

Report

	SOAPdenovo_2_results
# contigs (>= 0 bp)	1261822
# contigs (>= 1000 bp)	1372
# contigs (>= 5000 bp)	144
# contigs (>= 10000 bp)	13
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	96446830
Total length (>= 1000 bp)	3747854
Total length (>= 5000 bp)	1008262
Total length (>= 10000 bp)	155852
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	175148
Largest contig	16770
Total length	34265641
Reference length	4678760
GC (%)	43.84
Reference GC (%)	43.26
N50	194
NG50	2643
N75	153
NG75	1260
L50	55061
LG50	520
L75	105045
LG75	1161
# misassemblies	5
# misassembled contigs	5
Misassembled contigs length	21832
# local misassemblies	17
# unaligned mis. contigs	0
# unaligned contigs	171221 + 0 part
Unaligned length	29717303
Genome fraction (%)	94.347
Duplication ratio	1.030
# N's per 100 kbp	0.00
# mismatches per 100 kbp	24.22
# indels per 100 kbp	2.22
Largest alignment	16770
Total aligned length	4536846
NGA50	2642
NGA75	1246
LGA50	521
LGA75	1168

All statistics are based on contigs of size >= 100 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

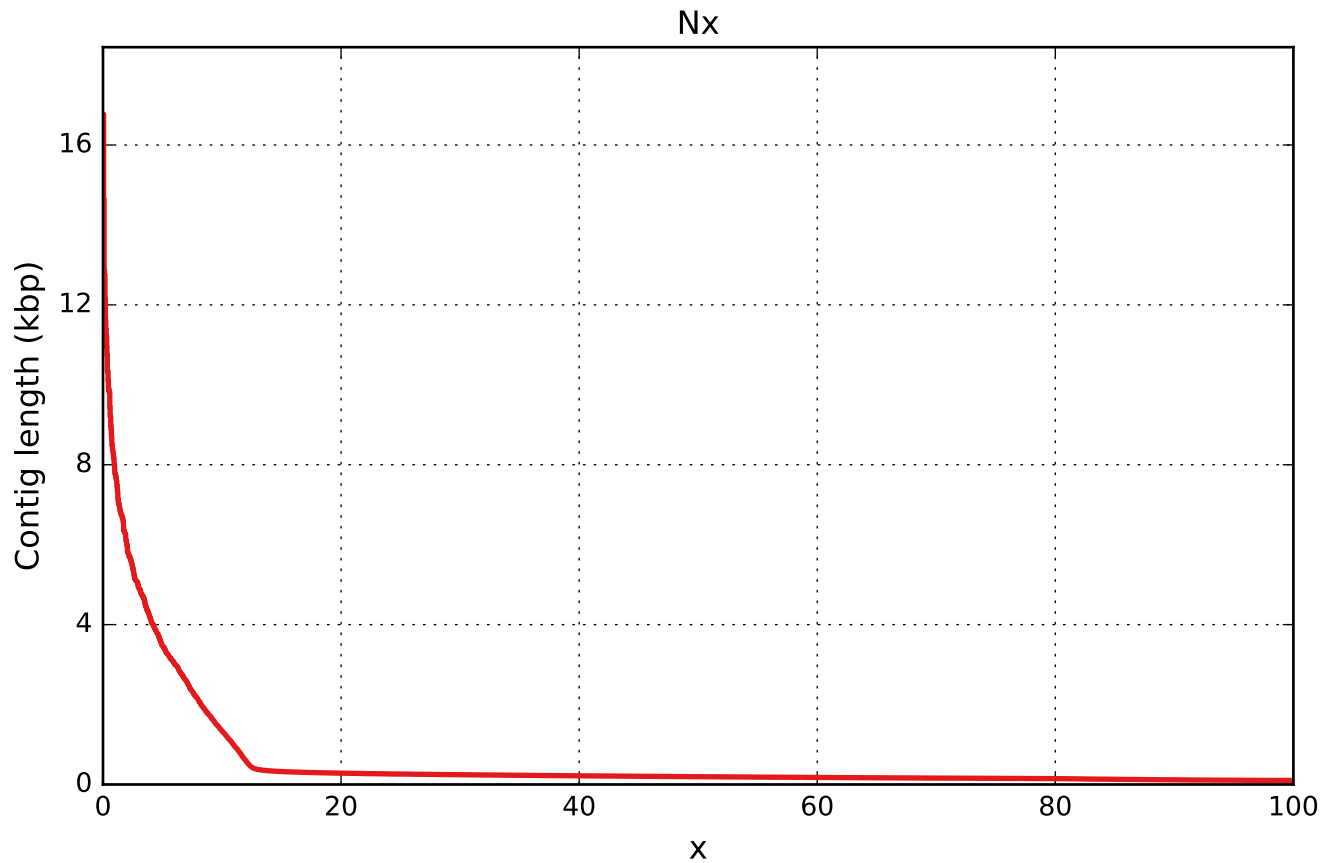
	SOAPdenovo_2_results
# misassemblies	5
# relocations	5
# translocations	0
# inversions	0
# misassembled contigs	5
Misassembled contigs length	21832
# local misassemblies	17
# unaligned mis. contigs	0
# mismatches	1069
# indels	98
# indels (≤ 5 bp)	82
# indels (> 5 bp)	16
Indels length	579

