

Report

	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# contigs (>= 0 bp)	42	56	18	7028
# contigs (>= 1000 bp)	14	36	11	621
# contigs (>= 5000 bp)	11	22	8	3
# contigs (>= 10000 bp)	10	18	8	0
# contigs (>= 25000 bp)	10	14	7	0
# contigs (>= 50000 bp)	8	12	4	0
Total length (>= 0 bp)	1831657	1965102	1811331	3320808
Total length (>= 1000 bp)	1821194	1955209	1808761	1071265
Total length (>= 5000 bp)	1816377	1924256	1802504	16099
Total length (>= 10000 bp)	1810330	1897645	1802504	0
Total length (>= 25000 bp)	1810330	1840422	1792310	0
Total length (>= 50000 bp)	1739635	1787121	1700270	0
# contigs	19	45	12	1590
Largest contig	545971	305868	1150911	5936
Total length	1824603	1961709	1809438	1738815
Reference length	1813033	1813033	1813033	1813033
GC (%)	37.88	38.25	37.91	38.00
Reference GC (%)	38.04	38.04	38.04	38.04
N50	444952	200368	1150911	1206
NG50	444952	200368	1150911	1164
N75	179754	79547	311459	786
NG75	179754	112073	311459	729
L50	2	4	1	437
LG50	2	4	1	469
L75	4	8	2	884
LG75	4	7	2	958
# misassemblies	15	33	74	10
# misassembled contigs	7	13	5	10
Misassembled contigs length	1603170	1761164	1566127	14304
# local misassemblies	42	56	32	14
# unaligned contigs	1 + 1 part	18 + 4 part	0 + 5 part	379 + 98 part
Unaligned length	3758	100343	121292	482149
Genome fraction (%)	94.515	88.477	55.453	63.972
Duplication ratio	1.063	1.160	1.679	1.083
# N's per 100 kbp	59.52	57.45	38.30	84.60
# mismatches per 100 kbp	1220.48	2447.07	3664.18	2084.45
# indels per 100 kbp	56.61	85.16	112.40	63.54
Largest alignment	427942	113381	69178	4706
NA50	117915	41216	7674	827
NGA50	117915	46032	7674	788
NA75	61004	16654	-	-
NGA75	61004	25415	-	-
LA50	4	15	48	587
LGA50	4	13	48	633
LA75	9	32	-	-
LGA75	9	27	-	-

