

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	1830138	1830138	1830138	1830138	1830138	1830138	1830138	1830138	1830138	1830138	1830138	1830138	1830138	1830138	1830138	1830138
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 (%)	38.15	38.15	38.15	38.15	38.15	38.15	38.15	38.15	38.15	38.15	38.15	38.15	38.15	38.15	38.15	38.15
N50	97979	80448	157960	82364	144973	103159	285281	100164	183050	141208	333934	138055	182978	141152	311520	125281
NG50	97979	84558	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	38074	63553	36285	60895	67108	83976	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	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	16	8	14	9	11	6	11	7	8	5	8	7	9	5	9
# misassemblies	32	35	49	30	43	42	54	37	47	45	73	38	45	43	68	38
# misassembled contigs	14	18	13	14	19	16	10	17	17	15	10	11	18	14	9	14
Misassembled contigs length	1385046	1353349	1274384	1140572	1644783	1592056	1323911	1448480	1766328	1756409	1748569	1581228	1685018	1676583	1642440	1579248
# local misassemblies	63	62	33	45	62	66	35	57	68	68	43	63	64	68	40	66
# unaligned contigs	6 + 2 part	30 + 9 part	1 + 10 part	15 + 10 part	5 + 0 part	23 + 9 part	1 + 7 part	9 + 4 part	3 + 0 part	15 + 6 part	1 + 2 part	5 + 3 part	5 + 0 part	16 + 7 part	1 + 5 part	6 + 3 part
Unaligned length	84481	233209	332786	125223	22076	198377	308187	98935	12276	181485	53718	60702	22862	199785	125346	66186
Genome fraction (%)	86.007	88.255	56.735	86.794	86.315	88.490	56.578	87.436	86.544	88.547	55.910	88.311	86.452	88.573	56.249	88.404
Duplication ratio	1.119	1.091	1.454	1.095	1.160	1.126	1.480	1.108	1.218	1.150	1.745	1.131	1.164	1.133	1.659	1.128
# 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	2503.11	2303.19	3746.77	2227.39	2499.48	2302.83	3747.89	2220.10	2492.05	2302.07	3736.68	2215.48	2499.43	2296.65	3745.16	2216.43
# indels per 100 kbp	75.09	73.86	101.32	72.59	75.46	74.78	102.08	72.93	76.08	74.30	100.86	73.75	76.03	74.52	100.64	73.55
Largest alignment	146760	110672	67112	111261	146760	110672	74272	125826	146760	112912	74272	125826	146760	110672	74272	125826
NA50	35835	29964	6591	35706	38389	36359	6605	36363	38389	38410	6805	41004	38765	36413	6988	38749
NGA50	35835	35717	6605	36395	38389	37887	6605	38749	40061	40982	6805	46355	40061	39695	6988	41004
NA75	12742	10251	-	14779	12889	10454	-	16870	12582	10254	-	18594	12893	10254	-	18594
NGA75	12857	17504	-	15584	13678	18944	-	17538	15134	22421	-	21672	13843	21762	-	21672
LA50	15	19	51	14	14	18	47	13	15	16	43	12	14	17	43	13
LGA50	15	16	50	13	14	15	47	12	13	13	43	11	13	14	43	12
LA75	36	44	-	33	35	41	-	30	36	39	-	28	33	39	-	29
LGA75	35	35	-	31	33	31	-	29	30	28	-	26	31	29	-	27