All statistics are based on contigs of size ≥ 100 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

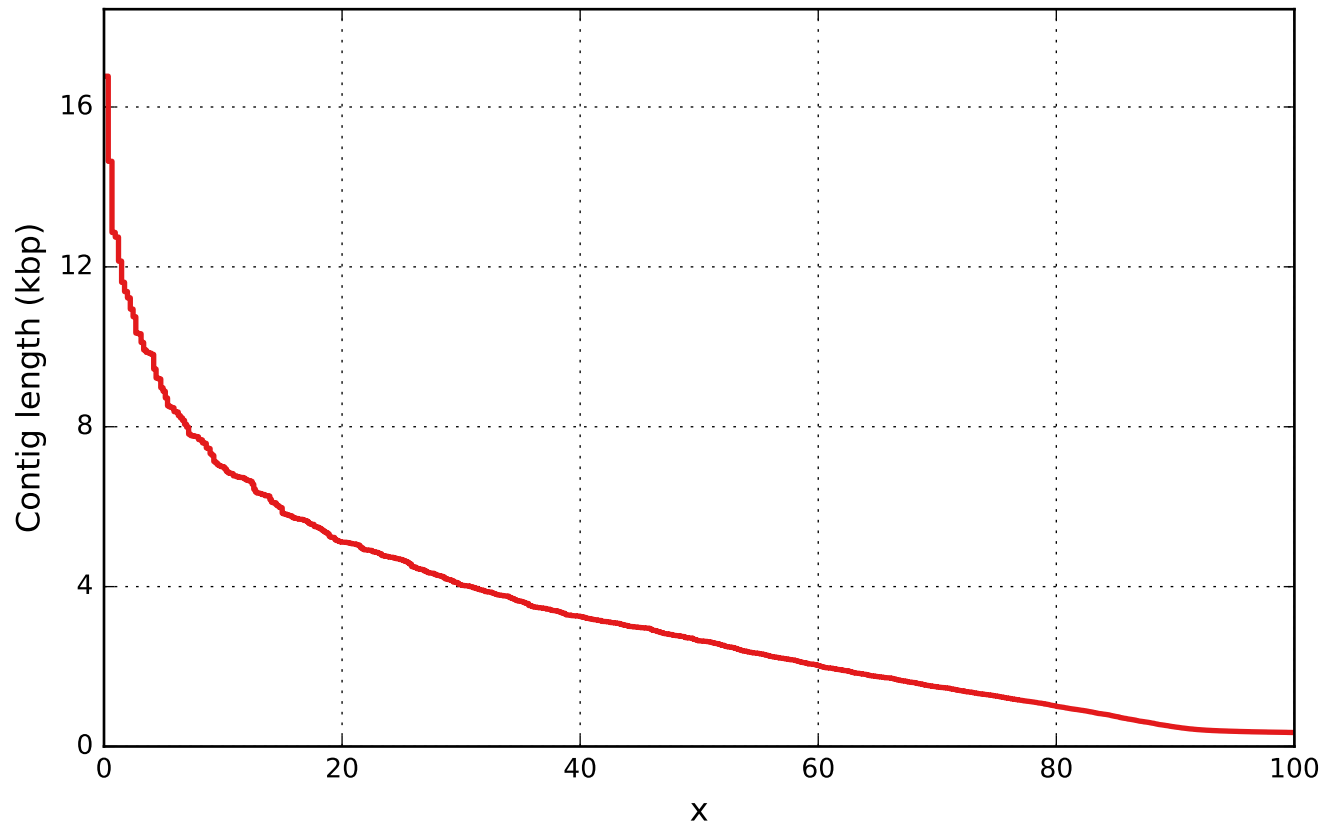
	SOAPdenovo_2_results
# fully unaligned contigs	171221
Fully unaligned length	29717303
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

All statistics are based on contigs of size ≥ 100 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

