

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	4401
# contigs ( $\geq 1000$ bp)	1288
Total length ( $\geq 0$ bp)	3979250
Total length ( $\geq 1000$ bp)	1783909
# contigs	4401
Largest contig	4132
Total length	3979250
Reference length	5478683
GC (%)	50.30
Reference GC (%)	50.49
N50	939
NG50	756
N75	704
L50	1501
LG50	2392
L75	2728
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	69.293
Duplication ratio	1.048
# N's per 100 kbp	0.00
# mismatches per 100 kbp	125.17
# indels per 100 kbp	0.21
Largest alignment	4132
NA50	939
NGA50	756
NA75	704
LA50	1501
LGA50	2392
LA75	2728

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

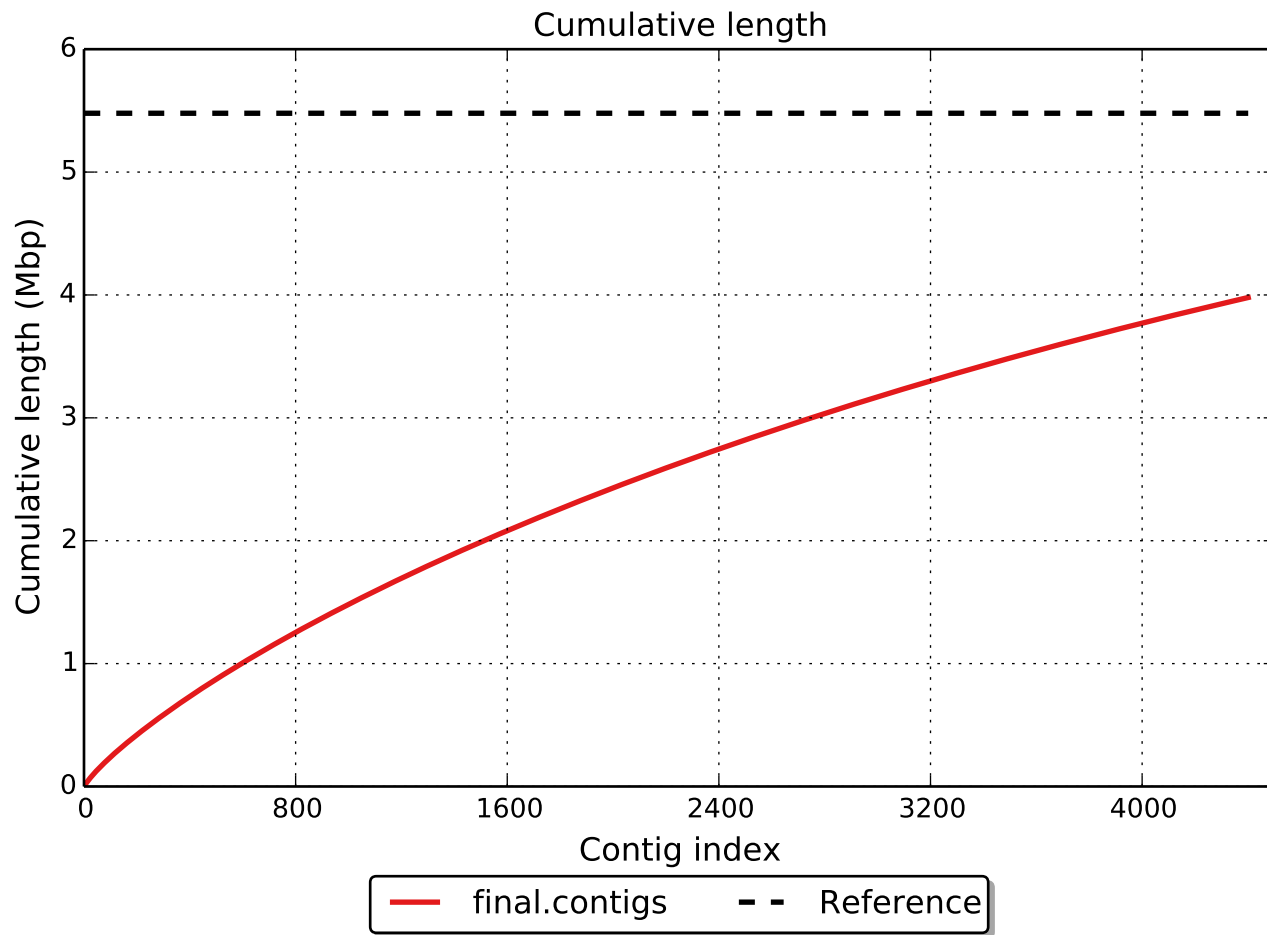
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	4752
# indels	8
# short indels	4
# long indels	4
Indels length	60

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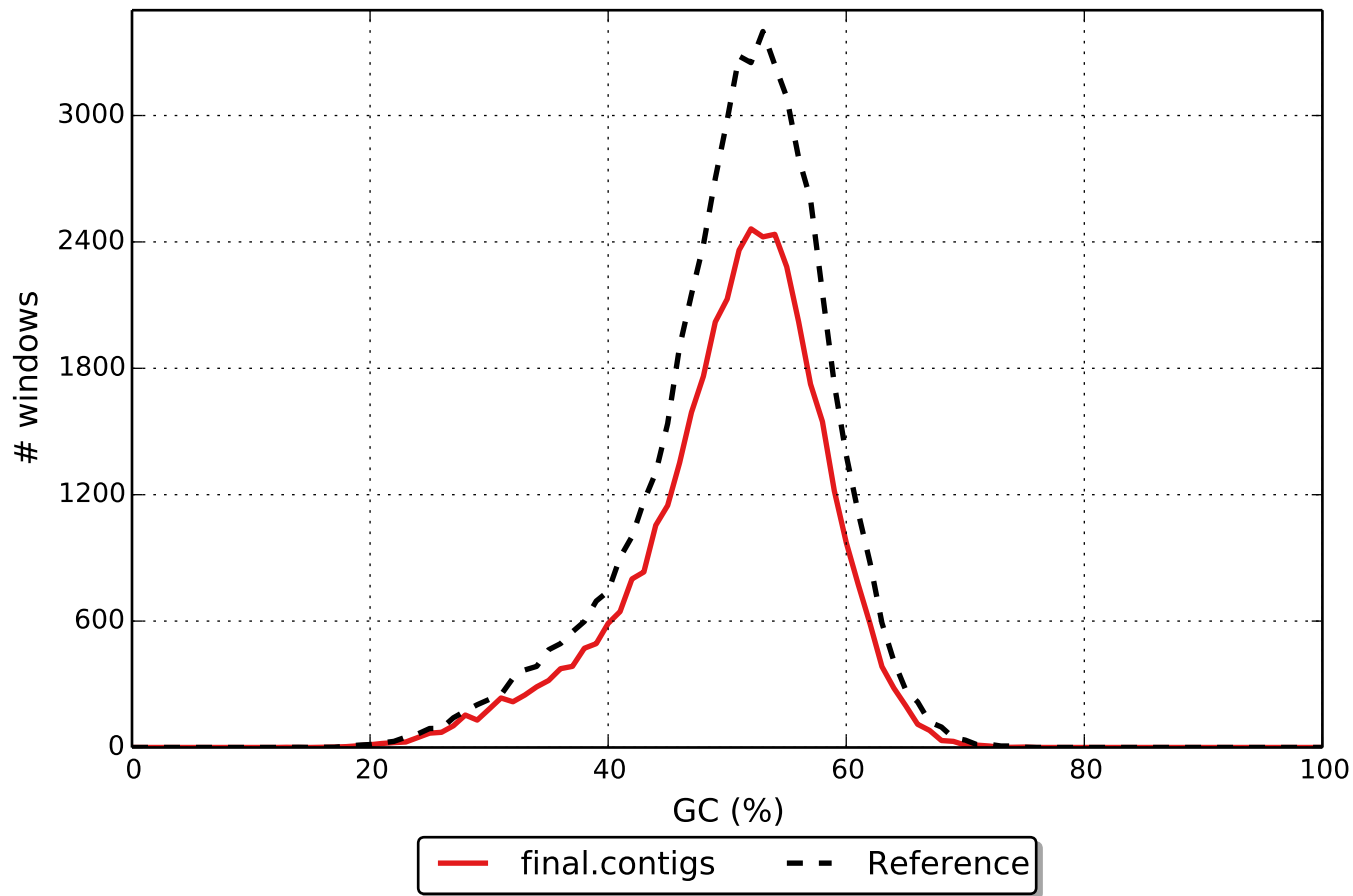
## Unaligned report

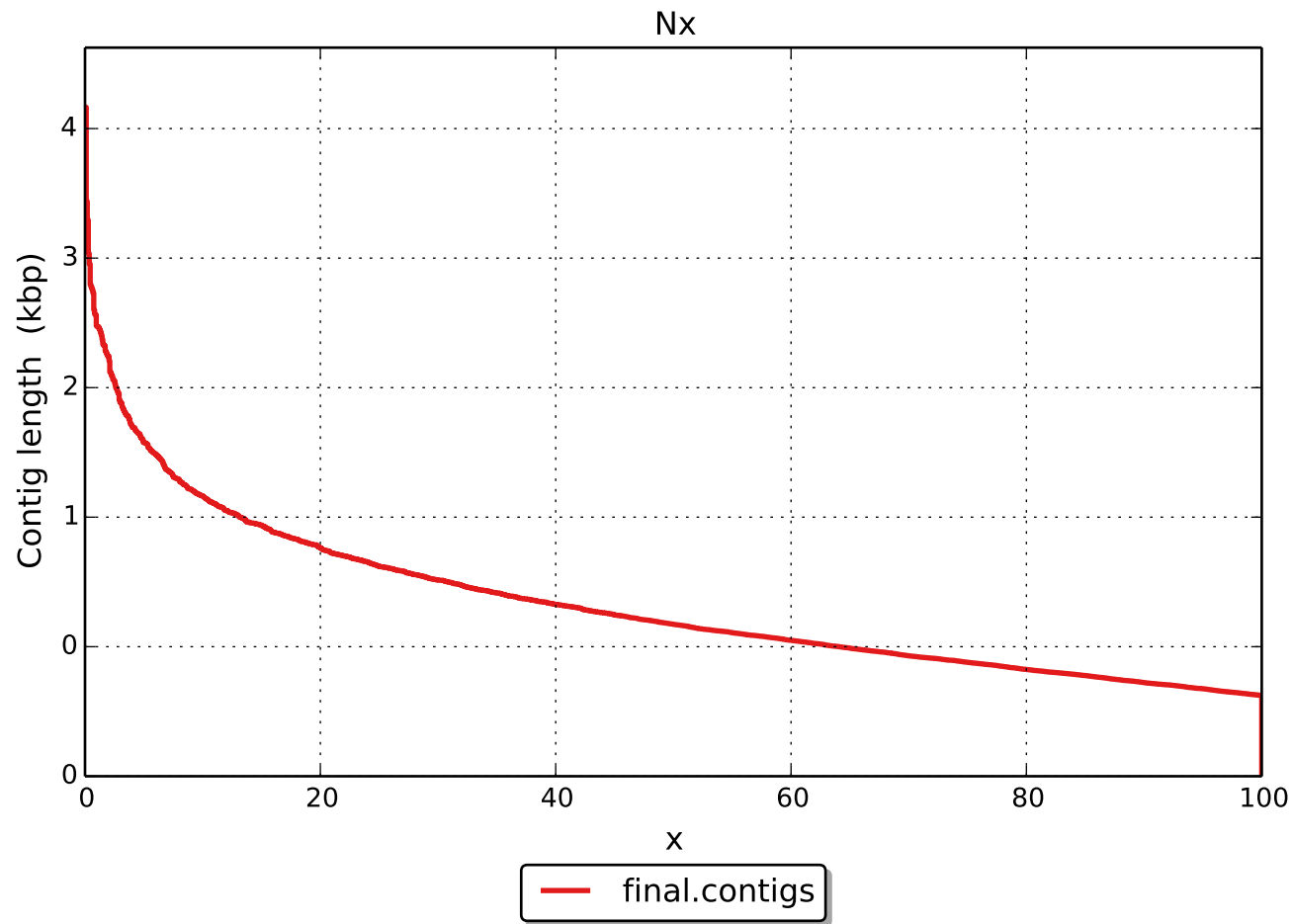
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

