

## Report

	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# contigs (>= 0 bp)	1385	1362	372	513
# contigs (>= 1000 bp)	144	163	37	76
# contigs (>= 5000 bp)	13	24	8	17
# contigs (>= 10000 bp)	12	20	8	13
# contigs (>= 25000 bp)	12	16	7	11
# contigs (>= 50000 bp)	9	12	4	10
Total length (>= 0 bp)	2661212	2781649	2014929	2219994
Total length (>= 1000 bp)	1985203	2119498	1846809	2009011
Total length (>= 5000 bp)	1810246	1910923	1802832	1886087
Total length (>= 10000 bp)	1804199	1884981	1802832	1859159
Total length (>= 25000 bp)	1804199	1812728	1792394	1833107
Total length (>= 50000 bp)	1693662	1688852	1700071	1805243
# contigs	762	775	159	211
Largest contig	503758	305777	1150417	398369
Total length	2404236	2538580	1927120	2098123
Reference length	1811802	1811802	1811802	1811802
GC (%)	41.19	41.57	37.84	37.98
Reference GC (%)	38.07	38.07	38.07	38.07
N50	120793	120675	1150417	165472
NG50	179983	140698	1150417	291100
N75	28168	5904	311604	100510
NG75	117636	111326	311604	134943
L50	5	7	1	4
LG50	3	5	1	3
L75	12	23	2	8
LG75	6	8	2	6
# misassemblies	46	42	84	46
# misassembled contigs	12	15	8	11
Misassembled contigs length	1764376	1784888	1728472	1811749
# local misassemblies	65	70	42	69
# unaligned contigs	740 + 1 part	745 + 4 part	91 + 16 part	145 + 20 part
Unaligned length	589601	703442	115362	196952
Genome fraction (%)	89.022	86.984	62.133	87.435
Duplication ratio	1.125	1.164	1.609	1.200
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	2571.45	2674.33	3599.81	2656.45
# indels per 100 kbp	70.87	65.67	92.65	70.95
Largest alignment	148362	226567	82059	226968
NA50	26066	21829	7696	29374
NGA50	59035	38532	10744	40791
NA75	-	-	-	1198
NGA75	18855	16241	-	14264
LA50	18	24	44	15
LGA50	10	11	38	12
LA75	-	-	-	64
LGA75	25	29	-	29

