Report

# contigs (>= 0 bp)		
# contigs (>= 1000 bp) 151 # contigs (>= 5000 bp) 100 # contigs (>= 25000 bp) 68 # contigs (>= 25000 bp) 68 # contigs (>= 50000 bp) 30 Total length (>= 0 bp) 4568828 Total length (>= 1000 bp) 4552910 Total length (>= 1000 bp) 4478121 Total length (>= 10000 bp) 4348753 Total length (>= 25000 bp) 3834342 Total length (>= 5000 bp) 4568828 Total length (>= 5000 bp) 4478121 Total length (>= 5000 bp) 4478121 Total length (>= 50000 bp) 3834342 Total length (>= 50000 bp) 2542059 # contigs 167 Largest contig 177939 Total length 4563894 Reference length 4641652 N50 55538 N75 30485 L50 26 L75 54 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # local misassemblies 11 # unaligned contigs 0 Genome fraction (%) 98.221 Duplication ratio 1.001 # N's per 100 kbp 9.00 # mismatches per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485		final.contigs
# contigs (>= 5000 bp) 118 # contigs (>= 10000 bp) 100 # contigs (>= 25000 bp) 68 # contigs (>= 50000 bp) 30 Total length (>= 0 bp) 4568828 Total length (>= 1000 bp) 4552910 Total length (>= 5000 bp) 4478121 Total length (>= 10000 bp) 4348753 Total length (>= 25000 bp) 3834342 Total length (>= 5000 bp) 4568828 Total length (>= 5000 bp) 4478121 Total length (>= 50000 bp) 4348753 Total length (>= 50000 bp) 2542059 # contigs 167 Largest contig 177939 Total length 4563894 Reference length 4641652 N50 55538 N75 30485 L50 26 L75 54 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 11 # unaligned contigs 0 # local misassemblies 11 # unaligned length 0 Genome fraction (%) 98.221 Duplication ratio 1.001 # N's per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485		186
# contigs (>= 10000 bp) 68 # contigs (>= 25000 bp) 68 # contigs (>= 50000 bp) 30 Total length (>= 0 bp) 4568828 Total length (>= 1000 bp) 4552910 Total length (>= 5000 bp) 4478121 Total length (>= 10000 bp) 4348753 Total length (>= 25000 bp) 3834342 Total length (>= 5000 bp) 2542059 # contigs 167 Largest contig 177939 Total length 4563894 Reference length 4641652 N50 55538 N75 30485 L50 266 L75 54 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 11 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.221 Duplication ratio 1.001 # N's per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485		151
# contigs (>= 25000 bp)		118
# contigs (>= 50000 bp) 30 Total length (>= 0 bp) 4568828 Total length (>= 1000 bp) 4552910 Total length (>= 5000 bp) 4478121 Total length (>= 10000 bp) 4348753 Total length (>= 25000 bp) 3834342 Total length (>= 50000 bp) 2542059 # contigs 167 Largest contig 177939 Total length 4563894 Reference length 4641652 N50 55538 N75 30485 L50 26 L75 54 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 10 # local misassemblies 11 # unaligned length 0 Genome fraction (%) 98.221 Duplication ratio 1.001 # N's per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485		100
Total length (>= 0 bp) 4568828 Total length (>= 1000 bp) 4552910 Total length (>= 5000 bp) 4478121 Total length (>= 10000 bp) 4348753 Total length (>= 25000 bp) 3834342 Total length (>= 50000 bp) 2542059 # contigs 167 Largest contig 177939 Total length 4563894 Reference length 4641652 N50 55538 N75 30485 L50 26 L75 54 # misassemblies 0 # sessembled contigs 0 Misassembled contigs length 0 # local misassemblies 11 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.221 Duplication ratio 1.001 # mismatches per 100 kbp 67.86 # indels per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485		68
Total length (>= 1000 bp) 4552910 Total length (>= 5000 bp) 4478121 Total length (>= 10000 bp) 4348753 Total length (>= 25000 bp) 3834342 Total length (>= 50000 bp) 2542059 # contigs 167 Largest contig 177939 Total length 4563894 Reference length 4641652 N50 55538 N75 30485 L50 26 L75 54 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 11 # unaligned length 0 Genome fraction (%) 98.221 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485		30
Total length (>= 5000 bp) 4478121 Total length (>= 10000 bp) 4348753 Total length (>= 25000 bp) 3834342 Total length (>= 50000 bp) 2542059 # contigs 167 Largest contig 177939 Total length 4563894 Reference length 4641652 N50 55538 N75 30485 L50 26 L75 54 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 11 # unaligned length 0 Genome fraction (%) 98.221 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 67.86 # indels per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485		4568828
Total length (>= 10000 bp) 4348753 Total length (>= 25000 bp) 3834342 Total length (>= 50000 bp) 2542059 # contigs 167 Largest contig 177939 Total length 4563894 Reference length 4641652 N50 55538 N75 30485 L50 26 L75 54 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 11 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.221 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 67.86 # indels per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485		4552910
Total length (>= 25000 bp) 3834342 Total length (>= 50000 bp) 2542059 # contigs 167 Largest contig 177939 Total length 4563894 Reference length 4641652 N50 55538 N75 30485 L50 26 L75 54 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 11 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.221 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 67.86 # indels per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485	Total length (>= 5000 bp)	4478121
Total length (>= 50000 bp) 2542059 # contigs 167 Largest contig 177939 Total length 4563894 Reference length 4641652 N50 55538 N75 30485 L50 26 L75 54 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 11 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.221 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 67.86 # indels per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485	Total length (>= 10000 bp)	4348753
# contigs 167 Largest contig 177939 Total length 4563894 Reference length 4641652 N50 55538 N75 30485 L50 26 L75 54 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 10 # local misassemblies 11 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.221 Duplication ratio 1.001 # N's per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485	Total length (>= 25000 bp)	3834342
Largest contig 177939 Total length 4563894 Reference length 4641652 N50 55538 N75 30485 L50 26 L75 54 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 11 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.221 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 67.86 # indels per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485	Total length (>= 50000 bp)	2542059
Total length 4563894 Reference length 4641652 N50 55538 N75 30485 L50 26 L75 54 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 11 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.221 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 67.86 # indels per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485	# contigs	167
Reference length 4641652 N50 55538 N75 30485 L50 26 L75 54 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 11 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.221 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 67.86 # indels per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485	Largest contig	177939
N50 55538 N75 30485 L50 26 L75 54 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 11 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.221 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 67.86 # indels per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485	Total length	4563894
N75 30485 L50 26 L75 54 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 11 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.221 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 67.86 # indels per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485	Reference length	4641652
L50 26 L75 54 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 11 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.221 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 67.86 # indels per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485	N50	55538
L75 54 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 11 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.221 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 67.86 # indels per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485	N75	30485
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 11 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.221 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 67.86 # indels per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485	L50	26
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 11 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.221 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 67.86 # indels per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485	L75	54
Misassembled contigs length0# local misassemblies11# unaligned contigs0 + 0 partUnaligned length0Genome fraction (%)98.221Duplication ratio1.001# N's per 100 kbp0.00# mismatches per 100 kbp67.86# indels per 100 kbp9.50Largest alignment177939NA5055538NA7530485	# misassemblies	0
# local misassemblies 11 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.221 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 67.86 # indels per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485	# misassembled contigs	0
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.221 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 67.86 # indels per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485	Misassembled contigs length	0
Unaligned length 0 Genome fraction (%) 98.221 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 67.86 # indels per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485	# local misassemblies	11
Genome fraction (%) 98.221 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 67.86 # indels per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485	# unaligned contigs	0 + 0 part
Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 67.86 # indels per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 67.86 # indels per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485	Genome fraction (%)	98.221
# mismatches per 100 kbp 67.86 # indels per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485	Duplication ratio	1.001
# indels per 100 kbp 9.50 Largest alignment 177939 NA50 55538 NA75 30485	# N's per 100 kbp	0.00
Largest alignment 177939 NA50 55538 NA75 30485	# mismatches per 100 kbp	67.86
NA50 55538 NA75 30485	# indels per 100 kbp	9.50
NA75 30485	Largest alignment	177939
	NA50	55538
	NA75	30485
LA50 26	LA50	26
LA75 54	LA75	54

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	11
# mismatches	3094
# indels	433
# short indels	432
# long indels	1
Indels length	727

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).









