Report

	k44_M05964-contigs	k44_M07572-contigs	k44_M10540-contigs	k44_M16180-contigs	k77_M05964-contigs	k77_M07572-contigs	k77_M10540-contigs	k77_M16180-contigs	k127_M05964-contigs	k127_M07572-contigs	k127_M10540-contigs	k127_M16180-contigs	k99_M05964-contigs	k99_M07572-contigs	k99_M10540-contigs	k99_M16180-contigs
# contigs (>= 0 bp)	134	261	69	141	84	126	38	69	41	55	19	36	61	72	23	42
# contigs (>= 1000 bp)	36	72	29	49	36	51	21	33	35	43	15	26	36	42	17	28
# contigs (>= 5000 bp)	31	47	27	39	27	34	20	31	21	35	14	22	23	36	15	26
# contigs (>= 10000 bp)	25	36	24	30	23	29	18	25	18	23	12	17	19	25	13	20
# contigs (>= 25000 bp)	19	26	16	22	18	20	13	21	16	17	10	15	15	18	11	18
# contigs (>= 50000 bp)	9	13	9	12	9	13	9	13	10	12	7	13	8	11	7	14
Total length (>= 0 bp)	1856487	2018561	1846668	1875236	1861765	2033998	1843463	1877718	1943458	2047751	1839699	1890630	1868767	2042415	1834414	1893788
Total length (>= 1000 bp)	1843001	1993863	1841807	1860135	1852825	2015592	1840271	1870234	1941913	2044301	1838715	1887625	1863738	2032406	1832278	1889956
Total length (>= 5000 bp)	1828185	1920860	1837035	1838044	1832670	1957892	1836531	1865087	1912787	2021558	1836960	1877331	1836604	2013233	1826810	1884609
Total length (>= 10000 bp)	1778633	1849422	1816581	1771774	1800812	1923302	1825488	1825390	1890847	1931796	1826417	1843900	1805426	1934655	1816267	1845458
Total length (>= 25000 bp)	1686546	1676512	1703942	1624648	1727524	1769021	1765750	1755503	1863980	1826189	1801233	1812508	1751712	1808181	1794781	1810534
Total length (>= 50000 bp)	1298668	1254806	1445343	1313950	1393482	1533445	1618312	1496920	1632852	1659461	1701763	1755696	1485927	1564002	1649111	1681577
# contigs	41	74	30	56	38	59	22	37	35	43	16	27	37	46	19	30
Largest contig	473423	217183	334836	369249	343779	312213	400731	369262	550439	312376	409689	401071	550431	312355	400825	401071
Total length	1846118	1995099	1842389	1864193	1854153	2022140	1840807	1872401	1941913	2044301	1839251	1888140	1864279	2035777	1833634	1891040
Reference length	1856176	1856176	1856176	1856176	1856176	1856176	1856176	1856176	1856176	1856176	1856176	1856176	1856176	1856176	1856176	1856176
GC (%)	37.95	38.36	38.10	38.08	37.95	38.40	38.10	38.09	38.00	38.44	38.07	38.18	38.00	38.44	38.04	38.18
Reference GC (%)	38.05	38.05	38.05	38.05	38.05	38.05	38.05	38.05	38.05	38.05	38.05	38.05	38.05	38.05	38.05	38.05
N50	97979	80448	157960	82364	144973	103159	285281	100164	183050	141208	333934	138055	182978	141152	311520	125281
NG50	97979	80448	157960	82364	144973	103159	285281	100164	183050	141208	333934	138055	182978	141152	311520	125281
N75	44883	33152	63553	33896	60895	52032	83976	52751	75809	77394	191716	96606	79438	53598	189976	73822
NG75	44883	37295	63553	33896	60895	67108	83976	52751	81560	81370	191716	116061	79438	81353	189976	73822
L50	5	9	4	7	4	6	3	5	3	5	3	5	3	5	3	5
LG50	5	9	4	7	4	6	3	5	3	5	3	5	3	5	3	5
L75	11	20	8	15	9	13	6	12	8	10	5	9	7	11	5	10
LG75	11	17	8	15	9	11	6	12	7	9	5	8	7	9	5	10
# misassemblies	59	46	7	38	72	53	8	45	75	61	8	43	75	59	8	46
# misassembled contigs	15	16	5	10	15	12	5	12	12	11	4	7	14	12	4	9
Misassembled contigs length	1272067	1174536	836399	928465	1314261	1204136	1063349	1181932	1388547	1403162	1174812	1032048	1372362	1401655	1061870	1129672
# local misassemblies	33	37	4	24	32	39	4	29	38	41	6	29	36	42	7	39
# unaligned contigs	11 + 8 part	32 + 18 part	0 + 0 part	20 + 20 part	9 + 6 part	26 + 15 part	0 + 0 part	9 + 13 part	6 + 8 part	18 + 9 part	0 + 0 part	5 + 9 part	8 + 4 part	18 + 11 part	0 + 0 part	6 + 11 part
Unaligned length	370233	537075	0	545986	335640	555785	0	425094	344900	467945	0	506615	314541	458575	0	447395
Genome fraction (%)	58.431	60.123	98.333	53.554	58.015	60.017	98.395	55.055	59.294	60.232	98.032	54.384	58.591	60.280	97.990	55.186
Duplication ratio	1.361	1.306	1.009	1.326	1.410	1.316	1.008	1.416	1.451	1.410	1.011	1.369	1.425	1.410	1.008	1.409
# N's per 100 kbp	8.29	8.32	0.05	1.45	1.19	0.49	0.00	0.80	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.05
# mismatches per 100 kbp	3664.25	3592.66	32.16	3663.39	3595.85	3580.88	32.14	3702.72	3606.58	3576.19	33.80	3673.94	3603.04	3574.20	32.88	3690.15
# indels per 100 kbp	88.88	85.13	2.74	90.24	86.73	84.92	3.56	91.30	87.13	85.78	3.52	92.72	87.63	85.44	3.68	92.06
Largest alignment	54188	57853	228094	48478	54188	57853	228096	48478	54188	57853	228096	48478	54188	57853	311121	48478
NA50	7557	6605	123728	4537	7353	6315	160610	5463	7557	6315	170342	4166	7353	6315	167101	5567
NGA50	7353	8628	123728	4537	7176	8666	160610	5792	8252	9018	170342	4678	7557	8683	167101	6107
NA75	-	-	52654	-	-	-	83976	-	-	-	109825	-	-	-	109875	-
NGA75	-	-	52654	-	-	-	58318	-	-	-	109825	-	-	-	109875	-
LA50	50	55	6	64	51	55	5	59	53	53	5	64	51	53	5	60
LGA50	51	46	6	64	52	44	5	57	48	41	5	60	50	41	5	57
LA75	-	-	11	-	-	-	9	-	-	-	8	-	-	-	8	-
LGA75	-	-	11	-	-	-	10	-	-	-	8	-	-	-	8	-

