Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/09 22:26:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124861.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR3124861 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124861_1.fastq.gz SRR3124861_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 09 22:26:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124861.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,173,904
Mapped reads	1,152,181 / 98.15%
Unmapped reads	21,723 / 1.85%
Mapped paired reads	1,152,181 / 98.15%
Mapped reads, first in pair	576,447 / 49.11%
Mapped reads, second in pair	575,734 / 49.04%
Mapped reads, both in pair	1,148,096 / 97.8%
Mapped reads, singletons	4,085 / 0.35%
Secondary alignments	0
Supplementary alignments	8,947 / 0.76%
Read min/max/mean length	30 / 151 / 151.38
Duplicated reads (estimated)	163,825 / 13.96%
Duplication rate	14.63%
Clipped reads	827,686 / 70.51%

2.2. ACGT Content

Number/percentage of A's	45,980,962 / 29.4%
Number/percentage of C's	31,485,556 / 20.13%
Number/percentage of T's	45,869,461 / 29.33%
Number/percentage of G's	33,059,358 / 21.14%
Number/percentage of N's	13,967 / 0.01%

GC Percentage	41.27%

2.3. Coverage

Mean	0.0506
Standard Deviation	0.5805

2.4. Mapping Quality

Mean Mapping Quality	53.55

2.5. Insert size

Mean	46,311.4
Standard Deviation	1,936,986.76
P25/Median/P75	141 / 176 / 223

2.6. Mismatches and indels

General error rate	1.17%
Mismatches	1,778,632
Insertions	25,464
Mapped reads with at least one insertion	2.14%
Deletions	50,700
Mapped reads with at least one deletion	4.28%
Homopolymer indels	47.9%

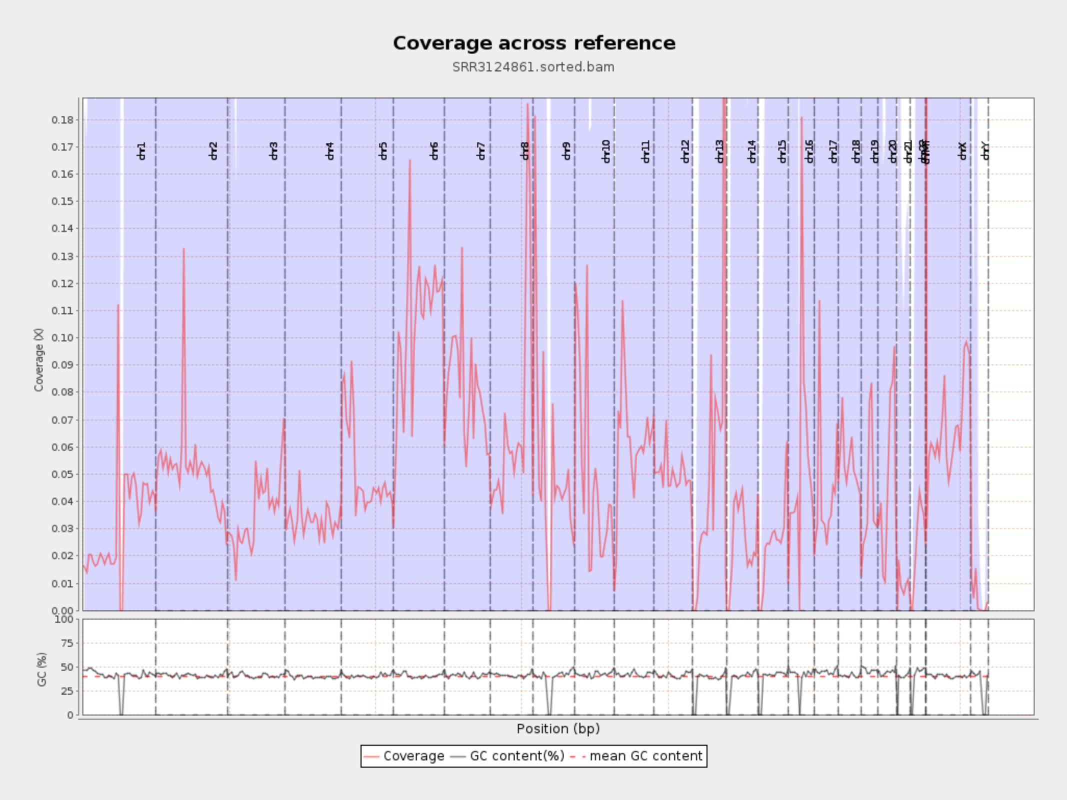
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