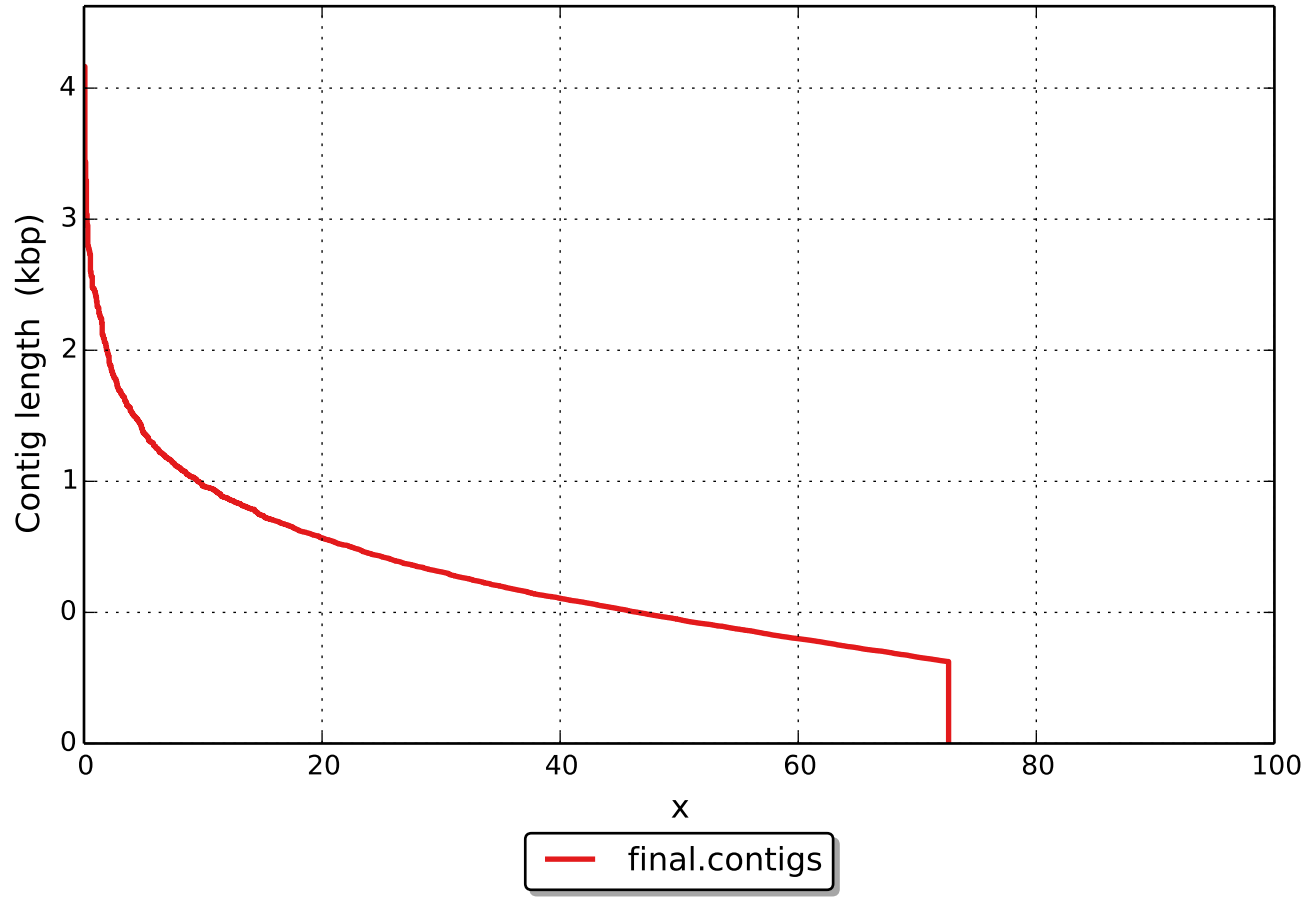


GC content





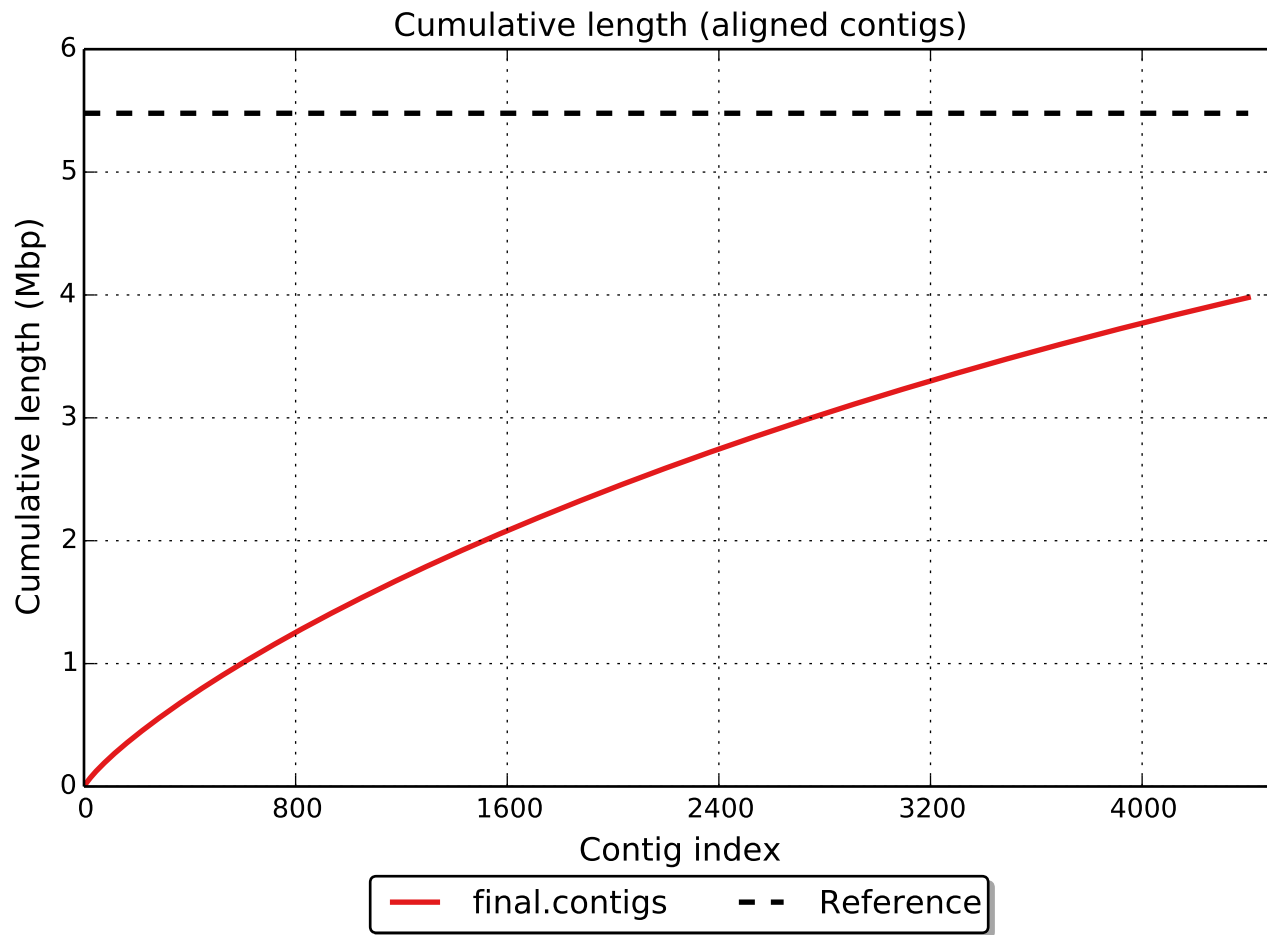
NGx



