

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	1257
# contigs ( $\geq 1000$ bp)	683
Total length ( $\geq 0$ bp)	10918009
Total length ( $\geq 1000$ bp)	10700510
# contigs	804
Largest contig	100879
Total length	10782533
Reference length	11094646
GC (%)	50.39
Reference GC (%)	50.48
N50	27581
NG50	26804
N75	15075
NG75	13958
L50	120
LG50	126
L75	253
LG75	269
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	169592
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.720
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	6.11
# indels per 100 kbp	0.12
Largest alignment	100879
NA50	27555
NGA50	26743
NA75	15070
NGA75	13937
LA50	121
LGA50	127
LA75	255
LGA75	271

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

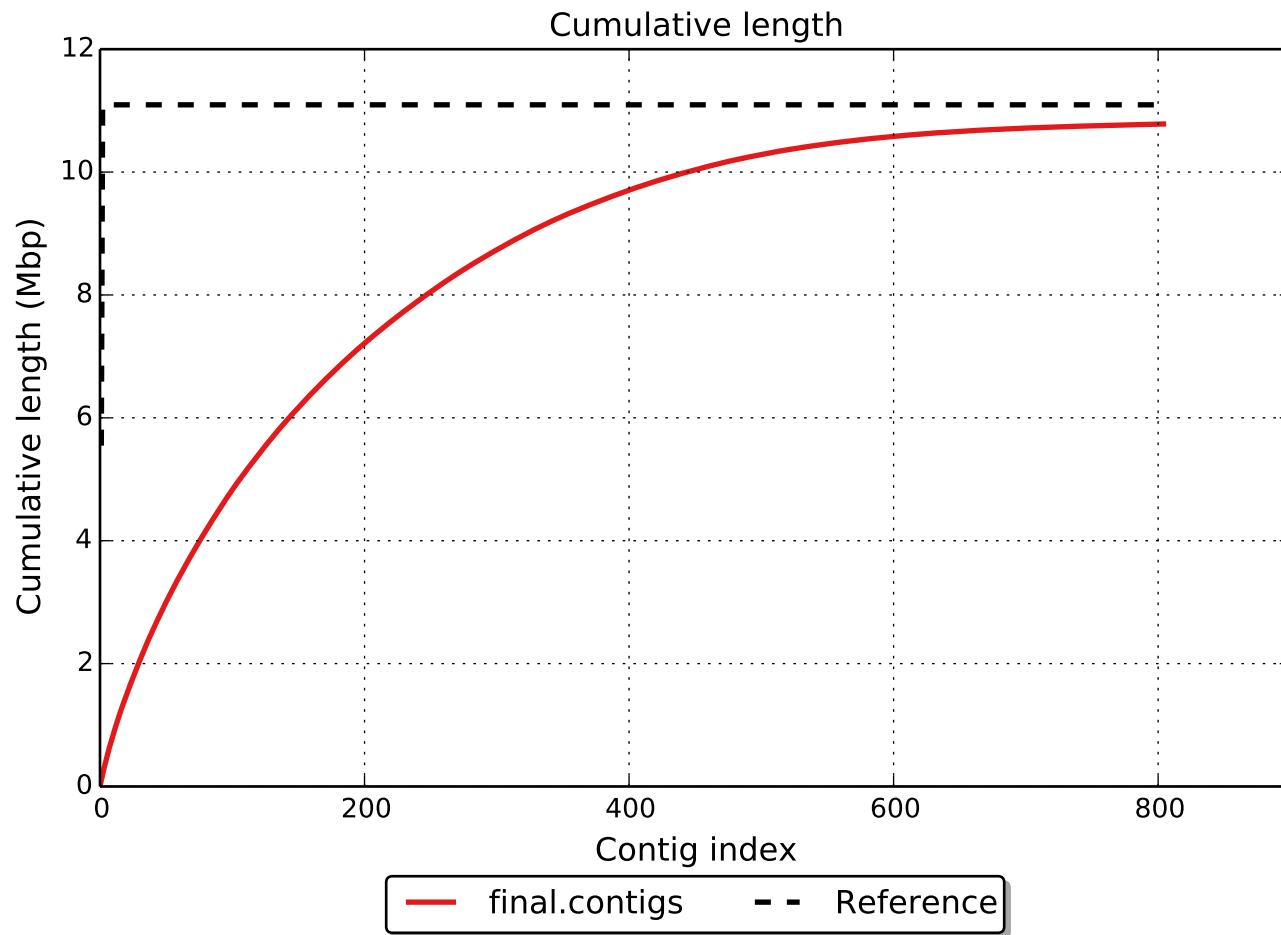
	final.contigs
# misassemblies	3
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	3
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	169592
# local misassemblies	1
# mismatches	656
# indels	13
# short indels	12
# long indels	1
Indels length	18

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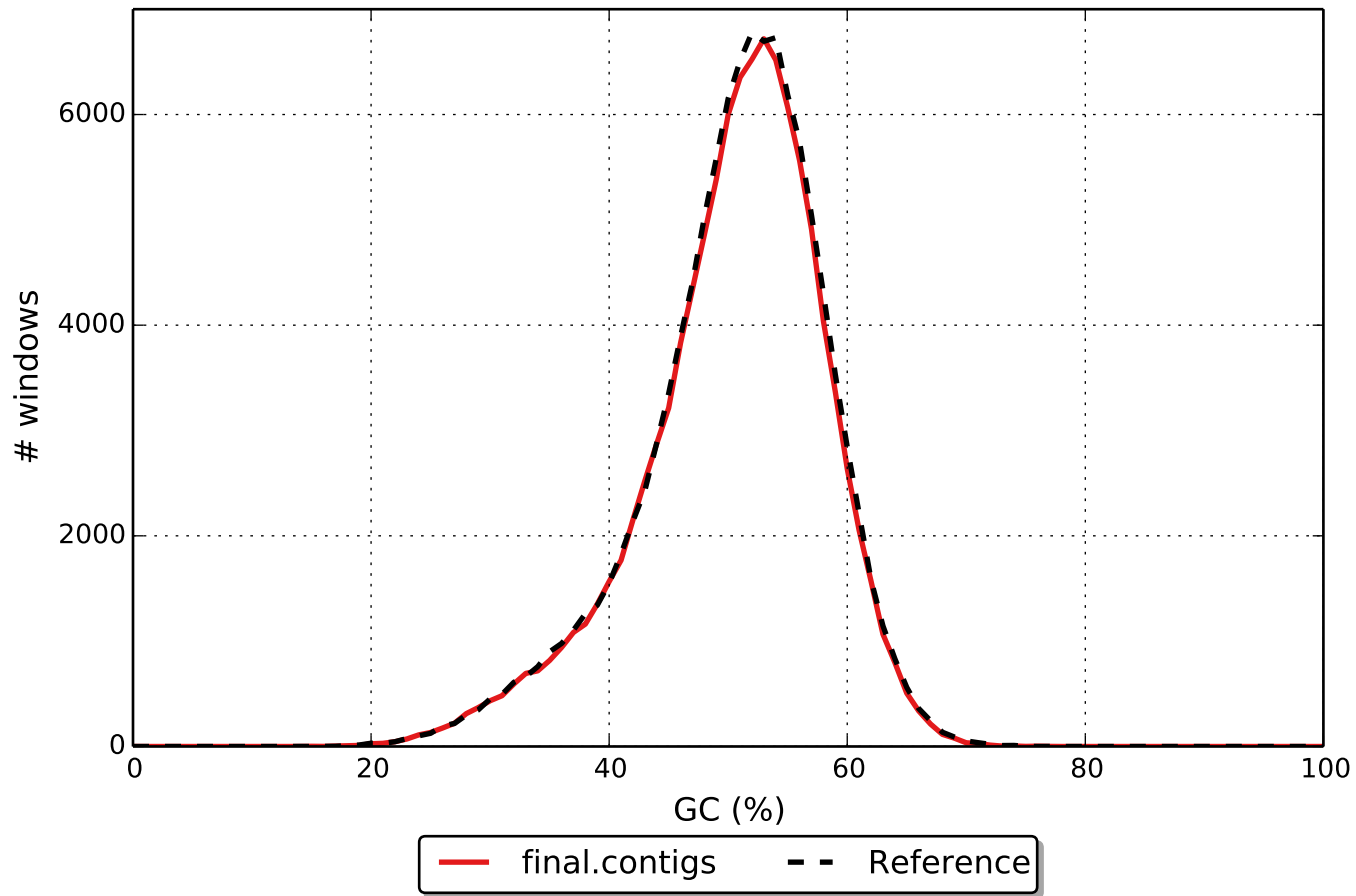
## Unaligned report

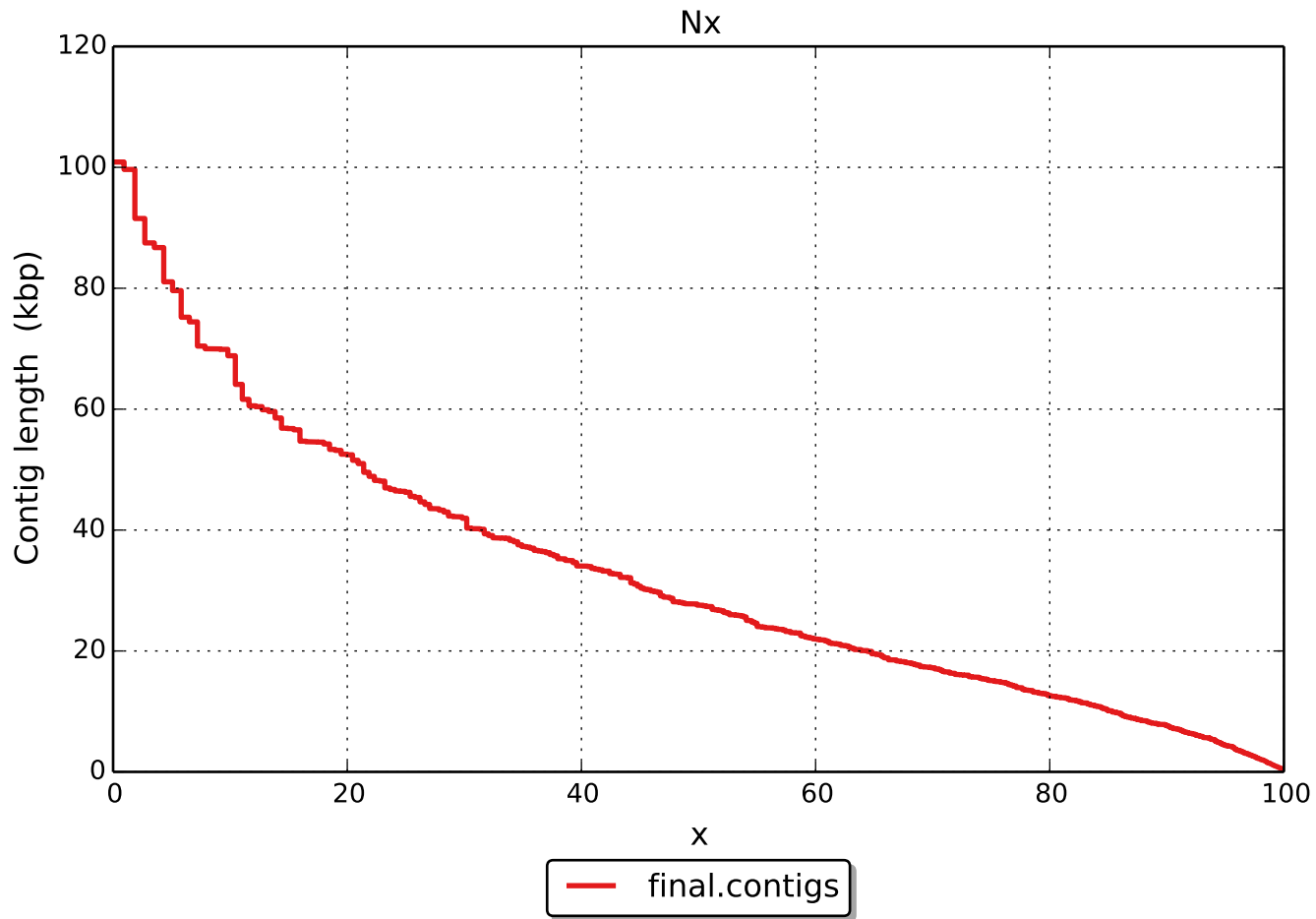
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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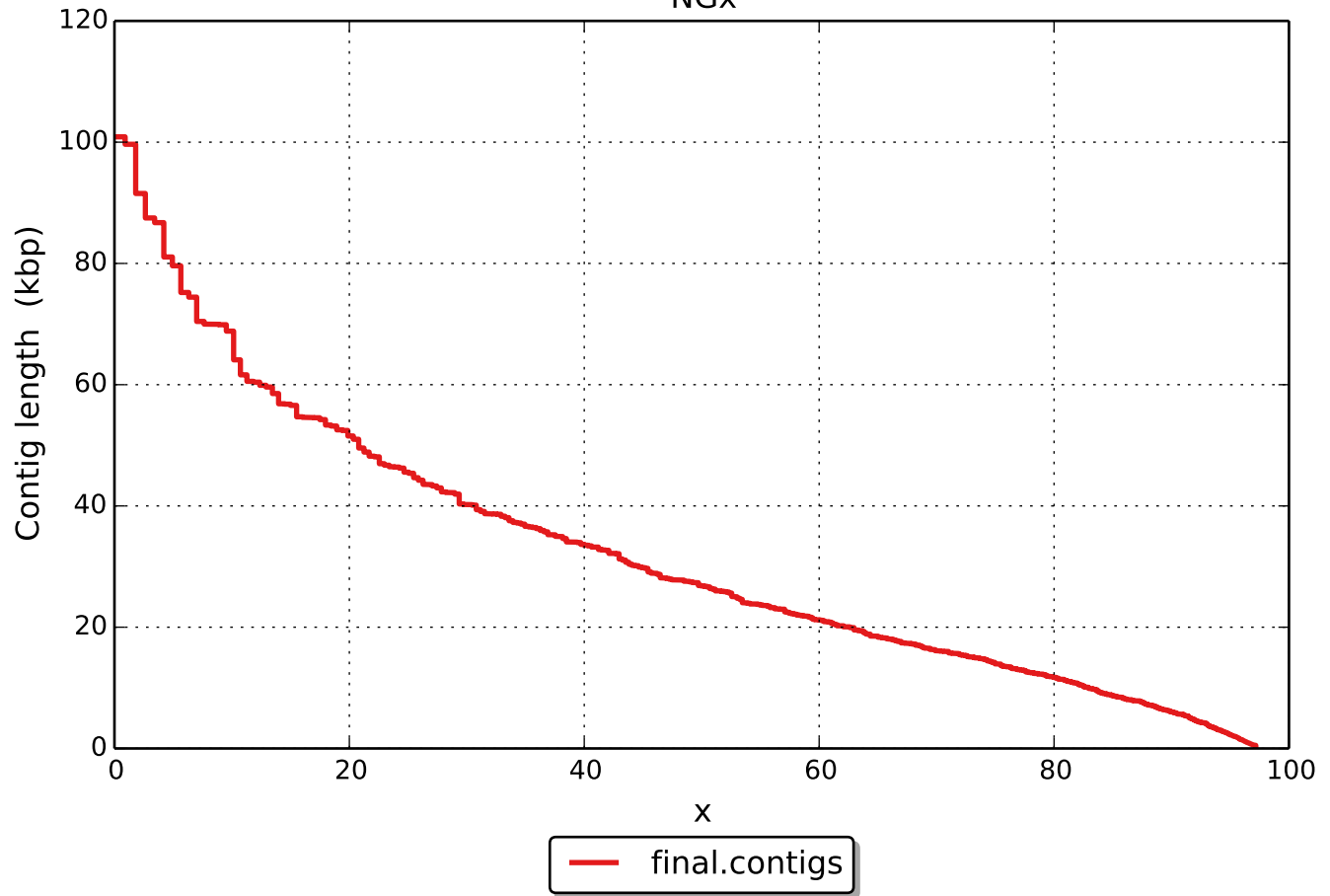


GC content

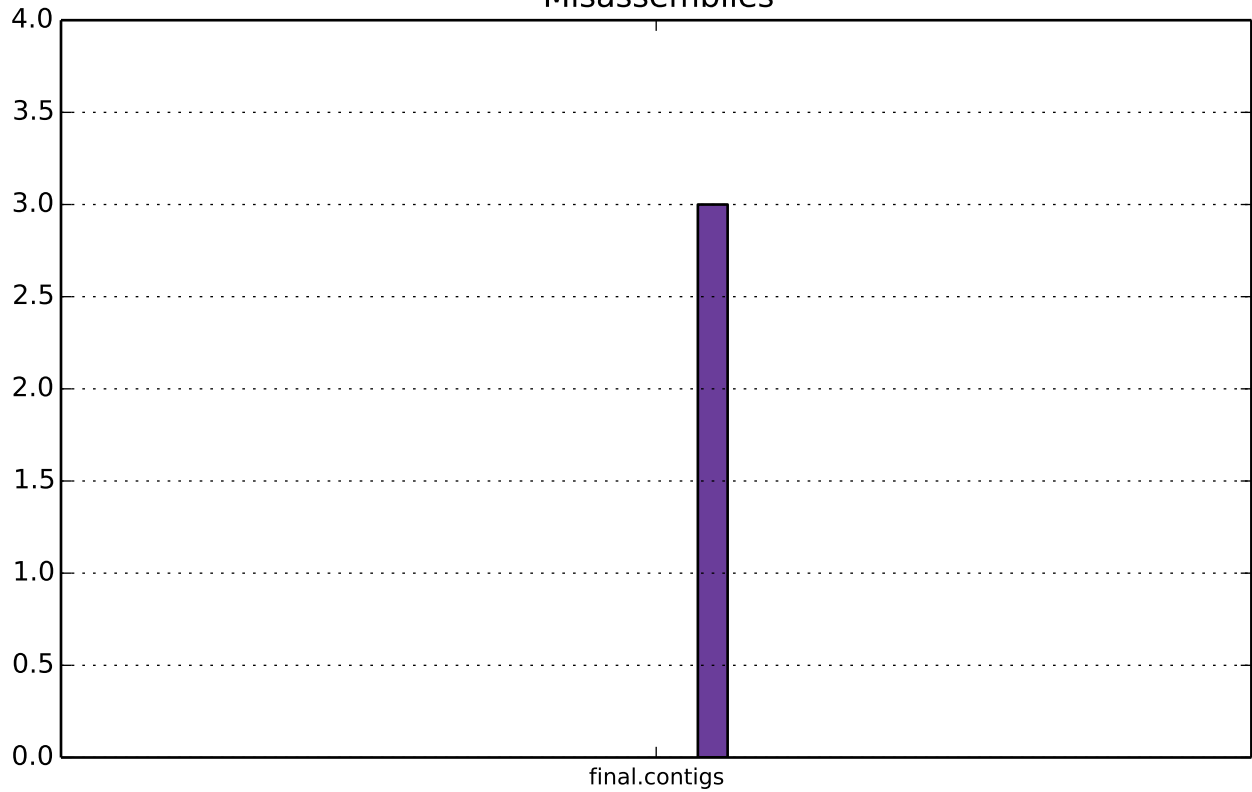





NGx

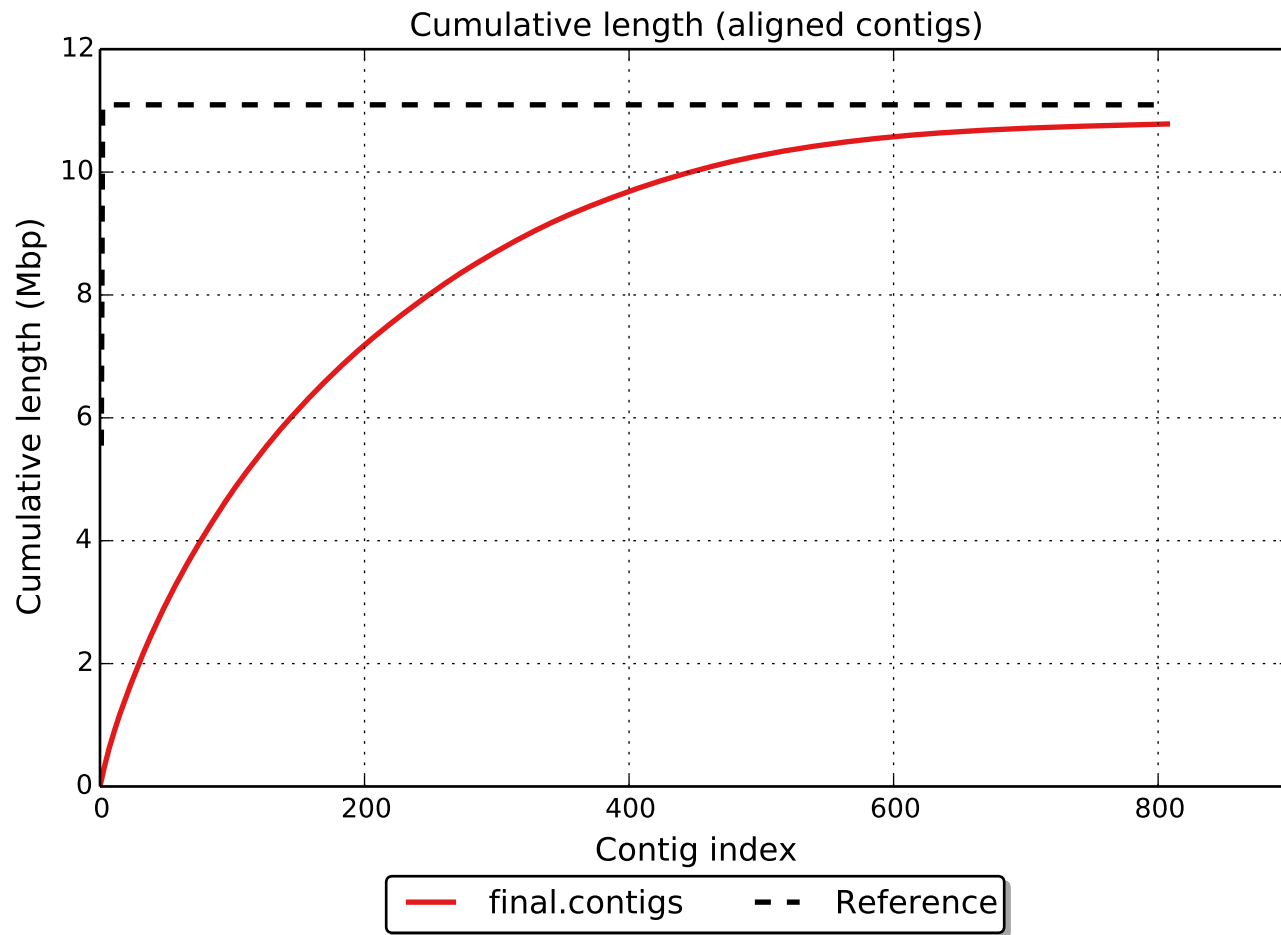


# Misassemblies

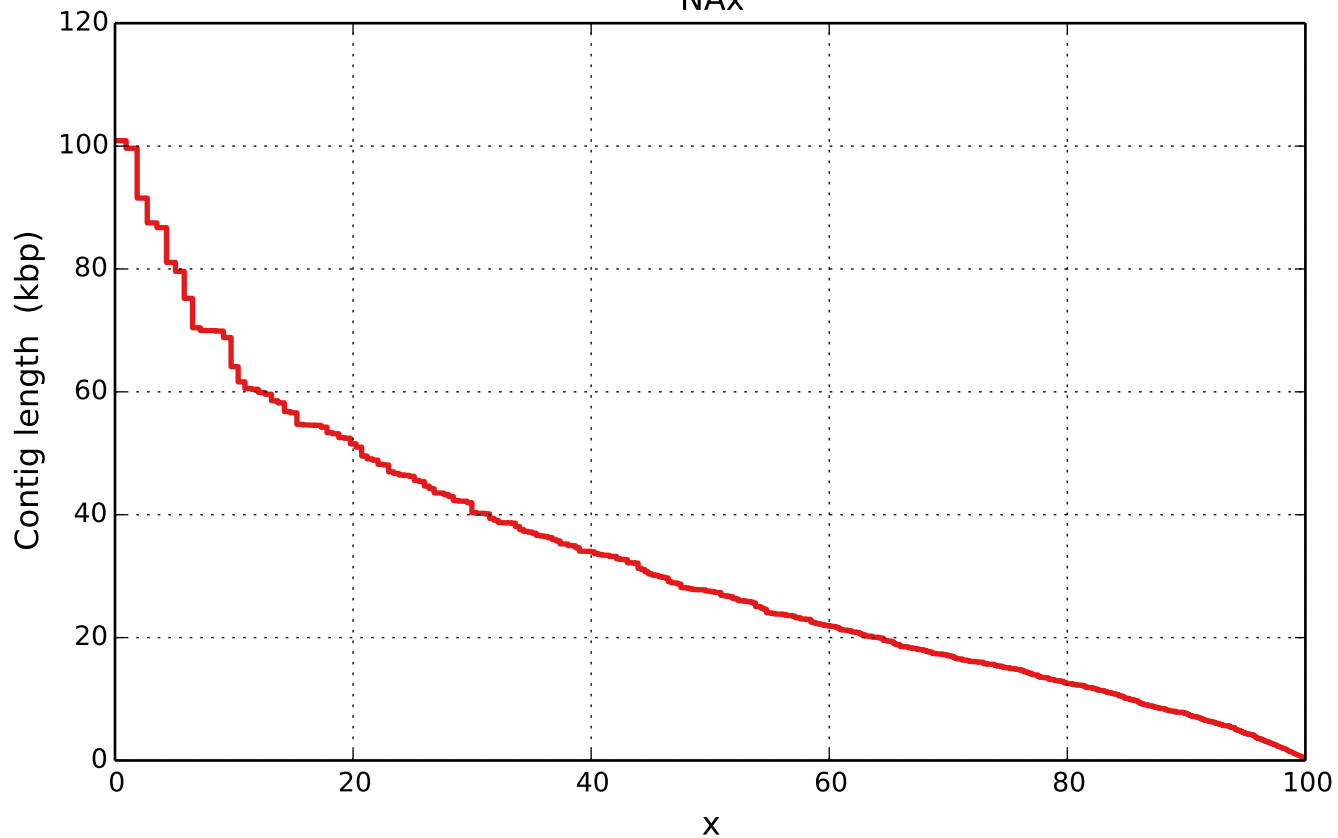


 # interspecies translocations





NAx



— final.contigs

# NGAx