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

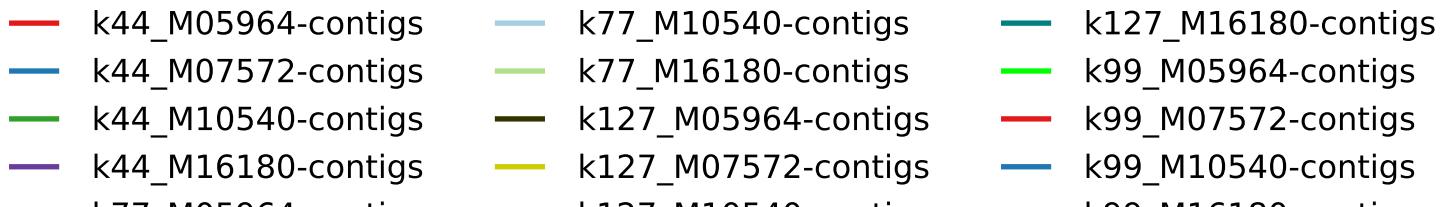
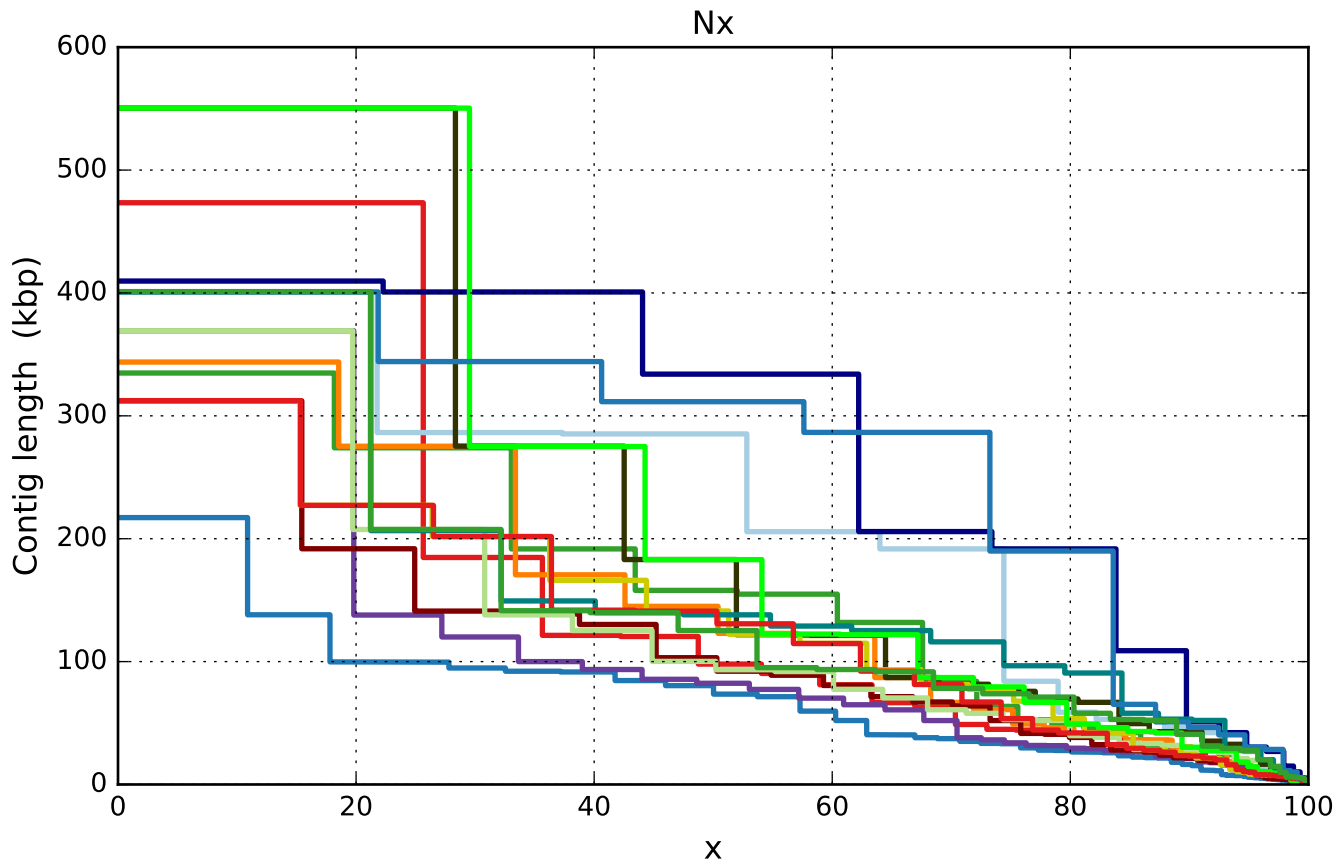
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# misassemblies	32	35	49	30	43	42	54	37	47	45	73	38	45	43	68	38
# relocations	31	35	48	30	43	42	53	37	46	45	73	38	44	43	68	38
# translocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# inversions	1	0	1	0	0	0	1	0	1	0	0	0	1	0	0	0
# misassembled contigs	14	18	13	14	19	16	10	17	17	15	10	11	18	14	9	14
Misassembled contigs length	1385046	1353349	1274384	1140572	1644783	1592056	1323911	1448480	1766328	1756409	1748569	1581228	1685018	1676583	1642440	1579248
# local misassemblies	63	62	33	45	62	66	35	57	68	68	43	63	64	68	40	66
# mismatches	39400	37201	38904	35381	39484	37294	38808	35526	39471	37306	38235	35807	39546	37229	38554	35860
# indels	1182	1193	1052	1153	1192	1211	1057	1167	1205	1204	1032	1192	1203	1208	1036	1190
# short indels	1069	1077	973	1054	1076	1097	979	1060	1086	1090	955	1085	1085	1092	958	1083
# long indels	113	116	79	99	116	114	78	107	119	114	77	107	118	116	78	107
Indels length	3101	3404	2236	3253	3183	3357	2183	3294	3279	3325	2162	3337	3181	3473	2214	3339

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).

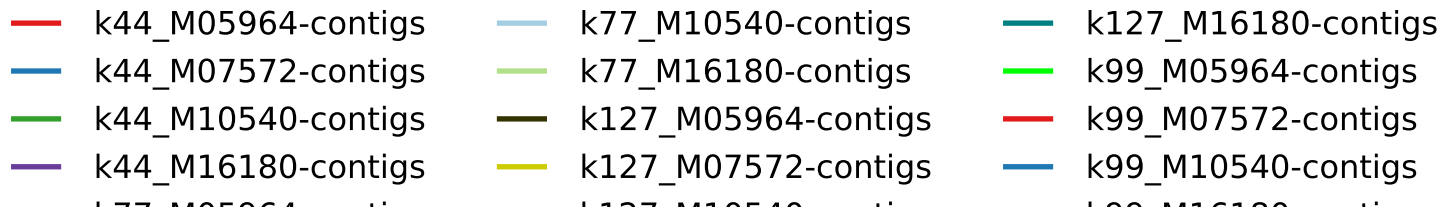
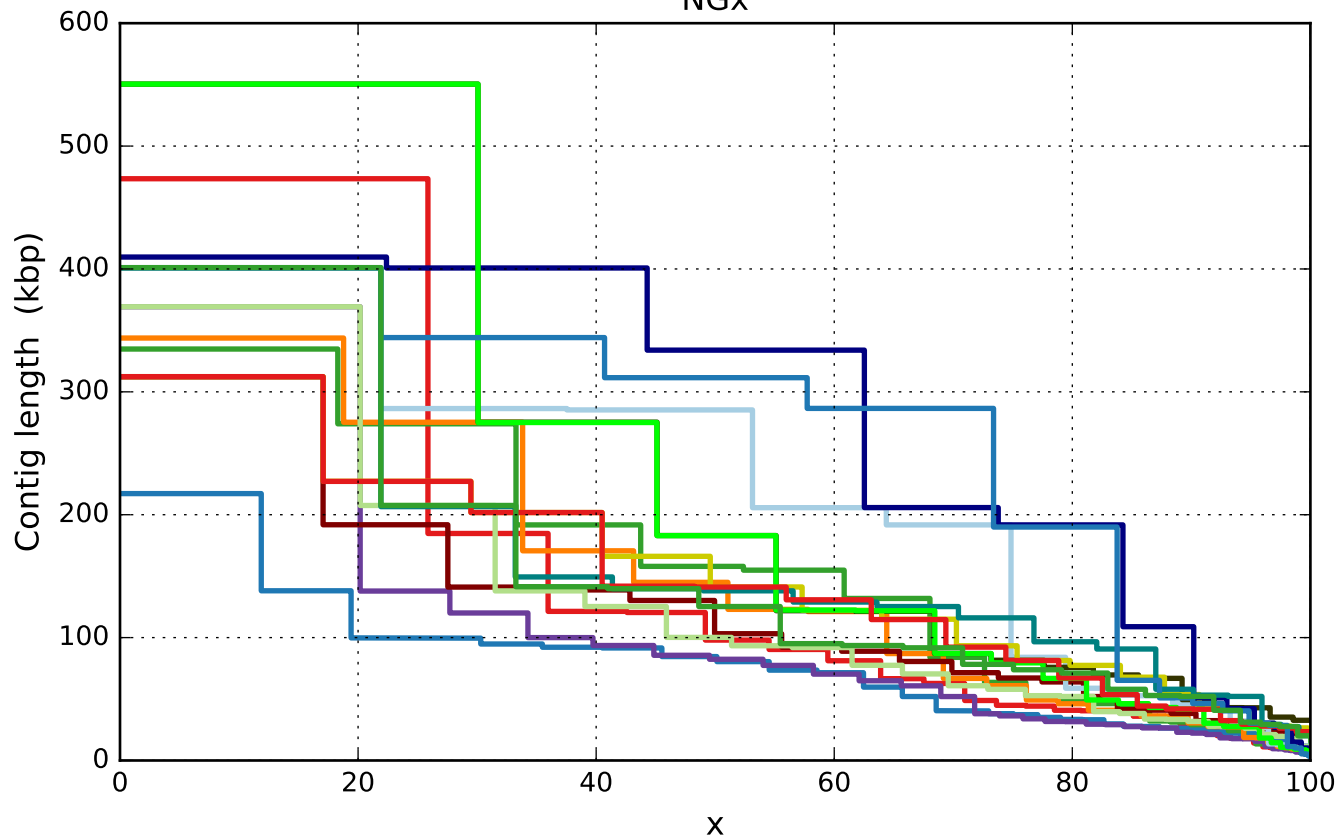
Unaligned report

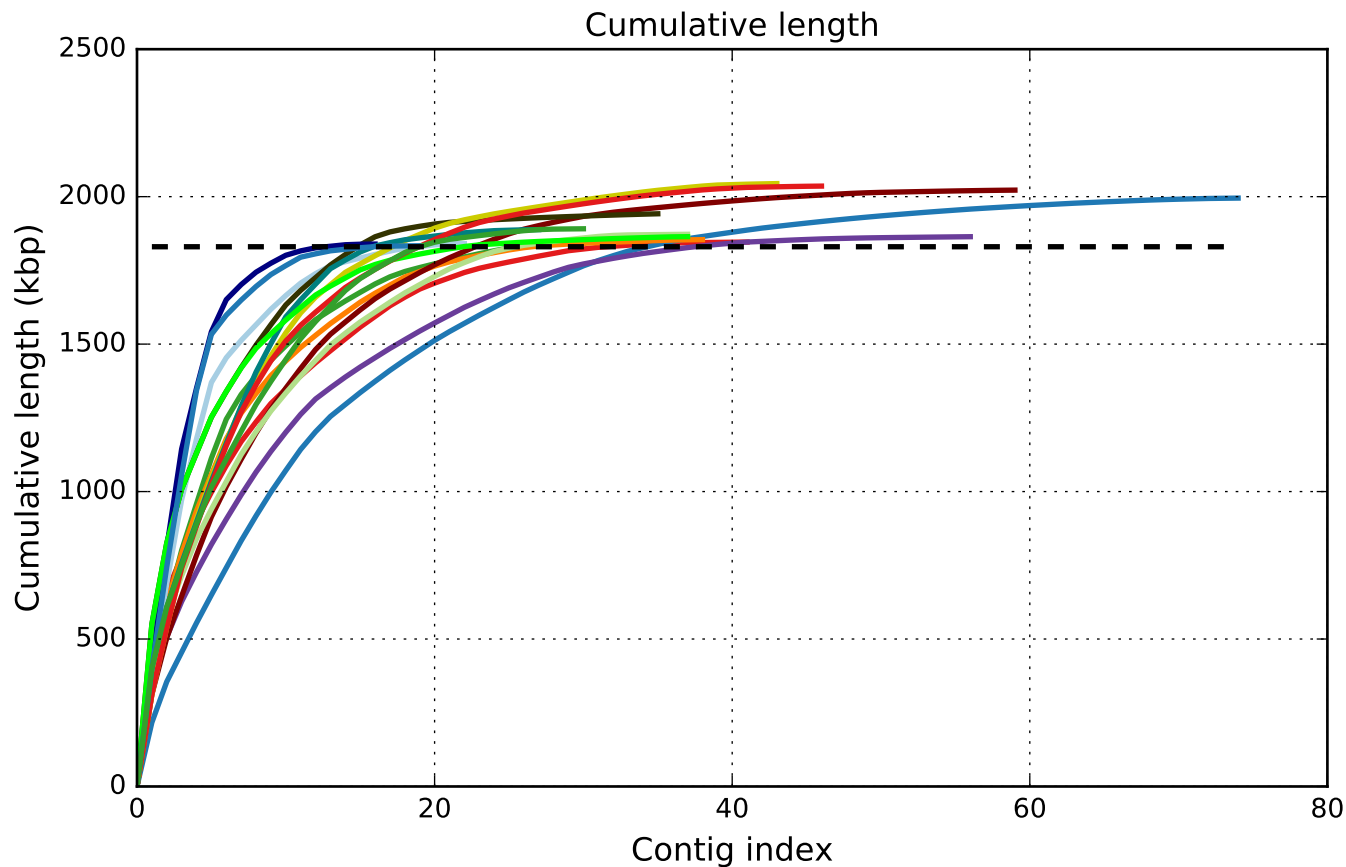
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# fully unaligned contigs	6	30	1	15	5	23	1	9	3	15	1	5	5	16	1	6
Fully unaligned length	65995	194956	582	58936	22076	114506	536	33318	12276	130694	536	24064	22862	117936	536	29812
# partially unaligned contigs	2	9	10	10	0	9	7	4	0	6	2	3	0	7	5	3
# with misassembly	1	1	6	2	0	1	6	1	0	1	2	1	0	1	3	1
# both parts are significant	2	5	8	8	0	3	6	4	0	2	2	3	0	2	3	3
Partially unaligned length	18486	38253	332204	66287	0	83871	307651	65617	0	50791	53182	36638	0	81849	124810	36374
# 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).



NGx





k44_M05964-contigs

k44_M07572-contigs

k44_M10540-contigs

k44_M16180-contigs

k77_M10540-contigs

k77_M16180-contigs

k127_M05964-contigs

k127_M07572-contigs

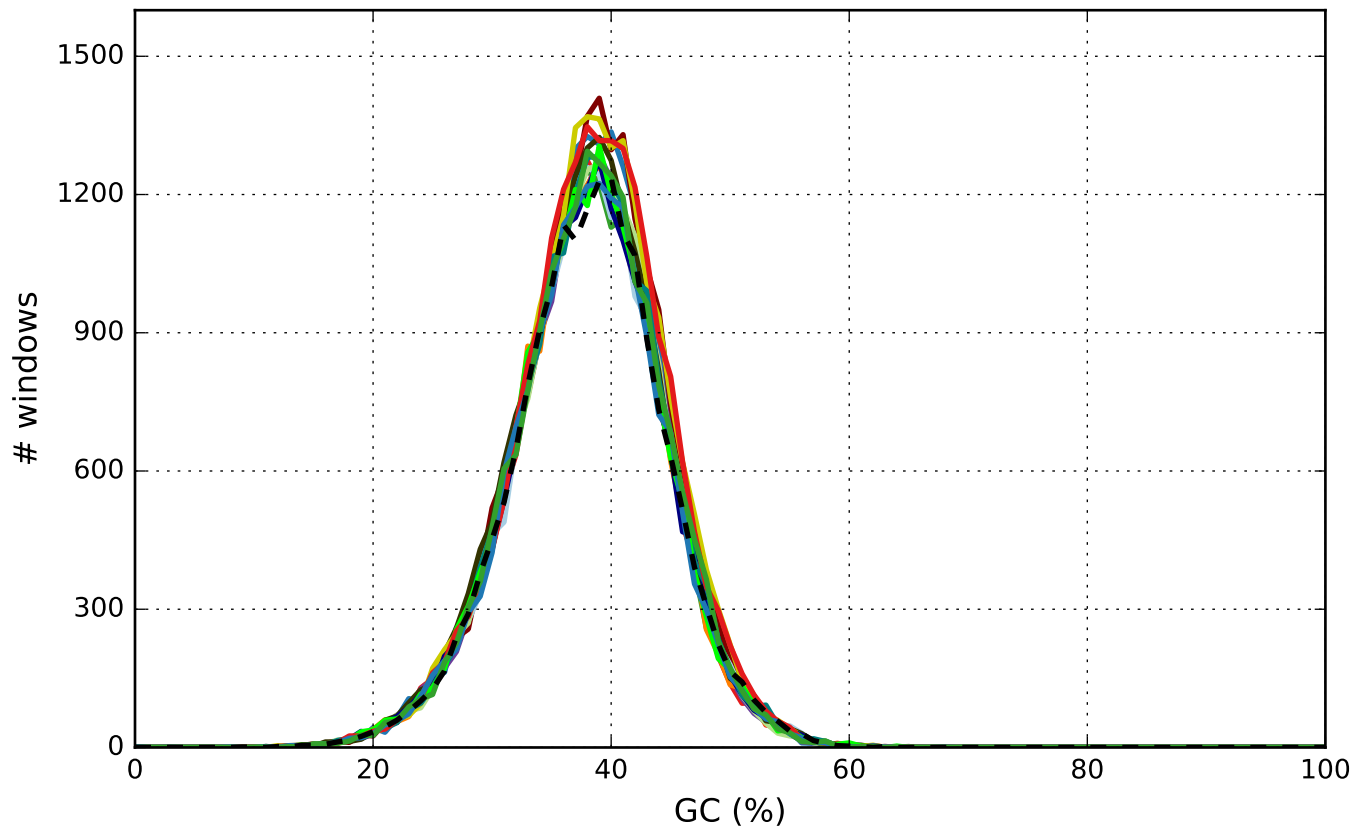
k99_M05964-contigs

k99_M07572-contigs

k99_M10540-contigs

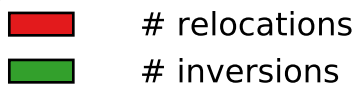
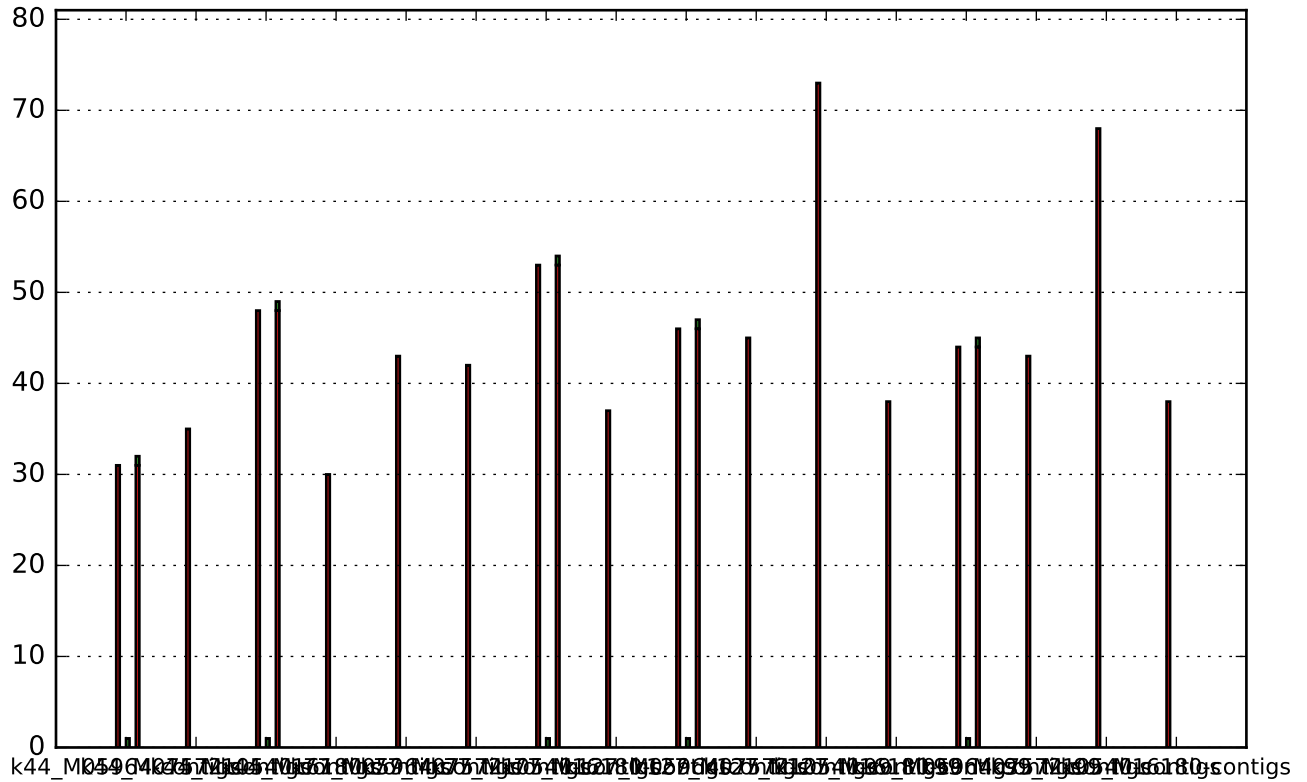
k99_M16180-contigs

GC content

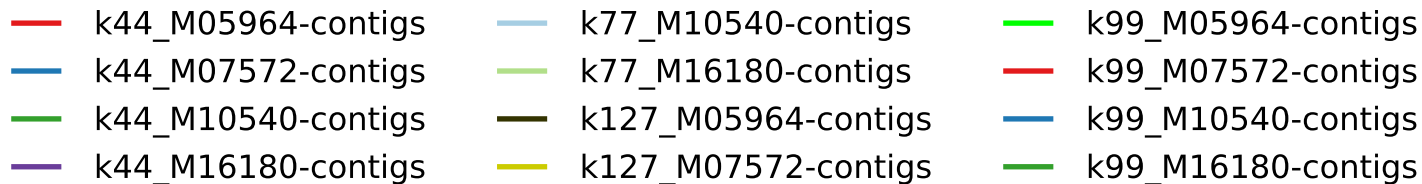
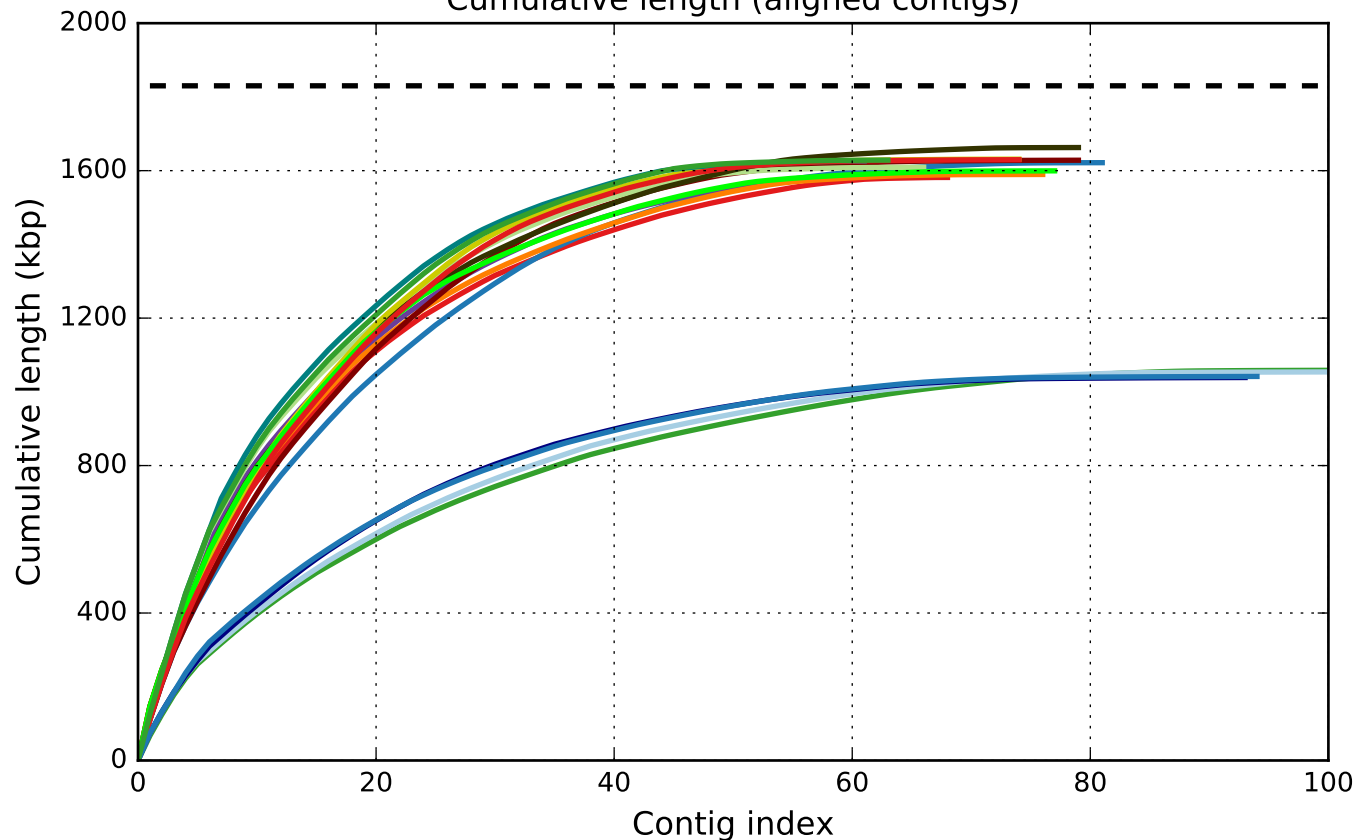


k44_M05964-contigs	k77_M10540-contigs	k99_M05964-contigs
k44_M07572-contigs	k77_M16180-contigs	k99_M07572-contigs
k44_M10540-contigs	k127_M05964-contigs	k99_M10540-contigs
k44_M16180-contigs	k127_M07572-contigs	k99_M16180-contigs

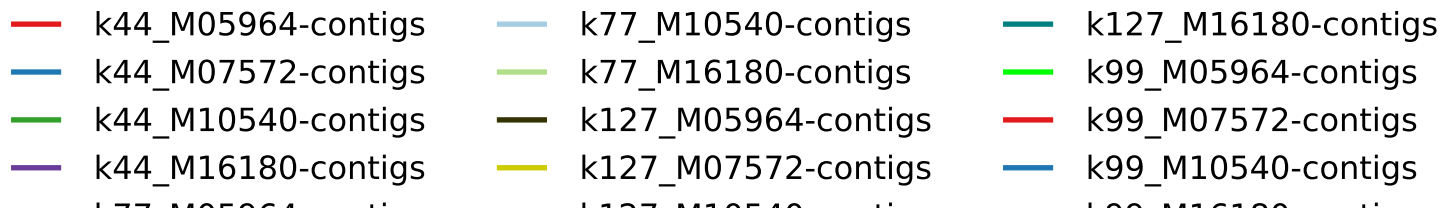
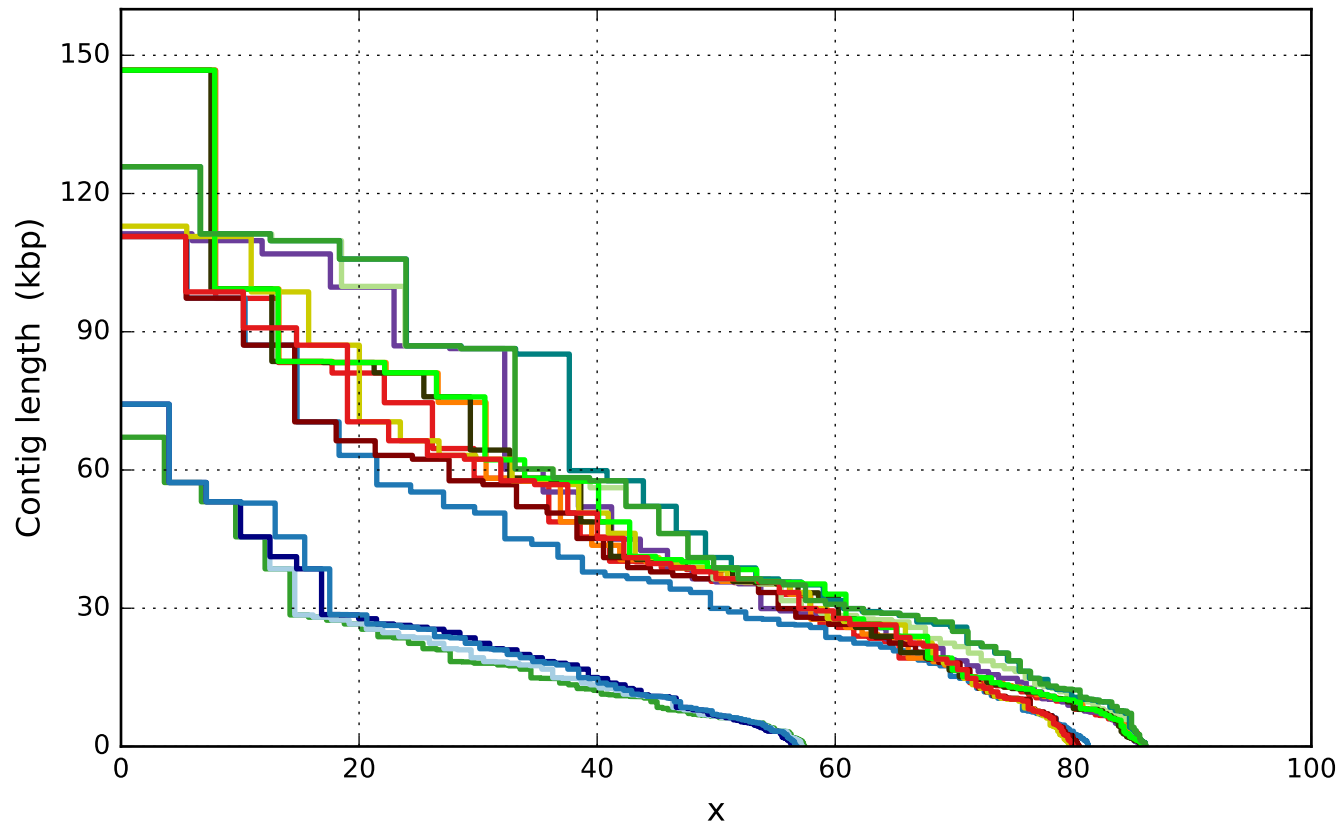
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

