

Report

	GAGE-B	abyss_134	abyss_136
# contigs (≥ 0 bp)	338	1115	1115
# contigs (≥ 1000 bp)	121	247	247
Total length (≥ 0 bp)	4115424	3980506	3980506
Total length (≥ 1000 bp)	4065299	3855718	3855718
# contigs	153	306	306
Largest contig	280277	145939	145939
Total length	4086478	3895189	3895189
Reference length	4033464	4033464	4033464
GC (%)	47.57	47.52	47.52
Reference GC (%)	47.49	47.49	47.49
N50	94508	25689	25689
NG50	94508	25448	25448
N75	58395	15919	15919
NG75	59821	14801	14801
L50	13	44	44
LG50	13	47	47
L75	27	93	93
LG75	26	100	100
# misassemblies	5	2	2
# misassembled contigs	5	2	2
Misassembled contigs length	376802	9653	9653
# local misassemblies	17	0	0
# unaligned contigs	1 + 0 part	1 + 0 part	1 + 0 part
Unaligned length	602	602	602
Genome fraction (%)	97.712	96.495	96.495
Duplication ratio	1.037	1.001	1.001
# N's per 100 kbp	100.94	0.00	0.00
# mismatches per 100 kbp	5.28	3.03	3.03
# indels per 100 kbp	4.92	2.60	2.60
# genes	3498 + 59 part	3322 + 133 part	3322 + 133 part
Largest alignment	246076	145939	145939
NA50	92996	25689	25689
NGA50	92996	25448	25448
NA75	58395	15919	15919
NGA75	59658	14801	14801
LA50	14	44	44
LGA50	14	47	47
LA75	28	93	93
LGA75	27	100	100

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

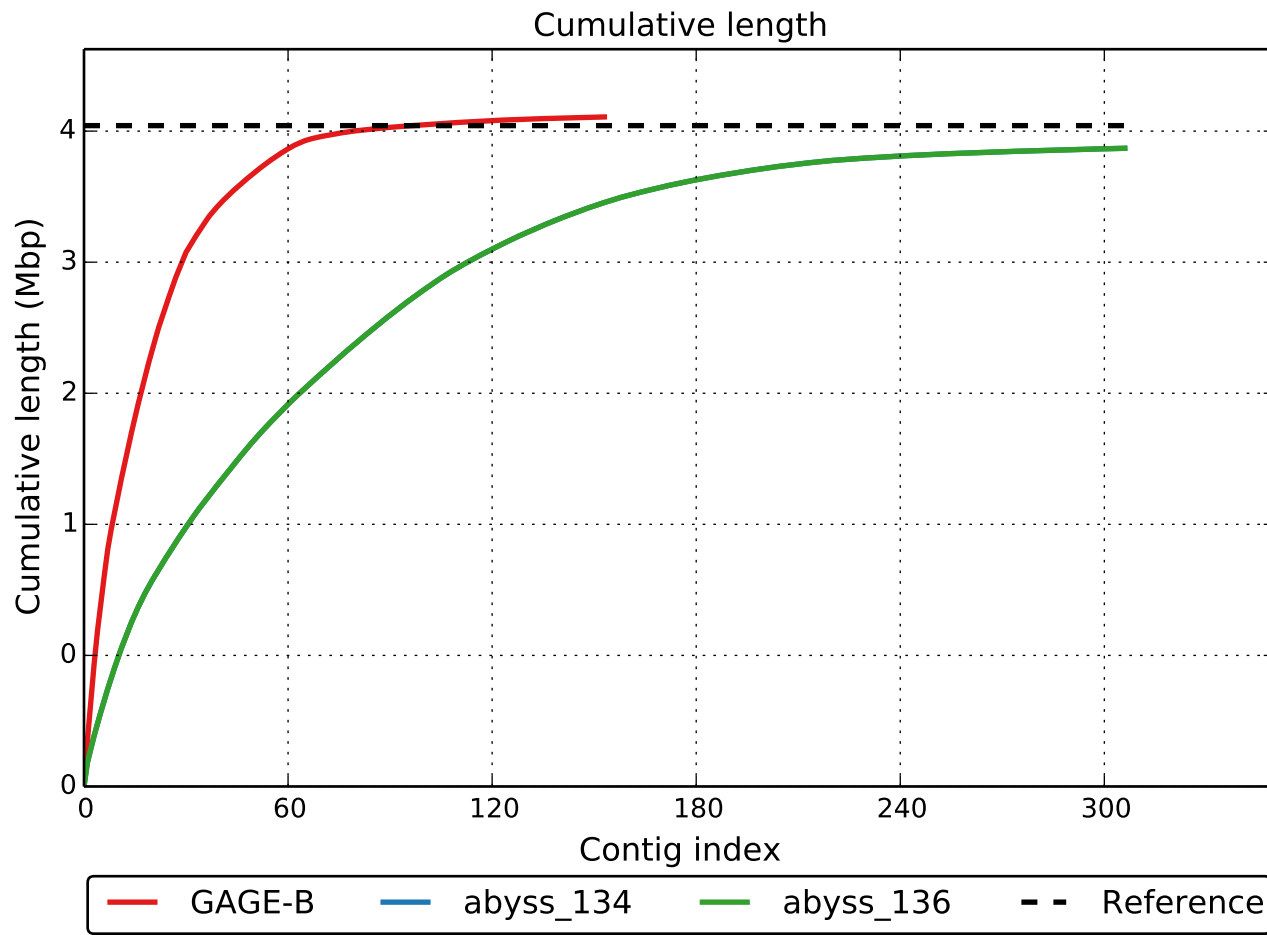
	GAGE-B	abyss_134	abyss_136
# misassemblies	5	2	2
# relocations	4	2	2
# translocations	1	0	0
# inversions	0	0	0
# misassembled contigs	5	2	2
Misassembled contigs length	376802	9653	9653
# local misassemblies	17	0	0
# mismatches	208	118	118
# indels	194	101	101
# short indels	155	99	99
# long indels	39	2	2
Indels length	703	119	119

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).

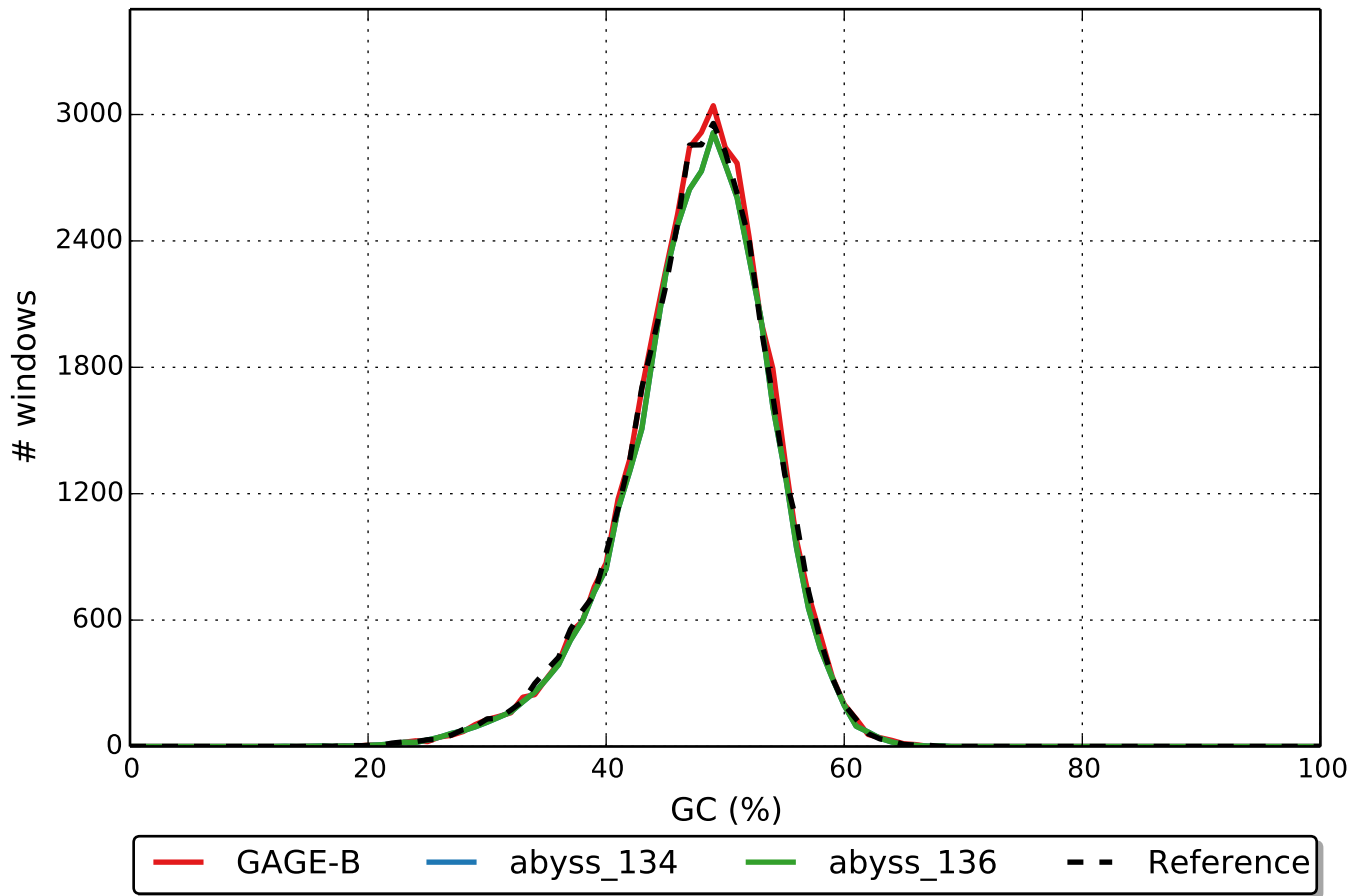
Unaligned report

	GAGE-B	abyss_134	abyss_136
# fully unaligned contigs	1	1	1
Fully unaligned length	602	602	602
# partially unaligned contigs	0	0	0
# with misassembly	0	0	0
# both parts are significant	0	0	0
Partially unaligned length	0	0	0
# N's	4125	0	0

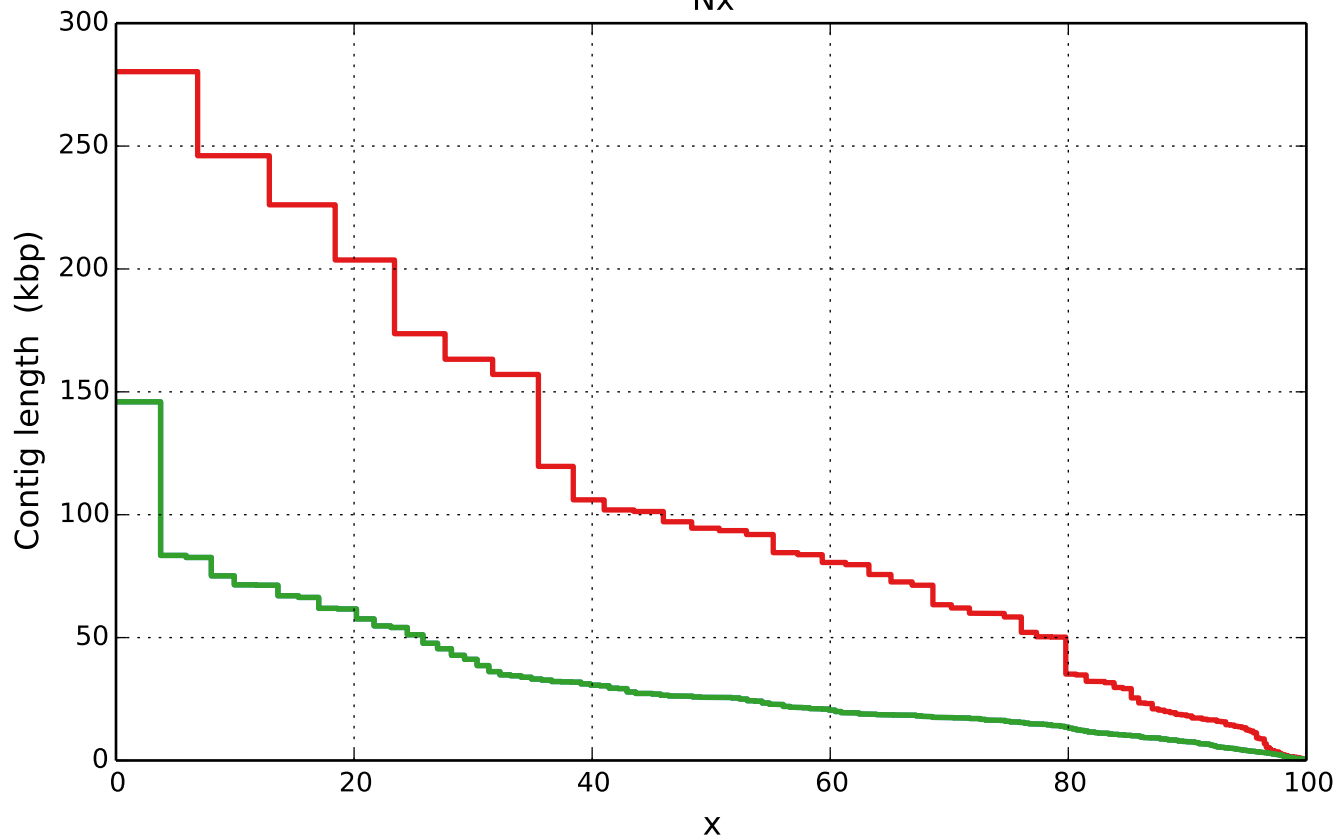
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



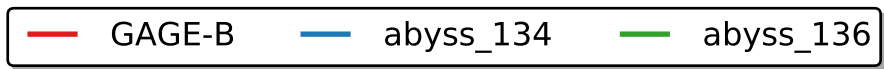
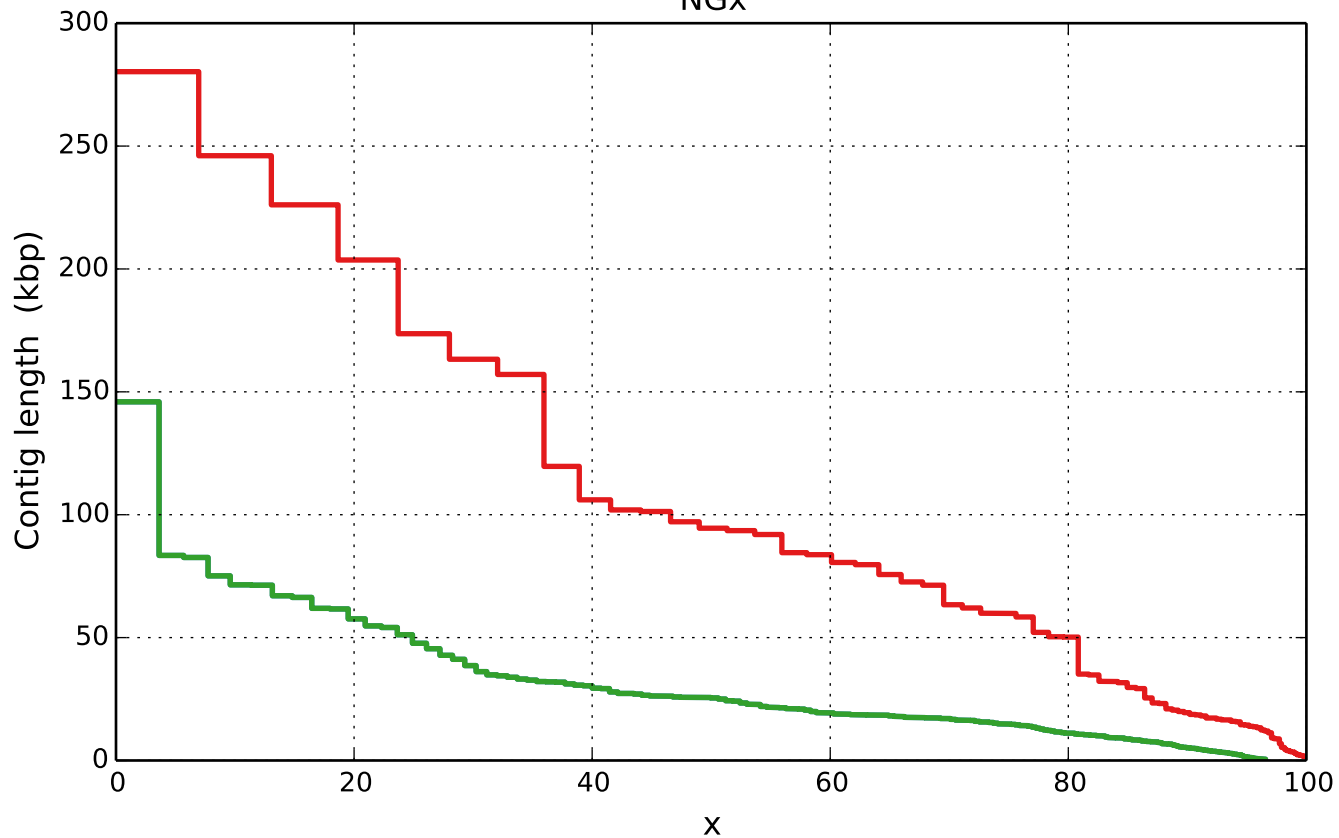
GC content

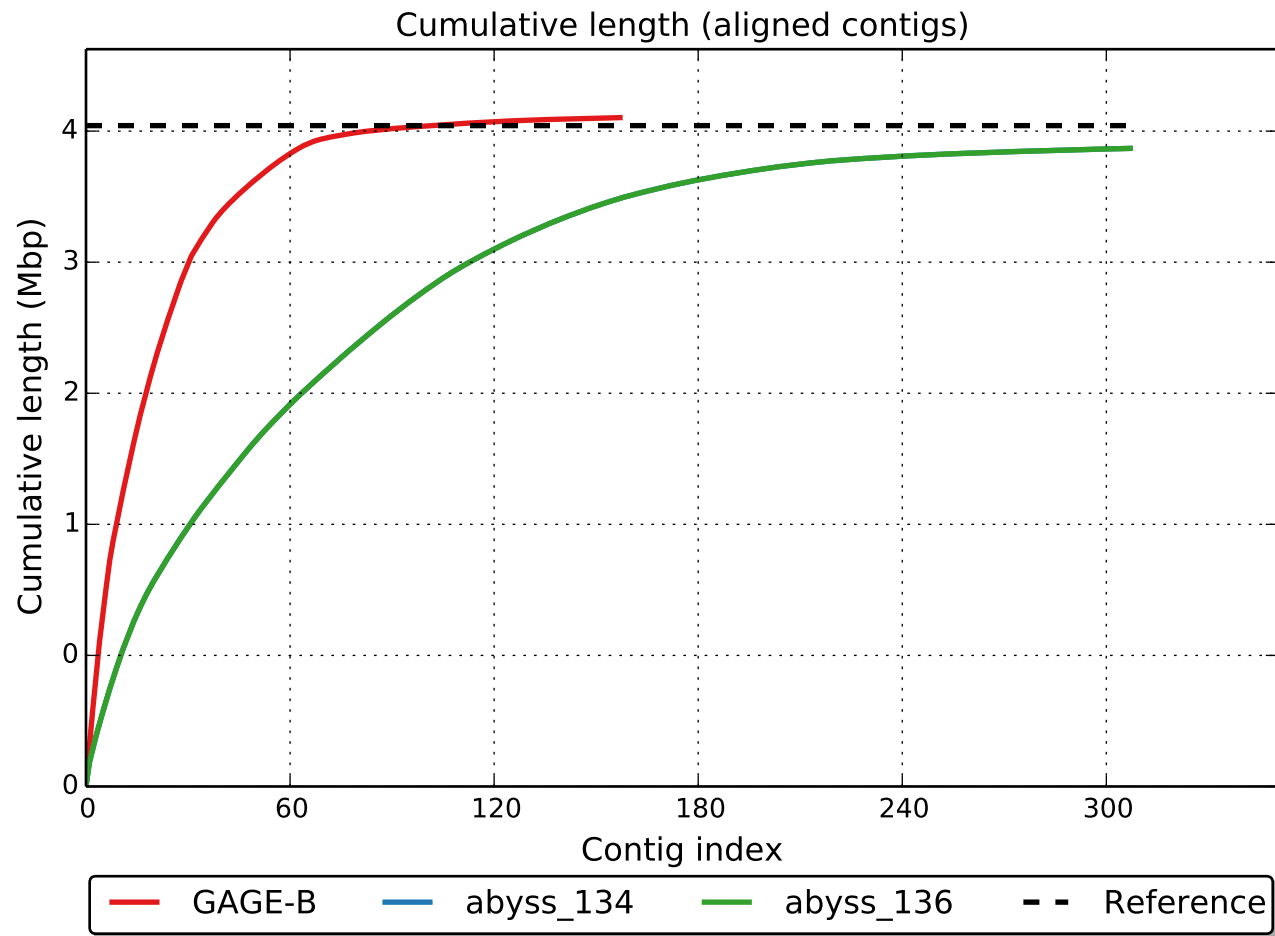


Nx

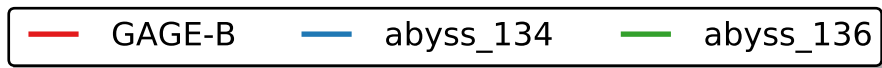
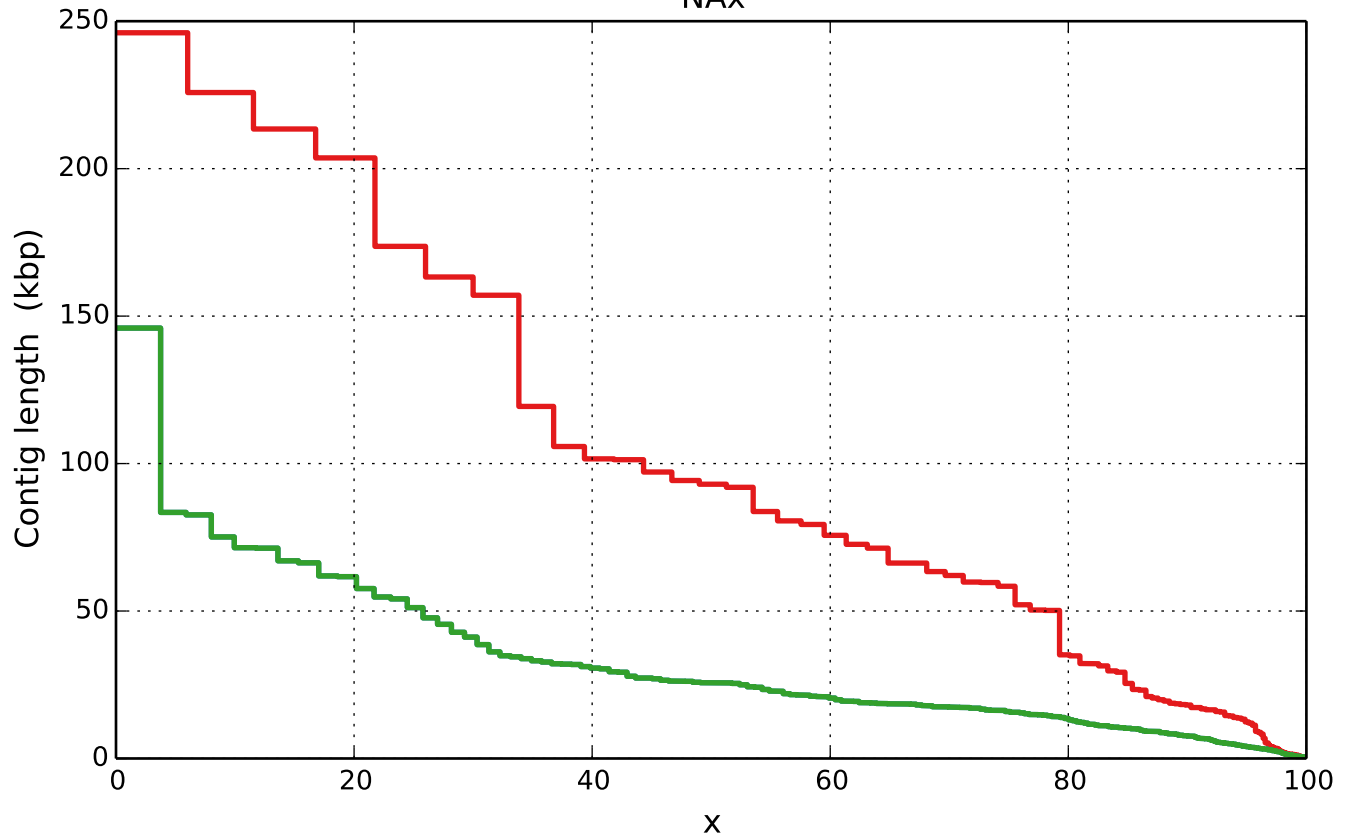


NGx

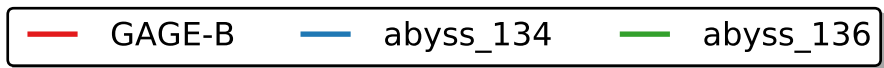
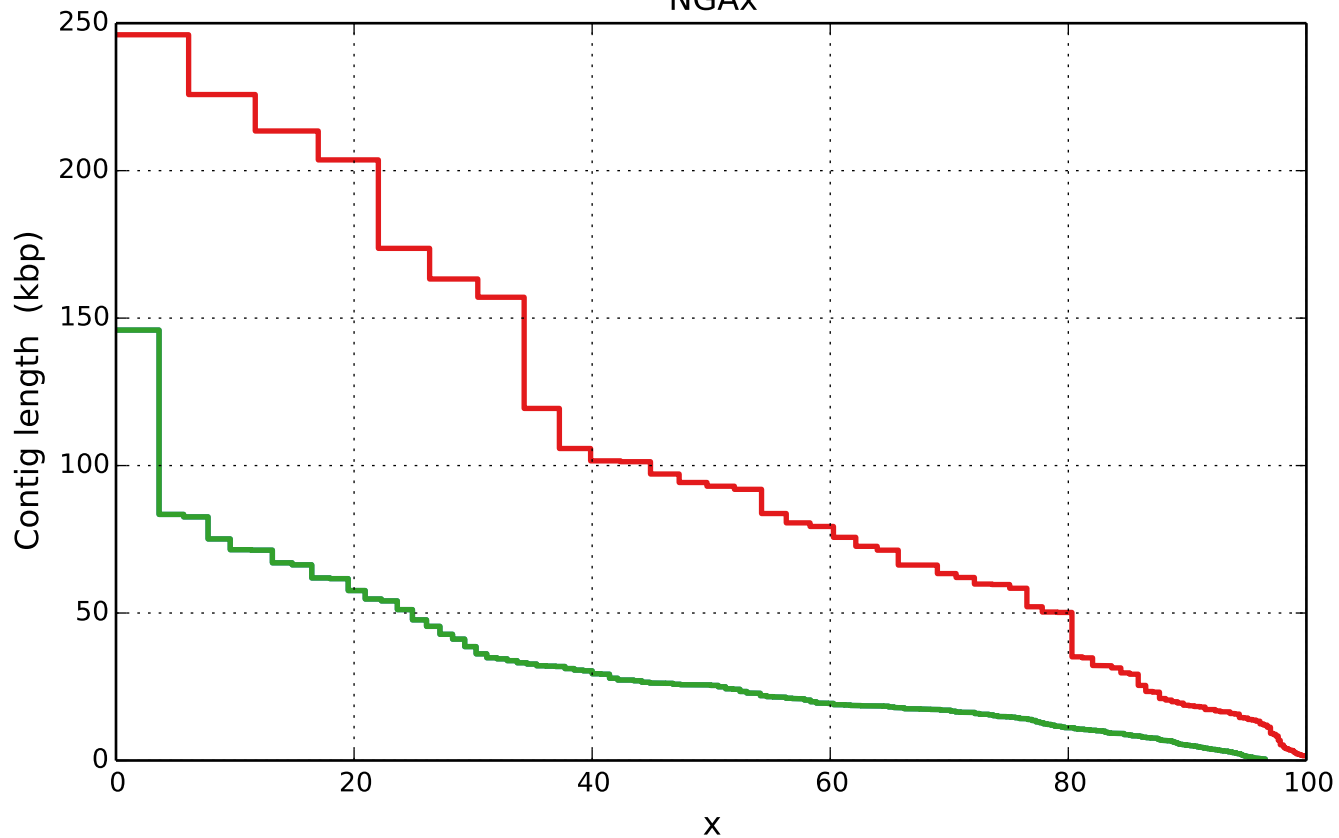




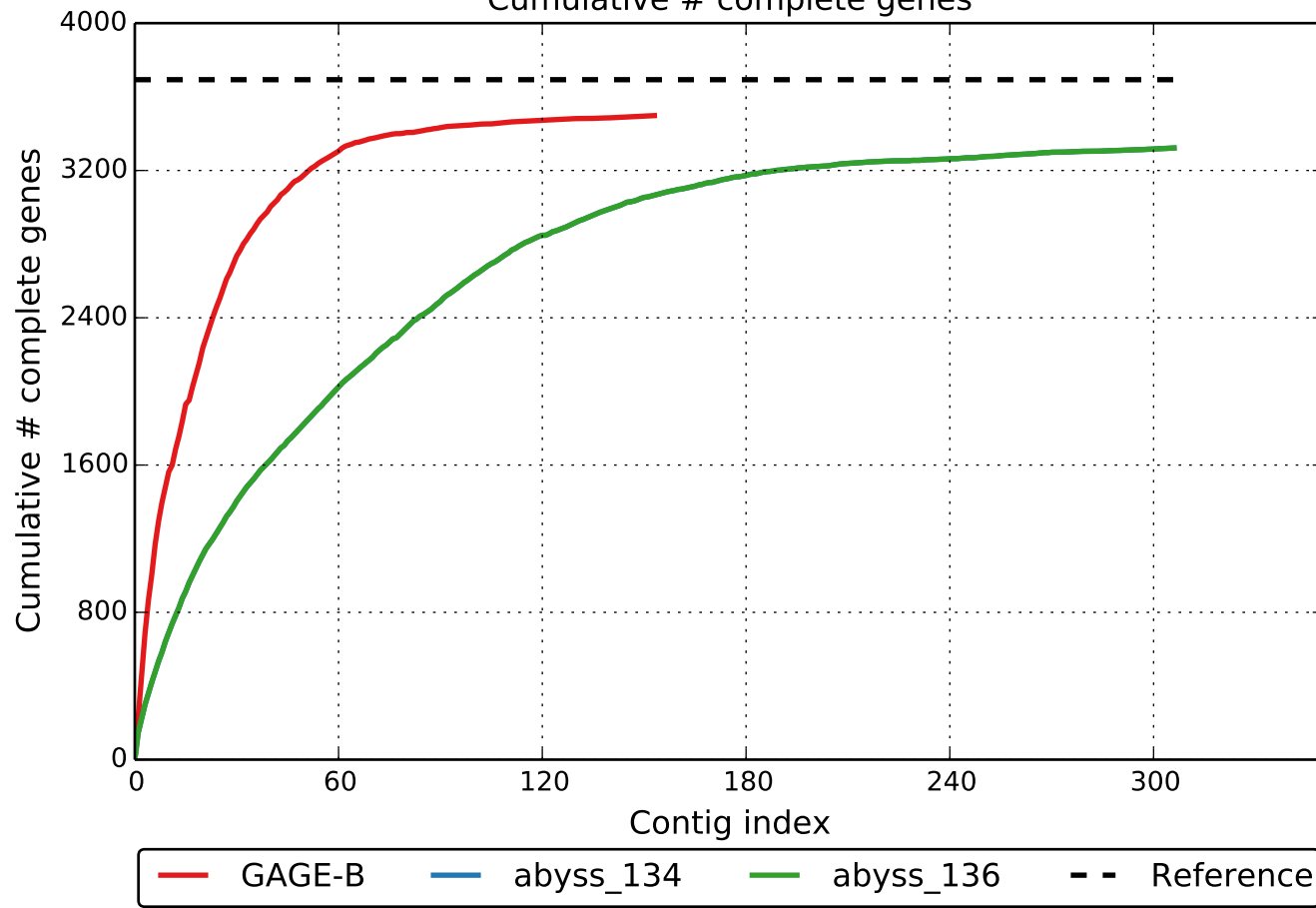
NAx



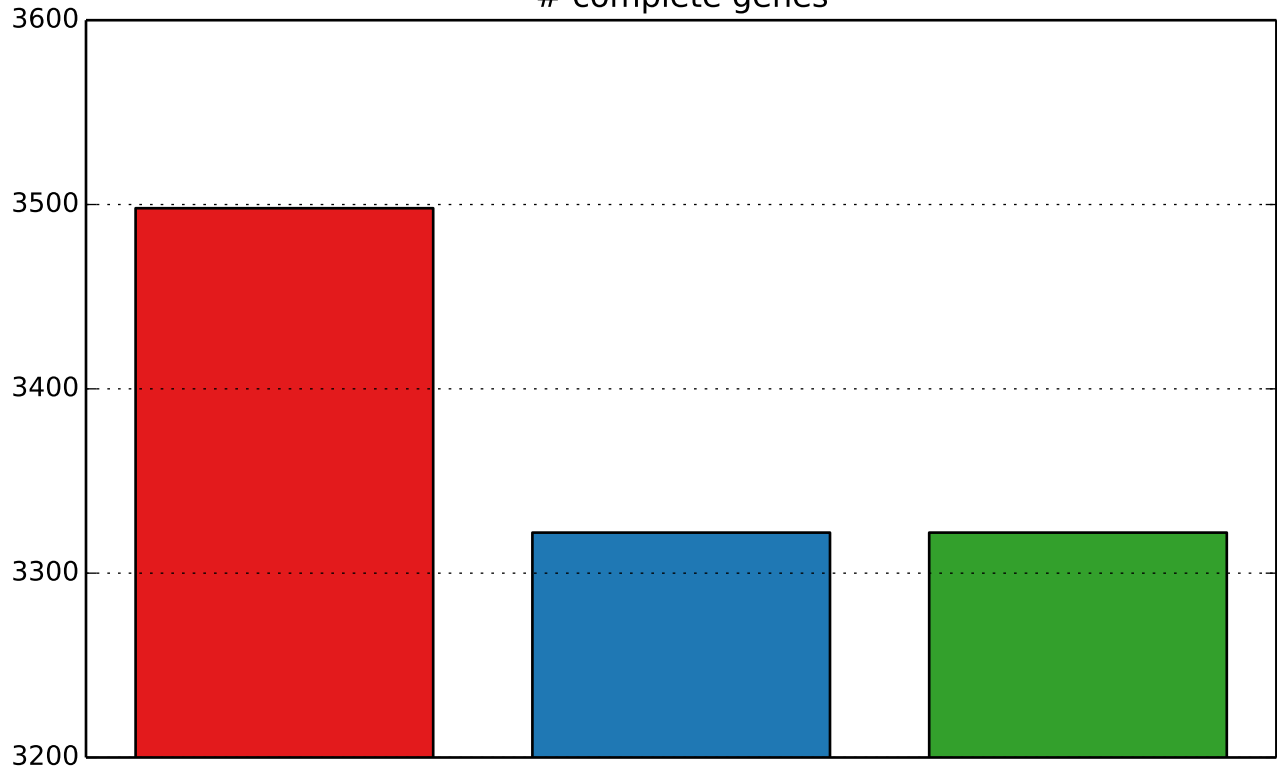
NGAx



Cumulative # complete genes



complete genes



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