

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	1932306	1932306	1932306	1932306
GC (%)	37.88	38.25	37.91	38.00
Reference GC (%)	38.08	38.08	38.08	38.08
N50	444952	200368	1150911	1206
NG50	444952	200368	1150911	1100
N75	179754	79547	311459	786
NG75	118299	79547	311459	670
L50	2	4	1	437
LG50	2	4	1	521
L75	4	8	2	884
LG75	5	8	2	1086
# misassemblies	53	32	93	11
# misassembled contigs	10	13	8	10
Misassembled contigs length	1810330	1777661	1795764	19454
# local misassemblies	58	59	35	15
# unaligned contigs	2 + 0 part	19 + 4 part	0 + 2 part	339 + 118 part
Unaligned length	8340	141685	564	422863
Genome fraction (%)	84.334	83.808	57.070	62.818
Duplication ratio	1.115	1.124	1.640	1.084
# N's per 100 kbp	59.52	57.45	38.30	84.60
# mismatches per 100 kbp	2511.07	2356.82	3655.55	2053.75
# indels per 100 kbp	62.16	61.94	85.60	40.12
Largest alignment	207278	140619	58344	4706
NA50	52826	40868	9573	874
NGA50	39404	40868	7127	777
NA75	20179	16984	-	339
NGA75	16539	21831	-	-
LA50	10	12	41	554
LGA50	11	12	48	671
LA75	25	28	-	1231
LGA75	29	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

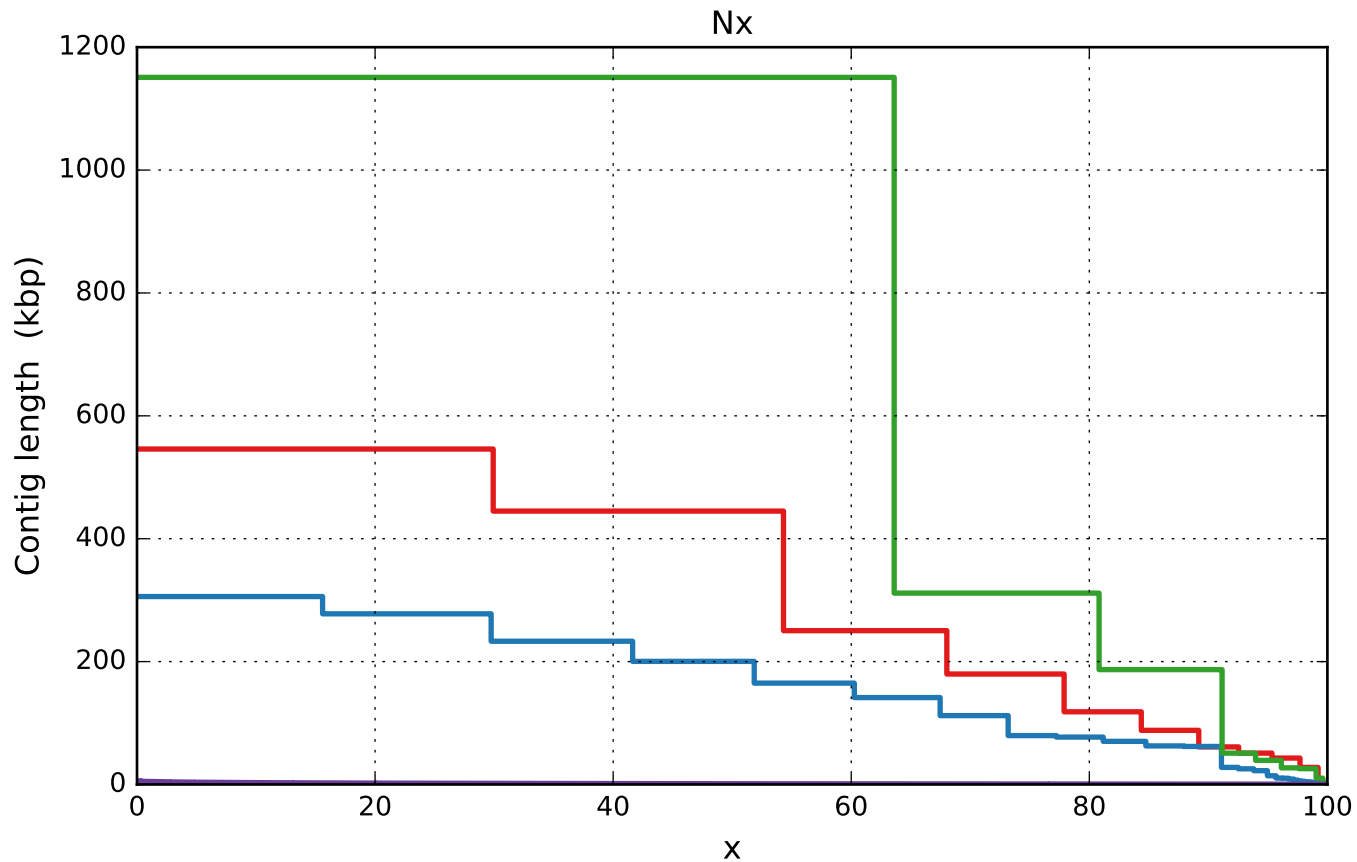
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	53	32	93	11
# relocations	51	32	93	11
# translocations	0	0	0	0
# inversions	2	0	0	0
# misassembled contigs	10	13	8	10
Misassembled contigs length	1810330	1777661	1795764	19454
# local misassemblies	58	59	35	15
# mismatches	40920	38167	40312	24929
# indels	1013	1003	944	487
# short indels	897	869	861	433
# long indels	116	134	83	54
Indels length	3319	3459	2441	1509