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

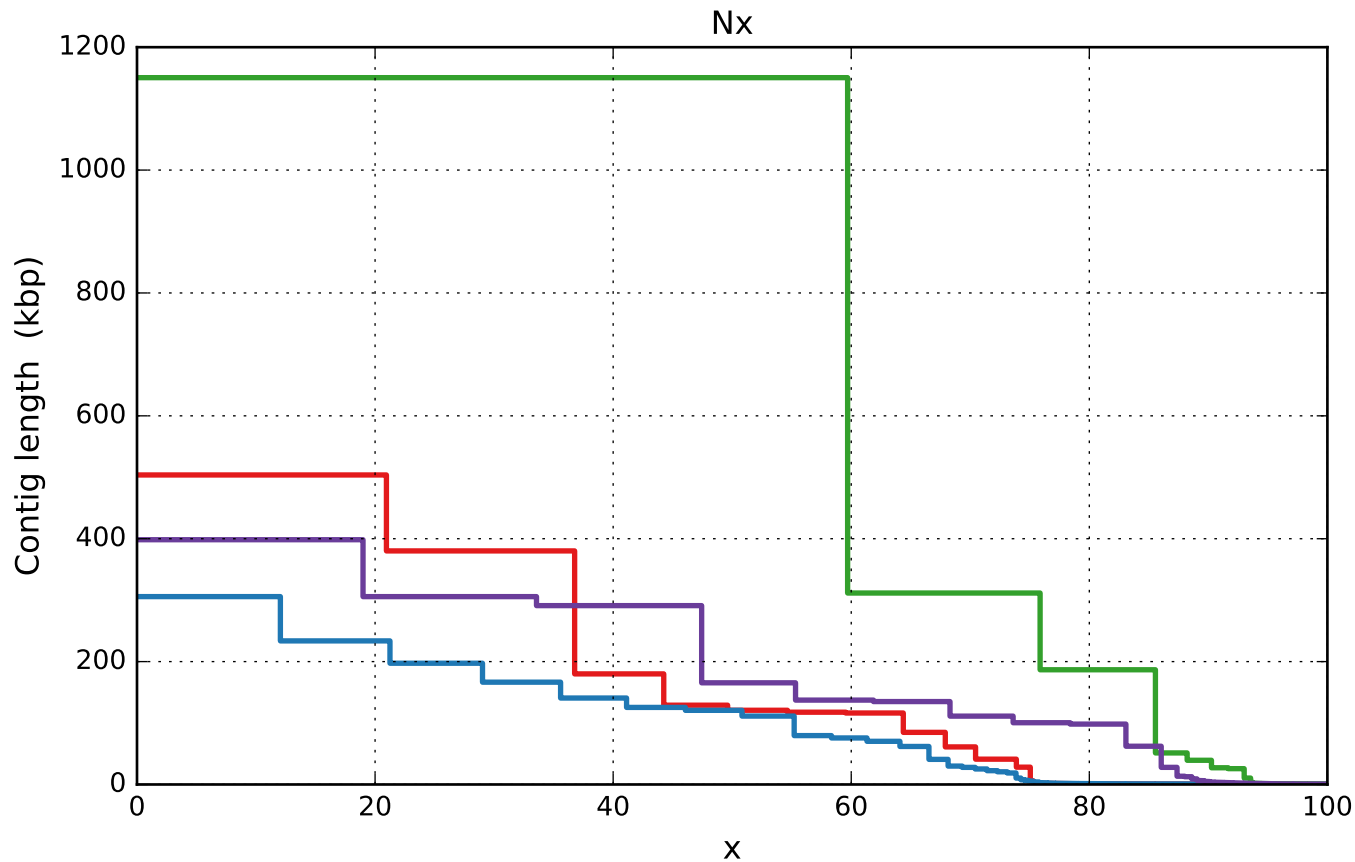
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	46	42	84	46
# relocations	46	42	84	46
# translocations	0	0	0	0
# inversions	0	0	0	0
# misassembled contigs	12	15	8	11
Misassembled contigs length	1764376	1784888	1728472	1811749
# local misassemblies	65	70	42	69
# mismatches	41475	42147	40524	42082
# indels	1143	1035	1043	1124
# short indels	1001	912	946	989
# long indels	142	123	97	135
Indels length	3553	3308	2543	3336

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

	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	740	745	91	145
Fully unaligned length	589529	673757	73021	164767
# partially unaligned contigs	1	4	16	20
# with misassembly	0	1	1	5
# both parts are significant	0	1	2	3
Partially unaligned length	72	29685	42341	32185
# N's	0	0	0	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).

