

Report

	VelvetAssembly	AbyssAssembly	SpadesAssembly
# contigs (>= 0 bp)	1032	9634	57
# contigs (>= 1000 bp)	560	94	37
Total length (>= 0 bp)	2227380	3223507	2291371
Total length (>= 1000 bp)	1984938	2339488	2283360
# contigs	1032	116	50
Largest contig	78205	136259	513400
Total length	2227380	2347273	2290300
Reference length	1667867	1667867	1667867
GC (%)	35.41	35.57	35.43
Reference GC (%)	38.87	38.87	38.87
N50	3862	50257	141550
NG50	5050	69385	165552
N75	1829	32771	65549
NG75	3359	49859	137248
L50	127	14	5
LG50	63	9	3
L75	334	28	11
LG75	165	15	6
# misassemblies	6	35	31
# misassembled contigs	6	16	15
Misassembled contigs length	31786	1086039	1139530
# local misassemblies	10	53	52
# unaligned contigs	352 + 92 part	75 + 9 part	23 + 5 part
Unaligned length	1002639	758353	745424
Genome fraction (%)	72.877	80.465	79.827
Duplication ratio	1.008	1.184	1.160
# N's per 100 kbp	0.00	22.24	0.00
# mismatches per 100 kbp	3221.64	3471.62	3475.14
# indels per 100 kbp	113.37	143.06	143.08
# genes	715 + 547 part	1258 + 65 part	1253 + 64 part
# predicted genes (unique)	3277	2641	2625
# predicted genes (>= 0 bp)	3277	2693	2634
# predicted genes (>= 300 bp)	2223	1990	1946
# predicted genes (>= 1500 bp)	115	239	230
# predicted genes (>= 3000 bp)	5	16	17
Largest alignment	10380	95355	151009
NA50	791	17529	17204
NGA50	1788	32588	32961
NGA75	-	13639	12740
LA50	465	33	28
LGA50	242	18	14
LGA75	-	38	35

All statistics are based on contigs of size >= 200 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	VelvetAssembly	AbyssAssembly	SpadesAssembly
# misassemblies	6	35	31
# relocations	6	33	29
# translocations	0	0	0
# inversions	0	2	2
# misassembled contigs	6	16	15
Misassembled contigs length	31786	1086039	1139530
# local misassemblies	10	53	52
# mismatches	39159	46591	46268
# indels	1378	1920	1905
# short indels	1253	1669	1664
# long indels	125	251	241
Indels length	3081	5366	5240

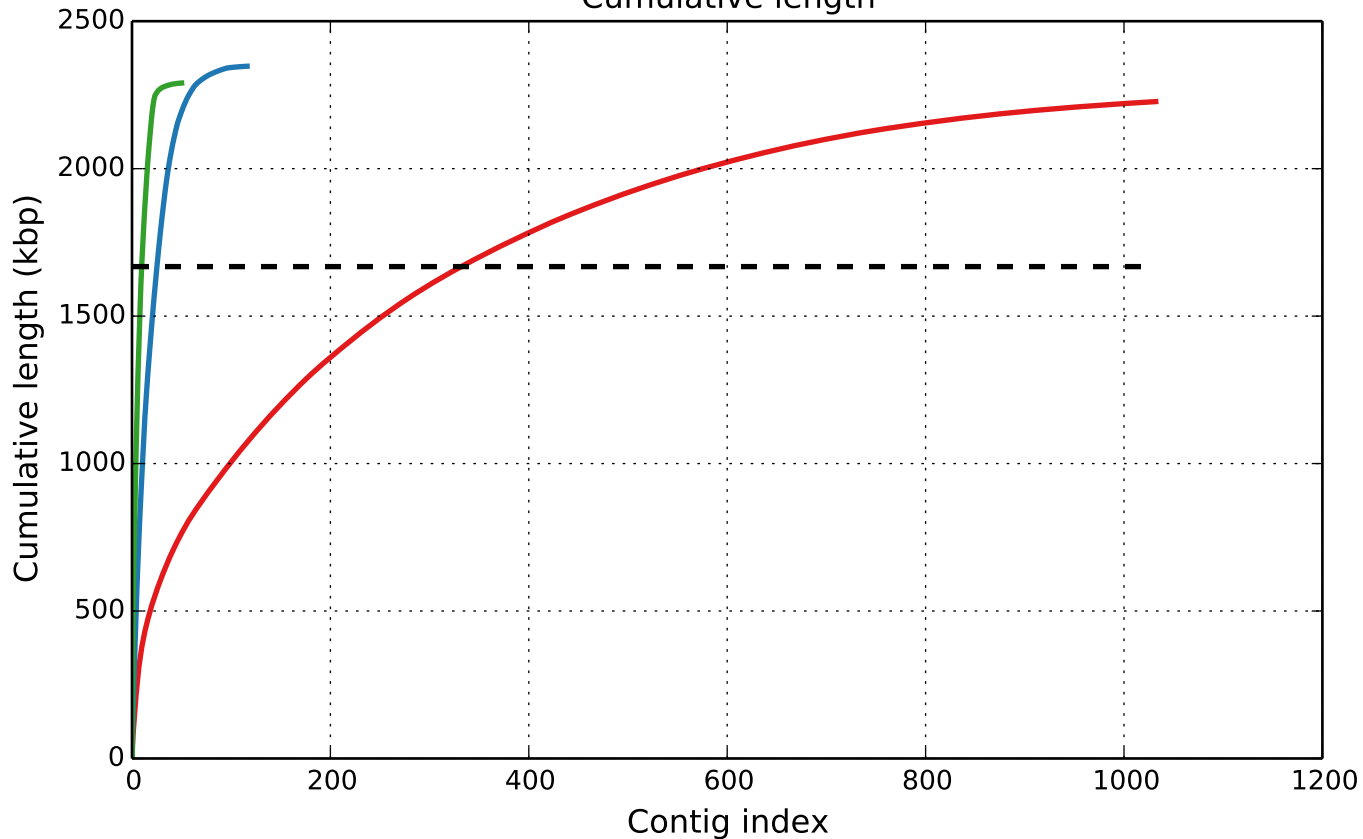
All statistics are based on contigs of size ≥ 200 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	VelvetAssembly	AbyssAssembly	SpadesAssembly
# fully unaligned contigs	352	75	23
Fully unaligned length	937121	719430	706562
# partially unaligned contigs	92	9	5
# with misassembly	4	1	1
# both parts are significant	52	5	4
Partially unaligned length	65518	38923	38862
# N's	0	522	0

All statistics are based on contigs of size ≥ 200 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Cumulative length



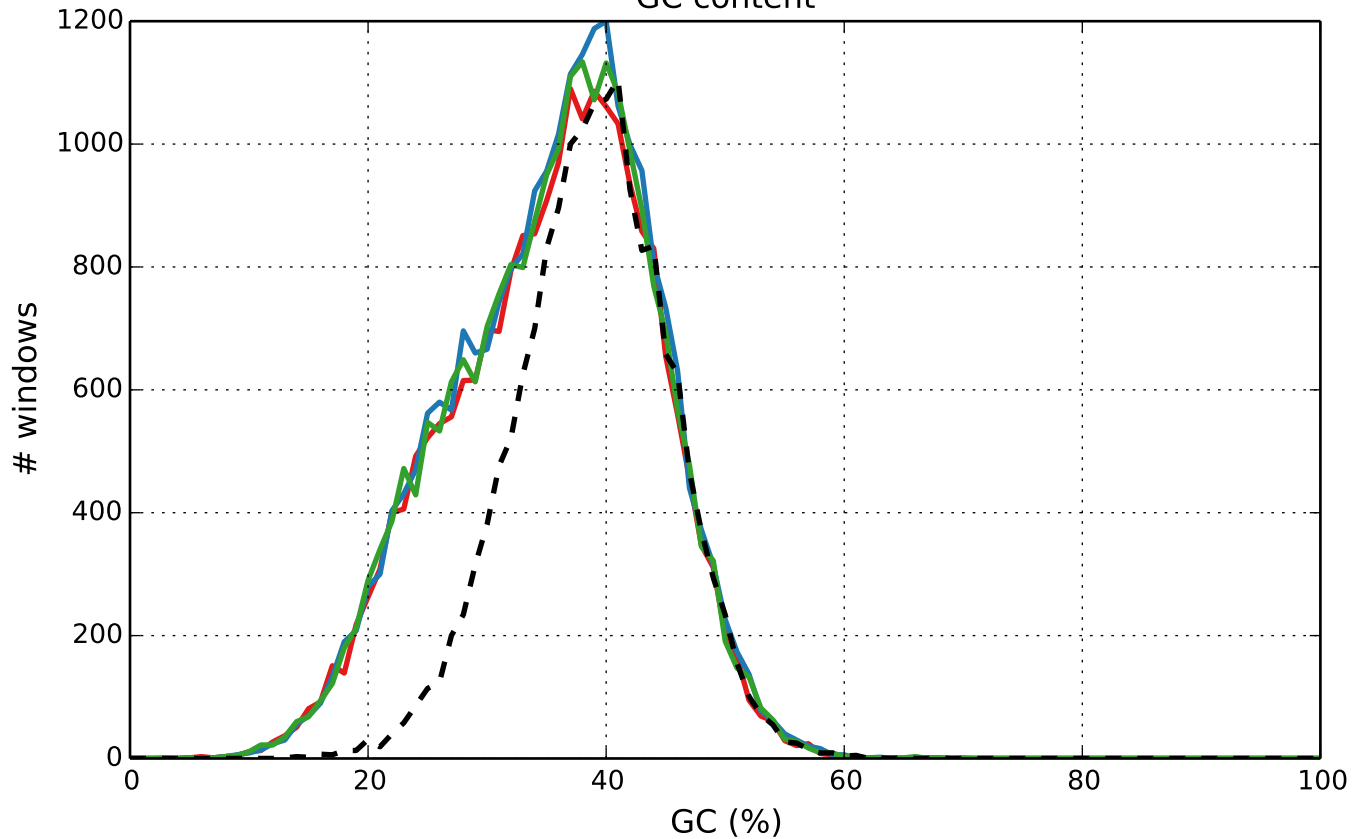
— VelvetAssembly

— SpadesAssembly

- - Reference

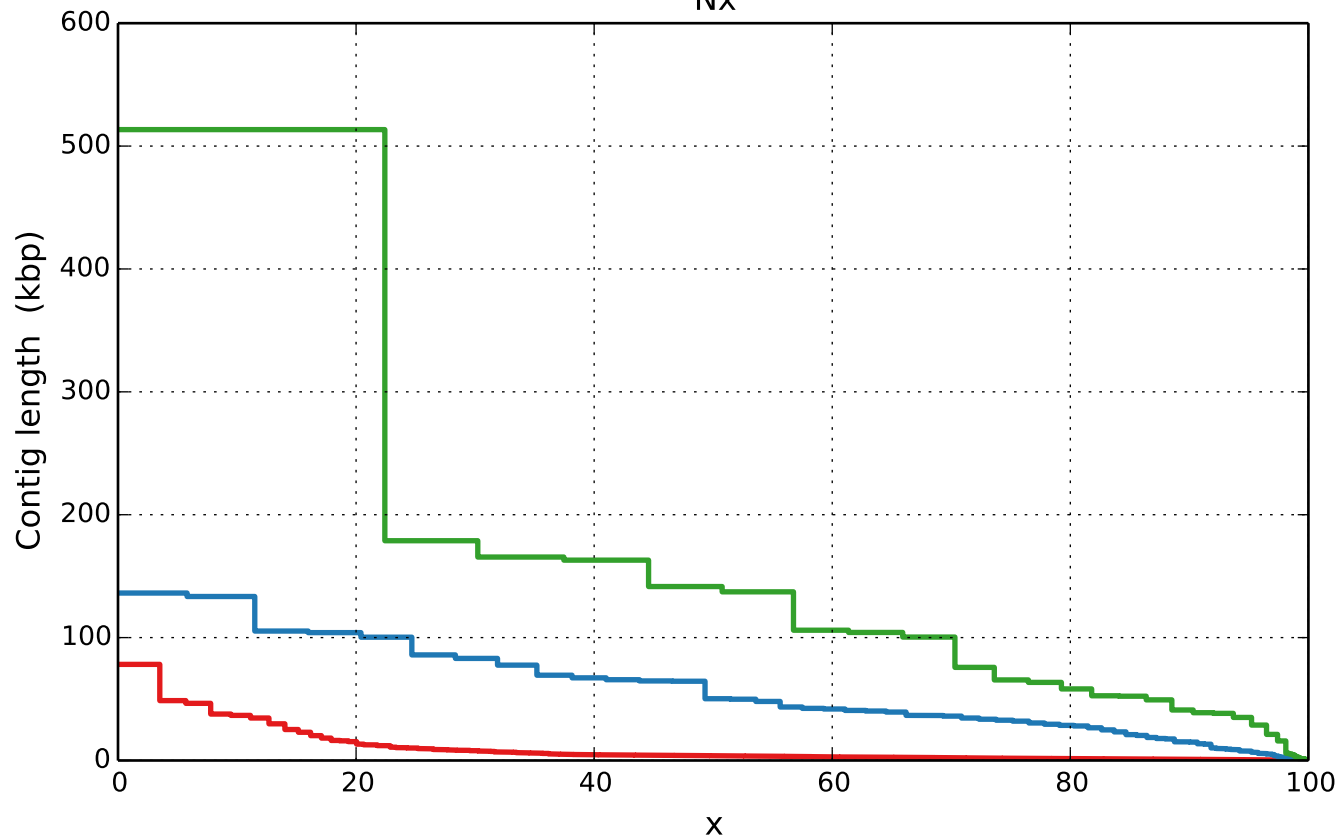
— AbyssAssembly

GC content



— VelvetAssembly — SpadesAssembly - - Reference
— AbyssAssembly

Nx

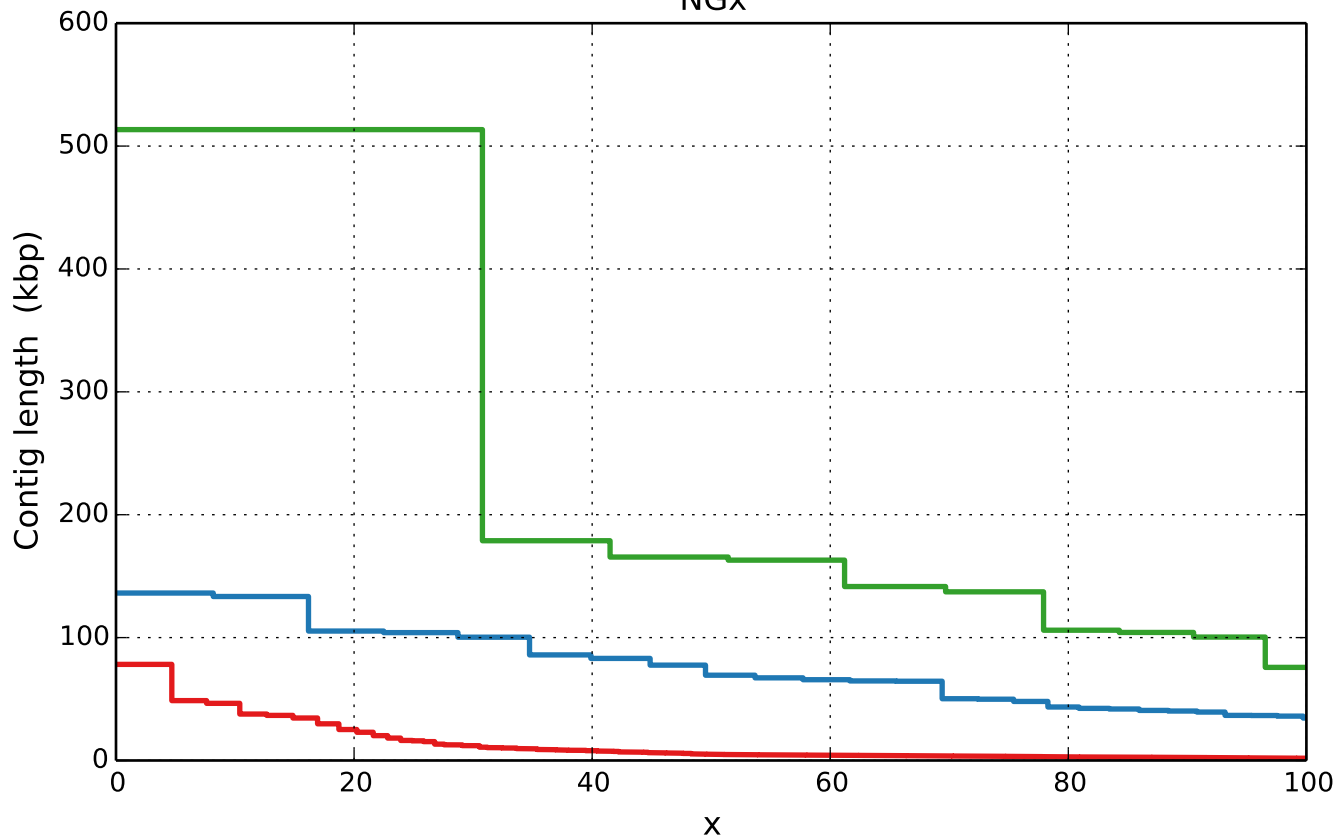


— VelvetAssembly

— AbyssAssembly

— SpadesAssembly

NGx

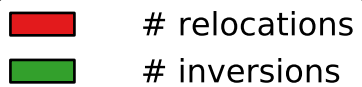
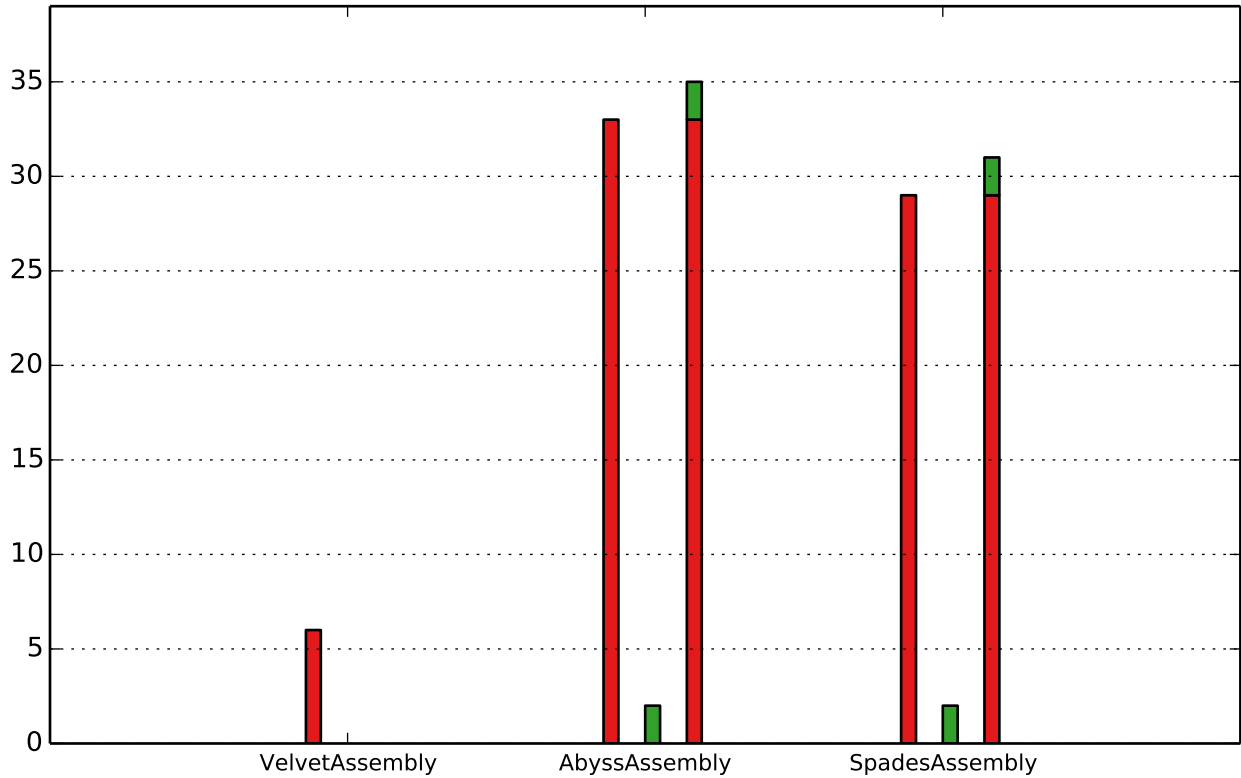


— VelvetAssembly

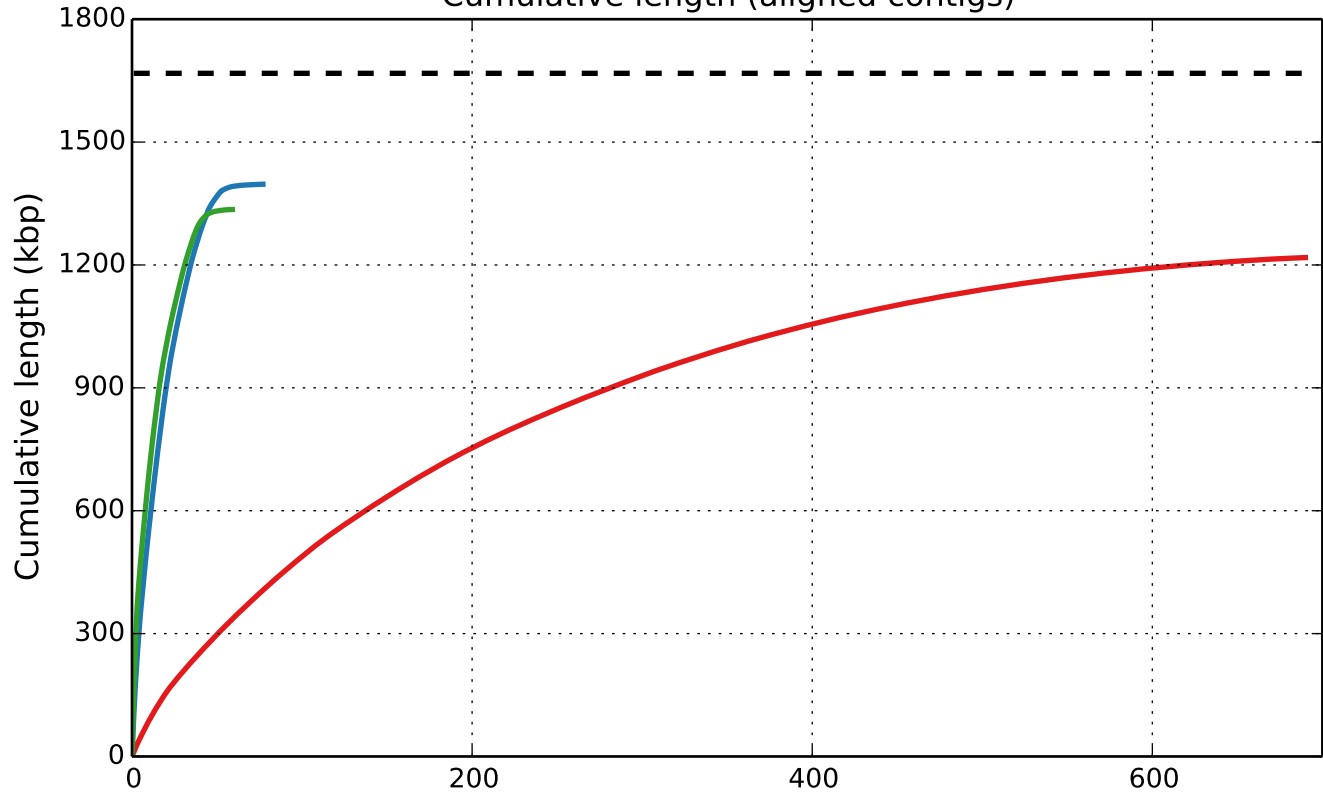
— AbyssAssembly

— SpadesAssembly

Misassemblies

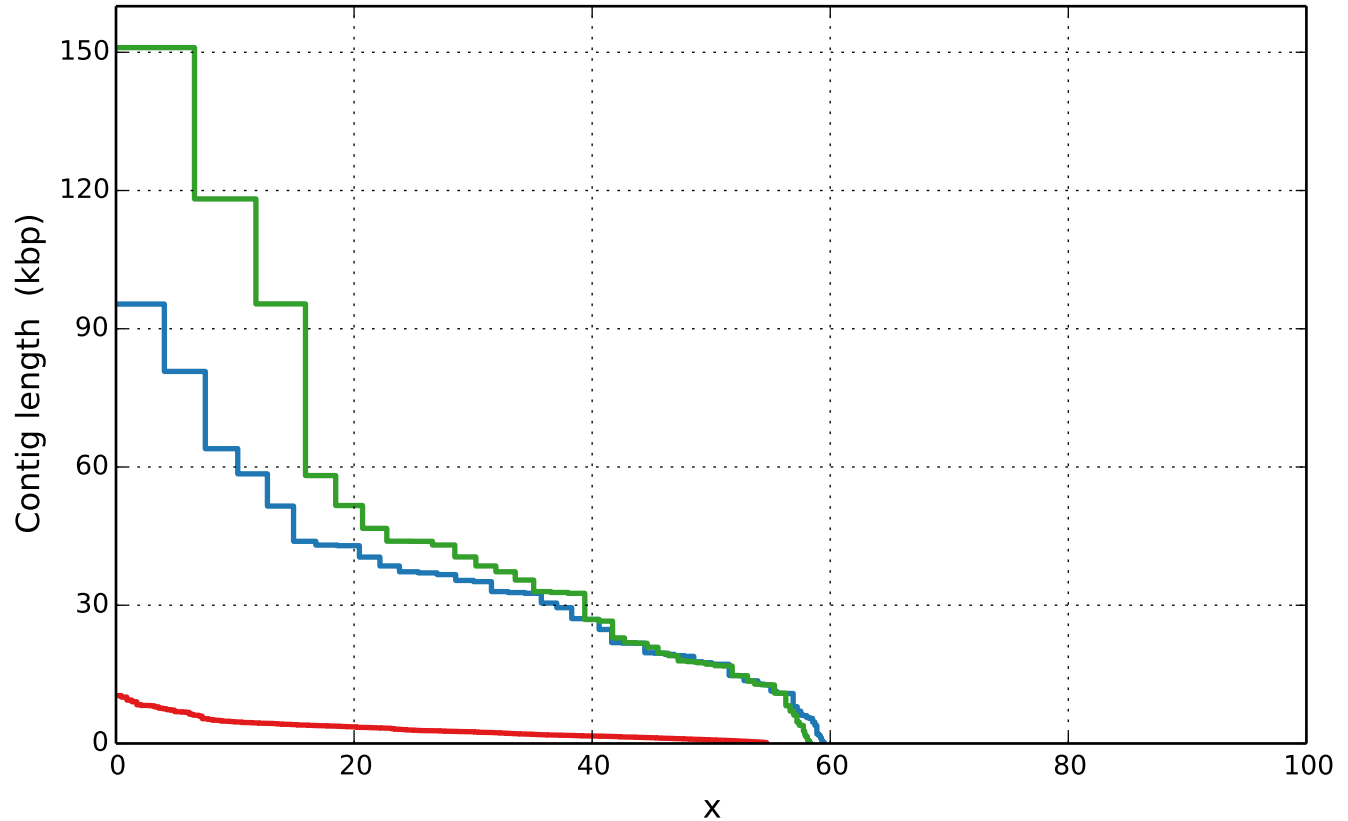


Cumulative length (aligned contigs)



— VelvetAssembly — SpadesAssembly - - Reference
— AbyssAssembly

NAx

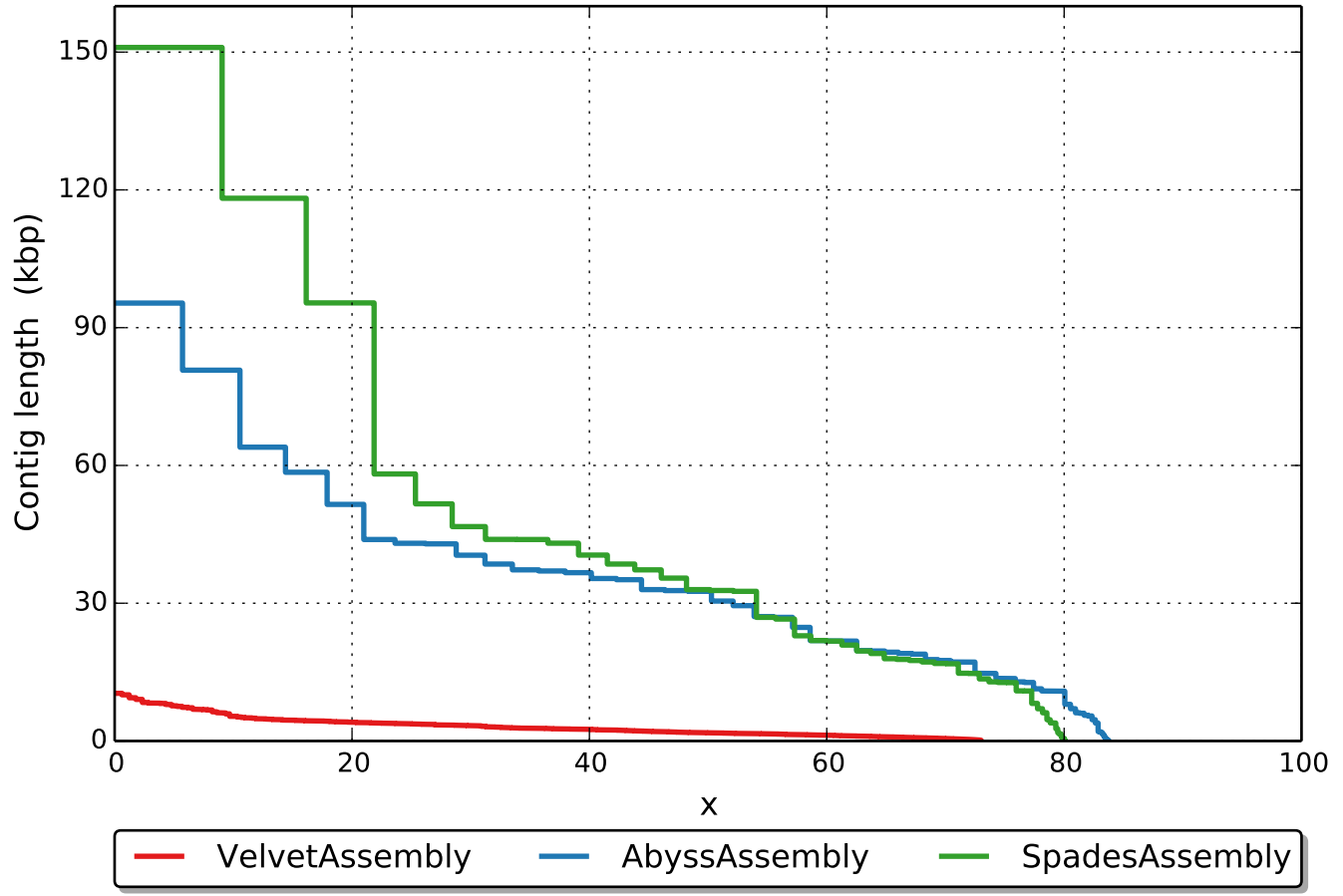


— VelvetAssembly

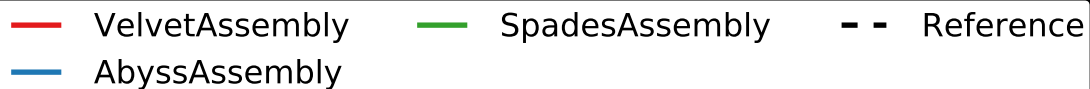
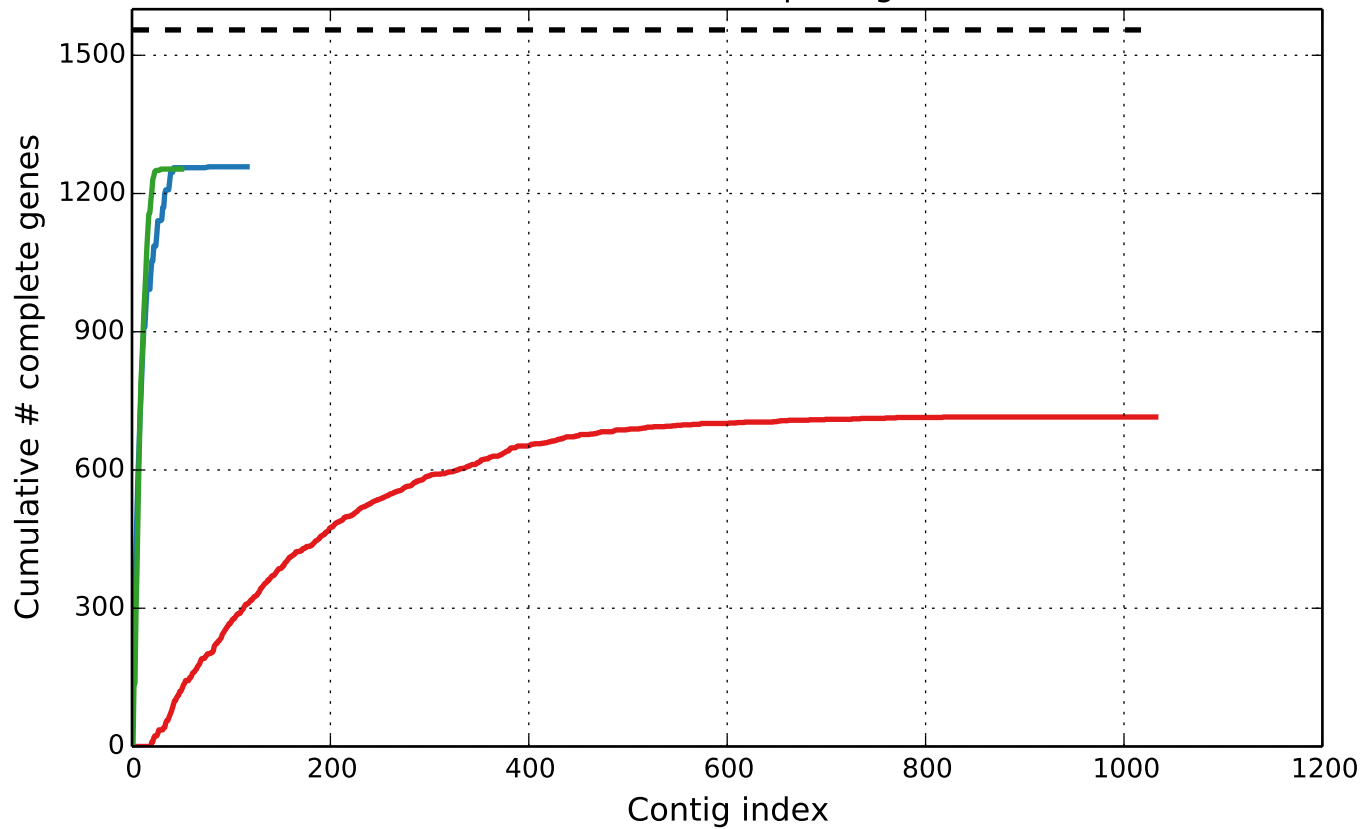
— AbyssAssembly

— SpadesAssembly

NGAx



Cumulative # complete genes



complete genes

