## Report

the sealth of the Ohea)	contigs
# contigs (>= 0 bp)	125
# contigs (>= 1000 bp)	73
# contigs (>= 5000 bp)	55
# contigs (>= 10000 bp)	50
# contigs (>= 25000 bp)	43
# contigs (>= 50000 bp)	27
Total length (>= 0 bp)	4576303
Total length (>= 1000 bp)	4558501
Total length (>= 5000 bp)	4517300
Total length (>= 10000 bp)	4480489
Total length (>= 25000 bp)	4375677
Total length (>= 50000 bp)	3825378
# contigs	86
Largest contig	327173
Total length	4567422
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	173566
NG50	133132
N75	78649
NG75	67379
L50	10
LG50	11
L75	21
LG75	22
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	8
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.328
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.95
# indels per 100 kbp	0.31
Largest alignment	327173
NA50	172028
NGA50	133132
NA75	78649
NGA75	67379
LA50	10
LGA50	11
LA75	21
LGA75	22
LOA73	

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

	contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	8
# mismatches	89
# indels	14
# short indels	13
# long indels	1
Indels length	101

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

	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).