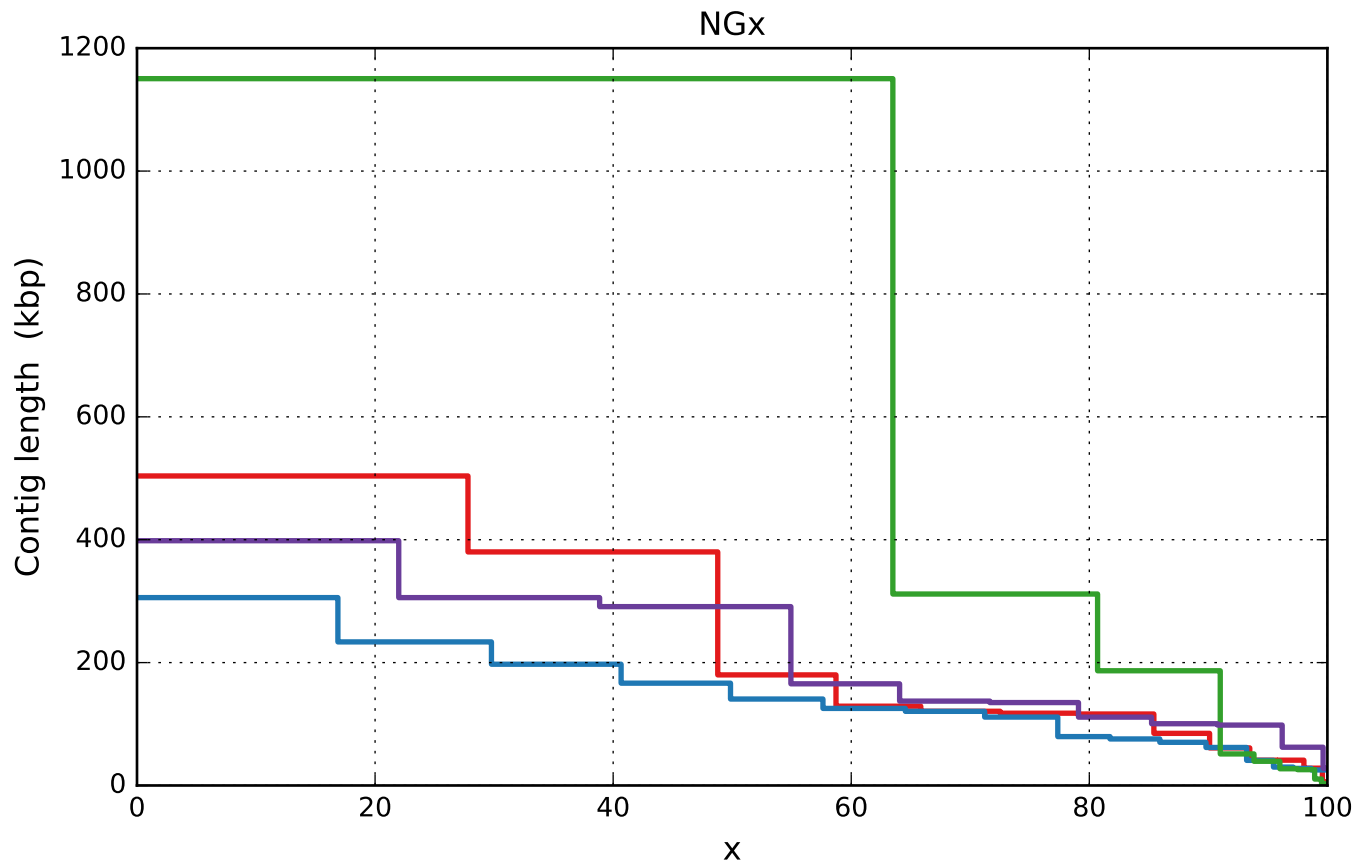


M05964\_contigs

M10540\_contigs

M16180\_contigs