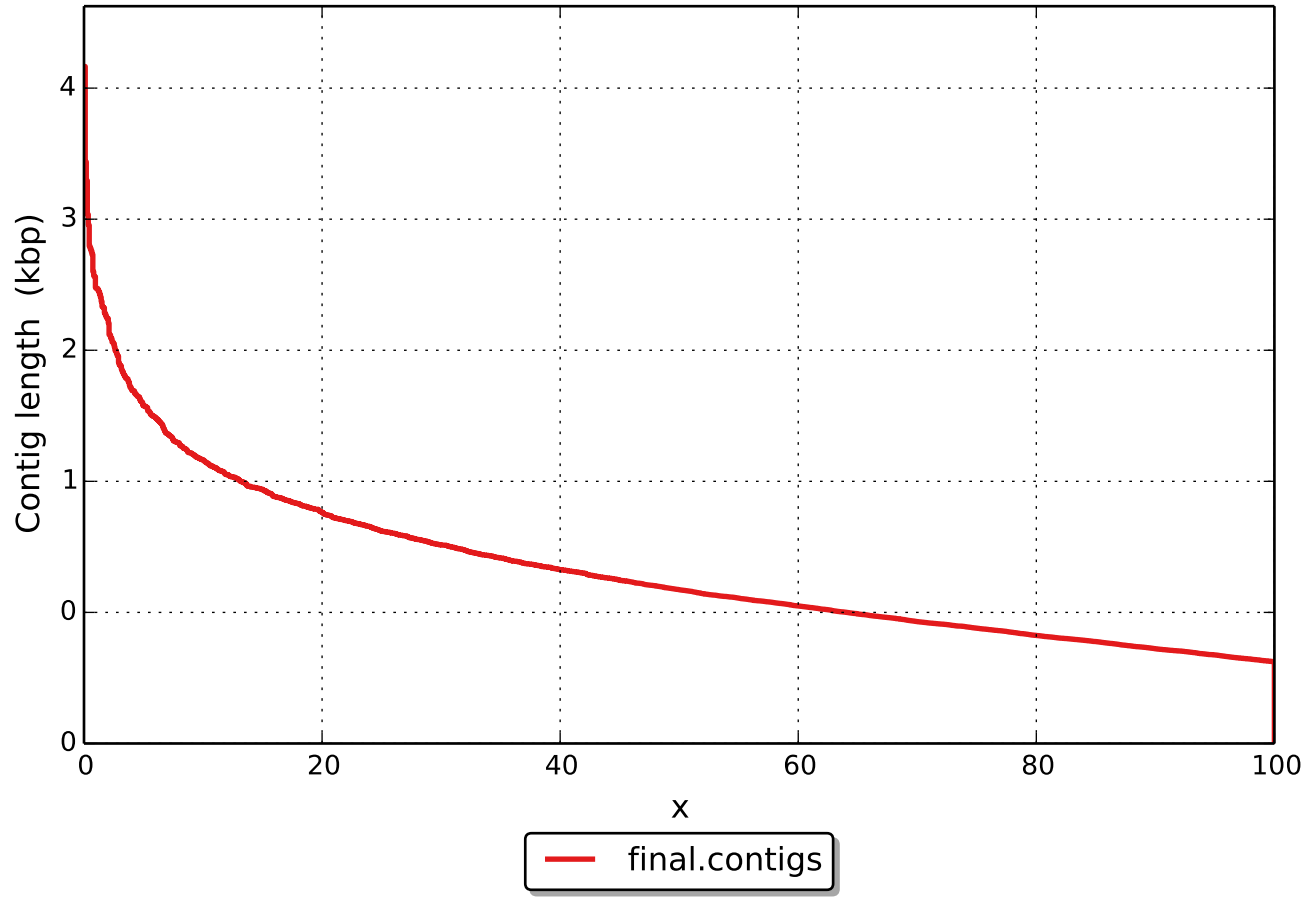
# Misassemblies







NAx



NGAx

