Report sim5M.SoDe2H # contigs (>= 0 bp) 1100 793 # contigs (>= 1000 bp) # contigs (>= 5000 bp) 329 # contigs (>= 10000 bp) 128 # contigs (>= 25000 bp) 9 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 4725731 Total length (>= 1000 bp) 4576364 Total length (>= 5000 bp) 3350958 1942020 Total length (>= 10000 bp) Total length (>= 25000 bp) 281174 Total length (>= 50000 bp) 0 934 # contigs 35592 Largest contig Total length 4679359 Reference length 5000040 GC (%) 35.09 Reference GC (%) 35.84 N50 8376 NG50 7761 N75 4520 NG75 3868 L50 172 LG50 192 L75 363 LG75 420 # misassemblies 0 0 # misassembled contigs Misassembled contigs length 0 66 # local misassemblies 13 # unaligned mis. contigs # unaligned contigs 144 + 92 part 463353 Unaligned length Genome fraction (%) 82.934 **Duplication ratio** 1.017 # N's per 100 kbp 3896.67 147.08 # mismatches per 100 kbp # indels per 100 kbp 120.67 Largest alignment 35307 4141792 Total aligned length NA50 7711 NGA50 7115 NA75 3519 NGA75 2643 LA50 180

LGA50

LGA75

LA75

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).

201

402 480

## Misassemblies report

	sim5M.SoDe2H
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	66
# unaligned mis. contigs	13
# mismatches	6099
# indels	5004
# indels (<= 5 bp)	3864
# indels (> 5 bp)	1140
Indels length	18819

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.SoDe2H
# fully unaligned contigs	144
Fully unaligned length	306256
# partially unaligned contigs	92
Partially unaligned length	157097
# N's	182339

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).



















