

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	1813033	1813033	1813033	1813033
GC (%)	41.19	41.57	37.84	37.98
Reference GC (%)	38.04	38.04	38.04	38.04
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	15	31	77	35
# misassembled contigs	8	15	7	11
Misassembled contigs length	1428378	1733449	1577471	1750314
# local misassemblies	40	54	33	66
# unaligned contigs	739 + 2 part	741 + 6 part	87 + 18 part	143 + 19 part
Unaligned length	585478	701849	198564	204864
Genome fraction (%)	94.573	88.693	57.352	90.921
Duplication ratio	1.061	1.142	1.662	1.149
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	1301.73	2445.66	3601.70	2470.42
# indels per 100 kbp	62.11	85.01	111.27	90.87
Largest alignment	427942	113381	69362	162803
NA50	98164	28953	4822	44330
NGA50	117636	45851	7674	52135
NA75	-	-	-	8294
NGA75	61005	25416	-	27772
LA50	7	23	57	14
LGA50	5	13	48	11
LA75	-	-	-	35
LGA75	10	27	-	22

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

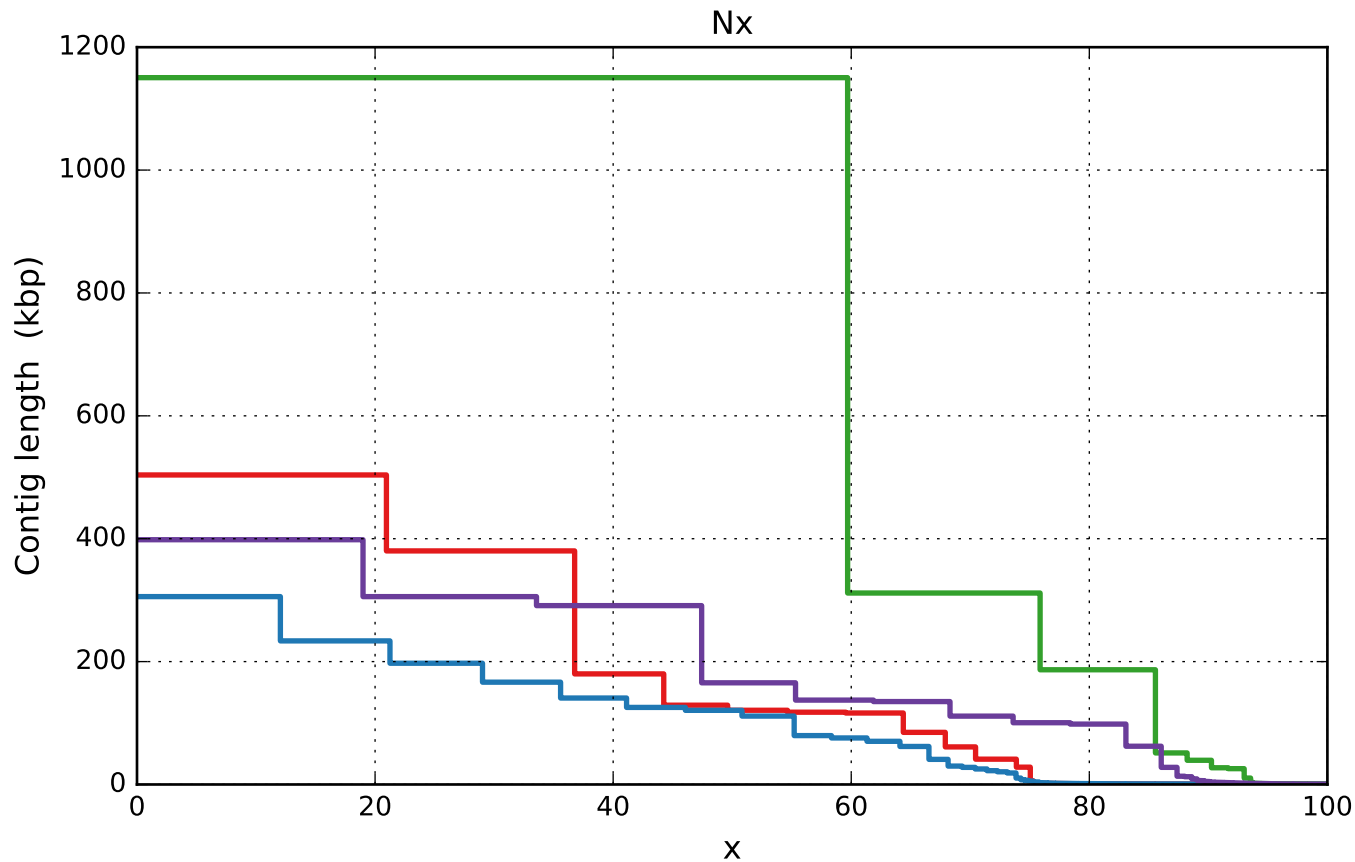
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	15	31	77	35
# relocations	15	31	77	35
# translocations	0	0	0	0
# inversions	0	0	0	0
# misassembled contigs	8	15	7	11
Misassembled contigs length	1428378	1733449	1577471	1750314
# local misassemblies	40	54	33	66
# mismatches	22320	39327	37451	40723
# indels	1065	1367	1157	1498
# short indels	981	1245	1082	1364
# long indels	84	122	75	134
Indels length	2644	3869	2498	3768

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

	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	739	741	87	143
Fully unaligned length	582974	669392	71737	184444
# partially unaligned contigs	2	6	18	19
# with misassembly	0	1	4	4
# both parts are significant	1	1	2	3
Partially unaligned length	2504	32457	126827	20420
# N's	0	0	0	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).

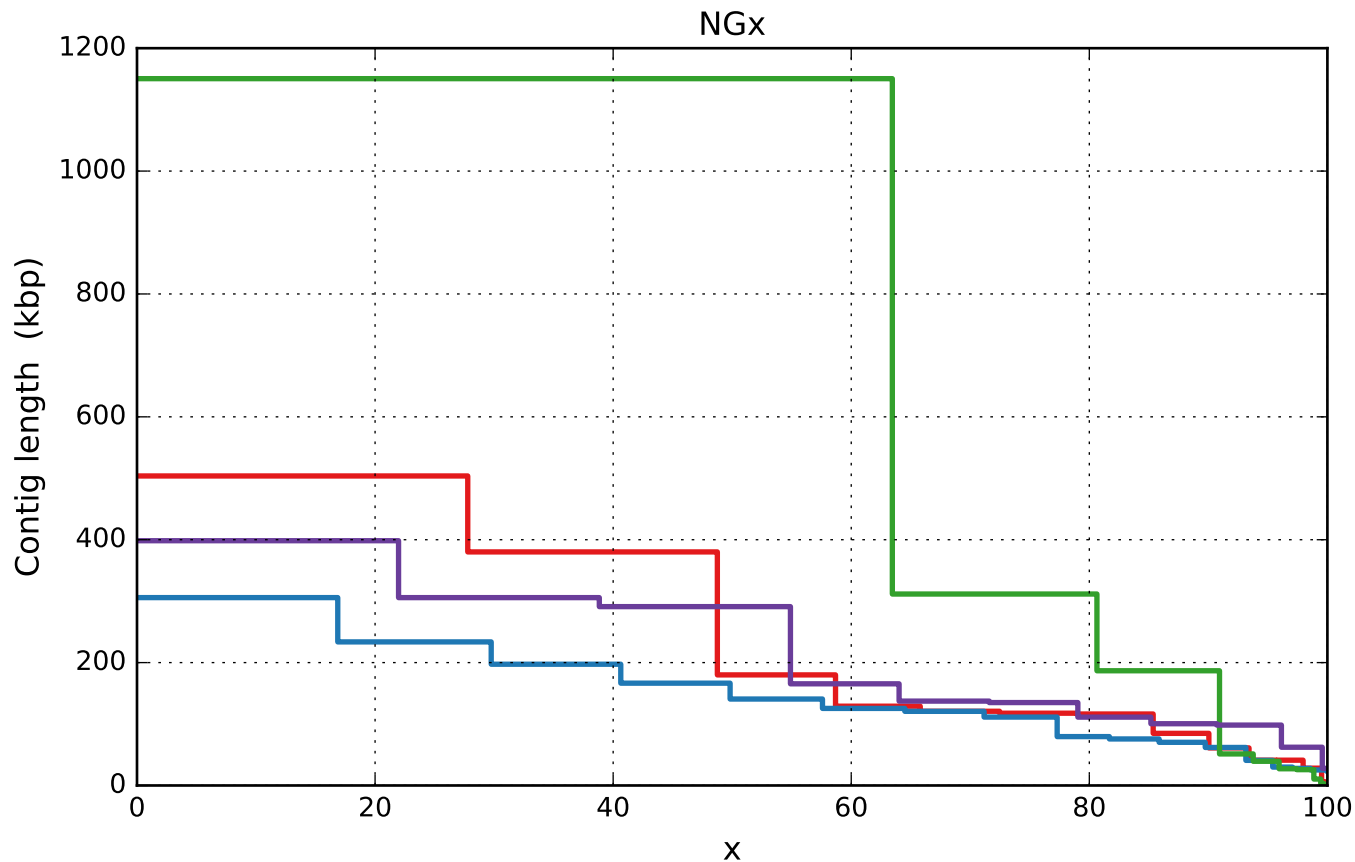


M05964_contigs

M10540_contigs

M16180_contigs

M07572_contigs

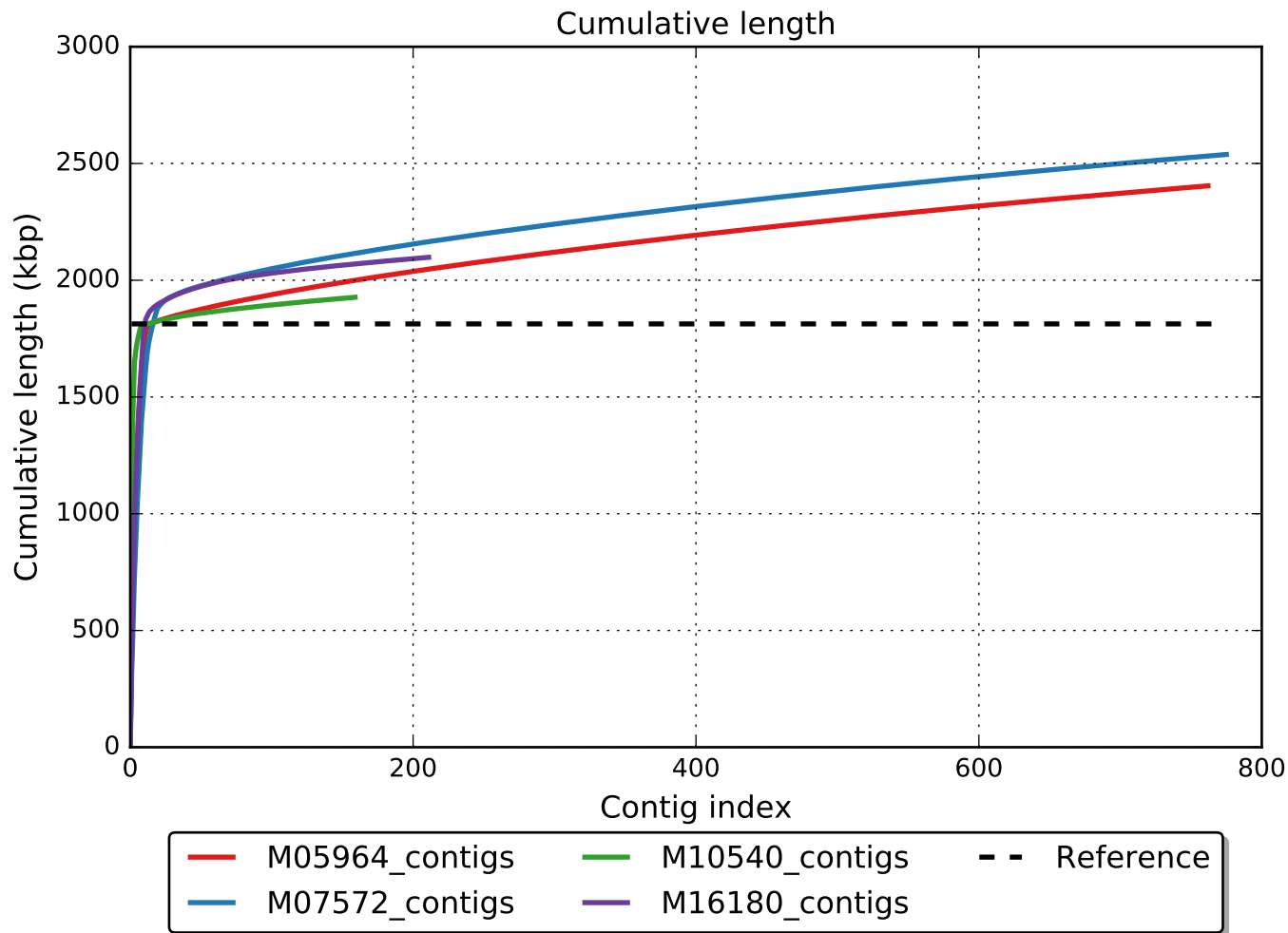


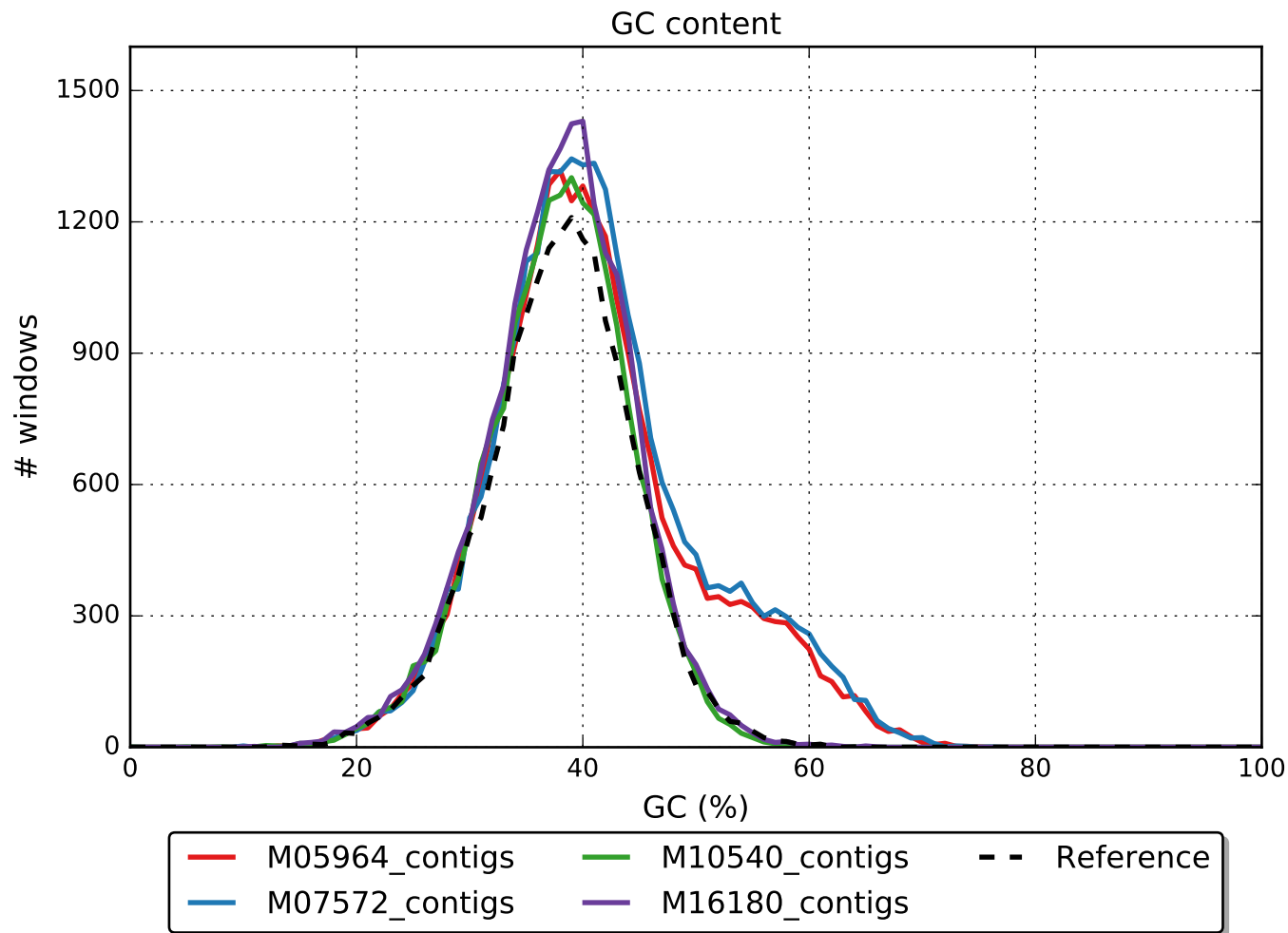
M05964_contigs

M10540_contigs

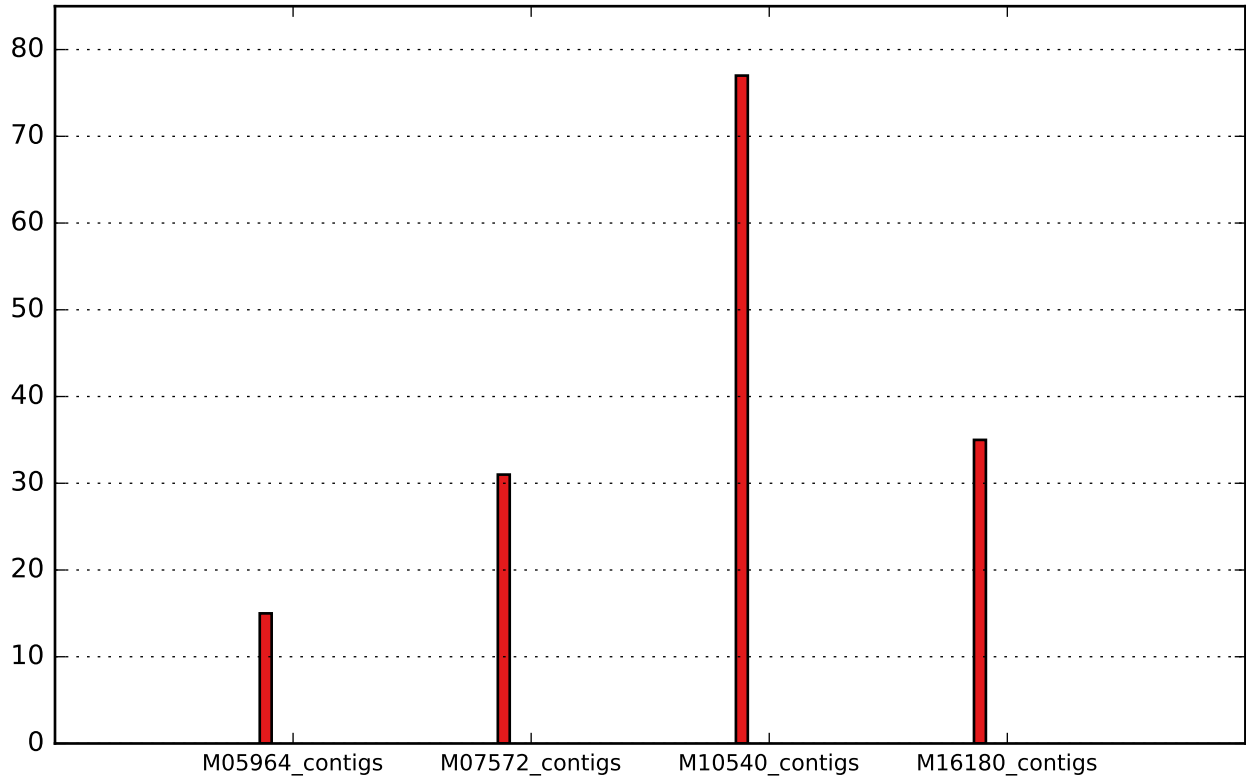
M16180_contigs

M07572_contigs



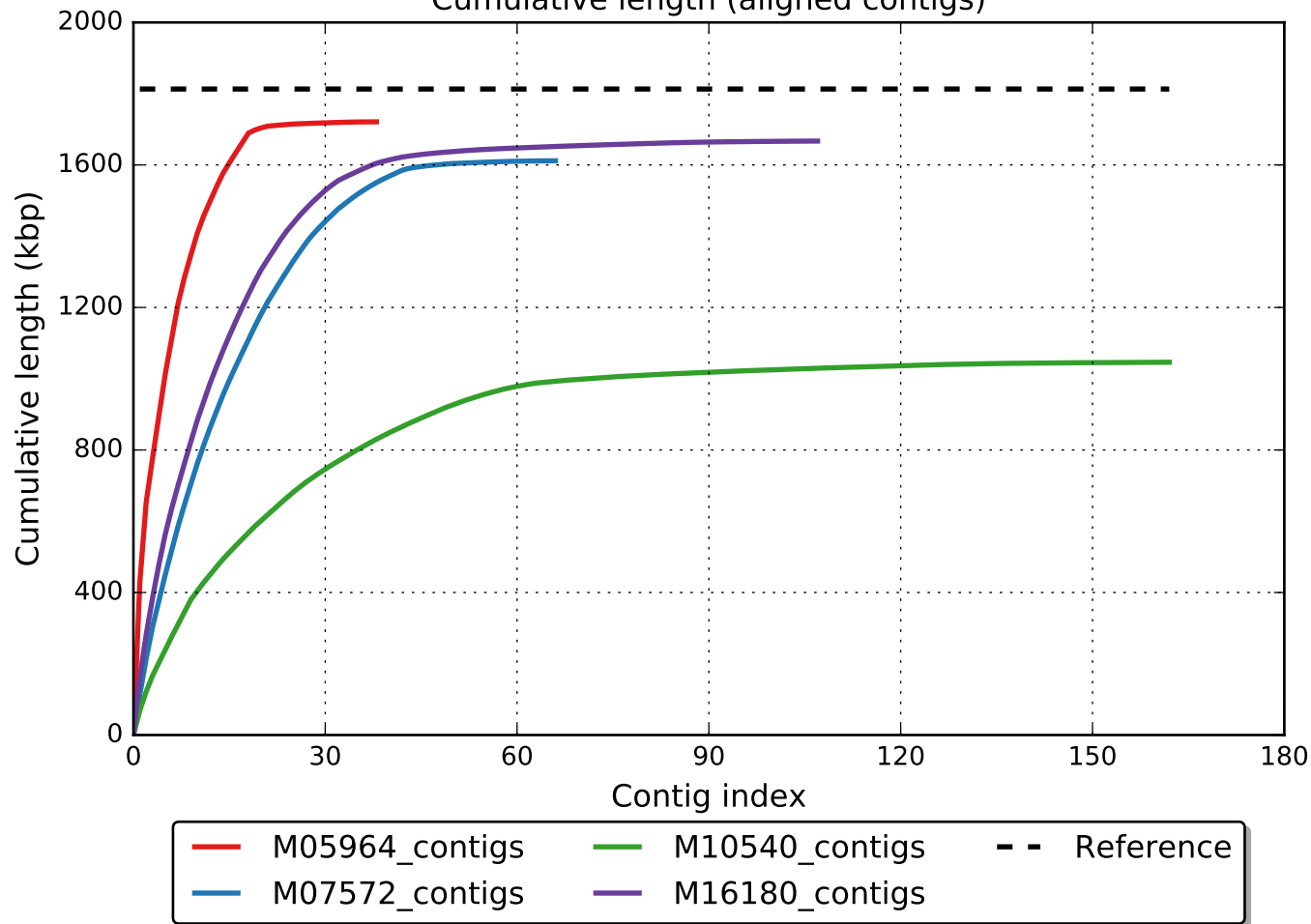


Misassemblies

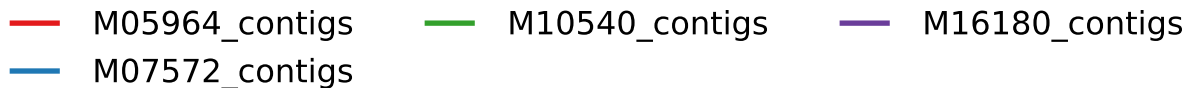
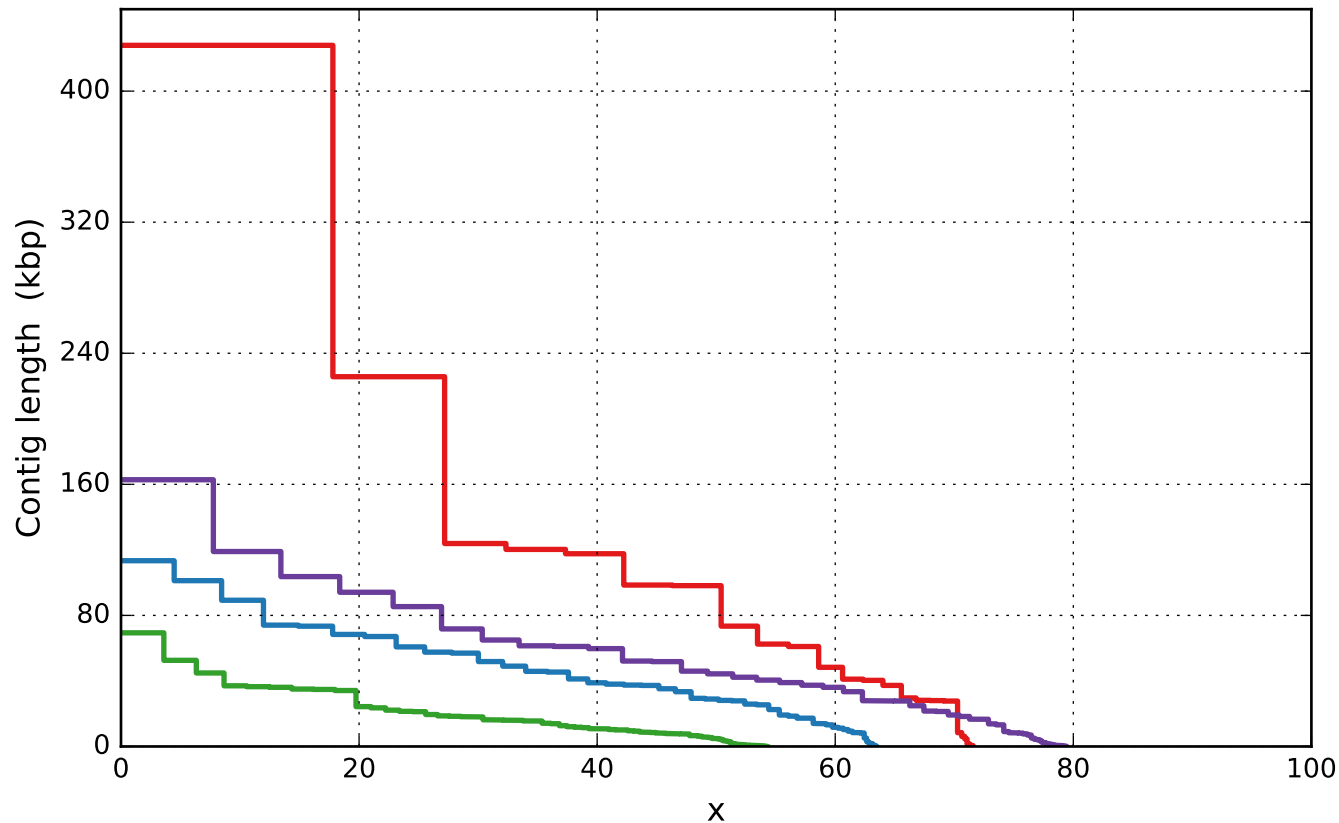


