

# 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	1819370	1819370	1819370	1819370
GC (%)	41.19	41.57	37.84	37.98
Reference GC (%)	38.02	38.02	38.02	38.02
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	25	30	32	35
# misassembled contigs	8	13	5	11
Misassembled contigs length	1471991	1533323	589768	1701433
# local misassemblies	43	65	17	72
# unaligned contigs	739 + 2 part	744 + 7 part	87 + 19 part	144 + 15 part
Unaligned length	584642	702493	709090	197230
Genome fraction (%)	93.062	88.171	52.435	89.987
Duplication ratio	1.075	1.145	1.277	1.161
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	1926.71	2341.42	3440.96	2391.60
# indels per 100 kbp	54.93	62.15	86.27	67.19
Largest alignment	300257	255415	68097	183344
NA50	44748	28726	-	49803
NGA50	98374	51885	1382	57400
NA75	-	-	-	7998
NGA75	38963	25638	-	27864
LA50	11	19	-	12
LGA50	6	10	83	9
LA75	-	-	-	33
LGA75	15	23	-	20

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

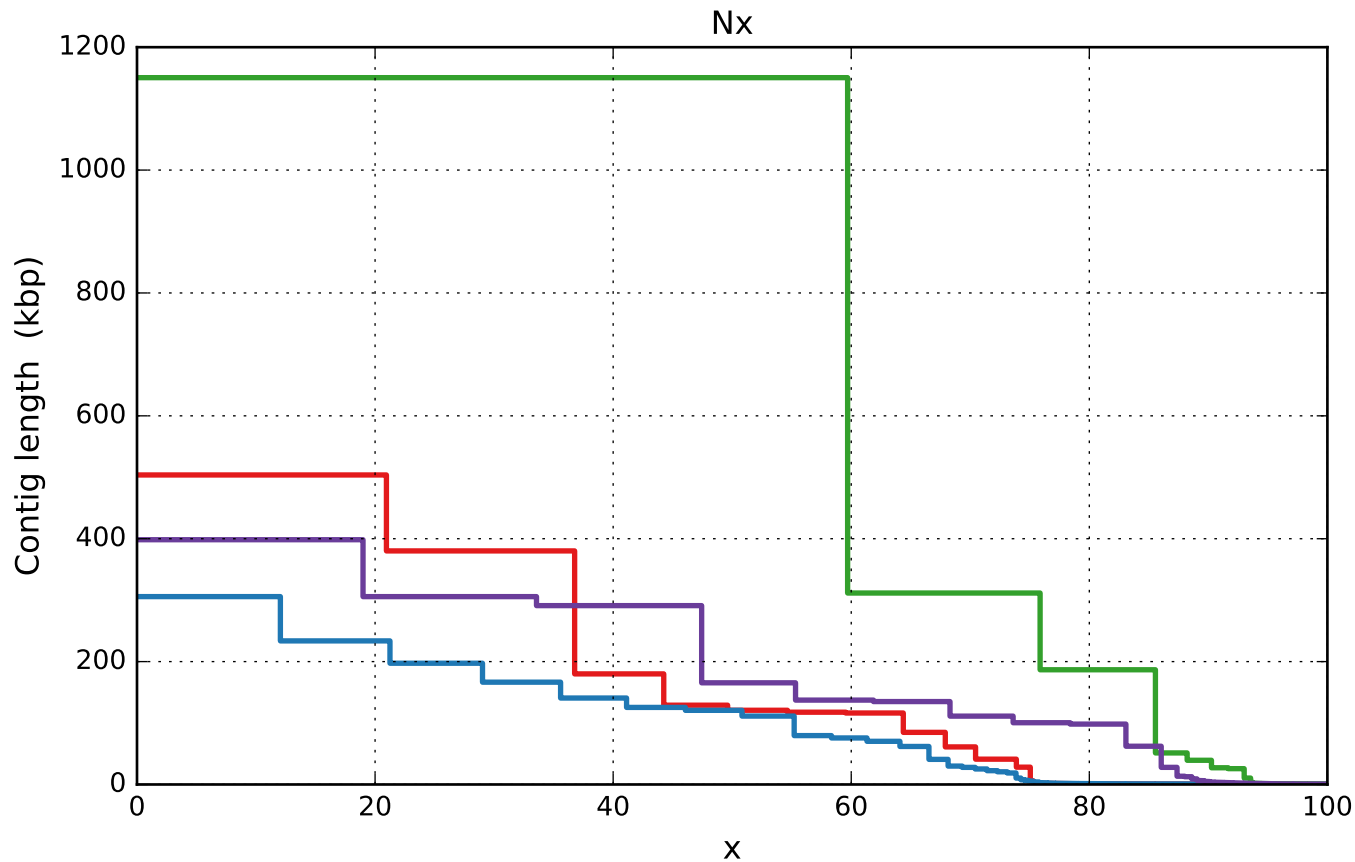
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	25	30	32	35
# relocations	24	30	32	35
# translocations	0	0	0	0
# inversions	1	0	0	0
# misassembled contigs	8	13	5	11
Misassembled contigs length	1471991	1533323	589768	1701433
# local misassemblies	43	65	17	72
# mismatches	32622	37560	32826	39155
# indels	930	997	823	1100
# short indels	816	875	745	972
# long indels	114	122	78	128
Indels length	3075	3414	1986	3494