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).

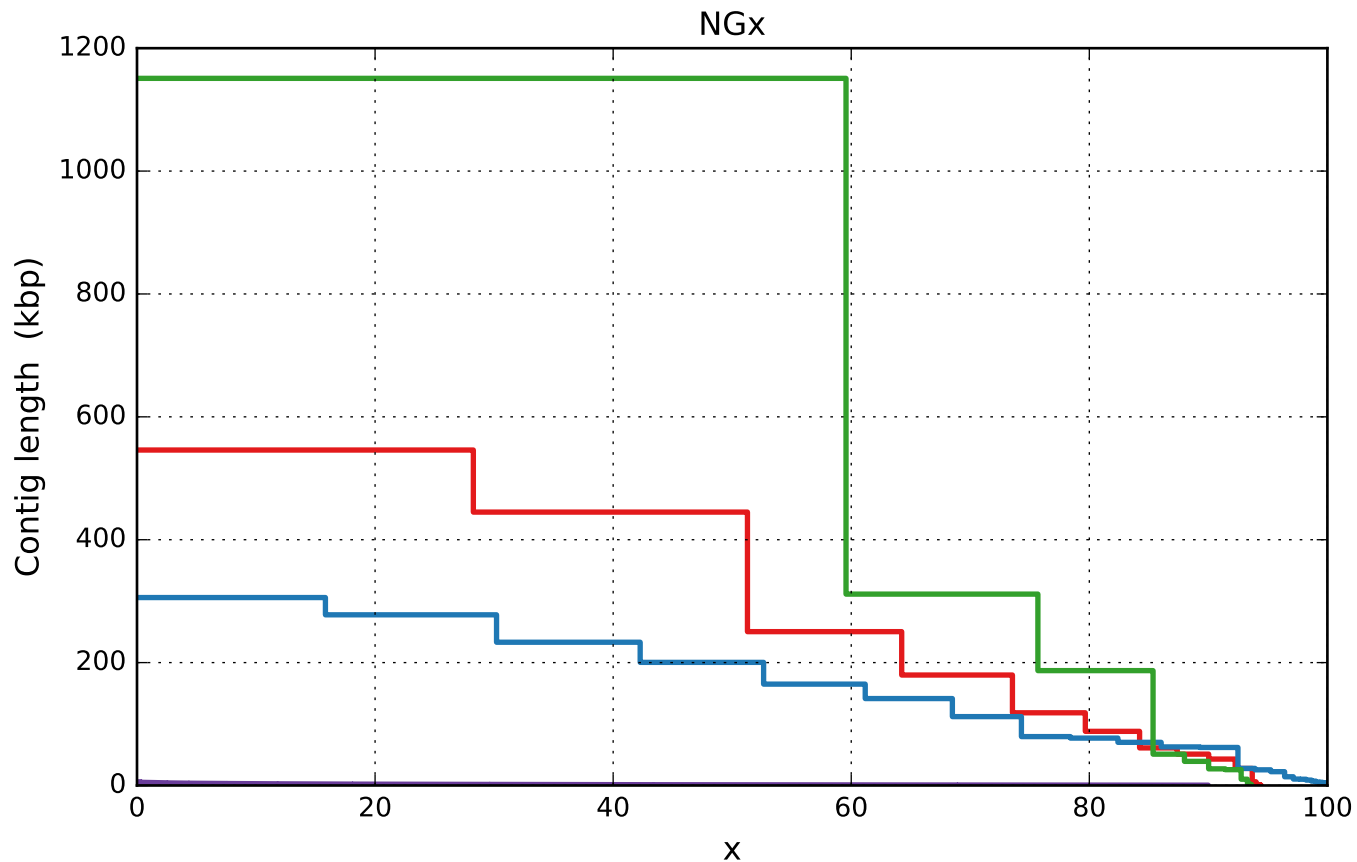
Unaligned report

	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	2	19	0	339
Fully unaligned length	8340	94767	0	364124
# partially unaligned contigs	0	4	2	118
# with misassembly	0	1	0	2
# both parts are significant	0	2	0	17
Partially unaligned length	0	46918	564	58739
# 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

