

	Report					
	sortie_medium	sortie_sequencage1	sortie_Hard	sortie_sequencage1_in	reads_sequencage1_in	reads_contaminant_in
# contigs (>= 0 bp)	6	586	2	1	736	7380
# contigs (>= 1000 bp)	2	1	2	1	0	0
# contigs (>= 5000 bp)	1	1	1	1	0	0
# contigs (>= 10000 bp)	0	1	0	1	0	0
# contigs (>= 25000 bp)	0	1	0	1	0	0
# contigs (>= 50000 bp)	0	0	0	0	0	0
Total length (>= 0 bp)	11310	62259	8034	45123	220800	2214000
Total length (>= 1000 bp)	11172	45261	8034	45123	0	0
Total length (>= 5000 bp)	7416	45261	5307	45123	0	0
Total length (>= 10000 bp)	0	45261	0	45123	0	0
Total length (>= 25000 bp)	0	45261	0	45123	0	0
Total length (>= 50000 bp)	0	0	0	0	0	0
# contigs	6	586	2	1	736	7380
Largest contig	7416	45261	5307	45123	300	300
Total length	11310	62259	8034	45123	220800	2214000
Reference length	48576	48576	48576	48576	48576	48576
GC (%)	38.01	50.53	39.38	49.54	51.22	49.64
Reference GC (%)	49.87	49.87	49.87	49.87	49.87	49.87
N50	7416	45261	5307	45123	300	300
NG50	-	45261	-	45123	300	300
N75	3756	39	2727	45123	300	300
NG75	-	45261	-	45123	300	300
L50	1	1	1	1	368	3690
LG50	-	1	-	1	81	81
L75	2	38	2	1	552	5535
LG75	-	1	-	1	122	122
# misassemblies	-	0	-	0	0	0
# misassembled contigs	-	0	-	0	0	0
Misassembled contigs length	-	0	-	0	0	0
# local misassemblies	-	0	-	0	0	0
# scaffold gap ext. mis.	-	0	-	0	0	0
# scaffold gap loc. mis.	-	0	-	0	0	0
# unaligned mis. contigs	-	1	-	0	0	0
# unaligned contigs	6 + 0 part	585 + 1 part	2 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part
Unaligned length	11310	41105	8034	0	0	0
Genome fraction (%)	-	43.505	-	92.850	84.196	99.212
Duplication ratio	-	1.001	-	1.000	5.399	45.940
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	-	331.24	-	0.00	8738.60	41744.65
# indels per 100 kbp	-	0.00	-	2.22	0.00	0.00
Largest alignment	-	429	-	45123	300	300
Total aligned length	-	21154	-	45123	220437	2210561
NA50	-	-	-	45123	300	300
NGA50	-	-	-	45123	300	300
NA75	-	-	-	45123	300	300
NGA75	-	-	-	45123	300	300
LA50	-	-	-	1	368	3690
LGA50	-	-	-	1	81	81
LA75	-	-	-	1	552	5535
LGA75	-	-	-	1	122	122

All statistics are based on contigs of size >= 1 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	sortie_medium	sortie_sequencage1	sortie_Hard	sortie_sequencage1_in	reads_sequencage1_in	reads_contaminant_in
# misassemblies	-	0	-	0	0	0
# contig misassemblies	-	0	-	0	0	0
# c. relocations	-	0	-	0	0	0
# c. translocations	-	0	-	0	0	0
# c. inversions	-	0	-	0	0	0
# scaffold misassemblies	-	0	-	0	0	0
# s. relocations	-	0	-	0	0	0
# s. translocations	-	0	-	0	0	0
# s. inversions	-	0	-	0	0	0
# misassembled contigs	-	0	-	0	0	0
Misassembled contigs length	-	0	-	0	0	0
# local misassemblies	-	0	-	0	0	0
# scaffold gap ext. mis.	-	0	-	0	0	0
# scaffold gap loc. mis.	-	0	-	0	0	0
# unaligned mis. contigs	-	1	-	0	0	0
# mismatches	-	70	-	0	3574	20118
# indels	-	0	-	1	0	0
# indels (<= 5 bp)	-	0	-	0	0	0
# indels (> 5 bp)	-	0	-	1	0	0
Indels length	-	0	-	20	0	0

