

Report	
	no_error_reads_hiseq_5k_olc
# contigs (>= 0 bp)	214
# contigs (>= 1000 bp)	17
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	113943
Total length (>= 1000 bp)	46500
Total length (>= 5000 bp)	8700
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	93
Largest contig	8700
Total length	85212
Reference length	30119
GC (%)	41.28
Reference GC (%)	41.24
N50	1234
NG50	4528
N90	355
NG90	3063
auN	2467.8
auNG	6981.9
L50	14
LG50	3
L90	68
LG90	6
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	45 + 0 part
Unaligned length	16898
Genome fraction (%)	97.812
Duplication ratio	2.319
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	8700
Total aligned length	68314
NA50	1234
NGA50	4528
NA90	-
NGA90	3063
auNA	2391.4
auNGA	6765.7
LA50	14
LGA50	3
LA90	-
LGA90	6

All statistics are based on contigs of size >= 300 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	no_error_reads_hiseq_5k_olc
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	0
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

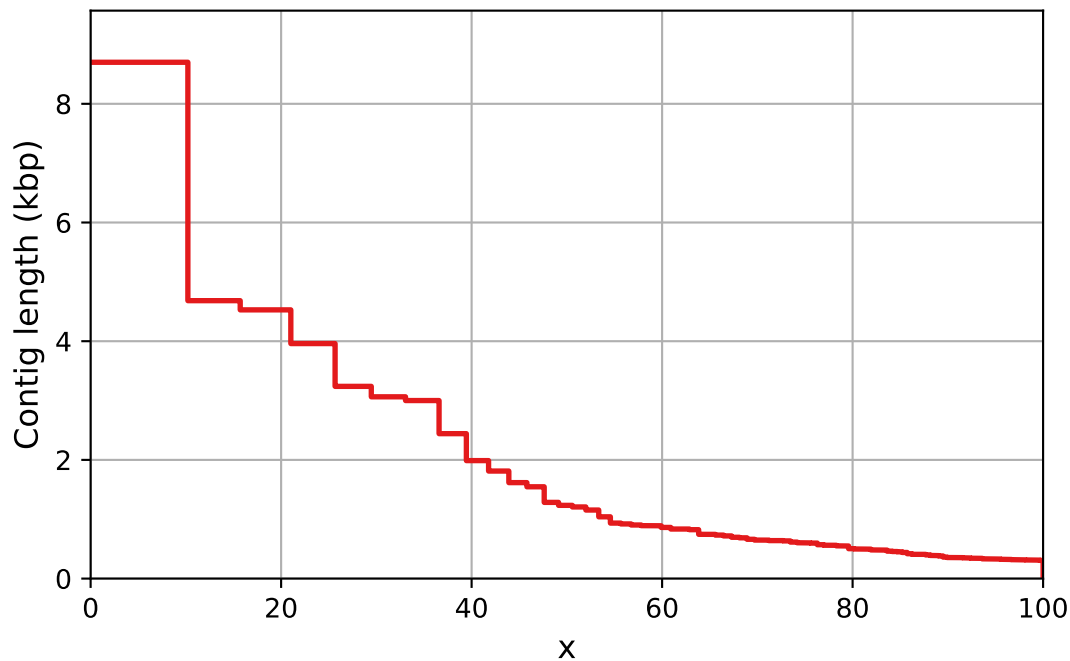
All statistics are based on contigs of size ≥ 300 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	no_error_reads_hiseq_5k_olc
# fully unaligned contigs	45
Fully unaligned length	16898
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

