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	1819370	1819370	1819370	1819370	1819370	1819370	1819370	1819370	1819370	1819370	1819370	1819370	1819370	1819370	1819370	1819370
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 (%)	38.02	38.02	38.02	38.02	38.02	38.02	38.02	38.02	38.02	38.02	38.02	38.02	38.02	38.02	38.02	38.02
N50	97979	80448	157960	82364	144973	103159	285281	100164	183050	141208	333934	138055	182978	141152	311520	125281
NG50	97979	84558	157960	82364	144973	130205	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	38074	63553	36285	60895	67108	191715	57916	81560	93346	191716	116061	79438	81353	189976	78232
L50	5	9	4	7	4	6	3	5	3	5	3	5	3	5	3	5
LG50	5	8	4	7	4	5	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	16	8	14	9	11	5	11	7	8	5	8	7	9	5	9
# misassemblies	15	21	40	21	19	27	51	26	25	29	38	27	18	29	46	27
# misassembled contigs	8	14	10	12	13	14	9	14	12	12	7	11	10	12	7	13
Misassembled contigs length	881744	1105204	770069	1117632	1294126	1391438	939232	1292145	1494625	1476437	619899	1472413	1338987	1416980	913230	1569617
# local misassemblies	43	58	28	59	46	62	30	65	41	64	23	69	46	65	29	67
# unaligned contigs	3 + 4 part	28 + 15 part	3 + 11 part	11 + 11 part	1 + 3 part	25 + 8 part	2 + 8 part	3 + 8 part	2 + 3 part	15 + 6 part	2 + 4 part	0 + 6 part	2 + 4 part	16 + 7 part	3 + 5 part	0 + 7 part
Unaligned length	57515	254793	589778	110689	7061	221226	497126	85160	9096	198836	623515	48538	10371	219456	484124	52968
Genome fraction (%)	92.953	88.172	52.039	87.928	93.351	88.390	52.018	87.698	93.607	88.562	51.715	88.736	93.596	88.480	52.062	88.910
Duplication ratio	1.058	1.085	1.323	1.096	1.088	1.120	1.420	1.120	1.135	1.145	1.292	1.139	1.089	1.128	1.425	1.136
# 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	1970.18	2350.80	3495.09	2421.16	1977.87	2348.54	3509.70	2425.56	1969.39	2348.90	3501.27	2396.20	1966.63	2347.71	3515.84	2396.08
# indels per 100 kbp	54.22	61.65	88.09	68.76	54.64	62.56	88.97	68.38	55.84	63.99	88.96	68.26	54.97	63.36	89.00	69.55
Largest alignment	183233	206866	39659	183383	255309	255395	39833	183363	255656	255411	39887	183344	255391	255407	68097	183344
NA50	71947	33471	2874	33438	60423	35008	2973	42937	58073	46185	2224	51788	74751	45093	2723	43069
NGA50	71947	35008	3236	40038	74751	45071	3637	46317	74751	51885	2697	57400	74751	51885	3236	46339
NA75	27502	11072	-	16250	27683	14058	-	19061	32484	14058	-	22478	31745	14058	-	22037
NGA75	27502	20478	-	19035	30252	22141	-	21536	41616	26518	-	25894	38878	22530	-	27937
LA50	8	15	74	13	8	13	70	11	8	12	77	10	7	12	68	11
LGA50	8	13	70	12	7	11	66	10	7	10	73	9	7	10	66	10
LA75	19	38	-	31	19	34	-	27	19	31	-	24	17	32	-	26
LGA75	19	30	-	29	18	26	-	25	16	23	-	22	16	24	-	23

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

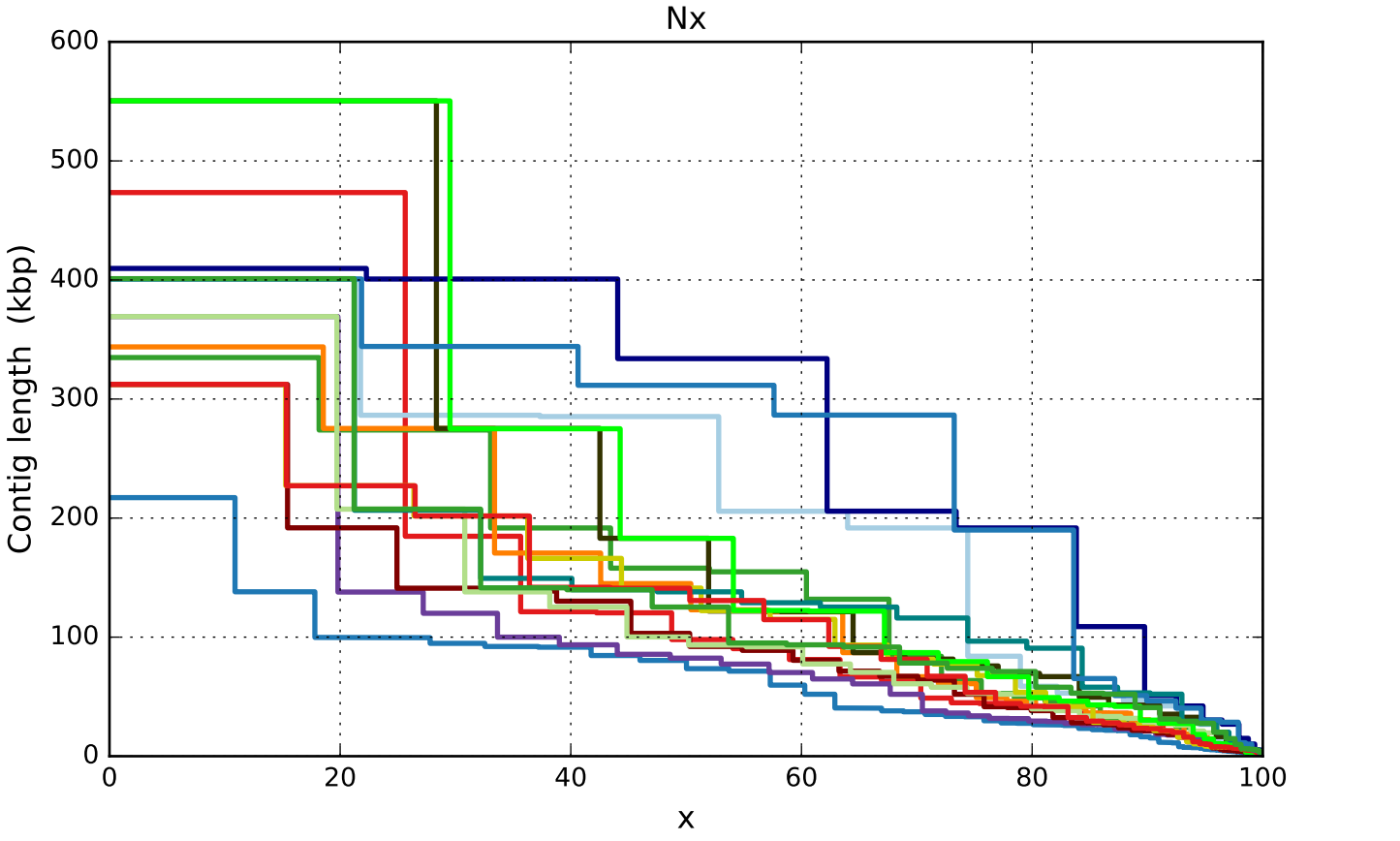
	k44_M05964-contigs	k44_M07572-contigs	k44_M10540-contigs	k44_M16180-contigs	k77_M05964-contigs	k77_M07572-contigs	k77_M10540-contigs	k77_M16180-contigs	k127_M05964-contigs	k127_M07572-contigs	k127_M10540-contigs	k127_M16180-contigs	k99_M05964-contigs	k99_M07572-contigs	k99_M10540-contigs	k99_M16180-contigs
# misassemblies	15	21	40	21	19	27	51	26	25	29	38	27	18	29	46	27
# relocations	15	21	40	21	18	27	50	26	25	29	38	27	18	29	46	27
# translocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# inversions	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0
# misassembled contigs	8	14	10	12	13	14	9	14	12	12	7	11	10	12	7	13
Misassembled contigs length	881744	1105204	770069	1117632	1294126	1391438	939232	1292145	1494625	1476437	619899	1472413	1338987	1416980	913230	1569617
# local misassemblies	43	58	28	59	46	62	30	65	41	64	23	69	46	65	29	67
# mismatches	33319	37711	33091	38732	33592	37768	33216	38701	33540	37847	32943	38685	33489	37793	33302	38759
# indels	917	989	834	1100	928	1006	842	1091	951	1031	837	1102	936	1020	843	1125
# short indels	811	872	755	979	818	885	763	964	840	903	757	969	824	897	763	984
# long indels	106	117	79	121	110	121	79	127	111	128	80	133	112	123	80	141
Indels length	3070	3337	2047	3523	3090	3382	2048	3496	3139	3475	2032	3592	3139	3467	2112	3737

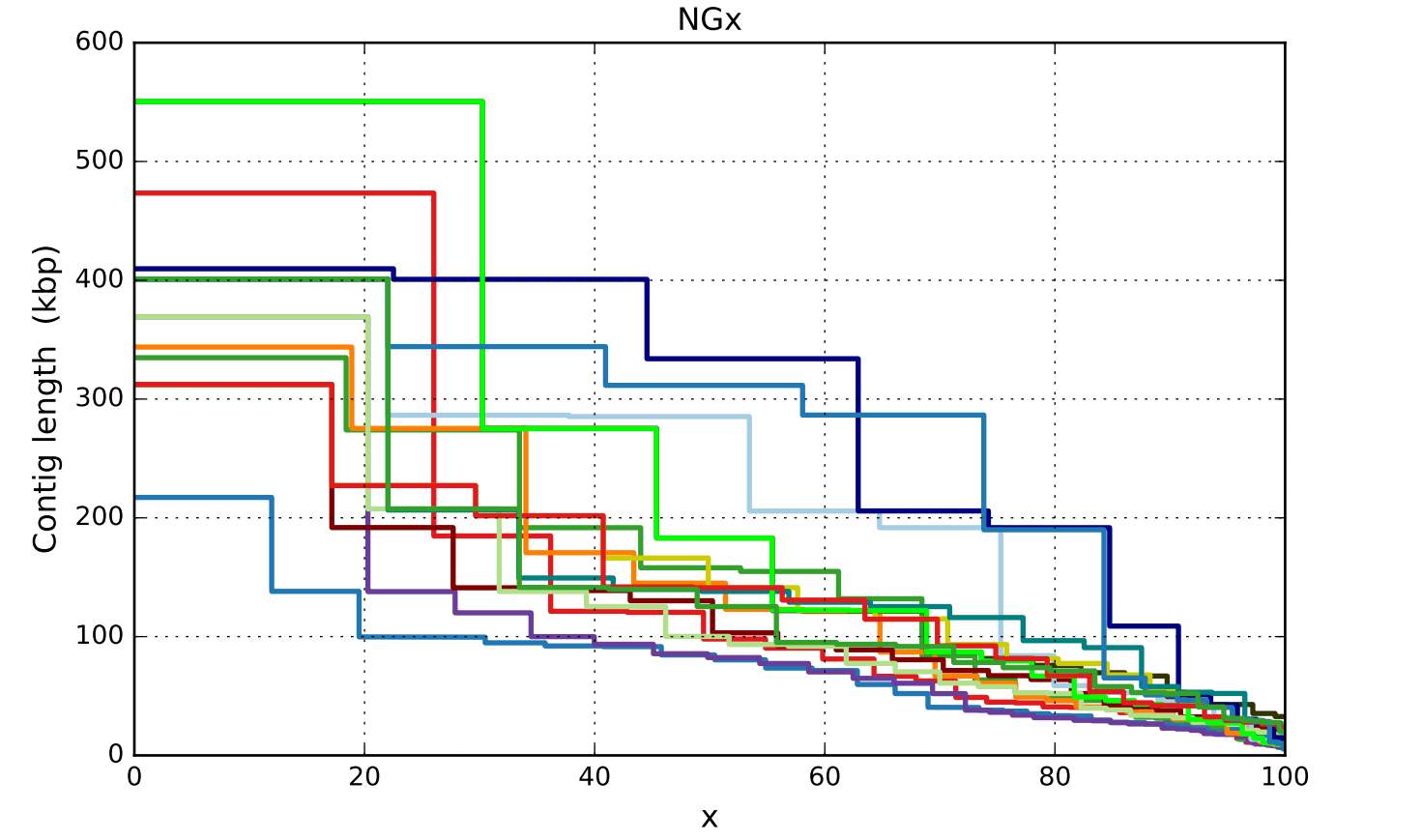
All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