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

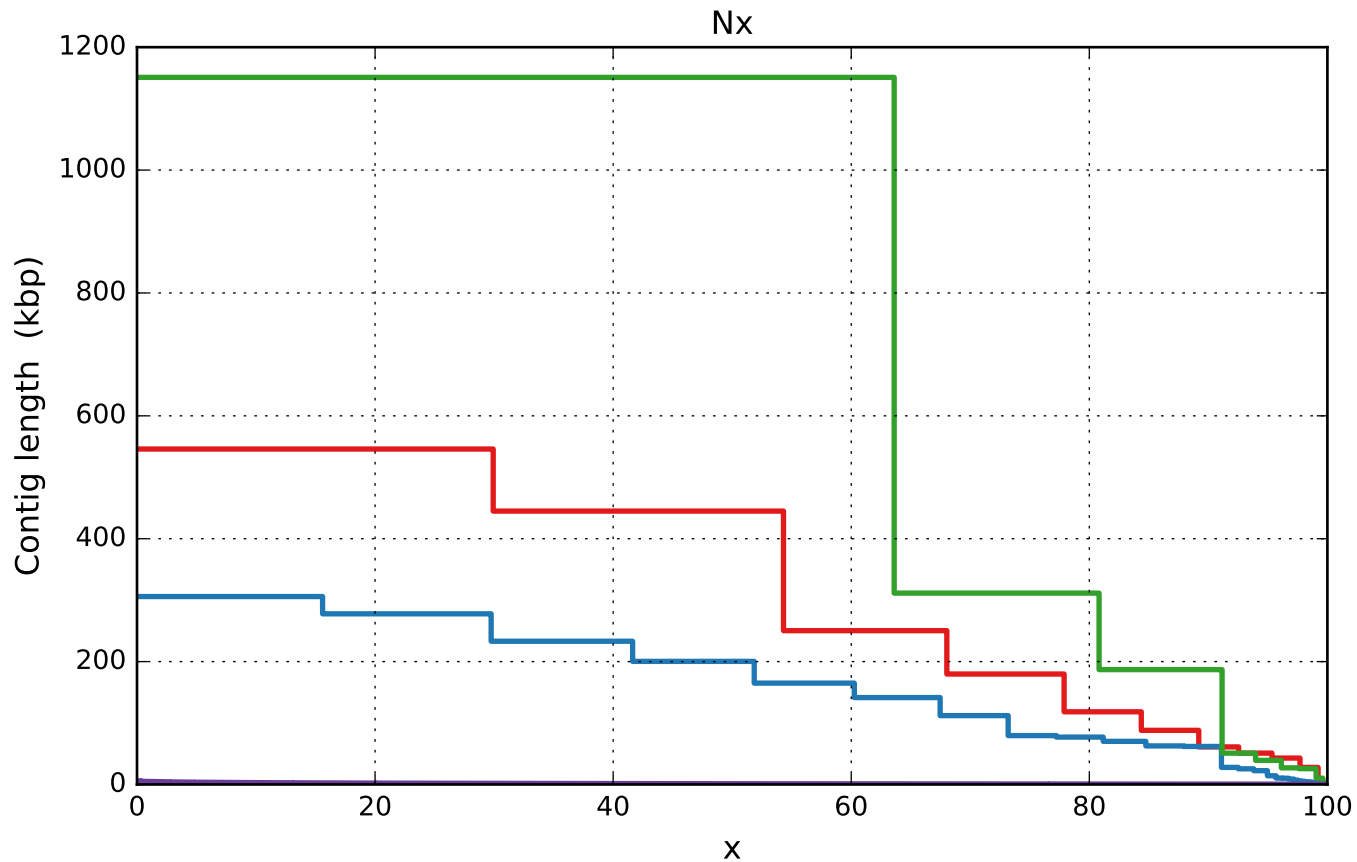
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	15	33	74	10
# relocations	15	32	74	10
# translocations	0	0	0	0
# inversions	0	1	0	0
# misassembled contigs	7	13	5	10
Misassembled contigs length	1603170	1761164	1566127	14304
# local misassemblies	42	56	32	14
# mismatches	20914	39254	36839	24176
# indels	970	1366	1130	737
# short indels	898	1241	1056	689
# long indels	72	125	74	48
Indels length	2458	3936	2486	1593

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Unaligned report

	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	1	18	0	379
Fully unaligned length	2293	83381	0	421902
# partially unaligned contigs	1	4	5	98
# with misassembly	0	1	3	5
# both parts are significant	1	2	3	18
Partially unaligned length	1465	16962	121292	60247
# N's	1086	1127	693	1471

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).

