Report

# contigs (>= 0 bp) 215 # contigs (>= 1000 bp) 198 Total length (>= 0 bp) 1267862 Total length (>= 1000 bp) 1254149 # contigs 215 Largest contig 36991 Total length 1267862 Reference length 615980 GC (%) 25.34 Reference GC (%) 25.35 N50 9274 NG50 16331 N75 5047 NG75 12035 L50 42 LG50 13 L75 86 LG75 25 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 10 # local misassemblies 0 # unaligned length 554414 Genome fraction (%) 99.618 Duplication ratio 1.163 # N's per 100 kbp 0.00 # mismatches per 100 kbp 173.23 # indels per 100 kbp 0.33 Largest alignment 36991 NA50 9274 NGA75 5569 LA50 94 LGA50 19 LGA50 19 LGA75 39		
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Total length (>= 1000 bp) 1254149 # contigs 215 Largest contig 36991 Total length 1267862 Reference length 615980 GC (%) 25.34 Reference GC (%) 25.35 N50 9274 NG50 16331 N75 5047 NG75 12035 L50 42 LG50 13 L75 86 LG75 25 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 2187 # local misassemblies 0 # unaligned contigs 70 + 22 part Unaligned length 554414 Genome fraction (%) 99.618 Duplication ratio 1.163 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.33 Largest alignment 36991 NA50 1725 NGA75 5569 LA50 94 LGA50 19	# contigs (>= 1000 bp)	198
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Largest contig 36991 Total length 1267862 Reference length 615980 GC (%) 25.34 Reference GC (%) 25.35 N50 9274 NG50 16331 N75 5047 NG75 12035 L50 42 LG50 13 L75 86 LG75 25 # misassemblies 1 # local misassembled contigs 1 # local misassembles 0 # unaligned contigs 70 + 22 part Unaligned length 554414 Genome fraction (%) 99.618 Duplication ratio 1.163 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.33 Largest alignment 36991 NA50 1725 NGA75 5569 LA50 94 LGA50 19	Total length (>= 1000 bp)	1254149
Total length 1267862 Reference length 615980 GC (%) 25.34 Reference GC (%) 25.35 N50 9274 NG50 16331 N75 5047 NG75 12035 L50 42 LG50 13 L75 86 LG75 25 # misassembled contigs 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 70 + 22 part Unaligned length 554414 Genome fraction (%) 99.618 Duplication ratio 1.163 # N's per 100 kbp 0.00 # mismatches per 100 kbp 173.23 # indels per 100 kbp 0.33 Largest alignment 36991 NA50 1725 NGA50 9274 NGA75 5569 LA50 94 LGA50 19	# contigs	215
Reference length 615980 GC (%) 25.34 Reference GC (%) 25.35 N50 9274 NG50 16331 N75 5047 NG75 12035 L50 42 LG50 13 L75 86 LG75 25 # misassemblies 1 # local misassembled contigs 1 # local misassemblies 0 # unaligned contigs 70 + 22 part Unaligned length 554414 Genome fraction (%) 99.618 Duplication ratio 1.163 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.33 Largest alignment 36991 NA50 1725 NGA75 5569 LA50 94 LGA50 19	Largest contig	36991
GC (%) 25.34 Reference GC (%) 25.35 N50 9274 NG50 16331 N75 5047 NG75 12035 L50 42 LG50 13 L75 86 LG75 25 # misassemblies 1 # local misassembled contigs 1 # local misassemblies 0 # unaligned contigs 70 + 22 part Unaligned length 554414 Genome fraction (%) 99.618 Duplication ratio 1.163 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.33 Largest alignment 36991 NA50 1725 NGA50 9274 NGA75 5569 LA50 94 LGA50 19	Total length	1267862
Reference GC (%) 25.35 N50 9274 NG50 16331 N75 5047 NG75 12035 L50 42 LG50 13 L75 86 LG75 25 # misassemblies 1 # local misassembled contigs 1 # local misassemblies 0 # unaligned contigs 70 + 22 part Unaligned length 554414 Genome fraction (%) 99.618 Duplication ratio 1.163 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.33 Largest alignment 36991 NA50 1725 NGA75 5569 LA50 94 LGA50 19	Reference length	615980
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NG50 16331 N75 5047 NG75 12035 L50 42 LG50 13 L75 86 LG75 25 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 2187 # local misassemblies 0 # unaligned contigs 70 + 22 part Unaligned length 554414 Genome fraction (%) 99.618 Duplication ratio 1.163 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.33 Largest alignment 36991 NA50 1725 NGA50 9274 NGA75 5569 LA50 94 LGA50 19	Reference GC (%)	25.35
N75 5047 NG75 12035 L50 42 LG50 13 L75 86 LG75 25 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 2187 # local misassemblies 0 # unaligned contigs 70 + 22 part Unaligned length 554414 Genome fraction (%) 99.618 Duplication ratio 1.163 # N's per 100 kbp 0.00 # mismatches per 100 kbp 173.23 # indels per 100 kbp 0.33 Largest alignment 36991 NA50 1725 NGA75 5569 LA50 94 LGA50 19	N50	9274
NG75 12035 L50 42 LG50 13 L75 86 LG75 25 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 2187 # local misassemblies 0 # unaligned contigs 70 + 22 part Unaligned length 554414 Genome fraction (%) 99.618 Duplication ratio 1.163 # N's per 100 kbp 0.00 # mismatches per 100 kbp 173.23 # indels per 100 kbp 0.33 Largest alignment 36991 NA50 1725 NGA70 9274 NGA75 5569 LA50 94 LGA50 19	NG50	16331
L50 42 LG50 13 L75 86 LG75 25 # misassemblies 1 Misassembled contigs 1 Misassembled contigs length 2187 # local misassemblies 0 # unaligned contigs 70 + 22 part Unaligned length 554414 Genome fraction (%) 99.618 Duplication ratio 1.163 # N's per 100 kbp 0.00 # mismatches per 100 kbp 173.23 # indels per 100 kbp 0.33 Largest alignment 36991 NA50 1725 NGA50 9274 NGA75 5569 LA50 94 LGA50 19	N75	5047
LG50 13 L75 86 LG75 25 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 2187 # local misassemblies 0 # unaligned contigs 70 + 22 part Unaligned length 554414 Genome fraction (%) 99.618 Duplication ratio 1.163 # N's per 100 kbp 0.00 # mismatches per 100 kbp 173.23 # indels per 100 kbp 0.33 Largest alignment 36991 NA50 1725 NGA50 9274 NGA75 5569 LA50 94 LGA50 19	NG75	12035
L75 86 LG75 25 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 2187 # local misassemblies 0 # unaligned contigs 70 + 22 part Unaligned length 554414 Genome fraction (%) 99.618 Duplication ratio 1.163 # N's per 100 kbp 0.00 # mismatches per 100 kbp 173.23 # indels per 100 kbp 0.33 Largest alignment 36991 NA50 1725 NGA50 9274 NGA75 5569 LA50 94 LGA50 19	L50	42
LG75 25 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 2187 # local misassemblies 0 # unaligned contigs 70 + 22 part Unaligned length 554414 Genome fraction (%) 99.618 Duplication ratio 1.163 # N's per 100 kbp 0.00 # mismatches per 100 kbp 173.23 # indels per 100 kbp 0.33 Largest alignment 36991 NA50 1725 NGA50 9274 NGA75 5569 LA50 94 LGA50 19	LG50	13
# misassemblies 1 # misassembled contigs 1 Misassembled contigs length 2187 # local misassemblies 0 # unaligned contigs 70 + 22 part Unaligned length 554414 Genome fraction (%) 99.618 Duplication ratio 1.163 # N's per 100 kbp 0.00 # mismatches per 100 kbp 173.23 # indels per 100 kbp 0.33 Largest alignment 36991 NA50 1725 NGA50 9274 NGA75 5569 LA50 94 LGA50 19	L75	86
# misassembled contigs 1 Misassembled contigs length 2187 # local misassemblies 0 # unaligned contigs 70 + 22 part Unaligned length 554414 Genome fraction (%) 99.618 Duplication ratio 1.163 # N's per 100 kbp 0.00 # mismatches per 100 kbp 173.23 # indels per 100 kbp 0.33 Largest alignment 36991 NA50 1725 NGA50 9274 NGA75 5569 LA50 94 LGA50 19	LG75	25
Misassembled contigs length 2187 # local misassemblies 0 # unaligned contigs 70 + 22 part Unaligned length 554414 Genome fraction (%) 99.618 Duplication ratio 1.163 # N's per 100 kbp 0.00 # mismatches per 100 kbp 173.23 # indels per 100 kbp 0.33 Largest alignment 36991 NA50 1725 NGA50 9274 NGA75 5569 LA50 94 LGA50 19	# misassemblies	1
# local misassemblies 0 # unaligned contigs 70 + 22 part Unaligned length 554414 Genome fraction (%) 99.618 Duplication ratio 1.163 # N's per 100 kbp 0.00 # mismatches per 100 kbp 173.23 # indels per 100 kbp 0.33 Largest alignment 36991 NA50 1725 NGA50 9274 NGA75 5569 LA50 94 LGA50 19	# misassembled contigs	1
# unaligned contigs 70 + 22 part Unaligned length 554414 Genome fraction (%) 99.618 Duplication ratio 1.163 # N's per 100 kbp 0.00 # mismatches per 100 kbp 173.23 # indels per 100 kbp 0.33 Largest alignment 36991 NA50 1725 NGA50 9274 NGA75 5569 LA50 94 LGA50 19	Misassembled contigs length	2187
Unaligned length 554414 Genome fraction (%) 99.618 Duplication ratio 1.163 # N's per 100 kbp 0.00 # mismatches per 100 kbp 173.23 # indels per 100 kbp 0.33 Largest alignment 36991 NA50 1725 NGA50 9274 NGA75 5569 LA50 94 LGA50 19	# local misassemblies	0
Genome fraction (%) 99.618 Duplication ratio 1.163 # N's per 100 kbp 0.00 # mismatches per 100 kbp 173.23 # indels per 100 kbp 0.33 Largest alignment 36991 NA50 1725 NGA50 9274 NGA75 5569 LA50 94 LGA50 19	# unaligned contigs	70 + 22 part
Duplication ratio 1.163 # N's per 100 kbp 0.00 # mismatches per 100 kbp 173.23 # indels per 100 kbp 0.33 Largest alignment 36991 NA50 1725 NGA50 9274 NGA75 5569 LA50 94 LGA50 19	Unaligned length	554414
# N's per 100 kbp 0.00 # mismatches per 100 kbp 173.23 # indels per 100 kbp 0.33 Largest alignment 36991 NA50 1725 NGA50 9274 NGA75 5569 LA50 94 LGA50 19	Genome fraction (%)	99.618
# mismatches per 100 kbp 173.23 # indels per 100 kbp 0.33 Largest alignment 36991 NA50 1725 NGA50 9274 NGA75 5569 LA50 94 LGA50 19	Duplication ratio	1.163
# indels per 100 kbp 0.33 Largest alignment 36991 NA50 1725 NGA50 9274 NGA75 5569 LA50 94 LGA50 19	# N's per 100 kbp	0.00
Largest alignment 36991 NA50 1725 NGA50 9274 NGA75 5569 LA50 94 LGA50 19	# mismatches per 100 kbp	173.23
NA50 1725 NGA50 9274 NGA75 5569 LA50 94 LGA50 19	# indels per 100 kbp	0.33
NGA50 9274 NGA75 5569 LA50 94 LGA50 19	Largest alignment	36991
NGA75 5569 LA50 94 LGA50 19	NA50	1725
LA50 94 LGA50 19	NGA50	9274
LGA50 19	NGA75	5569
	LA50	94
LGA75 39	LGA50	19
	LGA75	39

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	1
# translocations	0
# inversions	0
# possibly misassembled contigs	16
# misassembled contigs	1
Misassembled contigs length	2187
# local misassemblies	0
# mismatches	1063
# indels	2
# short indels	2
# long indels	0
Indels length	2

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	70
Fully unaligned length	382062
# partially unaligned contigs	22
# with misassembly	2
# both parts are significant	16
Partially unaligned length	172352
# 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).















