Report

# contigs (>= 0 bp)		anonymous_gsa
# contigs (>= 1000 bp)	# contigs (>= 0 hp)	
# contigs (>= 5000 bp)		
# contigs (>= 10000 bp)		
# contigs (>= 25000 bp) 1 # contigs (>= 50000 bp) 1 Total length (>= 0 bp) 4641592 Total length (>= 1000 bp) 4641592 Total length (>= 5000 bp) 4641592 Total length (>= 50000 bp) 4641592 Total length (>= 50000 bp) 4641592 # contigs 1 Largest contig 4641592 Reference length 4641652 GC (%) 50.79 Reference GC (%) 50.79 N50 4641592 NG50 4641592 NG50 4641592 NG75 4641592 LG50 1 LG50 1 LG50 1 LG75 1 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 99.999 Duplication ratio 1.0000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # and the series of the series		
# contigs (>= 50000 bp)		
Total length (>= 0 bp)		
Total length (>= 1000 bp)		_
Total length (>= 5000 bp)		
Total length (>= 10000 bp) 4641592 Total length (>= 25000 bp) 4641592 Total length (>= 50000 bp) 4641592 # contigs 1 Largest contig 4641592 Total length 4641592 Reference length 4641652 GC (%) 50.79 Reference GC (%) 50.79 N50 4641592 N75 4641592 N650 4641592 N75 4641592 L50 1 L75 1 LG75 1 # misassembled contigs 0 # indels per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 4641592 NGA75 4641592 NA75 4641592 DA50 1 L75 0.00 # N's per 100 kbp 0.00 Largest alignment 4641592 NA50 4641592 NA50 4641592 NA50 4641592 NA50 4641592 NA75 4641592		
Total length (>= 25000 bp) 4641592 Total length (>= 50000 bp) 4641592 # contigs 1 Largest contig 4641592 Total length 4641592 Reference length 4641652 GC (%) 50.79 Reference GC (%) 50.79 N50 4641592 NG50 4641592 NG75 4641592 NG75 4641592 LG50 1 L75 1 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.999 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 4641592 NA50 4641592 NA75 4641592 NGA50 4641592 </td <td></td> <td></td>		
Total length (>= 50000 bp) 4641592 # contigs 1 Largest contig 4641592 Total length 4641592 Reference length 4641652 GC (%) 50.79 Reference GC (%) 50.79 N50 4641592 NG50 4641592 NG75 4641592 LS0 1 LG50 1 LG75 1 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # unaligned length 0 Genome fraction (%) 99.999 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # and per 100 kbp 0.00 # models per 100 kbp 0.00 # notation ratio 4641592 NA50 4641592 NA50 4641592 NA75 4641592 NA75 4641592 NGA75		
# contigs 1 Largest contig 4641592 Total length 4641592 Reference length 4641652 GC (%) 50.79 Reference GC (%) 50.79 N50 4641592 NG50 4641592 N75 4641592 L50 1 LG50 1 LG75 1 LG75 1 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.999 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 4641592 NA50 4641592 NA50 4641592 NA75 4641592 NGA75 4641592 LA50 1 LGA50 1 LGA50 1 LGA50 1 LGA50 1		
Largest contig 4641592 Total length 4641592 Reference length 4641652 GC (%) 50.79 Reference GC (%) 50.79 N50 4641592 NG50 4641592 N75 4641592 NG75 4641592 L50 1 LG50 1 L75 1 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.999 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # add1592 NA50 4641592 NA50 4641592 NA75 4641592 NA75 4641592 NA75 4641592 NGA75 4641592 LA50 <td></td> <td></td>		
Total length 4641592 Reference length 4641652 GC (%) 50.79 Reference GC (%) 50.79 N50 4641592 NG50 4641592 NG75 4641592 L50 1 LG50 1 L75 1 LG75 1 # misassemblies 0 # misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.999 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 4641592 NA50 4641592 NA50 4641592 NA75 4641592 LA50 1 LGA50 1 LGA50 1 LA75 1		_
Reference length 4641652 GC (%) 50.79 Reference GC (%) 50.79 N50 4641592 NG50 4641592 N75 4641592 NG75 4641592 LS0 1 LG50 1 L75 1 LG75 1 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.999 Duplication ratio 1.000 # N's per 100 kbp 0.00 # indels per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 4641592 NA50 4641592 NA75 4641592 NGA75 4641592 LA50 1 LA75 1		
GC (%) 50.79 Reference GC (%) 50.79 N50 4641592 NG50 4641592 N75 4641592 NG75 4641592 LS0 1 LG50 1 L75 1 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.999 Duplication ratio 1.000 # N's per 100 kbp 0.00 # indels per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 4641592 NA50 4641592 NA75 4641592 NGA75 4641592 NGA75 4641592 LA50 1 LA75 1		
Reference GC (%) 50.79 N50 4641592 NG50 4641592 N75 4641592 NG75 4641592 LS0 1 LG50 1 L75 1 LG75 1 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.999 Duplication ratio 1.000 # N's per 100 kbp 0.00 # indels per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 4641592 NA50 4641592 NA75 4641592 NA75 4641592 NGA75 4641592 LA50 1 LA75 1		
N50 4641592 NG50 4641592 N75 4641592 NG75 4641592 L50 1 LG50 1 L75 1 LG75 1 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.999 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 4641592 NA50 4641592 NA75 4641592 NGA75 4641592 NGA75 4641592 LA50 1 LA75 1		
NG50 4641592 N75 4641592 NG75 4641592 L50 1 LG50 1 L75 1 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.999 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 4641592 NA50 4641592 NA75 4641592 NGA75 4641592 LA50 1 LGA50 1 LA75 1		
N75 4641592 NG75 4641592 L50 1 LG50 1 L75 1 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.999 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 4641592 NA50 4641592 NA75 4641592 NGA75 4641592 LA50 1 LA75 1		4641592
L50 1 LG50 1 L75 1 LG75 1 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.999 Duplication ratio 1.000 # N's per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 4641592 NA50 4641592 NA75 4641592 NGA75 4641592 LA50 1 LGA50 1 LA75 1	N75	4641592
LG50 1 L75 1 LG75 1 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.999 Duplication ratio 1.000 # N's per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 4641592 NA50 4641592 NA75 4641592 NGA75 4641592 LA50 1 LGA50 1 LA75 1	NG75	4641592
L75 1 LG75 1 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.999 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 4641592 NA50 4641592 NA75 4641592 NGA75 4641592 LA50 1 LGA50 1 LA75 1	L50	1
LG75 1 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.999 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 4641592 NA50 4641592 NA75 4641592 NGA75 4641592 LA50 1 LGA50 1 LA75 1	LG50	1
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.999 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 4641592 NA50 4641592 NA75 4641592 NA75 4641592 LA50 1 LGA50 1 LA75 1	L75	1
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.999 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 4641592 NA50 4641592 NA75 4641592 NA75 4641592 LA50 1 LGA50 1 LGA50 1	LG75	1
Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.999 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 4641592 NA50 4641592 NA75 4641592 NGA75 4641592 LA50 1 LGA50 1 LA75 1	# misassemblies	0
# local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.999 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 4641592 NA50 4641592 NA75 4641592 NA75 4641592 LA50 1 LGA50 1 LGA50 1	# misassembled contigs	0
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.999 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 4641592 NA50 4641592 NGA50 4641592 NA75 4641592 LA50 1 LGA50 1 LGA50 1	Misassembled contigs length	0
Unaligned length 0 Genome fraction (%) 99.999 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 4641592 NA50 4641592 NGA50 4641592 NA75 4641592 NGA75 4641592 LA50 1 LGA50 1 LA75 1	# local misassemblies	0
Genome fraction (%) 99.999 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 4641592 NA50 4641592 NGA50 4641592 NA75 4641592 NGA75 4641592 LA50 1 LGA50 1 LA75 1	# unaligned contigs	0 + 0 part
Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 4641592 NGA50 4641592 NA75 4641592 NGA75 4641592 LA50 1 LGA50 1 LA75 1	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 4641592 NA50 4641592 NA75 4641592 NGA75 4641592 LA50 1 LGA50 1 LA75 1	Genome fraction (%)	99.999
# mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 4641592 NA50 4641592 NGA50 4641592 NA75 4641592 NGA75 4641592 LA50 1 LGA50 1 LA75 1	Duplication ratio	1.000
# indels per 100 kbp 0.00 Largest alignment 4641592 NA50 4641592 NGA50 4641592 NA75 4641592 NGA75 4641592 LA50 1 LGA50 1 LA75 1	# N's per 100 kbp	0.00
Largest alignment 4641592 NA50 4641592 NGA50 4641592 NA75 4641592 NGA75 4641592 LA50 1 LGA50 1 LA75 1	# mismatches per 100 kbp	0.00
NA50 4641592 NGA50 4641592 NA75 4641592 NGA75 4641592 LA50 1 LGA50 1 LA75 1	# indels per 100 kbp	0.00
NGA50 4641592 NA75 4641592 NGA75 4641592 LA50 1 LGA50 1 LA75 1	Largest alignment	4641592
NA75 4641592 NGA75 4641592 LA50 1 LGA50 1 LA75 1	NA50	4641592
NGA75 4641592 LA50 1 LGA50 1 LA75 1	NGA50	4641592
LA50 1 LGA50 1 LA75 1	NA75	4641592
LGA50 1 LA75 1	NGA75	4641592
LA75 1	LA50	1
	LGA50	1
LGA75 1	LA75	1
	LGA75	1

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

	anonymous_gsa
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	0
# 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

	anonymous_gsa
# 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).















