

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	2007018	2007018	2007018	2007018
GC (%)	37.88	38.25	37.91	38.00
Reference GC (%)	38.22	38.22	38.22	38.22
N50	444952	200368	1150911	1206
NG50	250374	200368	1150911	1058
N75	179754	79547	311459	786
NG75	118299	79547	186938	629
L50	2	4	1	437
LG50	3	4	1	556
L75	4	8	2	884
LG75	5	8	3	1172
# misassemblies	70	79	9	14
# misassembled contigs	10	16	2	13
Misassembled contigs length	1810330	1791055	214010	22352
# local misassemblies	64	68	5	26
# unaligned contigs	2 + 0 part	10 + 8 part	0 + 8 part	355 + 143 part
Unaligned length	8340	117904	915166	472443
Genome fraction (%)	75.091	79.054	39.907	58.012
Duplication ratio	1.205	1.162	1.117	1.088
# N's per 100 kbp	59.52	57.45	38.30	84.60
# mismatches per 100 kbp	2681.59	2590.22	3888.45	2192.11
# indels per 100 kbp	76.44	76.20	92.89	50.50
Largest alignment	117001	120770	40371	5147
NA50	27278	28012	-	819
NGA50	23310	27382	-	689
NA75	11125	8665	-	-
NGA75	1212	6882	-	-
LA50	18	19	-	595
LGA50	21	20	-	774
LA75	43	49	-	-
LGA75	70	53	-	-

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

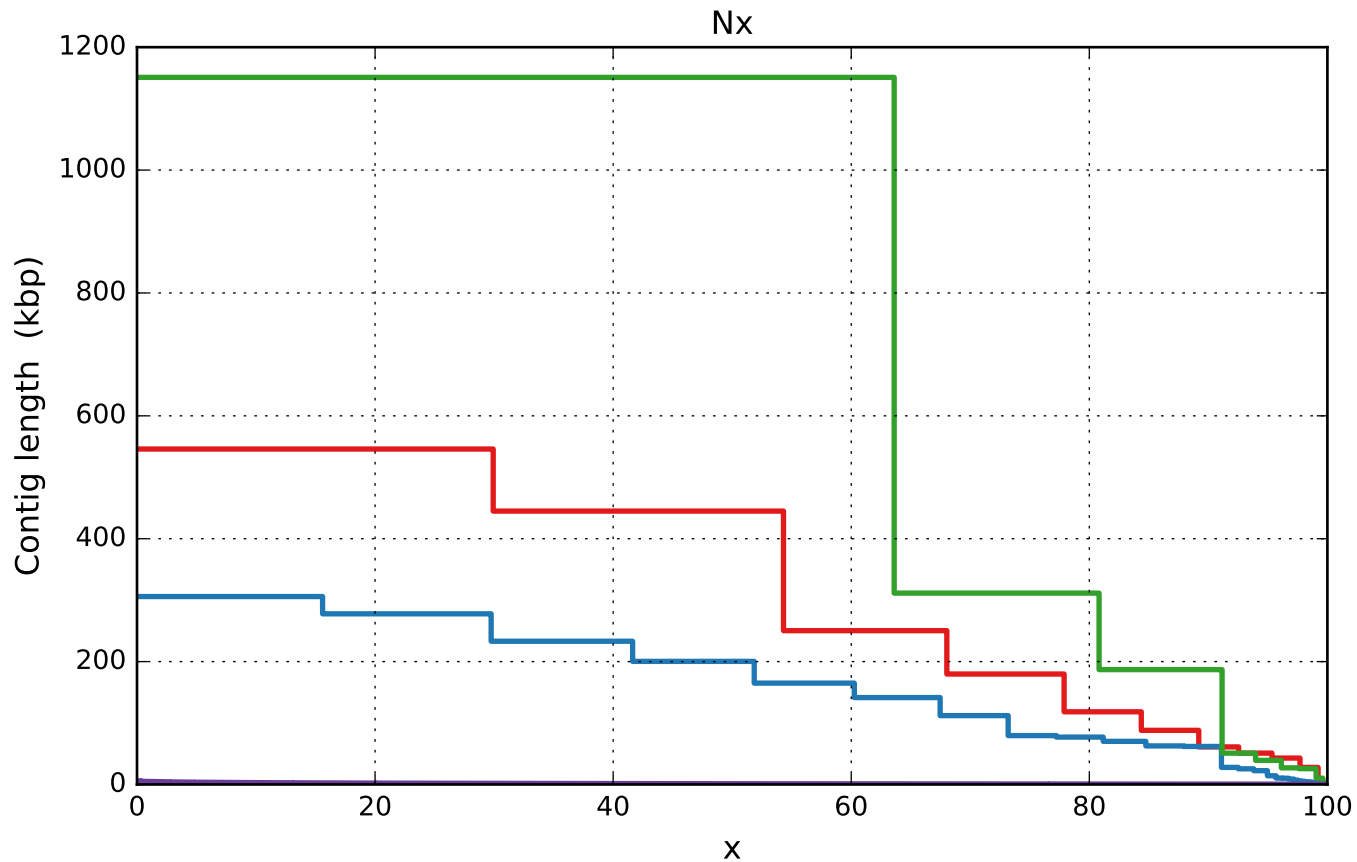
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	70	79	9	14
# relocations	69	79	9	14
# translocations	0	0	0	0
# inversions	1	0	0	0
# misassembled contigs	10	16	2	13
Misassembled contigs length	1810330	1791055	214010	22352
# local misassemblies	64	68	5	26
# mismatches	40414	41097	31144	25523
# indels	1152	1209	744	588
# short indels	1018	1064	679	530
# long indels	134	145	65	58
Indels length	3722	4035	1891	1718

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).

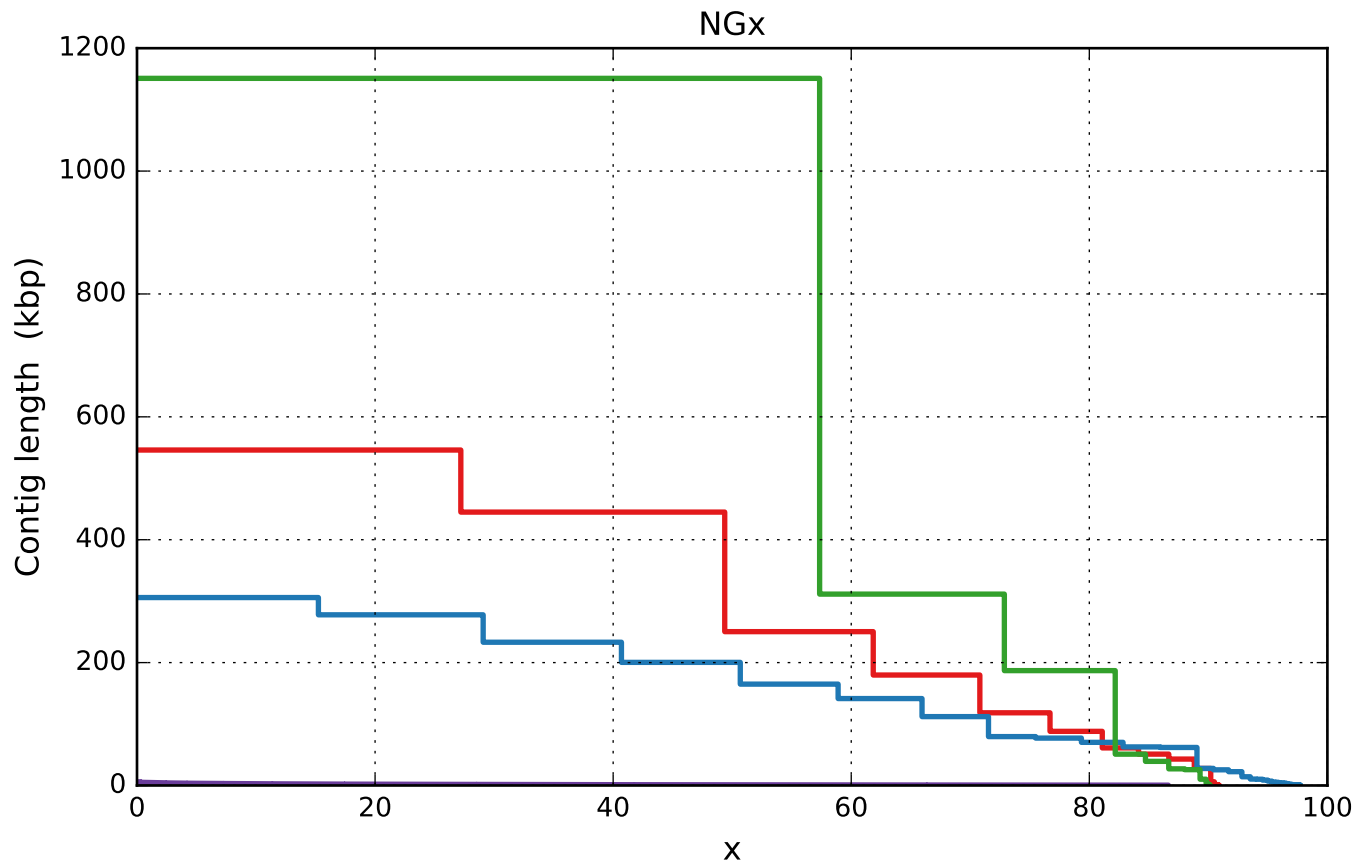
Unaligned report

	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	2	10	0	355
Fully unaligned length	8340	43825	0	381797
# partially unaligned contigs	0	8	8	143
# with misassembly	0	3	5	3
# both parts are significant	0	4	5	23
Partially unaligned length	0	74079	915166	90646
# N's	1086	1127	693	1471

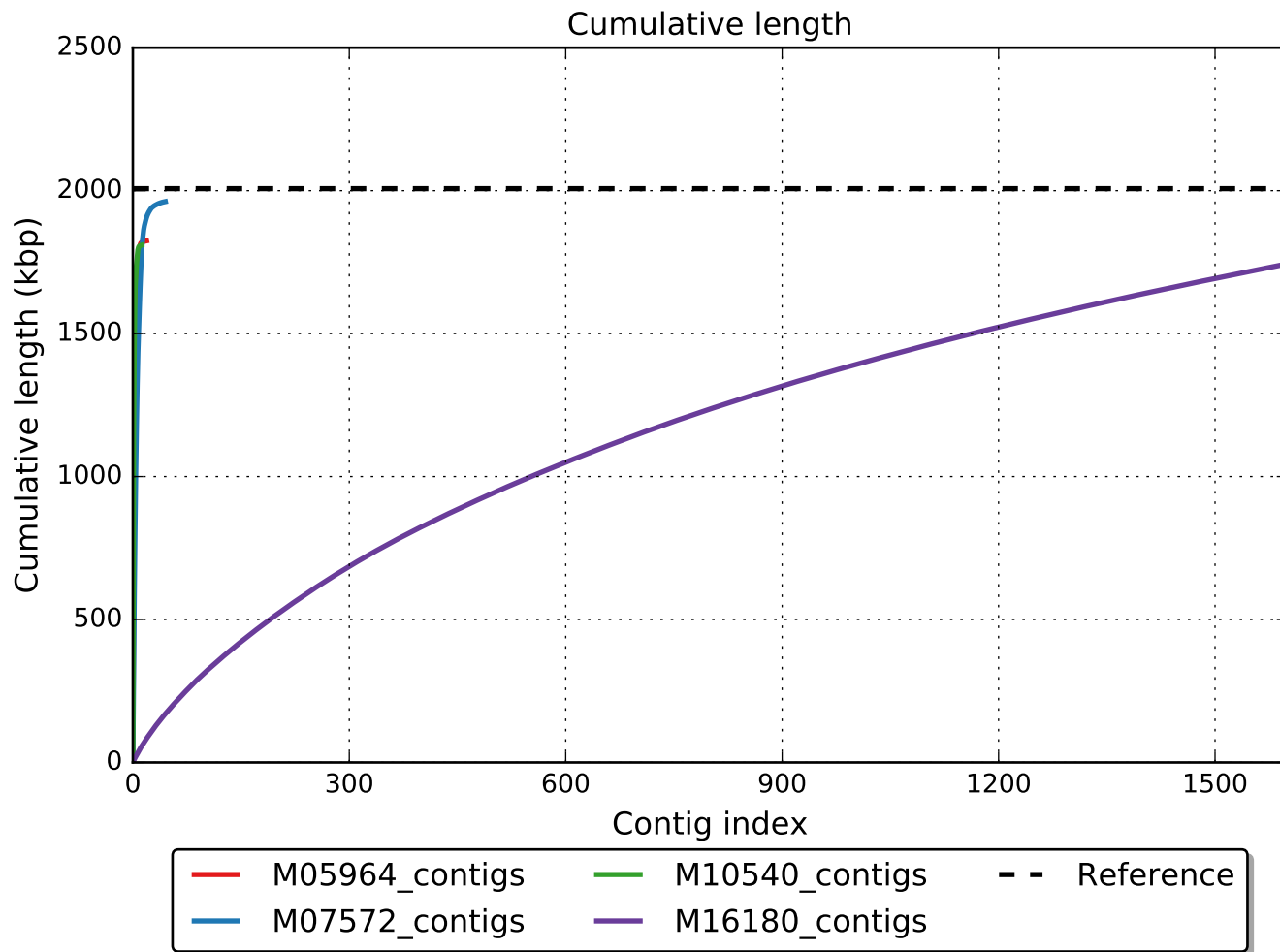
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

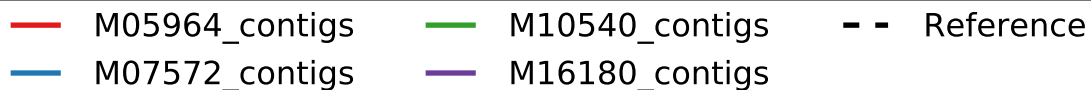
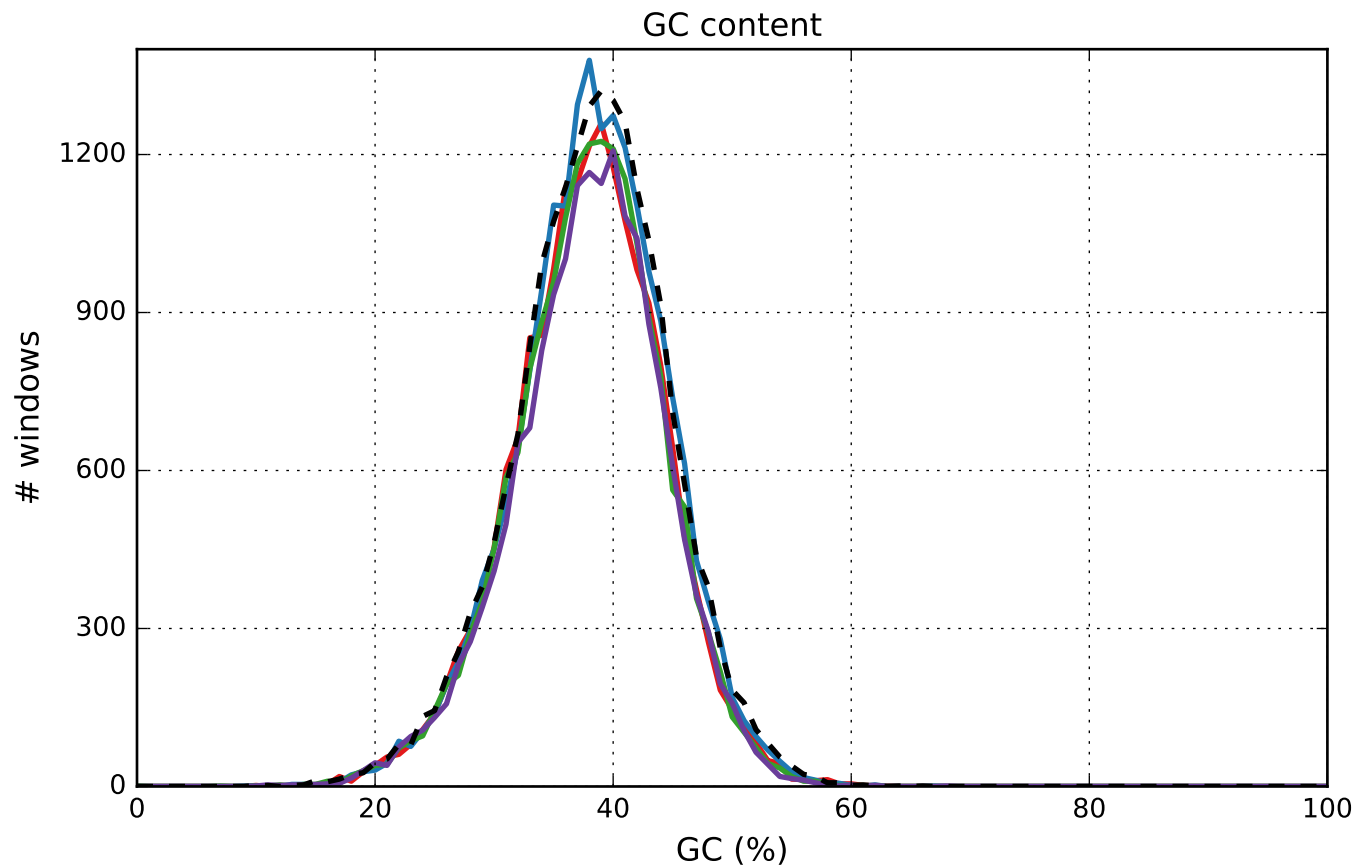


— M05964_contigs — M10540_contigs — M16180_contigs
— M07572_contigs

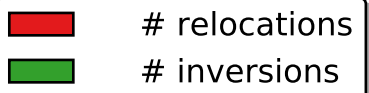
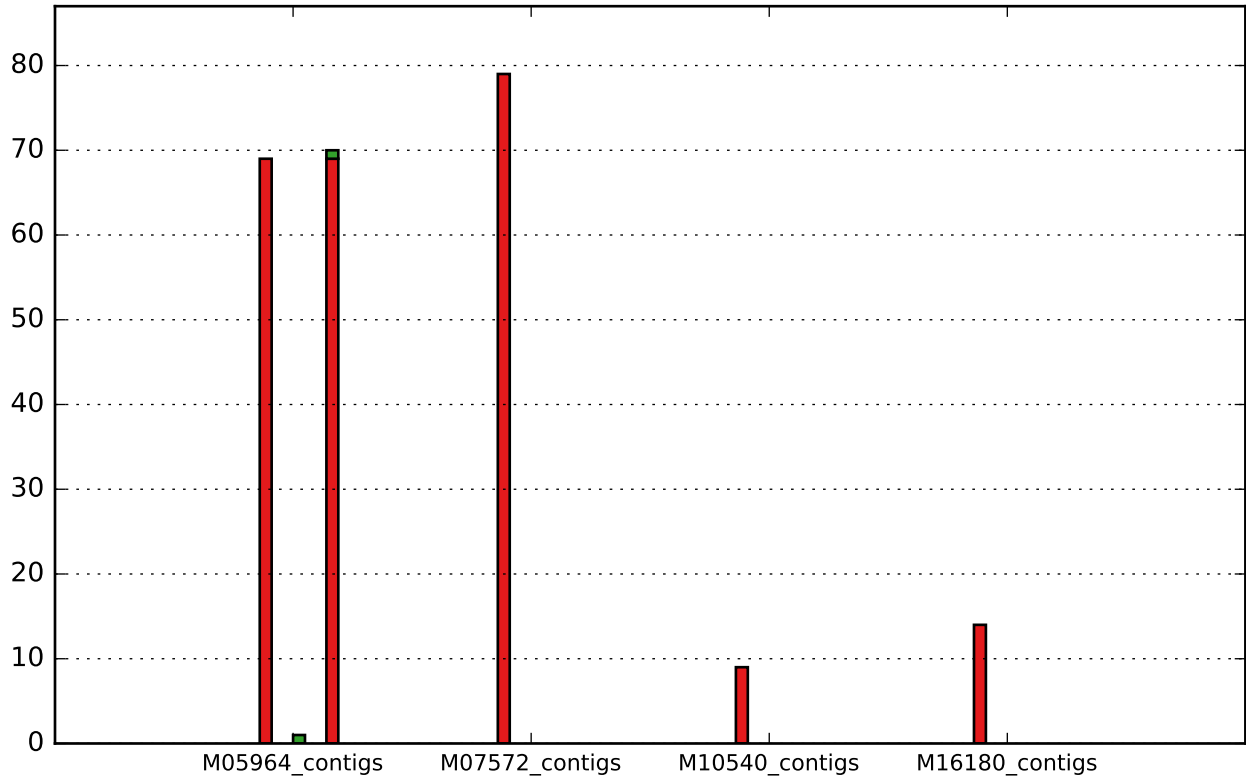


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M07572_contigs

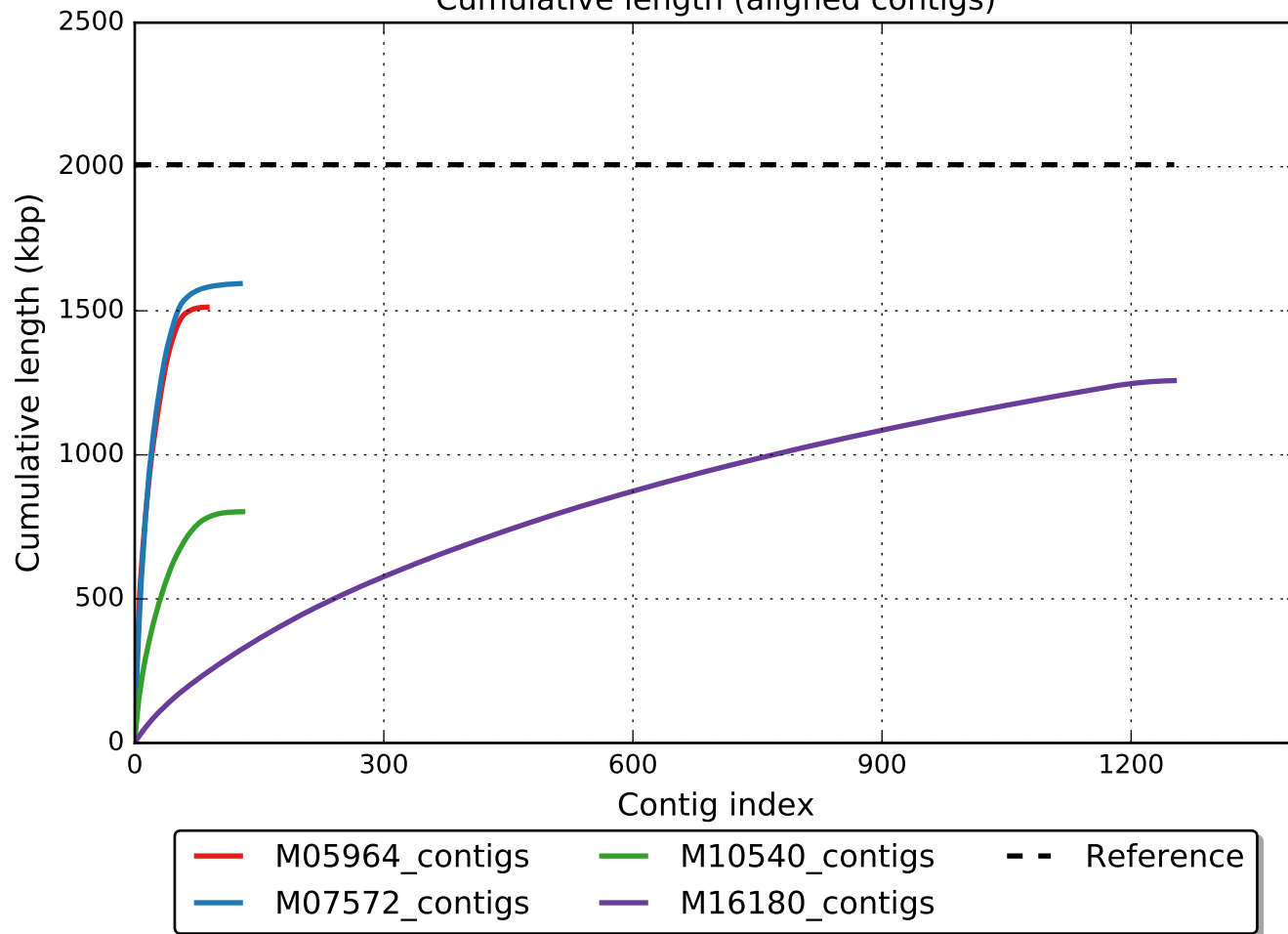




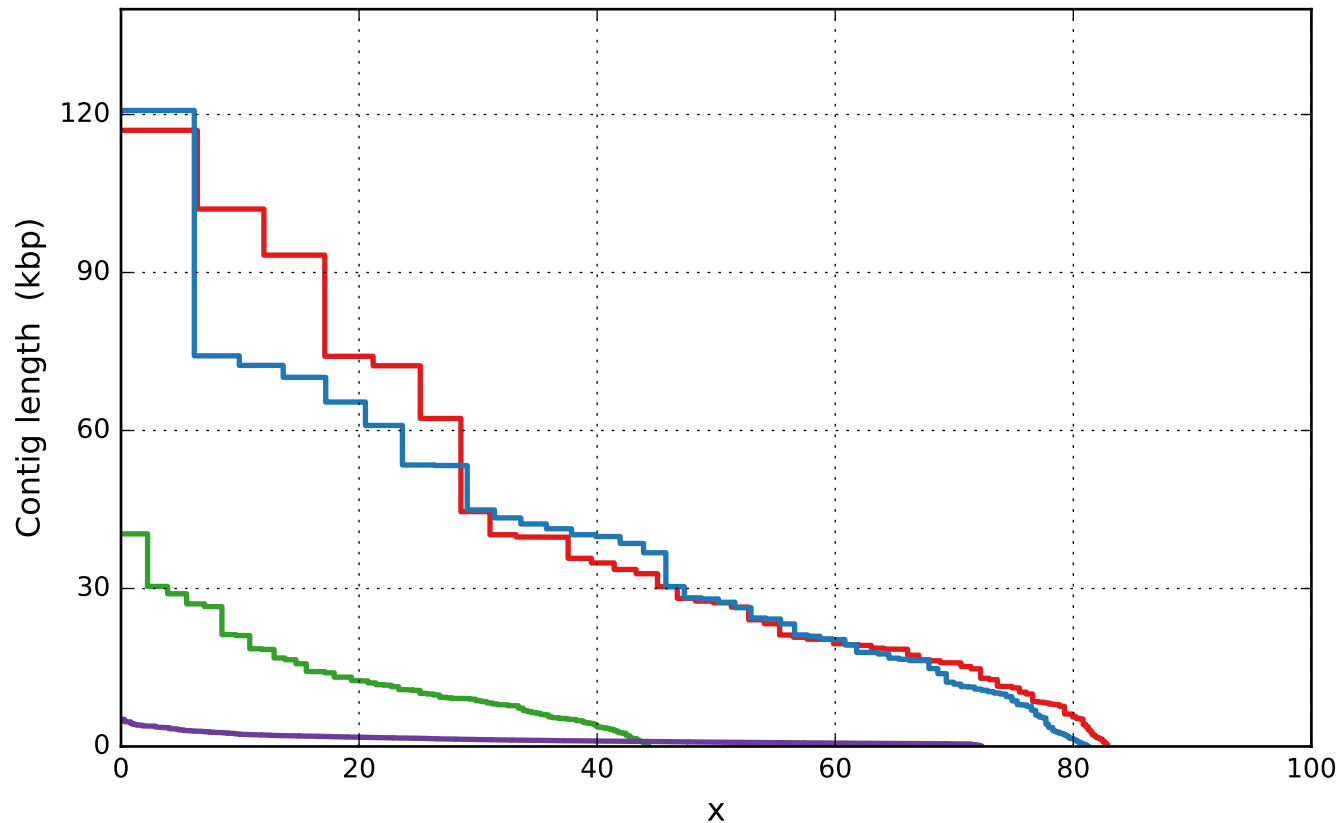
Misassemblies



Cumulative length (aligned contigs)

