Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/09 22:38:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124863.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_SRR3124863 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124863_1.fastq.gz SRR3124863_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 09 22:38:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124863.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,537,948
Mapped reads	4,380,829 / 96.54%
Unmapped reads	157,119 / 3.46%
Mapped paired reads	4,380,829 / 96.54%
Mapped reads, first in pair	2,194,288 / 48.35%
Mapped reads, second in pair	2,186,541 / 48.18%
Mapped reads, both in pair	4,365,190 / 96.19%
Mapped reads, singletons	15,639 / 0.34%
Secondary alignments	0
Supplementary alignments	14,530 / 0.32%
Read min/max/mean length	30 / 101 / 101.12
Duplicated reads (estimated)	397,759 / 8.77%
Duplication rate	6.82%
Clipped reads	2,089,166 / 46.04%

2.2. ACGT Content

Number/percentage of A's	106,477,306 / 27.98%
Number/percentage of C's	71,780,186 / 18.86%
Number/percentage of T's	112,235,676 / 29.49%
Number/percentage of G's	89,915,926 / 23.63%
Number/percentage of N's	143,447 / 0.04%

GC Percentage	42.49%

2.3. Coverage

Mean	0.123
Standard Deviation	0.9992

2.4. Mapping Quality

Mean Mapping Quality	52.8

2.5. Insert size

Mean	36,182.73
Standard Deviation	1,808,618.91
P25/Median/P75	143 / 192 / 267

2.6. Mismatches and indels

General error rate	0.79%
Mismatches	2,903,977
Insertions	53,539
Mapped reads with at least one insertion	1.19%
Deletions	128,550
Mapped reads with at least one deletion	2.87%
Homopolymer indels	47.92%

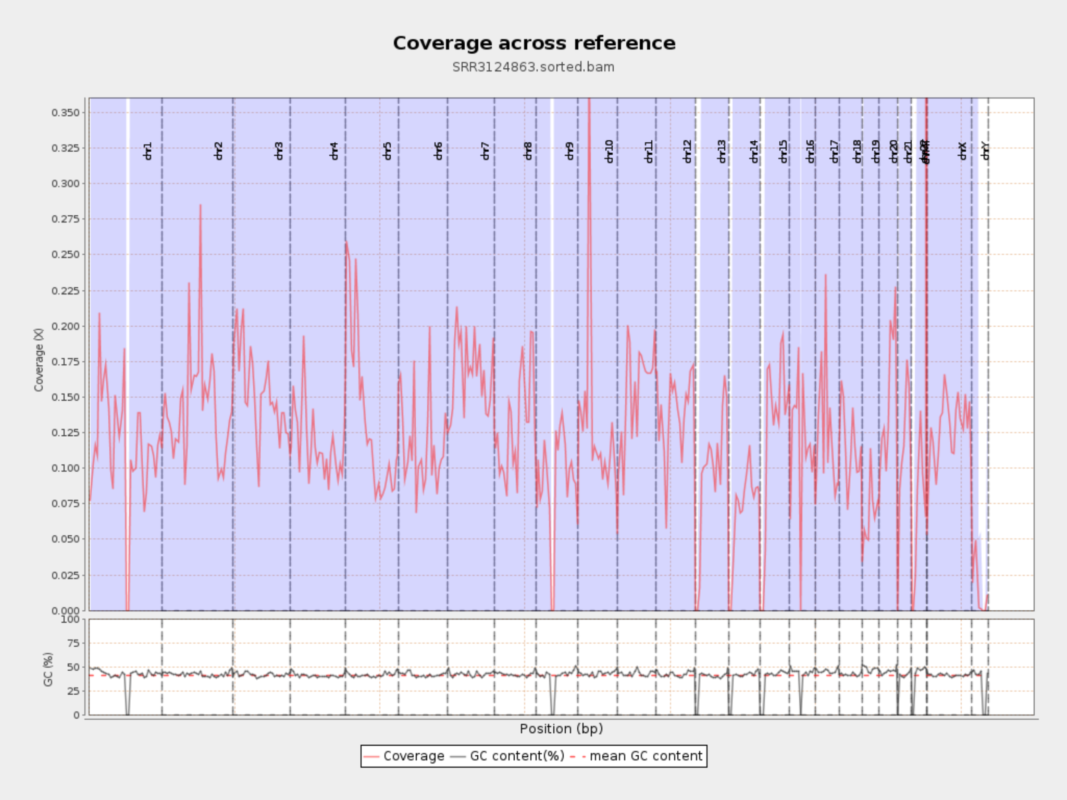
2.7. Chromosome stats

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

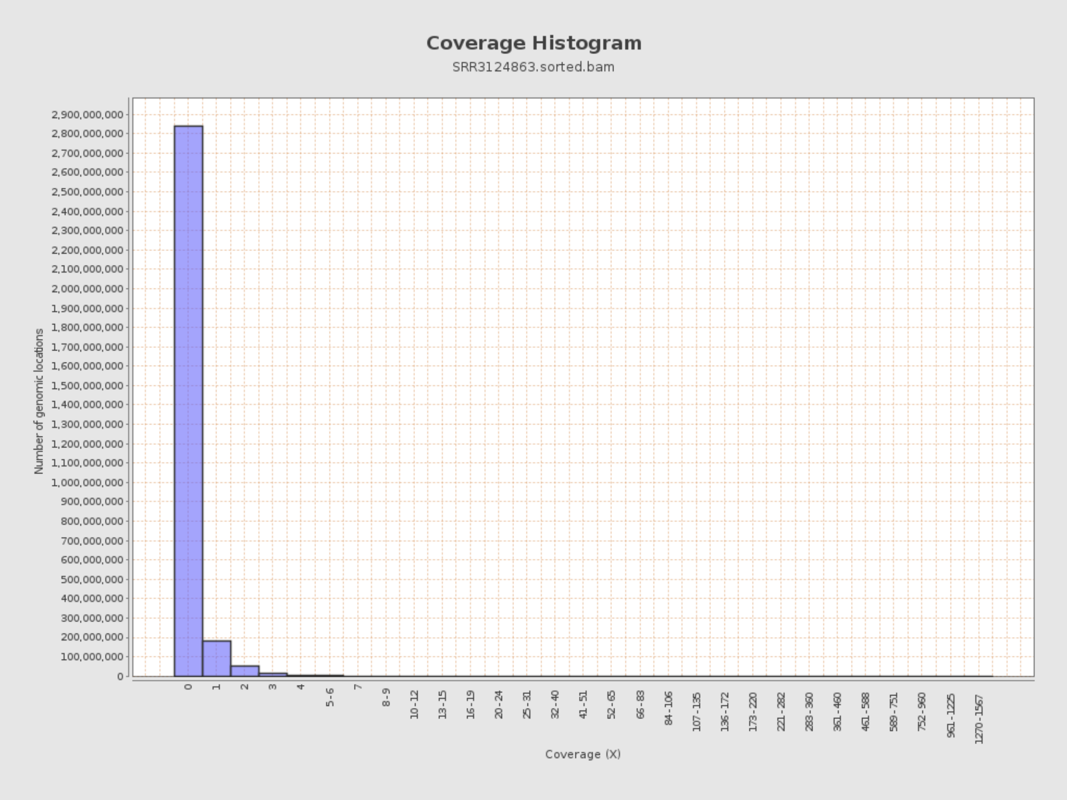
		bases	coverage	deviation
chr1	249250621	28592932	0.1147	1.0171
chr2	243199373	34773759	0.143	1.3403
chr3	198022430	30361607	0.1533	0.5388
chr4	191154276	22336580	0.1169	0.7319
chr5	180915260	24388130	0.1348	0.5207
chr6	171115067	20081439	0.1174	0.7875
chr7	159138663	26719283	0.1679	1.4812
chr8	146364022	19149047	0.1308	0.5688
chr9	141213431	12910142	0.0914	1.0372
chr10	135534747	17855952	0.1317	2.4199
chr11	135006516	20662381	0.153	0.8042
chr12	133851895	18464510	0.1379	0.5091
chr13	115169878	11001239	0.0955	0.4192
chr14	107349540	7545556	0.0703	0.4023
chr15	102531392	12902195	0.1258	0.5082
chr16	90354753	10649741	0.1179	1.0399
chr17	81195210	10209861	0.1257	1.3444
chr18	78077248	9169673	0.1174	1.2152
chr19	59128983	4047616	0.0685	0.6962
chr20	63025520	9482764	0.1505	0.5825
chr21	48129895	5378818	0.1118	0.5423
chr22	51304566	3398308	0.0662	0.3895
chrMT	16571	84397	5.0931	4.113
chrX	155270560	19736616	0.1271	0.6258

chrY	59373566	866921	0.0146	0.9782

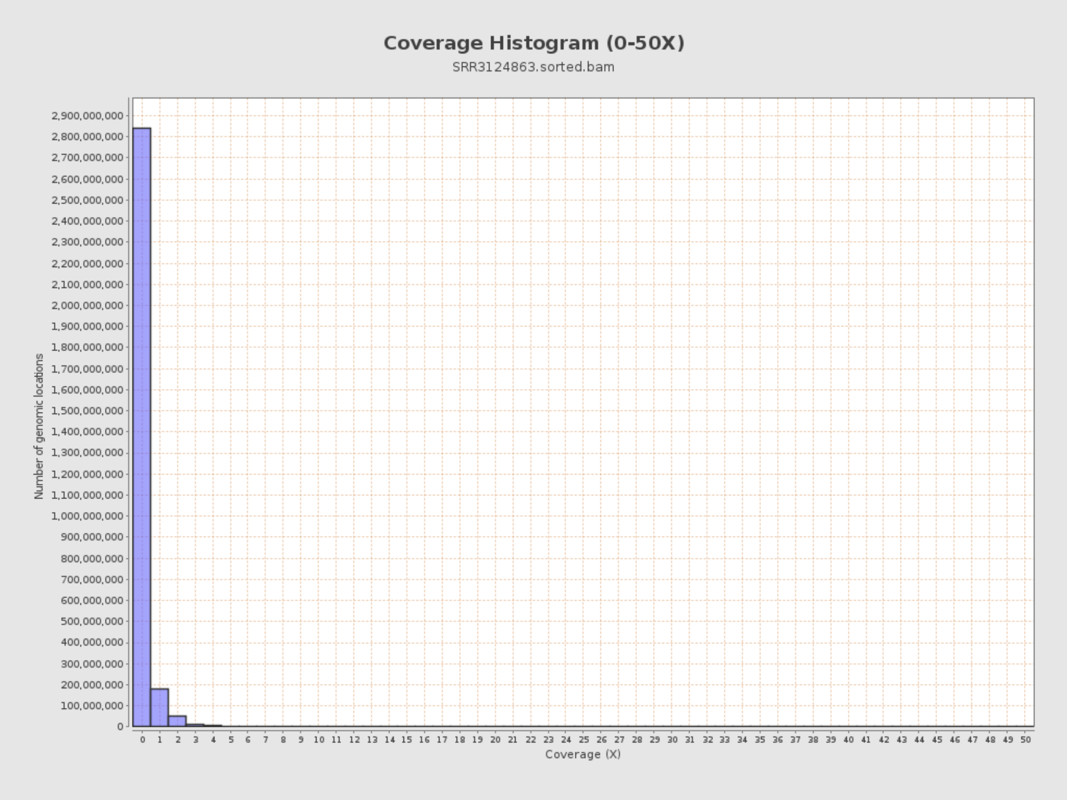
3. Results : Coverage across reference



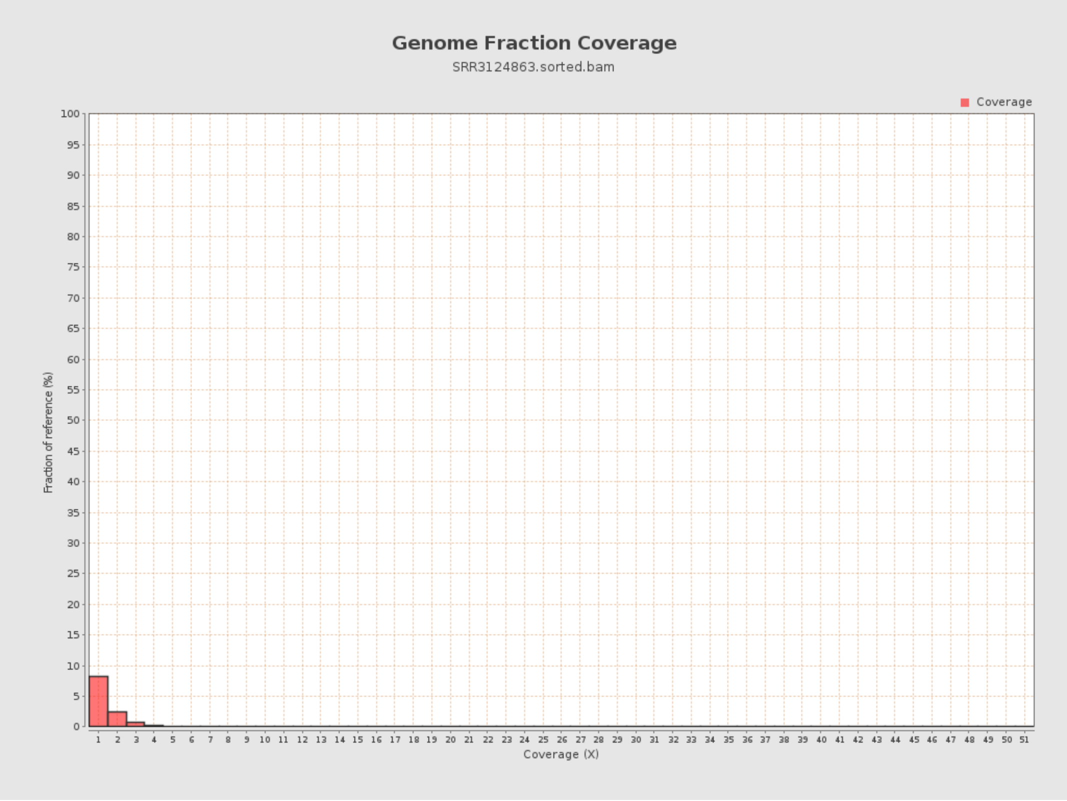
4. Results : Coverage Histogram



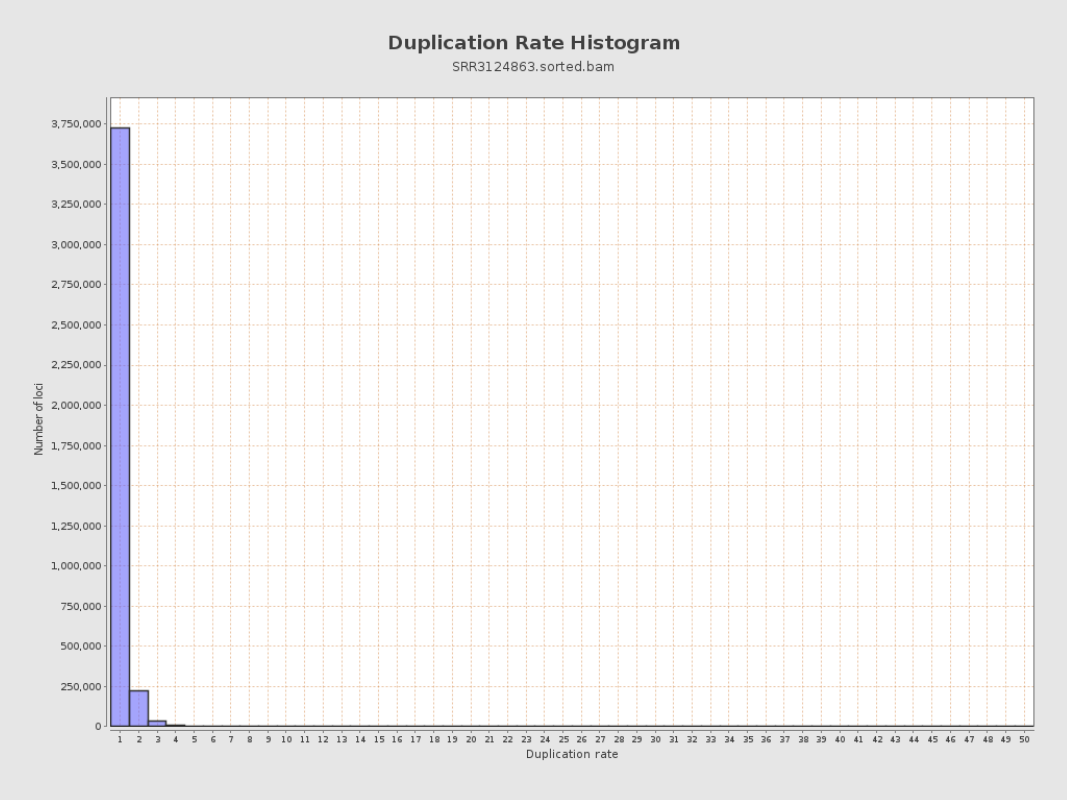
5. Results : Coverage Histogram (0-50X)



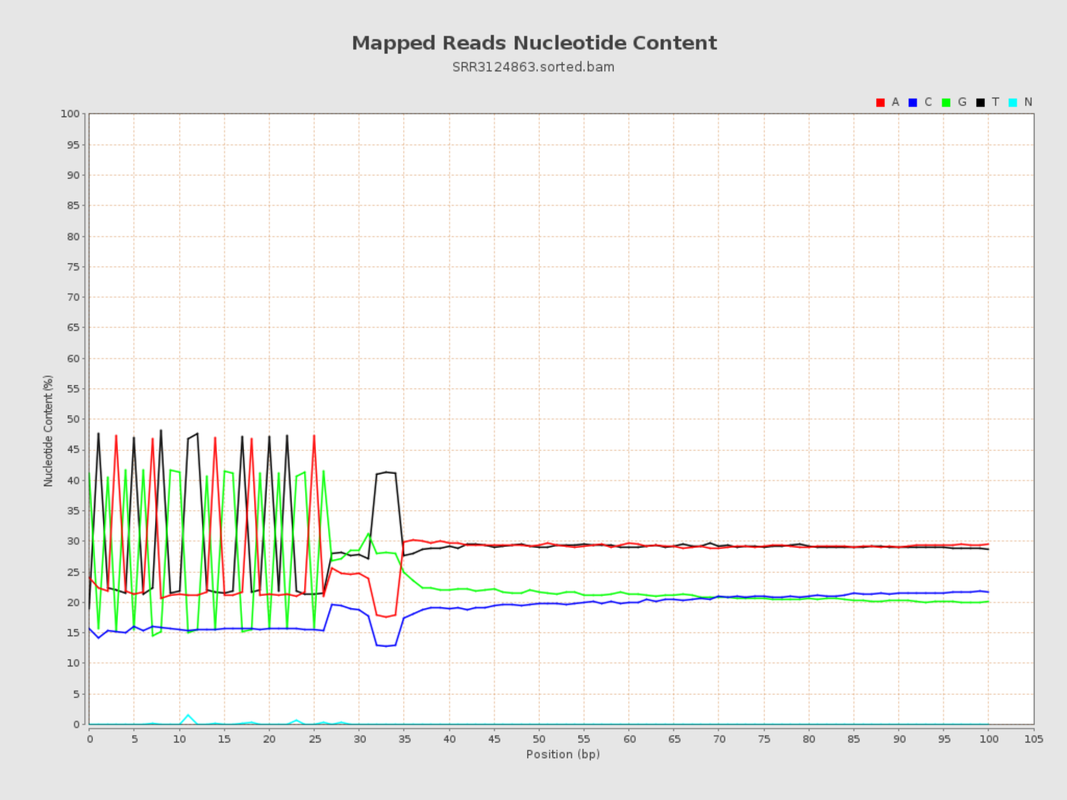
6. Results : Genome Fraction Coverage



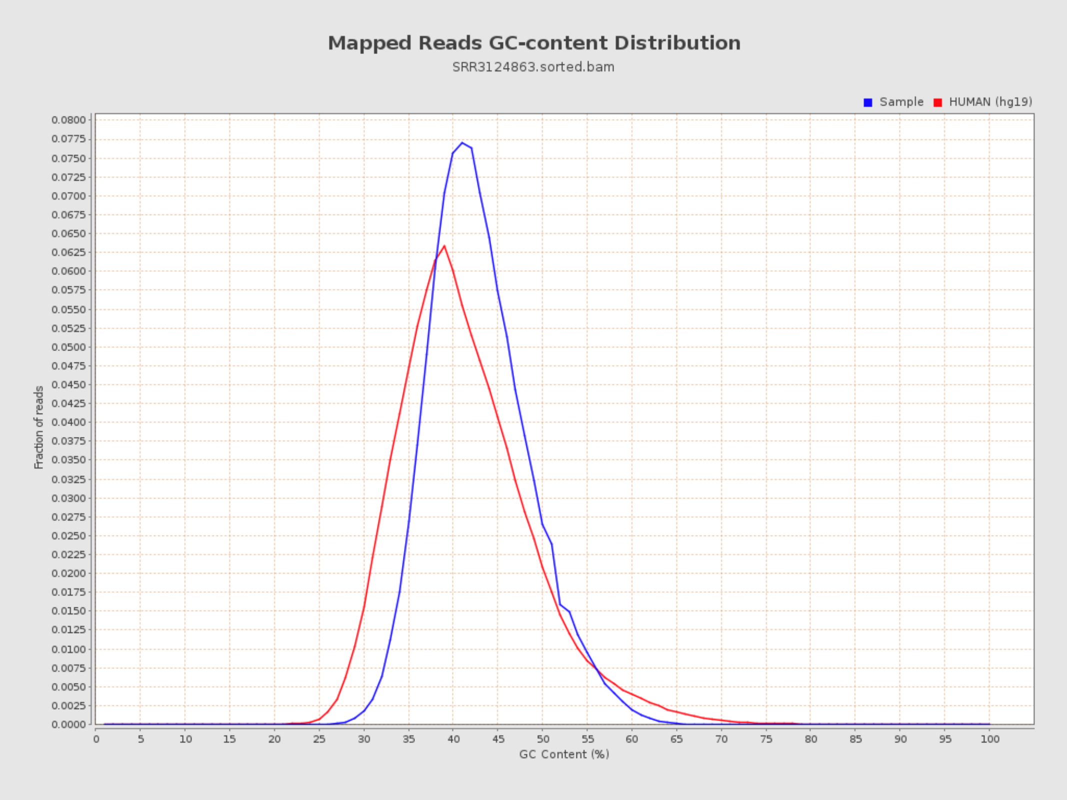
7. Results : Duplication Rate Histogram



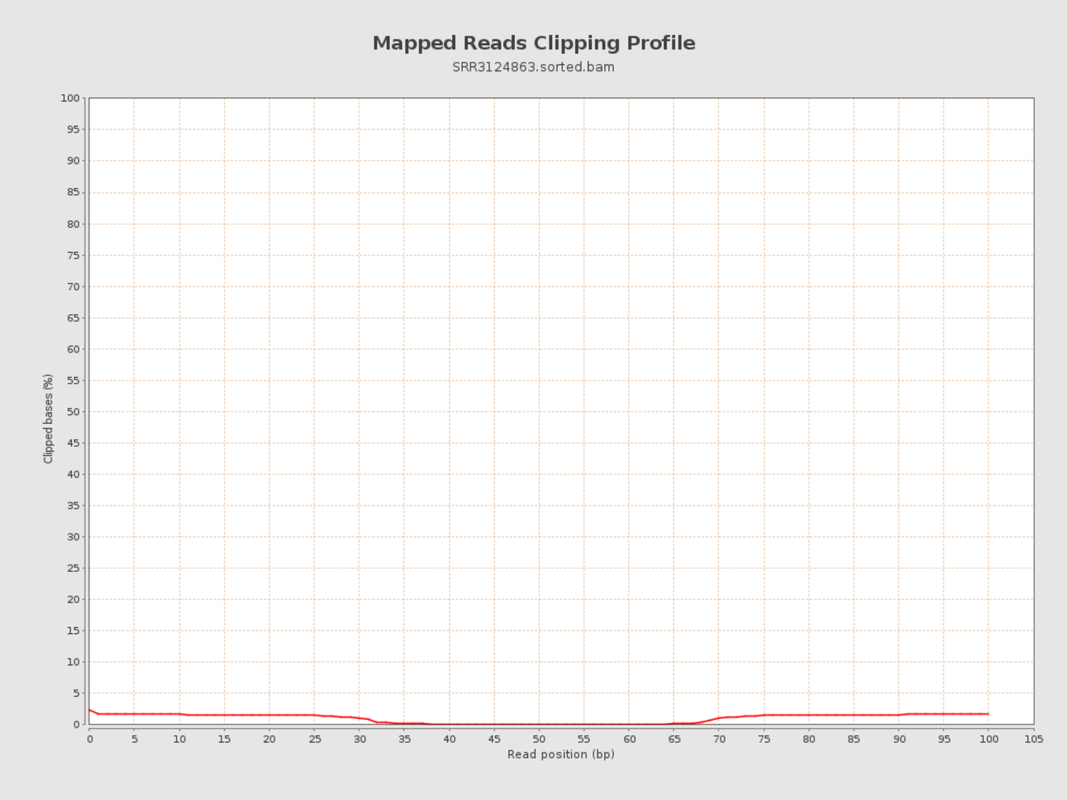
8. Results : Mapped Reads Nucleotide Content



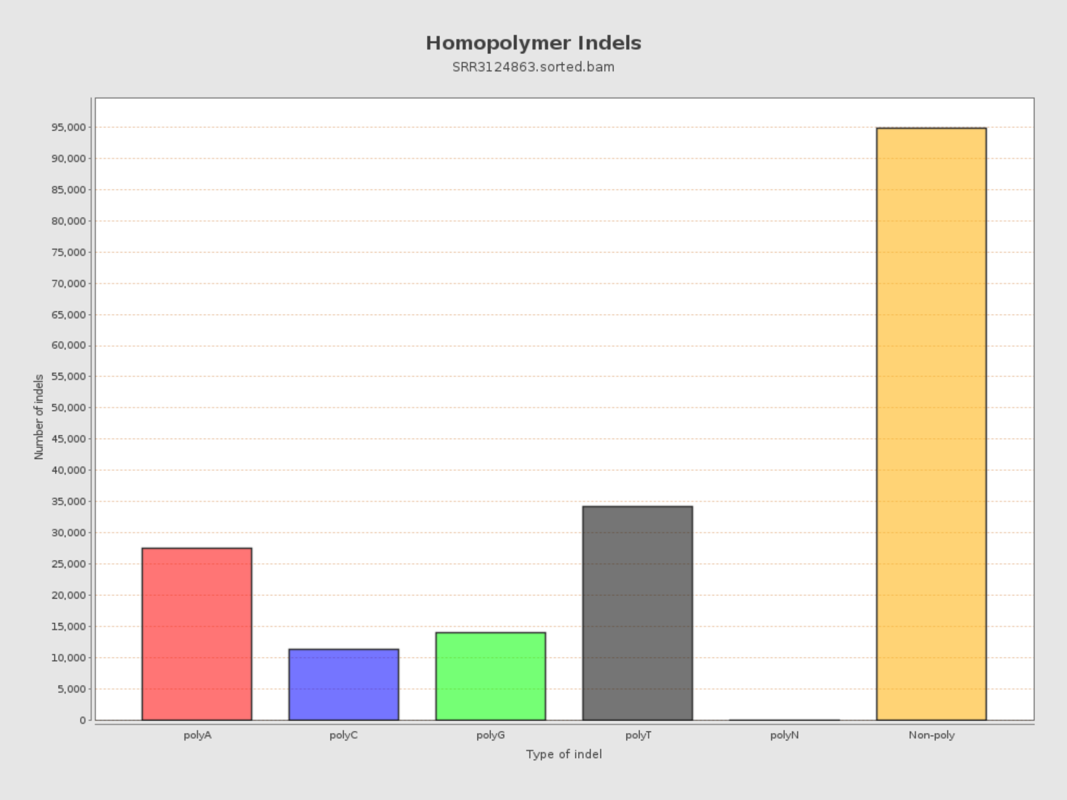
9. Results : Mapped Reads GC-content Distribution



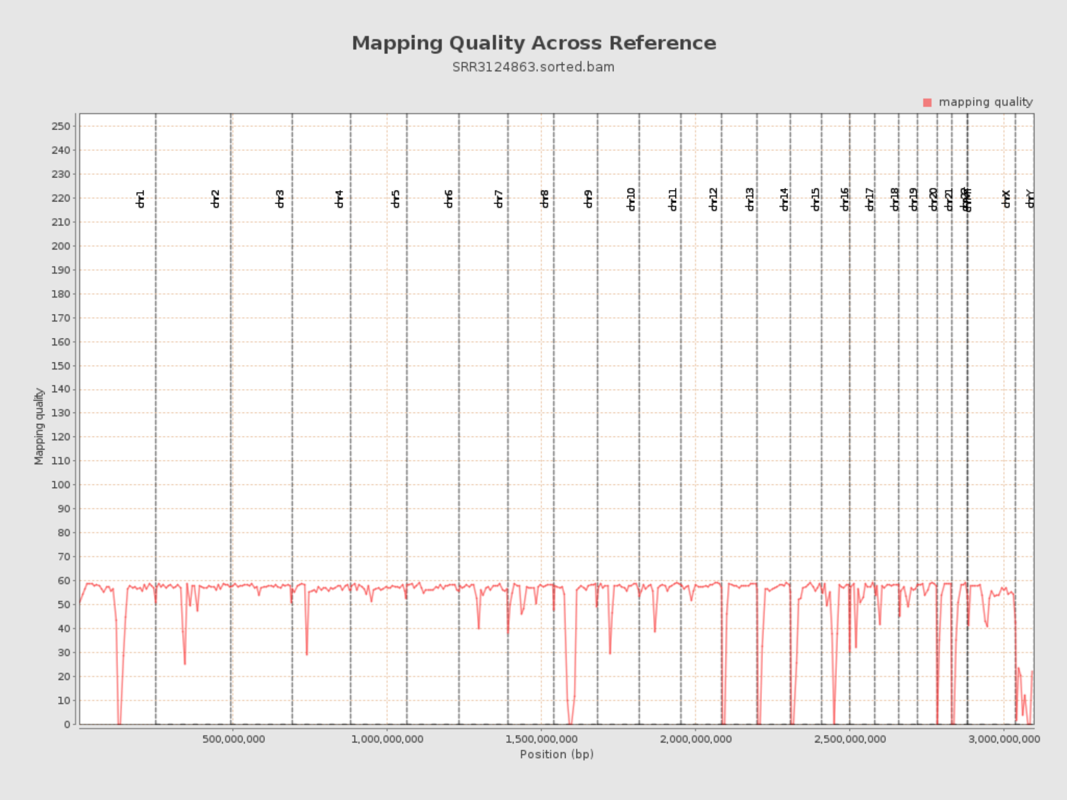
10. Results : Mapped Reads Clipping Profile



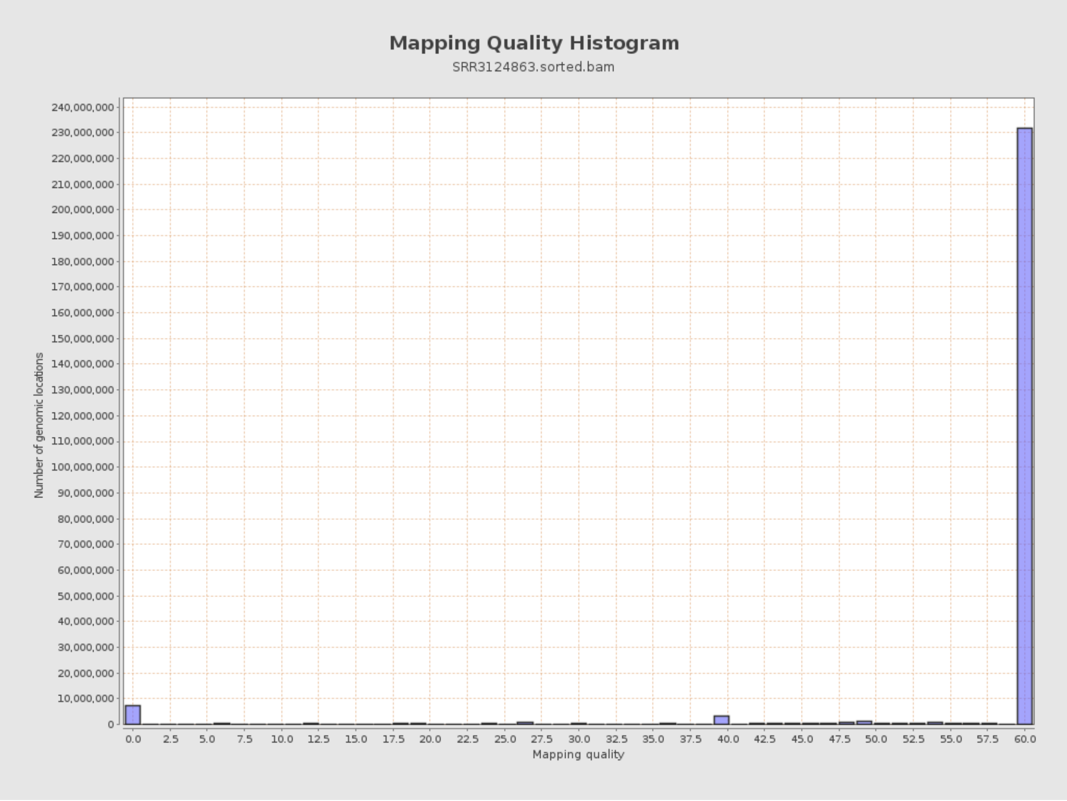
11. Results : Homopolymer Indels



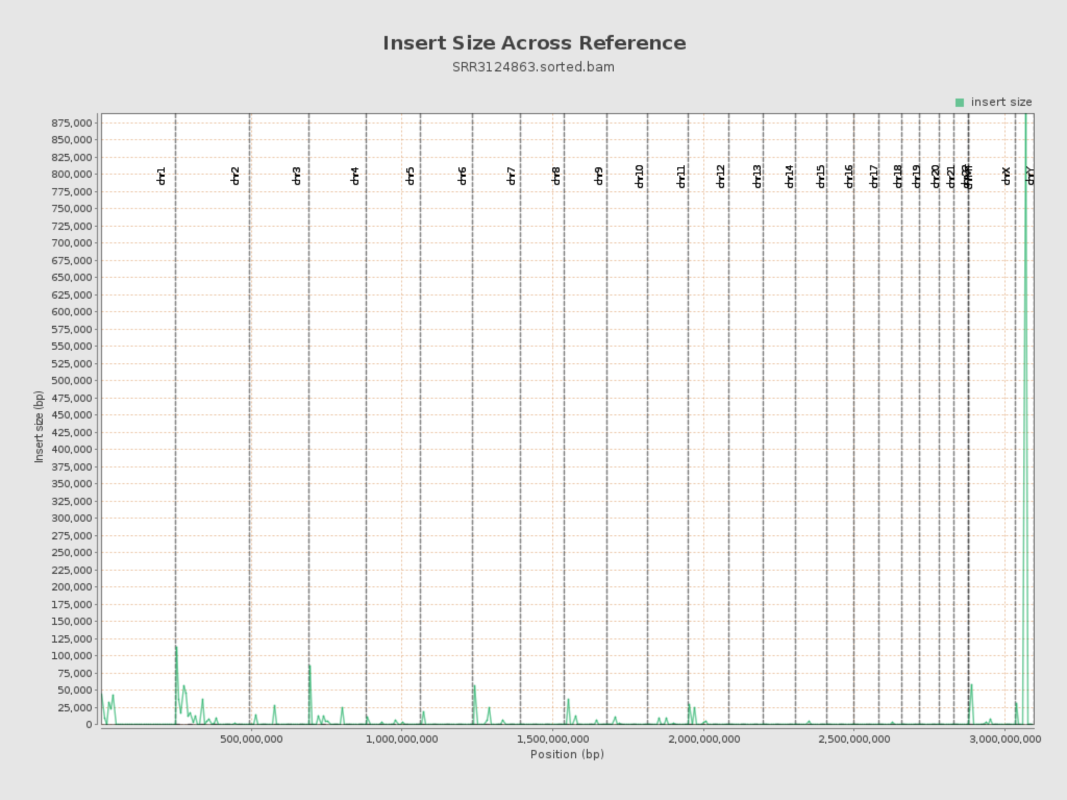
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram