

# 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	1856176	1856176	1856176	1856176
GC (%)	37.88	38.25	37.91	38.00
Reference GC (%)	38.05	38.05	38.05	38.05
N50	444952	200368	1150911	1206
NG50	444952	200368	1150911	1148
N75	179754	79547	311459	786
NG75	179754	112073	311459	706
L50	2	4	1	437
LG50	2	4	1	487
L75	4	8	2	884
LG75	4	7	2	1003
# misassemblies	74	57	7	7
# misassembled contigs	7	10	1	7
Misassembled contigs length	1292094	1353473	1150911	10672
# local misassemblies	31	35	8	12
# unaligned contigs	3 + 5 part	24 + 6 part	0 + 0 part	726 + 126 part
Unaligned length	361627	412819	0	872693
Genome fraction (%)	57.382	60.271	97.243	43.515
Duplication ratio	1.374	1.384	1.002	1.072
# N's per 100 kbp	59.52	57.45	38.30	84.60
# mismatches per 100 kbp	3498.59	3600.39	34.79	3008.15
# indels per 100 kbp	84.03	84.83	3.60	52.62
Largest alignment	54188	57853	334922	5148
NA50	7557	7882	201703	-
NGA50	7176	8672	201703	-
NA75	-	-	183005	-
NGA75	-	-	183005	-
LA50	49	47	4	-
LGA50	51	40	4	-
LA75	-	-	6	-
LGA75	-	-	6	-

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

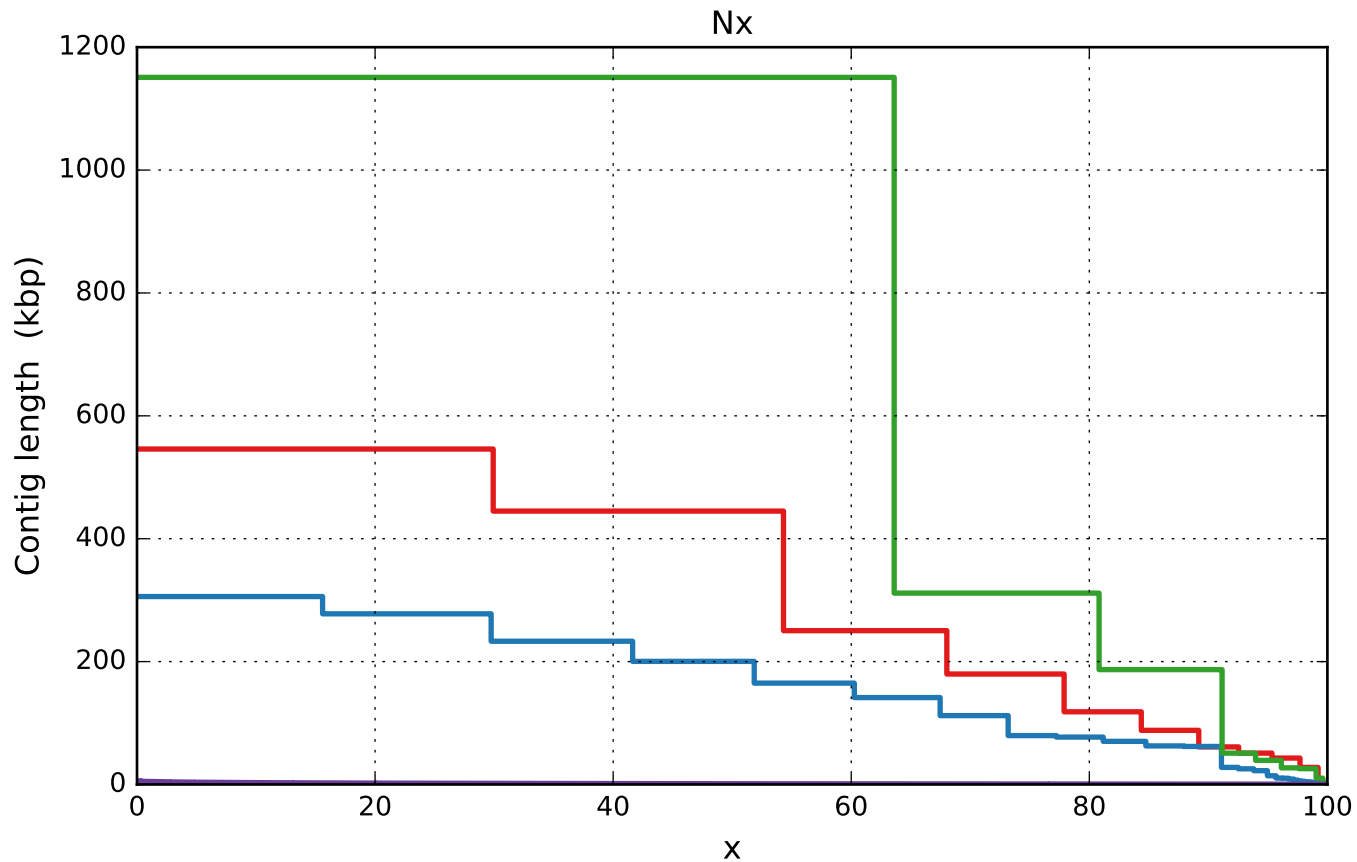
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	74	57	7	7
# relocations	74	57	6	7
# translocations	0	0	0	0
# inversions	0	0	1	0
# misassembled contigs	7	10	1	7
Misassembled contigs length	1292094	1353473	1150911	10672
# local misassemblies	31	35	8	12
# mismatches	37264	40279	628	24297
# indels	895	949	65	425
# short indels	822	868	40	398
# long indels	73	81	25	27
Indels length	2227	2329	673	863