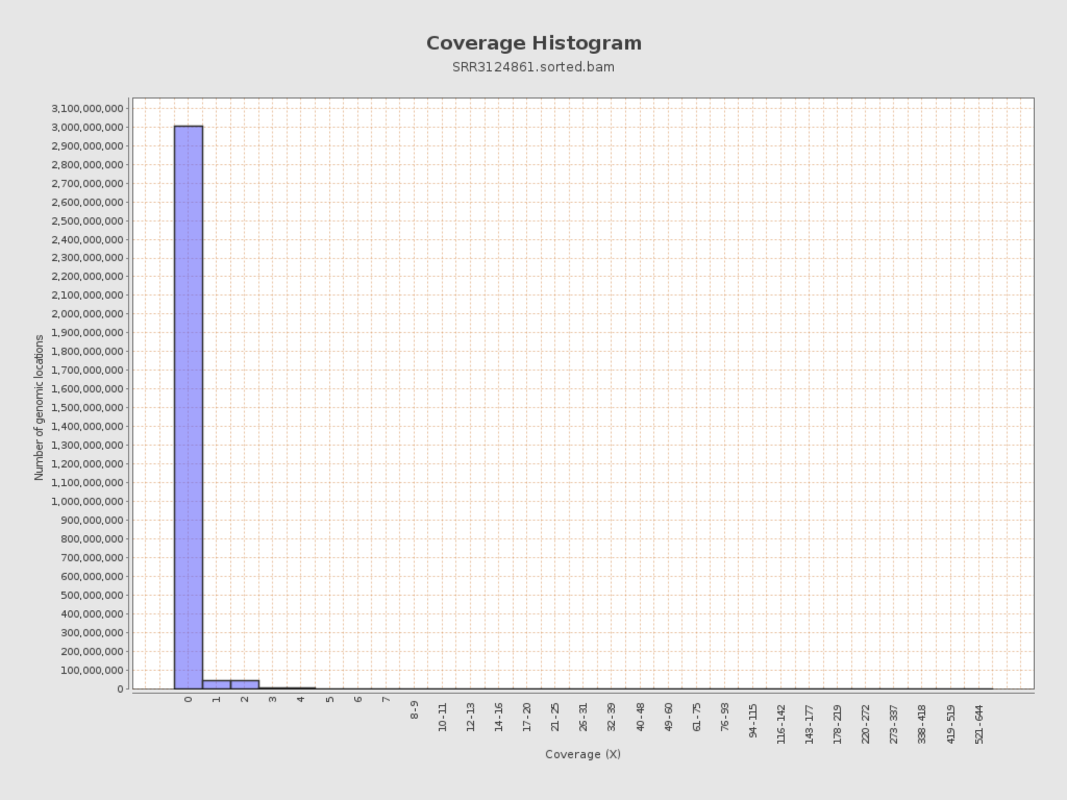
		bases	coverage	deviation
chr1	249250621	7836387	0.0314	0.7147
chr2	243199373	12652907	0.052	0.5744
chr3	198022430	7170962	0.0362	0.2585
chr4	191154276	6360452	0.0333	0.3133
chr5	180915260	9261176	0.0512	0.3063
chr6	171115067	18178497	0.1062	0.7181
chr7	159138663	12895845	0.081	1.1047
chr8	146364022	10177880	0.0695	0.3884
chr9	141213431	7285852	0.0516	0.7713
chr10	135534747	6775009	0.05	0.9338
chr11	135006516	8454151	0.0626	0.4968
chr12	133851895	6673156	0.0499	0.3007
chr13	115169878	7056253	0.0613	0.3848
chr14	107349540	2672268	0.0249	0.2187
chr15	102531392	2517174	0.0246	0.2097
chr16	90354753	4902298	0.0543	0.8147
chr17	81195210	3498618	0.0431	0.6919
chr18	78077248	4240567	0.0543	0.856
chr19	59128983	2488411	0.0421	0.4587
chr20	63025520	3113934	0.0494	0.3122
chr21	48129895	442996	0.0092	0.1721
chr22	51304566	1297702	0.0253	0.2135
chrMT	16571	58479	3.529	2.7586
chrX	155270560	10246403	0.066	0.3953

