Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 09:20:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472762.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_SRR3472762 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472762_1.fastq.gz SRR3472762_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 09:20:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472762.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,517,400
Mapped reads	15,398,552 / 99.23%
Unmapped reads	118,848 / 0.77%
Mapped paired reads	15,398,552 / 99.23%
Mapped reads, first in pair	7,723,938 / 49.78%
Mapped reads, second in pair	7,674,614 / 49.46%
Mapped reads, both in pair	15,322,212 / 98.74%
Mapped reads, singletons	76,340 / 0.49%
Secondary alignments	0
Supplementary alignments	53,970 / 0.35%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	10,508,946 / 67.72%
Duplication rate	48.14%
Clipped reads	1,207,564 / 7.78%

2.2. ACGT Content

Number/percentage of A's	425,167,734 / 28.01%
Number/percentage of C's	335,564,812 / 22.11%
Number/percentage of T's	422,968,852 / 27.87%
Number/percentage of G's	333,683,108 / 21.99%
Number/percentage of N's	296,038 / 0.02%

GC Percentage	44.1%

2.3. Coverage

Mean	0.4903
Standard Deviation	21.0269

2.4. Mapping Quality

Mean Mapping Quality	54.83

2.5. Insert size

Mean	21,244.53
Standard Deviation	1,439,761.53
P25/Median/P75	169 / 236 / 319

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	8,795,101
Insertions	87,155
Mapped reads with at least one insertion	0.56%
Deletions	85,745
Mapped reads with at least one deletion	0.53%
Homopolymer indels	45.87%

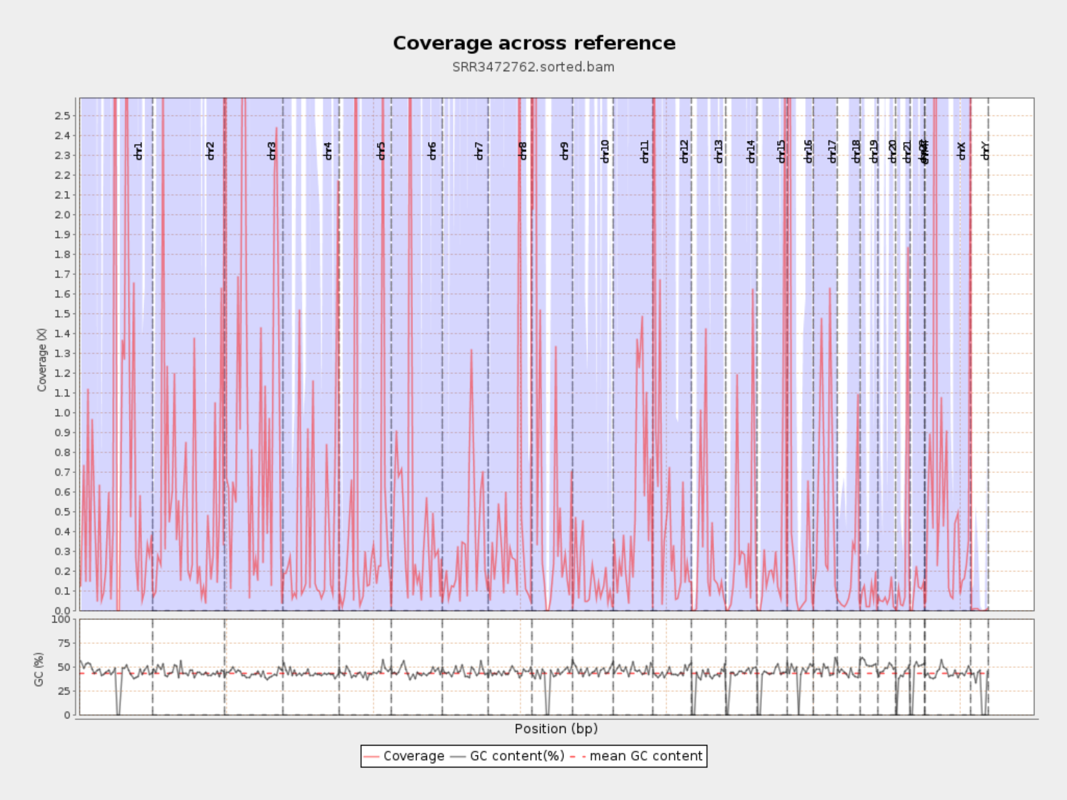
2.7. Chromosome stats

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

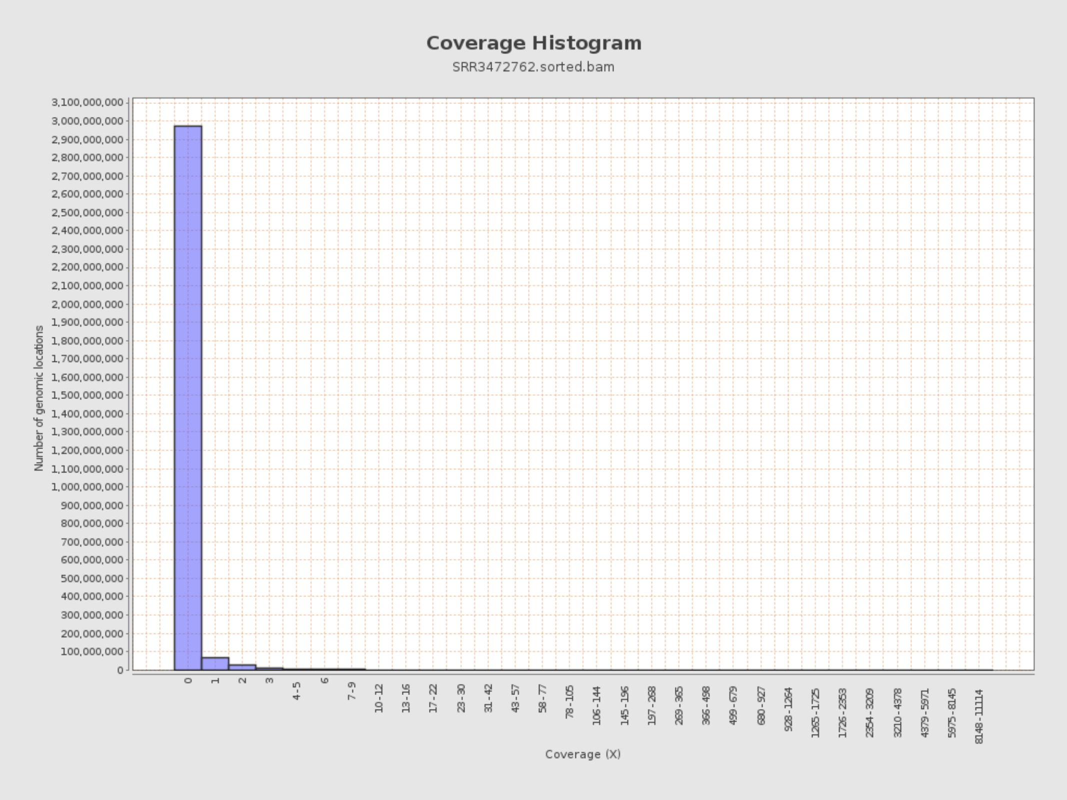
		bases	coverage	deviation
chr1	249250621	168656131	0.6767	28.5169
chr2	243199373	128734218	0.5293	23.8801
chr3	198022430	212583953	1.0735	31.1309
chr4	191154276	76056214	0.3979	15.3692
chr5	180915260	89483755	0.4946	23.6375
chr6	171115067	81946944	0.4789	16.6515
chr7	159138663	53855591	0.3384	13.5847
chr8	146364022	60794802	0.4154	20.6761
chr9	141213431	106331036	0.753	23.2491
chr10	135534747	20613474	0.1521	9.0141
chr11	135006516	72495356	0.537	20.0194
chr12	133851895	79862400	0.5966	23.8859
chr13	115169878	34603620	0.3005	17.3188
chr14	107349540	37112064	0.3457	25.7025
chr15	102531392	43093175	0.4203	20.3214
chr16	90354753	52817011	0.5846	19.6608
chr17	81195210	50093011	0.6169	19.138
chr18	78077248	16279848	0.2085	11.781
chr19	59128983	5097804	0.0862	2.7368
chr20	63025520	3935151	0.0624	2.9184
chr21	48129895	16852308	0.3501	30.2957
chr22	51304566	5552305	0.1082	4.1263
chrMT	16571	1471	0.0888	0.3084
chrX	155270560	100720258	0.6487	20.0558

chrY	59373566	306269	0.0052	0.3787

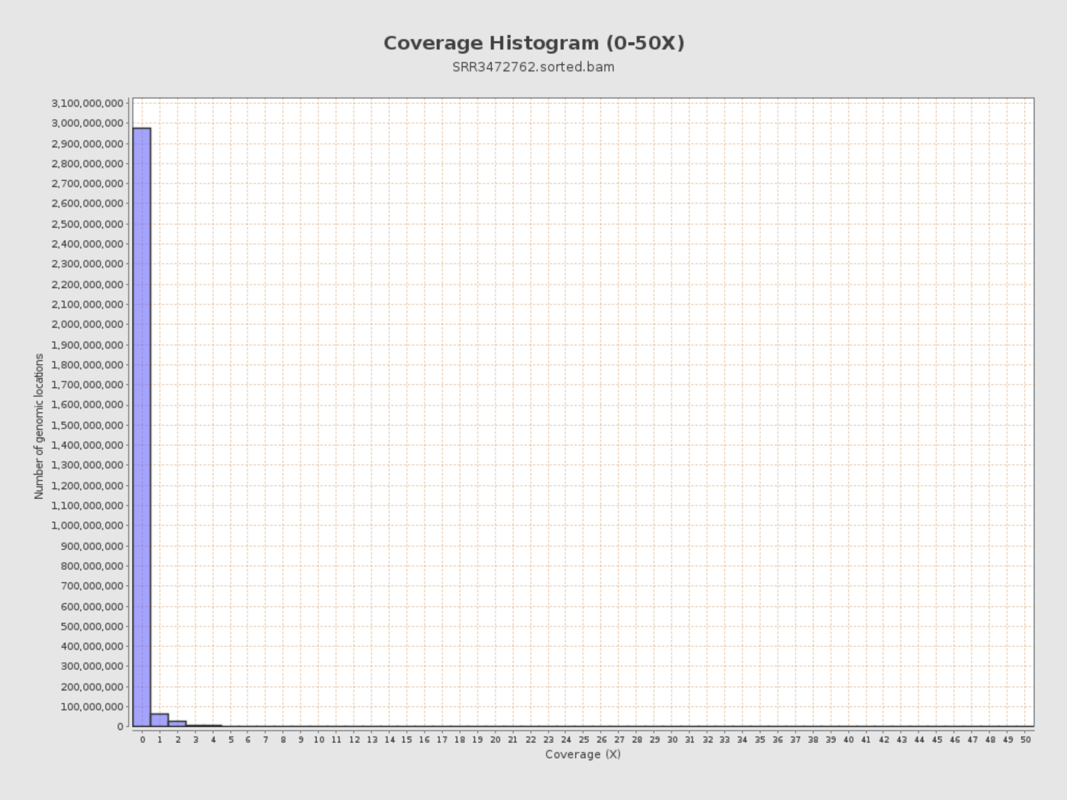
3. Results : Coverage across reference



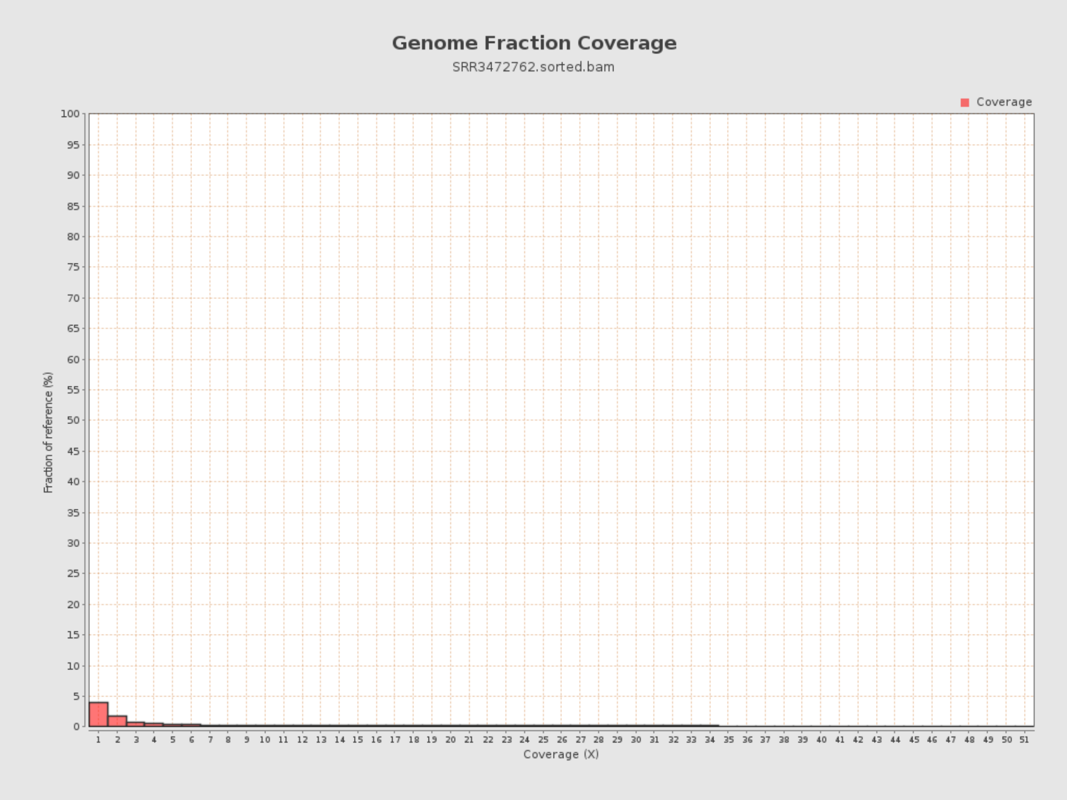
4. Results : Coverage Histogram



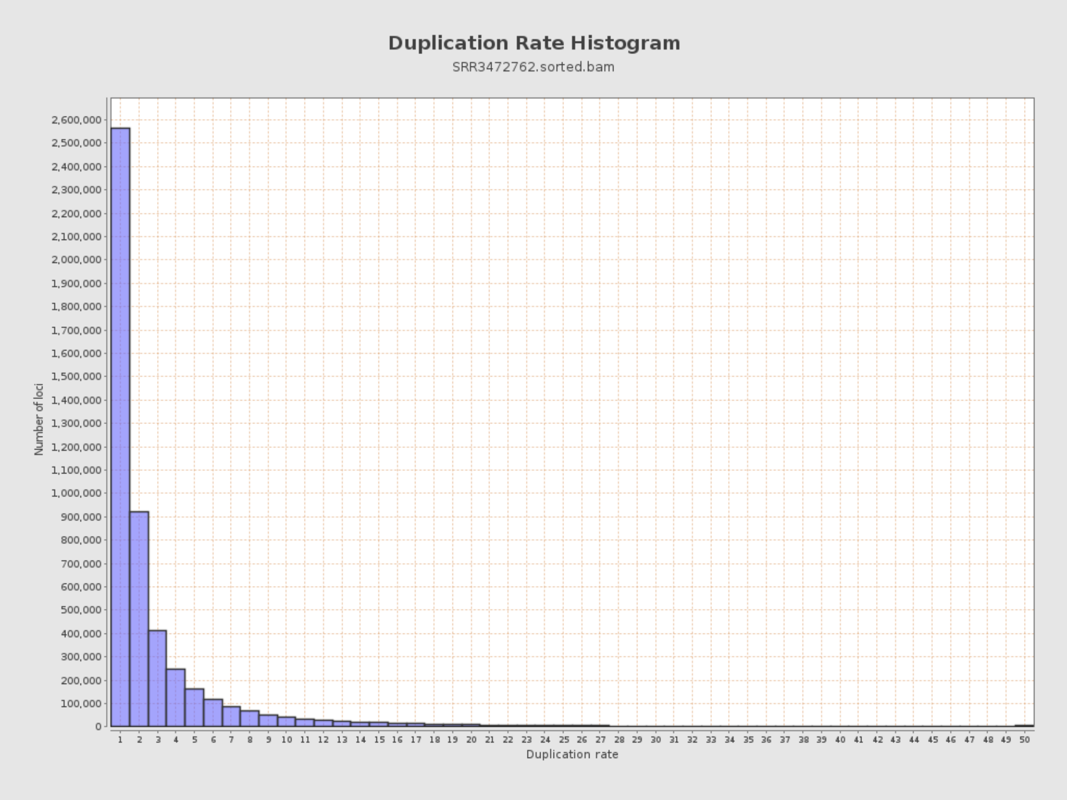
5. Results : Coverage Histogram (0-50X)



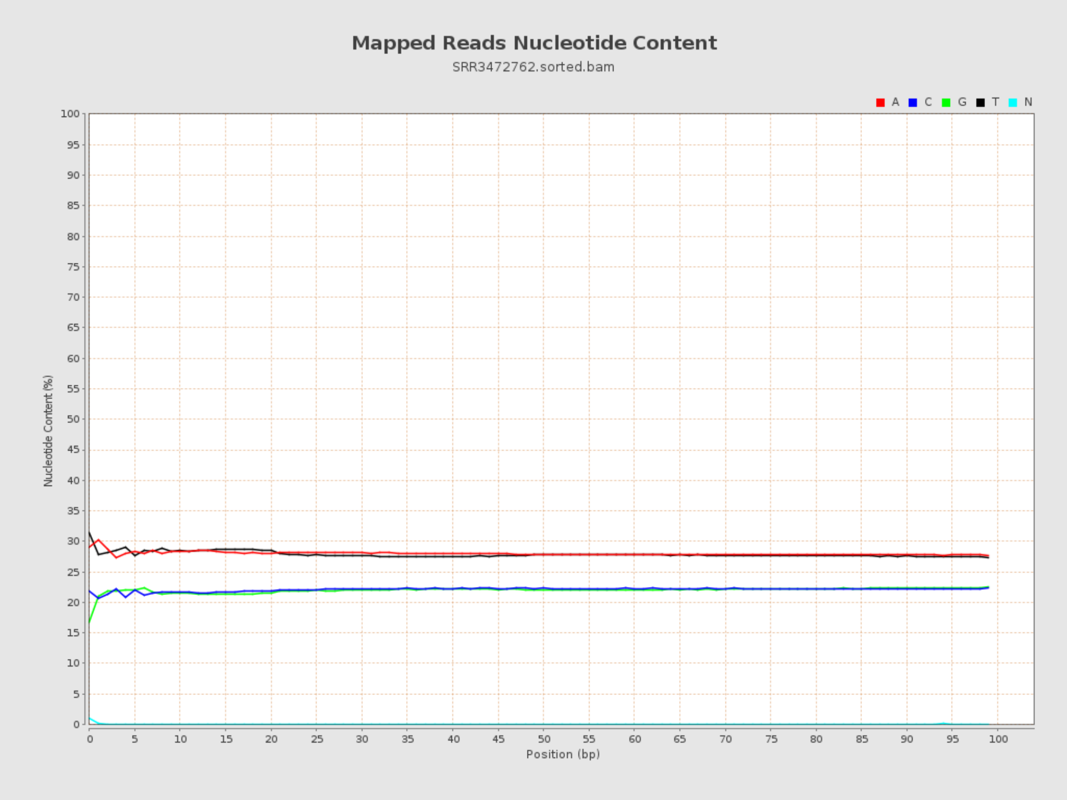
6. Results : Genome Fraction Coverage



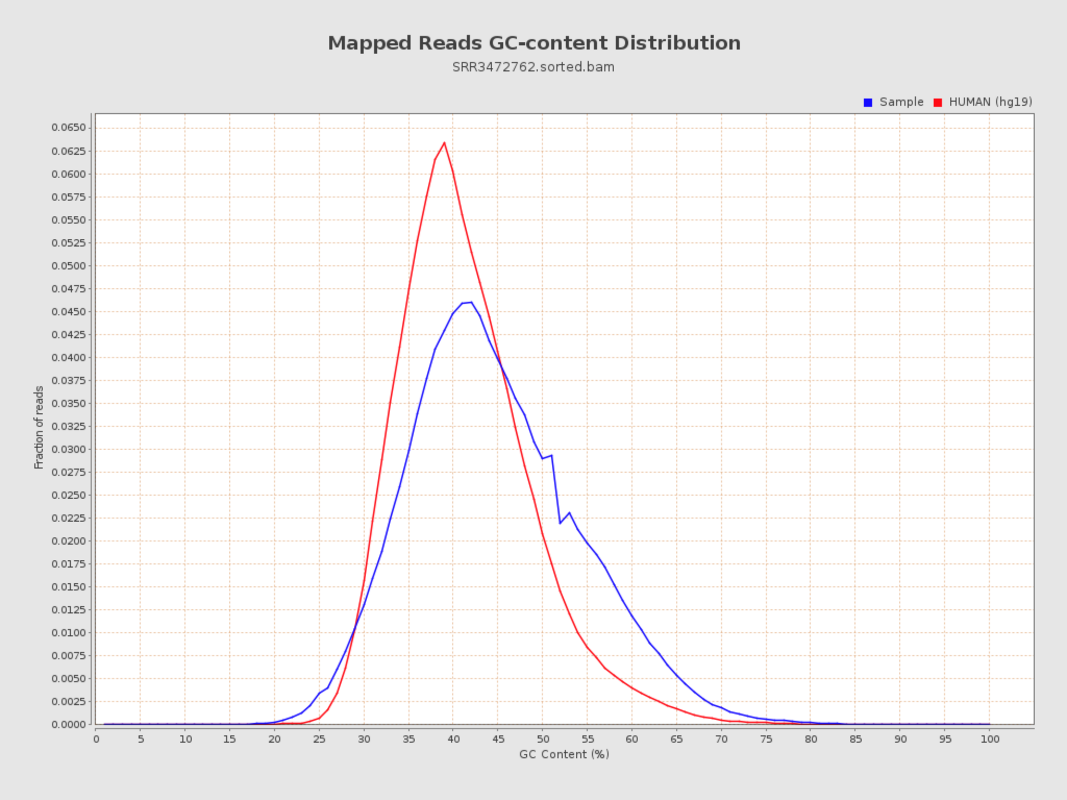
7. Results : Duplication Rate Histogram



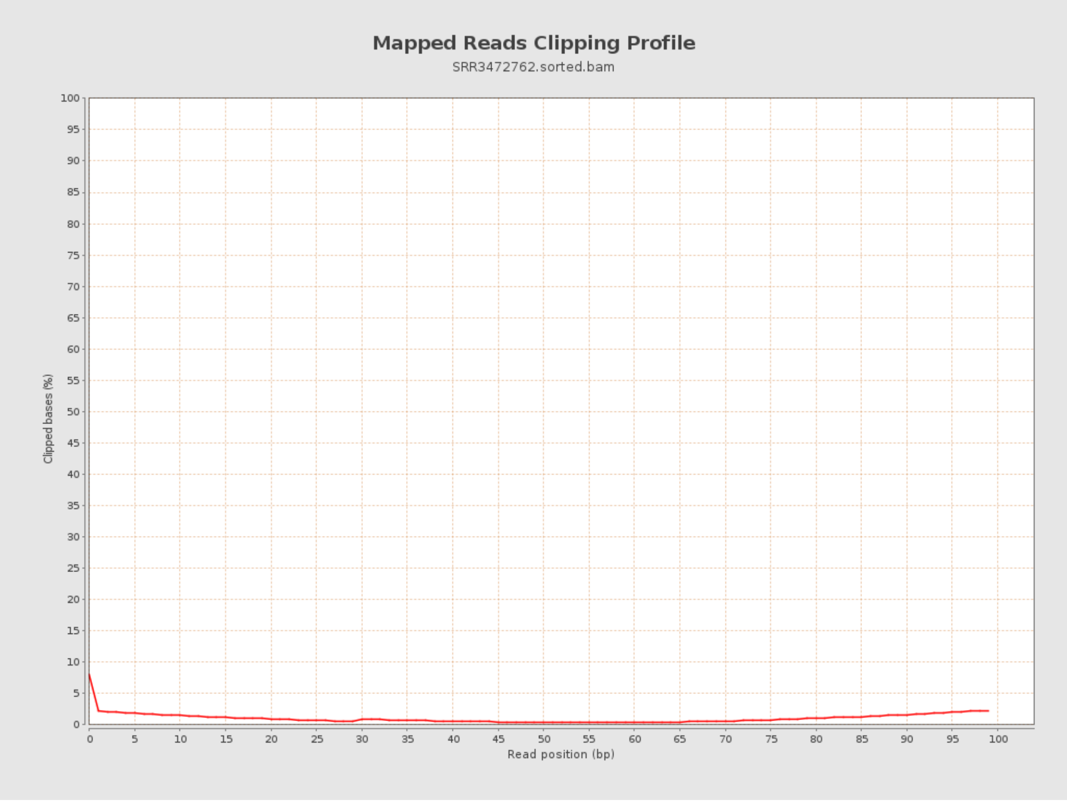
8. Results : Mapped Reads Nucleotide Content



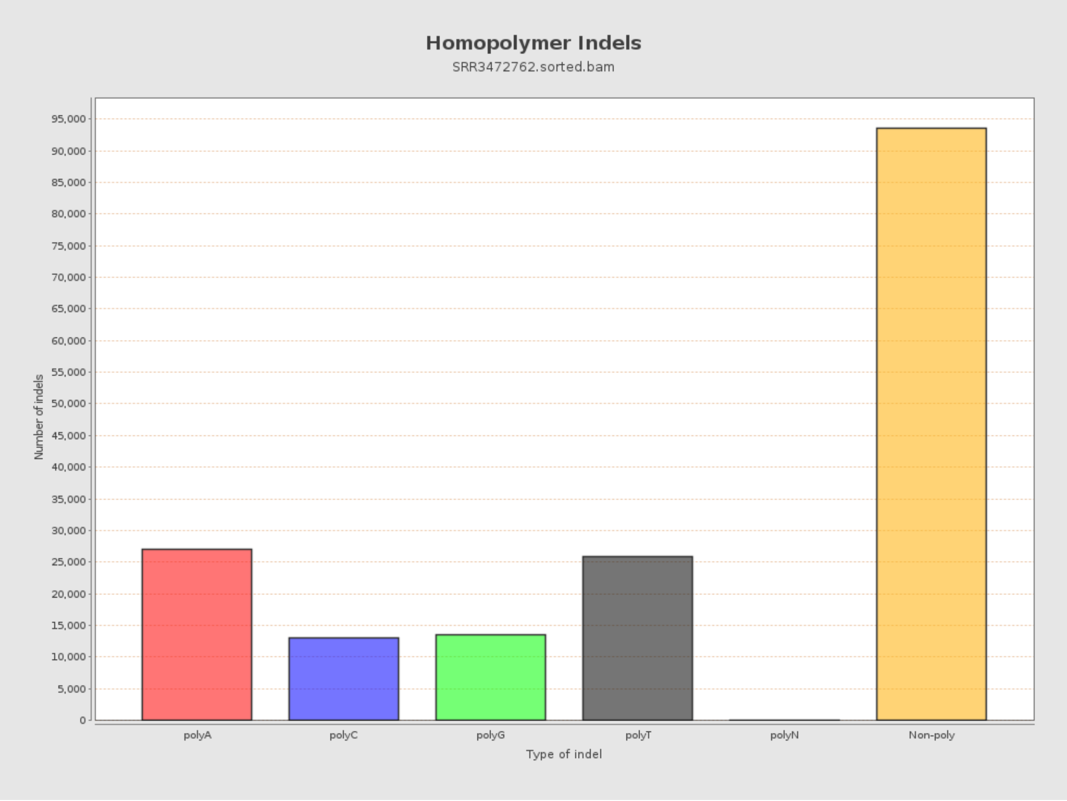
9. Results : Mapped Reads GC-content Distribution



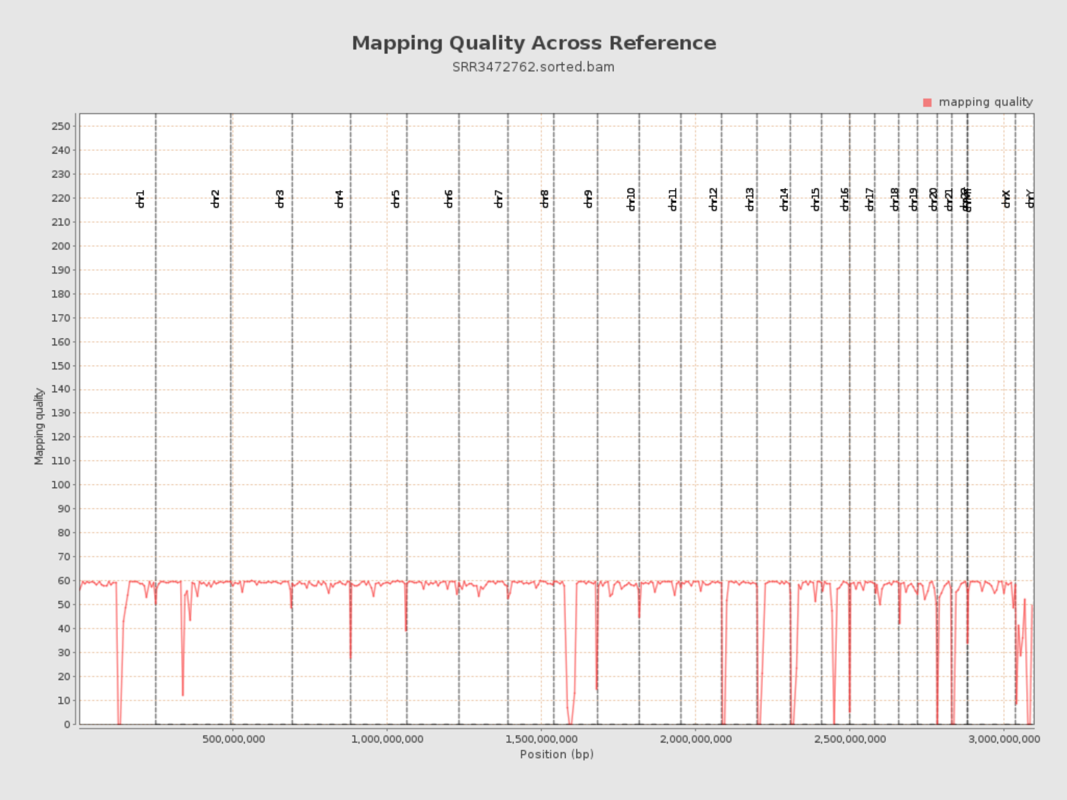
10. Results : Mapped Reads Clipping Profile



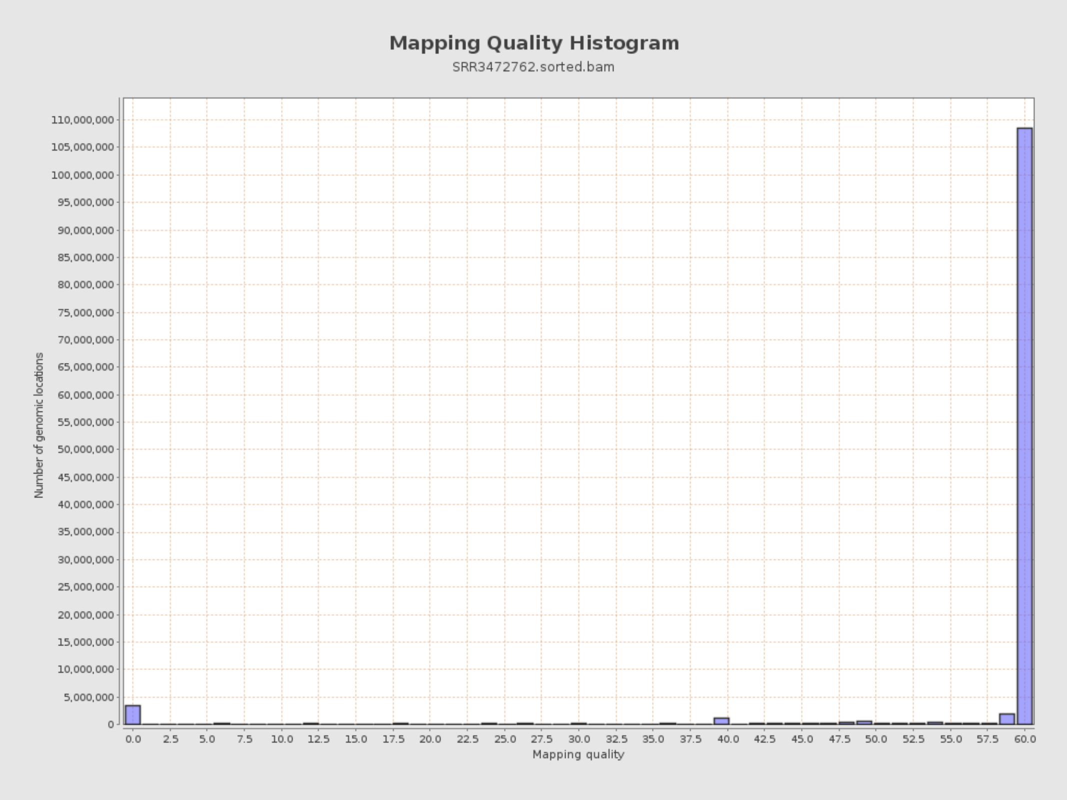
11. Results : Homopolymer Indels



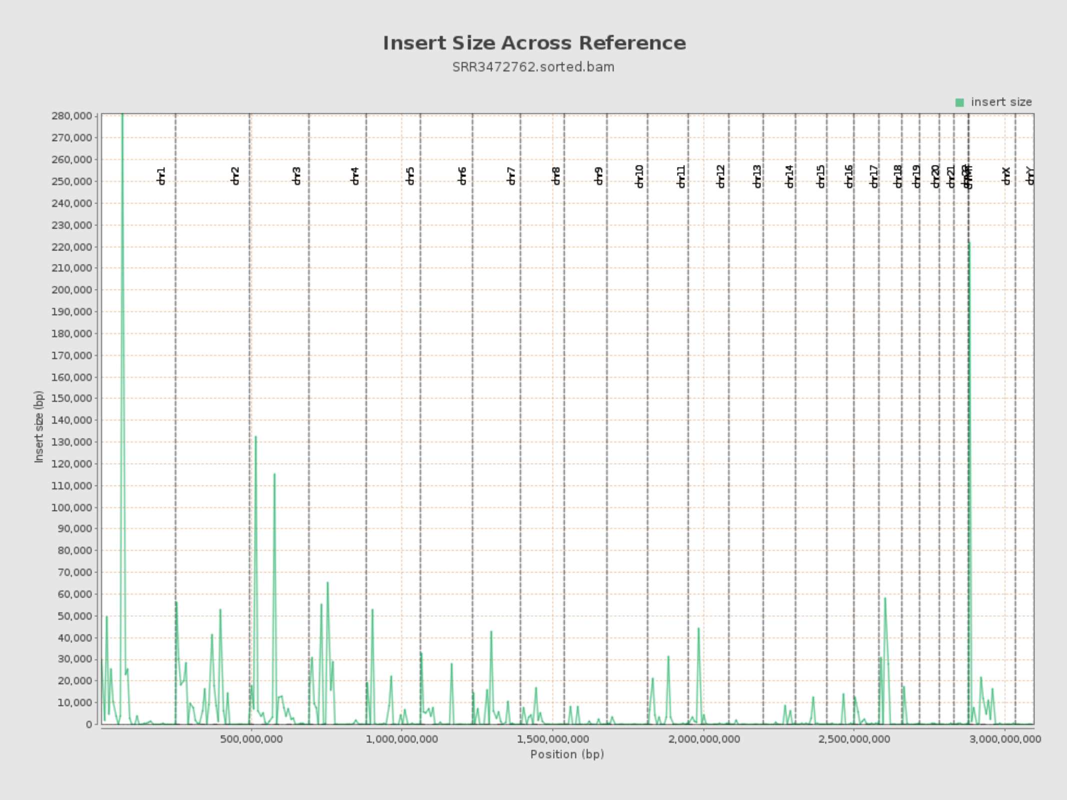
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram