

Report

	final.contigs
# contigs (>= 0 bp)	423
# contigs (>= 1000 bp)	324
Total length (>= 0 bp)	5200008
Total length (>= 1000 bp)	5131604
# contigs	423
Largest contig	107089
Total length	5200008
Reference length	5547323
GC (%)	50.29
Reference GC (%)	50.48
N50	32618
NG50	30514
N75	18536
NG75	15279
L50	51
LG50	57
L75	103
LG75	118
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	785
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	93.375
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	7.86
# indels per 100 kbp	0.27
Largest alignment	107089
NA50	32618
NGA50	30514
NA75	18536
NGA75	15279
LA50	51
LGA50	57
LA75	103
LGA75	118

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).

Misassemblies report

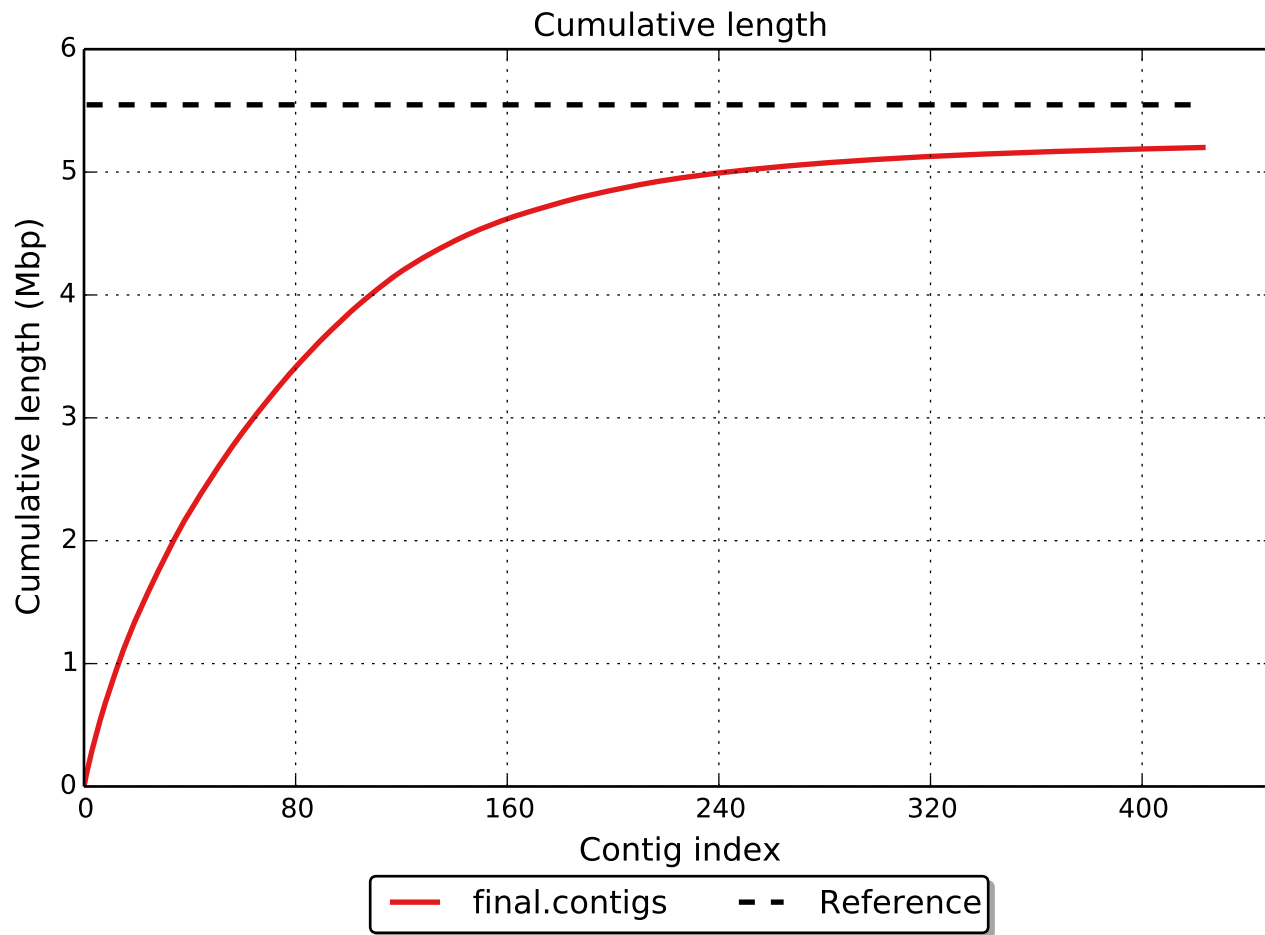
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	785
# local misassemblies	2
# mismatches	407
# indels	14
# short indels	12
# long indels	2
Indels length	33

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).

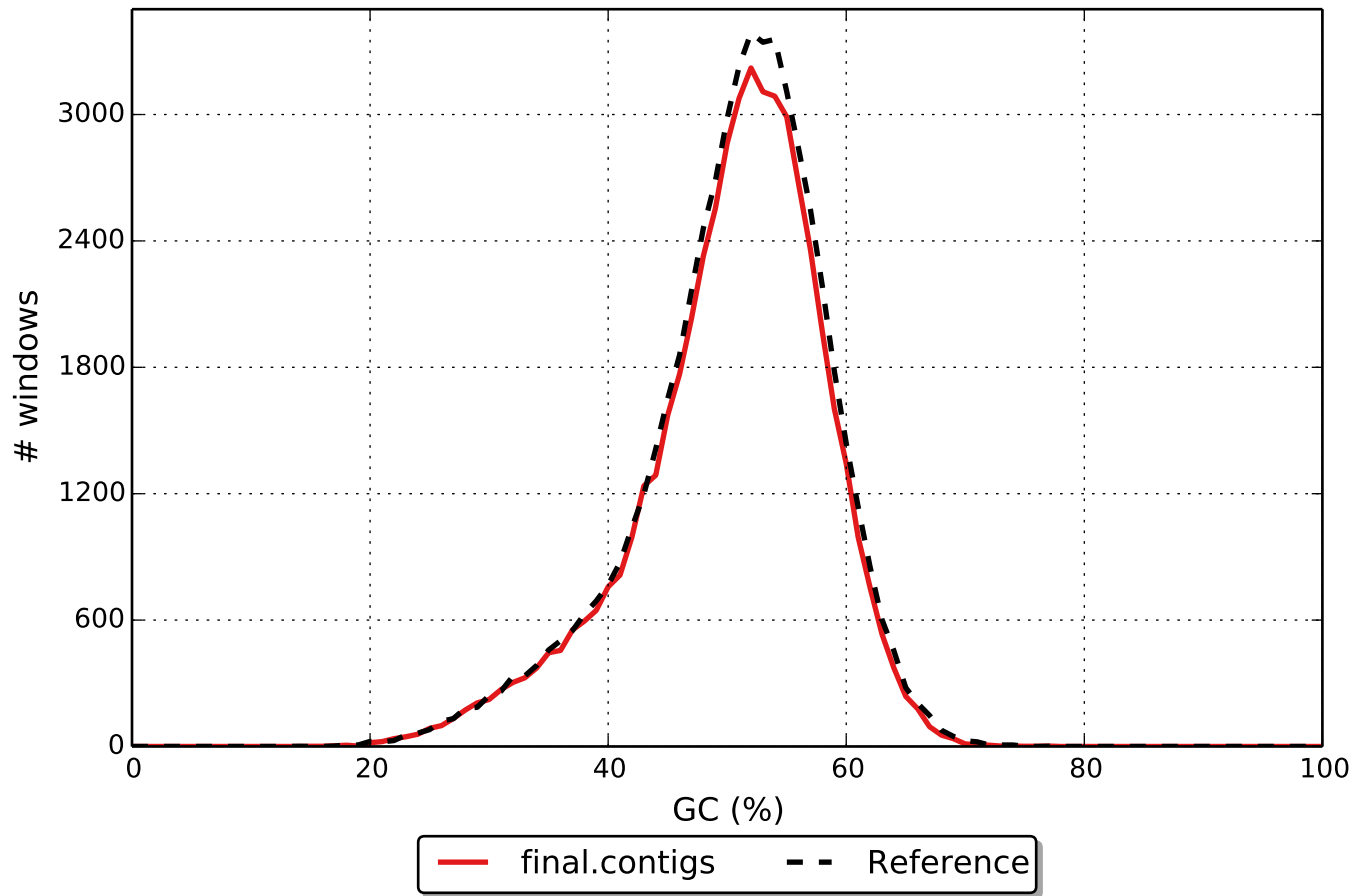
Unaligned report

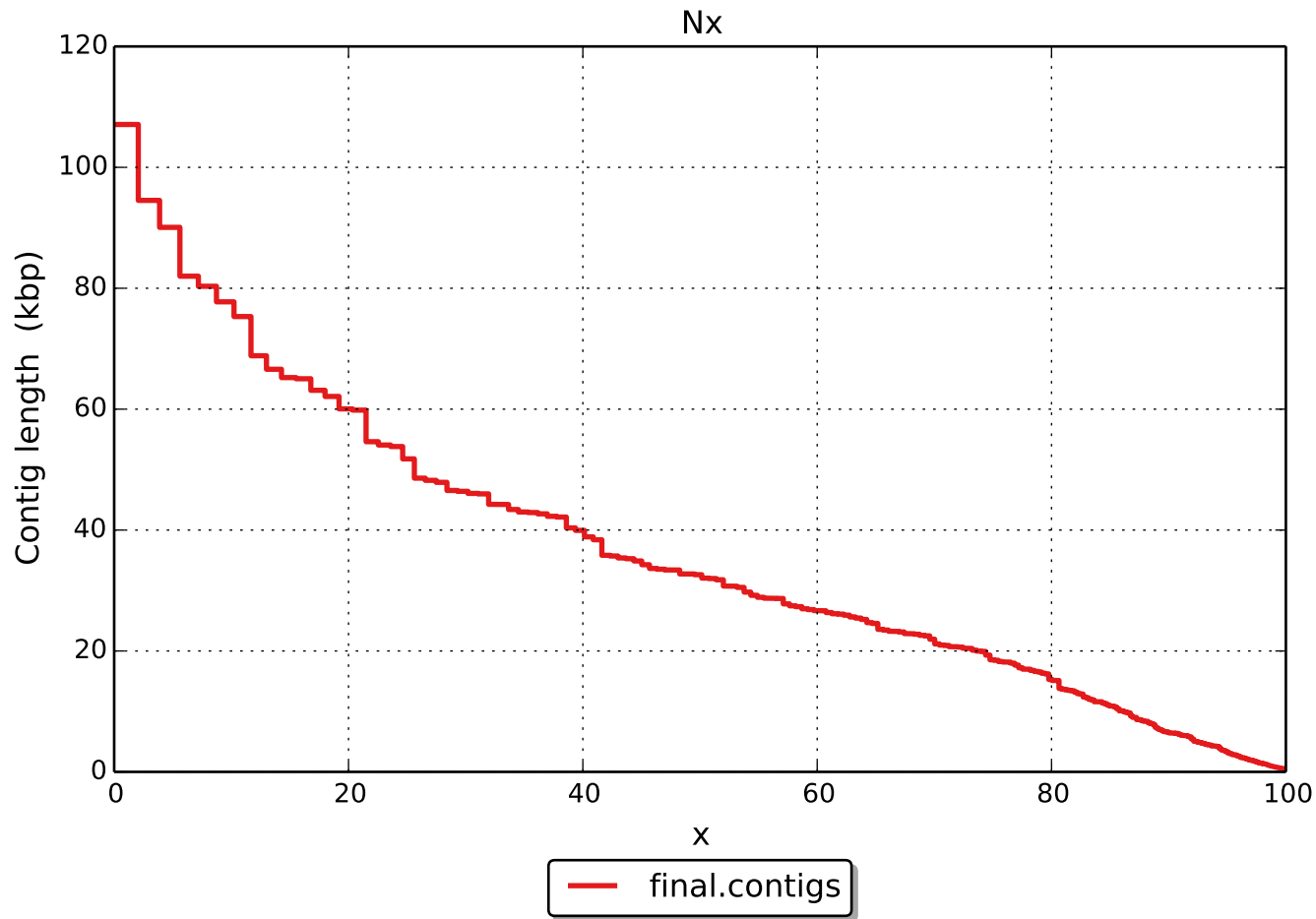
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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

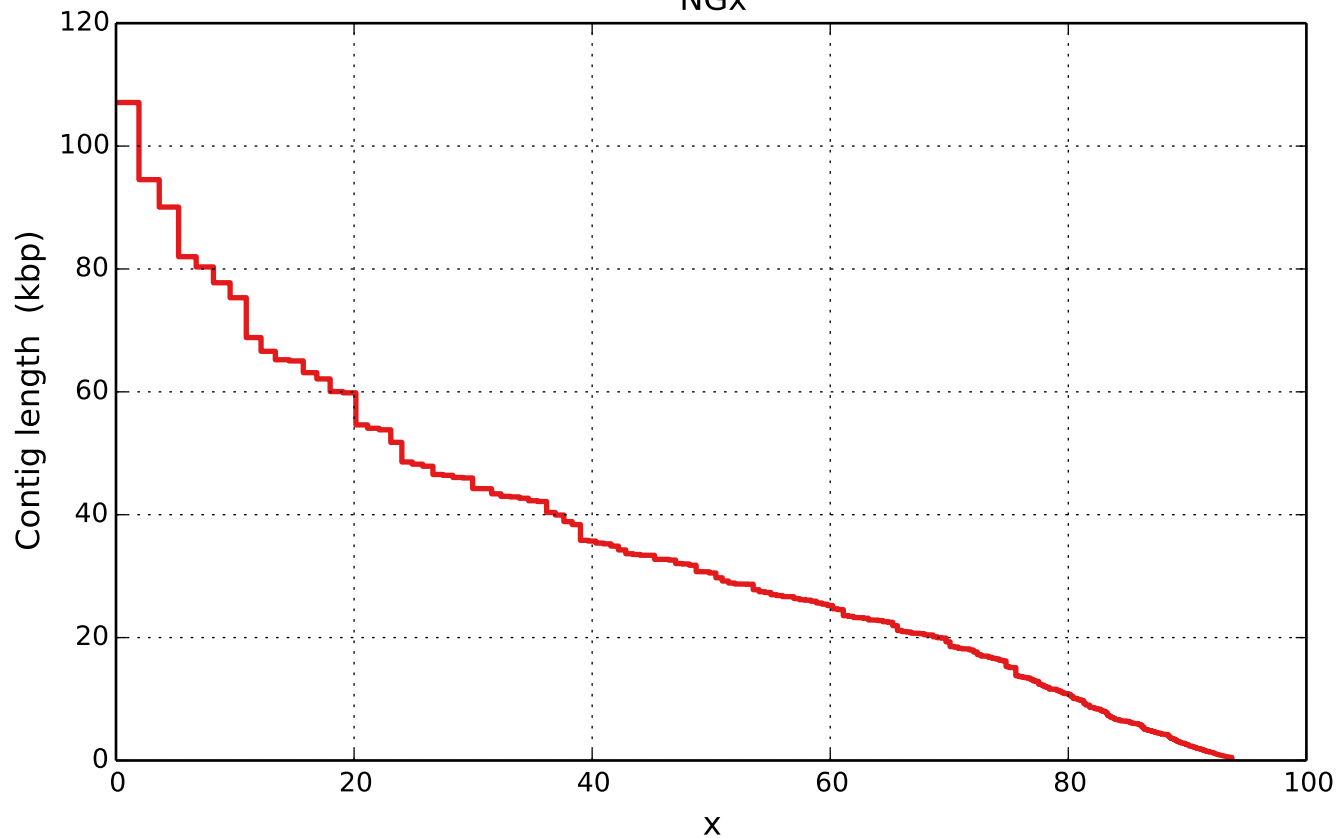


GC content





NGx

