

# Report

	scaffolds
# contigs ( $\geq 0$ bp)	4047
# contigs ( $\geq 1000$ bp)	271
# contigs ( $\geq 5000$ bp)	1
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	1960602
Total length ( $\geq 1000$ bp)	363536
Total length ( $\geq 5000$ bp)	5609
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	1399
Largest contig	5609
Total length	1127347
Reference length	4641652
N50	812
N75	618
L50	495
L75	892
# misassemblies	8
# misassembled contigs	8
Misassembled contigs length	12509
# local misassemblies	3
# unaligned contigs	138 + 15 part
Unaligned length	125380
Genome fraction (‰)	21.527
Duplication ratio	1.003
# N's per 100 kbp	1332.33
# mismatches per 100 kbp	368.10
# indels per 100 kbp	46.64
Largest alignment	5592
NA50	741
NA75	565
LA50	532
LA75	972

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

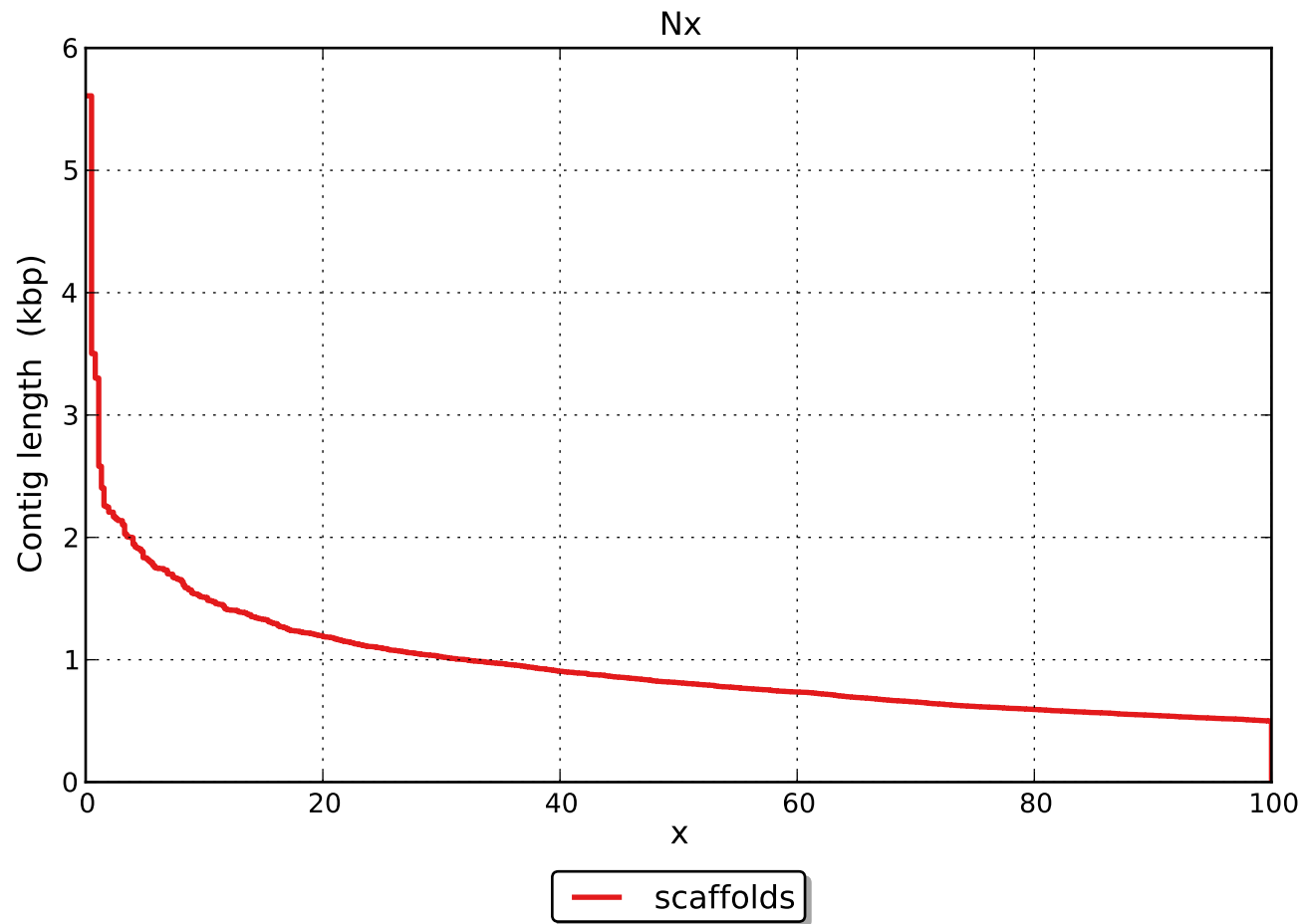
	scaffolds
# misassemblies	8
# relocations	8
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	8
Misassembled contigs length	12509
# local misassemblies	3
# mismatches	3678
# indels	466
# short indels	221
# long indels	245
Indels length	4110

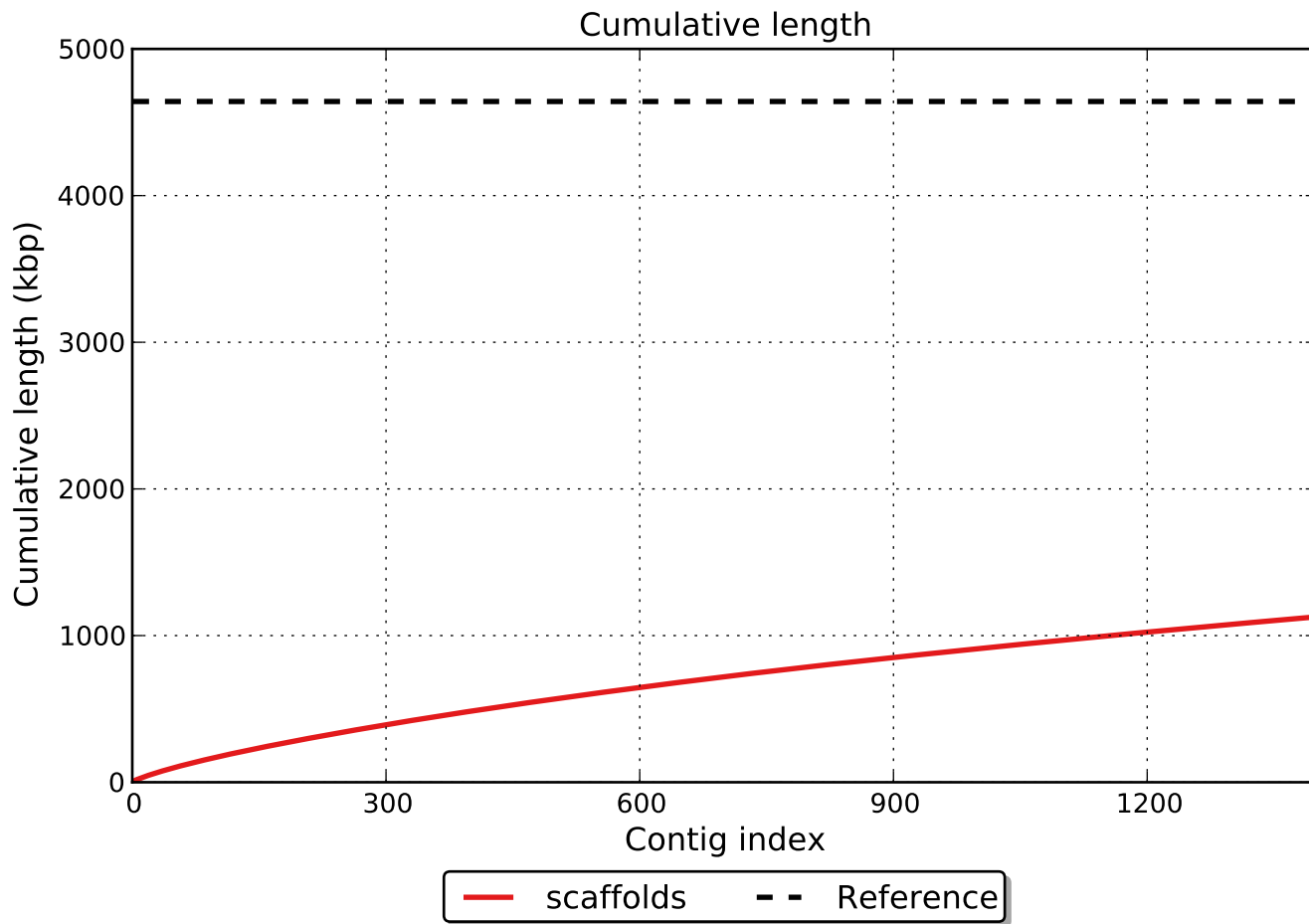
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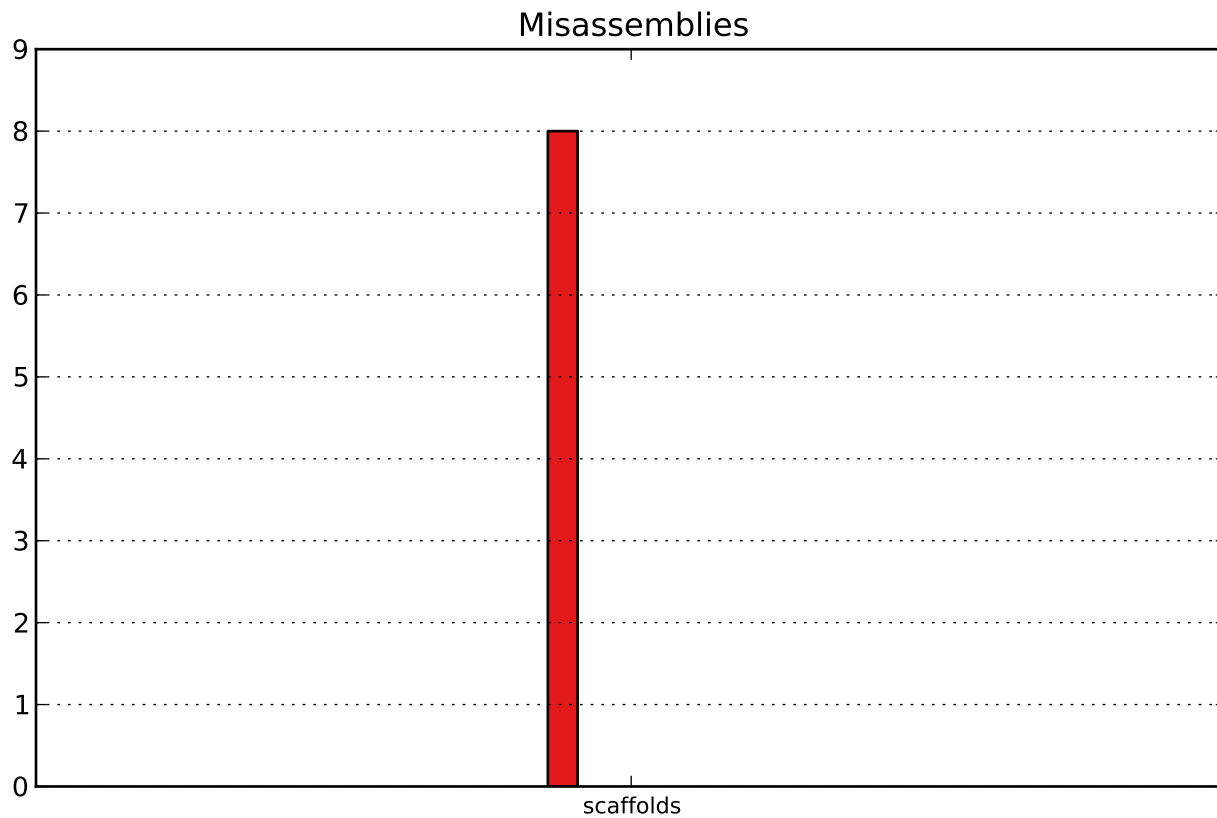
## Unaligned report

	scaffolds
# fully unaligned contigs	138
Fully unaligned length	119612
# partially unaligned contigs	15
# with misassembly	0
# both parts are significant	0
Partially unaligned length	5768
# N's	15020

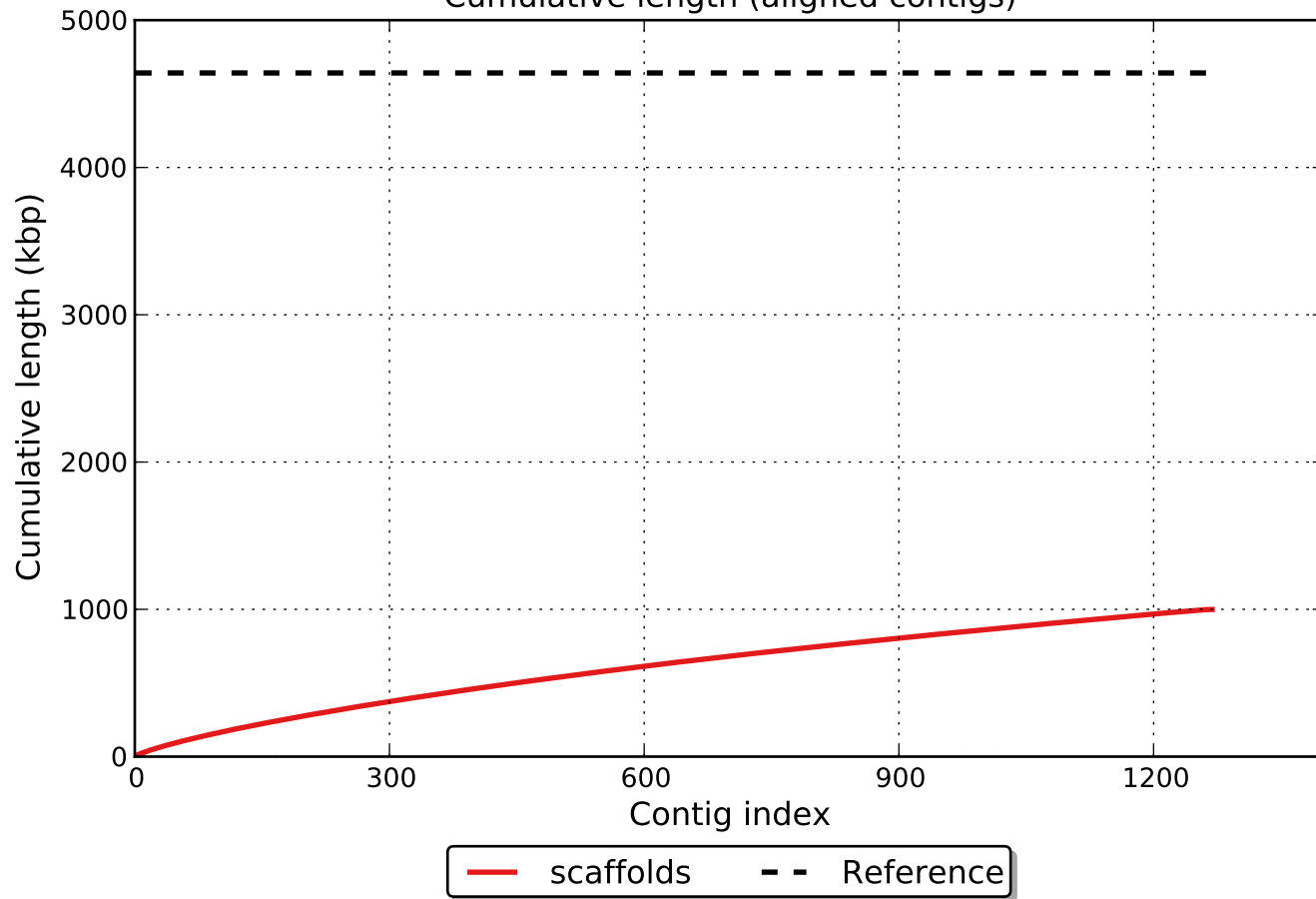
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



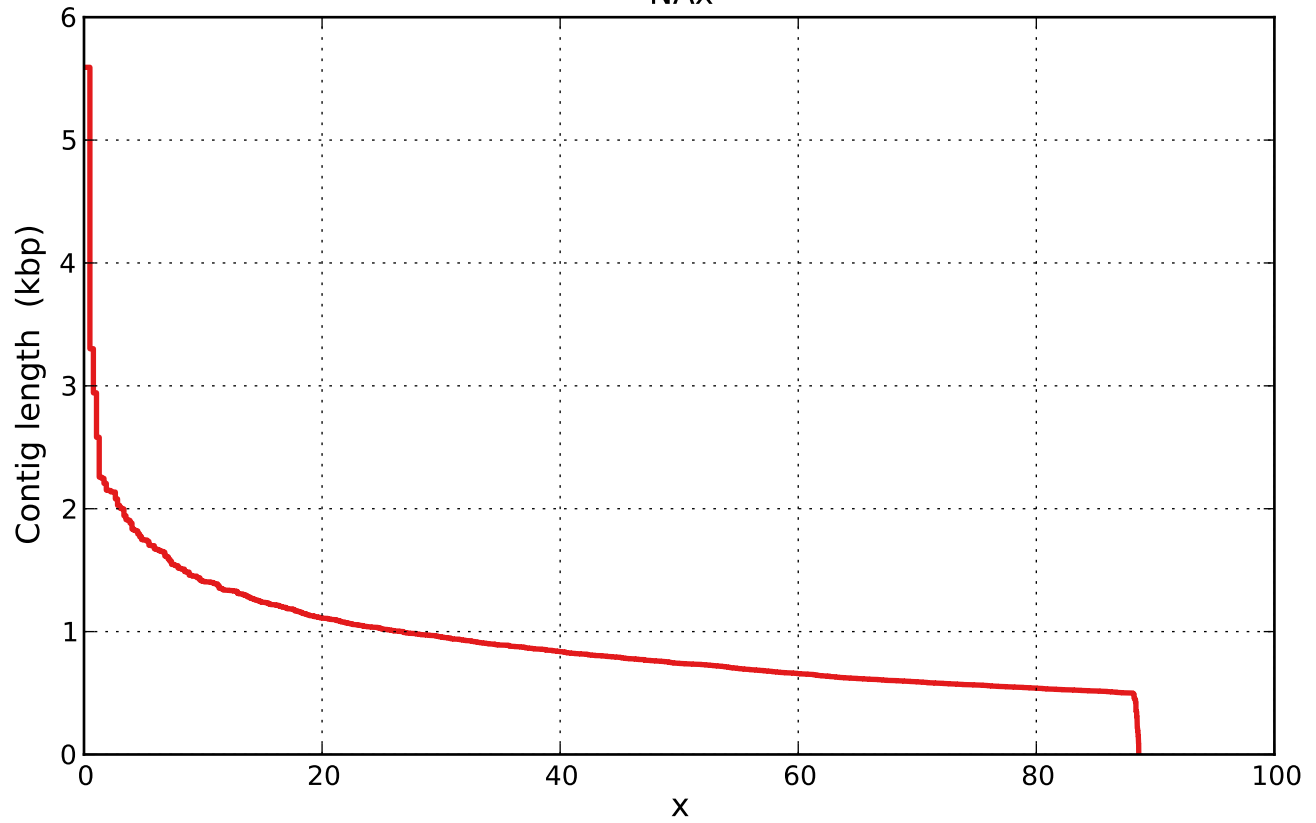




Cumulative length (aligned contigs)



NAx



— scaffolds