

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	1890645	1890645	1890645	1890645	1890645	1890645	1890645	1890645	1890645	1890645	1890645	1890645	1890645	1890645	1890645	1890645
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	63910	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	12	6	12	7	9	5	9	7	9	5	10
# misassemblies	32	9	68	14	44	15	77	18	51	14	87	17	42	15	76	17
# misassembled contigs	14	9	13	9	15	11	12	9	16	11	10	7	14	12	9	7
Misassembled contigs length	1442786	405156	1513028	958701	1513400	933408	1631232	1053236	1694504	961988	1755421	1169622	1553579	926616	1637433	1064799
# local misassemblies	60	12	46	25	61	15	52	30	68	16	57	31	62	15	49	33
# unaligned contigs	4 + 4 part	5 + 13 part	3 + 8 part	8 + 7 part	2 + 5 part	1 + 7 part	2 + 5 part	5 + 4 part	0 + 4 part	1 + 4 part	2 + 1 part	2 + 3 part	2 + 5 part	0 + 5 part	3 + 3 part	2 + 3 part
Unaligned length	67171	89900	175889	84176	16118	61499	123605	59446	9743	39067	45049	23285	16128	60582	110869	23217
Genome fraction (%)	84.892	95.209	58.940	89.365	85.091	96.428	59.493	89.424	85.396	96.913	59.335	90.249	85.295	96.411	59.113	90.562
Duplication ratio	1.108	1.058	1.145	1.054	1.143	1.075	1.527	1.072	1.197	1.094	1.599	1.093	1.146	1.084	1.541	1.091
# 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	2412.77	716.64	3544.32	1713.21	2415.38	737.92	3549.63	1664.65	2408.37	739.68	3546.23	1606.88	2414.75	734.43	3550.12	1606.65
# indels per 100 kbp	58.63	22.72	80.50	47.05	60.17	22.60	81.62	44.95	60.82	23.63	82.63	44.01	61.08	22.93	81.24	44.27
Largest alignment	121059	209662	47680	198664	121092	249008	47680	198677	155446	249008	47680	230485	155446	249008	47680	230485
NA50	36422	73059	9245	47072	38494	79124	9855	55615	38866	79783	10381	88044	38866	79783	9855	58338
NGA50	36422	73523	8526	47072	36418	79124	9245	55615	38866	92830	9404	88044	38866	92802	9245	58338