chrY	59373566	242036	0.0041	0.2373

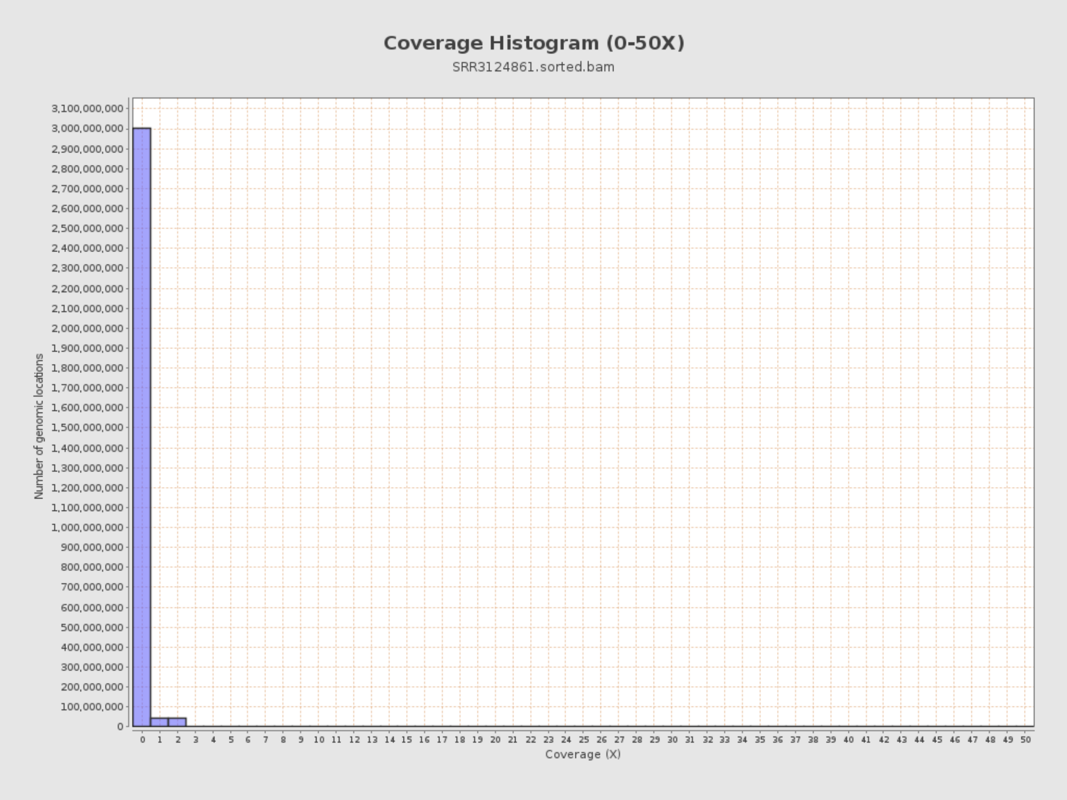
3. Results : Coverage across reference



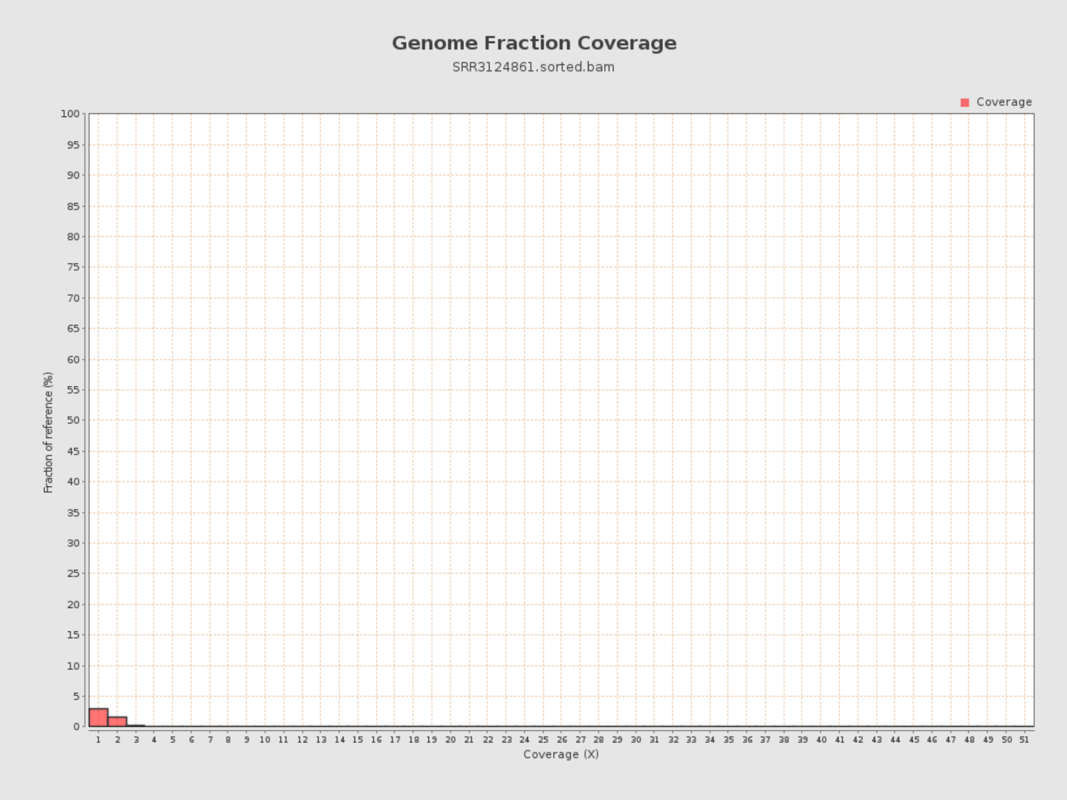
4. Results : Coverage Histogram



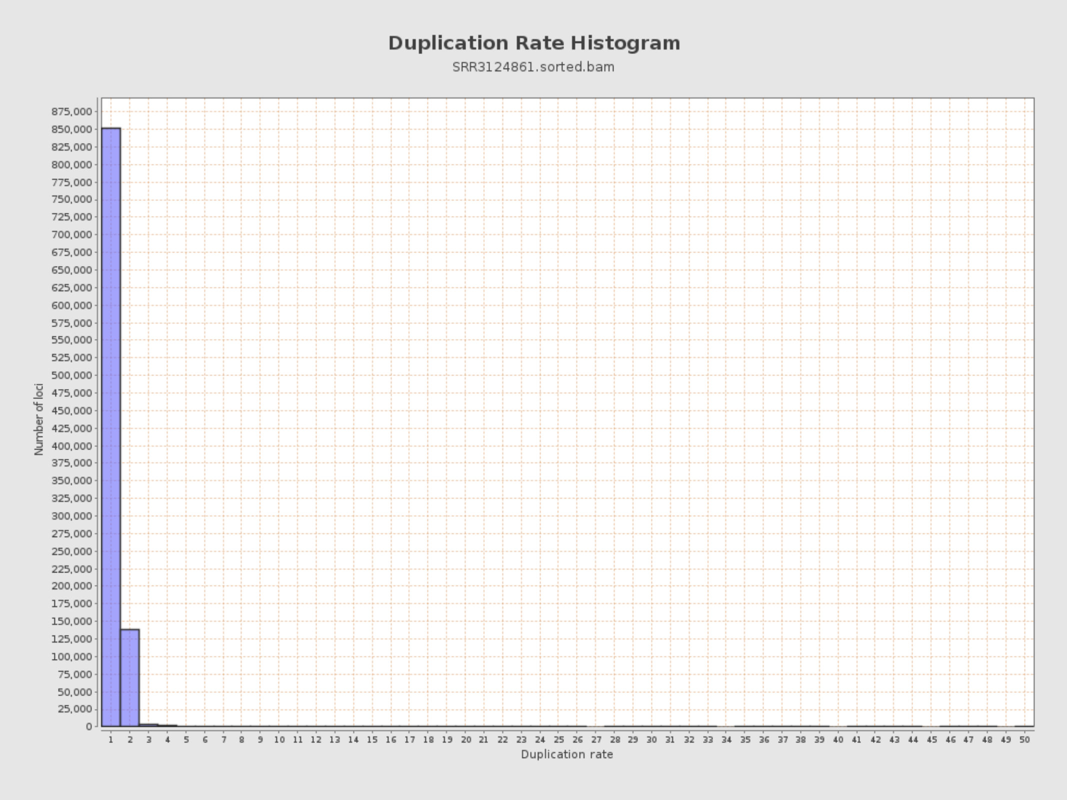
5. Results : Coverage Histogram (0-50X)



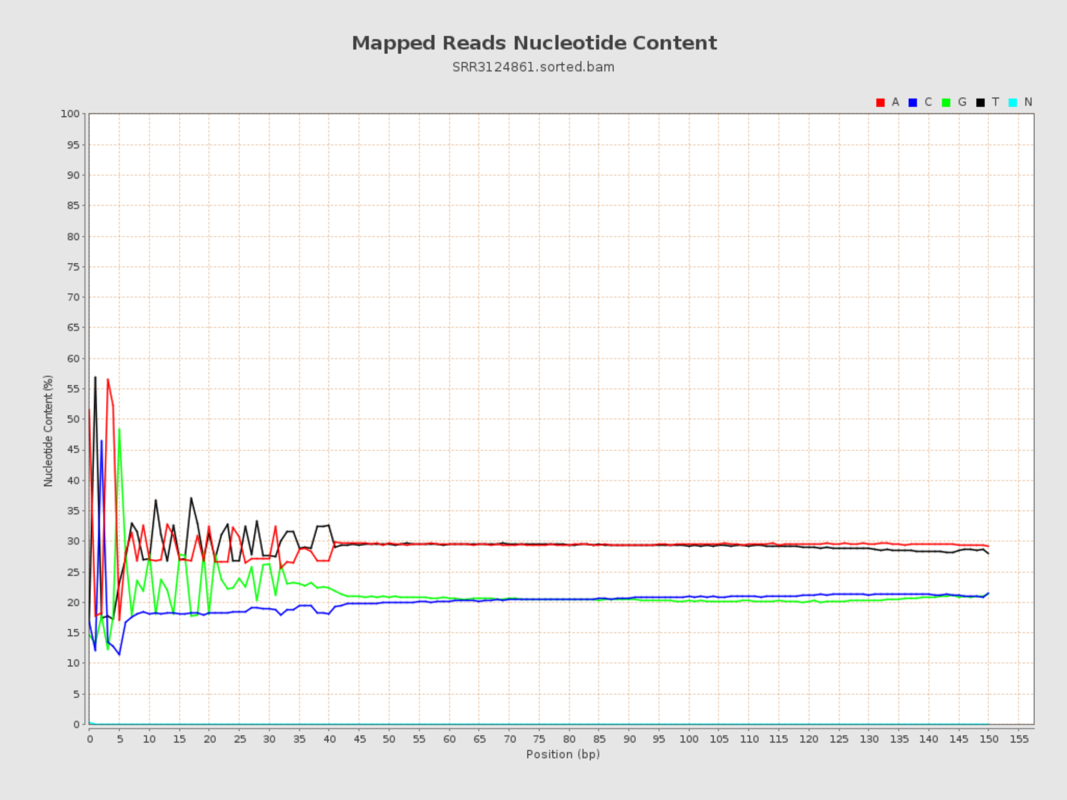
6. Results : Genome Fraction Coverage



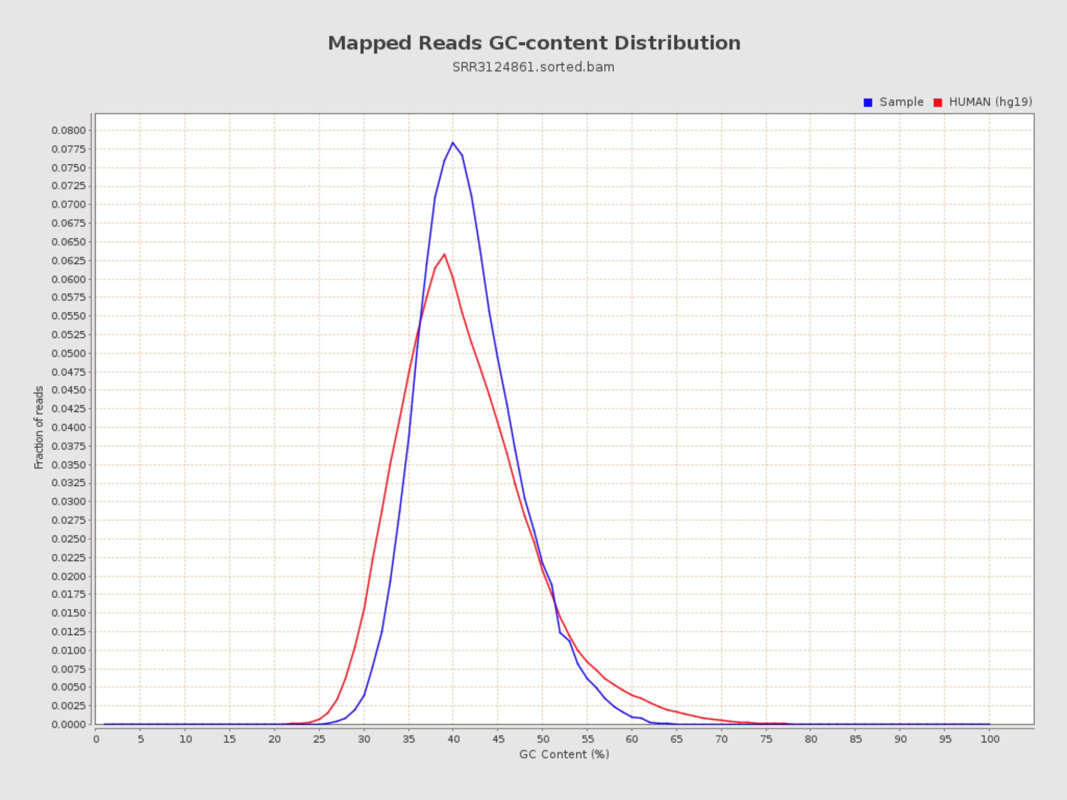
7. Results : Duplication Rate Histogram