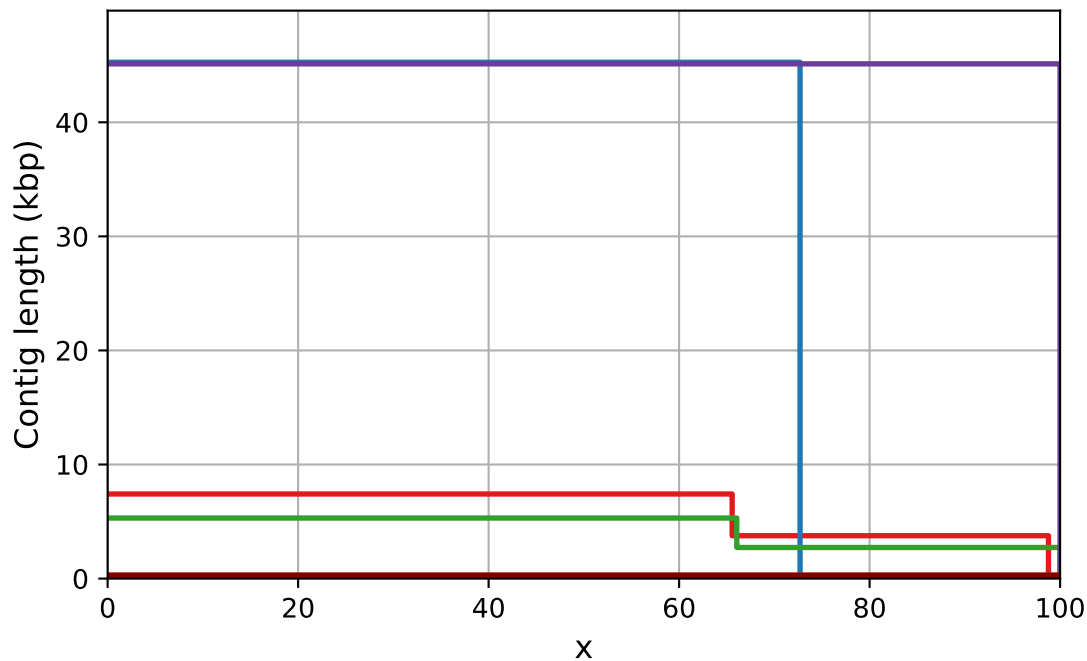
All statistics are based on contigs of size ≥ 1 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	sortie_medium	sortie_sequencage1	sortie_Hard	sortie_sequencage1_in	reads_sequencage1_in	reads_contaminant_in
# fully unaligned contigs	6	585	2	0	0	0
Fully unaligned length	11310	16998	8034	0	0	0
# partially unaligned contigs	-	1	-	0	0	0
Partially unaligned length	-	24107	-	0	0	0
# N's	0	0	0	0	0	0

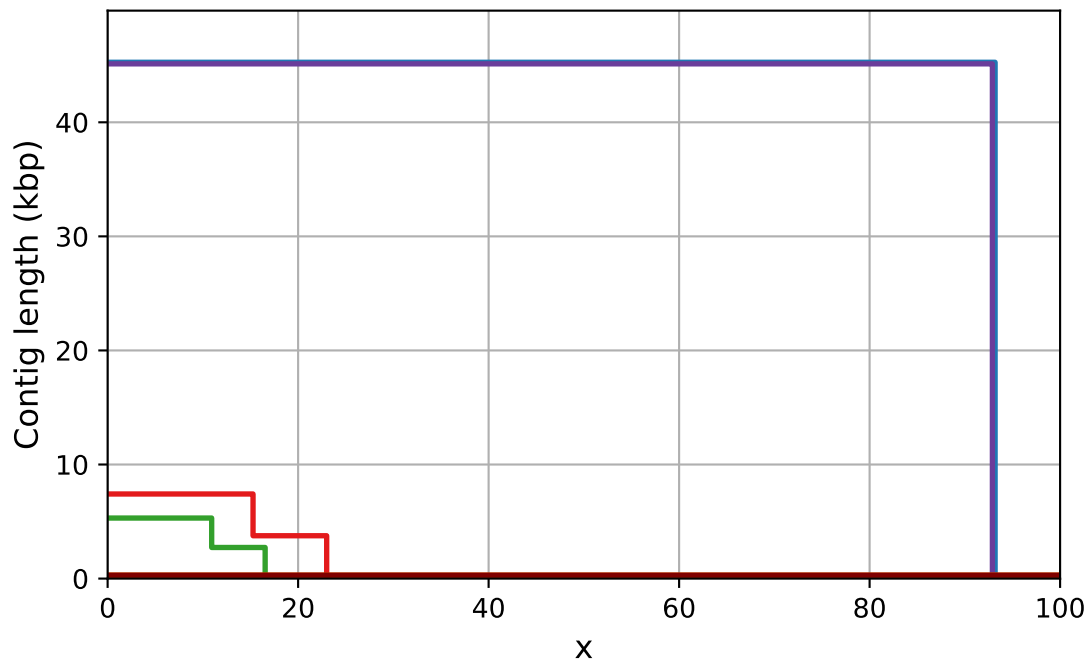
All statistics are based on contigs of size ≥ 1 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



sortie_medium sortie_Hard reads_sequencage1
sortie_sequencage1 sortie_sequencage1 reads_contaminant_i