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

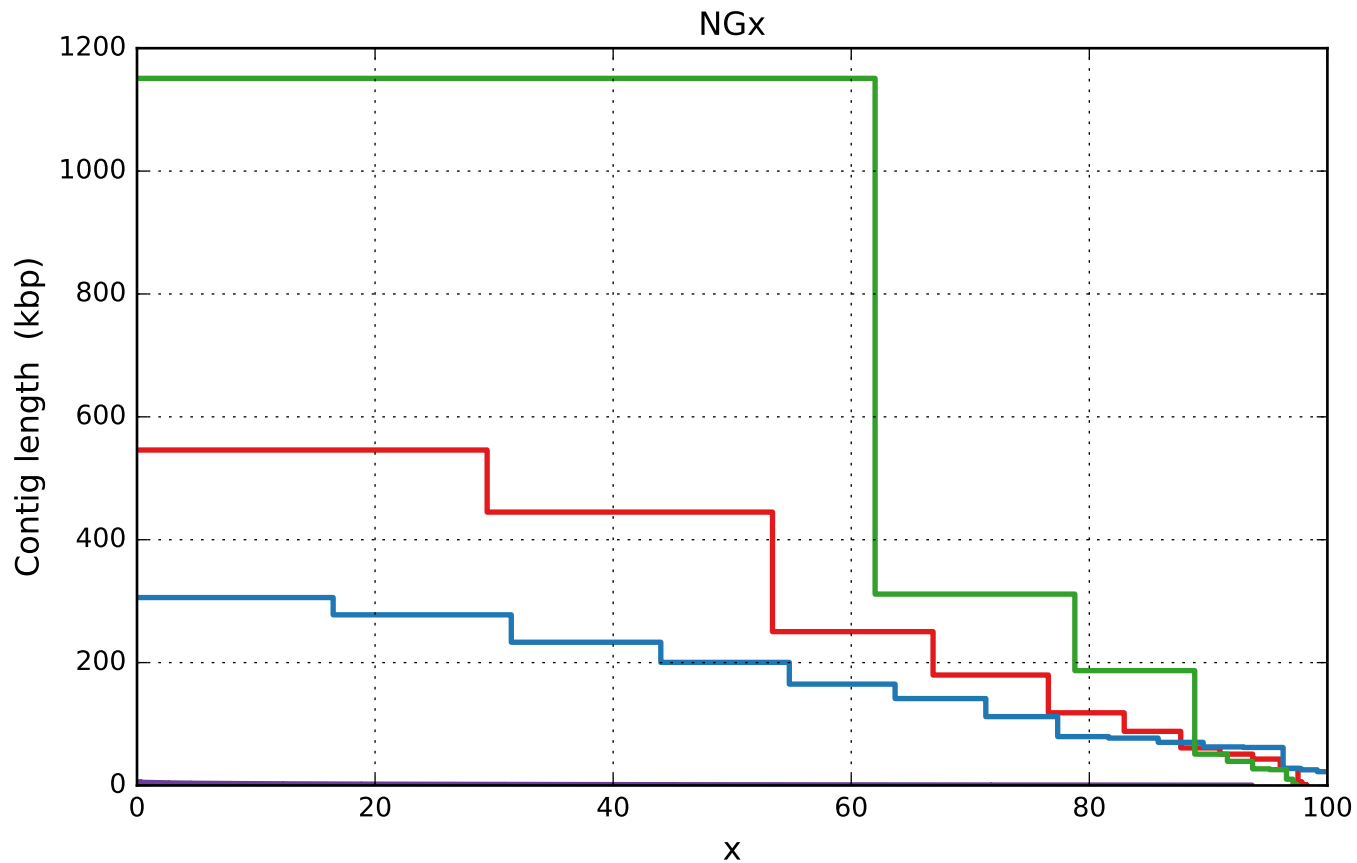
## Unaligned report

	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	3	24	0	726
Fully unaligned length	9652	104307	0	790855
# partially unaligned contigs	5	6	0	126
# with misassembly	3	5	0	6
# both parts are significant	3	4	0	28
Partially unaligned length	351975	308512	0	81838
# N's	1086	1127	693	1471

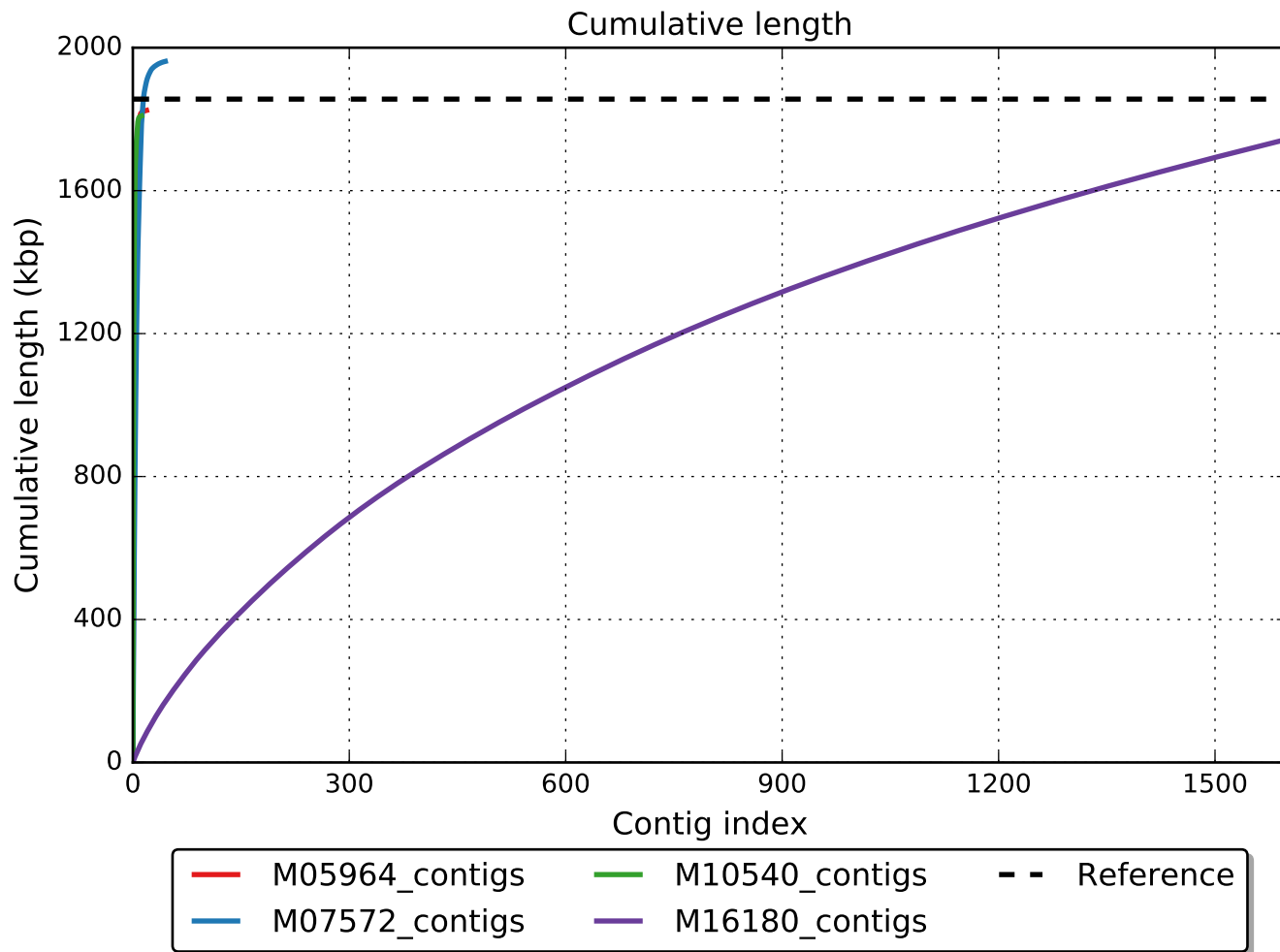
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