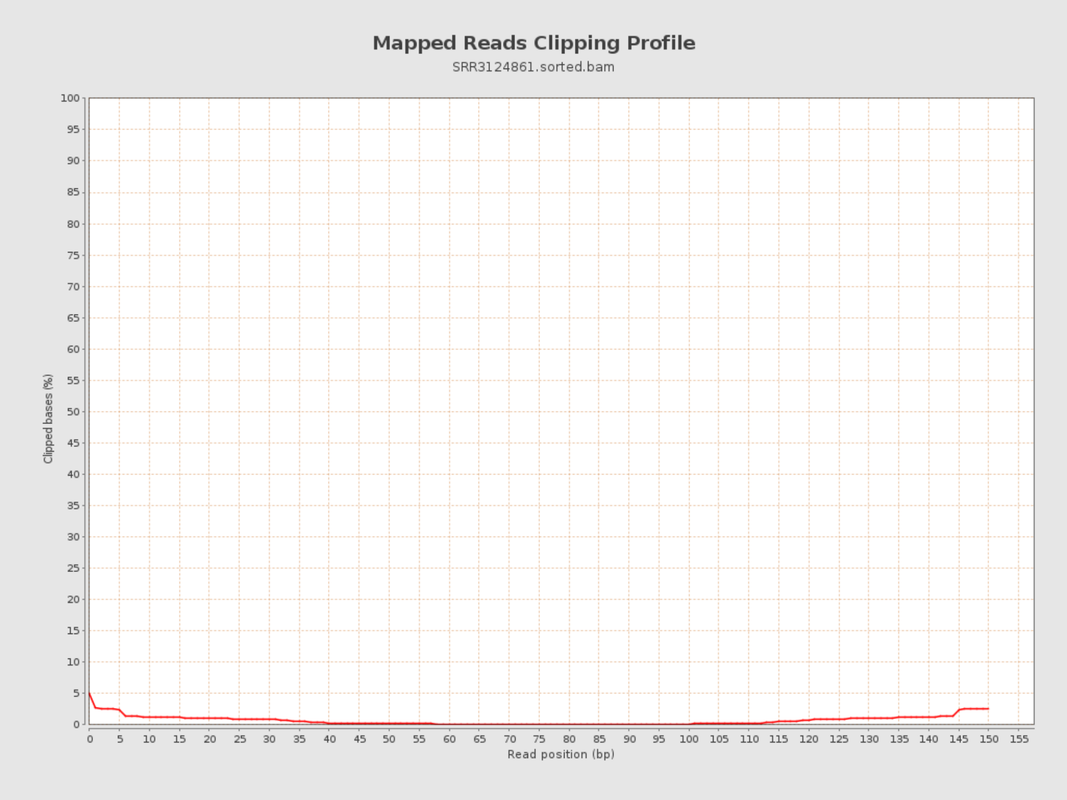
8. Results : Mapped Reads Nucleotide Content



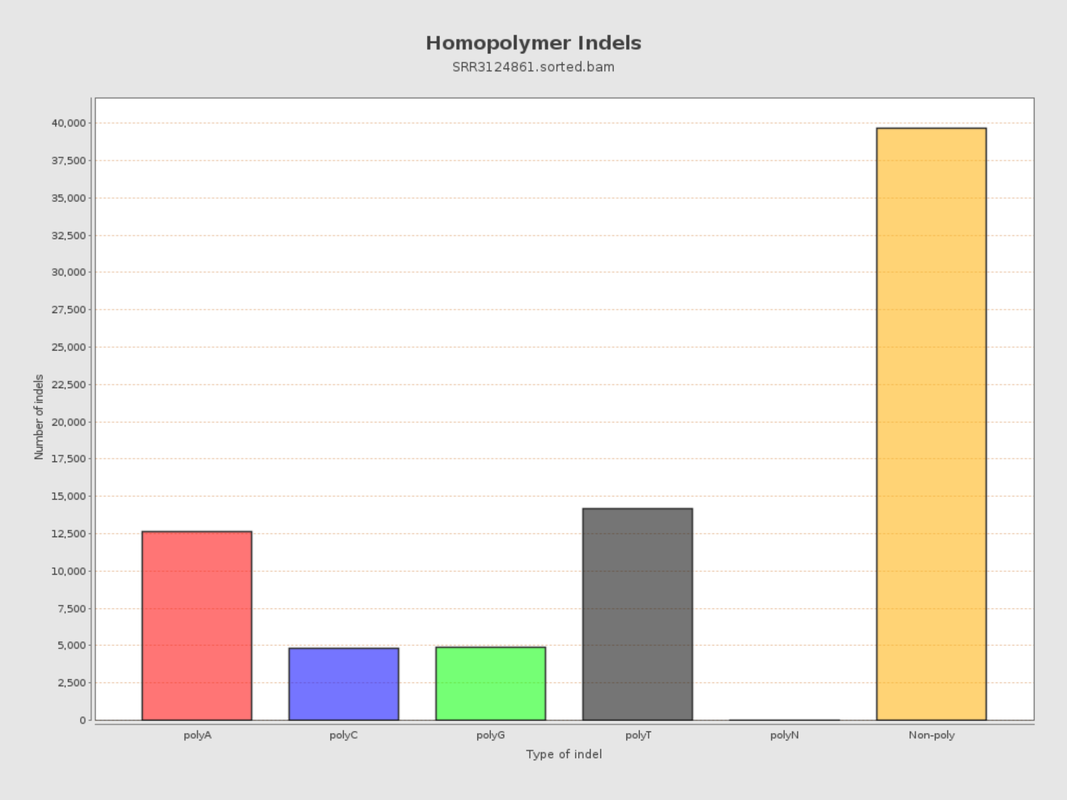
9. Results : Mapped Reads GC-content Distribution