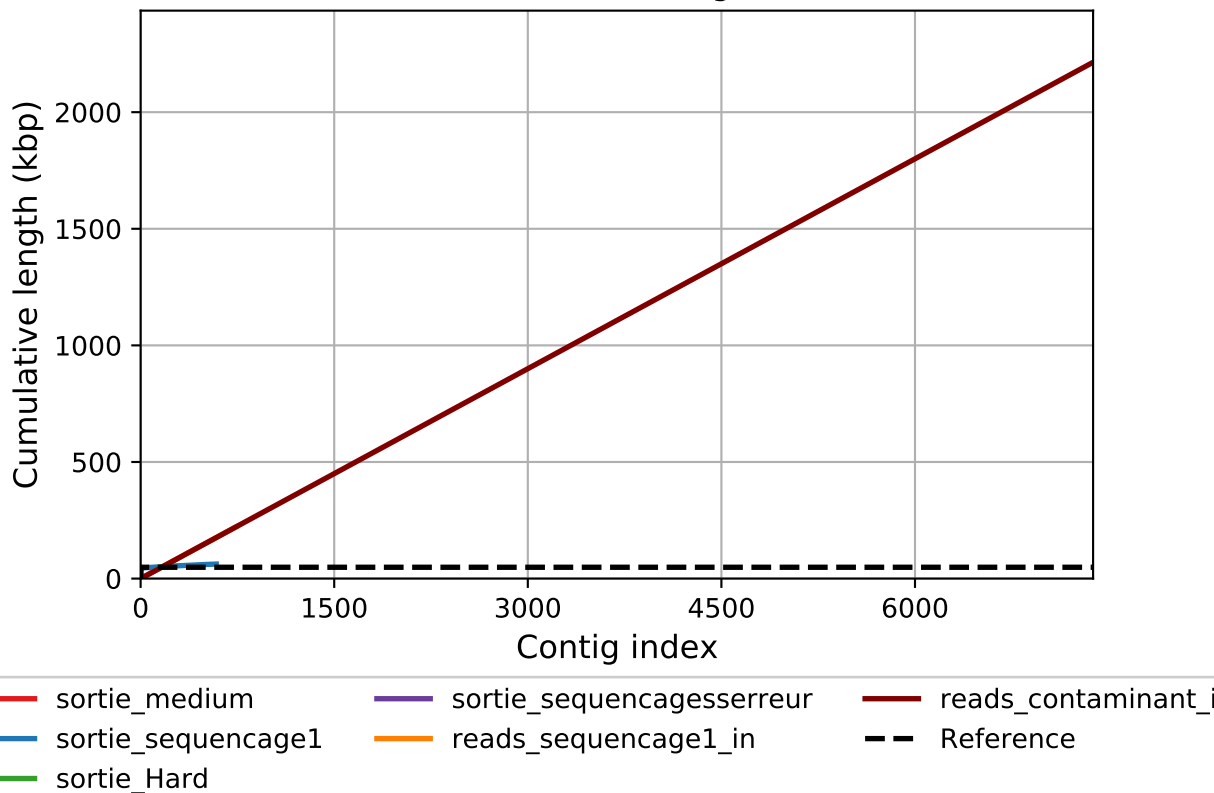
NGx



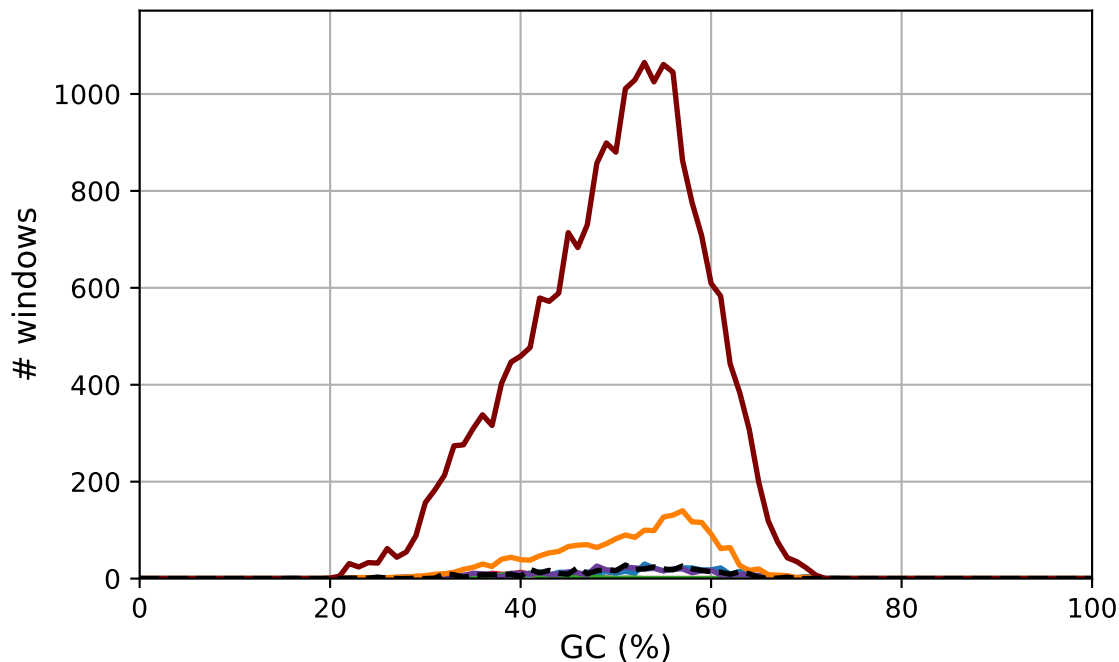
— sortie_medium — sortie_Hard — reads_sequencage1_

