

Report

	ABYSS_k96	ABYSS_k128	a5-miseq	megahit	SPAdes_def	velvetopt_data_97	idba_ud	omega	sga
# contigs (>= 0 bp)	52	45	29	83	44	48	57	86	189
# contigs (>= 1000 bp)	42	36	24	40	23	36	34	83	61
# contigs (>= 5000 bp)	37	33	18	30	19	31	24	71	42
# contigs (>= 10000 bp)	34	31	17	28	18	29	23	62	39
# contigs (>= 25000 bp)	27	23	16	25	17	24	20	42	29
# contigs (>= 50000 bp)	21	20	14	21	15	21	18	25	23
Total length (>= 0 bp)	3333623	3334167	3297786	3302864	3297390	3290412	3294507	3309777	3341618
Total length (>= 1000 bp)	3330672	3331593	3294340	3289376	3289008	3286633	3286908	3307250	3293078
Total length (>= 5000 bp)	3314497	3320081	3276990	3262440	3278167	3274486	3260140	3267705	3246906
Total length (>= 10000 bp)	3289458	3303922	3270720	3249183	3271897	3261862	3253870	3196926	3225949
Total length (>= 25000 bp)	3172423	3166177	3253349	3204771	3259206	3183316	3200922	2827267	3070921
Total length (>= 50000 bp)	2927072	3021896	3158299	3034363	3165087	3061935	3106884	2232371	2824294
# contigs	43	36	29	41	26	37	35	86	78
Largest contig	371505	371505	460304	439873	459976	439828	439855	207813	242670
Total length	3331667	3331593	3297786	3290098	3290913	3287449	3287724	3309777	3303020
Reference length	3310727	3310727	3310727	3310727	3310727	3310727	3310727	3310727	3310727
GC (%)	57.19	57.19	57.23	57.24	57.24	57.24	57.24	57.23	57.24
Reference GC (%)	57.22	57.22	57.22	57.22	57.22	57.22	57.22	57.22	57.22
N50	142571	189671	247335	139304	248333	181509	180386	65312	120995
NG50	142571	189671	247335	139304	248333	181509	180386	65312	116791
N75	80451	106281	170408	103933	170204	105340	116610	38126	71618
NG75	80451	106281	170408	103933	170204	79346	116610	38126	71618
L50	8	7	5	8	5	6	6	15	9
LG50	8	7	5	8	5	6	6	15	10
L75	15	13	9	14	9	12	11	32	18
LG75	15	13	9	14	9	13	11	32	18
# misassemblies	0	0	1	0	0	0	0	4	0
# misassembled contigs	0	0	1	0	0	0	0	4	0
Misassembled contigs length	0	0	267106	0	0	0	0	365987	0
# local misassemblies	1	0	1	0	0	0	0	4	0
# unaligned mis. contigs	0	0	0	0	0	0	0	0	0
# unaligned contigs	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	2 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	1 + 0 part
Unaligned length	0	0	0	0	1089	0	0	0	520
Genome fraction (%)	99.820	99.865	99.477	99.273	99.346	99.251	99.262	99.733	99.413
Duplication ratio	1.008	1.008	1.001	1.001	1.000	1.000	1.000	1.002	1.003
# N's per 100 kbp	7.14	2.85	0.88	0.00	0.00	8.21	0.00	0.24	0.00
# mismatches per 100 kbp	0.21	0.15	0.21	0.06	0.21	0.12	0.09	0.76	0.12
# indels per 100 kbp	0.45	0.45	0.67	0.40	0.52	0.52	0.46	0.42	1.15
# predicted genes (unique)	3218	3219	3228	3223	3217	3214	3212	3252	3264
# predicted genes (>= 0 bp)	3237	3237	3232	3225	3218	3215	3214	3261	3267
# predicted genes (>= 300 bp)	2851	2854	2842	2842	2843	2839	2834	2850	2860
# predicted genes (>= 1500 bp)	344	344	344	345	344	344	344	343	343
# predicted genes (>= 3000 bp)	34	34	34	33	34	34	34	34	34
Largest alignment	371505	371505	460304	439873	459976	439828	439855	207812	242670
Total aligned length	3330166	3331499	3297745	3288817	3289822	3287166	3287722	3309669	3302292
NA50	142571	189671	247335	139304	248333	181509	180386	63821	120995
NGA50	142571	189671	247335	139304	248333	181509	180386	63821	116791
NA75	80451	106281	170371	103812	170204	105340	116610	38126	71618
NGA75	80451	106281	170371	103812	170204	79258	116610	38126	71618
LA50	8	7	5	8	5	6	6	16	9
LGA50	8	7	5	8	5	6	6	16	10
LA75	15	13	9	14	9	12	11	33	18
LGA75	15	13	9	14	9	13	11	33	18

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

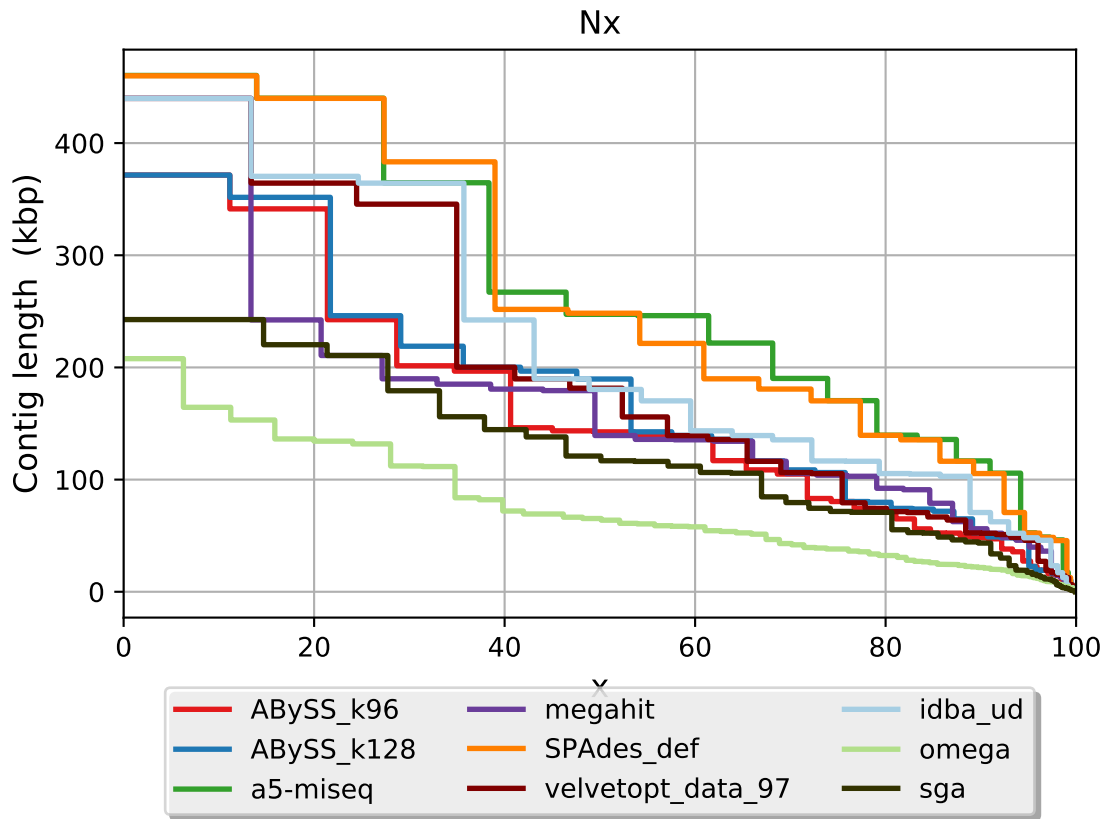
	ABYSS_k96	ABYSS_k128	a5-miseq	megahit	SPAdes_def	velvetopt_data_97	idba_ud	omega	sga
# misassemblies	0	0	1	0	0	0	0	4	0
# relocations	0	0	1	0	0	0	0	2	0
# translocations	0	0	0	0	0	0	0	2	0
# inversions	0	0	0	0	0	0	0	0	0
# misassembled contigs	0	0	1	0	0	0	0	4	0
Misassembled contigs length	0	0	267106	0	0	0	0	365987	0
# local misassemblies	1	0	1	0	0	0	0	4	0
# unaligned mis. contigs	0	0	0	0	0	0	0	0	0
# mismatches	7	5	7	2	7	4	3	25	4
# indels	15	15	22	13	17	17	15	14	38
# indels (<= 5 bp)	12	11	15	11	13	13	12	9	36
# indels (> 5 bp)	3	4	7	2	4	4	3	5	2
Indels length	39	119	176	28	104	143	95	68	54

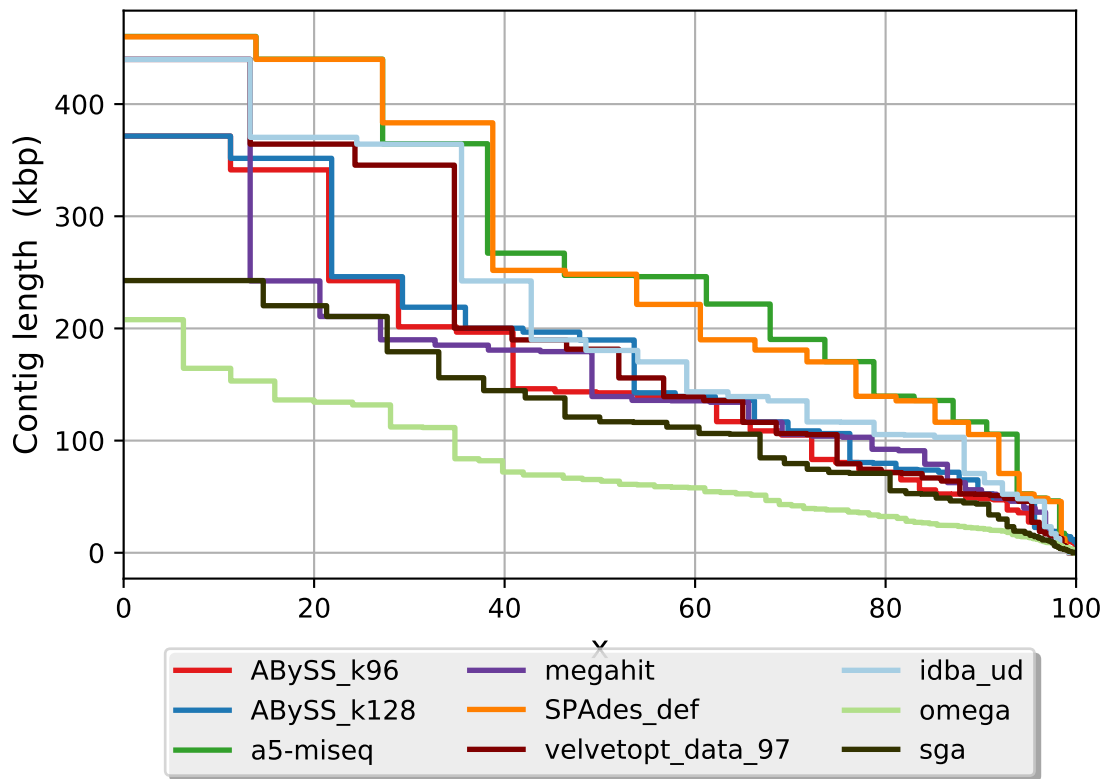
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

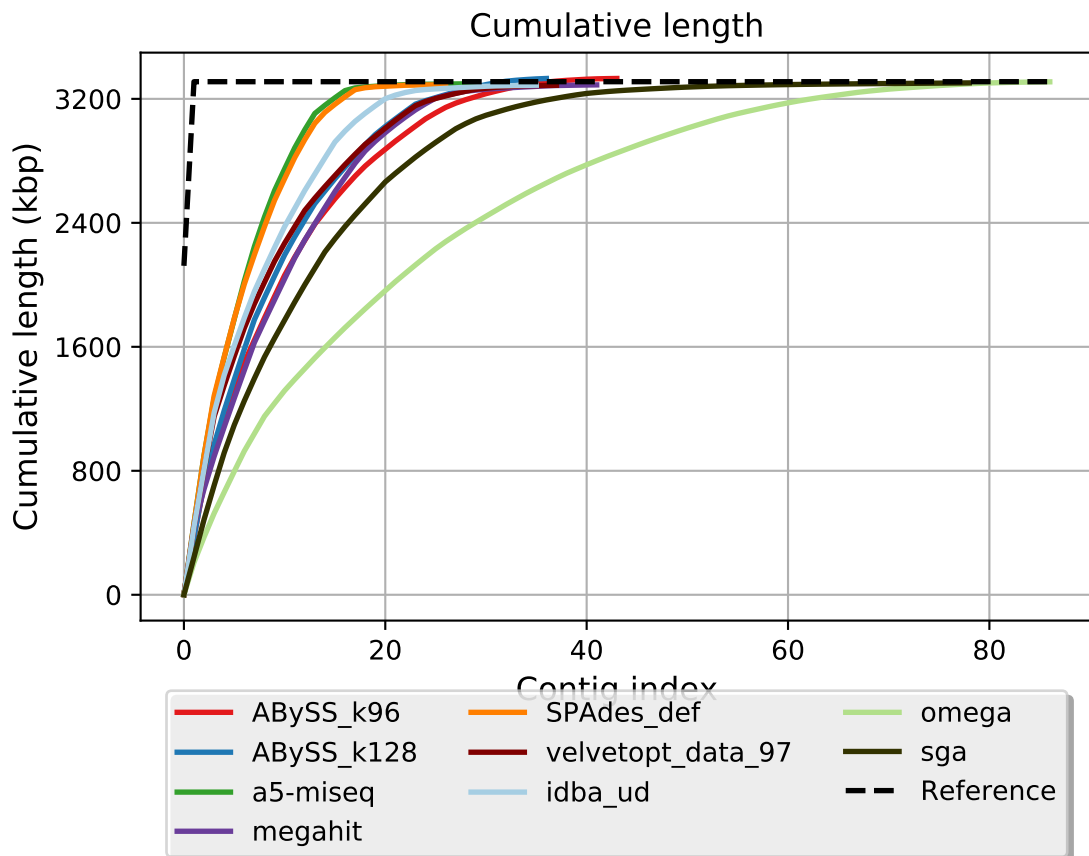
Unaligned report

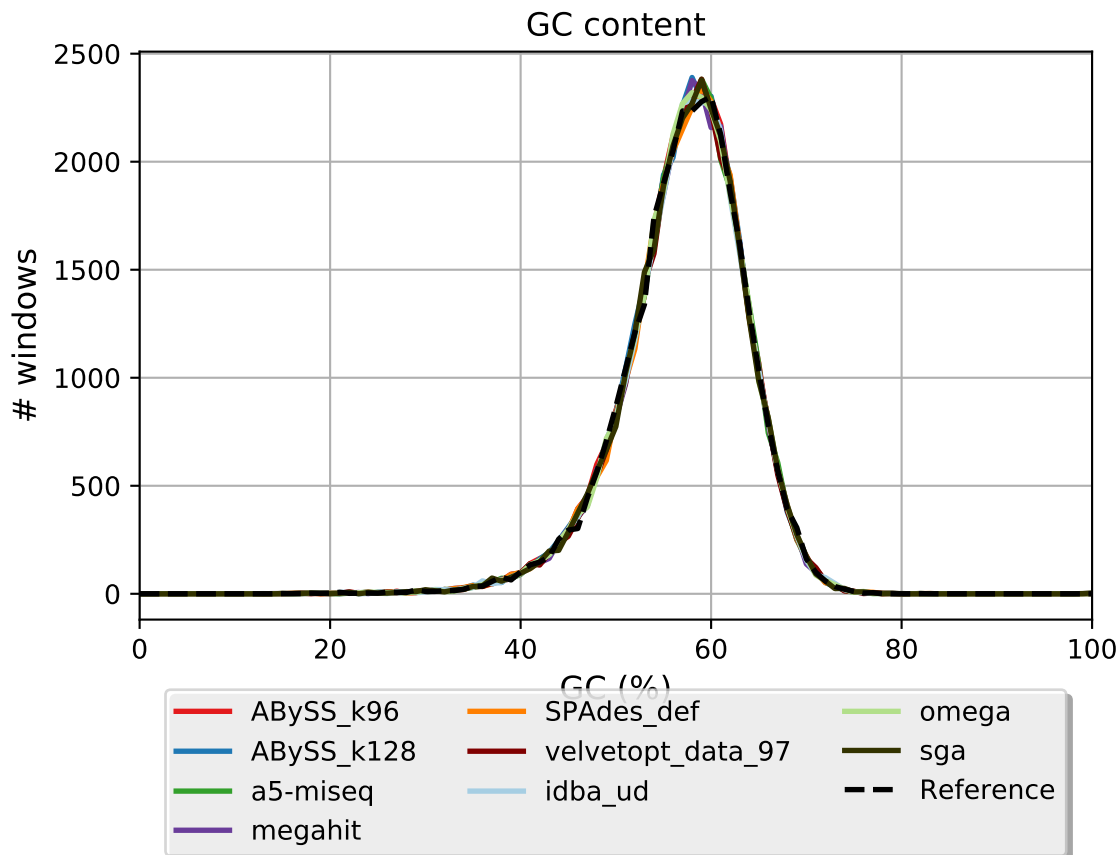
	ABYSS_k96	ABYSS_k128	a5-miseq	megahit	SPAdes_def	velvetopt_data_97	idba_ud	omega	sga
# fully unaligned contigs	0	0	0	0	2	0	0	0	1
Fully unaligned length	0	0	0	0	1089	0	0	0	520
# partially unaligned contigs	0	0	0	0	0	0	0	0	0
Partially unaligned length	0	0	0	0	0	0	0	0	0
# N's	238	95	29	0	0	270	0	8	0

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).

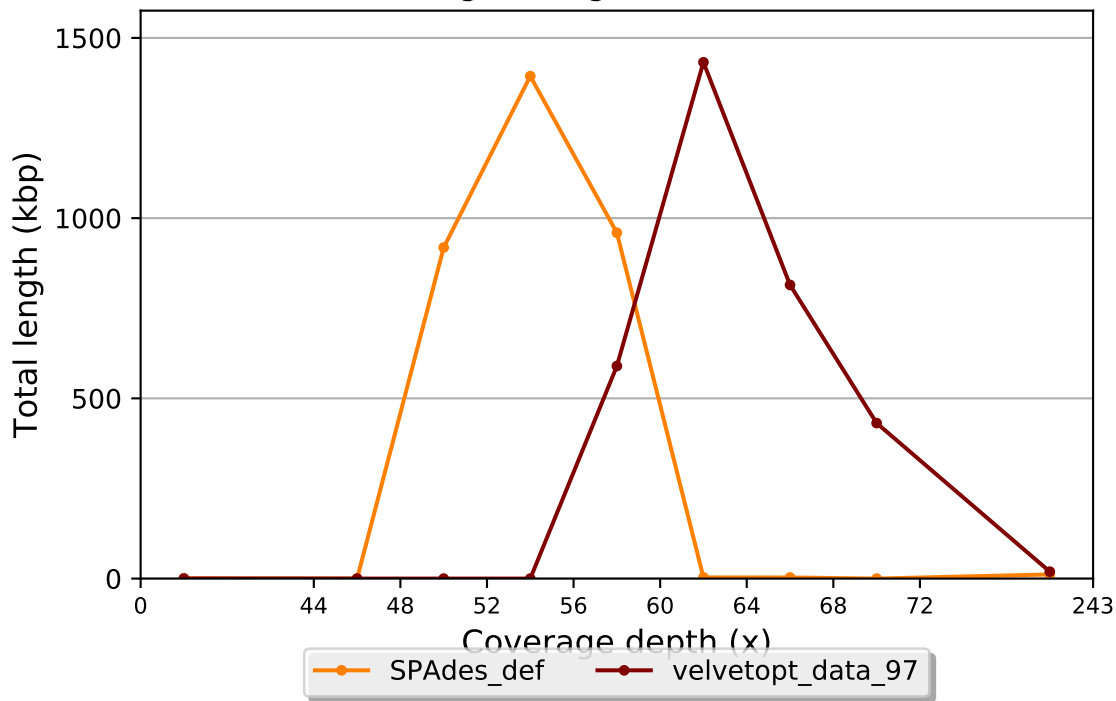




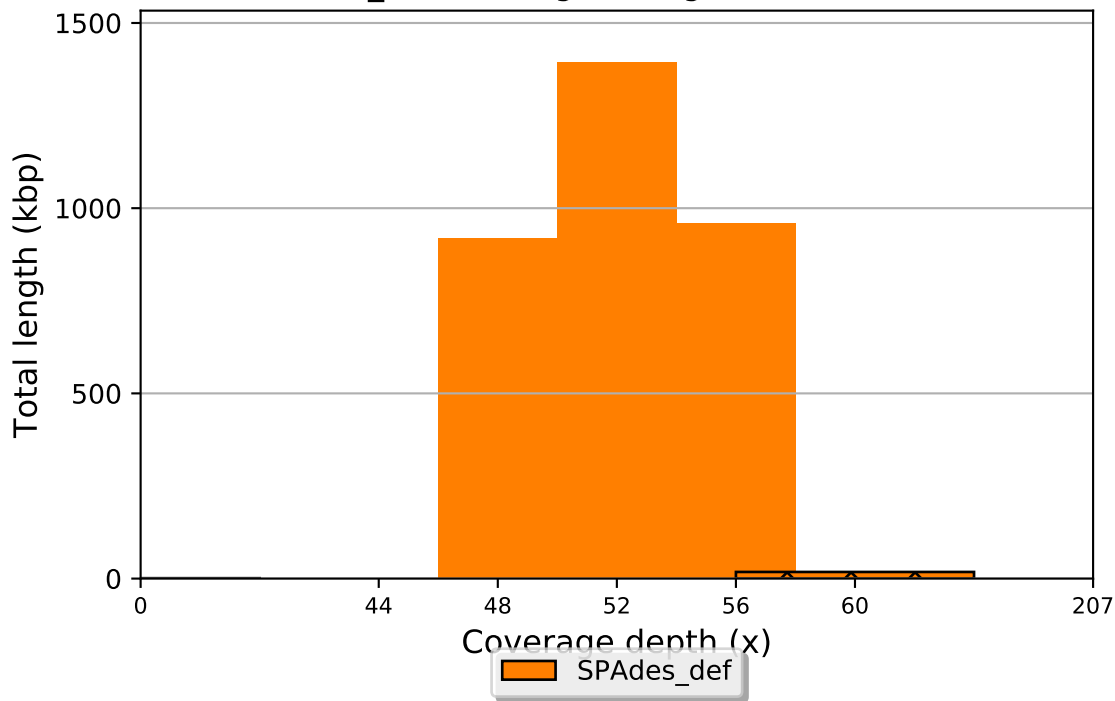




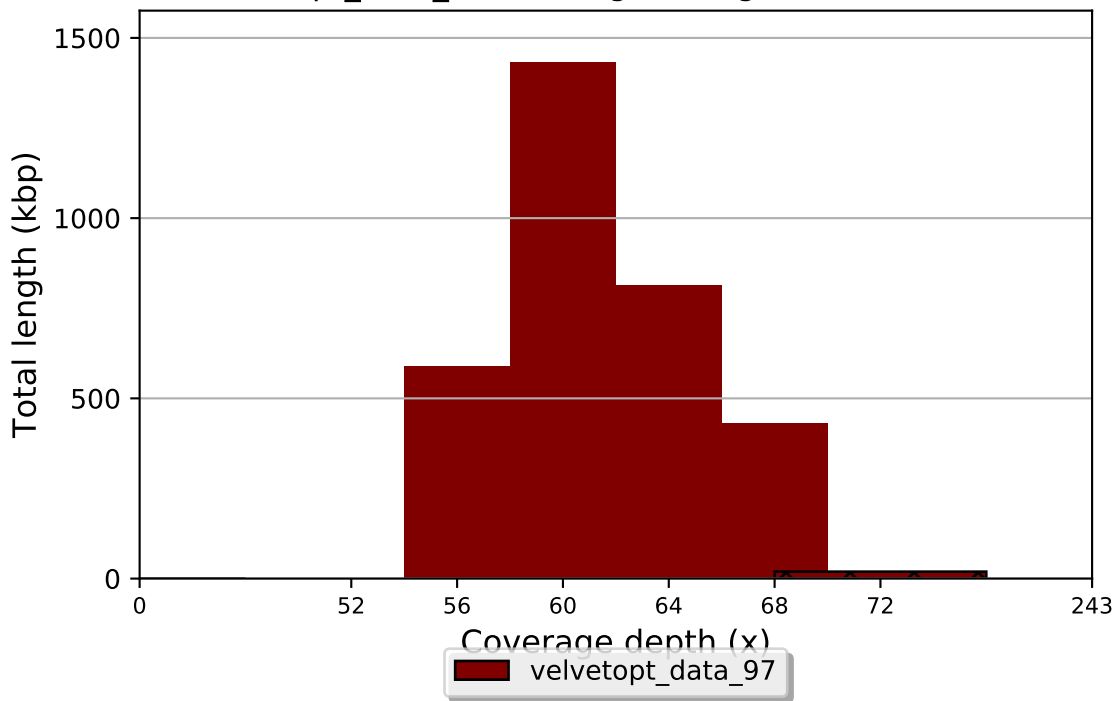
Coverage histogram (bin size: 4x)



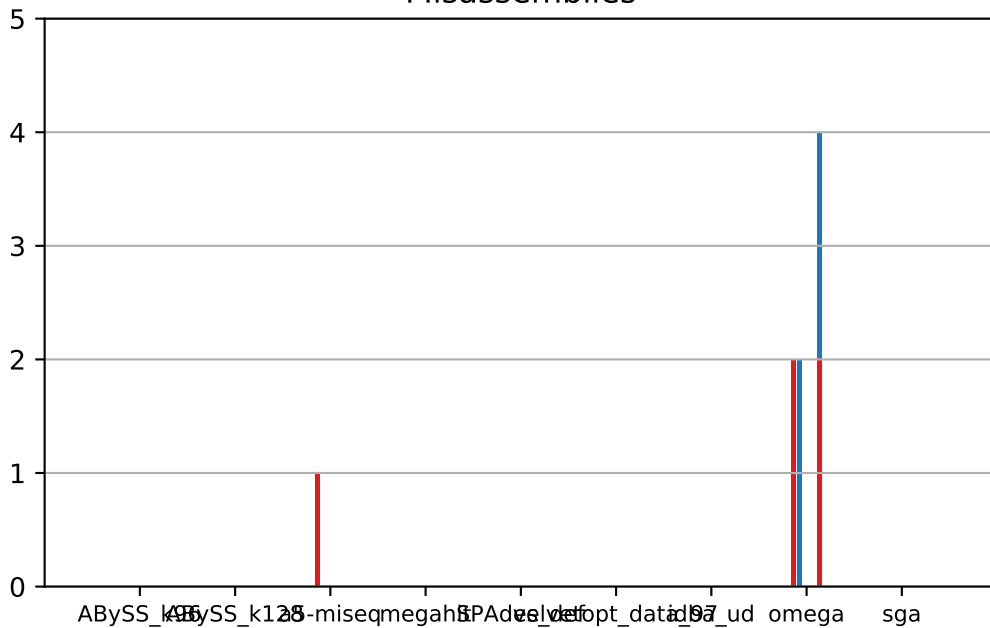
SPAdes_def coverage histogram (bin size: 4x)



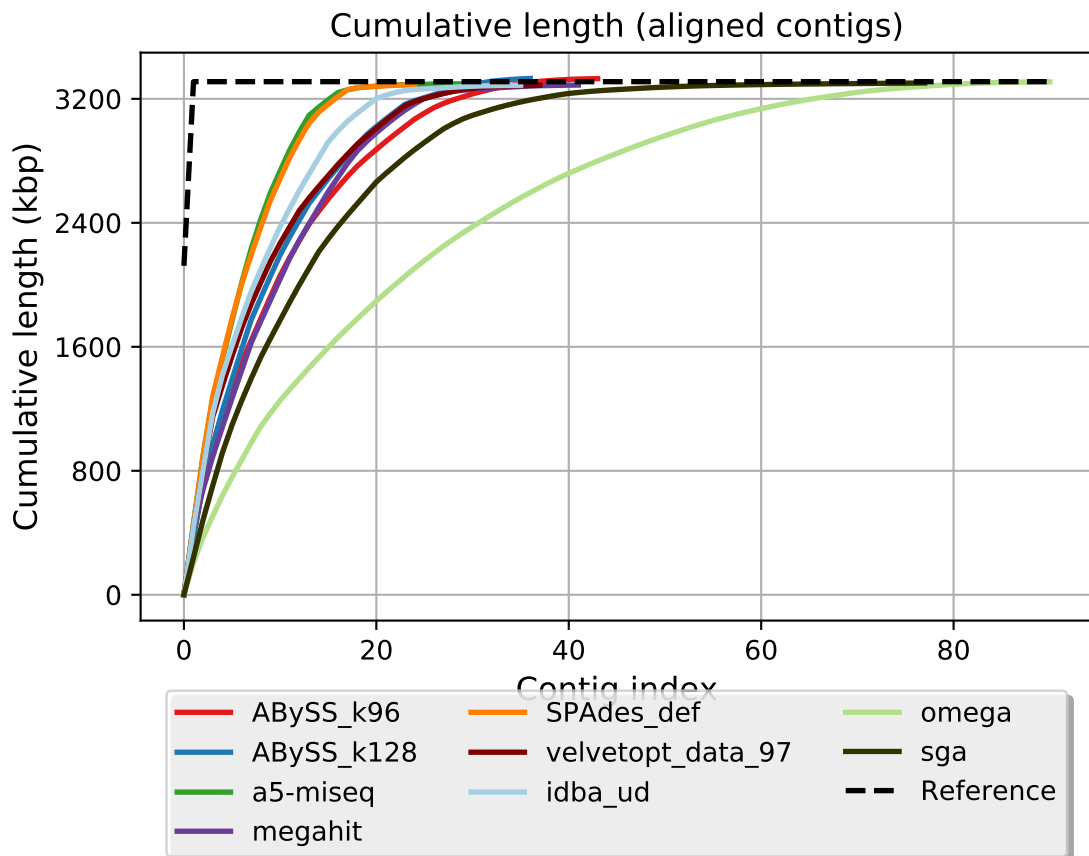
velvetopt_data_97 coverage histogram (bin size: 4x)

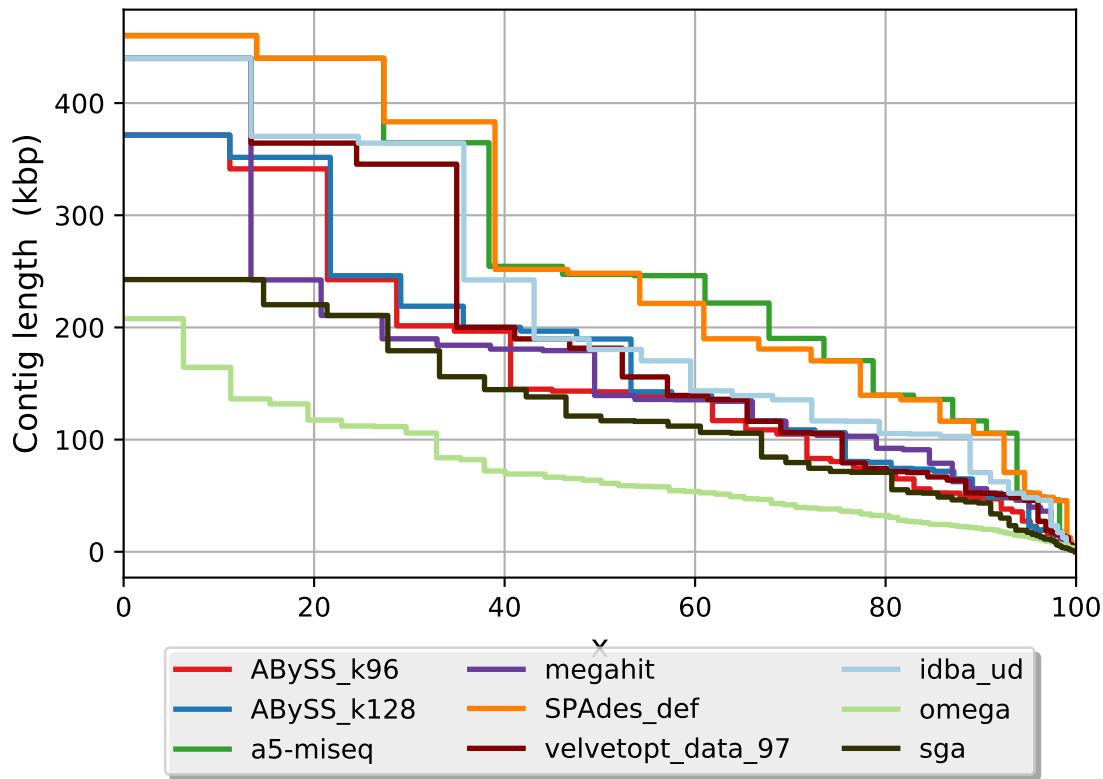


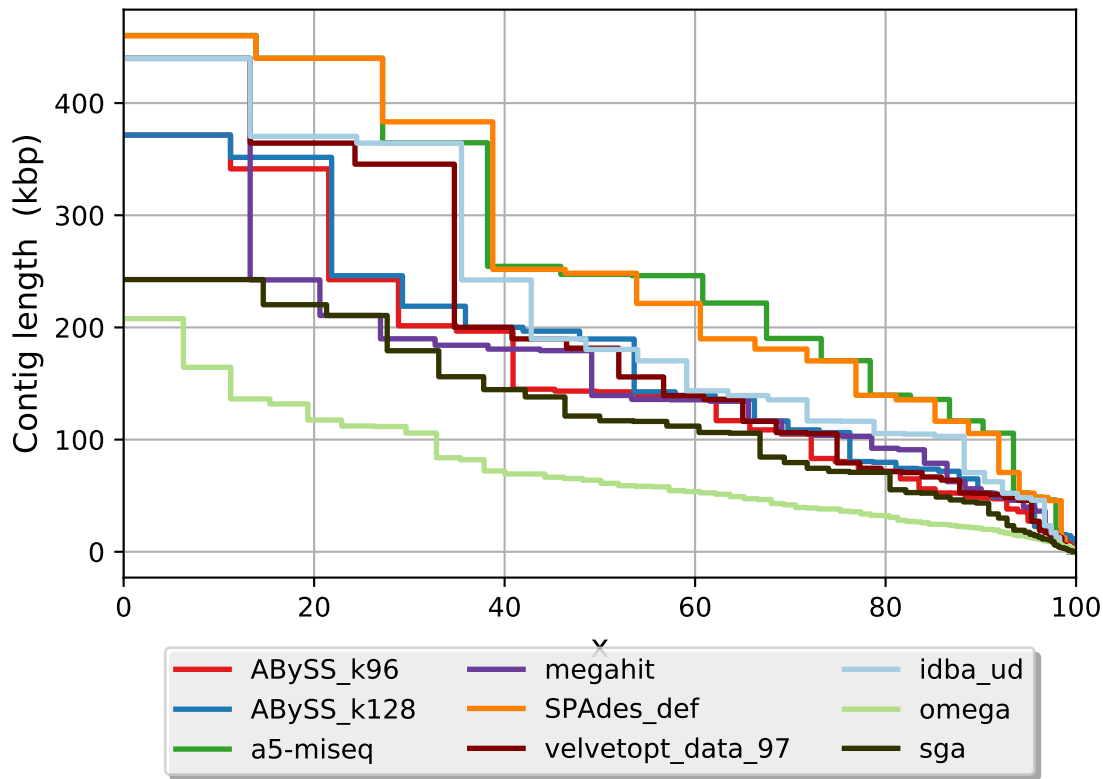
Misassemblies



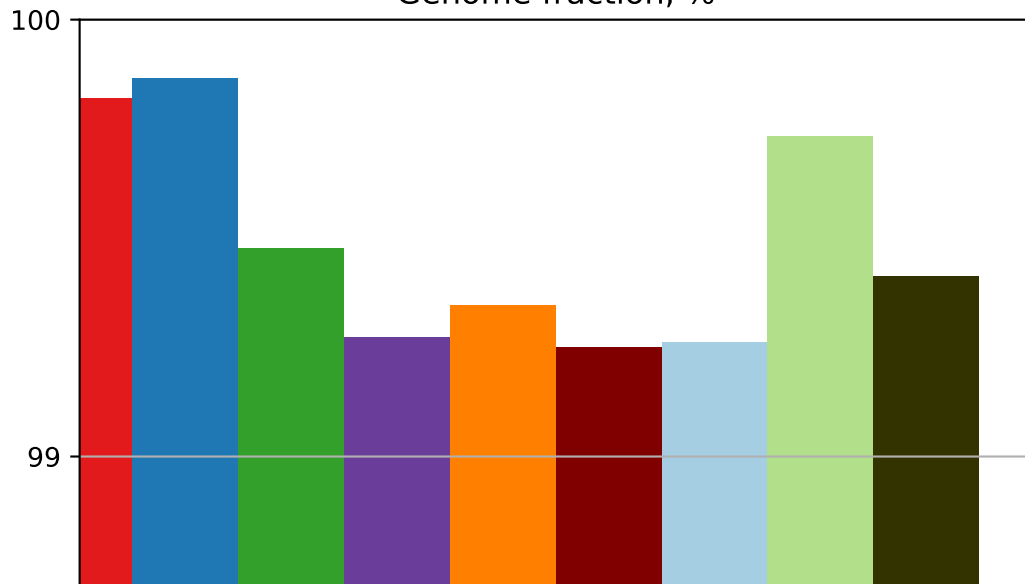
■ # relocations
■ # translocations







Genome fraction, %



ABySS_k96

ABySS_k128

a5-miseq

megahit

SPAdes_def

velvetopt_data_97

idba_ud

omega

sga