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

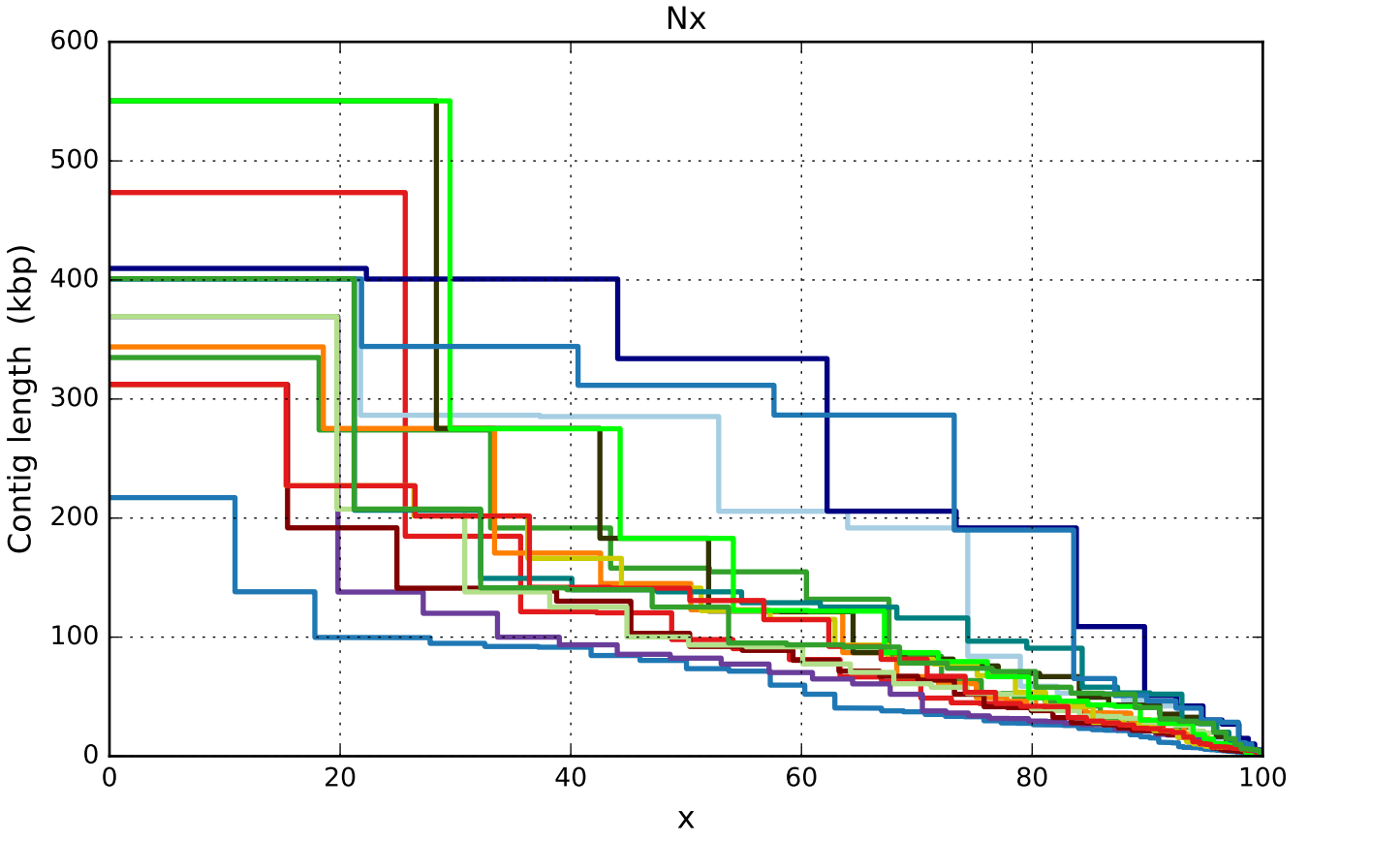
	k44_M05964-contigs	k44_M07572-contigs	k44_M10540-contigs	k44_M16180-contigs	k77_M05964-contigs	k77_M07572-contigs	k77_M10540-contigs	k77_M16180-contigs	k127_M05964-contigs	k127_M07572-contigs	k127_M10540-contigs	k127_M16180-contigs	k99_M05964-contigs	k99_M07572-contigs	k99_M10540-contigs	k99_M16180-contigs
# misassemblies	59	46	7	38	72	53	8	45	75	61	8	43	75	59	8	46
# relocations	59	45	6	38	72	53	8	45	75	61	8	43	75	59	8	46
# translocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# inversions	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
# misassembled contigs	15	16	5	10	15	12	5	12	12	11	4	7	14	12	4	9
Misassembled contigs length	1272067	1174536	836399	928465	1314261	1204136	1063349	1181932	1388547	1403162	1174812	1032048	1372362	1401655	1061870	1129672
# local misassemblies	33	37	4	24	32	39	4	29	38	41	6	29	36	42	7	39
# mismatches	39742	40094	587	36416	38722	39892	587	37839	39694	39982	615	37087	39185	39992	598	37800
# indels	964	950	50	897	934	946	65	933	959	959	64	936	953	956	67	943
# short indels	880	872	28	823	858	872	43	850	882	883	38	853	876	880	41	860
# long indels	84	78	22	74	76	74	22	83	77	76	26	83	77	76	26	83
Indels length	2361	2231	599	2046	2340	2215	551	2225	2316	2284	660	2178	2370	2279	720	2185

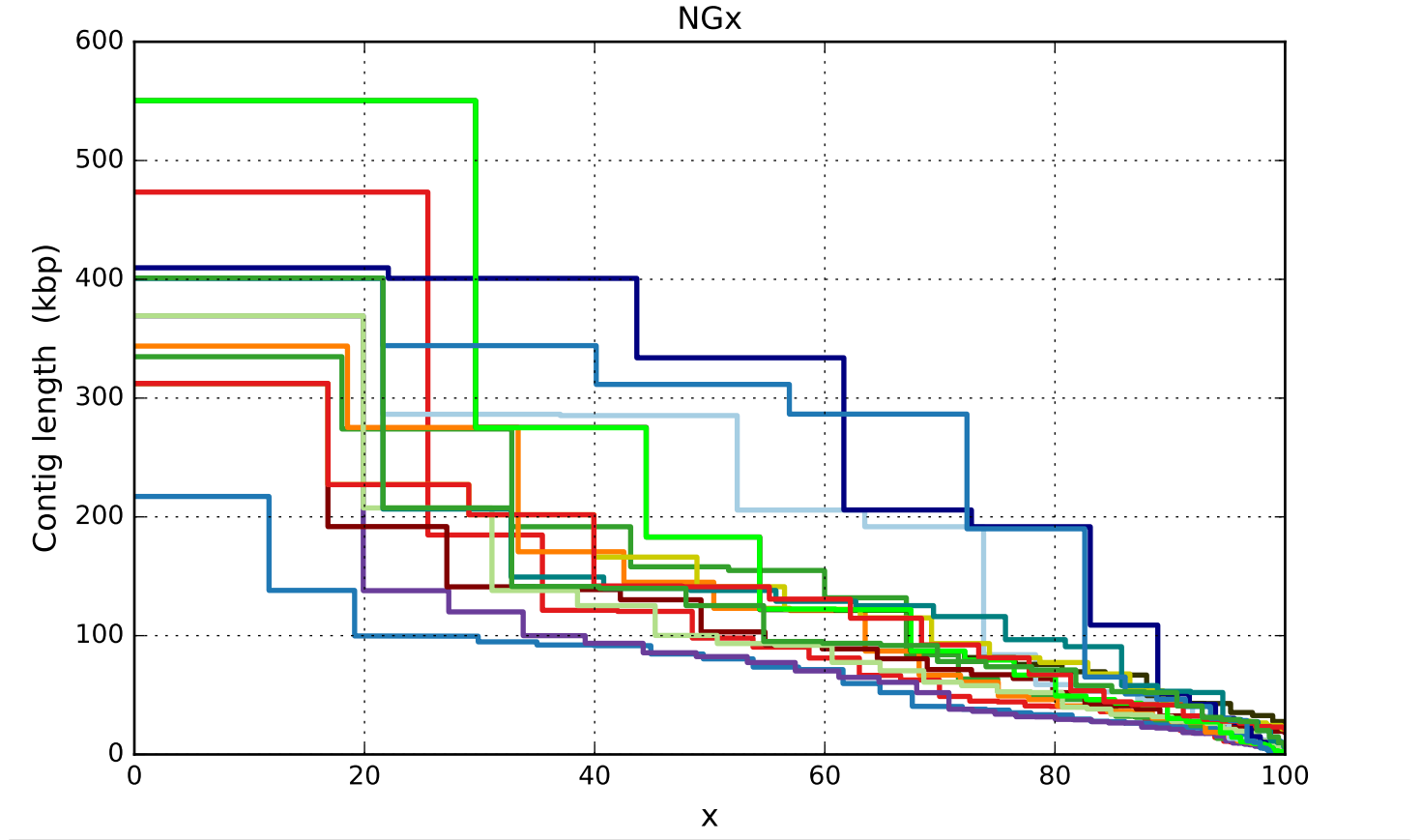
All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

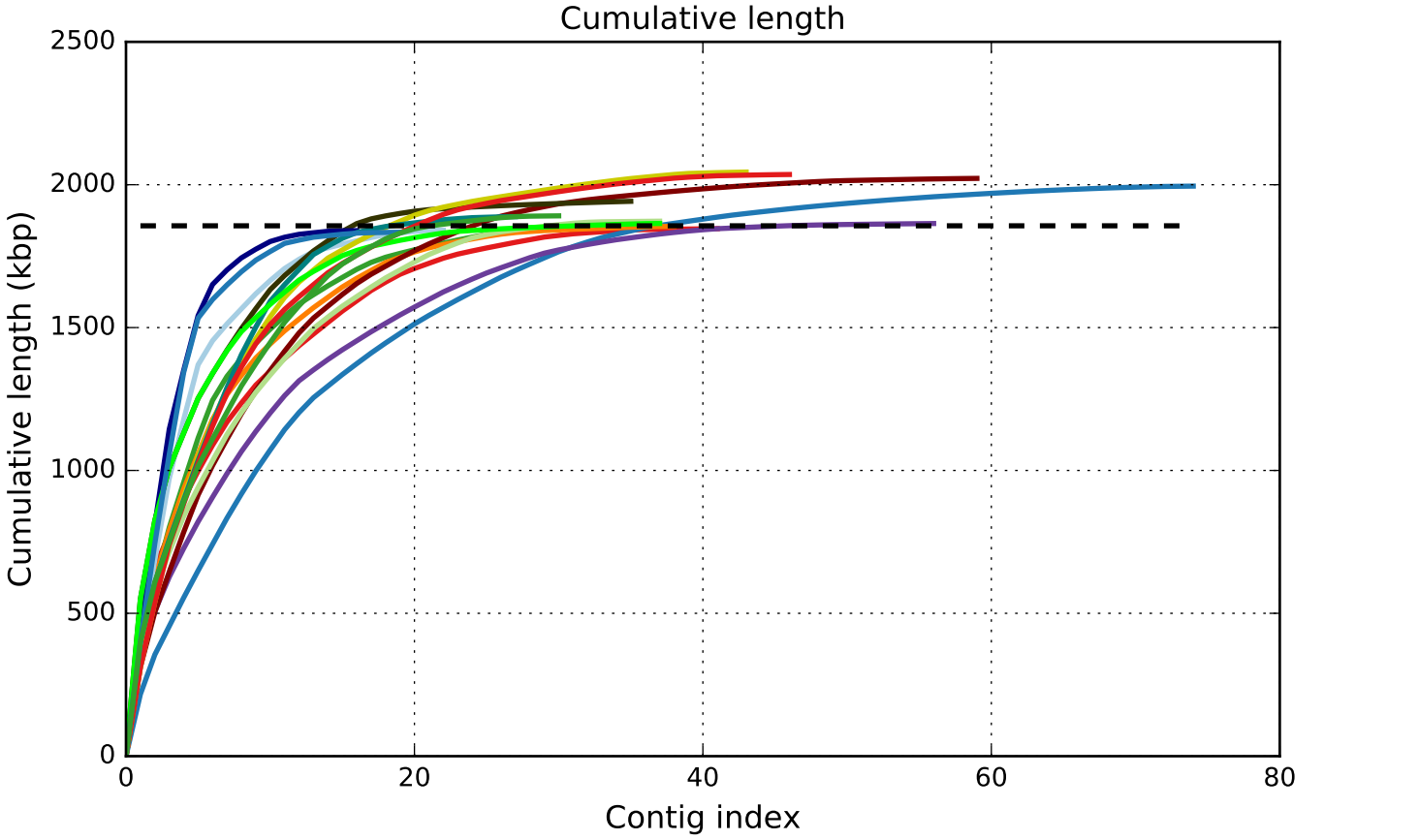
Unaligned report

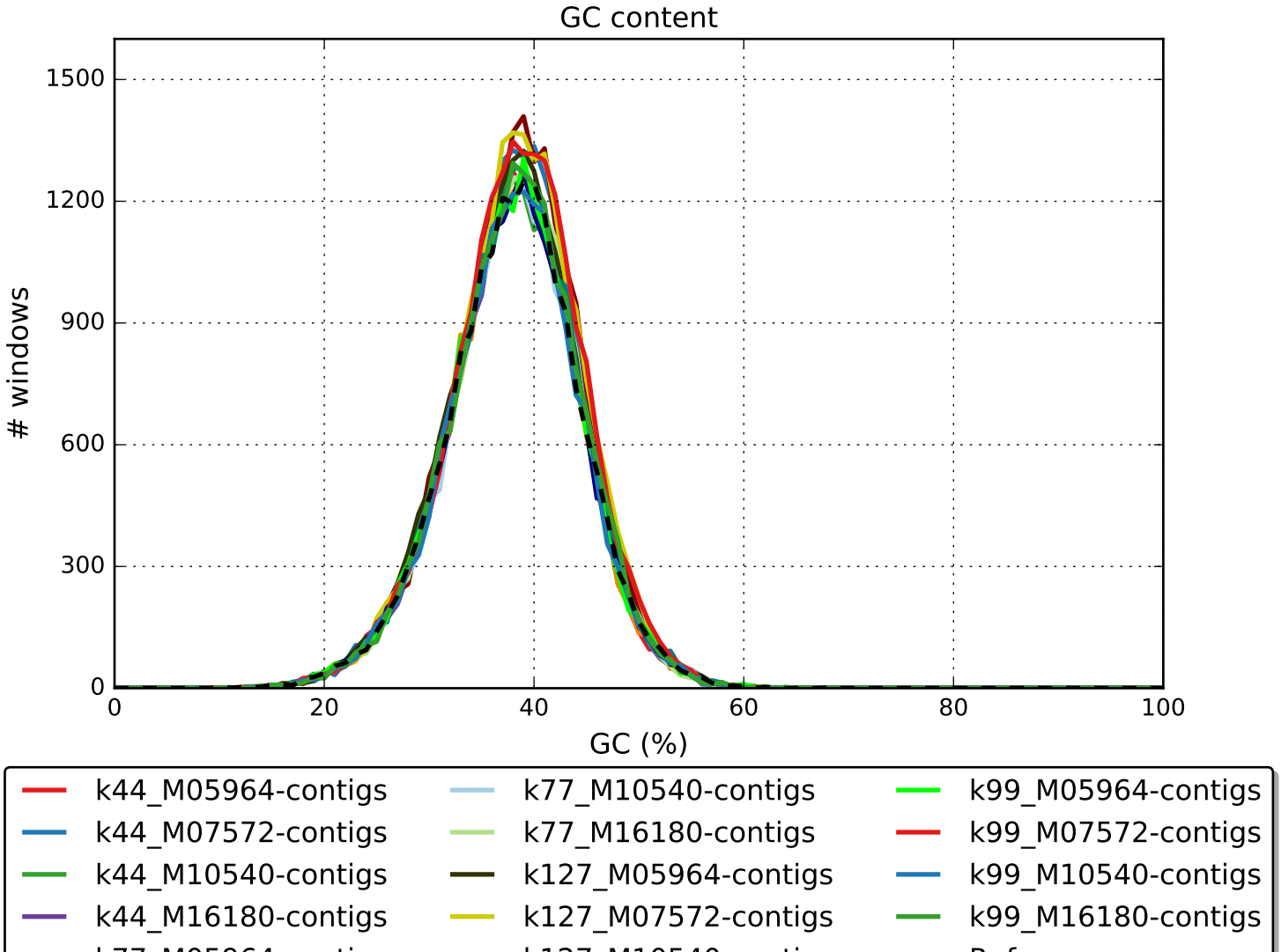
	k44_M05964-contigs	k44_M07572-contigs	k44_M10540-contigs	k44_M16180-contigs	k77_M05964-contigs	k77_M07572-contigs	k77_M10540-contigs	k77_M16180-contigs	k127_M05964-contigs	k127_M07572-contigs	k127_M10540-contigs	k127_M16180-contigs	k99_M05964-contigs	k99_M07572-contigs	k99_M10540-contigs	k99_M16180-contigs
# fully unaligned contigs	11	32	0	20	9	26	0	9	6	18	0	5	8	18	0	6
Fully unaligned length	76490	216029	0	101647	29306	144463	0	33318	18414	159174	0	24064	28916	152193	0	29812
# partially unaligned contigs	8	18	0	20	6	15	0	13	8	9	0	9	4	11	0	11
# with misassembly	7	8	0	9	5	10	0	7	5	7	0	7	3	7	0	7
# both parts are significant	7	16	0	15	6	13	0	10	6	8	0	9	4	11	0	9
Partially unaligned length	293743	321046	0	444339	306334	411322	0	391776	326486	308771	0	482551	285625	306382	0	417583
# N's	153	166	1	27	22	10	0	15	0	0	0	0	0	0	1	1

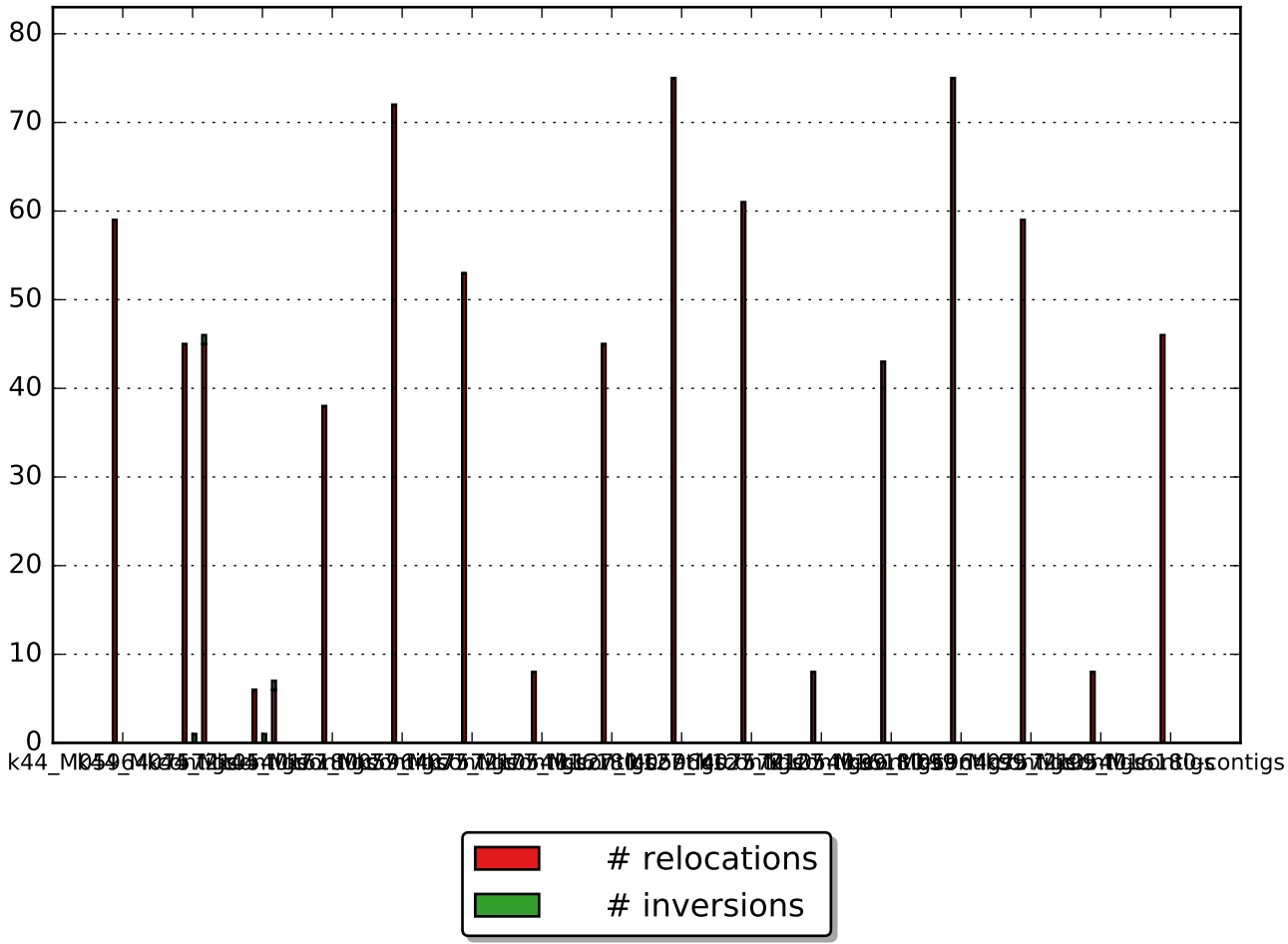
All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

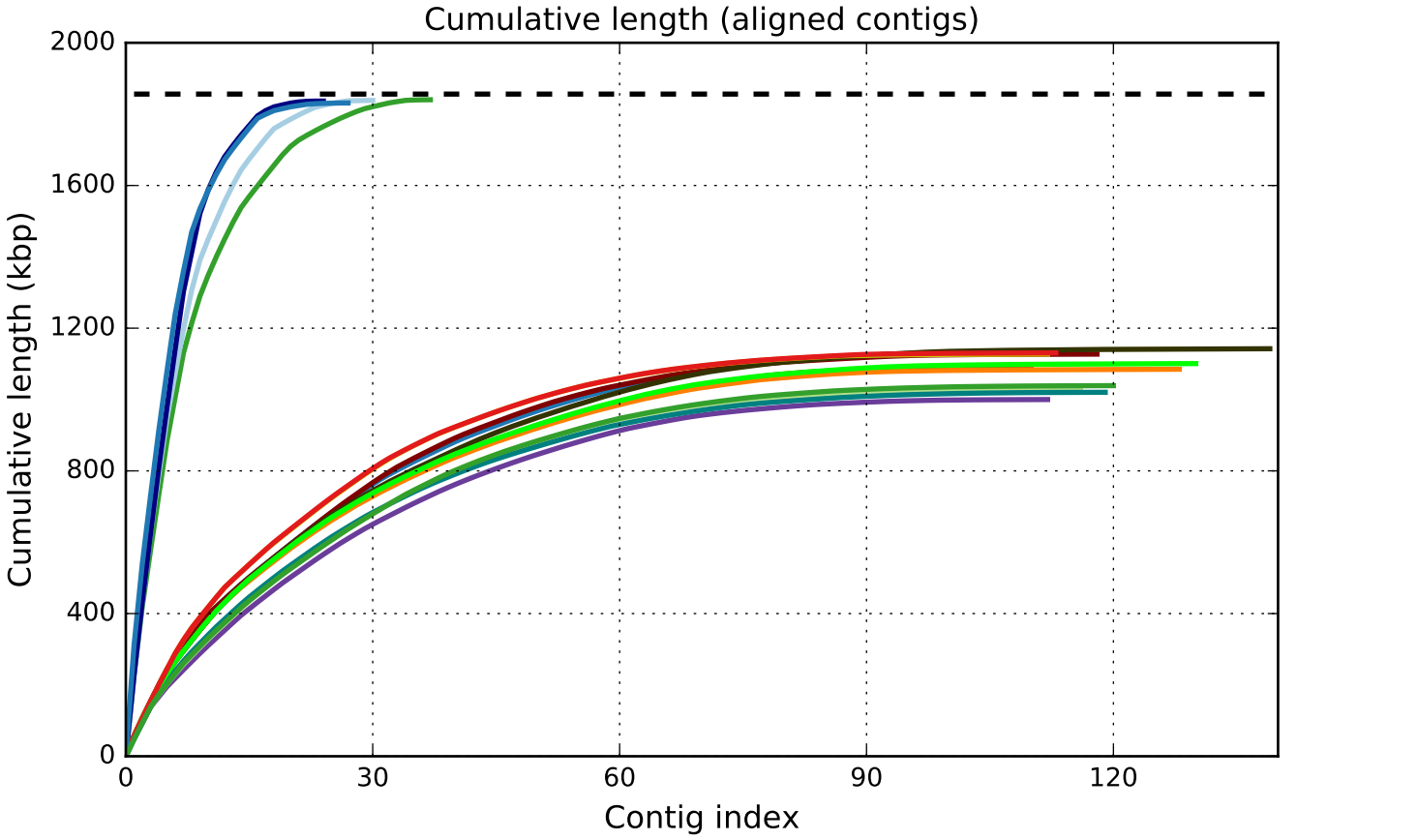

Nx
Contig length (kbp)
x
0
100
200
300
400
500
600
0
20
40
60
80
100
k44_M05964-contigs
k44_M07572-contigs
k44_M10540-contigs
k44_M16180-contigs
k77_M10540-contigs
k77_M16180-contigs
k127_M05964-contigs
k127_M07572-contigs
k127_M16180-contigs
k99_M05964-contigs
k99_M07572-contigs
k99_M10540-contigs

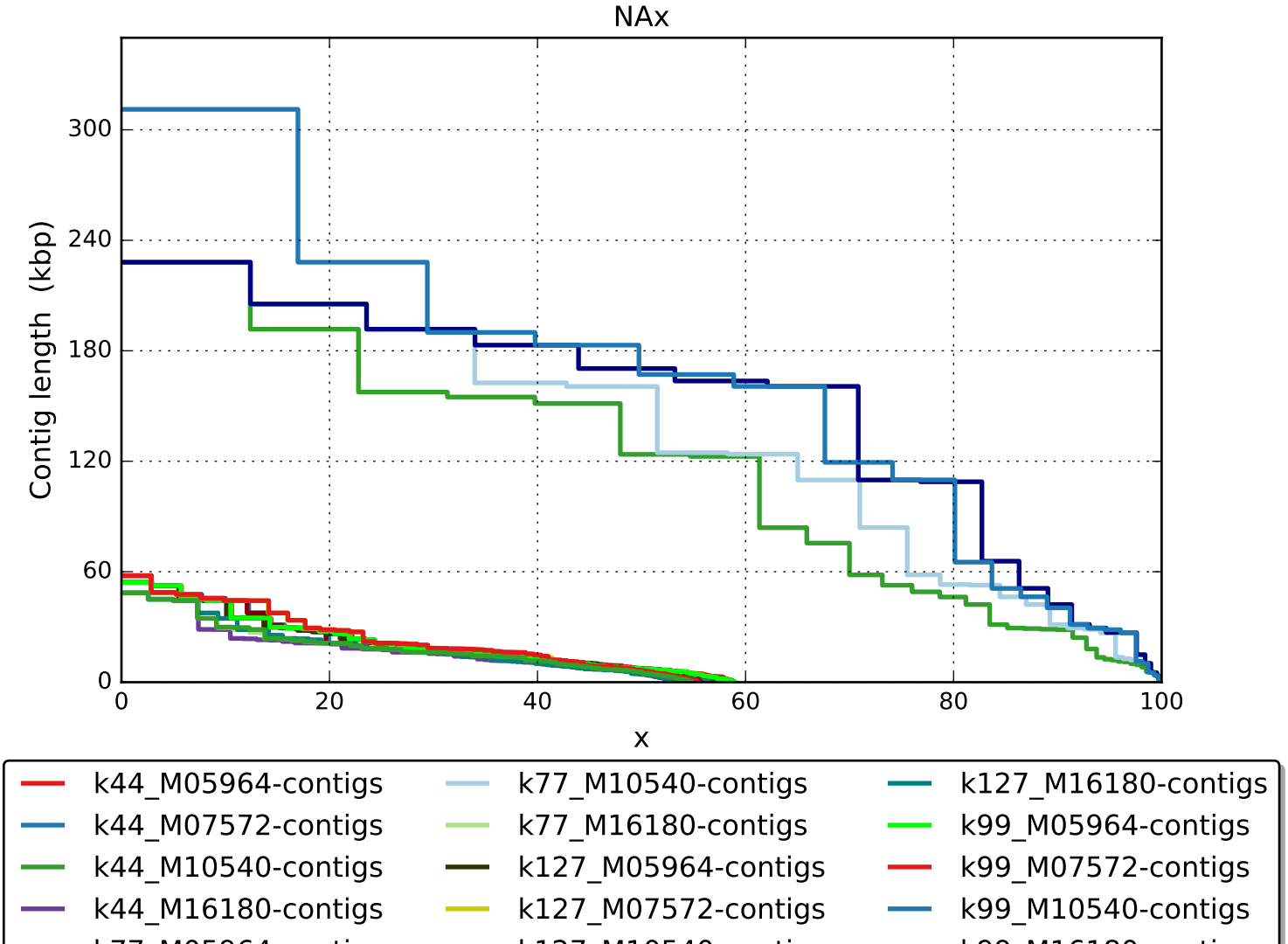

NGx
Contig length (kbp)
x
0
100
200
300
400
500
600
0
20
40
60
80
100
k44_M05964-contigs
k44_M07572-contigs
k44_M10540-contigs
k44_M16180-contigs
k77_M10540-contigs
k77_M16180-contigs
k127_M05964-contigs
k127_M07572-contigs
k127_M16180-contigs
k99_M05964-contigs
k99_M07572-contigs
k99_M10540-contigs

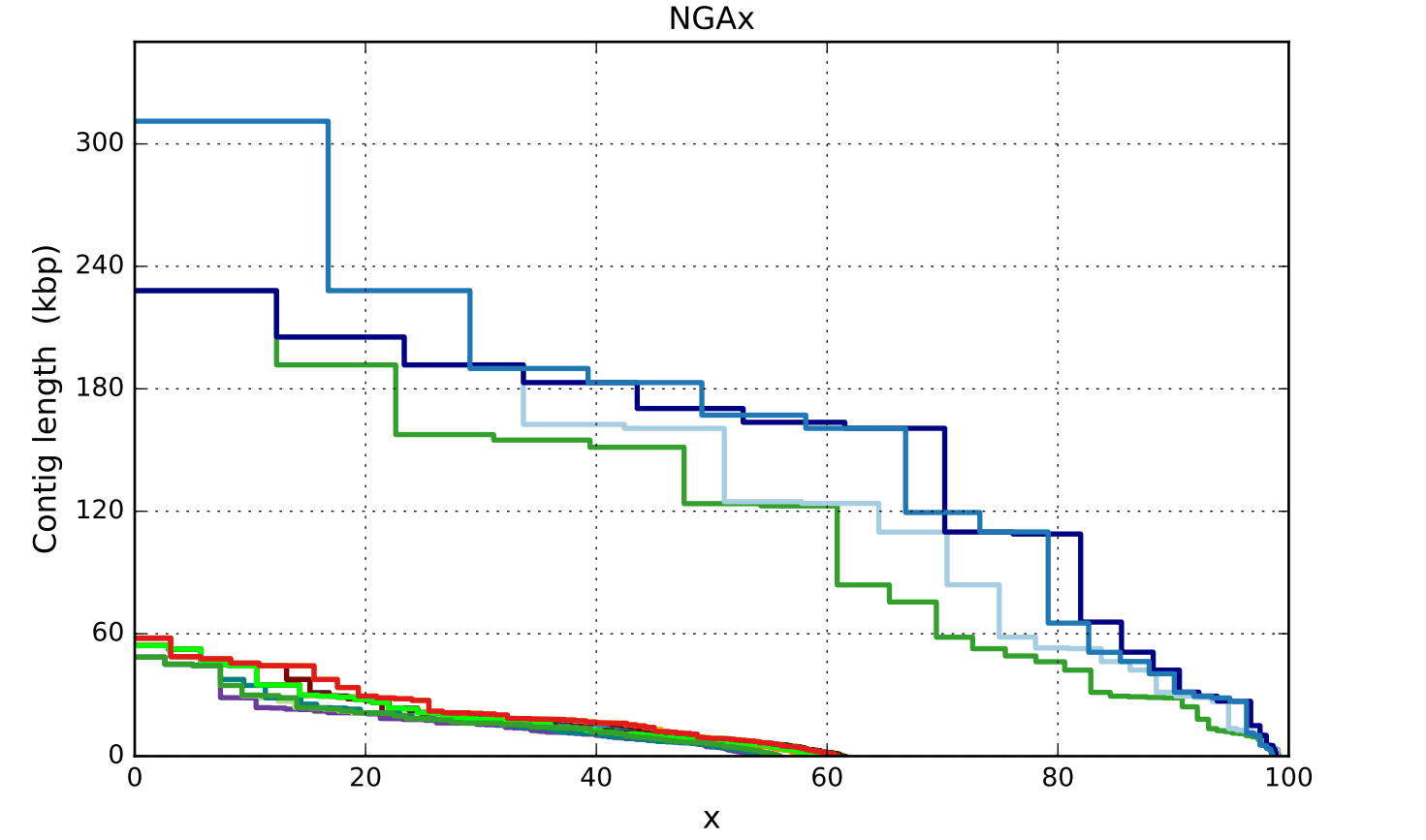

Cumulative length
Cumulative length (kbp)
Contig index
2500
2000
1500
1000
500
0
0
20
40
60
80
k44_M05964-contigs
k44_M07572-contigs
k44_M10540-contigs
k44_M16180-contigs
k77_M10540-contigs
k77_M16180-contigs
k127_M05964-contigs
k127_M07572-contigs
k99_M05964-contigs
k99_M07572-contigs
k99_M10540-contigs
k99_M16180-contigs