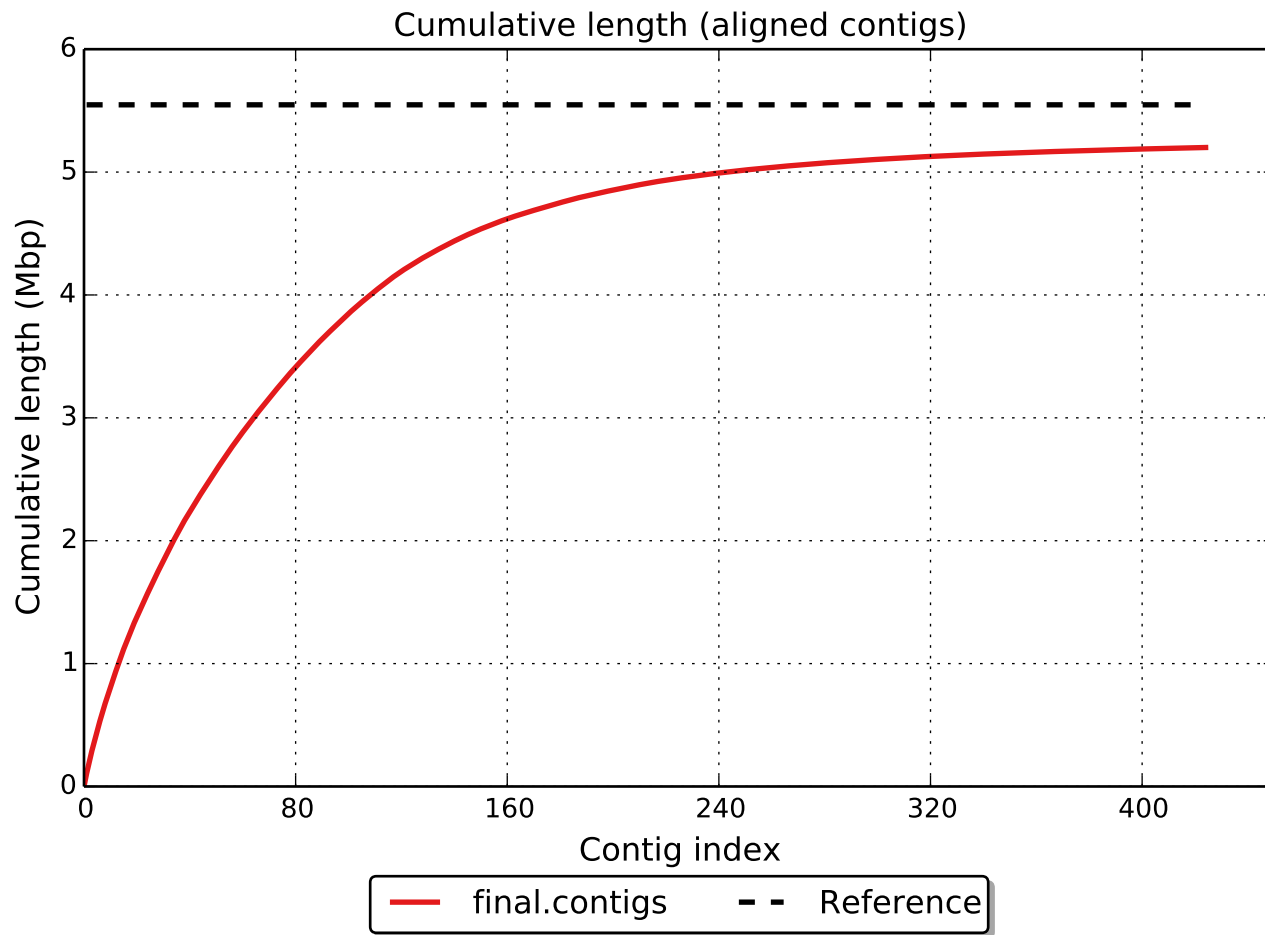


— final.contigs

