

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	1887620	1887620	1887620	1887620	1887620	1887620	1887620	1887620	1887620	1887620	1887620	1887620	1887620	1887620	1887620	1887620
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 (%)	38.23	38.23	38.23	38.23	38.23	38.23	38.23	38.23	38.23	38.23	38.23	38.23	38.23	38.23	38.23	38.23
N50	97979	80448	157960	82364	144973	103159	285281	100164	183050	141208	333934	138055	182978	141152	311520	125281
NG50	97979	80448	157960	82364	122974	103159	285281	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	44231	35070	52654	33896	49193	67108	83976	52751	81560	81370	191716	96606	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	5	6	3	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	12	18	9	15	10	11	6	12	7	9	5	9	7	9	5	10
# misassemblies	29	9	51	20	33	19	57	23	40	19	50	23	32	20	69	23
# misassembled contigs	13	9	11	15	13	14	10	11	13	10	7	9	10	11	8	10
Misassembled contigs length	1424804	389808	1233673	1218300	1492538	1024083	1340551	1287506	1682881	1012221	1231722	1356149	1523263	1033701	1632283	1361181
# local misassemblies	59	30	49	30	62	34	53	37	67	35	48	34	63	35	55	35
# unaligned contigs	5 + 5 part	5 + 16 part	3 + 9 part	6 + 8 part	2 + 6 part	3 + 9 part	2 + 6 part	5 + 3 part	1 + 6 part	1 + 8 part	2 + 3 part	2 + 4 part	3 + 6 part	0 + 9 part	3 + 3 part	2 + 4 part
Unaligned length	94609	99306	311369	79949	41974	79874	274655	57596	29835	54010	306596	82776	43166	77030	110121	82709
Genome fraction (%)	83.927	94.328	60.241	87.473	84.067	94.783	60.186	87.961	84.227	95.023	59.944	88.527	84.319	94.928	59.729	88.736
Duplication ratio	1.106	1.065	1.346	1.081	1.142	1.086	1.379	1.093	1.203	1.110	1.355	1.080	1.144	1.093	1.529	1.080
# 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	2365.64	1191.32	3558.70	1844.70	2361.95	1221.48	3559.69	1848.20	2339.73	1211.87	3560.12	1835.12	2361.18	1223.68	3558.07	1833.08
# indels per 100 kbp	61.61	32.07	82.84	49.66	63.08	32.47	82.92	50.23	63.28	32.17	85.81	50.45	63.52	32.54	82.66	50.03
Largest alignment	145100	216292	48752	191527	202907	288042	48752	191540	202935	288058	48752	223348	202963	288054	61112	223348
NA50	38866	71113	9570	41410	38590	82838	9582	47105	38866	93346	9404	92095	41226	92226	10803	57860
NGA50	38866	79041	8646	40366	38494	82838	8646	47105	41226	93346	8646	92095	41226	92226	9404	57860
NA75	16510	22445	-	18834	16563	25072	-	21108	16883	28434	-	22478	16852	29474	-	22478
NGA75	14342	27653	-	18648	14101	37585	-	21108	20262	45040	-	22478	16065	39946	-	22478
LA50	14	10	42	11	13	8	39	10	13	7	40	8	12	7	37	9
LGA50	14	9	45	12	14	8	42	10	12	7	43	8	12	7	40	9
LA75	31	25	-	27	31	19	-	24	30	17	-	19	28	17	-	22
LGA75	33	21	-	28	33	16	-	24	27	14	-	19	29	14	-	22

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	29	9	51	20	33	19	57	23	40	19	50	23	32	20	69	23
# relocations	29	9	51	20	32	19	57	23	40	19	49	23	32	20	68	23
# translocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# inversions	0	0	0	0	1	0	0	0	0	0	1	0	0	0	1	0
# misassembled contigs	13	9	11	15	13	14	10	11	13	10	7	9	10	11	8	10
Misassembled contigs length	1424804	389808	1233673	1218300	1492538	1024083	1340551	1287506	1682881	1012221	1231722	1356149	1523263	1033701	1632283	1361181
# local misassemblies	59	30	49	30	62	34	53	37	67	35	48	34	63	35	55	35
# mismatches	37477	21212	40467	30459	37481	21854	40441	30687	37199	21737	40283	30666	37581	21927	40116	30704
# indels	976	571	942	820	1001	581	942	834	1006	577	971	843	1011	583	932	838
# short indels	879	486	853	731	896	494	851	743	897	494	871	752	906	501	839	748
# long indels	97	85	89	89	105	87	91	91	109	83	100	91	105	82	93	90
Indels length	2802	2215	2315	2491	2994	2116	2342	2557	2994	2163	2507	2572	2935	2192	2373	2526

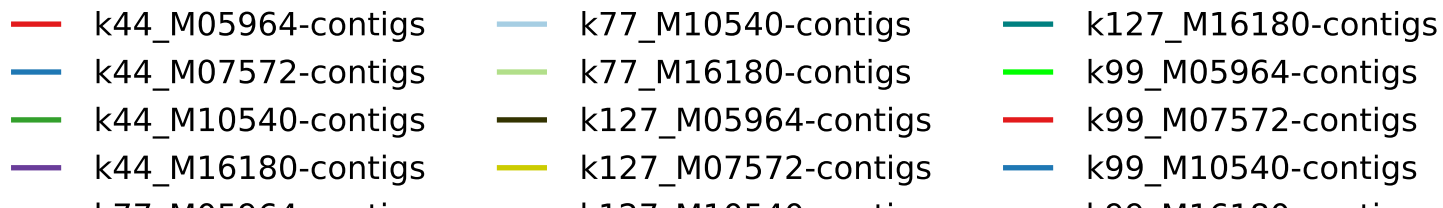
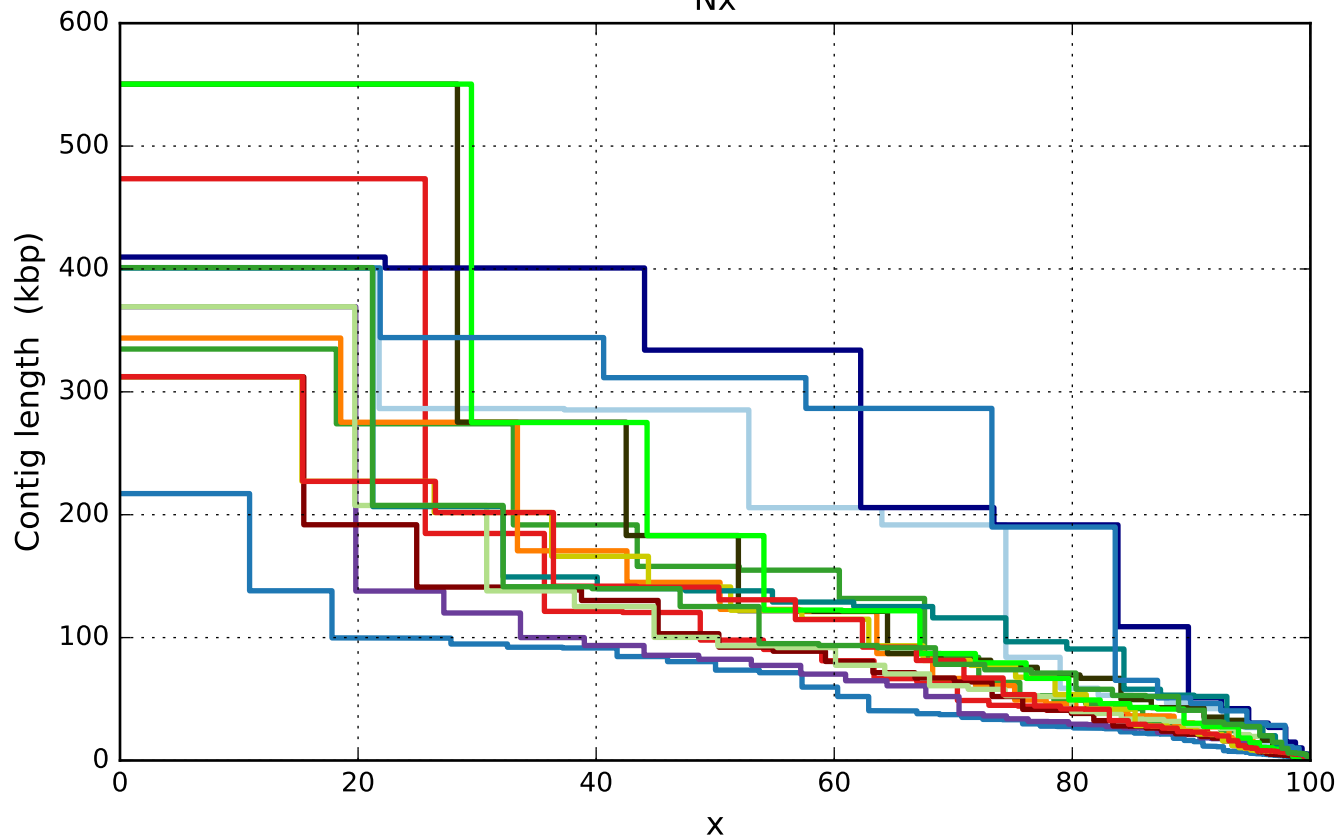
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

# Unaligned report

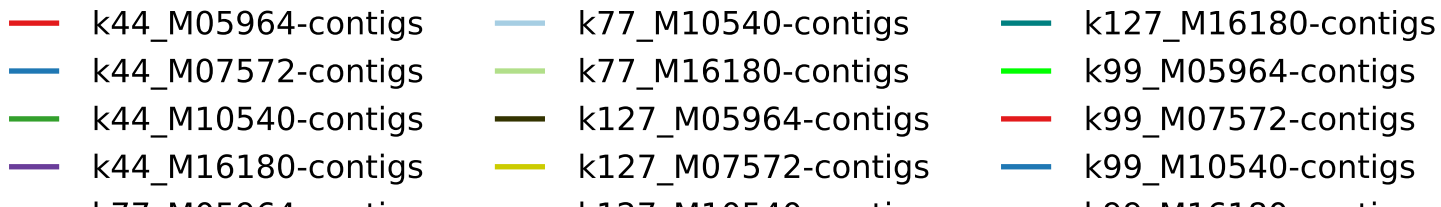
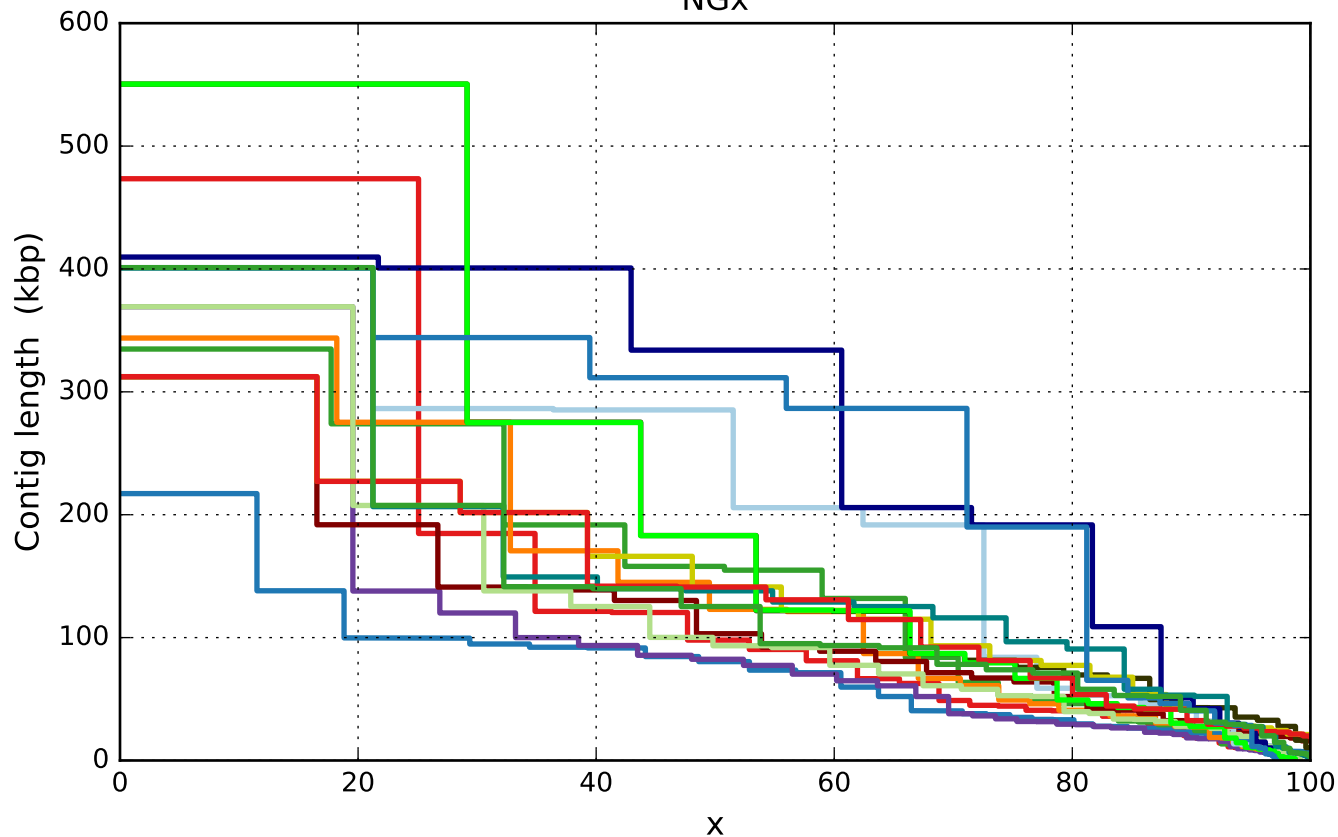
	k44_M05964-contigs	k44_M07572-contigs	k44_M10540-contigs	k44_M16180-contigs	k77_M05964-contigs	k77_M07572-contigs	k77_M10540-contigs	k77_M16180-contigs	k127_M05964-contigs	k127_M07572-contigs	k127_M10540-contigs	k127_M16180-contigs	k99_M05964-contigs	k99_M07572-contigs	k99_M10540-contigs	k99_M16180-contigs
# fully unaligned contigs	5	5	3	6	2	3	2	5	1	1	2	2	3	0	3	2
Fully unaligned length	50548	39636	11615	21985	5364	7617	10649	20746	3210	8429	10749	12653	7596	0	11513	12597
# partially unaligned contigs	5	16	9	8	6	9	6	3	6	8	3	4	6	9	3	4
# with misassembly	2	2	8	0	2	3	6	1	1	3	3	2	2	4	3	2
# both parts are significant	5	12	9	3	5	6	6	3	2	6	3	4	3	6	3	4
Partially unaligned length	44061	59670	299754	57964	36610	72257	264006	36850	26625	45581	295847	70123	35570	77030	98608	70112
# N's	153	166	1	27	22	10	0	15	0	0	0	0	0	0	1	1

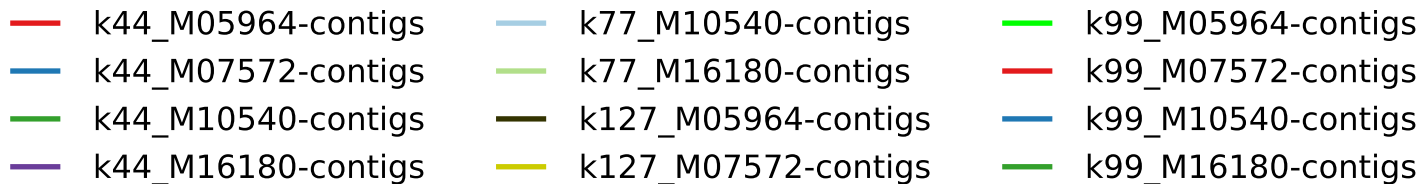
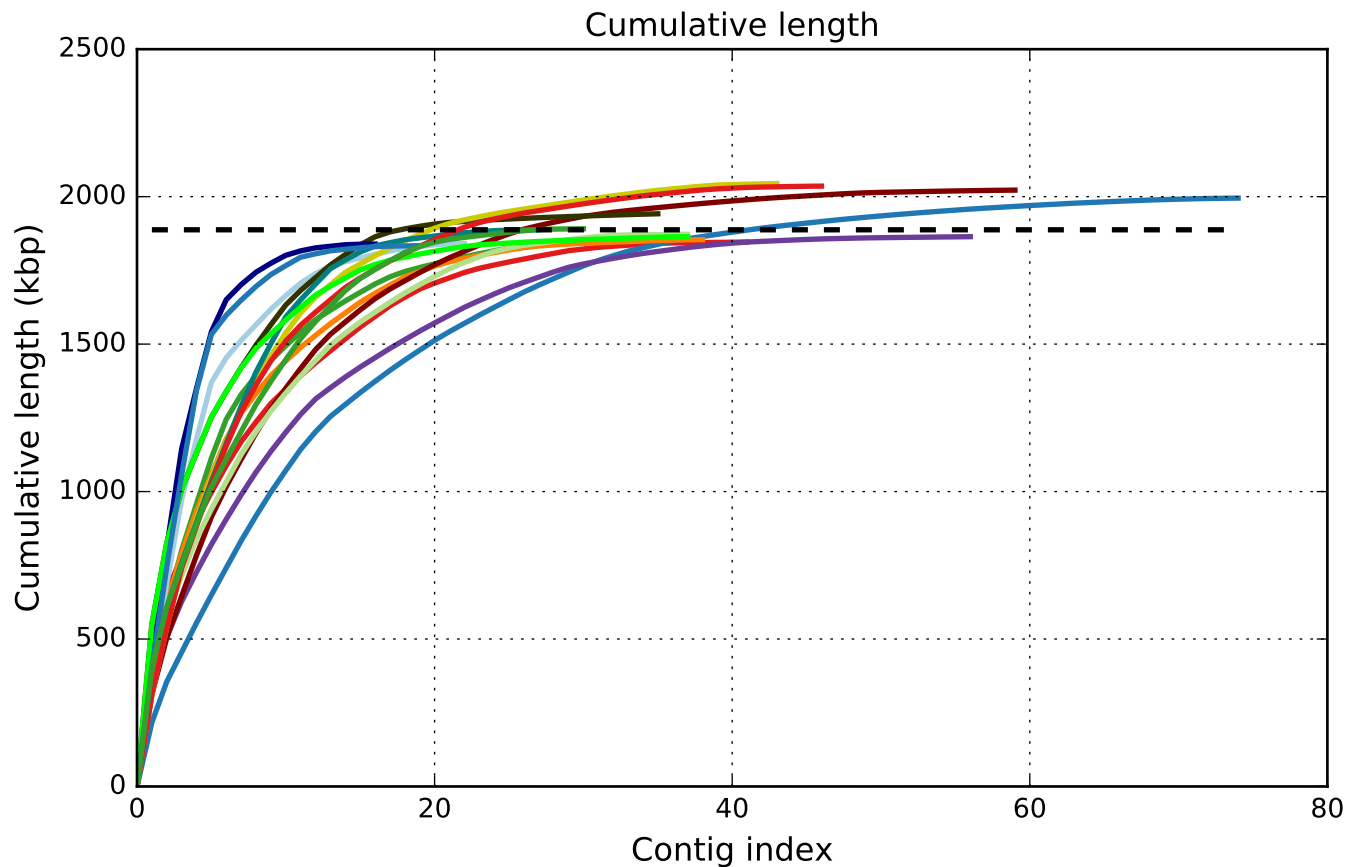
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Nx

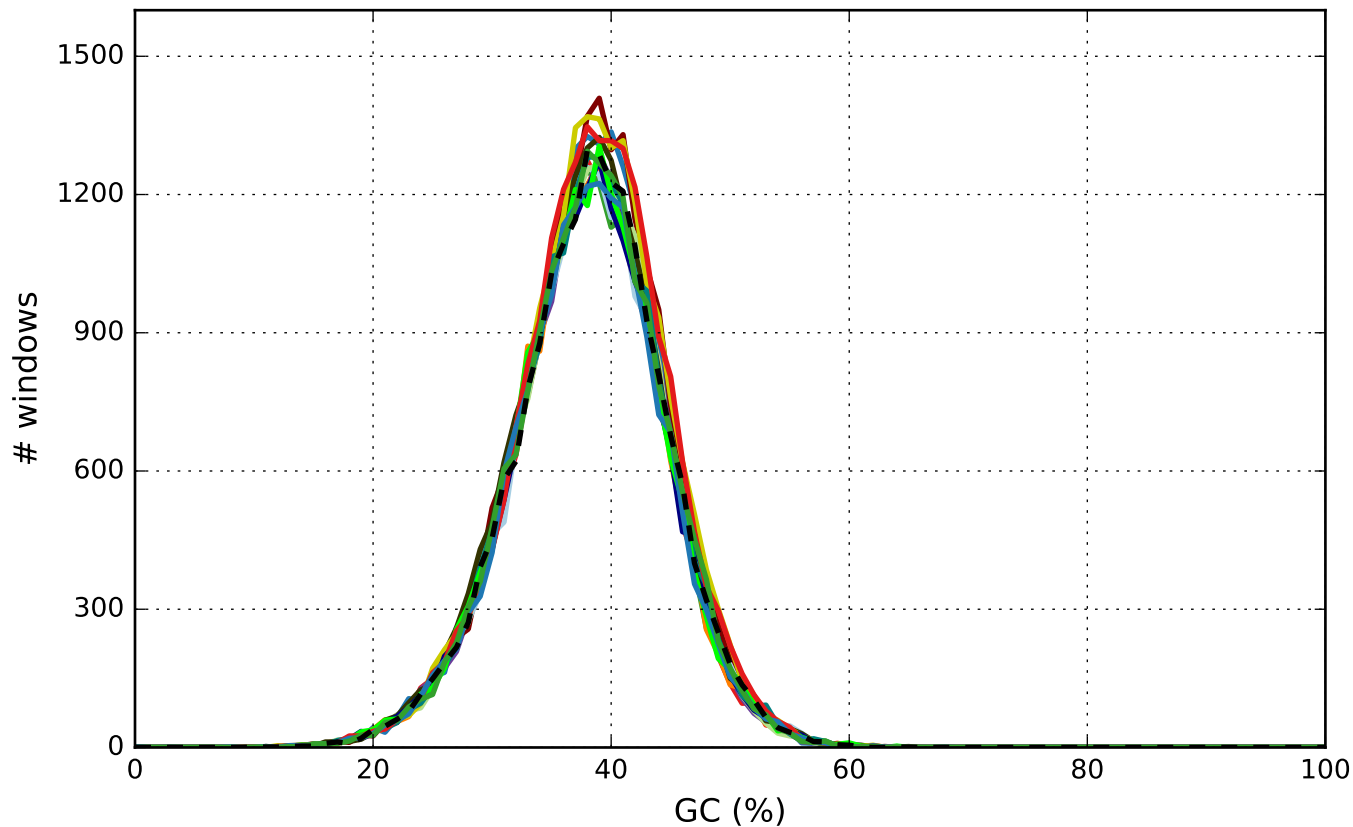


NGx



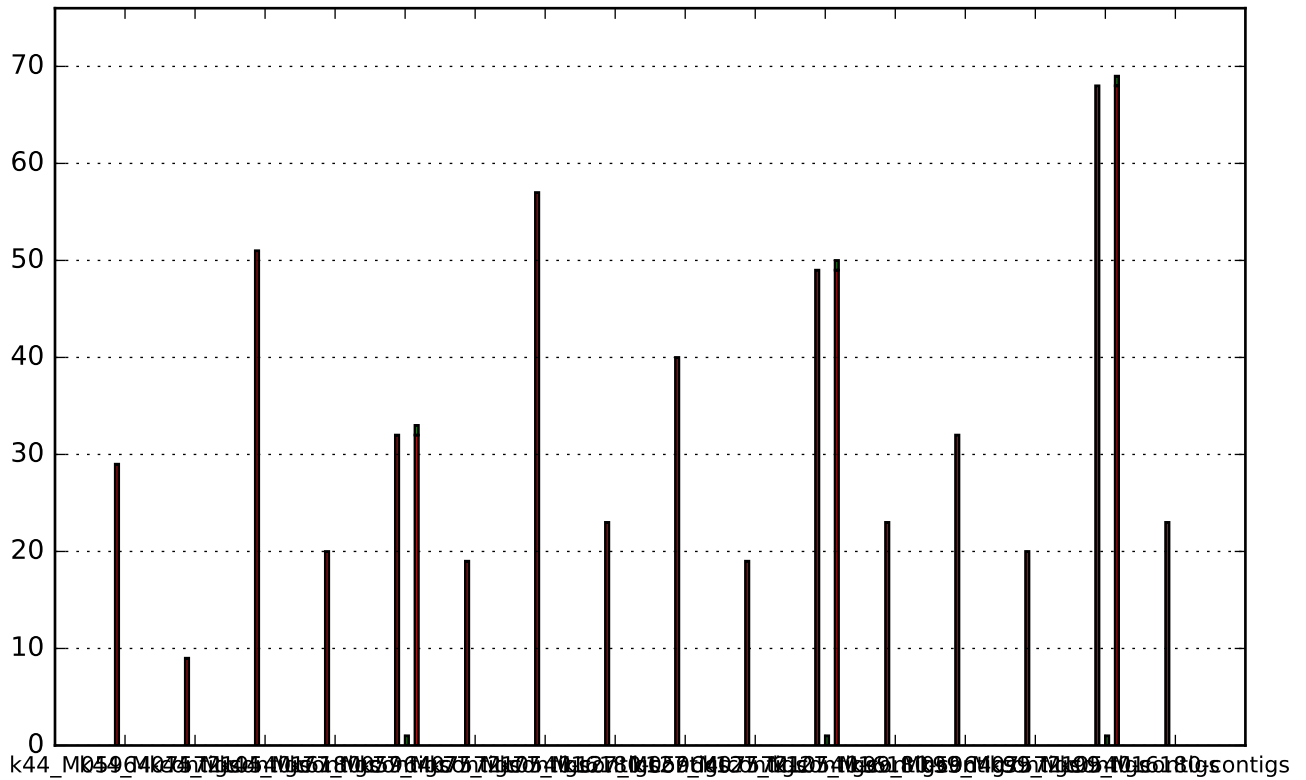


GC content



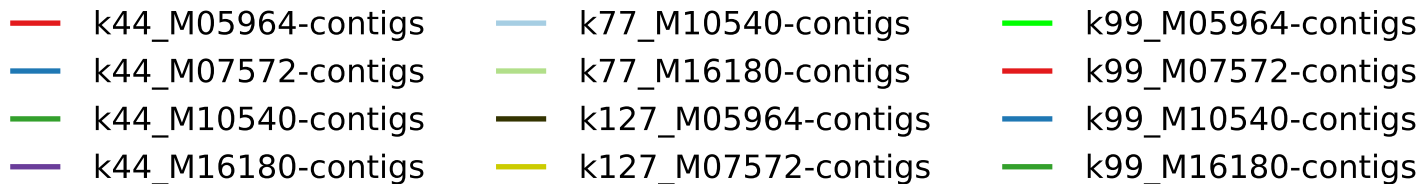
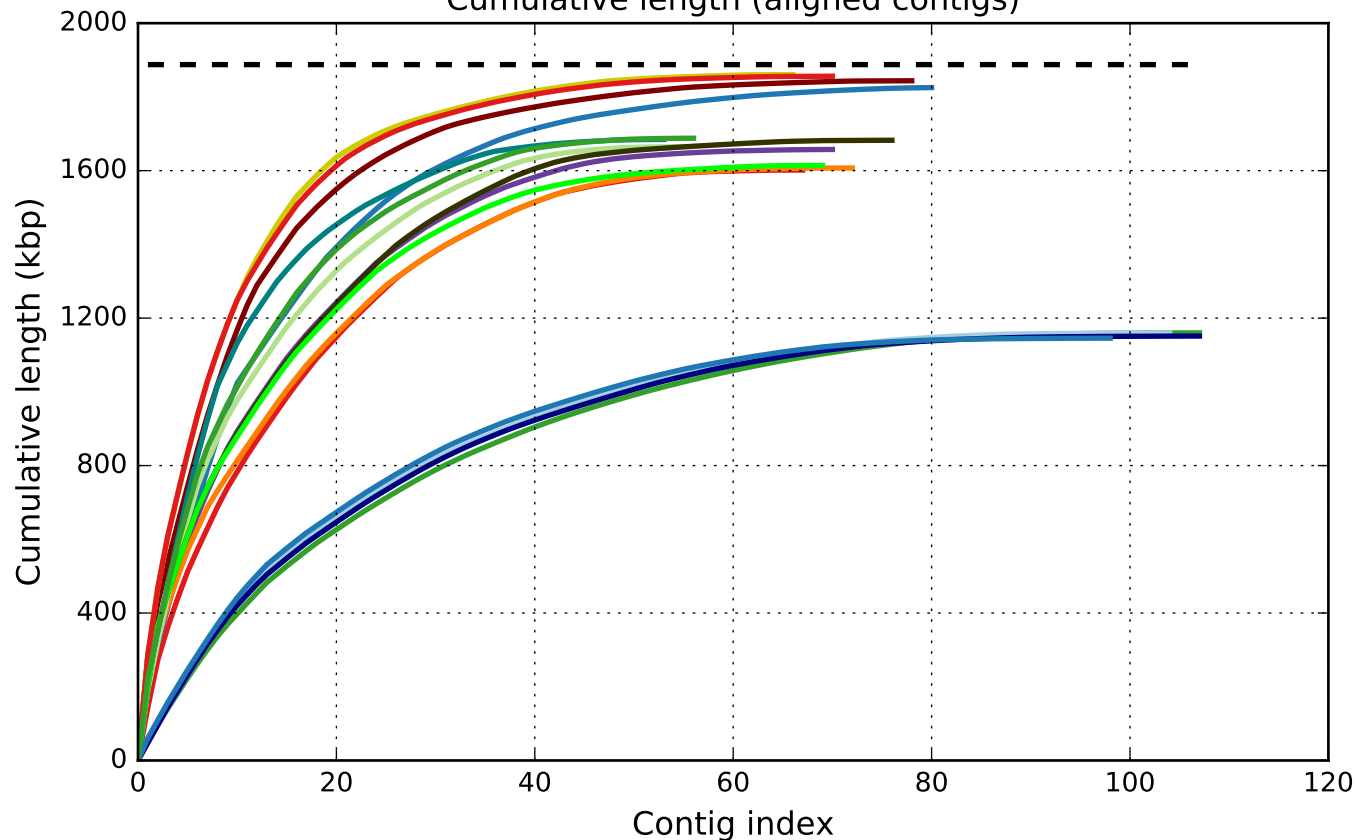
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|--------------------|---------------------|--------------------|
| k44_M05964-contigs | k77_M10540-contigs  | k99_M05964-contigs |
| k44_M07572-contigs | k77_M16180-contigs  | k99_M07572-contigs |
| k44_M10540-contigs | k127_M05964-contigs | k99_M10540-contigs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

# Misassemblies

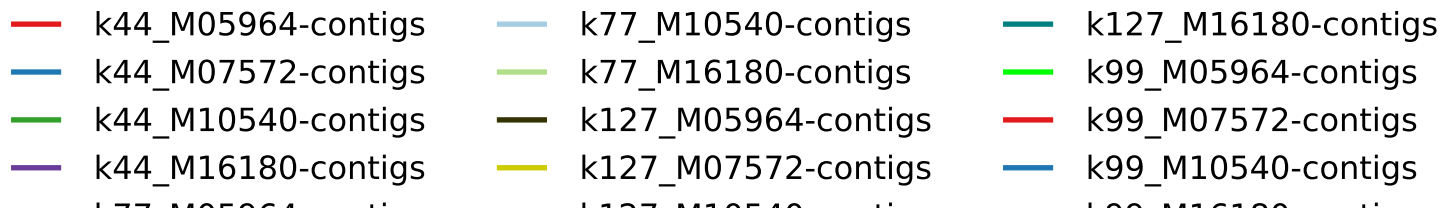
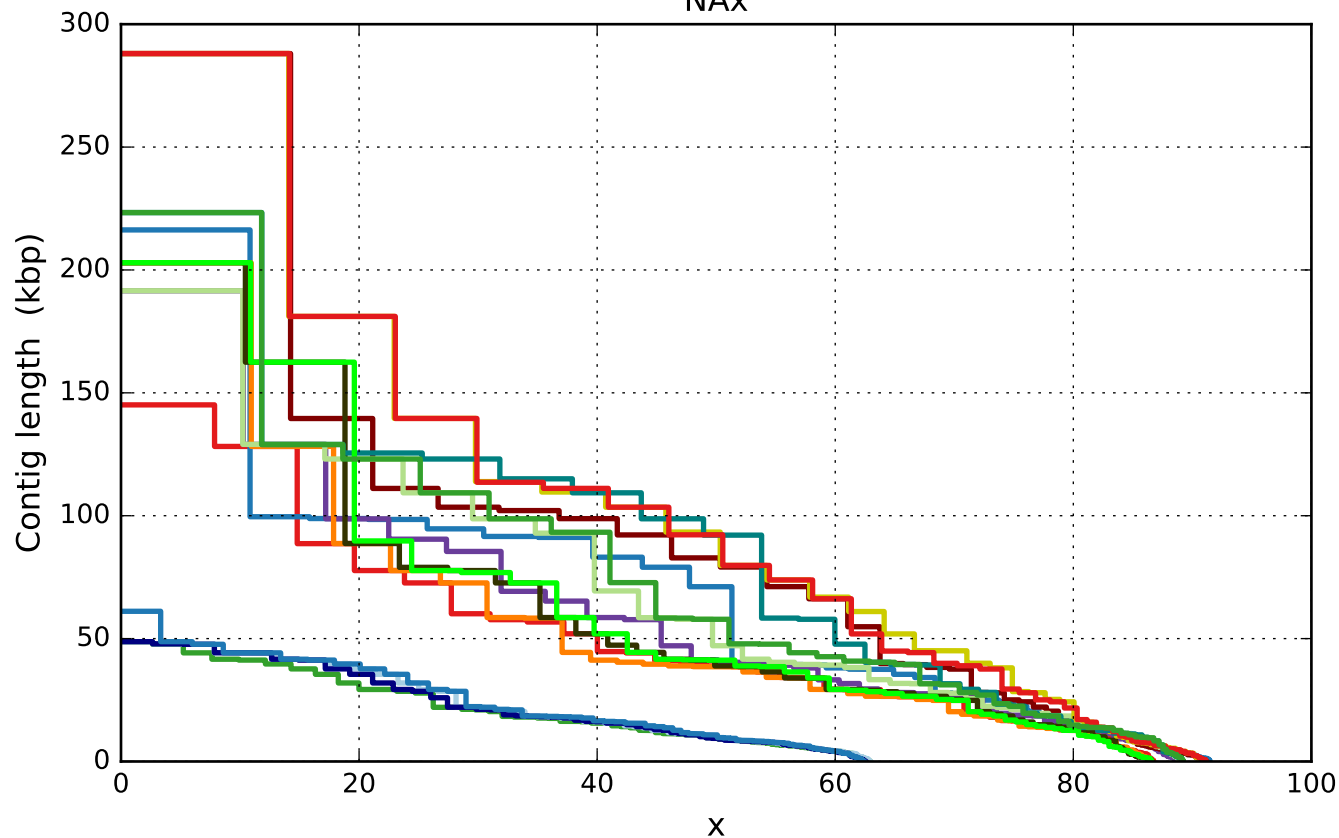




Cumulative length (aligned contigs)



NAx



# NGAx