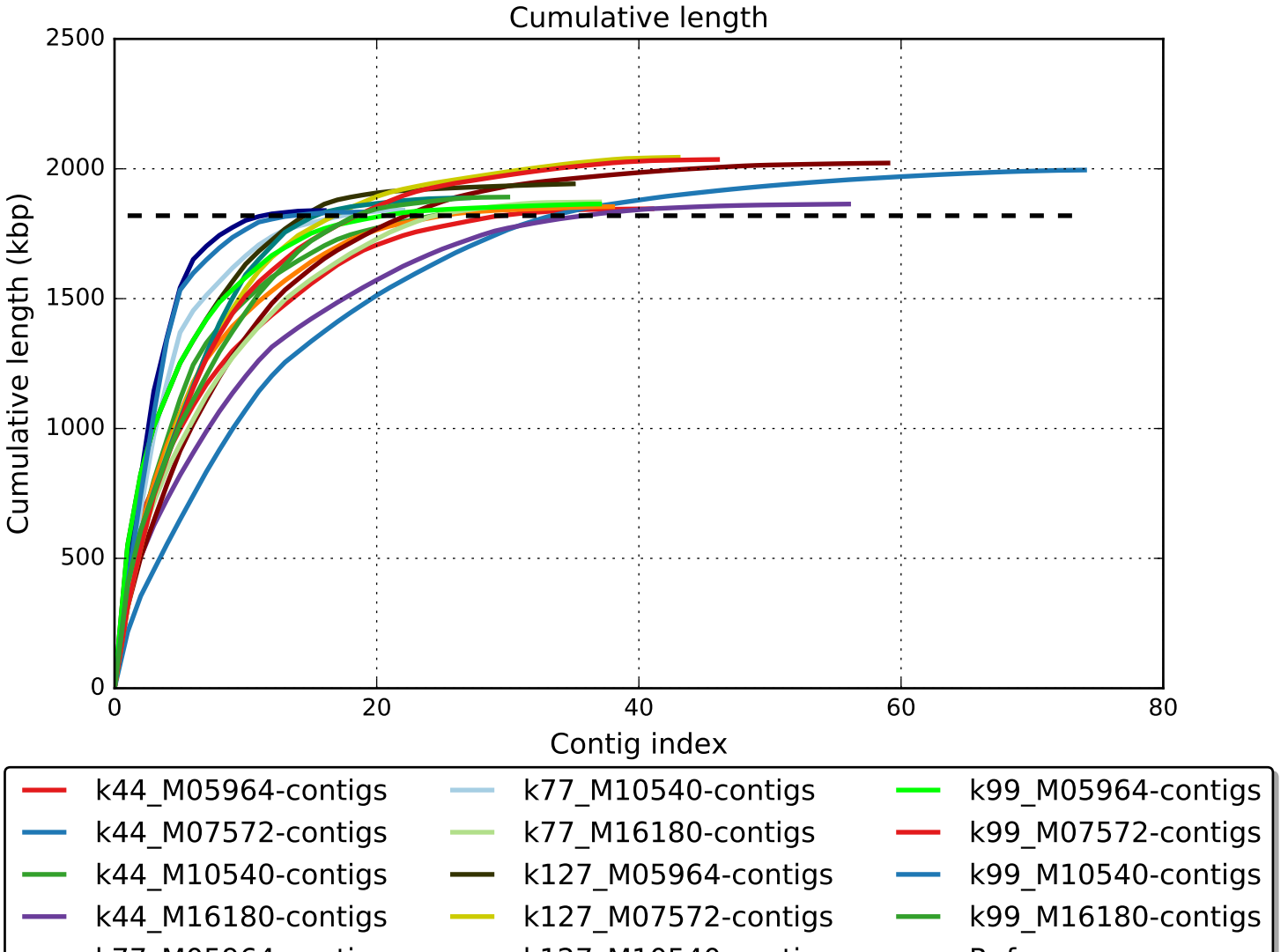
Unaligned report

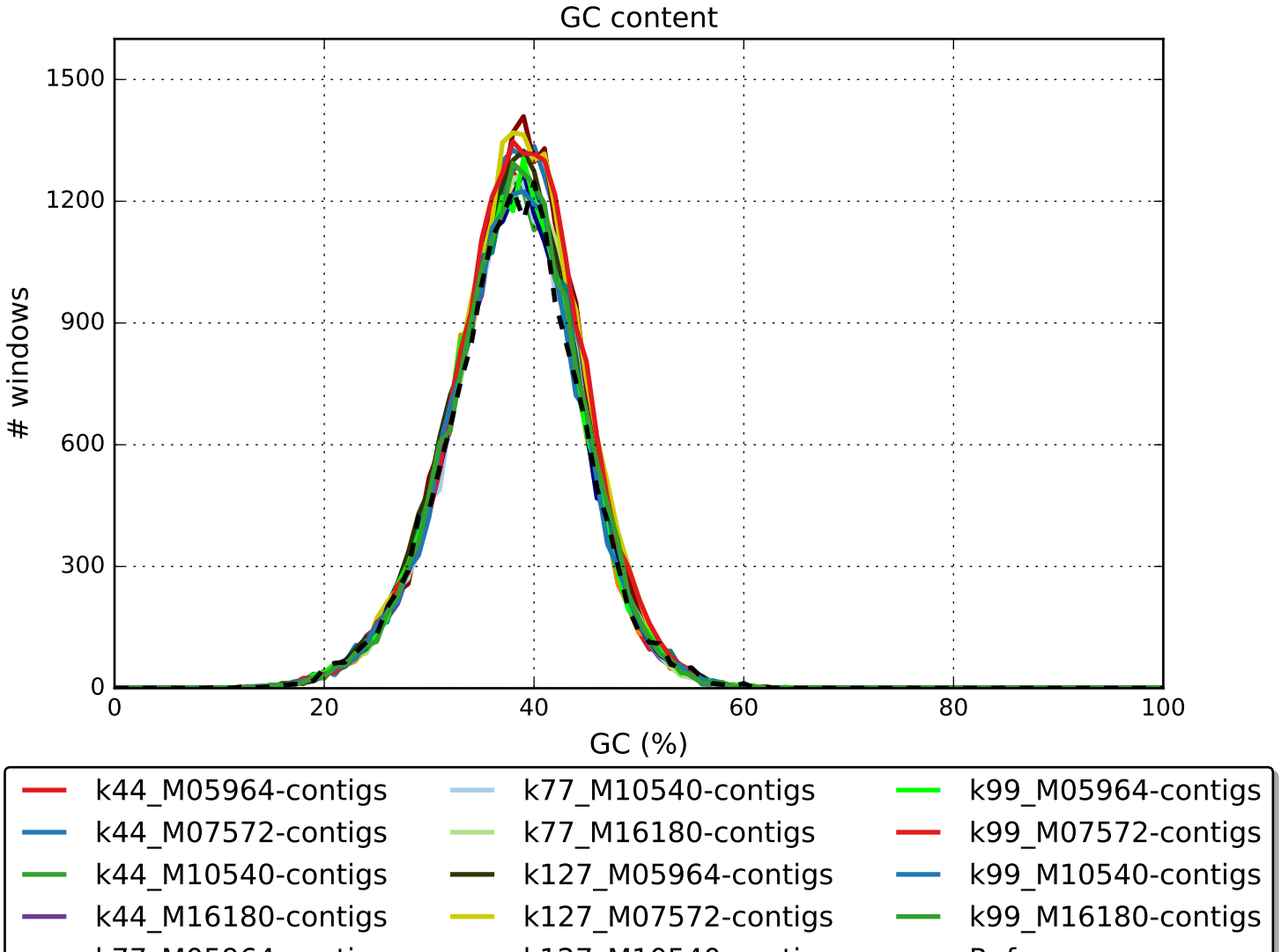
	k44_M05964-contigs	k44_M07572-contigs	k44_M10540-contigs	k44_M16180-contigs	k77_M05964-contigs	k77_M07572-contigs	k77_M10540-contigs	k77_M16180-contigs	k127_M05964-contigs	k127_M07572-contigs	k127_M10540-contigs	k127_M16180-contigs	k99_M05964-contigs	k99_M07572-contigs	k99_M10540-contigs	k99_M16180-contigs
# fully unaligned contigs	3	28	3	11	1	25	2	3	2	15	2	0	2	16	3	0
Fully unaligned length	46945	168145	11615	49652	1804	128924	10649	2770	4647	133749	10749	0	4414	128959	11513	0
# partially unaligned contigs	4	15	11	11	3	8	8	8	3	6	4	6	4	7	5	7
# with misassembly	0	3	8	2	0	2	7	1	1	1	4	0	1	1	4	1
# both parts are significant	3	11	11	9	2	4	8	6	2	3	4	5	2	2	5	6
Partially unaligned length	10570	86648	578163	61037	5257	92302	486477	82390	4449	65087	612766	48538	5957	90497	472611	52968
# N's	153	166	1	27	22	10	0	15	0	0	0	0	0	0	1	1