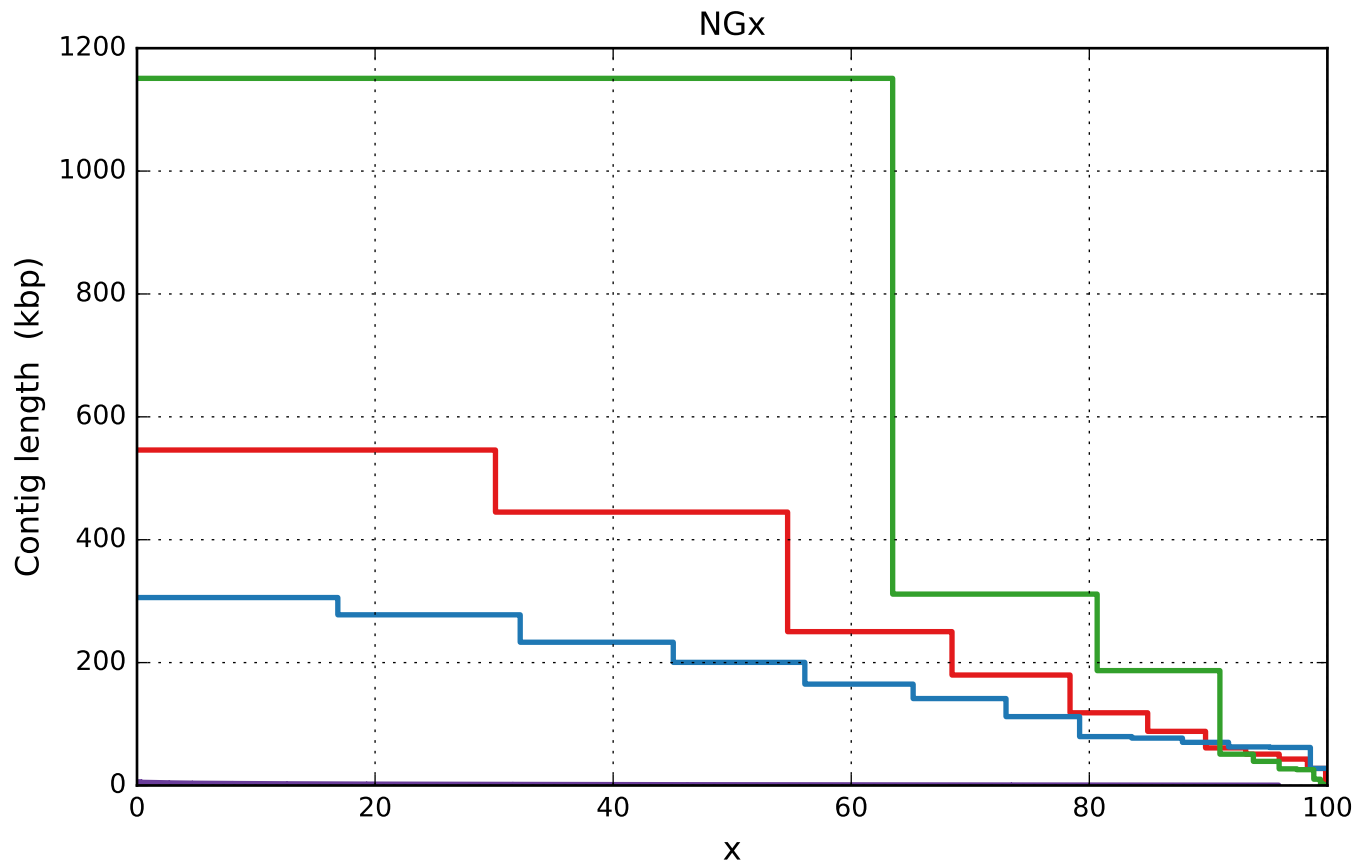


M05964_contigs

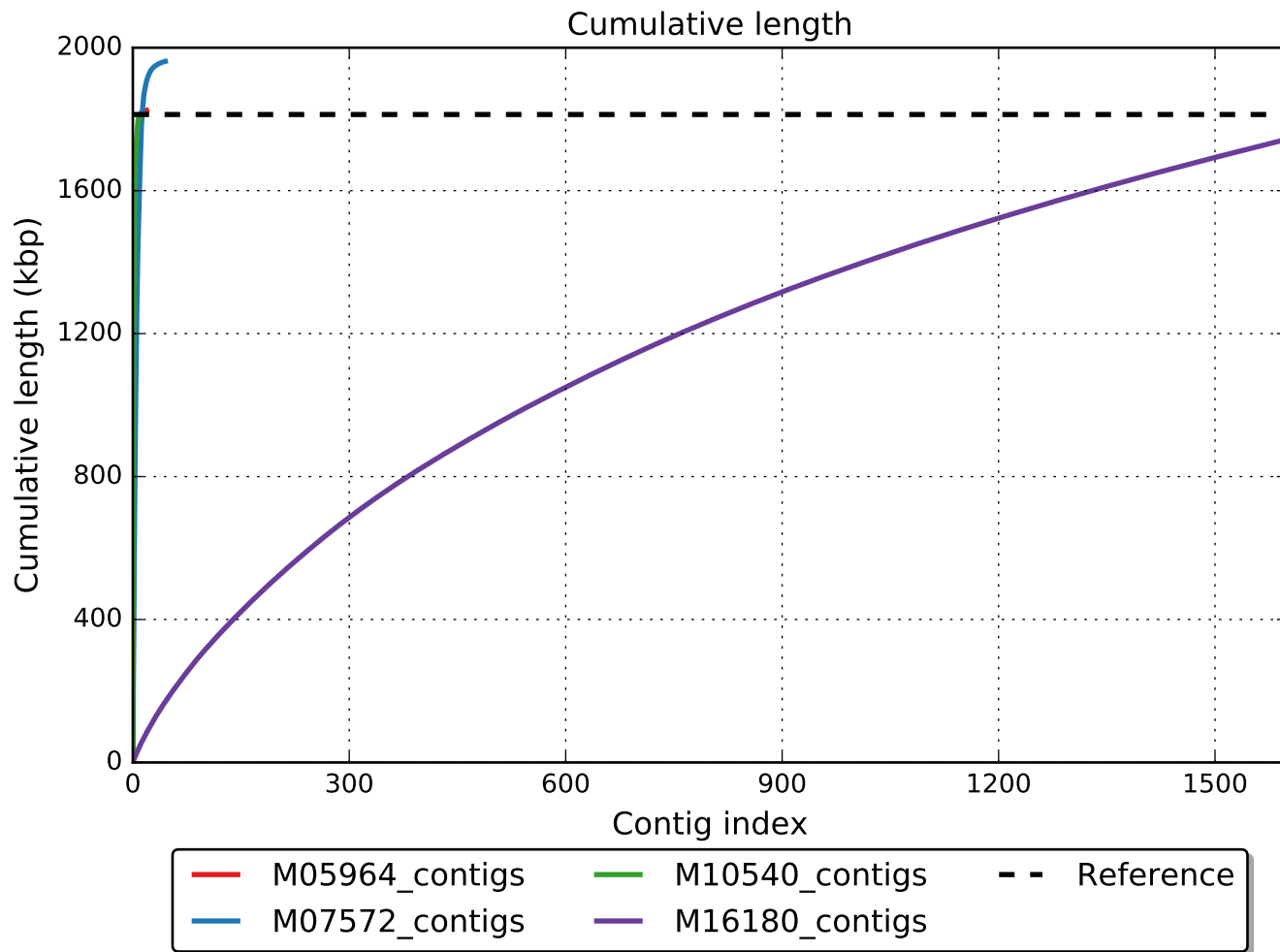
M10540_contigs

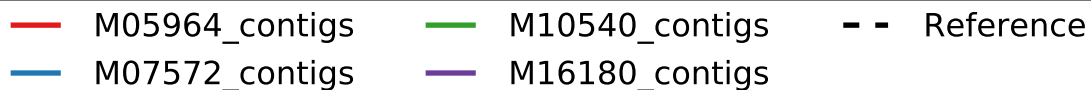
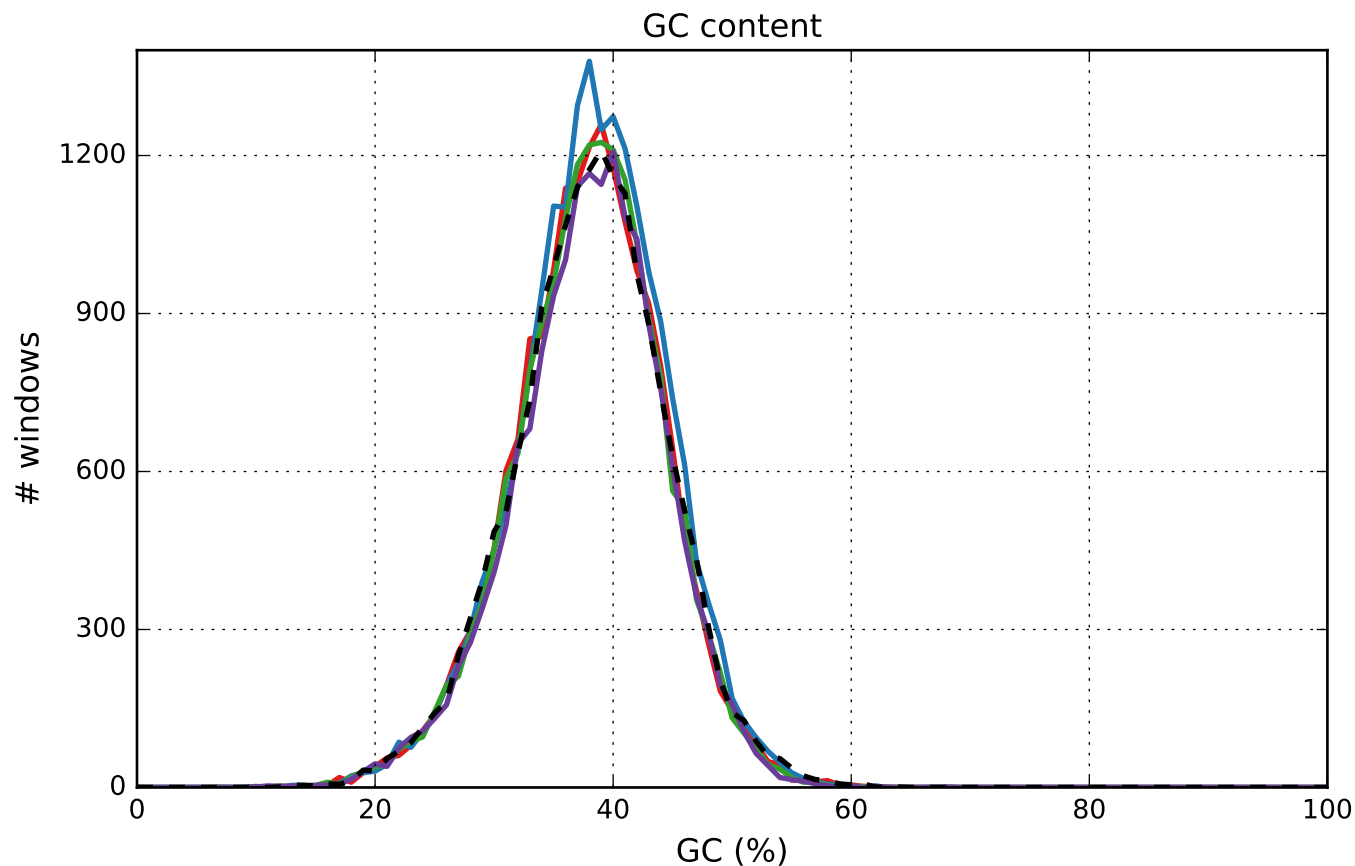
M16180_contigs

M07572_contigs

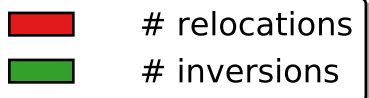
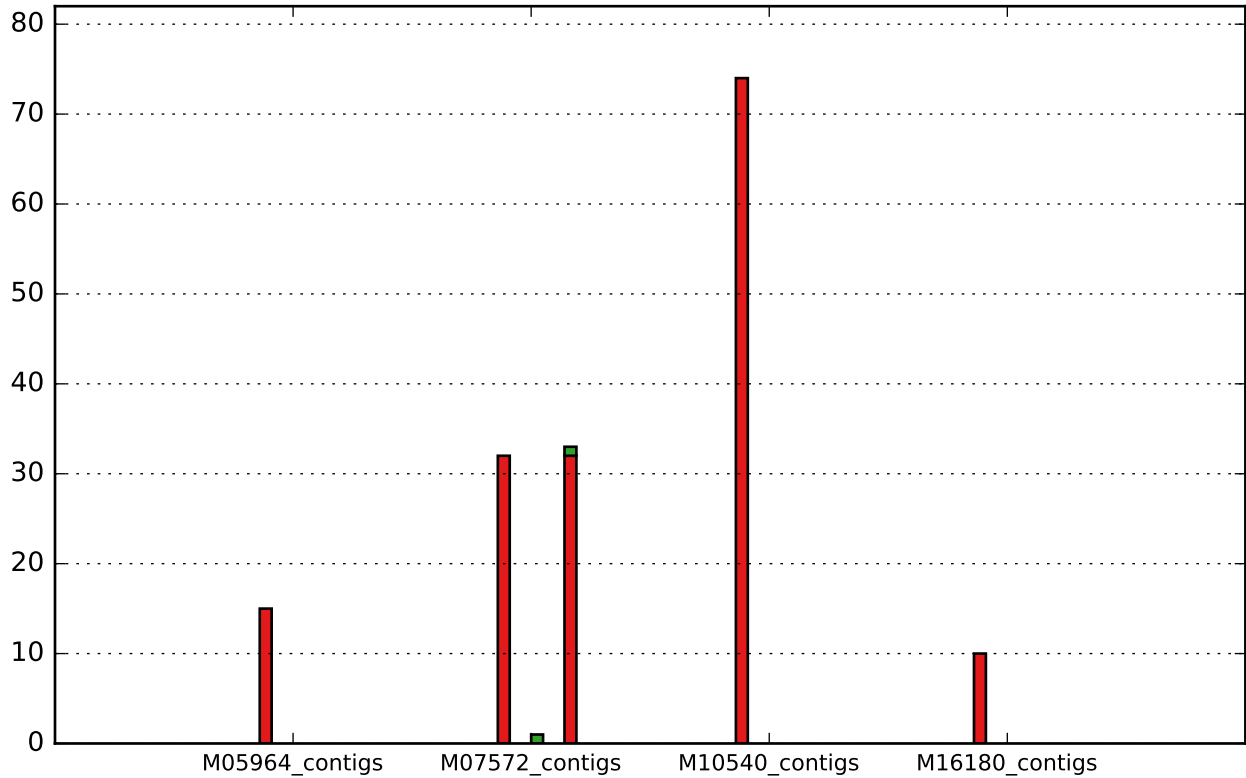


— M05964_contigs — M10540_contigs — M16180_contigs
— M07572_contigs

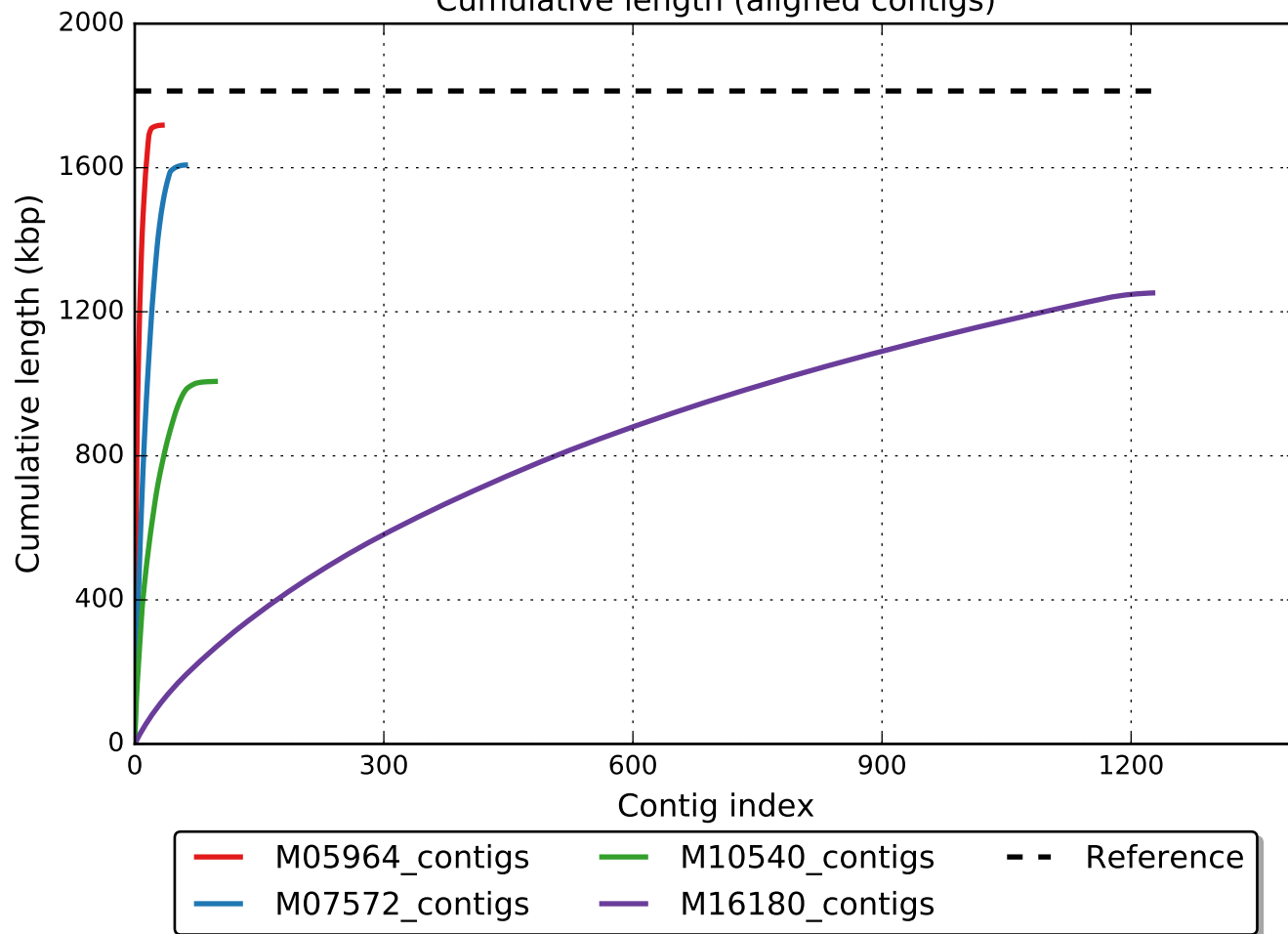




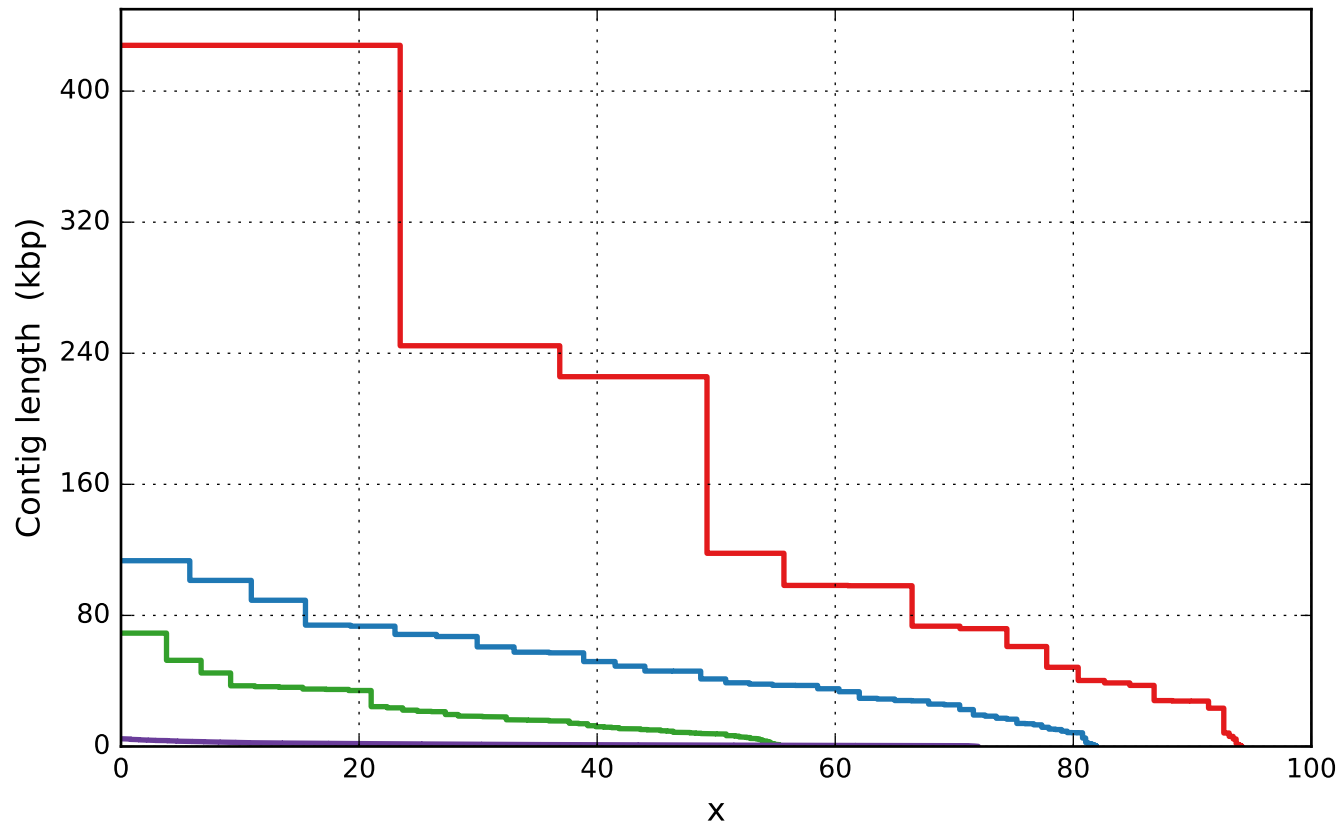
Misassemblies



Cumulative length (aligned contigs)