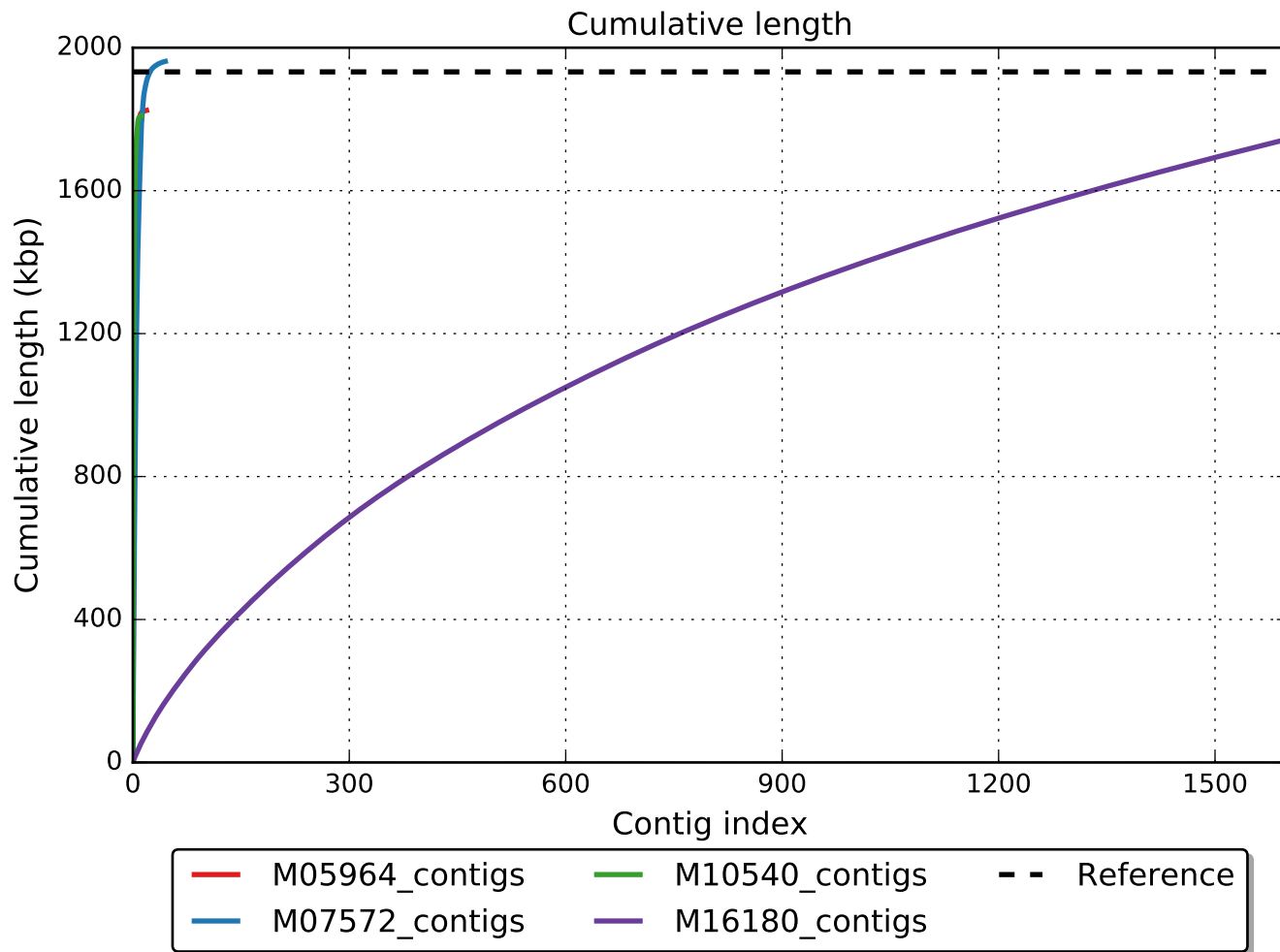


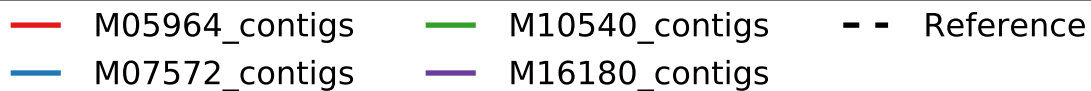
