Report

# contigs (>= 1000 bp)		scaffolds
# contigs (>= 10000 bp) 87 # contigs (>= 25000 bp) 75 # contigs (>= 50000 bp) 58 Total length (>= 10000 bp) 9007220 Total length (>= 50000 bp) 8960493 Total length (>= 10000 bp) 8921146 Total length (>= 25000 bp) 8704633 Total length (>= 50000 bp) 8130674 # contigs 137 Largest contig 527156 Total length 9019919 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.78 N50 132337 N75 86976 NG75 200796 L50 19 LG50 7 L75 39 LG75 13 # misassemblies 268 # misassembled contigs length 4251762 # local misassemblies 4 # unaligned length 7180 Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA75 89865 LA50 33 LGA50 8 LA75 98	# contigs (>= 1000 bp)	118
# contigs (>= 25000 bp)	# contigs (>= 5000 bp)	92
# contigs (>= 50000 bp) 58 Total length (>= 1000 bp) 9007220 Total length (>= 5000 bp) 8960493 Total length (>= 10000 bp) 8921146 Total length (>= 25000 bp) 8704633 Total length (>= 50000 bp) 8704633 Total length (>= 50000 bp) 8130674 # contigs 137 Largest contig 527156 Total length 9019919 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.78 N50 132337 NG50 263375 N75 86976 NG75 200796 L50 19 LG50 7 L75 39 LG75 13 # misassemblies 268 # misassembled contigs 42 Misassembled contigs 42 Misassembled contigs 42 Misassembled contigs 0 + 2 part Unaligned length 7180 Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8	# contigs (>= 10000 bp)	87
# contigs (>= 50000 bp) 58 Total length (>= 1000 bp) 9007220 Total length (>= 5000 bp) 8960493 Total length (>= 10000 bp) 8921146 Total length (>= 25000 bp) 8704633 Total length (>= 50000 bp) 8704633 Total length (>= 50000 bp) 8130674 # contigs 137 Largest contig 527156 Total length 9019919 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.78 N50 132337 NG50 263375 N75 86976 NG75 200796 L50 19 LG50 7 L75 39 LG75 13 # misassemblies 268 # misassembled contigs 42 Misassembled contigs 42 Misassembled contigs 42 Misassembled contigs 0 + 2 part Unaligned length 7180 Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8		75
Total length (>= 5000 bp) 8960493 Total length (>= 10000 bp) 8921146 Total length (>= 25000 bp) 8704633 Total length (>= 50000 bp) 8130674 # contigs 137 Largest contig 527156 Total length 9019919 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.78 N50 132337 NG50 263375 N75 86976 NG75 200796 L50 19 LG50 7 L75 39 LG75 13 # misassemblies 268 # misassembled contigs 42 Misassembled contigs 42 Misassembled contigs 42 Misassembled contigs 0 + 2 part Unaligned length 7180 Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LA50 8	# contigs (>= 50000 bp)	58
Total length (>= 10000 bp) 8921146 Total length (>= 25000 bp) 8704633 Total length (>= 50000 bp) 8130674 # contigs 137 Largest contig 527156 Total length 9019919 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.78 N50 132337 NG50 263375 N75 86976 NG75 200796 L50 19 LG50 7 L75 39 LG75 13 # misassemblies 268 # misassembled contigs 42 Misassembled contigs length 4251762 # local misassemblies 4 # unaligned length 7180 Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LA50 88	Total length (>= 1000 bp)	9007220
Total length (>= 25000 bp) 8704633 Total length (>= 50000 bp) 8130674 # contigs 137 Largest contig 527156 Total length 9019919 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.78 N50 132337 NG50 263375 N75 86976 NG75 200796 L50 19 LG50 7 L75 39 LG75 13 # misassemblies 268 # misassembled contigs 42 Misassembled contigs 42 Misassembled contigs 0 + 2 part Unaligned length 7180 Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8	Total length (>= 5000 bp)	8960493
# contigs 137 Largest contig 527156 Total length 9019919 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.78 N50 132337 NG50 263375 N75 86976 NG75 200796 L50 19 LG50 7 L75 39 LG75 13 # misassemblies 268 # misassembled contigs 42 Misassembled contigs 42 Misassembled contigs 0 + 2 part Unaligned length 7180 Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8	Total length (>= 10000 bp)	8921146
# contigs 137 Largest contig 527156 Total length 9019919 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.78 N50 132337 NG50 263375 N75 86976 NG75 200796 L50 19 LG50 7 L75 39 LG75 13 # misassemblies 268 # misassembled contigs 42 Misassembled contigs 42 Misassembled contigs 0 + 2 part Unaligned length 7180 Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8	Total length (>= 25000 bp)	8704633
# contigs 137 Largest contig 527156 Total length 9019919 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.78 N50 132337 NG50 263375 N75 86976 NG75 200796 L50 19 LG50 7 L75 39 LG75 13 # misassemblies 268 # misassembled contigs 42 Misassembled contigs 42 Misassembled contigs 42 # local misassemblies 4 # unaligned length 7180 Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8	Total length (>= 50000 bp)	8130674
Total length 9019919 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.78 N50 132337 NG50 263375 N75 86976 NG75 200796 L50 19 LG50 7 L75 39 LG75 13 # misassembled contigs 42 Misassembled contigs 42 Misassembled contigs 42 Misassembled contigs 0 + 2 part Unaligned length 7180 Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8		137
Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.78 N50 132337 NG50 263375 N75 86976 NG75 200796 L50 19 LG50 7 L75 39 LG75 13 # misassemblies 268 # misassembled contigs 42 Misassembled contigs length 4251762 # local misassemblies 4 # unaligned contigs 0 + 2 part Unaligned length 7180 Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8 LA75 98	Largest contig	527156
GC (%) 50.78 Reference GC (%) 50.78 N50 132337 NG50 263375 N75 86976 NG75 200796 L50 19 LG50 7 L75 39 LG75 13 # misassemblies 268 # misassembled contigs 42 Misassembled contigs 42 # local misassemblies 4 # unaligned contigs 0 + 2 part Unaligned length 7180 Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8 LA75 98	Total length	9019919
Reference GC (%) 50.78 N50 132337 NG50 263375 N75 86976 NG75 200796 L50 19 LG50 7 L75 39 LG75 13 # misassemblies 268 # misassembled contigs 42 Misassembled contigs length 4251762 # local misassemblies 4 # unaligned contigs 0 + 2 part Unaligned length 7180 Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8 LA75 98	Reference length	4641652
N50 132337 NG50 263375 N75 86976 NG75 200796 L50 19 LG50 7 L75 39 LG75 13 # misassemblies 268 # misassembled contigs 42 Misassembled contigs length 4251762 # local misassemblies 4 # unaligned contigs 0 + 2 part Unaligned length 7180 Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8 LA75 98	GC (%)	50.78
NG50 263375 N75 86976 NG75 200796 L50 19 LG50 7 L75 39 LG75 13 # misassemblies 268 # misassembled contigs 42 Misassembled contigs length 4251762 # local misassemblies 4 # unaligned contigs 0 + 2 part Unaligned length 7180 Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8 LA75 98	Reference GC (%)	50.78
N75 86976 NG75 200796 L50 19 LG50 7 L75 39 LG75 13 # misassemblies 268 # misassembled contigs 42 Misassembled contigs length 4251762 # local misassemblies 4 # unaligned contigs 0 + 2 part Unaligned length 7180 Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8 LA75 98	N50	132337
NG75 200796 L50 19 LG50 7 L75 39 LG75 13 # misassemblies 268 # misassembled contigs 42 Misassembled contigs length 4251762 # local misassemblies 4 # unaligned contigs 0 + 2 part Unaligned length 7180 Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8 LA75 98	NG50	263375
L50 19 LG50 7 L75 39 LG75 13 # misassemblies 268 # misassembled contigs 42 Misassembled contigs length 4251762 # local misassemblies 4 # unaligned contigs 0 + 2 part Unaligned length 7180 Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8 LA75 98	N75	86976
LG50 7 L75 39 LG75 13 # misassemblies 268 # misassembled contigs 42 Misassembled contigs length 4251762 # local misassemblies 4 # unaligned contigs 0 + 2 part Unaligned length 7180 Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8 LA75 98	NG75	200796
L75 39 LG75 13 # misassemblies 268 # misassembled contigs 42 Misassembled contigs length 4251762 # local misassemblies 4 # unaligned contigs 0 + 2 part Unaligned length 7180 Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8 LA75 98	L50	19
LG75 13 # misassemblies 268 # misassembled contigs 42 Misassembled contigs length 4251762 # local misassemblies 4 # unaligned contigs 0 + 2 part Unaligned length 7180 Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8 LA75 98	LG50	7
# misassemblies 268 # misassembled contigs 42 Misassembled contigs length 4251762 # local misassemblies 4 # unaligned contigs 0 + 2 part Unaligned length 7180 Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8	L75	39
# misassembled contigs 42 Misassembled contigs length 4251762 # local misassemblies 4 # unaligned contigs 0 + 2 part Unaligned length 7180 Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8 LA75 98	LG75	13
Misassembled contigs length 4251762 # local misassemblies 4 # unaligned contigs 0 + 2 part Unaligned length 7180 Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8 LA75 98	# misassemblies	268
# local misassemblies 4 # unaligned contigs 0 + 2 part Unaligned length 7180 Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8	# misassembled contigs	42
# unaligned contigs 0 + 2 part Unaligned length 7180 Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8 LA75 98	Misassembled contigs length	4251762
Unaligned length 7180 Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8 LA75 98	# local misassemblies	4
Genome fraction (%) 98.671 Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8 LA75 98	# unaligned contigs	0 + 2 part
Duplication ratio 1.968 # N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8 LA75 98	Unaligned length	7180
# N's per 100 kbp 0.00 # mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8 LA75 98	Genome fraction (%)	98.671
# mismatches per 100 kbp 853.00 # indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8 LA75 98		1.968
# indels per 100 kbp 1.24 Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8 LA75 98	# N's per 100 kbp	0.00
Largest alignment 527156 NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8 LA75 98	# mismatches per 100 kbp	853.00
NA50 61543 NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8 LA75 98	# indels per 100 kbp	1.24
NGA50 197358 NA75 20909 NGA75 89865 LA50 33 LGA50 8 LA75 98	Largest alignment	527156
NA75 20909 NGA75 89865 LA50 33 LGA50 8 LA75 98	NA50	61543
NGA75 89865 LA50 33 LGA50 8 LA75 98	NGA50	197358
LA50 33 LGA50 8 LA75 98	NA75	20909
LGA50 8 LA75 98	NGA75	89865
LA75 98	LA50	33
	LGA50	8
LGA75 19		98
	LGA75	19

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

	scaffolds
# misassemblies	268
# relocations	222
# translocations	0
# inversions	46
# possibly misassembled contigs	13
# misassembled contigs	42
Misassembled contigs length	4251762
# local misassemblies	4
# mismatches	39067
# indels	57
# short indels	57
# long indels	0
Indels length	58

All statistics are based on contigs of size \geq 500 bp, unless otherwise noted (e.g., "# contigs (\geq 0 bp)" and "Total length (\geq 0 bp)" include all contigs).

Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	1
Partially unaligned length	7180
# 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).

