 # relocations

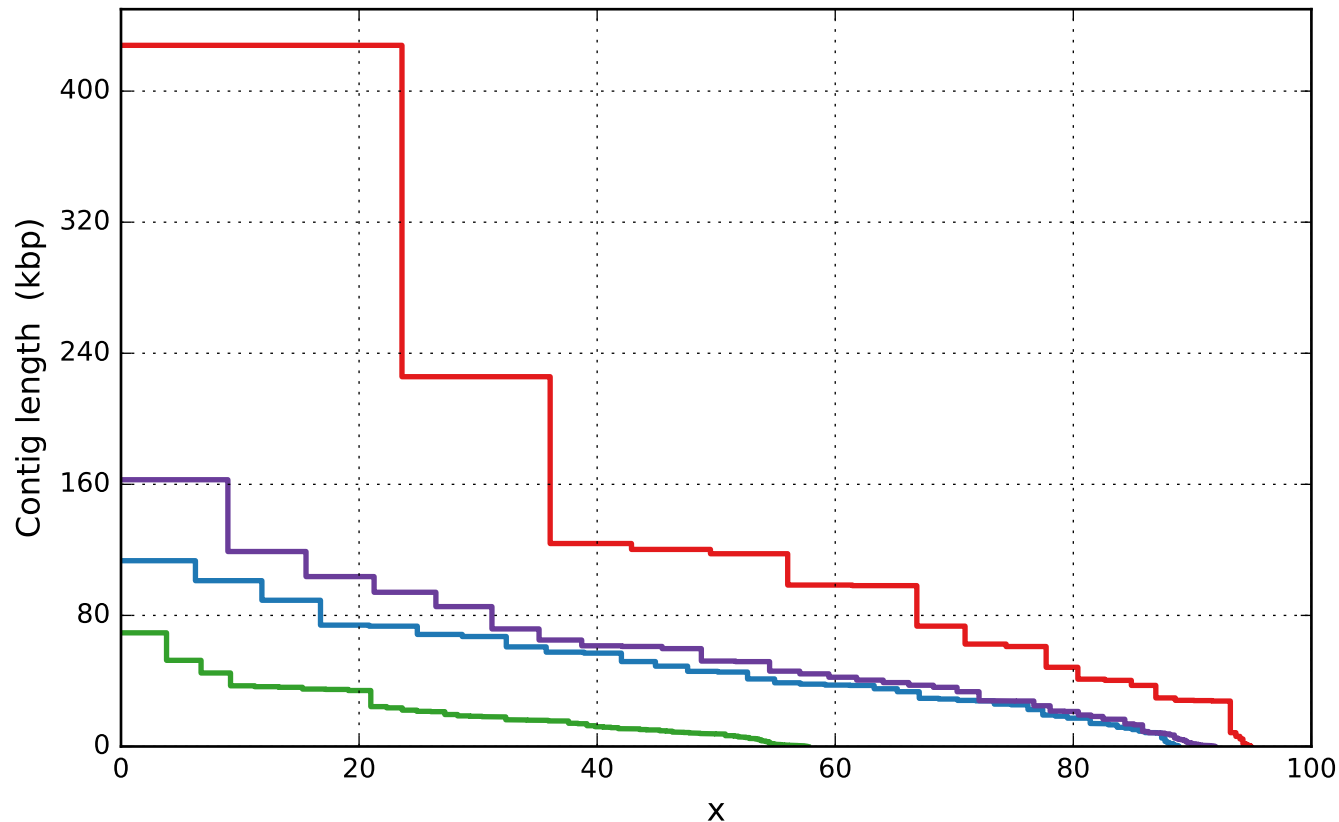
Cumulative length (aligned contigs)



NAx



NGAx



— M05964_contigs — M10540_contigs — M16180_contigs
— M07572_contigs