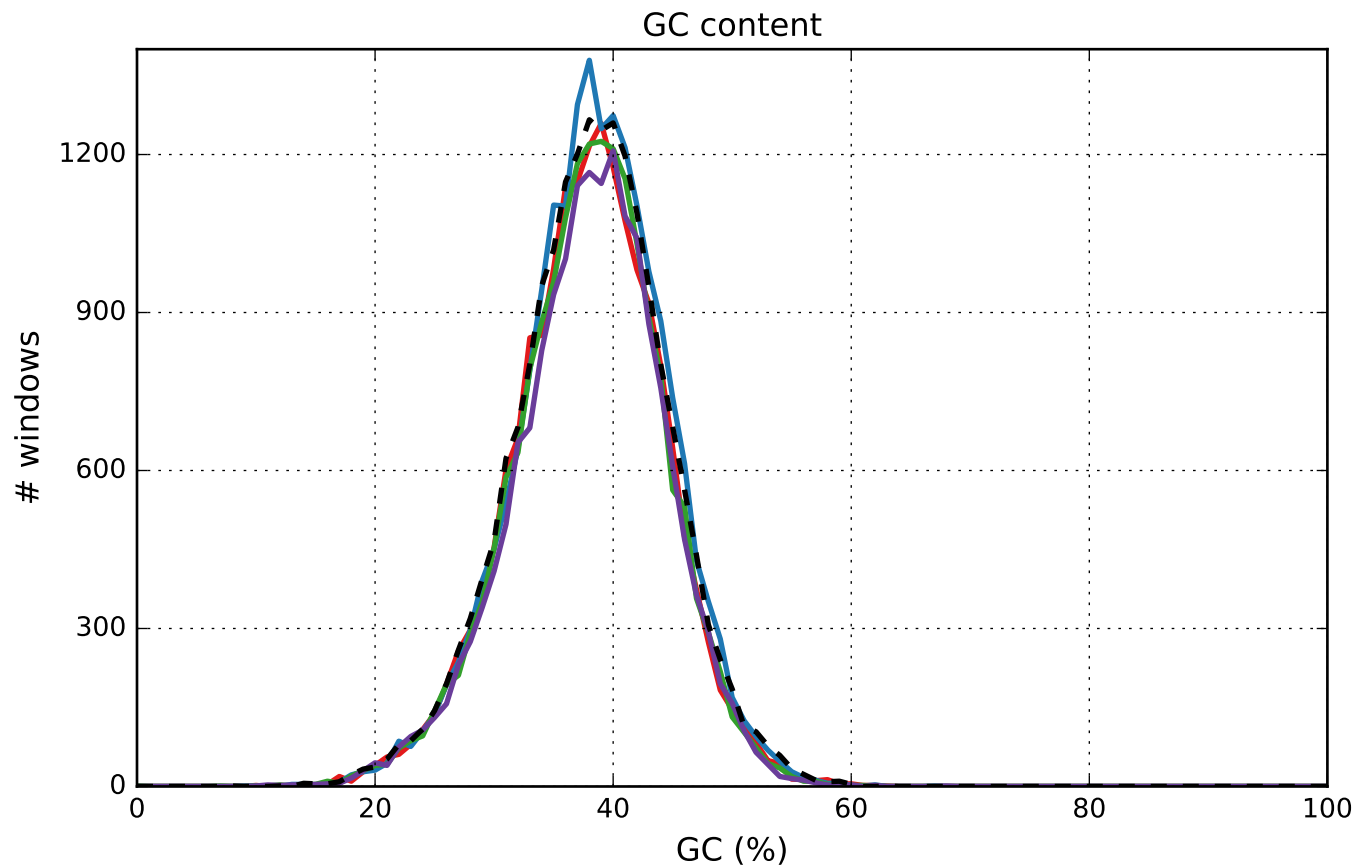
M05964_contigs

