

# Report

	scaffolds
# contigs ( $\geq 0$ bp)	4545
# contigs ( $\geq 1000$ bp)	1058
# contigs ( $\geq 5000$ bp)	0
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	3365052
Total length ( $\geq 1000$ bp)	1659424
Total length ( $\geq 5000$ bp)	0
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	2536
Largest contig	4985
Total length	2717422
Reference length	4641652
N50	1176
N75	819
L50	781
L75	1478
# misassemblies	8
# misassembled contigs	8
Misassembled contigs length	17085
# local misassemblies	1
# unaligned contigs	191 + 22 part
Unaligned length	209419
Genome fraction (‰)	53.792
Duplication ratio	1.004
# N's per 100 kbp	1081.65
# mismatches per 100 kbp	416.36
# indels per 100 kbp	47.18
Largest alignment	4985
NA50	1102
NA75	725
LA50	817
LA75	1579

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).

## Misassemblies report

	scaffolds
# misassemblies	8
# relocations	8
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	6
# misassembled contigs	8
Misassembled contigs length	17085
# local misassemblies	1
# mismatches	10396
# indels	1178
# short indels	601
# long indels	577
Indels length	9743

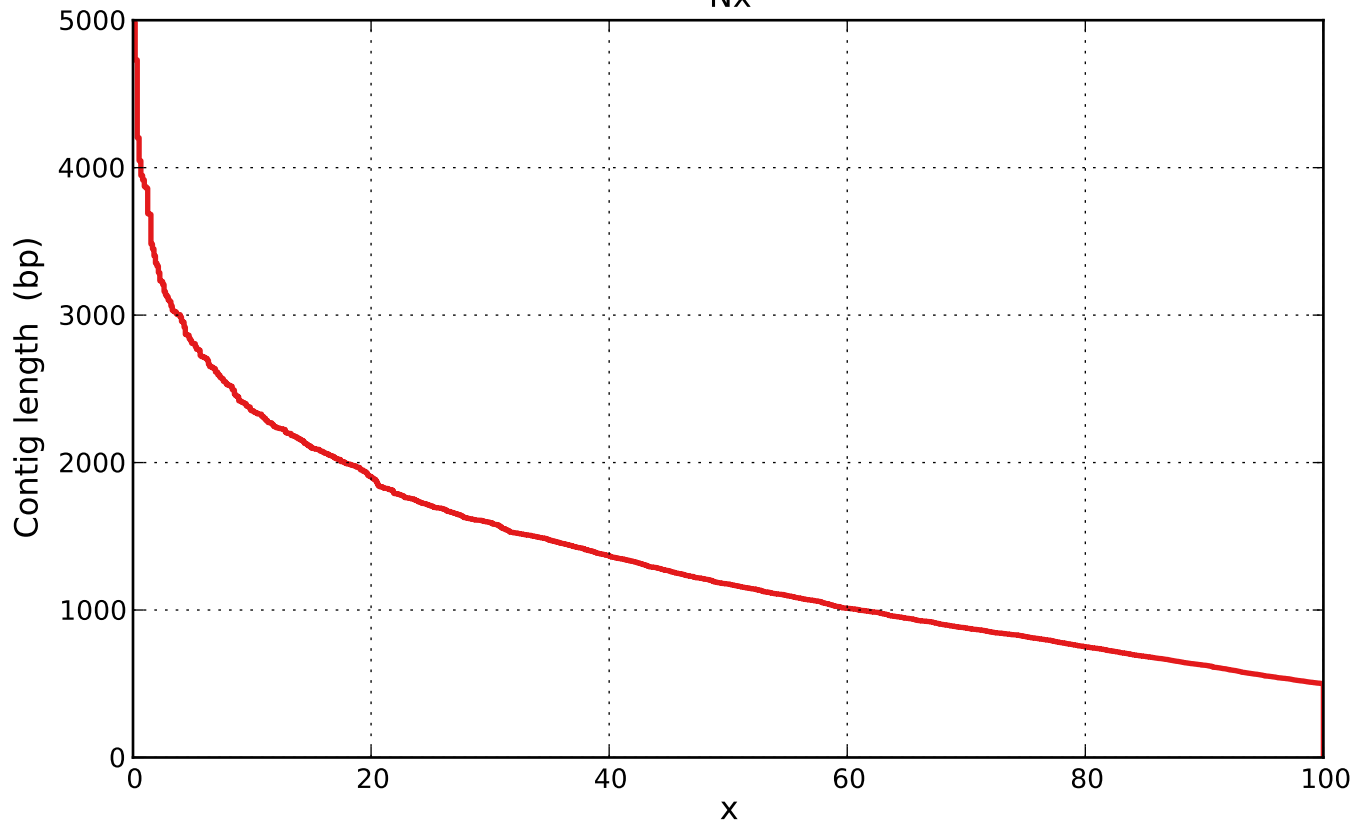
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

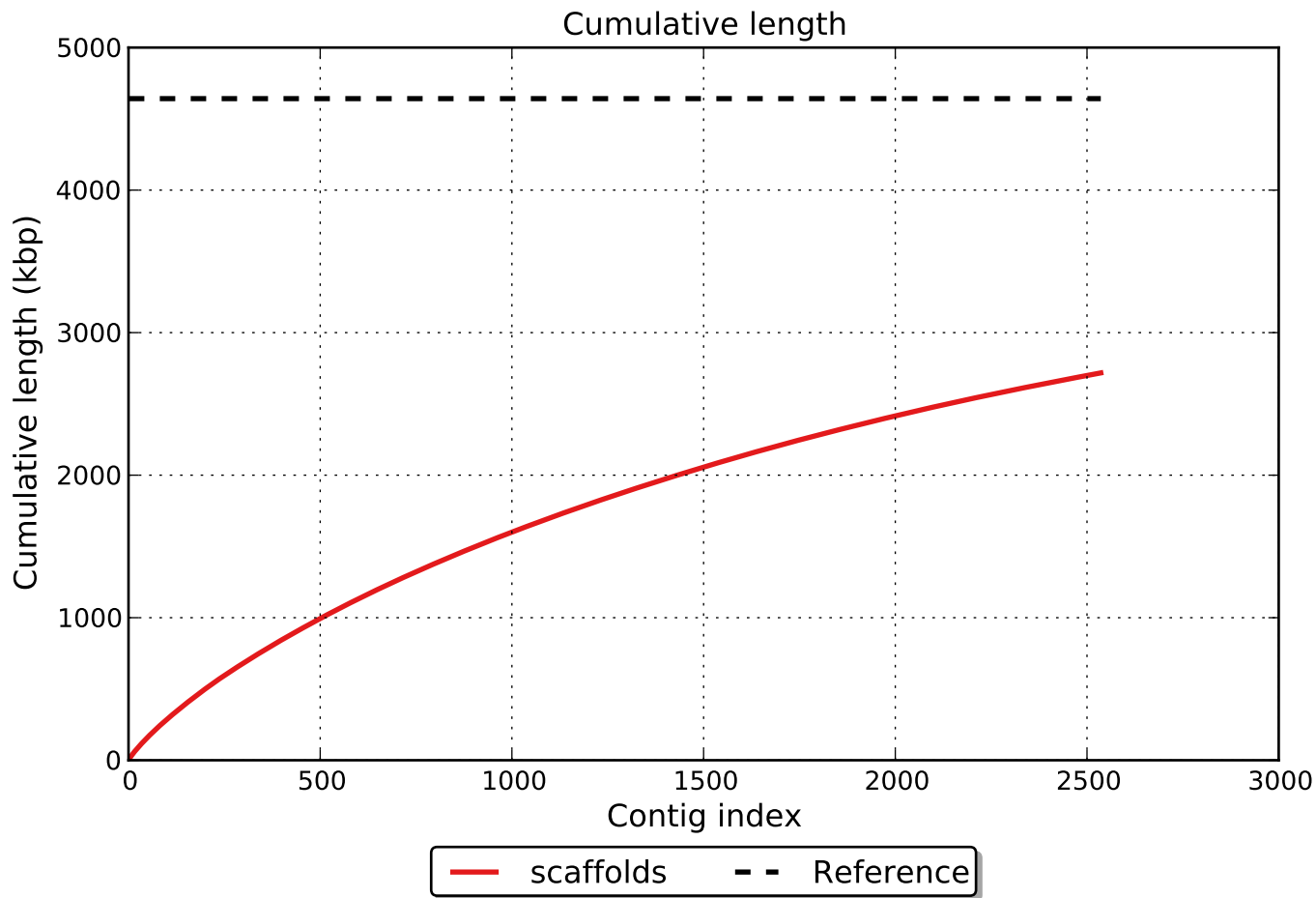
	scaffolds
# fully unaligned contigs	191
Fully unaligned length	197235
# partially unaligned contigs	22
# with misassembly	0
# both parts are significant	6
Partially unaligned length	12184
# N's	29393

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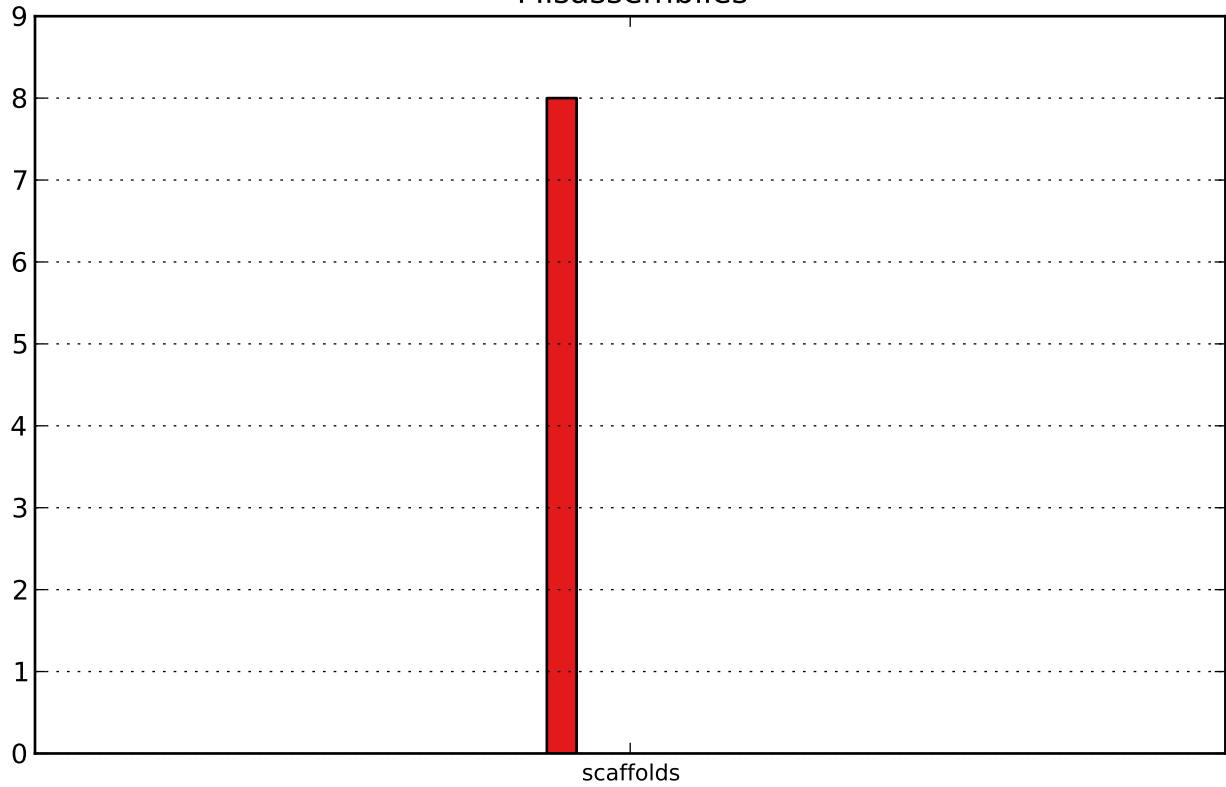
Nx



scaffolds

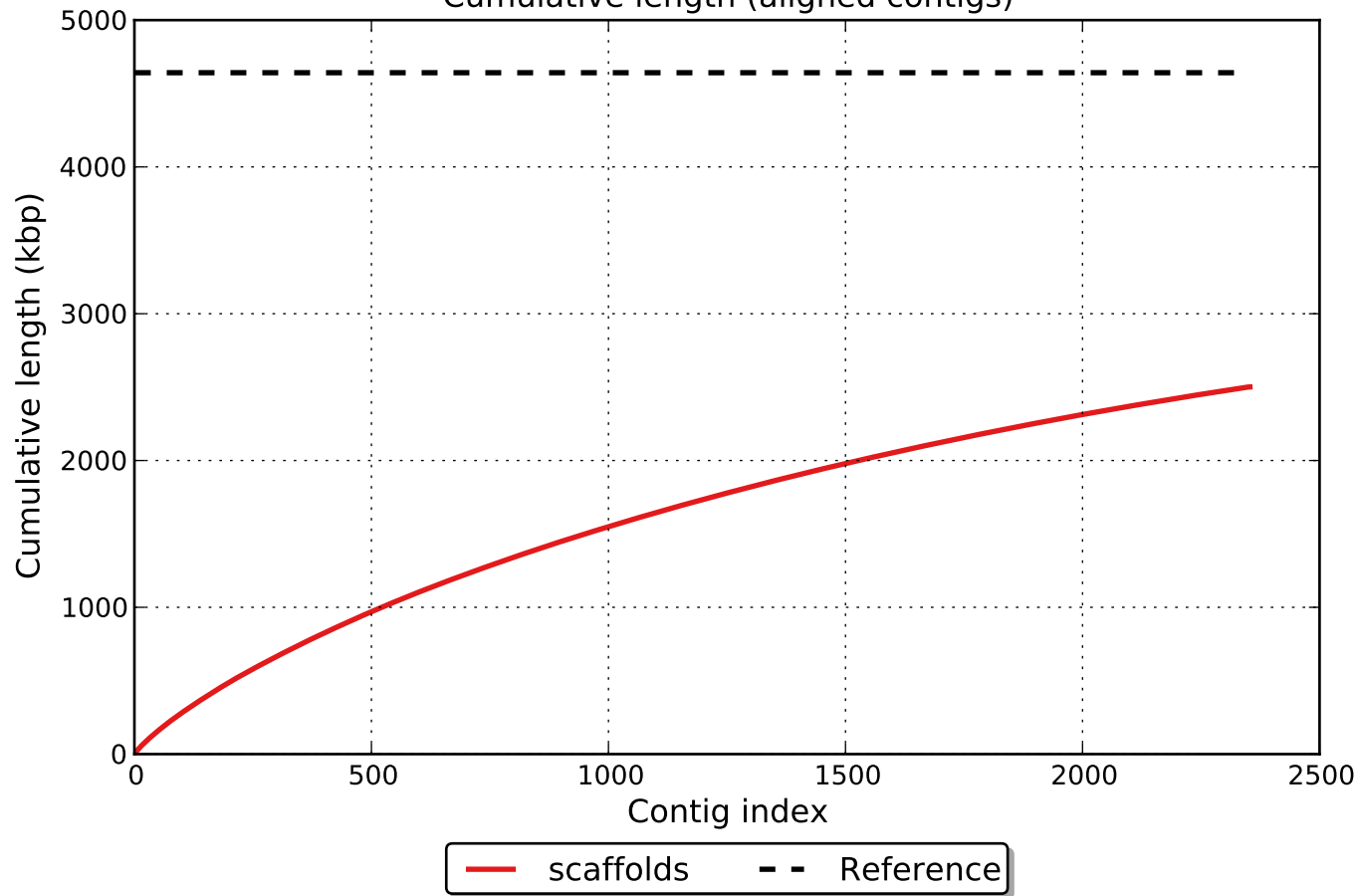


# Misassemblies

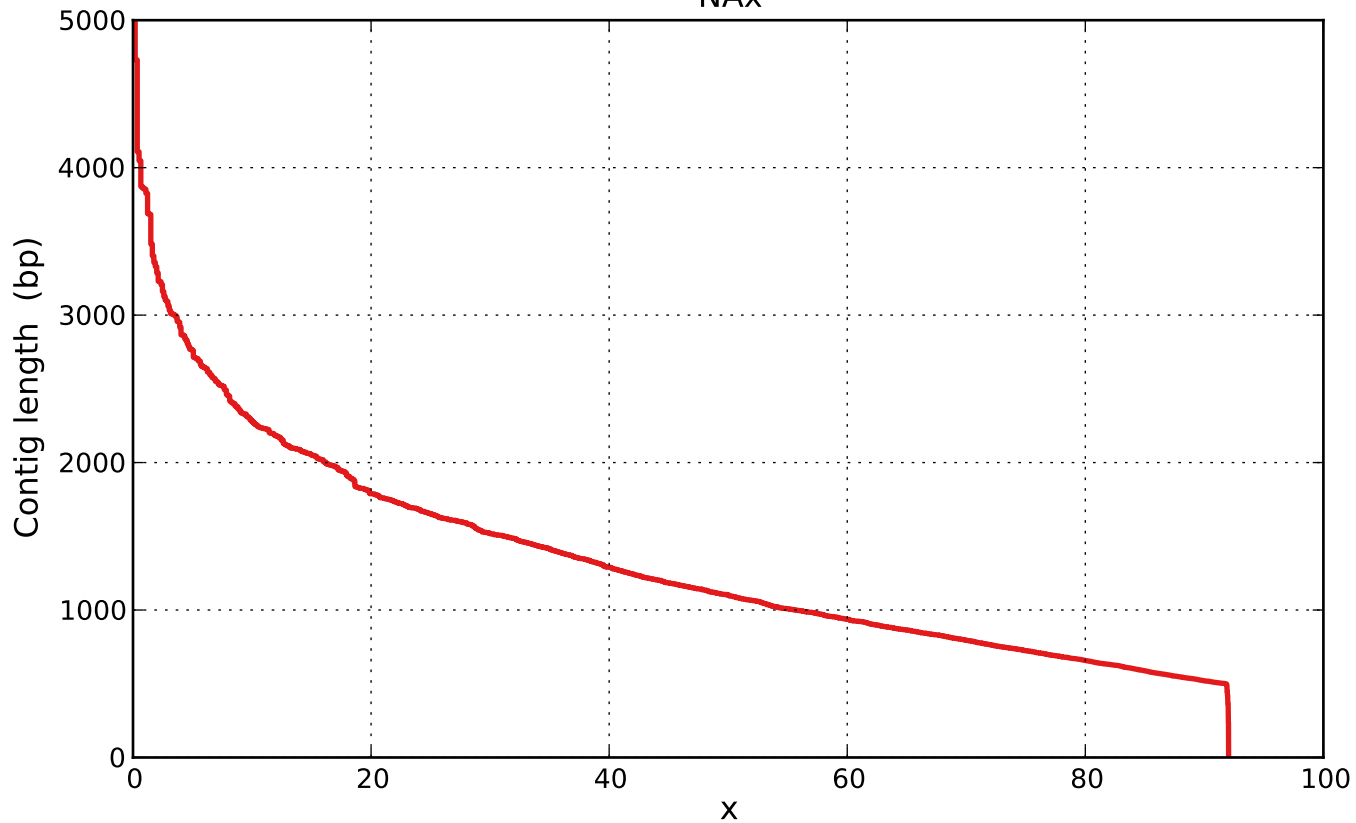


# relocations

Cumulative length (aligned contigs)



NAx



— scaffolds