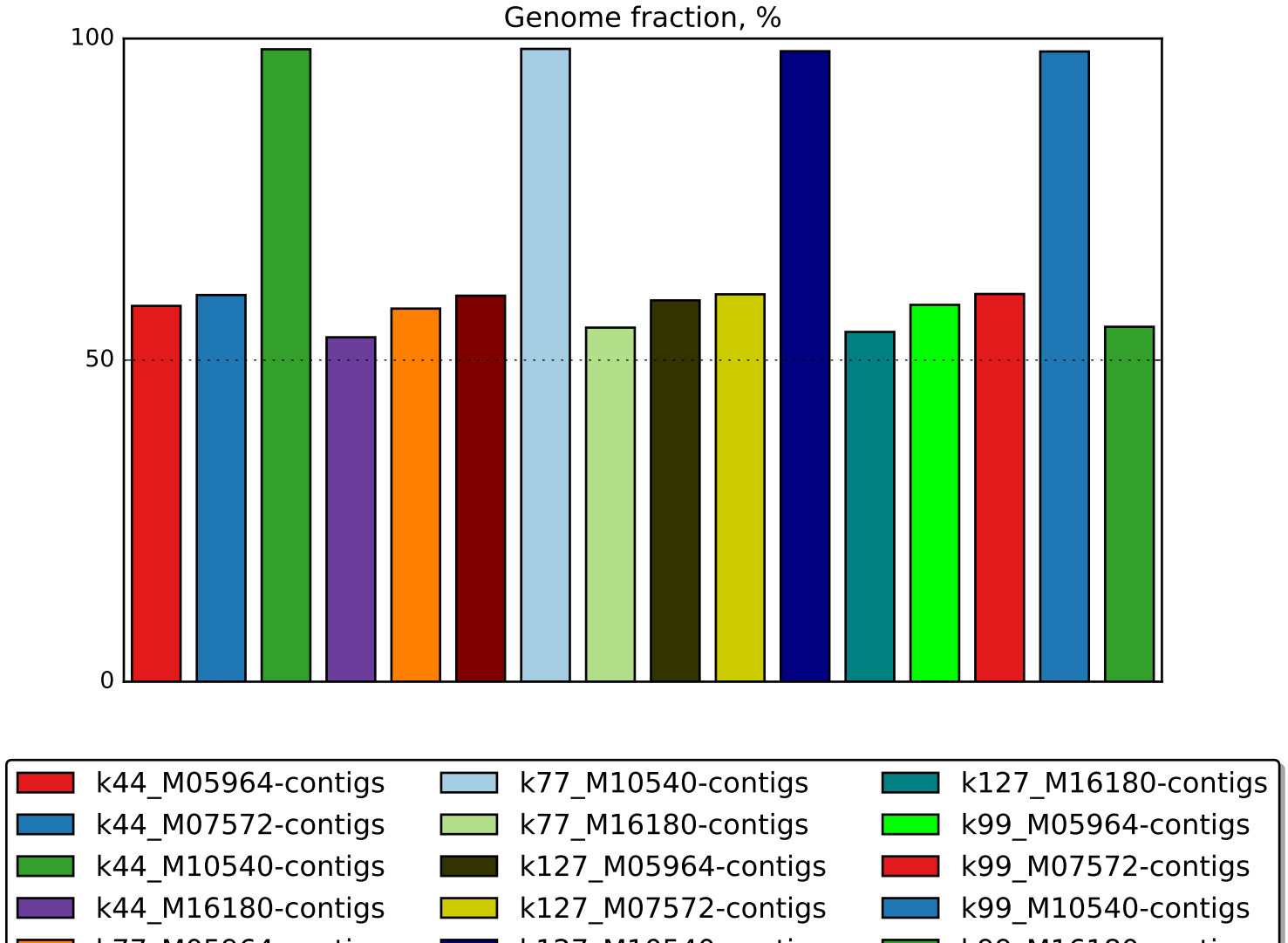

GC content
windows
GC (%)
0
300
600
900
1200
1500
0
20
40
60
80
100
k44_M05964-contigs
k44_M07572-contigs
k44_M10540-contigs
k44_M16180-contigs
k77_M10540-contigs
k77_M16180-contigs
k127_M05964-contigs
k127_M07572-contigs
k99_M05964-contigs
k99_M07572-contigs
k99_M10540-contigs
k99_M16180-contigs


Misassemblies
80
70
60
50
40
30
20
10
0
relocations
inversions


Cumulative length (aligned contigs)
Cumulative length (kbp)
Contig index
0
400
800
1200
1600
2000
0
30
60
90
120
k44_M05964-contigs
k44_M07572-contigs
k44_M10540-contigs
k44_M16180-contigs
k77_M10540-contigs
k77_M16180-contigs
k127_M05964-contigs
k127_M07572-contigs
k99_M05964-contigs
k99_M07572-contigs
k99_M10540-contigs
k99_M16180-contigs


NAx
Contig length (kbp)
0
60
120
180
240
300
0
20
40
60
80
100
x
k44_M05964-contigs
k44_M07572-contigs
k44_M10540-contigs
k44_M16180-contigs
k77_M10540-contigs
k77_M16180-contigs
k127_M05964-contigs
k127_M07572-contigs
k127_M16180-contigs
k99_M05964-contigs
k99_M07572-contigs
k99_M10540-contigs


NGAx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
k44_M05964-contigs
k44_M07572-contigs
k44_M10540-contigs
k44_M16180-contigs
k77_M10540-contigs
k77_M16180-contigs
k127_M05964-contigs
k127_M07572-contigs
k127_M16180-contigs
k99_M05964-contigs
k99_M07572-contigs
k99_M10540-contigs


Genome fraction, %
100
50
0
k44_M05964-contigs
k44_M07572-contigs
k44_M10540-contigs
k44_M16180-contigs
k77_M10540-contigs
k77_M16180-contigs
k127_M05964-contigs
k127_M07572-contigs
k127_M16180-contigs
k99_M05964-contigs
k99_M07572-contigs
k99_M10540-contigs