

## 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	1856176	1856176	1856176	1856176
GC (%)	41.19	41.57	37.84	37.98
Reference GC (%)	38.05	38.05	38.05	38.05
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	78	60	7	52
# misassembled contigs	8	10	1	8
Misassembled contigs length	1377429	1408655	1150417	1208360
# local misassemblies	34	37	7	30
# unaligned contigs	733 + 8 part	747 + 11 part	144 + 3 part	113 + 16 part
Unaligned length	881690	960689	116655	575361
Genome fraction (%)	58.946	60.336	97.293	57.479
Duplication ratio	1.392	1.409	1.003	1.427
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	3561.77	3505.19	32.12	3534.38
# indels per 100 kbp	84.91	82.59	3.77	88.10
Largest alignment	54188	57853	335033	48478
NA50	-	-	201703	662
NGA50	7883	8857	201703	5640
NA75	-	-	108663	-
NGA75	-	-	179223	-
LA50	-	-	4	128
LGA50	47	40	4	57
LA75	-	-	7	-
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

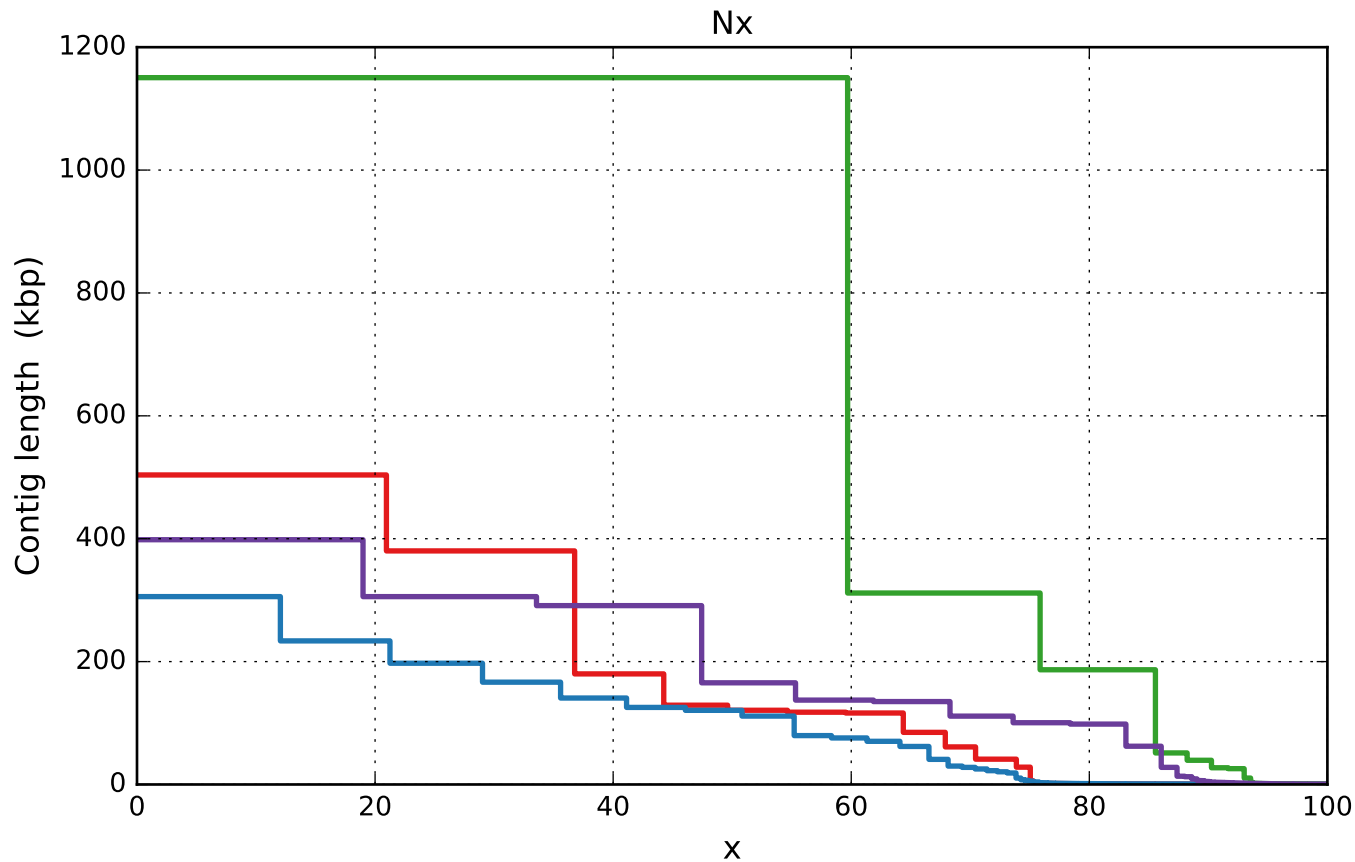
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	78	60	7	52
# relocations	78	60	7	52
# translocations	0	0	0	0
# inversions	0	0	0	0
# misassembled contigs	8	10	1	8
Misassembled contigs length	1377429	1408655	1150417	1208360
# local misassemblies	34	37	7	30
# mismatches	38971	39256	580	37709
# indels	929	925	68	940
# short indels	853	848	43	856
# long indels	76	77	25	84
Indels length	2262	2251	649	2227

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	733	747	144	113
Fully unaligned length	584741	683890	113828	153348
# partially unaligned contigs	8	11	3	16
# with misassembly	5	6	0	6
# both parts are significant	4	6	0	8
Partially unaligned length	296949	276799	2827	422013
# N's	0	0	0	0

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).

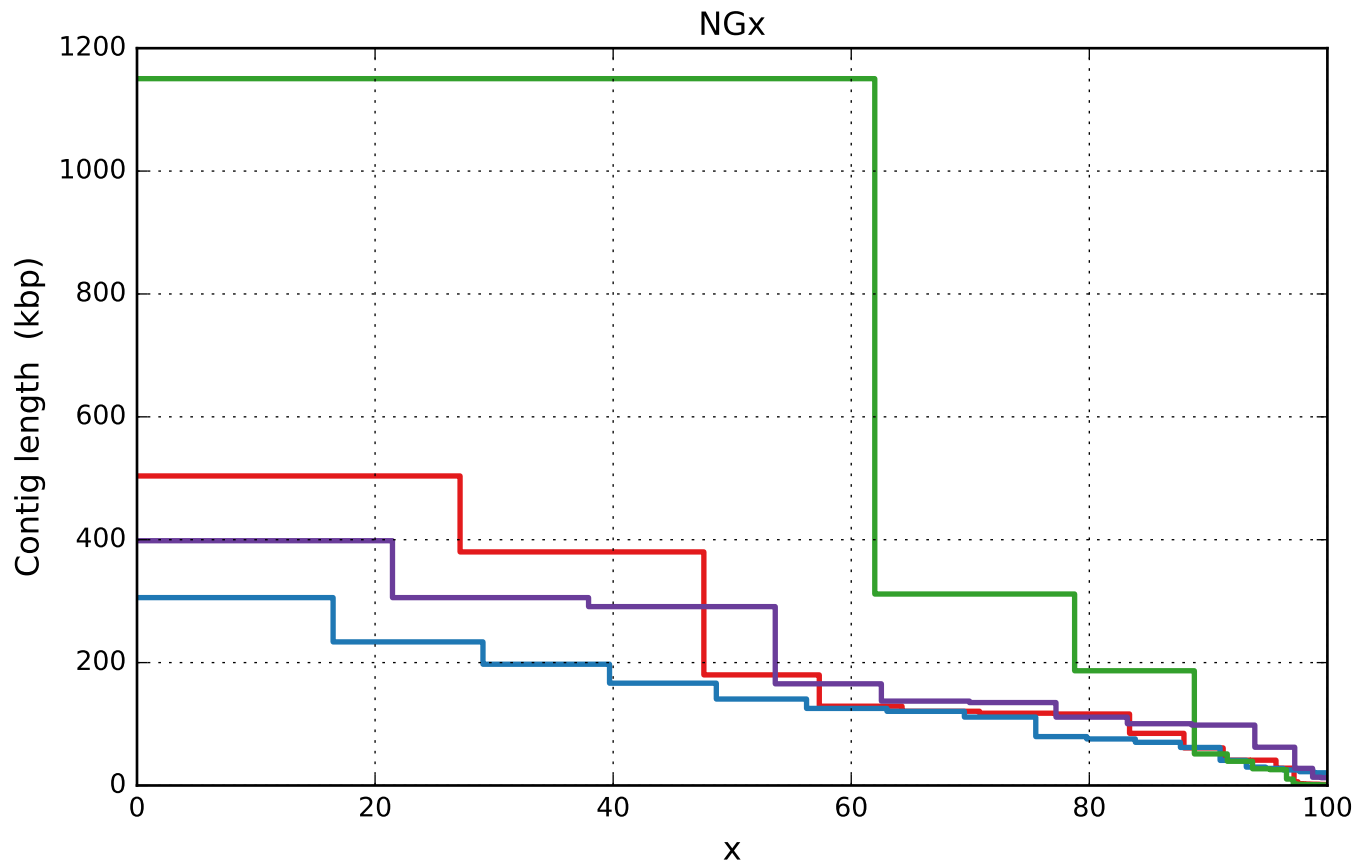


M05964\_contigs

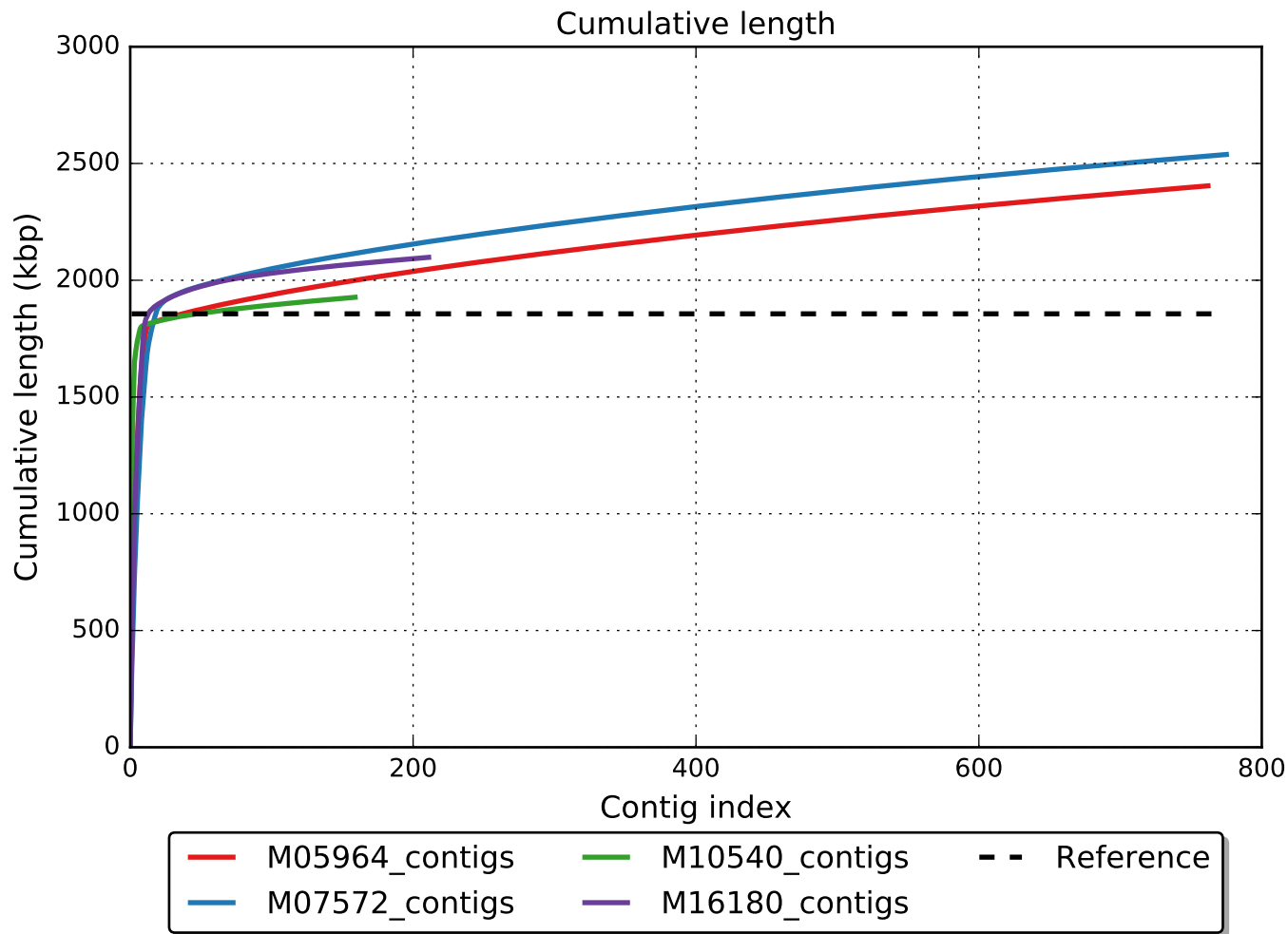