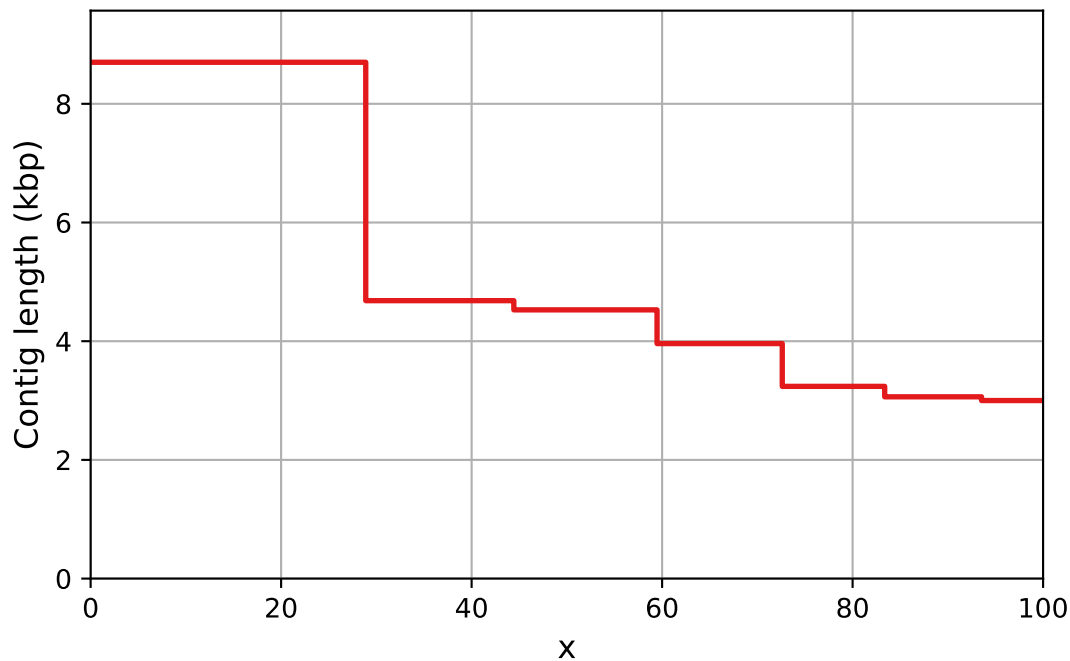
All statistics are based on contigs of size ≥ 300 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