— sortie_sequencage1 — sortie_sequencageerreur — reads_contaminant_i

Cumulative length

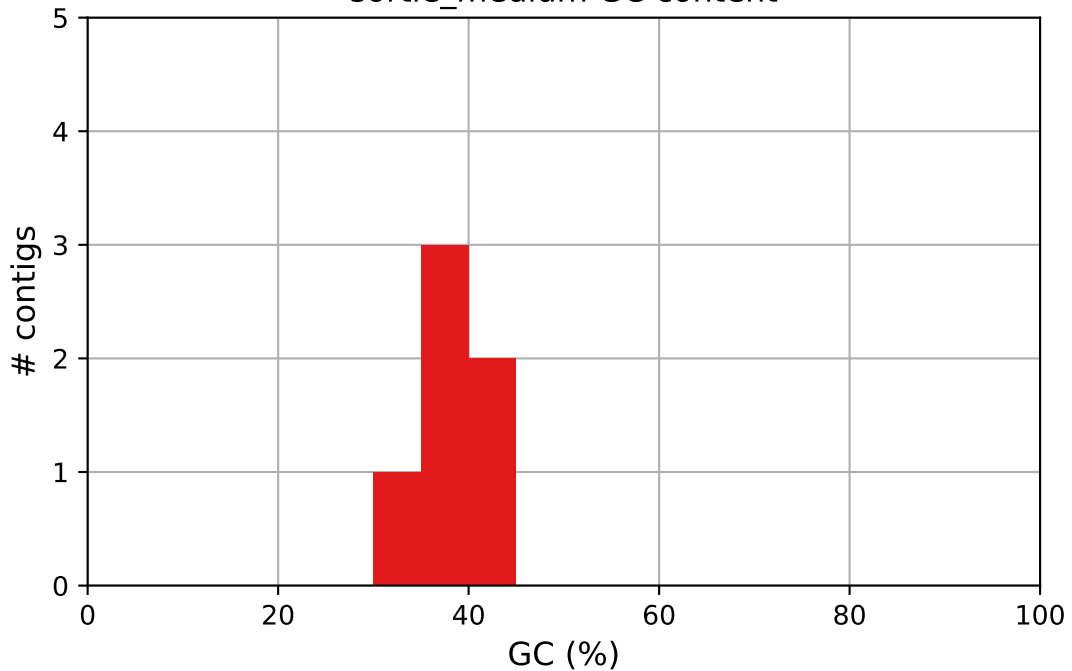


GC content



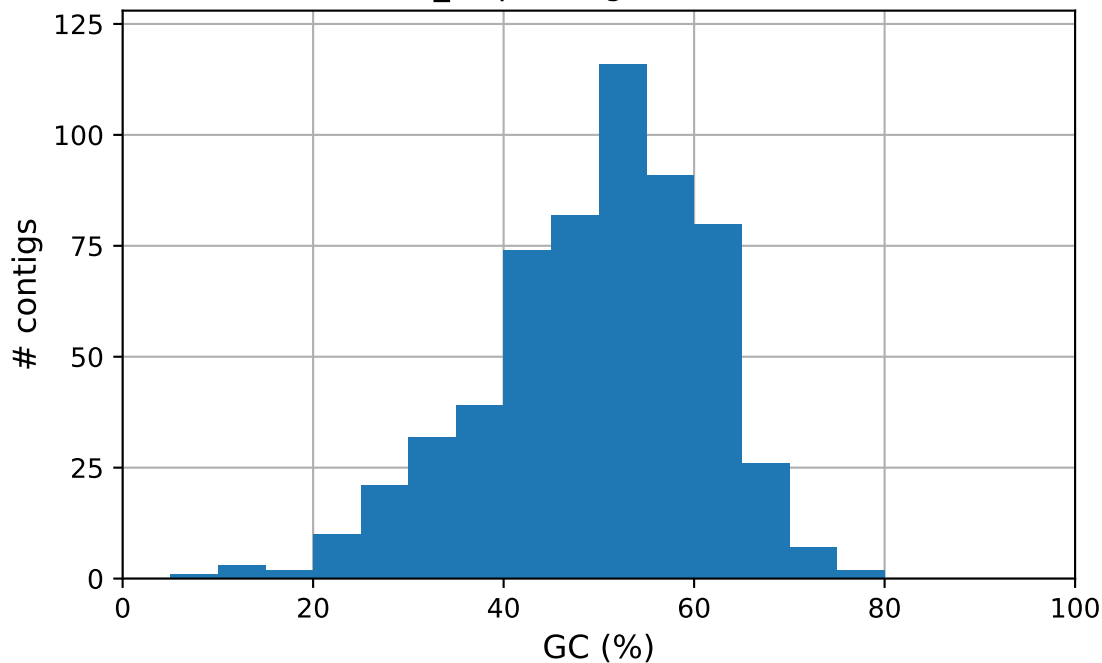
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 — sortie_sequencage1
 — reads_contaminant_i
 — sortie_sequencage1
 — reads_sequencage1_in
 - - Reference
 — sortie_Hard

sortie_medium GC content



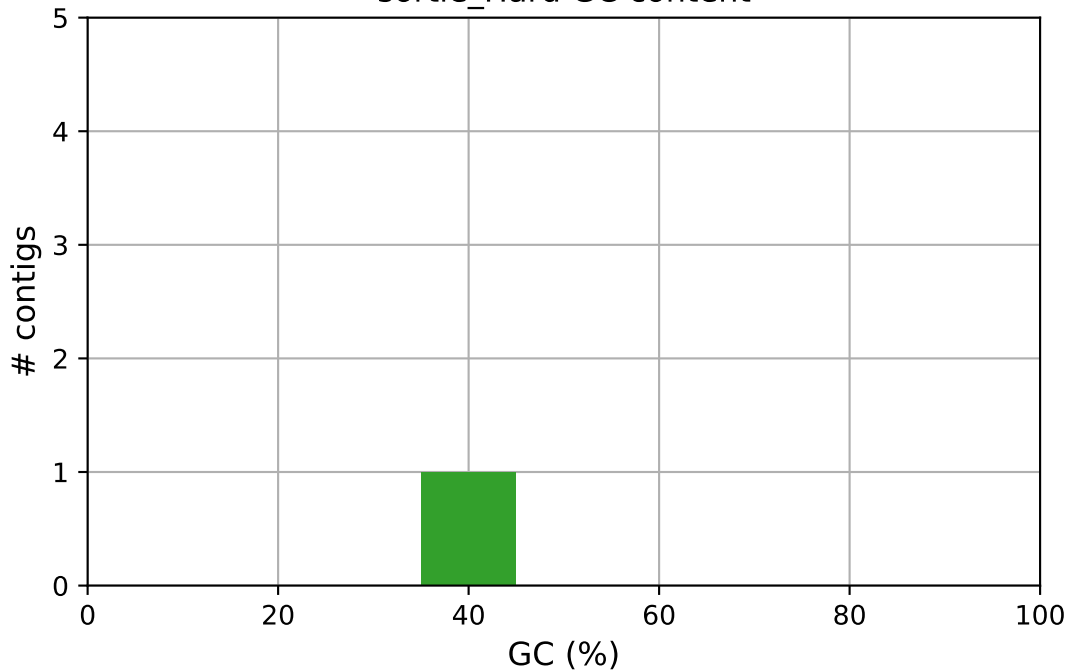
sortie_medium

sortie_sequencage1 GC content



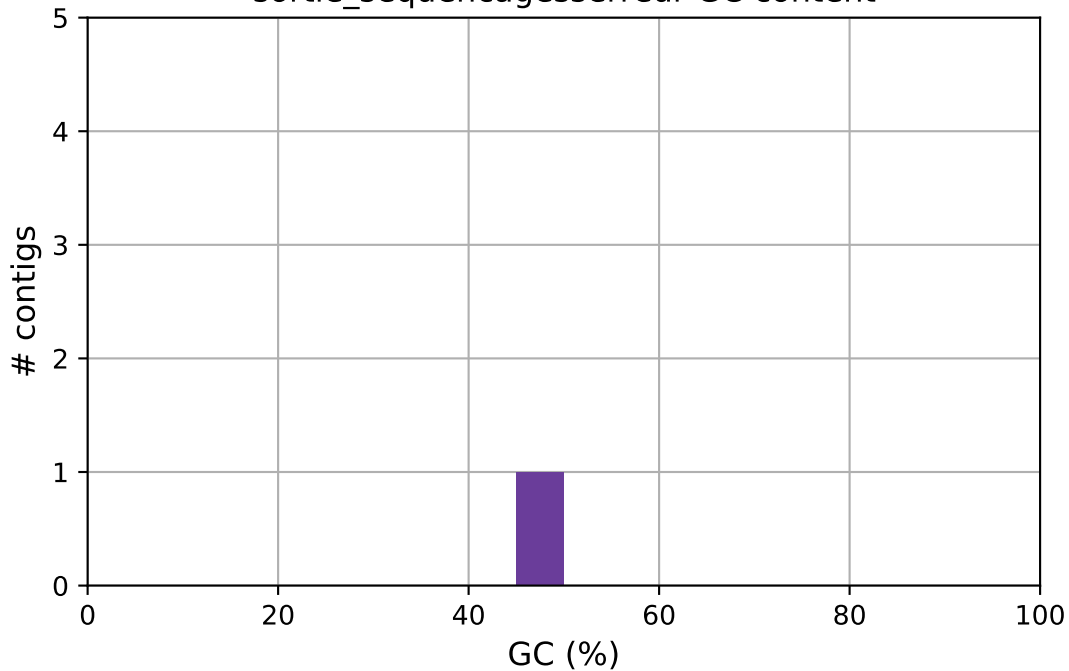
sortie_sequencage1

sortie_Hard GC content



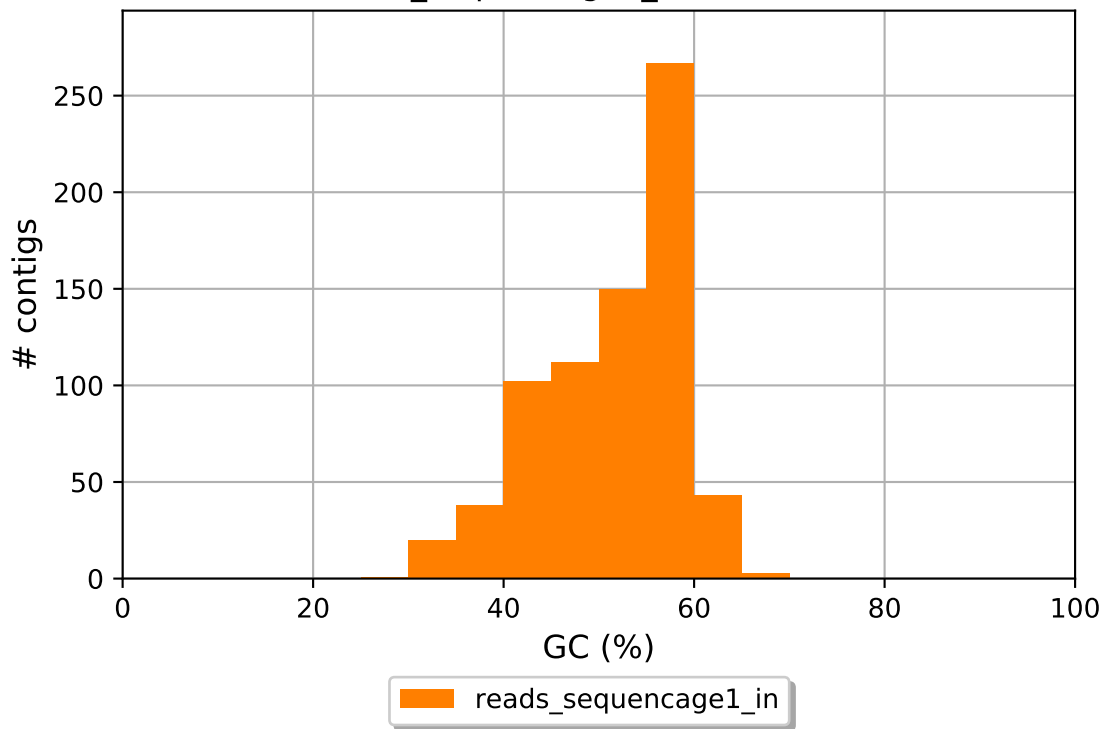
sortie_Hard