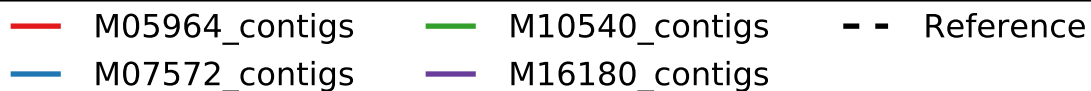
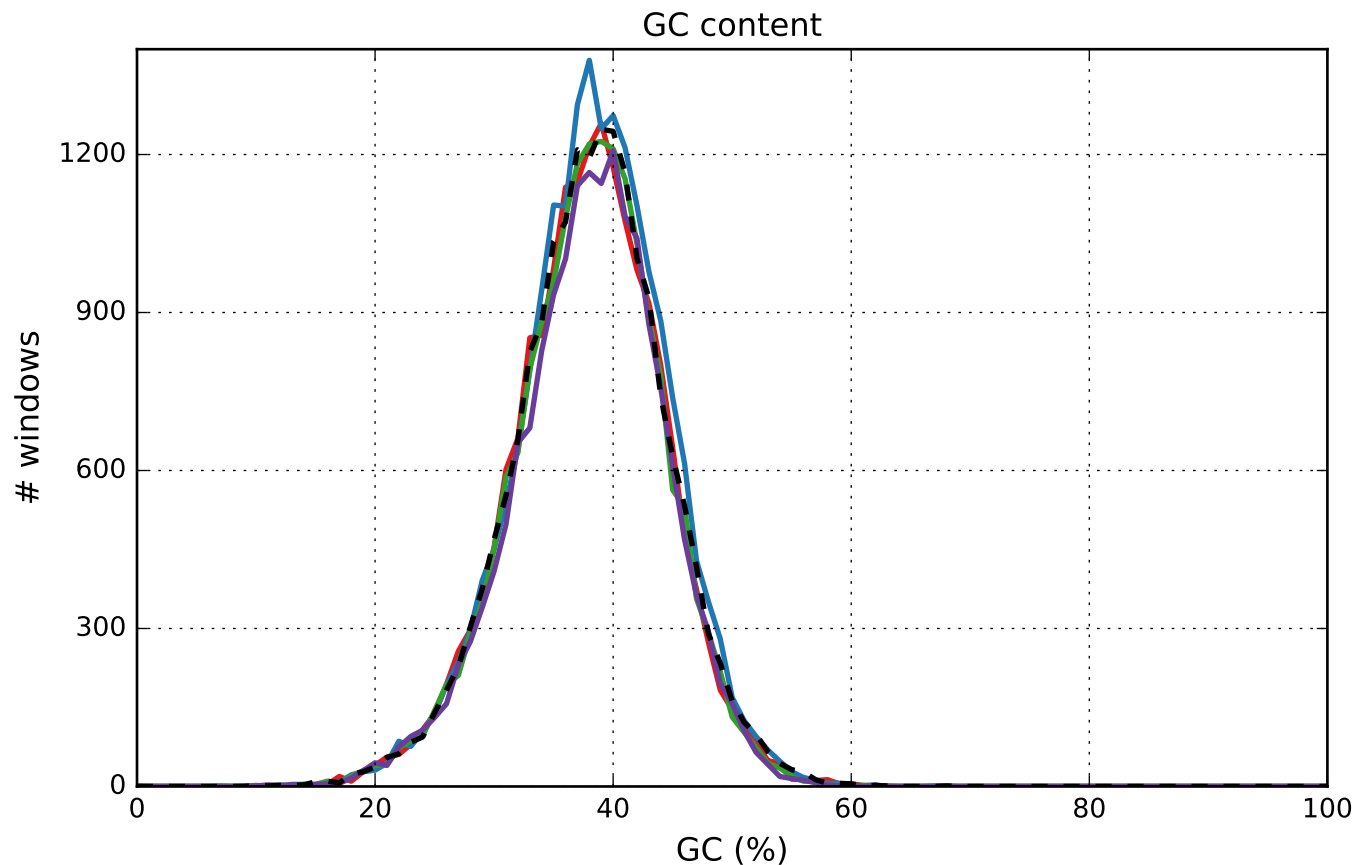


— M05964\_contigs    — M10540\_contigs    — M16180\_contigs  
— M07572\_contigs

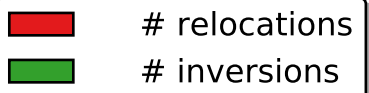
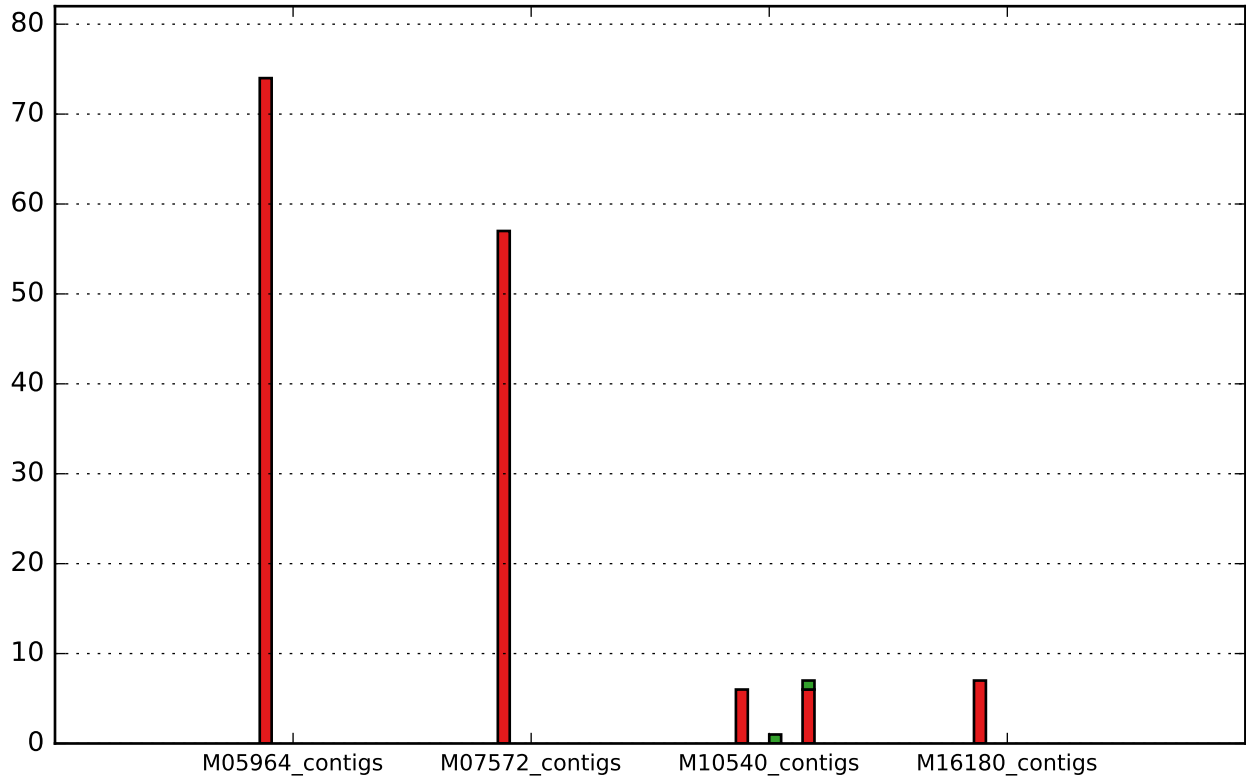


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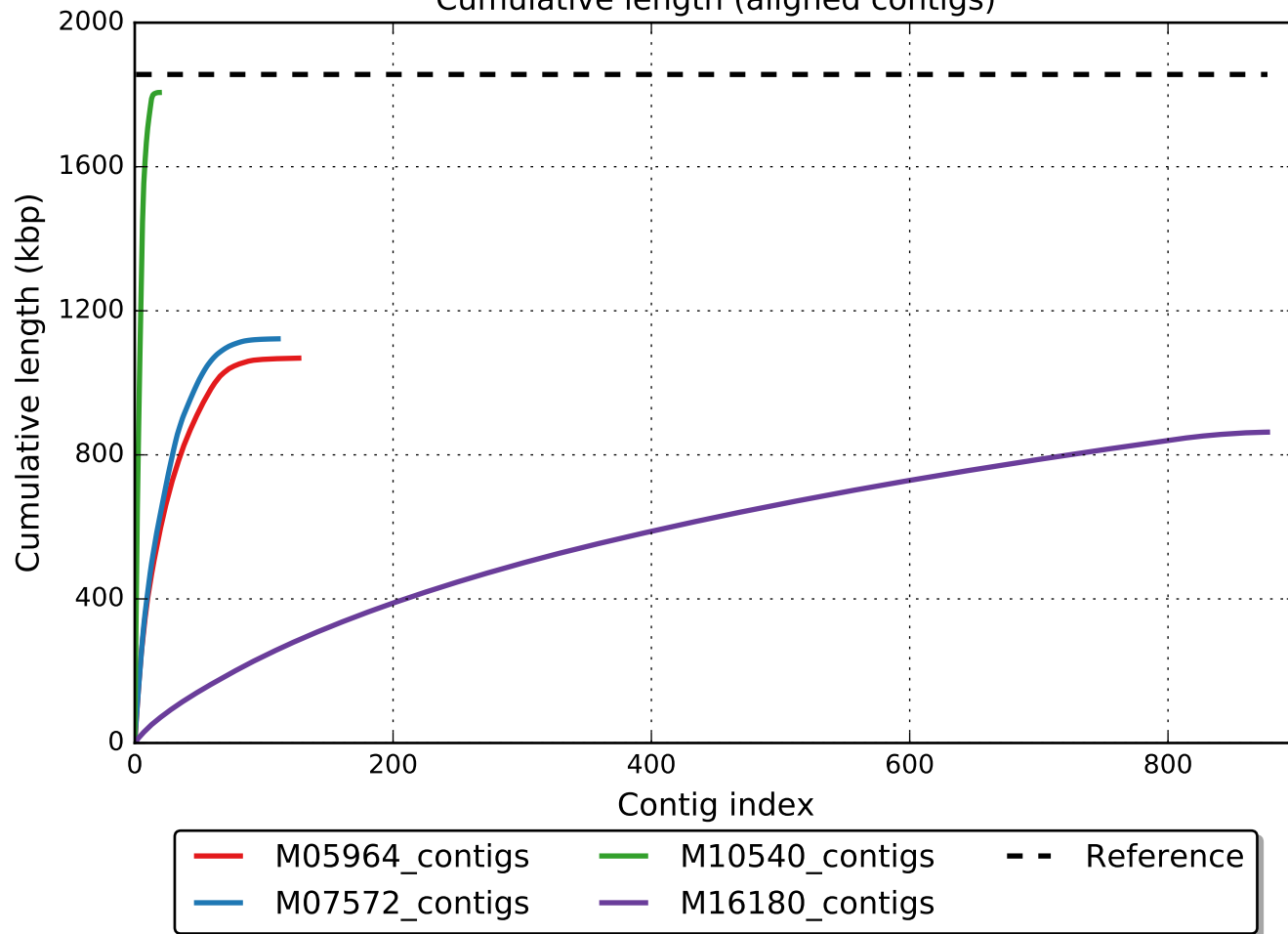


# Misassemblies

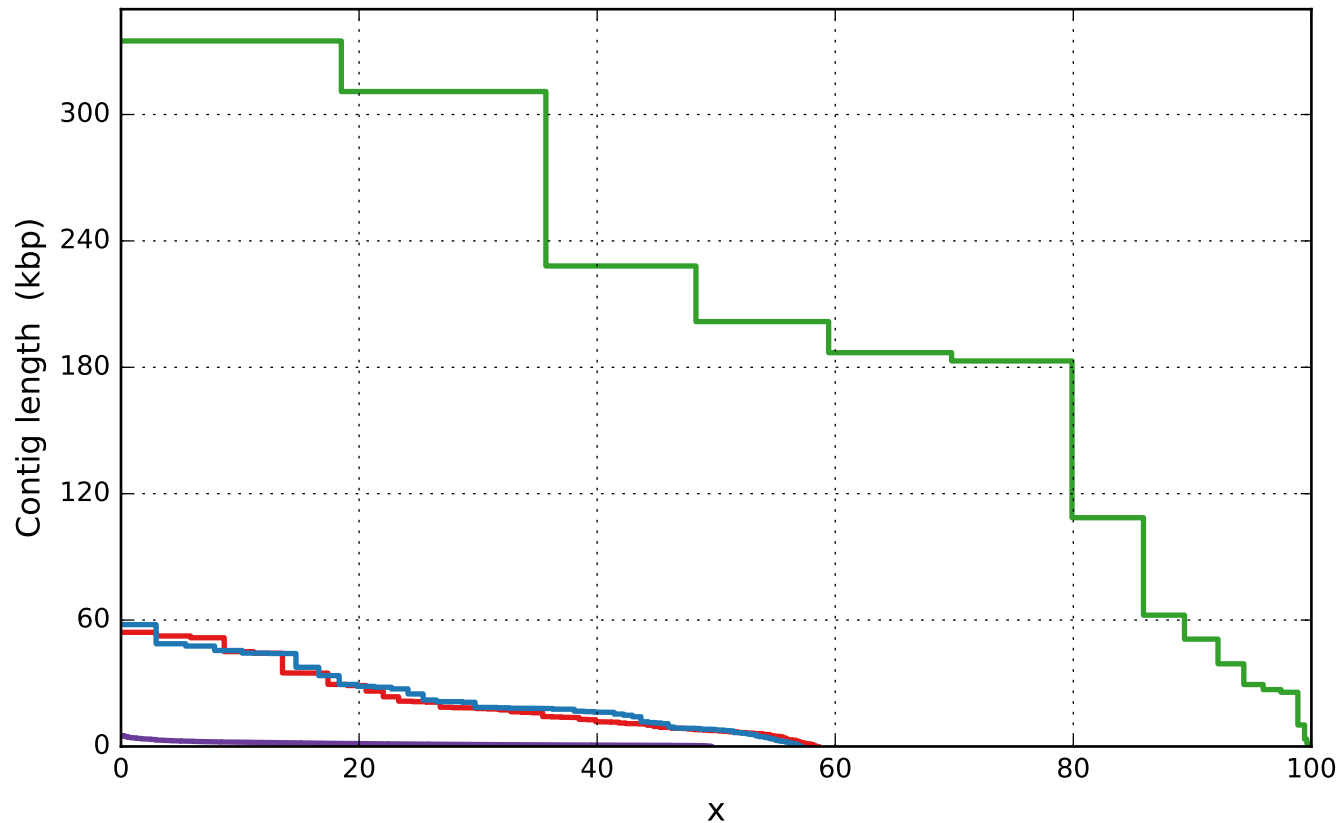




Cumulative length (aligned contigs)



