Г	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	1813033	1813033	1813033	1813033	1813033	1813033	1813033	1813033	1813033	1813033	1813033	1813033	1813033	1813033	1813033	1813033
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 (%)	38.04	38.04	38.04	38.04	38.04	38.04	38.04	38.04	38.04	38.04	38.04	38.04	38.04	38.04	38.04	38.04
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	166144	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	92226	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	4	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	8	5	9
# misassemblies	6	27	49	25	12	34	60	29	15	32	59	31	14	34	57	31
# misassembled contigs	5	17	12	11	11	17	11	14	11	14	10	11	11	15	9	14
Misassembled contigs length	802499	1206630	974478	1080401	1222644	1603582	1207166	1356967	1358015	1584320	1220192	1461347	1301381	1656042	1219662	1549249
# local misassemblies	36	50	23	55	40	52	28	60	41	54	27	63	39	55	30	63
# unaligned contigs	3 + 4 part	29 + 12 part	4 + 8 part	14 + 7 part	2 + 3 part	24 + 8 part	2 + 6 part	6 + 5 part	2 + 3 part	13 + 7 part	2 + 2 part	3 + 3 part	2 + 3 part	15 + 7 part	3 + 4 part	3 + 4 part
Unaligned length	61359	236162	447610	117857	9007	199522	333990	94710	11425	176482	316091	56178	9811	196173	334519	61286
Genome fraction (%)	94.824	88.648	55.967	89.311	94.727	89.067	57.300	89.445	95.355	89.165	56.669	90.234	95.134	89.044	56.433	90.025
Duplication ratio	1.038	1.094	1.375	1.078	1.074	1.129	1.450	1.096	1.117	1.155	1.483	1.120	1.075	1.139	1.465	1.121
# 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	1301.43	2465.51	3631.83	2496.90	1305.21	2462.96	3672.67	2499.21	1303.37	2448.10	3656.52	2470.84	1301.25	2446.92	3659.47	2473.44
# indels per 100 kbp	60.03	84.87	114.91	91.59	59.33	87.19	116.57	92.19	61.08	85.18	116.12	92.30	59.14	84.92	113.77	91.53
Largest alignment	427914	113400	52580	119011	329581	113381	52580	151223	427942	113381	52580	150238	427942	113381	69362	151223
NA50	74224	33470	6313	38993	98409	35233	6980	44375	100032	41216	6604	51788	100032	38868	6723	46341
NGA50	97979	35233	6604	38993	98409	38868	7559	44375	100032	46032	6980	52135	100032	45124	7559	46347
NA75	39961	11142	-	16610	40653	12836	-	16610	41727	11217	-	19207	41819	11189	-	19061
NGA75	39961	18784	-	19035	40653	19189	-	18809	50104	25482	-	24859	45914	22347	-	19996
LA50	6	19	56	14	6	17	52	12	5	16	54	12	5	16	51	12
LGA50	5	16	54	14	6	14	50	12	5	14	52	11	5	14	49	11
LA75	14	43	-	33	13	40	-	29	13	37		26	12	38	-	28
LGA75	14	34	-	31	13	31	_	27	11	27	-	23	11	28	-	25
		31	1		I						<u> </u>					<u> </u>

## Misassemblies report

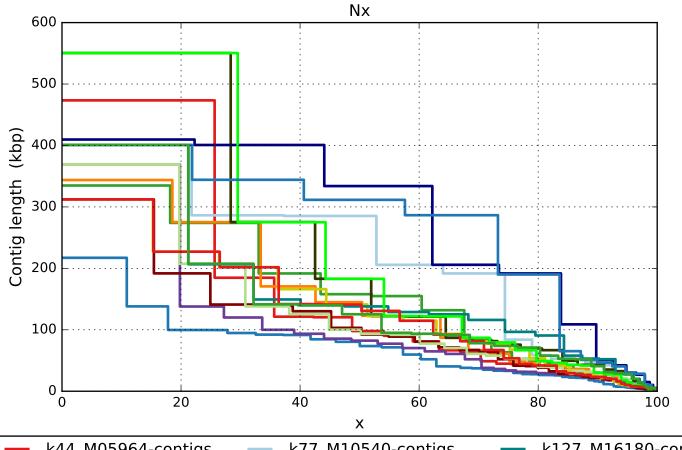
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# misassemblies	6	27	49	25	12	34	60	29	15	32	59	31	14	34	57	31
# relocations	6	26	49	24	12	33	58	28	15	31	59	30	14	33	57	31
# translocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# inversions	0	1	0	1	0	1	2	1	0	1	0	1	0	1	0	0
# misassembled contigs	5	17	12	11	11	17	11	14	11	14	10	11	11	15	9	14
Misassembled contigs length	802499	1206630	974478	1080401	1222644	1603582	1207166	1356967	1358015	1584320	1220192	1461347	1301381	1656042	1219662	1549249
# local misassemblies	36	50	23	55	40	52	28	60	41	54	27	63	39	55	30	63
# mismatches	22374	39626	36852	40431	22416	39772	38154	40529	22533	39576	37568	40422	22444	39503	37442	40371
# indels	1032	1364	1166	1483	1019	1408	1211	1495	1056	1377	1193	1510	1020	1371	1164	1494
# short indels	961	1244	1093	1356	947	1281	1137	1359	976	1252	1118	1371	948	1247	1088	1355
# long indels	71	120	73	127	72	127	74	136	80	125	75	139	72	124	76	139
Indels length	2444	3662	2466	3699	2478	3912	2588	3828	2583	3854	2591	3841	2463	3783	2625	3828

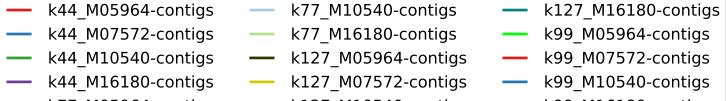
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

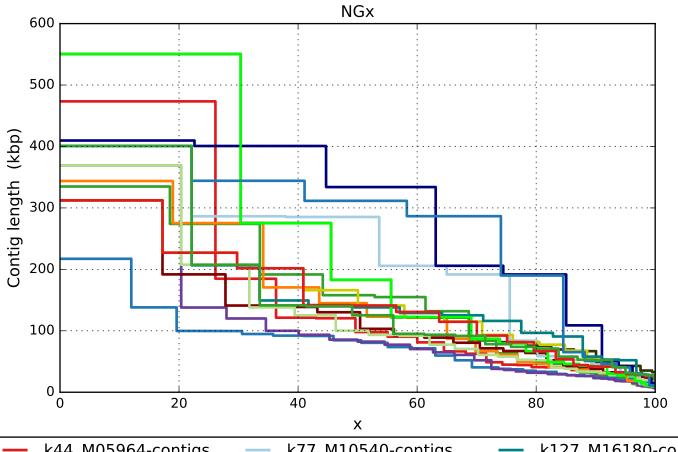
## Unaligned report

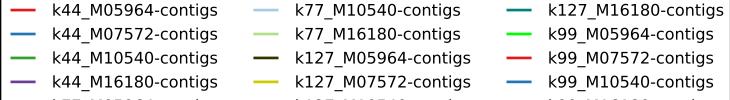
			<u> </u>							<del>1</del>					1	1
	k44_M05964-contigs	k44_M07572-contigs	k44_M10540-contigs	k44_M16180-contigs	k77_M05964-contigs	k77_M07572-contigs	k77_M10540-contigs	k77_M16180-contigs	k127_M05964-contigs	k127_M07572-contigs	k127_M10540-contigs	k127_M16180-contigs	k99_M05964-contigs	k99_M07572-contigs	k99_M10540-contigs	k99_M16180-contigs
# fully unaligned contigs	3	29	4	14	2	24	2	6	2	13	2	3	2	15	3	3
Fully unaligned length	46945	179638	24103	62327	3632	118033	10649	20149	4647	116876	10749	18430	4414	113166	11513	18318
# partially unaligned contigs	4	12	8	7	3	8	6	5	3	7	2	3	3	7	4	4
# with misassembly	0	1	6	0	0	2	5	1	0	2	2	1	0	2	3	1
# both parts are significant	4	7	7	6	2	4	6	4	3	5	2	3	2	4	4	3
Partially unaligned length	14414	56524	423507	55530	5375	81489	323341	74561	6778	59606	305342	37748	5397	83007	323006	42968
# N's	153	166	1	27	22	10	0	15	0	0	0	0	0	0	1	1

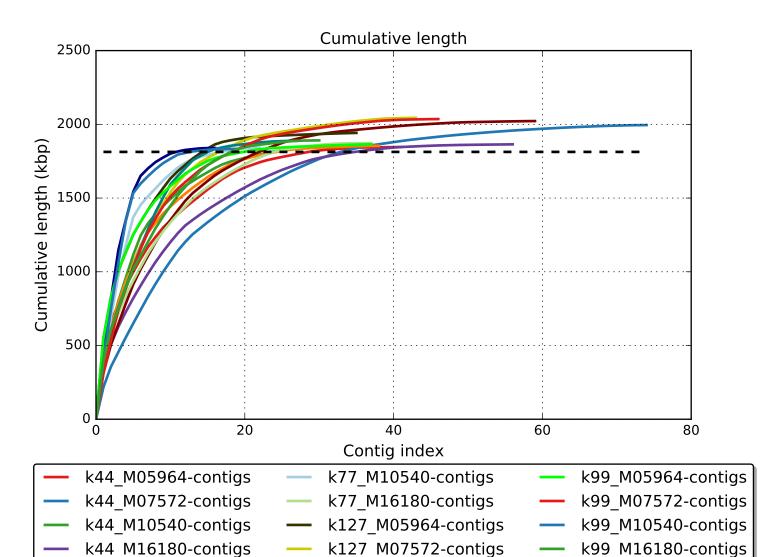
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

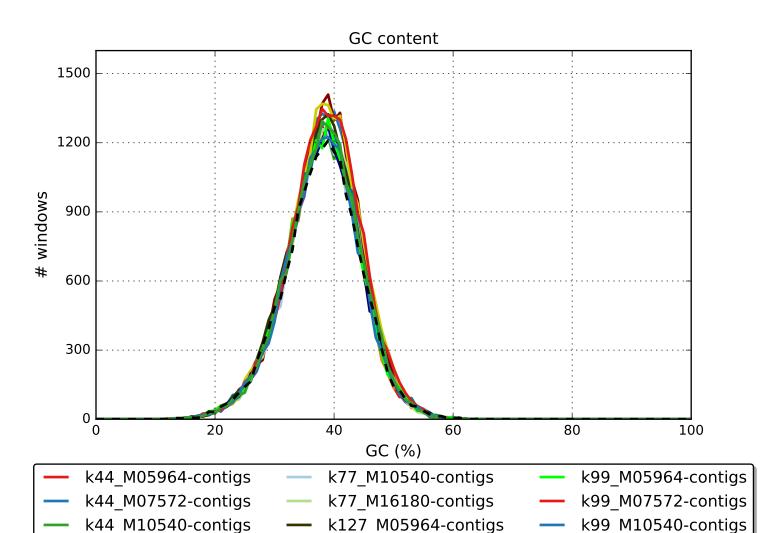








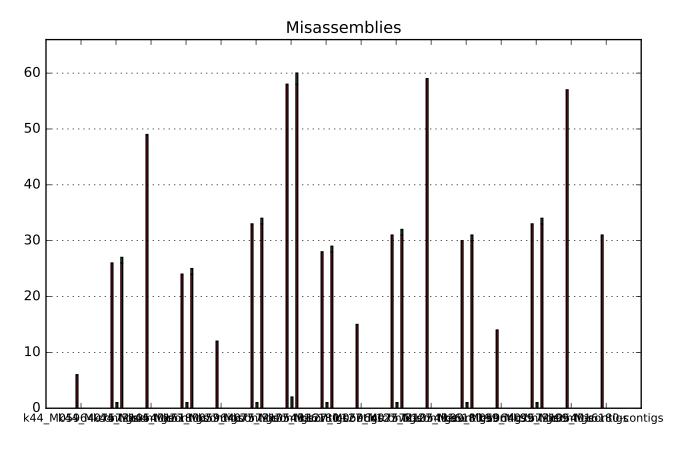




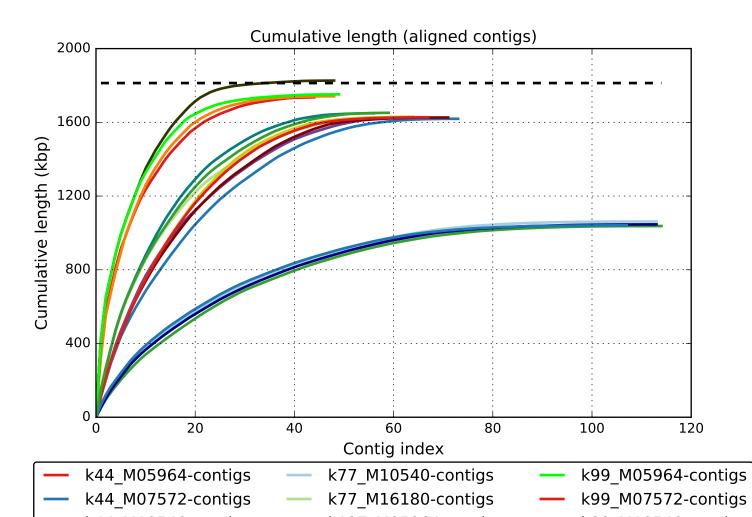
k127 M07572-contigs

k44 M16180-contigs

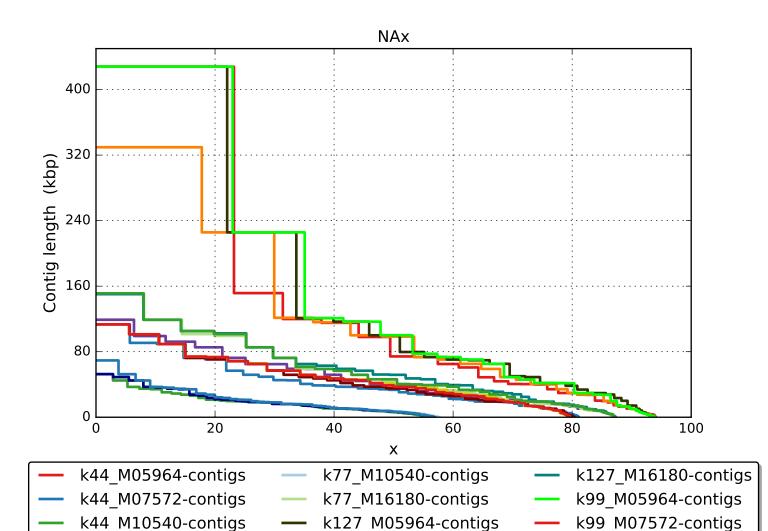
k99 M16180-contigs







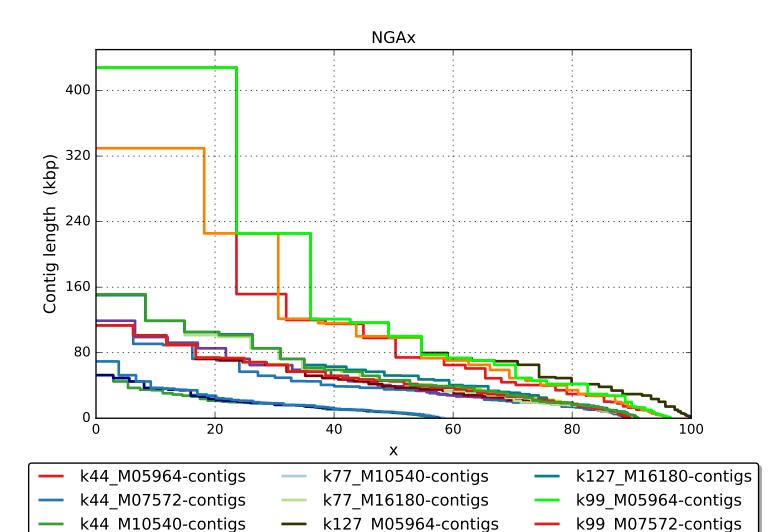
— k44\_M10540-contigs
— k127\_M05964-contigs
— k99\_M10540-contigs
— k99\_M16180-contigs
— k99\_M16180-contigs



k127 M07572-contigs

k99 M10540-contigs

k44 M16180-contigs



k127 M07572-contigs

k99 M10540-contigs

k44 M16180-contigs