M10540_contigs

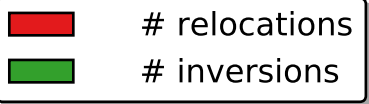
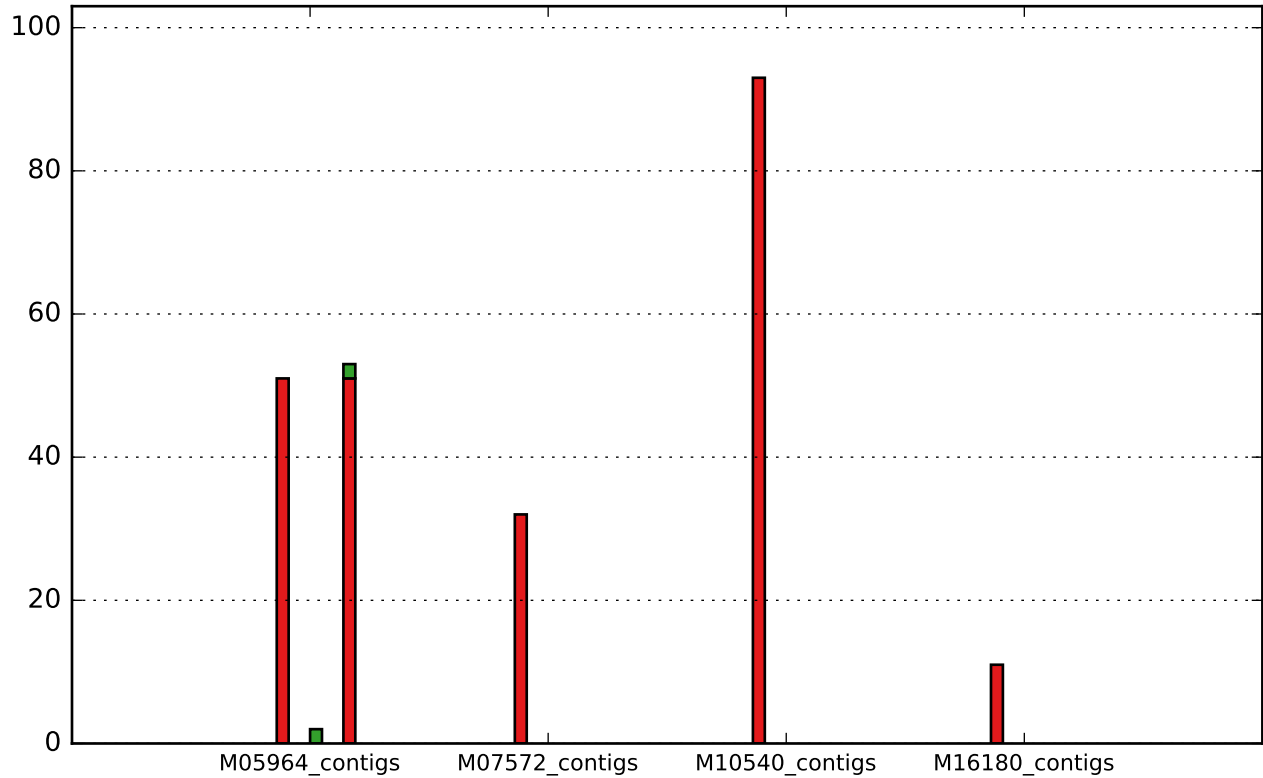
M16180_contigs