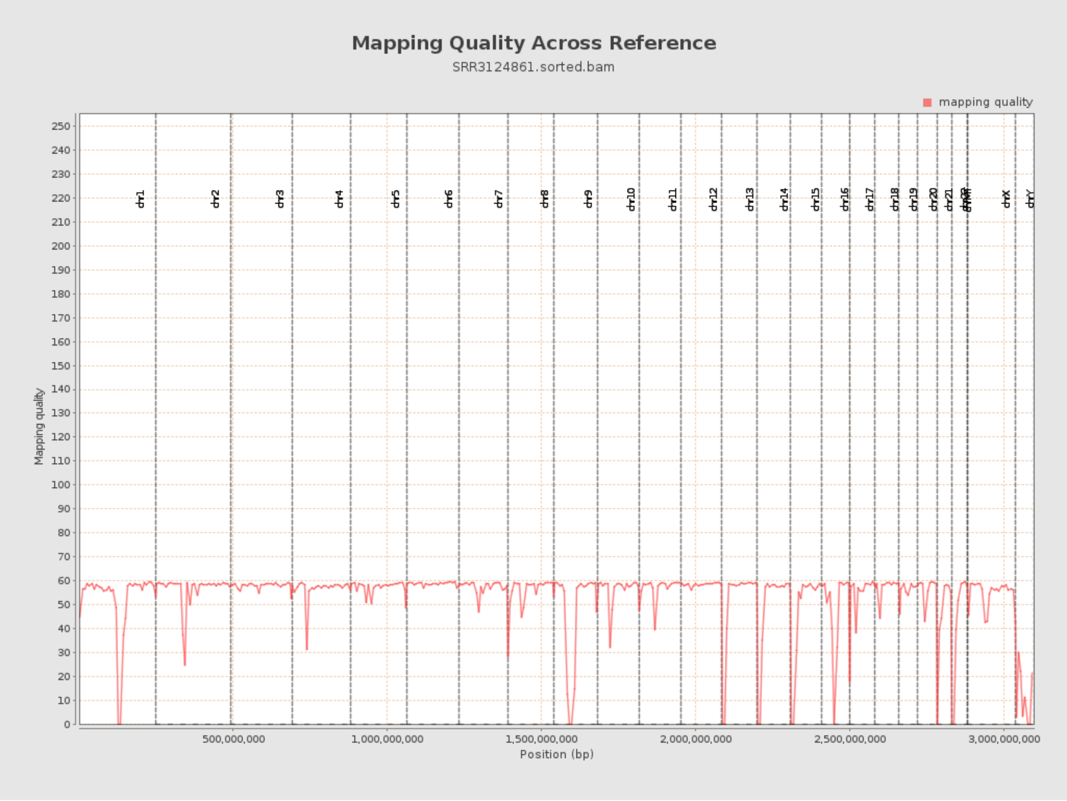
10. Results : Mapped Reads Clipping Profile