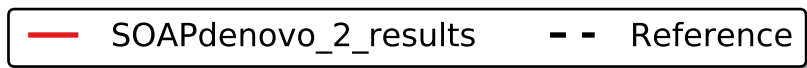
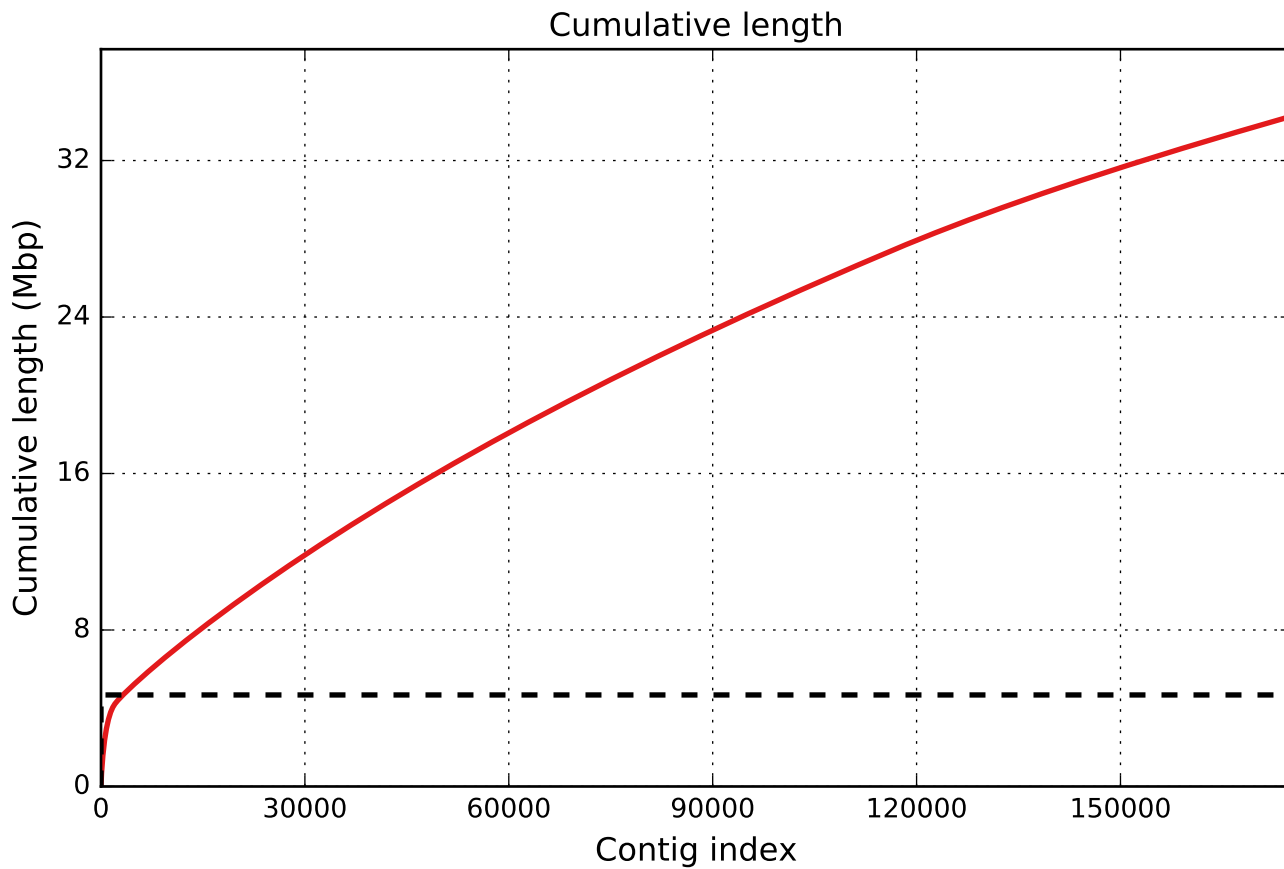


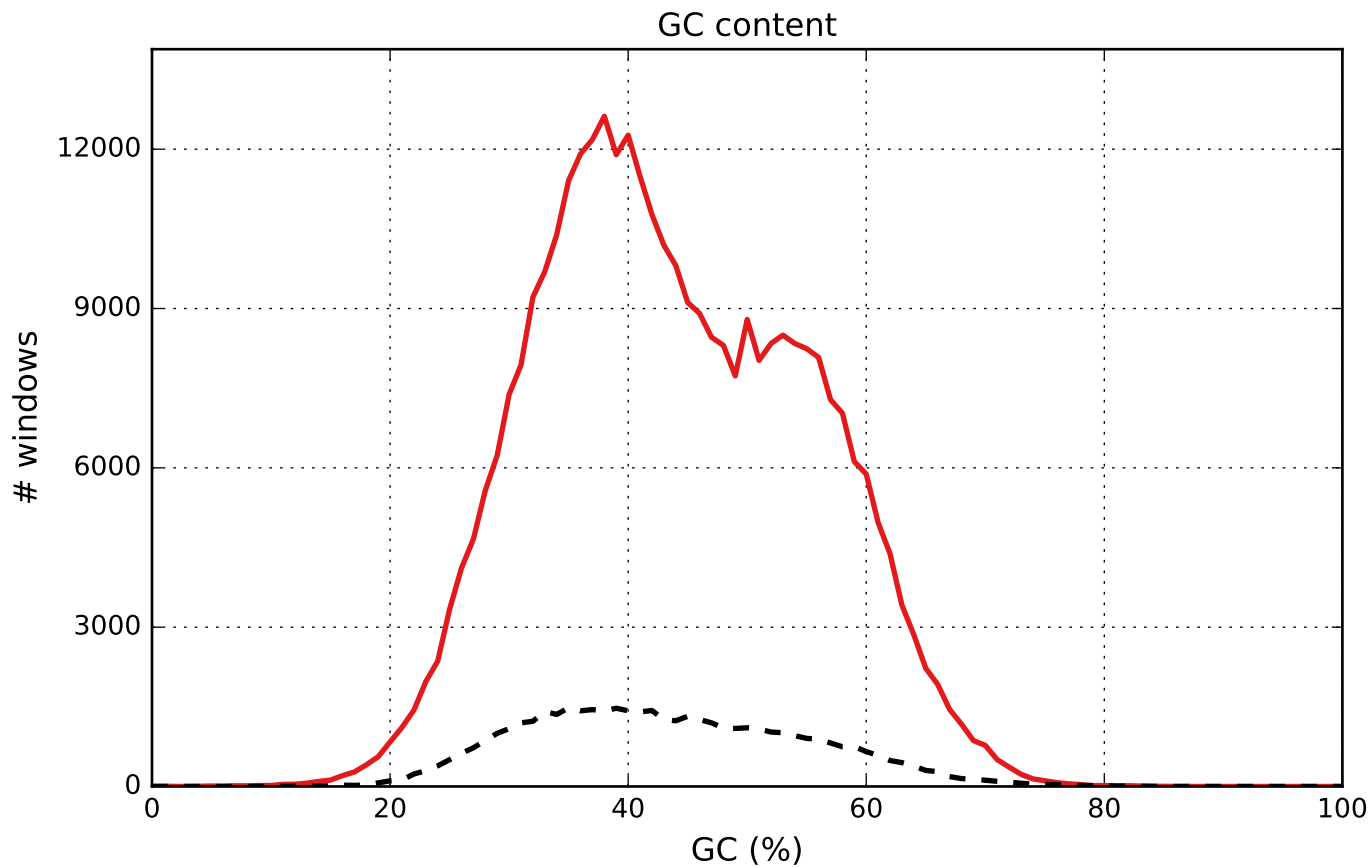
— SOAPdenovo_2_results

NGx



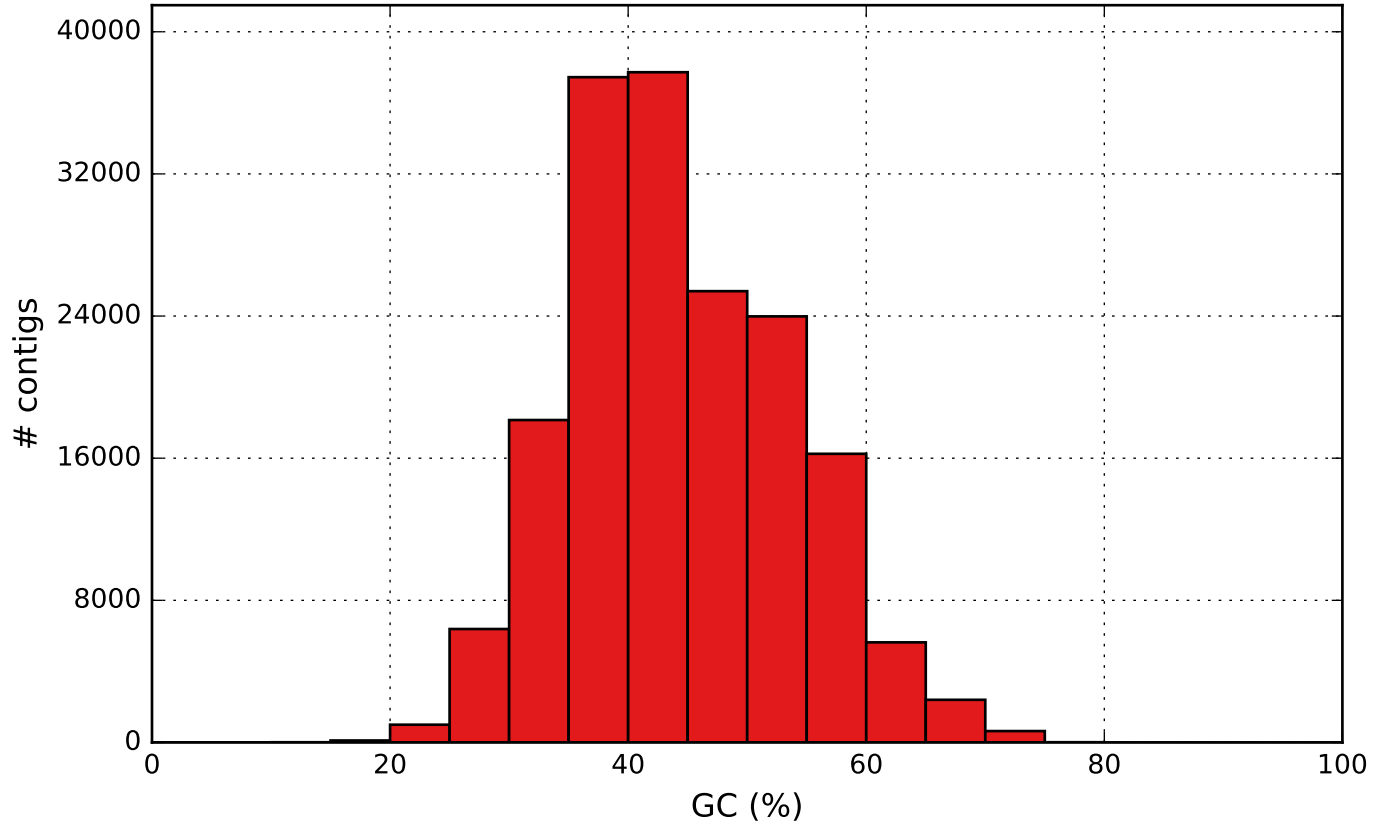
— SOAPdenovo_2_results



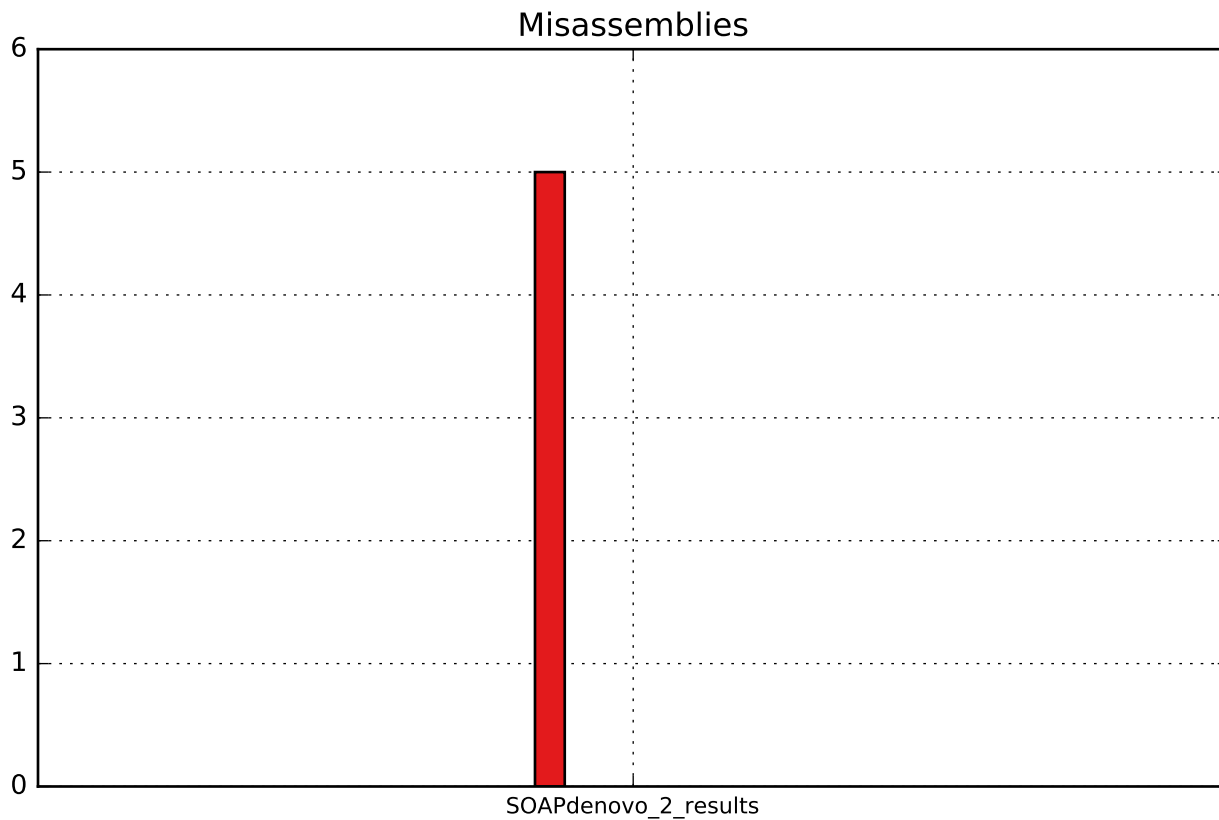