sortie_sequencagesserreur GC content

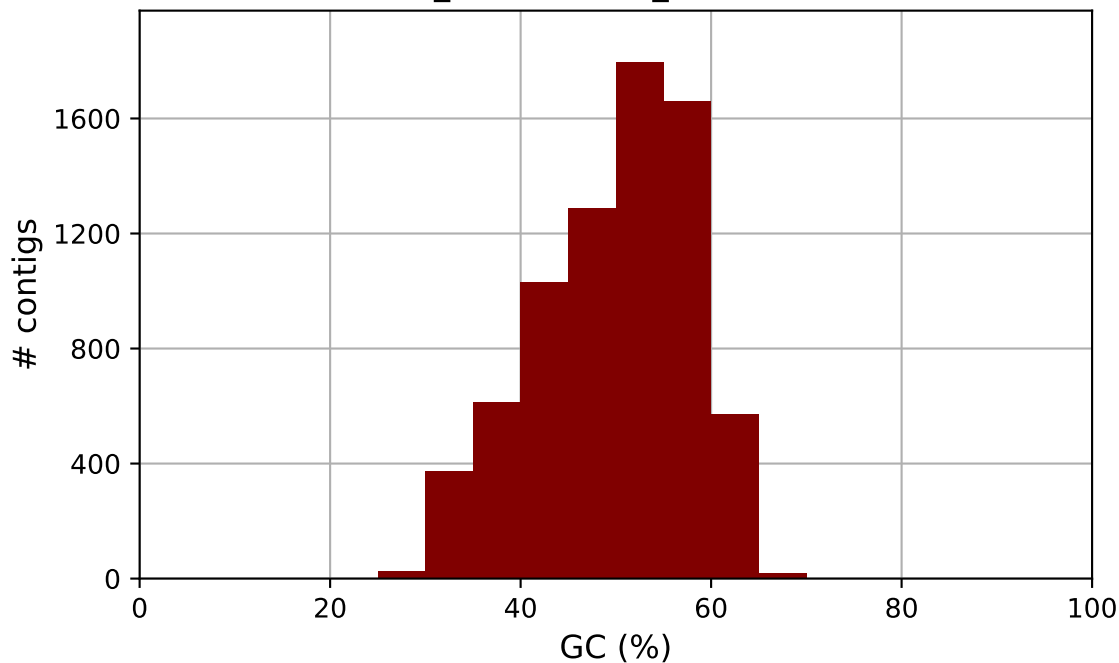


sortie_sequencagesserreur

reads_sequencage1_in GC content

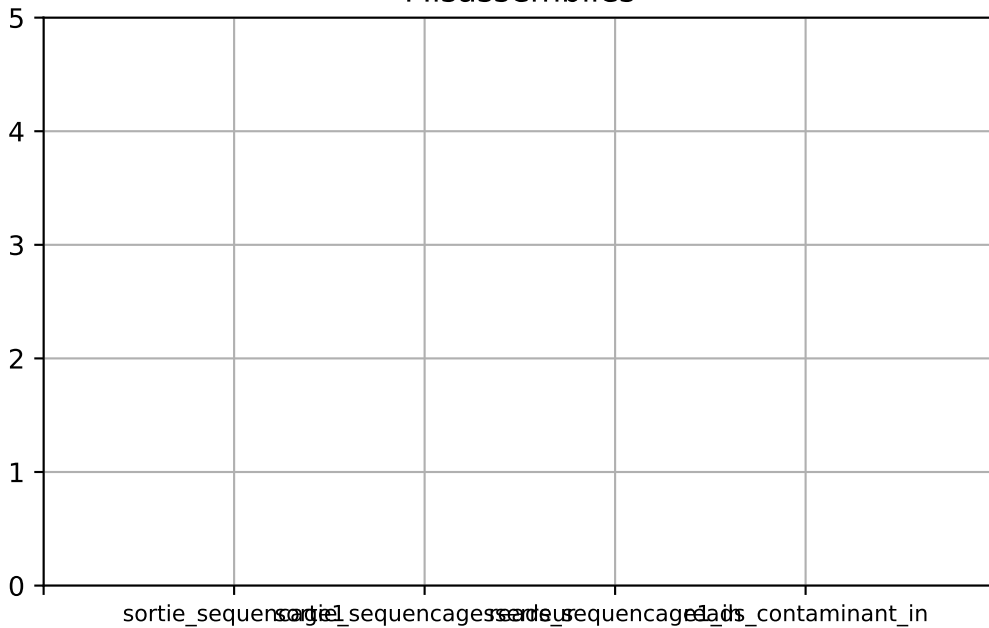


reads_contaminant_in GC content

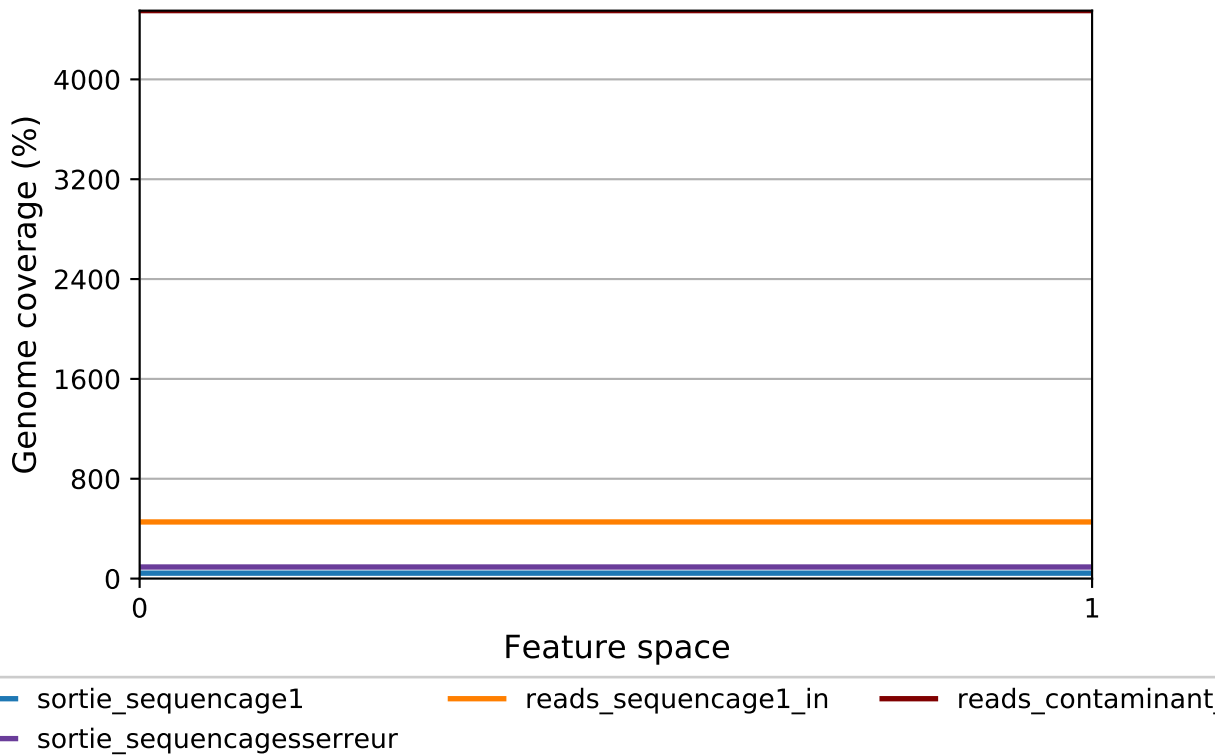


reads_contaminant_in

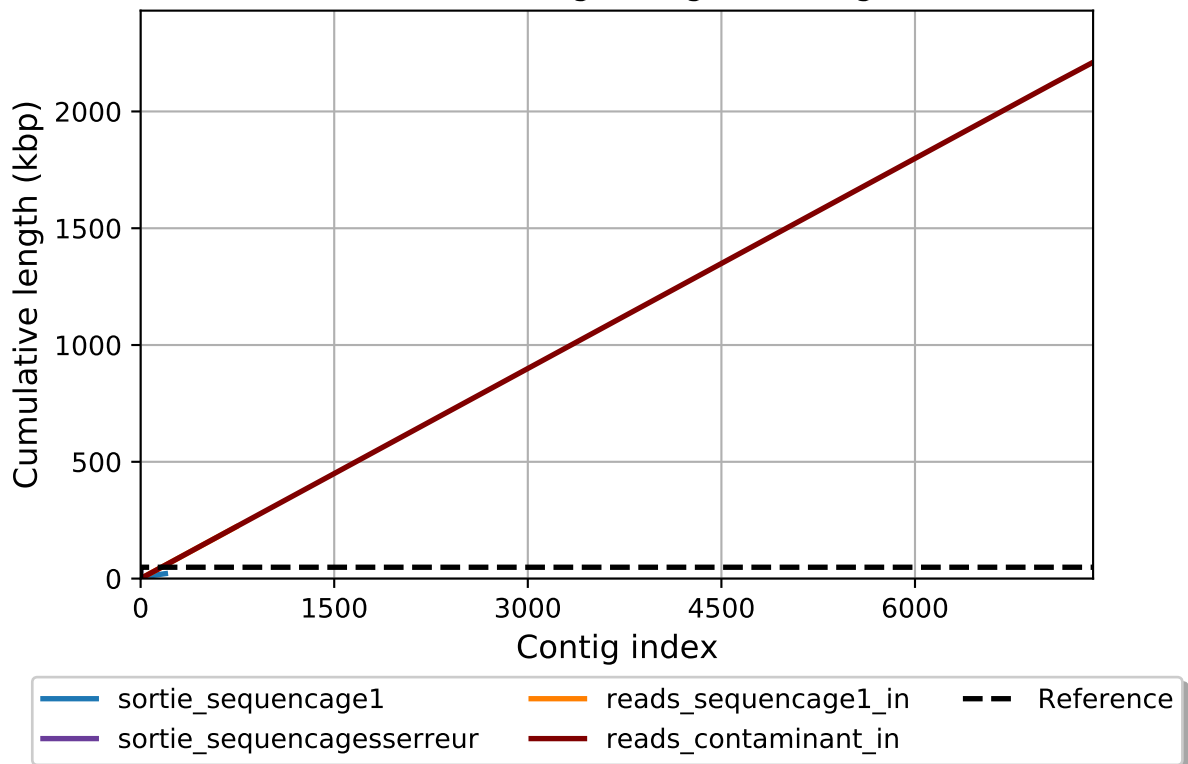
Misassemblies



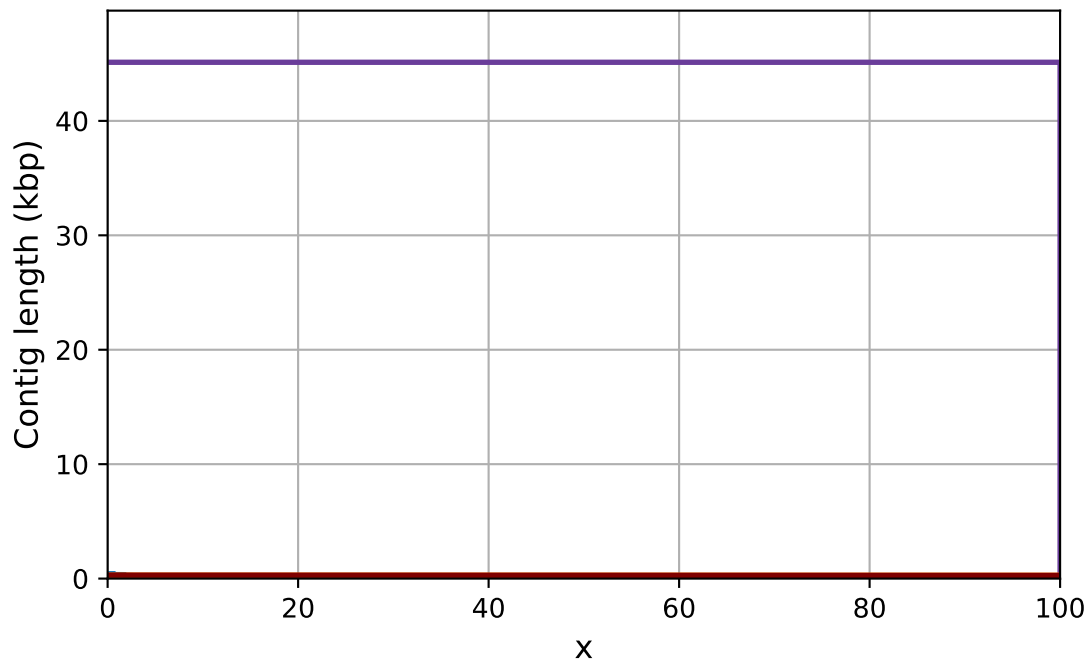
FRCurve (misassemblies)



Cumulative length (aligned contigs)

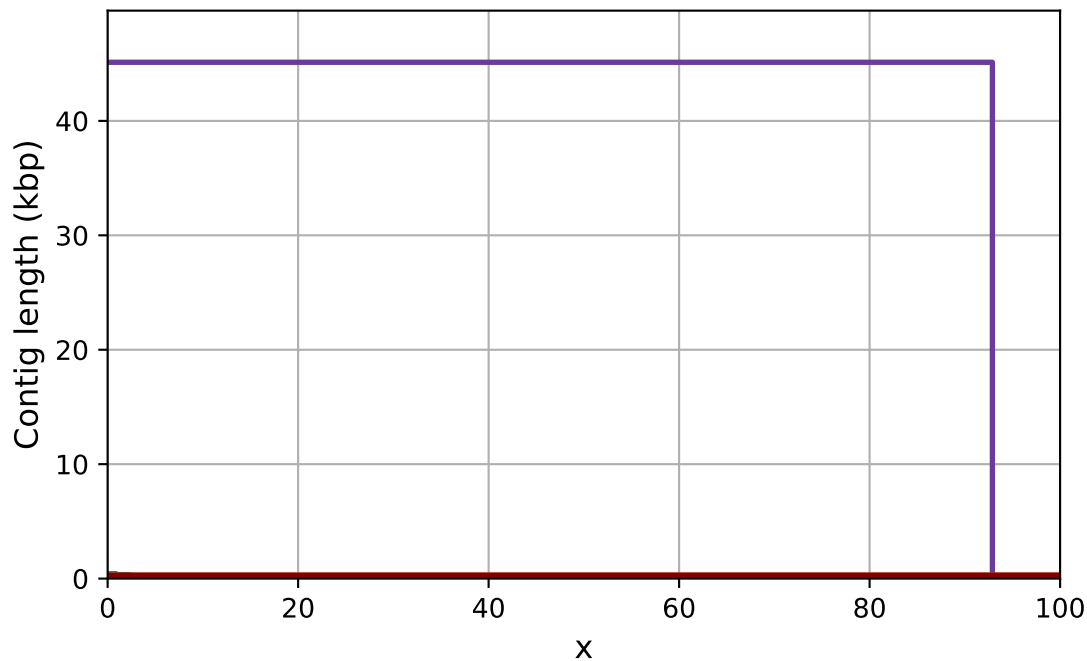


NAx



— sortie_sequencage1 — reads_sequencage1_in — reads_contaminant — sortie_sequencagesserreur

NGAx



— sortie_sequencage1 — reads_sequencage1_in — reads_contaminant — sortie_sequencagesserreur

Genome fraction, %

100

50

0

sortie_sequencage1
sortie_sequencagesserreur

reads_sequencage1_in

reads_contaminant