M10540\_contigs

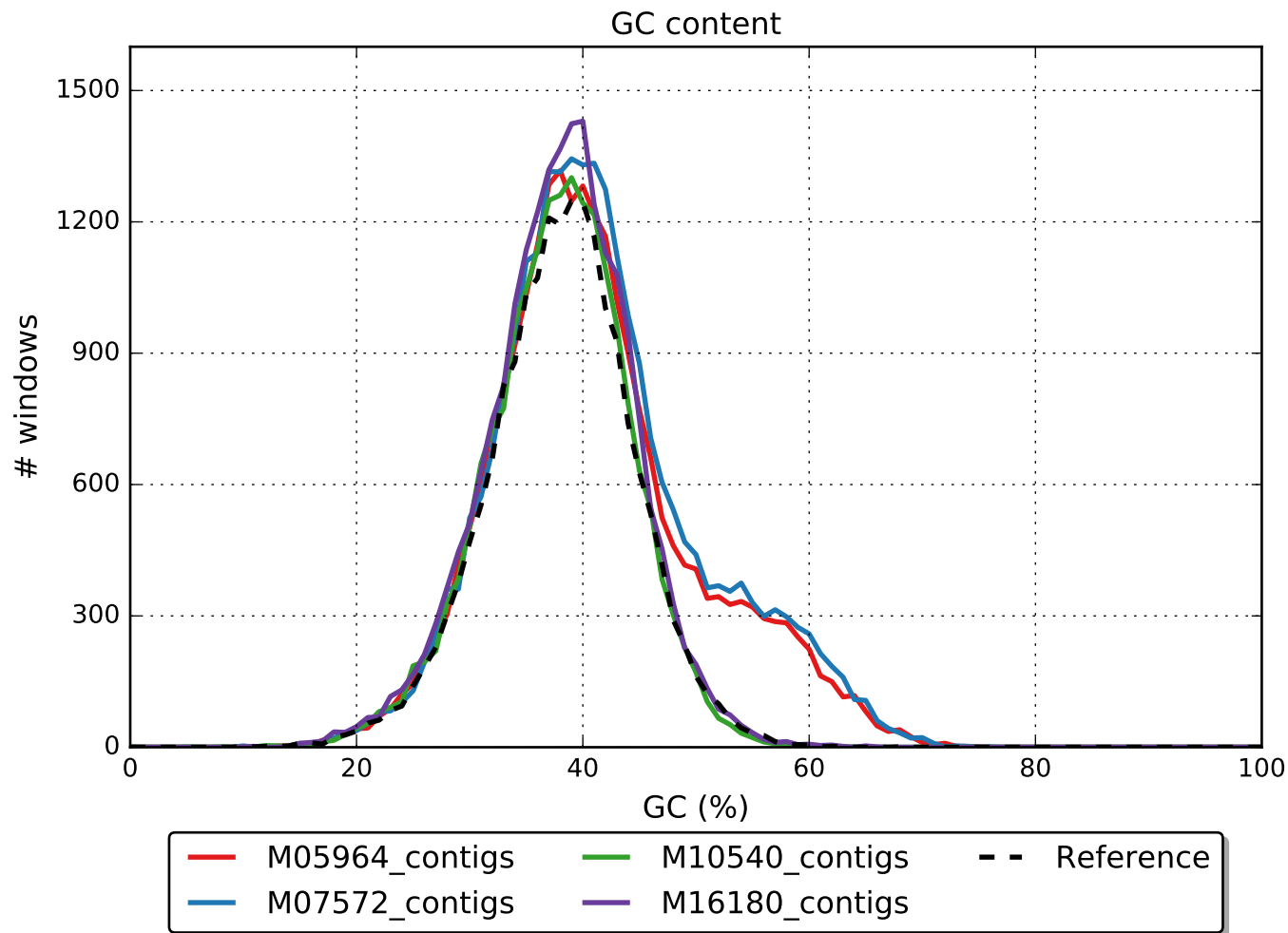
M16180\_contigs

M07572\_contigs

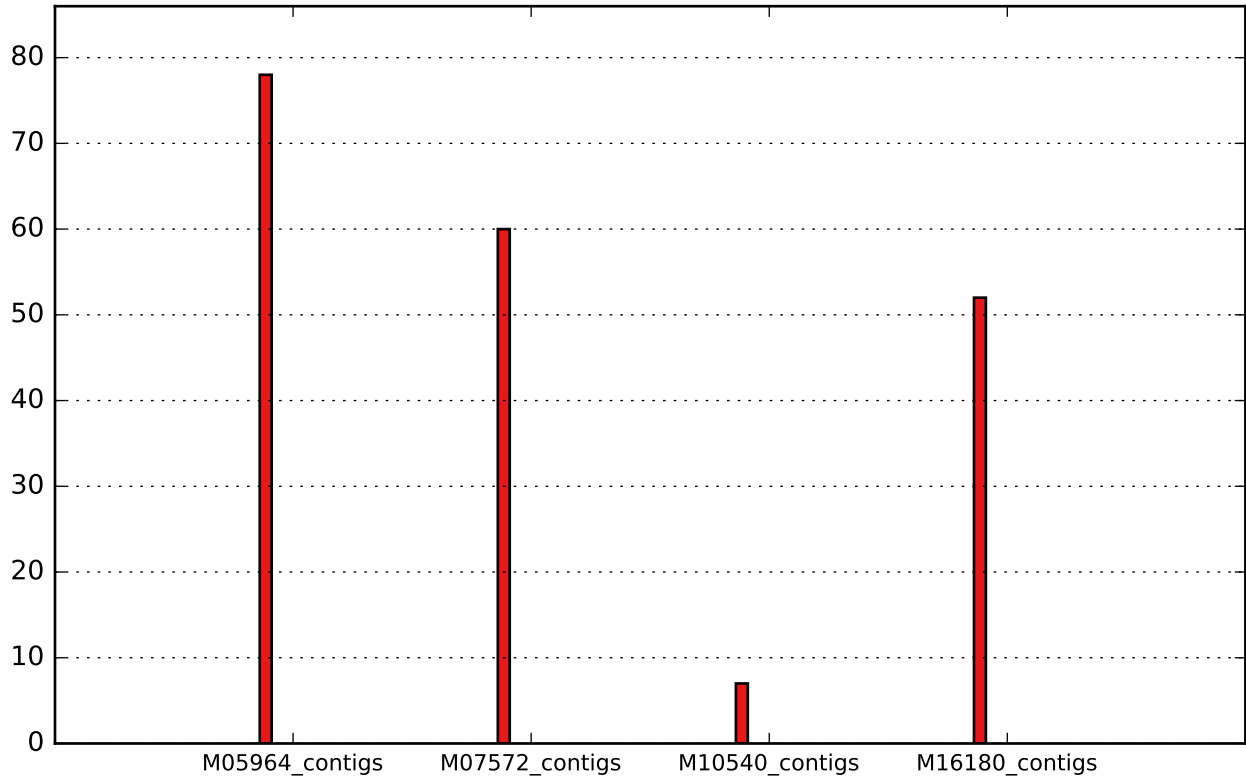


M05964\_contigs    M10540\_contigs    M16180\_contigs  
M07572\_contigs





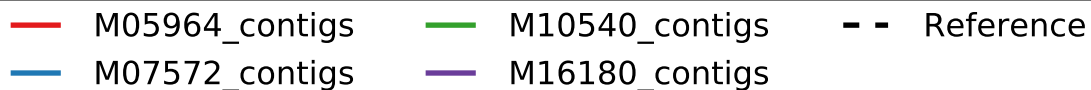
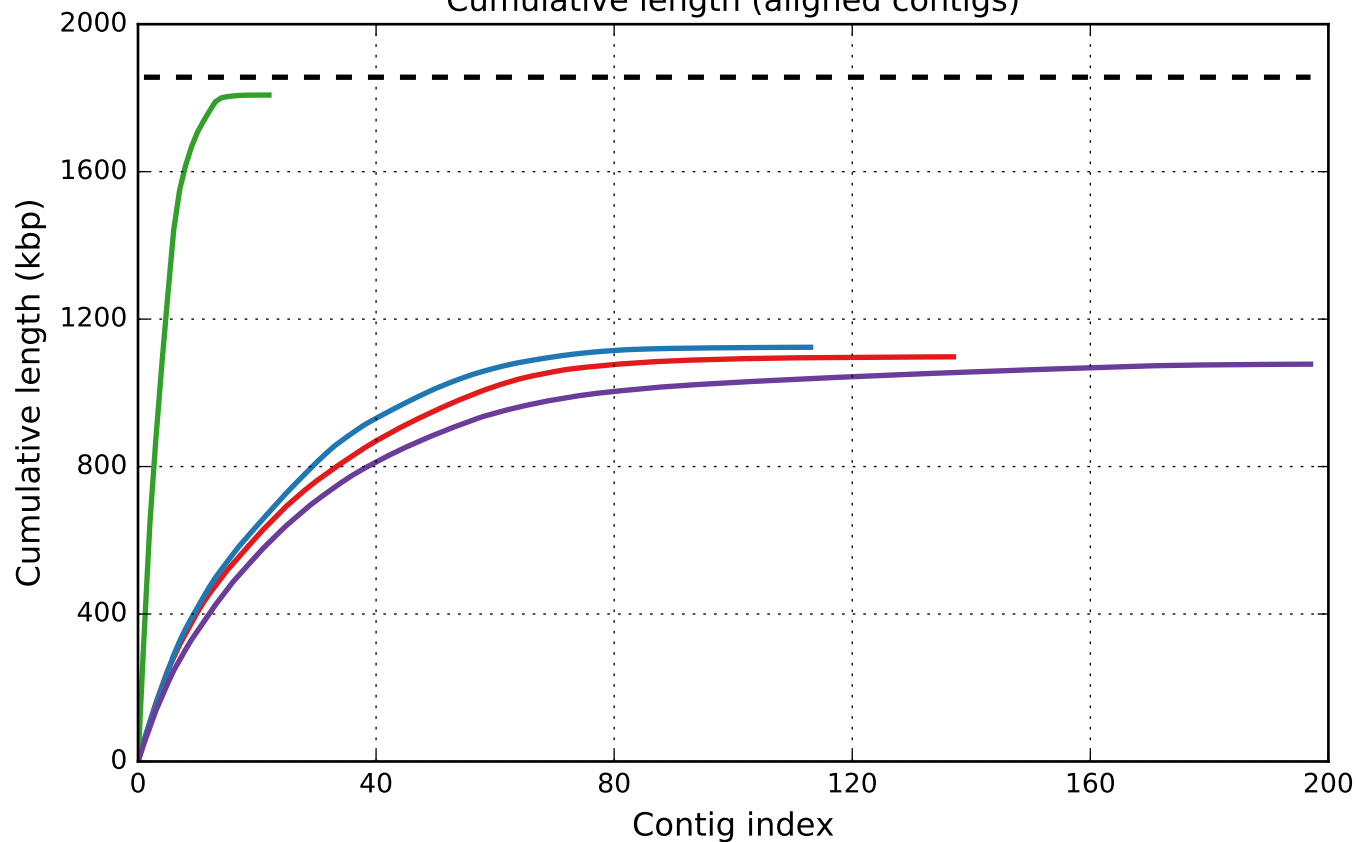
# Misassemblies



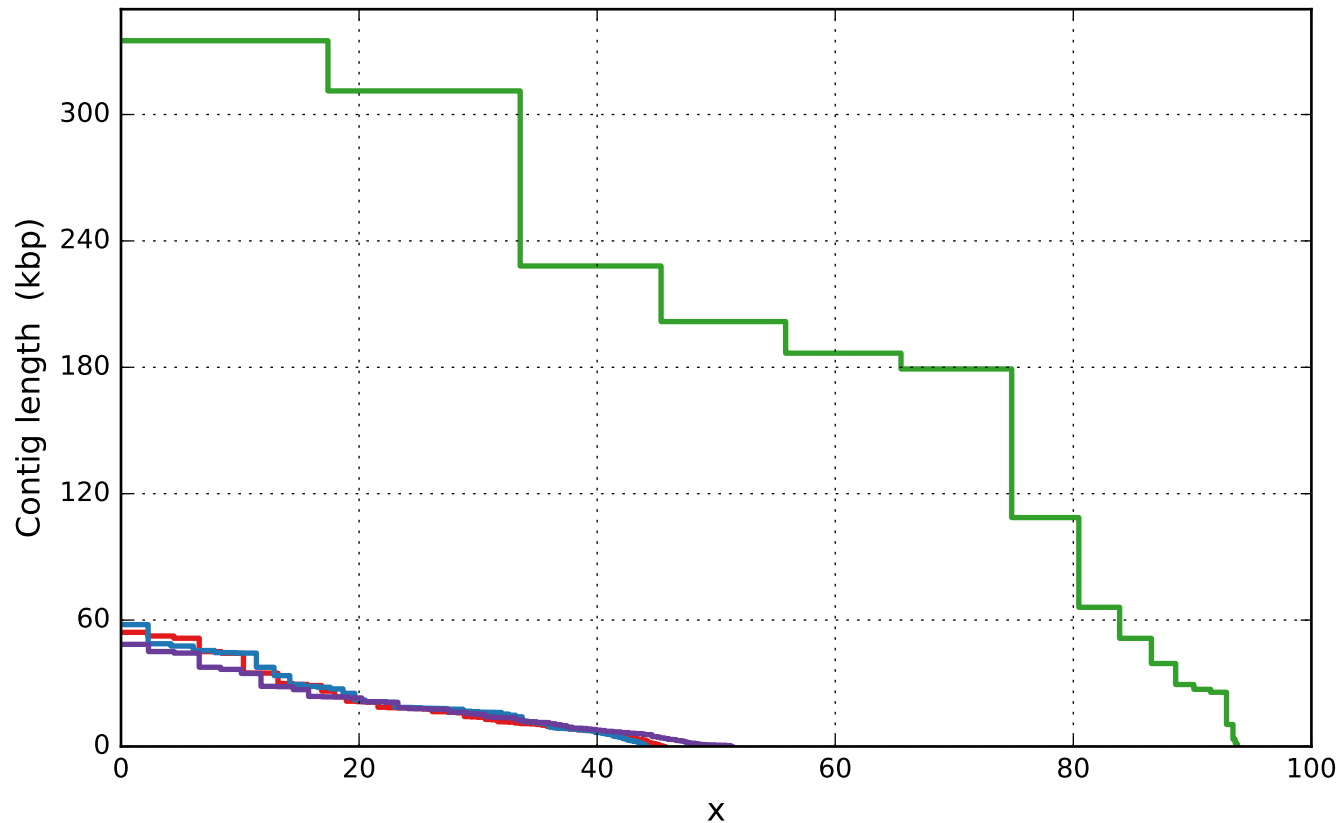
 # relocations



Cumulative length (aligned contigs)



NAx



M05964\_contigs

M10540\_contigs

M16180\_contigs

M07572\_contigs

# NGAx