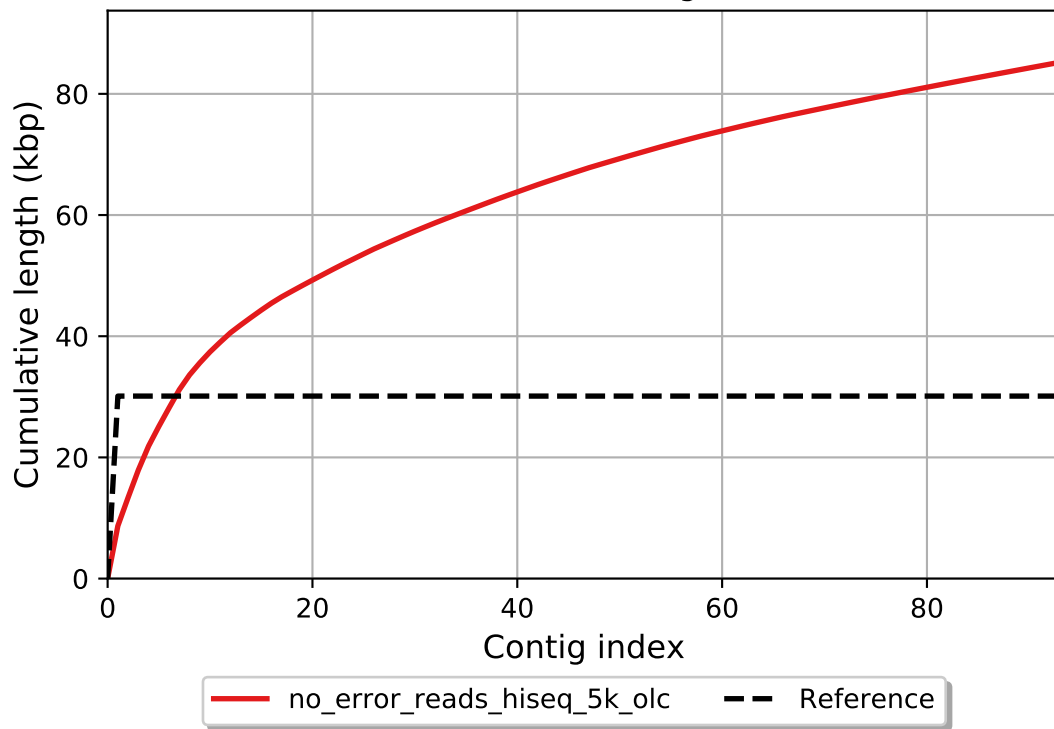
no_error_reads_hiseq_5k_olc

NGx

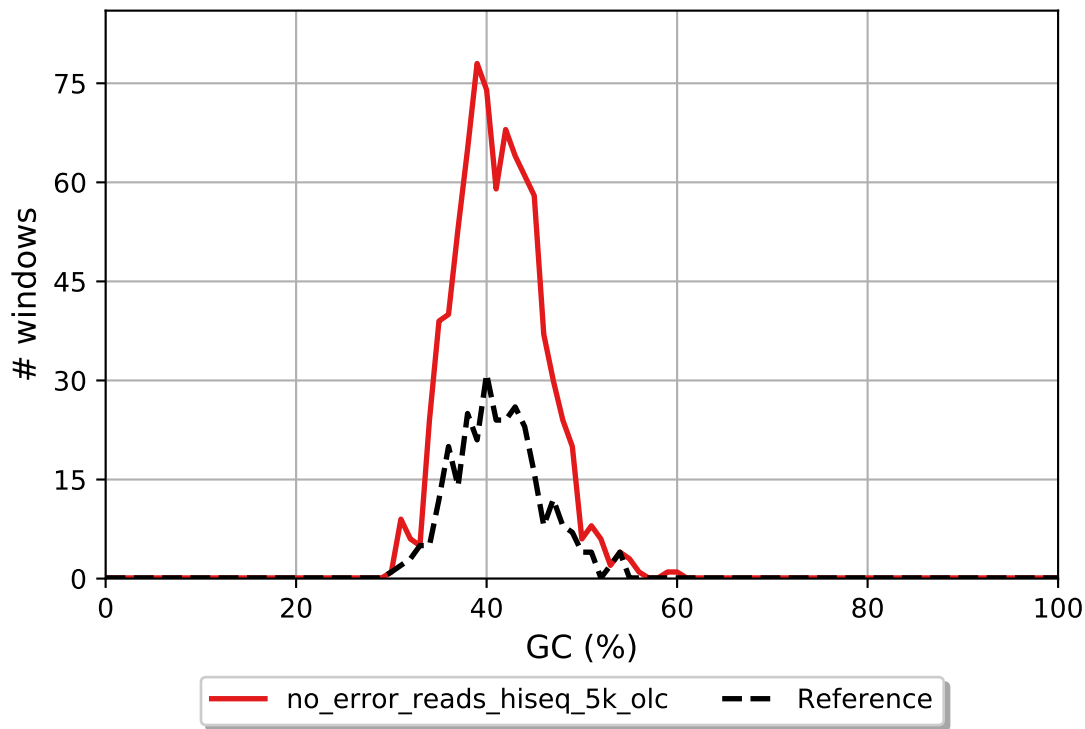


no_error_reads_hiseq_5k_olc

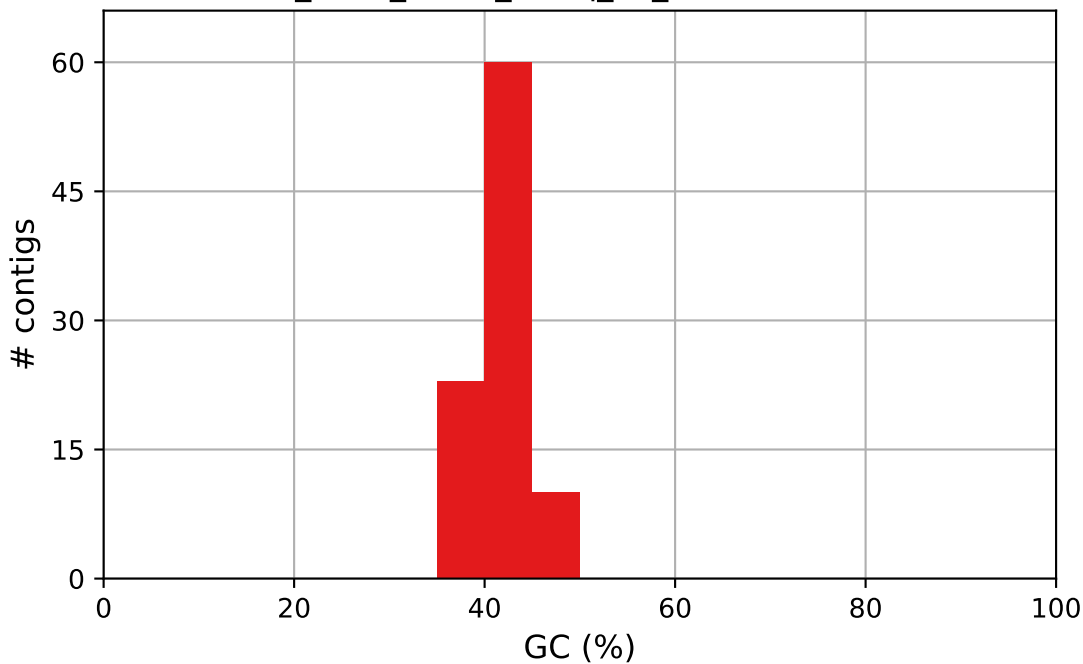
Cumulative length



GC content



no_error_reads_hiseq_5k_olc GC content

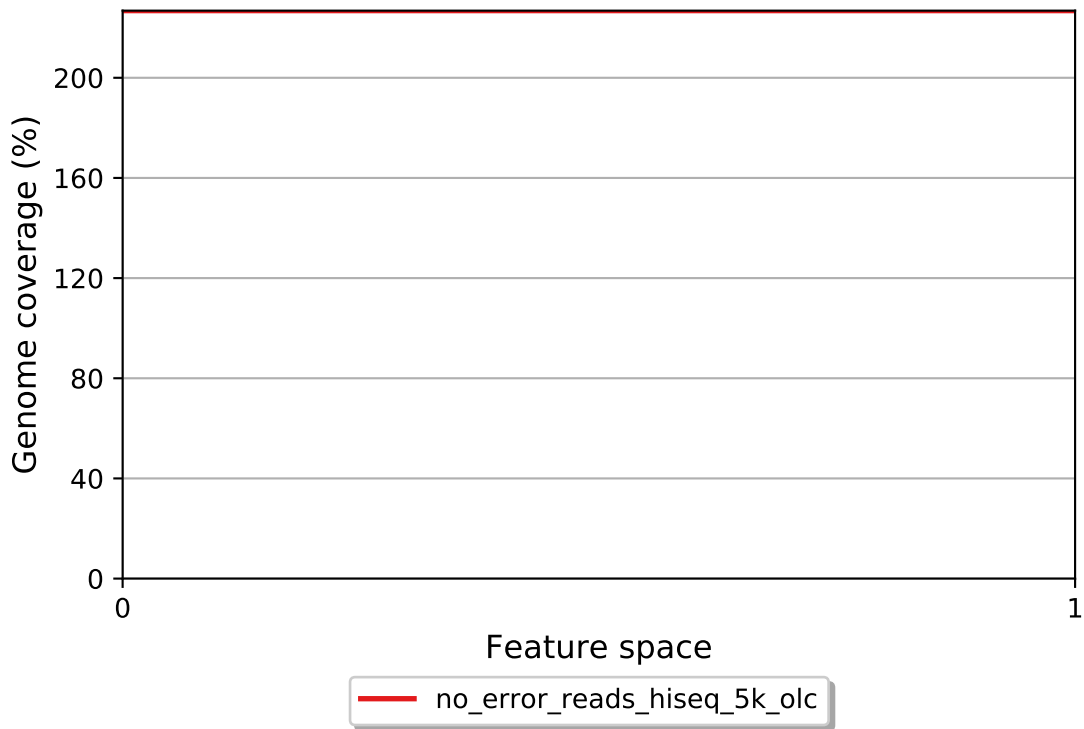


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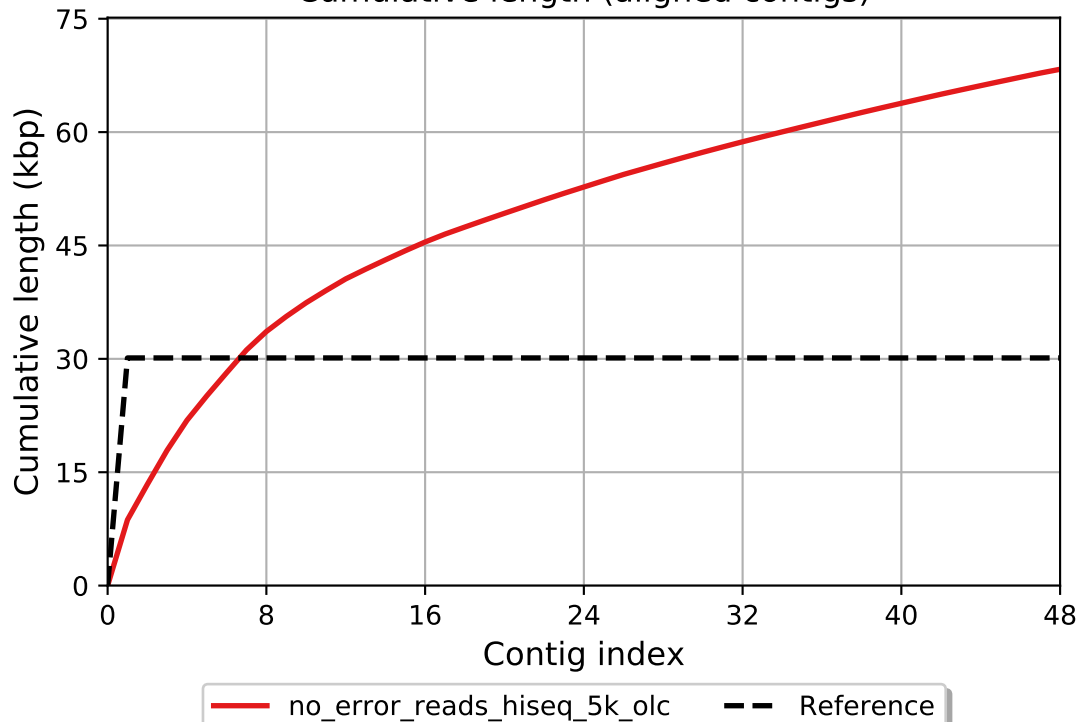
Misassemblies



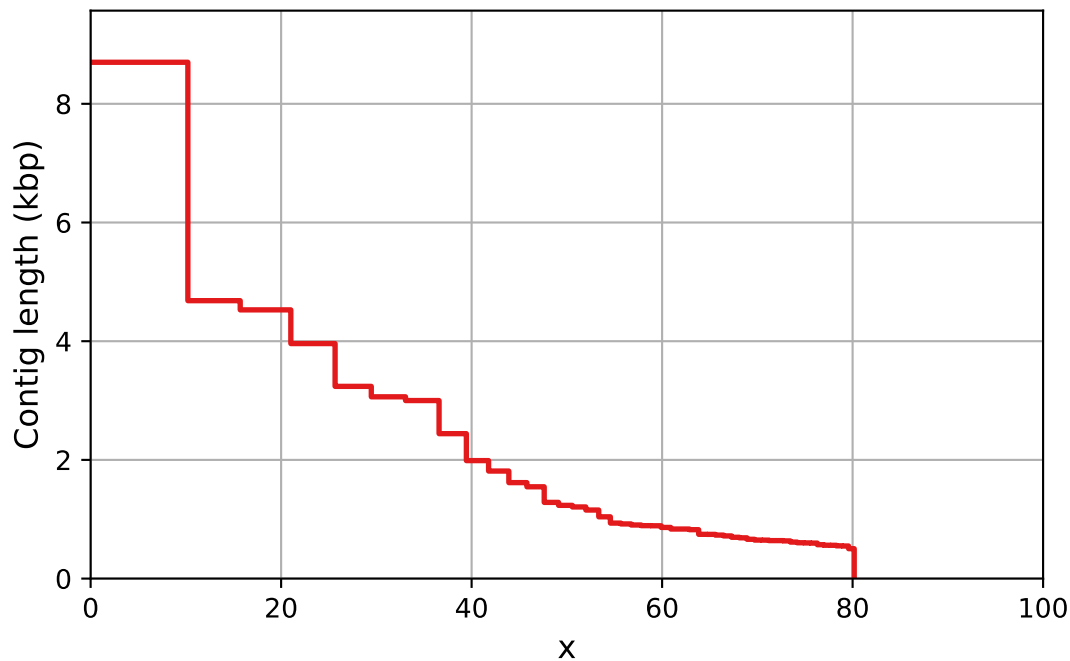
FRCurve (misassemblies)



Cumulative length (aligned contigs)

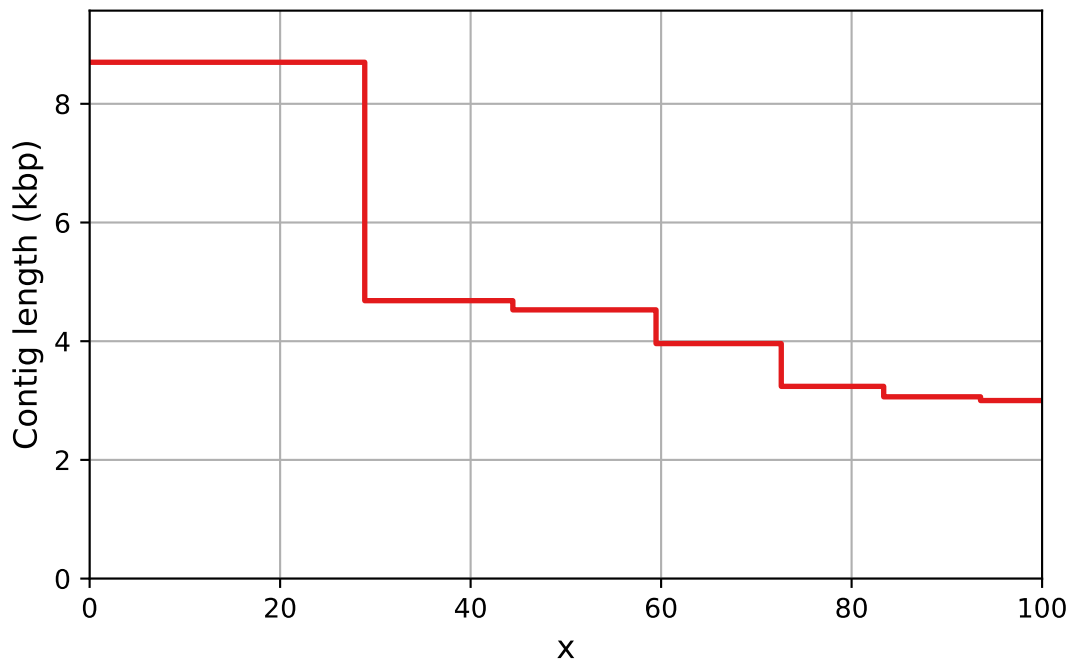


NAx



no_error_reads_hiseq_5k_olc

NGAx



— no_error_reads_hiseq_5k_olc