Report sim5M.SoDe2L # contigs (>= 0 bp) 2608 1240 # contigs (>= 1000 bp) # contigs (>= 5000 bp) 225 # contigs (>= 10000 bp) 35 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 4648392 Total length (>= 1000 bp) 4089447 Total length (>= 5000 bp) 1725228 443252 Total length (>= 10000 bp) Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 1681 Largest contig 20287 Total length 4413323 Reference length 5000040 GC (%) 34.85 Reference GC (%) 35.84 N50 3847 NG50 3373 N75 2118 NG75 1470 L50 336 LG50 417 L75 718 LG75 965 # misassemblies 0 0 # misassembled contigs Misassembled contigs length 0 12 # local misassemblies n # unaligned mis. contigs # unaligned contigs 128 + 19 part 151179 Unaligned length Genome fraction (%) 84.355 **Duplication ratio** 1.011 # N's per 100 kbp 1539.38 # mismatches per 100 kbp 34.40 # indels per 100 kbp 46.49 Largest alignment 20287 4221589 Total aligned length NA50 3751 NGA50 3269 NA75 2014 NGA75 1325 LA50 339

LGA50

LGA75

LA75

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).

423

733 998

## Misassemblies report

	sim5M.SoDe2L
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	12
# unaligned mis. contigs	0
# mismatches	1451
# indels	1961
# indels (<= 5 bp)	1509
# indels (> 5 bp)	452
Indels length	7390

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

	sim5M.SoDe2L
# fully unaligned contigs	128
Fully unaligned length	133022
# partially unaligned contigs	19
Partially unaligned length	18157
# N's	67938

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).



















