Largest contig Total length 5832055 Reference length N50 N75 Total length N50 1379 N75 L50 L75 2664 # misassemblies # misassembled contigs Misassembled contigs Misassembled contigs Unaligned length Genome fraction (%) Genome fraction (%) # N's per 100 kbp # indels per 100 kbp Largest alignment NA50 NA75 Total length 0 7141500 12589 7141500 714160 7141500 7141500 7	_	33
# contigs (>= 50000 bp) Total length (>= 0 bp) Total length (>= 1000 bp) Total length (>= 1000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 25000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp) Total length Tota		3
Total length (>= 0 bp) 7141500 Total length (>= 1000 bp) 3630565 Total length (>= 5000 bp) 215889 Total length (>= 10000 bp) 31260 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 5038 Largest contig 11097 Total length 5832055 Reference length 9714864 N50 1379 N75 765 L50 1190 L75 2664 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 # unaligned length 0 Genome fraction (♥) 85.433 Duplication ratio 1.065 # N's per 100 kbp 0.00 # mismatches per 100 kbp 545.06 # indels per 100 kbp 0.05 Largest alignment 11097 NA50 1379 NA75 765		0
Total length (>= 1000 bp) 3630565 Total length (>= 5000 bp) 215889 Total length (>= 10000 bp) 31260 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 5038 Largest contig 11097 Total length 5832055 Reference length 9714864 N50 1379 N75 765 L50 1190 L75 2664 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (♥) 85.433 Duplication ratio 1.065 # N's per 100 kbp 0.00 # indels per 100 kbp 545.06 # indels per 100 kbp 0.05 Largest alignment 11097 NA50 1379 NA75 765		0
Total length (>= 5000 bp) 215889 Total length (>= 10000 bp) 31260 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 5038 Largest contig 11097 Total length 5832055 Reference length 9714864 N50 1379 N75 765 L50 1190 L75 2664 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (♥) 85.433 Duplication ratio 1.065 # N's per 100 kbp 0.00 # indels per 100 kbp 545.06 # indels per 100 kbp 0.05 Largest alignment 11097 NA50 1379 NA75 765	_	7141500
Total length (>= 10000 bp) 31260 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 5038 Largest contig 11097 Total length 5832055 Reference length 9714864 N50 1379 N75 765 L50 1190 L75 2664 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (♥) 85.433 Duplication ratio 1.065 # N's per 100 kbp 0.00 # mismatches per 100 kbp 545.06 # indels per 100 kbp 0.05 Largest alignment 11097 NA50 1379 NA75 765	Total length (>= 1000 bp)	3630565
Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 5038 Largest contig 11097 Total length 5832055 Reference length 9714864 N50 1379 N75 765 L50 1190 L75 2664 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 # unaligned length 0 Genome fraction (%) 85.433 Duplication ratio 1.065 # N's per 100 kbp 0.00 # mismatches per 100 kbp 545.06 # indels per 100 kbp 0.05 Largest alignment 11097 NA50 1379 NA75 765	Total length (>= 5000 bp)	215889
Total length (>= 50000 bp) 0 # contigs 5038 Largest contig 11097 Total length 5832055 Reference length 9714864 N50 1379 N75 765 L50 1190 L75 2664 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 85.433 Duplication ratio 1.065 # N's per 100 kbp 0.00 # mismatches per 100 kbp 545.06 # indels per 100 kbp 0.05 Largest alignment 11097 NA50 1379 NA75 765	Total length (>= 10000 bp)	31260
# contigs 5038 Largest contig 11097 Total length 5832055 Reference length 9714864 N50 1379 N75 765 L50 1190 L75 2664 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 85.433 Duplication ratio 1.065 # N's per 100 kbp 0.00 # mismatches per 100 kbp 545.06 # indels per 100 kbp 0.05 Largest alignment 11097 NA50 1379 NA75	Total length (>= 25000 bp)	0
Largest contig 11097 Total length 5832055 Reference length 9714864 N50 1379 N75 765 L50 1190 L75 2664 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (♥) 85.433 Duplication ratio 1.065 # N's per 100 kbp 0.00 # mismatches per 100 kbp 545.06 # indels per 100 kbp 0.05 Largest alignment 11097 NA50 1379 NA75 765	Total length (>= 50000 bp)	0