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	739	744	87	144
Fully unaligned length	583486	667346	70270	174569
# partially unaligned contigs	2	7	19	15
# with misassembly	0	0	4	2
# both parts are significant	1	2	4	3
Partially unaligned length	1156	35147	638820	22661
# 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).

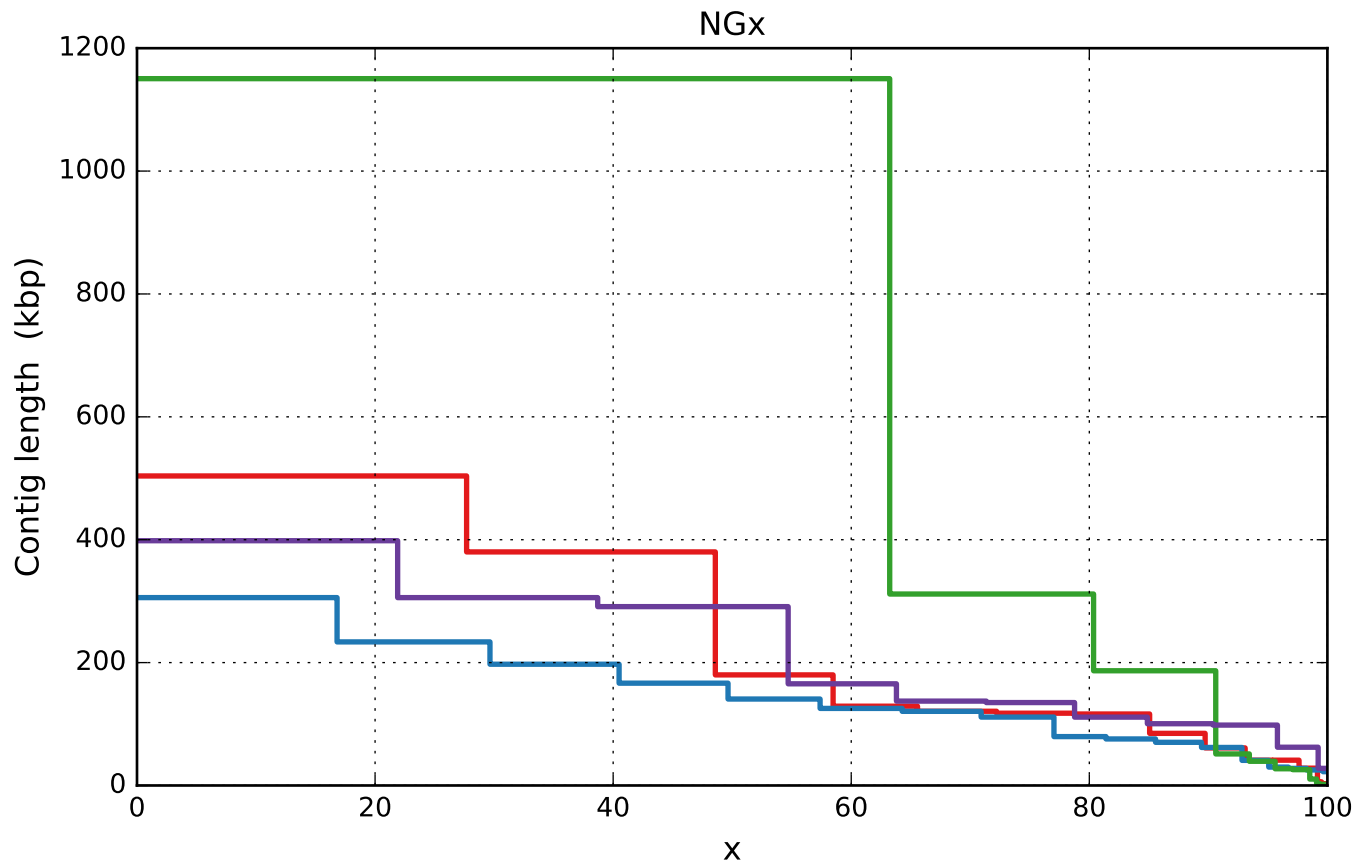


M05964\_contigs

M10540\_contigs

M16180\_contigs

M07572\_contigs

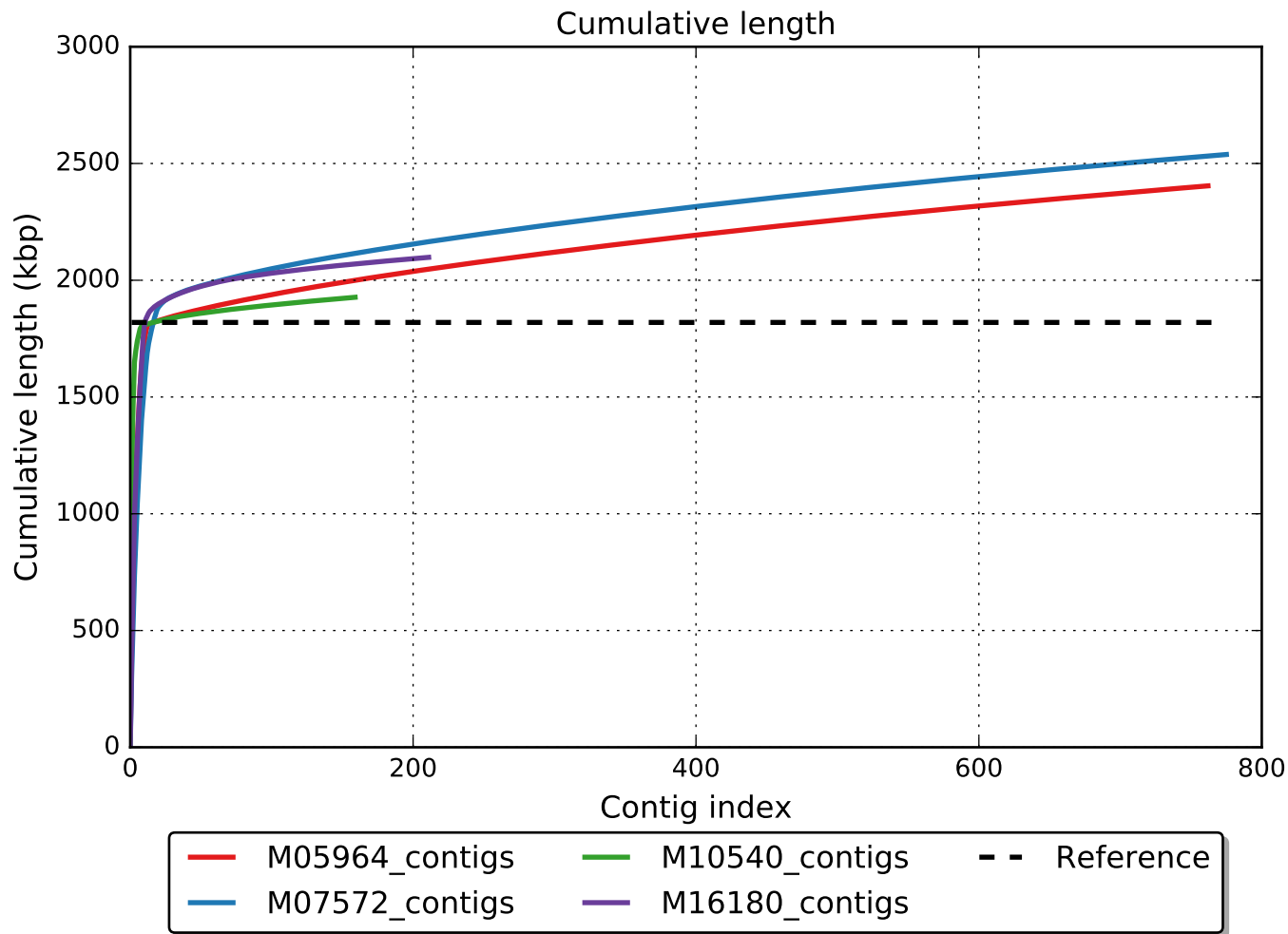


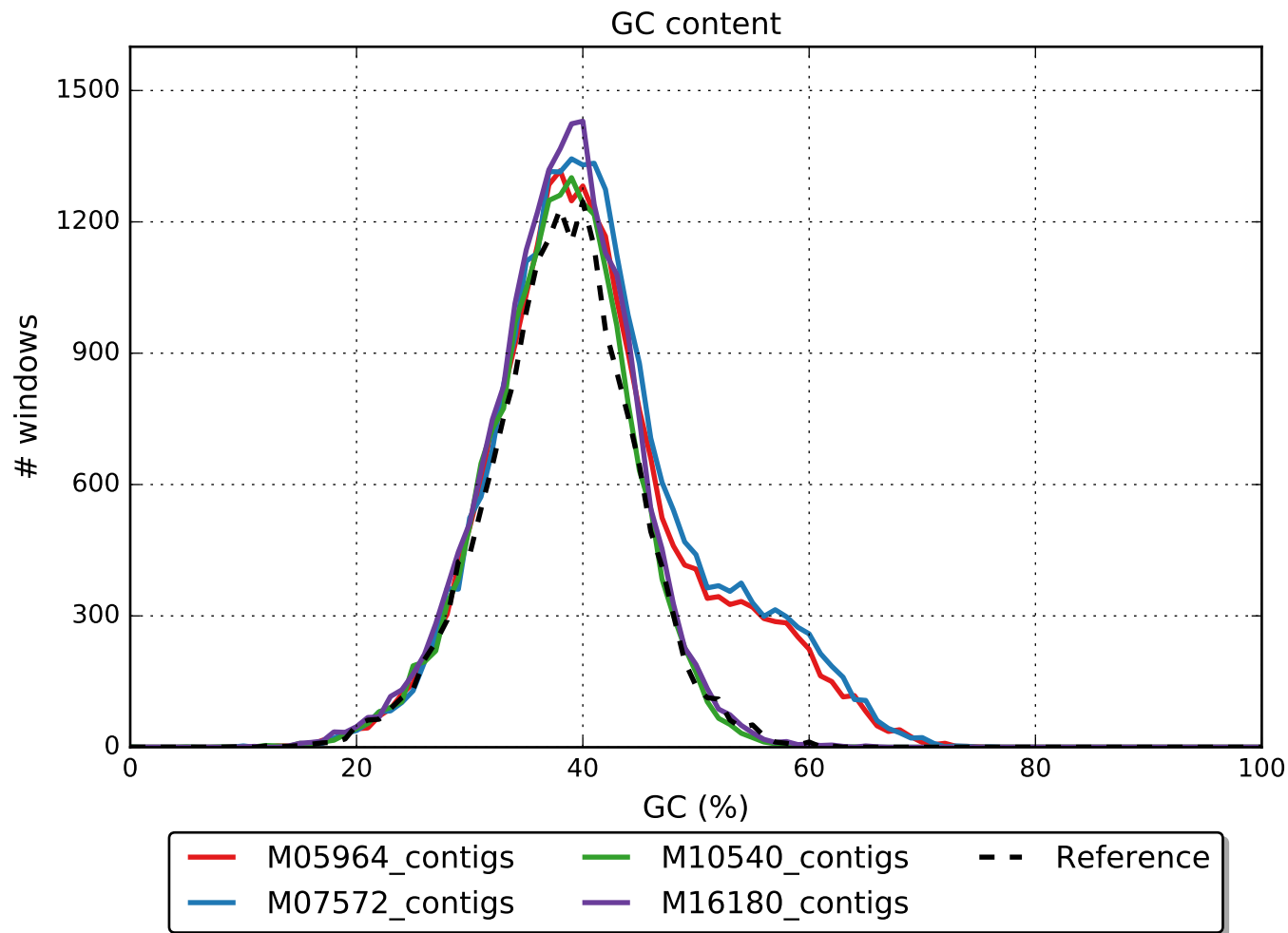
M05964\_contigs

M10540\_contigs

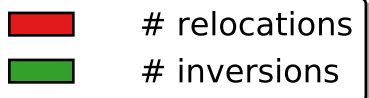
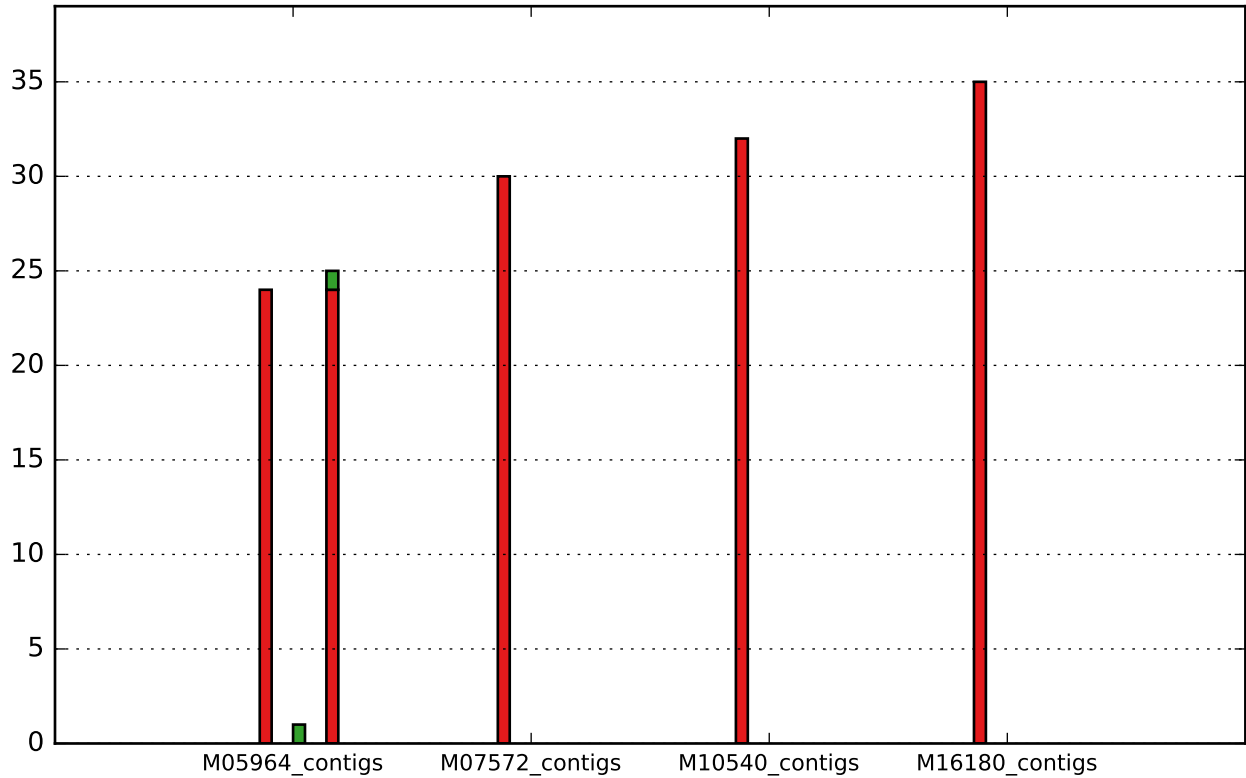
M16180\_contigs

M07572\_contigs



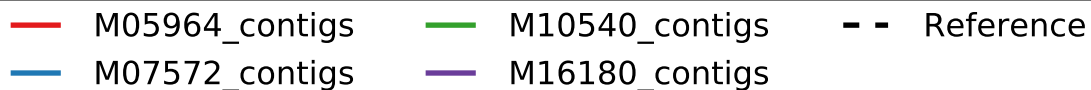
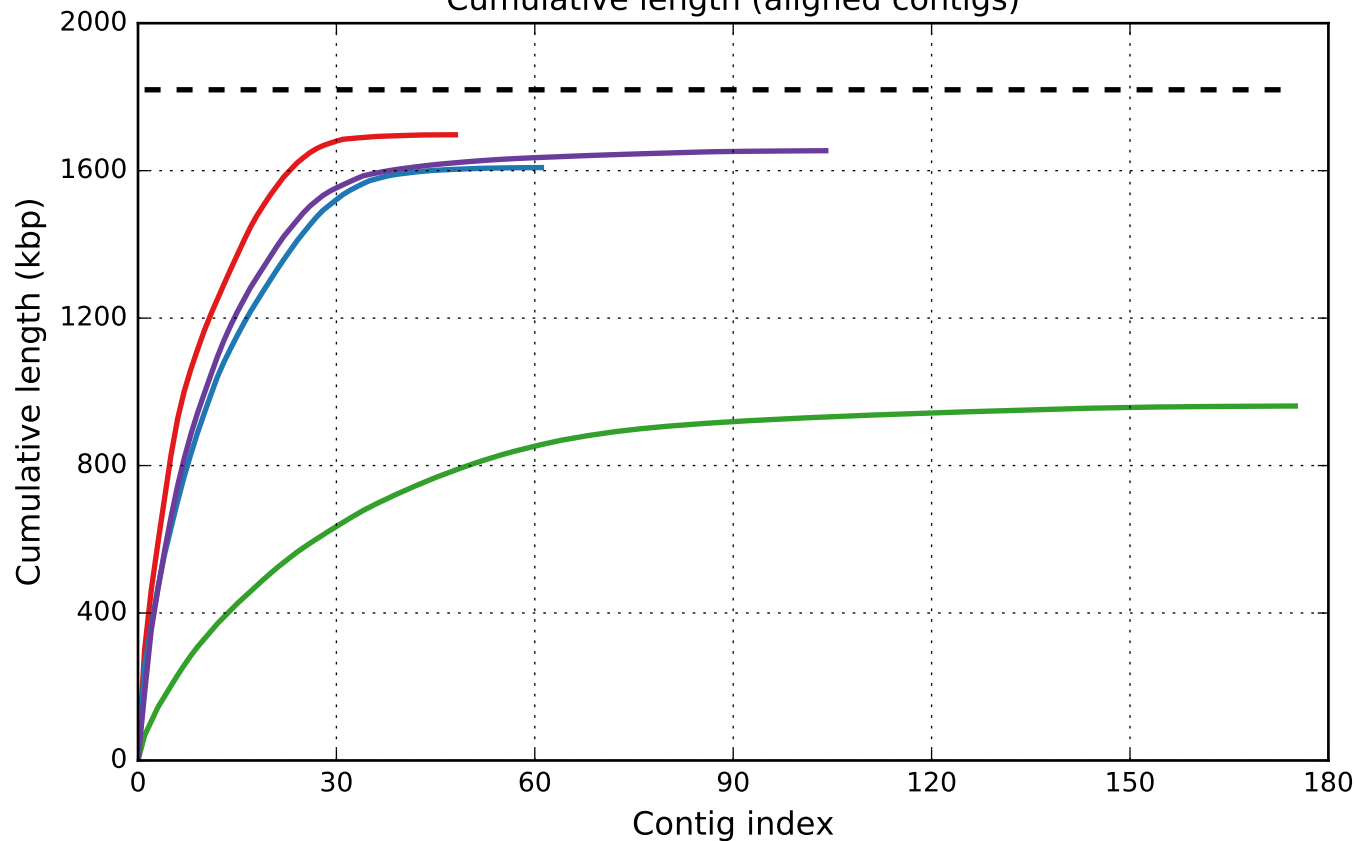