NAx



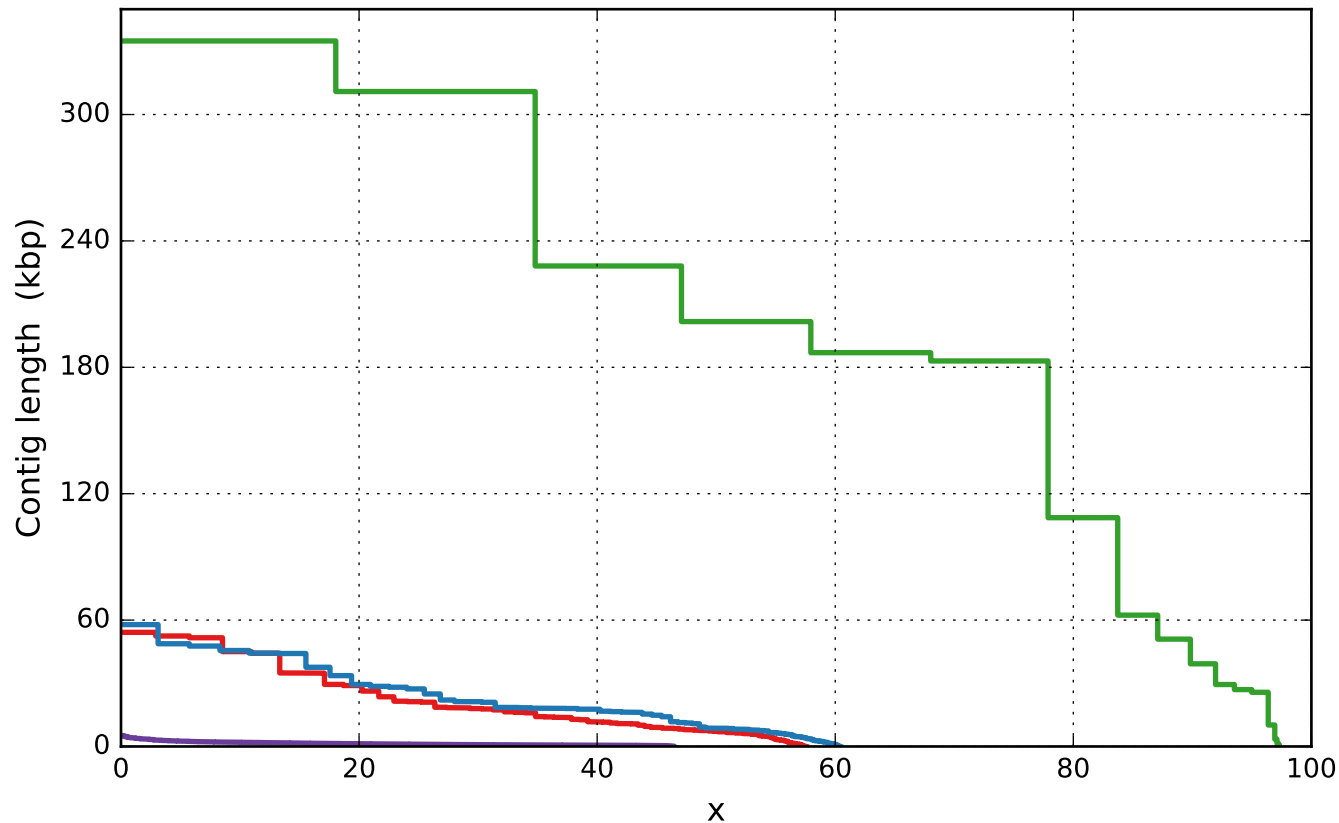
M05964\_contigs

M10540\_contigs

M16180\_contigs

M07572\_contigs

# NGAx



M05964\_contigs M10540\_contigs M16180\_contigs  
M07572\_contigs