M07572\_contigs

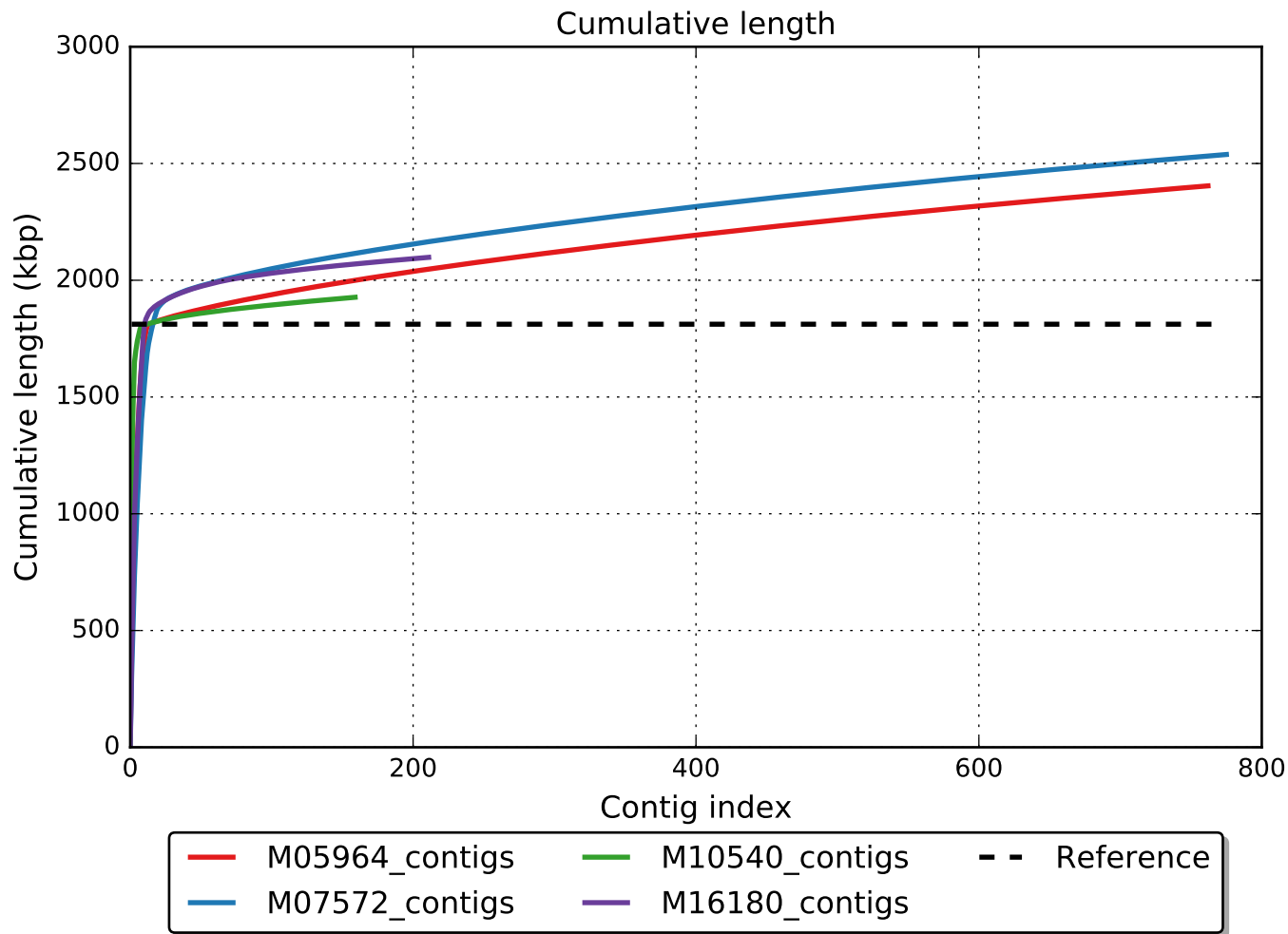


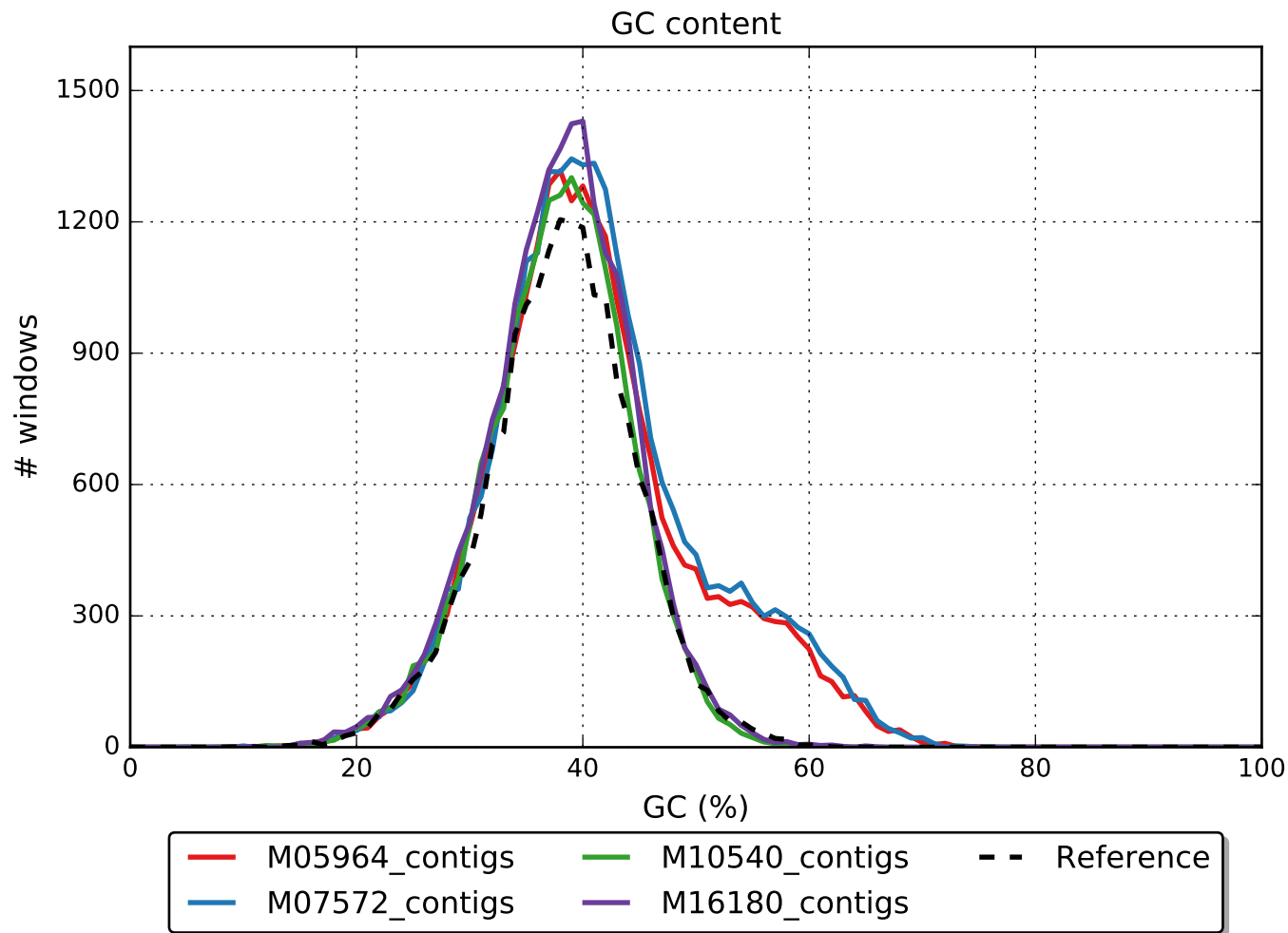