NA75	16510	27342	-	26468	14830	28370	-	27762	16065	39377	-	31629	16852	39377	-	31629
NGA75	14830	29567	-	22949	13879	39369	-	27762	19699	45040	-	31629	16065	43346	-	31629
LA50	16	10	45	11	15	8	43	10	14	7	42	8	14	7	42	9
LGA50	16	9	48	11	16	8	45	10	14	6	44	8	14	6	45	9
LA75	33	23	-	25	33	19	-	22	33	16	-	17	30	16	-	19
LGA75	35	20	-	26	35	16	-	22	30	13	-	17	31	14	-	19

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

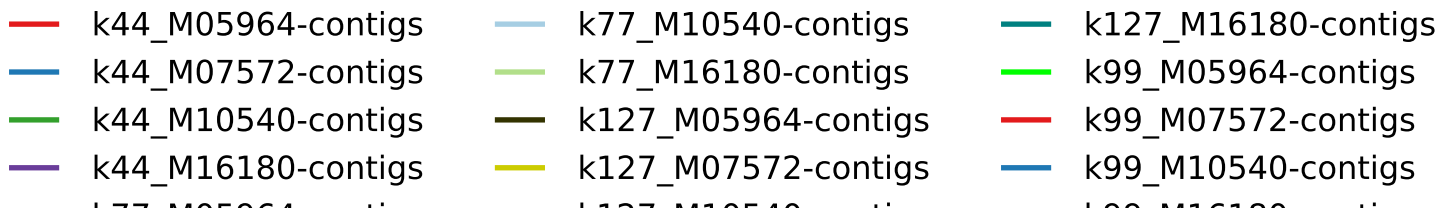
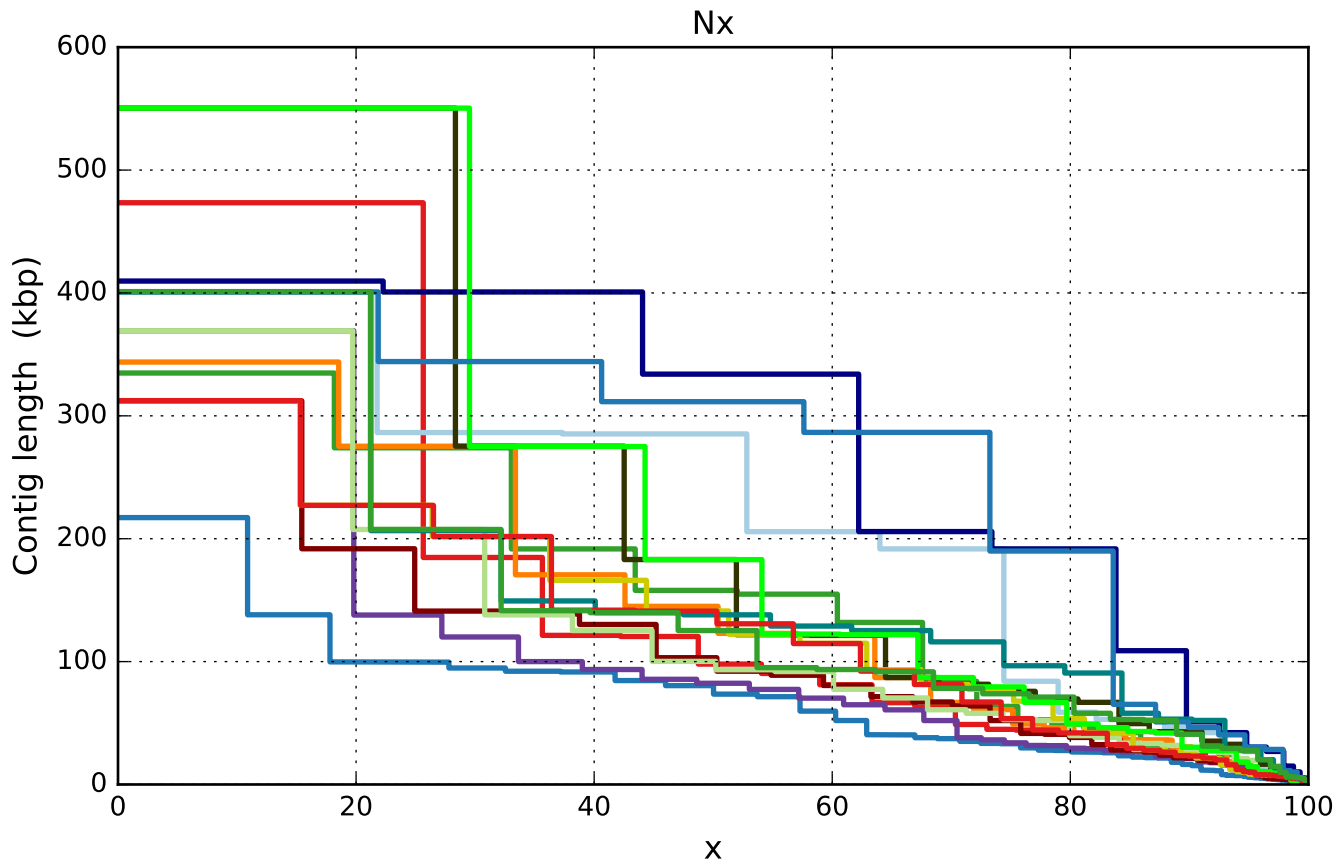
	k44_M05964-contigs	k44_M07572-contigs	k44_M10540-contigs	k44_M16180-contigs	k77_M05964-contigs	k77_M07572-contigs	k77_M10540-contigs	k77_M16180-contigs	k127_M05964-contigs	k127_M07572-contigs	k127_M10540-contigs	k127_M16180-contigs	k99_M05964-contigs	k99_M07572-contigs	k99_M10540-contigs	k99_M16180-contigs
# misassemblies	32	9	68	14	44	15	77	18	51	14	87	17	42	15	76	17
# relocations	32	9	66	14	43	15	75	18	51	14	87	17	42	15	76	17
# translocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# inversions	0	0	2	0	1	0	2	0	0	0	0	0	0	0	0	0
# misassembled contigs	14	9	13	9	15	11	12	9	16	11	10	7	14	12	9	7
Misassembled contigs length	1442786	405156	1513028	958701	1513400	933408	1631232	1053236	1694504	961988	1755421	1169622	1553579	926616	1637433	1064799
# local misassemblies	60	12	46	25	61	15	52	30	68	16	57	31	62	15	49	33
# mismatches	38725	12900	39496	28946	38858	13453	39926	28144	38884	13553	39782	27418	38941	13387	39677	27509
# indels	941	409	897	795	968	412	918	760	982	433	927	751	985	418	908	758
# short indels	837	347	809	693	857	350	829	660	870	365	834	649	870	352	818	655
# long indels	104	62	88	102	111	62	89	100	112	68	93	102	115	66	90	103
Indels length	2972	1750	2234	2838	3122	1879	2269	2793	3046	2095	2317	2831	3191	2045	2256	2841

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).

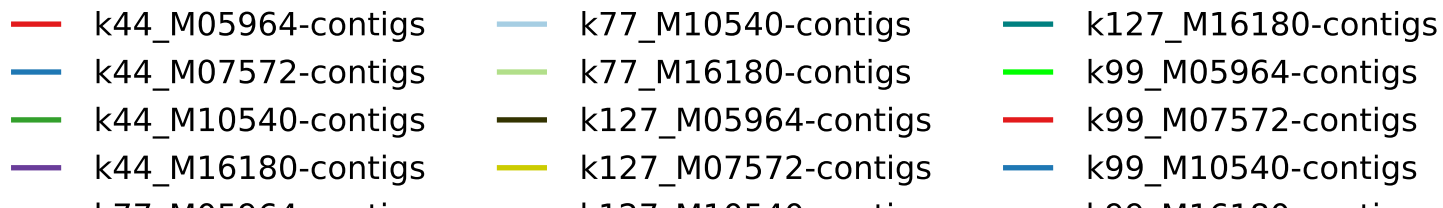
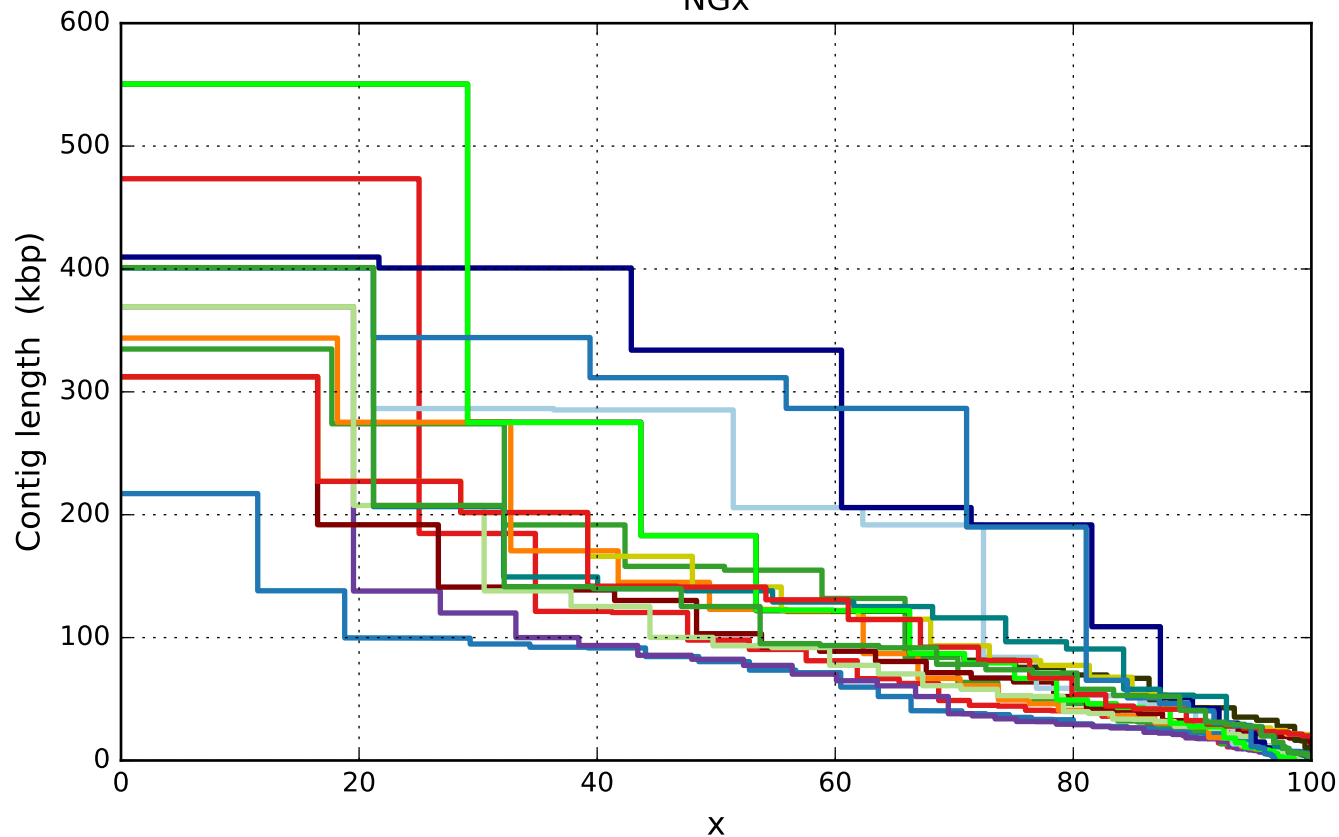
Unaligned report

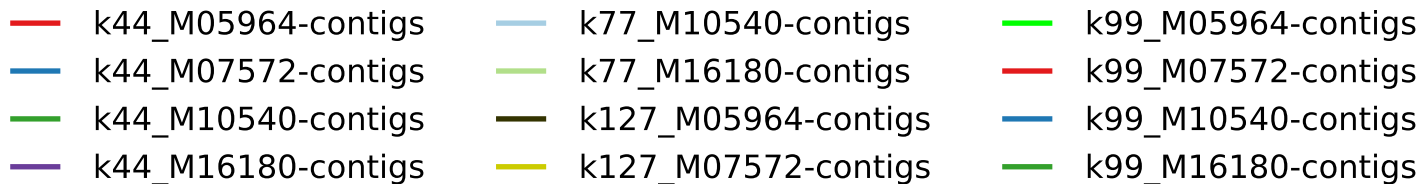
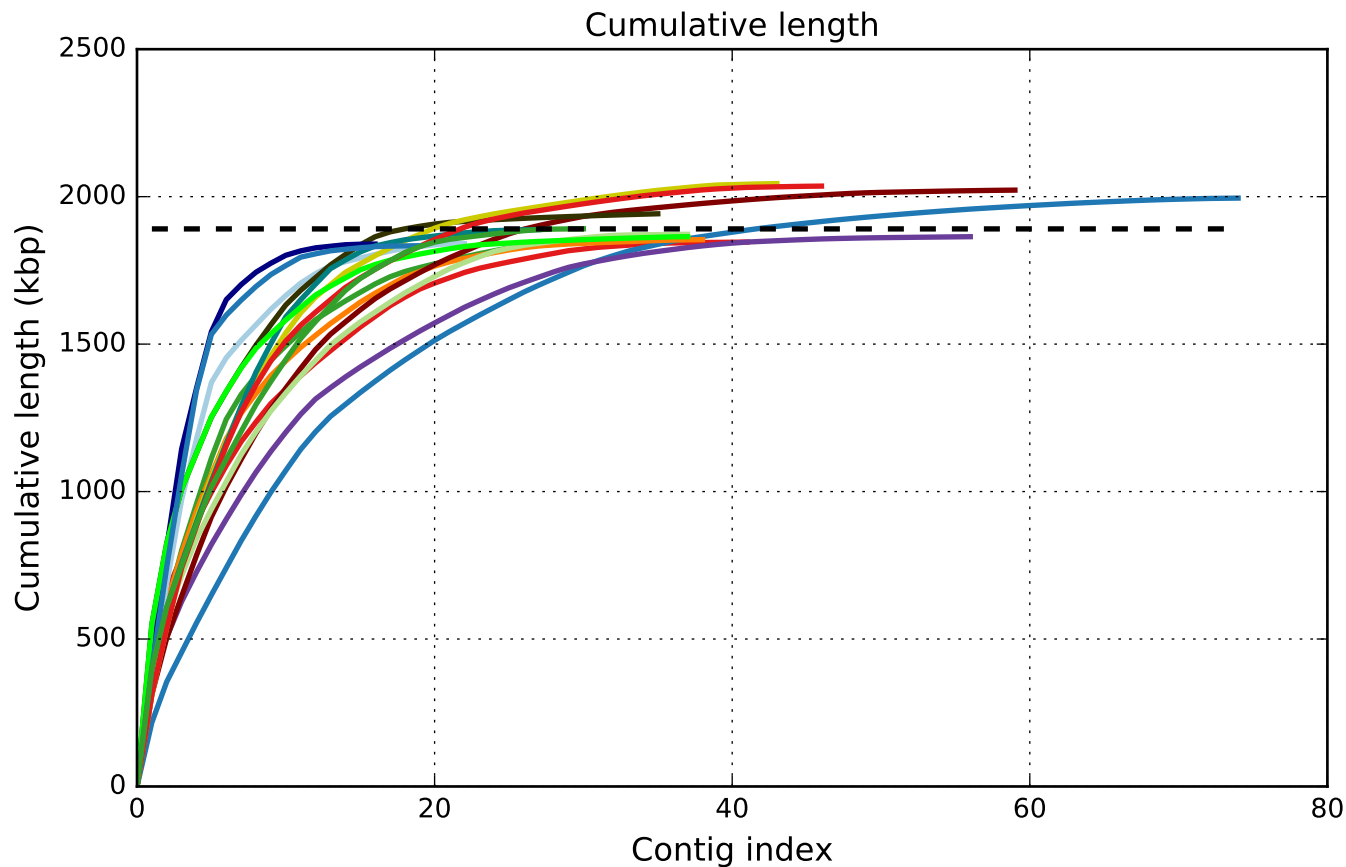
	k44_M05964-contigs	k44_M07572-contigs	k44_M10540-contigs	k44_M16180-contigs	k77_M05964-contigs	k77_M07572-contigs	k77_M10540-contigs	k77_M16180-contigs	k127_M05964-contigs	k127_M07572-contigs	k127_M10540-contigs	k127_M16180-contigs	k99_M05964-contigs	k99_M07572-contigs	k99_M10540-contigs	k99_M16180-contigs
# fully unaligned contigs	4	5	3	8	2	1	2	5	0	1	2	2	2	0	3	2
Fully unaligned length	47624	47933	11615	42615	3632	658	10649	20746	0	8429	10749	12653	4414	0	11513	12597
# partially unaligned contigs	4	13	8	7	5	7	5	4	4	4	1	3	5	5	3	3
# with misassembly	1	0	6	1	1	1	5	1	0	1	1	1	1	1	3	1
# both parts are significant	4	10	8	3	4	6	5	4	4	3	1	3	3	4	3	3
Partially unaligned length	19547	41967	164274	41561	12486	60841	112956	38700	9743	30638	34300	10632	11714	60582	99356	10620
# 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).

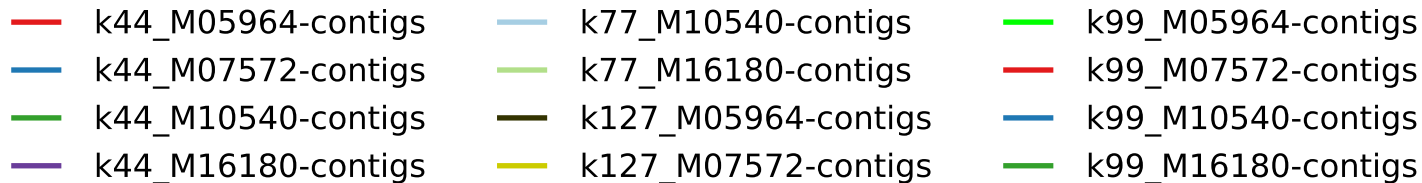
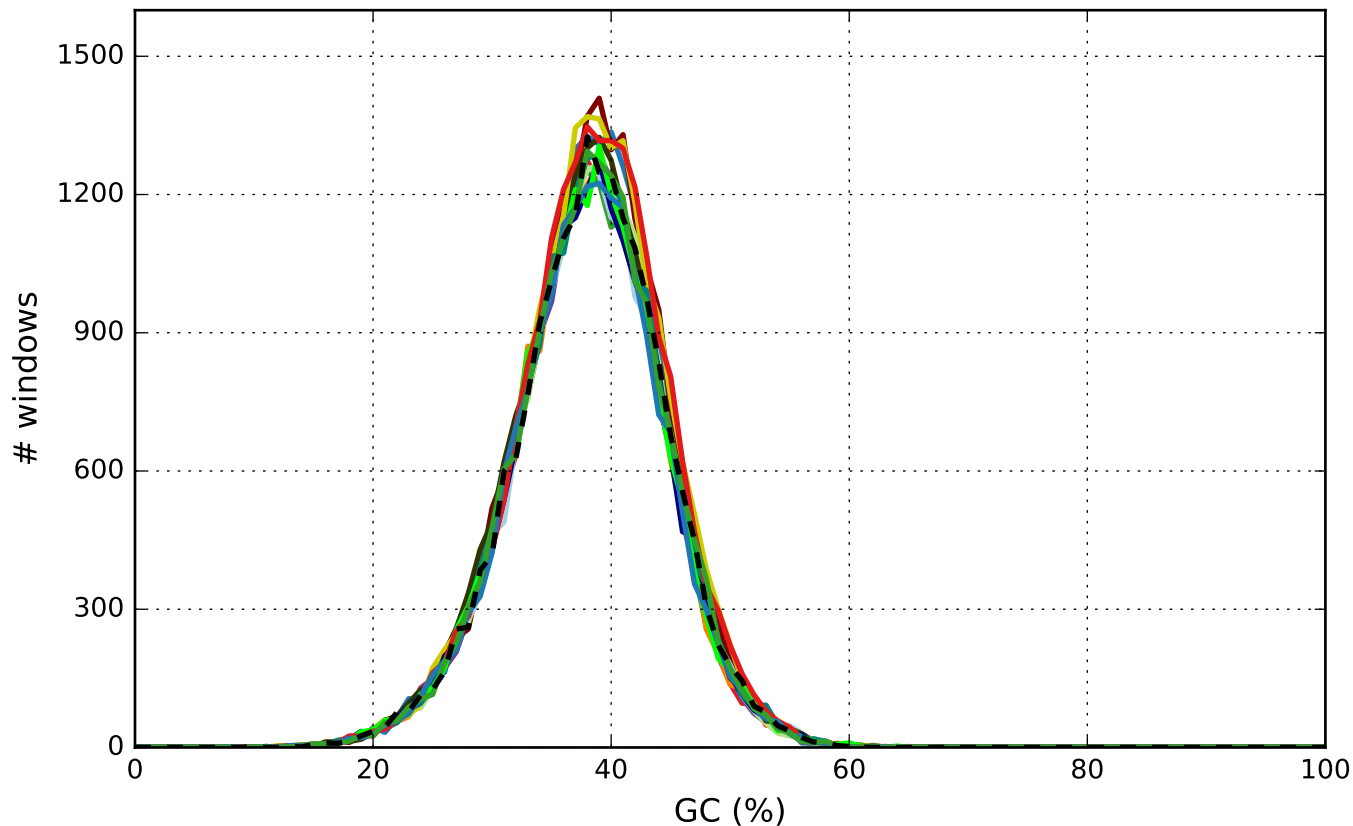


NGx

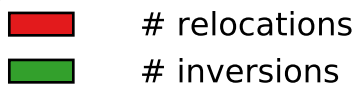
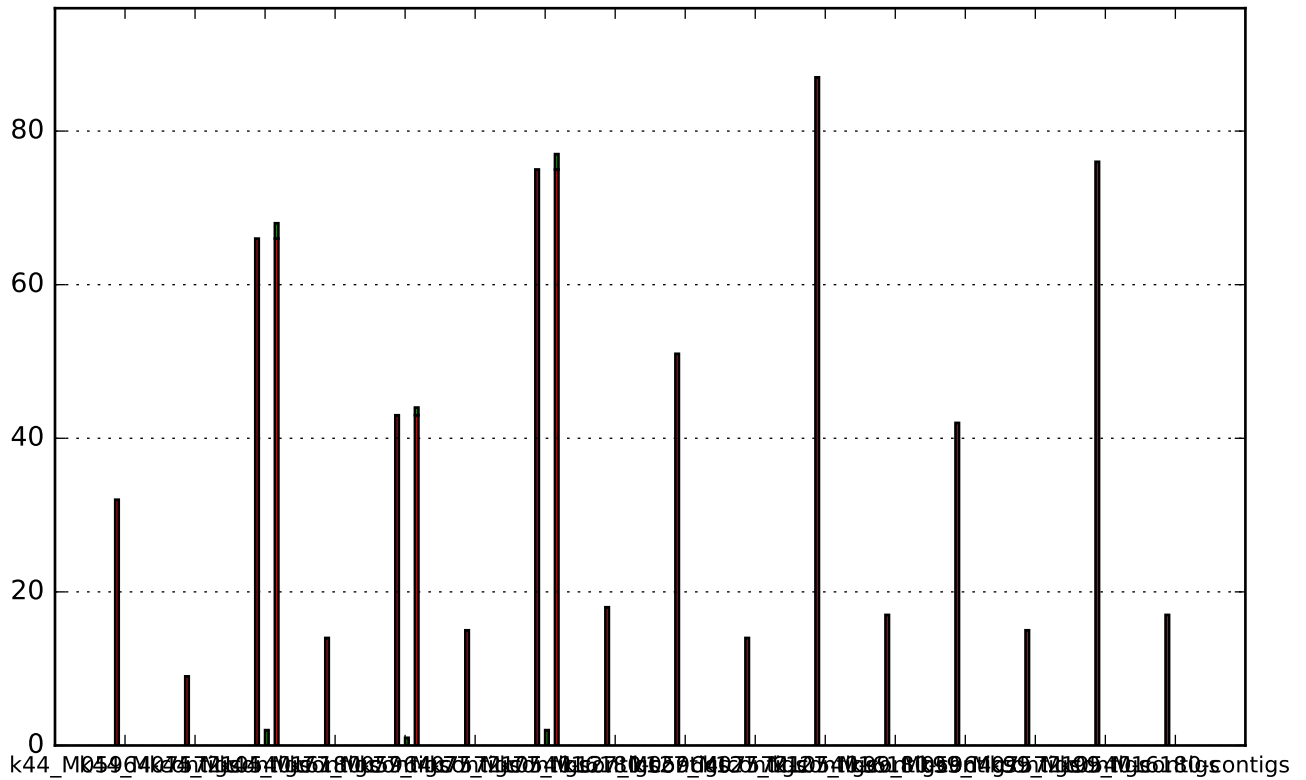




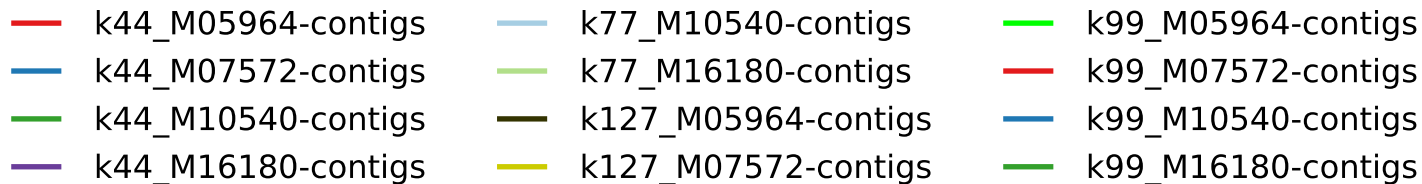
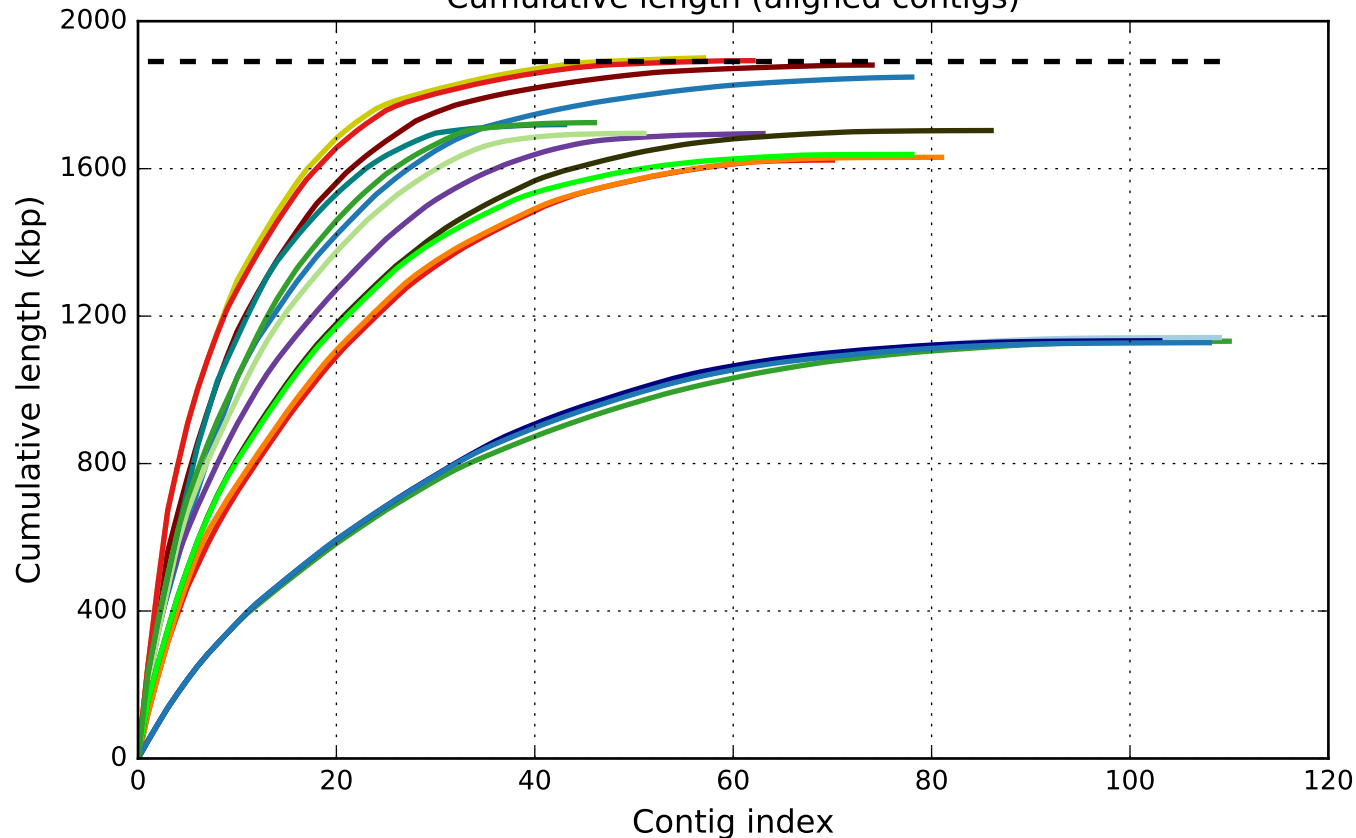
GC content



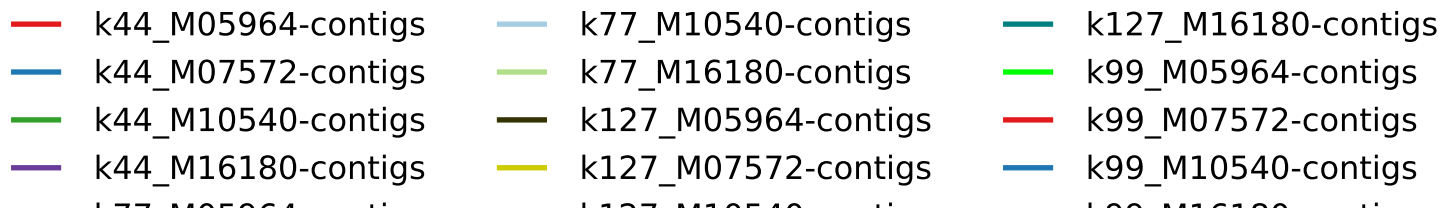
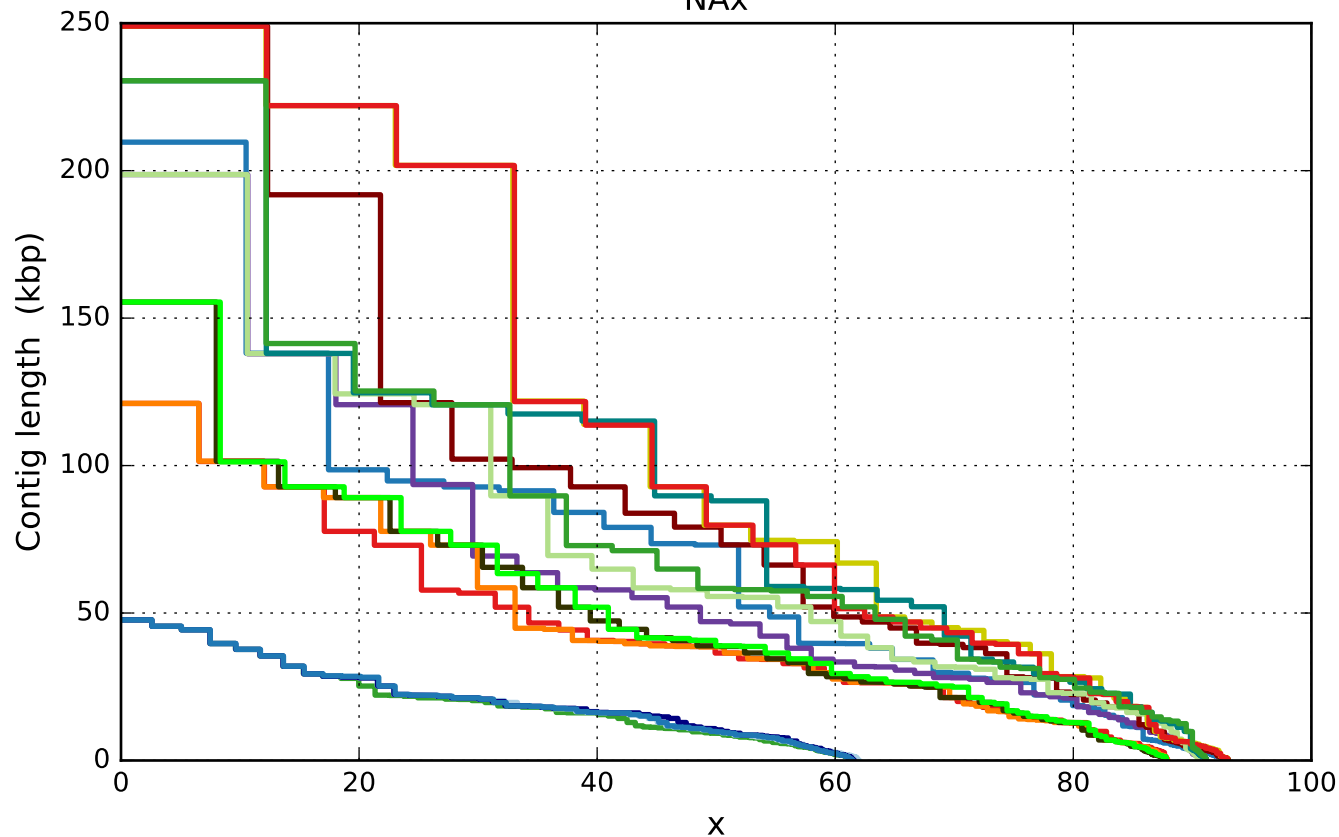
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

