

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	1850897	1850897	1850897	1850897
GC (%)	41.19	41.57	37.84	37.98
Reference GC (%)	38.16	38.16	38.16	38.16
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	6	85	22
# misassembled contigs	12	6	7	7
Misassembled contigs length	1777375	728252	1741781	1494429
# local misassemblies	67	22	44	38
# unaligned contigs	721 + 3 part	735 + 8 part	87 + 18 part	149 + 22 part
Unaligned length	573941	660428	122113	222660
Genome fraction (%)	87.375	95.842	61.487	91.646
Duplication ratio	1.132	1.059	1.586	1.106
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	2469.99	762.49	3530.84	1704.39
# indels per 100 kbp	63.07	23.90	84.27	45.45
Largest alignment	157919	251530	51516	221430
NA50	34017	79175	8632	68261
NGA50	44468	123248	10283	94334
NA75	-	-	-	27864
NGA75	21333	61872	-	47702
LA50	19	9	44	9
LGA50	12	5	40	7
LA75	-	-	-	20
LGA75	27	10	-	15

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

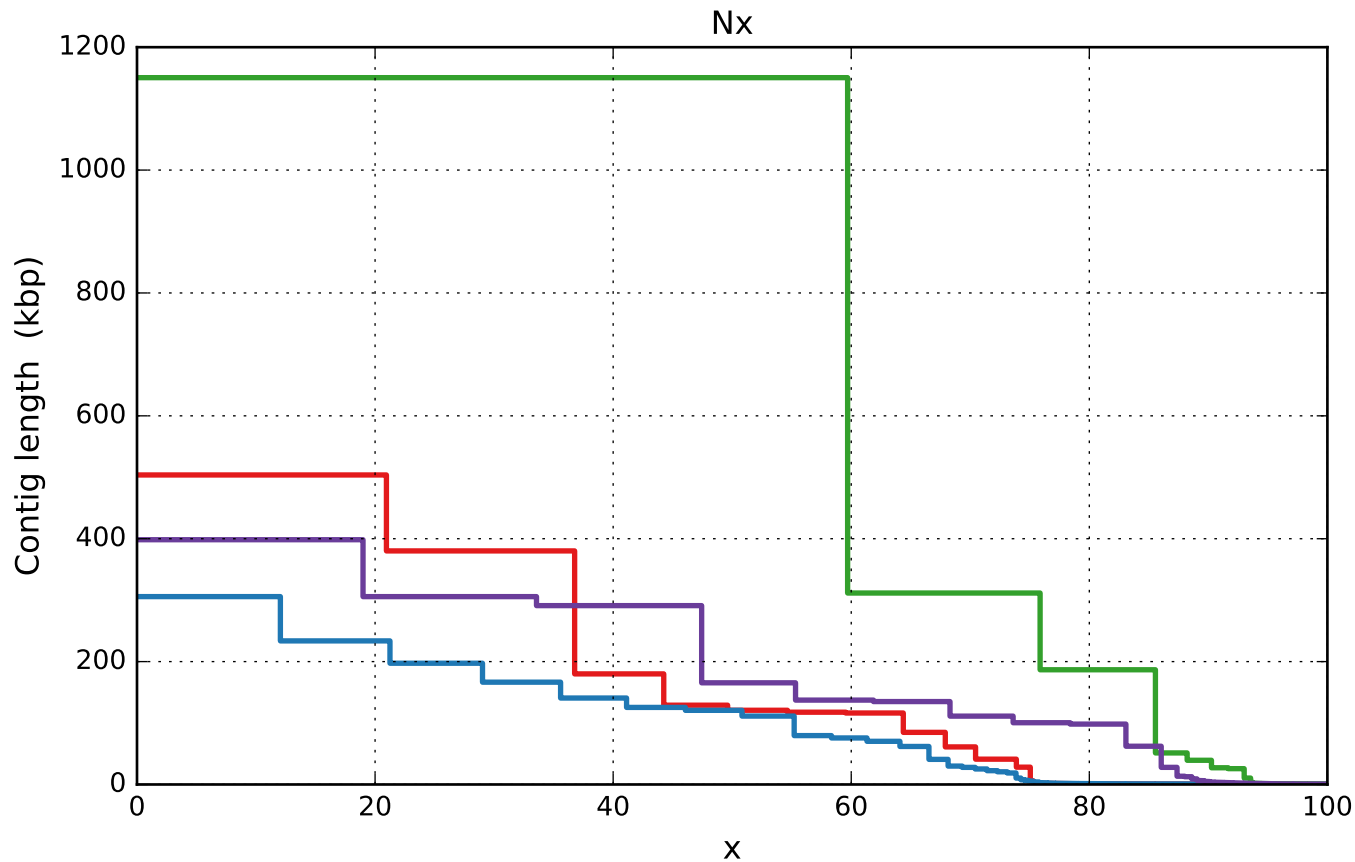
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	46	6	85	22
# relocations	45	6	85	22
# translocations	0	0	0	0
# inversions	1	0	0	0
# misassembled contigs	12	6	7	7
Misassembled contigs length	1777375	728252	1741781	1494429
# local misassemblies	67	22	44	38
# mismatches	39945	13526	40183	28911
# indels	1020	424	959	771
# short indels	907	352	868	665
# long indels	113	72	91	106
Indels length	3105	1937	2247	2698

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	721	735	87	149
Fully unaligned length	571358	621068	69895	187557
# partially unaligned contigs	3	8	18	22
# with misassembly	0	2	5	1
# both parts are significant	1	2	1	2
Partially unaligned length	2583	39360	52218	35103
# 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).

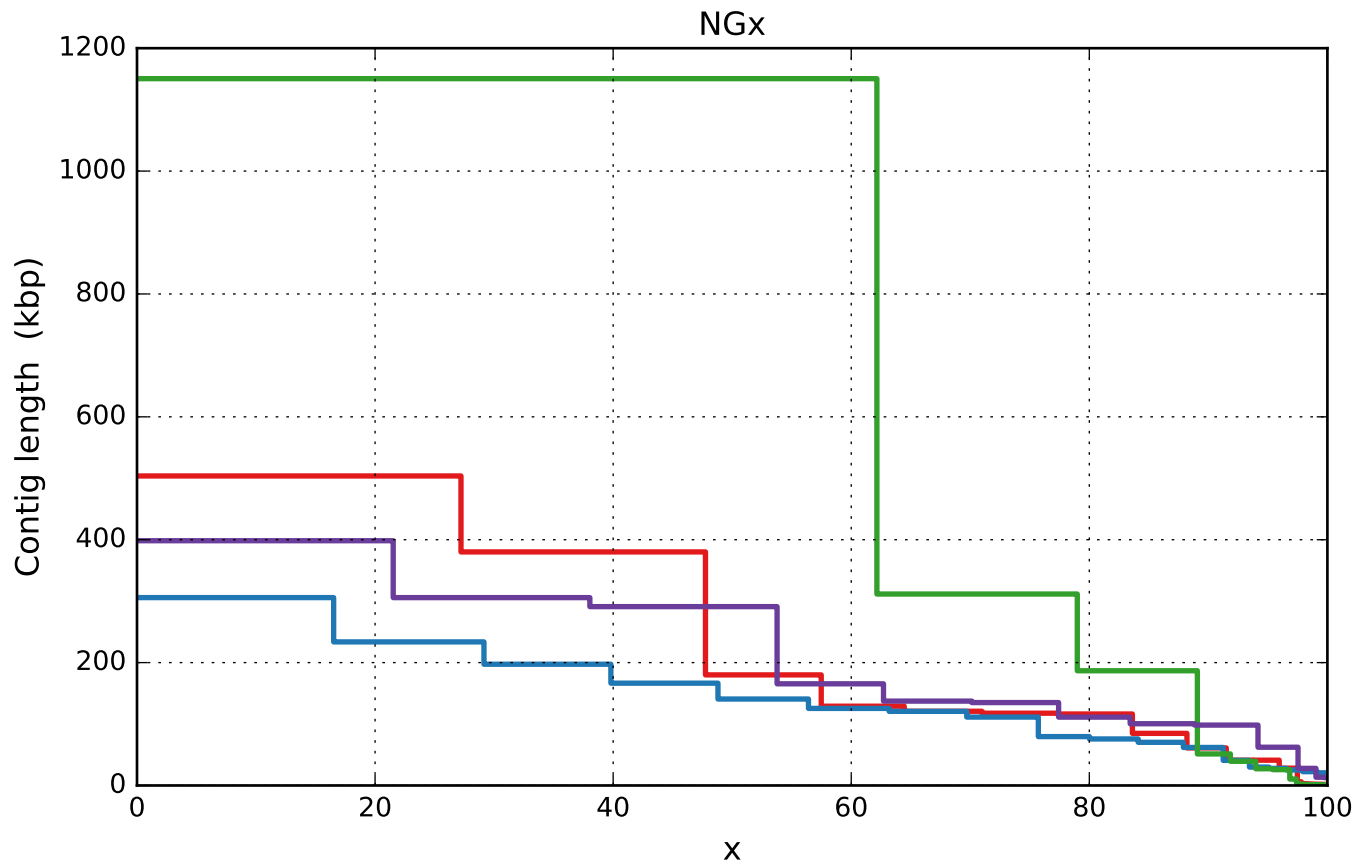


M05964_contigs

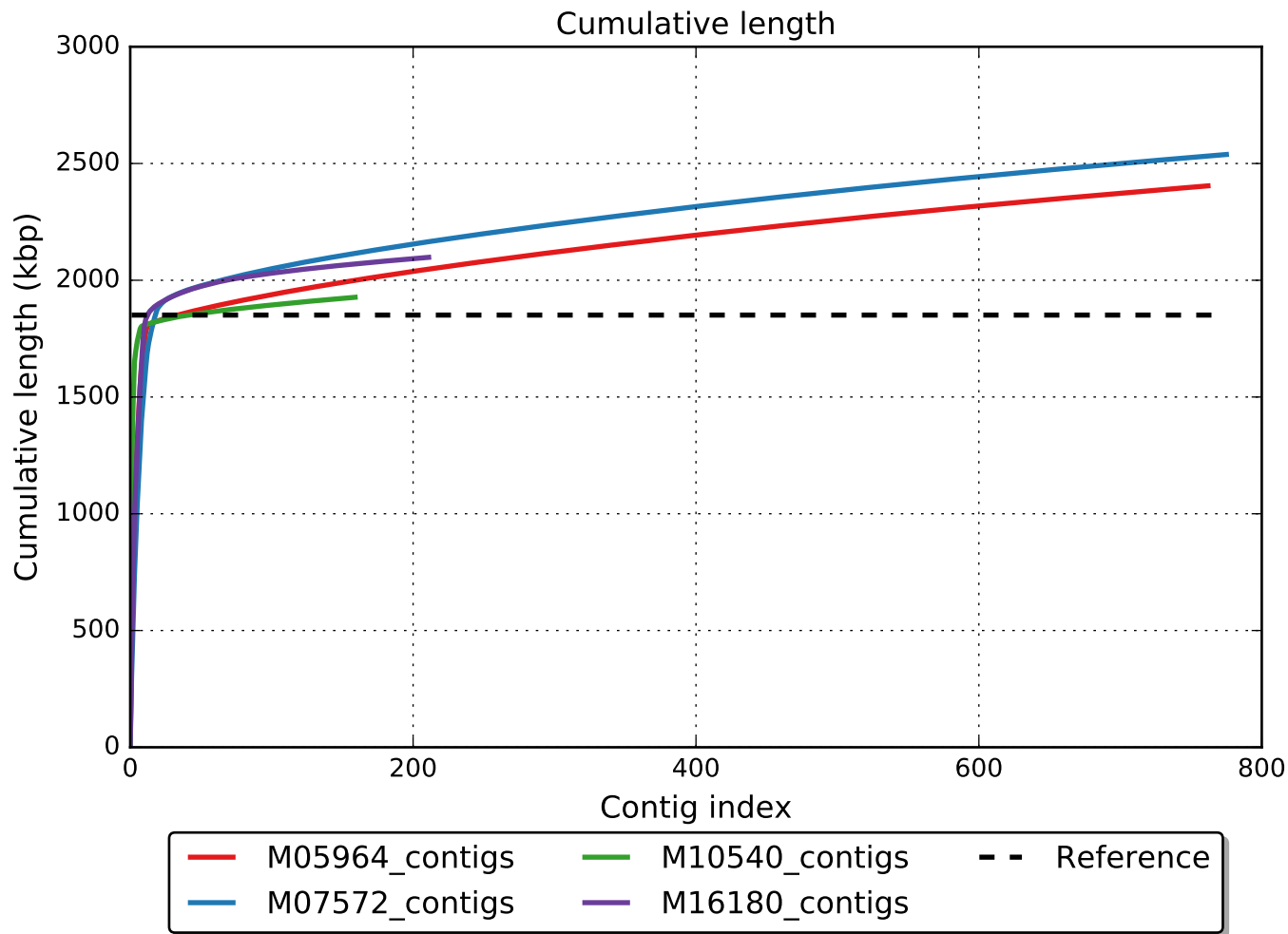
M10540_contigs

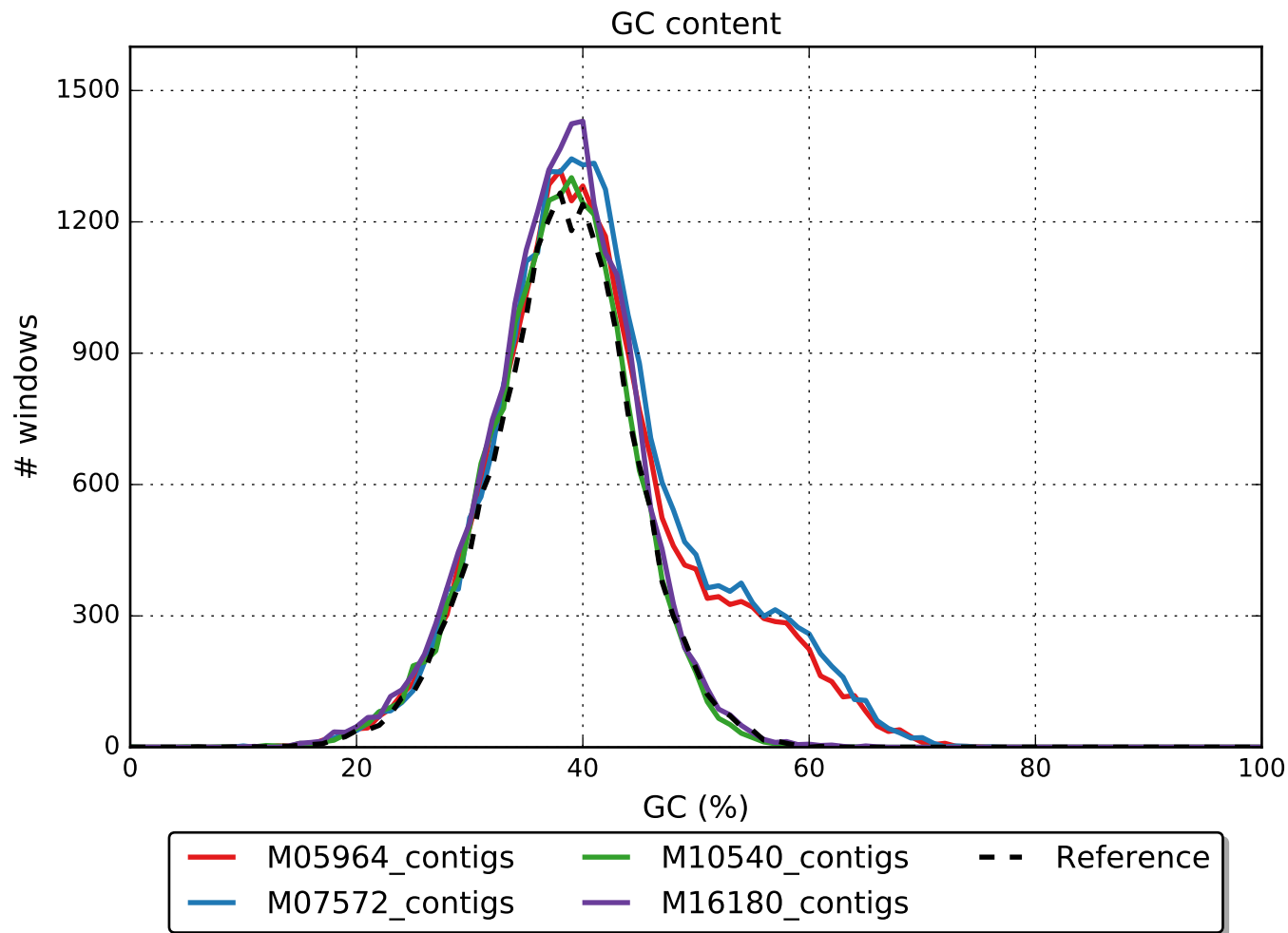
M16180_contigs

M07572_contigs

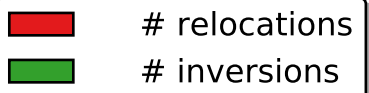
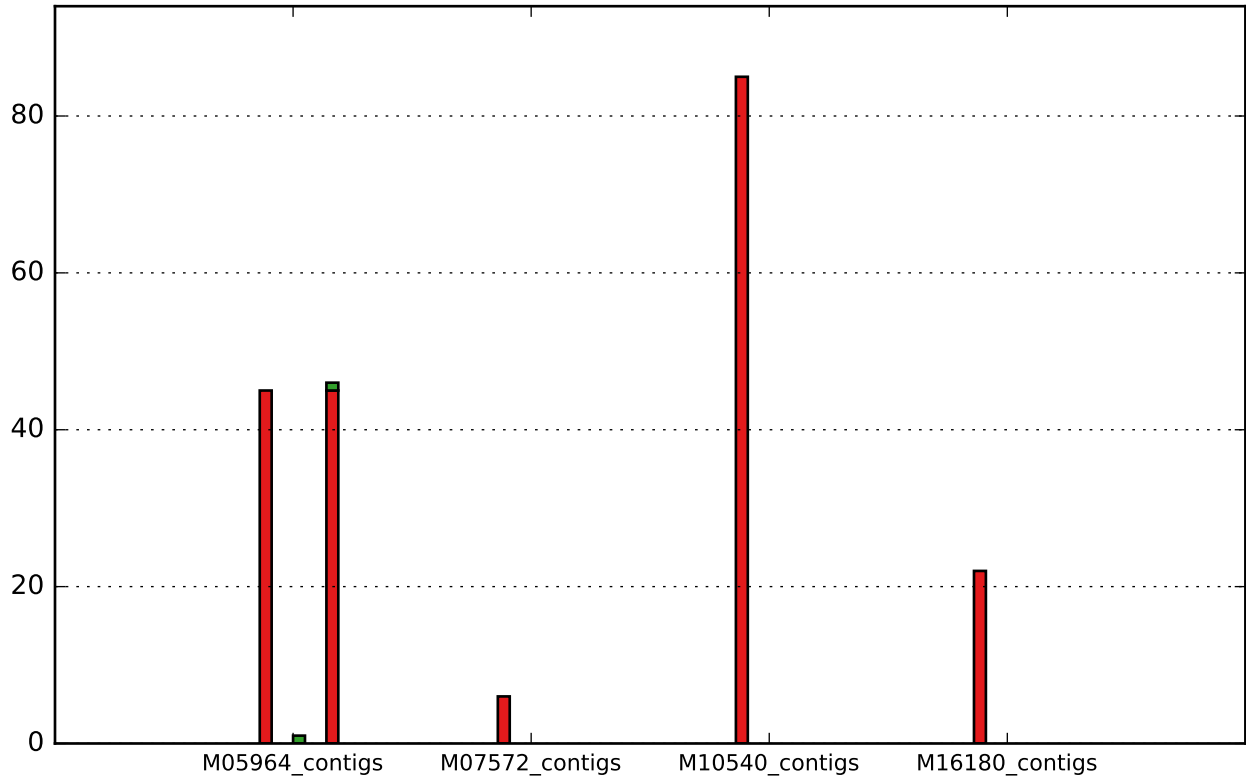


M05964_contigs M10540_contigs M16180_contigs
M07572_contigs

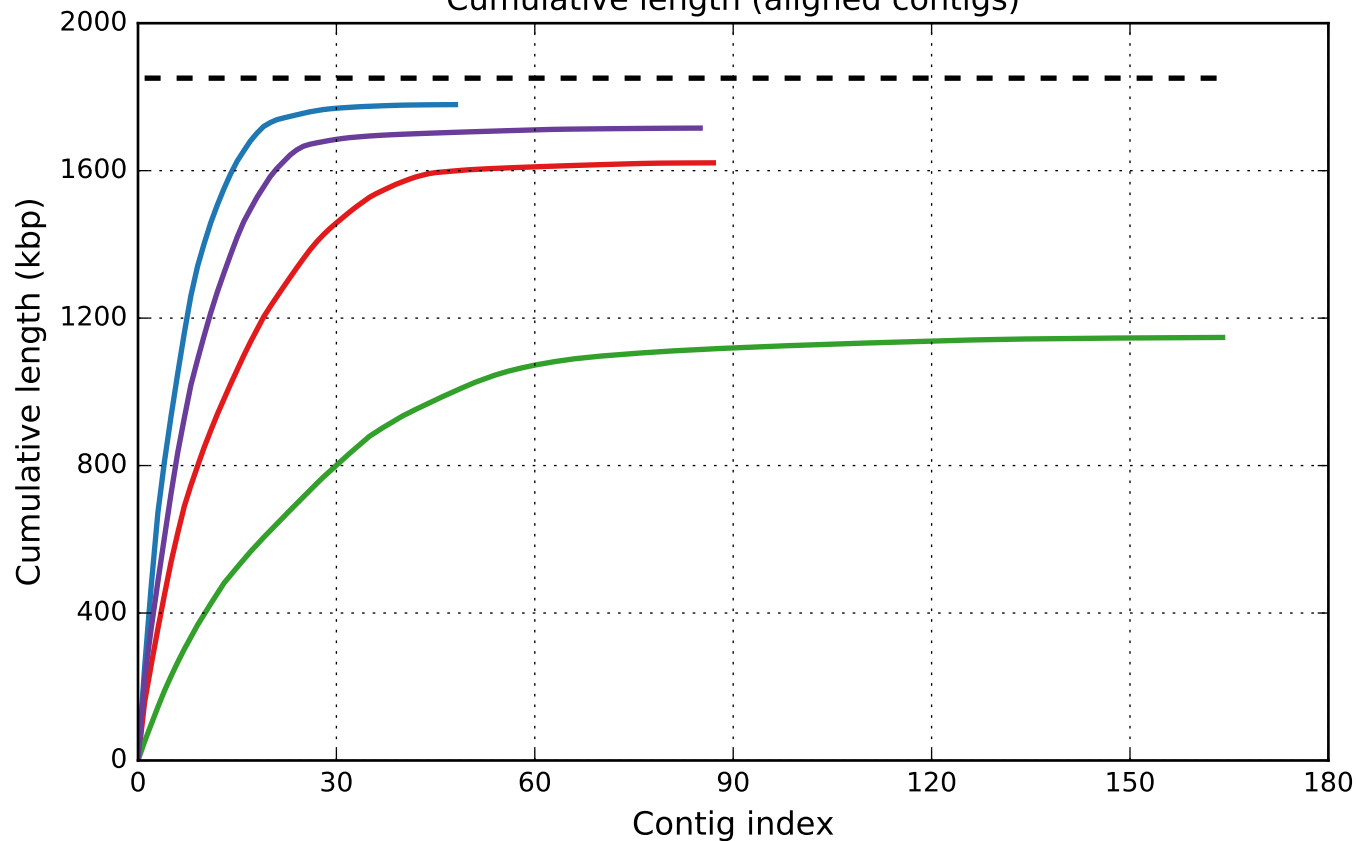




Misassemblies

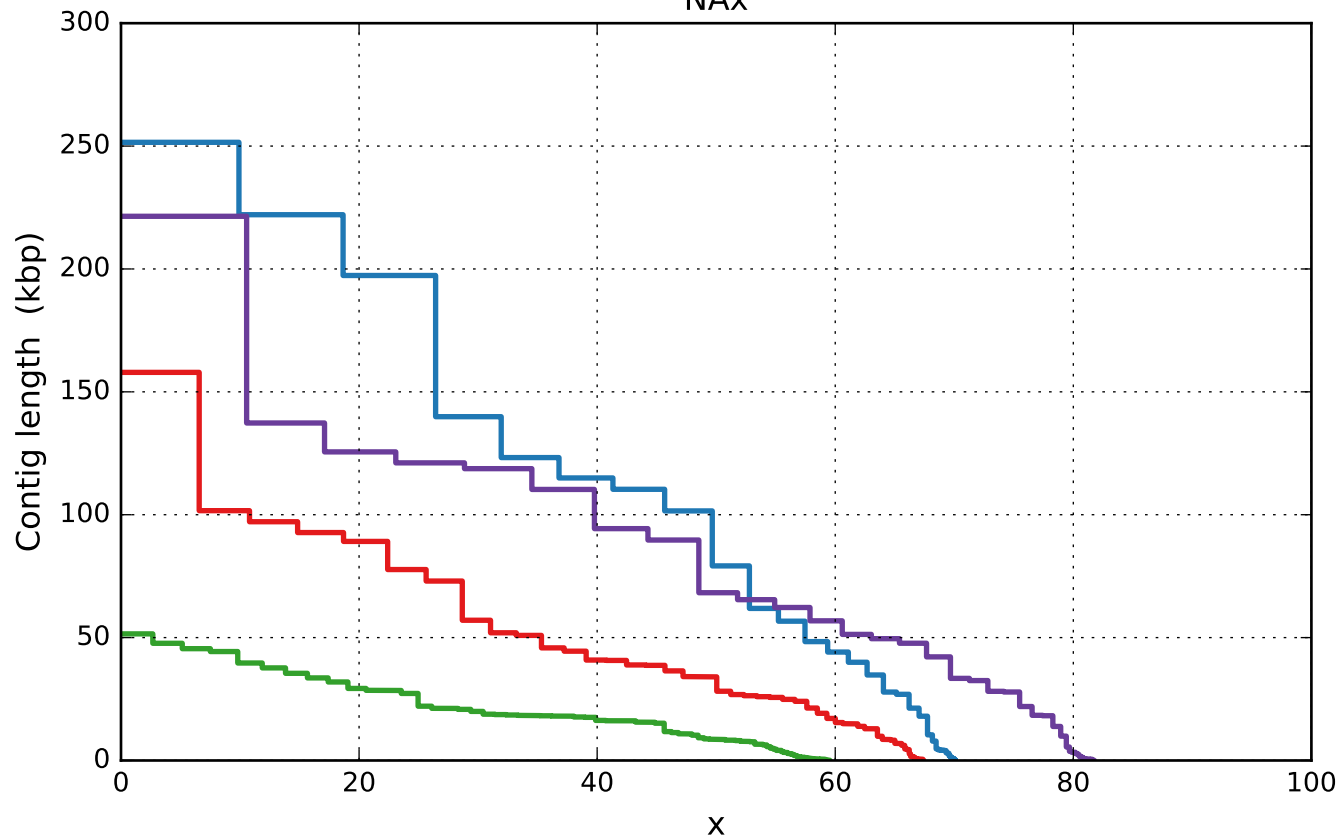


Cumulative length (aligned contigs)



— M05964_contigs — M10540_contigs - - Reference
— M07572_contigs — M16180_contigs

NAx



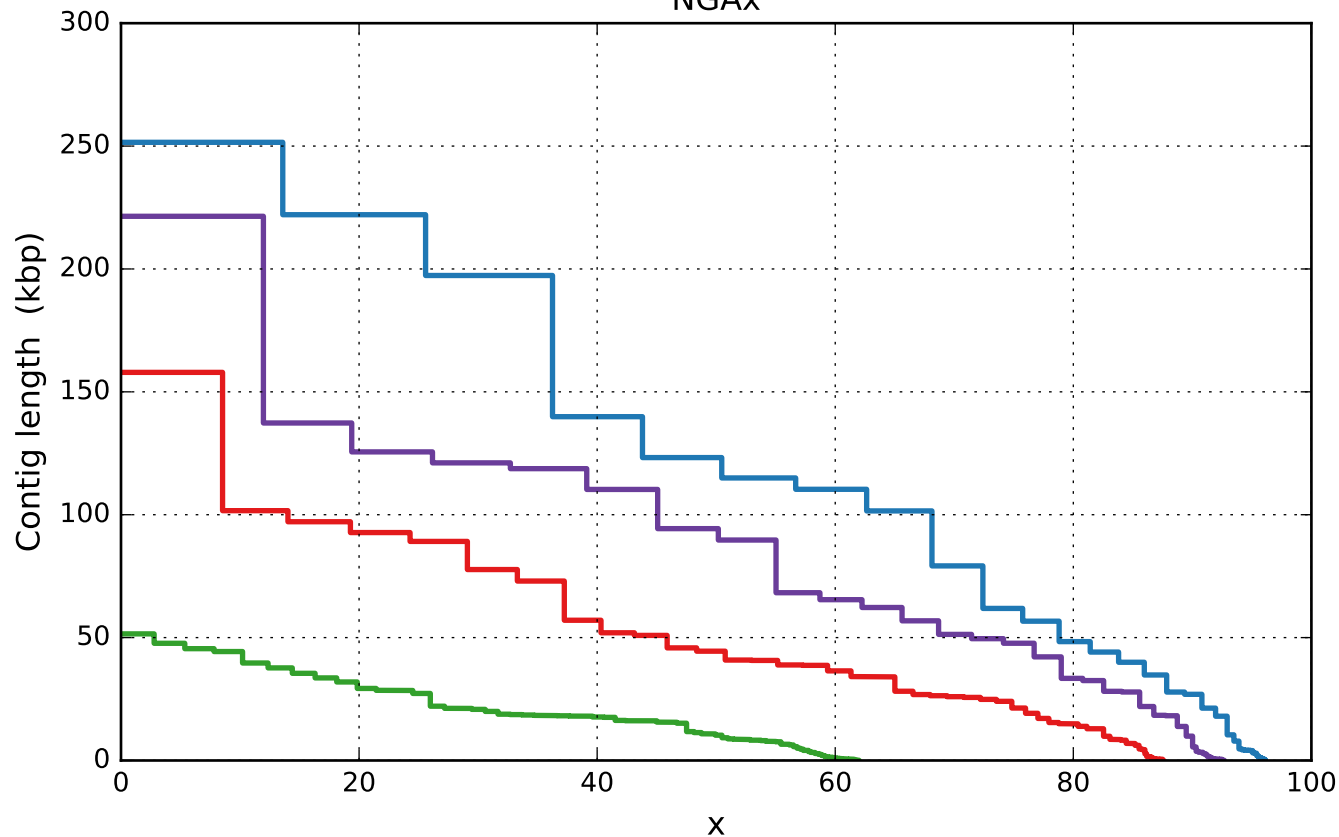
M05964_contigs

M10540_contigs

M16180_contigs

M07572_contigs

NGAx



M05964_contigs

M10540_contigs

M16180_contigs

M07572_contigs