Total length 5832055 Reference length 9714864 N50 1379 N75 765 L50 1190 L75 2664 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (♥) 85.433 Duplication ratio 1.065 # N's per 100 kbp 0.00 # mismatches per 100 kbp 545.06 # indels per 100 kbp 0.05 Largest alignment 11097 NA50 1379 NA75 765	# contigs	5038
Reference length 9714864 N50 1379 N75 765 L50 1190 L75 2664 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (♥) 85.433 Duplication ratio 1.065 # N's per 100 kbp 0.00 # mismatches per 100 kbp 545.06 # indels per 100 kbp 0.05 Largest alignment 11097 NA50 1379 NA75 765	Largest contig	11097
N50 1379 N75 765 L50 1190 L75 2664 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 85.433 Duplication ratio 1.065 # N's per 100 kbp 0.00 # mismatches per 100 kbp 545.06 # indels per 100 kbp 0.05 Largest alignment 11097 NA50 1379 NA75 765	Total length	5832055
N75 765 L50 1190 L75 2664 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 85.433 Duplication ratio 1.065 # N's per 100 kbp 0.00 # mismatches per 100 kbp 545.06 # indels per 100 kbp 0.05 Largest alignment 11097 NA50 1379 NA75 765	Reference length	9714864
L50 1190 L75 2664 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 85.433 Duplication ratio 1.065 # N's per 100 kbp 0.00 # mismatches per 100 kbp 545.06 # indels per 100 kbp 0.05 Largest alignment 11097 NA50 1379 NA75 765	N50	1379
L75 2664 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 85.433 Duplication ratio 1.065 # N's per 100 kbp 0.00 # mismatches per 100 kbp 545.06 # indels per 100 kbp 0.05 Largest alignment 11097 NA50 1379 NA75 765	N75	765
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 85.433 Duplication ratio 1.065 # N's per 100 kbp 0.00 # mismatches per 100 kbp 545.06 # indels per 100 kbp 0.05 Largest alignment 11097 NA50 1379 NA75 765	L50	1190
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 85.433 Duplication ratio 1.065 # N's per 100 kbp 0.00 # mismatches per 100 kbp 545.06 # indels per 100 kbp 0.05 Largest alignment 11097 NA50 1379 NA75 765	L75	2664
Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 85.433 Duplication ratio 1.065 # N's per 100 kbp 0.00 # mismatches per 100 kbp 545.06 # indels per 100 kbp 0.05 Largest alignment 11097 NA50 1379 NA75 765	# misassemblies	0
# local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 85.433 Duplication ratio 1.065 # N's per 100 kbp 0.00 # mismatches per 100 kbp 545.06 # indels per 100 kbp 0.05 Largest alignment 11097 NA50 1379 NA75 765	# misassembled contigs	0
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 85.433 Duplication ratio 1.065 # N's per 100 kbp 0.00 # mismatches per 100 kbp 545.06 # indels per 100 kbp 0.05 Largest alignment 11097 NA50 1379 NA75 765	Misassembled contigs length	0
Unaligned length 0 Genome fraction (♥) 85.433 Duplication ratio 1.065 # N's per 100 kbp 0.00 # mismatches per 100 kbp 545.06 # indels per 100 kbp 0.05 Largest alignment 11097 NA50 1379 NA75 765	# local misassemblies	0
Genome fraction (♥) 85.433 Duplication ratio 1.065 # N's per 100 kbp 0.00 # mismatches per 100 kbp 545.06 # indels per 100 kbp 0.05 Largest alignment 11097 NA50 1379 NA75 765	# unaligned contigs	0 + 0 part
Duplication ratio 1.065 # N's per 100 kbp 0.00 # mismatches per 100 kbp 545.06 # indels per 100 kbp 0.05 Largest alignment 11097 NA50 1379 NA75 765	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 545.06 # indels per 100 kbp 0.05 Largest alignment 11097 NA50 1379 NA75 765	Genome fraction (%)	85.433
# mismatches per 100 kbp 545.06 # indels per 100 kbp 0.05 Largest alignment 11097 NA50 1379 NA75 765	Duplication ratio	1.065
# indels per 100 kbp 0.05 Largest alignment 11097 NA50 1379 NA75 765	# N's per 100 kbp	0.00
Largest alignment 11097 NA50 1379 NA75 765	# mismatches per 100 kbp	545.06
Largest alignment 11097 NA50 1379 NA75 765	# indels per 100 kbp	0.05
NA50 1379 NA75 765		11097
+		1379
	NA75	765
LA50 1190	LA50	1190
LA75 2664	LA75	2664

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
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	45238
# indels	4
# short indels	4
# long indels	0
Indels length	4

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).