# Misassemblies

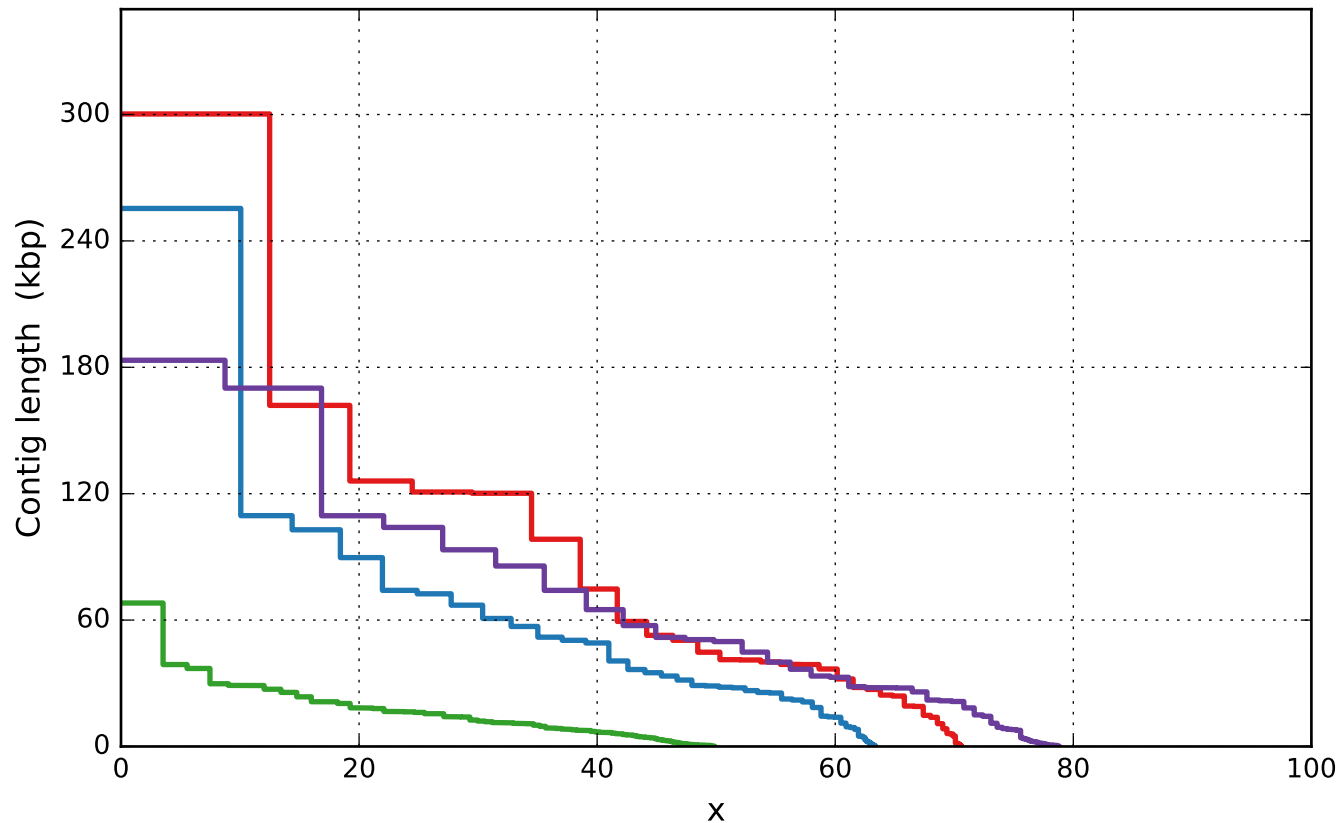




Cumulative length (aligned contigs)

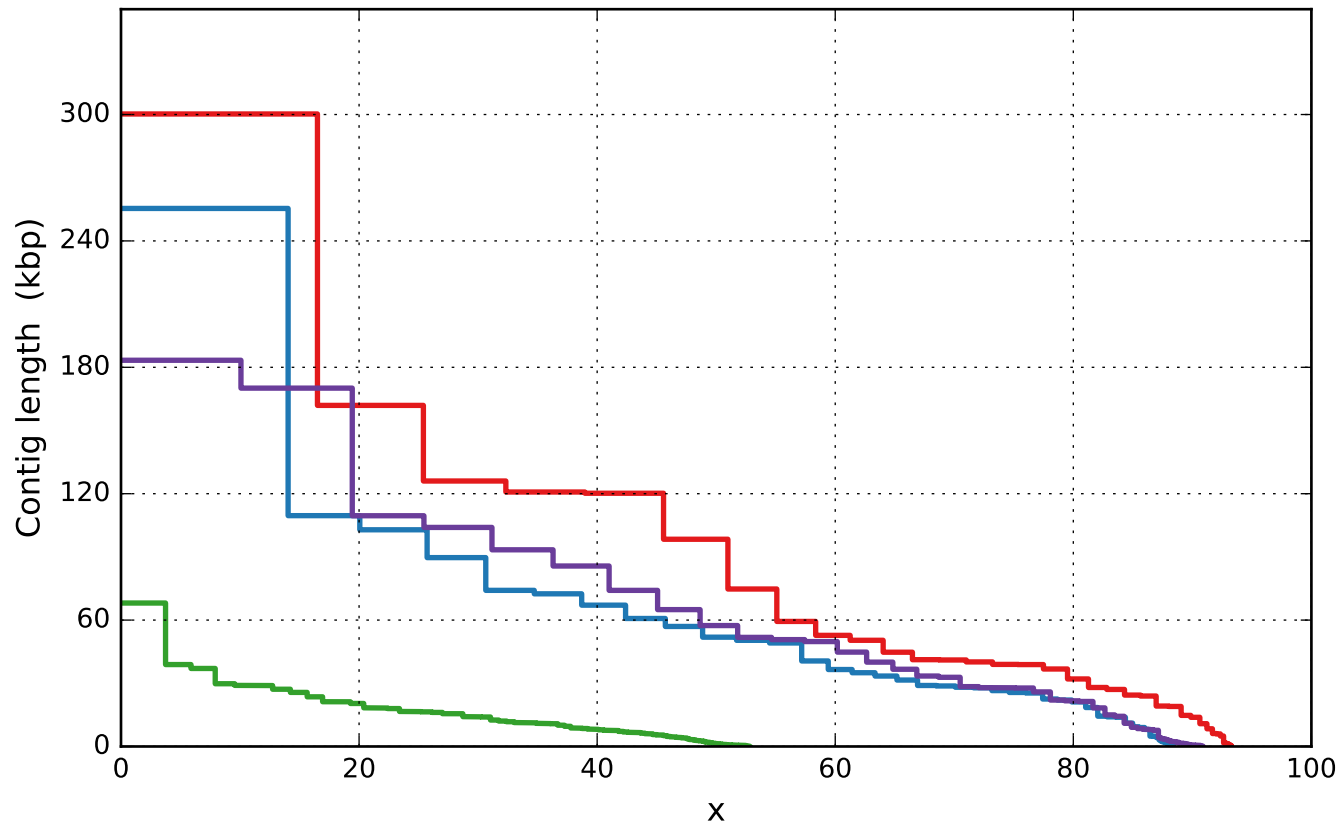


NAx



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

# NGAx



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