M05964\_contigs

M10540\_contigs

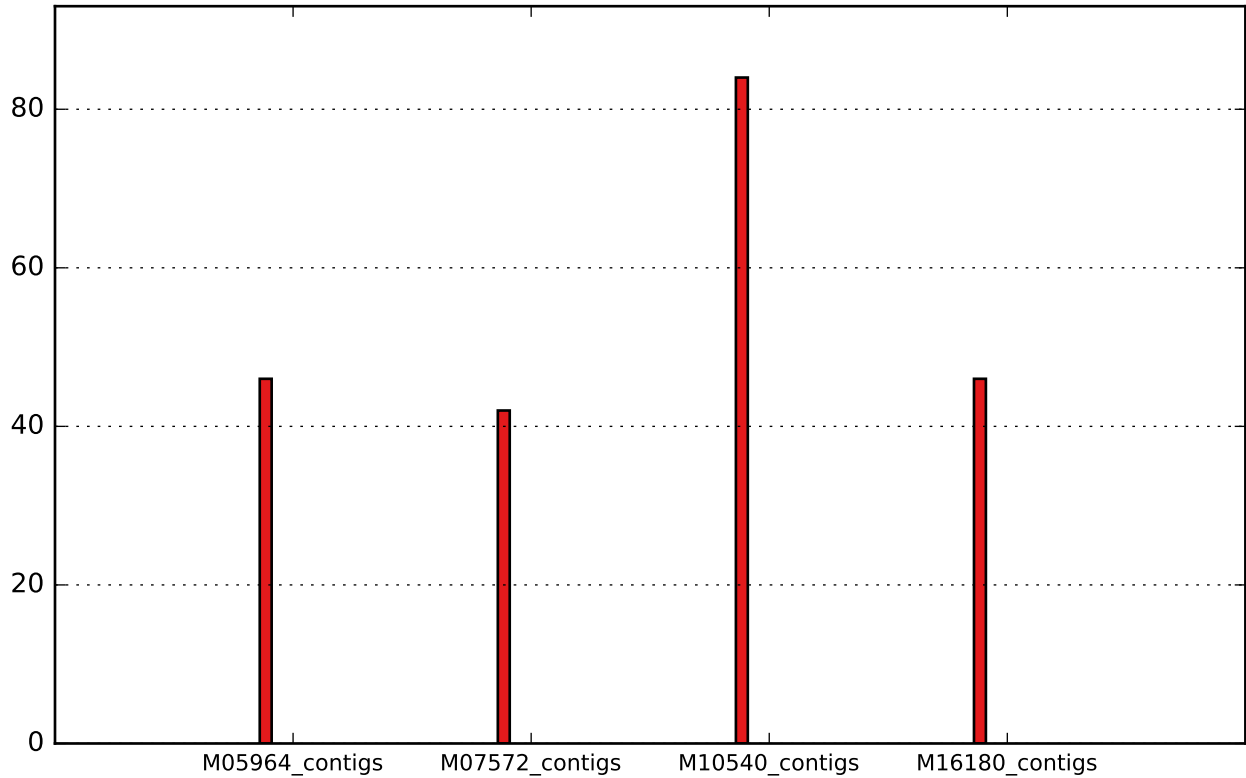
M16180\_contigs

M07572\_contigs





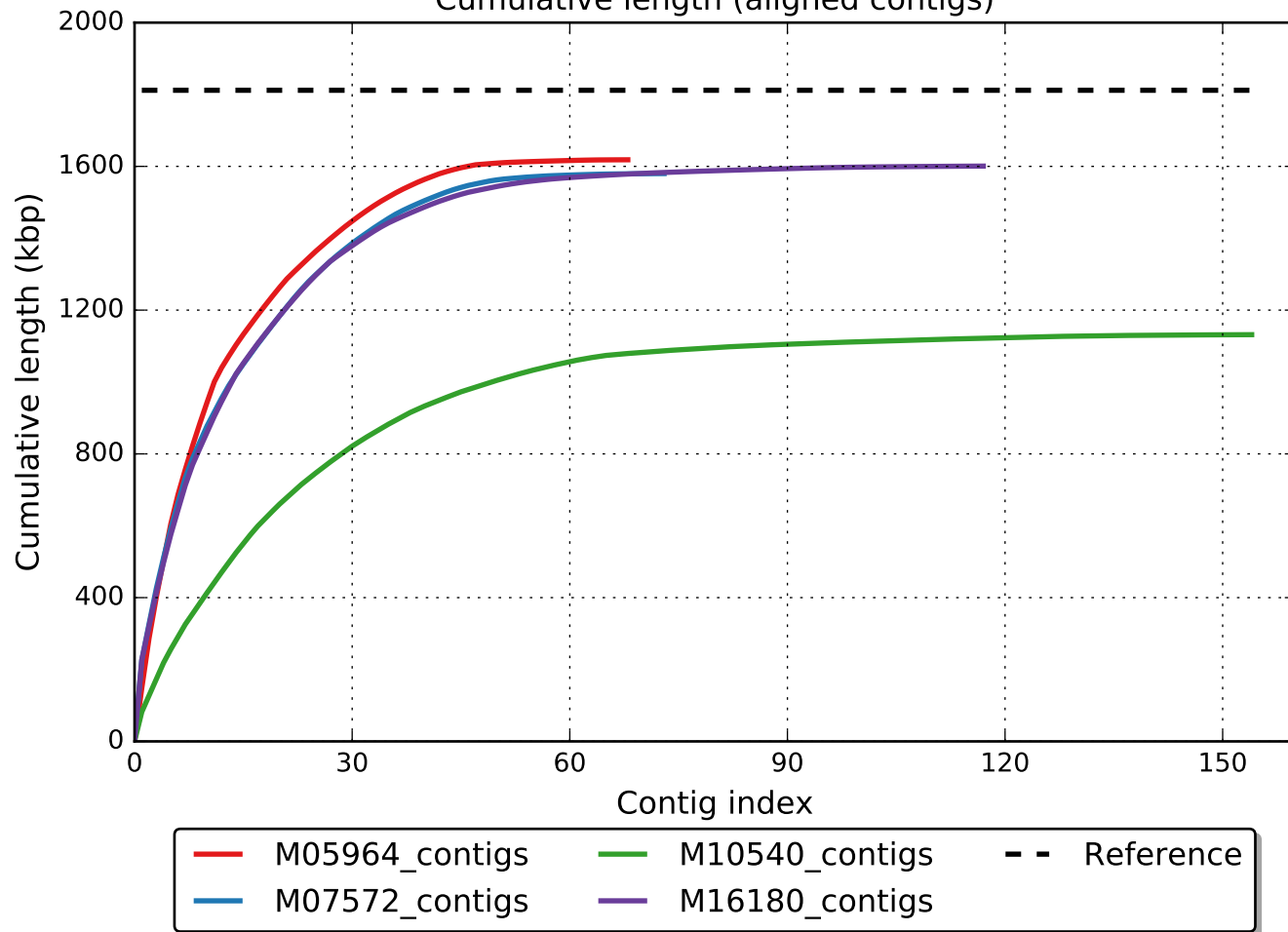
# Misassemblies