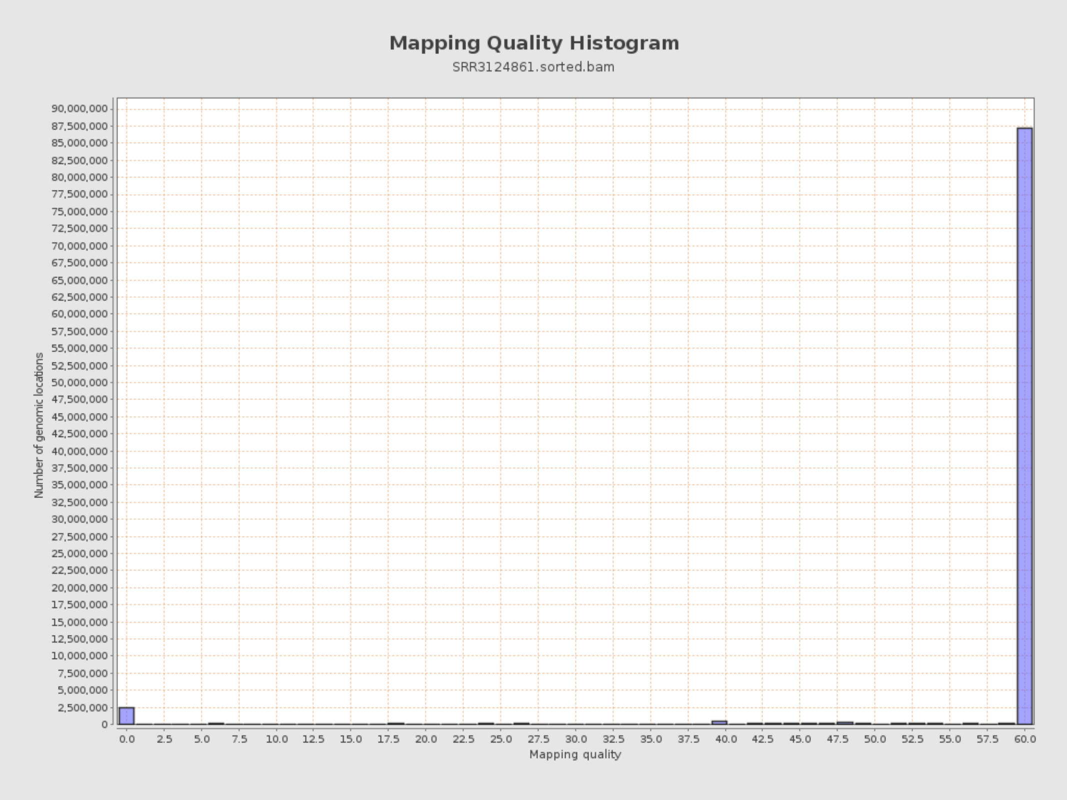
11. Results : Homopolymer Indels



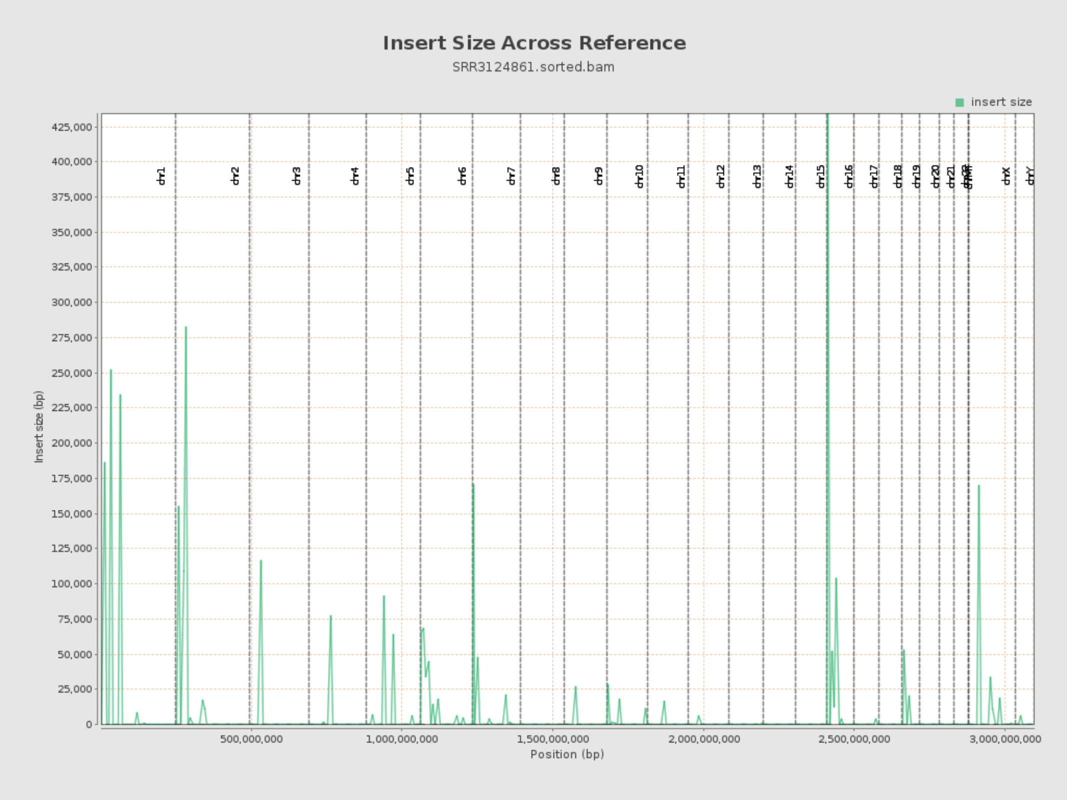
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram