Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 06:01:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124924.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_SRR3124924 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124924_1.fastq.gz SRR3124924_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 06:01:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124924.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,839,230
Mapped reads	3,792,609 / 98.79%
Unmapped reads	46,621 / 1.21%
Mapped paired reads	3,792,609 / 98.79%
Mapped reads, first in pair	1,899,686 / 49.48%
Mapped reads, second in pair	1,892,923 / 49.3%
Mapped reads, both in pair	3,777,576 / 98.39%
Mapped reads, singletons	15,033 / 0.39%
Secondary alignments	0
Supplementary alignments	20,194 / 0.53%
Read min/max/mean length	30 / 101 / 101.21
Duplicated reads (estimated)	259,747 / 6.77%
Duplication rate	4.95%
Clipped reads	1,812,325 / 47.21%

2.2. ACGT Content

Number/percentage of A's	92,611,511 / 28.12%
Number/percentage of C's	61,451,898 / 18.66%
Number/percentage of T's	98,172,106 / 29.81%
Number/percentage of G's	77,112,882 / 23.41%
Number/percentage of N's	4,748 / 0%

GC Percentage	42.07%

2.3. Coverage

Mean	0.1064
Standard Deviation	0.8934

2.4. Mapping Quality

Mean Mapping Quality	52.9

2.5. Insert size

Mean	51,294.96
Standard Deviation	2,117,715.29
P25/Median/P75	152 / 216 / 309

2.6. Mismatches and indels

General error rate	0.76%
Mismatches	2,425,751
Insertions	44,332
Mapped reads with at least one insertion	1.14%
Deletions	107,185
Mapped reads with at least one deletion	2.77%
Homopolymer indels	47.42%

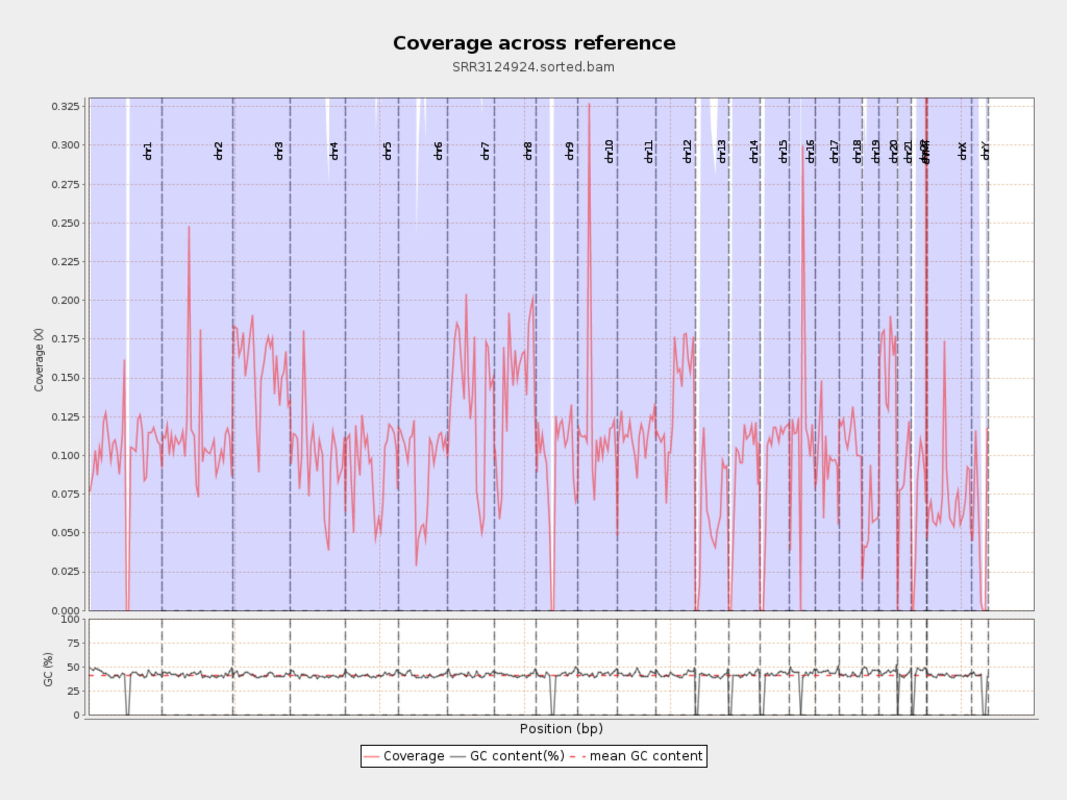
2.7. Chromosome stats

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

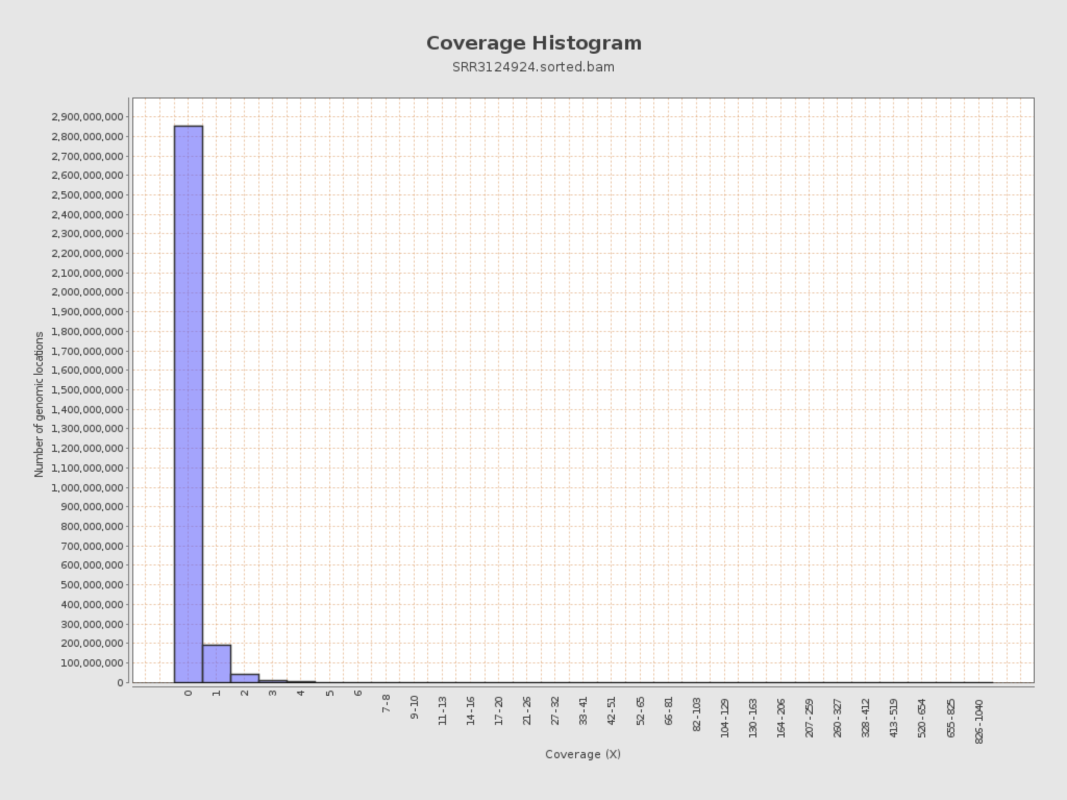
		bases	coverage	deviation
chr1	249250621	25122723	0.1008	0.8604
chr2	243199373	27194389	0.1118	1.198
chr3	198022430	31354356	0.1583	0.499
chr4	191154276	18656106	0.0976	0.6327
chr5	180915260	16985199	0.0939	0.3853
chr6	171115067	15970522	0.0933	0.6372
chr7	159138663	22174582	0.1393	1.6327
chr8	146364022	21191807	0.1448	0.598
chr9	141213431	13268754	0.094	1.0622
chr10	135534747	16150574	0.1192	1.7351
chr11	135006516	15138766	0.1121	0.7419
chr12	133851895	18188242	0.1359	0.4627
chr13	115169878	6934812	0.0602	0.2986
chr14	107349540	9481713	0.0883	0.408
chr15	102531392	9489265	0.0925	0.3823
chr16	90354753	10418927	0.1153	1.5101
chr17	81195210	7813709	0.0962	0.9094
chr18	78077248	8857793	0.1134	1.1125
chr19	59128983	3259926	0.0551	0.6133
chr20	63025520	10117764	0.1605	0.5253
chr21	48129895	3971599	0.0825	0.4509
chr22	51304566	3355971	0.0654	0.3367
chrMT	16571	199062	12.0127	7.9063
chrX	155270560	11215838	0.0722	0.4609

chrY	59373566	3022356	0.0509	1.0159

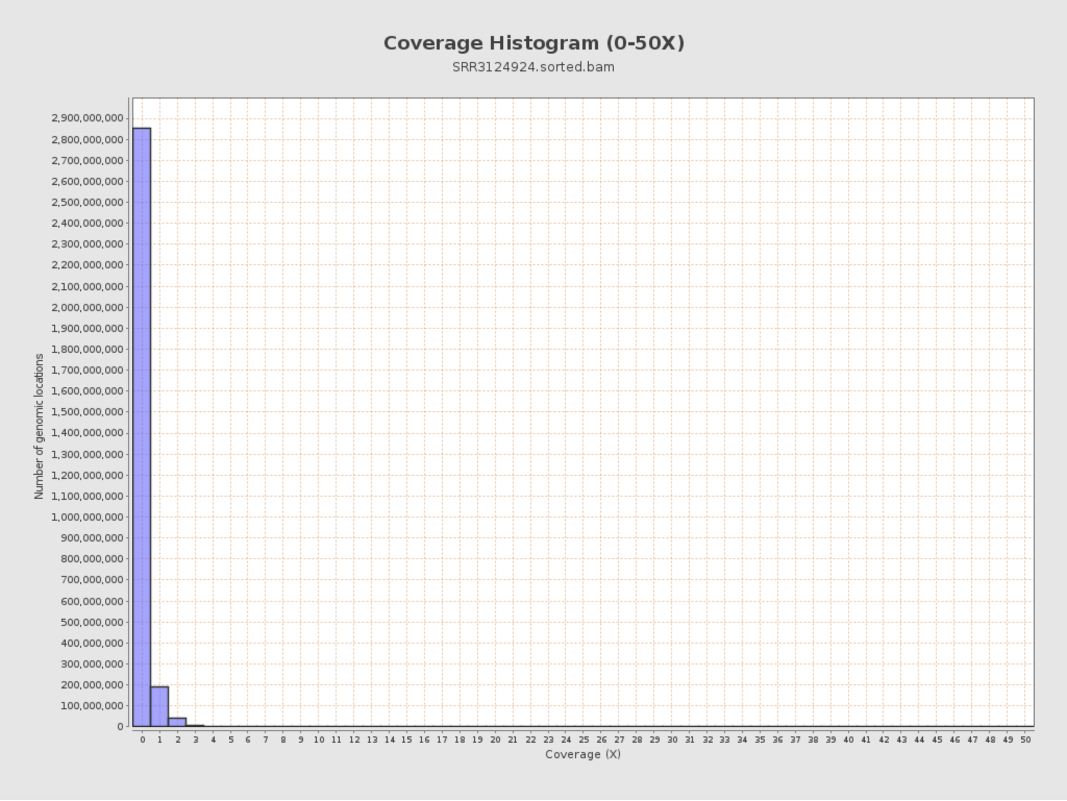
3. Results : Coverage across reference



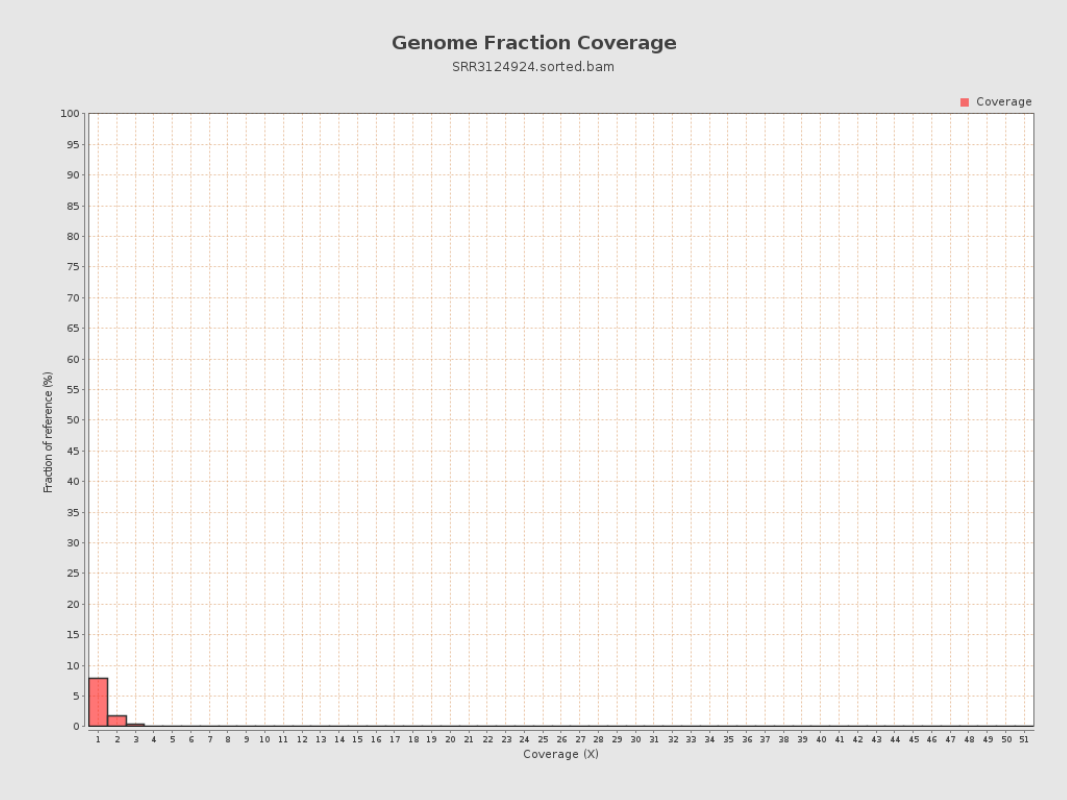
4. Results : Coverage Histogram



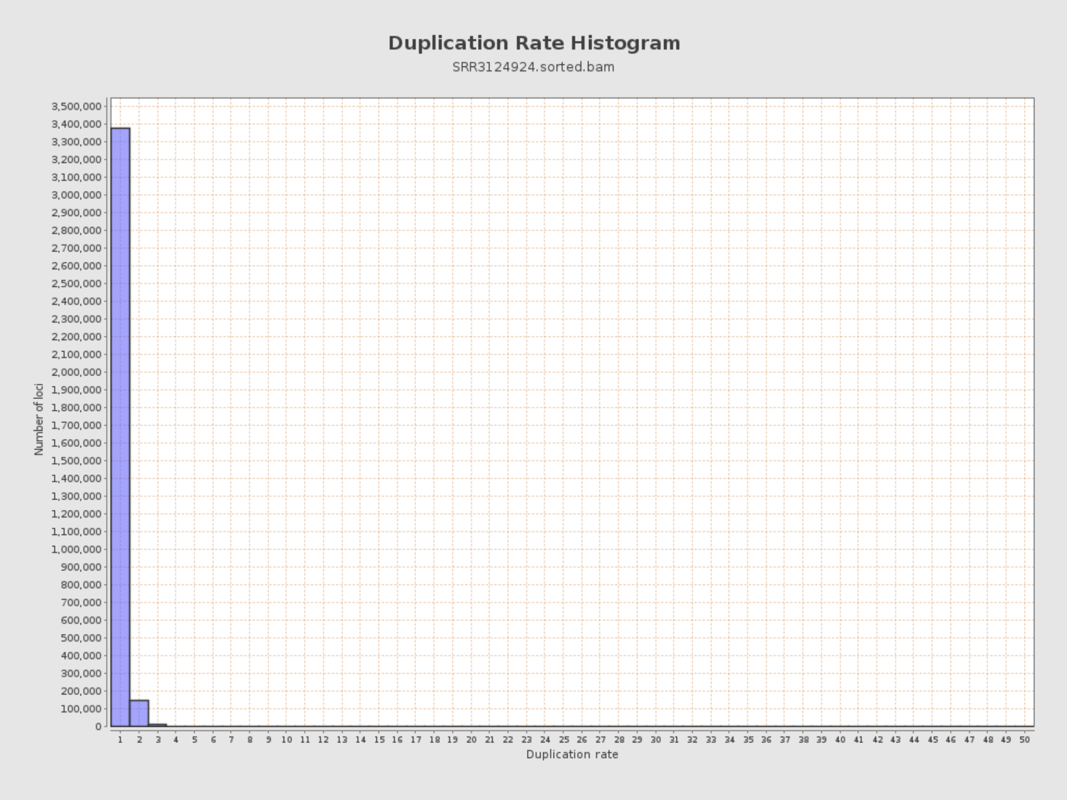
5. Results : Coverage Histogram (0-50X)



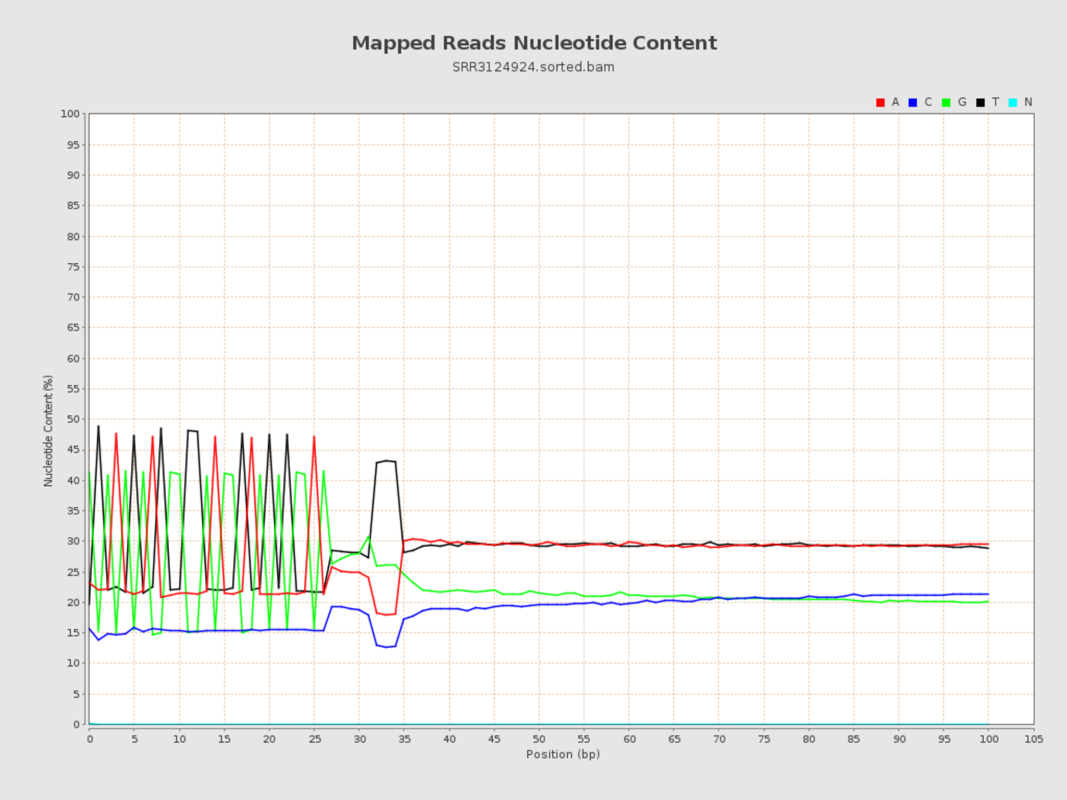
6. Results : Genome Fraction Coverage



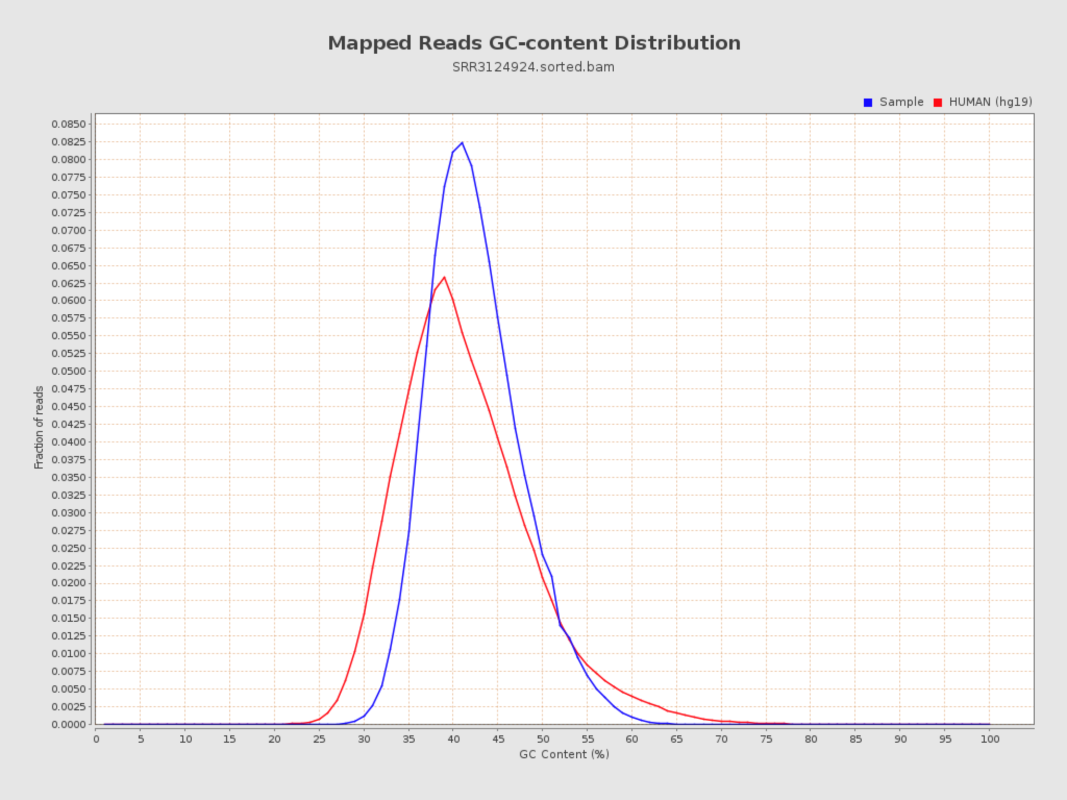
7. Results : Duplication Rate Histogram



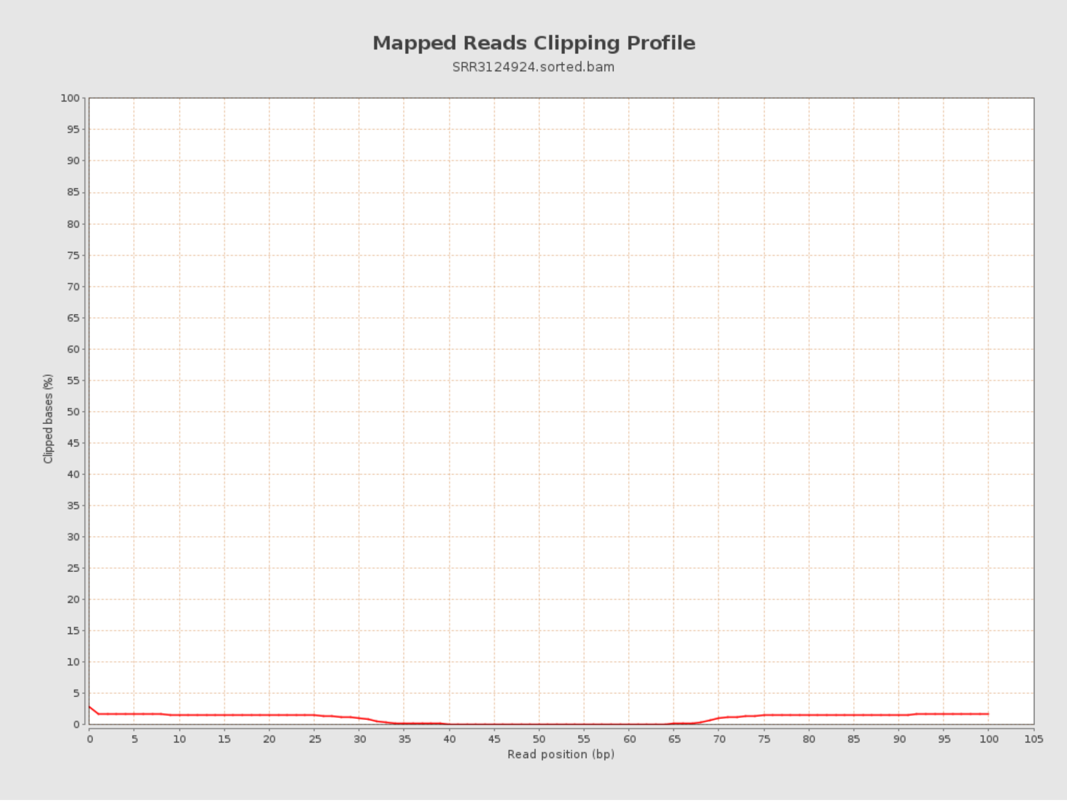
8. Results : Mapped Reads Nucleotide Content



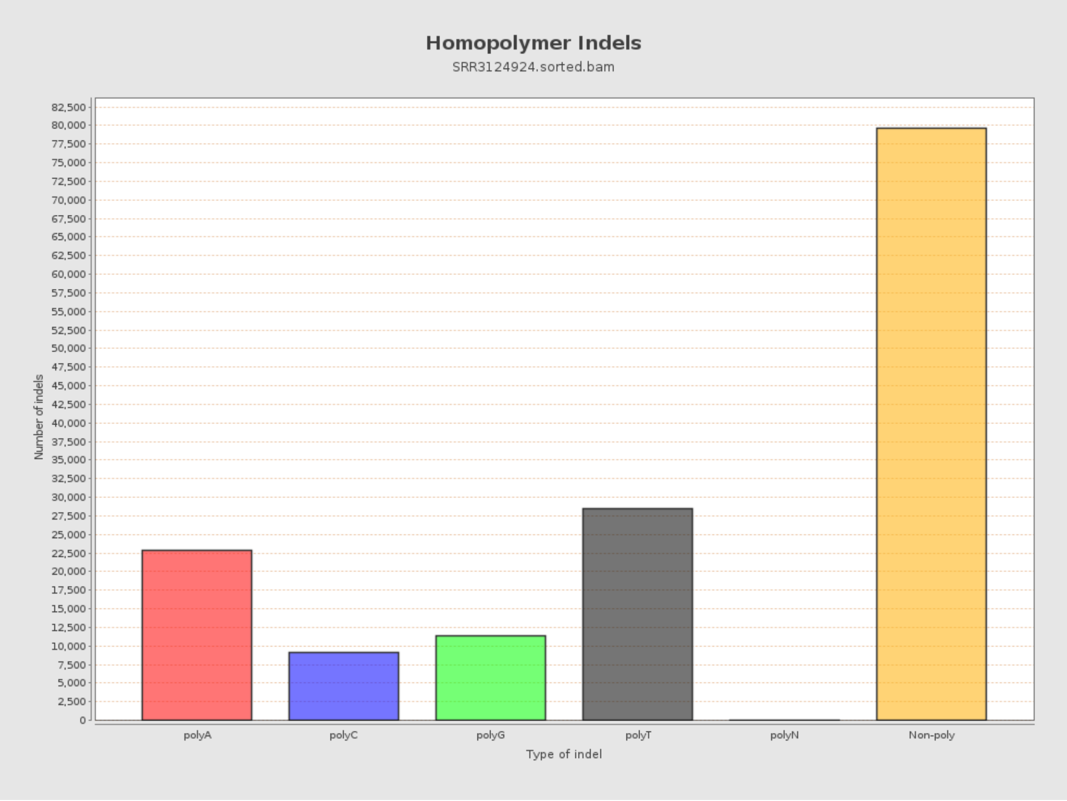
9. Results : Mapped Reads GC-content Distribution



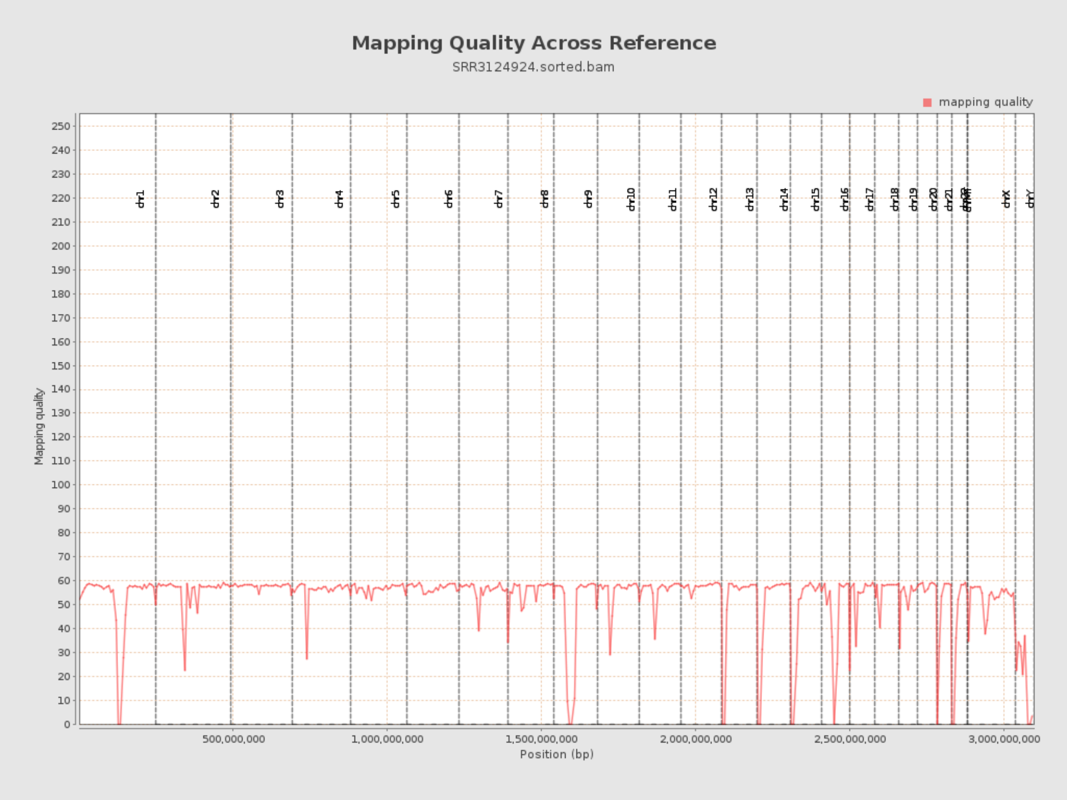
10. Results : Mapped Reads Clipping Profile



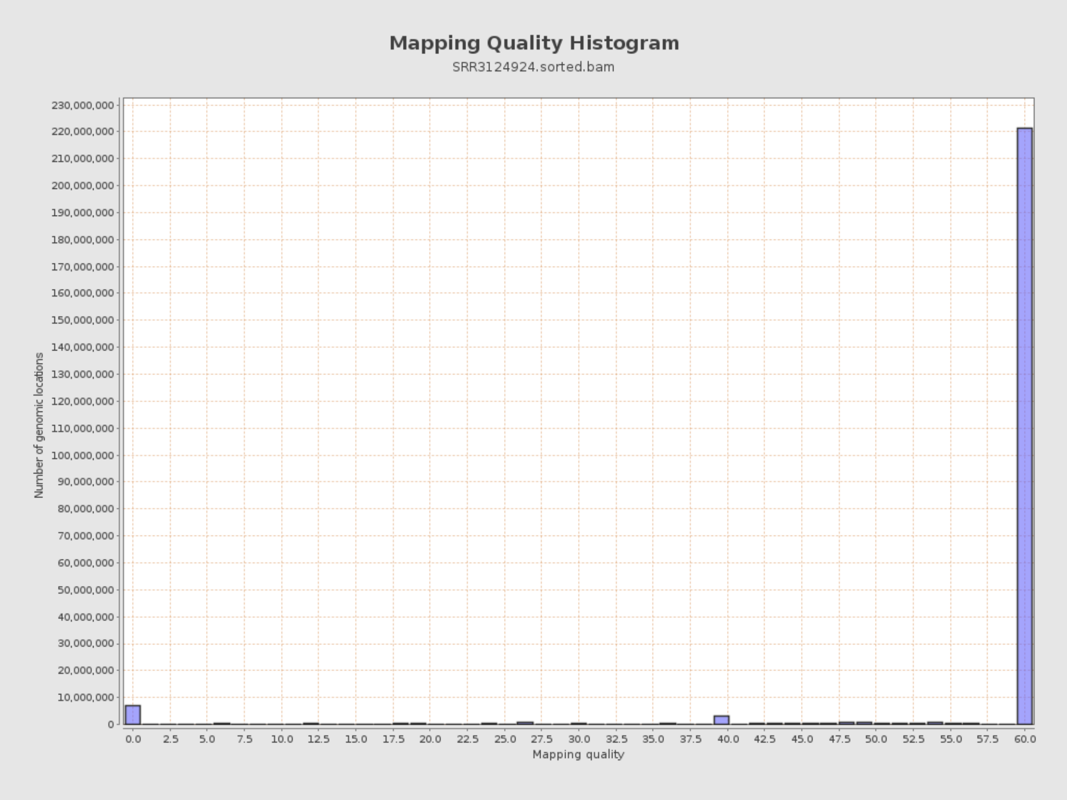
11. Results : Homopolymer Indels



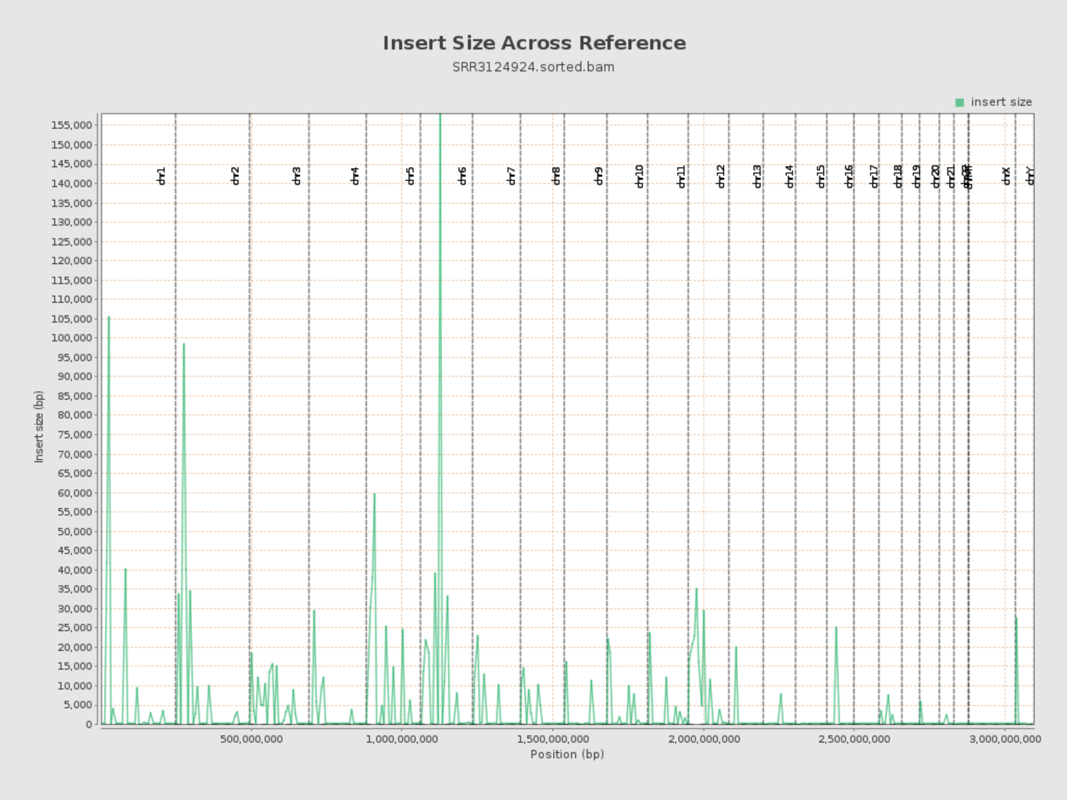
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram