Report

	meta_contigs_1	meta_contigs_2
# contigs (>= 1000 bp)	6	4
# contigs (>= 5000 bp)	3	4
# contigs (>= 10000 bp)	3	3
# contigs (>= 25000 bp)	1	1
# contigs (>= 50000 bp)	0	0
Total length (>= 1000 bp)	64988	60775
Total length (>= 5000 bp)	56606	60775
Total length (>= 10000 bp)	56606	53787
Total length (>= 25000 bp)	27969	27260
Total length (>= 50000 bp)	0	0
# contigs	11	7
Largest contig	27969	27260
Total length	69110	63015
Reference length	64999	64999
GC (%)	40.75	40.67
Reference GC (%)	40.73	40.73
N50	17535	16099
NG50	17535	16099
N75	11102	10428
NG75	11102	10428
L50	2	2
LG50	2	2
L75	3	3
LG75	3	3
# misassemblies	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# unaligned contigs	0 + 0 part	0 + 0 part
Unaligned length	0	0
Genome fraction (%)	98.397	96.609
Duplication ratio	1.081	1.004
# N's per 100 kbp	18.81	0.00
# mismatches per 100 kbp	46.91	12.74
# indels per 100 kbp	3.13	0.00
Largest alignment	27969	27260
NA50	17534	16099
NGA50	17534	16099
NA75	11101	10428
NGA75	11101	10428
LA50	2	2
LGA50	2	2
LA75	3	3
LGA75	3	3

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

	meta_contigs_1	meta_contigs_2
# misassemblies	0	0
# relocations	0	0
# translocations	0	0
# inversions	0	0
# possibly misassembled contigs	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# mismatches	30	8
# indels	2	0
# short indels	2	0
# long indels	0	0
Indels length	2	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

	meta_contigs_1	meta_contigs_2
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	0	0
# with misassembly	0	0
# both parts are significant	0	0
Partially unaligned length	0	0
# N's	13	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).

Nx

Contig length (kbp) vs x

Legend: meta_contigs_1, meta_contigs_2

GC content

Misassemblies

meta_contigs_1   meta_contigs_2

Cumulative length (aligned contigs)

Genome fraction, %