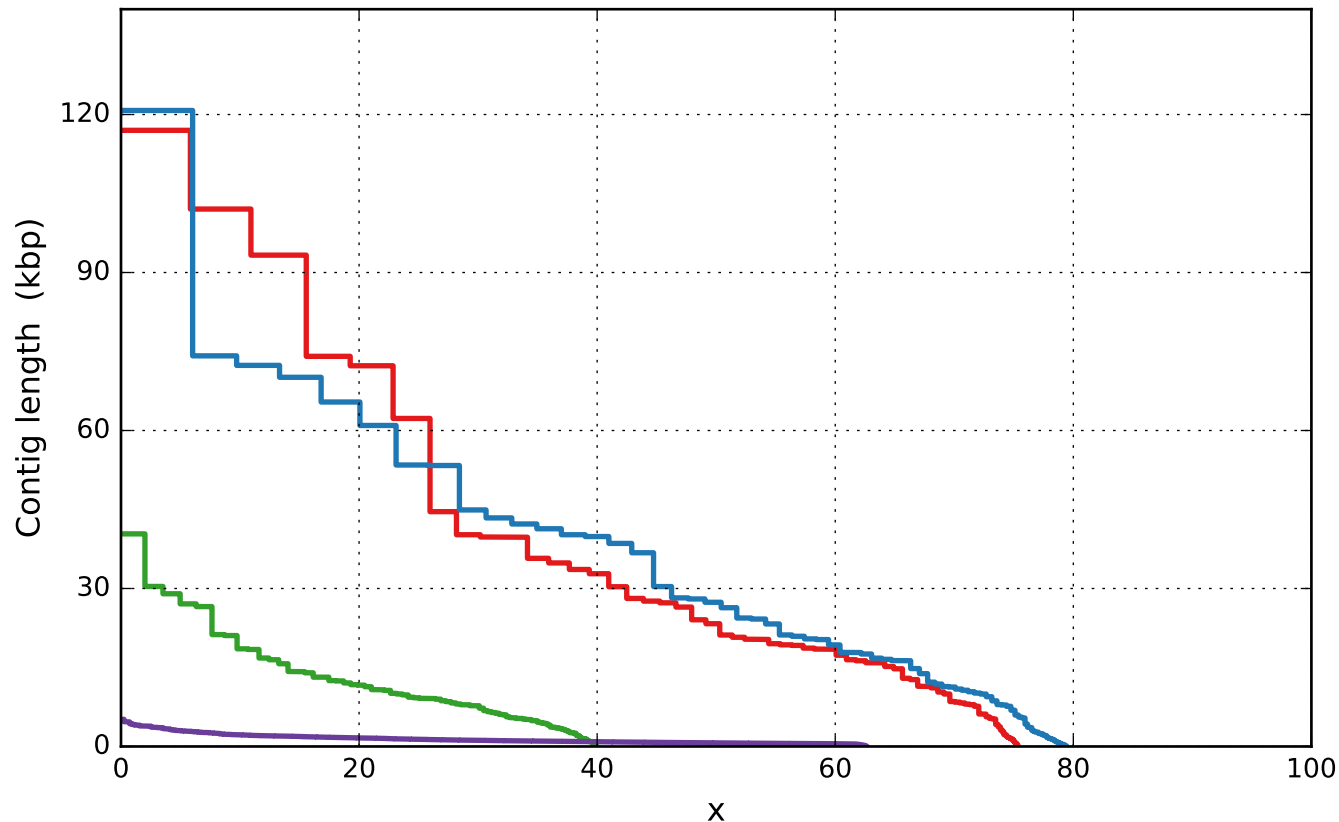


NAx



M05964_contigs M10540_contigs M16180_contigs
M07572_contigs

NGAx



— M05964_contigs — M10540_contigs — M16180_contigs
— M07572_contigs