M07572_contigs

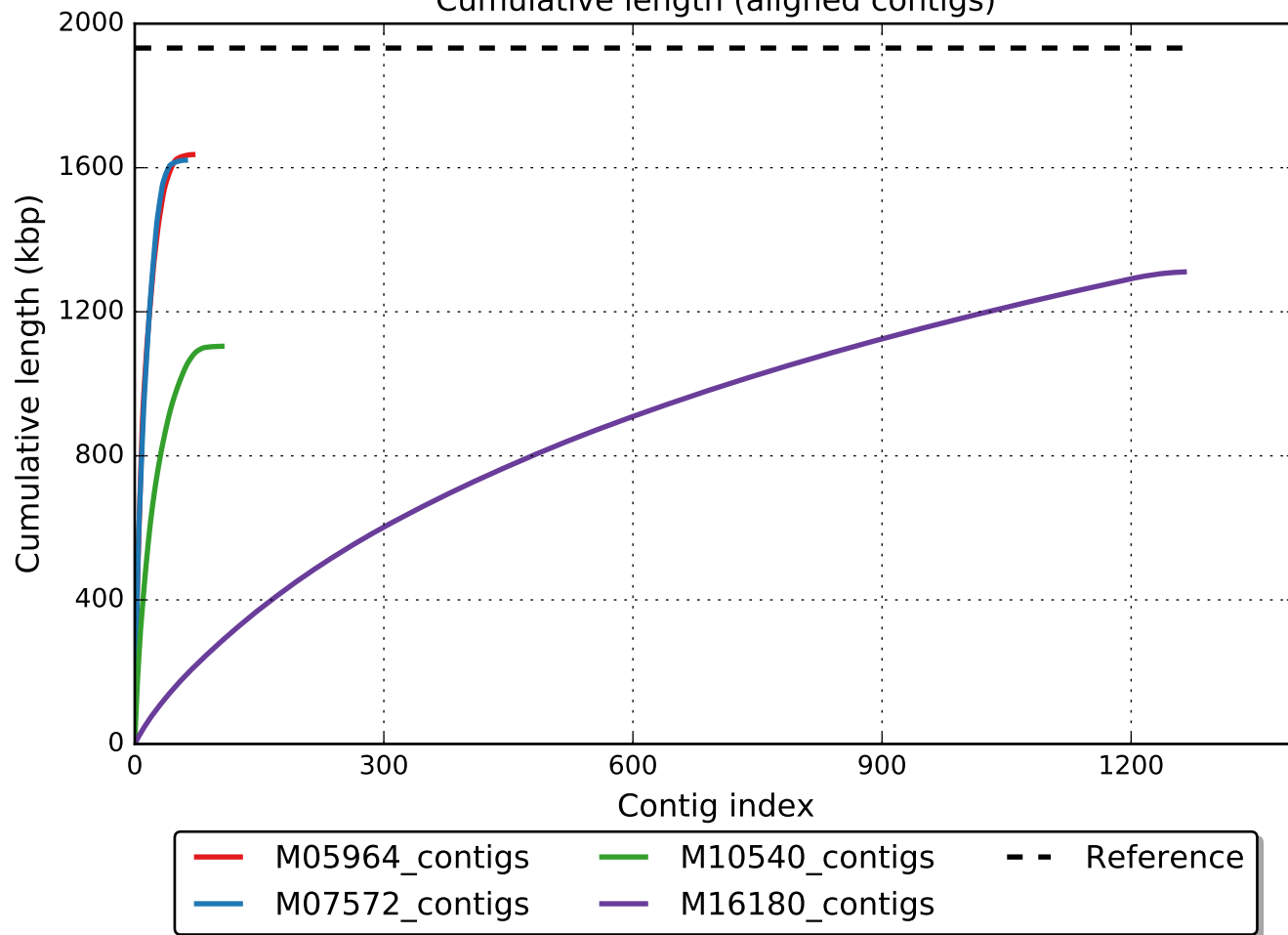




