Report

# contigs (>= 1000 bp) 1140 # contigs (>= 5000 bp) 335 # contigs (>= 10000 bp) 62 # contigs (>= 25000 bp) 1 # contigs (>= 50000 bp) 1 # contigs (>= 50000 bp) 1 # contigs (>= 50000 bp) 0 Total length (>= 10000 bp) 4788038 Total length (>= 10000 bp) 2679466 Total length (>= 10000 bp) 33760 Total length (>= 25000 bp) 33760 Total length (>= 50000 bp) 0 # contigs 1339 Largest contig 33760 Total length (>= 50000 bp) 0 # contigs 1339 Largest contig 33760 Total length (>= 50000 bp) 0 # contigs 1339 Largest contig 33760 Total length (>= 50000 bp) 0 # contigs 1339 Largest contig 33760 Total length (>= 50000 bp) 0 # contigs 1339 Largest contig 33760 Total length 4857432 GC (%) 52.24 Reference length 4857432 GC (%) 52.23 N50 5381 NG50 5381 NG50 5455 N75 3194 NG75 3276 L50 294 LG50 287 L75 591 LG75 573 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # misassembled contigs 0 # unaligned contigs 0 # unaligned length 0 Genome fraction (%) 99.493 Duplication ratio 1.021 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 33760 NA50 5381 NGA50 5455 NA75 3194 NGA75 3276 LGA50 287 LA75 591 LGA75 573		-
# contigs (>= 5000 bp)		final.contigs
# contigs (>= 10000 bp)	# contigs (>= 1000 bp)	
# contigs (>= 25000 bp)	# contigs (>= 5000 bp)	335
# contigs (>= 50000 bp)	# contigs (>= 10000 bp)	62
# contigs (>= 50000 bp)	# contigs (>= 25000 bp)	1
Total length (>= 5000 bp) 2679466 Total length (>= 10000 bp) 813583 Total length (>= 25000 bp) 33760 Total length (>= 50000 bp) 0 # contigs 1339 Largest contig 33760 Total length 4932156 Reference length 4857432 GC (%) 52.24 Reference GC (%) 52.23 N50 5381 NG50 5455 N75 3194 NG75 3276 L50 294 LG50 287 L75 591 LG75 573 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 99.493 Duplication ratio 1.021 # N's per 100 kbp 0.00 Largest alignment 33760 NA50 5381		0
Total length (>= 10000 bp) 813583 Total length (>= 25000 bp) 33760 Total length (>= 50000 bp) 0 # contigs 1339 Largest contig 33760 Total length 4932156 Reference length 4857432 GC (%) 52.24 Reference GC (%) 52.23 N50 5381 NG50 5455 N75 3194 NG75 3276 L50 294 LG50 287 L75 591 LG75 573 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 99.493 Duplication ratio 1.021 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 33760 NA50 5381	Total length (>= 1000 bp)	4788038
Total length (>= 25000 bp) 33760 Total length (>= 50000 bp) 0 # contigs 1339 Largest contig 33760 Total length 4932156 Reference length 4857432 GC (%) 52.24 Reference GC (%) 52.23 N50 5381 NG50 5455 N75 3194 NG75 3276 L50 294 LG50 287 L75 591 LG75 573 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 99.493 Duplication ratio 1.021 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.46 # indels per 100 kbp 0.00 Largest alignment 33760 NA50 5381 NGA5	Total length (>= 5000 bp)	2679466
Total length (>= 50000 bp) 0 # contigs 1339 Largest contig 33760 Total length 4932156 Reference length 4857432 GC (%) 52.24 Reference GC (%) 52.23 N50 5381 NG50 5455 N75 3194 NG75 3276 L50 294 LG50 287 L75 591 LG75 573 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 99.493 Duplication ratio 1.021 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.46 # indels per 100 kbp 0.54 NA50 5381 NGA50 5455 NA75 3194 NGA75 3276 <td>Total length (>= 10000 bp)</td> <td>813583</td>	Total length (>= 10000 bp)	813583
# contigs 1339 Largest contig 33760 Total length 4932156 Reference length 4857432 GC (%) 52.24 Reference GC (%) 52.23 N50 5381 NG50 5455 N75 3194 NG75 3276 L50 294 LG50 287 L75 591 LG75 573 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 99.493 Duplication ratio 1.021 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.46 # indels per 100 kbp 0.00 Largest alignment 33760 NA50 5381 NGA50 5455 NA75 3194 NGA75 3276 LA50 294 LA50 294	Total length (>= 25000 bp)	33760
Largest contig 33760 Total length 4932156 Reference length 4857432 GC (%) 52.24 Reference GC (%) 52.23 N50 5381 NG50 5455 N75 3194 NG75 3276 L50 294 LG50 287 L75 591 LG75 573 # misassemblies 0 # sassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.493 Duplication ratio 1.021 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.46 # indels per 100 kbp 0.00 Largest alignment 33760 NA50 5381 NGA50 5455 NA75 3194 NGA75 3276	Total length (>= 50000 bp)	0
Total length 4932156 Reference length 4857432 GC (%) 52.24 Reference GC (%) 52.23 N50 5381 NG50 5455 N75 3194 NG75 3276 L50 294 L650 287 L75 591 LG75 573 # misassemblies 0 # local misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.493 Duplication ratio 1.021 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.46 # indels per 100 kbp 0.00 Largest alignment 33760 NA50 5381 NGA50 5455 NA75 3194 NGA75 3276 LA50 294 <	# contigs	1339
Reference length 4857432 GC (%) 52.24 Reference GC (%) 52.23 N50 5381 NG50 5455 N75 3194 NG75 3276 L50 294 LG50 287 L75 591 LG75 573 # misassemblies 0 # local misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.493 Duplication ratio 1.021 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.46 # indels per 100 kbp 0.00 Largest alignment 33760 NA50 5381 NGA50 5455 NA75 3194 NGA75 3276 LA50 294 LA50 287 LA75 591	Largest contig	33760
GC (%) 52.24 Reference GC (%) 52.23 N50 5381 NG50 5455 N75 3194 NG75 3276 L50 294 LG50 287 L75 591 LG75 573 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.493 Duplication ratio 1.021 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.46 # indels per 100 kbp 0.00 Largest alignment 33760 NA50 5381 NGA50 5455 NA75 3194 NGA75 3276 LA50 294 LGA50 287 LA75 591	Total length	4932156
Reference GC (%) 52.23 N50 5381 NG50 5455 N75 3194 NG75 3276 L50 294 LG50 287 L75 591 LG75 573 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.493 Duplication ratio 1.021 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.46 # indels per 100 kbp 0.00 Largest alignment 33760 NA50 5381 NGA50 5455 NA75 3194 NGA75 3276 LA50 294 LGA50 287 LA75 591	Reference length	4857432
N50 5381 NG50 5455 N75 3194 NG75 3276 L50 294 LG50 287 L75 591 LG75 573 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.493 Duplication ratio 1.021 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.46 # indels per 100 kbp 0.00 Largest alignment 33760 NA50 5381 NGA50 5455 NA75 3194 NGA75 3276 LA50 294 LGA50 287 LA75 591	GC (%)	52.24
NG50 5455 N75 3194 NG75 3276 L50 294 LG50 287 L75 591 LG75 573 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.493 Duplication ratio 1.021 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.46 # indels per 100 kbp 0.00 Largest alignment 33760 NA50 5381 NGA50 5455 NA75 3194 NGA75 3276 LA50 294 LGA50 287 LA75 591	Reference GC (%)	52.23
N75 3194 NG75 3276 L50 294 LG50 287 L75 591 LG75 573 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.493 Duplication ratio 1.021 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.46 # indels per 100 kbp 0.00 Largest alignment 33760 NA50 5381 NGA50 5455 NA75 3194 NGA75 3276 LA50 294 LGA50 287 LA75 591	N50	5381
NG75 3276 L50 294 LG50 287 L75 591 LG75 573 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.493 Duplication ratio 1.021 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.46 # indels per 100 kbp 0.00 Largest alignment 33760 NA50 5381 NGA50 5455 NA75 3194 NGA75 3276 LA50 294 LGA50 287 LA75 591	NG50	5455
L50 294 LG50 287 L75 591 LG75 573 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.493 Duplication ratio 1.021 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.46 # indels per 100 kbp 0.00 Largest alignment 33760 NA50 5381 NGA50 5455 NA75 3194 NGA75 3276 LA50 294 LGA50 287 LA75 591	N75	3194
LG50 287 L75 591 LG75 573 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.493 Duplication ratio 1.021 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.46 # indels per 100 kbp 0.00 Largest alignment 33760 NA50 5381 NGA50 5455 NA75 3194 NGA75 3276 LA50 294 LGA50 287 LA75 591	NG75	3276
L75 591 LG75 573 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.493 Duplication ratio 1.021 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.46 # indels per 100 kbp 0.00 Largest alignment 33760 NA50 5381 NGA50 5455 NA75 3194 NGA75 3276 LA50 294 LGA50 287 LA75 591	L50	294
LG75 573 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.493 Duplication ratio 1.021 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.46 # indels per 100 kbp 0.00 Largest alignment 33760 NA50 5381 NGA50 5455 NA75 3194 NGA75 3276 LA50 294 LGA50 287 LA75 591	LG50	287
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.493 Duplication ratio 1.021 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.46 # indels per 100 kbp 0.00 Largest alignment 33760 NA50 5381 NGA50 5455 NA75 3194 NGA75 3276 LA50 294 LGA50 287 LA75 591	L75	591
# misassembled contigs	LG75	573
Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.493 Duplication ratio 1.021 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.46 # indels per 100 kbp 0.00 Largest alignment 33760 NA50 5381 NGA50 5455 NA75 3194 NGA75 3276 LA50 294 LGA50 287 LA75 591	# misassemblies	0
# local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.493 Duplication ratio 1.021 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.46 # indels per 100 kbp 33760 Largest alignment 33760 NA50 5381 NGA50 5455 NA75 3194 NGA75 3276 LA50 294 LGA50 287 LA75 591	# misassembled contigs	0
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.493 Duplication ratio 1.021 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.46 # indels per 100 kbp 33760 Largest alignment 33760 NA50 5381 NGA50 5455 NA75 3194 NGA75 3276 LA50 294 LGA50 287 LA75 591	Misassembled contigs length	0
Unaligned length 0 Genome fraction (%) 99.493 Duplication ratio 1.021 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.46 # indels per 100 kbp 0.00 Largest alignment 33760 NA50 5381 NGA50 5455 NA75 3194 NGA75 3276 LA50 294 LGA50 287 LA75 591	# local misassemblies	0
Genome fraction (%) 99.493 Duplication ratio 1.021 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.46 # indels per 100 kbp 0.00 Largest alignment 33760 NA50 5381 NGA50 5455 NA75 3194 NGA75 3276 LA50 294 LGA50 287 LA75 591		0 + 0 part
Duplication ratio 1.021 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.46 # indels per 100 kbp 0.00 Largest alignment 33760 NA50 5381 NGA50 5455 NA75 3194 NGA75 3276 LA50 294 LGA50 287 LA75 591		0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 0.46 # indels per 100 kbp 0.00 Largest alignment 33760 NA50 5381 NGA50 5455 NA75 3194 NGA75 3276 LA50 294 LGA50 287 LA75 591	Genome fraction (%)	99.493
# mismatches per 100 kbp 0.46 # indels per 100 kbp 0.00 Largest alignment 33760 NA50 5381 NGA50 5455 NA75 3194 NGA75 3276 LA50 294 LGA50 287 LA75 591	Duplication ratio	1.021
# indels per 100 kbp 0.00 Largest alignment 33760 NA50 5381 NGA50 5455 NA75 3194 NGA75 3276 LA50 294 LGA50 287 LA75 591		0.00
Largest alignment 33760 NA50 5381 NGA50 5455 NA75 3194 NGA75 3276 LA50 294 LGA50 287 LA75 591	# mismatches per 100 kbp	0.46
NA50 5381 NGA50 5455 NA75 3194 NGA75 3276 LA50 294 LGA50 287 LA75 591	# indels per 100 kbp	0.00
NGA50 5455 NA75 3194 NGA75 3276 LA50 294 LGA50 287 LA75 591	Largest alignment	33760
NA75 3194 NGA75 3276 LA50 294 LGA50 287 LA75 591	NA50	5381
NGA75 3276 LA50 294 LGA50 287 LA75 591	NGA50	5455
LA50 294 LGA50 287 LA75 591		3194
LGA50 287 LA75 591	NGA75	3276
LA75 591	LA50	294
i	LGA50	
LGA75 573	LA75	591
	LGA75	573

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	0
# mismatches	22
# 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).















