Report

	scaffolds
# contigs (>= 1000 bp)	202
# contigs (>= 5000 bp)	160
# contigs (>= 10000 bp)	130
# contigs (>= 25000 bp)	61
# contigs (>= 50000 bp)	12
Total length (>= 1000 bp)	3972819
Total length (>= 5000 bp)	3875821
Total length (>= 10000 bp)	3648554
Total length (>= 25000 bp)	2504220
Total length (>= 50000 bp)	821078
# contigs	219
Largest contig	125463
Total length	3983534
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.79
N50	31481
NG50	27383
N75	19554
NG75	12373
L50	43
LG50	55
L75	83
LG75	116
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	152553
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	83.379
Duplication ratio	1.029
# N's per 100 kbp	30.55
# mismatches per 100 kbp	906.47
# indels per 100 kbp	0.59
Largest alignment	125463
NA50	30519
NGA50	26933
NA75	18252
NGA75	12362
LA50	44
LGA50	56
LA75	86
LGA75	118

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

	scaffolds
# misassemblies	4
# relocations	4
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	152553
# local misassemblies	2
# mismatches	35082
# indels	23
# short indels	19
# long indels	4
Indels length	245

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

	scaffolds
# 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	1217

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).

