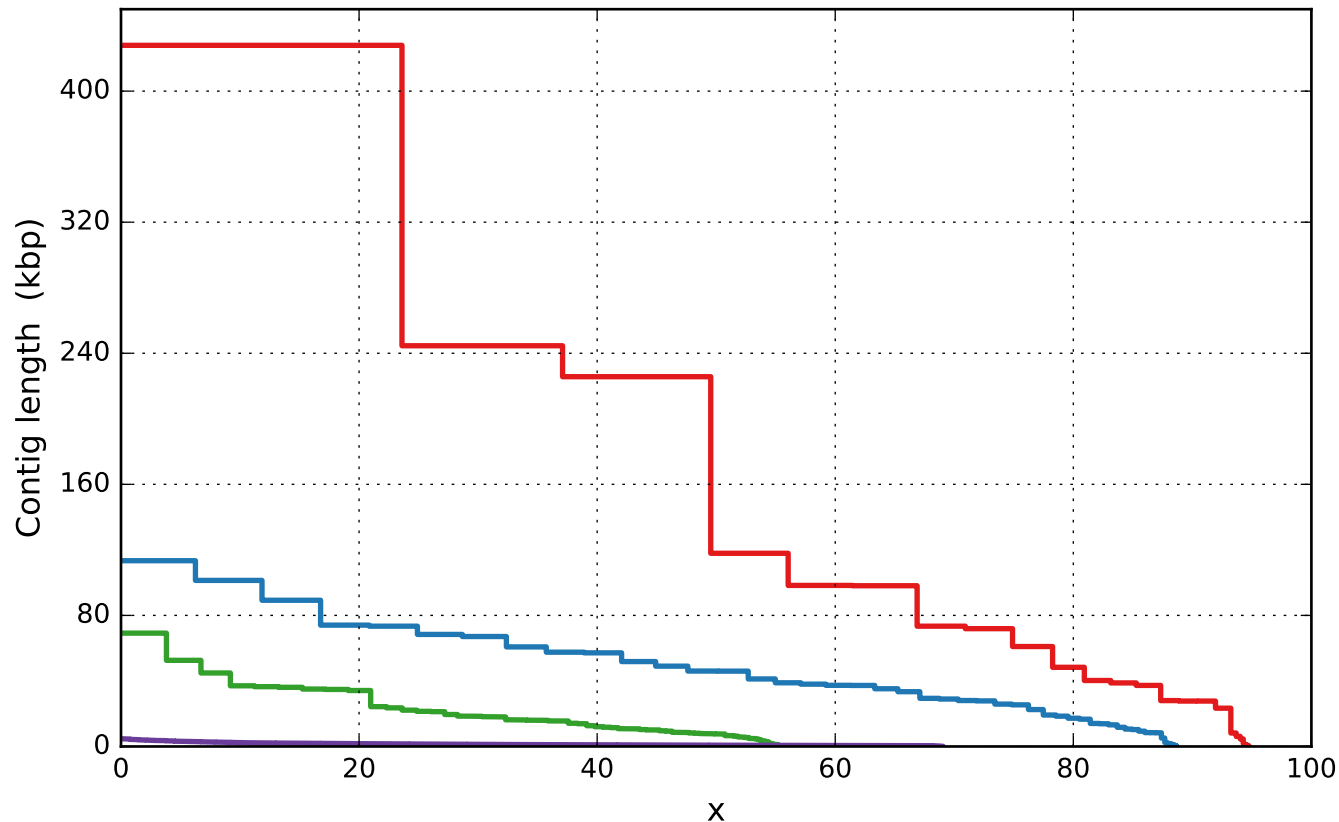


NAx



M05964_contigs M10540_contigs M16180_contigs
M07572_contigs

NGAx



— M05964_contigs — M10540_contigs — M16180_contigs
— M07572_contigs