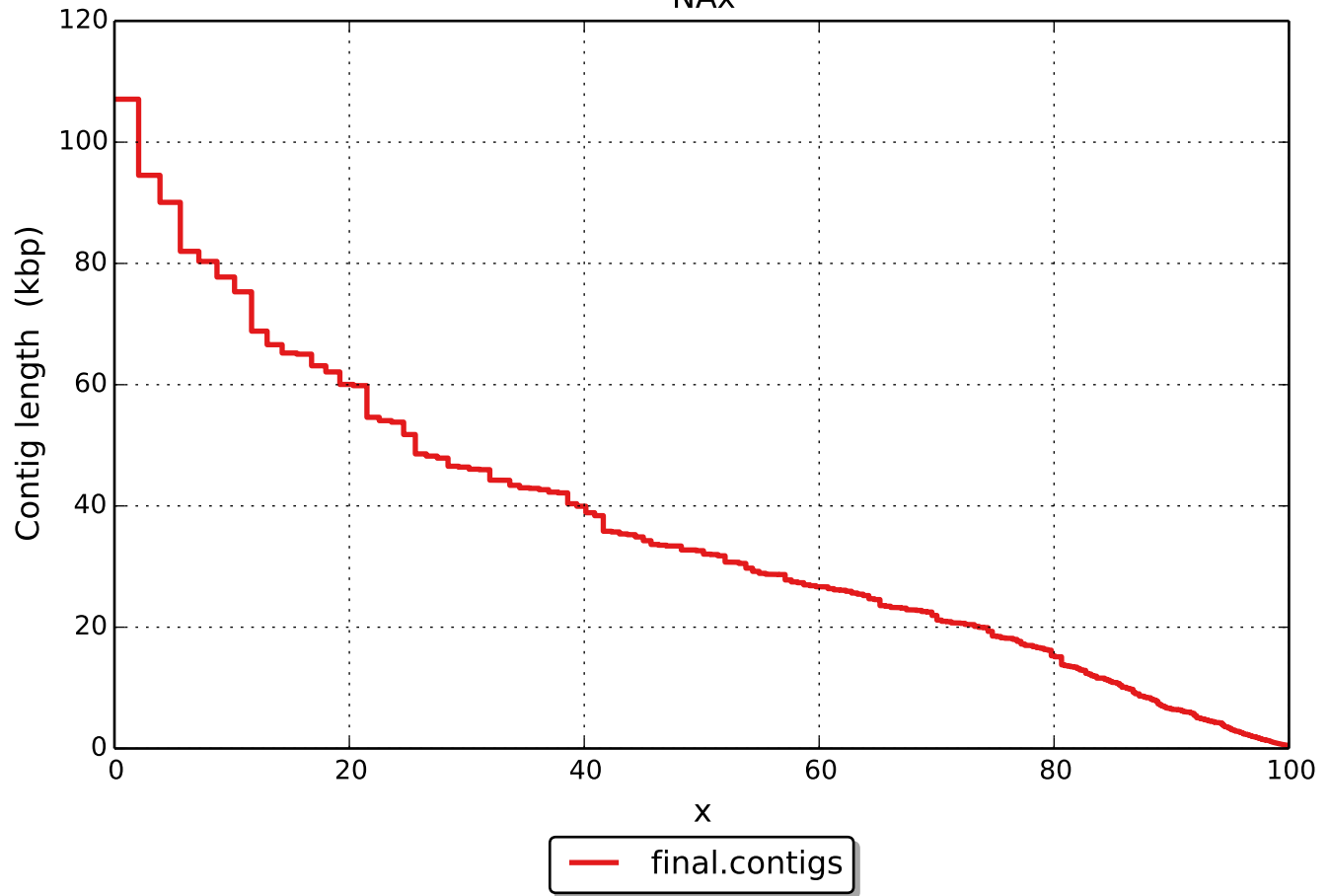
Misassemblies



 # relocations



NAx



NGAx