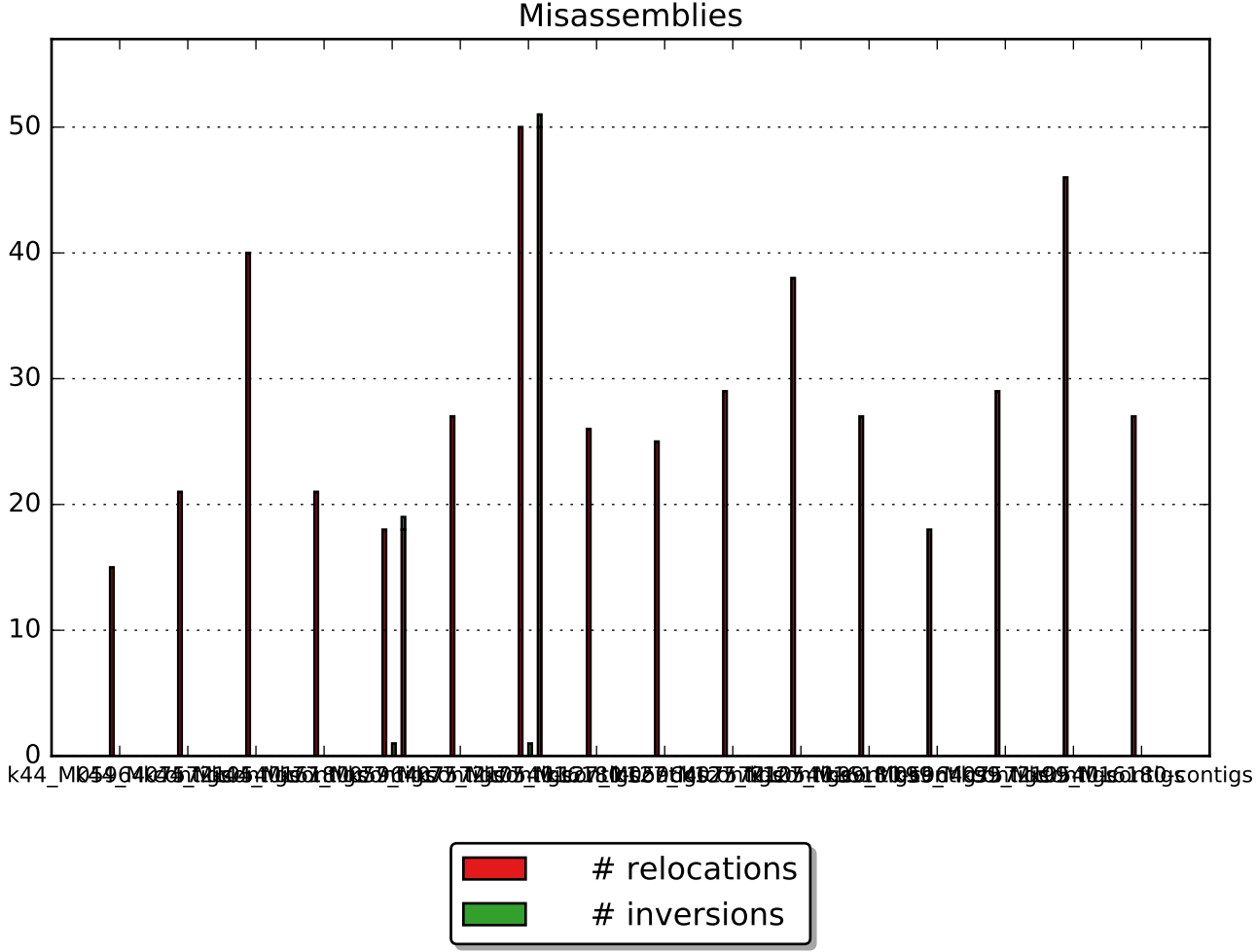
All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

