

## Report

	dataset_2.dat	dataset_3.dat
# contigs (>= 0 bp)	47	35
# contigs (>= 1000 bp)	11	7
Total length (>= 0 bp)	187773	179095
Total length (>= 1000 bp)	173623	169301
# contigs	20	12
Largest contig	55106	55421
Total length	180875	173140
Reference length	64999	64999
GC (%)	45.35	45.15
Reference GC (%)	40.73	40.73
N50	49658	49658
NG50	55106	55421
N75	17535	27260
NG75	55106	55421
L50	2	2
LG50	1	1
L75	4	3
LG75	1	1
# misassemblies	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# unaligned contigs	9 + 0 part	5 + 0 part
Unaligned length	111765	110125
Genome fraction (%)	98.397	97.782
Duplication ratio	1.081	1.004
# N's per 100 kbp	7.74	0.00
# mismatches per 100 kbp	46.91	29.89
# indels per 100 kbp	3.13	0.00
Largest alignment	27969	27260
NGA50	17534	16099
NGA75	11101	10428
LGA50	2	2
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

	dataset_2.dat	dataset_3.dat
# misassemblies	0	0
# relocations	0	0
# translocations	0	0
# inversions	0	0
# interspecies translocations	0	0
# possibly misassembled contigs	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# mismatches	30	19
# indels	2	0
# short indels	2	0
# long indels	0	0
Indels length	2	0

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

	dataset_2.dat	dataset_3.dat
# fully unaligned contigs	9	5
Fully unaligned length	111765	110125
# partially unaligned contigs	0	0
# with misassembly	0	0
# both parts are significant	0	0
Partially unaligned length	0	0
# N's	14	0

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).



