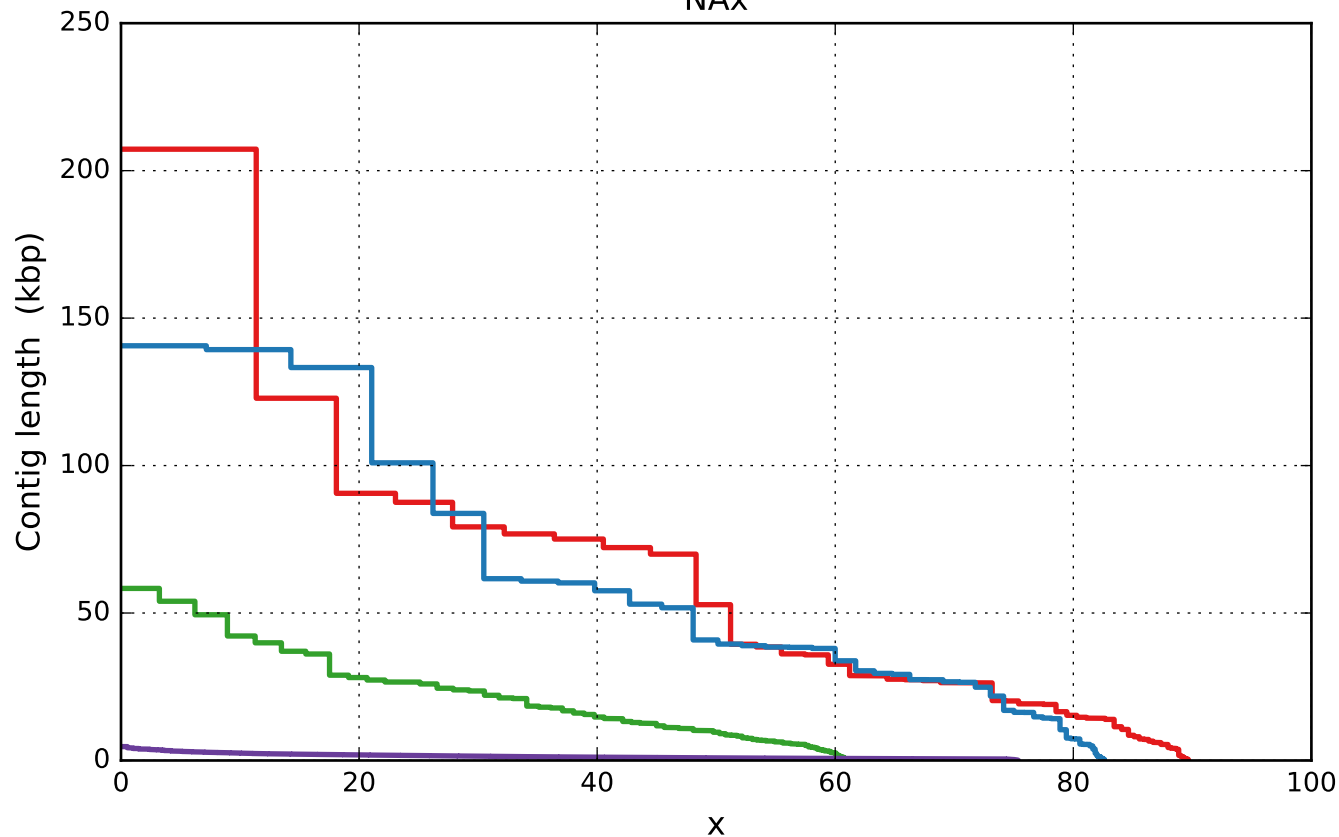
Misassemblies



Cumulative length (aligned contigs)



