Report

Report	L
	sim25M.SoDe2L
# contigs (>= 0 bp)	18513
# contigs (>= 1000 bp)	6139
# contigs (>= 5000 bp)	607
# contigs (>= 10000 bp)	67
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	21123668
Total length (>= 1000 bp)	16118235
Total length (>= 5000 bp)	4452589
Total length (>= 10000 bp)	871962
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	10029
Largest contig	22442
Total length	18923372
Reference length	25000020
GC (%)	43.03
Reference GC (%)	43.69
N50	2663
NG50	1779
N75	1388
NG75	530
L50	2021
LG50	3426
L75	4501
LG75	9692
# misassemblies	4
# misassembled contigs	10225
Misassembled contigs length	19335
# local misassemblies	43 7
# unaligned mis. contigs  # unaligned contigs	·
Unaligned length	888 + 56 part 856266
Genome fraction (%)	71.308
Duplication ratio	1.013
# N's per 100 kbp	1714.44
# mismatches per 100 kbp	43.83
# indels per 100 kbp	42.80
Largest alignment	22442
Total aligned length	17838734
NA50	2595
NGA50	1710
NA75	1284
LA50	2044
LGA50	3489
LA75	4626

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

	sim25M.SoDe2L
# misassemblies	4
# relocations	4
# translocations	0
# inversions	0
# misassembled contigs	4
Misassembled contigs length	19335
# local misassemblies	43
# unaligned mis. contigs	7
# mismatches	7814
# indels	7630
# indels (<= 5 bp)	5851
# indels (> 5 bp)	1779
Indels length	29152

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

	sim25M.SoDe2L
# fully unaligned contigs	888
Fully unaligned length	806809
# partially unaligned contigs	56
Partially unaligned length	49457
# N's	324429

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).





