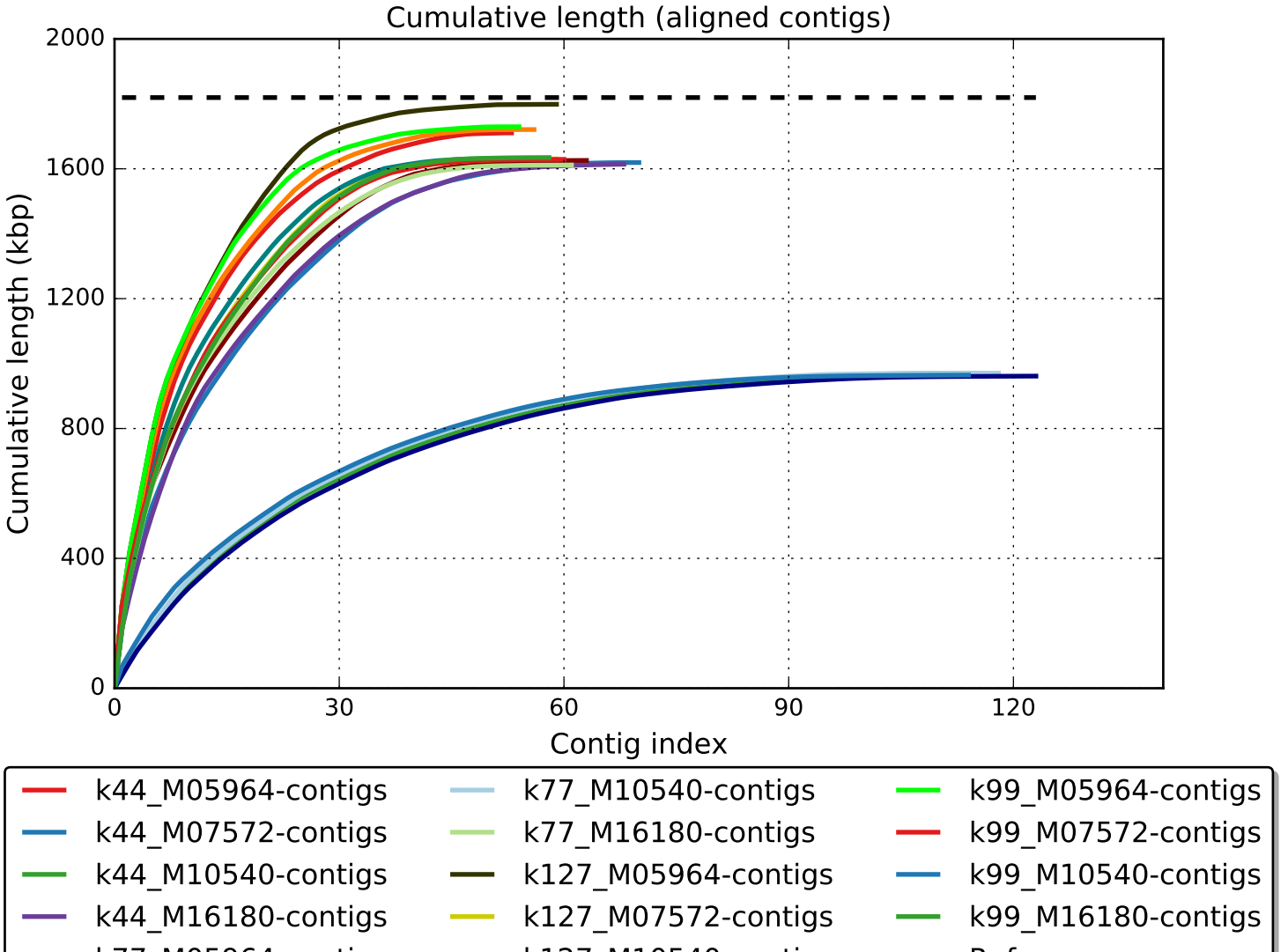

Nx
Contig length (kbp)
x
0
100
200
300
400
500
600
0
20
40
60
80
100
k44_M05964-contigs
k44_M07572-contigs
k44_M10540-contigs
k44_M16180-contigs
k77_M10540-contigs
k77_M16180-contigs
k127_M05964-contigs
k127_M07572-contigs
k127_M16180-contigs
k99_M05964-contigs
k99_M07572-contigs
k99_M10540-contigs

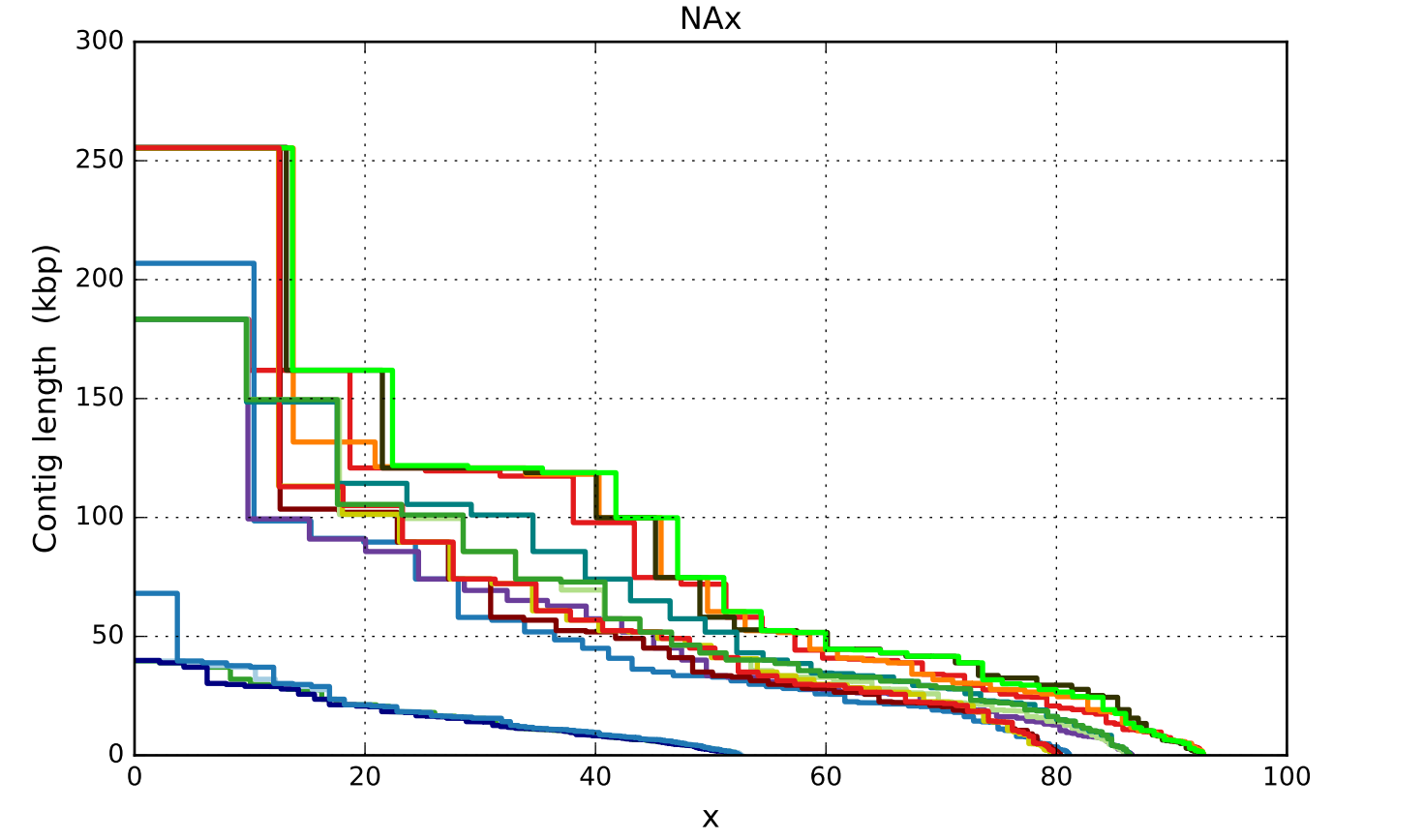

NGx
Contig length (kbp)
600
500
400
300
200
100
0
0
20
40
60
80
100
x
k44_M05964-contigs
k44_M07572-contigs
k44_M10540-contigs
k44_M16180-contigs
k77_M10540-contigs
k77_M16180-contigs
k127_M05964-contigs
k127_M07572-contigs
k127_M16180-contigs
k99_M05964-contigs
k99_M07572-contigs
k99_M10540-contigs

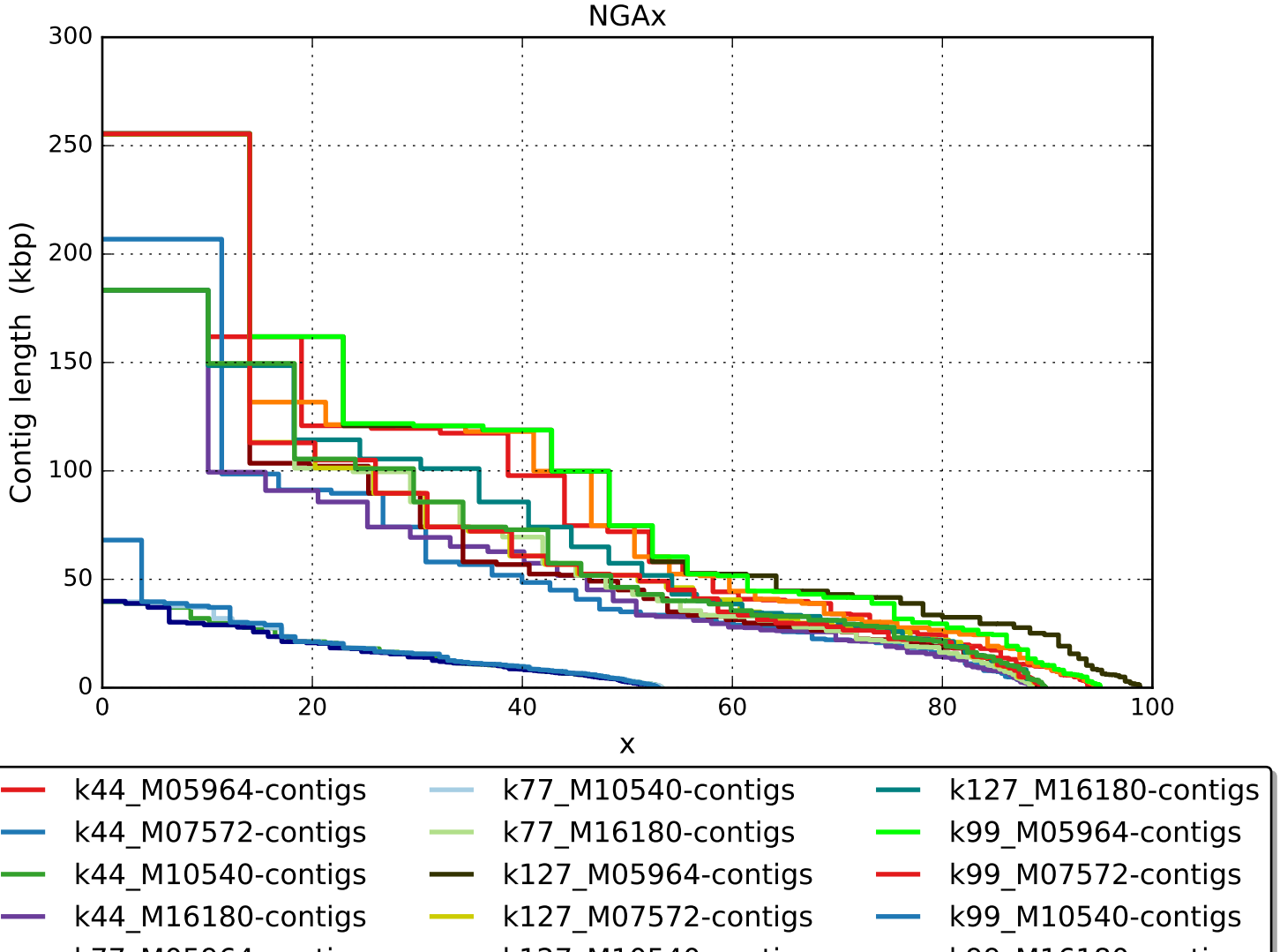

Cumulative length
Cumulative length (kbp)
Contig index
2500
2000
1500
1000
500
0
0
20
40
60
80
k44_M05964-contigs
k44_M07572-contigs
k44_M10540-contigs
k44_M16180-contigs
k77_M10540-contigs
k77_M16180-contigs
k127_M05964-contigs
k127_M07572-contigs
k99_M05964-contigs
k99_M07572-contigs
k99_M10540-contigs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

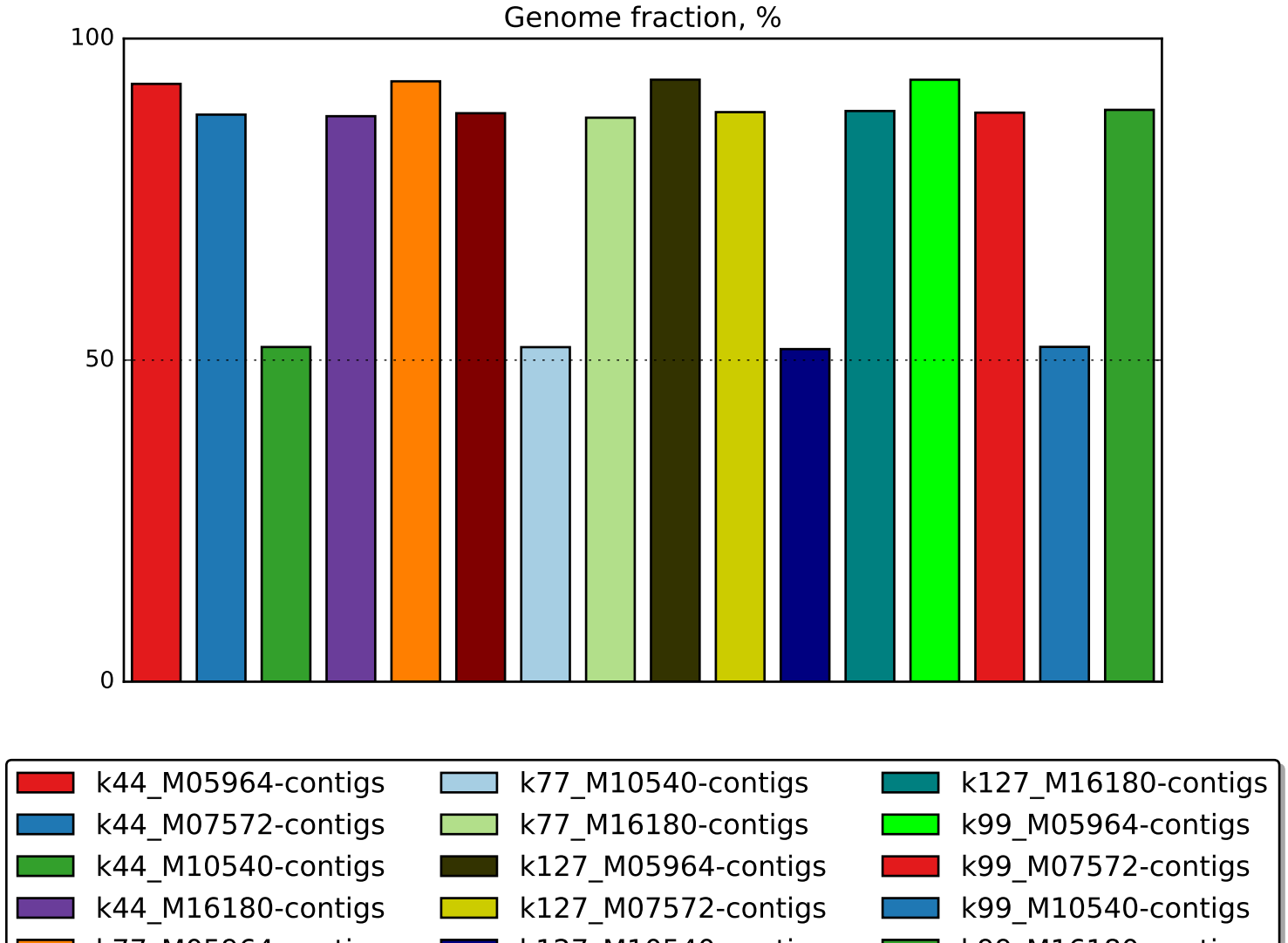

GC content
windows
GC (%)
0
300
600
900
1200
1500
0
20
40
60
80
100
k44_M05964-contigs
k44_M07572-contigs
k44_M10540-contigs
k44_M16180-contigs
k77_M10540-contigs
k77_M16180-contigs
k127_M05964-contigs
k127_M07572-contigs
k99_M05964-contigs
k99_M07572-contigs
k99_M10540-contigs
k99_M16180-contigs


Misassemblies
50
40
30
20
10
0
k44_M
contigs
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)
x
0
50
100
150
200
250
300
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


NGAx
Contig length (kbp)
x
0
50
100
150
200
250
300
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


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