— SOAPdenovo_2_results - - Reference

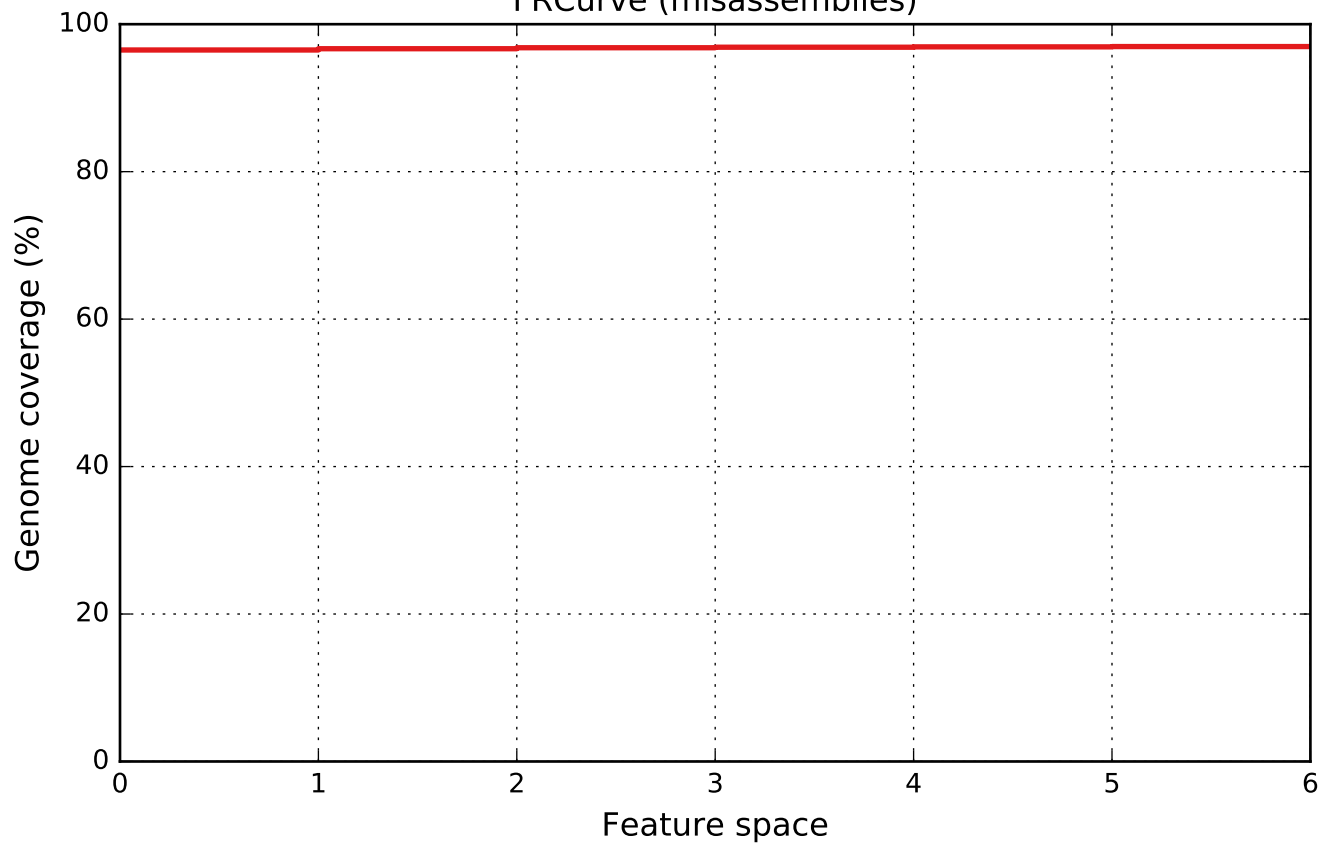
SOAPdenovo_2_results GC content



SOAPdenovo_2_results

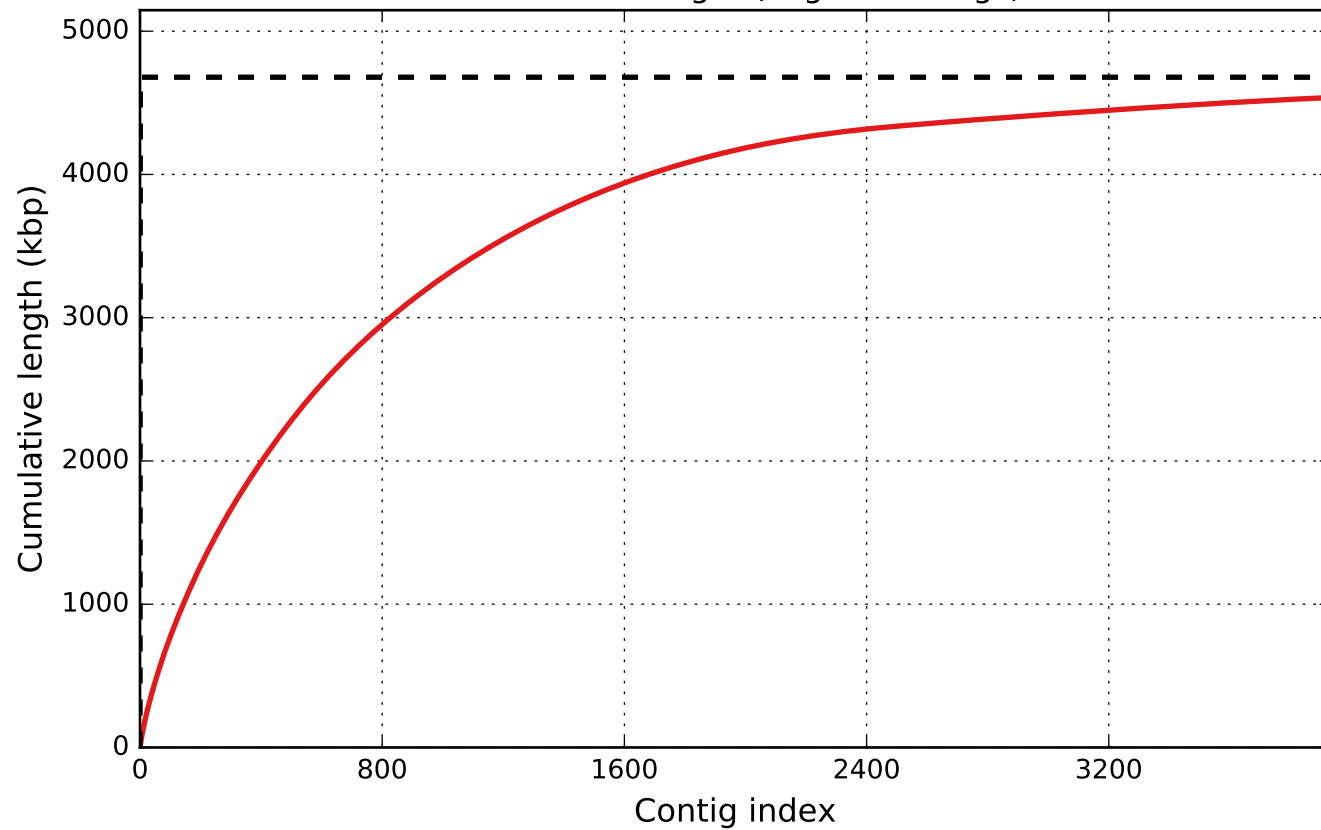


FRCurve (misassemblies)



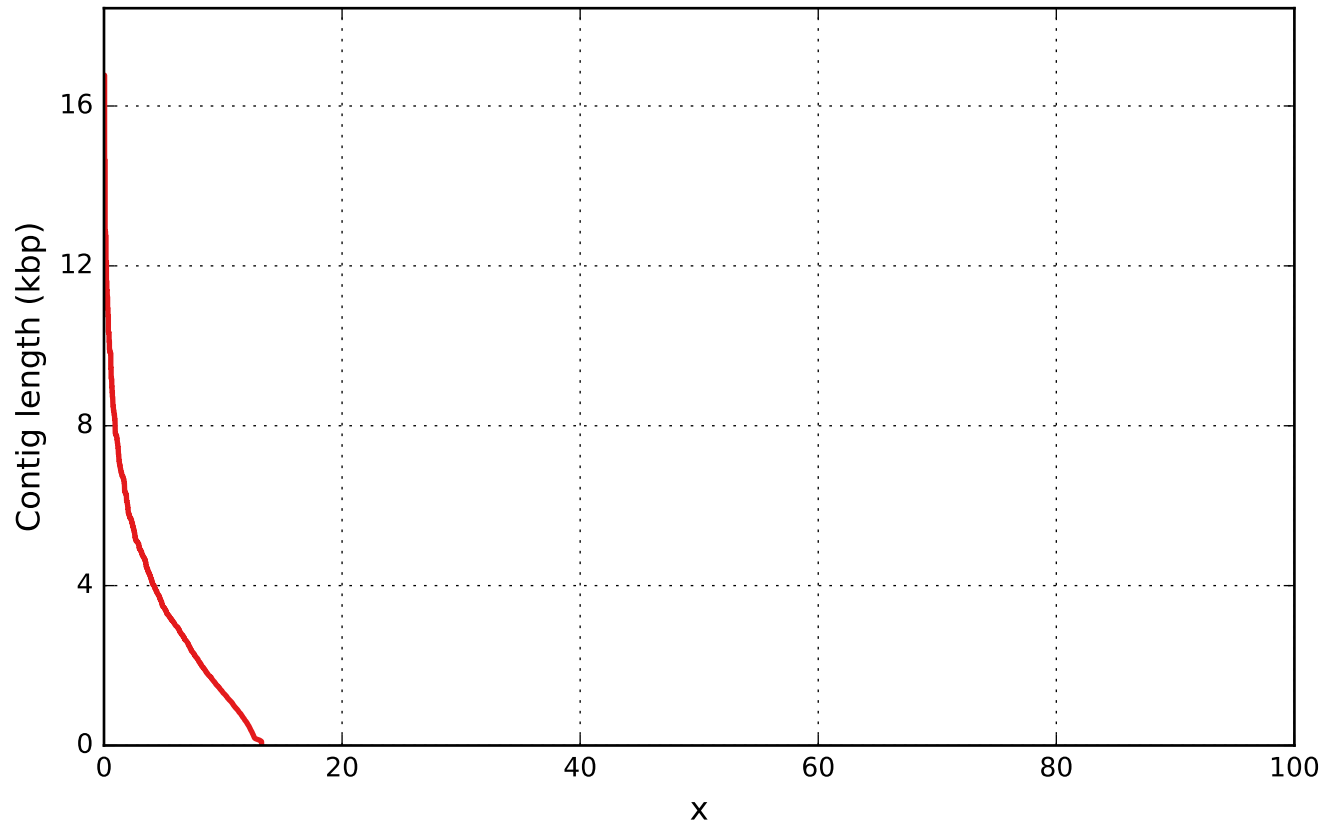
— SOAPdenovo_2_results

Cumulative length (aligned contigs)



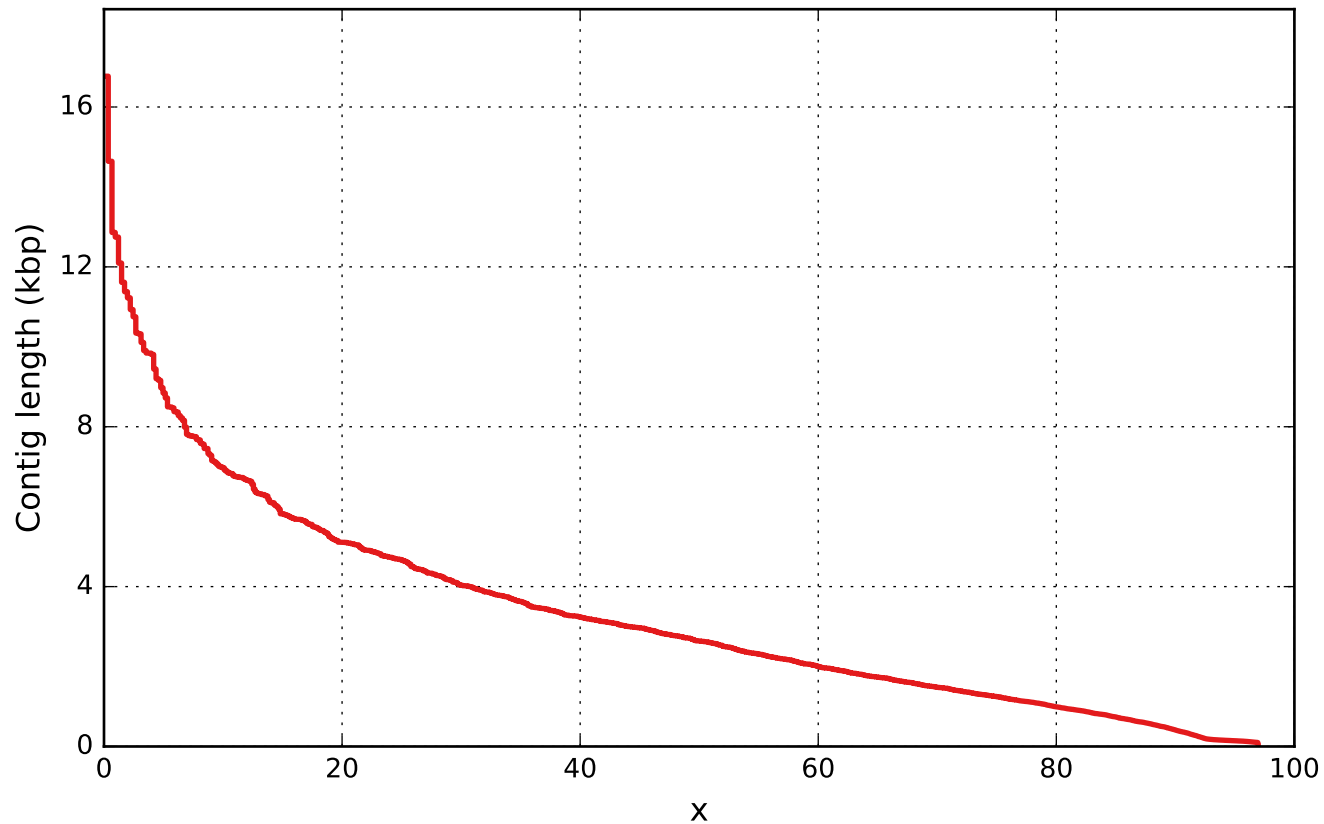
— SOAPdenovo_2_results - - Reference

NAx



— SOAPdenovo_2_results

NGAx



— SOAPdenovo_2_results