Report

Keport	
	AJ055.SoDe2L
# contigs (>= 0 bp)	25795
# contigs (>= 1000 bp)	948
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	7145906
Total length (>= 1000 bp)	1352478
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3607
Largest contig	4124
Total length	3190953
Reference length	5504133
GC (%)	56.21
Reference GC (%)	57.38
N50	907
NG50	589
N75	672
L50	1204
LG50	2801
L75	2230
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	197
# unaligned mis. contigs	0
# unaligned contigs	111 + 0 part
Unaligned length	118168
Genome fraction (%)	55.537
Duplication ratio	1.005
# N's per 100 kbp	95.30
# mismatches per 100 kbp	2.78
# indels per 100 kbp	1.01
Largest alignment	4124
Total aligned length	3069319
NA50	875
NGA50	568
NA75	645
LA50	1240
LGA50	2900
LA75	2305

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

	AJ055.SoDe2L
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	197
# unaligned mis. contigs	0
# mismatches	85
# indels	31
# indels (<= 5 bp)	29
# indels (> 5 bp)	2
Indels length	142

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

	AJ055.SoDe2L
# fully unaligned contigs	111
Fully unaligned length	118168
# partially unaligned contigs	0
Partially unaligned length	0
# N's	3041

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).



















