

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	1969659	1969659	1969659	1969659	1969659	1969659	1969659	1969659	1969659	1969659	1969659	1969659	1969659	1969659	1969659	1969659
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 (%)	38.31	38.31	38.31	38.31	38.31	38.31	38.31	38.31	38.31	38.31	38.31	38.31	38.31	38.31	38.31	38.31
N50	97979	80448	157960	82364	144973	103159	285281	100164	183050	141208	333934	138055	182978	141152	311520	125281
NG50	97979	80448	154878	82364	122974	103159	205735	93358	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	40839	33430	49096	31585	46134	63910	58778	52076	75809	77394	191716	96606	66805	67130	189976	71139
L50	5	9	4	7	4	6	3	5	3	5	3	5	3	5	3	5
LG50	5	9	5	7	5	6	4	6	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	13	19	10	17	11	12	7	13	8	10	5	9	8	10	5	11
# misassemblies	38	33	50	40	45	44	57	44	54	42	40	49	48	44	60	49
# misassembled contigs	16	18	11	18	16	17	9	14	16	15	6	13	15	18	6	15
Misassembled contigs length	1453233	1187855	1077196	1336486	1596414	1644834	1116152	1454405	1757633	1739273	785406	1723743	1638314	1785735	1257756	1678907
# local misassemblies	52	59	38	54	53	60	39	63	57	63	32	65	56	61	42	66
# unaligned contigs	2 + 6 part	20 + 15 part	3 + 10 part	3 + 12 part	2 + 7 part	13 + 16 part	2 + 7 part	2 + 5 part	2 + 3 part	6 + 13 part	2 + 4 part	3 + 4 part	2 + 7 part	7 + 12 part	3 + 5 part	4 + 5 part
Unaligned length	75588	193473	406276	56216	34428	174480	419050	37723	21840	181435	566779	33299	35256	151189	310903	39454
Genome fraction (%)	80.557	81.217	53.465	82.456	80.434	81.375	52.537	83.288	82.401	81.769	52.408	84.112	82.305	81.689	52.481	84.146
Duplication ratio	1.116	1.126	1.364	1.113	1.149	1.153	1.374	1.118	1.183	1.157	1.233	1.120	1.128	1.171	1.473	1.117
# 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	2471.35	2335.19	3461.11	2458.47	2476.16	2355.42	3453.82	2482.87	2507.24	2290.12	3449.92	2486.24	2513.06	2304.78	3455.43	2487.58
# indels per 100 kbp	64.66	56.89	78.53	64.65	67.16	62.08	79.05	69.43	71.29	60.79	78.76	71.59	70.69	60.85	78.55	71.98
Largest alignment	132027	123383	45472	124307	178313	157773	51034	138470	178366	157773	51084	156231	178366	157773	51055	156231
NA50	38702	33411	6729	33381	36942	34006	6313	35073	42872	34948	6104	37510	58566	34879	6313	36801
NGA50	34192	34042	5581	32065	34883	34868	4392	34774	42872	36850	3633	36801	40672	34948	4147	35994
NA75	14907	8540	-	15136	16550	13299	-	19207	18748	13299	-	20222	18748	13649	-	20023
NGA75	10547	10113	-	11147	13522	13685	-	15162	16455	14907	-	16333	14399	14907	-	16305
LA50	12	18	54	16	11	16	54	14	11	14	57	13	10	15	52	13
LGA50	14	17	64	18	13	15	65	15	11	13	70	14	11	14	64	14
LA75	31	43	-	36	29	39	-	31	28	37	-	28	26	37	-	29
LGA75	37	41	-	42	35	37	-	36	30	33	-	32	31	34	-	32

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

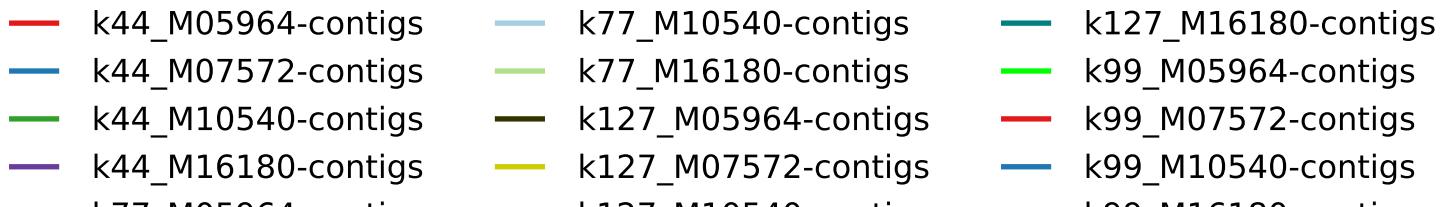
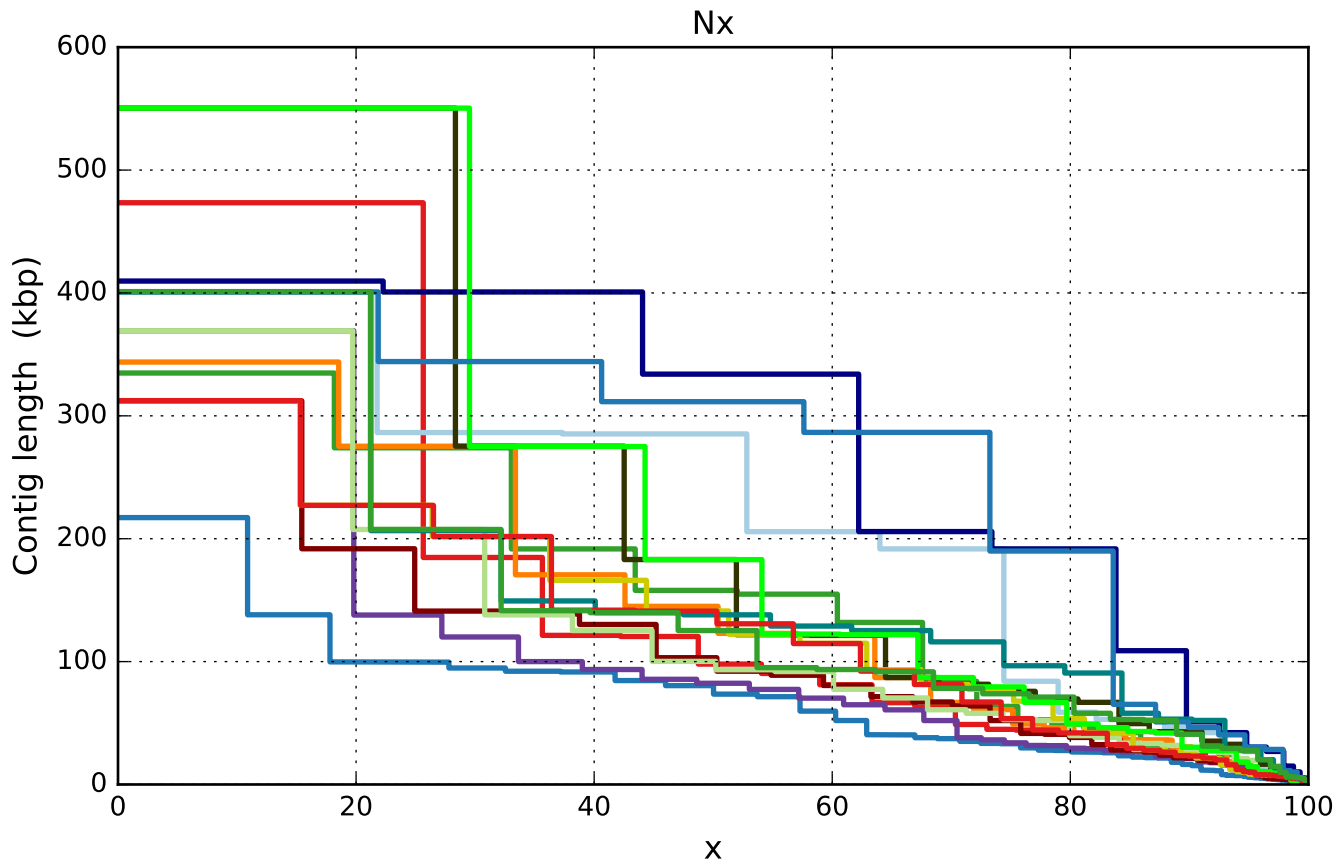
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# misassemblies	38	33	50	40	45	44	57	44	54	42	40	49	48	44	60	49
# relocations	38	33	50	40	45	44	57	44	54	42	40	49	48	44	59	48
# translocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# inversions	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
# misassembled contigs	16	18	11	18	16	17	9	14	16	15	6	13	15	18	6	15
Misassembled contigs length	1453233	1187855	1077196	1336486	1596414	1644834	1116152	1454405	1757633	1739273	785406	1723743	1638314	1785735	1257756	1678907
# local misassemblies	52	59	38	54	53	60	39	63	57	63	32	65	56	61	42	66
# mismatches	39213	37356	36448	39928	39229	37753	35740	40731	40693	36884	35612	41190	40740	37084	35719	41229
# indels	1026	910	827	1050	1064	995	818	1139	1157	979	813	1186	1146	979	812	1193
# short indels	911	824	767	941	943	887	760	1014	1021	871	754	1059	1011	872	753	1064
# long indels	115	86	60	109	121	108	58	125	136	108	59	127	135	107	59	129
Indels length	2963	2446	1881	2819	3160	2959	1821	3143	3518	3024	1844	3281	3508	2956	1829	3300

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).

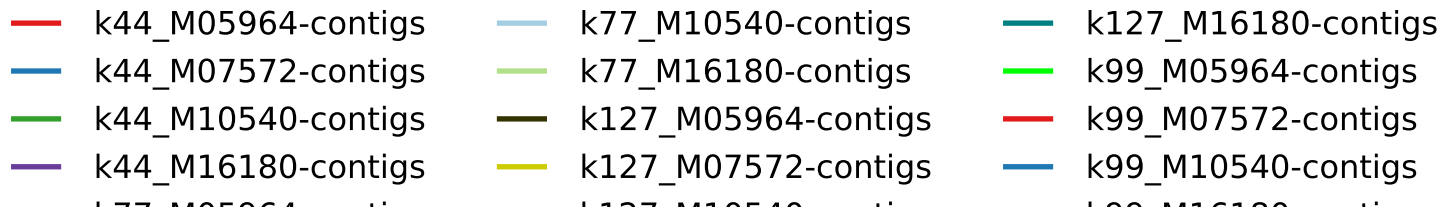
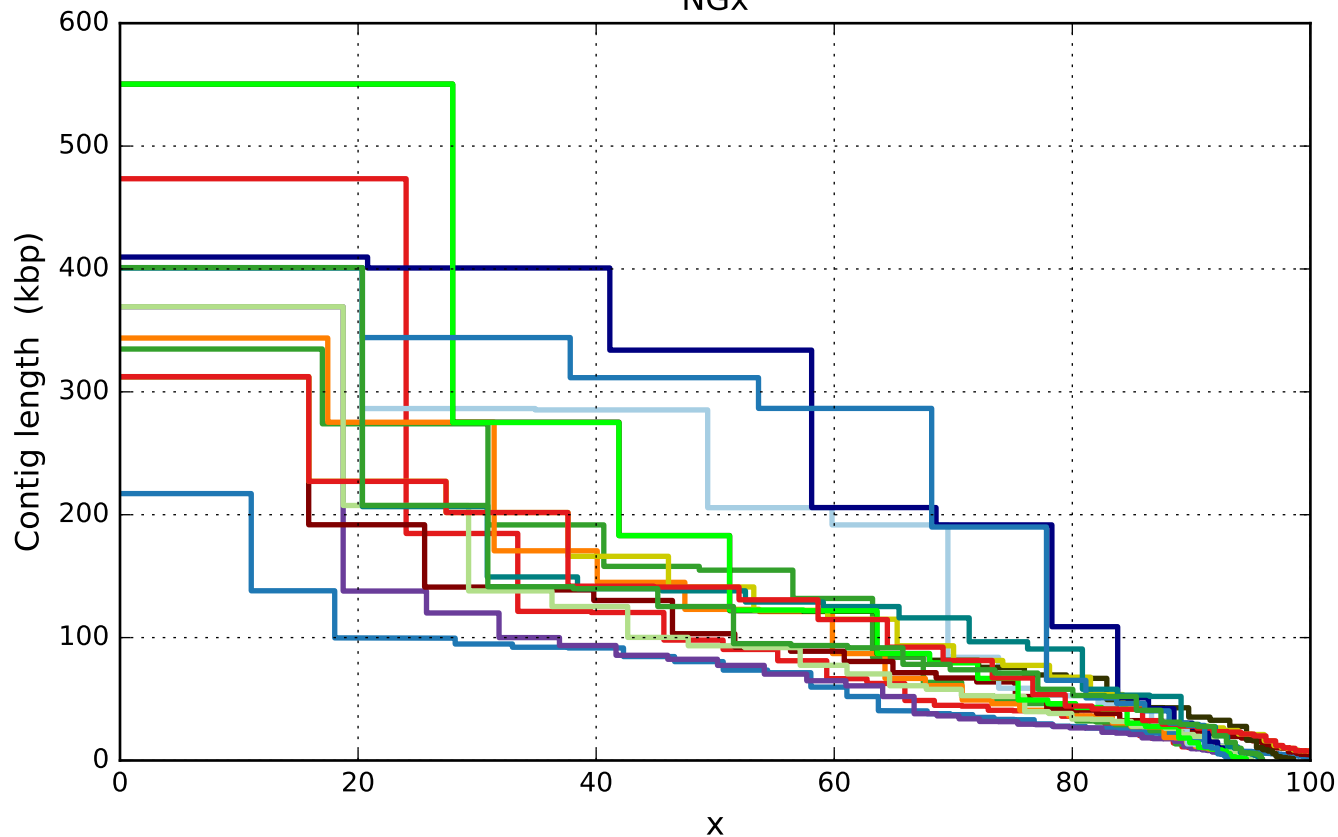
# Unaligned report

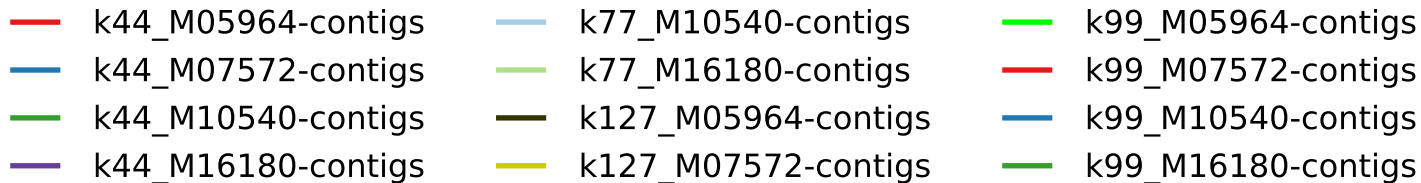
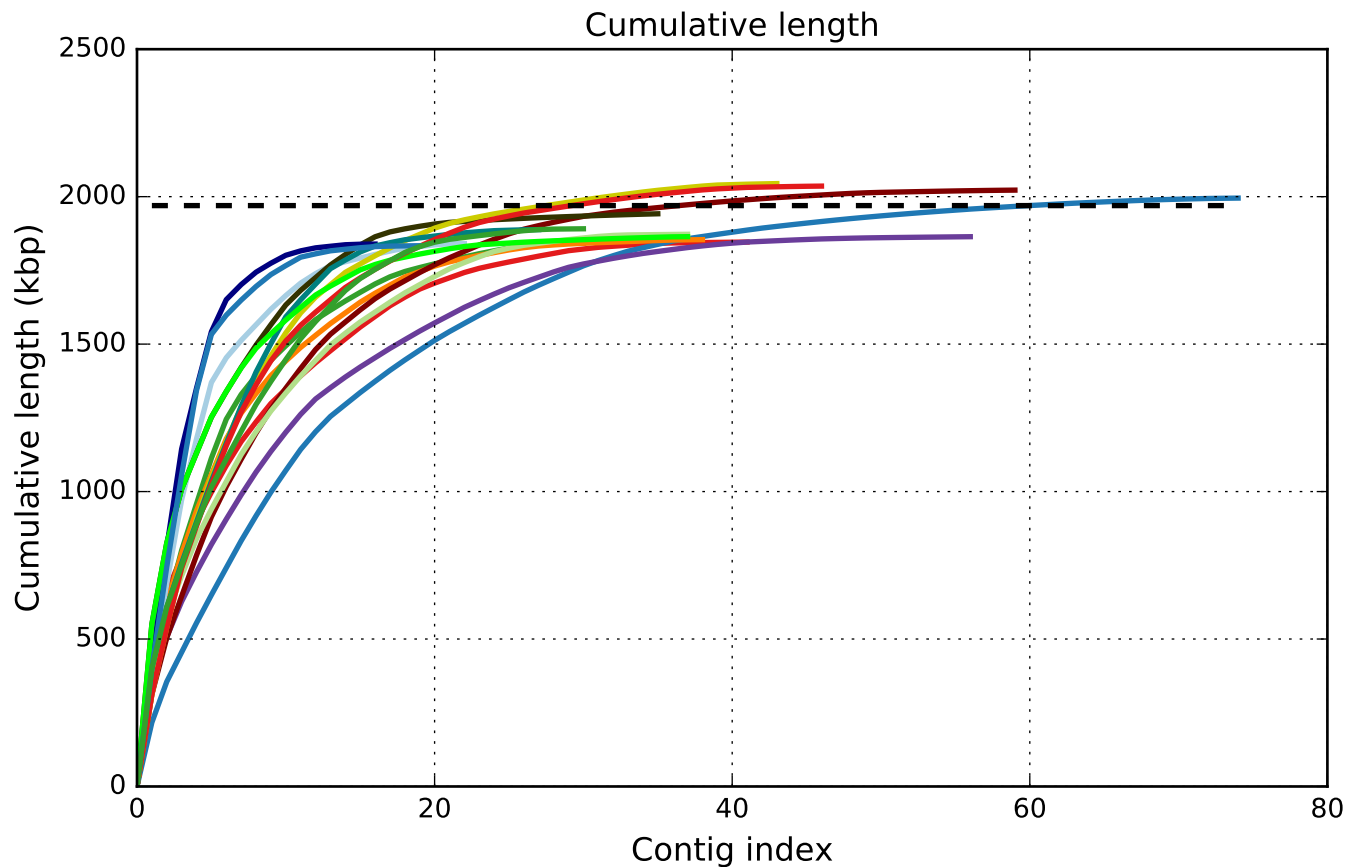
	k44_M05964-contigs	k44_M07572-contigs	k44_M10540-contigs	k44_M16180-contigs	k77_M05964-contigs	k77_M07572-contigs	k77_M10540-contigs	k77_M16180-contigs	k127_M05964-contigs	k127_M07572-contigs	k127_M10540-contigs	k127_M16180-contigs	k99_M05964-contigs	k99_M07572-contigs	k99_M10540-contigs	k99_M16180-contigs
# fully unaligned contigs	2	20	3	3	2	13	2	2	2	6	2	3	2	7	3	4
Fully unaligned length	45495	112747	11615	9325	3632	41546	10649	10769	4647	50310	10749	17113	4414	39137	11513	17589
# partially unaligned contigs	6	15	10	12	7	16	7	5	3	13	4	4	7	12	5	5
# with misassembly	3	2	6	1	2	4	6	1	1	5	4	1	2	5	4	1
# both parts are significant	4	11	10	8	4	10	7	3	3	10	4	2	5	9	5	2
Partially unaligned length	30093	80726	394661	46891	30796	132934	408401	26954	17193	131125	556030	16186	30842	112052	299390	21865
# 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  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

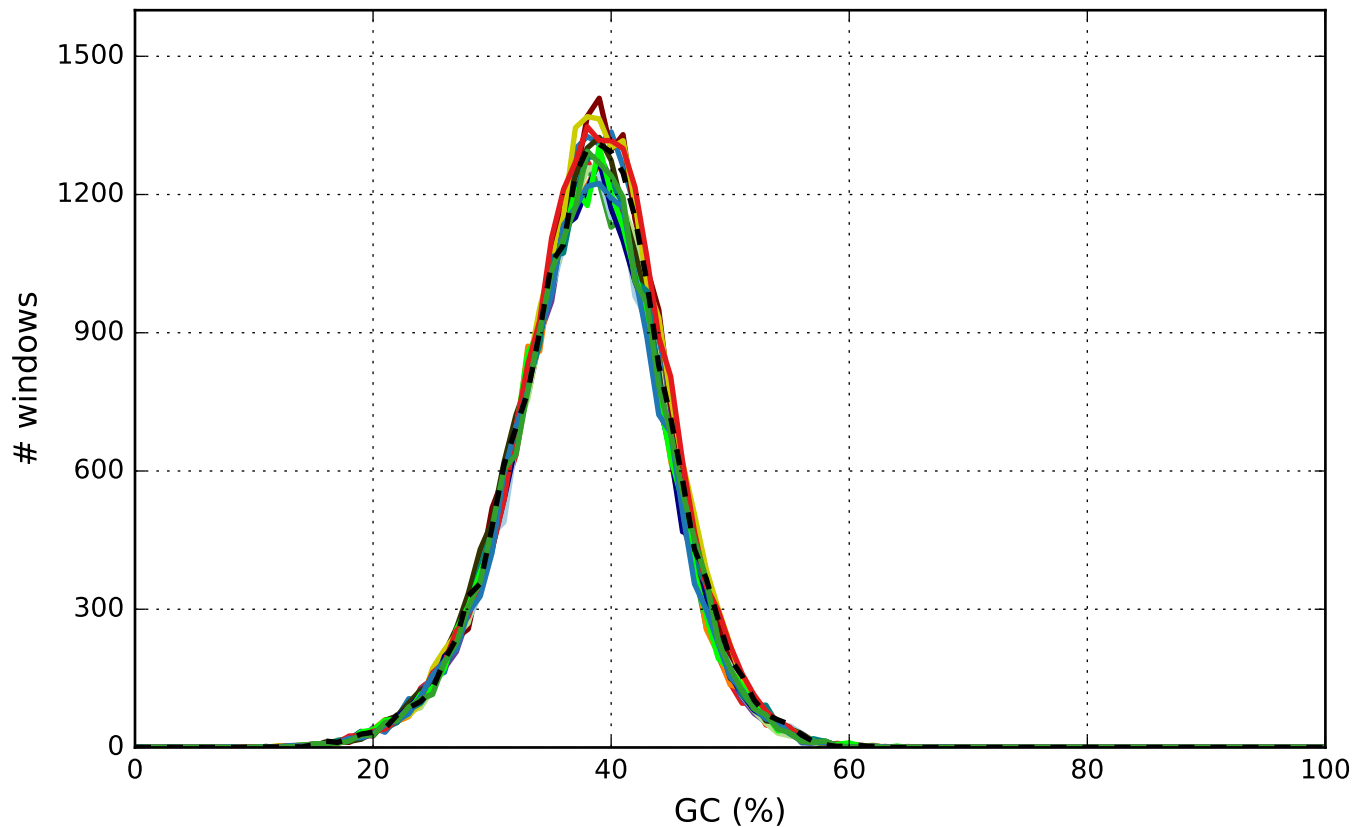


NGx



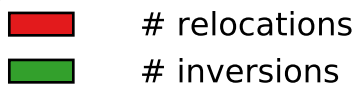
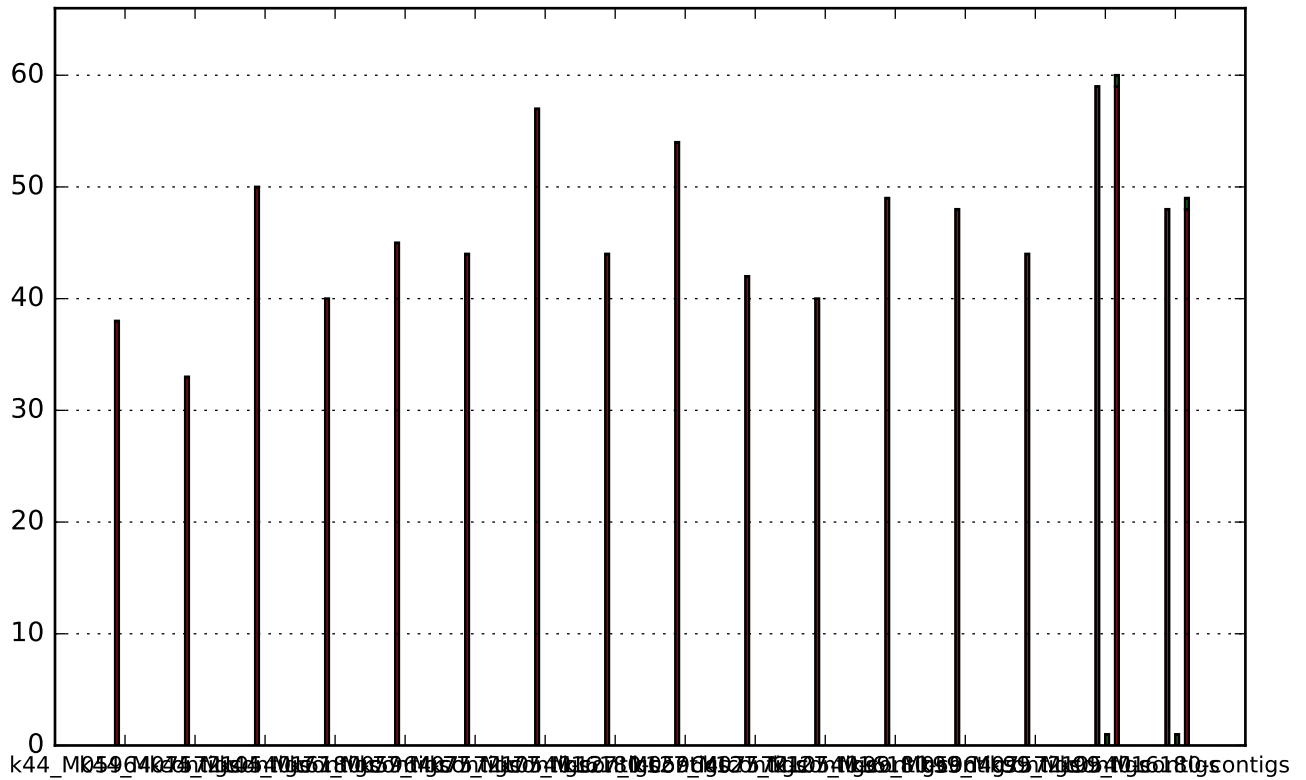


GC content



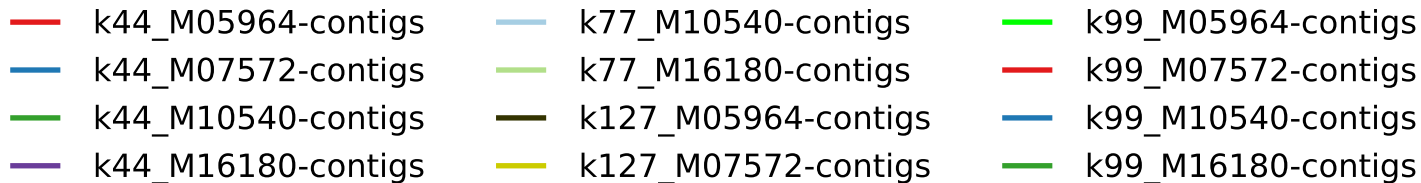
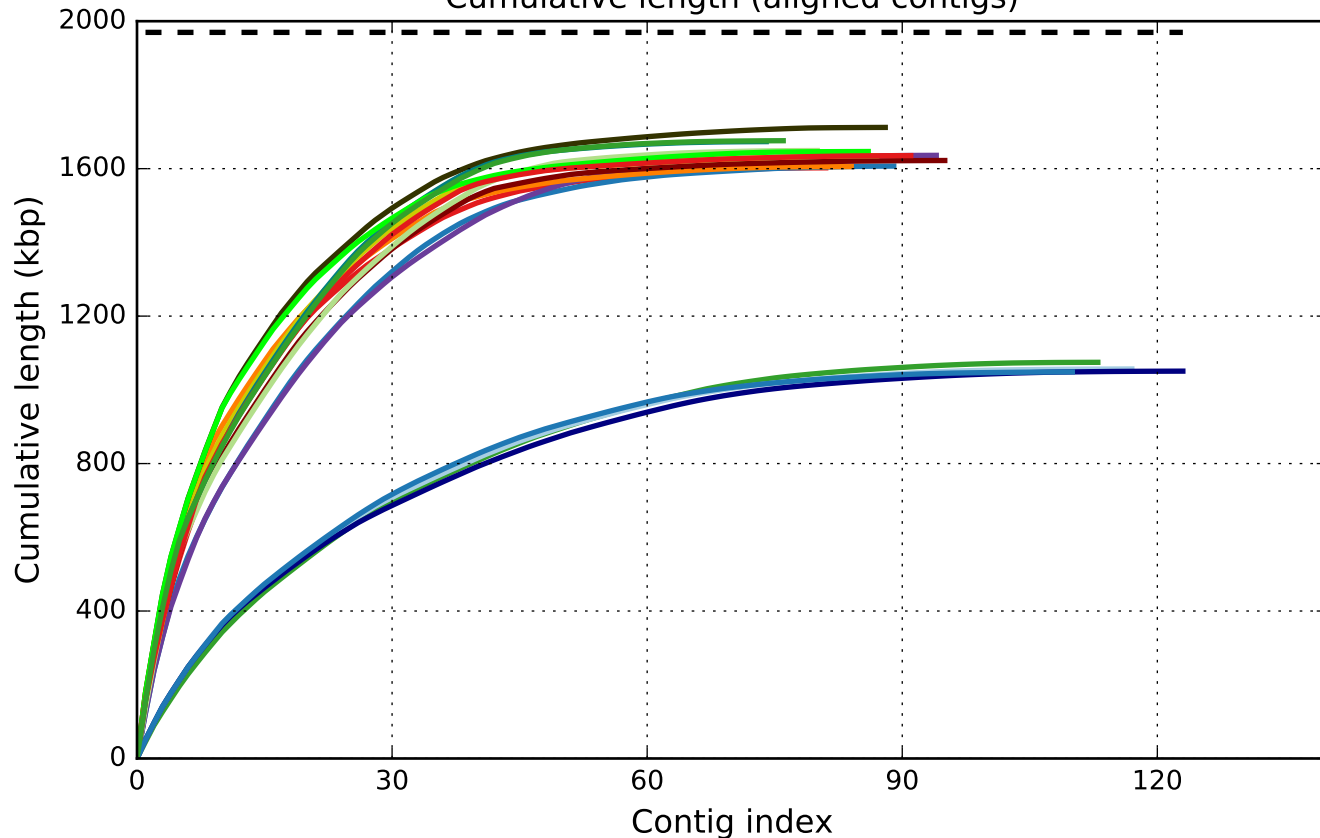
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k44_M07572-contigs	k77_M16180-contigs	k99_M07572-contigs
k44_M10540-contigs	k127_M05964-contigs	k99_M10540-contigs
k44_M16180-contigs	k127_M07572-contigs	k99_M16180-contigs
k77_M05964-contigs	k127_M10540-contigs	k99_M16180-contigs

# Misassemblies

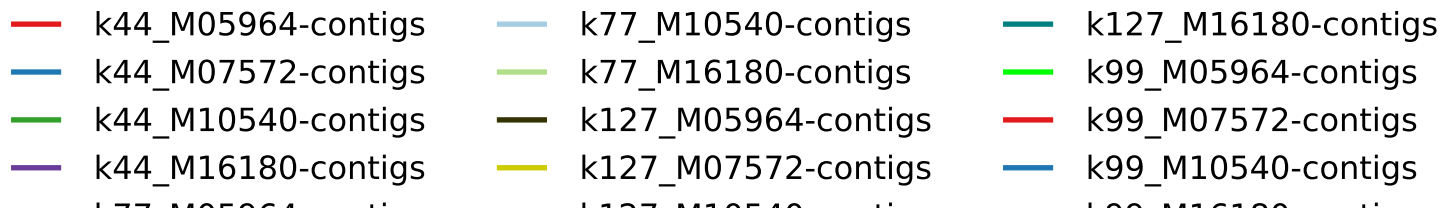
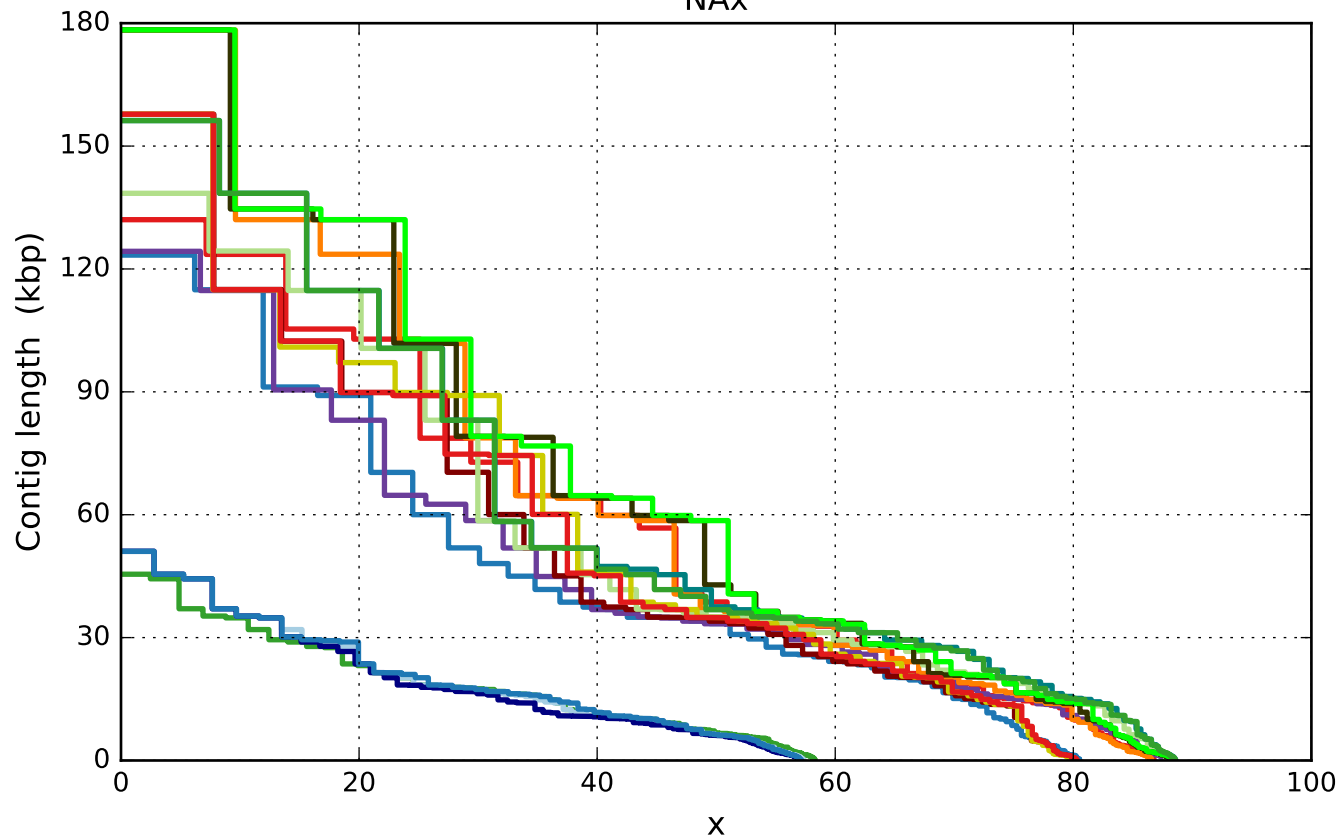




Cumulative length (aligned contigs)



NAx



# NGAx