NAx



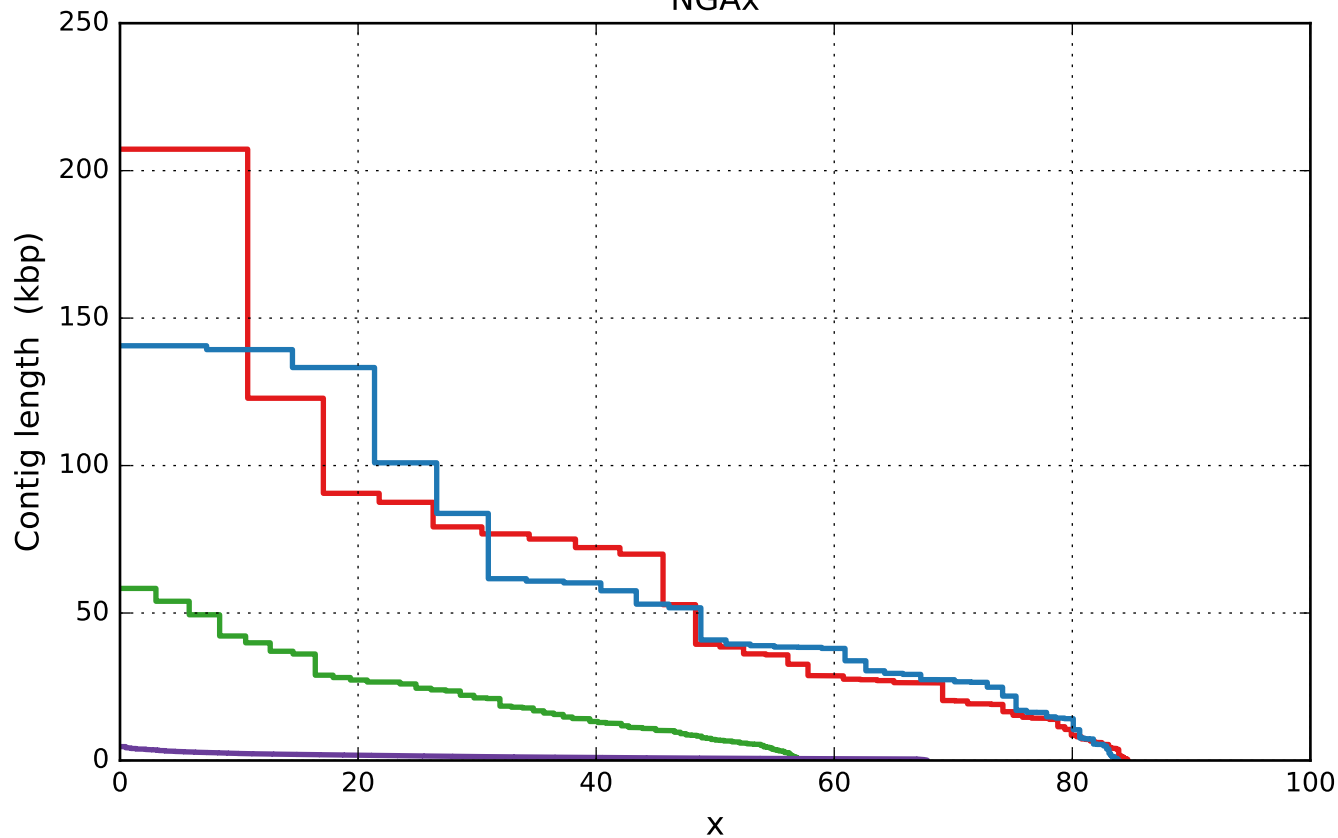
M05964_contigs

M10540_contigs

M16180_contigs

M07572_contigs

NGAx



— M05964_contigs — M10540_contigs — M16180_contigs
— M07572_contigs