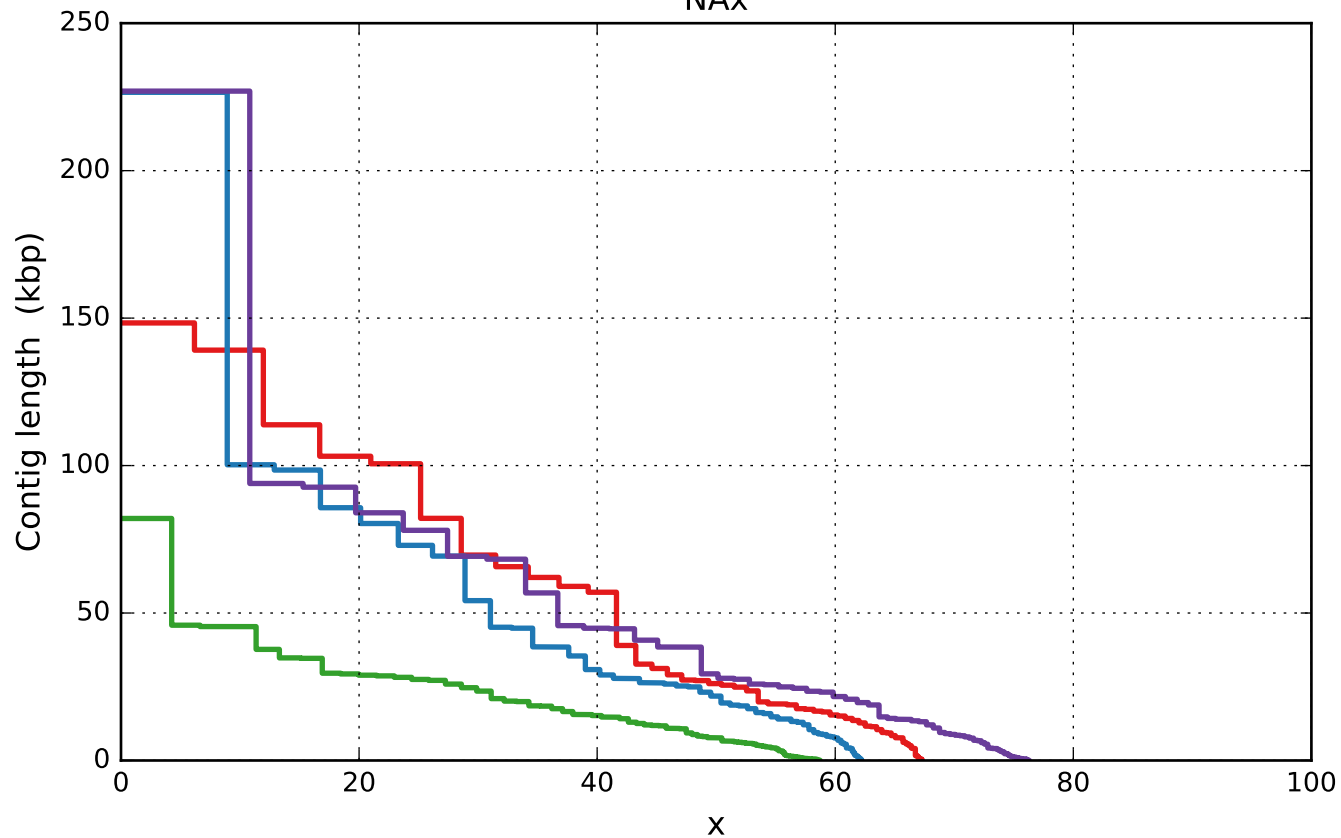
 # relocations



Cumulative length (aligned contigs)



NAx



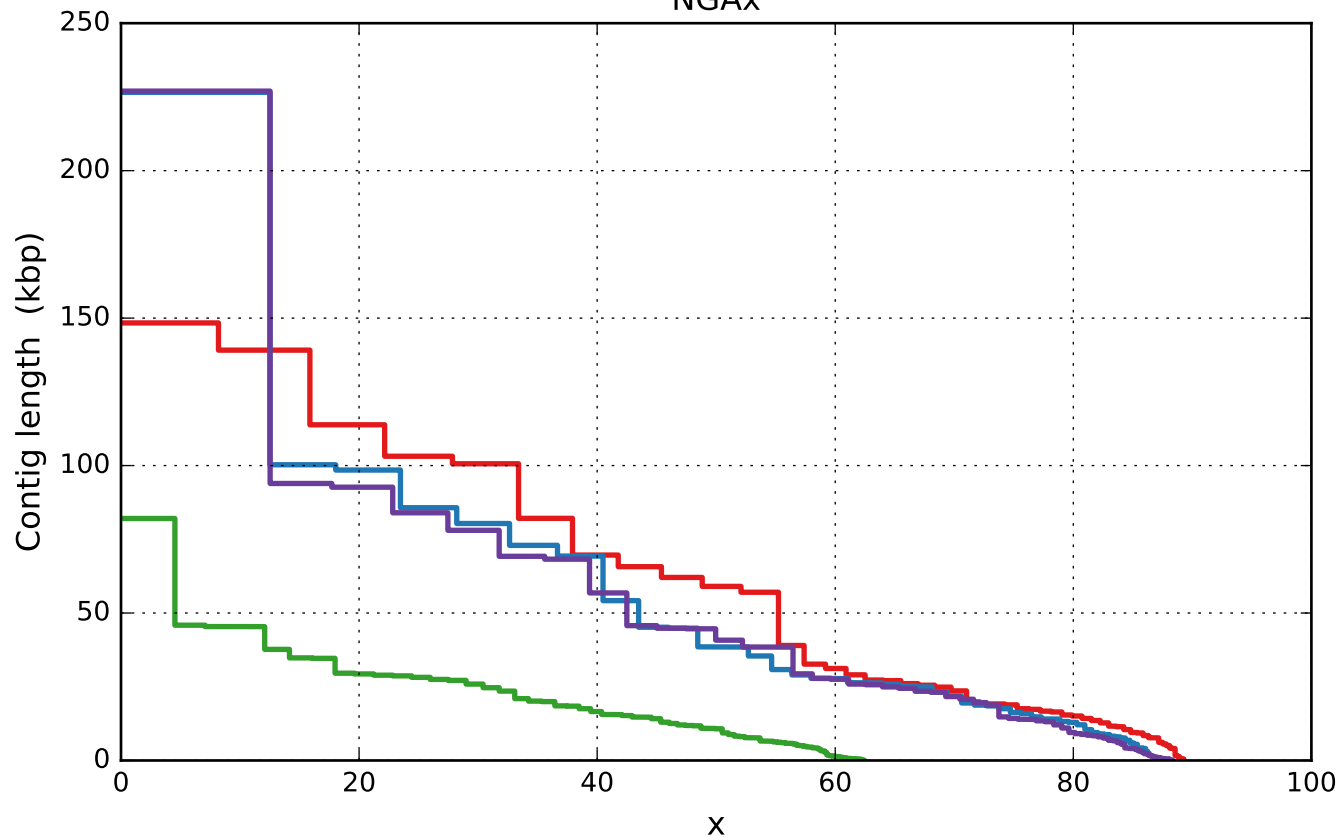
M05964\_contigs

M10540\_contigs

M16180\_contigs

M07572\_contigs

# NGAx



— M05964\_contigs    — M10540\_contigs    — M16180\_contigs  
— M07572\_contigs

