## Report

# contigs (>= 0 bp) 1314 # contigs (>= 1000 bp) 1047 # contigs (>= 5000 bp) 292 # contigs (>= 10000 bp) 63 # contigs (>= 25000 bp) 1 # contigs (>= 25000 bp) 1 # contigs (>= 50000 bp) 1 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 4497010 Total length (>= 1000 bp) 4325052 Total length (>= 5000 bp) 2393713 Total length (>= 10000 bp) 825519 Total length (>= 25000 bp) 26961 Total length (>= 50000 bp) 26961 Total length (>= 50000 bp) 3233 Largest contig 326961 Total length 4465552 Reference length 4641652 N50 5470 N75 3081 L50 262 L75 538 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 # local misassemblies 1 # local misassemblies 15 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.057 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.37 # indels per 100 kbp 0.34 Largest alignment 26961		
# contigs (>= 1000 bp) 292 # contigs (>= 5000 bp) 292 # contigs (>= 10000 bp) 63 # contigs (>= 25000 bp) 1 # contigs (>= 25000 bp) 1 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 4497010 Total length (>= 1000 bp) 4325052 Total length (>= 5000 bp) 2393713 Total length (>= 10000 bp) 825519 Total length (>= 25000 bp) 26961 Total length (>= 50000 bp) 0 # contigs 1233 Largest contig 26961 Total length 4465552 Reference length 4641652 N50 5470 N75 3081 L50 262 L75 538 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 1 # local misassemblies 1 # local misassemblies 15 # unaligned length 0 Genome fraction (%) 96.057 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.37 # indels per 100 kbp 0.34 Largest alignment 26961		final.contigs
# contigs (>= 5000 bp)     # contigs (>= 10000 bp)     # contigs (>= 25000 bp)     # contigs (>= 25000 bp)     # contigs (>= 50000 bp)     # contigs (>= 50000 bp)     Total length (>= 0 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 (>= 50000 bp)     # contigs     Largest contig     Total length     Total length     A465552 Reference length     A465552 Reference length     A4641652 N50     S470 N75     S381 L50     L50     L75     S38 # misassemblies     # misassemblies     # misassembled contigs     Misassembled contigs     # local misassemblies     # unaligned contigs     Unaligned length     Genome fraction (%)     96.057 Duplication ratio     # N's per 100 kbp     # mismatches per 100 kbp     # indels per 100 kbp     A37 # indels per 100 kbp     O.34 Largest alignment     26961	_	1314
# contigs (>= 10000 bp) 63 # contigs (>= 25000 bp) 1 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 4497010 Total length (>= 1000 bp) 4325052 Total length (>= 5000 bp) 2393713 Total length (>= 10000 bp) 825519 Total length (>= 25000 bp) 26961 Total length (>= 50000 bp) 0 # contigs 1233 Largest contig 26961 Total length 4465552 Reference length 4641652 N50 5470 N75 3081 L50 262 L75 538 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 1 # local misassemblies 15 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.057 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.37 # indels per 100 kbp 0.34 Largest alignment 26961		1047
# 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  4465552  Reference length  N50  N75  Solution  N75  L50  L75  # misassemblies  # misassembled contigs  # misassembled contigs  # local misassemblies  # unaligned contigs  Unaligned length  Genome fraction (%)  Genome fraction (%)  Picket  Picket		292
# contigs (>= 50000 bp)  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  Total length  # contigs  Largest contig  Total length  # 4465552  Reference length  # 4465552  Reference length  # 4461652  N50  N75  3081  L50  262  L75  # misassemblies  # misassembled contigs  # misassembled contigs  # misassembled contigs  # unaligned contigs  # unaligned contigs  Unaligned length  Genome fraction (%)  # O' 96.057  Duplication ratio  # N's per 100 kbp  # mismatches per 100 kbp  # indels per 100 kbp  0.34  Largest alignment  26961	# contigs (>= 10000 bp)	63
Total length (>= 0 bp)         4497010           Total length (>= 1000 bp)         4325052           Total length (>= 5000 bp)         2393713           Total length (>= 10000 bp)         825519           Total length (>= 25000 bp)         26961           Total length (>= 50000 bp)         0           # contigs         1233           Largest contig         26961           Total length         4465552           Reference length         4641652           N50         5470           N75         3081           L50         262           L75         538           # misassemblies         1           # local misassembled contigs         1           Misassembled contigs length         1211           # local misassemblies         15           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         96.057           Duplication ratio         1.002           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.34           Largest alignment         26961	# contigs (>= 25000 bp)	1
Total length (>= 1000 bp)	# contigs (>= 50000 bp)	0
Total length (>= 5000 bp)         2393713           Total length (>= 10000 bp)         825519           Total length (>= 25000 bp)         26961           Total length (>= 50000 bp)         0           # contigs         1233           Largest contig         26961           Total length         4465552           Reference length         4641652           N50         5470           N75         3081           L50         262           L75         538           # misassemblies         1           # local misassembled contigs         1           Misassembled contigs length         1211           # local misassemblies         15           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         96.057           Duplication ratio         1.002           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.34           Largest alignment         26961	Total length (>= 0 bp)	4497010
Total length (>= 10000 bp)         825519           Total length (>= 25000 bp)         26961           Total length (>= 50000 bp)         0           # contigs         1233           Largest contig         26961           Total length         4465552           Reference length         4641652           N50         5470           N75         3081           L50         262           L75         538           # misassemblies         1           # local misassembled contigs         1           Misassembled contigs length         1211           # local misassemblies         15           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         96.057           Duplication ratio         1.002           # N's per 100 kbp         0.00           # mismatches per 100 kbp         4.37           # indels per 100 kbp         0.34           Largest alignment         26961	Total length (>= 1000 bp)	4325052
Total length (>= 25000 bp)         26961           Total length (>= 50000 bp)         0           # contigs         1233           Largest contig         26961           Total length         4465552           Reference length         4641652           N50         5470           N75         3081           L50         262           L75         538           # misassemblies         1           # local misassembled contigs         1           Misassembled contigs length         1211           # local misassemblies         15           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         96.057           Duplication ratio         1.002           # N's per 100 kbp         0.00           # mismatches per 100 kbp         4.37           # indels per 100 kbp         0.34           Largest alignment         26961	Total length (>= 5000 bp)	2393713
Total length (>= 50000 bp)         0           # contigs         1233           Largest contig         26961           Total length         4465552           Reference length         4641652           N50         5470           N75         3081           L50         262           L75         538           # misassemblies         1           # local misassembled contigs         1           Misassembled contigs length         1211           # local misassemblies         15           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         96.057           Duplication ratio         1.002           # N's per 100 kbp         0.00           # mismatches per 100 kbp         4.37           # indels per 100 kbp         0.34           Largest alignment         26961	Total length (>= 10000 bp)	825519
# contigs 1233 Largest contig 26961 Total length 4465552 Reference length 4641652 N50 5470 N75 3081 L50 262 L75 538 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 # local misassemblies 15 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.057 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.37 # indels per 100 kbp 0.34 Largest alignment 26961	Total length (>= 25000 bp)	26961
Largest contig       26961         Total length       4465552         Reference length       4641652         N50       5470         N75       3081         L50       262         L75       538         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       1211         # local misassemblies       15         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.057         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4.37         # indels per 100 kbp       0.34         Largest alignment       26961	Total length (>= 50000 bp)	0
Total length         4465552           Reference length         4641652           N50         5470           N75         3081           L50         262           L75         538           # misassemblies         1           # misassembled contigs         1           Misassembled contigs length         1211           # local misassemblies         15           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         96.057           Duplication ratio         1.002           # N's per 100 kbp         0.00           # mismatches per 100 kbp         4.37           # indels per 100 kbp         0.34           Largest alignment         26961	# contigs	1233
Reference length       4641652         N50       5470         N75       3081         L50       262         L75       538         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       1211         # local misassemblies       15         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.057         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4.37         # indels per 100 kbp       0.34         Largest alignment       26961	Largest contig	26961
N50       5470         N75       3081         L50       262         L75       538         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       1211         # local misassemblies       15         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.057         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4.37         # indels per 100 kbp       0.34         Largest alignment       26961	Total length	4465552
N75       3081         L50       262         L75       538         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       1211         # local misassemblies       15         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.057         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4.37         # indels per 100 kbp       0.34         Largest alignment       26961	Reference length	4641652
L50       262         L75       538         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       1211         # local misassemblies       15         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       96.057         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4.37         # indels per 100 kbp       0.34         Largest alignment       26961	N50	5470
# misassemblies 1  # misassembled contigs 1  Misassembled contigs length 1211  # local misassemblies 15  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 96.057  Duplication ratio 1.002  # N's per 100 kbp 0.00  # mismatches per 100 kbp 4.37  # indels per 100 kbp 0.34  Largest alignment 26961	N75	3081
# misassemblies 1  # misassembled contigs 1  Misassembled contigs length 1211  # local misassemblies 15  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 96.057  Duplication ratio 1.002  # N's per 100 kbp 0.00  # mismatches per 100 kbp 4.37  # indels per 100 kbp 0.34  Largest alignment 26961	L50	262
# misassembled contigs 1 Misassembled contigs length 1211 # local misassemblies 15 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.057 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.37 # indels per 100 kbp 0.34 Largest alignment 26961	L75	538
Misassembled contigs length1211# local misassemblies15# unaligned contigs0 + 0 partUnaligned length0Genome fraction (%)96.057Duplication ratio1.002# N's per 100 kbp0.00# mismatches per 100 kbp4.37# indels per 100 kbp0.34Largest alignment26961	# misassemblies	1
# local misassemblies 15 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.057 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.37 # indels per 100 kbp 0.34 Largest alignment 26961	# misassembled contigs	1
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.057 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.37 # indels per 100 kbp 0.34 Largest alignment 26961	Misassembled contigs length	1211
Unaligned length         0           Genome fraction (%)         96.057           Duplication ratio         1.002           # N's per 100 kbp         0.00           # mismatches per 100 kbp         4.37           # indels per 100 kbp         0.34           Largest alignment         26961	# local misassemblies	15
Genome fraction (%)       96.057         Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4.37         # indels per 100 kbp       0.34         Largest alignment       26961	# unaligned contigs	0 + 0 part
Duplication ratio       1.002         # N's per 100 kbp       0.00         # mismatches per 100 kbp       4.37         # indels per 100 kbp       0.34         Largest alignment       26961	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 4.37 # indels per 100 kbp 0.34 Largest alignment 26961	Genome fraction (%)	96.057
# mismatches per 100 kbp       4.37         # indels per 100 kbp       0.34         Largest alignment       26961	Duplication ratio	1.002
# indels per 100 kbp 0.34 Largest alignment 26961	# N's per 100 kbp	0.00
Largest alignment 26961	# mismatches per 100 kbp	4.37
	# indels per 100 kbp	0.34
NA50 5470	Largest alignment	26961
10.55	NA50	5470
NA75 3081	NA75	3081
LA50 262	LA50	262
LA75 538	LA75	538

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
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1211
# local misassemblies	15
# mismatches	195
# indels	15
# short indels	14
# long indels	1
Indels length	83

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).











